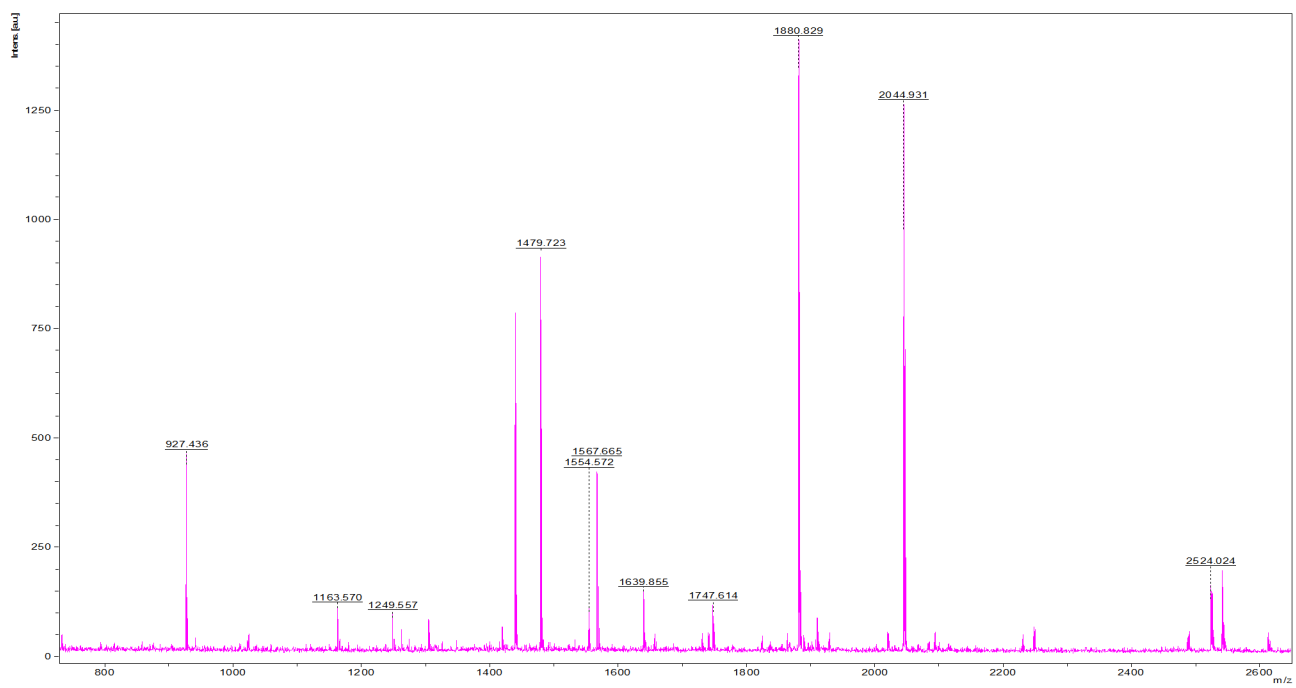
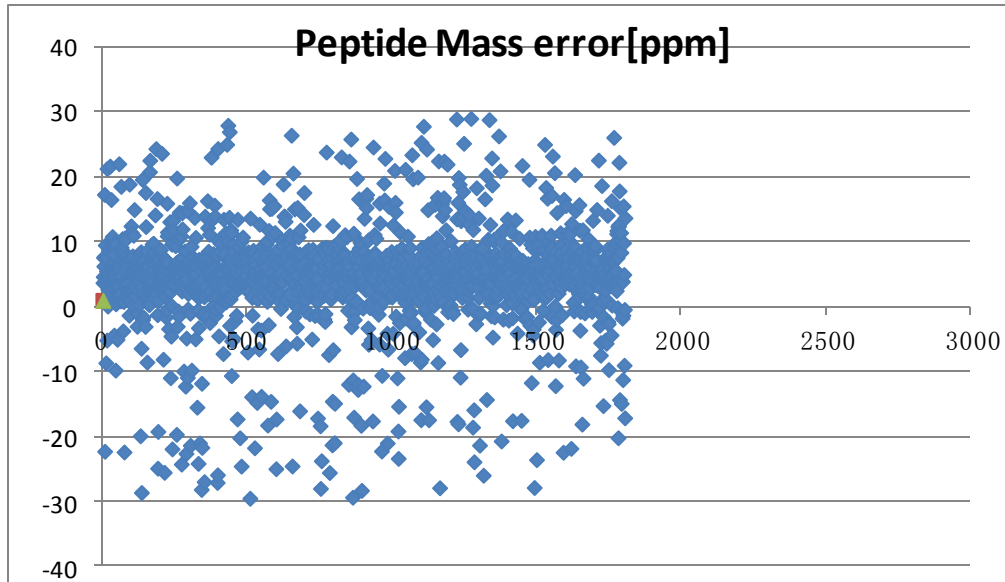


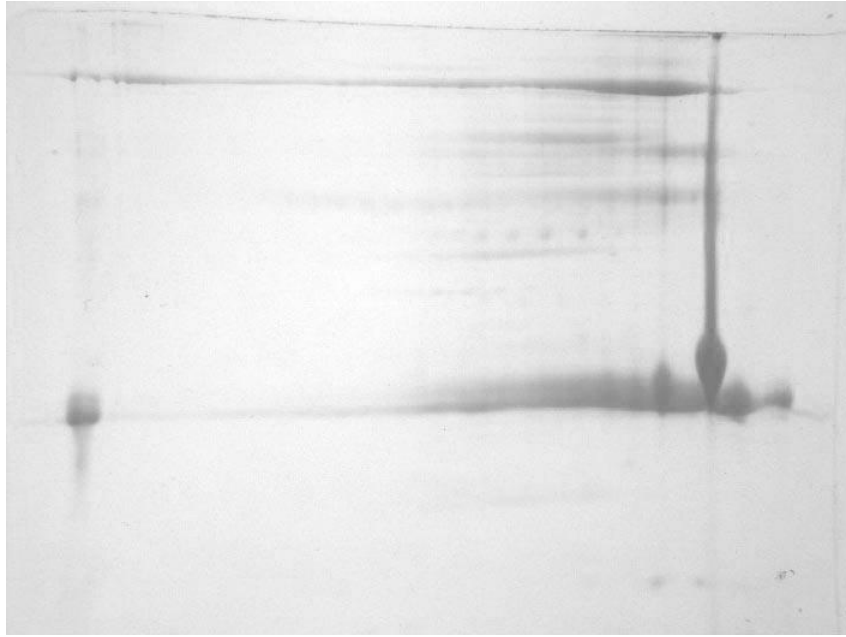
m/z	S/N	Quality Fac.	Res.	Intens.	Area
721.309	6	243	9851	62.8	8.33
927.436	45	2743	16069	434	50.1
1163.570	10	1143	18969	106	14.3
1249.557	8	257	17490	84.2	12.9
1305.650	7	325	18304	72.3	11.1
1439.738	73	20669	20664	754	133
1479.723	90	27984	21981	924	160
1554.572	9	665	22192	97.8	18.1
1567.665	43	7247	22513	448	83.3
1639.855	13	1079	23257	145	28.2
1747.614	9	511	18499	97.3	25.7
1880.829	131	71013	22243	1342	365
2044.931	104	8484	23127	973	279
2524.024	18	1251	22240	127	51.0
2541.052	18	1043	22501	123	47.6



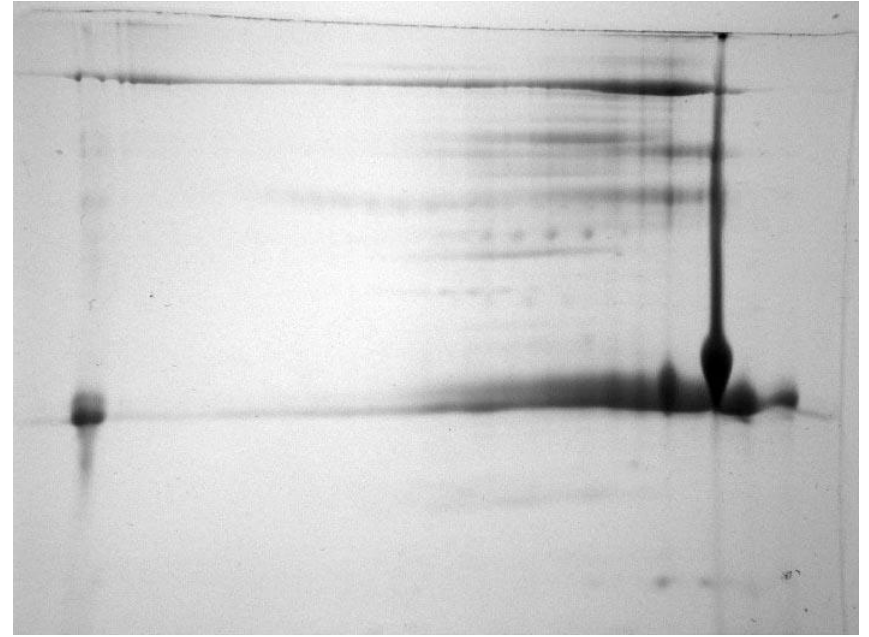
Supplementary Figure 1



Supplementary Figure 2



10 min



60 min

Supplementary Table 1A

Series Number	GO Term Name	Ensembl			GO Term Name	NCBI		
		0 min	10 min	1 h		0 min	10 min	1 h
1	metabolic process	27.3%	25%	24%	transport	28.5%	40%	19%
2	oxidation-reduction process	18.2%	8.3%	11%	metabolic process	14.3%	10%	18%
3	transport	45.5%	58.3%	10%	oxidation-reduction process	—	—	12%
4	signal transduction	—	—	10%	signal transduction	—	—	8%
5	proteolysis	9.1%	—	8%	glycolytic process	14.3%	20%	8%
6	small GTPase mediated signal transduction	—	—	8%	small GTPase mediated signal transduction	14.3%	—	8%
7	protein transport	—	—	8%	oxygen transport	14.3%	20%	8%
8	intracellular protein transport	—	—	7%	protein phosphorylation	14.3%	10%	7%
9	GTP catabolic process	—	—	7%	protein transport	—	—	6%
10	protein phosphorylation	—	8.3%	7%	proteolysis	—	—	6%

Supplementary Table 1B

Series Number	GO Term Name	Ensembl			GO Term Name	NCBI		
		0 min	10 min	1 h		0 min	10 min	1 h
1	protein binding	35%	38.5%	21%	nucleotide binding	10%	7.7%	20%
2	nucleotide binding	20%	7.7%	19%	ATP binding	10%	7.7%	13%
3	ATP binding	15%	15.4%	13%	transferase activity	10%	15.4%	10%
4	hydrolase activity	10%	7.7%	9%	catalytic activity	10%	30.8%	9%
5	transferase activity	—	7.7%	9%	protein binding	—	7.7%	8%
6	GTP binding	5%	—	7%	hydrolase activity	10%	—	8%
7	DNA binding	5%	—	6%	GTP binding	10%	—	8%
8	oxidoreductase activity	5%	7.7%	6%	DNA binding	—	15.4%	8%
9	structural molecule activity	—	—	5%	GTPase activity	10%	—	8%
10	metal ion binding	5%	15.4%	5%	metal ion binding	30%	15.4%	8%

