**Full title:**

# p62/SQSTM1 interacts with vimentin to enhance breast cancer metastasis

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## Abstract

The signalling adaptor p62 is frequently overexpressed in numerous cancer types. Here, we found that p62 expression was elevated in metastatic breast cancer and its overexpression correlated with reduced metastasis-free and relapse-free survival times. Analysis of p62 expression in breast cancer cell lines demonstrated that high p62 expression was associated with the invasive phenotypes of breast cancer. Indeed, silencing p62 expression attenuated the invasive phenotypes of highly metastatic cells, whereas overexpressing p62 promoted the invasion of non-metastatic cells in *in vitro* microfluidic model. Moreover, MDA-MB-231 cells with p62 depletion which were grown in a three-dimensional culture system exhibited a loss of invasive protrusions. Consistently, genetic ablation of p62 suppressed breast cancer metastasis in both zebrafish embryo and immunodeficient mouse models, as well as decreased tumorigenicity *in vivo*. To explore the molecular mechanism by which p62 promotes breast cancer invasion, we performed a co-immunoprecipitation (co-IP)-MS analysis and revealed that p62 interacted with vimentin, which mediated the function of p62 in promoting breast cancer invasion. Vimentin protein expression was downregulated upon p62 suppression and upregulated with p62 overexpression in breast cancer cells. Linear regression analysis of clinical breast cancer specimens showed a positive correlation between p62 and vimentin protein expression. Together, our findings provide strong evidence that p62 functions as a tumour metastasis promoter by binding vimentin and promoting its expression. This finding might help to develop novel molecular therapeutic strategies for breast cancer metastasis treatment.

**Summary**: p62 functions as a tumor metastasis promoter through its interaction with vimentin. This finding might help to develop novel molecular therapeutic strategies for breast cancer metastasis treatment.

## Introduction

Cancer metastasis is a complex multi-step cell biological process termed the invasion-metastasis cascade, by which primary tumour cells acquire the invasive ability and then spread to distant organs [1-3]. Metastases are responsible for more than 90% of cancer-related deaths in various solid malignancies, including breast cancer [4, 5]. Despite the early diagnostic methods, surgical resection and adjuvant therapy have improved, metastatic disease is largely incurable [6]. Recent studies have shown that the primary cause for cancer cells to drive the invasion-metastasis process is the acquisition of the genetic or epigenetic alterations [7, 8]. Thus, the exploration of key molecules and mechanisms underlying breast cancer metastasis regulation is urgently needed.

The adaptor protein p62 (also known as SQSTM1) is initially identified as a cytosolic 62kDa protein which can bind to the isolated src homology 2 (SH2) domain of $p56^{lck}$ [9]. This multidomain protein interacts selectively with different signalling intermediaries, such as Raptor [10], Nrf2-binding site on Keap1 [11], ubiquitin and LC3 [12, 13], to regulate metabolic reprogramming, antioxidant response and selective autophagy, respectively. Abnormal p62 overexpression has been documented in various neoplasms [14-19], especially in breast cancer [20-22]. For example, the scaffold p62 protein cooperates with the Wnt/PCP protein VANGL2 and recruits JNK to VANGL2, which is required for tumour growth in breast cancer [23]. In addition, high p62 expression is associated with breast tumours exhibiting the clinicopathological features of aggressive disease, as well as overexpression of EGF receptor (EGFR), HER2, HER3 and HER4 [21]. In triple-negative breast cancers, patients with p62 accumulation exhibit a higher risk of positive lymph node and lymphovascular invasion [22]. These findings highlight the potential of p62 as a therapeutic target during cancer progression. However, the detailed mechanism by which p62-mediates cancer cell invasion and metastasis remains largely unknown.

Studies of epithelial malignancies indicate that the acquisition of invasion and metastasis potential by the incipient cancer cell may depend on the transition of a mesenchymal phenotype [24]. Vimentin, a Type Ⅲ intermediate filament, serves as a classical mesenchymal phenotype biomarker [25, 26]. Furthermore, vimentin protein overexpression positively correlates with cell motility, induction of EMT, metastatic disease and poor prognosis [27-31]. *Vimentin*-deficient (-/-) mice reveal weakened wound healing ability in all stages of growth as a result of the seriously impaired fibroblasts in their capacity to migrate [32, 33]. In this study, we found that p62 binds to vimentin and regulates vimentin protein level, which in turn contributes to cancer cell invasion and metastasis. Thus, this p62-vimentin interaction may be a promising target and provide new opportunities for therapeutic intervention.

## Materials and methods

### *Clinical samples, cell culture and reagents*

All breast cancer specimens and adjacent normal tissues were obtained from clinical diagnosed patients with prior patient consent and the approval of the Institutional Clinical Ethics Review Board in the 2nd Affiliated Hospital of Dalian Medical University. Samples were kept in liquid nitrogen for protein extraction.

The human breast cancer cell lines (MDA-MB-231, SKBR-3, BT549 and MCF7), the immortalized human breast epithelial cell MCF-10A and human embryonic kidney HEK293T cell line were obtained from the American Type Culture Collection (ATCC). The SUM149 cell line was kindly provided by Prof. Zhi-Min Shao (Deparment of Medical Oncology, Cancer Hospital of Fudan University, Shanghai Medical College, Shanghai, China). All the cell lines were tested and authenticated by the standard short tandem repeat DNA typing methodology before used in this study [46]. Each cell line was cultured in its standard medium as recommended by ATCC. SUM149 cells were cultured in F-12 Hams (Gibco) supplemented with 5% FBS (Hyclone), 5 μg/ml insulin (Sigma-Aldrich), and 1 μg/ml hydrocortisone (Sigma-Aldrich). The cells were last tested in July 07th, 2015.

*Plasmid construction*

Full-length of p62 fragment was cloned from human genome cDNA and ligated into pLVX-DsRed-Monomer-N1 vector (Clontech). The primers were as followed: p62: 5' Xho I, 5'-CCGCTCGAGCGGGCCACCATGGCGTCGCTCACCGTGAAGGCC; 3' EcoR I, 5'-CCGGAATTCCGTCACAACGGCGGGGGATGCTTTGA. Flag-p62 was a gift from Prof. Song-Shu Meng (Department of Cancer Biology, Dalian Medical University, Dalian, China). The short hairpin RNA (shRNA) targeting p62 (1#, 2#) and the nontarget shRNA (SHC002) were kindly provided by Dr. Zi-Jie Long (Department of Hematology, the Third Affiliated Hospital, Sun Yat-sen University, Guangzhou, China) and packaged for lentivirus particles. The full-length vimentin plasmid was cloned from human genome cDNA and ligated into pcDNA6 vector in a frame with Myc and His tag

(Invitrogen). The primers were as followed: vimentin: 5’ Kpn I, 5’-GGGGTACCCCGCCACCATGTCCACCAGGTCCGTGTCC; 3’ EcoR I, 5’-CCGGAATTCGGTTCAAGGTCATCGTGATGCTGAGAAG. The constructs pLVX-GST-p62 and pLVX-GST-vimentin were generated by PCR and confirmed by sequencing. Flag-Ub was a gift from Dr. Muhammad Kamran (Department of Cancer Biology, Dalian Medical University, Dalian, China). The shRNA constructs targeting Vimentin and referring to the sequence is: Forward, CCGGCTCTGGTTGATACCCACTCAACTCGAGTTGAGTGGGTATCAACCAGAGTTTTTG; Reverse, AATTCAAAAACTCTGGTTGATACCCACTCAACTCGAGTTGAGTGGGTATCAACCAGAG. The above fragment was cloned into pLKO-Tet-On-shNC vector.

*RNAi and Transfection*

Transient RNAi transfection was carried out as previously described [47]. Two different target siRNA sequences of p62 were obtained from GenePharma Co. Ltd (1#, 5’-GUGACGAGGAAUUGACAAUTT; 2#, 5’-GGAGUCGGAUAACUGUUCATT). The negative control siRNA was 5’-UUCUCCGAACGUGUCACGUTT. RNAi was transfected into the culture cells using Lipofectamine 2000 Transfection Reagent (Invitrogen) according to the manufacturer’s instructions.

*Lentivirus preparation*

HEK293T cells were used for packaging lentivirus with the 2nd generation packaging system plasmid psPAX2 (Addgene) and pMD2.G (Addgene). Lentiviruses were concentrated by ultracentrifugation, and viral titer determined by serial dilutions. For infection with the lentivirus, infected cells were selected with Puromycin (2 μg/ml)

(Sigma-Aldrich).

*Microfluidic chips*

This microfluidic device consisting of one central chamber and two side channels was adopted in the present study and was modified for certain use (Supplementary Figure 1). Inlet and outlet ports of the PDMS (poly-dimethyl-siloxane; Silgard 184, Dow Chemical) devices were bored using disposable biopsy punches and the PDMS layer was bonded to a cover glass to create microfluidic channels 80mm deep with oxygen plasma treatment. These devices were subsequently sterilized by autoclave and dried in oven. Then, Matrigel (BD Biosciences) was mixed with same volume cell culture medium and was injected within the central channel using a 200 ul pipette. The chips were placed in the 10 cm petri dishes which contain 3 ml sterile water and were ready for use after 15 min standing.

*Transwell invasion assay*

Cells were placed into 10% matrigel (BD Biosciences) coated membrane in upper chamber (24-well insert, 8 μm, Corning Costar). Medium with 10% FBS was used as an attractant in the lower chamber. After being incubated for 36 hours, cells invaded through the membrane were fixed with 75% ethanol and stained with DAPI (1 μg/ml). The stained cell images were captured by microscope (Olympus), and five random fields at 10× magnification were counted. Results were shown as average from at least three independent experiments. Error bars represented the SD.

*Three-dimensional culture*

Three-dimensional culture was carried out as previously described [48]. Culture slides (BD BioCoat) were added with 80 μl Matrigel (BD Biosciences) per well and incubated at 37°C for 1 hour. Next, cells ($2\times10^3$) mixed with 2% Matrigel were added to each well and refed each 3 days. Finally, we observed the cell morphology under a fluorescence microscope (Olympus).

*Zebrafish embryo xenograft assay*

*Zebrafish maintenance*

Zebrafish adult specimens were maintained following the standard guidelines depicted in Nüsslein - Volhard and Dahm (2002). Zebrafish were kept in a self-recirculating aquarium at an average temperature of 28℃ with a 14-hours light 10-hour dark cycle. Adult specimens were fed twice a day on a diet of Hikari micropellets (Kyorin) and brine shrimp. Zebrafish embryos (1 dpf – 7 dpf) were kept in a solution composed of system water (chlorine deprived tap and distilled water mixture) with the addition of 0.0003% (v/v) methylene blue (antifungal) at a constant temperature of 28°C.

*CM-Dil labeling*

Cells lines were pre-seeded to obtain a culture with 80% level of confluency on the day of the CM-DiI (Invitrogen) cell labelling. CM-DiI dye was diluted in DMEM without solutes according to the concentrations defined during the DiI-labelling optimisation. Cell lines were individually trypsinised and centrifuged to obtain a pellet. Cell pellets were resuspended in 5μl/mL CM-DiI dilutions. Cells were left to incubate in the dye at 37°C at 10% $CO_2$ for 10 min. Following treatment, cells were rinsed once with PBS and centrifuged twice to remove all excess media prior to injection. The final pellet was then used for the zebrafish microinjection procedure.

*Microinjection of human tumour cells*

Zebrafish embryos developed in the chorion and have to be dechorionated at 24 hpf prior to injection. Human tumour cell lines (MCF-7 NSC and MCF-7 p62 siRNA) were pre-labelled with CM-DiI and centrifuged to obtain a dry pellet. The embryos were anaesthetized in a solution containing 0.003% tricane (Sigma) 10 min prior to injection. Injections were performed on an injection mould composed of 3% agarose in a solution of pre-warmed PBS (+Mg +Ca) 0.003% tricane, using a 12 mm gage borosilicate pipette fixed on a Narishige microinjector. Embryos were injected in the yolk sac region in proximity of the embryos sub-intestinal vessels with approximately 150 breast cancer cells. Injection were completed within 1 hour following which embryos were placed at 28℃ in a solution of system water with methylene blue for the duration of the experiment.

Embryos were imaged individually at 3dpi under a wide-field fluorescent microscope (Olympus CKX41). 0.05% tricaine was added to their water to prevent their movement during the live imaging procedure. Pictures were captured with Q Capture-Pro (QImaging). Any alteration of the original picture was performed with the aid of ImageJ. The corrected total cell fluorescence (CTCF) was measured using the formula: CTCF= Integrated Density – (Area of selected cell × Mean fluorescence of background readings) for each imaged zebrafish.

*Analysis of metastasis*

Female BALB/C-nu mice (4-6 weeks old) were tail intravenous injected with $1\times10^6$ cells per mouse. After 8 weeks, lungs were removed and examined macroscopically or detected in paraffin-embedded sections stained with H&E.

*Analysis of tumour growth*

Female BALB/C-nu mice (4-6 weeks old) were subcutaneously inoculated with equal amounts ($1\times10^6$/100 µl in PBS containing 50% Matrigel) of single cells. Tumour formation was monitored for 8 weeks. The tumour volumes and weights were determined by the method described previously [46]. All animal studies were approved by the Institute Animal Care and Use Committee of Dalian Medical University, and carried out in accordance with established institutional guidelines and approved protocols.

*RNA extraction, reverse transcription-PCR and real-time quantitative PCR*

Total RNA was extracted by using TRIzol reagent (Life technologies). cDNA was generated by using EasyScript One-Step gDNA Removal and cDNA Synthesis SuperMix Kit (TransGen Biotech) according to the manufacturer's instructions. Real-time quantitative PCR was performed by using the specific SYBR Select Master Mix (Life technologies) in a MX3000p cycler (Stratagene). Changes of mRNA levels were determined by the $2^{-\triangle\triangle CT}$ method using Actin for internal crossing normalization. Detailed primer sequences for qPCR were listed in Supplementary Table 1.

*Western blot analysis*

Samples were lysed on ice in RIPA buffer (50 mM Tris [pH 8.0], 150 mM sodium chloride, 0.5% sodium deoxycholate, 0.1% SDS, and 1% NP-40) supplemented with protease inhibitors (1 mM Na3VO4, 1 µg/mL leupeptin, and 1 mM PMSF). The protein concentration was determined by the Coomassie brilliant blue dye method. In all, equal amounts of protein per lane were run in 6% to 15% SDS–PAGE gels and subsequently transferred to a nitrocellulose membrane (Millipore) via submerged transfer. After blocking the membrane at room temperature for 1 hour, the membrane was incubated overnight at 4°C with various primary antibodies. After incubation with peroxidase-conjugated secondary antibodies (Thermo Scientific) for 1 hour at room temperature, the signals were visualized using an enhanced chemiluminescence Western blot detection kit (K-12045-D50; Apgbio, Beijing, China) according to the manufacturer's instructions. The blots were developed using the Bio-Rad Molecular Imager instrument (Bio-Rad, USA). The information of antibodies were listed as follows: Actin (Proteintech, #60008-1), GAPDH (KANGCHEN, KC-5G4), p62 (Santa Cruz, sc-28359), p62 (D5E2) (CST, 8025), Vimentin (ALBIOCHEM, #IF01), FLAG-TAG (Protein Tech, 66008-1-Ig), HIS-TAG (Protein Tech, 66005-1-Ig), HIS-TAG (BBI, D110002-0200), Ubiquitin (UBB) (Protein Tech, 60310-1-Ig), LC3B (Sigma-Aldrich, L7543), GOAT ANTI-MOUSE (ABB-Kinase, a25012-1), GOAT ANTI-RABBIT (Protein Tech, sa00001-2), Goat anti-Mouse IgG (HRP conjugated) (Thermo-Pierce, 31430), Goat anti-Rabbit IgG (HRP conjugated) (Thermo-Pierce, 31460).

*Co-immunoprecipitation analysis, In-Gel Trypsin Digestion, Mass Spectrometry, Immunofluorescence staining and Statistical analysis*

See Supplementary Materials and Methods.

## Results

*p62 expression is elevated in metastatic breast cancer and its overexpression correlates with poor prognosis.*

In an effort to explore the relationship between p62 expression and breast cancer metastatic capacity, we first collected 5 pairs of clinical metastatic breast cancer and adjacent normal tissues, and conducted Western blot analysis of p62 expression levels. Compared with adjacent normal tissues, p62 protein levels were up-regulated at varying degrees in all metastatic breast cancer tissues (Figure 1A). Consistently, analysis of gene expression value from TCGA showed that p62 mRNA expression levels in normal tissues (n=110) were significantly lower than that in both primary tumour (n=1065; -0.4355 versus -0.1485) and metastatic tumour tissues (n=7; -0.4355 versus -0.1423) (Figure 1B). Further, the Kaplan-Meier survival analysis of 87 breast carcinoma specimens revealed a correlation between the higher p62 expression and reduced metastasis-free survival times ($P=0.011$, GSE6532 from the GEO database) (Figure 1C). Moreover, 104 breast cancer samples from GEO database (GSE42568) by univariate analysis showed that high p62 expression was associated with decreased relapse-free survival times ($P<0.0001$) (Figure 1D). These data suggest that p62 is accumulated in metastatic breast cancer and its overexpression correlates with poor clinical outcome of breast cancer.

*p62 promotes invasive phenotypes of breast cancer cells in vitro.*

To investigate whether the expression level of p62 regulated invasive phenotypes of breast cancer cells, we first examined the expression of p62 in five breast cancer cell lines (SKBR-3, MDA-MB-231, BT-549, SUM149 and MCF-7), and a noncancerous breast epithelial cell line (MCF-10A). Here we found that both the mRNA and protein levels of p62 in metastatic group (SKBR-3, MDA-MB-231, BT-549, SUM149) were much higher than that in non-metastatic group (MCF-7, MCF-10A), indicating that the expression level of p62 positively correlated with the invasive phenotypes of breast cancer (Figure 2A and 2B). Then we used shRNA to mediate p62 depletion in metastatic MDA-MB-231 cells and lentivirus to facilitate ectopic overexpression of p62 in non-metastatic MCF-10A cells. The efficiencies of p62 knockdown and overexpression were assessed by western blotting. As shown in Figure 2C, p62 was effectively suppressed by two different p62 shRNA species in MDA-MB-231 cells, and significantly increased by lentivirus-infection in MCF-10A cells.

Herein, we built up a microfluidic model to observe local invasion of cancer cells in real time (Supplementary Figure 1) to assess the contribution of p62 in promoting breast cancer invasive ability. Silencing p62 expression dramatically reduced the invasive capacity of MDA-MB-231 cells as indicated by a decrease in both the area and distance of invasion (Figure 2D). Consistently, depletion of p62 impaired the ability of metastatic MDA-MB-231 cells to invade through matrigel pre-coated transwells (Supplementary Figure 2A). In contrast, overexpressing p62 in non-metastatic MCF-10A cells resulted in the acquisition of invasive ability as indicated by both the microfluidic and Transwell invasion assays (Figure 2E, Supplementary Figure 2B). Moreover, we examined the effect of p62 suppression on the ability of MDA-MB-231 cells to form colonies in three-dimensional matrigel culture. After ten days in culture, control cells formed multiple protrusions invading into the surrounding matrix while MDA-MB-231 cells with p62 depletion formed smooth edges around cell spheres (Figure 2F-a). These results were quantified by calculation of the perimeter, which showed a significant difference between control and p62 knockdown cells (Figure 2F-b). Together, these observations indicate that p62 enhances breast cancer cells invasion.

*Inhibition of p62 attenuates breast cancer metastasis and leads to decreased tumorigenicity in vivo.*

We next evaluated the *in vivo* effects of p62 depletion on breast cancer metastasis. In zebrafish embryo xenograft assay, we engrafted MCF-7 siNC and MCF-7 sip62 cells, stably expressing red fluorescent proteins, in a zebrafish embryo host. At 3 days post-implantation (dpi), silencing p62 expression in MCF-7 cells exhibited an obviously reduced invasive behavior when compared to control cells (Figure 3A). In addition, zebrafish embryo engrafted with p62 siRNA MCF-7 cells had a lower metastases incidence (20/90, 22.2%) compared to control cells (49/111, 44.1%) (Figure 3B). Quantification of the fluorescence intensity of invasive cells showed a significant decrease elicited by p62 knockdown (Figure 3C). In mice xenograft models, control shRNA MDA-MB-231 and p62 shRNA MDA-MB-231 cells were injected into the lateral tail vein of 4~6 weeks old BALB/C (nu/nu) female nude mice. Eight weeks after injection, mice injected with MDA-MB-231-shp62 cells had a markedly decreased metastatic burden as measured by macrography and H&E staining (Figure 4A-a&b). Consistently, the area and number of metastatic nodules in the lung of mice injected with MDA-MB-231-shp62 cells were significantly reduced as compared with that injected with MDA-MB-231-shNC cells (Figure 4A-c). These results indicate that silencing p62 expression attenuates the metastatic ability of breast cancer.

To determine the effect of p62 knockdown on tumour growth, equal number of control and p62 knockdown MDA-MB-231 cells ($1\times10^6$ cells) were subcutaneously injected into 4~6 weeks old BALB/C (nu/nu) female nude mice (5 mice in each group). Tumour xenografts were then measured every week and mice sacrificed after 8 weeks. As shown in Figure 4B, comparing with mice inoculated with MDA-MB-231-shNC cells, which formed large tumours within 56 days, the mice inoculated with MDA-MB-231-shp62-1 and shp62-2 cells showed a significant reduction in the tumour growth as indicated by the decreased tumour volumes and tumour weights. These results demonstrate that p62 suppression contributes to decreased tumorigenicity in breast cancer.

*Identification of vimentin as a novel p62 binding partner and p62 suppression downregulates vimentin protein expression.*

To further explore the mechanism for p62-mediated breast cancer invasion and metastasis, we sought to identify novel p62 binding proteins. Taking advantage of the proteomics-based approach, we analyzed endogenous p62 coimmunoprecipitated (co-IP) proteins by mass spectrometry to identify putative p62 protein binding partners (Figure 5A, Supplementary Table 2 and 3). Here, we focused our investigations on vimentin, which has been revealed to be a major intermediate filament in mediating cell movement [27, 34, 35]. To this end, we first examined whether endogenous p62 bound to vimentin by co-immunoprecipitation in MDA-MB-231 cells. In these cell extracts, we detected vimentin after immunoprecipitation with a p62 antibody, but not with the control IgG, indicating that p62 interacted with vimentin (Figure 5B). In addition, the p62-vimentin interaction was further confirmed by glutathione S-transferase pull-down assay, by which GST-tagged p62 co-precipitated with His-tagged vimentin, as well as GST-tagged vimentin cooperated with Flag-tagged p62 (Figure 5C and 5D). Furthermore, Immunofluorescence studies using p62 and vimentin specific antibodies showed that both proteins co-localized in the cytoplasm in MDA-MB-231 cells (Supplementary Figure 3). Together, these data suggest that p62 binds to vimentin in breast cancer cells.

Next, we examined the effects of silencing or overexpressing p62 on both the mRNA and protein levels of endogenous vimentin. As shown in Figure 5E-a and

Supplementary Figure 4A-a, shRNA or RNAi mediated depletion of p62 downregulated the protein expression levels of vimentin in both MDA-MB-231 and SK-BR-3 cells. In contrast, lentivirus-mediated overexpression of p62 upregulated vimentin protein levels in both MCF-10A and MCF-7 cells (Figure 5F-a and Supplementary Figure 4B-a). Interestingly, vimentin mRNA levels exhibited no significant differences whether in p62 knockdown MDA-MB-231 and SK-BR-3 cells or in p62 overexpression MCF-10A and MCF-7 cells compared with their relative controls (Figure 5E-b&5F-b, Supplementary Figure 4A-b&4B-b), suggesting that p62 promotes vimentin expression not at the transcriptional level.

*Vimentin plays an important role in p62-mediated breast cancer cells invasion.*

In order to test if vimentin acted as an important mediator in p62 promoting breast cancer cells invasion, we overexpressed vimentin in both MDA-MB-231-shNC and MDA-MB-231-shp62 cells. Western blot assays were conducted to evaluate the protein levels of p62 and vimentin. As shown in Figure 6A, depletion of p62 attenuated vimentin expression, but overexpression of vimentin increased vimentin protein levels in both shNC and shp62 cells. Next, we performed the microfluidic assay to verify the effect of vimentin on p62-mediated cancer cells invasion. In accordance with previous reports, overexpressing vimentin resulted in a significant increment in the invasive ability of MDA-MB-231 cells (Figure 6C). Critically, re-constitution of vimentin expression in MDA-MB-231-shp62 cells abolished the reduction in invasive capacity (Figure 6C). Transwell invasion assay showed that both the vimentin overexpressing shNC cells and shp62 cells exhibited an increased invasive ability when compared to their relative shNC and shp62 cells, and the difference in the invasive ability of vimentin overexpressed shNC and shp62 cells was not so dramatically as the difference in shNC and shp62 cells (Figure 6E).

In addition, we conducted shRNA-mediated vimentin suppression in both MDA-MB-231-Ctrl and MDA-MB-231-p62-OE cells. Notably, overexpressing p62 caused an increment in vimentin protein expression in MDA-MB-231 cells, along with an increased invasive phenotype as indicated by both the microfluidic and Transwell assays (Figure 6B, 6D, 6F). Interestingly, knockdown of vimentin in MDA-MB-231-p62-OE cells attenuated the increased invasive ability and exhibited no significant difference in the capacity of invasion compared with vimentin knockdown MDA-MB-231-Ctrl cells (Figure 6D and 6F). Taken together, these results demonstrate that vimentin plays an essential role in p62-mediated invasion in breast cancer cells.

### *p62 expression is positively correlated with vimentin protein levels in clinical breast cancer specimens.*

Finally, we assessed p62 and vimentin protein expression levels in clinical breast cancer specimens by Western blot analysis. The expression of vimentin was relatively higher in samples which showed much more abundant p62 expression (Figure 7A). Linear regression analysis showed a positive correlation between p62 and vimentin protein expression ($R^2=0.7539$, $P=0.0011$) (Figure 7B), indicating that p62 overexpression is associated with high vimentin levels in clinical breast cancer tissues.

## Discussion

Our recent work demonstrated that the signalling adaptor p62 enhances breast cancer stem-like properties through downregulating let7a/b expression to stabilize MYC mRNA [36]. In the present study, we further focus on the role of p62 in regulation of breast cancer metastasis. Several novel findings have been observed, and they include (a) p62 expression is elevated in metastatic breast cancer and its overexpression correlates with poor prognosis (Figure 1); (b) p62 promotes invasive phenotypes of breast cancer cells *in vitro* and inhibition of p62 attenuates breast cancer metastasis and leads to decreased tumorigenicity *in vivo* (Figure 2, 3, 4 and Supplementary Figure 2); (c) p62 binds to vimentin and p62 suppression downregulates vimentin protein expression (Figure 5, Supplementary Figure 3, 4); (d) Vimentin is required for p62-mediated breast cancer cells invasion (Figure 6); (e) p62 expression is positively correlated with vimentin protein levels in clinical breast cancer specimens (Figure 7).

Considering that metastases are responsible for more than 90% of breast cancer-related deaths and that no available strategies to interfere with the progress effectively, the verification of reliable prognostic biomarkers and novel therapeutic targets underlying tumour metastasis is urgently needed. We report here for the first time that clinical metastatic breast cancer tissues display high levels of p62 expression (Figure 1). Further analysis confirmed that p62 is required for the maintenance of breast cancer invasion and metastasis (Figure 2, 3, 4 and Supplementary Figure 2). Notably, the metastases incidence of zebrafish embryo engrafted with MCF-7 control cells was 44.1% (49/111), whereas MCF-7 cells with p62 depletion had a lower incidence of 22.2% (20/90) within the same time frame (Figure 3B). Silencing p62 expression attenuates breast cancer cells metastasis in both zebrafish embryo and mouse tail vein xenograft models

(Figure 3C, Figure 4A). Collectively, our data strongly suggest p62 as a potential target for limiting breast cancer metastasis.

Interestingly, a recent study showed that intramuscularly administered p62-encoding plasmid induces anti-p62 antibodies and exhibits strong antitumour activity in models of allogeneic mouse tumours, including the Ca755 breast carcinoma [37]. p62 DNA vaccine also decreases or stabilizes growth of locally advanced mammary tumours in dogs [38]. These two studies indicate that p62 might be a potential candidate antigen for cancer immunotherapy. A feasible cancer antigen should be immunogenic, essential for cancer cells but not for normal tissues to reduce the risk of toxicity, and overexpressed in tumours as compared to the normal tissues [39]. Here, our data show that p62 is overexpressed in breast cancer tissues relative to adjacent normal breast tissues (Figure 1A). High p62 expression levels correlate with reduced metastasis-free and relapse-free survival times (Figure 1C and D). In agreement, previous studies also implied that p62 is accumulated in Ras-transformed cells and it is required for Ras-induced survival and transformation [40]. Moreover, we identified a critical role of p62 in the maintenance of breast cancer stemness [36]. In combination, our observations reveal the dependence of breast tumours on p62 in contrast to normal breast tissues, further expanding the suggestion that p62 protein might be an excellent target as a cancer antigen.

The scaffold protein p62 includes several important functional domains, which mediate the interaction with different signalling molecules to regulate cancer initiation and progression [41, 42]. For example, p62 has been reported to promote engrafted human skin cancer cell growth through interacting with Twist-1 and inhibiting Twist-1 autophagic degradation [43]. p62 also specially associates with mTORC1 by binding to raptor to regulate cell growth and autophagy that integrates nutrient sensing and cell size control [10, 44, 45]. In an effort to investigate the mechanisms underlying the regulation of breast cancer metastasis by p62, we found that p62 binds to vimentin and silencing p62 expression downregulates vimentin protein expression (Figure 5 and Supplementary Figure 3, 4). Most importantly, vimentin is required for p62-promoted breast cancer metastasis (Figure 6). Linear regression analysis of clinical breast cancer specimens indicated that p62 is positively correlated with vimentin protein expression (Figure 7), while in adjacent normal samples, there is no such obviously correlation between p62 and vimentin expression (Supplementary Figure 5). Still, the molecular mechanism whereby p62 regulates vimentin expression remains to be unknown. We hypothesized that p62 regulates vimentin protein expression through ubiquitin-proteasome pathway. In order to test this conjecture, we performed reciprocal immunoprecipitation assay and analyzed proteins via immunoblotting. Ubiquitinated vimentin could be readily detected (Supplementary Figure 6A&B). Then we treated control and p62 knockdown MDA-MB-231 cells with MG132, a potent proteasome inhibitor, and found that the effect of p62 depletion mediated vimentin suppression was not reversed effectively (Supplementary Figure 6C). Moreover, treatment with MG132 in MCF-10A-Ctrl and MCF-10A-p62-OE cells, failed to prevent the upregulation of vimentin expression levels by p62 overexpression (Supplementary Figure 6D). Further, to confirm whether p62 upregulation influences the ubiquitin of vimentin, we overexpressed p62 in HEK-293T cells and used His-tagged vimentin to co-immunoprecipitate with Flag-tagged ubiquitin in the absence or presence of MG132. The IP/IB results showed that there were no significant differences in the vimentin ubiquitinated levels in both the control and p62 overexpressing cells (Supplementary Figure 6E). Together these data indicate that depletion of p62 downregulates vimentin protein expression independent of the ubiquitin-proteasome pathway.

In summary, we demonstrate that the signalling adaptor p62 enhances breast cancer metastasis through interacting with vimentin. Our findings also suggest that p62 could be used as both the potential prognostic biomarker of metastatic breast cancer and the therapeutic target for metastatic breast cancer treatment.

## Conflict of interest

No potential conflict of interest to disclose.

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## Figure Legends

**Figure 1** p62 expression is elevated in metastatic breast cancer and its overexpression correlates with poor prognosis. (A) p62 protein levels in five pairs of clinical metastatic breast cancer (T) and adjacent normal tissues (N) were subjected to western blot analysis. (B) p62 mRNA expression levels in normal tissues and primary tumour (left) or in metastatic tumour tissues (right) were shown by analysis of gene expression value from TCGA. ***P<0.001, two-tailed Student's t-tests. Error bars represented mean ± SD. (C) Kaplan-Meier survival analysis of 87 breast carcinoma specimens from the GEO database (GSE6532) (P=0.011). (D) Relapse-free survival times of 104 breast cancer samples from GEO database (GSE42568) by univariate analysis (P<0.0001).

**Figure 2** p62 is essential for breast cancer cells to maintain the invasive ability *in vitro*. (A) p62 protein expression was tested by Western blot and (B) p62 mRNA expression was examined by RT-qPCR assay in both the metastatic and nonmetastatic breast cancer cell lines. ***P<0.001, two-tailed Student's t-tests. Error bars represented mean ± SD. (C) Efficiencies for knockdown or overexpression of p62 were tested by Western blot analysis. (D) Comparison of the invasive capacity in the microfluidic model by silencing p62 expression in MDA-MB-231 cells and (E) overexpressing p62 in MCF-10A cells. Scale bar, 100 µm. *P<0.05, ***P<0.001, two-tailed Student's t-tests. Error bars represented mean ± SD. (F-a) Representative images of MDA-MB-231 control versus p62 knockdown cells embedded in three-dimensional matrigel culture. Scale bar, 500 µm. (F-b) Quantification of tumour-sphere perimeter. ***P<0.001, two-tailed Student's t-tests. Error bars represented mean ± SD.

**Figure 3** Effects of knockdown p62 on cell migration in Tra/Nac zebrafish embryos.

MCF-7 cells were transfected with non-specific control or p62 siRNA respectively. Thirty embryos were injected for each group and approximately 150 CM-Dil labelled MCF-7 cells were injected into each 2dpf Tra/Nac zebrafish embryos. Metastasis was measured under the fluorescent microscope at 3dpi. Some of the embryos were died at this stage. (A) Tra/Nac zebrafish embryos at 2dpf transplanted with MCF-7 non-specific control and MCF-7 p62 siRNA. The implanted tumour cells can be seen in red (red fluorescent microscope). Presence of migrated tumour cells from yolk sac to the tail is indicated with a black arrow. (B) Percentage of zebrafish which presented any form of metastasis in the total number of injected zebrafish in the experiment. (C) The corrected total cell fluorescence (CTCF) was measured using the formula: CTCF= Integrated Density – (Area of selected cell × Mean fluorescence of background readings) for each imaged zebrafish. Scale bar, 500 µm. **$P < 0.01$, two-tailed Student's t-tests. Error bars represented mean ± SD.

**Figure 4** Inhibition of p62 attenuates breast cancer metastasis and leads to decreased tumorigenicity *in vivo*. (A) Control shRNA MDA-MB-231 and p62 shRNA MDA-MB-231 cells were injected into the lateral tail vein of 4~6 weeks old BALB/C (nu/nu) female nude mice. Macrograph of representative lungs (a) and H&E staining of lung sections (b) were presented to show metastases in lungs. The metastatic nodules were indicated with yellow arrows. Scale bar, 100 µm. The area and number of metastatic nodules were presented as mean ± SD (n=6) (c). (B) Immunodeficient mice were subcutaneously inoculated with equal number of control and p62 knockdown MDA-MB-231 cells ($1\times10^6$ cells per mouse, n=5). Photographs of tumours (a), tumour volumes and tumour weights were shown (b). ***$P<0.001$, two-tailed Student's t-tests.

Error bars represented mean ± SD.

**Figure 5** p62 binds to vimentin and p62 suppression downregulates vimentin protein expression. (A) The endogenous p62 co-immunoprecipitated (co-IP) proteins were analyzed by mass spectrometry. (B) The interaction between endogenous p62 and vimentin protein was analyzed by co-immunoprecipitation in MDA-MB-231 cells. (C) (D) Protein interaction was analyzed by glutathione S-transferase pull-down assay. Vimentin protein and mRNA levels were examined in p62 knockdown MDA-MB-231 cells (E) or p62 overexpression MCF-10A cells (F). The protein and mRNA levels of p62 and vimentin were respectively tested by Western blot and RT-qPCR assay. $***P<0.001$, two-tailed Student's t-tests. Error bars represented mean ± SD.

**Figure 6** Vimentin is required for p62-mediated breast cancer cells invasion. p62 and vimentin expression levels were assessed by Western blot assay in vimentin overexpressed control and p62 knockdown cells (A), or in shRNA-mediated vimentin suppressed control and p62 upregulation cells (B). The invasive ability was analyzed by both the microfluidic assay (C and D) and the transwell invasion assay (E and F). Scale bar, 100 μm. $*P<0.05$, $**P<0.01$, $***P<0.001$, two-tailed Student's t-tests. Error bars represented mean ± SD.

**Figure 7** p62 expression is positively correlated with vimentin level in breast cancer specimens. (A) Both the p62 and vimentin protein expression in breast cancer specimens (n=10; T: tumour) were subjected to Western blot analysis. (B) Both the p62 and vimentin expression levels were normalized to relative GAPDH and linear regression analysis was shown. $R^2=0.7539$, $P=0.0011$.

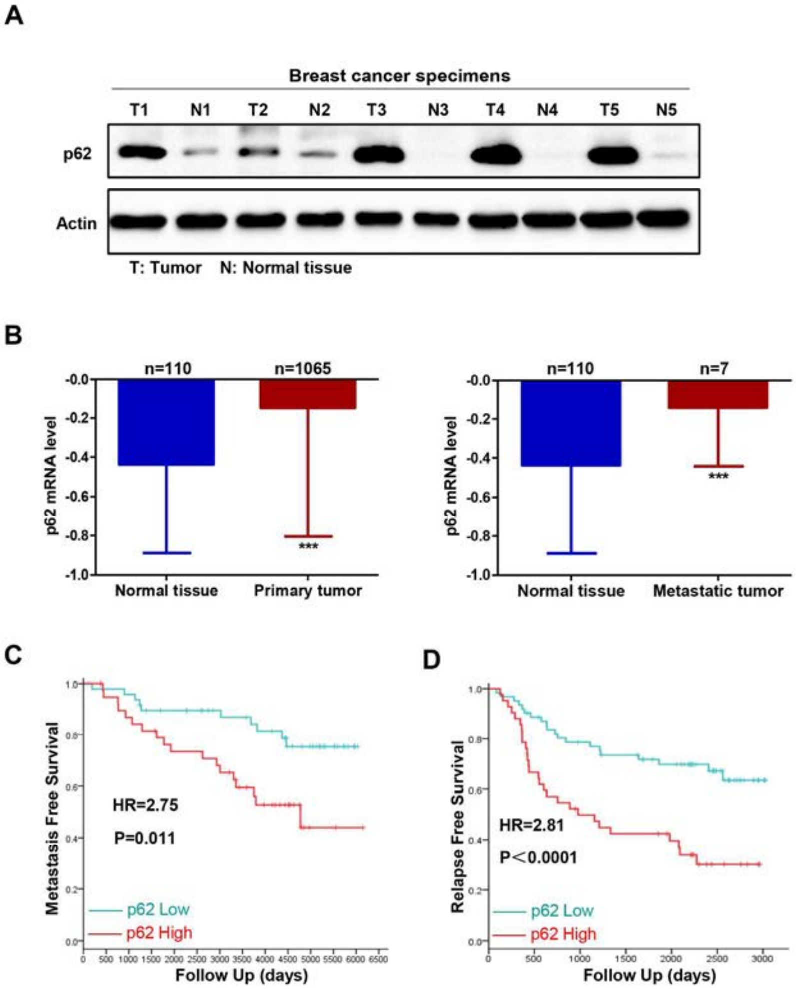

Figure 1

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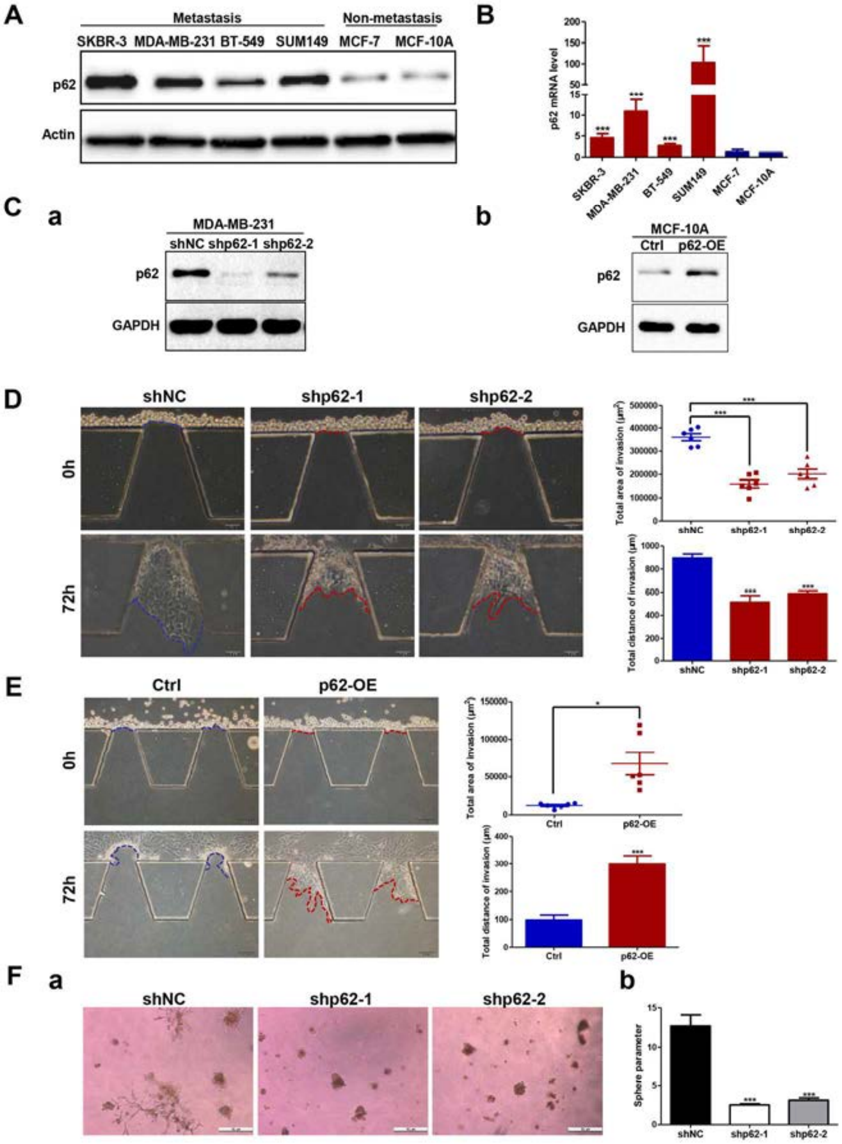

Figure 2

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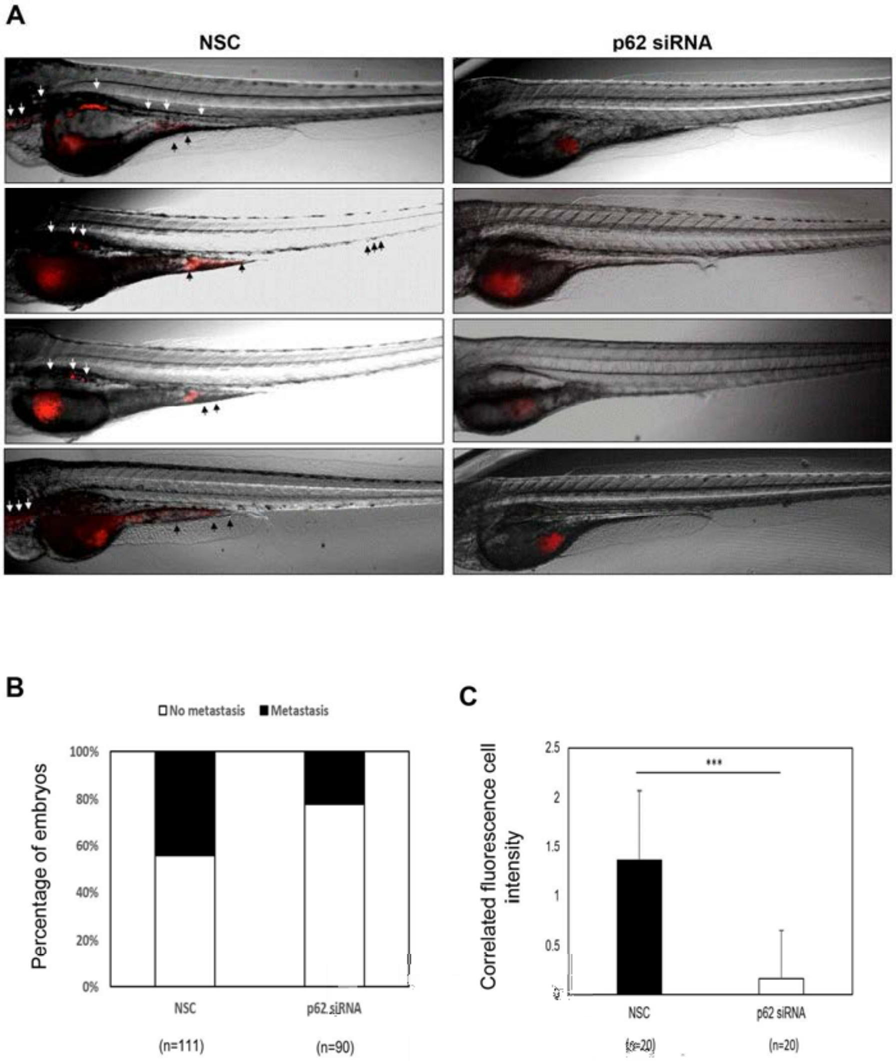

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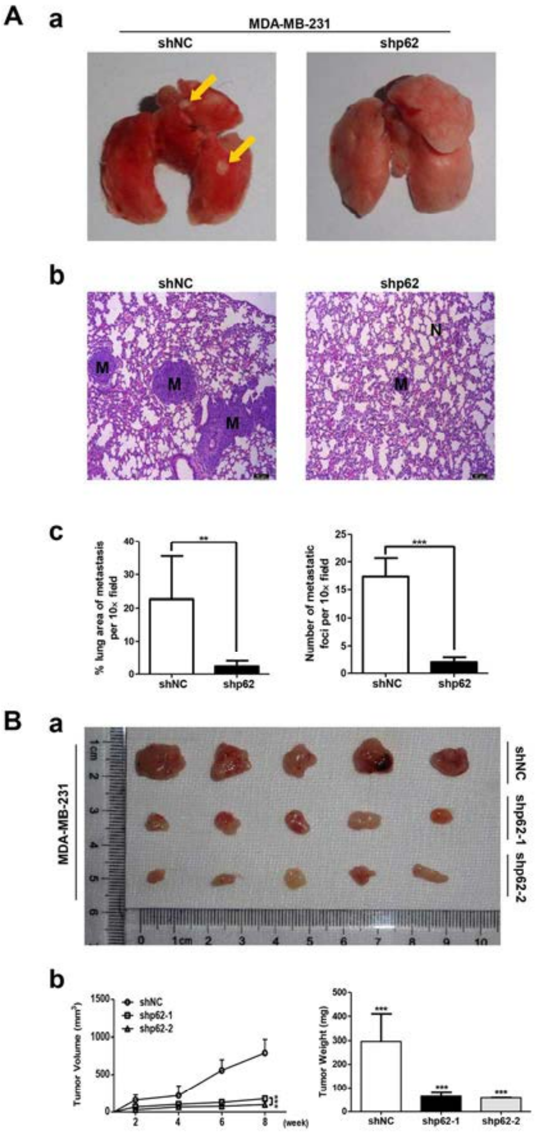

Figure 4

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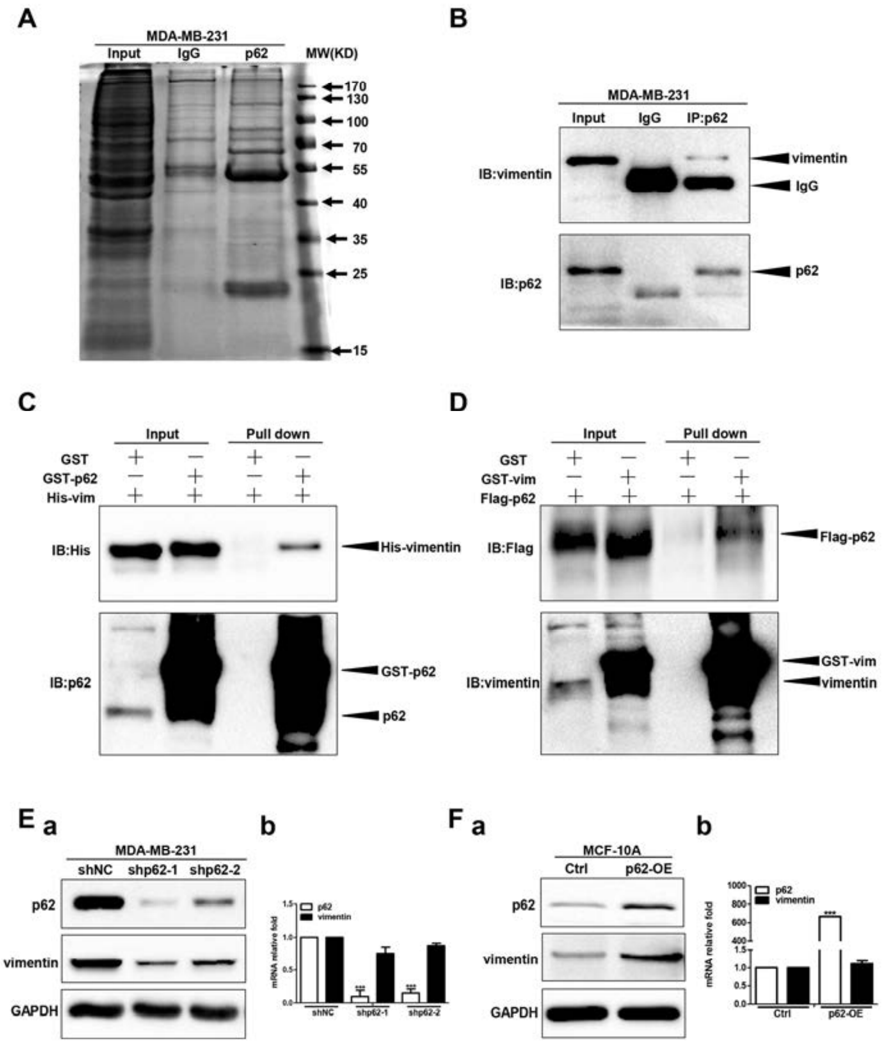

Figure 5

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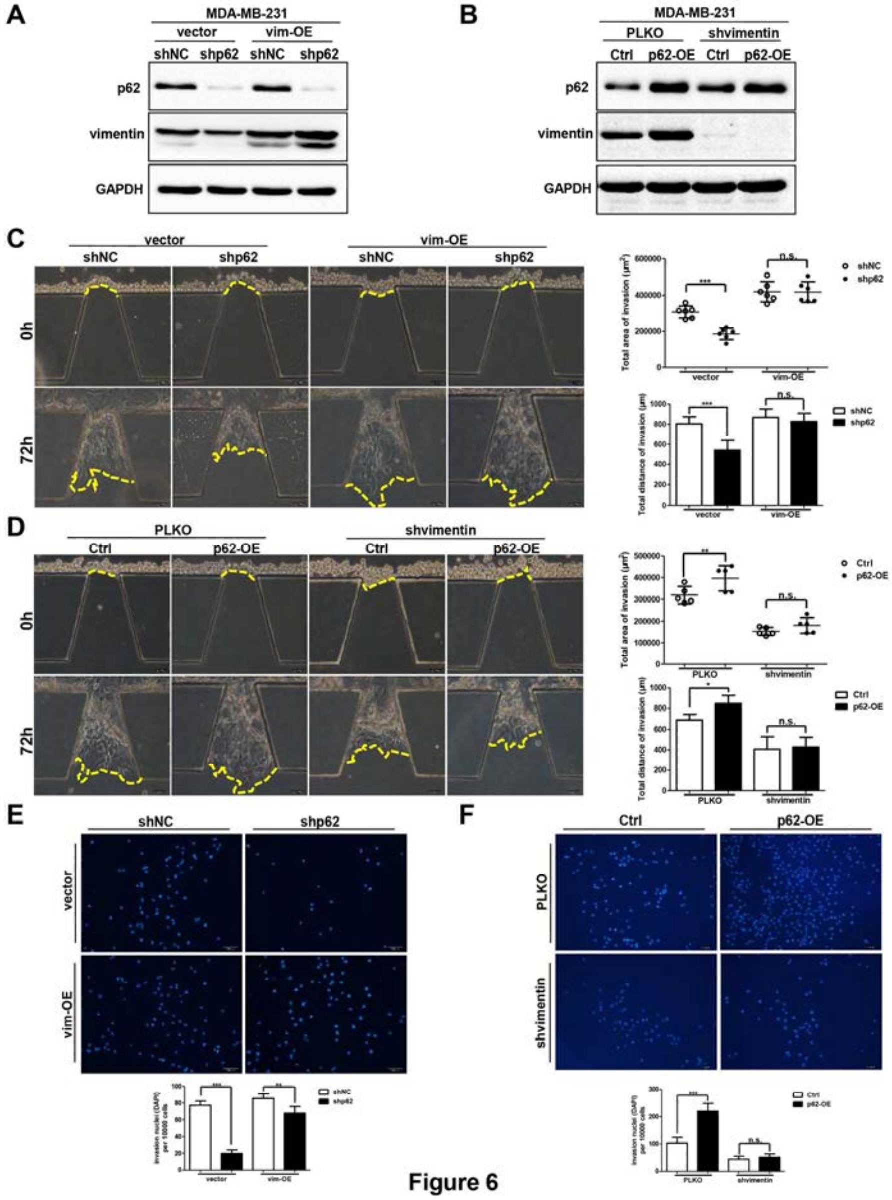

Figure 6

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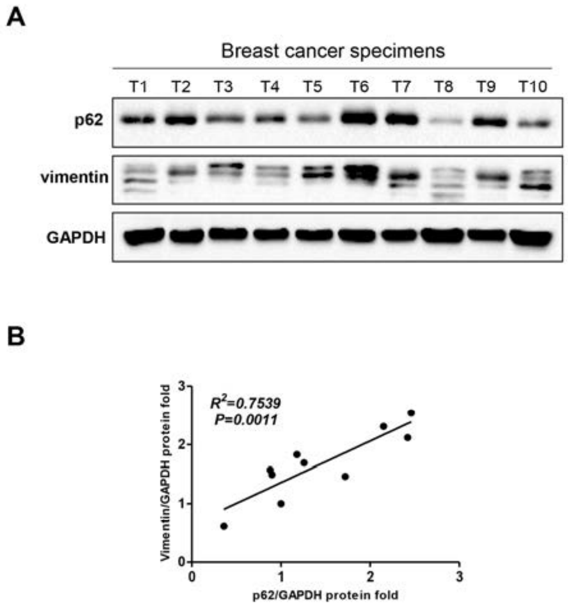

Figure 7

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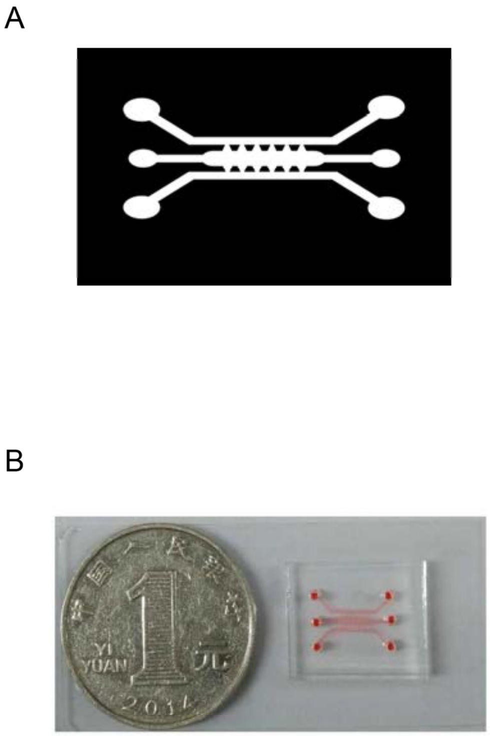

Supplementary Figure 1

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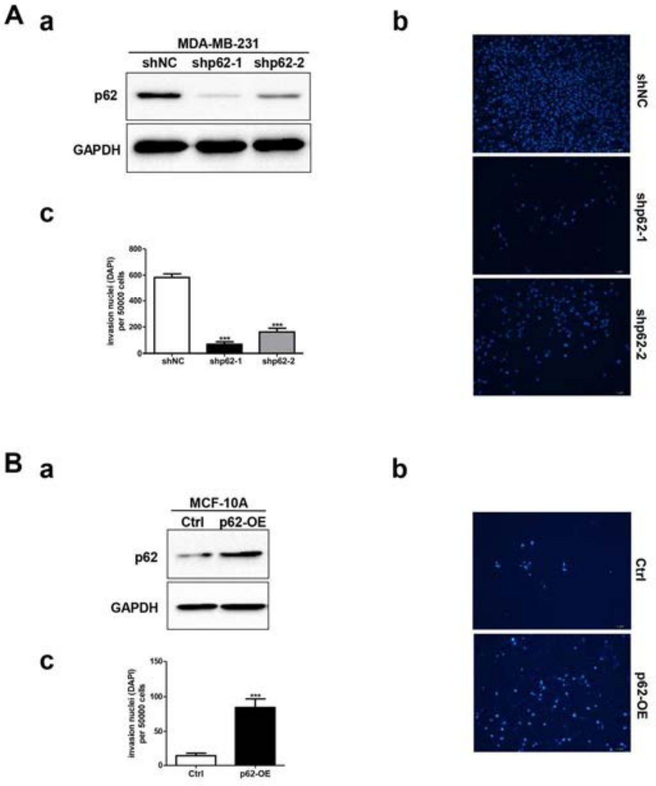

**Supplementary Figure 2**

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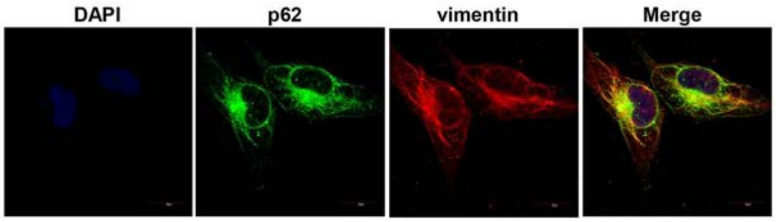

Supplementary Figure 3

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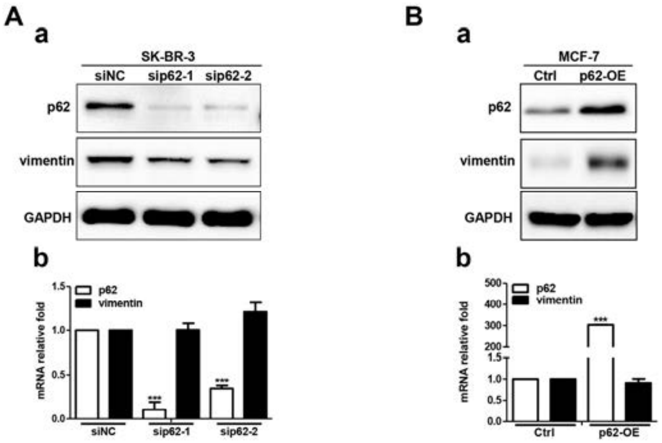

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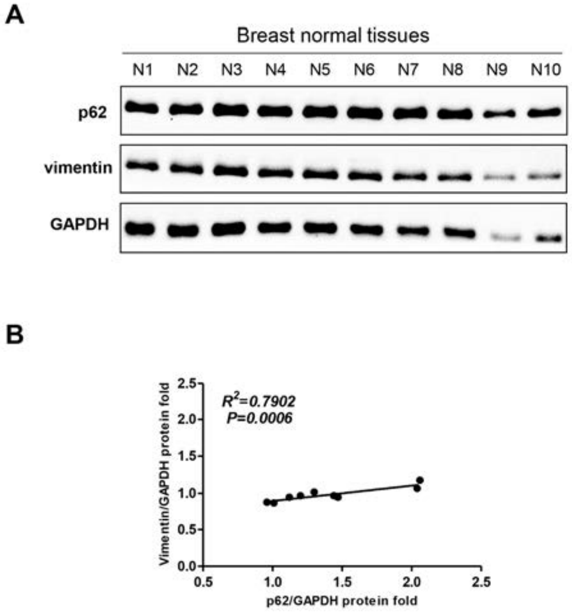

Supplementary Figure 5

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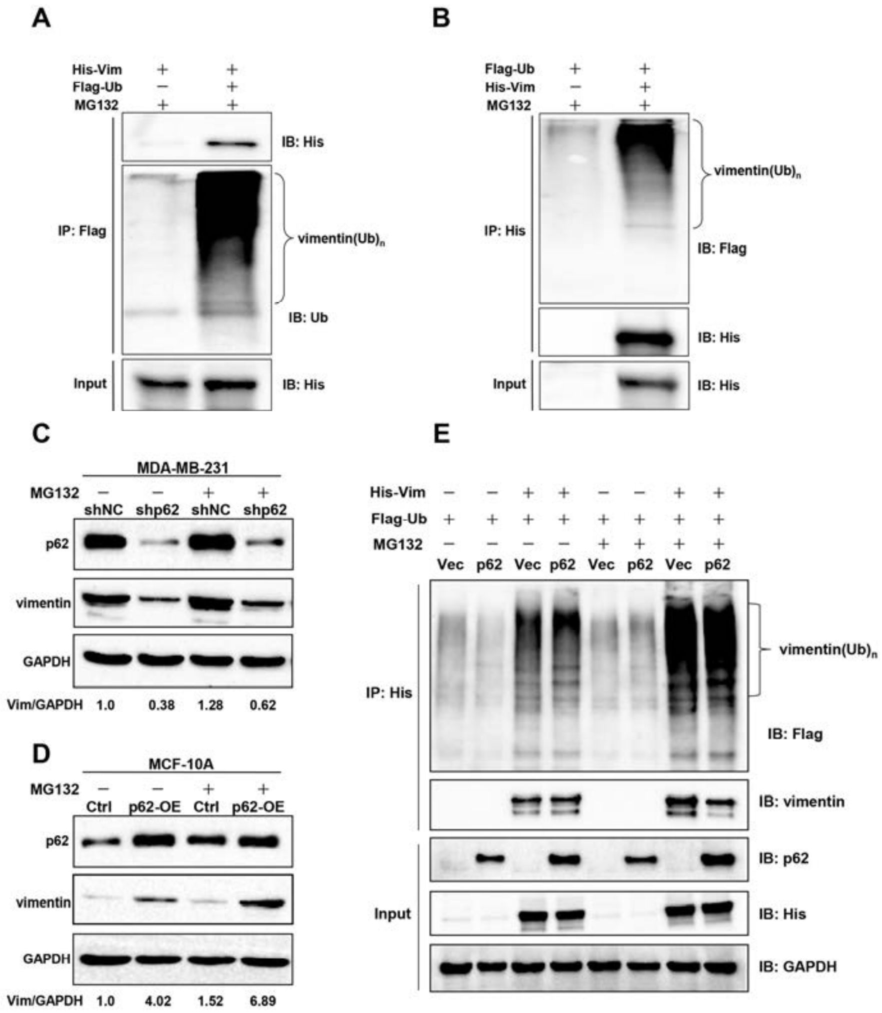

Supplementary Figure 6

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**Supplementary Figure 1** (A) Model diagram and (B) photograph of the microfluidic chip for testing cancer cells local invasion abilities. The chip is composed of one central chamber and two side channels. Cancer cells in which contained 1% FBS cell culture medium are seeded in one of the side channels and the other side channel is injected into 10% FBS containing cell culture medium. Matrigel is mixed with same volume 10% FBS containing cell culture medium and is injected into the central channel.

**Supplementary Figure 2** The invasive properties of MDA-MB-231-shp62 (A) and MCF-10A-p62-OE cells (B) together with their relative controls were analyzed by Transwell invasion assay. ***P<0.001, two-tailed Student's t-tests. Error bars represented mean ± SD.

**Supplementary Figure 3** Immunofluorescence staining of p62 (Green) and vimentin (Red) in MDA-MB-231 cells. Scale bars, 20 μm.

**Supplementary Figure 4** Vimentin protein and mRNA levels were examined in p62 knockdown SK-BR-3 cells or p62 overexpression MCF-7 cells. The protein and mRNA levels of p62 and vimentin were respectively tested by Western blot and RT-qPCR assay. ***P<0.001, two-tailed Student's t-tests. Error bars represented mean ± SD.

**Supplementary Figure 5** (A) Both the p62 and vimentin protein expression in breast cancer adjacent normal tissues (n=10; N: normal) was subjected to Western blot analysis. (B) Both the p62 and vimentin expression levels were normalized to relative GAPDH and linear regression analysis was shown. $R^2$=0.7902, P=0.0006.

**Supplementary Figure 6** (A) (B) HEK293T cells were co-transfected with His-Vimentin and Flag-Ubiquitin in the presence of MG132. Protein interaction was analyzed by co-immunoprecipitation and Western blot assay. (C) (D) The protein expression levels of p62 and vimentin were examined by Western blot assay. (E) Control and p62 overexpression HEK293T cells were co-transfected with Flag-Ubiquitin and His-Vimentin in the presence or absence of MG132. Vimentin ubiquitinated levels were analyzed by co-immunoprecipitation and Western blot assay.

## Supplementary Materials and Methods

### *Co-immunoprecipitation analysis*

Protein lysates (500-1000 μg) prepared from cultured cells. Immunocomplex pull-down was achieved via overnight incubation of protein lysates with relevant antibodies bound to Protein G-Agarose (Roche) or with Glutathione Sepharose beads (GE Healthcare) alone at 4℃. After careful washing, loading buffer was added, and the samples were boiled at 100℃ for 10 min. Co-immunoprecipitated proteins were then subjected to Western blot as described above.

### *In-Gel Trypsin Digestion*

p62 and interacting proteins that were co-immunoprecipitated as described above were solubilized in 1.5 × SDS sample buffer (15% glycerol, 60 mM Tris [pH 6.8], 3% SDS, 7.5% ß-mercaptoethanol) and run on SDS-PAGE. After migration, the gels were fixed, and proteins were detected with Coomassie blue staining. p62 immunoprecipitated protein bands and IgG control group protein bands were cut out of the gels and rinsed three times in deionized water. Gel slices (≤ 1 mm) were incubated with 100 mM ammonium bicarbonate buffer for 15 min at 4□. The supernatant was then removed, and samples were then mixed with 50% acetonitrile for shaking 10 min at 4□ to dehydrate the gel pieces. Re-incubate with 100 mM ammonium bicarbonate buffer for 15 min at 4□ and then mixed with 100% acetonitrile for shaking 10 min at 4□. After dehydrating the gels, samples were incubated with DTT for 2 hours at 37□. Following incubation, IAA was replaced with DTT and further incubated for 1 hour at 25□ in darkness. Then samples were dealt with 50% acetonitrile, 50 mM ammonium bicarbonate and 100% acetonitrile sequentially. Finally, dried gels were covered with 500 µl trypsin solution (12.5 ng/µl in 25 mM ammonium bicarbonate) and in-gel digestion was performed at 37□ overnight. The digested sample was prepared for mass spectrometry analysis as follows. Firstly, supernatant was transferred into a new tube and precipitants were incubated with 150 µl 25 mM ammonium bicarbonate for 10 min at 4□, then put the supernatant into the same tube. Secondly, precipitants were added 250 µl buffer (ACN : TFA=94 : 6) for shaking 10 min at 4□ and transferred into the same tube. Thirdly, dried the supernatant and store at -20□. Finally, dissolved the samples in 0.1% FA totally and then prepared for mass spectrometric analysis.

*Mass Spectrometry*

Peptides were analyzed on LTQ XL mass spectrometer (Thermo, San Jose, CA) with 1D RPLC separating system in the positive ion mode. The control and experiment group were respectively loaded onto and separated by a C18 capillary column (Thermo, BioBasic-18, 150*0.1) with a 120 min RP gradient elution. A Finnigan surveyor MS pump (Thermo, San Jose, CA, USA) was used to deliver the mobile phase consisted of mobile A, 0.1% (v/v) formic acid in water, and mobile phase B, 0.1% (v/v) formic acid in ACN. The flow rate was adjusted to 300μL/min without splitting. The gradients elution was performed with gradients of 2−35% B in 90 min, 35−80% B in 2 min, 80% B in 10 min, 80% B−98% A in 3 min and 98% A in 20 min. All MS and MS/MS spectra were acquired in the data-dependent analysis mode, in which the 10 most intense ions with MS scan were selected for MS/MS scan by collision-induced dissociation (CID). All MS/MS spectra were searched using Proteome Discoverer (Version 1.3.0.339) against NCBI protein database (human20141121) with 1% false discovery rate (FDR). The parameters were set as follows: precursor-ion mass tolerance, 2 Da; fragment-ion mass tolerance, 1 Da; enzyme, trypsin (KR/P); missed cleavage, 2; static modification, Cys (+57.021 Da); dynamic modifications methionine (+15.995 Da). The results were shown in Supplementary Table 2 and 3.

*Immunofluorescence staining*

To determine the localization of p62 and vimentin, we performed immunofluorescence assay. In brief, cells were plated on coverslips to 30% confluence and then fixed in 4% para-formaldehyde-PBS at room temperature for 20 minutes and permeabilized in 0.5% Triton X-100 in PBS for 10 minutes at 4℃. Cells were then blocked with 1% BSA and incubated with primary antibody against both p62 (Santa Cruz, sc-28359) and vimentin (Cell Signaling Technology, 5741s), followed by a FITC conjugated second antibody (Invitrogen), counterstained with DAPI (1 μg/μl), and visualized using a confocal microscope (Leica).

*Statistical analysis*

The two-tailed Student's t-tests was used to perform a statistical comparison between two groups. Statistical tests were performed using the SPSS software, version 16.0 (SPSS Inc.) or with GraphPad Prism 5.0 (GraphPad Software, Inc.). The level of statistical significance was set at *P < 0.05, **P <0.01, ***P <0.001.

| Gene | Formard (5'-3') | Reverse (5'-3') |
|---|---|---|
| p62 | AGGCGCACTACCGCGAT | CGTCACTGGAAAAGGCAACC |
| Actin | TTGCCGACAGGATGCAGAAGGA | AGGTGGACAGCGAGGCCAGGAT |
| Vimentin | GTCCACTGAGTACCGGAGACA | TAGTTAGCAGCTTCAACGGCAA |

| Accession | Description | Score | Coverage | # Proteins | # Unique Peptides | # Peptides | # PSMs | # AAs | MW [kDa] | calc. pI |
|---|---|---|---|---|---|---|---|---|---|---|
| 6166599 | RecName: Full=Myosin-9; AltName: Full=Cellular myosin heavy chai | 668.79 | 63.88 | 64 | 51 | 150 | 224 | 1960 | 226.4 | 5.60 |
| 239938886 | RecName: Full=Keratin, type I cytoskeletal 9; AltName: Full=Cytoke | 218.96 | 58.75 | 8 | 27 | 29 | 71 | 623 | 62.0 | 5.24 |
| 160332335 | RecName: Full=Neuroblast differentiation-associated protein AHNAK | 54.48 | 16.28 | 21 | 20 | 22 | 29 | 5890 | 628.7 | 6.15 |
| 123648 | RecName: Full=Heat shock cognate 71 kDa protein; AltName: Full= | 94.96 | 37.93 | 32 | 19 | 25 | 34 | 646 | 70.9 | 5.52 |
| 221042022 | unnamed protein product [Homo sapiens] | 74.88 | 34.74 | 14 | 19 | 20 | 25 | 665 | 72.4 | 5.94 |
| 63087903 | unnamed protein product [Homo sapiens] | 3027.34 | 66.67 | 17 | 17 | 17 | 914 | 231 | 24.3 | 7.91 |
| 238054406 | RecName: Full=Keratin, type II cytoskeletal 1; AltName: Full=67 kD | 577.20 | 64.60 | 52 | 17 | 52 | 196 | 644 | 66.0 | 8.12 |
| 194387918 | unnamed protein product [Homo sapiens] | 150.14 | 49.72 | 32 | 16 | 28 | 55 | 535 | 57.8 | 8.00 |
| 119614804 | clathrin, heavy polypeptide (Hc), isoform CRA_d [Homo sapiens] | 50.27 | 13.36 | 23 | 16 | 16 | 17 | 1639 | 187.8 | 5.69 |
| 386758 | GRP78 precursor, partial [Homo sapiens] | 53.50 | 32.77 | 12 | 15 | 18 | 19 | 653 | 72.1 | 5.14 |
| 90110781 | RecName: Full=Nucleolin; AltName: Full=Protein C23 | 39.85 | 23.10 | 12 | 15 | 17 | 18 | 710 | 76.6 | 4.70 |
| 485601457 | Chain C, Structure Of The Human 60s Ribosomal Proteins | 39.67 | 30.44 | 11 | 14 | 14 | 16 | 427 | 47.7 | 11.06 |
| 119581085 | keratin 10 (epidermolytic hyperkeratosis; keratosis palmaris et plant | 476.16 | 56.73 | 56 | 13 | 39 | 158 | 624 | 63.3 | 5.21 |
| 21757045 | unnamed protein product [Homo sapiens] | 73.04 | 48.90 | 72 | 13 | 20 | 24 | 454 | 52.4 | 5.06 |
| 52545822 | hypothetical protein [Homo sapiens] | 33.27 | 36.90 | 36 | 13 | 14 | 14 | 374 | 40.5 | 7.01 |
| 31092 | unnamed protein product [Homo sapiens] | 48.75 | 25.76 | 39 | 12 | 12 | 19 | 462 | 50.1 | 9.01 |
| 119578453 | alpha tubulin, isoform CRA_b [Homo sapiens] | 41.91 | 43.75 | 51 | 12 | 12 | 15 | 416 | 46.3 | 5.08 |
| 1195531 | type I keratin 16 [Homo sapiens] | 135.27 | 50.95 | 30 | 11 | 23 | 51 | 473 | 51.2 | 5.05 |
| 194382178 | unnamed protein product [Homo sapiens] | 63.06 | 21.70 | 9 | 10 | 10 | 20 | 530 | 56.8 | 6.87 |
| 425518 | anti-colorectal carcinoma heavy chain [Homo sapiens] | 61.27 | 30.35 | 5 | 10 | 10 | 21 | 458 | 50.6 | 6.67 |
| 190192184 | filamin A [Homo sapiens] | 34.55 | 7.56 | 33 | 10 | 13 | 13 | 2315 | 245.7 | 5.97 |
| 119605386 | DEAD (Asp-Glu-Ala-Asp) box polypeptide 41, isoform CRA_a [Homo | 30.60 | 24.40 | 11 | 10 | 10 | 10 | 496 | 55.4 | 8.18 |
| 332164777 | pyruvate kinase PKM isoform d [Homo sapiens] | 24.70 | 24.51 | 77 | 9 | 9 | 10 | 457 | 49.9 | 7.83 |
| 119597993 | annexin A2, isoform CRA_c [Homo sapiens] | 22.73 | 35.54 | 14 | 9 | 9 | 9 | 287 | 32.4 | 6.29 |
| 35903 | ribosomal protein L7 [Homo sapiens] | 19.91 | 34.68 | 14 | 9 | 9 | 9 | 248 | 29.2 | 10.61 |
| 109734611 | Myosin, heavy chain 10, non-muscle [Homo sapiens] | 102.34 | 15.69 | 65 | 8 | 29 | 39 | 1976 | 228.8 | 5.54 |
| 578804832 | PREDICTED: titin isoform X5 [Homo sapiens] | 51.02 | 0.63 | 31 | 8 | 16 | 24 | 35484 | 3935.9 | 6.43 |
| 431822406 | heat shock protein HSP 90-beta isoform b [Homo sapiens] | 40.55 | 19.97 | 49 | 8 | 14 | 17 | 676 | 78.2 | 5.05 |
| 378404908 | glyceraldehyde-3-phosphate dehydrogenase isoform 2 [Homo sapie | 32.55 | 29.35 | 13 | 8 | 8 | 13 | 293 | 31.5 | 7.61 |
| 27436948 | lamin isoform A-delta10 [Homo sapiens] | 23.74 | 18.14 | 27 | 8 | 9 | 9 | 634 | 70.6 | 8.40 |
| 119592222 | ribosomal protein S4, X-linked, isoform CRA_b, partial [Homo sapie | 23.72 | 31.17 | 17 | 8 | 8 | 10 | 231 | 26.1 | 9.99 |
| 189502784 | mitochondrial heat shock 60kD protein 1 variant 1 [Homo sapiens] | 23.65 | 17.40 | 19 | 8 | 8 | 8 | 569 | 60.6 | 6.04 |
| 119608213 | spectrin, alpha, non-erythrocytic 1 (alpha-fodrin), isoform CRA_c [H | 21.41 | 4.12 | 33 | 8 | 8 | 8 | 2427 | 279.3 | 5.36 |
| 119602167 | dynein, cytoplasmic 1, heavy chain 1, isoform CRA_c [Homo sapiens | 30.66 | 3.47 | 35 | 7 | 9 | 11 | 4236 | 485.7 | 6.35 |
| 18490263 | Ribosomal protein L6 [Homo sapiens] | 29.22 | 26.74 | 21 | 7 | 7 | 12 | 288 | 32.7 | 10.61 |
| 76496472 | 60S ribosomal protein L3 isoform b [Homo sapiens] | 23.97 | 22.03 | 23 | 7 | 8 | 9 | 354 | 40.1 | 10.23 |
| 40353734 | nucleophosmin isoform 2 [Homo sapiens] | 22.97 | 41.89 | 47 | 7 | 7 | 7 | 265 | 29.4 | 4.61 |
| 485601423 | Chain K, Structure Of The Human 60s Ribosomal Proteins | 21.59 | 53.33 | 10 | 7 | 7 | 9 | 165 | 17.8 | 9.42 |

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|---|---|---|---|---|---|---|---|---|---|---|
| 187281 | M4 protein [Homo sapiens] | 13.90 | 9.33 | 17 | 7 | 7 | 7 | 729 | 77.6 | 8.85 |
| 15431310 | keratin, type I cytoskeletal 14 [Homo sapiens] | 129.29 | 50.64 | 35 | 6 | 22 | 50 | 472 | 51.6 | 5.16 |
| 12654329 | HSP90AA1 protein [Homo sapiens] | 46.96 | 29.93 | 82 | 6 | 15 | 18 | 548 | 64.3 | 5.17 |
| 30354619 | YWHAZ protein, partial [Homo sapiens] | 28.40 | 34.69 | 43 | 6 | 9 | 10 | 320 | 35.3 | 7.21 |
| 119582143 | Treacher Collins-Franceschetti syndrome 1, isoform CRA_h [Homo s | 20.94 | 5.32 | 70 | 6 | 7 | 8 | 1411 | 144.2 | 9.04 |
| 221045062 | unnamed protein product [Homo sapiens] | 20.77 | 29.17 | 17 | 6 | 6 | 8 | 192 | 20.7 | 6.87 |
| 34849883 | TPA_exp: spectrin-like protein of the nuclear envelope and Golgi [H | 20.38 | 1.52 | 52 | 6 | 7 | 10 | 8407 | 965.7 | 5.55 |
| 119602459 | ribosomal protein L8, isoform CRA_e [Homo sapiens] | 17.31 | 24.66 | 14 | 6 | 6 | 7 | 223 | 24.1 | 11.24 |
| 119618578 | ribosomal protein, large, P0, isoform CRA_c [Homo sapiens] | 15.35 | 44.58 | 13 | 6 | 6 | 6 | 166 | 18.3 | 9.63 |
| 485601399 | Chain T, Structure Of The Human 40s Ribosomal Proteins | 15.18 | 33.79 | 4 | 6 | 6 | 6 | 145 | 16.1 | 10.32 |
| 12643409 | RecName: Full=Matrin-3 | 15.17 | 9.09 | 13 | 6 | 6 | 6 | 847 | 94.6 | 6.25 |
| 382546190 | ATP synthase subunit alpha, mitochondrial isoform c [Homo sapiens | 13.41 | 15.31 | 15 | 6 | 6 | 6 | 503 | 54.5 | 8.24 |
| 194384468 | unnamed protein product [Homo sapiens] | 92.91 | 45.73 | 6 | 5 | 13 | 36 | 234 | 27.3 | 4.89 |
| 119612227 | poly(A) binding protein, cytoplasmic 1, isoform CRA_c [Homo sapier | 27.66 | 19.33 | 19 | 5 | 8 | 11 | 419 | 47.3 | 8.92 |
| 56675570 | unnamed protein product [Homo sapiens] | 21.55 | 21.56 | 27 | 5 | 5 | 6 | 218 | 23.6 | 10.92 |
| 194385982 | unnamed protein product [Homo sapiens] | 18.69 | 15.67 | 17 | 5 | 6 | 7 | 638 | 72.2 | 5.10 |
| 57863259 | T-complex protein 1 subunit alpha isoform b [Homo sapiens] | 17.55 | 18.20 | 27 | 5 | 6 | 7 | 401 | 43.9 | 7.71 |
| 119624101 | ribosomal protein S18, isoform CRA_c [Homo sapiens] | 17.32 | 43.75 | 6 | 5 | 6 | 7 | 128 | 15.0 | 10.27 |
| 9022435 | ribosomal protein S3 [Homo sapiens] | 17.27 | 45.57 | 11 | 5 | 5 | 6 | 158 | 17.1 | 9.58 |
| 39644794 | EEF1G protein, partial [Homo sapiens] | 15.58 | 13.82 | 87 | 5 | 6 | 6 | 434 | 49.8 | 6.67 |
| 119601423 | hCG2028724 [Homo sapiens] | 14.38 | 16.92 | 18 | 5 | 5 | 6 | 266 | 30.1 | 10.74 |
| 17426161 | macrophin 1 isoform 4 [Homo sapiens] | 14.28 | 1.84 | 46 | 5 | 6 | 7 | 5314 | 599.5 | 5.14 |
| 40037762 | unnamed protein product [Homo sapiens] | 13.19 | 24.04 | 9 | 5 | 5 | 5 | 208 | 24.2 | 10.35 |
| 58761484 | T-complex protein 1 subunit gamma isoform c [Homo sapiens] | 12.99 | 10.65 | 9 | 5 | 5 | 5 | 507 | 56.4 | 6.49 |
| 158254970 | unnamed protein product [Homo sapiens] | 12.26 | 12.15 | 11 | 5 | 5 | 5 | 535 | 57.4 | 6.46 |
| 1310882 | Chain A, Cyclophilin B Complexed With [d-(Cholinylester)ser8]-Cycl | 12.17 | 29.78 | 37 | 5 | 5 | 5 | 178 | 19.6 | 9.16 |
| 119615473 | ribosomal protein L11, isoform CRA_a [Homo sapiens] | 11.86 | 36.09 | 7 | 5 | 5 | 5 | 133 | 15.1 | 8.87 |
| 31108 | human elongation factor 2 [Homo sapiens] | 11.75 | 9.09 | 8 | 5 | 5 | 5 | 858 | 95.3 | 6.83 |
| 119613715 | glutamyl-prolyl-tRNA synthetase, isoform CRA_a [Homo sapiens] | 11.37 | 4.04 | 16 | 5 | 5 | 5 | 1511 | 170.4 | 7.33 |
| 119588849 | hCG1992539, isoform CRA_b [Homo sapiens] | 9.27 | 17.53 | 46 | 5 | 5 | 5 | 251 | 27.3 | 9.96 |
| 194375299 | unnamed protein product [Homo sapiens] | 62.15 | 41.74 | 89 | 4 | 11 | 21 | 333 | 37.3 | 5.71 |
| 28590 | unnamed protein product [Homo sapiens] | 27.64 | 6.08 | 11 | 4 | 4 | 13 | 609 | 69.3 | 6.28 |
| 24417711 | nesprin-2 [Homo sapiens] | 19.95 | 1.39 | 42 | 4 | 8 | 10 | 6884 | 795.8 | 5.38 |
| 119617305 | myosin, light polypeptide 6, alkali, smooth muscle and non-muscle, | 18.08 | 37.93 | 16 | 4 | 4 | 6 | 116 | 12.9 | 4.87 |
| 119598260 | uveal autoantigen with coiled-coil domains and ankyrin repeats, isof | 17.35 | 5.37 | 15 | 4 | 6 | 6 | 1378 | 158.3 | 6.87 |
| 119585757 | filamin B, beta (actin binding protein 278), isoform CRA_b, partial [ | 17.17 | 3.45 | 36 | 4 | 7 | 7 | 2147 | 230.5 | 5.59 |
| 221043742 | unnamed protein product [Homo sapiens] | 15.39 | 16.12 | 7 | 4 | 6 | 6 | 484 | 54.6 | 6.60 |
| 114549 | RecName: Full=ATP synthase subunit beta, mitochondrial; Flags: Pr | 13.69 | 10.59 | 6 | 4 | 4 | 4 | 529 | 56.5 | 5.40 |
| 292435 | ribosomal protein L26 [Homo sapiens] | 13.64 | 22.07 | 9 | 4 | 4 | 5 | 145 | 17.3 | 10.55 |

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|---|---|---|---|---|---|---|---|---|---|---|
| 119578438 | myeloid/lymphoid or mixed-lineage leukemia 2, isoform CRA_a [Hor | 13.11 | 1.04 | 9 | 4 | 4 | 6 | 4539 | 487.1 | 6.58 |
| 116241330 | RecName: Full=ATP-dependent RNA helicase A; Short=RHA; AltNam | 13.03 | 4.96 | 13 | 4 | 5 | 5 | 1270 | 140.9 | 6.84 |
| 119580409 | hCG2010544 [Homo sapiens] | 12.77 | 40.74 | 101 | 4 | 5 | 5 | 135 | 15.6 | 9.61 |
| 179212 | Na+ K+ ATPase alpha subunit, partial [Homo sapiens] | 12.11 | 7.51 | 52 | 4 | 5 | 5 | 746 | 81.7 | 5.22 |
| 23491735 | ribosomal protein L10a [Homo sapiens] | 12.09 | 23.50 | 7 | 4 | 5 | 5 | 217 | 24.8 | 9.94 |
| 119615215 | karyopherin (importin) beta 1, isoform CRA_b [Homo sapiens] | 11.19 | 6.38 | 11 | 4 | 4 | 5 | 846 | 93.8 | 4.77 |
| 119569329 | hCG1640785, isoform CRA_a [Homo sapiens] | 10.88 | 27.42 | 5 | 4 | 4 | 6 | 124 | 13.6 | 9.99 |
| 23712 | myoblast antigen 24.1D5 [Homo sapiens] | 10.75 | 14.39 | 10 | 4 | 4 | 4 | 396 | 45.2 | 6.76 |
| 578829803 | PREDICTED: myosin phosphatase Rho-interacting protein isoform X | 10.04 | 2.13 | 26 | 4 | 4 | 4 | 2301 | 260.4 | 5.49 |
| 194378812 | unnamed protein product [Homo sapiens] | 10.03 | 14.77 | 7 | 4 | 4 | 4 | 352 | 38.9 | 4.94 |
| 119595171 | protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), | 9.93 | 7.52 | 21 | 4 | 4 | 4 | 917 | 103.7 | 6.76 |
| 915392 | fatty acid synthase [Homo sapiens] | 9.49 | 2.43 | 10 | 4 | 4 | 4 | 2509 | 272.9 | 6.42 |
| 15342049 | Ribosomal protein S6 [Homo sapiens] | 9.34 | 18.47 | 24 | 4 | 4 | 4 | 249 | 28.7 | 10.90 |
| 530418509 | PREDICTED: eukaryotic translation initiation factor 2 subunit 2 isofo | 9.26 | 19.11 | 11 | 4 | 4 | 4 | 314 | 36.2 | 5.48 |
| 4930167 | Chain A, Human Muscle Aldolase | 9.10 | 12.40 | 32 | 4 | 4 | 4 | 363 | 39.3 | 8.09 |
| 1096938 | ribosomal protein L5 | 8.52 | 12.46 | 9 | 4 | 4 | 4 | 297 | 34.4 | 9.74 |
| 158254664 | unnamed protein product [Homo sapiens] | 60.44 | 28.91 | 61 | 3 | 10 | 21 | 377 | 42.0 | 5.39 |
| 56757569 | RecName: Full=Tubulin beta chain; AltName: Full=Tubulin beta-5 cl | 48.50 | 36.94 | 52 | 3 | 13 | 17 | 444 | 49.6 | 4.89 |
| 114155144 | tropomyosin alpha-3 chain isoform 4 [Homo sapiens] | 28.90 | 35.89 | 72 | 3 | 10 | 10 | 248 | 28.9 | 4.75 |
| 386785 | heat shock protein [Homo sapiens] | 28.82 | 17.81 | 33 | 3 | 11 | 12 | 640 | 69.8 | 5.58 |
| 75517570 | HNRPA1 protein [Homo sapiens] | 25.17 | 26.22 | 36 | 3 | 6 | 8 | 267 | 29.4 | 9.14 |
| 578813467 | PREDICTED: heterogeneous nuclear ribonucleoproteins A2/B1 isofor | 19.20 | 15.34 | 13 | 3 | 5 | 6 | 313 | 33.9 | 9.03 |
| 45219787 | Ribosomal protein S3A [Homo sapiens] | 18.82 | 35.61 | 30 | 3 | 8 | 8 | 264 | 30.0 | 9.73 |
| 40788231 | KIAA0373 [Homo sapiens] | 17.51 | 2.27 | 26 | 3 | 5 | 10 | 1540 | 180.1 | 6.80 |
| 119607089 | protein kinase, DNA-activated, catalytic polypeptide, isoform CRA_d | 16.66 | 1.49 | 12 | 3 | 5 | 8 | 4033 | 458.5 | 7.08 |
| 47077415 | unnamed protein product [Homo sapiens] | 16.62 | 3.96 | 7 | 3 | 5 | 9 | 1340 | 150.9 | 8.22 |
| 14278227 | Chain B, Nmr Structure Of Dff40 And Dff45 N-Terminal Domain Com | 16.29 | 25.52 | 4 | 3 | 3 | 4 | 145 | 16.1 | 4.79 |
| 51476783 | hypothetical protein [Homo sapiens] | 15.59 | 2.66 | 8 | 3 | 4 | 8 | 1504 | 166.1 | 8.43 |
| 119621384 | tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation | 15.57 | 22.04 | 35 | 3 | 5 | 6 | 245 | 27.7 | 4.78 |
| 52545677 | hypothetical protein [Homo sapiens] | 15.48 | 8.90 | 22 | 3 | 5 | 6 | 652 | 72.5 | 8.59 |
| 209572633 | RecName: Full=Inositol 1,4,5-trisphosphate receptor type 3; AltNam | 15.25 | 2.73 | 32 | 3 | 5 | 7 | 2671 | 303.9 | 6.48 |
| 193786214 | unnamed protein product [Homo sapiens] | 14.07 | 4.80 | 15 | 3 | 4 | 7 | 688 | 78.6 | 8.84 |
| 34395763 | RecName: Full=Regulating synaptic membrane exocytosis protein 1 | 12.54 | 1.95 | 40 | 3 | 3 | 6 | 1692 | 189.0 | 9.66 |
| 4503507 | eukaryotic translation initiation factor 2 subunit 3 [Homo sapiens] | 12.19 | 13.14 | 7 | 3 | 5 | 5 | 472 | 51.1 | 8.40 |
| 119599909 | golgi autoantigen, golgin subfamily b, macrogolgin (with transmemb | 11.47 | 1.74 | 96 | 3 | 6 | 6 | 3225 | 372.0 | 5.01 |
| 119620549 | spectrin, beta, non-erythrocytic 1, isoform CRA_f [Homo sapiens] | 10.82 | 2.70 | 13 | 3 | 4 | 4 | 2150 | 250.8 | 5.43 |
| 578822859 | PREDICTED: L-lactate dehydrogenase B chain isoform X1 [Homo sa | 10.60 | 11.90 | 5 | 3 | 3 | 3 | 353 | 39.4 | 8.90 |
| 119580970 | ribosomal protein L19, isoform CRA_b [Homo sapiens] | 10.47 | 20.62 | 20 | 3 | 5 | 5 | 194 | 23.2 | 11.47 |
| 13097600 | Similar to ribosomal protein L23, partial [Homo sapiens] | 10.42 | 29.85 | 6 | 3 | 3 | 4 | 134 | 14.1 | 10.26 |

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|---|---|---|---|---|---|---|---|---|---|---|
| 119617760 | protein phosphatase 1, regulatory (inhibitor) subunit 12A, isoform C | 10.22 | 5.47 | 44 | 3 | 5 | 5 | 914 | 101.5 | 5.39 |
| 62896917 | proteasome 26S non-ATPase subunit 12 isoform 1 variant [Homo sa | 10.09 | 9.65 | 11 | 3 | 4 | 5 | 456 | 52.9 | 7.36 |
| 568245056 | AKAP350C [Homo sapiens] | 9.74 | 1.60 | 89 | 3 | 5 | 5 | 3126 | 362.2 | 4.89 |
| 40040850 | unnamed protein product [Homo sapiens] | 9.64 | 29.50 | 7 | 3 | 3 | 3 | 139 | 15.2 | 5.02 |
| 10047267 | KIAA1596 protein [Homo sapiens] | 9.64 | 2.87 | 9 | 3 | 3 | 5 | 1151 | 129.9 | 5.25 |
| 578832139 | PREDICTED: centrosomal protein of 192 kDa isoform X8 [Homo sap | 9.60 | 1.55 | 19 | 3 | 4 | 5 | 2448 | 270.0 | 5.95 |
| 119611612 | translocated promoter region (to activated MET oncogene), isoform | 9.54 | 1.96 | 27 | 3 | 4 | 5 | 2349 | 265.4 | 5.07 |
| 341604768 | 60S ribosomal protein L13 isoform 2 [Homo sapiens] | 9.43 | 19.27 | 24 | 3 | 4 | 4 | 192 | 22.2 | 11.65 |
| 13786856 | Chain H, Human Muscle L-Lactate Dehydrogenase M Chain, Ternary | 9.38 | 11.78 | 10 | 3 | 3 | 3 | 331 | 36.5 | 8.27 |
| 194374069 | unnamed protein product [Homo sapiens] | 9.30 | 19.25 | 31 | 3 | 4 | 4 | 213 | 22.9 | 6.92 |
| 1705725 | RecName: Full=B-cell receptor-associated protein 31; Short=BCR-as | 9.17 | 12.60 | 10 | 3 | 3 | 4 | 246 | 28.0 | 8.44 |
| 119610275 | solute carrier family 25 (mitochondrial carrier; adenine nucleotide tr | 9.00 | 14.74 | 18 | 3 | 3 | 3 | 251 | 27.6 | 9.57 |
| 224036253 | Chain F, Crystal Structure Of The Eif4a-Pdcd4 Complex | 8.84 | 10.05 | 17 | 3 | 3 | 3 | 388 | 44.2 | 5.68 |
| 119623706 | ATP-binding cassette, sub-family F (GCN20), member 1, isoform CR | 8.83 | 4.09 | 14 | 3 | 4 | 4 | 807 | 91.6 | 7.68 |
| 407944028 | Chain B, Crystal Structure Of A Truncated Soluble Form Of Human C | 8.71 | 7.92 | 13 | 3 | 3 | 3 | 530 | 58.9 | 6.93 |
| 194384036 | unnamed protein product [Homo sapiens] | 8.60 | 15.29 | 19 | 3 | 3 | 3 | 327 | 35.0 | 8.32 |
| 578810001 | PREDICTED: sperm flagellar protein 2 isoform X5 [Homo sapiens] | 8.41 | 1.43 | 12 | 3 | 3 | 5 | 1537 | 176.7 | 6.00 |
| 485601396 | Chain L, Structure Of The Human 40s Ribosomal Proteins | 8.40 | 19.62 | 3 | 3 | 3 | 3 | 158 | 18.4 | 10.30 |
| 121948325 | RecName: Full=Kinesin-like protein KIF26B | 8.40 | 1.52 | 6 | 3 | 3 | 5 | 2108 | 223.7 | 8.44 |
| 119599630 | hypothetical protein FLJ35880 [Homo sapiens] | 8.32 | 1.74 | 9 | 3 | 4 | 4 | 2531 | 280.4 | 7.20 |
| 219519934 | LONP2 protein [Homo sapiens] | 8.18 | 5.69 | 14 | 3 | 3 | 4 | 808 | 89.6 | 7.18 |
| 119569564 | antigen identified by monoclonal antibody Ki-67, isoform CRA_c [Ho | 7.97 | 1.42 | 57 | 3 | 4 | 4 | 2896 | 319.2 | 9.50 |
| 14603010 | EIF3B protein [Homo sapiens] | 7.73 | 7.07 | 8 | 3 | 3 | 3 | 622 | 72.9 | 7.18 |
| 193787899 | unnamed protein product [Homo sapiens] | 7.67 | 14.91 | 20 | 3 | 3 | 3 | 275 | 30.5 | 7.66 |
| 28175603 | TAF3 protein, partial [Homo sapiens] | 7.64 | 5.01 | 7 | 3 | 3 | 3 | 539 | 59.0 | 6.76 |
| 194386358 | unnamed protein product [Homo sapiens] | 7.32 | 3.94 | 14 | 3 | 3 | 4 | 762 | 86.0 | 6.14 |
| 119626284 | heterogeneous nuclear ribonucleoprotein D (AU-rich element RNA b | 7.31 | 15.52 | 31 | 3 | 3 | 3 | 277 | 30.2 | 9.03 |
| 119579121 | hCG27283 [Homo sapiens] | 7.21 | 26.96 | 15 | 3 | 3 | 3 | 115 | 13.0 | 10.70 |
| 58476967 | HNRPC protein [Homo sapiens] | 6.92 | 14.00 | 55 | 3 | 3 | 3 | 250 | 27.8 | 4.69 |
| 338700 | tat binding protein-1 (tbp-1) [Homo sapiens] | 6.86 | 11.63 | 8 | 3 | 3 | 3 | 404 | 45.1 | 5.44 |
| 119609484 | ATP-binding cassette, sub-family A (ABC1), member 10, isoform CR/ | 6.58 | 3.18 | 6 | 3 | 3 | 3 | 1543 | 175.6 | 6.65 |
| 119163 | RecName: Full=Elongation factor 1-beta; Short=EF-1-beta | 6.49 | 15.56 | 4 | 3 | 3 | 3 | 225 | 24.7 | 4.67 |
| 119596086 | ADP-ribosylation factor guanine nucleotide-exchange factor 2 (brefe | 6.31 | 2.08 | 15 | 3 | 3 | 3 | 1776 | 200.7 | 6.37 |
| 1585552 | glucose-regulated protein ERp57/GRP58 | 5.70 | 5.94 | 20 | 3 | 3 | 3 | 505 | 56.9 | 6.65 |
| 61744481 | 4F2 cell-surface antigen heavy chain isoform e [Homo sapiens] | 5.44 | 5.99 | 23 | 3 | 3 | 3 | 568 | 61.8 | 5.21 |
| 38114878 | RPL13A protein, partial [Homo sapiens] | 5.35 | 11.94 | 11 | 3 | 3 | 3 | 201 | 23.4 | 10.93 |
| 386854 | type II keratin subunit protein, partial [Homo sapiens] | 322.91 | 41.78 | 44 | 2 | 36 | 123 | 493 | 52.8 | 5.44 |
| 119579125 | protein tyrosine phosphatase, receptor type, D, isoform CRA_d [Hor | 161.11 | 2.07 | 36 | 2 | 2 | 76 | 1254 | 141.6 | 6.55 |
| 4583679 | vacuolar protein sorting [Homo sapiens] | 147.09 | 7.89 | 12 | 2 | 2 | 66 | 570 | 65.0 | 8.29 |

