

Supplementary Table S3

Relative Protein Abundance: Trabecular Meshwork Sample GTM304-04

Total Proteins Quantified = 401; Median Protein iTRAQ Ratio = 1.00; Mean Protein iTRAQ Ratio = 1.02; Standard Deviation = 0.29

SwissProtein Accession	Protein	Protein iTRAQ Ratio Dex/Control	Standard Deviation	P value	Unique Peptides	Sequence Coverage
P01011	Alpha-1-antichymotrypsin	5.45	NA	NA	2	4.73%
O94875	Sorbin and SH3 domain-containing protein 2	3.11	0.56	2.70E-02	4	5.27%
Q99972	Myocilin	2.49	NA	NA	2	3.57%
Q5SSJ5	Heterochromatin protein 1-binding protein 3	2.42	0.85	2.10E-01	3	6.33%
O00151	PDZ and LIM domain protein 1	2.27	NA	NA	2	8.21%
O75369	Filamin-B	2.16	0.32	6.90E-04	7	4.07%
P27144	Adenylate kinase isoenzyme 4, mitochondrial	2.13	NA	NA	2	9.87%
P00338	L-lactate dehydrogenase A chain	2.12	0.39	1.30E-02	5	12.95%
P38159	Heterogeneous nuclear ribonucleoprotein G	2.03	NA	NA	2	5.37%
O00159	Myosin-Ic	1.99	NA	NA	2	2.45%
Q9NSD9	Phenylalanyl-tRNA synthetase beta chain	1.98	NA	NA	2	3.06%
P39060	Collagen alpha-1(XVIII) chain	1.86	NA	NA	2	1.77%
P11166	Solute carrier family 2, facilitated glucose transporter member 1	1.84	NA	NA	2	3.66%
P43304	Glycerol-3-phosphate dehydrogenase, mitochondrial	1.81	NA	NA	2	3.44%
P62318	Small nuclear ribonucleoprotein Sm D3	1.80	NA	NA	2	15.08%
Q8LZP2	Protein FAM10A4	1.80	NA	NA	2	7.08%
P10909	Clusterin	1.80	NA	NA	2	5.12%
Q13740	CD166 antigen	1.73	0.24	9.20E-04	7	10.81%
P60900	Proteasome subunit alpha type-6	1.72	NA	NA	2	10.98%
P42765	3-ketoacyl-CoA thiolase, mitochondrial	1.68	NA	NA	2	4.03%
Q9BX66	Sorbin and SH3 domain-containing protein 1	1.67	NA	NA	2	1.86%
Q9UDY4	DnaJ homolog subfamily B member 4	1.67	NA	NA	2	7.42%
Q0ZGT2	Nexilin	1.66	NA	NA	2	2.81%
Q03135	Caveolin-1	1.64	0.49	8.80E-02	5	34.27%
Q13418	Integrin-linked protein kinase	1.61	0.27	3.80E-02	4	8.41%
Q9P0L0	Vesicle-associated membrane protein-associated protein A	1.58	NA	NA	2	11.24%
P63104	14-3-3 protein zeta/delta	1.56	0.40	1.10E-01	4	23.27%
Q9Y6N5	Sulfide:quinone oxidoreductase, mitochondrial	1.54	0.15	1.10E-02	4	11.56%
Q43570	Carbonic anhydrase 12	1.50	NA	NA	2	9.89%
P35613	Basigin	1.48	0.21	3.20E-02	4	15.58%
P37802	Transgelin-2	1.48	0.08	4.60E-04	5	30.65%
Q9UIJ7	GTP:AMP phosphotransferase mitochondrial	1.47	0.22	1.70E-02	5	23.35%
P54709	Sodium/potassium-transporting ATPase subunit beta-3	1.46	0.22	4.10E-02	4	15.77%
Q01844	RNA-binding protein EWS	1.46	NA	NA	2	2.29%
Q96I20	PRKC apoptosis WT1 regulator protein	1.45	NA	NA	2	6.47%
P26373	60S ribosomal protein L13	1.44	NA	NA	2	9.95%
P11177	Pyruvate dehydrogenase E1 component subunit beta, mitochondrial	1.43	NA	NA	2	6.41%
P30049	ATP synthase subunit delta, mitochondrial	1.42	0.07	1.50E-02	3	17.26%
Q969X5	Endoplasmic reticulum-Golgi intermediate compartment protein 1	1.42	0.17	7.10E-02	3	11.03%
P00558	Phosphoglycerate kinase 1	1.40	0.11	5.90E-04	6	15.59%
Q8N257	Histone H2B type 3-B	1.39	NA	NA	2	7.94%
P36542	ATP synthase subunit gamma, mitochondrial	1.38	NA	NA	2	9.06%
Q15942	Zyxin	1.37	0.13	2.30E-03	6	14.69%
P37837	Transaldolase	1.37	0.33	1.60E-01	4	10.68%
Q9UBR2	Cathepsin Z	1.36	NA	NA	2	7.26%
P06396	Gelsolin	1.35	0.49	3.90E-01	3	4.09%
O00148	ATP-dependent RNA helicase DDX39	1.35	NA	NA	2	4.22%
O00754	Lysosomal alpha-mannosidase	1.34	0.24	1.70E-01	3	3.46%