Supplementary Table 1C

Series Number	GO Term Name	Ensembl			GO Term Name	NCBI		
		0 min	10 min	1 h		0 min	10 min	1 h
1	membrane	16.7%	33.3%	18%	cytoplasm	33.3%	16.7%	17%
2	cytoplasm	49.9%	—	16%	extracellular	33.3%	33.3%	16%
3	intracellular	—	—	15%	membrane	—	16.7%	15%
4	nucleus	—	—	13%	plasma membrane	—	16.7%	12%
5	intermediate filament	—	33.3%	8%	intracellular	33.3%	—	8%
6	extracellular region	16.7%	33.3%	8%	nucleus	—	8.3%	8%
7	ribosome	—	—	7%	integral component of membrane	—	8.3%	7%
8	cytoskeleton	16.7%	—	6%	mitochondrion	—	—	7%
9	mitochondrion	—	—	5%	protein complex	—	—	7%
10	chromosome	—	—	4%	chromosome	—	—	3%

Ensembl database (fasting)

Spot No.	Ensembl ID	protein	Theoretical Mr/PI	Peptides matched	Sequence covered(%)	Score
1	ENSPMAP00000008289	plasma albumin prepeptide	13.3/6.64	1	6.70%	36.81
2	ENSPMAP00000005857	myoglobin	16.4/8.99	1	10.70%	98.48
3	ENSPMAP00000005910	myoglobin	16.4/9.00	5	52.70%	358.04
4	ENSPMAP00000005891	myoglobin	16.4/9.00	6	50.70%	334.62
5	ENSPMAP00000001744	myoglobin	16.4/6.14	2	19.30%	68.99
6	ENSPMAP00000008163	ARP2 actin-related protein 2a homolog (yeast)	31.2/5.90	1	2.20%	23.20
7	ENSPMAP00000005152	dihydrouridine synthase 2	31.2/9.92	1	3.60%	29.73
8	ENSPMAP00000002473	leucine-rich repeat transmembrane protein FLRT3	31.9/9.73	0	0.00%	36.11
9	ENSPMAP00000009725	coiled-coil domain containing 61	32.4/9.90	1	3.40%	24.60
11	ENSPMAP00000005159	Enoyl Coenzyme A hydratase domain containing 1	34.2/10.61	1	4.70%	29.20
10	ENSPMAP00000008415	translin-associated factor X interacting protein 1	37.2/5.40	1	1.50%	25.40
12	ENSPMAP00000001581	proteasome (prosome, macropain) 26S subunit, non-ATPase, 12	38.0/7.74	1	3.40%	31.55
13	ENSPMAP00000005508	Inter-alpha-trypsin inhibitor heavy chain H5-like protein	39.1/7.80	2	6.70%	121.65
14	ENSPMAP00000002471	leucine-rich repeat transmembrane protein	40.7/9.99	0	0.00%	36.14
15	ENSPMAP00000008937	secernin 3	45.0/6.04	1	3.60%	23.54
16	ENSPMAP00000001239	Proteasome (prosome, macropain) 26S subunit, ATPase 2	49.0/5.50	1	1.60%	25.36
17	ENSPMAP00000008411	adenylosuccinate synthase	50.8/9.20	1	1.50%	23.80
18	ENSPMAP00000009177	transient receptor potential cation channel, subfamily V, member 6	51.1/6.51	1	3.80%	28.82

19	ENSPMAP00000003132	fragile X mental retardation syndrome- related protein 1-like isoform X4	66.4/6.30	1	2.00%	23.2
20	ENSPMAP00000005361	Sidekick homolog 2b	77.3/6.12	1	1.00%	28.46
21	ENSPMAP00000000308	prominin 2(cd133/prominin)	79.0/9.21	1	1.50%	30.73
22	ENSPMAP00000009963	polymerase (DNA directed) kappa	83.8/9.10	1	0.90%	24.40
23	ENSPMAP00000003404	DEAD (Asp-Glu-Ala- Asp) box polypeptide 27	88.9/9.90	1	1.30%	25.30
24	ENSPMAP00000005992	CAP-GLY domain containing linker	111.0/5.22	1	0.80%	37.27
25	ENSPMAP00000009438	protein 1a tight junction protein	195.1/6.83	1	0.40%	24.45

NCBI database (fasting)						
Spot No.	NCBI ID	protein	Theoretical Mr/PI	Peptides matched	Sequence covered(%)	Score
1	gi 401705418	Hypothetical protein Y17_1183 [<i>Pectobacterium wasabiae</i> CFBP 3304]	12.1/9.70	1	8.90%	56.70
2	gi 297544925	hypothetical protein Tmath_1505 [<i>Thermoanaerobacter mathranii</i> subsp. <i>mathranii</i> str. Chain A, The 2.7 Angstrom	14.7/8.90	1	7.90%	72.00
3	gi 4389013	Crystal Structure Of Deoxygenated Hemoglobin [<i>Petromyzon marinus</i>]	16.3/6.20	2	20.80%	72.60
4	gi 30750169	Chain A, Crystal Structure Of Hemoglobin From River Lamprey	16.3/9.15	1	10.70%	95.36
5	gi 110825990	RecName: Full=Globin-1; AltName: Full=Globin I [<i>Petromyzon marinus</i>]	16.5/9.37	3	30.00%	98.69
6	gi 317062023	transcriptional regulator [<i>Fusobacterium ulcerans</i> ATCC 49185]	27.5/5.30	1	5.50%	57.00
7	gi 335058605	urea ABC transporter [uncultured <i>Acidobacteria bacterium</i> A3]	27.9/4.80	1	3.90%	53.60
8	gi 145046200	cysteine-rich secretory protein- buccal gland secretion [<i>Lethenteron camtschaticum</i>]	28.0/6.50	11	23.70%	425.00
9	gi 30248403	tRNA modification GTPase TrmE [<i>Nitrosomonas europaea</i> ATCC 19718]	48.6/4.80	1	2.40%	57.20
10	gi 313681747	pyruvate kinase [<i>Sulfuricurvum kujiense</i> DSM 16994]	55.0/5.49	1	2.00%	65.39
11	gi 126143340	plasma albumin [<i>Lethenteron camtschaticum</i>]	156.6/6.02	30	17.20%	1443.22

Ensembl database (feeding for 10 min)

Spot No.	Ensembl ID	protein	Theoretical Mr/PI	Peptides matched	Sequence covered(%)	Score
1	ENSPMAP00000007609	lamprey keratin	16.2/5.80	1	7.50%	69.50
2	ENSPMAP00000005910	myoglobin	16.4/8.99	5	52.70%	316.39
3	ENSPMAP00000005857	myoglobin	16.4/8.99	2	23.30%	74.39
4	ENSPMAP00000008005	myoglobin	16.4/8.99	5	52.70%	265.19
5	ENSPMAP00000001744	myoglobin	16.4/6.10	1	12.70%	47.61
6	ENSPMAP00000005891	Myoglobin	16.4/8.99	6	50.70%	334.62
		PREDICTED:				
7	ENSPMAP00000008821	uncharacterized protein C1orf50 homolog zgc:195245 protein	17.0/4.80	1	9.70%	21.60
8	ENSPMAP00000003872	FAM107B [<i>Rattus norvegicus</i>]	17.2/9.70	1	6.30%	24.14
9	ENSPMAP00000009056	PREDICTED: acid ceramidase	25.7/9.30	1	5.30%	67.80
10	ENSPMAP00000006073	Melanotransferrin, partial	28.5/5.88	1	5.60%	72.39
11	ENSPMAP00000000298	glutaminase kidney isoform, mitochondrial isoform X4	29.1/5.70	1	4.20%	24.60
12	ENSPMAP00000008259	erythrocyte band 7 integral membrane protein	31.5/7.70	1	4.90%	27.80
13	ENSPMAP00000008190	proactivator polypeptide	31.7/5.97	2	4.90%	36.03
14	ENSPMAP00000002473	leucine-rich repeat transmembrane protein FLRT3	31.9/9.70	1	4.00%	28.91
15	ENSPMAP00000008914	cytochrome P450, family 2, subfamily W, polypeptide 1	32.4/9.50	1	4.20%	24.90
16	ENSPMAP00000003316	PREDICTED: protein FAM118B isoform X3	35.5/6.24	1	2.20%	25.34
17	ENSPMAP00000005508	inter-alpha (globulin) inhibitor H2	39.1/7.84	1	3.60%	81.00
18	ENSPMAP00000002471	leucine-rich repeat transmembrane protein	40.7/10.00	1	3.20%	25.70
		PREDICTED: arf-GAP with GTPase, ANK				
19	ENSPMAP00000002352	repeat and PH domain-containing protein 1 isoform X4	47.3/10.20	1	2.10%	22.41

20	ENSPMAP00000003404	DEAD (Asp-Glu-Ala- Asp) box polypeptide 27	88.9/9.88	1	1.30%	25.30
21	ENSPMAP00000002451	titin	2097.2/6.89	1	0.00%	33.81

NCBI database (feeding for 10 min)

Spot No.	NCBI ID	protein	Theoretical Mr/PI	Peptides matched	Sequence covered(%)	Score
1	gi 30750169	Chain A, Crystal Structure Of Hemoglobin From River Lamprey	16.3/9.20	1	10.70%	72.94
2	gi 4389013	Chain A, The 2.7 Angstrom Crystal Structure Of Deoxygenated Hemoglobin From The Sea Lamprey (<i>Petromyzon Marinus</i>)	16.3/6.15	3	28.90%	212.09
3	gi 110825990	RecName: Full=Globin-1; AltName: Full=Globin I [<i>Petromyzon marinus</i>]	16.5/9.37	4	39.30%	226.19
4	gi 126143345	hemoglobin 2 [<i>Lethenteron camtschaticum</i>]	16.5/8.97	4	39.30%	175.82
5	gi 336451127	membrane protein [Idiomarina sp. A28L]	21.9/9.04	1	5.90%	54.50
6	gi 218461704	LysR family transcriptional regulator protein [<i>Rhizobium etli</i> bv. mimosae str. IE4771]	24.0/9.42	1	4.60%	57.02
7	gi 145046200	cysteine-rich secretory protein-buccal gland secretion [<i>Lethenteron camtschaticum</i>]	28.0/6.50	9	27.20%	431.37
8	gi 31581482	actin, partial [<i>Vanderwaltozyma polyspora</i>]	33.5/5.40	2	5.40%	119.00
9	gi 1703239	RecName: Full=Fructose-bisphosphate aldolase, muscle type [<i>Lethenteron camtschaticum</i>]	39.2/9.50	1	3.30%	54.20
10	gi 124027479	Cdc6-1 [<i>Hyperthermus butylicus</i> DSM 5456]	45.4/9.54	1	2.20%	50.84
11	gi 15991461	[<i>Pyrolobus fumarii</i>][<i>Metallosphaera yellowstonensis</i>]	46.9/4.96	1	2.60%	55.61
12	gi 313681747	RAG2, partial [<i>Triakis</i> sp. IMCB-2001]	55.0/5.50	1	2.00%	58.33
13	gi 7331218	pyruvate kinase [<i>Sulfuricurvum kujiense</i> DSM 16994]	66.0/8.80	6	10.10%	399.5
14	gi 16905189	keratin 1 [<i>Homo sapiens</i>]	77.2/9.48	1	1.00%	70.69
15	gi 378554473	putative gag-pol precursor [<i>Oryza sativa Japonica</i> Group]	95.0/9.19	1	1.20%	57.37
16	gi 308455280	ORF1a [Astrovirus wild boar/WBAstV-1/2011/HUN] hypothetical protein CRE_10724 [<i>Caenorhabditis remanei</i>]	111.3/5.10	1	1.00%	61.70

