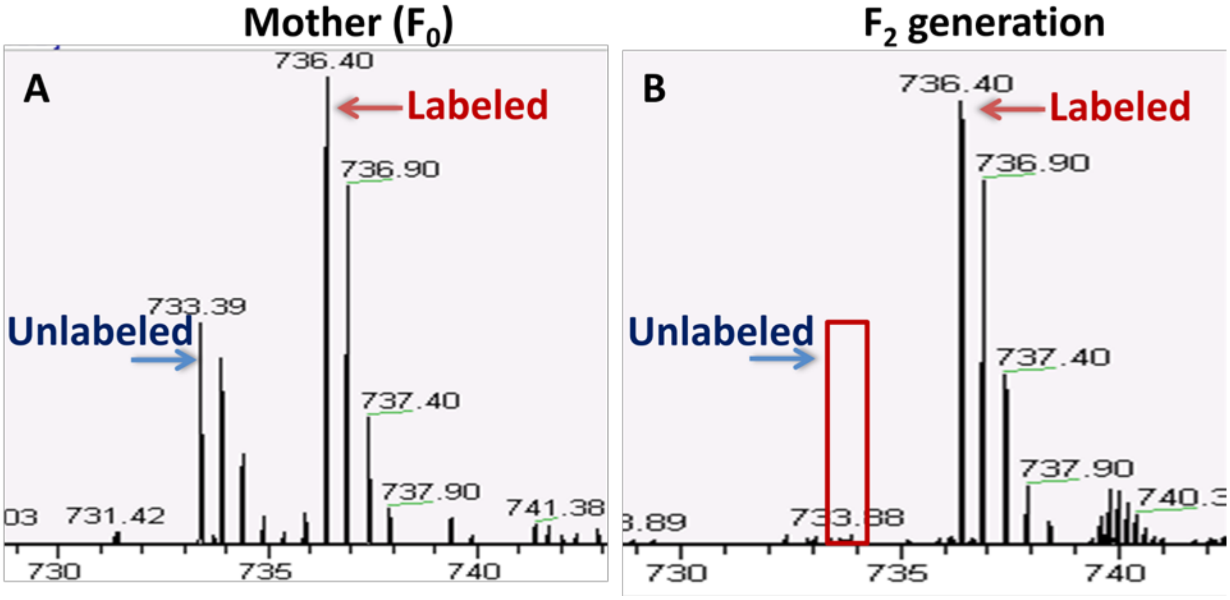
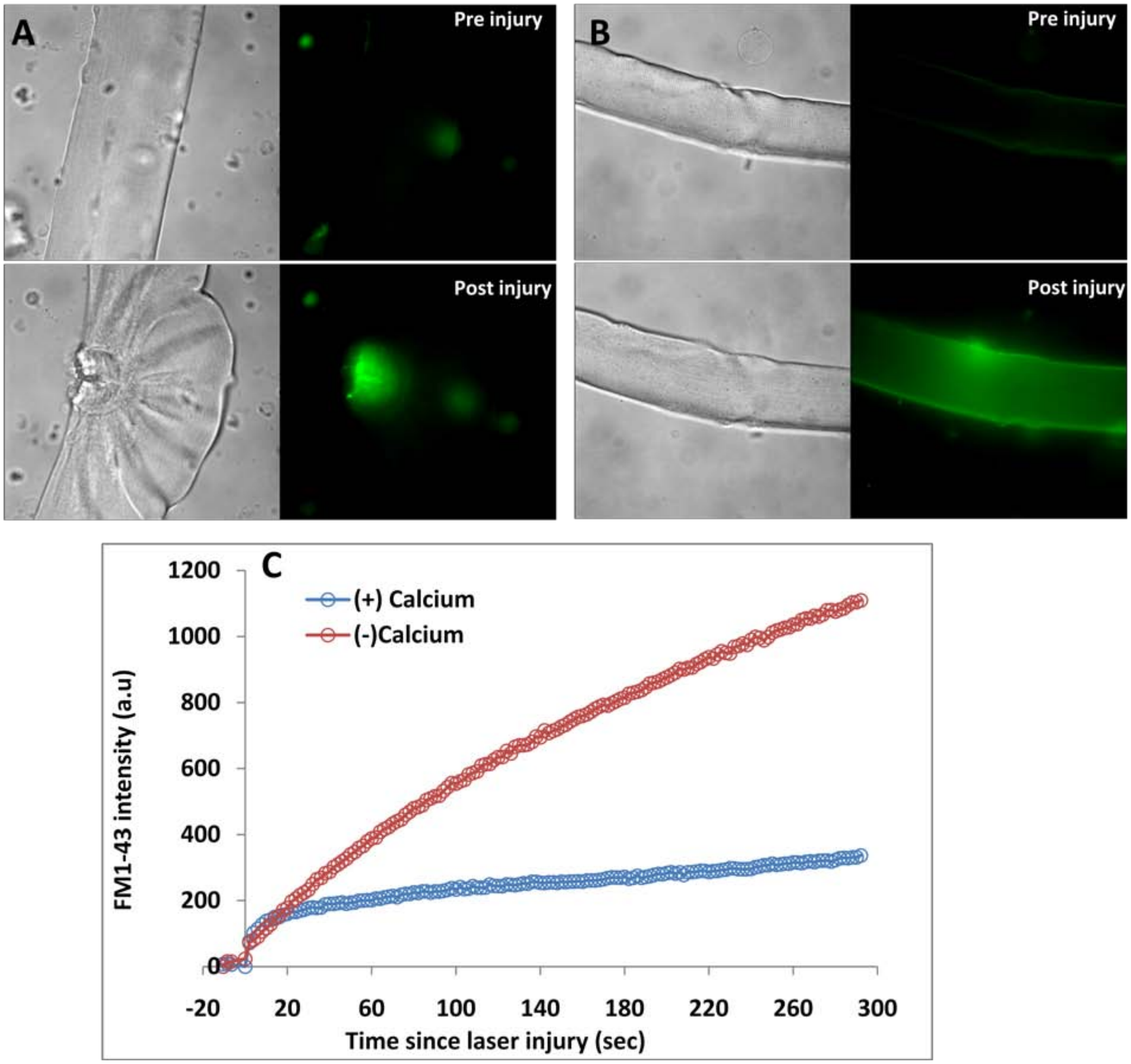
SUPPLEMENTARY DATA



Supplementary Figure 1: Mass spectrum showing incorporation efficiency for $^{13}C_6$–Lysine in skeletal muscle proteins in mice maintained on $^{13}C_6$–Lysine diet until F2 generation. The average labeling efficacy of all uniquely identified proteins from the gastrocnemius was 98.26±3.5%. The images show representative spectra for identified peptides in a narrow part of the mass spectra. This spectra shows the unlabeled (733.39 Da) and labeled (736.40 Da) peptide **LASADIETYLLEK** from myosin 4 protein from the gastrocnemius muscle of the mother (A) and a pup from the F2 (B) generation. Red box marks the region where (if present) we would have detected the peak for the unlabeled peptide spectra.



Supplementary Figure 2: Iamging healing of sarcolemma following laser injury. Sarcolemma of myofibers isolated from EDL muscle were injured using a high intensity pulsed laser in the presence of 2μM FM1-43 dye. The myofibers were maintained (A) in the presence of calcium (+ Calcium) or (B) in PBS with 1mM EGTA (- Calcium). Panels show the transmitted light (left panel) and the corresponding fluorescence (right panel) image of the fiber before injury and at the end of healing. (C) Plot of the FM1-43 intensity in the myofibers shows above during the course of healing.

Supplementary Video 1: Video showing MitoTracker labeled myofiber as it undergoes multiple rounds of injury. The mild injuries (shown in figure 4C) are followed by a larger injury (not shown in Figure 4c). Note while the milder injury causes minor accumulation of mitochondria, larger injury leads to greater accumulation of mitochondria at the site of injury.

Table S1: List of cell surface proteins identified from C2C12 cells in two independent biological replicate experiments. These proteins were isolated by cell surface biotinylation, followed by membrane solubilization using detergents. Subcellular classification of proteins is based on gene ontology annotation with reference to Uniprot database (http://www.uniprot.org) as well as literature search.

Table S2: List of plasma membrane proteins identified from C2C12 cells in two independent biological replicate experiments. These proteins were isolated by cell surface biotinylation, followed by mechanical lysis. Proteins were classified according to the GO annotation from the Uniprot database (http://www.uniprot.org) as well as literature search.

Table S3: Protein identification results for plasma membrane preparation from the H2K cells. The listed proteins were identified in two independent biological replicate experiments using the mechanical lysis method. Proteins were classified according to the GO annotation from the Uniprot database (http://www.uniprot.org) as well as literature search.

Table S4: Summary of cell surface proteins identified from two combined replicate experiments where EDL and Soleus muscle fibers were used together. Here, proteins were isolated using the cell surface biotinylation and mechanical lysis protocol. The subcellular localization of proteins was predicted on the basis of Gene Ontology (GO) information available from the Uniprot database (http://www.uniprot.org) as well as literature search.

Supplementary Figure 1: Mass spectrum showing incorporation efficiency for $^{13}C_6$–Lysine in skeletal muscle proteins in mice maintained on $^{13}C_6$–Lysine diet until F2 generation. The average labeling efficacy of all uniquely identified proteins from the gastrocnemius was 98.26±3.5%. The images show representative spectra for identified peptides in a narrow part of the mass spectra. This spectra shows the unlabeled (733.39 Da) and labeled (736.40 Da) peptide **LASADIETYLLEK** from myosin 4 protein from the gastrocnemius muscle of the mother (A) and a pup from the F2 (B) generation. Red box marks the region where (if present) we would have detected the peak for the unlabeled peptide spectrum.

Table S1

Accession	**Reference**	**P (pro)**	**Score**	**Coverage**	**Peptide (Hits)**	**Subcellular locations**
Q9QXS1	PLEC1_MOUSE Plectin-1 OS=Mus musculus GN=Plec1 PE=1 SV=2	1.0E-30	1668.3	33.10	323 (322 1 0 0 0)	Cytoplasm â€º cytoskeleton. Cell junction â€º hemidesmosome.
Q8VDD5	MYH9_MOUSE Myosin-9 OS=Mus musculus GN=Myh9 PE=1 SV=4	1.0E-30	1502.4	43.60	480 (471 8 1 0 0)	ND
Q61879	MYH10_MOUSE Myosin-10 OS=Mus musculus GN=Myh10 PE=1 SV=2	1.6E-14	606.3	30.40	96 (94 2 0 0 0)	ND
P20152	VIME_MOUSE Vimentin OS=Mus musculus GN=Vim PE=1 SV=3	1.0E-30	546.3	57.10	368 (364 2 2 0 0)	ND
P11276	FINC_MOUSE Fibronectin OS=Mus musculus GN=Fn1 PE=1 SV=3	3.3E-15	580.4	27.40	312 (312 0 0 0 0)	Secreted â€º extracellular space â€º extracellular matrix.
Q8BTM8	FLNA_MOUSE Filamin-A OS=Mus musculus GN=Flna PE=1 SV=4	4.4E-12	520.3	26.00	107 (107 0 0 0 0)	Cytoplasm â€º cell cortex. Cytoplasm â€º cytoskeleton.
P62737	ACTA_MOUSE Actin, aortic smooth muscle OS=Mus musculus GN=Acta2 PE=1 SV=1	7.8E-15	404.3	52.00	320 (317 3 0 0 0)	Cytoplasm â€º cytoskeleton.
Q91ZX7	LRP1_MOUSE Prolow-density lipoprotein receptor-related protein 1 OS=Mus musculus GN=Lrp1 PE=1 SV=1	3.4E-10	300.2	6.70	39 (39 0 0 0 0)	Cell membrane; Single-pass type I membrane protein. Membrane â€º coated pit. Cell membrane; Peripheral membrane protein; Extracellular side. Membrane â€º coated pit. Cytoplasm. Nucleus.
P20029	GRP78_MOUSE 78 kDa glucose-regulated protein OS=Mus musculus GN=Hspa5 PE=1 SV=3	1.1E-15	340.3	46.70	60 (60 0 0 0 0)	Endoplasmic reticulum lumen. Melanosome.
Q80X90	FLNB_MOUSE Filamin-B OS=Mus musculus GN=Flnb PE=1 SV=2	8.3E-14	340.3	15.40	39 (39 0 0 0 0)	Cytoplasm â€º cell cortex. Cytoplasm â€º myofibril â€º sarcomere â€º Z line. Cytoplasm â€º cytoskeleton.
Q62351	TFR1_MOUSE Transferrin receptor protein 1 OS=Mus musculus GN=Tfrc PE=1 SV=1	7.8E-15	290.3	29.40	45 (45 0 0 0 0)	Cell membrane; Single-pass type II membrane protein. Melanosome.

Q7TMM9	TBB2A_MOUSE Tubulin beta-2A chain OS=Mus musculus GN=Tubb2a PE=1 SV=1	1.3E-14	320.4	46.50	166 (161 4 1 0 0)	Cytoplasm â€º cytoskeleton.
P31001	DESM_MOUSE Desmin OS=Mus musculus GN=Des PE=1 SV=3	2.8E-12	306.3	54.60	113 (98 15 0 0 0)	Cytoplasm.
Q6P5H2	NEST_MOUSE Nestin OS=Mus musculus GN=Nes PE=1 SV=1	4.0E-12	270.3	18.40	47 (47 0 0 0 0)	ND
P38647	GRP75_MOUSE Stress-70 protein, mitochondrial OS=Mus musculus GN=Hspa9 PE=1 SV=2	3.5E-11	260.3	33.70	39 (39 0 0 0 0)	Mitochondrion.
Q8VHY0	CSPG4_MOUSE Chondroitin sulfate proteoglycan 4 OS=Mus musculus GN=Cspg4 PE=1 SV=2	7.7E-10	240.2	12.50	25 (25 0 0 0 0)	Apical cell membrane; Single-pass type I membrane protein; Extracellular side. Cell projection â€º lamellipodium membrane; Single-pass type I membrane protein; Extracellular side.
P48678	LMNA_MOUSE Lamin-A/C OS=Mus musculus GN=Lmna PE=1 SV=2	2.3E-13	260.3	36.20	63 (63 0 0 0 0)	Nucleus. Nucleus envelope.
Q05793	PGBM_MOUSE Basement membrane-specific heparan sulfate proteoglycan core protein OS=Mus musculus GN=Hspg2 PE=1 SV=1	9.7E-11	240.2	7.60	41 (41 0 0 0 0)	Secreted â€º extracellular space â€º extracellular matrix â€º basement membrane.
P26039	TLN1_MOUSE Talin-1 OS=Mus musculus GN=Tln1 PE=1 SV=1	1.5E-12	240.3	13.10	28 (28 0 0 0 0)	Cell projection â€º ruffle membrane; Peripheral membrane protein; Cytoplasmic side. Cytoplasm â€º cytoskeleton.
P08113	ENPL_MOUSE Endoplasmin OS=Mus musculus GN=Hsp90b1 PE=1 SV=2	5.5E-12	240.3	27.10	35 (35 0 0 0 0)	Endoplasmic reticulum lumen. Melanosome.
P13595	NCAM1_MOUSE Neural cell adhesion molecule 1 OS=Mus musculus GN=Ncam1 PE=1 SV=3	1.0E-30	230.3	21.20	68 (68 0 0 0 0)	Cell membrane; Single-pass type I membrane protein. Cell membrane; Lipid-anchor â€º GPI-anchor.
Q61738	ITA7_MOUSE Integrin alpha-7 OS=Mus musculus GN=Itga7 PE=1 SV=2	3.1E-12	200.3	19.40	58 (58 0 0 0 0)	Membrane; Single-pass type I membrane protein.
P43406	ITAV_MOUSE Integrin	5.6E-15	230.2	17.90	39 (39 0 0 0	Membrane; Single-

	alpha-V OS=Mus musculus GN=Itgav PE=1 SV=1				0)	pass type I membrane protein.
Q03145	EPHA2_MOUSE Ephrin type-A receptor 2 OS=Mus musculus GN=Epha2 PE=1 SV=2	1.2E-12	220.3	16.70	36 (36 0 0 0 0)	Cell membrane; Single-pass type I membrane protein. Cell projection â€º ruffle membrane; Single-pass type I membrane protein. Cell projection â€º lamellipodium membrane; Single-pass type I membrane protein. Cell junction â€º focal adhesion.
Q9JHU4	DYHC1_MOUSE Cytoplasmic dynein 1 heavy chain 1 OS=Mus musculus GN=Dync1h1 PE=1 SV=1	1.7E-10	200.2	4.20	28 (28 0 0 0 0)	Cytoplasm â€º cytoskeleton.
P63017	HSP7C_MOUSE Heat shock cognate 71 kDa protein OS=Mus musculus GN=Hspa8 PE=1 SV=1	5.7E-14	220.2	23.50	37 (37 0 0 0 0)	Cytoplasm. Melanosome.
P09055	ITB1_MOUSE Integrin beta-1 OS=Mus musculus GN=Itgb1 PE=1 SV=1	1.9E-11	208.3	16.20	102 (89 13 0 0 0)	Cell membrane; Single-pass type I membrane protein. Melanosome.
Q02257	PLAK_MOUSE Junction plakoglobin OS=Mus musculus GN=Jup PE=1 SV=3	9.4E-14	190.3	23.40	46 (46 0 0 0 0)	Cell junction â€º adherens junction. Cell junction â€º desmosome. Cytoplasm â€º cytoskeleton. Membrane; Peripheral membrane protein.
P07356	ANXA2_MOUSE Annexin A2 OS=Mus musculus GN=Anxa2 PE=1 SV=2	1.8E-12	200.3	46.00	46 (46 0 0 0 0)	Secreted â€º extracellular space â€º extracellular matrix â€º basement membrane. Melanosome.
Q8VDN2	AT1A1_MOUSE Sodium/potassium-transporting ATPase subunit alpha-1 OS=Mus musculus GN=Atp1a1 PE=1 SV=1	1.9E-12	200.3	21.60	37 (37 0 0 0 0)	Cell membrane; Multi-pass membrane protein.
Q80YX1	TENA_MOUSE Tenascin OS=Mus musculus GN=Tnc PE=1 SV=1	9.1E-12	200.2	9.60	22 (22 0 0 0 0)	Secreted â€º extracellular space â€º extracellular matrix.

Q9D0E1	HNRPM_MOUSE Heterogeneous nuclear ribonucleoprotein M OS=Mus musculus GN=Hnrnpm PE=1 SV=3	8.8E-11	198.2	22.20	33 (32 1 0 0 0)	Nucleus.
P07901	HS90A_MOUSE Heat shock protein HSP 90-alpha OS=Mus musculus GN=Hsp90aa1 PE=1 SV=4	3.0E-12	194.3	27.10	54 (38 16 0 0 0)	Cytoplasm. Melanosome.
Q8CAQ8	IMMT_MOUSE Mitochondrial inner membrane protein OS=Mus musculus GN=Immt PE=1 SV=1	3.6E-13	180.3	22.70	31 (31 0 0 0 0)	Mitochondrion inner membrane.
P14824	ANXA6_MOUSE Annexin A6 OS=Mus musculus GN=Anxa6 PE=1 SV=2	5.4E-13	180.2	28.20	21 (21 0 0 0 0)	Cytoplasm. Melanosome.
P63038	CH60_MOUSE 60 kDa heat shock protein, mitochondrial OS=Mus musculus GN=Hspd1 PE=1 SV=1	4.4E-15	190.3	30.70	24 (24 0 0 0 0)	Mitochondrion matrix.
P56480	ATPB_MOUSE ATP synthase subunit beta, mitochondrial OS=Mus musculus GN=Atp5b PE=1 SV=2	1.8E-13	190.3	39.30	26 (26 0 0 0 0)	Mitochondrion. Mitochondrion inner membrane.
O35516	NOTC2_MOUSE Neurogenic locus notch homolog protein 2 OS=Mus musculus GN=Notch2 PE=1 SV=1	2.5E-11	190.3	8.30	37 (37 0 0 0 0)	Cell membrane; Single-pass type I membrane protein. Nucleus.
P52480	KPYM_MOUSE Pyruvate kinase isozymes M1/M2 OS=Mus musculus GN=Pkm2 PE=1 SV=4	2.2E-15	170.3	33.50	20 (20 0 0 0 0)	Cytoplasm. Nucleus.
P33146	CAD15_MOUSE Cadherin-15 OS=Mus musculus GN=Cdh15 PE=1 SV=2	6.3E-14	170.3	25.30	57 (57 0 0 0 0)	Cell membrane; Single-pass type I membrane protein.
P27773	PDIA3_MOUSE Protein disulfide-isomerase A3 OS=Mus musculus GN=Pdia3 PE=1 SV=2	2.7E-11	190.2	37.80	21 (21 0 0 0 0)	Endoplasmic reticulum lumen. Melanosome.
P33146	CAD15_MOUSE Cadherin-15 OS=Mus musculus GN=Cdh15 PE=1 SV=2	4.5E-13	180.3	26.50	63 (63 0 0 0 0)	Cell membrane; Single-pass type I membrane protein.
Q02248	CTNB1_MOUSE Catenin beta-1 OS=Mus musculus GN=Ctnnb1 PE=1 SV=1	5.9E-09	170.2	19.80	30 (30 0 0 0 0)	Cytoplasm. Cytoplasm â€º cytoskeleton. Nucleus. Cell junction â€º adherens junction. Cell junction. Cell

						membrane.
Q05920	PYC_MOUSE Pyruvate carboxylase, mitochondrial OS=Mus musculus GN=Pc PE=1 SV=1	2.6E-10	180.3	17.70	23 (23 0 0 0 0)	Mitochondrion matrix.
Q9JKF1	IQGA1_MOUSE Ras GTPase-activating-like protein IQGAP1 OS=Mus musculus GN=Iqgap1 PE=1 SV=1	3.4E-14	160.3	10.70	17 (17 0 0 0 0)	Cell membrane.
Q64727	VINC_MOUSE Vinculin OS=Mus musculus GN=Vcl PE=1 SV=4	1.0E-09	180.2	19.80	18 (18 0 0 0 0)	Cytoplasm â€º cytoskeleton. Cell junction â€º adherens junction. Cell membrane; Peripheral membrane protein; Cytoplasmic side. Cell junction.
Q8VHX6	FLNC_MOUSE Filamin-C OS=Mus musculus GN=Flnc PE=1 SV=3	1.6E-13	160.3	7.60	24 (24 0 0 0 0)	Cytoplasm. Membrane; Peripheral membrane protein. Cytoplasm â€º cytoskeleton. Cytoplasm â€º myofibril â€º sarcomere â€º Z line.
P09103	PDIA1_MOUSE Protein disulfide-isomerase OS=Mus musculus GN=P4hb PE=1 SV=1	4.5E-12	160.3	31.40	19 (19 0 0 0 0)	Endoplasmic reticulum lumen. Melanosome. Cell membrane; Peripheral membrane protein.
P35441	TSP1_MOUSE Thrombospondin-1 OS=Mus musculus GN=Thbs1 PE=1 SV=1	1.9E-11	170.3	16.00	39 (39 0 0 0 0)	ND
Q9WTI7	MYO1C_MOUSE Myosin-Ic OS=Mus musculus GN=Myo1c PE=1 SV=2	2.9E-11	160.2	17.00	21 (21 0 0 0 0)	Cytoplasm. Cell membrane. Cell projection â€º stereocilium membrane. Nucleus â€º nucleolus. Nucleus â€º nucleoplasm. Nucleus â€º nuclear pore complex.
P11499	HS90B_MOUSE Heat shock protein HSP 90-beta OS=Mus musculus	7.0E-12	158.3	16.40	28 (27 1 0 0 0)	Cytoplasm. Melanosome.

	GN=Hsp90ab1 PE=1 SV=2					
Q9EPR5	SORC2_MOUSE VPS10 domain-containing receptor SorCS2 OS=Mus musculus GN=Sorcs2 PE=1 SV=1	3.7E-10	170.2	13.90	31 (31 0 0 0 0)	Membrane; Single-pass type I membrane protein.
Q8CIE6	COPA_MOUSE Coatomer subunit alpha OS=Mus musculus GN=Copa PE=1 SV=1	7.7E-12	170.2	16.00	17 (17 0 0 0 0)	Cytoplasm. Golgi apparatus membrane; Peripheral membrane protein; Cytoplasmic side. Cytoplasmic vesicle â€º COPI-coated vesicle membrane; Peripheral membrane protein; Cytoplasmic side. Secreted.
P60843	IF4A1_MOUSE Eukaryotic initiation factor 4A-I OS=Mus musculus GN=Eif4a1 PE=2 SV=1	2.5E-11	168.3	31.80	35 (34 1 0 0 0)	ND
P58252	EF2_MOUSE Elongation factor 2 OS=Mus musculus GN=Eef2 PE=1 SV=2	9.7E-11	160.3	14.80	20 (20 0 0 0 0)	Cytoplasm.
Q7TPR4	ACTN1_MOUSE Alpha-actinin-1 OS=Mus musculus GN=Actn1 PE=2 SV=1	1.6E-10	160.3	19.70	20 (20 0 0 0 0)	Cytoplasm â€º cytoskeleton. Cytoplasm â€º myofibril â€º sarcomere â€º Z line. Cell membrane. Cell projection â€º ruffle.
Q03265	ATPA_MOUSE ATP synthase subunit alpha, mitochondrial OS=Mus musculus GN=Atp5a1 PE=1 SV=1	1.9E-12	160.3	28.00	31 (31 0 0 0 0)	Mitochondrion inner membrane. Cell membrane; Peripheral membrane protein; Extracellular side.
P68369	TBA1A_MOUSE Tubulin alpha-1A chain OS=Mus musculus GN=Tuba1a PE=1 SV=1	3.3E-15	150.3	30.60	128 (128 0 0 0 0)	Cytoplasm â€º cytoskeleton.
Q9WV91	FPRP_MOUSE Prostaglandin F2 receptor negative regulator OS=Mus musculus GN=Ptgfrn PE=1 SV=1	1.7E-12	140.2	15.10	22 (22 0 0 0 0)	Endoplasmic reticulum membrane; Single-pass type I membrane protein. Golgi apparatus â€º trans-Golgi network membrane; Single-pass type I

						membrane protein.
P10107	ANXA1_MOUSE Annexin A1 OS=Mus musculus GN=Anxa1 PE=1 SV=2	2.5E-12	150.3	42.80	27 (27 0 0 0 0)	Nucleus. Cytoplasm. Cell projection â€º cilium. Basolateral cell membrane.
P16381	DDX3L_MOUSE Putative ATP-dependent RNA helicase Pl10 OS=Mus musculus GN=D1Pas1 PE=1 SV=1	6.8E-12	138.3	22.60	18 (17 1 0 0 0)	ND
P19324	SERPH_MOUSE Serpin H1 OS=Mus musculus GN=Serpinh1 PE=1 SV=2	6.0E-12	148.3	33.10	24 (23 1 0 0 0)	Endoplasmic reticulum lumen.
P02469	LAMB1_MOUSE Laminin subunit beta-1 OS=Mus musculus GN=Lamb1-1 PE=1 SV=2	4.3E-11	130.2	7.20	14 (14 0 0 0 0)	Secreted â€º extracellular space â€º extracellular matrix â€º basement membrane.
Q8CGC7	SYEP_MOUSE Bifunctional aminoacyl-tRNA synthetase OS=Mus musculus GN=Eprs PE=2 SV=3	1.1E-11	140.3	11.70	15 (15 0 0 0 0)	ND
P17182	ENOA_MOUSE Alpha-enolase OS=Mus musculus GN=Eno1 PE=1 SV=3	2.6E-13	136.3	26.50	16 (14 2 0 0 0)	Cytoplasm. Cell membrane.
P11688	ITA5_MOUSE Integrin alpha-5 OS=Mus musculus GN=Itga5 PE=1 SV=2	2.1E-11	130.2	14.30	26 (26 0 0 0 0)	Membrane; Single-pass type I membrane protein.
P08249	MDHM_MOUSE Malate dehydrogenase, mitochondrial OS=Mus musculus GN=Mdh2 PE=1 SV=3	1.0E-30	130.4	43.80	15 (15 0 0 0 0)	Mitochondrion matrix.
Q68FD5	CLH_MOUSE Clathrin heavy chain 1 OS=Mus musculus GN=Cltc PE=1 SV=3	1.2E-11	130.3	8.50	16 (16 0 0 0 0)	Cytoplasmic vesicle membrane; Peripheral membrane protein; Cytoplasmic side. Membrane â€º coated pit; Peripheral membrane protein; Cytoplasmic side. Melanosome.
P02468	LAMC1_MOUSE Laminin subunit gamma-1 OS=Mus musculus GN=Lamc1 PE=1 SV=2	1.2E-11	120.3	8.10	17 (17 0 0 0 0)	Secreted â€º extracellular space â€º extracellular matrix â€º basement

						membrane.
Q8JZQ9	EIF3B_MOUSE Eukaryotic translation initiation factor 3 subunit B OS=Mus musculus GN=Eif3b PE=1 SV=1	5.8E-10	120.3	17.20	12 (12 0 0 0 0)	Cytoplasm.
Q62470	ITA3_MOUSE Integrin alpha-3 OS=Mus musculus GN=Itga3 PE=1 SV=1	1.7E-11	110.2	10.60	17 (17 0 0 0 0)	Membrane; Single-pass type I membrane protein.
P62908	RS3_MOUSE 40S ribosomal protein S3 OS=Mus musculus GN=Rps3 PE=1 SV=1	1.6E-11	120.3	46.50	29 (29 0 0 0 0)	Cytoplasm.
P29533	VCAM1_MOUSE Vascular cell adhesion protein 1 OS=Mus musculus GN=Vcam1 PE=1 SV=1	6.1E-14	120.3	20.30	16 (16 0 0 0 0)	Cell membrane; Single-pass type I membrane protein. Cell membrane; Lipid-anchor â€º GPI-anchor.
P23116	EIF3A_MOUSE Eukaryotic translation initiation factor 3 subunit A OS=Mus musculus GN=Eif3a PE=1 SV=4	1.9E-09	120.2	7.40	13 (13 0 0 0 0)	Cytoplasm. Cytoplasm â€º cytoskeleton â€º centrosome. Nucleus.
Q922U2	K2C5_MOUSE Keratin, type II cytoskeletal 5 OS=Mus musculus GN=Krt5 PE=1 SV=1	2.8E-10	100.2	12.20	64 (64 0 0 0 0)	ND
Q99K48	NONO_MOUSE Non-POU domain-containing octamer-binding protein OS=Mus musculus GN=Nono PE=1 SV=3	2.1E-11	120.2	27.30	12 (12 0 0 0 0)	Nucleus.
P10852	4F2_MOUSE 4F2 cell-surface antigen heavy chain OS=Mus musculus GN=Slc3a2 PE=1 SV=1	1.4E-08	100.2	17.10	22 (22 0 0 0 0)	Apical cell membrane; Single-pass type II membrane protein. Melanosome.
Q8R422	CD109_MOUSE CD109 antigen OS=Mus musculus GN=Cd109 PE=2 SV=1	1.0E-13	110.3	9.50	16 (16 0 0 0 0)	Cell membrane; Lipid-anchor â€º GPI-anchor.
P37889	FBLN2_MOUSE Fibulin-2 OS=Mus musculus GN=Fbln2 PE=1 SV=1	2.2E-15	110.2	5.00	52 (52 0 0 0 0)	Secreted â€º extracellular space â€º extracellular matrix.
P16858	G3P_MOUSE Glyceraldehyde-3-phosphate dehydrogenase OS=Mus musculus GN=Gapdh PE=1 SV=2	2.0E-10	98.2	16.50	38 (35 3 0 0 0)	Cytoplasm â€º cytosol. Nucleus.

Q69ZN7	MYOF_MOUSE Myoferlin OS=Mus musculus GN=Myof PE=1 SV=2	1.8E-10	110.2	6.60	18 (18 0 0 0 0)	Cell membrane; Single-pass type II membrane protein. Nucleus membrane; Single-pass type II membrane protein. Cytoplasmic vesicle membrane; Single-pass type II membrane protein.
P26041	MOES_MOUSE Moesin OS=Mus musculus GN=Msn PE=1 SV=3	3.8E-11	110.2	18.40	11 (11 0 0 0 0)	Cell membrane; Peripheral membrane protein; Cytoplasmic side. Cytoplasm â€º cytoskeleton. Apical cell membrane; Peripheral membrane protein; Cytoplasmic side. Cell projection â€º microvillus membrane; Peripheral membrane protein; Cytoplasmic side.
Q64521	GPDM_MOUSE Glycerol-3-phosphate dehydrogenase, mitochondrial OS=Mus musculus GN=Gpd2 PE=1 SV=2	1.6E-07	110.2	15.30	18 (18 0 0 0 0)	Mitochondrion inner membrane.
Q9EP71	RAI14_MOUSE Ankycorbin OS=Mus musculus GN=Rai14 PE=1 SV=1	4.1E-09	110.2	12.90	12 (12 0 0 0 0)	Cytoplasm â€º cell cortex. Cytoplasm â€º cytoskeleton.
P61979	HNRPK_MOUSE Heterogeneous nuclear ribonucleoprotein K OS=Mus musculus GN=Hnrnpk PE=1 SV=1	2.9E-11	100.3	25.50	11 (11 0 0 0 0)	Cytoplasm. Nucleus â€º nucleoplasm.
P21981	TGM2_MOUSE Protein-glutamine gamma-glutamyltransferase 2 OS=Mus musculus GN=Tgm2 PE=1 SV=4	1.4E-11	90.3	13.80	12 (12 0 0 0 0)	ND
Q01853	TERA_MOUSE Transitional endoplasmic reticulum ATPase OS=Mus musculus GN=Vcp PE=1 SV=4	2.2E-11	100.3	15.60	10 (10 0 0 0 0)	Cytoplasm â€º cytosol. Nucleus.
Q9QXS6	DREB_MOUSE Drebrin OS=Mus musculus	2.6E-14	100.3	15.70	15 (15 0 0 0 0)	Cytoplasm.

	GN=Dbn1 PE=1 SV=4					
Q8R1B4	EIF3C_MOUSE Eukaryotic translation initiation factor 3 subunit C OS=Mus musculus GN=Eif3c PE=1 SV=1	2.4E-09	90.2	9.50	10 (10 0 0 0 0)	Cytoplasm.
Q9DB77	QCR2_MOUSE Cytochrome b-c1 complex subunit 2, mitochondrial OS=Mus musculus GN=Uqcrc2 PE=1 SV=1	9.7E-12	100.3	24.50	10 (10 0 0 0 0)	Mitochondrion inner membrane; Peripheral membrane protein; Matrix side.
P10126	EF1A1_MOUSE Elongation factor 1-alpha 1 OS=Mus musculus GN=Eef1a1 PE=1 SV=3	6.7E-10	100.2	19.00	56 (56 0 0 0 0)	Cytoplasm.
P02535	K1C10_MOUSE Keratin, type I cytoskeletal 10 OS=Mus musculus GN=Krt10 PE=1 SV=3	6.8E-11	90.2	11.10	145 (145 0 0 0 0)	ND
Q9D8E6	RL4_MOUSE 60S ribosomal protein L4 OS=Mus musculus GN=Rpl4 PE=1 SV=3	2.0E-08	100.2	25.30	17 (17 0 0 0 0)	ND
Q8BMK4	CKAP4_MOUSE Cytoskeleton-associated protein 4 OS=Mus musculus GN=Ckap4 PE=2 SV=2	3.0E-10	100.2	20.50	12 (12 0 0 0 0)	Endoplasmic reticulum-Golgi intermediate compartment membrane; Single-pass membrane protein.
Q99KI0	ACON_MOUSE Aconitate hydratase, mitochondrial OS=Mus musculus GN=Aco2 PE=1 SV=1	2.1E-12	100.2	17.30	13 (13 0 0 0 0)	Mitochondrion.
Q9JIK5	DDX21_MOUSE Nucleolar RNA helicase 2 OS=Mus musculus GN=Ddx21 PE=1 SV=2	1.6E-09	100.2	14.10	13 (13 0 0 0 0)	Nucleus â€º nucleolus.
Q99MR8	MCCA_MOUSE Methylcrotonoyl-CoA carboxylase subunit alpha, mitochondrial OS=Mus musculus GN=Mccc1 PE=2 SV=2	2.3E-14	80.3	11.20	10 (10 0 0 0 0)	Mitochondrion matrix.
Q6ZQ38	CAND1_MOUSE Cullin-associated NEDD8-dissociated protein 1 OS=Mus musculus GN=Cand1 PE=2 SV=2	7.6E-09	100.2	8.90	10 (10 0 0 0 0)	Nucleus.
O35129	PHB2_MOUSE Prohibitin-2 OS=Mus musculus GN=Phb2 PE=1 SV=1	4.8E-10	80.2	29.10	15 (15 0 0 0 0)	Mitochondrion inner membrane. Cytoplasm. Nucleus.
P60710	ACTB_MOUSE Actin, cytoplasmic 1 OS=Mus	1.0E-13	90.3	16.30	131 (125 6 0 0 0)	Cytoplasm â€º cytoskeleton.

	musculus GN=Actb PE=1 SV=1					
Q9QZF2	GPC1_MOUSE Glypican-1 OS=Mus musculus GN=Gpc1 PE=1 SV=1	4.9E-14	90.3	19.40	37 (37 0 0 0 0)	Cell membrane; Lipid-anchor â€º GPI-anchor; Extracellular side. Secreted â€º extracellular space.
Q8VEK3	HNRPU_MOUSE Heterogeneous nuclear ribonucleoprotein U OS=Mus musculus GN=Hnrnpu PE=1 SV=1	3.7E-10	90.3	13.30	13 (13 0 0 0 0)	Nucleus. Cytoplasm. Cell surface.
O54890	ITB3_MOUSE Integrin beta-3 OS=Mus musculus GN=Itgb3 PE=2 SV=1	1.4E-10	90.2	13.50	21 (21 0 0 0 0)	Membrane; Single-pass type I membrane protein.
P08121	CO3A1_MOUSE Collagen alpha-1(III) chain OS=Mus musculus GN=Col3a1 PE=2 SV=4	4.4E-10	80.2	7.50	12 (12 0 0 0 0)	Secreted â€º extracellular space â€º extracellular matrix.
Q91YQ5	RPN1_MOUSE Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1 OS=Mus musculus GN=Rpn1 PE=2 SV=1	1.1E-11	90.2	17.80	10 (10 0 0 0 0)	Endoplasmic reticulum membrane; Single-pass type I membrane protein. Melanosome.
Q3U7R1	ESYT1_MOUSE Extended synaptotagmin-1 OS=Mus musculus GN=Esyt1 PE=2 SV=2	4.1E-10	90.2	11.10	10 (10 0 0 0 0)	Membrane; Multi-pass membrane protein. Endomembrane system; Multi-pass membrane protein.
Q8BKG3	PTK7_MOUSE Tyrosine-protein kinase-like 7 OS=Mus musculus GN=Ptk7 PE=1 SV=1	3.5E-10	90.2	11.10	9 (9 0 0 0 0)	Membrane; Single-pass type I membrane protein. Cell junction.
P54116	STOM_MOUSE Erythrocyte band 7 integral membrane protein OS=Mus musculus GN=Stom PE=1 SV=3	1.1E-15	70.3	20.80	7 (7 0 0 0 0)	Cell membrane; Peripheral membrane protein; Cytoplasmic side. Cell membrane; Lipid-anchor; Cytoplasmic side. Melanosome.
P39061	COIA1_MOUSE Collagen alpha-1(XVIII) chain OS=Mus musculus GN=Col18a1 PE=1 SV=4	4.5E-11	70.3	5.80	13 (13 0 0 0 0)	Secreted â€º extracellular space â€º extracellular matrix.
P13020	GELS_MOUSE Gelsolin OS=Mus musculus GN=Gsn PE=1 SV=3	3.9E-09	90.2	14.40	10 (10 0 0 0 0)	Cytoplasm â€º cytoskeleton. Secreted.
P26443	DHE3_MOUSE Glutamate dehydrogenase 1, mitochondrial OS=Mus musculus GN=Glud1 PE=1	1.3E-10	90.2	17.90	10 (10 0 0 0 0)	Mitochondrion matrix.

	SV=1					
P15379	CD44_MOUSE CD44 antigen OS=Mus musculus GN=Cd44 PE=1 SV=3	5.8E-09	90.2	8.50	45 (45 0 0 0 0)	Membrane; Single-pass type I membrane protein.
P70206	PLXA1_MOUSE Plexin-A1 OS=Mus musculus GN=Plxna1 PE=1 SV=1	8.5E-09	90.2	4.60	9 (9 0 0 0 0)	Membrane; Single-pass type I membrane protein.
B0V2N1	PTPRS_MOUSE Receptor-type tyrosine-protein phosphatase S OS=Mus musculus GN=Ptprs PE=2 SV=1	3.5E-09	70.2	4.90	7 (7 0 0 0 0)	Membrane; Single-pass type I membrane protein.
P17710	HXK1_MOUSE Hexokinase-1 OS=Mus musculus GN=Hk1 PE=1 SV=2	2.5E-07	90.2	9.40	10 (10 0 0 0 0)	Mitochondrion outer membrane; Peripheral membrane protein. Membrane.
P42932	TCPQ_MOUSE T-complex protein 1 subunit theta OS=Mus musculus GN=Cct8 PE=1 SV=3	6.9E-11	70.2	14.10	7 (7 0 0 0 0)	Cytoplasm. Cytoplasm â€º cytoskeleton â€º centrosome.
O08638	MYH11_MOUSE Myosin-11 OS=Mus musculus GN=Myh11 PE=1 SV=1	2.4E-12	88.3	3.70	101 (72 29 0 0 0)	Melanosome. Cytoplasm â€º myofibril.
P14685	PSMD3_MOUSE 26S proteasome non-ATPase regulatory subunit 3 OS=Mus musculus GN=Psmd3 PE=2 SV=2	5.7E-10	70.2	17.20	7 (7 0 0 0 0)	ND
Q61881	MCM7_MOUSE DNA replication licensing factor MCM7 OS=Mus musculus GN=Mcm7 PE=2 SV=1	6.4E-08	70.2	10.00	8 (8 0 0 0 0)	Nucleus.
P68372	TBB2C_MOUSE Tubulin beta-2C chain OS=Mus musculus GN=Tubb2c PE=1 SV=1	9.0E-11	88.2	14.20	37 (34 3 0 0 0)	Cytoplasm â€º cytoskeleton.
Q8BFZ3	ACTBL_MOUSE Beta-actin-like protein 2 OS=Mus musculus GN=Actbl2 PE=2 SV=1	1.1E-16	82.3	21.80	105 (11 92 1 1 0)	Cytoplasm â€º cytoskeleton.
Q3TTY5	K22E_MOUSE Keratin, type II cytoskeletal 2 epidermal OS=Mus musculus GN=Krt2 PE=1 SV=1	1.6E-09	70.2	5.00	67 (67 0 0 0 0)	ND
Q62165	DAG1_MOUSE Dystroglycan OS=Mus musculus GN=Dag1 PE=1 SV=4	3.3E-15	70.2	8.40	11 (11 0 0 0 0)	Secreted â€º extracellular space. Cell membrane; Single-pass type I membrane protein. Cytoplasm â€º cytoskeleton. Nucleus â€º nucleoplasm.

Q9Z110	P5CS_MOUSE Delta-1-pyrroline-5-carboxylate synthetase OS=Mus musculus GN=Aldh18a1 PE=2 SV=1	3.1E-08	70.2	10.10	7 (7 0 0 0 0)	Mitochondrion inner membrane.
Q9DCN2	NB5R3_MOUSE NADH-cytochrome b5 reductase 3 OS=Mus musculus GN=Cyb5r3 PE=1 SV=3	5.1E-10	80.3	21.90	18 (18 0 0 0 0)	Endoplasmic reticulum membrane; Lipid-anchor; Cytoplasmic side. Mitochondrion outer membrane; Lipid-anchor; Cytoplasmic side. Cytoplasm â€º cytosol.
Q60875	ARHG2_MOUSE Rho guanine nucleotide exchange factor 2 OS=Mus musculus GN=Arhgef2 PE=1 SV=3	9.0E-12	80.3	9.10	10 (10 0 0 0 0)	Cytoplasm. Cell junction â€º tight junction. Golgi apparatus. Cytoplasm â€º cytoskeleton â€º spindle.
Q68FL6	SYMC_MOUSE Methionyl-tRNA synthetase, cytoplasmic OS=Mus musculus GN=Mars PE=2 SV=1	7.5E-12	80.3	11.00	8 (8 0 0 0 0)	Cytoplasm.
P67778	PHB_MOUSE Prohibitin OS=Mus musculus GN=Phb PE=1 SV=1	9.0E-10	80.3	32.70	8 (8 0 0 0 0)	Mitochondrion inner membrane.
P61161	ARP2_MOUSE Actin-related protein 2 OS=Mus musculus GN=Actr2 PE=1 SV=1	8.9E-15	80.3	21.30	8 (8 0 0 0 0)	Cytoplasm â€º cytoskeleton. Cell projection.
P14148	RL7_MOUSE 60S ribosomal protein L7 OS=Mus musculus GN=Rpl7 PE=2 SV=2	4.9E-10	70.2	28.10	13 (13 0 0 0 0)	ND
Q3THE2	ML12B_MOUSE Myosin regulatory light chain 12B OS=Mus musculus GN=Myl12b PE=1 SV=2	8.5E-09	70.2	29.70	9 (9 0 0 0 0)	ND
P09405	NUCL_MOUSE Nucleolin OS=Mus musculus GN=Ncl PE=1 SV=2	4.3E-13	80.2	13.60	12 (12 0 0 0 0)	Nucleus â€º nucleolus. Cytoplasm.
P15116	CADH2_MOUSE Cadherin-2 OS=Mus musculus GN=Cdh2 PE=1 SV=1	1.4E-12	80.2	12.80	14 (14 0 0 0 0)	Cell membrane; Single-pass type I membrane protein.
Q61982	NOTC3_MOUSE Neurogenic locus notch homolog protein 3 OS=Mus musculus GN=Notch3 PE=1 SV=1	1.3E-14	80.2	3.90	11 (11 0 0 0 0)	Cell membrane; Single-pass type I membrane protein. Nucleus.

Q8BMJ2	SYLC_MOUSE Leucyl-tRNA synthetase, cytoplasmic OS=Mus musculus GN=Lars PE=2 SV=2	2.4E-09	80.2	8.40	8 (8 0 0 0 0)	Cytoplasm.
P57780	ACTN4_MOUSE Alpha-actinin-4 OS=Mus musculus GN=Actn4 PE=1 SV=1	3.0E-10	80.2	9.90	8 (8 0 0 0 0)	Nucleus. Cytoplasm.
Q61781	K1C14_MOUSE Keratin, type I cytoskeletal 14 OS=Mus musculus GN=Krt14 PE=1 SV=2	1.1E-13	68.3	15.70	27 (25 2 0 0 0)	Cytoplasm. Nucleus.
Q920B9	SP16H_MOUSE FACT complex subunit SPT16 OS=Mus musculus GN=Supt16h PE=1 SV=2	1.9E-11	80.2	7.70	8 (8 0 0 0 0)	Nucleus. Chromosome.
Q922D8	C1TC_MOUSE C-1-tetrahydrofolate synthase, cytoplasmic OS=Mus musculus GN=Mthfd1 PE=1 SV=3	7.3E-09	80.2	10.10	8 (8 0 0 0 0)	Cytoplasm.
Q91YE6	IPO9_MOUSE Importin-9 OS=Mus musculus GN=Ipo9 PE=1 SV=3	4.1E-09	60.3	7.00	6 (6 0 0 0 0)	Cytoplasm. Nucleus.
Q01320	TOP2A_MOUSE DNA topoisomerase 2-alpha OS=Mus musculus GN=Top2a PE=1 SV=1	3.6E-07	80.2	5.80	9 (9 0 0 0 0)	Nucleus.
Q9D051	ODPB_MOUSE Pyruvate dehydrogenase E1 component subunit beta, mitochondrial OS=Mus musculus GN=Pdhb PE=1 SV=1	4.9E-11	60.2	13.90	6 (6 0 0 0 0)	Mitochondrion matrix.
Q8VIJ6	SFPQ_MOUSE Splicing factor, proline- and glutamine-rich OS=Mus musculus GN=Sfpq PE=1 SV=1	2.6E-06	80.2	14.20	8 (8 0 0 0 0)	Nucleus matrix.
Q07076	ANXA7_MOUSE Annexin A7 OS=Mus musculus GN=Anxa7 PE=2 SV=1	2.2E-06	80.2	15.60	9 (9 0 0 0 0)	ND
P35822	PTPRK_MOUSE Receptor-type tyrosine-protein phosphatase kappa OS=Mus musculus GN=Ptprk PE=1 SV=1	7.0E-10	60.2	5.90	6 (6 0 0 0 0)	Membrane; Single-pass type I membrane protein.
P58771	TPM1_MOUSE Tropomyosin alpha-1 chain OS=Mus musculus GN=Tpm1 PE=1 SV=1	1.3E-09	78.2	23.20	11 (10 1 0 0 0)	Cytoplasm â€º cytoskeleton.
Q9EQH3	VPS35_MOUSE Vacuolar protein sorting-associated protein 35 OS=Mus	8.5E-10	60.2	8.70	6 (6 0 0 0 0)	Cytoplasm. Membrane; Peripheral

	musculus GN=Vps35 PE=1 SV=1					membrane protein.
Q99PL5	RRBP1_MOUSE Ribosome-binding protein 1 OS=Mus musculus GN=Rrbp1 PE=2 SV=2	1.0E-30	70.3	5.50	7 (7 0 0 0 0)	Endoplasmic reticulum membrane; Single-pass type III membrane protein.
Q9WU78	PDC6I_MOUSE Programmed cell death 6-interacting protein OS=Mus musculus GN=Pdcd6ip PE=1 SV=2	8.9E-09	70.3	9.20	7 (7 0 0 0 0)	Cytoplasm â€º cytosol. Melanosome. Cytoplasm â€º cytoskeleton â€º centrosome.
Q8VDM4	PSMD2_MOUSE 26S proteasome non-ATPase regulatory subunit 2 OS=Mus musculus GN=Psmd2 PE=1 SV=1	6.6E-11	70.3	8.50	9 (9 0 0 0 0)	ND
O35639	ANXA3_MOUSE Annexin A3 OS=Mus musculus GN=Anxa3 PE=2 SV=3	3.3E-15	70.3	25.10	7 (7 0 0 0 0)	ND
Q61739	ITA6_MOUSE Integrin alpha-6 OS=Mus musculus GN=Itga6 PE=1 SV=2	2.1E-07	60.2	5.60	6 (6 0 0 0 0)	Membrane; Single-pass type I membrane protein.
Q569Z5	DDX46_MOUSE Probable ATP-dependent RNA helicase DDX46 OS=Mus musculus GN=Ddx46 PE=1 SV=2	2.6E-11	70.2	8.20	7 (7 0 0 0 0)	Nucleus speckle. Nucleus â€º Cajal body.
Q61753	SERA_MOUSE D-3-phosphoglycerate dehydrogenase OS=Mus musculus GN=Phgdh PE=1 SV=3	5.7E-08	60.2	12.40	8 (8 0 0 0 0)	ND
Q99JY9	ARP3_MOUSE Actin-related protein 3 OS=Mus musculus GN=Actr3 PE=1 SV=3	1.9E-12	70.2	19.60	14 (14 0 0 0 0)	Cytoplasm â€º cytoskeleton. Cell projection.
P62264	RS14_MOUSE 40S ribosomal protein S14 OS=Mus musculus GN=Rps14 PE=2 SV=3	1.6E-07	60.2	19.90	7 (7 0 0 0 0)	ND
P14602	HSPB1_MOUSE Heat shock protein beta-1 OS=Mus musculus GN=Hspb1 PE=1 SV=3	9.2E-13	70.2	39.20	20 (20 0 0 0 0)	Cytoplasm. Nucleus. Cytoplasm â€º cytoskeleton â€º spindle.
P80314	TCPB_MOUSE T-complex protein 1 subunit beta OS=Mus musculus GN=Cct2 PE=1 SV=4	1.4E-10	70.2	14.20	8 (8 0 0 0 0)	Cytoplasm.
Q8R366	IGSF8_MOUSE Immunoglobulin superfamily member 8 OS=Mus musculus	1.4E-10	70.2	11.50	10 (10 0 0 0 0)	Membrane; Single-pass membrane protein.

	GN=Igsf8 PE=1 SV=2					
Q9Z1Q9	SYVC_MOUSE Valyl-tRNA synthetase OS=Mus musculus GN=Vars PE=2 SV=1	9.6E-12	70.2	7.80	8 (8 0 0 0 0)	ND
P05202	AATM_MOUSE Aspartate aminotransferase, mitochondrial OS=Mus musculus GN=Got2 PE=1 SV=1	4.3E-09	70.2	12.60	9 (9 0 0 0 0)	Mitochondrion matrix. Cell membrane.
Q78PY7	SND1_MOUSE Staphylococcal nuclease domain-containing protein 1 OS=Mus musculus GN=Snd1 PE=1 SV=1	2.8E-08	70.2	9.70	8 (8 0 0 0 0)	Cytoplasm. Nucleus. Melanosome.
Q9WVM1	RGAP1_MOUSE Rac GTPase-activating protein 1 OS=Mus musculus GN=Racgap1 PE=2 SV=1	2.2E-08	70.2	11.90	9 (9 0 0 0 0)	Nucleus. Cytoplasm. Cytoplasm â€º cytoskeleton â€º spindle. Cytoplasmic vesicle â€º secretory vesicle â€º acrosome.
P11440	CDC2_MOUSE Cell division control protein 2 homolog OS=Mus musculus GN=Cdc2 PE=1 SV=3	1.3E-09	50.2	19.50	10 (10 0 0 0 0)	Nucleus.
P62702	RS4X_MOUSE 40S ribosomal protein S4, X isoform OS=Mus musculus GN=Rps4x PE=2 SV=2	1.9E-07	70.2	23.60	12 (12 0 0 0 0)	Cytoplasm.
Q04750	TOP1_MOUSE DNA topoisomerase 1 OS=Mus musculus GN=Top1 PE=1 SV=2	1.2E-08	70.2	9.10	12 (12 0 0 0 0)	Nucleus â€º nucleolus. Nucleus â€º nucleoplasm.
Q60854	SPB6_MOUSE Serpin B6 OS=Mus musculus GN=Serpinb6 PE=2 SV=1	1.1E-08	70.2	15.30	7 (7 0 0 0 0)	Cytoplasm.
Q62177	SEM3B_MOUSE Semaphorin-3B OS=Mus musculus GN=Sema3b PE=2 SV=1	3.9E-09	70.2	8.70	8 (8 0 0 0 0)	Secreted.
P19096	FAS_MOUSE Fatty acid synthase OS=Mus musculus GN=Fasn PE=1 SV=2	7.8E-08	50.2	2.10	5 (5 0 0 0 0)	Cytoplasm. Melanosome.
P61255	RL26_MOUSE 60S ribosomal protein L26 OS=Mus musculus GN=Rpl26 PE=2 SV=1	2.4E-07	70.2	31.00	9 (9 0 0 0 0)	ND
Q6PDM2	SFRS1_MOUSE Splicing factor, arginine/serine-rich 1 OS=Mus musculus GN=Sfrs1 PE=1 SV=3	3.2E-07	70.1	23.80	16 (16 0 0 0 0)	Cytoplasm. Nucleus. Nucleus speckle.

Q64475	H2B1B_MOUSE Histone H2B type 1-B OS=Mus musculus GN=Hist1h2bb PE=1 SV=3	9.6E-10	66.3	21.40	12 (9 3 0 0 0)	Nucleus. Chromosome.
Q9D379	HYEP_MOUSE Epoxide hydrolase 1 OS=Mus musculus GN=Ephx1 PE=1 SV=1	4.9E-07	50.2	9.70	7 (7 0 0 0 0)	Microsome membrane; Single-pass type II membrane protein. Endoplasmic reticulum membrane; Single-pass type II membrane protein.
P47738	ALDH2_MOUSE Aldehyde dehydrogenase, mitochondrial OS=Mus musculus GN=Aldh2 PE=1 SV=1	8.9E-12	60.3	15.00	10 (10 0 0 0 0)	Mitochondrion matrix.
P47963	RL13_MOUSE 60S ribosomal protein L13 OS=Mus musculus GN=Rpl13 PE=2 SV=3	2.5E-07	50.2	21.80	5 (5 0 0 0 0)	ND
Q501J6	DDX17_MOUSE Probable ATP-dependent RNA helicase DDX17 OS=Mus musculus GN=Ddx17 PE=2 SV=1	1.8E-10	50.2	5.40	8 (8 0 0 0 0)	Nucleus.
Q99JB2	STML2_MOUSE Stomatin-like protein 2 OS=Mus musculus GN=Stoml2 PE=1 SV=1	2.4E-10	60.3	22.40	6 (6 0 0 0 0)	Membrane; Peripheral membrane protein. Cytoplasm. Cytoplasm â€º cytoskeleton.
P62991	UBIQ_MOUSE Ubiquitin OS=Mus musculus GN=Rps27a PE=1 SV=1	9.6E-10	60.3	52.60	57 (57 0 0 0 0)	#N/A
Q922R8	PDIA6_MOUSE Protein disulfide-isomerase A6 OS=Mus musculus GN=Pdia6 PE=1 SV=3	1.3E-09	60.2	19.10	11 (11 0 0 0 0)	Endoplasmic reticulum lumen. Cell membrane. Melanosome.
P80318	TCPG_MOUSE T-complex protein 1 subunit gamma OS=Mus musculus GN=Cct3 PE=1 SV=1	2.4E-06	50.2	12.70	7 (7 0 0 0 0)	Cytoplasm.
Q9QWL7	K1C17_MOUSE Keratin, type I cytoskeletal 17 OS=Mus musculus GN=Krt17 PE=1 SV=3	1.0E-07	50.2	6.50	9 (9 0 0 0 0)	Cytoplasm.
P80315	TCPD_MOUSE T-complex protein 1 subunit delta OS=Mus musculus GN=Cct4 PE=1 SV=3	8.4E-11	60.2	12.80	6 (6 0 0 0 0)	Cytoplasm. Melanosome. Cytoplasm â€º cytoskeleton â€º centrosome.
P15864	H12_MOUSE Histone H1.2 OS=Mus musculus	7.8E-10	60.2	24.50	7 (7 0 0 0 0)	Nucleus. Chromosome.

	GN=Hist1h1c PE=1 SV=2					
Q6IFZ6	K2C1B_MOUSE Keratin, type II cytoskeletal 1b OS=Mus musculus GN=Krt77 PE=1 SV=1	2.8E-08	48.2	5.40	72 (69 3 0 0 0)	ND
Q9R118	HTRA1_MOUSE Serine protease HTRA1 OS=Mus musculus GN=Htra1 PE=2 SV=1	1.7E-10	60.2	10.40	8 (8 0 0 0 0)	Secreted.
P48036	ANXA5_MOUSE Annexin A5 OS=Mus musculus GN=Anxa5 PE=1 SV=1	2.3E-08	60.2	21.00	6 (6 0 0 0 0)	ND
P10493	NID1_MOUSE Nidogen-1 OS=Mus musculus GN=Nid1 PE=1 SV=1	1.7E-09	60.2	5.60	10 (10 0 0 0 0)	Secreted â€º extracellular space â€º extracellular matrix â€º basement membrane.
P62754	RS6_MOUSE 40S ribosomal protein S6 OS=Mus musculus GN=Rps6 PE=1 SV=1	5.0E-07	60.2	16.50	6 (6 0 0 0 0)	ND
P62196	PRS8_MOUSE 26S protease regulatory subunit 8 OS=Mus musculus GN=Psmc5 PE=1 SV=1	7.0E-10	60.2	15.30	6 (6 0 0 0 0)	Cytoplasm. Nucleus.
P46471	PRS7_MOUSE 26S protease regulatory subunit 7 OS=Mus musculus GN=Psmc2 PE=1 SV=5	2.0E-08	60.2	15.50	6 (6 0 0 0 0)	Cytoplasm. Nucleus.
P84099	RL19_MOUSE 60S ribosomal protein L19 OS=Mus musculus GN=Rpl19 PE=1 SV=1	2.2E-15	40.3	14.30	4 (4 0 0 0 0)	ND
Q9QZE5	COPG_MOUSE Coatomer subunit gamma OS=Mus musculus GN=Copg PE=2 SV=1	2.3E-06	60.2	8.50	6 (6 0 0 0 0)	Cytoplasm. Golgi apparatus membrane; Peripheral membrane protein; Cytoplasmic side. Cytoplasmic vesicle â€º COPI-coated vesicle membrane; Peripheral membrane protein; Cytoplasmic side.
P54761	EPHB4_MOUSE Ephrin type-B receptor 4 OS=Mus musculus GN=Ephb4 PE=1 SV=1	5.5E-11	40.3	5.00	6 (6 0 0 0 0)	Membrane; Single-pass type I membrane protein.
O08665	SEM3A_MOUSE Semaphorin-3A OS=Mus musculus GN=Sema3a PE=1 SV=1	3.7E-08	60.2	9.60	7 (7 0 0 0 0)	Secreted.

P35700	PRDX1_MOUSE Peroxiredoxin-1 OS=Mus musculus GN=Prdx1 PE=1 SV=1	1.5E-07	58.2	24.60	10 (6 4 0 0 0)	Cytoplasm. Melanosome.
P17156	HSP72_MOUSE Heat shock-related 70 kDa protein 2 OS=Mus musculus GN=Hspa2 PE=1 SV=1	1.1E-15	40.2	6.00	7 (7 0 0 0 0)	ND
Q8BWT1	THIM_MOUSE 3-ketoacyl-CoA thiolase, mitochondrial OS=Mus musculus GN=Acaa2 PE=1 SV=2	3.2E-10	58.2	15.60	6 (5 1 0 0 0)	Mitochondrion.
Q8CGP5	H2A1F_MOUSE Histone H2A type 1-F OS=Mus musculus GN=Hist1h2af PE=1 SV=3	3.9E-13	50.3	35.40	40 (40 0 0 0 0)	Nucleus. Chromosome.
O35737	HNRH1_MOUSE Heterogeneous nuclear ribonucleoprotein H OS=Mus musculus GN=Hnrnph1 PE=1 SV=3	1.5E-13	50.3	15.40	9 (9 0 0 0 0)	Nucleus â€º nucleoplasm.
Q9JIF7	COPB_MOUSE Coatomer subunit beta OS=Mus musculus GN=Copb1 PE=1 SV=1	3.2E-10	50.3	6.80	5 (5 0 0 0 0)	Cytoplasm. Golgi apparatus membrane; Peripheral membrane protein; Cytoplasmic side. Cytoplasmic vesicle â€º COPI-coated vesicle membrane; Peripheral membrane protein; Cytoplasmic side. Cell membrane. Endoplasmic reticulum-Golgi intermediate compartment.
P80317	TCPZ_MOUSE T-complex protein 1 subunit zeta OS=Mus musculus GN=Cct6a PE=1 SV=3	2.2E-10	50.3	8.90	6 (6 0 0 0 0)	Cytoplasm.
P68040	GBLP_MOUSE Guanine nucleotide-binding protein subunit beta-2-like 1 OS=Mus musculus GN=Gnb2l1 PE=1 SV=3	6.0E-11	50.3	18.60	8 (8 0 0 0 0)	Cell membrane; Peripheral membrane protein. Cytoplasm. Cytoplasm â€º perinuclear region. Cytoplasm â€º cytoskeleton. Nucleus. Perikaryon. Cell

						projection â€º dendrite.
P70696	H2B1A_MOUSE Histone H2B type 1-A OS=Mus musculus GN=Hist1h2ba PE=2 SV=3	3.7E-06	40.2	30.70	8 (8 0 0 0 0)	Nucleus. Chromosome.
P70168	IMB1_MOUSE Importin subunit beta-1 OS=Mus musculus GN=Kpnb1 PE=1 SV=1	3.9E-10	50.2	7.30	5 (5 0 0 0 0)	Cytoplasm. Nucleus envelope.
P70275	SEM3E_MOUSE Semaphorin-3E OS=Mus musculus GN=Sema3e PE=2 SV=2	3.0E-10	40.2	4.50	4 (4 0 0 0 0)	Secreted.
Q91ZA3	PCCA_MOUSE Propionyl-CoA carboxylase alpha chain, mitochondrial OS=Mus musculus GN=Pcca PE=2 SV=2	1.9E-11	50.2	9.80	6 (6 0 0 0 0)	Mitochondrion matrix.
P05064	ALDOA_MOUSE Fructose-bisphosphate aldolase A OS=Mus musculus GN=Aldoa PE=1 SV=2	5.0E-08	50.2	18.40	6 (6 0 0 0 0)	ND
P50446	K2C6A_MOUSE Keratin, type II cytoskeletal 6A OS=Mus musculus GN=Krt6a PE=2 SV=3	3.5E-07	40.2	6.00	8 (8 0 0 0 0)	ND
P35980	RL18_MOUSE 60S ribosomal protein L18 OS=Mus musculus GN=Rpl18 PE=2 SV=3	9.2E-09	40.2	18.60	7 (7 0 0 0 0)	Cytoplasm.
Q64487	PTPRD_MOUSE Receptor-type tyrosine-protein phosphatase delta OS=Mus musculus GN=Ptprd PE=2 SV=2	2.9E-10	50.2	3.40	7 (7 0 0 0 0)	Membrane; Single-pass type I membrane protein.
Q7TMB8	CYFP1_MOUSE Cytoplasmic FMR1-interacting protein 1 OS=Mus musculus GN=Cyfip1 PE=1 SV=1	1.7E-07	50.2	4.20	5 (5 0 0 0 0)	Cytoplasm. Cytoplasm â€º perinuclear region. Cell projection â€º lamellipodium. Cell projection â€º ruffle. Cell junction â€º synapse â€º synaptosome.
Q62371	DDR2_MOUSE Discoidin domain-containing receptor 2 OS=Mus musculus GN=Ddr2 PE=2 SV=2	3.0E-07	40.2	3.90	4 (4 0 0 0 0)	Cell membrane; Single-pass type I membrane protein.
P70698	PYRG1_MOUSE CTP synthase 1 OS=Mus	1.1E-11	50.2	9.50	5 (5 0 0 0 0)	ND

	musculus GN=Ctps PE=1 SV=2					
O88322	NID2_MOUSE Nidogen-2 OS=Mus musculus GN=Nid2 PE=1 SV=1	3.1E-08	50.2	4.80	5 (5 0 0 0 0)	Secreted â€º extracellular space â€º extracellular matrix â€º basement membrane.
Q8C2Q3	RBM14_MOUSE RNA-binding protein 14 OS=Mus musculus GN=Rbm14 PE=1 SV=1	1.5E-09	50.2	11.10	5 (5 0 0 0 0)	Nucleus.
P23927	CRYAB_MOUSE Alpha-crystallin B chain OS=Mus musculus GN=Cryab PE=1 SV=2	2.7E-09	40.2	18.30	4 (4 0 0 0 0)	Cytoplasm. Nucleus.
P57776	EF1D_MOUSE Elongation factor 1-delta OS=Mus musculus GN=Eef1d PE=1 SV=3	7.1E-09	50.2	26.70	6 (6 0 0 0 0)	ND
Q61656	DDX5_MOUSE Probable ATP-dependent RNA helicase DDX5 OS=Mus musculus GN=Ddx5 PE=1 SV=1	1.7E-07	50.2	7.20	5 (5 0 0 0 0)	Nucleus â€º nucleolus.
Q6ZWN5	RS9_MOUSE 40S ribosomal protein S9 OS=Mus musculus GN=Rps9 PE=2 SV=3	3.2E-04	40.2	14.90	4 (4 0 0 0 0)	Cytoplasm.
Q9D8N0	EF1G_MOUSE Elongation factor 1-gamma OS=Mus musculus GN=Eef1g PE=1 SV=3	3.2E-11	50.2	12.60	6 (6 0 0 0 0)	ND
P47911	RL6_MOUSE 60S ribosomal protein L6 OS=Mus musculus GN=Rpl6 PE=1 SV=3	1.3E-11	50.2	15.20	5 (5 0 0 0 0)	ND
O70309	ITB5_MOUSE Integrin beta-5 OS=Mus musculus GN=Itgb5 PE=2 SV=2	4.0E-06	40.2	5.50	4 (4 0 0 0 0)	Membrane; Single-pass type I membrane protein.
P27546	MAP4_MOUSE Microtubule-associated protein 4 OS=Mus musculus GN=Map4 PE=1 SV=3	1.3E-06	50.2	5.80	5 (5 0 0 0 0)	Cytoplasm â€º cytoskeleton.
P97351	RS3A_MOUSE 40S ribosomal protein S3a OS=Mus musculus GN=Rps3a PE=1 SV=3	1.1E-11	50.2	17.00	5 (5 0 0 0 0)	Cytoplasm. Nucleus.
Q61699	HS105_MOUSE Heat shock protein 105 kDa OS=Mus musculus GN=Hsph1 PE=1 SV=2	3.6E-08	50.2	6.40	5 (5 0 0 0 0)	Cytoplasm. Nucleus.
O35479	HNRPG_MOUSE Heterogeneous nuclear	1.1E-06	40.1	10.30	4 (4 0 0 0 0)	Nucleus.

	ribonucleoprotein G OS=Mus musculus GN=Rbmx PE=1 SV=1					
P06151	LDHA_MOUSE L-lactate dehydrogenase A chain OS=Mus musculus GN=Ldha PE=1 SV=3	1.7E-05	40.1	12.00	5 (5 0 0 0 0)	Cytoplasm.
P48962	ADT1_MOUSE ADP/ATP translocase 1 OS=Mus musculus GN=Slc25a4 PE=1 SV=4	3.0E-08	38.2	11.10	6 (5 1 0 0 0)	Mitochondrion inner membrane; Multi-pass membrane protein.
P26040	EZRI_MOUSE Ezrin OS=Mus musculus GN=Ezr PE=1 SV=3	2.9E-08	50.2	8.50	8 (8 0 0 0 0)	Apical cell membrane; Peripheral membrane protein; Cytoplasmic side. Cell projection. Cell projection â€º microvillus membrane; Peripheral membrane protein; Cytoplasmic side. Cell projection â€º ruffle membrane; Peripheral membrane protein; Cytoplasmic side. Cytoplasm â€º cell cortex. Cytoplasm â€º cytoskeleton.
P14733	LMNB1_MOUSE Lamin-B1 OS=Mus musculus GN=Lmnb1 PE=1 SV=3	6.4E-08	50.2	9.40	6 (6 0 0 0 0)	Nucleus inner membrane; Lipid-anchor; Nucleoplasmic side.
Q9D6R2	IDH3A_MOUSE Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial OS=Mus musculus GN=Idh3a PE=1 SV=1	1.0E-10	50.2	15.00	5 (5 0 0 0 0)	Mitochondrion.
Q9ERD7	TBB3_MOUSE Tubulin beta-3 chain OS=Mus musculus GN=Tubb3 PE=1 SV=1	5.7E-08	46.3	7.80	9 (7 0 2 0 0)	Cytoplasm â€º cytoskeleton.
Q8VH51	RBM39_MOUSE RNA-binding protein 39 OS=Mus musculus GN=Rbm39 PE=1 SV=1	1.5E-10	40.3	10.00	5 (5 0 0 0 0)	Nucleus.
P60335	PCBP1_MOUSE Poly(rC)-binding protein 1 OS=Mus musculus GN=Pcbp1 PE=1 SV=1	6.9E-12	40.3	12.40	5 (5 0 0 0 0)	Nucleus.

Q9Z1Q5	CLIC1_MOUSE Chloride intracellular channel protein 1 OS=Mus musculus GN=Clic1 PE=1 SV=3	4.1E-11	40.3	20.70	6 (6 0 0 0 0)	Nucleus. Nucleus membrane; Single-pass membrane protein. Cytoplasm. Cell membrane; Single-pass membrane protein.
Q6A0A9	F120A_MOUSE Constitutive coactivator of PPAR-gamma-like protein 1 OS=Mus musculus GN=FAM120A PE=1 SV=2	8.9E-11	30.2	3.40	4 (4 0 0 0 0)	Cytoplasm. Cell membrane; Peripheral membrane protein; Cytoplasmic side.
P35951	LDLR_MOUSE Low-density lipoprotein receptor OS=Mus musculus GN=Ldlr PE=1 SV=1	3.7E-13	40.3	6.30	4 (4 0 0 0 0)	Cell membrane; Single-pass type I membrane protein. Endomembrane system; Single-pass type I membrane protein. Membrane â€º clathrin-coated pit; Single-pass type I membrane protein.
Q9DCH4	EIF3F_MOUSE Eukaryotic translation initiation factor 3 subunit F OS=Mus musculus GN=Eif3f PE=1 SV=1	8.4E-12	40.3	13.30	5 (5 0 0 0 0)	Cytoplasm.
Q9CXW4	RL11_MOUSE 60S ribosomal protein L11 OS=Mus musculus GN=Rpl11 PE=1 SV=4	1.7E-08	30.2	17.40	3 (3 0 0 0 0)	Nucleus â€º nucleolus.
Q9CR57	RL14_MOUSE 60S ribosomal protein L14 OS=Mus musculus GN=Rpl14 PE=2 SV=3	8.4E-09	30.2	17.10	8 (8 0 0 0 0)	ND
Q9Z0M6	CD97_MOUSE CD97 antigen OS=Mus musculus GN=Cd97 PE=1 SV=2	2.3E-11	40.2	7.00	5 (5 0 0 0 0)	Cell membrane; Multi-pass membrane protein.
P08730	K1C13_MOUSE Keratin, type I cytoskeletal 13 OS=Mus musculus GN=Krt13 PE=1 SV=2	7.3E-07	30.2	4.60	25 (25 0 0 0 0)	ND
Q9CZD3	SYG_MOUSE Glycyl-tRNA synthetase OS=Mus musculus GN=Gars PE=1 SV=1	1.6E-12	40.2	6.90	4 (4 0 0 0 0)	Cytoplasm. Mitochondrion.
Q6IFX2	K1C42_MOUSE Keratin, type I cytoskeletal 42 OS=Mus musculus GN=Krt42 PE=1 SV=1	1.1E-07	30.2	6.90	15 (15 0 0 0 0)	Cytoplasm.
Q9Z127	LAT1_MOUSE Large neutral amino acids	6.0E-11	40.2	9.20	6 (6 0 0 0 0)	Cytoplasm â€º cytosol. Apical cell

	transporter small subunit 1 OS=Mus musculus GN=Slc7a5 PE=1 SV=1					membrane; Multi-pass membrane protein.
O70318	E41L2_MOUSE Band 4.1-like protein 2 OS=Mus musculus GN=Epb41l2 PE=1 SV=1	4.5E-09	40.2	4.90	4 (4 0 0 0 0)	Cytoplasm â€º cytoskeleton.
P51881	ADT2_MOUSE ADP/ATP translocase 2 OS=Mus musculus GN=Slc25a5 PE=1 SV=3	4.6E-09	30.2	8.10	5 (4 1 0 0 0)	Mitochondrion inner membrane; Multi-pass membrane protein.
Q8R2G6	CCD80_MOUSE Coiled-coil domain-containing protein 80 OS=Mus musculus GN=Ccdc80 PE=1 SV=2	1.0E-11	40.2	6.10	5 (5 0 0 0 0)	Secreted â€º extracellular space â€º extracellular matrix.
Q80UG5	SEPT9_MOUSE Septin-9 OS=Mus musculus GN=Sept9 PE=1 SV=1	5.1E-09	40.2	10.10	5 (5 0 0 0 0)	Cytoplasm â€º cytoskeleton.
Q91ZV3	DCBD2_MOUSE Discoidin, CUB and LCCL domain-containing protein 2 OS=Mus musculus GN=Dcbld2 PE=2 SV=1	1.9E-06	40.2	6.10	4 (4 0 0 0 0)	Membrane; Single-pass type I membrane protein.
P62242	RS8_MOUSE 40S ribosomal protein S8 OS=Mus musculus GN=Rps8 PE=1 SV=2	1.1E-06	30.2	17.30	3 (3 0 0 0 0)	Cytoplasm.
P62830	RL23_MOUSE 60S ribosomal protein L23 OS=Mus musculus GN=Rpl23 PE=2 SV=1	1.3E-07	40.2	20.00	4 (4 0 0 0 0)	ND
Q91VD9	NDUS1_MOUSE NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial OS=Mus musculus GN=Ndufs1 PE=1 SV=1	1.4E-09	40.2	6.50	4 (4 0 0 0 0)	Mitochondrion inner membrane.
Q8BP67	RL24_MOUSE 60S ribosomal protein L24 OS=Mus musculus GN=Rpl24 PE=2 SV=2	7.4E-10	30.2	14.00	6 (6 0 0 0 0)	ND
P35564	CALX_MOUSE Calnexin OS=Mus musculus GN=Canx PE=1 SV=1	2.7E-14	40.2	7.40	8 (8 0 0 0 0)	Endoplasmic reticulum membrane; Single-pass type I membrane protein. Melanosome.
P51660	DHB4_MOUSE Peroxisomal multifunctional enzyme type 2 OS=Mus musculus GN=Hsd17b4 PE=1 SV=3	1.7E-08	30.2	4.90	3 (3 0 0 0 0)	Peroxisome.
P04104	K2C1_MOUSE Keratin, type II cytoskeletal 1	3.0E-09	30.2	3.80	65 (65 0 0 0 0)	Cell membrane.

	OS=Mus musculus GN=Krt1 PE=1 SV=4					
Q01705	NOTC1_MOUSE Neurogenic locus notch homolog protein 1 OS=Mus musculus GN=Notch1 PE=1 SV=2	5.9E-08	40.2	1.70	7 (7 0 0 0 0)	Cell membrane; Single-pass type I membrane protein. Nucleus.
Q91V41	RAB14_MOUSE Ras-related protein Rab-14 OS=Mus musculus GN=Rab14 PE=1 SV=3	4.8E-05	30.2	18.10	3 (3 0 0 0 0)	Early endosome membrane; Lipid-anchor; Cytoplasmic side. Golgi apparatus membrane; Lipid-anchor; Cytoplasmic side. Golgi apparatus â€º trans-Golgi network membrane; Lipid-anchor; Cytoplasmic side.
P41105	RL28_MOUSE 60S ribosomal protein L28 OS=Mus musculus GN=Rpl28 PE=1 SV=2	5.6E-08	40.2	18.20	4 (4 0 0 0 0)	ND
P84078	ARF1_MOUSE ADP-ribosylation factor 1 OS=Mus musculus GN=Arf1 PE=1 SV=2	4.1E-10	40.2	25.40	4 (4 0 0 0 0)	Golgi apparatus. Cytoplasm â€º perinuclear region.
P47915	RL29_MOUSE 60S ribosomal protein L29 OS=Mus musculus GN=Rpl29 PE=2 SV=2	1.3E-06	40.2	21.30	5 (5 0 0 0 0)	ND
P84104	SFRS3_MOUSE Splicing factor, arginine/serine-rich 3 OS=Mus musculus GN=Sfrs3 PE=2 SV=1	2.2E-10	30.2	20.10	4 (4 0 0 0 0)	Nucleus.
P61022	CHP1_MOUSE Calcium-binding protein p22 OS=Mus musculus GN=Chp PE=2 SV=2	8.8E-08	30.2	18.50	3 (3 0 0 0 0)	Cytoplasm.
P17751	TPIS_MOUSE Triosephosphate isomerase OS=Mus musculus GN=Tpi1 PE=1 SV=3	3.1E-10	40.2	20.50	5 (5 0 0 0 0)	ND
Q61820	RANT_MOUSE GTP-binding nuclear protein Ran, testis-specific isoform OS=Mus musculus GN=Rasl2-9 PE=2 SV=1	5.9E-07	30.2	10.60	3 (3 0 0 0 0)	Nucleus.
P33175	KIF5A_MOUSE Kinesin heavy chain isoform 5A OS=Mus musculus GN=Kif5a PE=1 SV=3	5.9E-08	30.2	2.50	3 (3 0 0 0 0)	Cytoplasm â€º perinuclear region. Cytoplasm â€º cytoskeleton.
Q9D0I9	SYRC_MOUSE Arginyl-	1.8E-07	40.2	7.40	5 (5 0 0 0 0)	Cytoplasm.

	tRNA synthetase, cytoplasmic OS=Mus musculus GN=Rars PE=2 SV=2					
Q9WTR5	CAD13_MOUSE Cadherin-13 OS=Mus musculus GN=Cdh13 PE=2 SV=1	7.2E-13	40.2	5.70	9 (9 0 0 0 0)	Cell membrane; Lipid-anchor â€º GPI-anchor.
P62806	H4_MOUSE Histone H4 OS=Mus musculus GN=Hist1h4a PE=1 SV=2	1.3E-07	40.2	38.80	16 (16 0 0 0 0)	Nucleus. Chromosome.
P97311	MCM6_MOUSE DNA replication licensing factor MCM6 OS=Mus musculus GN=Mcm6 PE=1 SV=1	1.7E-10	40.2	5.20	4 (4 0 0 0 0)	Nucleus.
P70372	ELAV1_MOUSE ELAV-like protein 1 OS=Mus musculus GN=Elavl1 PE=1 SV=1	4.5E-08	40.2	13.50	6 (6 0 0 0 0)	Cytoplasm.
P46935	NEDD4_MOUSE E3 ubiquitin-protein ligase NEDD4 OS=Mus musculus GN=Nedd4 PE=1 SV=3	1.5E-08	40.2	6.30	4 (4 0 0 0 0)	Cytoplasm. Cell membrane; Peripheral membrane protein.
P54071	IDHP_MOUSE Isocitrate dehydrogenase [NADP], mitochondrial OS=Mus musculus GN=Idh2 PE=1 SV=3	1.4E-11	40.2	9.70	5 (5 0 0 0 0)	Mitochondrion.
Q07813	BAX_MOUSE Apoptosis regulator BAX OS=Mus musculus GN=Bax PE=1 SV=1	3.6E-07	40.2	19.30	4 (4 0 0 0 0)	Mitochondrion outer membrane; Single-pass membrane protein. Cytoplasm. Cytoplasm.
Q922B2	SYDC_MOUSE Aspartyl-tRNA synthetase, cytoplasmic OS=Mus musculus GN=Dars PE=2 SV=1	2.7E-07	40.2	11.00	5 (5 0 0 0 0)	Cytoplasm.
Q9R0E1	PLOD3_MOUSE Procollagen-lysine,2-oxoglutarate 5-dioxygenase 3 OS=Mus musculus GN=Plod3 PE=1 SV=1	1.2E-07	30.2	4.90	3 (3 0 0 0 0)	Rough endoplasmic reticulum membrane; Peripheral membrane protein; Lumenal side.
Q8BG32	PSD11_MOUSE 26S proteasome non-ATPase regulatory subunit 11 OS=Mus musculus GN=Psmd11 PE=1 SV=3	6.8E-07	40.2	11.40	4 (4 0 0 0 0)	ND
P62751	RL23A_MOUSE 60S ribosomal protein L23a OS=Mus musculus GN=Rpl23a PE=2 SV=1	1.0E-09	40.2	18.60	4 (4 0 0 0 0)	ND

P11087	CO1A1_MOUSE Collagen alpha-1(I) chain OS=Mus musculus GN=Col1a1 PE=1 SV=4	5.3E-10	40.2	3.50	4 (4 0 0 0 0)	Secreted â€º extracellular space â€º extracellular matrix.
O08532	CA2D1_MOUSE Voltage-dependent calcium channel subunit alpha-2/delta-1 OS=Mus musculus GN=Cacna2d1 PE=1 SV=1	4.4E-07	40.2	4.20	4 (4 0 0 0 0)	Membrane; Single-pass type I membrane protein.
Q91VR5	DDX1_MOUSE ATP-dependent RNA helicase DDX1 OS=Mus musculus GN=Ddx1 PE=2 SV=1	7.6E-06	30.2	5.40	3 (3 0 0 0 0)	Nucleus. Cytoplasm. Cytoplasmic granule.
Q80TS3	LPHN3_MOUSE Latrophilin-3 OS=Mus musculus GN=Lphn3 PE=1 SV=3	1.5E-08	40.2	3.20	5 (5 0 0 0 0)	Cell membrane; Multi-pass membrane protein.
Q61074	PPM1G_MOUSE Protein phosphatase 1G OS=Mus musculus GN=Ppm1g PE=2 SV=3	1.1E-06	40.2	8.70	4 (4 0 0 0 0)	Nucleus.
Q8BJ71	NUP93_MOUSE Nuclear pore complex protein Nup93 OS=Mus musculus GN=Nup93 PE=2 SV=1	7.0E-07	30.2	4.00	3 (3 0 0 0 0)	Nucleus â€º nuclear pore complex.
P12970	RL7A_MOUSE 60S ribosomal protein L7a OS=Mus musculus GN=Rpl7a PE=2 SV=2	2.8E-08	40.2	16.20	6 (6 0 0 0 0)	ND
P97807	FUMH_MOUSE Fumarate hydratase, mitochondrial OS=Mus musculus GN=Fh PE=1 SV=2	4.5E-07	30.2	7.10	3 (3 0 0 0 0)	Mitochondrion. Cytoplasm.
Q61171	PRDX2_MOUSE Peroxiredoxin-2 OS=Mus musculus GN=Prdx2 PE=1 SV=3	1.0E-07	40.2	23.20	5 (5 0 0 0 0)	Cytoplasm.
Q9CVB6	ARPC2_MOUSE Actin-related protein 2/3 complex subunit 2 OS=Mus musculus GN=Arpc2 PE=1 SV=3	4.1E-09	30.2	11.70	3 (3 0 0 0 0)	Cytoplasm â€º cytoskeleton. Cell projection.
Q9JKR6	HYOU1_MOUSE Hypoxia up-regulated protein 1 OS=Mus musculus GN=Hyou1 PE=1 SV=1	1.3E-07	40.2	4.80	4 (4 0 0 0 0)	Endoplasmic reticulum lumen.
P18572	BASI_MOUSE Basigin OS=Mus musculus GN=Bsg PE=1 SV=2	3.6E-06	40.2	10.30	8 (8 0 0 0 0)	Cell membrane; Single-pass type I membrane protein. Melanosome.
Q922Q8	LRC59_MOUSE Leucine-rich repeat-containing protein 59 OS=Mus musculus GN=Lrrc59 PE=2 SV=1	2.6E-07	30.2	13.00	3 (3 0 0 0 0)	Microsome membrane; Single-pass type II membrane protein. Endoplasmic

						reticulum membrane; Single-pass type II membrane protein.
Q62059	CSPG2_MOUSE Versican core protein OS=Mus musculus GN=Vcan PE=1 SV=2	1.0E-08	30.2	0.90	5 (5 0 0 0 0)	Secreted â€º extracellular space â€º extracellular matrix.
P53690	MMP14_MOUSE Matrix metalloproteinase-14 OS=Mus musculus GN=Mmp14 PE=2 SV=2	4.0E-08	40.2	7.00	7 (7 0 0 0 0)	Membrane; Single-pass type I membrane protein; Extracellular side. Melanosome.
Q61490	CD166_MOUSE CD166 antigen OS=Mus musculus GN=Alcam PE=1 SV=3	1.1E-07	30.2	4.30	7 (7 0 0 0 0)	Membrane; Single-pass type I membrane protein.
P62918	RL8_MOUSE 60S ribosomal protein L8 OS=Mus musculus GN=Rpl8 PE=2 SV=2	4.8E-07	40.2	12.50	8 (8 0 0 0 0)	Cytoplasm.
Q3V3R1	C1TM_MOUSE Monofunctional C1-tetrahydrofolate synthase, mitochondrial OS=Mus musculus GN=Mthfd1l PE=1 SV=2	2.1E-09	40.1	3.60	5 (5 0 0 0 0)	Mitochondrion.
O35295	PURB_MOUSE Transcriptional activator protein Pur-beta OS=Mus musculus GN=Purb PE=1 SV=3	6.1E-08	30.2	11.10	3 (3 0 0 0 0)	Nucleus.
P49717	MCM4_MOUSE DNA replication licensing factor MCM4 OS=Mus musculus GN=Mcm4 PE=2 SV=1	2.0E-08	30.2	4.20	3 (3 0 0 0 0)	Nucleus.
P62281	RS11_MOUSE 40S ribosomal protein S11 OS=Mus musculus GN=Rps11 PE=2 SV=3	5.9E-07	40.1	17.70	4 (4 0 0 0 0)	ND
Q99K51	PLST_MOUSE Plastin-3 OS=Mus musculus GN=Pls3 PE=1 SV=3	6.0E-05	40.1	7.80	4 (4 0 0 0 0)	Cytoplasm.
Q922F4	TBB6_MOUSE Tubulin beta-6 chain OS=Mus musculus GN=Tubb6 PE=1 SV=1	3.7E-11	36.3	9.40	6 (5 0 1 0 0)	Cytoplasm â€º cytoskeleton.
P12382	K6PL_MOUSE 6-phosphofructokinase, liver type OS=Mus musculus GN=Pfkl PE=1 SV=3	8.9E-14	30.3	3.60	3 (3 0 0 0 0)	ND
P99024	TBB5_MOUSE Tubulin beta-5 chain OS=Mus musculus GN=Tubb5 PE=1 SV=1	1.0E-10	30.3	9.90	32 (32 0 0 0 0)	Cytoplasm â€º cytoskeleton.