P08195	4F2 cell-surface antigen heavy chain	1.33	NA	NA	2	5.56%
Q8WX93	Palladin	1.33	0.23	1.60E-01	3	2.68%
Q15019	Septin-2	1.33	NA	NA	2	7.20%
P24844	Myosin regulatory light polypeptide 9	1.33	0.38	3.30E-01	3	17.44%
P20340	Ras-related protein Rab-6A	1.32	NA	NA	2	12.02%
Q9NR12	PDZ and LIM domain protein 7	1.32	0.55	3.80E-01	4	8.32%
Q9HBL0	Tensin-1	1.32	0.46	4.00E-01	3	2.71%
P21589	5'-nucleotidase	1.32	0.33	1.90E-02	11	22.13%
Q12797	Aspartyl/asparaginyl beta-hydroxylase	1.31	0.98	6.20E-01	4	6.73%
P13804	Electron transfer flavoprotein subunit alpha, mitochondrial	1.31	NA	NA	2	8.11%
P67936	Tropomyosin alpha-4 chain	1.31	0.27	6.50E-05	24	60.48%
P18206	Vinculin	1.31	0.26	9.10E-05	22	21.96%
P32119	Peroxioredoxin-2	1.30	0.32	2.80E-01	3	15.66%
P21333	Filamin-A	1.29	0.16	1.70E-17	58	29.17%
P98160	Basement membrane-specific heparan sulfate proteoglycan core protein	1.29	0.24	3.10E-02	7	1.96%
Q5QNW6	Histone H2B type 2-F	1.29	0.09	1.00E-02	4	26.98%
Q14847	LIM and SH3 domain protein 1	1.29	0.23	1.90E-01	3	12.26%
O60493	Sorting nexin-3	1.28	NA	NA	2	17.28%
P05023	Sodium/potassium-transporting ATPase subunit alpha-1	1.28	0.29	1.90E-01	4	5.38%
P00367	Glutamate dehydrogenase 1, mitochondrial	1.28	0.49	3.20E-01	5	9.68%
P40925	Malate dehydrogenase, cytoplasmic	1.28	NA	NA	2	7.78%
Q9BVC6	Transmembrane protein 109	1.28	NA	NA	2	8.64%
P29279	Connective tissue growth factor	1.28	NA	NA	2	6.30%
P61604	10 kDa heat shock protein, mitochondrial	1.27	0.04	1.40E-04	5	52.94%
P60660	Myosin light polypeptide 6	1.27	0.08	3.10E-03	5	40.40%
P02768	Serum albumin	1.27	NA	NA	2	3.61%
O94925	Glutaminase kidney isoform, mitochondrial	1.26	0.60	5.70E-01	3	5.38%
Q6NZI2	Polymerase I and transcript release factor	1.26	0.21	1.10E-03	14	32.05%
P50479	PDZ and LIM domain protein 4	1.26	0.36	2.90E-01	4	12.42%
Q9NZN4	EH domain-containing protein 2	1.26	0.36	3.80E-02	13	33.89%
Q13510	Acid ceramidase	1.25	NA	NA	2	4.81%
P60174	Triosephosphate isomerase	1.25	0.17	6.90E-03	8	36.95%
P35232	Prohibitin	1.24	0.37	1.20E-01	9	36.03%
O00483	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 4	1.24	NA	NA	2	22.22%
P36957	Dihydropyridyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex	1.24	0.50	3.90E-01	5	11.92%
Q96I99	Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial	1.23	NA	NA	2	6.25%
P04899	Guanine nucleotide-binding protein G(i), alpha-2 subunit	1.23	NA	NA	2	7.32%
Q16629	Splicing factor, arginine/serine-rich 7	1.23	NA	NA	2	15.97%
Q05682	Caldesmon	1.23	0.13	4.50E-08	25	29.00%
Q06830	Peroxioredoxin-1	1.21	0.33	8.20E-02	11	39.70%

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O00469	Procollagen-lysine,2-oxoglutarate 5-dioxygenase 2	1.21	0.17	1.00E-01	4	6.92%
P62263	40S ribosomal protein S14	1.21	0.37	4.70E-01	3	29.80%
P24752	Acetyl-CoA acetyltransferase, mitochondrial	1.21	NA	NA	2	4.92%
P60866	40S ribosomal protein S20	1.20	NA	NA	2	22.69%
Q9NYL9	Tropomodulin-3	1.20	NA	NA	2	11.08%
P48047	ATP synthase subunit O, mitochondrial	1.20	0.16	3.90E-02	6	30.05%
P49207	60S ribosomal protein L34	1.20	NA	NA	2	12.82%
P07951	Tropomyosin beta chain	1.20	0.20	4.00E-03	15	39.79%
P55084	Trifunctional enzyme subunit beta, mitochondrial	1.19	0.21	1.30E-01	5	9.07%
