

Supplementary Table S2

Relative Protein Abundance: Trabecular Meshwork Sample NTM496-05

Total Proteins Quantified = 485; Median Protein iTRAQ Ratio = 1.00; Mean Protein iTRAQ Ratio = 1.02; Standard Deviation = 0.38

SwissProtein Accession	Protein	Protein iTRAQ Ratio Dex/Control	Standard Deviation	P value	Unique Peptides	Sequence Coverage
P51858	Hepatoma-derived growth factor	3.60	NA	NA	2	8.75%
O94875	Sorbin and SH3 domain-containing protein 2	3.47	0.75	2.30E-03	8	8.91%
Q0ZGT2	Nexilin	3.39	0.34	1.30E-03	5	7.11%
P00325	Alcohol dehydrogenase 1B	3.02	NA	NA	2	4.53%
P07858	Cathepsin B	2.98	NA	NA	2	7.67%
Q13740	CD166 antigen	2.75	0.26	2.20E-02	3	5.83%
Q9HBL0	Tensin-1	2.66	NA	NA	2	1.27%
O75487	Glypican-4	2.63	NA	NA	2	4.50%
P36269	Gamma-glutamyltransferase 5	2.62	0.32	3.50E-02	3	6.14%
P98160	Basement membrane-specific heparan sulfate proteoglycan core protein	2.52	0.57	2.20E-02	5	1.21%
Q92734	Protein TFG	2.49	NA	NA	2	4.50%
Q16698	2,4-dienoyl-CoA reductase, mitochondrial	2.41	NA	NA	2	4.48%
Q99536	Synaptic vesicle membrane protein VAT-1 homolog	2.36	NA	NA	2	8.91%
P63010	AP-2 complex subunit beta-1	2.32	NA	NA	2	1.92%
Q9Y6C2	EMILIN-1	2.29	0.55	2.80E-02	5	5.12%
O75369	Filamin-B	2.29	0.40	3.00E-09	22	9.22%
P50479	PDZ and LIM domain protein 4	2.28	0.43	8.00E-02	3	8.18%
Q9UJ7	GTP:AMP phosphotransferase mitochondrial	2.26	0.53	2.60E-02	5	24.67%
Q16881	Thioredoxin reductase 1, cytoplasmic	2.19	0.61	1.60E-01	3	5.55%
P80723	Brain acid soluble protein 1	2.13	0.30	5.10E-03	5	41.41%
Q99497	Protein DJ-1	2.11	1.23	3.10E-01	4	21.16%
P30533	Alpha-2-macroglobulin receptor-associated protein	2.04	NA	NA	2	4.76%
Q9UJZ1	Stomatin-like protein 2	2.04	NA	NA	2	9.27%
Q9NR28	Diablo homolog, mitochondrial	2.03	NA	NA	2	8.79%
O14773	Tripeptidyl-peptidase 1	2.01	NA	NA	2	3.73%
P31513	Dimethylalanine monooxygenase [N-oxide-forming] 3	1.95	NA	NA	2	3.57%
Q15417	Calponin-3	1.94	0.42	5.00E-02	4	14.29%
Q16555	Dihydropyrimidinase-related protein 2	1.92	0.19	1.60E-03	5	10.66%
P61224	Ras-related protein Rap-1b	1.88	NA	NA	2	11.41%
Q96CX2	BTB/POZ domain-containing protein KCTD12	1.87	NA	NA	2	6.46%
Q04828	Aldo-keto reductase family 1 member C1	1.85	0.14	1.80E-02	3	7.43%
P10301	Ras-related protein R-Ras	1.85	NA	NA	2	12.39%
Q969G5	Protein kinase C delta-binding protein	1.84	NA	NA	2	8.05%
Q9Y6N5	Sulfide:quinone oxidoreductase, mitochondrial	1.83	0.08	5.10E-03	3	6.89%
Q14767	Latent-transforming growth factor beta-binding protein 2	1.82	NA	NA	2	1.59%
Q00839	Heterogeneous nuclear ribonucleoprotein U	1.79	NA	NA	2	1.94%
Q99715	Collagen alpha-1(XII) chain	1.79	NA	NA	2	0.65%
Q16891	Mitochondrial inner membrane protein	1.74	0.61	1.10E-01	5	7.65%
P51991	Heterogeneous nuclear ribonucleoprotein A3	1.69	NA	NA	2	3.44%
P21589	5'-nucleotidase	1.67	0.51	1.40E-01	4	6.10%
Q96HE7	ERO1-like protein alpha	1.66	NA	NA	2	4.06%
O15144	Actin-related protein 2/3 complex subunit 2	1.64	NA	NA	2	5.33%
P09497	Clathrin light chain B	1.64	NA	NA	2	8.30%
Q99714	3-hydroxyacyl-CoA dehydrogenase type-2	1.64	NA	NA	2	7.66%
Q13642	Four and a half LIM domains protein 1	1.63	NA	NA	2	7.12%
P61604	10 kDa heat shock protein, mitochondrial	1.63	0.13	2.80E-04	6	50.00%
P67936	Tropomyosin alpha-4 chain	1.63	0.26	4.10E-08	21	57.26%
P00367	Glutamate dehydrogenase 1, mitochondrial	1.63	0.18	3.80E-03	5	7.71%
P29692	Elongation factor 1-delta	1.63	0.20	5.40E-02	3	9.61%
P37837	Transaldolase	1.62	0.19	1.60E-03	6	15.73%
Q9NR12	PDZ and LIM domain protein 7	1.62	0.87	2.90E-01	5	9.85%
Q5QNW6	Histone H2B type 2-F	1.61	0.18	3.70E-04	7	46.03%
Q13442	28 kDa heat- and acid-stable phosphoprotein	1.61	NA	NA	2	14.36%
Q03252	Lamin-B2	1.61	0.25	3.30E-02	4	6.33%
P52272	Heterogeneous nuclear ribonucleoprotein M	1.61	0.18	1.30E-02	4	8.22%
O43678	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 2	1.61	NA	NA	2	10.10%
P20674	Cytochrome c oxidase subunit 5A, mitochondrial	1.60	NA	NA	2	14.67%
