

Supplementary Table 1 Target sequences used in shNrf2 and shMfn2 interference vectors

Target gene	Target sequence (DNA)
shMfn2-1	GCTGGACAGCTGGATTGATAA
shMfn2-2	GGCAGTTTGAGGAGTGCATTT
shMfn2-3	GCACTTTGTCAGTCCCAAGAA
shNrf2-1	GCAGCAGGACATTGAGCAA
shNrf2-2	GTAAGAAGCCAGATATTAA
shNrf2-3	GCAGGACATGGATTTGATTGA
Scrambled shRNA	GATGAAATGGGTAAAGTACAT

Supplementary Table 2 Primers used in quantitative real-time PCR analysis

Gene	Forward primer (5'-3')	Reverse primer (5'-3')
<i>Actb</i>	AGGGAAATCGTGCGTGACA	CCAAGAAGGAAGGCTGGAAA
<i>Bip</i>	TCATCGGACGCACTTGGA	AACCACCTTGAATGGCAAGAA
<i>Xbp1</i>	AGCAGCAAGTGGTGGATTTG	GAGTTTTCTCCCGTAAAAGCTGA
<i>sXbp1</i>	GGTCTGCTGAGTCCGCAGCAGG	AGGCTTGGTGTATACATGG
<i>p16</i>	TTGCCCATCATCATCACCT	GGGTTTTCTTGGTGAAGTTCTG
<i>p21</i>	CACAGCTCAGTGGACTGGAA	CCACCACCACACACCATAGA
<i>Il6</i>	AGTTGCCTTCTTGGGACTGATG	AACCTTTTTCTCATTTCACGATTT
<i>Ccl2</i>	AGGTCCCTGTCATGCTTCTGG	AGGTGAGTGGGGCGTTAACTG
<i>Nrf2</i>	AAGAAGTGGGCAACTGTGGTC	AAGGTGGGATTTGAGTCTAAGGA
<i>Gcl2</i>	GGCCACTATCTGCCCAATTGT	CCTCTCTCCTCCCGTGTCTATC
<i>Nqo1</i>	CTGGGAGGAGACCCCACTCTA	CACAGAGAGGCCAAACTTGTCT
<i>Mfn2</i>	CTTGAAGACACCCACAGGAACAC	GCACTTCGCTGATACCCCTG

Protein_ID	Protein_Qscore	Protein_Mass	PeptideSeqs	PeplsUni que	Uniqu e_Pep tide_ Num	Unique _Spectr a_Num	Coverage	Peptide_Query	Sameset	Description
sp Q922B2 SYD C_MOUSE	22.67344835	57111.18204	ALHHGIDLEK;AYIDSFR;EIVD AAEDYAK;FQTEIQT VSK;IISAA SEGGANVFTVSYFK;LEYCEAL AMLR;YGISSMIQSQEKPD	1;1;1;1;1; 1;1	7	8	0.1657	16585;16584;8843 ;19521;18144;359 26;24083;32141	-	Aspartate--tRNA ligase, cytoplasmic OS=Mus musculus OX=10090 GN=Dars1 PE=1 SV=2 Heat shock protein beta-1 OS=Mus musculus OX=10090 GN=Hspb1 PE=1 SV=3 Collagen alpha-1(IV) chain OS=Mus musculus OX=10090 GN=Col4a1 PE=1 SV=4 Glucose-6-phosphate 1- dehydrogenase X OS=Mus musculus OX=10090 GN=G6pdx PE=1 SV=3 26S proteasome regulatory subunit 7 OS=Mus musculus OX=10090 GN=Psmc2 PE=1 SV=5 Programmed cell death 6- interacting protein OS=Mus musculus OX=10090 GN=Pdc6ip PE=1 SV=3
sp P14602 HSPB 1_MOUSE	4.376559455	22999.72017	QLSSGVSEIR		1	1	0.0478	14746	-	
sp P02463 CO4 A1_MOUSE	3.33516677	160578.5105	ILYHGYSLLYVQGNER		1	1	0.0096	35329	-	
sp Q00612 G6P D1_MOUSE	2.487130441	59224.76624	LTVDDIR		1	1	0.0136	7687	-	
sp P46471 PRS7 _MOUSE	4.376559455	48617.13337	FDDGAGGDNEVQR		1	1	0.03	24412	-	
sp Q9WU78 PD C6I_MOUSE	4.376559455	95964.20877	LLDEEEATDNDLR HAF AQYNMDQFTPVK;ESCD SALR;FITHAPPGFEFNEFNDV R;FTITPPSAQVVGVLK;IEGYD DQVLITEHGD LGNSR;IQVHY YEDGNVQLVSHK;LLLNNNDNL	1;1;1;1;1; 1;0;0	1	1	0.015	28416	-	
sp P47753 CAZA 1_MOUSE	22.8760401	32919.30637	LR ISFLENNLEQLTK;LFVQDLATR ;SLSALGNVISALAEGSTYVPYR	1;1;1;1;1; 1;0;0	6	7	0.4266	28986;38342;3834 1;10701;37859;29 007;39657;37053; 37054;18683	-	F-actin-capping protein subunit alpha-1 OS=Mus musculus OX=10090 GN=Capza1 PE=1 SV=4 Kinesin-1 heavy chain OS=Mus musculus OX=10090 GN=Kif5b PE=1 SV=3 Calpain-2 catalytic subunit OS=Mus musculus OX=10090 GN=Capn2 PE=1 SV=4 Glutamine--fructose-6- phosphate aminotransferase [isomerizing] 2 OS=Mus musculus OX=10090 GN=Gfpt2 PE=1 SV=3
sp Q61768 KINH _MOUSE	15.6594622	109483.6735	;TGAEGAVLDEAK	1;1;1;1	4	5	0.0582	28811;14311;4013 8;40137;17488	-	
sp O08529 CAN 2_MOUSE	9.910394664	79821.76659	ALEEAGFK;EFYILWTK;YLNQD YETLR	1;1;1	3	3	0.0371	8631;15524;22429	-	
sp Q9Z2Z9 GFP T2_MOUSE	2.088488785	76959.72921	NTPVFR		1	1	0.0088	5349	sp P47856 G FPT1_MOUS E	

sp Q9JLI8 SART3_MOUSE	25.07034797	109549.8248	DLVLSVHSR;EAALVQQEEEEK; EFESAIVEAAR;EHVYELFER;EL WDSIMTR;VLSGAVAAEAAEA K;YANMWLEYYNLER	1;1;1;1;1; 1;1	7	7	0.079	13221;21112;1945 9;19455;17167;21 575;32599	-	antigen recognized by T-cells 3 OS=Mus musculus OX=10090 GN=Sart3 PE=1 SV=1 Developmentally-regulated GTP-binding protein 2 OS=Mus musculus OX=10090 GN=Drg2 PE=1 SV=1 Coatomer subunit gamma-1 OS=Mus musculus OX=10090 GN=Copg1 PE=1 SV=1 BAG family molecular chaperone regulator 3 OS=Mus musculus OX=10090 GN=Bag3 PE=1 SV=2 Nucleolar protein 56 OS=Mus musculus OX=10090 GN=Nop56 PE=1 SV=2 Leucine-rich repeat flightless- interacting protein 2 OS=Mus musculus OX=10090 GN=Lrrfip2 PE=1 SV=1 Eukaryotic translation initiation factor 4 gamma 1 OS=Mus musculus OX=10090 GN=Eif4g1 PE=1 SV=1 Eukaryotic translation initiation factor 4 gamma 3 OS=Mus musculus OX=10090 GN=Eif4g3 PE=1 SV=2 OX=10090 GN=Bgn PE=1 SV=1 Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial OS=Mus musculus OX=10090 GN=Dlat PE=1 SV=2
sp Q9QXB9 DRG2_MOUSE	4.376559455	40692.3582	TADVVMMLDATK ILHLLGQEGPK;SSPEPVALTES	1	1	1	0.0357	24813	-	
sp Q9QZE5 COPG1_MOUSE	14.56969932	97450.36435	ETEYVIR;TLEEAVGNIVK;VFNE TPINPR	1;1;1;1	4	4	0.0572	18944;36670;1790 1;18345	-	
sp Q9JLV1 BAG3_MOUSE	4.376559455	61822.18331	VQGLEQAVDSFEGK	1	1	1	0.0243	27760	-	
sp Q9D6Z1 NOP56_MOUSE	4.376559455	64424.10342	EAVVQAEEAAAEITR	1	1	1	0.0259	29481	-	
sp Q91WK0 LRRF2_MOUSE	4.376559455	47118.95182	AEQDIATLEQSISR;AMVSNA QLDNEK	1;0	1	1	0.0627	29073;22598	-	
sp Q6NZJ6 IF4G1_MOUSE	11.14175487	175967.4635	EAVGDLLDAFK;GVIDLIFEK;IH NAENIQPGEQK;LLTTIGK;QS NWVPR	1;1;1;0;1	4	5	0.0294	18044;13438;2703 7;27038;5602;925 9	-	
sp Q80XI3 IF4G3_MOUSE	22.66450094	174780.5953	DKADDDVFEK;ELIVEFSKPLLP VGR;ELSAEELSQR;GVIDLVFE K;LLTTIGK;SPAPVQTATTAPK; SPAIVATEVQR;VDTAVIK	1;1;1;1;0; 1;1;1	7	7	0.0513	18162;31378;1751 7;13065;5602;209 92;14143;5596	-	
sp P28653 PGS1_MOUSE	4.376559455	41612.60036	IQAIELEDLLR	1	1	1	0.0298	22384	-	
sp Q8BMF4 ODP2_MOUSE	22.22001487	67898.68002	AAPAAAAAMAPPGPR;ILVPE GTR;LQPHEFQGGTFTISNLG MFGIK;VAPAPAGVFTDIPISNI R;VPEANSSWMDTVIR;YLEKPI TMLL	1;1;1;1;1; 1	6	8	0.1355	22615;23134;2261 6;9217;42204;338 10;29777;19441	-	

sp Q80U63 MFN2_MOUSE	51.96307685	86132.78524	ISEVLAR;HMAEVNASPLK;IFFVSAK;LIMDSLHIAAQEQR;LSRPNIFILNNR;MFEFQNFER;NTELDPVTTEEQVLDVK;QFEECISQSAVK;QFVEYASEK;QITEEVE R;QLELLAQDYK;QVSTAMAE 1;1;1;0;1;IR;STVINAMLWDK;VG GTDG 1;1;1;1;1;HEAFLATEGSEEK;WDASASEP 1;1;1;1;1;EYMEEVR 1	15	16	0.2523	33037;8060;19160;7138;30121;26500;20300;20822;35403;25681;15547;12613;19436;20404;21774;36157;33188	-	Mitofusin-2 OS=Mus musculus OX=10090 GN=Mfn2 PE=1 SV=3
sp Q811U4 MFN1_MOUSE	26.21361191	83672.76182	HLEEEIAR;IASEDDLVEIQGYR;IFFVSAK;IKEVTEEVANK;LAVIGEVL SR;LTWTTR;QQFVNYAT 1;1;0;1;1;EK;TKFEQHTIR 1;1;1	7	7	0.1012	12419;29823;7138;20717;14125;6345;19649;17465	-	Mitofusin-1 OS=Mus musculus OX=10090 GN=Mfn1 PE=1 SV=3 Inverted formin-2 OS=Mus musculus OX=10090 GN=Inf2 PE=1 SV=1
sp Q0GNC1 INF2_MOUSE	4.376559455	138473.8521	SGQLLWEALENLVNR	1	1	0.0118	32200	-	sp Q9D646 KRT34_MOUSE E;sp Q61897 KT33B_MOUSE SE;sp Q8K0Y2 KT33A_MOUSE
sp Q61765 K1H1_MOUSE	2.353900435	47086.70197	LNVEVDAAPTVDLNR	1	1	0.0361	30132	USE	Keratin, type I cuticular Ha1 OS=Mus musculus OX=10090 GN=Krt31 PE=1 SV=2
sp Q9JIK5 DDX21_MOUSE	6.41119496	93493.23054	AAVIGDVIR;SGIDILVGTPGR 1;1	2	2	0.0247	10081;18283	-	Nucleolar RNA helicase 2 OS=Mus musculus OX=10090 GN=Ddx21 PE=1 SV=3
sp P07091 S10A4_MOUSE	2.30220692	11713.73981	ELPSFLGK	1	1	0.0792	9401	-	Protein S100-A4 OS=Mus musculus OX=10090 GN=S100a4 PE=1 SV=1
sp P14733 LMNB1_MOUSE	15.75591646	66744.75899	ASAPATPLSPTR;DAALATALGDKK;IQELEDMLAK;LSSEMNTSTVNSAR;NQNSWGTGEDVK 1;1;1;1;1	5	5	0.102	17748;17931;18442;27506;23088	-	Lamin-B1 OS=Mus musculus OX=10090 GN=Lmnb1 PE=1 SV=3
sp Q8VDM4 PSMD2_MOUSE	3.33516677	100138.6704	LNILDTLSK	1	1	0.0099	12982	-	26S proteasome non-ATPase regulatory subunit 2 OS=Mus musculus OX=10090 GN=Psm2 PE=1 SV=1
sp Q9WUA3 PFKAP_MOUSE	3.33516677	85400.31793	DLLFQPVAELK	1	1	0.014	21104	-	ATP-dependent 6-phosphofructokinase, platelet type OS=Mus musculus OX=10090 GN=Pfkp PE=1 SV=1
sp Q921U8 SMTN_MOUSE	15.73828299	100227.6823	AADGSTVGTVTK;LGSVTHVTFSHASPGNR;NTITHISNPGTVTR;TALASPTPTR 1;1;1;1	4	4	0.0585	15735;34314;27874;12908	-	Smoothelin OS=Mus musculus OX=10090 GN=Smtn PE=1 SV=2

sp P63101 1433 Z_MOUSE	4.376559455	27753.74364	SVTEQGAELSNEER	1	1	1	0.0571	28793	-	14-3-3 protein zeta/delta OS=Mus musculus OX=10090 GN=Ywhaz PE=1 SV=1 FERM, ARHGEF and pleckstrin domain-containing protein 1 OS=Mus musculus OX=10090 GN=Farp1 PE=1 SV=1 Protein S100-A11 OS=Mus musculus OX=10090 GN=S100a11 PE=1 SV=1 Protein PRRC2C OS=Mus musculus OX=10090 GN=Prrc2c PE=1 SV=3 Nck-associated protein 1 OS=Mus musculus OX=10090 GN=Nckap1 PE=1 SV=2 1 OS=Mus musculus OX=10090 GN=Pdlim1 PE=1 SV=4 Unconventional myosin-Va OS=Mus musculus OX=10090 GN=Myo5a PE=1 SV=2
sp F8VPU2 FARP 1_MOUSE	9.29065637	118800.5882	LALWEGR;QSIIVAASSR;SLIFP NFEPLHK	1;1;1	3	3	0.0277	8054;13385;26124	-	
sp P50543 S10A B_MOUSE	4.376559455	11075.48758	TEFLSFMNTELAATFK	1	1	1	0.1633	34019	-	
sp Q3TLH4 PRC 2C_MOUSE	7.043219307	310702.9989	SSSQIPAPPPVTK;TVNQSV AAPTvk	1;1	2	2	0.0091	23250;23347	-	
sp P28660 NCKP 1_MOUSE	3.33516677	128700.4028	NNNQQLAQLQK	1	1	1	0.0098	21945	-	
sp O70400 PDLI 1_MOUSE	3.33516677	35751.8869	QSTSFLVLQEILESDGKGDPN KPSGFR	1	1	1	0.0826	45938	-	
sp Q99104 MYO 5A_MOUSE	8.473555234	215401.5906	LTNLEGVYNSETEK;NQSIIVSG ESGAGK;YQNLLNEFSR	1;1;1	3	3	0.0205	29663;23449;2144 8	-	sp P26041 M OES_MOUSE Ezrin OS=Mus musculus ;sp P26043 R OX=10090 GN=Ezr PE=1 ADI_MOUSE SV=3
sp P26040 EZRI MOUSE	3.33516677	69363.62775	IGFPWSEIR	1	1	1	0.0154	15689	-	Phosphatidylcholine-sterol acyltransferase OS=Mus musculus OX=10090 GN=Lcat PE=1 SV=2
sp P16301 LCAT _MOUSE	3.07602819	49715.17637	TLEHINAILLGAYR	1	1	1	0.032	29417	-	Cullin-associated NEDD8- dissociated protein 1 OS=Mus musculus OX=10090 GN=Cand1 PE=1 SV=2
sp Q6ZQ38 CAN D1_MOUSE	4.376559455	136244.6062	ISGSILNELIGLVR	1	1	1	0.0114	27208	-	Ras-related protein Rab-15 OS=Mus musculus OX=10090 GN=Rab15 PE=1 SV=1
sp Q8K386 RAB 15_MOUSE	4.376559455	24303.14794	IQIWDTAGQER	1	1	1	0.0519	22510	-	Synaptic functional regulator FMR1 OS=Mus musculus OX=10090 GN=Fmr1 PE=1 SV=1
sp P35922 FMR1 _MOUSE	3.33516677	68946.88576	LQIDEQLR;TADGSLQSASSEG SR	0;1	1	1	0.0375	12909;26395	-	Fragile X mental retardation syndrome-related protein 2 OS=Mus musculus OX=10090 GN=Fxr2 PE=1 SV=1
sp Q9WVR4 FXR 2_MOUSE	11.28290275	73697.72562	AGYTTDESSSSSLHTTR;EITEG DEVEVYSR;LQIDEQLR;SYLEF SEDSVQVPR	1;1;0;1	3	4	0.0773	33206;33207;2821 9;12909;30663	-	

