

N°	Protein name	Entry ^a	Score ^b	Method						Location	GRAVY ^c index	Function	MW ^{d*}	MW ^{d**}	pI*	N° of pep ^e
				LC- MALDI TOF/T OF MS		IEF- LC- ESI- MS/MS		1D PAGE- LC- ESI- MS/MS								
				M	H	M	H	M	H							
Structural proteins																
1	Tubulin beta chain	gi 135490	1061	+	+	+	+	+	+	MT	-0.39	Cytoskeleton	50285	49861	4.78	68
2	Similar to AGAP005293-PA	gi 194037939	949	+	+	-	+	+	+	MT	-0.384	Cytoskeleton	56732	56255	4.69	74
3	Beta 5-tubulin	gi 41529175	947	+	-	-	-	+	+	MT	-0.348	Cytoskeleton	50095	49670	4.78	76
4	Tubulin alpha	gi 81174755	929	-	-	-	-	+	-	MT	-0.23	Cytoskeleton	50804	50151	4.94	51
5	Tubulin. alpha 1a	gi 194043861	920	+	+	+	+	+	+	MT	-0.247	Cytoskeleton	50990	50337	4.95	54
6	Chain A. Tubulin Alpha-Beta Dimer. Electron Diffraction	gi 3745821	785	-	-	-	+	+	+	MT	-0.195	Cytoskeleton	49469	48816	5.18	52
7	Tubulin alpha-3 chain (Fragment)	gi 88683157	687	-	-	-	-	+	+	MT	-0.18	Cytoskeleton	33321	32942	5.86	33
8	Tubulin alpha 3d	gi 194035320	483	+	-	+	+	+	+	MT	-0.2	Cytoskeleton	55763	54543	4.65	43
9	Tubulin alpha 4a	gi 194043859	483	+	-	+	-	+	+	MT	-0.252	Cytoskeleton	50634	49924	4.95	42
10	Sirtuin 2	gi 156779005	459	-	-	+	-	+	-	MT; C	-0.283	Cytoskeleton; Enzyme activity	40398	39796	7.08	37
11	Putative uncharacterized protein	gi 56792853	385	+	+	+	+	+	+	MT	-0.241	Cytoskeleton	21761	21490	5.59	28
12	Tubulin alpha-1A chain	gi 135435	377	+	-	+	-	-	+	MT	-0.245	Cytoskeleton	50721	50068	4.90	16
13	Tubulin. beta family 1	gi 147223311	317	+	-	-	+	+	+	MT; C	-0.177	Cytoskeleton	50206	49554	4.60	33
14	Tubulin alpha 3	gi 71559141	315	-	+	+	+	-	+	MT	-0.23	Cytoskeleton	50818	50165	4.90	18
15	Similar to ATP synthase. H+ transporting, mitochondrial F1 complex, alpha subunit	gi 194034970	312	-	-	-	-	-	+	M	-0.133	Cytoskeleton	59765	55310	8.46	15

	1, cardiac muscle															
16	Actin, alpha, cardiac muscle 1	gi 194034943	280	-	-	-	-	+	-	C	-0.241	Cytoskeleton	42334	41784	5.23	31
17	Skeletal alpha actin	gi 790202	280	+	-	-	+	+	+	C	-0.245	Cytoskeleton	42366	41816	5.23	30
18	Vascular smooth muscle alpha-actin	gi 194042452	268	-	-	-	+	+	+	C	-0.246	Cytoskeleton	38913	41774	5.08	28
19	Cytoskeletal beta actin	gi 45269029	267	-	-	-	+	-	+	C	-0.215	Cytoskeleton	45162	44792	5.55	28
20	Actin, cytoplasmic 1	gi 150438831	267	-	+	-	-	+	+	C	-0.177	Cytoskeleton	42052	49554	5.09	31
21	Glial fibrillary acidic protein	gi 223869	146	-	-	-	+	-	+	C	-0.826	Cytoskeleton	25004	24962	5.96	9
22	Cofilin-1	gi 116850	127	-	-	-	+	+	+	C; N	-0.339	Cytoskeleton; Signal transduction	18792	18518	8.16	29
23	Tubulin alpha	gi 90569223	222	-	-	-	-	+	-	MT	-0.08	Cytoskeleton	19848	19518	5.48	13
24	Tubulin polymerization promoting protein p25 alpha	gi 170178280	88	-	-	-	+	-	+	C	-0.795	Cytoskeleton	24126	23970	9.57	21
25	Similar to microtubule-associated protein 2	gi 194043795	84	-	-	-	+	-	+	C; MT	-0.846	Cytoskeleton	81748	81340	8.59	11
26	Beta actin	gi 94451600	83	-	-	-	-	+	-	C	-0.399	Cytoskeleton; Protein binding	20904	20859	9.10	9
27	Vesicle-associated membrane protein-associated protein B	gi 160210890	79	+	-	-	-	-	+	MP	-0.367	Tubulin and enzyme binding; Cytoskeleton	27042	27053	6.85	3
28	CD147	gi 166244451	75	-	-	-	-	+	-	MP	-0.36	Cytoskeleton; Protein binding	29631	29421	5.70	16
29	CD47 antigen/integrin-associated protein	gi 12061572	74	-	-	-	-	+	-	IMP	0.644	Cytoskeleton; Protein binding	33744	31405	8.38	5
30	Vascular smooth muscle alpha-actin	gi 88861940	64	-	-	-	-	+	-	C	-0.481	Cytoskeleton	7955	7902	8.12	11

31	Tubulin, beta isoform 2	gi 194040124	55	-	-	-	+		+	MT	-0.364	Cytoskeleton	50839	50415	4.80	3
32	Similar to microtubule-associated protein 1A	gi 194034848	53	-	-	-	-	+	-	MT	-1.025	Cytoskeleton	110597	110150	4.75	31
33	Ubiquitin/ribosomal fusion protein	gi 1628608	51	-	-	-	-	-	+	R	-0.703	Structural constituent of ribosome	15004	14728	9.87	1
34	Beta actin	gi 476332	48	-	-	-	+	-	+	C	0.001	Cytoskeleton	26330	26119	5.05	2
35	Stathmin-1	gi 49615355	47	-	+	-	-	-	+	C; MT	-1.311	Signal transduction	17292	17302	5.76	19
36	Moesin (Membrane-organizing extension spike protein)	gi 127236	47	-	-	-	-	-	+	C; MP	-0.989	Cytoskeleton; Cell-cell recognition, signaling and cell movement	67733	67660	6.30	2
37	Bridging integrator 1	gi 119352621	46	-	-	-	+	-	+	C	-0.715	Cytoskeleton; Protein binding	48032	47890	5.10	2
38	Similar to septin 5	gi 194043456	44	-	-	-	-	-	+	C	-0.578	Cytoskeleton; Nucleotide binding	44215	43787	6.21	4
39	Radixin (Moesin-B)	gi 131821	41	-	-	-	-	-	+	C; MP	-1.007	Cytoskeleton	68621	68549	5.95	5
40	Similar to Tetratricopeptide repeat protein 18	gi 194042804	41	-	-	-	-	+	-	C	-0.003	Cytoskeleton	23036	22993	4.67	5
41	Actin-related protein 2-like protein	gi 195562213	41	-	-	-	+	-	-	C	-0.185	Cytoskeleton	45017	44760	6.29	2
42	Microtubule-associated protein 2	gi 194043793	40	-	-	-	+	-	-	MT	-0.774	Cytoskeleton	130840	130635	4.48	5
43	Similar to Alpha-centractin (Centractin)	gi 194041937	40	-	-	-	-	-	+	C	-0.285	Cytoskeleton	42701	42613	6.19	2
44	Spectrin, alpha, erythrocytic 1 (elliptocytosis 2)	gi 194035905	35	-	-	-	-	+	-	C	-0.793	Cytoskeleton; Regulation of cell shape	281163	280308	4.89	99
45	Neurofibromatosis 2	gi 194043192	34	-	+	-	-	-	-	C; MP	-0.704	Cytoskeleton; Cytoskeletal protein binding	70035	69851	6.11	2
46	Similar to bromodomain and WD repeat domain containing 2	gi 194042152	33	-	-	-	-	-	+	IMP	-0.13	Cytoskeleton	138053	136314	6.80	3

