



The University of Bradford Institutional Repository

<http://bradscholars.brad.ac.uk>

This work is made available online in accordance with publisher policies. Please refer to the repository record for this item and our Policy Document available from the repository home page for further information.

To see the final version of this work please visit the publisher's website. Access to the published online version may require a subscription.

Link to original published version: <http://dx.doi.org/10.1016/j.dib.2015.02.005>

Citation: Brioschi M, Lento S, Barcell S et al (2015) Data for proteomic analysis of murine cardiomyocytic HL1 cells treated with siRNA against tissue factor. *Data in Brief*. 3: 117-119.

Copyright statement: © 2015 Elsevier B.V. Full-text reproduced in accordance with the publisher's self-archiving policy.

This manuscript version is made available under the CC-BY-NC-ND 4.0 license
<http://creativecommons.org/licenses/by-nc-nd/4.0/>



Data article

Title: Data for proteomic analysis of murine cardiomyocytic HL-1 cells treated with siRNA against Tissue Factor

Authors: Sabrina Lento¹, Maura Brioschi¹, Simona Barcella¹, Md. Talat Nasim^{2,3,4} Elena Tremoli^{1,5},
Cristina Banfi¹

Affiliations: ¹Centro Cardiologico Monzino IRCCS, Milano, Italy; ²National Institute for Health Research Comprehensive Biomedical Research Centre, King's College London, UK; ³Department of Medical and Molecular Genetics, King's College London, UK; ⁴Bradford School of Pharmacy, School of Life Sciences, University of Bradford, UK; ⁵Dipartimento di Scienze Farmacologiche e Biomolecolari, Università degli Studi di Milano, Milano, Italy.

Contact email: cristina.banfi@ccfm.it

Abstract

This data article is related to the research article entitled **Proteomics of Tissue Factor silencing in cardiomyocytic cells reveals a new role for this coagulation factor in splicing machinery control** by Lento et al [1].

Tissue Factor (TF) is the key player in the coagulation cascade, but it has additional functions ranging from angiogenesis, tumor invasion and, in the heart, the maintenance of the integrity of cardiac cells. This article reports the nano-LC-MS^E analysis of the cardiomyocytic HL-1 cell line proteome and describes the results obtained from a Gene Ontology analysis of those proteins affected by TF-gene silencing.

Specifications Table

Subject area	<i>Biology</i>
More specific subject area	<i>Cellular proteomics</i>
Type of data	<i>Excel files</i>
How data was acquired	<i>Experiments were performed on the hybrid quadrupole-time of flight mass spectrometer SYNAPT-G1 (Waters corporation, Milford, MA, USA) coupled to the nanoAQUITY UPLC system (Waters corporation, Milford, MA, USA)</i>
Data format	<i>Processed data</i>
Experimental factors	<i>Cardiomyocytic HL-1 cells were treated with TF siRNA or a non-silencing oligonucleotide sequence</i>
Experimental features	<i>Cell lysates were digested with trypsin and analyzed by nano-LC-MS^E and</i>

	<i>processed with PLGS 2.3 (Waters corporation, Milford, MA, USA)</i>
Data source location	<i>Milan, Italy</i>
Data accessibility	<i>Data are provided with this article and are related to [1]</i>

Value of the data

- **370 proteins were identified in the cardiomyocytic HL-1 cell line proteome**
- **The data are valuable for the understanding of the protein composition of cardiomyocytes and could be reused by other scientists investigating these cells under various conditions**
- **Computational analysis of differentially expressed proteins after TF gene silencing revealed a novel role of this coagulation factor in the splicing machinery control**

Data, Experimental Design, Materials and Methods

Cardiomyocytic HL-1 cells were treated with siRNA against TF in order to obtain a $83.7 \pm 5.6\%$ reduction of TF mRNA levels in comparison with cells treated with a non-silencing oligonucleotide sequence. Cell lysates were digested with trypsin and their proteome was compared by a label free nano-LC-MS^E analysis which allowed both a qualitative and quantitative analysis of 370 proteins (Supplementary Table 1). Differentially expressed proteins were further investigated with computational analysis for the identification of over-represented GO categories (Supplementary Table 2).

Cell cultures, RNA interference and cell transfection

The HL-1 cardiomyocytes, gift of Prof. Claycomb (LSU Health Sciences Center, New Orleans, LA, USA), were cultured according to Prof. Claycomb's instructions [2]. Gene silencing was performed using small interfering RNAs (siRNA) against TF or a nonsilencing oligonucleotide sequence provided by Qiagen Inc. following the manufacturer's instructions as described in [1].

Label-free LC-MS^E analysis

The cell lysates, dissolved in 25 mmol/L NH₄HCO₃ containing 0.1% RapiGest (Waters Corporation, Milford, MA, USA) were digested as previously described [3]. The tryptic peptides were analysed by means of a nanoACQUITY system coupled to a SYNAPT-MS, a hybrid Q-TOF mass spectrometer (Waters Corporation, Milford, MA, USA), for the LC-MS^E analysis as previously described [4].

ProteinLynx GlobalSERVER (PLGS) v 2.3 (Waters Corporation, Milford, MA, USA) was used for ion detection, data clustering, and database search of the data-independent LC-MS^E data as previously explained in detail [1, 5, 6]. The entire data set of differentially expressed proteins was further filtered by considering only the identifications from data with identified peptides that replicated at least two out of three technical instrument replicates and in two out of three biological replicates [1].

Computational analysis

The list of proteins down-regulated by TF-silencing were further analysed with the BiNGO plugin (v 2.3) in the Cytoscape (v 2.7) software platform in order to make gene ontology (GO) assignments and identify over-represented GO categories for cell component and biological, as previously described [3]. Statistical analysis was obtained using the hypergeometric analysis followed by Benjamini and Hochberg's false discovery rate correction ($p < 0.001$)[7].

References

- [1] Lento S, Brioschi M, Barcella S, Nasim T, Tremoli E, Banfi C. Proteomics of Tissue Factor silencing in cardiomyocytic cells reveals a new role for this coagulation factor in splicing machinery control. *Journal of Proteomics*. in press
- [2] White SM, Constantin PE, Claycomb WC. Cardiac physiology at the cellular level: use of cultured HL-1 cardiomyocytes for studies of cardiac muscle cell structure and function. *American journal of physiology Heart and circulatory physiology*. 2004;286:H823-9
- [3] Brioschi M, Lento S, Tremoli E, Banfi C. Proteomic analysis of endothelial cell secretome: a means of studying the pleiotropic effects of Hmg-CoA reductase inhibitors. *Journal of proteomics*. 2013;78:346-61
- [4] Brioschi M, Eligini S, Crisci M, Fiorelli S, Tremoli E, Colli S, et al. A mass spectrometry-based workflow for the proteomic analysis of in vitro cultured cell subsets isolated by means of laser capture microdissection. *Analytical and bioanalytical chemistry*. 2014;406:2817-25
- [5] Geromanos SJ, Vissers JP, Silva JC, Dorschel CA, Li GZ, Gorenstein MV, et al. The detection, correlation, and comparison of peptide precursor and product ions from data independent LC-MS with data dependant LC-MS/MS. *Proteomics*. 2009;9:1683-95
- [6] Li GZ, Vissers JP, Silva JC, Golick D, Gorenstein MV, Geromanos SJ. Database searching and accounting of multiplexed precursor and product ion spectra from the data independent analysis of simple and complex peptide mixtures. *Proteomics*. 2009;9:1696-719
- [7] Maere S, Heymans K, Kuiper M. BiNGO: a Cytoscape plugin to assess overrepresentation of gene ontology categories in biological networks. *Bioinformatics*. 2005;21:3448-9

Lento S, Brioschi M, Barcella S, Nasim T, Tremoli E, Banfi C. Proteomics of Tissue Factor silencing in cardiomyocytic cells reveals a new role for this coagulation factor in splicing machinery control. *J Proteomics* (in press)

Supplementary Table 1. List of all the identified proteins in control and TF-silenced cells from three independent experiments performed in triplicate.

