

Supplemental Table 1. BFA-sensitive proteins in cell lysates.

Accession	Protein name	Ratio ¹	SD Ratio ²	P-value ³	SP ⁴
P35441	Thrombospondin-1 precursor	28.08	8.50	1.67E-15	Y
Q61207	Sulfated glycoprotein 1 precursor	21.98	13.81	2.28E-05	Y
P08226	Apolipoprotein E precursor	21.19	6.10	8.66E-14	Y
P06797	Cathepsin L1 precursor	9.39	0.81	1.04E-14	Y
O70310	Glycylpeptide N-tetradecanoyltransferase 1	7.41	0.81	4.20E-11	N
P41233	ATP-binding cassette sub-family A member 1	5.63	2.15	1.01E-03	Y
P03995	Glial fibrillary acidic protein	3.31	0.41	4.58E-04	N
Q8BU30	Isoleucyl-tRNA synthetase, cytoplasmic	2.88	0.65	1.35E-02	N
P55937	Golgin subfamily A member 3	2.71	0.50	1.31E-02	N
Q9CZ44	NSFL1 cofactor p47	2.19	0.22	3.85E-02	N
Q99K01	Pyridoxal-dependent decarboxylase domain-containing protein 1	0.75	0.04	3.68E-02	N
Q62446	FK506-binding protein 3	0.71	0.08	3.35E-02	N
P17439	Glucosylceramidase precursor	0.67	0.01	1.01E-02	Y
Q9JIF7	Coatomer subunit beta	0.66	0.14	4.29E-02	N
P29758	Ornithine aminotransferase, mitochondrial precursor	0.64	0.10	1.86E-02	Y
Q61292	Laminin subunit beta-2 precursor	0.58	0.11	1.33E-02	Y
Q8CHG7	Rap guanine nucleotide exchange factor 2	0.58	0.03	1.73E-03	N
Q9QZE5	Coatomer subunit gamma	0.56	0.15	2.38E-02	N
Q8BYM7	Radial spokehead-like protein 3	0.44	0.10	1.54E-03	N
Q9DB41	Mitochondrial glutamate carrier 2	0.31	0.09	1.71E-04	N
Q8VDQ8	NAD-dependent deacetylase sirtuin-2	0.17	0.11	2.62E-03	N

Proteins are sorted in order of decreasing protein ratio.

¹Calculated from the intensity weighted average of individual peptide ratios. Represents fold change in relative protein abundance after BFA treatment.

²Standard deviation of the average protein ratio calculated from individual peptide ratios.

³P-value calculated by the complementary error function (see *Experimental Procedures*). P < 0.05 was required for significance.

⁴Indicates whether the protein contained a predicted N-terminal signal peptide (SignalP 3.0).

Supplemental Table 2. BFA-sensitive proteins in ACM.

Accession	Protein name	Ratio ¹	SD Ratio ²	P-value ³	SP ⁴
Q04857	Collagen alpha-1(VI) chain	0.01	0.01	1.62E-10	Y
Q6GQT1	Alpha-2-macroglobulin-P	0.01	0.02	1.27E-03	Y
Q61362	Chitinase-3-like protein 1	0.02	0.01	5.88E-15	Y
Q60847	Collagen alpha-1(XII) chain	0.02	0.01	1.22E-15	Y
P70663	SPARC-like protein 1	0.02	0.01	1.70E-07	Y
P01027	Complement C3	0.02	0.02	1.49E-05	Y
P07214	SPARC (Secreted protein acidic and rich in cysteine)	0.02	0.03	1.63E-03	Y
O88968	Transcobalamin-2	0.02	0.01	4.17E-14	Y
P12023	Amyloid beta A4 protein	0.02	0.01	3.56E-08	Y
P07141	Macrophage colony-stimulating factor 1	0.03	0.02	1.02E-05	Y
Q07079	Insulin-like growth factor-binding protein 5	0.03	0.01	1.20E-12	Y
P11087	Collagen alpha-1(I) chain	0.03	0.02	8.20E-06	Y
Q00493	Carboxypeptidase E	0.03	0.03	2.38E-05	Y
P97298	Pigment epithelium-derived factor (PEDF)	0.03	0.04	4.85E-03	Y
Q61147	Ceruloplasmin	0.04	0.02	1.12E-08	Y
Q9R0E2	Procollagen-lysine,2-oxoglutarate 5-dioxygenase 1	0.04	0.01	7.26E-10	Y
O09159	Lysosomal alpha-mannosidase	0.04	0.01	1.62E-09	Y
Q05895	Thrombospondin-3	0.04	0.02	4.91E-07	Y
P01029	Complement C4-B	0.04	0.07	2.79E-02	Y
P06797	Cathepsin L1	0.04	0.03	2.80E-06	Y
O09164	Extracellular superoxide dismutase [Cu-Zn]	0.05	0.02	2.17E-08	Y
P08226	Apolipoprotein E	0.06	0.07	6.07E-03	Y
P11276	Fibronectin	0.06	0.03	2.91E-06	Y
P47877	Insulin-like growth factor-binding protein 2	0.06	0.06	2.85E-03	Y
Q06890	Clusterin (Apo-J)	0.06	0.06	3.25E-03	Y
A2ASQ1	Agrin	0.06	0.03	6.50E-07	Y
Q02819	Nucleobindin-1	0.06	0.01	1.11E-08	Y
P08905	Lysozyme C-2	0.08	0.10	2.46E-02	Y
O89017	Legumain	0.08	0.09	1.31E-02	Y
P10605	Cathepsin B	0.10	0.12	1.76E-02	Y
P55066	Neurocan core protein	0.11	0.07	5.58E-04	Y
Q76KF0	Semaphorin-6D	0.11	0.12	1.77E-02	Y
Q9WVJ3	Plasma glutamate carboxypeptidase	0.11	0.04	2.52E-05	Y
Q9R0E1	Procollagen-lysine,2-oxoglutarate 5-dioxygenase 3	0.13	0.01	1.34E-06	Y
Q61508	Extracellular matrix protein 1	0.15	0.02	6.37E-06	Y
O88531	Palmitoyl-protein thioesterase 1 (PPT-1)	0.16	0.06	1.29E-04	Y
O88322	Nidogen-2	0.17	0.08	7.84E-04	Y
O70370	Cathepsin S	0.18	0.08	7.70E-04	Y