Q9NX63	Coiled-coil-helix-coiled-coil-helix domain-containing protein 3, mitochondrial	1.60	NA	NA	2	7.05%
P02751	Fibronectin	1.59	0.27	1.80E-10	30	15.00%
P47755	F-actin-capping protein subunit alpha-2	1.59	NA	NA	2	9.79%
Q8WX93	Palladin	1.58	NA	NA	2	1.52%
Q14847	LIM and SH3 domain protein 1	1.57	0.37	9.00E-02	4	15.71%
Q01105	Protein SET	1.57	NA	NA	2	7.93%
P40261	Nicotinamide N-methyltransferase	1.56	NA	NA	2	6.06%
Q9Y646	Plasma glutamate carboxypeptidase	1.55	NA	NA	2	4.24%
P22626	Heterogeneous nuclear ribonucleoproteins A2/B1	1.55	0.37	3.30E-02	6	16.71%
P30049	ATP synthase subunit delta, mitochondrial	1.52	NA	NA	2	13.69%
P08648	Integrin alpha-5	1.51	NA	NA	2	2.00%
Q15942	Zyxin	1.50	0.47	1.30E-01	5	7.52%
P05023	Sodium/potassium-transporting ATPase subunit alpha-1	1.50	0.53	1.60E-01	5	5.77%
P14866	Heterogeneous nuclear ribonucleoprotein L	1.50	0.27	1.20E-01	3	6.45%
Q14103	Heterogeneous nuclear ribonucleoprotein D0	1.47	NA	NA	2	7.32%
P37802	Transgelin-2	1.47	0.22	3.50E-03	7	39.70%
P62857	40S ribosomal protein S28	1.46	NA	NA	2	30.43%
P19338	Nucleolin	1.46	0.34	2.50E-03	12	17.04%
P15144	Aminopeptidase N	1.46	1.17	6.30E-01	3	3.10%
Q05682	Caldesmon	1.45	0.09	1.20E-08	12	13.49%
P0C0S8	Histone H2A type 1	1.45	0.50	2.30E-01	4	32.31%
P10606	Cytochrome c oxidase subunit 5B, mitochondrial	1.45	0.15	4.90E-02	3	20.16%
O14974	Protein phosphatase 1 regulatory subunit 12A	1.43	0.50	1.80E-01	5	6.50%
P00403	Cytochrome c oxidase subunit 2	1.43	NA	NA	2	7.49%
Q9P2R7	Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial	1.43	NA	NA	2	3.89%
Q15424	Scaffold attachment factor B1	1.42	NA	NA	2	1.86%
P0C0L4	Complement C4-A	1.42	NA	NA	2	0.92%
P11413	Glucose-6-phosphate 1-dehydrogenase	1.42	0.35	1.40E-01	4	7.77%
P29992	Guanine nucleotide-binding protein subunit alpha-11	1.41	0.28	1.70E-01	3	7.24%
Q5JWF2	Guanine nucleotide-binding protein G(s) subunit alpha isoforms XLas	1.41	NA	NA	2	2.31%
O00483	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 4	1.41	NA	NA	2	22.22%

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P48047	ATP synthase subunit O, mitochondrial	1.41	0.35	9.30E-02	5	24.41%
P29401	Transketolase	1.41	0.31	2.00E-03	13	23.27%
Q09666	Neuroblast differentiation-associated protein AHNAK	1.40	0.28	3.30E-22	103	15.33%
Q03135	Caveolin-1	1.40	0.44	1.60E-01	5	28.09%
P35241	Radixin	1.40	NA	NA	2	2.57%
Q06830	Peroxioredoxin-1	1.39	0.17	7.00E-05	11	47.24%
P07339	Cathepsin D	1.39	0.30	4.10E-02	6	15.78%
O75477	Erlin-1	1.38	NA	NA	2	6.94%
P61978	Heterogeneous nuclear ribonucleoprotein K	1.38	0.19	4.60E-03	7	18.14%
Q13011	Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial	1.38	NA	NA	2	4.88%
P60174	Triosephosphate isomerase	1.37	0.29	3.00E-02	7	27.71%
Q16851	UTP-glucose-1-phosphate uridylyltransferase	1.36	0.43	1.40E-01	6	11.22%
Q96AQ6	Pre-B-cell leukemia transcription factor-interacting protein 1	1.36	NA	NA	2	2.87%
Q6NZI2	Polymerase I and transcript release factor	1.35	0.20	2.80E-04	12	28.72%
Q86UP2	Kinectin	1.34	0.46	3.80E-01	3	2.80%
P21333	Filamin-A	1.34	0.24	7.20E-13	56	25.01%
Q07955	Splicing factor, arginine/serine-rich 1	1.34	0.09	6.90E-03	4	12.50%
P50991	T-complex protein 1 subunit delta	1.34	NA	NA	2	3.71%
Q02818	Nucleobindin-1	1.34	0.51	4.30E-01	3	8.68%
P29590	Probable transcription factor PML	1.33	0.22	1.50E-01	3	3.51%
P46783	40S ribosomal protein S10	1.33	NA	NA	2	10.91%
P16402	Histone H1.3	1.33	0.33	1.30E-01	5	15.38%
Q01130	Splicing factor, arginine/serine-rich 2	1.32	0.07	1.80E-02	3	14.48%
Q55S5J	Heterochromatin protein 1-binding protein 3	1.32	NA	NA	2	3.44%
P23246	Splicing factor, proline- and glutamine-rich	1.31	0.18	2.90E-02	5	6.65%
Q13510	Acid ceramidase	1.31	NA	NA	2	4.81%
P52209	6-phosphogluconate dehydrogenase, decarboxylating	1.30	0.70	5.10E-01	4	8.90%
P36957	Dihydropolyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase	1.30	0.26	9.00E-02	5	11.48%
Q16181	Septin-7	1.29	NA	NA	2	4.35%