Accession code	Entry name	Description	MW (Da)	pI	PLGS Score	# Peptides	Coverage (%)	Products	
								Precursor RMS Mass (ppm)	RMS Mass Error (ppm)
O08749	DLDH_MOUSE	Dihydrolipoyl dehydrogenase, mitochondrial precursor	54238	7.8	436.5	10	29.3	7.6	15.3
O35114	SCR2_MOUSE	Lysosome membrane protein 2	54009	4.8	162.3	5	17.8	7.2	17.3
O35737	HNRH1_MOUSE	Heterogeneous nuclear ribonucleoprotein H (hnRNP H)	49168	5.9	353.8	9	26.3	4.8	16.5
O55143	AT2A2_MOUSE	Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	114783	5.1	1563.6	32	40.8	5.3	15.8
O70133	DHX9_MOUSE	ATP-dependent RNA helicase A	149379	6.4	489.5	18	18.1	6.1	16.9
O70456	1433S_MOUSE	14-3-3 protein sigma (Stratifin)	27695	4.6	166.0	4	16.0	3.9	15.3
O88569	ROA2_MOUSE	Heterogeneous nuclear ribonucleoproteins A2/B1 (hnRNP A2 / hnRNP B1)	37379	9.2	705.6	14	47.0	6.4	17.5
O88990	ACTN3_MOUSE	Alpha-actinin-3	102977	5.2	431.5	12	19.6	7.4	17.3
P00405	COX2_MOUSE	Cytochrome c oxidase subunit 2	25959	4.4	204.9	3	22.7	5.8	14.1
P05202	AATM_MOUSE	Aspartate aminotransferase, mitochondrial precursor	47381	9.3	765.2	14	41.2	5.9	15.2
P05213	TBA2_MOUSE	Tubulin alpha-2 chain	50119	4.8	337.2	6	23.6	4.6	14.2
P07901	HS90A_MOUSE	Heat shock protein HSP 90-alpha	84734	4.7	381.4	8	14.8	5.4	16.5
P08003	PDIA4_MOUSE	Protein disulfide-isomerase A4 precursor	71928	5.0	306.6	10	23.5	5.9	17.9
P08113	ENPL_MOUSE	Endoplasmic precursor (Heat shock protein 90 kDa beta member 1)	92418	4.5	1113.7	27	37.1	5.4	15.8
P08249	MDHM_MOUSE	Malate dehydrogenase, mitochondrial precursor	35573	8.6	1527.0	16	55.9	5.6	15.6
P09055	ITB1_MOUSE	Integrin beta-1 precursor)	88173	5.6	253.7	9	16.3	6.3	16.9
P09405	NUCL_MOUSE	Nucleolin	76676	4.5	398.5	14	20.4	5.4	17.4
P09671	SODM_MOUSE	Superoxide dismutase [Mn], mitochondrial precursor	24587	8.8	252.0	4	29.2	5.0	17.1
P0C0S6	H2AZ_MOUSE	Histone H2A.Z (H2A/z)	13544	11.0	209.7	3	29.1	5.8	15.9
P10126	EF1A1_MOUSE	Elongation factor 1-alpha 1	50082	9.3	390.4	9	29.6	6.7	15.2
P10852	4F2_MOUSE	4F2 cell-surface antigen heavy chain	58300	5.5	274.3	10	27.3	5.2	16.9
P10853	H2B1F_MOUSE	Histone H2B type 1-F/J/L (H2B 291A)	13927	10.7	699.3	5	36.0	2.7	16.0
P10854	H2B1M_MOUSE	Histone H2B type 1-M (H2B 291B)	13927	10.7	720.0	5	37.3	3.3	15.9
P11370	ENV2_MOUSE	Retrovirus-related Env polyprotein from Fv-4 locus	74405	7.7	289.1	5	12.3	6.8	15.8
P11499	HS90B_MOUSE	Heat shock protein HSP 90-beta (HSP 84)	83273	4.8	504.3	16	29.6	5.4	16.7
P12787	COX5A_MOUSE	Cytochrome c oxidase subunit 5A, mitochondrial precursor	16020	6.1	112.4	3	24.5	5.8	17.6
P14211	CALR_MOUSE	Calreticulin precursor	47964	4.1	633.3	13	46.0	6.9	16.2
P14869	RLA0_MOUSE	60S acidic ribosomal protein P0	34194	5.8	293.3	9	41.3	5.1	15.2
P15331	PERI_MOUSE	Peripherin	54234	5.2	453.2	13	33.1	4.8	17.0
P15864	H12_MOUSE	Histone H1.2 (H1 VAR.1) (H1c)	21253	11.5	244.6	4	21.3	6.1	17.3
P16627	HS70L_MOUSE	Heat shock 70 kDa protein 1L	70593	5.8	582.7	8	19.5	5.8	16.5
P16858	G3P_MOUSE	Glyceraldehyde-3-phosphate dehydrogenase	35787	8.4	229.5	6	30.2	6.3	17.1
P17156	HSP72_MOUSE	Heat shock-related 70 kDa protein 2	69697	5.4	697.0	11	24.3	6.4	16.3
P17225	PTBP1_MOUSE	Polypyrimidine tract-binding protein 1	56443	8.5	218.9	8	33.6	6.7	17.2
P17742	PPIA_MOUSE	Peptidyl-prolyl cis-trans isomerase A	17959	8.0	187.0	6	52.0	5.0	16.5
P17879	HS70B_MOUSE	Heat shock 70 kDa protein 1B (HSP70.1)	70133	5.4	384.4	6	16.5	4.8	16.5
P18242	CATD_MOUSE	Cathepsin D precursor	44925	6.8	212.2	7	28.0	7.3	16.7
P19324	SERPH_MOUSE	Serpin H1 precursor	46560	9.2	981.0	14	44.4	7.0	15.6
P19783	COX41_MOUSE	Cytochrome c oxidase subunit 4 isoform 1, mitochondrial precursor	19517	9.6	254.4	7	42.1	5.7	16.5
P20029	GRP78_MOUSE	78 kDa glucose-regulated protein precursor	72377	4.9	1798.6	24	44.6	5.2	15.9
P20108	PRDX3_MOUSE	Thioredoxin-dependent peroxide reductase, mitochondrial precursor	28109	7.4	204.0	6	38.3	7.1	17.3
P20152	VIME_MOUSE	Vimentin	53655	4.9	1529.9	27	61.3	4.6	16.2
P22752	H2A1_MOUSE	Histone H2A type 1	14126	11.5	571.7	3	26.2	4.9	15.5
P27661	H2AX_MOUSE	Histone H2A.x (H2a/x)	15133	11.2	525.4	3	27.2	5.4	15.7
P27773	PDIA3_MOUSE	Protein disulfide-isomerase A3 precursor	56585	5.9	1115.6	19	44.0	4.4	15.1
P29758	OAT_MOUSE	Ornithine aminotransferase, mitochondrial precursor	48323	6.2	652.1	15	52.4	5.9	16.1
P31001	DESM_MOUSE	Desmin	53465	5.0	511.5	17	44.8	5.5	16.7
P35486	ODPA_MOUSE	Pyruvate dehydrogenase E1 component alpha subunit, somatic form, mitochondrial precursor	43203	8.1	350.3	10	31.5	5.7	16.4
P35564	CALX_MOUSE	Calnexin precursor	67235	4.3	314.1	12	26.9	6.4	16.9