Q61768	KINH_MOUSE Kinesin-1 heavy chain OS=Mus musculus GN=Kif5b PE=1 SV=2	7.0E-10	30.3	4.40	3 (3 0 0 0 0)	Cytoplasm â€º cytoskeleton.
O08749	DLDH_MOUSE Dihydrolipoyl dehydrogenase, mitochondrial OS=Mus musculus GN=Dld PE=1 SV=2	5.6E-10	30.3	6.50	3 (3 0 0 0 0)	Mitochondrion matrix.
P07091	S10A4_MOUSE Protein S100-A4 OS=Mus musculus GN=S100a4 PE=1 SV=1	2.3E-06	30.1	17.80	3 (3 0 0 0 0)	ND
Q9DCD0	6PGD_MOUSE 6-phosphogluconate dehydrogenase, decarboxylating OS=Mus musculus GN=Pgd PE=2 SV=3	1.9E-12	30.2	7.70	3 (3 0 0 0 0)	Cytoplasm.
P59999	ARPC4_MOUSE Actin-related protein 2/3 complex subunit 4 OS=Mus musculus GN=Arpc4 PE=1 SV=3	5.5E-06	30.1	16.70	5 (5 0 0 0 0)	Cytoplasm â€º cytoskeleton. Cell projection.
Q9CY58	PAIRB_MOUSE Plasminogen activator inhibitor 1 RNA-binding protein OS=Mus musculus GN=Serbp1 PE=1 SV=2	1.9E-09	30.2	9.60	5 (5 0 0 0 0)	Cytoplasm. Nucleus. Cytoplasm â€º perinuclear region.
Q99P72	RTN4_MOUSE Reticulon-4 OS=Mus musculus GN=Rtn4 PE=1 SV=2	2.0E-11	30.2	4.50	4 (4 0 0 0 0)	Endoplasmic reticulum membrane; Multi-pass membrane protein.
Q61390	TCPW_MOUSE T-complex protein 1 subunit zeta-2 OS=Mus musculus GN=Cct6b PE=2 SV=4	8.1E-09	30.1	4.30	3 (3 0 0 0 0)	Cytoplasm.
Q8BKC5	IPO5_MOUSE Importin-5 OS=Mus musculus GN=Ipo5 PE=1 SV=3	9.6E-06	30.1	2.60	3 (3 0 0 0 0)	Cytoplasm. Nucleus.
O35326	SFRS5_MOUSE Splicing factor, arginine/serine-rich 5 OS=Mus musculus GN=Sfrs5 PE=1 SV=1	4.7E-09	30.2	14.80	3 (3 0 0 0 0)	Nucleus.
Q6NVF9	CPSF6_MOUSE Cleavage and polyadenylation specificity factor subunit 6 OS=Mus musculus GN=Cpsf6 PE=1 SV=1	2.9E-10	30.2	5.10	3 (3 0 0 0 0)	Nucleus.
Q921F2	TADBP_MOUSE TAR DNA-binding protein 43 OS=Mus musculus GN=Tardbp PE=1 SV=1	3.3E-15	30.2	9.20	4 (4 0 0 0 0)	Nucleus.

Q60932	VDAC1_MOUSE Voltage-dependent anion-selective channel protein 1 OS=Mus musculus GN=Vdac1 PE=1 SV=3	4.4E-06	26.1	10.50	4 (2 2 0 0 0)	Mitochondrion outer membrane; Multi-pass membrane protein. Cell membrane; Multi-pass membrane protein.
Q9WUM4	COR1C_MOUSE Coronin-1C OS=Mus musculus GN=Coro1c PE=1 SV=2	4.3E-08	30.2	8.20	4 (4 0 0 0 0)	ND
Q6P542	ABCF1_MOUSE ATP-binding cassette sub-family F member 1 OS=Mus musculus GN=Abcf1 PE=1 SV=1	1.7E-08	20.3	3.50	2 (2 0 0 0 0)	Cytoplasm. Nucleus â€º nucleoplasm. Nucleus envelope.
Q99PT1	GDIR1_MOUSE Rho GDP-dissociation inhibitor 1 OS=Mus musculus GN=Arhgdia PE=1 SV=3	1.0E-11	30.2	23.50	3 (3 0 0 0 0)	Cytoplasm.
Q99MR6	SRRT_MOUSE Serrate RNA effector molecule homolog OS=Mus musculus GN=Srrt PE=1 SV=1	1.8E-09	30.2	3.80	3 (3 0 0 0 0)	Nucleus â€º nucleoplasm. Cytoplasm.
Q5SWU9	ACACA_MOUSE Acetyl-CoA carboxylase 1 OS=Mus musculus GN=Acaca PE=1 SV=1	3.9E-11	30.2	1.60	3 (3 0 0 0 0)	Cytoplasm.
P54754	EPHB3_MOUSE Ephrin type-B receptor 3 OS=Mus musculus GN=Ephb3 PE=2 SV=1	4.0E-11	20.2	2.60	2 (2 0 0 0 0)	Membrane; Single-pass type I membrane protein.
O08573	LEG9_MOUSE Galectin-9 OS=Mus musculus GN=Lgals9 PE=1 SV=1	1.9E-11	30.2	9.90	4 (4 0 0 0 0)	Cytoplasm. Secreted.
Q8BMS1	ECHA_MOUSE Trifunctional enzyme subunit alpha, mitochondrial OS=Mus musculus GN=Hadha PE=1 SV=1	3.7E-11	20.2	3.30	2 (2 0 0 0 0)	Mitochondrion matrix.
Q08943	SSRP1_MOUSE FACT complex subunit SSRP1 OS=Mus musculus GN=Ssrp1 PE=1 SV=2	1.3E-10	30.2	5.80	5 (5 0 0 0 0)	Nucleus. Chromosome.
P35979	RL12_MOUSE 60S ribosomal protein L12 OS=Mus musculus GN=Rpl12 PE=1 SV=2	8.6E-09	30.2	24.20	3 (3 0 0 0 0)	ND
O09167	RL21_MOUSE 60S ribosomal protein L21 OS=Mus musculus GN=Rpl21 PE=2 SV=3	4.0E-10	20.2	16.30	3 (3 0 0 0 0)	ND
Q8BNJ2	ATS4_MOUSE A disintegrin and	2.2E-08	20.2	4.00	2 (2 0 0 0 0)	Secreted â€º extracellular space

	metalloproteinase with thrombospondin motifs 4 OS=Mus musculus GN=Adamts4 PE=2 SV=2					â€º extracellular matrix.
P47753	CAZA1_MOUSE F-actin-capping protein subunit alpha-1 OS=Mus musculus GN=Capza1 PE=1 SV=4	1.6E-09	30.2	15.00	5 (5 0 0 0 0)	Cytoplasm â€º cytoskeleton.
O35375	NRP2_MOUSE Neuropilin-2 OS=Mus musculus GN=Nrp2 PE=2 SV=1	2.3E-08	20.2	2.80	3 (3 0 0 0 0)	Membrane; Single-pass type I membrane protein.
P14206	RSSA_MOUSE 40S ribosomal protein SA OS=Mus musculus GN=Rpsa PE=1 SV=4	9.6E-13	30.2	12.90	4 (4 0 0 0 0)	Cell membrane. Cytoplasm. Nucleus.
Q6IRU2	TPM4_MOUSE Tropomyosin alpha-4 chain OS=Mus musculus GN=Tpm4 PE=2 SV=3	1.8E-08	30.2	9.30	4 (4 0 0 0 0)	Cytoplasm â€º cytoskeleton.
O55222	ILK_MOUSE Integrin-linked protein kinase OS=Mus musculus GN=Ilk PE=1 SV=2	2.1E-08	30.2	8.60	3 (3 0 0 0 0)	Cell junction â€º focal adhesion. Cell membrane; Peripheral membrane protein; Cytoplasmic side.
P11679	K2C8_MOUSE Keratin, type II cytoskeletal 8 OS=Mus musculus GN=Krt8 PE=1 SV=4	1.0E-10	20.2	2.90	25 (25 0 0 0 0)	Cytoplasm. Nucleus â€º nucleoplasm. Nucleus matrix.
Q9R0E2	PLOD1_MOUSE Procollagen-lysine,2-oxoglutarate 5-dioxygenase 1 OS=Mus musculus GN=Plod1 PE=1 SV=1	1.7E-07	20.2	3.70	2 (2 0 0 0 0)	Rough endoplasmic reticulum membrane; Peripheral membrane protein; Lumenal side.
Q8K2B3	DHSA_MOUSE Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial OS=Mus musculus GN=Sdha PE=1 SV=1	6.0E-08	30.2	5.00	3 (3 0 0 0 0)	Mitochondrion inner membrane; Peripheral membrane protein; Matrix side.
P97370	AT1B3_MOUSE Sodium/potassium-transporting ATPase subunit beta-3 OS=Mus musculus GN=Atp1b3 PE=1 SV=1	4.1E-09	30.2	7.90	4 (4 0 0 0 0)	Membrane; Single-pass type II membrane protein. Melanosome.
Q9JIX8	ACINU_MOUSE Apoptotic chromatin condensation inducer in the nucleus OS=Mus musculus GN=Acin1 PE=1 SV=2	2.0E-11	30.2	2.80	4 (4 0 0 0 0)	Nucleus.
O08529	CAN2_MOUSE Calpain-2	1.4E-09	30.2	3.40	3 (3 0 0 0 0)	Cytoplasm. Cell

	catalytic subunit OS=Mus musculus GN=Capn2 PE=2 SV=4					membrane.
Q9Z1W8	AT12A_MOUSE Potassium-transporting ATPase alpha chain 2 OS=Mus musculus GN=Atp12a PE=1 SV=2	1.7E-11	20.2	1.30	3 (3 0 0 0 0)	Membrane; Multi-pass membrane protein.
O70475	UGDH_MOUSE UDP-glucose 6-dehydrogenase OS=Mus musculus GN=Ugdh PE=1 SV=1	4.3E-10	30.2	7.30	3 (3 0 0 0 0)	ND
Q6R0H7	GNAS1_MOUSE Guanine nucleotide-binding protein G(s) subunit alpha isoforms XLas OS=Mus musculus GN=Gnas PE=2 SV=1	6.7E-06	30.2	3.40	3 (3 0 0 0 0)	Cell membrane; Peripheral membrane protein.
Q569Z6	TR150_MOUSE Thyroid hormone receptor-associated protein 3 OS=Mus musculus GN=Thrap3 PE=1 SV=1	1.4E-08	30.2	3.20	3 (3 0 0 0 0)	Nucleus.
Q9CPW4	ARPC5_MOUSE Actin-related protein 2/3 complex subunit 5 OS=Mus musculus GN=Arpc5 PE=2 SV=3	1.8E-06	20.2	16.60	2 (2 0 0 0 0)	Cytoplasm â€º cytoskeleton. Cell projection.
P26516	PSD7_MOUSE 26S proteasome non-ATPase regulatory subunit 7 OS=Mus musculus GN=Psmd7 PE=1 SV=2	2.4E-09	30.2	10.60	3 (3 0 0 0 0)	ND
Q9R1C7	PR40A_MOUSE Pre-mRNA-processing factor 40 homolog A OS=Mus musculus GN=Prpf40a PE=1 SV=1	3.1E-05	30.2	4.20	3 (3 0 0 0 0)	Nucleus speckle. Nucleus matrix.
P62827	RAN_MOUSE GTP-binding nuclear protein Ran OS=Mus musculus GN=Ran PE=1 SV=3	2.2E-08	30.2	10.60	3 (3 0 0 0 0)	Nucleus. Cytoplasm. Melanosome.
P08003	PDIA4_MOUSE Protein disulfide-isomerase A4 OS=Mus musculus GN=Pdia4 PE=1 SV=2	1.9E-08	30.2	5.00	4 (4 0 0 0 0)	Endoplasmic reticulum lumen. Melanosome.
Q9CRB9	CHCH3_MOUSE Coiled-coil-helix-coiled-coil-helix domain-containing protein 3, mitochondrial OS=Mus musculus GN=Chchd3 PE=1 SV=1	7.2E-06	30.2	12.80	3 (3 0 0 0 0)	Mitochondrion inner membrane; Lipid-anchor; Intermembrane side.
Q9D0R2	SYTC_MOUSE Threonyl-tRNA synthetase, cytoplasmic OS=Mus musculus GN=Tars PE=1	2.2E-06	30.2	4.70	4 (4 0 0 0 0)	Cytoplasm.

	SV=2					
Q8BL97	SFRS7_MOUSE Splicing factor, arginine/serine-rich 7 OS=Mus musculus GN=Sfrs7 PE=1 SV=1	4.8E-10	30.2	18.40	3 (3 0 0 0 0)	Nucleus.
Q6NZJ6	IF4G1_MOUSE Eukaryotic translation initiation factor 4 gamma 1 OS=Mus musculus GN=Eif4g1 PE=1 SV=1	1.0E-11	30.2	3.70	3 (3 0 0 0 0)	ND
Q62181	SEM3C_MOUSE Semaphorin-3C OS=Mus musculus GN=Sema3c PE=2 SV=1	2.3E-06	20.2	2.90	2 (2 0 0 0 0)	Secreted.
Q61937	NPM_MOUSE Nucleophosmin OS=Mus musculus GN=Npm1 PE=1 SV=1	1.7E-05	20.2	7.90	3 (3 0 0 0 0)	Nucleus â€º nucleolus. Nucleus â€º nucleoplasm. Cytoplasm â€º cytoskeleton â€º centrosome.
Q3TEA8	HP1B3_MOUSE Heterochromatin protein 1-binding protein 3 OS=Mus musculus GN=Hp1bp3 PE=1 SV=1	4.9E-07	30.2	6.00	3 (3 0 0 0 0)	Nucleus. Chromosome.
P46460	NSF_MOUSE Vesicle-fusing ATPase OS=Mus musculus GN=Nsf PE=1 SV=2	2.0E-07	20.2	3.20	2 (2 0 0 0 0)	Cytoplasm.
Q5FWI3	TMEM2_MOUSE Transmembrane protein 2 OS=Mus musculus GN=Tmem2 PE=1 SV=1	3.9E-09	30.2	2.70	3 (3 0 0 0 0)	Membrane; Single-pass membrane protein.
P09411	PGK1_MOUSE Phosphoglycerate kinase 1 OS=Mus musculus GN=Pgk1 PE=1 SV=4	9.1E-11	20.2	7.20	2 (2 0 0 0 0)	Cytoplasm.
Q8BK67	RCC2_MOUSE Protein RCC2 OS=Mus musculus GN=Rcc2 PE=2 SV=1	2.1E-08	30.2	5.40	3 (3 0 0 0 0)	Nucleus â€º nucleolus. Chromosome â€º centromere. Cytoplasm â€º cytoskeleton â€º spindle.
Q8BJS4	UN84B_MOUSE Protein unc-84 homolog B OS=Mus musculus GN=Unc84b PE=1 SV=2	2.0E-07	20.2	3.40	2 (2 0 0 0 0)	Nucleus inner membrane; Single-pass type II membrane protein. Endosome membrane; Single-pass type II membrane protein.
Q9D2G2	ODO2_MOUSE Dihydrolipoyllysine-residue succinyltransferase	3.1E-08	30.2	5.10	3 (3 0 0 0 0)	Mitochondrion.

	component of 2-oxoglutarate dehydrogenase complex, mitochondrial OS=Mus musculus GN=Dlst PE=1 SV=1					
P27659	RL3_MOUSE 60S ribosomal protein L3 OS=Mus musculus GN=Rpl3 PE=2 SV=2	3.3E-07	20.2	6.20	7 (7 0 0 0 0)	Cytoplasm.
P35278	RAB5C_MOUSE Ras-related protein Rab-5C OS=Mus musculus GN=Rab5c PE=1 SV=2	5.7E-07	20.2	11.10	3 (3 0 0 0 0)	Cell membrane; Lipid-anchor; Cytoplasmic side. Early endosome membrane; Lipid-anchor. Melanosome.
P68433	H31_MOUSE Histone H3.1 OS=Mus musculus GN=Hist1h3a PE=1 SV=2	7.5E-08	30.2	17.60	7 (7 0 0 0 0)	Nucleus. Chromosome.
Q91VI7	RINI_MOUSE Ribonuclease inhibitor OS=Mus musculus GN=Rnh1 PE=2 SV=1	3.8E-08	20.2	4.80	3 (3 0 0 0 0)	Cytoplasm.
Q8N9S3	AHSA2_MOUSE Activator of 90 kDa heat shock protein ATPase homolog 2 OS=Mus musculus GN=Ahsa2 PE=2 SV=2	1.8E-07	20.2	6.00	2 (2 0 0 0 0)	ND
Q9R0U0	SF13A_MOUSE Splicing factor, arginine/serine-rich 13A OS=Mus musculus GN=Sfrs13a PE=1 SV=2	1.0E-04	30.2	13.70	4 (4 0 0 0 0)	Nucleus speckle.
P59222	SREC2_MOUSE Scavenger receptor class F member 2 OS=Mus musculus GN=Scarf2 PE=1 SV=1	1.0E-10	30.2	4.20	3 (3 0 0 0 0)	Membrane; Single-pass type I membrane protein.
Q61696	HS71A_MOUSE Heat shock 70 kDa protein 1A OS=Mus musculus GN=Hspa1a PE=1 SV=2	1.6E-10	30.2	4.80	7 (7 0 0 0 0)	Cytoplasm.
O70133	DHX9_MOUSE ATP-dependent RNA helicase A OS=Mus musculus GN=Dhx9 PE=1 SV=2	2.9E-09	30.2	2.40	3 (3 0 0 0 0)	Nucleus â€º nucleolus. Cytoplasm.
Q8R4U6	TOP1M_MOUSE DNA topoisomerase I, mitochondrial OS=Mus musculus GN=Top1mt PE=2 SV=1	1.8E-09	20.2	2.00	2 (2 0 0 0 0)	Mitochondrion.
Q80TF3	PCD19_MOUSE Protocadherin-19 OS=Mus musculus GN=Pcdh19 PE=2 SV=2	3.8E-05	30.2	3.70	3 (3 0 0 0 0)	Cell membrane; Single-pass type I membrane protein.
Q91VC3	IF4A3_MOUSE Eukaryotic	3.7E-05	20.2	5.10	2 (2 0 0 0 0)	Nucleus. Nucleus

	initiation factor 4A-III OS=Mus musculus GN=Eif4a3 PE=2 SV=3					speckle. Cytoplasm.
Q9JL15	LEG8_MOUSE Galectin-8 OS=Mus musculus GN=Lgals8 PE=2 SV=1	2.2E-09	30.2	10.80	3 (3 0 0 0 0)	Cytoplasm.
P47757	CAPZB_MOUSE F-actin-capping protein subunit beta OS=Mus musculus GN=Capzb PE=1 SV=3	2.7E-08	30.2	12.30	5 (5 0 0 0 0)	Cytoplasm â€º cytoskeleton.
O55029	COPB2_MOUSE Coatomer subunit beta' OS=Mus musculus GN=Copb2 PE=2 SV=2	4.2E-06	20.2	2.10	2 (2 0 0 0 0)	Cytoplasm. Golgi apparatus membrane; Peripheral membrane protein; Cytoplasmic side. Cytoplasmic vesicle â€º COPI-coated vesicle membrane; Peripheral membrane protein; Cytoplasmic side.
Q8VHE0	SEC63_MOUSE Translocation protein SEC63 homolog OS=Mus musculus GN=Sec63 PE=1 SV=3	4.2E-05	30.2	4.30	3 (3 0 0 0 0)	Endoplasmic reticulum membrane; Multi-pass membrane protein.
Q8BFR5	EFTU_MOUSE Elongation factor Tu, mitochondrial OS=Mus musculus GN=Tufm PE=1 SV=1	8.1E-08	30.2	9.30	4 (4 0 0 0 0)	Mitochondrion.
Q32MD9	CDON_MOUSE Cell adhesion molecule-related/down-regulated by oncogenes OS=Mus musculus GN=Cdon PE=1 SV=1	6.3E-07	30.2	2.90	3 (3 0 0 0 0)	Membrane; Single-pass membrane protein.
Q07079	IBP5_MOUSE Insulin-like growth factor-binding protein 5 OS=Mus musculus GN=Igfbp5 PE=1 SV=1	4.5E-09	30.2	8.10	5 (5 0 0 0 0)	Secreted.
Q7TPV4	MBB1A_MOUSE Myb-binding protein 1A OS=Mus musculus GN=Mybbp1a PE=1 SV=2	1.1E-07	20.2	2.20	2 (2 0 0 0 0)	Nucleus â€º nucleolus. Cytoplasm.
Q61001	LAMA5_MOUSE Laminin subunit alpha-5 OS=Mus musculus GN=Lama5 PE=1 SV=3	5.3E-07	20.2	0.60	3 (3 0 0 0 0)	Secreted â€º extracellular space â€º extracellular matrix â€º basement membrane.
Q9CZT5	VASN_MOUSE Vasorin OS=Mus musculus	3.4E-08	30.2	5.60	4 (4 0 0 0 0)	Membrane; Single-pass type I

	GN=Vasn PE=2 SV=2					membrane protein.
Q9CZM2	RL15_MOUSE 60S ribosomal protein L15 OS=Mus musculus GN=Rpl15 PE=2 SV=4	6.8E-09	30.2	4.40	3 (3 0 0 0 0)	ND
Q9D1D4	TMEDA_MOUSE Transmembrane emp24 domain-containing protein 10 OS=Mus musculus GN=Tmed10 PE=2 SV=1	3.1E-07	20.2	5.00	2 (2 0 0 0 0)	Golgi apparatus membrane; Single-pass type I membrane protein; Lumenal side. Melanosome.
P16460	ASSY_MOUSE Argininosuccinate synthase OS=Mus musculus GN=Ass1 PE=1 SV=1	3.5E-05	20.2	5.30	2 (2 0 0 0 0)	ND
Q9D6Z1	NOP56_MOUSE Nucleolar protein 56 OS=Mus musculus GN=Nop56 PE=1 SV=2	5.9E-10	30.2	6.20	3 (3 0 0 0 0)	Nucleus â€º nucleolus.
Q3UMU9	HDGR2_MOUSE Hepatoma-derived growth factor-related protein 2 OS=Mus musculus GN=Hdgfrp2 PE=1 SV=1	1.8E-07	30.2	6.00	3 (3 0 0 0 0)	ND
O54724	PTRF_MOUSE Polymerase I and transcript release factor OS=Mus musculus GN=Ptrf PE=1 SV=1	1.1E-05	30.2	5.60	3 (3 0 0 0 0)	Membrane â€º caveola. Cell membrane. Microsome. Endoplasmic reticulum. Cytoplasm â€º cytosol. Mitochondrion. Nucleus.
Q9WV55	VAPA_MOUSE Vesicle-associated membrane protein-associated protein A OS=Mus musculus GN=Vapa PE=1 SV=2	1.0E-05	20.2	9.60	2 (2 0 0 0 0)	Endoplasmic reticulum membrane; Single-pass type IV membrane protein.
P52795	EFNB1_MOUSE Ephrin-B1 OS=Mus musculus GN=Efnb1 PE=1 SV=1	7.2E-08	30.2	14.20	3 (3 0 0 0 0)	Membrane; Single-pass type I membrane protein.
Q9WVA4	TAGL2_MOUSE Transgelin-2 OS=Mus musculus GN=Tagln2 PE=1 SV=4	1.4E-07	20.2	11.60	2 (2 0 0 0 0)	ND
Q9DBV4	MXRA8_MOUSE Matrix-remodeling-associated protein 8 OS=Mus musculus GN=Mxra8 PE=2 SV=1	7.7E-07	30.2	7.20	3 (3 0 0 0 0)	Membrane; Single-pass type I membrane protein.
P19253	RL13A_MOUSE 60S ribosomal protein L13a OS=Mus musculus GN=Rpl13a PE=1 SV=4	5.0E-07	30.2	10.30	3 (3 0 0 0 0)	ND

P16110	LEG3_MOUSE Galectin-3 OS=Mus musculus GN=Lgals3 PE=1 SV=3	1.5E-06	30.2	14.00	3 (3 0 0 0 0)	Cytoplasm. Nucleus. Secreted.
Q9Z204	HNRPC_MOUSE Heterogeneous nuclear ribonucleoproteins C1/C2 OS=Mus musculus GN=Hnrnpc PE=1 SV=1	2.0E-07	20.2	8.60	2 (2 0 0 0 0)	Nucleus.
Q6ZWV7	RL35_MOUSE 60S ribosomal protein L35 OS=Mus musculus GN=Rpl35 PE=2 SV=1	1.3E-05	30.2	22.80	4 (4 0 0 0 0)	ND
Q9QYJ0	DNJA2_MOUSE DnaJ homolog subfamily A member 2 OS=Mus musculus GN=Dnaja2 PE=1 SV=1	5.4E-07	30.1	6.80	3 (3 0 0 0 0)	Membrane; Lipid-anchor.
Q6GU68	ISLR_MOUSE Immunoglobulin superfamily containing leucine-rich repeat protein OS=Mus musculus GN=Islr PE=1 SV=1	2.3E-07	30.1	7.70	4 (4 0 0 0 0)	Secreted.
Q01405	SC23A_MOUSE Protein transport protein Sec23A OS=Mus musculus GN=Sec23a PE=1 SV=2	1.5E-05	20.2	1.60	2 (2 0 0 0 0)	Smooth endoplasmic reticulum membrane; Peripheral membrane protein. Golgi apparatus membrane; Peripheral membrane protein.
P97434	MPRIP_MOUSE Myosin phosphatase Rho-interacting protein OS=Mus musculus GN=Mprip PE=1 SV=2	2.1E-06	20.2	2.50	2 (2 0 0 0 0)	Cytoplasm â€º cytoskeleton.
Q91ZW3	SMCA5_MOUSE SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5 OS=Mus musculus GN=Smarca5 PE=1 SV=1	8.8E-06	30.1	2.70	4 (4 0 0 0 0)	Nucleus.
Q61990	PCBP2_MOUSE Poly(rC)-binding protein 2 OS=Mus musculus GN=Pcbp2 PE=1 SV=1	2.6E-07	20.2	6.60	6 (6 0 0 0 0)	Nucleus. Cytoplasm.
P82347	SGCD_MOUSE Delta-sarcoglycan OS=Mus musculus GN=Sgcd PE=1 SV=1	3.6E-07	20.2	7.30	4 (4 0 0 0 0)	Cell membrane â€º sarcolemma; Single-pass type II membrane protein. Cytoplasm â€º cytoskeleton.

Q8CIB5	FERM2_MOUSE Fermitin family homolog 2 OS=Mus musculus GN=Fermt2 PE=1 SV=1	5.7E-06	30.1	5.10	3 (3 0 0 0 0)	Cytoplasm â€º cell cortex. Cytoplasm â€º cytoskeleton. Cell junction â€º focal adhesion.
P18406	CYR61_MOUSE Protein CYR61 OS=Mus musculus GN=Cyr61 PE=1 SV=1	2.9E-05	30.1	5.00	3 (3 0 0 0 0)	Secreted.
Q8C7R4	UBA6_MOUSE Ubiquitin-like modifier-activating enzyme 6 OS=Mus musculus GN=Uba6 PE=2 SV=1	3.8E-06	20.2	2.10	2 (2 0 0 0 0)	ND
Q99JR1	SFXN1_MOUSE Sideroflexin-1 OS=Mus musculus GN=Sfxn1 PE=1 SV=3	1.7E-07	28.2	9.90	4 (2 2 0 0 0)	Mitochondrion membrane; Multi-pass membrane protein.
P17225	PTBP1_MOUSE Polypyrimidine tract-binding protein 1 OS=Mus musculus GN=Ptbp1 PE=1 SV=2	1.5E-06	26.2	5.30	3 (1 2 0 0 0)	Nucleus.
P21107	TPM3_MOUSE Tropomyosin alpha-3 chain OS=Mus musculus GN=Tpm3 PE=1 SV=2	1.5E-06	20.1	8.50	2 (2 0 0 0 0)	Cytoplasm â€º cytoskeleton.
Q9CQD1	RAB5A_MOUSE Ras-related protein Rab-5A OS=Mus musculus GN=Rab5a PE=1 SV=1	4.8E-07	20.1	11.20	2 (2 0 0 0 0)	Cell membrane; Lipid-anchor; Cytoplasmic side. Early endosome membrane; Lipid-anchor. Melanosome.
Q9Z2X1	HNRPF_MOUSE Heterogeneous nuclear ribonucleoprotein F OS=Mus musculus GN=Hnrnpf PE=1 SV=3	3.5E-09	20.3	8.00	2 (2 0 0 0 0)	Nucleus â€º nucleoplasm.
Q8BG05	ROA3_MOUSE Heterogeneous nuclear ribonucleoprotein A3 OS=Mus musculus GN=Hnrnpa3 PE=1 SV=1	2.2E-16	20.3	8.40	4 (4 0 0 0 0)	Nucleus.
P63101	1433Z_MOUSE 14-3-3 protein zeta/delta OS=Mus musculus GN=Ywhaz PE=1 SV=1	9.1E-09	20.3	10.60	4 (4 0 0 0 0)	Cytoplasm. Melanosome.
Q8BGH2	SAM50_MOUSE Sorting and assembly machinery component 50 homolog OS=Mus musculus GN=Samm50 PE=1 SV=1	2.1E-09	20.1	4.50	3 (3 0 0 0 0)	Mitochondrion outer membrane; Multi-pass membrane protein. Cytoplasm.
P86048	RL10L_MOUSE 60S ribosomal protein L10-like OS=Mus musculus	1.5E-07	20.1	10.70	4 (4 0 0 0 0)	ND

	GN=Rpl10l PE=2 SV=1					
Q01721	GAS1_MOUSE Growth arrest-specific protein 1 OS=Mus musculus GN=Gas1 PE=2 SV=2	1.7E-13	20.3	14.60	3 (3 0 0 0 0)	Cell membrane; Lipid-anchor â€º GPI-anchor.
Q80T21	ATL4_MOUSE ADAMTS-like protein 4 OS=Mus musculus GN=Adamtsl4 PE=2 SV=1	5.9E-09	20.3	2.80	2 (2 0 0 0 0)	Secreted.
P46660	AINX_MOUSE Alpha-internexin OS=Mus musculus GN=Ina PE=1 SV=2	1.2E-08	20.3	2.40	13 (13 0 0 0 0)	ND
P03995	GFAP_MOUSE Glial fibrillary acidic protein OS=Mus musculus GN=Gfap PE=1 SV=4	2.1E-07	20.1	4.40	3 (3 0 0 0 0)	Cytoplasm.
Q62465	VAT1_MOUSE Synaptic vesicle membrane protein VAT-1 homolog OS=Mus musculus GN=Vat1 PE=2 SV=3	2.5E-09	20.2	7.40	3 (3 0 0 0 0)	Cytoplasm.
P97429	ANXA4_MOUSE Annexin A4 OS=Mus musculus GN=Anxa4 PE=2 SV=3	3.7E-09	20.2	8.20	2 (2 0 0 0 0)	ND
Q80UM3	NARG1_MOUSE NMDA receptor-regulated protein 1 OS=Mus musculus GN=Narg1 PE=1 SV=1	5.9E-05	20.1	2.50	2 (2 0 0 0 0)	Cytoplasm. Nucleus. Cytoplasm â€º perinuclear region.
Q8BGD9	IF4B_MOUSE Eukaryotic translation initiation factor 4B OS=Mus musculus GN=Eif4b PE=1 SV=1	9.6E-09	20.2	5.60	2 (2 0 0 0 0)	ND
Q9CQN1	TRAP1_MOUSE Heat shock protein 75 kDa, mitochondrial OS=Mus musculus GN=Trap1 PE=1 SV=1	7.1E-07	20.2	3.30	2 (2 0 0 0 0)	Mitochondrion.
Q8BWY3	ERF1_MOUSE Eukaryotic peptide chain release factor subunit 1 OS=Mus musculus GN=Etf1 PE=1 SV=4	3.2E-06	20.1	5.30	2 (2 0 0 0 0)	Cytoplasm.
P07724	ALBU_MOUSE Serum albumin OS=Mus musculus GN=Alb PE=1 SV=3	8.8E-10	20.2	4.30	86 (86 0 0 0 0)	Secreted.
Q05D44	IF2P_MOUSE Eukaryotic translation initiation factor 5B OS=Mus musculus GN=Eif5b PE=1 SV=2	9.9E-08	20.2	2.30	3 (3 0 0 0 0)	Cytoplasm.
Q9CPR4	RL17_MOUSE 60S ribosomal protein L17 OS=Mus musculus GN=Rpl17 PE=2 SV=3	1.8E-06	20.1	10.30	2 (2 0 0 0 0)	ND

Q69ZF7	CNNM4_MOUSE Metal transporter CNNM4 OS=Mus musculus GN=Cnnm4 PE=1 SV=2	5.0E-10	20.2	3.40	2 (2 0 0 0 0)	Cell membrane; Multi-pass membrane protein.
Q61468	MSLN_MOUSE Mesothelin OS=Mus musculus GN=Msln PE=1 SV=1	1.4E-04	20.1	3.40	2 (2 0 0 0 0)	Cell membrane; Lipid-anchor â€º GPI-anchor. Golgi apparatus. Secreted.
P53986	MOT1_MOUSE Monocarboxylate transporter 1 OS=Mus musculus GN=Slc16a1 PE=1 SV=1	3.0E-09	20.2	7.30	2 (2 0 0 0 0)	Cell membrane; Multi-pass membrane protein.
Q60605	MYL6_MOUSE Myosin light polypeptide 6 OS=Mus musculus GN=Myl6 PE=1 SV=3	3.1E-07	20.2	20.50	4 (4 0 0 0 0)	ND
Q9Z108	STAU1_MOUSE Double-stranded RNA-binding protein Staufen homolog 1 OS=Mus musculus GN=Stau1 PE=2 SV=1	5.3E-08	20.2	6.00	2 (2 0 0 0 0)	Cytoplasm. Rough endoplasmic reticulum.
P62874	GBB1_MOUSE Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1 OS=Mus musculus GN=Gnb1 PE=1 SV=3	1.1E-08	20.1	6.20	2 (2 0 0 0 0)	ND
Q5U3K5	PARF_MOUSE Putative GTP-binding protein Parf OS=Mus musculus GN=Parf PE=1 SV=2	4.5E-11	20.2	4.40	3 (3 0 0 0 0)	Nucleus. Cytoplasm.
Q99K01	PDXD1_MOUSE Pyridoxal-dependent decarboxylase domain-containing protein 1 OS=Mus musculus GN=Pdxdc1 PE=1 SV=2	1.6E-07	20.1	3.20	2 (2 0 0 0 0)	ND
Q8VDW0	DDX39_MOUSE ATP-dependent RNA helicase DDX39 OS=Mus musculus GN=Ddx39 PE=2 SV=1	1.0E-08	20.2	5.60	4 (4 0 0 0 0)	Nucleus.
Q61598	GDIB_MOUSE Rab GDP dissociation inhibitor beta OS=Mus musculus GN=Gdi2 PE=1 SV=1	7.4E-05	20.1	5.20	2 (2 0 0 0 0)	Cytoplasm. Membrane; Peripheral membrane protein.
P14869	RLA0_MOUSE 60S acidic ribosomal protein P0 OS=Mus musculus GN=Rplp0 PE=1 SV=3	6.7E-12	20.2	13.20	5 (5 0 0 0 0)	Nucleus. Cytoplasm.
P62270	RS18_MOUSE 40S ribosomal protein S18 OS=Mus musculus GN=Rps18 PE=2 SV=3	2.7E-05	20.1	13.20	2 (2 0 0 0 0)	Cytoplasm.
Q02053	UBA1_MOUSE Ubiquitin-	1.0E-09	20.2	2.50	3 (3 0 0 0 0)	ND

	like modifier-activating enzyme 1 OS=Mus musculus GN=Uba1 PE=1 SV=1					
P24452	CAPG_MOUSE Macrophage-capping protein OS=Mus musculus GN=Capg PE=1 SV=2	2.1E-08	20.2	7.10	2 (2 0 0 0 0)	Nucleus. Cytoplasm. Secreted. Melanosome.
Q8VE97	SFRS4_MOUSE Splicing factor, arginine/serine-rich 4 OS=Mus musculus GN=Sfrs4 PE=2 SV=1	5.1E-07	20.1	1.80	3 (3 0 0 0 0)	Nucleus speckle.
P18760	COF1_MOUSE Cofilin-1 OS=Mus musculus GN=Cfl1 PE=1 SV=3	6.8E-09	20.2	15.10	2 (2 0 0 0 0)	Nucleus matrix. Cytoplasm â€º cytoskeleton. Cell projection â€º ruffle membrane; Peripheral membrane protein; Cytoplasmic side. Cell projection â€º lamellipodium membrane; Peripheral membrane protein; Cytoplasmic side.
O35286	DHX15_MOUSE Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15 OS=Mus musculus GN=Dhx15 PE=2 SV=2	9.2E-06	20.1	2.90	2 (2 0 0 0 0)	Nucleus.
P17427	AP2A2_MOUSE AP-2 complex subunit alpha-2 OS=Mus musculus GN=Ap2a2 PE=1 SV=1	9.2E-04	20.1	2.30	2 (2 0 0 0 0)	Cell membrane. Membrane â€º coated pit; Peripheral membrane protein; Cytoplasmic side.
Q9Z0J7	GDF15_MOUSE Growth/differentiation factor 15 OS=Mus musculus GN=Gdf15 PE=2 SV=1	1.9E-09	20.2	9.20	2 (2 0 0 0 0)	Secreted.
P49718	MCM5_MOUSE DNA replication licensing factor MCM5 OS=Mus musculus GN=Mcm5 PE=2 SV=1	1.2E-11	20.2	3.70	2 (2 0 0 0 0)	Nucleus.
P62137	PP1A_MOUSE Serine/threonine-protein phosphatase PP1-alpha catalytic subunit OS=Mus musculus GN=Ppp1ca PE=1 SV=1	3.7E-06	20.1	8.50	2 (2 0 0 0 0)	Cytoplasm. Nucleus. Nucleus â€º nucleoplasm. Nucleus â€º nucleolus.
Q61686	CBX5_MOUSE Chromobox protein	1.0E-09	20.2	12.60	3 (3 0 0 0 0)	Nucleus. Chromosome.

	homolog 5 OS=Mus musculus GN=Cbx5 PE=1 SV=1					Chromosome â€º centromere.
P20108	PRDX3_MOUSE Thioredoxin-dependent peroxide reductase, mitochondrial OS=Mus musculus GN=Prdx3 PE=1 SV=1	1.4E-08	20.1	8.90	2 (2 0 0 0 0)	Mitochondrion.
Q8VEE4	RFA1_MOUSE Replication protein A 70 kDa DNA-binding subunit OS=Mus musculus GN=Rpa1 PE=2 SV=1	1.7E-06	20.2	4.50	2 (2 0 0 0 0)	Nucleus.
P18872	GNAO_MOUSE Guanine nucleotide-binding protein G(o) subunit alpha OS=Mus musculus GN=Gnao1 PE=1 SV=3	2.1E-06	20.2	7.30	2 (2 0 0 0 0)	ND
Q99L45	IF2B_MOUSE Eukaryotic translation initiation factor 2 subunit 2 OS=Mus musculus GN=Eif2s2 PE=1 SV=1	4.8E-08	20.1	5.40	2 (2 0 0 0 0)	ND
P25444	RS2_MOUSE 40S ribosomal protein S2 OS=Mus musculus GN=Rps2 PE=1 SV=3	2.5E-09	20.2	7.80	4 (4 0 0 0 0)	ND
O89079	COPE_MOUSE Coatomer subunit epsilon OS=Mus musculus GN=Cope PE=2 SV=3	2.3E-08	20.2	3.90	2 (2 0 0 0 0)	Cytoplasm. Golgi apparatus membrane; Peripheral membrane protein; Cytoplasmic side. Cytoplasmic vesicle â€º COPI-coated vesicle membrane; Peripheral membrane protein; Cytoplasmic side.
Q9CZX8	RS19_MOUSE 40S ribosomal protein S19 OS=Mus musculus GN=Rps19 PE=1 SV=3	6.0E-05	20.1	13.80	2 (2 0 0 0 0)	ND
Q9CZU6	CISY_MOUSE Citrate synthase, mitochondrial OS=Mus musculus GN=Cs PE=1 SV=1	1.1E-10	20.2	5.80	3 (3 0 0 0 0)	Mitochondrion matrix.
Q8BGQ7	SYAC_MOUSE Alanyl-tRNA synthetase, cytoplasmic OS=Mus musculus GN=Aars PE=2 SV=1	2.0E-06	20.1	2.90	2 (2 0 0 0 0)	Cytoplasm.
Q8QZY1	EIF3L_MOUSE Eukaryotic	6.1E-05	20.1	3.00	2 (2 0 0 0 0)	Cytoplasm.

	translation initiation factor 3 subunit L OS=Mus musculus GN=Eif3l PE=1 SV=1					
P62267	RS23_MOUSE 40S ribosomal protein S23 OS=Mus musculus GN=Rps23 PE=2 SV=3	1.8E-07	20.2	15.40	4 (4 0 0 0 0)	ND
Q64511	TOP2B_MOUSE DNA topoisomerase 2-beta OS=Mus musculus GN=Top2b PE=1 SV=2	9.6E-05	20.1	1.20	2 (2 0 0 0 0)	Nucleus â€º nucleolus.
P48999	LOX5_MOUSE Arachidonate 5-lipoxygenase OS=Mus musculus GN=Alox5 PE=1 SV=2	4.7E-04	20.1	2.50	2 (2 0 0 0 0)	Cytoplasm. Nucleus matrix. Nucleus membrane; Peripheral membrane protein.
Q91V61	SFXN3_MOUSE Sideroflexin-3 OS=Mus musculus GN=Sfxn3 PE=1 SV=1	4.1E-09	20.2	8.70	3 (3 0 0 0 0)	Mitochondrion membrane; Multi-pass membrane protein.
P63158	HMGB1_MOUSE High mobility group protein B1 OS=Mus musculus GN=Hmgb1 PE=1 SV=2	2.7E-08	20.2	13.50	2 (2 0 0 0 0)	Nucleus. Cytoplasm. Chromosome.
Q9R0N0	GALK1_MOUSE Galactokinase OS=Mus musculus GN=Galk1 PE=2 SV=1	4.7E-06	20.2	5.60	2 (2 0 0 0 0)	ND
B1AZI6	THOC2_MOUSE THO complex subunit 2 OS=Mus musculus GN=Thoc2 PE=3 SV=1	5.2E-06	20.2	1.40	2 (2 0 0 0 0)	Nucleus.
P15331	PERI_MOUSE Peripherin OS=Mus musculus GN=Prph PE=1 SV=2	2.7E-08	20.2	4.40	30 (30 0 0 0 0)	ND
Q3TXS7	PSMD1_MOUSE 26S proteasome non-ATPase regulatory subunit 1 OS=Mus musculus GN=Psmd1 PE=1 SV=1	3.3E-07	20.1	2.20	2 (2 0 0 0 0)	ND
P00405	COX2_MOUSE Cytochrome c oxidase subunit 2 OS=Mus musculus GN=Mtco2 PE=1 SV=1	6.7E-10	18.3	7.00	2 (1 1 0 0 0)	Mitochondrion inner membrane; Multi-pass membrane protein.
Q9CXW2	RT22_MOUSE 28S ribosomal protein S22, mitochondrial OS=Mus musculus GN=Mrps22 PE=2 SV=1	1.8E-06	20.2	5.60	2 (2 0 0 0 0)	Mitochondrion.
Q3UV17	K22O_MOUSE Keratin, type II cytoskeletal 2 oral OS=Mus musculus	1.0E-05	18.2	3.50	23 (22 1 0 0 0)	ND

	GN=Krt76 PE=2 SV=1					
Q9D880	TIM50_MOUSE Mitochondrial import inner membrane translocase subunit TIM50 OS=Mus musculus GN=Timm50 PE=1 SV=1	7.4E-09	20.2	6.20	2 (2 0 0 0 0)	Mitochondrion inner membrane; Single-pass membrane protein.
P53026	RL10A_MOUSE 60S ribosomal protein L10a OS=Mus musculus GN=Rpl10a PE=1 SV=3	5.3E-08	20.2	9.70	2 (2 0 0 0 0)	ND
P61027	RAB10_MOUSE Ras-related protein Rab-10 OS=Mus musculus GN=Rab10 PE=1 SV=1	1.8E-05	12.1	11.00	3 (0 1 0 2 0)	Cell membrane; Lipid-anchor; Cytoplasmic side.
O08807	PRDX4_MOUSE Peroxiredoxin-4 OS=Mus musculus GN=Prdx4 PE=1 SV=1	2.0E-08	20.2	8.80	2 (2 0 0 0 0)	Cytoplasm. Secreted.
Q641P0	ARP3B_MOUSE Actin-related protein 3B OS=Mus musculus GN=Actr3b PE=2 SV=1	5.4E-09	20.2	6.20	2 (2 0 0 0 0)	Cytoplasm â€º cytoskeleton. Cell projection.
O54734	OST48_MOUSE Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit OS=Mus musculus GN=Ddost PE=1 SV=1	5.2E-07	20.2	4.50	2 (2 0 0 0 0)	Endoplasmic reticulum membrane; Single-pass type I membrane protein.
P63037	DNJA1_MOUSE DnaJ homolog subfamily A member 1 OS=Mus musculus GN=Dnaja1 PE=1 SV=1	1.3E-08	20.2	6.50	2 (2 0 0 0 0)	Membrane; Lipid-anchor.
Q6P5E4	UGGG1_MOUSE UDP-glucose:glycoprotein glucosyltransferase 1 OS=Mus musculus GN=Uggt1 PE=1 SV=3	5.1E-10	20.2	1.60	2 (2 0 0 0 0)	Endoplasmic reticulum lumen. Endoplasmic reticulum-Golgi intermediate compartment.
O70194	EIF3D_MOUSE Eukaryotic translation initiation factor 3 subunit D OS=Mus musculus GN=Eif3d PE=1 SV=2	5.8E-05	20.2	4.70	2 (2 0 0 0 0)	Cytoplasm.
P35456	UPAR_MOUSE Urokinase plasminogen activator surface receptor OS=Mus musculus GN=Plaur PE=2 SV=1	3.9E-06	20.2	2.80	5 (5 0 0 0 0)	Cell membrane; Lipid-anchor â€º GPI-anchor. Secreted.
Q9DAW9	CNN3_MOUSE Calponin-3 OS=Mus musculus GN=Cnn3 PE=2 SV=1	2.5E-06	20.2	3.90	3 (3 0 0 0 0)	ND
Q60749	KHDR1_MOUSE KH domain-containing, RNA-	6.6E-06	20.2	5.40	3 (3 0 0 0 0)	Nucleus. Membrane.

	binding, signal transduction-associated protein 1 OS=Mus musculus GN=Khdrbs1 PE=1 SV=2					
P43276	H15_MOUSE Histone H1.5 OS=Mus musculus GN=Hist1h1b PE=1 SV=2	2.3E-06	20.2	5.80	2 (2 0 0 0 0)	Nucleus. Chromosome.
Q9QUR8	SEM7A_MOUSE Semaphorin-7A OS=Mus musculus GN=Sema7a PE=2 SV=1	9.2E-06	20.2	5.10	2 (2 0 0 0 0)	Cell membrane; Lipid-anchor â€º GPI-anchor; Extracellular side.
Q9WUA3	K6PP_MOUSE 6-phosphofructokinase type C OS=Mus musculus GN=Pfkp PE=1 SV=1	8.8E-06	20.2	2.60	2 (2 0 0 0 0)	ND
Q60931	VDAC3_MOUSE Voltage-dependent anion-selective channel protein 3 OS=Mus musculus GN=Vdac3 PE=1 SV=1	1.4E-07	20.2	11.00	2 (2 0 0 0 0)	Mitochondrion outer membrane.
P28660	NCKP1_MOUSE Nck-associated protein 1 OS=Mus musculus GN=Nckap1 PE=2 SV=2	9.4E-06	20.2	2.30	2 (2 0 0 0 0)	Cell membrane; Single-pass membrane protein; Cytoplasmic side. Cell projection â€º lamellipodium membrane; Single-pass membrane protein; Cytoplasmic side. Cytoplasm.
Q60865	CAPR1_MOUSE Caprin-1 OS=Mus musculus GN=Caprin1 PE=1 SV=2	1.6E-07	20.2	3.30	2 (2 0 0 0 0)	Cytoplasm â€º cytosol. Cell projection â€º dendrite.
Q921N6	DDX27_MOUSE Probable ATP-dependent RNA helicase DDX27 OS=Mus musculus GN=Ddx27 PE=1 SV=2	2.1E-06	20.2	3.30	2 (2 0 0 0 0)	Nucleus.
O70400	PDLI1_MOUSE PDZ and LIM domain protein 1 OS=Mus musculus GN=Pdlim1 PE=2 SV=4	3.1E-07	20.2	7.30	2 (2 0 0 0 0)	Cytoplasm â€º cytoskeleton.
Q9CPY7	AMPL_MOUSE Cytosol aminopeptidase OS=Mus musculus GN=Lap3 PE=1 SV=3	1.5E-06	20.2	4.60	2 (2 0 0 0 0)	Cytoplasm.
Q62523	ZYX_MOUSE Zyxin OS=Mus musculus GN=Zyx PE=1 SV=1	1.0E-08	20.2	5.50	3 (3 0 0 0 0)	Cytoplasm. Cytoplasm â€º cytoskeleton. Cell junction â€º focal adhesion. Nucleus.
Q9DB20	ATPO_MOUSE ATP	8.4E-05	20.2	11.70	3 (3 0 0 0 0)	Mitochondrion.

	synthase subunit O, mitochondrial OS=Mus musculus GN=Atp5o PE=1 SV=1					Mitochondrion inner membrane.
Q8VEM8	MPCP_MOUSE Phosphate carrier protein, mitochondrial OS=Mus musculus GN=Slc25a3 PE=1 SV=1	4.2E-07	20.2	6.20	4 (4 0 0 0 0)	Mitochondrion inner membrane; Multi-pass membrane protein.
P29391	FRIL1_MOUSE Ferritin light chain 1 OS=Mus musculus GN=Ftl1 PE=1 SV=2	1.3E-04	20.2	13.10	2 (2 0 0 0 0)	ND
Q91VR2	ATPG_MOUSE ATP synthase subunit gamma, mitochondrial OS=Mus musculus GN=Atp5c1 PE=1 SV=1	3.8E-05	20.2	8.40	2 (2 0 0 0 0)	Mitochondrion. Mitochondrion inner membrane; Peripheral membrane protein.
Q8C1S0	MED19_MOUSE Mediator of RNA polymerase II transcription subunit 19 OS=Mus musculus GN=Med19 PE=1 SV=1	6.5E-07	20.2	4.90	2 (2 0 0 0 0)	Nucleus.
P08553	NFM_MOUSE Neurofilament medium polypeptide OS=Mus musculus GN=Nefm PE=1 SV=4	1.6E-05	20.2	2.80	2 (2 0 0 0 0)	ND
P08551	NFL_MOUSE Neurofilament light polypeptide OS=Mus musculus GN=Nefl PE=1 SV=5	6.1E-07	20.2	3.70	2 (2 0 0 0 0)	ND
Q08879	FBLN1_MOUSE Fibulin-1 OS=Mus musculus GN=Fbln1 PE=1 SV=2	8.5E-06	20.2	3.10	5 (5 0 0 0 0)	Secreted â€º extracellular space â€º extracellular matrix.
Q921F4	HNRLL_MOUSE Heterogeneous nuclear ribonucleoprotein L-like OS=Mus musculus GN=Hnrpll PE=1 SV=3	3.9E-06	20.2	4.10	2 (2 0 0 0 0)	ND
Q8BFY9	TNPO1_MOUSE Transportin-1 OS=Mus musculus GN=Tnpo1 PE=1 SV=2	6.5E-06	20.2	2.70	2 (2 0 0 0 0)	Cytoplasm. Nucleus.
O88569	ROA2_MOUSE Heterogeneous nuclear ribonucleoproteins A2/B1 OS=Mus musculus GN=Hnrnpa2b1 PE=1 SV=2	3.5E-04	20.2	7.10	2 (2 0 0 0 0)	Nucleus â€º nucleoplasm. Cytoplasm.
Q9Z1D1	EIF3G_MOUSE Eukaryotic translation initiation factor 3 subunit G	2.4E-05	20.2	5.60	3 (3 0 0 0 0)	Cytoplasm. Nucleus. Cytoplasm â€º

	OS=Mus musculus GN=Eif3g PE=1 SV=2					perinuclear region.
Q61316	HSP74_MOUSE Heat shock 70 kDa protein 4 OS=Mus musculus GN=Hspa4 PE=1 SV=1	2.4E-07	20.2	2.90	2 (2 0 0 0 0)	Cytoplasm.
Q60930	VDAC2_MOUSE Voltage-dependent anion-selective channel protein 2 OS=Mus musculus GN=Vdac2 PE=1 SV=2	1.4E-06	20.2	10.80	2 (2 0 0 0 0)	Mitochondrion outer membrane.
P54775	PRS6B_MOUSE 26S protease regulatory subunit 6B OS=Mus musculus GN=Psmc4 PE=1 SV=1	2.6E-05	20.2	5.00	2 (2 0 0 0 0)	Cytoplasm. Nucleus.
Q99LD8	DDAH2_MOUSE N(G),N(G)-dimethylarginine dimethylaminohydrolase 2 OS=Mus musculus GN=Ddah2 PE=1 SV=1	7.7E-07	20.2	7.40	2 (2 0 0 0 0)	ND
Q9DBJ1	PGAM1_MOUSE Phosphoglycerate mutase 1 OS=Mus musculus GN=Pgam1 PE=1 SV=3	3.2E-08	20.2	8.30	2 (2 0 0 0 0)	ND
Q3V0K9	PLSI_MOUSE Plastin-1 OS=Mus musculus GN=Pls1 PE=2 SV=1	7.4E-08	20.2	4.10	2 (2 0 0 0 0)	Cytoplasm.
Q9JM76	ARPC3_MOUSE Actin-related protein 2/3 complex subunit 3 OS=Mus musculus GN=Arpc3 PE=1 SV=3	8.3E-06	20.2	10.10	2 (2 0 0 0 0)	Cytoplasm â€º cytoskeleton. Cell projection.
Q62167	DDX3X_MOUSE ATP-dependent RNA helicase DDX3X OS=Mus musculus GN=Ddx3x PE=1 SV=3	3.1E-08	20.2	4.20	2 (2 0 0 0 0)	Nucleus speckle. Cytoplasm.
Q61335	BAP31_MOUSE B-cell receptor-associated protein 31 OS=Mus musculus GN=Bcap31 PE=1 SV=3	1.1E-04	20.2	4.10	2 (2 0 0 0 0)	Endoplasmic reticulum membrane; Multi-pass membrane protein. Endoplasmic reticulum-Golgi intermediate compartment membrane; Multi-pass membrane protein.
Q32MW3	ACO10_MOUSE Acyl-coenzyme A thioesterase 10, mitochondrial OS=Mus musculus GN=Acot10 PE=2 SV=1	1.2E-04	20.2	2.30	2 (2 0 0 0 0)	Mitochondrion.
P80316	TCPE_MOUSE T-complex	3.6E-08	20.2	3.30	3 (3 0 0 0 0)	Cytoplasm.

	protein 1 subunit epsilon OS=Mus musculus GN=Cct5 PE=1 SV=1					Cytoplasm â€º cytoskeleton â€º centrosome.
Q91W97	HKDC1_MOUSE Putative hexokinase HKDC1 OS=Mus musculus GN=Hkdc1 PE=2 SV=1	5.4E-08	20.2	1.70	2 (2 0 0 0 0)	ND
Q62261	SPTB2_MOUSE Spectrin beta chain, brain 1 OS=Mus musculus GN=Sptbn1 PE=1 SV=2	8.0E-06	20.2	1.10	2 (2 0 0 0 0)	Cytoplasm â€º cytoskeleton. Cytoplasm â€º myofibril â€º sarcomere â€º M line. Cell membrane; Peripheral membrane protein; Cytoplasmic side.
P30285	CDK4_MOUSE Cell division protein kinase 4 OS=Mus musculus GN=Cdk4 PE=1 SV=1	1.0E-06	20.2	8.90	2 (2 0 0 0 0)	Cytoplasm. Nucleus. Membrane.
Q60751	IGF1R_MOUSE Insulin-like growth factor 1 receptor OS=Mus musculus GN=Igf1r PE=1 SV=3	7.6E-06	20.1	1.70	2 (2 0 0 0 0)	Membrane; Single-pass type I membrane protein.
Q8C0Z1	ITFG3_MOUSE Protein ITFG3 OS=Mus musculus GN=Itfg3 PE=1 SV=1	1.4E-06	20.1	3.60	2 (2 0 0 0 0)	Membrane; Single-pass type II membrane protein.
Q9QZN4	FBX6_MOUSE F-box only protein 6 OS=Mus musculus GN=Fbxo6 PE=1 SV=1	3.3E-07	20.1	7.50	2 (2 0 0 0 0)	Cytoplasm.
P22777	PAI1_MOUSE Plasminogen activator inhibitor 1 OS=Mus musculus GN=Serpine1 PE=1 SV=1	3.2E-06	20.1	5.00	2 (2 0 0 0 0)	Secreted.
Q61033	LAP2A_MOUSE Lamina-associated polypeptide 2, isoforms alpha/zeta OS=Mus musculus GN=Tmpo PE=1 SV=3	1.4E-04	20.1	3.50	3 (3 0 0 0 0)	Nucleus. Chromosome.
Q9D8V0	HM13_MOUSE Minor histocompatibility antigen H13 OS=Mus musculus GN=Hm13 PE=1 SV=1	8.6E-07	20.1	3.20	3 (3 0 0 0 0)	Endoplasmic reticulum membrane; Multi-pass membrane protein. Cell membrane; Multi-pass membrane protein.
Q9R1J0	NSDHL_MOUSE Sterol-4-alpha-carboxylate 3-dehydrogenase, decarboxylating OS=Mus musculus GN=Nsdhl PE=2	2.2E-06	20.1	6.60	2 (2 0 0 0 0)	Membrane; Single-pass membrane protein.

	SV=1					
Q9DCL9	PUR6_MOUSE Multifunctional protein ADE2 OS=Mus musculus GN=Paics PE=1 SV=3	2.6E-07	20.1	4.70	2 (2 0 0 0 0)	ND
Q9JLM8	DCLK1_MOUSE Serine/threonine-protein kinase DCLK1 OS=Mus musculus GN=Dclk1 PE=1 SV=1	2.3E-07	20.1	3.20	2 (2 0 0 0 0)	ND
Q91W90	TXND5_MOUSE Thioredoxin domain-containing protein 5 OS=Mus musculus GN=Txndc5 PE=1 SV=2	1.3E-05	20.1	4.30	2 (2 0 0 0 0)	Endoplasmic reticulum lumen.
P29341	PABP1_MOUSE Polyadenylate-binding protein 1 OS=Mus musculus GN=Pabpc1 PE=1 SV=1	2.1E-04	20.1	3.60	2 (2 0 0 0 0)	Cytoplasm. Nucleus.
Q9WTS6	TEN3_MOUSE Teneurin-3 OS=Mus musculus GN=Odz3 PE=1 SV=1	1.7E-05	20.1	1.40	2 (2 0 0 0 0)	Membrane; Single-pass type II membrane protein.
P62900	RL31_MOUSE 60S ribosomal protein L31 OS=Mus musculus GN=Rpl31 PE=2 SV=1	1.7E-04	20.1	15.20	2 (2 0 0 0 0)	ND
P51174	ACADL_MOUSE Long-chain specific acyl-CoA dehydrogenase, mitochondrial OS=Mus musculus GN=Acadl PE=2 SV=2	2.3E-08	20.1	5.10	3 (3 0 0 0 0)	Mitochondrion matrix.
P60229	EIF3E_MOUSE Eukaryotic translation initiation factor 3 subunit E OS=Mus musculus GN=Eif3e PE=1 SV=1	6.3E-04	20.1	4.50	2 (2 0 0 0 0)	Cytoplasm. Nucleus â€º PML body.
Q9DBG3	AP2B1_MOUSE AP-2 complex subunit beta OS=Mus musculus GN=Ap2b1 PE=1 SV=1	4.1E-06	20.1	2.20	2 (2 0 0 0 0)	Cell membrane. Membrane â€º coated pit; Peripheral membrane protein; Cytoplasmic side.
Q9WV32	ARC1B_MOUSE Actin-related protein 2/3 complex subunit 1B OS=Mus musculus GN=Arpc1b PE=1 SV=3	1.7E-04	20.1	5.40	2 (2 0 0 0 0)	Cytoplasm â€º cytoskeleton.
Q9JK48	SHLB1_MOUSE Endophilin-B1 OS=Mus musculus GN=Sh3glb1 PE=1 SV=1	1.6E-05	20.1	5.80	2 (2 0 0 0 0)	Cytoplasm. Golgi apparatus membrane; Peripheral membrane protein. Mitochondrion

						outer membrane; Peripheral membrane protein.
Q8CFI0	NED4L_MOUSE E3 ubiquitin-protein ligase NEDD4-like OS=Mus musculus GN=Nedd4l PE=1 SV=2	1.0E-06	18.2	2.00	2 (1 1 0 0 0)	Cytoplasm.
P62192	PRS4_MOUSE 26S protease regulatory subunit 4 OS=Mus musculus GN=Psmc1 PE=1 SV=1	1.2E-07	18.2	5.50	2 (1 1 0 0 0)	Cytoplasm. Nucleus.
P05977	MLE1_MOUSE Myosin light chain 1, skeletal muscle isoform OS=Mus musculus GN=Myl1 PE=1 SV=2	6.3E-10	16.2	8.50	3 (0 3 0 0 0)	ND
A8C756	THADA_MOUSE Thyroid adenoma-associated protein homolog OS=Mus musculus GN=Thada PE=2 SV=1	2.2E-05	16.1	0.80	2 (0 2 0 0 0)	ND
Q9JJN5	CBPN_MOUSE Carboxypeptidase N catalytic chain OS=Mus musculus GN=Cpn1 PE=2 SV=1	4.7E-04	16.1	2.00	2 (0 2 0 0 0)	Secreted â€º extracellular space.

Table S2

Accession	Reference	P (pro)	Score	Coverage	Peptide (Hits)	Subcellular locations
Q9QXS1	PLEC1_MOUSE Plectin-1 OS=Mus musculus GN=Plec1 PE=1 SV=2	3.11E-14	998.3	21.7	154 (153 1 0 0 0)	Cytoplasm â€º cytoskeleton. Cell junction â€º hemidesmosome.
P20152	VIME_MOUSE Vimentin OS=Mus musculus GN=Vim PE=1 SV=3	1.00E-30	594.3	57.9	784 (774 4 5 1 0)	ND
Q8BTM8	FLNA_MOUSE Filamin-A OS=Mus musculus GN=Flna PE=1 SV=4	2.11E-14	500.3	23.7	93 (92 1 0 0 0)	Cytoplasm â€º cell cortex. Cytoplasm â€º cytoskeleton.
Q69ZN7	MYOF_MOUSE Myoferlin OS=Mus musculus GN=Myof PE=1 SV=2	2.22E-16	370.3	22.7	108 (108 0 0 0 0)	Cell membrane; Single-pass type II membrane protein. Nucleus membrane; Single-pass type II membrane protein. Cytoplasmic vesicle membrane; Single-pass type II membrane protein.
Q6P5H2	NEST_MOUSE Nestin OS=Mus musculus GN=Nes PE=1 SV=1	2.82E-13	470.3	30.3	149 (149 0 0 0 0)	ND
P62737	ACTA_MOUSE Actin, aortic smooth muscle OS=Mus musculus GN=Acta2 PE=1 SV=1	6.66E-15	394.3	54.9	347 (343 4 0 0 0)	Cytoplasm â€º cytoskeleton.
P20029	GRP78_MOUSE 78 kDa glucose-regulated protein OS=Mus musculus GN=Hspa5 PE=1 SV=3	1.67E-13	360.3	44.3	217 (217 0 0 0 0)	Endoplasmic reticulum lumen. Melanosome.
P56480	ATPB_MOUSE ATP synthase subunit beta, mitochondrial OS=Mus musculus GN=Atp5b PE=1 SV=2	1.89E-14	346.3	58.6	116 (109 7 0 0 0)	Mitochondrion. Mitochondrion inner membrane.
Q8VDD5	MYH9_MOUSE Myosin-9 OS=Mus musculus GN=Myh9 PE=1 SV=4	2.91E-10	388.3	16.1	73 (72 1 0 0 0)	ND
Q5SWU9	ACACA_MOUSE Acetyl-CoA carboxylase 1 OS=Mus musculus GN=Acaca PE=1 SV=1	1.00E-30	380.3	18.6	71 (71 0 0 0 0)	Cytoplasm.
P31001	DESM_MOUSE Desmin OS=Mus musculus GN=Des PE=1 SV=3	1.78E-14	324.3	65.2	210 (194 15 1 0 0)	Cytoplasm.
P08113	ENPL_MOUSE Endoplasmin OS=Mus musculus GN=Hsp90b1	1.18E-11	318.2	29.8	112 (111 1 0 0 0)	Endoplasmic reticulum lumen. Melanosome.

	PE=1 SV=2					
P63038	CH60_MOUSE 60 kDa heat shock protein, mitochondrial OS=Mus musculus GN=Hspd1 PE=1 SV=1	8.88E-15	300.3	37.7	101 (101 0 0 0 0)	Mitochondrion matrix.
P13595	NCAM1_MOUSE Neural cell adhesion molecule 1 OS=Mus musculus GN=Ncam1 PE=1 SV=3	1.00E-30	278.3	25.3	64 (63 1 0 0 0)	Cell membrane; Single-pass type I membrane protein. Cell membrane; Lipid-anchor â€º GPI-anchor.
Q8BMK4	CKAP4_MOUSE Cytoskeleton-associated protein 4 OS=Mus musculus GN=Ckap4 PE=2 SV=2	7.77E-15	290.3	54.1	55 (55 0 0 0 0)	Endoplasmic reticulum-Golgi intermediate compartment membrane; Single-pass membrane protein.
Q61738	ITA7_MOUSE Integrin alpha-7 OS=Mus musculus GN=Itga7 PE=1 SV=2	2.78E-14	270.3	23.3	106 (106 0 0 0 0)	Membrane; Single-pass type I membrane protein.
Q8VDN2	AT1A1_MOUSE Sodium/potassium-transporting ATPase subunit alpha-1 OS=Mus musculus GN=Atp1a1 PE=1 SV=1	2.78E-14	270.3	22.0	95 (95 0 0 0 0)	Cell membrane; Multi-pass membrane protein.
P26041	MOES_MOUSE Moesin OS=Mus musculus GN=Msn PE=1 SV=3	4.45E-12	288.3	26.5	48 (44 4 0 0 0)	Cell membrane; Peripheral membrane protein; Cytoplasmic side. Cytoplasm â€º cytoskeleton. Apical cell membrane; Peripheral membrane protein; Cytoplasmic side. Cell projection â€º microvillus membrane; Peripheral membrane protein; Cytoplasmic side.
P63017	HSP7C_MOUSE Heat shock cognate 71 kDa protein OS=Mus musculus GN=Hspa8 PE=1 SV=1	3.32E-12	280.3	31.4	130 (130 0 0 0 0)	Cytoplasm. Melanosome.
P97449	AMPN_MOUSE Aminopeptidase N OS=Mus musculus GN=Anpep PE=1 SV=4	7.77E-15	260.3	30.2	47 (47 0 0 0 0)	Membrane; Single-pass type II membrane protein.
P35564	CALX_MOUSE Calnexin OS=Mus musculus GN=Canx PE=1 SV=1	1.35E-12	278.2	29.8	65 (64 1 0 0 0)	Endoplasmic reticulum membrane; Single-pass type I

						membrane protein. Melanosome.
Q02248	CTNB1_MOUSE Catenin beta-1 OS=Mus musculus GN=Ctnnb1 PE=1 SV=1	1.11E-16	260.3	28.3	58 (58 0 0 0 0)	Cytoplasm. Cytoplasm â€º cytoskeleton. Nucleus. Cell junction â€º adherens junction. Cell junction. Cell membrane.
P27773	PDIA3_MOUSE Protein disulfide-isomerase A3 OS=Mus musculus GN=Pdia3 PE=1 SV=2	5.45E-12	270.2	44.4	126 (126 0 0 0 0)	Endoplasmic reticulum lumen. Melanosome.
P43406	ITAV_MOUSE Integrin alpha-V OS=Mus musculus GN=Itgav PE=1 SV=1	3.44E-14	258.3	27.9	31 (30 1 0 0 0)	Membrane; Single-pass type I membrane protein.
P09103	PDIA1_MOUSE Protein disulfide-isomerase OS=Mus musculus GN=P4hb PE=1 SV=1	9.57E-11	260.3	39.5	97 (97 0 0 0 0)	Endoplasmic reticulum lumen. Melanosome. Cell membrane; Peripheral membrane protein.
P38647	GRP75_MOUSE Stress-70 protein, mitochondrial OS=Mus musculus GN=Hspa9 PE=1 SV=2	2.22E-14	240.3	34.6	93 (93 0 0 0 0)	Mitochondrion.
Q02257	PLAK_MOUSE Junction plakoglobin OS=Mus musculus GN=Jup PE=1 SV=3	5.77E-14	220.3	24.3	64 (64 0 0 0 0)	Cell junction â€º adherens junction. Cell junction â€º desmosome. Cytoplasm â€º cytoskeleton. Membrane; Peripheral membrane protein.
O08917	FLOT1_MOUSE Flotillin-1 OS=Mus musculus GN=Flot1 PE=1 SV=1	2.71E-13	200.3	47.2	48 (48 0 0 0 0)	Cell membrane; Peripheral membrane protein. Membrane â€º caveola; Peripheral membrane protein. Melanosome. Endosome.
P19324	SERPH_MOUSE Serpin H1 OS=Mus musculus GN=Serpinh1 PE=1 SV=2	4.44E-15	238.3	46.8	92 (91 1 0 0 0)	Endoplasmic reticulum lumen.
P33146	CAD15_MOUSE Cadherin-15 OS=Mus musculus GN=Cdh15 PE=1 SV=2	3.33E-16	190.3	29.0	47 (47 0 0 0 0)	Cell membrane; Single-pass type I membrane protein.

Q91ZX7	LRP1_MOUSE Prolow-density lipoprotein receptor-related protein 1 OS=Mus musculus GN=Lrp1 PE=1 SV=1	2.24E-09	220.2	4.6	33 (33 0 0 0 0)	Cell membrane; Single-pass type I membrane protein. Membrane â€º coated pit. Cell membrane; Peripheral membrane protein; Extracellular side. Membrane â€º coated pit. Cytoplasm. Nucleus.
P20029	GRP78_MOUSE 78 kDa glucose-regulated protein OS=Mus musculus GN=Hspa5 PE=1 SV=3	1.61E-13	190.3	34.8	28 (28 0 0 0 0)	Endoplasmic reticulum lumen. Melanosome.
Q99PL5	RRBP1_MOUSE Ribosome-binding protein 1 OS=Mus musculus GN=Rrbp1 PE=2 SV=2	1.00E-30	210.3	13.3	49 (49 0 0 0 0)	Endoplasmic reticulum membrane; Single-pass type III membrane protein.
P11276	FINC_MOUSE Fibronectin OS=Mus musculus GN=Fn1 PE=1 SV=3	1.44E-14	190.3	8.9	48 (48 0 0 0 0)	Secreted â€º extracellular space â€º extracellular matrix.
Q7TMM9	TBB2A_MOUSE Tubulin beta-2A chain OS=Mus musculus GN=Tubb2a PE=1 SV=1	3.46E-12	200.3	26.3	130 (130 0 0 0 0)	Cytoplasm â€º cytoskeleton.
P08003	PDIA4_MOUSE Protein disulfide-isomerase A4 OS=Mus musculus GN=Pdia4 PE=1 SV=2	1.27E-10	196.3	27.7	34 (30 4 0 0 0)	Endoplasmic reticulum lumen. Melanosome.
P11688	ITA5_MOUSE Integrin alpha-5 OS=Mus musculus GN=Itga5 PE=1 SV=2	6.07E-11	180.2	18.3	41 (41 0 0 0 0)	Membrane; Single-pass type I membrane protein.
Q9DBG6	RPN2_MOUSE Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2 OS=Mus musculus GN=Rpn2 PE=2 SV=1	1.11E-16	190.3	36.0	30 (30 0 0 0 0)	Endoplasmic reticulum membrane; Multi-pass membrane protein.
Q80X90	FLNB_MOUSE Filamin-B OS=Mus musculus GN=Flnb PE=1 SV=2	3.33E-15	170.3	7.8	19 (19 0 0 0 0)	Cytoplasm â€º cell cortex. Cytoplasm â€º myofibril â€º sarcomere â€º Z line. Cytoplasm â€º cytoskeleton.
Q03265	ATPA_MOUSE ATP synthase subunit alpha, mitochondrial OS=Mus musculus GN=Atp5a1 PE=1 SV=1	3.11E-14	180.3	30.6	87 (87 0 0 0 0)	Mitochondrion inner membrane. Cell membrane; Peripheral membrane protein; Extracellular side.

P16546	SPTA2_MOUSE Spectrin alpha chain, brain OS=Mus musculus GN=Sptan1 PE=1 SV=4	2.10E-07	170.2	6.3	21 (21 0 0 0 0)	Cytoplasm â€º cytoskeleton. Cytoplasm â€º cell cortex.
P09055	ITB1_MOUSE Integrin beta-1 OS=Mus musculus GN=Itgb1 PE=1 SV=1	1.15E-12	168.3	17.5	161 (128 33 0 0 0)	Cell membrane; Single-pass type I membrane protein. Melanosome.
Q9DCN2	NB5R3_MOUSE NADH-cytochrome b5 reductase 3 OS=Mus musculus GN=Cyb5r3 PE=1 SV=3	1.00E-30	170.4	48.5	36 (36 0 0 0 0)	Endoplasmic reticulum membrane; Lipid-anchor; Cytoplasmic side. Mitochondrion outer membrane; Lipid-anchor; Cytoplasmic side. Cytoplasm â€º cytosol.
P15116	CADH2_MOUSE Cadherin-2 OS=Mus musculus GN=Cdh2 PE=1 SV=1	8.88E-15	160.4	27.8	33 (33 0 0 0 0)	Cell membrane; Single-pass type I membrane protein.
P67778	PHB_MOUSE Prohibitin OS=Mus musculus GN=Phb PE=1 SV=1	6.66E-15	170.3	59.9	38 (38 0 0 0 0)	Mitochondrion inner membrane.
Q9WV91	FPRP_MOUSE Prostaglandin F2 receptor negative regulator OS=Mus musculus GN=Ptgfrn PE=1 SV=1	3.33E-14	160.3	15.2	31 (31 0 0 0 0)	Endoplasmic reticulum membrane; Single-pass type I membrane protein. Golgi apparatus â€º trans-Golgi network membrane; Single-pass type I membrane protein.
Q922R8	PDIA6_MOUSE Protein disulfide-isomerase A6 OS=Mus musculus GN=Pdia6 PE=1 SV=3	1.58E-12	170.2	32.7	55 (55 0 0 0 0)	Endoplasmic reticulum lumen. Cell membrane. Melanosome.
O08532	CA2D1_MOUSE Voltage-dependent calcium channel subunit alpha-2/delta-1 OS=Mus musculus GN=Cacna2d1 PE=1 SV=1	3.49E-13	158.3	18.0	24 (23 1 0 0 0)	Membrane; Single-pass type I membrane protein.
P26040	EZRI_MOUSE Ezrin OS=Mus musculus GN=Ezr PE=1 SV=3	1.98E-12	170.2	23.0	64 (64 0 0 0 0)	Apical cell membrane; Peripheral membrane protein; Cytoplasmic side. Cell projection. Cell projection â€º microvillus membrane; Peripheral

						membrane protein; Cytoplasmic side. Cell projection â€º ruffle membrane; Peripheral membrane protein; Cytoplasmic side. Cytoplasm â€º cell cortex. Cytoplasm â€º cytoskeleton.
Q91XV3	BASP1_MOUSE Brain acid soluble protein 1 OS=Mus musculus GN=Basp1 PE=1 SV=3	5.55E-15	160.3	92.9	31 (31 0 0 0 0)	Cell membrane; Lipid-anchor. Cell projection â€º growth cone.
P17182	ENOA_MOUSE Alpha-enolase OS=Mus musculus GN=Eno1 PE=1 SV=3	1.28E-13	156.3	31.3	23 (21 2 0 0 0)	Cytoplasm. Cell membrane.
Q62470	ITA3_MOUSE Integrin alpha-3 OS=Mus musculus GN=Itga3 PE=1 SV=1	8.88E-15	150.3	20.5	27 (27 0 0 0 0)	Membrane; Single-pass type I membrane protein.
P07901	HS90A_MOUSE Heat shock protein HSP 90-alpha OS=Mus musculus GN=Hsp90aa1 PE=1 SV=4	1.55E-11	154.3	19.6	61 (28 33 0 0 0)	Cytoplasm. Melanosome.
P52480	KPYM_MOUSE Pyruvate kinase isozymes M1/M2 OS=Mus musculus GN=Pkm2 PE=1 SV=4	3.00E-14	150.3	35.8	23 (23 0 0 0 0)	Cytoplasm. Nucleus.
Q62261	SPTB2_MOUSE Spectrin beta chain, brain 1 OS=Mus musculus GN=Sptbn1 PE=1 SV=2	7.83E-12	150.3	8.3	15 (15 0 0 0 0)	Cytoplasm â€º cytoskeleton. Cytoplasm â€º myofibril â€º sarcomere â€º M line. Cell membrane; Peripheral membrane protein; Cytoplasmic side.
P54116	STOM_MOUSE Erythrocyte band 7 integral membrane protein OS=Mus musculus GN=Stom PE=1 SV=3	4.44E-14	150.3	42.3	21 (21 0 0 0 0)	Cell membrane; Peripheral membrane protein; Cytoplasmic side. Cell membrane; Lipid-anchor; Cytoplasmic side. Melanosome.
Q9QZF2	GPC1_MOUSE Glypican-1 OS=Mus musculus GN=Gpc1 PE=1 SV=1	3.33E-16	140.3	31.1	41 (41 0 0 0 0)	Cell membrane; Lipid-anchor â€º GPI-anchor; Extracellular side. Secreted â€º extracellular space.
P60843	IF4A1_MOUSE Eukaryotic initiation factor 4A-I OS=Mus musculus	2.39E-12	150.3	27.3	24 (24 0 0 0 0)	ND

	GN=Eif4a1 PE=2 SV=1					
P58242	ASM3B_MOUSE Acid sphingomyelinase-like phosphodiesterase 3b OS=Mus musculus GN=Smpdl3b PE=1 SV=1	1.11E-15	136.3	28.7	28 (26 2 0 0 0)	Secreted.
P14211	CALR_MOUSE Calreticulin OS=Mus musculus GN=Calr PE=1 SV=1	2.55E-14	140.3	38.9	37 (37 0 0 0 0)	Endoplasmic reticulum lumen. Cytoplasmic granule.
P14602	HSPB1_MOUSE Heat shock protein beta-1 OS=Mus musculus GN=Hspb1 PE=1 SV=3	3.33E-16	130.4	68.9	122 (122 0 0 0 0)	Cytoplasm. Nucleus. Cytoplasm â€º cytoskeleton â€º spindle.
P47738	ALDH2_MOUSE Aldehyde dehydrogenase, mitochondrial OS=Mus musculus GN=Aldh2 PE=1 SV=1	6.17E-11	140.2	28.3	33 (33 0 0 0 0)	Mitochondrion matrix.
P48678	LMNA_MOUSE Lamin-A/C OS=Mus musculus GN=Lmna PE=1 SV=2	3.23E-12	130.2	21.8	20 (20 0 0 0 0)	Nucleus. Nucleus envelope.
P10852	4F2_MOUSE 4F2 cell-surface antigen heavy chain OS=Mus musculus GN=Slc3a2 PE=1 SV=1	4.03E-09	140.2	25.3	38 (38 0 0 0 0)	Apical cell membrane; Single-pass type II membrane protein. Melanosome.
Q8R422	CD109_MOUSE CD109 antigen OS=Mus musculus GN=Cd109 PE=2 SV=1	8.92E-13	120.3	12.8	24 (24 0 0 0 0)	Cell membrane; Lipid-anchor â€º GPI-anchor.
Q8VHX6	FLNC_MOUSE Filamin-C OS=Mus musculus GN=Flnc PE=1 SV=3	2.22E-11	120.3	6.5	17 (17 0 0 0 0)	Cytoplasm. Membrane; Peripheral membrane protein. Cytoplasm â€º cytoskeleton. Cytoplasm â€º myofibril â€º sarcomere â€º Z line.
Q62351	TFR1_MOUSE Transferrin receptor protein 1 OS=Mus musculus GN=Tfrc PE=1 SV=1	3.97E-12	140.2	14.8	18 (18 0 0 0 0)	Cell membrane; Single-pass type II membrane protein. Melanosome.
Q9DB77	QCR2_MOUSE Cytochrome b-c1 complex subunit 2, mitochondrial OS=Mus musculus GN=Uqcrc2 PE=1 SV=1	3.23E-11	140.2	30.5	19 (19 0 0 0 0)	Mitochondrion inner membrane; Peripheral membrane protein; Matrix side.
Q3U7R1	ESYT1_MOUSE Extended synaptotagmin-1 OS=Mus musculus GN=Esyt1 PE=2	2.22E-15	140.2	14.2	35 (35 0 0 0 0)	Membrane; Multi-pass membrane protein.

