

Supplementary Table 2: Listing of proteins identified in global proteomics experiments with high confidence and differential expression, $\leq / \geq 10\%$, $p \leq 0.1$, after exposure to BMP4 protein.

<u>RefSeq</u>	<u>IPI</u>	<u>Protein Name</u>	<u>Fold Change</u>	<u>p-value</u>	<u># of spectra utilized for quantification</u>	<u># of unique peptides</u>	<u>% Coverage*</u>
NP_002148	IPI00220362	10 kDa heat shock protein, mitochondrial	0.74	0.00	14	4	29.70%
NP_006102	IPI00001539	3-ketoacyl-CoA thiolase, mitochondrial	0.81	0.03	10	3	
	IPI00472102	60 kDa heat shock protein, mitochondrial precursor	0.74	0.00	144	15	42.10%
NP_000007	IPI00005040, IPI00513827	Acyl-CoA dehydrogenase, medium-chain specific, mitochondrial precursor	1.13	0.04	6	2	5.70%
NP_005754	IPI00033217	Alpha-aminoadipic semialdehyde synthase, mitochondrial precursor	0.54	0.00	25	7	10.20%
NP_001001937	IPI00440493	ATP synthase alpha chain, mitochondrial precursor	0.85	0.03	45	4	11.40%
NP_001677	IPI00303476	ATP synthase beta chain, mitochondrial precursor	0.87	0.01	79	12	33.60%
NP_006467	IPI00027448	ATP synthase g chain, mitochondrial	0.91	0.02	14	2	23.30%
NP_005989	IPI00290770, IPI00553185	Chaperonin Containing TCPI, subunit 3 isoform b	0.82	0.06	16	6	14.30%
NP_003312	IPI00027107	Elongation factor Tu, mitochondrial precursor	0.88	0.08	54	6	19.90%
NP_057376	IPI00030275, IPI00646055	Heat shock protein 75 kDa, mitochondrial precursor	0.79	0.02	15	5	8.67%
XP_944625.1	IPI00554788	Keratin, type I cytoskeletal 18	2.89	0.00	80	19	55.20%
NP_002264	IPI00554648	Keratin, type II cytoskeletal 8	3.48	0.00	115	23	49.80%
NP_004541	IPI00025239	NADH-ubiquinone oxidoreductase 49 kDa subunit, mitochondrial precursor	0.87	0.10	11	2	5.83%
NP_000265	IPI00022334	Ornithine aminotransferase, mitochondrial precursor	1.14	0.07	16	2	5.92%
NP_036531	IPI00334907, IPI00395939	PhosPhatidylinositol transfer Protein, beta	1.23	0.09	3	2	6.62%
NP_005403	IPI00002520	Serine hydroxymethyltransferase, mitochondrial precursor	0.83	0.05	3	3	7.74%
NP_003134	IPI00029744	Single-stranded DNA-binding protein, mitochondrial precursor	0.76	0.00	11	2	16.20%
NP_006507	IPI00220194, IPI00641837	Solute carrier family 2, facilitated glucose transporter member 1	1.60	0.10	22	2	3.60%
NP_008862	IPI00003909, IPI00152505, IPI00607720	Solute carrier family 2, facilitated glucose transporter member 3	3.05	0.03	5	2	5.58%
NP_001026854	IPI00003377, IPI00215907, IPI00332419	Splice Isoform 1 of Splicing factor, arginine/serine-rich 7	0.88	0.01	48	2	7.56%
NP_003760	IPI00012340	Splicing factor, arginine/serine-rich 9	0.83	0.04	12	2	9.96%
NP_004125	IPI00007765	Stress-70 protein, mitochondrial precursor	0.78	0.01	22	11	20.50%
NP_036205	IPI00010720	T-complex protein 1, epsilon subunit	0.88	0.03	23	5	12.60%
NP_006576.2	IPI00302925	T-complex protein 1, theta subunit	0.85	0.01	17	6	10.90%

* % Coverage = the # of amino acids in all unique peptides identified with 1 % FPR divided by the total # of amino acids in the protein listed. This is the largest % coverage identified for all three search algorithm identifications.

