

Table S1. Spot identifications on the gels, proteins names, NCBI accession ID, predicted isoelectric point and protein molecular weight, number of peptides matched against the data base, sequence data base used, molecular weight search score (MOWSE), and percent sequence coverage of 37 proteins that were identified using mass spectrometry.

Spot ID	Protein name	Predicted PI (Isoelectric point)	Predicted MW (molecular weight-Da)	Accession ID	Species name for which the protein was identified	Peptide matches	Database searched against	MOWSE score	Sequence percent coverage (%)	Modifications*	
										Fixed	Variable
295	Mitochondrial aconitase 2	5.88	66114.5	gi 226427149	<i>Gillichthys mirabilis</i>	1	EST_ <i>G.mirabilis</i>	48	4	(C)	(K), (M)
324	Serotransferrin	6.23	42280.31	gi 93275810	<i>Gillichthys mirabilis</i>	3	EST_ <i>G.mirabilis</i>	78	26		(C), (M)
353	Succinate dehydrogenase	7.31	73230.2	gi 284648	<i>Bos taurus</i>	1	Metazoa	104	3		(C), (M)
358	Warm-temperature acclimated protein 65-1 ^a	5.45	49095.47	gi 93276381	<i>Gillichthys mirabilis</i>	3	EST_ <i>G.mirabilis</i>	172	24	(C)	(K), (M)
388	Pyruvate kinase	5.97	57436.05	gi 224587654	<i>Salmo salar</i>	2	Metazoa	134	8	(C)	(K), (M)
404	Alpha tubulin ^a	5.23	30722.37	gi 93272711	<i>Gillichthys mirabilis</i>	3	EST_ <i>G.mirabilis</i>	133	17	(C)	(K), (M)
419	ATP synthase alpha subunit ^a	9.18	39510.91	gi 93272711	<i>Gillichthys mirabilis</i>	2	EST_ <i>G.mirabilis</i>	35	10	(C)	(K), (M)
446	ATP synthase beta subunit	5.09	53935.33	gi 226441959	<i>Gillichthys mirabilis</i>	3	EST_ <i>G.mirabilis</i>	194	20	(C)	(K), (M)
448	Hexa protein	5.37	52985.21	gi 126631876	<i>Danio rerio</i>	2	Metazoa	34	5	(C)	(K), (M)
455	Enolase ^a	6.7	51223.21	gi 93272692	<i>Gillichthys mirabilis</i>	3	EST_ <i>G.mirabilis</i>	64	12	(C)	(K), (M)
456	Ezrin/Moesin	5.73	67804.68	gi 348537470	<i>Oreochromis niloticus</i>	2	Metazoa	97	6	(C)	(K), (M)
472	Isocitrate dehydrogenase	7.12	50456.56	gi 225705994	<i>Osmerus mordax</i>	1	EST_ <i>G.mirabilis</i>	142	7	(C)	(K), (M)
486	Structure of actin bound WH-2 domains	5.1	40018.97	gi 297343122	<i>Oryctolagus cuniculus</i>	2	Metazoa	296	20	(C)	(K), (M)
498	Creatine Kinase B type	5.39	42693.03	gi 213513714	<i>Salmo salar</i>	3	Metazoa	149	14	(C)	(K), (M)
500	Structure of actin bound WH-2 domains (also Alpha cardiac actin matched with <i>Danio rerio</i>)	5.1	40018.97	gi 297343122	<i>Oryctolagus cuniculus</i>	2	Metazoa	290	20	(C)	(K), (M)
510	Fructose bisphosphate aldolase A ^a	8.26	39682.17	gi 93273258	<i>Gillichthys mirabilis</i>	3	EST_ <i>G.mirabilis</i>	139	19		(K), (C), (M)
512	Fructose bisphosphate aldolase C ^a	7.15	42997.74	gi 93273448	<i>Gillichthys mirabilis</i>	2	EST_ <i>G.mirabilis</i>	52	6	(C)	(K), (M)
520	Fructose-bisphosphate aldolase A	7.32	42983.06	gi 189039878	<i>Gillichthys mirabilis</i>	2	EST_ <i>G.mirabilis</i>	128	11	(C)	(K), (M)
528	Glyceraldehyde-3-phosphate dehydrogenase	7	21271.11	gi 93272727	<i>Gillichthys mirabilis</i>	1	EST_ <i>G.mirabilis</i>	89	9		(K), (C), (M)
531	Alpha Actin	5.47	41865.32	gi 5751	<i>Bombix mori</i>	2	Metazoa	132	9	(C)	(K), (M)