P38647	GRP75_MOUSE	Stress-70 protein, mitochondrial precursor	73482	5.8	969.1	22	44.9	4.8	15.3
P43274	H14_MOUSE	Histone H1.4 (H1 VAR.2) (H1e)	21964	11.6	205.5	3	16.1	4.5	16.9
P43277	H13_MOUSE	Histone H1.3 (H1 VAR.4) (H1d)	22086	11.5	257.8	4	19.7	5.6	16.5
P45952	ACADM_MOUSE	Medium-chain specific acyl-CoA dehydrogenase, mitochondrial precursor	46451	8.4	385.9	12	37.0	5.7	16.2
P47738	ALDH2_MOUSE	Aldehyde dehydrogenase, mitochondrial precursor	56501	7.5	292.1	11	33.2	6.1	17.2
P47955	RLA1_MOUSE	60S acidic ribosomal protein P1	11467	4.0	208.1	2	54.4	7.0	13.6
P48962	ADT1_MOUSE	ADP/ATP translocase 1	32883	10.0	960.8	14	52.7	4.5	15.6
P51150	RAB7_MOUSE	Ras-related protein Rab-7	23474	6.6	341.4	10	55.6	3.9	15.6
P51174	ACADL_MOUSE	Long-chain specific acyl-CoA dehydrogenase, mitochondrial precursor	47877	8.3	705.4	15	41.9	5.6	15.5
P51881	ADT2_MOUSE	ADP/ATP translocase 2	32910	10.0	1066.2	13	48.6	4.2	15.4
P54071	IDHP_MOUSE	Isocitrate dehydrogenase [NADP], mitochondrial precursor	58734	8.3	1027.1	21	45.0	5.8	15.8
P55258	RAB8A_MOUSE	Ras-related protein Rab-8A	23653	9.4	161.8	5	29.2	5.3	16.9
P56480	ATPB_MOUSE	ATP synthase subunit beta, mitochondrial precursor	56265	5.0	2075.3	25	70.3	5.9	15.1
P57780	ACTN4_MOUSE	Alpha-actinin-4	104911	5.1	905.8	23	36.6	6.5	17.0
P58771	TPM1_MOUSE	Tropomyosin-1 alpha chain	32660	4.5	256.6	8	27.5	4.7	17.1
P60710	ACTB_MOUSE	Actin, cytoplasmic 1	41709	5.1	1729.4	16	58.3	6.0	15.8
P61027	RAB10_MOUSE	Ras-related protein Rab-10	22526	8.6	229.5	5	29.1	4.1	16.8
P61028	RAB8B_MOUSE	Ras-related protein Rab-8B	23588	9.4	150.5	5	26.7	5.6	17.2
P61979	HNRPK_MOUSE	Heterogeneous nuclear ribonucleoprotein K	50944	5.2	414.5	13	41.2	6.2	16.4
P61982	1433G_MOUSE	14-3-3 protein gamma	28284	4.6	183.0	5	22.9	5.3	16.3
P62082	RS7_MOUSE	40S ribosomal protein S7	22113	10.6	183.1	4	34.5	7.0	15.8
P62259	1433E_MOUSE	14-3-3 protein epsilon (14-3-3E)	29155	4.4	254.0	6	32.8	4.5	16.2
P62631	EF1A2_MOUSE	Elongation factor 1-alpha 2	50422	9.3	261.4	5	16.1	5.9	15.9
P62737	ACTA_MOUSE	Actin, aortic smooth muscle	41981	5.1	1640.0	14	52.2	5.7	15.6
P62806	H4_MOUSE	Histone H4	11360	11.8	639.2	7	54.3	4.8	16.1
P62821	RAB1A_MOUSE	Ras-related protein Rab-1A	22663	5.8	204.3	4	30.3	3.9	17.0
P62897	CYC_MOUSE	Cytochrome c, somatic	11598	10.0	286.9	5	52.4	4.8	15.9
P62900	RL31_MOUSE	60S ribosomal protein L31	14453	11.0	149.0	2	18.6	3.8	14.4
P62991	UBIQ_MOUSE	Ubiquitin	8559	7.7	451.0	5	60.3	4.7	15.5
P63017	HSP7C_MOUSE	Heat shock cognate 71 kDa protein	70827	5.2	1330.3	22	48.7	5.2	15.7
P63038	CH60_MOUSE	60 kDa heat shock protein, mitochondrial precursor	60917	5.8	2569.8	27	64.9	6.1	15.9
P63101	1433Z_MOUSE	14-3-3 protein zeta/delta	27753	4.5	284.7	7	36.5	4.9	15.6
P63260	ACTG_MOUSE	Actin, cytoplasmic 2	41765	5.2	1716.8	16	59.3	5.9	15.9
P63268	ACTH_MOUSE	Actin, gamma-enteric smooth muscle	41849	5.2	1552.4	15	52.9	5.9	15.6
P68033	ACTC_MOUSE	Actin, alpha cardiac muscle 1	41991	5.1	1659.8	14	52.1	5.6	15.5
P68134	ACTS_MOUSE	Actin, alpha skeletal muscle	42023	5.1	1428.9	14	56.1	6.1	16.1
P68254	1433T_MOUSE	14-3-3 protein theta	27760	4.5	199.8	5	23.8	4.4	16.4
P68369	TBA1_MOUSE	Tubulin alpha-1 chain	50103	4.8	316.1	5	18.0	4.1	15.0
P68372	TBB2C_MOUSE	Tubulin beta-2C chain	49799	4.6	304.0	7	25.2	7.5	16.3
P68373	TBA6_MOUSE	Tubulin alpha-6 chain	49877	4.8	327.9	6	22.9	3.5	15.3
P68433	H31_MOUSE	Histone H3.1	15394	11.5	143.8	2	16.3	8.8	17.6
P68510	1433F_MOUSE	14-3-3 protein eta	28194	4.6	201.5	4	20.3	5.0	15.9
P84228	H32_MOUSE	Histone H3.2	15378	11.7	178.0	3	27.5	6.5	17.8
P84244	H33_MOUSE	Histone H3.3	15318	11.7	204.3	3	31.3	5.6	15.7
P97807	FUMH_MOUSE	Fumarate hydratase, mitochondrial precursor	54336	9.4	659.9	14	47.1	5.7	15.7
P99024	TBB5_MOUSE	Tubulin beta-5 chain	49638	4.6	346.8	8	28.5	5.6	15.3
P99027	RLA2_MOUSE	60S acidic ribosomal protein P2	11643	4.2	196.8	4	63.9	4.8	15.4
P99029	PRDX5_MOUSE	Peroxiredoxin-5, mitochondrial precursor	21883	9.1	252.5	5	40.7	5.1	16.3
O08756	HCD2_MOUSE	3-hydroxyacyl-CoA dehydrogenase type-2	27401	8.8	135.5	5	33.0	5.9	17.1
O08795	GLU2B_MOUSE	Glucosidase 2 subunit beta precursor	58755	4.2	215.1	6	15.9	5.3	17.1
O08807	PRDX4_MOUSE	Peroxiredoxin-4	31033	6.8	175.3	7	41.4	7.6	18.5
O35658	C1QBP_MOUSE	Complement component 1 Q subcomponent-binding protein, mitochondrial precursor	30993	4.6	108.7	4	11.8	6.6	15.0
O35887	CALU_MOUSE	Calumenin precursor	37040	4.3	197.9	6	34.1	7.7	18.3
O54734	OST48_MOUSE	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit precursor	48983	5.4	130.0	5	15.6	5.4	18.1