sp Q61584 FXR1_MOUSE	16.98050671	76175.31756	EISEGDEVEVYSR;LPPPPDIK;L QIDEQLR;RGPNYTSGYGTNS ELSNPSETESER;VIQEIVDK;V NILSDMHLR	1;1;0;1;1; 1	5	5	0.1064	27884;9010;12909 ;44813;10867;186 71	-	Fragile X mental retardation syndrome-related protein 1 OS=Mus musculus OX=10090 GN=Fxr1 PE=1 SV=2 axonemal microtubules protein 2 OS=Mus musculus OX=10090 GN=Togaram2 PE=2 SV=1 AP-2 complex subunit beta OS=Mus musculus OX=10090 GN=Ap2b1 PE=1 SV=1 AP-3 complex subunit beta-1 OS=Mus musculus OX=10090 GN=Ap3b1 PE=1 SV=2 Protein-lysine 6-oxidase OS=Mus musculus OX=10090 GN=Lox PE=1 SV=1 Collagen alpha-1(V) chain OS=Mus musculus OX=10090 GN=Col5a1 PE=1 SV=2 Extended synaptotagmin-1 OS=Mus musculus OX=10090 GN=Esyt1 PE=1 SV=2
sp Q3TYG6 TGRM2_MOUSE	2.150691262	108906.7948	EGLPLR	1	1	1	0.007	6793	-	
sp Q9DBG3 AP2B1_MOUSE	9.410885765	104516.0508	AAMIWIVGEYAER;LAPPLVTL LSGEPEVQYVALR;LQNNNVY TIAK	1;1;1	3	3	0.048	27808;40101;2126 0	-	
sp Q9Z1T1 AP3B1_MOUSE	6.375443949	122663.7427	EGSTAQLIINTEK;LLDSITVPV AR	1;1	2	2	0.0217	25089;18250	-	
sp P28301 LYOX_MOUSE	13.59176943	46671.46763	HWFAQGFSPSGAR;MVGDD PYNPYK;TPILLLR;VSVNPSYLV PESDYTNNVVR	1;1;1;1	4	4	0.1241	26261;21934;7518 ;39915	-	
sp O88207 CO5A1_MOUSE	2.563085783	183563.941	GDDGEVGPR	1	1	1	0.0049	9714	-	
sp Q3U7R1 ESYT1_MOUSE	3.33516677	121478.4252	SSELAALLSVFLER	1	1	1	0.0137	29796	-	

sp O08638 MYH11_MOUSE	144.4686962	226887.6756	LAHLEER;VCHLVGINVTDFT	1;0;1	37	58	0.323	4;28726;36606;36	-	Myosin-11 OS=Mus musculus OX=10090 GN=Myh11 PE=1 SV=1
			AAAER;TFHIFYLLAGAK;TGV	1;1;1;1;1;						
			MISELEVR;SLEADLMQLQEDL	0;0;1;1;1;						
			AIPK;SHEAQVQEMR;SKHES	1;1;1;1;0;						
			QQLTAMKVIQR;QRYEILAAAN	1;1;0;0;0;						
			AFGNAKTVK;QQQLTAMK;Q	1;1;1;1;1;						
			NPILEAFGNAK;QLLQANPILE	1;1;1;0;1;						
			K;QLHEYETELEDERK;QLLQA	1;1;1;1;0;						
			AEELASSLSGR;QGFEAASIKEE	0;0;1;0;1;						
			AQK;QACILMIK;QADLEKEEL	0;1;0;1;1;						
			WQWWWR;NTDQASMPDNTA	1;0;1;1;0;						
			QLFNHTMFILEQEEYQR;LRN							
			LQNEVESVTGMLNEAEGK;LQ							
			;LDAFLVLEQLR;LEVNMQALK;							
			VWVPSEK;KQELEEILHEMEAR							
			AQIAELK;KLEVQLQDLQSK;KL							
			NSK;KLEGDASDFHEQIADLQ							
			DQLLAEEK;KLEDDILVMDDQ							
			R;KATLQAEQLSNELATER;KF							
			QEDLDSER;ITDVIMAFQAMC							
			GANIETYLLEK;IRELEGHISDL							
			QLEEQVEQEAR;INFDVTGYIV							
			LEQFKR;HVSTLNIQLSDSK;IA							
			ELTEQLEQFK;HTQAVEELTEQ							
			QLLAEEK;FVADLWK;HTQAVE							
			PDNTAAQK;EVLLQVEDER;FD							
			QADFAIEALAK;ERNTDQASM							
			NEAMGR;EMEGLSQQYEEK;E							
			QSILCTGESGAGK;ELDEATES							
			SLGSQQLQDTQELLQEETR;ED							
			LGEELEALK;DRAEAEAR;DVA							
			DEIFATSK;DKTEFSIIHYAGK;D							
			ALEIQMEEMK;CNGVLEGIR;							

sp Q9JKF1 IQGA 1_MOUSE	89.67047523	188624.2412	VDYYK;ATGLHFR;EEVQAGV DAANSAAQQYQR;EEYLLLR;E KLEAYQHLYFYLLQTNPTYLAK; FALGISAINAEVDSGDVGR;F MDSVIFTLYNYASNQR;FQPG ETLTEILETPATNEQEAHQ; GLQTQNSDWYMK;IFYPETTD IYDR;ITLQDVVSHSK;LEGVLA EVAQHYQDTLIR;LFQTALQEE IK;LPYDVTPEQALSHEEVK;LQ QTYSALNSK;MFLGDNAHLSII NEYLSQSYQK;NGVYLAK;QIL APVVK;QSGQTDPLQKEEVQ AGVDAANSAAQQYQR;TDPV DIYK;TLQALQIPAAK;VDFTEE EINNMK;VNVNLLIFLLNK;YQ ELINDIAK	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;	25	28	0.2004	23179;27175;6895 ;37140;10669;445 00;44499;34708;3 7558;45617;26856 ;28420;19628;196 27;37399;22621;3 5830;35828;20463 ;43683;6050;8734; 46451;11092;1727 8;26804;24980;18 989	-	Ras GTPase-activating-like protein IQGAP1 OS=Mus musculus OX=10090 GN=lqgap1 PE=1 SV=2 Dolichyl- diphosphooligosaccharide-- protein glycosyltransferase subunit 2 OS=Mus musculus OX=10090 GN=Rpn2 PE=1 SV=1 Polypyrimidine tract-binding protein 1 OS=Mus musculus OX=10090 GN=Ptpb1 PE=1 SV=2 Tricarboxylate transport protein, mitochondrial OS=Mus musculus OX=10090 GN=Slc25a1 PE=1 SV=1
sp Q9DBG6 RPN 2_MOUSE	15.01203548	69020.03138	EETVLATVQALQTASHLSQQ ADLR;NIVEIEDLVAR;QEIQH LFR;TPFSLVGNVFEFNFK	1;1;1;1	4	4	0.0935	43966;24974;1455 6;31664	-	
sp P17225 PTBP 1_MOUSE	10.45227845	56442.95838	EGQEDQGLTK;NNQFQALLQ YADPVSAQHAK;VTPQSLFILF GVYGDVQR	1;1;1	3	4	0.0911	15678;39806;3718 2;37183	-	
sp Q8JZU2 TXTP _MOUSE	6.527250718	33909.9025	FGMFEFLSNHMR;GTYQGLTA TVLK	1;1	2	2	0.0772	27984;20435	-	

										Histone H2A type 1-B OS=Mus musculus OX=10090 GN=H2ac4 PE=1 SV=1 >sp C0HKE2 H2A1C_MOUSE Histone H2A type 1-C OS=Mus musculus OX=10090 GN=H2ac6 PE=1 SV=1 >sp C0HKE3 H2A1D_MOUSE Histone H2A type 1-D OS=Mus musculus OX=10090 GN=H2ac7 PE=1 SV=1
										sp Q64523 H2A2C_MOUSE Histone H2A type 1-E OS=Mus musculus OX=10090 GN=H2ac8 PE=1 SV=1 >sp P0C0S6 H2AZ_MOUSE Histone H2A type 1-G OS=Mus musculus OX=10090 GN=H2ac11 PE=1 SV=1 >sp Q8BFE H2A3_MOUSE Histone H2A type 1-I OS=Mus musculus OX=10090 GN=H2ac13 PE=1 SV=1 >sp C0HKE5 H2A1G_MOUSE Histone H2A type 1-N OS=Mus musculus OX=10090 GN=Hist1h2an PE=1 SV=1 >sp C0HKE6 H2A1I_MOUSE Histone H2A type 1-O OS=Mus musculus OX=10090 GN=Hist1h2ao PE=1 SV=1 >sp C0HKE7 H2A1N_MOUSE Histone H2A type 1-P OS=Mus musculus OX=10090 GN=Hist1h2ap PE=1 SV=1
sp C0HKE1 H2A1B_MOUSE	3.07602819	14126.94964	AGLQFPVGR	1	1	1	0.0692	10905		A1H_MOUSE Extracellular matrix protein 1 OS=Mus musculus OX=10090 GN=Ecm1 PE=1 SV=2 OX=10090 GN=Nes PE=1 SV=1
sp Q61508 ECM1_MOUSE	2.150691262	62791.85414	DILTLDLSR	1	1	1	0.0161	13767	-	
sp Q6P5H2 NES T_MOUSE	4.376559455	206999.6142	TLEEQNQLLSAELGGLR	1	1	1	0.0091	34362	-	protein 3 OS=Mus musculus OX=10090 GN=Fhl3 PE=1 SV=2
sp Q9R059 FHL3_MOUSE	2.150691262	31772.86874	HFHEGCFR	1	1	1	0.0277	15181	-	lyase 1 OS=Mus musculus OX=10090 GN=Sgpl1 PE=1 SV=1
sp Q8R0X7 SGPL1_MOUSE	5.025240252	63635.72731	GSSVVMYSNEK;GWNFNLYQ FPR	1;1	2	2	0.0387	18779;26113	-	

sp Q9R0P3 ESTD_MOUSE	12.08828568	31299.31594	AFSGYLGPDESK;LQEGYDHS YYFIATFIADHIR;SGYQQAASE HGLVVIAPDTSPR AAQAGVAVGDWVLNIDGEN AGSLTHIEAQNK;HSQPATPT PLQNR;ITGEIMHALK;SHAFS HV;TSIVQAAAGGGTGGGSN NGK;VLEEGGFEEK;VVLEGPA	1;1;1	3	3	0.195	21035;43593;4032 8	-	S-formylglutathione hydrolase OS=Mus musculus OX=10090 GN=Esd PE=1 SV=1
sp Q3TJD7 PDLI7_MOUSE	29.52572821	50086.72228	PWGFR;YTFAPSASLNK	1;1;1;1;1; 1;1;1	8	9	0.2516	46590;26243;1594 4;6450;31528;315 27;21442;22842;1 8712	-	PDZ and LIM domain protein 7 OS=Mus musculus OX=10090 GN=Pdlm7 PE=1 SV=1 Heterogeneous nuclear ribonucleoprotein F OS=Mus musculus OX=10090 GN=Hnrnpf PE=1 SV=3 Ras GTPase-activating protein-binding protein 2 OS=Mus musculus OX=10090 GN=G3bp2 PE=1 SV=2 T-complex protein 1 subunit theta OS=Mus musculus OX=10090 GN=Cct8 PE=1 SV=3 60S ribosomal protein L13 OS=Mus musculus OX=10090 GN=Rpl13 PE=1 SV=3 Cytoplasmic FMR1-interacting protein 1 OS=Mus musculus OX=10090 GN=Cyfp1 PE=1 SV=1
sp Q9Z2X1 HNRPF_MOUSE	6.678766375	45700.91426	ATENDIYNFFSPLNPVR;ITGEA FVQFASQELAEK;TEMDWVLK ;VHIEIGPDGR	0;1;1;0	2	2	0.1253	36513;34315;1311 1;15304	-	
sp P97379 G3BP2_MOUSE	10.78775442	54054.75892	HLEEEEEK;TEELKPQVEEK;VD AKPEVQSQPPR	1;1;1	3	4	0.0664	13232;22907;2635 1;26349	-	
sp P42932 TCPQ_MOUSE	7.711726226	59517.51014	DVDEVSSLLR;LATNAAVTVLR	1;1	2	2	0.0383	16578;16472	-	
sp P47963 RL13_MOUSE	10.0960393	24290.5042	GFSLEELR;LATQLTGPVMPPIR; STESLQANVQR	1;1;1	3	3	0.1517	11095;25341;1979 8	-	
sp Q7TMB8 CYFP1_MOUSE	6.67033354	145147.7548	TFLDDPIWR;TMLESLIADK EDL;DAVIQDLER;DSGDENEPI QER;EDAGWYTVSAK;FGPSQ TPAAFLSALLPSQPPPVAVNA LGLPK;IASDEEIQGTK;LDVYT QWHQQPQTTPK;LISEIEYR;L QNTGVADGYPVR;VSGVPPP	1;1 1;1;1;1;1; 1;1;1;1;1	2	2	0.0152	17551;16210	-	
sp Q9ET54 PALLD_MOUSE	32.11969528	152036.5045	QIFWK	1;1;1;1;1; 1;1;1;1;1	10	10	0.1051	43117;14175;2466 1;19612;46349;18 463;37974;13146; 24712;23693	-	Palladin OS=Mus musculus OX=10090 GN=Palld PE=1 SV=2 Pleckstrin homology-like domain family B member 2 OS=Mus musculus OX=10090 GN=Phldb2 PE=1 SV=2 Myeloid-associated differentiation marker OS=Mus musculus OX=10090 GN=Myadm PE=1 SV=2 Sideroflexin-3 OS=Mus musculus OX=10090 GN=Sfxn3 PE=1 SV=1
sp Q8K1N2 PHLB2_MOUSE	6.703511025	141397.7503	QSSETPQPVLRL;TPEDIGEEQR	1;1	2	2	0.0168	20096;17908	-	
sp O35682 MYADM_MOUSE	3.33516677	35261.32098	ALTQPLGLLR		1	1	0.0312	14951	-	
sp Q91V61 SFXN3_MOUSE	4.376559455	35383.52149	NLLLSGEQLEASR		1	1	0.0405	25804	-	

sp Q8CI51 PDLI 5_MOUSE	61.79196349	63259.09746	ASEGPESPGSSRPSVAGLR;DF NMPLTISSLK;EVVKPVPITSPA VSK;IGDVVLSIDGISAQGMTH LEAQNK;ILAQITGTEHLTESEN DNTK;ILGEVINALK;KILGEVIN ALK;LIEDTEDWRPR;NTEFYHI PTHSDASK;NTMAYIGFVEEK; QPTVTSVCSESAQELAEGQR; SAAAFKPVGSTSVK;SSGTGAS VGPPQPSDQDTLVQR;SWHP EEFNCAHCK;TPMCAHCNQV IR;VTSTTNMAYNK	1;1;1;1;1; 1;1;1;1;1; 1;1;1;1;1;	1	16	29	0.4247	48060;48059;2447 8;24027;28859;28 860;42928;42927; 39467;39470;3946 9;14537;18688;18 690;25801;32283; 32285;32284;2503 1;39001;38999;23 560;23556;39101; 31467;27267;2766 6;27268;19737	-	PDZ and LIM domain protein 5 OS=Mus musculus OX=10090 GN=Pdlm5 PE=1 SV=4 RuvB-like 1 OS=Mus musculus OX=10090 GN=Ruvbl1 PE=1 SV=1 Sterol O-acyltransferase 1 OS=Mus musculus OX=10090 GN=Soat1 PE=1 SV=2 Ubiquitin-associated protein 2-like OS=Mus musculus OX=10090 GN=Ubp2l PE=1 SV=1 Arginine--tRNA ligase, cytoplasmic OS=Mus musculus OX=10090 GN=Rars1 PE=1 SV=2 Heterogeneous nuclear ribonucleoprotein M OS=Mus musculus OX=10090 GN=Hnrrpm PE=1 SV=3 Eukaryotic translation initiation factor 3 subunit A OS=Mus musculus OX=10090 GN=Eif3a PE=1 SV=5 60S ribosomal protein L10a OS=Mus musculus OX=10090 GN=Rpl10a PE=1 SV=3 EMILIN-2 OS=Mus musculus OX=10090 GN=Emilin2 PE=1 SV=1 EMILIN-1 OS=Mus musculus OX=10090 GN=Emilin1 PE=1 SV=1
sp P60122 RUVB 1_MOUSE	4.376559455	50182.29751	TALALAI AQELGSK		1	1	1	0.0307	24595	-	
sp Q61263 SOA T1_MOUSE	8.753118911	63757.00628	FILILEQIR;NPTFLDYVRPR	1;1		2	2	0.037	16988;24365	-	
sp Q80X50 UBP 2L_MOUSE	2.923749796	116728.4078	IDLAVLLGK		1	1	1	0.0081	10818	-	
sp Q9D0I9 SYRC _MOUSE	7.11711168	75625.1451	FPEILQK;GFDILGIKPVQR ADILEDKDGK;FEPYSNPTK;G NFGGSFAGSFGGAGGHAPGV AR;LGSTVFVANLDYK;MGAN	1;1		2	2	0.0288	8955;23353	-	
sp Q9D0E1 HNR PM_MOUSE	17.5859506	77597.37505	SLER	1;1;1;1;1		5	6	0.0864	15653;15652;1496 1;37139;25712;90 22	-	
sp P23116 EIF3A _MOUSE	6.703511025	161838.2141	FSVLQYVVPEVK;LTSLVPFVD AFQLER	1;1		2	2	0.0201	25208;32068	-	
sp P53026 RL10 A_MOUSE	6.939645239	24900.59867	AVDIPHMDIEALK;ILGPGLNK	1;1		2	3	0.0968	26378;26380;7143	-	
sp Q8K482 EMIL 2_MOUSE	2.740552224	117236.6005	LDNEFDR		1	1	1	0.0065	9935	-	
sp Q99K41 EMIL 1_MOUSE	9.967477965	107518.2078	LQQEATEHVTSEER;LQQLSL K;VNEILSALER	1;1;1		3	3	0.0315	32962;7639;16950	-	