17	gi 330465484	hypothetical protein VAB18032_07535 [<i>Verrucosipora maris</i> AB- 18-032]	123.9/5.86	1	1.40%	55.99
18	gi 126143340	plasma albumin [<i>Lethenteron</i> <i>camtschaticum</i>]	156.6/6.00	23	14.80%	1116.07
19	gi 386111	plasma albumin prepeptide [<i>Petromyzon marinus</i>]	158.9/6.10	1	0.80%	55.30
20	gi 147784509	hypothetical protein VITISV_030622 [<i>Vitis</i> <i>vinifera</i>]	159.2/10.3 0	1	1.00%	60.38

Ensembl database (feeding for 60 min)

Spot No.	Ensembl ID	protein	Theoretical Mr/PI	Peptides matched	Sequence covered(%)	Score
1	ENSPMAP000000010145	Selenoprotein 15	6.7/5.16	2	49.20%	111.55
2	ENSPMAP000000010887	Glycine N-methyltransferase	7.7/7.56	2	42.00%	75.51
3	ENSPMAP000000001112	Diazepam binding inhibitor (GABA receptor modulator, acyl-CoA binding protein)	9.7/8.97	2	28.70%	70.81
4	ENSPMAP000000002361	Histone H4	11.0/12.03	4	40.40%	176.41
5	ENSPMAP000000009755	Cytochrome c, somatic b	11.7/10.19	1	10.50%	29.23
6	ENSPMAP000000000864	Ribosomal protein S26, like	13.3/12.19	1	12.70%	54.24
7	ENSPMAP000000008289	Uncharacterized protein plasma albumin propeptide [<i>Petromyzon marinus</i>]	13.3/6.64	1	6.70%	30.55
8	ENSPMAP000000005542	Ribosomal protein S20	13.6/10.63	3	22.50%	143.42
9	ENSPMAP000000011117	BLAST histone 2, H2a [<i>Danio rerio</i>]	13.6/11.73	2	30.20%	77.27
10	ENSPMAP000000000976	Ubiquinol-cytochrome c reductase binding protein	13.6/9.67	1	10.80%	45.99
11	ENSPMAP000000005647	Thioredoxin domain containing 17	13.6/4.62	1	15.40%	25.41
12	ENSPMAP000000006641	Uncharacterized protein sulfotransferase 6B1 [<i>Danio rerio</i>]	13.9/5.65	1	7.40%	39.98
13	ENSPMAP000000002376	PREDICTED: histone H2AX-like [<i>Lepisosteus oculatus</i>]	14.0/11.72	1	5.40%	41.48
14	ENSPMAP000000010426	Ribosomal protein L11	14.6/10.43	1	7.10%	44.28
15	ENSPMAP000000010392	Ribosomal protein S15a	14.8/10.69	1	10.80%	87.68
16	ENSPMAP000000011207	PREDICTED: histone H2A.x-like [<i>Oryzias latipes</i>]	14.9/11.18	2	11.30%	65.86
17	ENSPMAP000000004835	FK506 binding protein 2	15.4/9.74	1	10.50%	48.33

BLAST						
18	ENSPMAP000000002367	Uncharacterized protein Histone H3c [Culex quinquefasciatus]	15.6/11.63	3	19.00%	123.65
19	ENSPMAP000000002363	Histone H2B	15.7/10.73	5	35.90%	230.08
20	ENSPMAP000000008419	Peptidyl arginine deiminase, type II	15.8/6.52	1	5.90%	23.34
21	ENSPMAP000000009492	Ribosomal protein L28	16.0/12.47	1	7.90%	74.38
22	ENSPMAP000000007609	Uncharacterized protein type II keratin 3 [Lampetra fluviatilis]	16.2/5.78	1	7.50%	60.69
23	ENSPMAP000000005873	Myoglobin	16.3/7.62	4	39.30%	282.29
24	ENSPMAP000000005857	Myoglobin	16.4/8.99	4	41.30%	322.26
25	ENSPMAP000000001744	myoglobin	16.4/6.14	2	16.00%	98.12
26	ENSPMAP000000005910	Myoglobin	16.4/8.99	5	52.70%	358.04
27	ENSPMAP000000005891	Myoglobin	16.4/8.99	6	50.70%	334.62
28	ENSPMAP000000005163	Solute carrier family 48 (heme transporter), member 1	16.4/8.99	0	0.00%	33.85
29	ENSPMAP000000001812	Cytochrome c oxidase subunit Vaa	16.5/5.10	1	6.00%	26.35
30	ENSPMAP000000003636	Calmodulin 1	16.8/3.93	2	20.10%	65.55
31	ENSPMAP000000003698	Uncharacterized protein protein kinase C epsilon type, partial [Picoides pubescens]	16.9/9.02	1	4.80%	26.57
32	ENSPMAP000000001490	Deoxyribonuclease I	16.9/4.94	1	8.40%	39.03
33	ENSPMAP000000007215	cystatin (leukocystatin) F	17.1/10.31	2	11.10%	74.95
34	ENSPMAP000000003872	zgc:195245 protein FAM107B [Rattus norvegicus]	17.2/9.70	1	6.30%	24.14
35	ENSPMAP000000006690	Annexin	17.4/4.09	2	12.80%	75.97
36	ENSPMAP000000006483	Prohibitin 2b	17.5/10.43	1	6.30%	52.61
37	ENSPMAP000000002634	Ribosomal protein S25	17.7/11.50	2	13.30%	62.75
38	ENSPMAP000000010566	Translocase of inner mitochondrial membrane 17 homolog B (yeast)	17.8/10.22	1	5.30%	25.78
39	ENSPMAP000000007019	Malate dehydrogenase 1Aa, NAD (soluble)	18.0/9.81	2	7.80%	54.95

		Uncharacterized protein				
40	ENSPMAP00000006787	PREDICTED: legumain-like [<i>Oreochromis niloticus</i>]	18.1/6.35	1	9.90%	26.77
41	ENSPMAP00000003464	Uncharacterized protein olfactomedin 4 precursor [<i>Xenopus laevis</i>]	18.3/5.15	1	6.00%	27.09
42	ENSPMAP000000010483	Ribosomal protein L21	18.5/11.40	1	5.60%	24.36
43	ENSPMAP000000009791	Cofilin 1	18.6/7.47	1	8.40%	39.35
44	ENSPMAP000000000207	Zgc:165571 Anterior gradient protein 3, partial [<i>Chlamydotis macqueenii</i>]	18.7/6.52	1	10.90%	63.51
45	ENSPMAP000000010481	Nucleotide binding protein-like	19.3/5.28	1	5.60%	29.19
46	ENSPMAP000000007211	Annexin	19.3/5.04	1	9.10%	49.74
47	ENSPMAP000000004452	anterior gradient homolog 2 (<i>Xenopus laevis</i>)	19.5/9.15	2	12.20%	88.67
48	ENSPMAP000000010311	Uncharacterized protein PREDICTED: keratin, type II cytoskeletal 5-like [<i>Alligator mississippiensis</i>]	20.0/4.21	2	13.10%	108.69
49	ENSPMAP000000011072	ADP-ribosylation factor 6	20.2/9.70	0	0.00%	34.62
50	ENSPMAP000000002279	ADP-ribosylation factor-like 1	20.3/7.20	1	7.70%	35.7
51	ENSPMAP000000009400	Ferritin	20.3/5.04	6	42.90%	236.04
52	ENSPMAP000000009008	Uncharacterized protein ferritin heavy chain polypeptide 1 [<i>Petromyzon</i>]	20.5/5.15	1	6.20%	38.77
53	ENSPMAP000000002125	Glyoxalase 1	20.5/7.81	2	8.40%	50.59
54	ENSPMAP000000002230	ADP-ribosylation factor 3b	20.6/6.40	7	36.10%	290.98
55	ENSPMAP000000000590	Uncharacterized protein ADP-ribosylation factor 5 [<i>Xenopus (Silurana) tropicalis</i>]	20.7/6.40	2	13.80%	105.54

56	ENSPMAP00000003811	Uncharacterized protein type I keratin 18 [<i>Lampetra fluviatilis</i>] Proteasome	21.0/5.22	2	8.90%	108.22
57	ENSPMAP00000008784	(prosome, macropain) subunit, beta type, 2 RAB2A, member	21.0/6.35	1	5.90%	55.24
58	ENSPMAP00000009659	RAS oncogene family procollagen-proline, 2-oxoglutarate 4- dioxygenase (proline 4-hydroxylase), beta	21.0/6.25	2	14.70%	129.48
59	ENSPMAP00000010221	polypeptide BLAST PREDICTED: protein disulfide- isomerase [<i>Tarsius svrichta</i>]	21.0/4.75	3	21.20%	124.3
60	ENSPMAP00000003782	Neuropeptide S receptor 1	21.2/9.66	1	2.70%	24.93
61	ENSPMAP00000003895	Sorcini	21.5/4.67	3	14.00%	110.96
62	ENSPMAP00000010828	Glutathione peroxidase 2 (gastrointestinal) peroxiredoxin 2 buccal gland	21.6/7.74	1	4.70%	30.25
63	ENSPMAP00000008386	secretion peroxiredoxin [<i>Lethenteron camtschaticum</i>]	21.7/7.68	3	24.90%	133.02
64	ENSPMAP00000006967	Protein phosphatase 2, regulatory subunit B, delta	22.3/5.66	1	3.60%	29.23
65	ENSPMAP00000000223	Ribosomal protein S9	22.6/10.97	4	18.00%	113.39
66	ENSPMAP00000003933	SAR1 gene homolog Ab (<i>S. cerevisiae</i>) RAB1A, member	22.6/7.69	1	5.50%	65.74
67	ENSPMAP00000001989	RAS oncogene family Proteasome	22.7/5.44	1	3.90%	44.98
68	ENSPMAP00000002252	(prosome, macropain) subunit, beta type, 3 RAB11a, member	22.8/4.75	1	6.30%	48.00
69	ENSPMAP00000010262	RAS oncogene family, like	22.8/6.73	1	5.30%	25.29