P18242	Cathepsin D	0.18	0.12	4.92E-03	Y
P01887	Beta-2-microglobulin	0.20	0.06	2.99E-04	Y
P97290	Plasma protease C1 inhibitor	0.22	0.14	8.49E-03	Y
Q8K2I4	Beta-mannosidase	0.24	0.01	1.50E-04	Y
B2RXS8	Ptprz1 protein	0.26	0.18	2.05E-02	Y
P51655	Glypican-4 (K-glypican)	0.28	0.07	1.45E-03	Y
P70158	Acid sphingomyelinase-like phosphodiesterase 3a	0.28	0.12	5.84E-03	Y
Q9Z0J0	Epididymal secretory protein E1	0.31	0.11	4.87E-03	Y
Q9DBH5	Vesicular integral-membrane protein VIP36	0.31	0.05	1.37E-03	Y
Q9WTQ5	A-kinase anchor protein 12	0.33	0.19	2.37E-02	N
Q9QWR8	Alpha-N-acetylgalactosaminidase	0.38	0.10	7.42E-03	Y
P29416	Beta-hexosaminidase subunit alpha	0.44	0.06	8.67E-03	Y
A2BFA6	Alpha-N-acetylglucosaminidase	0.48	0.10	1.69E-02	Y
Q99M71	Mammalian ependymin-related protein 1	0.49	0.13	2.45E-02	Y
Q6PDJ1	VWFA and cache domain-containing protein 1	0.57	0.12	3.62E-02	N
P16858	Glyceraldehyde-3-phosphate dehydrogenase	0.63	0.10	4.63E-02	N
O54990	Prominin-1	0.63	0.10	4.66E-02	Y
Q9WVA4	Transgelin-2	7.90	0.49	1.64E-02	N

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²Standard deviation of the average protein ratio calculated from individual peptide ratios.

³P-value calculated by the complementary error function (see *Experimental Procedures*). P < 0.05 was required for significance.

⁴Indicates whether the protein contained a predicted N-terminal signal peptide (SignalP 3.0).

Supplemental Table 3. Quantified ACM proteins from control astrocytes.

Accession	Protein name	Ratio ¹	SD ²	Pep Count ³			SL ⁴
P08226	Apolipoprotein E	414.00	244.00	38	/	6	EM
O09164	Extracellular superoxide dismutase [Cu-Zn]	327.00	50.00	15	/	1	EM
P10923	Osteopontin	187.25	93.50	4	/	1	EM
Q8R422	CD109 antigen	76.00	22.50	50	/	1	EM
Q00493	Carboxypeptidase E	74.33	26.33	46	/	1	EM
P07214	SPARC	67.00	35.93	36	/	5	EM
A2APM1	CD44 antigen	65.33	4.33	3	/	1	EM
P47867	Secretogranin-3	64.00	16.00	29	/	1	EM
Q3UGY5	Fibronectin 1	57.67	87.06	119	/	6	EM
Q6GQT1	Alpha-2-macroglobulin-P	45.60	28.62	140	/	9	EM
P02463	Collagen alpha-1(IV) chain	41.89	12.13	9	/	2	EM
O88307	Sortilin-related receptor	31.45	5.76	42	/	6	EM
P43025	Tetranectin	30.62	5.62	8	/	1	EM
P29533	Vascular cell adhesion protein 1	30.15	4.23	21	/	1	EM
Q921T4	Phospholipase A2, group VII (Platelet-activating factor acetylhydrolase, plasma)	29.70	4.80	43	/	1	EM
P20152	Vimentin	27.43	19.36	61	/	8	O
Q80YX1	Tenascin	27.30	10.10	10	/	1	EM
Q9Z0J0	Epididymal secretory protein E1	22.00	12.65	19	/	7	EM
Q80W15	Insulin-like growth factor-binding protein-like 1	21.33	2.83	14	/	1	EM
Q9R0E1	Procollagen-lysine,2-oxoglutarate 5-dioxygenase 3	18.40	3.02	20	/	2	ER
P51655	Glypican-4	16.91	17.02	34	/	2	EM
P62806	Histone H4	16.17	4.64	9	/	7	O
Q06890	Clusterin	15.71	12.44	62	/	6	EM
Q61592	Growth arrest-specific protein 6	14.67	2.33	26	/	1	EM
P21460	Cystatin-C	14.00	2.45	37	/	1	EM
Q9WTR5	Cadherin-13	13.27	2.27	5	/	1	EM
Q02819	Nucleobindin-1	12.29	2.22	22	/	6	EM
Q3UHN9	Bifunctional heparan sulfate N-deacetylase/N-sulfotransferase 1	12.13	2.33	6	/	2	G
Q61147	Ceruloplasmin	12.00	14.40	37	/	2	EM
Q61361	Brevican core protein	11.23	2.39	14	/	2	EM
Q9WVJ3	Plasma glutamate carboxypeptidase	10.37	1.74	10	/	2	EM
P30412	Peptidyl-prolyl cis-trans isomerase C	10.36	0.57	4	/	2	EM
O70370	Cathepsin S	10.09	2.09	18	/	1	EL
Q80XP1	Complement component 3	9.75	11.25	130	/	5	EM
Q91ZX7	Prolow-density lipoprotein receptor-related protein 1	9.48	4.78	99	/	22	EM
Q9QXA3	Fat 1 cadherin (Fragment)	9.40	1.52	64	/	2	EM