sp P70460 VASP_MOUSE	6.67033354	39641.92638	ATQVGEKPPKDESASESEAR; LPAQSEPVR NEDNGIHK;KLDELYGTWR;LEA AATALATK;NIPGITLLNVSK;Q PYAVSELAGHQTSAESWGTG R;SGQGAFGNMCR;SNYNLP MHK ASAVGSSSDSGDPGCLEAEPGE LER;EDESTISGDR;EGEFTLSA MTSGIR;ELEVSEQYSQK;EN QELNAHNQELNNR;FFILYEH GLLR;GFAAMEETHQK;HVLPA SAPDVTSSLPEGK;LSTHELTSL LEK;LSTHELTSLLEKELEQSQK; MAVTSSSGSGSSSSSIPSAEK ;QEISSLKDELQTALR;QVPIAP LHLSLEDR;SPEGTTVSGYDIM K;SQISSINSIDIEALR;STEKQEA EPGEPDPEQK;STLWQEEMR;T QNVHVEIEQR;VESGYFSLEK; VKESEIQYLK;YKDIYTELSIAK	1;1 1;1;1;1;1; 1;1;1	2 8 21	3 10 26	0.08 0.2506 0.2754	39834;39835;1242 5 34205;29789;2135 0;14212;20995;40 867;40868;18255; 15642;15643 41550;15790;2756 7;26406;33521;25 206;25207;20338; 33292;33293;2414 6;24145;39456;36 565;32001;29504; 29237;27616;2842 8;34836;18090;23 635;23637;17415; 19953;26169	- - -	Vasodilator-stimulated phosphoprotein OS=Mus musculus OX=10090 GN=Vasp PE=1 SV=4 60S ribosomal protein L4 OS=Mus musculus OX=10090 GN=Rpl4 PE=1 SV=3 Myosin phosphatase Rho- interacting protein OS=Mus musculus OX=10090 GN=Mprip PE=1 SV=2	
sp P97434 MPRI_P_MOUSE	85.3340896	116336.5778								sp Q61011 G BB3_MOUSE; sp P62874 G BB1_MOUSE; sp P62880 G BB2_MOUSE	Guanine nucleotide-binding protein subunit beta-4 OS=Mus musculus OX=10090 GN=Gnb4 PE=1 SV=4
sp P29387 GBB4_MOUSE	3.33516677	37355.02105	LLVSASQDGK	1	1	1	0.0294	12999	-	Chloride intracellular channel protein 1 OS=Mus musculus OX=10090 GN=Clic1 PE=1 SV=3	
sp Q9Z1Q5 CLIC1_MOUSE	4.376559455	26995.73644	NSNPALNDNLEK	1	1	1	0.0498	22857	-	Elongation factor Tu, mitochondrial OS=Mus musculus OX=10090 GN=Tufm PE=1 SV=1	
sp Q8BFR5 EFTU_MOUSE	14.39223288	49476.96892	AEAGDNLGALVR;DLDKPFLL PVESVYSIPGR;GTVVTGTCLR; TVVTGIEMFHK	1;1;1;1	4	4	0.115	18309;38614;1340 2;20781	-	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform OS=Mus musculus OX=10090 GN=Ppp2r1a PE=1 SV=3	
sp Q76MZ3 2AA_A_MOUSE	4.376559455	65280.92774	LTQDQDQDVK	1	1	1	0.017	17486	-	CTP synthase 1 OS=Mus musculus OX=10090 GN=Ctps1 PE=1 SV=2	
sp P70698 PYRG1_MOUSE	7.711726226	66640.10264	ALEHSALAINHK;VPLLLLEEQG VVDYFLR	1;1	2	3	0.0474	22094;34697;3469 8	-		

sp Q8C0C7 SYF A_MOUSE	6.999819215	57562.74824	ALYQLAQK;DQHDTFFLR;LGI TQLR	1;1;1	3	3	0.0472	10642;18067;6882	-	Phenylalanine--tRNA ligase alpha subunit OS=Mus musculus OX=10090 GN=Farsa PE=1 SV=1 ATP-binding cassette sub- family D member 3 OS=Mus musculus OX=10090 GN=Abcd3 PE=1 SV=2 Histone H3.3 OS=Mus musculus OX=10090 GN=H3- 3a PE=1 SV=2 OX=10090 GN=Tes PE=1 SV=1 Dolichyl- diphosphooligosaccharide-- protein glycosyltransferase subunit 1 OS=Mus musculus OX=10090 GN=Rpn1 PE=1 SV=1 Eukaryotic translation initiation factor 3 subunit D OS=Mus musculus OX=10090 GN=Eif3d PE=1 SV=2 Cold shock domain- containing protein E1 OS=Mus musculus OX=10090 GN=Csde1 PE=1 SV=1 Galectin-1 OS=Mus musculus OX=10090 GN=Lgals1 PE=1 SV=3 Aspartyl/asparaginyl beta- hydroxylase OS=Mus musculus OX=10090 GN=Asph PE=1 SV=1 40S ribosomal protein S9 OS=Mus musculus OX=10090 GN=Rps9 PE=1 SV=3 Sarcoplasmic/endoplasmic reticulum calcium ATPase 2 OS=Mus musculus OX=10090 GN=Atp2a2 PE=1 SV=2 40S ribosomal protein SA OS=Mus musculus OX=10090 GN=Rpsa PE=1 SV=4
sp P55096 ABC D3_MOUSE	3.33516677	75426.26992	ITELMQVLK		1	1	0.0137	14719	-	
sp P84244 H33_ MOUSE	7.300309251	15318.50255	FQSAAIGALQEASEAYLVGLFE DTNLCAIHAK;STELLIR	1;1	2	2	0.2868	47617;7693		sp P02301 H 3C_MOUSE
sp P47226 TES_ MOUSE	3.07602819	47951.1195	SEALGVGDVK		1	1	0.0236	11809	-	
sp Q91YQ5 RPN 1_MOUSE	11.8291471	68485.73209	GEDEEDNNLEVR;IDHILDAL; QPDSGISSIR	1;1;1	3	3	0.0493	25504;9971;14204	-	
sp O70194 EIF3 D_MOUSE	2.529783838	63948.40067	IFHTVTTTDDPVIR		1	1	0.0255	29930	-	
sp Q91W50 CSD E1_MOUSE	4.376559455	88734.81875	ATNIEVLSNTFQFTNEAR		1	1	0.0226	37392	-	
sp P16045 LEG1 _MOUSE	11.046893	14856.19776	DSNNLCLHFNPR;FNAHGDA NTIVCNTK;SFVLNLGK	1;1;1	3	3	0.2593	27270;30769;9037	-	
sp Q8BSY0 ASP H_MOUSE	3.33516677	82990.99567	GLFLPEDENLR		1	1	0.0148	22061	-	
sp Q6ZWN5 RS9 _MOUSE	6.67033354	22577.55535	ELLTLDEK;MKLDYILGLK	1;1	2	2	0.0928	11375;18568	-	
sp O55143 AT2 A2_MOUSE	2.563085783	114783.6766	NAENAIEALK AIVAIENPADVSVISSR;FAAAT GATPIAGR;FTPGTFTNQIQAA		1	1	0.0096	14627	E	sp Q8R429 A T2A1_MOUS
sp P14206 RSSA _MOUSE	14.61806952	32817.43759	FR;LLVVTDPDR	1;1;1;1	4	4	0.1797	32178;18919;3141 6;10050	-	

sp Q6PHN9 RAB35_MOUSE	3.33516677	23010.7664	LLIIGDSGVGK	1	1	1	0.0547	14605	-	Ras-related protein Rab-35 OS=Mus musculus OX=10090 GN=Rab35 PE=1 SV=1
sp Q62523 ZYG_MOUSE	16.61005163	60506.78628	NQK;GPLSQAPTPAPK;QHPQ PPPAQNQNQVR;SPGGPGPL TLK	1;1;1;1;1	5	5	0.1082	5246;29129;17588 ;32144;13175	-	Zyxin OS=Mus musculus OX=10090 GN=Zyx PE=1 SV=2
sp Q61792 LASP1_MOUSE	5.898252554	29975.31053	GFSVVADTPELQR;TQDQISNI K	1;1	2	2	0.0837	25522;13792	-	1 OS=Mus musculus OX=10090 GN=Lasp1 PE=1 SV=1
sp Q9EP71 RAI14_MOUSE	43.61797848	108785.3223	EAQAELEDYRK;ESVFFAEAPF K;HHQEVISVYR;LQASLESEV NALATK;LSENAGIQNLLLSK; QLQDELQSQR;QSQQLDLLQ QQVK;QVSELSQLYR;SEEALS EMK;SSPPVEHPAGTSTTDND VIIR;VLNELTQLK	1;1;1;1;1; 1;1;1;1;1; 1	11	11	0.1359	23611;21072;2096 6;29289;27610;20 203;28977;19509; 13164;39204;1415 5	-	Ankycorbin OS=Mus musculus OX=10090 GN=Rai14 PE=1 SV=1
sp Q60875 ARHG2_MOUSE	2.32695157	111904.581	NNTALQSVSLR	1	1	1	0.0112	18872	-	Rho guanine nucleotide exchange factor 2 OS=Mus musculus OX=10090 GN=Arhgef2 PE=1 SV=4
sp O89079 COPE_MOUSE	4.376559455	34545.38144	APPVPGAVSGGSGEVDELFD VK	1	1	1	0.0714	38374	-	Coatomer subunit epsilon OS=Mus musculus OX=10090 GN=Cope PE=1 SV=3
sp Q99MJ9 DDX50_MOUSE	2.923749796	82124.8062	GAVDALAAALAHISGASSFEP R	1	1	1	0.03	38148	-	ATP-dependent RNA helicase DDX50 OS=Mus musculus OX=10090 GN=Ddx50 PE=2 SV=1
sp P35979 RL12_MOUSE	3.33516677	17793.52444	IGPLGLSPK	1	1	1	0.0545	9137	-	60S ribosomal protein L12 OS=Mus musculus OX=10090 GN=Rpl12 PE=1 SV=2
sp Q8VD75 HIP1_MOUSE	11.08007048	115130.2216	EIAASTAQLVAASK;GSLNLTQ LQQASR;QELQVLHSNLETSA QSEAK	1;1;1	3	3	0.0447	23857;25441;3815 8	-	1 OS=Mus musculus OX=10090 GN=Hip1 PE=1 SV=2
sp Q8VHE6 DYH5_MOUSE	2.384313076	527221.177	LKMLPTPAK	1	1	1	0.0019	12485	-	5 OS=Mus musculus OX=10090 GN=Dnah5 PE=1 SV=2
sp Q8BIA4 FBXW8_MOUSE	2.30220692	67913.22279	IQALALSQEKPIVATASAFDVV MLYPNEEGHWHVASEFEVQK LVDYLEIVPNTGR	1	1	1	0.092	49620	-	F-box/WD repeat-containing protein 8 OS=Mus musculus OX=10090 GN=Fbxw8 PE=1 SV=2

[illegible]

sp P60843 IF4A1_MOUSE	43.25466742	46124.55493	GIDVQQVSLVINYLPTNR;G VAINMVTEEDKR;GYDVIAQA QSGTGK;KEELTLEGIR;KVDWL TEK;LNSNTQVVLLSATMPD VLEVTK;MFVLDEADEMLSR;Q FYINVER;VFDMLNR;VLITTDL LAR	1;1;1;1;1; 1;1;1;1;1; 1;1	12	13	0.3374	17776;27646;3860 5;26647;24842;18 398;18396;13034; 42468;28963;1449 3;9523;16029	-	Eukaryotic initiation factor 4A- I OS=Mus musculus OX=10090 GN=Eif4a1 PE=1 SV=1
sp P01942 HBA_MOUSE	6.906343294	15075.7603	IGGHGAEGAEALER;LRVDPV NFK	1;1	2	2	0.169	28330;15148	-	Hemoglobin subunit alpha OS=Mus musculus OX=10090 GN=Hba PE=1 SV=2
sp Q8C8U0 LIPB1_MOUSE	8.402670565	108472.4806	ALHLVEDLR;DRLDYEDR;LDF NWWVTR	1;1;1	3	3	0.0258	14394;14925;1391 4	-	Liprin-beta-1 OS=Mus musculus OX=10090 GN=Ppfibp1 PE=1 SV=3
sp Q60930 VDA C2_MOUSE	2.088488785	31712.57741	YQLDPTASISAK		1	1	0.0407	21775	-	Voltage-dependent anion- selective channel protein 2 OS=Mus musculus OX=10090 GN=Vdac2 PE=1 SV=2
sp Q61554 FBN1_MOUSE	10.04086148	312083.352	GFVYKPDLDK;GTCWQTVIDGR; TLCCATVGR	1;1;1	3	3	0.0101	14424;21734;1352 9	-	Fibrillin-1 OS=Mus musculus OX=10090 GN=Fbn1 PE=1 SV=2
sp Q8VEK3 HNRPU_MOUSE	10.45227845	87862.72356	LLEQYKEESK;NGQDLGVAFK; VSELKEELK NR;GVPEELTGLLEYLR;NSASE EDHLPQLVLQSH;NSVLEIAF HCK;VEEVNWAWEK;VSLYD LSSVDSWEK;YLTDSAYTEGST GK	1;1;1 1;1;1;1;1; 1;1;1	3	3	0.0362	20938;13866;1471 6	-	Heterogeneous nuclear ribonucleoprotein U OS=Mus musculus OX=10090 GN=Hnrnpu PE=1 SV=1
sp Q9WTR1 TRPV2_MOUSE	32.89166793	85910.47002			8	10	0.1376	17990;17989;1773 2;29522;34934;34 935;25827;23876; 30151;27400	-	Transient receptor potential cation channel subfamily V member 2 OS=Mus musculus OX=10090 GN=Trpv2 PE=1 SV=2
sp O55142 RL35A_MOUSE	2.740552224	12545.74747	DETEFYLGK		1	1	0.0818	15584	-	60S ribosomal protein L35a OS=Mus musculus OX=10090 GN=Rpl35a PE=1 SV=2
sp P58774 TPM2_MOUSE	10.9687885	32816.55071	ATDAEADVASLNR;EDKYEEEI K;IQLVEEELDR;LDKENAIDR	1;0;1;1	3	3	0.1444	23011;18197;2017 6;14660	-	Tropomyosin beta chain OS=Mus musculus OX=10090 GN=Tpm2 PE=1 SV=1
sp Q6IRU2 TPM4_MOUSE	4.759295888	28450.43232	EDKYEEEIK;RIQLLEEELDR;TID DLEEK	0;1;1	2	2	0.1129	18197;25369;1142 5	-	Tropomyosin alpha-4 chain OS=Mus musculus OX=10090 GN=Tpm4 PE=1 SV=3
sp Q9QZL0 RIPK3_MOUSE	11.98240438	53288.93398	DLKPSNILLDPHELHAK;GGFGV VFR;KLEFVGK;QAQDTSVGPA TPAR	1;1;1;1	4	4	0.0926	33257;7895;7401; 24937	-	serine/threonine-protein kinase 3 OS=Mus musculus OX=10090 GN=Ripk3 PE=1 SV=2
sp Q91VH2 SNX9_MOUSE	3.33516677	66503.56851	HPVVSESEVFQQFLNFR		1	1	0.0286	37503	-	Sorting nexin-9 OS=Mus musculus OX=10090 GN=Snx9 PE=1 SV=1

sp Q6P542 ABC F1_MOUSE	6.67033354	94886.89222	GAVIVVSHDAR;STLLLLLTGK	1;1	2	2	0.0251	16307;14194	-	ATP-binding cassette sub- family F member 1 OS=Mus musculus OX=10090 GN=Abcf1 PE=1 SV=1
sp P08122 CO4 A2_MOUSE	7.711726226	167219.8865	GLDGFQGPSGPR;IAVQPGTL GPQGR	1;1	2	2	0.0146	18376;21793	-	Collagen alpha-2(IV) chain OS=Mus musculus OX=10090 GN=Col4a2 PE=1 SV=4
sp P62754 RS6_ MOUSE	9.498977689	28662.98612	DIPGLTDTTVPR;LIEVDDER;M ATEVAADALGEEWK	1;1;1	3	3	0.1406	7 21501;12185;3003	-	40S ribosomal protein S6 OS=Mus musculus OX=10090 GN=Rps6 PE=1 SV=1
sp P14148 RL7_ MOUSE	28.29399224	31399.74894	EANNFLWPFK;FGIICMEDLIH EIYTVGK;IVEPYIAWGYPNLK; QIFNGTFVK;TTHFVEGGDAG NR;TTHFVEGGDAGNREDQI NR;VPAVPETLK	1;1;1;1;1; 1;1	7	11	0.2926	0 20889;38531;3853 0;30797;14052;23 874;23873;38198; 38194;38196;1119	-	60S ribosomal protein L7 OS=Mus musculus OX=10090 GN=Rpl7 PE=1 SV=2
sp Q8QZY1 EIF3 L_MOUSE	9.028134024	66570.31994	TVSDLIDQK;VFSDEVQQQAQ LSTIR;YGDFFIR	1;1;1	3	3	0.0567	6 13028;33992;1018	-	Eukaryotic translation initiation factor 3 subunit L OS=Mus musculus OX=10090 GN=Eif3l PE=1 SV=1
sp P05064 ALD OA_MOUSE	4.376559455	39331.27392	IGEHTPSALAIMENANVLAR		1	1	0.0549		38087 -	aldolase A OS=Mus musculus OX=10090 GN=Aldoa PE=1 SV=2
sp Q00780 CO8 A1_MOUSE	3.07602819	73559.11606	GGNVWVALFK		1	1	0.0134		15233 -	Collagen alpha-1(VIII) chain OS=Mus musculus OX=10090 GN=Col8a1 PE=1 SV=3
sp P70398 USP9 X_MOUSE	2.384313076	290525.7485	GWLVDLLNK EDSVKPGAHLTVK;EDTEEYNL R;LFIGGLSFETDDSLREHFEK; SSGSPYGGGYGSGGGSGGYG		1	1	0.0035		14153 -	Probable ubiquitin carboxyl- terminal hydrolase FAF-X OS=Mus musculus OX=10090 GN=Usp9x PE=1 SV=2
sp Q8BG05 ROA 3_MOUSE	17.50623782	39627.6041	SR	1;1;1;1	4	5	0.1715	3;42227;35067	-	Heterogeneous nuclear ribonucleoprotein A3 OS=Mus musculus OX=10090 GN=Hnrnpa3 PE=1 SV=1
sp Q3UX10 TBA L3_MOUSE	4.376559455	49956.00585	SFGGGTSGGFTSLLMER		1	1	0.0381		31509 -	Tubulin alpha chain-like 3 OS=Mus musculus OX=10090 GN=Tubal3 PE=2 SV=2
sp O54734 OST 48_MOUSE	2.740552224	48996.99142	DTHSLFFR APSWIDTGLSEMR;EEKPAVA AAPK;QDEHGFISR;VLGDVIEV		1	1	0.0181		13139 -	Dolichyl- diphosphooligosaccharide-- protein glycosyltransferase 48 kDa subunit OS=Mus musculus OX=10090 GN=Ddost PE=1 SV=2
sp P23927 CRYA B_MOUSE	15.42345245	20056.40836	HGK	1;1;1;1	4	4	0.2514	7;17648	-	Alpha-crystallin B chain OS=Mus musculus OX=10090 GN=Cryab PE=1 SV=2