P07355	Annexin A2	1.19	0.19	3.20E-04	21	51.62%
Q14103	Heterogeneous nuclear ribonucleoprotein D0	1.19	0.18	2.50E-01	3	9.58%
Q01082	Spectrin beta chain, brain 1	1.19	0.27	8.90E-02	9	5.58%
P60709	Actin, cytoplasmic 1	1.19	0.22	2.20E-03	20	52.53%
P23142	Fibulin-1	1.19	0.14	1.80E-01	3	4.41%
O43707	Alpha-actinin-4	1.18	0.21	1.30E-03	21	26.78%
P12814	Alpha-actinin-1	1.18	0.22	2.20E-02	12	17.15%
P35579	Myosin-9	1.18	0.20	6.10E-05	33	17.04%
P07339	Cathepsin D	1.18	0.26	2.30E-01	5	12.86%
Q71D13	Histone H3.2	1.17	0.11	7.00E-02	4	19.85%
P49411	Elongation factor Tu, mitochondrial	1.17	0.43	4.10E-01	6	15.49%
Q12841	Follistatin-related protein 1	1.17	NA	NA	2	5.19%
P61981	14-3-3 protein gamma	1.17	0.26	2.60E-01	5	19.43%
P63244	Guanine nucleotide-binding protein subunit beta-2-like 1	1.17	0.58	6.90E-01	3	11.04%
Q9Y490	Talin-1	1.17	0.22	1.50E-02	16	7.79%
Q9H0U4	Ras-related protein Rab-1B	1.17	0.14	2.00E-01	3	14.43%
P52907	F-actin-capping protein subunit alpha-1	1.16	NA	NA	2	9.79%
P10412	Histone H1.4	1.16	0.21	3.30E-01	3	10.05%
P25705	ATP synthase subunit alpha, mitochondrial	1.16	0.24	5.40E-02	12	24.23%
P06753	Tropomyosin alpha-3 chain	1.16	0.26	1.60E-01	8	22.54%
P54819	Adenylate kinase 2, mitochondrial	1.16	NA	NA	2	11.30%
P52209	6-phosphogluconate dehydrogenase, decarboxylating	1.15	0.18	3.10E-01	3	7.04%
P06733	Alpha-enolase	1.15	0.15	5.60E-03	13	28.80%
A6NL28	Putative tropomyosin alpha-3 chain-like protein	1.15	0.27	4.60E-01	3	10.76%
O60763	General vesicular transport factor p115	1.15	0.39	5.90E-01	3	3.64%
P06576	ATP synthase subunit beta, mitochondrial	1.14	0.24	9.20E-02	12	28.36%
P40227	T-complex protein 1 subunit zeta	1.13	0.53	7.20E-01	3	6.21%
Q92945	Far upstream element-binding protein 2	1.13	0.35	5.20E-01	4	6.20%
Q09666	Neuroblast differentiation-associated protein AHNAK	1.13	0.20	1.50E-05	59	8.23%
P40939	Trifunctional enzyme subunit alpha, mitochondrial	1.13	NA	NA	2	2.10%
P18621	60S ribosomal protein L17	1.13	NA	NA	2	14.13%
P10809	60 kDa heat shock protein, mitochondrial	1.13	0.19	5.50E-02	12	21.99%
P59998	Actin-related protein 2/3 complex subunit 4	1.13	0.20	4.10E-01	3	16.07%
P08758	Annexin A5	1.13	0.27	2.20E-01	9	21.56%
P50990	T-complex protein 1 subunit theta	1.12	NA	NA	2	3.65%
P21912	Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial	1.12	NA	NA	2	5.71%
P30050	60S ribosomal protein L12	1.12	NA	NA	2	10.30%
P63010	AP-2 complex subunit beta-1	1.12	NA	NA	2	1.92%
Q8IV08	Phospholipase D3	1.12	0.67	8.00E-01	3	9.59%
P63267	Actin, gamma-enteric smooth muscle	1.11	0.09	3.40E-02	6	25.53%
P62244	40S ribosomal protein S15a	1.11	0.23	5.10E-01	3	20.77%
Q14344	Guanine nucleotide-binding protein subunit alpha-13	1.11	NA	NA	2	5.57%
P60903	Protein S100-A10	1.11	0.43	7.20E-01	3	32.99%
Q96FJ2	Dynein light chain 2, cytoplasmic	1.10	NA	NA	2	13.48%
Q00341	Vigilin	1.10	NA	NA	2	1.97%
P60842	Eukaryotic initiation factor 4A-I	1.09	0.18	4.80E-01	3	10.10%
Q16270	Insulin-like growth factor-binding protein 7	1.09	NA	NA	2	10.28%
Q53GG5	PDZ and LIM domain protein 3	1.09	0.57	8.20E-01	3	13.19%
O75947	ATP synthase subunit d, mitochondrial	1.09	0.13	4.00E-01	3	12.42%
P21796	Voltage-dependent anion-selective channel protein 1	1.09	0.21	4.30E-01	5	19.08%
P19338	Nucleolin	1.08	0.20	2.40E-01	11	16.76%