<u>RefSeq</u>	<u>IPI</u>	<u>Protein Name</u>	<u>Fold Change</u>	<u>p-value</u>	<u># of spectra utilized for quantification</u>	<u># of unique peptides</u>	<u>% Coverage*</u>
NP_689508	IPI00329633	Threonyl-tRNA synthetase, cytoplasmic	0.61	0.04	19	5	6.36%
	IPI00477182, IPI00556118	122 kDa protein	0.86	0.09	11	7	7.08%
NP_001002857	IPI00413331, IPI00418169, IPI00455315	36 kDa protein	1.77	0.00	16	5	17.60%
NP_001013454	IPI00165360	3-mercaptopyruvate sulfurtransferase	1.19	0.04	3	2	7.10%
NP_001008	IPI00221089	40S ribosomal protein S13	0.89	0.09	35	5	31.30%
NP_072045	IPI00013296	40S ribosomal protein S18	0.82	0.10	18	3	15.80%
NP_000996	IPI00011253	40S ribosomal protein S3	0.79	0.03	8	3	16.00%
NP_000997	IPI00419880, IPI00472119	40S ribosomal protein S3a	0.86	0.07	68	6	20.20%
NP_001001	IPI00021840	40S ribosomal protein S6	0.76	0.09	3	2	8.84%
NP_001002	IPI00013415	40S ribosomal protein S7	0.87	0.02	20	3	20.10%
NP_001004	IPI00221088	40S ribosomal protein S9	0.88	0.02	44	7	28.00%
	IPI00027493, IPI00554481, IPI00554611, IPI00554702,						24.40%
NP_001013269	IPI00554722, IPI00604710	4F2 cell-surface antigen heavy chain	1.15	0.03	106	11	
NP_006004	IPI00554723, IPI00646899	60S ribosomal protein L10	0.89	0.07	61	5	31.00%
NP_002939	IPI00470528, IPI00550032	60S ribosomal protein L15	0.86	0.03	80	7	29.60%
	IPI00413324, IPI00478208,	60S ribosomal protein L17	0.85	0.05	21	3	17.50%
NP_000976	IPI00514874, IPI00644171						
NP_000970	IPI00215719	60S ribosomal protein L18	0.67	0.01	8	2	13.40%
NP_000971	IPI00026202, IPI00176629	60S ribosomal protein L18a	0.81	0.03	55	6	24.40%
NP_000977	IPI00306332	60S ribosomal protein L24	0.86	0.05	17	2	
NP_000987	IPI00029731	60S ribosomal protein L35a	0.81	0.09	15	2	17.30%
NP_000961	IPI00329389	60S ribosomal protein L6	0.82	0.04	9	3	13.20%
	IPI00299573, IPI00397676, IPI00479315	60S ribosomal protein L7a	0.91	0.01	10	2	9.81%
NP_001093	IPI00013508	Alpha-actinin 1	1.25	0.00	64	14	16.30%
NP_004915	IPI00013808	Alpha-actinin 4	1.38	0.00	59	14	16.80%
NP_000691	IPI00218918, IPI00549413	Annexin A1	1.65	0.04	2	2	11.60%
NP_001145	IPI00329801	Annexin A5	1.18	0.03	29	6	27.00%
NP_066964	IPI00220834	ATP-dependent DNA helicase II 80 kDa subunit	0.88	0.05	118	16	25.00%
NP_005520	IPI00024284	Basement membrane-specific heparan sulfate proteoglycan core protein precursor	1.50	0.01	4	4	1.30%

* % Coverage = the # of amino acids in all unique peptides identified with 1 % FPR divided by the total # of amino acids in the protein listed. This is the largest % coverage identified for all three search algorithm identifications.