47	Similar to alpha 4 type IV collagen, partial	gi 194043877	33	-	-	+	-	-	-	MP; IMP	-0.295	Cytoskeleton	57687	57265	9.54	2
Transport proteins																
48	Similar to ATP synthase subunit beta, mitochondrial	gi 194037554	875	-	+	-	+	+	+	M	-0.020	Ion transport	56301	51769	5.00	54
49	Mitochondrial ATP synthase, H+ transporting F1 complex beta subunit	gi 89574051	875	-	+	+	-	+	+	M	0.020	Hydrogen transport	47060	51769	5.00	50
50	Cardiac muscle ATP synthase H+ transporting mitochondrial F1 complex alpha subunit 1	gi 187370717	704	+	-	+	+	+	-	M	-0.106	Hydrogen transport	59765	55209	8.28	67
51	Serum albumin	gi 164318	369	+	+	+	+	+	+	C	-0.412	Transport	71643	66797	5.84	31
52	Chain B. Structure Determination Of Aquomet Porcine Hemoglobin At 2.8 Angstrom Resolution	gi 809283	317	+	+	-	+	+	+	HC	-0.066	Oxygen transport	16082	16035	6.76	13
53	RAB5A	gi 115394760	283	-	-	-	-	+	-	MP	-0.422	Protein transport	24017	23615	8.30	11
54	Na+. K+-ATPase alpha-subunit precursor	gi 164382	280	+	-	+	+	+	+	MP	0.005	Ion transport	113920	112208	5.32	68
55	Rab-3A	gi 115394766	246	-	-	-	-	+	-	MP	-0.49	Protein transport	25182	24969	4.85	27
56	Voltage-dependent anion channel 1	gi 8745552	240	-	-	-	-	+	+	IMP	-0.404	Ion transport	30726	30726	8.62	30
57	ATPase alpha. Na/K	gi 225173	223	-	-	-	-	+	-	MP	0.010	Ion transport	113966	112208	5.32	54
58	Unnamed protein product	gi 1900	206	-	-	-	-	+	-	MP	-0.575	Ion transport	35475	35098	8.73	17
59	Clathrin heavy chain	gi 224492556	204	-	-	-	+	-	+	C; M	-0.243	Intracellular protein transport	193260	191614	5.48	15

60	ATP synthase subunit alpha liver isoform, mitochondrial	gi 18206369	194	-	-	+	-	+	-	M	0.047	Hydrogen transport	15546	15557	6.74	60
61	Na+. K+-ATPase alpha 2 subunit	gi 194035853	179	+	-	+	+	+	+	MP	-0.013	Ion transport	113448	111792	5.43	77
62	Sideroflexin-1	gi 146741302	170	+	-	-	-	+	-	MP; IMP	0.023	Iron ion transport	35886	35624	9.35	22
63	Similar to RAB2A. member RAS, oncogene family	gi 194036695	162	-	-	-	-	+	-	MP; ER	-0.469	Protein transport	31772	31677	9.72	33
64	Mitochondrial solute carrier family 25 member 6	gi 42565038	147	-	-	-	-	+	-	IMP	0.063	Transmembrane transport	33117	32779	9.82	38
65	Similar to calmodulin	gi 194038246	147	-	-	-	+	-	+	C	-0.654	Calcium-binding protein; Immune response; Metabolism	16827	16837	4.09	5
66	Valosin-containing protein	gi 164726	127	-	-	-	+	-	+	C; N	-0.346	Transport	89917	89288	5.13	8
67	Beta-globin	gi 806381	118	-	-	-	-	+	-	HC	-0.066	Oxygen transport	16212	16034	7.23	12
68	Voltage-dependent anion channel 3	gi 8745556	117	-	-	-	-	+	+	IMP	-0.277	Ion transport	30901	30577	8.85	14
69	Voltage-dependent anion channel 2	gi 8745554	115	-	-	-	-	+	-	MP; M	-0.296	Ion transport	32086	31461	7.66	10
70	Hemoglobin beta 115-146	gi 223958	103	-	-	-	+	-	+	HC	-0.266	Oxygen transport	3501	3503	9.70	6
71	Hemoglobin subunit alpha	gi 122465	101	-	+	-	+	+	+	HC	-0.064	Oxygen transport	15087	15039	8.76	12
72	Hemoglobin subunit beta	gi 3041678	98	-	+	-	-	-	+	HC	-0.053	Oxygen transport	16212	16165	7.10	4
73	Cytochrome c oxidase II	gi 755272	98	-	-	-	-	+	-	IMP	0.241	Electron transport	26281	26184	4.76	5
74	ATP synthase. H+ transporting mitochondrial F1 complex O. subunit	gi 87047636	94	-	-	-	-	+	-	MP	-0.041	Ion transport	23469	20920	9.83	43

75	Mitochondrial ATP50	gi 117660761	94	-	-	-	-	+	-	MP	0.008	Ion transport	23462	23362	9.90	41
76	Chain A. Crystal Structure Of Mitochondrial Respiratory Complex Ii From Porcine Heart At 2.4 Angstroms	gi 73535956	94	-	-	-	-	+	-	MP; M	0.273	Electron transport	69210	68227	6.32	31
77	Succinate dehydrogenase complex subunit A	gi 89574201	94	-	-	-	-	+	-	M	-0.215	Electron transport	60001	59069	6.11	23
78	Adenine nucleotide translocator 1	gi 4454540	91	-	-	-	-	+	-	IMP	0.111	Transport	18871	18768	9.79	20
79	Similar to adenine nucleotide translocator 2	gi 194044922	89	-	-	-	-	+	-	IMP	0.032	Transport	33162	32824	9.79	72
80	Clathrin light chain (CLTA) protein	gi 194595733	79	-	-	-	+	-	+	C; MP	-1.139	Cytoskeleton; Protein transport	18287	18240	4.96	2
81	Similar to ATPase. Na+/K+ transporting. alpha 4 polypeptide	gi 194035851	77	-	-	+	-	+	-	M	0.006	Ion transport	115123	114113	6.28	6
82	HPCA (Neuron-specific calcium-binding protein hippocalcin)	gi 115394790	76	-	-	-	-	+	+	C; M	-0.56	Neuronal calcium sensor and transport	22527	22427	4.87	10
83	Similar to ATP synthase. H+ transporting, mitochondrial F0 complex, subunit B1	gi 194036470	76	-	-	-	-	+	+	M	-0.279	Hydrogen transport	28666	24764	8.55	17
84	Putative oxoglutarate/malate carrier	gi 4102210	75	-	-	-	-	+	-	IMP	-0.082	Transport	9358	9363	9.86	4
85	Solute carrier family 6, member 17	gi 194036525	74	-	-	-	-	+	-	IMP	0.329	Neurotransmitter transport	81734	80988	6.07	15
86	ADP-ribosylation factor 5	gi 221327934	70	-	-	-	-	+	-	GA	-0.216	Protein transport	20631	20398	6.35	9