Q99LJ1	Tissue alpha-L-fucosidase	8.56	1.73	8	/	2	EL
P55066	Neurocan core protein	8.47	10.22	47	/	2	EM
P97298	Pigment epithelium-derived factor	7.65	9.26	34	/	3	EM
Q9ES89	Exostosin-like 2	7.50	0.38	3	/	1	ER
Q60847	Collagen alpha-1(XII) chain	7.25	16.12	109	/	4	EM
Q99M71	Mammalian ependymin-related protein 1	7.00	1.76	13	/	10	EM
P13595	Neural cell adhesion molecule 1	7.00	1.71	10	/	1	EM
P27661	Histone H2A.x	6.82	1.93	4	/	6	O
Q91VU0	Protein FAM3C	6.81	3.28	5	/	2	EM
Q8BND5	Sulfhydryl oxidase 1	5.88	1.08	27	/	1	EM
P18242	Cathepsin D	5.25	8.52	42	/	8	EL
Q8K2I4	Beta-mannosidase	5.03	1.31	5	/	1	EL
Q91WP6	Serine protease inhibitor A3N	5.02	2.23	20	/	2	EM
Q8BFR4	N-acetylglucosamine-6-sulfatase	4.92	1.18	18	/	4	EL
Q61599	Rho GDP-dissociation inhibitor 2	4.80	2.56	2	/	2	O
Q8R464	Cell adhesion molecule 4	3.83	0.50	9	/	1	EM
B2RXS4	Plexin B2 (MCG140951) (Plxn2 protein)	3.79	7.13	19	/	13	EM
Q04857	Collagen alpha-1(VI) chain	3.76	0.68	12	/	1	EM
Q3UCL5	Ferritin	3.75	0.79	9	/	1	O
Q61233	Plastin-2	3.75	1.04	12	/	2	O
P09528	Ferritin heavy chain	3.59	1.25	7	/	2	O
Q8K479	Complement C1q tumor necrosis factor-related protein 5	3.55	0.35	11	/	2	EM
O88325	Alpha-N-acetylglucosaminidase (Sanfilippo disease IIIB)	3.50	0.47	16	/	7	EL
Q9R0B9	Procollagen-lysine,2-oxoglutarate 5-dioxygenase 2	3.44	0.64	14	/	2	ER
Q9WUT8	DSD-1-proteoglycan	3.22	4.07	25	/	3	EM
Q61207	Sulfated glycoprotein 1	3.04	0.72	29	/	13	EM
O88668	Protein CREG1	2.95	0.71	5	/	2	EM
Q197W7	N-glycan processing alpha-mannosidase IIx	2.94	0.60	3	/	2	G
Q64191	N(4)-(beta-N-acetylglucosaminyl)-L-asparaginase	2.88	2.13	15	/	6	EL
O88531	Palmitoyl-protein thioesterase 1	2.79	0.41	17	/	12	EL
P20060	Beta-hexosaminidase subunit beta	2.78	1.77	32	/	4	EL
P70158	Acid sphingomyelinase-like phosphodiesterase 3a	2.77	0.36	8	/	3	EM
Q9ET22	Dipeptidyl-peptidase 2	2.70	0.66	9	/	4	EL
P00493	Hypoxanthine-guanine phosphoribosyltransferase	2.63	0.60	9	/	6	O
O89017	Legumain	2.60	0.57	16	/	1	EL
P17047	Lysosome-associated membrane glycoprotein 2	2.55	1.53	5	/	4	EL
Q3TCN2	Putative phospholipase B-like 2	2.43	0.58	14	/	10	EL

P80314	T-complex protein 1 subunit beta	2.40	0.39	5	/	2	O
A2ARV4	Low-density lipoprotein receptor-related protein 2	2.24	0.62	59	/	9	EM
Q9EQH2	Endoplasmic reticulum aminopeptidase 1	2.20	0.57	6	/	3	ER
P10605	Cathepsin B	2.16	1.34	43	/	13	EL
P50429	Arylsulfatase B	2.12	0.72	9	/	3	EL
O88569	Heterogeneous nuclear ribonucleoproteins A2/B1	2.06	0.65	3	/	2	O
P01029	Complement C4-B	2.03	0.77	109	/	1	EM
Q8CHQ7	UPF0727 protein C6orf115 homolog	2.01	0.01	2	/	2	O
Q9WV54	Acid ceramidase	1.96	0.36	16	/	7	EL
Q91XG3	Hexosaminidase A	1.93	1.36	13	/	3	EL
Q60648	Ganglioside GM2 activator	1.87	0.40	20	/	6	EL
P16675	Lysosomal protective protein	1.87	0.73	25	/	12	EL
Q07797	Galectin-3-binding protein	1.78	0.22	21	/	1	EM
O09159	Lysosomal alpha-mannosidase	1.69	0.21	23	/	1	EL
O54782	Epididymis-specific alpha-mannosidase	1.64	0.89	21	/	4	EM
Q9CT10	Ran-binding protein 3	1.64	0.01	2	/	2	O
P23780	Beta-galactosidase	1.55	0.38	10	/	1	EL
P97290	Plasma protease C1 inhibitor	1.54	1.53	34	/	2	EM
Q9WUU7	Cathepsin Z	1.53	0.48	15	/	3	EL
P10852	4F2 cell-surface antigen heavy chain	1.48	0.34	9	/	2	O
Q6P5H2	Nestin	1.44	0.29	14	/	5	O
P35441	Thrombospondin-1	1.42	0.50	15	/	5	EM
Q9CPT4	UPF0556 protein C19orf10 homolog	1.42	0.53	4	/	4	EM
Q7TPR4	Alpha-actinin-1	1.41	0.37	42	/	56	O
P57780	Alpha-actinin-4	1.39	0.33	35	/	48	O
P09470	Angiotensin-converting enzyme, somatic isoform	1.30	0.36	4	/	1	EM
P23492	Purine nucleoside phosphorylase	1.29	0.35	16	/	11	O
Q62422	Osteoclast-stimulating factor 1	1.23	0.39	4	/	4	O
Q9DBH5	Vesicular integral-membrane protein VIP36	1.23	0.30	9	/	2	G
Q9ERR7	15 kDa selenoprotein	1.19	0.03	3	/	2	EL
P11438	Lysosome-associated membrane glycoprotein 1	1.18	0.38	7	/	3	EL
P28063	Proteasome subunit beta type-8	1.12	0.94	2	/	1	O
P54818	Galactocerebrosidase	1.12	0.15	14	/	1	EL
Q62426	Cystatin-B	1.10	0.16	5	/	3	O
Q80YA8	Crumbs homolog 2	1.10	0.31	6	/	9	EM
O35955	Proteasome subunit beta type-10	1.07	0.65	3	/	2	O
P49935	Cathepsin H	1.07	0.27	9	/	4	EL
Q9WV32	Actin-related protein 2/3 complex subunit 1B	1.06	0.45	3	/	3	O
Q99020	Heterogeneous nuclear ribonucleoprotein	1.06	0.05	3	/	2	O