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|---|---|---|---|---|---|---|---|---|---|---|
| 256542310 | dynein heavy chain 17, axonemal [Homo sapiens] | 126.80 | 1.14 | 7 | 2 | 3 | 52 | 4462 | 509.0 | 5.72 |
| 41322910 | plectin isoform 1d [Homo sapiens] | 116.24 | 11.23 | 41 | 2 | 43 | 44 | 4515 | 512.3 | 5.77 |
| 119585106 | hCG1790160 [Homo sapiens] | 60.14 | 4.75 | 2 | 2 | 2 | 28 | 589 | 67.9 | 8.62 |
| 327478526 | RecName: Full=Myosin-14; AltName: Full=Myosin heavy chain 14; A | 50.36 | 6.12 | 60 | 2 | 13 | 20 | 1995 | 227.7 | 5.60 |
| 193785954 | unnamed protein product [Homo sapiens] | 45.37 | 14.83 | 55 | 2 | 7 | 17 | 445 | 49.0 | 5.48 |
| 193785596 | unnamed protein product [Homo sapiens] | 31.86 | 27.46 | 15 | 2 | 9 | 12 | 397 | 44.6 | 4.93 |
| 40225472 | CERCAM protein [Homo sapiens] | 20.73 | 12.00 | 11 | 2 | 2 | 9 | 275 | 31.2 | 5.33 |
| 62988667 | unknown [Homo sapiens] | 19.06 | 12.23 | 7 | 2 | 2 | 10 | 188 | 21.3 | 8.41 |
| 74750718 | RecName: Full=Ankyrin repeat and KH domain-containing protein 1; | 18.86 | 1.26 | 32 | 2 | 3 | 8 | 2542 | 269.3 | 5.73 |
| 119629468 | hCG2011852 [Homo sapiens] | 18.37 | 1.17 | 95 | 2 | 8 | 9 | 6929 | 784.5 | 8.88 |
| 29649737 | protease serine 1 [Homo sapiens] | 18.25 | 46.43 | 9 | 2 | 2 | 7 | 84 | 9.1 | 9.57 |
| 530392546 | PREDICTED: glycylpeptide N-tetradecanoyltransferase 2 isoform X1 | 16.33 | 6.87 | 20 | 2 | 2 | 7 | 495 | 56.7 | 7.75 |
| 308153675 | RecName: Full=Spectrin alpha chain, erythrocytic 1; AltName: Full= | 16.19 | 2.11 | 9 | 2 | 3 | 7 | 2419 | 279.8 | 5.05 |
| 109731497 | Myosin, heavy chain 1, skeletal muscle, adult [Homo sapiens] | 14.57 | 3.92 | 123 | 2 | 6 | 7 | 1939 | 223.0 | 5.78 |
| 108935939 | RecName: Full=Transferrin receptor protein 1; Short=TR; Short=Tfl | 13.79 | 4.47 | 9 | 2 | 2 | 6 | 760 | 84.8 | 6.61 |
| 76150625 | putative ribosomal RNA methyltransferase NOP2 isoform 1 [Homo sa | 13.67 | 4.83 | 8 | 2 | 3 | 7 | 808 | 88.9 | 9.23 |
| 40225951 | DIS3L protein [Homo sapiens] | 13.61 | 5.28 | 8 | 2 | 2 | 6 | 644 | 73.1 | 6.23 |
| 578836318 | PREDICTED: trafficking protein particle complex subunit 10-like [Ho | 13.59 | 16.87 | 9 | 2 | 2 | 6 | 249 | 27.5 | 6.05 |
| 193783825 | unnamed protein product [Homo sapiens] | 13.16 | 2.83 | 10 | 2 | 3 | 7 | 883 | 101.0 | 7.08 |
| 578829750 | PREDICTED: dynein heavy chain 9, axonemal isoform X1 [Homo sap | 13.14 | 1.16 | 28 | 2 | 4 | 7 | 3869 | 441.5 | 6.04 |
| 578832590 | PREDICTED: zinc finger protein 407 isoform X3 [Homo sapiens] | 13.01 | 1.23 | 8 | 2 | 2 | 7 | 1628 | 180.5 | 6.93 |
| 578809969 | PREDICTED: uncharacterized protein C5orf42 isoform X12 [Homo sa | 13.00 | 1.22 | 7 | 2 | 3 | 7 | 2792 | 316.0 | 6.95 |
| 1147783 | myosin-IXb [Homo sapiens] | 12.89 | 1.83 | 52 | 2 | 4 | 7 | 2022 | 228.5 | 9.29 |
| 34535977 | unnamed protein product [Homo sapiens] | 12.86 | 4.63 | 4 | 2 | 2 | 5 | 627 | 72.9 | 7.85 |
| 50409856 | aftiphilin isoform c [Homo sapiens] | 12.65 | 3.85 | 11 | 2 | 2 | 6 | 908 | 99.3 | 4.55 |
| 223462007 | CDC42BPA protein [Homo sapiens] | 12.44 | 2.88 | 22 | 2 | 3 | 5 | 1699 | 193.5 | 6.70 |
| 29865 | CENP-E [Homo sapiens] | 12.15 | 1.54 | 8 | 2 | 4 | 6 | 2663 | 311.9 | 5.58 |
| 119592825 | NACHT, leucine rich repeat and PYD containing 13, isoform CRA_a [ | 12.07 | 1.52 | 11 | 2 | 2 | 6 | 985 | 112.7 | 5.44 |
| 119584691 | TBC1 domain family, member 5, isoform CRA_a [Homo sapiens] | 12.00 | 6.04 | 7 | 2 | 3 | 5 | 795 | 89.0 | 6.70 |
| 119600270 | olfactory receptor, family 5, subfamily K, member 4 [Homo sapiens] | 11.87 | 8.72 | 1 | 2 | 2 | 6 | 321 | 36.7 | 8.10 |
| 78101741 | Chain A, 14-3-3 Protein Beta (human) In Complex With Exoenzyme | 11.84 | 19.59 | 31 | 2 | 4 | 5 | 245 | 28.2 | 4.91 |
| 229526 | protein Rei,Bence-Jones | 11.65 | 24.77 | 62 | 2 | 3 | 4 | 214 | 23.5 | 8.50 |
| 343183427 | coiled-coil domain-containing protein 40 isoform 2 [Homo sapiens] | 11.44 | 2.91 | 18 | 2 | 3 | 5 | 1030 | 116.7 | 5.43 |
| 118572619 | RecName: Full=Adenylate cyclase type 5; AltName: Full=ATP pyrop | 11.41 | 3.01 | 21 | 2 | 3 | 5 | 1261 | 138.8 | 7.24 |
| 119601288 | spectrin, beta, erythrocytic (includes spherocytosis, clinical type I), i | 11.16 | 2.15 | 67 | 2 | 5 | 6 | 2328 | 267.6 | 5.36 |
| 194381100 | unnamed protein product [Homo sapiens] | 11.10 | 7.42 | 15 | 2 | 5 | 5 | 701 | 81.5 | 5.81 |
| 119625664 | annexin A5, isoform CRA_c [Homo sapiens] | 10.98 | 20.82 | 11 | 2 | 4 | 4 | 293 | 32.9 | 5.05 |
| 3399676 | R31180_1 [Homo sapiens] | 10.91 | 2.82 | 15 | 2 | 4 | 6 | 1384 | 151.7 | 6.80 |
| 530426392 | PREDICTED: fatty-acid amide hydrolase 2 isoform X6 [Homo sapien | 10.72 | 9.09 | 9 | 2 | 2 | 4 | 341 | 37.1 | 9.10 |

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|---|---|---|---|---|---|---|---|---|---|---|
| 86651683 | myosin regulatory light chain [Homo sapiens] | 10.68 | 25.35 | 12 | 2 | 2 | 2 | 142 | 16.4 | 4.55 |
| 119625401 | LPS-responsive vesicle trafficking, beach and anchor containing [Ho | 10.51 | 0.75 | 15 | 2 | 2 | 5 | 2782 | 310.5 | 5.69 |
| 194390800 | unnamed protein product [Homo sapiens] | 10.30 | 5.26 | 46 | 2 | 4 | 6 | 589 | 69.3 | 7.15 |
| 285803631 | Chain B, The Crystal Structure Of Human Glia Maturation Factor, Ga | 10.24 | 27.94 | 9 | 2 | 2 | 5 | 136 | 16.1 | 5.24 |
| 594140535 | dmX-like protein 1 isoform 3 [Homo sapiens] | 10.22 | 1.54 | 11 | 2 | 4 | 5 | 2854 | 318.4 | 6.34 |
| 119597100 | transformation/transcription domain-associated protein, isoform CR/ | 10.14 | 1.85 | 9 | 2 | 4 | 6 | 3830 | 434.1 | 8.22 |
| 3282239 | rapamycin associated protein FRAP2 [Homo sapiens] | 10.09 | 1.88 | 15 | 2 | 4 | 5 | 2548 | 287.9 | 7.05 |
| 119621343 | Rho-associated, coiled-coil containing protein kinase 2, isoform CRA | 10.09 | 3.06 | 24 | 2 | 3 | 5 | 947 | 110.7 | 6.71 |
| 116242706 | RecName: Full=cAMP-specific 3',5'-cyclic phosphodiesterase 4A; Altl | 9.97 | 2.82 | 85 | 2 | 3 | 5 | 886 | 98.1 | 5.21 |
| 530365988 | PREDICTED: lysosomal-trafficking regulator isoform X2 [Homo sapie | 9.81 | 1.23 | 14 | 2 | 3 | 4 | 3755 | 423.5 | 6.58 |
| 578800920 | PREDICTED: hornerin isoform X1 [Homo sapiens] | 9.79 | 2.80 | 6 | 2 | 2 | 3 | 2146 | 213.3 | 9.86 |
| 530377893 | PREDICTED: la-related protein 1B isoform X8 [Homo sapiens] | 9.76 | 1.84 | 15 | 2 | 2 | 4 | 976 | 110.0 | 7.47 |
| 119624371 | dynein, axonemal, heavy polypeptide 8, isoform CRA_a, partial [Hor | 9.62 | 1.19 | 20 | 2 | 4 | 5 | 4358 | 499.3 | 6.19 |
| 119573774 | hCG1642996, isoform CRA_a [Homo sapiens] | 9.49 | 3.15 | 4 | 2 | 4 | 4 | 1365 | 174.4 | 6.60 |
| 119631904 | nebulin, isoform CRA_a [Homo sapiens] | 9.42 | 0.91 | 42 | 2 | 5 | 6 | 6391 | 740.0 | 9.11 |
| 34783670 | ZNF510 protein, partial [Homo sapiens] | 9.12 | 5.24 | 6 | 2 | 3 | 4 | 477 | 55.2 | 8.85 |
| 73909110 | KIAA1529 protein, partial [Homo sapiens] | 9.02 | 2.00 | 8 | 2 | 2 | 4 | 900 | 104.4 | 5.24 |
| 578837846 | PREDICTED: dystrophin isoform X9 [Homo sapiens] | 8.88 | 1.24 | 27 | 2 | 4 | 5 | 2913 | 337.2 | 5.80 |
| 801893 | leucine-rich PPR-motif containing protein [Homo sapiens] | 8.74 | 4.48 | 8 | 2 | 4 | 4 | 1273 | 145.1 | 5.68 |
| 119576757 | hCG39912, isoform CRA_b [Homo sapiens] | 8.72 | 13.04 | 13 | 2 | 2 | 3 | 184 | 21.4 | 10.20 |
| 51476583 | hypothetical protein [Homo sapiens] | 8.54 | 3.24 | 13 | 2 | 2 | 4 | 1017 | 116.7 | 6.74 |
| 119617755 | PRKC, apoptosis, WT1, regulator, isoform CRA_d [Homo sapiens] | 8.47 | 19.71 | 5 | 2 | 3 | 3 | 340 | 36.5 | 5.41 |
| 16075529 | immunoglobulin kappa chain variable region [Homo sapiens] | 8.46 | 36.90 | 120 | 2 | 3 | 3 | 84 | 9.3 | 7.28 |
| 119578788 | unc-13 homolog B (C. elegans), isoform CRA_b [Homo sapiens] | 8.42 | 1.67 | 7 | 2 | 2 | 4 | 1971 | 220.2 | 5.92 |
| 119598917 | SKI-like, isoform CRA_a [Homo sapiens] | 8.33 | 4.86 | 9 | 2 | 3 | 4 | 638 | 71.7 | 7.09 |
| 15430703 | testis specific serine/threonine kinase 2 [Homo sapiens] | 8.17 | 4.75 | 10 | 2 | 2 | 4 | 358 | 40.9 | 8.84 |
| 194387624 | unnamed protein product [Homo sapiens] | 8.11 | 2.82 | 26 | 2 | 3 | 4 | 816 | 93.8 | 8.75 |
| 34191672 | PLCH1 protein [Homo sapiens] | 8.09 | 4.43 | 7 | 2 | 3 | 4 | 768 | 83.2 | 8.09 |
| 194389344 | unnamed protein product [Homo sapiens] | 8.04 | 4.65 | 15 | 2 | 4 | 4 | 775 | 89.2 | 8.54 |
| 119630615 | Crn, crooked neck-like 1 (Drosophila), isoform CRA_e [Homo sapien | 8.03 | 4.13 | 15 | 2 | 3 | 4 | 848 | 100.3 | 8.00 |
| 194381190 | unnamed protein product [Homo sapiens] | 7.94 | 3.76 | 15 | 2 | 4 | 4 | 984 | 111.9 | 8.15 |
| 914302 | peroxisomal acyl-CoA oxidase, ACOX {C-terminal} [human, liver, Pe | 7.93 | 8.33 | 53 | 2 | 2 | 4 | 192 | 21.7 | 8.10 |
| 221040154 | unnamed protein product [Homo sapiens] | 7.81 | 8.48 | 22 | 2 | 3 | 3 | 389 | 42.3 | 7.61 |
| 194380132 | unnamed protein product [Homo sapiens] | 7.78 | 2.30 | 10 | 2 | 3 | 3 | 1348 | 162.3 | 6.99 |
| 226887852 | Chain C, Human Purine Nucleoside Phosphorylase Double Mutant E2 | 7.74 | 6.75 | 8 | 2 | 2 | 3 | 311 | 34.3 | 7.05 |
| 3789785 | yolk sac permease-like molecule 3 [Homo sapiens] | 7.71 | 9.20 | 13 | 2 | 2 | 4 | 598 | 64.5 | 6.98 |
| 459642365 | dynein heavy chain 11, axonemal [Homo sapiens] | 7.69 | 0.78 | 5 | 2 | 4 | 4 | 4516 | 520.0 | 6.44 |
| 166788546 | DYNC2H1 variant protein [Homo sapiens] | 7.53 | 0.74 | 80 | 2 | 4 | 4 | 4307 | 492.3 | 6.52 |
| 578832112 | PREDICTED: ankyrin repeat domain-containing protein 12 isoform X | 7.42 | 2.60 | 46 | 2 | 4 | 4 | 1769 | 202.9 | 6.90 |

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|---|---|---|---|---|---|---|---|---|---|---|
| 119580109 | myosin XVIIIB, isoform CRA_c [Homo sapiens] | 7.32 | 1.35 | 15 | 2 | 4 | 4 | 2080 | 233.5 | 6.71 |
| 119602845 | hypothetical protein FLJ20425, isoform CRA_a [Homo sapiens] | 7.30 | 7.12 | 4 | 2 | 3 | 3 | 379 | 43.6 | 9.57 |
| 296164 | 156 kDa Protein [Homo sapiens] | 7.28 | 3.24 | 1 | 2 | 3 | 3 | 1356 | 156.0 | 5.63 |
| 296453080 | RecName: Full=WD repeat-containing protein 87; AltName: Full=Te | 7.23 | 1.81 | 78 | 2 | 4 | 4 | 2873 | 333.0 | 7.28 |
| 74758950 | RecName: Full=Nucleolar protein 8; AltName: Full=Nucleolar protei | 7.21 | 2.74 | 84 | 2 | 4 | 4 | 1167 | 131.5 | 7.09 |
| 1710248 | protein disulfide isomerase-related protein 5 [Homo sapiens] | 7.15 | 9.26 | 15 | 2 | 2 | 2 | 421 | 46.2 | 5.08 |
| 119629155 | KIAA0853, isoform CRA_a [Homo sapiens] | 7.07 | 1.98 | 77 | 2 | 4 | 4 | 1564 | 184.7 | 9.47 |
| 232096 | RecName: Full=Peptidyl-prolyl cis-trans isomerase FKBP3; Short=P | 6.98 | 12.05 | 5 | 2 | 2 | 3 | 224 | 25.2 | 9.28 |
| 119597450 | KIAA1505 protein, isoform CRA_d [Homo sapiens] | 6.94 | 4.77 | 12 | 2 | 4 | 4 | 923 | 109.0 | 8.48 |
| 4455035 | pseudouridine synthase 1 [Homo sapiens] | 6.91 | 4.93 | 7 | 2 | 2 | 3 | 365 | 41.0 | 7.97 |
| 356168 | histone H1b | 6.88 | 12.84 | 7 | 2 | 3 | 3 | 218 | 21.7 | 11.03 |
| 578805858 | PREDICTED: CLIP-associating protein 2 isoform X24 [Homo sapiens | 6.88 | 2.73 | 35 | 2 | 2 | 3 | 1062 | 115.7 | 9.32 |
| 14250630 | XAB2 protein, partial [Homo sapiens] | 6.85 | 3.78 | 106 | 2 | 3 | 3 | 635 | 73.2 | 5.38 |
| 3121763 | RecName: Full=Actin-related protein 2/3 complex subunit 1B; AltNa | 6.81 | 6.72 | 1 | 2 | 2 | 3 | 372 | 40.9 | 8.35 |
| 57013082 | RecName: Full=Transcription initiation factor TFIID subunit 1-like; | 6.77 | 3.83 | 2 | 2 | 3 | 3 | 1826 | 207.2 | 5.40 |
| 62089472 | IQGAP1 protein, partial [Homo sapiens] | 6.74 | 2.65 | 7 | 2 | 3 | 4 | 943 | 107.5 | 5.91 |
| 119569007 | synaptotagmin binding, cytoplasmic RNA interacting protein, isofor | 6.72 | 6.83 | 18 | 2 | 3 | 3 | 410 | 46.3 | 8.88 |
| 578807160 | PREDICTED: MDS1 and EVI1 complex locus protein EVI1 isoform X1 | 6.64 | 5.35 | 32 | 2 | 3 | 3 | 841 | 93.9 | 6.62 |
| 119613451 | nuclear transcription factor, X-box binding-like 1, isoform CRA_e [H | 6.58 | 5.68 | 9 | 2 | 3 | 3 | 616 | 69.8 | 8.46 |
| 12006350 | 60S ribosomal protein L15 [Homo sapiens] | 6.53 | 14.22 | 11 | 2 | 2 | 2 | 204 | 24.1 | 11.62 |
| 194385134 | unnamed protein product [Homo sapiens] | 6.44 | 2.70 | 66 | 2 | 3 | 4 | 370 | 41.9 | 9.03 |
| 50512435 | HSPC069 isoform a [Homo sapiens] | 6.44 | 1.70 | 6 | 2 | 3 | 3 | 2061 | 231.0 | 5.68 |
| 158513765 | RecName: Full=Putative protein FAM90A9P | 6.36 | 5.17 | 20 | 2 | 2 | 3 | 464 | 49.7 | 9.86 |
| 119574171 | sequestosome 1, isoform CRA_a [Homo sapiens] | 6.34 | 9.39 | 10 | 2 | 2 | 2 | 394 | 42.5 | 5.44 |
| 578808176 | PREDICTED: SH3 domain and tetratricopeptide repeat-containing pr | 6.30 | 3.64 | 27 | 2 | 3 | 3 | 1043 | 115.0 | 6.58 |
| 181608 | desmoplakin, partial [Homo sapiens] | 6.27 | 2.23 | 13 | 2 | 3 | 3 | 1752 | 201.2 | 7.01 |
| 578824845 | PREDICTED: neurobeachin isoform X6 [Homo sapiens] | 6.25 | 2.07 | 14 | 2 | 2 | 3 | 1934 | 212.6 | 6.10 |
| 221042302 | unnamed protein product [Homo sapiens] | 6.22 | 10.20 | 7 | 2 | 3 | 3 | 392 | 44.9 | 7.87 |
| 519672462 | immunoglobulin A heavy chain variable region, partial [Homo sapien | 6.15 | 15.70 | 4 | 2 | 2 | 2 | 121 | 13.2 | 5.87 |
| 38014595 | RRBP1 protein, partial [Homo sapiens] | 6.10 | 4.27 | 10 | 2 | 2 | 2 | 655 | 73.6 | 4.93 |
| 120587027 | ubiquitin carboxyl-terminal hydrolase 31 [Homo sapiens] | 6.05 | 2.81 | 9 | 2 | 3 | 3 | 1352 | 146.6 | 9.22 |
| 194378958 | unnamed protein product [Homo sapiens] | 6.03 | 1.52 | 11 | 2 | 3 | 3 | 987 | 110.7 | 6.83 |
| 194380952 | unnamed protein product [Homo sapiens] | 6.03 | 12.82 | 8 | 2 | 3 | 3 | 234 | 26.4 | 8.82 |
| 221042358 | unnamed protein product [Homo sapiens] | 6.02 | 11.67 | 6 | 2 | 2 | 2 | 240 | 27.5 | 5.94 |
| 253722065 | Chain B, Human Platelet Profilin Complexed With The L-Pro10 Pepti | 5.99 | 23.19 | 5 | 2 | 2 | 2 | 138 | 14.8 | 8.27 |
| 119613224 | DEAH (Asp-Glu-Ala-His) box polypeptide 15, isoform CRA_e [Homo | 5.97 | 5.21 | 8 | 2 | 2 | 2 | 499 | 56.5 | 8.50 |
| 196049606 | Chain A, Pcbp2 Kh1-Kh2 Domains | 5.94 | 18.13 | 16 | 2 | 2 | 2 | 160 | 17.0 | 8.59 |
| 10435893 | unnamed protein product [Homo sapiens] | 5.93 | 3.43 | 17 | 2 | 3 | 4 | 1137 | 130.2 | 7.25 |
| 16552890 | unnamed protein product [Homo sapiens] | 5.80 | 6.09 | 17 | 2 | 2 | 3 | 345 | 37.1 | 9.03 |

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|---|---|---|---|---|---|---|---|---|---|---|
| 5542538 | Chain D, Mature Metal Chelatase Catalytic Antibody With Hapten | 5.71 | 15.74 | 1 | 2 | 2 | 2 | 216 | 23.1 | 9.20 |
| 257467639 | protein SOGA1 isoform 1 [Homo sapiens] | 5.70 | 1.44 | 14 | 2 | 3 | 3 | 1661 | 183.7 | 6.52 |
| 119589905 | ribosomal protein S15, isoform CRA_a [Homo sapiens] | 5.53 | 27.12 | 4 | 2 | 2 | 2 | 118 | 13.7 | 10.59 |
| 553790 | TFEB protein, partial [Homo sapiens] | 5.52 | 6.89 | 12 | 2 | 2 | 2 | 508 | 55.8 | 9.13 |
| 485601390 | Chain O, Structure Of The Human 40s Ribosomal Proteins | 5.45 | 17.88 | 2 | 2 | 2 | 2 | 151 | 16.3 | 10.05 |
| 1673514 | B-cell receptor associated protein, partial [Homo sapiens] | 5.44 | 12.32 | 4 | 2 | 2 | 2 | 211 | 23.6 | 9.57 |
| 119618140 | hCG2015269, isoform CRA_c [Homo sapiens] | 5.41 | 20.16 | 24 | 2 | 2 | 2 | 129 | 14.5 | 5.91 |
| 193787491 | unnamed protein product [Homo sapiens] | 5.37 | 5.58 | 35 | 2 | 2 | 2 | 538 | 62.7 | 6.30 |
| 51094952 | FLJ42526 protein [Homo sapiens] | 5.35 | 2.97 | 6 | 2 | 2 | 3 | 842 | 94.3 | 8.79 |
| 30583403 | eukaryotic translation initiation factor 4 gamma, 1 [Homo sapiens] | 5.32 | 4.34 | 23 | 2 | 2 | 2 | 645 | 72.2 | 6.34 |
| 1587352 | globin 245 | 5.29 | 1.34 | 15 | 2 | 2 | 2 | 2083 | 244.4 | 5.34 |
| 48146883 | PAI-RBP1 [Homo sapiens] | 5.29 | 6.98 | 16 | 2 | 2 | 2 | 387 | 42.4 | 8.44 |
| 347447331 | Chain F, Crystal Structure Of Human Nucleosome Core Particle Cont | 5.22 | 20.75 | 2 | 2 | 2 | 2 | 106 | 11.6 | 11.36 |
| 332138053 | Chain A, Solution Nmr Structure Of Rrm Domain Of Rna-Binding Pro | 5.20 | 16.16 | 19 | 2 | 2 | 2 | 99 | 10.9 | 6.89 |
| 530407008 | PREDICTED: A-kinase anchor protein 13 isoform X16 [Homo sapiens | 5.19 | 1.36 | 68 | 2 | 3 | 3 | 1473 | 165.7 | 6.89 |
| 119588997 | importin 7, isoform CRA_a [Homo sapiens] | 5.19 | 3.58 | 4 | 2 | 2 | 2 | 837 | 97.4 | 6.30 |
| 6739602 | talin [Homo sapiens] | 5.15 | 1.30 | 8 | 2 | 2 | 2 | 2540 | 269.5 | 6.07 |
| 119628806 | ribosomal protein L21, isoform CRA_f [Homo sapiens] | 5.15 | 29.89 | 16 | 2 | 2 | 2 | 87 | 9.9 | 10.29 |
| 159163435 | Chain A, Solution Structure Of The Third Spectrin Repeat Of Alpha- | 5.13 | 13.95 | 11 | 2 | 2 | 2 | 129 | 14.8 | 5.33 |
| 119588333 | myosin binding protein C, cardiac, isoform CRA_a [Homo sapiens] | 5.12 | 2.91 | 131 | 2 | 3 | 3 | 1273 | 140.5 | 6.65 |
| 119614392 | phosphodiesterase 1C, calmodulin-dependent 70kDa, isoform CRA_ | 5.10 | 11.32 | 12 | 2 | 2 | 2 | 521 | 58.9 | 6.92 |
| 7020305 | unnamed protein product [Homo sapiens] | 5.08 | 4.49 | 21 | 2 | 2 | 2 | 869 | 96.3 | 8.10 |
| 194374441 | unnamed protein product [Homo sapiens] | 4.98 | 6.86 | 18 | 2 | 2 | 2 | 452 | 50.6 | 4.97 |
| 558705212 | Chain B, X-ray Structure Of Receptor Interacting Protein 1 (rip1)kina | 4.95 | 12.01 | 13 | 2 | 2 | 2 | 333 | 38.1 | 5.43 |
| 3387899 | putative nuclear protein [Homo sapiens] | 4.95 | 9.18 | 5 | 2 | 2 | 2 | 294 | 33.6 | 7.72 |
| 119594897 | splicing factor 3b, subunit 2, 145kDa, isoform CRA_a [Homo sapiens | 4.95 | 7.74 | 17 | 2 | 2 | 2 | 349 | 37.7 | 5.15 |
| 7023756 | unnamed protein product [Homo sapiens] | 4.94 | 8.70 | 6 | 2 | 2 | 2 | 483 | 54.0 | 6.21 |
| 40047032 | unnamed protein product [Homo sapiens] | 4.93 | 10.71 | 95 | 2 | 2 | 3 | 112 | 12.3 | 7.43 |
| 15620863 | KIAA1902 protein [Homo sapiens] | 4.92 | 3.06 | 12 | 2 | 2 | 2 | 1112 | 126.2 | 8.18 |
| 119615395 | ubiquitin specific peptidase 48, isoform CRA_c, partial [Homo sapier | 4.89 | 3.61 | 24 | 2 | 2 | 3 | 526 | 60.0 | 5.97 |
| 28839596 | CDC42BPB protein, partial [Homo sapiens] | 4.82 | 2.04 | 10 | 2 | 2 | 2 | 933 | 108.5 | 5.82 |
| 119599184 | muscleblind-like (Drosophila), isoform CRA_d [Homo sapiens] | 4.81 | 16.67 | 29 | 2 | 2 | 4 | 210 | 22.5 | 8.68 |
| 578798776 | PREDICTED: E3 ubiquitin-protein ligase UBR4 isoform X13 [Homo sa | 4.80 | 0.44 | 14 | 2 | 3 | 3 | 5177 | 573.4 | 6.05 |
| 119590976 | ribosomal protein L37a, isoform CRA_b [Homo sapiens] | 4.79 | 27.59 | 5 | 2 | 2 | 2 | 58 | 6.6 | 10.45 |
| 56675654 | unnamed protein product [Homo sapiens] | 4.77 | 31.03 | 11 | 2 | 2 | 2 | 58 | 6.5 | 10.71 |
| 116241311 | RecName: Full=Coatomer subunit beta; AltName: Full=Beta-coat pr | 4.76 | 2.41 | 3 | 2 | 2 | 2 | 953 | 107.1 | 6.05 |
| 63994262 | unknown [Homo sapiens] | 4.65 | 8.15 | 5 | 2 | 2 | 2 | 356 | 40.5 | 8.05 |
| 21614542 | single-minded homolog 1 [Homo sapiens] | 4.64 | 4.96 | 2 | 2 | 2 | 2 | 766 | 85.5 | 7.43 |
| 1149513 | alpha3a subunit of laminin 5 [Homo sapiens] | 4.63 | 2.42 | 44 | 2 | 2 | 2 | 1238 | 137.8 | 6.98 |

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|---|---|---|---|---|---|---|---|---|---|---|
| 85397060 | Tyrosine hydroxylase [Homo sapiens] | 4.63 | 9.66 | 7 | 2 | 2 | 2 | 497 | 55.6 | 6.11 |
| 119625474 | hCG38879 [Homo sapiens] | 4.61 | 1.78 | 2 | 2 | 2 | 2 | 2186 | 243.3 | 6.39 |
| 3088338 | ribosomal protein S10 [Homo sapiens] | 4.58 | 32.05 | 8 | 2 | 2 | 2 | 78 | 9.4 | 9.44 |
| 221046210 | unnamed protein product [Homo sapiens] | 4.56 | 12.04 | 4 | 2 | 2 | 2 | 299 | 32.9 | 7.25 |
| 32425649 | EIF4B protein, partial [Homo sapiens] | 4.56 | 9.17 | 13 | 2 | 2 | 2 | 349 | 39.2 | 7.43 |
| 530365070 | PREDICTED: histone-lysine N-methyltransferase ASH1L isoform X2 [ | 4.52 | 1.24 | 9 | 2 | 2 | 2 | 2663 | 296.8 | 9.47 |
| 119600210 | ABI gene family, member 3 (NESH) binding protein, isoform CRA_a | 4.52 | 12.70 | 51 | 2 | 2 | 2 | 370 | 40.8 | 9.55 |
| 485601388 | Chain U, Structure Of The Human 40s Ribosomal Proteins | 4.51 | 15.13 | 3 | 2 | 2 | 2 | 119 | 13.4 | 9.94 |
| 13603893 | testis protein TEX15 [Homo sapiens] | 4.51 | 1.11 | 5 | 2 | 2 | 2 | 2789 | 315.2 | 6.20 |
| 56554487 | Chain B, Experimentally Phased Structure Of Human The Son Of Se | 4.48 | 2.48 | 16 | 2 | 2 | 2 | 847 | 98.7 | 6.52 |
| 20521660 | KIAA0788 protein [Homo sapiens] | 4.45 | 1.38 | 18 | 2 | 2 | 2 | 2026 | 231.6 | 5.88 |
| 530383144 | PREDICTED: unconventional myosin-VI isoform X2 [Homo sapiens] | 4.44 | 2.41 | 12 | 2 | 2 | 2 | 1285 | 148.5 | 8.53 |
| 119594856 | cofilin 1 (non-muscle), isoform CRA_a [Homo sapiens] | 4.42 | 16.78 | 8 | 2 | 2 | 2 | 149 | 16.8 | 8.35 |
| 1549241 | SWI/SNF complex 170 KDa subunit [Homo sapiens] | 4.40 | 1.98 | 13 | 2 | 2 | 2 | 1213 | 132.6 | 5.52 |
| 119620847 | hypothetical protein FLJ20272, isoform CRA_b, partial [Homo sapie | 4.38 | 4.91 | 9 | 2 | 2 | 2 | 753 | 86.4 | 6.32 |
| 194374597 | unnamed protein product [Homo sapiens] | 4.37 | 4.10 | 14 | 2 | 2 | 2 | 439 | 48.5 | 5.92 |
| 578809883 | PREDICTED: PDZ domain-containing protein 2 isoform X9 [Homo sa | 4.36 | 1.14 | 10 | 2 | 2 | 2 | 2542 | 269.5 | 7.85 |
| 194378486 | unnamed protein product [Homo sapiens] | 4.36 | 8.10 | 1 | 2 | 2 | 2 | 494 | 54.7 | 9.04 |
| 4091776 | Sam68-like phosphotyrosine protein beta, partial [Homo sapiens] | 4.36 | 7.58 | 18 | 2 | 2 | 2 | 264 | 29.3 | 9.58 |
| 62822526 | unknown [Homo sapiens] | 4.32 | 3.94 | 13 | 2 | 2 | 2 | 558 | 63.0 | 5.44 |
| 3970973 | similar to human HsGCN1 U77700 (PID:g2282576); similar to yeast | 4.31 | 1.30 | 10 | 2 | 2 | 2 | 2392 | 262.1 | 6.87 |
| 23396884 | RecName: Full=Tropomodulin-3; AltName: Full=Ubiquitous tropomo | 4.27 | 5.40 | 4 | 2 | 2 | 2 | 352 | 39.6 | 5.19 |
| 119588404 | hypothetical protein FLJ20294, isoform CRA_c [Homo sapiens] | 4.27 | 3.23 | 11 | 2 | 2 | 2 | 1238 | 135.4 | 7.18 |
| 105553088 | T-complex protein 10A homolog [Homo sapiens] | 4.27 | 13.50 | 4 | 2 | 2 | 2 | 326 | 35.6 | 9.50 |
| 1008856 | ribosomal protein L34 [Homo sapiens] | 4.26 | 15.38 | 6 | 2 | 2 | 2 | 117 | 13.3 | 11.37 |
| 237649049 | small nuclear ribonucleoprotein Sm D2 isoform 2 [Homo sapiens] | 4.22 | 23.15 | 2 | 2 | 2 | 2 | 108 | 12.4 | 9.89 |
| 1911429 | A0=heterogeneous nuclear ribonucleoprotein [human, placenta, Pe | 4.20 | 9.18 | 2 | 2 | 2 | 2 | 305 | 30.9 | 9.29 |
| 578821411 | PREDICTED: pecanex-like protein 3 isoform X6 [Homo sapiens] | 4.19 | 1.80 | 8 | 2 | 2 | 2 | 1946 | 212.6 | 6.39 |
| 18032008 | scribble [Homo sapiens] | 4.19 | 1.60 | 10 | 2 | 2 | 2 | 1630 | 174.8 | 5.08 |
| 119603735 | hCG18199, isoform CRA_a [Homo sapiens] | 4.11 | 3.87 | 6 | 2 | 2 | 2 | 568 | 65.9 | 9.07 |
| 194377440 | unnamed protein product [Homo sapiens] | 4.10 | 3.98 | 13 | 2 | 2 | 2 | 603 | 68.5 | 7.94 |
| 62955831 | small proline-rich protein 2B [Homo sapiens] | 4.09 | 43.06 | 11 | 2 | 2 | 2 | 72 | 8.0 | 8.43 |
| 119601362 | zinc finger, FYVE domain containing 26, isoform CRA_e [Homo sapie | 4.08 | 1.73 | 13 | 2 | 2 | 2 | 2481 | 278.2 | 6.29 |
| 31874813 | hypothetical protein [Homo sapiens] | 4.08 | 2.40 | 4 | 2 | 2 | 2 | 1210 | 136.0 | 6.68 |
| 194374105 | unnamed protein product [Homo sapiens] | 4.06 | 9.56 | 9 | 2 | 2 | 2 | 366 | 40.6 | 5.27 |
| 578819622 | PREDICTED: protein FAM178A isoform X2 [Homo sapiens] | 4.04 | 2.44 | 10 | 2 | 2 | 2 | 1147 | 128.9 | 9.01 |
| 194382292 | unnamed protein product [Homo sapiens] | 3.86 | 19.61 | 8 | 2 | 2 | 2 | 153 | 16.8 | 5.29 |
| 16551892 | unnamed protein product [Homo sapiens] | 3.81 | 2.98 | 4 | 2 | 2 | 2 | 637 | 72.3 | 4.93 |
| 194373601 | unnamed protein product [Homo sapiens] | 3.74 | 13.14 | 12 | 2 | 2 | 2 | 137 | 16.0 | 11.09 |

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|---|---|---|---|---|---|---|---|---|---|---|
| 119569889 | nebulin-related anchoring protein, isoform CRA_f [Homo sapiens] | 3.72 | 2.14 | 26 | 2 | 2 | 2 | 1170 | 133.1 | 9.35 |
| 57999483 | hypothetical protein [Homo sapiens] | 3.71 | 2.21 | 26 | 2 | 2 | 2 | 860 | 96.5 | 6.83 |
| 119577109 | hCG38659 [Homo sapiens] | 3.69 | 15.19 | 1 | 2 | 2 | 2 | 158 | 17.9 | 8.38 |
| 119576068 | myosin XVA, isoform CRA_b [Homo sapiens] | 3.67 | 0.77 | 9 | 2 | 2 | 2 | 2069 | 232.4 | 8.48 |
| 34535508 | unnamed protein product [Homo sapiens] | 3.65 | 1.37 | 9 | 2 | 2 | 2 | 1172 | 131.4 | 5.66 |
| 116283359 | MAP4 protein [Homo sapiens] | 3.65 | 7.85 | 6 | 2 | 2 | 2 | 382 | 41.5 | 4.54 |
| 124297731 | CPT1B protein [Homo sapiens] | 3.64 | 3.35 | 10 | 2 | 2 | 2 | 567 | 64.4 | 8.09 |
| 119569058 | dopey family member 1, isoform CRA_a [Homo sapiens] | 3.57 | 0.92 | 20 | 2 | 2 | 2 | 2275 | 255.6 | 6.30 |
| 189053832 | unnamed protein product [Homo sapiens] | 3.56 | 7.25 | 17 | 2 | 2 | 2 | 345 | 39.3 | 4.75 |
| 4323946 | immunoglobulin kappa light chain variable region [Homo sapiens] | 3.55 | 28.16 | 100 | 2 | 2 | 2 | 103 | 11.3 | 9.36 |
| 119580385 | Sfi1 homolog, spindle assembly associated (yeast), isoform CRA_b [ | 3.17 | 2.12 | 20 | 2 | 2 | 2 | 613 | 75.7 | 10.61 |
| 24899202 | KIAA2019 protein [Homo sapiens] | 3.12 | 0.43 | 18 | 2 | 2 | 2 | 2797 | 296.9 | 5.19 |
| 3426320 | OPA-containing protein [Homo sapiens] | 3.10 | 0.69 | 22 | 2 | 2 | 2 | 2023 | 225.7 | 6.77 |
| 30268331 | hypothetical protein [Homo sapiens] | 412.62 | 60.93 | 46 | 1 | 95 | 141 | 1331 | 154.1 | 6.19 |
| 119577203 | mitogen-activated protein kinase kinase kinase kinase 1, isoform CR | 380.22 | 11.45 | 4 | 1 | 1 | 131 | 166 | 18.3 | 6.67 |
| 623409 | keratin 10 [Homo sapiens] | 351.72 | 45.99 | 39 | 1 | 25 | 117 | 561 | 57.2 | 5.07 |
| 239938650 | RecName: Full=Keratin, type II cytoskeletal 2 epidermal; AltName: | 343.24 | 63.69 | 14 | 1 | 36 | 112 | 639 | 65.4 | 8.00 |
| 181402 | epidermal cytokeratin 2 [Homo sapiens] | 338.34 | 64.03 | 14 | 1 | 36 | 110 | 645 | 65.8 | 8.00 |
| 119602146 | hCG2036999 [Homo sapiens] | 286.42 | 18.18 | 1 | 1 | 1 | 112 | 99 | 11.2 | 10.29 |
| 221043440 | unnamed protein product [Homo sapiens] | 258.02 | 23.68 | 20 | 1 | 2 | 107 | 152 | 17.4 | 9.92 |
| 315583372 | Chain A, Solution Nmr Structure Of Pap248-286 In 30% Tfe | 229.75 | 48.72 | 14 | 1 | 1 | 89 | 39 | 4.5 | 10.39 |
| 74760207 | RecName: Full=Protein FAM83F | 181.71 | 3.80 | 1 | 1 | 1 | 75 | 500 | 55.5 | 8.19 |
| 14336717 | unknown [Homo sapiens] | 128.16 | 4.63 | 1 | 1 | 1 | 58 | 410 | 45.8 | 8.44 |
| 1296662 | plectin [Homo sapiens] | 112.74 | 10.57 | 17 | 1 | 42 | 43 | 4684 | 531.4 | 5.95 |
| 119612058 | matrix metallopeptidase 16 (membrane-inserted), isoform CRA_b [H | 110.89 | 2.19 | 3 | 1 | 1 | 49 | 457 | 52.5 | 8.50 |
| 2145062 | TTF-I interacting peptide 21 [Homo sapiens] | 107.21 | 4.92 | 1 | 1 | 1 | 40 | 590 | 62.1 | 6.79 |
| 119599126 | FLJ16641 protein, isoform CRA_c, partial [Homo sapiens] | 99.36 | 4.88 | 7 | 1 | 1 | 43 | 369 | 43.8 | 7.66 |
| 119610692 | F-box protein 39 [Homo sapiens] | 93.20 | 6.79 | 1 | 1 | 2 | 41 | 442 | 52.6 | 8.88 |
| 21754583 | unnamed protein product [Homo sapiens] | 84.05 | 23.00 | 33 | 1 | 13 | 36 | 426 | 47.6 | 5.02 |
| 196049862 | Chain C, Crystal Structure Of Fabox108 | 75.44 | 50.69 | 14 | 1 | 8 | 28 | 217 | 23.8 | 6.67 |
| 390136349 | Chain L, Structure Of Dengue Virus Diii In Complex With Fab 2h12 | 75.44 | 47.42 | 20 | 1 | 8 | 28 | 213 | 23.6 | 7.36 |
| 225733965 | Chain L, Human Thrombopoietin Neutralizing Antibody Tn1 Fab | 74.89 | 48.36 | 14 | 1 | 8 | 28 | 213 | 23.3 | 8.29 |
| 193786870 | unnamed protein product [Homo sapiens] | 70.30 | 14.47 | 41 | 1 | 10 | 30 | 456 | 49.2 | 4.77 |
| 996101 | Chain L, A Conformation Of Cyclosporin A In Aqueous Environment | 69.34 | 50.93 | 11 | 1 | 7 | 26 | 214 | 23.5 | 6.55 |
| 170026940 | myosin heavy chain 11 smooth muscle isoform [Homo sapiens] | 65.59 | 8.48 | 85 | 1 | 19 | 24 | 2029 | 234.1 | 5.80 |
| 21669511 | immunoglobulin lambda light chain VLJ region [Homo sapiens] | 49.34 | 6.69 | 1 | 1 | 1 | 21 | 269 | 28.1 | 8.21 |
| 193788435 | unnamed protein product [Homo sapiens] | 48.54 | 1.33 | 1 | 1 | 1 | 22 | 900 | 101.2 | 7.40 |
| 181400 | cytokeratin 8 [Homo sapiens] | 39.02 | 10.77 | 12 | 1 | 9 | 16 | 483 | 53.7 | 5.36 |
| 346704184 | unnamed protein product [Homo sapiens] | 34.77 | 6.26 | 8 | 1 | 2 | 14 | 543 | 61.2 | 5.83 |

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|---|---|---|---|---|---|---|---|---|---|---|
| 10434858 | unnamed protein product [Homo sapiens] | 34.29 | 19.35 | 6 | 1 | 1 | 13 | 155 | 17.1 | 6.37 |
| 189066668 | unnamed protein product [Homo sapiens] | 34.26 | 5.68 | 3 | 1 | 1 | 15 | 317 | 36.0 | 8.73 |
| 193787108 | unnamed protein product [Homo sapiens] | 31.81 | 21.12 | 1 | 1 | 6 | 12 | 251 | 28.6 | 4.72 |
| 27370697 | SGOL2 protein, partial [Homo sapiens] | 30.12 | 4.91 | 11 | 1 | 1 | 12 | 387 | 43.7 | 8.50 |
| 3309535 | liprin-alpha3 [Homo sapiens] | 29.58 | 8.13 | 7 | 1 | 2 | 13 | 443 | 49.4 | 8.97 |
| 119579661 | hCG1748768, isoform CRA_b, partial [Homo sapiens] | 26.65 | 10.67 | 13 | 1 | 4 | 11 | 450 | 50.6 | 7.52 |
| 194378760 | unnamed protein product [Homo sapiens] | 26.32 | 20.86 | 19 | 1 | 9 | 11 | 532 | 58.3 | 6.49 |
| 1297274 | beta-tubulin [Homo sapiens] | 24.19 | 18.44 | 21 | 1 | 7 | 9 | 450 | 50.5 | 4.97 |
| 10441386 | TPM4-ALK fusion oncoprotein type 2 [Homo sapiens] | 22.76 | 29.96 | 51 | 1 | 8 | 8 | 237 | 27.5 | 4.78 |
| 530415146 | PREDICTED: ubiquitin-60S ribosomal protein L40 isoform X2 [Homo | 21.80 | 10.86 | 2 | 1 | 1 | 11 | 175 | 19.4 | 9.22 |
| 119622550 | hCG2041657, partial [Homo sapiens] | 21.66 | 9.52 | 5 | 1 | 1 | 12 | 63 | 7.5 | 10.39 |
| 116242606 | RecName: Full=Kinesin-like protein KIF1C | 19.76 | 1.63 | 3 | 1 | 1 | 9 | 1103 | 122.9 | 6.90 |
| 296439440 | RecName: Full=Ankyrin repeat domain-containing protein 11; AltNa | 19.42 | 1.01 | 14 | 1 | 2 | 8 | 2663 | 297.7 | 7.11 |
| 578823928 | PREDICTED: stabilin-2 isoform X1 [Homo sapiens] | 19.32 | 0.98 | 5 | 1 | 1 | 7 | 2246 | 243.6 | 6.51 |
| 119629684 | pericentrin (kendrin), isoform CRA_c [Homo sapiens] | 18.71 | 2.17 | 32 | 1 | 5 | 9 | 3139 | 355.7 | 5.47 |
| 84201618 | SR140 protein [Homo sapiens] | 18.53 | 4.68 | 64 | 1 | 4 | 8 | 620 | 72.5 | 7.58 |
| 119606579 | hCG21545, isoform CRA_b [Homo sapiens] | 18.49 | 0.99 | 8 | 1 | 1 | 10 | 707 | 81.5 | 8.29 |
| 193785127 | unnamed protein product [Homo sapiens] | 18.41 | 4.23 | 12 | 1 | 1 | 8 | 449 | 49.7 | 6.86 |
| 119579872 | hCG1805190, partial [Homo sapiens] | 17.72 | 21.74 | 1 | 1 | 1 | 8 | 46 | 5.0 | 12.91 |
| 578827640 | PREDICTED: kinesin-like protein KIF23 isoform X8 [Homo sapiens] | 17.67 | 1.44 | 13 | 1 | 1 | 9 | 486 | 56.1 | 9.04 |
| 358439938 | Chain D, Crystal Structure Of Vimentin (fragment 144-251) From H | 17.59 | 39.50 | 1 | 1 | 6 | 6 | 119 | 14.3 | 5.07 |
| 285803112 | Chain A, Nmr Solution Structure Of The Caskin Sh3 Domain | 17.33 | 7.23 | 17 | 1 | 1 | 11 | 83 | 9.3 | 9.82 |
| 478885 | FR-gamma' [Homo sapiens] | 17.14 | 16.35 | 3 | 1 | 1 | 7 | 104 | 11.8 | 8.21 |
| 16266931 | Musashi1 [Homo sapiens] | 16.84 | 10.06 | 7 | 1 | 1 | 12 | 179 | 20.2 | 8.91 |
| 50949277 | hypothetical protein [Homo sapiens] | 16.73 | 9.01 | 11 | 1 | 2 | 7 | 344 | 39.7 | 6.68 |
| 62087794 | N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 1 variant [ | 16.48 | 3.44 | 10 | 1 | 2 | 8 | 698 | 80.4 | 7.74 |
| 119597114 | hCG40355, isoform CRA_a [Homo sapiens] | 15.76 | 47.53 | 13 | 1 | 7 | 7 | 162 | 18.6 | 9.33 |
| 20147759 | regulator of G protein signalling 9L [Homo sapiens] | 15.70 | 5.79 | 20 | 1 | 4 | 8 | 674 | 76.8 | 9.47 |
| 117558503 | KRT83 protein [Homo sapiens] | 15.57 | 7.16 | 40 | 1 | 5 | 8 | 447 | 49.6 | 5.39 |
| 119627670 | poly(A) binding protein, cytoplasmic 4 (inducible form), isoform CRA | 15.51 | 8.13 | 13 | 1 | 4 | 7 | 615 | 67.9 | 9.45 |
| 122937211 | proteasome-associated protein ECM29 homolog [Homo sapiens] | 15.47 | 1.24 | 8 | 1 | 2 | 7 | 2017 | 223.6 | 8.75 |
| 166007177 | Chain T, Solution Structure Of Human Immunoglobulin M | 15.08 | 7.46 | 167 | 1 | 3 | 5 | 523 | 56.7 | 8.41 |
| 119598029 | tropomyosin 1 (alpha), isoform CRA_e [Homo sapiens] | 15.07 | 19.18 | 51 | 1 | 5 | 5 | 245 | 28.4 | 4.77 |
| 30749678 | Chain A, Tr Receptor Mutations Conferring Hormone Resistance And | 15.00 | 7.98 | 1 | 1 | 1 | 7 | 263 | 29.6 | 5.49 |
| 157830410 | Chain A, Monocyte Chemoattractant Protein-3, Nmr, Minimized Aver | 14.95 | 21.05 | 5 | 1 | 1 | 7 | 76 | 8.9 | 9.69 |
| 119594669 | ribosomal protein S6 kinase, 90kDa, polypeptide 4, isoform CRA_d [ | 14.83 | 3.16 | 1 | 1 | 1 | 9 | 253 | 28.4 | 8.27 |
| 525343614 | replication factor C subunit 2 isoform 5 [Homo sapiens] | 14.69 | 9.13 | 1 | 1 | 1 | 6 | 219 | 24.7 | 6.39 |
| 3913958 | RecName: Full=Kinesin-like protein KIF3B; AltName: Full=HH0048; | 14.59 | 3.75 | 3 | 1 | 2 | 6 | 747 | 85.1 | 7.69 |
| 119593166 | interleukin-1 receptor-associated kinase 1, isoform CRA_a [Homo sa | 14.49 | 3.67 | 8 | 1 | 2 | 7 | 682 | 73.4 | 6.68 |

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|---|---|---|---|---|---|---|---|---|---|---|
| 30526194 | prostaglandin E receptor 1 subtype EP1 [Homo sapiens] | 14.38 | 3.23 | 3 | 1 | 1 | 6 | 402 | 41.8 | 11.72 |
| 309320007 | Chain A, Non-Phosphorylated Tyk2 Kinase With Cmp6 | 14.22 | 7.62 | 41 | 1 | 2 | 7 | 302 | 34.9 | 7.14 |
| 119581142 | keratin, hair, acidic, 6, isoform CRA_a [Homo sapiens] | 13.98 | 4.32 | 19 | 1 | 2 | 7 | 417 | 47.5 | 4.81 |
| 1205999 | YRRM, partial [Homo sapiens] | 13.65 | 18.60 | 1 | 1 | 1 | 8 | 43 | 4.5 | 11.74 |
| 19072647 | TPMsk1 [Homo sapiens] | 13.65 | 25.12 | 39 | 1 | 5 | 5 | 203 | 23.7 | 4.75 |
| 40977476 | unnamed protein product [Homo sapiens] | 13.49 | 11.48 | 1 | 1 | 1 | 8 | 61 | 6.3 | 12.13 |
| 915522 | T-cell receptor alpha V-J junction, partial [Homo sapiens] | 13.45 | 100.00 | 1 | 1 | 1 | 7 | 12 | 1.3 | 5.77 |
| 119625048 | KM-HN-1 protein, isoform CRA_a [Homo sapiens] | 13.32 | 8.48 | 9 | 1 | 6 | 7 | 578 | 68.0 | 7.94 |
| 344179024 | glycogen debranching enzyme [Homo sapiens] | 13.23 | 2.30 | 10 | 1 | 2 | 5 | 1262 | 143.6 | 6.64 |
| 21748769 | unnamed protein product [Homo sapiens] | 13.12 | 4.92 | 5 | 1 | 2 | 6 | 386 | 43.8 | 7.12 |
| 530363648 | PREDICTED: lysine-specific demethylase 4A isoform X3 [Homo sapie | 13.06 | 0.92 | 4 | 1 | 1 | 6 | 973 | 110.3 | 5.78 |
| 194373495 | unnamed protein product [Homo sapiens] | 12.88 | 6.27 | 12 | 1 | 2 | 6 | 399 | 43.2 | 6.13 |
| 13242739 | myelin P2 protein [Homo sapiens] | 12.76 | 12.82 | 7 | 1 | 1 | 6 | 117 | 13.1 | 9.99 |
| 1389559 | glycoprotein 330, partial [Homo sapiens] | 12.65 | 1.20 | 11 | 1 | 3 | 7 | 1751 | 198.3 | 4.91 |
| 588293127 | Chain L, Crystal Structure Of Human Fab Cap256-vrc26.10, A Potent | 12.46 | 14.29 | 107 | 1 | 3 | 4 | 217 | 23.0 | 8.06 |
| 550545747 | Chain C, Cqfd Meditope | 12.32 | 22.90 | 97 | 1 | 3 | 3 | 214 | 23.4 | 6.32 |
| 119631421 | titin, isoform CRA_c [Homo sapiens] | 12.21 | 0.54 | 4 | 1 | 3 | 6 | 5604 | 631.3 | 5.73 |
| 530377992 | PREDICTED: storkhead-box protein 2 isoform X1 [Homo sapiens] | 11.93 | 2.43 | 5 | 1 | 3 | 6 | 863 | 96.1 | 8.35 |
| 108250370 | unnamed protein product [Homo sapiens] | 11.88 | 4.97 | 17 | 1 | 1 | 5 | 161 | 17.4 | 8.95 |
| 119601262 | hCG2036758 [Homo sapiens] | 11.80 | 18.42 | 1 | 1 | 1 | 7 | 38 | 4.4 | 10.13 |
| 194384684 | unnamed protein product [Homo sapiens] | 11.69 | 6.92 | 7 | 1 | 1 | 6 | 130 | 15.1 | 8.88 |
| 23263572 | GPBP-interacting protein 90 [Homo sapiens] | 11.50 | 4.58 | 13 | 1 | 4 | 6 | 764 | 89.7 | 6.68 |
| 578804109 | PREDICTED: coiled-coil domain-containing protein 150 isoform X1 [I | 11.16 | 4.91 | 8 | 1 | 3 | 5 | 1080 | 126.4 | 6.99 |
| 63089918 | unnamed protein product [Homo sapiens] | 11.01 | 6.00 | 2 | 1 | 1 | 7 | 100 | 11.0 | 9.45 |
| 16551483 | unnamed protein product [Homo sapiens] | 10.94 | 3.85 | 1 | 1 | 1 | 5 | 545 | 58.7 | 6.57 |
| 34536060 | unnamed protein product [Homo sapiens] | 10.93 | 4.06 | 13 | 1 | 1 | 4 | 320 | 37.9 | 9.50 |
| 343197763 | Chain L, Structure Of Influenza A Neutralizing Antibody Selected Fro | 10.91 | 21.10 | 201 | 1 | 3 | 3 | 218 | 24.1 | 7.25 |
| 19575597 | unnamed protein product [Homo sapiens] | 10.78 | 13.91 | 1 | 1 | 1 | 4 | 151 | 16.8 | 5.82 |
| 158256198 | unnamed protein product [Homo sapiens] | 10.66 | 8.00 | 1 | 1 | 1 | 5 | 250 | 28.6 | 9.42 |
| 229892328 | IQ domain-containing protein C isoform 1 [Homo sapiens] | 10.60 | 4.95 | 1 | 1 | 2 | 5 | 546 | 61.9 | 8.43 |
| 6683500 | bromodomain adjacent to zinc finger domain 2B [Homo sapiens] | 10.57 | 1.37 | 22 | 1 | 3 | 5 | 1972 | 220.7 | 6.29 |
| 156230634 | ANKRD18A protein [Homo sapiens] | 10.50 | 2.62 | 34 | 1 | 4 | 6 | 992 | 115.6 | 7.99 |
| 40980420 | unnamed protein product [Homo sapiens] | 10.47 | 29.69 | 11 | 1 | 1 | 4 | 64 | 7.5 | 7.42 |
| 347954819 | ankyrin repeat domain-containing protein 18B [Homo sapiens] | 10.44 | 3.56 | 16 | 1 | 4 | 6 | 1010 | 118.1 | 8.15 |
| 2072951 | putative p150 [Homo sapiens] | 10.39 | 3.69 | 42 | 1 | 4 | 5 | 1275 | 149.1 | 9.69 |
| 62702310 | unknown [Homo sapiens] | 10.37 | 11.25 | 9 | 1 | 1 | 4 | 240 | 26.9 | 6.04 |
| 63089240 | unnamed protein product [Homo sapiens] | 10.37 | 7.60 | 10 | 1 | 1 | 4 | 329 | 36.3 | 9.16 |
| 3255987 | HIRIP3 [Homo sapiens] | 10.36 | 2.73 | 4 | 1 | 2 | 6 | 512 | 56.6 | 7.91 |
| 18031805 | estrogen-induced tag 6 [Homo sapiens] | 10.29 | 6.63 | 2 | 1 | 2 | 5 | 407 | 43.6 | 7.74 |

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|---|---|---|---|---|---|---|---|---|---|---|
| 29160170 | unnamed protein product [Homo sapiens] | 10.26 | 3.87 | 8 | 1 | 1 | 5 | 310 | 35.9 | 9.66 |
| 491668222 | Chain A, Crystal Structure Of The Human Cdkl5 Kinase Domain | 10.19 | 6.25 | 6 | 1 | 1 | 4 | 304 | 35.2 | 6.99 |
| 212675179 | anti-HIV-1 V3 immunoglobulin heavy chain [Homo sapiens] | 10.16 | 8.33 | 1 | 1 | 1 | 5 | 132 | 14.2 | 6.28 |
| 119582734 | RAD50 homolog (S. cerevisiae), isoform CRA_c [Homo sapiens] | 10.11 | 2.47 | 6 | 1 | 4 | 6 | 1173 | 138.3 | 6.55 |
| 239782025 | Chain D, Human Sahh-Like Domain Of Human Adenosylhomocystei | 10.08 | 3.22 | 9 | 1 | 1 | 4 | 435 | 48.4 | 7.46 |
| 530382430 | PREDICTED: dystonin isoform X7 [Homo sapiens] | 10.04 | 0.96 | 31 | 1 | 5 | 5 | 7723 | 875.9 | 5.26 |
| 119613590 | guanine nucleotide binding protein-like 3 (nucleolar)-like, isoform C | 10.00 | 2.71 | 25 | 1 | 2 | 5 | 516 | 58.0 | 7.05 |
| 84784317 | alpha-1-antitrypsin MBrescia variant [Homo sapiens] | 9.96 | 20.22 | 1 | 1 | 1 | 3 | 89 | 10.7 | 6.16 |
| 578828430 | PREDICTED: apolipophorins-like [Homo sapiens] | 9.87 | 2.18 | 13 | 1 | 2 | 5 | 688 | 74.4 | 7.01 |
| 6599138 | hypothetical protein [Homo sapiens] | 9.80 | 2.92 | 75 | 1 | 4 | 5 | 1132 | 129.0 | 5.57 |
| 578803637 | PREDICTED: xin actin-binding repeat-containing protein 2 isoform X | 9.70 | 1.42 | 16 | 1 | 5 | 5 | 3308 | 375.0 | 6.39 |
| 40976034 | unnamed protein product [Homo sapiens] | 9.59 | 7.07 | 1 | 1 | 1 | 6 | 99 | 10.5 | 9.33 |
| 46621647 | PHLDB2 protein, partial [Homo sapiens] | 9.51 | 3.31 | 16 | 1 | 3 | 5 | 1118 | 125.8 | 7.50 |
| 553243 | HSrel-1 (AA at 250), partial [Homo sapiens] | 9.48 | 17.14 | 6 | 1 | 1 | 5 | 105 | 12.0 | 6.11 |
| 2072948 | putative p150 [Homo sapiens] | 9.46 | 2.82 | 42 | 1 | 4 | 5 | 1275 | 149.0 | 9.67 |
| 119623235 | hCG2038876, partial [Homo sapiens] | 9.39 | 23.08 | 1 | 1 | 1 | 4 | 91 | 10.3 | 9.19 |
| 194379628 | unnamed protein product [Homo sapiens] | 9.39 | 3.43 | 5 | 1 | 2 | 4 | 1138 | 124.7 | 7.37 |
| 119597764 | hCG2045348, partial [Homo sapiens] | 9.38 | 27.54 | 1 | 1 | 2 | 5 | 69 | 7.9 | 10.70 |
| 119585568 | G protein-coupled receptor 62 [Homo sapiens] | 9.28 | 2.45 | 2 | 1 | 1 | 4 | 368 | 37.6 | 10.98 |
| 10433076 | unnamed protein product [Homo sapiens] | 9.25 | 10.98 | 9 | 1 | 1 | 4 | 164 | 18.7 | 6.09 |
| 119621885 | lipoxygenase homology domains 1, isoform CRA_d [Homo sapiens] | 9.21 | 2.63 | 104 | 1 | 2 | 5 | 457 | 52.5 | 5.47 |
| 38540973 | CCDC73 protein [Homo sapiens] | 9.18 | 14.88 | 2 | 1 | 3 | 4 | 383 | 45.5 | 5.49 |
| 1022786 | putative neuroD homolog protein, partial [Homo sapiens] | 9.13 | 25.00 | 7 | 1 | 1 | 4 | 52 | 5.7 | 8.56 |
| 119624835 | leucine rich repeat containing 1, isoform CRA_b [Homo sapiens] | 9.12 | 7.44 | 4 | 1 | 4 | 5 | 524 | 59.2 | 5.02 |
| 50897294 | POTE ankyrin domain family member A isoform 1 [Homo sapiens] | 9.09 | 3.10 | 2 | 1 | 1 | 4 | 452 | 51.2 | 6.62 |
| 7020699 | unnamed protein product [Homo sapiens] | 9.09 | 2.69 | 9 | 1 | 1 | 4 | 557 | 63.9 | 7.81 |
| 119605696 | hCG1658583, isoform CRA_b, partial [Homo sapiens] | 9.00 | 3.00 | 5 | 1 | 2 | 4 | 966 | 106.8 | 7.97 |
| 374074366 | Chain A, Crystal Structure Of 14-3-3 Epsilon With Mlf1 Peptide | 8.98 | 12.50 | 36 | 1 | 3 | 4 | 232 | 26.6 | 5.02 |
| 609412463 | Chain D, Crystal Structure Of Human Lnkh2b-h2a.z-anp32e | 8.87 | 14.83 | 61 | 1 | 3 | 3 | 209 | 22.5 | 10.23 |
| 578830293 | PREDICTED: DNA polymerase subunit gamma-2, mitochondrial isofo | 8.85 | 6.06 | 10 | 1 | 1 | 4 | 330 | 37.3 | 8.31 |
| 21669971 | immunoglobulin heavy chain VHDJ region [Homo sapiens] | 8.83 | 14.84 | 1 | 1 | 1 | 3 | 128 | 14.0 | 5.96 |
| 259121493 | MHC class I antigen [Homo sapiens] | 8.79 | 11.05 | 1 | 1 | 1 | 4 | 181 | 21.0 | 6.93 |
| 197725197 | Chain B, Crystal Structure Of Il-23 In Complex With Neutralizing Fab | 8.79 | 8.52 | 1 | 1 | 1 | 2 | 223 | 23.8 | 8.65 |
| 534286037 | Chain G, Crystal Structure Of Human Nucleosome Core Particle Lack | 8.79 | 28.23 | 40 | 1 | 3 | 3 | 124 | 13.6 | 10.84 |
| 194380910 | unnamed protein product [Homo sapiens] | 8.71 | 3.58 | 12 | 1 | 2 | 4 | 923 | 103.8 | 5.38 |
| 194383864 | unnamed protein product [Homo sapiens] | 8.69 | 10.06 | 9 | 1 | 2 | 2 | 338 | 37.2 | 6.05 |
| 34534815 | unnamed protein product [Homo sapiens] | 8.58 | 3.99 | 3 | 1 | 1 | 4 | 476 | 54.9 | 8.53 |
| 119630771 | phospholipase C, beta 4, isoform CRA_c [Homo sapiens] | 8.57 | 4.50 | 12 | 1 | 2 | 3 | 1022 | 117.1 | 7.08 |
| 194383918 | unnamed protein product [Homo sapiens] | 8.54 | 1.95 | 8 | 1 | 1 | 3 | 718 | 81.4 | 5.44 |

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|---|---|---|---|---|---|---|---|---|---|---|
| 146345435 | RecName: Full=Histone-lysine N-methyltransferase 2A; Short=Lysin | 8.44 | 0.86 | 93 | 1 | 5 | 5 | 3969 | 431.5 | 9.09 |
| 530371943 | PREDICTED: zinc finger CW-type PWWP domain protein 2 isoform X | 8.43 | 1.86 | 3 | 1 | 1 | 5 | 377 | 43.0 | 5.77 |
| 342350778 | Chain A, Human Annexin V With Incorporated Methionine Analogue | 8.38 | 14.37 | 1 | 1 | 3 | 3 | 320 | 35.7 | 5.05 |
| 239781734 | Chain C, Complement C3b In Complex With Factor H Domains 1-4 | 8.38 | 12.27 | 16 | 1 | 2 | 4 | 277 | 31.2 | 5.41 |
| 33877516 | ZNF598 protein, partial [Homo sapiens] | 8.31 | 3.63 | 7 | 1 | 2 | 4 | 661 | 70.5 | 8.88 |
| 315113204 | Chain H, Crystal Structure Of The Hk20 Fab In Complex With A Gp4 | 8.24 | 12.56 | 95 | 1 | 2 | 3 | 223 | 23.6 | 8.51 |
| 21757363 | unnamed protein product [Homo sapiens] | 8.21 | 2.32 | 1 | 1 | 1 | 4 | 518 | 58.8 | 6.58 |
| 572874814 | protein SDA1 homolog isoform 3 [Homo sapiens] | 8.19 | 4.24 | 82 | 1 | 3 | 4 | 590 | 68.4 | 9.39 |
| 21754724 | unnamed protein product [Homo sapiens] | 8.18 | 6.78 | 1 | 1 | 1 | 4 | 177 | 17.9 | 11.24 |
| 225897 | glycogen phosphorylase | 8.18 | 3.68 | 31 | 1 | 3 | 4 | 842 | 96.9 | 7.03 |
| 119570467 | exocyst complex component 6, isoform CRA_a [Homo sapiens] | 8.16 | 2.96 | 3 | 1 | 2 | 4 | 777 | 90.8 | 6.51 |
| 530371457 | PREDICTED: diacylglycerol kinase delta isoform X4 [Homo sapiens] | 8.14 | 0.88 | 11 | 1 | 1 | 5 | 680 | 75.5 | 7.36 |
| 183496 | glucose phosphate isomerase [Homo sapiens] | 8.05 | 8.45 | 7 | 1 | 1 | 5 | 71 | 8.6 | 8.65 |
| 223597 | actin beta related pseudogene | 8.01 | 2.70 | 1 | 1 | 1 | 4 | 371 | 41.8 | 6.74 |
| 773598 | immunoglobulin gamma heavy chain, partial [Homo sapiens] | 8.00 | 15.87 | 1 | 1 | 1 | 3 | 126 | 13.7 | 7.96 |
| 530378724 | PREDICTED: dynein heavy chain 5, axonemal isoform X1 [Homo sap | 7.98 | 0.50 | 26 | 1 | 3 | 4 | 4609 | 526.8 | 6.01 |
| 82469902 | trio-associated repeat on actin [Homo sapiens] | 7.82 | 1.94 | 46 | 1 | 4 | 4 | 2266 | 250.3 | 8.18 |
| 548923727 | lysM and putative peptidoglycan-binding domain-containing protein | 7.80 | 4.11 | 15 | 1 | 3 | 4 | 292 | 31.6 | 8.70 |
| 218103059 | unnamed protein product [Homo sapiens] | 7.76 | 2.99 | 9 | 1 | 4 | 4 | 2043 | 237.5 | 6.54 |
| 119609527 | hCG1641439 [Homo sapiens] | 7.71 | 10.49 | 2 | 1 | 1 | 3 | 143 | 16.5 | 7.78 |
| 194385806 | unnamed protein product [Homo sapiens] | 7.70 | 2.04 | 10 | 1 | 1 | 3 | 883 | 97.4 | 6.73 |
| 194386352 | unnamed protein product [Homo sapiens] | 7.67 | 4.73 | 6 | 1 | 2 | 3 | 634 | 72.1 | 9.67 |
| 530361876 | PREDICTED: zinc finger protein GLIS1 isoform X1 [Homo sapiens] | 7.67 | 1.38 | 5 | 1 | 2 | 5 | 795 | 84.4 | 7.88 |
| 119613557 | SMC1 structural maintenance of chromosomes 1-like 1 (yeast), isofc | 7.59 | 3.46 | 8 | 1 | 4 | 4 | 1099 | 128.2 | 7.01 |
| 2687853 | RAD50 homologue hsRAD50 [Homo sapiens] | 7.58 | 2.96 | 6 | 1 | 4 | 4 | 1318 | 154.3 | 6.58 |
| 211830808 | KRT18 protein [Homo sapiens] | 7.55 | 4.30 | 29 | 1 | 2 | 4 | 372 | 42.1 | 5.10 |
| 110227866 | SUN domain-containing protein 1 isoform b [Homo sapiens] | 7.55 | 6.27 | 14 | 1 | 2 | 3 | 702 | 77.9 | 7.08 |
| 57997526 | hypothetical protein [Homo sapiens] | 7.55 | 6.40 | 7 | 1 | 2 | 4 | 609 | 66.9 | 5.08 |
| 119568896 | fucosyltransferase 9 (alpha (1,3) fucosyltransferase), isoform CRA_a | 7.45 | 3.06 | 2 | 1 | 1 | 3 | 359 | 42.0 | 7.71 |
| 4758072 | cryptochrome-1 [Homo sapiens] | 7.43 | 3.92 | 6 | 1 | 3 | 4 | 586 | 66.4 | 8.00 |
| 578838717 | PREDICTED: THO complex subunit 2 isoform X11 [Homo sapiens] | 7.35 | 2.21 | 13 | 1 | 3 | 4 | 1582 | 181.2 | 8.28 |
| 119592378 | kallikrein 11, isoform CRA_c [Homo sapiens] | 7.25 | 18.71 | 5 | 1 | 2 | 4 | 139 | 15.0 | 8.06 |
| 164691107 | unnamed protein product [Homo sapiens] | 7.17 | 2.63 | 11 | 1 | 4 | 4 | 1217 | 141.4 | 7.18 |
| 119599949 | hCG21779, isoform CRA_b, partial [Homo sapiens] | 7.16 | 3.67 | 12 | 1 | 1 | 3 | 354 | 41.9 | 9.50 |
| 119628895 | furry homolog (Drosophila), isoform CRA_b [Homo sapiens] | 7.15 | 1.90 | 11 | 1 | 3 | 4 | 1737 | 193.4 | 5.40 |
| 74729423 | RecName: Full=Putative uncharacterized protein encoded by MAPKA | 7.09 | 14.39 | 1 | 1 | 1 | 5 | 139 | 13.2 | 11.41 |
| 194379678 | unnamed protein product [Homo sapiens] | 7.06 | 1.97 | 7 | 1 | 1 | 3 | 559 | 61.1 | 6.80 |
| 119582253 | leucyl-tRNA synthetase, isoform CRA_b [Homo sapiens] | 7.05 | 5.63 | 17 | 1 | 3 | 3 | 710 | 80.2 | 7.14 |
| 116283433 | RDX protein [Homo sapiens] | 7.05 | 8.48 | 18 | 1 | 3 | 3 | 342 | 40.7 | 9.38 |

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|---|---|---|---|---|---|---|---|---|---|---|
| 3859998 | unknown [Homo sapiens] | 7.04 | 4.75 | 13 | 1 | 2 | 4 | 316 | 36.6 | 6.09 |
| 119572141 | spen homolog, transcriptional regulator (Drosophila) [Homo sapiens | 6.99 | 0.96 | 70 | 1 | 4 | 4 | 3664 | 402.0 | 7.58 |
| 119586250 | mirror-image polydactyly 1, isoform CRA_a [Homo sapiens] | 6.88 | 8.25 | 8 | 1 | 4 | 4 | 424 | 49.7 | 6.37 |
| 38541875 | BRDT protein, partial [Homo sapiens] | 6.86 | 5.82 | 77 | 1 | 3 | 4 | 464 | 53.0 | 9.36 |
| 119578686 | zinc finger and BTB domain containing 5 [Homo sapiens] | 6.85 | 2.07 | 2 | 1 | 1 | 3 | 677 | 74.2 | 6.19 |
| 578827509 | PREDICTED: E3 ubiquitin-protein ligase HERC2 isoform X5 [Homo sa | 6.84 | 1.31 | 10 | 1 | 3 | 3 | 4748 | 517.6 | 6.30 |
| 116283819 | HIRA protein [Homo sapiens] | 6.83 | 2.64 | 8 | 1 | 2 | 4 | 643 | 70.5 | 8.10 |
| 189096240 | Chain A, Structure Of Map Kinase P38 In Complex With A 1-O-Tolyl- | 6.81 | 14.37 | 27 | 1 | 3 | 3 | 348 | 39.7 | 6.47 |
| 563379 | mucin [Homo sapiens] | 6.80 | 21.67 | 1 | 1 | 1 | 3 | 60 | 6.4 | 8.21 |
| 578802575 | PREDICTED: peroxidasin homolog isoform X2 [Homo sapiens] | 6.80 | 2.38 | 5 | 1 | 2 | 3 | 1388 | 155.5 | 7.31 |
| 40042522 | unnamed protein product [Homo sapiens] | 6.77 | 21.80 | 8 | 1 | 2 | 3 | 133 | 15.2 | 9.38 |
| 119621322 | hCG1990625, isoform CRA_b [Homo sapiens] | 6.77 | 15.83 | 2 | 1 | 1 | 4 | 120 | 13.7 | 6.10 |
| 119574194 | heterogeneous nuclear ribonucleoprotein H1 (H), isoform CRA_b [H | 6.73 | 8.40 | 13 | 1 | 2 | 2 | 393 | 43.7 | 6.95 |
| 119612193 | vacuolar protein sorting 13B (yeast), isoform CRA_b [Homo sapiens | 6.70 | 0.64 | 6 | 1 | 1 | 3 | 2352 | 262.1 | 6.68 |
| 13540565 | dendritic cell-specific transmembrane protein isoform 1 [Homo sapie | 6.70 | 8.72 | 2 | 1 | 2 | 3 | 470 | 53.4 | 9.29 |
| 119574562 | hCG2024326, isoform CRA_b [Homo sapiens] | 6.61 | 3.30 | 9 | 1 | 2 | 3 | 880 | 94.3 | 8.29 |
| 119610501 | arachidonate 12-lipoxygenase, 12R type [Homo sapiens] | 6.59 | 4.42 | 1 | 1 | 2 | 3 | 701 | 80.3 | 7.64 |
| 6466068 | ATP sulfurylase/APS kinase isoform SK2 [Homo sapiens] | 6.55 | 7.92 | 8 | 1 | 1 | 3 | 265 | 30.1 | 8.24 |
| 62087652 | proteasome 26S ATPase subunit 5 variant [Homo sapiens] | 6.55 | 11.30 | 9 | 1 | 3 | 3 | 345 | 38.7 | 6.47 |
| 221044806 | unnamed protein product [Homo sapiens] | 6.54 | 6.00 | 11 | 1 | 1 | 3 | 200 | 22.7 | 7.21 |
| 119600012 | dopamine receptor D3, isoform CRA_b, partial [Homo sapiens] | 6.54 | 3.22 | 25 | 1 | 2 | 4 | 342 | 37.9 | 8.41 |
| 15559471 | ATAD3A protein [Homo sapiens] | 6.51 | 7.34 | 14 | 1 | 3 | 3 | 586 | 66.2 | 9.17 |
| 194384396 | unnamed protein product [Homo sapiens] | 6.51 | 2.54 | 6 | 1 | 1 | 3 | 433 | 46.3 | 8.97 |
| 117558519 | Phosphoinositide-3-kinase, regulatory subunit 4 [Homo sapiens] | 6.48 | 2.43 | 3 | 1 | 3 | 3 | 1358 | 153.1 | 7.23 |
| 119594722 | CDC42 binding protein kinase gamma (DMPK-like), partial [Homo sa | 6.48 | 3.19 | 5 | 1 | 3 | 3 | 1503 | 166.9 | 6.30 |
| 119603341 | hypothetical protein LOC92922 [Homo sapiens] | 6.46 | 7.27 | 2 | 1 | 3 | 3 | 550 | 62.6 | 5.58 |
| 74762377 | RecName: Full=Leucine-rich repeat and immunoglobulin-like domair | 6.45 | 6.91 | 2 | 1 | 2 | 3 | 593 | 63.7 | 8.18 |
| 119582715 | apical protein 2, isoform CRA_b [Homo sapiens] | 6.44 | 2.48 | 4 | 1 | 1 | 3 | 847 | 90.2 | 6.15 |
| 119568993 | hCG1640214, isoform CRA_b [Homo sapiens] | 6.44 | 1.16 | 126 | 1 | 4 | 4 | 2583 | 288.7 | 7.83 |
| 1091688 | heat shock protein | 6.43 | 21.77 | 5 | 1 | 3 | 3 | 124 | 13.7 | 8.13 |
| 119568026 | radial spokehead-like 2, isoform CRA_a [Homo sapiens] | 6.43 | 7.76 | 26 | 1 | 3 | 3 | 464 | 52.7 | 5.92 |
| 33570004 | immunoglobulin kappa chain variable region [Homo sapiens] | 6.42 | 21.35 | 1 | 1 | 1 | 3 | 89 | 9.7 | 4.78 |
| 119590349 | hCG1791982, isoform CRA_b [Homo sapiens] | 6.39 | 10.53 | 2 | 1 | 1 | 3 | 190 | 21.4 | 8.09 |
| 221044466 | unnamed protein product [Homo sapiens] | 6.38 | 6.60 | 12 | 1 | 2 | 3 | 485 | 55.3 | 7.94 |
| 62420299 | unknown [Homo sapiens] | 6.37 | 5.76 | 4 | 1 | 3 | 3 | 538 | 61.4 | 8.51 |
| 172046176 | RecName: Full=Protein FAM179A | 6.37 | 3.83 | 5 | 1 | 3 | 3 | 1019 | 111.1 | 9.42 |
| 371447579 | immunoglobulin G heavy chain variable region, partial [Homo sapier | 6.36 | 26.89 | 58 | 1 | 2 | 2 | 119 | 13.3 | 5.45 |
| 194373809 | unnamed protein product [Homo sapiens] | 6.33 | 6.75 | 3 | 1 | 3 | 3 | 563 | 64.4 | 9.50 |
| 530404104 | PREDICTED: exonuclease 3'-5' domain-containing protein 2 isoform | 6.30 | 10.93 | 8 | 1 | 2 | 3 | 366 | 42.3 | 8.69 |

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|---|---|---|---|---|---|---|---|---|---|---|
| 608785551 | FANCD2/FANCI-associated nuclease 1 isoform A, partial [Homo sapi | 6.28 | 6.97 | 29 | 1 | 3 | 3 | 531 | 59.1 | 6.65 |
| 119577506 | POU domain, class 2, transcription factor 2, isoform CRA_e [Homo s | 6.27 | 4.75 | 20 | 1 | 2 | 3 | 400 | 43.5 | 8.51 |
| 46852026 | hypothetical rhabdomyosarcoma antigen MU-RMS-40.15 [Homo sap | 6.26 | 1.21 | 1 | 1 | 1 | 4 | 578 | 64.1 | 5.14 |
| 15213542 | NSD1 [Homo sapiens] | 6.25 | 1.66 | 13 | 1 | 3 | 3 | 2596 | 284.8 | 7.55 |
| 119613529 | hCG1642860 [Homo sapiens] | 6.25 | 9.41 | 5 | 1 | 2 | 3 | 255 | 29.1 | 9.76 |
| 28278558 | TUBGCP5 protein [Homo sapiens] | 6.22 | 4.82 | 1 | 1 | 2 | 3 | 477 | 55.2 | 6.73 |
| 119573820 | cingulin, isoform CRA_b [Homo sapiens] | 6.20 | 2.92 | 30 | 1 | 3 | 3 | 1062 | 120.1 | 5.69 |
| 33338102 | MSTP147 protein [Homo sapiens] | 6.17 | 10.28 | 1 | 1 | 1 | 3 | 214 | 22.3 | 12.15 |
| 400977233 | Chain A, Solution Nmr Structure Of Ph Domain Of Tyrosine-Protein | 6.17 | 4.88 | 4 | 1 | 1 | 3 | 164 | 19.5 | 9.36 |
| 194381742 | unnamed protein product [Homo sapiens] | 6.16 | 4.11 | 11 | 1 | 3 | 3 | 584 | 67.0 | 6.32 |
| 119611431 | chromosome 1 open reading frame 49, isoform CRA_c [Homo sapie | 6.07 | 11.94 | 7 | 1 | 2 | 3 | 201 | 23.1 | 9.14 |
| 194373933 | unnamed protein product [Homo sapiens] | 6.06 | 4.06 | 26 | 1 | 2 | 3 | 813 | 92.9 | 7.17 |
| 40038107 | unnamed protein product [Homo sapiens] | 6.04 | 8.84 | 1 | 1 | 1 | 3 | 147 | 16.7 | 9.32 |
| 221040072 | unnamed protein product [Homo sapiens] | 6.03 | 1.80 | 14 | 1 | 2 | 3 | 1057 | 116.0 | 7.46 |
| 26080431 | ATPase family AAA domain-containing protein 5 [Homo sapiens] | 6.01 | 1.68 | 6 | 1 | 3 | 3 | 1844 | 207.4 | 9.19 |
| 578842345 | PREDICTED: serine/threonine-protein phosphatase 1 regulatory sub | 5.97 | 2.31 | 3 | 1 | 2 | 3 | 910 | 96.3 | 9.17 |
| 193786115 | unnamed protein product [Homo sapiens] | 5.95 | 3.03 | 9 | 1 | 2 | 3 | 561 | 65.1 | 7.71 |
| 1098059 | brain factor 2 | 5.94 | 7.04 | 99 | 1 | 3 | 3 | 469 | 50.5 | 9.47 |
| 119624469 | chromosome 6 open reading frame 49, isoform CRA_c [Homo sapie | 5.94 | 6.73 | 1 | 1 | 1 | 2 | 312 | 33.3 | 7.99 |
| 116283877 | IL16 protein [Homo sapiens] | 5.92 | 3.30 | 22 | 1 | 2 | 3 | 576 | 61.0 | 6.86 |
| 187936349 | monoacylglycerol lipase isoform 2 [Homo sapiens] | 5.89 | 13.19 | 14 | 1 | 2 | 3 | 273 | 30.1 | 6.84 |
| 119588262 | hCG2039930, isoform CRA_a [Homo sapiens] | 5.84 | 7.86 | 3 | 1 | 1 | 2 | 369 | 41.2 | 6.90 |
| 14715009 | LIMA1 protein [Homo sapiens] | 5.83 | 9.06 | 16 | 1 | 3 | 3 | 276 | 30.8 | 5.00 |
| 119630693 | chromosome 20 open reading frame 23, isoform CRA_b [Homo sapi | 5.82 | 3.07 | 148 | 1 | 3 | 3 | 1303 | 150.6 | 6.34 |
| 119613723 | hCG1985901 [Homo sapiens] | 5.80 | 3.85 | 74 | 1 | 3 | 3 | 805 | 88.8 | 6.92 |
| 221043242 | unnamed protein product [Homo sapiens] | 5.76 | 5.87 | 10 | 1 | 3 | 3 | 443 | 48.9 | 7.66 |
| 119616102 | microtubule-associated protein 1B, isoform CRA_a [Homo sapiens] | 5.75 | 1.07 | 82 | 1 | 3 | 3 | 2342 | 256.6 | 4.78 |
| 34532387 | unnamed protein product [Homo sapiens] | 5.75 | 3.89 | 11 | 1 | 3 | 3 | 978 | 114.2 | 5.64 |
| 51873980 | HNRPA3 protein, partial [Homo sapiens] | 5.72 | 15.34 | 11 | 1 | 2 | 2 | 189 | 17.9 | 9.39 |
| 578835374 | PREDICTED: ninein-like protein isoform X6 [Homo sapiens] | 5.72 | 2.76 | 49 | 1 | 3 | 3 | 762 | 86.2 | 5.40 |
| 530404931 | PREDICTED: thyroid receptor-interacting protein 11 isoform X2 [Ho | 5.71 | 1.76 | 24 | 1 | 3 | 3 | 1537 | 177.3 | 5.35 |
| 158258613 | unnamed protein product [Homo sapiens] | 5.70 | 5.81 | 24 | 1 | 3 | 3 | 671 | 75.9 | 8.98 |
| 119583824 | hCG1993117, partial [Homo sapiens] | 5.69 | 10.82 | 1 | 1 | 3 | 3 | 231 | 26.6 | 8.03 |
| 194385284 | unnamed protein product [Homo sapiens] | 5.68 | 5.69 | 4 | 1 | 2 | 3 | 439 | 45.4 | 9.35 |
| 296453021 | RecName: Full=Probable helicase senataxin; AltName: Full=Amyotr | 5.68 | 1.16 | 171 | 1 | 4 | 4 | 2677 | 302.7 | 7.17 |
| 54780770 | immunoglobulin mu heavy chain [Homo sapiens] | 5.67 | 30.19 | 1 | 1 | 1 | 2 | 106 | 10.9 | 7.90 |
| 530410168 | PREDICTED: telomerase-binding protein EST1A isoform X2 [Homo s | 5.64 | 2.67 | 12 | 1 | 2 | 3 | 899 | 101.9 | 9.28 |
| 389886545 | protein regulator of cytokinesis 1 isoform 4 [Homo sapiens] | 5.61 | 5.14 | 112 | 1 | 3 | 3 | 525 | 61.4 | 7.65 |
| 149693029 | jakmip1 [Homo sapiens] | 5.60 | 4.04 | 10 | 1 | 3 | 3 | 569 | 67.0 | 7.20 |

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|---|---|---|---|---|---|---|---|---|---|---|
| 1438954 | neuronal pentraxin 1 [Homo sapiens] | 5.60 | 4.88 | 5 | 1 | 2 | 3 | 430 | 47.0 | 6.55 |
| 40044130 | unnamed protein product [Homo sapiens] | 5.56 | 32.20 | 3 | 1 | 1 | 2 | 59 | 6.3 | 8.16 |
| 13276699 | hypothetical protein [Homo sapiens] | 5.55 | 2.95 | 1 | 1 | 2 | 2 | 984 | 112.2 | 6.55 |
| 208436347 | TCF7L2 isoform pFC8A_TCF7L2_D5_ex3-11,12,13a,14 [Homo sapie | 5.55 | 6.12 | 4 | 1 | 1 | 2 | 490 | 53.8 | 9.42 |
| 118142839 | TTLL5 protein [Homo sapiens] | 5.54 | 3.24 | 10 | 1 | 2 | 3 | 709 | 80.0 | 9.16 |
| 119621549 | retinoblastoma binding protein 8, isoform CRA_b [Homo sapiens] | 5.49 | 2.08 | 5 | 1 | 1 | 2 | 867 | 98.4 | 6.64 |
| 194386848 | unnamed protein product [Homo sapiens] | 5.48 | 4.07 | 9 | 1 | 1 | 2 | 565 | 63.0 | 6.77 |
| 10334526 | WTAP protein [Homo sapiens] | 5.48 | 5.67 | 7 | 1 | 2 | 2 | 388 | 43.4 | 5.19 |
| 8569618 | Chain B, Crystal Structure Of The Moesin Ferm DomainTAIL DOMAI | 5.47 | 6.46 | 17 | 1 | 2 | 2 | 294 | 34.4 | 8.87 |
| 119591210 | phenylalanine-tRNA synthetase-like, beta subunit, isoform CRA_c [H | 5.47 | 3.06 | 14 | 1 | 2 | 3 | 490 | 54.8 | 7.50 |
| 119619736 | hCG2005374 [Homo sapiens] | 5.46 | 48.48 | 1 | 1 | 1 | 2 | 66 | 7.1 | 8.25 |
| 530405878 | PREDICTED: protein unc-13 homolog C isoform X2 [Homo sapiens] | 5.45 | 1.05 | 5 | 1 | 3 | 3 | 2188 | 247.7 | 5.91 |
| 119630259 | chromosome 21 open reading frame 62, isoform CRA_b, partial [Ho | 5.42 | 11.97 | 2 | 1 | 1 | 2 | 234 | 26.3 | 7.78 |
| 485601450 | Chain e, Structure Of The Human 60s Ribosomal Proteins | 5.40 | 15.56 | 5 | 1 | 2 | 3 | 135 | 15.8 | 11.33 |
| 55507560 | unknown [Homo sapiens] | 5.39 | 5.80 | 16 | 1 | 2 | 2 | 362 | 40.2 | 7.88 |
| 7023538 | unnamed protein product [Homo sapiens] | 5.37 | 5.85 | 6 | 1 | 1 | 3 | 171 | 19.6 | 5.68 |
| 327478596 | RecName: Full=Uncharacterized protein C6orf132 | 5.37 | 2.27 | 2 | 1 | 2 | 3 | 1188 | 124.0 | 9.45 |
| 266635280 | truncated PRUNE2 [Homo sapiens] | 5.36 | 0.99 | 25 | 1 | 3 | 3 | 2733 | 299.7 | 4.39 |
| 58331185 | T-complex protein 1 subunit eta isoform b [Homo sapiens] | 5.36 | 7.37 | 6 | 1 | 2 | 3 | 339 | 37.5 | 6.46 |
| 16552114 | unnamed protein product [Homo sapiens] | 5.36 | 6.08 | 1 | 1 | 2 | 2 | 707 | 81.4 | 6.16 |
| 530373337 | PREDICTED: leucine-rich repeat flightless-interacting protein 2 isofo | 5.32 | 5.16 | 28 | 1 | 3 | 3 | 465 | 53.2 | 5.47 |
| 14423824 | RecName: Full=Olfactory receptor 14J1; AltName: Full=Hs6M1-28; | 5.31 | 5.92 | 1 | 1 | 1 | 2 | 321 | 35.9 | 8.59 |
| 530380590 | PREDICTED: prefoldin subunit 1 isoform X1 [Homo sapiens] | 5.30 | 8.70 | 1 | 1 | 1 | 3 | 115 | 13.2 | 6.32 |
| 1195528 | 26S protease subunit S8=SUG1 homolog [human, erythrocytes, Pep | 5.28 | 5.43 | 8 | 1 | 2 | 3 | 405 | 45.2 | 9.01 |
| 530432132 | PREDICTED: B-cell CLL/lymphoma 9 protein isoform X3 [Homo sapi | 5.28 | 2.44 | 5 | 1 | 1 | 3 | 1352 | 141.9 | 8.72 |
| 154091032 | ankyrin repeat domain-containing protein 22 [Homo sapiens] | 5.27 | 7.85 | 2 | 1 | 1 | 2 | 191 | 21.8 | 8.84 |
| 5174449 | histone H1x [Homo sapiens] | 5.27 | 7.04 | 1 | 1 | 1 | 2 | 213 | 22.5 | 10.76 |
| 63089484 | unnamed protein product [Homo sapiens] | 5.26 | 45.83 | 10 | 1 | 1 | 2 | 72 | 7.2 | 7.18 |
| 404248892 | immunoglobulin gamma heavy chain variable region, partial [Homo | 5.25 | 9.82 | 1 | 1 | 1 | 2 | 112 | 12.2 | 8.81 |
| 40041152 | unnamed protein product [Homo sapiens] | 5.25 | 10.38 | 10 | 1 | 1 | 2 | 106 | 12.1 | 6.52 |
| 197927452 | dynein heavy chain 1, axonemal [Homo sapiens] | 5.24 | 0.66 | 24 | 1 | 3 | 3 | 4265 | 487.2 | 5.83 |
| 194377758 | unnamed protein product [Homo sapiens] | 5.24 | 1.29 | 7 | 1 | 1 | 3 | 465 | 51.7 | 7.21 |
| 33150550 | HUMEEP [Homo sapiens] | 5.24 | 6.62 | 2 | 1 | 1 | 2 | 453 | 50.5 | 6.25 |
| 116283983 | SMC5 protein [Homo sapiens] | 5.22 | 3.61 | 9 | 1 | 2 | 2 | 941 | 109.9 | 8.63 |
| 371570899 | immunoglobulin heavy variable 5-51*01, partial [Homo sapiens] | 5.22 | 39.62 | 12 | 1 | 2 | 2 | 106 | 12.1 | 9.36 |
| 10437384 | unnamed protein product [Homo sapiens] | 5.22 | 3.59 | 17 | 1 | 2 | 3 | 696 | 81.6 | 5.33 |
| 119602645 | nicotinate phosphoribosyltransferase domain containing 1, isoform | 5.21 | 2.74 | 1 | 1 | 1 | 2 | 584 | 62.1 | 6.73 |
| 119612624 | DENN/MADD domain containing 3, isoform CRA_c [Homo sapiens] | 5.21 | 3.97 | 12 | 1 | 1 | 2 | 554 | 63.5 | 8.51 |
| 40976100 | unnamed protein product [Homo sapiens] | 5.20 | 22.22 | 1 | 1 | 1 | 3 | 54 | 6.2 | 9.19 |