P12814	Alpha-actinin-1	1.29	0.20	7.30E-04	13	19.28%
P38646	Stress-70 protein, mitochondrial	1.29	0.27	1.60E-02	10	17.82%
Q99439	Calponin-2	1.29	0.21	9.70E-02	4	12.30%
Q15019	Septin-2	1.28	0.55	4.40E-01	4	11.36%
P15586	N-acetylglucosamine-6-sulfatase	1.28	NA	NA	2	3.26%
P11216	Glycogen phosphorylase, brain form	1.27	NA	NA	2	2.25%
P24752	Acetyl-CoA acetyltransferase, mitochondrial	1.27	NA	NA	2	4.22%
Q96QR8	Transcriptional activator protein Pur-beta	1.27	NA	NA	2	4.49%
Q9NYL9	Tropomodulin-3	1.26	0.20	1.90E-01	3	9.94%
P42765	3-ketoacyl-CoA thiolase, mitochondrial	1.26	0.53	5.30E-01	3	5.54%
Q13813	Spectrin alpha chain, brain	1.26	0.31	2.20E-03	22	9.83%
Q63ZY3	KN motif and ankyrin repeat domain-containing protein 2	1.26	0.25	1.10E-01	5	5.64%
Q15233	Non-POU domain-containing octamer-binding protein	1.25	0.18	5.20E-02	5	8.70%
P40926	Malate dehydrogenase, mitochondrial	1.24	0.10	1.20E-03	7	23.08%
O00469	Procollagen-lysine,2-oxoglutarate 5-dioxygenase 2	1.24	1.06	7.60E-01	3	5.29%
P82979	Nuclear protein Hcc-1	1.24	NA	NA	2	9.52%
P02545	Lamin-A/C	1.24	0.22	1.80E-05	29	32.83%
Q14315	Filamin-C	1.24	0.74	5.50E-01	5	1.98%
P62158	Calmodulin	1.23	0.38	3.50E-01	4	21.48%
O75367	Core histone macro-H2A.1	1.23	0.18	1.90E-01	3	9.68%
Q13418	Integrin-linked protein kinase	1.23	0.63	5.00E-01	5	10.18%
Q16643	Drebrin	1.23	0.63	5.60E-01	4	7.86%
P24534	Elongation factor 1-beta	1.23	NA	NA	2	7.11%
P17844	Probable ATP-dependent RNA helicase DDX5	1.22	0.20	1.40E-01	4	6.19%
P55010	Eukaryotic translation initiation factor 5	1.22	NA	NA	2	4.87%
Q9BS26	Endoplasmic reticulum resident protein ERp44	1.22	NA	NA	2	4.43%
P35613	Basigin	1.22	NA	NA	2	7.27%
P05387	60S acidic ribosomal protein P2	1.22	NA	NA	2	24.35%
Q71DI3	Histone H3.2	1.22	0.17	1.00E-01	4	19.12%
P27824	Calnexin	1.22	NA	NA	2	3.89%
A6NL28	Putative tropomyosin alpha-3 chain-like protein	1.21	0.19	2.30E-01	3	10.76%
P09651	Heterogeneous nuclear ribonucleoprotein A1	1.21	0.30	3.80E-01	3	8.87%
Q9NSD9	Phenylalanyl-tRNA synthetase beta chain	1.21	0.48	5.60E-01	3	4.92%
Q13557	Calcium/calmodulin-dependent protein kinase type II delta chain	1.21	NA	NA	2	3.81%
Q9H223	EH domain-containing protein 4	1.21	0.25	3.20E-01	3	7.02%
P06748	Nucleophosmin	1.20	0.46	3.80E-01	6	12.93%
P00441	Superoxide dismutase [Cu-Zn]	1.20	NA	NA	2	18.18%
P60709	Actin, cytoplasmic 1	1.20	0.38	7.10E-02	17	47.20%
P20700	Lamin-B1	1.19	0.19	1.10E-01	5	7.85%
Q02878	60S ribosomal protein L6	1.19	0.59	5.40E-01	5	14.93%
Q9P0K7	Ankyrin	1.19	NA	NA	2	1.73%
P21980	Protein-glutamine gamma-glutamyltransferase 2	1.19	NA	NA	2	2.33%
Q07666	KH domain-containing, RNA-binding, signal transduction-associated protein 1	1.18	0.50	5.50E-01	4	6.32%
Q01082	Spectrin beta chain, brain 1	1.18	0.49	3.10E-01	10	4.27%
O14950	Myosin regulatory light chain 12B	1.18	0.22	2.30E-01	4	17.44%
P60842	Eukaryotic initiation factor 4A-I	1.18	NA	NA	2	6.40%
Q5JTV8	Torsin-1A-interacting protein 1	1.18	NA	NA	2	3.26%
P46821	Microtubule-associated protein 1B	1.18	0.34	8.70E-02	15	7.25%
P09622	Dihydropolyl dehydrogenase, mitochondrial	1.18	NA	NA	2	3.34%
Q99733	Nucleosome assembly protein 1-like 4	1.17	NA	NA	2	5.60%
P49411	Elongation factor Tu, mitochondrial	1.17	0.24	1.70E-01	6	13.72%
O43707	Alpha-actinin-4	1.17	0.17	1.60E-02	10	15.04%
P11047	Laminin subunit gamma-1	1.17	0.18	2.80E-01	3	2.24%
P35611	Alpha-adducin	1.17	NA	NA	2	2.99%
P60660	Myosin light polypeptide 6	1.17	0.15	8.00E-02	5	34.44%
P06753	Tropomyosin alpha-3 chain	1.16	0.71	7.50E-01	3	11.27%
P35268	60S ribosomal protein L22	1.16	NA	NA	2	18.75%
P62258	14-3-3 protein epsilon	1.16	1.40	7.90E-01	7	23.92%
P00558	Phosphoglycerate kinase 1	1.16	0.23	8.20E-02	10	24.46%
Q16836	Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial	1.15	NA	NA	2	6.69%
P46779	60S ribosomal protein L28	1.15	NA	NA	2	13.14%
O15173	Membrane-associated progesterone receptor component 2	1.15	NA	NA	2	6.28%