538	glyceraldehyde 3-phosphate dehydrogenase	7.24	33670.31	gi 93272727	<i>Gillichthys mirabilis</i>	1	EST_ <i>G.mirabilis</i>	66	6		(K), (C), (M)
548	L-lactate dehydrogenase A chain ^a	8.1	36374.78	gi 93274906	<i>Gillichthys mirabilis</i>	1	EST_ <i>G.mirabilis</i>	48	14		(K), (C), (M)
552	Keratin-like type 1	4.94	35515.12	gi 224796285	<i>Sparus aurata</i>	1	Metazoa	114	8	(C)	(K), (M)
569	Malate dehydrogenase ^a	5.49	42888.36	gi 93277532	<i>Gillichthys mirabilis</i>	2	EST_ <i>G.mirabilis</i>	65	39		(K), (C), (M)
571	Actin A3	5.47	41865.32	gi 5751	<i>Bombix mori</i>	3	Metazoa	326	20	(C)	(K), (M)
573	Alpha actin (cardiac isoform) ^a	5.26	37157.5	gi 93277509	<i>Gillichthys mirabilis</i>	2	EST_ <i>G.mirabilis</i>	78	7	(C)	(K), (M)
605	Voltage dependent anion channel	8.65	30253.27	gi 111146880	<i>Paralichthys olivaceus</i>	1	Metazoa	87	6	(C)	(K), (M)
614	Voltage-dependent anion-selective channel protein 2	8.44	30283.2	gi 209156096	<i>Salmo salar</i>	2	Metazoa	54	3	(C)	(K), (M)
619	Cathepsin B	5.69	36244.16	gi 226821413	<i>Lutjanus argentimaculatus</i>	1	Metazoa	85	10	(C)	(K), (M)
620	Hydroxyacyl-coenzyme A dehydrogenase	8.26	33170.34	gi 348529544	<i>Oreochromis niloticus</i>	1	Metazoa	61	4	(C)	(K), (M)
623	Cathepsin B	5.04	38015.11	gi 298392281	<i>Ovis aries</i>	1	Metazoa	49	2		(C), (M)
636	Phosphoglycerate mutase 2	8.82	28805.98	gi 41056123	<i>Danio rerio</i>	2	Metazoa	76	8	(C)	(K), (M)
641	Proteasome beta-3 subunit	5.02	23005.41	gi 56541012	<i>Xenopus laevis</i>	1	Metazoa	80	11		
677	Adenylate kinase	6.2	21335.12	gi 47218682	<i>Tetraodon nigroviridis</i>	1	Metazoa	101	17	(C)	(K), (M)
3277	Glyceraldehyde-3-phosphate dehydrogenase	7	21217.11	gi 93272727	<i>Gillichthys mirabilis</i>	1	EST_ <i>G.mirabilis</i>	40	6		(K), (C), (M)
8770	Selenium binding protein ^a	5.42	52893.24	gi 93275515	<i>Gillichthys mirabilis</i>	1	EST_ <i>G.mirabilis</i>	42	13		(K), (C), (M)
10195	Thioredoxin-dependent peroxide reductase, mitochondrial precursor	7.74	27388.04	gi 225715944	<i>Esox lucius</i>	2	Metazoa	86	12	(C)	(K), (M)

Notes: *(C) - Carbamidomethyl, (K)- Acetyl, (M) – Oxidation.

^aPeptide sequence(s) that showed sequence homology to an un-annotated *Gillichthys mirabilis* EST. These EST sequences were identified using BLAST.