70	ENSPMAP00000000757	Abhydrolase domain containing 14B RAB29, member	22.9/6.24	1	6.10%	46.46
71	ENSPMAP000000006576	RAS oncogene family	23.0/7.73	2	5.90%	42.38
72	ENSPMAP000000010385	ADP-ribosylation factor-like 6	23.2/10.00	1	3.40%	24.47
73	ENSPMAP000000001612	interacting protein 1 Peroxiredoxin 3	23.2/5.53	2	12.40%	77.47
74	ENSPMAP000000007595	Gdnf family receptor alpha 1b (glial cell line-derived neurotrophic factor,GDNF)	23.4/7.76	1	4.30%	33.88
75	ENSPMAP000000005276	Integrator complex subunit 10	23.8/6.11	1	4.30%	32.55
76	ENSPMAP000000009910	Methyltransferase like 5	23.9/6.22	1	4.70%	25.19
77	ENSPMAP000000006436	Cystathionine-beta- synthase b	24.2/9.63	1	4.10%	28.36
78	ENSPMAP000000007890	Superoxide dismutase 2, mitochondrial	25.3/9.43	2	12.10%	86.89
79	ENSPMAP000000001201	BLAST PREDICTED: LOW QUALITY PROTEIN: protein FAM161A [<i>Melopsittacus undulatus</i>]	25.4/10.76	1	2.70%	28.6
80	ENSPMAP000000002785	Adipocyte plasma membrane associated protein	25.5/6.35	1	3.10%	29.01
81	ENSPMAP000000009056	N-acylsphingosine amidohydrolase (acid ceramidase) 1b	25.7/9.33	1	5.30%	72.46
82	ENSPMAP000000009520	BLAST PREDICTED: guanine nucleotide- binding protein subunit beta-4-like [<i>Felis catus</i>]	25.8/7.85	2	7.30%	78.53
83	ENSPMAP000000006678	Tyrosine 3- monooxygenase/tryp tophan 5- monooxygenase activation protein, epsilon polypeptide 1	26.6/4.60	2	8.90%	64.70

84	ENSPMAP00000000724	Triosephosphate isomerase 1b	26.8/7.86	1	6.00%	48.50
85	ENSPMAP000000006138	ADP-ribosylation factor 5	27.2/9.76	1	7.40%	29.54
		Uncharacterized protein				
		PREDICTED: guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2 isoform X1				
86	ENSPMAP000000008362	[<i>Pelodiscus sinensis</i>] BLAST	27.2/4.78	1	4.00%	50.90
		PREDICTED: EGF-like repeat and discoidin I-like domain-containing protein 3, partial				
87	ENSPMAP000000009728	[<i>Tarsius sylvaticus</i>] Cathepsin Z	27.2/9.76	1	3.60%	28.38
88	ENSPMAP000000000605	Glyceraldehyde-3-phosphate dehydrogenase	27.3/10.86	1	4.90%	40.35
89	ENSPMAP000000010249	Carnosine dipeptidase 1	27.3/9.45	1	5.90%	25.92
90	ENSPMAP000000009936	CNDP dipeptidase 2	27.3/4.81	1	4.40%	39.73
91	ENSPMAP000000009538	(metallopeptidase M20 family)	27.3/6.52	7	20.30%	239.79
92	ENSPMAP000000000145	Actinin, alpha 4	27.6/4.47	1	5.00%	64.66
93	ENSPMAP000000003475	syndecan binding protein (syntenin) 2	27.8/9.35	1	4.30%	29.59
		Uncharacterized protein				
94	ENSPMAP000000009298	PREDICTED: rho-related GTP-binding protein RhoE	28.2/9.52	1	2.70%	27.25
		[<i>Alliaator sinensis</i>] Uncharacterized protein				
		PREDICTED: protein phosphatase 1 regulatory inhibitor subunit 16B isoform X1				
95	ENSPMAP000000003319	[<i>Callorhinchus</i>	28.3/5.86	1	2.30%	27.73

		Uncharacterized protein				
		PREDICTED: 14-3-				
96	ENSPMAP00000005888	3 protein gamma-1-like isoform X2 [<i>Xiphophorus maculatus</i> l Erythrocyte	28.4/4.59	4	14.10%	157.02
97	ENSPMAP00000002193	membrane protein band 4.1 like 5	28.5/9.99	1	2.90%	27.14
98	ENSPMAP00000006073	Otolith matrix protein	28.5/5.88	1	3.40%	23.70
99	ENSPMAP00000008360	ribonuclease T2	28.8/6.28	1	6.00%	54.74
100	ENSPMAP00000000478	TatD DNase domain containing 3	29.1/9.07	1	2.60%	26.74
101	ENSPMAP00000008589	Dipeptidyl-peptidase 7	29.2/5.25	1	5.30%	30.65
		Uncharacterized protein				
		PREDICTED: 14-3-				
102	ENSPMAP00000007305	3 protein epsilon isoform X1 [<i>Callorhinchus milii</i> l	29.4/4.59	10	32.60%	417.11
		Uncharacterized protein				
		PREDICTED:				
103	ENSPMAP00000008802	ADP/ATP translocase 3-like [<i>Haplochromis burtoni</i> l	29.5/10.50	1	5.70%	64.09
		Proteasome (prosome, macropain) subunit, beta type, 5				
104	ENSPMAP00000009424		30.0/6.27	2	8.40%	63.78
105	ENSPMAP00000003783	Voltage-dependent anion channel 3	30.2/9.03	3	12.00%	99.29
106	ENSPMAP00000003114	ankyrin repeat and SOCS box-containing 7	30.2/11.92	0	0.00%	37.92
107	ENSPMAP00000010567	Polyglutamine binding protein 1	30.2/4.98	1	2.60%	29.19
		ATP synthase, H ⁺ transporting,				
108	ENSPMAP00000006476	mitochondrial F1 complex, gamma polypeptide 1	30.6/10.04	1	4.00%	24.34
109	ENSPMAP00000005235	stromal cell derived factor 4	30.9/4.39	1	5.00%	86.64

		Seven in absentia homolog 1 (<i>Drosophila</i>) BLAST				
110	ENSPMAP00000001842	PREDICTED: E3 ubiquitin-protein ligase SIAH1 isoform X2 [<i>Felis catus</i>]	31.5/6.22	0	0.00%	36.59
111	ENSPMAP00000008259	Stomatin VPS9 domain containing 1	31.5/7.67	2	8.40%	76.90
112	ENSPMAP00000006978	(vacuolar protein sorting, May bind a Rab GTPase such as VPS21)	31.5/10.61	1	1.80%	24.20
113	ENSPMAP00000002253	sarcoglycan, gamma	31.6/5.61	1	5.40%	26.73
114	ENSPMAP00000008190	Prosaposin BLAST	31.7/5.97	2	9.10%	83.22
115	ENSPMAP00000009988	PREDICTED: sperm-associated antigen 1 [<i>Larimichthys crocea</i>]	32.0/5.22	1	4.20%	25.67
116	ENSPMAP00000005370	BLAST keratin alpha [<i>Lampetra fluviatilis</i>]	32.1/9.63	1	2.90%	67.58
117	ENSPMAP00000001254	Glutaminyl-peptide cyclotransferase	32.1/5.96	1	4.00%	32.82
118	ENSPMAP00000008914	Blast Cytochrome P450 2H2, partial [<i>Columba livia</i>] Zgc:136930 keratin	32.4/9.49	1	4.20%	24.92
119	ENSPMAP00000008118	gamma3 [<i>Lampetra fluviatilis</i>]	32.6/5.53	3	9.80%	119.76
120	ENSPMAP00000011279	Glyceraldehyde-3- phosphate dehydrogenase	32.7/7.82	2	8.50%	68.86
121	ENSPMAP00000005709	BLAST cathepsin Z precursor [<i>Xenopus laevis</i>] BLAST	32.8/5.91	1	3.40%	66.87
122	ENSPMAP00000003198	PREDICTED: netrin-G2, partial [<i>Pelecanus crispus</i>]	33.5/9.47	1	2.70%	23.21
123	ENSPMAP00000006739	Aurora kinase A	33.6/10.01	1	2.70%	24.00
124	ENSPMAP00000005779	Sulfotransferase family 5A, member	34.0/7.79	1	5.70%	37.75

		zgc:73340 BLAST putative				
125	ENSPMAP000000008676	methyltransferase KIAA1456 homolog [<i>Danio rerio</i>]	34.0/10.96	1	2.30%	28.33
126	ENSPMAP000000006316	Angiotensin II receptor, type 1a	34.0/12.03	1	2.60%	33.85
127	ENSPMAP000000011213	Ribosomal protein, large, P0 Uncharacterized protein	34.2/5.72	3	11.10%	151.04
128	ENSPMAP000000011002	PREDICTED: natterin-like protein- like [<i>Astyanax mexicanus</i>]	34.2/9.25	10	40.30%	451.92
129	ENSPMAP000000004119	Uncharacterized protein natterin-like protein [<i>Lethenteron camtschaticum</i>]	34.4/9.38	1	2.50%	81.87
130	ENSPMAP000000000696	poly(U)-specific endoribonuclease-C- like	34.4/6.17	1	2.60%	52.60
131	ENSPMAP000000007179	Pyridoxal (pyridoxine, vitamin B6) kinase b UDP-	34.5/6.01	5	15.70%	187.65
132	ENSPMAP000000004981	Gal:betaGlcNAc beta 1,4- galactosyltransferase , polypeptide 2 Phospholipase A2, group VII (platelet- activating factor acetylhydrolase, plasma)	34.6/7.79	3	10.60%	145.13
133	ENSPMAP000000003361	2-deoxyribose-5- phosphate aldolase homolog (C. elegans)	34.6/9.14	1	4.20%	36.47
134	ENSPMAP000000010582	Uncharacterized protein natterin-like protein [<i>Lethenteron camtschaticum</i>]	34.6/10.03	1	5.00%	28.92
135	ENSPMAP000000001233	protein phosphatase 1, catalytic subunit, alpha isoform a	34.7/6.44	3	9.80%	101.27
136	ENSPMAP000000005532		34.9/6.75	1	5.60%	43.28