O54962	BAF_MOUSE	Barrier-to-autointegration factor	10096	5.7	75.0	2	36.2	8.1	13.6
O88844	IDHC_MOUSE	Isocitrate dehydrogenase [NADP] cytoplasmic	46630	6.5	150.8	5	18.8	7.2	17.3
P03930	ATP8_MOUSE	ATP synthase protein 8	7761	10.4	61.5	2	22.8	1.8	16.2
P05064	ALDOA_MOUSE	Fructose-bisphosphate aldolase A	39331	8.1	229.3	5	28.2	6.2	16.6
P05214	TBA3_MOUSE	Tubulin alpha-3/alpha-7 chain	49927	4.8	205.0	8	29.0	7.1	18.3
P06151	LDHA_MOUSE	L-lactate dehydrogenase A chain	36475	7.7	179.6	6	29.1	6.0	16.7
P06745	G6PI_MOUSE	Glucose-6-phosphate isomerase	62728	7.9	179.6	7	21.7	5.6	16.6
P09103	PDIA1_MOUSE	Protein disulfide-isomerase precursor	57107	4.6	313.3	12	32.9	5.9	17.4
P09411	PGK1_MOUSE	Phosphoglycerate kinase 1	44507	7.6	219.4	10	35.3	6.9	16.9
P09541	MYL4_MOUSE	Myosin light polypeptide 4	21145	4.8	142.2	4	27.9	4.6	17.5
P12970	RL7A_MOUSE	60S ribosomal protein L7a	29957	11.0	143.9	4	18.8	4.9	16.2
P14094	AT1B1_MOUSE	Sodium/potassium-transporting ATPase subunit beta-1	35171	8.8	149.4	6	25.8	5.3	17.7
P14115	RL27A_MOUSE	60S ribosomal protein L27a (L29)	16578	11.5	79.6	2	17.1	5.7	17.3
P14131	RS16_MOUSE	40S ribosomal protein S16	16435	10.6	139.6	2	17.7	3.5	17.4
P14148	RL7_MOUSE	60S ribosomal protein L7	31399	11.3	158.6	5	18.3	3.9	15.6
P14206	RSSA_MOUSE	40S ribosomal protein SA	32698	4.5	246.8	6	28.8	6.0	17.1
P14733	LMNB1_MOUSE	Lamin-B1	66744	4.9	409.1	13	31.6	6.2	17.7
P14824	ANXA6_MOUSE	Annexin A6	75838	5.2	357.6	12	25.2	6.2	17.7
P15532	NDKA_MOUSE	Nucleoside diphosphate kinase A	17196	7.3	120.6	4	36.5	6.6	15.2
P16381	PL10_MOUSE	Putative ATP-dependent RNA helicase P110	73095	6.8	267.7	6	13.7	5.2	16.5
P17047	LAMP2_MOUSE	Lysosome-associated membrane glycoprotein 2 precursor	45618	7.1	126.3	4	15.4	6.2	17.4
P17182	ENOA_MOUSE	Alpha-enolase	47111	6.4	213.7	9	35.0	6.2	17.4
P17183	ENOG_MOUSE	Gamma-enolase	47267	4.8	151.5	9	28.9	7.1	17.3
P17710	HXK1_MOUSE	Hexokinase-1	108232	6.4	420.2	13	18.7	5.9	17.6
P17751	TPIS_MOUSE	Triosephosphate isomerase	26695	7.1	137.6	7	36.0	6.3	16.8
P18572	BASI_MOUSE	Basigin precursor	42418	5.5	258.2	7	21.4	6.1	16.1
P21550	ENOB_MOUSE	Beta-enolase	46995	6.8	145.0	7	20.7	7.3	16.4
P24369	PPIB_MOUSE	Peptidyl-prolyl cis-trans isomerase B precursor	22699	9.9	152.9	6	30.7	4.8	18.3
P25444	RS2_MOUSE	40S ribosomal protein S2	31211	10.6	220.9	6	23.3	5.8	17.2
P26443	DHE3_MOUSE	Glutamate dehydrogenase 1, mitochondrial precursor	61298	8.0	218.7	9	26.5	6.8	17.6
P30999	CTND1_MOUSE	Catenin delta-1	101668	6.5	246.9	7	13.2	5.4	16.7
P32020	NLTP_MOUSE	Nonspecific lipid-transfer protein	59087	7.2	187.2	6	17.7	6.1	15.9
P35276	RAB3D_MOUSE	Ras-related protein Rab-3D	24400	4.6	123.5	4	22.6	7.9	18.0
P35700	PRDX1_MOUSE	Peroxiredoxin-1	22162	8.2	123.3	5	35.6	7.5	18.1
P35762	CD81_MOUSE	CD81 antigen	25811	5.4	68.3	2	17.4	6.9	17.3
P35980	RL18_MOUSE	60S ribosomal protein L18	21631	12.2	126.5	3	19.0	4.7	15.4
P41216	ACSL1_MOUSE	Long-chain-fatty-acid--CoA ligase 1	77873	6.8	263.1	10	19.7	7.4	17.9
P42125	D3D2_MOUSE	3,2-trans-enoyl-CoA isomerase, mitochondrial precursor	32057	8.9	196.3	6	27.7	5.1	15.7
P43275	H11_MOUSE	Histone H1.1 (H1 VAR.3) (H1a)	21771	11.4	103.6	2	13.6	6.3	17.9
P45878	FKBP2_MOUSE	FK506-binding protein 2 precursor	15334	9.3	73.2	2	17.1	3.2	15.3
P47911	RL6_MOUSE	60S ribosomal protein L6	33488	11.1	145.1	6	22.3	5.1	16.9
P47962	RL5_MOUSE	60S ribosomal protein L5	34378	10.1	117.0	4	19.7	5.6	18.2
P47963	RL13_MOUSE	60S ribosomal protein L13 (A52)	24290	12.0	176.8	6	23.5	4.8	16.4
P49312	ROA1_MOUSE	Heterogeneous nuclear ribonucleoprotein A1	34175	9.5	191.8	8	34.6	6.8	17.4
P51863	VA0D_MOUSE	Vacuolar ATP synthase subunit d	40275	4.7	117.2	6	29.6	5.4	17.1
P53986	MOT1_MOUSE	Monocarboxylate transporter 1	53232	7.4	151.5	4	13.4	4.3	14.6
P53994	RAB2A_MOUSE	Ras-related protein Rab-2A	23532	6.1	159.8	6	42.7	5.9	16.7
P56135	ATPK_MOUSE	ATP synthase f chain, mitochondrial	10337	10.2	106.3	2	27.1	1.3	16.2
P56371	RAB4A_MOUSE	Ras-related protein Rab-4A	23922	5.7	145.1	3	19.9	7.0	17.1
P56391	CX6B1_MOUSE	Cytochrome c oxidase subunit VIb isoform 1	10064	9.0	94.5	4	51.1	6.5	17.6
P56394	COX17_MOUSE	Cytochrome c oxidase copper chaperone	6779	7.7	82.3	2	38.3	5.1	15.5
P57759	ERP29_MOUSE	Endoplasmic reticulum protein ERp29 precursor	28805	5.8	110.2	4	20.3	4.8	15.7
P58252	EF2_MOUSE	Elongation factor 2 (EF-2)	95252	6.4	378.1	14	23.9	6.9	18.3
P58774	TPM2_MOUSE	Tropomyosin beta chain	32816	4.5	222.7	5	21.9	4.2	16.4

