

Supplementary Table S1

Relative Protein Abundance: Trabecular Meshwork Sample NTM416-07

Total Proteins Quantified = 513; Median Protein iTRAQ Ratio = 1.00; Mean Protein iTRAQ Ratio = 1.00; Standard Deviation = 0.30

SwissProtein Accession	Protein	Protein iTRAQ Ratio Dex/Control	Standard Deviation	P value	Unique Peptides	Sequence Coverage
O94875	Sorbin and SH3 domain-containing protein 2	3.41	0.61	2.80E-02	4	5.27%
Q99972	Myocilin	3.33	NA	NA	2	4.76%
Q13740	CD166 antigen	2.51	0.17	2.50E-04	5	8.75%
P30038	Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial	2.37	NA	NA	2	6.04%
Q15121	Astrocytic phosphoprotein PEA-15	2.24	NA	NA	2	10.00%
P78417	Glutathione S-transferase omega-1	2.05	NA	NA	2	9.54%
P29590	Probable transcription factor PML	2.04	NA	NA	2	3.63%
Q9Y6N5	Sulfide:quinone oxidoreductase, mitochondrial	2.02	0.25	1.10E-02	4	8.44%
P39060	Collagen alpha-1(XVIII) chain	2.00	NA	NA	2	1.60%
P54819	Adenylate kinase 2, mitochondrial	1.98	NA	NA	2	11.30%
P02768	Serum albumin	1.98	0.99	2.00E-01	5	7.88%
O00151	PDZ and LIM domain protein 1	1.97	NA	NA	2	9.42%
P11216	Glycogen phosphorylase, brain form	1.97	0.65	2.10E-01	3	3.68%
P46976	Glycogenin-1	1.90	NA	NA	2	4.86%
Q9HBL0	Tensin-1	1.86	NA	NA	2	1.79%
Q96HY6	DDRKG domain-containing protein 1	1.85	NA	NA	2	10.19%
P07195	L-lactate dehydrogenase B chain	1.85	0.79	1.10E-01	6	18.26%
P05455	Lupus La protein	1.82	NA	NA	2	3.43%
P68371	Tubulin beta-2C chain	1.82	NA	NA	2	6.07%
Q03135	Caveolin-1	1.81	0.18	1.90E-03	5	26.97%
Q14247	Src substrate cortactin	1.71	NA	NA	2	3.27%
P61604	10 kDa heat shock protein, mitochondrial	1.70	0.47	6.40E-03	10	77.45%
P04792	Heat shock protein beta-1	1.69	0.45	2.10E-02	7	45.85%
P11047	Laminin subunit gamma-1	1.67	0.31	4.50E-02	4	2.73%
P60981	Destrin	1.67	NA	NA	2	10.30%
Q04828	Aldo-keto reductase family 1 member C1	1.66	0.41	3.00E-02	6	16.10%
Q58A63	BNIP2 motif-containing molecule at the C-terminal region 1	1.66	0.20	4.90E-02	3	1.58%
P28070	Proteasome subunit beta type-4	1.66	NA	NA	2	9.09%
Q0ZGT2	Nexilin	1.65	0.24	9.40E-03	5	5.33%
O14558	Heat shock protein beta-6	1.65	NA	NA	2	16.25%
P52209	6-phosphogluconate dehydrogenase, decarboxylating	1.64	0.70	2.50E-01	4	10.56%
Q15942	Zyxin	1.63	0.89	2.90E-01	5	12.94%
P54709	Sodium/potassium-transporting ATPase subunit beta-3	1.62	0.34	6.40E-02	4	15.05%
Q16851	UTP--glucose-1-phosphate uridylyltransferase	1.61	NA	NA	2	3.15%
P43490	Nicotinamide phosphoribosyltransferase	1.59	NA	NA	2	3.87%
Q9UN86	Ras GTPase-activating protein-binding protein 2	1.59	0.66	3.50E-01	3	6.02%
P28482	Mitogen-activated protein kinase 1	1.57	NA	NA	2	8.33%
Q9UIJ7	GTP:AMP phosphotransferase mitochondrial	1.57	0.14	8.00E-03	4	20.26%
Q9BRA2	Thioredoxin domain-containing protein 17	1.56	NA	NA	2	18.70%
P18669	Phosphoglycerate mutase 1	1.52	0.22	7.90E-02	3	15.75%
Q99715	Collagen alpha-1(XII) chain	1.51	0.35	1.80E-01	3	2.12%
Q53GG5	PDZ and LIM domain protein 3	1.51	NA	NA	2	9.07%
Q13510	Acid ceramidase	1.50	NA	NA	2	3.54%
P10301	Ras-related protein R-Ras	1.50	NA	NA	2	14.68%
Q92734	Protein TFG	1.50	NA	NA	2	4.50%
Q99439	Calponin-2	1.49	NA	NA	2	4.21%
A6NL28	Putative tropomyosin alpha-3 chain-like protein	1.47	NA	NA	2	10.76%
P60174	Triosephosphate isomerase	1.46	0.22	8.20E-03	6	27.31%
O75947	ATP synthase subunit d, mitochondrial	1.46	0.46	2.90E-01	3	12.42%
P38117	Electron transfer flavoprotein subunit beta	1.46	0.46	5.60E-02	8	32.94%
Q969X5	Endoplasmic reticulum-Golgi intermediate compartment protein 1	1.45	0.55	3.60E-01	3	11.03%
P62258	14-3-3 protein epsilon	1.45	0.04	3.40E-03	3	14.90%
Q14847	LIM and SH3 domain protein 1	1.44	0.40	2.60E-01	3	11.49%
P42765	3-ketoacyl-CoA thiolase, mitochondrial	1.44	0.33	2.00E-01	3	6.30%
Q9NX63	Coiled-coil-helix-coiled-coil-helix domain-containing protein 3, mitochondrial	1.44	NA	NA	2	7.05%
O75369	Filamin-B	1.43	0.17	7.40E-06	13	5.88%
P00390	Glutathione reductase, mitochondrial	1.39	NA	NA	2	6.32%
P09496	Clathrin light chain A	1.38	0.33	2.30E-01	3	10.48%
Q6NZI2	Polymerase I and transcript release factor	1.37	0.18	1.10E-05	15	27.95%
P22314	Ubiquitin-like modifier-activating enzyme 1	1.36	NA	NA	2	1.23%
Q09666	Neuroblast differentiation-associated protein AHNAK	1.35	0.28	5.10E-17	92	13.34%