137	ENSPMAP000000002494	Guanine nucleotide binding protein (G protein), beta polypeptide 2-like 1	35.1/7.90	1	3.50%	37.61
138	ENSPMAP000000003520	ATP synthase, H ⁺ transporting, mitochondrial F1 complex, beta polypeptide Family with sequence similarity	35.7/4.77	4	17.00%	218.19
139	ENSPMAP000000002059	185, member A Blast protein FAM185A isoform Gamma-glutamyl hydrolase	35.7/9.62	0	0.00%	35.45
140	ENSPMAP000000007960	(conjugase, folylpolygammaglutamyl hydrolase) UEV and	36.0/9.45	1	4.30%	44.14
141	ENSPMAP000000002676	lactate/malate dehydrogenase domains	36.4/7.02	1	4.50%	50.59
142	ENSPMAP000000006408	Serine carboxypeptidase 1	36.8/5.29	1	3.30%	57.77
143	ENSPMAP000000001757	RNA methyltransferase like 1a	37.5/10.22	1	1.80%	27.92
144	ENSPMAP000000006470	BLAST cathepsin L2 precursor [Xenopus laevis]	37.6/5.89	1	3.20%	43.06
145	ENSPMAP000000006718	Calcium/calmodulin -dependent protein kinase (CaM kinase) II alpha	37.7/6.19	1	3.60%	30.62
146	ENSPMAP000000010248	aminocarboxymuconate semialdehyde decarboxylase	37.8/5.78	2	8.30%	118.84
147	ENSPMAP000000002162	BLAST serpin [Lampetra fluviatilis]	38.2/6.19	2	7.30%	82.20
148	ENSPMAP000000001895	Leucine rich repeat containing 41	38.4/11.03	1	2.90%	37.09
149	ENSPMAP000000007456	Tubulin, alpha 7 like	38.9/5.51	2	6.60%	63.38

BLAST						
PREDICTED: D-						
beta-						
150	ENSPMAP00000004300	hydroxybutyrate dehydrogenase, mitochondrial-like	38.9/9.62	1	2.00%	27.01
[<i>Latimeria</i>						
Guanine nucleotide binding protein (G						
151	ENSPMAP00000007243	protein), alpha transducing activity	38.9/5.12	1	3.20%	61.81
polypeptide 2						
152	ENSPMAP00000001644	Calcium binding protein 39, like 1	39.1/8.97	2	6.50%	59.88
Inter-alpha						
153	ENSPMAP00000005508	(globulin) inhibitor H5	39.1/7.84	1	3.60%	45.09
Fructose-						
154	ENSPMAP00000004397	bisphosphate aldolase	39.2/9.37	10	21.00%	375.8
155	ENSPMAP00000003735	Aminoacylase 1	39.9/5.14			
Prolyl 4-						
156	ENSPMAP00000000210	hydroxylase, alpha polypeptide I b	40.0/4.75	1	2.20%	34.81
Abhydrolase domain						
157	ENSPMAP000000010369	containing 3	40.1/7.12	1	1.40%	27.34
ATP synthase, H+						
transporting,						
158	ENSPMAP00000006362	mitochondrial F1 complex, alpha subunit 1, cardiac muscle	40.4/9.60	3	9.90%	117.99
ATP synthase, H+						
transporting,						
159	ENSPMAP00000002549	mitochondrial F1 complex, alpha subunit 1, cardiac muscle	40.5/9.88	3	9.90%	113.68
Replication factor C						
160	ENSPMAP00000008580	(activator 1) 2	40.6/6.30	1	6.00%	31.89
G patch domain and						
161	ENSPMAP000000011255	ankyrin repeats 1	40.6/10.33	1	2.50%	25.90
PREDICTED:						
leucine-rich repeat						
162	ENSPMAP00000002471	transmembrane protein FLRT3	40.7/9.99	1	3.20%	28.28
[<i>Poecilia reticulata</i>]						
Galactose-3-O-						
163	ENSPMAP00000007858	sulfotransferase 1	41.6/9.76	1	3.40%	32.76

164	ENSPMAP000000004567	Uncharacterized protein cytoplasmic actin [<i>Lethenteron camtschaticum</i>]	41.7/5.10	5	13.30%	210.15
165	ENSPMAP000000000348	Tubulin, beta 4B class Ivb	41.7/5.62	6	21.30%	271.04
166	ENSPMAP000000011067	Uncharacterized protein cytoplasmic actin [<i>Lethenteron camtschaticum</i>]	41.8/5.19	14	38.30%	657.59
167	ENSPMAP000000004873	Uncharacterized protein type I keratin 10 [<i>Lampetra fluviatilis</i>]	42.5/4.76	3	6.50%	120.56
168	ENSPMAP000000004933	Uncharacterized protein type II keratin 2 [<i>Lampetra fluviatilis</i>]	43.9/5.06	1	3.10%	74.18
169	ENSPMAP000000007519	Uncharacterized protein PREDICTED: zinc finger BED domain- containing protein 1- like [<i>Callorhinchus mili</i>]	44.4/6.96	1	2.30%	25.05
170	ENSPMAP000000009021	Chitinase domain containing 1 Proteasome	44.8/9.95	1	2.00%	29.22
171	ENSPMAP000000006869	(prosome, macropain) 26S subunit, non- ATPase, 6	45.3/5.79	1	3.30%	30.20
172	ENSPMAP000000008862	Uncharacterized protein Protein PTHB1 [<i>Pelecopus crispus</i>]	45.4/6.68	1	2.00%	27.44
173	ENSPMAP000000010238	Thyroid hormone receptor associated protein 3b	45.7/9.81	1	1.80%	24.47
174	ENSPMAP000000002661	Uncharacterized protein type I keratin 18 [<i>Lampetra fluviatilis</i>]	45.8/5.74	1	1.70%	58.66
175	ENSPMAP000000008365	Epoxide hydrolase 2, cytoplasmic	45.8/8.79	2	8.00%	51.52
176	ENSPMAP000000007847	FERM domain containing 4Ba	45.8/9.73	1	3.00%	27.84
177	ENSPMAP000000004211	Enolase 1b, (alpha)	46.9/4.75	2	6.90%	62.76

178	ENSPMAP000000007938	Uncharacterized protein Ubc protein [<i>Rattus norvegicus</i>]	47.1/8.95	2	6.00%	64.10
179	ENSPMAP000000005835	SIL1 nucleotide exchange factor	47.5/4.92	3	9.00%	216.41
180	ENSPMAP000000006606	Echinoderm microtubule associated protein like 2	48.2/9.34	1	1.60%	25.31
181	ENSPMAP000000003032	Protein disulfide isomerase-related protein (provisional)	48.3/5.42	2	5.40%	75.62
182	ENSPMAP000000003029	N-sulfoglucosamine sulfohydrolase (sulfamidase)	48.4/5.76	1	3.10%	40.10
183	ENSPMAP000000001808	Uncharacterized protein PREDICTED: arginine-glutamic acid dipeptide repeats protein [<i>Capra hircus</i>]	48.6/9.93	1	2.10%	34.29
184	ENSPMAP000000009146	Serine/threonine kinase 25a	48.9/5.51	1	3.40%	49.34
185	ENSPMAP000000001461	Uncharacterized protein keratin type II Lfl-K 1 [<i>Lampetra fluviatilis</i>]	49.6/9.45	9	15.20%	352.61
186	ENSPMAP000000001463	Uncharacterized protein keratin type II Lfl-K 1 [<i>Lampetra fluviatilis</i>]	49.7/9.38	3	5.50%	118.52
187	ENSPMAP000000001329	Fibulin 5	49.8/5.19	1	2.40%	47.76
188	ENSPMAP000000007379	Dolichyl- diphosphooligosacch aride-protein glycosyltransferase	49.9/5.50	1	2.70%	52.09
189	ENSPMAP000000000545	Chaperonin containing TCP1, subunit 7	50.0/5.34	1	2.40%	31.22
190	ENSPMAP000000011381	Eukaryotic translation elongation factor 1 alpha 2	50.2/9.68	1	2.60%	80.51
191	ENSPMAP000000001701	Uncharacterized protein rab GDP dissociation inhibitor alpha-like	52.1/5.08	1	2.00%	48.74

192	ENSPMAP00000009361	Chromosome 9 open reading frame 72 zgc:136930 keratin	52.9/6.52	1	2.30%	27.91
193	ENSPMAP00000007934	gamma3[<i>Lampetra fluviatilis</i>]	53.2/4.60	20	34.00%	1110.93
194	ENSPMAP00000000074	TNF receptor- associated factor 3 Uncharacterized protein	53.3/9.39	1	1.50%	25.62
195	ENSPMAP00000007275	PREDICTED: phosphatidylinositid e phosphatase SAC2-like [<i>Mustela nutorius furo</i>]	53.8/6.09	1	1.40%	28.34
196	ENSPMAP00000007263	Mixed lineage kinase domain-like RAB guanine nucleotide exchange factor (GEF) 1	53.9/6.95	1	2.60%	25.93
197	ENSPMAP00000005875	PREDICTED: rab5 GDP/GTP exchange factor [<i>Latimeria chalumnae</i>]	54.6/9.48	1	1.70%	24.75
198	ENSPMAP00000008152	Leucine rich repeat containing 6	54.8/5.74	0	0.00%	37.56
199	ENSPMAP00000002228	Eyes shut homolog (<i>Drosophila</i>) BLAST	54.8/10.32	0	0.00%	37.56
200	ENSPMAP00000007474	PREDICTED: spastin isoform X4 [<i>Camelus bactrianus</i>] protein disulfide	55.0/10.06	1	2.20%	24.12
201	ENSPMAP00000008501	isomerase family A, member 3 Uncharacterized protein	55.6/5.19	1	2.60%	28.66
202	ENSPMAP00000003563	PREDICTED: collagen alpha-3(VI) chain [<i>Tarsius svrichta</i>]	57.2/10.36	7	16.60%	461.37
203	ENSPMAP00000003743	Catalase BLAST	57.2/6.55	1	2.80%	24.63
204	ENSPMAP00000008572	PREDICTED: putative aminopeptidase W07G4.4-like [<i>Latimeria chalumnae</i>]	57.3/5.97	3	6.30%	82.97

205	ENSPMAP000000011159	Uncharacterized protein cytochrome P450, family 2, subfamily AA, polypeptide 12 [<i>Danio rerio</i>]	57.6/6.63	1	1.40%	32.32
206	ENSPMAP000000010058	Uncharacterized protein type II keratin 2 [<i>Lampetra fluviatilis</i>]	57.8/8.64	8	11.00%	336.14
207	ENSPMAP000000001210	Uncharacterized protein Leucine-rich repeats and immunoglobulin- like domains protein	58.3/9.97	2	2.60%	35.78
208	ENSPMAP000000010787	3. partial zgc:136930 keratin gamma 2 [<i>Lampetra fluviatilis</i>]	58.4/4.68	9	18.10%	491.83
209	ENSPMAP000000001207	Uncharacterized protein zinc finger and BTB domain- containing protein 39 [<i>Chrysochloris asiatica</i>]	58.4/6.03	2	3.00%	42.85
210	ENSPMAP000000000233	Pyruvate kinase, muscle, b Chaperonin	58.6/5.88	1	2.40%	32.76
211	ENSPMAP000000004078	containing TCP1, subunit 4 (delta) Zgc:136930 keratin	58.8/9.14	1	2.40%	53.11
212	ENSPMAP000000002685	gamma [<i>Lampetra fluviatilis</i>]	59.1/5.13	9	18.00%	526.10
213	ENSPMAP000000004386	Poly(A)-specific ribonuclease (deadenylation nuclease)	59.2/5.90	1	1.50%	28.90
214	ENSPMAP000000009730	Golgin A4	59.4/5.43	1	1.20%	47.83
215	ENSPMAP000000006100	Katanin p60 subunit A-like 2 NOP56	60.0/8.57	1	1.50%	24.48
216	ENSPMAP000000003566	ribonucleoprotein homolog MCM5 minichromosome maintenance	60.5/9.94	1	1.50%	26.15
217	ENSPMAP000000002357	deficient 5 (S. <i>cerevisiae</i>) DNA replication licensing factor	60.9/9.81	0	0.00%	36.69