<u>RefSeq</u>	<u>IPI</u>	<u>Protein Name</u>	<u>Fold Change</u>	<u>p-value</u>	<u># of spectra utilized for quantification</u>	<u># of unique peptides</u>	<u>% Coverage*</u>
NP_006308	IPI00299024	Brain acid soluble protein 1	1.57	0.00	40	9	69.50%
NP_005611	IPI00013895, IPI00029574	Calcizzarin	3.18	0.08	3	2	25.70%
NP_004369	IPI00219930	Cellular retinoic acid binding protein 1	0.61	0.01	9	3	16.90%
NP_001279	IPI00010896, IPI00554767, IPI00640548, IPI00646484, IPI00647593	Chloride intracellular channel protein 1	1.09	0.03	22	3	10.80%
NP_001814	IPI00022977	Creatine kinase B-type	0.72	0.01	11	5	17.30%
NP_001312	IPI00002824	Cysteine and glycine-rich protein 2	0.64	0.09	13	2	16.10%
NP_061820	IPI00465315	Cytochrome c	0.82	0.01	60	3	25.00%
NP_004146	IPI00032139	Cytoplasmic antiproteinase 3	2.07	0.00	16	7	23.10%
NP_112487	IPI00009922	DC50	0.80	0.08	43	2	20.20%
NP_001377	IPI00257508	Dihydropyrimidinase-related protein 2	0.72	0.00	4	4	8.92%
NP_001805	IPI00022810	Dipeptidyl-peptidase I precursor	0.80	0.00	49	5	11.50%
NP_004517	IPI00184330	DNA replication licensing factor MCM2	0.78	0.01	20	4	3.98%
NP_002379	IPI00013214	DNA replication licensing factor MCM3	0.79	0.07	5	4	5.94%
NP_005905	IPI00018349	DNA replication licensing factor MCM4	0.85	0.02	16	6	8.34%
NP_006730	IPI00018350	DNA replication licensing factor MCM5	0.81	0.05	6	4	7.08%
NP_005906	IPI00031517	DNA replication licensing factor MCM6	0.82	0.01	22	6	8.53%
NP_001378	IPI00029111	DPYSL3 protein	0.71	0.00	31	6	11.40%
NP_004386	IPI00003406	Drebrin	0.79	0.04	7	4	6.94%
NP_002746	IPI00219604	Dual specificity mitogen-activated protein kinase kinase 1	1.22	0.09	2	2	5.87%
NP_001952	IPI00186290	Elongation factor 2	0.84	0.00	133	20	26.60%
NP_001559	IPI00013068	Eukaryotic translation initiation factor 3 subunit 6	1.14	0.09	2	2	6.07%
NP_003370	IPI00479359	Ezrin	1.69	0.00	105	12	19.00%
NP_001427	IPI00025039	Fibrillarin	0.78	0.01	80	6	24.60%
NP_002005	IPI00219005	FK506-binding protein 4	0.83	0.05	22	5	17.50%
NP_036525.1	IPI00465260	GARS protein	0.83	0.10	13	4	6.26%
NP_000166	IPI00027497	Glucose-6-phosphate isomerase	0.87	0.08	16	5	10.20%
NP_000843	IPI00219757	Glutathione S-transferase P	0.91	0.09	72	7	45.00%
NP_004823	IPI00019755, IPI00642936	Glutathione transferase omega 1	1.73	0.02	4	2	7.47%
NP_002037	IPI00219018	Glyceraldehyde-3-phosphate dehydrogenase	0.85	0.00	130	11	45.80%
NP_001439	IPI00232571	Glypican-4 precursor	0.59	0.06	23	2	5.58%
NP_006316	IPI00012507, IPI00643041	GTP-binding nuclear protein RAN	0.84	0.02	32	7	28.90%
NP_001017963	IPI00382470	Heat shock protein HSP 90-alpha 2	0.90	0.03	167	22	29.20%

* % Coverage = the # of amino acids in all unique peptides identified with 1 % FPR divided by the total # of amino acids in the protein listed. This is the largest % coverage identified for all three search algorithm identifications.