Q6NUK1	Calcium-binding mitochondrial carrier protein SCAcMC-1	1.14	NA	NA	2	3.35%
P69905	Hemoglobin subunit alpha	1.14	NA	NA	2	11.27%
P08107	Heat shock 70 kDa protein 1	1.13	0.44	5.70E-01	5	8.42%
P52597	Heterogeneous nuclear ribonucleoprotein F	1.12	NA	NA	2	1.93%
O14745	Na(+)/H(+) exchange regulatory cofactor NHE-RF1	1.12	NA	NA	2	7.54%

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Q9BRK5	45 kDa calcium-binding protein	1.12	NA	NA	2	5.80%
Q12904	Multisynthetase complex auxiliary component p43	1.12	NA	NA	2	8.01%
P09669	Cytochrome c oxidase subunit 6C	1.12	NA	NA	2	20.00%
Q15181	Inorganic pyrophosphatase	1.12	NA	NA	2	5.54%
P35232	Prohibitin	1.11	0.22	2.80E-01	6	20.96%
Q9NX24	H/ACA ribonucleoprotein complex subunit 2	1.11	NA	NA	2	13.07%
P35579	Myosin-9	1.11	0.30	6.30E-02	33	14.44%
P00338	L-lactate dehydrogenase A chain	1.10	0.36	4.60E-01	8	22.29%
Q8WW11	LIM domain only protein 7	1.10	0.16	4.10E-01	3	2.32%
P04843	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	1.10	0.49	7.20E-01	4	6.43%
Q04760	Lactoylglutathione lyase	1.10	0.08	1.90E-01	3	14.13%
P10515	Dihydrolypolyllysine-residue acetyltransferase component of pyruvate dehydrogen	1.09	NA	NA	2	2.47%
P26440	Isovaleryl-CoA dehydrogenase, mitochondrial	1.09	NA	NA	2	4.49%
O60664	Mannose-6-phosphate receptor-binding protein 1	1.08	0.76	8.20E-01	5	15.44%
Q969X5	Endoplasmic reticulum-Golgi intermediate compartment protein 1	1.08	0.45	7.90E-01	3	9.31%
Q96HC4	PDZ and LIM domain protein 5	1.08	0.30	5.40E-01	6	13.09%
P25705	ATP synthase subunit alpha, mitochondrial	1.08	0.28	3.60E-01	11	20.43%
Q15370	Transcription elongation factor B polypeptide 2	1.08	NA	NA	2	12.71%
P06733	Alpha-enolase	1.08	0.28	2.90E-01	15	35.94%
P62917	60S ribosomal protein L8	1.08	NA	NA	2	8.95%
P04179	Superoxide dismutase [Mn], mitochondrial	1.07	NA	NA	2	9.46%
P61981	14-3-3 protein gamma	1.07	0.35	7.60E-01	3	13.77%
P15880	40S ribosomal protein S2	1.07	NA	NA	2	5.80%
O75396	Vesicle-trafficking protein SEC22b	1.07	0.16	4.60E-01	4	20.47%
Q9Y3Y2	Uncharacterized protein C1orf77	1.07	NA	NA	2	11.69%
P07951	Tropomyosin beta chain	1.06	0.14	1.90E-01	10	28.52%
P24844	Myosin regulatory light polypeptide 9	1.06	0.67	8.90E-01	3	17.44%
P62750	60S ribosomal protein L23a	1.06	0.33	7.80E-01	3	19.87%
Q14247	Src substrate cactactin	1.06	0.17	6.10E-01	3	5.27%
P06396	Gelsolin	1.05	0.13	5.00E-01	4	4.73%
P13798	Acylamino-acid-releasing enzyme	1.05	NA	NA	2	2.32%
P06454	Prothymosin alpha	1.04	NA	NA	2	12.61%
P07910	Heterogeneous nuclear ribonucleoproteins C1/C2	1.04	0.20	6.40E-01	6	20.59%
Q15149	Plectin-1	1.04	0.27	3.30E-01	42	8.90%
Q40939	Trifunctional enzyme subunit alpha, mitochondrial	1.04	0.05	3.40E-01	3	3.54%
Q8WUP2	Filamin-binding LIM protein 1	1.04	0.13	6.60E-01	3	9.38%
P62937	Peptidyl-prolyl cis-trans isomerase A	1.03	0.23	7.40E-01	6	28.48%
P43307	Translocon-associated protein subunit alpha	1.03	NA	NA	2	6.64%
Q12906	Interleukin enhancer-binding factor 3	1.03	0.44	9.00E-01	4	4.81%
P06576	ATP synthase subunit beta, mitochondrial	1.03	0.45	8.20E-01	14	30.43%
P54819	Adenylate kinase 2, mitochondrial	1.03	NA	NA	2	11.30%
P43686	26S protease regulatory subunit 6B	1.03	NA	NA	2	4.31%
P62424	60S ribosomal protein L7a	1.02	NA	NA	2	7.52%
P38159	Heterogeneous nuclear ribonucleoprotein G	1.02	NA	NA	2	5.37%
Q13561	Dynactin subunit 2	1.02	0.30	9.20E-01	4	8.73%
P35580	Myosin-10	1.02	0.12	8.50E-01	3	1.47%
Q9Y2B0	Protein canopy homolog 2	1.01	NA	NA	2	14.29%
P07355	Annexin A2	1.01	0.19	7.70E-01	18	48.67%
P11142	Heat shock cognate 71 kDa protein	1.01	0.17	7.90E-01	12	18.58%
P68371	Tubulin beta-2C chain	1.01	NA	NA	2	6.07%
P25398	40S ribosomal protein S12	1.01	NA	NA	2	13.64%
P10809	60 kDa heat shock protein, mitochondrial	1.01	0.32	9.10E-01	14	20.42%
P62851	40S ribosomal protein S25	1.01	0.05	7.90E-01	3	20.80%
Q15365	Poly(rC)-binding protein 1	1.01	NA	NA	2	4.78%
P11177	Pyruvate dehydrogenase E1 component subunit beta, mitochondrial	1.01	NA	NA	2	4.18%