P10909	Clusterin	1.35	0.17	9.50E-02	3	6.68%
P43686	26S protease regulatory subunit 6B	1.34	0.32	2.60E-01	3	7.89%
P07355	Annexin A2	1.33	0.20	5.30E-07	23	54.87%
P29992	Guanine nucleotide-binding protein subunit alpha-11	1.33	0.12	5.40E-02	3	7.24%
P50914	60S ribosomal protein L14	1.33	0.22	1.60E-01	3	14.88%
Q02952	A-kinase anchor protein 12	1.32	NA	NA	2	1.85%
P18206	Vinculin	1.32	0.37	3.00E-03	21	24.07%
Q13509	Tubulin beta-3 chain	1.32	NA	NA	2	5.33%
P16152	Carbonyl reductase [NADPH] 1	1.31	0.18	1.10E-01	3	12.64%
P16615	Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	1.31	NA	NA	2	2.78%
Q8WWV1	LIM domain only protein 7	1.31	0.26	5.20E-02	6	4.22%
Q92896	Golgi apparatus protein 1	1.30	NA	NA	2	1.70%
O60664	Mannose-6-phosphate receptor-binding protein 1	1.30	0.43	2.00E-01	6	20.97%
P02511	Alpha-crystallin B chain	1.30	0.17	5.80E-02	4	24.00%
P52565	Rho GDP-dissociation inhibitor 1	1.29	0.31	2.90E-01	3	22.06%
P00558	Phosphoglycerate kinase 1	1.29	0.40	6.50E-02	11	20.86%
Q06830	Peroxiredoxin-1	1.27	0.34	3.00E-02	12	51.76%
P25398	40S ribosomal protein S12	1.27	NA	NA	2	13.64%
P40926	Malate dehydrogenase, mitochondrial	1.27	0.17	2.70E-03	9	28.11%
Q9NSD9	Phenylalanyl-tRNA synthetase beta chain	1.27	0.24	2.30E-01	3	4.58%
Q99442	Translocation protein SEC62	1.27	NA	NA	2	4.51%

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Q16698	2,4-dienoyl-CoA reductase, mitochondrial	1.26	0.27	2.70E-01	3	12.54%
P61981	14-3-3 protein gamma	1.26	0.19	1.70E-01	3	16.60%
P11413	Glucose-6-phosphate 1-dehydrogenase	1.26	0.40	2.70E-01	5	9.32%
P00338	L-lactate dehydrogenase A chain	1.26	0.25	1.10E-01	5	12.95%
P62899	60S ribosomal protein L31	1.26	NA	NA	2	14.40%
P35268	60S ribosomal protein L22	1.26	0.08	4.20E-02	3	19.53%
P30049	ATP synthase subunit delta, mitochondrial	1.25	0.18	1.60E-01	3	17.26%
P47756	F-actin-capping protein subunit beta	1.25	NA	NA	2	7.22%
P05141	ADP/ATP translocase 2	1.25	0.19	1.80E-01	3	9.40%
P07951	Tropomyosin beta chain	1.25	0.32	6.10E-02	10	31.34%
P52907	F-actin-capping protein subunit alpha-1	1.24	NA	NA	2	9.79%
P28838	Cytosol aminopeptidase	1.24	0.38	2.70E-01	5	10.98%
P35613	Basigin	1.24	0.06	4.80E-03	4	13.25%
O60716	Catenin delta-1	1.24	NA	NA	2	2.17%
P10606	Cytochrome c oxidase subunit 5B, mitochondrial	1.24	0.18	1.00E-01	4	20.93%
Q13418	Integrin-linked protein kinase	1.24	0.35	4.00E-01	3	6.19%
P62158	Calmodulin	1.23	0.44	4.10E-01	4	26.17%
P10809	60 kDa heat shock protein, mitochondrial	1.23	0.38	5.40E-02	15	28.80%
P23528	Cofilin-1	1.23	0.15	1.50E-01	3	21.69%
P29401	Transketolase	1.23	0.19	1.40E-02	9	16.21%
P83731	60S ribosomal protein L24	1.23	0.34	3.10E-01	4	21.66%
Q8N1G4	Leucine-rich repeat-containing protein 47	1.22	NA	NA	2	4.12%
O15460	Prolyl 4-hydroxylase subunit alpha-2	1.22	NA	NA	2	5.05%
Q8IVF2	Protein AHNAK2	1.22	0.23	2.70E-01	3	0.31%
P84103	Splicing factor, arginine/serine-rich 3	1.22	NA	NA	2	18.29%
P30086	Phosphatidylethanolamine-binding protein 1	1.22	0.15	1.50E-01	3	11.76%
P09669	Cytochrome c oxidase subunit 6C	1.22	0.47	4.60E-01	4	48.00%
P24534	Elongation factor 1-beta	1.21	0.17	2.70E-02	7	14.22%
O43491	Band 4.1-like protein 2	1.21	0.40	4.10E-01	4	4.88%
P12109	Collagen alpha-1(VI) chain	1.21	0.14	6.70E-02	4	4.67%
Q9C0E8	Protein lunapark	1.21	NA	NA	2	2.10%
P04040	Catalase	1.21	NA	NA	2	4.74%
P21333	Filamin-A	1.21	0.24	2.70E-07	58	27.28%
P36542	ATP synthase subunit gamma, mitochondrial	1.21	0.14	1.50E-01	3	12.08%
Q03252	Lamin-B2	1.20	0.21	2.20E-02	10	18.00%
Q07157	Tight junction protein ZO-1	1.20	NA	NA	2	1.89%
O95881	Thioredoxin domain-containing protein 12	1.20	0.45	5.60E-01	3	22.09%
Q96I99	Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial	1.20	0.31	2.60E-01	5	12.73%
P08238	Heat shock protein HSP 90-beta	1.20	0.56	4.00E-01	8	13.12%
P06733	Alpha-enolase	1.20	0.21	2.10E-03	18	35.02%
P46939	Utrophin	1.20	NA	NA	2	0.93%
P35222	Catenin beta-1	1.19	NA	NA	2	3.20%
P36957	Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex	1.19	0.34	2.60E-01	6	13.25%
P30041	Peroxioredoxin-6	1.19	0.19	1.60E-01	4	11.61%
P51571	Translocon-associated protein subunit delta	1.19	NA	NA	2	6.94%
P26038	Moesin	1.19	0.35	6.60E-02	16	25.13%