87	Similar to Ras-related protein Rab-13 (Cell growth-inhibiting gene 4 protein)	gi 194036119	69	-	-	-	-	+	-	GA	-0.519	Protein transport	30447	30237	9.55	17
88	Similar to vesicle trafficking protein sec22b	gi 194036349	68	-	-	-	-	+	-	IMP	-0.192	Protein transport	24912	24609	8.68	29
89	RAB1B	gi 115394758	69	-	-	-	-	+	+	C; IMP	-0.331	Protein transport	22269	22112	5.55	11
90	Electron transfer flavoprotein beta subunit precursor	gi 35384838	68	-	-	-	-	-	+	M	-0.048	Electron transport	27974	27763	8.58	5
91	Succinate dehydrogenase complex subunit B	gi 115522027	66	-	-	-	-	+	-	MP; M	-0.513	Electron transport	32420	28725	8.48	91
92	Chain B. Crystal Structure Of Mitochondrial Respiratory Complex Ii From Porcine Heart At 2.4 Angstroms	gi 73535957	66	-	-	-	-	+	-	MP; M	-0.501	Electron transport	29475	28753	8.48	21
93	Hemoglobin subunit theta	gi 122784	64	-	+	-	-	-	-	HC	-0.027	Oxygen transport	16027	15980	8.05	3
94	Hemoglobin epsilon	gi 223756	62	-	+	-	-	-	+	HC	-0.045	Oxygen transport	16169	16122	8.06	5
95	Similar to RAB2B protein	gi 194038961	63	-	-	-	-	+	-	MP; ER	-0.351	Protein transport	24506	24236	6.96	23
96	Similar to Vacuolar proton pump subunit E 1 (V-ATPase 31 kDa subunit)	gi 194037904	63	-	-	-	-	-	+	C; MP	-0.448	Hydrogen ion transport	25453	25411	8.79	2
97	Mitochondrial ATP5I	gi 117660446	60	-	-	-	-	+	+	M	-0.648	Hydrogen ion transport	8287	8291	9.30	6
98	ATP synthase subunit e. mitochondrial	gi 148887343	60	-	-	-	-	+	-	M	-0.736	Ion transport	8226	8100	9.30	6
99	Similar to Neurocalcin-delta isoform 1	gi 194036961	59	-	-	-	-	+	-	C	-0.57	Vesicle-mediated transport	22345	22245	5.23	8

100	Similar to Selenium-binding protein 1	gi 194036227	59	-	-	-	-	-	+	C; MP	-0.303	Protein transport	53185	52534	6.17	2
101	Similar to NADH dehydrogenase	gi 194037175	58	-	-	-	-	+	-	MP; M	-0.591	Neuronal calcium-binding protein	14933	14922	10.04	3
102	RHOB	gi 115394776	57	-	-	-	-	+	-	MP	-0.285	Electron transport	22565	21782	5.00	4
103	Alpha-fetoprotein precursor	gi 21617495	54	+	+	-	-	-	+	E	-0.295	Copper, nickel, fatty acids transport	70405	66503	5.47	3
104	Fatty acid-binding protein	gi 2143386	49	-	-	-	-	-	+	C	-0.209	Transport; Lipid metabolic process	14797	14748	6.11	1
105	Steroid membrane binding protein	gi 1657409	48	+	-	+	-	-	-	MP	-0.209	Steroid binding	21710	14748	4.56	3
106	Serotransferrin	gi 136192	47	-	+	-	-	-	+	S	-0.47	Iron ion transport	78971	76967	6.93	4
107	Electron transfer flavoprotein alpha subunit precursor	gi 35384836	47	-	-	-	-	+	-	M	0.154	Electron transport	33206	32884	8.16	19
108	Similar to Beta-soluble NSF attachment protein (SNAP-beta) (N-ethylmaleimide-sensitive factor attachment protein beta)	gi 194044361	46	-	-	-	-	+	-	GA; ER	-0.442	Intracellular protein transport; Syntaxin binding	33792	33470	5.31	15
109	ADP-ribosylation factor family-like protein	gi 62208269	46	-	-	-	-	+	-	MP; C	-0.197	Protein transport; Signal transduction	20587	20485	5.50	7
110	Transferrin	gi 833800	45	-	-	-	-	-	+	E	-0.464	Iron ion transport	78954	76951	6.73	3
111	Solute carrier family 25. member 5	gi 148879235	44	-	-	-	-	+	-	IMP	-0.077	Transport	18721	18618	9.92	52
112	Ras-related protein Rab-11A	gi 62868644	42	-	-	-	-	+	-	MP	-0.426	Protein transport; Signal transduction	24492	23906	6.14	13
113	Aquaporin 6	gi 184073657	42	+	-	-	-	+	-	MP; IMP	0.649	Transport	29840	29630	6.31	1
114	Guanosine diphosphate dissociation inhibitor 2	gi 45758488	39	-	-	-	+	-	+	C; MP	-0.291	Protein transport	50749	50267	6.31	2

115	Diazepam-binding inhibitor (32-86)	gi 415513	38	-	-	-	-	-	+	C	-0.876	Transport	6150	6150	9.48	1
116	Ferritin heavy chain 2 – pig (fragment)	gi 89197	38	-	-	-	-	-	-	IFC	-0.595	Iron ion transport; Immune response	9255	9147	5.16	1
117	Calbindin 1 (Vitamin D-dependent calcium-binding protein)	gi 190888872	37	-	-	-	-	-	+	N	-0.508	Calcium transport; Vitamin D binding	30183	29974	4.70	3
118	Similar to sodium/potassium/calcium exchanger 2 precursor	gi 194034346	37	-	-	+	-	+	-	IMP	0.288	Ion transport	38433	38115	5.35	2
119	Similar to Plasma membrane calcium-transporting ATPase 2 (PMCA2)	gi 194041349	36	-	-	+	-	-	-	MP; IMP	-0.427	Ion transport	30613	30289	9.32	2
120	Plasma membrane Ca ²⁺ pump (PMCA1b)	gi 2061	36	-	-	+	-	-	-	MP; IMP	-0.156	Ion transport	135651	134709	5.62	2
121	Similar to NADH dehydrogenase (ubiquinone) Fe-S protein 2	gi 194036880	35	-	-	-	-	+	-	MP; M	-0.278	Electron transport	52852	52486	6.37	24
122	SUR1 (Fragment)	gi 187692589	32	-	-	-	-	+	+	IMP	0.547	Potassium ion transport	22938	22839	9.32	1
123	H ⁺ -transporting ATP synthase (ATP synthase subunit e, mitochondrial)	gi 8546969	28	+	-	-	-	-	-	M	-0.772	Hydrogen transport	8214	8219	9.30	3
124	Apolipoprotein E	gi 311233	19	-	+	-	-	-	-	S	-0.875	Lipid transport; Antioxidant activity	36634	34615	5.40	5
125	U1 small nuclear ribonucleoprotein A	gi 122131847	17	-	+	-	-	-	-	N	-0.44	Nucleic acid binding	31259	31148	9.81	1
126	Plasma membrane calcium-transporting ATPase 1	gi 114319	14	+	-	-	-	+	-	MP	-0.153	Calcium transport	135651	134709	5.62	7
127	Apolipoprotein B	gi 951375	14	+	-	-	-	-	-	MP	-0.279	Cholesterol transport; Lipid metabolism and transport	300251	300095	6.16	8