218	ENSPMAP000000002526	CDC-like kinase 2b wu:fb15e04 keratin	61.0/9.90	0	0.00%	33.57
219	ENSPMAP000000002817	alpha [<i>Lampetra fluviatilis</i>] Cell division cycle 6	61.8/5.46	15	23.90%	697.75
220	ENSPMAP000000009602	homolog (S. <i>cerevisiae</i>)	62.5/10.74	1	1.70%	24.97
221	ENSPMAP000000004917	Vasorin b Uncharacterized protein PREDICTED: receptor-type	63.3/8.77	1	1.10%	29.72
222	ENSPMAP000000002725	tyrosine-protein phosphatase mu, partial [<i>Balearica regulorum aihericens</i>] tumor necrosis	63.7/6.97	1	1.20%	30.27
223	ENSPMAP000000008795	factor receptor superfamily, member 21 POC1 centriolar	65.7/10.04	1	1.80%	25.14
224	ENSPMAP000000008691	protein homolog B (<i>Chlamydomonas</i>), like	67.0/6.33	1	1.90%	37.09
225	ENSPMAP000000004130	syntaxin binding protein 1a	67.3/8.43	1	1.20%	29.83
226	ENSPMAP000000000659	Formin-like 3 Moesin	67.4/5.92	1	1.20%	32.31
227	ENSPMAP000000008006	b(membrane- organizing extension spike protein)	68.6/6.37	1	1.50%	43.62
228	ENSPMAP000000009479	Immunoglobulin mu binding protein 2 Echinoderm	70.4/7.29	1	1.40%	24.80
229	ENSPMAP000000001624	microtubule associated protein like 2	70.6/5.29	1	1.50%	27.90
230	ENSPMAP000000000670	chromosome 10 open reading frame Transcription	71.0/9.87	1	0.90%	31.04
231	ENSPMAP000000001070	elongation regulator 1a (CA150) intraflagellar	71.2/9.41	1	1.50%	32.36
232	ENSPMAP000000003688	transport protein 172 homolog, partial	72.0/5.81	1	1.60%	24.64
233	ENSPMAP000000005081	Heat shock protein 5	72.7/4.91	2	3.90%	86.87

234	ENSPMAP00000007015	ATP-binding cassette, sub-family G (WHITE), member 2d	73.9/9.81	1	1.50%	39.00
235	ENSPMAP00000005970	Bardet-Biedl syndrome 2	79.1/5.71	1	1.50%	26.69
236	ENSPMAP00000009078	Sperm antigen with calponin homology and coiled-coil domains 1-like a	79.9/4.64	1	0.80%	28.94
237	ENSPMAP00000009994	transferrin-a	80.3/9.47	2	3.10%	55.11
238	ENSPMAP00000003384	Heat shock protein 90, alpha (cytosolic), class A member 1, tandem duplicate 1	80.9/4.86	3	5.40%	95.52
239	ENSPMAP00000003753	Uncharacterized protein PREDICTED: collagen alpha-1(XXII) chain isoform X3 [<i>Xenopus (Silurana) tronicalis</i>]	81.2/9.55	1	1.30%	26.34
240	ENSPMAP00000003104	cysteine and glycine-rich protein 2	83.5/7.94	1	0.80%	43.41
241	ENSPMAP00000008238	binding protein Exocyst complex component 8	84.2/8.41	1	1.00%	29.45
242	ENSPMAP00000008526	Catenin (cadherin-associated protein), beta 1, 88kDa	85.2/5.44	1	1.50%	38.10
243	ENSPMAP00000008329	Cyclin M2a Blast PREDICTED: metal transporter CNNM2 [<i>Latimeria chalumnae</i>]	85.5/6.20	1	0.80%	26.84
244	ENSPMAP00000004431	SUN domain containing ossification factor dystonin-like, partial [<i>Felis catus</i>](anchoring	86.0/4.96	1	0.60%	40.18
245	ENSPMAP00000006477	neural intermediate filaments to the actin	86.7/9.39	1	1.30%	38.68
246	ENSPMAP00000001105	cytoskeleton) SLIT and NTRK-like family, member	87.8/6.08	1	1.00%	27.37

247	ENSPMAP00000003404	DEAD (Asp-Glu-Ala-Asp) box polypeptide 27	88.9/9.88	1	1.30%	25.30
248	ENSPMAP00000001240	Heat shock protein 90, beta (grp94), member 1	89.3/4.60	2	2.90%	95.37
249	ENSPMAP00000005404	Protein phosphatase 1, regulatory subunit 9A	90.8/4.69	1	1.20%	27.57
250	ENSPMAP000000010708	Tubulin, gamma complex associated protein 5	92.6/10.45	0	0.00%	35.33
251	ENSPMAP00000005505	Threonyl-tRNA synthetase	93.1/9.14	1	1.00%	26.67
252	ENSPMAP000000001332	N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 2a	93.7/9.84	1	0.60%	47.81
253	ENSPMAP000000004863	Helicase, POLQ-like Eukaryotic	94.2/9.23	1	1.30%	25.32
254	ENSPMAP000000001330	translation elongation factor 2, like 2	95.4/6.35	2	2.90%	121.92
255	ENSPMAP000000010154	Oxoglutarate (alpha-ketoglutarate) dehydrogenase a (lipoamide)	96.4/8.51	1	0.60%	27.14
256	ENSPMAP000000007886	Karyopherin (importin) beta 1	97.4/4.51	1	1.70%	33.54
257	ENSPMAP000000002931	prominin 1 b (CD133)	97.7/7.75	1	1.50%	58.95
258	ENSPMAP000000006065	bicaudal C homolog 1a (<i>Drosophila</i>)	100.0/10.14	1	1.10%	30.20
259	ENSPMAP000000000662	inositol polyphosphate-4-phosphatase, type Ia	102.9/9.73	1	1.00%	44.65
260	ENSPMAP000000009480	Myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, <i>Drosophila</i>)	108.7/9.72	1	0.60%	24.58
261	ENSPMAP000000000904	Dishevelled associated activator of morphogenesis 2	109.3/9.52	1	0.80%	38.67
262	ENSPMAP000000000475	Smg-5 homolog, nonsense mediated mRNA decay factor (<i>C. elegans</i>)	114.1/5.50	2	0.90%	34.29
263	ENSPMAP000000004255	Tumor protein p53 binding protein, 2	115.3/9.89	1	0.60%	33.24

		Uncharacterized protein				
264	ENSPMAP000000009524	PREDICTED: protocadherin Fat 1- like, partial	115.8/5.49	1	1.40%	23.55
265	ENSPMAP000000004604	[<i>Pelecanus crispus</i>] RAD50 homolog (<i>S. cerevisiae</i>)	120.2/6.35	2	1.70%	31.76
266	ENSPMAP000000001007	Myosin, heavy chain 10, non-muscle	120.3/6.36	1	1.50%	29.64
267	ENSPMAP000000001305	5-oxoprolinase (ATP-hydrolysing)	127.4/6.01	1	0.60%	32.62
268	ENSPMAP000000006009	Protein tyrosine phosphatase, non- receptor type 21	127.7/9.00	1	0.50%	26.64
269	ENSPMAP000000008605	Uncharacterized protein AF4/FMR2 family member 2 isoform X2	130.5/10.03	0	0.00%	33.25
		[<i>Callorhinchus mili</i>]				
270	ENSPMAP000000003639	non-SMC condensin II complex, subunit G2	131.6/6.39	1	0.90%	26.76
271	ENSPMAP000000005601	Ubiquitin- conjugating enzyme E2O	133.0/5.30	1	0.70%	28.35
272	ENSPMAP000000008534	DNA-directed RNA polymerase	133.3/8.86	1	0.80%	26.10
273	ENSPMAP000000007731	Adenylate cyclase 9	135.7/8.97	1	1.30%	24.81
		Uncharacterized protein				
274	ENSPMAP000000006147	PREDICTED: interferon-induced very large GTPase 1-like isoform X2	137.1/6.13	0	0.00%	36.17
275	ENSPMAP000000007534	Dmx-like 2	140.6/6.19	1	1.10%	27.44
276	ENSPMAP000000001026	Polybromo 1, like Serine/threonine	142.8/7.02	1	0.60%	24.10
277	ENSPMAP000000005602	kinase 36 (fused homolog, <i>Drosophila</i>)	144.9/5.74	2	1.40%	40.45
		Structural				
278	ENSPMAP000000008570	maintenance of chromosomes 4	147.0/6.41	1	0.50%	46.03

		TBC1 domain family, member 32 BLAST				
279	ENSPMAP000000008843	PREDICTED: protein broad- minded-like isoform X1 [<i>Latimeria chalumnae</i>] protein phosphatase	147.1/6.26	0	0.00%	33.71
280	ENSPMAP000000004719	Slingshot homolog 2 isoform 1	150.7/5.91	1	0.90%	27.01
281	ENSPMAP000000000569	Golgi autoantigen, golgin subfamily a, Rho-associated,	153.3/5.31	0	0.00%	32.00
282	ENSPMAP000000004576	coiled-coil containing protein kinase 1 ATP-binding	157.1/5.78	0	0.00%	34.57
283	ENSPMAP000000000990	cassette, sub-family C (CFTR/MRP), member 3 Uncharacterized protein	166.3/7.16	1	0.30%	26.29
284	ENSPMAP000000009592	PREDICTED: collagen alpha-3(VI) chain isoform X3 [<i>Chrysemys picta bellii</i>]	168.3/10.12	13	9.20%	734.76
285	ENSPMAP000000002751	Dual oxidase	171.9/8.69	1	0.40%	25.18
286	ENSPMAP000000008992	Tudor domain containing 6	180.5/5.66	1	0.50%	25.35
287	ENSPMAP000000010336	SET binding factor 2 Uncharacterized protein	181.9/9.68	1	0.30%	40.45
288	ENSPMAP000000010244	PREDICTED: ras GTPase-activating- like protein IQGAP1 isoform X1 [<i>Chrysemys picta bellii</i>] Eukaryotic	187.1/5.08	1	0.40%	24.1
289	ENSPMAP000000007704	translation initiation factor 2 alpha kinase 4	189.2/6.12	1	0.50%	27.16
290	ENSPMAP000000002280	Sodium channel protein	189.3/9.87	1	0.50%	25.55
291	ENSPMAP000000001826	C-type lectin domain family 19, member	192.5/4.13	4	1.60%	130.76