Q9UKS6	Protein kinase C and casein kinase substrate in neurons protein 3	1.08	NA	NA	2	7.55%
P62857	40S ribosomal protein S28	1.08	NA	NA	2	23.19%
P35268	60S ribosomal protein L22	1.08	NA	NA	2	18.75%
P25398	40S ribosomal protein S12	1.08	0.27	6.80E-01	3	17.42%
P51911	Calponin-1	1.08	0.36	7.10E-01	4	11.78%
P21980	Protein-glutamine gamma-glutamyltransferase 2	1.07	0.43	7.70E-01	4	7.86%
P29401	Transketolase	1.07	0.20	4.80E-01	5	8.67%
P04075	Fructose-bisphosphate aldolase A	1.07	0.20	3.00E-01	11	28.30%
Q14773	Tripeptidyl-peptidase 1	1.07	NA	NA	2	3.73%
Q12906	Interleukin enhancer-binding factor 3	1.06	0.27	6.80E-01	4	5.59%
P09651	Heterogeneous nuclear ribonucleoprotein A1	1.06	0.35	6.80E-01	6	20.97%
P48735	Iso citrate dehydrogenase [NADP], mitochondrial	1.06	0.15	5.50E-01	3	8.19%
P52272	Heterogeneous nuclear ribonucleoprotein M	1.06	0.17	6.20E-01	3	6.58%
P02751	Fibronectin	1.06	0.20	1.10E-01	34	18.36%
P27816	Microtubule-associated protein 4	1.06	0.16	4.40E-01	6	7.47%
Q07955	Splicing factor, arginine/serine-rich 1	1.06	0.08	3.50E-01	3	12.50%
P36578	60S ribosomal protein L4	1.06	0.22	6.60E-01	4	8.20%
P62899	60S ribosomal protein L31	1.05	NA	NA	2	14.40%
P04792	Heat shock protein beta-1	1.05	0.14	3.70E-01	7	29.76%
P55072	Transitional endoplasmic reticulum ATPase	1.05	0.47	8.20E-01	6	7.32%
Q96HC4	PDZ and LIM domain protein 5	1.04	0.06	3.80E-01	3	6.88%
P09622	Dihydropyridyl dehydrogenase, mitochondrial	1.04	0.31	8.10E-01	4	9.63%
P78417	Glutathione S-transferase omega-1	1.04	NA	NA	2	9.54%
P10253	Lysosomal alpha-glucosidase	1.04	0.27	7.30E-01	7	8.30%
Q53GQ0	Estradiol 17-beta-dehydrogenase 12	1.04	NA	NA	2	8.97%
Q02952	A-kinase anchor protein 12	1.04	0.29	8.00E-01	5	4.83%
P61224	Ras-related protein Rap-1b	1.04	0.39	8.50E-01	5	27.72%
P38646	Stress-70 protein, mitochondrial	1.03	0.16	5.30E-01	10	17.23%
P08865	40S ribosomal protein SA	1.03	0.33	8.50E-01	5	18.98%
P08107	Heat shock 70 kDa protein 1	1.03	0.25	8.50E-01	3	6.86%
P18085	ADP-ribosylation factor 4	1.03	NA	NA	2	11.67%
Q16643	Drebrin	1.03	0.07	5.50E-01	3	7.55%
P40926	Malate dehydrogenase, mitochondrial	1.03	0.26	7.40E-01	10	34.62%
P35580	Myosin-10	1.03	0.08	4.60E-01	6	3.80%
P46940	Ras GTPase-activating-like protein IQGAP1	1.03	0.15	6.60E-01	7	4.47%
O43491	Band 4.1-like protein 2	1.03	0.41	8.90E-01	5	7.36%

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Q12904	Multisynthetase complex auxiliary component p43	1.02	NA	NA	2	11.22%
P30837	Aldehyde dehydrogenase X, mitochondrial	1.02	0.47	9.00E-01	8	19.34%
Q99497	Protein DJ-1	1.02	0.09	7.10E-01	4	19.58%
P51149	Ras-related protein Rab-7a	1.02	0.14	8.40E-01	3	16.43%
P07437	Tubulin beta chain	1.02	0.21	7.70E-01	11	27.25%
P09493	Tropomyosin alpha-1 chain	1.02	0.38	9.00E-01	10	25.70%
P62805	Histone H4	1.01	0.13	8.70E-01	7	52.43%
P29692	Elongation factor 1-delta	1.01	0.16	9.20E-01	5	18.51%
P61247	40S ribosomal protein S3a	1.01	0.05	8.60E-01	3	12.88%
P11142	Heat shock cognate 71 kDa protein	1.01	0.16	9.10E-01	10	18.27%
P14618	Pyruvate kinase isozymes M1/M2	1.00	0.23	9.40E-01	14	30.89%
Q9P2E9	Ribosome-binding protein 1	1.00	0.20	9.40E-01	16	11.70%
O75367	Core histone macro-H2A.1	1.00	0.20	9.80E-01	3	9.68%
P80723	Brain acid soluble protein 1	1.00	0.29	9.80E-01	4	38.33%