128	Apolipoprotein A-IV	gi 164614632	14	-	+	-	-	-	-	S	-0.749	Lipid transport	43268	41281	5.51	2
Intermediary metabolism enzymes																
129	Similar to pyruvate kinase 3 isoform 3	gi 194038730	347	-	+	-	-	-	+	M	-0.111	Enzyme activity	58509	58033	7.61	46
130	Aspartate aminotransferase, cytoplasmic	gi 112976	286	-	+	-	+	-	+	C	-0.301	Enzyme activity	46731	46474	6.73	16
131	Aspartate aminotransferase, mitochondrial	gi 112985	234	+	-	-	+	+	+	M; MP	-0.289	Enzyme activity; Lipid transport	47805	44664	8.98	20
132	Triosephosphate isomerase 1	gi 74275492	267	-	-	-	-	-	+	C	-0.157	Enzyme activity	26941	26598	7.19	10
133	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide	gi 194036973	234	-	+	-	+	-	+	M; N	-0.621	Enzyme activity	27899	27745	4.73	13
134	Glucosephosphate isomerase	gi 1364248	213	-	-	-	-	-	+	C; S	-0.344	Enzyme activity	62227	62994	7.89	11
135	Similar to hexokinase 1	gi 194042320	187	-	-	-	+	-	+	M; MP	-0.184	Enzyme activity	103497	102365	6.31	17
136	Glyceraldehyde-3-phosphate dehydrogenase	gi 89573945	167	-	-	-	-	+	-	C	-0.001	Enzyme and catalytic activity	24342	24187	8.71	21
137	Glyceraldehyde-3-phosphate dehydrogenase	gi 2506441	167	-	-	-	-	+	+	C	-0.075	Enzyme activity	36041	35704	8.51	24
138	Glyceraldehyde-3-phosphate dehydrogenase (phosphorylating)	gi 65987	167	-	-	-	+	+	+	C	-0.075	Enzyme activity	35914	35704	8.52	25
139	Similar to Gamma-enolase (2-phospho-D-glycerate hydro-lyase) (Neural enolase)	gi 194037873	165	-	-	-	+	-	+	C	-0.228	Enzyme and catalytic activity	67961	67489	6.39	19

140	Beta-enolase 3	gi 85720739	159	-	-	-	+	-	+	C	-0.214	Enzyme and catalytic activity	47443	46998	8.11	15
141	Malate dehydrogenase	gi 164543	157	-	-	-	+	-	+	C	-0.038	Enzyme activity	36978	36323	6.15	7
142	Transketolase	gi 159502444	150	-	+	-	+	-	+	C	-0.177	Enzyme and catalytic activity; Ion binding	68479	67837	7.21	8
143	Glutamine synthetase	gi 452437	150	-	+	-	+	-	+	C	-0.62	Enzyme activity	42630	41899	6.30	9
144	Malate dehydrogenase. mitochondrial. precursor	gi 2506849	148	+	-	+	-	+	+	M	0.145	Enzyme activity	36029	33082	8.55	25
145	Structure Of Porcine Class Pi Glutathione S-Transferase, Chain A	gi 1943418	148	-	+	-	-	-	-	C	-0.334	Enzyme activity; Protein binding	23724	23511	8.07	6
146	Muscle phosphofructokinase	gi 86371672	143	-	-	-	-	-	+	C	-0.171	Enzyme activity	86128	85195	8.41	7
147	Glutathione S-transferase P	gi 544445	126	-	-	-	-	+	+	C	-0.334	Enzyme activity	23710	23496	8.07	12
148	Aconitate hydratase, mitochondrial	gi 113159	125	-	+	-	+	-	+	M	-0.375	Citrate metabolic process	86449	82761	8.24	3
149	Phosphohexose isomerase	gi 120742	119	-	-	-	-	-	+	C; S	-0.344	Enzyme activity	63617	62994	7.89	5
150	Puromycin sensitive aminopeptidase	gi 45268993	107	-	-	-	+	-	+	C; N	-0.248	Enzyme activity	34121	33970	6.60	4
151	Citrate synthase, mitochondrial	gi 116470	106	-	-	-	-	-	+	M	-0.211	Enzyme activity	51882	48919	7.01	43
152	Lactate dehydrogenase-B	gi 473575	103	+	-	-	-	+	+	C	0.046	Enzyme activity	36874	36481	5.57	7
153	Nm23-H2	gi 87047646	102	-	-	-	-	-	+	C; N	-0.163	Enzyme and catalytic activity	17279	17175	7.76	4
154	Ubiquitin carboxyl-terminal hydrolase L1	gi 38492203	96	-	-	-	+	-	+	C	-0.309	Enzyme activity	25186	24859	5.22	6
155	Fructose-bisphosphate aldolase A	gi 38230151	96	-	+	-	+	-	+	C	-0.334	Enzyme and catalytic activity	12254	12033	5.41	3
156	Calcineurin catalytic subunit delta isoform	gi 14209665	92	-	-	-	-	+	+	N	-0.319	Enzyme activity; Calcium ion binding	58284	57636	5.87	22