P59279	RAB2B_MOUSE	Ras-related protein Rab-2B	24183	6.2	140.2	4	31.7	5.7	16.5
P60335	PCBP1_MOUSE	Poly(rC)-binding protein 1	37473	6.7	156.9	6	34.7	5.2	18.4
P60843	IF4A1_MOUSE	Eukaryotic initiation factor 4A-I	46124	5.2	218.4	6	22.3	5.2	17.7
P61205	ARF3_MOUSE	ADP-ribosylation factor 3	20587	7.4	144.8	3	27.0	4.8	14.6
P61358	RL27_MOUSE	60S ribosomal protein L27	15787	11.0	97.9	3	31.3	5.3	15.8
P61750	ARF4_MOUSE	ADP-ribosylation factor 4	20383	7.0	132.8	3	30.0	6.4	16.8
P62075	TIM13_MOUSE	Mitochondrial import inner membrane translocase subunit Tim13	10450	8.3	81.1	2	27.7	4.8	14.6
P62242	RS8_MOUSE	40S ribosomal protein S8	24190	10.7	165.9	4	27.1	4.8	15.2
P62264	RS14_MOUSE	40S ribosomal protein S14	16262	10.5	116.2	4	32.4	6.5	17.4
P62267	RS23_MOUSE	40S ribosomal protein S23	15797	11.0	91.5	3	28.4	6.2	17.7
P62270	RS18_MOUSE	40S ribosomal protein S18	17707	11.4	133.5	4	26.1	2.7	16.0
P62301	RS13_MOUSE	40S ribosomal protein S13	17211	10.9	130.7	4	30.5	7.2	16.8
P62305	RUXE_MOUSE	Small nuclear ribonucleoprotein E	10796	9.8	80.9	2	20.5	4.1	14.7
P62309	RUXG_MOUSE	Small nuclear ribonucleoprotein G	8490	9.6	60.7	1	15.8	2.7	14.4
P62315	SMD1_MOUSE	Small nuclear ribonucleoprotein Sm D1	13273	12.0	74.2	3	38.2	6.2	15.0
P62317	SMD2_MOUSE	Small nuclear ribonucleoprotein Sm D2	13518	10.4	121.3	4	37.6	6.0	16.5
P62320	SMD3_MOUSE	Small nuclear ribonucleoprotein Sm D3	13907	10.7	112.3	4	37.4	5.9	15.9
P62702	RS4X_MOUSE	40S ribosomal protein S4, X isoform	29579	10.6	159.0	6	26.7	4.9	15.8
P62827	RAN_MOUSE	GTP-binding nuclear protein Ran	24407	7.3	140.8	4	26.3	5.5	16.5
P62830	RL23_MOUSE	60S ribosomal protein L23	14856	10.9	89.1	4	39.8	6.2	16.1
P62835	RAP1A_MOUSE	Ras-related protein Rap-1A precursor	20973	6.5	133.5	2	23.8	4.2	16.3
P62852	RS25_MOUSE	40S ribosomal protein S25	13733	10.6	96.0	2	12.8	2.3	14.7
P62874	GBB1_MOUSE	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta 1	37353	5.5	157.6	5	20.6	5.6	17.2
P62880	GBB2_MOUSE	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta 2	37307	5.5	163.4	5	18.6	3.5	17.1
P62889	RL30_MOUSE	60S ribosomal protein L30	12775	10.0	122.5	4	46.5	6.5	15.8
P62908	RS3_MOUSE	40S ribosomal protein S3	26657	10.0	244.9	9	43.3	4.4	16.5
P62918	RL8_MOUSE	60S ribosomal protein L8	28007	11.5	110.0	4	24.0	5.7	15.7
P62962	PROF1_MOUSE	Profilin-1 (Profilin I)	14947	8.5	101.2	4	39.6	5.2	15.3
P63011	RAB3A_MOUSE	Ras-related protein Rab-3A	24954	4.7	135.4	4	21.4	5.8	17.7
P63323	RS12_MOUSE	40S ribosomal protein S12	14515	7.0	110.3	4	34.3	5.3	16.6
P67778	PHB_MOUSE	Prohibitin	29801	5.4	165.6	7	35.3	6.0	16.0
P67984	RL22_MOUSE	60S ribosomal protein L22	14749	9.6	79.0	3	35.0	4.9	14.2
P68040	GBLP_MOUSE	Guanine nucleotide-binding protein subunit beta 2-like 1	35054	7.6	243.7	9	45.8	7.0	16.2
P68368	TBA4_MOUSE	Tubulin alpha-4 chain	49892	4.8	136.4	5	19.7	5.7	16.1
P70168	IMB1_MOUSE	Importin beta-1 subunit	97090	4.5	235.8	7	16.9	6.8	16.8
P70333	HNRH2_MOUSE	Heterogeneous nuclear ribonucleoprotein H' (hnRNP H')	49248	5.9	296.2	8	24.3	5.5	16.2
P70372	ELAV1_MOUSE	ELAV-like protein 1	36046	9.5	245.5	8	31.5	6.7	15.6
P70404	IDH3G_MOUSE	Isocitrate dehydrogenase [NAD] subunit gamma, mitochondrial precursor	42758	9.3	170.2	9	37.5	7.6	18.2
P70696	H2B1A_MOUSE	Histone H2B type 1-A	14227	10.7	234.5	4	28.8	7.9	16.0
P84078	ARF1_MOUSE	ADP-ribosylation factor 1	20683	6.4	125.5	2	17.1	3.3	14.4
P84104	SFRS3_MOUSE	Splicing factor, arginine/serine-rich 3 (Pre-mRNA-splicing factor SRP20)	19317	12.0	118.6	4	28.0	5.2	15.5
P97351	RS3A_MOUSE	40S ribosomal protein S3a	29865	10.2	240.3	7	34.2	6.5	15.8
P97370	AT1B3_MOUSE	Sodium/potassium-transporting ATPase subunit beta-3	31755	8.6	102.0	4	20.5	6.9	18.8
P97450	ATP5J_MOUSE	ATP synthase coupling factor 6, mitochondrial precursor	12488	9.8	131.4	3	37.4	3.8	14.6
P99028	UCRH_MOUSE	Ubiquinol-cytochrome c reductase complex 11 kDa protein, mitochondrial precursor	10427	4.6	111.9	2	24.7	8.8	14.0
Q00P19	HNRL2_MOUSE	Heterogeneous nuclear ribonucleoprotein U-like protein 2	84947	4.6	200.7	6	12.0	7.5	16.1
Q01768	NDKB_MOUSE	Nucleoside diphosphate kinase B	17351	7.4	121.5	4	39.4	6.8	16.6
Q01853	TERA_MOUSE	Transitional endoplasmic reticulum ATPase	89251	5.0	426.7	14	30.4	6.3	17.3
Q02566	MYH6_MOUSE	Myosin-6 (Myosin heavy chain 6)	223425	5.4	890.5	25	18.3	5.8	16.5
Q03265	ATPA_MOUSE	ATP synthase subunit alpha, mitochondrial precursor	59715	9.5	1905.0	25	54.2	5.1	15.7
Q05920	PYC_MOUSE	Pyruvate carboxylase, mitochondrial precursor	129602	6.2	341.9	12	17.5	7.6	17.5
Q06185	ATP5I_MOUSE	ATP synthase e chain, mitochondrial	8230	9.7	100.1	3	46.3	6.6	15.8
Q07133	H1T_MOUSE	Histone H1t	21527	12.1	150.4	3	18.4	4.2	17.4
Q07417	ACADS_MOUSE	Short-chain specific acyl-CoA dehydrogenase, mitochondrial precursor	44918	9.0	309.0	10	36.6	5.8	17.3

Q3THW5	H2AV_MOUSE	Histone H2AV (H2A.F/Z)	13500	11.0	191.6	2	15.2	8.4	15.1
Q501J6	DDX17_MOUSE	Probable ATP-dependent RNA helicase DDX17	72354	8.6	360.4	8	15.9	5.3	16.2
Q60597	ODO1_MOUSE	2-oxoglutarate dehydrogenase E1 component, mitochondrial precursor	116043	6.5	708.4	23	32.6	7.1	16.5
Q60668	HNRPD_MOUSE	Heterogeneous nuclear ribonucleoprotein D0 (hnRNP D0)	38330	7.9	217.8	6	20.6	5.4	16.9
Q60749	SAM68_MOUSE	KH domain-containing, RNA-binding, signal transduction-associated protein 1	48340	8.9	135.1	5	17.6	6.8	15.6
Q60930	VDAC2_MOUSE	Voltage-dependent anion-selective channel protein 2	31712	7.4	379.8	10	45.9	6.1	16.3
Q60931	VDAC3_MOUSE	Voltage-dependent anion-selective channel protein 3	30733	9.0	290.6	7	39.7	6.0	15.9
Q60932	VDAC1_MOUSE	Voltage-dependent anion-selective channel protein 1	32331	8.7	400.8	10	52.4	6.3	16.2
Q60961	LAP4A_MOUSE	Lysosomal-associated transmembrane protein 4A	26839	6.1	119.0	3	17.4	7.1	13.2
Q61029	LAP2B_MOUSE	Lamina-associated polypeptide 2 isoforms beta/delta/epsilon/gamma	50264	9.8	244.5	8	28.1	6.8	17.2
Q61207	SAP_MOUSE	Sulfated glycoprotein 1 precursor	61381	4.9	374.7	6	16.5	5.3	16.8
Q61595	KTN1_MOUSE	Kinectin	152497	5.5	683.4	17	22.0	6.9	17.5
Q61656	DDX5_MOUSE	Probable ATP-dependent RNA helicase DDX5	69276	9.1	413.3	11	20.6	5.4	16.4
Q61696	HS70A_MOUSE	Heat shock 70 kDa protein 1A	70036	5.4	402.7	8	20.7	5.9	16.4
Q61879	MYH10_MOUSE	Myosin-10	228853	5.3	767.3	32	25.1	6.6	17.4
Q61937	NPM_MOUSE	Nucleophosmin	32539	4.4	326.3	6	34.1	7.4	16.0
Q61990	PCBP2_MOUSE	Poly(rC)-binding protein 2	38197	6.3	138.4	4	19.9	4.8	16.6
Q62095	DDX3Y_MOUSE	ATP-dependent RNA helicase DDX3Y	73382	7.3	254.7	6	15.6	6.6	16.0
Q62167	DDX3X_MOUSE	ATP-dependent RNA helicase DDX3X	73056	6.8	254.7	7	16.3	6.2	16.6
Q62425	NDUA4_MOUSE	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 4	9320	9.9	208.4	3	32.5	3.1	16.5
Q64012	RALY_MOUSE	RNA-binding protein Raly	33137	9.1	142.1	6	23.6	5.8	17.4
Q64310	SURF4_MOUSE	Surfeit locus protein 4	30360	7.8	131.9	3	15.7	4.5	14.9
Q64433	CH10_MOUSE	10 kDa heat shock protein, mitochondrial	10955	9.1	360.5	6	50.5	4.5	16.0
Q64436	ATP4A_MOUSE	Potassium-transporting ATPase alpha chain 1	113942	5.5	281.9	8	13.9	6.8	16.5
Q64475	H2B1B_MOUSE	Histone H2B type 1-B	13943	10.7	723.4	5	36.3	4.2	15.8
Q64478	H2B1H_MOUSE	Histone H2B type 1-H	13911	10.7	644.3	5	32.3	3.1	16.0
Q64516	GLPK_MOUSE	Glycerol kinase	57421	5.3	230.9	7	25.6	6.0	19.0
Q64518	AT2A3_MOUSE	Sarcoplasmic/endoplasmic reticulum calcium ATPase 3	113535	5.5	498.6	12	17.8	6.4	16.3
Q64522	H2A2B_MOUSE	Histone H2A type 2-B	14004	11.3	563.1	2	26.4	4.1	15.7
Q64523	H2A2C_MOUSE	Histone H2A type 2-C	13979	11.3	646.6	3	27.1	4.1	15.0
Q64524	H2B2E_MOUSE	Histone H2B type 2-E	13984	10.7	519.8	3	29.5	3.0	16.1
Q64525	H2B2B_MOUSE	Histone H2B type 2-B	13911	10.7	720.8	6	38.1	5.1	16.4
Q68FD5	CLH_MOUSE	Clathrin heavy chain	191433	5.4	732.8	23	22.3	6.8	18.2
Q6GSS7	H2A2A_MOUSE	Histone H2A type 2-A	14095	10.9	528.0	3	25.1	4.1	15.0
Q6PHN9	RAB35_MOUSE	Ras-related protein Rab-35	23010	8.4	142.5	3	24.5	4.8	16.2
Q6PIC6	AT1A3_MOUSE	Sodium/potassium-transporting ATPase alpha-3 chain	111620	5.1	514.2	12	19.0	5.3	16.1
Q6PIE5	AT1A2_MOUSE	Sodium/potassium-transporting ATPase alpha-2 chain precursor	112145	5.2	572.4	13	19.9	5.5	16.3
Q6ZWN5	RS9_MOUSE	40S ribosomal protein S9	22577	11.1	147.8	4	18.4	3.3	15.1
Q6ZWY9	H2B1C_MOUSE	Histone H2B type 1-C/E/G	13897	10.7	784.4	6	41.3	4.4	16.0
Q7TMK9	HNRPQ_MOUSE	Heterogeneous nuclear ribonucleoprotein Q	69589	8.8	240.3	8	20.4	6.7	18.3
Q7TMM9	TBB2A_MOUSE	Tubulin beta-2A chain	49874	4.6	314.5	6	22.4	5.9	15.1
Q7TPR4	ACTN1_MOUSE	Alpha-actinin-1	103003	5.1	857.5	21	33.0	6.0	16.2
Q7TPV4	MBB1A_MOUSE	Myb-binding protein 1A	151941	9.3	424.3	16	20.2	6.9	18.3
Q8BFR5	EFTU_MOUSE	Elongation factor Tu, mitochondrial precursor	49477	7.3	354.6	11	35.6	6.1	16.1
Q8BFU2	H2A3_MOUSE	Histone H2A type 3	14121	11.1	528.0	3	25.1	4.1	15.0
Q8BG05	ROA3_MOUSE	Heterogeneous nuclear ribonucleoprotein A3	39627	9.2	237.1	8	31.4	7.1	17.4
Q8BH59	CMC1_MOUSE	Calcium-binding mitochondrial carrier protein Aralar1	74522	8.3	251.1	10	26.1	6.3	17.1
Q8BH95	ECHM_MOUSE	Enoyl-CoA hydratase, mitochondrial precursor	31454	8.6	211.6	6	28.0	5.7	17.2
Q8BH97	RCN3_MOUSE	Reticulocalbin-3 precursor	37978	4.6	133.7	4	17.1	6.5	16.0
Q8BHC1	RB39B_MOUSE	Ras-related protein Rab-39B	24620	7.8	137.3	4	26.6	8.5	17.9
Q8BHN3	GANAB_MOUSE	Neutral alpha-glucosidase AB precursor	106843	5.6	278.2	12	17.9	6.4	16.7
Q8BIG7	CMTD1_MOUSE	Catechol-O-methyltransferase domain-containing protein 1	28942	8.4	107.5	4	29.0	6.3	15.2
Q8BL97	SFRS7_MOUSE	Splicing factor, arginine/serine-rich 7	30798	12.3	100.0	5	16.2	6.2	16.7
Q8BLF1	ADCL1_MOUSE	Arylacetamide deacetylase-like 1	45710	6.6	248.1	7	30.0	7.2	15.2