	SV=2					Endomembrane system; Multi-pass membrane protein.
Q60634	FLOT2_MOUSE Flotillin-2 OS=Mus musculus GN=Flot2 PE=1 SV=2	7.03E-11	120.2	23.4	38 (38 0 0 0 0)	Cell membrane; Peripheral membrane protein. Membrane â€º caveola; Peripheral membrane protein. Endosome.
O35129	PHB2_MOUSE Prohibitin-2 OS=Mus musculus GN=Phb2 PE=1 SV=1	9.99E-14	130.3	50.5	34 (34 0 0 0 0)	Mitochondrion inner membrane. Cytoplasm. Nucleus.
P39688	FYN_MOUSE Proto-oncogene tyrosine-protein kinase Fyn OS=Mus musculus GN=Fyn PE=1 SV=3	2.90E-09	118.3	23.1	17 (15 2 0 0 0)	Cell membrane.
P26039	TLN1_MOUSE Talin-1 OS=Mus musculus GN=Tln1 PE=1 SV=1	5.53E-10	130.2	6.1	23 (23 0 0 0 0)	Cell projection â€º ruffle membrane; Peripheral membrane protein; Cytoplasmic side. Cytoplasm â€º cytoskeleton.
Q61335	BAP31_MOUSE B-cell receptor-associated protein 31 OS=Mus musculus GN=Bcap31 PE=1 SV=3	1.11E-15	128.3	34.7	16 (15 1 0 0 0)	Endoplasmic reticulum membrane; Multi-pass membrane protein. Endoplasmic reticulum-Golgi intermediate compartment membrane; Multi-pass membrane protein.
Q07076	ANXA7_MOUSE Annexin A7 OS=Mus musculus GN=Anxa7 PE=2 SV=1	1.34E-11	120.3	24.4	15 (15 0 0 0 0)	ND
Q922U2	K2C5_MOUSE Keratin, type II cytoskeletal 5 OS=Mus musculus GN=Krt5 PE=1 SV=1	8.74E-09	118.2	17.4	61 (60 1 0 0 0)	ND
P48962	ADT1_MOUSE ADP/ATP translocase 1 OS=Mus musculus GN=Slc25a4 PE=1 SV=4	2.19E-11	120.3	33.6	43 (43 0 0 0 0)	Mitochondrion inner membrane; Multi-pass membrane protein.
P70206	PLXA1_MOUSE Plexin-A1 OS=Mus musculus GN=Plxna1 PE=1 SV=1	1.49E-11	110.3	7.1	13 (13 0 0 0 0)	Membrane; Single-pass type I membrane protein.
P10107	ANXA1_MOUSE Annexin A1 OS=Mus musculus GN=Anxa1 PE=1 SV=2	5.50E-11	110.3	31.5	13 (13 0 0 0 0)	Nucleus. Cytoplasm. Cell projection â€º

						cilium. Basolateral cell membrane.
Q9WVK4	EHD1_MOUSE EH domain-containing protein 1 OS=Mus musculus GN=Ehd1 PE=1 SV=1	9.98E-10	120.2	21.0	13 (13 0 0 0 0)	Cell membrane; Peripheral membrane protein; Cytoplasmic side. Early endosome membrane; Peripheral membrane protein. Recycling endosome membrane; Peripheral membrane protein.
Q9D379	HYEP_MOUSE Epoxide hydrolase 1 OS=Mus musculus GN=Ephx1 PE=1 SV=1	5.94E-10	120.2	26.8	15 (15 0 0 0 0)	Microsome membrane; Single-pass type II membrane protein. Endoplasmic reticulum membrane; Single-pass type II membrane protein.
Q8CAQ8	IMMT_MOUSE Mitochondrial inner membrane protein OS=Mus musculus GN=Immt PE=1 SV=1	8.64E-11	120.2	18.4	24 (24 0 0 0 0)	Mitochondrion inner membrane.
Q9EPR5	SORC2_MOUSE VPS10 domain-containing receptor SorCS2 OS=Mus musculus GN=Sorcs2 PE=1 SV=1	2.63E-10	110.2	10.5	19 (19 0 0 0 0)	Membrane; Single-pass type I membrane protein.
Q60932	VDAC1_MOUSE Voltage-dependent anion-selective channel protein 1 OS=Mus musculus GN=Vdac1 PE=1 SV=3	1.00E-30	116.3	40.9	25 (21 4 0 0 0)	Mitochondrion outer membrane; Multi-pass membrane protein. Cell membrane; Multi-pass membrane protein.
Q99P72	RTN4_MOUSE Reticulon-4 OS=Mus musculus GN=Rtn4 PE=1 SV=2	1.00E-30	110.4	15.7	28 (28 0 0 0 0)	Endoplasmic reticulum membrane; Multi-pass membrane protein.
Q8R366	IGSF8_MOUSE Immunoglobulin superfamily member 8 OS=Mus musculus GN=Igsf8 PE=1 SV=2	3.00E-14	100.3	17.3	24 (24 0 0 0 0)	Membrane; Single-pass membrane protein.
P08249	MDHM_MOUSE Malate dehydrogenase, mitochondrial OS=Mus musculus GN=Mdh2 PE=1	1.11E-15	110.3	40.8	28 (28 0 0 0 0)	Mitochondrion matrix.

	SV=3					
Q62165	DAG1_MOUSE Dystroglycan OS=Mus musculus GN=Dag1 PE=1 SV=4	7.77E-15	90.3	10.3	14 (14 0 0 0 0)	Secreted â€º extracellular space. Cell membrane; Single-pass type I membrane protein. Cytoplasm â€º cytoskeleton. Nucleus â€º nucleoplasm.
Q9JKF1	IQGA1_MOUSE Ras GTPase-activating-like protein IQGAP1 OS=Mus musculus GN=Iqgap1 PE=1 SV=1	5.96E-11	110.2	8.0	14 (14 0 0 0 0)	Cell membrane.
Q9QUR8	SEM7A_MOUSE Semaphorin-7A OS=Mus musculus GN=Sema7a PE=2 SV=1	1.56E-09	90.3	17.8	13 (13 0 0 0 0)	Cell membrane; Lipid-anchor â€º GPI-anchor; Extracellular side.
Q6P5E4	UGGG1_MOUSE UDP-glucose:glycoprotein glucosyltransferase 1 OS=Mus musculus GN=Uggt1 PE=1 SV=3	6.71E-09	110.2	7.4	11 (11 0 0 0 0)	Endoplasmic reticulum lumen. Endoplasmic reticulum-Golgi intermediate compartment.
P08752	GNAI2_MOUSE Guanine nucleotide-binding protein G(i), alpha-2 subunit OS=Mus musculus GN=Gnai2 PE=1 SV=4	6.67E-13	90.3	21.4	37 (37 0 0 0 0)	Cytoplasm. Cytoplasm â€º cytoskeleton â€º centrosome. Cell membrane.
Q9JKR6	HYOU1_MOUSE Hypoxia up-regulated protein 1 OS=Mus musculus GN=Hyou1 PE=1 SV=1	6.08E-12	110.2	10.3	15 (15 0 0 0 0)	Endoplasmic reticulum lumen.
O35516	NOTC2_MOUSE Neurogenic locus notch homolog protein 2 OS=Mus musculus GN=Notch2 PE=1 SV=1	2.03E-10	90.3	4.5	14 (14 0 0 0 0)	Cell membrane; Single-pass type I membrane protein. Nucleus.
Q02819	NUCB1_MOUSE Nucleobindin-1 OS=Mus musculus GN=Nucb1 PE=1 SV=2	4.21E-13	110.2	28.5	12 (12 0 0 0 0)	Golgi apparatus â€º cis-Golgi network membrane; Peripheral membrane protein; Lumenal side. Cytoplasm.
O54890	ITB3_MOUSE Integrin beta-3 OS=Mus musculus GN=Itgb3 PE=2 SV=1	6.58E-10	90.3	11.4	15 (15 0 0 0 0)	Membrane; Single-pass type I membrane protein.
Q8BH59	CMC1_MOUSE Calcium-binding mitochondrial carrier protein Aralar1 OS=Mus musculus GN=Slc25a12	1.31E-10	108.2	17.1	11 (10 1 0 0 0)	Mitochondrion inner membrane; Multi-pass membrane protein.

	PE=1 SV=1					
P26231	CTNA1_MOUSE Catenin alpha-1 OS=Mus musculus GN=Ctnna1 PE=1 SV=1	2.03E-12	90.2	12.3	12 (12 0 0 0 0)	Cytoplasm â€º cytoskeleton. Cell junction â€º adherens junction. Cell membrane; Peripheral membrane protein; Cytoplasmic side. Cell junction.
P68369	TBA1A_MOUSE Tubulin alpha-1A chain OS=Mus musculus GN=Tuba1a PE=1 SV=1	1.67E-14	100.3	29.7	91 (91 0 0 0 0)	Cytoplasm â€º cytoskeleton.
P11499	HS90B_MOUSE Heat shock protein HSP 90-beta OS=Mus musculus GN=Hsp90ab1 PE=1 SV=2	3.36E-12	100.3	11.7	31 (31 0 0 0 0)	Cytoplasm. Melanosome.
Q8VEM8	MPCP_MOUSE Phosphate carrier protein, mitochondrial OS=Mus musculus GN=Slc25a3 PE=1 SV=1	9.25E-10	100.2	21.8	43 (43 0 0 0 0)	Mitochondrion inner membrane; Multi-pass membrane protein.
P15379	CD44_MOUSE CD44 antigen OS=Mus musculus GN=Cd44 PE=1 SV=3	2.64E-10	90.2	8.1	93 (93 0 0 0 0)	Membrane; Single-pass type I membrane protein.
Q9CRB9	CHCH3_MOUSE Coiled-coil-helix-coiled-coil-helix domain-containing protein 3, mitochondrial OS=Mus musculus GN=Chchd3 PE=1 SV=1	8.95E-12	100.2	32.2	11 (11 0 0 0 0)	Mitochondrion inner membrane; Lipid-anchor; Intermembrane side.
P60710	ACTB_MOUSE Actin, cytoplasmic 1 OS=Mus musculus GN=Actb PE=1 SV=1	7.77E-15	88.3	16.3	218 (211 7 0 0 0)	Cytoplasm â€º cytoskeleton.
Q9D024	CC47_MOUSE Coiled-coil domain-containing protein 47 OS=Mus musculus GN=Ccdc47 PE=2 SV=2	9.31E-07	100.2	15.9	13 (13 0 0 0 0)	Membrane; Single-pass membrane protein.
Q9EQP2	EHD4_MOUSE EH domain-containing protein 4 OS=Mus musculus GN=Ehd4 PE=1 SV=1	1.09E-07	100.2	18.1	10 (10 0 0 0 0)	Early endosome membrane; Peripheral membrane protein. Recycling endosome membrane; Peripheral membrane protein.
Q60875	ARHG2_MOUSE Rho guanine nucleotide exchange factor 2 OS=Mus musculus GN=Arhgef2 PE=1 SV=3	2.38E-09	100.2	8.3	14 (14 0 0 0 0)	Cytoplasm. Cell junction â€º tight junction. Golgi apparatus. Cytoplasm â€º

						cytoskeleton â€º spindle.
P08551	NFL_MOUSE Neurofilament light polypeptide OS=Mus musculus GN=Nefl PE=1 SV=5	5.11E-12	80.2	14.9	8 (8 0 0 0 0)	ND
O35887	CALU_MOUSE Calumenin OS=Mus musculus GN=Calu PE=1 SV=1	8.88E-15	90.3	33.7	15 (15 0 0 0 0)	Endoplasmic reticulum lumen. Melanosome. Sarcoplasmic reticulum lumen. Secreted.
Q04736	YES_MOUSE Proto-oncogene tyrosine-protein kinase Yes OS=Mus musculus GN=Yes1 PE=1 SV=3	2.04E-12	80.2	20.7	9 (9 0 0 0 0)	Cytoplasm â€º cytosol.
Q91VD9	NDUS1_MOUSE NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial OS=Mus musculus GN=Ndufs1 PE=1 SV=1	6.47E-10	90.2	11.7	11 (11 0 0 0 0)	Mitochondrion inner membrane.
Q05793	PGBM_MOUSE Basement membrane-specific heparan sulfate proteoglycan core protein OS=Mus musculus GN=Hspg2 PE=1 SV=1	1.63E-10	80.2	2.1	8 (8 0 0 0 0)	Secreted â€º extracellular space â€º extracellular matrix â€º basement membrane.
Q60715	P4HA1_MOUSE Prolyl 4-hydroxylase subunit alpha-1 OS=Mus musculus GN=P4ha1 PE=2 SV=2	4.12E-12	90.2	18.9	14 (14 0 0 0 0)	Endoplasmic reticulum lumen.
Q91YQ5	RPN1_MOUSE Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1 OS=Mus musculus GN=Rpn1 PE=2 SV=1	1.89E-12	90.2	18.4	27 (27 0 0 0 0)	Endoplasmic reticulum membrane; Single-pass type I membrane protein. Melanosome.
Q8VDZ4	ZDHC5_MOUSE Probable palmitoyltransferase ZDHHC5 OS=Mus musculus GN=Zdhhc5 PE=1 SV=1	4.44E-15	70.4	16.8	11 (11 0 0 0 0)	Membrane; Multi-pass membrane protein.
Q03145	EPHA2_MOUSE Ephrin type-A receptor 2 OS=Mus musculus GN=Epha2 PE=1 SV=2	4.95E-09	90.2	7.7	12 (12 0 0 0 0)	Cell membrane; Single-pass type I membrane protein. Cell projection â€º ruffle membrane; Single-pass type I membrane protein. Cell projection â€º lamellipodium

						membrane; Single-pass type I membrane protein. Cell junction â€º focal adhesion.
Q61739	ITA6_MOUSE Integrin alpha-6 OS=Mus musculus GN=Itga6 PE=1 SV=2	2.55E-14	70.3	8.3	8 (8 0 0 0 0)	Membrane; Single-pass type I membrane protein.
Q9CZ13	QCR1_MOUSE Cytochrome b-c1 complex subunit 1, mitochondrial OS=Mus musculus GN=Uqcrc1 PE=1 SV=1	1.33E-14	80.3	13.3	17 (17 0 0 0 0)	Mitochondrion inner membrane.
Q99KI0	ACON_MOUSE Aconitate hydratase, mitochondrial OS=Mus musculus GN=Aco2 PE=1 SV=1	8.22E-14	80.3	13.8	24 (24 0 0 0 0)	Mitochondrion.
Q9Z0P4	PALM_MOUSE Paralemmin OS=Mus musculus GN=Palm PE=1 SV=1	8.65E-11	70.3	22.2	17 (17 0 0 0 0)	Cell membrane; Lipid-anchor; Cytoplasmic side. Cell projection â€º filopodium membrane; Lipid-anchor. Cell projection â€º axon. Cell projection â€º dendrite. Cell projection â€º dendritic spine. Basolateral cell membrane; Lipid-anchor. Apicolateral cell membrane; Lipid-anchor.
Q7TPR4	ACTN1_MOUSE Alpha-actinin-1 OS=Mus musculus GN=Actn1 PE=2 SV=1	1.86E-09	70.2	9.8	10 (10 0 0 0 0)	Cytoplasm â€º cytoskeleton. Cytoplasm â€º myofibril â€º sarcomere â€º Z line. Cell membrane. Cell projection â€º ruffle.
P63321	RALA_MOUSE Ras-related protein Ral-A OS=Mus musculus GN=Rala PE=1 SV=1	2.59E-11	80.3	30.6	11 (11 0 0 0 0)	Cell surface. Cell membrane; Lipid-anchor; Cytoplasmic side. Cleavage furrow. Midbody.
P07356	ANXA2_MOUSE Annexin A2 OS=Mus musculus GN=Anxa2 PE=1 SV=2	8.73E-09	80.2	24.5	30 (30 0 0 0 0)	Secreted â€º extracellular space â€º extracellular matrix â€º

						basement membrane. Melanosome.
P17809	GTR1_MOUSE Solute carrier family 2, facilitated glucose transporter member 1 OS=Mus musculus GN=Slc2a1 PE=1 SV=3	6.07E-11	80.2	9.3	39 (39 0 0 0 0)	Cell membrane; Multi-pass membrane protein. Melanosome.
P50544	ACADV_MOUSE Very long-chain specific acyl-CoA dehydrogenase, mitochondrial OS=Mus musculus GN=Acadvl PE=1 SV=3	9.87E-12	80.2	13.6	8 (8 0 0 0 0)	Mitochondrion inner membrane.
Q61595	KTN1_MOUSE Kinectin OS=Mus musculus GN=Ktn1 PE=1 SV=1	1.72E-07	80.2	6.8	10 (10 0 0 0 0)	Endoplasmic reticulum membrane; Single-pass type II membrane protein.
P18572	BASI_MOUSE Basigin OS=Mus musculus GN=Bsg PE=1 SV=2	2.09E-08	80.2	18.0	22 (22 0 0 0 0)	Cell membrane; Single-pass type I membrane protein. Melanosome.
Q8VHY0	CSPG4_MOUSE Chondroitin sulfate proteoglycan 4 OS=Mus musculus GN=Cspg4 PE=1 SV=2	1.04E-08	70.2	3.5	8 (8 0 0 0 0)	Apical cell membrane; Single-pass type I membrane protein; Extracellular side. Cell projection â€º lamellipodium membrane; Single-pass type I membrane protein; Extracellular side.
O08795	GLU2B_MOUSE Glucosidase 2 subunit beta OS=Mus musculus GN=Prkcsh PE=1 SV=1	8.72E-11	80.2	10.0	10 (10 0 0 0 0)	Endoplasmic reticulum.
P15864	H12_MOUSE Histone H1.2 OS=Mus musculus GN=Hist1h1c PE=1 SV=2	2.31E-11	68.2	19.8	8 (7 1 0 0 0)	Nucleus. Chromosome.
P61979	HNRPK_MOUSE Heterogeneous nuclear ribonucleoprotein K OS=Mus musculus GN=Hnrnpk PE=1 SV=1	1.12E-11	60.3	17.7	6 (6 0 0 0 0)	Cytoplasm. Nucleus â€º nucleoplasm.
P02535	K1C10_MOUSE Keratin, type I cytoskeletal 10 OS=Mus musculus GN=Krt10 PE=1 SV=3	7.79E-10	80.2	11.1	85 (85 0 0 0 0)	ND
P39061	COIA1_MOUSE Collagen alpha-1(XVIII) chain OS=Mus musculus GN=Col18a1 PE=1 SV=4	4.77E-13	80.2	5.5	8 (8 0 0 0 0)	Secreted â€º extracellular space â€º extracellular matrix.

P05202	AATM_MOUSE Aspartate aminotransferase, mitochondrial OS=Mus musculus GN=Got2 PE=1 SV=1	2.10E-08	80.2	16.5	14 (14 0 0 0 0)	Mitochondrion matrix. Cell membrane.
Q99MN9	PCCB_MOUSE Propionyl-CoA carboxylase beta chain, mitochondrial OS=Mus musculus GN=Pccb PE=1 SV=1	1.46E-11	60.3	14.8	8 (8 0 0 0 0)	Mitochondrion matrix.
Q9Z0M6	CD97_MOUSE CD97 antigen OS=Mus musculus GN=Cd97 PE=1 SV=2	1.15E-13	60.3	11.0	15 (15 0 0 0 0)	Cell membrane; Multi-pass membrane protein.
Q9ERE2	KRT81_MOUSE Keratin, type II cuticular Hb1 (Fragment) OS=Mus musculus GN=Krt81 PE=2 SV=1	8.48E-07	80.2	15.1	25 (25 0 0 0 0)	ND
P54761	EPHB4_MOUSE Ephrin type-B receptor 4 OS=Mus musculus GN=Ephb4 PE=1 SV=1	7.77E-15	60.3	8.4	6 (6 0 0 0 0)	Membrane; Single-pass type I membrane protein.
P68372	TBB2C_MOUSE Tubulin beta-2C chain OS=Mus musculus GN=Tubb2c PE=1 SV=1	1.48E-11	78.2	14.2	56 (55 1 0 0 0)	Cytoplasm â€º cytoskeleton.
Q3V0J1	AL2S4_MOUSE Amyotrophic lateral sclerosis 2 chromosomal region candidate gene 4 protein homolog OS=Mus musculus GN=Als2cr4 PE=2 SV=1	9.63E-13	60.3	19.9	10 (10 0 0 0 0)	Membrane; Multi-pass membrane protein.
O09044	SNP23_MOUSE Synaptosomal-associated protein 23 OS=Mus musculus GN=Snap23 PE=1 SV=1	1.59E-12	70.3	29.5	8 (8 0 0 0 0)	Cell membrane; Peripheral membrane protein. Cell membrane; Lipid-anchor. Cell junction â€º synapse â€º synaptosome.
Q9JL15	LEG8_MOUSE Galectin-8 OS=Mus musculus GN=Lgals8 PE=2 SV=1	9.11E-11	60.2	20.3	8 (8 0 0 0 0)	Cytoplasm.
O54724	PTRF_MOUSE Polymerase I and transcript release factor OS=Mus musculus GN=Ptrf PE=1 SV=1	1.40E-10	70.2	18.6	9 (9 0 0 0 0)	Membrane â€º caveola. Cell membrane. Microsome. Endoplasmic reticulum. Cytoplasm â€º cytosol. Mitochondrion. Nucleus.

Q9WV55	VAPA_MOUSE Vesicle-associated membrane protein-associated protein A OS=Mus musculus GN=Vapa PE=1 SV=2	3.40E-13	70.2	25.7	41 (41 0 0 0 0)	Endoplasmic reticulum membrane; Single-pass type IV membrane protein.
Q9R0K7	AT2B2_MOUSE Plasma membrane calcium-transporting ATPase 2 OS=Mus musculus GN=Atp2b2 PE=1 SV=2	2.38E-09	70.2	7.3	23 (23 0 0 0 0)	Cell membrane; Multi-pass membrane protein.
Q9WVM1	RGAP1_MOUSE Rac GTPase-activating protein 1 OS=Mus musculus GN=Racgap1 PE=2 SV=1	8.99E-09	60.2	9.6	11 (11 0 0 0 0)	Nucleus. Cytoplasm. Cytoplasm â€º cytoskeleton â€º spindle. Cytoplasmic vesicle â€º secretory vesicle â€º acrosome.
Q01705	NOTC1_MOUSE Neurogenic locus notch homolog protein 1 OS=Mus musculus GN=Notch1 PE=1 SV=2	3.42E-09	60.2	2.3	6 (6 0 0 0 0)	Cell membrane; Single-pass type I membrane protein. Nucleus.
Q921F2	TADBP_MOUSE TAR DNA-binding protein 43 OS=Mus musculus GN=Tardbp PE=1 SV=1	8.10E-14	70.2	17.9	13 (13 0 0 0 0)	Nucleus.
Q9WTY4	AQP5_MOUSE Aquaporin-5 OS=Mus musculus GN=Aqp5 PE=2 SV=1	7.69E-08	60.2	19.2	13 (13 0 0 0 0)	Membrane; Multi-pass membrane protein.
Q62371	DDR2_MOUSE Discoidin domain-containing receptor 2 OS=Mus musculus GN=Ddr2 PE=2 SV=2	9.54E-08	60.2	8.3	6 (6 0 0 0 0)	Cell membrane; Single-pass type I membrane protein.
P10126	EF1A1_MOUSE Elongation factor 1-alpha 1 OS=Mus musculus GN=Eef1a1 PE=1 SV=3	9.44E-08	70.2	14.1	41 (41 0 0 0 0)	Cytoplasm.
P35822	PTPRK_MOUSE Receptor-type tyrosine-protein phosphatase kappa OS=Mus musculus GN=Ptprk PE=1 SV=1	6.45E-07	60.2	4.3	8 (8 0 0 0 0)	Membrane; Single-pass type I membrane protein.
P53994	RAB2A_MOUSE Ras-related protein Rab-2A OS=Mus musculus GN=Rab2a PE=1 SV=1	2.78E-12	70.2	37.7	20 (20 0 0 0 0)	Endoplasmic reticulum-Golgi intermediate compartment membrane; Lipid-anchor. Melanosome. Endoplasmic reticulum membrane; Lipid-anchor. Golgi

						apparatus membrane; Lipid-anchor.
Q68FD5	CLH_MOUSE Clathrin heavy chain 1 OS=Mus musculus GN=Cltc PE=1 SV=3	8.22E-11	60.2	4.1	6 (6 0 0 0 0)	Cytoplasmic vesicle membrane; Peripheral membrane protein; Cytoplasmic side. Membrane â€º coated pit; Peripheral membrane protein; Cytoplasmic side. Melanosome.
P35278	RAB5C_MOUSE Ras-related protein Rab-5C OS=Mus musculus GN=Rab5c PE=1 SV=2	3.46E-09	70.2	34.7	12 (12 0 0 0 0)	Cell membrane; Lipid-anchor; Cytoplasmic side. Early endosome membrane; Lipid-anchor. Melanosome.
Q922J9	FACR1_MOUSE Fatty acyl-CoA reductase 1 OS=Mus musculus GN=Far1 PE=1 SV=1	3.97E-09	70.2	16.3	14 (14 0 0 0 0)	Peroxisome membrane; Single-pass membrane protein.
P24369	PPIB_MOUSE Peptidyl-prolyl cis-trans isomerase B OS=Mus musculus GN=Ppib PE=2 SV=2	5.43E-11	70.2	31.9	10 (10 0 0 0 0)	Endoplasmic reticulum lumen. Melanosome.
P80318	TCPG_MOUSE T-complex protein 1 subunit gamma OS=Mus musculus GN=Cct3 PE=1 SV=1	3.76E-06	60.2	12.7	8 (8 0 0 0 0)	Cytoplasm.
Q64521	GPDM_MOUSE Glycerol-3-phosphate dehydrogenase, mitochondrial OS=Mus musculus GN=Gpd2 PE=1 SV=2	6.81E-09	70.2	8.3	15 (15 0 0 0 0)	Mitochondrion inner membrane.
P62270	RS18_MOUSE 40S ribosomal protein S18 OS=Mus musculus GN=Rps18 PE=2 SV=3	7.89E-09	70.2	30.3	14 (14 0 0 0 0)	Cytoplasm.
Q8BFZ3	ACTBL_MOUSE Beta-actin-like protein 2 OS=Mus musculus GN=Actbl2 PE=2 SV=1	1.00E-30	50.3	18.9	84 (15 68 1 0 0)	Cytoplasm â€º cytoskeleton.
O35598	ADA10_MOUSE Disintegrin and metalloproteinase domain-containing protein 10 OS=Mus musculus GN=Adam10 PE=1 SV=1	3.67E-08	70.2	10.1	7 (7 0 0 0 0)	Membrane; Single-pass type I membrane protein.

Q61490	CD166_MOUSE CD166 antigen OS=Mus musculus GN=Alcam PE=1 SV=3	3.88E-08	70.2	10.6	12 (12 0 0 0 0)	Membrane; Single-pass type I membrane protein.
Q3UEB3	PUF60_MOUSE Poly(U)-binding-splicing factor PUF60 OS=Mus musculus GN=Puf60 PE=2 SV=2	4.18E-11	50.3	15.4	7 (7 0 0 0 0)	Nucleus.
Q99JY0	ECHB_MOUSE Trifunctional enzyme subunit beta, mitochondrial OS=Mus musculus GN=Hadhb PE=1 SV=1	1.19E-05	70.2	13.1	7 (7 0 0 0 0)	Mitochondrion matrix.
P80314	TCPB_MOUSE T-complex protein 1 subunit beta OS=Mus musculus GN=Cct2 PE=1 SV=4	4.54E-13	50.3	13.6	6 (6 0 0 0 0)	Cytoplasm.
P82347	SGCD_MOUSE Delta-sarcoglycan OS=Mus musculus GN=Sgcd PE=1 SV=1	1.49E-09	50.2	21.1	11 (11 0 0 0 0)	Cell membrane â€º sarcolemma; Single-pass type II membrane protein. Cytoplasm â€º cytoskeleton.
Q9DBS1	TMM43_MOUSE Transmembrane protein 43 OS=Mus musculus GN=Tmem43 PE=1 SV=1	6.11E-14	68.2	20.0	12 (11 1 0 0 0)	Endoplasmic reticulum. Nucleus inner membrane; Multi-pass membrane protein.
P18872	GNAO_MOUSE Guanine nucleotide-binding protein G(o) subunit alpha OS=Mus musculus GN=Gnao1 PE=1 SV=3	5.90E-11	50.2	17.2	9 (9 0 0 0 0)	ND
P62821	RAB1A_MOUSE Ras-related protein Rab-1A OS=Mus musculus GN=Rab1A PE=1 SV=3	4.40E-11	68.2	28.3	13 (12 1 0 0 0)	Golgi apparatus. Endoplasmic reticulum.
P97384	ANX11_MOUSE Annexin A11 OS=Mus musculus GN=Anxa11 PE=1 SV=1	1.49E-09	68.2	13.7	12 (9 3 0 0 0)	Cytoplasm. Melanosome. Nucleus envelope. Nucleus â€º nucleoplasm. Cytoplasm â€º cytoskeleton â€º spindle.
P61161	ARP2_MOUSE Actin-related protein 2 OS=Mus musculus GN=Actr2 PE=1 SV=1	3.05E-11	50.2	10.4	5 (5 0 0 0 0)	Cytoplasm â€º cytoskeleton. Cell projection.
Q9Z127	LAT1_MOUSE Large neutral amino acids transporter small subunit 1 OS=Mus musculus GN=Slc7a5 PE=1 SV=1	8.11E-11	50.2	8.6	10 (10 0 0 0 0)	Cytoplasm â€º cytosol. Apical cell membrane; Multi-pass membrane protein.

Q9CQD1	RAB5A_MOUSE Ras-related protein Rab-5A OS=Mus musculus GN=Rab5a PE=1 SV=1	1.26E-06	66.2	29.3	10 (7 3 0 0 0)	Cell membrane; Lipid-anchor; Cytoplasmic side. Early endosome membrane; Lipid-anchor. Melanosome.
Q61765	K1H1_MOUSE Keratin, type I cuticular Ha1 OS=Mus musculus GN=Krt31 PE=2 SV=2	1.34E-07	66.2	16.3	7 (5 2 0 0 0)	ND
Q8R464	CADM4_MOUSE Cell adhesion molecule 4 OS=Mus musculus GN=Cadm4 PE=1 SV=1	2.48E-09	50.2	14.9	6 (6 0 0 0 0)	Membrane; Single-pass type I membrane protein.
P17156	HSP72_MOUSE Heat shock-related 70 kDa protein 2 OS=Mus musculus GN=Hspa2 PE=1 SV=1	1.00E-30	60.3	8.5	33 (33 0 0 0 0)	ND
Q91V61	SFXN3_MOUSE Sideroflexin-3 OS=Mus musculus GN=Sfxn3 PE=1 SV=1	1.98E-11	60.3	24.6	6 (6 0 0 0 0)	Mitochondrion membrane; Multi-pass membrane protein.
Q9EPK2	XRP2_MOUSE Protein XRP2 OS=Mus musculus GN=Rp2 PE=2 SV=3	2.68E-09	50.2	9.5	11 (11 0 0 0 0)	Cell membrane; Lipid-anchor; Cytoplasmic side.
P97855	G3BP1_MOUSE Ras GTPase-activating protein-binding protein 1 OS=Mus musculus GN=G3bp1 PE=1 SV=1	1.11E-15	60.3	15.5	6 (6 0 0 0 0)	Cytoplasm. Cytoplasm â€º cytosol. Cell membrane. Nucleus.
Q9JIM1	S29A1_MOUSE Equilibrative nucleoside transporter 1 OS=Mus musculus GN=Slc29a1 PE=1 SV=3	2.89E-14	60.3	12.4	17 (17 0 0 0 0)	Basolateral cell membrane; Multi-pass membrane protein. Apical cell membrane; Multi-pass membrane protein.
Q9WTS6	TEN3_MOUSE Teneurin-3 OS=Mus musculus GN=Odz3 PE=1 SV=1	2.77E-06	50.2	1.8	6 (6 0 0 0 0)	Membrane; Single-pass type II membrane protein.
P97807	FUMH_MOUSE Fumarate hydratase, mitochondrial OS=Mus musculus GN=Fh PE=1 SV=2	3.53E-11	60.3	13.0	8 (8 0 0 0 0)	Mitochondrion. Cytoplasm.
Q01853	TERA_MOUSE Transitional endoplasmic reticulum ATPase OS=Mus musculus GN=Vcp PE=1 SV=4	2.20E-09	50.2	5.5	5 (5 0 0 0 0)	Cytoplasm â€º cytosol. Nucleus.
P57776	EF1D_MOUSE Elongation factor 1-delta OS=Mus musculus GN=Eef1d PE=1 SV=3	6.29E-09	50.2	26.3	7 (7 0 0 0 0)	ND

Q99JB2	STML2_MOUSE Stomatin-like protein 2 OS=Mus musculus GN=Stoml2 PE=1 SV=1	1.07E-12	60.3	22.9	7 (7 0 0 0 0)	Membrane; Peripheral membrane protein. Cytoplasm. Cytoplasm â€º cytoskeleton.
Q61576	FKB10_MOUSE FK506-binding protein 10 OS=Mus musculus GN=Fkbp10 PE=1 SV=1	3.76E-10	60.2	10.7	8 (8 0 0 0 0)	Endoplasmic reticulum lumen.
P16858	G3P_MOUSE Glyceraldehyde-3-phosphate dehydrogenase OS=Mus musculus GN=Gapdh PE=1 SV=2	4.61E-10	48.2	19.5	8 (7 1 0 0 0)	Cytoplasm â€º cytosol. Nucleus.
Q80X50	UBP2L_MOUSE Ubiquitin-associated protein 2-like OS=Mus musculus GN=Ubap2l PE=1 SV=1	2.45E-08	60.2	6.4	7 (7 0 0 0 0)	ND
Q02013	AQP1_MOUSE Aquaporin-1 OS=Mus musculus GN=Aqp1 PE=1 SV=3	1.67E-14	40.3	17.8	26 (26 0 0 0 0)	Membrane; Multi-pass membrane protein.
P51150	RAB7A_MOUSE Ras-related protein Rab-7a OS=Mus musculus GN=Rab7a PE=1 SV=2	9.61E-12	60.2	33.3	28 (28 0 0 0 0)	Late endosome. Lysosome. Cytoplasmic vesicle â€º phagosome. Melanosome.
Q05186	RCN1_MOUSE Reticulocalbin-1 OS=Mus musculus GN=Rcn1 PE=1 SV=1	1.33E-10	60.2	22.2	9 (9 0 0 0 0)	Endoplasmic reticulum lumen.
Q3TTY5	K22E_MOUSE Keratin, type II cytoskeletal 2 epidermal OS=Mus musculus GN=Krt2 PE=1 SV=1	1.86E-08	60.2	6.2	35 (35 0 0 0 0)	ND
P80316	TCPE_MOUSE T-complex protein 1 subunit epsilon OS=Mus musculus GN=Cct5 PE=1 SV=1	1.14E-10	40.3	10.9	5 (5 0 0 0 0)	Cytoplasm. Cytoplasm â€º cytoskeleton â€º centrosome.
P70452	STX4_MOUSE Syntaxin-4 OS=Mus musculus GN=Stx4 PE=1 SV=1	9.11E-09	60.2	25.8	6 (6 0 0 0 0)	Cell membrane; Single-pass type IV membrane protein.
P80317	TCPZ_MOUSE T-complex protein 1 subunit zeta OS=Mus musculus GN=Cct6a PE=1 SV=3	2.12E-13	40.3	10.9	5 (5 0 0 0 0)	Cytoplasm.
O35737	HNRH1_MOUSE Heterogeneous nuclear ribonucleoprotein H OS=Mus musculus GN=Hnrnph1 PE=1 SV=3	5.98E-09	40.3	13.4	7 (7 0 0 0 0)	Nucleus â€º nucleoplasm.
P62492	RB11A_MOUSE Ras-related protein Rab-11A OS=Mus musculus	3.02E-10	60.2	25.5	17 (17 0 0 0 0)	Cell membrane; Peripheral membrane protein.

	GN=Rab11a PE=1 SV=3					Recycling endosome membrane; Peripheral membrane protein.
P51174	ACADL_MOUSE Long-chain specific acyl-CoA dehydrogenase, mitochondrial OS=Mus musculus GN=Acadl PE=2 SV=2	6.94E-09	60.2	14.0	7 (7 0 0 0 0)	Mitochondrion matrix.
P80315	TCPD_MOUSE T-complex protein 1 subunit delta OS=Mus musculus GN=Cct4 PE=1 SV=3	3.02E-12	40.3	10.9	4 (4 0 0 0 0)	Cytoplasm. Melanosome. Cytoplasm â€º cytoskeleton â€º centrosome.
P51881	ADT2_MOUSE ADP/ATP translocase 2 OS=Mus musculus GN=Slc25a5 PE=1 SV=3	4.11E-09	60.2	16.1	45 (42 3 0 0 0)	Mitochondrion inner membrane; Multi-pass membrane protein.
P62908	RS3_MOUSE 40S ribosomal protein S3 OS=Mus musculus GN=Rps3 PE=1 SV=1	6.88E-08	60.2	23.5	7 (7 0 0 0 0)	Cytoplasm.
P11984	TCPA1_MOUSE T-complex protein 1 subunit alpha A OS=Mus musculus GN=Tcp1 PE=1 SV=2	5.44E-14	40.2	9.2	4 (4 0 0 0 0)	#N/A
P26443	DHE3_MOUSE Glutamate dehydrogenase 1, mitochondrial OS=Mus musculus GN=Glud1 PE=1 SV=1	2.98E-09	60.2	11.5	8 (8 0 0 0 0)	Mitochondrion matrix.
Q99K48	NONO_MOUSE Non-POU domain-containing octamer-binding protein OS=Mus musculus GN=Nono PE=1 SV=3	4.84E-11	40.2	13.5	4 (4 0 0 0 0)	Nucleus.
Q99JY9	ARP3_MOUSE Actin-related protein 3 OS=Mus musculus GN=Actr3 PE=1 SV=3	3.08E-06	40.2	10.5	5 (5 0 0 0 0)	Cytoplasm â€º cytoskeleton. Cell projection.
Q3TZZ7	ESYT2_MOUSE Extended synaptotagmin-2 OS=Mus musculus GN=Esyt2 PE=1 SV=1	9.62E-10	60.2	8.8	7 (7 0 0 0 0)	Cell membrane; Multi-pass membrane protein.
P15331	PERI_MOUSE Peripherin OS=Mus musculus GN=Prph PE=1 SV=2	5.15E-08	40.2	4.8	74 (74 0 0 0 0)	ND
Q7TQ95	LNP_MOUSE Protein lunapark OS=Mus musculus GN=Lnp PE=1 SV=1	3.70E-08	60.2	15.1	8 (8 0 0 0 0)	Membrane; Multi-pass membrane protein.
P53690	MMP14_MOUSE Matrix metalloproteinase-14 OS=Mus musculus	1.24E-08	40.2	7.6	4 (4 0 0 0 0)	Membrane; Single-pass type I membrane protein;

	GN=Mmp14 PE=2 SV=2					Extracellular side. Melanosome.
A2APV2	FMNL2_MOUSE Formin-like protein 2 OS=Mus musculus GN=Fmnl2 PE=2 SV=2	8.64E-09	40.2	4.3	4 (4 0 0 0 0)	Cytoplasm.
Q99KE1	MAOM_MOUSE NAD-dependent malic enzyme, mitochondrial OS=Mus musculus GN=Me2 PE=2 SV=1	1.16E-06	60.2	10.5	6 (6 0 0 0 0)	Mitochondrion matrix.
P14869	RLA0_MOUSE 60S acidic ribosomal protein P0 OS=Mus musculus GN=Rplp0 PE=1 SV=3	6.66E-07	40.2	19.9	6 (6 0 0 0 0)	Nucleus. Cytoplasm.
Q6P9J9	ANO6_MOUSE Anoctamin-6 OS=Mus musculus GN=Ano6 PE=1 SV=1	2.73E-08	60.2	7.1	10 (10 0 0 0 0)	Membrane; Multi-pass membrane protein.
Q8BHN3	GANAB_MOUSE Neutral alpha-glucosidase AB OS=Mus musculus GN=Ganab PE=1 SV=1	4.28E-07	60.1	6.1	7 (7 0 0 0 0)	Endoplasmic reticulum. Golgi apparatus. Melanosome.
P50446	K2C6A_MOUSE Keratin, type II cytoskeletal 6A OS=Mus musculus GN=Krt6a PE=2 SV=3	1.73E-05	40.2	4.3	4 (4 0 0 0 0)	ND
Q60930	VDAC2_MOUSE Voltage-dependent anion-selective channel protein 2 OS=Mus musculus GN=Vdac2 PE=1 SV=2	8.10E-14	58.2	19.0	14 (12 2 0 0 0)	Mitochondrion outer membrane.
Q8VI59	PCX3_MOUSE Pecanex-like protein 3 OS=Mus musculus GN=Pcnxl3 PE=1 SV=2	1.39E-06	40.2	1.8	5 (5 0 0 0 0)	Membrane; Multi-pass membrane protein.
Q99JR1	SFXN1_MOUSE Sideroflexin-1 OS=Mus musculus GN=Sfxn1 PE=1 SV=3	3.65E-08	58.2	22.7	7 (6 1 0 0 0)	Mitochondrion membrane; Multi-pass membrane protein.
Q61879	MYH10_MOUSE Myosin-10 OS=Mus musculus GN=Myh10 PE=1 SV=2	1.56E-12	50.3	3.1	10 (10 0 0 0 0)	ND
P42932	TCPQ_MOUSE T-complex protein 1 subunit theta OS=Mus musculus GN=Cct8 PE=1 SV=3	1.00E-07	40.2	7.8	5 (5 0 0 0 0)	Cytoplasm. Cytoplasm â€º cytoskeleton â€º centrosome.
Q91ZV3	DCBD2_MOUSE Discoidin, CUB and LCCL domain-containing protein 2 OS=Mus musculus GN=Dcbld2 PE=2 SV=1	2.03E-10	40.2	5.2	5 (5 0 0 0 0)	Membrane; Single-pass type I membrane protein.
O08749	DLDH_MOUSE Dihydrolipoyl dehydrogenase,	6.66E-15	50.3	11.2	6 (6 0 0 0 0)	Mitochondrion matrix.

	mitochondrial OS=Mus musculus GN=Dld PE=1 SV=2					
Q8K2K6	AGFG1_MOUSE Arf-GAP domain and FG repeats-containing protein 1 OS=Mus musculus GN=Agfg1 PE=1 SV=2	1.59E-09	50.3	11.6	7 (7 0 0 0 0)	Nucleus. Cytoplasmic vesicle.
P80313	TCPH_MOUSE T-complex protein 1 subunit eta OS=Mus musculus GN=Cct7 PE=1 SV=1	1.11E-15	30.3	7.2	4 (4 0 0 0 0)	Cytoplasm.
Q80W54	FACE1_MOUSE CAAX prenyl protease 1 homolog OS=Mus musculus GN=Zmpste24 PE=1 SV=2	4.32E-13	50.3	10.1	7 (7 0 0 0 0)	Endoplasmic reticulum membrane; Multi-pass membrane protein. Golgi apparatus membrane; Multi-pass membrane protein.
P97333	NRP1_MOUSE Neuropilin-1 OS=Mus musculus GN=Nrp1 PE=1 SV=1	1.56E-11	30.3	5.7	3 (3 0 0 0 0)	Membrane; Single-pass type I membrane protein.
Q9Z2K1	K1C16_MOUSE Keratin, type I cytoskeletal 16 OS=Mus musculus GN=Krt16 PE=1 SV=3	2.11E-14	30.3	9.2	4 (4 0 0 0 0)	ND
Q8BMD8	SCMC1_MOUSE Calcium-binding mitochondrial carrier protein SCaMC-1 OS=Mus musculus GN=Slc25a24 PE=2 SV=1	1.20E-10	50.3	12.4	10 (10 0 0 0 0)	Mitochondrion inner membrane; Multi-pass membrane protein.
B0V2N1	PTPRS_MOUSE Receptor-type tyrosine-protein phosphatase S OS=Mus musculus GN=Ptprs PE=2 SV=1	1.67E-09	30.3	3.0	3 (3 0 0 0 0)	Membrane; Single-pass type I membrane protein.
P10810	CD14_MOUSE Monocyte differentiation antigen CD14 OS=Mus musculus GN=Cd14 PE=1 SV=1	2.22E-14	30.3	10.7	4 (4 0 0 0 0)	Cell membrane; Lipid-anchor â€º GPI-anchor.
P62991	UBIQ_MOUSE Ubiquitin OS=Mus musculus GN=Rps27a PE=1 SV=1	9.22E-10	50.2	61.8	50 (50 0 0 0 0)	#N/A
Q01721	GAS1_MOUSE Growth arrest-specific protein 1 OS=Mus musculus GN=Gas1 PE=2 SV=2	7.11E-13	30.3	17.8	3 (3 0 0 0 0)	Cell membrane; Lipid-anchor â€º GPI-anchor.
Q922Q8	LRC59_MOUSE Leucine-rich repeat-containing protein 59 OS=Mus musculus GN=Lrrc59 PE=2 SV=1	4.05E-10	50.2	16.9	22 (22 0 0 0 0)	Microsome membrane; Single-pass type II membrane protein. Endoplasmic reticulum

						membrane; Single-pass type II membrane protein.
P53986	MOT1_MOUSE Monocarboxylate transporter 1 OS=Mus musculus GN=Slc16a1 PE=1 SV=1	2.15E-13	50.2	13.4	12 (12 0 0 0 0)	Cell membrane; Multi-pass membrane protein.
P97370	AT1B3_MOUSE Sodium/potassium-transporting ATPase subunit beta-3 OS=Mus musculus GN=Atp1b3 PE=1 SV=1	9.49E-11	30.2	11.9	8 (8 0 0 0 0)	Membrane; Single-pass type II membrane protein. Melanosome.
Q8BKE6	CP20A_MOUSE Cytochrome P450 20A1 OS=Mus musculus GN=Cyp20a1 PE=2 SV=1	7.87E-11	50.2	10.8	5 (5 0 0 0 0)	Membrane; Single-pass membrane protein.
Q91VR2	ATPG_MOUSE ATP synthase subunit gamma, mitochondrial OS=Mus musculus GN=Atp5c1 PE=1 SV=1	2.29E-10	50.2	17.1	6 (6 0 0 0 0)	Mitochondrion. Mitochondrion inner membrane; Peripheral membrane protein.
P26645	MARCS_MOUSE Myristoylated alanine-rich C-kinase substrate OS=Mus musculus GN=Marcks PE=1 SV=2	4.57E-10	50.2	18.1	12 (12 0 0 0 0)	Cytoplasm â€º cytoskeleton. Membrane; Lipid-anchor.
P19096	FAS_MOUSE Fatty acid synthase OS=Mus musculus GN=Fasn PE=1 SV=2	3.27E-08	30.2	1.4	3 (3 0 0 0 0)	Cytoplasm. Melanosome.
Q8BMF4	ODP2_MOUSE Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial OS=Mus musculus GN=Dlat PE=1 SV=2	1.11E-15	50.2	10.0	9 (9 0 0 0 0)	Mitochondrion matrix.
P21278	GNA11_MOUSE Guanine nucleotide-binding protein subunit alpha-11 OS=Mus musculus GN=Gna11 PE=1 SV=1	1.11E-10	50.2	17.0	9 (9 0 0 0 0)	Cell membrane; Lipid-anchor.
Q8BHL4	RAI3_MOUSE Retinoic acid-induced protein 3 OS=Mus musculus GN=Gprc5a PE=2 SV=1	6.38E-12	30.2	7.6	24 (24 0 0 0 0)	Cell membrane; Multi-pass membrane protein.
Q3U9G9	LBR_MOUSE Lamin-B receptor OS=Mus musculus GN=Lbr PE=1 SV=2	2.92E-10	50.2	6.9	5 (5 0 0 0 0)	Nucleus inner membrane; Multi-pass membrane protein.
P35456	UPAR_MOUSE Urokinase plasminogen activator surface receptor OS=Mus musculus GN=Plaur PE=2 SV=1	3.85E-09	30.2	6.7	12 (12 0 0 0 0)	Cell membrane; Lipid-anchor â€º GPI-anchor. Secreted.

Q8BR92	PALM2_MOUSE Paralemmin-2 OS=Mus musculus GN=Palm2 PE=1 SV=1	1.53E-09	30.2	12.8	3 (3 0 0 0 0)	Cell membrane; Lipid-anchor; Cytoplasmic side.
P59326	YTHD1_MOUSE YTH domain family protein 1 OS=Mus musculus GN=Ythdf1 PE=2 SV=1	2.26E-11	50.2	11.1	7 (7 0 0 0 0)	ND
O54734	OST48_MOUSE Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit OS=Mus musculus GN=Ddost PE=1 SV=1	1.12E-07	50.2	9.3	10 (10 0 0 0 0)	Endoplasmic reticulum membrane; Single-pass type I membrane protein.
Q9CQQ7	AT5F1_MOUSE ATP synthase subunit b, mitochondrial OS=Mus musculus GN=Atp5f1 PE=1 SV=1	2.04E-08	50.2	13.7	6 (6 0 0 0 0)	Mitochondrion. Mitochondrion inner membrane.
Q3V3R1	C1TM_MOUSE Monofunctional C1-tetrahydrofolate synthase, mitochondrial OS=Mus musculus GN=Mthfd1l PE=1 SV=2	4.35E-10	50.2	4.1	7 (7 0 0 0 0)	Mitochondrion.
Q6IFX2	K1C42_MOUSE Keratin, type I cytoskeletal 42 OS=Mus musculus GN=Krt42 PE=1 SV=1	2.23E-06	30.2	6.9	4 (4 0 0 0 0)	Cytoplasm.
P97300	NPTN_MOUSE Neuroplastin OS=Mus musculus GN=Nptn PE=1 SV=2	2.97E-08	50.2	16.4	14 (14 0 0 0 0)	Cell membrane; Single-pass type I membrane protein.
P47963	RL13_MOUSE 60S ribosomal protein L13 OS=Mus musculus GN=Rpl13 PE=2 SV=3	3.13E-09	50.2	20.9	9 (9 0 0 0 0)	ND
Q9CRD0	OCAD1_MOUSE OCIA domain-containing protein 1 OS=Mus musculus GN=Ociad1 PE=1 SV=1	3.81E-07	50.2	17.0	5 (5 0 0 0 0)	Endosome.
P11440	CDC2_MOUSE Cell division control protein 2 homolog OS=Mus musculus GN=Cdc2 PE=1 SV=3	1.57E-09	30.2	13.1	3 (3 0 0 0 0)	Nucleus.
Q9DBH5	LMAN2_MOUSE Vesicular integral-membrane protein VIP36 OS=Mus musculus GN=Lman2 PE=2 SV=1	2.36E-10	50.2	13.4	6 (6 0 0 0 0)	Golgi apparatus membrane; Single-pass type I membrane protein.
Q9WTR5	CAD13_MOUSE Cadherin-13 OS=Mus musculus GN=Cdh13 PE=2 SV=1	1.77E-09	30.2	5.2	5 (5 0 0 0 0)	Cell membrane; Lipid-anchor â€º GPI-anchor.
P57716	NICA_MOUSE Nicastrin OS=Mus musculus GN=Ncstn PE=1 SV=2	4.25E-07	50.2	7.6	9 (9 0 0 0 0)	Membrane; Single-pass type I membrane protein.

						Melanosome.
O88207	CO5A1_MOUSE Collagen alpha-1(V) chain OS=Mus musculus GN=Col5a1 PE=2 SV=2	7.95E-09	30.2	2.2	3 (3 0 0 0 0)	Secreted â€º extracellular space â€º extracellular matrix.
P48678	LMNA_MOUSE Lamin-A/C OS=Mus musculus GN=Lmna PE=1 SV=2	4.16E-09	50.2	8.9	5 (5 0 0 0 0)	Nucleus. Nucleus envelope.
P29341	PABP1_MOUSE Polyadenylate-binding protein 1 OS=Mus musculus GN=Pabpc1 PE=1 SV=1	3.20E-10	50.2	7.2	7 (7 0 0 0 0)	Cytoplasm. Nucleus.
P58252	EF2_MOUSE Elongation factor 2 OS=Mus musculus GN=Eef2 PE=1 SV=2	2.26E-07	30.1	3.1	3 (3 0 0 0 0)	Cytoplasm.
P47753	CAZA1_MOUSE F-actin-capping protein subunit alpha-1 OS=Mus musculus GN=Capza1 PE=1 SV=4	3.09E-10	30.1	14.0	4 (4 0 0 0 0)	Cytoplasm â€º cytoskeleton.
P62751	RL23A_MOUSE 60S ribosomal protein L23a OS=Mus musculus GN=Rpl23a PE=2 SV=1	3.24E-07	50.2	32.1	5 (5 0 0 0 0)	ND
P46978	STT3A_MOUSE Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3A OS=Mus musculus GN=Stt3a PE=1 SV=1	1.33E-07	50.2	5.5	10 (10 0 0 0 0)	Endoplasmic reticulum membrane; Multi-pass membrane protein.
Q01149	CO1A2_MOUSE Collagen alpha-2(I) chain OS=Mus musculus GN=Col1a2 PE=2 SV=2	8.65E-08	30.1	2.6	4 (4 0 0 0 0)	Secreted â€º extracellular space â€º extracellular matrix.
P35279	RAB6A_MOUSE Ras-related protein Rab-6A OS=Mus musculus GN=Rab6a PE=1 SV=4	2.04E-07	50.2	18.3	6 (6 0 0 0 0)	Golgi apparatus membrane; Lipid-anchor.
P14824	ANXA6_MOUSE Annexin A6 OS=Mus musculus GN=Anxa6 PE=1 SV=2	9.22E-07	30.1	4.3	3 (3 0 0 0 0)	Cytoplasm. Melanosome.
Q9CQY5	MAGT1_MOUSE Magnesium transporter protein 1 OS=Mus musculus GN=Magt1 PE=2 SV=1	1.40E-06	50.2	14.3	6 (6 0 0 0 0)	Endoplasmic reticulum membrane; Multi-pass membrane protein.
Q91YT0	NDUV1_MOUSE NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial OS=Mus musculus GN=Ndufv1 PE=1 SV=1	1.73E-08	50.2	9.3	7 (7 0 0 0 0)	Mitochondrion inner membrane; Peripheral membrane protein; Matrix side.
Q64487	PTPRD_MOUSE Receptor-type tyrosine-protein phosphatase delta OS=Mus musculus GN=Ptprd PE=2	2.15E-09	28.3	2.2	4 (3 1 0 0 0)	Membrane; Single-pass type I membrane protein.

	SV=2					
O35435	PYRD_MOUSE Dihydroorotate dehydrogenase, mitochondrial OS=Mus musculus GN=Dhodh PE=2 SV=2	2.92E-06	50.2	12.7	5 (5 0 0 0 0)	Mitochondrion inner membrane; Single-pass membrane protein.
P62874	GBB1_MOUSE Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1 OS=Mus musculus GN=Gnb1 PE=1 SV=3	7.99E-08	50.2	12.4	6 (6 0 0 0 0)	ND
Q61390	TCPW_MOUSE T-complex protein 1 subunit zeta-2 OS=Mus musculus GN=Cct6b PE=2 SV=4	1.72E-07	28.2	8.1	3 (2 1 0 0 0)	Cytoplasm.
Q8JZQ9	EIF3B_MOUSE Eukaryotic translation initiation factor 3 subunit B OS=Mus musculus GN=Eif3b PE=1 SV=1	4.96E-08	50.2	5.0	5 (5 0 0 0 0)	Cytoplasm.
P30999	CTND1_MOUSE Catenin delta-1 OS=Mus musculus GN=Ctnnd1 PE=1 SV=2	6.17E-08	50.1	5.0	20 (20 0 0 0 0)	Cytoplasm. Nucleus. Cell membrane.
Q64337	SQSTM_MOUSE Sequestosome-1 OS=Mus musculus GN=Sqstm1 PE=1 SV=1	1.25E-10	20.3	5.9	4 (4 0 0 0 0)	Cytoplasm. Late endosome. Nucleus.
O70318	E41L2_MOUSE Band 4.1-like protein 2 OS=Mus musculus GN=Epb41l2 PE=1 SV=1	1.07E-08	48.2	5.5	7 (4 3 0 0 0)	Cytoplasm â€º cytoskeleton.
P70168	IMB1_MOUSE Importin subunit beta-1 OS=Mus musculus GN=Kpnb1 PE=1 SV=1	2.68E-09	20.3	3.1	2 (2 0 0 0 0)	Cytoplasm. Nucleus envelope.
Q9D1G1	RAB1B_MOUSE Ras-related protein Rab-1B OS=Mus musculus GN=Rab1b PE=1 SV=1	2.35E-09	46.2	29.9	5 (4 0 1 0 0)	Membrane; Lipid-anchor; Cytoplasmic side. Cytoplasm.
Q80WJ7	LYRIC_MOUSE Protein LYRIC OS=Mus musculus GN=Mtdh PE=1 SV=1	3.14E-13	40.3	7.3	8 (8 0 0 0 0)	Endoplasmic reticulum membrane; Single-pass membrane protein. Nucleus membrane; Single-pass membrane protein. Cell junction â€º tight junction. Nucleus â€º nucleolus. Cytoplasm â€º perinuclear region.

P21981	TGM2_MOUSE Protein-glutamine gamma-glutamyltransferase 2 OS=Mus musculus GN=Tgm2 PE=1 SV=4	1.54E-11	20.3	4.5	3 (3 0 0 0 0)	ND
O35682	MYADM_MOUSE Myeloid-associated differentiation marker OS=Mus musculus GN=Myadm PE=2 SV=2	9.19E-12	20.3	8.4	46 (46 0 0 0 0)	Membrane; Multi-pass membrane protein.
P62960	YBOX1_MOUSE Nuclease-sensitive element-binding protein 1 OS=Mus musculus GN=Ybx1 PE=1 SV=3	6.66E-15	40.3	22.7	4 (4 0 0 0 0)	Cytoplasm. Nucleus. Cytoplasmic granule. Secreted.
P46660	AINX_MOUSE Alpha-internexin OS=Mus musculus GN=Ina PE=1 SV=2	6.54E-09	20.2	4.0	4 (4 0 0 0 0)	ND
Q8VH51	RBM39_MOUSE RNA-binding protein 39 OS=Mus musculus GN=Rbm39 PE=1 SV=1	1.18E-09	20.2	6.0	3 (3 0 0 0 0)	Nucleus.
P62071	RRAS2_MOUSE Ras-related protein R-Ras2 OS=Mus musculus GN=Rras2 PE=1 SV=1	3.70E-13	40.3	19.1	20 (20 0 0 0 0)	Cell membrane; Lipid-anchor; Cytoplasmic side.
P70670	NACAM_MOUSE Nascent polypeptide-associated complex subunit alpha, muscle-specific form OS=Mus musculus GN=Naca PE=1 SV=1	8.85E-10	20.2	1.3	3 (3 0 0 0 0)	Cytoplasm. Nucleus.
Q8BXA1	GOLI4_MOUSE Golgi integral membrane protein 4 OS=Mus musculus GN=Golim4 PE=1 SV=1	1.77E-08	40.2	8.2	4 (4 0 0 0 0)	Golgi apparatus â€º Golgi stack membrane; Single-pass type II membrane protein. Endosome membrane; Single-pass type II membrane protein.
Q8BGD9	IF4B_MOUSE Eukaryotic translation initiation factor 4B OS=Mus musculus GN=Eif4b PE=1 SV=1	3.07E-06	20.2	5.6	2 (2 0 0 0 0)	ND
Q68FD9	K1549_MOUSE UPF0606 protein KIAA1549 OS=Mus musculus GN=Kiaa1549 PE=1 SV=2	2.99E-10	20.2	1.6	2 (2 0 0 0 0)	Membrane; Multi-pass membrane protein.
Q9CZU6	CISY_MOUSE Citrate synthase, mitochondrial OS=Mus musculus GN=Cs PE=1 SV=1	1.91E-11	40.2	8.2	11 (11 0 0 0 0)	Mitochondrion matrix.

Q6F3F9	GP126_MOUSE Probable G-protein coupled receptor 126 OS=Mus musculus GN=Gpr126 PE=1 SV=1	1.33E-14	20.2	2.3	4 (4 0 0 0 0)	Cell membrane; Multi-pass membrane protein.
Q9CRD2	TTC35_MOUSE Tetratricopeptide repeat protein 35 OS=Mus musculus GN=Ttc35 PE=2 SV=1	6.68E-11	40.2	19.9	5 (5 0 0 0 0)	Nucleus.
P63101	1433Z_MOUSE 14-3-3 protein zeta/delta OS=Mus musculus GN=Ywhaz PE=1 SV=1	2.24E-09	20.2	10.6	2 (2 0 0 0 0)	Cytoplasm. Melanosome.
Q9D1M7	FKB11_MOUSE FK506-binding protein 11 OS=Mus musculus GN=Fkbp11 PE=2 SV=1	2.36E-12	40.2	14.4	4 (4 0 0 0 0)	Membrane; Single-pass membrane protein.
Q9QZD8	DIC_MOUSE Mitochondrial dicarboxylate carrier OS=Mus musculus GN=Slc25a10 PE=2 SV=2	1.68E-07	40.2	19.5	5 (5 0 0 0 0)	Mitochondrion inner membrane; Multi-pass membrane protein.
Q9QXS6	DREB_MOUSE Drebrin OS=Mus musculus GN=Dbn1 PE=1 SV=4	1.65E-11	20.2	5.4	2 (2 0 0 0 0)	Cytoplasm.
Q9DC16	ERGI1_MOUSE Endoplasmic reticulum-Golgi intermediate compartment protein 1 OS=Mus musculus GN=Ergic1 PE=1 SV=1	7.21E-13	40.2	20.3	5 (5 0 0 0 0)	Endoplasmic reticulum membrane; Multi-pass membrane protein. Endoplasmic reticulum-Golgi intermediate compartment membrane; Multi-pass membrane protein. Golgi apparatus membrane; Multi-pass membrane protein.
Q91V41	RAB14_MOUSE Ras-related protein Rab-14 OS=Mus musculus GN=Rab14 PE=1 SV=3	2.28E-08	40.2	20.0	7 (7 0 0 0 0)	Early endosome membrane; Lipid-anchor; Cytoplasmic side. Golgi apparatus membrane; Lipid-anchor; Cytoplasmic side. Golgi apparatus â€º trans-Golgi network membrane; Lipid-anchor; Cytoplasmic side.
P16110	LEG3_MOUSE Galectin-3	1.41E-10	40.2	14.0	5 (5 0 0 0 0)	Cytoplasm.

	OS=Mus musculus GN=Lgals3 PE=1 SV=3					Nucleus. Secreted.
P14685	PSMD3_MOUSE 26S proteasome non-ATPase regulatory subunit 3 OS=Mus musculus GN=Psmd3 PE=2 SV=2	1.94E-10	20.2	5.7	2 (2 0 0 0 0)	ND
Q9DC51	GNAI3_MOUSE Guanine nucleotide-binding protein G(k) subunit alpha OS=Mus musculus GN=Gnai3 PE=1 SV=3	4.26E-07	20.2	7.1	5 (5 0 0 0 0)	Cytoplasm. Cell membrane. Cytoplasm â€º cytoskeleton â€º centrosome.
P70696	H2B1A_MOUSE Histone H2B type 1-A OS=Mus musculus GN=Hist1h2ba PE=2 SV=3	1.11E-12	40.2	34.6	10 (10 0 0 0 0)	Nucleus. Chromosome.
P40237	CD82_MOUSE CD82 antigen OS=Mus musculus GN=Cd82 PE=1 SV=1	2.29E-06	40.2	13.2	12 (12 0 0 0 0)	Membrane; Multi-pass membrane protein.
Q91ZA3	PCCA_MOUSE Propionyl-CoA carboxylase alpha chain, mitochondrial OS=Mus musculus GN=Pcca PE=2 SV=2	8.53E-11	20.2	4.0	3 (3 0 0 0 0)	Mitochondrion matrix.
O08547	SC22B_MOUSE Vesicle-trafficking protein SEC22b OS=Mus musculus GN=Sec22b PE=1 SV=3	2.18E-10	40.2	21.4	7 (7 0 0 0 0)	Endoplasmic reticulum-Golgi intermediate compartment membrane; Single-pass type IV membrane protein. Golgi apparatus membrane; Single-pass type IV membrane protein. Endoplasmic reticulum membrane; Single-pass type IV membrane protein. Melanosome.
Q8BYK6	YTHD3_MOUSE YTH domain family protein 3 OS=Mus musculus GN=Ythdf3 PE=1 SV=2	1.67E-11	40.2	8.7	7 (7 0 0 0 0)	ND
Q9WVL3	S12A7_MOUSE Solute carrier family 12 member 7 OS=Mus musculus GN=Slc12a7 PE=1 SV=1	3.29E-09	40.2	4.9	4 (4 0 0 0 0)	Membrane; Multi-pass membrane protein.
P57759	ERP29_MOUSE Endoplasmic reticulum protein ERp29 OS=Mus musculus GN=Erp29 PE=1 SV=2	1.17E-12	40.2	17.9	5 (5 0 0 0 0)	Endoplasmic reticulum lumen. Melanosome.

Q9QY76	VAPB_MOUSE Vesicle-associated membrane protein-associated protein B OS=Mus musculus GN=Vapb PE=2 SV=3	1.40E-08	40.2	20.2	7 (7 0 0 0 0)	Endoplasmic reticulum membrane; Single-pass type IV membrane protein.
Q9D074	MGRN1_MOUSE Probable E3 ubiquitin-protein ligase MGRN1 OS=Mus musculus GN=Mgrn1 PE=1 SV=2	5.50E-09	20.2	6.6	3 (3 0 0 0 0)	Early endosome. Cytoplasm. Cell membrane. Cytoplasm. Nucleus.
O35609	SCAM3_MOUSE Secretory carrier-associated membrane protein 3 OS=Mus musculus GN=Scamp3 PE=1 SV=2	1.53E-12	40.2	13.5	6 (6 0 0 0 0)	Membrane; Multi-pass membrane protein.
Q8K0C4	CP51A_MOUSE Lanosterol 14-alpha demethylase OS=Mus musculus GN=Cyp51a1 PE=2 SV=1	4.59E-08	40.2	10.5	4 (4 0 0 0 0)	Endoplasmic reticulum membrane. Microsome membrane.
Q8K224	NAT10_MOUSE N-acetyltransferase 10 OS=Mus musculus GN=Nat10 PE=2 SV=1	6.80E-11	20.2	2.3	3 (3 0 0 0 0)	Nucleus â€º nucleolus.
Q9DB20	ATPO_MOUSE ATP synthase subunit O, mitochondrial OS=Mus musculus GN=Atp5o PE=1 SV=1	7.25E-08	40.2	22.5	5 (5 0 0 0 0)	Mitochondrion. Mitochondrion inner membrane.
Q9WUM4	COR1C_MOUSE Coronin-1C OS=Mus musculus GN=Coro1c PE=1 SV=2	6.56E-07	20.2	4.9	2 (2 0 0 0 0)	ND
Q9WV32	ARC1B_MOUSE Actin-related protein 2/3 complex subunit 1B OS=Mus musculus GN=Arpc1b PE=1 SV=3	9.08E-10	20.2	8.3	2 (2 0 0 0 0)	Cytoplasm â€º cytoskeleton.
P70227	ITPR3_MOUSE Inositol 1,4,5-trisphosphate receptor type 3 OS=Mus musculus GN=Itpr3 PE=1 SV=3	3.29E-07	40.2	2.0	4 (4 0 0 0 0)	Endoplasmic reticulum membrane; Multi-pass membrane protein.
Q9D8B3	CHM4B_MOUSE Charged multivesicular body protein 4b OS=Mus musculus GN=Chmp4b PE=2 SV=2	4.28E-08	20.2	11.2	2 (2 0 0 0 0)	Cytoplasm â€º cytosol. Late endosome membrane; Peripheral membrane protein.
Q9R0A0	PEX14_MOUSE Peroxisomal membrane protein PEX14 OS=Mus musculus GN=Pex14 PE=1 SV=1	1.23E-10	40.2	13.3	4 (4 0 0 0 0)	Peroxisome membrane; Peripheral membrane protein; Cytoplasmic side.
Q8VIJ6	SFPQ_MOUSE Splicing factor, proline- and glutamine-rich OS=Mus	1.65E-04	20.2	3.7	2 (2 0 0 0 0)	Nucleus matrix.

	musculus GN=Sfpq PE=1 SV=1					
Q62465	VAT1_MOUSE Synaptic vesicle membrane protein VAT-1 homolog OS=Mus musculus GN=Vat1 PE=2 SV=3	2.11E-09	40.2	10.1	4 (4 0 0 0 0)	Cytoplasm.
Q61656	DDX5_MOUSE Probable ATP-dependent RNA helicase DDX5 OS=Mus musculus GN=Ddx5 PE=1 SV=1	8.46E-07	20.2	3.4	2 (2 0 0 0 0)	Nucleus â€º nucleolus.
P03995	GFAP_MOUSE Glial fibrillary acidic protein OS=Mus musculus GN=Gfap PE=1 SV=4	7.39E-09	20.2	4.4	8 (8 0 0 0 0)	Cytoplasm.
Q8C7X2	K0090_MOUSE Uncharacterized protein KIAA0090 OS=Mus musculus GN=Kiaa0090 PE=1 SV=1	3.68E-06	40.2	4.2	6 (6 0 0 0 0)	Membrane; Single-pass type I membrane protein.
P47740	AL3A2_MOUSE Fatty aldehyde dehydrogenase OS=Mus musculus GN=Aldh3a2 PE=2 SV=1	3.05E-09	40.2	11.6	4 (4 0 0 0 0)	Endoplasmic reticulum membrane; Single-pass membrane protein; Cytoplasmic side.
Q91W90	TXND5_MOUSE Thioredoxin domain-containing protein 5 OS=Mus musculus GN=Txndc5 PE=1 SV=2	7.87E-10	40.2	11.0	7 (7 0 0 0 0)	Endoplasmic reticulum lumen.
Q9Z0X1	AIFM1_MOUSE Apoptosis-inducing factor 1, mitochondrial OS=Mus musculus GN=Aifm1 PE=1 SV=1	2.51E-07	40.2	8.5	6 (6 0 0 0 0)	Mitochondrion intermembrane space. Mitochondrion inner membrane. Cytoplasm. Cytoplasm â€º perinuclear region. Nucleus.
Q91WB7	UBTD1_MOUSE Ubiquitin domain-containing protein 1 OS=Mus musculus GN=Ubtd1 PE=2 SV=1	1.33E-07	20.2	11.0	2 (2 0 0 0 0)	ND
P50247	SAHH_MOUSE Adenosylhomocysteinase OS=Mus musculus GN=Ahcy PE=1 SV=3	8.52E-08	20.2	5.3	2 (2 0 0 0 0)	Cytoplasm. Melanosome.
Q9QYA2	TOM40_MOUSE Mitochondrial import receptor subunit TOM40 homolog OS=Mus musculus GN=Tomm40 PE=1 SV=3	2.48E-06	40.2	9.4	4 (4 0 0 0 0)	Mitochondrion outer membrane; Multi-pass membrane protein.

O55143	AT2A2_MOUSE Sarcoplasmic/endoplasmic reticulum calcium ATPase 2 OS=Mus musculus GN=Atp2a2 PE=1 SV=2	4.20E-10	40.2	4.7	12 (12 0 0 0 0)	Endoplasmic reticulum membrane; Multi-pass membrane protein. Sarcoplasmic reticulum membrane; Multi-pass membrane protein.
Q9R233	TPSN_MOUSE Tapasin OS=Mus musculus GN=Tapbp PE=2 SV=2	1.20E-07	40.2	6.7	4 (4 0 0 0 0)	Endoplasmic reticulum membrane; Single-pass type I membrane protein.
Q99K28	ARFG2_MOUSE ADP-ribosylation factor GTPase-activating protein 2 OS=Mus musculus GN=Arfgap2 PE=1 SV=1	2.10E-08	40.2	8.1	4 (4 0 0 0 0)	Cytoplasm. Golgi apparatus membrane; Peripheral membrane protein; Cytoplasmic side.
Q9Z247	FKBP9_MOUSE FK506-binding protein 9 OS=Mus musculus GN=Fkbp9 PE=1 SV=1	5.65E-11	40.2	8.6	5 (5 0 0 0 0)	Endoplasmic reticulum lumen.
Q00993	UFO_MOUSE Tyrosine-protein kinase receptor UFO OS=Mus musculus GN=Axl PE=1 SV=1	1.88E-07	20.2	2.9	2 (2 0 0 0 0)	Membrane; Single-pass type I membrane protein.
P17710	HXK1_MOUSE Hexokinase-1 OS=Mus musculus GN=Hk1 PE=1 SV=2	3.57E-07	40.2	3.4	4 (4 0 0 0 0)	Mitochondrion outer membrane; Peripheral membrane protein. Membrane.
Q9CZQ6	RAE1E_MOUSE Retinoic acid early-inducible protein 1-epsilon OS=Mus musculus GN=Raet1e PE=2 SV=1	1.00E-05	20.2	4.8	3 (3 0 0 0 0)	Cell membrane; Lipid-anchor â€º GPI-anchor.
Q9QYE6	GOGA5_MOUSE Golgin subfamily A member 5 OS=Mus musculus GN=Golga5 PE=1 SV=2	2.65E-07	40.2	6.0	4 (4 0 0 0 0)	Golgi apparatus membrane; Single-pass type IV membrane protein.
Q61781	K1C14_MOUSE Keratin, type I cytoskeletal 14 OS=Mus musculus GN=Krt14 PE=1 SV=2	2.96E-10	40.2	6.8	19 (19 0 0 0 0)	Cytoplasm. Nucleus.
Q8VDM4	PSMD2_MOUSE 26S proteasome non-ATPase regulatory subunit 2 OS=Mus musculus GN=Psmd2 PE=1 SV=1	2.49E-08	20.2	3.0	2 (2 0 0 0 0)	ND
P06151	LDHA_MOUSE L-lactate dehydrogenase A chain OS=Mus musculus GN=Ldha PE=1 SV=3	1.81E-05	20.2	6.0	2 (2 0 0 0 0)	Cytoplasm.

Q9D2G2	ODO2_MOUSE Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial OS=Mus musculus GN=Dlst PE=1 SV=1	2.10E-09	40.2	7.7	7 (7 0 0 0 0)	Mitochondrion.
Q62318	TIF1B_MOUSE Transcription intermediary factor 1-beta OS=Mus musculus GN=Trim28 PE=1 SV=3	3.67E-09	20.2	3.8	2 (2 0 0 0 0)	Nucleus.
P56695	WFS1_MOUSE Wolframin OS=Mus musculus GN=Wfs1 PE=1 SV=1	3.80E-05	40.2	4.6	5 (5 0 0 0 0)	Endoplasmic reticulum membrane; Multi-pass membrane protein.
P97379	G3BP2_MOUSE Ras GTPase-activating protein-binding protein 2 OS=Mus musculus GN=G3bp2 PE=1 SV=2	2.83E-08	40.2	8.9	5 (5 0 0 0 0)	ND
P62806	H4_MOUSE Histone H4 OS=Mus musculus GN=Hist1h4a PE=1 SV=2	2.78E-08	40.2	38.8	6 (6 0 0 0 0)	Nucleus. Chromosome.
Q9QZD9	EIF3I_MOUSE Eukaryotic translation initiation factor 3 subunit I OS=Mus musculus GN=Eif3i PE=1 SV=1	3.57E-07	20.2	8.6	2 (2 0 0 0 0)	Cytoplasm.
Q9D6R2	IDH3A_MOUSE Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial OS=Mus musculus GN=Idh3a PE=1 SV=1	8.15E-10	40.2	8.5	13 (13 0 0 0 0)	Mitochondrion.
P05064	ALDOA_MOUSE Fructose-bisphosphate aldolase A OS=Mus musculus GN=Aldoa PE=1 SV=2	2.85E-07	20.2	6.3	3 (3 0 0 0 0)	ND
P02469	LAMB1_MOUSE Laminin subunit beta-1 OS=Mus musculus GN=Lamb1-1 PE=1 SV=2	1.26E-06	40.2	2.1	4 (4 0 0 0 0)	Secreted â€º extracellular space â€º extracellular matrix â€º basement membrane.
P29758	OAT_MOUSE Ornithine aminotransferase, mitochondrial OS=Mus musculus GN=Oat PE=1 SV=1	1.67E-09	40.2	7.3	5 (5 0 0 0 0)	Mitochondrion matrix.
P24452	CAPG_MOUSE Macrophage-capping protein OS=Mus musculus GN=Capg PE=1 SV=2	9.11E-10	20.2	7.7	2 (2 0 0 0 0)	Nucleus. Cytoplasm. Secreted. Melanosome.
P56959	FUS_MOUSE RNA-binding	3.18E-08	20.2	4.4	2 (2 0 0 0 0)	Nucleus.

	protein FUS OS=Mus musculus GN=Fus PE=2 SV=1					
P68433	H31_MOUSE Histone H3.1 OS=Mus musculus GN=Hist1h3a PE=1 SV=2	1.70E-08	40.1	23.5	4 (4 0 0 0 0)	Nucleus. Chromosome.
Q6IFZ6	K2C1B_MOUSE Keratin, type II cytoskeletal 1b OS=Mus musculus GN=Krt77 PE=1 SV=1	1.31E-09	38.2	5.4	54 (53 1 0 0 0)	ND
Q9R0Y5	KAD1_MOUSE Adenylate kinase isoenzyme 1 OS=Mus musculus GN=Ak1 PE=1 SV=1	1.16E-06	20.2	11.3	4 (4 0 0 0 0)	Cytoplasm.
O08602	RAE1A_MOUSE Retinoic acid early-inducible protein 1-alpha OS=Mus musculus GN=Raet1a PE=1 SV=1	8.11E-08	20.2	4.7	5 (5 0 0 0 0)	Cell membrane; Lipid-anchor â€º GPI-anchor.
Q8R317	UBQL1_MOUSE Ubiquilin-1 OS=Mus musculus GN=Ubqln1 PE=1 SV=1	1.99E-05	38.2	7.0	4 (3 1 0 0 0)	Nucleus. Cytoplasm.
P35951	LDLR_MOUSE Low-density lipoprotein receptor OS=Mus musculus GN=Ldlr PE=1 SV=1	3.22E-06	20.2	3.6	2 (2 0 0 0 0)	Cell membrane; Single-pass type I membrane protein. Endomembrane system; Single-pass type I membrane protein. Membrane â€º clathrin-coated pit; Single-pass type I membrane protein.
P61027	RAB10_MOUSE Ras-related protein Rab-10 OS=Mus musculus GN=Rab10 PE=1 SV=1	1.66E-08	32.2	17.0	29 (11 3 0 15 0)	Cell membrane; Lipid-anchor; Cytoplasmic side.
Q9Z0L0	TPBG_MOUSE Trophoblast glycoprotein OS=Mus musculus GN=Tpbg PE=1 SV=2	1.46E-08	20.2	5.6	3 (3 0 0 0 0)	Membrane; Single-pass type I membrane protein.
P62196	PRS8_MOUSE 26S protease regulatory subunit 8 OS=Mus musculus GN=Psmc5 PE=1 SV=1	1.37E-07	20.2	5.4	2 (2 0 0 0 0)	Cytoplasm. Nucleus.
O35874	SATT_MOUSE Neutral amino acid transporter A OS=Mus musculus GN=Slc1a4 PE=1 SV=1	1.11E-16	30.3	9.0	5 (5 0 0 0 0)	Membrane; Multi-pass membrane protein. Melanosome.
P25911	LYN_MOUSE Tyrosine-protein kinase Lyn OS=Mus musculus GN=Lyn PE=1 SV=4	1.79E-07	20.2	4.9	2 (2 0 0 0 0)	Cell membrane. Nucleus. Cytoplasm. Cytoplasm â€º perinuclear region. Golgi apparatus.

Q8VCH8	UBXN4_MOUSE UBX domain-containing protein 4 OS=Mus musculus GN=Ubxn4 PE=1 SV=1	1.89E-11	30.3	7.7	3 (3 0 0 0 0)	Endoplasmic reticulum membrane; Peripheral membrane protein. Nucleus envelope.
Q9JIW9	RALB_MOUSE Ras-related protein Ral-B OS=Mus musculus GN=Ralb PE=2 SV=1	1.62E-11	30.3	19.9	5 (5 0 0 0 0)	Cell membrane; Lipid-anchor; Cytoplasmic side.
Q9CR62	M2OM_MOUSE Mitochondrial 2-oxoglutarate/malate carrier protein OS=Mus musculus GN=Slc25a11 PE=1 SV=3	1.18E-10	30.3	15.9	5 (5 0 0 0 0)	Mitochondrion inner membrane; Multi-pass membrane protein.
P27659	RL3_MOUSE 60S ribosomal protein L3 OS=Mus musculus GN=Rpl3 PE=2 SV=2	1.34E-07	20.2	5.2	2 (2 0 0 0 0)	Cytoplasm.
P84099	RL19_MOUSE 60S ribosomal protein L19 OS=Mus musculus GN=Rpl19 PE=1 SV=1	5.22E-14	30.3	17.3	4 (4 0 0 0 0)	ND
P06837	NEUM_MOUSE Neuromodulin OS=Mus musculus GN=Gap43 PE=1 SV=1	6.71E-13	30.3	23.3	3 (3 0 0 0 0)	Cell membrane; Peripheral membrane protein; Cytoplasmic side. Cell projection â€º growth cone membrane; Peripheral membrane protein; Cytoplasmic side. Cell junction â€º synapse. Cell projection â€º filopodium membrane; Peripheral membrane protein.
P97350	PKP1_MOUSE Plakophilin-1 OS=Mus musculus GN=Pkp1 PE=1 SV=1	7.58E-09	30.2	5.1	3 (3 0 0 0 0)	Nucleus. Cell junction â€º desmosome.
Q7TPV4	MBB1A_MOUSE Myb-binding protein 1A OS=Mus musculus GN=Mybbp1a PE=1 SV=2	4.19E-06	20.1	1.8	2 (2 0 0 0 0)	Nucleus â€º nucleolus. Cytoplasm.
O08638	MYH11_MOUSE Myosin-11 OS=Mus musculus GN=Myh11 PE=1 SV=1	5.56E-13	30.2	1.8	7 (7 0 0 0 0)	Melanosome. Cytoplasm â€º myofibril.
Q9JI59	JAM2_MOUSE Junctional adhesion molecule B OS=Mus musculus GN=Jam2 PE=1 SV=1	2.89E-07	20.1	7.0	2 (2 0 0 0 0)	Cell junction â€º tight junction. Cell membrane; Single-pass type I membrane protein.

P32507	PVRL2_MOUSE Poliovirus receptor-related protein 2 OS=Mus musculus GN=Pvrl2 PE=1 SV=2	2.44E-08	30.2	8.9	3 (3 0 0 0 0)	Cell membrane; Single-pass type I membrane protein.
P48036	ANXA5_MOUSE Annexin A5 OS=Mus musculus GN=Anxa5 PE=1 SV=1	1.73E-08	30.2	12.2	3 (3 0 0 0 0)	ND
P62702	RS4X_MOUSE 40S ribosomal protein S4, X isoform OS=Mus musculus GN=Rps4x PE=2 SV=2	5.13E-05	20.1	7.6	2 (2 0 0 0 0)	Cytoplasm.
Q78IK4	APOOL_MOUSE Apolipoprotein O-like OS=Mus musculus GN=Apool PE=2 SV=1	1.21E-09	30.2	10.2	3 (3 0 0 0 0)	Secreted.
Q3UM83	KLRG2_MOUSE Killer cell lectin-like receptor subfamily G member 2 OS=Mus musculus GN=Klrg2 PE=2 SV=1	3.24E-07	20.1	6.5	2 (2 0 0 0 0)	Membrane; Single-pass membrane protein.
Q61503	5NTD_MOUSE 5'-nucleotidase OS=Mus musculus GN=Nt5e PE=1 SV=2	2.31E-07	20.1	3.5	2 (2 0 0 0 0)	Cell membrane; Lipid-anchor â€º GPI-anchor.
P16110	LEG3_MOUSE Galectin-3 OS=Mus musculus GN=Lgals3 PE=1 SV=3	2.33E-06	20.1	8.3	2 (2 0 0 0 0)	Cytoplasm. Nucleus. Secreted.
Q9WTI7	MYO1C_MOUSE Myosin-Ic OS=Mus musculus GN=Myo1c PE=1 SV=2	1.45E-11	30.2	4.7	5 (5 0 0 0 0)	Cytoplasm. Cell membrane. Cell projection â€º stereocilium membrane. Nucleus â€º nucleolus. Nucleus â€º nucleoplasm. Nucleus â€º nuclear pore complex.
Q61990	PCBP2_MOUSE Poly(rC)-binding protein 2 OS=Mus musculus GN=Pcbp2 PE=1 SV=1	4.10E-06	20.1	6.6	2 (2 0 0 0 0)	Nucleus. Cytoplasm.
Q6ZWV7	RL35_MOUSE 60S ribosomal protein L35 OS=Mus musculus GN=Rpl35 PE=2 SV=1	1.32E-09	30.2	12.2	4 (4 0 0 0 0)	ND
P63101	1433Z_MOUSE 14-3-3 protein zeta/delta OS=Mus musculus GN=Ywhaz PE=1 SV=1	6.25E-10	30.2	16.3	4 (4 0 0 0 0)	Cytoplasm. Melanosome.
P54763	EPHB2_MOUSE Ephrin type-B receptor 2 OS=Mus musculus GN=Ephb2 PE=1 SV=2	1.83E-07	20.1	2.8	2 (2 0 0 0 0)	Membrane; Single-pass type I membrane protein.