157	Peptidyl-Pro cis trans isomerase	gi 226256	92	-	-	-	+	-	+	C; N	-0.303	Enzyme activity; Peptide binding	18086	17738	8.37	4
158	Hypoxanthine phosphoribosyltransferase	gi 4809241	92	-	-	-	-	-	+	C	-0.064	Enzyme activity	16126	15965	6.33	3
159	Stratifin	gi 90811815	91	-	-	-	-	-	+	C; E	-0.617	Enzyme activity	28032	27935	4.78	16
160	Hypoxanthine phosphoribosyltransferase 1	gi 71842219	89	-	-	-	-	-	+	C	-0.153	Enzyme activity	24768	24424	6.33	4
161	Similar to phosphoglycerate mutase 1 (Phosphoglycerate mutase isozyme B)	gi 194041793	88	-	+	-	+	-	+	C	-0.498	Enzyme activity	28900	28672	6.75	6
162	Glyceraldehyde-3-phosphate dehydrogenase	gi 2506446	88	+	+	+	-	+	+	C; MP	-0.087	Enzyme activity; Protein binding	36041	35836	8.57	2
163	Muscle glycogen phosphorylase	gi 106073338	88	-	-	-	-	-	+	M	-0.351	Enzyme activity	84382	84036	6.10	6
164	Adenylate kinase isoenzyme 1	gi 125151	84	-	-	-	+	-	+	C	-0.467	Enzyme activity	21739	21638	8.38	2
165	Similar to glutamate dehydrogenase 1, partial	gi 194042272	82	-	-	-	+	-	-	M	-0.255	Enzyme activity	32829	32678	6.57	2
166	L-lactate dehydrogenase B chain	gi 157837048	82	-	-	-	-	+	+	C	0.048	Enzyme activity	36707	36481	5.58	7
167	Dehydrogenase H4. lactate	gi 229620	82	-	-	-	-	-	+	C	0.046	Enzyme activity	36709	36481	5.58	7
168	Pyruvate dehydrogenase (lipoamide)	gi 1851	81	-	-	-	-	-	+	M	-0.349	Enzyme activity	43835	40286	6.51	2
169	NDUFV2	gi 117660947	80	-	-	-	+	+	+	M	-0.312	Enzyme activity; Transport	27748	27423	8.16	36
170	Similar to Isocitrate dehydrogenase 3 (NAD+) alpha	gi 194039491	79	-	-	-	-	+	-	M	-0.095	Enzyme activity	40062	36640	5.71	194

171	Aminotransferase, Asp	gi 223046	79	-	-	-	-	+	-	M; MP	-0.301	Enzyme activity; Lipid transport	45003	44664	8.98	55
172	Pyruvate dehydrogenase, beta subunit	gi 448581	77	-	-	-	-	-	+	M	0.022	Enzyme activity	36107	35801	5.38	3
173	Protein carboxyl-o-methyltransferase	gi 19070126	77	-	-	-	+	-	+	C	-0.183	Enzyme activity	24745	24515	6.78	7
174	Superoxide dismutase	gi 122064583	77	-	-	-	-	-	+	M	-0.406	Enzyme and catalytic activity	16053	15760	6.03	4
175	Cytochrome c oxidase subunit 4 isoform 1, mitochondrial	gi 6166026	75	-	-	-	-	-	+	M	-0.821	Enzyme activity; Transport	11098	8602	6.98	31
176	Mitochondrial creatine kinase 1B	gi 187370721	73	-	-	-	-	-	+	M	-0.55	Enzyme activity	47319	42978	7.29	3
177	Similar to ubiquinol-cytochrome c reductase	gi 194041191	70	+	-	+	-	+	+	M; MP	-0.116	Enzyme activity; Transport	53349	52698	5.76	5
178	Oligosaccharyltransferase OST48	gi 10638222	69	-	-	-	-	+	-	IMP; ER	-0.085	Enzyme and catalytic activity	48889	46245	5.43	8
179	Calcineurin A protein isoform 1	gi 194042808	69	-	-	-	-	-	+	N	-0.302	Enzyme activity; Calcium ion binding	59645	58998	5.60	5
180	Isocitrate dehydrogenase 2 (NADP+), mitochondrial	gi 194039662	65	-	-	-	-	+	-	M	-0.388	Enzyme and catalytic activity	57937	46614	8.32	18
181	Similar to GLUD1 protein	gi 194042282	64	-	-	-	-	-	+	M	-0.809	Enzyme activity	38664	38345	10.28	2
182	Glyceraldehyde-3-phosphate dehydrogenase	gi 6690050	63	-	-	-	-	+	-	C	-0.095	Enzyme and catalytic activity	17099	16995	9.15	10
183	Similar to Putative hexokinase HKDC1	gi 194042318	64	-	-	-	-	-	+	M	-0.193	Enzyme activity	103569	102437	6.33	3
184	Phosphoglycerate mutase 2	gi 157093850	64	-	-	-	+	-	-	C; N	-0.563	Enzyme and catalytic activity	28830	28634	9.00	2
185	Protein phosphatase 2A 65 kDa regulatory subunit, alpha isoform	gi 510469	62	+	-	+	-	+	-	C	0.072	Enzyme activity	66079	65191	5.00	6

186	GTP-binding protein p21 - pig (fragment)	gi 108221	62	-	-	-	-	+	+	C	-0.178	Enzyme activity	5313	5202	9.45	8
187	Similar to Carbonic anhydrase 2	gi 194037097	60	-	-	-	-	-	+	C	-0.588	Enzyme and catalytic activity	29297	29114	6.86	3
188	Mitochondrial NAD+isocitrate dehydrogenase 3 beta variant 2	gi 98283613	58	-	-	-	-	+	-	M	-0.145	Enzyme activity;	42646	38793	7.82	13
189	4-aminobutyrate aminotransferase	gi 255327	57	-	-	-	-	-	+	M	-0.307	Enzyme activity	53833	53297	7.20	4
190	Mitochondrial creatine kinase 2	gi 86371674	57	-	-	-	-	-	+	M	-0.493	Enzyme activity	47961	43200	7.73	2
191	Similar to phosphoserine aminotransferase isoform 1	gi 194033990	57	+	-	-	-	+	+	C	0.033	Enzyme activity	40885	40511	7.56	3
192	Similar to 14-3-3 protein beta/alpha (Protein kinase C inhibitor protein 1) (KCIP-1)	gi 194044626	55	-	-	-	+	-	+	C	-0.739	Enzyme activity	28209	28112	4.76	20
193	Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial	gi 3023985	55	-	-	+	-	-	-	M	0.183	Enzyme and catalytic activity	10027	9691	4.68	2
194	Chain A. Refined Structure Of Mitochondrial Malate Dehydrogenase From Porcine Heart And The Consensus Structure For Dicarboxylic Acid Oxidoreductases	gi 999617	55	+	-	-	-	-	+	M	0.145	Enzyme and catalytic activity	33518	33082	8.55	4
195	Similar to peptidylprolyl isomerase B	gi 194035031	52	-	-	-	-	-	+	ER	-0.437	Enzyme activity	22936	20218	9.42	2
196	Mitochondrial cytochrome c oxidase subunit Vb	gi 55583747	52	-	-	-	+	-	+	M	-0.432	Enzyme activity; Ion transport	14002	10649	6.07	2