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|---|---|---|---|---|---|---|---|---|---|---|
| 158430383 | Chain A, Structure Of C8a-Macpf Reveals Mechanism Of Membrane | 5.19 | 2.99 | 10 | 1 | 1 | 3 | 334 | 37.8 | 6.13 |
| 119581999 | ADAM metallopeptidase domain 19 (meltrin beta), isoform CRA_a [H | 5.18 | 2.61 | 9 | 1 | 3 | 3 | 918 | 100.9 | 8.21 |
| 323433092 | immunoglobulin variable region [Homo sapiens] | 5.18 | 12.32 | 1 | 1 | 1 | 2 | 138 | 14.7 | 8.60 |
| 378405232 | RecName: Full=StAR-related lipid transfer protein 9; AltName: Full= | 5.17 | 0.79 | 2 | 1 | 3 | 3 | 4700 | 516.0 | 6.32 |
| 300637759 | apolipoprotein E, partial [Homo sapiens] | 5.15 | 23.08 | 16 | 1 | 2 | 2 | 91 | 10.3 | 9.70 |
| 21755922 | unnamed protein product [Homo sapiens] | 5.15 | 2.60 | 6 | 1 | 2 | 3 | 539 | 60.2 | 6.49 |
| 119622222 | ring finger protein 149, isoform CRA_a [Homo sapiens] | 5.14 | 8.50 | 10 | 1 | 2 | 2 | 400 | 43.2 | 6.54 |
| 116283844 | IRGC protein [Homo sapiens] | 5.13 | 11.93 | 3 | 1 | 2 | 2 | 285 | 31.1 | 6.09 |
| 1096609 | Na channel:SUBUNIT=gamma | 5.12 | 5.23 | 14 | 1 | 2 | 2 | 1033 | 113.9 | 5.88 |
| 119582430 | WD repeat domain 55, isoform CRA_c [Homo sapiens] | 5.10 | 12.36 | 3 | 1 | 1 | 2 | 259 | 28.7 | 4.88 |
| 119597878 | hCG2044149 [Homo sapiens] | 5.10 | 12.16 | 1 | 1 | 1 | 3 | 74 | 8.9 | 9.41 |
| 10438712 | unnamed protein product [Homo sapiens] | 5.09 | 3.19 | 13 | 1 | 1 | 4 | 565 | 64.6 | 9.67 |
| 311484712 | unnamed protein product [Homo sapiens] | 5.07 | 15.93 | 1 | 1 | 1 | 2 | 113 | 12.2 | 7.96 |
| 194387658 | unnamed protein product [Homo sapiens] | 5.06 | 1.75 | 4 | 1 | 1 | 2 | 571 | 63.1 | 9.07 |
| 194388774 | unnamed protein product [Homo sapiens] | 5.06 | 2.60 | 35 | 1 | 2 | 3 | 423 | 46.8 | 8.31 |
| 194379610 | unnamed protein product [Homo sapiens] | 5.06 | 4.00 | 13 | 1 | 2 | 2 | 874 | 97.5 | 5.31 |
| 119569978 | chromosome 10 open reading frame 80, isoform CRA_a [Homo sapi | 5.04 | 6.17 | 4 | 1 | 2 | 2 | 470 | 55.4 | 6.58 |
| 530401185 | PREDICTED: citron Rho-interacting kinase isoform X3 [Homo sapien | 5.03 | 1.04 | 8 | 1 | 2 | 2 | 1545 | 177.1 | 6.58 |
| 63994935 | unknown [Homo sapiens] | 5.01 | 3.65 | 71 | 1 | 2 | 3 | 329 | 36.3 | 6.60 |
| 145585268 | unnamed protein product [Homo sapiens] | 4.96 | 3.30 | 1 | 1 | 1 | 3 | 212 | 24.3 | 5.81 |
| 6730102 | Chain A, Solution Structure Of Human Thioltransferase Complex Wit | 4.96 | 13.33 | 3 | 1 | 2 | 3 | 105 | 11.6 | 8.79 |
| 7243231 | KIAA1425 protein [Homo sapiens] | 4.96 | 11.11 | 9 | 1 | 2 | 2 | 495 | 55.8 | 9.50 |
| 4512275 | immunoglobulin heavy chain variable region [Homo sapiens] | 4.95 | 35.04 | 33 | 1 | 2 | 2 | 117 | 12.8 | 7.85 |
| 82802781 | rcADH5 [Homo sapiens] | 4.94 | 4.62 | 1 | 1 | 1 | 2 | 368 | 39.0 | 7.99 |
| 119595837 | hCG2018376 [Homo sapiens] | 4.94 | 12.39 | 1 | 1 | 2 | 3 | 113 | 12.8 | 9.31 |
| 122892406 | immunoglobulin heavy chain variable region [Homo sapiens] | 4.91 | 32.56 | 3 | 1 | 2 | 2 | 129 | 14.5 | 9.29 |
| 508123612 | Chain B, Crystal Structure Of Jmjc Domain Of Human Histone Deme | 4.90 | 4.81 | 186 | 1 | 2 | 2 | 478 | 54.9 | 7.81 |
| 261399877 | T-complex protein 1 subunit eta isoform d [Homo sapiens] | 4.89 | 3.81 | 9 | 1 | 2 | 2 | 499 | 54.8 | 7.68 |
| 119589501 | KH-type splicing regulatory protein (FUSE binding protein 2), isofor | 4.89 | 4.35 | 1 | 1 | 1 | 2 | 345 | 34.4 | 8.90 |
| 530381140 | PREDICTED: arginine--tRNA ligase, cytoplasmic isoform X2 [Homo s | 4.87 | 5.73 | 5 | 1 | 2 | 2 | 454 | 52.3 | 6.64 |
| 15029567 | PR/SET domain-containing protein 07 [Homo sapiens] | 4.86 | 5.60 | 1 | 1 | 1 | 2 | 393 | 43.0 | 9.80 |
| 26985936 | protein tyrosine phosphatase short form [Homo sapiens] | 4.86 | 20.69 | 5 | 1 | 1 | 2 | 87 | 10.5 | 10.33 |
| 4163853 | inducible nitric oxide synthase [Homo sapiens] | 4.86 | 1.44 | 8 | 1 | 1 | 2 | 1114 | 126.7 | 7.96 |
| 194380354 | unnamed protein product [Homo sapiens] | 4.85 | 2.46 | 15 | 1 | 2 | 2 | 935 | 109.5 | 5.31 |
| 194374763 | unnamed protein product [Homo sapiens] | 4.84 | 3.75 | 6 | 1 | 2 | 3 | 347 | 39.5 | 8.72 |
| 311484708 | unnamed protein product [Homo sapiens] | 4.84 | 30.09 | 1 | 1 | 2 | 2 | 113 | 12.6 | 5.38 |
| 1881852 | Sry-related HMG box gene [Homo sapiens] | 4.81 | 2.31 | 15 | 1 | 1 | 3 | 347 | 38.8 | 7.02 |
| 164691047 | unnamed protein product [Homo sapiens] | 4.81 | 2.29 | 5 | 1 | 2 | 2 | 1353 | 156.7 | 7.09 |
| 119628728 | spastic ataxia of Charlevoix-Saguenay (sacsin), partial [Homo sapie | 4.80 | 2.67 | 1 | 1 | 2 | 2 | 1313 | 146.2 | 8.13 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 194385986 | unnamed protein product [Homo sapiens] | 4.80 | 6.09 | 7 | 1 | 2 | 2 | 476 | 54.4 | 8.87 |
| 54400344 | TPA_exp: tight junction protein occludin TM4 minus [Homo sapiens] | 4.79 | 8.12 | 8 | 1 | 2 | 2 | 468 | 52.7 | 6.11 |
| 119628727 | hCG1774880 [Homo sapiens] | 4.78 | 0.31 | 71 | 1 | 2 | 3 | 3829 | 436.7 | 7.18 |
| 194390454 | unnamed protein product [Homo sapiens] | 4.78 | 2.17 | 35 | 1 | 2 | 3 | 554 | 61.4 | 5.99 |
| 194380728 | unnamed protein product [Homo sapiens] | 4.76 | 5.72 | 6 | 1 | 1 | 2 | 367 | 42.0 | 6.48 |
| 482014 | Ig kappa chain - human | 4.76 | 31.58 | 3 | 1 | 2 | 2 | 114 | 12.5 | 7.39 |
| 119601403 | hCG21972, isoform CRA_a [Homo sapiens] | 4.75 | 4.35 | 2 | 1 | 2 | 2 | 506 | 59.2 | 6.44 |
| 28175590 | PASK protein, partial [Homo sapiens] | 4.73 | 4.30 | 16 | 1 | 2 | 2 | 953 | 103.1 | 4.63 |
| 119595726 | hCG2045320 [Homo sapiens] | 4.73 | 7.79 | 1 | 1 | 1 | 3 | 77 | 9.1 | 9.04 |
| 158261227 | unnamed protein product [Homo sapiens] | 4.72 | 4.35 | 1 | 1 | 1 | 2 | 276 | 31.5 | 8.12 |
| 46253814 | immunoglobulin heavy chain [Homo sapiens] | 4.72 | 4.96 | 1 | 1 | 1 | 3 | 141 | 15.4 | 7.96 |
| 3088336 | ribosomal protein S5 [Homo sapiens] | 4.71 | 27.27 | 5 | 1 | 1 | 1 | 55 | 6.0 | 8.97 |
| 532598 | Ig J-chain, partial [Homo sapiens] | 4.70 | 17.52 | 3 | 1 | 2 | 2 | 137 | 15.6 | 4.73 |
| 134105213 | Chain A, Crystal Structure Of Alix V Domain | 4.70 | 5.46 | 18 | 1 | 2 | 2 | 348 | 38.8 | 5.29 |
| 211827073 | HECTD3 protein [Homo sapiens] | 4.70 | 16.43 | 6 | 1 | 2 | 2 | 213 | 24.3 | 4.87 |
| 158261441 | unnamed protein product [Homo sapiens] | 4.70 | 2.70 | 6 | 1 | 2 | 2 | 963 | 109.9 | 5.57 |
| 221041748 | unnamed protein product [Homo sapiens] | 4.69 | 8.66 | 2 | 1 | 1 | 3 | 127 | 13.8 | 5.24 |
| 119621476 | tumor suppressing subtransferable candidate 1, isoform CRA_a [Hor | 4.69 | 5.68 | 4 | 1 | 2 | 2 | 387 | 43.6 | 5.06 |
| 119627767 | mitochondrial ribosomal protein S15, isoform CRA_d [Homo sapiens | 4.69 | 10.00 | 4 | 1 | 1 | 2 | 100 | 11.8 | 10.78 |
| 19575325 | unnamed protein product [Homo sapiens] | 4.69 | 2.67 | 2 | 1 | 2 | 2 | 1013 | 114.2 | 7.39 |
| 119603084 | hCG1642576, isoform CRA_a [Homo sapiens] | 4.69 | 11.50 | 1 | 1 | 1 | 2 | 113 | 12.4 | 6.67 |
| 193785274 | unnamed protein product [Homo sapiens] | 4.68 | 6.97 | 7 | 1 | 2 | 2 | 330 | 37.7 | 5.40 |
| 156076916 | immunoglobulin heavy chain variable region 6 [Homo sapiens] | 4.68 | 17.82 | 2 | 1 | 1 | 2 | 101 | 11.4 | 8.91 |
| 119616473 | calpastatin, isoform CRA_c [Homo sapiens] | 4.68 | 4.69 | 49 | 1 | 2 | 2 | 683 | 73.0 | 5.64 |
| 221042518 | unnamed protein product [Homo sapiens] | 4.67 | 5.35 | 99 | 1 | 2 | 2 | 635 | 70.1 | 8.15 |
| 56967015 | Chain A, Human Lamin Coil 2b | 4.65 | 23.26 | 5 | 1 | 2 | 2 | 86 | 10.2 | 5.01 |
| 50949298 | hypothetical protein [Homo sapiens] | 4.65 | 4.01 | 11 | 1 | 2 | 2 | 873 | 99.0 | 6.29 |
| 614458217 | FRAS1-related extracellular matrix protein 2 precursor [Homo sapier | 4.64 | 1.45 | 2 | 1 | 2 | 2 | 3169 | 350.9 | 5.03 |
| 14040075 | caspase recruitment domain protein 12 [Homo sapiens] | 4.64 | 3.81 | 7 | 1 | 2 | 2 | 1024 | 116.1 | 6.77 |
| 194384194 | unnamed protein product [Homo sapiens] | 4.64 | 3.07 | 1 | 1 | 1 | 2 | 522 | 60.0 | 7.42 |
| 508123592 | Chain C, Bace2 Fab Complex | 4.63 | 15.38 | 6 | 1 | 2 | 2 | 221 | 23.6 | 8.90 |
| 40980772 | unnamed protein product [Homo sapiens] | 4.63 | 23.08 | 5 | 1 | 2 | 2 | 91 | 10.7 | 10.26 |
| 194374607 | unnamed protein product [Homo sapiens] | 4.63 | 4.35 | 1 | 1 | 1 | 2 | 207 | 24.3 | 4.60 |
| 119574016 | hCG2003971, isoform CRA_a, partial [Homo sapiens] | 4.59 | 10.53 | 1 | 1 | 1 | 2 | 95 | 11.1 | 9.50 |
| 371447767 | immunoglobulin G heavy chain variable region, partial [Homo sapier | 4.59 | 17.21 | 1 | 1 | 1 | 2 | 122 | 13.3 | 8.46 |
| 530375745 | PREDICTED: activated CDC42 kinase 1 isoform X5 [Homo sapiens] | 4.59 | 1.83 | 3 | 1 | 1 | 2 | 1040 | 114.9 | 7.99 |
| 119570958 | hCG1805634 [Homo sapiens] | 4.59 | 15.63 | 1 | 1 | 2 | 2 | 96 | 11.0 | 4.84 |
| 119610899 | Tax1 (human T-cell leukemia virus type I) binding protein 3, isoform | 4.59 | 38.30 | 1 | 1 | 1 | 2 | 47 | 5.5 | 10.87 |
| 307066 | inosine-5'-monophosphate dehydrogenase (EC 1.1.1.205) [Homo sa | 4.58 | 6.61 | 6 | 1 | 2 | 2 | 514 | 55.9 | 7.08 |

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|---|---|---|---|---|---|---|---|---|---|---|
| 10436376 | unnamed protein product [Homo sapiens] | 4.56 | 1.81 | 6 | 1 | 1 | 2 | 498 | 57.0 | 6.83 |
| 62088980 | cytochrome P450, family 2, subfamily E, polypeptide 1 variant [Hom | 4.56 | 10.12 | 11 | 1 | 2 | 2 | 336 | 38.9 | 6.16 |
| 30722352 | hypothetical protein [Homo sapiens] | 4.55 | 4.51 | 12 | 1 | 2 | 2 | 820 | 90.4 | 7.30 |
| 119575392 | hCG2002943, partial [Homo sapiens] | 4.54 | 8.87 | 1 | 1 | 1 | 2 | 124 | 14.1 | 9.38 |
| 15559717 | AP2A1 protein [Homo sapiens] | 4.54 | 3.46 | 3 | 1 | 2 | 2 | 982 | 107.9 | 7.64 |
| 194375824 | unnamed protein product [Homo sapiens] | 4.50 | 1.43 | 1 | 1 | 1 | 2 | 977 | 110.1 | 6.19 |
| 152012538 | CASP8AP2 protein [Homo sapiens] | 4.49 | 2.22 | 7 | 1 | 2 | 2 | 1981 | 222.4 | 6.57 |
| 530405989 | PREDICTED: 1-phosphatidylinositol 4,5-bisphosphate phosphodieste | 4.47 | 1.50 | 12 | 1 | 2 | 2 | 1070 | 120.6 | 6.61 |
| 194383974 | unnamed protein product [Homo sapiens] | 4.45 | 2.78 | 18 | 1 | 1 | 2 | 396 | 44.2 | 5.06 |
| 21261451 | unnamed protein product [Homo sapiens] | 4.44 | 4.80 | 8 | 1 | 2 | 2 | 396 | 44.2 | 7.90 |
| 31874826 | hypothetical protein [Homo sapiens] | 4.43 | 6.47 | 10 | 1 | 2 | 2 | 618 | 71.0 | 7.53 |
| 119613364 | Nedd4 binding protein 2, isoform CRA_b [Homo sapiens] | 4.43 | 2.03 | 11 | 1 | 2 | 2 | 1722 | 193.4 | 5.17 |
| 119612528 | coiled-coil domain containing 26, isoform CRA_a [Homo sapiens] | 4.43 | 16.51 | 1 | 1 | 1 | 2 | 109 | 13.2 | 9.45 |
| 3421045 | transcription repressor [Homo sapiens] | 4.43 | 3.59 | 42 | 1 | 2 | 2 | 752 | 82.6 | 4.60 |
| 21756834 | unnamed protein product [Homo sapiens] | 4.42 | 10.39 | 7 | 1 | 1 | 2 | 231 | 24.8 | 9.42 |
| 530389399 | PREDICTED: protein LYRIC isoform X3 [Homo sapiens] | 4.41 | 3.94 | 7 | 1 | 1 | 1 | 381 | 41.2 | 9.72 |
| 158431160 | Chain A, Structure Of N-Terminal Actin Depolymerizing Factor Homo | 4.41 | 5.22 | 18 | 1 | 1 | 2 | 134 | 15.2 | 5.88 |
| 74748429 | RecName: Full=IQ motif and SEC7 domain-containing protein 1; Alt | 4.41 | 2.60 | 3 | 1 | 2 | 2 | 963 | 108.2 | 6.93 |
| 10436325 | unnamed protein product [Homo sapiens] | 4.40 | 2.41 | 2 | 1 | 1 | 2 | 332 | 37.5 | 8.57 |
| 57997563 | hypothetical protein [Homo sapiens] | 4.40 | 2.49 | 12 | 1 | 2 | 2 | 923 | 104.7 | 7.25 |
| 221039400 | unnamed protein product [Homo sapiens] | 4.40 | 4.05 | 23 | 1 | 2 | 2 | 716 | 81.1 | 7.24 |
| 156630449 | RecName: Full=Fas-binding factor 1; Short=FBF-1; AltName: Full=F | 4.40 | 1.77 | 7 | 1 | 2 | 2 | 1133 | 125.4 | 7.08 |
| 67107032 | leucine-rich repeat kinase 1 [Homo sapiens] | 4.40 | 1.29 | 2 | 1 | 2 | 2 | 2014 | 225.0 | 6.64 |
| 568786799 | Chain C, Human Mhf1-mhf2 Complex | 4.40 | 15.05 | 2 | 1 | 1 | 2 | 93 | 10.6 | 8.29 |
| 116283612 | DMXL1 protein [Homo sapiens] | 4.40 | 5.80 | 3 | 1 | 2 | 2 | 621 | 70.1 | 9.13 |
| 119580789 | hCG2011046, partial [Homo sapiens] | 4.39 | 13.16 | 1 | 1 | 1 | 2 | 76 | 8.2 | 10.01 |
| 7328160 | hypothetical protein [Homo sapiens] | 4.37 | 4.51 | 9 | 1 | 1 | 2 | 355 | 39.1 | 8.05 |
| 343794315 | anti-HIV-1 immunoglobulin heavy chain variable region, partial [Hor | 4.36 | 15.00 | 1 | 1 | 1 | 2 | 140 | 15.6 | 8.88 |
| 115556 | RecName: Full=Cartilage matrix protein; AltName: Full=Matrilin-1; F | 4.36 | 7.06 | 5 | 1 | 2 | 2 | 496 | 53.7 | 7.69 |
| 194378708 | unnamed protein product [Homo sapiens] | 4.35 | 2.19 | 1 | 1 | 1 | 3 | 594 | 65.9 | 7.30 |
| 119605660 | cytokine-like nuclear factor n-pac, isoform CRA_d [Homo sapiens] | 4.34 | 3.77 | 10 | 1 | 2 | 2 | 478 | 51.8 | 8.97 |
| 119597064 | zinc finger protein 95 homolog (mouse), isoform CRA_b [Homo sapi | 4.34 | 2.09 | 9 | 1 | 1 | 2 | 575 | 66.3 | 8.84 |
| 119607610 | hCG1993380, isoform CRA_c [Homo sapiens] | 4.34 | 2.52 | 8 | 1 | 2 | 2 | 1152 | 129.0 | 5.99 |
| 578808733 | PREDICTED: serine/threonine-protein kinase PLK4 isoform X2 [Hom | 4.33 | 2.71 | 14 | 1 | 2 | 2 | 923 | 103.9 | 8.60 |
| 211830824 | METTL4 protein [Homo sapiens] | 4.33 | 6.80 | 8 | 1 | 2 | 2 | 353 | 40.4 | 7.77 |
| 148342506 | ITGAV protein [Homo sapiens] | 4.33 | 3.53 | 15 | 1 | 2 | 2 | 1048 | 116.0 | 5.74 |
| 21928237 | seven transmembrane helix receptor [Homo sapiens] | 4.33 | 12.85 | 55 | 1 | 2 | 2 | 249 | 28.3 | 8.37 |
| 21439340 | unnamed protein product [Homo sapiens] | 4.32 | 0.82 | 5 | 1 | 2 | 2 | 4263 | 469.6 | 5.15 |
| 578835955 | PREDICTED: glucocorticoid modulatory element-binding protein 2 is | 4.32 | 1.77 | 5 | 1 | 1 | 2 | 452 | 48.5 | 6.47 |

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|---|---|---|---|---|---|---|---|---|---|---|
| 38014011 | EHMT1 protein, partial [Homo sapiens] | 4.31 | 2.09 | 20 | 1 | 1 | 2 | 716 | 78.9 | 5.77 |
| 119583281 | hCG1813839 [Homo sapiens] | 4.30 | 14.14 | 1 | 1 | 1 | 2 | 99 | 11.8 | 10.01 |
| 460417544 | Chain B, Crystal Strucure Of The Dh-ph-ph Domain Of Farp1 | 4.29 | 6.59 | 5 | 1 | 2 | 2 | 501 | 57.8 | 7.37 |
| 119619478 | family with sequence similarity 47, member B [Homo sapiens] | 4.29 | 4.81 | 3 | 1 | 2 | 2 | 645 | 73.9 | 8.73 |
| 34536022 | unnamed protein product [Homo sapiens] | 4.28 | 5.51 | 14 | 1 | 2 | 2 | 526 | 58.0 | 8.47 |
| 219841912 | TACC2 protein [Homo sapiens] | 4.28 | 1.34 | 24 | 1 | 2 | 2 | 2826 | 296.6 | 4.79 |
| 119591837 | protein inhibitor of activated STAT, 3, isoform CRA_c [Homo sapiens | 4.28 | 5.73 | 3 | 1 | 2 | 2 | 628 | 68.0 | 7.69 |
| 106575 | Ig kappa chain V region (Vx O11 and Vx O1) - human (fragment) | 4.28 | 25.62 | 3 | 1 | 2 | 2 | 121 | 13.3 | 4.61 |
| 119610447 | chromosome 17 open reading frame 38, isoform CRA_d [Homo sapi | 4.27 | 6.65 | 7 | 1 | 2 | 2 | 376 | 42.0 | 9.20 |
| 21998598 | immunoglobulin heavy chain variable region [Homo sapiens] | 4.26 | 15.45 | 2 | 1 | 1 | 2 | 123 | 13.3 | 4.67 |
| 119570224 | CWF19-like 1, cell cycle control (S. pombe), isoform CRA_b [Homo s | 4.26 | 3.99 | 3 | 1 | 1 | 2 | 401 | 45.5 | 7.66 |
| 194375538 | unnamed protein product [Homo sapiens] | 4.25 | 7.29 | 36 | 1 | 2 | 2 | 288 | 30.0 | 9.67 |
| 40981668 | unnamed protein product [Homo sapiens] | 4.25 | 30.77 | 1 | 1 | 1 | 2 | 52 | 5.9 | 10.30 |
| 167745132 | Chain A, Human Poly(Adp-Ribose) Polymerase 3, Catalytic Fragment | 4.24 | 7.84 | 1 | 1 | 2 | 2 | 357 | 39.7 | 6.27 |
| 119571294 | aldehyde dehydrogenase 3 family, memberA1, isoform CRA_b [Hom | 4.24 | 6.18 | 20 | 1 | 2 | 2 | 453 | 50.3 | 6.54 |
| 119571005 | hCG1994859 [Homo sapiens] | 4.24 | 14.18 | 1 | 1 | 1 | 2 | 141 | 14.9 | 6.70 |
| 530386299 | PREDICTED: PERQ amino acid-rich with GYF domain-containing pro | 4.24 | 1.64 | 29 | 1 | 2 | 2 | 1034 | 114.4 | 5.39 |
| 21748512 | FLJ00310 protein [Homo sapiens] | 4.23 | 9.97 | 1 | 1 | 2 | 2 | 291 | 34.5 | 5.53 |
| 298286915 | RecName: Full=Maestro heat-like repeat-containing protein family m | 4.23 | 2.05 | 98 | 1 | 2 | 2 | 1706 | 193.1 | 6.68 |
| 126632187 | RAPGEF6 protein [Homo sapiens] | 4.23 | 2.26 | 19 | 1 | 2 | 2 | 1504 | 168.8 | 6.42 |
| 119609196 | chromosome condensation-related SMC-associated protein 1, isofor | 4.23 | 2.03 | 9 | 1 | 2 | 2 | 937 | 104.4 | 5.87 |
| 51094807 | LOC401407 [Homo sapiens] | 4.22 | 10.94 | 1 | 1 | 2 | 2 | 265 | 30.3 | 9.26 |
| 119609629 | cerebellar degeneration-related protein 2-like, isoform CRA_a [Hom | 4.21 | 6.52 | 6 | 1 | 2 | 2 | 414 | 47.1 | 6.80 |
| 390979647 | beta/gamma crystallin domain-containing protein 3 [Homo sapiens] | 4.21 | 0.94 | 6 | 1 | 2 | 2 | 2970 | 330.4 | 5.20 |
| 159147879 | Par6 beta short form [Homo sapiens] | 4.20 | 17.39 | 3 | 1 | 1 | 2 | 115 | 13.0 | 9.35 |
| 221042054 | unnamed protein product [Homo sapiens] | 4.20 | 5.57 | 14 | 1 | 1 | 2 | 323 | 36.0 | 7.52 |
| 119573448 | hCG1997332, isoform CRA_a [Homo sapiens] | 4.19 | 6.28 | 2 | 1 | 1 | 2 | 207 | 22.0 | 5.43 |
| 530369556 | PREDICTED: activin receptor type-2A isoform X1 [Homo sapiens] | 4.19 | 9.14 | 4 | 1 | 2 | 2 | 361 | 40.5 | 6.81 |
| 119592618 | ribosomal protein S9, isoform CRA_c [Homo sapiens] | 4.19 | 10.79 | 16 | 1 | 2 | 2 | 139 | 16.6 | 11.06 |
| 133777825 | PB1 protein [Homo sapiens] | 4.18 | 1.24 | 31 | 1 | 2 | 2 | 1615 | 184.5 | 6.79 |
| 119598373 | zinc finger protein 680, isoform CRA_b [Homo sapiens] | 4.18 | 2.88 | 4 | 1 | 1 | 2 | 452 | 52.7 | 9.04 |
| 392583868 | SRA stem-loop-interacting RNA-binding protein, mitochondrial isofor | 4.17 | 15.22 | 5 | 1 | 1 | 2 | 92 | 10.3 | 10.23 |
| 112180685 | C20orf132 protein [Homo sapiens] | 4.17 | 3.56 | 12 | 1 | 2 | 2 | 956 | 108.1 | 8.07 |
| 547234890 | PIN2/TERF1-interacting telomerase inhibitor 1 isoform 2 [Homo sap | 4.17 | 9.20 | 6 | 1 | 1 | 2 | 174 | 19.7 | 8.82 |
| 530386990 | PREDICTED: WD repeat-containing protein 86 isoform X3 [Homo sa | 4.17 | 4.28 | 6 | 1 | 1 | 2 | 327 | 35.6 | 7.68 |
| 18676660 | FLJ00229 protein [Homo sapiens] | 4.16 | 1.91 | 1 | 1 | 1 | 2 | 627 | 71.5 | 8.62 |
| 371446725 | immunoglobulin G heavy chain variable region, partial [Homo sapier | 4.16 | 16.10 | 1 | 1 | 1 | 2 | 118 | 12.4 | 9.41 |
| 119583441 | WD repeat domain 7, isoform CRA_a, partial [Homo sapiens] | 4.15 | 2.36 | 8 | 1 | 2 | 2 | 1398 | 153.8 | 6.79 |
| 312050 | myosin I homologue [Homo sapiens] | 4.15 | 2.96 | 23 | 1 | 2 | 2 | 812 | 96.0 | 9.39 |

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|---|---|---|---|---|---|---|---|---|---|---|
| 133777284 | Membrane metallo-endopeptidase-like 1 [Homo sapiens] | 4.14 | 3.51 | 13 | 1 | 2 | 2 | 770 | 88.4 | 5.87 |
| 119595337 | hCG1802847, isoform CRA_b [Homo sapiens] | 4.14 | 4.39 | 8 | 1 | 2 | 2 | 683 | 75.5 | 8.98 |
| 119594172 | yippee-like 4 (Drosophila), isoform CRA_b [Homo sapiens] | 4.14 | 31.94 | 1 | 1 | 2 | 2 | 72 | 7.7 | 9.19 |
| 119618177 | cytoskeleton-associated protein 4, isoform CRA_b [Homo sapiens] | 4.14 | 5.69 | 8 | 1 | 1 | 1 | 334 | 37.4 | 4.94 |
| 578815344 | PREDICTED: pericentriolar material 1 protein isoform X27 [Homo sa | 4.14 | 1.78 | 27 | 1 | 2 | 2 | 1970 | 222.2 | 4.98 |
| 630869349 | immunoglobulin light chain variable region, partial [Homo sapiens] | 4.13 | 14.56 | 6 | 1 | 1 | 1 | 103 | 11.4 | 5.25 |
| 530375317 | PREDICTED: centrosomal protein of 63 kDa isoform X1 [Homo sapie | 4.13 | 3.37 | 13 | 1 | 2 | 2 | 712 | 82.6 | 6.40 |
| 193787623 | unnamed protein product [Homo sapiens] | 4.13 | 2.87 | 9 | 1 | 1 | 2 | 557 | 64.0 | 7.25 |
| 119581945 | hCG1979388, isoform CRA_a [Homo sapiens] | 4.13 | 20.75 | 3 | 1 | 2 | 2 | 106 | 11.9 | 8.87 |
| 119624345 | TBC1 domain family, member 22B, isoform CRA_b [Homo sapiens] | 4.13 | 5.92 | 82 | 1 | 2 | 2 | 591 | 67.6 | 8.43 |
| 22760006 | unnamed protein product [Homo sapiens] | 4.12 | 3.07 | 6 | 1 | 1 | 2 | 261 | 29.3 | 6.02 |
| 119601461 | pecanex homolog (Drosophila), isoform CRA_d [Homo sapiens] | 4.12 | 2.07 | 95 | 1 | 2 | 2 | 1641 | 181.2 | 7.77 |
| 62088012 | bromodomain containing protein 1 variant [Homo sapiens] | 4.12 | 4.25 | 16 | 1 | 1 | 2 | 471 | 53.8 | 9.95 |
| 10434519 | unnamed protein product [Homo sapiens] | 4.11 | 2.58 | 1 | 1 | 1 | 2 | 543 | 59.9 | 5.49 |
| 10439816 | unnamed protein product [Homo sapiens] | 4.10 | 2.42 | 6 | 1 | 2 | 2 | 991 | 109.6 | 7.68 |
| 18490229 | DMGDH protein, partial [Homo sapiens] | 4.10 | 3.10 | 1 | 1 | 2 | 2 | 613 | 69.2 | 6.60 |
| 119569197 | chromosome 6 open reading frame 57, isoform CRA_a [Homo sapie | 4.08 | 15.74 | 2 | 1 | 1 | 2 | 108 | 12.2 | 9.36 |
| 425906070 | RecName: Full=Coiled-coil domain-containing protein 177; AltName | 4.07 | 2.12 | 2 | 1 | 1 | 2 | 707 | 79.7 | 10.74 |
| 38195903 | fat-like cadherin FATJ protein [Homo sapiens] | 4.07 | 0.68 | 5 | 1 | 1 | 2 | 3222 | 351.0 | 5.08 |
| 5051248 | immunoglobulin gamma heavy chain variable region [Homo sapiens | 4.07 | 12.07 | 1 | 1 | 1 | 2 | 116 | 13.0 | 7.96 |
| 519674680 | immunoglobulin A heavy chain variable region, partial [Homo sapie | 4.07 | 12.80 | 1 | 1 | 1 | 2 | 125 | 13.9 | 8.94 |
| 31874464 | hypothetical protein [Homo sapiens] | 4.07 | 2.18 | 6 | 1 | 2 | 2 | 917 | 105.7 | 9.50 |
| 247424357 | immunoglobulin heavy chain variable region [Homo sapiens] | 4.07 | 6.61 | 1 | 1 | 1 | 2 | 121 | 13.0 | 8.47 |
| 193787818 | unnamed protein product [Homo sapiens] | 4.06 | 5.87 | 6 | 1 | 2 | 2 | 511 | 58.4 | 4.34 |
| 58045557 | 2-5-3p [Homo sapiens] | 4.06 | 3.08 | 9 | 1 | 2 | 2 | 616 | 70.2 | 6.98 |
| 110611233 | collagen alpha-1(XVIII) chain isoform 2 precursor [Homo sapiens] | 4.05 | 2.02 | 18 | 1 | 2 | 2 | 1336 | 135.4 | 6.47 |
| 190410954 | RecName: Full=Transmembrane and coiled-coil domain-containing | 4.05 | 6.84 | 1 | 1 | 2 | 2 | 307 | 35.7 | 5.03 |
| 429544581 | Chain D, Crystal Structure Of The Tetratricopeptide Repeat (Tpr) M | 4.03 | 5.59 | 5 | 1 | 1 | 2 | 161 | 18.2 | 8.92 |
| 2735849 | G protein-coupled receptor Edg-4 [Homo sapiens] | 4.02 | 1.57 | 1 | 1 | 1 | 2 | 382 | 42.6 | 9.13 |
| 52545679 | hypothetical protein [Homo sapiens] | 4.00 | 3.74 | 25 | 1 | 2 | 2 | 508 | 58.0 | 4.98 |
| 50833998 | unnamed protein product [Homo sapiens] | 4.00 | 2.70 | 8 | 1 | 1 | 2 | 445 | 52.7 | 7.53 |
| 119622230 | TBC1 domain family, member 8 (with GRAM domain), isoform CRA_ | 3.99 | 2.20 | 26 | 1 | 2 | 2 | 727 | 83.5 | 5.44 |
| 253722206 | Chain L, Free And Liganded Form Of An Esterolytic Catalytic Antibo | 3.98 | 8.41 | 1 | 1 | 1 | 1 | 214 | 23.4 | 7.27 |
| 119597183 | hCG1741805, isoform CRA_a [Homo sapiens] | 3.96 | 1.37 | 79 | 1 | 2 | 2 | 1314 | 147.2 | 5.50 |
| 578844510 | PREDICTED: putative exonuclease GOR-like protein-like [Homo sapi | 3.96 | 2.12 | 5 | 1 | 1 | 2 | 944 | 103.8 | 9.31 |
| 30268309 | hypothetical protein [Homo sapiens] | 3.94 | 3.28 | 3 | 1 | 2 | 2 | 641 | 74.4 | 9.14 |
| 119578807 | valosin-containing protein, isoform CRA_a [Homo sapiens] | 3.93 | 3.80 | 13 | 1 | 2 | 2 | 632 | 69.8 | 5.58 |
| 119631344 | FLJ44048 protein, isoform CRA_a [Homo sapiens] | 3.90 | 0.20 | 96 | 1 | 2 | 2 | 6049 | 681.9 | 6.54 |
| 119569102 | pleckstrin homology domain interacting protein, isoform CRA_a [Ho | 3.90 | 1.36 | 51 | 1 | 2 | 2 | 1546 | 177.0 | 9.11 |

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|---|---|---|---|---|---|---|---|---|---|---|
| 10436696 | unnamed protein product [Homo sapiens] | 3.90 | 3.60 | 7 | 1 | 2 | 2 | 639 | 71.8 | 8.72 |
| 4501959 | alpha-1B adrenergic receptor [Homo sapiens] | 3.88 | 2.88 | 7 | 1 | 2 | 2 | 520 | 56.8 | 9.41 |
| 578841606 | PREDICTED: E3 ubiquitin-protein ligase TRIM31 isoform X3 [Homo s | 3.88 | 6.90 | 68 | 1 | 2 | 2 | 261 | 30.0 | 6.99 |
| 40042310 | unnamed protein product [Homo sapiens] | 3.87 | 21.93 | 9 | 1 | 2 | 2 | 114 | 12.8 | 11.34 |
| 34811402 | Chain B, Crystal Structure Of Human Cathepsin F | 3.87 | 7.94 | 8 | 1 | 2 | 2 | 214 | 23.6 | 6.19 |
| 255917908 | Chain C, Crystal Structure Of The Cbc-Importin Alpha Complex. | 3.86 | 3.85 | 7 | 1 | 1 | 1 | 467 | 50.7 | 5.17 |
| 24899178 | KIAA2006 protein [Homo sapiens] | 3.86 | 1.83 | 22 | 1 | 2 | 2 | 1367 | 151.0 | 5.15 |
| 126030570 | Chain A, Structural And Functional Insights Into The Human Upf1 H | 3.85 | 3.53 | 8 | 1 | 2 | 2 | 624 | 69.9 | 8.48 |
| 19578161 | unnamed protein product [Homo sapiens] | 3.84 | 2.64 | 8 | 1 | 2 | 2 | 682 | 78.0 | 8.68 |
| 450469 | type 2 inositol 1,4,5-trisphosphate receptor [Homo sapiens] | 3.83 | 0.85 | 13 | 1 | 2 | 2 | 2701 | 307.9 | 6.46 |
| 30269262 | pol protein [Homo sapiens] | 3.83 | 2.11 | 1 | 1 | 2 | 2 | 1183 | 131.4 | 9.04 |
| 51094479 | similar to 60S ribosomal protein L35 [Homo sapiens] | 3.82 | 15.15 | 16 | 1 | 2 | 2 | 99 | 11.5 | 10.96 |
| 143928063 | RecName: Full=Serine/arginine repetitive matrix protein 2; AltName | 3.81 | 1.13 | 80 | 1 | 2 | 2 | 2752 | 299.4 | 12.06 |
| 119620329 | RAB1A, member RAS oncogene family, isoform CRA_f [Homo sapien | 3.81 | 9.73 | 7 | 1 | 2 | 2 | 257 | 28.1 | 8.57 |
| 119596076 | staufen, RNA binding protein, homolog 1 (Drosophila), isoform CRA_ | 3.80 | 3.79 | 31 | 1 | 2 | 2 | 317 | 35.4 | 9.89 |
| 257297088 | unnamed protein product [Homo sapiens] | 3.79 | 20.29 | 8 | 1 | 2 | 2 | 138 | 15.1 | 9.70 |
| 530360940 | PREDICTED: OTU domain-containing protein 3 isoform X2 [Homo sa | 3.78 | 3.65 | 7 | 1 | 2 | 2 | 384 | 42.5 | 7.62 |
| 4884358 | hypothetical protein [Homo sapiens] | 3.78 | 4.18 | 18 | 1 | 2 | 2 | 502 | 55.4 | 9.63 |
| 374414629 | Chain D, Crystal Structure Of Human Pnpase | 3.77 | 2.54 | 9 | 1 | 2 | 2 | 630 | 68.7 | 6.58 |
| 74734680 | RecName: Full=Uncharacterized protein C2orf42 | 3.77 | 3.31 | 5 | 1 | 2 | 2 | 574 | 64.0 | 8.92 |
| 755748 | RB protein binding protein [Homo sapiens] | 3.76 | 2.11 | 5 | 1 | 2 | 2 | 948 | 107.1 | 9.95 |
| 193785179 | unnamed protein product [Homo sapiens] | 3.76 | 2.65 | 9 | 1 | 2 | 2 | 491 | 55.0 | 9.06 |
| 119596753 | hCG2019498, isoform CRA_b [Homo sapiens] | 3.76 | 1.31 | 92 | 1 | 2 | 2 | 1068 | 120.9 | 8.95 |
| 119594879 | testis specific, 10 interacting protein, partial [Homo sapiens] | 3.75 | 3.60 | 6 | 1 | 2 | 2 | 556 | 62.3 | 10.05 |
| 119574994 | discs, large homolog 5 (Drosophila), isoform CRA_a [Homo sapiens] | 3.75 | 4.01 | 16 | 1 | 2 | 2 | 674 | 74.9 | 8.22 |
| 194386984 | unnamed protein product [Homo sapiens] | 3.75 | 2.92 | 62 | 1 | 2 | 2 | 753 | 83.2 | 7.20 |
| 429509414 | MHC class I antigen, partial [Homo sapiens] | 3.74 | 3.31 | 2 | 1 | 1 | 2 | 181 | 20.9 | 5.73 |
| 645986066 | Chain D, Crystal Structure Of The Human Cdk12-cyclink Complex | 3.74 | 1.84 | 11 | 1 | 1 | 2 | 326 | 37.7 | 6.93 |
| 119620760 | MORN repeat containing 2, partial [Homo sapiens] | 3.74 | 1.74 | 39 | 1 | 2 | 2 | 976 | 109.5 | 7.47 |
| 193788489 | unnamed protein product [Homo sapiens] | 3.73 | 4.37 | 17 | 1 | 2 | 2 | 504 | 56.6 | 9.19 |
| 164691209 | unnamed protein product [Homo sapiens] | 3.73 | 14.75 | 6 | 1 | 2 | 2 | 122 | 13.5 | 5.21 |
| 1729764 | dynein-related protein [Homo sapiens] | 3.72 | 2.63 | 1 | 1 | 2 | 2 | 798 | 91.0 | 5.69 |
| 1585676 | acyl-CoA/cholesterol acyltransferase | 3.71 | 2.91 | 7 | 1 | 2 | 2 | 550 | 64.8 | 9.07 |
| 10438885 | unnamed protein product [Homo sapiens] | 3.71 | 7.27 | 10 | 1 | 2 | 2 | 289 | 32.0 | 9.66 |
| 38196995 | DUS1L protein, partial [Homo sapiens] | 3.71 | 7.36 | 96 | 1 | 2 | 2 | 299 | 33.8 | 8.91 |
| 10437232 | unnamed protein product [Homo sapiens] | 3.71 | 10.70 | 11 | 1 | 2 | 2 | 215 | 24.5 | 5.14 |
| 119571060 | coiled-coil domain containing 22, isoform CRA_b, partial [Homo sapi | 3.70 | 1.32 | 4 | 1 | 1 | 2 | 606 | 68.6 | 7.08 |
| 469096 | microsomal triglyceride transfer protein [Homo sapiens] | 3.70 | 2.01 | 1 | 1 | 2 | 2 | 894 | 99.3 | 8.41 |
| 578808153 | PREDICTED: myb/SANT-like DNA-binding domain-containing protein | 3.69 | 4.15 | 3 | 1 | 1 | 2 | 265 | 30.5 | 8.57 |

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|---|---|---|---|---|---|---|---|---|---|---|
| 119612929 | spectrin, beta, non-erythrocytic 5 [Homo sapiens] | 3.69 | 0.33 | 4 | 1 | 2 | 2 | 3674 | 416.6 | 6.67 |
| 194373715 | unnamed protein product [Homo sapiens] | 3.69 | 4.86 | 9 | 1 | 1 | 1 | 370 | 40.3 | 10.74 |
| 178057337 | homeobox protein Mohawk [Homo sapiens] | 3.69 | 5.11 | 30 | 1 | 2 | 2 | 352 | 39.3 | 9.64 |
| 194373539 | unnamed protein product [Homo sapiens] | 3.68 | 8.92 | 12 | 1 | 1 | 2 | 157 | 17.2 | 8.97 |
| 578807194 | PREDICTED: transmembrane and coiled-coil domains protein 1 isof | 3.68 | 3.67 | 17 | 1 | 2 | 2 | 463 | 51.6 | 6.55 |
| 14035906 | unnamed protein product [Homo sapiens] | 3.68 | 6.13 | 38 | 1 | 2 | 2 | 310 | 33.6 | 8.43 |
| 119596610 | centrosomal protein 250kDa, isoform CRA_a [Homo sapiens] | 3.67 | 1.05 | 9 | 1 | 2 | 2 | 1810 | 208.3 | 5.02 |
| 194376194 | unnamed protein product [Homo sapiens] | 3.66 | 4.51 | 4 | 1 | 1 | 2 | 244 | 27.7 | 7.25 |
| 34596303 | GRINL1A combined protein Gcom11 precursor [Homo sapiens] | 3.65 | 4.79 | 8 | 1 | 2 | 2 | 397 | 46.2 | 5.92 |
| 62897403 | MAPK13 protein (Fragment) variant [Homo sapiens] | 3.64 | 7.82 | 11 | 1 | 2 | 2 | 307 | 35.6 | 7.91 |
| 119630026 | Down syndrome cell adhesion molecule, isoform CRA_b, partial [Ho | 3.63 | 0.75 | 16 | 1 | 2 | 2 | 1732 | 190.7 | 7.84 |
| 266250 | tetanus toxoid-specific T-cell receptor beta chain [human, periphera | 3.63 | 14.41 | 9 | 1 | 2 | 2 | 118 | 13.7 | 7.75 |
| 119617805 | peptidylglycine alpha-amidating monooxygenase COOH-terminal int | 3.63 | 3.91 | 2 | 1 | 2 | 2 | 435 | 50.0 | 5.31 |
| 194390244 | unnamed protein product [Homo sapiens] | 3.63 | 4.21 | 11 | 1 | 1 | 1 | 356 | 41.2 | 9.41 |
| 119623981 | tenascin XB, isoform CRA_e [Homo sapiens] | 3.62 | 0.58 | 7 | 1 | 2 | 2 | 3451 | 375.6 | 5.14 |
| 119618060 | UTP20, small subunit (SSU) processome component, homolog (yeas | 3.61 | 0.90 | 8 | 1 | 2 | 2 | 1772 | 201.3 | 7.59 |
| 56675578 | unnamed protein product [Homo sapiens] | 3.61 | 12.03 | 6 | 1 | 1 | 1 | 133 | 14.8 | 4.86 |
| 15825717 | Chain B, Crystal Structure Of The Ku Heterodimer Bound To Dna | 3.61 | 4.07 | 7 | 1 | 1 | 1 | 565 | 64.1 | 6.40 |
| 119608738 | ATP-binding cassette, sub-family A (ABC1), member 2, isoform CRA | 3.60 | 1.06 | 10 | 1 | 2 | 2 | 1978 | 218.2 | 6.61 |
| 8648885 | integrin-linked kinase-2 [Homo sapiens] | 3.60 | 3.76 | 12 | 1 | 2 | 2 | 452 | 51.4 | 8.07 |
| 194378470 | unnamed protein product [Homo sapiens] | 3.59 | 7.29 | 77 | 1 | 2 | 2 | 247 | 28.3 | 7.62 |
| 6841480 | HSPC129 [Homo sapiens] | 3.59 | 2.58 | 6 | 1 | 2 | 2 | 466 | 53.1 | 6.58 |
| 172044680 | RecName: Full=Dynein heavy chain 2, axonemal; AltName: Full=Ax | 3.57 | 0.38 | 3 | 1 | 2 | 2 | 4427 | 507.4 | 6.37 |
| 62089274 | caspase recruitment domain family, member 6 variant [Homo sapie | 3.57 | 1.61 | 16 | 1 | 2 | 2 | 872 | 98.6 | 5.34 |
| 34530195 | unnamed protein product [Homo sapiens] | 3.57 | 3.46 | 10 | 1 | 2 | 2 | 809 | 87.8 | 9.50 |
| 83318446 | CCDC141 protein [Homo sapiens] | 3.57 | 3.47 | 4 | 1 | 1 | 2 | 202 | 23.8 | 8.05 |
| 194374255 | unnamed protein product [Homo sapiens] | 3.57 | 5.25 | 31 | 1 | 2 | 2 | 400 | 43.2 | 9.51 |
| 239938605 | RecName: Full=Bromodomain-containing protein 9; AltName: Full= | 3.56 | 2.01 | 85 | 1 | 2 | 2 | 597 | 67.0 | 6.19 |
| 7739449 | hnRNP 2H9E [Homo sapiens] | 3.54 | 12.23 | 10 | 1 | 1 | 1 | 139 | 15.4 | 6.40 |
| 145579989 | Chain B, Stefin B (Cystatin B) Tetramer | 3.54 | 9.18 | 2 | 1 | 1 | 2 | 98 | 11.1 | 8.43 |
| 119578127 | XK, Kell blood group complex subunit-related family, member 3 [Ho | 3.52 | 2.40 | 83 | 1 | 2 | 2 | 459 | 53.4 | 8.95 |
| 62087264 | Integrin alpha-6 precursor variant [Homo sapiens] | 3.52 | 4.24 | 13 | 1 | 2 | 2 | 566 | 64.6 | 8.40 |
| 119850921 | MBD5 protein [Homo sapiens] | 3.50 | 19.09 | 4 | 1 | 1 | 1 | 110 | 12.2 | 4.65 |
| 40041056 | unnamed protein product [Homo sapiens] | 3.48 | 24.53 | 11 | 1 | 1 | 1 | 53 | 5.7 | 5.71 |
| 20150236 | Chain H, Crystal Structure Of The Mrp14 Complexed With Chaps | 3.46 | 13.27 | 5 | 1 | 1 | 1 | 113 | 13.1 | 6.13 |
| 24987241 | Chain L, Variable Light Chain Dimer Of Anti-Ferritin Antibody | 3.39 | 11.40 | 1 | 1 | 1 | 1 | 114 | 12.7 | 8.47 |
| 320089846 | Chain G, Crystal Structure Of Mica-Specific Human Gamma Delta T | 3.38 | 3.86 | 1 | 1 | 2 | 2 | 259 | 29.2 | 9.23 |
| 578804438 | PREDICTED: ankyrin repeat and MYND domain-containing protein 1 | 3.36 | 2.84 | 8 | 1 | 1 | 1 | 703 | 77.6 | 6.92 |
| 194388818 | unnamed protein product [Homo sapiens] | 3.34 | 1.87 | 75 | 1 | 3 | 3 | 801 | 90.5 | 8.28 |

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|---|---|---|---|---|---|---|---|---|---|---|
| 327478577 | RecName: Full=Interferon-related developmental regulator 2; AltNa | 3.34 | 1.19 | 2 | 1 | 1 | 2 | 506 | 54.8 | 7.94 |
| 71051976 | MYH11 protein [Homo sapiens] | 3.33 | 11.71 | 1 | 1 | 1 | 1 | 222 | 25.0 | 7.02 |
| 119569715 | chromosome 10 open reading frame 86, isoform CRA_a, partial [Ho | 3.33 | 2.85 | 4 | 1 | 1 | 2 | 316 | 35.8 | 5.76 |
| 609412241 | Chain A, The Structure Of 1na In Complex With Src T338g | 3.32 | 4.91 | 2 | 1 | 1 | 1 | 448 | 51.0 | 6.47 |
| 119631103 | hCG2003116, isoform CRA_c [Homo sapiens] | 3.31 | 1.87 | 13 | 1 | 2 | 2 | 643 | 74.0 | 8.32 |
| 158061661 | unnamed protein product [Homo sapiens] | 3.31 | 0.59 | 10 | 1 | 2 | 2 | 3069 | 334.8 | 5.99 |
| 221040986 | unnamed protein product [Homo sapiens] | 3.27 | 0.42 | 16 | 1 | 1 | 2 | 1415 | 163.5 | 6.21 |
| 13529083 | ARG1 protein [Homo sapiens] | 3.26 | 2.97 | 12 | 1 | 2 | 2 | 236 | 25.3 | 8.51 |
| 98956399 | immunoglobulin kappa light chain variable region [Homo sapiens] | 3.23 | 11.61 | 1 | 1 | 1 | 1 | 112 | 12.3 | 9.35 |
| 119570989 | eukaryotic elongation factor-2 kinase [Homo sapiens] | 3.22 | 1.10 | 3 | 1 | 1 | 2 | 725 | 82.1 | 5.36 |
| 158714178 | C-type lectin family 2 member A variant 2 [Homo sapiens] | 3.22 | 16.33 | 5 | 1 | 1 | 1 | 147 | 17.1 | 8.47 |
| 194376218 | unnamed protein product [Homo sapiens] | 3.22 | 13.23 | 1 | 1 | 1 | 1 | 189 | 22.2 | 5.24 |
| 114147509 | immunoglobulin heavy chain variable region [Homo sapiens] | 3.20 | 10.48 | 1 | 1 | 1 | 1 | 124 | 13.6 | 5.99 |
| 119608376 | hCG30195, isoform CRA_c [Homo sapiens] | 3.19 | 0.61 | 17 | 1 | 2 | 2 | 1955 | 214.1 | 7.72 |
| 180631 | calnexin, partial [Homo sapiens] | 3.19 | 4.21 | 5 | 1 | 1 | 1 | 356 | 40.8 | 4.34 |
| 485601395 | Chain N, Structure Of The Human 40s Ribosomal Proteins | 3.18 | 9.93 | 1 | 1 | 1 | 1 | 151 | 17.2 | 10.54 |
| 300116271 | 3-oxo-5-beta-steroid 4-dehydrogenase isoform 2 [Homo sapiens] | 3.18 | 4.56 | 6 | 1 | 1 | 2 | 285 | 32.9 | 6.62 |
| 221040266 | unnamed protein product [Homo sapiens] | 3.17 | 11.86 | 18 | 1 | 1 | 1 | 118 | 13.5 | 8.60 |
| 320042386 | immunoglobulin heavy chain variable region [Homo sapiens] | 3.17 | 15.45 | 1 | 1 | 1 | 1 | 123 | 13.6 | 7.77 |
| 556695373 | TBC1 domain family member 21 isoform 2 [Homo sapiens] | 3.17 | 4.33 | 5 | 1 | 1 | 2 | 300 | 34.9 | 6.04 |
| 353558907 | RecName: Full=Proline-rich basic protein 1 | 3.15 | 1.87 | 1 | 1 | 2 | 2 | 1015 | 106.9 | 9.63 |
| 428698207 | Chain G, Dcnl Complex With N-terminally Acetylated Nedd8 E2 Pept | 3.15 | 28.00 | 1 | 1 | 1 | 2 | 25 | 2.6 | 9.70 |
| 530388682 | PREDICTED: collectin-10 isoform X1 [Homo sapiens] | 3.14 | 3.85 | 4 | 1 | 1 | 2 | 208 | 23.3 | 7.66 |
| 387936154 | glutaminyl-tRNA synthetase, partial [Homo sapiens] | 3.14 | 25.93 | 9 | 1 | 1 | 1 | 108 | 11.5 | 9.99 |
| 119618933 | splicing factor, arginine/serine-rich 8 (suppressor-of-white-apricot h | 3.14 | 1.82 | 10 | 1 | 2 | 2 | 825 | 90.7 | 9.09 |
| 40039698 | unnamed protein product [Homo sapiens] | 3.13 | 12.73 | 1 | 1 | 1 | 2 | 55 | 5.6 | 12.00 |
| 119622426 | aggrecan 1 (chondroitin sulfate proteoglycan 1, large aggregating p | 3.13 | 1.62 | 7 | 1 | 1 | 1 | 2165 | 224.6 | 4.20 |
| 116496933 | Zinc finger protein 37 homolog (mouse) [Homo sapiens] | 3.13 | 2.06 | 15 | 1 | 2 | 2 | 630 | 71.2 | 9.06 |
| 34529199 | unnamed protein product [Homo sapiens] | 3.12 | 1.62 | 108 | 1 | 2 | 2 | 677 | 78.4 | 6.65 |
| 62988906 | unknown [Homo sapiens] | 3.12 | 0.56 | 14 | 1 | 2 | 2 | 2151 | 235.0 | 6.60 |
| 1942180 | Chain H, Free And Liganded Form Of An Esterolytic Catalytic Antibo | 3.11 | 8.76 | 2 | 1 | 1 | 1 | 217 | 23.2 | 8.66 |
| 119584509 | vestigial like 4 (Drosophila), isoform CRA_f [Homo sapiens] | 3.10 | 5.02 | 48 | 1 | 2 | 2 | 219 | 23.1 | 9.31 |
| 119596687 | S-adenosylhomocysteine hydrolase, isoform CRA_b [Homo sapiens] | 3.09 | 5.26 | 8 | 1 | 1 | 1 | 285 | 30.9 | 5.26 |
| 119568064 | AT rich interactive domain 1B (SWI1-like), isoform CRA_b [Homo sa | 3.09 | 1.89 | 8 | 1 | 1 | 2 | 529 | 51.9 | 7.71 |
| 264673 | gp39=CD40 ligand [human, hyper-IgM syndrome patient CD, T cells | 3.08 | 3.31 | 6 | 1 | 1 | 2 | 151 | 16.4 | 9.51 |
| 119623578 | hCG1811792, isoform CRA_a [Homo sapiens] | 3.07 | 17.17 | 2 | 1 | 1 | 1 | 99 | 11.0 | 9.50 |
| 304562566 | immunoglobulin gamma 1 heavy chain variable region [Homo sapie | 3.07 | 12.98 | 1 | 1 | 1 | 1 | 131 | 13.9 | 7.94 |
| 578814737 | PREDICTED: diacylglycerol kinase iota isoform X3 [Homo sapiens] | 3.06 | 2.82 | 9 | 1 | 1 | 1 | 496 | 55.6 | 6.11 |
| 537368169 | immunoglobulin heavy chain variable region, partial [Homo sapiens] | 3.06 | 11.96 | 1 | 1 | 1 | 1 | 92 | 10.5 | 6.55 |

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|---|---|---|---|---|---|---|---|---|---|---|---|
| 119591738 | ankyrin repeat domain 23, isoform CRA_b [Homo sapiens] | 3.06 | 5.84 | 7 | 1 | 1 | 1 | 257 | 28.8 | 9.42 |
| 34531561 | unnamed protein product [Homo sapiens] | 3.04 | 0.47 | 1 | 1 | 1 | 2 | 1268 | 143.5 | 6.58 |
| 119572383 | Tu translation elongation factor, mitochondrial, isoform CRA_b [Hon | 3.04 | 5.44 | 5 | 1 | 1 | 1 | 349 | 37.4 | 6.60 |
| 212675169 | anti-HIV-1 V3 immunoglobulin heavy chain [Homo sapiens] | 3.04 | 18.57 | 1 | 1 | 1 | 1 | 140 | 15.3 | 8.15 |
| 119585587 | ribosomal protein L29, isoform CRA_a [Homo sapiens] | 3.03 | 9.55 | 9 | 1 | 1 | 1 | 157 | 17.5 | 11.66 |
| 553615 | alpha-1 collagen type I, partial [Homo sapiens] | 3.03 | 6.36 | 12 | 1 | 1 | 1 | 472 | 44.7 | 5.16 |
| 64653183 | Serpin peptidase inhibitor, clade B (ovalbumin), member 10 [Homo | 3.03 | 6.80 | 1 | 1 | 1 | 1 | 397 | 45.4 | 5.87 |
| 7020957 | unnamed protein product [Homo sapiens] | 3.02 | 1.11 | 104 | 1 | 2 | 2 | 993 | 109.2 | 5.43 |
| 119618006 | solute carrier family 25 (mitochondrial carrier; phosphate carrier), m | 3.00 | 5.19 | 7 | 1 | 1 | 1 | 231 | 26.0 | 9.48 |
| 270047085 | immunoglobulin heavy chain variable region [Homo sapiens] | 2.99 | 31.82 | 1 | 1 | 1 | 1 | 88 | 9.8 | 9.04 |
| 40040218 | unnamed protein product [Homo sapiens] | 2.94 | 32.95 | 1 | 1 | 1 | 1 | 88 | 9.6 | 5.19 |
| 119623333 | apoptosis-inducing factor like, isoform CRA_d [Homo sapiens] | 2.94 | 3.63 | 7 | 1 | 1 | 1 | 578 | 63.7 | 9.86 |
| 221040506 | unnamed protein product [Homo sapiens] | 2.94 | 16.18 | 1 | 1 | 1 | 1 | 136 | 14.7 | 10.01 |
| 270053266 | immunoglobulin heavy chain variable region [Homo sapiens] | 2.93 | 22.90 | 1 | 1 | 1 | 2 | 131 | 14.7 | 9.01 |
| 123829 | RecName: Full=Ig heavy chain V-II region SESS; Flags: Precursor | 2.93 | 10.88 | 3 | 1 | 1 | 1 | 147 | 16.3 | 7.09 |
| 37927289 | Chain A, A Chemical, Genetic, And Structural Analysis Of The Nuclea | 2.92 | 13.79 | 1 | 1 | 1 | 1 | 232 | 27.0 | 5.72 |
| 296275 | HLA-DRB4$0101 [Homo sapiens] | 2.91 | 82.76 | 1 | 1 | 1 | 1 | 29 | 2.9 | 8.00 |
| 119583278 | hCG2038568, partial [Homo sapiens] | 2.91 | 15.18 | 1 | 1 | 1 | 1 | 112 | 12.7 | 8.63 |
| 2853277 | WD splicing factor Hprp4p [Homo sapiens] | 2.90 | 2.50 | 7 | 1 | 1 | 1 | 520 | 58.2 | 7.40 |
| 112694586 | immunoglobulin heavy chain variable region [Homo sapiens] | 2.90 | 18.81 | 1 | 1 | 1 | 1 | 101 | 10.9 | 8.31 |
| 119571921 | formin-like 1, isoform CRA_c [Homo sapiens] | 2.90 | 13.21 | 2 | 1 | 1 | 1 | 212 | 23.2 | 9.35 |
| 34535327 | unnamed protein product [Homo sapiens] | 2.90 | 14.88 | 1 | 1 | 1 | 1 | 215 | 21.8 | 8.70 |
| 40881289 | unnamed protein product [Homo sapiens] | 2.90 | 4.21 | 8 | 1 | 1 | 1 | 309 | 34.9 | 8.38 |
| 194389826 | unnamed protein product [Homo sapiens] | 2.89 | 8.75 | 5 | 1 | 1 | 1 | 160 | 17.7 | 7.71 |
| 361129718 | Chain A, Solution Structure Of The Dimerization Domain Of Human | 2.89 | 23.19 | 6 | 1 | 1 | 1 | 69 | 7.1 | 4.55 |
| 194380566 | unnamed protein product [Homo sapiens] | 2.88 | 9.60 | 6 | 1 | 1 | 1 | 125 | 14.6 | 8.69 |
| 119574690 | DEAD (Asp-Glu-Ala-Asp) box polypeptide 21, isoform CRA_a [Homo | 2.88 | 7.54 | 5 | 1 | 1 | 1 | 199 | 22.6 | 8.79 |
| 4323920 | immunoglobulin kappa light chain variable region [Homo sapiens] | 2.88 | 20.00 | 2 | 1 | 1 | 1 | 100 | 10.8 | 5.96 |
| 1335249 | carboxy-propeptide of alpha 1 (III) procollagen [Homo sapiens] | 2.87 | 13.06 | 10 | 1 | 1 | 1 | 245 | 27.4 | 5.52 |
| 197725196 | Chain A, Crystal Structure Of Il-23 In Complex With Neutralizing Fab | 2.87 | 8.41 | 1 | 1 | 1 | 1 | 214 | 23.4 | 6.99 |
| 112699833 | immunoglobulin heavy chain variable region [Homo sapiens] | 2.87 | 23.76 | 1 | 1 | 1 | 1 | 101 | 10.8 | 8.29 |
| 194379836 | unnamed protein product [Homo sapiens] | 2.86 | 4.72 | 7 | 1 | 1 | 1 | 254 | 29.5 | 8.82 |
| 545762836 | cytochrome b (mitochondrion) [Homo sapiens] | 2.86 | 7.63 | 1 | 1 | 1 | 1 | 380 | 42.7 | 8.15 |
| 183448389 | Chain B, Crystal Structure Of Human Eukaryotic Translation Initiatio | 2.86 | 17.39 | 3 | 1 | 1 | 1 | 138 | 15.1 | 6.18 |
| 119621461 | ribosomal protein S7, isoform CRA_a [Homo sapiens] | 2.85 | 6.47 | 3 | 1 | 1 | 1 | 170 | 19.4 | 10.26 |
| 404249076 | immunoglobulin gamma heavy chain variable region, partial [Homo | 2.85 | 25.44 | 1 | 1 | 1 | 1 | 114 | 12.8 | 8.60 |
| 119616544 | C-type lectin domain family 12 member B, isoform CRA_b [Homo sa | 2.85 | 11.64 | 6 | 1 | 1 | 1 | 232 | 26.7 | 5.88 |
| 119628414 | hCG1807616 [Homo sapiens] | 2.85 | 14.65 | 1 | 1 | 1 | 1 | 198 | 21.8 | 5.55 |
| 124504581 | SAMD13 protein [Homo sapiens] | 2.84 | 19.05 | 3 | 1 | 1 | 1 | 147 | 16.1 | 5.48 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 284174 | Ig heavy chain V region (DP-1) - human (fragment) | 2.84 | 11.22 | 9 | 1 | 1 | 1 | 98 | 10.9 | 9.13 |
| 119598316 | hCG2036668, partial [Homo sapiens] | 2.84 | 13.43 | 1 | 1 | 1 | 1 | 216 | 21.9 | 5.60 |
| 519674316 | immunoglobulin A heavy chain variable region, partial [Homo sapier | 2.84 | 23.58 | 1 | 1 | 1 | 1 | 123 | 13.1 | 7.94 |
| 40982484 | unnamed protein product [Homo sapiens] | 2.83 | 24.74 | 1 | 1 | 1 | 1 | 97 | 11.5 | 9.10 |
| 12620919 | prosomal P27K protein [Homo sapiens] | 2.82 | 18.97 | 7 | 1 | 1 | 1 | 58 | 6.2 | 8.97 |
| 221044848 | unnamed protein product [Homo sapiens] | 2.82 | 3.45 | 3 | 1 | 1 | 2 | 579 | 63.1 | 7.85 |
| 530362593 | PREDICTED: protein FAM73A isoform X5 [Homo sapiens] | 2.81 | 4.55 | 6 | 1 | 1 | 1 | 593 | 66.5 | 5.55 |
| 61679988 | Chain B, Crystal Structure Of The TollINTERLEUKIN-1 Receptor (Tir) | 2.81 | 11.95 | 1 | 1 | 1 | 1 | 159 | 18.8 | 6.79 |
| 194381766 | unnamed protein product [Homo sapiens] | 2.81 | 11.52 | 4 | 1 | 1 | 1 | 165 | 19.2 | 9.77 |
| 221044944 | unnamed protein product [Homo sapiens] | 2.81 | 3.09 | 8 | 1 | 1 | 1 | 518 | 59.3 | 6.49 |
| 119607958 | zinc finger protein 482 [Homo sapiens] | 2.80 | 6.60 | 1 | 1 | 1 | 1 | 424 | 48.2 | 6.76 |
| 194390448 | unnamed protein product [Homo sapiens] | 2.79 | 8.21 | 3 | 1 | 1 | 1 | 280 | 32.2 | 9.20 |
| 119587014 | ATPase, Class II, type 9B, isoform CRA_b, partial [Homo sapiens] | 2.79 | 9.39 | 1 | 1 | 1 | 1 | 330 | 35.5 | 10.46 |
| 40041124 | unnamed protein product [Homo sapiens] | 2.79 | 11.36 | 8 | 1 | 1 | 1 | 132 | 14.1 | 6.92 |
| 40037956 | unnamed protein product [Homo sapiens] | 2.79 | 18.80 | 1 | 1 | 1 | 1 | 117 | 13.1 | 4.64 |
| 75765948 | Chain C, Structure Of The Third Kh Domain Of Hnrnp K In Complex | 2.79 | 18.29 | 1 | 1 | 1 | 1 | 82 | 8.9 | 8.50 |
| 189054432 | unnamed protein product [Homo sapiens] | 2.79 | 6.44 | 1 | 1 | 1 | 1 | 295 | 31.6 | 6.38 |
| 6599075 | caveolin-1 [Homo sapiens] | 2.78 | 21.54 | 5 | 1 | 1 | 1 | 65 | 7.4 | 5.78 |
| 304563754 | immunoglobulin gamma 4 heavy chain variable region [Homo sapier | 2.78 | 19.23 | 1 | 1 | 1 | 1 | 130 | 14.1 | 8.87 |
| 18676690 | FLJ00244 protein [Homo sapiens] | 2.78 | 2.49 | 9 | 1 | 1 | 1 | 1124 | 125.8 | 8.50 |
| 28193122 | unnamed protein product [Homo sapiens] | 2.78 | 8.14 | 6 | 1 | 1 | 1 | 221 | 25.5 | 6.52 |
| 148921621 | FOXN4 protein [Homo sapiens] | 2.78 | 4.84 | 1 | 1 | 1 | 1 | 517 | 55.2 | 6.48 |
| 4732139 | smoothened [Homo sapiens] | 2.76 | 30.00 | 3 | 1 | 1 | 1 | 80 | 8.6 | 5.24 |
| 62088078 | DHX57 protein variant [Homo sapiens] | 2.76 | 2.86 | 9 | 1 | 1 | 1 | 733 | 82.6 | 7.97 |
| 4960030 | Rab GDP dissociation inhibitor beta [Homo sapiens] | 2.76 | 4.18 | 6 | 1 | 1 | 1 | 359 | 41.0 | 7.88 |
| 119601895 | solute carrier family 24 (sodium/potassium/calcium exchanger), mer | 2.76 | 3.16 | 11 | 1 | 1 | 1 | 316 | 35.2 | 6.57 |
| 40977724 | unnamed protein product [Homo sapiens] | 2.74 | 58.18 | 1 | 1 | 1 | 1 | 55 | 5.7 | 8.28 |
| 62630166 | unknown [Homo sapiens] | 2.74 | 6.59 | 4 | 1 | 1 | 1 | 425 | 46.9 | 4.75 |
| 6624942 | hypothetical protein [Homo sapiens] | 2.74 | 14.21 | 4 | 1 | 1 | 1 | 190 | 22.2 | 5.48 |
| 10433952 | unnamed protein product [Homo sapiens] | 2.74 | 4.00 | 3 | 1 | 1 | 1 | 525 | 59.3 | 5.01 |
| 41350956 | C12orf51 protein [Homo sapiens] | 2.73 | 3.90 | 11 | 1 | 1 | 1 | 564 | 62.9 | 6.65 |
| 119579508 | hydroxysteroid dehydrogenase like 2, isoform CRA_a, partial [Homo | 2.73 | 5.64 | 6 | 1 | 1 | 1 | 319 | 34.8 | 7.36 |
| 578802666 | PREDICTED: STAM-binding protein isoform X6 [Homo sapiens] | 2.73 | 4.16 | 1 | 1 | 1 | 1 | 457 | 51.7 | 6.19 |
| 385271660 | anti-group 1 influenza HA immunoglobulin heavy chain variable regi | 2.72 | 25.41 | 1 | 1 | 1 | 1 | 122 | 13.2 | 7.94 |
| 119625759 | diacylglycerol O-acyltransferase 2-like 6 [Homo sapiens] | 2.72 | 11.15 | 3 | 1 | 1 | 1 | 296 | 33.8 | 9.91 |
| 895845 | p64 CLCP [Homo sapiens] | 2.72 | 8.57 | 17 | 1 | 1 | 1 | 210 | 23.5 | 5.21 |
| 2914183 | Chain B, Mature Oxy-Cope Catalytic Antibody With Hapten | 2.72 | 8.60 | 1 | 1 | 1 | 1 | 221 | 23.6 | 8.38 |
| 365813387 | Chain B, Crystal Structure Of A Raver1 Pri4 Peptide In Complex With | 2.71 | 15.38 | 12 | 1 | 1 | 1 | 130 | 14.1 | 7.99 |
| 119583896 | hCG1994156 [Homo sapiens] | 2.71 | 22.06 | 1 | 1 | 1 | 1 | 68 | 7.9 | 10.68 |

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|---|---|---|---|---|---|---|---|---|---|---|
| 7959167 | KIAA1454 protein [Homo sapiens] | 2.69 | 1.58 | 1 | 1 | 1 | 1 | 1265 | 142.6 | 7.61 |
| 386873 | hla antigen, partial [Homo sapiens] | 2.69 | 6.41 | 2 | 1 | 1 | 1 | 359 | 40.5 | 6.30 |
| 119589968 | ATP-binding cassette, sub-family A (ABC1), member 7, isoform CRA | 2.69 | 1.46 | 2 | 1 | 1 | 1 | 1505 | 163.8 | 7.47 |
| 10046711 | 8.2 kDa differentiation factor [Homo sapiens] | 2.68 | 24.74 | 1 | 1 | 1 | 1 | 97 | 11.0 | 9.99 |
| 572153151 | Chain I, Crystal Structure Of Ephb1 | 2.68 | 7.38 | 9 | 1 | 1 | 1 | 298 | 33.6 | 6.39 |
| 195539356 | proteasome subunit beta type-5 isoform 2 [Homo sapiens] | 2.68 | 7.50 | 5 | 1 | 1 | 1 | 160 | 17.8 | 7.24 |
| 70798312 | immunoglobulin heavy chain variable region [Homo sapiens] | 2.68 | 13.79 | 1 | 1 | 1 | 1 | 116 | 12.9 | 9.07 |
| 156633254 | immunoglobulin lambda 6 light chain [Homo sapiens] | 2.68 | 26.79 | 1 | 1 | 1 | 1 | 112 | 11.9 | 5.01 |
| 14017851 | KIAA1817 protein [Homo sapiens] | 2.68 | 3.11 | 3 | 1 | 1 | 1 | 997 | 108.8 | 9.19 |
| 119579173 | relaxin 1, isoform CRA_c [Homo sapiens] | 2.67 | 11.11 | 3 | 1 | 1 | 1 | 99 | 11.3 | 8.72 |
| 2495724 | RecName: Full=Phosphatidate phosphatase LPIN2; AltName: Full=L | 2.67 | 4.91 | 3 | 1 | 1 | 1 | 896 | 99.3 | 5.33 |
| 6650816 | PRO1975 [Homo sapiens] | 2.67 | 5.34 | 7 | 1 | 1 | 2 | 393 | 44.1 | 9.03 |
| 119604840 | glycoprotein, synaptic 2, isoform CRA_a, partial [Homo sapiens] | 2.67 | 18.37 | 1 | 1 | 1 | 1 | 98 | 10.4 | 8.73 |
| 322510055 | RecName: Full=Ileal sodium/bile acid cotransporter; AltName: Full= | 2.67 | 6.03 | 2 | 1 | 1 | 1 | 348 | 37.7 | 7.09 |
| 3171053 | immunoglobulin heavy chain variable region [Homo sapiens] | 2.67 | 23.77 | 2 | 1 | 1 | 1 | 122 | 13.1 | 9.17 |
| 399758 | FBRNP [Homo sapiens] | 2.67 | 11.90 | 1 | 1 | 1 | 1 | 269 | 29.3 | 8.29 |
| 50949842 | hypothetical protein [Homo sapiens] | 2.67 | 27.08 | 1 | 1 | 1 | 1 | 96 | 11.1 | 6.52 |
| 194384456 | unnamed protein product [Homo sapiens] | 2.67 | 6.86 | 2 | 1 | 1 | 1 | 350 | 39.6 | 9.31 |
| 181238 | cytochrome c1, partial [Homo sapiens] | 2.66 | 9.25 | 6 | 1 | 1 | 1 | 227 | 25.7 | 7.46 |
| 119630681 | destrin (actin depolymerizing factor), isoform CRA_a [Homo sapiens | 2.66 | 8.11 | 3 | 1 | 1 | 1 | 148 | 16.6 | 8.34 |
| 578840688 | PREDICTED: D-dopachrome decarboxylase isoform X1 [Homo sapie | 2.66 | 14.35 | 1 | 1 | 1 | 1 | 209 | 22.5 | 6.54 |
| 119618258 | acetyl-Coenzyme A carboxylase beta, isoform CRA_a [Homo sapiens | 2.66 | 1.84 | 1 | 1 | 1 | 1 | 1307 | 147.1 | 8.18 |
| 221046052 | unnamed protein product [Homo sapiens] | 2.66 | 30.43 | 29 | 1 | 1 | 1 | 552 | 62.1 | 11.30 |
| 48425167 | Chain B, Three-Dimensional Solution Structure Of Apo-S100p Protei | 2.65 | 31.58 | 1 | 1 | 1 | 1 | 95 | 10.4 | 4.88 |
| 40980046 | unnamed protein product [Homo sapiens] | 2.65 | 37.97 | 1 | 1 | 1 | 1 | 79 | 8.5 | 11.00 |
| 221046216 | unnamed protein product [Homo sapiens] | 2.65 | 5.65 | 13 | 1 | 1 | 1 | 372 | 41.4 | 5.02 |
| 193783585 | unnamed protein product [Homo sapiens] | 2.65 | 5.95 | 2 | 1 | 1 | 1 | 370 | 41.5 | 6.54 |
| 545773382 | cytochrome c oxidase subunit I, partial (mitochondrion) [Homo sapi | 2.65 | 6.65 | 1 | 1 | 1 | 1 | 466 | 51.9 | 6.76 |
| 56417715 | SCL/TAL1 interrupting locus [Homo sapiens] | 2.65 | 13.81 | 1 | 1 | 1 | 1 | 210 | 23.0 | 4.68 |
| 194383268 | unnamed protein product [Homo sapiens] | 2.64 | 7.33 | 9 | 1 | 1 | 1 | 150 | 16.9 | 10.67 |
| 22209024 | Chromosome 2 open reading frame 69 [Homo sapiens] | 2.64 | 5.20 | 2 | 1 | 1 | 1 | 269 | 30.9 | 8.43 |
| 148753391 | TTF1 protein [Homo sapiens] | 2.64 | 6.72 | 1 | 1 | 1 | 1 | 461 | 53.1 | 8.22 |
| 113472394 | immunoglobulin heavy chain variable region [Homo sapiens] | 2.64 | 22.61 | 1 | 1 | 1 | 1 | 115 | 12.9 | 7.74 |
| 62913991 | SSBP3 protein, partial [Homo sapiens] | 2.64 | 17.59 | 10 | 1 | 1 | 1 | 216 | 21.8 | 6.13 |
| 519672770 | immunoglobulin A heavy chain variable region, partial [Homo sapie | 2.64 | 25.64 | 1 | 1 | 1 | 1 | 117 | 12.8 | 8.85 |
| 60219220 | hypothetical protein [Homo sapiens] | 2.64 | 6.16 | 14 | 1 | 1 | 1 | 357 | 40.0 | 7.09 |
| 88683029 | PROM2 protein [Homo sapiens] | 2.64 | 8.33 | 3 | 1 | 1 | 1 | 360 | 40.6 | 6.42 |
| 119581314 | ribosomal protein L27, isoform CRA_b [Homo sapiens] | 2.64 | 11.25 | 5 | 1 | 1 | 1 | 80 | 9.7 | 10.59 |
| 252092 | HLBP14=14-kDa laminin binding protein [human, melanoma cells, P | 2.64 | 100.00 | 11 | 1 | 1 | 1 | 15 | 1.6 | 7.18 |

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|---|---|---|---|---|---|---|---|---|---|---|
| 194318520 | soluble IGF1R variant 2 [Homo sapiens] | 2.64 | 3.56 | 10 | 1 | 1 | 1 | 759 | 85.8 | 6.81 |
| 119595343 | phosphoglucomutase 2-like 1 [Homo sapiens] | 2.64 | 3.22 | 4 | 1 | 1 | 1 | 622 | 70.4 | 7.15 |
| 448261618 | low-density lipoprotein receptor class A domain-containing protein 1 | 2.64 | 19.75 | 1 | 1 | 1 | 1 | 162 | 17.7 | 5.15 |
| 119585176 | hCG1777807 [Homo sapiens] | 2.63 | 16.96 | 1 | 1 | 1 | 1 | 171 | 18.7 | 9.39 |
| 27900369 | unnamed protein product [Homo sapiens] | 2.63 | 17.61 | 5 | 1 | 1 | 1 | 142 | 16.1 | 8.87 |
| 119611557 | nicotinamide nucleotide adenylyltransferase 2, isoform CRA_d, parti | 2.63 | 12.94 | 1 | 1 | 1 | 1 | 255 | 29.0 | 7.62 |
| 21336160 | unnamed protein product [Homo sapiens] | 2.63 | 1.66 | 1 | 1 | 1 | 1 | 1082 | 121.6 | 8.15 |
| 75765955 | Chain A, Solution Structure Of The F-Actin Binding Domain Of Bcr- | 2.63 | 12.31 | 1 | 1 | 1 | 1 | 130 | 14.1 | 8.66 |
| 1685239 | immunoglobulin variable region, partial [Homo sapiens] | 2.63 | 19.67 | 1 | 1 | 1 | 1 | 122 | 13.7 | 8.37 |
| 159164174 | Chain A, Solution Structure Of The First Ig-Like Domain Of Human | 2.63 | 21.54 | 4 | 1 | 1 | 1 | 130 | 14.0 | 6.54 |
| 299856865 | Chain D, Crystal Structure Of Epha2 Ectodomain In Complex With E | 2.63 | 13.77 | 6 | 1 | 1 | 1 | 138 | 16.3 | 7.71 |
| 6808044 | hypothetical protein [Homo sapiens] | 2.63 | 4.88 | 5 | 1 | 1 | 1 | 635 | 69.4 | 6.21 |
| 119613730 | hCG2045588 [Homo sapiens] | 2.63 | 54.90 | 1 | 1 | 1 | 1 | 51 | 6.2 | 10.01 |
| 40976616 | unnamed protein product [Homo sapiens] | 2.62 | 17.69 | 1 | 1 | 1 | 1 | 130 | 14.6 | 4.46 |
| 530383948 | PREDICTED: DNA polymerase zeta catalytic subunit isoform X4 [Ho | 2.62 | 0.78 | 8 | 1 | 1 | 1 | 2679 | 301.0 | 8.00 |
| 21670687 | immunoglobulin heavy chain VHDJ region [Homo sapiens] | 2.62 | 28.00 | 2 | 1 | 1 | 1 | 125 | 13.8 | 4.75 |
| 14336733 | unknown [Homo sapiens] | 2.62 | 14.23 | 1 | 1 | 1 | 1 | 246 | 25.5 | 7.90 |
| 2654488 | dopamine transporter [Homo sapiens] | 2.62 | 31.58 | 4 | 1 | 1 | 1 | 95 | 10.4 | 8.47 |
| 10437965 | unnamed protein product [Homo sapiens] | 2.62 | 8.57 | 3 | 1 | 1 | 1 | 210 | 23.6 | 7.61 |
| 578805875 | PREDICTED: stabilin-1 isoform X5 [Homo sapiens] | 2.62 | 1.51 | 14 | 1 | 1 | 1 | 1521 | 162.4 | 7.72 |
| 18027474 | TRIMLESS beta [Homo sapiens] | 2.61 | 9.68 | 3 | 1 | 1 | 1 | 279 | 32.0 | 6.73 |
| 7245821 | Chain L, Unliganded Mature Oxy-Cope Catalytic Antibody | 2.61 | 7.11 | 1 | 1 | 1 | 1 | 211 | 23.5 | 7.20 |
| 17942622 | Chain B, The Unliganded Germline Precursor To The Sulfide Oxidase | 2.61 | 4.11 | 1 | 1 | 1 | 1 | 219 | 23.4 | 8.63 |
| 119597329 | ADAM metallopeptidase domain 22, isoform CRA_h, partial [Homo s | 2.61 | 14.49 | 1 | 1 | 1 | 1 | 214 | 23.3 | 11.44 |
| 1388000 | bradykinin receptor [Homo sapiens] | 2.61 | 8.24 | 4 | 1 | 1 | 1 | 364 | 41.4 | 8.25 |
| 4324472 | 5c5-2 protein [Homo sapiens] | 2.61 | 28.28 | 1 | 1 | 1 | 1 | 99 | 10.5 | 7.24 |
| 40976460 | unnamed protein product [Homo sapiens] | 2.60 | 68.63 | 1 | 1 | 1 | 1 | 51 | 5.6 | 8.60 |
| 21465965 | Chain D, Structure Of The Human Replication Protein A (Rpa) Trime | 2.60 | 17.36 | 2 | 1 | 1 | 1 | 121 | 13.6 | 5.08 |
| 119622789 | hCG1778301 [Homo sapiens] | 2.60 | 23.49 | 2 | 1 | 1 | 1 | 149 | 14.9 | 9.20 |
| 158259349 | unnamed protein product [Homo sapiens] | 2.60 | 2.90 | 5 | 1 | 1 | 1 | 828 | 94.0 | 9.07 |
| 155722998 | sodium-driven chloride bicarbonate exchanger isoform 2 [Homo sap | 2.60 | 2.57 | 5 | 1 | 1 | 1 | 1088 | 122.6 | 6.34 |
| 28447472 | unnamed protein product [Homo sapiens] | 2.60 | 3.62 | 3 | 1 | 1 | 1 | 387 | 42.8 | 8.46 |
| 25091738 | RecName: Full=AN1-type zinc finger protein 5; AltName: Full=Zinc | 2.60 | 11.74 | 4 | 1 | 1 | 1 | 213 | 23.1 | 8.51 |
| 578836106 | PREDICTED: retinoblastoma-like protein 1 isoform X1 [Homo sapien | 2.60 | 3.24 | 5 | 1 | 1 | 1 | 896 | 101.1 | 7.56 |
| 7650413 | immunoglobulin heavy chain variable region [Homo sapiens] | 2.59 | 37.04 | 1 | 1 | 1 | 1 | 81 | 9.2 | 8.13 |
| 107558 | R15 gamma peptide - human | 2.59 | 43.24 | 1 | 1 | 1 | 1 | 37 | 4.5 | 4.53 |
| 10697072 | immunoglobulin heavy chain variable region [Homo sapiens] | 2.59 | 26.72 | 1 | 1 | 1 | 1 | 116 | 12.9 | 8.07 |
| 80975571 | immunoglobulin heavy chain variable region VH [Homo sapiens] | 2.59 | 24.37 | 1 | 1 | 1 | 1 | 119 | 12.7 | 5.96 |
| 119620238 | hCG1812972 [Homo sapiens] | 2.59 | 28.70 | 1 | 1 | 1 | 1 | 115 | 12.1 | 11.18 |

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|---|---|---|---|---|---|---|---|---|---|---|
| 194384980 | unnamed protein product [Homo sapiens] | 2.58 | 15.82 | 1 | 1 | 1 | 1 | 177 | 20.9 | 9.60 |
| 194378534 | unnamed protein product [Homo sapiens] | 2.58 | 6.22 | 9 | 1 | 1 | 1 | 450 | 50.2 | 8.53 |
| 1498576 | immunoglobulin heavy chain variable region, partial [Homo sapiens] | 2.58 | 29.21 | 1 | 1 | 1 | 1 | 89 | 9.9 | 5.95 |
| 353251634 | Chain B, Orientation Of Rna Polymerase Ii Within The Human Vp16- | 2.58 | 2.21 | 1 | 1 | 1 | 1 | 1224 | 138.7 | 6.52 |
| 5689521 | KIAA1092 protein [Homo sapiens] | 2.58 | 2.43 | 1 | 1 | 1 | 1 | 1154 | 128.3 | 7.20 |
| 10440006 | unnamed protein product [Homo sapiens] | 2.58 | 5.47 | 1 | 1 | 1 | 1 | 548 | 62.0 | 8.66 |
| 484973 | Ig kappa chain V region (clone LUNm03) - human (fragment) | 2.58 | 21.62 | 1 | 1 | 1 | 1 | 111 | 11.9 | 6.60 |
| 143745282 | RecName: Full=Rod outer segment membrane protein 1; Short=RO | 2.58 | 4.27 | 2 | 1 | 1 | 1 | 351 | 37.2 | 6.05 |
| 158257478 | unnamed protein product [Homo sapiens] | 2.57 | 4.74 | 5 | 1 | 1 | 1 | 380 | 41.6 | 5.27 |
| 585379891 | H1/H5 cross-reactive influenza antibody heavy chain VDJ region imr | 2.57 | 24.41 | 1 | 1 | 1 | 1 | 127 | 14.0 | 8.44 |
| 564730862 | Chain D, Crystal Structure Of The N Terminal Domain Of Wild Type | 2.57 | 20.51 | 1 | 1 | 1 | 1 | 156 | 17.0 | 5.38 |
| 119622919 | transient receptor potential cation channel, subfamily M, member 5, | 2.57 | 1.29 | 9 | 1 | 1 | 2 | 1088 | 123.1 | 6.76 |
| 57157123 | G-protein coupled receptor [Homo sapiens] | 2.57 | 3.83 | 1 | 1 | 1 | 1 | 915 | 102.1 | 8.44 |
| 239916002 | lens fiber membrane intrinsic protein isoform 2 [Homo sapiens] | 2.57 | 15.61 | 2 | 1 | 1 | 1 | 173 | 19.7 | 9.52 |
| 19575559 | unnamed protein product [Homo sapiens] | 2.57 | 2.43 | 1 | 1 | 1 | 1 | 370 | 41.0 | 10.07 |
| 48425472 | Chain D, Structure Of The Signal Recognition Particle Interacting Wi | 2.57 | 12.26 | 6 | 1 | 1 | 1 | 106 | 12.1 | 10.04 |
| 473714 | RNA helicase [Homo sapiens] | 2.57 | 4.56 | 1 | 1 | 1 | 1 | 439 | 47.4 | 10.01 |
| 297787757 | Chain A, Metabotropic Glutamate Receptor Mglur7 Complexed With | 2.57 | 3.95 | 7 | 1 | 1 | 1 | 481 | 53.5 | 5.78 |
| 221044864 | unnamed protein product [Homo sapiens] | 2.57 | 7.03 | 7 | 1 | 1 | 1 | 427 | 46.8 | 8.25 |
| 2689443 | R28830_2 [Homo sapiens] | 2.57 | 2.33 | 6 | 1 | 1 | 1 | 557 | 63.8 | 8.87 |
| 73909040 | FMN1 protein [Homo sapiens] | 2.56 | 6.16 | 3 | 1 | 1 | 1 | 503 | 53.6 | 4.82 |
| 34536355 | unnamed protein product [Homo sapiens] | 2.56 | 14.62 | 1 | 1 | 1 | 1 | 260 | 28.8 | 7.74 |
| 56675533 | unnamed protein product [Homo sapiens] | 2.56 | 29.41 | 1 | 1 | 1 | 1 | 102 | 10.8 | 8.38 |
| 62088938 | MCF.2 cell line derived transforming sequence variant [Homo sapier | 2.56 | 4.60 | 21 | 1 | 1 | 1 | 435 | 51.2 | 6.42 |
| 221041914 | unnamed protein product [Homo sapiens] | 2.56 | 5.93 | 9 | 1 | 1 | 1 | 388 | 44.6 | 5.00 |
| 40042188 | unnamed protein product [Homo sapiens] | 2.56 | 31.76 | 8 | 1 | 1 | 1 | 85 | 9.4 | 10.21 |
| 119591253 | collagen, type IV, alpha 4, isoform CRA_b [Homo sapiens] | 2.56 | 2.02 | 12 | 1 | 1 | 1 | 1189 | 115.6 | 8.24 |
| 361131805 | Chain B, Crystal Structure Of Lrh-1/beta-catenin Complex | 2.56 | 9.09 | 1 | 1 | 1 | 1 | 352 | 39.9 | 6.04 |
| 530398119 | PREDICTED: cell surface glycoprotein MUC18 isoform X2 [Homo sap | 2.55 | 7.28 | 12 | 1 | 1 | 1 | 412 | 45.4 | 5.19 |
| 221039834 | unnamed protein product [Homo sapiens] | 2.55 | 10.54 | 2 | 1 | 1 | 1 | 313 | 34.8 | 8.94 |
| 40046624 | unnamed protein product [Homo sapiens] | 2.55 | 15.89 | 3 | 1 | 1 | 1 | 107 | 11.6 | 9.99 |
| 28827807 | NACHT, LRR and PYD domains-containing protein 10 [Homo sapiens | 2.55 | 4.27 | 1 | 1 | 1 | 1 | 655 | 75.0 | 7.20 |
| 193786297 | unnamed protein product [Homo sapiens] | 2.55 | 3.75 | 12 | 1 | 1 | 1 | 506 | 56.8 | 8.34 |
| 48257075 | BCAT2 protein, partial [Homo sapiens] | 2.55 | 5.54 | 4 | 1 | 1 | 1 | 379 | 42.9 | 8.34 |
| 119620454 | hCG1815165, isoform CRA_c [Homo sapiens] | 2.55 | 20.00 | 1 | 1 | 1 | 1 | 100 | 11.5 | 8.37 |
| 119616996 | hCG2009555 [Homo sapiens] | 2.55 | 13.71 | 1 | 1 | 1 | 1 | 124 | 14.0 | 9.44 |
| 109730579 | Collagen, type XXIV, alpha 1 [Homo sapiens] | 2.55 | 1.75 | 3 | 1 | 1 | 1 | 1714 | 175.4 | 8.27 |
| 40040382 | unnamed protein product [Homo sapiens] | 2.55 | 12.88 | 1 | 1 | 1 | 1 | 132 | 14.8 | 8.91 |
| 189030349 | RecName: Full=Putative uncharacterized protein ENSP00000381961 | 2.54 | 37.88 | 2 | 1 | 1 | 1 | 66 | 7.5 | 11.49 |

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|---|---|---|---|---|---|---|---|---|---|---|
| 320042358 | immunoglobulin heavy chain variable region [Homo sapiens] | 2.54 | 23.77 | 2 | 1 | 1 | 1 | 122 | 13.4 | 7.12 |
| 632933512 | RNA-specific adenosine deaminase [Homo sapiens] | 2.54 | 2.77 | 1 | 1 | 1 | 1 | 1226 | 135.9 | 8.56 |
| 119587019 | ATPase, Class II, type 9B, isoform CRA_g [Homo sapiens] | 2.54 | 11.42 | 19 | 1 | 1 | 1 | 254 | 28.2 | 5.44 |
| 163869660 | immunoglobulin light chain variable region [Homo sapiens] | 2.54 | 29.63 | 2 | 1 | 1 | 1 | 108 | 11.4 | 4.78 |
| 2145156 | IgM rheumatoid factor RF-DI2, variable heavy chain [Homo sapiens | 2.54 | 24.17 | 1 | 1 | 1 | 1 | 120 | 13.2 | 7.94 |
| 119600648 | ras homolog gene family, member T1, isoform CRA_a [Homo sapie | 2.54 | 3.05 | 1 | 1 | 1 | 1 | 459 | 52.8 | 8.16 |
| 4337084 | immunoglobulin lambda light chain variable region [Homo sapiens] | 2.54 | 75.68 | 1 | 1 | 1 | 1 | 37 | 4.1 | 8.22 |
| 112702748 | immunoglobulin heavy chain variable region [Homo sapiens] | 2.54 | 23.76 | 1 | 1 | 1 | 1 | 101 | 10.8 | 7.87 |
| 28799745 | unnamed protein product [Homo sapiens] | 2.54 | 7.17 | 1 | 1 | 1 | 1 | 307 | 34.5 | 7.83 |
| 219517915 | Neuropilin 2 [Homo sapiens] | 2.54 | 3.24 | 1 | 1 | 1 | 1 | 926 | 104.1 | 5.17 |
| 57157119 | G-protein coupled receptor [Homo sapiens] | 2.54 | 2.95 | 1 | 1 | 1 | 1 | 542 | 60.0 | 6.28 |
| 119602114 | likely ortholog of rat brain-enriched guanylate kinase-associated pro | 2.54 | 5.10 | 6 | 1 | 1 | 1 | 529 | 56.9 | 5.33 |
| 119605709 | DnaJ (Hsp40) homolog, subfamily A, member 3, isoform CRA_a, pa | 2.53 | 5.11 | 9 | 1 | 1 | 1 | 450 | 49.3 | 9.29 |
| 119599423 | calsyntenin 2, isoform CRA_b [Homo sapiens] | 2.53 | 6.41 | 5 | 1 | 1 | 1 | 608 | 67.8 | 6.52 |
| 58223096 | anti-tetanus toxoid immunoglobulin light chain variable region [Hom | 2.53 | 27.78 | 1 | 1 | 1 | 1 | 108 | 11.6 | 8.50 |
| 62702328 | unknown [Homo sapiens] | 2.53 | 21.49 | 4 | 1 | 1 | 1 | 121 | 12.5 | 8.84 |
| 444733215 | alternative protein TTYH2 [Homo sapiens] | 2.53 | 38.60 | 1 | 1 | 1 | 2 | 57 | 6.1 | 11.41 |
| 84105516 | C21orf123 protein [Homo sapiens] | 2.53 | 9.42 | 1 | 1 | 1 | 1 | 138 | 15.0 | 9.83 |
| 49168450 | ANXA9 [Homo sapiens] | 2.53 | 9.17 | 2 | 1 | 1 | 1 | 338 | 37.6 | 5.76 |
| 532164692 | vacuolar protein-sorting-associated protein 36 isoform 3 [Homo sap | 2.53 | 7.01 | 5 | 1 | 1 | 1 | 328 | 36.9 | 7.49 |
| 33570506 | immunoglobulin kappa chain variable region [Homo sapiens] | 2.53 | 23.96 | 1 | 1 | 1 | 1 | 96 | 10.7 | 5.06 |
| 109730461 | Syntaxin binding protein 5 (tomosyn) [Homo sapiens] | 2.53 | 2.69 | 1 | 1 | 1 | 1 | 1115 | 123.4 | 7.11 |
| 10444345 | CIG30 [Homo sapiens] | 2.53 | 12.71 | 2 | 1 | 1 | 1 | 236 | 27.3 | 9.79 |
| 4557501 | cathepsin O preproprotein [Homo sapiens] | 2.53 | 7.79 | 2 | 1 | 1 | 1 | 321 | 35.9 | 7.42 |
| 119595384 | serpin peptidase inhibitor, clade H (heat shock protein 47), member | 2.53 | 3.05 | 8 | 1 | 1 | 1 | 361 | 40.7 | 8.41 |
| 157829395 | ubiquitously transcribed tetratricopeptide repeat protein Y-linked tra | 2.53 | 23.02 | 3 | 1 | 1 | 1 | 126 | 14.1 | 5.33 |
| 119589203 | olfactory receptor, family 51, subfamily M, member 1 [Homo sapien | 2.53 | 8.57 | 4 | 1 | 1 | 1 | 315 | 35.4 | 8.84 |
| 119577274 | interleukin 28A (interferon, lambda 2) [Homo sapiens] | 2.53 | 7.50 | 1 | 1 | 1 | 1 | 400 | 42.4 | 9.73 |
| 112696692 | immunoglobulin heavy chain variable region [Homo sapiens] | 2.53 | 21.78 | 1 | 1 | 1 | 1 | 101 | 10.9 | 8.97 |
| 578837112 | PREDICTED: oxysterol-binding protein 2 isoform X9 [Homo sapiens] | 2.52 | 4.34 | 1 | 1 | 1 | 1 | 461 | 52.5 | 7.21 |
| 388326835 | Chain B, Crystal Structure Of The Two N-terminal Rrm Domains Of | 2.52 | 6.21 | 6 | 1 | 1 | 1 | 177 | 19.8 | 9.41 |
| 44894233 | TCR alpha chain [Homo sapiens] | 2.52 | 12.41 | 1 | 1 | 1 | 1 | 274 | 30.9 | 6.24 |
| 119588586 | GPI-anchored membrane protein 1, isoform CRA_d [Homo sapiens] | 2.52 | 2.87 | 6 | 1 | 1 | 1 | 628 | 70.3 | 5.02 |
| 41281429 | basic leucine zipper and W2 domain-containing protein 1 isoform 4 | 2.52 | 7.65 | 6 | 1 | 1 | 1 | 353 | 40.5 | 6.46 |
| 119625999 | UDP glucuronosyltransferase 2 family, polypeptide A1, isoform CRA_ | 2.52 | 7.02 | 6 | 1 | 1 | 1 | 527 | 59.9 | 8.92 |
| 119617856 | decorin, isoform CRA_a [Homo sapiens] | 2.52 | 9.13 | 3 | 1 | 1 | 1 | 252 | 28.0 | 8.13 |
| 13487375 | inwardly-rectifying potassium channel Kir1.2 [Homo sapiens] | 2.52 | 79.41 | 6 | 1 | 1 | 1 | 34 | 3.9 | 10.95 |
| 119571227 | hCG2043388 [Homo sapiens] | 2.52 | 16.41 | 7 | 1 | 1 | 1 | 195 | 21.3 | 7.64 |
| 40032048 | unnamed protein product [Homo sapiens] | 2.52 | 9.64 | 1 | 1 | 1 | 1 | 197 | 21.6 | 11.12 |