P27144	Adenylate kinase isoenzyme 4, mitochondrial	1.18	NA	NA	2	9.87%
P48047	ATP synthase subunit O, mitochondrial	1.18	0.31	2.50E-01	6	29.58%
Q15019	Septin-2	1.18	0.25	3.70E-01	3	9.42%
Q9Y3U8	60S ribosomal protein L36	1.18	0.21	3.00E-01	3	17.14%
P37802	Transgelin-2	1.18	0.21	2.30E-01	4	21.61%
O95168	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 4	1.18	NA	NA	2	17.83%
P25705	ATP synthase subunit alpha, mitochondrial	1.18	0.36	1.00E-01	15	31.10%
P62266	40S ribosomal protein S23	1.17	NA	NA	2	11.89%
P62913	60S ribosomal protein L11	1.17	0.23	3.60E-01	3	13.48%
P15153	Ras-related C3 botulinum toxin substrate 2	1.17	NA	NA	2	10.42%
P35998	26S protease regulatory subunit 7	1.17	NA	NA	2	5.08%
Q9BR76	Coronin-1B	1.17	NA	NA	2	5.11%
Q9Y2W1	Thyroid hormone receptor-associated protein 3	1.17	NA	NA	2	3.35%
P35579	Myosin-9	1.17	0.34	1.20E-02	34	16.99%
P98160	Basement membrane-specific heparan sulfate proteoglycan core protein	1.16	0.27	1.80E-01	7	2.14%
Q14315	Filamin-C	1.15	0.31	1.40E-01	12	5.21%
P08579	U2 small nuclear ribonucleoprotein B	1.15	0.91	8.10E-01	3	8.89%
P00367	Glutamate dehydrogenase 1, mitochondrial	1.15	0.12	2.50E-02	7	13.80%
P25789	Proteasome subunit alpha type-4	1.15	0.25	4.30E-01	3	11.88%
P49368	T-complex protein 1 subunit gamma	1.15	0.60	6.30E-01	5	8.44%
P50402	Emerin	1.15	NA	NA	2	9.84%
O43678	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 2	1.15	NA	NA	2	10.10%
P30050	60S ribosomal protein L12	1.15	0.29	5.00E-01	3	20.00%
P67936	Tropomyosin alpha-4 chain	1.15	0.27	1.60E-02	27	64.92%
P10253	Lysosomal alpha-glucosidase	1.15	NA	NA	2	2.42%
P24752	Acetyl-CoA acetyltransferase, mitochondrial	1.14	0.53	5.60E-01	6	13.82%
P29692	Elongation factor 1-delta	1.14	0.25	2.50E-01	6	27.05%
P21912	Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial	1.14	0.05	5.40E-02	3	10.36%
P07942	Laminin subunit beta-1	1.14	0.76	6.70E-01	7	4.82%
Q15233	Non-POU domain-containing octamer-binding protein	1.14	NA	NA	2	2.76%
P62263	40S ribosomal protein S14	1.14	0.11	1.80E-01	3	30.46%
P61106	Ras-related protein Rab-14	1.13	NA	NA	2	10.70%
P06396	Gelsolin	1.13	0.70	6.80E-01	6	6.91%
P00403	Cytochrome c oxidase subunit 2	1.13	NA	NA	2	7.49%
Q05682	Caldesmon	1.13	0.24	6.00E-02	17	20.81%
Q9UMX5	Neudesin	1.12	0.15	3.00E-01	3	20.35%
P11498	Pyruvate carboxylase, mitochondrial	1.12	NA	NA	2	2.55%
P60866	40S ribosomal protein S20	1.12	0.25	5.10E-01	3	22.69%
P50895	Lutheran blood group glycoprotein	1.12	NA	NA	2	5.10%
P13489	Ribonuclease inhibitor	1.12	NA	NA	2	6.51%
Q9UJZ1	Stomatin-like protein 2	1.12	0.20	3.60E-01	4	15.17%
P48643	T-complex protein 1 subunit epsilon	1.11	0.06	8.60E-02	3	4.99%
P62424	60S ribosomal protein L7a	1.11	0.27	5.60E-01	3	10.53%

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O14974	Protein phosphatase 1 regulatory subunit 12A	1.11	0.38	6.20E-01	4	5.44%
P32119	Peroxioredoxin-2	1.11	0.25	3.50E-01	6	32.83%
P37837	Transaldolase	1.11	0.41	5.00E-01	8	19.29%
P62249	40S ribosomal protein S16	1.11	0.36	6.00E-01	4	25.34%
O43707	Alpha-actinin-4	1.11	0.20	4.10E-02	18	24.37%
Q8NBJ7	Sulfatase-modifying factor 2	1.11	NA	NA	2	7.64%
P18085	ADP-ribosylation factor 4	1.11	NA	NA	2	11.67%
Q9UHD8	Septin-9	1.11	NA	NA	2	3.92%
P50991	T-complex protein 1 subunit delta	1.11	0.08	1.50E-01	3	6.68%
P08758	Annexin A5	1.10	0.51	5.00E-01	13	36.88%
O75390	Citrate synthase, mitochondrial	1.10	NA	NA	2	4.51%
Q9H299	SH3 domain-binding glutamic acid-rich-like protein 3	1.10	NA	NA	2	31.18%
O75915	PRA1 family protein 3	1.10	NA	NA	2	9.57%
Q92945	Far upstream element-binding protein 2	1.10	0.82	7.80E-01	7	11.55%
P11940	Polyadenylate-binding protein 1	1.09	NA	NA	2	2.83%
P10599	Thioredoxin	1.09	0.21	5.40E-01	3	19.05%
O75396	Vesicle-trafficking protein SEC22b	1.09	0.27	4.30E-01	7	38.14%
P49755	Transmembrane emp24 domain-containing protein 10	1.09	0.20	4.50E-01	4	21.46%
P04075	Fructose-bisphosphate aldolase A	1.09	0.42	3.80E-01	19	51.10%
O00170	AH receptor-interacting protein	1.09	NA	NA	2	8.79%
P02786	Transferrin receptor protein 1	1.08	0.21	5.70E-01	3	5.26%
Q15149	Plectin-1	1.08	0.26	1.20E-02	70	15.61%
P08195	4F2 cell-surface antigen heavy chain	1.08	0.05	1.20E-01	3	7.46%