Q80WW9	DDRGK_MOUSE DDRGK domain-containing protein 1 OS=Mus musculus GN=Ddrgk1 PE=1 SV=2	7.05E-11	30.2	11.4	3 (3 0 0 0 0)	Endoplasmic reticulum.
Q61468	MSLN_MOUSE Mesothelin OS=Mus musculus GN=Msln PE=1 SV=1	8.50E-05	20.1	1.6	2 (2 0 0 0 0)	Cell membrane; Lipid-anchor â€º GPI-anchor. Golgi apparatus. Secreted.
P35293	RAB18_MOUSE Ras-related protein Rab-18 OS=Mus musculus GN=Rab18 PE=2 SV=2	2.75E-09	30.2	18.0	4 (4 0 0 0 0)	Apical cell membrane; Lipid-anchor. Basal cell membrane; Lipid-anchor.
Q9R1Q9	VAS1_MOUSE V-type proton ATPase subunit S1 OS=Mus musculus GN=Atp6ap1 PE=1 SV=1	5.32E-08	30.2	8.9	3 (3 0 0 0 0)	Vacuole membrane; Single-pass membrane protein.
Q8BY89	CTL2_MOUSE Choline transporter-like protein 2 OS=Mus musculus GN=Slc44a2 PE=1 SV=1	4.06E-04	18.1	2.3	2 (1 1 0 0 0)	Membrane; Multi-pass membrane protein.
Q9CYL5	GAPR1_MOUSE Golgi-associated plant pathogenesis-related protein 1 OS=Mus musculus GN=Glipr2 PE=2 SV=3	1.99E-08	30.2	24.7	5 (5 0 0 0 0)	Golgi apparatus membrane; Lipid-anchor.
P99024	TBB5_MOUSE Tubulin beta-5 chain OS=Mus musculus GN=Tubb5 PE=1 SV=1	1.27E-08	30.2	9.9	24 (24 0 0 0 0)	Cytoplasm â€º cytoskeleton.
P61022	CHP1_MOUSE Calcium-binding protein p22 OS=Mus musculus GN=Chp PE=2 SV=2	9.16E-08	30.2	17.9	3 (3 0 0 0 0)	Cytoplasm.
Q91WD5	NDUS2_MOUSE NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial OS=Mus musculus GN=Ndufs2 PE=1 SV=1	9.58E-07	30.2	5.2	3 (3 0 0 0 0)	Mitochondrion inner membrane; Peripheral membrane protein; Matrix side.
O35857	TIM44_MOUSE Mitochondrial import inner membrane translocase subunit TIM44 OS=Mus musculus GN=Timm44 PE=2 SV=1	6.37E-08	30.2	8.4	3 (3 0 0 0 0)	Mitochondrion inner membrane.
Q9Z2T6	KRT85_MOUSE Keratin, type II cuticular Hb5 OS=Mus musculus GN=Krt85 PE=2 SV=2	8.36E-07	30.2	3.9	7 (7 0 0 0 0)	ND
Q9Z127	LAT1_MOUSE Large neutral amino acids transporter small subunit 1 OS=Mus musculus	1.31E-12	30.2	6.1	14 (14 0 0 0 0)	Cytoplasm â€º cytosol. Apical cell membrane; Multi-pass membrane

	GN=Slc7a5 PE=1 SV=1					protein.
P55302	AMRP_MOUSE Alpha-2-macroglobulin receptor-associated protein OS=Mus musculus GN=Lrpap1 PE=1 SV=1	6.76E-12	30.2	9.4	3 (3 0 0 0 0)	Endoplasmic reticulum. Cytoplasm. Cell surface.
Q64133	AOFA_MOUSE Amine oxidase [flavin-containing] A OS=Mus musculus GN=Maoa PE=1 SV=2	2.41E-12	30.2	8.0	4 (4 0 0 0 0)	Mitochondrion outer membrane; Single-pass type IV membrane protein; Cytoplasmic side.
Q99KN9	EPN4_MOUSE Clathrin interactor 1 OS=Mus musculus GN=Clint1 PE=1 SV=2	1.19E-07	30.2	7.8	3 (3 0 0 0 0)	Cytoplasm. Cytoplasm â€º perinuclear region. Membrane; Peripheral membrane protein. Cytoplasmic vesicle â€º clathrin-coated vesicle.
Q99J47	DRS7B_MOUSE Dehydrogenase/reductase SDR family member 7B OS=Mus musculus GN=Dhrs7b PE=2 SV=1	9.32E-10	30.2	13.0	3 (3 0 0 0 0)	Peroxisome membrane; Single-pass type II membrane protein.
Q9WTS2	FUT8_MOUSE Alpha-(1,6)-fucosyltransferase OS=Mus musculus GN=Fut8 PE=2 SV=1	8.50E-13	30.2	6.3	3 (3 0 0 0 0)	Golgi apparatus â€º Golgi stack membrane; Single-pass type II membrane protein.
Q91X78	ERLN1_MOUSE Erlin-1 OS=Mus musculus GN=Erlin1 PE=2 SV=1	2.16E-08	30.2	9.8	6 (6 0 0 0 0)	Endoplasmic reticulum membrane; Single-pass type II membrane protein.
Q64727	VINC_MOUSE Vinculin OS=Mus musculus GN=Vcl PE=1 SV=4	6.61E-08	30.2	3.7	6 (6 0 0 0 0)	Cytoplasm â€º cytoskeleton. Cell junction â€º adherens junction. Cell membrane; Peripheral membrane protein; Cytoplasmic side. Cell junction.
Q9ES97	RTN3_MOUSE Reticulon-3 OS=Mus musculus GN=Rtn3 PE=1 SV=2	7.91E-09	30.2	2.3	5 (5 0 0 0 0)	Endoplasmic reticulum membrane; Multi-pass membrane protein. Golgi apparatus membrane; Multi-pass membrane protein.

Q9JHU4	DYHC1_MOUSE Cytoplasmic dynein 1 heavy chain 1 OS=Mus musculus GN=Dync1h1 PE=1 SV=1	8.08E-09	30.2	0.9	3 (3 0 0 0 0)	Cytoplasm â€º cytoskeleton.
Q9DCX2	ATP5H_MOUSE ATP synthase subunit d, mitochondrial OS=Mus musculus GN=Atp5h PE=1 SV=3	9.50E-08	30.2	20.5	5 (5 0 0 0 0)	Mitochondrion. Mitochondrion inner membrane.
P26043	RADI_MOUSE Radixin OS=Mus musculus GN=Rdx PE=1 SV=2	2.96E-05	30.2	3.8	4 (4 0 0 0 0)	Cell membrane; Peripheral membrane protein; Cytoplasmic side. Cytoplasm â€º cytoskeleton. Cleavage furrow.
Q9R0E1	PLOD3_MOUSE Procollagen-lysine,2-oxoglutarate 5-dioxygenase 3 OS=Mus musculus GN=Plod3 PE=1 SV=1	1.30E-09	30.2	3.2	4 (4 0 0 0 0)	Rough endoplasmic reticulum membrane; Peripheral membrane protein; Lumenal side.
Q8BGH2	SAM50_MOUSE Sorting and assembly machinery component 50 homolog OS=Mus musculus GN=Samm50 PE=1 SV=1	3.03E-08	30.2	7.0	3 (3 0 0 0 0)	Mitochondrion outer membrane; Multi-pass membrane protein. Cytoplasm.
Q7TN29	SMAP2_MOUSE Stromal membrane-associated protein 2 OS=Mus musculus GN=Smap2 PE=1 SV=1	8.35E-10	30.2	9.3	7 (7 0 0 0 0)	Cytoplasm.
P21279	GNAQ_MOUSE Guanine nucleotide-binding protein G(q) subunit alpha OS=Mus musculus GN=Gnaq PE=1 SV=4	3.20E-10	30.2	10.0	3 (3 0 0 0 0)	ND
P30412	PPIC_MOUSE Peptidyl-prolyl cis-trans isomerase C OS=Mus musculus GN=Ppic PE=1 SV=1	6.08E-11	30.2	18.9	4 (4 0 0 0 0)	Cytoplasm.
Q80U72	SCRIB_MOUSE Protein scribble homolog OS=Mus musculus GN=Scrib PE=1 SV=2	1.72E-10	30.2	2.8	4 (4 0 0 0 0)	Cell membrane; Peripheral membrane protein. Cell junction â€º adherens junction. Cytoplasm.
P04104	K2C1_MOUSE Keratin, type II cytoskeletal 1 OS=Mus musculus GN=Krt1 PE=1 SV=4	5.18E-09	30.2	3.6	28 (28 0 0 0 0)	Cell membrane.
P27046	MA2A1_MOUSE Alpha-mannosidase 2 OS=Mus musculus GN=Man2a1 PE=1 SV=1	6.22E-08	30.2	3.0	3 (3 0 0 0 0)	Golgi apparatus membrane; Single-pass type II membrane protein.

Q99KF1	TMED9_MOUSE Transmembrane emp24 domain-containing protein 9 OS=Mus musculus GN=Tmed9 PE=2 SV=2	7.87E-09	30.2	15.7	5 (5 0 0 0 0)	Endoplasmic reticulum membrane; Single-pass type I membrane protein.
Q9WV92	E41L3_MOUSE Band 4.1-like protein 3 OS=Mus musculus GN=Epb41l3 PE=1 SV=1	1.72E-06	30.2	3.4	6 (6 0 0 0 0)	Cytoplasm â€º cytoskeleton.
Q6PB66	LPPRC_MOUSE Leucine-rich PPR motif-containing protein, mitochondrial OS=Mus musculus GN=Lrpprc PE=1 SV=2	3.61E-09	30.2	2.9	5 (5 0 0 0 0)	Mitochondrion. Nucleus. Nucleus â€º nucleoplasm. Nucleus inner membrane. Nucleus outer membrane.
Q8BKC5	IPO5_MOUSE Importin-5 OS=Mus musculus GN=Ipo5 PE=1 SV=3	6.70E-08	30.2	3.3	3 (3 0 0 0 0)	Cytoplasm. Nucleus.
Q64213	SF01_MOUSE Splicing factor 1 OS=Mus musculus GN=Sf1 PE=1 SV=5	5.12E-10	30.2	6.1	6 (6 0 0 0 0)	Nucleus.
Q7TQH0	ATX2L_MOUSE Ataxin-2-like protein OS=Mus musculus GN=Atxn2l PE=1 SV=1	3.67E-10	30.2	3.1	4 (4 0 0 0 0)	Membrane; Peripheral membrane protein.
Q8BXZ1	TMX3_MOUSE Protein disulfide-isomerase TMX3 OS=Mus musculus GN=Tmx3 PE=1 SV=2	1.79E-07	30.2	9.0	3 (3 0 0 0 0)	Endoplasmic reticulum membrane; Single-pass membrane protein.
P14206	RSSA_MOUSE 40S ribosomal protein SA OS=Mus musculus GN=Rpsa PE=1 SV=4	3.22E-06	30.2	12.9	3 (3 0 0 0 0)	Cell membrane. Cytoplasm. Nucleus.
P08730	K1C13_MOUSE Keratin, type I cytoskeletal 13 OS=Mus musculus GN=Krt13 PE=1 SV=2	1.12E-06	30.2	4.6	23 (23 0 0 0 0)	ND
Q3UVK0	ERMP1_MOUSE Endoplasmic reticulum metallopeptidase 1 OS=Mus musculus GN=Ermp1 PE=1 SV=2	1.56E-08	30.2	3.9	3 (3 0 0 0 0)	Endoplasmic reticulum membrane; Multi-pass membrane protein.
Q60716	P4HA2_MOUSE Prolyl 4-hydroxylase subunit alpha-2 OS=Mus musculus GN=P4ha2 PE=2 SV=1	6.74E-09	30.2	6.7	5 (5 0 0 0 0)	Endoplasmic reticulum lumen.
Q6ZQ38	CAND1_MOUSE Cullin-associated NEDD8-dissociated protein 1 OS=Mus musculus GN=Cand1 PE=2 SV=2	1.22E-08	30.2	3.0	3 (3 0 0 0 0)	Nucleus.

P54071	IDHP_MOUSE Isocitrate dehydrogenase [NADP], mitochondrial OS=Mus musculus GN=Idh2 PE=1 SV=3	2.53E-11	30.2	7.3	9 (9 0 0 0 0)	Mitochondrion.
P25444	RS2_MOUSE 40S ribosomal protein S2 OS=Mus musculus GN=Rps2 PE=1 SV=3	5.18E-07	30.2	10.6	3 (3 0 0 0 0)	ND
Q91VX2	UBAP2_MOUSE Ubiquitin-associated protein 2 OS=Mus musculus GN=Ubap2 PE=2 SV=1	6.09E-08	30.2	3.6	3 (3 0 0 0 0)	ND
O08807	PRDX4_MOUSE Peroxiredoxin-4 OS=Mus musculus GN=Prdx4 PE=1 SV=1	1.25E-06	30.2	12.4	7 (7 0 0 0 0)	Cytoplasm. Secreted.
Q9CR68	UCRI_MOUSE Cytochrome b-c1 complex subunit Rieske, mitochondrial OS=Mus musculus GN=Uqcrfs1 PE=1 SV=1	5.98E-10	30.2	16.1	4 (4 0 0 0 0)	Mitochondrion inner membrane.
P13020	GELS_MOUSE Gelsolin OS=Mus musculus GN=Gsn PE=1 SV=3	5.71E-07	30.2	5.3	4 (4 0 0 0 0)	Cytoplasm â€º cytoskeleton. Secreted.
Q9EP72	CO024_MOUSE UPF0480 protein C15orf24 homolog OS=Mus musculus GN=ORF3 PE=2 SV=1	8.24E-10	30.2	16.6	5 (5 0 0 0 0)	Membrane; Single-pass type I membrane protein.
Q9D7N9	APMAP_MOUSE Adipocyte plasma membrane-associated protein OS=Mus musculus GN=Apmap PE=1 SV=1	1.61E-08	30.2	8.2	4 (4 0 0 0 0)	Membrane; Single-pass type II membrane protein.
O08579	EMD_MOUSE Emerin OS=Mus musculus GN=Emd PE=1 SV=1	8.10E-08	30.2	16.2	3 (3 0 0 0 0)	Nucleus inner membrane; Single-pass membrane protein; Nucleoplasmic side. Nucleus outer membrane.
Q9R099	TBL2_MOUSE Transducin beta-like protein 2 OS=Mus musculus GN=Tbl2 PE=2 SV=1	1.24E-09	30.2	8.1	4 (4 0 0 0 0)	ND
Q9D1D4	TMEDA_MOUSE Transmembrane emp24 domain-containing protein 10 OS=Mus musculus GN=Tmed10 PE=2 SV=1	1.66E-07	30.2	15.1	4 (4 0 0 0 0)	Golgi apparatus membrane; Single-pass type I membrane protein; Lumenal side. Melanosome.
Q8VDP6	CDIPT_MOUSE CDP-diacylglycerol--inositol 3-phosphatidyltransferase OS=Mus musculus	1.42E-05	30.2	9.9	3 (3 0 0 0 0)	Endoplasmic reticulum membrane; Multi-pass membrane

	GN=Cdipt PE=1 SV=1					protein. Golgi apparatus membrane; Multi-pass membrane protein. Cell membrane; Multi-pass membrane protein.
P62835	RAP1A_MOUSE Ras-related protein Rap-1A OS=Mus musculus GN=Rap1a PE=2 SV=1	1.46E-09	30.2	19.0	9 (9 0 0 0 0)	Cell membrane; Lipid-anchor.
Q9Z2I0	LETM1_MOUSE LETM1 and EF-hand domain-containing protein 1, mitochondrial OS=Mus musculus GN=Letm1 PE=2 SV=1	1.99E-08	30.2	4.6	3 (3 0 0 0 0)	Mitochondrion inner membrane; Single-pass membrane protein.
Q9D880	TIM50_MOUSE Mitochondrial import inner membrane translocase subunit TIM50 OS=Mus musculus GN=Timm50 PE=1 SV=1	1.62E-07	30.2	9.3	5 (5 0 0 0 0)	Mitochondrion inner membrane; Single-pass membrane protein.
Q921G7	ETFD_MOUSE Electron transfer flavoprotein-ubiquinone oxidoreductase, mitochondrial OS=Mus musculus GN=Etfdh PE=1 SV=1	3.25E-05	30.2	5.5	3 (3 0 0 0 0)	Mitochondrion inner membrane.
Q6R0H7	GNAS1_MOUSE Guanine nucleotide-binding protein G(s) subunit alpha isoforms XLas OS=Mus musculus GN=Gnas PE=2 SV=1	1.44E-08	30.2	3.1	3 (3 0 0 0 0)	Cell membrane; Peripheral membrane protein.
Q80UM7	MOGS_MOUSE Mannosyl-oligosaccharide glucosidase OS=Mus musculus GN=Mogs PE=2 SV=1	2.50E-09	30.2	4.1	4 (4 0 0 0 0)	Endoplasmic reticulum membrane; Single-pass type II membrane protein.
Q8VHE0	SEC63_MOUSE Translocation protein SEC63 homolog OS=Mus musculus GN=Sec63 PE=1 SV=3	2.53E-06	30.2	4.3	3 (3 0 0 0 0)	Endoplasmic reticulum membrane; Multi-pass membrane protein.
Q497I4	KRT35_MOUSE Keratin, type I cuticular Ha5 OS=Mus musculus GN=Krt35 PE=2 SV=1	7.65E-07	30.1	4.6	3 (3 0 0 0 0)	ND
Q9D0E1	HNRPM_MOUSE Heterogeneous nuclear ribonucleoprotein M OS=Mus musculus GN=Hnrnpm PE=1 SV=3	5.53E-06	30.1	4.9	4 (4 0 0 0 0)	Nucleus.

Q6PD26	PIGS_MOUSE GPI transamidase component PIG-S OS=Mus musculus GN=Pigs PE=1 SV=3	6.24E-07	30.1	5.9	4 (4 0 0 0 0)	Endoplasmic reticulum membrane; Multi-pass membrane protein.
Q61941	NNTM_MOUSE NAD(P) transhydrogenase, mitochondrial OS=Mus musculus GN=Nnt PE=1 SV=2	1.03E-06	30.1	2.6	5 (5 0 0 0 0)	Mitochondrion inner membrane; Multi-pass membrane protein; Matrix side.
Q61033	LAP2A_MOUSE Lamina-associated polypeptide 2, isoforms alpha/zeta OS=Mus musculus GN=Tmpo PE=1 SV=3	4.39E-08	30.1	5.9	4 (4 0 0 0 0)	Nucleus. Chromosome.
Q8C3X8	LMF2_MOUSE Lipase maturation factor 2 OS=Mus musculus GN=Lmf2 PE=2 SV=1	2.14E-04	30.1	2.1	3 (3 0 0 0 0)	Endoplasmic reticulum membrane; Multi-pass membrane protein.
P61620	S61A1_MOUSE Protein transport protein Sec61 subunit alpha isoform 1 OS=Mus musculus GN=Sec61a1 PE=2 SV=2	2.74E-07	30.1	4.4	3 (3 0 0 0 0)	Endoplasmic reticulum membrane; Multi-pass membrane protein.
Q8VCM8	NCLN_MOUSE Nicalin OS=Mus musculus GN=Ncln PE=2 SV=2	6.21E-05	30.1	4.8	4 (4 0 0 0 0)	Endoplasmic reticulum membrane; Single-pass membrane protein.
P11679	K2C8_MOUSE Keratin, type II cytoskeletal 8 OS=Mus musculus GN=Krt8 PE=1 SV=4	3.88E-10	28.2	2.9	27 (26 1 0 0 0)	Cytoplasm. Nucleus â€º nucleoplasm. Nucleus matrix.
P35762	CD81_MOUSE CD81 antigen OS=Mus musculus GN=Cd81 PE=1 SV=1	3.16E-13	20.3	8.5	5 (5 0 0 0 0)	Membrane; Multi-pass membrane protein.
Q9JII5	DAZP1_MOUSE DAZ-associated protein 1 OS=Mus musculus GN=Dazap1 PE=2 SV=2	1.56E-10	20.3	7.6	2 (2 0 0 0 0)	Cytoplasm. Nucleus.
Q99KI3	TM111_MOUSE Transmembrane protein 111 OS=Mus musculus GN=Tmem111 PE=2 SV=3	3.29E-10	20.3	11.9	3 (3 0 0 0 0)	Membrane; Multi-pass membrane protein.
Q8C7E7	STBD1_MOUSE Starch-binding domain-containing protein 1 OS=Mus musculus GN=Stbd1 PE=1 SV=1	1.56E-07	20.3	8.0	2 (2 0 0 0 0)	Membrane; Single-pass type III membrane protein.
P24668	MPRD_MOUSE Cation-dependent mannose-6-phosphate receptor OS=Mus musculus GN=M6pr PE=1 SV=1	9.94E-12	20.3	8.6	2 (2 0 0 0 0)	Lysosome membrane; Single-pass type I membrane protein.

Q99KV1	DJB11_MOUSE DnaJ homolog subfamily B member 11 OS=Mus musculus GN=Dnajb11 PE=1 SV=1	1.58E-11	20.2	9.8	2 (2 0 0 0 0)	Endoplasmic reticulum lumen.
Q924Z4	LASS2_MOUSE LAG1 longevity assurance homolog 2 OS=Mus musculus GN=Lass2 PE=1 SV=1	1.11E-14	20.2	4.7	2 (2 0 0 0 0)	Nucleus membrane; Multi-pass membrane protein. Endoplasmic reticulum membrane; Multi-pass membrane protein.
Q9WUQ2	PREB_MOUSE Prolactin regulatory element-binding protein OS=Mus musculus GN=Preb PE=1 SV=1	1.28E-09	20.2	6.2	2 (2 0 0 0 0)	Nucleus. Membrane; Single-pass membrane protein. Endoplasmic reticulum.
P47758	SRPRB_MOUSE Signal recognition particle receptor subunit beta OS=Mus musculus GN=Srprb PE=1 SV=1	9.33E-14	20.2	11.9	3 (3 0 0 0 0)	Endoplasmic reticulum membrane; Single-pass membrane protein.
P62259	1433E_MOUSE 14-3-3 protein epsilon OS=Mus musculus GN=Ywhae PE=1 SV=1	2.18E-10	20.2	13.3	2 (2 0 0 0 0)	Cytoplasm. Melanosome.
P07214	SPRC_MOUSE SPARC OS=Mus musculus GN=Sparc PE=1 SV=1	6.29E-09	20.2	4.6	3 (3 0 0 0 0)	Secreted â€º extracellular space â€º extracellular matrix â€º basement membrane.
Q9JKB3	DBPA_MOUSE DNA-binding protein A OS=Mus musculus GN=Csda PE=1 SV=2	2.62E-09	20.2	8.9	2 (2 0 0 0 0)	Cytoplasm. Nucleus.
Q9Z0R9	FADS2_MOUSE Fatty acid desaturase 2 OS=Mus musculus GN=Fads2 PE=2 SV=1	1.38E-12	20.2	6.1	2 (2 0 0 0 0)	Endoplasmic reticulum membrane; Multi-pass membrane protein.
Q9CY58	PAIRB_MOUSE Plasminogen activator inhibitor 1 RNA-binding protein OS=Mus musculus GN=Serbp1 PE=1 SV=2	9.70E-09	20.2	6.6	3 (3 0 0 0 0)	Cytoplasm. Nucleus. Cytoplasm â€º perinuclear region.
Q9JJI8	RL38_MOUSE 60S ribosomal protein L38 OS=Mus musculus GN=Rpl38 PE=2 SV=3	1.34E-08	20.2	35.7	3 (3 0 0 0 0)	ND
Q8BP67	RL24_MOUSE 60S ribosomal protein L24	8.84E-10	20.2	8.3	8 (8 0 0 0 0)	ND

	OS=Mus musculus GN=Rpl24 PE=2 SV=2					
Q8VDL4	ADPGK_MOUSE ADP-dependent glucokinase OS=Mus musculus GN=Adpgk PE=1 SV=2	1.11E-14	20.2	6.3	3 (3 0 0 0 0)	Secreted.
Q9D0F3	LMAN1_MOUSE Protein ERGIC-53 OS=Mus musculus GN=Lman1 PE=2 SV=1	1.14E-12	20.2	6.0	2 (2 0 0 0 0)	Endoplasmic reticulum-Golgi intermediate compartment membrane; Single-pass type I membrane protein. Golgi apparatus membrane; Single-pass membrane protein. Endoplasmic reticulum membrane; Single-pass membrane protein.
P50431	GLYC_MOUSE Serine hydroxymethyltransferase, cytosolic OS=Mus musculus GN=Shmt1 PE=1 SV=2	1.33E-09	20.2	2.9	4 (4 0 0 0 0)	Cytoplasm.
Q6ZQI3	MLEC_MOUSE Malectin OS=Mus musculus GN=Mlec PE=2 SV=2	4.91E-09	20.2	8.6	2 (2 0 0 0 0)	Endoplasmic reticulum membrane; Single-pass type I membrane protein.
Q8JZN5	ACAD9_MOUSE Acyl-CoA dehydrogenase family member 9, mitochondrial OS=Mus musculus GN=Acad9 PE=2 SV=1	2.69E-11	20.2	4.2	4 (4 0 0 0 0)	Mitochondrion.
P62830	RL23_MOUSE 60S ribosomal protein L23 OS=Mus musculus GN=Rpl23 PE=2 SV=1	5.57E-13	20.2	17.9	9 (9 0 0 0 0)	ND
Q9CQF9	PCYOX_MOUSE Prenylcysteine oxidase OS=Mus musculus GN=Pcyox1 PE=1 SV=1	2.54E-06	20.2	5.0	2 (2 0 0 0 0)	Lysosome.
Q80V26	IMPA3_MOUSE Inositol monophosphatase 3 OS=Mus musculus GN=Impad1 PE=2 SV=1	4.66E-11	20.2	3.9	2 (2 0 0 0 0)	Membrane; Single-pass membrane protein.
O88967	YMEL1_MOUSE ATP-dependent metalloprotease YME1L1 OS=Mus musculus GN=Yme1l1 PE=2 SV=1	9.90E-09	20.2	3.8	4 (4 0 0 0 0)	Mitochondrion.
Q8VCL2	SCO2_MOUSE Protein SCO2 homolog, mitochondrial OS=Mus	1.17E-10	20.2	9.4	2 (2 0 0 0 0)	Mitochondrion.

	musculus GN=Sco2 PE=2 SV=1					
Q9CR57	RL14_MOUSE 60S ribosomal protein L14 OS=Mus musculus GN=Rpl14 PE=2 SV=3	1.37E-08	20.2	11.5	2 (2 0 0 0 0)	ND
P40240	CD9_MOUSE CD9 antigen OS=Mus musculus GN=Cd9 PE=1 SV=2	1.48E-08	20.2	10.2	4 (4 0 0 0 0)	Membrane; Multi-pass membrane protein.
Q9CR60	GOT1B_MOUSE Vesicle transport protein GOT1B OS=Mus musculus GN=Golt1b PE=2 SV=1	3.48E-08	20.2	19.6	2 (2 0 0 0 0)	Golgi apparatus membrane; Multi-pass membrane protein.
Q9CQN1	TRAP1_MOUSE Heat shock protein 75 kDa, mitochondrial OS=Mus musculus GN=Trap1 PE=1 SV=1	4.61E-06	20.2	3.3	3 (3 0 0 0 0)	Mitochondrion.
O88696	CLPP_MOUSE Putative ATP-dependent Clp protease proteolytic subunit, mitochondrial OS=Mus musculus GN=Clpp PE=2 SV=1	1.01E-10	20.2	9.6	2 (2 0 0 0 0)	Mitochondrion matrix.
Q5FWK3	RHG01_MOUSE Rho GTPase-activating protein 1 OS=Mus musculus GN=Arhgap1 PE=1 SV=1	7.95E-07	20.2	4.6	2 (2 0 0 0 0)	Cytoplasm.
P17751	TPIS_MOUSE Triosephosphate isomerase OS=Mus musculus GN=Tpi1 PE=1 SV=3	4.92E-10	20.2	10.8	2 (2 0 0 0 0)	ND
Q8BFZ9	ERLN2_MOUSE Erlin-2 OS=Mus musculus GN=Erlin2 PE=1 SV=1	3.21E-11	20.2	7.9	2 (2 0 0 0 0)	Endoplasmic reticulum membrane; Single-pass type II membrane protein.
Q9D051	ODPB_MOUSE Pyruvate dehydrogenase E1 component subunit beta, mitochondrial OS=Mus musculus GN=Pdhb PE=1 SV=1	5.83E-12	20.2	4.5	2 (2 0 0 0 0)	Mitochondrion matrix.
Q8BWT1	THIM_MOUSE 3-ketoacyl-CoA thiolase, mitochondrial OS=Mus musculus GN=Acaa2 PE=1 SV=2	1.93E-07	20.2	6.8	2 (2 0 0 0 0)	Mitochondrion.
P37040	NCPR_MOUSE NADPH--cytochrome P450 reductase OS=Mus musculus GN=Por PE=1 SV=2	3.25E-09	20.2	2.8	10 (10 0 0 0 0)	Endoplasmic reticulum membrane; Peripheral membrane protein.
P62242	RS8_MOUSE 40S ribosomal protein S8 OS=Mus	3.07E-05	20.2	11.5	2 (2 0 0 0 0)	Cytoplasm.

	musculus GN=Rps8 PE=1 SV=2					
P16381	DDX3L_MOUSE Putative ATP-dependent RNA helicase Pl10 OS=Mus musculus GN=D1Pas1 PE=1 SV=1	4.06E-08	20.2	3.9	10 (10 0 0 0 0)	ND
Q32MW3	ACO10_MOUSE Acyl-coenzyme A thioesterase 10, mitochondrial OS=Mus musculus GN=Acot10 PE=2 SV=1	4.98E-08	20.2	4.8	2 (2 0 0 0 0)	Mitochondrion.
Q9Z1W8	AT12A_MOUSE Potassium-transporting ATPase alpha chain 2 OS=Mus musculus GN=Atp12a PE=1 SV=2	1.53E-10	20.2	1.3	8 (8 0 0 0 0)	Membrane; Multi-pass membrane protein.
Q9ER00	STX12_MOUSE Syntaxin-12 OS=Mus musculus GN=Stx12 PE=1 SV=1	1.07E-07	20.2	11.3	2 (2 0 0 0 0)	Endomembrane system; Single-pass type IV membrane protein; Cytoplasmic side. Golgi apparatus membrane; Single-pass type IV membrane protein.
Q8R3H7	HS2ST_MOUSE Heparan sulfate 2-O-sulfotransferase 1 OS=Mus musculus GN=Hs2st1 PE=1 SV=2	4.17E-08	20.2	3.4	3 (3 0 0 0 0)	Golgi apparatus membrane; Single-pass type II membrane protein.
P40124	CAP1_MOUSE Adenylyl cyclase-associated protein 1 OS=Mus musculus GN=Cap1 PE=1 SV=3	1.90E-06	20.2	4.6	2 (2 0 0 0 0)	Cell membrane; Peripheral membrane protein.
Q61029	LAP2B_MOUSE Lamina-associated polypeptide 2, isoforms beta/delta/epsilon/gamma OS=Mus musculus GN=Tmpo PE=1 SV=3	1.45E-06	20.2	6.2	2 (2 0 0 0 0)	Nucleus inner membrane; Single-pass type II membrane protein. Chromosome.
P61255	RL26_MOUSE 60S ribosomal protein L26 OS=Mus musculus GN=Rpl26 PE=2 SV=1	6.18E-07	20.2	15.9	4 (4 0 0 0 0)	ND
P63001	RAC1_MOUSE Ras-related C3 botulinum toxin substrate 1 OS=Mus musculus GN=Rac1 PE=1 SV=1	3.23E-07	20.2	14.1	2 (2 0 0 0 0)	Cell membrane; Lipid-anchor; Cytoplasmic side. Melanosome.
O70456	1433S_MOUSE 14-3-3 protein sigma OS=Mus musculus GN=Sfn PE=1 SV=1	5.04E-09	20.2	5.2	2 (2 0 0 0 0)	Cytoplasm. Nucleus. Secreted.

P42208	SEPT2_MOUSE Septin-2 OS=Mus musculus GN=Sept2 PE=1 SV=2	4.19E-07	20.2	7.8	2 (2 0 0 0 0)	Cytoplasm. Cytoplasm â€º cytoskeleton. Cytoplasm â€º cytoskeleton â€º spindle. Chromosome â€º centromere â€º kinetochore. Cleavage furrow. Midbody. Cytoplasm â€º cell cortex.
Q9DB15	RM12_MOUSE 39S ribosomal protein L12, mitochondrial OS=Mus musculus GN=Mrpl12 PE=1 SV=2	1.99E-04	20.2	12.4	2 (2 0 0 0 0)	Mitochondrion.
Q8R429	AT2A1_MOUSE Sarcoplasmic/endoplasmic reticulum calcium ATPase 1 OS=Mus musculus GN=Atp2a1 PE=2 SV=1	1.94E-09	20.2	2.8	7 (7 0 0 0 0)	Endoplasmic reticulum membrane; Multi-pass membrane protein. Sarcoplasmic reticulum membrane; Multi-pass membrane protein.
P63037	DNJA1_MOUSE DnaJ homolog subfamily A member 1 OS=Mus musculus GN=Dnaja1 PE=1 SV=1	6.38E-08	20.2	6.5	2 (2 0 0 0 0)	Membrane; Lipid-anchor.
Q91W92	BORG5_MOUSE Cdc42 effector protein 1 OS=Mus musculus GN=Cdc42ep1 PE=1 SV=1	8.20E-10	20.2	4.6	2 (2 0 0 0 0)	Endomembrane system; Peripheral membrane protein. Cytoplasm â€º cytoskeleton.
Q9DC69	NDUA9_MOUSE NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial OS=Mus musculus GN=Ndufa9 PE=1 SV=1	1.84E-07	20.2	7.2	2 (2 0 0 0 0)	Mitochondrion matrix.
P12970	RL7A_MOUSE 60S ribosomal protein L7a OS=Mus musculus GN=Rpl7a PE=2 SV=2	6.99E-06	20.2	9.4	2 (2 0 0 0 0)	ND
Q501J7	PHAR4_MOUSE Phosphatase and actin regulator 4 OS=Mus musculus GN=Phactr4 PE=1 SV=2	3.11E-14	20.2	4.9	2 (2 0 0 0 0)	ND

O35704	SPTC1_MOUSE Serine palmitoyltransferase 1 OS=Mus musculus GN=Sptlc1 PE=2 SV=1	2.86E-05	20.2	4.9	2 (2 0 0 0 0)	Endoplasmic reticulum membrane; Single-pass membrane protein.
Q501J6	DDX17_MOUSE Probable ATP-dependent RNA helicase DDX17 OS=Mus musculus GN=Ddx17 PE=2 SV=1	7.82E-10	20.2	3.5	11 (11 0 0 0 0)	Nucleus.
Q8CFE4	SCYL2_MOUSE SCY1-like protein 2 OS=Mus musculus GN=Scyl2 PE=1 SV=1	2.59E-06	20.2	2.8	2 (2 0 0 0 0)	Cytoplasm â€º perinuclear region. Cytoplasmic vesicle â€º clathrin-coated vesicle. Golgi apparatus â€º trans-Golgi network membrane. Endosome membrane.
Q9D646	KRT34_MOUSE Keratin, type I cuticular Ha4 OS=Mus musculus GN=Krt34 PE=2 SV=1	6.49E-07	20.2	5.4	3 (3 0 0 0 0)	ND
Q9CYZ2	TPD54_MOUSE Tumor protein D54 OS=Mus musculus GN=Tpd52l2 PE=1 SV=1	2.69E-06	20.2	11.4	2 (2 0 0 0 0)	ND
P35980	RL18_MOUSE 60S ribosomal protein L18 OS=Mus musculus GN=Rpl18 PE=2 SV=3	3.93E-07	20.2	13.8	3 (3 0 0 0 0)	Cytoplasm.
Q61753	SERA_MOUSE D-3-phosphoglycerate dehydrogenase OS=Mus musculus GN=Phgdh PE=1 SV=3	1.28E-05	20.2	4.7	4 (4 0 0 0 0)	ND
Q8BTY2	S4A7_MOUSE Sodium bicarbonate cotransporter 3 OS=Mus musculus GN=Slc4a7 PE=1 SV=2	7.29E-08	20.2	2.9	2 (2 0 0 0 0)	Basolateral cell membrane; Multi-pass membrane protein. Apical cell membrane; Multi-pass membrane protein. Cell projection â€º stereocilium.
Q60931	VDAC3_MOUSE Voltage-dependent anion-selective channel protein 3 OS=Mus musculus GN=Vdac3 PE=1 SV=1	1.87E-08	20.2	8.5	5 (5 0 0 0 0)	Mitochondrion outer membrane.
Q8R0X7	SGPL1_MOUSE Sphingosine-1-phosphate lyase 1 OS=Mus musculus	3.03E-11	20.2	2.6	3 (3 0 0 0 0)	Endoplasmic reticulum membrane; Single-

	GN=Sgpl1 PE=2 SV=1					pass type III membrane protein.
P14148	RL7_MOUSE 60S ribosomal protein L7 OS=Mus musculus GN=Rpl7 PE=2 SV=2	4.12E-10	20.2	8.9	2 (2 0 0 0 0)	ND
P58021	TM9S2_MOUSE Transmembrane 9 superfamily member 2 OS=Mus musculus GN=Tm9sf2 PE=2 SV=1	8.39E-07	20.2	3.3	2 (2 0 0 0 0)	Endosome membrane; Multi-pass membrane protein.
Q8BFR5	EFTU_MOUSE Elongation factor Tu, mitochondrial OS=Mus musculus GN=Tufm PE=1 SV=1	1.21E-08	20.2	5.5	3 (3 0 0 0 0)	Mitochondrion.
Q9Z110	P5CS_MOUSE Delta-1-pyrroline-5-carboxylate synthetase OS=Mus musculus GN=Aldh18a1 PE=2 SV=1	5.63E-09	20.2	2.5	7 (7 0 0 0 0)	Mitochondrion inner membrane.
Q6IMF0	KRT83_MOUSE Keratin, type II cuticular Hb3 OS=Mus musculus GN=Krt83 PE=2 SV=2	6.71E-05	20.2	1.8	3 (3 0 0 0 0)	ND
P59017	B2L13_MOUSE Bcl-2-like protein 13 OS=Mus musculus GN=Bcl2l13 PE=1 SV=1	3.33E-06	20.2	5.1	3 (3 0 0 0 0)	Mitochondrion membrane; Single-pass membrane protein.
Q9CXW2	RT22_MOUSE 28S ribosomal protein S22, mitochondrial OS=Mus musculus GN=Mrps22 PE=2 SV=1	2.69E-11	20.2	6.7	2 (2 0 0 0 0)	Mitochondrion.
P62918	RL8_MOUSE 60S ribosomal protein L8 OS=Mus musculus GN=Rpl8 PE=2 SV=2	9.65E-07	20.2	8.9	4 (4 0 0 0 0)	Cytoplasm.
Q5F2E7	NUFP2_MOUSE Nuclear fragile X mental retardation-interacting protein 2 OS=Mus musculus GN=Nufip2 PE=1 SV=1	2.23E-06	20.2	3.9	2 (2 0 0 0 0)	Nucleus. Cytoplasm.
P60335	PCBP1_MOUSE Poly(rC)-binding protein 1 OS=Mus musculus GN=Pcbp1 PE=1 SV=1	2.27E-06	20.2	6.7	3 (3 0 0 0 0)	Nucleus.
P28667	MRP_MOUSE MARCKS-related protein OS=Mus musculus GN=Marcksl1 PE=1 SV=2	6.60E-07	20.2	14.0	2 (2 0 0 0 0)	ND
P11438	LAMP1_MOUSE Lysosome-associated membrane glycoprotein 1 OS=Mus musculus	9.61E-07	20.2	5.7	3 (3 0 0 0 0)	Cell membrane; Single-pass type I membrane protein. Endosome

	GN=Lamp1 PE=1 SV=2					membrane; Single-pass type I membrane protein. Lysosome membrane; Single-pass type I membrane protein.
Q8C7K6	PCYXL_MOUSE Prenylcysteine oxidase-like OS=Mus musculus GN=Pcyox1l PE=2 SV=1	4.79E-05	20.2	5.1	3 (3 0 0 0 0)	Secreted.
P10493	NID1_MOUSE Nidogen-1 OS=Mus musculus GN=Nid1 PE=1 SV=1	6.11E-07	20.2	1.8	2 (2 0 0 0 0)	Secreted â€º extracellular space â€º extracellular matrix â€º basement membrane.
Q99M74	KRT82_MOUSE Keratin, type II cuticular Hb2 OS=Mus musculus GN=Krt82 PE=2 SV=1	6.72E-05	20.2	4.3	3 (3 0 0 0 0)	ND
P81117	NUCB2_MOUSE Nucleobindin-2 OS=Mus musculus GN=Nucb2 PE=1 SV=2	2.49E-06	20.2	5.2	2 (2 0 0 0 0)	Perikaryon. Endoplasmic reticulum. Nucleus envelope.
Q00262	STX2_MOUSE Syntaxin-2 OS=Mus musculus GN=Stx2 PE=2 SV=1	9.39E-07	20.2	6.6	2 (2 0 0 0 0)	Membrane; Single-pass type IV membrane protein.
P15331	PERI_MOUSE Peripherin OS=Mus musculus GN=Prph PE=1 SV=2	9.40E-09	20.2	4.4	23 (23 0 0 0 0)	ND
Q9WVE8	PACN2_MOUSE Protein kinase C and casein kinase substrate in neurons protein 2 OS=Mus musculus GN=Pacsin2 PE=2 SV=1	7.66E-08	20.2	4.1	2 (2 0 0 0 0)	Cytoplasmic vesicle.
Q91VZ6	SMAP1_MOUSE Stromal membrane-associated protein 1 OS=Mus musculus GN=Smap1 PE=1 SV=1	1.16E-06	20.2	2.5	2 (2 0 0 0 0)	Cell membrane; Peripheral membrane protein; Cytoplasmic side.
Q8CIV2	MBRL_MOUSE Membralin OS=Mus musculus GN=ORF61 PE=1 SV=2	1.33E-07	20.2	3.8	2 (2 0 0 0 0)	Membrane; Multi-pass membrane protein.
Q9R049	AMFR_MOUSE Autocrine motility factor receptor OS=Mus musculus GN=Amfr PE=1 SV=2	6.12E-08	20.2	3.7	2 (2 0 0 0 0)	Endoplasmic reticulum membrane; Multi-pass membrane protein.
Q9WTQ8	TIM23_MOUSE Mitochondrial import inner membrane translocase subunit Tim23 OS=Mus musculus GN=Timm23 PE=2 SV=1	4.94E-06	20.2	4.8	3 (3 0 0 0 0)	Mitochondrion inner membrane; Multi-pass membrane protein.
Q6ZPF4	FMNL3_MOUSE Formin-	9.63E-08	20.2	2.1	2 (2 0 0 0 0)	ND

	like protein 3 OS=Mus musculus GN=Fmnl3 PE=2 SV=2					
O70378	CX4NB_MOUSE Neighbor of COX4 OS=Mus musculus GN=Cox4nb PE=1 SV=1	4.67E-06	20.2	10.1	2 (2 0 0 0 0)	ND
Q60865	CAPR1_MOUSE Caprin-1 OS=Mus musculus GN=Caprin1 PE=1 SV=2	4.91E-07	20.2	3.1	2 (2 0 0 0 0)	Cytoplasm â€º cytosol. Cell projection â€º dendrite.
Q9DBG7	SRPR_MOUSE Signal recognition particle receptor subunit alpha OS=Mus musculus GN=Srpr PE=1 SV=1	2.58E-05	20.1	3.9	2 (2 0 0 0 0)	Endoplasmic reticulum membrane; Peripheral membrane protein.
P61021	RAB5B_MOUSE Ras-related protein Rab-5B OS=Mus musculus GN=Rab5b PE=1 SV=1	4.29E-07	20.1	12.1	2 (2 0 0 0 0)	Cell membrane; Lipid-anchor; Cytoplasmic side. Early endosome membrane; Lipid-anchor. Melanosome.
Q791T5	MTCH1_MOUSE Mitochondrial carrier homolog 1 OS=Mus musculus GN=Mtch1 PE=1 SV=1	4.85E-07	20.1	2.8	2 (2 0 0 0 0)	Mitochondrion inner membrane; Multi-pass membrane protein.
Q61712	DNJC1_MOUSE DnaJ homolog subfamily C member 1 OS=Mus musculus GN=Dnajc1 PE=1 SV=1	1.05E-04	20.1	3.8	2 (2 0 0 0 0)	Endoplasmic reticulum membrane; Single-pass type I membrane protein. Nucleus membrane; Single-pass type I membrane protein. Microsome membrane; Single-pass type I membrane protein.
Q9CZW5	TOM70_MOUSE Mitochondrial import receptor subunit TOM70 OS=Mus musculus GN=Tomm70a PE=1 SV=1	2.08E-07	20.1	3.3	4 (4 0 0 0 0)	Mitochondrion outer membrane; Single-pass membrane protein.
Q9D8V0	HM13_MOUSE Minor histocompatibility antigen H13 OS=Mus musculus GN=Hm13 PE=1 SV=1	2.73E-06	20.1	3.2	2 (2 0 0 0 0)	Endoplasmic reticulum membrane; Multi-pass membrane protein. Cell membrane; Multi-pass membrane protein.

Q61696	HS71A_MOUSE Heat shock 70 kDa protein 1A OS=Mus musculus GN=Hspa1a PE=1 SV=2	1.01E-10	20.1	3.4	16 (16 0 0 0 0)	Cytoplasm.
Q3TDQ1	STT3B_MOUSE Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3B OS=Mus musculus GN=Stt3b PE=1 SV=2	1.37E-07	20.1	2.8	2 (2 0 0 0 0)	Endoplasmic reticulum membrane; Multi-pass membrane protein.
Q09143	CTR1_MOUSE High affinity cationic amino acid transporter 1 OS=Mus musculus GN=Slc7a1 PE=2 SV=1	1.01E-07	20.1	1.8	5 (5 0 0 0 0)	Membrane; Multi-pass membrane protein.
Q9QZ23	NFU1_MOUSE NFU1 iron-sulfur cluster scaffold homolog, mitochondrial OS=Mus musculus GN=Nfu1 PE=1 SV=2	4.14E-07	20.1	4.7	2 (2 0 0 0 0)	Mitochondrion. Cytoplasm â€º cytosol.
Q9CR23	TMEM9_MOUSE Transmembrane protein 9 OS=Mus musculus GN=Tmem9 PE=2 SV=1	9.90E-08	20.1	7.1	3 (3 0 0 0 0)	Late endosome membrane; Single-pass type I membrane protein. Lysosome membrane; Single-pass type I membrane protein.
P08074	CBR2_MOUSE Carbonyl reductase [NADPH] 2 OS=Mus musculus GN=Cbr2 PE=1 SV=1	1.13E-05	20.1	4.5	2 (2 0 0 0 0)	Mitochondrion matrix.
Q9EP69	SAC1_MOUSE Phosphatidylinositide phosphatase SAC1 OS=Mus musculus GN=Sacm1l PE=2 SV=1	1.46E-07	20.1	3.4	2 (2 0 0 0 0)	Endoplasmic reticulum membrane; Multi-pass membrane protein.
Q60870	REEP5_MOUSE Receptor expression-enhancing protein 5 OS=Mus musculus GN=Reep5 PE=1 SV=1	4.68E-04	20.1	11.4	2 (2 0 0 0 0)	Membrane; Multi-pass membrane protein.
Q9CY50	SSRA_MOUSE Translocon-associated protein subunit alpha OS=Mus musculus GN=Ssr1 PE=1 SV=1	9.06E-06	20.1	8.0	2 (2 0 0 0 0)	Endoplasmic reticulum membrane; Single-pass type I membrane protein.
Q8BI84	MIA3_MOUSE Melanoma inhibitory activity protein 3 OS=Mus musculus GN=Mia3 PE=1 SV=2	1.08E-04	20.1	1.2	2 (2 0 0 0 0)	Endoplasmic reticulum membrane; Single-pass type I membrane protein.
Q62523	ZYX_MOUSE Zyxin OS=Mus musculus GN=Zyx PE=1 SV=1	1.01E-09	20.1	3.9	2 (2 0 0 0 0)	Cytoplasm. Cytoplasm â€º cytoskeleton. Cell junction â€º focal

						adhesion. Nucleus.
Q80U93	NU214_MOUSE Nuclear pore complex protein Nup214 OS=Mus musculus GN=Nup214 PE=1 SV=2	2.65E-05	20.1	0.5	2 (2 0 0 0 0)	Nucleus â€º nuclear pore complex.
Q6ZWN5	RS9_MOUSE 40S ribosomal protein S9 OS=Mus musculus GN=Rps9 PE=2 SV=3	9.67E-05	20.1	9.8	2 (2 0 0 0 0)	Cytoplasm.
Q9R1J0	NSDHL_MOUSE Sterol-4-alpha-carboxylate 3-dehydrogenase, decarboxylating OS=Mus musculus GN=Nsdhl PE=2 SV=1	5.39E-07	20.1	6.6	3 (3 0 0 0 0)	Membrane; Single-pass membrane protein.
Q9D1N9	RM21_MOUSE 39S ribosomal protein L21, mitochondrial OS=Mus musculus GN=Mrpl21 PE=2 SV=1	9.86E-06	20.1	9.1	2 (2 0 0 0 0)	Mitochondrion.
Q6PHN9	RAB35_MOUSE Ras-related protein Rab-35 OS=Mus musculus GN=Rab35 PE=1 SV=1	8.09E-07	20.1	11.9	2 (2 0 0 0 0)	Cell membrane; Lipid-anchor; Cytoplasmic side. Membrane â€º clathrin-coated pit. Cytoplasmic vesicle â€º clathrin-coated vesicle. Endosome. Melanosome.
Q9CQU3	RER1_MOUSE Protein RER1 OS=Mus musculus GN=Rer1 PE=1 SV=1	1.60E-05	20.1	11.2	2 (2 0 0 0 0)	Golgi apparatus membrane; Multi-pass membrane protein.
Q5SXY1	CYTSB_MOUSE Cytospin-B OS=Mus musculus GN=Cytsb PE=1 SV=2	6.33E-05	20.1	0.9	2 (2 0 0 0 0)	Nucleus.
Q3TLH4	BA2D1_MOUSE BAT2 domain-containing protein 1 OS=Mus musculus GN=Bat2d1 PE=1 SV=2	3.39E-05	20.1	0.7	2 (2 0 0 0 0)	ND
P62267	RS23_MOUSE 40S ribosomal protein S23 OS=Mus musculus GN=Rps23 PE=2 SV=3	3.27E-08	20.1	15.4	2 (2 0 0 0 0)	ND
P70403	CASP_MOUSE Protein CASP OS=Mus musculus GN=Cux1 PE=2 SV=2	1.42E-05	20.1	3.1	2 (2 0 0 0 0)	Golgi apparatus membrane; Single-pass type IV membrane protein.
Q8BGZ7	K2C75_MOUSE Keratin, type II cytoskeletal 75 OS=Mus musculus GN=Krt75 PE=1 SV=1	2.33E-10	18.3	6.7	16 (3 9 4 0 0)	ND

P35700	PRDX1_MOUSE Peroxiredoxin-1 OS=Mus musculus GN=Prdx1 PE=1 SV=1	2.83E-05	18.1	11.6	4 (1 3 0 0 0)	Cytoplasm. Melanosome.
Q3UIW5	RNF10_MOUSE RING finger protein 10 OS=Mus musculus GN=Rnf10 PE=2 SV=2	3.31E-04	16.1	1.1	2 (0 2 0 0 0)	Cytoplasm. Nucleus.

Table s3

Accession	Reference	P (pro)	Score	Coverage	Peptide (Hits)	Subcellular locations
Q9CQV8	1433B_MOUSE 14-3-3 protein beta/alpha OS=Mus musculus GN=Ywhab PE=1 SV=3	1.1E-13	96.2	34.6	10 (8 2 0 0 0)	Cytoplasm. Melanosome.
P62259	1433E_MOUSE 14-3-3 protein epsilon OS=Mus musculus GN=Ywhae PE=1 SV=1	9.3E-13	110.3	45.9	14 (14 0 0 0 0)	Cytoplasm. Melanosome.
P68510	1433F_MOUSE 14-3-3 protein eta OS=Mus musculus GN=Ywhah PE=1 SV=2	1.1E-09	40.2	18.7	4 (4 0 0 0 0)	Cytoplasm.
P61982	1433G_MOUSE 14-3-3 protein gamma OS=Mus musculus GN=Ywhag PE=1 SV=2	1.2E-09	40.2	14.2	4 (4 0 0 0 0)	Cytoplasm.
P68254	1433T_MOUSE 14-3-3 protein theta OS=Mus musculus GN=Ywhaq PE=1 SV=1	1.5E-12	20.3	13.1	3 (3 0 0 0 0)	Cytoplasm.
P63101	1433Z_MOUSE 14-3-3 protein zeta/delta OS=Mus musculus GN=Ywhaz PE=1 SV=1	2.2E-12	70.3	29.0	7 (7 0 0 0 0)	Cytoplasm. Melanosome.
Q76MZ3	2AAA_MOUSE Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform OS=Mus musculus GN=Ppp2r1a PE=1 SV=3	1.1E-14	60.3	13.8	11 (11 0 0 0 0)	Cytoplasm. Chromosome â€º centromere.
P10852	4F2_MOUSE 4F2 cell-surface antigen heavy chain OS=Mus musculus GN=Slc3a2 PE=1 SV=1	5.0E-14	170.3	37.6	118 (118 0 0 0 0)	Apical cell membrane; Single-pass type II membrane protein. Melanosome.
Q571I9	A16A1_MOUSE Aldehyde dehydrogenase family 16 member A1 OS=Mus musculus GN=Aldh16a1 PE=2 SV=2	9.1E-06	20.1	3.7	3 (3 0 0 0 0)	ND
P51912	AAAT_MOUSE Neutral amino acid transporter B(0) OS=Mus musculus GN=Slc1a5 PE=2 SV=2	4.9E-13	80.3	14.6	23 (23 0 0 0 0)	Membrane; Multi-pass membrane protein. Melanosome.
Q5EG47	AAPK1_MOUSE 5'-AMP-activated protein kinase catalytic subunit alpha-1 OS=Mus musculus GN=Prkaa1 PE=1 SV=2	1.3E-06	30.2	6.6	4 (4 0 0 0 0)	ND

P05202	AATM_MOUSE Aspartate aminotransferase, mitochondrial OS=Mus musculus GN=Got2 PE=1 SV=1	3.3E-09	60.2	19.1	8 (8 0 0 0 0)	Mitochondrion matrix. Cell membrane.
P55096	ABCD3_MOUSE ATP-binding cassette sub-family D member 3 OS=Mus musculus GN=Abcd3 PE=1 SV=1	4.3E-14	90.2	14.6	9 (9 0 0 0 0)	Peroxisome membrane; Multi-pass membrane protein.
P61222	ABCE1_MOUSE ATP-binding cassette sub-family E member 1 OS=Mus musculus GN=Abce1 PE=2 SV=1	5.5E-09	20.2	4.0	2 (2 0 0 0 0)	Cytoplasm. Mitochondrion.
Q7TMS5	ABCG2_MOUSE ATP-binding cassette sub-family G member 2 OS=Mus musculus GN=Abcg2 PE=2 SV=1	3.6E-08	40.2	6.7	7 (7 0 0 0 0)	Cell membrane; Multi-pass membrane protein.
Q8R2Y0	ABHD6_MOUSE Monoacylglycerol lipase ABHD6 OS=Mus musculus GN=Abhd6 PE=2 SV=1	3.7E-06	20.2	7.4	2 (2 0 0 0 0)	Membrane; Single-pass type II membrane protein.
Q5SSL4	ABR_MOUSE Active breakpoint cluster region-related protein OS=Mus musculus GN=Abr PE=2 SV=1	1.1E-05	30.1	3.6	3 (3 0 0 0 0)	ND
Q5SWU9	ACACA_MOUSE Acetyl-CoA carboxylase 1 OS=Mus musculus GN=Acaca PE=1 SV=1	1.1E-16	570.4	27.5	94 (94 0 0 0 0)	Cytoplasm.
Q8JZN5	ACAD9_MOUSE Acyl-CoA dehydrogenase family member 9, mitochondrial OS=Mus musculus GN=Acad9 PE=2 SV=1	1.5E-10	20.2	4.5	2 (2 0 0 0 0)	Mitochondrion.
P51174	ACADL_MOUSE Long-chain specific acyl-CoA dehydrogenase, mitochondrial OS=Mus musculus GN=Acadl PE=2 SV=2	2.7E-10	50.2	13.3	6 (6 0 0 0 0)	Mitochondrion matrix.
Q07417	ACADS_MOUSE Short-chain specific acyl-CoA dehydrogenase, mitochondrial OS=Mus musculus GN=Acads PE=2 SV=1	5.2E-06	20.2	7.3	2 (2 0 0 0 0)	Mitochondrion matrix.
P50544	ACADV_MOUSE Very long-chain specific acyl-CoA dehydrogenase, mitochondrial OS=Mus musculus GN=Acadvl PE=1	1.6E-11	50.3	12.0	5 (5 0 0 0 0)	Mitochondrion inner membrane.

	SV=3					
Q91V92	ACLY_MOUSE ATP-citrate synthase OS=Mus musculus GN=Acly PE=1 SV=1	6.2E-06	30.2	3.1	3 (3 0 0 0 0)	Cytoplasm.
P13516	ACOD1_MOUSE Acyl-CoA desaturase 1 OS=Mus musculus GN=Scd1 PE=2 SV=2	6.6E-09	20.1	6.2	3 (3 0 0 0 0)	Endoplasmic reticulum membrane; Multi-pass membrane protein.
Q99KI0	ACON_MOUSE Aconitate hydratase, mitochondrial OS=Mus musculus GN=Aco2 PE=1 SV=1	1.1E-16	212.4	27.7	36 (33 2 1 0 0)	Mitochondrion.
Q9CZW4	ACSL3_MOUSE Long-chain-fatty-acid--CoA ligase 3 OS=Mus musculus GN=Acsl3 PE=2 SV=1	2.2E-15	80.2	14.6	9 (9 0 0 0 0)	Mitochondrion outer membrane; Single-pass type III membrane protein. Peroxisome membrane; Single-pass type III membrane protein. Microsome membrane; Single-pass type III membrane protein. Endoplasmic reticulum membrane; Single-pass type III membrane protein.
Q9QUJ7	ACSL4_MOUSE Long-chain-fatty-acid--CoA ligase 4 OS=Mus musculus GN=Acsl4 PE=2 SV=1	1.1E-15	30.2	6.5	5 (5 0 0 0 0)	Mitochondrion outer membrane; Single-pass type III membrane protein. Peroxisome membrane; Single-pass type III membrane protein. Microsome membrane; Single-pass type III membrane protein. Endoplasmic reticulum membrane; Single-pass type III membrane protein.
P62737	ACTA_MOUSE Actin, aortic smooth muscle OS=Mus musculus GN=Acta2 PE=1 SV=1	1.0E-30	286.3	57.6	66 (64 2 0 0 0)	Cytoplasm â€º cytoskeleton.
P60710	ACTB_MOUSE Actin, cytoplasmic 1 OS=Mus	8.3E-14	90.3	24.0	32 (32 0 0 0 0)	Cytoplasm â€º cytoskeleton.

	musculus GN=Actb PE=1 SV=1					
Q8BFZ3	ACTBL_MOUSE Beta-actin-like protein 2 OS=Mus musculus GN=Actbl2 PE=2 SV=1	1.0E-30	46.4	15.7	28 (11 17 0 0 0)	Cytoplasm â€º cytoskeleton.
Q7TPR4	ACTN1_MOUSE Alpha-actinin-1 OS=Mus musculus GN=Actn1 PE=2 SV=1	2.3E-12	190.3	22.3	24 (24 0 0 0 0)	Cytoplasm â€º cytoskeleton. Cytoplasm â€º myofibril â€º sarcomere â€º Z line. Cell membrane. Cell projection â€º ruffle.
Q9JI91	ACTN2_MOUSE Alpha-actinin-2 OS=Mus musculus GN=Actn2 PE=1 SV=1	6.6E-07	20.2	1.1	3 (3 0 0 0 0)	Cytoplasm â€º myofibril â€º sarcomere â€º Z line.
P57780	ACTN4_MOUSE Alpha-actinin-4 OS=Mus musculus GN=Actn4 PE=1 SV=1	1.2E-11	60.3	10.3	7 (7 0 0 0 0)	Nucleus. Cytoplasm.
O35598	ADA10_MOUSE Disintegrin and metalloproteinase domain-containing protein 10 OS=Mus musculus GN=Adam10 PE=1 SV=1	9.4E-09	40.2	5.2	7 (7 0 0 0 0)	Membrane; Single-pass type I membrane protein.
Q9Z0F8	ADA17_MOUSE Disintegrin and metalloproteinase domain-containing protein 17 OS=Mus musculus GN=Adam17 PE=1 SV=2	3.5E-06	20.1	2.4	4 (4 0 0 0 0)	Cell membrane; Single-pass type I membrane protein. Secreted.
Q8VDL4	ADPGK_MOUSE ADP-dependent glucokinase OS=Mus musculus GN=Adpgk PE=1 SV=2	1.7E-10	60.2	14.9	6 (6 0 0 0 0)	Secreted.
P48962	ADT1_MOUSE ADP/ATP translocase 1 OS=Mus musculus GN=Slc25a4 PE=1 SV=4	4.8E-11	108.2	32.9	25 (24 1 0 0 0)	Mitochondrion inner membrane; Multi-pass membrane protein.
P51881	ADT2_MOUSE ADP/ATP translocase 2 OS=Mus musculus GN=Slc25a5 PE=1 SV=3	3.6E-10	48.2	11.4	22 (21 1 0 0 0)	Mitochondrion inner membrane; Multi-pass membrane protein.
Q920A7	AFG31_MOUSE AFG3-like protein 1 OS=Mus musculus GN=Afg3l1 PE=2 SV=2	7.1E-05	30.2	4.1	3 (3 0 0 0 0)	Mitochondrion membrane; Multi-pass membrane protein.
Q8JZQ2	AFG32_MOUSE AFG3-like protein 2 OS=Mus musculus GN=Afg3l2 PE=1 SV=1	4.1E-08	30.1	4.1	3 (3 0 0 0 0)	Mitochondrion membrane; Multi-pass membrane protein.

Q8K2K6	AGFG1_MOUSE Arf-GAP domain and FG repeats-containing protein 1 OS=Mus musculus GN=Agfg1 PE=1 SV=2	3.9E-11	20.2	5.3	2 (2 0 0 0 0)	Nucleus. Cytoplasmic vesicle.
Q9Z0X1	AIFM1_MOUSE Apoptosis-inducing factor 1, mitochondrial OS=Mus musculus GN=Aifm1 PE=1 SV=1	3.9E-12	110.2	23.5	17 (17 0 0 0 0)	Mitochondrion intermembrane space. Mitochondrion inner membrane. Cytoplasm. Cytoplasm â€º perinuclear region. Nucleus.
Q8R010	AIMP2_MOUSE Aminoacyl tRNA synthetase complex-interacting multifunctional protein 2 OS=Mus musculus GN=Aimp2 PE=1 SV=1	9.2E-08	20.2	11.6	3 (3 0 0 0 0)	Cytoplasm â€º cytosol. Nucleus.
Q9DBR0	AKAP8_MOUSE A-kinase anchor protein 8 OS=Mus musculus GN=Akap8 PE=1 SV=1	5.9E-07	30.1	4.9	3 (3 0 0 0 0)	Nucleus matrix.
Q3V0J1	AL2S4_MOUSE Amyotrophic lateral sclerosis 2 chromosomal region candidate gene 4 protein homolog OS=Mus musculus GN=Als2cr4 PE=2 SV=1	1.4E-10	20.2	7.3	2 (2 0 0 0 0)	Membrane; Multi-pass membrane protein.
P47740	AL3A2_MOUSE Fatty aldehyde dehydrogenase OS=Mus musculus GN=Aldh3a2 PE=2 SV=1	3.3E-08	40.2	8.5	4 (4 0 0 0 0)	Endoplasmic reticulum membrane; Single-pass membrane protein; Cytoplasmic side.
P07724	ALBU_MOUSE Serum albumin OS=Mus musculus GN=Alb PE=1 SV=3	5.8E-10	20.2	4.3	30 (30 0 0 0 0)	Secreted.
P47738	ALDH2_MOUSE Aldehyde dehydrogenase, mitochondrial OS=Mus musculus GN=Aldh2 PE=1 SV=1	6.9E-11	70.3	19.7	7 (7 0 0 0 0)	Mitochondrion matrix.
P05064	ALDOA_MOUSE Fructose-bisphosphate aldolase A OS=Mus musculus GN=Aldoa PE=1 SV=2	1.1E-15	50.3	16.5	7 (7 0 0 0 0)	ND
P45376	ALDR_MOUSE Aldose reductase OS=Mus musculus GN=Akr1b1 PE=1 SV=3	1.6E-08	20.2	7.9	2 (2 0 0 0 0)	Cytoplasm.
Q9DB25	ALG5_MOUSE Dolichyl-phosphate beta-glucosyltransferase OS=Mus musculus GN=Alg5 PE=2 SV=1	1.1E-07	30.2	12.3	3 (3 0 0 0 0)	Endoplasmic reticulum membrane; Single-pass type II membrane protein.

Q9CPY7	AMPL_MOUSE Cytosol aminopeptidase OS=Mus musculus GN=Lap3 PE=1 SV=3	4.3E-07	30.2	7.3	3 (3 0 0 0 0)	Cytoplasm.
P55302	AMRP_MOUSE Alpha-2-macroglobulin receptor-associated protein OS=Mus musculus GN=Lrpap1 PE=1 SV=1	2.5E-07	30.2	10.0	3 (3 0 0 0 0)	Endoplasmic reticulum. Cytoplasm. Cell surface.
Q9JHZ2	ANKH_MOUSE Progressive ankylosis protein OS=Mus musculus GN=Ankh PE=2 SV=1	4.6E-10	50.3	11.8	5 (5 0 0 0 0)	Membrane; Multi-pass membrane protein.
Q6P9J9	ANO6_MOUSE Anoctamin-6 OS=Mus musculus GN=Ano6 PE=1 SV=1	1.8E-12	90.2	11.1	19 (19 0 0 0 0)	Membrane; Multi-pass membrane protein.
Q6VVW5	ANPRB_MOUSE Atrial natriuretic peptide receptor B OS=Mus musculus GN=Npr2 PE=2 SV=1	7.8E-12	30.2	4.1	4 (4 0 0 0 0)	Membrane; Single-pass type I membrane protein.
P97384	ANX11_MOUSE Annexin A11 OS=Mus musculus GN=Anxa11 PE=1 SV=1	2.1E-10	88.3	20.3	13 (12 1 0 0 0)	Cytoplasm. Melanosome. Nucleus envelope. Nucleus â€º nucleoplasm. Cytoplasm â€º cytoskeleton â€º spindle.
P10107	ANXA1_MOUSE Annexin A1 OS=Mus musculus GN=Anxa1 PE=1 SV=2	4.2E-14	250.3	55.2	114 (114 0 0 0 0)	Nucleus. Cytoplasm. Cell projection â€º cilium. Basolateral cell membrane.
P07356	ANXA2_MOUSE Annexin A2 OS=Mus musculus GN=Anxa2 PE=1 SV=2	1.1E-15	260.3	53.7	114 (114 0 0 0 0)	Secreted â€º extracellular space â€º extracellular matrix â€º basement membrane. Melanosome.
O35639	ANXA3_MOUSE Annexin A3 OS=Mus musculus GN=Anxa3 PE=2 SV=3	1.2E-14	230.3	54.8	32 (32 0 0 0 0)	ND
P97429	ANXA4_MOUSE Annexin A4 OS=Mus musculus GN=Anxa4 PE=2 SV=3	1.1E-11	140.3	40.1	29 (29 0 0 0 0)	ND
P48036	ANXA5_MOUSE Annexin A5 OS=Mus musculus GN=Anxa5 PE=1 SV=1	2.2E-15	230.3	68.0	65 (65 0 0 0 0)	ND
P14824	ANXA6_MOUSE Annexin A6 OS=Mus musculus GN=Anxa6 PE=1 SV=2	2.2E-16	616.3	58.1	243 (241 2 0 0 0)	Cytoplasm. Melanosome.
Q07076	ANXA7_MOUSE Annexin A7 OS=Mus musculus GN=Anxa7 PE=2 SV=1	4.1E-09	100.2	20.1	13 (13 0 0 0 0)	ND

Q64133	AOFA_MOUSE Amine oxidase [flavin-containing] A OS=Mus musculus GN=Maoa PE=1 SV=2	1.3E-10	40.2	10.3	5 (5 0 0 0 0)	Mitochondrion outer membrane; Single-pass type IV membrane protein; Cytoplasmic side.
O35643	AP1B1_MOUSE AP-1 complex subunit beta-1 OS=Mus musculus GN=Ap1b1 PE=1 SV=1	2.0E-07	30.2	4.1	3 (3 0 0 0 0)	Golgi apparatus. Cytoplasmic vesicle â€º clathrin-coated vesicle membrane; Peripheral membrane protein; Cytoplasmic side. Golgi apparatus.
P22892	AP1G1_MOUSE AP-1 complex subunit gamma-1 OS=Mus musculus GN=Ap1g1 PE=1 SV=3	4.1E-06	20.2	2.4	2 (2 0 0 0 0)	Golgi apparatus. Cytoplasmic vesicle â€º clathrin-coated vesicle membrane; Peripheral membrane protein; Cytoplasmic side.
P17426	AP2A1_MOUSE AP-2 complex subunit alpha-1 OS=Mus musculus GN=Ap2a1 PE=1 SV=1	1.3E-11	118.3	12.3	12 (11 1 0 0 0)	Cell membrane. Membrane â€º coated pit; Peripheral membrane protein; Cytoplasmic side.
P17427	AP2A2_MOUSE AP-2 complex subunit alpha-2 OS=Mus musculus GN=Ap2a2 PE=1 SV=1	8.7E-10	60.2	8.3	6 (6 0 0 0 0)	Cell membrane. Membrane â€º coated pit; Peripheral membrane protein; Cytoplasmic side.
Q9DBG3	AP2B1_MOUSE AP-2 complex subunit beta OS=Mus musculus GN=Ap2b1 PE=1 SV=1	7.8E-15	30.2	4.4	3 (3 0 0 0 0)	Cell membrane. Membrane â€º coated pit; Peripheral membrane protein; Cytoplasmic side.
Q9D7N9	APMAP_MOUSE Adipocyte plasma membrane-associated protein OS=Mus musculus GN=Apmap PE=1 SV=1	1.3E-06	40.2	12.0	5 (5 0 0 0 0)	Membrane; Single-pass type II membrane protein.
Q78IK4	APOOL_MOUSE Apolipoprotein O-like OS=Mus musculus GN=Apool PE=2 SV=1	3.1E-08	30.2	10.2	3 (3 0 0 0 0)	Secreted.
P84078	ARF1_MOUSE ADP-ribosylation factor 1 OS=Mus musculus GN=Arf1 PE=1 SV=2	5.2E-10	50.2	24.3	5 (5 0 0 0 0)	Golgi apparatus. Cytoplasm â€º perinuclear region.
Q60875	ARHG2_MOUSE Rho guanine nucleotide exchange factor 2 OS=Mus musculus	1.8E-08	30.1	3.1	5 (5 0 0 0 0)	Cytoplasm. Cell junction â€º tight junction. Golgi

	GN=Arhgef2 PE=1 SV=3					apparatus. Cytoplasm â€º cytoskeleton â€º spindle.
P59999	ARPC4_MOUSE Actin-related protein 2/3 complex subunit 4 OS=Mus musculus GN=Arpc4 PE=1 SV=3	9.8E-06	20.1	11.9	4 (4 0 0 0 0)	Cytoplasm â€º cytoskeleton. Cell projection.
P58242	ASM3B_MOUSE Acid sphingomyelinase-like phosphodiesterase 3b OS=Mus musculus GN=Smpdl3b PE=1 SV=1	5.4E-14	100.2	27.9	23 (23 0 0 0 0)	Secreted.
Q61024	ASNS_MOUSE Asparagine synthetase [glutamine-hydrolyzing] OS=Mus musculus GN=Asns PE=2 SV=3	2.5E-08	20.2	6.2	2 (2 0 0 0 0)	ND
Q8BSY0	ASPH_MOUSE Aspartyl/asparaginyl beta-hydroxylase OS=Mus musculus GN=Asph PE=2 SV=1	4.0E-14	60.2	10.5	8 (8 0 0 0 0)	Endoplasmic reticulum membrane; Single-pass type II membrane protein.
P16460	ASSY_MOUSE Argininosuccinate synthase OS=Mus musculus GN=Ass1 PE=1 SV=1	2.4E-07	20.2	7.3	2 (2 0 0 0 0)	ND
Q9Z1W8	AT12A_MOUSE Potassium-transporting ATPase alpha chain 2 OS=Mus musculus GN=Atp12a PE=1 SV=2	8.8E-11	20.2	1.3	12 (12 0 0 0 0)	Membrane; Multi-pass membrane protein.
Q9EPE9	AT131_MOUSE Probable cation-transporting ATPase 13A1 OS=Mus musculus GN=Atp13a1 PE=1 SV=1	2.4E-07	60.2	5.9	6 (6 0 0 0 0)	Membrane; Multi-pass membrane protein.
Q8VDN2	AT1A1_MOUSE Sodium/potassium-transporting ATPase subunit alpha-1 OS=Mus musculus GN=Atp1a1 PE=1 SV=1	1.3E-14	300.3	29.6	190 (190 0 0 0 0)	Cell membrane; Multi-pass membrane protein.
Q9WV27	AT1A4_MOUSE Sodium/potassium-transporting ATPase subunit alpha-4 OS=Mus musculus GN=Atp1a4 PE=1 SV=2	4.3E-07	16.2	1.6	2 (0 2 0 0 0)	Cell membrane; Multi-pass membrane protein.
P97370	AT1B3_MOUSE Sodium/potassium-transporting ATPase subunit beta-3 OS=Mus musculus GN=Atp1b3 PE=1 SV=1	1.0E-10	50.2	16.9	15 (15 0 0 0 0)	Membrane; Single-pass type II membrane protein. Melanosome.
Q8R429	AT2A1_MOUSE Sarcoplasmic/endoplasmic reticulum calcium ATPase 1 OS=Mus musculus GN=Atp2a1 PE=2 SV=1	4.3E-14	110.3	8.9	27 (27 0 0 0 0)	Endoplasmic reticulum membrane; Multi-pass membrane protein.

						Sarcoplasmic reticulum membrane; Multi-pass membrane protein.
O55143	AT2A2_MOUSE Sarcoplasmic/endoplasmic reticulum calcium ATPase 2 OS=Mus musculus GN=Atp2a2 PE=1 SV=2	1.2E-14	190.3	16.5	32 (32 0 0 0 0)	Endoplasmic reticulum membrane; Multi-pass membrane protein. Sarcoplasmic reticulum membrane; Multi-pass membrane protein.
Q9R0K7	AT2B2_MOUSE Plasma membrane calcium-transporting ATPase 2 OS=Mus musculus GN=Atp2b2 PE=1 SV=2	1.1E-10	130.3	5.8	35 (35 0 0 0 0)	Cell membrane; Multi-pass membrane protein.
Q9CQQ7	AT5F1_MOUSE ATP synthase subunit b, mitochondrial OS=Mus musculus GN=Atp5f1 PE=1 SV=1	2.6E-08	98.2	40.2	10 (9 1 0 0 0)	Mitochondrion. Mitochondrion inner membrane.
Q9D5T0	ATAD1_MOUSE ATPase family AAA domain-containing protein 1 OS=Mus musculus GN=Atad1 PE=1 SV=1	3.3E-05	18.2	5.8	2 (1 1 0 0 0)	Peroxisome.
Q925I1	ATAD3_MOUSE ATPase family AAA domain-containing protein 3 OS=Mus musculus GN=Atad3 PE=1 SV=1	1.9E-06	80.2	14.9	9 (9 0 0 0 0)	ND
Q6PA06	ATLA2_MOUSE Atlastin-2 OS=Mus musculus GN=Atl2 PE=1 SV=1	1.8E-09	40.3	8.6	4 (4 0 0 0 0)	Endoplasmic reticulum membrane; Multi-pass membrane protein.
Q91YH5	ATLA3_MOUSE Atlastin-3 OS=Mus musculus GN=Atl3 PE=2 SV=1	9.0E-13	100.3	20.1	10 (10 0 0 0 0)	Endoplasmic reticulum membrane; Multi-pass membrane protein.
Q9DCX2	ATP5H_MOUSE ATP synthase subunit d, mitochondrial OS=Mus musculus GN=Atp5h PE=1 SV=3	1.1E-11	70.2	43.5	15 (15 0 0 0 0)	Mitochondrion. Mitochondrion inner membrane.
Q64430	ATP7A_MOUSE Copper-transporting ATPase 1 OS=Mus musculus GN=Atp7a PE=1 SV=2	2.7E-06	20.1	1.3	3 (3 0 0 0 0)	Golgi apparatus â€º trans-Golgi network membrane; Multi-pass membrane

						protein. Cell membrane; Multi-pass membrane protein.
Q03265	ATPA_MOUSE ATP synthase subunit alpha, mitochondrial OS=Mus musculus GN=Atp5a1 PE=1 SV=1	3.3E-15	220.3	48.1	42 (42 0 0 0 0)	Mitochondrion inner membrane. Cell membrane; Peripheral membrane protein; Extracellular side.
P56480	ATPB_MOUSE ATP synthase subunit beta, mitochondrial OS=Mus musculus GN=Atp5b PE=1 SV=2	1.0E-30	268.3	59.7	36 (35 1 0 0 0)	Mitochondrion. Mitochondrion inner membrane.
Q9D3D9	ATPD_MOUSE ATP synthase subunit delta, mitochondrial OS=Mus musculus GN=Atp5d PE=1 SV=1	8.7E-11	40.2	20.2	6 (6 0 0 0 0)	Mitochondrion. Mitochondrion inner membrane.
Q91VR2	ATPG_MOUSE ATP synthase subunit gamma, mitochondrial OS=Mus musculus GN=Atp5c1 PE=1 SV=1	2.6E-12	70.2	24.2	9 (9 0 0 0 0)	Mitochondrion. Mitochondrion inner membrane; Peripheral membrane protein.
Q9DB20	ATPO_MOUSE ATP synthase subunit O, mitochondrial OS=Mus musculus GN=Atp5o PE=1 SV=1	4.8E-10	60.2	30.5	11 (11 0 0 0 0)	Mitochondrion. Mitochondrion inner membrane.
P70295	AUP1_MOUSE Ancient ubiquitous protein 1 OS=Mus musculus GN=Aup1 PE=2 SV=1	5.9E-11	30.3	11.7	3 (3 0 0 0 0)	Endoplasmic reticulum membrane; Single-pass type III membrane protein; Cytoplasmic side.
P01887	B2MG_MOUSE Beta-2-microglobulin OS=Mus musculus GN=B2m PE=1 SV=1	5.8E-07	20.2	16.0	10 (10 0 0 0 0)	Secreted.
O08734	BAK_MOUSE Bcl-2 homologous antagonist/killer OS=Mus musculus GN=Bak1 PE=1 SV=1	2.4E-09	20.2	10.1	3 (3 0 0 0 0)	Mitochondrion membrane; Single-pass membrane protein.
Q61335	BAP31_MOUSE B-cell receptor-associated protein 31 OS=Mus musculus GN=Bcap31 PE=1 SV=3	1.0E-30	188.4	36.3	30 (29 1 0 0 0)	Endoplasmic reticulum membrane; Multi-pass membrane protein. Endoplasmic reticulum-Golgi intermediate compartment membrane; Multi-pass membrane

						protein.
P18572	BASI_MOUSE Basigin OS=Mus musculus GN=Bsg PE=1 SV=2	2.2E-14	80.2	21.6	32 (32 0 0 0 0)	Cell membrane; Single-pass type I membrane protein. Melanosome.
Q91XV3	BASP1_MOUSE Brain acid soluble protein 1 OS=Mus musculus GN=Basp1 PE=1 SV=3	7.8E-15	100.3	69.0	22 (22 0 0 0 0)	Cell membrane; Lipid-anchor. Cell projection â€º growth cone.
Q9Z1R2	BAT3_MOUSE Large proline-rich protein BAT3 OS=Mus musculus GN=Bat3 PE=1 SV=1	1.8E-07	30.2	3.2	3 (3 0 0 0 0)	Cytoplasm â€º cytosol. Nucleus.
Q91ZU6	BPA1_MOUSE Bullous pemphigoid antigen 1, isoforms 1/2/3/4 OS=Mus musculus GN=Dst PE=1 SV=1	3.1E-09	40.2	0.5	4 (4 0 0 0 0)	Cytoplasm â€º cytoskeleton. Cell projection â€º axon. Membrane. Cytoplasm â€º cytoskeleton. Cell membrane â€º sarcolemma. Cytoplasm â€º myofibril â€º sarcomere â€º Z line. Cytoplasm â€º myofibril â€º sarcomere â€º H zone. Cytoplasm â€º cytoskeleton. Cytoplasm â€º cytoskeleton. Cell junction â€º hemidesmosome. Nucleus. Nucleus envelope. Membrane; Single-pass membrane protein. Endoplasmic reticulum membrane; Single-pass membrane protein. Cytoplasm â€º cytoskeleton. Cytoplasm â€º cytoskeleton. Cytoplasm â€º cell cortex. Cell membrane; Lipid-anchor.

Q8BXV2	BRI3B_MOUSE BRI3-binding protein OS=Mus musculus GN=Bri3bp PE=2 SV=1	3.6E-11	30.3	11.5	5 (5 0 0 0 0)	Mitochondrion outer membrane; Multi-pass membrane protein.
Q8R2Q8	BST2_MOUSE Bone marrow stromal antigen 2 OS=Mus musculus GN=Bst2 PE=1 SV=1	1.9E-13	50.3	17.4	29 (29 0 0 0 0)	Cell membrane; Lipid-anchor â€º GPI-anchor. Cell membrane; Single-pass type II membrane protein. Golgi apparatus â€º trans-Golgi network.
O35658	C1QBP_MOUSE Complement component 1 Q subcomponent-binding protein, mitochondrial OS=Mus musculus GN=C1qbp PE=1 SV=1	2.1E-12	30.2	10.1	3 (3 0 0 0 0)	Mitochondrion matrix.
Q3V3R1	C1TM_MOUSE Monofunctional C1-tetrahydrofolate synthase, mitochondrial OS=Mus musculus GN=Mthfd1l PE=1 SV=2	8.9E-10	100.2	10.4	11 (11 0 0 0 0)	Mitochondrion.
Q3V3R1	C1TM_MOUSE Monofunctional C1-tetrahydrofolate synthase, mitochondrial OS=Mus musculus GN=Mthfd1l PE=1 SV=2	3.8E-08	30.1	3.8	3 (3 0 0 0 0)	Mitochondrion.
O08532	CA2D1_MOUSE Voltage-dependent calcium channel subunit alpha-2/delta-1 OS=Mus musculus GN=Cacna2d1 PE=1 SV=1	1.4E-13	80.3	9.9	10 (10 0 0 0 0)	Membrane; Single-pass type I membrane protein.
Q8CGU1	CACO1_MOUSE Calcium-binding and coiled-coil domain-containing protein 1 OS=Mus musculus GN=Calcoco1 PE=1 SV=2	1.5E-06	30.2	5.2	3 (3 0 0 0 0)	Cytoplasm. Nucleus.
Q8CGU1	CACO1_MOUSE Calcium-binding and coiled-coil domain-containing protein 1 OS=Mus musculus GN=Calcoco1 PE=1 SV=2	6.7E-07	50.2	8.5	7 (7 0 0 0 0)	Cytoplasm. Nucleus.
P55288	CAD11_MOUSE Cadherin-11 OS=Mus musculus GN=Cdh11 PE=1 SV=1	2.2E-07	70.2	10.3	8 (8 0 0 0 0)	Cell membrane; Single-pass type I membrane protein.
Q9WTR5	CAD13_MOUSE Cadherin-13 OS=Mus musculus GN=Cdh13 PE=2 SV=1	1.5E-09	30.2	5.2	3 (3 0 0 0 0)	Cell membrane; Lipid-anchor â€º GPI-anchor.
P33146	CAD15_MOUSE Cadherin-15 OS=Mus musculus GN=Cdh15 PE=1 SV=2	1.4E-12	170.3	29.5	61 (61 0 0 0 0)	Cell membrane; Single-pass type I membrane protein.

P15116	CADH2_MOUSE Cadherin-2 OS=Mus musculus GN=Cdh2 PE=1 SV=1	4.7E-14	90.3	15.6	27 (27 0 0 0 0)	Cell membrane; Single-pass type I membrane protein.
Q9D6P8	CALL3_MOUSE Calmodulin-like protein 3 OS=Mus musculus GN=Calml3 PE=2 SV=1	8.6E-06	20.2	8.1	3 (3 0 0 0 0)	ND
P62204	CALM_MOUSE Calmodulin OS=Mus musculus GN=Calm1 PE=1 SV=2	1.6E-12	20.3	25.5	4 (4 0 0 0 0)	Cytoplasm â€º cytoskeleton â€º spindle. Cytoplasm â€º cytoskeleton â€º spindle pole.
P14211	CALR_MOUSE Calreticulin OS=Mus musculus GN=Calr PE=1 SV=1	8.7E-12	130.3	32.5	29 (29 0 0 0 0)	Endoplasmic reticulum lumen. Cytoplasmic granule.
O35887	CALU_MOUSE Calumenin OS=Mus musculus GN=Calu PE=1 SV=1	3.4E-10	70.2	22.5	12 (12 0 0 0 0)	Endoplasmic reticulum lumen. Melanosome. Sarcoplasmic reticulum lumen. Secreted.
P35564	CALX_MOUSE Calnexin OS=Mus musculus GN=Canx PE=1 SV=1	1.3E-14	210.2	29.3	85 (85 0 0 0 0)	Endoplasmic reticulum membrane; Single-pass type I membrane protein. Melanosome.
O08529	CAN2_MOUSE Calpain-2 catalytic subunit OS=Mus musculus GN=Capn2 PE=2 SV=4	7.6E-08	30.2	5.6	4 (4 0 0 0 0)	Cytoplasm. Cell membrane.
Q6ZQ38	CAND1_MOUSE Cullin-associated NEDD8-dissociated protein 1 OS=Mus musculus GN=Cand1 PE=2 SV=2	2.7E-07	80.2	8.2	8 (8 0 0 0 0)	Nucleus.
P40124	CAP1_MOUSE Adenylyl cyclase-associated protein 1 OS=Mus musculus GN=Cap1 PE=1 SV=3	3.0E-06	30.2	8.4	3 (3 0 0 0 0)	Cell membrane; Peripheral membrane protein.
Q60865	CAPR1_MOUSE Caprin-1 OS=Mus musculus GN=Caprin1 PE=1 SV=2	1.2E-06	40.2	6.1	4 (4 0 0 0 0)	Cytoplasm â€º cytosol. Cell projection â€º dendrite.
P70403	CASP_MOUSE Protein CASP OS=Mus musculus GN=Cux1 PE=2 SV=2	1.3E-11	50.2	10.0	6 (6 0 0 0 0)	Golgi apparatus membrane; Single-pass type IV membrane protein.
P49817	CAV1_MOUSE Caveolin-1 OS=Mus musculus GN=Cav1 PE=1 SV=1	3.8E-10	40.2	27.0	11 (11 0 0 0 0)	Golgi apparatus membrane; Peripheral membrane protein. Cell membrane; Peripheral

						membrane protein. Membrane â€º caveola; Peripheral membrane protein. Membrane raft.
O89001	CBPD_MOUSE Carboxypeptidase D OS=Mus musculus GN=Cpd PE=1 SV=1	4.4E-13	90.3	7.6	10 (10 0 0 0 0)	Membrane; Single-pass type I membrane protein.
Q3U4G3	CC021_MOUSE Uncharacterized protein C3orf21 homolog OS=Mus musculus PE=2 SV=1	6.5E-05	20.1	2.6	3 (3 0 0 0 0)	Membrane; Single-pass membrane protein.
Q3USZ8	CC058_MOUSE UPF0672 protein C3orf58 homolog OS=Mus musculus PE=2 SV=1	3.1E-08	20.2	6.1	2 (2 0 0 0 0)	Secreted.
Q9D024	CC47_MOUSE Coiled-coil domain-containing protein 47 OS=Mus musculus GN=Ccdc47 PE=2 SV=2	4.7E-08	140.2	35.6	15 (15 0 0 0 0)	Membrane; Single-pass membrane protein.
Q8BGU5	CCNY_MOUSE Cyclin-Y OS=Mus musculus GN=Ccny PE=1 SV=1	6.0E-05	20.2	9.4	2 (2 0 0 0 0)	Cell membrane; Lipid-anchor; Cytoplasmic side.
O35566	CD151_MOUSE CD151 antigen OS=Mus musculus GN=Cd151 PE=2 SV=2	3.0E-09	20.2	9.1	6 (6 0 0 0 0)	Membrane; Multi-pass membrane protein.
Q61490	CD166_MOUSE CD166 antigen OS=Mus musculus GN=Alcam PE=1 SV=3	2.3E-11	60.3	11.7	8 (8 0 0 0 0)	Membrane; Single-pass type I membrane protein.
P51480	CD2A1_MOUSE Cyclin-dependent kinase inhibitor 2A, isoforms 1/2 OS=Mus musculus GN=Cdkn2a PE=1 SV=2	1.6E-07	20.2	15.5	3 (3 0 0 0 0)	Cytoplasm. Nucleus.
P15379	CD44_MOUSE CD44 antigen OS=Mus musculus GN=Cd44 PE=1 SV=3	1.1E-09	60.2	5.3	26 (26 0 0 0 0)	Membrane; Single-pass type I membrane protein.
Q61735	CD47_MOUSE Leukocyte surface antigen CD47 OS=Mus musculus GN=Cd47 PE=1 SV=2	1.6E-11	20.2	8.9	6 (6 0 0 0 0)	Cell membrane; Multi-pass membrane protein.
P41731	CD63_MOUSE CD63 antigen OS=Mus musculus GN=Cd63 PE=1 SV=2	8.4E-09	20.2	8.8	10 (10 0 0 0 0)	Cell membrane; Multi-pass membrane protein. Lysosome membrane; Multi-pass membrane protein. Late endosome membrane; Multi-pass membrane protein.