sp D3YWJ0 SLIP_MOUSE	2.037040553	91211.94072	LLALIEK	1	1	1	0.0088	6851	-	Nuclear GTPase SLIP-GC OS=Mus musculus OX=10090 GN=Nuggc PE=3 SV=1 RNA cytosine C(5)-methyltransferase NSUN2 OS=Mus musculus OX=10090 GN=Nsun2 PE=1 SV=2 Protein argonaute-2 OS=Mus musculus OX=10090 GN=Ago2 PE=1 SV=3 Caveolae-associated protein 2 OS=Mus musculus OX=10090 GN=Cavin2 PE=1 SV=3 Nucleophosmin OS=Mus musculus OX=10090 GN=Npm1 PE=1 SV=1 Leucine zipper protein 1 OS=Mus musculus OX=10090 GN=Luzp1 PE=1 SV=2 Fascin OS=Mus musculus OX=10090 GN=Fscn1 PE=1 SV=4
sp Q1HFZ0 NSU_N2_MOUSE	4.376559455	85397.17316	TLTQENPFFR	1	1	1	0.0145	24029	-	
sp Q8CJG0 AGO2_MOUSE	6.41119496	97241.92071	DGVSEGGFQQVLHHELLAIR; ELLIQFYK	1;1	2	2	0.0326	40251;14017	-	
sp Q63918 CAV_N2_MOUSE	12.83789779	46735.37849	DNSQVNAVTVHTLLDK;GIQ NDLTk;LVNMLDAVR;VSPLSF GR	1;1;1;1	4	4	0.0981	32415;9336;13355 ;8568	-	
sp Q61937 NPM_MOUSE	2.740552224	32539.81247	VTLATLK	1	1	1	0.024	5601	-	
sp Q8R4U7 LUZ_P1_MOUSE	3.33516677	119238.6725	NASTFLER	1	1	1	0.0075	10709	-	
sp Q61553 FSC_N1_MOUSE	4.376559455	54473.93217	WSLQSEHR	1	1	1	0.0183	15968	-	
sp Q9EPU0 REN_T1_MOUSE	28.15328942	123888.51	AGAKPDQIGIITPYEGQR;AGL SQLFER;ALVEGPLNNLR;DET GELSSADEK;EAIIPGSVYDR;QI TAQQINK;TFAVDETSVSGYIY HK;TVTSATIVYHLAR	1;1;1;1;1; 1;1;1	8	9	0.089	35126;15775;1862 3;21335;19395;13 712;33447;25855; 25854	-	Regulator of nonsense transcripts 1 OS=Mus musculus OX=10090 GN=Upf1 PE=1 SV=2
sp Q54724 CAV_N1_MOUSE	19.91290217	43927.01431	ATEMVEVGPEDDEVGAER;EG EVEVLK;KLEVNEAELLR;QAE MEGAVQSIQGELSK;SFTPDH VYAR;VMIQDEVK	1;1;1;1;1; 1	6	6	0.1888	35452;9757;22411 ;33286;21710;168 03	-	Caveolae-associated protein 1 OS=Mus musculus OX=10090 GN=Cavin1 PE=1 SV=1 Probable global transcription activator SNF2L1 OS=Mus musculus OX=10090 GN=Smarca1 PE=1 SV=1 Asparagine--tRNA ligase, cytoplasmic OS=Mus musculus OX=10090 GN=NARS1 PE=1 SV=2 protein 7 OS=Mus musculus OX=10090 GN=Dock7 PE=1 SV=3 Heterogeneous nuclear ribonucleoprotein K OS=Mus musculus OX=10090 GN=Hnrnpk PE=1 SV=1
sp Q6PGB8 SMC_A1_MOUSE	2.563085783	121637.6106	FDWFIK	1	1	1	0.0057	8377	-	
sp Q8BP47 SYN_C_MOUSE	5.486835579	64238.00907	SPVASIVYELNPNFKPPK;SWD SEEILEGYK	1;1	2	2	0.0537	36560;26460	-	
sp Q8R1A4 DOC_K7_MOUSE	14.37301237	241285.632	AHGELHEQFK;EAYTAVVYHN R;ESILGGVLK;FGEDVLEVIK;LE GFYGER	1;1;1;1;1	5	5	0.0225	18611;22694;1014 1;17106;11656	-	
sp P61979 HNR_PK_MOUSE	9.830093089	50944.4019	IILDLIESPik;LLIHQSLAGGIIG VK;TDYNASVSPDSSGPER	1;1;1	3	3	0.095	23300;28091;3285 6	-	

sp P56480 ATPB_MOUSE	22.8760401	56265.46521	AHGGYSVFAGVGER;AIAELGI YPAVDPLDSTSR;IPVGPETLG R;TVLIMELINNVAK;VALTGLT VAEYFR;VVDLLAPYAK APNSPDVLEIEFK;EFVEEFIWP AVQSSALYEDR;FAELVYTGF WHSPECEFVR;KVFIEDVSK;N QAPPGLYTK;QVEIAQR;VFIED VSK;VQVSVFK	1;1;1;1;1; 1 1;1;1;1;1; 1;1;1	6 7 8	7 7 9	0.1493 0.075;15178 0.2063	25166;25165;3637 6;13573;26539;26 26562;41874;4189 0;41359;14359;15 168;8017;10690;7 022	- - -	ATP synthase subunit beta, mitochondrial OS=Mus musculus OX=10090 GN=Atp5f1b PE=1 SV=2		
sp P16460 ASSY_MOUSE	24.5615922	46555.00971								-	Argininosuccinate synthase OS=Mus musculus OX=10090 GN=Ass1 PE=1 SV=1	
sp O08788 DCTN1_MOUSE	4.376559455	141588.0585	ELTNQQEASVER		1	1	1	0.0094		25079	-	Dynactin subunit 1 OS=Mus musculus OX=10090 GN=Dctn1 PE=1 SV=3
sp P14873 MAP1B_MOUSE	3.33516677	270088.9326	NVDVEFFK		1	1	1	0.0032		12445	-	Microtubule-associated protein 1B OS=Mus musculus OX=10090 GN=Map1b PE=1 SV=2
sp Q9Z0N1 IF2G_MOUSE	6.678766375	51033.19088	NEVLMVNIGSLSTGGR;VGQE IEVRPGIVSK	1;1		2	2	0.0636	30503;27879		sp Q9Z0N2 F2H_MOUSE	initiation factor 2 subunit 3, X- linked OS=Mus musculus OX=10090 GN=Eif2s3x PE=1 SV=2
sp Q8BH04 PCKGM_MOUSE	2.740552224	70482.4469	FLWPGFGENAR		1	1	1	0.0172		21773	-	Phosphoenolpyruvate carboxykinase [GTP], mitochondrial OS=Mus musculus OX=10090 GN=Pck2 PE=1 SV=1
sp Q922Q4 P5CR2_MOUSE	3.33516677	33637.62497	LGAQALLGAAK		1	1	1	0.0344		12870	sp Q922W5 P5CR1_MOUSE SE	Pyrroline-5-carboxylate reductase 2 OS=Mus musculus OX=10090 GN=Pycr2 PE=1 SV=1
sp Q61398 PCOC1_MOUSE	7.711726226	50136.09994	ESALSPGEDVQR;SNQDQILN NLSK	1;1		2	2	0.0513	21591;24255		-	Procollagen C-endopeptidase enhancer 1 OS=Mus musculus OX=10090 GN=Pcolce PE=1 SV=2
sp Q9Z108 STAU1_MOUSE	3.07602819	53890.79014	SNISSGHVPHGPR		1	1	1	0.0267		23402	-	binding protein Staufen homolog 1 OS=Mus musculus OX=10090 GN=Stau1 PE=1 SV=1
sp Q61820 RANT_MOUSE	2.037040553	24436.46552	FNVWDTAGQEK		1	1	1	0.0509		21807	sp P62827 RAN_MOUSE	GTP-binding nuclear protein Ran, testis-specific isoform OS=Mus musculus OX=10090 GN=Rasl2-9 PE=2 SV=1
sp Q6ZQM8 UD17_MOUSE	4.376559455	59718.73071	TYAVSHTQEDLNR		1	1	1	0.0245		28453	-	UDP-glucuronosyltransferase 1A7 OS=Mus musculus OX=10090 GN=Ugt1a7 PE=1 SV=1

sp Q9D8N0 EF1 G_MOUSE	14.13135402	50029.15714	EYFSWEGTFQHVGK;ILGLLDT HLK;STFVLDEFKR;TFLVGER	1;1;1;1	4	6	0.0938	15	31702;16288;1628 5;20093;20094;74	-	Elongation factor 1-gamma OS=Mus musculus OX=10090 GN=Eef1g PE=1 SV=3
sp Q8CGB6 TNS 2_MOUSE	2.162498145	151917.3268	VSAQGITLTDNQ		1	1	0.0093	25063	7;46;81;46;82;12 471;12472;12470; 12899;39643;3983 2;39816;39815;18 695;18694;18744; 18697;18696;2367 8;17528;16515;18 372;18370;17846; 6754;6750;13518; 27992;27989;2799 1;27993;28018;28 019;41130;41131; 43362;27621;2762 2;27619;27620;27 178;33043;33041; 33040;33065;3304 2;33063;46804;46 763;46761;46760; 46802;46762;3585 4;35853;35920;35 922;36180;35921; 36179;36181;3591	E	sp Q5SSZ5 T ENS3_MOUSE SV=1 Tensin-2 OS=Mus musculus OX=10090 GN=Tns2 PE=1
sp P68033 ACTC _MOUSE	4.376559455	41991.88007	AGFAGDDAPR;AVFPSIVGRP R;CPETLFQPSFIGMESAGIHET TYNSIMK;DLTDYLMK;DLYAN NVLSGGTTMYPGIADR;DSYV GDEAQSK;DSYVGDEAQSKR; EITALAPSTMK;GYSFVTTAER; HQGVMVGMGQK;IIAPPER;IK IIAPPER;IWHHTFYNELR;KDLY ANNVLSGGTTMYPGIADR;LC YVALDFENEMATAASSSSLEK; QEYDEAGPSIVHR;SYELPDG QVITIGNER;TTGIVLDSGDGV THNVPIYEGYALPHAIMR;VAP EEHPTLLTEAPLNPK;YPIEHGII TNWDDMEK;YPIEHGIITNWD	0;0;0;0;0; 0;0;0;0;0; 0;0;0;0;0; 0;0;0;0;0;	1	1	4	0.687	0;12899;24357;18 372;18370;17846; 6754;6750;13518; 28648;28649;2864 6;33043;33041;33 040;33065;33042; 33063;46705;4677 0;46709;46710;46 708;46772;46706; 46707;46771	-	Actin, alpha cardiac muscle 1 OS=Mus musculus OX=10090 GN=Actc1 PE=1 SV=1
sp Q8BFZ3 ACT BL_MOUSE	7.300309251	41976.98704	DLTDYLMK;GIHETTFNSIMK; HQGVMVGMGQK;IIAPPER;IK IIAPPER;IWYHTFYNELR;SYEL PDGQVITIGNER;TTGIVMDSG DGVTHTVPIYEGYALPHAILR	0;1;0;0;0; 1;0;0	2	4	0.258	46707;46771	-	Beta-actin-like protein 2 OS=Mus musculus OX=10090 GN=Actbl2 PE=1 SV=1 2 OS=Mus musculus OX=10090 GN=Angptl2 PE=2 SV=2	
sp Q9R045 ANG L2_MOUSE	4.376559455	57069.37933	IINQISTNEIQSDQNLK		1	1	0.0345	35884	-	Cysteine and glycine-rich protein 1 OS=Mus musculus OX=10090 GN=Csrp1 PE=1 SV=3	
sp P97315 CSRP 1_MOUSE	2.150691262	20569.75742	GFGFGQGAGALVHSE		1	1	0.0777	25903	-		

sp Q61941 NNT M_MOUSE	4.376559455	113765.0796	FFTGQITAAGK	1	1	1	0.0101	16813	-	NAD(P) transhydrogenase, mitochondrial OS=Mus musculus OX=10090 GN=Nnt PE=1 SV=2
sp O08663 MAP 2_MOUSE	6.258916566	52888.25353	ALDQASEEIWNDFR;YDILLTA VK	1;1	2	2	0.0481	31331;13484	-	Methionine aminopeptidase 2 OS=Mus musculus OX=10090 GN=Metap2 PE=1 SV=1
sp O35286 DHX 15_MOUSE	2.25575174	90949.20113	TLATDILMGVLK	1	1	1	0.0151	21175	-	ATP-dependent RNA helicase DHX15 OS=Mus musculus OX=10090 GN=Dhx15 PE=1 SV=2
sp Q99KN9 EPN 4_MOUSE	3.07602819	68468.76679	SLLLLAYLIR	1	1	1	0.0158	17968	-	Clathrin interactor 1 OS=Mus musculus OX=10090 GN=Clint1 PE=1 SV=2
sp Q9QUI0 RHO A_MOUSE	2.740552224	21768.08745	EVFEMATR	1	1	1	0.0415	11997	E	sp Q62159 R HOC_MOUS Transforming protein RhoA OS=Mus musculus OX=10090 GN=Rhoa PE=1 SV=1
sp Q8C0T5 SI1L 1_MOUSE	4.376559455	196908.6542	QGTSGDSFFDLLK	1	1	1	0.0073	25384	-	Signal-induced proliferation- associated 1-like protein 1 OS=Mus musculus OX=10090 GN=Sipa1l1 PE=1 SV=2
sp P58252 EF2_ MOUSE	22.27792129	95252.88587	L;ETVSEESNVLCLSK;FSVSPV VR;NPADLPK;WLPAGDALLQ MITIHLPSPVTAQK;YEWDAE AR	1;1;1;1;1; 1;1	7	8	0.0991	21172;21174;2619 5;29625;9403;576 8;43899;16746	-	Elongation factor 2 OS=Mus musculus OX=10090 GN=Eef2 PE=1 SV=2
sp Q68FD5 CLH 1_MOUSE	91.02824593	191434.5045	QLCEK;AHMGMFTELAILYSK; ALEHFTDLYDIK;EHLELFSWR; FDFVHDLVLYLR;GQFSTDEL VAEVEK;HDVVFLITK;IVLDNS VFSEHR;KDPELWGSVLLESNP YR;LASTLVHLGEYQAAVDGA R;LLYNNVSNFGR;NNLAGAE ELFAR;RPISADSAIMNPASK;S VDPTLALSYYLR;SVNESLNNL FITEEDYQALR;TLQIFNIEMK;V DKLDASESLR;VGEQAQVVIID MNDPSNPIR;VGYPDWIFLL R;VIQCFAETGQVQK;VSQPIE GHAASFAQFK;YHEQLSTQSLI ELFESFK;YIEIYVQK	1;1;1;1;1; 1;1;1;1;1; 1;1;1;1;1; 1;1;1;1;1; 1;1;1;1	24	29	0.194	35690;14522;3165 6;26721;19288;19 289;31441;28872; 14602;25428;2542 9;36608;36089;36 088;21881;22123; 29021;25916;4110 3;41102;19949;19 802;39233;27089; 27789;31748;3928 4;39281;14077	-	Clathrin heavy chain 1 OS=Mus musculus OX=10090 GN=Cltc PE=1 SV=3
sp P62892 RL39 _MOUSE	3.33516677	6402.650395	QNRPIPWIR	1	1	1	0.1961	22232	-	60S ribosomal protein L39 OS=Mus musculus OX=10090 GN=Rpl39 PE=1 SV=2