292	ENSPMAP000000001591	Rho GTPase activating protein 23b Uncharacterized protein PREDICTED: nuclear pore complex protein Nup98-Nup96 isoform X2 [<i>Oryctolagus cuniculus</i>]	193.1/32.36	1	0.30%	32.36
293	ENSPMAP000000002335	Calcineurin binding protein 1	198.5/5.82	1	0.50%	30.97
294	ENSPMAP000000008791	Periaxin	205.6/8.99	0	0.00%	34.23
295	ENSPMAP000000001899	rotatin	211.9/5.07	3	1.80%	133.98
296	ENSPMAP000000007161	Tectorin alpha	212.2/8.66	1	0.30%	27.53
297	ENSPMAP000000003251	Uncharacterized protein PREDICTED: interferon-induced very large GTPase 1-like [<i>Chrysemys picta bellii</i>]	218.3/5.27	2	1.00%	88.13
298	ENSPMAP000000009803	Neuron navigator 2b RANBP2-like and GRIP domain containing 2	235.2/6.33	1	0.20%	36.93
299	ENSPMAP000000000553	Dynein, cytoplasmic 2, heavy chain 1 Uncharacterized protein PREDICTED: nebulin [<i>Struthio camelus australis</i>]	250.6/9.98	1	0.40%	50.74
300	ENSPMAP000000007926	Uncharacterized protein PREDICTED: plectin-like isoform X2 [<i>Lepisosteus oculatus</i>]	268.7/5.67	1	0.30%	28.39
301	ENSPMAP000000000599	novel transcript LOW QUALITY PROTEIN: ryanodine receptor 2, partial [<i>Latimeria chalumnae</i>]	279.7/6.44	1	0.30%	25.16
302	ENSPMAP000000009365	HYDIN, axonemal central pair apparatus protein	335.9/9.87	1	0.30%	24.99
303	ENSPMAP000000010203		336.4/5.53	1	0.30%	25.59
304	ENSPMAP000000010556		439.6/5.96	1	0.30%	24.62
305	ENSPMAP000000001794		571.0/6.28	2	0.20%	38.93

306	ENSPMAP00000002451	titin	2097.2/6.89	1	0.00%	33.81
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NCBI database (feeding for 60 min)

Spot No.	NCBI ID	protein	Theoretical Mr/PI	Peptides matched	Sequence covered(%)	Score
1	gi 127525	RecName: Full=Major outer membrane lipoprotein; AltName: Full=Murein-lipoprotein; Flags: Precursor	8.2/9.76	2	33.80%	94.24
2	gi 158767	ubiquitin, partial [<i>Drosophila melanogaster</i>]	8.5/7.58	2	32.90%	67.86
3	gi 16974825	Chain A, Solution Structure Of Calcium-Calmodulin N-Terminal Domain	8.5/3.84	2	39.50%	99
4	gi 3201828	major outer membrane lipoprotein I [<i>Pseudomonas oleovorans</i>]	8.8/9.30	1	12.00%	72.35
5	gi 535709	HU protein [<i>Pseudomonas aeruginosa</i>]	9.0/10.15	2	32.60%	74.04
6	gi 157368539	transcriptional regulator HU subunit alpha [<i>Serratia proteamaculans</i> 568]	9.6/10.10	3	47.80%	154.45
7	gi 511116	G-protein beta subunit [<i>Mus musculus</i>]	13.5/5.37	2	17.10%	93.39
8	gi 220950	lysozyme [synthetic construct]	14.8/10.52	1	6.90%	62.20
9	gi 3891470	Chain A, Crystal Structure Of Human Galectin-7 In Complex With Galactosamine	14.9/7.93	1	11.90%	56.04
10	gi 229751	Chain A, Structure Of Haemoglobin In The Deoxy Quaternary State With Ligand Bound At The Alpha Haems	15.1/9.50	4	31.20%	176.07
11	gi 122298	RecName: Full=Hemoglobin subunit alpha-3; AltName: Full=Alpha-3-globin; AltName: Full=Hemoglobin alpha-2 chain	15.2/10.27	2	14.20%	74.86
12	gi 9909951	ATP synthase beta subunit [<i>Rhizobium leguminosarum</i>]	15.6/6.72	1	8.80%	63.61
13	gi 4929993	Chain A, Module-Substituted Chimera Hemoglobin Beta-Alpha (F133v)	15.8/8.00	6	44.50%	254.12
14	gi 122629	RecName: Full=Hemoglobin subunit beta; AltName: Full=Beta-globin; AltName: Full=Hemoglobin beta chain	15.9/9.10	2	15.80%	112.93
15	gi 229149	hemoglobin beta	15.9/5.14	4	35.60%	103.76
16	gi 122634	RecName: Full=Hemoglobin subunit beta; AltName: Full=Beta-globin; AltName: Full=Hemoglobin beta chain	16.0/6.91	2	15.80%	95.58

17	gi 13241083	hemoglobin beta chain [<i>Silurus asotus</i>]	16.1/9.11	3	20.40%	139.66
18	gi 30750169	Chain A, Crystal Structure Of Hemoglobin From River Lamprey	16.3/9.15	5	51.00%	355.01
19	gi 157835321	Chain A, Refinement Of A Molecular Model For Lamprey Hemoglobin From Petromyzon Marinus	16.3/5.62	6	44.00%	280.07
20	gi 126143345	hemoglobin 2 [<i>Lethenteron camtschaticum</i>]	16.5/8.97	9	59.30%	425.11
21	gi 110825990	RecName: Full=Globin-1; AltName: Full=Globin I	16.5/9.37	8	59.30%	427.41
22	gi 320167770	calmodulin [<i>Capsaspora owczarzaki</i> ATCC 30864]	16.9/4.01	2	19.50%	101.51
23	gi 320583470	Nucleoside diphosphate kinase [<i>Ogataea parapolymorpha</i> DL-1]	17.1/8.98	2	17.20%	81.38
24	gi 4127588	sodium chloride cotransporter [<i>Bos taurus</i>]	17.2/10.85	1	6.80%	60.41
25	gi 188572482	putative 40S ribosomal protein RPS18 [<i>Phoronis muelleri</i>]	17.7/11.25	2	12.50%	89.81
26	gi 14719272	15 kDa cytosolic selenoprotein [<i>Rattus norvegicus</i>]	17.8/5.15	2	13.60%	75.58
27	gi 126143347	hemoglobin 4 [<i>Lethenteron camtschaticum</i>]	18.0/4.82	7	45.90%	312.12
28	gi 158451345	putative dopa decarboxylase protein [<i>Apha aequalis</i>]	18.2/9.64	2	9.20%	71.72
29	gi 152969309	peptidoglycan-associated outer membrane lipoprotein [<i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i> MGH 78578]	18.9/6.37	3	20.07%	99.41
30	gi 16517086	voltage-dependent anion channel [<i>Gillichthys mirabilis</i>]	19.0/9.23	1	5.60%	62.73
31	gi 198424347	PREDICTED: similar to nucleoside diphosphate kinase [<i>Ciona intestinalis</i>]	19.3/9.69	1	6.70%	90.04
32	gi 221126247	PREDICTED: similar to ADP-Ribosylation Factor related family member (arf-3) [<i>Hydra magnipapillata</i>]	20.2/6.18	4	24.00%	147.96
33	gi 156322163	hypothetical protein NEMVEDRAFT_v1g225293 [<i>Nematostella vectensis</i>]	20.2/11.56	8	38.30%	387.84
34	gi 391344825	PREDICTED: ADP-ribosylation factor 4-like [<i>Metaseiulus occidentalis</i>]	20.4/5.44	5	26.00%	211.64
35	gi 114056	RecName: Full=Blood plasma apolipoprotein LAL2; Flags: Precursor	20.5/5.98	4	2300.00%	167.31

36	gi 1065361	Chain A, Human Adp- Ribosylation Factor 1 Complexed With Gdp, Full Length Non-Myristoylated	20.6/6.39	2	13.90%	105.54
37	gi 595280	Rap1b [<i>Rattus norvegicus</i>]	20.9/5.22	2	14.10%	131.74
38	gi 188497677	ras-related protein Rap-1A [<i>Taeniopygia guttata</i>]	21.0/5.57	3	13.60%	102.56
39	gi 194772468	GF20391 [<i>Drosophila ananassae</i>]	21.2/11.08	13	45.80%	539.87
40	gi 28630356	ribosomal protein L18 [<i>Petromyzon marinus</i>]	21.5/12.32	2	21.80%	190.52
41	gi 260944114	peroxiredoxin TSA1 [<i>Clavisporea lusitaniae</i> ATCC 42720]	21.6/5.03	2	12.80%	93.84
42	gi 33863962	TPR repeat-containing protein [<i>Prochlorococcus marinus</i> str. MIT 9313]	21.8/5.38	1	3.90%	56.28
43	gi 293392580	alkyl hydroperoxide reductase [<i>Serratia odorifera</i> DSM 4582]	22.1/5.47	2	13.00%	82.22
44	gi 332264562	PREDICTED: 40S ribosomal protein S9-like [<i>Nomascus leucogenys</i>]	22.4/10.94	1	4.60%	61.57
45	gi 5146	YPT1-related protein [<i>Schizosaccharomyces pombe</i>]	23.1/5.88	2	9.20%	73.58
46	gi 2500360	RecName: Full=60S ribosomal protein L14	23.3/11.82	1	5.60%	86.03
47	gi 156555012	PREDICTED: ras-related protein Rab-2-like [<i>Nasonia vitripennis</i>]	23.5/5.97	1	6.50%	129.48
48	gi 3318722	Chain E, Leech-Derived Trypsin Inhibitor TRYPSIN COMPLEX	23.5/9.53	3	8.10%	130.02
49	gi 218296871	Nicotinate-nucleotide-- dimethylbenzimidazole phosphoribosyltransferase [<i>Thermus aquaticus</i> Y51MC23]	23.8/10.42	1	4.40%	56.69
50	gi 218461704	LysR family transcriptional regulator [<i>Rhizobium etli</i> Kim 5]	24.0/9.42	1	4.60%	62.95
51	gi 225632	casein alphaS1	24.4/4.70	3	15.40%	100.52
52	gi 136429	RecName: Full=Trypsin; Flags: Precursor	24.4/7.71	2	7.80%	96.89
53	gi 2055301	proteasome subunit Y [<i>Lethenteron camtschaticum</i>]	24.9/5.80	2	10.80%	108.46
54	gi 52345832	glutathione S-transferase mu 1 [<i>Xenopus (Silurana) tropicalis</i>]	25.2/6.40	2	11.10%	67.92