P35762	CD81_MOUSE CD81 antigen OS=Mus musculus GN=Cd81 PE=1 SV=1	2.6E-13	40.3	9.7	11 (11 0 0 0 0)	Membrane; Multi-pass membrane protein.
P40237	CD82_MOUSE CD82 antigen OS=Mus musculus GN=Cd82 PE=1 SV=1	9.8E-08	30.2	12.8	7 (7 0 0 0 0)	Membrane; Multi-pass membrane protein.
P40240	CD9_MOUSE CD9 antigen OS=Mus musculus GN=Cd9 PE=1 SV=2	1.2E-07	20.2	10.2	7 (7 0 0 0 0)	Membrane; Multi-pass membrane protein.
Q9Z0M6	CD97_MOUSE CD97 antigen OS=Mus musculus GN=Cd97 PE=1 SV=2	4.4E-12	70.3	13.7	18 (18 0 0 0 0)	Cell membrane; Multi-pass membrane protein.
P11440	CDC2_MOUSE Cell division control protein 2 homolog OS=Mus musculus GN=Cdc2 PE=1 SV=3	1.2E-10	90.2	33.3	9 (9 0 0 0 0)	Nucleus.
P60766	CDC42_MOUSE Cell division control protein 42 homolog OS=Mus musculus GN=Cdc42 PE=1 SV=1	2.3E-09	20.2	11.0	8 (8 0 0 0 0)	Cell membrane; Lipid-anchor; Cytoplasmic side. Cytoplasm â€º cytoskeleton â€º centrosome.
Q8VDP6	CDIPT_MOUSE CDP-diacylglycerol--inositol 3-phosphatidyltransferase OS=Mus musculus GN=Cdipt PE=1 SV=1	1.1E-10	50.2	16.0	8 (8 0 0 0 0)	Endoplasmic reticulum membrane; Multi-pass membrane protein. Golgi apparatus membrane; Multi-pass membrane protein. Cell membrane; Multi-pass membrane protein.
P63038	CH60_MOUSE 60 kDa heat shock protein, mitochondrial OS=Mus musculus GN=Hspd1 PE=1 SV=1	1.0E-30	300.3	52.4	67 (67 0 0 0 0)	Mitochondrion matrix.
Q9CRB9	CHCH3_MOUSE Coiled-coil-helix-coiled-coil-helix domain-containing protein 3, mitochondrial OS=Mus musculus GN=Chchd3 PE=1 SV=1	1.1E-07	60.2	16.3	7 (7 0 0 0 0)	Mitochondrion inner membrane; Lipid-anchor; Intermembrane side.
Q9D8B3	CHM4B_MOUSE Charged multivesicular body protein 4b OS=Mus musculus GN=Chmp4b PE=2 SV=2	2.1E-06	30.2	15.6	5 (5 0 0 0 0)	Cytoplasm â€º cytosol. Late endosome membrane; Peripheral membrane protein.
P0C0A3	CHMP6_MOUSE Charged multivesicular body protein 6 OS=Mus musculus GN=Chmp6 PE=2 SV=2	1.7E-09	20.2	10.5	2 (2 0 0 0 0)	Endomembrane system. Endosome membrane; Lipid-anchor. Late endosome

						membrane.
P61022	CHP1_MOUSE Calcium-binding protein p22 OS=Mus musculus GN=Chp PE=2 SV=2	3.2E-13	70.3	44.6	9 (9 0 0 0 0)	Cytoplasm.
Q9CZU6	CISY_MOUSE Citrate synthase, mitochondrial OS=Mus musculus GN=Cs PE=1 SV=1	7.5E-10	80.2	17.2	8 (8 0 0 0 0)	Mitochondrion matrix.
Q8BMK4	CKAP4_MOUSE Cytoskeleton-associated protein 4 OS=Mus musculus GN=Ckap4 PE=2 SV=2	1.0E-30	338.3	53.6	88 (87 1 0 0 0)	Endoplasmic reticulum-Golgi intermediate compartment membrane; Single-pass membrane protein.
A2AGT5	CKAP5_MOUSE Cytoskeleton-associated protein 5 OS=Mus musculus GN=Ckap5 PE=2 SV=1	1.6E-06	20.2	1.3	2 (2 0 0 0 0)	ND
Q9WVD4	CLCN5_MOUSE H(+)/Cl(-) exchange transporter 5 OS=Mus musculus GN=Clcn5 PE=2 SV=1	3.3E-14	20.2	3.8	3 (3 0 0 0 0)	Golgi apparatus membrane; Multi-pass membrane protein. Endosome membrane; Multi-pass membrane protein. Cell membrane; Multi-pass membrane protein.
Q9CQX5	CLDN1_MOUSE Claudin domain-containing protein 1 OS=Mus musculus GN=Cldnd1 PE=1 SV=1	2.0E-11	20.3	8.7	3 (3 0 0 0 0)	Membrane; Multi-pass membrane protein.
Q68FD5	CLH_MOUSE Clathrin heavy chain 1 OS=Mus musculus GN=Cltc PE=1 SV=3	5.4E-14	420.3	31.5	75 (75 0 0 0 0)	Cytoplasmic vesicle membrane; Peripheral membrane protein; Cytoplasmic side. Membrane â€º coated pit; Peripheral membrane protein; Cytoplasmic side. Melanosome.
Q9Z1Q5	CLIC1_MOUSE Chloride intracellular channel protein 1 OS=Mus musculus GN=Clic1 PE=1 SV=3	7.3E-10	20.2	12.4	2 (2 0 0 0 0)	Nucleus. Nucleus membrane; Single-pass membrane protein. Cytoplasm. Cell membrane; Single-pass membrane protein.

Q8VBZ3	CLPT1_MOUSE Cleft lip and palate transmembrane protein 1 homolog OS=Mus musculus GN=Clptm1 PE=1 SV=1	1.8E-12	60.2	11.4	13 (13 0 0 0 0)	Membrane; Multi-pass membrane protein.
Q8BH59	CMC1_MOUSE Calcium-binding mitochondrial carrier protein Aralar1 OS=Mus musculus GN=Slc25a12 PE=1 SV=1	4.7E-14	40.2	9.6	4 (4 0 0 0 0)	Mitochondrion inner membrane; Multi-pass membrane protein.
Q08093	CNN2_MOUSE Calponin-2 OS=Mus musculus GN=Cnn2 PE=2 SV=1	1.1E-06	20.1	6.9	3 (3 0 0 0 0)	ND
Q9QXT0	CNPY2_MOUSE Protein canopy homolog 2 OS=Mus musculus GN=Cnpy2 PE=2 SV=1	3.6E-12	20.2	15.4	3 (3 0 0 0 0)	Endoplasmic reticulum.
Q9EP72	CO024_MOUSE UPF0480 protein C15orf24 homolog OS=Mus musculus GN=ORF3 PE=2 SV=1	3.4E-10	30.1	16.2	5 (5 0 0 0 0)	Membrane; Single-pass type I membrane protein.
Q01149	CO1A2_MOUSE Collagen alpha-2(I) chain OS=Mus musculus GN=Col1a2 PE=2 SV=2	2.2E-16	160.3	20.9	16 (16 0 0 0 0)	Secreted â€º extracellular space â€º extracellular matrix.
P08121	CO3A1_MOUSE Collagen alpha-1(III) chain OS=Mus musculus GN=Col3a1 PE=2 SV=4	2.2E-15	110.3	11.7	14 (14 0 0 0 0)	Secreted â€º extracellular space â€º extracellular matrix.
O88207	CO5A1_MOUSE Collagen alpha-1(V) chain OS=Mus musculus GN=Col5a1 PE=2 SV=2	9.3E-06	20.2	1.6	4 (4 0 0 0 0)	Secreted â€º extracellular space â€º extracellular matrix.
Q3U962	CO5A2_MOUSE Collagen alpha-2(V) chain OS=Mus musculus GN=Col5a2 PE=1 SV=1	2.1E-09	20.1	2.2	2 (2 0 0 0 0)	Secreted â€º extracellular space â€º extracellular matrix.
Q60847	COCA1_MOUSE Collagen alpha-1(XII) chain OS=Mus musculus GN=Col12a1 PE=2 SV=3	1.3E-10	180.2	6.3	18 (18 0 0 0 0)	Secreted â€º extracellular space â€º extracellular matrix.
P18760	COF1_MOUSE Cofilin-1 OS=Mus musculus GN=Cfl1 PE=1 SV=3	5.2E-12	40.3	42.2	6 (6 0 0 0 0)	Nucleus matrix. Cytoplasm â€º cytoskeleton. Cell projection â€º ruffle membrane; Peripheral membrane protein; Cytoplasmic side. Cell projection â€º lamellipodium membrane; Peripheral membrane protein; Cytoplasmic side.

Q8K4Q8	COL12_MOUSE Collectin-12 OS=Mus musculus GN=Colec12 PE=1 SV=1	3.4E-08	30.2	5.1	3 (3 0 0 0 0)	Membrane; Single-pass type II membrane protein.
Q8CIE6	COPA_MOUSE Coatomer subunit alpha OS=Mus musculus GN=Copa PE=1 SV=1	3.3E-10	80.2	7.3	9 (9 0 0 0 0)	Cytoplasm. Golgi apparatus membrane; Peripheral membrane protein; Cytoplasmic side. Cytoplasmic vesicle â€º COPI-coated vesicle membrane; Peripheral membrane protein; Cytoplasmic side. Secreted.
Q9JIF7	COPB_MOUSE Coatomer subunit beta OS=Mus musculus GN=Copb1 PE=1 SV=1	4.1E-10	60.2	7.6	6 (6 0 0 0 0)	Cytoplasm. Golgi apparatus membrane; Peripheral membrane protein; Cytoplasmic side. Cytoplasmic vesicle â€º COPI-coated vesicle membrane; Peripheral membrane protein; Cytoplasmic side. Cell membrane. Endoplasmic reticulum-Golgi intermediate compartment.
O55029	COPB2_MOUSE Coatomer subunit beta' OS=Mus musculus GN=Copb2 PE=2 SV=2	4.4E-11	30.2	4.2	3 (3 0 0 0 0)	Cytoplasm. Golgi apparatus membrane; Peripheral membrane protein; Cytoplasmic side. Cytoplasmic vesicle â€º COPI-coated vesicle membrane; Peripheral membrane protein; Cytoplasmic side.
Q9QZE5	COPG_MOUSE Coatomer subunit gamma OS=Mus musculus GN=Copg PE=2 SV=1	1.4E-07	30.2	5.9	4 (4 0 0 0 0)	Cytoplasm. Golgi apparatus membrane; Peripheral membrane protein; Cytoplasmic side. Cytoplasmic

						vesicle â€º COPI-coated vesicle membrane; Peripheral membrane protein; Cytoplasmic side.
Q9WUM4	COR1C_MOUSE Coronin-1C OS=Mus musculus GN=Coro1c PE=1 SV=2	2.0E-11	20.2	6.1	4 (4 0 0 0 0)	ND
P00405	COX2_MOUSE Cytochrome c oxidase subunit 2 OS=Mus musculus GN=Mtco2 PE=1 SV=1	3.6E-14	48.3	23.3	8 (7 1 0 0 0)	Mitochondrion inner membrane; Multi-pass membrane protein.
P19783	COX41_MOUSE Cytochrome c oxidase subunit 4 isoform 1, mitochondrial OS=Mus musculus GN=Cox4i1 PE=1 SV=2	2.3E-13	40.2	26.6	7 (7 0 0 0 0)	Mitochondrion inner membrane.
P12787	COX5A_MOUSE Cytochrome c oxidase subunit 5A, mitochondrial OS=Mus musculus GN=Cox5a PE=1 SV=2	9.8E-07	30.2	12.3	3 (3 0 0 0 0)	Mitochondrion inner membrane.
P19536	COX5B_MOUSE Cytochrome c oxidase subunit 5B, mitochondrial OS=Mus musculus GN=Cox5b PE=1 SV=1	2.7E-05	20.2	8.6	3 (3 0 0 0 0)	Mitochondrion inner membrane.
Q8BKE6	CP20A_MOUSE Cytochrome P450 20A1 OS=Mus musculus GN=Cyp20a1 PE=2 SV=1	3.2E-09	40.2	9.7	4 (4 0 0 0 0)	Membrane; Single-pass membrane protein.
Q8K0C4	CP51A_MOUSE Lanosterol 14-alpha demethylase OS=Mus musculus GN=Cyp51a1 PE=2 SV=1	5.8E-12	100.2	25.0	11 (11 0 0 0 0)	Endoplasmic reticulum membrane. Microsome membrane.
Q8C166	CPNE1_MOUSE Copine-1 OS=Mus musculus GN=Cpne1 PE=1 SV=1	1.1E-09	80.2	17.9	17 (17 0 0 0 0)	ND
P59108	CPNE2_MOUSE Copine-2 OS=Mus musculus GN=Cpne2 PE=2 SV=1	8.6E-12	40.2	9.9	5 (5 0 0 0 0)	ND
Q8BT60	CPNE3_MOUSE Copine-3 OS=Mus musculus GN=Cpne3 PE=1 SV=2	6.8E-12	40.2	8.1	4 (4 0 0 0 0)	ND
Q9CQF3	CPSF5_MOUSE Cleavage and polyadenylation specificity factor subunit 5 OS=Mus musculus GN=Nudt21 PE=2 SV=1	1.2E-04	20.1	7.5	2 (2 0 0 0 0)	Nucleus.
Q9D136	CQ101_MOUSE PKHD domain-containing transmembrane protein	1.7E-06	20.1	5.7	2 (2 0 0 0 0)	Membrane; Single-pass type II membrane protein.

	C17orf101 homolog OS=Mus musculus PE=2 SV=1					
P23927	CRYAB_MOUSE Alpha-crystallin B chain OS=Mus musculus GN=Cryab PE=1 SV=2	1.4E-11	40.2	18.3	4 (4 0 0 0 0)	Cytoplasm. Nucleus.
O70589	CSKP_MOUSE Peripheral plasma membrane protein CASK OS=Mus musculus GN=Cask PE=1 SV=2	4.1E-06	40.2	5.0	5 (5 0 0 0 0)	Nucleus. Cytoplasm. Cell membrane; Peripheral membrane protein.
P58466	CTDS1_MOUSE Carboxy-terminal domain RNA polymerase II polypeptide A small phosphatase 1 OS=Mus musculus GN=Ctdsp1 PE=1 SV=1	7.3E-05	20.2	7.3	3 (3 0 0 0 0)	Nucleus.
Q6X893	CTL1_MOUSE Choline transporter-like protein 1 OS=Mus musculus GN=Slc44a1 PE=1 SV=2	1.1E-10	30.2	6.3	3 (3 0 0 0 0)	Cell membrane; Multi-pass membrane protein. Mitochondrion outer membrane; Multi-pass membrane protein.
Q8BY89	CTL2_MOUSE Choline transporter-like protein 2 OS=Mus musculus GN=Slc44a2 PE=1 SV=1	4.3E-10	60.2	7.8	15 (15 0 0 0 0)	Membrane; Multi-pass membrane protein.
P26231	CTNA1_MOUSE Catenin alpha-1 OS=Mus musculus GN=Ctnna1 PE=1 SV=1	6.7E-15	290.3	36.0	67 (67 0 0 0 0)	Cytoplasm â€º cytoskeleton. Cell junction â€º adherens junction. Cell membrane; Peripheral membrane protein; Cytoplasmic side. Cell junction.
Q02248	CTNB1_MOUSE Catenin beta-1 OS=Mus musculus GN=Ctnnb1 PE=1 SV=1	1.0E-30	190.3	24.6	43 (43 0 0 0 0)	Cytoplasm. Cytoplasm â€º cytoskeleton. Nucleus. Cell junction â€º adherens junction. Cell junction. Cell membrane.
P30999	CTND1_MOUSE Catenin delta-1 OS=Mus musculus GN=Ctnnd1 PE=1 SV=2	7.1E-14	260.3	25.9	56 (56 0 0 0 0)	Cytoplasm. Nucleus. Cell membrane.
Q09143	CTR1_MOUSE High affinity cationic amino acid transporter 1 OS=Mus musculus GN=Slc7a1 PE=2 SV=1	4.1E-11	40.2	8.5	12 (12 0 0 0 0)	Membrane; Multi-pass membrane protein.
Q8VE73	CUL7_MOUSE Cullin-7	1.9E-09	30.2	2.2	3 (3 0 0 0 0)	ND

	OS=Mus musculus GN=Cul7 PE=1 SV=2					
Q99LF4	CV028_MOUSE UPF0027 protein C22orf28 homolog OS=Mus musculus GN=D10Wsu52e PE=2 SV=1	8.4E-07	20.1	5.7	2 (2 0 0 0 0)	Cytoplasm.
O70378	CX4NB_MOUSE Neighbor of COX4 OS=Mus musculus GN=Cox4nb PE=1 SV=1	5.0E-10	30.3	18.4	5 (5 0 0 0 0)	ND
P97792	CXAR_MOUSE Coxsackievirus and adenovirus receptor homolog OS=Mus musculus GN=Cxadr PE=1 SV=1	4.1E-06	20.1	6.6	2 (2 0 0 0 0)	Cell membrane; Single-pass type I membrane protein. Cell junction â€º adherens junction. Cell junction â€º tight junction. Basolateral cell membrane; Single-pass type I membrane protein. Secreted.
Q9D0M3	CY1_MOUSE Cytochrome c1, heme protein, mitochondrial OS=Mus musculus GN=Cyc1 PE=1 SV=1	7.8E-15	30.3	16.0	7 (7 0 0 0 0)	Mitochondrion inner membrane; Single-pass membrane protein; Intermembrane side.
Q9CQX2	CYB5B_MOUSE Cytochrome b5 type B OS=Mus musculus GN=Cyb5b PE=1 SV=1	1.0E-30	70.3	51.4	14 (14 0 0 0 0)	Mitochondrion outer membrane.
Q7TMB8	CYFP1_MOUSE Cytoplasmic FMR1-interacting protein 1 OS=Mus musculus GN=Cyfip1 PE=1 SV=1	9.9E-11	70.2	7.0	7 (7 0 0 0 0)	Cytoplasm. Cytoplasm â€º perinuclear region. Cell projection â€º lamellipodium. Cell projection â€º ruffle. Cell junction â€º synapse â€º synaptosome.
Q5SXY1	CYTSB_MOUSE Cytospin-B OS=Mus musculus GN=Cytsb PE=1 SV=2	1.3E-07	70.2	6.1	10 (10 0 0 0 0)	Nucleus.
Q8BPM0	DAAM1_MOUSE Disheveled-associated activator of morphogenesis 1 OS=Mus musculus GN=Daam1 PE=2 SV=3	9.0E-07	40.2	4.6	4 (4 0 0 0 0)	Cytoplasm.
Q62165	DAG1_MOUSE Dystroglycan OS=Mus musculus GN=Dag1 PE=1 SV=4	4.4E-15	50.2	9.0	8 (8 0 0 0 0)	Secreted â€º extracellular space. Cell membrane; Single-pass type I membrane protein. Cytoplasm â€º

						cytoskeleton. Nucleus â€º nucleoplasm.
Q9JII5	DAZP1_MOUSE DAZ-associated protein 1 OS=Mus musculus GN=Dazap1 PE=2 SV=2	2.6E-10	20.3	8.4	2 (2 0 0 0 0)	Cytoplasm. Nucleus.
Q8BHC4	DCAKD_MOUSE Dephospho-CoA kinase domain-containing protein OS=Mus musculus GN=Dcakd PE=2 SV=1	3.9E-12	80.3	35.5	9 (9 0 0 0 0)	ND
Q91ZV3	DCBD2_MOUSE Discoidin, CUB and LCCL domain-containing protein 2 OS=Mus musculus GN=Dcbld2 PE=2 SV=1	2.5E-05	20.1	3.0	3 (3 0 0 0 0)	Membrane; Single-pass type I membrane protein.
O08788	DCTN1_MOUSE Dynactin subunit 1 OS=Mus musculus GN=Dctn1 PE=1 SV=2	7.7E-09	20.2	2.3	2 (2 0 0 0 0)	Cytoplasm. Cytoplasm â€º cytoskeleton.
Q9CWS0	DDAH1_MOUSE N(G),N(G)-dimethylarginine dimethylaminohydrolase 1 OS=Mus musculus GN=Ddah1 PE=1 SV=3	1.4E-07	20.2	7.0	2 (2 0 0 0 0)	ND
Q99LD8	DDAH2_MOUSE N(G),N(G)-dimethylarginine dimethylaminohydrolase 2 OS=Mus musculus GN=Ddah2 PE=1 SV=1	1.1E-16	70.3	36.8	12 (12 0 0 0 0)	ND
Q80WW9	DDRGK_MOUSE DDRGK domain-containing protein 1 OS=Mus musculus GN=Ddrgk1 PE=1 SV=2	1.4E-14	40.2	16.8	5 (5 0 0 0 0)	Endoplasmic reticulum.
Q501J6	DDX17_MOUSE Probable ATP-dependent RNA helicase DDX17 OS=Mus musculus GN=Ddx17 PE=2 SV=1	8.2E-11	20.2	3.5	11 (11 0 0 0 0)	Nucleus.
Q9JIK5	DDX21_MOUSE Nucleolar RNA helicase 2 OS=Mus musculus GN=Ddx21 PE=1 SV=2	5.1E-04	20.2	1.3	2 (2 0 0 0 0)	Nucleus â€º nucleolus.
P16381	DDX3L_MOUSE Putative ATP-dependent RNA helicase Pl10 OS=Mus musculus GN=D1Pas1 PE=1 SV=1	1.5E-12	80.3	15.5	13 (13 0 0 0 0)	ND
Q61656	DDX5_MOUSE Probable ATP-dependent RNA helicase DDX5 OS=Mus musculus GN=Ddx5 PE=1 SV=1	1.6E-13	40.3	6.8	5 (5 0 0 0 0)	Nucleus â€º nucleolus.

O09005	DEGS1_MOUSE Sphingolipid delta(4)-desaturase DES1 OS=Mus musculus GN=Degs1 PE=2 SV=1	4.2E-13	20.2	10.5	2 (2 0 0 0 0)	Endoplasmic reticulum membrane; Multi-pass membrane protein.
P31001	DESM_MOUSE Desmin OS=Mus musculus GN=Des PE=1 SV=3	1.2E-14	238.3	51.4	49 (46 3 0 0 0)	Cytoplasm.
O70503	DHB12_MOUSE Estradiol 17-beta-dehydrogenase 12 OS=Mus musculus GN=Hsd17b12 PE=2 SV=1	3.4E-14	50.2	19.2	10 (10 0 0 0 0)	Endoplasmic reticulum membrane; Multi-pass membrane protein.
P26443	DHE3_MOUSE Glutamate dehydrogenase 1, mitochondrial OS=Mus musculus GN=Glud1 PE=1 SV=1	6.4E-11	110.3	24.4	12 (12 0 0 0 0)	Mitochondrion matrix.
Q5SS80	DHR13_MOUSE Dehydrogenase/reductase SDR family member 13 OS=Mus musculus GN=Dhrs13 PE=1 SV=1	3.2E-06	20.1	5.9	2 (2 0 0 0 0)	Secreted.
Q8K2B3	DHSA_MOUSE Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial OS=Mus musculus GN=Sdha PE=1 SV=1	3.7E-09	40.2	6.6	6 (6 0 0 0 0)	Mitochondrion inner membrane; Peripheral membrane protein; Matrix side.
Q9CQA3	DHSB_MOUSE Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial OS=Mus musculus GN=Sdhb PE=1 SV=1	1.6E-10	60.2	18.8	6 (6 0 0 0 0)	Mitochondrion inner membrane; Peripheral membrane protein; Matrix side.
Q9QZD8	DIC_MOUSE Mitochondrial dicarboxylate carrier OS=Mus musculus GN=Slc25a10 PE=2 SV=2	2.1E-14	50.3	23.0	7 (7 0 0 0 0)	Mitochondrion inner membrane; Multi-pass membrane protein.
Q99KV1	DJB11_MOUSE DnaJ homolog subfamily B member 11 OS=Mus musculus GN=Dnajb11 PE=1 SV=1	3.7E-06	30.2	8.7	3 (3 0 0 0 0)	Endoplasmic reticulum lumen.
Q80TN4	DJC16_MOUSE DnaJ homolog subfamily C member 16 OS=Mus musculus GN=Dnajc16 PE=1 SV=2	4.2E-05	20.1	2.5	2 (2 0 0 0 0)	Membrane; Single-pass type IV membrane protein.
O08749	DLDH_MOUSE Dihydrolipoyl dehydrogenase, mitochondrial OS=Mus musculus GN=Dld PE=1 SV=2	2.7E-09	50.3	10.6	5 (5 0 0 0 0)	Mitochondrion matrix.

Q811D0	DLG1_MOUSE Disks large homolog 1 OS=Mus musculus GN=Dlg1 PE=1 SV=1	5.3E-09	30.2	3.8	6 (6 0 0 0 0)	Membrane; Peripheral membrane protein. Basolateral cell membrane. Endoplasmic reticulum membrane. Cell junction â€º synapse â€º postsynaptic cell membrane â€º postsynaptic density. Cell junction â€º synapse.
P63037	DNJA1_MOUSE DnaJ homolog subfamily A member 1 OS=Mus musculus GN=Dnaja1 PE=1 SV=1	5.0E-08	40.2	12.6	4 (4 0 0 0 0)	Membrane; Lipid-anchor.
P13864	DNMT1_MOUSE DNA (cytosine-5)-methyltransferase 1 OS=Mus musculus GN=Dnmt1 PE=1 SV=5	2.8E-05	20.1	0.7	3 (3 0 0 0 0)	Nucleus. Cytoplasm.
O70152	DPM1_MOUSE Dolichol-phosphate mannosyltransferase OS=Mus musculus GN=Dpm1 PE=2 SV=1	2.1E-08	20.2	9.6	2 (2 0 0 0 0)	Endoplasmic reticulum.
Q9QXS6	DREB_MOUSE Drebrin OS=Mus musculus GN=Dbn1 PE=1 SV=4	2.1E-14	30.3	6.7	3 (3 0 0 0 0)	Cytoplasm.
Q99J47	DRS7B_MOUSE Dehydrogenase/reductase SDR family member 7B OS=Mus musculus GN=Dhrs7b PE=2 SV=1	8.8E-05	20.1	9.6	2 (2 0 0 0 0)	Peroxisome membrane; Single-pass type II membrane protein.
Q9JHU4	DYHC1_MOUSE Cytoplasmic dynein 1 heavy chain 1 OS=Mus musculus GN=Dync1h1 PE=1 SV=1	2.7E-14	440.3	10.7	47 (47 0 0 0 0)	Cytoplasm â€º cytoskeleton.
Q9Z2H5	E41L1_MOUSE Band 4.1-like protein 1 OS=Mus musculus GN=Epb41l1 PE=1 SV=2	5.6E-06	30.2	4.2	3 (3 0 0 0 0)	Cytoplasm â€º cytoskeleton.
O70318	E41L2_MOUSE Band 4.1-like protein 2 OS=Mus musculus GN=Epb41l2 PE=1 SV=1	1.1E-15	220.3	28.4	26 (26 0 0 0 0)	Cytoplasm â€º cytoskeleton.
Q9WV92	E41L3_MOUSE Band 4.1-like protein 3 OS=Mus musculus GN=Epb41l3 PE=1 SV=1	1.6E-10	120.3	17.9	19 (19 0 0 0 0)	Cytoplasm â€º cytoskeleton.

Q4PZA2	ECE1_MOUSE Endothelin-converting enzyme 1 OS=Mus musculus GN=Ece1 PE=1 SV=1	1.7E-13	70.3	12.4	16 (16 0 0 0 0)	Cell membrane; Single-pass type II membrane protein.
Q8BMS1	ECHA_MOUSE Trifunctional enzyme subunit alpha, mitochondrial OS=Mus musculus GN=Hadha PE=1 SV=1	2.2E-15	150.3	24.9	18 (18 0 0 0 0)	Mitochondrion matrix.
Q99JY0	ECHB_MOUSE Trifunctional enzyme subunit beta, mitochondrial OS=Mus musculus GN=Hadhb PE=1 SV=1	9.6E-06	30.1	6.1	3 (3 0 0 0 0)	Mitochondrion matrix.
Q8BH95	ECHM_MOUSE Enoyl-CoA hydratase, mitochondrial OS=Mus musculus GN=Echs1 PE=1 SV=1	1.6E-07	38.2	8.6	4 (3 1 0 0 0)	Mitochondrion matrix.
Q3UJB9	EDC4_MOUSE Enhancer of mRNA-decapping protein 4 OS=Mus musculus GN=Edc4 PE=1 SV=2	1.7E-12	30.2	3.5	3 (3 0 0 0 0)	Cytoplasm â€º P-body. Nucleus.
P10126	EF1A1_MOUSE Elongation factor 1-alpha 1 OS=Mus musculus GN=Eef1a1 PE=1 SV=3	2.9E-09	70.2	15.8	22 (22 0 0 0 0)	Cytoplasm.
O70251	EF1B_MOUSE Elongation factor 1-beta OS=Mus musculus GN=Eef1b PE=1 SV=5	7.8E-13	20.3	12.4	3 (3 0 0 0 0)	ND
P57776	EF1D_MOUSE Elongation factor 1-delta OS=Mus musculus GN=Eef1d PE=1 SV=3	2.6E-09	50.2	26.3	6 (6 0 0 0 0)	ND
Q9D8N0	EF1G_MOUSE Elongation factor 1-gamma OS=Mus musculus GN=Eef1g PE=1 SV=3	5.5E-08	30.2	7.6	6 (6 0 0 0 0)	ND
P58252	EF2_MOUSE Elongation factor 2 OS=Mus musculus GN=Eef2 PE=1 SV=2	7.0E-12	110.3	14.3	20 (20 0 0 0 0)	Cytoplasm.
P52795	EFNB1_MOUSE Ephrin-B1 OS=Mus musculus GN=Efnb1 PE=1 SV=1	9.2E-07	30.2	14.2	8 (8 0 0 0 0)	Membrane; Single-pass type I membrane protein.
Q8BG67	EFR3A_MOUSE Protein EFR3 homolog A OS=Mus musculus GN=Efr3a PE=1 SV=1	2.3E-08	30.2	6.3	3 (3 0 0 0 0)	Cell membrane.
Q8BFR5	EFTU_MOUSE Elongation factor Tu, mitochondrial OS=Mus musculus GN=Tufm PE=1 SV=1	1.6E-09	30.2	9.1	3 (3 0 0 0 0)	Mitochondrion.

Q01279	EGFR_MOUSE Epidermal growth factor receptor OS=Mus musculus GN=Egfr PE=1 SV=1	7.7E-07	30.2	2.7	4 (4 0 0 0 0)	Membrane; Single-pass type I membrane protein. Endoplasmic reticulum membrane; Single-pass type I membrane protein. Golgi apparatus membrane; Single-pass type I membrane protein. Nucleus membrane; Single-pass type I membrane protein. Endosome.
Q9WVK4	EHD1_MOUSE EH domain-containing protein 1 OS=Mus musculus GN=Ehd1 PE=1 SV=1	4.8E-06	60.2	13.3	8 (8 0 0 0 0)	Cell membrane; Peripheral membrane protein; Cytoplasmic side. Early endosome membrane; Peripheral membrane protein. Recycling endosome membrane; Peripheral membrane protein.
Q8BH64	EHD2_MOUSE EH domain-containing protein 2 OS=Mus musculus GN=Ehd2 PE=1 SV=1	4.6E-08	40.2	7.0	5 (5 0 0 0 0)	Cell membrane; Peripheral membrane protein; Cytoplasmic side. Endosome membrane; Peripheral membrane protein.
Q9EQP2	EHD4_MOUSE EH domain-containing protein 4 OS=Mus musculus GN=Ehd4 PE=1 SV=1	4.5E-08	80.2	17.0	8 (8 0 0 0 0)	Early endosome membrane; Peripheral membrane protein. Recycling endosome membrane; Peripheral membrane protein.
P23116	EIF3A_MOUSE Eukaryotic translation initiation factor 3 subunit A OS=Mus musculus GN=Eif3a PE=1 SV=4	1.1E-11	50.2	4.6	8 (8 0 0 0 0)	Cytoplasm. Cytoplasm â€º cytoskeleton â€º centrosome. Nucleus.
Q8JZQ9	EIF3B_MOUSE Eukaryotic translation initiation factor 3 subunit B OS=Mus musculus	4.6E-11	60.2	9.6	6 (6 0 0 0 0)	Cytoplasm.

	GN=Eif3b PE=1 SV=1					
O70194	EIF3D_MOUSE Eukaryotic translation initiation factor 3 subunit D OS=Mus musculus GN=Eif3d PE=1 SV=2	2.0E-06	30.2	6.6	3 (3 0 0 0 0)	Cytoplasm.
Q9Z1D1	EIF3G_MOUSE Eukaryotic translation initiation factor 3 subunit G OS=Mus musculus GN=Eif3g PE=1 SV=2	3.7E-05	20.2	5.6	2 (2 0 0 0 0)	Cytoplasm. Nucleus. Cytoplasm â€º perinuclear region.
Q8QZY1	EIF3L_MOUSE Eukaryotic translation initiation factor 3 subunit L OS=Mus musculus GN=Eif3l PE=1 SV=1	9.4E-10	30.2	6.7	3 (3 0 0 0 0)	Cytoplasm.
P70290	EM55_MOUSE 55 kDa erythrocyte membrane protein OS=Mus musculus GN=Mpp1 PE=1 SV=1	1.5E-06	20.1	4.5	3 (3 0 0 0 0)	Membrane; Peripheral membrane protein. Cell projection â€º stereocilium.
O08579	EMD_MOUSE Emerin OS=Mus musculus GN=Emd PE=1 SV=1	1.2E-07	20.1	8.9	2 (2 0 0 0 0)	Nucleus inner membrane; Single-pass membrane protein; Nucleoplasmic side. Nucleus outer membrane.
P17182	ENOA_MOUSE Alpha-enolase OS=Mus musculus GN=Eno1 PE=1 SV=3	4.8E-11	68.2	16.6	8 (7 1 0 0 0)	Cytoplasm. Cell membrane.
P08113	ENPL_MOUSE Endoplasmin OS=Mus musculus GN=Hsp90b1 PE=1 SV=2	1.2E-13	318.3	33.0	58 (57 1 0 0 0)	Endoplasmic reticulum lumen. Melanosome.
P10404	ENV1_MOUSE MLV-related proviral Env polyprotein OS=Mus musculus PE=2 SV=3	8.5E-12	80.3	12.2	14 (14 0 0 0 0)	Virion membrane; Single-pass type I membrane protein. Cell membrane; Single-pass type I membrane protein. Virion membrane; Peripheral membrane protein. Cell membrane; Peripheral membrane protein.
Q60750	EPHA1_MOUSE Ephrin type-A receptor 1 OS=Mus musculus GN=Epha1 PE=1 SV=2	6.4E-07	40.2	4.7	5 (5 0 0 0 0)	Membrane; Single-pass type I membrane protein.
Q03145	EPHA2_MOUSE Ephrin type-A receptor 2 OS=Mus musculus GN=Epha2 PE=1 SV=2	5.1E-14	170.3	20.0	43 (43 0 0 0 0)	Cell membrane; Single-pass type I membrane protein. Cell projection â€º ruffle membrane;

						Single-pass type I membrane protein. Cell projection â€º lamellipodium membrane; Single-pass type I membrane protein. Cell junction â€º focal adhesion.
Q99KN9	EPN4_MOUSE Clathrin interactor 1 OS=Mus musculus GN=Clint1 PE=1 SV=2	5.6E-09	40.2	7.6	4 (4 0 0 0 0)	Cytoplasm. Cytoplasm â€º perinuclear region. Membrane; Peripheral membrane protein. Cytoplasmic vesicle â€º clathrin-coated vesicle.
Q9EQH2	ERAP1_MOUSE Endoplasmic reticulum aminopeptidase 1 OS=Mus musculus GN=Erap1 PE=2 SV=1	5.3E-09	30.2	4.0	4 (4 0 0 0 0)	Endoplasmic reticulum membrane; Single-pass type II membrane protein.
Q9DC16	ERGI1_MOUSE Endoplasmic reticulum-Golgi intermediate compartment protein 1 OS=Mus musculus GN=Ergic1 PE=1 SV=1	1.1E-13	70.2	26.9	7 (7 0 0 0 0)	Endoplasmic reticulum membrane; Multi-pass membrane protein. Endoplasmic reticulum-Golgi intermediate compartment membrane; Multi-pass membrane protein. Golgi apparatus membrane; Multi-pass membrane protein.
Q9CQE7	ERGI3_MOUSE Endoplasmic reticulum-Golgi intermediate compartment protein 3 OS=Mus musculus GN=Ergic3 PE=2 SV=1	3.4E-07	30.2	7.3	3 (3 0 0 0 0)	Endoplasmic reticulum-Golgi intermediate compartment membrane; Multi-pass membrane protein. Golgi apparatus â€º cis-Golgi network membrane; Multi-pass membrane protein. Endoplasmic reticulum membrane; Multi-pass membrane

						protein.
Q91X78	ERLN1_MOUSE Erlin-1 OS=Mus musculus GN=Erlin1 PE=2 SV=1	6.8E-09	60.2	17.3	6 (6 0 0 0 0)	Endoplasmic reticulum membrane; Single-pass type II membrane protein.
Q8BFZ9	ERLN2_MOUSE Erlin-2 OS=Mus musculus GN=Erlin2 PE=1 SV=1	3.5E-13	30.3	13.2	4 (4 0 0 0 0)	Endoplasmic reticulum membrane; Single-pass type II membrane protein.
Q3UVK0	ERMP1_MOUSE Endoplasmic reticulum metallopeptidase 1 OS=Mus musculus GN=Ermp1 PE=1 SV=2	5.5E-07	20.2	2.2	3 (3 0 0 0 0)	Endoplasmic reticulum membrane; Multi-pass membrane protein.
P57759	ERP29_MOUSE Endoplasmic reticulum protein ERp29 OS=Mus musculus GN=Erp29 PE=1 SV=2	3.6E-06	30.2	12.2	5 (5 0 0 0 0)	Endoplasmic reticulum lumen. Melanosome.
Q3U7R1	ESYT1_MOUSE Extended synaptotagmin-1 OS=Mus musculus GN=Esyt1 PE=2 SV=2	1.0E-30	360.3	38.7	71 (71 0 0 0 0)	Membrane; Multi-pass membrane protein. Endomembrane system; Multi-pass membrane protein.
Q3TZZ7	ESYT2_MOUSE Extended synaptotagmin-2 OS=Mus musculus GN=Esyt2 PE=1 SV=1	1.1E-14	180.3	29.2	27 (27 0 0 0 0)	Cell membrane; Multi-pass membrane protein.
Q99LC5	ETFA_MOUSE Electron transfer flavoprotein subunit alpha, mitochondrial OS=Mus musculus GN=Etfa PE=1 SV=2	1.2E-12	30.3	13.8	3 (3 0 0 0 0)	Mitochondrion matrix.
Q9DCW4	ETFB_MOUSE Electron transfer flavoprotein subunit beta OS=Mus musculus GN=Etfb PE=1 SV=3	5.3E-06	50.2	24.7	5 (5 0 0 0 0)	Mitochondrion matrix.
P70428	EXT2_MOUSE Exostosin-2 OS=Mus musculus GN=Ext2 PE=1 SV=1	3.3E-05	20.1	2.8	3 (3 0 0 0 0)	Endoplasmic reticulum membrane; Single-pass type II membrane protein. Golgi apparatus membrane; Single-pass type II membrane protein.

P26040	EZRI_MOUSE Ezrin OS=Mus musculus GN=Ezr PE=1 SV=3	5.4E-09	60.2	7.7	8 (8 0 0 0 0)	Apical cell membrane; Peripheral membrane protein; Cytoplasmic side. Cell projection. Cell projection â€º microvillus membrane; Peripheral membrane protein; Cytoplasmic side. Cell projection â€º ruffle membrane; Peripheral membrane protein; Cytoplasmic side. Cytoplasm â€º cell cortex. Cytoplasm â€º cytoskeleton.
Q8VE91	F134B_MOUSE Protein FAM134B OS=Mus musculus GN=Fam134b PE=1 SV=1	3.5E-06	30.2	9.8	3 (3 0 0 0 0)	Golgi apparatus â€º cis-Golgi network membrane; Single-pass membrane protein.
Q9CQV4	F134C_MOUSE Protein FAM134C OS=Mus musculus GN=Fam134c PE=2 SV=1	3.5E-10	30.2	8.4	3 (3 0 0 0 0)	Membrane; Multi-pass membrane protein.
Q9D6U8	F162A_MOUSE UPF0389 protein FAM162A OS=Mus musculus GN=Fam162a PE=2 SV=1	2.7E-08	20.2	16.1	4 (4 0 0 0 0)	Membrane; Single-pass membrane protein.
Q921M7	FA49B_MOUSE Protein FAM49B OS=Mus musculus GN=Fam49b PE=2 SV=1	2.0E-14	30.3	13.9	3 (3 0 0 0 0)	ND
Q80W54	FACE1_MOUSE CAAX prenyl protease 1 homolog OS=Mus musculus GN=Zmpste24 PE=1 SV=2	1.6E-13	58.3	12.2	9 (8 1 0 0 0)	Endoplasmic reticulum membrane; Multi-pass membrane protein. Golgi apparatus membrane; Multi-pass membrane protein.
Q922J9	FACR1_MOUSE Fatty acyl-CoA reductase 1 OS=Mus musculus GN=Far1 PE=1 SV=1	1.0E-09	150.2	29.7	15 (15 0 0 0 0)	Peroxisome membrane; Single-pass membrane protein.
Q9Z0R9	FADS2_MOUSE Fatty acid desaturase 2 OS=Mus musculus GN=Fads2 PE=2 SV=1	7.9E-09	40.2	10.6	4 (4 0 0 0 0)	Endoplasmic reticulum membrane; Multi-pass membrane protein.

Q3TDN2	FAF2_MOUSE FAS-associated factor 2 OS=Mus musculus GN=Faf2 PE=2 SV=2	5.5E-08	40.3	10.6	4 (4 0 0 0 0)	Cytoplasm. Lipid droplet. Endoplasmic reticulum.
Q91VU0	FAM3C_MOUSE Protein FAM3C OS=Mus musculus GN=Fam3c PE=1 SV=1	7.4E-08	40.2	20.7	6 (6 0 0 0 0)	Secreted. Cytoplasmic vesicle.
P19096	FAS_MOUSE Fatty acid synthase OS=Mus musculus GN=Fasn PE=1 SV=2	1.4E-11	160.2	8.3	20 (20 0 0 0 0)	Cytoplasm. Melanosome.
Q8CIB5	FERM2_MOUSE Fermitin family homolog 2 OS=Mus musculus GN=Fermt2 PE=1 SV=1	4.5E-12	20.2	4.7	3 (3 0 0 0 0)	Cytoplasm â€º cell cortex. Cytoplasm â€º cytoskeleton. Cell junction â€º focal adhesion.
P11276	FINC_MOUSE Fibronectin OS=Mus musculus GN=Fn1 PE=1 SV=3	3.3E-16	240.3	11.7	76 (76 0 0 0 0)	Secreted â€º extracellular space â€º extracellular matrix.
Q9D1M7	FKB11_MOUSE FK506-binding protein 11 OS=Mus musculus GN=Fkbp11 PE=2 SV=1	3.9E-10	30.2	14.4	3 (3 0 0 0 0)	Membrane; Single-pass membrane protein.
O35465	FKBP8_MOUSE FK506-binding protein 8 OS=Mus musculus GN=Fkbp8 PE=1 SV=2	2.6E-11	20.2	7.7	3 (3 0 0 0 0)	Mitochondrion membrane; Single-pass membrane protein; Cytoplasmic side.
Q8BTM8	FLNA_MOUSE Filamin-A OS=Mus musculus GN=Flna PE=1 SV=4	1.7E-14	790.3	36.5	162 (162 0 0 0 0)	Cytoplasm â€º cell cortex. Cytoplasm â€º cytoskeleton.
Q80X90	FLNB_MOUSE Filamin-B OS=Mus musculus GN=Flnb PE=1 SV=2	1.1E-16	360.3	17.2	37 (37 0 0 0 0)	Cytoplasm â€º cell cortex. Cytoplasm â€º myofibril â€º sarcomere â€º Z line. Cytoplasm â€º cytoskeleton.
Q8VHX6	FLNC_MOUSE Filamin-C OS=Mus musculus GN=Flnc PE=1 SV=3	1.1E-11	310.3	14.7	37 (37 0 0 0 0)	Cytoplasm. Membrane; Peripheral membrane protein. Cytoplasm â€º cytoskeleton. Cytoplasm â€º myofibril â€º sarcomere â€º Z line.
O08917	FLOT1_MOUSE Flotillin-1 OS=Mus musculus GN=Flot1 PE=1 SV=1	2.1E-13	30.3	10.3	3 (3 0 0 0 0)	Cell membrane; Peripheral membrane protein. Membrane â€º caveola; Peripheral membrane protein. Melanosome. Endosome.

Q60634	FLOT2_MOUSE Flotillin-2 OS=Mus musculus GN=Flot2 PE=1 SV=2	3.7E-10	80.2	19.9	9 (9 0 0 0 0)	Cell membrane; Peripheral membrane protein. Membrane â€º caveola; Peripheral membrane protein. Endosome.
Q6ZPF4	FMNL3_MOUSE Formin-like protein 3 OS=Mus musculus GN=Fmnl3 PE=2 SV=2	2.2E-07	50.2	4.2	6 (6 0 0 0 0)	ND
P50285	FMO1_MOUSE Dimethylaniline monooxygenase [N-oxide-forming] 1 OS=Mus musculus GN=Fmo1 PE=1 SV=1	2.6E-08	20.2	3.6	2 (2 0 0 0 0)	Microsome membrane. Endoplasmic reticulum membrane.
Q6NWW9	FND3B_MOUSE Fibronectin type III domain-containing protein 3B OS=Mus musculus GN=Fndc3b PE=1 SV=1	2.6E-06	20.1	2.5	2 (2 0 0 0 0)	Membrane; Single-pass membrane protein.
Q9WV91	FPRP_MOUSE Prostaglandin F2 receptor negative regulator OS=Mus musculus GN=Ptgfrn PE=1 SV=1	7.0E-10	110.2	10.6	11 (11 0 0 0 0)	Endoplasmic reticulum membrane; Single-pass type I membrane protein. Golgi apparatus â€º trans-Golgi network membrane; Single-pass type I membrane protein.
P29391	FRIL1_MOUSE Ferritin light chain 1 OS=Mus musculus GN=Ftl1 PE=1 SV=2	1.6E-07	20.2	15.8	2 (2 0 0 0 0)	ND
Q61553	FSCN1_MOUSE Fascin OS=Mus musculus GN=Fscn1 PE=1 SV=4	1.3E-08	60.2	13.0	6 (6 0 0 0 0)	Cytoplasm â€º cytoskeleton. Cell projection â€º filopodium. Cell projection â€º invadopodium.
Q3U0V1	FUBP2_MOUSE Far upstream element-binding protein 2 OS=Mus musculus GN=Khsrp PE=1 SV=1	3.2E-07	30.1	4.8	3 (3 0 0 0 0)	Nucleus. Cytoplasm.
Q9WTS2	FUT8_MOUSE Alpha-(1,6)-fucosyltransferase OS=Mus musculus GN=Fut8 PE=2 SV=1	3.0E-12	30.2	6.3	3 (3 0 0 0 0)	Golgi apparatus â€º Golgi stack membrane; Single-pass type II membrane protein.
P39688	FYN_MOUSE Proto-oncogene tyrosine-protein kinase Fyn OS=Mus	3.8E-08	28.2	6.7	4 (2 2 0 0 0)	Cell membrane.

	musculus GN=Fyn PE=1 SV=3					
P97855	G3BP1_MOUSE Ras GTPase-activating protein-binding protein 1 OS=Mus musculus GN=G3bp1 PE=1 SV=1	3.2E-12	60.3	19.8	11 (11 0 0 0 0)	Cytoplasm. Cytoplasm â€º cytosol. Cell membrane. Nucleus.
P97379	G3BP2_MOUSE Ras GTPase-activating protein-binding protein 2 OS=Mus musculus GN=G3bp2 PE=1 SV=2	6.7E-15	40.3	11.8	5 (5 0 0 0 0)	ND
P16858	G3P_MOUSE Glyceraldehyde-3-phosphate dehydrogenase OS=Mus musculus GN=Gapdh PE=1 SV=2	1.1E-15	60.3	18.9	9 (9 0 0 0 0)	Cytoplasm â€º cytosol. Nucleus.
Q9CR59	G45IP_MOUSE Growth arrest and DNA-damage-inducible proteins-interacting protein 1 OS=Mus musculus GN=Gadd45gip1 PE=2 SV=1	4.9E-06	30.1	12.2	3 (3 0 0 0 0)	Nucleus.
P11365	GAG_IPMA Retrovirus-related Gag polyprotein OS=Mouse intracisternal a-particle MIA14 GN=gag PE=4 SV=2	6.6E-11	20.3	4.0	2 (2 0 0 0 0)	ND
O08912	GALT1_MOUSE Polypeptide N-acetylgalactosaminyltransferase 1 OS=Mus musculus GN=Galnt1 PE=1 SV=1	2.7E-08	30.2	6.1	3 (3 0 0 0 0)	Golgi apparatus â€º Golgi stack membrane; Single-pass type II membrane protein. Secreted.
Q6PB93	GALT2_MOUSE Polypeptide N-acetylgalactosaminyltransferase 2 OS=Mus musculus GN=Galnt2 PE=2 SV=1	1.4E-14	50.3	11.9	6 (6 0 0 0 0)	Golgi apparatus â€º Golgi stack membrane; Single-pass type II membrane protein. Secreted.
Q8BHN3	GANAB_MOUSE Neutral alpha-glucosidase AB OS=Mus musculus GN=Ganab PE=1 SV=1	1.2E-12	210.2	25.3	25 (25 0 0 0 0)	Endoplasmic reticulum. Golgi apparatus. Melanosome.
Q9CYL5	GAPR1_MOUSE Golgi-associated plant pathogenesis-related protein 1 OS=Mus musculus GN=Glipr2 PE=2 SV=3	1.0E-09	50.2	45.5	8 (8 0 0 0 0)	Golgi apparatus membrane; Lipid-anchor.
P62874	GBB1_MOUSE Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1 OS=Mus musculus GN=Gnb1 PE=1 SV=3	6.6E-09	50.2	12.4	12 (12 0 0 0 0)	ND

P68040	GBLP_MOUSE Guanine nucleotide-binding protein subunit beta-2-like 1 OS=Mus musculus GN=Gnb2l1 PE=1 SV=3	1.6E-12	50.2	18.9	8 (8 0 0 0 0)	Cell membrane; Peripheral membrane protein. Cytoplasm. Cytoplasm â€º perinuclear region. Cytoplasm â€º cytoskeleton. Nucleus. Perikaryon. Cell projection â€º dendrite.
Q01514	GBP1_MOUSE Interferon-induced guanylate-binding protein 1 OS=Mus musculus GN=Gbp1 PE=1 SV=1	1.3E-08	30.2	7.3	4 (4 0 0 0 0)	Cell membrane; Lipid-anchor; Cytoplasmic side.
Q9Z0E6	GBP2_MOUSE Interferon-induced guanylate-binding protein 2 OS=Mus musculus GN=Gbp2 PE=1 SV=1	7.0E-10	40.3	9.0	6 (6 0 0 0 0)	Cell membrane; Lipid-anchor; Cytoplasmic side.
Q61598	GDIB_MOUSE Rab GDP dissociation inhibitor beta OS=Mus musculus GN=Gdi2 PE=1 SV=1	2.6E-07	20.1	5.2	3 (3 0 0 0 0)	Cytoplasm. Membrane; Peripheral membrane protein.
Q99PT1	GDIR1_MOUSE Rho GDP-dissociation inhibitor 1 OS=Mus musculus GN=Arhgdia PE=1 SV=3	4.2E-10	30.2	23.5	3 (3 0 0 0 0)	Cytoplasm.
O08795	GLU2B_MOUSE Glucosidase 2 subunit beta OS=Mus musculus GN=Prkcsh PE=1 SV=1	2.6E-09	50.2	10.0	8 (8 0 0 0 0)	Endoplasmic reticulum.
P50431	GLYC_MOUSE Serine hydroxymethyltransferase, cytosolic OS=Mus musculus GN=Shmt1 PE=1 SV=2	4.1E-10	20.2	2.9	2 (2 0 0 0 0)	Cytoplasm.
P21278	GNA11_MOUSE Guanine nucleotide-binding protein subunit alpha-11 OS=Mus musculus GN=Gna11 PE=1 SV=1	5.6E-15	130.3	43.7	18 (18 0 0 0 0)	Cell membrane; Lipid-anchor.
P27601	GNA13_MOUSE Guanine nucleotide-binding protein subunit alpha-13 OS=Mus musculus GN=Gna13 PE=1 SV=1	4.6E-11	110.2	26.5	21 (21 0 0 0 0)	Membrane; Lipid-anchor. Melanosome.
P30677	GNA14_MOUSE Guanine nucleotide-binding protein subunit alpha-14 OS=Mus musculus GN=Gna14 PE=1 SV=1	4.1E-11	56.3	7.9	8 (5 3 0 0 0)	ND
P08752	GNAI2_MOUSE Guanine nucleotide-binding protein G(i), alpha-2 subunit OS=Mus musculus	1.2E-14	110.3	27.0	25 (25 0 0 0 0)	Cytoplasm. Cytoplasm â€º cytoskeleton â€º centrosome. Cell

	GN=Gnai2 PE=1 SV=4					membrane.
Q9DC51	GNAI3_MOUSE Guanine nucleotide-binding protein G(k) subunit alpha OS=Mus musculus GN=Gnai3 PE=1 SV=3	8.7E-13	50.2	18.9	9 (9 0 0 0 0)	Cytoplasm. Cell membrane. Cytoplasm â€º cytoskeleton â€º centrosome.
P21279	GNAQ_MOUSE Guanine nucleotide-binding protein G(q) subunit alpha OS=Mus musculus GN=Gnaq PE=1 SV=4	3.6E-14	70.3	25.1	10 (10 0 0 0 0)	ND
Q6R0H7	GNAS1_MOUSE Guanine nucleotide-binding protein G(s) subunit alpha isoforms XLas OS=Mus musculus GN=Gnas PE=2 SV=1	1.2E-08	80.2	5.9	13 (13 0 0 0 0)	Cell membrane; Peripheral membrane protein.
P98192	GNPAT_MOUSE Dihydroxyacetone phosphate acyltransferase OS=Mus musculus GN=Gnpat PE=2 SV=1	2.5E-08	20.2	4.7	2 (2 0 0 0 0)	Peroxisome membrane; Peripheral membrane protein; Matrix side.
Q9QYE6	GOGA5_MOUSE Golgin subfamily A member 5 OS=Mus musculus GN=Golga5 PE=1 SV=2	4.4E-15	90.3	13.7	12 (12 0 0 0 0)	Golgi apparatus membrane; Single-pass type IV membrane protein.
Q91W53	GOGA7_MOUSE Golgin subfamily A member 7 OS=Mus musculus GN=Golga7 PE=2 SV=1	3.0E-11	20.2	19.0	2 (2 0 0 0 0)	Golgi apparatus membrane; Lipid-anchor.
Q8BXA1	GOLI4_MOUSE Golgi integral membrane protein 4 OS=Mus musculus GN=Golim4 PE=1 SV=1	1.3E-08	80.3	15.7	15 (15 0 0 0 0)	Golgi apparatus â€º Golgi stack membrane; Single-pass type II membrane protein. Endosome membrane; Single-pass type II membrane protein.
O88630	GOSR1_MOUSE Golgi SNAP receptor complex member 1 OS=Mus musculus GN=Gosr1 PE=1 SV=1	1.9E-11	30.3	15.2	4 (4 0 0 0 0)	Golgi apparatus membrane; Single-pass type IV membrane protein.
O35166	GOSR2_MOUSE Golgi SNAP receptor complex member 2 OS=Mus musculus GN=Gosr2 PE=2 SV=2	5.9E-08	30.2	12.7	3 (3 0 0 0 0)	Golgi apparatus membrane; Single-pass type IV membrane protein.
Q9QZF2	GPC1_MOUSE Glypican-1 OS=Mus musculus GN=Gpc1 PE=1 SV=1	1.0E-30	100.3	24.2	28 (28 0 0 0 0)	Cell membrane; Lipid-anchor â€º GPI-anchor; Extracellular side. Secreted â€º

						extracellular space.
Q9R087	GPC6_MOUSE Glypican-6 OS=Mus musculus GN=Gpc6 PE=2 SV=1	1.9E-11	20.2	4.5	4 (4 0 0 0 0)	Cell membrane; Lipid-anchor â€º GPI-anchor; Extracellular side. Secreted â€º extracellular space.
Q64521	GPDM_MOUSE Glycerol-3-phosphate dehydrogenase, mitochondrial OS=Mus musculus GN=Gpd2 PE=1 SV=2	2.1E-13	110.3	13.1	12 (12 0 0 0 0)	Mitochondrion inner membrane.
Q9CXY9	GPI8_MOUSE GPI-anchor transamidase OS=Mus musculus GN=Pigk PE=2 SV=2	1.0E-08	20.1	5.8	2 (2 0 0 0 0)	Endoplasmic reticulum membrane; Single-pass type I membrane protein.
Q9D7B7	GPX8_MOUSE Probable glutathione peroxidase 8 OS=Mus musculus GN=Gpx8 PE=2 SV=1	2.5E-07	20.1	10.5	3 (3 0 0 0 0)	Membrane; Single-pass membrane protein.
P38647	GRP75_MOUSE Stress-70 protein, mitochondrial OS=Mus musculus GN=Hspa9 PE=1 SV=2	1.0E-14	240.3	39.3	42 (42 0 0 0 0)	Mitochondrion.
P20029	GRP78_MOUSE 78 kDa glucose-regulated protein OS=Mus musculus GN=Hspa5 PE=1 SV=3	1.1E-15	420.3	49.3	99 (99 0 0 0 0)	Endoplasmic reticulum lumen. Melanosome.
Q61543	GSLG1_MOUSE Golgi apparatus protein 1 OS=Mus musculus GN=Glg1 PE=1 SV=1	1.1E-15	100.3	8.2	18 (18 0 0 0 0)	Cell membrane; Single-pass type I membrane protein. Golgi apparatus membrane; Single-pass type I membrane protein.
P17809	GTR1_MOUSE Solute carrier family 2, facilitated glucose transporter member 1 OS=Mus musculus GN=Slc2a1 PE=1 SV=3	3.0E-07	40.2	5.7	9 (9 0 0 0 0)	Cell membrane; Multi-pass membrane protein. Melanosome.
Q80SU7	GVIN1_MOUSE Interferon-induced very large GTPase 1 OS=Mus musculus GN=Gvin1 PE=1 SV=1	1.0E-13	220.3	10.8	26 (26 0 0 0 0)	Cytoplasm â€º cytosol. Nucleus.
Q8CGP5	H2A1F_MOUSE Histone H2A type 1-F OS=Mus musculus GN=Hist1h2af PE=1 SV=3	3.0E-14	50.3	35.4	25 (25 0 0 0 0)	Nucleus. Chromosome.
P70696	H2B1A_MOUSE Histone H2B type 1-A OS=Mus musculus GN=Hist1h2ba PE=2 SV=3	4.6E-11	40.2	36.2	6 (6 0 0 0 0)	Nucleus. Chromosome.

Q64475	H2B1B_MOUSE Histone H2B type 1-B OS=Mus musculus GN=Hist1h2bb PE=1 SV=3	2.2E-11	76.2	21.4	10 (8 2 0 0 0)	Nucleus. Chromosome.
P68433	H31_MOUSE Histone H3.1 OS=Mus musculus GN=Hist1h3a PE=1 SV=2	3.8E-09	60.2	27.2	8 (8 0 0 0 0)	Nucleus. Chromosome.
P62806	H4_MOUSE Histone H4 OS=Mus musculus GN=Hist1h4a PE=1 SV=2	1.5E-07	30.2	31.1	6 (6 0 0 0 0)	Nucleus. Chromosome.
P62806	H4_MOUSE Histone H4 OS=Mus musculus GN=Hist1h4a PE=1 SV=2	7.1E-09	110.2	60.2	12 (12 0 0 0 0)	Nucleus. Chromosome.
P01898	HA10_MOUSE H-2 class I histocompatibility antigen, Q10 alpha chain OS=Mus musculus GN=H2-Q10 PE=1 SV=3	4.4E-11	70.2	20.9	21 (21 0 0 0 0)	Membrane; Single-pass type I membrane protein.
P01899	HA11_MOUSE H-2 class I histocompatibility antigen, D-B alpha chain OS=Mus musculus GN=H2-D1 PE=1 SV=2	6.5E-12	160.2	36.5	61 (61 0 0 0 0)	Membrane; Single-pass type I membrane protein.
P01900	HA12_MOUSE H-2 class I histocompatibility antigen, D-D alpha chain OS=Mus musculus GN=H2-D1 PE=1 SV=1	1.8E-05	20.2	5.5	3 (3 0 0 0 0)	Membrane; Single-pass type I membrane protein.
P14426	HA13_MOUSE H-2 class I histocompatibility antigen, D-K alpha chain OS=Mus musculus GN=H2-D1 PE=1 SV=1	1.0E-09	48.2	10.8	12 (11 1 0 0 0)	Membrane; Single-pass type I membrane protein.
P06339	HA15_MOUSE H-2 class I histocompatibility antigen, D-37 alpha chain OS=Mus musculus GN=H2-T23 PE=1 SV=1	5.1E-05	20.2	3.6	3 (3 0 0 0 0)	Membrane; Single-pass type I membrane protein.
P14429	HA17_MOUSE H-2 class I histocompatibility antigen, Q7 alpha chain OS=Mus musculus GN=H2-Q7 PE=1 SV=1	7.8E-10	50.2	11.1	5 (5 0 0 0 0)	Membrane; Single-pass type I membrane protein.
P01901	HA1B_MOUSE H-2 class I histocompatibility antigen, K-B alpha chain OS=Mus musculus GN=H2-K1 PE=1 SV=1	2.4E-14	100.3	16.0	36 (36 0 0 0 0)	Membrane; Single-pass type I membrane protein.
P01902	HA1D_MOUSE H-2 class I histocompatibility antigen, K-D alpha chain OS=Mus musculus GN=H2-K1 PE=1 SV=1	6.7E-08	16.2	4.9	3 (0 3 0 0 0)	Membrane; Single-pass type I membrane protein.

P14434	HA2B_MOUSE H-2 class II histocompatibility antigen, A-B alpha chain OS=Mus musculus GN=H2-Aa PE=1 SV=2	3.9E-11	20.2	10.5	2 (2 0 0 0 0)	Membrane; Single-pass type I membrane protein.
P14483	HB2A_MOUSE H-2 class II histocompatibility antigen, A beta chain OS=Mus musculus GN=H2-Ab1 PE=1 SV=1	3.7E-11	50.2	27.2	9 (9 0 0 0 0)	Membrane; Single-pass type I membrane protein.
O08756	HCD2_MOUSE 3-hydroxyacyl-CoA dehydrogenase type-2 OS=Mus musculus GN=Hsd17b10 PE=1 SV=4	8.5E-11	40.2	27.2	5 (5 0 0 0 0)	Mitochondrion.
Q9D8V0	HM13_MOUSE Minor histocompatibility antigen H13 OS=Mus musculus GN=Hm13 PE=1 SV=1	1.0E-30	40.3	8.2	5 (5 0 0 0 0)	Endoplasmic reticulum membrane; Multi-pass membrane protein. Cell membrane; Multi-pass membrane protein.
P14901	HMOX1_MOUSE Heme oxygenase 1 OS=Mus musculus GN=Hmox1 PE=2 SV=1	4.2E-09	60.3	14.5	6 (6 0 0 0 0)	Microsome. Endoplasmic reticulum.
O70252	HMOX2_MOUSE Heme oxygenase 2 OS=Mus musculus GN=Hmox2 PE=2 SV=1	2.2E-14	120.3	40.3	13 (13 0 0 0 0)	Microsome. Endoplasmic reticulum.
O35737	HNRH1_MOUSE Heterogeneous nuclear ribonucleoprotein H OS=Mus musculus GN=Hnrnph1 PE=1 SV=3	3.2E-09	30.2	11.1	4 (4 0 0 0 0)	Nucleus â€º nucleoplasm.
Q9Z2X1	HNRPF_MOUSE Heterogeneous nuclear ribonucleoprotein F OS=Mus musculus GN=Hnrnpf PE=1 SV=3	4.3E-09	20.3	9.2	2 (2 0 0 0 0)	Nucleus â€º nucleoplasm.
P61979	HNRPK_MOUSE Heterogeneous nuclear ribonucleoprotein K OS=Mus musculus GN=Hnrnpk PE=1 SV=1	2.1E-10	90.3	28.1	11 (11 0 0 0 0)	Cytoplasm. Nucleus â€º nucleoplasm.
Q9D0E1	HNRPM_MOUSE Heterogeneous nuclear ribonucleoprotein M OS=Mus musculus GN=Hnrnpm PE=1 SV=3	4.6E-13	240.3	27.2	37 (37 0 0 0 0)	Nucleus.
Q7TMK9	HNRPQ_MOUSE Heterogeneous nuclear ribonucleoprotein Q OS=Mus musculus	1.6E-10	30.2	6.7	3 (3 0 0 0 0)	Nucleus. Cytoplasm.

	GN=Syncrip PE=1 SV=2					
Q8VEK3	HNRPU_MOUSE Heterogeneous nuclear ribonucleoprotein U OS=Mus musculus GN=Hnrnpu PE=1 SV=1	1.0E-09	50.2	5.6	5 (5 0 0 0 0)	Nucleus. Cytoplasm. Cell surface.
Q8R3H7	HS2ST_MOUSE Heparan sulfate 2-O-sulfotransferase 1 OS=Mus musculus GN=Hs2st1 PE=1 SV=2	1.1E-06	20.1	5.9	2 (2 0 0 0 0)	Golgi apparatus membrane; Single-pass type II membrane protein.
Q61696	HS71A_MOUSE Heat shock 70 kDa protein 1A OS=Mus musculus GN=Hspa1a PE=1 SV=2	1.5E-13	30.3	7.2	7 (7 0 0 0 0)	Cytoplasm.
P07901	HS90A_MOUSE Heat shock protein HSP 90-alpha OS=Mus musculus GN=Hsp90aa1 PE=1 SV=4	1.2E-12	244.3	30.3	53 (38 15 0 0 0)	Cytoplasm. Melanosome.
P11499	HS90B_MOUSE Heat shock protein HSP 90-beta OS=Mus musculus GN=Hsp90ab1 PE=1 SV=2	3.9E-12	108.3	16.9	31 (30 1 0 0 0)	Cytoplasm. Melanosome.
P17156	HSP72_MOUSE Heat shock-related 70 kDa protein 2 OS=Mus musculus GN=Hspa2 PE=1 SV=1	1.8E-13	50.2	8.5	16 (16 0 0 0 0)	ND
Q61316	HSP74_MOUSE Heat shock 70 kDa protein 4 OS=Mus musculus GN=Hspa4 PE=1 SV=1	4.4E-08	20.2	3.8	3 (3 0 0 0 0)	Cytoplasm.
P63017	HSP7C_MOUSE Heat shock cognate 71 kDa protein OS=Mus musculus GN=Hspa8 PE=1 SV=1	3.3E-15	240.3	27.9	63 (63 0 0 0 0)	Cytoplasm. Melanosome.
P14602	HSPB1_MOUSE Heat shock protein beta-1 OS=Mus musculus GN=Hspb1 PE=1 SV=3	4.9E-06	30.1	20.6	3 (3 0 0 0 0)	Cytoplasm. Nucleus. Cytoplasm â€º cytoskeleton â€º spindle.
O08528	HXK2_MOUSE Hexokinase-2 OS=Mus musculus GN=Hk2 PE=1 SV=1	2.1E-06	30.2	4.7	3 (3 0 0 0 0)	ND
Q9JKR6	HYOU1_MOUSE Hypoxia up-regulated protein 1 OS=Mus musculus GN=Hyou1 PE=1 SV=1	2.2E-15	230.3	28.1	30 (30 0 0 0 0)	Endoplasmic reticulum lumen.
Q9D6R2	IDH3A_MOUSE Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial OS=Mus musculus GN=Idh3a PE=1 SV=1	1.3E-10	100.2	31.1	12 (12 0 0 0 0)	Mitochondrion.

P54071	IDHP_MOUSE Isocitrate dehydrogenase [NADP], mitochondrial OS=Mus musculus GN=Idh2 PE=1 SV=3	2.0E-09	90.2	22.6	9 (9 0 0 0 0)	Mitochondrion.
Q6ZWX6	IF2A_MOUSE Eukaryotic translation initiation factor 2 subunit 1 OS=Mus musculus GN=Eif2s1 PE=1 SV=3	9.4E-08	20.2	8.6	2 (2 0 0 0 0)	Cytoplasmic granule.
P60843	IF4A1_MOUSE Eukaryotic initiation factor 4A-I OS=Mus musculus GN=Eif4a1 PE=2 SV=1	1.9E-11	140.3	29.1	17 (17 0 0 0 0)	ND
P63242	IF5A1_MOUSE Eukaryotic translation initiation factor 5A-1 OS=Mus musculus GN=Eif5a PE=1 SV=2	6.9E-11	20.1	15.6	3 (3 0 0 0 0)	Cytoplasm. Nucleus. Endoplasmic reticulum membrane; Peripheral membrane protein; Cytoplasmic side. Nucleus â€º nuclear pore complex.
P03975	IGEB_MOUSE IgE-binding protein OS=Mus musculus GN=Iap PE=2 SV=1	3.2E-11	20.2	4.8	2 (2 0 0 0 0)	ND
Q60751	IGF1R_MOUSE Insulin-like growth factor 1 receptor OS=Mus musculus GN=Igf1r PE=1 SV=3	1.7E-08	80.2	7.5	12 (12 0 0 0 0)	Membrane; Single-pass type I membrane protein.
Q8R366	IGSF8_MOUSE Immunoglobulin superfamily member 8 OS=Mus musculus GN=Igsf8 PE=1 SV=2	2.8E-08	90.2	18.5	10 (10 0 0 0 0)	Membrane; Single-pass membrane protein.
Q9QZ85	IIGP1_MOUSE Interferon-inducible GTPase 1 OS=Mus musculus GN=Iigp1 PE=1 SV=2	1.0E-30	230.3	55.4	39 (39 0 0 0 0)	Cytoplasm. Nucleus membrane; Peripheral membrane protein. Endoplasmic reticulum membrane; Peripheral membrane protein. Golgi apparatus â€º Golgi stack membrane; Peripheral membrane protein. Parasitophorous vacuole membrane.

Q9DBZ1	IKIP_MOUSE Inhibitor of nuclear factor kappa-B kinase-interacting protein OS=Mus musculus GN=Ikip PE=1 SV=2	7.8E-10	70.2	21.4	10 (10 0 0 0 0)	Endoplasmic reticulum membrane; Single-pass membrane protein.
O55222	ILK_MOUSE Integrin-linked protein kinase OS=Mus musculus GN=Ilk PE=1 SV=2	6.4E-08	60.2	15.7	6 (6 0 0 0 0)	Cell junction â€º focal adhesion. Cell membrane; Peripheral membrane protein; Cytoplasmic side.
Q8BU33	ILVBL_MOUSE Acetolactate synthase-like protein OS=Mus musculus GN=Ilvbl PE=2 SV=1	6.7E-15	30.3	8.5	5 (5 0 0 0 0)	Membrane; Single-pass membrane protein.
P52293	IMA2_MOUSE Importin subunit alpha-2 OS=Mus musculus GN=Kpna2 PE=1 SV=2	3.5E-09	50.2	14.0	5 (5 0 0 0 0)	Cytoplasm. Nucleus.
P70168	IMB1_MOUSE Importin subunit beta-1 OS=Mus musculus GN=Kpnb1 PE=1 SV=1	1.6E-10	160.3	20.0	18 (18 0 0 0 0)	Cytoplasm. Nucleus envelope.
P24547	IMDH2_MOUSE Inosine-5'-monophosphate dehydrogenase 2 OS=Mus musculus GN=Impdh2 PE=1 SV=2	4.3E-09	20.2	4.5	2 (2 0 0 0 0)	Cytoplasm. Nucleus.
Q8CAQ8	IMMT_MOUSE Mitochondrial inner membrane protein OS=Mus musculus GN=Immt PE=1 SV=1	1.3E-13	360.3	43.5	54 (54 0 0 0 0)	Mitochondrion inner membrane.
Q80V26	IMPA3_MOUSE Inositol monophosphatase 3 OS=Mus musculus GN=Impad1 PE=2 SV=1	8.7E-06	50.2	12.6	5 (5 0 0 0 0)	Membrane; Single-pass membrane protein.
Q0GNC1	INF2_MOUSE Inverted formin-2 OS=Mus musculus GN=Inf2 PE=1 SV=1	1.0E-06	20.1	1.6	2 (2 0 0 0 0)	Cytoplasm â€º perinuclear region.
Q3TAS6	INM02_MOUSE UPF0510 protein INM02 OS=Mus musculus GN=Inm02 PE=2 SV=2	5.2E-14	20.2	9.7	3 (3 0 0 0 0)	Membrane; Single-pass type I membrane protein. Secreted.
Q8VI75	IPO4_MOUSE Importin-4 OS=Mus musculus GN=Ipo4 PE=1 SV=1	1.5E-07	20.1	2.6	3 (3 0 0 0 0)	Cytoplasm. Nucleus.
Q8BKC5	IPO5_MOUSE Importin-5 OS=Mus musculus GN=Ipo5 PE=1 SV=3	9.7E-11	80.2	8.3	8 (8 0 0 0 0)	Cytoplasm. Nucleus.
Q8BKC5	IPO5_MOUSE Importin-5 OS=Mus musculus GN=Ipo5 PE=1 SV=3	4.3E-13	30.3	4.6	4 (4 0 0 0 0)	Cytoplasm. Nucleus.
Q9EPL8	IPO7_MOUSE Importin-7 OS=Mus musculus GN=Ipo7	7.8E-08	20.1	2.3	2 (2 0 0 0 0)	Cytoplasm. Nucleus.

	PE=1 SV=2					
Q9JKF1	IQGA1_MOUSE Ras GTPase-activating-like protein IQGAP1 OS=Mus musculus GN=Iqgap1 PE=1 SV=1	1.4E-14	220.3	16.1	25 (25 0 0 0 0)	Cell membrane.
Q60766	IRGM_MOUSE Immunity-related GTPase family M protein OS=Mus musculus GN=Irgm PE=1 SV=1	1.0E-30	164.3	35.0	37 (35 1 1 0 0)	Golgi apparatus membrane. Cell membrane. Cytoplasmic vesicle â€º phagosome membrane. Cytoplasmic vesicle â€º autophagosome membrane. Lysosome membrane. Late endosome membrane. Cell projection â€º phagocytic cup.
Q6GU68	ISLR_MOUSE Immunoglobulin superfamily containing leucine-rich repeat protein OS=Mus musculus GN=Islr PE=1 SV=1	3.5E-11	60.2	11.7	14 (14 0 0 0 0)	Secreted.
Q62470	ITA3_MOUSE Integrin alpha-3 OS=Mus musculus GN=Itga3 PE=1 SV=1	1.6E-12	80.2	9.4	10 (10 0 0 0 0)	Membrane; Single-pass type I membrane protein.
P11688	ITA5_MOUSE Integrin alpha-5 OS=Mus musculus GN=Itga5 PE=1 SV=2	4.2E-11	180.3	17.9	30 (30 0 0 0 0)	Membrane; Single-pass type I membrane protein.
Q61739	ITA6_MOUSE Integrin alpha-6 OS=Mus musculus GN=Itga6 PE=1 SV=2	4.0E-14	120.3	14.6	17 (17 0 0 0 0)	Membrane; Single-pass type I membrane protein.
Q61738	ITA7_MOUSE Integrin alpha-7 OS=Mus musculus GN=Itga7 PE=1 SV=2	6.0E-14	180.3	16.0	47 (47 0 0 0 0)	Membrane; Single-pass type I membrane protein.
P43406	ITAV_MOUSE Integrin alpha-V OS=Mus musculus GN=Itgav PE=1 SV=1	5.6E-11	110.2	11.6	13 (13 0 0 0 0)	Membrane; Single-pass type I membrane protein.
P09055	ITB1_MOUSE Integrin beta-1 OS=Mus musculus GN=Itgb1 PE=1 SV=1	1.8E-12	148.3	15.2	85 (82 3 0 0 0)	Cell membrane; Single-pass type I membrane protein. Melanosome.
O54890	ITB3_MOUSE Integrin beta-3 OS=Mus musculus GN=Itgb3 PE=2 SV=1	7.0E-09	20.2	3.3	3 (3 0 0 0 0)	Membrane; Single-pass type I membrane protein.
Q8C0Z1	ITFG3_MOUSE Protein ITFG3 OS=Mus musculus GN=Itfg3 PE=1 SV=1	7.5E-07	30.2	6.5	4 (4 0 0 0 0)	Membrane; Single-pass type II membrane protein.