sp Q6A0A9 F120 A_MOUSE	9.830093089	121568.7429	NIHDTSDLDAIAK;QSILEGLSF SR;QTAQQIVSHVQNK	1;1;1	3	5	0.0333	25332;25331;1994 6;27121;27120	-	Constitutive coactivator of PPAR-gamma-like protein 1 OS=Mus musculus OX=10090 GN=FAM120A PE=1 SV=2 Mitochondrial amidoxime reducing component 2 OS=Mus musculus OX=10090 GN=Mtarc2 PE=1 SV=1 Eukaryotic translation initiation factor 3 subunit B OS=Mus musculus OX=10090 GN=Eif3b PE=1 SV=1 Glutamine--tRNA ligase OS=Mus musculus OX=10090 GN=Qars1 PE=1 SV=1 Heterogeneous nuclear ribonucleoprotein L OS=Mus musculus OX=10090 GN=Hnrnp1 PE=1 SV=2 PML-RARA-regulated adapter molecule 1 OS=Mus musculus OX=10090 GN=Pram1 PE=1 SV=2 Leiomodin-1 OS=Mus musculus OX=10090 GN=Lmod1 PE=1 SV=1 eIF-2-alpha kinase activator GCN1 OS=Mus musculus OX=10090 GN=Gcn1 PE=1 SV=1 26S proteasome non-ATPase regulatory subunit 7 OS=Mus musculus OX=10090 GN=Psm7 PE=1 SV=2 kDa OS=Mus musculus OX=10090 GN=Cep55 PE=1 SV=2 60 kDa heat shock protein, mitochondrial OS=Mus musculus OX=10090 GN=Hspd1 PE=1 SV=1 Thyroid hormone receptor- associated protein 3 OS=Mus musculus OX=10090 GN=Thrap3 PE=1 SV=1
sp Q922Q1 MA RC2_MOUSE	2.740552224	38169.60784	LFGLDIK		1	1	1	0.0207	6995 -	
sp Q8JZQ9 EIF3 B_MOUSE	11.046893	91313.13698	GTQGVVTNFEIFR;GTYLATFH QR;VNLFTDFDK	1;1;1	3	3	0.0399	26781;18553;1549 1	-	
sp Q8BML9 SYQ _MOUSE	2.608604626	87620.86687	ATGVLLYDLVSR		1	1	1	0.0155	22191 -	
sp Q8R081 HNR PL_MOUSE	4.376559455	63923.24864	TPASPVVHIR		1	1	1	0.0171	14784 -	
sp Q6BCL1 PRA M_MOUSE	4.376559455	75461.21447	KPESCNPQSHSPLPDFNAFPK		1	1	1	0.0311	41668 -	
sp Q8BVA4 LM OD1_MOUSE	2.384313076	66269.62619	TITSLNLDNSNHITGK		1	1	1	0.0252	29929 -	
sp E9PVA8 GCN 1_MOUSE	4.376559455	292834.2934	AALLETLSLLLGK		1	1	1	0.0049	23329 -	
sp P26516 PSM D7_MOUSE	4.376559455	36517.21183	VVHPLVLLSVVDHFN		1	1	1	0.053	35630 -	
sp Q8BT07 CEP5 5_MOUSE	11.48917106	53896.97333	IQVLEAER;SEELLSQVR;SQIT QLES�K;TSLDEITSGK	1;1;1;1	4	4	0.0801	11278;14231;1704 4;13913	-	
sp P63038 CH60 _MOUSE	3.33516677	60917.38866	TLNDELEHIEGMK		1	1	1	0.0227	27714 -	
sp Q569Z6 TR15 0_MOUSE	4.376559455	108113.6944	EQTFSGGTSQDIK		1	1	1	0.0137	24908 -	

sp Q9ES74 NEK7_MOUSE	2.529783838	34514.46918	LGDLGLGR		1	1	1	0.0265	6874	sp Q9ES70 NEK7_MOUSE	Serine/threonine-protein kinase Nek7 OS=Mus musculus OX=10090 GN=Nek7 PE=1 SV=1
sp Q7TPH6 MYC_B2_MOUSE	6.863689897	520899.7455	R	GIPIGMLVLGNK;VYENYSFEEL	1;1		2	2	0.0048	19150;26283	E3 ubiquitin-protein ligase MYCBP2 OS=Mus musculus OX=10090 GN=Mycbp2 PE=1 SV=3
sp Q9QXL2 KI21A_MOUSE	2.529783838	186420.2799	YAASGNAVR	TLTSSGQVTLGEACSASTSRT VAIPSGESQINQIALNPTGTFL		1	1	1	0.0311	48933	Kinesin-like protein KIF21A OS=Mus musculus OX=10090 GN=Kif21a PE=1 SV=2
sp Q8BX10 PGAM5_MOUSE	2.25575174	31974.5998	HIFLIR			1	1	1	0.0208	6826	Serine/threonine-protein phosphatase PGAM5, mitochondrial OS=Mus musculus OX=10090 GN=Pgam5 PE=1 SV=1
sp Q9R0P5 DEST_MOUSE	4.376559455	18509.48504	HEYQANGPEDLNR			1	1	2	0.0788	28665;28666	Destrin OS=Mus musculus OX=10090 GN=Dstn PE=1 SV=3
sp O08709 PRDX6_MOUSE	6.985164081	24854.97443	LPFPIIDDK;NFDEILR		1;1		2	2	0.0714	14146;9885	Peroxiredoxin-6 OS=Mus musculus OX=10090 GN=Prdx6 PE=1 SV=3
sp O09167 RL21_MOUSE	4.376559455	18550.06091	VYNVTQHAVGIIVNK			1	1	2	0.0938	30653;30654	60S ribosomal protein L21 OS=Mus musculus OX=10090 GN=Rpl21 PE=1 SV=3
sp P62137 PP1A_MOUSE	3.33516677	37515.80971	LNLDSIIGR			1	1	1	0.0273	12537	Serine/threonine-protein phosphatase PP1-alpha catalytic subunit OS=Mus musculus OX=10090 GN=Ppp1ca PE=1 SV=1
sp P09103 PDIA1_MOUSE	2.413332988	57022.76721	ILEFFGLK			1	1	1	0.0157	11569	Protein disulfide-isomerase OS=Mus musculus OX=10090 GN=P4hb PE=1 SV=2
sp P62960 YBOX1_MOUSE	12.86561144	35708.56953	NGYGFNR	EDGNEEDKENQGDDETQGQQ PPQR;GAEEANVTGPGGVPV QGSK;NDTKEDVFVHQTAIK;	1;1;1;1		4	5	0.2019	44108;31362;3225 8;10801;10774	Y-box-binding protein 1 OS=Mus musculus OX=10090 GN=Ybx1 PE=1 SV=3
sp Q60847 COL1A1_MOUSE	31.26648329	340004.1376	R	PQTTYDITVLPAMYK;NIGVEVF SLGIK;QNSVLLQK;VPAPTNL QFTEVTPESFR;VSDATTSTLK; VTDETTDSFK;VYDPSTSSLSV	1;1;1;1;1; 1;1;1;1		9	9	0.0337	16907;12917;3510 7;21210;10500;37 107;13143;16900;	Collagen alpha-1(XII) chain OS=Mus musculus OX=10090 GN=Col12a1 PE=2 SV=3
sp P14869 RLA0_MOUSE	16.9118436	34194.7504	K	K;GHLENNPALEK;GNVGFVFT K;GTIEILSDVQLIK;IIQLDDYP	1;1;1;1;1		5	5	0.205	39043;19463;1160 6;25783;19334	P0 OS=Mus musculus OX=10090 GN=Rplp0 PE=1 SV=3

sp Q8K310 MATR3_MOUSE	4.376559455	94571.84259	TEEGPTLSYGR CDENILWLDYK;EAEAAIYHLQ LFEELRR;FGVEQDQDVMVFASF IR;GADFLVTEVENGGSLGSK;L APITSDPTEAAAVGAVEASFK; LNFSHGTHEYHAETIK ELEFYLR;IIDVVYNASNELVR ;LDVGNFSWGSECCTR;LTPEE EEILNK;NCIVLIDSTPYR;QWY ESHYALPLGR	1 1 1 1 1 1 1	1 1 1 6 6 6 6	1 1 1 6 6 6 6	0.013 0.013 0.013 0.1883 0.1883 0.1883 0.351	19062 19062 19062 595 595 595 020	- - - - - - -	Matrin-3 OS=Mus musculus OX=10090 GN=Matr3 PE=1 SV=1
sp P52480 KPYM_MOUSE	23.58195682	57808.00344	AVTEQGHLSNEER LKDENGALIR;LYEQILAENEK; NSSINEGSTYHR;QGVDIEAAR ;QWLNSGHISDVR;SASYSYLE DR;SGGTALHVAAAK;SYLTPV RDEESQSR;VGQTAQFDVADE DILGYLEELQK	1 1 1 1 1 1 1	1 1 1 6 6 6 9	1 1 1 6 6 6 13	0.0569 0.0569 0.0569 0.1098 0.1098 0.1098 0.1098	29700 29700 29700 2,42397;42396 2,42397;42396 2,42397;42396 2,42397;42396	- - - - - - -	Pyruvate kinase PKM OS=Mus musculus OX=10090 GN=Pkm PE=1 SV=4
sp P62242 RS8_MOUSE	23.50806444	24190.16227	AVTEQGHLSNEER LKDENGALIR;LYEQILAENEK; NSSINEGSTYHR;QGVDIEAAR ;QWLNSGHISDVR;SASYSYLE DR;SGGTALHVAAAK;SYLTPV RDEESQSR;VGQTAQFDVADE DILGYLEELQK	1 1 1 1 1 1 1	1 1 1 6 6 6 6	1 1 1 6 6 6 6	0.0569 0.0569 0.0569 0.351 0.351 0.351 0.351	29700 29700 29700 020 020 020 020	- - - - - - -	40S ribosomal protein S8 OS=Mus musculus OX=10090 GN=Rps8 PE=1 SV=2 14-3-3 protein beta/alpha OS=Mus musculus OX=10090 GN=Ywhab PE=1 SV=3
sp Q9CQV8 1433B_MOUSE	3.07602819	28068.86156	AVTEQGHLSNEER LKDENGALIR;LYEQILAENEK; NSSINEGSTYHR;QGVDIEAAR ;QWLNSGHISDVR;SASYSYLE DR;SGGTALHVAAAK;SYLTPV RDEESQSR;VGQTAQFDVADE DILGYLEELQK	1 1 1 1 1 1 1	1 1 1 6 6 6 6	1 1 1 6 6 6 6	0.0569 0.0569 0.0569 0.351 0.351 0.351 0.351	29700 29700 29700 020 020 020 020	- - - - - - -	40S ribosomal protein S8 OS=Mus musculus OX=10090 GN=Rps8 PE=1 SV=2 14-3-3 protein beta/alpha OS=Mus musculus OX=10090 GN=Ywhab PE=1 SV=3
sp Q9DBR7 MYP T1_MOUSE	32.90346806	114927.0483	AVTEQGHLSNEER LKDENGALIR;LYEQILAENEK; NSSINEGSTYHR;QGVDIEAAR ;QWLNSGHISDVR;SASYSYLE DR;SGGTALHVAAAK;SYLTPV RDEESQSR;VGQTAQFDVADE DILGYLEELQK	1 1 1 1 1 1 1	1 1 1 6 6 6 6	1 1 1 6 6 6 6	0.0569 0.0569 0.0569 0.351 0.351 0.351 0.351	29700 29700 29700 020 020 020 020	- - - - - - -	Protein phosphatase 1 regulatory subunit 12A OS=Mus musculus OX=10090 GN=Ppp1r12a PE=1 SV=2 E3 ubiquitin-protein ligase NEDD4 OS=Mus musculus OX=10090 GN=Nedd4 PE=1 SV=3
sp P46935 NEDD4_MOUSE	17.57414371	102641.6558	ANILEDYSR;DFVLHPR;EGFFE LIPQDLIK;FIIDEELFGQTHQH ELK;TGGSEIVVTNK	1 1 1 1 1 1 1	1 1 1 6 6 6 6	1 1 1 6 6 6 6	0.0643 0.0643 0.0643 0.37785 0.37785 0.37785 0.37785	14899;9173;28810 14899;9173;28810 14899;9173;28810 ;37785;15690 ;37785;15690 ;37785;15690 ;37785;15690	- - - - - - -	Amyloid beta A4 precursor protein-binding family B member 1-interacting protein OS=Mus musculus OX=10090 GN=Apbb1ip PE=1 SV=2 T-complex protein 1 subunit zeta OS=Mus musculus OX=10090 GN=Cct6a PE=1 SV=3
sp Q8R5A3 AB11P_MOUSE	2.529783838	74272.34537	DVLNLFK	1	1	1	0.0134	15291	-	4'-phosphopantetheine phosphatase OS=Mus musculus OX=10090 GN=Pank4 PE=1 SV=2 Serpine B6 OS=Mus musculus OX=10090 GN=Serpineb6 PE=1 SV=1 NEDD8-conjugating enzyme Ubc12 OS=Mus musculus OX=10090 GN=Ube2m PE=1 SV=1
sp P80317 TCPZ_MOUSE	4.376559455	57967.66786	SETDTSLR	1	1	1	0.0169	13114	-	
sp Q80YV4 PAN K4_MOUSE	8.428036392	91463.93982	GEVQALFLR;GLLAGNVFDW GAK;KFDELLQLASR	1;1;1	3	3	0.0402	0	-	
sp Q60854 SPB6_MOUSE	8.753118911	42571.17087	FCADHPFLFFIHHVK;LGMTD AFGGR	1;1	2	2	0.0661	35149;13191	-	
sp P61082 UBC12_MOUSE	2.608604626	20886.6484	LFEQNVQR	1	1	1	0.0437	13429	-	

sp Q8BMA6 SRP68_MOUSE	2.088488785	70530.32735	VEEISPNIR	1	1	1	0.0144	14113	-	Signal recognition particle subunit SRP68 OS=Mus musculus OX=10090 GN=Srp68 PE=1 SV=2
sp P08113 ENPL_MOUSE	3.33516677	92418.25449	LGVIEDHSNR	1	1	2	0.0125	16783;16782	-	Endoplasmin OS=Mus musculus OX=10090 GN=Hsp90b1 PE=1 SV=2
sp Q9251 ATAD3_MOUSE	3.07602819	66700.56235	QQQLLNEENLR	1	1	1	0.0186	24558	-	ATPase family AAA domain-containing protein 3 OS=Mus musculus OX=10090 GN=Atad3 PE=1 SV=1
sp P46735 MYO1B_MOUSE	5.864950608	128483.0006	LGNIEFKPESR;TLFQLEDLRK AENSQALTER;AMEALALAER;A SMVQSQEAPK;ETSYEEALAN QR;HLEDIVEK;HMAAASAEC QNYAK;LIEILSEK;LLATEQEDA AVAK;QVLQLQASHK;SAILEA TPK;SIEALLEAGQAQDTQAS HAEANQQQTR;TLVSTVGSM VFSEGEAQR;VEPAVSSIVNSI QVLASK;VGAAEEELHK	1;1 1;1;1;1;1; 1;1;1;1;1; 1;1;1;1	2	2	0.019	21649;20819	-	Unconventional myosin-Ib OS=Mus musculus OX=10090 GN=Myo1b PE=1 SV=3
sp Q99PL5 RRBP1_MOUSE	51.07742985	172775.8334	QVLASK;VGAAEEELHK	1;1;1;1;1; 1;1;1;1;1; 1;1;1;1	14	15	0.1103	13804;14707;1797 6;25257;12009;28 862;10914;23810; 17205;10496;4572 3;34825;33863;14 963;14964	-	Ribosome-binding protein 1 OS=Mus musculus OX=10090 GN=Rrbp1 PE=1 SV=2
sp O70579 PMP34_MOUSE	2.740552224	34390.77019	NVLSELLHQR	1	1	1	0.0293	14877	-	Peroxisomal membrane protein PMP34 OS=Mus musculus OX=10090 GN=Slc25a17 PE=1 SV=1
sp Q80SW1 SAH2_MOUSE	4.376559455	58913.44134	GIVEESVTGVHR	1	1	2	0.0226	21410;21411	-	S-adenosylhomocysteine hydrolase-like protein 1 OS=Mus musculus OX=10090 GN=Ahcyl1 PE=1 SV=1
sp P60867 RS20_MOUSE	4.376559455	13364.30823	TPVEPEVAIHR	1	1	1	0.0924	20324	-	40S ribosomal protein S20 OS=Mus musculus OX=10090 GN=Rps20 PE=1 SV=1
sp P80316 TCPE_MOUSE	2.413332988	59585.92275	FSELTSEK	1	1	1	0.0148	10775	-	T-complex protein 1 subunit epsilon OS=Mus musculus OX=10090 GN=Cct5 PE=1 SV=1
sp Q9CZM2 RL15_MOUSE	8.53161046	24131.08353	NTLQLHR;QGYVIYR;SLQSVA EER	1;1;1	3	3	0.1127	9135;9627;13022	-	60S ribosomal protein L15 OS=Mus musculus OX=10090 GN=Rpl15 PE=1 SV=4
sp Q9WVA4 TAGL2_MOUSE	4.376559455	22381.15642	NFSDNQLQEGK	1	1	1	0.0553	21308	-	Transgelin-2 OS=Mus musculus OX=10090 GN=Tagln2 PE=1 SV=4