A/B							
P16110	Galectin-3	1.05	0.22	10	/	7	O
Q9D7V9	N-acylethanolamine-hydrolyzing acid amidase	1.04	0.12	7	/	4	EL
Q921M7	Protein FAM49B	1.02	0.08	4	/	4	O
Q9Z1N5	Spliceosome RNA helicase Bat1	1.01	0.60	3	/	2	O
P05201	Aspartate aminotransferase, cytoplasmic	0.98	0.18	13	/	3	O
P20108	Thioredoxin-dependent peroxide reductase, mitochondrial	0.96	0.31	13	/	16	M
P62962	Profilin-1	0.96	0.15	9	/	12	O
P26041	Moesin	0.95	0.32	27	/	15	O
Q01768	Nucleoside diphosphate kinase B	0.93	0.13	5	/	11	O
P70665	Sialate O-acetyltransferase	0.92	0.09	5	/	2	EL
Q93092	Transaldolase	0.91	0.21	10	/	12	O
P16045	Galectin-1	0.87	0.13	6	/	11	O
P17439	Glucosylceramidase	0.86	0.01	2	/	1	EL
P14901	Heme oxygenase 1	0.86	0.01	2	/	1	O
Q6NXZ0	Dipeptidylpeptidase 3	0.86	0.14	7	/	1	O
P06151	L-lactate dehydrogenase A chain	0.85	0.20	21	/	19	O
P62991	Ubiquitin	0.85	0.24	5	/	7	O
P63028	Translationally-controlled tumor protein	0.85	0.14	7	/	6	O
P70699	Lysosomal alpha-glucosidase	0.84	0.33	7	/	5	O
Q05816	Fatty acid-binding protein, epidermal	0.83	0.28	2	/	2	O
Q06138	Calcium-binding protein 39	0.82	0.82	7	/	2	O
Q9QWR8	Alpha-N-acetylgalactosaminidase	0.82	0.16	15	/	7	EL
Q60709	Amyloid-like protein 2, isoform 751	0.82	0.20	8	/	1	EM
Q3TW96	UDP-N-acetylhexosamine pyrophosphorylase-like protein 1	0.78	0.01	2	/	1	O
P10639	Thioredoxin	0.78	0.37	3	/	5	O
P00920	Carbonic anhydrase 2	0.78	0.12	6	/	7	O
Q9JII6	Alcohol dehydrogenase [NADP+]	0.78	0.26	6	/	5	O
Q920E5	Farnesyl pyrophosphate synthetase	0.78	0.12	5	/	2	O
Q9CQF3	Cleavage and polyadenylation specificity factor subunit 5	0.78	0.09	2	/	1	O
Q8C845	Efh2 protein	0.77	0.54	7	/	4	O
P21107	Tropomyosin alpha-3 chain	0.77	0.20	9	/	7	O
Q60854	Serpin B6	0.77	0.10	9	/	3	O
Q9DCJ9	N-acetylneuraminate lyase	0.77	0.13	7	/	2	O
P97822	Acidic leucine-rich nuclear phosphoprotein 32 family member E	0.76	0.23	3	/	4	O
P15532	Nucleoside diphosphate kinase A	0.74	0.09	5	/	9	O
Q60631	Growth factor receptor-bound protein 2	0.73	0.36	4	/	2	O
P08228	Superoxide dismutase [Cu-Zn]	0.72	0.07	6	/	9	O
Q9CVB6	Actin-related protein 2/3 complex subunit 2	0.72	0.18	6	/	7	O