P22307	Non-specific lipid-transfer protein	1.01	NA	NA	2	3.84%
P21796	Voltage-dependent anion-selective channel protein 1	1.00	0.05	8.60E-01	4	13.43%
P50552	Vasodilator-stimulated phosphoprotein	1.00	NA	NA	2	5.53%
P07602	Proactivator polypeptide	1.00	0.38	9.90E-01	3	4.58%
P39023	60S ribosomal protein L3	1.00	NA	NA	2	3.72%
P26641	Elongation factor 1-gamma	1.00	0.27	1.00E+00	5	7.09%
Q9BUF5	Tubulin beta-6 chain	1.00	NA	NA	2	6.73%
Q9NVA2	Septin-11	1.00	NA	NA	2	3.96%
P31946	14-3-3 protein beta/alpha	0.99	0.12	9.30E-01	4	17.07%
P15531	Nucleoside diphosphate kinase A	0.99	NA	NA	2	19.08%
P49368	T-complex protein 1 subunit gamma	0.99	0.80	9.90E-01	4	6.61%
P18206	Vinculin	0.99	0.28	8.90E-01	24	23.46%
P04792	Heat shock protein beta-1	0.99	0.18	8.40E-01	7	36.10%
P49207	60S ribosomal protein L34	0.98	NA	NA	2	12.82%
P07585	Decorin	0.98	NA	NA	2	5.01%
Q9Y490	Talin-1	0.98	0.27	7.40E-01	17	7.24%
P07686	Beta-hexosaminidase subunit beta	0.97	0.20	8.40E-01	3	4.50%
P30086	Phosphatidylethanolamine-binding protein 1	0.97	0.14	6.60E-01	4	26.74%
P55084	Trifunctional enzyme subunit beta, mitochondrial	0.97	0.17	6.90E-01	5	8.44%
P04075	Fructose-bisphosphate aldolase A	0.97	0.17	4.80E-01	12	36.54%
Q15056	Eukaryotic translation initiation factor 4H	0.96	NA	NA	2	9.27%
Q96AE4	Far upstream element-binding protein 1	0.96	0.15	6.60E-01	4	5.75%
P09382	Galectin-1	0.96	0.23	7.60E-01	4	26.67%
P30837	Aldehyde dehydrogenase X, mitochondrial	0.96	NA	NA	2	3.48%
Q13263	Transcription intermediary factor 1-beta	0.96	0.18	6.50E-01	4	5.27%
O75521	Peroxisomal 3,2-trans-enoyl-CoA isomerase	0.96	NA	NA	2	6.60%
Q9NZN4	EH domain-containing protein 2	0.96	0.31	7.40E-01	6	9.94%
P16401	Histone H1.5	0.95	NA	NA	2	10.18%
Q9H299	SH3 domain-binding glutamic acid-rich-like protein 3	0.95	NA	NA	2	31.18%
P62805	Histone H4	0.95	0.35	7.00E-01	8	52.43%
Q7KZF4	Staphylococcal nuclease domain-containing protein 1	0.95	0.25	7.20E-01	4	4.18%
Q99623	Prohibitin-2	0.95	0.10	3.70E-01	4	14.72%
P27348	14-3-3 protein theta	0.95	NA	NA	2	8.16%
P62753	40S ribosomal protein S6	0.95	NA	NA	2	5.22%
Q13765	Nascent polypeptide-associated complex subunit alpha	0.95	NA	NA	2	13.49%
Q12797	Aspartyl/asparaginyl beta-hydroxylase	0.95	0.12	4.50E-01	4	5.15%
P32969	60S ribosomal protein L9	0.94	NA	NA	2	8.85%
P55786	Puromycin-sensitive aminopeptidase	0.94	0.45	8.30E-01	3	3.16%
P05556	Integrin beta-1	0.94	0.20	4.40E-01	7	8.90%
P27816	Microtubule-associated protein 4	0.93	0.43	6.90E-01	7	7.03%
O94925	Glutaminase kidney isoform, mitochondrial	0.93	NA	NA	2	3.74%

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P50995	Annexin A11	0.93	0.24	6.60E-01	3	7.52%
P35221	Catenin alpha-1	0.93	NA	NA	2	1.88%
Q14764	Major vault protein	0.93	0.13	2.80E-01	5	5.71%
P30044	Peroxisome oxidase, mitochondrial	0.93	NA	NA	2	10.28%
P38117	Electron transfer flavoprotein subunit beta	0.93	0.46	7.60E-01	4	13.33%
P08758	Annexin A5	0.93	0.62	6.90E-01	11	28.44%
P07195	L-lactate dehydrogenase B chain	0.92	0.27	5.10E-01	6	16.77%
Q04917	14-3-3 protein eta	0.92	0.31	6.90E-01	3	10.57%
P51149	Ras-related protein Rab-7a	0.92	0.25	6.10E-01	3	14.98%
Q16658	Fascin	0.91	NA	NA	2	5.68%
P09936	Ubiquitin carboxyl-terminal hydrolase isozyme L1	0.91	0.15	3.00E-01	4	21.52%
P62244	40S ribosomal protein S15a	0.91	NA	NA	2	13.08%
O43852	Calumenin	0.91	0.49	7.70E-01	3	8.25%
P49419	Alpha-aminoacidic semialdehyde dehydrogenase	0.91	0.25	5.70E-01	3	5.87%
P10599	Thioredoxin	0.91	0.62	8.10E-01	3	22.86%
Q9UUK9	ADP-sugar pyrophosphatase	0.91	NA	NA	2	8.22%
P30084	Enoyl-CoA hydratase, mitochondrial	0.91	0.10	2.10E-01	3	8.62%
P09493	Tropomyosin alpha-1 chain	0.90	0.92	8.00E-01	6	14.79%
Q94826	Mitochondrial import receptor subunit TOM70	0.90	0.17	4.10E-01	3	3.78%
Q15145	Actin-related protein 2/3 complex subunit 3	0.90	NA	NA	2	10.11%
Q9H2U2	Inorganic pyrophosphatase 2, mitochondrial	0.90	NA	NA	2	5.09%