Q03252	Laminin-B2	1.00	NA	NA	2	3.83%
P62241	40S ribosomal protein S8	1.00	NA	NA	2	8.65%
P23528	Cofilin-1	1.00	NA	NA	2	15.06%
P04406	Glyceraldehyde-3-phosphate dehydrogenase	1.00	0.09	9.90E-01	9	29.85%
P07942	Laminin subunit beta-1	1.00	0.44	1.00E+00	3	1.79%
O00571	ATP-dependent RNA helicase DDX3X	1.00	NA	NA	2	3.02%
P26038	Moesin	1.00	0.32	9.90E-01	13	21.14%
Q14315	Filamin-C	1.00	0.32	9.90E-01	10	4.37%
Q16891	Mitochondrial inner membrane protein	1.00	0.22	9.80E-01	4	7.12%
Q9BS26	Thioredoxin domain-containing protein 4	1.00	NA	NA	2	4.68%
P08133	Annexin A6	0.99	0.16	9.20E-01	8	12.04%
Q9NR28	Diablo homolog, mitochondrial	0.99	NA	NA	2	8.79%
P61978	Heterogeneous nuclear ribonucleoprotein K	0.99	0.35	9.70E-01	4	9.94%
O75396	Vesicle-trafficking protein SEC22b	0.99	0.34	9.60E-01	5	28.84%
Q14247	Src substrate cortactin	0.99	0.04	7.60E-01	3	3.27%
P30041	Peroxioredoxin-6	0.99	0.16	9.10E-01	5	19.20%
Q9UHD8	Septin-9	0.99	NA	NA	2	2.90%
Q6NUK1	Calcium-binding mitochondrial carrier protein SCAmC-1	0.99	NA	NA	2	3.35%
P62913	60S ribosomal protein L11	0.99	NA	NA	2	5.62%
O75390	Citrate synthase, mitochondrial	0.99	0.19	8.90E-01	4	9.44%
P00387	NADH-cytochrome b5 reductase 3	0.99	0.15	8.60E-01	4	19.60%
P22626	Heterogeneous nuclear ribonucleoproteins A2/B1	0.98	0.26	8.60E-01	8	25.21%
Q00839	Heterogeneous nuclear ribonucleoprotein U	0.98	NA	NA	2	1.21%
O14950	Myosin regulatory light chain MRLC2	0.98	0.23	8.80E-01	4	17.44%
Q99623	Prohibitin-2	0.98	NA	NA	2	5.35%
P17844	Probable ATP-dependent RNA helicase DDX5	0.97	0.38	8.90E-01	5	8.14%
P83731	60S ribosomal protein L24	0.97	0.28	8.80E-01	3	19.11%
P09211	Glutathione S-transferase P	0.97	0.17	7.30E-01	5	34.29%
P05556	Integrin beta-1	0.97	0.16	5.60E-01	9	12.16%
Q9UII2	ATPase inhibitor, mitochondrial	0.97	NA	NA	2	15.09%
P00441	Superoxide dismutase [Cu-Zn]	0.97	NA	NA	2	12.99%
P62277	40S ribosomal protein S13	0.96	0.16	6.90E-01	4	21.85%
P62851	40S ribosomal protein S25	0.96	0.15	6.40E-01	4	25.60%
P50552	Vasodilator-stimulated phosphoprotein	0.96	0.17	7.30E-01	3	9.47%
P78371	T-complex protein 1 subunit beta	0.96	0.17	6.60E-01	4	11.03%
O95571	Protein ETHE1, mitochondrial	0.96	NA	NA	2	12.20%
Q9UMX5	Neudesin	0.96	0.49	8.90E-01	3	20.35%
P42766	60S ribosomal protein L35	0.96	0.30	8.20E-01	3	17.07%
P13073	Cytochrome c oxidase subunit 4 isoform 1, mitochondrial	0.96	NA	NA	2	13.02%
P00505	Aspartate aminotransferase, mitochondrial	0.95	0.07	3.00E-01	3	6.98%
Q96JB5	CDK5 regulatory subunit-associated protein 3	0.95	NA	NA	2	4.15%
P15880	40S ribosomal protein S2	0.95	NA	NA	2	6.14%
P20674	Cytochrome c oxidase subunit 5A, mitochondrial	0.95	NA	NA	2	10.00%
Q00610	Clathrin heavy chain 1	0.94	0.17	4.20E-01	7	6.03%
O95816	BAG family molecular chaperone regulator 2	0.94	NA	NA	2	12.80%
Q13813	Spectrin alpha chain, brain	0.94	0.29	2.20E-01	35	18.61%
Q7L7L0	Histone H2A type 3	0.94	0.36	7.90E-01	3	30.00%
P62258	14-3-3 protein epsilon	0.94	0.11	1.50E-01	8	35.69%
P14406	Cytochrome c oxidase polypeptide 7A2, mitochondrial	0.93	NA	NA	2	27.71%
Q96AQ6	Pre-B-cell leukemia transcription factor-interacting protein 1	0.93	0.17	5.60E-01	3	4.24%
P51991	Heterogeneous nuclear ribonucleoprotein A3	0.93	NA	NA	2	8.20%
P24534	Elongation factor 1-beta	0.93	0.33	7.30E-01	3	10.22%