55	gi 126310937	PREDICTED: glutathione S-transferase Yb-3-like isoform 1 [<i>Monodelphis domestica</i>]	25.6/5.97	1	4.60%	57.64
56	gi 530049	14-3-3 protein, partial [<i>Ovis aries</i>]	26.3/4.65	2	9.50%	171.26
57	gi 145046200	cysteine-rich secretory protein-buccal gland secretion [<i>Lethenteron camtschaticum</i>]	28.0/6.50	7	26.80%	273.53
58	gi 391340828	PREDICTED: uncharacterized protein LOC100900270 [<i>Metaseiulus occidentalis</i>]	28.1/11.38	4	13.80%	172.94
59	gi 148260723	short-chain dehydrogenase/reductase SDR [<i>Acidiphilium cryptum</i> JF-5]	28.2/10.69	2	4.50%	70.35
60	gi 118403700	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, gamma polypeptide [<i>Xenopus (Silurana) tropicalis</i>]	28.2/4.65	1	5.70%	102.83
61	gi 1197463	14-3-3 [Dictyostelium discoideum]	28.7/4.67	1	7.50%	83.31
62	gi 157128413	14-3-3 protein sigma, gamma, zeta, beta/alpha [<i>Aedes aegypti</i>]	29.4/4.59	2	12.00%	142.98
63	gi 345561222	hypothetical protein AOL_s00193g46 [<i>Arthrobotrys oligospora</i>]	29.4/4.66	0	0.00%	62.08
64	gi 1405323	LMPX of lamprey [<i>Petromyzon marinus</i>]	30.0/5.99	2	8.40%	63.78
65	gi 87303693	possible ATP adenyltransferase [<i>Synechococcus</i> sp. WH 5701]	30.8/9.90	1	2.90%	63.13
66	gi 118099442	PREDICTED: erythrocyte band 7 integral membrane protein [<i>Gallus gallus</i>]	30.8/7.63	2	13.90%	84.3
67	gi 307109985	hypothetical protein CHLNCDRAFT_142100 [<i>Chlorella variabilis</i>]	31.5/9.51	2	3.70%	65.07
68	gi 146386352	cathepsin D [<i>Oryctolagus cuniculus</i>]	31.7/6.64	2	6.50%	62.29
69	gi 239937499	adenine nucleotide translocator s254 [<i>Takifugu rubripes</i>]	33.1/10.29	3	13.00%	132.95
70	gi 313200575	hypothetical protein MPQ_0825 [<i>Methylovorus</i> sp.]	33.3/10.35	1	3.10%	55.42
71	gi 374368554	ABC transporter substrate-binding protein [<i>Cupriavidus basilensis</i> OR 16]	33.7/9.52	1	2.50%	59.73

72	gi 291238366	PREDICTED: sulfotransferase family 1B, member 1-like [<i>Saccoglossus kowalevskii</i>]	35.4/6.36	1	3.60%	60.34
73	gi 270262170	glyceraldehyde-3-phosphate dehydrogenase [<i>Serratia odorifera</i> 4Rx13]	35.5/7.80	2	6.90%	143.3
74	gi 163113	guanine nucleotide-binding regulatory protein-beta-2 subunit, partial [<i>Bos taurus</i>]	35.6/6.06	2	6.10%	117.85
75	gi 147899037	malate dehydrogenase 2, NAD (mitochondrial) [<i>Xenopus laevis</i>]	35.8/9.52	2	7.10%	97.96
76	gi 25989185	glyceraldehyde 3-phosphate dehydrogenase [<i>Gadus morhua</i>]	36.1/8.73	4	18.30%	200.05
77	gi 29242787	cytosolic malate dehydrogenase [<i>Acipenser brevirostrum</i>]	36.2/7.72	3	6.90%	93.08
78	gi 13936898	glyceraldehyde phosphate dehydrogenase [<i>Oncorhynchus mykiss</i>]	36.3/7.91	4	17.70%	176.51
79	gi 462494	RecName: Full=L-lactate dehydrogenase; Short=LDH fructose-1,6-bisphosphate	36.4/7.02	3	11.70%	194.4
80	gi 387970584	aldolase [<i>Pseudomonas stutzeri</i> TS44]	38.4/5.22	1	2.30%	70.26
81	gi 1703239	RecName: Full=Fructose-bisphosphate aldolase, muscle type	39.2/9.49	10	22.60%	449.89
82	gi 120972532	alpha enolase [<i>Priapulus caudatus</i>]	39.7/5.73	2	8.70%	76.1
83	gi 2143483	hypothetical calcium-binding protein - mouse	39.8/6.83	3	9.10%	130.46
84	gi 120407311	SPARCB [<i>Petromyzon marinus</i>]	39.9/4.25	2	7.10%	56.97
85	gi 113213	RecName: Full=Actin-1	41.6/5.27	1	2.70%	61.7
86	gi 113273	RecName: Full=Actin, cytoplasmic; Flags: Precursor	41.8/5.19	10	29.50%	418.44
87	gi 374314355	tuf1 gene product [<i>Serratia symbiotica</i> str. 'Cinara cedri']	43.3/5.30	2	7.60%	103.14
88	gi 251772958	putative methyl-accepting chemotaxis protein [<i>Leptospirillum ferrodiazotrophum</i>]	43.5/5.58	2	3.70%	58.03
89	gi 395830813	PREDICTED: serpin B4 [<i>Otolemur garnettii</i>]	44.6/6.55	2	4.10%	88.77
90	gi 488838	CaBP1 [<i>Rattus norvegicus</i>]	47.2/4.80	1	3.20%	76.4
91	gi 167534702	hypothetical protein [<i>Monosiga brevicollis</i> MX1]	47.6/4.77	1	2.10%	62.07
92	gi 402501996	putative two-component sensor [<i>Rhodovulum</i> sp. PH10]	51.4/9.28	2	3.70%	61.8

93	gi 238053993	aromatic-L-amino-acid decarboxylase [<i>Oryzias latipes</i>]	54.2/6.73	2	4.80%	103.54
94	gi 402078132	hypothetical protein GGTG_10319 [<i>Gaeumannomyces graminis</i> <i>var. tritici</i> R3-111a-1]	54.5/5.28	1	2.30%	59.61
95	gi 313681747	pyruvate kinase [<i>Sulfuricurvum</i> <i>kujense</i> DSM 16994]	55.0/5.49	1	2.00%	65.39
96	gi 47575824	mitochondrial ATP synthase beta subunit [<i>Xenopus</i> (<i>Silurana</i>) <i>tropicalis</i>]	56.2/5.27	5	12.80%	264.92
97	gi 318067305	secretory M20A dipeptidase [<i>Lethenteron reissneri</i>]	57.7/5.36	11	19.50%	449.39
98	gi 14009437	mitochondrial ATP synthase alpha-subunit [<i>Cyprinus</i> <i>carpio</i>]	59.5/9.82	7	15.80%	268.46
99	gi 125550515	hypothetical protein OsI_18115 [<i>Oryza sativa Indica</i> Group]	60.4/5.82	1	1.10%	60.06
100	gi 66563290	PREDICTED: t-complex protein 1 subunit gamma [<i>Apis</i> <i>mellifera</i>]	61.0/6.17	1	2.00%	58.77
101	gi 227538423	signal transduction histidine kinase [<i>Sphingobacterium</i> <i>spiritivorum</i> ATCC 33300]	61.2/4.87	1	1.70%	64.99
102	gi 83592964	hypothetical protein Rru_A1629 [<i>Rhodospirillum</i> <i>rubrum</i> ATCC 11170]	64.8/4.93	1	1.40%	59.13
103	gi 229552	albumin	66.1/5.71	2	4.80%	86.19
104	gi 2492797	RecName: Full=Serum albumin; Flags: Precursor	67.8/5.81	2	4.20%	83.27
105	gi 240142573	hypothetical protein MexAM1_META2p0946 [<i>Methylobacterium extorquens</i> AM1]	68.8/9.68	2	2.10%	71.6
106	gi 71987784	Protein GLY-6, isoform a [<i>Caenorhabditis elegans</i>]	71.1/9.60	1	1.80%	66.69
107	gi 113931558	ATP-binding cassette, sub- family G (WHITE), member 2 [<i>Xenopus (Silurana) tropicalis</i>]	73.5/9.64	2	3.30%	72.59
108	gi 76818381	hypothetical protein [<i>Burkholderia pseudomallei</i> 1710b]	76.1/12.39	1	1.00%	59.45
109	gi 295660730	conserved hypothetical protein [<i>Paracoccidioides sp.</i> 'lutzii' Pb01]	90.6/6.60	2	2.90%	67.22
110	gi 262195396	serine/threonine protein kinase [<i>Haliangium ochraceum</i> DSM 14365]	105.6/7.00	0	0.00%	56.82

		hypothetical protein				
111	gi 145479413	[<i>Paramecium tetraurelia</i> strain d4-2]	117.3/9.67	2	0.80%	58.43
112	gi 357613203	Moesin [<i>Danaus plexippus</i>]	121.6/5.66	2	2.20%	72.55
113	gi 390461147	PREDICTED: uncharacterized protein LOC100406435 [<i>Callithrix jacchus</i>]	136.5/11.12	3	2.50%	102.75
114	gi 29378311	subtilisin-like protease [<i>Toxoplasma gondii</i>]	141.4/5.38	2	1.90%	57.04
115	gi 373493775	DNA-directed RNA polymerase, beta' subunit [<i>Eubacterium infirmum</i> F0142]	144.3/5.79	1	0.90%	58.19
116	gi 149068757	Rho guanine nucleotide exchange factor (GEF) 17 (predicted), isoform CRA_a [<i>Rattus norvegicus</i>]	154.6/7.98	1	0.70%	57.55
117	gi 339897150	putative pumilio protein 4 [<i>Leishmania infantum</i> JPCM5]	155.0/8.83	1	0.70%	62.2
118	gi 126143340	plasma albumin [<i>Lethenteron camtschaticum</i>]	156.6/6.02	46	26.60%	1977
119	gi 195173563	GL18391 [<i>Drosophila persimilis</i>]	167.2/6.36	1	0.50%	55.39
120	gi 322705180	Metarhizium anisopliae ARSEF 23	170.7/6.77	1	1.00%	67.7
121	gi 350427672	PREDICTED: ATP-dependent RNA helicase hrpA-like [<i>Bombus impatiens</i>]	170.8/9.55	1	0.50%	64.09
122	gi 164511455	putative non-ribosomal peptide synthetase [<i>Streptomyces collinus</i> Tu 365]	264.9/5.85	1	0.30%	57.04
123	gi 308487754	CRE-MEL-28 protein [<i>Caenorhabditis remanei</i>]	268.2/5.28	1	0.80%	58.09
124	gi 145355563	predicted protein [<i>Ostreococcus lucimarinus</i> CCE9901]	442.4/4.62	1	0.20%	59.74
125	gi 397517241	PREDICTED: neuroblast differentiation-associated protein AHNAK [<i>Pan paniscus</i>]	556.9/5.74	5	1.50%	198.13