197	Phosphoglycerate dehydrogenase	gi 147223383	53	-	-	+	-	+	+	C	0.098	Enzyme activity	57515	56678	6.46	19
198	Endonuclease/reverse transcriptase	gi 148645276	48	-	-	-	+	-	+	M	-0.547	Enzyme activity	149478	148716	9.59	6
199	Creatine kinase B chain	gi 3183054	48	-	-	-	-	-	+	C	-0.285	Enzyme activity	11670	11566	5.19	1
200	Novel protein similar to vertebrate phosphoglycerate dehydrogenase (PHGDH)	gi 147223381	47	-	-	+	-	-	-	C	0.041	Enzyme and catalytic activity	30575	30308	7.29	3
201	Similar to protein phosphatase 3, catalytic subunit, gamma	gi 194041451	47	+	-	-	-	-	-	C	-0.355	Enzyme activity	66137	65323	6.59	3
202	Cytosolic malate dehydrogenase	gi 1469402	46	-	-	-	+	-	+	C	-0.033	Enzyme activity	36716	36454	6.16	2
203	Chain A. Crystal Structure of Pig Muscle Phosphoglycerate Kinase Ternary Complex With Amp-Pcp And 3pg	gi 22219037	46	-	-	-	-	-	+	C	-0.081	Enzyme activity; Cytoskeleton	44837	44471	8.74	6
204	Lactate dehydrogenase-A	gi 473571	46	-	-	+	-	-	-	C	0.027	Enzyme activity	36880	36487	8.22	13
205	NADPH-specific isocitrate dehydrogenase	gi 294223	45	-	-	-	-	-	+	C	-0.384	Enzyme activity	47895	46629	8.50	4
206	Similar to dihydropyrimidinase	gi 194036930	45	-	+	-	-	-	+	C	-0.162	Enzyme activity; Metal-binding	62489	61957	6.45	2
207	Proteasome subunit alpha type 6	gi 210062872	44	-	-	-	-	-	+	C	-0.161	Enzyme activity	27884	27445	6.35	2
208	Quinoid dihydropteridine reductase	gi 22094813	43	-	-	-	-	-	+	C	0.002	Enzyme activity	25969	25626	7.87	3
209	Dihydrolipoamide acetyltransferase	gi 14587786	43	-	-	-	-	-	+	M	-0.034	Enzyme activity	69561	59620	5.50	6

210	ATPase family. AAA domain containing 1	gi 194042439	42	-	-	-	+	-	-	N	-0.253	Catalytic activity	40354	40744	6.43	3
211	Glycogen storage disease type VI-related protein	gi 167834153	42	-	-	-	-	-	+	C	-0.341	Enzyme activity; Glycogen metabolism	97843	97324	6.70	2
212	Similar to Carboxypeptidase A6 precursor (Carboxypeptidase B)	gi 194036655	41	-	-	-	-	-	+	E	-0.369	Enzyme activity	50796	36196	9.50	2
213	Similar to succinic semialdehyde dehydrogenase	gi 194039730	40	-	-	-	-	+	+	M	0.037	Enzyme activity	58603	52165	6.47	2
214	Proteasome (prosome. macropain) 26S subunit, non-ATPase,1	gi 194043678	39	-	-	-	+	-	+	C	-0.225	Enzyme activity; Protein binding	106773	105814	5.25	2
215	Superoxide dismutase [Mn], mitochondrial	gi 134677	39	-	-	-	-	-	+	M	-0.33	Enzyme and catalytic activity	15686	15638	6.39	1
216	Adenosine monophosphate deaminase1	gi 164707699	39	-	-	-	-	-	+	C; N	-0.454	Enzyme activity	87081	86509	6.53	2
217	Putative V-ATPase G subunit	gi 6624727	38	-	-	-	+	-	+	M	-1.121	Enzyme and catalytic activity	13628	13579	10.26	2
218	Type III iodothyronine deiodinase	gi 44889701	38	-	+	-	-	-	-	IMP	-0.308	Enzyme activity; Ion binding	31910	31322	5.98	2
219	Similar to pyruvate kinase 3 isoform 2	gi 194038726	37	-	-	-	+	-	-	M	-0.132	Enzyme activity; Ion binding	58411	57805	7.96	6
220	Aminotransferase, Asp	gi 222979	79	-	-	-	+	-	+	C	-0.301	Enzyme activity	44690	44664	9.02	49
221	Glutamyl-tRNA synthetase	gi 52631983	35	-	-	-	-	-	+	C; M	-0.249	Enzyme and catalytic activity	38043	37496	5.91	2
222	Monoamine oxidase B	gi 46909483	35	-	-	-	-	+	-	IMP	-0.194	Enzyme and catalytic activity	58798	58134	8.36	20
223	Similar to Lipoamide acyltransferase component of branched-chain alpha-keto acid	gi 194035688	35	-	-	-	-	+	-	M	-0.289	Enzyme and catalytic activity	68792	68150	8.53	42

	dehydrogenase complex. mitochondrial precursor															
224	Chain A. Refinement And Comparison Of The Crystal Structures Of Pig Cytosolic Aspartate Aminotransferase And Its Complex With 2- Methylaspartate	gi 2392156	34	-	-	-	-	+	-	C	-0.285	Enzyme and catalytic activity	46580	46323	7.81	9
225	Acylglycerol kinase	gi 217314883	34	-	-	-	-	+	-	MP; M	-0.321	Enzyme and catalytic activity	47366	43354	7.72	10
226	Similar to KIAA1379 protein	gi 194040336	34	-	-	-	+	-	+	C	-0.926	Enzyme activity; Transport	59511	59205	5.20	2
227	Similar to glutamate dehydrogenase 1. partial	gi 194042284	34	-	-	-	+	-	-	M	-0.124	Enzyme activity; Protein binding	35320	35057	6.14	2
228	Similar to dolichyl pyrophosphate phosphatase 1	gi 194033684	34	-	-	+	-	-	-	ER; IMP	0.394	Enzyme and catalytic activity	27178	27081	9.48	1
229	Dopamine beta- hydroxylase	gi 71361891	27	+	-	-	-	-	-	MP	-0.16	Enzyme activity; Transport	62328	62626	5.76	2
230	Calpain-3 (skeletal muscle specific calpain)	gi 2827424	25	-	+	-	-	-	-	C	-0.58	Signal transducer activity; Calcium-binding	95460	94551	5.70	2
231	Carbonyl reductase [NADPH] 1	gi 47522960	18	+	-	-	-	-	-	C	-0.221	Enzyme activity	32015	31562	7.58	4
Antioxidant enzymes																
232	Peroxiredoxin-2	gi 1717797	79	-	+	-	-	-	+	C	0.078	Antioxidant enzyme activity	14272	14168	4.70	5
233	Peroxiredoxin 5	gi 10305336	58	-	-	-	-	-	+	M	0.123	Antioxidant enzyme activity	17484	17324	5.72	3
234	Similar to antioxidant protein isoform 1	gi 194042132	47	-	-	-	-	-	+	M	-0.023	Antioxidant enzyme activity	28682	21529	5.73	4