Q5XKN4	JAGN1_MOUSE Protein jagunal homolog 1 OS=Mus musculus GN=Jagn1 PE=2 SV=2	4.1E-08	20.2	13.1	2 (2 0 0 0 0)	Endoplasmic reticulum membrane; Multi-pass membrane protein.
P52332	JAK1_MOUSE Tyrosine-protein kinase JAK1 OS=Mus musculus GN=Jak1 PE=1 SV=1	6.9E-13	60.2	5.1	6 (6 0 0 0 0)	Endomembrane system; Peripheral membrane protein.
Q9D8B7	JAM3_MOUSE Junctional adhesion molecule C OS=Mus musculus GN=Jam3 PE=1 SV=2	2.4E-10	20.2	8.4	4 (4 0 0 0 0)	Cell membrane; Single-pass type I membrane protein. Cell junction â€º desmosome. Secreted â€º extracellular space.
Q9ET78	JPH2_MOUSE Junctophilin-2 OS=Mus musculus GN=Jph2 PE=1 SV=2	1.0E-07	20.2	4.5	2 (2 0 0 0 0)	Cell membrane; Peripheral membrane protein. Endoplasmic reticulum membrane; Single-pass type IV membrane protein. Sarcoplasmic reticulum membrane; Single-pass type IV membrane protein.
Q8C7X2	K0090_MOUSE Uncharacterized protein KIAA0090 OS=Mus musculus GN=Kiaa0090 PE=1 SV=1	2.9E-14	120.3	19.4	14 (14 0 0 0 0)	Membrane; Single-pass type I membrane protein.
Q8C7X2	K0090_MOUSE Uncharacterized protein KIAA0090 OS=Mus musculus GN=Kiaa0090 PE=1 SV=1	1.3E-13	100.2	15.6	14 (14 0 0 0 0)	Membrane; Single-pass type I membrane protein.
Q69ZQ1	K1161_MOUSE Uncharacterized family 31 glucosidase KIAA1161 OS=Mus musculus GN=Kiaa1161 PE=1 SV=2	2.6E-07	20.1	2.8	2 (2 0 0 0 0)	Membrane; Single-pass type II membrane protein.
P02535	K1C10_MOUSE Keratin, type I cytoskeletal 10 OS=Mus musculus GN=Krt10 PE=1 SV=3	9.9E-09	50.2	5.3	27 (27 0 0 0 0)	ND
P04104	K2C1_MOUSE Keratin, type II cytoskeletal 1 OS=Mus musculus GN=Krt1 PE=1 SV=4	2.7E-06	18.1	3.6	4 (3 1 0 0 0)	Cell membrane.
Q6IFZ6	K2C1B_MOUSE Keratin, type II cytoskeletal 1b OS=Mus musculus	8.3E-09	20.2	3.8	20 (20 0 0 0 0)	ND

	GN=Krt77 PE=1 SV=1					
P11679	K2C8_MOUSE Keratin, type II cytoskeletal 8 OS=Mus musculus GN=Krt8 PE=1 SV=4	3.7E-12	30.2	2.9	6 (6 0 0 0 0)	Cytoplasm. Nucleus â€º nucleoplasm. Nucleus matrix.
Q9R0Y5	KAD1_MOUSE Adenylate kinase isoenzyme 1 OS=Mus musculus GN=Ak1 PE=1 SV=1	1.3E-08	30.2	18.6	4 (4 0 0 0 0)	Cytoplasm.
Q8BX02	KANK2_MOUSE KN motif and ankyrin repeat domain-containing protein 2 OS=Mus musculus GN=Kank2 PE=1 SV=1	1.5E-13	50.2	8.5	5 (5 0 0 0 0)	ND
P31324	KAP3_MOUSE cAMP-dependent protein kinase type II-beta regulatory subunit OS=Mus musculus GN=Prkar2b PE=1 SV=3	3.0E-06	20.2	7.9	2 (2 0 0 0 0)	Cytoplasm. Cell membrane.
P11798	KCC2A_MOUSE Calcium/calmodulin-dependent protein kinase type II alpha chain OS=Mus musculus GN=Camk2a PE=1 SV=2	4.7E-12	30.2	6.5	4 (4 0 0 0 0)	Cytoplasm. Cell junction â€º synapse â€º presynaptic cell membrane. Cell junction â€º synapse.
Q6PHZ2	KCC2D_MOUSE Calcium/calmodulin-dependent protein kinase type II delta chain OS=Mus musculus GN=Camk2d PE=1 SV=1	2.7E-11	30.2	7.0	5 (5 0 0 0 0)	Cell membrane â€º sarcolemma; Peripheral membrane protein; Cytoplasmic side. Sarcoplasmic reticulum membrane; Peripheral membrane protein; Cytoplasmic side.
Q60749	KHDR1_MOUSE KH domain-containing, RNA-binding, signal transduction-associated protein 1 OS=Mus musculus GN=Khdrbs1 PE=1 SV=2	1.1E-07	20.2	5.4	2 (2 0 0 0 0)	Nucleus. Membrane.
P33175	KIF5A_MOUSE Kinesin heavy chain isoform 5A OS=Mus musculus GN=Kif5a PE=1 SV=3	1.6E-06	50.2	4.6	5 (5 0 0 0 0)	Cytoplasm â€º perinuclear region. Cytoplasm â€º cytoskeleton.
Q61768	KINH_MOUSE Kinesin-1 heavy chain OS=Mus musculus GN=Kif5b PE=1 SV=2	3.4E-06	40.2	5.4	4 (4 0 0 0 0)	Cytoplasm â€º cytoskeleton.
Q80W68	KIRR1_MOUSE Kin of IRRE-like protein 1 OS=Mus	8.0E-10	20.2	4.2	3 (3 0 0 0 0)	Cell membrane; Single-pass type I

	musculus GN=Kirrel PE=1 SV=1					membrane protein.
P52480	KPYM_MOUSE Pyruvate kinase isozymes M1/M2 OS=Mus musculus GN=Pkm2 PE=1 SV=4	1.0E-30	230.3	45.4	42 (42 0 0 0 0)	Cytoplasm. Nucleus.
Q61595	KTN1_MOUSE Kinectin OS=Mus musculus GN=Ktn1 PE=1 SV=1	1.0E-30	340.3	30.4	52 (52 0 0 0 0)	Endoplasmic reticulum membrane; Single-pass type II membrane protein.
P02469	LAMB1_MOUSE Laminin subunit beta-1 OS=Mus musculus GN=Lamb1-1 PE=1 SV=2	1.1E-10	80.2	5.9	10 (10 0 0 0 0)	Secreted â€º extracellular space â€º extracellular matrix â€º basement membrane.
P02468	LAMC1_MOUSE Laminin subunit gamma-1 OS=Mus musculus GN=Lamc1 PE=1 SV=2	6.5E-10	40.2	3.3	6 (6 0 0 0 0)	Secreted â€º extracellular space â€º extracellular matrix â€º basement membrane.
Q80TH2	LAP2_MOUSE Protein LAP2 OS=Mus musculus GN=Erbb2ip PE=1 SV=2	2.3E-09	50.3	5.1	9 (9 0 0 0 0)	Cell junction â€º hemidesmosome.
Q61029	LAP2B_MOUSE Lamina-associated polypeptide 2, isoforms beta/delta/epsilon/gamma OS=Mus musculus GN=Tmpo PE=1 SV=3	3.5E-13	20.2	5.8	2 (2 0 0 0 0)	Nucleus inner membrane; Single-pass type II membrane protein. Chromosome.
Q924Z4	LASS2_MOUSE LAG1 longevity assurance homolog 2 OS=Mus musculus GN=Lass2 PE=1 SV=1	1.1E-15	20.3	4.7	2 (2 0 0 0 0)	Nucleus membrane; Multi-pass membrane protein. Endoplasmic reticulum membrane; Multi-pass membrane protein.
Q8C172	LASS6_MOUSE LAG1 longevity assurance homolog 6 OS=Mus musculus GN=Lass6 PE=1 SV=1	7.4E-05	20.1	2.9	2 (2 0 0 0 0)	Nucleus membrane; Multi-pass membrane protein. Endoplasmic reticulum membrane; Multi-pass membrane protein.
Q9Z127	LAT1_MOUSE Large neutral amino acids transporter small subunit 1 OS=Mus musculus	3.8E-11	60.2	8.6	13 (13 0 0 0 0)	Cytoplasm â€º cytosol. Apical cell membrane; Multi-pass membrane

	GN=Slc7a5 PE=1 SV=1					protein.
Q8C129	LCAP_MOUSE Leucyl-cystinyl aminopeptidase OS=Mus musculus GN=Lnpep PE=1 SV=1	1.2E-09	170.3	16.2	20 (20 0 0 0 0)	Cell membrane; Single-pass type II membrane protein. Endomembrane system; Single-pass type II membrane protein.
Q3UN02	LCLT1_MOUSE Lysocardiolipin acyltransferase 1 OS=Mus musculus GN=Lclat1 PE=2 SV=2	3.1E-06	30.1	8.8	3 (3 0 0 0 0)	Endoplasmic reticulum membrane; Multi-pass membrane protein.
P06151	LDHA_MOUSE L-lactate dehydrogenase A chain OS=Mus musculus GN=Ldha PE=1 SV=3	2.3E-07	30.1	9.0	3 (3 0 0 0 0)	Cytoplasm.
P35951	LDLR_MOUSE Low-density lipoprotein receptor OS=Mus musculus GN=Ldlr PE=1 SV=1	4.1E-12	60.3	10.6	7 (7 0 0 0 0)	Cell membrane; Single-pass type I membrane protein. Endomembrane system; Single-pass type I membrane protein. Membrane â€º clathrin-coated pit; Single-pass type I membrane protein.
P16110	LEG3_MOUSE Galectin-3 OS=Mus musculus GN=Lgals3 PE=1 SV=3	1.2E-12	50.2	19.7	6 (6 0 0 0 0)	Cytoplasm. Nucleus. Secreted.
Q9JL15	LEG8_MOUSE Galectin-8 OS=Mus musculus GN=Lgals8 PE=2 SV=1	4.6E-06	20.1	6.3	2 (2 0 0 0 0)	Cytoplasm.
Q9JL15	LEG8_MOUSE Galectin-8 OS=Mus musculus GN=Lgals8 PE=2 SV=1	1.2E-08	30.2	10.4	3 (3 0 0 0 0)	Cytoplasm.
Q9Z2I0	LETM1_MOUSE LETM1 and EF-hand domain-containing protein 1, mitochondrial OS=Mus musculus GN=Letm1 PE=2 SV=1	2.3E-14	70.3	17.9	7 (7 0 0 0 0)	Mitochondrion inner membrane; Single-pass membrane protein.
P15702	LEUK_MOUSE Leukosialin OS=Mus musculus GN=Spn PE=1 SV=1	2.2E-13	30.2	12.4	3 (3 0 0 0 0)	Membrane; Single-pass type I membrane protein.
Q8C8U0	LIPB1_MOUSE Liprin-beta-1 OS=Mus musculus GN=Ppfibp1 PE=1 SV=3	4.7E-06	30.2	4.1	3 (3 0 0 0 0)	ND

Q9D0F3	LMAN1_MOUSE Protein ERGIC-53 OS=Mus musculus GN=Lman1 PE=2 SV=1	1.0E-30	110.3	26.1	15 (15 0 0 0 0)	Endoplasmic reticulum-Golgi intermediate compartment membrane; Single-pass type I membrane protein. Golgi apparatus membrane; Single-pass membrane protein. Endoplasmic reticulum membrane; Single-pass membrane protein.
Q9DBH5	LMAN2_MOUSE Vesicular integral-membrane protein VIP36 OS=Mus musculus GN=Lman2 PE=2 SV=1	4.4E-15	90.3	26.8	16 (16 0 0 0 0)	Golgi apparatus membrane; Single-pass type I membrane protein.
Q8C3X8	LMF2_MOUSE Lipase maturation factor 2 OS=Mus musculus GN=Lmf2 PE=2 SV=1	1.5E-07	20.2	4.7	2 (2 0 0 0 0)	Endoplasmic reticulum membrane; Multi-pass membrane protein.
P48678	LMNA_MOUSE Lamin-A/C OS=Mus musculus GN=Lmna PE=1 SV=2	4.4E-10	40.2	7.2	4 (4 0 0 0 0)	Nucleus. Nucleus envelope.
Q7TQ95	LNP_MOUSE Protein lunapark OS=Mus musculus GN=Lnp PE=1 SV=1	1.1E-06	20.2	5.6	2 (2 0 0 0 0)	Membrane; Multi-pass membrane protein.
Q8CGK3	LONM_MOUSE Lon protease homolog, mitochondrial OS=Mus musculus GN=Lonp1 PE=1 SV=2	1.9E-11	40.2	5.5	4 (4 0 0 0 0)	Mitochondrion matrix.
Q8JZZ7	LPHN2_MOUSE Latrophilin-2 (Fragment) OS=Mus musculus GN=Lphn2 PE=1 SV=2	8.2E-09	40.2	5.8	6 (6 0 0 0 0)	Cell membrane; Multi-pass membrane protein.
Q6PB66	LPPRC_MOUSE Leucine-rich PPR motif-containing protein, mitochondrial OS=Mus musculus GN=Lrpprc PE=1 SV=2	1.6E-06	80.2	6.7	8 (8 0 0 0 0)	Mitochondrion. Nucleus. Nucleus â€º nucleoplasm. Nucleus inner membrane. Nucleus outer membrane.
Q922Q8	LRC59_MOUSE Leucine-rich repeat-containing protein 59 OS=Mus musculus GN=Lrrc59 PE=2 SV=1	1.0E-30	90.4	30.9	23 (23 0 0 0 0)	Microsome membrane; Single-pass type II membrane protein. Endoplasmic reticulum membrane; Single-pass type II

						membrane protein.
Q80WG5	LRC8A_MOUSE Leucine-rich repeat-containing protein 8A OS=Mus musculus GN=Lrrc8a PE=1 SV=1	2.6E-08	30.2	4.4	3 (3 0 0 0 0)	Membrane; Multi-pass membrane protein.
Q8BGR2	LRC8D_MOUSE Leucine-rich repeat-containing protein 8D OS=Mus musculus GN=Lrrc8d PE=2 SV=1	1.1E-06	20.2	2.8	2 (2 0 0 0 0)	Membrane; Multi-pass membrane protein.
Q91ZX7	LRP1_MOUSE Prolow-density lipoprotein receptor-related protein 1 OS=Mus musculus GN=Lrp1 PE=1 SV=1	1.6E-14	600.3	13.7	87 (87 0 0 0 0)	Cell membrane; Single-pass type I membrane protein. Membrane â€º coated pit. Cell membrane; Peripheral membrane protein; Extracellular side. Membrane â€º coated pit. Cytoplasm. Nucleus.
Q60767	LY75_MOUSE Lymphocyte antigen 75 OS=Mus musculus GN=Ly75 PE=1 SV=1	5.8E-10	80.3	6.0	10 (10 0 0 0 0)	Membrane; Single-pass type I membrane protein.
Q80WJ7	LYRIC_MOUSE Protein LYRIC OS=Mus musculus GN=Mtdh PE=1 SV=1	1.3E-06	30.2	6.9	3 (3 0 0 0 0)	Endoplasmic reticulum membrane; Single-pass membrane protein. Nucleus membrane; Single-pass membrane protein. Cell junction â€º tight junction. Nucleus â€º nucleolus. Cytoplasm â€º perinuclear region.
Q9CR62	M2OM_MOUSE Mitochondrial 2-oxoglutarate/malate carrier protein OS=Mus musculus GN=Slc25a11 PE=1 SV=3	3.0E-12	40.3	19.7	6 (6 0 0 0 0)	Mitochondrion inner membrane; Multi-pass membrane protein.
P39098	MA1A2_MOUSE Mannosyl-oligosaccharide 1,2-alpha-mannosidase IB OS=Mus musculus GN=Man1a2 PE=2 SV=1	1.3E-10	30.2	7.8	3 (3 0 0 0 0)	Golgi apparatus membrane; Single-pass type II membrane protein.
P27046	MA2A1_MOUSE Alpha-mannosidase 2 OS=Mus musculus GN=Man2a1 PE=1	7.0E-14	150.3	18.0	27 (27 0 0 0 0)	Golgi apparatus membrane; Single-pass type II

	SV=1					membrane protein.
Q9QXZ0	MACF1_MOUSE Microtubule-actin cross-linking factor 1 OS=Mus musculus GN=Macf1 PE=1 SV=1	1.2E-10	130.2	2.9	18 (18 0 0 0 0)	Cytoplasm. Cytoplasm â€º cytoskeleton. Golgi apparatus. Cell membrane. Cell projection â€º ruffle membrane. Cytoplasm. Golgi apparatus.
Q9CQY5	MAGT1_MOUSE Magnesium transporter protein 1 OS=Mus musculus GN=Magt1 PE=2 SV=1	4.7E-07	30.2	10.1	4 (4 0 0 0 0)	Endoplasmic reticulum membrane; Multi-pass membrane protein.
Q99KE1	MAOM_MOUSE NAD-dependent malic enzyme, mitochondrial OS=Mus musculus GN=Me2 PE=2 SV=1	9.8E-05	20.1	1.7	2 (2 0 0 0 0)	Mitochondrion matrix.
P26645	MARCS_MOUSE Myristoylated alanine-rich C-kinase substrate OS=Mus musculus GN=Marcks PE=1 SV=2	1.0E-30	60.2	28.8	16 (16 0 0 0 0)	Cytoplasm â€º cytoskeleton. Membrane; Lipid-anchor.
Q61166	MARE1_MOUSE Microtubule-associated protein RP/EB family member 1 OS=Mus musculus GN=Mapre1 PE=1 SV=3	3.2E-07	20.2	14.2	2 (2 0 0 0 0)	Cytoplasm. Cytoplasm â€º cytoskeleton. Cytoplasm â€º cytoskeleton â€º centrosome.
P97310	MCM2_MOUSE DNA replication licensing factor MCM2 OS=Mus musculus GN=Mcm2 PE=1 SV=3	2.2E-05	40.2	3.9	4 (4 0 0 0 0)	Nucleus.
P49717	MCM4_MOUSE DNA replication licensing factor MCM4 OS=Mus musculus GN=Mcm4 PE=2 SV=1	6.1E-08	30.2	5.0	5 (5 0 0 0 0)	Nucleus.
P49718	MCM5_MOUSE DNA replication licensing factor MCM5 OS=Mus musculus GN=Mcm5 PE=2 SV=1	6.6E-09	70.2	14.6	8 (8 0 0 0 0)	Nucleus.
P97311	MCM6_MOUSE DNA replication licensing factor MCM6 OS=Mus musculus GN=Mcm6 PE=1 SV=1	9.7E-09	20.2	2.8	2 (2 0 0 0 0)	Nucleus.
Q61881	MCM7_MOUSE DNA replication licensing factor MCM7 OS=Mus musculus GN=Mcm7 PE=2 SV=1	9.4E-13	110.2	21.4	12 (12 0 0 0 0)	Nucleus.

P08249	MDHM_MOUSE Malate dehydrogenase, mitochondrial OS=Mus musculus GN=Mdh2 PE=1 SV=3	7.8E-15	120.4	37.3	17 (17 0 0 0 0)	Mitochondrion matrix.
P06795	MDR1_MOUSE Multidrug resistance protein 1 OS=Mus musculus GN=Abcb1 PE=1 SV=1	1.7E-14	68.2	7.8	9 (8 1 0 0 0)	Membrane; Multi-pass membrane protein.
Q07646	MEST_MOUSE Mesoderm-specific transcript protein OS=Mus musculus GN=Mest PE=2 SV=1	9.1E-06	20.2	2.7	4 (4 0 0 0 0)	Endoplasmic reticulum membrane; Multi-pass membrane protein.
Q811U4	MFN1_MOUSE Mitofusin-1 OS=Mus musculus GN=Mfn1 PE=1 SV=2	5.4E-08	40.2	6.6	4 (4 0 0 0 0)	Mitochondrion outer membrane; Multi-pass membrane protein.
Q80U63	MFN2_MOUSE Mitofusin-2 OS=Mus musculus GN=Mfn2 PE=1 SV=3	1.6E-08	20.2	2.6	2 (2 0 0 0 0)	Mitochondrion outer membrane; Multi-pass membrane protein.
P27808	MGAT1_MOUSE Alpha-1,3-mannosyl-glycoprotein 2-beta-N-acetylglucosaminyltransferase OS=Mus musculus GN=Mgat1 PE=2 SV=1	7.0E-11	20.2	6.9	3 (3 0 0 0 0)	Golgi apparatus membrane; Single-pass type II membrane protein.
Q8BI84	MIA3_MOUSE Melanoma inhibitory activity protein 3 OS=Mus musculus GN=Mia3 PE=1 SV=2	8.7E-08	30.2	2.0	5 (5 0 0 0 0)	Endoplasmic reticulum membrane; Single-pass type I membrane protein.
Q3THE2	ML12B_MOUSE Myosin regulatory light chain 12B OS=Mus musculus GN=Myl12b PE=1 SV=2	1.3E-05	20.1	12.2	3 (3 0 0 0 0)	ND
Q6ZQI3	MLEC_MOUSE Malectin OS=Mus musculus GN=Mlec PE=2 SV=2	9.9E-09	30.2	14.1	5 (5 0 0 0 0)	Endoplasmic reticulum membrane; Single-pass type I membrane protein.
P53690	MMP14_MOUSE Matrix metalloproteinase-14 OS=Mus musculus GN=Mmp14 PE=2 SV=2	1.8E-07	50.1	8.8	5 (5 0 0 0 0)	Membrane; Single-pass type I membrane protein; Extracellular side. Melanosome.
P26041	MOES_MOUSE Moesin OS=Mus musculus GN=Msn PE=1 SV=3	4.6E-11	118.3	21.8	15 (14 1 0 0 0)	Cell membrane; Peripheral membrane protein; Cytoplasmic side. Cytoplasm â€º cytoskeleton. Apical cell membrane;

						Peripheral membrane protein; Cytoplasmic side. Cell projection â€º microvillus membrane; Peripheral membrane protein; Cytoplasmic side.
Q80UM7	MOGS_MOUSE Mannosyl-oligosaccharide glucosidase OS=Mus musculus GN=Mogs PE=2 SV=1	3.9E-11	80.2	11.6	12 (12 0 0 0 0)	Endoplasmic reticulum membrane; Single-pass type II membrane protein.
P53986	MOT1_MOUSE Monocarboxylate transporter 1 OS=Mus musculus GN=Slc16a1 PE=1 SV=1	1.1E-15	60.3	14.0	44 (44 0 0 0 0)	Cell membrane; Multi-pass membrane protein.
Q8VEM8	MPCP_MOUSE Phosphate carrier protein, mitochondrial OS=Mus musculus GN=Slc25a3 PE=1 SV=1	7.5E-13	90.2	18.8	20 (20 0 0 0 0)	Mitochondrion inner membrane; Multi-pass membrane protein.
P24668	MPRD_MOUSE Cation-dependent mannose-6-phosphate receptor OS=Mus musculus GN=M6pr PE=1 SV=1	4.6E-14	40.3	19.8	8 (8 0 0 0 0)	Lysosome membrane; Single-pass type I membrane protein.
Q07113	MPRI_MOUSE Cation-independent mannose-6-phosphate receptor OS=Mus musculus GN=Igf2r PE=1 SV=1	9.7E-08	100.2	3.6	12 (12 0 0 0 0)	Lysosome membrane; Single-pass type I membrane protein.
Q64449	MRC2_MOUSE C-type mannose receptor 2 OS=Mus musculus GN=Mrc2 PE=1 SV=2	1.3E-11	60.2	4.7	10 (10 0 0 0 0)	Membrane; Single-pass type I membrane protein.
Q7TT50	MRCKB_MOUSE Serine/threonine-protein kinase MRCK beta OS=Mus musculus GN=Cdc42bpb PE=1 SV=1	1.3E-09	40.2	3.4	4 (4 0 0 0 0)	Cytoplasm. Cell membrane; Peripheral membrane protein; Cytoplasmic side. Cell junction.
O35379	MRP1_MOUSE Multidrug resistance-associated protein 1 OS=Mus musculus GN=Abcc1 PE=1 SV=1	2.9E-14	110.3	9.8	28 (28 0 0 0 0)	Cell membrane; Multi-pass membrane protein.
Q791T5	MTCH1_MOUSE Mitochondrial carrier homolog 1 OS=Mus musculus GN=Mtch1 PE=1 SV=1	1.9E-07	30.1	8.2	3 (3 0 0 0 0)	Mitochondrion inner membrane; Multi-pass membrane protein.
Q791V5	MTCH2_MOUSE Mitochondrial carrier homolog 2 OS=Mus musculus GN=Mtch2 PE=1	1.2E-10	40.2	20.5	4 (4 0 0 0 0)	Mitochondrion inner membrane; Multi-pass membrane protein.

	SV=1					
P47802	MTX1_MOUSE Metaxin-1 OS=Mus musculus GN=Mtx1 PE=1 SV=1	3.3E-09	20.1	9.5	2 (2 0 0 0 0)	Mitochondrion outer membrane.
Q9CZH7	MXRA7_MOUSE Matrix-remodeling-associated protein 7 OS=Mus musculus GN=Mxra7 PE=1 SV=2	3.0E-14	20.2	16.3	4 (4 0 0 0 0)	Membrane; Single-pass membrane protein.
Q9DBV4	MXRA8_MOUSE Matrix-remodeling-associated protein 8 OS=Mus musculus GN=Mxra8 PE=2 SV=1	1.6E-08	30.2	7.5	3 (3 0 0 0 0)	Membrane; Single-pass type I membrane protein.
O35682	MYADM_MOUSE Myeloid-associated differentiation marker OS=Mus musculus GN=Myadm PE=2 SV=2	3.0E-12	30.2	8.4	24 (24 0 0 0 0)	Membrane; Multi-pass membrane protein.
Q61879	MYH10_MOUSE Myosin-10 OS=Mus musculus GN=Myh10 PE=1 SV=2	2.7E-12	100.3	5.5	12 (12 0 0 0 0)	ND
O08638	MYH11_MOUSE Myosin-11 OS=Mus musculus GN=Myh11 PE=1 SV=1	3.6E-12	68.2	3.6	11 (10 1 0 0 0)	Melanosome. Cytoplasm â€º myofibril.
Q8VDD5	MYH9_MOUSE Myosin-9 OS=Mus musculus GN=Myh9 PE=1 SV=4	1.2E-14	758.3	33.5	104 (103 1 0 0 0)	ND
Q60605	MYL6_MOUSE Myosin light polypeptide 6 OS=Mus musculus GN=Myl6 PE=1 SV=3	9.4E-12	30.2	20.5	8 (8 0 0 0 0)	ND
P46735	MYO1B_MOUSE Myosin-Ib OS=Mus musculus GN=Myo1b PE=2 SV=2	6.0E-10	50.2	5.0	5 (5 0 0 0 0)	ND
Q9WTI7	MYO1C_MOUSE Myosin-Ic OS=Mus musculus GN=Myo1c PE=1 SV=2	8.0E-12	190.2	22.9	37 (37 0 0 0 0)	Cytoplasm. Cell membrane. Cell projection â€º stereocilium membrane. Nucleus â€º nucleolus. Nucleus â€º nucleoplasm. Nucleus â€º nuclear pore complex.
Q5SYD0	MYO1D_MOUSE Myosin-Id OS=Mus musculus GN=Myo1d PE=1 SV=1	3.6E-05	18.1	1.8	2 (1 1 0 0 0)	ND
Q69ZN7	MYOF_MOUSE Myoferlin OS=Mus musculus GN=Myof PE=1 SV=2	3.3E-15	880.3	36.8	216 (216 0 0 0 0)	Cell membrane; Single-pass type II membrane protein. Nucleus membrane; Single-pass type II

						membrane protein. Cytoplasmic vesicle membrane; Single-pass type II membrane protein.
Q9DBR7	MYPT1_MOUSE Protein phosphatase 1 regulatory subunit 12A OS=Mus musculus GN=Ppp1r12a PE=1 SV=2	5.0E-07	20.2	2.3	2 (2 0 0 0 0)	Cytoplasm.
Q9DCN2	NB5R3_MOUSE NADH-cytochrome b5 reductase 3 OS=Mus musculus GN=Cyb5r3 PE=1 SV=3	1.2E-14	190.3	41.5	40 (40 0 0 0 0)	Endoplasmic reticulum membrane; Lipid-anchor; Cytoplasmic side. Mitochondrion outer membrane; Lipid-anchor; Cytoplasmic side. Cytoplasm â€º cytosol.
P13595	NCAM1_MOUSE Neural cell adhesion molecule 1 OS=Mus musculus GN=Ncam1 PE=1 SV=3	1.0E-30	250.3	20.7	112 (112 0 0 0 0)	Cell membrane; Single-pass type I membrane protein. Cell membrane; Lipid-anchor â€º GPI-anchor.
P28660	NCKP1_MOUSE Nck-associated protein 1 OS=Mus musculus GN=Nckap1 PE=2 SV=2	2.3E-06	20.2	1.9	2 (2 0 0 0 0)	Cell membrane; Single-pass membrane protein; Cytoplasmic side. Cell projection â€º lamellipodium membrane; Single-pass membrane protein; Cytoplasmic side. Cytoplasm.
Q8VCM8	NCLN_MOUSE Nicalin OS=Mus musculus GN=Ncln PE=2 SV=2	1.2E-09	70.3	15.5	13 (13 0 0 0 0)	Endoplasmic reticulum membrane; Single-pass membrane protein.
P37040	NCPR_MOUSE NADPH--cytochrome P450 reductase OS=Mus musculus GN=Por PE=1 SV=2	2.6E-14	110.3	23.3	18 (18 0 0 0 0)	Endoplasmic reticulum membrane; Peripheral membrane protein.
Q9Z1P6	NDUA7_MOUSE NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 7 OS=Mus musculus GN=Ndufa7 PE=1 SV=3	7.3E-06	20.2	19.5	2 (2 0 0 0 0)	Mitochondrion inner membrane; Peripheral membrane protein; Matrix side.

Q9DCJ5	NDUA8_MOUSE NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 8 OS=Mus musculus GN=Ndufa8 PE=1 SV=3	1.8E-07	20.3	18.6	3 (3 0 0 0 0)	Mitochondrion. Mitochondrion intermembrane space.
Q9DC69	NDUA9_MOUSE NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial OS=Mus musculus GN=Ndufa9 PE=1 SV=1	4.6E-11	40.2	17.2	5 (5 0 0 0 0)	Mitochondrion matrix.
Q99LC3	NDUAA_MOUSE NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial OS=Mus musculus GN=Ndufa10 PE=1 SV=1	4.4E-08	20.2	9.3	2 (2 0 0 0 0)	Mitochondrion matrix.
Q7TMF3	NDUAC_MOUSE NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 12 OS=Mus musculus GN=Ndufa12 PE=1 SV=2	1.5E-11	20.2	20.0	3 (3 0 0 0 0)	Mitochondrion inner membrane; Peripheral membrane protein; Matrix side.
Q9ERS2	NDUAD_MOUSE NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 13 OS=Mus musculus GN=Ndufa13 PE=1 SV=3	1.9E-08	40.2	33.3	5 (5 0 0 0 0)	Mitochondrion inner membrane; Single-pass membrane protein; Matrix side. Nucleus.
Q9CQC7	NDUB4_MOUSE NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 4 OS=Mus musculus GN=Ndufb4 PE=1 SV=3	1.7E-14	20.3	29.5	3 (3 0 0 0 0)	Mitochondrion inner membrane; Single-pass membrane protein; Matrix side.
Q9DCS9	NDUBA_MOUSE NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 10 OS=Mus musculus GN=Ndufb10 PE=1 SV=3	1.1E-14	20.3	17.0	2 (2 0 0 0 0)	Mitochondrion inner membrane; Peripheral membrane protein; Matrix side.
Q9DCS9	NDUBA_MOUSE NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 10 OS=Mus musculus GN=Ndufb10 PE=1 SV=3	5.6E-16	20.2	17.0	2 (2 0 0 0 0)	Mitochondrion inner membrane; Peripheral membrane protein; Matrix side.
Q91VD9	NDUS1_MOUSE NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial OS=Mus musculus GN=Ndufs1 PE=1 SV=1	3.1E-09	90.2	15.7	9 (9 0 0 0 0)	Mitochondrion inner membrane.
Q9DCT2	NDUS3_MOUSE NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial OS=Mus musculus GN=Ndufs3 PE=1 SV=2	8.4E-11	60.2	28.9	8 (8 0 0 0 0)	Mitochondrion inner membrane.

Q8K3J1	NDUS8_MOUSE NADH dehydrogenase [ubiquinone] iron-sulfur protein 8, mitochondrial OS=Mus musculus GN=Ndufs8 PE=1 SV=1	4.4E-05	20.1	4.2	2 (2 0 0 0 0)	Mitochondrion.
P46935	NEDD4_MOUSE E3 ubiquitin-protein ligase NEDD4 OS=Mus musculus GN=Nedd4 PE=1 SV=3	4.7E-14	50.2	8.5	5 (5 0 0 0 0)	Cytoplasm. Cell membrane; Peripheral membrane protein.
Q6P5H2	NEST_MOUSE Nestin OS=Mus musculus GN=Nes PE=1 SV=1	1.3E-12	310.3	24.1	88 (88 0 0 0 0)	ND
Q8R1F1	NIBL1_MOUSE Niban-like protein 1 OS=Mus musculus GN=Fam129b PE=2 SV=2	6.2E-08	30.1	4.1	4 (4 0 0 0 0)	Cytoplasm â€º cytosol. Cell junction â€º adherens junction.
P57716	NICA_MOUSE Nicastrin OS=Mus musculus GN=Ncstn PE=1 SV=2	6.7E-14	60.2	8.1	22 (22 0 0 0 0)	Membrane; Single-pass type I membrane protein. Melanosome.
Q01705	NOTC1_MOUSE Neurogenic locus notch homolog protein 1 OS=Mus musculus GN=Notch1 PE=1 SV=2	2.4E-05	20.1	0.4	2 (2 0 0 0 0)	Cell membrane; Single-pass type I membrane protein. Nucleus.
P28656	NP1L1_MOUSE Nucleosome assembly protein 1-like 1 OS=Mus musculus GN=Nap1l1 PE=1 SV=2	3.1E-11	30.2	9.7	3 (3 0 0 0 0)	Nucleus. Melanosome.
P97300	NPTN_MOUSE Neuroplastin OS=Mus musculus GN=Nptn PE=1 SV=2	1.0E-09	60.2	21.0	23 (23 0 0 0 0)	Cell membrane; Single-pass type I membrane protein.
Q9R1J0	NSDHL_MOUSE Sterol-4-alpha-carboxylate 3-dehydrogenase, decarboxylating OS=Mus musculus GN=Nsdhl PE=2 SV=1	6.0E-10	50.2	17.7	6 (6 0 0 0 0)	Membrane; Single-pass membrane protein.
P46460	NSF_MOUSE Vesicle-fusing ATPase OS=Mus musculus GN=Nsf PE=1 SV=2	6.8E-09	50.2	7.5	5 (5 0 0 0 0)	Cytoplasm.
Q99P88	NU155_MOUSE Nuclear pore complex protein Nup155 OS=Mus musculus GN=Nup155 PE=2 SV=1	3.2E-08	20.2	2.5	2 (2 0 0 0 0)	Nucleus â€º nuclear pore complex. Nucleus membrane; Peripheral membrane protein; Cytoplasmic side. Nucleus membrane; Peripheral

						membrane protein; Nucleoplasmic side.
Q80U93	NU214_MOUSE Nuclear pore complex protein Nup214 OS=Mus musculus GN=Nup214 PE=1 SV=2	6.0E-07	40.2	2.6	5 (5 0 0 0 0)	Nucleus â€º nuclear pore complex.
Q9R061	NUBP2_MOUSE Cytosolic Fe-S cluster assembly factor NUBP2 OS=Mus musculus GN=Nubp2 PE=1 SV=1	2.4E-09	20.2	11.3	2 (2 0 0 0 0)	Nucleus. Cytoplasm â€º cytoskeleton â€º centrosome.
Q02819	NUCB1_MOUSE Nucleobindin-1 OS=Mus musculus GN=Nucb1 PE=1 SV=2	4.9E-12	200.2	42.3	37 (37 0 0 0 0)	Golgi apparatus â€º cis-Golgi network membrane; Peripheral membrane protein; Lumenal side. Cytoplasm.
P81117	NUCB2_MOUSE Nucleobindin-2 OS=Mus musculus GN=Nucb2 PE=1 SV=2	3.2E-06	30.2	7.4	3 (3 0 0 0 0)	Perikaryon. Endoplasmic reticulum. Nucleus envelope.
P09405	NUCL_MOUSE Nucleolin OS=Mus musculus GN=Ncl PE=1 SV=2	3.2E-10	30.2	6.4	6 (6 0 0 0 0)	Nucleus â€º nucleolus. Cytoplasm.
O35685	NUDC_MOUSE Nuclear migration protein nudC OS=Mus musculus GN=Nudc PE=1 SV=1	2.2E-05	20.1	6.0	2 (2 0 0 0 0)	Cytoplasm â€º cytoskeleton. Nucleus.
Q63850	NUP62_MOUSE Nuclear pore glycoprotein p62 OS=Mus musculus GN=Nup62 PE=1 SV=2	6.8E-07	20.2	4.6	2 (2 0 0 0 0)	Nucleus â€º nuclear pore complex. Cytoplasm â€º cytoskeleton â€º spindle pole.
Q8CEC0	NUP88_MOUSE Nuclear pore complex protein Nup88 OS=Mus musculus GN=Nup88 PE=2 SV=1	1.2E-06	60.2	9.7	6 (6 0 0 0 0)	Nucleus â€º nuclear pore complex.
Q8BJ71	NUP93_MOUSE Nuclear pore complex protein Nup93 OS=Mus musculus GN=Nup93 PE=2 SV=1	4.8E-08	40.2	5.5	4 (4 0 0 0 0)	Nucleus â€º nuclear pore complex.
P29758	OAT_MOUSE Ornithine aminotransferase, mitochondrial OS=Mus musculus GN=Oat PE=1 SV=1	3.5E-11	40.3	11.6	4 (4 0 0 0 0)	Mitochondrion matrix.
Q60597	ODO1_MOUSE 2-oxoglutarate dehydrogenase E1 component, mitochondrial OS=Mus musculus GN=Ogdh PE=1 SV=3	3.1E-10	60.2	5.0	6 (6 0 0 0 0)	Mitochondrion matrix.

Q9D2G2	ODO2_MOUSE Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial OS=Mus musculus GN=Dlst PE=1 SV=1	2.2E-07	30.2	7.7	3 (3 0 0 0 0)	Mitochondrion.
Q8BMF4	ODP2_MOUSE Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial OS=Mus musculus GN=Dlat PE=1 SV=2	6.7E-15	80.2	16.0	10 (10 0 0 0 0)	Mitochondrion matrix.
Q9D051	ODPB_MOUSE Pyruvate dehydrogenase E1 component subunit beta, mitochondrial OS=Mus musculus GN=Pdhb PE=1 SV=1	3.8E-12	30.2	12.3	4 (4 0 0 0 0)	Mitochondrion matrix.
P58281	OPA1_MOUSE Dynamin-like 120 kDa protein, mitochondrial OS=Mus musculus GN=Opa1 PE=1 SV=1	1.2E-07	30.1	3.2	3 (3 0 0 0 0)	Mitochondrion inner membrane; Single-pass membrane protein. Mitochondrion intermembrane space.
O54734	OST48_MOUSE Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit OS=Mus musculus GN=Ddost PE=1 SV=1	1.0E-30	80.3	25.6	13 (13 0 0 0 0)	Endoplasmic reticulum membrane; Single-pass type I membrane protein.
O54901	OX2G_MOUSE OX-2 membrane glycoprotein OS=Mus musculus GN=Cd200 PE=1 SV=1	2.4E-08	70.2	21.2	8 (8 0 0 0 0)	Cell membrane; Single-pass type I membrane protein.
Q3V1T4	P3H1_MOUSE Prolyl 3-hydroxylase 1 OS=Mus musculus GN=Lepre1 PE=2 SV=2	4.3E-07	18.2	3.2	2 (1 1 0 0 0)	Endoplasmic reticulum. Secreted â€º extracellular space â€º extracellular matrix.
Q60715	P4HA1_MOUSE Prolyl 4-hydroxylase subunit alpha-1 OS=Mus musculus GN=P4ha1 PE=2 SV=2	1.9E-07	40.2	9.0	4 (4 0 0 0 0)	Endoplasmic reticulum lumen.
Q9Z110	P5CS_MOUSE Delta-1-pyrroline-5-carboxylate synthetase OS=Mus musculus GN=Aldh18a1 PE=2 SV=1	7.8E-15	130.3	19.1	15 (15 0 0 0 0)	Mitochondrion inner membrane.

P47713	PA24A_MOUSE Cytosolic phospholipase A2 OS=Mus musculus GN=Pla2g4a PE=1 SV=1	7.6E-05	20.1	3.3	2 (2 0 0 0 0)	Cytoplasm. Cytoplasmic vesicle.
P29341	PABP1_MOUSE Polyadenylate-binding protein 1 OS=Mus musculus GN=Pabpc1 PE=1 SV=1	1.6E-11	40.2	11.2	5 (5 0 0 0 0)	Cytoplasm. Nucleus.
Q9CY58	PAIRB_MOUSE Plasminogen activator inhibitor 1 RNA-binding protein OS=Mus musculus GN=Serbp1 PE=1 SV=2	1.1E-11	50.3	14.0	6 (6 0 0 0 0)	Cytoplasm. Nucleus. Cytoplasm â€º perinuclear region.
Q8BR92	PALM2_MOUSE Paralemmin-2 OS=Mus musculus GN=Palm2 PE=1 SV=1	6.9E-12	20.3	8.0	4 (4 0 0 0 0)	Cell membrane; Lipid-anchor; Cytoplasmic side.
Q2EMV9	PAR14_MOUSE Poly [ADP-ribose] polymerase 14 OS=Mus musculus GN=Parp14 PE=1 SV=2	2.9E-10	30.2	2.3	3 (3 0 0 0 0)	Nucleus. Cytoplasm.
Q8CAS9	PARP9_MOUSE Poly [ADP-ribose] polymerase 9 OS=Mus musculus GN=Parp9 PE=1 SV=2	1.1E-08	20.2	2.8	2 (2 0 0 0 0)	Cytoplasm â€º cytosol. Nucleus.
Q3TVI8	PBIP1_MOUSE Pre-B-cell leukemia transcription factor-interacting protein 1 OS=Mus musculus GN=Pbxip1 PE=1 SV=2	7.1E-08	60.2	8.7	6 (6 0 0 0 0)	Cytoplasm â€º cytoskeleton. Nucleus.
Q3TFD2	PCAT1_MOUSE Lysophosphatidylcholine acyltransferase 1 OS=Mus musculus GN=Lpcat1 PE=1 SV=1	1.6E-08	30.2	5.8	5 (5 0 0 0 0)	Endoplasmic reticulum membrane; Single-pass type II membrane protein. Golgi apparatus membrane; Single-pass type II membrane protein.
P60335	PCBP1_MOUSE Poly(rC)-binding protein 1 OS=Mus musculus GN=Pcbp1 PE=1 SV=1	6.0E-12	30.3	12.4	3 (3 0 0 0 0)	Nucleus.
Q61990	PCBP2_MOUSE Poly(rC)-binding protein 2 OS=Mus musculus GN=Pcbp2 PE=1 SV=1	8.6E-11	30.2	10.5	5 (5 0 0 0 0)	Nucleus. Cytoplasm.
Q8BH04	PCKGM_MOUSE Phosphoenolpyruvate carboxykinase [GTP], mitochondrial OS=Mus musculus GN=Pck2 PE=2 SV=1	8.9E-14	90.3	20.6	9 (9 0 0 0 0)	Mitochondrion.

Q9R0L6	PCM1_MOUSE Pericentriolar material 1 protein OS=Mus musculus GN=Pcm1 PE=1 SV=1	3.7E-09	40.2	2.0	6 (6 0 0 0 0)	Cytoplasm â€º cytoskeleton. Cytoplasm â€º cytoskeleton â€º centrosome. Cytoplasmic granule.
P48725	PCNT_MOUSE Pericentrin OS=Mus musculus GN=Pcnt PE=1 SV=1	9.4E-06	40.2	2.0	4 (4 0 0 0 0)	Cytoplasm â€º cytoskeleton â€º centrosome.
Q9CQF9	PCYOX_MOUSE Prenylcysteine oxidase OS=Mus musculus GN=Pcyox1 PE=1 SV=1	4.8E-06	30.2	8.5	3 (3 0 0 0 0)	Lysosome.
Q8C7K6	PCYXL_MOUSE Prenylcysteine oxidase-like OS=Mus musculus GN=Pcyox1l PE=2 SV=1	4.0E-07	20.2	2.2	3 (3 0 0 0 0)	Secreted.
Q9WU78	PDC6I_MOUSE Programmed cell death 6-interacting protein OS=Mus musculus GN=Pdcd6ip PE=1 SV=2	2.2E-12	130.3	18.4	14 (14 0 0 0 0)	Cytoplasm â€º cytosol. Melanosome. Cytoplasm â€º cytoskeleton â€º centrosome.
P09103	PDIA1_MOUSE Protein disulfide-isomerase OS=Mus musculus GN=P4hb PE=1 SV=1	1.0E-13	230.3	46.4	33 (33 0 0 0 0)	Endoplasmic reticulum lumen. Melanosome. Cell membrane; Peripheral membrane protein.
P27773	PDIA3_MOUSE Protein disulfide-isomerase A3 OS=Mus musculus GN=Pdia3 PE=1 SV=2	2.7E-14	290.3	48.5	58 (58 0 0 0 0)	Endoplasmic reticulum lumen. Melanosome.
P08003	PDIA4_MOUSE Protein disulfide-isomerase A4 OS=Mus musculus GN=Pdia4 PE=1 SV=2	7.8E-15	188.3	31.2	19 (18 1 0 0 0)	Endoplasmic reticulum lumen. Melanosome.
Q922R8	PDIA6_MOUSE Protein disulfide-isomerase A6 OS=Mus musculus GN=Pdia6 PE=1 SV=3	5.7E-12	80.3	25.0	12 (12 0 0 0 0)	Endoplasmic reticulum lumen. Cell membrane. Melanosome.
O70400	PDLI1_MOUSE PDZ and LIM domain protein 1 OS=Mus musculus GN=Pdlim1 PE=2 SV=4	5.3E-06	20.1	7.6	2 (2 0 0 0 0)	Cytoplasm â€º cytoskeleton.
P15331	PERI_MOUSE Peripherin OS=Mus musculus GN=Prph PE=1 SV=2	1.2E-07	20.2	4.4	8 (8 0 0 0 0)	ND
Q9R0A0	PEX14_MOUSE Peroxisomal membrane protein PEX14 OS=Mus musculus GN=Pex14 PE=1 SV=1	1.3E-08	50.2	16.2	6 (6 0 0 0 0)	Peroxisome membrane; Peripheral membrane protein; Cytoplasmic side.

Q9DBJ1	PGAM1_MOUSE Phosphoglycerate mutase 1 OS=Mus musculus GN=Pgam1 PE=1 SV=3	6.5E-09	60.2	32.7	6 (6 0 0 0 0)	ND
Q05793	PGBM_MOUSE Basement membrane-specific heparan sulfate proteoglycan core protein OS=Mus musculus GN=Hspg2 PE=1 SV=1	8.3E-09	80.2	3.0	13 (13 0 0 0 0)	Secreted â€º extracellular space â€º extracellular matrix â€º basement membrane.
P05622	PGFRB_MOUSE Beta-type platelet-derived growth factor receptor OS=Mus musculus GN=Pdgfrb PE=1 SV=1	2.5E-11	170.2	19.2	32 (32 0 0 0 0)	Membrane; Single-pass type I membrane protein.
O55022	PGRC1_MOUSE Membrane-associated progesterone receptor component 1 OS=Mus musculus GN=Pgrmc1 PE=1 SV=4	8.9E-15	50.3	22.6	7 (7 0 0 0 0)	Microsome membrane; Single-pass membrane protein. Endoplasmic reticulum membrane; Single-pass membrane protein.
Q80UU9	PGRC2_MOUSE Membrane-associated progesterone receptor component 2 OS=Mus musculus GN=Pgrmc2 PE=1 SV=2	1.0E-30	20.3	18.0	3 (3 0 0 0 0)	Membrane; Single-pass membrane protein.
P67778	PHB_MOUSE Prohibitin OS=Mus musculus GN=Phb PE=1 SV=1	2.7E-12	110.3	42.6	16 (16 0 0 0 0)	Mitochondrion inner membrane.
O35129	PHB2_MOUSE Prohibitin-2 OS=Mus musculus GN=Phb2 PE=1 SV=1	2.8E-14	130.3	40.5	29 (29 0 0 0 0)	Mitochondrion inner membrane. Cytoplasm. Nucleus.
Q6PD26	PIGS_MOUSE GPI transamidase component PIG-S OS=Mus musculus GN=Pigs PE=1 SV=3	2.8E-14	120.3	33.2	16 (16 0 0 0 0)	Endoplasmic reticulum membrane; Multi-pass membrane protein.
Q8BXQ2	PIGT_MOUSE GPI transamidase component PIG-T OS=Mus musculus GN=Pigt PE=1 SV=2	5.2E-08	20.2	5.3	3 (3 0 0 0 0)	Endoplasmic reticulum membrane; Single-pass type I membrane protein.
Q02257	PLAK_MOUSE Junction plakoglobin OS=Mus musculus GN=Jup PE=1 SV=3	1.2E-11	100.2	16.5	15 (15 0 0 0 0)	Cell junction â€º adherens junction. Cell junction â€º desmosome. Cytoplasm â€º cytoskeleton. Membrane; Peripheral

						membrane protein.
Q8K2J0	PLCD3_MOUSE 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase delta-3 OS=Mus musculus GN=Plcd3 PE=1 SV=2	1.2E-05	40.2	6.1	4 (4 0 0 0 0)	Membrane; Peripheral membrane protein. Cytoplasm. Cleavage furrow.
Q9QXS1	PLEC1_MOUSE Plectin-1 OS=Mus musculus GN=Plec1 PE=1 SV=2	8.5E-14	450.2	10.8	67 (67 0 0 0 0)	Cytoplasm â€º cytoskeleton. Cell junction â€º hemidesmosome.
Q07832	PLK1_MOUSE Serine/threonine-protein kinase PLK1 OS=Mus musculus GN=Plk1 PE=2 SV=2	5.8E-07	40.2	7.6	4 (4 0 0 0 0)	Nucleus. Chromosome â€º centromere â€º kinetochore. Cytoplasm â€º cytoskeleton â€º centrosome.
Q9R0E1	PLOD3_MOUSE Procollagen-lysine,2-oxoglutarate 5-dioxygenase 3 OS=Mus musculus GN=Plod3 PE=1 SV=1	5.5E-06	30.2	5.8	4 (4 0 0 0 0)	Rough endoplasmic reticulum membrane; Peripheral membrane protein; Lumenal side.
Q3TRM4	PLPL6_MOUSE Neuropathy target esterase OS=Mus musculus GN=Pnpla6 PE=2 SV=2	1.2E-07	30.2	3.2	3 (3 0 0 0 0)	Endoplasmic reticulum membrane; Single-pass type I membrane protein; Cytoplasmic side.
Q9JJ00	PLS1_MOUSE Phospholipid scramblase 1 OS=Mus musculus GN=Plscr1 PE=2 SV=1	2.7E-06	20.1	6.1	3 (3 0 0 0 0)	Membrane; Single-pass type II membrane protein.
Q9JIZ9	PLS3_MOUSE Phospholipid scramblase 3 OS=Mus musculus GN=Plscr3 PE=2 SV=1	3.9E-13	30.3	11.1	6 (6 0 0 0 0)	Membrane; Single-pass type II membrane protein.
P70206	PLXA1_MOUSE Plexin-A1 OS=Mus musculus GN=Plxna1 PE=1 SV=1	4.9E-10	50.2	3.1	5 (5 0 0 0 0)	Membrane; Single-pass type I membrane protein.
P70207	PLXA2_MOUSE Plexin-A2 OS=Mus musculus GN=Plxna2 PE=1 SV=2	6.8E-09	20.1	1.1	2 (2 0 0 0 0)	Membrane; Single-pass type I membrane protein.
P62137	PP1A_MOUSE Serine/threonine-protein phosphatase PP1-alpha catalytic subunit OS=Mus musculus GN=Ppp1ca PE=1 SV=1	8.5E-08	30.2	11.8	3 (3 0 0 0 0)	Cytoplasm. Nucleus. Nucleus â€º nucleoplasm. Nucleus â€º nucleolus.

P17742	PPIA_MOUSE Peptidyl-prolyl cis-trans isomerase A OS=Mus musculus GN=Ppia PE=1 SV=2	9.0E-10	50.2	20.7	8 (8 0 0 0 0)	Cytoplasm.
P24369	PPIB_MOUSE Peptidyl-prolyl cis-trans isomerase B OS=Mus musculus GN=Ppib PE=2 SV=2	2.2E-12	130.2	47.2	19 (19 0 0 0 0)	Endoplasmic reticulum lumen. Melanosome.
P30412	PPIC_MOUSE Peptidyl-prolyl cis-trans isomerase C OS=Mus musculus GN=Ppic PE=1 SV=1	1.0E-10	50.2	22.6	7 (7 0 0 0 0)	Cytoplasm.
Q9JIG8	PRAF2_MOUSE PRA1 family protein 2 OS=Mus musculus GN=Praf2 PE=2 SV=1	2.8E-10	30.3	16.3	6 (6 0 0 0 0)	Endosome membrane; Multi-pass membrane protein.
Q8R5J9	PRAF3_MOUSE PRA1 family protein 3 OS=Mus musculus GN=Arl6ip5 PE=1 SV=2	1.1E-14	50.4	16.5	13 (13 0 0 0 0)	Endoplasmic reticulum membrane; Multi-pass membrane protein. Cytoplasm. Cytoplasm â€º cytoskeleton.
P35700	PRDX1_MOUSE Peroxiredoxin-1 OS=Mus musculus GN=Prdx1 PE=1 SV=1	9.7E-08	58.2	33.7	9 (6 3 0 0 0)	Cytoplasm. Melanosome.
Q61171	PRDX2_MOUSE Peroxiredoxin-2 OS=Mus musculus GN=Prdx2 PE=1 SV=3	1.5E-07	30.2	19.2	3 (3 0 0 0 0)	Cytoplasm.
O08807	PRDX4_MOUSE Peroxiredoxin-4 OS=Mus musculus GN=Prdx4 PE=1 SV=1	4.2E-09	40.2	17.2	4 (4 0 0 0 0)	Cytoplasm. Secreted.
P99029	PRDX5_MOUSE Peroxiredoxin-5, mitochondrial OS=Mus musculus GN=Prdx5 PE=1 SV=2	2.9E-10	30.2	18.6	3 (3 0 0 0 0)	Mitochondrion. Cytoplasm. Peroxisome.
Q9WUQ2	PREB_MOUSE Prolactin regulatory element-binding protein OS=Mus musculus GN=Preb PE=1 SV=1	1.6E-06	30.2	9.4	3 (3 0 0 0 0)	Nucleus. Membrane; Single-pass membrane protein. Endoplasmic reticulum.
P62334	PRS10_MOUSE 26S protease regulatory subunit S10B OS=Mus musculus GN=Psmc6 PE=1 SV=1	2.0E-08	40.2	13.9	4 (4 0 0 0 0)	Cytoplasm. Nucleus.
P62192	PRS4_MOUSE 26S protease regulatory subunit 4 OS=Mus musculus GN=Psmc1 PE=1 SV=1	9.4E-13	108.3	32.3	11 (10 1 0 0 0)	Cytoplasm. Nucleus.

O88685	PRS6A_MOUSE 26S protease regulatory subunit 6A OS=Mus musculus GN=Psmc3 PE=2 SV=1	7.5E-09	60.2	19.9	7 (7 0 0 0 0)	Cytoplasm. Nucleus.
P54775	PRS6B_MOUSE 26S protease regulatory subunit 6B OS=Mus musculus GN=Psmc4 PE=1 SV=1	1.0E-30	60.4	25.4	7 (7 0 0 0 0)	Cytoplasm. Nucleus.
P46471	PRS7_MOUSE 26S protease regulatory subunit 7 OS=Mus musculus GN=Psmc2 PE=1 SV=5	8.0E-10	58.3	18.9	8 (7 1 0 0 0)	Cytoplasm. Nucleus.
P62196	PRS8_MOUSE 26S protease regulatory subunit 8 OS=Mus musculus GN=Psmc5 PE=1 SV=1	2.2E-08	80.2	24.4	8 (8 0 0 0 0)	Cytoplasm. Nucleus.
Q11011	PSA_MOUSE Puromycin-sensitive aminopeptidase OS=Mus musculus GN=Npepps PE=1 SV=1	7.6E-08	20.2	2.5	2 (2 0 0 0 0)	Cytoplasm â€º cytosol. Nucleus.
P49722	PSA2_MOUSE Proteasome subunit alpha type-2 OS=Mus musculus GN=Psma2 PE=1 SV=2	1.1E-07	20.2	13.2	3 (3 0 0 0 0)	Cytoplasm. Nucleus.
O70435	PSA3_MOUSE Proteasome subunit alpha type-3 OS=Mus musculus GN=Psma3 PE=1 SV=3	2.0E-08	30.2	14.1	3 (3 0 0 0 0)	Cytoplasm. Nucleus.
Q9Z2U1	PSA5_MOUSE Proteasome subunit alpha type-5 OS=Mus musculus GN=Psma5 PE=1 SV=1	2.2E-10	30.2	14.9	3 (3 0 0 0 0)	Cytoplasm. Nucleus.
Q9Z2U0	PSA7_MOUSE Proteasome subunit alpha type-7 OS=Mus musculus GN=Psma7 PE=1 SV=1	5.4E-07	20.2	10.5	2 (2 0 0 0 0)	Cytoplasm. Nucleus.
Q9CWH6	PSA7L_MOUSE Proteasome subunit alpha type-7-like OS=Mus musculus GN=Psma8 PE=2 SV=1	7.2E-06	20.1	11.2	2 (2 0 0 0 0)	Cytoplasm. Nucleus.
O35955	PSB10_MOUSE Proteasome subunit beta type-10 OS=Mus musculus GN=Psmb10 PE=2 SV=1	8.9E-15	20.3	14.7	3 (3 0 0 0 0)	Cytoplasm. Nucleus.
Q9R1P3	PSB2_MOUSE Proteasome subunit beta type-2 OS=Mus musculus GN=Psmb2 PE=1 SV=1	4.9E-10	20.2	13.9	2 (2 0 0 0 0)	Cytoplasm. Nucleus.
Q9D8W5	PSD12_MOUSE 26S proteasome non-ATPase regulatory subunit 12 OS=Mus musculus GN=Psmd12 PE=2 SV=3	8.9E-08	20.2	5.0	2 (2 0 0 0 0)	ND

P26516	PSD7_MOUSE 26S proteasome non-ATPase regulatory subunit 7 OS=Mus musculus GN=Psmd7 PE=1 SV=2	2.9E-07	50.2	18.4	5 (5 0 0 0 0)	ND
Q3TXS7	PSMD1_MOUSE 26S proteasome non-ATPase regulatory subunit 1 OS=Mus musculus GN=Psmd1 PE=1 SV=1	2.0E-06	20.1	2.5	4 (4 0 0 0 0)	ND
Q8VDM4	PSMD2_MOUSE 26S proteasome non-ATPase regulatory subunit 2 OS=Mus musculus GN=Psmd2 PE=1 SV=1	3.2E-05	20.2	3.4	2 (2 0 0 0 0)	ND
P14685	PSMD3_MOUSE 26S proteasome non-ATPase regulatory subunit 3 OS=Mus musculus GN=Psmd3 PE=2 SV=2	6.6E-07	30.2	4.5	3 (3 0 0 0 0)	ND
P97372	PSME2_MOUSE Proteasome activator complex subunit 2 OS=Mus musculus GN=Psme2 PE=2 SV=4	2.5E-11	30.2	17.2	3 (3 0 0 0 0)	ND
P49769	PSN1_MOUSE Presenilin-1 OS=Mus musculus GN=Psen1 PE=1 SV=1	2.4E-13	60.3	12.6	7 (7 0 0 0 0)	Endoplasmic reticulum membrane; Multi-pass membrane protein. Golgi apparatus membrane; Multi-pass membrane protein. Cell surface.
Q8R2Y8	PTH2_MOUSE Peptidyl-tRNA hydrolase 2, mitochondrial OS=Mus musculus GN=Ptrh2 PE=2 SV=1	8.9E-13	20.2	16.0	5 (5 0 0 0 0)	Mitochondrion.
Q8BKG3	PTK7_MOUSE Tyrosine-protein kinase-like 7 OS=Mus musculus GN=Ptk7 PE=1 SV=1	2.2E-15	90.2	9.4	14 (14 0 0 0 0)	Membrane; Single-pass type I membrane protein. Cell junction.
P18052	PTPRA_MOUSE Receptor-type tyrosine-protein phosphatase alpha OS=Mus musculus GN=Ptpra PE=1 SV=2	5.3E-09	60.3	8.0	7 (7 0 0 0 0)	Membrane; Single-pass type I membrane protein.
O54724	PTRF_MOUSE Polymerase I and transcript release factor OS=Mus musculus GN=Ptrf PE=1 SV=1	3.2E-12	40.3	15.6	4 (4 0 0 0 0)	Membrane â€º caveola. Cell membrane. Microsome. Endoplasmic reticulum.

						Cytoplasm â€º cytosol. Mitochondrion. Nucleus.
P32507	PVRL2_MOUSE Poliovirus receptor-related protein 2 OS=Mus musculus GN=Pvrl2 PE=1 SV=2	7.2E-10	30.2	10.6	5 (5 0 0 0 0)	Cell membrane; Single-pass type I membrane protein.
O35435	PYRD_MOUSE Dihydroorotate dehydrogenase, mitochondrial OS=Mus musculus GN=Dhodh PE=2 SV=2	1.3E-05	30.1	8.4	3 (3 0 0 0 0)	Mitochondrion inner membrane; Single-pass membrane protein.
P70698	PYRG1_MOUSE CTP synthase 1 OS=Mus musculus GN=Ctps PE=1 SV=2	4.9E-12	30.3	8.5	4 (4 0 0 0 0)	ND
Q9CZ13	QCR1_MOUSE Cytochrome b-c1 complex subunit 1, mitochondrial OS=Mus musculus GN=Uqcrc1 PE=1 SV=1	1.0E-30	60.3	12.9	6 (6 0 0 0 0)	Mitochondrion inner membrane.
Q9DB77	QCR2_MOUSE Cytochrome b-c1 complex subunit 2, mitochondrial OS=Mus musculus GN=Uqcrc2 PE=1 SV=1	6.2E-13	70.2	21.6	10 (10 0 0 0 0)	Mitochondrion inner membrane; Peripheral membrane protein; Matrix side.
Q9D855	QCR7_MOUSE Cytochrome b-c1 complex subunit 7 OS=Mus musculus GN=Uqcrb PE=1 SV=3	1.4E-10	20.2	22.5	2 (2 0 0 0 0)	Mitochondrion inner membrane.
Q3TMX7	QSOX2_MOUSE Sulfhydryl oxidase 2 OS=Mus musculus GN=Qsox2 PE=2 SV=1	3.2E-09	30.2	6.1	5 (5 0 0 0 0)	Membrane; Single-pass membrane protein.
P61027	RAB10_MOUSE Ras-related protein Rab-10 OS=Mus musculus GN=Rab10 PE=1 SV=1	8.9E-15	68.3	40.5	22 (11 4 1 6 0)	Cell membrane; Lipid-anchor; Cytoplasmic side.
P35283	RAB12_MOUSE Ras-related protein Rab-12 OS=Mus musculus GN=Rab12 PE=1 SV=3	1.1E-05	20.2	8.2	2 (2 0 0 0 0)	Golgi apparatus membrane; Lipid-anchor.
Q91V41	RAB14_MOUSE Ras-related protein Rab-14 OS=Mus musculus GN=Rab14 PE=1 SV=3	1.3E-12	100.3	51.6	17 (17 0 0 0 0)	Early endosome membrane; Lipid-anchor; Cytoplasmic side. Golgi apparatus membrane; Lipid-anchor; Cytoplasmic side. Golgi apparatus â€º trans-Golgi network membrane; Lipid-

						anchor; Cytoplasmic side.
P35293	RAB18_MOUSE Ras-related protein Rab-18 OS=Mus musculus GN=Rab18 PE=2 SV=2	2.7E-10	70.2	34.0	8 (8 0 0 0 0)	Apical cell membrane; Lipid-anchor. Basal cell membrane; Lipid-anchor.
P62821	RAB1A_MOUSE Ras-related protein Rab-1A OS=Mus musculus GN=Rab1A PE=1 SV=3	2.2E-12	110.3	34.1	32 (20 7 5 0 0)	Golgi apparatus. Endoplasmic reticulum.
Q9D1G1	RAB1B_MOUSE Ras-related protein Rab-1B OS=Mus musculus GN=Rab1b PE=1 SV=1	3.4E-12	100.3	27.9	28 (12 7 9 0 0)	Membrane; Lipid-anchor; Cytoplasmic side. Cytoplasm.
P35282	RAB21_MOUSE Ras-related protein Rab-21 OS=Mus musculus GN=Rab21 PE=1 SV=4	7.8E-15	60.3	27.9	7 (7 0 0 0 0)	Endoplasmic reticulum membrane; Lipid-anchor. Golgi apparatus membrane. Early endosome membrane. Cytoplasmic vesicle membrane.
P35288	RAB23_MOUSE Ras-related protein Rab-23 OS=Mus musculus GN=Rab23 PE=1 SV=2	3.5E-09	30.3	18.1	3 (3 0 0 0 0)	Cell membrane; Lipid-anchor; Cytoplasmic side.
P53994	RAB2A_MOUSE Ras-related protein Rab-2A OS=Mus musculus GN=Rab2a PE=1 SV=1	3.2E-10	90.3	43.4	14 (14 0 0 0 0)	Endoplasmic reticulum-Golgi intermediate compartment membrane; Lipid-anchor. Melanosome. Endoplasmic reticulum membrane; Lipid-anchor. Golgi apparatus membrane; Lipid-anchor.
Q921E2	RAB31_MOUSE Ras-related protein Rab-31 OS=Mus musculus GN=Rab31 PE=1 SV=1	2.2E-12	80.2	53.1	16 (16 0 0 0 0)	Cell membrane; Lipid-anchor; Cytoplasmic side.
Q64008	RAB34_MOUSE Ras-related protein Rab-34 OS=Mus musculus GN=Rab34 PE=1 SV=2	3.9E-09	30.2	17.0	3 (3 0 0 0 0)	Cytoplasm. Golgi apparatus.

Q6PHN9	RAB35_MOUSE Ras-related protein Rab-35 OS=Mus musculus GN=Rab35 PE=1 SV=1	1.0E-12	50.2	23.9	10 (10 0 0 0 0)	Cell membrane; Lipid-anchor; Cytoplasmic side. Membrane â€º clathrin-coated pit. Cytoplasmic vesicle â€º clathrin-coated vesicle. Endosome. Melanosome.
Q9CQD1	RAB5A_MOUSE Ras-related protein Rab-5A OS=Mus musculus GN=Rab5a PE=1 SV=1	1.0E-30	86.3	44.2	15 (12 3 0 0 0)	Cell membrane; Lipid-anchor; Cytoplasmic side. Early endosome membrane; Lipid-anchor. Melanosome.
P61021	RAB5B_MOUSE Ras-related protein Rab-5B OS=Mus musculus GN=Rab5b PE=1 SV=1	6.2E-14	40.3	26.5	6 (6 0 0 0 0)	Cell membrane; Lipid-anchor; Cytoplasmic side. Early endosome membrane; Lipid-anchor. Melanosome.
P35278	RAB5C_MOUSE Ras-related protein Rab-5C OS=Mus musculus GN=Rab5c PE=1 SV=2	8.9E-15	128.3	56.0	20 (19 1 0 0 0)	Cell membrane; Lipid-anchor; Cytoplasmic side. Early endosome membrane; Lipid-anchor. Melanosome.
P35279	RAB6A_MOUSE Ras-related protein Rab-6A OS=Mus musculus GN=Rab6a PE=1 SV=4	1.9E-10	70.2	34.1	10 (10 0 0 0 0)	Golgi apparatus membrane; Lipid-anchor.
P51150	RAB7A_MOUSE Ras-related protein Rab-7a OS=Mus musculus GN=Rab7a PE=1 SV=2	6.0E-10	120.2	55.6	28 (28 0 0 0 0)	Late endosome. Lysosome. Cytoplasmic vesicle â€º phagosome. Melanosome.
P55258	RAB8A_MOUSE Ras-related protein Rab-8A OS=Mus musculus GN=Rab8a PE=1 SV=2	7.1E-08	40.2	19.8	5 (5 0 0 0 0)	Cell membrane; Lipid-anchor; Cytoplasmic side. Golgi apparatus. Cytoplasm â€º perinuclear region. Cell projection.
P61028	RAB8B_MOUSE Ras-related protein Rab-8B OS=Mus musculus GN=Rab8b PE=1 SV=1	3.2E-10	20.2	6.8	2 (2 0 0 0 0)	Cell membrane; Lipid-anchor; Cytoplasmic side.
P63001	RAC1_MOUSE Ras-related C3 botulinum toxin substrate 1 OS=Mus musculus	3.2E-11	60.3	22.9	11 (11 0 0 0 0)	Cell membrane; Lipid-anchor; Cytoplasmic side.

	GN=Rac1 PE=1 SV=1					Melanosome.
P63321	RALA_MOUSE Ras-related protein Ral-A OS=Mus musculus GN=Rala PE=1 SV=1	4.1E-12	90.3	30.6	13 (13 0 0 0 0)	Cell surface. Cell membrane; Lipid-anchor; Cytoplasmic side. Cleavage furrow. Midbody.
Q9JIW9	RALB_MOUSE Ras-related protein Ral-B OS=Mus musculus GN=Ralb PE=2 SV=1	3.1E-12	60.3	25.2	11 (11 0 0 0 0)	Cell membrane; Lipid-anchor; Cytoplasmic side.
P62827	RAN_MOUSE GTP-binding nuclear protein Ran OS=Mus musculus GN=Ran PE=1 SV=3	6.8E-07	30.2	11.6	3 (3 0 0 0 0)	Nucleus. Cytoplasm. Melanosome.
P34022	RANG_MOUSE Ran-specific GTPase-activating protein OS=Mus musculus GN=Ranbp1 PE=1 SV=2	1.0E-07	40.2	20.7	4 (4 0 0 0 0)	ND
P62835	RAP1A_MOUSE Ras-related protein Rap-1A OS=Mus musculus GN=Rap1a PE=2 SV=1	3.5E-08	60.3	28.3	10 (10 0 0 0 0)	Cell membrane; Lipid-anchor.
Q99JI6	RAP1B_MOUSE Ras-related protein Rap-1b OS=Mus musculus GN=Rap1b PE=2 SV=2	1.2E-09	20.3	8.2	3 (3 0 0 0 0)	Cell membrane. Cytoplasm â€º cytosol. Cell junction.
Q80ZJ1	RAP2A_MOUSE Ras-related protein Rap-2a OS=Mus musculus GN=Rap2a PE=1 SV=2	6.8E-10	30.2	29.0	3 (3 0 0 0 0)	Recycling endosome membrane; Lipid-anchor; Cytoplasmic side.
P61226	RAP2B_MOUSE Ras-related protein Rap-2b OS=Mus musculus GN=Rap2b PE=1 SV=1	4.9E-11	40.2	15.3	4 (4 0 0 0 0)	Recycling endosome membrane; Lipid-anchor; Cytoplasmic side.
Q8BU31	RAP2C_MOUSE Ras-related protein Rap-2c OS=Mus musculus GN=Rap2c PE=1 SV=1	7.7E-13	20.2	8.7	3 (3 0 0 0 0)	Cytoplasm. Recycling endosome membrane; Lipid-anchor; Cytoplasmic side.
Q60790	RASA3_MOUSE Ras GTPase-activating protein 3 OS=Mus musculus GN=Rasa3 PE=1 SV=1	2.2E-07	50.2	6.4	5 (5 0 0 0 0)	ND
Q61411	RASH_MOUSE GTPase HRas OS=Mus musculus GN=Hras1 PE=1 SV=1	6.9E-09	40.2	21.2	6 (6 0 0 0 0)	Cell membrane. Cell membrane; Lipid-anchor; Cytoplasmic side. Golgi apparatus. Golgi apparatus

						membrane; Lipid-anchor.
P62492	RB11A_MOUSE Ras-related protein Rab-11A OS=Mus musculus GN=Rab11a PE=1 SV=3	8.5E-09	90.2	32.4	19 (19 0 0 0 0)	Cell membrane; Peripheral membrane protein. Recycling endosome membrane; Peripheral membrane protein.
Q8BMG7	RBGPR_MOUSE Rab3 GTPase-activating protein non-catalytic subunit OS=Mus musculus GN=Rab3gap2 PE=1 SV=2	5.7E-09	20.2	1.7	2 (2 0 0 0 0)	Cytoplasm.
Q05186	RCN1_MOUSE Reticulocalbin-1 OS=Mus musculus GN=Rcn1 PE=1 SV=1	2.1E-07	40.2	15.7	5 (5 0 0 0 0)	Endoplasmic reticulum lumen.
Q8BP92	RCN2_MOUSE Reticulocalbin-2 OS=Mus musculus GN=Rcn2 PE=2 SV=1	1.0E-30	20.3	8.4	2 (2 0 0 0 0)	Endoplasmic reticulum lumen.
Q8BH97	RCN3_MOUSE Reticulocalbin-3 OS=Mus musculus GN=Rcn3 PE=2 SV=1	7.4E-11	50.2	15.5	5 (5 0 0 0 0)	Endoplasmic reticulum lumen.
Q9QYF1	RDH11_MOUSE Retinol dehydrogenase 11 OS=Mus musculus GN=Rdh11 PE=2 SV=2	1.7E-10	30.2	11.7	3 (3 0 0 0 0)	Endoplasmic reticulum membrane; Single-pass type II membrane protein.
Q60870	REEP5_MOUSE Receptor expression-enhancing protein 5 OS=Mus musculus GN=Reep5 PE=1 SV=1	3.4E-08	20.1	10.8	6 (6 0 0 0 0)	Membrane; Multi-pass membrane protein.
Q9CQU3	RER1_MOUSE Protein RER1 OS=Mus musculus GN=Rer1 PE=1 SV=1	5.3E-11	20.3	14.8	2 (2 0 0 0 0)	Golgi apparatus membrane; Multi-pass membrane protein.
Q8CHX7	RFTN2_MOUSE Raftlin-2 OS=Mus musculus GN=Rftn2 PE=2 SV=3	8.0E-11	30.2	7.2	3 (3 0 0 0 0)	Cell membrane; Lipid-anchor.
Q9WVM1	RGAP1_MOUSE Rac GTPase-activating protein 1 OS=Mus musculus GN=Racgap1 PE=2 SV=1	2.2E-08	40.2	7.2	7 (7 0 0 0 0)	Nucleus. Cytoplasm. Cytoplasm â€º cytoskeleton â€º spindle. Cytoplasmic vesicle â€º secretory vesicle â€º acrosome.

Q9QUI0	RHOA_MOUSE Transforming protein RhoA OS=Mus musculus GN=Rhoa PE=1 SV=1	5.6E-13	60.3	25.9	10 (10 0 0 0 0)	Cell membrane; Lipid-anchor; Cytoplasmic side. Cytoplasm â€º cytoskeleton.
P84096	RHOG_MOUSE Rho-related GTP-binding protein RhoG OS=Mus musculus GN=Rhog PE=2 SV=1	4.3E-14	50.2	34.0	7 (7 0 0 0 0)	Cell membrane; Lipid-anchor; Cytoplasmic side.
P07742	RIR1_MOUSE Ribonucleoside-diphosphate reductase large subunit OS=Mus musculus GN=Rrm1 PE=2 SV=1	8.5E-11	40.2	6.7	5 (5 0 0 0 0)	Cytoplasm.
Q6ZWV3	RL10_MOUSE 60S ribosomal protein L10 OS=Mus musculus GN=Rpl10 PE=2 SV=3	9.3E-11	30.2	6.5	6 (6 0 0 0 0)	ND
P53026	RL10A_MOUSE 60S ribosomal protein L10a OS=Mus musculus GN=Rpl10a PE=1 SV=3	2.7E-10	20.2	12.4	4 (4 0 0 0 0)	ND
P86048	RL10L_MOUSE 60S ribosomal protein L10-like OS=Mus musculus GN=Rpl10l PE=2 SV=1	1.5E-08	80.2	17.8	14 (14 0 0 0 0)	ND
Q9CXW4	RL11_MOUSE 60S ribosomal protein L11 OS=Mus musculus GN=Rpl11 PE=1 SV=4	1.4E-10	30.2	15.7	3 (3 0 0 0 0)	Nucleus â€º nucleolus.
P35979	RL12_MOUSE 60S ribosomal protein L12 OS=Mus musculus GN=Rpl12 PE=1 SV=2	1.0E-12	30.3	24.2	7 (7 0 0 0 0)	ND
P47963	RL13_MOUSE 60S ribosomal protein L13 OS=Mus musculus GN=Rpl13 PE=2 SV=3	5.0E-11	110.2	38.9	27 (27 0 0 0 0)	ND
P19253	RL13A_MOUSE 60S ribosomal protein L13a OS=Mus musculus GN=Rpl13a PE=1 SV=4	1.2E-06	20.2	5.4	4 (4 0 0 0 0)	ND
Q9CR57	RL14_MOUSE 60S ribosomal protein L14 OS=Mus musculus GN=Rpl14 PE=2 SV=3	1.2E-09	30.2	17.1	6 (6 0 0 0 0)	ND
Q9CZM2	RL15_MOUSE 60S ribosomal protein L15 OS=Mus musculus GN=Rpl15 PE=2 SV=4	1.6E-12	40.2	16.7	8 (8 0 0 0 0)	ND
Q9CPR4	RL17_MOUSE 60S ribosomal protein L17 OS=Mus musculus GN=Rpl17 PE=2 SV=3	8.7E-11	80.3	27.2	15 (15 0 0 0 0)	ND

P35980	RL18_MOUSE 60S ribosomal protein L18 OS=Mus musculus GN=Rpl18 PE=2 SV=3	3.2E-08	60.2	30.3	12 (12 0 0 0 0)	Cytoplasm.
P84099	RL19_MOUSE 60S ribosomal protein L19 OS=Mus musculus GN=Rpl19 PE=1 SV=1	1.8E-14	70.3	22.4	11 (11 0 0 0 0)	ND
O09167	RL21_MOUSE 60S ribosomal protein L21 OS=Mus musculus GN=Rpl21 PE=2 SV=3	1.7E-11	30.2	16.3	4 (4 0 0 0 0)	ND
P62830	RL23_MOUSE 60S ribosomal protein L23 OS=Mus musculus GN=Rpl23 PE=2 SV=1	1.1E-09	104.3	27.9	15 (12 3 0 0 0)	ND
P62751	RL23A_MOUSE 60S ribosomal protein L23a OS=Mus musculus GN=Rpl23a PE=2 SV=1	1.3E-08	60.2	31.4	6 (6 0 0 0 0)	ND
Q8BP67	RL24_MOUSE 60S ribosomal protein L24 OS=Mus musculus GN=Rpl24 PE=2 SV=2	3.9E-11	60.2	22.3	18 (18 0 0 0 0)	ND
P61255	RL26_MOUSE 60S ribosomal protein L26 OS=Mus musculus GN=Rpl26 PE=2 SV=1	2.7E-07	70.2	26.9	12 (12 0 0 0 0)	ND
P61358	RL27_MOUSE 60S ribosomal protein L27 OS=Mus musculus GN=Rpl27 PE=2 SV=2	2.9E-12	40.2	40.4	4 (4 0 0 0 0)	ND
P14115	RL27A_MOUSE 60S ribosomal protein L27a OS=Mus musculus GN=Rpl27a PE=2 SV=4	1.6E-08	20.2	16.2	10 (10 0 0 0 0)	ND
P41105	RL28_MOUSE 60S ribosomal protein L28 OS=Mus musculus GN=Rpl28 PE=1 SV=2	1.2E-07	60.2	23.4	6 (6 0 0 0 0)	ND
P47915	RL29_MOUSE 60S ribosomal protein L29 OS=Mus musculus GN=Rpl29 PE=2 SV=2	6.2E-08	40.2	16.9	5 (5 0 0 0 0)	ND
P62900	RL31_MOUSE 60S ribosomal protein L31 OS=Mus musculus GN=Rpl31 PE=2 SV=1	7.7E-08	30.2	35.2	3 (3 0 0 0 0)	ND
Q9D1R9	RL34_MOUSE 60S ribosomal protein L34 OS=Mus musculus GN=Rpl34 PE=3 SV=2	1.0E-06	30.2	20.5	3 (3 0 0 0 0)	ND
Q6ZWV7	RL35_MOUSE 60S ribosomal protein L35 OS=Mus musculus	6.1E-09	40.2	11.4	9 (9 0 0 0 0)	ND

	GN=Rpl35 PE=2 SV=1					
P47964	RL36_MOUSE 60S ribosomal protein L36 OS=Mus musculus GN=Rpl36 PE=2 SV=2	1.9E-07	20.1	8.6	3 (3 0 0 0 0)	ND
P83882	RL36A_MOUSE 60S ribosomal protein L36a OS=Mus musculus GN=Rpl36a PE=3 SV=2	1.8E-05	20.2	10.4	3 (3 0 0 0 0)	Cytoplasm.
Q9D8E6	RL4_MOUSE 60S ribosomal protein L4 OS=Mus musculus GN=Rpl4 PE=1 SV=3	3.9E-08	100.2	26.7	11 (11 0 0 0 0)	ND
P47962	RL5_MOUSE 60S ribosomal protein L5 OS=Mus musculus GN=Rpl5 PE=1 SV=3	8.3E-09	40.2	15.8	4 (4 0 0 0 0)	Cytoplasm. Nucleus â€º nucleolus.
P47911	RL6_MOUSE 60S ribosomal protein L6 OS=Mus musculus GN=Rpl6 PE=1 SV=3	2.2E-12	40.2	12.2	5 (5 0 0 0 0)	ND
P14148	RL7_MOUSE 60S ribosomal protein L7 OS=Mus musculus GN=Rpl7 PE=2 SV=2	6.9E-09	70.2	28.5	9 (9 0 0 0 0)	ND
P12970	RL7A_MOUSE 60S ribosomal protein L7a OS=Mus musculus GN=Rpl7a PE=2 SV=2	4.5E-13	50.3	18.8	11 (11 0 0 0 0)	ND
P62918	RL8_MOUSE 60S ribosomal protein L8 OS=Mus musculus GN=Rpl8 PE=2 SV=2	1.9E-07	50.2	15.2	6 (6 0 0 0 0)	Cytoplasm.
P51410	RL9_MOUSE 60S ribosomal protein L9 OS=Mus musculus GN=Rpl9 PE=2 SV=2	1.0E-11	20.2	15.1	3 (3 0 0 0 0)	ND
P14869	RLA0_MOUSE 60S acidic ribosomal protein P0 OS=Mus musculus GN=Rplp0 PE=1 SV=3	1.1E-14	60.3	29.3	10 (10 0 0 0 0)	Nucleus. Cytoplasm.
P99027	RLA2_MOUSE 60S acidic ribosomal protein P2 OS=Mus musculus GN=Rplp2 PE=1 SV=3	6.2E-10	40.3	69.6	5 (5 0 0 0 0)	ND
Q9DB15	RM12_MOUSE 39S ribosomal protein L12, mitochondrial OS=Mus musculus GN=Mrpl12 PE=1 SV=2	3.0E-06	40.2	23.9	4 (4 0 0 0 0)	Mitochondrion.
Q9CPR5	RM15_MOUSE 39S ribosomal protein L15, mitochondrial OS=Mus	1.8E-07	20.1	8.1	2 (2 0 0 0 0)	Mitochondrion.

	musculus GN=Mrpl15 PE=1 SV=1					
Q99N93	RM16_MOUSE 39S ribosomal protein L16, mitochondrial OS=Mus musculus GN=Mrpl16 PE=2 SV=1	1.1E-05	20.1	10.4	2 (2 0 0 0 0)	Mitochondrion.
Q91YQ5	RPN1_MOUSE Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1 OS=Mus musculus GN=Rpn1 PE=2 SV=1	5.6E-15	200.3	42.1	43 (43 0 0 0 0)	Endoplasmic reticulum membrane; Single-pass type I membrane protein. Melanosome.
Q9DBG6	RPN2_MOUSE Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2 OS=Mus musculus GN=Rpn2 PE=2 SV=1	1.0E-30	150.3	30.9	34 (34 0 0 0 0)	Endoplasmic reticulum membrane; Multi-pass membrane protein.
P10833	RRAS_MOUSE Ras-related protein R-Ras OS=Mus musculus GN=Rras PE=2 SV=1	2.8E-14	60.3	28.9	8 (8 0 0 0 0)	Cell membrane; Lipid-anchor; Cytoplasmic side.
P62071	RRAS2_MOUSE Ras-related protein R-Ras2 OS=Mus musculus GN=Rras2 PE=1 SV=1	7.7E-13	140.3	40.2	30 (30 0 0 0 0)	Cell membrane; Lipid-anchor; Cytoplasmic side.
P63325	RS10_MOUSE 40S ribosomal protein S10 OS=Mus musculus GN=Rps10 PE=1 SV=1	4.8E-07	20.1	8.5	2 (2 0 0 0 0)	Cytoplasm. Nucleus â€º nucleolus.
P62281	RS11_MOUSE 40S ribosomal protein S11 OS=Mus musculus GN=Rps11 PE=2 SV=3	6.8E-10	40.2	15.8	4 (4 0 0 0 0)	ND
P62301	RS13_MOUSE 40S ribosomal protein S13 OS=Mus musculus GN=Rps13 PE=1 SV=2	1.2E-11	90.2	52.3	13 (13 0 0 0 0)	ND
P62264	RS14_MOUSE 40S ribosomal protein S14 OS=Mus musculus GN=Rps14 PE=2 SV=3	9.9E-08	40.2	18.5	5 (5 0 0 0 0)	ND
P62843	RS15_MOUSE 40S ribosomal protein S15 OS=Mus musculus GN=Rps15 PE=2 SV=2	1.9E-13	40.2	31.0	8 (8 0 0 0 0)	ND
P62245	RS15A_MOUSE 40S ribosomal protein S15a OS=Mus musculus GN=Rps15a PE=2 SV=2	2.5E-05	30.2	25.4	5 (5 0 0 0 0)	ND
P63276	RS17_MOUSE 40S ribosomal protein S17 OS=Mus musculus GN=Rps17 PE=1 SV=2	2.7E-14	60.2	37.8	10 (10 0 0 0 0)	ND

P62270	RS18_MOUSE 40S ribosomal protein S18 OS=Mus musculus GN=Rps18 PE=2 SV=3	1.2E-09	140.2	56.6	39 (39 0 0 0 0)	Cytoplasm.
Q9CZX8	RS19_MOUSE 40S ribosomal protein S19 OS=Mus musculus GN=Rps19 PE=1 SV=3	5.4E-07	80.2	44.1	10 (10 0 0 0 0)	ND
P25444	RS2_MOUSE 40S ribosomal protein S2 OS=Mus musculus GN=Rps2 PE=1 SV=3	5.1E-10	40.2	14.3	8 (8 0 0 0 0)	ND
P60867	RS20_MOUSE 40S ribosomal protein S20 OS=Mus musculus GN=Rps20 PE=1 SV=1	3.8E-09	20.2	19.3	3 (3 0 0 0 0)	ND
P62267	RS23_MOUSE 40S ribosomal protein S23 OS=Mus musculus GN=Rps23 PE=2 SV=3	6.4E-09	40.2	30.1	6 (6 0 0 0 0)	ND
P62849	RS24_MOUSE 40S ribosomal protein S24 OS=Mus musculus GN=Rps24 PE=1 SV=1	2.2E-09	40.2	20.3	5 (5 0 0 0 0)	ND
P62852	RS25_MOUSE 40S ribosomal protein S25 OS=Mus musculus GN=Rps25 PE=2 SV=1	2.7E-10	40.2	28.8	5 (5 0 0 0 0)	ND
P62908	RS3_MOUSE 40S ribosomal protein S3 OS=Mus musculus GN=Rps3 PE=1 SV=1	1.2E-14	90.2	47.3	13 (13 0 0 0 0)	Cytoplasm.
P62862	RS30_MOUSE 40S ribosomal protein S30 OS=Mus musculus GN=Fau PE=3 SV=1	2.8E-06	20.2	20.3	2 (2 0 0 0 0)	ND
P97351	RS3A_MOUSE 40S ribosomal protein S3a OS=Mus musculus GN=Rps3a PE=1 SV=3	6.2E-09	110.2	39.4	16 (16 0 0 0 0)	Cytoplasm. Nucleus.
P62702	RS4X_MOUSE 40S ribosomal protein S4, X isoform OS=Mus musculus GN=Rps4x PE=2 SV=2	7.1E-11	110.2	40.7	19 (19 0 0 0 0)	Cytoplasm.
P62754	RS6_MOUSE 40S ribosomal protein S6 OS=Mus musculus GN=Rps6 PE=1 SV=1	4.3E-13	110.3	32.1	14 (14 0 0 0 0)	ND
P62082	RS7_MOUSE 40S ribosomal protein S7 OS=Mus musculus GN=Rps7 PE=2 SV=1	9.5E-09	20.2	19.1	2 (2 0 0 0 0)	Cytoplasm â€º cytoskeleton â€º centrosome.
P62242	RS8_MOUSE 40S ribosomal protein S8 OS=Mus musculus GN=Rps8 PE=1	3.6E-11	80.2	38.5	15 (15 0 0 0 0)	Cytoplasm.

	SV=2					
Q6ZWN5	RS9_MOUSE 40S ribosomal protein S9 OS=Mus musculus GN=Rps9 PE=2 SV=3	1.7E-07	70.2	27.8	10 (10 0 0 0 0)	Cytoplasm.
P14206	RSSA_MOUSE 40S ribosomal protein SA OS=Mus musculus GN=Rpsa PE=1 SV=4	5.8E-14	30.2	15.3	3 (3 0 0 0 0)	Cell membrane. Cytoplasm. Nucleus.
Q80X85	RT07_MOUSE 28S ribosomal protein S7, mitochondrial OS=Mus musculus GN=Mrps7 PE=2 SV=1	7.4E-08	30.2	17.4	3 (3 0 0 0 0)	Mitochondrion.
O70622	RTN2_MOUSE Reticulon-2 OS=Mus musculus GN=Rtn2 PE=1 SV=1	1.1E-15	60.3	17.8	8 (8 0 0 0 0)	Endoplasmic reticulum membrane; Single-pass membrane protein.
Q9ES97	RTN3_MOUSE Reticulon-3 OS=Mus musculus GN=Rtn3 PE=1 SV=2	2.0E-10	20.2	1.3	7 (7 0 0 0 0)	Endoplasmic reticulum membrane; Multi-pass membrane protein. Golgi apparatus membrane; Multi-pass membrane protein.
Q99P72	RTN4_MOUSE Reticulon-4 OS=Mus musculus GN=Rtn4 PE=1 SV=2	1.0E-30	170.3	23.8	52 (52 0 0 0 0)	Endoplasmic reticulum membrane; Multi-pass membrane protein.
P60122	RUVB1_MOUSE RuvB-like 1 OS=Mus musculus GN=Ruvbl1 PE=1 SV=1	3.6E-10	30.2	9.0	3 (3 0 0 0 0)	Nucleus.
P08207	S10AA_MOUSE Protein S100-A10 OS=Mus musculus GN=S100a10 PE=2 SV=2	4.2E-09	20.2	14.4	2 (2 0 0 0 0)	ND
P55012	S12A2_MOUSE Solute carrier family 12 member 2 OS=Mus musculus GN=Slc12a2 PE=1 SV=1	1.8E-09	90.2	10.5	15 (15 0 0 0 0)	Membrane; Multi-pass membrane protein.
Q9JIS8	S12A4_MOUSE Solute carrier family 12 member 4 OS=Mus musculus GN=Slc12a4 PE=1 SV=2	1.5E-07	40.2	4.6	6 (6 0 0 0 0)	Membrane; Multi-pass membrane protein.
Q9WVL3	S12A7_MOUSE Solute carrier family 12 member 7 OS=Mus musculus GN=Slc12a7 PE=1 SV=1	2.3E-13	180.3	19.1	40 (40 0 0 0 0)	Membrane; Multi-pass membrane protein.