Q9DCD0	6-phosphogluconate dehydrogenase, decarboxylating	0.72	0.27	8	/	4	O
P24369	Peptidyl-prolyl cis-trans isomerase B	0.69	0.15	9	/	8	ER
P61982	14-3-3 protein gamma	0.69	0.14	15	/	10	O
P68510	14-3-3 protein eta	0.68	0.17	14	/	8	O
P47791	Glutathione reductase, mitochondrial	0.68	0.13	4	/	1	O
Q9Z2U0	Proteasome subunit alpha type-7	0.68	0.18	14	/	12	O
Q9JMH6	Thioredoxin reductase 1, cytoplasmic	0.67	0.08	6	/	4	O
Q01279	Epidermal growth factor receptor	0.67	0.03	3	/	1	EM
Q8BHG1	Nardilysin	0.67	0.28	2	/	11	O
P05064	Fructose-bisphosphate aldolase A	0.67	0.14	29	/	17	O
P63280	SUMO-conjugating enzyme UBC9	0.67	0.01	2	/	1	O
Q99LB4	Capping protein (Actin filament), gelsolin-like	0.66	0.55	6	/	4	O
P49722	Proteasome subunit alpha type-2	0.66	0.12	12	/	11	O
P54923	[Protein ADP-ribosylarginine] hydrolase	0.66	0.24	3	/	1	O
Q3U962	Collagen alpha-2(V) chain	0.65	0.31	14	/	1	EM
Q99K51	Plastin-3	0.64	0.59	4	/	4	O
Q3TIH9	Ubiquitin carrier protein	0.64	0.11	5	/	5	O
Q9D0B6	UPF0368 protein Cxorf26 homolog	0.63	0.01	2	/	1	O
P06745	Glucose-6-phosphate isomerase	0.63	0.11	30	/	13	O
O88958	Glucosamine-6-phosphate isomerase 1	0.63	0.25	7	/	4	O
O70435	Proteasome subunit alpha type-3	0.62	0.21	6	/	6	O
O55135	Eukaryotic translation initiation factor 6	0.62	0.28	3	/	3	O
P62897	Cytochrome c, somatic	0.61	0.15	6	/	6	O
P17742	Peptidyl-prolyl cis-trans isomerase A	0.61	0.14	20	/	17	O
Q3TH46	Putative uncharacterized protein (Fragment)	0.60	0.16	13	/	4	O
P59999	Actin-related protein 2/3 complex subunit 4	0.60	0.07	8	/	7	O
P51880	Fatty acid-binding protein, brain	0.59	0.60	4	/	6	O
Q9Z2W0	Aspartyl aminopeptidase	0.59	0.11	5	/	5	O
P14602	Heat shock protein beta-1	0.58	0.03	3	/	2	O
Q9JJU8	SH3 domain-binding glutamic acid-rich-like protein	0.58	0.27	4	/	5	O
Q9CR09	Ufm1-conjugating enzyme 1	0.58	0.12	4	/	5	O
P61161	Actin-related protein 2	0.57	0.23	5	/	3	O
P14211	Calreticulin	0.57	0.09	15	/	7	ER
Q9R1P3	Proteasome subunit beta type-2	0.57	0.09	5	/	7	O
P46664	Adenylosuccinate synthetase isozyme 2	0.57	0.06	5	/	1	O
O09061	Proteasome subunit beta type-1	0.57	0.17	13	/	11	O
O89023	Tripeptidyl-peptidase 1	0.57	0.15	16	/	2	EL
Q91VI7	Ribonuclease inhibitor	0.57	0.32	4	/	3	O
Q61035	Histidyl-tRNA synthetase, cytoplasmic	0.55	0.20	2	/	1	O
Q4FJY5	Ltb4dh protein	0.55	0.07	9	/	11	O

P27773	Protein disulfide-isomerase A3	0.55	0.11	25	/	16	ER
P53810	Phosphatidylinositol transfer protein alpha isoform	0.55	0.09	3	/	2	O
Q9QUM9	Proteasome subunit alpha type-6	0.55	0.13	9	/	11	O
O08795	Glucosidase 2 subunit beta	0.55	0.01	2	/	2	ER
Q9R1P1	Proteasome subunit beta type-3	0.55	0.13	7	/	6	O
P24527	Leukotriene A-4 hydrolase	0.54	0.14	12	/	4	O
P63101	14-3-3 protein zeta/delta	0.54	0.12	25	/	22	O
P10518	Delta-aminolevulinic acid dehydratase	0.53	0.15	3	/	3	O
Q9D8S4	Oligoribonuclease, mitochondrial	0.53	0.11	4	/	5	O
Q6WVG3	BTB/POZ domain-containing protein KCTD12	0.53	0.64	2	/	1	O
Q64727	Vinculin	0.52	0.18	22	/	33	O
P61979	Heterogeneous nuclear ribonucleoprotein K	0.52	0.53	4	/	3	O
Q61508	Extracellular matrix protein 1	0.52	0.09	23	/	1	EM
Q9JHW2	Nitrilase homolog 2	0.52	0.19	5	/	7	M
Q3TGE1	Putative uncharacterized protein	0.52	0.11	7	/	4	O
Q9R1P0	Proteasome subunit alpha type-4	0.52	0.16	9	/	9	O
Q9DBJ1	Phosphoglycerate mutase 1	0.52	0.10	17	/	16	O
P62204	Calmodulin	0.51	0.26	4	/	2	O
Q9CQV8	14-3-3 protein beta/alpha	0.51	0.15	11	/	11	O
Q6IRU2	Tropomyosin alpha-4 chain	0.51	0.10	19	/	24	O
Q9R1P4	Proteasome subunit alpha type-1	0.50	0.11	7	/	10	O
P57759	Endoplasmic reticulum protein Erp29	0.50	0.05	6	/	5	ER
Q3U561	Ribosomal protein L1	0.49	0.17	7	/	5	O
O54983	Mu-crystallin homolog	0.48	0.24	2	/	3	O
P13020	Gelsolin	0.48	0.15	17	/	4	EM
O35215	D-dopachrome decarboxylase	0.48	0.06	5	/	1	O
Q60692	Proteasome subunit beta type-6	0.48	0.25	7	/	7	O
Q9D1K7	Uncharacterized protein C20orf27 homolog	0.48	0.51	2	/	2	O
Q9CQI6	Coactosin-like protein	0.47	0.11	5	/	6	O
P58044	Isopentenyl-diphosphate Delta-isomerase 1	0.47	0.08	5	/	5	O
Q3TI11	Putative uncharacterized protein	0.47	0.10	4	/	5	O
O55234	Proteasome subunit beta type-5	0.46	0.06	10	/	11	O
Q921S3	Malic enzyme	0.46	0.09	9	/	13	O
P70195	Proteasome subunit beta type-7	0.46	0.09	6	/	5	O
Q9CQ60	6-phosphogluconolactonase	0.45	0.11	8	/	8	O
Q9CPY7	Cytosol aminopeptidase	0.45	0.22	7	/	3	O
Q07813	Apoptosis regulator BAX	0.45	0.03	2	/	4	O
Q9D967	Magnesium-dependent phosphatase 1	0.45	0.14	5	/	2	O
O88844	Isocitrate dehydrogenase [NADP] cytoplasmic	0.45	0.02	10	/	3	O
Q64010	Proto-oncogene C-crk	0.45	0.14	4	/	4	O
Q3U136	Putative uncharacterized protein (Fragment)	0.44	0.18	10	/	3	O