<u>RefSeq</u>	<u>IPI</u>	<u>Protein Name</u>	<u>Fold Change</u>	<u>p-value</u>	<u># of spectra utilized for quantification</u>	<u># of unique peptides</u>	<u>% Coverage*</u>
NP_031381	IPI00334775, IPI00414676	Heat shock protein HSP 90-beta	0.80	0.00	215	28	43.90%
NP_003474	IPI00005996	High mobility group protein HMGI-C	0.90	0.09	17	4	41.30%
NP_254280	IPI00031562, IPI00255316, IPI00303315	Histone H2A	0.81	0.03	96	3	24.60%
NP_778235	IPI00216730	Histone H2A	0.82	0.00	35	4	27.10%
NP_003510	IPI00018534,	Histone H2B.c	0.90	0.07	183	7	48.00%
NP_003519	IPI00003935	Histone H2B.q	0.87	0.02	24	2	20.80%
NP_001005464	IPI00171611	Histone H3	0.92	0.07	11	2	13.20%
NP_524147	IPI00413922	Hypothetical protein	1.23	0.05	15	7	63.60%
NP_997647	IPI00339227	Hypothetical protein DKFZp686O1166	2.84	0.00	147	23	12.00%
NP_078950	IPI00002948	Hypothetical protein FLJ12457	0.81	0.01	33	5	28.70%
NP_001001521.1	IPI00329331	Hypothetical protein UGP2	0.69	0.00	22	5	15.80%
NP_002257	IPI00002214	Importin alpha-2 subunit	0.65	0.05	12	2	5.86%
NP_002262.3	IPI00329200	Importin beta-3	0.81	0.07	4	2	1.91%
NP_002221	IPI00554711	Junction plakoglobin	1.58	0.03	20	4	8.75%
NP_058642	IPI00001754, IPI00069985, IPI00294993	Junctional adhesion molecule A precursor	1.39	0.01	13	2	12.70%
NP_002267	IPI00479145	Keratin 19	3.57	0.00	198	19	57.00%
NP_002264.1	IPI00418411	Keratin 8 variant	3.45	0.00	107	23	56.10%
NP_002297	IPI00465431, IPI00556088	LGALS3 protein	1.49	0.05	10	3	16.00%
NP_002291	IPI00219217	L-lactate dehydrogenase B chain	0.83	0.00	32	7	21.60%
NP_002323	IPI00020557	Low-density lipoprotein receptor	1.25	0.01	3	2	0.73%
NP_002289	IPI00010471	L-plastin	2.18	0.01	7	4	6.38%
NP_075385	IPI00641181	MARCKS-related protein	0.85	0.03	8	3	32.00%
NP_006658	IPI00220739	Membrane associated progesterone receptor component 1	0.86	0.08	15	2	7.73%
NP_060530	IPI00017283, IPI00181469	Mitochondrial isoleucine tRNA synthetase	1.17	0.09	3	2	2.37%
NP_002435	IPI00219365	Moesin	1.70	0.03	6	2	3.47%
NP_006294	IPI00011916	Multisynthetase complex auxiliary component p38	0.82	0.04	2	2	5.00%
NP_291024	IPI00033494, IPI00220573, IPI00604523	Myosin regulatory light chain	1.28	0.06	7	2	16.30%
NP_002464	IPI00019502	Myosin-9	1.34	0.00	53	13	7.66%
NP_006608	IPI00513769	Nestin	0.72	0.03	8	3	2.84%
NP_001611	IPI00021812	Neuroblast differentiation-associated protein AHNAK	3.44	0.01	8	3	0.85%
NP_055113	IPI00300086	Nicotinate-nucleotide pyrophosphorylase	1.26	0.03	19	3	11.80%
NP_001018146	IPI00604590	NME2 protein	0.83	0.03	45	4	16.80%

* % Coverage = the # of amino acids in all unique peptides identified with 1 % FPR divided by the total # of amino acids in the protein listed. This is the largest % coverage identified for all three search algorithm identifications.