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|---|---|---|---|---|---|---|---|---|---|---|
| 119612450 | hCG1779572 [Homo sapiens] | 2.52 | 26.36 | 1 | 1 | 1 | 1 | 110 | 12.8 | 10.15 |
| 58202664 | rotavirus-specific intestinal-homing antibody heavy chain variable re | 2.52 | 26.05 | 1 | 1 | 1 | 1 | 119 | 12.7 | 8.88 |
| 29823335 | unnamed protein product [Homo sapiens] | 2.52 | 1.18 | 4 | 1 | 1 | 1 | 2367 | 257.2 | 5.71 |
| 578846035 | PREDICTED: polycystin-1-like [Homo sapiens] | 2.52 | 4.32 | 2 | 1 | 1 | 1 | 509 | 53.6 | 7.01 |
| 343791333 | anti-HIV-1 immunoglobulin heavy chain variable region, partial [Ho | 2.51 | 24.00 | 3 | 1 | 1 | 1 | 125 | 14.1 | 9.01 |
| 159163499 | Chain A, Solution Structure Of The Ph Domain Of Human Docking P | 2.51 | 18.79 | 4 | 1 | 1 | 1 | 149 | 17.0 | 6.02 |
| 194384446 | unnamed protein product [Homo sapiens] | 2.51 | 12.21 | 5 | 1 | 1 | 1 | 303 | 34.0 | 10.90 |
| 296434449 | RecName: Full=UPF0723 protein C11orf83; Flags: Precursor | 2.51 | 31.18 | 2 | 1 | 1 | 1 | 93 | 10.1 | 9.41 |
| 84569966 | Unknown (protein for MGC:131531) [Homo sapiens] | 2.51 | 12.50 | 1 | 1 | 1 | 1 | 192 | 21.7 | 10.07 |
| 112699896 | immunoglobulin heavy chain variable region [Homo sapiens] | 2.51 | 14.15 | 1 | 1 | 1 | 1 | 106 | 11.5 | 7.83 |
| 524454108 | IgG H chain [Homo sapiens] | 2.51 | 10.55 | 1 | 1 | 1 | 1 | 275 | 29.4 | 8.16 |
| 91979634 | immunoglobulin heavy chain variable region [Homo sapiens] | 2.50 | 24.74 | 1 | 1 | 1 | 1 | 97 | 10.8 | 9.28 |
| 119621847 | hCG2040428, partial [Homo sapiens] | 2.50 | 10.42 | 1 | 1 | 1 | 1 | 240 | 27.2 | 7.88 |
| 578846966 | PREDICTED: putative uncharacterized protein LOC388882-like isofo | 2.50 | 11.63 | 1 | 1 | 1 | 1 | 215 | 24.6 | 4.42 |
| 324022755 | potassium voltage-gated channel subfamily A member 2 isoform b [ | 2.50 | 5.62 | 3 | 1 | 1 | 1 | 356 | 40.9 | 5.05 |
| 119597532 | heterogeneous nuclear ribonucleoprotein U (scaffold attachment fa | 2.48 | 2.14 | 11 | 1 | 1 | 1 | 513 | 57.6 | 9.36 |
| 578801287 | PREDICTED: prospero homeobox protein 1 isoform X4 [Homo sapie | 2.47 | 2.35 | 5 | 1 | 1 | 1 | 680 | 76.5 | 7.61 |
| 169249224 | immunoglobulin heavy chain constant alpha 1 membrane bound iso | 2.47 | 5.71 | 58 | 1 | 1 | 1 | 175 | 19.6 | 5.00 |
| 6525168 | concentrative nucleoside transporter [Homo sapiens] | 2.47 | 3.08 | 2 | 1 | 1 | 1 | 649 | 71.5 | 7.74 |
| 119584301 | cereblon, isoform CRA_g [Homo sapiens] | 2.46 | 7.50 | 11 | 1 | 1 | 1 | 120 | 13.9 | 5.24 |
| 159164158 | Chain A, Solution Structures Of The Whep-Trs Domain Of Human M | 2.46 | 18.99 | 8 | 1 | 1 | 1 | 79 | 8.2 | 9.74 |
| 40041380 | unnamed protein product [Homo sapiens] | 2.45 | 6.79 | 4 | 1 | 1 | 1 | 221 | 25.3 | 5.35 |
| 194373853 | unnamed protein product [Homo sapiens] | 2.44 | 8.61 | 2 | 1 | 1 | 1 | 244 | 26.4 | 7.18 |
| 530375417 | PREDICTED: ruvB-like 1 isoform X1 [Homo sapiens] | 2.44 | 2.78 | 5 | 1 | 1 | 1 | 396 | 43.9 | 5.78 |
| 6573673 | Chain A, Crystal Structure Of The Pten Tumor Suppressor | 2.43 | 2.47 | 10 | 1 | 1 | 1 | 324 | 38.4 | 8.59 |
| 119612184 | NIPA-like domain containing 2, isoform CRA_b [Homo sapiens] | 2.42 | 3.53 | 2 | 1 | 1 | 1 | 368 | 40.8 | 8.92 |
| 119625336 | fibrinogen beta chain, isoform CRA_b [Homo sapiens] | 2.42 | 6.48 | 1 | 1 | 1 | 1 | 247 | 27.7 | 7.99 |
| 32394712 | interferon-induced ISG12c delta isoform [Homo sapiens] | 2.42 | 22.81 | 7 | 1 | 1 | 1 | 57 | 5.4 | 10.84 |
| 119590886 | hCG2040938, partial [Homo sapiens] | 2.42 | 18.69 | 1 | 1 | 1 | 1 | 107 | 11.8 | 11.75 |
| 116283351 | CCDC6 protein [Homo sapiens] | 2.41 | 3.89 | 4 | 1 | 1 | 1 | 334 | 38.1 | 9.39 |
| 119632165 | hypoxanthine phosphoribosyltransferase 1 (Lesch-Nyhan syndrome) | 2.41 | 6.07 | 10 | 1 | 1 | 1 | 214 | 24.1 | 6.40 |
| 119604151 | KIAA0265 protein, isoform CRA_b [Homo sapiens] | 2.40 | 4.76 | 7 | 1 | 1 | 1 | 231 | 26.1 | 7.80 |
| 194376544 | unnamed protein product [Homo sapiens] | 2.40 | 15.20 | 1 | 1 | 1 | 2 | 125 | 14.3 | 5.60 |
| 10121865 | topoisomerase II alpha-4 [Homo sapiens] | 2.38 | 2.24 | 1 | 1 | 1 | 1 | 581 | 64.8 | 8.91 |
| 119569482 | solute carrier organic anion transporter family, member 6A1, isofor | 2.38 | 1.80 | 6 | 1 | 1 | 1 | 445 | 49.2 | 8.68 |
| 7959893 | PRO2242 [Homo sapiens] | 2.38 | 16.44 | 4 | 1 | 1 | 1 | 73 | 8.4 | 5.34 |
| 119615677 | hCG1818253, partial [Homo sapiens] | 2.37 | 15.87 | 1 | 1 | 1 | 1 | 126 | 14.1 | 7.02 |
| 119621016 | solute carrier family 30 (zinc transporter), member 3, isoform CRA_ | 2.37 | 2.60 | 1 | 1 | 1 | 1 | 500 | 53.5 | 8.19 |
| 1495423 | B-HLH DNA binding protein [Homo sapiens] | 2.37 | 14.56 | 1 | 1 | 1 | 1 | 206 | 21.2 | 9.44 |

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|---|---|---|---|---|---|---|---|---|---|---|---|
| 62988897 | unknown [Homo sapiens] | 2.36 | 2.53 | 7 | 1 | 1 | 1 | 711 | 79.0 | 8.10 |
| 39939605 | immunoglobulin heavy chain variable region [Homo sapiens] | 2.36 | 11.28 | 1 | 1 | 1 | 1 | 133 | 14.1 | 5.14 |
| 40040938 | unnamed protein product [Homo sapiens] | 2.36 | 5.88 | 13 | 1 | 1 | 1 | 170 | 19.1 | 6.54 |
| 119588867 | hCG1992268 [Homo sapiens] | 2.36 | 17.82 | 1 | 1 | 1 | 1 | 101 | 11.8 | 8.60 |
| 119582347 | hCG1982215, isoform CRA_v [Homo sapiens] | 2.35 | 1.71 | 2 | 1 | 1 | 1 | 817 | 89.7 | 4.73 |
| 187385 | myristoylated alanine-rich C-kinase substrate, partial [Homo sapiens | 2.35 | 55.88 | 6 | 1 | 1 | 1 | 34 | 3.3 | 8.73 |
| 343478275 | B9 domain-containing protein 1 isoform a [Homo sapiens] | 2.35 | 6.61 | 1 | 1 | 1 | 1 | 257 | 27.8 | 10.99 |
| 399227406 | sterile alpha motif domain containing 11 splice variant ASV11 [Hom | 2.34 | 1.78 | 1 | 1 | 1 | 1 | 619 | 65.6 | 8.46 |
| 485601410 | Chain f, Structure Of The Human 40s Ribosomal Proteins | 2.33 | 16.25 | 5 | 1 | 1 | 1 | 80 | 9.4 | 9.83 |
| 119583073 | kinesin family member 27, isoform CRA_c [Homo sapiens] | 2.33 | 3.34 | 10 | 1 | 1 | 1 | 389 | 45.5 | 7.14 |
| 14290586 | TIMM50 protein [Homo sapiens] | 2.33 | 3.49 | 6 | 1 | 1 | 1 | 344 | 38.8 | 8.37 |
| 119624289 | hypothetical protein DKFZp779B1540 [Homo sapiens] | 2.33 | 3.37 | 1 | 1 | 1 | 1 | 652 | 71.9 | 8.47 |
| 34533442 | unnamed protein product [Homo sapiens] | 2.32 | 3.04 | 1 | 1 | 1 | 1 | 493 | 55.3 | 9.45 |
| 193806376 | RecName: Full=Tetratricopeptide repeat protein GNN; Short=TPR re | 2.32 | 0.83 | 1 | 1 | 1 | 1 | 1318 | 151.6 | 8.25 |
| 115305981 | unnamed protein product [Homo sapiens] | 2.31 | 13.73 | 12 | 1 | 1 | 1 | 153 | 16.5 | 7.75 |
| 223972627 | 3-oxoacyl-[acyl-carrier-protein] synthase, mitochondrial isoform 2 p | 2.31 | 4.79 | 4 | 1 | 1 | 2 | 376 | 40.0 | 7.88 |
| 119583325 | hCG2039004 [Homo sapiens] | 2.30 | 10.00 | 2 | 1 | 1 | 1 | 140 | 15.1 | 8.34 |
| 259596 | immunoglobulin VL region=humanized bispecific antibody [human, | 2.30 | 7.48 | 3 | 1 | 1 | 1 | 107 | 11.9 | 8.44 |
| 578823589 | PREDICTED: ras association domain-containing protein 3 isoform X1 | 2.30 | 7.02 | 2 | 1 | 1 | 1 | 228 | 26.3 | 7.78 |
| 114794318 | Chain B, Acidic Residues At The Active Sites Of Cd38 And Adp-Ribos | 2.29 | 7.63 | 2 | 1 | 1 | 1 | 262 | 30.2 | 6.62 |
| 40041958 | unnamed protein product [Homo sapiens] | 2.29 | 8.13 | 11 | 1 | 1 | 1 | 123 | 14.1 | 5.01 |
| 615276301 | nephrocystin-4 isoform b [Homo sapiens] | 2.29 | 2.41 | 10 | 1 | 1 | 1 | 913 | 100.9 | 8.16 |
| 50834176 | unnamed protein product [Homo sapiens] | 2.29 | 1.09 | 10 | 1 | 1 | 1 | 733 | 83.6 | 8.56 |
| 119589872 | hCG1814070, partial [Homo sapiens] | 2.28 | 16.06 | 1 | 1 | 1 | 1 | 137 | 15.1 | 11.94 |
| 119622336 | hCG1796123 [Homo sapiens] | 2.28 | 3.49 | 3 | 1 | 1 | 1 | 372 | 43.4 | 9.01 |
| 119628858 | katanin p60 subunit A-like 1, isoform CRA_a [Homo sapiens] | 2.27 | 2.65 | 3 | 1 | 1 | 1 | 490 | 55.4 | 6.74 |
| 119597419 | hCG2042174, partial [Homo sapiens] | 2.27 | 14.63 | 10 | 1 | 1 | 1 | 82 | 9.4 | 10.14 |
| 40039462 | unnamed protein product [Homo sapiens] | 2.27 | 10.20 | 11 | 1 | 1 | 1 | 147 | 16.4 | 3.95 |
| 530381706 | PREDICTED: NAD-dependent protein deacylase sirtuin-5, mitochond | 2.27 | 5.65 | 1 | 1 | 1 | 1 | 283 | 31.7 | 9.98 |
| 119611947 | receptor interacting protein kinase 5, isoform CRA_b [Homo sapiens | 2.27 | 5.10 | 10 | 1 | 1 | 1 | 255 | 29.2 | 6.24 |
| 304562429 | immunoglobulin gamma 2 heavy chain variable region [Homo sapie | 2.27 | 11.36 | 1 | 1 | 1 | 1 | 132 | 14.4 | 8.62 |
| 38197069 | PFKL protein, partial [Homo sapiens] | 2.27 | 2.26 | 12 | 1 | 1 | 1 | 486 | 53.6 | 8.32 |
| 111494163 | Mediator complex subunit 26 [Homo sapiens] | 2.26 | 2.00 | 4 | 1 | 1 | 1 | 600 | 65.4 | 9.09 |
| 62420306 | unknown [Homo sapiens] | 2.26 | 1.55 | 8 | 1 | 1 | 1 | 1291 | 145.1 | 8.24 |
| 41472460 | unknown [Homo sapiens] | 2.26 | 2.76 | 11 | 1 | 1 | 1 | 326 | 35.8 | 7.88 |
| 21740345 | hypothetical protein [Homo sapiens] | 2.26 | 9.28 | 11 | 1 | 1 | 1 | 237 | 26.2 | 6.52 |
| 37781128 | UEF3 [Homo sapiens] | 2.26 | 5.42 | 6 | 1 | 1 | 1 | 406 | 46.8 | 8.75 |
| 40041454 | unnamed protein product [Homo sapiens] | 2.25 | 6.43 | 6 | 1 | 1 | 1 | 140 | 15.3 | 10.24 |
| 119625039 | sorbin and SH3 domain containing 2, isoform CRA_d, partial [Homo | 2.25 | 22.37 | 1 | 1 | 1 | 1 | 76 | 8.3 | 7.25 |

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|---|---|---|---|---|---|---|---|---|---|---|
| 40030410 | unnamed protein product [Homo sapiens] | 2.25 | 9.94 | 6 | 1 | 1 | 1 | 171 | 19.4 | 6.55 |
| 119610509 | guanylate cyclase 2D, membrane (retina-specific) [Homo sapiens] | 2.25 | 1.04 | 4 | 1 | 1 | 1 | 862 | 93.4 | 7.52 |
| 145911175 | immunoglobulin heavy chain variable region [Homo sapiens] | 2.25 | 18.48 | 1 | 1 | 1 | 1 | 92 | 10.3 | 6.64 |
| 194386918 | unnamed protein product [Homo sapiens] | 2.25 | 4.35 | 1 | 1 | 1 | 1 | 230 | 26.5 | 10.39 |
| 40046890 | unnamed protein product [Homo sapiens] | 2.25 | 6.88 | 1 | 1 | 1 | 1 | 160 | 18.5 | 8.35 |
| 119571225 | hCG2042779 [Homo sapiens] | 2.25 | 16.18 | 1 | 1 | 1 | 1 | 136 | 15.0 | 6.25 |
| 519673328 | immunoglobulin A heavy chain variable region, partial [Homo sapie | 2.24 | 13.01 | 1 | 1 | 1 | 1 | 123 | 13.8 | 8.85 |
| 119620409 | AHA1, activator of heat shock 90kDa protein ATPase homolog 2 (ye | 2.24 | 14.29 | 3 | 1 | 1 | 1 | 112 | 12.5 | 9.35 |
| 20150918 | Chain A, Crystal Structure Of The N-Terminal Segment Of Human E | 2.24 | 6.04 | 3 | 1 | 1 | 1 | 182 | 21.2 | 7.34 |
| 18041762 | immunoglobulin kappa light chain variable region [Homo sapiens] | 2.24 | 17.39 | 2 | 1 | 1 | 1 | 92 | 10.1 | 8.47 |
| 33667089 | ligand-dependent nuclear receptor corepressor-like protein isoform | 2.24 | 6.60 | 2 | 1 | 1 | 1 | 318 | 35.4 | 5.10 |
| 296439575 | RecName: Full=Uncharacterized protein C11orf95 | 2.23 | 1.62 | 1 | 1 | 1 | 1 | 678 | 73.2 | 6.16 |
| 119614073 | hCG2009678 [Homo sapiens] | 2.23 | 13.59 | 1 | 1 | 1 | 1 | 103 | 12.5 | 10.33 |
| 40981068 | unnamed protein product [Homo sapiens] | 2.23 | 22.22 | 1 | 1 | 1 | 1 | 72 | 8.1 | 5.29 |
| 390136348 | Chain H, Structure Of Dengue Virus Diii In Complex With Fab 2h12 | 2.23 | 12.90 | 1 | 1 | 1 | 1 | 217 | 23.0 | 6.74 |
| 115430239 | spectrin beta chain, non-erythrocytic 4 isoform sigma5 [Homo sapie | 2.23 | 2.06 | 9 | 1 | 1 | 1 | 678 | 77.1 | 5.35 |
| 16549375 | unnamed protein product [Homo sapiens] | 2.23 | 7.14 | 1 | 1 | 1 | 1 | 168 | 18.9 | 12.31 |
| 119577179 | hCG2041100, partial [Homo sapiens] | 2.22 | 22.95 | 1 | 1 | 1 | 1 | 61 | 6.5 | 6.92 |
| 401015111 | tumor necrosis factor receptor superfamily member 11A isoform 2 p | 2.22 | 5.70 | 10 | 1 | 1 | 1 | 263 | 28.9 | 8.24 |
| 39645003 | AKR7A2 protein, partial [Homo sapiens] | 2.22 | 4.19 | 3 | 1 | 1 | 1 | 358 | 39.4 | 7.17 |
| 348204 | immunoglobulin light-chain V-J region, partial [Homo sapiens] | 2.22 | 16.51 | 1 | 1 | 1 | 1 | 109 | 11.7 | 8.94 |
| 296179386 | clathrin light chain A isoform e [Homo sapiens] | 2.22 | 5.95 | 6 | 1 | 1 | 1 | 168 | 18.1 | 4.44 |
| 16554278 | unnamed protein product [Homo sapiens] | 2.22 | 4.85 | 7 | 1 | 1 | 1 | 206 | 24.0 | 8.81 |
| 2232013 | zinc finger protein [Homo sapiens] | 2.22 | 1.90 | 1 | 1 | 1 | 1 | 474 | 54.4 | 8.34 |
| 163931089 | Chain B, Ap2 Clathrin Adaptor Core | 2.22 | 3.55 | 15 | 1 | 1 | 1 | 591 | 66.8 | 5.31 |
| 40040316 | unnamed protein product [Homo sapiens] | 2.21 | 14.29 | 5 | 1 | 1 | 1 | 91 | 10.6 | 10.15 |
| 530427583 | PREDICTED: protein FAM27D1-like [Homo sapiens] | 2.21 | 7.59 | 1 | 1 | 1 | 1 | 237 | 26.5 | 11.11 |
| 211828173 | VPS37D protein [Homo sapiens] | 2.21 | 7.56 | 3 | 1 | 1 | 1 | 238 | 26.3 | 8.48 |
| 119609155 | COP9 constitutive photomorphogenic homolog subunit 7A (Arabidop | 2.21 | 8.66 | 5 | 1 | 1 | 1 | 127 | 13.7 | 9.28 |
| 14549677 | immunoglobulin heavy chain variable region, partial [Homo sapiens] | 2.21 | 12.30 | 1 | 1 | 1 | 1 | 122 | 13.1 | 9.10 |
| 39938062 | immunoglobulin heavy chain variable region [Homo sapiens] | 2.21 | 10.74 | 1 | 1 | 1 | 1 | 149 | 16.2 | 8.95 |
| 21756038 | unnamed protein product [Homo sapiens] | 2.21 | 7.07 | 5 | 1 | 1 | 1 | 184 | 19.9 | 6.60 |
| 119623105 | testis expressed sequence 13B [Homo sapiens] | 2.20 | 6.41 | 1 | 1 | 1 | 1 | 312 | 33.9 | 6.18 |
| 74745319 | RecName: Full=Keratinocyte proline-rich protein; Short=hKPRP | 2.20 | 2.07 | 1 | 1 | 1 | 1 | 579 | 64.1 | 8.27 |
| 40039256 | unnamed protein product [Homo sapiens] | 2.20 | 14.58 | 3 | 1 | 1 | 1 | 96 | 9.5 | 9.25 |
| 119570637 | hCG1818005, isoform CRA_b, partial [Homo sapiens] | 2.20 | 17.72 | 2 | 1 | 1 | 1 | 79 | 8.8 | 5.39 |
| 530395950 | PREDICTED: MAP kinase-activating death domain protein isoform X | 2.20 | 0.97 | 36 | 1 | 1 | 1 | 1231 | 136.1 | 6.10 |
| 119630989 | nucleolar protein 5A (56kDa with KKE/D repeat), isoform CRA_a [Ho | 2.20 | 1.22 | 1 | 1 | 1 | 1 | 654 | 72.7 | 9.41 |
| 2258128 | complement 9 [Homo sapiens] | 2.20 | 3.94 | 4 | 1 | 1 | 1 | 533 | 60.4 | 5.59 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 119626983 | hCG2041610, partial [Homo sapiens] | 2.20 | 14.29 | 1 | 1 | 1 | 1 | 84 | 9.4 | 9.35 |
| 6453436 | hypothetical protein [Homo sapiens] | 2.20 | 0.68 | 8 | 1 | 1 | 1 | 1908 | 208.2 | 6.23 |
| 119615746 | SFT2 domain containing 3, isoform CRA_a [Homo sapiens] | 2.19 | 9.30 | 3 | 1 | 1 | 1 | 215 | 21.8 | 9.89 |
| 308153674 | RecName: Full=Zinc finger and BTB domain-containing protein 34 | 2.19 | 3.00 | 4 | 1 | 1 | 1 | 500 | 55.5 | 6.44 |
| 40033114 | unnamed protein product [Homo sapiens] | 2.19 | 5.86 | 1 | 1 | 1 | 1 | 222 | 24.7 | 9.16 |
| 119608588 | potassium channel, subfamily T, member 1, isoform CRA_f, partial [ | 2.19 | 1.49 | 13 | 1 | 1 | 1 | 1005 | 113.0 | 7.30 |
| 55670733 | Chain A, Crystal Structure Of Human Trp14 | 2.19 | 9.76 | 1 | 1 | 1 | 1 | 123 | 13.9 | 5.52 |
| 119627432 | hypothetical LOC339541, isoform CRA_b [Homo sapiens] | 2.19 | 6.19 | 6 | 1 | 1 | 1 | 307 | 33.9 | 6.92 |
| 530421172 | PREDICTED: phosphorylase b kinase regulatory subunit alpha, liver | 2.19 | 0.58 | 6 | 1 | 1 | 1 | 1207 | 135.4 | 6.38 |
| 21753693 | unnamed protein product [Homo sapiens] | 2.18 | 5.16 | 3 | 1 | 1 | 1 | 349 | 38.4 | 7.42 |
| 37182623 | MMP27 [Homo sapiens] | 2.18 | 2.53 | 1 | 1 | 1 | 1 | 513 | 59.0 | 8.87 |
| 20530135 | growth differentiation factor 3A [Homo sapiens] | 2.18 | 5.79 | 3 | 1 | 1 | 1 | 363 | 41.4 | 8.21 |
| 40043478 | unnamed protein product [Homo sapiens] | 2.18 | 10.67 | 10 | 1 | 1 | 1 | 150 | 17.6 | 5.48 |
| 70913399 | T cell receptor alpha variable 7 [Homo sapiens] | 2.18 | 100.00 | 1 | 1 | 1 | 1 | 17 | 2.0 | 8.63 |
| 209402728 | epididymis luminal protein 123 [Homo sapiens] | 2.18 | 1.56 | 1 | 1 | 1 | 1 | 1026 | 110.3 | 9.06 |
| 119572848 | transient receptor potential cation channel, subfamily M, member 4, | 2.18 | 4.38 | 1 | 1 | 1 | 1 | 160 | 17.5 | 8.09 |
| 578845789 | PREDICTED: COMM domain-containing protein 4-like [Homo sapiens | 2.18 | 8.00 | 1 | 1 | 1 | 1 | 175 | 19.2 | 9.58 |
| 68161840 | hypothetical protein [Homo sapiens] | 2.18 | 5.06 | 6 | 1 | 1 | 1 | 237 | 25.7 | 8.27 |
| 119577337 | hypothetical BC331191_1, isoform CRA_b [Homo sapiens] | 2.17 | 10.47 | 1 | 1 | 1 | 1 | 86 | 10.3 | 5.12 |
| 1800287 | anti-HIV-1 gp120 V3 loop antibody DO142-10 light chain variable re | 2.17 | 14.78 | 1 | 1 | 1 | 1 | 115 | 12.7 | 7.94 |
| 119574344 | ankyrin repeat domain 30B, partial [Homo sapiens] | 2.17 | 0.85 | 3 | 1 | 1 | 1 | 826 | 91.9 | 6.15 |
| 21748490 | FLJ00278 protein [Homo sapiens] | 2.17 | 10.80 | 1 | 1 | 1 | 1 | 176 | 19.8 | 10.48 |
| 119582059 | hCG1980758, partial [Homo sapiens] | 2.17 | 6.18 | 1 | 1 | 1 | 1 | 275 | 29.7 | 7.52 |
| 110832790 | RecName: Full=Centromere protein L; Short=CENP-L; AltName: Full | 2.17 | 3.49 | 1 | 1 | 1 | 1 | 344 | 39.0 | 6.52 |
| 160285841 | Chain B, Ephb2SNEW ANTAGONISTIC PEPTIDE COMPLEX | 2.17 | 10.10 | 15 | 1 | 1 | 1 | 208 | 23.6 | 6.84 |
| 262118589 | Chain A, Crystal Structure Of Hnf4a Lbd In Complex With The Ligan | 2.17 | 5.65 | 22 | 1 | 1 | 1 | 230 | 25.9 | 5.21 |
| 40046942 | unnamed protein product [Homo sapiens] | 2.17 | 8.06 | 8 | 1 | 1 | 1 | 124 | 13.8 | 6.76 |
| 221043596 | unnamed protein product [Homo sapiens] | 2.17 | 9.72 | 4 | 1 | 1 | 1 | 144 | 16.4 | 8.19 |
| 221045894 | unnamed protein product [Homo sapiens] | 2.17 | 8.06 | 5 | 1 | 1 | 1 | 186 | 21.1 | 10.13 |
| 25990364 | P-glycoprotein [Homo sapiens] | 2.16 | 1.03 | 9 | 1 | 1 | 1 | 681 | 75.3 | 8.48 |
| 119625706 | zinc finger, MYM-type 3, isoform CRA_a [Homo sapiens] | 2.16 | 0.66 | 3 | 1 | 1 | 1 | 1358 | 151.0 | 6.35 |
| 194381686 | unnamed protein product [Homo sapiens] | 2.16 | 1.57 | 5 | 1 | 1 | 1 | 446 | 50.4 | 6.25 |
| 193785455 | unnamed protein product [Homo sapiens] | 2.16 | 2.80 | 1 | 1 | 1 | 1 | 572 | 66.6 | 9.44 |
| 62630129 | unknown [Homo sapiens] | 2.16 | 1.90 | 6 | 1 | 1 | 1 | 579 | 67.5 | 8.38 |
| 194381590 | unnamed protein product [Homo sapiens] | 2.16 | 3.75 | 15 | 1 | 1 | 1 | 293 | 32.8 | 5.72 |
| 177926 | nicotinic receptor alpha 5 subunit [Homo sapiens] | 2.16 | 3.63 | 3 | 1 | 1 | 1 | 468 | 53.3 | 7.72 |
| 3600098 | aconitase precursor [Homo sapiens] | 2.16 | 2.33 | 1 | 1 | 1 | 1 | 600 | 65.3 | 7.84 |
| 194384004 | unnamed protein product [Homo sapiens] | 2.16 | 6.02 | 6 | 1 | 1 | 1 | 266 | 29.9 | 4.88 |
| 158431483 | Chain B, Human Ubiquitin-Conjugating Enzyme E2 H | 2.16 | 5.59 | 1 | 1 | 1 | 1 | 179 | 20.2 | 6.43 |

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|---|---|---|---|---|---|---|---|---|---|---|
| 119587093 | zinc finger protein 276, isoform CRA_c [Homo sapiens] | 2.15 | 2.68 | 13 | 1 | 1 | 1 | 373 | 41.8 | 8.24 |
| 51850711 | unnamed protein product [Homo sapiens] | 2.15 | 2.00 | 2 | 1 | 1 | 1 | 701 | 78.1 | 6.16 |
| 28799163 | unnamed protein product [Homo sapiens] | 2.15 | 9.25 | 5 | 1 | 1 | 1 | 173 | 19.6 | 6.84 |
| 33341718 | PP10513 [Homo sapiens] | 2.15 | 19.80 | 1 | 1 | 1 | 1 | 101 | 10.9 | 10.43 |
| 22652550 | pyrin-domain containing protein [Homo sapiens] | 2.15 | 11.24 | 2 | 1 | 1 | 1 | 89 | 10.0 | 8.44 |
| 47076986 | unnamed protein product [Homo sapiens] | 2.15 | 4.76 | 1 | 1 | 1 | 1 | 357 | 38.9 | 5.94 |
| 115528754 | ACAD11 protein [Homo sapiens] | 2.15 | 4.59 | 1 | 1 | 1 | 1 | 305 | 33.8 | 9.06 |
| 578817416 | PREDICTED: alpha-N-acetylgalactosaminide alpha-2,6-sialyltransfera | 2.15 | 6.47 | 3 | 1 | 1 | 1 | 340 | 37.0 | 10.29 |
| 119614841 | hCG1642624, isoform CRA_a [Homo sapiens] | 2.15 | 5.00 | 2 | 1 | 1 | 1 | 340 | 39.1 | 5.86 |
| 29334005 | unnamed protein product [Homo sapiens] | 2.15 | 0.51 | 1 | 1 | 1 | 1 | 2334 | 258.2 | 6.60 |
| 530427222 | PREDICTED: nuclear pore complex protein Nup214 isoform X3 [Hom | 2.14 | 0.43 | 1 | 1 | 1 | 1 | 2083 | 213.2 | 8.10 |
| 558026207 | MHC class I antigen, partial [Homo sapiens] | 2.14 | 15.28 | 1 | 1 | 1 | 1 | 72 | 8.4 | 4.81 |
| 49259285 | Chain R, Structure Of The Human Mcad:etf Complex | 2.14 | 2.10 | 1 | 1 | 1 | 1 | 333 | 35.1 | 8.38 |
| 119630076 | hCG1812836, isoform CRA_b, partial [Homo sapiens] | 2.14 | 8.40 | 1 | 1 | 1 | 1 | 131 | 14.5 | 10.84 |
| 1154674 | MHC type I antigen [Homo sapiens] | 2.14 | 6.08 | 4 | 1 | 1 | 1 | 181 | 21.0 | 5.67 |
| 4884138 | hypothetical protein [Homo sapiens] | 2.14 | 2.54 | 13 | 1 | 1 | 1 | 394 | 43.7 | 8.81 |
| 194386786 | unnamed protein product [Homo sapiens] | 2.14 | 8.06 | 4 | 1 | 1 | 1 | 186 | 21.0 | 9.79 |
| 530407730 | PREDICTED: protein disulfide-isomerase-like protein of the testis isc | 2.14 | 6.17 | 3 | 1 | 1 | 1 | 308 | 34.7 | 6.46 |
| 530396754 | PREDICTED: dnaJ homolog subfamily B member 13 isoform X2 [Hoi | 2.14 | 4.58 | 3 | 1 | 1 | 1 | 262 | 30.1 | 8.21 |
| 78101144 | Chain B, Crystal Structure Of The Catalytic Domain Of An Adenosine | 2.14 | 3.97 | 17 | 1 | 1 | 1 | 403 | 44.9 | 9.31 |
| 119585962 | hCG1989330 [Homo sapiens] | 2.14 | 7.41 | 1 | 1 | 1 | 1 | 162 | 16.6 | 8.65 |
| 45708762 | MIA2 protein, partial [Homo sapiens] | 2.14 | 3.00 | 1 | 1 | 1 | 1 | 434 | 48.9 | 4.45 |
| 119594460 | chromosome 11 open reading frame 48, isoform CRA_c [Homo sapi | 2.13 | 10.57 | 2 | 1 | 1 | 1 | 123 | 14.2 | 11.53 |
| 530376869 | PREDICTED: homeodomain-only protein isoform X1 [Homo sapiens] | 2.13 | 16.22 | 2 | 1 | 1 | 1 | 111 | 12.2 | 7.30 |
| 119615575 | transmembrane protein 50A, isoform CRA_b [Homo sapiens] | 2.13 | 12.86 | 1 | 1 | 1 | 1 | 140 | 15.3 | 6.27 |
| 904790 | unnamed protein product [Homo sapiens] | 2.13 | 13.04 | 2 | 1 | 1 | 1 | 115 | 13.3 | 8.41 |
| 194378596 | unnamed protein product [Homo sapiens] | 2.13 | 2.96 | 3 | 1 | 1 | 1 | 676 | 72.1 | 6.29 |
| 3421130 | E6-AP ubiquitin-protein ligase [Homo sapiens] | 2.13 | 13.24 | 9 | 1 | 1 | 1 | 68 | 7.8 | 6.51 |
| 193786774 | unnamed protein product [Homo sapiens] | 2.13 | 1.90 | 13 | 1 | 1 | 1 | 630 | 73.2 | 6.06 |
| 159164351 | Chain A, Solution Structure Of The Ch Domain From Human Mical-2 | 2.13 | 15.70 | 14 | 1 | 1 | 1 | 121 | 13.6 | 5.03 |
| 119576935 | Mov10, Moloney leukemia virus 10, homolog (mouse), isoform CRA_ | 2.13 | 3.39 | 10 | 1 | 1 | 1 | 561 | 63.8 | 8.51 |
| 371446035 | immunoglobulin G heavy chain variable region, partial [Homo sapier | 2.13 | 11.54 | 1 | 1 | 1 | 1 | 130 | 14.5 | 7.91 |
| 119580349 | ring finger protein 185, isoform CRA_c, partial [Homo sapiens] | 2.13 | 16.52 | 1 | 1 | 1 | 1 | 115 | 12.9 | 9.70 |
| 11177516 | tandem pore domain potassium channel THIK-1 [Homo sapiens] | 2.13 | 3.68 | 2 | 1 | 1 | 1 | 408 | 45.4 | 8.25 |
| 48476355 | rhabdomyosarcoma antigen MU-RMS-40.22 [Homo sapiens] | 2.13 | 7.14 | 7 | 1 | 1 | 1 | 154 | 17.2 | 9.79 |
| 10438914 | unnamed protein product [Homo sapiens] | 2.13 | 3.11 | 3 | 1 | 1 | 1 | 322 | 35.0 | 4.88 |
| 119605525 | hCG1654197 [Homo sapiens] | 2.13 | 6.70 | 3 | 1 | 1 | 1 | 224 | 24.5 | 8.84 |
| 578817973 | PREDICTED: E3 ubiquitin-protein ligase LRSAM1 isoform X2 [Homo | 2.13 | 1.16 | 6 | 1 | 1 | 1 | 690 | 79.5 | 5.85 |
| 194378362 | unnamed protein product [Homo sapiens] | 2.13 | 4.05 | 4 | 1 | 1 | 1 | 222 | 24.6 | 8.44 |

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|---|---|---|---|---|---|---|---|---|---|---|---|
| 119622131 | clusterin-like 1 (retinal), isoform CRA_c [Homo sapiens] | 2.12 | 4.51 | 7 | 1 | 1 | 1 | 288 | 33.9 | 5.01 |
| 119593997 | polymerase (RNA) I polypeptide B, 128kDa, isoform CRA_b [Homo s | 2.12 | 1.33 | 10 | 1 | 1 | 1 | 824 | 93.5 | 7.44 |
| 259016156 | RecName: Full=THO complex subunit 5 homolog; AltName: Full=Fu | 2.12 | 2.20 | 6 | 1 | 1 | 1 | 683 | 78.5 | 6.87 |
| 442565693 | otopetrin-3 isoform 2 [Homo sapiens] | 2.12 | 2.08 | 5 | 1 | 1 | 1 | 578 | 64.4 | 7.97 |
| 40976374 | unnamed protein product [Homo sapiens] | 2.12 | 25.00 | 7 | 1 | 1 | 1 | 88 | 9.9 | 5.10 |
| 197692625 | methyl-CpG binding domain protein 3-like [Homo sapiens] | 2.12 | 5.67 | 2 | 1 | 1 | 1 | 194 | 21.5 | 7.94 |
| 896476 | hormone-sensitive lipase [Homo sapiens] | 2.12 | 2.97 | 10 | 1 | 1 | 1 | 775 | 84.1 | 6.71 |
| 28800915 | unnamed protein product [Homo sapiens] | 2.12 | 2.02 | 1 | 1 | 1 | 1 | 939 | 103.4 | 7.61 |
| 119609635 | ATP synthase, H+ transporting, mitochondrial F0 complex, subunit | 2.12 | 8.76 | 1 | 1 | 1 | 1 | 137 | 15.8 | 7.18 |
| 444738547 | alternative protein SPRY1 [Homo sapiens] | 2.12 | 25.00 | 1 | 1 | 1 | 1 | 52 | 5.7 | 9.47 |
| 221045258 | unnamed protein product [Homo sapiens] | 2.12 | 4.46 | 6 | 1 | 1 | 1 | 224 | 24.0 | 10.87 |
| 21757857 | unnamed protein product [Homo sapiens] | 2.12 | 7.49 | 5 | 1 | 1 | 1 | 334 | 37.8 | 9.03 |
| 119574444 | ATP-binding cassette, sub-family B (MDR/TAP), member 8, isoform | 2.12 | 11.05 | 12 | 1 | 1 | 1 | 190 | 20.7 | 6.89 |
| 189053760 | unnamed protein product [Homo sapiens] | 2.12 | 3.75 | 5 | 1 | 1 | 1 | 427 | 48.5 | 7.75 |
| 550029 | methylmalonyl CoA mutase, MCM {EC 5.4.99.2} [human, mut- meth | 2.11 | 5.47 | 2 | 1 | 1 | 1 | 274 | 29.6 | 6.55 |
| 315488052 | immunoglobulin variable region [Homo sapiens] | 2.11 | 11.81 | 1 | 1 | 1 | 1 | 127 | 13.8 | 5.33 |
| 408773052 | truncated breast and ovarian cancer susceptibility protein 2, partial | 2.11 | 52.00 | 1 | 1 | 1 | 1 | 25 | 3.0 | 4.72 |
| 578820330 | PREDICTED: cyclic nucleotide-gated cation channel alpha-4 isoform | 2.11 | 3.55 | 3 | 1 | 1 | 1 | 535 | 61.4 | 5.45 |
| 6114718 | T cell receptor beta chain variable region [Homo sapiens] | 2.11 | 16.90 | 1 | 1 | 1 | 1 | 71 | 7.6 | 7.34 |
| 440575999 | alternative protein SETD1A [Homo sapiens] | 2.11 | 4.41 | 1 | 1 | 1 | 1 | 340 | 39.1 | 12.23 |
| 6254142 | chondromodulin-I [Homo sapiens] | 2.11 | 12.50 | 5 | 1 | 1 | 1 | 120 | 13.7 | 7.91 |
| 15293621 | olfactory receptor [Homo sapiens] | 2.11 | 5.09 | 8 | 1 | 1 | 1 | 216 | 24.5 | 8.51 |
| 119601012 | hCG2026668, partial [Homo sapiens] | 2.10 | 24.53 | 1 | 1 | 1 | 1 | 53 | 6.3 | 5.97 |
| 358248275 | Bardet-Biedl syndrome 4 protein isoform 2 [Homo sapiens] | 2.10 | 6.05 | 12 | 1 | 1 | 1 | 347 | 38.3 | 6.87 |
| 24430155 | 26S protease regulatory subunit 6B isoform 2 [Homo sapiens] | 2.10 | 5.43 | 4 | 1 | 1 | 1 | 387 | 43.5 | 5.26 |
| 578807499 | PREDICTED: DNA-directed RNA polymerases I, II, and III subunit R | 2.10 | 12.95 | 2 | 1 | 1 | 1 | 139 | 15.6 | 4.56 |
| 254575045 | Chain A, Crystal Structure Of Human Mocs3 Rhodanese-Like Domai | 2.10 | 5.51 | 2 | 1 | 1 | 1 | 127 | 14.1 | 6.93 |
| 34535952 | unnamed protein product [Homo sapiens] | 2.10 | 7.69 | 1 | 1 | 1 | 1 | 143 | 16.0 | 9.57 |
| 40043704 | unnamed protein product [Homo sapiens] | 2.10 | 8.33 | 4 | 1 | 1 | 1 | 120 | 14.4 | 4.84 |
| 224808238 | B cell antibody heavy chain variable region, partial [Homo sapiens] | 2.10 | 16.80 | 1 | 1 | 1 | 1 | 125 | 13.6 | 9.20 |
| 119569966 | hCG1781035, partial [Homo sapiens] | 2.10 | 8.91 | 1 | 1 | 1 | 1 | 101 | 11.0 | 8.60 |
| 197304953 | Chain B, Dj-1 Activation By Catechol Quinone Modification | 2.10 | 8.02 | 24 | 1 | 1 | 1 | 187 | 19.6 | 7.33 |
| 530395980 | PREDICTED: serine/threonine-protein kinase BRSK2 isoform X3 [Ho | 2.09 | 3.53 | 8 | 1 | 1 | 1 | 453 | 49.5 | 9.33 |
| 119623752 | general transcription factor IIH, polypeptide 4, 52kDa [Homo sapien | 2.09 | 4.98 | 3 | 1 | 1 | 1 | 462 | 52.2 | 9.04 |
| 194387930 | unnamed protein product [Homo sapiens] | 2.09 | 4.46 | 5 | 1 | 1 | 1 | 314 | 36.8 | 8.79 |
| 194374039 | unnamed protein product [Homo sapiens] | 2.09 | 3.08 | 11 | 1 | 1 | 1 | 260 | 30.6 | 9.06 |
| 122892272 | immunoglobulin heavy chain variable region [Homo sapiens] | 2.09 | 13.95 | 1 | 1 | 1 | 1 | 129 | 14.3 | 7.96 |
| 10438861 | unnamed protein product [Homo sapiens] | 2.09 | 1.96 | 6 | 1 | 1 | 1 | 917 | 102.7 | 6.76 |
| 205689966 | RecName: Full=Putative cathepsin L-like protein 6 | 2.09 | 6.86 | 2 | 1 | 1 | 1 | 277 | 30.9 | 6.15 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 47057390 | unnamed protein product [Homo sapiens] | 2.09 | 5.44 | 1 | 1 | 1 | 1 | 239 | 26.1 | 7.72 |
| 29611624 | G protein-coupled receptor PGR23 [Homo sapiens] | 2.09 | 4.79 | 1 | 1 | 1 | 1 | 146 | 16.0 | 8.72 |
| 353251640 | Chain H, Orientation Of Rna Polymerase Ii Within The Human Vp16- | 2.08 | 8.22 | 1 | 1 | 1 | 1 | 146 | 16.5 | 4.70 |
| 119572729 | KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention rec | 2.08 | 11.11 | 5 | 1 | 1 | 1 | 153 | 17.5 | 7.90 |
| 145580569 | Chain B, Human Bir3 Domain Of Baculoviral Inhibitor Of Apoptosis R | 2.08 | 18.75 | 5 | 1 | 1 | 1 | 96 | 11.1 | 7.72 |
| 10636660 | immunoglobulin heavy chain variable region [Homo sapiens] | 2.08 | 11.96 | 2 | 1 | 1 | 1 | 92 | 10.3 | 10.15 |
| 18676712 | FLJ00255 protein [Homo sapiens] | 2.08 | 2.59 | 20 | 1 | 1 | 1 | 733 | 80.8 | 7.03 |
| 14583147 | Kelch-like protein 1 [Homo sapiens] | 2.08 | 1.20 | 4 | 1 | 1 | 1 | 582 | 65.0 | 6.04 |
| 119594502 | TAF6-like RNA polymerase II, p300/CBP-associated factor (PCAF)-as | 2.08 | 2.16 | 4 | 1 | 1 | 1 | 509 | 54.7 | 9.28 |
| 119610369 | elaC homolog 2 (E. coli), isoform CRA_c [Homo sapiens] | 2.08 | 4.19 | 11 | 1 | 1 | 1 | 501 | 56.1 | 7.43 |
| 49457368 | TBCA [Homo sapiens] | 2.08 | 16.67 | 2 | 1 | 1 | 1 | 108 | 12.8 | 5.29 |
| 545746392 | serine-rich coiled-coil domain-containing protein 2 isoform 3 [Homo | 2.08 | 2.47 | 7 | 1 | 1 | 1 | 567 | 62.7 | 6.86 |
| 119608560 | chromosome 9 open reading frame 116, isoform CRA_a, partial [Hor | 2.08 | 25.97 | 1 | 1 | 1 | 1 | 77 | 8.4 | 11.14 |
| 298508744 | Chain A, Crystal Structure Of Human Mitochondrial Mterf Fragment | 2.08 | 3.23 | 9 | 1 | 1 | 1 | 310 | 35.6 | 9.28 |
| 119628607 | hCG18126, isoform CRA_b [Homo sapiens] | 2.08 | 0.86 | 2 | 1 | 1 | 1 | 816 | 88.9 | 8.43 |
| 3169156 | BC269730_4 [Homo sapiens] | 2.08 | 2.07 | 17 | 1 | 1 | 1 | 482 | 53.5 | 8.94 |
| 40044704 | unnamed protein product [Homo sapiens] | 2.08 | 24.19 | 5 | 1 | 1 | 1 | 62 | 7.1 | 7.30 |
| 10434865 | unnamed protein product [Homo sapiens] | 2.08 | 8.96 | 3 | 1 | 1 | 1 | 212 | 24.4 | 7.39 |
| 119630255 | hCG2040581, partial [Homo sapiens] | 2.08 | 6.70 | 1 | 1 | 1 | 1 | 179 | 19.5 | 9.54 |
| 529481788 | Chain C, Human Vps33a In Complex With A Fragment Of Human Vp | 2.07 | 15.15 | 12 | 1 | 1 | 1 | 99 | 11.3 | 8.56 |
| 40044046 | unnamed protein product [Homo sapiens] | 2.07 | 18.18 | 3 | 1 | 1 | 1 | 110 | 12.1 | 8.78 |
| 20380408 | INTS5 protein [Homo sapiens] | 2.07 | 1.56 | 3 | 1 | 1 | 1 | 833 | 88.4 | 7.25 |
| 6841220 | HSPC285 [Homo sapiens] | 2.07 | 10.38 | 3 | 1 | 1 | 1 | 212 | 22.1 | 5.58 |
| 38493111 | Chain H, Structure Of A Complex Of The Golgin-245 Grip Domain W | 2.07 | 21.67 | 1 | 1 | 1 | 1 | 60 | 7.1 | 6.70 |
| 51094831 | plexin A4 [Homo sapiens] | 2.07 | 1.18 | 4 | 1 | 1 | 1 | 850 | 93.6 | 6.93 |
| 41472389 | unknown [Homo sapiens] | 2.07 | 9.23 | 9 | 1 | 1 | 1 | 195 | 22.6 | 6.96 |
| 62822422 | unknown [Homo sapiens] | 2.07 | 7.25 | 2 | 1 | 1 | 1 | 193 | 21.6 | 8.50 |
| 194385444 | unnamed protein product [Homo sapiens] | 2.07 | 3.11 | 1 | 1 | 1 | 1 | 450 | 51.2 | 8.27 |
| 7019867 | unnamed protein product [Homo sapiens] | 2.07 | 4.60 | 7 | 1 | 1 | 1 | 391 | 44.7 | 6.67 |
| 15825656 | Chain A, Crystal Structure Of Fibroblast Growth Factor 4 (fgf4) | 2.07 | 7.81 | 1 | 1 | 1 | 1 | 128 | 14.2 | 9.89 |
| 16550798 | unnamed protein product [Homo sapiens] | 2.07 | 2.91 | 7 | 1 | 1 | 1 | 412 | 46.9 | 9.52 |
| 119628022 | hCG1787699 [Homo sapiens] | 2.07 | 7.86 | 2 | 1 | 1 | 1 | 140 | 15.4 | 5.67 |
| 194379176 | unnamed protein product [Homo sapiens] | 2.07 | 5.24 | 6 | 1 | 1 | 1 | 191 | 21.6 | 7.97 |
| 119601859 | KIAA2010, isoform CRA_b [Homo sapiens] | 2.07 | 3.78 | 2 | 1 | 1 | 1 | 556 | 63.5 | 4.82 |
| 194353946 | homeobox protein Hox-D12 [Homo sapiens] | 2.07 | 2.59 | 2 | 1 | 1 | 1 | 270 | 29.0 | 9.80 |
| 189083866 | bile acid-CoA:amino acid N-acyltransferase [Homo sapiens] | 2.06 | 4.78 | 1 | 1 | 1 | 1 | 418 | 46.3 | 6.99 |
| 119604418 | zinc finger protein 317, isoform CRA_c [Homo sapiens] | 2.06 | 2.39 | 12 | 1 | 1 | 1 | 419 | 48.4 | 9.73 |
| 62088436 | p21-activated kinase 2 variant [Homo sapiens] | 2.06 | 5.02 | 9 | 1 | 1 | 1 | 279 | 31.1 | 7.71 |
| 119567882 | hCG2029440, partial [Homo sapiens] | 2.06 | 12.06 | 1 | 1 | 1 | 1 | 141 | 15.8 | 7.88 |

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|---|---|---|---|---|---|---|---|---|---|---|
| 388778229 | immunoglobulin heavy chain variable region, partial [Homo sapiens] | 2.06 | 20.39 | 1 | 1 | 1 | 1 | 103 | 11.3 | 6.51 |
| 119623206 | hCG18775, isoform CRA_b, partial [Homo sapiens] | 2.06 | 3.85 | 1 | 1 | 1 | 1 | 441 | 51.0 | 6.74 |
| 194387728 | unnamed protein product [Homo sapiens] | 2.06 | 3.83 | 1 | 1 | 1 | 1 | 392 | 43.1 | 5.43 |
| 2654431 | type XII collagen, partial [Homo sapiens] | 2.06 | 3.87 | 6 | 1 | 1 | 1 | 517 | 56.7 | 5.03 |
| 239582759 | equatorin isoform 2 precursor [Homo sapiens] | 2.06 | 6.42 | 5 | 1 | 1 | 1 | 265 | 29.5 | 4.98 |
| 194381176 | unnamed protein product [Homo sapiens] | 2.06 | 1.69 | 3 | 1 | 1 | 1 | 415 | 45.0 | 6.14 |
| 40046834 | unnamed protein product [Homo sapiens] | 2.06 | 7.41 | 5 | 1 | 1 | 1 | 108 | 12.7 | 9.50 |
| 119604088 | hypothetical protein DKFZp434G156, isoform CRA_b [Homo sapiens | 2.06 | 2.30 | 17 | 1 | 1 | 1 | 434 | 49.4 | 4.40 |
| 84798094 | immunoglobulin light chain variable region EV3-4-LC-5 [Homo sapie | 2.06 | 14.81 | 1 | 1 | 1 | 1 | 108 | 11.6 | 7.39 |
| 2340097 | 60% similarity to Z49912 (PID:g872093), match to Z41881 (NID:g5 | 2.06 | 5.43 | 8 | 1 | 1 | 1 | 184 | 21.2 | 9.45 |
| 530429173 | PREDICTED: death domain-associated protein 6 isoform X3 [Homo s | 2.06 | 4.57 | 1 | 1 | 1 | 1 | 372 | 40.1 | 4.32 |
| 229892345 | zinc finger protein GLI1 isoform 2 [Homo sapiens] | 2.06 | 1.94 | 6 | 1 | 1 | 1 | 978 | 104.6 | 7.12 |
| 68566217 | RecName: Full=Protein tyrosine phosphatase type IVA 1; AltName: | 2.06 | 8.67 | 1 | 1 | 1 | 1 | 173 | 19.8 | 8.97 |
| 194379382 | unnamed protein product [Homo sapiens] | 2.06 | 1.86 | 1 | 1 | 1 | 1 | 751 | 82.1 | 8.63 |
| 27753165 | immunoglobulin heavy chain variable region [Homo sapiens] | 2.06 | 7.25 | 1 | 1 | 1 | 1 | 138 | 14.9 | 8.62 |
| 62630195 | unknown [Homo sapiens] | 2.05 | 8.44 | 2 | 1 | 1 | 1 | 154 | 16.5 | 5.24 |
| 21757047 | unnamed protein product [Homo sapiens] | 2.05 | 13.39 | 2 | 1 | 1 | 1 | 127 | 13.6 | 8.54 |
| 51094855 | family with sequence similarity 40, member B [Homo sapiens] | 2.05 | 2.24 | 1 | 1 | 1 | 1 | 893 | 101.7 | 6.04 |
| 40043190 | unnamed protein product [Homo sapiens] | 2.05 | 8.24 | 11 | 1 | 1 | 1 | 85 | 8.8 | 10.80 |
| 119629117 | hCG2020499, partial [Homo sapiens] | 2.05 | 14.89 | 1 | 1 | 1 | 1 | 94 | 10.2 | 9.88 |
| 194378580 | unnamed protein product [Homo sapiens] | 2.05 | 3.46 | 5 | 1 | 1 | 1 | 376 | 42.6 | 5.45 |
| 182676484 | RecName: Full=Putative proline dehydrogenase-like protein | 2.05 | 9.68 | 18 | 1 | 1 | 1 | 186 | 21.1 | 8.12 |
| 530391245 | PREDICTED: SHC-transforming protein 3 isoform X1 [Homo sapiens | 2.05 | 3.35 | 1 | 1 | 1 | 1 | 448 | 49.5 | 7.77 |
| 578817848 | PREDICTED: transducin-like enhancer protein 4 isoform X18 [Homo | 2.05 | 1.83 | 6 | 1 | 1 | 1 | 764 | 83.2 | 7.61 |
| 22095217 | immunoglobulin light chain variable region [Homo sapiens] | 2.05 | 10.83 | 2 | 1 | 1 | 1 | 120 | 12.4 | 7.24 |
| 530379851 | PREDICTED: AF4/FMR2 family member 4 isoform X2 [Homo sapiens | 2.05 | 1.78 | 5 | 1 | 1 | 1 | 785 | 85.8 | 9.16 |
| 221316716 | proteasome subunit alpha type-1 isoform 3 [Homo sapiens] | 2.05 | 11.54 | 6 | 1 | 1 | 1 | 130 | 14.6 | 8.51 |
| 221042434 | unnamed protein product [Homo sapiens] | 2.05 | 2.36 | 17 | 1 | 1 | 1 | 381 | 42.4 | 7.68 |
| 119578216 | hCG1775001, isoform CRA_a [Homo sapiens] | 2.05 | 1.12 | 7 | 1 | 1 | 1 | 717 | 79.7 | 6.64 |
| 4321151 | formiminotransferase cyclodeaminase [Homo sapiens] | 2.04 | 6.85 | 8 | 1 | 1 | 1 | 146 | 16.1 | 5.35 |
| 14424095 | RecName: Full=NUAK family SNF1-like kinase 1; AltName: Full=AMP | 2.04 | 1.82 | 2 | 1 | 1 | 1 | 661 | 74.3 | 8.82 |
| 119591549 | hCG1777462, isoform CRA_a [Homo sapiens] | 2.04 | 5.11 | 1 | 1 | 1 | 1 | 137 | 14.6 | 8.76 |
| 119619642 | hCG1731070, partial [Homo sapiens] | 2.04 | 16.04 | 1 | 1 | 1 | 1 | 106 | 12.0 | 5.78 |
| 40044514 | unnamed protein product [Homo sapiens] | 2.04 | 17.65 | 3 | 1 | 1 | 1 | 51 | 6.1 | 10.42 |
| 325053894 | Chain H, Egfr Kinase Domain Complexed With An Imidazo[2,1-B]thia | 2.04 | 5.20 | 5 | 1 | 1 | 1 | 327 | 37.0 | 8.19 |
| 40040960 | unnamed protein product [Homo sapiens] | 2.04 | 17.35 | 4 | 1 | 1 | 1 | 98 | 11.0 | 9.51 |
| 194386284 | unnamed protein product [Homo sapiens] | 2.04 | 8.16 | 31 | 1 | 1 | 1 | 196 | 21.1 | 9.58 |
| 194381152 | unnamed protein product [Homo sapiens] | 2.04 | 3.15 | 2 | 1 | 1 | 1 | 572 | 64.8 | 9.10 |
| 119602022 | T-cell leukemia/lymphoma 6, isoform CRA_b [Homo sapiens] | 2.04 | 9.22 | 1 | 1 | 1 | 1 | 141 | 15.8 | 9.23 |

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|---|---|---|---|---|---|---|---|---|---|---|
| 145579474 | Chain B, Diabetes Mellitus Due To A Frustrated Schellman Motif In H | 2.04 | 69.70 | 1 | 1 | 1 | 1 | 33 | 3.6 | 4.46 |
| 119598104 | pleckstrin homology domain containing, family Q member 1, isoform | 2.04 | 6.16 | 1 | 1 | 1 | 1 | 211 | 23.4 | 7.77 |
| 205371873 | RecName: Full=Protein ANKUB1; AltName: Full=Ankyrin repeat and | 2.04 | 2.83 | 3 | 1 | 1 | 1 | 424 | 47.6 | 8.95 |
| 221046254 | unnamed protein product [Homo sapiens] | 2.04 | 4.09 | 2 | 1 | 1 | 1 | 514 | 58.6 | 7.12 |
| 21740259 | hypothetical protein [Homo sapiens] | 2.04 | 1.39 | 5 | 1 | 1 | 1 | 794 | 87.9 | 6.79 |
| 544711067 | T-complex protein 1 subunit theta isoform 4 [Homo sapiens] | 2.04 | 2.32 | 8 | 1 | 1 | 1 | 475 | 51.6 | 5.24 |
| 37196758 | mitochondrial methionyl-tRNA synthetase [Homo sapiens] | 2.04 | 3.37 | 1 | 1 | 1 | 1 | 593 | 66.6 | 8.09 |
| 119629031 | hCG2020245 [Homo sapiens] | 2.04 | 14.05 | 1 | 1 | 1 | 1 | 121 | 13.0 | 7.21 |
| 119597538 | hCG2041487, partial [Homo sapiens] | 2.04 | 8.27 | 1 | 1 | 1 | 1 | 254 | 28.0 | 8.41 |
| 119629779 | hCG1817323, isoform CRA_b [Homo sapiens] | 2.04 | 8.26 | 1 | 1 | 1 | 1 | 218 | 23.5 | 9.17 |
| 7106894 | HSPC252 [Homo sapiens] | 2.04 | 5.88 | 1 | 1 | 1 | 1 | 323 | 36.0 | 5.50 |
| 33604112 | CCDC102B protein [Homo sapiens] | 2.04 | 5.76 | 10 | 1 | 1 | 1 | 139 | 16.3 | 5.50 |
| 62088678 | N-glycanase 1 variant [Homo sapiens] | 2.04 | 4.44 | 10 | 1 | 1 | 1 | 225 | 26.1 | 6.54 |
| 119584828 | CKLF-like MARVEL transmembrane domain containing 7, isoform CR | 2.03 | 8.16 | 2 | 1 | 1 | 1 | 147 | 15.1 | 12.00 |
| 119596625 | integrin beta 4 binding protein, isoform CRA_a [Homo sapiens] | 2.03 | 12.18 | 5 | 1 | 1 | 1 | 197 | 21.3 | 4.77 |
| 519672838 | immunoglobulin A heavy chain variable region, partial [Homo sapien | 2.03 | 15.57 | 1 | 1 | 1 | 1 | 122 | 13.5 | 4.81 |
| 119623033 | hCG1644442 [Homo sapiens] | 2.03 | 8.46 | 1 | 1 | 1 | 1 | 201 | 23.2 | 8.37 |
| 594149486 | Chain B, Crystal Structure Of Cbp Bromodomain | 2.03 | 6.03 | 19 | 1 | 1 | 1 | 116 | 13.8 | 5.27 |
| 119586943 | F-box protein 15, isoform CRA_a [Homo sapiens] | 2.03 | 3.69 | 3 | 1 | 1 | 1 | 434 | 49.4 | 7.85 |
| 371446853 | immunoglobulin G heavy chain variable region, partial [Homo sapien | 2.03 | 13.82 | 1 | 1 | 1 | 1 | 123 | 13.5 | 7.12 |
| 40979276 | unnamed protein product [Homo sapiens] | 2.03 | 35.09 | 1 | 1 | 1 | 1 | 57 | 6.2 | 5.78 |
| 40040786 | unnamed protein product [Homo sapiens] | 2.03 | 6.92 | 11 | 1 | 1 | 1 | 130 | 14.8 | 4.68 |
| 221040502 | unnamed protein product [Homo sapiens] | 2.03 | 9.52 | 8 | 1 | 1 | 1 | 147 | 17.4 | 9.52 |
| 14589153 | immunoglobulin heavy chain variable region [Homo sapiens] | 2.03 | 20.48 | 1 | 1 | 1 | 1 | 83 | 9.5 | 10.07 |
| 119570587 | FLJ39237 protein [Homo sapiens] | 2.03 | 3.24 | 1 | 1 | 1 | 1 | 525 | 57.0 | 6.27 |
| 112697869 | immunoglobulin heavy chain variable region [Homo sapiens] | 2.03 | 22.00 | 1 | 1 | 1 | 1 | 100 | 10.7 | 5.33 |
| 119589132 | sphingomyelin phosphodiesterase 1, acid lysosomal (acid sphingomy | 2.03 | 4.63 | 1 | 1 | 1 | 1 | 324 | 36.5 | 8.65 |
| 512393278 | fragile X mental retardation 1 [Homo sapiens] | 2.03 | 1.94 | 1 | 1 | 1 | 1 | 566 | 63.9 | 8.40 |
| 119625903 | signal recognition particle 72kDa, isoform CRA_c [Homo sapiens] | 2.03 | 2.13 | 3 | 1 | 1 | 1 | 610 | 67.8 | 9.41 |
| 38488440 | immunoglobulin heavy chain V-D-J region [Homo sapiens] | 2.03 | 12.04 | 1 | 1 | 1 | 1 | 108 | 11.9 | 9.22 |
| 21756433 | unnamed protein product [Homo sapiens] | 2.02 | 7.10 | 3 | 1 | 1 | 1 | 183 | 21.0 | 9.83 |
| 119570279 | secreted frizzled-related protein 5 [Homo sapiens] | 2.02 | 5.36 | 2 | 1 | 1 | 1 | 317 | 35.5 | 8.56 |
| 119568149 | hCG1772243, partial [Homo sapiens] | 2.02 | 6.15 | 1 | 1 | 1 | 1 | 130 | 14.5 | 7.83 |
| 119619611 | chromosome 15 open reading frame 5 [Homo sapiens] | 2.02 | 17.02 | 1 | 1 | 1 | 2 | 94 | 11.5 | 7.75 |
| 50949538 | hypothetical protein [Homo sapiens] | 2.02 | 4.66 | 14 | 1 | 1 | 1 | 408 | 45.8 | 6.79 |
| 119614526 | chromosome 7 open reading frame 36 [Homo sapiens] | 2.02 | 5.75 | 3 | 1 | 1 | 1 | 226 | 25.3 | 5.59 |
| 221316769 | ELAV-like protein 4 isoform 3 [Homo sapiens] | 2.02 | 3.39 | 2 | 1 | 1 | 1 | 383 | 42.4 | 9.39 |
| 74726650 | RecName: Full=BolA-like protein 3 | 2.02 | 13.08 | 1 | 1 | 1 | 1 | 107 | 12.1 | 9.64 |
| 119593222 | hCG2042264, partial [Homo sapiens] | 2.02 | 5.76 | 1 | 1 | 1 | 1 | 191 | 20.8 | 6.43 |

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|---|---|---|---|---|---|---|---|---|---|---|
| 578800821 | PREDICTED: digestive organ expansion factor homolog isoform X1 [ | 2.02 | 2.11 | 1 | 1 | 1 | 1 | 568 | 64.9 | 5.16 |
| 354686630 | immunoglobulin heavy chain variable region [Homo sapiens] | 2.02 | 12.82 | 1 | 1 | 1 | 1 | 78 | 9.0 | 9.14 |
| 371927701 | Chain D, Crystal Structure Of Apo Human Ck1d | 2.02 | 5.07 | 20 | 1 | 1 | 1 | 296 | 34.3 | 9.29 |
| 33356967 | Chain B, Crystal Structure Of Human Angiogenin In Complex With F | 2.02 | 8.52 | 1 | 1 | 1 | 1 | 223 | 23.6 | 8.05 |
| 119588589 | hCG1785179 [Homo sapiens] | 2.02 | 18.85 | 1 | 1 | 1 | 1 | 122 | 13.7 | 10.27 |
| 564731264 | Chain B, Crystal Structure Of The Extracellular Domain Of Human Ga | 2.02 | 1.85 | 11 | 1 | 1 | 1 | 433 | 49.0 | 7.12 |
| 530384843 | PREDICTED: WD repeat-containing protein mio isoform X5 [Homo s | 2.02 | 2.07 | 6 | 1 | 1 | 1 | 484 | 55.1 | 6.54 |
| 221040592 | unnamed protein product [Homo sapiens] | 2.02 | 2.91 | 4 | 1 | 1 | 1 | 619 | 68.7 | 8.72 |
| 119614192 | insulin-like growth factor 2 mRNA binding protein 3, isoform CRA_a | 2.02 | 3.32 | 13 | 1 | 1 | 1 | 422 | 46.1 | 9.48 |
| 21756595 | unnamed protein product [Homo sapiens] | 2.02 | 8.18 | 1 | 1 | 1 | 1 | 269 | 29.5 | 11.55 |
| 530403617 | PREDICTED: DNA-(apurinic or apyrimidinic site) lyase isoform X2 [H | 2.02 | 2.66 | 1 | 1 | 1 | 1 | 301 | 33.8 | 7.91 |
| 194379564 | unnamed protein product [Homo sapiens] | 2.02 | 8.24 | 8 | 1 | 1 | 1 | 255 | 26.3 | 9.51 |
| 209572622 | RecName: Full=cTAGE family member 2; Short=Protein cTAGE-2; A | 2.02 | 2.68 | 4 | 1 | 1 | 1 | 745 | 85.2 | 6.16 |
| 14017817 | KIAA1800 protein [Homo sapiens] | 2.01 | 3.13 | 1 | 1 | 1 | 1 | 736 | 84.2 | 7.30 |
| 119597580 | hCG1983020, isoform CRA_e [Homo sapiens] | 2.01 | 2.52 | 3 | 1 | 1 | 1 | 515 | 60.1 | 8.65 |
| 59807731 | TDRD5 protein, partial [Homo sapiens] | 2.01 | 2.03 | 4 | 1 | 1 | 1 | 787 | 88.0 | 7.37 |
| 1362826 | Ig heavy chain V-J region - human (fragment) | 2.01 | 6.09 | 1 | 1 | 1 | 1 | 115 | 12.7 | 9.17 |
| 2960071 | acyl-CoA synthetase-like protein [Homo sapiens] | 2.01 | 12.96 | 3 | 1 | 1 | 1 | 54 | 6.2 | 10.42 |
| 221042490 | unnamed protein product [Homo sapiens] | 2.01 | 1.97 | 5 | 1 | 1 | 1 | 557 | 61.4 | 5.11 |
| 5689744 | T-box transcription factor [Homo sapiens] | 2.01 | 6.50 | 6 | 1 | 1 | 1 | 200 | 23.1 | 9.31 |
| 91979430 | immunoglobulin heavy chain variable region [Homo sapiens] | 2.01 | 23.08 | 2 | 1 | 1 | 1 | 91 | 10.1 | 9.16 |
| 194387332 | unnamed protein product [Homo sapiens] | 2.01 | 2.47 | 1 | 1 | 1 | 1 | 324 | 37.1 | 11.71 |
| 341838320 | MHC class I antigen [Homo sapiens] | 2.01 | 11.05 | 1 | 1 | 1 | 1 | 181 | 20.9 | 6.89 |
| 119574473 | hepatocellular carcinoma-associated antigen 112, isoform CRA_a [H | 2.01 | 5.12 | 4 | 1 | 1 | 1 | 215 | 23.5 | 6.99 |
| 221043214 | unnamed protein product [Homo sapiens] | 2.01 | 2.35 | 6 | 1 | 1 | 1 | 638 | 72.1 | 8.97 |
| 532138042 | Chain B, Structure Of C-terminal Coiled Coil Of Rasgrp1 | 2.01 | 26.79 | 11 | 1 | 1 | 1 | 56 | 6.6 | 6.52 |
| 119599724 | hCG2045407, partial [Homo sapiens] | 2.01 | 20.97 | 1 | 1 | 1 | 1 | 62 | 6.9 | 5.94 |
| 530416023 | PREDICTED: zinc finger protein 30 homolog isoform X7 [Homo sapi | 2.01 | 3.09 | 5 | 1 | 1 | 1 | 518 | 61.4 | 8.91 |
| 525458843 | cytochrome P450 3A43 isoform 4 [Homo sapiens] | 2.01 | 2.54 | 5 | 1 | 1 | 1 | 393 | 44.8 | 9.13 |
| 119620519 | hypothetical protein FLJ31438, isoform CRA_c [Homo sapiens] | 2.01 | 18.25 | 14 | 1 | 1 | 1 | 137 | 15.5 | 4.49 |
| 51094740 | LOC392659 [Homo sapiens] | 2.01 | 14.44 | 1 | 1 | 1 | 1 | 90 | 9.2 | 8.65 |
| 578814590 | PREDICTED: zinc finger and SCAN domain-containing protein 21 iso | 2.01 | 2.33 | 3 | 1 | 1 | 1 | 386 | 42.8 | 7.28 |
| 288965868 | Chain B, Ligand Binding Domain Of Metabotropoc Glutamate Recept | 2.01 | 1.83 | 10 | 1 | 1 | 1 | 492 | 55.3 | 6.43 |
| 887360 | ORF; putative, partial [Homo sapiens] | 2.00 | 7.33 | 1 | 1 | 1 | 1 | 273 | 30.8 | 5.06 |
| 37728216 | immunoglobulin heavy chain variable region [Homo sapiens] | 2.00 | 16.38 | 1 | 1 | 1 | 1 | 116 | 12.9 | 7.96 |
| 34201 | unnamed protein product [Homo sapiens] | 2.00 | 12.73 | 5 | 1 | 1 | 1 | 110 | 12.5 | 10.90 |
| 10436952 | unnamed protein product [Homo sapiens] | 2.00 | 3.75 | 5 | 1 | 1 | 1 | 267 | 31.1 | 7.05 |
| 4827036 | peptidoglycan recognition protein 1 precursor [Homo sapiens] | 2.00 | 7.14 | 1 | 1 | 1 | 1 | 196 | 21.7 | 8.59 |
| 159164066 | Chain A, Solution Structure Of Rsgi Ruh-051, A C1 Domain Of Stac3 | 2.00 | 24.32 | 3 | 1 | 1 | 1 | 74 | 8.3 | 9.11 |

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|---|---|---|---|---|---|---|---|---|---|---|---|
| 40982180 | unnamed protein product [Homo sapiens] | 2.00 | 15.38 | 1 | 1 | 1 | 1 | 91 | 10.1 | 8.31 |
| 119627965 | chromosome 1 open reading frame 91, isoform CRA_d [Homo sapie | 2.00 | 8.20 | 5 | 1 | 1 | 1 | 122 | 13.7 | 7.59 |
| 1772345 | ras-related GTP-binding protein [Homo sapiens] | 2.00 | 5.98 | 1 | 1 | 1 | 1 | 184 | 20.6 | 5.92 |
| 119598288 | GRAM domain containing 2, isoform CRA_a [Homo sapiens] | 2.00 | 3.33 | 3 | 1 | 1 | 1 | 300 | 34.4 | 8.00 |
| 194376796 | unnamed protein product [Homo sapiens] | 2.00 | 2.58 | 17 | 1 | 1 | 1 | 426 | 46.6 | 8.13 |
| 46325261 | microcephalin [Homo sapiens] | 2.00 | 5.21 | 5 | 1 | 1 | 1 | 384 | 41.9 | 7.37 |
| 93007481 | anti-Rh(D) antibody immunoglobulin heavy chain variable region [H | 2.00 | 13.11 | 1 | 1 | 1 | 1 | 122 | 13.7 | 8.44 |
| 194375502 | unnamed protein product [Homo sapiens] | 2.00 | 3.46 | 7 | 1 | 1 | 1 | 405 | 44.8 | 8.53 |
| 119605238 | cartilage intermediate layer protein 2, isoform CRA_a [Homo sapien | 2.00 | 1.38 | 4 | 1 | 1 | 1 | 1156 | 126.2 | 8.22 |
| 13183305 | MIL1 protein isoform 1 [Homo sapiens] | 2.00 | 7.96 | 8 | 1 | 1 | 1 | 201 | 22.6 | 4.93 |
| 189231268 | anti-fluorescein immunoglobulin light chain variable region [Homo s | 2.00 | 25.00 | 1 | 1 | 1 | 1 | 28 | 3.1 | 10.26 |
| 119629688 | chromosome 21 open reading frame 58, isoform CRA_b, partial [Ho | 1.96 | 3.90 | 1 | 1 | 1 | 1 | 154 | 16.8 | 12.07 |
| 50812437 | regulated in COPD kinase transcript variant 3 [Homo sapiens] | 1.94 | 0.53 | 3 | 1 | 1 | 1 | 1127 | 127.9 | 6.86 |
| 40041160 | unnamed protein product [Homo sapiens] | 1.93 | 19.64 | 2 | 1 | 1 | 1 | 56 | 6.2 | 11.44 |
| 221044936 | unnamed protein product [Homo sapiens] | 1.90 | 1.79 | 10 | 1 | 1 | 1 | 559 | 62.7 | 7.77 |
| 17226648 | immunoglobulin heavy chain variable region, partial [Homo sapiens] | 1.89 | 6.35 | 1 | 1 | 1 | 1 | 126 | 14.0 | 9.06 |
| 119625936 | hCG1640454 [Homo sapiens] | 1.89 | 4.65 | 8 | 1 | 1 | 1 | 129 | 14.9 | 10.11 |
| 119631998 | hCG1812664, partial [Homo sapiens] | 1.88 | 14.29 | 1 | 1 | 1 | 1 | 56 | 6.3 | 4.26 |
| 578812294 | PREDICTED: uncharacterized protein LOC102724585 [Homo sapien | 1.83 | 2.24 | 1 | 1 | 1 | 1 | 268 | 28.3 | 9.77 |
| 30802096 | LSM11 protein, partial [Homo sapiens] | 1.82 | 2.55 | 2 | 1 | 1 | 1 | 353 | 38.6 | 11.08 |
| 119593268 | biglycan, isoform CRA_b [Homo sapiens] | 1.82 | 3.30 | 2 | 1 | 1 | 1 | 394 | 44.3 | 7.52 |
| 296434473 | RecName: Full=Homeobox protein DBX2; AltName: Full=Developin | 1.82 | 2.36 | 3 | 1 | 1 | 1 | 339 | 36.5 | 9.35 |
| 2656123 | p53 binding protein [Homo sapiens] | 1.81 | 1.23 | 5 | 1 | 1 | 1 | 815 | 93.4 | 9.52 |
| 3088352 | ribosomal protein L31 [Homo sapiens] | 1.79 | 21.28 | 5 | 1 | 1 | 1 | 47 | 5.6 | 9.32 |
| 119625674 | PR domain containing 5, isoform CRA_c [Homo sapiens] | 1.78 | 3.17 | 5 | 1 | 1 | 1 | 221 | 25.6 | 9.54 |
| 21903375 | RecName: Full=Collagen alpha-1(VIII) chain; AltName: Full=Endoth | 1.76 | 0.94 | 3 | 1 | 1 | 1 | 744 | 73.3 | 9.61 |
| 193783630 | unnamed protein product [Homo sapiens] | 1.74 | 11.76 | 1 | 1 | 1 | 1 | 102 | 11.9 | 10.29 |
| 157836397 | Chain A, Rna Binding Domain 2 Of Human U1a Protein, Nmr, 20 Str | 1.72 | 7.95 | 9 | 1 | 1 | 1 | 88 | 9.9 | 5.83 |
| 119614816 | yippee-like 2 (Drosophila), isoform CRA_d [Homo sapiens] | 1.72 | 8.77 | 3 | 1 | 1 | 1 | 114 | 12.0 | 8.48 |
| 194379742 | unnamed protein product [Homo sapiens] | 1.71 | 2.83 | 6 | 1 | 1 | 1 | 212 | 24.3 | 5.11 |
| 194389854 | unnamed protein product [Homo sapiens] | 1.70 | 2.48 | 14 | 1 | 1 | 1 | 282 | 31.2 | 6.95 |
| 119595460 | hypothetical protein LOC283219, isoform CRA_b [Homo sapiens] | 1.70 | 2.13 | 2 | 1 | 1 | 1 | 329 | 37.0 | 8.43 |
| 30962605 | histamine N-methyltransferase [Homo sapiens] | 1.67 | 3.17 | 9 | 1 | 1 | 1 | 221 | 25.4 | 7.08 |
| 47123516 | C10orf118 protein, partial [Homo sapiens] | 1.67 | 4.59 | 1 | 1 | 1 | 1 | 218 | 24.4 | 5.53 |
| 194380152 | unnamed protein product [Homo sapiens] | 1.66 | 3.38 | 10 | 1 | 1 | 1 | 207 | 24.2 | 4.72 |
| 194379320 | unnamed protein product [Homo sapiens] | 1.66 | 3.14 | 1 | 1 | 1 | 1 | 287 | 30.8 | 11.31 |
| 4056412 | BRG-1-HUMAN [AA 812-1440] [Homo sapiens] | 1.66 | 1.75 | 28 | 1 | 1 | 1 | 628 | 73.2 | 8.73 |
| 39644467 | LANCL2 protein, partial [Homo sapiens] | 1.65 | 4.37 | 7 | 1 | 1 | 1 | 252 | 28.7 | 8.40 |
| 119610319 | hCG1647425, partial [Homo sapiens] | 1.63 | 3.54 | 1 | 1 | 1 | 1 | 254 | 28.3 | 9.54 |

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|---|---|---|---|---|---|---|---|---|---|---|
| 91979682 | immunoglobulin heavy chain variable region [Homo sapiens] | 1.63 | 10.87 | 1 | 1 | 1 | 1 | 92 | 10.4 | 9.33 |
| 119597552 | hCG1806822 [Homo sapiens] | 1.63 | 1.55 | 1 | 1 | 1 | 1 | 1032 | 95.1 | 10.86 |
| 119611340 | chromosome 1 open reading frame 9, isoform CRA_d [Homo sapien | 1.61 | 0.57 | 5 | 1 | 1 | 1 | 1405 | 156.3 | 5.41 |
| 578826089 | PREDICTED: tumor necrosis factor alpha-induced protein 2 isoform | 1.61 | 1.12 | 1 | 1 | 1 | 1 | 716 | 79.7 | 8.28 |
| 119610596 | transmembrane protein 102, isoform CRA_a [Homo sapiens] | 1.61 | 1.57 | 1 | 1 | 1 | 1 | 508 | 54.1 | 5.91 |
| 119603716 | hCG2044641, partial [Homo sapiens] | 1.61 | 17.39 | 3 | 1 | 1 | 1 | 46 | 5.0 | 7.44 |
| 119632275 | hCG1793821, isoform CRA_a [Homo sapiens] | 1.61 | 7.48 | 1 | 1 | 1 | 1 | 107 | 12.1 | 5.49 |
| 6102931 | hypothetical protein [Homo sapiens] | 1.60 | 2.67 | 11 | 1 | 1 | 1 | 262 | 29.9 | 6.32 |
| 221043670 | unnamed protein product [Homo sapiens] | 1.60 | 6.45 | 1 | 1 | 1 | 1 | 155 | 16.1 | 6.13 |
| 1517907 | RAGE-3 ORF5; one of 3 possible coding regions [Homo sapiens] | 1.60 | 8.22 | 7 | 1 | 1 | 1 | 73 | 7.9 | 10.77 |
| 157874535 | Chain A, Nmr Structure Of The Alpha-Helical Hairpin Of P8mtcp1 | 1.60 | 18.42 | 1 | 1 | 1 | 1 | 38 | 4.2 | 8.19 |
| 119607043 | hCG1644292 [Homo sapiens] | 1.59 | 1.41 | 1 | 1 | 1 | 1 | 709 | 78.1 | 6.90 |
| 119594952 | actinin, alpha 3 [Homo sapiens] | 1.59 | 1.22 | 5 | 1 | 1 | 1 | 576 | 66.4 | 5.80 |
| 11640574 | MSTP033 [Homo sapiens] | 1.59 | 13.33 | 1 | 1 | 1 | 1 | 60 | 7.0 | 10.45 |
| 28071038 | unnamed protein product [Homo sapiens] | 1.59 | 20.93 | 1 | 1 | 1 | 1 | 43 | 5.2 | 11.05 |
| 255918079 | versican core protein isoform 4 precursor [Homo sapiens] | 1.58 | 0.61 | 3 | 1 | 1 | 1 | 1642 | 181.9 | 4.89 |
| 20521005 | KIAA0342 protein [Homo sapiens] | 1.58 | 0.32 | 4 | 1 | 1 | 1 | 2467 | 283.5 | 6.48 |
| 371446332 | immunoglobulin G heavy chain variable region, partial [Homo sapien | 1.58 | 3.97 | 2 | 1 | 1 | 1 | 126 | 13.8 | 7.05 |
| 40042660 | unnamed protein product [Homo sapiens] | 1.58 | 11.27 | 11 | 1 | 1 | 1 | 71 | 8.1 | 8.02 |
| 7023067 | unnamed protein product [Homo sapiens] | 1.58 | 1.41 | 24 | 1 | 1 | 1 | 354 | 39.9 | 4.97 |
| 119570164 | hCG2044982 [Homo sapiens] | 1.58 | 4.92 | 1 | 1 | 1 | 1 | 122 | 13.4 | 10.81 |
| 553281 | erythropoietin receptor, partial [Homo sapiens] | 1.58 | 7.29 | 11 | 1 | 1 | 1 | 96 | 10.5 | 4.61 |
| 119615334 | chromosome 1 open reading frame 166, isoform CRA_b, partial [Ho | 1.57 | 1.50 | 1 | 1 | 1 | 1 | 400 | 41.6 | 11.36 |
| 34327986 | KIAA1894 protein [Homo sapiens] | 1.57 | 0.24 | 10 | 1 | 1 | 1 | 2977 | 325.4 | 5.82 |
| 119619594 | TBC1 domain family, member 2B, isoform CRA_a [Homo sapiens] | 1.57 | 1.92 | 10 | 1 | 1 | 1 | 312 | 36.4 | 5.86 |
| 16548917 | unnamed protein product [Homo sapiens] | 1.57 | 4.41 | 7 | 1 | 1 | 1 | 136 | 15.0 | 6.70 |
| 119628585 | solute carrier family 12 (potassium/chloride transporters), member | 1.56 | 1.00 | 21 | 1 | 1 | 1 | 501 | 57.5 | 9.16 |
| 930044 | unnamed protein product [Homo sapiens] | 1.56 | 9.09 | 2 | 1 | 1 | 1 | 77 | 8.2 | 10.01 |
| 119613734 | hCG1985681 [Homo sapiens] | 1.56 | 7.69 | 1 | 1 | 1 | 1 | 130 | 14.6 | 8.75 |
| 247426073 | immunoglobulin heavy chain variable region [Homo sapiens] | 1.56 | 5.51 | 2 | 1 | 1 | 1 | 127 | 13.9 | 6.62 |
| 194390218 | unnamed protein product [Homo sapiens] | 1.56 | 2.05 | 3 | 1 | 1 | 1 | 293 | 32.4 | 6.62 |
| 4009513 | protoporphyrinogen oxidase mutant [Homo sapiens] | 1.55 | 25.00 | 13 | 1 | 1 | 1 | 32 | 3.3 | 6.32 |
| 124504629 | EGFR protein [Homo sapiens] | 1.55 | 1.80 | 1 | 1 | 1 | 1 | 388 | 42.1 | 7.49 |
| 119615739 | LIM and senescent cell antigen-like domains 2, isoform CRA_b, part | 1.55 | 3.25 | 17 | 1 | 1 | 1 | 154 | 16.2 | 10.04 |
| 21752253 | unnamed protein product [Homo sapiens] | 1.55 | 2.07 | 6 | 1 | 1 | 1 | 484 | 57.6 | 8.50 |
| 578824856 | PREDICTED: serine/threonine-protein kinase Nek5 isoform X3 [Hom | 1.55 | 1.49 | 4 | 1 | 1 | 1 | 402 | 46.0 | 9.55 |
| 119593870 | hCG1987469, isoform CRA_a, partial [Homo sapiens] | 1.54 | 1.91 | 1 | 1 | 1 | 1 | 314 | 33.4 | 9.36 |
| 119589078 | olfactory receptor, family 2, subfamily D, member 3 [Homo sapiens] | 1.54 | 1.91 | 13 | 1 | 1 | 1 | 314 | 35.7 | 8.97 |
| 119621301 | DEAD (Asp-Glu-Ala-Asp) box polypeptide 1, isoform CRA_c [Homo s | 1.54 | 1.86 | 8 | 1 | 1 | 1 | 377 | 41.5 | 7.17 |

| | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 51095136 | similar to Argininosuccinate synthase (Citrulline--aspartate ligase) [H | 1.54 | 3.29 | 1 | 1 | 1 | 1 | 213 | 24.2 | 7.75 |
| 119576360 | hCG1778706 [Homo sapiens] | 1.54 | 2.53 | 1 | 1 | 1 | 1 | 277 | 31.6 | 7.08 |
| 119600179 | nuclear factor of kappa light polypeptide gene enhancer in B-cells in | 1.54 | 1.01 | 3 | 1 | 1 | 1 | 596 | 64.3 | 7.06 |
| 194380996 | unnamed protein product [Homo sapiens] | 1.54 | 2.64 | 17 | 1 | 1 | 1 | 227 | 26.2 | 8.90 |
| 119622900 | hCG1648122 [Homo sapiens] | 1.53 | 1.63 | 3 | 1 | 1 | 1 | 368 | 39.1 | 12.04 |
| 40976252 | unnamed protein product [Homo sapiens] | 1.53 | 6.03 | 6 | 1 | 1 | 1 | 116 | 12.3 | 9.29 |
| 119620568 | chromosome 2 open reading frame 30, isoform CRA_a [Homo sapie | 1.53 | 1.63 | 5 | 1 | 1 | 1 | 429 | 48.9 | 6.25 |
| 6841066 | calcium-binding transporter [Homo sapiens] | 1.53 | 1.22 | 10 | 1 | 1 | 1 | 411 | 45.8 | 5.47 |
| 7020012 | unnamed protein product [Homo sapiens] | 1.53 | 2.30 | 10 | 1 | 1 | 1 | 261 | 30.1 | 7.33 |
| 34528547 | unnamed protein product [Homo sapiens] | 1.53 | 8.13 | 1 | 1 | 1 | 1 | 123 | 14.3 | 9.85 |
| 119571434 | nitric oxide synthase 2A (inducible, hepatocytes), isoform CRA_b, pa | 1.53 | 2.94 | 1 | 1 | 1 | 1 | 306 | 34.2 | 9.14 |
| 22095219 | immunoglobulin light chain variable region [Homo sapiens] | 1.52 | 6.42 | 1 | 1 | 1 | 1 | 109 | 11.8 | 5.99 |
| 9802308 | iron regulatory protein 1 [Homo sapiens] | 1.52 | 0.76 | 1 | 1 | 1 | 1 | 790 | 87.0 | 6.55 |
| 50949614 | hypothetical protein [Homo sapiens] | 1.52 | 1.88 | 2 | 1 | 1 | 1 | 533 | 60.8 | 8.88 |
| 39962935 | ROBO2 protein, partial [Homo sapiens] | 1.52 | 2.05 | 10 | 1 | 1 | 1 | 341 | 37.2 | 5.69 |
| 119592203 | malate dehydrogenase 2, NAD (mitochondrial), isoform CRA_b [Hon | 1.52 | 2.60 | 45 | 1 | 1 | 1 | 231 | 24.6 | 7.99 |
| 40043026 | unnamed protein product [Homo sapiens] | 1.52 | 6.35 | 10 | 1 | 1 | 1 | 126 | 14.4 | 9.44 |
| 1093622 | Id3 gene | 1.52 | 5.04 | 4 | 1 | 1 | 1 | 119 | 13.0 | 5.83 |
| 340780553 | Chain A, Crystal Structure Of Faf1 Ubx Domain In Complex With P97 | 1.51 | 2.81 | 2 | 1 | 1 | 1 | 178 | 20.2 | 5.52 |
| 311771787 | uncharacterized protein C8orf58 isoform 3 [Homo sapiens] | 1.51 | 2.00 | 3 | 1 | 1 | 1 | 300 | 32.0 | 6.24 |
| 22760973 | unnamed protein product [Homo sapiens] | 1.51 | 1.68 | 2 | 1 | 1 | 1 | 357 | 41.3 | 9.72 |
| 119630471 | hCG2042829, partial [Homo sapiens] | 1.51 | 3.85 | 1 | 1 | 1 | 1 | 156 | 17.3 | 7.77 |
| 14249280 | N-alpha-acetyltransferase 11 [Homo sapiens] | 1.51 | 2.62 | 4 | 1 | 1 | 1 | 229 | 26.0 | 5.17 |
| 578826539 | PREDICTED: magnesium transporter NIPA2 isoform X13 [Homo sap | 1.51 | 2.55 | 8 | 1 | 1 | 1 | 274 | 30.1 | 6.40 |
| 38541852 | CMYA5 protein, partial [Homo sapiens] | 1.51 | 1.63 | 1 | 1 | 1 | 1 | 369 | 41.7 | 5.54 |
| 34531444 | unnamed protein product [Homo sapiens] | 1.51 | 3.02 | 2 | 1 | 1 | 1 | 298 | 32.9 | 5.40 |
| 930048 | collagen-like protein (447 AA) [Homo sapiens] | 1.51 | 1.79 | 1 | 1 | 1 | 1 | 447 | 41.8 | 8.02 |
| 39644924 | LRIG1 protein, partial [Homo sapiens] | 1.51 | 2.40 | 11 | 1 | 1 | 1 | 417 | 44.5 | 6.52 |
| 221046018 | unnamed protein product [Homo sapiens] | 1.51 | 3.35 | 5 | 1 | 1 | 1 | 179 | 19.5 | 6.44 |
| 18676784 | unnamed protein product [Homo sapiens] | 1.50 | 3.40 | 6 | 1 | 1 | 1 | 235 | 26.6 | 6.64 |
| 578842780 | PREDICTED: neurogenic locus notch homolog protein 2-like isoform | 1.50 | 1.57 | 1 | 1 | 1 | 1 | 446 | 48.7 | 7.94 |
| 300087065 | anti-Venezuelan equine encephalitis virus immunoglobulin light chai | 1.50 | 8.11 | 1 | 1 | 1 | 1 | 111 | 11.6 | 4.78 |
| 30583297 | eukaryotic translation initiation factor 2C, 2 [Homo sapiens] | 1.50 | 1.20 | 10 | 1 | 1 | 1 | 585 | 66.2 | 9.28 |
| 21756090 | unnamed protein product [Homo sapiens] | 1.50 | 0.97 | 10 | 1 | 1 | 1 | 515 | 57.2 | 9.32 |
| 119585666 | inter-alpha (globulin) inhibitor H3, isoform CRA_a [Homo sapiens] | 1.50 | 1.04 | 9 | 1 | 1 | 1 | 670 | 75.0 | 5.94 |

| Accession | Description | Score | Coverage |
|---|---|---|---|
| 6166599 | RecName: Full=Myosin-9; AltName: Full=Cellular myosin heavy chai | 182.70 | 34.34 |
| 181402 | epidermal cytokeratin 2 [Homo sapiens] | 246.67 | 55.50 |
| 41322916 | plectin isoform 1 [Homo sapiens] | 66.29 | 7.28 |
| 123648 | RecName: Full=Heat shock cognate 71 kDa protein; AltName: Full= | 101.10 | 40.40 |
| 239938886 | RecName: Full=Keratin, type I cytoskeletal 9; AltName: Full=Cytoke | 193.59 | 56.18 |
| 74735628 | RecName: Full=Sequestosome-1; AltName: Full=EBI3-associated pr | 225.01 | 72.27 |
| 63087903 | unnamed protein product [Homo sapiens] | 3229.72 | 65.37 |
| 194388850 | unnamed protein product [Homo sapiens] | 89.05 | 43.51 |
| 113950 | RecName: Full=Annexin A2; AltName: Full=Annexin II; AltName: Fu | 38.83 | 37.46 |
| 119631419 | titin, isoform CRA_a [Homo sapiens] | 64.95 | 0.74 |
| 225733965 | Chain L, Human Thrombopoietin Neutralizing Antibody Tn1 Fab | 344.40 | 52.11 |
| 119581085 | keratin 10 (epidermolytic hyperkeratosis; keratosis palmaris et plant | 312.72 | 58.33 |
| 189306 | nucleolin [Homo sapiens] | 37.38 | 19.24 |
| 425518 | anti-colorectal carcinoma heavy chain [Homo sapiens] | 737.73 | 44.98 |
| 578837003 | PREDICTED: histone acetyltransferase p300 isoform X1 [Homo sapie | 31.12 | 7.58 |
| 146345444 | RecName: Full=Kelch-like ECH-associated protein 1; AltName: Full= | 42.33 | 23.24 |
| 119614804 | clathrin, heavy polypeptide (Hc), isoform CRA_d [Homo sapiens] | 30.03 | 8.54 |
| 169404698 | Chain D, Pyruvate Kinase M2 Is A Phosphotyrosine Binding Protein | 31.73 | 24.13 |
| 189502784 | mitochondrial heat shock 60kD protein 1 variant 1 [Homo sapiens] | 25.23 | 19.16 |
| 221042022 | unnamed protein product [Homo sapiens] | 28.03 | 19.70 |
| 119608213 | spectrin, alpha, non-erythrocytic 1 (alpha-fodrin), isoform CRA_c [H | 24.00 | 4.90 |
| 1195531 | type I keratin 16 [Homo sapiens] | 99.01 | 47.99 |
| 2769254 | NIPSNAP2 protein [Homo sapiens] | 35.16 | 38.25 |
| 378404908 | glyceraldehyde-3-phosphate dehydrogenase isoform 2 [Homo sapie | 32.83 | 40.61 |
| 119578453 | alpha tubulin, isoform CRA_b [Homo sapiens] | 22.51 | 25.48 |
| 194382178 | unnamed protein product [Homo sapiens] | 29.11 | 17.74 |
| 23491735 | ribosomal protein L10a [Homo sapiens] | 23.33 | 37.33 |
| 239938658 | RecName: Full=Protein kinase C iota type; AltName: Full=Atypical p | 26.45 | 15.27 |
| 15341992 | Unknown (protein for IMAGE:4347401), partial [Homo sapiens] | 15.32 | 26.86 |
| 516764 | motor protein [Homo sapiens] | 20.29 | 13.18 |
| 190192192 | filamin B [Homo sapiens] | 18.51 | 3.92 |
| 568786378 | Chain A, Structure Of The Mammalian Ribosomal Pre-termination Co | 13.48 | 16.67 |
| 485601393 | Chain S, Structure Of The Human 40s Ribosomal Proteins | 14.18 | 31.58 |
| 190192184 | filamin A [Homo sapiens] | 15.02 | 3.15 |
| 221045062 | unnamed protein product [Homo sapiens] | 18.61 | 50.00 |
| 300669711 | RecName: Full=Fibrous sheath-interacting protein 2 | 20.16 | 1.22 |
| 119602167 | dynein, cytoplasmic 1, heavy chain 1, isoform CRA_c [Homo sapiens | 17.64 | 2.31 |
| 119598181 | ribosomal protein L4, isoform CRA_a [Homo sapiens] | 23.10 | 21.92 |
| 14042692 | unnamed protein product [Homo sapiens] | 15.82 | 13.18 |
| 337580 | ribosomal protein L3, partial [Homo sapiens] | 15.07 | 13.07 |
| 39644662 | HSP90AB1 protein [Homo sapiens] | 43.69 | 26.62 |
| 34392 | unnamed protein product [Homo sapiens] | 13.12 | 27.15 |
| 119582734 | RAD50 homolog (S. cerevisiae), isoform CRA_c [Homo sapiens] | 13.33 | 3.50 |
| 31108 | human elongation factor 2 [Homo sapiens] | 12.27 | 7.34 |
| 194379998 | unnamed protein product [Homo sapiens] | 26.88 | 24.43 |
| 1827593 | Chain B, Recombinant Cyclophilin A From Human T Cell | 15.20 | 32.93 |
| 119577296 | ribosomal protein S16, isoform CRA_a [Homo sapiens] | 12.07 | 34.88 |
| 119612227 | poly(A) binding protein, cytoplasmic 1, isoform CRA_c [Homo sapier | 20.57 | 17.42 |
| 119601423 | hCG2028724 [Homo sapiens] | 17.91 | 25.94 |
| 119594430 | eukaryotic translation elongation factor 1 gamma, isoform CRA_b [H | 10.34 | 14.91 |
| 119582155 | hCG1783090 [Homo sapiens] | 13.78 | 18.55 |
| 340219 | vimentin [Homo sapiens] | 23.77 | 17.38 |
| 56675570 | unnamed protein product [Homo sapiens] | 18.18 | 24.31 |
| 825671 | B23 nucleophosmin (280 AA) [Homo sapiens] | 20.52 | 28.57 |
| 32488 | unnamed protein product [Homo sapiens] | 38.69 | 20.49 |
| 530420475 | PREDICTED: protein NipSnap homolog 1 isoform X1 [Homo sapiens] | 18.27 | 20.77 |
| 40031212 | unnamed protein product [Homo sapiens] | 14.54 | 35.61 |
| 403234036 | eukaryotic translation initiation factor 3 [Homo sapiens] | 15.71 | 5.28 |

| | | | |
|---|---|---|---|
| 31873360 | hypothetical protein [Homo sapiens] | 11.03 | 5.23 |
| 160332335 | RecName: Full=Neuroblast differentiation-associated protein AHNAK | 17.65 | 6.59 |
| 58530842 | desmoplakin isoform II [Homo sapiens] | 10.05 | 2.90 |
| 485601397 | Chain R, Structure Of The Human 40s Ribosomal Proteins | 17.31 | 48.89 |
| 119615022 | leucine rich repeat containing 59, isoform CRA_a [Homo sapiens] | 13.88 | 16.61 |
| 49257460 | PTRF protein [Homo sapiens] | 11.04 | 19.33 |
| 21620099 | Treacher Collins-Franceschetti syndrome 1 [Homo sapiens] | 9.60 | 4.07 |
| 48735185 | EEF1A1 protein [Homo sapiens] | 59.05 | 41.50 |
| 375151597 | 60S ribosomal protein L10 isoform c [Homo sapiens] | 8.84 | 23.03 |
| 15431310 | keratin, type I cytoskeletal 14 [Homo sapiens] | 75.69 | 31.78 |
| 157829895 | Chain A, Crystal Structure Of Human Annexin I At 2.5 Angstroms Re | 15.21 | 19.75 |
| 119621461 | ribosomal protein S7, isoform CRA_a [Homo sapiens] | 10.88 | 27.06 |
| 119631904 | nebulin, isoform CRA_a [Homo sapiens] | 12.94 | 1.36 |
| 119626065 | albumin, isoform CRA_b [Homo sapiens] | 24.04 | 10.23 |
| 119602460 | ribosomal protein L8, isoform CRA_f [Homo sapiens] | 13.70 | 23.18 |
| 119569562 | antigen identified by monoclonal antibody Ki-67, isoform CRA_a [Ho | 11.45 | 2.36 |
| 119569329 | hCG1640785, isoform CRA_a [Homo sapiens] | 10.34 | 19.35 |
| 221045918 | unnamed protein product [Homo sapiens] | 55.35 | 42.17 |
| 10435150 | unnamed protein product [Homo sapiens] | 8.80 | 9.42 |
| 63102283 | CKAP4 protein [Homo sapiens] | 10.21 | 12.07 |
| 62204505 | RPL13 protein [Homo sapiens] | 11.62 | 25.59 |
| 38014351 | EEF1D protein, partial [Homo sapiens] | 8.78 | 6.91 |
| 34785048 | RPS6 protein, partial [Homo sapiens] | 8.37 | 14.17 |
| 40040444 | unnamed protein product [Homo sapiens] | 9.85 | 16.28 |
| 530392193 | PREDICTED: 6-phosphofructokinase type C isoform X3 [Homo sapie | 11.23 | 10.59 |
| 55507560 | unknown [Homo sapiens] | 10.13 | 11.60 |
| 50513340 | Chain A, Nmr Structure Of Human Cofilin | 6.01 | 16.27 |
| 12643540 | RecName: Full=Proteasome subunit alpha type-7; AltName: Full=Pr | 7.53 | 13.71 |
| 485601396 | Chain L, Structure Of The Human 40s Ribosomal Proteins | 5.81 | 19.62 |
| 485601390 | Chain O, Structure Of The Human 40s Ribosomal Proteins | 7.59 | 18.54 |
| 122937211 | proteasome-associated protein ECM29 homolog [Homo sapiens] | 9.12 | 2.38 |
| 33341236 | polytrophin [Homo sapiens] | 12.15 | 0.81 |
| 118498368 | kinectin isoform c [Homo sapiens] | 13.50 | 3.38 |
| 296439473 | RecName: Full=Dynein heavy chain 10, axonemal; AltName: Full=A | 14.01 | 1.72 |
| 75517570 | HNRPA1 protein [Homo sapiens] | 21.53 | 20.97 |
| 119574650 | hect domain and RLD 4, isoform CRA_e [Homo sapiens] | 6.59 | 3.70 |
| 194386084 | unnamed protein product [Homo sapiens] | 8.84 | 21.34 |
| 259016354 | RecName: Full=Protein ELYS; AltName: Full=Embryonic large molec | 7.35 | 2.12 |
| 119590009 | cytoplasmic linker 2, isoform CRA_a [Homo sapiens] | 7.00 | 3.36 |
| 374532823 | Golgin subfamily B member 1 isoform 4 [Homo sapiens] | 7.57 | 0.82 |
| 4930167 | Chain A, Human Muscle Aldolase | 6.55 | 8.26 |
| 166007177 | Chain T, Solution Structure Of Human Immunoglobulin M | 21.94 | 10.13 |
| 225733966 | Chain H, Human Thrombopoietin Neutralizing Antibody Tn1 Fab | 414.86 | 40.55 |
| 1587352 | globin 245 | 12.97 | 2.35 |
| 2661039 | alpha enolase [Homo sapiens] | 21.49 | 27.08 |
| 119619469 | dystrophin (muscular dystrophy, Duchenne and Becker types), isofo | 15.08 | 1.60 |
| 119615215 | karyopherin (importin) beta 1, isoform CRA_b [Homo sapiens] | 8.53 | 5.08 |
| 119612228 | hCG15685 [Homo sapiens] | 9.85 | 26.96 |
| 119607089 | protein kinase, DNA-activated, catalytic polypeptide, isoform CRA_d | 8.43 | 1.59 |
| 119600702 | hCG1989166, isoform CRA_c, partial [Homo sapiens] | 9.72 | 5.11 |
| 119590272 | obscurin, cytoskeletal calmodulin and titin-interacting RhoGEF, isofo | 11.52 | 0.48 |
| 119582699 | heat shock 70kDa protein 4, isoform CRA_b [Homo sapiens] | 14.03 | 7.82 |
| 119576069 | myosin XVA, isoform CRA_c [Homo sapiens] | 5.35 | 0.74 |
| 21754583 | unnamed protein product [Homo sapiens] | 37.71 | 22.30 |
| 39645240 | HNRPU protein, partial [Homo sapiens] | 8.87 | 6.24 |
| 38114878 | RPL13A protein, partial [Homo sapiens] | 5.65 | 11.44 |
| 21619981 | LMNA protein [Homo sapiens] | 9.41 | 10.32 |
| 116283708 | DHX9 protein [Homo sapiens] | 9.41 | 6.58 |
| 40040430 | unnamed protein product [Homo sapiens] | 9.43 | 12.11 |