P45591	Cofilin-2	0.44	0.03	7	/	5	O
O55023	Inositol monophosphatase	0.44	0.14	9	/	6	O
Q8BFS6	Uncharacterized metallophosphoesterase CSTP1	0.44	0.12	2	/	1	O
Q66JR7	Pgm2 protein (Fragment)	0.43	0.16	2	/	2	O
P58252	Elongation factor 2	0.43	0.13	22	/	16	O
Q8C0E2	Vacuolar protein sorting-associated protein 26B	0.43	0.01	2	/	1	O
O09131	Glutathione S-transferase omega-1	0.43	0.01	2	/	2	O
Q3U6V5	Putative uncharacterized protein	0.43	0.02	3	/	1	O
Q9Z2U1	Proteasome subunit alpha type-5	0.43	0.18	6	/	7	O
Q99KQ4	Nicotinamide phosphoribosyltransferase	0.43	0.11	2	/	2	O
Q9WTQ5	A-kinase anchor protein 12	0.42	0.12	4	/	4	O
P60843	Eukaryotic initiation factor 4A-I	0.42	0.20	10	/	6	O
Q3U449	Putative uncharacterized protein	0.41	0.14	4	/	6	O
P09103	Protein disulfide-isomerase	0.41	0.05	11	/	4	ER
P97371	Proteasome activator complex subunit 1	0.40	0.07	5	/	4	O
Q3U1J4	DNA damage-binding protein 1	0.40	0.35	3	/	10	O
Q99LS3	Phosphoserine phosphatase	0.40	0.10	5	/	4	O
Q99PT1	Rho GDP-dissociation inhibitor 1	0.40	0.13	7	/	7	O
Q62348	Translin	0.39	0.09	10	/	12	O
P31786	Acyl-CoA-binding protein	0.39	0.29	4	/	5	O
P97372	Proteasome activator complex subunit 2	0.39	0.06	8	/	8	O
P05202	Aspartate aminotransferase, mitochondrial	0.39	0.11	20	/	12	M
Q9CRC9	Glucosamine-6-phosphate isomerase 2	0.39	0.11	2	/	5	O
Q8C1A5	Thimet oligopeptidase	0.38	0.08	5	/	2	O
Q8BHN3	Neutral alpha-glucosidase AB	0.38	0.16	8	/	21	M
P61087	Ubiquitin-conjugating enzyme E2 K	0.38	0.23	4	/	4	O
Q9JM76	Actin-related protein 2/3 complex subunit 3	0.37	0.08	3	/	3	O
P58389	Serine/threonine-protein phosphatase 2A regulatory subunit B'	0.37	0.15	4	/	4	O
Q61598	Rab GDP dissociation inhibitor beta	0.36	0.08	22	/	17	O
P20029	78 kDa glucose-regulated protein	0.36	0.13	13	/	14	ER
P47753	F-actin-capping protein subunit alpha-1	0.36	0.20	3	/	4	O
P58771	Tropomyosin alpha-1 chain	0.36	0.05	8	/	7	O
P26040	Ezrin	0.36	0.12	15	/	12	O
Q8BKC5	Importin-5	0.36	0.09	4	/	9	O
P62259	14-3-3 protein epsilon	0.36	0.06	24	/	24	O
P34884	Macrophage migration inhibitory factor	0.35	0.05	4	/	4	O
Q9DBP5	UMP-CMP kinase	0.35	0.04	3	/	3	O
P63242	Eukaryotic translation initiation factor 5A-1	0.34	0.07	5	/	5	O
P45376	Aldose reductase	0.34	0.05	12	/	9	O
P42932	T-complex protein 1 subunit theta	0.34	0.44	2	/	2	O

Q922R8	Protein disulfide-isomerase A6	0.34	0.06	7	/	5	ER
P05063	Fructose-bisphosphate aldolase C	0.34	0.06	27	/	15	O
Q8CDN6	Thioredoxin-like protein 1	0.34	0.14	4	/	6	O
Q66JR8	Ptms protein	0.34	0.07	4	/	5	O
P24472	Glutathione S-transferase A4	0.34	0.05	9	/	10	O
P09671	Superoxide dismutase [Mn], mitochondrial	0.34	0.15	4	/	5	O
Q99LP6	GrpE protein homolog 1, mitochondrial	0.33	0.13	7	/	4	M
P62257	Ubiquitin-conjugating enzyme E2 H	0.33	0.16	3	/	4	O
Q8BHG2	UPF0587 protein C1orf123 homolog	0.33	0.05	2	/	2	O
Q8CHP8	Phosphoglycolate phosphatase	0.33	0.36	2	/	1	O
Q9ERK4	Exportin-2	0.32	0.30	3	/	2	O
B1AXW7	Peroxiredoxin 1	0.32	0.04	20	/	19	O
Q99JI4	26S proteasome non-ATPase regulatory subunit 6	0.32	0.12	9	/	4	O
O88456	Calpain small subunit 1	0.32	0.17	2	/	1	O
Q9JKB1	Ubiquitin carboxyl-terminal hydrolase isozyme L3	0.32	0.41	3	/	1	O
Q9CXI5	Protein ARMET	0.32	0.13	3	/	6	EM
O55013	Trafficking protein particle complex subunit 3	0.31	0.01	2	/	1	O
Q61171	Peroxiredoxin-2	0.31	0.07	9	/	14	O
Q9DAW9	Calponin-3	0.31	0.38	2	/	5	O
P47955	60S acidic ribosomal protein P1	0.30	0.01	2	/	2	O
Q9Z2Y8	Proline synthetase co-transcribed bacterial homolog protein	0.30	0.05	4	/	3	O
Q9DB16	Calcium-binding protein 39-like	0.30	0.21	4	/	3	O
O88851	Retinoblastoma-binding protein 9	0.30	0.02	7	/	8	O
P61089	Ubiquitin-conjugating enzyme E2 N	0.30	0.11	2	/	7	O
Q9CZY3	Ubiquitin-conjugating enzyme E2 variant 1	0.29	0.01	2	/	2	O
Q8BG32	26S proteasome non-ATPase regulatory subunit 11	0.29	0.07	4	/	1	O
O88543	COP9 signalosome complex subunit 3	0.29	0.01	2	/	2	O
Q9JKR6	Hypoxia up-regulated protein 1	0.29	0.07	8	/	16	ER
O35381	Acidic leucine-rich nuclear phosphoprotein 32 family member A	0.28	0.10	4	/	5	O
O08807	Peroxiredoxin-4	0.28	0.22	6	/	7	M
P23506	Protein-L-isoaspartate(D-aspartate) O-methyltransferase	0.28	0.15	4	/	3	O
Q9D1Q6	Thioredoxin domain-containing protein 4	0.28	0.01	2	/	1	ER
P50396	Rab GDP dissociation inhibitor alpha	0.28	0.06	13	/	9	O
P29341	Polyadenylate-binding protein 1	0.28	0.02	4	/	2	O
Q91W90	Thioredoxin domain-containing protein 5	0.28	0.04	4	/	7	ER
Q9WVJ2	26S proteasome non-ATPase regulatory subunit 13	0.27	0.25	2	/	2	O