P62854	40S ribosomal protein S26	1.08	0.25	6.50E-01	3	33.91%
P18124	60S ribosomal protein L7	1.08	0.26	4.70E-01	7	16.13%
P49411	Elongation factor Tu, mitochondrial	1.08	0.24	3.50E-01	10	29.20%
P60709	Actin, cytoplasmic 1	1.08	0.34	3.40E-01	20	44.00%
P62937	Peptidyl-prolyl cis-trans isomerase A	1.08	0.49	7.00E-01	7	33.94%
Q5JXB2	Putative ubiquitin-conjugating enzyme E2 N-like	1.08	NA	NA	2	13.73%
P50995	Annexin A11	1.08	NA	NA	2	3.56%
Q16881	Thioredoxin reductase 1, cytoplasmic	1.08	0.20	4.70E-01	5	11.09%
P48735	Isocitrate dehydrogenase [NADP], mitochondrial	1.07	0.13	4.60E-01	3	7.52%
Q15046	Lysyl-tRNA synthetase	1.07	NA	NA	2	3.85%
P27348	14-3-3 protein theta	1.07	0.21	5.70E-01	4	16.33%
P09525	Annexin A4	1.07	0.47	7.90E-01	4	11.91%
P40429	60S ribosomal protein L13a	1.07	NA	NA	2	8.37%
P34897	Serine hydroxymethyltransferase, mitochondrial	1.07	NA	NA	2	4.17%
P62280	40S ribosomal protein S11	1.07	0.32	7.50E-01	3	16.46%
Q16555	Dihydropyrimidinase-related protein 2	1.07	0.20	5.20E-01	5	9.79%
P35580	Myosin-10	1.07	0.17	3.90E-01	6	3.59%
P04406	Glyceraldehyde-3-phosphate dehydrogenase	1.06	0.54	7.30E-01	10	29.85%
O15173	Membrane-associated progesterone receptor component 2	1.06	NA	NA	2	9.87%
P51665	26S proteasome non-ATPase regulatory subunit 7	1.05	NA	NA	2	6.17%
P49419	Alpha-aminoacidic semialdehyde dehydrogenase	1.05	NA	NA	2	3.91%
Q969G5	Protein kinase C delta-binding protein	1.05	0.22	7.40E-01	3	8.43%
Q16629	Splicing factor, arginine/serine-rich 7	1.05	0.20	6.70E-01	4	24.37%
P15880	40S ribosomal protein S2	1.05	NA	NA	2	7.85%
P78559	Microtubule-associated protein 1A	1.05	0.19	5.80E-01	6	2.78%
P05091	Aldehyde dehydrogenase, mitochondrial	1.04	0.46	8.40E-01	5	10.44%
Q9BRK5	45 kDa calcium-binding protein	1.04	NA	NA	2	5.80%
P46821	Microtubule-associated protein 1B	1.04	0.25	5.00E-01	17	7.86%
O00469	Procollagen-lysine,2-oxoglutarate 5-dioxygenase 2	1.04	0.38	8.20E-01	5	9.63%
O43390	Heterogeneous nuclear ribonucleoprotein R	1.04	0.41	8.60E-01	4	7.11%
P39023	60S ribosomal protein L3	1.04	0.32	8.30E-01	4	6.20%
P17844	Probable ATP-dependent RNA helicase DDX5	1.04	0.77	9.10E-01	6	9.45%
Q9Y2B0	Protein canopy homolog 2	1.04	NA	NA	2	14.29%
Q9P2E9	Ribosome-binding protein 1	1.04	0.41	6.70E-01	24	16.88%
Q16836	Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial	1.04	NA	NA	2	5.41%
Q13813	Spectrin alpha chain, brain	1.04	0.26	5.20E-01	24	12.38%
P10644	cAMP-dependent protein kinase type I-alpha regulatory subunit	1.03	NA	NA	2	9.19%
Q99798	Aconitase hydratase, mitochondrial	1.03	0.20	8.10E-01	3	5.90%
P23634	Plasma membrane calcium-transporting ATPase 4	1.03	NA	NA	2	2.34%
P19367	Hexokinase-1	1.03	0.69	9.30E-01	5	5.78%
P60660	Myosin light polypeptide 6	1.03	0.14	6.90E-01	4	34.44%
P31937	3-hydroxyisobutyrate dehydrogenase, mitochondrial	1.03	0.42	9.00E-01	4	19.64%
Q5QNW6	Histone H2B type 2-F	1.03	0.05	2.50E-01	5	37.30%
P46778	60S ribosomal protein L21	1.03	NA	NA	2	13.75%
P60900	Proteasome subunit alpha type-6	1.03	0.22	8.60E-01	3	16.26%
P52272	Heterogeneous nuclear ribonucleoprotein M	1.02	0.24	8.30E-01	5	9.86%
Q01082	Spectrin beta chain, brain 1	1.02	0.33	8.30E-01	12	6.05%
P55072	Transitional endoplasmic reticulum ATPase	1.02	0.57	9.20E-01	10	14.27%
Q14240	Eukaryotic initiation factor 4A-II	1.02	0.22	9.00E-01	3	10.07%
Q9Y680	FK506-binding protein 7	1.02	NA	NA	2	5.79%
O95816	BAG family molecular chaperone regulator 2	1.02	NA	NA	2	12.80%
Q5VTE0	Putative elongation factor 1-alpha-like 3	1.02	0.46	9.40E-01	5	9.09%
P07237	Protein disulfide-isomerase	1.02	0.38	8.40E-01	24	36.02%
P59998	Actin-related protein 2/3 complex subunit 4	1.01	0.42	9.60E-01	3	16.07%
O60218	Aldo-keto reductase family 1 member B10	1.01	0.39	9.60E-01	3	9.18%
P13674	Prolyl 4-hydroxylase subunit alpha-1	1.01	0.46	9.70E-01	3	6.55%
P14314	Glucosidase 2 subunit beta	1.00	0.24	9.70E-01	7	13.26%
P49257	Protein ERGIC-53	1.00	NA	NA	2	3.92%
P61978	Heterogeneous nuclear ribonucleoprotein K	1.00	0.29	9.90E-01	6	14.69%
O43852	Calumenin	1.00	0.18	9.90E-01	7	17.46%
P20674	Cytochrome c oxidase subunit 5A, mitochondrial	1.00	0.21	9.90E-01	3	10.00%
P62701	40S ribosomal protein S4, X isoform	1.00	0.46	1.00E+00	4	11.79%