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|---|---|---|---|
| 20521005 | KIAA0342 protein [Homo sapiens] | 11.41 | 1.42 |
| 161172139 | Chain B, Phosphorylation Independent Interactions Between 14-3-3 | 9.70 | 20.00 |
| 298508322 | Chain F, Structure Of P97 N-D1 R95g Mutant In Complex With Atpgs | 7.81 | 10.02 |
| 13097600 | Similar to ribosomal protein L23, partial [Homo sapiens] | 6.22 | 20.15 |
| 645912958 | major vault protein isoform 2 [Homo sapiens] | 10.03 | 7.44 |
| 578801447 | PREDICTED: tropomyosin alpha-3 chain isoform X6 [Homo sapiens] | 6.61 | 11.27 |
| 89574029 | mitochondrial ATP synthase, H+ transporting F1 complex beta subu | 8.79 | 12.36 |
| 29334005 | unnamed protein product [Homo sapiens] | 5.46 | 1.20 |
| 119581825 | ribosomal protein L26-like 1, isoform CRA_a [Homo sapiens] | 5.38 | 15.86 |
| 153792663 | myosin-2 [Homo sapiens] | 5.64 | 1.80 |
| 2506816 | RecName: Full=Versican core protein; AltName: Full=Chondroitin su | 5.37 | 0.62 |
| 485601388 | Chain U, Structure Of The Human 40s Ribosomal Proteins | 4.93 | 15.13 |
| 4503513 | eukaryotic translation initiation factor 3 subunit I [Homo sapiens] | 4.25 | 6.15 |
| 118572681 | RecName: Full=Phosphatidylinositol 3-kinase regulatory subunit alpl | 11.37 | 7.04 |
| 4501889 | actin, gamma-enteric smooth muscle isoform 1 precursor [Homo sap | 32.38 | 28.46 |
| 119627197 | zinc finger, FYVE domain containing 9, isoform CRA_c [Homo sapier | 21.82 | 3.67 |
| 14589854 | protein tyrosine phosphatase type IVA 3 isoform 2 [Homo sapiens] | 4.02 | 20.95 |
| 119613293 | hCG2027030, partial [Homo sapiens] | 22.56 | 33.33 |
| 21758964 | unnamed protein product [Homo sapiens] | 4.04 | 5.92 |
| 485601399 | Chain T, Structure Of The Human 40s Ribosomal Proteins | 4.65 | 13.79 |
| 308153582 | RecName: Full=Neuron navigator 2; AltName: Full=Helicase APC do | 12.78 | 1.29 |
| 121925 | RecName: Full=Histone H1.3; AltName: Full=Histone H1c; AltName: | 9.78 | 19.91 |
| 238054406 | RecName: Full=Keratin, type II cytoskeletal 1; AltName: Full=67 kD | 405.11 | 58.70 |
| 485601395 | Chain N, Structure Of The Human 40s Ribosomal Proteins | 5.79 | 15.89 |
| 296439461 | RecName: Full=Protein broad-minded; AltName: Full=TBC1 domain | 6.13 | 2.23 |
| 118572619 | RecName: Full=Adenylate cyclase type 5; AltName: Full=ATP pyropl | 5.65 | 2.14 |
| 119598471 | optic atrophy 1 (autosomal dominant), isoform CRA_b [Homo sapier | 5.23 | 3.79 |
| 21928473 | seven transmembrane helix receptor [Homo sapiens] | 4.21 | 16.42 |
| 126362947 | sodium channel protein type 3 subunit alpha isoform 2 [Homo sapie | 4.05 | 1.49 |
| 578835066 | PREDICTED: liprin-alpha-3 isoform X1 [Homo sapiens] | 36.04 | 3.12 |
| 74756116 | RecName: Full=Zinc finger and BTB domain-containing protein 41 | 13.25 | 2.75 |
| 47076897 | unnamed protein product [Homo sapiens] | 4.33 | 11.66 |
| 119577859 | hypothetical protein FLJ20512 [Homo sapiens] | 9.00 | 15.96 |
| 58761484 | T-complex protein 1 subunit gamma isoform c [Homo sapiens] | 6.86 | 3.75 |
| 193786214 | unnamed protein product [Homo sapiens] | 3.71 | 2.33 |
| 18375644 | tyrosine-protein phosphatase non-receptor type 11 isoform 2 [Homo | 4.17 | 5.22 |
| 182627587 | RecName: Full=Putative ankyrin repeat domain-containing protein 3 | 4.65 | 1.55 |
| 119614677 | proteasome (prosome, macropain) 26S subunit, ATPase, 5, isoform | 4.49 | 9.05 |
| 27436873 | E3 ubiquitin-protein ligase SHPRH isoform b [Homo sapiens] | 9.48 | 2.29 |
| 24660442 | MYO18A protein [Homo sapiens] | 9.68 | 1.60 |
| 172044680 | RecName: Full=Dynein heavy chain 2, axonemal; AltName: Full=Axo | 6.47 | 0.86 |
| 119599446 | coatomer protein complex, subunit beta 2 (beta prime), isoform CRA | 3.82 | 2.74 |
| 119608075 | ribosomal protein L12, isoform CRA_d [Homo sapiens] | 7.77 | 22.73 |
| 205371795 | RecName: Full=BAH and coiled-coil domain-containing protein 1; Alt | 6.57 | 1.65 |
| 530377992 | PREDICTED: storkhead-box protein 2 isoform X1 [Homo sapiens] | 11.49 | 1.39 |
| 119592618 | ribosomal protein S9, isoform CRA_c [Homo sapiens] | 4.68 | 11.51 |
| 119598167 | hypothetical protein MGC4562, isoform CRA_d [Homo sapiens] | 10.44 | 4.24 |
| 172046085 | RecName: Full=Dynein heavy chain 14, axonemal; AltName: Full=A | 9.70 | 1.51 |
| 194384416 | unnamed protein product [Homo sapiens] | 5.97 | 15.82 |
| 554790420 | NAD(P)H dehydrogenase [quinone] 1 isoform d [Homo sapiens] | 5.04 | 8.42 |
| 194385216 | unnamed protein product [Homo sapiens] | 7.01 | 9.69 |
| 219518228 | Unknown (protein for MGC:177866) [Homo sapiens] | 5.11 | 35.11 |
| 260099727 | L-lactate dehydrogenase A chain isoform 5 [Homo sapiens] | 7.82 | 14.94 |
| 194379468 | unnamed protein product [Homo sapiens] | 9.40 | 8.26 |
| 194375492 | unnamed protein product [Homo sapiens] | 9.10 | 4.52 |
| 221044142 | unnamed protein product [Homo sapiens] | 14.39 | 2.81 |
| 10436376 | unnamed protein product [Homo sapiens] | 5.24 | 7.43 |
| 321117084 | RPS10-NUDT3 protein [Homo sapiens] | 10.51 | 10.65 |
| 119597906 | testis expressed sequence 9 [Homo sapiens] | 3.63 | 6.01 |

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|---|---|---|---|
| 331284176 | nuclear receptor corepressor 2 isoform 2 [Homo sapiens] | 7.23 | 1.67 |
| 194378812 | unnamed protein product [Homo sapiens] | 5.16 | 8.52 |
| 256542310 | dynein heavy chain 17, axonemal [Homo sapiens] | 134.15 | 0.90 |
| 20150918 | Chain A, Crystal Structure Of The N-Terminal Segment Of Human Eu | 4.16 | 11.54 |
| 157883792 | Chain A, Nmr Structure Of The Second Qrrm Domain Of Human Hnr | 9.93 | 24.60 |
| 315583650 | Chain A, Crystal Structure Of Human Dnmt1(646-1600) In Complex | 6.15 | 4.50 |
| 223673784 | Chain A, Human Acylphosphatase(Acph) Surface Charge-Optimized | 3.62 | 20.20 |
| 284232 | Ig heavy chain V region - human | 16.94 | 45.13 |
| 224053 | macroglobulin alpha2 | 8.30 | 2.69 |
| 119613451 | nuclear transcription factor, X-box binding-like 1, isoform CRA_e [Ho | 7.00 | 3.57 |
| 337451 | hnRNP type A/B protein [Homo sapiens] | 3.95 | 7.04 |
| 1136741 | KIAA0002 [Homo sapiens] | 5.27 | 4.08 |
| 551411917 | DBF4-type zinc finger-containing protein 2 isoform 2 [Homo sapiens | 10.86 | 3.10 |
| 120538705 | ATP2B3 protein [Homo sapiens] | 3.56 | 2.86 |
| 109734611 | Myosin, heavy chain 10, non-muscle [Homo sapiens] | 30.30 | 5.41 |
| 10438219 | unnamed protein product [Homo sapiens] | 6.26 | 4.80 |
| 4388965 | Chain L, Antibody To Campath-1h Humanized Fab | 22.72 | 23.36 |
| 119629468 | hCG2011852 [Homo sapiens] | 15.91 | 0.91 |
| 119629071 | KIAA0564 protein, isoform CRA_b [Homo sapiens] | 3.68 | 5.35 |
| 119628802 | ribosomal protein L21, isoform CRA_c [Homo sapiens] | 5.16 | 28.45 |
| 119625048 | KM-HN-1 protein, isoform CRA_a [Homo sapiens] | 11.01 | 8.30 |
| 119623948 | euchromatic histone-lysine N-methyltransferase 2, isoform CRA_d [H | 5.15 | 2.68 |
| 119623343 | hCG1999854, isoform CRA_a [Homo sapiens] | 3.70 | 1.75 |
| 119618140 | hCG2015269, isoform CRA_c [Homo sapiens] | 4.62 | 27.13 |
| 119617634 | chaperonin containing TCP1, subunit 2 (beta), isoform CRA_a [Hom | 4.92 | 4.69 |
| 119616102 | microtubule-associated protein 1B, isoform CRA_a [Homo sapiens] | 6.77 | 2.01 |
| 119614240 | heterogeneous nuclear ribonucleoprotein A2/B1, isoform CRA_a [Ho | 16.50 | 12.96 |
| 119613723 | hCG1985901 [Homo sapiens] | 13.92 | 5.59 |
| 119613335 | ribosomal protein L9, isoform CRA_c [Homo sapiens] | 4.45 | 14.07 |
| 119612929 | spectrin, beta, non-erythrocytic 5 [Homo sapiens] | 8.51 | 1.14 |
| 119612251 | E3 ubiquitin protein ligase, HECT domain containing, 1, isoform CRA | 113.25 | 1.76 |
| 119611612 | translocated promoter region (to activated MET oncogene), isoform | 9.20 | 1.62 |
| 119611276 | kinesin-associated protein 3, isoform CRA_b [Homo sapiens] | 3.08 | 1.68 |
| 119610957 | TSR1, 20S rRNA accumulation, homolog (yeast), isoform CRA_d [Ho | 9.69 | 6.51 |
| 119610275 | solute carrier family 25 (mitochondrial carrier; adenine nucleotide tr | 11.67 | 16.73 |
| 119609433 | proteasome (prosome, macropain) 26S subunit, non-ATPase, 12, iso | 3.97 | 7.05 |
| 119609377 | Jumonji, AT rich interactive domain 1A (RBBP2-like), isoform CRA_b | 7.29 | 1.83 |
| 119609186 | nucleolar protein 1, 120kDa [Homo sapiens] | 17.99 | 4.46 |
| 119604554 | dynamin 2, isoform CRA_e [Homo sapiens] | 4.00 | 3.33 |
| 119600676 | neurofibromin 1 (neurofibromatosis, von Recklinghausen disease, W | 6.02 | 0.69 |
| 119598667 | eukaryotic translation initiation factor 4 gamma, 1, isoform CRA_e [ | 5.32 | 1.60 |
| 119598006 | vacuolar protein sorting 13C (yeast), isoform CRA_b [Homo sapiens | 13.91 | 1.42 |
| 119597394 | hCG19253, isoform CRA_d [Homo sapiens] | 9.02 | 0.65 |
| 119592222 | ribosomal protein S4, X-linked, isoform CRA_b, partial [Homo sapier | 7.72 | 14.72 |
| 119591307 | thyroid hormone receptor interactor 12, isoform CRA_f [Homo sapie | 3.64 | 2.16 |
| 119590595 | hCG1653748 [Homo sapiens] | 3.87 | 44.74 |
| 119590527 | dynein, axonemal, heavy polypeptide 7, isoform CRA_b [Homo sapie | 13.29 | 1.52 |
| 119579125 | protein tyrosine phosphatase, receptor type, D, isoform CRA_d [Hor | 180.52 | 2.07 |
| 119576757 | hCG39912, isoform CRA_b [Homo sapiens] | 5.50 | 15.22 |
| 119574194 | heterogeneous nuclear ribonucleoprotein H1 (H), isoform CRA_b [Ho | 6.85 | 8.65 |
| 119573054 | Rho GTPase activating protein 30, isoform CRA_c [Homo sapiens] | 23.68 | 2.23 |
| 119572456 | diaphanous homolog 3 (Drosophila), isoform CRA_c [Homo sapiens] | 4.61 | 7.42 |
| 119570361 | tolloid-like 2, isoform CRA_b [Homo sapiens] | 9.19 | 3.84 |
| 119569863 | tudor domain containing 1, isoform CRA_c [Homo sapiens] | 5.29 | 3.00 |
| 119569579 | dedicator of cytokinesis 1 [Homo sapiens] | 4.72 | 1.60 |
| 221046404 | unnamed protein product [Homo sapiens] | 4.72 | 16.96 |
| 33096800 | hypothetical protein [Homo sapiens] | 5.88 | 6.90 |
| 194388520 | unnamed protein product [Homo sapiens] | 5.35 | 29.06 |
| 194381188 | unnamed protein product [Homo sapiens] | 3.66 | 2.08 |

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|---|---|---|---|
| 194374917 | unnamed protein product [Homo sapiens] | 4.63 | 9.63 |
| 194374597 | unnamed protein product [Homo sapiens] | 4.24 | 4.56 |
| 193788435 | unnamed protein product [Homo sapiens] | 36.09 | 3.11 |
| 193787899 | unnamed protein product [Homo sapiens] | 6.37 | 10.55 |
| 193785065 | unnamed protein product [Homo sapiens] | 10.49 | 8.30 |
| 158259305 | unnamed protein product [Homo sapiens] | 8.03 | 3.45 |
| 21756441 | unnamed protein product [Homo sapiens] | 10.25 | 9.17 |
| 7023915 | unnamed protein product [Homo sapiens] | 7.28 | 7.87 |
| 18676660 | FLJ00229 protein [Homo sapiens] | 6.89 | 2.87 |
| 47939143 | YBX1 protein, partial [Homo sapiens] | 4.68 | 11.65 |
| 28838367 | LOXHD1 protein [Homo sapiens] | 9.82 | 3.71 |
| 507898 | glutamate transporter [Homo sapiens] | 10.26 | 8.78 |
| 158253421 | DNAH9 protein [Homo sapiens] | 8.08 | 0.94 |
| 189053448 | unnamed protein product [Homo sapiens] | 12.58 | 5.90 |
| 47077415 | unnamed protein product [Homo sapiens] | 10.41 | 1.94 |
| 34533879 | unnamed protein product [Homo sapiens] | 9.21 | 5.81 |
| 34531561 | unnamed protein product [Homo sapiens] | 5.55 | 1.18 |
| 80476693 | NBN protein [Homo sapiens] | 3.56 | 4.03 |
| 12232589 | TFNR [Homo sapiens] | 4.65 | 1.14 |
| 40788890 | KIAA0165 [Homo sapiens] | 5.36 | 1.15 |
| 519882971 | RecName: Full=Putative ciliary rootlet coiled-coil protein-like 3 prote | 44.54 | 1.11 |
| 444738577 | alternative protein IPO7 [Homo sapiens] | 4.81 | 23.08 |
| 109730579 | Collagen, type XXIV, alpha 1 [Homo sapiens] | 7.98 | 2.39 |
| 56078799 | Ribosomal protein S27a [Homo sapiens] | 39.43 | 44.87 |
| 33440522 | FBXO38 protein [Homo sapiens] | 4.96 | 10.33 |
| 15928389 | Unknown (protein for IMAGE:4158571), partial [Homo sapiens] | 10.28 | 15.60 |
| 15680023 | B-cell receptor-associated protein 31 [Homo sapiens] | 5.32 | 16.67 |
| 13938339 | ATP5A1 protein, partial [Homo sapiens] | 6.09 | 4.90 |
| 847816 | interferon omega-1, partial [Homo sapiens] | 4.79 | 21.84 |
| 1147783 | myosin-IXb [Homo sapiens] | 8.27 | 1.19 |
| 1049053 | encodes region of fatty acid synthase activity; FAS; multifunctional | 4.47 | 0.76 |
| 183272 | glutamate decarboxylase [Homo sapiens] | 9.80 | 5.73 |
| 5805196 | Fas associated factor 1 [Homo sapiens] | 7.52 | 4.08 |
| 2104553 | Myosin heavy chain (MHY11) (5'partial) [Homo sapiens] | 32.57 | 8.02 |
| 62822517 | unknown [Homo sapiens] | 4.20 | 8.05 |
| 62822099 | unknown [Homo sapiens] | 5.97 | 5.18 |
| 62630102 | unknown [Homo sapiens] | 5.90 | 0.76 |
| 11890755 | RNA helicase II/Gu protein [Homo sapiens] | 5.55 | 4.62 |
| 4583679 | vacuolar protein sorting [Homo sapiens] | 106.07 | 7.89 |
| 40807213 | FAM179B protein [Homo sapiens] | 9.17 | 3.51 |
| 62088708 | ATP-binding cassette, sub-family F, member 1 variant [Homo sapier | 6.55 | 5.06 |
| 62087794 | N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 1 variant | 16.35 | 5.16 |
| 115333997 | 145 kDa nucleolar protein [Homo sapiens] | 4.68 | 4.93 |
| 39644893 | FOXRED1 protein [Homo sapiens] | 4.20 | 7.90 |
| 63089650 | unnamed protein product [Homo sapiens] | 5.09 | 13.13 |
| 40980242 | unnamed protein product [Homo sapiens] | 8.51 | 42.00 |
| 40976912 | unnamed protein product [Homo sapiens] | 5.71 | 16.08 |
| 40976232 | unnamed protein product [Homo sapiens] | 4.68 | 25.81 |
| 313223 | transcription elongation factor [Homo sapiens] | 3.93 | 7.97 |
| 20521792 | KIAA1208 protein [Homo sapiens] | 3.74 | 2.21 |
| 1663704 | KIAA0242 protein [Homo sapiens] | 25.68 | 7.56 |
| 550545215 | Chain D, 14-3-3gamma Complexed With The N-terminal Sequence | 10.30 | 24.71 |
| 296863377 | Chain A, Crystal Structure Of The Catalytic Domain Of Flj14393 | 7.17 | 4.98 |
| 530418458 | PREDICTED: cytochrome c oxidase subunit 4 isoform 2, mitochondri | 3.86 | 18.11 |
| 530411223 | PREDICTED: Golgi SNAP receptor complex member 1 isoform X2 [H | 3.72 | 7.72 |
| 530404104 | PREDICTED: exonuclease 3'-5' domain-containing protein 2 isoform | 4.21 | 10.93 |
| 530392546 | PREDICTED: glycylpeptide N-tetradecanoyltransferase 2 isoform X1 | 18.56 | 6.87 |
| 530382430 | PREDICTED: dystonin isoform X7 [Homo sapiens] | 16.43 | 1.13 |
| 578806816 | PREDICTED: 26S proteasome non-ATPase regulatory subunit 6 isofo | 6.98 | 8.82 |

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|---|---|---:|---:|
| 530369227 | PREDICTED: rho guanine nucleotide exchange factor 4 isoform X2 [ | 3.14 | 0.65 |
| 530363026 | PREDICTED: outer dense fiber protein 2-like isoform X4 [Homo sapi | 7.18 | 6.50 |
| 519674682 | immunoglobulin A heavy chain variable region, partial [Homo sapien | 49.28 | 11.97 |
| 381142222 | immunoglobulin light chain variable region, partial [Homo sapiens] | 4.42 | 30.19 |
| 459214638 | KIF5B-RET(NM_020630)_K24;R11 fusion protein [Homo sapiens] | 10.77 | 4.10 |
| 442564354 | von Willebrand factor [Homo sapiens] | 3.65 | 0.59 |
| 374074366 | Chain A, Crystal Structure Of 14-3-3 Epsilon With Mlf1 Peptide | 6.71 | 16.81 |
| 319443270 | Chain A, Nmr Structure Of Calcium-Loaded Stim2 Ef-Sam. | 10.11 | 7.33 |
| 190406 | profilaggrin, partial [Homo sapiens] | 4.12 | 1.40 |
| 14625824 | moesin/anaplastic lymphoma kinase fusion protein [Homo sapiens] | 4.56 | 3.61 |
| 403456 | 26S protease (S4) regulatory subunit [Homo sapiens] | 3.71 | 3.41 |
| 62871194 | immunoglobulin alpha heavy chain variable region [Homo sapiens] | 10.43 | 11.73 |
| 609412463 | Chain D, Crystal Structure Of Human Lnkh2b-h2a.z-anp32e | 10.86 | 15.31 |
| 578837382 | PREDICTED: putative SEC14-like protein 6 isoform X3 [Homo sapien | 3.61 | 5.59 |
| 578837055 | PREDICTED: calcineurin-binding protein cabin-1 isoform X12 [Homo | 12.19 | 2.10 |
| 578832590 | PREDICTED: zinc finger protein 407 isoform X3 [Homo sapiens] | 7.82 | 1.66 |
| 578831328 | PREDICTED: actin, cytoplasmic 2 isoform X1 [Homo sapiens] | 40.33 | 21.15 |
| 578826913 | PREDICTED: SHC-transforming protein 4 isoform X3 [Homo sapiens | 4.12 | 5.64 |
| 578808176 | PREDICTED: SH3 domain and tetratricopeptide repeat-containing pr | 6.01 | 1.63 |
| 578807393 | PREDICTED: leucine-, glutamate- and lysine-rich protein 1 isoform X | 56.25 | 5.28 |
| 578804532 | PREDICTED: telomere-associated protein RIF1 isoform X4 [Homo sa | 4.58 | 0.90 |
| 38305350 | antigen MLAA-44 [Homo sapiens] | 3.10 | 4.02 |
| 2253417 | Trip230 [Homo sapiens] | 13.38 | 1.97 |
| 284930095 | Treslin [Homo sapiens] | 3.16 | 0.58 |
| 11527207 | CGI-85 [Homo sapiens] | 3.66 | 7.92 |
| 40286771 | brain leucine zipper protein [Homo sapiens] | 6.36 | 9.77 |
| 52545570 | hypothetical protein [Homo sapiens] | 3.15 | 1.09 |
| 21739524 | hypothetical protein [Homo sapiens] | 26.00 | 3.82 |
| 13093781 | hypothetical protein [Homo sapiens] | 3.17 | 3.17 |
| 12052969 | hypothetical protein [Homo sapiens] | 4.34 | 6.65 |
| 51476290 | hypothetical protein [Homo sapiens] | 3.60 | 1.73 |
| 23712 | myoblast antigen 24.1D5 [Homo sapiens] | 4.38 | 6.57 |
| 62897645 | eukaryotic translation elongation factor 1 alpha 1 variant [Homo sap | 55.32 | 35.57 |
| 133251534 | piwi-like 1 [Homo sapiens] | 6.44 | 3.77 |
| 29823335 | unnamed protein product [Homo sapiens] | 7.32 | 1.65 |
| 2804273 | alpha actinin 4 [Homo sapiens] | 13.52 | 7.13 |
| 7643786 | HDCMD34P [Homo sapiens] | 1.51 | 3.64 |
| 119583237 | ankyrin repeat domain 19, isoform CRA_a [Homo sapiens] | 11.28 | 7.95 |
| 74720814 | RecName: Full=AF4/FMR2 family member 4; AltName: Full=ALL1-fu | 5.62 | 0.95 |
| 119578686 | zinc finger and BTB domain containing 5 [Homo sapiens] | 4.20 | 2.07 |
| 8569517 | Chain B, Migration Inhibitory Factor-Related Protein 8 From Human | 2.03 | 12.90 |
| 146387470 | Chain F, The Crystal Structure Of Human Gins Core Complex | 2.53 | 8.11 |
| 226246523 | fanconi-associated nuclease 1 isoform a [Homo sapiens] | 10.59 | 1.47 |
| 22653683 | RecName: Full=Chromatin accessibility complex protein 1; Short=C | 2.26 | 11.45 |
| 28380027 | RecName: Full=Putative dimethylaniline monooxygenase [N-oxide-f | 2.20 | 2.78 |
| 21542000 | RecName: Full=Hsp90 co-chaperone Cdc37; AltName: Full=Hsp90 c | 2.26 | 2.38 |
| 158519875 | RecName: Full=Cation channel sperm-associated protein subunit be | 2.56 | 2.33 |
| 12643409 | RecName: Full=Matrin-3 | 6.34 | 3.78 |
| 205831135 | RecName: Full=Putative GTP-binding protein FLJ12595 | 3.59 | 10.81 |
| 7328086 | hypothetical protein [Homo sapiens] | 2.50 | 12.45 |
| 1170862 | RecName: Full=Melanoma-associated antigen 9; AltName: Full=Can | 4.80 | 4.76 |
| 119608307 | paired related homeobox 2 [Homo sapiens] | 3.55 | 5.53 |
| 1586821 | sulphamidase | 2.10 | 2.79 |
| 119630629 | chromosome 20 open reading frame 79 [Homo sapiens] | 2.96 | 16.67 |
| 7717443 | PRED58 [Homo sapiens] | 2.27 | 9.02 |
| 1705750 | RecName: Full=CCAAT/enhancer-binding protein gamma; Short=C/ | 2.26 | 11.33 |
| 32469765 | RecName: Full=Dedicator of cytokinesis protein 2 | 6.09 | 1.69 |
| 75706636 | ubiquitously transcribed tetratricopeptide repeat protein Y-linked tra | 15.73 | 1.39 |
| 131616 | RecName: Full=Trifunctional purine biosynthetic protein adenosine- | 4.57 | 3.47 |

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|---|---|---|---|
| 130370 | RecName: Full=Pneumadin; Short=PNM | 1.53 | 50.00 |
| 52783599 | RecName: Full=Guanine nucleotide-binding protein G(I)/G(S)/G(O) | 2.04 | 16.18 |
| 4503041 | corticoliberin preproprotein [Homo sapiens] | 2.19 | 10.71 |
| 119601616 | eukaryotic translation initiation factor 2B, subunit 2 beta, 39kDa [Ho | 2.15 | 5.13 |
| 13124319 | RecName: Full=Kinesin heavy chain isoform 5C; AltName: Full=Kine | 7.59 | 3.13 |
| 119607932 | mitochondrial ribosome recycling factor, isoform CRA_e [Homo sapi | 2.56 | 17.26 |
| 3183214 | RecName: Full=Uncharacterized protein KIAA0087 | 4.37 | 10.14 |
| 24418479 | RecName: Full=Potassium voltage-gated channel subfamily G memb | 2.53 | 6.24 |
| 7959923 | PRO2738 [Homo sapiens] | 2.04 | 11.29 |
| 119618007 | IKK interacting protein, isoform CRA_a [Homo sapiens] | 4.78 | 3.71 |
| 14250487 | EML4 protein [Homo sapiens] | 1.51 | 17.74 |
| 119579805 | nyctalopin, isoform CRA_a [Homo sapiens] | 2.01 | 2.49 |
| 357528797 | RecName: Full=FRAS1-related extracellular matrix protein 3; Flags: | 2.81 | 1.03 |
| 118197270 | RANBP2-like and GRIP domain-containing protein 5/6 isoform 2 [Ho | 2.04 | 2.32 |
| 154091032 | ankyrin repeat domain-containing protein 22 [Homo sapiens] | 9.45 | 10.99 |
| 20806097 | nucleolar complex protein 3 homolog [Homo sapiens] | 14.39 | 4.88 |
| 119569197 | chromosome 6 open reading frame 57, isoform CRA_a [Homo sapie | 2.69 | 15.74 |
| 223718169 | transmembrane O-methyltransferase isoform LRTOMT2b [Homo sap | 2.61 | 10.36 |
| 37537558 | nuclear apoptosis-inducing factor 1 [Homo sapiens] | 7.03 | 3.98 |
| 119595722 | chromosome 20 open reading frame 59, isoform CRA_c, partial [Ho | 2.52 | 8.80 |
| 119600375 | potassium channel tetramerisation domain containing 13, isoform C | 9.44 | 9.42 |
| 119617055 | keratin 5b, isoform CRA_a [Homo sapiens] | 37.90 | 8.54 |
| 33872248 | Unknown (protein for IMAGE:3632616), partial [Homo sapiens] | 2.01 | 4.52 |
| 119610692 | F-box protein 39 [Homo sapiens] | 52.00 | 4.07 |
| 21758935 | unnamed protein product [Homo sapiens] | 5.18 | 4.69 |
| 74729423 | RecName: Full=Putative uncharacterized protein encoded by MAPKA | 7.12 | 14.39 |
| 119595512 | hypothetical protein FLJ38159 [Homo sapiens] | 1.58 | 1.87 |
| 119612054 | cyclic nucleotide binding domain containing 1 [Homo sapiens] | 2.03 | 3.44 |
| 21750654 | unnamed protein product [Homo sapiens] | 2.06 | 14.94 |
| 74762570 | RecName: Full=Putative protein FAM10A5; AltName: Full=Suppressi | 3.94 | 4.61 |
| 119622951 | chromosome 11 open reading frame 36, isoform CRA_a [Homo sapi | 2.04 | 5.06 |
| 30172728 | unknown [Homo sapiens] | 2.07 | 23.88 |
| 119163 | RecName: Full=Elongation factor 1-beta; Short=EF-1-beta | 1.89 | 3.11 |
| 18606290 | VPRBP protein [Homo sapiens] | 3.16 | 1.13 |
| 7739449 | hnRNP 2H9E [Homo sapiens] | 3.89 | 12.23 |
| 49457368 | TBCA [Homo sapiens] | 4.22 | 16.67 |
| 13623191 | KIAA0652 protein [Homo sapiens] | 6.30 | 3.70 |
| 119612058 | matrix metallopeptidase 16 (membrane-inserted), isoform CRA_b [H | 116.07 | 2.19 |
| 149240951 | Chain D, Human Milk Xanthine Oxidoreductase | 6.41 | 1.43 |
| 119629135 | hCG1641173 [Homo sapiens] | 2.52 | 9.65 |
| 156071462 | ADP/ATP translocase 3 [Homo sapiens] | 6.92 | 10.07 |
| 121945944 | RecName: Full=La-related protein 7; AltName: Full=La ribonucleopr | 2.62 | 4.98 |
| 120587027 | ubiquitin carboxyl-terminal hydrolase 31 [Homo sapiens] | 4.44 | 2.14 |
| 48146637 | FLJ10525 [Homo sapiens] | 2.26 | 4.86 |
| 71153032 | RecName: Full=Olfactory receptor 7D4; AltName: Full=OR19-B; Alt | 3.05 | 2.88 |
| 21928237 | seven transmembrane helix receptor [Homo sapiens] | 6.61 | 13.25 |
| 119606123 | MPF-like, isoform CRA_b [Homo sapiens] | 3.62 | 2.56 |
| 578836199 | PREDICTED: polyadenylate-binding protein 1-like isoform X3 [Homo | 14.03 | 5.45 |
| 119570368 | zinc finger protein 518 [Homo sapiens] | 2.59 | 1.62 |
| 28193122 | unnamed protein product [Homo sapiens] | 2.86 | 8.14 |
| 218512159 | RecName: Full=Putative zinc finger protein 840 | 8.02 | 0.98 |
| 21730760 | Chain V, Structure Of A Hif-1a-Pvhl-Elonginb-Elonginc Complex | 2.02 | 10.00 |
| 327478526 | RecName: Full=Myosin-14; AltName: Full=Myosin heavy chain 14; A | 14.41 | 2.51 |
| 172048422 | RecName: Full=Importin subunit alpha-8; AltName: Full=Karyopher | 3.90 | 3.68 |
| 189041198 | RecName: Full=Putative uncharacterized protein C6orf183 | 2.53 | 6.82 |
| 31874135 | hypothetical protein [Homo sapiens] | 8.65 | 10.20 |
| 152012941 | Interferon induced transmembrane protein 5 [Homo sapiens] | 2.55 | 22.73 |
| 31074637 | type I inner root sheath specific keratin 25 irs1 [Homo sapiens] | 29.35 | 5.33 |
| 119631244 | myosin IB, isoform CRA_a [Homo sapiens] | 5.38 | 1.58 |

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|---|---|---|---|
| 119582013 | family with sequence similarity 71, member B [Homo sapiens] | 2.10 | 3.80 |
| 189364 | long overlapping ORF; NH2 terminus uncertain, partial [Homo sapie | 2.08 | 8.27 |
| 119614428 | hCG2010019, partial [Homo sapiens] | 2.03 | 9.58 |
| 3859988 | proteasome subunit p58 [Homo sapiens] | 2.10 | 10.43 |
| 30269262 | pol protein [Homo sapiens] | 2.67 | 2.28 |
| 546231210 | serine/threonine-protein phosphatase 4 regulatory subunit 3A isofor | 3.80 | 3.37 |
| 21739618 | hypothetical protein [Homo sapiens] | 3.78 | 2.60 |
| 48146497 | TNFRSF21 [Homo sapiens] | 2.05 | 8.06 |
| 22002426 | brain peptide A1 [Homo sapiens] | 3.13 | 24.44 |
| 237757312 | synaptojanin-1 isoform c [Homo sapiens] | 3.86 | 1.16 |
| 119626181 | nucleoporin 54kDa, isoform CRA_b [Homo sapiens] | 1.86 | 2.41 |
| 166919564 | RecName: Full=Actin filament-associated protein 1; AltName: Full= | 17.92 | 3.15 |
| 119621549 | retinoblastoma binding protein 8, isoform CRA_b [Homo sapiens] | 2.51 | 2.08 |
| 194377758 | unnamed protein product [Homo sapiens] | 7.96 | 2.80 |
| 160017591 | RecName: Full=Coiled-coil domain-containing protein 15 | 9.60 | 5.15 |
| 119581560 | polypyrimidine tract binding protein 1, isoform CRA_e [Homo sapien | 2.19 | 4.06 |
| 148277111 | putative oncomodulin-2 [Homo sapiens] | 1.58 | 8.26 |
| 117949375 | RecName: Full=Calpain-13; AltName: Full=Calcium-activated neutra | 1.75 | 1.64 |
| 34532125 | unnamed protein product [Homo sapiens] | 2.21 | 8.03 |
| 113414869 | TBC1 domain family, member 8B (with GRAM domain) [Homo sapie | 1.51 | 1.11 |
| 37782410 | FP17581 [Homo sapiens] | 4.55 | 18.58 |
| 194294556 | SET-binding protein isoform b [Homo sapiens] | 1.67 | 3.31 |
| 34527615 | unnamed protein product [Homo sapiens] | 7.45 | 10.94 |
| 34527153 | unnamed protein product [Homo sapiens] | 2.23 | 13.67 |
| 34526674 | unnamed protein product [Homo sapiens] | 1.69 | 6.67 |
| 34535305 | unnamed protein product [Homo sapiens] | 4.25 | 7.36 |
| 34531380 | unnamed protein product [Homo sapiens] | 2.85 | 13.50 |
| 119625299 | guanylate cyclase 1, soluble, alpha 3, isoform CRA_c [Homo sapiens | 8.46 | 9.09 |
| 34189915 | RBM26 protein [Homo sapiens] | 3.49 | 21.31 |
| 62122911 | interleukin-31 precursor [Homo sapiens] | 1.55 | 3.66 |
| 440575863 | alternative protein GRINL1A [Homo sapiens] | 3.01 | 37.21 |
| 62088078 | DHX57 protein variant [Homo sapiens] | 2.60 | 2.86 |
| 109255232 | centrosomal protein of 170 kDa isoform gamma [Homo sapiens] | 5.59 | 1.30 |
| 119609753 | hCG1989313, isoform CRA_g, partial [Homo sapiens] | 10.39 | 2.87 |
| 119593568 | protein kinase N2, isoform CRA_b [Homo sapiens] | 5.65 | 3.64 |
| 34596303 | GRINL1A combined protein Gcom11 precursor [Homo sapiens] | 2.50 | 5.54 |
| 119577949 | piggyBac transposable element derived 2, isoform CRA_b [Homo sa | 2.50 | 8.21 |
| 62088124 | Abl-philin 2 isoform 3 variant [Homo sapiens] | 1.99 | 4.90 |
| 62089276 | transcription termination factor, RNA polymerase II variant [Homo s | 2.55 | 15.76 |
| 194382676 | unnamed protein product [Homo sapiens] | 2.04 | 6.18 |
| 62087632 | solute carrier family 37 (glycerol-6-phosphate transporter), member | 4.93 | 3.08 |
| 62087594 | RNA binding motif protein 14 variant [Homo sapiens] | 2.31 | 1.27 |
| 530421763 | PREDICTED: protein PBDC1 isoform X1 [Homo sapiens] | 1.55 | 3.02 |
| 23271324 | CMIP protein [Homo sapiens] | 2.08 | 2.10 |
| 194374751 | unnamed protein product [Homo sapiens] | 2.04 | 11.02 |
| 157829345 | ubiquitously transcribed tetratricopeptide repeat protein X-linked tra | 2.89 | 2.55 |
| 194383268 | unnamed protein product [Homo sapiens] | 2.51 | 7.33 |
| 84708830 | TUBB6 protein [Homo sapiens] | 27.96 | 12.75 |
| 194387516 | unnamed protein product [Homo sapiens] | 2.08 | 7.02 |
| 119613529 | hCG1642860 [Homo sapiens] | 8.47 | 6.27 |
| 119613673 | hCG25333, isoform CRA_a [Homo sapiens] | 5.70 | 6.88 |
| 88999767 | autogenous vein graft remodeling associated protein 5 [Homo sapie | 2.68 | 4.09 |
| 112891 | RecName: Full=Putative alpha-1-antitrypsin-related protein; AltNam | 2.05 | 4.29 |
| 475808427 | POTE ankyrin domain family member I [Homo sapiens] | 12.75 | 3.26 |
| 18089180 | LOC644246 protein, partial [Homo sapiens] | 4.12 | 24.14 |
| 205831107 | RecName: Full=Protein FAM196B | 5.46 | 4.86 |
| 21754281 | unnamed protein product [Homo sapiens] | 1.53 | 2.86 |
| 143928063 | RecName: Full=Serine/arginine repetitive matrix protein 2; AltName | 25.49 | 1.89 |
| 215274269 | RecName: Full=Spectrin beta chain, erythrocytic; AltName: Full=Bet | 5.31 | 1.12 |

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|---|---|---|---|
| 56675094 | cathepsin L-like protein [Homo sapiens] | 1.52 | 2.75 |
| 62087622 | BM-010 variant [Homo sapiens] | 2.16 | 23.88 |
| 190410954 | RecName: Full=Transmembrane and coiled-coil domain-containing | 2.01 | 3.91 |
| 193787670 | unnamed protein product [Homo sapiens] | 34.60 | 5.74 |
| 119580802 | hypothetical protein LOC63929, isoform CRA_b [Homo sapiens] | 4.14 | 5.61 |
| 119585275 | coiled-coil domain containing 51, isoform CRA_a [Homo sapiens] | 3.27 | 11.26 |
| 221043670 | unnamed protein product [Homo sapiens] | 1.74 | 6.45 |
| 4514403 | squamous cell carcinoma antigen 2 [Homo sapiens] | 2.54 | 13.73 |
| 194384240 | unnamed protein product [Homo sapiens] | 108.64 | 26.31 |
| 116283351 | CCDC6 protein [Homo sapiens] | 2.84 | 3.89 |
| 313104224 | RecName: Full=LON peptidase N-terminal domain and RING finger | 3.73 | 3.05 |
| 71297232 | PPM1K protein [Homo sapiens] | 1.68 | 4.67 |
| 154426306 | kinesin-like protein KIF24 [Homo sapiens] | 3.24 | 0.44 |
| 28302161 | CCBE1 protein [Homo sapiens] | 2.01 | 8.37 |
| 51094451 | FLJ42291 protein [Homo sapiens] | 2.16 | 1.48 |
| 540344531 | acetylcholinesterase isoform 3 precursor [Homo sapiens] | 10.26 | 2.09 |
| 119586982 | hCG14941, isoform CRA_a [Homo sapiens] | 5.69 | 1.55 |
| 215273970 | RecName: Full=Protein diaphanous homolog 1; AltName: Full=Diap | 8.51 | 2.20 |
| 73621116 | RecName: Full=Protein KIAA1045 | 2.00 | 4.25 |
| 155030220 | sister chromatid cohesion protein PDS5 homolog A isoform 3 [Hom | 1.53 | 0.83 |
| 151347347 | MUC1 isoform M8 [Homo sapiens] | 2.24 | 7.91 |
| 119630988 | isocitrate dehydrogenase 3 (NAD+) beta, isoform CRA_b [Homo sa | 2.23 | 8.15 |
| 194375209 | unnamed protein product [Homo sapiens] | 2.02 | 3.16 |
| 634743229 | inhibitor of growth protein 2 isoform 2 [Homo sapiens] | 2.16 | 7.08 |
| 17511715 | FLYWCH1 protein [Homo sapiens] | 2.09 | 3.84 |
| 530403029 | PREDICTED: protein AHNAK2 isoform X1 [Homo sapiens] | 4.83 | 1.86 |
| 211059433 | telomere repeats-binding bouquet formation protein 1 [Homo sapie | 8.59 | 3.44 |
| 1515452 | tissue plasminogen activator, partial [Homo sapiens] | 2.08 | 13.25 |
| 194382670 | unnamed protein product [Homo sapiens] | 2.54 | 10.70 |
| 119627029 | hypothetical protein FLJ10986, isoform CRA_d [Homo sapiens] | 5.20 | 4.10 |
| 194378698 | unnamed protein product [Homo sapiens] | 4.18 | 5.16 |
| 194383408 | unnamed protein product [Homo sapiens] | 2.23 | 9.50 |
| 193787232 | unnamed protein product [Homo sapiens] | 9.93 | 7.00 |
| 194386226 | unnamed protein product [Homo sapiens] | 4.02 | 12.90 |
| 194387020 | unnamed protein product [Homo sapiens] | 2.80 | 11.17 |
| 194384530 | unnamed protein product [Homo sapiens] | 2.77 | 14.11 |
| 194384124 | unnamed protein product [Homo sapiens] | 2.04 | 1.47 |
| 194377112 | unnamed protein product [Homo sapiens] | 2.22 | 6.56 |
| 194379488 | unnamed protein product [Homo sapiens] | 1.50 | 1.86 |
| 194389024 | unnamed protein product [Homo sapiens] | 2.14 | 7.59 |
| 194381310 | unnamed protein product [Homo sapiens] | 2.61 | 5.86 |
| 194382494 | unnamed protein product [Homo sapiens] | 4.80 | 7.34 |
| 194377718 | unnamed protein product [Homo sapiens] | 2.17 | 8.06 |
| 194384754 | unnamed protein product [Homo sapiens] | 2.07 | 2.01 |
| 194374107 | unnamed protein product [Homo sapiens] | 2.67 | 10.29 |
| 194373459 | unnamed protein product [Homo sapiens] | 2.64 | 11.35 |
| 194389532 | unnamed protein product [Homo sapiens] | 25.17 | 7.24 |
| 194384220 | unnamed protein product [Homo sapiens] | 2.18 | 1.46 |
| 194386174 | unnamed protein product [Homo sapiens] | 2.53 | 5.81 |
| 194383904 | unnamed protein product [Homo sapiens] | 1.67 | 5.69 |
| 194387024 | unnamed protein product [Homo sapiens] | 3.01 | 4.65 |
| 300116271 | 3-oxo-5-beta-steroid 4-dehydrogenase isoform 2 [Homo sapiens] | 1.69 | 4.56 |
| 194382774 | unnamed protein product [Homo sapiens] | 2.59 | 8.10 |
| 194377168 | unnamed protein product [Homo sapiens] | 4.57 | 13.66 |
| 194375932 | unnamed protein product [Homo sapiens] | 216.61 | 6.42 |
| 194384396 | unnamed protein product [Homo sapiens] | 3.64 | 2.54 |
| 194388594 | unnamed protein product [Homo sapiens] | 4.47 | 5.95 |
| 194375063 | unnamed protein product [Homo sapiens] | 9.65 | 12.67 |
| 194389318 | unnamed protein product [Homo sapiens] | 2.12 | 2.42 |

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|---|---|---|---|
| 194378362 | unnamed protein product [Homo sapiens] | 2.14 | 4.05 |
| 214010191 | ribonuclease H2 subunit B isoform 2 [Homo sapiens] | 2.03 | 7.39 |
| 300669606 | RecName: Full=Rho guanine nucleotide exchange factor 33 | 2.01 | 1.54 |
| 119591539 | ubiquitin-conjugating enzyme E2F (putative), isoform CRA_f [Homo | 1.57 | 9.52 |
| 119613486 | oxoglutarate dehydrogenase-like, isoform CRA_a [Homo sapiens] | 3.75 | 2.12 |
| 221316674 | dimethylaniline monooxygenase [N-oxide-forming] 5 isoform 2 [Hon | 2.63 | 4.53 |
| 219520978 | MYBPHL protein [Homo sapiens] | 2.63 | 8.46 |
| 354548834 | zinc transporter 5 isoform 3 [Homo sapiens] | 3.16 | 7.79 |
| 221039610 | unnamed protein product [Homo sapiens] | 3.61 | 4.79 |
| 221045258 | unnamed protein product [Homo sapiens] | 2.28 | 4.46 |
| 221041774 | unnamed protein product [Homo sapiens] | 4.46 | 5.26 |
| 221041900 | unnamed protein product [Homo sapiens] | 1.58 | 4.73 |
| 221043242 | unnamed protein product [Homo sapiens] | 6.19 | 6.09 |
| 195928000 | nuclear factor of activated T-cells c4 isoform IC-IXS [Homo sapiens] | 7.27 | 2.30 |
| 119590976 | ribosomal protein L37a, isoform CRA_b [Homo sapiens] | 2.07 | 12.07 |
| 52545699 | hypothetical protein [Homo sapiens] | 10.71 | 2.23 |
| 119584380 | bromodomain and PHD finger containing, 1, isoform CRA_e [Homo s | 4.33 | 1.73 |
| 119590674 | amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candi | 11.11 | 8.39 |
| 220897513 | LUC7-like (S. cerevisiae) [Homo sapiens] | 1.54 | 21.88 |
| 193785596 | unnamed protein product [Homo sapiens] | 27.29 | 25.94 |
| 194388148 | unnamed protein product [Homo sapiens] | 3.88 | 5.88 |
| 194391382 | unnamed protein product [Homo sapiens] | 4.18 | 7.34 |
| 545479145 | mediator of RNA polymerase II transcription subunit 30 isoform 2 [H | 2.52 | 13.29 |
| 378405228 | RecName: Full=Tetratricopeptide repeat protein 40 | 4.76 | 1.62 |
| 194377158 | unnamed protein product [Homo sapiens] | 2.02 | 6.94 |
| 119629284 | integrator complex subunit 6, isoform CRA_b [Homo sapiens] | 4.53 | 4.23 |
| 378405232 | RecName: Full=StAR-related lipid transfer protein 9; AltName: Full= | 4.41 | 0.72 |
| 193786637 | unnamed protein product [Homo sapiens] | 4.91 | 10.68 |
| 119615050 | pyruvate dehydrogenase kinase, isozyme 2, isoform CRA_c [Homo s | 3.01 | 5.83 |
| 578825442 | PREDICTED: egl nine homolog 3 isoform X1 [Homo sapiens] | 2.40 | 8.97 |
| 21322210 | MHC class II HLA-DQ [Homo sapiens] | 1.51 | 7.50 |
| 194383974 | unnamed protein product [Homo sapiens] | 2.07 | 4.29 |
| 119588806 | general transcription factor IIH, polypeptide 1, 62kDa, isoform CRA_ | 2.67 | 4.63 |
| 6815237 | 5-hydroxytryptamine (serotonin) receptor 1F [Homo sapiens] | 2.55 | 8.22 |
| 119632249 | hCG2044193 [Homo sapiens] | 2.18 | 1.41 |
| 119588809 | Hermansky-Pudlak syndrome 5, isoform CRA_b, partial [Homo sapie | 2.19 | 3.00 |
| 28375611 | unnamed protein product [Homo sapiens] | 7.03 | 8.12 |
| 194378470 | unnamed protein product [Homo sapiens] | 2.02 | 4.86 |
| 194378082 | unnamed protein product [Homo sapiens] | 1.55 | 3.23 |
| 221046300 | unnamed protein product [Homo sapiens] | 2.03 | 7.51 |
| 193787268 | unnamed protein product [Homo sapiens] | 5.78 | 3.09 |
| 9587153 | xeroderma pigmentosum complementation group G protein splice va | 1.50 | 3.02 |
| 193787064 | unnamed protein product [Homo sapiens] | 2.65 | 6.74 |
| 62088934 | CDC10 protein variant [Homo sapiens] | 1.51 | 2.10 |
| 75517448 | TMC1 protein [Homo sapiens] | 6.05 | 2.20 |
| 194386170 | unnamed protein product [Homo sapiens] | 2.24 | 5.63 |
| 221043808 | unnamed protein product [Homo sapiens] | 2.35 | 4.39 |
| 194385852 | unnamed protein product [Homo sapiens] | 3.88 | 4.05 |
| 194388748 | unnamed protein product [Homo sapiens] | 2.05 | 3.95 |
| 221040478 | unnamed protein product [Homo sapiens] | 6.75 | 3.50 |
| 58041810 | tRNA isopentenylpyrophosphate transferase isoform 6 [Homo sapier | 3.43 | 6.75 |
| 221044102 | unnamed protein product [Homo sapiens] | 8.41 | 3.52 |
| 164691199 | unnamed protein product [Homo sapiens] | 2.24 | 6.64 |
| 332164666 | caveolin-2 isoform d [Homo sapiens] | 2.63 | 46.84 |
| 30722352 | hypothetical protein [Homo sapiens] | 2.04 | 1.95 |
| 194383366 | unnamed protein product [Homo sapiens] | 2.33 | 3.34 |
| 17372671 | RecName: Full=Ataxin-10; AltName: Full=Brain protein E46 homolog | 8.21 | 9.47 |
| 221042358 | unnamed protein product [Homo sapiens] | 3.46 | 5.42 |
| 119621321 | hCG1990625, isoform CRA_a [Homo sapiens] | 3.93 | 17.81 |

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|---|---|---|---|
| 40035509 | unnamed protein product [Homo sapiens] | 2.62 | 5.99 |
| 86577744 | HSPA5 protein [Homo sapiens] | 26.15 | 19.24 |
| 119589905 | ribosomal protein S15, isoform CRA_a [Homo sapiens] | 2.52 | 11.02 |
| 117414137 | retinitis pigmentosa 1-like 1 protein [Homo sapiens] | 4.30 | 0.33 |
| 119593515 | bromodomain, testis-specific, isoform CRA_b [Homo sapiens] | 8.44 | 2.75 |
| 119612282 | collagen triple helix repeat containing 1, isoform CRA_c [Homo sapie | 2.07 | 6.55 |
| 172046061 | RecName: Full=Immunoglobulin superfamily member 3; Short=IgS | 2.14 | 0.75 |
| 347954819 | ankyrin repeat domain-containing protein 18B [Homo sapiens] | 1.57 | 1.09 |
| 10437855 | unnamed protein product [Homo sapiens] | 6.63 | 9.92 |
| 119604261 | nucleoporin 205kDa, isoform CRA_a [Homo sapiens] | 3.11 | 0.94 |
| 449061866 | RecName: Full=Protein C9orf69; AltName: Full=Herpes virus UL25- | 4.13 | 6.47 |
| 353251637 | Chain E, Orientation Of Rna Polymerase Ii Within The Human Vp16- | 1.68 | 3.26 |
| 12803397 | ATRX protein [Homo sapiens] | 1.84 | 7.78 |
| 73920089 | RecName: Full=Potassium channel subfamily T member 1; AltName | 2.05 | 0.65 |
| 145585268 | unnamed protein product [Homo sapiens] | 3.49 | 3.30 |
| 119595343 | phosphoglucomutase 2-like 1 [Homo sapiens] | 2.01 | 2.41 |
| 119604667 | zinc finger protein 625, isoform CRA_a [Homo sapiens] | 2.89 | 6.21 |
| 401015109 | tumor necrosis factor receptor superfamily member 11A isoform 4 p | 2.41 | 4.01 |
| 78101501 | Chain D, Crystal Structure Of Kh1 Domain Of Human Poly(C)-Bindin | 3.52 | 17.81 |
| 157880239 | Chain B, Crystal Structure Of Human Trypsin 1: Unexpected Phosph | 23.23 | 8.04 |
| 157831398 | Chain A, Human Mannose Binding Protein Carbohydrate Recognition | 2.68 | 9.22 |
| 401817558 | Chain B, Human Igg1 Fc Fragment Heterodimer | 16.14 | 12.56 |
| 239782025 | Chain D, Human Sahh-Like Domain Of Human Adenosylhomocystei | 8.95 | 3.22 |
| 61679820 | Chain A, Solution Structure Of Human Prolactin | 2.14 | 8.04 |
| 13786848 | Chain B, Human Heart L-Lactate Dehydrogenase H Chain, Ternary | 6.09 | 8.11 |
| 342350991 | Chain B, Crystal Structure Of Human Nadph-Cytochrome P450 Redu | 6.42 | 3.72 |
| 119610899 | Tax1 (human T-cell leukemia virus type I) binding protein 3, isofor | 2.53 | 38.30 |
| 544192134 | Chain F, Structural Basis For Autoactivation Of Human Mst2 Kinase | 5.00 | 4.68 |
| 532138036 | Chain B, Crystal Structure Of Mers-cov Complexed With Human Dpp | 1.51 | 2.94 |
| 413915762 | Chain A, Homologous Domain Of Human Fkbp25 | 3.82 | 11.21 |
| 167745132 | Chain A, Human Poly(Adp-Ribose) Polymerase 3, Catalytic Fragment | 2.02 | 3.36 |
| 110590621 | Chain B, Structure Of Human Mip-3a Chemokine | 2.01 | 11.59 |
| 349587833 | Chain J, Crystal Structure Of Full-Length Human Peroxiredoxin 4 Wi | 3.06 | 8.54 |
| 238828124 | Chain C, Crystal Structure Of The Human Rad9-Hus1-Rad1 Complex | 2.02 | 6.46 |
| 78101741 | Chain A, 14-3-3 Protein Beta (human) In Complex With Exoenzyme | 8.27 | 14.29 |
| 61679988 | Chain B, Crystal Structure Of The TollINTERLEUKIN-1 Receptor (Tir | 8.32 | 11.95 |
| 512125429 | Chain B, Protease-induced Heterodimer Of Human Triosephosphate | 3.81 | 8.13 |
| 491668222 | Chain A, Crystal Structure Of The Human Cdkl5 Kinase Domain | 11.29 | 8.88 |
| 157835957 | Chain A, Crystal Structure Of The Extracellular Domain Of Human G | 2.23 | 9.63 |
| 564731264 | Chain B, Crystal Structure Of The Extracellular Domain Of Human G | 2.08 | 1.85 |
| 159163949 | Chain A, Solution Structure Of J-Domain From Human Dnaj Subfami | 1.55 | 11.54 |
| 159163860 | Chain A, Solution Structure Of Rsgi Ruh-039, A Fragment Of C- Terr | 2.00 | 21.05 |
| 7245805 | Chain D, Human Erythrocyte Catalase | 1.73 | 1.41 |
| 534286037 | Chain G, Crystal Structure Of Human Nucleosome Core Particle Lack | 9.76 | 22.58 |
| 42543655 | Chain D, Crystal Structure Of Human Anti-hiv-1 Gp120 Reactive Anti | 13.27 | 14.02 |
| 361129718 | Chain A, Solution Structure Of The Dimerization Domain Of Human | 4.30 | 23.19 |
| 179744 | voltage-dependent calcium channel beta-2 subunit [Homo sapiens] | 2.54 | 6.28 |
| 232472 | nucleotide diphosphate kinase subunit A, p19/nm23-H1 [human, Pe | 2.31 | 100.00 |
| 252092 | HLBP14=14-kDa laminin binding protein [human, melanoma cells, P | 3.89 | 100.00 |
| 2135467 | Ig heavy chain - human (fragment) | 7.05 | 15.70 |
| 345758 | lamin B2 - human (fragment) | 7.66 | 4.27 |
| 284187 | Ig heavy chain V region (DP-30) - human (fragment) | 4.41 | 19.00 |
| 87330 | DNA-binding protein GRF-1 - human | 3.57 | 1.80 |
| 300197 | V gamma 9JP/V delta 2DJ1 T cell receptor {cytotoxic clone SC1, rea | 8.46 | 80.00 |
| 87804 | Ig heavy chain precursor V-D-J region (JP-FL-5) - human | 2.73 | 18.92 |
| 223429 | tubulin beta | 33.62 | 17.34 |
| 449754 | MLL-AF4 fusion protein | 8.82 | 1.25 |
| 311772087 | Chain E, Structure Of Il-13 Antibody H2l6, A Humanized Variant Of | 6.95 | 9.82 |
| 2689443 | R28830_2 [Homo sapiens] | 2.17 | 2.33 |

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|---|---|---|---|
| 391358156 | RecName: Full=Kinetochore protein Spc24; Short=hSpc24 | 4.27 | 7.11 |
| 3482907 | CTF5 [Homo sapiens] | 2.87 | 45.45 |
| 10438968 | unnamed protein product [Homo sapiens] | 1.56 | 3.31 |
| 10437189 | unnamed protein product [Homo sapiens] | 2.62 | 5.19 |
| 10437000 | unnamed protein product [Homo sapiens] | 2.16 | 3.36 |
| 4406651 | h-sco1 [Homo sapiens] | 3.80 | 11.05 |
| 49168450 | ANXA9 [Homo sapiens] | 5.16 | 9.17 |
| 119609484 | ATP-binding cassette, sub-family A (ABC1), member 10, isoform CR | 8.37 | 2.53 |
| 1699038 | ABC3 [Homo sapiens] | 2.68 | 1.70 |
| 2826857 | KIF3C [Homo sapiens] | 2.54 | 38.46 |
| 525343614 | replication factor C subunit 2 isoform 5 [Homo sapiens] | 12.85 | 9.13 |
| 452722259 | immunoglobulin kappa light chain variable region, partial [Homo sap | 5.92 | 12.86 |
| 119622276 | thioredoxin domain containing 9, isoform CRA_c [Homo sapiens] | 6.41 | 2.66 |
| 119622225 | ring finger protein 149, isoform CRA_d [Homo sapiens] | 3.63 | 4.08 |
| 119615402 | heparan sulfate proteoglycan 2 (perlecan), isoform CRA_b [Homo sa | 5.81 | 0.78 |
| 119610699 | solute carrier family 13 (sodium-dependent citrate transporter), me | 8.22 | 4.03 |
| 119590731 | hCG2036623, isoform CRA_a [Homo sapiens] | 2.04 | 0.74 |
| 119589968 | ATP-binding cassette, sub-family A (ABC1), member 7, isoform CRA | 2.25 | 1.46 |
| 115529031 | SCNN1D protein [Homo sapiens] | 2.84 | 6.61 |
| 115527741 | NOX5 protein [Homo sapiens] | 6.46 | 6.54 |
| 588282802 | zona pellucida sperm-binding protein 2 isoform 2 preproprotein [Ho | 2.54 | 3.40 |
| 125858928 | DLEC1 protein [Homo sapiens] | 3.28 | 1.26 |
| 20530135 | growth differentiation factor 3A [Homo sapiens] | 2.00 | 5.79 |
| 6648144 | neurexin III [Homo sapiens] | 1.52 | 2.85 |
| 208606797 | unnamed protein product [Homo sapiens] | 3.15 | 2.83 |
| 193786834 | unnamed protein product [Homo sapiens] | 2.06 | 2.12 |
| 152061071 | LIN28B protein [Homo sapiens] | 7.28 | 6.61 |
| 124504581 | SAMD13 protein [Homo sapiens] | 2.59 | 19.05 |
| 18676915 | unnamed protein product [Homo sapiens] | 4.07 | 2.34 |
| 16554278 | unnamed protein product [Homo sapiens] | 4.76 | 4.85 |
| 16553682 | unnamed protein product [Homo sapiens] | 6.19 | 5.20 |
| 10437815 | unnamed protein product [Homo sapiens] | 1.64 | 2.16 |
| 557357735 | adenosine 3'-phospho 5'-phosphosulfate transporter 1 isoform b [H | 2.86 | 3.75 |
| 544186123 | dimethylaniline monooxygenase [N-oxide-forming] 1 isoform a [Ho | 1.89 | 1.31 |
| 526118181 | surfeit locus protein 4 isoform 6 [Homo sapiens] | 4.35 | 8.55 |
| 119621383 | tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation | 5.59 | 19.86 |
| 119621343 | Rho-associated, coiled-coil containing protein kinase 2, isoform CRA | 1.81 | 1.27 |
| 119621160 | hCG22390, isoform CRA_a [Homo sapiens] | 4.01 | 5.20 |
| 119620547 | spectrin, beta, non-erythrocytic 1, isoform CRA_e [Homo sapiens] | 4.49 | 8.31 |
| 119620491 | polyribonucleotide nucleotidyltransferase 1, isoform CRA_a [Homo s | 8.12 | 2.00 |
| 119620455 | hCG1783369 [Homo sapiens] | 2.47 | 16.92 |
| 119620409 | AHA1, activator of heat shock 90kDa protein ATPase homolog 2 (ye | 24.36 | 14.29 |
| 119577251 | seryl-tRNA synthetase 2, isoform CRA_c [Homo sapiens] | 1.68 | 2.44 |
| 119577203 | mitogen-activated protein kinase kinase kinase kinase 1, isoform CR | 369.83 | 11.45 |
| 119632275 | hCG1793821, isoform CRA_a [Homo sapiens] | 1.68 | 7.48 |
| 119632132 | DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 26B, isoform CRA_c | 4.53 | 6.03 |
| 119632103 | hCG1646178, isoform CRA_a, partial [Homo sapiens] | 1.56 | 4.62 |
| 119631973 | hCG1647962, isoform CRA_a, partial [Homo sapiens] | 2.30 | 6.00 |
| 119631874 | hCG2007338, isoform CRA_b, partial [Homo sapiens] | 3.11 | 4.03 |
| 119631669 | hCG15219, isoform CRA_a, partial [Homo sapiens] | 2.08 | 21.24 |
| 119631525 | chimerin (chimaerin) 1, isoform CRA_d [Homo sapiens] | 7.06 | 6.56 |
| 119631421 | titin, isoform CRA_c [Homo sapiens] | 15.86 | 0.79 |
| 119631077 | TBC1 domain family, member 20, isoform CRA_c [Homo sapiens] | 2.27 | 7.96 |
| 119630700 | hCG2038614, partial [Homo sapiens] | 1.54 | 6.03 |
| 119630031 | hCG1812841, isoform CRA_a, partial [Homo sapiens] | 2.59 | 10.00 |
| 119630026 | Down syndrome cell adhesion molecule, isoform CRA_b, partial [Ho | 3.80 | 1.15 |
| 119629967 | ubiquitin associated and SH3 domain containing, A, isoform CRA_c, | 4.95 | 8.20 |
| 119629319 | hCG2041314, partial [Homo sapiens] | 2.33 | 14.39 |
| 119629073 | hCG1644029, partial [Homo sapiens] | 2.01 | 6.49 |

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|---|---|---|---|
| 119628926 | hCG32806, isoform CRA_e [Homo sapiens] | 2.05 | 0.55 |
| 119628728 | spastic ataxia of Charlevoix-Saguenay (sacsin), partial [Homo sapie | 4.85 | 4.04 |
| 119628614 | hCG1791068, isoform CRA_b, partial [Homo sapiens] | 2.16 | 2.54 |
| 119628610 | hCG18315, isoform CRA_c [Homo sapiens] | 2.57 | 8.26 |
| 119628541 | iroquois homeobox protein 2, partial [Homo sapiens] | 2.00 | 3.63 |
| 119628538 | hCG1989689, partial [Homo sapiens] | 2.12 | 13.08 |
| 119628507 | hCG1990016 [Homo sapiens] | 14.00 | 9.09 |
| 119628379 | chaperonin containing TCP1, subunit 6A (zeta 1), isoform CRA_b [H | 2.26 | 7.08 |
| 119627737 | hCG2041179, partial [Homo sapiens] | 2.59 | 36.14 |
| 119627245 | hCG1643513 [Homo sapiens] | 2.44 | 2.30 |
| 119625915 | homeodomain-only protein, isoform CRA_i, partial [Homo sapiens] | 4.68 | 32.20 |
| 119625687 | hCG2036595 [Homo sapiens] | 1.61 | 1.48 |
| 119625447 | OTU domain containing 4, isoform CRA_a [Homo sapiens] | 5.79 | 3.63 |
| 119625403 | mab-21-like 2 (C. elegans), isoform CRA_a [Homo sapiens] | 3.03 | 5.46 |
| 119625162 | hCG2041080, partial [Homo sapiens] | 9.98 | 14.12 |
| 119624765 | polycystic kidney and hepatic disease 1 (autosomal recessive), isofo | 2.53 | 0.62 |
| 119623591 | olfactory receptor, family 5, subfamily U, member 1 [Homo sapiens] | 2.53 | 8.45 |
| 119623229 | hCG1989619, isoform CRA_a [Homo sapiens] | 2.57 | 17.53 |
| 119623210 | protocadherin 19, isoform CRA_b [Homo sapiens] | 11.48 | 1.31 |
| 119623206 | hCG18775, isoform CRA_b, partial [Homo sapiens] | 2.27 | 3.85 |
| 119622706 | proprotein convertase subtilisin/kexin type 6, isoform CRA_a [Homo | 2.03 | 2.18 |
| 119622691 | hCG2045702, partial [Homo sapiens] | 2.00 | 13.46 |
| 119622550 | hCG2041657, partial [Homo sapiens] | 18.67 | 9.52 |
| 119622113 | hCG1644617 [Homo sapiens] | 2.00 | 18.95 |
| 119622000 | RAB31, member RAS oncogene family, isoform CRA_a [Homo sapie | 2.64 | 10.47 |
| 119619806 | hCG39240, isoform CRA_b [Homo sapiens] | 4.76 | 13.89 |
| 119619572 | hCG2005369, partial [Homo sapiens] | 2.52 | 16.87 |
| 119619444 | hCG2036884 [Homo sapiens] | 2.74 | 12.06 |
| 119619407 | hypothetical protein MGC4825, isoform CRA_a [Homo sapiens] | 3.32 | 14.04 |
| 119619137 | hCG1981372, isoform CRA_a [Homo sapiens] | 2.62 | 14.74 |
| 119618553 | coiled-coil domain containing 60, isoform CRA_a [Homo sapiens] | 2.53 | 19.55 |
| 119618310 | ATPase, Ca++ transporting, cardiac muscle, slow twitch 2, isoform | 2.42 | 1.49 |
| 119618067 | hCG1815253 [Homo sapiens] | 2.06 | 20.34 |
| 119618010 | apoptotic peptidase activating factor, isoform CRA_b, partial [Homo | 5.59 | 2.06 |
| 119617982 | hCG2042157, partial [Homo sapiens] | 2.11 | 2.96 |
| 119617754 | PRKC, apoptosis, WT1, regulator, isoform CRA_c [Homo sapiens] | 2.59 | 43.75 |
| 119617334 | ubiquitin specific peptidase 52, isoform CRA_a [Homo sapiens] | 5.22 | 1.42 |
| 119617311 | myosin, light polypeptide 6, alkali, smooth muscle and non-muscle, | 2.33 | 15.53 |
| 119617203 | hCG21937, isoform CRA_b [Homo sapiens] | 9.18 | 6.01 |
| 119616788 | hCG2040433 [Homo sapiens] | 2.01 | 4.84 |
| 119616523 | C-type lectin domain family 2, member D, isoform CRA_b [Homo sa | 6.63 | 12.39 |
| 119616286 | single-stranded DNA binding protein 2, isoform CRA_d [Homo sapie | 2.17 | 13.54 |
| 119616244 | PAP associated domain containing 4, isoform CRA_b, partial [Homo | 7.29 | 2.73 |
| 119616019 | hCG1979897, isoform CRA_b [Homo sapiens] | 2.03 | 8.16 |
| 119616018 | hCG1979897, isoform CRA_a, partial [Homo sapiens] | 8.28 | 12.12 |
| 119615473 | ribosomal protein L11, isoform CRA_a [Homo sapiens] | 2.26 | 5.26 |
| 119615116 | tubulin tyrosine ligase-like family, member 6, isoform CRA_b [Homo | 3.32 | 1.25 |
| 119614967 | mbt domain containing 1, isoform CRA_b, partial [Homo sapiens] | 1.70 | 8.00 |
| 119614760 | EF-hand calcium binding domain 3, partial [Homo sapiens] | 2.51 | 2.90 |
| 119614392 | phosphodiesterase 1C, calmodulin-dependent 70kDa, isoform CRA_ | 5.31 | 5.57 |
| 119613593 | inter-alpha (globulin) inhibitor H5-like, isoform CRA_b, partial [Hom | 2.59 | 5.16 |
| 119612728 | hCG1787519 [Homo sapiens] | 1.62 | 7.62 |
| 119612617 | PTK2 protein tyrosine kinase 2, isoform CRA_b [Homo sapiens] | 5.38 | 2.27 |
| 119612447 | F-box protein 32, isoform CRA_b, partial [Homo sapiens] | 3.07 | 11.81 |
| 119612325 | eukaryotic translation initiation factor 3, subunit 6 48kDa, isoform C | 2.09 | 2.78 |
| 119611721 | kinesin family member 14, isoform CRA_a [Homo sapiens] | 1.53 | 0.51 |
| 119611588 | chromosome 1 open reading frame 22, isoform CRA_e [Homo sapie | 32.39 | 9.90 |
| 119611381 | hCG2040409 [Homo sapiens] | 6.41 | 20.36 |
| 119611364 | chromosome 1 open reading frame 155, isoform CRA_b, partial [Ho | 2.70 | 16.20 |

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|---|---|---|---|
| 119611340 | chromosome 1 open reading frame 9, isoform CRA_d [Homo sapien | 1.61 | 0.57 |
| 119610429 | hCG57025, isoform CRA_c [Homo sapiens] | 2.49 | 1.63 |
| 574270145 | alpha-N-acetylgalactosaminide alpha-2,6-sialyltransferase 1 isoform | 4.76 | 2.99 |
| 119609527 | hCG1641439 [Homo sapiens] | 7.05 | 10.49 |
| 119608942 | hCG2041489, partial [Homo sapiens] | 5.01 | 3.98 |
| 119608652 | EGF-like-domain, multiple 7, isoform CRA_a, partial [Homo sapiens] | 2.02 | 8.60 |
| 119608609 | hCG2040469 [Homo sapiens] | 2.61 | 13.30 |
| 119608259 | nucleoporin 188kDa, isoform CRA_d, partial [Homo sapiens] | 2.62 | 1.83 |
| 119607432 | junctophilin 1, isoform CRA_a, partial [Homo sapiens] | 1.52 | 2.43 |
| 119607075 | hCG2042370, partial [Homo sapiens] | 2.09 | 15.09 |
| 119606579 | hCG21545, isoform CRA_b [Homo sapiens] | 16.79 | 1.98 |
| 119606543 | armadillo repeat containing 3, isoform CRA_a [Homo sapiens] | 5.11 | 2.64 |
| 119606115 | CTF18, chromosome transmission fidelity factor 18 homolog (S. cere | 2.62 | 6.09 |
| 119606064 | hypothetical protein LOC283951, isoform CRA_b [Homo sapiens] | 2.00 | 5.06 |
| 119605696 | hCG1658583, isoform CRA_b, partial [Homo sapiens] | 4.81 | 1.86 |
| 119605531 | hCG2042874, isoform CRA_b, partial [Homo sapiens] | 2.09 | 3.04 |
| 119605415 | solute carrier family 34 (sodium phosphate), member 1, isoform CR | 2.11 | 3.72 |
| 119604587 | dedicator of cytokinesis 6, isoform CRA_c, partial [Homo sapiens] | 3.37 | 0.60 |
| 119604409 | hCG21930, isoform CRA_f [Homo sapiens] | 3.03 | 0.16 |
| 119604207 | coiled-coil-helix-coiled-coil-helix domain containing 3, isoform CRA_ | 2.51 | 8.70 |
| 119602547 | hCG1993037, isoform CRA_h [Homo sapiens] | 4.26 | 2.32 |
| 119602406 | hCG2038924, partial [Homo sapiens] | 3.56 | 6.98 |
| 119602251 | protein phosphatase 1, regulatory (inhibitor) subunit 13B, isoform C | 2.02 | 1.46 |
| 119602146 | hCG2036999 [Homo sapiens] | 278.74 | 18.18 |
| 119601675 | KIAA1737, isoform CRA_a [Homo sapiens] | 4.66 | 8.31 |
| 119601482 | D4, zinc and double PHD fingers, family 3, isoform CRA_a [Homo sa | 1.51 | 2.59 |
| 119601262 | hCG2036758 [Homo sapiens] | 6.81 | 18.42 |
| 119601239 | hCG1651220 [Homo sapiens] | 1.51 | 6.02 |
| 119601150 | hCG22233 [Homo sapiens] | 2.10 | 6.07 |
| 119600904 | hCG2026504, partial [Homo sapiens] | 6.44 | 11.83 |
| 119600833 | hCG2044005 [Homo sapiens] | 2.19 | 8.30 |
| 119600697 | chromosome 17 open reading frame 42, isoform CRA_b [Homo sapi | 2.22 | 7.60 |
| 119600622 | amiloride-sensitive cation channel 1, neuronal (degenerin) [Homo sa | 3.29 | 2.83 |
| 119600566 | hCG1989262, partial [Homo sapiens] | 1.63 | 5.98 |
| 119599993 | hCG2022736, isoform CRA_a [Homo sapiens] | 3.22 | 8.21 |
| 119599875 | poly (ADP-ribose) polymerase family, member 14, isoform CRA_a [H | 1.53 | 0.91 |
| 119599768 | hCG1798119 [Homo sapiens] | 1.66 | 1.60 |
| 119599748 | G protein-coupled receptor 175, isoform CRA_c [Homo sapiens] | 2.50 | 4.04 |
| 119599587 | hCG2038396, partial [Homo sapiens] | 2.01 | 21.51 |
| 119598646 | chordin, isoform CRA_b, partial [Homo sapiens] | 1.55 | 3.33 |
| 119598639 | KIAA0804, isoform CRA_a [Homo sapiens] | 5.55 | 7.19 |
| 119598573 | hCG1792419, isoform CRA_b, partial [Homo sapiens] | 2.38 | 3.02 |
| 119597481 | fatty acid binding protein 1, liver, isoform CRA_a [Homo sapiens] | 2.57 | 21.74 |
| 119597386 | hCG2045330 [Homo sapiens] | 2.75 | 80.00 |
| 119597096 | SMAD specific E3 ubiquitin protein ligase 1, isoform CRA_a [Homo s | 2.53 | 3.44 |
| 119596610 | centrosomal protein 250kDa, isoform CRA_a [Homo sapiens] | 1.57 | 0.33 |
| 119596606 | ERGIC and golgi 3, isoform CRA_b [Homo sapiens] | 2.37 | 6.28 |
| 119596419 | hCG2019858, isoform CRA_a, partial [Homo sapiens] | 2.60 | 3.76 |
| 119595939 | hCG2043550 [Homo sapiens] | 7.47 | 14.01 |
| 119595726 | hCG2045320 [Homo sapiens] | 1.55 | 7.79 |
| 119595045 | phosphatidylinositol transfer protein, membrane-associated 1, isofor | 2.23 | 3.23 |
| 119594973 | RCE1 homolog, prenyl protein peptidase (S. cerevisiae), isoform CR | 2.04 | 6.12 |
| 119594826 | hCG23294, isoform CRA_b, partial [Homo sapiens] | 2.05 | 1.06 |
| 119594502 | TAF6-like RNA polymerase II, p300/CBP-associated factor (PCAF)-as | 7.13 | 2.16 |
| 119593011 | tripartite motif-containing 28, isoform CRA_a [Homo sapiens] | 3.84 | 2.71 |
| 119592825 | NACHT, leucine rich repeat and PYD containing 13, isoform CRA_a [ | 9.50 | 1.93 |
| 119592517 | zinc finger protein 160, isoform CRA_b [Homo sapiens] | 2.84 | 2.43 |
| 119592486 | hCG2040446 [Homo sapiens] | 2.08 | 15.57 |
| 119591468 | hCG2012694, isoform CRA_a [Homo sapiens] | 4.24 | 11.59 |

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|---|---|---|---|
| 119590969 | X-ray repair complementing defective repair in Chinese hamster cell | 7.19 | 4.35 |
| 119590934 | 5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase/I | 5.02 | 4.61 |
| 119590616 | hCG2038227, partial [Homo sapiens] | 2.02 | 8.70 |
| 119589501 | KH-type splicing regulatory protein (FUSE binding protein 2), isofor | 2.16 | 4.35 |
| 119589376 | hCG2003956 [Homo sapiens] | 2.09 | 15.54 |
| 119588908 | BTB (POZ) domain containing 10, isoform CRA_e, partial [Homo sap | 2.07 | 8.84 |
| 119588859 | hCG1992264, isoform CRA_b [Homo sapiens] | 2.03 | 1.55 |
| 119588717 | hCG2045250 [Homo sapiens] | 2.14 | 45.10 |
| 119588714 | leucine zipper protein 2, partial [Homo sapiens] | 1.53 | 7.14 |
| 119587781 | hCG2043599, isoform CRA_a [Homo sapiens] | 3.68 | 100.00 |
| 119587173 | hCG1980844, isoform CRA_e, partial [Homo sapiens] | 1.70 | 1.19 |
| 119587011 | hCG1654128, partial [Homo sapiens] | 5.38 | 1.39 |
| 119586299 | hCG2033479, isoform CRA_e [Homo sapiens] | 2.72 | 10.26 |
| 119585701 | choline dehydrogenase, isoform CRA_a [Homo sapiens] | 2.08 | 3.37 |
| 119585620 | dynein, axonemal, heavy polypeptide 1, isoform CRA_b [Homo sapie | 4.85 | 0.70 |
| 119585568 | G protein-coupled receptor 62 [Homo sapiens] | 11.41 | 2.45 |
| 119585538 | dedicator of cytokinesis 3, isoform CRA_a [Homo sapiens] | 3.87 | 0.97 |
| 119585025 | hCG2042883, isoform CRA_c [Homo sapiens] | 2.08 | 4.25 |
| 119584932 | solute carrier family 22 (organic cation transporter), member 13, is | 1.53 | 1.32 |
| 119584319 | inositol 1,4,5-triphosphate receptor, type 1, isoform CRA_e [Homo s | 3.79 | 0.63 |
| 119584255 | deleted in liver cancer 1, isoform CRA_a [Homo sapiens] | 2.01 | 3.46 |
| 119584178 | hCG1656107 [Homo sapiens] | 1.59 | 4.31 |
| 119583954 | epoxide hydrolase 2, cytoplasmic, isoform CRA_d [Homo sapiens] | 2.17 | 6.33 |
| 119583929 | hCG2042278, partial [Homo sapiens] | 3.18 | 13.04 |
| 119583683 | hCG1785549, isoform CRA_a [Homo sapiens] | 2.06 | 40.74 |
| 119583508 | phorbol-12-myristate-13-acetate-induced protein 1, isoform CRA_a [ | 3.28 | 12.33 |
| 119583478 | neural precursor cell expressed, developmentally down-regulated 4- | 3.57 | 1.73 |
| 119583303 | hCG1793638, partial [Homo sapiens] | 2.70 | 9.82 |
| 119583128 | hCG1817457 [Homo sapiens] | 4.29 | 24.53 |
| 119582828 | basonuclin 1, partial [Homo sapiens] | 2.70 | 3.25 |
| 119582526 | catenin (cadherin-associated protein), alpha 1, 102kDa, isoform CR | 3.84 | 1.78 |
| 119582240 | hCG2045132 [Homo sapiens] | 1.52 | 14.63 |
| 119582176 | casein kinase 1, alpha 1, isoform CRA_f [Homo sapiens] | 2.13 | 8.25 |
| 119581798 | hCG2045156, partial [Homo sapiens] | 3.15 | 7.46 |
| 119581314 | ribosomal protein L27, isoform CRA_b [Homo sapiens] | 2.21 | 11.25 |
| 119581311 | RUN domain containing 1, isoform CRA_a [Homo sapiens] | 2.43 | 4.18 |
| 119581212 | RAB5C, member RAS oncogene family, isoform CRA_b, partial [Hom | 2.29 | 11.52 |
| 119580816 | l(3)mbt-like 2 (Drosophila), isoform CRA_c [Homo sapiens] | 2.27 | 3.69 |
| 119580774 | trinucleotide repeat containing 6B, isoform CRA_c [Homo sapiens] | 3.60 | 2.57 |
| 119580589 | TRIO and F-actin binding protein, isoform CRA_e [Homo sapiens] | 6.53 | 2.72 |
| 119580349 | ring finger protein 185, isoform CRA_c, partial [Homo sapiens] | 2.32 | 16.52 |
| 119580109 | myosin XVIIIB, isoform CRA_c [Homo sapiens] | 1.51 | 0.58 |
| 119579820 | hCG1789581, isoform CRA_b [Homo sapiens] | 64.45 | 16.67 |
| 119579789 | hCG1643051, isoform CRA_b, partial [Homo sapiens] | 2.61 | 7.46 |
| 119579731 | hCG29146, partial [Homo sapiens] | 1.60 | 1.27 |
| 119579661 | hCG1748768, isoform CRA_b, partial [Homo sapiens] | 10.51 | 8.44 |
| 119579548 | hCG201489, isoform CRA_b [Homo sapiens] | 1.57 | 9.46 |
| 119579339 | hCG1654432 [Homo sapiens] | 2.05 | 13.79 |
| 119578438 | myeloid/lymphoid or mixed-lineage leukemia 2, isoform CRA_a [Ho | 15.94 | 0.99 |
| 119578198 | hCG1773636 [Homo sapiens] | 2.57 | 16.76 |
| 119578149 | hCG1817588 [Homo sapiens] | 2.60 | 26.42 |
| 119577954 | X antigen family, member 5, isoform CRA_a, partial [Homo sapiens] | 2.09 | 11.90 |
| 119576911 | DEAD (Asp-Glu-Ala-Asp) box polypeptide 20, isoform CRA_a [Homo | 2.00 | 2.08 |
| 119576743 | hCG2045076 [Homo sapiens] | 2.03 | 22.22 |
| 119576684 | tumor necrosis factor receptor superfamily, member 4, isoform CRA | 2.21 | 6.19 |
| 119576538 | hCG2045069 [Homo sapiens] | 2.10 | 16.47 |
| 119576503 | pantothenate kinase 4, isoform CRA_c [Homo sapiens] | 2.03 | 10.24 |
| 119576425 | hCG2006035 [Homo sapiens] | 2.59 | 27.50 |
| 119576063 | lethal giant larvae homolog 1 (Drosophila), isoform CRA_c [Homo sa | 4.59 | 1.19 |

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|---|---|---|---|
| 119575615 | hCG15865, isoform CRA_a, partial [Homo sapiens] | 3.49 | 2.99 |
| 119575351 | hypothetical protein MGC33648, isoform CRA_a [Homo sapiens] | 2.02 | 22.22 |
| 119575327 | interleukin 31 receptor A, isoform CRA_c [Homo sapiens] | 4.25 | 4.43 |
| 119575183 | zinc finger protein 140 (clone pHZ-39), isoform CRA_c, partial [Hom | 2.17 | 17.33 |
| 119575171 | hCG1724266 [Homo sapiens] | 2.62 | 19.86 |
| 119574613 | AT rich interactive domain 5B (MRF1-like), isoform CRA_c [Homo sa | 4.15 | 1.23 |
| 119574016 | hCG2003971, isoform CRA_a, partial [Homo sapiens] | 4.10 | 10.53 |
| 119573663 | solute carrier family 27 (fatty acid transporter), member 3, isoform | 2.07 | 18.26 |
| 119573320 | G patch domain containing 4, isoform CRA_a [Homo sapiens] | 2.05 | 3.28 |
| 119572988 | succinate dehydrogenase complex, subunit C, integral membrane pr | 3.06 | 12.50 |
| 119572861 | hypothetical protein FLJ32658, isoform CRA_a [Homo sapiens] | 2.26 | 7.39 |
| 119572748 | ribosomal protein L18, isoform CRA_e [Homo sapiens] | 6.46 | 22.06 |
| 119572729 | KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention re | 4.63 | 11.11 |
| 119572383 | Tu translation elongation factor, mitochondrial, isoform CRA_b [Ho | 2.31 | 4.30 |
| 119571874 | myomesin (M-protein) 2, 165kDa, isoform CRA_b [Homo sapiens] | 2.07 | 0.81 |
| 119571612 | carboxypeptidase D, isoform CRA_a [Homo sapiens] | 2.10 | 1.11 |
| 119571365 | hCG2038550, partial [Homo sapiens] | 2.01 | 3.57 |
| 119571209 | hCG1755149, isoform CRA_b [Homo sapiens] | 2.56 | 16.11 |
| 119571047 | protein tyrosine phosphatase, non-receptor type 20B [Homo sapien | 1.58 | 3.91 |
| 119570910 | otoancorin, isoform CRA_b, partial [Homo sapiens] | 2.14 | 2.70 |
| 119570469 | exocyst complex component 6, isoform CRA_c [Homo sapiens] | 4.05 | 1.98 |
| 119570260 | hCG1642531 [Homo sapiens] | 1.68 | 7.55 |
| 119569824 | hCG2036773, isoform CRA_a [Homo sapiens] | 4.31 | 5.13 |
| 119569625 | hCG1641490, partial [Homo sapiens] | 1.61 | 3.55 |
| 119569496 | hCG2041837, partial [Homo sapiens] | 2.02 | 20.27 |
| 119569485 | solute carrier organic anion transporter family, member 4C1, isofor | 1.57 | 1.81 |
| 119569417 | calcium/calmodulin-dependent protein kinase IV, isoform CRA_a [H | 3.73 | 5.07 |
| 119569383 | hCG2039564, isoform CRA_b [Homo sapiens] | 2.00 | 24.36 |
| 119569230 | lamin B1, isoform CRA_a [Homo sapiens] | 17.42 | 6.69 |
| 119569069 | hCG2040303, partial [Homo sapiens] | 4.63 | 10.71 |
| 119568896 | fucosyltransferase 9 (alpha (1,3) fucosyltransferase), isoform CRA_ | 2.74 | 3.06 |
| 119568499 | R-spondin 3 homolog (Xenopus laevis), isoform CRA_a [Homo sapie | 2.10 | 4.74 |
| 119568002 | t-complex 1, isoform CRA_b [Homo sapiens] | 2.64 | 7.10 |
| 133777549 | Dystrophin related protein 2 [Homo sapiens] | 3.58 | 2.10 |
| 84627501 | UNC13B protein [Homo sapiens] | 2.51 | 2.26 |
| 38541875 | BRDT protein, partial [Homo sapiens] | 3.81 | 3.23 |
| 3108019 | NFI-X_HUMAN NUCLEAR FACTOR 1/X (NFI-X) [Homo sapiens] | 2.00 | 8.06 |
| 184556 | insulin-degrading enzyme [Homo sapiens] | 2.03 | 1.96 |
| 3831611 | olfactory receptor [Homo sapiens] | 2.50 | 8.87 |
| 34596117 | central open reading frame [Homo sapiens] | 1.65 | 6.67 |
| 221046346 | unnamed protein product [Homo sapiens] | 4.20 | 10.33 |
| 221045894 | unnamed protein product [Homo sapiens] | 2.19 | 8.06 |
| 221045112 | unnamed protein product [Homo sapiens] | 2.44 | 2.03 |
| 221044806 | unnamed protein product [Homo sapiens] | 7.14 | 6.00 |
| 221044746 | unnamed protein product [Homo sapiens] | 2.59 | 5.56 |
| 221044626 | unnamed protein product [Homo sapiens] | 2.20 | 7.75 |
| 221044340 | unnamed protein product [Homo sapiens] | 2.11 | 4.16 |
| 221042302 | unnamed protein product [Homo sapiens] | 2.05 | 2.30 |
| 221042248 | unnamed protein product [Homo sapiens] | 11.33 | 6.08 |
| 221041662 | unnamed protein product [Homo sapiens] | 3.86 | 4.97 |
| 221041614 | unnamed protein product [Homo sapiens] | 2.58 | 4.13 |
| 221040986 | unnamed protein product [Homo sapiens] | 6.48 | 2.19 |
| 221040152 | unnamed protein product [Homo sapiens] | 1.50 | 3.23 |
| 221040022 | unnamed protein product [Homo sapiens] | 2.05 | 1.79 |
| 34365000 | hypothetical protein [Homo sapiens] | 2.08 | 6.02 |
| 31874064 | hypothetical protein [Homo sapiens] | 5.39 | 4.86 |
| 31874003 | hypothetical protein [Homo sapiens] | 9.31 | 1.45 |
| 30722358 | hypothetical protein [Homo sapiens] | 6.00 | 1.46 |
| 30268309 | hypothetical protein [Homo sapiens] | 3.19 | 1.09 |