<u>RefSeq</u>	<u>IPI</u>	<u>Protein Name</u>	<u>Fold Change</u>	<u>p-value</u>	<u># of spectra utilized for quantification</u>	<u># of unique peptides</u>	<u>% Coverage*</u>
NP_004550	IPI00031812, IPI00643351	Nuclease sensitive element binding protein 1	0.73	0.00	34	6	22.20%
NP_004732	IPI00292387	Nucleolar and coiled-body phosphoprotein 1	0.61	0.00	66	9	13.70%
NP_005372.2	IPI00604620	Nucleolin	0.63	0.05	24	13	18.20%
NP_005959	IPI00171903, IPI00383296	ORF protein	0.90	0.03	88	15	26.30%
NP_653080	IPI00217683, IPI00237884, IPI00479064	OTTHUMP00000017427	0.82	0.01	5	4	2.73%
NP_004593	IPI00218609,	OTTHUMP00000031235	0.80	0.06	16	2	6.86%
NP_066953	IPI00419585	Peptidyl-prolyl cis-trans isomerase A	0.81	0.02	24	7	58.50%
NP_002565	IPI00000874	Peroxiredoxin 1	0.88	0.03	83	9	53.30%
NP_004896	IPI00220301	Peroxiredoxin 6	0.82	0.03	17	8	48.90%
NP_002558	IPI00219446	Phosphatidylethanolamine-binding protein	0.80	0.01	13	3	21.00%
NP_005388	IPI00299116, IPI00604773	Podocalyxin-like protein 1 precursor	0.64	0.01	4	3	5.30%
NP_001609	IPI00449049	Poly [ADP-ribose] polymerase 1	0.85	0.04	19	5	6.81%
NP_005007	IPI00012066	Poly(rC)-binding protein 2, isoform b	0.83	0.03	8	4	21.60%
NP_002943.2]	IPI00455532, IPI00479366	PREDICTED: similar to ribosomal protein S2	0.87	0.00	11	3	11.40%
NP_055555	IPI00009328	Probable ATP-dependent RNA helicase DDX48	0.90	0.09	78	4	11.70%
NP_004387	IPI00017617	Probable ATP-dependent RNA helicase DDX5	0.84	0.02	13	5	11.70%
NP_005013	IPI00216691	Profilin-1	0.89	0.02	74	6	44.60%
NP_002625	IPI00017334	Prohibitin	0.78	0.02	30	3	18.40%
NP_009204	IPI00027252	Prohibitin-2	0.87	0.02	18	4	18.70%
NP_003463	IPI00020021	Protein DEK	0.68	0.04	14	2	5.33%
NP_005304	IPI00025252	Protein disulfide-isomerase A3 precursor	0.84	0.05	69	18	38.40%
NP_000909	IPI00010796	Protein disulfide-isomerase precursor	1.16	0.04	64	11	23.40%
NP_061185	IPI00465044	Protein RCC2	0.79	0.08	43	4	9.00%
NP_000261	IPI00017672	Purine nucleoside phosphorylase	1.16	0.06	6	2	11.80%
NP_002873	IPI00414127	Ran-specific GTPase-activating protein	0.86	0.03	5	2	15.90%
NP_112243	IPI00008964	Ras-related protein Rab-1B	1.24	0.05	7	4	20.90%
NP_002892	IPI00015842	Reticulocalbin-1 precursor	1.29	0.03	7	2	9.67%
NP_005398	IPI00144003	Sal-like protein 2	0.77	0.04	12	2	1.29%
NP_055464	IPI00005648	Scaffold attachment factor B2	0.92	0.05	7	3	5.14%
NP_004850.1	IPI00024067, IPI00455383 IPI00034283,	Similar to Clathrin heavy chain	1.13	0.02	37	17	13.90%
NP_115914	IPI00641706, IPI00643158, IPI00646779	Similar to Tubulin beta-5 chain	0.84	0.00	122	9	24.70%
NP_001895	IPI00017292	Splice Isoform 1 of Beta-catenin	1.29	0.00	33	5	10.90%

* % Coverage = the # of amino acids in all unique peptides identified with 1 % FPR divided by the total # of amino acids in the protein listed. This is the largest % coverage identified for all three search algorithm identifications.