sp P19253 RL13 A_MOUSE	4.376559455	23449.33256	CEGINISGNFYR		1	1	1	0.0591	25795	-	60S ribosomal protein L13a OS=Mus musculus OX=10090 GN=Rpl13a PE=1 SV=4
sp Q9ERE2 KRT8 1_MOUSE	6.703511025	52828.52058	ATAENEFVALK;FAAFIDK	1;1		2	2	0.0374	18531;7131	E	sp P97861 K RT86_MOUSE Keratin, type II cuticular Hb1 OS=Mus musculus OX=10090 GN=Krt81 PE=2 SV=2
sp Q3UV17 K22 O_MOUSE	2.740552224	62805.96022	AQYEDIAQK;FASFIDKVR;LAL DVEIATYR	1;0;0		1	1	0.0488	14383;14974;2084 7	-	Keratin, type II cytoskeletal 2 oral OS=Mus musculus OX=10090 GN=Krt76 PE=1 SV=1
sp Q6NXH9 K2C 73_MOUSE	2.608604626	58874.69536	FASFIDKVR;FLEQQNQVLQTK ;LALDIEIATYR	0;0;1		1	2	0.0594	14974;26990;2699 1;21262;21264	-	Keratin, type II cytoskeletal 73 OS=Mus musculus OX=10090 GN=Krt73 PE=1 SV=1
sp P50446 K2C6 A_MOUSE	4.376559455	59298.61673	LDVEIATYR;SLDLDSIIAEVK;T AAENEFVTLK;YEDEINK;YEDEI NKR	0;0;0;0;1; 0;0		1	1	0.1085	13228;14974;2084 7;22067;19504;99 84;14408	-	Keratin, type II cytoskeletal 6A OS=Mus musculus OX=10090 GN=Krt6a PE=1 SV=3
sp O55222 ILK_ MOUSE	18.47883522	51339.91862	GDDTPLHLAASHGHR;GMAF LHTLEPLIPR;LNENHSGELWK; SAVVEMLIMR;WQGNDIVVK	1;1;1;1;1		5	6	0.1305	29412;29640;2281 2;22813;17104;14 177	-	Integrin-linked protein kinase OS=Mus musculus OX=10090 GN=Ilk PE=1 SV=2
sp Q2KN98 CYT SA_MOUSE	31.62915901	124411.5073	FSLEQR;SDIQDLLESVR;SEAQ EEIGDLK;SEAQEEIGDLKR;SFD SASQVPNAAAAAIPR;SLLDE HHISYVIDEDVK;SNYGELPVQ EHLLR	1;1;1;1;1; 1;1;1		8	9	0.0877	31590;20328;2116 3;19346;24279;32 741;36752;30644; 30692	-	Cytospin-A OS=Mus musculus OX=10090 GN=Specc1l PE=1 SV=1
sp Q8VDJ3 VIGL N_MOUSE	15.42586582	141655.2719	ASVITQVFHVPLEER;ELLELAS R;IIFPAAEDKDQDLITIIGK;LQT QASATVPIPK;SGLVPQQIK	1;1;1;1;1		5	5	0.0505	31897;10532;3799 9;23673;11639	-	Vigilin OS=Mus musculus OX=10090 GN=Hdlbp PE=1 SV=1
sp B2RQC6 PYR 1_MOUSE	6.41119496	243083.6162	EAAAGNIGGQTVR;LSLDDLL QR	1;1		2	2	0.0099	20174;14637	-	musculus OX=10090 GN=Cad PE=1 SV=1
sp Q8BU30 SYIC _MOUSE	7.711726226	144178.9396	DVLLPWYNAYR;QESDYEILER	1;1		2	2	0.0166	25239;21363	-	Isoleucine--tRNA ligase, cytoplasmic OS=Mus musculus OX=10090 GN=lars1 PE=1 SV=2
sp P12382 PFKA L_MOUSE	9.398497069	85305.40883	EQWWLNLNLR;GQVQEVGWH DVAGWLGR;NEWGSLLEELVK	1;1;1		3	3	0.0474	16968;34774;2545 3	-	phosphofructokinase, liver type OS=Mus musculus OX=10090 GN=Pfkl PE=1 SV=4
sp P11983 TCPA _MOUSE	7.117111168	60410.66862	AFHNEAQVNPER;WIGLDLVH GKPR	1;1		2	2	0.0432	25300;24747	-	T-complex protein 1 subunit alpha OS=Mus musculus OX=10090 GN=Tcp1 PE=1 SV=3
sp Q08879 FBLN 1_MOUSE	2.150691262	77980.57644	DSFDIIK		1	1	1	0.0099	7866	-	Fibulin-1 OS=Mus musculus OX=10090 GN=Fbln1 PE=1 SV=2

sp P70372 ELAV1_MOUSE	6.906343294	36146.13183	SR	SLFSSIGEVE\$AK;VLVDQTTGL	1;1	2	2	0.0736	23661;18419	-	ELAV-like protein 1 OS=Mus musculus OX=10090 GN=Elavl1 PE=1 SV=2
sp P61027 RAB10_MOUSE	4.376559455	22526.58867	NIDEHANEDVER		1	1	1	0.06	26082	-	Ras-related protein Rab-10 OS=Mus musculus OX=10090 GN=Rab10 PE=1 SV=1
sp Q8BMS1 ECHA_MOUSE	16.46484514	82617.45908	PEVLLGILPGAGGTQR	FVDLYGAQK;LPAKPEVSSDE DVQYR;MQLLEIITTDK;TVLGV	1;1;1;1	4	6	0.0747	13615;33710;33711;22131;37263;37264	-	Trifunctional enzyme subunit alpha, mitochondrial OS=Mus musculus OX=10090 GN=Hadha PE=1 SV=1
sp Q8C1B7 SEP11_MOUSE	2.529783838	49663.31263	STLMDTLFNTK		1	1	1	0.0255	21040	E	sp Q9R1T4 SEPTIN11_MOUSE Septin-11 OS=Mus musculus OX=10090 GN=Septin11 PE=1 SV=4
sp Q9Z1Z0 USO1_MOUSE	2.740552224	106916.595	LLTSLLK		1	1	1	0.0073	6557	-	General vesicular transport factor p115 OS=Mus musculus OX=10090 GN=Uso1 PE=1 SV=2
sp Q99LF4 RTCB_MOUSE	17.04667098	55213.86602	SHNIAK	VME\$EAPESYK;QIGNVAALPGI VHR;VFNTTPDDL\$DLHVIYDV	1;1;1;1;1	5	6	0.1347	19423;11339;21834;26199;26198;44103	-	RNA-splicing ligase RtcB homolog OS=Mus musculus OX=10090 GN=Rtcb PE=1 SV=1
sp O70475 UGDH_MOUSE	36.13572572	54797.26613	QR	ESSSIYISK;IFDANTKPNLNLQ VLSNPEFLAEGTAIK;IIDS\$LFNT VTDK;IIDS\$LFNTVTDKK;ILTTN TWSS\$ELSK;INAWNSPTLPIYE PGLK;NLFFSTNIDDAIR;VLIGG DETPEGQK;YWQQVIDMNDY	1;1;1;1;1;1;1;1;1;1	10	11	0.2819	38693;12881;46256;24030;27436;27437;27084;35110;28224;23342;32500	-	UDP-glucose 6-dehydrogenase OS=Mus musculus OX=10090 GN=Ugdh PE=1 SV=1
sp A3KGW5 GT253_MOUSE	2.25575174	67629.3278	TLNSSILK		1	1	1	0.0135	8983	-	Inactive glycosyltransferase 25 family member 3 OS=Mus musculus OX=10090 GN=Cercam PE=3 SV=1
sp P10078 ZFP28_MOUSE	2.076765906	93249.55458	AFSHHASLTQHQR		1	1	1	0.0158	28099	-	Zinc finger protein 28 OS=Mus musculus OX=10090 GN=Zfp28 PE=2 SV=3
sp Q3KNJ2 NHEJ1_MOUSE	2.413332988	32718.81157	SLALQSHVR	GEEGLILRVQSELSGLPFSWHF HCIPASSSLVSQHLIHLPMGV	1	1	1	0.1763	49461	-	Non-homologous end-joining factor 1 OS=Mus musculus OX=10090 GN=Nhej1 PE=1 SV=1
sp Q9DCN2 NB5R3_MOUSE	4.376559455	34105.74552	STPAITLENPDIK		1	1	1	0.0432	24948	-	NADH-cytochrome b5 reductase 3 OS=Mus musculus OX=10090 GN=Cyb5r3 PE=1 SV=3

sp Q3TDQ1 STT3B_MOUSE	7.452587645	93185.4719	EAYFWLR;EGDYFTQQGEFR	1;1	2	2	0.0231	12054;26995	-	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3B OS=Mus musculus OX=10090 GN=Stt3b PE=1 SV=2	
sp Q62261 SPTB2_MOUSE	18.16400468	274052.4505	EIEELQSQAQALSQEGK;LLEVLSGER;LTTLELLEVR;LVSDGNI NSDR;SALPAQSAATLPAR	1;1;1;1;1	5	5	0.0258	34656;12950;1836 3;18435;23672	-	Spectrin beta chain, non-erythrocytic 1 OS=Mus musculus OX=10090 GN=Sptbn1 PE=1 SV=2	
sp P61222 ABCE1_MOUSE	4.376559455	67271.01644	GSELQNYFTK		1	1	0.0167		18334	-	ATP-binding cassette sub-family E member 1 OS=Mus musculus OX=10090 GN=Abce1 PE=1 SV=1
sp P52332 JAK1_MOUSE	3.07602819	133281.6339	NVLVESEHQVK		1	1	0.0095		21377	-	Tyrosine-protein kinase JAK1 OS=Mus musculus OX=10090 GN=Jak1 PE=1 SV=1
sp Q08091 CNN1_MOUSE	12.45310335	33334.60343	EWIEGVTGR;IGNNFMDGLK;NIIGLQMGTNK;VNESTQNW HQLNIGNFIK	1;1;1;1	4	4	0.165	13787;15802;1841 4;40172	-	Calponin-1 OS=Mus musculus OX=10090 GN=Cnn1 PE=1 SV=1	
sp Q8CGC7 SYEP_MOUSE	18.87817812	169971.601	FVELPGAEMGK;KEENLAEWY SQVITK;SQGSGLSSGGAGEG QGPK;TGQEYKPGNPSAAAV QTVSTK;VYEELLAIPVVR	1;1;1;1;1	5	5	0.0509	18041;33803;2907 1;38485;25016	-	glutamate/proline--tRNA ligase OS=Mus musculus OX=10090 GN=Eprs1 PE=1 SV=4	
sp Q8CGP1 H2B1K_MOUSE	11.49367114	13911.57292	AMGIMNSFVNDIFER;EIQTAV R;QVHPDTGISSK	1;1;1	3	3	0.2619	32237;7298;17737	SE	2B1H_MOUSE E;sp P10854 H2B1M_MOUSE;sp P10853 H2B1F_MOUSE;sp Q8CGP2 H2B1P_MOUSE;sp Q64475 H2B1B_MOUSE;sp Q6ZWY9 H2B1C_MOUSE E;sp Q64525 H2B2B_MOUSE Histone H2B type 1-K OS=Mus musculus OX=10090 GN=H2bc12 PE=1 SV=3	

sp P21981 TGM2_MOUSE	62.38067698	77012.26341	;DLYLENPEIK;EYVLTQQGFIY QGSVK;GLLIEPAANSYLLAER; GYEASVDSLTFGAVTGPDPSE EAGTK;KLVAEVSLK;LAEKEET GVAMR;NEFGELESNK;NPLS DPLYDCIFTVEGAGLTK;SVEV SDPVPAGDLVK;VDLFPTDIGL HK;VVSAMVNCNDDQGVLL GR;VVTNYN SAHDQNSNLLIE 1;1;1;1;1; YFR;WDNNYGDGISPMAWIG 1;1;1;1;1; SVDILR;YPEGSPEER;YSGCLTE 1;1;1;1;1; SNLIK 1;1	17	17	0.3644	17973;24776;1983 7;34183;31982;43 810;12137;23056; 17661;40634;2789 2;23691;35683;42 933;42701;14323; 24548	-	Protein-glutamine gamma-glutamyltransferase 2 OS=Mus musculus OX=10090 GN=Tgm2 PE=1 SV=4
			DGQAMLWDLNEGK;FSPNSS NPIIVSCGWDK;GHNGWVTQ IATTPQFPDMILSASR;HLYTLD GGDIINALCFSPNR;IIVDELKQ EVISTSSK;LWDLTTGTTR;YT 1;1;1;1;1; VQDESHSEWVSCVR 1;1				27007;35005;4411 2;40244;40228;33 020;33019;20868; 36266		
sp P68040 RACK1_MOUSE	25.21194458	35054.55748	ELDTVTLEDIKEHVR;EQQDLE FAK;ISLADIAQK;VYEFLDKLD VVR 1;1;1;1	4	5	0.0849	33167;15762;1131 5;27492;27494	-	Receptor of activated protein C kinase 1 OS=Mus musculus OX=10090 GN=Rack1 PE=1 SV=3 26S proteasome non-ATPase regulatory subunit 3 OS=Mus musculus OX=10090 GN=Psmc3 PE=1 SV=3 Glutamate dehydrogenase 1, mitochondrial OS=Mus musculus OX=10090 GN=Glud1 PE=1 SV=1 Peroxisomal oxidoreductase 2 OS=Mus musculus OX=10090 GN=Prdx2 PE=1 SV=3 Latent-transforming growth factor beta-binding protein 2 OS=Mus musculus OX=10090 GN=Ltbp2 PE=1 SV=2 Sequestosome-1 OS=Mus musculus OX=10090 GN=Sqstm1 PE=1 SV=1
sp P14685 PSMD3_MOUSE	14.82883791	60680.34501							
sp P26443 DHE3_MOUSE	4.376559455	61298.17174	TAAYVNAIEK	1	1	1	0.0179	14870	-
sp Q61171 PRDX2_MOUSE	4.376559455	21765.0581	QITVNDLPVGR	1	1	1	0.0556	19144	-
sp O08999 LTBP2_MOUSE	2.923749796	195700.3731	TLEGPLK	1	1	1	0.0044	8833	-
sp Q64337 SQSTM1_MOUSE	4.829041009	48132.15795	LTPPTPESSTGTEDK;NYDIGA ALDTIQYSK 1;1 AFVHWYVGEEMEEGFSEAR; AVCMLSNTTAAIEAWAR;AVF VDLEPTVIDEVR;EDAANNYA R;EIIDLVLDR;FDGALNVDLTE FQTNLVPPYR;IHFPLATYAPVI SAEK;LIGQIVSSITASLR;NLDIE RPTYTNLNR;QLFHPEQLITGK; 0;0;0;0;0; QLFHPEQLITGKEDAANNYAR 0;0;1;0;0; ;TIGGGDDSFNTFFSETGAGK 0;0	2	2	0.0701	30565;30922 40846;41019;3426 5;34264;31478;31 477;13162;15065; 41790;32484;3248 3;32482;26541;31 788;31787;25280; 25282;41877;4187 6;36687;36686	-	
sp P68369 TUBA1A_MOUSE	4.376559455	50103.60889		1	1	0.3703	6;36687;36686	-	Tubulin alpha-1A chain OS=Mus musculus OX=10090 GN=Tuba1a PE=1 SV=1

sp Q61595 KTN1_MOUSE	5.402979759	152497.9664	EQDVLLSHQDTK;VEPVLVTK	1;1	2	2	0.0151	25334;9220	-	Kinectin OS=Mus musculus OX=10090 GN=Ktn1 PE=1 SV=1 Phospholipid-transporting ATPase IA OS=Mus musculus OX=10090 GN=Atp8a1 PE=1 SV=2	
sp P70704 AT8A1_MOUSE	2.076765906	131329.5368	IWILTGDK		1	1	1	0.0069	10941	-	TRIO and F-actin-binding protein OS=Mus musculus OX=10090 GN=Triobp PE=1 SV=3
sp Q99KW3 TARA_MOUSE	2.740552224	223231.9355	TVRPTSAPDVTK		1	1	1	0.006	21082	-	Nucleolar protein 58 OS=Mus musculus OX=10090 GN=Nop58 PE=1 SV=1
sp Q6DFW4 NOP58_MOUSE	4.376559455	60304.71515	HAASTVQILGAEK DNETLMELK;DRDDYVPYTGE		1	1	1	0.0243	22779	-	Tropomodulin-3 OS=Mus musculus OX=10090 GN=Tmod3 PE=1 SV=1
sp Q9JHJ0 TMO D3_MOUSE	16.65079362	39478.33193	K;FGYQFTQQGPR;HFSLAATR ;NIPIPTLK;QQLGTSVELEMAK	1;1;1;1;1; 1	6	6	0.1733	15281;26508;2285 5;9756;9571;2590 9	-	SWI/SNF-related matrix- associated actin-dependent regulator of chromatin subfamily A-like protein 1 OS=Mus musculus OX=10090 GN=Smarcal1 PE=1 SV=1	
sp Q8BJL0 SMAL1_MOUSE	2.413332988	100777.2611	AAVPILK		1	1	1	0.0077	4891	-	60S ribosomal protein L28 OS=Mus musculus OX=10090 GN=Rpl28 PE=1 SV=2
sp P41105 RL28_MOUSE	5.411932676	15723.65511	NCSSFLIK;QTYSTEPNNLK	1;1	2	2	0.1387	11603;21810	-	60S ribosomal protein L8 OS=Mus musculus OX=10090 GN=Rpl8 PE=1 SV=2	
sp P62918 RL8_MOUSE	6.413600008	28007.28818	RTELFIAAEGIHGTGFVYCGK;T ELFIAAEGIHGTGFVYCGK	1;1	2	2	0.0817	41635;39791	-	Nucleosome assembly protein 1-like 1 OS=Mus musculus OX=10090 GN=Nap1l1 PE=1 SV=2	
sp P28656 NP1L1_MOUSE	7.711726226	45316.90632	FYEEVHDLER;GIPEFWLTVFK	1;1	2	2	0.0537	23149;23164	-	A-kinase anchor protein 9 OS=Mus musculus OX=10090 GN=Akap9 PE=1 SV=2	
sp Q70FJ1 AKAP9_MOUSE	3.33516677	435944.1812	SLLAEIEDLR		1	1	1	0.0026	17439	-	60S ribosomal protein L18 OS=Mus musculus OX=10090 GN=Rpl18 PE=1 SV=3
sp P35980 RL18_MOUSE	8.753118911	21631.17874	ILTFDQLALESPK;TNRPPLSLS R	1;1	2	3	0.1223	26972;16819;1682 0	-	2 OS=Mus musculus OX=10090 GN=Rock2 PE=1 SV=1	
sp P70336 ROCK2_MOUSE	5.63737369	160484.6252	LEGWLSLPVR;QIQQLESNNR	1;1	2	2	0.0144	17793;19721	-	sp Q60972 RBBP7 OS=Mus musculus BBP4_MOUSE OX=10090 GN=Rbbp7 PE=1 E SV=1	
sp Q60973 RBBP7_MOUSE	7.711726226	47760.16816	LNVDWLSK;TPSSDVLVFDYT K	1;1	2	2	0.0494	11815;26882			