Q9QZ88	Vacuolar protein sorting-associated protein 29	0.27	0.06	6	/	5	O
Q01730	Ras suppressor protein 1	0.27	0.06	8	/	5	O
Q04447	Creatine kinase B-type	0.27	0.07	25	/	23	O
Q8C0M9	L-asparaginase	0.27	0.17	4	/	5	O
P37804	Transgelin	0.27	0.12	22	/	21	O
P68254	14-3-3 protein theta	0.27	0.09	14	/	13	O
Q8C1B7	Septin-11	0.27	0.44	2	/	2	O
O35593	26S proteasome non-ATPase regulatory subunit 14	0.27	0.22	3	/	3	O
Q9WTX5	S-phase kinase-associated protein 1	0.27	0.04	4	/	6	O
Q7TQI3	Ubiquitin thioesterase OTUB1	0.26	0.04	9	/	7	O
Q01405	Protein transport protein Sec23A	0.26	0.02	2	/	2	O
Q3UGR5	Haloacid dehalogenase-like hydrolase domain-containing protein 2	0.26	0.12	3	/	5	O
Q99LX0	Protein DJ-1	0.26	0.15	12	/	8	O
P14869	60S acidic ribosomal protein P0	0.26	0.17	6	/	8	O
P70168	Importin subunit beta-1	0.25	0.07	7	/	8	O
Q9DBG3	AP-2 complex subunit beta-1	0.25	0.07	2	/	5	O
Q91V76	Ester hydrolase C11orf54 homolog	0.25	0.03	6	/	5	O
P70296	Phosphatidylethanolamine-binding protein 1	0.25	0.06	20	/	26	O
Q9CPU0	Lactoylglutathione lyase	0.25	0.04	15	/	17	O
Q9JI75	Ribosyldihydronicotinamide dehydrogenase [quinone]	0.25	0.01	2	/	2	O
Q9CPV4	Glyoxalase domain-containing protein 4	0.25	0.05	13	/	10	O
P11499	Heat shock protein HSP 90-beta	0.25	0.10	31	/	29	O
Q6P1F6	Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B alpha isoform	0.25	0.05	4	/	1	O
Q7TMB8	Cytoplasmic FMR1-interacting protein 1	0.24	0.09	4	/	6	O
P52480	Pyruvate kinase isozymes M1/M2	0.24	0.08	32	/	14	O
Q01853	Transitional endoplasmic reticulum ATPase	0.24	0.07	18	/	16	O
Q9CX56	26S proteasome non-ATPase regulatory subunit 8	0.24	0.10	3	/	4	O
Q9QYR9	Acyl-coenzyme A thioesterase 2, mitochondrial	0.23	0.07	6	/	6	O
Q60605	Myosin light polypeptide 6	0.23	0.04	7	/	10	O
O08553	Dihydropyrimidinase-related protein 2	0.23	0.13	17	/	11	O
Q6P5E4	UDP-glucose:glycoprotein glucosyltransferase 1	0.23	0.05	3	/	9	M
Q8BJY1	26S proteasome non-ATPase regulatory subunit 5	0.23	0.05	4	/	2	O
Q8R0Y6	10-formyltetrahydrofolate dehydrogenase	0.23	0.06	8	/	19	O
Q9EQH3	Vacuolar protein sorting-associated protein 35	0.23	0.07	14	/	10	O
P17156	Heat shock-related 70 kDa protein 2	0.23	0.18	12	/	14	O