Q8WX93	Palladin	1.00	0.34	1.00E+00	3	1.88%
P61224	Ras-related protein Rap-1b	1.00	NA	NA	2	14.13%
P08133	Annexin A6	1.00	0.31	9.70E-01	10	14.56%
P07858	Cathepsin B	1.00	NA	NA	2	7.67%

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Q07955	Splicing factor, arginine/serine-rich 1	0.99	0.27	9.70E-01	5	21.77%
P13861	cAMP-dependent protein kinase type II-alpha regulatory subunit	0.99	0.11	9.30E-01	3	8.91%
P49458	Signal recognition particle 9 kDa protein	0.99	NA	NA	2	22.09%
Q9UBR2	Cathepsin Z	0.99	0.26	9.60E-01	3	10.56%
P12814	Alpha-actinin-1	0.99	0.09	7.40E-01	8	9.64%
P09211	Glutathione S-transferase P	0.99	0.31	9.50E-01	3	16.19%
P51149	Ras-related protein Rab-7a	0.99	0.40	9.50E-01	4	21.74%
P11142	Heat shock cognate 71 kDa protein	0.99	0.17	7.90E-01	12	21.83%
P69905	Hemoglobin subunit alpha	0.99	0.16	8.90E-01	3	21.83%
P62244	40S ribosomal protein S15a	0.98	NA	NA	2	13.08%
Q13232	Nucleoside diphosphate kinase 3	0.98	NA	NA	2	10.06%
P38646	Stress-70 protein, mitochondrial	0.98	0.38	8.30E-01	17	24.30%
P49756	RNA-binding protein 25	0.98	NA	NA	2	2.49%
Q13557	Calcium/calmodulin-dependent protein kinase type II delta chain	0.98	0.25	8.60E-01	4	7.41%
Q13435	Splicing factor 3B subunit 2	0.97	NA	NA	2	2.41%
Q9NR28	Diablo homolog, mitochondrial	0.97	NA	NA	2	8.79%
P07437	Tubulin beta chain	0.97	0.27	7.50E-01	11	26.13%
P06753	Tropomyosin alpha-3 chain	0.97	0.26	7.50E-01	9	23.24%
P51659	Peroxisomal multifunctional enzyme type 2	0.97	NA	NA	2	3.53%
O43809	Cleavage and polyadenylation specificity factor subunit 5	0.97	0.20	8.10E-01	3	12.78%
Q96CX2	BTB/POZ domain-containing protein KCTD12	0.96	NA	NA	2	10.46%
Q7KZF4	Staphylococcal nuclease domain-containing protein 1	0.96	0.43	8.60E-01	5	7.58%
O95202	LETM1 and EF-hand domain-containing protein 1, mitochondrial	0.96	NA	NA	2	3.25%
O00571	ATP-dependent RNA helicase DDX3X	0.96	NA	NA	2	2.57%
Q07960	Rho GTPase-activating protein 1	0.96	0.37	8.80E-01	3	6.15%
P24844	Myosin regulatory light polypeptide 9	0.96	0.57	9.20E-01	3	17.44%
P51572	B-cell receptor-associated protein 31	0.96	0.15	5.90E-01	5	22.36%
P62736	Actin, aortic smooth muscle	0.96	0.38	8.20E-01	5	17.51%
A0FGR8	Extended synaptotagmin-2	0.96	NA	NA	2	2.82%
P22626	Heterogeneous nuclear ribonucleoproteins A2/B1	0.96	0.30	7.30E-01	6	18.70%
P13073	Cytochrome c oxidase subunit 4 isoform 1, mitochondrial	0.96	0.36	8.50E-01	3	13.61%
Q02252	Methylmalonate-semialdehyde dehydrogenase [acylating], mitochondrial	0.95	NA	NA	2	3.74%
P14618	Pyruvate kinase isozymes M1/M2	0.95	0.24	4.40E-01	14	27.87%
P14927	Cytochrome b-c1 complex subunit 7	0.95	NA	NA	2	15.32%
P04083	Annexin A1	0.95	0.43	6.50E-01	13	40.17%
Q13217	DnaJ homolog subfamily C member 3	0.95	NA	NA	2	3.17%
Q16822	Phosphoenolpyruvate carboxykinase [GTP], mitochondrial	0.94	NA	NA	2	3.13%
P06576	ATP synthase subunit beta, mitochondrial	0.94	0.32	4.90E-01	14	27.98%
O00264	Membrane-associated progesterone receptor component 1	0.94	0.40	7.50E-01	5	26.67%
Q96HC4	PDZ and LIM domain protein 5	0.94	0.30	7.60E-01	3	6.04%
P31040	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial	0.94	NA	NA	2	2.86%
Q16891	Mitochondrial inner membrane protein	0.94	0.18	4.30E-01	6	8.71%
P50479	PDZ and LIM domain protein 4	0.94	0.50	8.20E-01	4	9.70%
Q9Y490	Talin-1	0.94	0.42	5.30E-01	18	7.32%
Q9BS26	Thioredoxin domain-containing protein 4	0.94	0.11	2.70E-01	5	9.85%
P80723	Brain acid soluble protein 1	0.93	0.07	5.90E-02	6	50.22%
P35052	Glypican-1	0.93	NA	NA	2	4.66%
P62906	60S ribosomal protein L10a	0.93	0.09	2.10E-01	4	14.75%
P11233	Ras-related protein Ral-A	0.93	0.01	9.70E-03	3	18.45%
Q14974	Importin subunit beta-1	0.93	0.19	5.70E-01	3	3.42%
P36578	60S ribosomal protein L4	0.93	0.34	5.80E-01	7	12.65%
P20700	Lamin-B1	0.93	NA	NA	2	2.39%
P78371	T-complex protein 1 subunit beta	0.92	0.26	5.90E-01	4	6.92%
P63104	14-3-3 protein zeta/delta	0.92	0.37	6.30E-01	6	28.57%
Q01995	Transgelin	0.92	0.68	7.50E-01	8	36.32%
P30044	Peroxioredoxin-5, mitochondrial	0.92	0.42	7.30E-01	4	20.56%
P35232	Prohibitin	0.92	0.24	3.60E-01	8	31.99%
Q9Y3I0	UPF0027 protein C22orf28	0.92	NA	NA	2	5.94%
P00387	NADH-cytochrome b5 reductase 3	0.92	0.31	6.70E-01	3	15.61%