sp Q91VR5 DDX1_MOUSE	6.67033354	82447.76632	FGFGFGGTGK;LDDLVTGK	1;1	2	2	0.0257	11795;10993	-	ATP-dependent RNA helicase DDX1 OS=Mus musculus OX=10090 GN=Ddx1 PE=1 SV=1
sp P01029 CO4B_MOUSE	10.25660266	192793.5912	ASAGLLGAHAAAITAYALT LK;DHAVDLIQK;DSSTWLTAFV	1;1;1	3	3	0.0247	37802;13568;2407 0	-	Complement C4-B OS=Mus musculus OX=10090 GN=C4b PE=1 SV=3
sp Q8K2B3 SDHA_MOUSE	3.33516677	72539.17051	GEGGILINSQGER		1	1	0.0196		22930 -	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial OS=Mus musculus OX=10090 GN=Sdha PE=1 SV=1
sp P63330 PP2A_MOUSE	2.666659851	35585.4118	YSFLQFDPAPR		1	1	0.0356		23274 E	Serine/threonine-protein phosphatase 2A catalytic subunit alpha isoform OS=Mus musculus OX=10090 GN=Ppp2ca PE=1 SV=1
sp Q5SYD0 MYO1D_MOUSE	15.69276415	116007.3507	HQVEYLGLLENVR;IGELVGVL VNHF;NSMIALVDNLASK;VT DGMFLEALNSK	1;1;1;1	4	4	0.0517	29218;25674;2430 4;25658	-	Unconventional myosin-1d OS=Mus musculus OX=10090 GN=Myo1d PE=1 SV=1
sp P20029 BIP_MOUSE	14.53601928	72377.4615	ELEEIVQPIISK;IINEPTAAAIY GLDK;IINEPTAAAIYGLDKR;I TITNDQNR;ITPSYVAFTPEGE R;VEIIANDQGNR	1;0;1;1;1; 0	4	4	0.0962	24930;30746;3343 9;14706;29156;19 695	-	Endoplasmic reticulum chaperone BiP OS=Mus musculus OX=10090 GN=Hspa5 PE=1 SV=3
sp O35129 PHB2_MOUSE	4.376559455	33275.91554	IVQAEGEAEAAK		1	1	0.0401		19251 -	Prohibitin-2 OS=Mus musculus OX=10090 GN=Phb2 PE=1 SV=1
sp Q9Z1Q9 SYVC_MOUSE	3.07602819	140127.084	QLWWGHR		1	1	0.0055		12006 -	Valine--tRNA ligase OS=Mus musculus OX=10090 GN=Vars1 PE=1 SV=1
sp A2ABU4 MYOM3_MOUSE	2.234022521	161677.7746	FTVPGLR		1	1	0.0049		6607 -	Myomesin-3 OS=Mus musculus OX=10090 GN=Myom3 PE=1 SV=1
sp P17427 AP2A2_MOUSE	9.061929987	103951.0575	ALLLSTYIK;IAGDYVSEEVWYR ;YGGTFQNVSVK	1;1;1	3	3	0.0352	13130;29473;1875 6	-	2 OS=Mus musculus OX=10090 GN=Ap2a2 PE=1 SV=2
sp P63037 DNJA1_MOUSE	2.529783838	44839.45178	TIVITSHPGQIVK		1	1	0.0327		24805 -	DnaJ homolog subfamily A member 1 OS=Mus musculus OX=10090 GN=Dnaja1 PE=1 SV=1
sp Q91VR2 ATPG_MOUSE	7.711726226	32865.14218	HLIIGVSSDR;VYGTGSLALYEK	1;1	2	3	0.0738	15439;15441;2200 6	-	ATP synthase subunit gamma, mitochondrial OS=Mus musculus OX=10090 GN=Atp5f1c PE=1 SV=1

[illegible]

sp Q8K4L3 SVIL_MOUSE	36.10413763	243011.2063	ADV KPYDVTR;ATYIQTIEEGIN THTHAAK;EFGETTSEQTEVAA R;FLDWTELK;GAANDSTQFTV AGR;GAQVQVLQGK;LLGGQT SYQSAGDPK;NALTVAEDSG VQTR;QQESSEQLAEK;REEEE ENVQSEWR;VTEHNETILFK	1;1;1;1;1; 1;1;1;1;1; 1	11	12	0.065	17578;37972;3063 6;13951;24841;13 259;28119;28395; 21215;31801;2293 9;22938	-	Supervillin OS=Mus musculus OX=10090 GN=Swil PE=1 SV=1
sp Q3TDN2 FAF2_MOUSE	2.076765906	52438.446	LLQFQDLTGIESMEQCRLALE QHNWNMEAAVQDR	1	1	1	0.0764	48243	-	FAS-associated factor 2 OS=Mus musculus OX=10090 GN=Faf2 PE=1 SV=2
sp Q6PDQ2 CHD4_MOUSE	7.711726226	217613.785	GPFLVSAPLSTIINWER;HHYE QQQEDLAR	1;1	2	2	0.0151	34870;28905	-	Chromodomain-helicase- DNA-binding protein 4 OS=Mus musculus OX=10090 GN=Chd4 PE=1 SV=1
sp P67984 RL22_MOUSE	4.376559455	14749.77256	AGNLGGGVVTIER	1	1	1	0.1016	20143	-	60S ribosomal protein L22 OS=Mus musculus OX=10090 GN=Rpl22 PE=1 SV=2
sp Q99JW4 LIMS1_MOUSE	4.376559455	37214.82621	VIEGDVVSALNK	1	1	1	0.0369	20186	-	antigen-like-containing domain protein 1 OS=Mus musculus OX=10090 GN=Lims1 PE=1 SV=3
sp Q3TJZ6 FA98A_MOUSE	4.376559455	55021.20133	AQEGGGSEVFQELK	1	1	1	0.0272	27051	-	Protein FAM98A OS=Mus musculus OX=10090 GN=Fam98a PE=1 SV=1
sp Q91YR1 TWF1_MOUSE	4.376559455	40054.47028	HQTLQGVAFPISR	1	1	1	0.0371	26430	-	Twinfilin-1 OS=Mus musculus OX=10090 GN=Twf1 PE=1 SV=2
sp O08553 DPYL2_MOUSE	4.376559455	62238.58995	NLHQSGFSLSGAQIDDNIPR	1	1	1	0.035	38914	-	Dihydropyrimidinase-related protein 2 OS=Mus musculus OX=10090 GN=Dpysl2 PE=1 SV=2
sp Q4VAC9 PKHG3_MOUSE	4.376559455	148427.8387	LQEIQSLLINWK	1	1	1	0.0089	27233	-	Pleckstrin homology domain- containing family G member 3 OS=Mus musculus OX=10090 GN=Plekhg3 PE=1 SV=2
sp Q9CQQ7 AT5F1_MOUSE	2.740552224	28930.4413	IAQLEEVK	1	1	1	0.0312	10494	-	ATP synthase F(0) complex subunit B1, mitochondrial OS=Mus musculus OX=10090 GN=Atp5pb PE=1 SV=1
sp Q8BP92 RCN2_MOUSE	3.07602819	37247.84231	QLHDDYFYHDEL	1	1	1	0.0375	29617	-	Reticulocalbin-2 OS=Mus musculus OX=10090 GN=Rcn2 PE=1 SV=1
sp Q9CR00 PSMD9_MOUSE	2.740552224	24704.56949	VNSISPGSPASIAGLQVDDEIV EFGSVNTQNFQSVQNVGT VQHSEGKPLNVTVIRR	1	1	1	0.2568	49581	-	26S proteasome non-ATPase regulatory subunit 9 OS=Mus musculus OX=10090 GN=Psm9 PE=1 SV=1

sp Q3UZ39 LRRF1_MOUSE	2.215669586	79201.21721	AMVSNAQLDNEK;ETLQNSE QE QPKPNTGK	0;1	1	1	0.0398	22598;35372	-	Leucine-rich repeat flightless-interacting protein 1 OS=Mus musculus OX=10090 GN=Lrrfip1 PE=1 SV=2
sp P80318 TCPG_MOUSE	17.43744253	60591.36039	AVAQALEVIPR;EIQVQH PAAK ;ELGIWEPLAVK;KGESQTDIEIT R;TAVETAVLLLLR	1;1;1;1;1	5	5	0.1009	17685;16218;2053 1;24329;18324	-	T-complex protein 1 subunit gamma OS=Mus musculus OX=10090 GN=Cct3 PE=1 SV=1
sp Q62417 SRBS1_MOUSE	3.07602819	142982.4208	FGDLLNIDDTAK		1	1	0.0093	22673	-	Sorbin and SH3 domain-containing protein 1 OS=Mus musculus OX=10090 GN=Sorbs1 PE=1 SV=2
sp Q8R1F1 NIBA2_MOUSE	7.711726226	84764.9648	FDSVSTSVFK;FQELIFEDFAR	1;1	2	2	0.028	16071;25385	-	Protein Niban 2 OS=Mus musculus OX=10090 GN=Niban2 PE=1 SV=2
sp P68254 1433T_MOUSE	7.11711168	27760.78201	AVTEQGAELSNEER;YLAEVAC GDDR	1;1	2	3	0.102	28419;28417;2097 9	-	14-3-3 protein theta OS=Mus musculus OX=10090 GN=Ywhaq PE=1 SV=1
sp P16546 SPTN1_MOUSE	25.25354554	284422.2789	ADVVESWIGEK;LGESQTLQQ FSR;LSDDNTIGQEEIQQR;NT TGVTEEALK;QWELLLEK;SQLL GSAHEVQR;SSEEIESAFR	1;1;1;1;1; 1;1	7	7	0.032	19796;24812;3227 1;17552;14186;22 772;17287	-	Spectrin alpha chain, non-erythrocytic 1 OS=Mus musculus OX=10090 GN=Sptan1 PE=1 SV=4
sp P80315 TCPD_MOUSE	8.753118911	58029.73251	ALIAGGGAPEIELALR;GIHPTII SESFQK	1;1	2	2	0.0538	28858;26494	-	T-complex protein 1 subunit delta OS=Mus musculus OX=10090 GN=Cct4 PE=1 SV=3
sp Q7TPV4 MBB1A_MOUSE	21.49917145	151941.5219	AQDASLNVPER;ATQTLQTLG EAQSK;LITGLGVGR;LPNVAL DLLR;LVQLADMLLNHNHNR;NV TSVTSLTTQQR	1;1;1;1;1; 1	6	6	0.0521	18757;26988;9247 ;16314;28517;259 30	-	Myb-binding protein 1A OS=Mus musculus OX=10090 GN=Mybbp1a PE=1 SV=2
sp Q00547 HMMR_MOUSE	2.150691262	91729.23806	YNDTAQSLR AEGTTYRDELLTK;ALDLLYGM VSK;FAVSQMSSLLDSAHLVA SSTQR;ILIEDSDQNLK;NYLSL		1	1	0.0113	14439	-	Hyaluronan mediated motility receptor OS=Mus musculus OX=10090 GN=Hmnr PE=1 SV=4
sp O54774 AP3D1_MOUSE	18.91257874	134995.9812	APLFFK	1;1;1;1;1	5	5	0.0567	27514;19085;4089 1;21600;22380	-	AP-3 complex subunit delta-1 OS=Mus musculus OX=10090 GN=Ap3d1 PE=1 SV=1
sp Q69Z38 PEAK1_MOUSE	12.08828568	190978.3654	EDLFQIFTTSATLAQK;FGVDS WSDFR;STEAESILHSEGSR	1;1;1	3	3	0.0231	33410;19242;2766 8	-	Inactive tyrosine-protein kinase PEAK1 OS=Mus musculus OX=10090 GN=Peak1 PE=1 SV=4
sp Q8BX02 KAN K2_MOUSE	6.453325361	90189.59127	VAVLETQLK;VPAPENVASGPD PEEEIR	1;1	2	2	0.0308	12539;33064	-	KN motif and ankyrin repeat domain-containing protein 2 OS=Mus musculus OX=10090 GN=Kank2 PE=1 SV=1

sp P09411 PGK1_MOUSE	14.8923007	44521.98545	ALESPERPFLAILGGAK;ELNYF AK;FHVEEEGK;LGDVYVNDAF GTAHR	1;1;1;1	4	4	0.1127	32693;9208;11793 ;30277	-	Phosphoglycerate kinase 1 OS=Mus musculus OX=10090 GN=Pgk1 PE=1 SV=4 Synaptopodin OS=Mus musculus OX=10090 GN=Synpo PE=1 SV=2 Pyruvate dehydrogenase protein X component, mitochondrial OS=Mus musculus OX=10090 GN=Pdhx PE=1 SV=1 Caprin-1 OS=Mus musculus OX=10090 GN=Caprin1 PE=1 SV=2 Eukaryotic translation initiation factor 3 subunit C OS=Mus musculus OX=10090 GN=Eif3c PE=1 SV=1 Very-long-chain 3-oxoacyl-CoA reductase OS=Mus musculus OX=10090 GN=Hsd17b12 PE=1 SV=1 Trifunctional enzyme subunit beta, mitochondrial OS=Mus musculus OX=10090 GN=Hadhb PE=1 SV=1 60S ribosomal protein L14 OS=Mus musculus OX=10090 GN=Rpl14 PE=1 SV=3 Protein flightless-1 homolog OS=Mus musculus OX=10090 GN=Flii PE=1 SV=1 Coatomer subunit alpha OS=Mus musculus OX=10090 GN=Copa PE=1 SV=2	
sp Q8CC35 SYNPO_MOUSE	5.816580414	99490.36571	LVDLEEEGTSQSR;SSILLIDK	1;1	2	2	0.0226	26667;9343	-		
sp Q8BKZ9 ODPX_MOUSE	6.075718995	53965.22661	HSLDASQGTATGPR;VSVNDF IIR	1;1	2	3	0.0459	24917;24915;1431 6	-		
sp Q60865 CAPR1_MOUSE	4.376559455	78120.80125	LNEQYEHASIHLWDLLEGK		1	1	1	0.0269	40470	-	
sp Q8R1B4 EIF3C_MOUSE	9.200117379	105464.7601	DAHNALLDIQSSGR;ELLGQG LLLR;LNEILQVR	1;1;1	3	4	0.0351	27508;27512;1591 7;12074	-		
sp O70503 DHB12_MOUSE	8.044190232	34719.42714	AYAEELAK;IQKPTLDKPSAETF VK;LVLPGMVER	1;1;1	3	3	0.1058	9527;33243;12890	-		
sp Q99JY0 ECHB_MOUSE	4.376559455	51353.40812	IPFLLSGTSYK		1	1	1	0.0232	19598	-	
sp Q9CR57 RL14_MOUSE	6.539057601	23549.20234	CMQLTDFILK;LVAIVDVIDQN R ADLTALFLPR;EGEEAAAEAE K;LLQSLLDTR;NAEAVLQGQG LSGK;NWDDVLTVDYTR;RWD QGLEKPR;VPECLYLTPSLR ASNLNSTYDLYTIPIK;CLFTLL GHLDYIR;FEEAVEK;GVNWAA FHPTMPLIVSGADDR;ISPLQF R;LDALCNIHENIR;LLELGPKPE VAQQTR;LSFLYLITGNLEK;LV GQSIIAYLQK;NLSPGAVESDV R;QELILSNSEDK;SGAWDESG VFIYTTSNHIK;TGVQTFR;TLDL PIYVTR;TTFFHHIEYPWILSASD DQTIR;VLTIDPTEFK;VTTVTEI GK;VTTVTEIGKDVIGLR	1;1 1;1;1;1;1; 1;1	2	2	0.1014	20985;23694 16104;20794;1419 1;24187;27504;21 502;26273	- -		
sp Q9JJ28 FLII_MOUSE	27.00521551	144711.6184			7	7	0.0622			-	
sp Q8CIE6 COPA_MOUSE	66.97088182	138343.8526			18	21	0.1806	33638;30045;8256 ;39934;8524;2677 8;31058;31059;27 877;23030;20171; 21194;38154;7057 ;18478;43639;436 38;43640;17560;1 1000;29735	-		