Q8BMK4	CKAP4_MOUSE	Cytoskeleton-associated protein 4	63653	5.3	300.6	10	23.8	7.0	18.8
Q8BSL7	ARF2_MOUSE	ADP-ribosylation factor 2	20732	6.2	137.4	4	32.8	4.6	14.2
Q8BWT1	THIM_MOUSE	3-ketoacyl-CoA thiolase, mitochondrial	41831	8.1	520.4	13	56.9	6.7	14.9
Q8CAQ8	IMMT_MOUSE	Mitochondrial inner membrane protein	83848	6.2	307.5	12	21.5	7.4	17.6
Q8CG50	RAB43_MOUSE	Ras-related protein Rab-43	23248	5.5	139.8	4	28.0	6.8	16.0
Q8CGC7	SYEP_MOUSE	Bifunctional aminoacyl-tRNA synthetase	169828	7.4	504.0	18	19.2	6.9	18.3
Q8CGP0	H2B3B_MOUSE	Histone H2B type 3-B	13899	10.7	506.3	4	31.3	4.1	15.9
Q8CGP1	H2B1K_MOUSE	Histone H2B type 1-K	13911	10.7	733.9	6	38.1	3.7	16.1
Q8CGP2	H2B1P_MOUSE	Histone H2B type 1-P	13983	10.7	731.0	5	37.5	3.6	16.1
Q8CGP5	H2A1F_MOUSE	Histone H2A type 1-F	14152	11.5	487.3	2	28.5	3.9	14.6
Q8CGP6	H2A1H_MOUSE	Histone H2A type 1-H	13941	11.5	584.5	3	26.6	4.3	16.0
Q8CGP7	H2A1K_MOUSE	Histone H2A type 1-K	14140	11.5	529.1	4	48.5	6.3	15.3
Q8K0D5	EFG1_MOUSE	Elongation factor G 1, mitochondrial precursor	83496	6.5	310.1	12	26.1	6.5	16.5
Q8K2B3	DHSA_MOUSE	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial precursor	72539	7.0	367.8	14	35.4	6.4	16.9
Q8K310	MATR3_MOUSE	Matrin-3	94571	5.8	264.3	11	19.8	7.9	17.4
Q8K386	RAB15_MOUSE	Ras-related protein Rab-15	24303	5.4	145.0	4	29.4	6.1	17.2
Q8QZT1	THIL_MOUSE	Acetyl-CoA acetyltransferase, mitochondrial precursor	44787	8.7	358.4	9	36.8	5.3	16.1
Q8R081	HNRPL_MOUSE	Heterogeneous nuclear ribonucleoprotein L	60085	6.7	260.7	10	29.4	7.6	17.5
Q8R2G4	NAR3_MOUSE	Ecto-ADP-ribosyltransferase 3 precursor	48270	9.2	140.5	3	20.0	5.8	15.4
Q8R429	AT2A1_MOUSE	Sarcoplasmic/endoplasmic reticulum calcium ATPase 1	109355	4.9	704.2	11	17.4	5.2	15.5
Q8VDN2	AT1A1_MOUSE	Sodium/potassium-transporting ATPase alpha-1 chain precursor	112909	5.1	959.7	25	30.2	4.4	14.9
Q8VDW0	DDX39_MOUSE	ATP-dependent RNA helicase DDX39	49036	5.3	239.4	6	24.3	6.0	15.7
Q8VEM8	MPCP_MOUSE	Phosphate carrier protein, mitochondrial precursor (PTP)	39606	9.5	212.2	8	32.2	5.9	17.0
Q8VII6	SFPQ_MOUSE	Splicing factor, proline- and glutamine-rich	75394	9.8	245.1	9	18.2	5.9	15.9
Q91V41	RAB14_MOUSE	Ras-related protein Rab-14	23881	5.8	154.4	5	31.2	5.9	17.2
Q91VD9	NDUS1_MOUSE	NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial precursor	79697	5.4	245.7	10	24.4	6.9	17.5
Q91VR2	ATPG_MOUSE	ATP synthase gamma chain, mitochondrial precursor	32865	9.4	167.3	6	24.0	5.4	16.0
Q91W90	TXND5_MOUSE	Thioredoxin domain-containing protein 5 precursor	46385	5.4	115.1	6	18.2	5.1	16.3
Q91WD5	NDUS2_MOUSE	NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial precursor	52591	6.5	190.9	7	24.5	6.4	17.7
Q91YQ5	RIB1_MOUSE	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 67 kDa subunit precursor	68485	6.0	251.8	8	20.0	6.4	17.5
Q91YT0	NDUV1_MOUSE	NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial precursor	50801	8.2	166.9	7	24.5	6.4	17.2
Q91Z83	MYH7_MOUSE	Myosin-7	222739	5.5	862.6	22	17.6	5.8	16.3
Q91ZR1	RAB4B_MOUSE	Ras-related protein Rab-4B	23613	5.7	117.5	4	21.9	7.0	19.9
Q921F2	TADBP_MOUSE	TAR DNA-binding protein 43	44519	6.3	247.0	7	24.8	5.0	16.4
Q921H8	THIKA_MOUSE	3-ketoacyl-CoA thiolase A, peroxisomal precursor	43925	8.5	133.6	5	19.2	5.3	17.1
Q921M3	SF3B3_MOUSE	Splicing factor 3B subunit 3	135464	5.0	261.4	12	15.8	8.0	19.3
Q922F4	TBB6_MOUSE	Tubulin beta-6 chain	50058	4.6	246.4	5	16.3	6.1	15.9
Q922Q8	LRC59_MOUSE	Leucine-rich repeat-containing protein 59	34855	10.0	129.1	4	16.6	6.5	15.8
Q922R8	PDIA6_MOUSE	Protein disulfide-isomerase A6 precursor	48070	4.8	417.0	10	31.5	6.0	15.5
Q923S9	RAB30_MOUSE	Ras-related protein Rab-30	23043	4.7	109.5	3	27.1	5.0	16.9
Q99020	ROAA_MOUSE	Heterogeneous nuclear ribonucleoprotein A/B	30812	8.1	403.1	7	29.1	5.0	15.9
Q99JI6	RAP1B_MOUSE	Ras-related protein Rap-1b precursor	20811	5.5	131.5	2	31.0	4.5	17.2
Q99JY0	ECHB_MOUSE	Trifunctional enzyme subunit beta, mitochondrial precursor	51353	9.7	351.5	11	31.4	5.5	16.6
Q99K48	NONO_MOUSE	Non-POU domain-containing octamer-binding protein	54506	9.4	202.9	6	16.9	5.6	17.5
Q99KF1	TMED9_MOUSE	Transmembrane emp24 domain-containing protein 9 precursor	24993	6.8	133.7	4	36.4	6.9	16.2
Q99KI0	ACON_MOUSE	Aconitate hydratase, mitochondrial precursor	85410	7.8	1716.5	31	51.4	5.9	16.0
Q99KV1	DNJBB_MOUSE	DnaJ homolog subfamily B member 11 precursor	40529	5.9	111.9	5	22.2	6.4	18.1
Q99LC5	ETFA_MOUSE	Electron transfer flavoprotein subunit alpha, mitochondrial precursor	35017	8.5	469.6	13	53.7	4.8	15.5
Q99LP6	GRPE1_MOUSE	GrpE protein homolog 1, mitochondrial precursor	24291	8.6	147.9	4	22.3	4.5	16.8
Q9CQ62	DECR_MOUSE	2,4-dienoyl-CoA reductase, mitochondrial precursor	36190	9.3	183.2	7	27.3	6.0	15.9
Q9CQA3	DHSB_MOUSE	Succinate dehydrogenase [ubiquinone] iron-sulfur protein, mitochondrial precursor	31792	8.7	147.5	4	18.7	5.2	15.7
Q9CQQ7	AT5F1_MOUSE	ATP synthase B chain, mitochondrial precursor	28930	9.4	147.9	4	21.0	4.8	15.6
Q9CQR4	THEM2_MOUSE	Thioesterase superfamily member 2	15172	9.3	143.0	4	30.6	5.1	15.2
Q9CQV8	1433B_MOUSE	14-3-3 protein beta/alpha	28068	4.6	204.0	5	27.8	5.3	17.1