Q15691	Microtubule-associated protein RP/EB family member 1	0.91	NA	NA	2	7.09%
P30084	Enoyl-CoA hydratase, mitochondrial	0.91	NA	NA	2	6.55%
P30101	Protein disulfide-isomerase A3	0.91	0.17	3.00E-02	19	41.39%
Q99714	3-hydroxyacyl-CoA dehydrogenase type-2	0.91	NA	NA	2	7.66%
Q9Y2Q3	Glutathione S-transferase kappa 1	0.91	NA	NA	2	11.95%
P19338	Nucleolin	0.91	0.27	2.60E-01	11	15.77%
P80303	Nucleobindin-2	0.91	NA	NA	2	3.81%
P30048	Thioredoxin-dependent peroxide reductase, mitochondrial	0.91	NA	NA	2	7.42%
Q9BQE5	Apolipoprotein L2	0.91	0.16	3.90E-01	3	9.79%
Q15005	Signal peptidase complex subunit 2	0.90	NA	NA	2	11.95%
P07737	Profilin-1	0.90	0.16	2.90E-01	4	30.71%
P27816	Microtubule-associated protein 4	0.90	0.30	4.00E-01	7	6.34%
Q96AQ6	Pre-B-cell leukemia transcription factor-interacting protein 1	0.90	NA	NA	2	2.87%
Q07065	Cytoskeleton-associated protein 4	0.90	0.23	5.50E-02	21	42.69%
Q8NBS9	Thioredoxin domain-containing protein 5	0.90	0.21	1.90E-01	8	16.44%
Q15907	Ras-related protein Rab-11B	0.90	0.40	5.90E-01	5	21.56%
O14950	Myosin regulatory light chain MRLC2	0.90	0.60	7.50E-01	4	17.44%
P62988	Ubiquitin	0.90	0.39	4.70E-01	8	88.16%
P08865	40S ribosomal protein SA	0.90	0.28	5.70E-01	3	13.22%
Q8IZP2	Protein FAM10A4	0.90	NA	NA	2	7.08%
P46940	Ras GTPase-activating-like protein IQGAP1	0.90	0.46	6.70E-01	4	2.72%
Q14195	Dihydropyrimidinase-related protein 3	0.89	0.37	5.40E-01	5	11.23%
P21796	Voltage-dependent anion-selective channel protein 1	0.89	0.28	4.20E-01	5	18.37%
P62269	40S ribosomal protein S18	0.89	0.42	6.20E-01	4	25.00%
Q9UII2	ATPase inhibitor, mitochondrial	0.89	NA	NA	2	7.55%
P13639	Elongation factor 2	0.89	0.31	5.70E-01	3	3.61%
Q3SY69	Probable 10-formyltetrahydrofolate dehydrogenase ALDH1L2	0.89	NA	NA	2	1.95%
Q9BQE3	Tubulin alpha-1C chain	0.89	0.26	2.30E-01	8	21.83%
P25788	Proteasome subunit alpha type-3	0.88	0.32	5.80E-01	3	13.73%
O43617	Trafficking protein particle complex subunit 3	0.88	NA	NA	2	12.78%

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P02545	Lamin-A/C	0.88	0.15	2.40E-05	35	41.42%
Q02818	Nucleobindin-1	0.88	0.34	3.50E-01	7	16.49%
Q9BXX3	Ankyrin repeat domain-containing protein 30A	0.88	NA	NA	2	1.00%
Q13838	Spliceosome RNA helicase BAT1	0.88	0.09	1.30E-01	3	8.41%
P26440	Isovaleryl-CoA dehydrogenase, mitochondrial	0.87	NA	NA	2	4.49%
P11021	78 kDa glucose-regulated protein	0.87	0.34	3.40E-02	30	47.09%
Q9UNM6	26S proteasome non-ATPase regulatory subunit 13	0.87	NA	NA	2	4.26%
P04439	HLA class I histocompatibility antigen, A-3 alpha chain	0.87	NA	NA	2	3.84%
P26373	60S ribosomal protein L13	0.86	0.38	3.90E-01	6	27.96%
P06730	Eukaryotic translation initiation factor 4E	0.86	NA	NA	2	9.68%
O00754	Lysosomal alpha-mannosidase	0.86	NA	NA	2	2.37%
Q96AY3	FK506-binding protein 10	0.86	0.28	1.70E-01	8	14.09%
Q86UP2	Kinectin	0.86	0.37	1.70E-01	13	10.91%
P04899	Guanine nucleotide-binding protein G(i), alpha-2 subunit	0.86	NA	NA	2	7.32%
P26641	Elongation factor 1-gamma	0.85	0.42	5.00E-01	4	10.07%
P25786	Proteasome subunit alpha type-1	0.85	0.13	4.40E-02	5	23.95%
Q13185	Chromobox protein homolog 3	0.85	0.31	4.60E-01	3	23.50%
Q99497	Protein DJ-1	0.85	0.79	7.60E-01	3	11.64%
O15145	Actin-related protein 2/3 complex subunit 3	0.85	NA	NA	2	9.55%
P62277	40S ribosomal protein S13	0.85	0.57	5.60E-01	5	32.45%
P17931	Galectin-3	0.85	0.19	1.80E-01	4	15.60%
P05023	Sodium/potassium-transporting ATPase subunit alpha-1	0.85	0.52	5.10E-01	5	4.99%
Q71DI3	Histone H3.2	0.85	0.17	9.20E-02	5	24.26%
Q9NZM1	Myoferlin	0.84	0.21	3.90E-02	9	5.48%
Q9NR12	PDZ and LIM domain protein 7	0.84	0.55	5.90E-01	4	7.44%
O14773	Tripeptidyl-peptidase 1	0.84	0.20	2.70E-01	3	6.22%
P23396	40S ribosomal protein S3	0.84	0.25	2.10E-01	5	21.40%
P05556	Integrin beta-1	0.84	0.49	4.30E-01	6	7.77%
Q15075	Early endosome antigen 1	0.84	0.40	3.30E-01	6	4.18%
P54289	Voltage-dependent calcium channel subunit alpha-2/delta-1	0.84	NA	NA	2	2.09%
Q99623	Prohibitin-2	0.84	0.35	2.00E-01	8	29.10%
P16402	Histone H1.3	0.84	0.34	3.70E-01	4	10.41%
P07686	Beta-hexosaminidase subunit beta	0.83	0.42	5.30E-01	3	6.12%
P09936	Ubiquitin carboxyl-terminal hydrolase isozyme L1	0.83	0.14	7.90E-02	4	18.83%