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|---|---|---|---|
| 42406435 | VPS13D-2A protein [Homo sapiens] | 3.57 | 0.80 |
| 194390268 | unnamed protein product [Homo sapiens] | 2.01 | 4.94 |
| 194389166 | unnamed protein product [Homo sapiens] | 3.87 | 3.19 |
| 194384684 | unnamed protein product [Homo sapiens] | 4.39 | 6.92 |
| 194384094 | unnamed protein product [Homo sapiens] | 2.57 | 3.10 |
| 194384024 | unnamed protein product [Homo sapiens] | 3.05 | 4.74 |
| 194382090 | unnamed protein product [Homo sapiens] | 3.69 | 5.07 |
| 194378708 | unnamed protein product [Homo sapiens] | 2.04 | 2.02 |
| 194375834 | unnamed protein product [Homo sapiens] | 2.12 | 1.23 |
| 194375079 | unnamed protein product [Homo sapiens] | 2.05 | 2.44 |
| 194387756 | unnamed protein product [Homo sapiens] | 2.15 | 14.66 |
| 194389828 | unnamed protein product [Homo sapiens] | 6.86 | 6.13 |
| 194389800 | unnamed protein product [Homo sapiens] | 4.35 | 3.59 |
| 194387450 | unnamed protein product [Homo sapiens] | 1.59 | 1.29 |
| 194387346 | unnamed protein product [Homo sapiens] | 2.76 | 4.57 |
| 194386918 | unnamed protein product [Homo sapiens] | 4.14 | 4.35 |
| 194386686 | unnamed protein product [Homo sapiens] | 1.74 | 1.99 |
| 194385806 | unnamed protein product [Homo sapiens] | 7.92 | 2.04 |
| 194385786 | unnamed protein product [Homo sapiens] | 4.64 | 17.82 |
| 194385736 | unnamed protein product [Homo sapiens] | 2.16 | 1.33 |
| 194385632 | unnamed protein product [Homo sapiens] | 7.51 | 7.75 |
| 194385420 | unnamed protein product [Homo sapiens] | 39.84 | 38.96 |
| 194384468 | unnamed protein product [Homo sapiens] | 111.97 | 36.75 |
| 194383918 | unnamed protein product [Homo sapiens] | 10.79 | 1.95 |
| 194381558 | unnamed protein product [Homo sapiens] | 3.16 | 1.54 |
| 194380558 | unnamed protein product [Homo sapiens] | 2.52 | 2.57 |
| 194379872 | unnamed protein product [Homo sapiens] | 9.43 | 4.03 |
| 194377340 | unnamed protein product [Homo sapiens] | 4.25 | 1.93 |
| 194376800 | unnamed protein product [Homo sapiens] | 2.05 | 3.70 |
| 194375468 | unnamed protein product [Homo sapiens] | 8.65 | 3.17 |
| 194373809 | unnamed protein product [Homo sapiens] | 2.33 | 2.13 |
| 194373719 | unnamed protein product [Homo sapiens] | 4.56 | 6.42 |
| 577019450 | glucose-6-phosphate isomerase isoform 4 [Homo sapiens] | 6.48 | 2.45 |
| 194373539 | unnamed protein product [Homo sapiens] | 8.45 | 8.92 |
| 194373535 | unnamed protein product [Homo sapiens] | 2.53 | 5.01 |
| 193787134 | unnamed protein product [Homo sapiens] | 10.95 | 6.77 |
| 193783700 | unnamed protein product [Homo sapiens] | 5.15 | 1.37 |
| 193787783 | unnamed protein product [Homo sapiens] | 2.61 | 11.02 |
| 193787582 | unnamed protein product [Homo sapiens] | 17.91 | 13.69 |
| 193786597 | unnamed protein product [Homo sapiens] | 3.77 | 6.25 |
| 193786389 | unnamed protein product [Homo sapiens] | 2.57 | 3.43 |
| 193785905 | unnamed protein product [Homo sapiens] | 4.16 | 11.03 |
| 193785471 | unnamed protein product [Homo sapiens] | 9.78 | 5.24 |
| 193785014 | unnamed protein product [Homo sapiens] | 2.27 | 6.98 |
| 193785647 | unnamed protein product [Homo sapiens] | 4.07 | 1.00 |
| 189066668 | unnamed protein product [Homo sapiens] | 9.18 | 5.68 |
| 189054902 | unnamed protein product [Homo sapiens] | 2.54 | 15.92 |
| 158261765 | unnamed protein product [Homo sapiens] | 5.75 | 1.68 |
| 158260377 | unnamed protein product [Homo sapiens] | 4.65 | 9.26 |
| 158260107 | unnamed protein product [Homo sapiens] | 5.34 | 3.41 |
| 158258340 | unnamed protein product [Homo sapiens] | 5.25 | 1.22 |
| 158256976 | unnamed protein product [Homo sapiens] | 2.15 | 2.90 |
| 158255298 | unnamed protein product [Homo sapiens] | 1.52 | 3.22 |
| 22760973 | unnamed protein product [Homo sapiens] | 3.12 | 3.36 |
| 21757363 | unnamed protein product [Homo sapiens] | 4.56 | 2.32 |
| 21755136 | unnamed protein product [Homo sapiens] | 6.29 | 10.49 |
| 21753522 | unnamed protein product [Homo sapiens] | 2.89 | 16.67 |
| 21752832 | unnamed protein product [Homo sapiens] | 3.61 | 4.83 |
| 21752165 | unnamed protein product [Homo sapiens] | 2.01 | 4.89 |

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|---|---|---|---|
| 21752113 | unnamed protein product [Homo sapiens] | 4.29 | 3.51 |
| 21751586 | unnamed protein product [Homo sapiens] | 13.06 | 2.87 |
| 21750841 | unnamed protein product [Homo sapiens] | 6.07 | 2.60 |
| 21749605 | unnamed protein product [Homo sapiens] | 1.95 | 1.93 |
| 16551959 | unnamed protein product [Homo sapiens] | 4.25 | 6.38 |
| 16551483 | unnamed protein product [Homo sapiens] | 23.11 | 3.85 |
| 16549875 | unnamed protein product [Homo sapiens] | 2.51 | 2.88 |
| 16549375 | unnamed protein product [Homo sapiens] | 4.11 | 7.14 |
| 10435134 | unnamed protein product [Homo sapiens] | 2.67 | 6.73 |
| 10434667 | unnamed protein product [Homo sapiens] | 9.06 | 3.86 |
| 10433360 | unnamed protein product [Homo sapiens] | 17.59 | 4.37 |
| 7023630 | unnamed protein product [Homo sapiens] | 4.10 | 5.36 |
| 7022948 | unnamed protein product [Homo sapiens] | 2.92 | 6.05 |
| 7022861 | unnamed protein product [Homo sapiens] | 5.11 | 4.10 |
| 18676688 | FLJ00243 protein [Homo sapiens] | 2.70 | 4.57 |
| 10440389 | FLJ00030 protein [Homo sapiens] | 24.07 | 7.63 |
| 76879741 | putative protein product of Nbla00650 [Homo sapiens] | 5.89 | 2.89 |
| 68533135 | ABCA4 variant protein [Homo sapiens] | 5.61 | 1.04 |
| 34364852 | hypothetical protein [Homo sapiens] | 2.17 | 3.22 |
| 559709 | KIAA0075 [Homo sapiens] | 2.65 | 8.05 |
| 425906070 | RecName: Full=Coiled-coil domain-containing protein 177; AltName | 5.51 | 3.54 |
| 30749678 | Chain A, Tr Receptor Mutations Conferring Hormone Resistance And | 12.92 | 7.98 |
| 291463381 | Chain A, Crystal Structure Of Human4-1bb Ligand Ectodomain | 1.52 | 3.59 |
| 158254191 | GCN1 general control of amino-acid synthesis 1-like 1 (yeast) [Hom | 4.27 | 1.20 |
| 156230634 | ANKRD18A protein [Homo sapiens] | 10.77 | 1.51 |
| 152012995 | ZNF536 protein [Homo sapiens] | 3.30 | 1.08 |
| 152012538 | CASP8AP2 protein [Homo sapiens] | 5.87 | 2.02 |
| 148745671 | MAN2A1 protein [Homo sapiens] | 1.72 | 0.79 |
| 73909096 | LRRC4B protein, partial [Homo sapiens] | 1.53 | 4.35 |
| 47123516 | C10orf118 protein, partial [Homo sapiens] | 4.95 | 4.59 |
| 46249807 | PRDM4 protein [Homo sapiens] | 1.77 | 2.22 |
| 38174254 | GOLGA3 protein, partial [Homo sapiens] | 9.04 | 2.97 |
| 34783093 | SGOL1 protein, partial [Homo sapiens] | 3.63 | 4.54 |
| 29792202 | ARFGEF2 protein, partial [Homo sapiens] | 4.30 | 2.88 |
| 28839788 | BCLAF1 protein, partial [Homo sapiens] | 5.05 | 3.19 |
| 28374332 | COBL protein, partial [Homo sapiens] | 5.37 | 2.62 |
| 26251962 | ARHGEF10 protein [Homo sapiens] | 4.69 | 2.89 |
| 26251781 | TEX14 protein [Homo sapiens] | 3.29 | 1.00 |
| 17389922 | SLC16A10 protein [Homo sapiens] | 4.24 | 4.98 |
| 17389503 | CHORDC1 protein [Homo sapiens] | 4.83 | 10.34 |
| 17389198 | KIAA1524 protein, partial [Homo sapiens] | 2.09 | 2.46 |
| 15341851 | RHBDL2 protein [Homo sapiens] | 8.53 | 16.53 |
| 14250440 | EPHA2 protein, partial [Homo sapiens] | 2.37 | 7.51 |
| 12652757 | XPO5 protein [Homo sapiens] | 2.63 | 9.29 |
| 882290 | immunoglobulin light chain variable region, partial [Homo sapiens] | 8.39 | 17.76 |
| 553168 | acrosin, partial [Homo sapiens] | 2.55 | 18.52 |
| 386758 | GRP78 precursor, partial [Homo sapiens] | 28.94 | 19.75 |
| 1297330 | DOC-2 [Homo sapiens] | 2.11 | 1.04 |
| 235590 | lysosomal acid beta-galactosidase [Homo sapiens] | 1.63 | 46.15 |
| 40067573 | immunoglobulin heavy chain variable region [Homo sapiens] | 9.34 | 31.63 |
| 15430703 | testis specific serine/threonine kinase 2 [Homo sapiens] | 2.07 | 2.79 |
| 4545137 | G protein-coupled receptor [Homo sapiens] | 17.06 | 4.70 |
| 2394178 | P-glycoprotein [Homo sapiens] | 8.10 | 89.19 |
| 2282576 | HsGCN1 [Homo sapiens] | 4.75 | 2.02 |
| 62988667 | unknown [Homo sapiens] | 12.90 | 4.26 |
| 33150792 | ATP-dependent RNA helicase [Homo sapiens] | 2.01 | 2.86 |
| 15293591 | olfactory receptor [Homo sapiens] | 4.04 | 7.34 |
| 40362722 | inosine monophosphate dehydrogenase type II [Homo sapiens] | 1.84 | 10.61 |
| 12620919 | prosomal P27K protein [Homo sapiens] | 3.03 | 22.41 |

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|---|---|---|---|
| 45643115 | hypothetical protein [Homo sapiens] | 1.56 | 2.16 |
| 211825727 | FAM62B protein [Homo sapiens] | 2.44 | 3.07 |
| 193785898 | unnamed protein product [Homo sapiens] | 2.12 | 2.75 |
| 193785859 | unnamed protein product [Homo sapiens] | 2.17 | 2.78 |
| 193785127 | unnamed protein product [Homo sapiens] | 4.08 | 4.23 |
| 47682880 | C2orf67 protein [Homo sapiens] | 6.25 | 3.51 |
| 189054612 | unnamed protein product [Homo sapiens] | 3.03 | 1.60 |
| 189054269 | unnamed protein product [Homo sapiens] | 5.15 | 5.91 |
| 34536208 | unnamed protein product [Homo sapiens] | 2.86 | 11.41 |
| 34536075 | unnamed protein product [Homo sapiens] | 7.26 | 3.77 |
| 34534922 | unnamed protein product [Homo sapiens] | 7.00 | 1.04 |
| 34534815 | unnamed protein product [Homo sapiens] | 6.11 | 3.99 |
| 34533483 | unnamed protein product [Homo sapiens] | 3.53 | 5.11 |
| 34533179 | unnamed protein product [Homo sapiens] | 2.74 | 14.14 |
| 34532249 | unnamed protein product [Homo sapiens] | 3.25 | 0.63 |
| 34532000 | unnamed protein product [Homo sapiens] | 3.97 | 2.37 |
| 116283583 | UGCGL2 protein [Homo sapiens] | 1.63 | 2.77 |
| 91979518 | immunoglobulin heavy chain variable region [Homo sapiens] | 2.13 | 23.26 |
| 34849883 | TPA_exp: spectrin-like protein of the nuclear envelope and Golgi [H | 22.37 | 1.23 |
| 312050 | myosin I homologue [Homo sapiens] | 2.53 | 2.96 |
| 32335 | HMG2B [Homo sapiens] | 2.11 | 5.91 |
| 24899200 | KIAA2018 protein [Homo sapiens] | 4.06 | 2.79 |
| 18916861 | KIAA1976 protein [Homo sapiens] | 4.11 | 6.27 |
| 14017861 | KIAA1822 protein [Homo sapiens] | 3.36 | 1.88 |
| 14017851 | KIAA1817 protein [Homo sapiens] | 2.67 | 2.11 |
| 10047341 | KIAA1632 protein [Homo sapiens] | 2.70 | 1.99 |
| 10047267 | KIAA1596 protein [Homo sapiens] | 3.69 | 1.04 |
| 7959259 | KIAA1499 protein [Homo sapiens] | 3.20 | 2.12 |
| 12698023 | KIAA1739 protein [Homo sapiens] | 1.52 | 0.93 |
| 557804845 | Chain B, Crystal Structure Of Eif4aiii-cwc22 Complex | 2.27 | 2.06 |
| 157829395 | ubiquitously transcribed tetratricopeptide repeat protein Y-linked tra | 6.07 | 23.02 |
| 444739075 | alternative protein KIAA1704 [Homo sapiens] | 2.71 | 33.33 |
| 444738631 | alternative protein SCN3A [Homo sapiens] | 4.17 | 22.08 |
| 444738587 | alternative protein POLR3G [Homo sapiens] | 2.51 | 30.86 |
| 444738203 | alternative protein HRC [Homo sapiens] | 2.03 | 2.62 |
| 444737907 | alternative protein TCHHL1 [Homo sapiens] | 2.02 | 12.23 |
| 444733343 | alternative protein KHDRBS2 [Homo sapiens] | 2.03 | 24.44 |
| 538260951 | Chain B, Crystal Structure Of A0-domain Of P5 From H. Sapiens | 3.20 | 12.07 |
| 537368331 | immunoglobulin heavy chain variable region, partial [Homo sapiens] | 2.41 | 22.22 |
| 537368226 | immunoglobulin heavy chain variable region, partial [Homo sapiens] | 2.95 | 15.45 |
| 428698207 | Chain G, Dcnl Complex With N-terminally Acetylated Nedd8 E2 Pepti | 3.14 | 28.00 |
| 161172286 | Chain V, Vti1b Habc Domain - Epsinr Enth Domain Complex | 2.11 | 12.50 |
| 440576043 | alternative protein TGM7 [Homo sapiens] | 2.20 | 24.56 |
| 253722224 | Chain A, Irs-1 Ptb Domain Complexed With A Il-4 Receptor Phospho | 4.20 | 26.79 |
| 197304953 | Chain B, Dj-1 Activation By Catechol Quinone Modification | 2.61 | 8.56 |
| 2780883 | Chain N, Proteasome Activator Reg(Alpha) | 2.32 | 7.86 |
| 404248974 | immunoglobulin gamma heavy chain variable region, partial [Homo | 2.62 | 26.19 |
| 223462007 | CDC42BPA protein [Homo sapiens] | 11.80 | 3.41 |
| 223460494 | Myosin phosphatase Rho interacting protein [Homo sapiens] | 6.02 | 4.24 |
| 219519058 | CAMTA2 protein [Homo sapiens] | 4.20 | 2.21 |
| 187952395 | Plexin A2 [Homo sapiens] | 9.95 | 2.59 |
| 118142820 | TWISTNB protein [Homo sapiens] | 1.54 | 3.10 |
| 71051965 | SLC18A2 protein [Homo sapiens] | 2.52 | 20.10 |
| 61970223 | anti-oxLDL immunoglobulin heavy chain variable region, partial [Ho | 7.81 | 12.71 |
| 45946348 | WDR78 protein, partial [Homo sapiens] | 2.58 | 1.70 |
| 45708577 | Kruppel-like factor 3 (basic) [Homo sapiens] | 5.17 | 1.74 |
| 40225490 | ZNF343 protein, partial [Homo sapiens] | 5.04 | 2.27 |
| 39644518 | CLSTN2 protein, partial [Homo sapiens] | 8.21 | 8.86 |
| 37589111 | KIAA1370 protein, partial [Homo sapiens] | 1.53 | 1.52 |

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|---|---|---|---|
| 36338349 | SNX9 protein, partial [Homo sapiens] | 1.55 | 2.47 |
| 34784468 | CAMSAP1L1 protein, partial [Homo sapiens] | 4.32 | 1.92 |
| 34783670 | ZNF510 protein, partial [Homo sapiens] | 2.33 | 2.31 |
| 33872592 | NCOA7 protein, partial [Homo sapiens] | 2.05 | 3.34 |
| 30046835 | TRPM7 protein, partial [Homo sapiens] | 2.68 | 3.55 |
| 29387268 | ILF3 protein, partial [Homo sapiens] | 2.48 | 2.56 |
| 29127019 | HMHA1 protein, partial [Homo sapiens] | 2.15 | 4.56 |
| 27882448 | AGAP3 protein [Homo sapiens] | 3.06 | 2.43 |
| 16198423 | STT3B protein [Homo sapiens] | 1.64 | 2.67 |
| 16041846 | EF-hand calcium binding domain 7 [Homo sapiens] | 5.68 | 3.50 |
| 15426553 | ADD1 protein [Homo sapiens] | 2.55 | 5.75 |
| 14495707 | Jun B proto-oncogene [Homo sapiens] | 2.27 | 3.17 |
| 13111947 | SF3B3 protein [Homo sapiens] | 2.09 | 2.76 |
| 1276428 | FAC1 [Homo sapiens] | 10.58 | 2.59 |
| 1001945 | serine palmitoyltransferase, partial [Homo sapiens] | 1.60 | 1.70 |
| 897824 | AHNAK, partial [Homo sapiens] | 6.14 | 3.60 |
| 553281 | erythropoietin receptor, partial [Homo sapiens] | 1.55 | 7.29 |
| 553243 | HSrel-1 (AA at 250), partial [Homo sapiens] | 15.18 | 17.14 |
| 386854 | type II keratin subunit protein, partial [Homo sapiens] | 224.41 | 39.35 |
| 386850 | keratin K5, partial [Homo sapiens] | 89.16 | 24.80 |
| 386820 | interleukin-2 receptor precursor, partial [Homo sapiens] | 2.52 | 8.76 |
| 292775 | T-cell receptor beta, partial [Homo sapiens] | 2.00 | 14.49 |
| 180394 | collagen 1 pro-alpha-2 chain, partial [Homo sapiens] | 2.55 | 32.14 |
| 178281 | AHNAK nucleoprotein, partial [Homo sapiens] | 10.02 | 4.58 |
| 6466068 | ATP sulfurylase/APS kinase isoform SK2 [Homo sapiens] | 9.09 | 7.92 |
| 82802728 | KIF4B [Homo sapiens] | 2.07 | 1.27 |
| 197115729 | immunoglobulin heavy chain variable region [Homo sapiens] | 4.34 | 17.53 |
| 247426213 | immunoglobulin heavy chain variable region [Homo sapiens] | 2.29 | 9.32 |
| 247425909 | immunoglobulin heavy chain variable region [Homo sapiens] | 21.42 | 15.83 |
| 247425468 | immunoglobulin heavy chain variable region [Homo sapiens] | 2.80 | 15.83 |
| 603074 | ATP:citrate lyase [Homo sapiens] | 4.71 | 1.00 |
| 4689154 | neuronal cell death-related protein [Homo sapiens] | 1.59 | 3.98 |
| 4689134 | 60S ribosomal protein L36 [Homo sapiens] | 2.35 | 12.38 |
| 4454688 | FtsH homolog [Homo sapiens] | 4.76 | 7.74 |
| 2072953 | putative p150 [Homo sapiens] | 16.25 | 3.14 |
| 1881852 | Sry-related HMG box gene [Homo sapiens] | 3.47 | 2.31 |
| 1684931 | immunoglobulin lambda light chain [Homo sapiens] | 2.58 | 12.21 |
| 1620561 | C-1 [Homo sapiens] | 2.04 | 9.23 |
| 1438954 | neuronal pentraxin 1 [Homo sapiens] | 6.14 | 4.88 |
| 1066753 | galactose-1-phosphate uridyl transferase [Homo sapiens] | 5.29 | 32.08 |
| 685061 | calcium sensor protein [Homo sapiens] | 7.78 | 2.99 |
| 623409 | keratin 10 [Homo sapiens] | 221.84 | 48.13 |
| 190706 | parathyroid-like protein precursor [Homo sapiens] | 2.57 | 20.13 |
| 188586 | myosin light chain 2 [Homo sapiens] | 1.52 | 4.07 |
| 260513560 | T cell receptor alpha chain [Homo sapiens] | 1.54 | 9.62 |
| 5052950 | unknown [Homo sapiens] | 3.52 | 7.10 |
| 122892406 | immunoglobulin heavy chain variable region [Homo sapiens] | 2.56 | 20.16 |
| 116283844 | IRGC protein [Homo sapiens] | 2.78 | 8.07 |
| 82802708 | eFI-2-gamma [Homo sapiens] | 2.10 | 2.97 |
| 46325377 | microcephalin [Homo sapiens] | 2.02 | 33.33 |
| 33332354 | HLC-6 [Homo sapiens] | 2.57 | 4.13 |
| 28626027 | N-acetyltransferase-like protein [Homo sapiens] | 1.56 | 0.84 |
| 6841372 | HSPC067 [Homo sapiens] | 2.05 | 7.42 |
| 4680683 | CGI-22 protein [Homo sapiens] | 5.94 | 5.95 |
| 2735849 | G protein-coupled receptor Edg-4 [Homo sapiens] | 1.87 | 1.57 |
| 33570004 | immunoglobulin kappa chain variable region [Homo sapiens] | 2.43 | 21.35 |
| 14336717 | unknown [Homo sapiens] | 101.72 | 4.63 |
| 189041712 | RecName: Full=Putative zinc finger protein ENSP00000344568 | 7.07 | 3.26 |
| 91980140 | immunoglobulin heavy chain variable region [Homo sapiens] | 17.32 | 23.47 |

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|---|---|---|---|
| 91980098 | immunoglobulin heavy chain variable region [Homo sapiens] | 2.02 | 22.83 |
| 63990112 | unknown [Homo sapiens] | 126.37 | 1.41 |
| 62988906 | unknown [Homo sapiens] | 2.24 | 0.56 |
| 62988890 | unknown [Homo sapiens] | 2.33 | 1.52 |
| 62822367 | unknown [Homo sapiens] | 2.07 | 1.57 |
| 62822150 | unknown [Homo sapiens] | 7.49 | 11.93 |
| 62702324 | unknown [Homo sapiens] | 2.50 | 12.12 |
| 62702310 | unknown [Homo sapiens] | 5.46 | 11.25 |
| 62702215 | unknown [Homo sapiens] | 4.44 | 5.03 |
| 62630090 | unknown [Homo sapiens] | 10.16 | 2.02 |
| 41393471 | unknown [Homo sapiens] | 2.78 | 1.48 |
| 22000462 | immunoglobulin heavy chain variable region [Homo sapiens] | 2.52 | 33.33 |
| 19744564 | immunoglobulin light chain variable region [Homo sapiens] | 1.62 | 6.60 |
| 14009267 | N-myc downstream regulator 2 [Homo sapiens] | 2.60 | 7.84 |
| 13123512 | mitochondrial ribosomal protein-L5 heart-specific splice-variant [Hor | 4.35 | 7.84 |
| 12044071 | immunoglobulin lambda chain variable region [Homo sapiens] | 9.33 | 20.25 |
| 37182448 | CCNL1 [Homo sapiens] | 1.68 | 2.34 |
| 4883586 | TSHR [Homo sapiens] | 2.64 | 14.94 |
| 5919228 | Na,K-ATPase catalytic subunit alpha-A protein [Homo sapiens] | 2.16 | 40.63 |
| 450469 | type 2 inositol 1,4,5-trisphosphate receptor [Homo sapiens] | 8.81 | 0.85 |
| 211830808 | KRT18 protein [Homo sapiens] | 4.07 | 5.11 |
| 1617312 | UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase (GalNAc | 6.06 | 3.16 |
| 98956308 | immunoglobulin kappa light chain variable region [Homo sapiens] | 2.52 | 22.22 |
| 66347234 | retinoid X receptor, beta [Homo sapiens] | 5.39 | 4.77 |
| 27552819 | KANK4 protein [Homo sapiens] | 4.13 | 5.50 |
| 166408625 | immunoglobulin lambda variable region [Homo sapiens] | 2.58 | 26.04 |
| 62089198 | G patch domain and KOW motifs variant [Homo sapiens] | 4.06 | 6.74 |
| 62089058 | Inositol 1,4,5-trisphosphate receptor type 3 variant [Homo sapiens] | 8.13 | 1.54 |
| 62088938 | MCF.2 cell line derived transforming sequence variant [Homo sapier | 2.73 | 4.60 |
| 62088878 | Protein 4.1 variant [Homo sapiens] | 6.43 | 3.39 |
| 62088678 | N-glycanase 1 variant [Homo sapiens] | 2.31 | 4.44 |
| 62088386 | iron-responsive element binding protein 2 variant [Homo sapiens] | 1.50 | 0.87 |
| 62087786 | ATP-binding cassette C5 splicing variant A variant [Homo sapiens] | 8.55 | 3.38 |
| 62087140 | scaffold attachment factor B variant [Homo sapiens] | 1.50 | 0.78 |
| 118600887 | RNF20 protein [Homo sapiens] | 5.80 | 7.11 |
| 116283836 | RBM16 protein [Homo sapiens] | 8.32 | 3.25 |
| 77747996 | EIF2S2 protein [Homo sapiens] | 5.49 | 42.53 |
| 54780770 | immunoglobulin mu heavy chain [Homo sapiens] | 2.59 | 30.19 |
| 145309046 | POTE-2 alpha-actin [Homo sapiens] | 19.49 | 5.30 |
| 32822886 | SMC2 protein [Homo sapiens] | 2.60 | 12.92 |
| 109693321 | immunglobulin heavy chain variable region [Homo sapiens] | 2.80 | 16.53 |
| 112702683 | immunoglobulin heavy chain variable region [Homo sapiens] | 5.98 | 7.29 |
| 112702549 | immunoglobulin heavy chain variable region [Homo sapiens] | 2.01 | 20.20 |
| 112699381 | immunoglobulin heavy chain variable region [Homo sapiens] | 2.17 | 19.00 |
| 112697538 | immunoglobulin heavy chain variable region [Homo sapiens] | 15.35 | 28.28 |
| 112697352 | immunoglobulin heavy chain variable region [Homo sapiens] | 33.52 | 18.81 |
| 112696974 | immunoglobulin heavy chain variable region [Homo sapiens] | 75.33 | 30.69 |
| 112696000 | immunoglobulin heavy chain variable region [Homo sapiens] | 2.03 | 14.00 |
| 112694704 | immunoglobulin heavy chain variable region [Homo sapiens] | 12.86 | 23.76 |
| 112694612 | immunoglobulin heavy chain variable region [Homo sapiens] | 7.81 | 15.00 |
| 1565257 | cerebroside sulfate activator [Homo sapiens] | 2.92 | 5.71 |
| 1340149 | adrenoleukodystropy [Homo sapiens] | 6.89 | 2.01 |
| 74146878 | immunoglobulin epsilon heavy chain variable region [Homo sapiens] | 1.68 | 8.80 |
| 95007527 | immunoglobulin variable kappa chain [Homo sapiens] | 2.51 | 23.89 |
| 71891770 | KIAA0430 protein [Homo sapiens] | 3.57 | 0.86 |
| 63089918 | unnamed protein product [Homo sapiens] | 9.18 | 6.00 |
| 63089534 | unnamed protein product [Homo sapiens] | 2.36 | 4.06 |
| 63089484 | unnamed protein product [Homo sapiens] | 5.42 | 45.83 |
| 31179 | enolase [Homo sapiens] | 14.07 | 12.01 |

| | | | |
|---|---|---|---|
| 28557150 | hornerin [Homo sapiens] | 12.14 | 3.25 |
| 56675639 | unnamed protein product [Homo sapiens] | 2.04 | 17.00 |
| 42759878 | immunoglobulin lambda-1 variable region [Homo sapiens] | 2.11 | 14.81 |
| 40983044 | unnamed protein product [Homo sapiens] | 1.56 | 12.73 |
| 40982542 | unnamed protein product [Homo sapiens] | 3.12 | 20.93 |
| 40981914 | unnamed protein product [Homo sapiens] | 5.23 | 22.22 |
| 40981658 | unnamed protein product [Homo sapiens] | 2.02 | 23.33 |
| 40980420 | unnamed protein product [Homo sapiens] | 18.73 | 29.69 |
| 40980098 | unnamed protein product [Homo sapiens] | 2.01 | 16.80 |
| 40979676 | unnamed protein product [Homo sapiens] | 2.03 | 8.60 |
| 40977632 | unnamed protein product [Homo sapiens] | 6.35 | 16.42 |
| 40977326 | unnamed protein product [Homo sapiens] | 2.63 | 30.23 |
| 40977210 | unnamed protein product [Homo sapiens] | 2.99 | 21.78 |
| 40976806 | unnamed protein product [Homo sapiens] | 2.07 | 15.84 |
| 40976308 | unnamed protein product [Homo sapiens] | 2.29 | 14.43 |
| 40976260 | unnamed protein product [Homo sapiens] | 1.53 | 3.90 |
| 40976188 | unnamed protein product [Homo sapiens] | 2.00 | 12.70 |
| 40976100 | unnamed protein product [Homo sapiens] | 6.29 | 22.22 |
| 40976098 | unnamed protein product [Homo sapiens] | 2.08 | 17.78 |
| 40976034 | unnamed protein product [Homo sapiens] | 5.36 | 7.07 |
| 40975666 | unnamed protein product [Homo sapiens] | 2.02 | 13.33 |
| 40047186 | unnamed protein product [Homo sapiens] | 2.08 | 13.86 |
| 40047060 | unnamed protein product [Homo sapiens] | 2.21 | 15.69 |
| 40046916 | unnamed protein product [Homo sapiens] | 2.73 | 23.85 |
| 40046616 | unnamed protein product [Homo sapiens] | 2.10 | 13.33 |
| 40046356 | unnamed protein product [Homo sapiens] | 1.64 | 7.78 |
| 40046294 | unnamed protein product [Homo sapiens] | 3.42 | 17.24 |
| 40046010 | unnamed protein product [Homo sapiens] | 2.10 | 16.25 |
| 40045048 | unnamed protein product [Homo sapiens] | 2.23 | 31.37 |
| 40044556 | unnamed protein product [Homo sapiens] | 2.16 | 18.75 |
| 40043814 | unnamed protein product [Homo sapiens] | 4.13 | 9.35 |
| 40043348 | unnamed protein product [Homo sapiens] | 3.82 | 9.93 |
| 40042992 | unnamed protein product [Homo sapiens] | 2.28 | 10.75 |
| 40042932 | unnamed protein product [Homo sapiens] | 2.16 | 13.10 |
| 40042720 | unnamed protein product [Homo sapiens] | 2.26 | 11.83 |
| 40042484 | unnamed protein product [Homo sapiens] | 2.01 | 8.80 |
| 40042292 | unnamed protein product [Homo sapiens] | 2.87 | 11.21 |
| 40041898 | unnamed protein product [Homo sapiens] | 2.88 | 11.89 |
| 40041828 | unnamed protein product [Homo sapiens] | 2.57 | 33.33 |
| 40041812 | unnamed protein product [Homo sapiens] | 2.10 | 16.33 |
| 40041348 | unnamed protein product [Homo sapiens] | 2.13 | 7.59 |
| 40041274 | unnamed protein product [Homo sapiens] | 2.56 | 24.17 |
| 40041050 | unnamed protein product [Homo sapiens] | 3.75 | 18.84 |
| 40041032 | unnamed protein product [Homo sapiens] | 1.78 | 15.09 |
| 40040964 | unnamed protein product [Homo sapiens] | 2.09 | 15.58 |
| 40040600 | unnamed protein product [Homo sapiens] | 3.63 | 15.84 |
| 40040594 | unnamed protein product [Homo sapiens] | 3.77 | 31.18 |
| 40040382 | unnamed protein product [Homo sapiens] | 5.16 | 12.88 |
| 40039184 | unnamed protein product [Homo sapiens] | 2.11 | 20.69 |
| 27900479 | unnamed protein product [Homo sapiens] | 12.89 | 24.36 |
| 27529704 | KIAA0239 [Homo sapiens] | 2.11 | 1.88 |
| 23385949 | unnamed protein product [Homo sapiens] | 4.67 | 1.71 |
| 473714 | RNA helicase [Homo sapiens] | 2.76 | 4.56 |
| 21998781 | immunoglobulin lambda chain variable region [Homo sapiens] | 2.03 | 17.27 |
| 21697811 | unnamed protein product [Homo sapiens] | 3.84 | 2.76 |
| 21669915 | immunoglobulin heavy chain VHDJ region [Homo sapiens] | 7.79 | 8.94 |
| 21669671 | immunoglobulin lambda light chain VLJ region [Homo sapiens] | 2.54 | 7.22 |
| 21669511 | immunoglobulin lambda light chain VLJ region [Homo sapiens] | 42.72 | 6.69 |
| 21669043 | immunoglobulin heavy chain VHDJ region [Homo sapiens] | 13.65 | 16.13 |

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|---|---|---|---|
| 20521075 | KIAA0539 protein [Homo sapiens] | 7.43 | 0.78 |
| 18698403 | immunoglobulin light chain variable region [Homo sapiens] | 2.46 | 14.04 |
| 4432756 | ribosomal protein L34 [Homo sapiens] | 1.76 | 15.56 |
| 3088336 | ribosomal protein S5 [Homo sapiens] | 4.65 | 27.27 |
| 18098062 | unnamed protein product [Homo sapiens] | 2.65 | 2.09 |
| 16266931 | Musashi1 [Homo sapiens] | 9.20 | 10.06 |
| 16076426 | immunoglobulin heavy chain variable region [Homo sapiens] | 155.38 | 22.99 |
| 16076402 | immunoglobulin heavy chain variable region [Homo sapiens] | 1.53 | 13.10 |
| 16076293 | immunoglobulin heavy chain variable region [Homo sapiens] | 4.04 | 23.53 |
| 12309812 | unnamed protein product [Homo sapiens] | 4.21 | 6.38 |
| 8250273 | IgG heavy chain variable region [Homo sapiens] | 2.56 | 21.23 |
| 3790366 | MNB/DYRK protein kinase [Homo sapiens] | 2.39 | 10.07 |
| 7243041 | KIAA1330 protein [Homo sapiens] | 3.95 | 2.12 |
| 6526769 | HRIHFB2003 [Homo sapiens] | 3.82 | 3.83 |
| 6330854 | KIAA1249 protein [Homo sapiens] | 1.55 | 1.16 |
| 3882181 | KIAA0730 protein [Homo sapiens] | 2.54 | 2.89 |
| 3327176 | KIAA0681 protein [Homo sapiens] | 2.05 | 2.04 |
| 1097157 | familial Alzheimer's disease protein 1 | 2.61 | 6.82 |
| 229585 | Ig A1 Bur | 4.48 | 4.23 |
| 929609 | unnamed protein product [Homo sapiens] | 2.09 | 7.69 |
| 602023 | unnamed protein product [Homo sapiens] | 2.25 | 7.30 |
| 563379 | mucin [Homo sapiens] | 4.75 | 21.67 |
| 37589 | unnamed protein product [Homo sapiens] | 2.75 | 5.11 |
| 578797420 | PREDICTED: uncharacterized protein LOC101930546 [Homo sapiens | 2.27 | 3.61 |
| 530429173 | PREDICTED: death domain-associated protein 6 isoform X3 [Homo s | 2.13 | 4.57 |
| 530426677 | PREDICTED: zinc finger MYND domain-containing protein 19 isoforn | 3.13 | 5.90 |
| 530422989 | PREDICTED: melatonin-related receptor isoform X1 [Homo sapiens] | 2.46 | 7.05 |
| 530420498 | PREDICTED: THO complex subunit 5 homolog isoform X4 [Homo sa | 10.95 | 3.66 |
| 530418855 | PREDICTED: biotin--protein ligase isoform X2 [Homo sapiens] | 2.30 | 2.13 |
| 530417365 | PREDICTED: ankyrin repeat domain-containing protein 27 isoform X | 2.02 | 2.58 |
| 530416474 | PREDICTED: intermediate conductance calcium-activated potassium | 2.13 | 5.22 |
| 530416023 | PREDICTED: zinc finger protein 30 homolog isoform X7 [Homo sapie | 2.07 | 3.09 |
| 530415146 | PREDICTED: ubiquitin-60S ribosomal protein L40 isoform X2 [Homo | 46.05 | 42.29 |
| 530414784 | PREDICTED: protein Hook homolog 2 isoform X6 [Homo sapiens] | 3.15 | 4.02 |
| 530410977 | PREDICTED: flotillin-2 isoform X4 [Homo sapiens] | 1.53 | 1.71 |
| 530409203 | PREDICTED: 3 beta-hydroxysteroid dehydrogenase type 7 isoform X | 2.57 | 5.96 |
| 530408236 | PREDICTED: polycystin-1 isoform X5 [Homo sapiens] | 4.79 | 1.22 |
| 530407818 | PREDICTED: uncharacterized protein KIAA0556 isoform X8 [Homo s | 8.96 | 1.98 |
| 530405878 | PREDICTED: protein unc-13 homolog C isoform X2 [Homo sapiens] | 5.65 | 1.92 |
| 530401067 | PREDICTED: ubiquitin carboxyl-terminal hydrolase 15 isoform X3 [H | 1.67 | 1.70 |
| 530399966 | PREDICTED: UHRF1-binding protein 1-like isoform X1 [Homo sapien | 6.42 | 1.11 |
| 530399511 | PREDICTED: C2 domain-containing protein 5 isoform X8 [Homo sap | 2.59 | 4.31 |
| 530398206 | PREDICTED: sialate O-acetylesterase isoform X1 [Homo sapiens] | 1.53 | 2.92 |
| 530397581 | PREDICTED: synaptotagmin-7 isoform X7 [Homo sapiens] | 2.58 | 6.51 |
| 530394820 | PREDICTED: janus kinase and microtubule-interacting protein 3 isof | 3.52 | 1.42 |
| 530389632 | PREDICTED: izumo sperm-egg fusion protein 3 isoform X2 [Homo sa | 9.25 | 8.33 |
| 530388682 | PREDICTED: collectin-10 isoform X1 [Homo sapiens] | 3.30 | 3.85 |
| 530387087 | PREDICTED: zinc finger protein 862 isoform X2 [Homo sapiens] | 36.08 | 3.23 |
| 530386907 | PREDICTED: GTPase IMAP family member 8 isoform X2 [Homo sapi | 3.62 | 4.17 |
| 530383912 | PREDICTED: E3 ubiquitin-protein ligase HACE1 isoform X3 [Homo sa | 1.68 | 1.57 |
| 530383351 | PREDICTED: kelch-like protein 32 isoform X6 [Homo sapiens] | 2.66 | 2.27 |
| 530380047 | PREDICTED: E3 ubiquitin-protein ligase TRIM36 isoform X4 [Homo s | 3.95 | 5.77 |
| 530378158 | PREDICTED: DNA transposase THAP9 isoform X1 [Homo sapiens] | 2.13 | 2.37 |
| 530377909 | PREDICTED: la-related protein 1B isoform X16 [Homo sapiens] | 12.73 | 1.49 |
| 530373508 | PREDICTED: serine/threonine-protein kinase OSR1 isoform X1 [Hom | 8.67 | 6.74 |
| 530373461 | PREDICTED: TBC1 domain family member 5 isoform X6 [Homo sapi | 1.53 | 1.03 |
| 530372382 | PREDICTED: acylamino-acid-releasing enzyme isoform X2 [Homo sa | 1.59 | 1.58 |
| 530371943 | PREDICTED: zinc finger CW-type PWWP domain protein 2 isoform X | 16.84 | 1.86 |
| 530371457 | PREDICTED: diacylglycerol kinase delta isoform X4 [Homo sapiens] | 8.51 | 0.88 |

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|---|---|---|---|
| 530368845 | PREDICTED: interleukin-18 receptor 1 isoform X2 [Homo sapiens] | 2.05 | 4.10 |
| 530368776 | PREDICTED: E3 SUMO-protein ligase RanBP2 isoform X5 [Homo sa | 4.58 | 1.08 |
| 530367826 | PREDICTED: girdin isoform X9 [Homo sapiens] | 6.35 | 3.36 |
| 530367324 | PREDICTED: dystrobrevin beta isoform X6 [Homo sapiens] | 5.00 | 11.32 |
| 530366678 | PREDICTED: unhealthy ribosome biogenesis protein 2 homolog isof | 2.97 | 1.68 |
| 578801162 | PREDICTED: protoporphyrinogen oxidase isoform X11 [Homo sapie | 2.74 | 5.88 |
| 530363331 | PREDICTED: SH3 domain-containing protein 21 isoform X2 [Homo s | 1.56 | 1.49 |
| 519674472 | immunoglobulin A heavy chain variable region, partial [Homo sapie | 2.00 | 11.11 |
| 519674244 | immunoglobulin A heavy chain variable region, partial [Homo sapie | 2.52 | 23.58 |
| 519674180 | immunoglobulin A heavy chain variable region, partial [Homo sapie | 5.64 | 15.83 |
| 519674088 | immunoglobulin A heavy chain variable region, partial [Homo sapie | 2.53 | 15.83 |
| 519673838 | immunoglobulin A heavy chain variable region, partial [Homo sapie | 66.85 | 7.44 |
| 519673812 | immunoglobulin A heavy chain variable region, partial [Homo sapie | 4.50 | 15.83 |
| 519673648 | immunoglobulin A heavy chain variable region, partial [Homo sapie | 7.56 | 20.51 |
| 519673468 | immunoglobulin A heavy chain variable region, partial [Homo sapie | 11.50 | 9.09 |
| 519672710 | immunoglobulin A heavy chain variable region, partial [Homo sapie | 2.78 | 15.45 |
| 519672644 | immunoglobulin A heavy chain variable region, partial [Homo sapie | 5.17 | 21.14 |
| 519672366 | immunoglobulin A heavy chain variable region, partial [Homo sapie | 2.01 | 9.32 |
| 519672308 | immunoglobulin A heavy chain variable region, partial [Homo sapie | 2.61 | 20.63 |
| 519672238 | immunoglobulin A heavy chain variable region, partial [Homo sapie | 4.88 | 5.13 |
| 389604444 | MHC class II antigen, partial [Homo sapiens] | 2.09 | 11.48 |
| 385843546 | immunoglobulin G4 heavy chain variable region, partial [Homo sapi | 13.61 | 11.70 |
| 479274698 | casein kinase II b subunit splicing isoform 318 [Homo sapiens] | 2.17 | 23.76 |
| 294979767 | Chain E, Crystal Structure Of P120 Catenin In Complex With E-cadh | 2.11 | 3.42 |
| 163310782 | Chain A, Crystal Structure Of Cert Start Domain In Complex With C1 | 2.02 | 4.71 |
| 146386490 | Chain A, Discovery Of 2-pyrimidyl-5-amidothiophenes As Novel And | 2.22 | 4.45 |
| 448262603 | Chain B, Crystal Structure Of Hbrap1 N-bar Domain | 7.65 | 7.24 |
| 372467016 | Chain F, Crystal Structure Of A Linear-Specific Ubiquitin Fab Bound | 2.60 | 11.89 |
| 422920087 | Chain A, U7ub7 Disulfide Variant | 10.39 | 40.26 |
| 152149455 | Chain D, Design And Synthesis Of Novel, Conformationally Restrict | 2.11 | 3.63 |
| 410698506 | pro-opiomelanocortin, partial [Homo sapiens] | 2.01 | 10.11 |
| 149242231 | Chain A, Beta Appendage In Complex With B-Arrestin Peptide | 2.53 | 11.34 |
| 355333098 | Chain A, Iap Antagonist-Induced Conformational Change In Ciap1 P | 2.62 | 7.54 |
| 310942977 | Chain P, Cf Im25-Cf Im68-Uguaa Complex | 2.02 | 15.56 |
| 364505846 | Chain A, Structure Of The Noxo1b Px Domain | 2.04 | 9.40 |
| 315583372 | Chain A, Solution Nmr Structure Of Pap248-286 In 30% Tfe | 193.91 | 48.72 |
| 291191168 | Chain H, Crystal Structure Of Li33 Igg1 Fab | 8.23 | 8.37 |
| 283135299 | Chain A, Solution Structure Of Eif3b-Rrm Bound To Eif3j Peptide | 2.46 | 22.22 |
| 224983568 | Chain B, Glycogen Synthase Kinase 3beta Inhibitor Complex | 2.04 | 2.87 |
| 183448317 | Chain A, Complex Between Pp2a-Specific Methylesterase Pme-1 An | 2.52 | 10.78 |
| 159794776 | Chain A, Solution Structure Of First Pdz Domain Of Pdz Domain Co | 1.52 | 8.00 |
| 159163891 | Chain A, Solution Structure Of Wgr Domain Of Poly(Adp-Ribose) Pol | 4.23 | 18.71 |
| 159163791 | Chain A, Nmr Solution Structure Of Phospholipase C Epsilon Ra 1 D | 2.62 | 25.45 |
| 157830410 | Chain A, Monocyte Chemoattractant Protein-3, Nmr, Minimized Aver | 2.13 | 21.05 |
| 14278227 | Chain B, Nmr Structure Of Dff40 And Dff45 N-Terminal Domain Co | 3.42 | 10.34 |
| 260656175 | Chain A, Crystal Structure Of The Catalytic Core Domain Of Jmjd2d | 2.59 | 7.91 |
| 400653669 | immunoglobulin heavy chain variable region, partial [Homo sapiens] | 2.09 | 19.35 |
| 379030845 | BCL6 corepressor-cyclin B3 fusion protein [Homo sapiens] | 3.63 | 0.86 |
| 113195993 | T-cell receptor beta chain variable region, partial [Homo sapiens] | 2.57 | 44.44 |
| 73426694 | immunoglobulin kappa chain, partial [Homo sapiens] | 5.05 | 90.00 |
| 2896146 | transcriptional coactivator ALY, partial [Homo sapiens] | 2.02 | 8.15 |
| 1800303 | HIV-1 Nef interacting protein, partial [Homo sapiens] | 2.48 | 1.94 |
| 1685102 | NifU-like protein, partial [Homo sapiens] | 1.51 | 5.79 |
| 1658578 | ribosomal L5 protein, partial [Homo sapiens] | 2.21 | 8.28 |
| 1280308 | T-cell receptor beta chain, partial [Homo sapiens] | 1.62 | 30.77 |
| 1061310 | valyl-tRNA synthetase, partial [Homo sapiens] | 7.80 | 3.67 |
| 987255 | Menkes disease gene, partial [Homo sapiens] | 2.64 | 2.07 |
| 726469 | voltage-gated potassium channel beta subunit, partial [Homo sapie | 2.65 | 21.05 |
| 726044 | VT4, partial [Homo sapiens] | 8.54 | 7.27 |

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|---|---|---|---|
| 185262 | Ig H-chain 2A4 precursor V4-D-J6 region, partial [Homo sapiens] | 4.03 | 12.42 |
| 181033 | retinol-binding protein, partial [Homo sapiens] | 2.52 | 18.18 |
| 375314773 | keratin 1 [Homo sapiens] | 360.69 | 58.70 |
| 375004613 | EPRSN1 [Homo sapiens] | 2.10 | 1.85 |
| 371447985 | immunoglobulin G heavy chain variable region, partial [Homo sapien | 2.29 | 14.88 |
| 371447973 | immunoglobulin G heavy chain variable region, partial [Homo sapien | 2.19 | 18.18 |
| 371446332 | immunoglobulin G heavy chain variable region, partial [Homo sapien | 1.55 | 3.97 |
| 354686620 | immunoglobulin heavy chain variable region [Homo sapiens] | 2.05 | 27.03 |
| 353255736 | anti-tetanus toxoid immunoglobulin light chain variable region [Hom | 2.09 | 11.54 |
| 346704184 | unnamed protein product [Homo sapiens] | 59.55 | 6.26 |
| 328942848 | immunoglobulin heavy chain variable region [Homo sapiens] | 4.08 | 22.47 |
| 329581998 | MHC class I antigen [Homo sapiens] | 2.59 | 7.42 |
| 259121493 | MHC class I antigen [Homo sapiens] | 11.05 | 11.05 |
| 323433006 | immunoglobulin variable region [Homo sapiens] | 2.10 | 15.32 |
| 323432331 | immunoglobulin variable region [Homo sapiens] | 2.52 | 14.71 |
| 323431376 | immunoglobulin variable region [Homo sapiens] | 2.27 | 15.00 |
| 224028035 | MHC class I antigen [Homo sapiens] | 2.01 | 4.40 |
| 238684834 | MHC class II antigen [Homo sapiens] | 3.67 | 30.34 |
| 166897665 | BCR/ABL e14a2 fusion protein [Homo sapiens] | 2.83 | 19.75 |
| 37021685 | MHC class II antigen [Homo sapiens] | 2.12 | 25.00 |
| 33319654 | Ig heavy chain variable region, VH3 family [Homo sapiens] | 5.30 | 23.48 |
| 33319542 | Ig heavy chain variable region, VH3 family [Homo sapiens] | 2.19 | 11.38 |
| 33319008 | Ig heavy chain variable region, VH3 family [Homo sapiens] | 4.19 | 15.45 |
| 264668688 | gamma-aminobutyric acid A receptor beta 2 [Homo sapiens] | 4.75 | 27.16 |
| 304563748 | immunoglobulin gamma 4 heavy chain variable region [Homo sapien | 16.47 | 14.73 |
| 304563442 | immunoglobulin gamma 1 heavy chain variable region [Homo sapien | 2.59 | 17.07 |
| 304563158 | immunoglobulin gamma 1 heavy chain variable region [Homo sapien | 2.81 | 23.97 |
| 304562832 | immunoglobulin gamma 1 heavy chain variable region [Homo sapien | 2.66 | 21.09 |
| 304562636 | immunoglobulin gamma 1 heavy chain variable region [Homo sapien | 2.10 | 13.49 |
| 304562630 | immunoglobulin gamma 1 heavy chain variable region [Homo sapien | 2.71 | 12.10 |
| 304562501 | immunoglobulin gamma 2 heavy chain variable region [Homo sapien | 2.87 | 22.31 |
| 304562401 | immunoglobulin gamma 2 heavy chain variable region [Homo sapien | 2.55 | 21.71 |
| 304561958 | immunoglobulin gamma 3 heavy chain variable region [Homo sapien | 4.67 | 33.90 |
| 304561900 | immunoglobulin gamma 3 heavy chain variable region [Homo sapien | 17.57 | 16.00 |
| 114147670 | immunoglobulin heavy chain variable region [Homo sapiens] | 1.69 | 7.56 |
| 46852026 | hypothetical rhabdomyosarcoma antigen MU-RMS-40.15 [Homo sap | 11.52 | 2.42 |
| 633926 | APK1 antigen [Homo sapiens] | 2.01 | 5.32 |
| 478885 | FR-gamma' [Homo sapiens] | 9.75 | 16.35 |
| 189397 | ORF [Homo sapiens] | 4.34 | 6.38 |
| 44887465 | T cell antigen receptor alpha chain [Homo sapiens] | 2.52 | 9.93 |
| 10643592 | centrosomal P4.1-associated protein [Homo sapiens] | 5.55 | 2.17 |
| 2145062 | TTF-I interacting peptide 21 [Homo sapiens] | 97.94 | 4.92 |
| 4587127 | unnamed protein product [Homo sapiens] | 4.37 | 12.03 |
| 636666479 | Chain B, Steroid Receptor Rna Activator (sra) Modification By The H | 4.76 | 3.83 |
| 570359685 | Chain A, A Thermostable Variant Of Human Nudt18 Nudix Domain C | 2.71 | 16.05 |
| 584277117 | excitatory amino acid transporter 1 isoform 5 [Homo sapiens] | 4.19 | 8.84 |
| 608785746 | G protein-coupled receptor 89B isoform A [Homo sapiens] | 2.55 | 54.55 |
| 608785541 | nudE neurodevelopment protein 1 isoform D, partial [Homo sapiens | 2.15 | 3.17 |
| 608785229 | contactin associated protein-like 2 isoform B, partial [Homo sapiens] | 4.40 | 1.93 |
| 578829816 | PREDICTED: telomerase-binding protein EST1A isoform X4 [Homo s | 3.10 | 1.11 |
| 578827039 | PREDICTED: myelin expression factor 2 isoform X3 [Homo sapiens] | 8.09 | 11.09 |
| 578823928 | PREDICTED: stabilin-2 isoform X1 [Homo sapiens] | 8.21 | 0.98 |
| 578802129 | PREDICTED: lysosomal-trafficking regulator isoform X5 [Homo sapie | 4.62 | 1.09 |
| 632933512 | RNA-specific adenosine deaminase [Homo sapiens] | 2.56 | 2.77 |
| 615276301 | nephrocystin-4 isoform b [Homo sapiens] | 7.07 | 2.41 |
| 612406815 | anti-HIV-1 immunoglobulin cap256-059-137547 chain variable regio | 2.05 | 8.33 |
| 612406323 | anti-HIV-1 immunoglobulin cap256-048-012148 chain variable regio | 13.42 | 13.19 |
| 612405920 | anti-HIV-1 immunoglobulin 119-075862 chain variable region, partia | 2.56 | 21.30 |
| 608073328 | interferon regulatory factor 1 isoform +I9 [Homo sapiens] | 2.42 | 5.92 |

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|---|---|---|---|
| 380041936 | SETDB2-PHF11 fusion protein variant 6, partial [Homo sapiens] | 2.06 | 7.78 |
| 578846035 | PREDICTED: polycystin-1-like [Homo sapiens] | 1.61 | 1.18 |
| 578843125 | PREDICTED: protein piccolo-like [Homo sapiens] | 1.60 | 2.43 |
| 578840717 | PREDICTED: T-box transcription factor TBX22 isoform X3 [Homo sa | 2.38 | 4.57 |
| 578840688 | PREDICTED: D-dopachrome decarboxylase isoform X1 [Homo sapie | 11.00 | 14.35 |
| 578839183 | PREDICTED: gamma-glutamyltranspeptidase 2-like isoform X9 [Hom | 6.33 | 5.42 |
| 578838365 | PREDICTED: ADP-ribosylation factor-like protein 13A isoform X2 [Ho | 2.04 | 8.00 |
| 578836486 | PREDICTED: GDP-fucose protein O-fucosyltransferase 2 isoform X2 | 2.51 | 6.54 |
| 578836465 | PREDICTED: Lebercilin-like protein isoform X9 [Homo sapiens] | 3.85 | 2.41 |
| 578832531 | PREDICTED: nuclear factor of activated T-cells, cytoplasmic 1 isofor | 2.62 | 4.69 |
| 578831093 | PREDICTED: protein FAM20A isoform X3 [Homo sapiens] | 6.30 | 8.03 |
| 578830653 | PREDICTED: polycomb protein SUZ12 isoform X3 [Homo sapiens] | 1.62 | 1.49 |
| 578830621 | PREDICTED: arylsulfatase G isoform X8 [Homo sapiens] | 4.27 | 7.25 |
| 578830460 | PREDICTED: RNA binding protein fox-1 homolog 3 isoform X7 [Hom | 2.06 | 4.27 |
| 578830293 | PREDICTED: DNA polymerase subunit gamma-2, mitochondrial isof | 12.67 | 6.06 |
| 578830152 | PREDICTED: rho GTPase-activating protein 44 isoform X5 [Homo sa | 2.01 | 1.88 |
| 578830040 | PREDICTED: PHD finger protein 23 isoform X4 [Homo sapiens] | 2.02 | 1.72 |
| 578829793 | PREDICTED: lysine-specific demethylase 6B isoform X8 [Homo sapie | 6.23 | 1.34 |
| 578828959 | PREDICTED: ankyrin repeat domain-containing protein 11 isoform X | 25.86 | 1.17 |
| 578827640 | PREDICTED: kinesin-like protein KIF23 isoform X8 [Homo sapiens] | 14.94 | 1.44 |
| 578827191 | PREDICTED: unconventional myosin-Vc isoform X1 [Homo sapiens] | 10.57 | 1.64 |
| 578826600 | PREDICTED: probable threonine--tRNA ligase 2, cytoplasmic isoform | 4.99 | 2.47 |
| 578825877 | PREDICTED: dapper homolog 1 isoform X1 [Homo sapiens] | 15.89 | 3.21 |
| 578825333 | PREDICTED: transmembrane and coiled-coil domain-containing prot | 2.53 | 6.81 |
| 578824341 | PREDICTED: coiled-coil domain-containing protein 62 isoform X4 [H | 9.55 | 4.27 |
| 578824259 | PREDICTED: centrosomal protein of 290 kDa isoform X6 [Homo sap | 26.34 | 3.36 |
| 578823704 | PREDICTED: ADP-ribosylation factor 3 isoform X2 [Homo sapiens] | 2.37 | 7.30 |
| 578823287 | PREDICTED: coiled-coil domain-containing protein 38 isoform X2 [H | 3.74 | 6.22 |
| 578823068 | PREDICTED: liprin-beta-1 isoform X14 [Homo sapiens] | 3.13 | 3.28 |
| 578821565 | PREDICTED: serine/threonine-protein phosphatase 6 regulatory sub | 20.12 | 2.19 |
| 578818557 | PREDICTED: supervillin isoform X15 [Homo sapiens] | 3.03 | 0.54 |
| 578816882 | PREDICTED: cortactin-binding protein 2-like [Homo sapiens] | 2.12 | 4.27 |
| 578815689 | PREDICTED: zinc finger protein 704 isoform X2 [Homo sapiens] | 2.82 | 6.88 |
| 578814737 | PREDICTED: diacylglycerol kinase iota isoform X3 [Homo sapiens] | 2.11 | 2.82 |
| 578814353 | PREDICTED: phosphatidylinositol 4,5-bisphosphate 3-kinase catalyt | 2.09 | 0.80 |
| 578812604 | PREDICTED: nesprin-1 isoform X19 [Homo sapiens] | 22.36 | 1.18 |
| 578812547 | PREDICTED: protein dopey-1 isoform X8 [Homo sapiens] | 4.14 | 0.99 |
| 578812030 | PREDICTED: receptor-interacting serine/threonine-protein kinase 1 | 4.33 | 6.46 |
| 578811659 | PREDICTED: trem-like transcript 1 protein isoform X1 [Homo sapien | 2.00 | 13.17 |
| 578810422 | PREDICTED: cyclin-dependent kinase-like 3 isoform X10 [Homo sapi | 10.79 | 6.51 |
| 578810298 | PREDICTED: E3 ubiquitin-protein ligase RNF180 isoform X3 [Homo | 2.04 | 4.10 |
| 578809969 | PREDICTED: uncharacterized protein C5orf42 isoform X12 [Homo s | 5.83 | 1.00 |
| 578809149 | PREDICTED: serine/threonine-protein kinase Nek1 isoform X2 [Hom | 1.50 | 0.57 |
| 578808887 | PREDICTED: coiled-coil domain-containing protein 111 isoform X3 [ | 3.72 | 2.39 |
| 578807573 | PREDICTED: intraflagellar transport protein 122 homolog isoform X | 2.08 | 1.14 |
| 578807124 | PREDICTED: protein ECT2 isoform X8 [Homo sapiens] | 3.85 | 3.04 |
| 578806122 | PREDICTED: microtubule-associated protein 4 isoform X51 [Homo s | 2.06 | 1.39 |
| 578805209 | PREDICTED: nuclear body protein SP140-like protein isoform X6 [H | 4.17 | 8.13 |
| 578804810 | PREDICTED: trafficking kinesin-binding protein 2 isoform X1 [Homo | 7.19 | 1.14 |
| 578804640 | PREDICTED: E3 ubiquitin-protein ligase HECW2 isoform X4 [Homo s | 8.73 | 1.91 |
| 578804299 | PREDICTED: ankyrin repeat domain-containing protein 36A isoform | 4.32 | 2.79 |
| 578802318 | PREDICTED: probable methyltransferase TARBP1 isoform X2 [Homo | 5.04 | 2.06 |
| 578802311 | PREDICTED: ryanodine receptor 2 isoform X8 [Homo sapiens] | 4.86 | 1.32 |
| 578801002 | PREDICTED: pre-B-cell leukemia transcription factor 1 isoform X4 [ | 2.59 | 6.72 |
| 578800972 | PREDICTED: metaxin-1 isoform X1 [Homo sapiens] | 1.56 | 4.15 |
| 578799998 | PREDICTED: uncharacterized protein KIAA1751 isoform X3 [Homo s | 3.73 | 1.42 |
| 578799700 | PREDICTED: solute carrier family 35 member E2B isoform X2 [Hom | 4.23 | 4.52 |
| 578798828 | PREDICTED: microtubule-actin cross-linking factor 1 isoform X24 [H | 7.48 | 0.61 |
| 578798776 | PREDICTED: E3 ubiquitin-protein ligase UBR4 isoform X13 [Homo s | 4.58 | 0.58 |

| | | | |
|---|---|---|---|
| 578798666 | PREDICTED: polycomb protein SCMH1 isoform X10 [Homo sapiens] | 4.90 | 5.62 |
| 578796804 | PREDICTED: filaggrin-like isoform X5 [Homo sapiens] | 5.39 | 1.00 |
| 578794871 | PREDICTED: serine/arginine repetitive matrix protein 1-like [Homo s | 3.55 | 5.57 |
| 568779352 | PJA2/FER fusion protein [Homo sapiens] | 4.18 | 2.21 |
| 568245056 | AKAP350C [Homo sapiens] | 5.42 | 1.02 |
| 564730730 | Chain C, Hiv-1 Vif Socs-box And Elongin Bc Solution Structure | 4.81 | 21.98 |
| 118406061 | immunoglobulin heavy chain variable region [Homo sapiens] | 2.20 | 15.87 |
| 47088185 | AIDA-1bDAnk [Homo sapiens] | 4.28 | 3.87 |
| 34396082 | cell death activator [Homo sapiens] | 2.97 | 10.96 |
| 21666318 | cervical cancer suppressor gene 5 [Homo sapiens] | 2.40 | 14.41 |
| 18001260 | CKII beta binding protein 2 [Homo sapiens] | 2.51 | 16.13 |
| 16326438 | pregnancy-associated plasma protein E2 [Homo sapiens] | 5.22 | 0.73 |
| 15029567 | PR/SET domain-containing protein 07 [Homo sapiens] | 2.26 | 5.60 |
| 14289323 | LIP isoform of BLIP [Homo sapiens] | 4.70 | 1.30 |
| 11526821 | nuclear receptor coactivator CIA [Homo sapiens] | 1.52 | 1.13 |
| 5813799 | Che-1 [Homo sapiens] | 5.59 | 2.15 |
| 5106572 | transcriptional activator SRCAP [Homo sapiens] | 8.84 | 0.98 |
| 5059425 | RIP-like kinase [Homo sapiens] | 4.18 | 5.21 |
| 4732139 | smoothened [Homo sapiens] | 5.12 | 30.00 |
| 4240391 | lecithin retinol acyltransferase [Homo sapiens] | 2.52 | 14.35 |
| 3659901 | F1F0-type ATP synthase subunit g [Homo sapiens] | 3.61 | 23.30 |
| 146330322 | immunoglobulin heavy chain variable region [Homo sapiens] | 2.03 | 11.11 |
| 270054608 | immunoglobulin heavy chain variable region [Homo sapiens] | 8.00 | 20.87 |
| 270054355 | immunoglobulin heavy chain variable region [Homo sapiens] | 2.73 | 24.56 |
| 270053188 | immunoglobulin heavy chain variable region [Homo sapiens] | 130.54 | 9.17 |
| 270053146 | immunoglobulin heavy chain variable region [Homo sapiens] | 2.11 | 16.96 |
| 270053106 | immunoglobulin heavy chain variable region [Homo sapiens] | 8.80 | 9.91 |
| 270052393 | immunoglobulin heavy chain variable region [Homo sapiens] | 2.01 | 11.40 |
| 270047366 | immunoglobulin heavy chain variable region [Homo sapiens] | 2.37 | 13.10 |
| 270046664 | immunoglobulin heavy chain variable region [Homo sapiens] | 22.53 | 8.33 |
| 28269794 | factor VII active site mutant immunoconjugate [Homo sapiens] | 4.80 | 5.89 |
| 13991483 | psoriasis vulgaris immunoglobulin heavy chain [Homo sapiens] | 2.56 | 17.53 |
| 11275612 | CTCL tumor antigen se2-5 [Homo sapiens] | 2.61 | 2.55 |
| 55139084 | MHC class II antigen [Homo sapiens] | 2.76 | 11.65 |
| 46254063 | immunoglobulin heavy chain [Homo sapiens] | 2.81 | 16.36 |
| 46253885 | immunoglobulin heavy chain [Homo sapiens] | 4.36 | 13.10 |
| 40388596 | immunoglobulin light chain [Homo sapiens] | 1.60 | 11.94 |
| 39939605 | immunoglobulin heavy chain variable region [Homo sapiens] | 2.20 | 11.28 |
| 37789670 | immunoglobulin lambda light chain variable region [Homo sapiens] | 9.19 | 19.51 |
| 4097704 | unknown protein [Homo sapiens] | 2.79 | 7.80 |
| 3560559 | cellular apoptosis susceptibilty protein [Homo sapiens] | 1.51 | 3.79 |
| 2145178 | IgM rheumatoid factor RF-TT3, variable heavy chain [Homo sapiens | 2.17 | 10.34 |
| 261385167 | unnamed protein product [Homo sapiens] | 1.53 | 3.70 |
| 257297088 | unnamed protein product [Homo sapiens] | 3.27 | 8.70 |
| 145939086 | immunoglobulin heavy chain variable region [Homo sapiens] | 2.56 | 41.30 |
| 145911945 | immunoglobulin heavy chain variable region [Homo sapiens] | 1.50 | 10.47 |
| 28375607 | unnamed protein product [Homo sapiens] | 2.65 | 1.42 |
| 28193156 | unnamed protein product [Homo sapiens] | 3.69 | 3.02 |
| 21740354 | hypothetical protein [Homo sapiens] | 2.25 | 3.11 |
| 21740309 | hypothetical protein [Homo sapiens] | 2.57 | 22.93 |
| 6808437 | hypothetical protein [Homo sapiens] | 2.01 | 4.49 |
| 6599262 | hypothetical protein [Homo sapiens] | 2.56 | 2.33 |
| 5911879 | hypothetical protein [Homo sapiens] | 2.54 | 5.33 |
| 5911871 | hypothetical protein [Homo sapiens] | 2.11 | 12.90 |
| 51476814 | hypothetical protein [Homo sapiens] | 6.27 | 5.08 |
| 50949930 | hypothetical protein [Homo sapiens] | 2.05 | 1.99 |
| 9663119 | PEX5 related protein [Homo sapiens] | 2.16 | 2.91 |
| 3255987 | HIRIP3 [Homo sapiens] | 1.78 | 1.37 |
| 639693 | transcription factor [Homo sapiens] | 5.71 | 3.16 |

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|---|---|---|---|
| 505033 | mitogen inducible gene mig-2 [Homo sapiens] | 8.51 | 8.19 |
| 62550765 | killer cell immunoglobulin-like receptor [Homo sapiens] | 2.59 | 23.15 |
| 32177 | HLA-B27 [Homo sapiens] | 1.55 | 2.21 |
| 171853469 | immunoglobulin heavy chain variable region [Homo sapiens] | 2.00 | 22.06 |
| 156633220 | immunoglobulin kappa 1 light chain [Homo sapiens] | 6.35 | 12.04 |
| 156632946 | immunoglobulin lambda 2 light chain [Homo sapiens] | 2.03 | 14.41 |
| 161727494 | T cell receptor beta variable 7 [Homo sapiens] | 2.04 | 8.51 |
| 62897719 | calcium binding protein Cab45 precursor variant [Homo sapiens] | 2.12 | 5.52 |
| 118640476 | KIR3DL2 [Homo sapiens] | 2.52 | 7.69 |
| 134254698 | peroxiredoxin 6 [Homo sapiens] | 2.07 | 12.50 |
| 5420190 | hypothetical protein [Homo sapiens] | 2.18 | 2.21 |
| 3326993 | SNF5/INI1 protein [Homo sapiens] | 2.58 | 6.20 |
| 1524099 | TFE3 transcription factor [Homo sapiens] | 6.64 | 2.77 |
| 111922752 | unnamed protein product [Homo sapiens] | 2.02 | 1.56 |
| 108250378 | unnamed protein product [Homo sapiens] | 2.37 | 3.49 |
| 108250370 | unnamed protein product [Homo sapiens] | 4.66 | 4.97 |
| 37998957 | chimeric MOZ-ASXH2 fusion protein [Homo sapiens] | 4.58 | 1.62 |
| 31044222 | TPA_exp: MICAL-like 2 [Homo sapiens] | 11.59 | 1.56 |
| 84784317 | alpha-1-antitrypsin MBrescia variant [Homo sapiens] | 6.92 | 20.22 |
| 78927052 | mitochondrial steroid acute regulatory protein [Homo sapiens] | 4.26 | 39.47 |
| 73810004 | MYO9 isoform 2 [Homo sapiens] | 5.25 | 3.70 |
| 71273688 | immunoglobulin heavy chain variable region [Homo sapiens] | 5.65 | 26.26 |
| 66349786 | unnamed protein product [Homo sapiens] | 2.13 | 2.35 |
| 31873859 | hypothetical protein [Homo sapiens] | 1.50 | 4.44 |
| 21739582 | hypothetical protein [Homo sapiens] | 1.63 | 1.66 |
| 60221954 | unnamed protein product [Homo sapiens] | 2.66 | 8.82 |
| 56675533 | unnamed protein product [Homo sapiens] | 5.22 | 29.41 |
| 54304382 | unnamed protein product [Homo sapiens] | 3.07 | 9.69 |
| 50949358 | hypothetical protein [Homo sapiens] | 5.39 | 5.31 |
| 6808239 | hypothetical protein [Homo sapiens] | 2.02 | 5.69 |
| 50834324 | unnamed protein product [Homo sapiens] | 2.31 | 3.58 |
| 47846703 | immunoglobulin heavy chain variable region [Homo sapiens] | 34.32 | 15.83 |
| 45503834 | unnamed protein product [Homo sapiens] | 1.77 | 2.45 |
| 44845565 | unnamed protein product [Homo sapiens] | 2.77 | 100.00 |
| 2439517 | putative RHO/RAC effector protein; 95% similarity to P49205 (PID:g | 5.87 | 1.71 |
| 40038843 | unnamed protein product [Homo sapiens] | 4.31 | 7.72 |
| 40037705 | unnamed protein product [Homo sapiens] | 1.51 | 4.29 |
| 40037540 | unnamed protein product [Homo sapiens] | 2.15 | 2.48 |
| 40037234 | unnamed protein product [Homo sapiens] | 2.06 | 16.22 |
| 40035594 | unnamed protein product [Homo sapiens] | 4.30 | 3.86 |
| 40035148 | unnamed protein product [Homo sapiens] | 2.52 | 16.50 |
| 40034191 | unnamed protein product [Homo sapiens] | 4.26 | 3.92 |
| 40032318 | unnamed protein product [Homo sapiens] | 2.57 | 14.93 |
| 40032084 | unnamed protein product [Homo sapiens] | 2.67 | 3.45 |
| 40031121 | unnamed protein product [Homo sapiens] | 1.50 | 1.65 |
| 40030670 | unnamed protein product [Homo sapiens] | 2.08 | 6.56 |
| 39722653 | unnamed protein product [Homo sapiens] | 5.04 | 2.48 |
| 38502079 | OPK VI-weel/mikl family [Homo sapiens] | 5.95 | 1.53 |
| 38502045 | CaMK II KIN1/SNFl/Niml family [Homo sapiens] | 4.42 | 3.34 |
| 38502003 | AGC I Cyclic nucleotide regulated protein kinase family [Homo sapie | 2.17 | 1.45 |
| 33352800 | L1 cell adhesion molecule [Homo sapiens] | 2.67 | 19.28 |
| 31338696 | immunoglobulin gamma heavy chain variable region [Homo sapiens | 2.55 | 15.50 |
| 29161458 | unnamed protein product [Homo sapiens] | 4.18 | 3.19 |
| 28800861 | unnamed protein product [Homo sapiens] | 2.13 | 12.22 |
| 28800447 | unnamed protein product [Homo sapiens] | 4.54 | 14.57 |
| 28799826 | unnamed protein product [Homo sapiens] | 2.51 | 14.01 |
| 23343183 | unnamed protein product [Homo sapiens] | 6.15 | 1.79 |
| 21739444 | hypothetical protein [Homo sapiens] | 2.07 | 2.95 |
| 21439304 | unnamed protein product [Homo sapiens] | 2.05 | 5.19 |

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|---|---|---|---|
| 21336432 | unnamed protein product [Homo sapiens] | 2.02 | 3.33 |
| 21336348 | unnamed protein product [Homo sapiens] | 4.41 | 2.45 |
| 19773321 | immunoglobulin heavy chain variable region [Homo sapiens] | 4.63 | 10.87 |
| 18617760 | unnamed protein product [Homo sapiens] | 7.15 | 4.49 |
| 12655593 | immunoglobulin lambda chain variable region [Homo sapiens] | 3.06 | 19.27 |
| 14589165 | immunoglobulin heavy chain variable region [Homo sapiens] | 2.12 | 18.68 |
| 12733986 | immunoglobulin gamma heavy chain variable region [Homo sapiens | 2.56 | 27.27 |
| 11121485 | immunoglobulin heavy chain variable region [Homo sapiens] | 3.83 | 13.77 |
| 5051248 | immunoglobulin gamma heavy chain variable region [Homo sapiens | 2.34 | 12.07 |
| 6482350 | CAC-1 [Homo sapiens] | 5.43 | 13.46 |
| 1617094 | heavy chain of IgD variable region [Homo sapiens] | 20.08 | 14.06 |
| 1200067 | immunoglobulin heavy chain [Homo sapiens] | 2.03 | 19.13 |
| 2896033 | PCF11p homolog [Homo sapiens] | 7.12 | 1.38 |
| 226343 | beta amyloid peptide precursor | 3.63 | 3.83 |
| 1235763 | immunoglobulin heavy chain V-D-J region [Homo sapiens] | 4.05 | 7.32 |

| # Proteins | # Unique Peptides | # Peptides | # PSMs | Molecular Function | Cellular Component |
|---|---|---|---|---|---|
| 27 | 44 | 56 | 57 | | |
| 21 | 29 | 37 | 87 | | |
| 84 | 26 | 30 | 30 | | |
| 34 | 24 | 30 | 38 | | |
| 19 | 23 | 26 | 64 | | |
| 354 | 23 | 24 | 68 | | |
| 16 | 16 | 17 | 938 | | |
| 38 | 14 | 23 | 33 | | |
| 30 | 13 | 14 | 14 | | |
| 128 | 13 | 24 | 33 | | |
| 17 | 12 | 12 | 114 | | |
| 73 | 12 | 35 | 115 | | |
| 15 | 12 | 12 | 14 | | |
| 16 | 12 | 16 | 245 | | |
| 35 | 12 | 12 | 12 | | |
| 12 | 11 | 11 | 13 | | |
| 21 | 11 | 11 | 11 | | |
| 56 | 11 | 11 | 14 | | |
| 18 | 10 | 10 | 11 | | |
| 14 | 9 | 10 | 10 | | |
| 32 | 9 | 9 | 11 | | |
| 54 | 9 | 21 | 39 | | |
| 4 | 9 | 11 | 15 | | |
| 12 | 8 | 9 | 12 | | |
| 50 | 8 | 8 | 8 | | |
| 9 | 8 | 8 | 10 | | |
| 13 | 8 | 8 | 9 | | |
| 25 | 7 | 7 | 8 | | |
| 12 | 7 | 7 | 7 | | |
| 24 | 7 | 7 | 7 | | |
| 42 | 7 | 7 | 7 | | |
| 33 | 7 | 7 | 7 | | |
| 6 | 6 | 6 | 6 | | |
| 19 | 6 | 6 | 6 | | |
| 16 | 6 | 6 | 6 | | |
| 123 | 6 | 9 | 11 | | |
| 11 | 6 | 6 | 6 | | |
| 10 | 6 | 6 | 8 | | |
| 11 | 6 | 6 | 6 | | |
| 22 | 6 | 6 | 7 | | |
| 122 | 6 | 16 | 18 | | |
| 43 | 6 | 7 | 7 | | |
| 10 | 5 | 5 | 7 | | |
| 9 | 5 | 5 | 5 | | |
| 36 | 5 | 11 | 11 | | |
| 49 | 5 | 5 | 6 | | |
| 8 | 5 | 5 | 5 | | |
| 28 | 5 | 6 | 9 | | |
| 13 | 5 | 6 | 7 | | |
| 18 | 5 | 5 | 5 | | |
| 12 | 5 | 5 | 5 | | |
| 45 | 5 | 8 | 9 | | |
| 26 | 5 | 5 | 7 | | |
| 45 | 5 | 8 | 9 | | |
| 121 | 5 | 13 | 15 | | |
| 21 | 5 | 8 | 9 | | |
| 4 | 5 | 6 | 6 | | |
| 9 | 5 | 6 | 6 | | |

| | | | | | |
|---|---|---|---|---|---|
| 30 | 5 | 5 | 5 | | |
| 17 | 4 | 9 | 11 | | |
| 18 | 4 | 4 | 4 | | |
| 5 | 4 | 4 | 5 | | |
| 1 | 4 | 4 | 4 | | |
| 14 | 4 | 4 | 4 | | |
| 30 | 4 | 4 | 4 | | |
| 17 | 4 | 15 | 25 | | |
| 18 | 4 | 4 | 4 | | |
| 56 | 4 | 17 | 32 | | |
| 23 | 4 | 5 | 5 | | |
| 4 | 4 | 4 | 4 | | |
| 43 | 4 | 6 | 6 | | |
| 51 | 4 | 5 | 10 | | |
| 10 | 4 | 4 | 4 | | |
| 13 | 4 | 6 | 6 | | |
| 5 | 4 | 4 | 5 | | |
| 78 | 4 | 14 | 19 | | |
| 4 | 4 | 4 | 4 | | |
| 19 | 4 | 5 | 5 | | |
| 8 | 4 | 5 | 5 | | |
| 18 | 4 | 4 | 4 | | |
| 19 | 4 | 4 | 4 | | |
| 26 | 4 | 4 | 4 | | |
| 21 | 4 | 5 | 5 | | |
| 16 | 4 | 4 | 4 | | |
| 12 | 3 | 3 | 3 | | |
| 12 | 3 | 3 | 3 | | |
| 2 | 3 | 3 | 3 | | |
| 2 | 3 | 3 | 3 | | |
| 8 | 3 | 3 | 4 | | |
| 58 | 3 | 6 | 6 | | |
| 74 | 3 | 5 | 7 | | |
| 8 | 3 | 4 | 6 | | |
| 37 | 3 | 6 | 6 | | |
| 12 | 3 | 3 | 3 | | |
| 11 | 3 | 3 | 4 | | |
| 15 | 3 | 3 | 3 | | |
| 5 | 3 | 3 | 3 | | |
| 25 | 3 | 3 | 4 | | |
| 31 | 3 | 3 | 3 | | |
| 261 | 3 | 4 | 9 | | |
| 10 | 3 | 6 | 136 | | |
| 17 | 3 | 6 | 7 | | |
| 28 | 3 | 8 | 9 | | |
| 213 | 3 | 7 | 8 | | |
| 11 | 3 | 3 | 3 | | |
| 14 | 3 | 3 | 4 | | |
| 11 | 3 | 4 | 4 | | |
| 6 | 3 | 4 | 4 | | |
| 96 | 3 | 4 | 6 | | |
| 20 | 3 | 5 | 6 | | |
| 8 | 3 | 3 | 3 | | |
| 61 | 3 | 11 | 17 | | |
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| 10 | 3 | 3 | 3 | | |
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| 10 | 3 | 3 | 3 | | |
| 19 | 3 | 3 | 5 | | |

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| 89 | 3 | 3 | 3 | | |
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| 7 | 2 | 3 | 3 | | |
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| 343 | 1 | 2 | 3 | | |
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| 19 | 1 | 6 | 6 | | |
| 2 | 1 | 2 | 2 | | |
| 1 | 1 | 1 | 1 | | |
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| 8 | 1 | 3 | 13 | | |
| 42 | 1 | 3 | 3 | | |

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| 16 | 1 | 2 | 2 | | |
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| 73 | 1 | 2 | 9 | | |
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| 7 | 1 | 4 | 6 | | |
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| 5 | 1 | 1 | 1 | | |
| 15 | 1 | 1 | 1 | | |
| 3 | 1 | 3 | 3 | | |
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| 5 | 1 | 1 | 1 | | |

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| 2 | 1 | 2 | 2 | | |

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| 1 | 1 | 1 | 1 | | |
| 10 | 1 | 3 | 3 | | |
| 5 | 1 | 1 | 1 | | |
| 1 | 1 | 1 | 4 | | |
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| 69 | 1 | 2 | 7 | | |
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| 14 | 1 | 2 | 3 | | |
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| 12 | 1 | 3 | 3 | | |
| 11 | 1 | 1 | 1 | | |
| 343 | 1 | 2 | 4 | | |
| 1 | 1 | 1 | 1 | | |
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| 15 | 1 | 1 | 1 | | |
| 48 | 1 | 2 | 4 | | |
| 1 | 1 | 1 | 1 | | |
| 4 | 1 | 2 | 4 | | |
| 7 | 1 | 1 | 1 | | |
| 5 | 1 | 1 | 2 | | |
| 1 | 1 | 1 | 1 | | |
| 2 | 1 | 1 | 1 | | |
| 11 | 1 | 1 | 2 | | |
| 3 | 1 | 1 | 1 | | |
| 9 | 1 | 1 | 1 | | |
| 2 | 1 | 1 | 2 | | |
| 4 | 1 | 1 | 1 | | |
| 6 | 1 | 1 | 1 | | |
| 6 | 1 | 1 | 1 | | |
| 11 | 1 | 3 | 13 | | |
| 1 | 1 | 2 | 3 | | |
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| 8 | 1 | 2 | 9 | | |
| 23 | 1 | 3 | 3 | | |
| 12 | 1 | 1 | 1 | | |
| 2 | 1 | 1 | 1 | | |
| 5 | 1 | 1 | 2 | | |
| 3 | 1 | 1 | 1 | | |
| 7 | 1 | 1 | 1 | | |
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| 5 | 1 | 3 | 4 | | |
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| 5 | 1 | 1 | 1 | | |
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| 4 | 1 | 1 | 3 | | |
| 5 | 1 | 2 | 2 | | |
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| 1 | 1 | 1 | 28 | | |
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| 1 | 1 | 1 | 1 | | |
| 1 | 1 | 1 | 1 | | |
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| 8 | 1 | 1 | 1 | | |

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| 5 | 1 | 1 | 2 | | |
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| 139 | 1 | 2 | 2 | | |
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| 11 | 1 | 1 | 5 | | |
| 13 | 1 | 1 | 1 | | |
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| 21 | 1 | 4 | 4 | | |
| 6 | 1 | 2 | 2 | | |
| 2 | 1 | 1 | 1 | | |
| 21 | 1 | 3 | 3 | | |
| 13 | 1 | 1 | 1 | | |
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| 6 | 1 | 1 | 2 | | |
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| 12 | 1 | 1 | 1 | | |
| 5 | 1 | 2 | 3 | | |
| 7 | 1 | 9 | 17 | | |
| 14 | 1 | 9 | 46 | | |
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| 3 | 1 | 1 | 1 | | |
| 8 | 1 | 1 | 1 | | |
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| 12 | 1 | 1 | 5 | | |
| 18 | 1 | 1 | 1 | | |
| 1 | 1 | 1 | 5 | | |
| 13 | 1 | 2 | 3 | | |
| 3 | 1 | 1 | 1 | | |
| 12 | 1 | 7 | 8 | | |
| 8 | 1 | 2 | 2 | | |
| 8 | 1 | 1 | 1 | | |
| 6 | 1 | 2 | 2 | | |
| 26 | 1 | 2 | 5 | | |
| 7 | 1 | 1 | 2 | | |
| 1 | 1 | 2 | 2 | | |
| 3 | 1 | 1 | 4 | | |
| 5 | 1 | 1 | 1 | | |
| 5 | 1 | 2 | 3 | | |
| 11 | 1 | 2 | 2 | | |
| 13 | 1 | 3 | 3 | | |
| 1 | 1 | 2 | 3 | | |
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| 4 | 1 | 1 | 1 | | |
| 13 | 1 | 2 | 2 | | |
| 1 | 1 | 1 | 2 | | |
| 4 | 1 | 2 | 3 | | |
| 7 | 1 | 1 | 1 | | |
| 9 | 1 | 2 | 2 | | |
| 7 | 1 | 1 | 1 | | |

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| 9 | 1 | 1 | 4 | | |
| 10 | 1 | 1 | 7 | | |
| 5 | 1 | 1 | 2 | | |
| 9 | 1 | 1 | 1 | | |
| 11 | 1 | 1 | 2 | | |
| 1 | 1 | 1 | 1 | | |
| 4 | 1 | 1 | 9 | | |
| 12 | 1 | 1 | 3 | | |
| 9 | 1 | 2 | 3 | | |
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| 8 | 1 | 1 | 1 | | |
| 2 | 1 | 2 | 3 | | |
| 1 | 1 | 1 | 6 | | |
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| 9 | 1 | 2 | 2 | | |
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| 5 | 1 | 2 | 2 | | |
| 16 | 1 | 3 | 3 | | |
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| 10 | 1 | 2 | 2 | | |
| 9 | 1 | 2 | 2 | | |
| 14 | 1 | 3 | 3 | | |
| 18 | 1 | 3 | 3 | | |
| 85 | 1 | 2 | 3 | | |
| 13 | 1 | 2 | 2 | | |
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| 8 | 1 | 2 | 3 | | |
| 12 | 1 | 1 | 1 | | |
| 6 | 1 | 2 | 4 | | |
| 63 | 1 | 1 | 1 | | |
| 14 | 1 | 1 | 1 | | |
| 3 | 1 | 1 | 4 | | |
| 2 | 1 | 1 | 1 | | |
| 9 | 1 | 10 | 10 | | |
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| 1 | 1 | 1 | 1 | | |
| 183 | 1 | 2 | 4 | | |
| 8 | 1 | 1 | 1 | | |
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| 4 | 1 | 2 | 2 | | |
| 5 | 1 | 1 | 7 | | |
| 2 | 1 | 1 | 1 | | |
| 5 | 1 | 1 | 2 | | |
| 36 | 1 | 1 | 1 | | |
| 9 | 1 | 1 | 1 | | |

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| 12 | 1 | 1 | 2 | | |
| 12 | 1 | 1 | 3 | | |
| 1 | 1 | 1 | 2 | | |
| 4 | 1 | 1 | 2 | | |
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| 8 | 1 | 2 | 3 | | |
| 81 | 1 | 2 | 4 | | |
| 3 | 1 | 1 | 3 | | |
| 26 | 1 | 2 | 2 | | |
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| 3 | 1 | 1 | 2 | | |
| 5 | 1 | 2 | 2 | | |
| 1 | 1 | 1 | 1 | | |
| 1 | 1 | 1 | 1 | | |
| 36 | 1 | 8 | 11 | | |
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| 10 | 1 | 2 | 2 | | |
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| 77 | 1 | 2 | 2 | | |
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| 7 | 1 | 2 | 2 | | |
| 26 | 1 | 1 | 1 | | |
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| 23 | 1 | 4 | 5 | | |
| 23 | 1 | 3 | 3 | | |
| 18 | 1 | 2 | 2 | | |
| 12 | 1 | 2 | 4 | | |
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| 5 | 1 | 1 | 1 | | |
| 1 | 1 | 1 | 3 | | |
| 2 | 1 | 1 | 1 | | |
| 1 | 1 | 1 | 3 | | |
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| 5 | 1 | 1 | 4 | | |
| 16 | 1 | 1 | 1 | | |

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| 11 | 1 | 1 | 1 | | |
| 31 | 1 | 1 | 1 | | |
| 17 | 1 | 1 | 1 | | |
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| 3 | 1 | 1 | 1 | | |
| 6 | 1 | 2 | 3 | | |
| 14 | 1 | 1 | 1 | | |
| 3 | 1 | 1 | 1 | | |
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| 25 | 1 | 1 | 5 | | |
| 4 | 1 | 1 | 1 | | |
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| 11 | 1 | 1 | 1 | | |
| 6 | 1 | 1 | 6 | | |
| 22 | 1 | 27 | 87 | | |
| 27 | 1 | 15 | 32 | | |
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| 3 | 1 | 5 | 5 | | |
| 8 | 1 | 1 | 4 | | |
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| 9 | 1 | 2 | 2 | | |
| 35 | 1 | 4 | 9 | | |
| 15 | 1 | 1 | 2 | | |
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| 3 | 1 | 1 | 1 | | |
| 6 | 1 | 2 | 3 | | |
| 14 | 1 | 1 | 2 | | |
| 10 | 1 | 1 | 4 | | |
| 66 | 1 | 24 | 82 | | |
| 2 | 1 | 1 | 1 | | |
| 1 | 1 | 1 | 1 | | |
| 2 | 1 | 1 | 1 | | |
| 19 | 1 | 2 | 2 | | |
| 1 | 1 | 1 | 1 | | |
| 2 | 1 | 1 | 1 | | |
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| 9 | 1 | 1 | 1 | | |
| 19 | 1 | 1 | 1 | | |
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| 3 | 1 | 1 | 1 | | |
| 8 | 1 | 2 | 3 | | |
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| 78 | 1 | 2 | 4 | | |
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| 100 | 1 | 1 | 4 | | |
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| 20 | 1 | 3 | 5 | | |
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| 5 | 1 | 2 | 3 | | |
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| 1 | 1 | 1 | 1 | | |
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| 24 | 1 | 3 | 4 | | |
| 21 | 1 | 1 | 1 | | |
| 69 | 1 | 3 | 3 | | |
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| 12 | 1 | 2 | 3 | | |
| 13 | 1 | 2 | 5 | | |
| 7 | 1 | 2 | 2 | | |
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| 14 | 1 | 5 | 8 | | |
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| 54 | 1 | 2 | 5 | | |
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| 11 | 1 | 6 | 6 | | |

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| 7 | 1 | 1 | 6 | | |
| 91 | 1 | 2 | 61 | | |
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| 5 | 1 | 1 | 1 | | |
| 42 | 1 | 6 | 19 | | |
| 8 | 1 | 1 | 1 | | |
| 7 | 1 | 1 | 1 | | |
| 1 | 1 | 1 | 1 | | |
| 18 | 1 | 2 | 2 | | |
| 11 | 1 | 2 | 4 | | |
| 5 | 1 | 3 | 3 | | |
| 8 | 1 | 1 | 1 | | |
| 12 | 1 | 2 | 3 | | |
| 22 | 1 | 1 | 1 | | |
| 4 | 1 | 1 | 1 | | |
| 5 | 1 | 1 | 1 | | |
| 17 | 1 | 2 | 2 | | |
| 3 | 1 | 1 | 4 | | |
| 4 | 1 | 1 | 2 | | |
| 5 | 1 | 3 | 18 | | |
| 35 | 1 | 2 | 2 | | |
| 7 | 1 | 1 | 1 | | |
| 10 | 1 | 1 | 1 | | |
| 8 | 1 | 2 | 2 | | |
| 3 | 1 | 1 | 1 | | |
| 12 | 1 | 1 | 5 | | |
| 31 | 1 | 2 | 4 | | |
| 6 | 1 | 1 | 1 | | |
| 5 | 1 | 1 | 1 | | |
| 3 | 1 | 1 | 10 | | |
| 11 | 1 | 1 | 5 | | |

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|---|---|---|---|---|---|
| 1 | 1 | 1 | 1 | | |
| 13 | 1 | 2 | 2 | | |
| 15 | 1 | 3 | 4 | | |
| 20 | 1 | 2 | 2 | | |
| 1 | 1 | 1 | 1 | | |
| 1 | 1 | 1 | 1 | | |
| 7 | 1 | 1 | 1 | | |
| 1 | 1 | 1 | 1 | | |
| 1 | 1 | 1 | 1 | | |
| 1 | 1 | 1 | 2 | | |
| 1 | 1 | 1 | 1 | | |
| 1 | 1 | 1 | 28 | | |
| 1 | 1 | 1 | 2 | | |
| 159 | 1 | 2 | 4 | | |
| 2 | 1 | 1 | 4 | | |
| 2 | 1 | 1 | 1 | | |
| 1 | 1 | 1 | 2 | | |
| 1 | 1 | 1 | 1 | | |
| 1 | 1 | 1 | 1 | | |
| 1 | 1 | 1 | 3 | | |
| 2 | 1 | 1 | 1 | | |
| 6 | 1 | 1 | 6 | | |
| 5 | 1 | 1 | 1 | | |
| 24 | 1 | 1 | 1 | | |
| 7 | 1 | 1 | 1 | | |
| 1 | 1 | 1 | 1 | | |
| 1 | 1 | 1 | 3 | | |
| 1 | 1 | 1 | 1 | | |
| 2 | 1 | 3 | 5 | | |
| 7 | 1 | 1 | 1 | | |
| 1 | 1 | 1 | 1 | | |
| 14 | 1 | 1 | 1 | | |
| 5 | 1 | 1 | 1 | | |
| 9 | 1 | 1 | 1 | | |
| 6 | 1 | 1 | 1 | | |
| 14 | 1 | 1 | 79 | | |
| 2 | 1 | 1 | 3 | | |
| 11 | 1 | 1 | 1 | | |
| 32 | 1 | 1 | 1 | | |
| 16 | 1 | 1 | 1 | | |
| 2 | 1 | 1 | 1 | | |
| 12 | 1 | 2 | 2 | | |
| 16 | 1 | 1 | 1 | | |
| 5 | 1 | 1 | 1 | | |
| 4 | 1 | 1 | 1 | | |
| 3 | 1 | 1 | 1 | | |
| 1 | 1 | 1 | 1 | | |
| 10 | 1 | 2 | 2 | | |
| 4 | 1 | 1 | 1 | | |
| 1 | 1 | 1 | 2 | | |
| 4 | 1 | 1 | 1 | | |
| 7 | 1 | 1 | 1 | | |
| 9 | 1 | 1 | 1 | | |
| 7 | 1 | 1 | 1 | | |
| 30 | 1 | 1 | 1 | | |
| 40 | 1 | 4 | 4 | | |
| 1 | 1 | 1 | 1 | | |
| 3 | 1 | 1 | 1 | | |
| 8 | 1 | 3 | 4 | | |