Q9CQX2	CYB5B_MOUSE	Cytochrome b5 type B precursor	16307	4.6	106.1	4	44.3	7.8	16.9
Q9CR57	RL14_MOUSE	60S ribosomal protein L14	23549	11.5	115.9	5	23.5	5.4	15.1
Q9CR68	UCRI_MOUSE	Ubiquinol-cytochrome c reductase iron-sulfur subunit, mitochondrial precursor	29349	8.9	112.9	4	26.2	6.6	15.3
Q9CWF2	TBB2B_MOUSE	Tubulin beta-2B chain	49920	4.6	288.6	6	23.8	6.4	15.9
Q9CXW4	RL11_MOUSE	60S ribosomal protein L11	20239	10.0	176.5	3	21.6	3.8	14.2
Q9CXY6	ILF2_MOUSE	Interleukin enhancer-binding factor 2	43035	5.0	147.2	5	29.1	6.1	17.1
Q9CZ13	UQCR1_MOUSE	Ubiquinol-cytochrome-c reductase complex core protein 1, mitochondrial precursor	52735	5.7	254.3	9	31.8	7.5	17.8
Q9CZS1	AL1B1_MOUSE	Aldehyde dehydrogenase X, mitochondrial precursor	57516	6.6	318.2	11	31.9	6.4	15.7
Q9CZU6	CISY_MOUSE	Citrate synthase, mitochondrial precursor	51703	8.7	548.2	11	28.9	5.8	15.7
Q9CZX8	RS19_MOUSE	40S ribosomal protein S19	16075	10.8	148.5	5	33.8	5.3	16.4
Q9D051	ODPB_MOUSE	Pyruvate dehydrogenase E1 component subunit beta, mitochondrial precursor	38912	6.4	472.1	10	40.3	5.5	15.3
Q9D0E1	HNRPM_MOUSE	Heterogeneous nuclear ribonucleoprotein M	77597	8.9	369.7	16	30.2	6.6	16.8
Q9D0K2	SCOT_MOUSE	Succinyl-CoA:3-ketoacid-coenzyme A transferase 1, mitochondrial precursor	55953	8.7	570.4	14	40.1	5.2	16.4
Q9D0M3	CY1_MOUSE	Cytochrome c1 heme protein, mitochondrial precursor	35304	9.4	155.8	5	32.3	6.0	15.7
Q9D1G1	RAB1B_MOUSE	Ras-related protein Rab-1B	22173	5.4	208.1	5	36.2	5.6	17.6
Q9D2G2	ODO2_MOUSE	Dihydropolyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial precursor	21902	5.6	112.5	2	10.9	7.4	15.5
Q9D2U9	H2B3A_MOUSE	Histone H2B type 3-A	13985	10.8	509.8	4	32.5	5.0	16.4
Q9D6F9	TBB4_MOUSE	Tubulin beta-4 chain	49519	4.6	265.4	5	19.8	6.9	14.3
Q9D6R2	IDH3A_MOUSE	Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial precursor	39613	6.3	512.0	9	31.3	5.0	15.7
Q9D8E6	RL4_MOUSE	60S ribosomal protein L4 (L1)	47124	11.4	222.6	9	26.6	5.1	15.8
Q9DB20	ATPO_MOUSE	ATP synthase O subunit, mitochondrial precursor	23348	10.4	312.4	8	51.5	7.1	16.0
Q9DB77	UQCR2_MOUSE	Ubiquinol-cytochrome-c reductase complex core protein 2, mitochondrial precursor	48205	9.6	293.8	11	35.8	5.5	15.5
Q9DBG6	RPN2_MOUSE	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 63 kDa subunit precursor	69020	5.4	267.9	10	26.8	5.8	16.2
Q9DBJ1	PGAM1_MOUSE	Phosphoglycerate mutase 1	28813	6.8	132.0	4	26.0	4.9	17.0
Q9DCN2	NCB5R_MOUSE	NADH-cytochrome b5 reductase	34105	8.5	135.3	5	27.1	4.7	17.0
Q9DCS9	NDUBA_MOUSE	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 10	21010	8.1	167.2	4	26.0	3.7	14.7
Q9DCT2	NDUS3_MOUSE	NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial precursor	30188	6.4	173.3	6	31.4	6.6	16.3
Q9DCW4	ETFB_MOUSE	Electron transfer flavoprotein subunit beta	27605	8.2	507.5	11	53.9	5.9	15.2
Q9DCX2	ATP5H_MOUSE	ATP synthase D chain, mitochondrial	18737	5.4	193.7	6	50.8	7.2	16.0
Q9DD03	RAB13_MOUSE	Ras-related protein Rab-13	22755	9.9	120.7	2	19.6	5.1	17.0
Q9ERD7	TBB3_MOUSE	Tubulin beta-3 chain	50386	4.6	261.7	5	19.5	6.3	15.6
Q9ES82	POPD2_MOUSE	Popeye domain-containing protein 2	41224	5.5	98.8	4	15.1	5.2	16.5
Q9JI91	ACTN2_MOUSE	Alpha-actinin-2	103588	5.2	456.5	13	22.1	6.6	17.4
Q9JIK5	DDX21_MOUSE	Nucleolar RNA helicase 2	93524	9.5	307.9	8	17.0	6.3	16.3
Q9JJZ2	TBA8_MOUSE	Tubulin alpha-8 chain	50019	4.8	140.1	6	20.8	4.8	15.6
Q9JLZ6	HIC2_MOUSE	Hypermethylated in cancer 2 protein	72626	6.1	167.5	5	9.7	6.6	16.4
Q9QVP4	MLRA_MOUSE	Myosin regulatory light chain 2, atrial isoform	19437	4.5	100.7	4	38.6	7.0	15.4
Q9QXY1	ZO3_MOUSE	Tight junction protein ZO-3	99264	6.4	205.6	8	14.4	6.2	18.4
Q9QY76	VAPB_MOUSE	Vesicle-associated membrane protein-associated protein B	26929	7.8	116.5	3	24.3	6.0	17.0
Q9QZ23	NFU1_MOUSE	NFU1 iron-sulfur cluster scaffold homolog	22125	4.0	113.2	3	22.4	6.4	14.8
Q9WTP6	KAD2_MOUSE	Adenylate kinase isoenzyme 2, mitochondrial	25589	7.2	271.0	8	42.8	5.6	15.7
Q9WUM5	SUCA_MOUSE	Succinyl-CoA ligase [GDP-forming] subunit alpha, mitochondrial precursor	34972	9.8	149.8	6	25.9	6.2	16.2
Q9WV27	AT1A4_MOUSE	Sodium/potassium-transporting ATPase alpha-4 chain	114742	5.4	307.6	8	14.6	7.1	17.3
Q9WV55	VAPA_MOUSE	Vesicle-associated membrane protein-associated protein A	27837	8.6	151.4	5	30.1	6.5	15.7
Q9Z0X1	AIFM1_MOUSE	Apoptosis-inducing factor 1, mitochondrial precursor	66723	9.5	355.2	13	31.3	6.0	16.0
Q9Z110	P5CS_MOUSE	Delta 1-pyrroline-5-carboxylate synthetase	87242	7.2	291.2	9	17.6	6.1	17.7
Q9Z1N5	UAP56_MOUSE	Spliceosome RNA helicase Bat1	49004	5.3	284.4	9	29.8	6.1	17.3
Q9Z1W8	AT12A_MOUSE	Potassium-transporting ATPase alpha chain 2	114653	6.1	338.2	9	15.0	6.5	17.2
Q9Z204	HNRPC_MOUSE	Heterogeneous nuclear ribonucleoproteins C1/C2	34363	4.7	242.6	7	24.3	4.1	14.7
Q9Z219	SUCB1_MOUSE	Succinyl-CoA ligase [ADP-forming] beta-chain, mitochondrial precursor	50082	6.6	195.7	8	22.7	5.3	17.9
Q9Z2X1	HNRPF_MOUSE	Heterogeneous nuclear ribonucleoprotein F	45700	5.2	371.8	7	25.0	5.4	16.8