P62280	40S ribosomal protein S11	0.90	NA	NA	2	9.49%
P11940	Polyadenylate-binding protein 1	0.89	0.53	6.60E-01	5	8.02%
O94979	Protein transport protein Sec31A	0.89	0.33	6.00E-01	3	2.46%
Q15907	Ras-related protein Rab-11B	0.88	0.42	5.50E-01	5	21.56%
Q9UNX3	60S ribosomal protein L26-like 1	0.88	0.15	2.00E-01	4	22.07%
Q9UHG3	Prenylcysteine oxidase 1	0.88	NA	NA	2	4.36%
P50990	T-complex protein 1 subunit theta	0.88	0.19	1.30E-01	7	14.78%
P26599	Polypyrimidine tract-binding protein 1	0.88	0.41	6.50E-01	3	4.71%
P19320	Vascular cell adhesion protein 1	0.88	NA	NA	2	2.71%
P62249	40S ribosomal protein S16	0.88	0.49	6.90E-01	3	17.81%
Q9P2E9	Ribosome-binding protein 1	0.88	0.51	3.30E-01	15	10.50%
Q9NZM1	Myoferlin	0.87	0.52	5.20E-01	7	3.40%
Q9UHD8	Septin-9	0.87	0.51	6.40E-01	4	5.97%
Q8NBS9	Thioredoxin domain-containing protein 5	0.87	0.36	3.90E-01	6	12.27%
P07437	Tubulin beta chain	0.87	0.25	3.60E-01	4	9.23%
Q14818	Proteasome subunit alpha type-7	0.87	NA	NA	2	9.27%
P06756	Integrin alpha-V	0.87	0.29	3.90E-01	4	3.53%
P62277	40S ribosomal protein S13	0.86	0.18	2.00E-01	4	23.84%
P00505	Aspartate aminotransferase, mitochondrial	0.86	NA	NA	2	3.49%
P07737	Profilin-1	0.86	0.72	6.30E-01	6	40.71%
P40429	60S ribosomal protein L13a	0.86	0.20	3.20E-01	3	12.81%
P06865	Beta-hexosaminidase subunit alpha	0.86	NA	NA	2	2.84%
Q15121	Astrocytic phosphoprotein PEA-15	0.86	NA	NA	2	14.62%
Q5JXB2	Putative ubiquitin-conjugating enzyme E2 N-like	0.86	NA	NA	2	13.73%
P83731	60S ribosomal protein L24	0.86	NA	NA	2	14.01%
P50395	Rab GDP dissociation inhibitor beta	0.86	0.21	3.30E-01	3	7.42%
P46777	60S ribosomal protein L5	0.86	0.34	5.10E-01	3	8.75%
P11021	78 kDa glucose-regulated protein	0.86	0.19	1.10E-03	21	36.09%
O00231	26S proteasome non-ATPase regulatory subunit 11	0.85	NA	NA	2	3.55%
P23142	Fibulin-1	0.85	0.12	8.20E-02	4	5.69%
P61247	40S ribosomal protein S3a	0.85	0.15	5.20E-02	6	19.32%
Q14108	Lysosome membrane protein 2	0.85	NA	NA	2	3.14%
O60493	Sorting nexin-3	0.85	NA	NA	2	11.11%
P46778	60S ribosomal protein L21	0.85	NA	NA	2	13.75%
P46781	40S ribosomal protein S9	0.85	0.33	3.20E-01	5	22.16%
P61160	Actin-related protein 2	0.84	NA	NA	2	4.82%
P28838	Cytosol aminopeptidase	0.84	0.67	6.50E-01	4	8.29%
P52565	Rho GDP-dissociation inhibitor 1	0.84	NA	NA	2	15.20%
P40925	Malate dehydrogenase, cytoplasmic	0.84	0.18	1.50E-01	4	11.08%
P54727	UV excision repair protein RAD23 homolog B	0.84	0.31	4.40E-01	3	6.60%
P61006	Ras-related protein Rab-8A	0.84	0.14	9.00E-02	4	17.87%
P47756	F-actin-capping protein subunit beta	0.84	NA	NA	2	6.50%
P16070	CD44 antigen	0.84	0.36	4.80E-01	3	4.85%
P09211	Glutathione S-transferase P	0.84	0.16	2.00E-01	3	16.19%
Q14974	Importin subunit beta-1	0.84	0.21	2.70E-01	3	3.42%
Q14195	Dihydropyrimidinase-related protein 3	0.83	0.14	5.00E-03	9	18.42%
Q15075	Early endosome antigen 1	0.83	0.14	4.10E-02	5	3.47%
P62988	Ubiquitin	0.83	0.10	1.50E-02	5	65.79%
Q9UGI8	Testin	0.83	0.40	5.00E-01	3	7.36%
P36578	60S ribosomal protein L4	0.83	0.09	9.90E-03	5	10.30%
P08670	Vimentin	0.83	0.32	5.50E-04	39	61.80%
P51911	Calponin-1	0.82	0.37	2.10E-01	7	22.56%
P46940	Ras GTPase-activating-like protein IQGAP1	0.82	0.01	1.80E-03	3	1.51%
P48643	T-complex protein 1 subunit epsilon	0.82	NA	NA	2	2.77%
P26038	Moesin	0.82	0.23	9.00E-02	6	10.23%
P07954	Fumarate hydratase, mitochondrial	0.82	0.18	1.20E-01	4	8.43%
P62241	40S ribosomal protein S8	0.82	NA	NA	2	8.65%
P62701	40S ribosomal protein S4, X isoform	0.82	0.16	2.90E-02	6	15.97%
P22314	Ubiquitin-like modifier-activating enzyme 1	0.82	0.06	2.80E-02	3	3.21%
Q07065	Cytoskeleton-associated protein 4	0.81	0.32	7.50E-03	21	37.04%
Q99436	Proteasome subunit beta type-7	0.81	NA	NA	2	6.86%
P34897	Serine hydroxymethyltransferase, mitochondrial	0.81	NA	NA	2	3.57%
P48735	Isocitrate dehydrogenase [NADP], mitochondrial	0.81	0.32	2.10E-01	5	11.06%
P62195	26S proteasome regulatory subunit 8	0.80	NA	NA	2	3.45%