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|---|---|---|---|---|---|
| 1 | 1 | 1 | 2 | | |
| 3 | 1 | 1 | 1 | | |
| 22 | 1 | 41 | 125 | | |
| 1 | 1 | 1 | 1 | | |
| 1 | 1 | 1 | 1 | | |
| 1 | 1 | 1 | 1 | | |
| 2 | 1 | 1 | 1 | | |
| 1 | 1 | 1 | 1 | | |
| 1 | 1 | 1 | 1 | | |
| 8 | 1 | 2 | 23 | | |
| 1 | 1 | 1 | 2 | | |
| 1 | 1 | 1 | 1 | | |
| 1 | 1 | 1 | 5 | | |
| 1 | 1 | 1 | 1 | | |
| 1 | 1 | 1 | 1 | | |
| 1 | 1 | 1 | 2 | | |
| 1 | 1 | 1 | 1 | | |
| 1 | 1 | 2 | 2 | | |
| 1 | 1 | 1 | 1 | | |
| 12 | 1 | 1 | 1 | | |
| 1 | 1 | 1 | 2 | | |
| 1 | 1 | 1 | 1 | | |
| 1 | 1 | 1 | 2 | | |
| 8 | 1 | 2 | 2 | | |
| 1 | 1 | 1 | 5 | | |
| 2 | 1 | 1 | 1 | | |
| 1 | 1 | 1 | 1 | | |
| 1 | 1 | 1 | 1 | | |
| 1 | 1 | 1 | 1 | | |
| 1 | 1 | 1 | 1 | | |
| 1 | 1 | 1 | 1 | | |
| 1 | 1 | 1 | 1 | | |
| 1 | 1 | 2 | 2 | | |
| 1 | 1 | 2 | 8 | | |
| 1 | 1 | 1 | 1 | | |
| 1 | 1 | 2 | 7 | | |
| 6 | 1 | 1 | 1 | | |
| 3 | 1 | 1 | 4 | | |
| 8 | 1 | 2 | 2 | | |
| 1 | 1 | 1 | 1 | | |
| 9 | 1 | 3 | 3 | | |
| 1 | 1 | 1 | 37 | | |
| 1 | 1 | 1 | 2 | | |
| 7 | 1 | 1 | 2 | | |
| 1 | 1 | 1 | 1 | | |
| 10 | 1 | 2 | 2 | | |
| 1 | 1 | 1 | 1 | | |
| 11 | 1 | 1 | 1 | | |
| 4 | 1 | 1 | 2 | | |
| 12 | 1 | 2 | 2 | | |
| 13 | 1 | 2 | 6 | | |
| 5 | 1 | 1 | 3 | | |
| 5 | 1 | 2 | 2 | | |
| 1 | 1 | 1 | 2 | | |
| 10 | 1 | 1 | 3 | | |
| 7 | 1 | 1 | 1 | | |
| 3 | 1 | 1 | 4 | | |
| 1 | 1 | 1 | 1 | | |
| 1 | 1 | 1 | 1 | | |

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|---|---|---|---|---|---|
| 1 | 1 | 1 | 1 | | |
| 1 | 1 | 1 | 1 | | |
| 1 | 1 | 1 | 1 | | |
| 5 | 1 | 1 | 1 | | |
| 1 | 1 | 1 | 4 | | |
| 18 | 1 | 2 | 3 | | |
| 1 | 1 | 1 | 1 | | |
| 1 | 1 | 1 | 1 | | |
| 7 | 1 | 2 | 2 | | |
| 16 | 1 | 1 | 1 | | |
| 8 | 1 | 2 | 4 | | |
| 1 | 1 | 1 | 1 | | |
| 8 | 1 | 1 | 2 | | |
| 4 | 1 | 1 | 1 | | |
| 10 | 1 | 1 | 5 | | |
| 10 | 1 | 1 | 1 | | |
| 1 | 1 | 1 | 1 | | |
| 9 | 1 | 2 | 3 | | |
| 41 | 1 | 2 | 11 | | |
| 13 | 1 | 1 | 7 | | |
| 13 | 1 | 3 | 5 | | |
| 6 | 1 | 1 | 2 | | |
| 17 | 1 | 3 | 8 | | |
| 11 | 1 | 1 | 1 | | |
| 51 | 1 | 3 | 5 | | |
| 102 | 1 | 7 | 13 | | |
| 14 | 1 | 1 | 1 | | |
| 3 | 1 | 2 | 2 | | |
| 25 | 1 | 2 | 2 | | |
| 1 | 1 | 1 | 9 | | |
| 94 | 1 | 2 | 2 | | |
| 1 | 1 | 1 | 1 | | |
| 2 | 1 | 1 | 1 | | |
| 9 | 1 | 1 | 1 | | |
| 20 | 1 | 1 | 1 | | |
| 58 | 1 | 8 | 11 | | |
| 13 | 1 | 2 | 3 | | |
| 11 | 1 | 2 | 3 | | |
| 1 | 1 | 1 | 1 | | |
| 7 | 1 | 1 | 5 | | |
| 3 | 1 | 1 | 1 | | |
| 10 | 1 | 3 | 3 | | |
| 5 | 1 | 1 | 1 | | |
| 40 | 1 | 2 | 2 | | |
| 16 | 1 | 1 | 1 | | |
| 21 | 1 | 2 | 2 | | |
| 4 | 1 | 1 | 1 | | |
| 67 | 1 | 2 | 2 | | |
| 7 | 1 | 1 | 4 | | |
| 20 | 1 | 2 | 4 | | |
| 21 | 1 | 2 | 2 | | |
| 3 | 1 | 1 | 2 | | |
| 15 | 1 | 2 | 2 | | |
| 1 | 1 | 1 | 1 | | |
| 4 | 1 | 1 | 1 | | |
| 17 | 1 | 2 | 2 | | |
| 2 | 1 | 1 | 2 | | |
| 44 | 1 | 4 | 4 | | |
| 18 | 1 | 2 | 2 | | |

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|---|---|---|---|---|---|
| 9 | 1 | 2 | 2 | | |
| 7 | 1 | 2 | 3 | | |
| 47 | 1 | 2 | 2 | | |
| 13 | 1 | 2 | 2 | | |
| 57 | 1 | 3 | 3 | | |
| 5 | 1 | 1 | 2 | | |
| 1 | 1 | 1 | 1 | | |
| 42 | 1 | 2 | 2 | | |
| 2 | 1 | 1 | 1 | | |
| 1 | 1 | 1 | 1 | | |
| 6 | 1 | 1 | 1 | | |
| 5 | 1 | 1 | 3 | | |
| 1 | 1 | 1 | 1 | | |
| 1 | 1 | 2 | 2 | | |
| 1 | 1 | 1 | 1 | | |
| 2 | 1 | 1 | 3 | | |
| 8 | 1 | 2 | 4 | | |
| 1 | 1 | 1 | 3 | | |
| 3 | 1 | 1 | 2 | | |
| 2 | 1 | 1 | 1 | | |
| 73 | 1 | 2 | 2 | | |
| 2 | 1 | 1 | 1 | | |
| 1 | 1 | 1 | 3 | | |
| 1 | 1 | 1 | 1 | | |
| 1 | 1 | 1 | 45 | | |
| 1 | 1 | 1 | 1 | | |
| 1 | 1 | 1 | 5 | | |
| 1 | 1 | 1 | 1 | | |
| 5 | 1 | 1 | 1 | | |
| 3 | 1 | 1 | 13 | | |
| 9 | 1 | 2 | 2 | | |
| 1 | 1 | 1 | 1 | | |
| 20 | 1 | 1 | 1 | | |
| 1 | 1 | 1 | 1 | | |
| 1 | 1 | 1 | 1 | | |
| 1 | 1 | 1 | 2 | | |
| 19 | 1 | 1 | 1 | | |
| 1 | 1 | 1 | 1 | | |
| 1 | 1 | 1 | 4 | | |
| 5 | 1 | 1 | 1 | | |
| 12 | 1 | 1 | 1 | | |
| 1 | 1 | 1 | 1 | | |
| 3 | 1 | 1 | 1 | | |
| 1 | 1 | 1 | 2 | | |
| 1 | 1 | 1 | 1 | | |
| 1 | 1 | 1 | 1 | | |
| 1 | 1 | 1 | 1 | | |
| 12 | 1 | 2 | 2 | | |
| 12 | 1 | 1 | 1 | | |
| 10 | 1 | 1 | 1 | | |
| 32 | 1 | 1 | 1 | | |
| 7 | 1 | 1 | 1 | | |
| 7 | 1 | 1 | 1 | | |
| 10 | 1 | 1 | 1 | | |
| 12 | 1 | 3 | 6 | | |
| 8 | 1 | 1 | 2 | | |
| 17 | 1 | 1 | 1 | | |
| 4 | 1 | 1 | 1 | | |
| 8 | 1 | 3 | 3 | | |

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|---|---|---|---|---|---|
| 12 | 1 | 4 | 4 | | |
| 3 | 1 | 1 | 1 | | |
| 3 | 1 | 1 | 1 | | |
| 1 | 1 | 1 | 1 | | |
| 1 | 1 | 1 | 2 | | |
| 1 | 1 | 1 | 1 | | |
| 1 | 1 | 1 | 1 | | |
| 1 | 1 | 1 | 1 | | |
| 2 | 1 | 1 | 1 | | |
| 3 | 1 | 1 | 1 | | |
| 10 | 1 | 1 | 1 | | |
| 6 | 1 | 1 | 1 | | |
| 58 | 1 | 3 | 4 | | |
| 7 | 1 | 1 | 1 | | |
| 5 | 1 | 1 | 1 | | |
| 17 | 1 | 1 | 2 | | |
| 17 | 1 | 2 | 2 | | |
| 9 | 1 | 2 | 6 | | |
| 1 | 1 | 1 | 2 | | |
| 7 | 1 | 1 | 2 | | |
| 2 | 1 | 1 | 3 | | |
| 1 | 1 | 1 | 2 | | |
| 11 | 1 | 1 | 1 | | |
| 10 | 1 | 1 | 1 | | |
| 5 | 1 | 1 | 1 | | |
| 6 | 1 | 1 | 1 | | |
| 1 | 1 | 1 | 2 | | |
| 5 | 1 | 1 | 1 | | |
| 5 | 1 | 2 | 2 | | |
| 11 | 1 | 1 | 1 | | |
| 1 | 1 | 1 | 1 | | |
| 1 | 1 | 1 | 10 | | |
| 1 | 1 | 1 | 1 | | |
| 17 | 1 | 1 | 1 | | |
| 5 | 1 | 2 | 3 | | |
| 11 | 1 | 1 | 2 | | |
| 6 | 1 | 1 | 1 | | |
| 9 | 1 | 1 | 1 | | |
| 1 | 1 | 1 | 1 | | |
| 7 | 1 | 1 | 2 | | |
| 9 | 1 | 1 | 1 | | |
| 9 | 1 | 2 | 2 | | |
| 4 | 1 | 1 | 1 | | |
| 11 | 1 | 1 | 1 | | |
| 49 | 1 | 1 | 1 | | |
| 1 | 1 | 1 | 1 | | |
| 8 | 1 | 1 | 3 | | |
| 1 | 1 | 1 | 3 | | |
| 8 | 1 | 2 | 2 | | |
| 5 | 1 | 1 | 1 | | |
| 10 | 1 | 1 | 1 | | |
| 1 | 1 | 1 | 1 | | |
| 4 | 1 | 1 | 2 | | |
| 1 | 1 | 1 | 1 | | |
| 1 | 1 | 1 | 2 | | |
| 2 | 1 | 1 | 1 | | |
| 3 | 1 | 1 | 3 | | |
| 1 | 1 | 1 | 1 | | |
| 21 | 1 | 1 | 1 | | |

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|---|---|---|---|---|---|
| 1 | 1 | 1 | 1 | | |
| 6 | 1 | 2 | 2 | | |
| 1 | 1 | 1 | 2 | | |
| 6 | 1 | 2 | 3 | | |
| 1 | 1 | 1 | 1 | | |
| 1 | 1 | 1 | 1 | | |
| 1 | 1 | 1 | 1 | | |
| 1 | 1 | 1 | 1 | | |
| 1 | 1 | 1 | 1 | | |
| 2 | 1 | 1 | 2 | | |
| 1 | 1 | 1 | 9 | | |
| 1 | 1 | 1 | 1 | | |
| 7 | 1 | 1 | 4 | | |
| 22 | 1 | 2 | 2 | | |
| 3 | 1 | 1 | 2 | | |

| Biological Process | Pfam IDs | # AAs | MW [kDa] | calc. pI |
|---|---|---|---|---|
| | Retrival Error | 1960 | 226.4 | 5.60 |
| | Retrival Error | 645 | 65.8 | 8.00 |
| | Retrival Error | 4684 | 531.5 | 5.96 |
| | Retrival Error | 646 | 70.9 | 5.52 |
| | Retrival Error | 623 | 62.0 | 5.24 |
| | Retrival Error | 440 | 47.7 | 5.22 |
| | Retrival Error | 231 | 24.3 | 7.91 |
| | Retrival Error | 547 | 58.6 | 7.72 |
| | Retrival Error | 339 | 38.6 | 7.75 |
| | Retrival Error | 34942 | 3878.8 | 6.38 |
| | Retrival Error | 213 | 23.3 | 8.29 |
| | Retrival Error | 624 | 63.3 | 5.21 |
| | Retrival Error | 707 | 76.3 | 4.69 |
| | Retrival Error | 458 | 50.6 | 6.67 |
| | Retrival Error | 2388 | 261.2 | 8.47 |
| | Retrival Error | 624 | 69.6 | 6.44 |
| | Retrival Error | 1639 | 187.8 | 5.69 |
| | Retrival Error | 518 | 56.5 | 7.83 |
| | Retrival Error | 569 | 60.6 | 6.04 |
| | Retrival Error | 665 | 72.4 | 5.94 |
| | Retrival Error | 2427 | 279.3 | 5.36 |
| | Retrival Error | 473 | 51.2 | 5.05 |
| | Retrival Error | 285 | 33.7 | 9.36 |
| | Retrival Error | 293 | 31.5 | 7.61 |
| | Retrival Error | 416 | 46.3 | 5.08 |
| | Retrival Error | 530 | 56.8 | 6.87 |
| | Retrival Error | 217 | 24.8 | 9.94 |
| | Retrival Error | 596 | 68.2 | 5.85 |
| | Retrival Error | 242 | 26.5 | 9.66 |
| | Retrival Error | 721 | 79.7 | 5.99 |
| | Retrival Error | 2578 | 275.5 | 5.81 |
| | Retrival Error | 414 | 46.4 | 7.47 |
| | Retrival Error | 152 | 17.7 | 10.99 |
| | Retrival Error | 2315 | 245.7 | 5.97 |
| | Retrival Error | 192 | 20.7 | 6.87 |
| | Retrival Error | 6907 | 780.1 | 6.71 |
| | Retrival Error | 4236 | 485.7 | 6.35 |
| | Retrival Error | 333 | 37.6 | 11.03 |
| | Retrival Error | 622 | 69.8 | 6.55 |
| | Retrival Error | 398 | 45.4 | 10.15 |
| | Retrival Error | 650 | 74.7 | 5.14 |
| | Retrival Error | 221 | 24.2 | 9.79 |
| | Retrival Error | 1173 | 138.3 | 6.55 |
| | Retrival Error | 858 | 95.3 | 6.83 |
| | Retrival Error | 618 | 67.5 | 5.50 |
| | Retrival Error | 164 | 17.9 | 7.81 |
| | Retrival Error | 129 | 14.4 | 10.23 |
| | Retrival Error | 419 | 47.3 | 8.92 |
| | Retrival Error | 266 | 30.1 | 10.74 |
| | Retrival Error | 389 | 44.6 | 6.47 |
| | Retrival Error | 248 | 29.2 | 10.65 |
| | Retrival Error | 466 | 53.7 | 5.10 |
| | Retrival Error | 218 | 23.6 | 10.92 |
| | Retrival Error | 280 | 30.9 | 4.84 |
| | Retrival Error | 732 | 84.6 | 5.02 |
| | Retrival Error | 260 | 31.2 | 9.06 |
| | Retrival Error | 278 | 29.7 | 5.68 |
| | Retrival Error | 1382 | 166.4 | 6.79 |

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|---|---|---|---|---|
| | Retrival Error | 1262 | 144.4 | 6.04 |
| | Retrival Error | 5890 | 628.7 | 6.15 |
| | Retrival Error | 2272 | 260.0 | 6.96 |
| | Retrival Error | 135 | 15.5 | 9.85 |
| | Retrival Error | 307 | 34.9 | 9.57 |
| | Retrival Error | 300 | 33.3 | 5.07 |
| | Retrival Error | 958 | 96.7 | 5.62 |
| | Retrival Error | 441 | 47.8 | 9.03 |
| | Retrival Error | 178 | 20.5 | 10.52 |
| | Retrival Error | 472 | 51.6 | 5.16 |
| | Retrival Error | 314 | 35.0 | 7.78 |
| | Retrival Error | 170 | 19.4 | 10.26 |
| | Retrival Error | 6391 | 740.0 | 9.11 |
| | Retrival Error | 518 | 59.6 | 7.24 |
| | Retrival Error | 151 | 16.3 | 10.89 |
| | Retrival Error | 2801 | 308.6 | 9.51 |
| | Retrival Error | 124 | 13.6 | 9.99 |
| | Retrival Error | 415 | 46.5 | 4.93 |
| | Retrival Error | 669 | 74.2 | 8.54 |
| | Retrival Error | 522 | 58.2 | 5.29 |
| | Retrival Error | 211 | 24.3 | 11.65 |
| | Retrival Error | 550 | 60.8 | 7.55 |
| | Retrival Error | 247 | 28.4 | 10.84 |
| | Retrival Error | 258 | 29.3 | 9.77 |
| | Retrival Error | 746 | 81.7 | 7.55 |
| | Retrival Error | 362 | 40.2 | 7.88 |
| | Retrival Error | 166 | 18.5 | 8.09 |
| | Retrival Error | 248 | 27.9 | 8.46 |
| | Retrival Error | 158 | 18.4 | 10.30 |
| | Retrival Error | 151 | 16.3 | 10.05 |
| | Retrival Error | 2017 | 223.6 | 8.75 |
| | Retrival Error | 6825 | 788.0 | 5.47 |
| | Retrival Error | 1300 | 149.5 | 5.71 |
| | Retrival Error | 4471 | 514.5 | 5.88 |
| | Retrival Error | 267 | 29.4 | 9.14 |
| | Retrival Error | 947 | 106.6 | 6.47 |
| | Retrival Error | 164 | 19.3 | 11.93 |
| | Retrival Error | 2266 | 252.3 | 6.60 |
| | Retrival Error | 1011 | 111.7 | 6.76 |
| | Retrival Error | 3184 | 367.2 | 5.02 |
| | Retrival Error | 363 | 39.3 | 8.09 |
| | Retrival Error | 523 | 56.7 | 8.41 |
| | Retrival Error | 217 | 23.3 | 6.90 |
| | Retrival Error | 2083 | 244.4 | 5.34 |
| | Retrival Error | 336 | 36.3 | 6.90 |
| | Retrival Error | 3562 | 412.2 | 5.86 |
| | Retrival Error | 846 | 93.8 | 4.77 |
| | Retrival Error | 115 | 13.0 | 11.00 |
| | Retrival Error | 4033 | 458.5 | 7.08 |
| | Retrival Error | 1349 | 152.0 | 9.42 |
| | Retrival Error | 6616 | 720.7 | 5.81 |
| | Retrival Error | 780 | 87.7 | 5.17 |
| | Retrival Error | 3528 | 394.8 | 9.19 |
| | Retrival Error | 426 | 47.6 | 5.02 |
| | Retrival Error | 705 | 78.3 | 7.27 |
| | Retrival Error | 201 | 23.4 | 10.93 |
| | Retrival Error | 465 | 53.2 | 6.40 |
| | Retrival Error | 593 | 66.7 | 5.63 |
| | Retrival Error | 223 | 25.1 | 10.99 |

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|---|---|---|---|---|
| | Retrival Error | 2467 | 283.5 | 6.48 |
| | Retrival Error | 230 | 26.3 | 5.06 |
| | Retrival Error | 489 | 54.4 | 5.68 |
| | Retrival Error | 134 | 14.1 | 10.26 |
| | Retrival Error | 833 | 92.5 | 5.44 |
| | Retrival Error | 284 | 33.1 | 4.79 |
| | Retrival Error | 445 | 48.1 | 5.07 |
| | Retrival Error | 2334 | 258.2 | 6.60 |
| | Retrival Error | 145 | 17.2 | 10.55 |
| | Retrival Error | 1941 | 222.9 | 5.82 |
| | Retrival Error | 3396 | 372.6 | 4.51 |
| | Retrival Error | 119 | 13.4 | 9.94 |
| | Retrival Error | 325 | 36.5 | 5.64 |
| | Retrival Error | 724 | 83.5 | 6.16 |
| | Retrival Error | 376 | 41.8 | 5.48 |
| | Retrival Error | 762 | 83.7 | 4.74 |
| | Retrival Error | 148 | 16.8 | 9.38 |
| | Retrival Error | 51 | 5.6 | 10.13 |
| | Retrival Error | 439 | 49.6 | 9.03 |
| | Retrival Error | 145 | 16.1 | 10.32 |
| | Retrival Error | 2488 | 268.0 | 9.03 |
| | Retrival Error | 221 | 22.3 | 11.02 |
| | Retrival Error | 644 | 66.0 | 8.12 |
| | Retrival Error | 151 | 17.2 | 10.54 |
| | Retrival Error | 1257 | 144.7 | 6.74 |
| | Retrival Error | 1261 | 138.8 | 7.24 |
| | Retrival Error | 924 | 107.5 | 7.99 |
| | Retrival Error | 201 | 23.3 | 8.24 |
| | Retrival Error | 1951 | 221.3 | 5.72 |
| | Retrival Error | 1185 | 132.3 | 5.74 |
| | Retrival Error | 909 | 105.1 | 7.93 |
| | Retrival Error | 283 | 31.3 | 6.99 |
| | Retrival Error | 188 | 19.6 | 8.03 |
| | Retrival Error | 507 | 56.4 | 6.49 |
| | Retrival Error | 688 | 78.6 | 8.84 |
| | Retrival Error | 460 | 52.8 | 7.44 |
| | Retrival Error | 1873 | 210.7 | 6.20 |
| | Retrival Error | 398 | 44.8 | 8.18 |
| | Retrival Error | 1659 | 190.4 | 7.62 |
| | Retrival Error | 2002 | 226.5 | 6.20 |
| | Retrival Error | 4427 | 507.4 | 6.37 |
| | Retrival Error | 877 | 99.0 | 5.16 |
| | Retrival Error | 132 | 14.2 | 8.65 |
| | Retrival Error | 2608 | 276.8 | 8.81 |
| | Retrival Error | 863 | 96.1 | 8.35 |
| | Retrival Error | 139 | 16.6 | 11.06 |
| | Retrival Error | 920 | 104.9 | 6.10 |
| | Retrival Error | 3507 | 399.6 | 6.93 |
| | Retrival Error | 158 | 17.6 | 4.86 |
| | Retrival Error | 202 | 22.8 | 8.50 |
| | Retrival Error | 196 | 22.0 | 5.63 |
| | Retrival Error | 94 | 10.7 | 8.72 |
| | Retrival Error | 241 | 26.7 | 8.15 |
| | Retrival Error | 448 | 49.5 | 6.19 |
| | Retrival Error | 442 | 50.3 | 7.99 |
| | Retrival Error | 498 | 54.9 | 10.07 |
| | Retrival Error | 498 | 57.0 | 6.83 |
| | Retrival Error | 291 | 33.1 | 9.29 |
| | Retrival Error | 316 | 36.5 | 6.37 |

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|---|---|---|---|---|
| | Retrival Error | 2458 | 267.9 | 7.83 |
| | Retrival Error | 352 | 38.9 | 4.94 |
| | Retrival Error | 4462 | 509.0 | 5.72 |
| | Retrival Error | 182 | 21.2 | 7.34 |
| | Retrival Error | 126 | 13.7 | 7.30 |
| | Retrival Error | 956 | 107.8 | 8.48 |
| | Retrival Error | 99 | 11.2 | 9.44 |
| | Retrival Error | 113 | 12.0 | 8.94 |
| | Retrival Error | 1450 | 160.7 | 6.37 |
| | Retrival Error | 616 | 69.8 | 8.46 |
| | Retrival Error | 284 | 31.2 | 9.32 |
| | Retrival Error | 539 | 58.5 | 6.09 |
| | Retrival Error | 2352 | 264.9 | 6.11 |
| | Retrival Error | 874 | 95.4 | 5.73 |
| | Retrival Error | 1976 | 228.8 | 5.54 |
| | Retrival Error | 563 | 64.6 | 5.87 |
| | Retrival Error | 214 | 23.6 | 8.29 |
| | Retrival Error | 6929 | 784.5 | 8.88 |
| | Retrival Error | 486 | 54.4 | 8.98 |
| | Retrival Error | 116 | 13.4 | 10.20 |
| | Retrival Error | 578 | 68.0 | 7.94 |
| | Retrival Error | 1156 | 127.3 | 5.63 |
| | Retrival Error | 1257 | 140.7 | 6.96 |
| | Retrival Error | 129 | 14.5 | 5.91 |
| | Retrival Error | 426 | 46.1 | 6.54 |
| | Retrival Error | 2342 | 256.6 | 4.78 |
| | Retrival Error | 301 | 32.5 | 8.72 |
| | Retrival Error | 805 | 88.8 | 6.92 |
| | Retrival Error | 135 | 15.2 | 9.44 |
| | Retrival Error | 3674 | 416.6 | 6.67 |
| | Retrival Error | 1647 | 184.1 | 5.54 |
| | Retrival Error | 2349 | 265.4 | 5.07 |
| | Retrival Error | 772 | 89.2 | 5.20 |
| | Retrival Error | 599 | 68.2 | 6.02 |
| | Retrival Error | 251 | 27.6 | 9.57 |
| | Retrival Error | 397 | 46.4 | 8.31 |
| | Retrival Error | 1641 | 186.7 | 6.84 |
| | Retrival Error | 606 | 67.1 | 9.89 |
| | Retrival Error | 872 | 98.2 | 7.65 |
| | Retrival Error | 2330 | 261.7 | 7.58 |
| | Retrival Error | 1310 | 145.5 | 5.22 |
| | Retrival Error | 2884 | 324.6 | 6.79 |
| | Retrival Error | 4919 | 535.9 | 6.30 |
| | Retrival Error | 231 | 26.1 | 9.99 |
| | Retrival Error | 1019 | 110.0 | 9.29 |
| | Retrival Error | 38 | 4.5 | 10.54 |
| | Retrival Error | 4024 | 460.8 | 5.99 |
| | Retrival Error | 1254 | 141.6 | 6.55 |
| | Retrival Error | 184 | 21.4 | 10.20 |
| | Retrival Error | 393 | 43.7 | 6.95 |
| | Retrival Error | 539 | 58.7 | 6.34 |
| | Retrival Error | 418 | 47.4 | 6.71 |
| | Retrival Error | 963 | 107.8 | 5.67 |
| | Retrival Error | 1066 | 119.1 | 6.62 |
| | Retrival Error | 1752 | 202.0 | 7.55 |
| | Retrival Error | 171 | 20.0 | 9.42 |
| | Retrival Error | 406 | 46.0 | 8.34 |
| | Retrival Error | 117 | 12.9 | 6.15 |
| | Retrival Error | 1008 | 113.4 | 9.77 |

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| | Retrival Error | 270 | 29.9 | 7.85 |
| | Retrival Error | 439 | 48.5 | 5.92 |
| | Retrival Error | 900 | 101.2 | 7.40 |
| | Retrival Error | 275 | 30.5 | 7.66 |
| | Retrival Error | 470 | 53.6 | 5.47 |
| | Retrival Error | 406 | 47.6 | 8.69 |
| | Retrival Error | 327 | 36.8 | 9.23 |
| | Retrival Error | 254 | 28.7 | 5.71 |
| | Retrival Error | 627 | 71.5 | 8.62 |
| | Retrival Error | 266 | 29.4 | 10.23 |
| | Retrival Error | 512 | 58.7 | 5.58 |
| | Retrival Error | 524 | 57.0 | 5.55 |
| | Retrival Error | 2992 | 340.2 | 6.16 |
| | Retrival Error | 424 | 48.5 | 5.69 |
| | Retrival Error | 1340 | 150.9 | 8.22 |
| | Retrival Error | 1033 | 119.4 | 6.98 |
| | Retrival Error | 1268 | 143.5 | 6.58 |
| | Retrival Error | 471 | 52.5 | 8.51 |
| | Retrival Error | 2187 | 245.6 | 5.15 |
| | Retrival Error | 2093 | 229.8 | 7.34 |
| | Retrival Error | 2252 | 248.2 | 5.83 |
| | Retrival Error | 104 | 12.7 | 11.93 |
| | Retrival Error | 1714 | 175.4 | 8.27 |
| | Retrival Error | 156 | 17.9 | 9.60 |
| | Retrival Error | 426 | 48.6 | 7.18 |
| | Retrival Error | 250 | 27.0 | 7.69 |
| | Retrival Error | 246 | 28.0 | 7.42 |
| | Retrival Error | 408 | 44.4 | 9.39 |
| | Retrival Error | 174 | 20.2 | 8.50 |
| | Retrival Error | 2022 | 228.5 | 9.29 |
| | Retrival Error | 2504 | 272.9 | 6.67 |
| | Retrival Error | 593 | 66.8 | 7.75 |
| | Retrival Error | 490 | 55.9 | 5.16 |
| | Retrival Error | 1857 | 214.2 | 5.54 |
| | Retrival Error | 472 | 53.4 | 8.59 |
| | Retrival Error | 367 | 42.3 | 8.63 |
| | Retrival Error | 3929 | 441.5 | 7.46 |
| | Retrival Error | 715 | 79.6 | 9.35 |
| | Retrival Error | 570 | 65.0 | 8.29 |
| | Retrival Error | 798 | 88.3 | 8.82 |
| | Retrival Error | 593 | 67.4 | 7.71 |
| | Retrival Error | 698 | 80.4 | 7.74 |
| | Retrival Error | 812 | 93.5 | 5.69 |
| | Retrival Error | 367 | 40.7 | 5.69 |
| | Retrival Error | 198 | 22.2 | 10.76 |
| | Retrival Error | 50 | 5.9 | 9.70 |
| | Retrival Error | 143 | 16.7 | 10.52 |
| | Retrival Error | 124 | 14.8 | 6.39 |
| | Retrival Error | 301 | 34.0 | 8.05 |
| | Retrival Error | 950 | 108.7 | 7.12 |
| | Retrival Error | 529 | 59.1 | 6.95 |
| | Retrival Error | 255 | 29.1 | 5.00 |
| | Retrival Error | 442 | 50.4 | 6.39 |
| | Retrival Error | 127 | 14.6 | 9.60 |
| | Retrival Error | 298 | 34.2 | 9.85 |
| | Retrival Error | 366 | 42.3 | 8.69 |
| | Retrival Error | 495 | 56.7 | 7.75 |
| | Retrival Error | 7723 | 875.9 | 5.26 |
| | Retrival Error | 340 | 40.0 | 6.02 |

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| | Retrival Error | 1839 | 201.3 | 6.62 |
| | Retrival Error | 554 | 64.1 | 6.42 |
| | Retrival Error | 117 | 12.6 | 7.96 |
| | Retrival Error | 106 | 11.4 | 7.28 |
| | Retrival Error | 1366 | 155.7 | 6.54 |
| | Retrival Error | 2715 | 298.2 | 5.48 |
| | Retrival Error | 232 | 26.6 | 5.02 |
| | Retrival Error | 150 | 17.8 | 5.73 |
| | Retrival Error | 1218 | 133.5 | 9.64 |
| | Retrival Error | 527 | 61.8 | 7.81 |
| | Retrival Error | 440 | 49.2 | 5.96 |
| | Retrival Error | 162 | 17.4 | 5.14 |
| | Retrival Error | 209 | 22.5 | 10.23 |
| | Retrival Error | 322 | 35.9 | 8.06 |
| | Retrival Error | 1189 | 134.8 | 5.92 |
| | Retrival Error | 1628 | 180.5 | 6.93 |
| | Retrival Error | 468 | 51.2 | 7.20 |
| | Retrival Error | 585 | 63.6 | 7.24 |
| | Retrival Error | 1043 | 115.0 | 6.58 |
| | Retrival Error | 568 | 65.5 | 8.94 |
| | Retrival Error | 2436 | 270.5 | 5.53 |
| | Retrival Error | 373 | 42.8 | 5.21 |
| | Retrival Error | 1978 | 227.4 | 5.30 |
| | Retrival Error | 1909 | 210.6 | 8.78 |
| | Retrival Error | 265 | 30.3 | 9.14 |
| | Retrival Error | 399 | 45.0 | 7.58 |
| | Retrival Error | 1198 | 136.3 | 8.59 |
| | Retrival Error | 1230 | 140.1 | 6.80 |
| | Retrival Error | 410 | 48.5 | 7.93 |
| | Retrival Error | 331 | 38.2 | 5.44 |
| | Retrival Error | 1385 | 155.7 | 7.20 |
| | Retrival Error | 396 | 45.2 | 6.76 |
| | Retrival Error | 433 | 46.9 | 9.11 |
| | Retrival Error | 530 | 61.0 | 9.74 |
| | Retrival Error | 2367 | 257.2 | 5.71 |
| | Retrival Error | 884 | 102.2 | 5.44 |
| | Retrival Error | 165 | 18.4 | 6.18 |
| | Retrival Error | 264 | 30.4 | 8.95 |
| | Retrival Error | 1163 | 127.4 | 9.31 |
| | Retrival Error | 677 | 74.2 | 6.19 |
| | Retrival Error | 93 | 10.8 | 7.03 |
| | Retrival Error | 185 | 21.4 | 5.44 |
| | Retrival Error | 1017 | 114.2 | 7.34 |
| | Retrival Error | 131 | 14.7 | 5.10 |
| | Retrival Error | 539 | 61.3 | 6.39 |
| | Retrival Error | 378 | 44.4 | 5.25 |
| | Retrival Error | 1116 | 126.8 | 7.17 |
| | Retrival Error | 847 | 94.6 | 6.25 |
| | Retrival Error | 148 | 16.4 | 8.46 |
| | Retrival Error | 233 | 24.5 | 6.05 |
| | Retrival Error | 315 | 35.1 | 4.53 |
| | Retrival Error | 253 | 27.1 | 10.14 |
| | Retrival Error | 502 | 56.7 | 6.95 |
| | Retrival Error | 156 | 17.7 | 9.33 |
| | Retrival Error | 244 | 26.6 | 9.33 |
| | Retrival Error | 150 | 16.4 | 9.77 |
| | Retrival Error | 1830 | 211.8 | 6.87 |
| | Retrival Error | 1363 | 151.3 | 7.80 |
| | Retrival Error | 1010 | 107.7 | 6.70 |

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| | Retrival Error | 10 | 1.0 | 4.50 |
| | Retrival Error | 68 | 7.3 | 9.85 |
| | Retrival Error | 196 | 21.4 | 9.96 |
| | Retrival Error | 351 | 39.0 | 6.16 |
| | Retrival Error | 957 | 109.4 | 6.19 |
| | Retrival Error | 168 | 18.8 | 9.86 |
| | Retrival Error | 138 | 14.9 | 8.72 |
| | Retrival Error | 513 | 57.9 | 6.29 |
| | Retrival Error | 124 | 13.4 | 9.50 |
| | Retrival Error | 377 | 43.1 | 4.92 |
| | Retrival Error | 62 | 7.5 | 8.47 |
| | Retrival Error | 481 | 52.0 | 8.68 |
| | Retrival Error | 2139 | 238.0 | 5.33 |
| | Retrival Error | 904 | 103.3 | 7.18 |
| | Retrival Error | 191 | 21.8 | 8.84 |
| | Retrival Error | 800 | 92.5 | 9.17 |
| | Retrival Error | 108 | 12.2 | 9.36 |
| | Retrival Error | 251 | 27.5 | 8.25 |
| | Retrival Error | 327 | 35.1 | 7.21 |
| | Retrival Error | 216 | 23.7 | 8.07 |
| | Retrival Error | 329 | 36.3 | 7.23 |
| | Retrival Error | 410 | 45.0 | 5.20 |
| | Retrival Error | 221 | 23.8 | 10.54 |
| | Retrival Error | 442 | 52.6 | 8.88 |
| | Retrival Error | 320 | 33.3 | 6.47 |
| | Retrival Error | 139 | 13.2 | 11.41 |
| | Retrival Error | 374 | 43.8 | 5.36 |
| | Retrival Error | 436 | 50.2 | 9.07 |
| | Retrival Error | 154 | 16.5 | 11.90 |
| | Retrival Error | 369 | 41.4 | 5.05 |
| | Retrival Error | 158 | 16.4 | 7.20 |
| | Retrival Error | 67 | 7.5 | 5.97 |
| | Retrival Error | 225 | 24.7 | 4.67 |
| | Retrival Error | 1058 | 118.2 | 4.94 |
| | Retrival Error | 139 | 15.4 | 6.40 |
| | Retrival Error | 108 | 12.8 | 5.29 |
| | Retrival Error | 405 | 44.5 | 5.39 |
| | Retrival Error | 457 | 52.5 | 8.50 |
| | Retrival Error | 1333 | 146.3 | 7.66 |
| | Retrival Error | 259 | 29.9 | 7.06 |
| | Retrival Error | 298 | 32.8 | 9.74 |
| | Retrival Error | 582 | 66.9 | 9.55 |
| | Retrival Error | 1352 | 146.6 | 9.22 |
| | Retrival Error | 247 | 28.0 | 9.70 |
| | Retrival Error | 312 | 34.4 | 7.37 |
| | Retrival Error | 249 | 28.3 | 8.37 |
| | Retrival Error | 1053 | 112.1 | 8.13 |
| | Retrival Error | 330 | 37.7 | 9.22 |
| | Retrival Error | 1483 | 166.7 | 9.28 |
| | Retrival Error | 221 | 25.5 | 6.52 |
| | Retrival Error | 716 | 83.2 | 9.61 |
| | Retrival Error | 160 | 18.5 | 8.51 |
| | Retrival Error | 1995 | 227.7 | 5.60 |
| | Retrival Error | 516 | 56.9 | 6.04 |
| | Retrival Error | 396 | 45.7 | 5.62 |
| | Retrival Error | 343 | 38.0 | 8.60 |
| | Retrival Error | 132 | 14.4 | 8.29 |
| | Retrival Error | 450 | 49.3 | 5.08 |
| | Retrival Error | 1136 | 131.9 | 9.38 |

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| | Retrival Error | 605 | 64.7 | 9.48 |
| | Retrival Error | 278 | 30.5 | 7.91 |
| | Retrival Error | 167 | 19.0 | 9.45 |
| | Retrival Error | 115 | 13.3 | 5.34 |
| | Retrival Error | 1183 | 131.4 | 9.04 |
| | Retrival Error | 594 | 67.8 | 5.17 |
| | Retrival Error | 615 | 66.5 | 7.53 |
| | Retrival Error | 124 | 14.6 | 6.13 |
| | Retrival Error | 45 | 5.1 | 11.62 |
| | Retrival Error | 1295 | 143.2 | 7.33 |
| | Retrival Error | 291 | 33.2 | 6.37 |
| | Retrival Error | 730 | 80.7 | 8.68 |
| | Retrival Error | 867 | 98.4 | 6.64 |
| | Retrival Error | 465 | 51.7 | 7.21 |
| | Retrival Error | 951 | 110.4 | 6.47 |
| | Retrival Error | 197 | 21.9 | 9.55 |
| | Retrival Error | 109 | 12.1 | 4.27 |
| | Retrival Error | 669 | 76.6 | 7.39 |
| | Retrival Error | 274 | 30.1 | 9.57 |
| | Retrival Error | 632 | 72.6 | 6.34 |
| | Retrival Error | 113 | 12.3 | 10.74 |
| | Retrival Error | 242 | 26.4 | 8.10 |
| | Retrival Error | 265 | 29.7 | 9.23 |
| | Retrival Error | 139 | 15.4 | 9.52 |
| | Retrival Error | 120 | 14.1 | 9.47 |
| | Retrival Error | 299 | 32.5 | 8.16 |
| | Retrival Error | 200 | 22.0 | 11.08 |
| | Retrival Error | 143 | 16.1 | 7.64 |
| | Retrival Error | 61 | 7.3 | 9.73 |
| | Retrival Error | 164 | 18.2 | 5.50 |
| | Retrival Error | 86 | 8.8 | 8.25 |
| | Retrival Error | 733 | 82.6 | 7.97 |
| | Retrival Error | 1460 | 161.3 | 7.01 |
| | Retrival Error | 662 | 69.1 | 7.75 |
| | Retrival Error | 604 | 68.3 | 9.48 |
| | Retrival Error | 397 | 46.2 | 5.92 |
| | Retrival Error | 341 | 39.5 | 9.51 |
| | Retrival Error | 204 | 23.3 | 9.92 |
| | Retrival Error | 165 | 18.4 | 9.32 |
| | Retrival Error | 178 | 18.7 | 7.39 |
| | Retrival Error | 195 | 21.1 | 8.18 |
| | Retrival Error | 552 | 55.6 | 9.48 |
| | Retrival Error | 232 | 26.6 | 9.36 |
| | Retrival Error | 620 | 69.2 | 6.43 |
| | Retrival Error | 127 | 13.7 | 10.35 |
| | Retrival Error | 1293 | 141.4 | 8.02 |
| | Retrival Error | 150 | 16.9 | 10.67 |
| | Retrival Error | 447 | 50.1 | 4.89 |
| | Retrival Error | 299 | 34.9 | 5.02 |
| | Retrival Error | 255 | 29.1 | 9.76 |
| | Retrival Error | 785 | 87.4 | 6.83 |
| | Retrival Error | 465 | 54.0 | 9.83 |
| | Retrival Error | 420 | 47.9 | 7.90 |
| | Retrival Error | 1075 | 121.2 | 6.21 |
| | Retrival Error | 58 | 5.8 | 9.09 |
| | Retrival Error | 535 | 59.2 | 8.13 |
| | Retrival Error | 210 | 24.2 | 9.66 |
| | Retrival Error | 2752 | 299.4 | 12.06 |
| | Retrival Error | 2137 | 246.3 | 5.27 |

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| | Retrival Error | 218 | 25.0 | 7.15 |
| | Retrival Error | 67 | 7.7 | 5.35 |
| | Retrival Error | 307 | 35.7 | 5.03 |
| | Retrival Error | 122 | 14.4 | 5.17 |
| | Retrival Error | 428 | 48.1 | 5.62 |
| | Retrival Error | 302 | 33.6 | 6.96 |
| | Retrival Error | 155 | 16.1 | 6.13 |
| | Retrival Error | 102 | 11.4 | 6.95 |
| | Retrival Error | 555 | 58.8 | 5.97 |
| | Retrival Error | 334 | 38.1 | 9.39 |
| | Retrival Error | 754 | 83.6 | 5.90 |
| | Retrival Error | 150 | 16.7 | 6.90 |
| | Retrival Error | 1368 | 151.8 | 7.14 |
| | Retrival Error | 215 | 22.6 | 8.59 |
| | Retrival Error | 474 | 52.2 | 7.12 |
| | Retrival Error | 526 | 58.3 | 6.95 |
| | Retrival Error | 1163 | 124.2 | 8.72 |
| | Retrival Error | 1272 | 141.3 | 5.41 |
| | Retrival Error | 400 | 45.2 | 5.67 |
| | Retrival Error | 600 | 69.0 | 7.08 |
| | Retrival Error | 215 | 22.9 | 7.46 |
| | Retrival Error | 233 | 25.5 | 9.06 |
| | Retrival Error | 412 | 45.0 | 8.57 |
| | Retrival Error | 240 | 28.0 | 8.13 |
| | Retrival Error | 391 | 44.6 | 9.14 |
| | Retrival Error | 5695 | 605.3 | 5.36 |
| | Retrival Error | 727 | 83.0 | 7.46 |
| | Retrival Error | 166 | 18.0 | 9.26 |
| | Retrival Error | 243 | 28.2 | 7.49 |
| | Retrival Error | 439 | 47.7 | 6.64 |
| | Retrival Error | 446 | 50.9 | 6.68 |
| | Retrival Error | 179 | 20.9 | 8.22 |
| | Retrival Error | 643 | 72.0 | 9.52 |
| | Retrival Error | 155 | 17.6 | 5.31 |
| | Retrival Error | 179 | 21.0 | 9.88 |
| | Retrival Error | 241 | 25.9 | 9.14 |
| | Retrival Error | 611 | 67.9 | 9.38 |
| | Retrival Error | 305 | 34.5 | 5.72 |
| | Retrival Error | 485 | 55.5 | 4.97 |
| | Retrival Error | 224 | 24.1 | 8.88 |
| | Retrival Error | 324 | 37.5 | 8.90 |
| | Retrival Error | 259 | 28.8 | 5.36 |
| | Retrival Error | 186 | 21.2 | 4.39 |
| | Retrival Error | 896 | 102.1 | 6.52 |
| | Retrival Error | 243 | 25.4 | 7.06 |
| | Retrival Error | 229 | 26.1 | 7.81 |
| | Retrival Error | 373 | 43.2 | 9.06 |
| | Retrival Error | 685 | 79.5 | 7.75 |
| | Retrival Error | 396 | 43.1 | 4.87 |
| | Retrival Error | 123 | 14.2 | 9.94 |
| | Retrival Error | 301 | 33.8 | 9.92 |
| | Retrival Error | 285 | 32.9 | 6.62 |
| | Retrival Error | 284 | 31.3 | 9.73 |
| | Retrival Error | 227 | 25.9 | 9.17 |
| | Retrival Error | 265 | 29.2 | 7.91 |
| | Retrival Error | 433 | 46.3 | 8.97 |
| | Retrival Error | 269 | 29.7 | 9.07 |
| | Retrival Error | 221 | 24.4 | 9.38 |
| | Retrival Error | 372 | 40.5 | 9.66 |

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| | Retrival Error | 222 | 24.6 | 8.44 |
| | Retrival Error | 257 | 29.0 | 8.82 |
| | Retrival Error | 844 | 94.6 | 6.81 |
| | Retrival Error | 63 | 6.9 | 9.42 |
| | Retrival Error | 801 | 91.2 | 6.83 |
| | Retrival Error | 464 | 52.4 | 8.66 |
| | Retrival Error | 331 | 36.2 | 8.48 |
| | Retrival Error | 77 | 8.2 | 9.92 |
| | Retrival Error | 334 | 36.7 | 5.14 |
| | Retrival Error | 224 | 24.0 | 10.87 |
| | Retrival Error | 304 | 35.3 | 5.25 |
| | Retrival Error | 148 | 15.8 | 10.58 |
| | Retrival Error | 443 | 48.9 | 7.66 |
| | Retrival Error | 826 | 87.2 | 5.40 |
| | Retrival Error | 58 | 6.6 | 10.45 |
| | Retrival Error | 942 | 107.5 | 7.61 |
| | Retrival Error | 1213 | 137.3 | 7.93 |
| | Retrival Error | 143 | 17.3 | 6.61 |
| | Retrival Error | 32 | 3.8 | 4.51 |
| | Retrival Error | 397 | 44.6 | 4.93 |
| | Retrival Error | 323 | 34.2 | 8.10 |
| | Retrival Error | 354 | 40.2 | 5.22 |
| | Retrival Error | 143 | 16.3 | 9.20 |
| | Retrival Error | 2715 | 303.3 | 7.36 |
| | Retrival Error | 173 | 19.2 | 7.43 |
| | Retrival Error | 709 | 80.5 | 8.72 |
| | Retrival Error | 4700 | 516.0 | 6.32 |
| | Retrival Error | 103 | 12.6 | 9.73 |
| | Retrival Error | 343 | 38.8 | 5.94 |
| | Retrival Error | 145 | 16.8 | 7.01 |
| | Retrival Error | 80 | 9.1 | 5.83 |
| | Retrival Error | 396 | 44.2 | 5.06 |
| | Retrival Error | 432 | 48.7 | 7.81 |
| | Retrival Error | 365 | 41.6 | 8.92 |
| | Retrival Error | 993 | 109.7 | 8.79 |
| | Retrival Error | 400 | 45.1 | 6.68 |
| | Retrival Error | 431 | 46.4 | 6.47 |
| | Retrival Error | 247 | 28.3 | 7.62 |
| | Retrival Error | 186 | 21.9 | 8.87 |
| | Retrival Error | 173 | 20.1 | 5.66 |
| | Retrival Error | 648 | 71.7 | 8.25 |
| | Retrival Error | 232 | 27.2 | 8.38 |
| | Retrival Error | 193 | 22.4 | 6.80 |
| | Retrival Error | 381 | 43.8 | 7.78 |
| | Retrival Error | 727 | 83.7 | 6.96 |
| | Retrival Error | 160 | 17.6 | 10.07 |
| | Retrival Error | 547 | 60.7 | 9.14 |
| | Retrival Error | 296 | 34.7 | 4.34 |
| | Retrival Error | 228 | 26.1 | 5.72 |
| | Retrival Error | 943 | 107.2 | 5.74 |
| | Retrival Error | 163 | 18.7 | 9.42 |
| | Retrival Error | 938 | 103.5 | 5.35 |
| | Retrival Error | 256 | 28.5 | 4.91 |
| | Retrival Error | 79 | 8.7 | 8.21 |
| | Retrival Error | 820 | 90.4 | 7.30 |
| | Retrival Error | 629 | 70.2 | 5.53 |
| | Retrival Error | 475 | 53.5 | 5.25 |
| | Retrival Error | 240 | 27.5 | 5.94 |
| | Retrival Error | 146 | 16.6 | 6.13 |

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| | Retrival Error | 167 | 19.6 | 10.13 |
| | Retrival Error | 655 | 72.4 | 5.16 |
| | Retrival Error | 118 | 13.7 | 10.59 |
| | Retrival Error | 2400 | 252.1 | 4.45 |
| | Retrival Error | 874 | 99.3 | 8.73 |
| | Retrival Error | 229 | 24.8 | 7.94 |
| | Retrival Error | 1194 | 135.1 | 6.07 |
| | Retrival Error | 1010 | 118.1 | 8.15 |
| | Retrival Error | 383 | 42.1 | 4.94 |
| | Retrival Error | 2012 | 227.8 | 6.21 |
| | Retrival Error | 139 | 16.1 | 10.46 |
| | Retrival Error | 215 | 25.1 | 9.10 |
| | Retrival Error | 90 | 9.8 | 5.91 |
| | Retrival Error | 1230 | 138.3 | 7.52 |
| | Retrival Error | 212 | 24.3 | 5.81 |
| | Retrival Error | 622 | 70.4 | 7.15 |
| | Retrival Error | 306 | 34.7 | 8.98 |
| | Retrival Error | 299 | 32.3 | 7.93 |
| | Retrival Error | 73 | 7.9 | 8.79 |
| | Retrival Error | 224 | 24.0 | 7.55 |
| | Retrival Error | 141 | 15.6 | 5.29 |
| | Retrival Error | 207 | 23.6 | 7.44 |
| | Retrival Error | 435 | 48.4 | 7.46 |
| | Retrival Error | 199 | 22.9 | 6.61 |
| | Retrival Error | 333 | 36.5 | 6.05 |
| | Retrival Error | 618 | 70.0 | 5.81 |
| | Retrival Error | 47 | 5.5 | 10.87 |
| | Retrival Error | 299 | 33.9 | 5.58 |
| | Retrival Error | 204 | 22.5 | 5.48 |
| | Retrival Error | 116 | 12.9 | 9.45 |
| | Retrival Error | 357 | 39.7 | 6.27 |
| | Retrival Error | 69 | 7.9 | 9.63 |
| | Retrival Error | 246 | 28.0 | 6.47 |
| | Retrival Error | 263 | 29.5 | 5.21 |
| | Retrival Error | 245 | 28.2 | 4.91 |
| | Retrival Error | 159 | 18.8 | 6.79 |
| | Retrival Error | 246 | 26.4 | 6.90 |
| | Retrival Error | 304 | 35.2 | 6.99 |
| | Retrival Error | 135 | 15.4 | 6.89 |
| | Retrival Error | 433 | 49.0 | 7.12 |
| | Retrival Error | 78 | 8.3 | 9.00 |
| | Retrival Error | 95 | 10.0 | 6.76 |
| | Retrival Error | 497 | 56.5 | 7.20 |
| | Retrival Error | 124 | 13.6 | 10.84 |
| | Retrival Error | 214 | 23.4 | 8.05 |
| | Retrival Error | 69 | 7.1 | 4.55 |
| | Retrival Error | 478 | 52.9 | 9.26 |
| | Retrival Error | 12 | 1.3 | 9.00 |
| | Retrival Error | 15 | 1.6 | 7.18 |
| | Retrival Error | 121 | 12.9 | 7.97 |
| | Retrival Error | 515 | 59.0 | 6.14 |
| | Retrival Error | 100 | 10.9 | 8.46 |
| | Retrival Error | 835 | 94.1 | 6.48 |
| | Retrival Error | 20 | 2.3 | 4.46 |
| | Retrival Error | 148 | 16.6 | 6.06 |
| | Retrival Error | 444 | 49.8 | 4.78 |
| | Retrival Error | 2311 | 249.9 | 10.07 |
| | Retrival Error | 224 | 24.1 | 8.50 |
| | Retrival Error | 557 | 63.8 | 8.87 |

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| | Retrival Error | 197 | 22.5 | 4.70 |
| | Retrival Error | 66 | 7.2 | 7.52 |
| | Retrival Error | 181 | 19.9 | 6.62 |
| | Retrival Error | 366 | 39.2 | 7.06 |
| | Retrival Error | 476 | 52.2 | 8.70 |
| | Retrival Error | 190 | 21.9 | 6.07 |
| | Retrival Error | 338 | 37.6 | 5.76 |
| | Retrival Error | 1543 | 175.6 | 6.65 |
| | Retrival Error | 1704 | 191.3 | 7.62 |
| | Retrival Error | 39 | 4.7 | 4.55 |
| | Retrival Error | 219 | 24.7 | 6.39 |
| | Retrival Error | 70 | 7.9 | 8.92 |
| | Retrival Error | 188 | 22.2 | 5.83 |
| | Retrival Error | 392 | 42.4 | 6.14 |
| | Retrival Error | 4346 | 463.7 | 6.51 |
| | Retrival Error | 694 | 76.3 | 8.35 |
| | Retrival Error | 2285 | 261.8 | 6.24 |
| | Retrival Error | 1505 | 163.8 | 7.47 |
| | Retrival Error | 378 | 41.7 | 8.59 |
| | Retrival Error | 719 | 82.0 | 8.73 |
| | Retrival Error | 736 | 81.2 | 6.32 |
| | Retrival Error | 873 | 98.0 | 6.80 |
| | Retrival Error | 363 | 41.4 | 8.21 |
| | Retrival Error | 351 | 39.5 | 7.74 |
| | Retrival Error | 389 | 44.1 | 7.49 |
| | Retrival Error | 520 | 55.4 | 6.02 |
| | Retrival Error | 227 | 24.9 | 9.35 |
| | Retrival Error | 147 | 16.1 | 5.48 |
| | Retrival Error | 599 | 66.5 | 5.00 |
| | Retrival Error | 206 | 24.0 | 8.81 |
| | Retrival Error | 481 | 52.8 | 8.57 |
| | Retrival Error | 416 | 46.8 | 8.70 |
| | Retrival Error | 427 | 46.3 | 8.59 |
| | Retrival Error | 536 | 60.8 | 7.01 |
| | Retrival Error | 152 | 16.9 | 9.48 |
| | Retrival Error | 141 | 16.3 | 7.80 |
| | Retrival Error | 947 | 110.7 | 6.71 |
| | Retrival Error | 269 | 31.8 | 9.22 |
| | Retrival Error | 313 | 36.6 | 5.33 |
| | Retrival Error | 500 | 55.0 | 7.99 |
| | Retrival Error | 65 | 7.5 | 10.93 |
| | Retrival Error | 112 | 12.5 | 9.35 |
| | Retrival Error | 328 | 36.3 | 8.35 |
| | Retrival Error | 166 | 18.3 | 6.67 |
| | Retrival Error | 107 | 12.1 | 5.49 |
| | Retrival Error | 365 | 40.8 | 6.24 |
| | Retrival Error | 130 | 14.3 | 8.65 |
| | Retrival Error | 200 | 22.6 | 4.86 |
| | Retrival Error | 298 | 33.6 | 6.43 |
| | Retrival Error | 113 | 12.9 | 9.16 |
| | Retrival Error | 427 | 49.4 | 6.90 |
| | Retrival Error | 5604 | 631.3 | 5.73 |
| | Retrival Error | 226 | 25.8 | 6.21 |
| | Retrival Error | 116 | 13.1 | 10.24 |
| | Retrival Error | 280 | 30.9 | 7.85 |
| | Retrival Error | 1732 | 190.7 | 7.84 |
| | Retrival Error | 451 | 50.5 | 7.61 |
| | Retrival Error | 132 | 14.5 | 7.50 |
| | Retrival Error | 262 | 30.3 | 9.48 |

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| | Retrival Error | 1284 | 145.8 | 8.72 |
| | Retrival Error | 1313 | 146.2 | 8.13 |
| | Retrival Error | 670 | 72.9 | 7.03 |
| | Retrival Error | 351 | 38.2 | 8.22 |
| | Retrival Error | 358 | 37.7 | 5.00 |
| | Retrival Error | 107 | 12.2 | 7.30 |
| | Retrival Error | 110 | 12.0 | 8.07 |
| | Retrival Error | 353 | 39.3 | 7.24 |
| | Retrival Error | 83 | 9.2 | 10.29 |
| | Retrival Error | 434 | 42.2 | 5.67 |
| | Retrival Error | 59 | 6.9 | 11.82 |
| | Retrival Error | 473 | 50.5 | 8.19 |
| | Retrival Error | 1048 | 116.9 | 6.67 |
| | Retrival Error | 348 | 38.6 | 9.63 |
| | Retrival Error | 85 | 9.5 | 6.73 |
| | Retrival Error | 3396 | 371.4 | 6.30 |
| | Retrival Error | 343 | 38.4 | 8.70 |
| | Retrival Error | 194 | 19.0 | 6.77 |
| | Retrival Error | 996 | 109.6 | 5.21 |
| | Retrival Error | 441 | 51.0 | 6.74 |
| | Retrival Error | 733 | 80.9 | 7.55 |
| | Retrival Error | 104 | 11.7 | 8.32 |
| | Retrival Error | 63 | 7.5 | 10.39 |
| | Retrival Error | 95 | 11.0 | 8.62 |
| | Retrival Error | 172 | 19.3 | 7.42 |
| | Retrival Error | 108 | 13.1 | 10.11 |
| | Retrival Error | 83 | 9.3 | 11.49 |
| | Retrival Error | 141 | 15.6 | 9.44 |
| | Retrival Error | 114 | 13.1 | 7.28 |
| | Retrival Error | 190 | 20.2 | 6.76 |
| | Retrival Error | 133 | 15.2 | 10.14 |
| | Retrival Error | 872 | 95.6 | 6.16 |
| | Retrival Error | 118 | 13.0 | 11.91 |
| | Retrival Error | 1163 | 132.4 | 6.58 |
| | Retrival Error | 304 | 33.5 | 7.83 |
| | Retrival Error | 48 | 5.7 | 4.54 |
| | Retrival Error | 1196 | 134.7 | 5.87 |
| | Retrival Error | 103 | 11.6 | 4.53 |
| | Retrival Error | 549 | 61.8 | 6.29 |
| | Retrival Error | 248 | 26.9 | 9.54 |
| | Retrival Error | 218 | 23.8 | 5.34 |
| | Retrival Error | 96 | 11.0 | 6.51 |
| | Retrival Error | 440 | 50.5 | 9.16 |
| | Retrival Error | 147 | 16.6 | 10.74 |
| | Retrival Error | 132 | 14.6 | 12.06 |
| | Retrival Error | 133 | 15.1 | 8.87 |
| | Retrival Error | 560 | 64.6 | 8.98 |
| | Retrival Error | 100 | 10.9 | 4.77 |
| | Retrival Error | 449 | 51.3 | 9.26 |
| | Retrival Error | 521 | 58.9 | 6.92 |
| | Retrival Error | 523 | 57.7 | 6.74 |
| | Retrival Error | 105 | 12.3 | 10.48 |
| | Retrival Error | 1013 | 114.9 | 6.62 |
| | Retrival Error | 144 | 16.9 | 9.39 |
| | Retrival Error | 396 | 46.4 | 6.46 |
| | Retrival Error | 975 | 111.1 | 6.95 |
| | Retrival Error | 515 | 58.5 | 6.27 |
| | Retrival Error | 167 | 17.8 | 11.71 |
| | Retrival Error | 179 | 19.9 | 7.83 |

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| | Retrival Error | 1405 | 156.3 | 5.41 |
| | Retrival Error | 551 | 60.2 | 9.92 |
| | Retrival Error | 468 | 53.5 | 9.82 |
| | Retrival Error | 143 | 16.5 | 7.78 |
| | Retrival Error | 251 | 27.7 | 9.23 |
| | Retrival Error | 186 | 18.3 | 7.64 |
| | Retrival Error | 188 | 19.6 | 10.01 |
| | Retrival Error | 1531 | 171.8 | 6.33 |
| | Retrival Error | 371 | 40.5 | 8.85 |
| | Retrival Error | 53 | 6.5 | 9.00 |
| | Retrival Error | 707 | 81.5 | 8.29 |
| | Retrival Error | 681 | 74.4 | 5.55 |
| | Retrival Error | 493 | 55.4 | 9.54 |
| | Retrival Error | 316 | 34.0 | 9.36 |
| | Retrival Error | 966 | 106.8 | 7.97 |
| | Retrival Error | 395 | 44.1 | 7.43 |
| | Retrival Error | 215 | 22.7 | 7.91 |
| | Retrival Error | 1677 | 186.3 | 6.95 |
| | Retrival Error | 12622 | 1310.2 | 5.07 |
| | Retrival Error | 138 | 15.5 | 8.63 |
| | Retrival Error | 1120 | 124.2 | 6.60 |
| | Retrival Error | 129 | 14.4 | 9.26 |
| | Retrival Error | 957 | 104.4 | 7.42 |
| | Retrival Error | 99 | 11.2 | 10.29 |
| | Retrival Error | 301 | 32.0 | 8.34 |
| | Retrival Error | 193 | 22.2 | 6.55 |
| | Retrival Error | 38 | 4.4 | 10.13 |
| | Retrival Error | 83 | 9.4 | 9.69 |
| | Retrival Error | 214 | 23.6 | 4.92 |
| | Retrival Error | 93 | 10.9 | 9.63 |
| | Retrival Error | 241 | 26.1 | 11.58 |
| | Retrival Error | 171 | 19.7 | 9.67 |
| | Retrival Error | 318 | 35.6 | 4.61 |
| | Retrival Error | 117 | 12.6 | 10.86 |
| | Retrival Error | 268 | 30.7 | 5.76 |
| | Retrival Error | 1424 | 160.1 | 8.35 |
| | Retrival Error | 561 | 65.4 | 8.41 |
| | Retrival Error | 272 | 29.7 | 8.48 |
| | Retrival Error | 93 | 10.9 | 7.88 |
| | Retrival Error | 420 | 43.9 | 7.61 |
| | Retrival Error | 167 | 18.7 | 4.51 |
| | Retrival Error | 331 | 35.1 | 10.26 |
| | Retrival Error | 115 | 12.9 | 7.93 |
| | Retrival Error | 30 | 3.4 | 10.01 |
| | Retrival Error | 582 | 66.8 | 6.34 |
| | Retrival Error | 1810 | 208.3 | 5.02 |
| | Retrival Error | 239 | 26.5 | 9.73 |
| | Retrival Error | 745 | 82.3 | 7.01 |
| | Retrival Error | 157 | 17.6 | 9.85 |
| | Retrival Error | 77 | 9.1 | 9.04 |
| | Retrival Error | 496 | 54.5 | 5.05 |
| | Retrival Error | 147 | 16.5 | 8.03 |
| | Retrival Error | 942 | 101.8 | 6.70 |
| | Retrival Error | 509 | 54.7 | 9.28 |
| | Retrival Error | 701 | 75.8 | 5.91 |
| | Retrival Error | 985 | 112.7 | 5.44 |
| | Retrival Error | 782 | 89.7 | 9.33 |
| | Retrival Error | 122 | 14.2 | 9.33 |
| | Retrival Error | 302 | 33.6 | 8.69 |

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| | Retrival Error | 827 | 93.5 | 8.10 |
| | Retrival Error | 456 | 49.2 | 6.65 |
| | Retrival Error | 92 | 10.3 | 9.36 |
| | Retrival Error | 345 | 34.4 | 8.90 |
| | Retrival Error | 148 | 15.6 | 7.78 |
| | Retrival Error | 147 | 16.9 | 9.61 |
| | Retrival Error | 1033 | 117.0 | 9.63 |
| | Retrival Error | 51 | 5.9 | 11.65 |
| | Retrival Error | 84 | 9.9 | 7.94 |
| | Retrival Error | 21 | 2.3 | 8.84 |
| | Retrival Error | 505 | 55.0 | 8.69 |
| | Retrival Error | 792 | 86.1 | 4.64 |
| | Retrival Error | 341 | 37.9 | 9.80 |
| | Retrival Error | 594 | 65.4 | 8.38 |
| | Retrival Error | 3272 | 372.0 | 6.06 |
| | Retrival Error | 368 | 37.6 | 10.98 |
| | Retrival Error | 1643 | 188.3 | 6.71 |
| | Retrival Error | 400 | 44.7 | 9.17 |
| | Retrival Error | 454 | 49.6 | 9.00 |
| | Retrival Error | 2695 | 306.6 | 6.35 |
| | Retrival Error | 463 | 50.9 | 5.22 |
| | Retrival Error | 255 | 27.9 | 9.89 |
| | Retrival Error | 221 | 25.6 | 6.29 |
| | Retrival Error | 46 | 5.5 | 9.63 |
| | Retrival Error | 54 | 6.1 | 6.23 |
| | Retrival Error | 73 | 8.9 | 6.02 |
| | Retrival Error | 750 | 86.9 | 5.74 |
| | Retrival Error | 275 | 27.9 | 12.21 |
| | Retrival Error | 53 | 5.8 | 9.99 |
| | Retrival Error | 862 | 96.4 | 7.39 |
| | Retrival Error | 841 | 92.7 | 5.52 |
| | Retrival Error | 41 | 4.8 | 9.72 |
| | Retrival Error | 206 | 24.3 | 9.60 |
| | Retrival Error | 67 | 7.5 | 7.39 |
| | Retrival Error | 80 | 9.7 | 10.59 |
| | Retrival Error | 383 | 42.2 | 8.78 |
| | Retrival Error | 165 | 18.1 | 9.47 |
| | Retrival Error | 407 | 46.4 | 7.46 |
| | Retrival Error | 1091 | 116.5 | 6.52 |
| | Retrival Error | 1215 | 135.2 | 6.54 |
| | Retrival Error | 115 | 12.9 | 9.70 |
| | Retrival Error | 2080 | 233.5 | 6.71 |
| | Retrival Error | 120 | 13.9 | 8.24 |
| | Retrival Error | 228 | 25.4 | 8.41 |
| | Retrival Error | 474 | 53.4 | 6.61 |
| | Retrival Error | 450 | 50.6 | 7.52 |
| | Retrival Error | 74 | 8.6 | 6.51 |
| | Retrival Error | 116 | 13.2 | 8.73 |
| | Retrival Error | 4539 | 487.1 | 6.58 |
| | Retrival Error | 179 | 20.5 | 7.27 |
| | Retrival Error | 106 | 12.0 | 5.26 |
| | Retrival Error | 168 | 18.6 | 4.78 |
| | Retrival Error | 432 | 49.3 | 6.48 |
| | Retrival Error | 45 | 5.3 | 8.35 |
| | Retrival Error | 307 | 31.7 | 8.18 |
| | Retrival Error | 85 | 10.0 | 11.12 |
| | Retrival Error | 166 | 18.3 | 9.66 |
| | Retrival Error | 80 | 9.2 | 9.52 |
| | Retrival Error | 1011 | 109.0 | 6.06 |

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| | Retrival Error | 468 | 52.1 | 7.58 |
| | Retrival Error | 90 | 10.2 | 4.59 |
| | Retrival Error | 745 | 84.3 | 7.27 |
| | Retrival Error | 75 | 8.5 | 5.10 |
| | Retrival Error | 141 | 15.1 | 8.54 |
| | Retrival Error | 1139 | 127.2 | 8.68 |
| | Retrival Error | 95 | 11.1 | 9.50 |
| | Retrival Error | 115 | 12.8 | 11.34 |
| | Retrival Error | 335 | 37.7 | 9.54 |
| | Retrival Error | 64 | 6.8 | 8.05 |
| | Retrival Error | 284 | 30.9 | 4.39 |
| | Retrival Error | 136 | 15.2 | 11.72 |
| | Retrival Error | 153 | 17.5 | 7.90 |
| | Retrival Error | 349 | 37.4 | 6.60 |
| | Retrival Error | 1227 | 137.5 | 5.67 |
| | Retrival Error | 1079 | 120.5 | 6.02 |
| | Retrival Error | 364 | 42.0 | 9.48 |
| | Retrival Error | 180 | 20.6 | 4.96 |
| | Retrival Error | 179 | 20.7 | 8.79 |
| | Retrival Error | 444 | 49.0 | 6.79 |
| | Retrival Error | 706 | 82.4 | 6.29 |
| | Retrival Error | 106 | 12.1 | 10.21 |
| | Retrival Error | 390 | 42.6 | 5.92 |
| | Retrival Error | 169 | 19.5 | 9.58 |
| | Retrival Error | 74 | 8.4 | 11.66 |
| | Retrival Error | 609 | 66.2 | 7.43 |
| | Retrival Error | 276 | 30.3 | 5.45 |
| | Retrival Error | 78 | 8.9 | 10.29 |
| | Retrival Error | 329 | 37.6 | 5.34 |
| | Retrival Error | 112 | 13.0 | 10.21 |
| | Retrival Error | 359 | 42.0 | 7.71 |
| | Retrival Error | 274 | 31.1 | 9.51 |
| | Retrival Error | 324 | 35.4 | 6.93 |
| | Retrival Error | 954 | 107.5 | 6.23 |
| | Retrival Error | 1197 | 136.3 | 7.17 |
| | Retrival Error | 464 | 53.0 | 9.36 |
| | Retrival Error | 186 | 21.9 | 9.23 |
| | Retrival Error | 1019 | 117.9 | 6.76 |
| | Retrival Error | 327 | 36.0 | 8.13 |
| | Retrival Error | 105 | 11.8 | 10.23 |
| | Retrival Error | 184 | 20.8 | 7.52 |
| | Retrival Error | 186 | 21.1 | 10.13 |
| | Retrival Error | 492 | 55.6 | 9.32 |
| | Retrival Error | 200 | 22.7 | 7.21 |
| | Retrival Error | 396 | 42.5 | 9.55 |
| | Retrival Error | 284 | 31.5 | 5.97 |
| | Retrival Error | 409 | 44.7 | 9.67 |
| | Retrival Error | 392 | 44.9 | 7.87 |
| | Retrival Error | 822 | 94.7 | 5.69 |
| | Retrival Error | 382 | 43.8 | 8.63 |
| | Retrival Error | 606 | 68.9 | 6.35 |
| | Retrival Error | 1415 | 163.5 | 6.21 |
| | Retrival Error | 217 | 24.8 | 6.74 |
| | Retrival Error | 836 | 93.7 | 7.55 |
| | Retrival Error | 216 | 24.9 | 6.37 |
| | Retrival Error | 555 | 62.6 | 8.06 |
| | Retrival Error | 2210 | 245.5 | 8.03 |
| | Retrival Error | 1509 | 172.7 | 5.12 |
| | Retrival Error | 641 | 74.4 | 9.14 |

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| | Retrival Error | 4363 | 488.7 | 6.55 |
| | Retrival Error | 324 | 36.6 | 6.55 |
| | Retrival Error | 752 | 85.7 | 6.16 |
| | Retrival Error | 130 | 15.1 | 8.88 |
| | Retrival Error | 451 | 52.8 | 5.80 |
| | Retrival Error | 548 | 62.0 | 8.88 |
| | Retrival Error | 335 | 38.9 | 9.25 |
| | Retrival Error | 594 | 65.9 | 7.30 |
| | Retrival Error | 974 | 110.5 | 6.90 |
| | Retrival Error | 328 | 35.8 | 7.59 |
| | Retrival Error | 116 | 13.0 | 10.52 |
| | Retrival Error | 163 | 18.1 | 9.61 |
| | Retrival Error | 557 | 64.0 | 8.05 |
| | Retrival Error | 541 | 62.0 | 8.76 |
| | Retrival Error | 394 | 45.5 | 7.24 |
| | Retrival Error | 230 | 26.5 | 10.39 |
| | Retrival Error | 402 | 45.5 | 8.32 |
| | Retrival Error | 883 | 97.4 | 6.73 |
| | Retrival Error | 202 | 23.8 | 8.47 |
| | Retrival Error | 828 | 89.1 | 6.87 |
| | Retrival Error | 426 | 47.1 | 8.82 |
| | Retrival Error | 308 | 33.2 | 8.75 |
| | Retrival Error | 234 | 27.3 | 4.89 |
| | Retrival Error | 718 | 81.4 | 5.44 |
| | Retrival Error | 454 | 49.2 | 6.60 |
| | Retrival Error | 623 | 71.4 | 9.07 |
| | Retrival Error | 273 | 32.1 | 10.39 |
| | Retrival Error | 724 | 84.3 | 5.95 |
| | Retrival Error | 216 | 22.6 | 7.96 |
| | Retrival Error | 378 | 41.6 | 8.69 |
| | Retrival Error | 563 | 64.4 | 9.50 |
| | Retrival Error | 296 | 30.9 | 8.43 |
| | Retrival Error | 530 | 60.1 | 8.15 |
| | Retrival Error | 157 | 17.2 | 8.97 |
| | Retrival Error | 379 | 42.9 | 8.24 |
| | Retrival Error | 310 | 35.0 | 5.34 |
| | Retrival Error | 952 | 103.0 | 8.34 |
| | Retrival Error | 236 | 27.1 | 4.45 |
| | Retrival Error | 643 | 70.9 | 6.14 |
| | Retrival Error | 416 | 48.0 | 6.64 |
| | Retrival Error | 846 | 95.3 | 5.96 |
| | Retrival Error | 263 | 29.3 | 6.54 |
| | Retrival Error | 382 | 43.2 | 5.73 |
| | Retrival Error | 215 | 24.2 | 8.03 |
| | Retrival Error | 1401 | 157.1 | 6.61 |
| | Retrival Error | 317 | 36.0 | 8.73 |
| | Retrival Error | 201 | 21.9 | 9.64 |
| | Retrival Error | 1307 | 151.8 | 9.48 |
| | Retrival Error | 367 | 42.8 | 7.53 |
| | Retrival Error | 908 | 102.4 | 7.61 |
| | Retrival Error | 1395 | 157.8 | 6.74 |
| | Retrival Error | 449 | 50.8 | 5.38 |
| | Retrival Error | 311 | 34.2 | 5.92 |
| | Retrival Error | 357 | 41.3 | 9.72 |
| | Retrival Error | 518 | 58.8 | 6.58 |
| | Retrival Error | 267 | 30.5 | 8.29 |
| | Retrival Error | 126 | 14.2 | 7.81 |
| | Retrival Error | 600 | 69.6 | 7.61 |
| | Retrival Error | 450 | 52.9 | 7.47 |

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|---|---|---|---|---|
| | Retrival Error | 797 | 92.6 | 6.33 |
| | Retrival Error | 627 | 70.4 | 5.58 |
| | Retrival Error | 885 | 99.0 | 4.63 |
| | Retrival Error | 362 | 41.5 | 7.56 |
| | Retrival Error | 423 | 47.0 | 5.07 |
| | Retrival Error | 545 | 58.7 | 6.57 |
| | Retrival Error | 799 | 89.7 | 5.83 |
| | Retrival Error | 168 | 18.9 | 12.31 |
| | Retrival Error | 431 | 48.6 | 6.79 |
| | Retrival Error | 440 | 47.7 | 5.45 |
| | Retrival Error | 435 | 46.1 | 4.61 |
| | Retrival Error | 373 | 43.2 | 7.96 |
| | Retrival Error | 446 | 49.0 | 9.23 |
| | Retrival Error | 659 | 73.8 | 4.87 |
| | Retrival Error | 503 | 53.8 | 5.52 |
| | Retrival Error | 249 | 27.4 | 8.31 |
| | Retrival Error | 381 | 40.7 | 10.15 |
| | Retrival Error | 2303 | 258.8 | 6.32 |
| | Retrival Error | 590 | 67.3 | 10.59 |
| | Retrival Error | 174 | 19.1 | 4.41 |
| | Retrival Error | 707 | 79.7 | 10.74 |
| | Retrival Error | 263 | 29.6 | 5.49 |
| | Retrival Error | 167 | 17.6 | 7.65 |
| | Retrival Error | 2671 | 292.6 | 7.43 |
| | Retrival Error | 992 | 115.6 | 7.99 |
| | Retrival Error | 1298 | 141.2 | 7.23 |
| | Retrival Error | 1981 | 222.4 | 6.57 |
| | Retrival Error | 1143 | 131.0 | 7.58 |
| | Retrival Error | 161 | 17.0 | 7.11 |
| | Retrival Error | 218 | 24.4 | 5.53 |
| | Retrival Error | 316 | 32.9 | 5.33 |
| | Retrival Error | 843 | 93.0 | 5.05 |
| | Retrival Error | 507 | 57.7 | 9.23 |
| | Retrival Error | 832 | 92.9 | 6.02 |
| | Retrival Error | 689 | 79.0 | 10.17 |
| | Retrival Error | 1146 | 122.4 | 6.80 |
| | Retrival Error | 380 | 43.7 | 5.62 |
| | Retrival Error | 1497 | 167.8 | 5.15 |
| | Retrival Error | 201 | 21.9 | 7.71 |
| | Retrival Error | 116 | 13.2 | 8.62 |
| | Retrival Error | 285 | 33.2 | 6.33 |
| | Retrival Error | 121 | 14.2 | 8.10 |
| | Retrival Error | 253 | 28.7 | 8.24 |
| | Retrival Error | 280 | 31.4 | 5.44 |
| | Retrival Error | 107 | 11.8 | 7.12 |
| | Retrival Error | 162 | 18.0 | 9.35 |
| | Retrival Error | 653 | 72.1 | 5.14 |
| | Retrival Error | 770 | 82.5 | 5.69 |
| | Retrival Error | 13 | 1.5 | 9.99 |
| | Retrival Error | 98 | 11.3 | 7.91 |
| | Retrival Error | 358 | 40.9 | 8.84 |
| | Retrival Error | 319 | 36.3 | 8.27 |
| | Retrival Error | 37 | 3.9 | 4.75 |
| | Retrival Error | 1928 | 211.4 | 7.24 |
| | Retrival Error | 188 | 21.3 | 8.41 |
| | Retrival Error | 454 | 52.7 | 9.60 |
| | Retrival Error | 218 | 24.6 | 8.68 |
| | Retrival Error | 66 | 7.3 | 5.41 |
| | Retrival Error | 58 | 6.2 | 8.97 |

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|---|---|---|---|---|
| | Retrival Error | 416 | 46.0 | 9.01 |
| | Retrival Error | 489 | 54.4 | 8.28 |
| | Retrival Error | 545 | 60.9 | 8.25 |
| | Retrival Error | 540 | 59.0 | 6.83 |
| | Retrival Error | 449 | 49.7 | 6.86 |
| | Retrival Error | 342 | 38.5 | 7.40 |
| | Retrival Error | 564 | 63.7 | 7.77 |
| | Retrival Error | 474 | 54.8 | 9.03 |
| | Retrival Error | 263 | 28.9 | 4.88 |
| | Retrival Error | 531 | 58.4 | 8.31 |
| | Retrival Error | 1345 | 148.8 | 7.39 |
| | Retrival Error | 476 | 54.9 | 8.53 |
| | Retrival Error | 509 | 57.6 | 6.70 |
| | Retrival Error | 191 | 21.6 | 6.98 |
| | Retrival Error | 1264 | 136.4 | 9.17 |
| | Retrival Error | 1394 | 157.9 | 6.13 |
| | Retrival Error | 361 | 41.1 | 9.35 |
| | Retrival Error | 86 | 9.7 | 8.15 |
| | Retrival Error | 8407 | 965.7 | 5.55 |
| | Retrival Error | 812 | 96.0 | 9.39 |
| | Retrival Error | 186 | 21.4 | 6.30 |
| | Retrival Error | 1685 | 181.3 | 7.25 |
| | Retrival Error | 351 | 38.5 | 8.69 |
| | Retrival Error | 533 | 58.6 | 8.24 |
| | Retrival Error | 997 | 108.8 | 9.19 |
| | Retrival Error | 1457 | 165.1 | 6.55 |
| | Retrival Error | 1151 | 129.9 | 5.25 |
| | Retrival Error | 660 | 73.7 | 7.15 |
| | Retrival Error | 963 | 106.7 | 7.97 |
| | Retrival Error | 291 | 33.4 | 7.49 |
| | Retrival Error | 126 | 14.1 | 5.33 |
| | Retrival Error | 60 | 7.1 | 10.21 |
| | Retrival Error | 77 | 8.9 | 7.27 |
| | Retrival Error | 81 | 10.1 | 12.03 |
| | Retrival Error | 305 | 34.3 | 11.99 |
| | Retrival Error | 139 | 17.1 | 10.62 |
| | Retrival Error | 45 | 5.3 | 11.08 |
| | Retrival Error | 116 | 12.8 | 6.30 |
| | Retrival Error | 108 | 11.8 | 8.73 |
| | Retrival Error | 110 | 12.2 | 8.29 |
| | Retrival Error | 25 | 2.6 | 9.70 |
| | Retrival Error | 96 | 11.2 | 6.33 |
| | Retrival Error | 57 | 6.3 | 12.22 |
| | Retrival Error | 112 | 12.6 | 8.51 |
| | Retrival Error | 187 | 19.6 | 7.33 |
| | Retrival Error | 140 | 16.3 | 7.50 |
| | Retrival Error | 126 | 14.0 | 8.44 |
| | Retrival Error | 1699 | 193.5 | 6.70 |
| | Retrival Error | 1037 | 118.0 | 6.39 |
| | Retrival Error | 1178 | 128.5 | 7.14 |
| | Retrival Error | 1894 | 210.9 | 6.52 |
| | Retrival Error | 226 | 24.6 | 5.19 |
| | Retrival Error | 209 | 23.0 | 7.37 |
| | Retrival Error | 118 | 12.8 | 8.00 |
| | Retrival Error | 530 | 59.6 | 5.36 |
| | Retrival Error | 345 | 38.7 | 9.44 |
| | Retrival Error | 485 | 56.1 | 9.11 |
| | Retrival Error | 237 | 26.9 | 4.87 |
| | Retrival Error | 396 | 45.1 | 8.73 |

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|---|---|---|---|---|
| | Retrival Error | 283 | 32.7 | 6.46 |
| | Retrival Error | 678 | 76.9 | 6.98 |
| | Retrival Error | 477 | 55.2 | 8.85 |
| | Retrival Error | 329 | 36.2 | 5.10 |
| | Retrival Error | 535 | 62.6 | 9.14 |
| | Retrival Error | 351 | 38.8 | 6.47 |
| | Retrival Error | 526 | 57.3 | 5.47 |
| | Retrival Error | 576 | 61.8 | 10.74 |
| | Retrival Error | 225 | 26.3 | 9.72 |
| | Retrival Error | 629 | 71.9 | 6.38 |
| | Retrival Error | 400 | 44.0 | 6.54 |
| | Retrival Error | 347 | 35.8 | 9.22 |
| | Retrival Error | 399 | 44.6 | 5.34 |
| | Retrival Error | 810 | 91.7 | 4.75 |
| | Retrival Error | 411 | 46.2 | 7.96 |
| | Retrival Error | 1277 | 132.4 | 8.27 |
| | Retrival Error | 96 | 10.5 | 4.61 |
| | Retrival Error | 105 | 12.0 | 6.11 |
| | Retrival Error | 493 | 52.8 | 5.44 |
| | Retrival Error | 508 | 54.5 | 5.76 |
| | Retrival Error | 251 | 28.4 | 6.52 |
| | Retrival Error | 138 | 15.2 | 5.20 |
| | Retrival Error | 56 | 5.2 | 10.93 |
| | Retrival Error | 1683 | 179.9 | 6.20 |
| | Retrival Error | 265 | 30.1 | 8.24 |
| | Retrival Error | 1185 | 134.6 | 5.96 |
| | Retrival Error | 97 | 11.4 | 7.97 |
| | Retrival Error | 118 | 12.6 | 8.88 |
| | Retrival Error | 120 | 12.8 | 5.06 |
| | Retrival Error | 120 | 13.0 | 7.11 |
| | Retrival Error | 1101 | 120.7 | 7.33 |
| | Retrival Error | 251 | 27.6 | 9.47 |
| | Retrival Error | 105 | 12.2 | 11.50 |
| | Retrival Error | 517 | 57.6 | 9.04 |
| | Retrival Error | 1275 | 148.9 | 9.69 |
| | Retrival Error | 347 | 38.8 | 7.02 |
| | Retrival Error | 131 | 13.7 | 7.80 |
| | Retrival Error | 130 | 14.9 | 4.53 |
| | Retrival Error | 430 | 47.0 | 6.55 |
| | Retrival Error | 53 | 6.2 | 8.85 |
| | Retrival Error | 268 | 30.9 | 6.54 |
| | Retrival Error | 561 | 57.2 | 5.07 |
| | Retrival Error | 159 | 18.3 | 10.13 |
| | Retrival Error | 172 | 19.9 | 5.24 |
| | Retrival Error | 104 | 11.1 | 8.50 |
| | Retrival Error | 338 | 40.0 | 9.45 |
| | Retrival Error | 129 | 14.5 | 9.29 |
| | Retrival Error | 285 | 31.1 | 6.09 |
| | Retrival Error | 471 | 51.1 | 8.50 |
| | Retrival Error | 36 | 4.1 | 9.31 |
| | Retrival Error | 508 | 55.0 | 5.49 |
| | Retrival Error | 834 | 93.4 | 5.94 |
| | Retrival Error | 283 | 32.6 | 6.33 |
| | Retrival Error | 353 | 38.4 | 9.98 |
| | Retrival Error | 382 | 42.6 | 9.13 |
| | Retrival Error | 89 | 9.7 | 4.78 |
| | Retrival Error | 410 | 45.8 | 8.44 |
| | Retrival Error | 614 | 72.1 | 9.22 |
| | Retrival Error | 98 | 11.1 | 8.10 |

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| | Retrival Error | 92 | 10.3 | 7.17 |
| | Retrival Error | 2407 | 268.8 | 6.98 |
| | Retrival Error | 2151 | 235.0 | 6.60 |
| | Retrival Error | 922 | 105.3 | 6.20 |
| | Retrival Error | 826 | 91.7 | 7.94 |
| | Retrival Error | 218 | 24.9 | 9.92 |
| | Retrival Error | 231 | 26.1 | 6.83 |
| | Retrival Error | 240 | 26.9 | 6.04 |
| | Retrival Error | 537 | 58.8 | 8.73 |
| | Retrival Error | 1583 | 184.5 | 5.11 |
| | Retrival Error | 1081 | 115.3 | 7.78 |
| | Retrival Error | 57 | 6.6 | 5.19 |
| | Retrival Error | 106 | 11.6 | 9.41 |
| | Retrival Error | 357 | 39.2 | 5.63 |
| | Retrival Error | 204 | 23.5 | 6.43 |
| | Retrival Error | 79 | 8.5 | 7.17 |
| | Retrival Error | 299 | 34.7 | 11.43 |
| | Retrival Error | 174 | 19.7 | 7.49 |
| | Retrival Error | 32 | 3.6 | 4.17 |
| | Retrival Error | 2701 | 307.9 | 6.46 |
| | Retrival Error | 372 | 42.1 | 5.10 |
| | Retrival Error | 633 | 72.6 | 8.07 |
| | Retrival Error | 108 | 11.9 | 8.00 |
| | Retrival Error | 482 | 51.8 | 8.62 |
| | Retrival Error | 527 | 56.4 | 6.15 |
| | Retrival Error | 96 | 10.4 | 7.28 |
| | Retrival Error | 475 | 52.1 | 6.15 |
| | Retrival Error | 2341 | 266.9 | 6.33 |
| | Retrival Error | 435 | 51.2 | 6.42 |
| | Retrival Error | 827 | 92.1 | 5.55 |
| | Retrival Error | 225 | 26.1 | 6.54 |
| | Retrival Error | 802 | 87.7 | 6.96 |
| | Retrival Error | 799 | 89.2 | 8.72 |
| | Retrival Error | 772 | 86.6 | 5.06 |
| | Retrival Error | 394 | 46.2 | 6.18 |
| | Retrival Error | 461 | 52.1 | 9.73 |
| | Retrival Error | 87 | 10.2 | 5.15 |
| | Retrival Error | 106 | 10.9 | 7.90 |
| | Retrival Error | 1075 | 121.3 | 6.24 |
| | Retrival Error | 209 | 24.5 | 9.14 |
| | Retrival Error | 121 | 13.3 | 5.99 |
| | Retrival Error | 96 | 10.1 | 8.32 |
| | Retrival Error | 99 | 10.5 | 9.03 |
| | Retrival Error | 100 | 10.9 | 8.66 |
| | Retrival Error | 99 | 10.7 | 5.31 |
| | Retrival Error | 101 | 11.0 | 7.83 |
| | Retrival Error | 101 | 11.0 | 7.84 |
| | Retrival Error | 100 | 10.8 | 5.01 |
| | Retrival Error | 101 | 10.9 | 7.84 |
| | Retrival Error | 100 | 10.7 | 5.33 |
| | Retrival Error | 210 | 23.4 | 4.94 |
| | Retrival Error | 745 | 82.9 | 8.95 |
| | Retrival Error | 125 | 13.8 | 4.88 |
| | Retrival Error | 113 | 12.5 | 5.96 |
| | Retrival Error | 1506 | 167.6 | 7.83 |
| | Retrival Error | 100 | 11.0 | 9.45 |
| | Retrival Error | 197 | 21.4 | 9.66 |
| | Retrival Error | 72 | 7.2 | 7.18 |
| | Retrival Error | 458 | 49.4 | 6.11 |

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| | Retrival Error | 493 | 48.6 | 9.69 |
| | Retrival Error | 100 | 10.7 | 10.27 |
| | Retrival Error | 108 | 11.3 | 5.19 |
| | Retrival Error | 55 | 6.5 | 4.65 |
| | Retrival Error | 86 | 8.9 | 4.07 |
| | Retrival Error | 72 | 8.4 | 10.15 |
| | Retrival Error | 60 | 6.7 | 6.95 |
| | Retrival Error | 64 | 7.5 | 7.42 |
| | Retrival Error | 125 | 14.3 | 5.99 |
| | Retrival Error | 93 | 10.8 | 9.00 |
| | Retrival Error | 67 | 7.5 | 11.93 |
| | Retrival Error | 86 | 9.8 | 8.81 |
| | Retrival Error | 101 | 11.1 | 11.09 |
| | Retrival Error | 101 | 11.0 | 7.46 |
| | Retrival Error | 97 | 10.6 | 8.34 |
| | Retrival Error | 154 | 18.2 | 4.64 |
| | Retrival Error | 126 | 13.1 | 9.54 |
| | Retrival Error | 54 | 6.2 | 9.19 |
| | Retrival Error | 90 | 9.9 | 9.48 |
| | Retrival Error | 99 | 10.5 | 9.33 |
| | Retrival Error | 120 | 13.0 | 6.16 |
| | Retrival Error | 101 | 12.0 | 10.20 |
| | Retrival Error | 102 | 11.6 | 9.13 |
| | Retrival Error | 109 | 12.7 | 4.27 |
| | Retrival Error | 105 | 12.2 | 7.77 |
| | Retrival Error | 90 | 10.0 | 8.63 |
| | Retrival Error | 87 | 9.6 | 4.93 |
| | Retrival Error | 80 | 9.1 | 6.51 |
| | Retrival Error | 51 | 5.6 | 8.03 |
| | Retrival Error | 64 | 7.3 | 4.20 |
| | Retrival Error | 107 | 12.9 | 5.63 |
| | Retrival Error | 141 | 15.4 | 10.55 |
| | Retrival Error | 93 | 10.2 | 5.76 |
| | Retrival Error | 84 | 9.3 | 5.19 |
| | Retrival Error | 93 | 10.3 | 8.15 |
| | Retrival Error | 125 | 14.6 | 4.92 |
| | Retrival Error | 107 | 11.7 | 7.05 |
| | Retrival Error | 143 | 15.4 | 8.27 |
| | Retrival Error | 54 | 5.7 | 11.60 |
| | Retrival Error | 98 | 11.2 | 10.70 |
| | Retrival Error | 145 | 15.8 | 7.37 |
| | Retrival Error | 120 | 13.5 | 5.34 |
| | Retrival Error | 69 | 8.0 | 8.40 |
| | Retrival Error | 53 | 6.2 | 11.80 |
| | Retrival Error | 77 | 8.7 | 7.12 |
| | Retrival Error | 101 | 11.4 | 10.70 |
| | Retrival Error | 93 | 10.6 | 10.33 |
| | Retrival Error | 132 | 14.8 | 8.91 |
| | Retrival Error | 58 | 6.5 | 10.87 |
| | Retrival Error | 78 | 8.5 | 10.68 |
| | Retrival Error | 849 | 93.6 | 5.68 |
| | Retrival Error | 934 | 108.2 | 5.74 |
| | Retrival Error | 439 | 47.4 | 10.01 |
| | Retrival Error | 110 | 11.4 | 7.11 |
| | Retrival Error | 1161 | 126.7 | 5.77 |
| | Retrival Error | 123 | 13.7 | 5.01 |
| | Retrival Error | 263 | 28.0 | 5.35 |
| | Retrival Error | 269 | 28.1 | 8.21 |
| | Retrival Error | 124 | 13.4 | 6.61 |