<u>RefSeq</u>	<u>IPI</u>	<u>Protein Name</u>	<u>Fold Change</u>	<u>p-value</u>	<u># of spectra utilized for quantification</u>	<u># of unique peptides</u>	<u>% Coverage*</u>
NP_149129	IPI00014516, IPI00218694, IPI00218695, IPI00218696, IPI00333771 IPI00010415,	Splice Isoform 1 of Caldesmon	1.37	0.00	20	3	9.02%
NP_863654	IPI00219452, IPI00395469, IPI00395748, IPI00413603	Splice Isoform 1 of Cytosolic acyl coenzyme A thioester hydrolase	0.84	0.04	4	2	8.16%
NP_005907	IPI00299904	Splice Isoform 1 of DNA replication licensing factor MCM7	0.85	0.07	14	3	5.70%
NP_001102	IPI00394665, IPI00394668,	Splice Isoform 1 of Double-stranded RNA-specific adenosine deaminase	0.84	0.07	18	4	4.73%
NP_001008493	IPI00411623 IPI00289334, IPI00382696,	Splice Isoform 1 of Enabled protein homolog	0.85	0.02	15	3	6.26%
NP_001448	IPI00382697, IPI00382700, IPI00477536, IPI00480131	Splice Isoform 1 of Filamin-B	1.28	0.00	97	17	7.80%
XP_499363.2	IPI00178352, IPI00413958	Splice Isoform 1 of Filamin-C	1.16	0.07	27	7	3.23%
NP_006588	IPI00003865	Splice Isoform 1 of Heat shock cognate 71 kDa protein	0.84	0.00	201	20	39.90%
NP_653171	IPI00027397, IPI00607796, IPI00607884 IPI00028888, IPI00220683,	Splice Isoform 1 of Hematological and neurological expressed 1-like protein	0.76	0.03	2	2	8.95%
NP_112738	IPI00220684, IPI00220685, IPI00382617, IPI00477150	Splice Isoform 1 of Heterogeneous nuclear ribonucleoprotein D0	0.78	0.00	51	7	16.30%
NP_036350	IPI00298788, IPI00418313	Splice Isoform 1 of Interleukin enhancer-binding factor 3	0.83	0.04	75	12	21.00%
NP_002473	IPI00179953	Splice Isoform 1 of Nuclear autoantigenic sperm protein	0.78	0.04	5	4	19.20%
NP_078862	IPI00077853, IPI00170891, IPI00218449, IPI00307359	Splice Isoform 1 of Oxysterol binding protein-related protein 9	1.27	0.01	6	3	4.34%
NP_150091	IPI00028122	Splice Isoform 1 of PC4 and SFRS1 interacting protein	0.62	0.01	9	4	8.87%

* % Coverage = the # of amino acids in all unique peptides identified with 1 % FPR divided by the total # of amino acids in the protein listed. This is the largest % coverage identified for all three search algorithm identifications.