O00264	Membrane-associated progesterone receptor component 1	0.80	NA	NA	2	11.28%
P30101	Protein disulfide-isomerase A3	0.80	0.22	3.70E-03	13	25.74%
P62269	40S ribosomal protein S18	0.80	0.17	1.40E-01	3	19.08%
P13489	Ribonuclease inhibitor	0.79	NA	NA	2	4.12%
Q15293	Reticulocalbin-1	0.79	0.17	1.30E-01	3	8.46%
P49458	Signal recognition particle 9 kDa protein	0.79	NA	NA	2	22.09%
O75083	WD repeat-containing protein 1	0.79	0.41	2.60E-01	5	8.58%
P63104	14-3-3 protein zeta/delta	0.79	0.32	9.20E-02	7	30.61%
P25788	Proteasome subunit alpha type-3	0.78	NA	NA	2	5.49%
P16152	Carbonyl reductase [NADPH] 1	0.78	0.29	2.80E-01	3	15.52%
O15511	Actin-related protein 2/3 complex subunit 5	0.78	NA	NA	2	11.92%

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P07942	Laminin subunit beta-1	0.78	0.34	1.80E-01	5	3.08%
P50502	Hsc70-interacting protein	0.78	NA	NA	2	5.69%
P30153	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isofo	0.78	0.03	4.50E-03	3	4.41%
P62829	60S ribosomal protein L23	0.78	NA	NA	2	12.86%
P13667	Protein disulfide-isomerase A4	0.77	0.24	7.60E-03	10	14.73%
P62906	60S ribosomal protein L10a	0.77	NA	NA	2	7.37%
Q13162	Peroxisredoxin-4	0.77	NA	NA	2	7.75%
P25786	Proteasome subunit alpha type-1	0.76	NA	NA	2	6.46%
P55072	Transitional endoplasmic reticulum ATPase	0.76	0.38	1.10E-01	7	8.44%
P53999	Activated RNA polymerase II transcriptional coactivator p15	0.76	NA	NA	2	9.45%
P08865	40S ribosomal protein SA	0.76	0.62	5.20E-01	3	12.88%
P62736	Actin, aortic smooth muscle	0.76	0.49	3.40E-01	4	17.24%
P29966	Myristoylated alanine-rich C-kinase substrate	0.75	0.26	2.00E-01	3	13.55%
Q00341	Vigilin	0.75	0.33	2.70E-01	3	2.68%
O14910	Lin-7 homolog A	0.75	NA	NA	2	5.58%
P62318	Small nuclear ribonucleoprotein Sm D3	0.75	NA	NA	2	15.08%
P32119	Peroxisredoxin-2	0.75	0.42	2.00E-01	5	22.22%
P11586	C-1-tetrahydrofolate synthase, cytoplasmic	0.75	0.19	1.20E-01	3	3.64%
P21964	Catechol O-methyltransferase	0.75	NA	NA	2	7.38%
P49755	Transmembrane emp24 domain-containing protein 10	0.74	NA	NA	2	9.59%
P13674	Prolyl 4-hydroxylase subunit alpha-1	0.74	0.35	8.70E-02	6	11.61%
P04083	Annexin A1	0.74	0.11	8.90E-05	8	21.10%
P30041	Peroxisredoxin-6	0.74	0.58	2.60E-01	6	22.77%
O95816	BAG family molecular chaperone regulator 2	0.74	NA	NA	2	8.06%
P02768	Serum albumin	0.74	0.44	2.60E-01	4	6.40%
P07237	Protein disulfide-isomerase	0.73	0.22	4.80E-04	12	23.23%
Q92945	Far upstream element-binding protein 2	0.73	0.07	1.70E-02	3	3.38%
P40227	T-complex protein 1 subunit zeta	0.73	NA	NA	2	4.14%
P05388	60S acidic ribosomal protein P0	0.73	0.36	2.60E-01	3	5.99%
Q01518	Adenylyl cyclase-associated protein 1	0.73	NA	NA	2	3.16%
O75718	Cartilage-associated protein	0.72	NA	NA	2	3.74%
Q9BQE3	Tubulin alpha-1C chain	0.72	0.49	1.00E-01	8	20.71%
Q14697	Neutral alpha-glucosidase AB	0.72	NA	NA	2	1.69%
O15212	Prefoldin subunit 6	0.72	NA	NA	2	15.50%
P54578	Ubiquitin carboxyl-terminal hydrolase 14	0.72	0.43	3.20E-01	3	5.47%
Q9UIG0	Bromodomain adjacent to zinc finger domain protein 1B	0.72	NA	NA	2	0.74%
Q96AG4	Leucine-rich repeat-containing protein 59	0.72	NA	NA	2	5.54%
P62081	40S ribosomal protein S7	0.72	NA	NA	2	8.76%
O00148	ATP-dependent RNA helicase DDX39	0.72	0.19	9.30E-02	3	5.85%
P59998	Actin-related protein 2/3 complex subunit 4	0.72	0.44	3.20E-01	3	16.07%
P18085	ADP-ribosylation factor 4	0.72	0.19	9.00E-02	3	15.00%
P06703	Protein S100-A6	0.71	0.19	9.20E-02	3	24.44%
O43491	Band 4.1-like protein 2	0.71	0.34	9.20E-02	5	4.78%
Q13509	Tubulin beta-3 chain	0.71	0.34	3.90E-02	7	18.44%
Q96AY3	FK506-binding protein 10	0.71	0.23	5.60E-02	4	5.84%
Q9UNM6	26S proteasome non-ATPase regulatory subunit 13	0.71	0.05	8.40E-04	4	9.31%
Q07960	Rho GTPase-activating protein 1	0.70	0.09	2.10E-02	3	5.47%
O15460	Prolyl 4-hydroxylase subunit alpha-2	0.70	0.17	9.20E-03	5	12.15%
P14618	Pyruvate kinase isozymes M1/M2	0.70	0.35	7.60E-03	11	22.79%