Q9JIM1	S29A1_MOUSE Equilibrative nucleoside transporter 1 OS=Mus musculus GN=Slc29a1 PE=1 SV=3	1.9E-14	60.3	12.0	26 (26 0 0 0 0)	Basolateral cell membrane; Multi-pass membrane protein. Apical cell membrane; Multi-pass membrane protein.
Q91ZN5	S35B2_MOUSE Adenosine 3'-phospho 5'-phosphosulfate transporter 1 OS=Mus musculus GN=Slc35b2 PE=2 SV=1	3.6E-06	20.2	4.9	2 (2 0 0 0 0)	Golgi apparatus membrane; Multi-pass membrane protein.
Q8BTY2	S4A7_MOUSE Sodium bicarbonate cotransporter 3 OS=Mus musculus GN=Slc4a7 PE=1 SV=2	4.6E-13	90.2	10.7	17 (17 0 0 0 0)	Basolateral cell membrane; Multi-pass membrane protein. Apical cell membrane; Multi-pass membrane protein. Cell projection â€º stereocilium.
P61620	S61A1_MOUSE Protein transport protein Sec61 subunit alpha isoform 1 OS=Mus musculus GN=Sec61a1 PE=2 SV=2	3.3E-07	20.1	2.3	2 (2 0 0 0 0)	Endoplasmic reticulum membrane; Multi-pass membrane protein.
Q9EP69	SAC1_MOUSE Phosphatidylinositide phosphatase SAC1 OS=Mus musculus GN=Sacm1l PE=2 SV=1	1.8E-11	60.2	8.7	6 (6 0 0 0 0)	Endoplasmic reticulum membrane; Multi-pass membrane protein.
Q8BGH2	SAM50_MOUSE Sorting and assembly machinery component 50 homolog OS=Mus musculus GN=Samm50 PE=1 SV=1	5.3E-08	30.2	7.0	3 (3 0 0 0 0)	Mitochondrion outer membrane; Multi-pass membrane protein. Cytoplasm.
O35874	SATT_MOUSE Neutral amino acid transporter A OS=Mus musculus GN=Slc1a4 PE=1 SV=1	1.1E-16	40.3	10.9	7 (7 0 0 0 0)	Membrane; Multi-pass membrane protein. Melanosome.
Q9R0P6	SC11A_MOUSE Signal peptidase complex catalytic subunit SEC11A OS=Mus musculus GN=Sec11a PE=2 SV=1	2.0E-07	30.2	18.4	3 (3 0 0 0 0)	Microsome membrane; Single-pass type II membrane protein. Endoplasmic reticulum membrane; Single-pass type II membrane protein.
O08547	SC22B_MOUSE Vesicle-trafficking protein SEC22b OS=Mus musculus GN=Sec22b PE=1 SV=3	1.1E-16	120.2	39.5	17 (17 0 0 0 0)	Endoplasmic reticulum-Golgi intermediate compartment membrane; Single-pass type IV

						membrane protein. Golgi apparatus membrane; Single-pass type IV membrane protein. Endoplasmic reticulum membrane; Single-pass type IV membrane protein. Melanosome.
Q01405	SC23A_MOUSE Protein transport protein Sec23A OS=Mus musculus GN=Sec23a PE=1 SV=2	3.2E-12	20.2	4.1	2 (2 0 0 0 0)	Smooth endoplasmic reticulum membrane; Peripheral membrane protein. Golgi apparatus membrane; Peripheral membrane protein.
Q9D662	SC23B_MOUSE Protein transport protein Sec23B OS=Mus musculus GN=Sec23b PE=2 SV=1	7.1E-09	20.2	3.3	2 (2 0 0 0 0)	Golgi apparatus membrane. Endoplasmic reticulum membrane. Endoplasmic reticulum-Golgi intermediate compartment membrane.
O35609	SCAM3_MOUSE Secretory carrier-associated membrane protein 3 OS=Mus musculus GN=Scamp3 PE=1 SV=2	6.3E-11	30.2	12.9	11 (11 0 0 0 0)	Membrane; Multi-pass membrane protein.
Q8BRF7	SCFD1_MOUSE Sec1 family domain-containing protein 1 OS=Mus musculus GN=Scfd1 PE=2 SV=1	6.0E-05	20.1	3.6	2 (2 0 0 0 0)	Cytoplasm. Endoplasmic reticulum membrane; Peripheral membrane protein. Golgi apparatus â€º Golgi stack membrane; Peripheral membrane protein.
Q8BMD8	SCMC1_MOUSE Calcium-binding mitochondrial carrier protein SCaMC-1 OS=Mus musculus GN=Slc25a24 PE=2 SV=1	2.6E-11	40.2	12.6	5 (5 0 0 0 0)	Mitochondrion inner membrane; Multi-pass membrane protein.
Q80U72	SCRIB_MOUSE Protein scribble homolog OS=Mus musculus GN=Scrib PE=1 SV=2	5.4E-14	40.3	2.8	5 (5 0 0 0 0)	Cell membrane; Peripheral membrane protein. Cell junction â€º

						adherens junction. Cytoplasm.
Q8CFE4	SCYL2_MOUSE SCY1-like protein 2 OS=Mus musculus GN=Scyl2 PE=1 SV=1	2.5E-05	30.2	4.8	3 (3 0 0 0 0)	Cytoplasm â€º perinuclear region. Cytoplasmic vesicle â€º clathrin-coated vesicle. Golgi apparatus â€º trans-Golgi network membrane. Endosome membrane.
O08992	SDCB1_MOUSE Syntenin-1 OS=Mus musculus GN=Sdcbp PE=2 SV=1	5.2E-08	20.2	11.4	2 (2 0 0 0 0)	Membrane; Peripheral membrane protein. Melanosome.
Q9Z2G6	SE1L1_MOUSE Protein sel-1 homolog 1 OS=Mus musculus GN=Sel1l PE=2 SV=2	1.4E-08	20.3	3.7	2 (2 0 0 0 0)	Endoplasmic reticulum membrane; Single-pass type I membrane protein.
Q6QD59	SEC20_MOUSE Vesicle transport protein SEC20 OS=Mus musculus GN=Bnip1 PE=2 SV=1	1.2E-06	40.1	17.5	4 (4 0 0 0 0)	Endoplasmic reticulum membrane; Single-pass type IV membrane protein. Golgi apparatus membrane; Single-pass type IV membrane protein.
Q8VHE0	SEC63_MOUSE Translocation protein SEC63 homolog OS=Mus musculus GN=Sec63 PE=1 SV=3	1.4E-09	190.2	22.9	23 (23 0 0 0 0)	Endoplasmic reticulum membrane; Multi-pass membrane protein.
Q9QUR8	SEM7A_MOUSE Semaphorin-7A OS=Mus musculus GN=Sema7a PE=2 SV=1	2.1E-09	20.2	5.1	2 (2 0 0 0 0)	Cell membrane; Lipid-anchor â€º GPI-anchor; Extracellular side.
Q8C1B7	SEP11_MOUSE Septin-11 OS=Mus musculus GN=Sept11 PE=1 SV=4	2.3E-11	30.2	9.3	3 (3 0 0 0 0)	Cytoplasm. Cytoplasm â€º cytoskeleton. Cell junction â€º synapse. Cell projection â€º dendritic spine. Cell projection â€º axon.
P42208	SEPT2_MOUSE Septin-2 OS=Mus musculus GN=Sept2 PE=1 SV=2	4.2E-08	20.3	7.5	2 (2 0 0 0 0)	Cytoplasm. Cytoplasm â€º cytoskeleton. Cytoplasm â€º cytoskeleton â€º

						spindle. Chromosome â€º centromere â€º kinetochore. Cleavage furrow. Midbody. Cytoplasm â€º cell cortex.
O55131	SEPT7_MOUSE Septin-7 OS=Mus musculus GN=Sept7 PE=1 SV=1	4.0E-06	20.1	4.4	2 (2 0 0 0 0)	Cytoplasm. Chromosome â€º centromere â€º kinetochore. Cytoplasm â€º cytoskeleton â€º spindle. Cleavage furrow. Midbody. Cytoplasm â€º cytoskeleton â€º cilium axoneme.
Q61753	SERA_MOUSE D-3-phosphoglycerate dehydrogenase OS=Mus musculus GN=Phgdh PE=1 SV=3	2.3E-09	70.2	15.2	13 (13 0 0 0 0)	ND
P19324	SERPH_MOUSE Serpin H1 OS=Mus musculus GN=Serpinh1 PE=1 SV=2	4.0E-12	158.3	39.3	24 (23 1 0 0 0)	Endoplasmic reticulum lumen.
Q64213	SF01_MOUSE Splicing factor 1 OS=Mus musculus GN=Sf1 PE=1 SV=5	1.3E-07	30.2	8.1	3 (3 0 0 0 0)	Nucleus.
Q99JR1	SFXN1_MOUSE Sideroflexin-1 OS=Mus musculus GN=Sfxn1 PE=1 SV=3	7.2E-13	58.3	22.7	6 (5 1 0 0 0)	Mitochondrion membrane; Multi-pass membrane protein.
Q91V61	SFXN3_MOUSE Sideroflexin-3 OS=Mus musculus GN=Sfxn3 PE=1 SV=1	6.7E-10	20.2	8.1	2 (2 0 0 0 0)	Mitochondrion membrane; Multi-pass membrane protein.
Q8R0X7	SGPL1_MOUSE Sphingosine-1-phosphate lyase 1 OS=Mus musculus GN=Sgpl1 PE=2 SV=1	1.4E-11	80.2	14.3	10 (10 0 0 0 0)	Endoplasmic reticulum membrane; Single-pass type III membrane protein.
Q9JK48	SHLB1_MOUSE Endophilin-B1 OS=Mus musculus GN=Sh3glb1 PE=1 SV=1	1.2E-05	30.1	9.6	3 (3 0 0 0 0)	Cytoplasm. Golgi apparatus membrane; Peripheral membrane protein. Mitochondrion outer membrane; Peripheral membrane protein.
Q9CU62	SMC1A_MOUSE Structural maintenance of chromosomes protein 1A	2.9E-08	60.2	6.0	7 (7 0 0 0 0)	Nucleus. Chromosome. Chromosome â€º

	OS=Mus musculus GN=Smc1a PE=1 SV=3					centromere.
Q9CW03	SMC3_MOUSE Structural maintenance of chromosomes protein 3 OS=Mus musculus GN=Smc3 PE=1 SV=2	2.7E-09	70.2	7.4	7 (7 0 0 0 0)	Nucleus. Chromosome. Chromosome â€º centromere.
Q78PY7	SND1_MOUSE Staphylococcal nuclease domain-containing protein 1 OS=Mus musculus GN=Snd1 PE=1 SV=1	2.3E-06	40.2	7.5	4 (4 0 0 0 0)	Cytoplasm. Nucleus. Melanosome.
O09044	SNP23_MOUSE Synaptosomal-associated protein 23 OS=Mus musculus GN=Snap23 PE=1 SV=1	3.1E-14	100.3	48.6	23 (23 0 0 0 0)	Cell membrane; Peripheral membrane protein. Cell membrane; Lipid-anchor. Cell junction â€º synapse â€º synaptosome.
Q61235	SNTB2_MOUSE Beta-2-syntrophin OS=Mus musculus GN=Sntb2 PE=1 SV=2	7.7E-08	30.2	6.9	3 (3 0 0 0 0)	Membrane. Cytoplasmic vesicle â€º secretory vesicle membrane; Peripheral membrane protein. Cell junction. Cytoplasm â€º cytoskeleton.
Q61263	SOAT1_MOUSE Sterol O-acyltransferase 1 OS=Mus musculus GN=Soat1 PE=2 SV=1	8.9E-11	20.2	5.0	2 (2 0 0 0 0)	Endoplasmic reticulum membrane; Multi-pass membrane protein.
Q3UPH7	SOLO_MOUSE Protein SOLO OS=Mus musculus GN=Solo PE=2 SV=1	1.1E-08	20.1	1.6	2 (2 0 0 0 0)	Cytoplasm.
Q9EPR5	SORC2_MOUSE VPS10 domain-containing receptor SorCS2 OS=Mus musculus GN=Sorcs2 PE=1 SV=1	5.9E-11	110.2	10.6	15 (15 0 0 0 0)	Membrane; Single-pass type I membrane protein.
Q9CYN2	SPCS2_MOUSE Signal peptidase complex subunit 2 OS=Mus musculus GN=Spcs2 PE=2 SV=1	9.4E-12	70.3	28.8	8 (8 0 0 0 0)	Microsome membrane; Multi-pass membrane protein. Endoplasmic reticulum membrane; Multi-pass membrane protein.
P16546	SPTA2_MOUSE Spectrin alpha chain, brain OS=Mus musculus GN=Sptan1 PE=1	1.5E-12	360.3	21.2	46 (46 0 0 0 0)	Cytoplasm â€º cytoskeleton. Cytoplasm â€º cell

	SV=4					cortex.
P15508	SPTB1_MOUSE Spectrin beta chain, erythrocyte OS=Mus musculus GN=Sptb PE=1 SV=4	8.0E-05	20.2	0.8	2 (2 0 0 0 0)	Cytoplasm â€º cytoskeleton. Cytoplasm â€º cell cortex.
Q62261	SPTB2_MOUSE Spectrin beta chain, brain 1 OS=Mus musculus GN=Sptbn1 PE=1 SV=2	4.4E-15	350.4	20.9	45 (45 0 0 0 0)	Cytoplasm â€º cytoskeleton. Cytoplasm â€º myofibril â€º sarcomere â€º M line. Cell membrane; Peripheral membrane protein; Cytoplasmic side.
O35704	SPTC1_MOUSE Serine palmitoyltransferase 1 OS=Mus musculus GN=Sptlc1 PE=2 SV=1	6.3E-06	20.2	4.9	3 (3 0 0 0 0)	Endoplasmic reticulum membrane; Single-pass membrane protein.
P97363	SPTC2_MOUSE Serine palmitoyltransferase 2 OS=Mus musculus GN=Sptlc2 PE=2 SV=2	3.3E-16	20.2	6.6	3 (3 0 0 0 0)	Endoplasmic reticulum membrane; Single-pass membrane protein.
Q64337	SQSTM_MOUSE Sequestosome-1 OS=Mus musculus GN=Sqstm1 PE=1 SV=1	2.0E-07	20.2	7.5	2 (2 0 0 0 0)	Cytoplasm. Late endosome. Nucleus.
Q9DBG7	SRPR_MOUSE Signal recognition particle receptor subunit alpha OS=Mus musculus GN=Srpr PE=1 SV=1	4.3E-11	110.2	11.6	12 (12 0 0 0 0)	Endoplasmic reticulum membrane; Peripheral membrane protein.
P47758	SRPRB_MOUSE Signal recognition particle receptor subunit beta OS=Mus musculus GN=Srprb PE=1 SV=1	3.2E-13	70.2	34.2	12 (12 0 0 0 0)	Endoplasmic reticulum membrane; Single-pass membrane protein.
Q9CY50	SSRA_MOUSE Translocon-associated protein subunit alpha OS=Mus musculus GN=Ssr1 PE=1 SV=1	2.1E-10	40.2	21.0	10 (10 0 0 0 0)	Endoplasmic reticulum membrane; Single-pass type I membrane protein.
Q62186	SSRD_MOUSE Translocon-associated protein subunit delta OS=Mus musculus GN=Ssr4 PE=2 SV=1	3.1E-08	40.2	30.8	4 (4 0 0 0 0)	Endoplasmic reticulum membrane; Single-pass type I membrane protein.
Q9DCF9	SSRG_MOUSE Translocon-associated protein subunit gamma OS=Mus musculus GN=Ssr3 PE=1 SV=1	2.8E-10	30.2	15.1	3 (3 0 0 0 0)	Endoplasmic reticulum membrane; Multi-pass membrane

						protein.
P42225	STAT1_MOUSE Signal transducer and activator of transcription 1 OS=Mus musculus GN=Stat1 PE=1 SV=1	9.7E-12	100.3	17.8	13 (13 0 0 0 0)	Cytoplasm. Nucleus.
Q8BWB6	STEA2_MOUSE Metalloreductase STEAP2 OS=Mus musculus GN=Steap2 PE=2 SV=1	5.2E-10	40.2	8.8	5 (5 0 0 0 0)	Cell membrane; Multi-pass membrane protein. Endosome membrane; Multi-pass membrane protein.
Q60864	STIP1_MOUSE Stress-induced-phosphoprotein 1 OS=Mus musculus GN=Stip1 PE=1 SV=1	1.3E-05	40.2	7.6	4 (4 0 0 0 0)	Cytoplasm. Nucleus.
Q99JB2	STML2_MOUSE Stomatin-like protein 2 OS=Mus musculus GN=Stoml2 PE=1 SV=1	7.0E-14	80.3	28.9	10 (10 0 0 0 0)	Membrane; Peripheral membrane protein. Cytoplasm. Cytoplasm â€º cytoskeleton.
P54116	STOM_MOUSE Erythrocyte band 7 integral membrane protein OS=Mus musculus GN=Stom PE=1 SV=3	1.2E-14	138.4	43.0	23 (22 1 0 0 0)	Cell membrane; Peripheral membrane protein; Cytoplasmic side. Cell membrane; Lipid-anchor; Cytoplasmic side. Melanosome.
P46978	STT3A_MOUSE Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3A OS=Mus musculus GN=Stt3a PE=1 SV=1	7.0E-08	60.2	5.7	11 (11 0 0 0 0)	Endoplasmic reticulum membrane; Multi-pass membrane protein.
Q3TDQ1	STT3B_MOUSE Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3B OS=Mus musculus GN=Stt3b PE=1 SV=2	3.8E-12	50.2	6.2	6 (6 0 0 0 0)	Endoplasmic reticulum membrane; Multi-pass membrane protein.
Q9ER00	STX12_MOUSE Syntaxin-12 OS=Mus musculus GN=Stx12 PE=1 SV=1	6.8E-11	80.3	33.6	9 (9 0 0 0 0)	Endomembrane system; Single-pass type IV membrane protein; Cytoplasmic side. Golgi apparatus membrane; Single-pass type IV membrane protein.

Q8VDS8	STX18_MOUSE Syntaxin-18 OS=Mus musculus GN=Stx18 PE=2 SV=2	7.5E-10	40.2	17.7	5 (5 0 0 0 0)	Endoplasmic reticulum membrane; Single-pass type IV membrane protein. Golgi apparatus membrane; Single-pass type IV membrane protein.
Q00262	STX2_MOUSE Syntaxin-2 OS=Mus musculus GN=Stx2 PE=2 SV=1	1.1E-06	30.2	11.4	4 (4 0 0 0 0)	Membrane; Single-pass type IV membrane protein.
P70452	STX4_MOUSE Syntaxin-4 OS=Mus musculus GN=Stx4 PE=1 SV=1	2.8E-09	80.2	31.2	15 (15 0 0 0 0)	Cell membrane; Single-pass type IV membrane protein.
Q8K1E0	STX5_MOUSE Syntaxin-5 OS=Mus musculus GN=Stx5 PE=2 SV=3	7.2E-09	20.2	9.9	4 (4 0 0 0 0)	Endoplasmic reticulum-Golgi intermediate compartment membrane; Single-pass type IV membrane protein. Golgi apparatus membrane; Single-pass type IV membrane protein.
O70439	STX7_MOUSE Syntaxin-7 OS=Mus musculus GN=Stx7 PE=1 SV=3	2.6E-11	20.2	11.1	3 (3 0 0 0 0)	Early endosome membrane; Single-pass type IV membrane protein.
O88983	STX8_MOUSE Syntaxin-8 OS=Mus musculus GN=Stx8 PE=2 SV=1	1.9E-11	20.3	11.9	2 (2 0 0 0 0)	Membrane; Single-pass type IV membrane protein.
O08599	STXB1_MOUSE Syntaxin-binding protein 1 OS=Mus musculus GN=Stxbp1 PE=1 SV=2	6.8E-08	50.2	9.9	5 (5 0 0 0 0)	ND
Q60770	STXB3_MOUSE Syntaxin-binding protein 3 OS=Mus musculus GN=Stxbp3 PE=1 SV=1	1.9E-05	20.1	3.4	2 (2 0 0 0 0)	Cytoplasm â€º cytosol. Cell membrane.
Q9WUM5	SUCA_MOUSE Succinyl-CoA ligase [GDP-forming] subunit alpha, mitochondrial OS=Mus musculus GN=Suclg1 PE=1 SV=4	3.6E-08	40.2	11.6	4 (4 0 0 0 0)	Mitochondrion.
Q64310	SURF4_MOUSE Surfeit locus protein 4 OS=Mus musculus GN=Surf4 PE=2 SV=1	2.4E-08	40.2	9.7	9 (9 0 0 0 0)	Endoplasmic reticulum membrane; Multi-pass membrane protein. Endoplasmic reticulum-Golgi intermediate compartment

						membrane; Multi-pass membrane protein. Golgi apparatus membrane; Multi-pass membrane protein.
Q8BGQ7	SYAC_MOUSE Alanyl-tRNA synthetase, cytoplasmic OS=Mus musculus GN=Aars PE=2 SV=1	1.1E-06	30.2	4.8	3 (3 0 0 0 0)	Cytoplasm.
Q922B2	SYDC_MOUSE Aspartyl-tRNA synthetase, cytoplasmic OS=Mus musculus GN=Dars PE=2 SV=1	4.1E-12	60.2	14.2	7 (7 0 0 0 0)	Cytoplasm.
Q8CGC7	SYEP_MOUSE Bifunctional aminoacyl-tRNA synthetase OS=Mus musculus GN=Eprs PE=2 SV=3	3.2E-12	90.3	7.9	10 (10 0 0 0 0)	ND
Q9CZD3	SYG_MOUSE Glycyl-tRNA synthetase OS=Mus musculus GN=Gars PE=1 SV=1	5.9E-07	30.2	4.9	4 (4 0 0 0 0)	Cytoplasm. Mitochondrion.
Q9D6K5	SYJ2B_MOUSE Synaptojanin-2-binding protein OS=Mus musculus GN=Synj2bp PE=1 SV=1	1.0E-05	20.2	15.9	2 (2 0 0 0 0)	Mitochondrion outer membrane; Single-pass type IV membrane protein; Cytoplasmic side. Cytoplasm â€º perinuclear region.
Q8BMJ2	SYLC_MOUSE Leucyl-tRNA synthetase, cytoplasmic OS=Mus musculus GN=Lars PE=2 SV=2	8.3E-12	30.2	3.6	3 (3 0 0 0 0)	Cytoplasm.
Q68FL6	SYMC_MOUSE Methionyl-tRNA synthetase, cytoplasmic OS=Mus musculus GN=Mars PE=2 SV=1	3.9E-10	30.3	4.9	3 (3 0 0 0 0)	Cytoplasm.
Q9D0R2	SYTC_MOUSE Threonyl-tRNA synthetase, cytoplasmic OS=Mus musculus GN=Tars PE=1 SV=2	1.8E-07	20.1	3.3	2 (2 0 0 0 0)	Cytoplasm.
Q9Z1Q9	SYVC_MOUSE Valyl-tRNA synthetase OS=Mus musculus GN=Vars PE=2 SV=1	1.7E-12	50.2	5.0	5 (5 0 0 0 0)	ND
Q921F2	TADBP_MOUSE TAR DNA-binding protein 43 OS=Mus musculus GN=Tardbp PE=1 SV=1	4.7E-14	60.2	17.9	8 (8 0 0 0 0)	Nucleus.

Q9WVA4	TAGL2_MOUSE Transgelin-2 OS=Mus musculus GN=Tagln2 PE=1 SV=4	9.7E-07	50.2	24.1	5 (5 0 0 0 0)	ND
P21958	TAP1_MOUSE Antigen peptide transporter 1 OS=Mus musculus GN=Tap1 PE=2 SV=2	3.4E-14	150.4	27.8	23 (23 0 0 0 0)	Endoplasmic reticulum membrane; Multi-pass membrane protein.
P36371	TAP2_MOUSE Antigen peptide transporter 2 OS=Mus musculus GN=Tap2 PE=2 SV=1	7.8E-15	160.3	23.4	33 (33 0 0 0 0)	Endoplasmic reticulum membrane; Multi-pass membrane protein.
P68369	TBA1A_MOUSE Tubulin alpha-1A chain OS=Mus musculus GN=Tuba1a PE=1 SV=1	3.0E-14	160.3	43.7	100 (100 0 0 0 0)	Cytoplasm â€º cytoskeleton.
Q7TMM9	TBB2A_MOUSE Tubulin beta-2A chain OS=Mus musculus GN=Tubb2a PE=1 SV=1	1.0E-30	312.4	48.3	105 (99 3 3 0 0)	Cytoplasm â€º cytoskeleton.
P68372	TBB2C_MOUSE Tubulin beta-2C chain OS=Mus musculus GN=Tubb2c PE=1 SV=1	1.0E-30	90.3	20.2	19 (19 0 0 0 0)	Cytoplasm â€º cytoskeleton.
Q9ERD7	TBB3_MOUSE Tubulin beta-3 chain OS=Mus musculus GN=Tubb3 PE=1 SV=1	3.5E-07	36.3	9.1	4 (3 0 1 0 0)	Cytoplasm â€º cytoskeleton.
P99024	TBB5_MOUSE Tubulin beta-5 chain OS=Mus musculus GN=Tubb5 PE=1 SV=1	1.8E-13	60.3	10.1	22 (22 0 0 0 0)	Cytoplasm â€º cytoskeleton.
Q922F4	TBB6_MOUSE Tubulin beta-6 chain OS=Mus musculus GN=Tubb6 PE=1 SV=1	1.0E-30	70.3	19.7	7 (7 0 0 0 0)	Cytoplasm â€º cytoskeleton.
P11984	TCPA1_MOUSE T-complex protein 1 subunit alpha A OS=Mus musculus GN=Tcp1 PE=1 SV=2	1.0E-30	160.3	34.9	28 (28 0 0 0 0)	#N/A
P11983	TCPA2_MOUSE T-complex protein 1 subunit alpha B OS=Mus musculus GN=Tcp1 PE=1 SV=3	6.7E-15	40.3	10.1	6 (6 0 0 0 0)	Cytoplasm. Cytoplasm â€º cytoskeleton â€º centrosome.
P80314	TCPB_MOUSE T-complex protein 1 subunit beta OS=Mus musculus GN=Cct2 PE=1 SV=4	6.2E-14	180.3	42.2	25 (25 0 0 0 0)	Cytoplasm.
P80315	TCPD_MOUSE T-complex protein 1 subunit delta OS=Mus musculus GN=Cct4 PE=1 SV=3	3.9E-12	110.3	30.2	13 (13 0 0 0 0)	Cytoplasm. Melanosome. Cytoplasm â€º cytoskeleton â€º centrosome.

P80316	TCPE_MOUSE T-complex protein 1 subunit epsilon OS=Mus musculus GN=Cct5 PE=1 SV=1	1.7E-10	70.3	16.6	9 (9 0 0 0 0)	Cytoplasm. Cytoplasm â€º cytoskeleton â€º centrosome.
P80318	TCPG_MOUSE T-complex protein 1 subunit gamma OS=Mus musculus GN=Cct3 PE=1 SV=1	1.1E-12	224.3	34.7	34 (32 1 1 0 0)	Cytoplasm.
P80313	TCPH_MOUSE T-complex protein 1 subunit eta OS=Mus musculus GN=Cct7 PE=1 SV=1	5.0E-14	120.3	28.9	16 (16 0 0 0 0)	Cytoplasm.
P42932	TCPQ_MOUSE T-complex protein 1 subunit theta OS=Mus musculus GN=Cct8 PE=1 SV=3	3.2E-12	110.2	22.8	15 (15 0 0 0 0)	Cytoplasm. Cytoplasm â€º cytoskeleton â€º centrosome.
Q61390	TCPW_MOUSE T-complex protein 1 subunit zeta-2 OS=Mus musculus GN=Cct6b PE=2 SV=4	3.1E-09	46.2	10.0	10 (8 2 0 0 0)	Cytoplasm.
P80317	TCPZ_MOUSE T-complex protein 1 subunit zeta OS=Mus musculus GN=Cct6a PE=1 SV=3	2.5E-13	110.3	25.2	19 (19 0 0 0 0)	Cytoplasm.
P63028	TCTP_MOUSE Translationally-controlled tumor protein OS=Mus musculus GN=Tpt1 PE=1 SV=1	4.2E-11	20.2	14.0	3 (3 0 0 0 0)	Cytoplasm.
Q9CY27	TECR_MOUSE Trans-2,3-enoyl-CoA reductase OS=Mus musculus GN=Tecr PE=1 SV=1	7.1E-09	30.2	10.7	7 (7 0 0 0 0)	Endoplasmic reticulum membrane; Multi-pass membrane protein.
Q01853	TERA_MOUSE Transitional endoplasmic reticulum ATPase OS=Mus musculus GN=Vcp PE=1 SV=4	3.6E-13	130.3	22.3	36 (36 0 0 0 0)	Cytoplasm â€º cytosol. Nucleus.
Q62351	TFR1_MOUSE Transferrin receptor protein 1 OS=Mus musculus GN=Tfrc PE=1 SV=1	3.3E-13	320.2	35.4	65 (65 0 0 0 0)	Cell membrane; Single-pass type II membrane protein. Melanosome.
Q8QZT1	THIL_MOUSE Acetyl-CoA acetyltransferase, mitochondrial OS=Mus musculus GN=Acat1 PE=1 SV=1	7.6E-11	30.3	12.5	4 (4 0 0 0 0)	Mitochondrion.
Q8BWT1	THIM_MOUSE 3-ketoacyl-CoA thiolase, mitochondrial OS=Mus musculus GN=Acaa2 PE=1 SV=2	2.3E-11	50.2	21.2	5 (5 0 0 0 0)	Mitochondrion.
Q62318	TIF1B_MOUSE Transcription intermediary factor 1-beta OS=Mus musculus GN=Trim28 PE=1	2.9E-11	30.2	5.5	3 (3 0 0 0 0)	Nucleus.

	SV=3					
Q9CQV1	TIM16_MOUSE Mitochondrial import inner membrane translocase subunit Tim16 OS=Mus musculus GN=Timm16 PE=2 SV=1	1.2E-07	20.2	34.4	2 (2 0 0 0 0)	Mitochondrion inner membrane; Peripheral membrane protein.
O35857	TIM44_MOUSE Mitochondrial import inner membrane translocase subunit TIM44 OS=Mus musculus GN=Timm44 PE=2 SV=1	4.8E-11	30.2	8.0	3 (3 0 0 0 0)	Mitochondrion inner membrane.
Q9D880	TIM50_MOUSE Mitochondrial import inner membrane translocase subunit TIM50 OS=Mus musculus GN=Timm50 PE=1 SV=1	2.7E-13	60.3	23.2	8 (8 0 0 0 0)	Mitochondrion inner membrane; Single-pass membrane protein.
P26039	TLN1_MOUSE Talin-1 OS=Mus musculus GN=Tln1 PE=1 SV=1	1.6E-14	350.3	18.7	58 (58 0 0 0 0)	Cell projection â€º ruffle membrane; Peripheral membrane protein; Cytoplasmic side. Cytoplasm â€º cytoskeleton.
Q3UBX0	TM109_MOUSE Transmembrane protein 109 OS=Mus musculus GN=Tmem109 PE=1 SV=2	1.5E-08	20.2	5.3	3 (3 0 0 0 0)	Nucleus outer membrane; Multi-pass membrane protein. Endoplasmic reticulum membrane; Multi-pass membrane protein. Sarcoplasmic reticulum membrane; Multi-pass membrane protein.
Q99KI3	TM111_MOUSE Transmembrane protein 111 OS=Mus musculus GN=Tmem111 PE=2 SV=3	2.6E-10	40.3	17.2	4 (4 0 0 0 0)	Membrane; Multi-pass membrane protein.
Q9WUH1	TM115_MOUSE Transmembrane protein 115 OS=Mus musculus GN=Tmem115 PE=1 SV=1	7.3E-08	20.1	9.4	2 (2 0 0 0 0)	Membrane; Multi-pass membrane protein.
Q8R138	TM119_MOUSE Transmembrane protein 119 OS=Mus musculus GN=Tmem119 PE=2 SV=1	1.4E-13	20.3	8.2	6 (6 0 0 0 0)	Membrane; Single-pass type I membrane protein.

Q3TBT3	TM173_MOUSE Transmembrane protein 173 OS=Mus musculus GN=Tmem173 PE=1 SV=2	9.9E-14	30.3	12.4	3 (3 0 0 0 0)	Endoplasmic reticulum membrane; Multi-pass membrane protein. Mitochondrion outer membrane; Multi-pass membrane protein. Cell membrane; Multi-pass membrane protein. Cytoplasm â€º perinuclear region.
Q8BM55	TM214_MOUSE Transmembrane protein 214 OS=Mus musculus GN=Tmem214 PE=2 SV=1	1.1E-06	30.1	4.9	3 (3 0 0 0 0)	Membrane; Multi-pass membrane protein.
P58021	TM9S2_MOUSE Transmembrane 9 superfamily member 2 OS=Mus musculus GN=Tm9sf2 PE=2 SV=1	4.0E-12	40.3	7.3	7 (7 0 0 0 0)	Endosome membrane; Multi-pass membrane protein.
Q8BH24	TM9S4_MOUSE Transmembrane 9 superfamily member 4 OS=Mus musculus GN=Tm9sf4 PE=2 SV=1	4.1E-09	40.2	6.4	4 (4 0 0 0 0)	Membrane; Multi-pass membrane protein.
Q921L3	TMCO1_MOUSE Transmembrane and coiled-coil domain-containing protein 1 OS=Mus musculus GN=Tmco1 PE=2 SV=1	2.9E-11	30.2	21.3	5 (5 0 0 0 0)	Endoplasmic reticulum membrane; Multi-pass membrane protein. Golgi apparatus membrane; Multi-pass membrane protein.
Q3V009	TMED1_MOUSE Transmembrane emp24 domain-containing protein 1 OS=Mus musculus GN=Tmed1 PE=2 SV=1	5.5E-06	50.2	14.1	7 (7 0 0 0 0)	Cell membrane; Single-pass type I membrane protein.
Q9R0Q3	TMED2_MOUSE Transmembrane emp24 domain-containing protein 2 OS=Mus musculus GN=Tmed2 PE=1 SV=1	6.8E-07	40.2	10.9	7 (7 0 0 0 0)	Cytoplasmic vesicle membrane; Single-pass type I membrane protein. Cytoplasmic vesicle â€º COPI-coated vesicle membrane; Single-pass type I membrane protein. Golgi apparatus membrane; Single-pass type I

						membrane protein.
Q8R1V4	TMED4_MOUSE Transmembrane emp24 domain-containing protein 4 OS=Mus musculus GN=Tmed4 PE=2 SV=1	7.0E-13	58.2	20.3	7 (6 1 0 0 0)	Endoplasmic reticulum membrane; Single-pass type I membrane protein.
Q9CXE7	TMED5_MOUSE Transmembrane emp24 domain-containing protein 5 OS=Mus musculus GN=Tmed5 PE=2 SV=1	7.6E-06	20.1	9.2	2 (2 0 0 0 0)	Endoplasmic reticulum membrane; Single-pass type I membrane protein.
Q99KF1	TMED9_MOUSE Transmembrane emp24 domain-containing protein 9 OS=Mus musculus GN=Tmed9 PE=2 SV=2	1.1E-16	98.3	25.1	15 (14 1 0 0 0)	Endoplasmic reticulum membrane; Single-pass type I membrane protein.
Q9D1D4	TMEDA_MOUSE Transmembrane emp24 domain-containing protein 10 OS=Mus musculus GN=Tmed10 PE=2 SV=1	3.8E-14	100.3	36.5	21 (21 0 0 0 0)	Golgi apparatus membrane; Single-pass type I membrane protein; Lumenal side. Melanosome.
Q5FWI3	TMEM2_MOUSE Transmembrane protein 2 OS=Mus musculus GN=Tmem2 PE=1 SV=1	3.9E-05	20.2	1.9	2 (2 0 0 0 0)	Membrane; Single-pass membrane protein.
Q9CR67	TMM33_MOUSE Transmembrane protein 33 OS=Mus musculus GN=Tmem33 PE=2 SV=1	1.2E-08	30.2	12.6	7 (7 0 0 0 0)	Membrane; Multi-pass membrane protein. Melanosome.
Q9DBS1	TMM43_MOUSE Transmembrane protein 43 OS=Mus musculus GN=Tmem43 PE=1 SV=1	7.4E-14	70.2	26.0	8 (8 0 0 0 0)	Endoplasmic reticulum. Nucleus inner membrane; Multi-pass membrane protein.
Q9CZX9	TMM85_MOUSE Transmembrane protein 85 OS=Mus musculus GN=Tmem85 PE=2 SV=1	2.2E-08	20.2	15.8	2 (2 0 0 0 0)	Membrane; Multi-pass membrane protein.
Q8BRH0	TMTC3_MOUSE Transmembrane and TPR repeat-containing protein 3 OS=Mus musculus GN=Tmtc3 PE=2 SV=2	2.7E-08	50.2	7.6	5 (5 0 0 0 0)	Membrane; Multi-pass membrane protein.
Q8VBT0	TMX1_MOUSE Thioredoxin-related transmembrane protein 1 OS=Mus musculus GN=Tmx1 PE=1 SV=1	1.4E-09	30.2	12.9	6 (6 0 0 0 0)	Membrane; Single-pass type I membrane protein. Endoplasmic reticulum membrane; Single-pass type I

						membrane protein.
Q9D710	TMX2_MOUSE Thioredoxin-related transmembrane protein 2 OS=Mus musculus GN=Tmx2 PE=2 SV=1	1.5E-05	20.1	7.5	2 (2 0 0 0 0)	Membrane; Single-pass type I membrane protein.
Q8BXZ1	TMX3_MOUSE Protein disulfide-isomerase TMX3 OS=Mus musculus GN=Tmx3 PE=1 SV=2	1.0E-11	40.2	9.0	6 (6 0 0 0 0)	Endoplasmic reticulum membrane; Single-pass membrane protein.
Q8BFY9	TNPO1_MOUSE Transportin-1 OS=Mus musculus GN=Tnpo1 PE=1 SV=2	9.6E-07	30.1	3.7	3 (3 0 0 0 0)	Cytoplasm. Nucleus.
Q8BYU6	TOIP2_MOUSE Torsin-1A-interacting protein 2 OS=Mus musculus GN=Tor1aip2 PE=1 SV=1	4.2E-08	50.2	12.5	6 (6 0 0 0 0)	Endoplasmic reticulum membrane; Single-pass membrane protein.
Q9CPQ3	TOM22_MOUSE Mitochondrial import receptor subunit TOM22 homolog OS=Mus musculus GN=Tomm22 PE=2 SV=3	5.6E-15	70.3	62.7	10 (10 0 0 0 0)	Mitochondrion outer membrane; Single-pass membrane protein.
Q9QYA2	TOM40_MOUSE Mitochondrial import receptor subunit TOM40 homolog OS=Mus musculus GN=Tomm40 PE=1 SV=3	2.3E-10	70.3	18.0	7 (7 0 0 0 0)	Mitochondrion outer membrane; Multi-pass membrane protein.
Q9CZW5	TOM70_MOUSE Mitochondrial import receptor subunit TOM70 OS=Mus musculus GN=Tomm70a PE=1 SV=1	8.0E-11	130.2	16.7	17 (17 0 0 0 0)	Mitochondrion outer membrane; Single-pass membrane protein.
Q9Z0L0	TPBG_MOUSE Trophoblast glycoprotein OS=Mus musculus GN=Tpbg PE=1 SV=2	3.0E-08	30.2	10.8	4 (4 0 0 0 0)	Membrane; Single-pass type I membrane protein.
P17751	TPIS_MOUSE Triosephosphate isomerase OS=Mus musculus GN=Tpi1 PE=1 SV=3	7.2E-11	30.2	16.1	3 (3 0 0 0 0)	ND
P58771	TPM1_MOUSE Tropomyosin alpha-1 chain OS=Mus musculus GN=Tpm1 PE=1 SV=1	3.3E-08	50.2	13.4	7 (7 0 0 0 0)	Cytoplasm â€º cytoskeleton.
P21107	TPM3_MOUSE Tropomyosin alpha-3 chain OS=Mus musculus GN=Tpm3 PE=1 SV=2	7.0E-08	30.2	11.3	3 (3 0 0 0 0)	Cytoplasm â€º cytoskeleton.

Q6IRU2	TPM4_MOUSE Tropomyosin alpha-4 chain OS=Mus musculus GN=Tpm4 PE=2 SV=3	3.4E-10	50.2	25.4	7 (7 0 0 0 0)	Cytoplasm â€º cytoskeleton.
Q64514	TPP2_MOUSE Tripeptidyl-peptidase 2 OS=Mus musculus GN=Tpp2 PE=2 SV=3	7.4E-08	20.1	1.7	2 (2 0 0 0 0)	Cytoplasm. Nucleus.
Q9R233	TPSN_MOUSE Tapasin OS=Mus musculus GN=Tapbp PE=2 SV=2	4.6E-13	90.3	17.8	29 (29 0 0 0 0)	Endoplasmic reticulum membrane; Single-pass type I membrane protein.
O88856	TPST2_MOUSE Protein-tyrosine sulfotransferase 2 OS=Mus musculus GN=Tpst2 PE=1 SV=1	8.4E-06	30.2	8.8	4 (4 0 0 0 0)	Golgi apparatus membrane; Single-pass type II membrane protein.
Q9CQN1	TRAP1_MOUSE Heat shock protein 75 kDa, mitochondrial OS=Mus musculus GN=Trap1 PE=1 SV=1	2.7E-12	80.2	14.7	8 (8 0 0 0 0)	Mitochondrion.
Q7TN37	TRPM4_MOUSE Transient receptor potential cation channel subfamily M member 4 OS=Mus musculus GN=Trpm4 PE=2 SV=1	7.3E-09	30.2	3.8	3 (3 0 0 0 0)	Cell membrane; Multi-pass membrane protein. Endoplasmic reticulum. Golgi apparatus.
P35441	TSP1_MOUSE Thrombospondin-1 OS=Mus musculus GN=Thbs1 PE=1 SV=1	1.0E-05	40.1	3.6	4 (4 0 0 0 0)	ND
Q9CRD2	TTC35_MOUSE Tetratricopeptide repeat protein 35 OS=Mus musculus GN=Ttc35 PE=2 SV=1	2.1E-08	60.2	25.9	7 (7 0 0 0 0)	Nucleus.
Q8K2W3	TXD11_MOUSE Thioredoxin domain-containing protein 11 OS=Mus musculus GN=Txndc11 PE=2 SV=1	4.5E-05	20.1	2.1	2 (2 0 0 0 0)	Endoplasmic reticulum membrane; Single-pass membrane protein.
Q91W90	TXND5_MOUSE Thioredoxin domain-containing protein 5 OS=Mus musculus GN=Txndc5 PE=1 SV=2	3.8E-09	30.2	7.7	5 (5 0 0 0 0)	Endoplasmic reticulum lumen.
Q8CGB3	UACA_MOUSE Uveal autoantigen with coiled-coil domains and ankyrin repeats OS=Mus musculus GN=Uaca PE=1 SV=2	6.4E-09	20.2	1.7	2 (2 0 0 0 0)	Nucleus. Cytoplasm. Cytoplasm â€º cytoskeleton.
Q9CZY3	UB2V1_MOUSE Ubiquitin-conjugating enzyme E2 variant 1 OS=Mus musculus	1.1E-04	20.1	13.6	2 (2 0 0 0 0)	Nucleus.

	GN=Ube2v1 PE=1 SV=1					
Q02053	UBA1_MOUSE Ubiquitin-like modifier-activating enzyme 1 OS=Mus musculus GN=Uba1 PE=1 SV=1	4.3E-09	40.2	5.9	5 (5 0 0 0 0)	ND
P61089	UBE2N_MOUSE Ubiquitin-conjugating enzyme E2 N OS=Mus musculus GN=Ube2n PE=1 SV=1	1.4E-05	30.2	25.0	3 (3 0 0 0 0)	Nucleus. Cytoplasm.
P62991	UBIQ_MOUSE Ubiquitin OS=Mus musculus GN=Rps27a PE=1 SV=1	1.1E-09	50.2	61.8	81 (81 0 0 0 0)	ND
P21126	UBL4A_MOUSE Ubiquitin-like protein 4A OS=Mus musculus GN=Ubl4a PE=2 SV=1	8.7E-07	20.2	15.9	3 (3 0 0 0 0)	Cytoplasm â€º cytosol.
Q9JMA1	UBP14_MOUSE Ubiquitin carboxyl-terminal hydrolase 14 OS=Mus musculus GN=Usp14 PE=1 SV=3	2.1E-08	20.1	4.9	2 (2 0 0 0 0)	Cytoplasm. Cell membrane; Peripheral membrane protein.
Q91WB7	UBTD1_MOUSE Ubiquitin domain-containing protein 1 OS=Mus musculus GN=Ubtd1 PE=2 SV=1	1.1E-07	40.2	16.3	5 (5 0 0 0 0)	ND
Q6PGH0	UBTD2_MOUSE Ubiquitin domain-containing protein 2 OS=Mus musculus GN=Ubtd2 PE=2 SV=1	1.7E-08	30.2	9.8	3 (3 0 0 0 0)	Cytoplasm.
Q8VCH8	UBXN4_MOUSE UBX domain-containing protein 4 OS=Mus musculus GN=Ubxn4 PE=1 SV=1	2.1E-14	30.3	9.7	3 (3 0 0 0 0)	Endoplasmic reticulum membrane; Peripheral membrane protein. Nucleus envelope.
Q9CR68	UCRI_MOUSE Cytochrome b-c1 complex subunit Rieske, mitochondrial OS=Mus musculus GN=Uqcrfs1 PE=1 SV=1	7.1E-08	30.2	11.3	3 (3 0 0 0 0)	Mitochondrion inner membrane.
O70475	UGDH_MOUSE UDP-glucose 6-dehydrogenase OS=Mus musculus GN=Ugdh PE=1 SV=1	1.9E-07	30.2	7.3	3 (3 0 0 0 0)	ND
Q6P5E4	UGGG1_MOUSE UDP-glucose:glycoprotein glucosyltransferase 1 OS=Mus musculus GN=Uggt1 PE=1 SV=3	4.4E-15	150.3	14.1	17 (17 0 0 0 0)	Endoplasmic reticulum lumen. Endoplasmic reticulum-Golgi intermediate compartment.
Q9CQ56	USE1_MOUSE Vesicle transport protein USE1 OS=Mus musculus GN=Use1 PE=2 SV=1	3.1E-08	40.2	17.0	4 (4 0 0 0 0)	Endoplasmic reticulum membrane; Single-pass type IV

						membrane protein.
Q9Z1Z0	USO1_MOUSE General vesicular transport factor p115 OS=Mus musculus GN=Uso1 PE=1 SV=2	9.6E-11	20.2	2.6	2 (2 0 0 0 0)	Cytoplasm â€º cytosol. Golgi apparatus membrane; Peripheral membrane protein.
P51863	VA0D1_MOUSE V-type proton ATPase subunit d 1 OS=Mus musculus GN=Atp6v0d1 PE=1 SV=2	5.5E-09	20.2	6.8	3 (3 0 0 0 0)	ND
P63044	VAMP2_MOUSE Vesicle-associated membrane protein 2 OS=Mus musculus GN=Vamp2 PE=1 SV=2	1.3E-11	20.3	20.7	5 (5 0 0 0 0)	Cytoplasmic vesicle â€º secretory vesicle â€º synaptic vesicle membrane; Single-pass type IV membrane protein. Cell junction â€º synapse â€º synaptosome.
P63024	VAMP3_MOUSE Vesicle-associated membrane protein 3 OS=Mus musculus GN=Vamp3 PE=1 SV=1	3.1E-11	20.3	16.5	4 (4 0 0 0 0)	Membrane; Single-pass type IV membrane protein. Cell junction â€º synapse â€º synaptosome.
O70480	VAMP4_MOUSE Vesicle-associated membrane protein 4 OS=Mus musculus GN=Vamp4 PE=1 SV=1	1.2E-09	20.2	10.6	2 (2 0 0 0 0)	Golgi apparatus â€º trans-Golgi network membrane; Single-pass type IV membrane protein.
O70404	VAMP8_MOUSE Vesicle-associated membrane protein 8 OS=Mus musculus GN=Vamp8 PE=1 SV=1	5.9E-07	40.2	40.6	4 (4 0 0 0 0)	Membrane; Single-pass type IV membrane protein.
Q9WV55	VAPA_MOUSE Vesicle-associated membrane protein-associated protein A OS=Mus musculus GN=Vapa PE=1 SV=2	5.6E-15	140.3	29.3	37 (37 0 0 0 0)	Endoplasmic reticulum membrane; Single-pass type IV membrane protein.
Q9QY76	VAPB_MOUSE Vesicle-associated membrane protein-associated protein B OS=Mus musculus GN=Vapb PE=2 SV=3	2.6E-09	40.2	16.9	6 (6 0 0 0 0)	Endoplasmic reticulum membrane; Single-pass type IV membrane protein.
Q9R1Q9	VAS1_MOUSE V-type proton ATPase subunit S1 OS=Mus musculus GN=Atp6ap1 PE=1 SV=1	1.0E-10	30.3	9.1	3 (3 0 0 0 0)	Vacuole membrane; Single-pass membrane protein.
Q62465	VAT1_MOUSE Synaptic vesicle membrane protein	1.9E-08	40.2	10.8	4 (4 0 0 0 0)	Cytoplasm.

	VAT-1 homolog OS=Mus musculus GN=Vat1 PE=2 SV=3					
P29533	VCAM1_MOUSE Vascular cell adhesion protein 1 OS=Mus musculus GN=Vcam1 PE=1 SV=1	8.5E-12	160.3	22.3	25 (25 0 0 0 0)	Cell membrane; Single-pass type I membrane protein. Cell membrane; Lipid-anchor â€º GPI-anchor.
Q60932	VDAC1_MOUSE Voltage-dependent anion-selective channel protein 1 OS=Mus musculus GN=Vdac1 PE=1 SV=3	1.0E-30	116.3	51.7	25 (20 5 0 0 0)	Mitochondrion outer membrane; Multi-pass membrane protein. Cell membrane; Multi-pass membrane protein.
Q60930	VDAC2_MOUSE Voltage-dependent anion-selective channel protein 2 OS=Mus musculus GN=Vdac2 PE=1 SV=2	8.8E-12	68.2	21.7	14 (11 3 0 0 0)	Mitochondrion outer membrane.
Q60931	VDAC3_MOUSE Voltage-dependent anion-selective channel protein 3 OS=Mus musculus GN=Vdac3 PE=1 SV=1	8.9E-15	40.3	17.7	5 (5 0 0 0 0)	Mitochondrion outer membrane.
Q8VDJ3	VIGLN_MOUSE Vigilin OS=Mus musculus GN=Hdlbp PE=1 SV=1	1.7E-08	20.2	2.1	2 (2 0 0 0 0)	Cytoplasm. Nucleus.
P20152	VIME_MOUSE Vimentin OS=Mus musculus GN=Vim PE=1 SV=3	5.6E-15	314.3	52.1	99 (97 1 0 1 0)	ND
Q64727	VINC_MOUSE Vinculin OS=Mus musculus GN=Vcl PE=1 SV=4	1.0E-30	260.3	29.0	26 (26 0 0 0 0)	Cytoplasm â€º cytoskeleton. Cell junction â€º adherens junction. Cell membrane; Peripheral membrane protein; Cytoplasmic side. Cell junction.
P15920	VPP2_MOUSE V-type proton ATPase 116 kDa subunit a isoform 2 OS=Mus musculus GN=Atp6v0a2 PE=1 SV=2	1.0E-11	30.2	4.4	3 (3 0 0 0 0)	Cell membrane; Multi-pass membrane protein. Endosome membrane.
Q9EQH3	VPS35_MOUSE Vacuolar protein sorting-associated protein 35 OS=Mus musculus GN=Vps35 PE=1 SV=1	2.1E-06	20.2	3.1	2 (2 0 0 0 0)	Cytoplasm. Membrane; Peripheral membrane protein.
P97390	VPS45_MOUSE Vacuolar protein sorting-associated protein 45 OS=Mus musculus GN=Vps45 PE=1	9.1E-07	30.1	6.1	3 (3 0 0 0 0)	Golgi apparatus membrane; Peripheral membrane protein.

	SV=1					Endosome membrane; Peripheral membrane protein.
O88342	WDR1_MOUSE WD repeat-containing protein 1 OS=Mus musculus GN=Wdr1 PE=1 SV=3	4.7E-06	20.1	3.1	2 (2 0 0 0 0)	Cytoplasm â€º cytoskeleton.
P56695	WFS1_MOUSE Wolframin OS=Mus musculus GN=Wfs1 PE=1 SV=1	1.5E-07	50.2	7.6	8 (8 0 0 0 0)	Endoplasmic reticulum membrane; Multi-pass membrane protein.
Q6P5F9	XPO1_MOUSE Exportin-1 OS=Mus musculus GN=Xpo1 PE=1 SV=1	9.6E-05	20.2	2.1	2 (2 0 0 0 0)	Cytoplasm. Nucleus â€º nucleoplasm. Nucleus â€º Cajal body. Nucleus â€º nucleolus.
Q924C1	XPO5_MOUSE Exportin-5 OS=Mus musculus GN=Xpo5 PE=2 SV=1	8.5E-08	20.2	2.1	2 (2 0 0 0 0)	Nucleus. Cytoplasm.
Q9EPK2	XRP2_MOUSE Protein XRP2 OS=Mus musculus GN=Rp2 PE=2 SV=3	1.6E-06	30.2	8.9	3 (3 0 0 0 0)	Cell membrane; Lipid-anchor; Cytoplasmic side.
P62960	YBOX1_MOUSE Nuclease-sensitive element-binding protein 1 OS=Mus musculus GN=Ybx1 PE=1 SV=3	1.0E-14	20.2	15.2	3 (3 0 0 0 0)	Cytoplasm. Nucleus. Cytoplasmic granule. Secreted.
Q9CX30	YIF1B_MOUSE Protein YIF1B OS=Mus musculus GN=Yif1b PE=2 SV=2	1.6E-09	30.2	12.2	4 (4 0 0 0 0)	Membrane; Multi-pass membrane protein.
O88967	YMEL1_MOUSE ATP-dependent metalloprotease YME1L1 OS=Mus musculus GN=Yme1l1 PE=2 SV=1	1.9E-12	80.3	17.2	8 (8 0 0 0 0)	Mitochondrion.
Q9CWU2	ZDH13_MOUSE Probable palmitoyltransferase ZDHHC13 OS=Mus musculus GN=Zdhhc13 PE=2 SV=2	6.3E-06	20.2	3.7	2 (2 0 0 0 0)	Golgi apparatus membrane; Multi-pass membrane protein. Cytoplasmic vesicle membrane; Multi-pass membrane protein.
Q9DB43	ZFPL1_MOUSE Zinc finger protein-like 1 OS=Mus musculus GN=Zfpl1 PE=2 SV=1	1.4E-07	20.2	5.8	2 (2 0 0 0 0)	Golgi apparatus â€º cis-Golgi network membrane; Single-pass membrane protein.
Q62523	ZYX_MOUSE Zyxin OS=Mus musculus GN=Zyx PE=1 SV=1	2.0E-10	30.2	8.3	4 (4 0 0 0 0)	Cytoplasm. Cytoplasm â€º cytoskeleton. Cell junction â€º focal adhesion. Nucleus.

Table s4

Accession	Reference	P (pro)	Score	Coverage	Peptide (Hits)	Subcellular locations
Q9CQV8	1433B_MOUSE 14-3-3 protein beta/alpha OS=Mus musculus GN=Ywhab PE=1 SV=3	1.7E-11	38.2	15.4	5 (4 1 0 0 0)	Cytoplasm. Melanosome.
P62259	1433E_MOUSE 14-3-3 protein epsilon OS=Mus musculus GN=Ywhae PE=1 SV=1	3.8E-09	98.2	32.5	12 (11 1 0 0 0)	Cytoplasm. Melanosome.
P68510	1433F_MOUSE 14-3-3 protein eta OS=Mus musculus GN=Ywhah PE=1 SV=2	5.8E-04	14.2	6.5	2 (0 1 1 0 0)	Cytoplasm.
P61982	1433G_MOUSE 14-3-3 protein gamma OS=Mus musculus GN=Ywhag PE=1 SV=2	1.0E-30	50.3	25.9	6 (6 0 0 0 0)	Cytoplasm.
P63101	1433Z_MOUSE 14-3-3 protein zeta/delta OS=Mus musculus GN=Ywhaz PE=1 SV=1	2.6E-09	20.2	10.6	2 (2 0 0 0 0)	Cytoplasm. Melanosome.
Q76MZ3	2AAA_MOUSE Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform OS=Mus musculus GN=Ppp2r1a PE=1 SV=3	1.3E-14	140.3	27.0	19 (19 0 0 0 0)	Cytoplasm. Chromosome â€º centromere.
Q99L13	3HIDH_MOUSE 3-hydroxyisobutyrate dehydrogenase, mitochondrial OS=Mus musculus GN=Hibadh PE=2 SV=1	1.4E-12	20.2	7.2	4 (4 0 0 0 0)	Mitochondrion.
Q61838	A2M_MOUSE Alpha-2-macroglobulin OS=Mus musculus GN=A2m PE=1 SV=2	6.1E-11	50.3	4.7	5 (5 0 0 0 0)	Secreted.
P05201	AATC_MOUSE Aspartate aminotransferase, cytoplasmic OS=Mus musculus GN=Got1 PE=1 SV=2	8.8E-11	90.2	27.4	12 (12 0 0 0 0)	Cytoplasm.
P05202	AATM_MOUSE Aspartate aminotransferase, mitochondrial OS=Mus musculus GN=Got2 PE=1 SV=1	7.4E-09	100.3	21.6	26 (26 0 0 0 0)	Mitochondrion matrix. Cell membrane.
P61222	ABCE1_MOUSE ATP-binding cassette sub-family E member 1 OS=Mus musculus GN=Abce1 PE=2 SV=1	3.9E-06	30.2	6.0	3 (3 0 0 0 0)	Cytoplasm. Mitochondrion.
Q9WV35	ABEC2_MOUSE Probable	5.9E-04	20.1	9.8	2 (2 0 0 0	ND

	C->U-editing enzyme APOBEC-2 OS=Mus musculus GN=Apobec2 PE=1 SV=1				0)	
Q5SWU9	ACACA_MOUSE Acetyl-CoA carboxylase 1 OS=Mus musculus GN=Acaca PE=1 SV=1	7.2E-08	40.2	2.0	4 (4 0 0 0 0)	Cytoplasm.
P51174	ACADL_MOUSE Long-chain specific acyl-CoA dehydrogenase, mitochondrial OS=Mus musculus GN=Acadl PE=2 SV=2	3.4E-10	110.2	19.5	22 (22 0 0 0 0)	Mitochondrion matrix.
P45952	ACADM_MOUSE Medium-chain specific acyl-CoA dehydrogenase, mitochondrial OS=Mus musculus GN=Acadm PE=1 SV=1	4.2E-10	60.2	15.9	11 (11 0 0 0 0)	Mitochondrion matrix.
Q07417	ACADS_MOUSE Short-chain specific acyl-CoA dehydrogenase, mitochondrial OS=Mus musculus GN=Acads PE=2 SV=1	1.2E-08	50.2	12.9	5 (5 0 0 0 0)	Mitochondrion matrix.
P50544	ACADV_MOUSE Very long-chain specific acyl-CoA dehydrogenase, mitochondrial OS=Mus musculus GN=Acadvl PE=1 SV=3	1.8E-12	150.3	36.1	30 (30 0 0 0 0)	Mitochondrion inner membrane.
Q8K370	ACD10_MOUSE Acyl-CoA dehydrogenase family member 10 OS=Mus musculus GN=Acad10 PE=2 SV=1	8.0E-08	20.2	2.2	2 (2 0 0 0 0)	ND
P09470	ACE_MOUSE Angiotensin-converting enzyme OS=Mus musculus GN=Ace PE=1 SV=3	2.8E-09	20.2	2.1	2 (2 0 0 0 0)	Secreted. Cell membrane; Single-pass type I membrane protein.
Q99KI0	ACON_MOUSE Aconitate hydratase, mitochondrial OS=Mus musculus GN=Aco2 PE=1 SV=1	3.7E-14	214.3	28.6	62 (55 3 4 0 0)	Mitochondrion.
P41216	ACSL1_MOUSE Long-chain-fatty-acid--CoA ligase 1 OS=Mus musculus GN=Acsl1 PE=1 SV=1	1.1E-15	150.3	21.3	37 (37 0 0 0 0)	Mitochondrion outer membrane; Single-pass type III membrane protein. Peroxisome membrane; Single-pass type III membrane protein. Microsome membrane; Single-

						pass type III membrane protein. Endoplasmic reticulum membrane; Single-pass type III membrane protein.
P62737	ACTA_MOUSE Actin, aortic smooth muscle OS=Mus musculus GN=Acta2 PE=1 SV=1	1.0E-30	246.3	48.5	209 (207 2 0 0 0)	Cytoplasm â€º cytoskeleton.
P60710	ACTB_MOUSE Actin, cytoplasmic 1 OS=Mus musculus GN=Actb PE=1 SV=1	7.0E-13	50.3	16.0	23 (23 0 0 0 0)	Cytoplasm â€º cytoskeleton.
Q8BFZ3	ACTBL_MOUSE Beta-actin-like protein 2 OS=Mus musculus GN=Actbl2 PE=2 SV=1	1.0E-30	44.3	21.5	13 (7 5 1 0 0)	Cytoplasm â€º cytoskeleton.
Q7TPR4	ACTN1_MOUSE Alpha-actinin-1 OS=Mus musculus GN=Actn1 PE=2 SV=1	1.9E-08	90.2	10.1	27 (27 0 0 0 0)	Cytoplasm â€º cytoskeleton. Cytoplasm â€º myofibril â€º sarcomere â€º Z line. Cell membrane. Cell projection â€º ruffle.
Q9JI91	ACTN2_MOUSE Alpha-actinin-2 OS=Mus musculus GN=Actn2 PE=1 SV=1	2.2E-15	340.3	38.0	131 (131 0 0 0 0)	Cytoplasm â€º myofibril â€º sarcomere â€º Z line.
O88990	ACTN3_MOUSE Alpha-actinin-3 OS=Mus musculus GN=Actn3 PE=2 SV=1	1.0E-30	320.3	33.2	143 (141 2 0 0 0)	ND
P68134	ACTS_MOUSE Actin, alpha skeletal muscle OS=Mus musculus GN=Acta1 PE=1 SV=1	5.7E-14	60.3	5.8	16 (12 4 0 0 0)	Cytoplasm â€º cytoskeleton.
Q60936	ADCK3_MOUSE Chaperone activity of bc1 complex-like, mitochondrial OS=Mus musculus GN=Cabc1 PE=2 SV=2	2.2E-13	60.3	13.0	19 (19 0 0 0 0)	Mitochondrion.
Q8BLF1	ADCL1_MOUSE Neutral cholesterol ester hydrolase 1 OS=Mus musculus GN=Nceh1 PE=1 SV=1	1.0E-30	20.4	9.8	4 (4 0 0 0 0)	Membrane; Single-pass type II membrane protein. Microsome.
P48962	ADT1_MOUSE ADP/ATP translocase 1 OS=Mus musculus GN=Slc25a4 PE=1 SV=4	5.5E-11	98.2	25.8	123 (122 1 0 0 0)	Mitochondrion inner membrane; Multi-pass membrane protein.
P51881	ADT2_MOUSE ADP/ATP translocase 2 OS=Mus musculus GN=Slc25a5 PE=1	5.0E-08	18.2		3 (1 2 0 0 0)	Mitochondrion inner membrane; Multi-pass

	SV=3					membrane protein.
Q9Z0X1	AIFM1_MOUSE Apoptosis-inducing factor 1, mitochondrial OS=Mus musculus GN=Aifm1 PE=1 SV=1	7.4E-14	130.3	21.2	16 (16 0 0 0 0)	Mitochondrion intermembrane space. Mitochondrion inner membrane. Cytoplasm. Cytoplasm â€º perinuclear region. Nucleus.
P31230	AIMP1_MOUSE Aminoacyl tRNA synthetase complex-interacting multifunctional protein 1 OS=Mus musculus GN=Aimp1 PE=1 SV=2	3.4E-09	30.2	15.2	4 (4 0 0 0 0)	Nucleus. Cytoplasm â€º cytosol. Cytoplasmic vesicle â€º secretory vesicle. Secreted. Endoplasmic reticulum. Golgi apparatus.
Q8CHT0	AL4A1_MOUSE Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial OS=Mus musculus GN=Aldh4a1 PE=1 SV=2	3.3E-09	30.2	7.7	4 (4 0 0 0 0)	Mitochondrion matrix.
P07724	ALBU_MOUSE Serum albumin OS=Mus musculus GN=Alb PE=1 SV=3	1.5E-10	70.2	13.8	34 (34 0 0 0 0)	Secreted.
P47738	ALDH2_MOUSE Aldehyde dehydrogenase, mitochondrial OS=Mus musculus GN=Aldh2 PE=1 SV=1	9.8E-13	120.3	29.9	21 (21 0 0 0 0)	Mitochondrion matrix.
P05064	ALDOA_MOUSE Fructose-bisphosphate aldolase A OS=Mus musculus GN=Aldoa PE=1 SV=2	1.0E-30	270.3	57.4	409 (407 2 0 0 0)	ND
Q3V1D3	AMPD1_MOUSE AMP deaminase 1 OS=Mus musculus GN=Ampd1 PE=2 SV=1	4.7E-11	180.3	31.7	36 (36 0 0 0 0)	ND
P16406	AMPE_MOUSE Glutamyl aminopeptidase OS=Mus musculus GN=Enpep PE=1 SV=1	1.7E-13	30.2	5.3	3 (3 0 0 0 0)	Membrane; Single-pass type II membrane protein.
Q9CPY7	AMPL_MOUSE Cytosol aminopeptidase OS=Mus musculus GN=Lap3 PE=1 SV=3	2.5E-07	20.2	4.6	2 (2 0 0 0 0)	Cytoplasm.
P97449	AMPN_MOUSE Aminopeptidase N OS=Mus musculus GN=Anpep PE=1 SV=4	3.4E-13	50.3	9.2	10 (10 0 0 0 0)	Membrane; Single-pass type II membrane protein.

Q9WV06	ANKR2_MOUSE Ankyrin repeat domain-containing protein 2 OS=Mus musculus GN=Ankrd2 PE=2 SV=2	8.2E-11	40.3	13.1	9 (9 0 0 0 0)	ND
P97384	ANX11_MOUSE Annexin A11 OS=Mus musculus GN=Anxa11 PE=1 SV=1	2.1E-07	38.2	8.0	7 (3 4 0 0 0)	Cytoplasm. Melanosome. Nucleus envelope. Nucleus â€º nucleoplasm. Cytoplasm â€º cytoskeleton â€º spindle.
P10107	ANXA1_MOUSE Annexin A1 OS=Mus musculus GN=Anxa1 PE=1 SV=2	2.4E-11	40.3	15.6	9 (9 0 0 0 0)	Nucleus. Cytoplasm. Cell projection â€º cilium. Basolateral cell membrane.
P07356	ANXA2_MOUSE Annexin A2 OS=Mus musculus GN=Anxa2 PE=1 SV=2	2.8E-12	110.3	31.6	24 (24 0 0 0 0)	Secreted â€º extracellular space â€º extracellular matrix â€º basement membrane. Melanosome.
O35639	ANXA3_MOUSE Annexin A3 OS=Mus musculus GN=Anxa3 PE=2 SV=3	8.8E-07	20.2	7.7	4 (4 0 0 0 0)	ND
P97429	ANXA4_MOUSE Annexin A4 OS=Mus musculus GN=Anxa4 PE=2 SV=3	2.1E-09	40.2	16.0	6 (6 0 0 0 0)	ND
P48036	ANXA5_MOUSE Annexin A5 OS=Mus musculus GN=Anxa5 PE=1 SV=1	3.6E-11	140.3	43.3	28 (28 0 0 0 0)	ND
P14824	ANXA6_MOUSE Annexin A6 OS=Mus musculus GN=Anxa6 PE=1 SV=2	1.2E-12	408.3	53.5	102 (101 1 0 0 0)	Cytoplasm. Melanosome.
Q07076	ANXA7_MOUSE Annexin A7 OS=Mus musculus GN=Anxa7 PE=2 SV=1	1.3E-07	20.2	6.5	4 (4 0 0 0 0)	ND
O35643	AP1B1_MOUSE AP-1 complex subunit beta-1 OS=Mus musculus GN=Ap1b1 PE=1 SV=1	1.1E-14	50.3	8.3	10 (10 0 0 0 0)	Golgi apparatus. Cytoplasmic vesicle â€º clathrin-coated vesicle membrane; Peripheral membrane protein; Cytoplasmic side. Golgi apparatus.
P17426	AP2A1_MOUSE AP-2 complex subunit alpha-1 OS=Mus musculus GN=Ap2a1 PE=1 SV=1	2.3E-10	60.3	7.2	12 (12 0 0 0 0)	Cell membrane. Membrane â€º coated pit; Peripheral membrane protein; Cytoplasmic side.

P17427	AP2A2_MOUSE AP-2 complex subunit alpha-2 OS=Mus musculus GN=Ap2a2 PE=1 SV=1	1.5E-08	30.2	5.1	4 (4 0 0 0 0)	Cell membrane. Membrane â€º coated pit; Peripheral membrane protein; Cytoplasmic side.
P84091	AP2M1_MOUSE AP-2 complex subunit mu OS=Mus musculus GN=Ap2m1 PE=1 SV=1	2.6E-04	20.1	6.7	2 (2 0 0 0 0)	Cell membrane. Membrane â€º coated pit; Peripheral membrane protein; Cytoplasmic side.
Q9Z1T1	AP3B1_MOUSE AP-3 complex subunit beta-1 OS=Mus musculus GN=Ap3b1 PE=1 SV=1	5.8E-04	16.1	2.2	2 (1 0 1 0 0)	Golgi apparatus. Cytoplasmic vesicle â€º clathrin-coated vesicle membrane; Peripheral membrane protein; Cytoplasmic side. Golgi apparatus.
P16460	ASSY_MOUSE Argininosuccinate synthase OS=Mus musculus GN=Ass1 PE=1 SV=1	8.1E-11	30.2	7.5	17 (17 0 0 0 0)	ND
Q9Z1W8	AT12A_MOUSE Potassium-transporting ATPase alpha chain 2 OS=Mus musculus GN=Atp12a PE=1 SV=2	7.1E-09	30.1	3.1	7 (7 0 0 0 0)	Membrane; Multi-pass membrane protein.
Q8VDN2	AT1A1_MOUSE Sodium/potassium-transporting ATPase subunit alpha-1 OS=Mus musculus GN=Atp1a1 PE=1 SV=1	3.8E-14	110.3	12.2	58 (58 0 0 0 0)	Cell membrane; Multi-pass membrane protein.
Q6PIE5	AT1A2_MOUSE Sodium/potassium-transporting ATPase subunit alpha-2 OS=Mus musculus GN=Atp1a2 PE=1 SV=1	8.4E-10	198.3	17.9	91 (90 1 0 0 0)	Membrane; Multi-pass membrane protein. Cell membrane; Multi-pass membrane protein.
P14094	AT1B1_MOUSE Sodium/potassium-transporting ATPase subunit beta-1 OS=Mus musculus GN=Atp1b1 PE=1 SV=1	5.2E-07	20.2	7.2	8 (8 0 0 0 0)	Membrane; Single-pass type II membrane protein.
Q8R429	AT2A1_MOUSE Sarcoplasmic/endoplasmic reticulum calcium ATPase 1 OS=Mus musculus GN=Atp2a1 PE=2 SV=1	1.0E-30	814.4	40.6	5708 (5614 94 0 0 0)	Endoplasmic reticulum membrane; Multi-pass membrane protein. Sarcoplasmic reticulum membrane; Multi-pass membrane protein.

O55143	AT2A2_MOUSE Sarcoplasmic/endoplasmic reticulum calcium ATPase 2 OS=Mus musculus GN=Atp2a2 PE=1 SV=2	6.7E-15	138.3	11.1	55 (53 2 0 0 0)	Endoplasmic reticulum membrane; Multi-pass membrane protein. Sarcoplasmic reticulum membrane; Multi-pass membrane protein.
Q9CQQ7	AT5F1_MOUSE ATP synthase subunit b, mitochondrial OS=Mus musculus GN=Atp5f1 PE=1 SV=1	1.0E-08	60.2	20.3	8 (8 0 0 0 0)	Mitochondrion. Mitochondrion inner membrane.
Q6PA06	ATLA2_MOUSE Atlastin-2 OS=Mus musculus GN=Atl2 PE=1 SV=1	1.2E-09	40.2	9.3	5 (5 0 0 0 0)	Endoplasmic reticulum membrane; Multi-pass membrane protein.
Q9DCX2	ATP5H_MOUSE ATP synthase subunit d, mitochondrial OS=Mus musculus GN=Atp5h PE=1 SV=3	1.1E-09	40.2	15.5	6 (6 0 0 0 0)	Mitochondrion. Mitochondrion inner membrane.
Q06185	ATP5I_MOUSE ATP synthase subunit e, mitochondrial OS=Mus musculus GN=Atp5i PE=1 SV=2	2.3E-04	20.2	21.1	3 (3 0 0 0 0)	Mitochondrion. Mitochondrion inner membrane.
Q03265	ATPA_MOUSE ATP synthase subunit alpha, mitochondrial OS=Mus musculus GN=Atp5a1 PE=1 SV=1	1.1E-15	420.4	61.5	306 (304 2 0 0 0)	Mitochondrion inner membrane. Cell membrane; Peripheral membrane protein; Extracellular side.
P56480	ATPB_MOUSE ATP synthase subunit beta, mitochondrial OS=Mus musculus GN=Atp5b PE=1 SV=2	1.0E-30	450.3	75.2	325 (313 12 0 0 0)	Mitochondrion. Mitochondrion inner membrane.
Q9D3D9	ATPD_MOUSE ATP synthase subunit delta, mitochondrial OS=Mus musculus GN=Atp5d PE=1 SV=1	1.6E-08	20.2	13.7	2 (2 0 0 0 0)	Mitochondrion. Mitochondrion inner membrane.
Q91VR2	ATPG_MOUSE ATP synthase subunit gamma, mitochondrial OS=Mus musculus GN=Atp5c1 PE=1 SV=1	2.8E-09	70.3	24.5	15 (15 0 0 0 0)	Mitochondrion. Mitochondrion inner membrane; Peripheral membrane protein.
P56135	ATPK_MOUSE ATP synthase subunit f, mitochondrial OS=Mus musculus GN=Atp5j2 PE=1	9.0E-04	20.1	26.1	2 (2 0 0 0 0)	Mitochondrion. Mitochondrion inner membrane.

	SV=3					
Q9DB20	ATPO_MOUSE ATP synthase subunit O, mitochondrial OS=Mus musculus GN=Atp5o PE=1 SV=1	6.1E-09	78.2	26.3	12 (11 1 0 0 0)	Mitochondrion. Mitochondrion inner membrane.
Q61335	BAP31_MOUSE B-cell receptor-associated protein 31 OS=Mus musculus GN=Bcap31 PE=1 SV=3	4.5E-05	20.1		2 (2 0 0 0 0)	Endoplasmic reticulum membrane; Multi-pass membrane protein. Endoplasmic reticulum-Golgi intermediate compartment membrane; Multi-pass membrane protein.
P18572	BASI_MOUSE Basigin OS=Mus musculus GN=Bsg PE=1 SV=2	3.5E-07	30.2	9.8	6 (6 0 0 0 0)	Cell membrane; Single-pass type I membrane protein. Melanosome.
Q80XN0	BDH_MOUSE D-beta-hydroxybutyrate dehydrogenase, mitochondrial OS=Mus musculus GN=Bdh1 PE=1 SV=1	1.3E-14	30.3	8.7	4 (4 0 0 0 0)	Mitochondrion matrix.
P82198	BGH3_MOUSE Transforming growth factor-beta-induced protein ig-h3 OS=Mus musculus GN=Tgfbi PE=2 SV=1	2.7E-08	20.2	5.0	3 (3 0 0 0 0)	Secreted â€º extracellular space â€º extracellular matrix.
O35490	BHMT1_MOUSE Betaine--homocysteine S-methyltransferase 1 OS=Mus musculus GN=Bhmt PE=2 SV=1	1.2E-14	20.3	4.9	200 (200 0 0 0 0)	Cytoplasm.
O08539	BIN1_MOUSE Myc box-dependent-interacting protein 1 OS=Mus musculus GN=Bin1 PE=1 SV=1	4.5E-12	88.3	22.1	22 (21 1 0 0 0)	Cytoplasm. Nucleus.
O08532	CA2D1_MOUSE Voltage-dependent calcium channel subunit alpha-2/delta-1 OS=Mus musculus GN=Cacna2d1 PE=1 SV=1	1.3E-14	238.3	25.8	46 (45 1 0 0 0)	Membrane; Single-pass type I membrane protein.
Q02789	CAC1S_MOUSE Voltage-dependent L-type calcium channel subunit alpha-1S OS=Mus musculus GN=Cacna1s PE=1 SV=2	2.9E-10	40.2	2.2	8 (8 0 0 0 0)	Membrane; Multi-pass membrane protein.
P47934	CACP_MOUSE Carnitine O-acetyltransferase OS=Mus musculus GN=Crat PE=1	2.9E-12	50.2	10.1	5 (5 0 0 0 0)	Endoplasmic reticulum. Peroxisome.

	SV=2					Mitochondrion inner membrane; Peripheral membrane protein; Matrix side.
Q9WTR5	CAD13_MOUSE Cadherin-13 OS=Mus musculus GN=Cdh13 PE=2 SV=1	7.4E-10	20.2	4.9	9 (9 0 0 0 0)	Cell membrane; Lipid-anchor â€º GPI-anchor.
P16015	CAH3_MOUSE Carbonic anhydrase 3 OS=Mus musculus GN=Ca3 PE=1 SV=3	1.3E-12	50.2	29.2	9 (9 0 0 0 0)	Cytoplasm.
P35564	CALX_MOUSE Calnexin OS=Mus musculus GN=Canx PE=1 SV=1	5.2E-12	50.2	9.3	12 (12 0 0 0 0)	Endoplasmic reticulum membrane; Single-pass type I membrane protein. Melanosome.
O35350	CAN1_MOUSE Calpain-1 catalytic subunit OS=Mus musculus GN=Capn1 PE=2 SV=1	3.0E-07	30.2	4.3	3 (3 0 0 0 0)	Cytoplasm. Cell membrane.
Q6ZQ73	CAND2_MOUSE Cullin-associated NEDD8-dissociated protein 2 OS=Mus musculus GN=Cand2 PE=1 SV=2	9.1E-13	50.3	6.3	8 (8 0 0 0 0)	Nucleus.
O09165	CASQ1_MOUSE Calsequestrin-1 OS=Mus musculus GN=Casq1 PE=2 SV=2	1.0E-30	60.3	18.3	12 (12 0 0 0 0)	Sarcoplasmic reticulum lumen.
P24270	CATA_MOUSE Catalase OS=Mus musculus GN=Cat PE=1 SV=3	3.7E-09	50.2	14.2	5 (5 0 0 0 0)	Peroxisome.
Q9D024	CC47_MOUSE Coiled-coil domain-containing protein 47 OS=Mus musculus GN=Ccdc47 PE=2 SV=2	6.3E-05	30.2	3.9	3 (3 0 0 0 0)	Membrane; Single-pass membrane protein.
Q08857	CD36_MOUSE Platelet glycoprotein 4 OS=Mus musculus GN=Cd36 PE=2 SV=2	8.2E-13	40.3	10.4	9 (9 0 0 0 0)	Membrane; Multi-pass membrane protein.
P63038	CH60_MOUSE 60 kDa heat shock protein, mitochondrial OS=Mus musculus GN=Hspd1 PE=1 SV=1	2.2E-15	160.3	27.4	28 (28 0 0 0 0)	Mitochondrion matrix.
O55226	CHAD_MOUSE Chondroadherin OS=Mus musculus GN=Chad PE=2 SV=1	1.0E-11	30.2	10.3	4 (4 0 0 0 0)	Secreted â€º extracellular space â€º extracellular matrix.
Q9CRB9	CHCH3_MOUSE Coiled-coil-helix-coiled-coil-helix domain-containing protein 3, mitochondrial OS=Mus musculus GN=Chchd3 PE=1	2.0E-08	50.2	9.3	6 (6 0 0 0 0)	Mitochondrion inner membrane; Lipid-anchor; Intermembrane side.

	SV=1					
Q9CZU6	CISY_MOUSE Citrate synthase, mitochondrial OS=Mus musculus GN=Cs PE=1 SV=1	2.2E-15	218.3	39.4	44 (38 4 2 0 0)	Mitochondrion matrix.
Q68FD5	CLH_MOUSE Clathrin heavy chain 1 OS=Mus musculus GN=Cltc PE=1 SV=3	1.0E-30	424.3	31.7	107 (103 2 2 0 0)	Cytoplasmic vesicle membrane; Peripheral membrane protein; Cytoplasmic side. Membrane â€º coated pit; Peripheral membrane protein; Cytoplasmic side. Melanosome.
Q8BH59	CMC1_MOUSE Calcium-binding mitochondrial carrier protein Aralar1 OS=Mus musculus GN=Slc25a12 PE=1 SV=1	1.0E-30	298.4	49.2	76 (73 3 0 0 0)	Mitochondrion inner membrane; Multi-pass membrane protein.
P11087	CO1A1_MOUSE Collagen alpha-1(I) chain OS=Mus musculus GN=Col1a1 PE=1 SV=4	2.6E-14	30.2	2.1	19 (19 0 0 0 0)	Secreted â€º extracellular space â€º extracellular matrix.
Q01149	CO1A2_MOUSE Collagen alpha-2(I) chain OS=Mus musculus GN=Col1a2 PE=2 SV=2	1.6E-14	40.2	4.2	23 (23 0 0 0 0)	Secreted â€º extracellular space â€º extracellular matrix.
P01027	CO3_MOUSE Complement C3 OS=Mus musculus GN=C3 PE=1 SV=2	2.0E-08	30.2	2.0	5 (5 0 0 0 0)	Secreted.
Q04857	CO6A1_MOUSE Collagen alpha-1(VI) chain OS=Mus musculus GN=Col6a1 PE=2 SV=1	8.9E-15	140.3	15.9	71 (71 0 0 0 0)	Secreted â€º extracellular space â€º extracellular matrix.
Q02788	CO6A2_MOUSE Collagen alpha-2(VI) chain OS=Mus musculus GN=Col6a2 PE=2 SV=3	1.0E-30	190.3	18.2	63 (63 0 0 0 0)	Secreted â€º extracellular space â€º extracellular matrix. Membrane; Peripheral membrane protein.
Q8C6K9	CO6A6_MOUSE Collagen alpha-6(VI) chain OS=Mus musculus GN=Col6a6 PE=1 SV=2	9.2E-07	20.2	1.0	2 (2 0 0 0 0)	Secreted â€º extracellular space â€º extracellular matrix.
Q60847	COCA1_MOUSE Collagen alpha-1(XII) chain OS=Mus musculus GN=Col12a1 PE=2 SV=3	2.2E-15	110.3	6.2	17 (17 0 0 0 0)	Secreted â€º extracellular space â€º extracellular matrix.
P00405	COX2_MOUSE Cytochrome c oxidase subunit 2 OS=Mus musculus GN=Mtco2 PE=1 SV=1	4.7E-10	28.3	7.0	7 (6 1 0 0 0)	Mitochondrion inner membrane; Multi-pass membrane protein.

P19783	COX41_MOUSE Cytochrome c oxidase subunit 4 isoform 1, mitochondrial OS=Mus musculus GN=Cox4i1 PE=1 SV=2	3.8E-11	40.2	23.7	10 (10 0 0 0 0)	Mitochondrion inner membrane.
P12787	COX5A_MOUSE Cytochrome c oxidase subunit 5A, mitochondrial OS=Mus musculus GN=Cox5a PE=1 SV=2	1.7E-05	20.2	6.8	9 (9 0 0 0 0)	Mitochondrion inner membrane.
Q9CPQ1	COX6C_MOUSE Cytochrome c oxidase subunit 6C OS=Mus musculus GN=Cox6c PE=1 SV=3	6.2E-04	20.1	27.6	2 (2 0 0 0 0)	Mitochondrion inner membrane.
Q8C196	CPSM_MOUSE Carbamoyl-phosphate synthase [ammonia], mitochondrial OS=Mus musculus GN=Cps1 PE=1 SV=2	1.0E-30	50.4	4.3	377 (377 0 0 0 0)	Mitochondrion.
Q924X2	CPT1B_MOUSE Carnitine O-palmitoyltransferase 1, muscle isoform OS=Mus musculus GN=Cpt1b PE=2 SV=1	4.6E-13	130.2	16.2	27 (27 0 0 0 0)	Mitochondrion outer membrane; Multi-pass membrane protein.
P52825	CPT2_MOUSE Carnitine O-palmitoyltransferase 2, mitochondrial OS=Mus musculus GN=Cpt2 PE=1 SV=1	1.7E-12	80.3	13.4	11 (11 0 0 0 0)	Mitochondrion inner membrane; Peripheral membrane protein; Matrix side.
Q9D5V5	CUL5_MOUSE Cullin-5 OS=Mus musculus GN=Cul5 PE=2 SV=3	8.1E-09	30.2	4.6	3 (3 0 0 0 0)	ND
Q9D0M3	CY1_MOUSE Cytochrome c1, heme protein, mitochondrial OS=Mus musculus GN=Cyc1 PE=1 SV=1	1.1E-15	86.3	28.9	13 (9 2 1 1 0)	Mitochondrion inner membrane; Single-pass membrane protein; Intermembrane side.
P42125	D3D2_MOUSE 3,2-trans-enoyl-CoA isomerase, mitochondrial OS=Mus musculus GN=Dci PE=2 SV=1	9.5E-09	60.2	21.5	7 (7 0 0 0 0)	Mitochondrion matrix.
Q99KJ8	DCTN2_MOUSE Dynactin subunit 2 OS=Mus musculus GN=Dctn2 PE=1 SV=3	1.1E-05	20.2	7.2	2 (2 0 0 0 0)	Cytoplasm â€º cytoskeleton â€º centrosome. Membrane; Peripheral membrane protein.
Q9CQ62	DECR_MOUSE 2,4-dienoyl-CoA reductase, mitochondrial OS=Mus musculus GN=Decr1 PE=1	1.1E-15	40.3	15.8	9 (9 0 0 0 0)	Mitochondrion.