235	Non-selenium glutathione phospholipid hydroperoxide peroxidase (PHGPx)	gi 6689393	47	-	-	-	+	-	+	C	-0.294	Antioxidant enzyme activity; Lipid catabolic process	25078	24905	5.73	1
236	Similar to peroxiredoxin-4	gi 194044822	44	-	+	-	-	-	+	C	-0.231	Antioxidant enzyme activity	30764	30555	6.01	2
Structurally related cell regulatory proteins																
237	Myelin basic protein	gi 224358	213	+	+	+	+	+	+	IMP; MP	-1.047	Synaptic transmission; Immune response	18585	18599	11.28	19
238	Inhibin beta A chain (Activin beta-A chain)	gi 124280	26	+	-	-	-	-	-	S	-0.258	Growth factor activity; Cell-cell signaling	48244	12975	7.07	3
239	Ciliary neurotrophic factor (CNTF)	gi 2072395	24	+	-	-	-	-	-	C; E	-0.35	Growth factor activity	22761	22717	6.30	3
Glycoproteins																
240	Myelin proteolipid protein	gi 5679718	1037	-	-	+	-	+	+	IMP; MP	0.005	Signaling pathways	30855	25165	8.33	50
241	Myelin-oligodendrocyte glycoprotein (Precursor)	gi 56805528	340	+	-	-	-	+	+	IMP	0.102	Myelination of nerves	28196	27871	8.56	15
242	Similar to neuronal membrane glycoprotein M6-a	gi 194044039	73	-	-	+	-	+	-	IMP; MP	0.222	Cytoskeleton; Signaling pathways	17155	16880	6.06	5
243	Similar to MAL2 proteolipid protein	gi 194035646	34	-	-	-	-	+	-	IMP	0.724	Protein binding	19321	19048	6.79	2
Cytokines																
244	C-C motif chemokine 2	gi 1170889	29	-	+	-	-	-	-	S; E	-0.661	Inflammatory response; Signaling pathway	11311	8612	9.61	2
245	Interleukin 2 receptor, gamma	gi 148747300	16	+	-	-	-	-	-	MP	-0.474	Cytokine receptor activity	42384	39920	5.80	2
246	Interleukin 1 receptor	gi 38304066	16	+	-	-	-	-	-	MP	-0.115	Cytokine receptor activity	12263	11986	8.41	1
247	Interleukin 19	gi 116292413	16	+	-	-	-	-	-	S; E	-0.54	Receptor activity; Signal transduction	5579	5468	5.38	1

248	Tumor necrosis factor superfamily member 18	gi 116270707	14	+	-	-	-	-	-	MP; E	-0.294	Signal transduction	11836	11836	5.42	1
249	Interleukin 20	gi 116270713	13	-	+	-	-	-	-	S; E	-0.325	Cytokine receptor activity	4893	4895	10.61	2
Neurotransmitter and neuron-specific proteins																
250	Ras-related protein Rab-1A	gi 62868642	188	-	-	-	-	+	+	MP	-0.279	Signal transduction	22819	22605	6.6	9
251	GBI1	gi 115394798	176	-	-	-	-	+	+	N; MP	-0.371	Signal transduction	41117	40319	5.34	38
252	GBAK	gi 115394796	176	-	-	-	-	+	-	MP	-0.362	Signaling pathways	41091	40546	5.50	36
253	Similar to transducin-alpha	gi 194041214	163	-	-	+	-	+	-	MP	-0.285	Signal transduction	40410	39909	5.41	29
254	Synapsin Ia	gi 212525786	158	-	-	-	+	-	+	GA	-0.603	Neurotransmitter secretion	74928	74803	9.84	10
255	Similar to 14-3-3 protein eta	gi 194043292	100	-	-	-	-	+	+	C	-0.607	Signal transduction	28365	28211	4.81	17
256	Neuriblastoma ras oncogene	gi 84322432	95	-	-	-	-	+	-	MP	0.317	Signal transduction	21501	21229	5.01	6
257	Similar to syntaxin-binding protein 1	gi 194033625	84	+	+	+	+	+	+	IMP; MP; C	-0.45	Signal transduction; Protein transport	72006	71595	6.23	34
258	Similar to Ras-related protein Rab-35 (Rab-1C) (GTP-binding protein RAY)	gi 194043062	69	-	-	-	-	+	+	MP	-0.471	Signal transduction	23296	23025	8.53	12
259	GNAS complex locus	gi 147223307	66	-	-	+	-	-	+	C	-0.586	Signal transduction	108321	107475	5.01	3
260	DJ-1 protein (Parkinson disease protein 7)	gi 67038668	61	-	-	-	-	-	+	C; N	-0.003	Signal transduction	20095	19936	6.33	3
261	Chain A. Porcine Neuropeptide Y Bound To Dpc Micelles	gi 253722841	53	+	-	-	-	-	-	M	-1.11	Neurotransmitter	4200	4366	6.76	3

262	Similar to p87	gi 194036298	51	-	-	+	-	-	-	IMP; MP	0.021	Neurotransmitter transport	83378	82633	5.38	2
263	Guanine nucleotide-binding protein G(s) subunit alpha	gi 1958	50	-	-	+	-	-	-	MP	-0.534	Signaling pathways	72006	46476	5.59	2
264	HPCL4	gi 115394804	47	-	-	-	-	+	-	C; N	-0.478	Central nervous system development	22415	22071	4.76	11
265	GNAS complex locus	gi 147223306	46	-	-	-	-	+	-	MP	-0.593	Signaling pathways	112654	111810	5.15	19
266	Guanine nucleotide-binding protein. alpha-stimulating activity polypeptide 1	gi 138752615	46	-	-	-	-	+	-	MP	-0.39	Signaling pathways	13198	13148	6.80	7
267	Guanine nucleotide binding protein alpha 11	gi 84688557	41	-	-	-	-	+	-	MP; C	-0.331	Signaling pathway	42323	42064	5.90	16
268	Guanine nucleotide-binding protein alpha q	gi 83939812	41	-	-	-	-	+	-	MP	-0.44	Signaling pathway	42400	42142	5.48	7
269	Guanine nucleotide-binding protein alpha 14	gi 134038934	41	-	-	-	-	+	-	C	-0.388	Signaling pathway	41943	41513	5.67	12
270	CD90 protein	gi 224697007	41	-	-	-	-	+	-	IMP; ER	0.134	Signaling pathway	18072	12553	9.16	8
271	Chain A. Structure Of Pig Heart Citrate Synthase At 1.78 A Resolution	gi 222447060	36	-	-	-	-	+	-	M	-0.211	Signal transduction	49227	48919	7.01	45
272	Similar to Synaptogyrin-1	gi 194037211	33	-	-	-	-	+	-	IMP	-0.305	Neuronal synaptic plasticity	19605	19560	4.29	5
273	Similar to SH3-domain GRB2-like 2	gi 194034104	33	-	+	-	-	-	+	C	-0.629	Signal transduction	55745	55323	8.04	4
274	Similar to calcineurin-binding protein cabin-1	gi 194043342	31	-	+	-	-	-	-	N	-0.456	Signal transduction	191421	189259	6.15	2
276	Muscarinic acetylcholine receptor	gi 113120	16	+	-	-	-	-	-	IMP	-0.076	Signaling pathway	52241	51418	9.46	2