Supplementary Table 2: BiNGO analysis of biological process and cell component categories for the proteins down-regulated after TF silencing, or unique in control cells.

Selected ontology file :GO_Cellular_Component

Selected annotation file : M_musculus_default

Overrepresentation

Selected statistical test : Hypergeometric test

Selected correction : Benjamini & Hochberg False Discovery Rate (FDR) correction

Selected significance level : 0.05

Testing option : Test cluster versus whole annotation

GO-ID	p-value	corr p-value	x	nX	N	Description	Genes in test set
5681	6.35E-05	2.48E-03	3	118	11	spliceosome	Q9Z1N5 Q921M3 Q64012
30529	1.55E-04	3.03E-03	4	433	11	ribonucleoprotein complex	Q9Z1N5 Q921M3 Q64012 Q60668
43231	7.61E-04	7.49E-03	10	6369	11	intracellular membrane-bounded organelle	Q8VIJ6 Q9Z1N5 Q8VDW0 Q501J6 Q8K310 Q921M3 Q05920 P63011 C
43227	7.68E-04	7.49E-03	10	6375	11	membrane-bounded organelle	Q8VIJ6 Q9Z1N5 Q8VDW0 Q501J6 Q8K310 Q921M3 Q05920 P63011 C
5634	1.23E-03	8.49E-03	8	3987	11	nucleus	Q8VIJ6 Q9Z1N5 Q8VDW0 Q501J6 Q8K310 Q921M3 Q64012 Q60668
44424	1.31E-03	8.49E-03	11	8672	11	intracellular part	Q8VIJ6 Q9Z1N5 P10126 Q8VDW0 Q501J6 Q8K310 Q921M3 Q05920 F
5622	1.91E-03	1.06E-02	11	8975	11	intracellular	Q8VIJ6 Q9Z1N5 P10126 Q8VDW0 Q501J6 Q8K310 Q921M3 Q05920 F
43229	2.46E-03	1.08E-02	10	7219	11	intracellular organelle	Q8VIJ6 Q9Z1N5 Q8VDW0 Q501J6 Q8K310 Q921M3 Q05920 P63011 C
43226	2.48E-03	1.08E-02	10	7225	11	organelle	Q8VIJ6 Q9Z1N5 Q8VDW0 Q501J6 Q8K310 Q921M3 Q05920 P63011 C

Selected ontology file : GO_Biological_Process

Selected annotation file : M_musculus_default

Overrepresentation

Selected statistical test : Hypergeometric test

Selected correction : Benjamini & Hochberg False Discovery Rate (FDR) correction

Selected significance level : 0.05

Testing option : Test cluster versus whole annotation

GO-ID	p-value	corr p-value	x	nX	N	Description	Genes in test set
16071	1.15E-09	1.62E-07	6	267	8	mRNA metabolic process	Q8VIJ6 Q9Z1N5 Q8VDW0 Q921M3 Q64012 Q60668
6395	1.80E-08	1.27E-06	5	182	8	RNA splicing	Q8VIJ6 Q9Z1N5 Q8VDW0 Q921M3 Q64012
6397	6.34E-08	2.61E-06	5	234	8	mRNA processing	Q8VIJ6 Q9Z1N5 Q8VDW0 Q921M3 Q64012
16070	7.41E-08	2.61E-06	6	535	8	RNA metabolic process	Q8VIJ6 Q9Z1N5 Q8VDW0 Q921M3 Q64012 Q60668
6394	5.35E-07	1.51E-05	5	359	8	RNA processing	Q8VIJ6 Q9Z1N5 Q8VDW0 Q921M3 Q64012
10467	2.48E-04	5.82E-03	6	2135	8	gene expression	Q8VIJ6 Q9Z1N5 Q8VDW0 Q921M3 Q64012 Q60668
6139	4.39E-04	8.85E-03	6	2361	8	nucleobase, nucleoside, nucleotide and nucleic acid	Q8VIJ6 Q9Z1N5 Q8VDW0 Q921M3 Q64012 Q60668
48790	5.65E-04	8.85E-03	1	1	8	maintenance of presynaptic active zone structure	P63011

50975	5.65E-04	8.85E-03	1	1	8 sensory perception of touch	P63011
31338	1.13E-03	1.33E-02	1	2	8 regulation of vesicle fusion	P63011
51602	1.13E-03	1.33E-02	1	2	8 response to electrical stimulus	P63011
31630	1.13E-03	1.33E-02	1	2	8 regulation of synaptic vesicle fusion to presynaptic	P63011
16188	2.82E-03	3.06E-02	1	5	8 synaptic vesicle maturation	P63011
43283	3.65E-03	3.67E-02	6	3449	8 biopolymer metabolic process	Q8VIJ6 Q9Z1N5 Q8VDW0 Q921M3 Q64012 Q60668
8099	4.51E-03	4.24E-02	1	8	8 synaptic vesicle endocytosis	P63011
43488	5.63E-03	4.76E-02	1	10	8 regulation of mRNA stability	Q60668
44238	5.74E-03	4.76E-02	7	5333	8 primary metabolic process	Q8VIJ6 Q9Z1N5 Q8VDW0 Q921M3 Q05920 Q64012 Q60668
43487	6.76E-03	4.79E-02	1	12	8 regulation of RNA stability	Q60668
3016	6.76E-03	4.79E-02	1	12	8 respiratory system process	P63011
44237	6.79E-03	4.79E-02	7	5473	8 cellular metabolic process	Q8VIJ6 Q9Z1N5 Q8VDW0 Q921M3 Q05920 Q64012 Q60668
16079	7.32E-03	4.91E-02	1	13	8 synaptic vesicle exocytosis	P63011

Q64012|Q60668
Q64012|Q60668

Q63011|Q64012|Q60668
Q63011|Q64012|Q60668
Q64012|Q60668
Q64012|Q60668