<u>RefSeq</u>	<u>IPI</u>	<u>Protein Name</u>	<u>Fold Change</u>	<u>p-value</u>	<u># of spectra utilized for quantification</u>	<u># of unique peptides</u>	<u>% Coverage*</u>
NP_478059	IPI00001734	Splice Isoform 1 of Phosphoserine aminotransferase	0.57	0.02	27	4	8.65%
NP_001018077	IPI00410693, IPI00412714, IPI00470497, IPI00470498	Splice Isoform 1 of Plasminogen activator inhibitor 1 RNA-binding protein	0.78	0.01	19	4	11.50%
NP_000436.2	IPI00014898, IPI00186711, IPI00215942, IPI00215943, IPI00398002, IPI00398775, IPI00398776, IPI00398777, IPI00398778, IPI00398779, IPI00420096	Splice Isoform 1 of Plectin 1	1.33	0.08	2	2	0.45%
NP_006377	IPI00023785, IPI00651653, IPI00651677	Splice Isoform 1 of Probable ATP-dependent RNA helicase DDX17	0.87	0.07	21	6	10.90%
NP_056374.1	IPI00072377	Splice Isoform 1 of SET protein	0.82	0.04	73	8	33.10%
NP_005753	IPI00438229, IPI00438230	Splice Isoform 1 of Transcription intermediary factor 1-beta	0.85	0.04	54	10	15.10%
NP_000382	IPI00298237, IPI00554538, IPI00554617	Splice Isoform 1 of Tripeptidyl-peptidase I precursor	1.40	0.01	15	3	7.46%
NP_003366.2	IPI00024145, IPI00216024, IPI00216026, IPI00216027, IPI00411815, IPI00455531, IPI00642484	Splice Isoform 1 of Voltage-dependent anion-selective channel protein 2	0.78	0.03	53	3	10.40%
NP_001322.1	IPI00182469, IPI00182540, IPI00219725, IPI00219726, IPI00219727, IPI00219728, IPI00219730, IPI00219731, IPI00219732, IPI00219733,	Splice Isoform 1AB of Catenin delta-1	1.25	0.01	25	5	8.17%
NP_112556	IPI00334587, IPI00334713	Splice Isoform 2 of Heterogeneous nuclear ribonucleoprotein A/B	0.85	0.02	30	5	15.70%
NP_006176.2	IPI00006196, IPI00292771, IPI00619936	Splice Isoform 2 of Nuclear mitotic apparatus protein 1	1.18	0.09	7	2	1.48%
NP_954654	IPI00220740	Splice Isoform 2 of Nucleophosmin	0.86	0.03	104	12	57.40%
XP_001133946.1	IPI00451401	Splice Isoform 2 of Triosephosphate isomerase	0.84	0.03	44	9	46.40%
NP_001014157.1	IPI00216256	Splice Isoform 2 of WD-repeat protein 1	1.19	0.04	6	4	9.94%
NP_787045	IPI00218358	Splice Isoform 3 of DNA	0.71	0.06	7	5	7.53%
NP_127493	IPI00217449, IPI00217450, IPI00293242	Splice Isoform 3 of General transcription factor II-I	0.69	0.02	10	5	

* % Coverage = the # of amino acids in all unique peptides identified with 1 % FPR divided by the total # of amino acids in the protein listed. This is the largest % coverage identified for all three search algorithm identifications.