Q07954	Prolong-density lipoprotein receptor-related protein 1	0.93	0.48	7.70E-01	4	1.06%
Q9NZM1	Myoferlin	0.93	0.44	7.20E-01	5	3.06%
P10606	Cytochrome c oxidase subunit 5B, mitochondrial	0.92	0.17	4.80E-01	3	20.16%
Q01995	Transgelin	0.92	0.28	4.00E-01	9	39.30%
P23246	Splicing factor, proline- and glutamine-rich	0.92	0.10	1.90E-01	4	6.22%
Q02878	60S ribosomal protein L6	0.92	0.28	5.90E-01	4	11.81%
P30084	Enoyl-CoA hydratase, mitochondrial	0.92	0.05	1.00E-01	3	10.34%
P02545	Laminin-A/C	0.92	0.15	3.00E-03	31	41.27%
Q8WW11	LIM domain only protein 7	0.92	0.34	4.70E-01	9	6.89%
O75083	WD repeat-containing protein 1	0.92	0.24	5.90E-01	3	7.59%
Q14257	Reticulocalbin-2	0.91	0.24	5.80E-01	3	13.88%
Q13561	Dynactin subunit 2	0.91	0.54	8.00E-01	3	5.99%
O00231	26S proteasome non-ATPase regulatory subunit 11	0.91	0.19	4.90E-01	3	6.40%
P07737	Profilin-1	0.91	0.24	3.90E-01	6	40.71%
P80303	Nucleobindin-2	0.91	NA	NA	2	3.81%
P23396	40S ribosomal protein S3	0.91	0.41	5.50E-01	7	25.51%
P07996	Thrombospondin-1	0.91	0.17	3.40E-01	4	3.59%
P09936	Ubiquitin carboxyl-terminal hydrolase isozyme L1	0.91	0.19	4.60E-01	3	13.00%
O75477	Erlin-1	0.91	NA	NA	2	6.94%
Q14195	Dihydropyrimidinase-related protein 3	0.90	0.06	2.10E-02	5	10.70%
Q15149	Plectin-1	0.90	0.35	4.00E-02	53	13.43%
P04179	Superoxide dismutase [Mn], mitochondrial	0.90	0.07	1.40E-01	3	15.77%
P55209	Nucleosome assembly protein 1-like 1	0.90	0.41	7.10E-01	3	11.51%
P11047	Laminin subunit gamma-1	0.90	NA	NA	2	1.74%
P38117	Electron transfer flavoprotein subunit beta	0.90	0.30	5.00E-01	5	20.78%
Q5VTE0	Putative elongation factor 1-alpha-like 3	0.90	0.21	2.80E-01	6	14.50%
Q9NQC3	Reticulon-4	0.90	NA	NA	2	1.76%
P61106	Ras-related protein Rab-14	0.90	NA	NA	2	13.02%
P62988	Ubiquitin	0.89	0.08	3.50E-02	5	60.53%
P51688	N-sulphoglucosamine sulphohydrolase	0.89	NA	NA	2	4.78%

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O43852	Calumenin	0.89	0.25	3.10E-01	6	21.27%
P05091	Aldehyde dehydrogenase, mitochondrial	0.89	NA	NA	2	4.26%
P49368	T-complex protein 1 subunit gamma	0.89	NA	NA	2	6.79%
P10599	Thioredoxin	0.89	0.20	4.20E-01	3	31.43%
O15173	Membrane-associated progesterone receptor component 2	0.89	0.10	1.80E-01	3	13.00%
P31937	3-hydroxyisobutyrate dehydrogenase, mitochondrial	0.88	NA	NA	2	9.52%
P50991	T-complex protein 1 subunit delta	0.88	0.36	5.30E-01	4	10.02%
P62937	Peptidyl-prolyl cis-trans isomerase A	0.88	0.24	1.70E-01	8	35.15%
P04216	Thy-1 membrane glycoprotein	0.88	NA	NA	2	16.15%
O43678	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 2	0.88	NA	NA	2	10.10%
P49257	Protein ERGIC-53	0.88	NA	NA	2	3.92%
Q8NHV5	60S acidic ribosomal protein P0-like	0.88	0.20	3.70E-01	3	8.83%
O43399	Tumor protein D54	0.88	0.04	8.30E-03	4	18.93%
P43307	Translocon-associated protein subunit alpha	0.87	0.05	3.60E-02	3	11.89%
P62158	Calmodulin	0.87	0.20	2.00E-01	5	36.24%
Q969G5	Protein kinase C delta-binding protein	0.87	0.01	1.10E-03	3	8.43%
P04843	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	0.87	0.41	5.40E-01	4	8.24%
P62269	40S ribosomal protein S18	0.87	0.21	2.60E-01	4	23.68%
P28838	Cytosol aminopeptidase	0.86	NA	NA	2	5.01%
P07686	Beta-hexosaminidase subunit beta	0.86	0.35	4.60E-01	4	5.04%