sp O70251 EF1B_MOUSE	4.376559455	24678.24504	TPAGLQVLNDYLADK EAESCDCLQGQQLTHSLGGG TGSGMGTLISK;EIVHIQAGQ CGNQIGAK;EVDEQMLNVQN K;FPGQLNADLR;FWEVISDEH GIDPTGTYHGDSLQLDR;GH YTEGAELVDSVLDVVR;ISEQF TAMFR;ISVYYNEATGGK;LTP TYGDLNHLVSATMSGVTTCL R;NSSYFVEWIPNNVK;SGPFG QIFRPDNFVFGQSGAGNNW AK;TAVCDIPPR;YLTVAAVFR ATSNVFAMFDQSQIQEFK;DG FIDKEDLHDMLASLGK;FTDEE VDEMYR;LNGTDPEDVIR;NAF ACFDEEASGFIHEDHLR EIVHIQAGQCGNQIGAK;EVD EQMLNVQNK;FPGQLNADLR ;GHYTEGAELVDSVLDVVR;IN VYYNEATGNK;ISEQFTAMFR; LTPPTYGDLNHLVSATMSGVT TCLR;MSATFIGNSTAIQELFK; NSSYFVEWIPNNVK;SGPFGQI FRPDNFVFGQSGAGNNWAK; TAVCDIPPR EIVHIQAGQCGNQIGAK;EVD EQMLNVQNK;FPGQLNADLR ;GHYTEGAELVDSVLDVVR;IN VYYNEAAGNK;ISEQFTAMFR; LTPPTYGDLNHLVSATMSGVT TCLR;MSATFIGNSTAIQELFK; NSSYFVEWIPNNVK;SGPFGQI FRPDNFVFGQSGAGNNWAK; TAVCDIPPR AGQCGNQIGTK;EVDEQMLAI QNK;FPGQLNADLR;FWEVIS DEHGIDQAGGYVGDSALQLE R;GHYTEGAELVDSVLDVVR;IS EQFSAMFR;ISVYYNESSK;LT TPTYGDLNHLVSATMSGVTT LR;NSSYFVEWIPNNVK;YLT ATVFR	1	1	1	0.0667	29989	-	Elongation factor 1-beta OS=Mus musculus OX=10090 GN=Eef1b PE=1 SV=5
sp P99024 TBB5_MOUSE	8.753118911	49638.97066	AK;TAVCDIPPR;YLTVAAVFR ATSNVFAMFDQSQIQEFK;DG FIDKEDLHDMLASLGK;FTDEE VDEMYR;LNGTDPEDVIR;NAF ACFDEEASGFIHEDHLR EIVHIQAGQCGNQIGAK;EVD EQMLNVQNK;FPGQLNADLR ;GHYTEGAELVDSVLDVVR;IN VYYNEATGNK;ISEQFTAMFR; LTPPTYGDLNHLVSATMSGVT TCLR;MSATFIGNSTAIQELFK; NSSYFVEWIPNNVK;SGPFGQI FRPDNFVFGQSGAGNNWAK; TAVCDIPPR EIVHIQAGQCGNQIGAK;EVD EQMLNVQNK;FPGQLNADLR ;GHYTEGAELVDSVLDVVR;IN VYYNEAAGNK;ISEQFTAMFR; LTPPTYGDLNHLVSATMSGVT TCLR;MSATFIGNSTAIQELFK; NSSYFVEWIPNNVK;SGPFGQI FRPDNFVFGQSGAGNNWAK; TAVCDIPPR AGQCGNQIGTK;EVDEQMLAI QNK;FPGQLNADLR;FWEVIS DEHGIDQAGGYVGDSALQLE R;GHYTEGAELVDSVLDVVR;IS EQFSAMFR;ISVYYNESSK;LT TPTYGDLNHLVSATMSGVTT LR;NSSYFVEWIPNNVK;YLT ATVFR	0;0;0;0;1; 0;0;1;0;0; 0;0;0	2	2	0.4977	13276;13596 37899;38079;3789 8;36629;26306;25 896;19692;19719; 41235;41236 33527;26236;1652 4;16523;35898;35 899;24635;19718; 20235;44670;4467 2;34395;31373;45 270;45271;13276	-	Tubulin beta-5 chain OS=Mus musculus OX=10090 GN=Tubb5 PE=1 SV=1 Myosin regulatory light polypeptide 9 OS=Mus musculus OX=10090 GN=MyI9 PE=1 SV=3
sp Q9CQ19 MYL9_MOUSE	7.711726226	19841.45846	ACFDEEASGFIHEDHLR EIVHIQAGQCGNQIGAK;EVD EQMLNVQNK;FPGQLNADLR ;GHYTEGAELVDSVLDVVR;IN VYYNEATGNK;ISEQFTAMFR; LTPPTYGDLNHLVSATMSGVT TCLR;MSATFIGNSTAIQELFK; NSSYFVEWIPNNVK;SGPFGQI FRPDNFVFGQSGAGNNWAK; TAVCDIPPR EIVHIQAGQCGNQIGAK;EVD EQMLNVQNK;FPGQLNADLR ;GHYTEGAELVDSVLDVVR;IN VYYNEAAGNK;ISEQFTAMFR; LTPPTYGDLNHLVSATMSGVT TCLR;MSATFIGNSTAIQELFK; NSSYFVEWIPNNVK;SGPFGQI FRPDNFVFGQSGAGNNWAK; TAVCDIPPR AGQCGNQIGTK;EVDEQMLAI QNK;FPGQLNADLR;FWEVIS DEHGIDQAGGYVGDSALQLE R;GHYTEGAELVDSVLDVVR;IS EQFSAMFR;ISVYYNESSK;LT TPTYGDLNHLVSATMSGVTT LR;NSSYFVEWIPNNVK;YLT ATVFR	0;0;1;0;1	2	4	0.4535	41235;41236 33527;26236;1652 4;16523;35898;35 899;24635;19718; 20235;44670;4467 2;34395;31373;45 270;45271;13276	-	Tubulin beta-2B chain OS=Mus musculus OX=10090 GN=Tubb2b PE=1 SV=1
sp Q9CWF2 TBB2B_MOUSE	2.563085783	49920.94358	TAVCDIPPR EIVHIQAGQCGNQIGAK;EVD EQMLNVQNK;FPGQLNADLR ;GHYTEGAELVDSVLDVVR;IN VYYNEAAGNK;ISEQFTAMFR; LTPPTYGDLNHLVSATMSGVT TCLR;MSATFIGNSTAIQELFK; NSSYFVEWIPNNVK;SGPFGQI FRPDNFVFGQSGAGNNWAK; TAVCDIPPR EIVHIQAGQCGNQIGAK;EVD EQMLNVQNK;FPGQLNADLR ;GHYTEGAELVDSVLDVVR;IN VYYNEAAGNK;ISEQFTAMFR; LTPPTYGDLNHLVSATMSGVT TCLR;MSATFIGNSTAIQELFK; NSSYFVEWIPNNVK;SGPFGQI FRPDNFVFGQSGAGNNWAK; TAVCDIPPR AGQCGNQIGTK;EVDEQMLAI QNK;FPGQLNADLR;FWEVIS DEHGIDQAGGYVGDSALQLE R;GHYTEGAELVDSVLDVVR;IS EQFSAMFR;ISVYYNESSK;LT TPTYGDLNHLVSATMSGVTT LR;NSSYFVEWIPNNVK;YLT ATVFR	0 0;0;0;0;0; 0	1	1	0.382	270;45271;13276	-	Tubulin beta-2A chain OS=Mus musculus OX=10090 GN=Tubb2a PE=1 SV=1
sp Q7TMM9 TBB2A_MOUSE	4.376559455	49874.95585	TAVCDIPPR EIVHIQAGQCGNQIGAK;EVD EQMLNVQNK;FPGQLNADLR ;GHYTEGAELVDSVLDVVR;IN VYYNEAAGNK;ISEQFTAMFR; LTPPTYGDLNHLVSATMSGVT TCLR;MSATFIGNSTAIQELFK; NSSYFVEWIPNNVK;SGPFGQI FRPDNFVFGQSGAGNNWAK; TAVCDIPPR EIVHIQAGQCGNQIGAK;EVD EQMLNVQNK;FPGQLNADLR ;GHYTEGAELVDSVLDVVR;IN VYYNEAAGNK;ISEQFTAMFR; LTPPTYGDLNHLVSATMSGVT TCLR;MSATFIGNSTAIQELFK; NSSYFVEWIPNNVK;SGPFGQI FRPDNFVFGQSGAGNNWAK; TAVCDIPPR AGQCGNQIGTK;EVDEQMLAI QNK;FPGQLNADLR;FWEVIS DEHGIDQAGGYVGDSALQLE R;GHYTEGAELVDSVLDVVR;IS EQFSAMFR;ISVYYNESSK;LT TPTYGDLNHLVSATMSGVTT LR;NSSYFVEWIPNNVK;YLT ATVFR	0 0;0;0;0;1; 0;0;0;0;0; 0	1	1	0.382	270;45271;13276	-	Tubulin beta-6 chain OS=Mus musculus OX=10090 GN=Tubb6 PE=1 SV=1
sp Q922F4 TBB6_MOUSE	26.91712359	50058.12554	ATVFR	0;1;1;0;1; 0;1;1;1;0; 1	7	7	0.3758	5;31373;14528	-	Tubulin beta-6 chain OS=Mus musculus OX=10090 GN=Tubb6 PE=1 SV=1

sp Q91Z31 PTBP2_MOUSE	3.33516677	57452.8152	VTNILMLK	1	1	1	0.0151	10563	-	Polypyrimidine tract-binding protein 2 OS=Mus musculus OX=10090 GN=Ptbp2 PE=1 SV=2
sp Q8BHB0 NOD1_MOUSE	2.037040553	107671.2002	SMLLQR	1	1	1	0.0063	5640	-	Nucleotide-binding oligomerization domain-containing protein 1 OS=Mus musculus OX=10090 GN=Nod1 PE=1 SV=1
sp P01808 HVM38_MOUSE	2.413332988	13160.49815	YWMSWVR	1	1	1	0.0588	13248	sp P01810 HVM40_MOUSE;sp P01806 HVM36_MOUSE;sp P01807 HVM37_MOUSE;sp P01812 HVM42_MOUSE;sp P14234 FGR_MOUSE;s p Q04736 YES_MOUSE;sp Q61851 FGFR3_MOUSE;s p P39688 FYN_MOUSE;s p P08103 HCK_MOUSE;sp Q04859 MAK_MOUSE;sp P21803 FGFR2_MOUSE;s p P16277 BLK_MOUSE;sp P25911 LYN_MOUSE;sp P16092 FGFR1_MOUSE;s p Q9JHU3 CDK20_MOUSE;sp Q03142 FGFR4_MOUSE;sp P0624	ig heavy chain V region T601 OS=Mus musculus OX=10090 PE=1 SV=1
sp Q9JKV2 CILK1_MOUSE	2.529783838	70547.88067	IADFLAR	1	1	1	0.0127	8567	SE;sp P0624	Serine/threonine-protein kinase ICK OS=Mus musculus OX=10090 GN=Cilk1 PE=1 SV=2
sp P62911 RL32_MOUSE	6.760872531	15849.80395	FLVHNVK;SYCAEIAHNVSSK	1;1	2	3	0.1481	8407;26740;26739	-	60S ribosomal protein L32 OS=Mus musculus OX=10090 GN=Rpl32 PE=1 SV=2

sp Q9QZD9 EIF3 I_MOUSE	3.33516677	36437.5865	QINDIQLSR	1	1	1	0.0277	15102	-	Eukaryotic translation initiation factor 3 subunit I OS=Mus musculus OX=10090 GN=Eif3i PE=1 SV=1
sp P97447 FHL1 _MOUSE	7.043219307	31866.82357	AIVAGDQNVEYK;CLHPLASET FVSK	1;1	2	2	0.0893	22178;27319	-	protein 1 OS=Mus musculus OX=10090 GN=Fhl1 PE=1 SV=3
sp P47738 ALDH 2_MOUSE	6.760872531	56501.75081	LLCGGGAAADR;TEQGPQVD ETQFK	1;1	2	2	0.0462	14224;27752	-	Aldehyde dehydrogenase, mitochondrial OS=Mus musculus OX=10090 GN=Aldh2 PE=1 SV=1
sp Q9Z130 HNR DL_MOUSE	3.33516677	33538.09087	GFGFVLFK EHVIEALR;FNADEFEDMVAEK	1	1	1	0.0266	10106	SE	sp Q60668 H NRPD_MOU OS=Mus musculus OX=10090 GN=HnrrpdI PE=1 SV=1
sp Q6ZWV3 RL1 0_MOUSE	10.63547602	24587.86717	;VDEFPLCGHMSDEYEQLSS EALEAAR	1;1;1	3	3	0.2243	2	-	60S ribosomal protein L10 OS=Mus musculus OX=10090 GN=Rpl10 PE=1 SV=3
sp P84091 AP2 M1_MOUSE	7.452587645	49623.02468	EEQSQITSQVTGQIGWR;LNY SDHDEVK	1;1	2	3	0.0621	35685;18906;1890 8	-	AP-2 complex subunit mu OS=Mus musculus OX=10090 GN=Ap2m1 PE=1 SV=1
sp P26369 U2AF 2_MOUSE	2.529783838	53483.22158	NFAFLEFR	1	1	1	0.0168	13699	-	Splicing factor U2AF 65 kDa subunit OS=Mus musculus OX=10090 GN=U2af2 PE=1 SV=3
sp P80313 TCPH _MOUSE	6.527250718	59614.10673	LPIGDVATQYFADR;TLVDIAK EFSPFGTITSAK;FSPAGPILSR;	1;1	2	2	0.0386	29130;5922	-	T-complex protein 1 subunit eta OS=Mus musculus OX=10090 GN=Cct7 PE=1 SV=1
sp P29341 PABP 1_MOUSE	22.46462312	70625.86835	GFGFVSFER;NLDDGIDDER;SL GYAYVNFQPPADAER;VDEA VAVLQAHQAK	1;1;1;1;1; 1	6	6	0.1148	21491;17389;1374 9;17507;35381;27 065	-	Polyadenylate-binding protein 1 OS=Mus musculus OX=10090 GN=Pabpc1 PE=1 SV=2
sp Q9ERU9 RBP 2_MOUSE	2.353900435	340906.8511	TGSSLNSFYDQR	1	1	1	0.0039	24273	-	E3 SUMO-protein ligase RanBP2 OS=Mus musculus OX=10090 GN=Ranbp2 PE=1 SV=2
sp Q9QYJ0 DNJ A2_MOUSE	4.376559455	45716.58983	VSLEDLYNGK	1	1	1	0.0243	16726	-	DnaJ homolog subfamily A member 2 OS=Mus musculus OX=10090 GN=Dnaja2 PE=1 SV=1
sp P56959 FUS_ MOUSE	2.529783838	52641.50811	AAIDWFDGK	1	1	1	0.0174	13137	-	RNA-binding protein FUS OS=Mus musculus OX=10090 GN=Fus PE=1 SV=1

sp Q8BFW7 LPP_MOUSE	8.753118911	65847.91553	STGEPLGHVPAR;YYEPYYAAG PSYGGR	1;1	2	3	0.044	7	19427;19426;3168	-	homolog OS=Mus musculus OX=10090 GN=Lpp PE=1 SV=1
sp Q9QY06 MYO9B_MOUSE	3.33516677	238685.4156	ETLVEVLTK		1	1	1	0.0043	13390	-	Unconventional myosin-IXb OS=Mus musculus OX=10090 GN=Myo9b PE=1 SV=2
sp Q9CQE8 RTRAF_MOUSE	7.711726226	28134.77536	EGLPVALEK;QEAI DWLLGLAV R	1;1	2	2	0.0902	11229;27190		-	RNA transcription, translation and transport factor protein OS=Mus musculus OX=10090 GN=RTRAF PE=1 SV=1
sp Q9QXS6 DREB_MOUSE	30.6416196	77239.23298	EQFWEQAK;KSESEVEEAAAI AQRPDNPR;LAASGEGGLQEL SGHFENQK;LELLAAYEEVIR;L REDENAEPVGT TYQK;SESEVE EAAAI AQRPDNPR;SPSDSST ASTPIAEQIER;TDAAVEMK	1;1;1;1;1;1;1;1	8	10	0.1459	14378;40637;4063 6;37607;25527;34 016;34017;39067; 34427;8624		-	Drebrin OS=Mus musculus OX=10090 GN=Dbrn1 PE=1 SV=4
sp Q9DB20 ATPO_MOUSE	2.740552224	23348.73849	SFLSPNQILK		1	1	1	0.0469	17046	-	ATP synthase subunit O, mitochondrial OS=Mus musculus OX=10090 GN=Atp5po PE=1 SV=1
sp Q61235 SNTB2_MOUSE	3.33516677	56346.18911	AGLVELLLR		1	1	1	0.0173	12041	-	Beta-2-syntrophin OS=Mus musculus OX=10090 GN=Sntb2 PE=1 SV=2
sp Q7TMK9 HNRPQ_MOUSE	8.112035621	69589.60683	AGPIWDLR;DLFEDELVPLFEK; TGYTL DVT TGQR	1;1;1	3	3	0.053	10424;29605;2234 7		-	Heterogeneous nuclear ribonucleoprotein Q OS=Mus musculus OX=10090 GN=Syncrip PE=1 SV=2
sp Q8CFW1 ANO2_MOUSE	2.666659851	114062.1413	MAAPGLR		1	1	1	0.007	4947	-	Anoctamin-2 OS=Mus musculus OX=10090 GN=Ano2 PE=1 SV=2
sp P84099 RL19_MOUSE	11.046893	23451.24625	HMYHSLYLK;ILMEHIHK;VWL DPNETNEIANANSR	1;1;1	3	4	0.1735	18498;13097;1351 0;35617		-	60S ribosomal protein L19 OS=Mus musculus OX=10090 GN=Rpl19 PE=1 SV=1
sp A2AHJ4 BRWD3_MOUSE	2.608604626	202815.5787	IGPLLDK		1	1	1	0.0039	5801	-	Bromodomain and WD repeat-containing protein 3 OS=Mus musculus OX=10090 GN=Brwd3 PE=1 SV=1
sp Q02053 UBA1_MOUSE	2.666659851	117734.0068	QNSLDEDLIR		1	1	1	0.0095	18864	-	Ubiquitin-like modifier-activating enzyme 1 OS=Mus musculus OX=10090 GN=Uba1 PE=1 SV=1
sp O88685 PR56A_MOUSE	4.376559455	49517.555	VDILDALLR		1	1	1	0.0226	16345	-	26S proteasome regulatory subunit 6A OS=Mus musculus OX=10090 GN=Psmc3 PE=1 SV=2

sp P84078 ARF1_MOUSE	3.33516677	20683.66809	DAVLLVFANK;HYFQNTQGLI FVVDSDNRER;TTILYK	1;0;0	1	1	0.1989	15203;42203;5437	sp P61205 A RF3_MOUSE; ADP-ribosylation factor 1 sp P84084 A OS=Mus musculus OX=10090 RF5_MOUSE GN=Arf1 PE=1 SV=2
sp P61750 ARF4_MOUSE	4.376559455	20383.61347	HYFQNTQGLIFVVDSDNRER;I QEGAAVLQK;TTILYK	0;1;0	1	1	0.2	42203;14120;5437	ADP-ribosylation factor 4 OS=Mus musculus OX=10090 GN=Arf4 PE=1 SV=2
sp Q9JHH6 CBP B2_MOUSE	2.529783838	48839.63222	YPLYVLK		1	1	1	0.0166	9567 - Carboxypeptidase B2 OS=Mus musculus OX=10090 GN=Cpb2 PE=1 SV=1
sp P29268 CCN 2_MOUSE	2.150691262	37797.72133	VTNDNTFCR		1	1	1	0.0259	16386 - CCN family member 2 OS=Mus musculus OX=10090 GN=Ccn2 PE=1 SV=3
sp Q9WVJ2 PSD 13_MOUSE	2.076765906	42782.08604	LNIGDLQATK		1	1	1	0.0266	14638 - 26S proteasome non-ATPase regulatory subunit 13 OS=Mus musculus OX=10090 GN=Psm13 PE=1 SV=1