P06744	Glucose-6-phosphate isomerase	0.70	NA	NA	2	2.87%
P14314	Glucosidase 2 subunit beta	0.69	0.52	1.40E-01	6	11.74%
Q01995	Transgelin	0.68	0.49	3.40E-02	10	48.26%
Q9UBQ0	Vacuolar protein sorting-associated protein 29	0.68	NA	NA	2	8.24%
O75964	ATP synthase subunit g, mitochondrial	0.68	NA	NA	2	18.45%
P08238	Heat shock protein HSP 90-beta	0.67	0.39	4.90E-03	12	16.57%
P23284	Peptidyl-prolyl cis-trans isomerase B	0.67	0.36	6.70E-03	10	37.96%
P23528	Cofilin-1	0.67	0.32	8.70E-02	4	23.49%
P60900	Proteasome subunit alpha type-6	0.67	NA	NA	2	8.94%
P61158	Actin-related protein 3	0.67	NA	NA	2	5.26%
O95302	FK506-binding protein 9	0.66	0.26	1.10E-01	3	4.39%
P13639	Elongation factor 2	0.66	0.09	4.30E-04	5	5.36%
P04439	HLA class I histocompatibility antigen, A-3 alpha chain	0.66	NA	NA	2	3.84%
P14625	Endoplasmic reticulum chaperone protein BiP	0.65	0.26	1.50E-05	15	16.81%
Q07954	Prolow-density lipoprotein receptor-related protein 1	0.64	0.24	2.90E-03	7	1.54%
P62913	60S ribosomal protein L11	0.64	NA	NA	2	8.99%
Q02952	A-kinase anchor protein 12	0.63	0.40	1.00E-01	4	2.69%
P60228	Eukaryotic translation initiation factor 3 subunit E	0.63	NA	NA	2	4.27%
P18124	60S ribosomal protein L7	0.63	0.62	1.70E-01	5	16.53%
P62263	40S ribosomal protein S14	0.62	NA	NA	2	15.89%
Q96D15	Reticulocalbin-3	0.62	0.25	7.80E-02	3	14.63%
Q16576	Histone-binding protein RBBP7	0.61	NA	NA	2	4.24%
P23396	40S ribosomal protein S3	0.60	0.18	9.90E-04	6	20.58%
Q92841	Probable ATP-dependent RNA helicase DDX17	0.60	NA	NA	2	3.54%
P31949	Protein S100-A11	0.60	NA	NA	2	17.14%
Q32P28	Prolyl 3-hydroxylase 1	0.59	0.36	1.30E-01	3	3.53%
P08133	Annexin A6	0.59	0.16	8.50E-06	9	14.86%
P04406	Glyceraldehyde-3-phosphate dehydrogenase	0.59	0.15	3.30E-04	6	18.21%
O43399	Tumor protein D54	0.59	NA	NA	2	10.68%
P27797	Calreticulin	0.59	0.33	2.20E-02	5	12.23%
P50454	Serpin H1	0.58	0.51	7.70E-02	5	13.40%
P78371	T-complex protein 1 subunit beta	0.58	0.59	1.60E-01	4	8.60%
P15084	Protein disulfide-isomerase A6	0.58	0.29	1.40E-02	5	9.09%
O43175	D-3-phosphoglycerate dehydrogenase	0.58	0.52	2.10E-01	3	6.57%
P20962	Parathyromin	0.58	NA	NA	2	21.57%
P00387	NADH-cytochrome b5 reductase 3	0.57	0.67	2.80E-01	3	14.29%
O75874	Isocitrate dehydrogenase [NADP] cytoplasmic	0.56	0.65	2.60E-01	3	7.49%
P12110	Collagen alpha-2(VI) chain	0.55	NA	NA	2	1.86%
P30040	Endoplasmic reticulum protein ERp29	0.55	0.57	7.50E-02	5	20.69%
P07900	Heat shock protein HSP 90-alpha	0.54	0.48	2.50E-02	6	6.97%
P01023	Alpha-2-macroglobulin	0.53	NA	NA	2	1.09%
O60506	Heterogeneous nuclear ribonucleoprotein Q	0.52	0.50	8.10E-02	4	5.78%
Q5VTE0	Putative elongation factor 1-alpha-like 3	0.52	0.40	1.00E-02	6	10.82%
O00299	Chloride intracellular channel protein 1	0.51	0.37	8.60E-02	3	11.20%
P20618	Proteasome subunit beta type-1	0.51	0.74	1.60E-01	4	20.33%
Q70UQ0	Inhibitor of nuclear factor kappa-B kinase-interacting protein	0.50	NA	NA	2	6.00%
Q9NQC3	Reticulon-4	0.47	NA	NA	2	1.76%

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Q00610	Clathrin heavy chain 1	0.46	0.83	2.50E-01	3	1.49%
P18621	60S ribosomal protein L17	0.46	0.65	1.70E-01	3	16.30%
Q8TED1	Probable glutathione peroxidase 8	0.45	NA	NA	2	10.53%
P10319	HLA class I histocompatibility antigen, B-58 alpha chain	0.45	0.57	6.60E-02	4	15.47%
P78417	Glutathione S-transferase omega-1	0.45	NA	NA	2	9.54%
P02461	Collagen alpha-1(III) chain	0.45	0.62	1.50E-01	3	2.73%
P13797	Plastin-3	0.45	0.36	2.10E-02	4	7.30%
P31948	Stress-induced-phosphoprotein 1	0.44	NA	NA	2	4.05%
P08123	Collagen alpha-2(I) chain	0.42	0.37	1.80E-02	4	3.44%
P49257	Protein ERGIC-53	0.41	NA	NA	2	3.73%
O60701	UDP-glucose 6-dehydrogenase	0.39	0.59	5.20E-02	4	10.73%
P02452	Collagen alpha-1(I) chain	0.36	0.98	5.10E-02	6	6.22%
Q14019	Coactosin-like protein	0.29	NA	NA	2	11.97%

Average false discovery rate = 2.9% peptide identity, 3.6% peptide homology; NA = not applicable because < 3 peptides.