P11766	Alcohol dehydrogenase class-3	0.86	NA	NA	2	4.81%
Q86UP2	Kinectin	0.86	0.25	2.50E-01	5	4.35%
P69905	Hemoglobin subunit alpha	0.86	NA	NA	2	11.27%
P27824	Calnexin	0.86	0.24	2.30E-01	5	12.33%
P04083	Annexin A1	0.86	0.24	3.90E-02	13	41.91%
P15586	N-acetylglucosamine-6-sulfatase	0.85	0.18	2.60E-01	3	5.43%
P18124	60S ribosomal protein L7	0.85	0.31	4.70E-01	3	11.69%
P46821	Microtubule-associated protein 1B	0.85	0.41	3.80E-01	6	3.36%
Q14108	Lysosome membrane protein 2	0.85	0.21	3.20E-01	3	5.65%
P39019	40S ribosomal protein S19	0.84	0.21	7.00E-02	7	34.48%
Q07065	Cytoskeleton-associated protein 4	0.84	0.16	3.90E-05	22	44.35%
Q12907	Vesicular integral-membrane protein VIP36	0.84	NA	NA	2	7.87%
Q9C0E8	Protein lunapark	0.84	NA	NA	2	4.67%
O60506	Heterogeneous nuclear ribonucleoprotein Q	0.83	0.41	4.40E-01	4	9.47%
P08238	Heat shock protein HSP 90-beta	0.83	0.25	1.30E-01	6	9.12%
P22307	Non-specific lipid-transfer protein	0.83	0.42	4.50E-01	4	5.48%
Q15907	Ras-related protein Rab-11B	0.83	0.14	1.40E-01	3	13.30%
P10644	cAMP-dependent protein kinase type I-alpha regulatory subunit	0.83	0.46	5.40E-01	3	11.55%
P30153	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isofo	0.83	NA	NA	2	4.75%
P07910	Heterogeneous nuclear ribonucleoproteins C1/C2	0.82	0.18	7.50E-02	5	17.32%
P39656	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit	0.82	0.46	5.40E-01	3	6.80%
O95202	LETM1 and EF-hand domain-containing protein 1, mitochondrial	0.82	0.07	4.40E-02	3	4.60%
O00264	Membrane-associated progesterone receptor component 1	0.82	0.18	1.10E-01	4	14.87%
Q14697	Neutral alpha-glucosidase AB	0.82	0.16	5.50E-02	5	6.04%
P46783	40S ribosomal protein S10	0.82	NA	NA	2	14.55%
P11021	78 kDa glucose-regulated protein	0.81	0.19	4.10E-06	28	41.90%
Q9BQE3	Tubulin alpha-1C chain	0.81	0.44	3.00E-01	6	17.59%
Q9Y6C2	EMILIN-1	0.81	0.14	1.30E-02	6	7.97%
Q9Y4L1	Hypoxia up-regulated protein 1	0.81	0.06	2.20E-02	3	2.90%
P30086	Phosphatidylethanolamine-binding protein 1	0.81	0.15	6.60E-02	4	19.25%
P51572	B-cell receptor-associated protein 31	0.81	NA	NA	2	11.79%
P49755	Transmembrane emp24 domain-containing protein 10	0.80	0.15	1.30E-01	3	13.70%
P62750	60S ribosomal protein L23a	0.80	0.42	3.80E-01	4	20.51%
Q92896	Golgi apparatus protein 1	0.80	0.57	5.70E-01	3	2.88%
Q96AE4	Far upstream element-binding protein 1	0.80	NA	NA	2	3.26%
P08670	Vimentin	0.80	0.27	2.20E-07	51	73.61%
P04181	Ornithine aminotransferase, mitochondrial	0.80	NA	NA	2	5.24%
O60664	Mannose-6-phosphate receptor-binding protein 1	0.80	0.44	3.70E-01	4	15.44%
Q9Y2B0	Protein canopy homolog 2	0.79	NA	NA	2	14.29%
O94973	AP-2 complex subunit alpha-2	0.79	NA	NA	2	2.02%
Q9UNX3	60S ribosomal protein L26-like 1	0.79	0.34	3.50E-01	3	16.55%
P15531	Nucleoside diphosphate kinase A	0.78	NA	NA	2	16.45%
Q96D15	Reticulocalbin-3	0.78	0.19	2.50E-02	6	18.90%
P06748	Nucleophosmin	0.78	0.26	9.70E-02	5	14.63%
P49419	Alpha-aminoadipic semialdehyde dehydrogenase	0.78	NA	NA	2	3.91%
P62906	60S ribosomal protein L10a	0.77	0.21	1.70E-01	3	10.14%
P10619	Lysosomal protective protein	0.77	0.20	1.60E-01	3	6.88%
P26599	Polypyrimidine tract-binding protein 1	0.77	NA	NA	2	2.45%
P16401	Histone H1.5	0.77	NA	NA	2	10.18%
O75915	PRA1 family protein 3	0.77	NA	NA	2	9.57%