<u>RefSeq</u>	<u>IPI</u>	<u>Protein Name</u>	<u>Fold Change</u>	<u>p-value</u>	<u># of spectra utilized for quantification</u>	<u># of unique peptides</u>	<u>% Coverage*</u>
NP_898868	IPI00216542, IPI00385321, IPI00418316, IPI00552796, IPI00640598	Splice Isoform 5 of Protein kinase C binding protein 1	0.79	0.00	3	2	1.61%
NP_112533	IPI00396378, IPI00414696, IPI00477522	Splice Isoform B1 of Heterogeneous nuclear ribonucleoproteins A2/B1	0.90	0.10	364	18	55.50%
NP_057441	IPI00008918	Splice Isoform Beta of Epithelial protein lost in neoplasm	2.10	0.10	3	2	3.95%
NP_000170	IPI00106847, IPI00384456	Splice Isoform GTBP-alt of DNA mismatch repair protein MSH6	0.80	0.08	4	2	1.62%
NP_000810	IPI00025273	Splice Isoform Long of Trifunctional purine biosynthetic protein adenosine-3	0.83	0.01	12	3	3.56%
NP_005868	IPI00017451	Splicing factor 3 subunit 1	0.90	0.01	8	2	3.91%
NP_009096	IPI00017341	Splicing factor 3A subunit 2	0.81	0.09	8	2	3.66%
NP_036565	IPI00026089	Splicing factor 3B subunit 1	0.68	0.10	3	2	1.92%
NP_003137	IPI00005154	Structure-specific recognition protein 1	0.76	0.00	44	6	6.63%
NP_006592	IPI00015029, IPI00479875, IPI00656118	Telomerase-binding protein p23	0.85	0.07	8	2	16.90%
NP_009057	IPI00022774, IPI00478540	Transitional endoplasmic reticulum ATPase	1.15	0.01	48	10	16.30%
NP_001055	IPI00021716, IPI00643920, IPI00646755	Transketolase	1.21	0.00	34	13	29.40%
NP_009145	IPI00218922, IPI00643718	Translocation protein SEC63 homolog	0.87	0.01	6	2	3.43%
NP_000356	IPI00465028	Triosephosphate isomerase 1 variant	0.84	0.02	54	9	45.80%
NP_000357	IPI00018853, IPI00216135, IPI00296039	Tropomyosin isoform	1.22	0.05	8	3	14.40%
NP_004175	IPI00295400	Tryptophanyl-tRNA synthetase	0.82	0.02	11	3	6.79%
NP_006000	IPI00180675	Tubulin alpha-3 chain	0.86	0.00	151	19	61.40%
NP_006073	IPI00387144	Tubulin alpha-ubiquitous chain	0.85	0.00	199	19	61.40%
NP_821133	IPI00011654	Tubulin beta-2 chain	0.82	0.00	375	19	61.50%
NP_006079	IPI00007752	Tubulin beta-2C chain	0.78	0.00	69	7	24.00%
NP_006077	IPI00013683	Tubulin beta-3 chain	0.80	0.00	152	14	39.10%
NP_005142	IPI00219913, IPI00640357	Ubiquitin carboxyl-terminal hydrolase 14	0.89	0.00	2	2	5.48%
NP_004172	IPI00018352	Ubiquitin carboxyl-terminal hydrolase isozyme L1	0.68	0.00	26	5	29.60%
NP_003325	IPI00645078	Ubiquitin-activating enzyme E1	0.85	0.08	18	4	4.35%
NP_002865	IPI00008223	UV excision repair protein RAD23, homolog B	1.44	0.06	11	3	12.00%
NP_003371	IPI00418471, IPI00646867	Vimentin	0.75	0.08	48	10	26.90%

* % Coverage = the # of amino acids in all unique peptides identified with 1 % FPR divided by the total # of amino acids in the protein listed. This is the largest % coverage identified for all three search algorithm identifications.

<u>RefSeq</u>	<u>IPI</u>	<u>Protein Name</u>	<u>Fold Change</u>	<u>p-value</u>	<u># of spectra utilized for quantification</u>	<u># of unique peptides</u>	<u>% Coverage*</u>
NP_057085	IPI00000733	WD-repeat protein 50	0.73	0.07	24	2	5.76%
NP_057396	IPI00170786	WW domain-binding protein 11	0.76	0.03	9	2	5.30%
NP_001203	IPI00014230	Complement component 1, Q subcomponent binding protein, mitochondrial precursor	0.61	0.04	10	3	19.20%
NP_006550	IPI00008575	Splice Isoform 1 of KH domain containing, RNA binding, signal transduction associated protein 1	0.86	0.05	7	4	10.40%
NP_000692	IPI00006482	Splice Isoform Long of Sodium/potassium-transporting ATPase alpha-1 chain precursor	1.10	0.01	18	3	2.93%

* % Coverage = the # of amino acids in all unique peptides identified with 1 % FPR divided by the total # of amino acids in the protein listed. This is the largest % coverage identified for all three search algorithm identifications.