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| | Retrival Error | 2046 | 229.5 | 6.29 |
| | Retrival Error | 114 | 12.1 | 5.01 |
| | Retrival Error | 45 | 5.1 | 11.39 |
| | Retrival Error | 55 | 6.0 | 8.97 |
| | Retrival Error | 814 | 89.1 | 7.78 |
| | Retrival Error | 179 | 20.2 | 8.91 |
| | Retrival Error | 87 | 9.7 | 9.03 |
| | Retrival Error | 84 | 9.7 | 8.75 |
| | Retrival Error | 85 | 9.8 | 8.84 |
| | Retrival Error | 298 | 33.5 | 8.13 |
| | Retrival Error | 146 | 15.7 | 8.47 |
| | Retrival Error | 139 | 16.3 | 9.31 |
| | Retrival Error | 945 | 99.1 | 5.55 |
| | Retrival Error | 261 | 29.6 | 8.69 |
| | Retrival Error | 949 | 105.1 | 7.40 |
| | Retrival Error | 1004 | 115.2 | 7.61 |
| | Retrival Error | 538 | 60.4 | 7.59 |
| | Retrival Error | 440 | 47.0 | 11.00 |
| | Retrival Error | 686 | 73.3 | 9.03 |
| | Retrival Error | 104 | 11.9 | 9.09 |
| | Retrival Error | 233 | 27.6 | 11.09 |
| | Retrival Error | 60 | 6.4 | 8.21 |
| | Retrival Error | 528 | 60.5 | 8.91 |
| | Retrival Error | 332 | 35.0 | 9.73 |
| | Retrival Error | 372 | 40.1 | 4.32 |
| | Retrival Error | 288 | 33.5 | 8.25 |
| | Retrival Error | 241 | 26.7 | 7.80 |
| | Retrival Error | 410 | 46.4 | 6.68 |
| | Retrival Error | 751 | 83.7 | 5.78 |
| | Retrival Error | 854 | 94.4 | 6.93 |
| | Retrival Error | 364 | 39.7 | 10.95 |
| | Retrival Error | 518 | 61.4 | 8.91 |
| | Retrival Error | 175 | 19.4 | 9.22 |
| | Retrival Error | 646 | 75.1 | 5.53 |
| | Retrival Error | 351 | 38.7 | 5.41 |
| | Retrival Error | 470 | 51.3 | 9.19 |
| | Retrival Error | 3288 | 356.7 | 7.37 |
| | Retrival Error | 1211 | 135.4 | 6.07 |
| | Retrival Error | 2188 | 247.7 | 5.91 |
| | Retrival Error | 648 | 74.4 | 5.22 |
| | Retrival Error | 1443 | 161.8 | 6.32 |
| | Retrival Error | 673 | 74.0 | 5.68 |
| | Retrival Error | 274 | 29.7 | 8.19 |
| | Retrival Error | 415 | 44.5 | 9.80 |
| | Retrival Error | 916 | 105.7 | 6.48 |
| | Retrival Error | 168 | 19.8 | 8.43 |
| | Retrival Error | 208 | 23.3 | 7.66 |
| | Retrival Error | 1085 | 122.2 | 7.20 |
| | Retrival Error | 456 | 51.3 | 8.18 |
| | Retrival Error | 573 | 64.4 | 6.98 |
| | Retrival Error | 397 | 45.0 | 7.66 |
| | Retrival Error | 381 | 43.6 | 7.65 |
| | Retrival Error | 759 | 87.2 | 8.82 |
| | Retrival Error | 536 | 59.6 | 8.78 |
| | Retrival Error | 460 | 50.6 | 7.02 |
| | Retrival Error | 681 | 75.3 | 5.90 |
| | Retrival Error | 631 | 69.9 | 5.55 |
| | Retrival Error | 377 | 43.0 | 5.77 |
| | Retrival Error | 680 | 75.5 | 7.36 |

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| | Retrival Error | 488 | 56.2 | 8.25 |
| | Retrival Error | 3136 | 348.8 | 6.16 |
| | Retrival Error | 1311 | 153.6 | 5.39 |
| | Retrival Error | 318 | 36.7 | 8.60 |
| | Retrival Error | 1487 | 166.5 | 7.20 |
| | Retrival Error | 357 | 38.5 | 8.16 |
| | Retrival Error | 603 | 66.0 | 5.82 |
| | Retrival Error | 117 | 12.7 | 8.73 |
| | Retrival Error | 123 | 12.9 | 5.36 |
| | Retrival Error | 120 | 13.0 | 4.88 |
| | Retrival Error | 120 | 13.2 | 5.14 |
| | Retrival Error | 121 | 13.2 | 7.97 |
| | Retrival Error | 120 | 13.4 | 9.76 |
| | Retrival Error | 117 | 12.9 | 8.44 |
| | Retrival Error | 121 | 13.2 | 5.99 |
| | Retrival Error | 123 | 13.6 | 7.28 |
| | Retrival Error | 123 | 13.5 | 7.37 |
| | Retrival Error | 118 | 12.9 | 6.28 |
| | Retrival Error | 126 | 13.6 | 5.11 |
| | Retrival Error | 117 | 12.7 | 7.28 |
| | Retrival Error | 183 | 21.7 | 5.78 |
| | Retrival Error | 94 | 10.5 | 9.48 |
| | Retrival Error | 101 | 11.9 | 4.56 |
| | Retrival Error | 584 | 65.2 | 7.52 |
| | Retrival Error | 255 | 28.9 | 6.52 |
| | Retrival Error | 337 | 39.2 | 8.66 |
| | Retrival Error | 221 | 26.0 | 6.11 |
| | Retrival Error | 227 | 24.0 | 8.53 |
| | Retrival Error | 77 | 8.7 | 8.48 |
| | Retrival Error | 441 | 47.4 | 7.74 |
| | Retrival Error | 89 | 9.8 | 8.21 |
| | Retrival Error | 238 | 26.9 | 7.88 |
| | Retrival Error | 345 | 39.2 | 6.14 |
| | Retrival Error | 90 | 10.1 | 6.96 |
| | Retrival Error | 149 | 16.6 | 11.00 |
| | Retrival Error | 39 | 4.5 | 10.39 |
| | Retrival Error | 227 | 24.3 | 8.72 |
| | Retrival Error | 81 | 9.2 | 7.50 |
| | Retrival Error | 349 | 39.5 | 8.76 |
| | Retrival Error | 232 | 25.9 | 6.40 |
| | Retrival Error | 100 | 10.1 | 8.98 |
| | Retrival Error | 139 | 15.4 | 9.19 |
| | Retrival Error | 110 | 12.8 | 5.95 |
| | Retrival Error | 76 | 8.9 | 9.69 |
| | Retrival Error | 145 | 16.1 | 4.79 |
| | Retrival Error | 354 | 40.7 | 7.97 |
| | Retrival Error | 124 | 13.7 | 5.17 |
| | Retrival Error | 3038 | 337.5 | 6.28 |
| | Retrival Error | 63 | 6.9 | 4.42 |
| | Retrival Error | 20 | 2.2 | 6.16 |
| | Retrival Error | 233 | 24.5 | 11.55 |
| | Retrival Error | 412 | 45.2 | 7.33 |
| | Retrival Error | 121 | 12.9 | 8.66 |
| | Retrival Error | 145 | 16.8 | 9.72 |
| | Retrival Error | 26 | 2.9 | 8.73 |
| | Retrival Error | 1063 | 119.0 | 7.49 |
| | Retrival Error | 1447 | 157.5 | 6.46 |
| | Retrival Error | 133 | 14.3 | 8.94 |
| | Retrival Error | 344 | 38.1 | 8.75 |

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| | Retrival Error | 153 | 16.5 | 9.63 |
| | Retrival Error | 121 | 14.3 | 4.88 |
| | Retrival Error | 644 | 66.0 | 7.80 |
| | Retrival Error | 863 | 97.5 | 7.39 |
| | Retrival Error | 121 | 13.2 | 9.22 |
| | Retrival Error | 121 | 13.4 | 8.48 |
| | Retrival Error | 126 | 13.8 | 7.05 |
| | Retrival Error | 74 | 8.3 | 7.18 |
| | Retrival Error | 104 | 11.3 | 8.88 |
| | Retrival Error | 543 | 61.2 | 5.83 |
| | Retrival Error | 89 | 9.7 | 8.84 |
| | Retrival Error | 337 | 38.1 | 6.14 |
| | Retrival Error | 181 | 21.0 | 6.93 |
| | Retrival Error | 111 | 12.4 | 9.33 |
| | Retrival Error | 136 | 14.8 | 9.55 |
| | Retrival Error | 140 | 15.3 | 9.74 |
| | Retrival Error | 273 | 31.7 | 5.82 |
| | Retrival Error | 89 | 10.8 | 7.88 |
| | Retrival Error | 162 | 18.1 | 5.82 |
| | Retrival Error | 52 | 6.2 | 7.18 |
| | Retrival Error | 115 | 12.5 | 7.28 |
| | Retrival Error | 123 | 13.5 | 5.45 |
| | Retrival Error | 123 | 13.6 | 7.97 |
| | Retrival Error | 81 | 9.2 | 9.17 |
| | Retrival Error | 129 | 13.7 | 8.47 |
| | Retrival Error | 123 | 13.4 | 8.43 |
| | Retrival Error | 121 | 13.1 | 5.99 |
| | Retrival Error | 128 | 14.1 | 9.17 |
| | Retrival Error | 126 | 13.7 | 8.00 |
| | Retrival Error | 124 | 13.3 | 7.96 |
| | Retrival Error | 130 | 14.2 | 9.17 |
| | Retrival Error | 129 | 14.1 | 9.07 |
| | Retrival Error | 118 | 13.3 | 9.64 |
| | Retrival Error | 125 | 14.2 | 8.69 |
| | Retrival Error | 119 | 13.3 | 7.83 |
| | Retrival Error | 578 | 64.1 | 5.14 |
| | Retrival Error | 263 | 30.5 | 5.19 |
| | Retrival Error | 104 | 11.8 | 8.21 |
| | Retrival Error | 298 | 33.4 | 5.19 |
| | Retrival Error | 272 | 30.7 | 5.12 |
| | Retrival Error | 1338 | 152.9 | 6.67 |
| | Retrival Error | 590 | 62.1 | 6.79 |
| | Retrival Error | 158 | 18.3 | 9.17 |
| | Retrival Error | 313 | 35.6 | 8.48 |
| | Retrival Error | 162 | 18.3 | 7.05 |
| | Retrival Error | 430 | 47.1 | 9.03 |
| | Retrival Error | 55 | 5.8 | 12.00 |
| | Retrival Error | 284 | 32.4 | 4.83 |
| | Retrival Error | 1294 | 144.4 | 6.52 |
| | Retrival Error | 1357 | 153.3 | 6.57 |
| | Retrival Error | 559 | 60.3 | 8.75 |
| | Retrival Error | 2246 | 243.6 | 6.51 |
| | Retrival Error | 3022 | 340.9 | 6.40 |
| | Retrival Error | 1226 | 135.9 | 8.56 |
| | Retrival Error | 913 | 100.9 | 8.16 |
| | Retrival Error | 144 | 16.2 | 7.05 |
| | Retrival Error | 144 | 15.7 | 5.24 |
| | Retrival Error | 108 | 11.2 | 7.96 |
| | Retrival Error | 321 | 35.9 | 5.63 |

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|---|---|---|---|---|
| | Retrival Error | 167 | 19.1 | 7.77 |
| | Retrival Error | 509 | 53.6 | 7.01 |
| | Retrival Error | 288 | 30.4 | 10.96 |
| | Retrival Error | 350 | 39.7 | 8.94 |
| | Retrival Error | 209 | 22.5 | 6.54 |
| | Retrival Error | 517 | 56.3 | 6.99 |
| | Retrival Error | 250 | 28.3 | 9.03 |
| | Retrival Error | 321 | 37.0 | 8.87 |
| | Retrival Error | 540 | 61.8 | 9.58 |
| | Retrival Error | 639 | 69.4 | 8.95 |
| | Retrival Error | 386 | 43.5 | 9.29 |
| | Retrival Error | 603 | 69.4 | 8.07 |
| | Retrival Error | 276 | 29.9 | 6.05 |
| | Retrival Error | 281 | 30.4 | 7.69 |
| | Retrival Error | 330 | 37.3 | 8.31 |
| | Retrival Error | 692 | 76.4 | 6.20 |
| | Retrival Error | 407 | 44.5 | 7.25 |
| | Retrival Error | 1638 | 176.1 | 8.50 |
| | Retrival Error | 2564 | 286.8 | 6.83 |
| | Retrival Error | 486 | 56.1 | 9.04 |
| | Retrival Error | 1712 | 199.1 | 8.05 |
| | Retrival Error | 446 | 51.3 | 5.62 |
| | Retrival Error | 747 | 80.9 | 9.35 |
| | Retrival Error | 411 | 46.5 | 6.32 |
| | Retrival Error | 632 | 72.0 | 6.32 |
| | Retrival Error | 1997 | 233.4 | 6.52 |
| | Retrival Error | 137 | 15.6 | 7.25 |
| | Retrival Error | 370 | 42.7 | 8.66 |
| | Retrival Error | 580 | 65.3 | 5.17 |
| | Retrival Error | 866 | 96.6 | 4.61 |
| | Retrival Error | 1866 | 209.9 | 7.11 |
| | Retrival Error | 351 | 38.5 | 9.89 |
| | Retrival Error | 378 | 41.1 | 6.87 |
| | Retrival Error | 496 | 55.6 | 6.11 |
| | Retrival Error | 878 | 100.9 | 7.56 |
| | Retrival Error | 8721 | 1002.8 | 5.52 |
| | Retrival Error | 2434 | 273.7 | 6.28 |
| | Retrival Error | 526 | 58.3 | 9.11 |
| | Retrival Error | 205 | 22.1 | 4.79 |
| | Retrival Error | 307 | 35.3 | 8.95 |
| | Retrival Error | 537 | 61.4 | 8.73 |
| | Retrival Error | 2792 | 316.0 | 6.95 |
| | Retrival Error | 1227 | 139.3 | 6.16 |
| | Retrival Error | 502 | 58.1 | 7.69 |
| | Retrival Error | 877 | 99.4 | 6.35 |
| | Retrival Error | 889 | 100.7 | 7.68 |
| | Retrival Error | 865 | 91.4 | 8.72 |
| | Retrival Error | 455 | 52.0 | 8.81 |
| | Retrival Error | 703 | 77.2 | 6.06 |
| | Retrival Error | 1414 | 157.7 | 5.36 |
| | Retrival Error | 1865 | 208.3 | 8.76 |
| | Retrival Error | 1165 | 132.4 | 7.36 |
| | Retrival Error | 2735 | 307.0 | 6.15 |
| | Retrival Error | 357 | 38.8 | 8.24 |
| | Retrival Error | 241 | 27.5 | 5.35 |
| | Retrival Error | 1553 | 174.6 | 7.11 |
| | Retrival Error | 465 | 50.6 | 9.26 |
| | Retrival Error | 7553 | 856.3 | 5.36 |
| | Retrival Error | 5177 | 573.4 | 6.05 |

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|---|---|---|---|---|
| | Retrival Error | 569 | 63.1 | 9.76 |
| | Retrival Error | 1694 | 181.0 | 9.01 |
| | Retrival Error | 413 | 45.0 | 11.47 |
| | Retrival Error | 858 | 96.2 | 4.67 |
| | Retrival Error | 3126 | 362.2 | 4.89 |
| | Retrival Error | 91 | 10.2 | 5.76 |
| | Retrival Error | 126 | 13.7 | 7.96 |
| | Retrival Error | 750 | 83.4 | 6.79 |
| | Retrival Error | 219 | 24.7 | 9.23 |
| | Retrival Error | 111 | 11.5 | 4.28 |
| | Retrival Error | 124 | 14.5 | 9.61 |
| | Retrival Error | 826 | 92.0 | 6.30 |
| | Retrival Error | 393 | 43.0 | 9.80 |
| | Retrival Error | 2392 | 269.3 | 6.19 |
| | Retrival Error | 621 | 69.7 | 9.80 |
| | Retrival Error | 558 | 62.2 | 4.87 |
| | Retrival Error | 2971 | 315.4 | 5.66 |
| | Retrival Error | 518 | 56.9 | 6.28 |
| | Retrival Error | 80 | 8.6 | 5.24 |
| | Retrival Error | 230 | 25.7 | 8.16 |
| | Retrival Error | 103 | 11.4 | 9.60 |
| | Retrival Error | 126 | 13.5 | 9.35 |
| | Retrival Error | 115 | 12.9 | 8.84 |
| | Retrival Error | 114 | 12.6 | 7.97 |
| | Retrival Error | 120 | 13.2 | 5.45 |
| | Retrival Error | 112 | 12.4 | 8.85 |
| | Retrival Error | 111 | 12.3 | 8.48 |
| | Retrival Error | 114 | 12.6 | 8.91 |
| | Retrival Error | 84 | 9.5 | 9.04 |
| | Retrival Error | 72 | 8.2 | 6.55 |
| | Retrival Error | 679 | 75.5 | 7.01 |
| | Retrival Error | 97 | 10.5 | 8.53 |
| | Retrival Error | 667 | 73.5 | 8.09 |
| | Retrival Error | 266 | 30.0 | 7.47 |
| | Retrival Error | 165 | 17.6 | 5.03 |
| | Retrival Error | 145 | 16.1 | 8.56 |
| | Retrival Error | 67 | 7.3 | 8.18 |
| | Retrival Error | 133 | 14.1 | 5.14 |
| | Retrival Error | 82 | 8.8 | 7.97 |
| | Retrival Error | 218 | 25.4 | 8.97 |
| | Retrival Error | 211 | 24.1 | 6.52 |
| | Retrival Error | 116 | 12.8 | 9.13 |
| | Retrival Error | 162 | 18.8 | 9.77 |
| | Retrival Error | 138 | 15.1 | 9.70 |
| | Retrival Error | 92 | 10.3 | 6.61 |
| | Retrival Error | 86 | 9.6 | 9.00 |
| | Retrival Error | 705 | 78.5 | 8.21 |
| | Retrival Error | 497 | 58.0 | 6.96 |
| | Retrival Error | 386 | 43.3 | 8.75 |
| | Retrival Error | 157 | 17.2 | 7.12 |
| | Retrival Error | 356 | 39.4 | 5.50 |
| | Retrival Error | 1159 | 130.0 | 8.32 |
| | Retrival Error | 450 | 47.4 | 6.05 |
| | Retrival Error | 186 | 21.4 | 8.38 |
| | Retrival Error | 590 | 68.2 | 9.39 |
| | Retrival Error | 351 | 39.5 | 5.31 |
| | Retrival Error | 344 | 38.4 | 5.19 |
| | Retrival Error | 512 | 56.6 | 7.91 |
| | Retrival Error | 886 | 101.2 | 9.57 |

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|---|---|---|---|---|
| | Retrival Error | 720 | 81.9 | 7.47 |
| | Retrival Error | 108 | 11.9 | 7.47 |
| | Retrival Error | 362 | 40.6 | 6.25 |
| | Retrival Error | 68 | 7.6 | 9.19 |
| | Retrival Error | 108 | 11.9 | 5.06 |
| | Retrival Error | 111 | 11.5 | 6.44 |
| | Retrival Error | 188 | 20.9 | 6.19 |
| | Retrival Error | 362 | 41.8 | 4.89 |
| | Retrival Error | 442 | 49.0 | 8.40 |
| | Retrival Error | 80 | 9.0 | 5.15 |
| | Retrival Error | 723 | 77.7 | 9.45 |
| | Retrival Error | 355 | 40.7 | 6.38 |
| | Retrival Error | 470 | 50.6 | 6.55 |
| | Retrival Error | 449 | 50.8 | 6.15 |
| | Retrival Error | 344 | 39.1 | 5.53 |
| | Retrival Error | 161 | 17.4 | 8.95 |
| | Retrival Error | 2228 | 244.3 | 8.78 |
| | Retrival Error | 895 | 96.6 | 9.52 |
| | Retrival Error | 89 | 10.7 | 6.16 |
| | Retrival Error | 38 | 4.3 | 12.31 |
| | Retrival Error | 135 | 16.1 | 6.52 |
| | Retrival Error | 99 | 10.9 | 7.99 |
| | Retrival Error | 554 | 62.7 | 8.75 |
| | Retrival Error | 270 | 27.7 | 5.34 |
| | Retrival Error | 362 | 42.6 | 9.16 |
| | Retrival Error | 170 | 19.1 | 8.75 |
| | Retrival Error | 102 | 10.8 | 8.38 |
| | Retrival Error | 196 | 21.3 | 4.75 |
| | Retrival Error | 716 | 82.6 | 7.52 |
| | Retrival Error | 246 | 27.0 | 5.54 |
| | Retrival Error | 699 | 79.6 | 9.29 |
| | Retrival Error | 120 | 13.2 | 6.29 |
| | Retrival Error | 326 | 36.5 | 5.06 |
| | Retrival Error | 20 | 2.3 | 7.25 |
| | Retrival Error | 1286 | 146.4 | 6.92 |
| | Retrival Error | 246 | 27.3 | 6.52 |
| | Retrival Error | 140 | 15.6 | 8.10 |
| | Retrival Error | 644 | 73.3 | 5.77 |
| | Retrival Error | 111 | 12.5 | 11.40 |
| | Retrival Error | 389 | 43.6 | 6.57 |
| | Retrival Error | 103 | 11.2 | 8.75 |
| | Retrival Error | 663 | 74.0 | 5.08 |
| | Retrival Error | 201 | 23.4 | 4.98 |
| | Retrival Error | 551 | 65.0 | 5.96 |
| | Retrival Error | 425 | 47.9 | 8.88 |
| | Retrival Error | 122 | 14.2 | 9.69 |
| | Retrival Error | 363 | 41.5 | 9.04 |
| | Retrival Error | 782 | 85.3 | 8.79 |
| | Retrival Error | 1078 | 120.0 | 9.67 |
| | Retrival Error | 415 | 46.7 | 6.48 |
| | Retrival Error | 83 | 9.7 | 9.25 |
| | Retrival Error | 129 | 14.4 | 9.01 |
| | Retrival Error | 313 | 35.0 | 8.50 |
| | Retrival Error | 180 | 19.5 | 11.34 |
| | Retrival Error | 151 | 17.2 | 8.87 |
| | Retrival Error | 157 | 17.9 | 9.45 |
| | Retrival Error | 446 | 49.8 | 8.85 |
| | Retrival Error | 440 | 50.2 | 8.32 |
| | Retrival Error | 308 | 34.1 | 10.77 |

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|---|---|---|---|---|
| | Retrival Error | 451 | 51.0 | 5.80 |
| | Retrival Error | 980 | 111.4 | 6.84 |
| | Retrival Error | 92 | 10.1 | 9.44 |
| | Retrival Error | 847 | 92.3 | 9.19 |
| | Retrival Error | 109 | 11.5 | 8.66 |
| | Retrival Error | 91 | 10.4 | 8.15 |
| | Retrival Error | 121 | 12.9 | 7.12 |
| | Retrival Error | 138 | 14.7 | 8.46 |
| | Retrival Error | 116 | 13.0 | 7.96 |
| | Retrival Error | 208 | 22.4 | 7.21 |
| | Retrival Error | 128 | 14.0 | 8.51 |
| | Retrival Error | 115 | 12.7 | 8.97 |
| | Retrival Error | 725 | 82.6 | 9.83 |
| | Retrival Error | 574 | 65.1 | 4.72 |
| | Retrival Error | 123 | 13.6 | 9.17 |

| Accession | Description |
|---|---|
| 6166599 | RecName: Full=Myosin-9; AltName: Full=Cellular myosin heavy chain, type A; AltName: Full=Myosin heavy chain 9; Alt |
| 181402 | epidermal cytokeratin 2 [Homo sapiens] |
| 41322916 | plectin isoform 1 [Homo sapiens] |
| 123648 | RecName: Full=Heat shock cognate 71 kDa protein; AltName: Full=Heat shock 70 kDa protein 8; AltName: Full=Lipopo |
| 239938886 | RecName: Full=Keratin, type I cytoskeletal 9; AltName: Full=Cytokeratin-9; Short=CK-9; AltName: Full=Keratin-9; Shor |
| 74735628 | RecName: Full=Sequestosome-1; AltName: Full=EBI3-associated protein of 60 kDa; Short=EBIAP; Short=p60; AltName |
| 63087903 | unnamed protein product [Homo sapiens] |
| 194388850 | unnamed protein product [Homo sapiens] |
| 113950 | RecName: Full=Annexin A2; AltName: Full=Annexin II; AltName: Full=Annexin-2; AltName: Full=Calpactin I heavy chai |
| 119631419 | titin, isoform CRA_a [Homo sapiens] |
| 225733965 | Chain L, Human Thrombopoietin Neutralizing Antibody Tn1 Fab |
| 119581085 | keratin 10 (epidermolytic hyperkeratosis; keratosis palmaris et plantaris), isoform CRA_b [Homo sapiens] |
| 189306 | nucleolin [Homo sapiens] |
| 425518 | anti-colorectal carcinoma heavy chain [Homo sapiens] |
| 578837003 | PREDICTED: histone acetyltransferase p300 isoform X1 [Homo sapiens] |
| 146345444 | RecName: Full=Kelch-like ECH-associated protein 1; AltName: Full=Cytosolic inhibitor of Nrf2; Short=INrf2; AltName: F |
| 119614804 | clathrin, heavy polypeptide (Hc), isoform CRA_d [Homo sapiens] |
| 169404698 | Chain D, Pyruvate Kinase M2 Is A Phosphotyrosine Binding Protein |
| 189502784 | mitochondrial heat shock 60kD protein 1 variant 1 [Homo sapiens] |
| 221042022 | unnamed protein product [Homo sapiens] |
| 119608213 | spectrin, alpha, non-erythrocytic 1 (alpha-fodrin), isoform CRA_c [Homo sapiens] |
| 1195531 | type I keratin 16 [Homo sapiens] |
| 2769254 | NIPSNAP2 protein [Homo sapiens] |
| 378404908 | glyceraldehyde-3-phosphate dehydrogenase isoform 2 [Homo sapiens] |
| 119578453 | alpha tubulin, isoform CRA_b [Homo sapiens] |
| 194382178 | unnamed protein product [Homo sapiens] |
| 23491735 | ribosomal protein L10a [Homo sapiens] |
| 239938658 | RecName: Full=Protein kinase C iota type; AltName: Full=Atypical protein kinase C-lambda/iota; Short=PRKC-lambda/io |
| 15341992 | Unknown (protein for IMAGE:4347401), partial [Homo sapiens] |
| 516764 | motor protein [Homo sapiens] |
| 190192192 | filamin B [Homo sapiens] |
| 568786378 | Chain A, Structure Of The Mammalian Ribosomal Pre-termination Complex Associated With Erf1-erf3-gdpnp |
| 485601393 | Chain S, Structure Of The Human 40s Ribosomal Proteins |
| 190192184 | filamin A [Homo sapiens] |
| 221045062 | unnamed protein product [Homo sapiens] |
| 300669711 | RecName: Full=Fibrous sheath-interacting protein 2 |
| 119602167 | dynein, cytoplasmic 1, heavy chain 1, isoform CRA_c [Homo sapiens] |
| 119598181 | ribosomal protein L4, isoform CRA_a [Homo sapiens] |
| 14042692 | unnamed protein product [Homo sapiens] |
| 337580 | ribosomal protein L3, partial [Homo sapiens] |
| 39644662 | HSP90AB1 protein [Homo sapiens] |
| 34392 | unnamed protein product [Homo sapiens] |
| 119582734 | RAD50 homolog (S. cerevisiae), isoform CRA_c [Homo sapiens] |
| 31108 | human elongation factor 2 [Homo sapiens] |
| 194379998 | unnamed protein product [Homo sapiens] |
| 1827593 | Chain B, Recombinant Cyclophilin A From Human T Cell |
| 119577296 | ribosomal protein S16, isoform CRA_a [Homo sapiens] |
| 119612227 | poly(A) binding protein, cytoplasmic 1, isoform CRA_c [Homo sapiens] |
| 119601423 | hCG2028724 [Homo sapiens] |
| 119594430 | eukaryotic translation elongation factor 1 gamma, isoform CRA_b [Homo sapiens] |
| 119582155 | hCG1783090 [Homo sapiens] |
| 340219 | vimentin [Homo sapiens] |
| 56675570 | unnamed protein product [Homo sapiens] |
| 825671 | B23 nucleophosmin (280 AA) [Homo sapiens] |

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|---|---|
| 32488 | unnamed protein product [Homo sapiens] |
| 530420475 | PREDICTED: protein NipSnap homolog 1 isoform X1 [Homo sapiens] |
| 40031212 | unnamed protein product [Homo sapiens] |
| 403234036 | eukaryotic translation initiation factor 3 [Homo sapiens] |
| 31873360 | hypothetical protein [Homo sapiens] |
| 160332335 | RecName: Full=Neuroblast differentiation-associated protein AHNAK; AltName: Full=Desmoyokin |
| 58530842 | desmoplakin isoform II [Homo sapiens] |
| 485601397 | Chain R, Structure Of The Human 40s Ribosomal Proteins |
| 119615022 | leucine rich repeat containing 59, isoform CRA_a [Homo sapiens] |
| 49257460 | PTRF protein [Homo sapiens] |
| 21620099 | Treacher Collins-Franceschetti syndrome 1 [Homo sapiens] |
| 48735185 | EEF1A1 protein [Homo sapiens] |
| 375151597 | 60S ribosomal protein L10 isoform c [Homo sapiens] |
| 15431310 | keratin, type I cytoskeletal 14 [Homo sapiens] |
| 157829895 | Chain A, Crystal Structure Of Human Annexin I At 2.5 Angstroms Resolution |
| 119621461 | ribosomal protein S7, isoform CRA_a [Homo sapiens] |
| 119631904 | nebulin, isoform CRA_a [Homo sapiens] |
| 119626065 | albumin, isoform CRA_b [Homo sapiens] |
| 119602460 | ribosomal protein L8, isoform CRA_f [Homo sapiens] |
| 119569562 | antigen identified by monoclonal antibody Ki-67, isoform CRA_a [Homo sapiens] |
| 119569329 | hCG1640785, isoform CRA_a [Homo sapiens] |
| 221045918 | unnamed protein product [Homo sapiens] |
| 10435150 | unnamed protein product [Homo sapiens] |
| 63102283 | CKAP4 protein [Homo sapiens] |
| 62204505 | RPL13 protein [Homo sapiens] |
| 38014351 | EEF1D protein, partial [Homo sapiens] |
| 34785048 | RPS6 protein, partial [Homo sapiens] |
| 40040444 | unnamed protein product [Homo sapiens] |
| 530392193 | PREDICTED: 6-phosphofructokinase type C isoform X3 [Homo sapiens] |
| 55507560 | unknown [Homo sapiens] |
| 50513340 | Chain A, Nmr Structure Of Human Cofilin |
| 12643540 | RecName: Full=Proteasome subunit alpha type-7; AltName: Full=Proteasome subunit RC6-1; AltName: Full=Proteasom |
| 485601396 | Chain L, Structure Of The Human 40s Ribosomal Proteins |
| 485601390 | Chain O, Structure Of The Human 40s Ribosomal Proteins |
| 122937211 | proteasome-associated protein ECM29 homolog [Homo sapiens] |
| 33341236 | polytrophin [Homo sapiens] |
| 118498368 | kinectin isoform c [Homo sapiens] |
| 296439473 | RecName: Full=Dynein heavy chain 10, axonemal; AltName: Full=Axonemal beta dynein heavy chain 10; AltName: Full |
| 75517570 | HNRPA1 protein [Homo sapiens] |
| 119574650 | hect domain and RLD 4, isoform CRA_e [Homo sapiens] |
| 194386084 | unnamed protein product [Homo sapiens] |
| 259016354 | RecName: Full=Protein ELYS; AltName: Full=Embryonic large molecule derived from yolk sac; AltName: Full=Protein M |
| 119590009 | cytoplasmic linker 2, isoform CRA_a [Homo sapiens] |
| 374532823 | Golgin subfamily B member 1 isoform 4 [Homo sapiens] |
| 4930167 | Chain A, Human Muscle Aldolase |
| 166007177 | Chain T, Solution Structure Of Human Immunoglobulin M |
| 225733966 | Chain H, Human Thrombopoietin Neutralizing Antibody Tn1 Fab |
| 1587352 | globin 245 |
| 2661039 | alpha enolase [Homo sapiens] |
| 119619469 | dystrophin (muscular dystrophy, Duchenne and Becker types), isoform CRA_c [Homo sapiens] |
| 119615215 | karyopherin (importin) beta 1, isoform CRA_b [Homo sapiens] |
| 119612228 | hCG15685 [Homo sapiens] |
| 119607089 | protein kinase, DNA-activated, catalytic polypeptide, isoform CRA_d [Homo sapiens] |
| 119600702 | hCG1989166, isoform CRA_c, partial [Homo sapiens] |
| 119590272 | obscurin, cytoskeletal calmodulin and titin-interacting RhoGEF, isoform CRA_a [Homo sapiens] |

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|---|---|
| 119582699 | heat shock 70kDa protein 4, isoform CRA_b [Homo sapiens] |
| 119576069 | myosin XVA, isoform CRA_c [Homo sapiens] |
| 21754583 | unnamed protein product [Homo sapiens] |
| 39645240 | HNRPU protein, partial [Homo sapiens] |
| 38114878 | RPL13A protein, partial [Homo sapiens] |
| 21619981 | LMNA protein [Homo sapiens] |
| 116283708 | DHX9 protein [Homo sapiens] |
| 40040430 | unnamed protein product [Homo sapiens] |
| 20521005 | KIAA0342 protein [Homo sapiens] |
| 161172139 | Chain B, Phosphorylation Independent Interactions Between 14-3-3 And Exoenzyme S: From Structure To Pathogenesis |
| 298508322 | Chain F, Structure Of P97 N-D1 R95g Mutant In Complex With Atpgs |
| 13097600 | Similar to ribosomal protein L23, partial [Homo sapiens] |
| 645912958 | major vault protein isoform 2 [Homo sapiens] |
| 578801447 | PREDICTED: tropomyosin alpha-3 chain isoform X6 [Homo sapiens] |
| 89574029 | mitochondrial ATP synthase, H+ transporting F1 complex beta subunit [Homo sapiens] |
| 29334005 | unnamed protein product [Homo sapiens] |
| 119581825 | ribosomal protein L26-like 1, isoform CRA_a [Homo sapiens] |
| 153792663 | myosin-2 [Homo sapiens] |
| 2506816 | RecName: Full=Versican core protein; AltName: Full=Chondroitin sulfate proteoglycan core protein 2; Short=Chondroiti |
| 485601388 | Chain U, Structure Of The Human 40s Ribosomal Proteins |
| 4503513 | eukaryotic translation initiation factor 3 subunit I [Homo sapiens] |
| 118572681 | RecName: Full=Phosphatidylinositol 3-kinase regulatory subunit alpha; Short=PI3-kinase regulatory subunit alpha; Shor |
| 4501889 | actin, gamma-enteric smooth muscle isoform 1 precursor [Homo sapiens] |
| 119627197 | zinc finger, FYVE domain containing 9, isoform CRA_c [Homo sapiens] |
| 14589854 | protein tyrosine phosphatase type IVA 3 isoform 2 [Homo sapiens] |
| 119613293 | hCG2027030, partial [Homo sapiens] |
| 21758964 | unnamed protein product [Homo sapiens] |
| 485601399 | Chain T, Structure Of The Human 40s Ribosomal Proteins |
| 308153582 | RecName: Full=Neuron navigator 2; AltName: Full=Helicase APC down-regulated 1; AltName: Full=Pore membrane and |
| 121925 | RecName: Full=Histone H1.3; AltName: Full=Histone H1c; AltName: Full=Histone H1s-2 |
| 238054406 | RecName: Full=Keratin, type II cytoskeletal 1; AltName: Full=67 kDa cytokeratin; AltName: Full=Cytokeratin-1; Short= |
| 485601395 | Chain N, Structure Of The Human 40s Ribosomal Proteins |
| 296439461 | RecName: Full=Protein broad-minded; AltName: Full=TBC1 domain family member 32 |
| 118572619 | RecName: Full=Adenylate cyclase type 5; AltName: Full=ATP pyrophosphate-lyase 5; AltName: Full=Adenylate cyclase |
| 119598471 | optic atrophy 1 (autosomal dominant), isoform CRA_b [Homo sapiens] |
| 21928473 | seven transmembrane helix receptor [Homo sapiens] |
| 126362947 | sodium channel protein type 3 subunit alpha isoform 2 [Homo sapiens] |
| 578835066 | PREDICTED: liprin-alpha-3 isoform X1 [Homo sapiens] |
| 74756116 | RecName: Full=Zinc finger and BTB domain-containing protein 41 |
| 47076897 | unnamed protein product [Homo sapiens] |
| 119577859 | hypothetical protein FLJ20512 [Homo sapiens] |
| 58761484 | T-complex protein 1 subunit gamma isoform c [Homo sapiens] |
| 193786214 | unnamed protein product [Homo sapiens] |
| 18375644 | tyrosine-protein phosphatase non-receptor type 11 isoform 2 [Homo sapiens] |
| 182627587 | RecName: Full=Putative ankyrin repeat domain-containing protein 31 |
| 119614677 | proteasome (prosome, macropain) 26S subunit, ATPase, 5, isoform CRA_b [Homo sapiens] |
| 27436873 | E3 ubiquitin-protein ligase SHPRH isoform b [Homo sapiens] |
| 24660442 | MYO18A protein [Homo sapiens] |
| 172044680 | RecName: Full=Dynein heavy chain 2, axonemal; AltName: Full=Axonemal beta dynein heavy chain 2; AltName: Full=C |
| 119599446 | coatomer protein complex, subunit beta 2 (beta prime), isoform CRA_b [Homo sapiens] |
| 119608075 | ribosomal protein L12, isoform CRA_d [Homo sapiens] |
| 205371795 | RecName: Full=BAH and coiled-coil domain-containing protein 1; AltName: Full=Bromo adjacent homology domain-con |
| 530377992 | PREDICTED: storkhead-box protein 2 isoform X1 [Homo sapiens] |
| 119592618 | ribosomal protein S9, isoform CRA_c [Homo sapiens] |
| 119598167 | hypothetical protein MGC4562, isoform CRA_d [Homo sapiens] |

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|---|---|
| 172046085 | RecName: Full=Dynein heavy chain 14, axonemal; AltName: Full=Axonemal beta dynein heavy chain 14; AltName: Full |
| 194384416 | unnamed protein product [Homo sapiens] |
| 554790420 | NAD(P)H dehydrogenase [quinone] 1 isoform d [Homo sapiens] |
| 194385216 | unnamed protein product [Homo sapiens] |
| 219518228 | Unknown (protein for MGC:177866) [Homo sapiens] |
| 260099727 | L-lactate dehydrogenase A chain isoform 5 [Homo sapiens] |
| 194379468 | unnamed protein product [Homo sapiens] |
| 194375492 | unnamed protein product [Homo sapiens] |
| 221044142 | unnamed protein product [Homo sapiens] |
| 10436376 | unnamed protein product [Homo sapiens] |
| 321117084 | RPS10-NUDT3 protein [Homo sapiens] |
| 119597906 | testis expressed sequence 9 [Homo sapiens] |
| 331284176 | nuclear receptor corepressor 2 isoform 2 [Homo sapiens] |
| 194378812 | unnamed protein product [Homo sapiens] |
| 256542310 | dynein heavy chain 17, axonemal [Homo sapiens] |
| 20150918 | Chain A, Crystal Structure Of The N-Terminal Segment Of Human Eukaryotic Initiation Factor 2alpha |
| 157883792 | Chain A, Nmr Structure Of The Second Qrrm Domain Of Human Hnrnp F |
| 315583650 | Chain A, Crystal Structure Of Human Dnmt1(646-1600) In Complex With Dna |
| 223673784 | Chain A, Human Acylphosphatase(Acph) Surface Charge-Optimized |
| 284232 | Ig heavy chain V region - human |
| 224053 | macroglobulin alpha2 |
| 119613451 | nuclear transcription factor, X-box binding-like 1, isoform CRA_e [Homo sapiens] |
| 337451 | hnRNP type A/B protein [Homo sapiens] |
| 1136741 | KIAA0002 [Homo sapiens] |
| 551411917 | DBF4-type zinc finger-containing protein 2 isoform 2 [Homo sapiens] |
| 120538705 | ATP2B3 protein [Homo sapiens] |
| 109734611 | Myosin, heavy chain 10, non-muscle [Homo sapiens] |
| 10438219 | unnamed protein product [Homo sapiens] |
| 4388965 | Chain L, Antibody To Campath-1h Humanized Fab |
| 119629468 | hCG2011852 [Homo sapiens] |
| 119629071 | KIAA0564 protein, isoform CRA_b [Homo sapiens] |
| 119628802 | ribosomal protein L21, isoform CRA_c [Homo sapiens] |
| 119625048 | KM-HN-1 protein, isoform CRA_a [Homo sapiens] |
| 119623948 | euchromatic histone-lysine N-methyltransferase 2, isoform CRA_d [Homo sapiens] |
| 119623343 | hCG1999854, isoform CRA_a [Homo sapiens] |
| 119618140 | hCG2015269, isoform CRA_c [Homo sapiens] |
| 119617634 | chaperonin containing TCP1, subunit 2 (beta), isoform CRA_a [Homo sapiens] |
| 119616102 | microtubule-associated protein 1B, isoform CRA_a [Homo sapiens] |
| 119614240 | heterogeneous nuclear ribonucleoprotein A2/B1, isoform CRA_a [Homo sapiens] |
| 119613723 | hCG1985901 [Homo sapiens] |
| 119613335 | ribosomal protein L9, isoform CRA_c [Homo sapiens] |
| 119612929 | spectrin, beta, non-erythrocytic 5 [Homo sapiens] |
| 119612251 | E3 ubiquitin protein ligase, HECT domain containing, 1, isoform CRA_c [Homo sapiens] |
| 119611612 | translocated promoter region (to activated MET oncogene), isoform CRA_d [Homo sapiens] |
| 119611276 | kinesin-associated protein 3, isoform CRA_b [Homo sapiens] |
| 119610957 | TSR1, 20S rRNA accumulation, homolog (yeast), isoform CRA_d [Homo sapiens] |
| 119610275 | solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 5, isoform CRA_b [Homo sapie |
| 119609433 | proteasome (prosome, macropain) 26S subunit, non-ATPase, 12, isoform CRA_b [Homo sapiens] |
| 119609377 | Jumonji, AT rich interactive domain 1A (RBBP2-like), isoform CRA_b [Homo sapiens] |
| 119609186 | nucleolar protein 1, 120kDa [Homo sapiens] |
| 119604554 | dynamin 2, isoform CRA_e [Homo sapiens] |
| 119600676 | neurofibromin 1 (neurofibromatosis, von Recklinghausen disease, Watson disease), isoform CRA_c [Homo sapiens] |
| 119598667 | eukaryotic translation initiation factor 4 gamma, 1, isoform CRA_e [Homo sapiens] |
| 119598006 | vacuolar protein sorting 13C (yeast), isoform CRA_b [Homo sapiens] |
| 119597394 | hCG19253, isoform CRA_d [Homo sapiens] |

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|---|---|
| 119592222 | ribosomal protein S4, X-linked, isoform CRA_b, partial [Homo sapiens] |
| 119591307 | thyroid hormone receptor interactor 12, isoform CRA_f [Homo sapiens] |
| 119590595 | hCG1653748 [Homo sapiens] |
| 119590527 | dynein, axonemal, heavy polypeptide 7, isoform CRA_b [Homo sapiens] |
| 119579125 | protein tyrosine phosphatase, receptor type, D, isoform CRA_d [Homo sapiens] |
| 119576757 | hCG39912, isoform CRA_b [Homo sapiens] |
| 119574194 | heterogeneous nuclear ribonucleoprotein H1 (H), isoform CRA_b [Homo sapiens] |
| 119573054 | Rho GTPase activating protein 30, isoform CRA_c [Homo sapiens] |
| 119572456 | diaphanous homolog 3 (Drosophila), isoform CRA_c [Homo sapiens] |
| 119570361 | tolloid-like 2, isoform CRA_b [Homo sapiens] |
| 119569863 | tudor domain containing 1, isoform CRA_c [Homo sapiens] |
| 119569579 | dedicator of cytokinesis 1 [Homo sapiens] |
| 221046404 | unnamed protein product [Homo sapiens] |
| 33096800 | hypothetical protein [Homo sapiens] |
| 194388520 | unnamed protein product [Homo sapiens] |
| 194381188 | unnamed protein product [Homo sapiens] |
| 194374917 | unnamed protein product [Homo sapiens] |
| 194374597 | unnamed protein product [Homo sapiens] |
| 193788435 | unnamed protein product [Homo sapiens] |
| 193787899 | unnamed protein product [Homo sapiens] |
| 193785065 | unnamed protein product [Homo sapiens] |
| 158259305 | unnamed protein product [Homo sapiens] |
| 21756441 | unnamed protein product [Homo sapiens] |
| 7023915 | unnamed protein product [Homo sapiens] |
| 18676660 | FLJ00229 protein [Homo sapiens] |
| 47939143 | YBX1 protein, partial [Homo sapiens] |
| 28838367 | LOXHD1 protein [Homo sapiens] |
| 507898 | glutamate transporter [Homo sapiens] |
| 158253421 | DNAH9 protein [Homo sapiens] |
| 189053448 | unnamed protein product [Homo sapiens] |
| 47077415 | unnamed protein product [Homo sapiens] |
| 34533879 | unnamed protein product [Homo sapiens] |
| 34531561 | unnamed protein product [Homo sapiens] |
| 80476693 | NBN protein [Homo sapiens] |
| 12232589 | TFNR [Homo sapiens] |
| 40788890 | KIAA0165 [Homo sapiens] |
| 519882971 | RecName: Full=Putative ciliary rootlet coiled-coil protein-like 3 protein |
| 444738577 | alternative protein IPO7 [Homo sapiens] |
| 109730579 | Collagen, type XXIV, alpha 1 [Homo sapiens] |
| 56078799 | Ribosomal protein S27a [Homo sapiens] |
| 33440522 | FBXO38 protein [Homo sapiens] |
| 15928389 | Unknown (protein for IMAGE:4158571), partial [Homo sapiens] |
| 15680023 | B-cell receptor-associated protein 31 [Homo sapiens] |
| 13938339 | ATP5A1 protein, partial [Homo sapiens] |
| 847816 | interferon omega-1, partial [Homo sapiens] |
| 1147783 | myosin-IXb [Homo sapiens] |
| 1049053 | encodes region of fatty acid synthase activity; FAS; multifunctional protein [Homo sapiens] |
| 183272 | glutamate decarboxylase [Homo sapiens] |
| 5805196 | Fas associated factor 1 [Homo sapiens] |
| 2104553 | Myosin heavy chain (MHY11) (5'partial) [Homo sapiens] |
| 62822517 | unknown [Homo sapiens] |
| 62822099 | unknown [Homo sapiens] |
| 62630102 | unknown [Homo sapiens] |
| 11890755 | RNA helicase II/Gu protein [Homo sapiens] |
| 4583679 | vacuolar protein sorting [Homo sapiens] |

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|---|---|
| 40807213 | FAM179B protein [Homo sapiens] |
| 62088708 | ATP-binding cassette, sub-family F, member 1 variant [Homo sapiens] |
| 62087794 | N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 1 variant [Homo sapiens] |
| 115333997 | 145 kDa nucleolar protein [Homo sapiens] |
| 39644893 | FOXRED1 protein [Homo sapiens] |
| 63089650 | unnamed protein product [Homo sapiens] |
| 40980242 | unnamed protein product [Homo sapiens] |
| 40976912 | unnamed protein product [Homo sapiens] |
| 40976232 | unnamed protein product [Homo sapiens] |
| 313223 | transcription elongation factor [Homo sapiens] |
| 20521792 | KIAA1208 protein [Homo sapiens] |
| 1663704 | KIAA0242 protein [Homo sapiens] |
| 550545215 | Chain D, 14-3-3gamma Complexed With The N-terminal Sequence Of Tyrosine Hydroxylase (residues 1-43) |
| 296863377 | Chain A, Crystal Structure Of The Catalytic Domain Of Flj14393 |
| 530418458 | PREDICTED: cytochrome c oxidase subunit 4 isoform 2, mitochondrial isoform X3 [Homo sapiens] |
| 530411223 | PREDICTED: Golgi SNAP receptor complex member 1 isoform X2 [Homo sapiens] |
| 530404104 | PREDICTED: exonuclease 3'-5' domain-containing protein 2 isoform X4 [Homo sapiens] |
| 530392546 | PREDICTED: glycylpeptide N-tetradecanoyltransferase 2 isoform X1 [Homo sapiens] |
| 530382430 | PREDICTED: dystonin isoform X7 [Homo sapiens] |
| 578806816 | PREDICTED: 26S proteasome non-ATPase regulatory subunit 6 isoform X3 [Homo sapiens] |
| 530369227 | PREDICTED: rho guanine nucleotide exchange factor 4 isoform X2 [Homo sapiens] |
| 530363026 | PREDICTED: outer dense fiber protein 2-like isoform X4 [Homo sapiens] |
| 519674682 | immunoglobulin A heavy chain variable region, partial [Homo sapiens] |
| 381142222 | immunoglobulin light chain variable region, partial [Homo sapiens] |
| 459214638 | KIF5B-RET(NM_020630)_K24;R11 fusion protein [Homo sapiens] |
| 442564354 | von Willebrand factor [Homo sapiens] |
| 374074366 | Chain A, Crystal Structure Of 14-3-3 Epsilon With Mlf1 Peptide |
| 319443270 | Chain A, Nmr Structure Of Calcium-Loaded Stim2 Ef-Sam. |
| 190406 | profilaggrin, partial [Homo sapiens] |
| 14625824 | moesin/anaplastic lymphoma kinase fusion protein [Homo sapiens] |
| 403456 | 26S protease (S4) regulatory subunit [Homo sapiens] |
| 62871194 | immunoglobulin alpha heavy chain variable region [Homo sapiens] |
| 609412463 | Chain D, Crystal Structure Of Human Lnkh2b-h2a.z-anp32e |
| 578837382 | PREDICTED: putative SEC14-like protein 6 isoform X3 [Homo sapiens] |
| 578837055 | PREDICTED: calcineurin-binding protein cabin-1 isoform X12 [Homo sapiens] |
| 578832590 | PREDICTED: zinc finger protein 407 isoform X3 [Homo sapiens] |
| 578831328 | PREDICTED: actin, cytoplasmic 2 isoform X1 [Homo sapiens] |
| 578826913 | PREDICTED: SHC-transforming protein 4 isoform X3 [Homo sapiens] |
| 578808176 | PREDICTED: SH3 domain and tetratricopeptide repeat-containing protein 1 isoform X7 [Homo sapiens] |
| 578807393 | PREDICTED: leucine-, glutamate- and lysine-rich protein 1 isoform X7 [Homo sapiens] |
| 578804532 | PREDICTED: telomere-associated protein RIF1 isoform X4 [Homo sapiens] |
| 38305350 | antigen MLAA-44 [Homo sapiens] |
| 2253417 | Trip230 [Homo sapiens] |
| 284930095 | Treslin [Homo sapiens] |
| 11527207 | CGI-85 [Homo sapiens] |
| 40286771 | brain leucine zipper protein [Homo sapiens] |
| 52545570 | hypothetical protein [Homo sapiens] |
| 21739524 | hypothetical protein [Homo sapiens] |
| 13093781 | hypothetical protein [Homo sapiens] |
| 12052969 | hypothetical protein [Homo sapiens] |
| 51476290 | hypothetical protein [Homo sapiens] |
| 23712 | myoblast antigen 24.1D5 [Homo sapiens] |
| 62897645 | eukaryotic translation elongation factor 1 alpha 1 variant [Homo sapiens] |
| 133251534 | piwi-like 1 [Homo sapiens] |
| 29823335 | unnamed protein product [Homo sapiens] |

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|---|---|
| 2804273 | alpha actinin 4 [Homo sapiens] |

| Score | Coverage | # Proteins | # Unique Peptide | # Peptides | # PSMs | Molecular Function | llular Compon | ological Proce |
|---|---|---|---|---|---|---|---|---|
| 182.70 | 34.34 | 27 | 44 | 56 | 57 | | | |
| 246.67 | 55.50 | 21 | 29 | 37 | 87 | | | |
| 66.29 | 7.28 | 84 | 26 | 30 | 30 | | | |
| 101.10 | 40.40 | 34 | 24 | 30 | 38 | | | |
| 193.59 | 56.18 | 19 | 23 | 26 | 64 | | | |
| 225.01 | 72.27 | 354 | 23 | 24 | 68 | | | |
| 3229.72 | 65.37 | 16 | 16 | 17 | 938 | | | |
| 89.05 | 43.51 | 38 | 14 | 23 | 33 | | | |
| 38.83 | 37.46 | 30 | 13 | 14 | 14 | | | |
| 64.95 | 0.74 | 128 | 13 | 24 | 33 | | | |
| 344.40 | 52.11 | 17 | 12 | 12 | 114 | | | |
| 312.72 | 58.33 | 73 | 12 | 35 | 115 | | | |
| 37.38 | 19.24 | 15 | 12 | 12 | 14 | | | |
| 737.73 | 44.98 | 16 | 12 | 16 | 245 | | | |
| 31.12 | 7.58 | 35 | 12 | 12 | 12 | | | |
| 42.33 | 23.24 | 12 | 11 | 11 | 13 | | | |
| 30.03 | 8.54 | 21 | 11 | 11 | 11 | | | |
| 31.73 | 24.13 | 56 | 11 | 11 | 14 | | | |
| 25.23 | 19.16 | 18 | 10 | 10 | 11 | | | |
| 28.03 | 19.70 | 14 | 9 | 10 | 10 | | | |
| 24.00 | 4.90 | 32 | 9 | 9 | 11 | | | |
| 99.01 | 47.99 | 54 | 9 | 21 | 39 | | | |
| 35.16 | 38.25 | 4 | 9 | 11 | 15 | | | |
| 32.83 | 40.61 | 12 | 8 | 9 | 12 | | | |
| 22.51 | 25.48 | 50 | 8 | 8 | 8 | | | |
| 29.11 | 17.74 | 9 | 8 | 8 | 10 | | | |
| 23.33 | 37.33 | 13 | 8 | 8 | 9 | | | |
| 26.45 | 15.27 | 25 | 7 | 7 | 8 | | | |
| 15.32 | 26.86 | 12 | 7 | 7 | 7 | | | |
| 20.29 | 13.18 | 24 | 7 | 7 | 7 | | | |
| 18.51 | 3.92 | 42 | 7 | 7 | 7 | | | |
| 13.48 | 16.67 | 33 | 7 | 7 | 7 | | | |
| 14.18 | 31.58 | 6 | 6 | 6 | 6 | | | |
| 15.02 | 3.15 | 19 | 6 | 6 | 6 | | | |
| 18.61 | 50.00 | 16 | 6 | 6 | 6 | | | |
| 20.16 | 1.22 | 123 | 6 | 9 | 11 | | | |
| 17.64 | 2.31 | 11 | 6 | 6 | 6 | | | |
| 23.10 | 21.92 | 10 | 6 | 6 | 8 | | | |
| 15.82 | 13.18 | 11 | 6 | 6 | 6 | | | |
| 15.07 | 13.07 | 22 | 6 | 6 | 7 | | | |
| 43.69 | 26.62 | 122 | 6 | 16 | 18 | | | |
| 13.12 | 27.15 | 43 | 6 | 7 | 7 | | | |
| 13.33 | 3.50 | 10 | 5 | 5 | 7 | | | |
| 12.27 | 7.34 | 9 | 5 | 5 | 5 | | | |
| 26.88 | 24.43 | 36 | 5 | 11 | 11 | | | |
| 15.20 | 32.93 | 49 | 5 | 5 | 6 | | | |
| 12.07 | 34.88 | 8 | 5 | 5 | 5 | | | |
| 20.57 | 17.42 | 28 | 5 | 6 | 9 | | | |
| 17.91 | 25.94 | 13 | 5 | 6 | 7 | | | |
| 10.34 | 14.91 | 18 | 5 | 5 | 5 | | | |
| 13.78 | 18.55 | 12 | 5 | 5 | 5 | | | |
| 23.77 | 17.38 | 45 | 5 | 8 | 9 | | | |
| 18.18 | 24.31 | 26 | 5 | 5 | 7 | | | |
| 20.52 | 28.57 | 45 | 5 | 8 | 9 | | | |

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|---|---|---|---|---|---|---|---|---|
| 38.69 | 20.49 | 121 | 5 | 13 | 15 | | | |
| 18.27 | 20.77 | 21 | 5 | 8 | 9 | | | |
| 14.54 | 35.61 | 4 | 5 | 6 | 6 | | | |
| 15.71 | 5.28 | 9 | 5 | 6 | 6 | | | |
| 11.03 | 5.23 | 30 | 5 | 5 | 5 | | | |
| 17.65 | 6.59 | 17 | 4 | 9 | 11 | | | |
| 10.05 | 2.90 | 18 | 4 | 4 | 4 | | | |
| 17.31 | 48.89 | 5 | 4 | 4 | 5 | | | |
| 13.88 | 16.61 | 1 | 4 | 4 | 4 | | | |
| 11.04 | 19.33 | 14 | 4 | 4 | 4 | | | |
| 9.60 | 4.07 | 30 | 4 | 4 | 4 | | | |
| 59.05 | 41.50 | 17 | 4 | 15 | 25 | | | |
| 8.84 | 23.03 | 18 | 4 | 4 | 4 | | | |
| 75.69 | 31.78 | 56 | 4 | 17 | 32 | | | |
| 15.21 | 19.75 | 23 | 4 | 5 | 5 | | | |
| 10.88 | 27.06 | 4 | 4 | 4 | 4 | | | |
| 12.94 | 1.36 | 43 | 4 | 6 | 6 | | | |
| 24.04 | 10.23 | 51 | 4 | 5 | 10 | | | |
| 13.70 | 23.18 | 10 | 4 | 4 | 4 | | | |
| 11.45 | 2.36 | 13 | 4 | 6 | 6 | | | |
| 10.34 | 19.35 | 5 | 4 | 4 | 5 | | | |
| 55.35 | 42.17 | 78 | 4 | 14 | 19 | | | |
| 8.80 | 9.42 | 4 | 4 | 4 | 4 | | | |
| 10.21 | 12.07 | 19 | 4 | 5 | 5 | | | |
| 11.62 | 25.59 | 8 | 4 | 5 | 5 | | | |
| 8.78 | 6.91 | 18 | 4 | 4 | 4 | | | |
| 8.37 | 14.17 | 19 | 4 | 4 | 4 | | | |
| 9.85 | 16.28 | 26 | 4 | 4 | 4 | | | |
| 11.23 | 10.59 | 21 | 4 | 5 | 5 | | | |
| 10.13 | 11.60 | 16 | 4 | 4 | 4 | | | |
| 6.01 | 16.27 | 12 | 3 | 3 | 3 | | | |
| 7.53 | 13.71 | 12 | 3 | 3 | 3 | | | |
| 5.81 | 19.62 | 2 | 3 | 3 | 3 | | | |
| 7.59 | 18.54 | 2 | 3 | 3 | 3 | | | |
| 9.12 | 2.38 | 8 | 3 | 3 | 4 | | | |
| 12.15 | 0.81 | 58 | 3 | 6 | 6 | | | |
| 13.50 | 3.38 | 74 | 3 | 5 | 7 | | | |
| 14.01 | 1.72 | 8 | 3 | 4 | 6 | | | |
| 21.53 | 20.97 | 37 | 3 | 6 | 6 | | | |
| 6.59 | 3.70 | 12 | 3 | 3 | 3 | | | |
| 8.84 | 21.34 | 11 | 3 | 3 | 4 | | | |
| 7.35 | 2.12 | 15 | 3 | 3 | 3 | | | |
| 7.00 | 3.36 | 5 | 3 | 3 | 3 | | | |
| 7.57 | 0.82 | 25 | 3 | 3 | 4 | | | |
| 6.55 | 8.26 | 31 | 3 | 3 | 3 | | | |
| 21.94 | 10.13 | 261 | 3 | 4 | 9 | | | |
| 414.86 | 40.55 | 10 | 3 | 6 | 136 | | | |
| 12.97 | 2.35 | 17 | 3 | 6 | 7 | | | |
| 21.49 | 27.08 | 28 | 3 | 8 | 9 | | | |
| 15.08 | 1.60 | 213 | 3 | 7 | 8 | | | |
| 8.53 | 5.08 | 11 | 3 | 3 | 3 | | | |
| 9.85 | 26.96 | 14 | 3 | 3 | 4 | | | |
| 8.43 | 1.59 | 11 | 3 | 4 | 4 | | | |
| 9.72 | 5.11 | 6 | 3 | 4 | 4 | | | |
| 11.52 | 0.48 | 96 | 3 | 4 | 6 | | | |

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|---|---|---|---|---|---|---|---|---|
| 14.03 | 7.82 | 20 | 3 | 5 | 6 | | | |
| 5.35 | 0.74 | 8 | 3 | 3 | 3 | | | |
| 37.71 | 22.30 | 61 | 3 | 11 | 17 | | | |
| 8.87 | 6.24 | 11 | 3 | 4 | 4 | | | |
| 5.65 | 11.44 | 10 | 3 | 3 | 3 | | | |
| 9.41 | 10.32 | 21 | 3 | 4 | 4 | | | |
| 9.41 | 6.58 | 10 | 3 | 3 | 3 | | | |
| 9.43 | 12.11 | 19 | 3 | 3 | 5 | | | |
| 11.41 | 1.42 | 7 | 3 | 3 | 6 | | | |
| 9.70 | 20.00 | 20 | 3 | 4 | 4 | | | |
| 7.81 | 10.02 | 23 | 3 | 3 | 3 | | | |
| 6.22 | 20.15 | 8 | 3 | 3 | 3 | | | |
| 10.03 | 7.44 | 18 | 3 | 4 | 4 | | | |
| 6.61 | 11.27 | 89 | 3 | 3 | 3 | | | |
| 8.79 | 12.36 | 6 | 3 | 3 | 3 | | | |
| 5.46 | 1.20 | 2 | 3 | 3 | 3 | | | |
| 5.38 | 15.86 | 9 | 2 | 2 | 2 | | | |
| 5.64 | 1.80 | 46 | 2 | 3 | 3 | | | |
| 5.37 | 0.62 | 6 | 2 | 2 | 3 | | | |
| 4.93 | 15.13 | 13 | 2 | 2 | 2 | | | |
| 4.25 | 6.15 | 5 | 2 | 2 | 2 | | | |
| 11.37 | 7.04 | 105 | 2 | 5 | 6 | | | |
| 32.38 | 28.46 | 39 | 2 | 8 | 13 | | | |
| 21.82 | 3.67 | 6 | 2 | 2 | 10 | | | |
| 4.02 | 20.95 | 7 | 2 | 2 | 2 | | | |
| 22.56 | 33.33 | 1 | 2 | 2 | 10 | | | |
| 4.04 | 5.92 | 7 | 2 | 2 | 2 | | | |
| 4.65 | 13.79 | 4 | 2 | 2 | 2 | | | |
| 12.78 | 1.29 | 95 | 2 | 3 | 7 | | | |
| 9.78 | 19.91 | 7 | 2 | 3 | 4 | | | |
| 405.11 | 58.70 | 29 | 2 | 42 | 138 | | | |
| 5.79 | 15.89 | 2 | 2 | 2 | 2 | | | |
| 6.13 | 2.23 | 19 | 2 | 3 | 3 | | | |
| 5.65 | 2.14 | 29 | 2 | 2 | 3 | | | |
| 5.23 | 3.79 | 14 | 2 | 3 | 3 | | | |
| 4.21 | 16.42 | 1 | 2 | 2 | 2 | | | |
| 4.05 | 1.49 | 27 | 2 | 2 | 2 | | | |
| 36.04 | 3.12 | 22 | 2 | 3 | 17 | | | |
| 13.25 | 2.75 | 6 | 2 | 2 | 5 | | | |
| 4.33 | 11.66 | 6 | 2 | 2 | 2 | | | |
| 9.00 | 15.96 | 2 | 2 | 2 | 3 | | | |
| 6.86 | 3.75 | 9 | 2 | 2 | 3 | | | |
| 3.71 | 2.33 | 10 | 2 | 2 | 2 | | | |
| 4.17 | 5.22 | 18 | 2 | 2 | 2 | | | |
| 4.65 | 1.55 | 1 | 2 | 2 | 2 | | | |
| 4.49 | 9.05 | 8 | 2 | 2 | 2 | | | |
| 9.48 | 2.29 | 13 | 2 | 3 | 4 | | | |
| 9.68 | 1.60 | 15 | 2 | 3 | 4 | | | |
| 6.47 | 0.86 | 3 | 2 | 3 | 3 | | | |
| 3.82 | 2.74 | 2 | 2 | 2 | 2 | | | |
| 7.77 | 22.73 | 7 | 2 | 2 | 2 | | | |
| 6.57 | 1.65 | 7 | 2 | 3 | 3 | | | |
| 11.49 | 1.39 | 36 | 2 | 3 | 6 | | | |
| 4.68 | 11.51 | 12 | 2 | 2 | 2 | | | |
| 10.44 | 4.24 | 38 | 2 | 3 | 6 | | | |

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|---|---|---|---|---|---|---|---|---|
| 9.70 | 1.51 | 10 | 2 | 5 | 5 | | | |
| 5.97 | 15.82 | 76 | 2 | 2 | 3 | | | |
| 5.04 | 8.42 | 13 | 2 | 2 | 2 | | | |
| 7.01 | 9.69 | 49 | 2 | 2 | 3 | | | |
| 5.11 | 35.11 | 2 | 2 | 2 | 2 | | | |
| 7.82 | 14.94 | 23 | 2 | 3 | 3 | | | |
| 9.40 | 8.26 | 15 | 2 | 3 | 3 | | | |
| 9.10 | 4.52 | 22 | 2 | 2 | 5 | | | |
| 14.39 | 2.81 | 32 | 2 | 2 | 7 | | | |
| 5.24 | 7.43 | 10 | 2 | 2 | 2 | | | |
| 10.51 | 10.65 | 11 | 2 | 3 | 5 | | | |
| 3.63 | 6.01 | 2 | 2 | 2 | 2 | | | |
| 7.23 | 1.67 | 16 | 2 | 3 | 4 | | | |
| 5.16 | 8.52 | 7 | 2 | 2 | 2 | | | |
| 134.15 | 0.90 | 22 | 2 | 4 | 56 | | | |
| 4.16 | 11.54 | 3 | 2 | 2 | 2 | | | |
| 9.93 | 24.60 | 1 | 2 | 2 | 3 | | | |
| 6.15 | 4.50 | 41 | 2 | 3 | 3 | | | |
| 3.62 | 20.20 | 1 | 2 | 2 | 2 | | | |
| 16.94 | 45.13 | 279 | 2 | 4 | 8 | | | |
| 8.30 | 2.69 | 14 | 2 | 2 | 3 | | | |
| 7.00 | 3.57 | 9 | 2 | 2 | 4 | | | |
| 3.95 | 7.04 | 8 | 2 | 2 | 2 | | | |
| 5.27 | 4.08 | 8 | 2 | 2 | 2 | | | |
| 10.86 | 3.10 | 6 | 2 | 3 | 4 | | | |
| 3.56 | 2.86 | 10 | 2 | 2 | 2 | | | |
| 30.30 | 5.41 | 66 | 2 | 11 | 13 | | | |
| 6.26 | 4.80 | 44 | 2 | 3 | 3 | | | |
| 22.72 | 23.36 | 111 | 2 | 4 | 6 | | | |
| 15.91 | 0.91 | 170 | 2 | 8 | 8 | | | |
| 3.68 | 5.35 | 13 | 2 | 2 | 2 | | | |
| 5.16 | 28.45 | 14 | 2 | 2 | 2 | | | |
| 11.01 | 8.30 | 8 | 2 | 4 | 6 | | | |
| 5.15 | 2.68 | 27 | 2 | 2 | 2 | | | |
| 3.70 | 1.75 | 8 | 2 | 2 | 2 | | | |
| 4.62 | 27.13 | 25 | 2 | 2 | 2 | | | |
| 4.92 | 4.69 | 10 | 2 | 2 | 2 | | | |
| 6.77 | 2.01 | 13 | 2 | 3 | 3 | | | |
| 16.50 | 12.96 | 16 | 2 | 5 | 5 | | | |
| 13.92 | 5.59 | 3 | 2 | 3 | 6 | | | |
| 4.45 | 14.07 | 9 | 2 | 2 | 2 | | | |
| 8.51 | 1.14 | 7 | 2 | 3 | 4 | | | |
| 113.25 | 1.76 | 13 | 2 | 3 | 49 | | | |
| 9.20 | 1.62 | 144 | 2 | 4 | 5 | | | |
| 3.08 | 1.68 | 6 | 2 | 2 | 2 | | | |
| 9.69 | 6.51 | 77 | 2 | 4 | 5 | | | |
| 11.67 | 16.73 | 9 | 2 | 4 | 4 | | | |
| 3.97 | 7.05 | 5 | 2 | 2 | 2 | | | |
| 7.29 | 1.83 | 88 | 2 | 3 | 4 | | | |
| 17.99 | 4.46 | 8 | 2 | 2 | 8 | | | |
| 4.00 | 3.33 | 20 | 2 | 2 | 2 | | | |
| 6.02 | 0.69 | 18 | 2 | 2 | 3 | | | |
| 5.32 | 1.60 | 33 | 2 | 3 | 3 | | | |
| 13.91 | 1.42 | 18 | 2 | 5 | 8 | | | |
| 9.02 | 0.65 | 9 | 2 | 3 | 4 | | | |

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|---|---|---|---|---|---|---|---|---|
| 7.72 | 14.72 | 20 | 2 | 4 | 4 | | | |
| 3.64 | 2.16 | 28 | 2 | 2 | 2 | | | |
| 3.87 | 44.74 | 1 | 2 | 2 | 2 | | | |
| 13.29 | 1.52 | 8 | 2 | 4 | 6 | | | |
| 180.52 | 2.07 | 36 | 2 | 2 | 85 | | | |
| 5.50 | 15.22 | 13 | 2 | 2 | 2 | | | |
| 6.85 | 8.65 | 15 | 2 | 2 | 3 | | | |
| 23.68 | 2.23 | 50 | 2 | 3 | 15 | | | |
| 4.61 | 7.42 | 12 | 2 | 2 | 2 | | | |
| 9.19 | 3.84 | 4 | 2 | 3 | 5 | | | |
| 5.29 | 3.00 | 181 | 2 | 4 | 4 | | | |
| 4.72 | 1.60 | 7 | 2 | 2 | 2 | | | |
| 4.72 | 16.96 | 8 | 2 | 2 | 2 | | | |
| 5.88 | 6.90 | 20 | 2 | 2 | 2 | | | |
| 5.35 | 29.06 | 12 | 2 | 2 | 2 | | | |
| 3.66 | 2.08 | 8 | 2 | 2 | 2 | | | |
| 4.63 | 9.63 | 5 | 2 | 2 | 2 | | | |
| 4.24 | 4.56 | 14 | 2 | 2 | 2 | | | |
| 36.09 | 3.11 | 13 | 2 | 2 | 16 | | | |
| 6.37 | 10.55 | 19 | 2 | 3 | 3 | | | |
| 10.49 | 8.30 | 29 | 2 | 4 | 5 | | | |
| 8.03 | 3.45 | 3 | 2 | 2 | 4 | | | |
| 10.25 | 9.17 | 13 | 2 | 2 | 5 | | | |
| 7.28 | 7.87 | 2 | 2 | 2 | 4 | | | |
| 6.89 | 2.87 | 6 | 2 | 2 | 3 | | | |
| 4.68 | 11.65 | 22 | 2 | 2 | 2 | | | |
| 9.82 | 3.71 | 88 | 2 | 3 | 5 | | | |
| 10.26 | 8.78 | 7 | 2 | 2 | 4 | | | |
| 8.08 | 0.94 | 13 | 2 | 2 | 4 | | | |
| 12.58 | 5.90 | 11 | 2 | 3 | 6 | | | |
| 10.41 | 1.94 | 6 | 2 | 3 | 6 | | | |
| 9.21 | 5.81 | 1 | 2 | 3 | 4 | | | |
| 5.55 | 1.18 | 12 | 2 | 2 | 3 | | | |
| 3.56 | 4.03 | 11 | 2 | 2 | 2 | | | |
| 4.65 | 1.14 | 19 | 2 | 2 | 2 | | | |
| 5.36 | 1.15 | 6 | 2 | 3 | 3 | | | |
| 44.54 | 1.11 | 4 | 2 | 2 | 20 | | | |
| 4.81 | 23.08 | 2 | 2 | 2 | 7 | | | |
| 7.98 | 2.39 | 3 | 2 | 2 | 3 | | | |
| 39.43 | 44.87 | 103 | 2 | 7 | 16 | | | |
| 4.96 | 10.33 | 13 | 2 | 2 | 3 | | | |
| 10.28 | 15.60 | 13 | 2 | 3 | 3 | | | |
| 5.32 | 16.67 | 10 | 2 | 2 | 2 | | | |
| 6.09 | 4.90 | 11 | 2 | 2 | 2 | | | |
| 4.79 | 21.84 | 6 | 2 | 2 | 2 | | | |
| 8.27 | 1.19 | 11 | 2 | 3 | 5 | | | |
| 4.47 | 0.76 | 8 | 2 | 2 | 2 | | | |
| 9.80 | 5.73 | 90 | 2 | 3 | 5 | | | |
| 7.52 | 4.08 | 9 | 2 | 2 | 4 | | | |
| 32.57 | 8.02 | 30 | 2 | 13 | 13 | | | |
| 4.20 | 8.05 | 11 | 2 | 2 | 2 | | | |
| 5.97 | 5.18 | 29 | 2 | 2 | 3 | | | |
| 5.90 | 0.76 | 32 | 2 | 3 | 3 | | | |
| 5.55 | 4.62 | 4 | 2 | 2 | 2 | | | |
| 106.07 | 7.89 | 12 | 2 | 2 | 47 | | | |

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|---|---|---|---|---|---|---|---|---|
| 9.17 | 3.51 | 5 | 2 | 2 | 4 | | | |
| 6.55 | 5.06 | 57 | 2 | 3 | 3 | | | |
| 16.35 | 5.16 | 19 | 2 | 3 | 8 | | | |
| 4.68 | 4.93 | 3 | 2 | 2 | 2 | | | |
| 4.20 | 7.90 | 13 | 2 | 2 | 2 | | | |
| 5.09 | 13.13 | 1 | 2 | 2 | 2 | | | |
| 8.51 | 42.00 | 1 | 2 | 3 | 5 | | | |
| 5.71 | 16.08 | 10 | 2 | 2 | 2 | | | |
| 4.68 | 25.81 | 11 | 2 | 2 | 2 | | | |
| 3.93 | 7.97 | 10 | 2 | 2 | 2 | | | |
| 3.74 | 2.21 | 12 | 2 | 2 | 2 | | | |
| 25.68 | 7.56 | 6 | 2 | 2 | 11 | | | |
| 10.30 | 24.71 | 42 | 2 | 5 | 5 | | | |
| 7.17 | 4.98 | 37 | 2 | 3 | 4 | | | |
| 3.86 | 18.11 | 6 | 2 | 2 | 2 | | | |
| 3.72 | 7.72 | 7 | 2 | 2 | 2 | | | |
| 4.21 | 10.93 | 8 | 2 | 2 | 2 | | | |
| 18.56 | 6.87 | 20 | 2 | 2 | 8 | | | |
| 16.43 | 1.13 | 35 | 2 | 6 | 7 | | | |
| 6.98 | 8.82 | 7 | 2 | 3 | 3 | | | |
| 3.14 | 0.65 | 17 | 2 | 2 | 2 | | | |
| 7.18 | 6.50 | 14 | 2 | 3 | 3 | | | |
| 49.28 | 11.97 | 1 | 2 | 2 | 22 | | | |
| 4.42 | 30.19 | 1 | 2 | 2 | 2 | | | |
| 10.77 | 4.10 | 45 | 2 | 5 | 5 | | | |
| 3.65 | 0.59 | 30 | 2 | 2 | 2 | | | |
| 6.71 | 16.81 | 16 | 2 | 3 | 3 | | | |
| 10.11 | 7.33 | 12 | 2 | 2 | 6 | | | |
| 4.12 | 1.40 | 13 | 2 | 2 | 2 | | | |
| 4.56 | 3.61 | 35 | 2 | 2 | 2 | | | |
| 3.71 | 3.41 | 10 | 2 | 2 | 2 | | | |
| 10.43 | 11.73 | 13 | 2 | 2 | 5 | | | |
| 10.86 | 15.31 | 65 | 2 | 3 | 4 | | | |
| 3.61 | 5.59 | 17 | 2 | 2 | 2 | | | |
| 12.19 | 2.10 | 42 | 2 | 2 | 6 | | | |
| 7.82 | 1.66 | 8 | 2 | 3 | 4 | | | |
| 40.33 | 21.15 | 108 | 2 | 9 | 16 | | | |
| 4.12 | 5.64 | 20 | 2 | 2 | 2 | | | |
| 6.01 | 1.63 | 16 | 2 | 2 | 3 | | | |
| 56.25 | 5.28 | 10 | 2 | 3 | 24 | | | |
| 4.58 | 0.90 | 29 | 2 | 3 | 3 | | | |
| 3.10 | 4.02 | 26 | 2 | 2 | 2 | | | |
| 13.38 | 1.97 | 11 | 2 | 4 | 6 | | | |
| 3.16 | 0.58 | 19 | 2 | 2 | 2 | | | |
| 3.66 | 7.92 | 10 | 2 | 2 | 2 | | | |
| 6.36 | 9.77 | 8 | 2 | 3 | 3 | | | |
| 3.15 | 1.09 | 15 | 2 | 2 | 2 | | | |
| 26.00 | 3.82 | 12 | 2 | 5 | 13 | | | |
| 3.17 | 3.17 | 10 | 2 | 2 | 2 | | | |
| 4.34 | 6.65 | 2 | 2 | 2 | 2 | | | |
| 3.60 | 1.73 | 15 | 2 | 2 | 2 | | | |
| 4.38 | 6.57 | 10 | 2 | 2 | 2 | | | |
| 55.32 | 35.57 | 6 | 2 | 13 | 25 | | | |
| 6.44 | 3.77 | 49 | 2 | 3 | 4 | | | |
| 7.32 | 1.65 | 4 | 2 | 2 | 3 | | | |

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|---|---|---|---|---|---|---|---|---|
| 13.52 | 7.13 | 22 | 2 | 5 | 5 |  |  |  |

| Pfam IDs | # AAs | MW [kDa] | calc. pI |
|---|---|---|---|
| Retrival Error | 1960 | 226.4 | 5.60 |
| Retrival Error | 645 | 65.8 | 8.00 |
| Retrival Error | 4684 | 531.5 | 5.96 |
| Retrival Error | 646 | 70.9 | 5.52 |
| Retrival Error | 623 | 62.0 | 5.24 |
| Retrival Error | 440 | 47.7 | 5.22 |
| Retrival Error | 231 | 24.3 | 7.91 |
| Retrival Error | 547 | 58.6 | 7.72 |
| Retrival Error | 339 | 38.6 | 7.75 |
| Retrival Error | 34942 | 3878.8 | 6.38 |
| Retrival Error | 213 | 23.3 | 8.29 |
| Retrival Error | 624 | 63.3 | 5.21 |
| Retrival Error | 707 | 76.3 | 4.69 |
| Retrival Error | 458 | 50.6 | 6.67 |
| Retrival Error | 2388 | 261.2 | 8.47 |
| Retrival Error | 624 | 69.6 | 6.44 |
| Retrival Error | 1639 | 187.8 | 5.69 |
| Retrival Error | 518 | 56.5 | 7.83 |
| Retrival Error | 569 | 60.6 | 6.04 |
| Retrival Error | 665 | 72.4 | 5.94 |
| Retrival Error | 2427 | 279.3 | 5.36 |
| Retrival Error | 473 | 51.2 | 5.05 |
| Retrival Error | 285 | 33.7 | 9.36 |
| Retrival Error | 293 | 31.5 | 7.61 |
| Retrival Error | 416 | 46.3 | 5.08 |
| Retrival Error | 530 | 56.8 | 6.87 |
| Retrival Error | 217 | 24.8 | 9.94 |
| Retrival Error | 596 | 68.2 | 5.85 |
| Retrival Error | 242 | 26.5 | 9.66 |
| Retrival Error | 721 | 79.7 | 5.99 |
| Retrival Error | 2578 | 275.5 | 5.81 |
| Retrival Error | 414 | 46.4 | 7.47 |
| Retrival Error | 152 | 17.7 | 10.99 |
| Retrival Error | 2315 | 245.7 | 5.97 |
| Retrival Error | 192 | 20.7 | 6.87 |
| Retrival Error | 6907 | 780.1 | 6.71 |
| Retrival Error | 4236 | 485.7 | 6.35 |
| Retrival Error | 333 | 37.6 | 11.03 |
| Retrival Error | 622 | 69.8 | 6.55 |
| Retrival Error | 398 | 45.4 | 10.15 |
| Retrival Error | 650 | 74.7 | 5.14 |
| Retrival Error | 221 | 24.2 | 9.79 |
| Retrival Error | 1173 | 138.3 | 6.55 |
| Retrival Error | 858 | 95.3 | 6.83 |
| Retrival Error | 618 | 67.5 | 5.50 |
| Retrival Error | 164 | 17.9 | 7.81 |
| Retrival Error | 129 | 14.4 | 10.23 |
| Retrival Error | 419 | 47.3 | 8.92 |
| Retrival Error | 266 | 30.1 | 10.74 |
| Retrival Error | 389 | 44.6 | 6.47 |
| Retrival Error | 248 | 29.2 | 10.65 |
| Retrival Error | 466 | 53.7 | 5.10 |
| Retrival Error | 218 | 23.6 | 10.92 |
| Retrival Error | 280 | 30.9 | 4.84 |

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| Retrival Error | 732 | 84.6 | 5.02 |
| Retrival Error | 260 | 31.2 | 9.06 |
| Retrival Error | 278 | 29.7 | 5.68 |
| Retrival Error | 1382 | 166.4 | 6.79 |
| Retrival Error | 1262 | 144.4 | 6.04 |
| Retrival Error | 5890 | 628.7 | 6.15 |
| Retrival Error | 2272 | 260.0 | 6.96 |
| Retrival Error | 135 | 15.5 | 9.85 |
| Retrival Error | 307 | 34.9 | 9.57 |
| Retrival Error | 300 | 33.3 | 5.07 |
| Retrival Error | 958 | 96.7 | 5.62 |
| Retrival Error | 441 | 47.8 | 9.03 |
| Retrival Error | 178 | 20.5 | 10.52 |
| Retrival Error | 472 | 51.6 | 5.16 |
| Retrival Error | 314 | 35.0 | 7.78 |
| Retrival Error | 170 | 19.4 | 10.26 |
| Retrival Error | 6391 | 740.0 | 9.11 |
| Retrival Error | 518 | 59.6 | 7.24 |
| Retrival Error | 151 | 16.3 | 10.89 |
| Retrival Error | 2801 | 308.6 | 9.51 |
| Retrival Error | 124 | 13.6 | 9.99 |
| Retrival Error | 415 | 46.5 | 4.93 |
| Retrival Error | 669 | 74.2 | 8.54 |
| Retrival Error | 522 | 58.2 | 5.29 |
| Retrival Error | 211 | 24.3 | 11.65 |
| Retrival Error | 550 | 60.8 | 7.55 |
| Retrival Error | 247 | 28.4 | 10.84 |
| Retrival Error | 258 | 29.3 | 9.77 |
| Retrival Error | 746 | 81.7 | 7.55 |
| Retrival Error | 362 | 40.2 | 7.88 |
| Retrival Error | 166 | 18.5 | 8.09 |
| Retrival Error | 248 | 27.9 | 8.46 |
| Retrival Error | 158 | 18.4 | 10.30 |
| Retrival Error | 151 | 16.3 | 10.05 |
| Retrival Error | 2017 | 223.6 | 8.75 |
| Retrival Error | 6825 | 788.0 | 5.47 |
| Retrival Error | 1300 | 149.5 | 5.71 |
| Retrival Error | 4471 | 514.5 | 5.88 |
| Retrival Error | 267 | 29.4 | 9.14 |
| Retrival Error | 947 | 106.6 | 6.47 |
| Retrival Error | 164 | 19.3 | 11.93 |
| Retrival Error | 2266 | 252.3 | 6.60 |
| Retrival Error | 1011 | 111.7 | 6.76 |
| Retrival Error | 3184 | 367.2 | 5.02 |
| Retrival Error | 363 | 39.3 | 8.09 |
| Retrival Error | 523 | 56.7 | 8.41 |
| Retrival Error | 217 | 23.3 | 6.90 |
| Retrival Error | 2083 | 244.4 | 5.34 |
| Retrival Error | 336 | 36.3 | 6.90 |
| Retrival Error | 3562 | 412.2 | 5.86 |
| Retrival Error | 846 | 93.8 | 4.77 |
| Retrival Error | 115 | 13.0 | 11.00 |
| Retrival Error | 4033 | 458.5 | 7.08 |
| Retrival Error | 1349 | 152.0 | 9.42 |
| Retrival Error | 6616 | 720.7 | 5.81 |

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|---|---|---|---|
| Retrival Error | 780 | 87.7 | 5.17 |
| Retrival Error | 3528 | 394.8 | 9.19 |
| Retrival Error | 426 | 47.6 | 5.02 |
| Retrival Error | 705 | 78.3 | 7.27 |
| Retrival Error | 201 | 23.4 | 10.93 |
| Retrival Error | 465 | 53.2 | 6.40 |
| Retrival Error | 593 | 66.7 | 5.63 |
| Retrival Error | 223 | 25.1 | 10.99 |
| Retrival Error | 2467 | 283.5 | 6.48 |
| Retrival Error | 230 | 26.3 | 5.06 |
| Retrival Error | 489 | 54.4 | 5.68 |
| Retrival Error | 134 | 14.1 | 10.26 |
| Retrival Error | 833 | 92.5 | 5.44 |
| Retrival Error | 284 | 33.1 | 4.79 |
| Retrival Error | 445 | 48.1 | 5.07 |
| Retrival Error | 2334 | 258.2 | 6.60 |
| Retrival Error | 145 | 17.2 | 10.55 |
| Retrival Error | 1941 | 222.9 | 5.82 |
| Retrival Error | 3396 | 372.6 | 4.51 |
| Retrival Error | 119 | 13.4 | 9.94 |
| Retrival Error | 325 | 36.5 | 5.64 |
| Retrival Error | 724 | 83.5 | 6.16 |
| Retrival Error | 376 | 41.8 | 5.48 |
| Retrival Error | 762 | 83.7 | 4.74 |
| Retrival Error | 148 | 16.8 | 9.38 |
| Retrival Error | 51 | 5.6 | 10.13 |
| Retrival Error | 439 | 49.6 | 9.03 |
| Retrival Error | 145 | 16.1 | 10.32 |
| Retrival Error | 2488 | 268.0 | 9.03 |
| Retrival Error | 221 | 22.3 | 11.02 |
| Retrival Error | 644 | 66.0 | 8.12 |
| Retrival Error | 151 | 17.2 | 10.54 |
| Retrival Error | 1257 | 144.7 | 6.74 |
| Retrival Error | 1261 | 138.8 | 7.24 |
| Retrival Error | 924 | 107.5 | 7.99 |
| Retrival Error | 201 | 23.3 | 8.24 |
| Retrival Error | 1951 | 221.3 | 5.72 |
| Retrival Error | 1185 | 132.3 | 5.74 |
| Retrival Error | 909 | 105.1 | 7.93 |
| Retrival Error | 283 | 31.3 | 6.99 |
| Retrival Error | 188 | 19.6 | 8.03 |
| Retrival Error | 507 | 56.4 | 6.49 |
| Retrival Error | 688 | 78.6 | 8.84 |
| Retrival Error | 460 | 52.8 | 7.44 |
| Retrival Error | 1873 | 210.7 | 6.20 |
| Retrival Error | 398 | 44.8 | 8.18 |
| Retrival Error | 1659 | 190.4 | 7.62 |
| Retrival Error | 2002 | 226.5 | 6.20 |
| Retrival Error | 4427 | 507.4 | 6.37 |
| Retrival Error | 877 | 99.0 | 5.16 |
| Retrival Error | 132 | 14.2 | 8.65 |
| Retrival Error | 2608 | 276.8 | 8.81 |
| Retrival Error | 863 | 96.1 | 8.35 |
| Retrival Error | 139 | 16.6 | 11.06 |
| Retrival Error | 920 | 104.9 | 6.10 |

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| Retrival Error | 3507 | 399.6 | 6.93 |
| Retrival Error | 158 | 17.6 | 4.86 |
| Retrival Error | 202 | 22.8 | 8.50 |
| Retrival Error | 196 | 22.0 | 5.63 |
| Retrival Error | 94 | 10.7 | 8.72 |
| Retrival Error | 241 | 26.7 | 8.15 |
| Retrival Error | 448 | 49.5 | 6.19 |
| Retrival Error | 442 | 50.3 | 7.99 |
| Retrival Error | 498 | 54.9 | 10.07 |
| Retrival Error | 498 | 57.0 | 6.83 |
| Retrival Error | 291 | 33.1 | 9.29 |
| Retrival Error | 316 | 36.5 | 6.37 |
| Retrival Error | 2458 | 267.9 | 7.83 |
| Retrival Error | 352 | 38.9 | 4.94 |
| Retrival Error | 4462 | 509.0 | 5.72 |
| Retrival Error | 182 | 21.2 | 7.34 |
| Retrival Error | 126 | 13.7 | 7.30 |
| Retrival Error | 956 | 107.8 | 8.48 |
| Retrival Error | 99 | 11.2 | 9.44 |
| Retrival Error | 113 | 12.0 | 8.94 |
| Retrival Error | 1450 | 160.7 | 6.37 |
| Retrival Error | 616 | 69.8 | 8.46 |
| Retrival Error | 284 | 31.2 | 9.32 |
| Retrival Error | 539 | 58.5 | 6.09 |
| Retrival Error | 2352 | 264.9 | 6.11 |
| Retrival Error | 874 | 95.4 | 5.73 |
| Retrival Error | 1976 | 228.8 | 5.54 |
| Retrival Error | 563 | 64.6 | 5.87 |
| Retrival Error | 214 | 23.6 | 8.29 |
| Retrival Error | 6929 | 784.5 | 8.88 |
| Retrival Error | 486 | 54.4 | 8.98 |
| Retrival Error | 116 | 13.4 | 10.20 |
| Retrival Error | 578 | 68.0 | 7.94 |
| Retrival Error | 1156 | 127.3 | 5.63 |
| Retrival Error | 1257 | 140.7 | 6.96 |
| Retrival Error | 129 | 14.5 | 5.91 |
| Retrival Error | 426 | 46.1 | 6.54 |
| Retrival Error | 2342 | 256.6 | 4.78 |
| Retrival Error | 301 | 32.5 | 8.72 |
| Retrival Error | 805 | 88.8 | 6.92 |
| Retrival Error | 135 | 15.2 | 9.44 |
| Retrival Error | 3674 | 416.6 | 6.67 |
| Retrival Error | 1647 | 184.1 | 5.54 |
| Retrival Error | 2349 | 265.4 | 5.07 |
| Retrival Error | 772 | 89.2 | 5.20 |
| Retrival Error | 599 | 68.2 | 6.02 |
| Retrival Error | 251 | 27.6 | 9.57 |
| Retrival Error | 397 | 46.4 | 8.31 |
| Retrival Error | 1641 | 186.7 | 6.84 |
| Retrival Error | 606 | 67.1 | 9.89 |
| Retrival Error | 872 | 98.2 | 7.65 |
| Retrival Error | 2330 | 261.7 | 7.58 |
| Retrival Error | 1310 | 145.5 | 5.22 |
| Retrival Error | 2884 | 324.6 | 6.79 |
| Retrival Error | 4919 | 535.9 | 6.30 |

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| Retrival Error | 231 | 26.1 | 9.99 |
| Retrival Error | 1019 | 110.0 | 9.29 |
| Retrival Error | 38 | 4.5 | 10.54 |
| Retrival Error | 4024 | 460.8 | 5.99 |
| Retrival Error | 1254 | 141.6 | 6.55 |
| Retrival Error | 184 | 21.4 | 10.20 |
| Retrival Error | 393 | 43.7 | 6.95 |
| Retrival Error | 539 | 58.7 | 6.34 |
| Retrival Error | 418 | 47.4 | 6.71 |
| Retrival Error | 963 | 107.8 | 5.67 |
| Retrival Error | 1066 | 119.1 | 6.62 |
| Retrival Error | 1752 | 202.0 | 7.55 |
| Retrival Error | 171 | 20.0 | 9.42 |
| Retrival Error | 406 | 46.0 | 8.34 |
| Retrival Error | 117 | 12.9 | 6.15 |
| Retrival Error | 1008 | 113.4 | 9.77 |
| Retrival Error | 270 | 29.9 | 7.85 |
| Retrival Error | 439 | 48.5 | 5.92 |
| Retrival Error | 900 | 101.2 | 7.40 |
| Retrival Error | 275 | 30.5 | 7.66 |
| Retrival Error | 470 | 53.6 | 5.47 |
| Retrival Error | 406 | 47.6 | 8.69 |
| Retrival Error | 327 | 36.8 | 9.23 |
| Retrival Error | 254 | 28.7 | 5.71 |
| Retrival Error | 627 | 71.5 | 8.62 |
| Retrival Error | 266 | 29.4 | 10.23 |
| Retrival Error | 512 | 58.7 | 5.58 |
| Retrival Error | 524 | 57.0 | 5.55 |
| Retrival Error | 2992 | 340.2 | 6.16 |
| Retrival Error | 424 | 48.5 | 5.69 |
| Retrival Error | 1340 | 150.9 | 8.22 |
| Retrival Error | 1033 | 119.4 | 6.98 |
| Retrival Error | 1268 | 143.5 | 6.58 |
| Retrival Error | 471 | 52.5 | 8.51 |
| Retrival Error | 2187 | 245.6 | 5.15 |
| Retrival Error | 2093 | 229.8 | 7.34 |
| Retrival Error | 2252 | 248.2 | 5.83 |
| Retrival Error | 104 | 12.7 | 11.93 |
| Retrival Error | 1714 | 175.4 | 8.27 |
| Retrival Error | 156 | 17.9 | 9.60 |
| Retrival Error | 426 | 48.6 | 7.18 |
| Retrival Error | 250 | 27.0 | 7.69 |
| Retrival Error | 246 | 28.0 | 7.42 |
| Retrival Error | 408 | 44.4 | 9.39 |
| Retrival Error | 174 | 20.2 | 8.50 |
| Retrival Error | 2022 | 228.5 | 9.29 |
| Retrival Error | 2504 | 272.9 | 6.67 |
| Retrival Error | 593 | 66.8 | 7.75 |
| Retrival Error | 490 | 55.9 | 5.16 |
| Retrival Error | 1857 | 214.2 | 5.54 |
| Retrival Error | 472 | 53.4 | 8.59 |
| Retrival Error | 367 | 42.3 | 8.63 |
| Retrival Error | 3929 | 441.5 | 7.46 |
| Retrival Error | 715 | 79.6 | 9.35 |
| Retrival Error | 570 | 65.0 | 8.29 |

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|---|---|---|---|
| Retrival Error | 798 | 88.3 | 8.82 |
| Retrival Error | 593 | 67.4 | 7.71 |
| Retrival Error | 698 | 80.4 | 7.74 |
| Retrival Error | 812 | 93.5 | 5.69 |
| Retrival Error | 367 | 40.7 | 5.69 |
| Retrival Error | 198 | 22.2 | 10.76 |
| Retrival Error | 50 | 5.9 | 9.70 |
| Retrival Error | 143 | 16.7 | 10.52 |
| Retrival Error | 124 | 14.8 | 6.39 |
| Retrival Error | 301 | 34.0 | 8.05 |
| Retrival Error | 950 | 108.7 | 7.12 |
| Retrival Error | 529 | 59.1 | 6.95 |
| Retrival Error | 255 | 29.1 | 5.00 |
| Retrival Error | 442 | 50.4 | 6.39 |
| Retrival Error | 127 | 14.6 | 9.60 |
| Retrival Error | 298 | 34.2 | 9.85 |
| Retrival Error | 366 | 42.3 | 8.69 |
| Retrival Error | 495 | 56.7 | 7.75 |
| Retrival Error | 7723 | 875.9 | 5.26 |
| Retrival Error | 340 | 40.0 | 6.02 |
| Retrival Error | 1839 | 201.3 | 6.62 |
| Retrival Error | 554 | 64.1 | 6.42 |
| Retrival Error | 117 | 12.6 | 7.96 |
| Retrival Error | 106 | 11.4 | 7.28 |
| Retrival Error | 1366 | 155.7 | 6.54 |
| Retrival Error | 2715 | 298.2 | 5.48 |
| Retrival Error | 232 | 26.6 | 5.02 |
| Retrival Error | 150 | 17.8 | 5.73 |
| Retrival Error | 1218 | 133.5 | 9.64 |
| Retrival Error | 527 | 61.8 | 7.81 |
| Retrival Error | 440 | 49.2 | 5.96 |
| Retrival Error | 162 | 17.4 | 5.14 |
| Retrival Error | 209 | 22.5 | 10.23 |
| Retrival Error | 322 | 35.9 | 8.06 |
| Retrival Error | 1189 | 134.8 | 5.92 |
| Retrival Error | 1628 | 180.5 | 6.93 |
| Retrival Error | 468 | 51.2 | 7.20 |
| Retrival Error | 585 | 63.6 | 7.24 |
| Retrival Error | 1043 | 115.0 | 6.58 |
| Retrival Error | 568 | 65.5 | 8.94 |
| Retrival Error | 2436 | 270.5 | 5.53 |
| Retrival Error | 373 | 42.8 | 5.21 |
| Retrival Error | 1978 | 227.4 | 5.30 |
| Retrival Error | 1909 | 210.6 | 8.78 |
| Retrival Error | 265 | 30.3 | 9.14 |
| Retrival Error | 399 | 45.0 | 7.58 |
| Retrival Error | 1198 | 136.3 | 8.59 |
| Retrival Error | 1230 | 140.1 | 6.80 |
| Retrival Error | 410 | 48.5 | 7.93 |
| Retrival Error | 331 | 38.2 | 5.44 |
| Retrival Error | 1385 | 155.7 | 7.20 |
| Retrival Error | 396 | 45.2 | 6.76 |
| Retrival Error | 433 | 46.9 | 9.11 |
| Retrival Error | 530 | 61.0 | 9.74 |
| Retrival Error | 2367 | 257.2 | 5.71 |

| | | | |
|---|---|---|---|
| Retrival Error | 884 | 102.2 | 5.44 |