Q8TED1	Probable glutathione peroxidase 8	0.77	NA	NA	2	10.53%
Q13162	Peroxiredoxin-4	0.77	0.27	2.40E-01	3	12.92%
P61970	Nuclear transport factor 2	0.76	NA	NA	2	18.90%
O00461	Golgi integral membrane protein 4	0.75	NA	NA	2	3.88%
P45880	Voltage-dependent anion-selective channel protein 2	0.74	NA	NA	2	10.88%
P14625	Endoplasmic	0.74	0.24	3.20E-05	19	22.42%
P30044	Peroxiredoxin-5, mitochondrial	0.74	0.45	2.70E-01	4	20.56%
Q02818	Nucleobindin-1	0.73	0.25	5.30E-02	5	14.10%
Q9HAV0	Guanine nucleotide-binding protein subunit beta-4	0.73	NA	NA	2	6.18%
P30101	Protein disulfide-isomerase A3	0.73	0.18	1.40E-06	18	35.84%
P13667	Protein disulfide-isomerase A4	0.73	0.31	1.80E-02	9	13.18%
P07195	L-lactate dehydrogenase B chain	0.73	0.60	4.60E-01	3	9.28%
Q96AY3	FK506-binding protein 10	0.73	0.33	1.50E-01	4	6.53%
Q15084	Protein disulfide-isomerase A6	0.72	0.21	1.70E-03	9	25.91%
Q8NBS9	Thioredoxin domain-containing protein 5	0.72	0.16	2.50E-04	9	21.06%
P06703	Protein S100-A6	0.72	NA	NA	2	17.78%
P17931	Galectin-3	0.72	0.15	6.00E-02	3	15.60%
P07237	Protein disulfide-isomerase	0.72	0.21	4.10E-08	25	45.08%
P26641	Elongation factor 1-gamma	0.71	0.53	2.90E-01	4	8.92%
P04844	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2	0.71	NA	NA	2	5.71%
P14314	Glucosidase 2 subunit beta	0.70	0.24	4.00E-03	8	17.99%
P78559	Microtubule-associated protein 1A	0.70	0.50	2.50E-01	4	2.14%
O15460	Prolyl 4-hydroxylase subunit alpha-2	0.70	0.20	9.00E-02	3	6.36%
O75964	ATP synthase subunit g, mitochondrial	0.70	NA	NA	2	21.36%
Q04637	Eukaryotic translation initiation factor 4 gamma 1	0.69	NA	NA	2	1.13%
Q15293	Reticulocalbin-1	0.69	0.18	1.00E-02	5	17.22%

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P27797	Calreticulin	0.68	0.16	1.30E-05	11	29.26%
P09382	Galectin-1	0.68	0.27	3.20E-02	5	26.67%
P13797	Plastin-3	0.67	0.13	3.20E-02	3	6.83%
P13674	Prolyl 4-hydroxylase subunit alpha-1	0.67	0.23	1.90E-02	5	12.55%
P99999	Cytochrome c	0.67	0.88	5.20E-01	3	24.76%
P30040	Endoplasmic reticulum protein ERp29	0.65	0.58	1.30E-01	6	24.52%
Q15075	Early endosome antigen 1	0.65	NA	NA	2	1.28%
P48681	Nestin	0.65	0.34	1.30E-04	16	12.40%
P10301	Ras-related protein R-Ras	0.64	0.31	1.30E-01	3	17.89%
P07093	Glia-derived nexin	0.63	NA	NA	2	6.53%
Q99584	Protein S100-A13	0.63	NA	NA	2	20.41%
P08559	Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondr	0.61	NA	NA	2	4.87%
Q9BRK5	45 kDa calcium-binding protein	0.61	NA	NA	2	5.80%
O95302	FK506-binding protein 9	0.60	NA	NA	2	3.16%
P68871	Hemoglobin subunit beta	0.60	NA	NA	2	15.65%
P55145	Protein ARMET	0.58	NA	NA	2	6.15%
Q9BVK6	Transmembrane emp24 domain-containing protein 9	0.57	NA	NA	2	6.81%
O94979	Protein transport protein Sec31A	0.57	NA	NA	2	1.31%
P30533	Alpha-2-macroglobulin receptor-associated protein	0.56	0.46	1.60E-01	3	6.72%
P23284	Peptidyl-prolyl cis-trans isomerase B	0.55	0.25	4.20E-06	12	39.81%
Q14764	Major vault protein	0.54	0.75	2.90E-01	3	2.69%
O75718	Cartilage-associated protein	0.51	0.41	2.10E-02	5	12.22%
P29966	Myristoylated alanine-rich C-kinase substrate	0.51	NA	NA	2	7.83%
P21810	Biglycan	0.48	NA	NA	2	5.43%
P50454	Serpin H1	0.44	0.22	6.50E-05	7	23.44%

Average false discovery rate = 1.01% peptide identity, 2.19% peptide homology; NA = not applicable because < 3 peptides.