	M1															
277	Corticoliberin precursor	gi 172046780	14	-	+	-	-	-	+	S; E	-0.344	Signaling pathway	21143		5.50	2
Coagulation factors																
278	Coagulation factor VIII	gi 47523422	17	-	+	-	-	-	-	S; E	-0.489	Blood coagulation; Acute-phase response	240467	237208	6.53	7
279	Coagulation factor VII isoform b protein	gi 106647515	17	-	+	-	-	-	-	S; E	-0.308	Blood coagulation; Proteolysis	50688	49237	5.99	3
Inhibitors																
280	Aprotinin	gi 166153972	53	-	-	-	+	-	+	S	-0.634	Protease inhibitor activity	7037	6699	7.75	2
281	Rab GDP dissociation inhibitor beta	gi 75043802	35	-	+	-	+	-	+	C	-0.291	Inhibitor activity	50749	50267	6.31	2
282	Inter-alpha-trypsin inhibitor heavy chain H2	gi 3024050	28	-	+	-	-	-	+	S	-0.278	Inhibitor activity	105012	71082	6.11	2
283	Amyloid protein variant 2	gi 82542245	23	+	-	-	-	-	-	IMP	-0.631	Inhibitor activity	85771	85180	4.72	5
284	Inter-alpha-trypsin inhibitor heavy chain H4	gi 48374067	14	-	+	-	-	-	+	S	-0.245	Protease inhibitor activity	102254	102146	6.42	10
Immunoglobulins																
285	Neuroplastin	gi 194038709	89	-	-	+	-	+	-	IMP	-0.424	Immune response; Synaptic transmission	44840	44525	8.11	13
286	Immunoglobulin VDJ region	gi 1022923	81	-	-	-	+	-	+	E	-0.033	Immune response	14732	14627	4.56	2
287	Mutated immunoglobulin heavy chain	gi 161511655	81	-	-	-	+	-	+	S; E	-0.156	Immune response	29106	28668	9.1	3
288	Immunoglobulin heavy chain variable region	gi 54888536	81	-	-	-	+	-	+	S; E	-0.01	Immune response	29106	13509	4.5	3
289	Immunoglobulin heavy chain variable region	gi 119663001	80	-	-	-	+	-	+	S; E	-0.157	Immune response	12880	12774	5.74	3
290	Macrophage migration inhibitory factor	gi 5739517	59	-	+	-	+	-	+	C; S	0.082	Signal transduction; Immune response	12388	12320	8.24	3

[illegible]

307	Similar to collapsin response mediator protein-2A isoform 2	gi 194041525	569	-	+	-	+	+	+	C	-0.373	Regulation of microtubule assembly in neurons	73998	73530	5.94	23
308	Similar to Adipocyte plasma membrane-associated protein	gi 194044373	167	-	-	-	-	+	-	IMP	-0.123	Biosynthetic process	43437	43292	6.36	66
309	Alpha synuclein	gi 71068492	164	-	-	-	-	-	+	C	-0.476	Molecular chaperone	14511	14520	4.62	6
310	Similar to collapsin response mediator protein-2A isoform 1	gi 194041527	118	-	-	-	-	+	-	C; M	-0.27	Cell differentiation	62682	62321	5.95	10
311	Beta-synuclein	gi 144227406	90	-	-	-	-	-	+	C	-0.491	Molecular chaperone	14106	14114	4.46	3
312	Cathepsin D protein	gi 56417363	85	-	-	-	-	+	-	ER	-0.049	Proteolysis; Cell death	43192	37852	5.60	13
313	Similar to SFLQ611 isoform 4	gi 194042195	66	-	-	-	-	+	-	S	-0.271	Unknown	26037	22307	9.08	21
314	Eukaryotic translation elongation factor 1 alpha 2	gi 222066102	60	-	-	-	-	+	-	C	-0.306	Protein biosynthesis	50780	50470	9.11	27
315	Eukaryotic translation elongation factor 1 alpha 1	gi 110287842	60	-	-	-	-	+	-	C	-0.257	Protein biosynthesis	50451	50140	9.10	21
315	CCT3 protein	gi 194036006	56	-	-	-	-	-	+	C	-0.281	Molecular chaperone	59961	59257	7.09	2
316	NADH-cytochrome b5 reductase 3	gi 39931643	51	-	-	-	-	+	-	MP; M; ER	-0.336	Lipid synthesis	31039	30830	6.50	19
317	Similar to arylacetamide deacetylase-like 1	gi 194040972	48	-	-	-	-	+	-	IMP; ER	0.026	Lipid catabolic process	42980	45807	6.76	14
318	Monoglyceride lipase	gi 217314901	39	-	-	-	-	+	-	MP	0.017	Inflammatory response;	33562	33298	6.89	17
319	Gi-alpha-1 protein	gi 562016	38	-	-	-	-	+	-	GPC	-0.271	Lipid metabolic process	24320	24050	5.87	9
320	Gi-alpha-3 protein	gi 562020	38	-	-	-	-	+	-	GPC	-0.402	Signaling pathway	15902	15797	5.59	5
321	BM88 antigen	gi 557673	38	-	-	-	-	+	-	IMP	-0.526	Signaling pathway	14016	13967	9.10	5

322	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein zeta polypeptide	gi 112980823	37	-	-	-	-	+	-	C	-0.357	Cell differentiation	20073	19971	4.53	13
323	Similar to Acyl-coenzyme A thioesterase 4	gi 194038530	35	-	-	-	-	+	-	Peroxisome	-0.061	Carboxylic acid metabolic process	46321	45951	7.21	12
324	DSPP593	gi 37725365	34	-	-	-	+	-	-	C	-1.279	Calcium binding; Dentinogenesis	62200	62122	4.25	2
325	Similar to SDCCAG33 variant protein	gi 194034548	33	-	-	+	-	-	-	N	-0.531	Metal ion binding	170108	168217	6.98	3
326	Similar to MGC137953 protein isoform 2	gi 194037149	33	-	-	-	-	-	+	C	-0.834	Phosphoprotein	35688	35083	9.88	2
327	Similar to retinitis pigmentosa GTP-ase regulator RPGR	gi 194045071	31	-	+	-	-	-	-	GA	-0.783	Sensory transduction	99510	99512	4.78	3
306	Annexin A2	gi 54020966	28	+	-	-	-	-	-	MP; S	-0.509	Calcium and cytoskeletal protein binding; Inhibitor activity	38795	38534	6.49	2
328	Similar to FDPS protein	gi 194036063	27	+	-	-	-	-	-	C	-0.243	Host-virus interaction; Steroid and lipid biosynthesis	48333	48599	6.06	1
329	Similar to keratocan sulfate proteoglycan core protein 37A	gi 194037685	27	+	-	-	-	-	-	S; E	-0.323	Development and maintenance of corneal transparency	40509	38192	7.78	1
330	TNF-receptor associated factor 6	gi 38304068	16	+	-	-	-	-	-	C	0.092	T cell receptor signaling pathway	32180	31648	6.13	2
331	Parathyroid hormone	gi 131548	15	-	+	-	-	-	-	C	-0.312	Growth factor	12852	12871	9.88	1

^a NCBI knowledge entry;

^b Proteins were found and identified by integral mascot database batch search of all MS/MS in Swissprot (v 56.1). All matches are identified significantly. Identified proteins are considered as positive match on at least a 95% MudPIT MASCOT scoring ($p \leq 0.05$);

^c Grand average of hydrophobicity;

^d Molecular weight in Da;

MW^{d*} Molecular weight of proteins according to UniProt

MW^{d}** Molecular weight of proteins calculated based on its primary amino acid sequence after excluding signal and propeptide chains;

^e Number of tryptic peptides that match the identified protein. At least one matching peptide for each identified protein must fulfill significance criteria;