P51991	Heterogeneous nuclear ribonucleoprotein A3	0.83	0.24	2.30E-01	4	7.67%
P38159	Heterogeneous nuclear ribonucleoprotein G	0.83	NA	NA	2	5.63%
Q9Y6C2	EMILIN-1	0.83	0.17	3.30E-03	12	14.37%
P62318	Small nuclear ribonucleoprotein Sm D3	0.83	NA	NA	2	15.08%
P13667	Protein disulfide-isomerase A4	0.83	0.17	8.70E-03	10	13.64%
Q9NYU2	UDP-glucose:glycoprotein glucosyltransferase 1	0.83	NA	NA	2	1.54%
O75718	Cartilage-associated protein	0.83	0.19	2.40E-01	3	7.73%
Q96D15	Reticulocalbin-3	0.83	0.24	2.10E-01	4	17.07%
Q5SSJ5	Heterochromatin protein 1-binding protein 3	0.83	NA	NA	2	3.44%
P07910	Heterogeneous nuclear ribonucleoproteins C1/C2	0.83	0.24	1.60E-01	5	18.63%
Q9NZN4	EH domain-containing protein 2	0.83	0.23	6.70E-02	7	15.29%
Q9Y6G9	Cytoplasmic dynein 1 light intermediate chain 1	0.83	NA	NA	2	4.21%
P53621	Coatamer subunit alpha	0.83	NA	NA	2	2.45%
P62851	40S ribosomal protein S25	0.83	0.15	8.60E-02	4	25.60%
Q8TED1	Probable glutathione peroxidase 8	0.83	0.23	2.80E-01	3	11.00%
P40227	T-complex protein 1 subunit zeta	0.82	NA	NA	2	3.39%
P61254	60S ribosomal protein L26	0.82	0.39	3.10E-01	5	26.21%
P30153	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isofo	0.82	0.24	2.80E-01	3	5.60%
P27105	Erythrocyte band 7 integral membrane protein	0.82	0.39	3.80E-01	4	12.85%
P99999	Cytochrome c	0.82	0.46	5.30E-01	3	15.24%
P16401	Histone H1.5	0.81	NA	NA	2	5.75%
P08670	Vimentin	0.81	0.34	3.00E-05	55	75.11%
P26006	Integrin alpha-3	0.81	NA	NA	2	2.44%
P0C7M2	Putative heterogeneous nuclear ribonucleoprotein A1-like protein 3	0.81	NA	NA	2	7.19%
P09493	Tropomyosin alpha-1 chain	0.81	0.22	2.30E-01	3	9.86%
O94979	Protein transport protein Sec31A	0.81	NA	NA	2	1.39%
P07954	Fumarate hydratase, mitochondrial	0.80	NA	NA	2	3.73%
P13797	Plastin-3	0.80	0.03	5.00E-04	4	8.41%
P00505	Aspartate aminotransferase, mitochondrial	0.80	NA	NA	2	5.35%
Q14204	Cytoplasmic dynein 1 heavy chain 1	0.80	NA	NA	2	0.47%
Q02878	60S ribosomal protein L6	0.80	0.09	4.50E-03	5	14.93%
P08107	Heat shock 70 kDa protein 1	0.79	0.10	6.00E-02	3	5.46%
Q95302	FK506-binding protein 9	0.79	0.21	1.10E-01	4	6.84%
P06748	Nucleophosmin	0.79	0.47	2.40E-01	7	16.33%
P15586	N-acetylglucosamine-6-sulfatase	0.79	0.28	1.30E-01	5	9.06%
O60763	General vesicular transport factor p115	0.79	0.43	3.40E-01	4	3.64%
P55084	Trifunctional enzyme subunit beta, mitochondrial	0.79	0.07	1.70E-03	5	7.38%
Q7L7L0	Histone H2A type 3	0.79	0.28	2.80E-01	3	17.69%
P02751	Fibronectin	0.78	0.18	5.00E-08	30	16.55%
P40939	Trifunctional enzyme subunit alpha, mitochondrial	0.78	NA	NA	2	2.23%
P45880	Voltage-dependent anion-selective channel protein 2	0.78	0.61	3.70E-01	6	23.81%
Q96AE4	Far upstream element-binding protein 1	0.78	NA	NA	2	3.26%
P62241	40S ribosomal protein S8	0.78	NA	NA	2	8.65%
Q9NQC3	Reticulon-4	0.78	0.24	1.30E-01	4	4.28%
P23246	Splicing factor, proline- and glutamine-rich	0.78	0.62	3.60E-01	6	8.77%
P30837	Aldehyde dehydrogenase X, mitochondrial	0.78	0.23	2.00E-01	3	6.96%
P29279	Connective tissue growth factor	0.77	NA	NA	2	6.30%
P04843	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	0.77	0.34	1.70E-01	5	9.39%
Q92841	Probable ATP-dependent RNA helicase DDX17	0.77	0.14	3.40E-02	4	6.62%
O15400	Syntaxin-7	0.77	NA	NA	2	7.66%
O75083	WD repeat-containing protein 1	0.77	0.10	1.20E-02	4	5.45%
O43399	Tumor protein D54	0.77	0.50	3.00E-01	5	26.21%
Q12906	Interleukin enhancer-binding factor 3	0.77	0.32	9.60E-02	6	8.61%
P50990	T-complex protein 1 subunit theta	0.76	0.51	2.30E-01	6	10.77%
P61006	Ras-related protein Rab-8A	0.75	0.19	6.00E-02	4	17.87%

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Q9UHG3	Prenylcysteine oxidase 1	0.75	NA	NA	2	5.54%
P09622	Dihydrolipoyl dehydrogenase, mitochondrial	0.75	0.26	1.20E-01	4	8.06%
P01033	Metalloproteinase inhibitor 1	0.75	NA	NA	2	7.25%
P21589	5'-phosphonucleotidase	0.75	0.52	1.10E-01	10	21.25%
P17987	T-complex protein 1 subunit alpha	0.75	0.44	3.70E-01	3	5.58%
Q969H8	UPF0556 protein C19orf10	0.75	0.21	1.40E-01	3	17.34%
P46776	60S ribosomal protein L27a	0.75	0.63	5.00E-01	3	16.22%
O95336	6-phosphogluconolactonase	0.74	0.64	5.10E-01	3	14.73%
Q96HE7	ERO1-like protein alpha	0.74	NA	NA	2	5.13%
P49748	Very long-chain specific acyl-CoA dehydrogenase, mitochondrial	0.74	NA	NA	2	2.90%