	SV=1					
P31001	DESM_MOUSE Desmin OS=Mus musculus GN=Des PE=1 SV=3	1.5E-11	190.3	32.8	47 (47 0 0 0 0)	Cytoplasm.
Q99LB2	DHRS4_MOUSE Dehydrogenase/reductase SDR family member 4 OS=Mus musculus GN=Dhrs4 PE=2 SV=1	1.2E-11	50.2	18.8	7 (7 0 0 0 0)	Peroxisome.
Q8K2B3	DHSA_MOUSE Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial OS=Mus musculus GN=Sdha PE=1 SV=1	9.0E-14	90.3	17.0	19 (19 0 0 0 0)	Mitochondrion inner membrane; Peripheral membrane protein; Matrix side.
Q9CQA3	DHSB_MOUSE Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial OS=Mus musculus GN=Sdhb PE=1 SV=1	1.8E-08	50.2	18.8	5 (5 0 0 0 0)	Mitochondrion inner membrane; Peripheral membrane protein; Matrix side.
O08749	DLDH_MOUSE Dihydrolipoyl dehydrogenase, mitochondrial OS=Mus musculus GN=Dld PE=1 SV=2	1.1E-14	90.3	18.9	13 (13 0 0 0 0)	Mitochondrion matrix.
P11531	DMD_MOUSE Dystrophin OS=Mus musculus GN=Dmd PE=1 SV=2	1.0E-11	20.2	1.0	4 (4 0 0 0 0)	Cell membrane â€º sarcolemma; Peripheral membrane protein; Cytoplasmic side. Cytoplasm â€º cytoskeleton.
Q8K1M6	DNM1L_MOUSE Dynamin-1-like protein OS=Mus musculus GN=Dnm1l PE=1 SV=2	4.8E-14	30.3	7.1	4 (4 0 0 0 0)	Cytoplasm â€º cytosol. Golgi apparatus. Endomembrane system; Peripheral membrane protein.
Q9Z2W0	DNPEP_MOUSE Aspartyl aminopeptidase OS=Mus musculus GN=Dnpep PE=2 SV=1	5.1E-05	20.2	8.2	2 (2 0 0 0 0)	Cytoplasm.
O08553	DPYL2_MOUSE Dihydropyrimidinase-related protein 2 OS=Mus musculus GN=Dpysl2 PE=1 SV=2	6.3E-09	40.2	7.7	5 (5 0 0 0 0)	Cytoplasm.
Q8CHS7	DRS7C_MOUSE Dehydrogenase/reductase SDR family member 7C OS=Mus musculus GN=Dhrs7c PE=2 SV=3	8.9E-10	60.3	19.3	6 (6 0 0 0 0)	Secreted.
Q9JHU4	DYHC1_MOUSE Cytoplasmic dynein 1 heavy	6.7E-15	260.4	7.5	38 (38 0 0 0 0)	Cytoplasm â€º cytoskeleton.

	chain 1 OS=Mus musculus GN=Dync1h1 PE=1 SV=1					
Q9ESD7	DYSF_MOUSE Dysferlin OS=Mus musculus GN=Dysf PE=1 SV=3	2.8E-09	20.3	1.5	2 (2 0 0 0 0)	Cell membrane â€º sarcolemma; Single-pass type II membrane protein. Cytoplasmic vesicle membrane; Single-pass type II membrane protein.
O35459	ECH1_MOUSE Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial OS=Mus musculus GN=Ech1 PE=2 SV=1	2.0E-10	30.2	8.9	3 (3 0 0 0 0)	Mitochondrion. Peroxisome.
Q8BMS1	ECHA_MOUSE Trifunctional enzyme subunit alpha, mitochondrial OS=Mus musculus GN=Hadha PE=1 SV=1	1.0E-30	344.4	43.6	107 (104 3 0 0 0)	Mitochondrion matrix.
Q99JY0	ECHB_MOUSE Trifunctional enzyme subunit beta, mitochondrial OS=Mus musculus GN=Hadhb PE=1 SV=1	1.9E-13	220.3	44.4	33 (33 0 0 0 0)	Mitochondrion matrix.
Q8BH95	ECHM_MOUSE Enoyl-CoA hydratase, mitochondrial OS=Mus musculus GN=Echs1 PE=1 SV=1	1.0E-30	50.3	15.9	8 (6 2 0 0 0)	Mitochondrion matrix.
Q6PDI5	ECM29_MOUSE Proteasome-associated protein ECM29 homolog OS=Mus musculus GN=Ecm29 PE=1 SV=2	9.4E-07	20.2	1.5	3 (3 0 0 0 0)	Endoplasmic reticulum. Endoplasmic reticulum-Golgi intermediate compartment. Endosome. Cytoplasm â€º cytoskeleton â€º centrosome. Nucleus. Endosome â€º multivesicular body. Cytoplasmic vesicle.
P10126	EF1A1_MOUSE Elongation factor 1-alpha 1 OS=Mus musculus GN=Eef1a1 PE=1 SV=3	2.5E-11	100.2	21.9	95 (95 0 0 0 0)	Cytoplasm.
P62631	EF1A2_MOUSE Elongation factor 1-alpha 2 OS=Mus musculus GN=Eef1a2 PE=1 SV=1	8.2E-13	140.3	27.9	102 (101 1 0 0 0)	Nucleus.
P57776	EF1D_MOUSE Elongation factor 1-delta OS=Mus musculus GN=Eef1d PE=1	5.1E-08	40.2	21.7	8 (8 0 0 0 0)	ND

	SV=3					
Q9D8N0	EF1G_MOUSE Elongation factor 1-gamma OS=Mus musculus GN=Eef1g PE=1 SV=3	2.4E-11	60.2	18.1	13 (13 0 0 0 0)	ND
P58252	EF2_MOUSE Elongation factor 2 OS=Mus musculus GN=Eef2 PE=1 SV=2	5.7E-12	120.3	17.4	29 (29 0 0 0 0)	Cytoplasm.
Q8BFR5	EFTU_MOUSE Elongation factor Tu, mitochondrial OS=Mus musculus GN=Tufm PE=1 SV=1	3.2E-12	60.2	15.7	12 (12 0 0 0 0)	Mitochondrion.
Q9WVK4	EHD1_MOUSE EH domain-containing protein 1 OS=Mus musculus GN=Ehd1 PE=1 SV=1	4.5E-10	20.2	6.2	2 (2 0 0 0 0)	Cell membrane; Peripheral membrane protein; Cytoplasmic side. Early endosome membrane; Peripheral membrane protein. Recycling endosome membrane; Peripheral membrane protein.
Q8BH64	EHD2_MOUSE EH domain-containing protein 2 OS=Mus musculus GN=Ehd2 PE=1 SV=1	1.1E-14	220.3	37.2	35 (35 0 0 0 0)	Cell membrane; Peripheral membrane protein; Cytoplasmic side. Endosome membrane; Peripheral membrane protein.
Q9EQP2	EHD4_MOUSE EH domain-containing protein 4 OS=Mus musculus GN=Ehd4 PE=1 SV=1	6.6E-08	20.2	3.5	2 (2 0 0 0 0)	Early endosome membrane; Peripheral membrane protein. Recycling endosome membrane; Peripheral membrane protein.
P17182	ENOA_MOUSE Alpha-enolase OS=Mus musculus GN=Eno1 PE=1 SV=3	7.3E-14	60.3	19.6	9 (9 0 0 0 0)	Cytoplasm. Cell membrane.
P21550	ENOB_MOUSE Beta-enolase OS=Mus musculus GN=Eno3 PE=1 SV=3	2.0E-14	166.3	29.5	33 (27 6 0 0 0)	Cytoplasm.
P08113	ENPL_MOUSE Endoplasmin OS=Mus musculus GN=Hsp90b1 PE=1 SV=2	1.8E-11	20.3	3.9	7 (7 0 0 0 0)	Endoplasmic reticulum lumen. Melanosome.
O55026	ENTP2_MOUSE Ectonucleoside triphosphate diphosphohydrolase 2	2.3E-06	20.2	4.8	3 (3 0 0 0 0)	Membrane; Multi-pass membrane protein.

	OS=Mus musculus GN=Entpd2 PE=1 SV=2					
Q9R0P3	ESTD_MOUSE S-formylglutathione hydrolase OS=Mus musculus GN=Esd PE=2 SV=1	3.0E-12	20.2	8.2	4 (4 0 0 0 0)	Cytoplasm. Cytoplasmic vesicle.
Q99LC5	ETFA_MOUSE Electron transfer flavoprotein subunit alpha, mitochondrial OS=Mus musculus GN=Etfa PE=1 SV=2	1.1E-10	50.2	19.8	6 (6 0 0 0 0)	Mitochondrion matrix.
Q9DCW4	ETFB_MOUSE Electron transfer flavoprotein subunit beta OS=Mus musculus GN=Etfb PE=1 SV=3	6.9E-07	50.2	25.1	5 (5 0 0 0 0)	Mitochondrion matrix.
Q921G7	ETFD_MOUSE Electron transfer flavoprotein-ubiquinone oxidoreductase, mitochondrial OS=Mus musculus GN=Etfdh PE=1 SV=1	6.9E-10	70.2	13.1	15 (15 0 0 0 0)	Mitochondrion inner membrane.
P26040	EZRI_MOUSE Ezrin OS=Mus musculus GN=Ezr PE=1 SV=3	2.2E-08	40.2	5.3	11 (11 0 0 0 0)	Apical cell membrane; Peripheral membrane protein; Cytoplasmic side. Cell projection. Cell projection â€º microvillus membrane; Peripheral membrane protein; Cytoplasmic side. Cell projection â€º ruffle membrane; Peripheral membrane protein; Cytoplasmic side. Cytoplasm â€º cell cortex. Cytoplasm â€º cytoskeleton.
P19096	FAS_MOUSE Fatty acid synthase OS=Mus musculus GN=Fasn PE=1 SV=2	1.1E-15	20.2	1.4	5 (5 0 0 0 0)	Cytoplasm. Melanosome.
Q61554	FBN1_MOUSE Fibrillin-1 OS=Mus musculus GN=Fbn1 PE=1 SV=1	9.7E-06	20.2	0.6	7 (7 0 0 0 0)	Secreted â€º extracellular space â€º extracellular matrix.
P97447	FHL1_MOUSE Four and a half LIM domains protein 1 OS=Mus musculus GN=Fhl1 PE=2 SV=3	4.1E-06	30.2	8.2	6 (6 0 0 0 0)	Cytoplasm. Nucleus.
Q8BTM8	FLNA_MOUSE Filamin-A OS=Mus musculus GN=Flna PE=1 SV=4	5.7E-12	50.2	1.6	9 (9 0 0 0 0)	Cytoplasm â€º cell cortex. Cytoplasm â€º cytoskeleton.

Q8VHX6	FLNC_MOUSE Filamin-C OS=Mus musculus GN=Flnc PE=1 SV=3	1.1E-15	540.3	26.9	190 (190 0 0 0 0)	Cytoplasm. Membrane; Peripheral membrane protein. Cytoplasm â€º cytoskeleton. Cytoplasm â€º myofibril â€º sarcomere â€º Z line.
P50608	FMOD_MOUSE Fibromodulin OS=Mus musculus GN=Fmod PE=2 SV=1	1.0E-12	40.3	11.7	16 (16 0 0 0 0)	Secreted â€º extracellular space â€º extracellular matrix.
P97807	FUMH_MOUSE Fumarate hydratase, mitochondrial OS=Mus musculus GN=Fh PE=1 SV=2	2.3E-12	90.3	20.3	16 (16 0 0 0 0)	Mitochondrion. Cytoplasm.
P16858	G3P_MOUSE Glyceraldehyde-3-phosphate dehydrogenase OS=Mus musculus GN=Gapdh PE=1 SV=2	1.0E-30	226.4	39.9	115 (110 5 0 0 0)	Cytoplasm â€º cytosol. Nucleus.
P06745	G6PI_MOUSE Glucose-6-phosphate isomerase OS=Mus musculus GN=Gpi PE=1 SV=4	2.4E-11	110.3	19.5	18 (18 0 0 0 0)	Cytoplasm. Secreted.
P62874	GBB1_MOUSE Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1 OS=Mus musculus GN=Gnb1 PE=1 SV=3	2.0E-04	20.1		2 (2 0 0 0 0)	ND
Q9D6Y9	GLGB_MOUSE 1,4-alpha-glucan-branching enzyme OS=Mus musculus GN=Gbe1 PE=2 SV=1	1.6E-08	50.2	8.5	7 (7 0 0 0 0)	ND
P15105	GLNA_MOUSE Glutamine synthetase OS=Mus musculus GN=Glul PE=1 SV=6	2.3E-12	20.3	5.6	2 (2 0 0 0 0)	Cytoplasm. Mitochondrion.
Q9DCZ1	GMPR1_MOUSE GMP reductase 1 OS=Mus musculus GN=Gmpr PE=2 SV=1	8.2E-05	20.2	7.0	2 (2 0 0 0 0)	ND
P13707	GPDA_MOUSE Glycerol-3-phosphate dehydrogenase [NAD+], cytoplasmic OS=Mus musculus GN=Gpd1 PE=1 SV=3	1.0E-30	170.3	41.5	48 (44 4 0 0 0)	Cytoplasm.
Q64521	GPDM_MOUSE Glycerol-3-phosphate dehydrogenase, mitochondrial OS=Mus musculus GN=Gpd2 PE=1 SV=2	7.5E-10	60.2	9.8	9 (9 0 0 0 0)	Mitochondrion inner membrane.
Q91Z53	GRHPR_MOUSE	2.0E-08	20.2	8.5	3 (3 0 0 0	ND

	Glyoxylate reductase/hydroxypyruvate reductase OS=Mus musculus GN=Grhpr PE=1 SV=1				0)	
P38647	GRP75_MOUSE Stress-70 protein, mitochondrial OS=Mus musculus GN=Hspa9 PE=1 SV=2	9.7E-14	140.3	27.0	18 (18 0 0 0 0)	Mitochondrion.
P20029	GRP78_MOUSE 78 kDa glucose-regulated protein OS=Mus musculus GN=Hspa5 PE=1 SV=3	4.2E-11	120.2	25.0	17 (17 0 0 0 0)	Endoplasmic reticulum lumen. Melanosome.
Q9Z1E4	GYS1_MOUSE Glycogen [starch] synthase, muscle OS=Mus musculus GN=Gys1 PE=1 SV=2	7.8E-15	170.3	27.2	48 (48 0 0 0 0)	ND
P15864	H12_MOUSE Histone H1.2 OS=Mus musculus GN=Hist1h1c PE=1 SV=2	1.3E-07	20.1		4 (4 0 0 0 0)	Nucleus. Chromosome.
Q8CGP5	H2A1F_MOUSE Histone H2A type 1-F OS=Mus musculus GN=Hist1h2af PE=1 SV=3	6.4E-09	20.2	21.5	4 (4 0 0 0 0)	Nucleus. Chromosome.
P01942	HBA_MOUSE Hemoglobin subunit alpha OS=Mus musculus GN=Hba PE=1 SV=2	2.8E-13	20.2	10.6	23 (23 0 0 0 0)	ND
P02088	HBB1_MOUSE Hemoglobin subunit beta-1 OS=Mus musculus GN=Hbb-b1 PE=1 SV=2	1.0E-30	30.4	19.7	91 (91 0 0 0 0)	ND
O08756	HCD2_MOUSE 3-hydroxyacyl-CoA dehydrogenase type-2 OS=Mus musculus GN=Hsd17b10 PE=1 SV=4	1.0E-14	20.3	14.2	21 (21 0 0 0 0)	Mitochondrion.
Q61425	HCDH_MOUSE Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial OS=Mus musculus GN=Hadh PE=1 SV=2	4.7E-08	40.2	15.3	6 (6 0 0 0 0)	Mitochondrion matrix.
Q9D1G3	HHATL_MOUSE Protein-cysteine N-palmitoyltransferase HHAT-like protein OS=Mus musculus GN=Hhatl PE=1 SV=2	1.0E-30	80.3	17.7	27 (27 0 0 0 0)	Endoplasmic reticulum membrane; Multi-pass membrane protein.
Q61696	HS71A_MOUSE Heat shock 70 kDa protein 1A OS=Mus musculus GN=Hspa1a PE=1 SV=2	2.2E-13	30.2	5.9	7 (7 0 0 0 0)	Cytoplasm.
P07901	HS90A_MOUSE Heat shock protein HSP 90-alpha OS=Mus musculus	6.7E-10	36.2	6.5	9 (4 5 0 0 0)	Cytoplasm. Melanosome.

	GN=Hsp90aa1 PE=1 SV=4					
P11499	HS90B_MOUSE Heat shock protein HSP 90-beta OS=Mus musculus GN=Hsp90ab1 PE=1 SV=2	1.8E-14	80.3	13.5	22 (22 0 0 0 0)	Cytoplasm. Melanosome.
P17156	HSP72_MOUSE Heat shock-related 70 kDa protein 2 OS=Mus musculus GN=Hspa2 PE=1 SV=1	1.0E-14	50.3	8.5	13 (13 0 0 0 0)	ND
P63017	HSP7C_MOUSE Heat shock cognate 71 kDa protein OS=Mus musculus GN=Hspa8 PE=1 SV=1	4.5E-12	230.3	29.4	47 (47 0 0 0 0)	Cytoplasm. Melanosome.
P14602	HSPB1_MOUSE Heat shock protein beta-1 OS=Mus musculus GN=Hspb1 PE=1 SV=3	1.1E-09	30.2	16.7	6 (6 0 0 0 0)	Cytoplasm. Nucleus. Cytoplasm â€º cytoskeleton â€º spindle.
Q5EBG6	HSPB6_MOUSE Heat shock protein beta-6 OS=Mus musculus GN=Hspb6 PE=1 SV=1	8.2E-09	20.2	8.0	13 (13 0 0 0 0)	Cytoplasm. Nucleus.
O08528	HXK2_MOUSE Hexokinase-2 OS=Mus musculus GN=Hk2 PE=1 SV=1	2.5E-07	20.2	3.2	4 (4 0 0 0 0)	ND
Q9D379	HYEP_MOUSE Epoxide hydrolase 1 OS=Mus musculus GN=Ephx1 PE=1 SV=1	2.2E-07	60.1	11.4	7 (7 0 0 0 0)	Microsome membrane; Single-pass type II membrane protein. Endoplasmic reticulum membrane; Single-pass type II membrane protein.
Q9D6R2	IDH3A_MOUSE Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial OS=Mus musculus GN=Idh3a PE=1 SV=1	3.4E-12	188.3	31.4	75 (62 11 2 0 0)	Mitochondrion.
P54071	IDHP_MOUSE Isocitrate dehydrogenase [NADP], mitochondrial OS=Mus musculus GN=Idh2 PE=1 SV=3	1.2E-10	100.2	21.7	20 (20 0 0 0 0)	Mitochondrion.
Q6ZWX6	IF2A_MOUSE Eukaryotic translation initiation factor 2 subunit 1 OS=Mus musculus GN=Eif2s1 PE=1 SV=3	7.3E-08	20.2	8.6	3 (3 0 0 0 0)	Cytoplasmic granule.
Q9Z0N1	IF2G_MOUSE Eukaryotic translation initiation factor 2 subunit 3, X-linked OS=Mus musculus GN=Eif2s3x PE=1 SV=2	1.4E-08	30.1	7.4	3 (3 0 0 0 0)	ND

P60843	IF4A1_MOUSE Eukaryotic initiation factor 4A-I OS=Mus musculus GN=Eif4a1 PE=2 SV=1	6.5E-10	40.2	9.4	5 (5 0 0 0 0)	ND
Q8CAQ8	IMMT_MOUSE Mitochondrial inner membrane protein OS=Mus musculus GN=Immt PE=1 SV=1	1.4E-13	140.2	17.0	27 (27 0 0 0 0)	Mitochondrion inner membrane.
Q8BKC5	IPO5_MOUSE Importin-5 OS=Mus musculus GN=Ipo5 PE=1 SV=3	2.2E-08	50.2	6.4	7 (7 0 0 0 0)	Cytoplasm. Nucleus.
Q9EPL8	IPO7_MOUSE Importin-7 OS=Mus musculus GN=Ipo7 PE=1 SV=2	2.5E-06	30.2	3.8	3 (3 0 0 0 0)	Cytoplasm. Nucleus.
Q61738	ITA7_MOUSE Integrin alpha-7 OS=Mus musculus GN=Itga7 PE=1 SV=2	1.5E-08	30.2	2.8	3 (3 0 0 0 0)	Membrane; Single-pass type I membrane protein.
P09055	ITB1_MOUSE Integrin beta-1 OS=Mus musculus GN=Itgb1 PE=1 SV=1	1.4E-09	48.2	9.8	9 (7 2 0 0 0)	Cell membrane; Single-pass type I membrane protein. Melanosome.
Q9JHI5	IVD_MOUSE Isovaleryl-CoA dehydrogenase, mitochondrial OS=Mus musculus GN=Ivd PE=1 SV=1	2.0E-07	30.2	7.5	3 (3 0 0 0 0)	Mitochondrion matrix.
Q9ET78	JPH2_MOUSE Junctophilin-2 OS=Mus musculus GN=Jph2 PE=1 SV=2	1.0E-06	20.1		2 (2 0 0 0 0)	Cell membrane; Peripheral membrane protein. Endoplasmic reticulum membrane; Single-pass type IV membrane protein. Sarcoplasmic reticulum membrane; Single-pass type IV membrane protein.
Q3MI48	JSPR1_MOUSE Junctional sarcoplasmic reticulum protein 1 OS=Mus musculus GN=Jsrp1 PE=1 SV=2	1.3E-12	50.2	15.1	7 (7 0 0 0 0)	Sarcoplasmic reticulum membrane. Endoplasmic reticulum membrane.
Q8C7X2	K0090_MOUSE Uncharacterized protein KIAA0090 OS=Mus musculus GN=Kiaa0090 PE=1 SV=1	3.8E-09	30.2	4.7	4 (4 0 0 0 0)	Membrane; Single-pass type I membrane protein.
P02535	K1C10_MOUSE Keratin, type I cytoskeletal 10 OS=Mus musculus GN=Krt10 PE=1 SV=3	2.4E-09	68.2	9.5	55 (54 1 0 0 0)	ND

Q61781	K1C14_MOUSE Keratin, type I cytoskeletal 14 OS=Mus musculus GN=Krt14 PE=1 SV=2	4.9E-05	20.2	4.5	2 (2 0 0 0 0)	Cytoplasm. Nucleus.
Q3TTY5	K22E_MOUSE Keratin, type II cytoskeletal 2 epidermal OS=Mus musculus GN=Krt2 PE=1 SV=1	2.1E-07	30.2	4.5	13 (13 0 0 0 0)	ND
P04104	K2C1_MOUSE Keratin, type II cytoskeletal 1 OS=Mus musculus GN=Krt1 PE=1 SV=4	9.8E-08	20.2	1.7	15 (15 0 0 0 0)	Cell membrane.
Q6IFZ6	K2C1B_MOUSE Keratin, type II cytoskeletal 1b OS=Mus musculus GN=Krt77 PE=1 SV=1	1.3E-08	30.2	3.8	25 (25 0 0 0 0)	ND
Q922U2	K2C5_MOUSE Keratin, type II cytoskeletal 5 OS=Mus musculus GN=Krt5 PE=1 SV=1	6.9E-08	30.2	5.2	30 (30 0 0 0 0)	ND
P11679	K2C8_MOUSE Keratin, type II cytoskeletal 8 OS=Mus musculus GN=Krt8 PE=1 SV=4	2.0E-08	28.2	2.9	17 (16 1 0 0 0)	Cytoplasm. Nucleus â€º nucleoplasm. Nucleus matrix.
P47857	K6PF_MOUSE 6-phosphofructokinase, muscle type OS=Mus musculus GN=Pfkm PE=1 SV=3	1.0E-30	444.3	45.3	325 (311 14 0 0 0)	ND
Q9R0Y5	KAD1_MOUSE Adenylate kinase isoenzyme 1 OS=Mus musculus GN=Ak1 PE=1 SV=1	9.7E-11	30.2	20.6	16 (16 0 0 0 0)	Cytoplasm.
Q9D783	KBTB5_MOUSE Kelch repeat and BTB domain-containing protein 5 OS=Mus musculus GN=Kbtbd5 PE=2 SV=1	2.3E-09	50.2	10.6	6 (6 0 0 0 0)	ND
Q04447	KCRB_MOUSE Creatine kinase B-type OS=Mus musculus GN=Ckb PE=1 SV=1	7.2E-09	20.2	3.4	2 (2 0 0 0 0)	Cytoplasm.
P07310	KCRM_MOUSE Creatine kinase M-type OS=Mus musculus GN=Ckm PE=1 SV=1	6.7E-15	150.3	44.4	175 (175 0 0 0 0)	Cytoplasm.
Q6P8J7	KCRS_MOUSE Creatine kinase S-type, mitochondrial OS=Mus musculus GN=Ckmt2 PE=1 SV=1	3.3E-15	120.3	24.1	91 (91 0 0 0 0)	Mitochondrion inner membrane; Peripheral membrane protein; Intermembrane side.
O35367	KERA_MOUSE Keratocan OS=Mus musculus GN=Kera PE=2 SV=1	3.0E-09	40.3	17.1	10 (10 0 0 0 0)	Secreted â€º extracellular space â€º extracellular matrix.

P33175	KIF5A_MOUSE Kinesin heavy chain isoform 5A OS=Mus musculus GN=Kif5a PE=1 SV=3	3.0E-07	30.2	3.3	3 (3 0 0 0 0)	Cytoplasm â€º perinuclear region. Cytoplasm â€º cytoskeleton.
Q61768	KINH_MOUSE Kinesin-1 heavy chain OS=Mus musculus GN=Kif5b PE=1 SV=2	2.8E-09	30.2	5.3	3 (3 0 0 0 0)	Cytoplasm â€º cytoskeleton.
P18826	KPB1_MOUSE Phosphorylase b kinase regulatory subunit alpha, skeletal muscle isoform OS=Mus musculus GN=Phka1 PE=1 SV=2	6.1E-08	30.2	2.8	10 (10 0 0 0 0)	Cell membrane; Lipid-anchor; Cytoplasmic side.
Q7TSH2	KPBB_MOUSE Phosphorylase b kinase regulatory subunit beta OS=Mus musculus GN=Phkb PE=1 SV=1	4.2E-09	100.2	8.8	15 (15 0 0 0 0)	Cell membrane; Lipid-anchor; Cytoplasmic side.
P52480	KPYM_MOUSE Pyruvate kinase isozymes M1/M2 OS=Mus musculus GN=Pkm2 PE=1 SV=4	1.3E-14	240.3	33.5	151 (151 0 0 0 0)	Cytoplasm. Nucleus.
Q61595	KTN1_MOUSE Kinectin OS=Mus musculus GN=Ktn1 PE=1 SV=1	2.7E-10	20.2	3.2	2 (2 0 0 0 0)	Endoplasmic reticulum membrane; Single-pass type II membrane protein.
Q60675	LAMA2_MOUSE Laminin subunit alpha-2 OS=Mus musculus GN=Lama2 PE=1 SV=1	1.0E-30	250.4	10.2	49 (49 0 0 0 0)	Secreted â€º extracellular space â€º extracellular matrix â€º basement membrane.
Q61001	LAMA5_MOUSE Laminin subunit alpha-5 OS=Mus musculus GN=Lama5 PE=1 SV=3	2.6E-06	20.2	0.7	3 (3 0 0 0 0)	Secreted â€º extracellular space â€º extracellular matrix â€º basement membrane.
P02469	LAMB1_MOUSE Laminin subunit beta-1 OS=Mus musculus GN=Lamb1-1 PE=1 SV=2	4.4E-15	110.3	7.8	34 (34 0 0 0 0)	Secreted â€º extracellular space â€º extracellular matrix â€º basement membrane.
Q61292	LAMB2_MOUSE Laminin subunit beta-2 OS=Mus musculus GN=Lamb2 PE=2 SV=1	1.1E-12	170.2	10.3	33 (33 0 0 0 0)	Secreted â€º extracellular space â€º extracellular matrix â€º basement membrane.
P02468	LAMC1_MOUSE Laminin subunit gamma-1 OS=Mus musculus GN=Lamc1 PE=1	6.5E-13	140.3	10.5	37 (37 0 0 0 0)	Secreted â€º extracellular space â€º extracellular

	SV=2					matrix â€º basement membrane.
Q9JKS4	LDB3_MOUSE LIM domain-binding protein 3 OS=Mus musculus GN=Ldb3 PE=1 SV=1	1.9E-10	128.3	18.0	36 (35 1 0 0 0)	Cytoplasm â€º perinuclear region. Cell projection â€º pseudopodium. Cytoplasm â€º cytoskeleton. Cytoplasm â€º myofibril â€º sarcomere â€º Z line.
P06151	LDHA_MOUSE L-lactate dehydrogenase A chain OS=Mus musculus GN=Ldha PE=1 SV=3	2.7E-13	156.3	32.5	57 (55 2 0 0 0)	Cytoplasm.
P16125	LDHB_MOUSE L-lactate dehydrogenase B chain OS=Mus musculus GN=Ldhb PE=1 SV=2	1.8E-08	80.2	25.4	15 (15 0 0 0 0)	Cytoplasm.
P24527	LKHA4_MOUSE Leukotriene A-4 hydrolase OS=Mus musculus GN=Lta4h PE=1 SV=3	1.1E-07	20.2	3.9	2 (2 0 0 0 0)	Cytoplasm.
Q9D0F3	LMAN1_MOUSE Protein ERGIC-53 OS=Mus musculus GN=Lman1 PE=2 SV=1	1.2E-08	20.1		2 (2 0 0 0 0)	Endoplasmic reticulum-Golgi intermediate compartment membrane; Single-pass type I membrane protein. Golgi apparatus membrane; Single-pass membrane protein. Endoplasmic reticulum membrane; Single-pass membrane protein.
P48678	LMNA_MOUSE Prelamin-A/C OS=Mus musculus GN=Lmna PE=1 SV=2	2.3E-07	20.2	2.9	4 (4 0 0 0 0)	Nucleus. Nucleus envelope.
Q6PB66	LPPRC_MOUSE Leucine-rich PPR motif-containing protein, mitochondrial OS=Mus musculus GN=Lrpprc PE=1 SV=2	4.8E-06	30.1	2.2	4 (4 0 0 0 0)	Mitochondrion. Nucleus. Nucleus â€º nucleoplasm. Nucleus inner membrane. Nucleus outer membrane.
Q9CR62	M2OM_MOUSE Mitochondrial 2-oxoglutarate/malate carrier protein OS=Mus musculus	2.8E-12	60.2	21.7	12 (12 0 0 0 0)	Mitochondrion inner membrane; Multi-pass membrane protein.

	GN=Slc25a11 PE=1 SV=3					
Q91W89	MA2C1_MOUSE Alpha-mannosidase 2C1 OS=Mus musculus GN=Man2c1 PE=1 SV=1	5.0E-10	20.2	2.5	2 (2 0 0 0 0)	ND
P06801	MAOX_MOUSE NADP-dependent malic enzyme OS=Mus musculus GN=Me1 PE=1 SV=1	4.0E-10	40.2	6.3	6 (6 0 0 0 0)	Cytoplasm.
Q9Z2Z6	MCAT_MOUSE Mitochondrial carnitine/acylcarnitine carrier protein OS=Mus musculus GN=Slc25a20 PE=1 SV=1	2.9E-04	20.1	3.0	2 (2 0 0 0 0)	Mitochondrion inner membrane; Multi-pass membrane protein.
Q99MR8	MCCA_MOUSE Methylcrotonoyl-CoA carboxylase subunit alpha, mitochondrial OS=Mus musculus GN=Mccc1 PE=2 SV=2	2.5E-09	20.2	4.6	5 (5 0 0 0 0)	Mitochondrion matrix.
Q3ULD5	MCCB_MOUSE Methylcrotonoyl-CoA carboxylase beta chain, mitochondrial OS=Mus musculus GN=Mccc2 PE=2 SV=1	3.8E-09	90.2	14.0	11 (11 0 0 0 0)	Mitochondrion matrix.
P14152	MDHC_MOUSE Malate dehydrogenase, cytoplasmic OS=Mus musculus GN=Mdh1 PE=1 SV=3	2.6E-12	60.2	23.1	16 (16 0 0 0 0)	Cytoplasm.
P08249	MDHM_MOUSE Malate dehydrogenase, mitochondrial OS=Mus musculus GN=Mdh2 PE=1 SV=3	8.9E-15	140.3	39.9	51 (51 0 0 0 0)	Mitochondrion matrix.
Q62000	MIME_MOUSE Mimecan OS=Mus musculus GN=Ogn PE=2 SV=1	3.4E-08	30.2	16.4	4 (4 0 0 0 0)	Secreted â€º extracellular space â€º extracellular matrix.
P05977	MLE1_MOUSE Myosin light chain 1, skeletal muscle isoform OS=Mus musculus GN=Myl1 PE=1 SV=2	1.5E-10	60.2	24.5	47 (47 0 0 0 0)	ND
P97457	MLRS_MOUSE Myosin regulatory light chain 2, skeletal muscle isoform OS=Mus musculus GN=Mylpf PE=1 SV=3	1.2E-05	30.2	16.6	3 (3 0 0 0 0)	ND
P26041	MOES_MOUSE Moesin OS=Mus musculus GN=Msn PE=1 SV=3	1.4E-14	118.3	19.2	24 (22 2 0 0 0)	Cell membrane; Peripheral membrane protein; Cytoplasmic side. Cytoplasm â€º cytoskeleton. Apical cell

						membrane; Peripheral membrane protein; Cytoplasmic side. Cell projection â€º microvillus membrane; Peripheral membrane protein; Cytoplasmic side.
Q8VEM8	MPCP_MOUSE Phosphate carrier protein, mitochondrial OS=Mus musculus GN=Slc25a3 PE=1 SV=1	1.9E-12	100.2	23.8	29 (29 0 0 0 0)	Mitochondrion inner membrane; Multi-pass membrane protein.
P28665	MUG1_MOUSE Murinoglobulin-1 OS=Mus musculus GN=Mug1 PE=1 SV=3	6.1E-06	20.2	1.1	2 (2 0 0 0 0)	Secreted.
P11588	MUP1_MOUSE Major urinary protein 1 OS=Mus musculus GN=Mup1 PE=1 SV=1	1.5E-10	20.3	18.9	26 (26 0 0 0 0)	Secreted.
Q9EQK5	MVP_MOUSE Major vault protein OS=Mus musculus GN=Mvp PE=1 SV=3	2.6E-07	30.2	4.4	3 (3 0 0 0 0)	Cytoplasm. Nucleus.
P70402	MYBPH_MOUSE Myosin-binding protein H OS=Mus musculus GN=Mybph PE=1 SV=1	5.3E-08	20.2	8.1	2 (2 0 0 0 0)	ND
Q5SX40	MYH1_MOUSE Myosin-1 OS=Mus musculus GN=Myh1 PE=1 SV=1	1.0E-30	1434.4	51.3	986 (878 108 0 0 0)	Cytoplasm â€º myofibril.
O08638	MYH11_MOUSE Myosin-11 OS=Mus musculus GN=Myh11 PE=1 SV=1	9.2E-12	60.3	3.9	8 (8 0 0 0 0)	Melanosome. Cytoplasm â€º myofibril.
P13541	MYH3_MOUSE Myosin-3 OS=Mus musculus GN=Myh3 PE=2 SV=2	1.1E-10	66.4	3.7	16 (14 2 0 0 0)	Cytoplasm â€º myofibril.
Q5SX39	MYH4_MOUSE Myosin-4 OS=Mus musculus GN=Myh4 PE=1 SV=1	1.1E-15	608.3	21.1	333 (332 1 0 0 0)	Cytoplasm â€º myofibril.
Q02566	MYH6_MOUSE Myosin-6 OS=Mus musculus GN=Myh6 PE=1 SV=2	1.1E-15	256.4	12.8	74 (70 4 0 0 0)	Cytoplasm â€º myofibril.
Q91Z83	MYH7_MOUSE Myosin-7 OS=Mus musculus GN=Myh7 PE=1 SV=1	2.2E-14	228.3	12.1	64 (63 1 0 0 0)	Cytoplasm â€º myofibril.
P13542	MYH8_MOUSE Myosin-8 OS=Mus musculus GN=Myh8 PE=1 SV=2	7.1E-14	56.3	4.0	14 (9 5 0 0 0)	Cytoplasm â€º myofibril.
Q8VDD5	MYH9_MOUSE Myosin-9 OS=Mus musculus GN=Myh9 PE=1 SV=4	4.3E-11	20.2	1.7	2 (2 0 0 0 0)	ND
P05977	MYL1_MOUSE Myosin light chain 1/3, skeletal	7.6E-12	124.2	50.5	58 (54 4 0 0 0)	ND

	muscle isoform OS=Mus musculus GN=Myl1 PE=1 SV=2					
P09542	MYL3_MOUSE Myosin light chain 3 OS=Mus musculus GN=Myl3 PE=2 SV=4	8.2E-14	50.3	37.3	24 (24 0 0 0 0)	ND
Q8CI43	MYL6B_MOUSE Myosin light chain 6B OS=Mus musculus GN=Myl6b PE=2 SV=1	5.4E-05	20.2	14.0	2 (2 0 0 0 0)	ND
Q62234	MYOM1_MOUSE Myomesin-1 OS=Mus musculus GN=Myom1 PE=1 SV=2	2.8E-14	150.4	11.8	52 (52 0 0 0 0)	ND
A2ABU4	MYOM3_MOUSE Myomesin-3 OS=Mus musculus GN=Myom3 PE=2 SV=1	2.6E-13	120.3	13.3	15 (15 0 0 0 0)	ND
Q9JIF9	MYOTI_MOUSE Myotilin OS=Mus musculus GN=Myot PE=2 SV=1	3.6E-09	40.2	7.1	5 (5 0 0 0 0)	Cell membrane â€º sarcolemma. Cytoplasm â€º cytoskeleton. Cytoplasm â€º myofibril â€º sarcomere â€º Z line.
Q9JK37	MYOZ1_MOUSE Myozenin-1 OS=Mus musculus GN=Myoz1 PE=1 SV=1	5.1E-07	20.2	4.4	2 (2 0 0 0 0)	Nucleus. Cell projection â€º pseudopodium.
P27573	MYP0_MOUSE Myelin protein P0 OS=Mus musculus GN=Mpz PE=1 SV=1	1.7E-06	20.1	9.3	2 (2 0 0 0 0)	Membrane; Single-pass type I membrane protein.
Q5XKE0	MYPC2_MOUSE Myosin-binding protein C, fast-type OS=Mus musculus GN=Mybpc2 PE=1 SV=1	3.3E-16	550.3	50.1	321 (321 0 0 0 0)	ND
Q99KQ4	NAMPT_MOUSE Nicotinamide phosphoribosyltransferase OS=Mus musculus GN=Nampt PE=1 SV=1	2.7E-14	30.3	12.0	3 (3 0 0 0 0)	Cytoplasm.
Q9DB73	NB5R1_MOUSE NADH-cytochrome b5 reductase 1 OS=Mus musculus GN=Cyb5r1 PE=2 SV=1	3.3E-06	30.1	10.2	3 (3 0 0 0 0)	Membrane; Single-pass membrane protein.
Q9DCN2	NB5R3_MOUSE NADH-cytochrome b5 reductase 3 OS=Mus musculus GN=Cyb5r3 PE=1 SV=3	6.2E-10	30.2	14.6	4 (4 0 0 0 0)	Endoplasmic reticulum membrane; Lipid-anchor; Cytoplasmic side. Mitochondrion outer membrane;

						Lipid-anchor; Cytoplasmic side. Cytoplasm â€º cytosol.
Q8VCM8	NCLN_MOUSE Nicalin OS=Mus musculus GN=Ncln PE=2 SV=2	8.0E-05	20.2	1.4	2 (2 0 0 0 0)	Endoplasmic reticulum membrane; Single-pass membrane protein.
P15532	NDKA_MOUSE Nucleoside diphosphate kinase A OS=Mus musculus GN=Nme1 PE=1 SV=1	4.3E-06	20.2	19.1	8 (8 0 0 0 0)	Cytoplasm. Nucleus.
Q9QYG0	NDRG2_MOUSE Protein NDRG2 OS=Mus musculus GN=Ndrg2 PE=1 SV=1	1.0E-30	50.3	15.9	16 (16 0 0 0 0)	Cytoplasm.
Q9CQ75	NDUA2_MOUSE NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 2 OS=Mus musculus GN=Ndufa2 PE=1 SV=3	1.7E-11	30.2	38.4	5 (5 0 0 0 0)	Mitochondrion inner membrane; Peripheral membrane protein; Matrix side.
Q9DCJ5	NDUA8_MOUSE NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 8 OS=Mus musculus GN=Ndufa8 PE=1 SV=3	4.8E-06	20.3	9.9	3 (3 0 0 0 0)	Mitochondrion. Mitochondrion intermembrane space.
Q9DC69	NDUA9_MOUSE NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial OS=Mus musculus GN=Ndufa9 PE=1 SV=1	2.2E-14	110.3	41.4	21 (21 0 0 0 0)	Mitochondrion matrix.
Q99LC3	NDUAA_MOUSE NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial OS=Mus musculus GN=Ndufa10 PE=1 SV=1	1.4E-12	60.2	23.1	9 (9 0 0 0 0)	Mitochondrion matrix.
Q9ERS2	NDUAD_MOUSE NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 13 OS=Mus musculus GN=Ndufa13 PE=1 SV=3	7.5E-05	20.1	13.2	4 (4 0 0 0 0)	Mitochondrion inner membrane; Single-pass membrane protein; Matrix side. Nucleus.
Q9CQJ8	NDUB9_MOUSE NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 9 OS=Mus musculus GN=Ndufb9 PE=1 SV=3	4.2E-08	20.2	11.7	2 (2 0 0 0 0)	Mitochondrion inner membrane; Peripheral membrane protein; Matrix side.
Q9DCS9	NDUBA_MOUSE NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 10 OS=Mus musculus GN=Ndufb10 PE=1 SV=3	7.0E-13	20.2	17.0	2 (2 0 0 0 0)	Mitochondrion inner membrane; Peripheral membrane protein; Matrix side.
Q91VD9	NDUS1_MOUSE NADH-	9.4E-13	300.3	34.3	59 (59 0 0	Mitochondrion

	ubiquinone oxidoreductase 75 kDa subunit, mitochondrial OS=Mus musculus GN=Ndufs1 PE=1 SV=1				0 0)	inner membrane.
Q91WD5	NDUS2_MOUSE NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial OS=Mus musculus GN=Ndufs2 PE=1 SV=1	4.6E-12	170.3	41.0	26 (26 0 0 0 0)	Mitochondrion inner membrane; Peripheral membrane protein; Matrix side.
Q9DCT2	NDUS3_MOUSE NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial OS=Mus musculus GN=Ndufs3 PE=1 SV=2	1.4E-11	70.2	30.4	19 (19 0 0 0 0)	Mitochondrion inner membrane.
Q9DC70	NDUS7_MOUSE NADH dehydrogenase [ubiquinone] iron-sulfur protein 7, mitochondrial OS=Mus musculus GN=Ndufs7 PE=1 SV=1	2.3E-04	20.2	8.0	6 (6 0 0 0 0)	Mitochondrion.
Q91YT0	NDUV1_MOUSE NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial OS=Mus musculus GN=Ndufv1 PE=1 SV=1	1.2E-14	120.2	24.1	23 (23 0 0 0 0)	Mitochondrion inner membrane; Peripheral membrane protein; Matrix side.
Q9D6J6	NDUV2_MOUSE NADH dehydrogenase [ubiquinone] flavoprotein 2, mitochondrial OS=Mus musculus GN=Ndufv2 PE=1 SV=2	4.5E-05	30.2	4.4	5 (5 0 0 0 0)	Mitochondrion inner membrane.
P10493	NID1_MOUSE Nidogen-1 OS=Mus musculus GN=Nid1 PE=1 SV=1	1.5E-12	70.2	6.5	18 (18 0 0 0 0)	Secreted â€º extracellular space â€º extracellular matrix â€º basement membrane.
O55126	NIPS2_MOUSE Protein NipSnap homolog 2 OS=Mus musculus GN=Gbas PE=2 SV=1	2.8E-08	50.2	16.4	7 (7 0 0 0 0)	ND
P60670	NPL4_MOUSE Nuclear protein localization protein 4 homolog OS=Mus musculus GN=Nploc4 PE=1 SV=3	1.1E-13	20.2	5.4	2 (2 0 0 0 0)	Cytoplasm â€º cytosol. Endoplasmic reticulum. Nucleus.
P03911	NU4M_MOUSE NADH-ubiquinone oxidoreductase chain 4 OS=Mus musculus GN=Mtnd4 PE=1 SV=1	8.6E-07	20.2	5.2	2 (2 0 0 0 0)	Mitochondrion membrane; Multi-pass membrane protein.
P03921	NU5M_MOUSE NADH-ubiquinone oxidoreductase chain 5 OS=Mus musculus GN=Mtnd5 PE=2 SV=2	8.9E-07	20.2	2.8	3 (3 0 0 0 0)	Mitochondrion inner membrane; Multi-pass membrane protein.

A2AAJ9	OBSCN_MOUSE Obscurin OS=Mus musculus GN=Obscn PE=2 SV=2	9.2E-09	60.3	0.9	9 (9 0 0 0 0)	ND
P53395	ODB2_MOUSE Lipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex, mitochondrial OS=Mus musculus GN=Dbt PE=2 SV=1	4.6E-09	20.2	5.8	2 (2 0 0 0 0)	Mitochondrion matrix.
Q60597	ODO1_MOUSE 2-oxoglutarate dehydrogenase E1 component, mitochondrial OS=Mus musculus GN=Ogdh PE=1 SV=3	1.0E-30	328.4	32.0	115 (114 1 0 0 0)	Mitochondrion matrix.
Q9D2G2	ODO2_MOUSE Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial OS=Mus musculus GN=Dlst PE=1 SV=1	1.3E-14	116.3	22.5	29 (25 4 0 0 0)	Mitochondrion.
Q8BMF4	ODP2_MOUSE Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial OS=Mus musculus GN=Dlat PE=1 SV=2	4.4E-16	160.3	23.1	63 (63 0 0 0 0)	Mitochondrion matrix.
P35486	ODPA_MOUSE Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial OS=Mus musculus GN=Pdha1 PE=1 SV=1	1.4E-10	80.2	29.0	13 (13 0 0 0 0)	Mitochondrion matrix.
Q9D051	ODPB_MOUSE Pyruvate dehydrogenase E1 component subunit beta, mitochondrial OS=Mus musculus GN=Pdhb PE=1 SV=1	6.2E-12	160.2	28.7	26 (26 0 0 0 0)	Mitochondrion matrix.
Q8BKZ9	ODPX_MOUSE Pyruvate dehydrogenase protein X component, mitochondrial OS=Mus musculus GN=Pdhx PE=2 SV=1	6.4E-12	60.2	16.8	12 (11 1 0 0 0)	Mitochondrion matrix.
Q8K010	OPLA_MOUSE 5-oxoprolinase OS=Mus musculus GN=Oplah PE=2 SV=1	3.3E-08	20.2	2.2	2 (2 0 0 0 0)	ND
O54734	OST48_MOUSE Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit OS=Mus	2.5E-08	30.2	7.5	3 (3 0 0 0 0)	Endoplasmic reticulum membrane; Single-pass type I

	musculus GN=Ddost PE=1 SV=1					membrane protein.
Q99JB8	PACN3_MOUSE Protein kinase C and casein kinase II substrate protein 3 OS=Mus musculus GN=Pacsin3 PE=1 SV=1	7.2E-08	40.2	7.5	7 (7 0 0 0 0)	Cytoplasm. Cell membrane; Peripheral membrane protein; Cytoplasmic side.
Q08642	PADI2_MOUSE Protein-arginine deiminase type-2 OS=Mus musculus GN=Padi2 PE=1 SV=1	3.3E-09	40.2	7.3	6 (6 0 0 0 0)	Cytoplasm.
Q3TVI8	PBIP1_MOUSE Pre-B-cell leukemia transcription factor-interacting protein 1 OS=Mus musculus GN=Pbxip1 PE=1 SV=2	8.1E-12	70.2	14.3	19 (19 0 0 0 0)	Cytoplasm â€º cytoskeleton. Nucleus.
Q91ZA3	PCCA_MOUSE Propionyl-CoA carboxylase alpha chain, mitochondrial OS=Mus musculus GN=Pcca PE=2 SV=2	6.1E-12	20.2	4.0	4 (4 0 0 0 0)	Mitochondrion matrix.
Q99MN9	PCCB_MOUSE Propionyl-CoA carboxylase beta chain, mitochondrial OS=Mus musculus GN=Pccb PE=1 SV=1	3.4E-12	70.3	18.3	13 (13 0 0 0 0)	Mitochondrion matrix.
Q9CQF9	PCYOX_MOUSE Prenylcysteine oxidase OS=Mus musculus GN=Pcyox1 PE=1 SV=1	1.2E-06	30.2	5.0	3 (3 0 0 0 0)	Lysosome.
P27773	PDIA3_MOUSE Protein disulfide-isomerase A3 OS=Mus musculus GN=Pdia3 PE=1 SV=2	5.9E-06	20.1	5.3	2 (2 0 0 0 0)	Endoplasmic reticulum lumen. Melanosome.
Q9DBJ1	PGAM1_MOUSE Phosphoglycerate mutase 1 OS=Mus musculus GN=Pgam1 PE=1 SV=3	3.0E-08	60.2	15.0	8 (8 0 0 0 0)	ND
O70250	PGAM2_MOUSE Phosphoglycerate mutase 2 OS=Mus musculus GN=Pgam2 PE=1 SV=3	5.8E-08	70.2	21.3	12 (12 0 0 0 0)	ND
Q05793	PGBM_MOUSE Basement membrane-specific heparan sulfate proteoglycan core protein OS=Mus musculus GN=Hspg2 PE=1 SV=1	8.8E-08	130.2	4.2	18 (18 0 0 0 0)	Secreted â€º extracellular space â€º extracellular matrix â€º basement membrane.
Q9D0F9	PGM1_MOUSE Phosphoglucomutase-1 OS=Mus musculus GN=Pgm1 PE=1 SV=3	9.7E-08	40.2	7.3	5 (5 0 0 0 0)	Cytoplasm.
Q8BZF8	PGM5_MOUSE Phosphoglucomutase-like protein 5 OS=Mus musculus	2.6E-10	20.3	4.6	4 (4 0 0 0 0)	Cell junction â€º adherens junction. Cytoplasm â€º

	GN=Pgm5 PE=1 SV=2					cytoskeleton.
P28653	PGS1_MOUSE Biglycan OS=Mus musculus GN=Bgn PE=2 SV=1	2.2E-15	50.3	16.0	11 (11 0 0 0 0)	Secreted â€º extracellular space â€º extracellular matrix.
P28654	PGS2_MOUSE Decorin OS=Mus musculus GN=Dcn PE=2 SV=1	9.8E-09	80.2	26.0	15 (15 0 0 0 0)	Secreted â€º extracellular space â€º extracellular matrix.
P67778	PHB_MOUSE Prohibitin OS=Mus musculus GN=Phb PE=1 SV=1	3.4E-08	100.2	30.1	13 (13 0 0 0 0)	Mitochondrion inner membrane.
O35129	PHB2_MOUSE Prohibitin-2 OS=Mus musculus GN=Phb2 PE=1 SV=1	5.7E-13	100.3	37.1	16 (16 0 0 0 0)	Mitochondrion inner membrane. Cytoplasm. Nucleus.
P07934	PHKG1_MOUSE Phosphorylase b kinase gamma catalytic chain, skeletal muscle isoform OS=Mus musculus GN=Phkg1 PE=2 SV=3	9.9E-06	30.1	7.7	3 (3 0 0 0 0)	ND
Q6PD26	PIGS_MOUSE GPI transamidase component PIG-S OS=Mus musculus GN=Pigs PE=1 SV=3	3.2E-13	20.3	6.8	4 (4 0 0 0 0)	Endoplasmic reticulum membrane; Multi-pass membrane protein.
Q9QXS1	PLEC1_MOUSE Plectin-1 OS=Mus musculus GN=Plec1 PE=1 SV=2	4.1E-11	248.3	6.0	39 (38 1 0 0 0)	Cytoplasm â€º cytoskeleton. Cell junction â€º hemidesmosome.
P24369	PPIB_MOUSE Peptidyl-prolyl cis-trans isomerase B OS=Mus musculus GN=Ppib PE=2 SV=2	2.6E-05	30.2	10.2	3 (3 0 0 0 0)	Endoplasmic reticulum lumen. Melanosome.
P35700	PRDX1_MOUSE Peroxiredoxin-1 OS=Mus musculus GN=Prdx1 PE=1 SV=1	5.2E-07	28.1	14.6	4 (2 2 0 0 0)	Cytoplasm. Melanosome.
Q61171	PRDX2_MOUSE Peroxiredoxin-2 OS=Mus musculus GN=Prdx2 PE=1 SV=3	3.3E-05	20.1		3 (3 0 0 0 0)	Cytoplasm.
Q9JK53	PRELP_MOUSE Prolargin OS=Mus musculus GN=Prelp PE=2 SV=2	1.0E-07	50.2	14.3	16 (16 0 0 0 0)	Secreted â€º extracellular space â€º extracellular matrix.
Q9D7G0	PRPS1_MOUSE Ribose-phosphate pyrophosphokinase 1 OS=Mus musculus GN=Prps1 PE=1 SV=3	1.4E-07	20.2	8.8	2 (2 0 0 0 0)	ND
P62334	PRS10_MOUSE 26S protease regulatory subunit	4.4E-10	50.2	18.8	6 (6 0 0 0 0)	Cytoplasm. Nucleus.

	S10B OS=Mus musculus GN=Psmc6 PE=1 SV=1					
P62192	PRS4_MOUSE 26S protease regulatory subunit 4 OS=Mus musculus GN=Psmc1 PE=1 SV=1	1.8E-08	40.2	10.5	6 (6 0 0 0 0)	Cytoplasm. Nucleus.
O88685	PRS6A_MOUSE 26S protease regulatory subunit 6A OS=Mus musculus GN=Psmc3 PE=2 SV=1	7.4E-12	68.3	17.2	9 (8 1 0 0 0)	Cytoplasm. Nucleus.
P54775	PRS6B_MOUSE 26S protease regulatory subunit 6B OS=Mus musculus GN=Psmc4 PE=1 SV=1	1.1E-12	50.3	17.7	13 (13 0 0 0 0)	Cytoplasm. Nucleus.
P46471	PRS7_MOUSE 26S protease regulatory subunit 7 OS=Mus musculus GN=Psmc2 PE=1 SV=5	4.0E-11	50.3	16.6	6 (6 0 0 0 0)	Cytoplasm. Nucleus.
P62196	PRS8_MOUSE 26S protease regulatory subunit 8 OS=Mus musculus GN=Psmc5 PE=1 SV=1	1.7E-11	50.2	15.3	6 (6 0 0 0 0)	Cytoplasm. Nucleus.
Q11011	PSA_MOUSE Puromycin-sensitive aminopeptidase OS=Mus musculus GN=Npepps PE=1 SV=1	3.7E-07	30.2	3.9	6 (6 0 0 0 0)	Cytoplasm â€º cytosol. Nucleus.
Q9R1P0	PSA4_MOUSE Proteasome subunit alpha type-4 OS=Mus musculus GN=Psma4 PE=1 SV=1	6.3E-07	20.2	6.9	2 (2 0 0 0 0)	Cytoplasm. Nucleus.
Q9Z2U0	PSA7_MOUSE Proteasome subunit alpha type-7 OS=Mus musculus GN=Psma7 PE=1 SV=1	5.2E-06	20.1		2 (2 0 0 0 0)	Cytoplasm. Nucleus.
Q9CWH6	PSA7L_MOUSE Proteasome subunit alpha type-7-like OS=Mus musculus GN=Psma8 PE=2 SV=1	5.0E-10	20.2	10.0	3 (3 0 0 0 0)	Cytoplasm. Nucleus.
O09061	PSB1_MOUSE Proteasome subunit beta type-1 OS=Mus musculus GN=Psmb1 PE=1 SV=1	2.6E-10	20.2	11.7	3 (3 0 0 0 0)	Cytoplasm. Nucleus.
O55234	PSB5_MOUSE Proteasome subunit beta type-5 OS=Mus musculus GN=Psmb5 PE=1 SV=3	2.1E-07	60.2	17.4	6 (6 0 0 0 0)	Cytoplasm. Nucleus.
Q60692	PSB6_MOUSE Proteasome subunit beta type-6 OS=Mus musculus GN=Psmb6 PE=1 SV=3	2.4E-07	20.1		2 (2 0 0 0 0)	Cytoplasm. Nucleus.
Q8BG32	PSD11_MOUSE 26S proteasome non-ATPase regulatory subunit 11 OS=Mus musculus GN=Psmd11 PE=1 SV=3	2.2E-06	70.2	20.6	10 (10 0 0 0 0)	ND

Q9D8W5	PSD12_MOUSE 26S proteasome non-ATPase regulatory subunit 12 OS=Mus musculus GN=Psmd12 PE=2 SV=3	6.7E-15	40.2	9.9	6 (6 0 0 0 0)	ND
Q9WVJ2	PSD13_MOUSE 26S proteasome non-ATPase regulatory subunit 13 OS=Mus musculus GN=Psmd13 PE=1 SV=1	4.9E-06	20.2	8.0	2 (2 0 0 0 0)	ND
P26516	PSD7_MOUSE 26S proteasome non-ATPase regulatory subunit 7 OS=Mus musculus GN=Psmd7 PE=1 SV=2	1.9E-09	20.2	7.5	2 (2 0 0 0 0)	ND
O35593	PSDE_MOUSE 26S proteasome non-ATPase regulatory subunit 14 OS=Mus musculus GN=Psmd14 PE=1 SV=2	2.3E-09	20.2	12.6	2 (2 0 0 0 0)	ND
Q8VDM4	PSMD2_MOUSE 26S proteasome non-ATPase regulatory subunit 2 OS=Mus musculus GN=Psmd2 PE=1 SV=1	2.2E-08	60.2	7.6	9 (9 0 0 0 0)	ND
P14685	PSMD3_MOUSE 26S proteasome non-ATPase regulatory subunit 3 OS=Mus musculus GN=Psmd3 PE=2 SV=2	1.0E-11	70.3	14.9	11 (11 0 0 0 0)	ND
O54724	PTRF_MOUSE Polymerase I and transcript release factor OS=Mus musculus GN=Ptrf PE=1 SV=1	4.4E-15	110.3	32.4	22 (22 0 0 0 0)	Membrane â€º caveola. Cell membrane. Microsome. Endoplasmic reticulum. Cytoplasm â€º cytosol. Mitochondrion. Nucleus.
Q9DCL9	PUR6_MOUSE Multifunctional protein ADE2 OS=Mus musculus GN=Paics PE=1 SV=3	1.7E-11	20.2	5.9	3 (3 0 0 0 0)	ND
P54822	PUR8_MOUSE Adenylosuccinate lyase OS=Mus musculus GN=Adsl PE=2 SV=1	3.3E-15	110.3	28.5	17 (17 0 0 0 0)	ND
P28650	PURA1_MOUSE Adenylosuccinate synthetase isozyme 1 OS=Mus musculus GN=Adssl1 PE=1 SV=2	1.4E-13	40.3	12.5	9 (9 0 0 0 0)	Cytoplasm. Membrane; Peripheral membrane protein.
Q8CI94	PYGB_MOUSE Glycogen phosphorylase, brain form	4.0E-11	76.3	7.7	55 (36 19 0 0 0)	ND

	OS=Mus musculus GN=Pygb PE=1 SV=3					
Q9ET01	PYGL_MOUSE Glycogen phosphorylase, liver form OS=Mus musculus GN=Pygl PE=1 SV=3	3.0E-09	20.2	2.0	13 (13 0 0 0 0)	ND
Q9WUB3	PYGM_MOUSE Glycogen phosphorylase, muscle form OS=Mus musculus GN=Pygm PE=1 SV=3	4.4E-16	418.3	38.2	362 (351 11 0 0 0)	ND
Q9CZ13	QCR1_MOUSE Cytochrome b-c1 complex subunit 1, mitochondrial OS=Mus musculus GN=Uqcrc1 PE=1 SV=1	1.0E-30	244.4	41.5	59 (56 3 0 0 0)	Mitochondrion inner membrane.
Q9DB77	QCR2_MOUSE Cytochrome b-c1 complex subunit 2, mitochondrial OS=Mus musculus GN=Uqcrc2 PE=1 SV=1	1.3E-14	180.3	40.0	49 (49 0 0 0 0)	Mitochondrion inner membrane; Peripheral membrane protein; Matrix side.
P61027	RAB10_MOUSE Ras-related protein Rab-10 OS=Mus musculus GN=Rab10 PE=1 SV=1	2.8E-08	20.2	11.5	2 (2 0 0 0 0)	Cell membrane; Lipid-anchor; Cytoplasmic side.
P53994	RAB2A_MOUSE Ras-related protein Rab-2A OS=Mus musculus GN=Rab2a PE=1 SV=1	1.0E-08	20.2	11.8	2 (2 0 0 0 0)	Endoplasmic reticulum-Golgi intermediate compartment membrane; Lipid-anchor. Melanosome. Endoplasmic reticulum membrane; Lipid-anchor. Golgi apparatus membrane; Lipid-anchor.
P26043	RADI_MOUSE Radixin OS=Mus musculus GN=Rdx PE=1 SV=2	2.8E-07	50.2	10.8	6 (6 0 0 0 0)	Cell membrane; Peripheral membrane protein; Cytoplasmic side. Cytoplasm â€º cytoskeleton. Cleavage furrow.
P47963	RL13_MOUSE 60S ribosomal protein L13 OS=Mus musculus GN=Rpl13 PE=2 SV=3	3.2E-08	40.2	16.1	5 (5 0 0 0 0)	ND
P84099	RL19_MOUSE 60S ribosomal protein L19 OS=Mus musculus GN=Rpl19 PE=1 SV=1	6.9E-05	20.2		4 (4 0 0 0 0)	ND
P62751	RL23A_MOUSE 60S ribosomal protein L23a	9.8E-09	20.2	16.0	2 (2 0 0 0 0)	ND

	OS=Mus musculus GN=Rpl23a PE=1 SV=1					
Q8BP67	RL24_MOUSE 60S ribosomal protein L24 OS=Mus musculus GN=Rpl24 PE=2 SV=2	4.2E-08	20.2	8.3	2 (2 0 0 0 0)	ND
P61255	RL26_MOUSE 60S ribosomal protein L26 OS=Mus musculus GN=Rpl26 PE=2 SV=1	7.5E-07	30.2	17.2	3 (3 0 0 0 0)	ND
P14148	RL7_MOUSE 60S ribosomal protein L7 OS=Mus musculus GN=Rpl7 PE=2 SV=2	7.2E-08	30.2	9.3	3 (3 0 0 0 0)	ND
Q91YQ5	RPN1_MOUSE Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1 OS=Mus musculus GN=Rpn1 PE=2 SV=1	9.9E-09	90.2	18.3	12 (12 0 0 0 0)	Endoplasmic reticulum membrane; Single-pass type I membrane protein. Melanosome.
Q9DBG6	RPN2_MOUSE Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2 OS=Mus musculus GN=Rpn2 PE=2 SV=1	3.3E-16	70.4	17.9	9 (9 0 0 0 0)	Endoplasmic reticulum membrane; Multi-pass membrane protein.
P62264	RS14_MOUSE 40S ribosomal protein S14 OS=Mus musculus GN=Rps14 PE=2 SV=3	2.0E-07	20.2	15.9	3 (3 0 0 0 0)	ND
P62908	RS3_MOUSE 40S ribosomal protein S3 OS=Mus musculus GN=Rps3 PE=1 SV=1	1.1E-06	30.1	12.8	5 (5 0 0 0 0)	Cytoplasm.
P97351	RS3A_MOUSE 40S ribosomal protein S3a OS=Mus musculus GN=Rps3a PE=1 SV=3	4.1E-06	50.2	15.5	5 (5 0 0 0 0)	Cytoplasm. Nucleus.
P62702	RS4X_MOUSE 40S ribosomal protein S4, X isoform OS=Mus musculus GN=Rps4x PE=2 SV=2	8.5E-06	40.1	15.2	4 (4 0 0 0 0)	Cytoplasm.
P62754	RS6_MOUSE 40S ribosomal protein S6 OS=Mus musculus GN=Rps6 PE=1 SV=1	5.4E-09	20.1		4 (4 0 0 0 0)	ND
P62242	RS8_MOUSE 40S ribosomal protein S8 OS=Mus musculus GN=Rps8 PE=1 SV=2	9.3E-09	30.2	18.8	3 (3 0 0 0 0)	Cytoplasm.
Q6ZWN5	RS9_MOUSE 40S ribosomal protein S9 OS=Mus musculus GN=Rps9 PE=2 SV=3	1.6E-05	20.2	10.3	3 (3 0 0 0 0)	Cytoplasm.
O70622	RTN2_MOUSE Reticulon-2 OS=Mus musculus GN=Rtn2	7.8E-13	40.3	11.7	48 (48 0 0 0 0)	Endoplasmic reticulum

	PE=1 SV=1					membrane; Single-pass membrane protein.
Q99P72	RTN4_MOUSE Reticulon-4 OS=Mus musculus GN=Rtn4 PE=1 SV=2	3.8E-11	20.2	2.4	2 (2 0 0 0 0)	Endoplasmic reticulum membrane; Multi-pass membrane protein.
Q9EP69	SAC1_MOUSE Phosphatidylinositide phosphatase SAC1 OS=Mus musculus GN=Sacm1l PE=2 SV=1	4.1E-07	20.2	3.4	3 (3 0 0 0 0)	Endoplasmic reticulum membrane; Multi-pass membrane protein.
Q8BGH2	SAM50_MOUSE Sorting and assembly machinery component 50 homolog OS=Mus musculus GN=Samm50 PE=1 SV=1	2.4E-09	40.2	10.7	4 (4 0 0 0 0)	Mitochondrion outer membrane; Multi-pass membrane protein. Cytoplasm.
Q01405	SC23A_MOUSE Protein transport protein Sec23A OS=Mus musculus GN=Sec23a PE=1 SV=2	5.2E-09	20.2	3.3	2 (2 0 0 0 0)	Smooth endoplasmic reticulum membrane; Peripheral membrane protein. Golgi apparatus membrane; Peripheral membrane protein.
Q9D0K2	SCOT1_MOUSE Succinyl-CoA:3-ketoacid-coenzyme A transferase 1, mitochondrial OS=Mus musculus GN=Oxct1 PE=1 SV=1	3.1E-09	70.3	11.0	7 (7 0 0 0 0)	Mitochondrion matrix.
Q63918	SDPR_MOUSE Serum deprivation-response protein OS=Mus musculus GN=Sdpr PE=1 SV=3	2.1E-09	20.2	7.2	2 (2 0 0 0 0)	Cytoplasm â€º cytosol. Membrane â€º caveola.
O55131	SEPT7_MOUSE Septin-7 OS=Mus musculus GN=Sept7 PE=1 SV=1	3.9E-06	20.2	4.8	3 (3 0 0 0 0)	Cytoplasm. Chromosome â€º centromere â€º kinetochore. Cytoplasm â€º cytoskeleton â€º spindle. Cleavage furrow. Midbody. Cytoplasm â€º cytoskeleton â€º cilium axoneme.
P19324	SERPH_MOUSE Serpin H1 OS=Mus musculus GN=Serpinh1 PE=1 SV=2	1.4E-12	30.2	9.8	6 (6 0 0 0 0)	Endoplasmic reticulum lumen.
P82350	SGCA_MOUSE Alpha-sarcoglycan OS=Mus musculus GN=Sgca PE=1 SV=1	2.1E-11	40.3	12.7	13 (13 0 0 0 0)	Cell membrane â€º sarcolemma; Single-pass type I membrane protein.

						Cytoplasm â€º cytoskeleton.
P82347	SGCD_MOUSE Delta-sarcoglycan OS=Mus musculus GN=Sgcd PE=1 SV=1	8.1E-09	20.1		2 (2 0 0 0 0)	Cell membrane â€º sarcolemma; Single-pass type II membrane protein. Cytoplasm â€º cytoskeleton.
P82348	SGCG_MOUSE Gamma-sarcoglycan OS=Mus musculus GN=Sgcg PE=1 SV=2	1.9E-10	20.2	11.3	4 (4 0 0 0 0)	Cell membrane â€º sarcolemma; Single-pass type II membrane protein. Cytoplasm â€º cytoskeleton.
P97443	SMYD1_MOUSE SET and MYND domain-containing protein 1 OS=Mus musculus GN=Smyd1 PE=1 SV=2	4.2E-11	100.2	25.6	20 (20 0 0 0 0)	Cytoplasm. Nucleus.
Q61234	SNTA1_MOUSE Alpha-1-syntrophin OS=Mus musculus GN=Snta1 PE=1 SV=1	5.7E-14	20.3	5.6	2 (2 0 0 0 0)	Cell membrane â€º sarcolemma; Peripheral membrane protein; Cytoplasmic side. Cell junction. Cytoplasm â€º cytoskeleton.
Q60854	SPB6_MOUSE Serpin B6 OS=Mus musculus GN=Serpinb6 PE=2 SV=1	8.8E-06	20.1	4.8	2 (2 0 0 0 0)	Cytoplasm.
P16546	SPTA2_MOUSE Spectrin alpha chain, brain OS=Mus musculus GN=Sptan1 PE=1 SV=4	1.6E-14	60.3	5.3	11 (11 0 0 0 0)	Cytoplasm â€º cytoskeleton. Cytoplasm â€º cell cortex.
Q62261	SPTB2_MOUSE Spectrin beta chain, brain 1 OS=Mus musculus GN=Sptbn1 PE=1 SV=2	7.1E-10	20.2	1.3	2 (2 0 0 0 0)	Cytoplasm â€º cytoskeleton. Cytoplasm â€º myofibril â€º sarcomere â€º M line. Cell membrane; Peripheral membrane protein; Cytoplasmic side.
Q7TQ48	SRCA_MOUSE Sarcalumenin OS=Mus musculus GN=Srl PE=1 SV=1	1.0E-30	330.3	33.2	128 (128 0 0 0 0)	Sarcoplasmic reticulum lumen.
O35400	ST2B1_MOUSE Sulfotransferase family cytosolic 2B member 1 OS=Mus musculus GN=Sult2b1 PE=2 SV=2	8.1E-04	20.1	5.0	2 (2 0 0 0 0)	Cytoplasm.
P70302	STIM1_MOUSE Stromal interaction molecule 1	5.0E-06	50.2	5.3	5 (5 0 0 0 0)	Cell membrane; Single-pass type I

	OS=Mus musculus GN=Stim1 PE=1 SV=1					membrane protein. Endoplasmic reticulum membrane; Single-pass type I membrane protein. Cytoplasm â€º cytoskeleton.
Q60864	STIP1_MOUSE Stress-induced-phosphoprotein 1 OS=Mus musculus GN=Stip1 PE=1 SV=1	1.7E-08	60.2	13.6	6 (6 0 0 0 0)	Cytoplasm. Nucleus.
Q9WUM5	SUCA_MOUSE Succinyl-CoA ligase [GDP-forming] subunit alpha, mitochondrial OS=Mus musculus GN=Suclg1 PE=1 SV=4	5.9E-09	50.2	11.8	5 (5 0 0 0 0)	Mitochondrion.
Q9Z2I9	SUCB1_MOUSE Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial OS=Mus musculus GN=Sucla2 PE=1 SV=2	1.1E-06	60.2	17.1	8 (8 0 0 0 0)	Mitochondrion.
Q8R086	SUOX_MOUSE Sulfite oxidase, mitochondrial OS=Mus musculus GN=Suox PE=1 SV=2	4.7E-11	30.3	11.7	4 (4 0 0 0 0)	Mitochondrion intermembrane space.
Q922B2	SYDC_MOUSE Aspartyl-tRNA synthetase, cytoplasmic OS=Mus musculus GN=Dars PE=2 SV=1	4.9E-12	130.2	26.7	21 (21 0 0 0 0)	Cytoplasm.
Q8CGC7	SYEP_MOUSE Bifunctional aminoacyl-tRNA synthetase OS=Mus musculus GN=Eprs PE=2 SV=3	4.7E-12	220.3	22.2	34 (34 0 0 0 0)	ND
Q9CZD3	SYG_MOUSE Glycyl-tRNA synthetase OS=Mus musculus GN=Gars PE=1 SV=1	1.0E-09	20.2	3.3	2 (2 0 0 0 0)	Cytoplasm. Mitochondrion.
Q8BU30	SYIC_MOUSE Isoleucyl-tRNA synthetase, cytoplasmic OS=Mus musculus GN=Iars PE=2 SV=1	2.7E-13	110.3	11.3	16 (16 0 0 0 0)	Cytoplasm.
O89104	SYPL2_MOUSE Synaptophysin-like protein 2 OS=Mus musculus GN=Sypl2 PE=2 SV=1	1.6E-05	20.1	8.7	2 (2 0 0 0 0)	Membrane; Multi-pass membrane protein.
Q9D0I9	SYRC_MOUSE Arginyl-tRNA synthetase, cytoplasmic OS=Mus musculus GN=Rars PE=2 SV=2	1.5E-11	130.2	22.1	13 (13 0 0 0 0)	Cytoplasm.
Q9D0R2	SYTC_MOUSE Threonyl-tRNA synthetase,	5.0E-07	20.2	3.5	3 (3 0 0 0 0)	Cytoplasm.

	cytoplasmic OS=Mus musculus GN=Tars PE=1 SV=2					
Q8BLY2	SYTC2_MOUSE Probable threonyl-tRNA synthetase 2, cytoplasmic OS=Mus musculus GN=Tarsl2 PE=2 SV=1	1.3E-05	40.2	4.9	6 (6 0 0 0 0)	Cytoplasm.
Q9Z1Q9	SYVC_MOUSE Valyl-tRNA synthetase OS=Mus musculus GN=Vars PE=2 SV=1	1.0E-30	110.4	12.7	16 (16 0 0 0 0)	ND
P68369	TBA1A_MOUSE Tubulin alpha-1A chain OS=Mus musculus GN=Tuba1a PE=1 SV=1	3.3E-13	110.3	37.5	38 (38 0 0 0 0)	Cytoplasm â€º cytoskeleton.
P68368	TBA4A_MOUSE Tubulin alpha-4A chain OS=Mus musculus GN=Tuba4a PE=1 SV=1	4.8E-10	30.2	6.7	15 (15 0 0 0 0)	Cytoplasm â€º cytoskeleton.
Q7TMM9	TBB2A_MOUSE Tubulin beta-2A chain OS=Mus musculus GN=Tubb2a PE=1 SV=1	1.7E-06	20.2	2.2	3 (3 0 0 0 0)	Cytoplasm â€º cytoskeleton.
Q7TMM9	TBB2A_MOUSE Tubulin beta-2A chain OS=Mus musculus GN=Tubb2a PE=1 SV=1	2.5E-13	148.3	26.7	69 (68 1 0 0 0)	Cytoplasm â€º cytoskeleton.
P68372	TBB2C_MOUSE Tubulin beta-2C chain OS=Mus musculus GN=Tubb2c PE=1 SV=1	2.3E-12	80.2	12.1	33 (33 0 0 0 0)	Cytoplasm â€º cytoskeleton.
P11984	TCPA1_MOUSE T-complex protein 1 subunit alpha A OS=Mus musculus GN=Tcp1 PE=1 SV=2	8.9E-15	140.3	22.8	21 (21 0 0 0 0)	ND
P11983	TCPA2_MOUSE T-complex protein 1 subunit alpha B OS=Mus musculus GN=Tcp1 PE=1 SV=3	2.1E-09	30.2	6.3	4 (4 0 0 0 0)	Cytoplasm. Cytoplasm â€º cytoskeleton â€º centrosome.
P80314	TCPB_MOUSE T-complex protein 1 subunit beta OS=Mus musculus GN=Cct2 PE=1 SV=4	2.6E-14	220.3	49.9	37 (37 0 0 0 0)	Cytoplasm.
P80315	TCPD_MOUSE T-complex protein 1 subunit delta OS=Mus musculus GN=Cct4 PE=1 SV=3	3.6E-11	120.2	22.6	15 (15 0 0 0 0)	Cytoplasm. Melanosome. Cytoplasm â€º cytoskeleton â€º centrosome.
P80316	TCPE_MOUSE T-complex protein 1 subunit epsilon OS=Mus musculus GN=Cct5 PE=1 SV=1	1.0E-14	146.3	30.3	25 (21 3 1 0 0)	Cytoplasm. Cytoplasm â€º cytoskeleton â€º centrosome.
P80318	TCPG_MOUSE T-complex protein 1 subunit gamma	1.0E-14	194.3	32.8	27 (25 1 1 0 0)	Cytoplasm.

	OS=Mus musculus GN=Cct3 PE=1 SV=1					
P80313	TCPH_MOUSE T-complex protein 1 subunit eta OS=Mus musculus GN=Cct7 PE=1 SV=1	8.9E-15	110.3	22.4	15 (15 0 0 0 0)	Cytoplasm.
P42932	TCPQ_MOUSE T-complex protein 1 subunit theta OS=Mus musculus GN=Cct8 PE=1 SV=3	3.7E-10	130.2	19.5	22 (22 0 0 0 0)	Cytoplasm. Cytoplasm â€º cytoskeleton â€º centrosome.
Q61390	TCPW_MOUSE T-complex protein 1 subunit zeta-2 OS=Mus musculus GN=Cct6b PE=2 SV=4	1.0E-12	66.3	10.5	12 (8 4 0 0 0)	Cytoplasm.
P80317	TCPZ_MOUSE T-complex protein 1 subunit zeta OS=Mus musculus GN=Cct6a PE=1 SV=3	3.5E-13	100.3	23.9	15 (15 0 0 0 0)	Cytoplasm.
Q9CY27	TECR_MOUSE Trans-2,3-enoyl-CoA reductase OS=Mus musculus GN=Tecr PE=1 SV=1	6.9E-10	20.2	6.8	3 (3 0 0 0 0)	Endoplasmic reticulum membrane; Multi-pass membrane protein.
Q01853	TERA_MOUSE Transitional endoplasmic reticulum ATPase OS=Mus musculus GN=Vcp PE=1 SV=4	3.2E-13	160.3	24.3	27 (27 0 0 0 0)	Cytoplasm â€º cytosol. Nucleus.
P21981	TGM2_MOUSE Protein-glutamine gamma-glutamyltransferase 2 OS=Mus musculus GN=Tgm2 PE=1 SV=4	3.1E-12	20.2	4.1	6 (6 0 0 0 0)	ND
Q8QZT1	THIL_MOUSE Acetyl-CoA acetyltransferase, mitochondrial OS=Mus musculus GN=Acat1 PE=1 SV=1	1.0E-12	50.3	20.0	8 (8 0 0 0 0)	Mitochondrion.
Q8BWT1	THIM_MOUSE 3-ketoacyl-CoA thiolase, mitochondrial OS=Mus musculus GN=Acaa2 PE=1 SV=2	5.6E-15	130.3	37.5	31 (31 0 0 0 0)	Mitochondrion.
A2ASS6	TITIN_MOUSE Titin OS=Mus musculus GN=Ttn PE=1 SV=1	1.0E-30	7190.4	23.1	1881 (1850 23 8 0 0)	Cytoplasm. Nucleus.
P26039	TLN1_MOUSE Talin-1 OS=Mus musculus GN=Tln1 PE=1 SV=1	4.7E-06	20.2	1.4	3 (3 0 0 0 0)	Cell projection â€º ruffle membrane; Peripheral membrane protein; Cytoplasmic side. Cytoplasm â€º cytoskeleton.
Q3TMP8	TM38A_MOUSE Trimeric intracellular cation channel type A OS=Mus musculus GN=Tmem38a PE=1 SV=2	1.9E-09	40.3	16.1	15 (15 0 0 0 0)	Sarcoplasmic reticulum membrane; Multi-pass membrane

						protein. Nucleus membrane.
Q9R0Q3	TMED2_MOUSE Transmembrane emp24 domain-containing protein 2 OS=Mus musculus GN=Tmed2 PE=1 SV=1	1.5E-04	20.1		2 (2 0 0 0 0)	Cytoplasmic vesicle membrane; Single-pass type I membrane protein. Cytoplasmic vesicle â€º COPI-coated vesicle membrane; Single-pass type I membrane protein. Golgi apparatus membrane; Single-pass type I membrane protein.
Q9D1D4	TMEDA_MOUSE Transmembrane emp24 domain-containing protein 10 OS=Mus musculus GN=Tmed10 PE=2 SV=1	7.7E-06	20.2	9.1	2 (2 0 0 0 0)	Golgi apparatus membrane; Single-pass type I membrane protein; Lumenal side. Melanosome.
P13412	TNNI2_MOUSE Troponin I, fast skeletal muscle OS=Mus musculus GN=Tnni2 PE=1 SV=2	2.8E-08	20.2	13.7	2 (2 0 0 0 0)	ND
O88346	TNNT1_MOUSE Troponin T, slow skeletal muscle OS=Mus musculus GN=Tnnt1 PE=2 SV=3	1.8E-07	30.2	10.7	3 (3 0 0 0 0)	ND
Q9QZ47	TNNT3_MOUSE Troponin T, fast skeletal muscle OS=Mus musculus GN=Tnnt3 PE=1 SV=3	1.8E-13	100.3	29.8	35 (35 0 0 0 0)	ND
P17751	TPIS_MOUSE Triosephosphate isomerase OS=Mus musculus GN=Tpi1 PE=1 SV=3	2.5E-12	100.2	38.2	40 (40 0 0 0 0)	ND
P58771	TPM1_MOUSE Tropomyosin alpha-1 chain OS=Mus musculus GN=Tpm1 PE=1 SV=1	3.8E-13	176.2	48.9	39 (37 2 0 0 0)	Cytoplasm â€º cytoskeleton.
P58774	TPM2_MOUSE Tropomyosin beta chain OS=Mus musculus GN=Tpm2 PE=1 SV=1	2.4E-08	90.2	29.9	13 (13 0 0 0 0)	Cytoplasm â€º cytoskeleton.
P21107	TPM3_MOUSE Tropomyosin alpha-3 chain OS=Mus musculus GN=Tpm3 PE=1 SV=2	6.1E-08	30.2	14.8	3 (3 0 0 0 0)	Cytoplasm â€º cytoskeleton.
Q921I1	TRFE_MOUSE Serotransferrin OS=Mus musculus GN=Tf PE=1 SV=1	6.7E-05	20.2	2.9	3 (3 0 0 0 0)	Secreted.
Q1XH17	TRI72_MOUSE Tripartite	2.2E-16	200.3	40.5	56 (55 1 0	Cell membrane â€º

	motif-containing protein 72 OS=Mus musculus GN=Trim72 PE=1 SV=1				0 0)	sarcolemma. Cytoplasmic vesicle membrane.
Q9JMH6	TRXR1_MOUSE Thioredoxin reductase 1, cytoplasmic OS=Mus musculus GN=Txnrd1 PE=1 SV=3	1.9E-06	20.2	4.2	2 (2 0 0 0 0)	Cytoplasm.
Q9CRD2	TTC35_MOUSE Tetratricopeptide repeat protein 35 OS=Mus musculus GN=Ttc35 PE=2 SV=1	3.3E-09	20.2	7.4	2 (2 0 0 0 0)	Nucleus.
Q02053	UBA1_MOUSE Ubiquitin-like modifier-activating enzyme 1 OS=Mus musculus GN=Uba1 PE=1 SV=1	1.7E-14	50.3	8.7	12 (12 0 0 0 0)	ND
P62991	UBIQ_MOUSE Ubiquitin OS=Mus musculus GN=Rps27a PE=1 SV=1	2.4E-07	20.2	32.9	8 (8 0 0 0 0)	ND
Q9CR68	UCRI_MOUSE Cytochrome b-c1 complex subunit Rieske, mitochondrial OS=Mus musculus GN=Uqcrfs1 PE=1 SV=1	1.8E-09	50.2	33.9	14 (14 0 0 0 0)	Mitochondrion inner membrane.
Q91ZJ5	UGPA_MOUSE UTP--glucose-1-phosphate uridylyltransferase OS=Mus musculus GN=Ugp2 PE=2 SV=3	1.1E-15	340.3	61.8	105 (105 0 0 0 0)	Cytoplasm.
Q9WV55	VAPA_MOUSE Vesicle-associated membrane protein-associated protein A OS=Mus musculus GN=Vapa PE=1 SV=2	3.5E-08	20.2	10.4	2 (2 0 0 0 0)	Endoplasmic reticulum membrane; Single-pass type IV membrane protein.
Q9QY76	VAPB_MOUSE Vesicle-associated membrane protein-associated protein B OS=Mus musculus GN=Vapb PE=2 SV=3	1.5E-07	20.2	11.1	3 (3 0 0 0 0)	Endoplasmic reticulum membrane; Single-pass type IV membrane protein.
P50516	VATA_MOUSE V-type proton ATPase catalytic subunit A OS=Mus musculus GN=Atp6v1a PE=1 SV=2	8.3E-09	30.2	6.2	3 (3 0 0 0 0)	ND
Q60932	VDAC1_MOUSE Voltage-dependent anion-selective channel protein 1 OS=Mus musculus GN=Vdac1 PE=1 SV=3	5.6E-11	106.3	38.2	26 (18 8 0 0 0)	Mitochondrion outer membrane; Multi-pass membrane protein. Cell membrane; Multi-pass membrane protein.
Q60930	VDAC2_MOUSE Voltage-dependent anion-selective channel protein 2 OS=Mus musculus GN=Vdac2 PE=1	5.8E-09	38.2	14.2	10 (8 2 0 0 0)	Mitochondrion outer membrane.

	SV=2					
Q60931	VDAC3_MOUSE Voltage-dependent anion-selective channel protein 3 OS=Mus musculus GN=Vdac3 PE=1 SV=1	4.3E-09	30.2	15.5	5 (5 0 0 0 0)	Mitochondrion outer membrane.
P20152	VIME_MOUSE Vimentin OS=Mus musculus GN=Vim PE=1 SV=3	9.8E-11	30.1	7.3	3 (3 0 0 0 0)	ND
Q9EQH3	VPS35_MOUSE Vacuolar protein sorting-associated protein 35 OS=Mus musculus GN=Vps35 PE=1 SV=1	1.3E-08	20.2	2.9	3 (3 0 0 0 0)	Cytoplasm. Membrane; Peripheral membrane protein.