Q07954	Prolow-density lipoprotein receptor-related protein 1	0.74	0.46	1.00E-01	8	2.09%
P07339	Cathepsin D	0.73	0.41	3.20E-01	3	7.28%
Q14103	Heterogeneous nuclear ribonucleoprotein D0	0.73	0.34	2.50E-01	3	8.45%
P27824	Calnexin	0.73	0.57	3.50E-01	4	7.43%
Q9UKS6	Protein kinase C and casein kinase substrate in neurons protein 3	0.73	NA	NA	2	6.60%
P27797	Calreticulin	0.73	0.34	3.10E-02	8	15.35%
P02452	Collagen alpha-1(I) chain	0.72	NA	NA	2	2.19%
O95571	Protein ETHE1, mitochondrial	0.72	NA	NA	2	12.20%
P22307	Non-specific lipid-transfer protein	0.72	0.25	2.30E-02	6	7.50%
P30040	Endoplasmic reticulum protein ERp29	0.72	0.30	4.30E-02	6	24.52%
P05388	60S acidic ribosomal protein P0	0.72	0.41	2.10E-01	4	11.04%
Q00839	Heterogeneous nuclear ribonucleoprotein U	0.72	NA	NA	2	2.67%
O00483	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 4	0.72	0.40	2.90E-01	3	32.10%
Q12907	Vesicular integral-membrane protein VIP36	0.72	NA	NA	2	5.34%
P62805	Histone H4	0.71	0.47	1.40E-01	6	42.72%
O94925	Glutaminase kidney isoform, mitochondrial	0.71	0.09	2.30E-02	3	5.38%
P55786	Puromycin-sensitive aminopeptidase	0.70	NA	NA	2	2.39%
Q9GZY8	Mitochondrial fission factor	0.70	NA	NA	2	6.43%
Q15293	Reticulocalbin-1	0.70	0.30	9.50E-02	4	14.20%
Q14697	Neutral alpha-glucosidase AB	0.69	0.27	7.30E-02	4	4.45%
Q14108	Lysosome membrane protein 2	0.69	NA	NA	2	3.14%
P37108	Signal recognition particle 14 kDa protein	0.69	NA	NA	2	16.18%
P10619	Lysosomal protective protein	0.69	NA	NA	2	2.71%
P61247	40S ribosomal protein S3a	0.68	0.43	1.20E-01	5	18.18%
P40925	Malate dehydrogenase, cytoplasmic	0.68	NA	NA	2	4.79%
Q99536	Synaptic vesicle membrane protein VAT-1 homolog	0.68	0.22	9.40E-02	3	11.45%
P14625	Endoplasmic	0.67	0.33	7.60E-06	23	23.91%
Q9ULV4	Coronin-1C	0.67	NA	NA	2	3.80%
Q9HDC9	Adipocyte plasma membrane-associated protein	0.66	NA	NA	2	5.29%
O15144	Actin-related protein 2/3 complex subunit 2	0.66	NA	NA	2	5.33%
Q12797	Aspartyl/asparaginyl beta-hydroxylase	0.66	0.18	6.10E-03	5	6.73%
P15121	Aldose reductase	0.65	NA	NA	2	4.43%
P06703	Protein S100-A6	0.65	0.42	1.40E-01	4	25.56%
P02792	Ferritin light chain	0.65	NA	NA	2	12.57%
Q15084	Protein disulfide-isomerase A6	0.65	0.46	2.10E-02	9	21.14%
Q14764	Major vault protein	0.65	0.56	1.10E-01	6	6.27%
P09382	Galectin-1	0.65	0.12	5.50E-03	4	26.67%
P0C0L4	Complement C4-A	0.64	NA	NA	2	1.32%
Q08211	ATP-dependent RNA helicase A	0.64	0.21	6.90E-02	3	2.76%
Q07666	KH domain-containing, RNA-binding, signal transduction-associated protein 1	0.64	NA	NA	2	2.71%
P07900	Heat shock protein HSP 90-alpha	0.63	NA	NA	2	3.01%
P16070	CD44 antigen	0.61	0.66	3.30E-01	3	4.85%
P30533	Alpha-2-macroglobulin receptor-associated protein	0.61	0.22	2.00E-02	4	11.20%
P39019	40S ribosomal protein S19	0.61	0.40	1.60E-01	3	11.72%
P23142	Fibulin-1	0.60	NA	NA	2	3.27%
P07996	Thrombospondin-1	0.60	NA	NA	2	1.97%
P23284	Peptidyl-prolyl cis-trans isomerase B	0.59	0.27	3.40E-05	12	41.20%
P04216	Thy-1 membrane glycoprotein	0.59	NA	NA	2	15.53%
P48681	Nestin	0.58	0.52	7.70E-02	5	3.52%
Q00610	Clathrin heavy chain 1	0.56	0.18	7.40E-03	4	1.85%
O60701	UDP-glucose 6-dehydrogenase	0.56	0.50	1.90E-01	3	8.10%
Q9Y4L1	Hypoxia up-regulated protein 1	0.55	0.42	6.40E-02	4	3.90%
P50454	Serpin H1	0.55	0.17	5.30E-03	4	12.20%
Q9BVK6	Transmembrane emp24 domain-containing protein 9	0.54	0.49	1.60E-01	3	10.64%
Q13561	Dynactin subunit 2	0.53	0.64	2.30E-01	3	5.99%
P10319	HLA class I histocompatibility antigen, B-58 alpha chain	0.50	NA	NA	2	9.39%
P46781	40S ribosomal protein S9	0.50	0.56	1.60E-01	3	13.92%
Q9BS40	Latexin	0.48	NA	NA	2	12.16%
O75964	ATP synthase subunit g, mitochondrial	0.48	NA	NA	2	21.36%
Q16181	Septin-7	0.48	NA	NA	2	7.32%
P39656	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit	0.44	NA	NA	2	3.51%
P04179	Superoxide dismutase [Mn], mitochondrial	0.43	0.25	1.60E-03	5	21.17%
Q13162	Peroxisome dismutase 4	0.43	0.65	1.50E-01	3	12.92%
Q99584	Protein S100-A13	0.43	NA	NA	2	20.41%
P29966	Myristoylated alanine-rich C-kinase substrate	0.33	NA	NA	2	5.42%

Average false discovery rate = 1.9% peptide identity, 2.9% peptide homology; NA = not applicable because < 3 peptides.