Q61205	Platelet-activating factor acetylhydrolase IB subunit gamma	0.23	0.01	2	/	2	O
P48758	Carbonyl reductase [NADPH] 1	0.23	0.32	2	/	4	O
Q61553	Fascin	0.22	0.05	6	/	3	O
Q922B2	Aspartyl-tRNA synthetase, cytoplasmic	0.22	0.08	3	/	2	O
Q61425	Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial	0.22	0.07	2	/	4	O
Q9CZD3	Glycyl-tRNA synthetase	0.21	0.01	2	/	3	M
O88545	COP9 signalosome complex subunit 6	0.21	0.05	2	/	3	O
Q9D898	Actin-related protein 2/3 complex subunit 5-like protein	0.21	0.01	2	/	2	O
P62137	Serine/threonine-protein phosphatase PP1-alpha catalytic subunit	0.21	0.15	9	/	4	O
Q9D8N0	Elongation factor 1-gamma	0.21	0.08	10	/	4	O
Q6P5F9	Exportin-1	0.20	0.02	5	/	7	O
Q6ZQ38	Cullin-associated NEDD8-dissociated protein 1	0.20	0.04	14	/	21	O
Q9CQM5	Thioredoxin domain-containing protein 17	0.20	0.01	2	/	1	O
P14152	Malate dehydrogenase, cytoplasmic	0.20	0.04	7	/	13	O
O55137	Acyl-coenzyme A thioesterase 1	0.20	0.07	8	/	8	O
Q9WU78	Programmed cell death 6-interacting protein	0.20	0.05	3	/	7	O
Q80Y52	Heat shock protein 90, alpha (Cytosolic), class A member 1	0.19	0.07	24	/	29	O
Q9CZ04	COP9 signalosome complex subunit 7a	0.19	0.03	3	/	4	O
Q8K4Z3	Apolipoprotein A-I-binding protein	0.19	0.05	6	/	7	M
Q9Z1Z2	Serine-threonine kinase receptor-associated protein	0.19	0.04	2	/	2	O
Q564P4	Adenine phosphoribosyl transferase	0.19	0.03	4	/	4	O
O08749	Dihydrolipoyl dehydrogenase, mitochondrial	0.18	0.05	8	/	5	O
Q61206	Platelet-activating factor acetylhydrolase IB subunit beta	0.18	0.03	4	/	4	O
Q6ZWX6	Eukaryotic translation initiation factor 2 subunit 1	0.18	0.10	2	/	2	O
P60122	RuvB-like 1	0.18	0.01	2	/	3	O
P08113	Endoplasmic	0.18	0.07	13	/	24	ER
O70251	Elongation factor 1-beta	0.17	0.06	3	/	3	O
P40142	Transketolase	0.17	0.04	7	/	9	O
Q64433	10 kDa heat shock protein, mitochondrial	0.17	0.02	4	/	5	O
Q6PJ91	Gstm7 protein	0.17	0.04	7	/	7	O
Q99KC8	Loss of heterozygosity 11 chromosomal region 2 gene A protein homolog	0.17	0.09	6	/	4	O
Q62048	Astrocytic phosphoprotein PEA-15	0.17	0.04	12	/	14	O
P40124	Adenylyl cyclase-associated protein 1	0.17	0.02	5	/	3	O
P17710	Hexokinase-1	0.17	0.07	7	/	10	O
P68040	Guanine nucleotide-binding protein subunit	0.17	0.09	8	/	5	O

beta-2-like 1							
P47754	F-actin-capping protein subunit alpha-2	0.17	0.07	4	/	5	O
P09411	Phosphoglycerate kinase 1	0.17	0.05	19	/	15	O
Q8VHX6	Filamin-C	0.17	0.06	50	/	66	O
Q9R0Y5	Adenylate kinase isoenzyme 1	0.16	0.08	4	/	5	O
Q76M23	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform	0.16	0.12	7	/	7	O
P26516	26S proteasome non-ATPase regulatory subunit 7	0.16	0.06	3	/	5	O
O35643	AP-1 complex subunit beta-1	0.16	0.10	2	/	6	O
Q99P72	Reticulon-4	0.16	0.08	3	/	4	O
P99029	Peroxisredoxin-5, mitochondrial	0.16	0.04	12	/	13	O
Q9R0P9	Ubiquitin carboxyl-terminal hydrolase isozyme L1	0.16	0.04	6	/	8	O
P99027	60S acidic ribosomal protein P2	0.16	0.03	2	/	3	O
Q91ZJ5	UTP--glucose-1-phosphate uridylyltransferase	0.16	0.20	7	/	3	O
P80315	T-complex protein 1 subunit delta	0.16	0.24	4	/	2	O
P14685	26S proteasome non-ATPase regulatory subunit 3	0.16	0.07	2	/	4	O
Q9Z1Q5	Chloride intracellular channel protein 1	0.15	0.03	3	/	7	O
Q80X90	Filamin-B	0.15	0.05	105	/	115	O
P61164	Alpha-centractin	0.15	0.01	2	/	1	O
P70202	Latexin	0.15	0.04	8	/	7	O
P08003	Protein disulfide-isomerase A4	0.15	0.05	9	/	6	ER
P10649	Glutathione S-transferase Mu 1	0.15	0.03	25	/	24	O
P15626	Glutathione S-transferase Mu 2	0.14	0.05	11	/	13	O
P97823	Acyl-protein thioesterase 1	0.14	0.01	2	/	1	O
P16125	L-lactate dehydrogenase B chain	0.14	0.05	21	/	17	O
P60710	Actin, cytoplasmic 1	0.14	0.04	27	/	27	O
Q9QXT0	Protein canopy homolog 2	0.13	0.11	3	/	3	ER
P48774	Glutathione S-transferase Mu 5	0.13	0.02	10	/	8	O
Q9WVA4	Transgelin-2	0.13	0.03	10	/	8	O
Q9JIF7	Coatomer subunit beta	0.13	0.01	2	/	3	O
P18760	Cofilin-1	0.13	0.02	17	/	17	O
Q62261	Spectrin beta chain, brain 1	0.13	0.08	22	/	40	O
P63017	Heat shock cognate 71 kDa protein	0.13	0.06	38	/	19	O
P50247	Adenosylhomocysteinase	0.12	0.05	4	/	4	O
Q11011	Puromycin-sensitive aminopeptidase	0.12	0.05	3	/	9	M
Q9DBE0	Cysteine sulfinic acid decarboxylase	0.12	0.01	2	/	1	O
P34022	Ran-specific GTPase-activating protein	0.12	0.04	2	/	3	O
Q68FD5	Clathrin heavy chain 1	0.12	0.03	31	/	56	O
P68033	Actin, alpha cardiac muscle 1	0.12	0.05	23	/	25	O
P12815	Programmed cell death protein 6	0.12	0.04	3	/	5	O

Q6P069	Sorcin	0.12	0.05	5	/	10	O
Q99L47	Hsc70-interacting protein	0.12	0.01	4	/	1	O
P70670	Nascent polypeptide-associated complex subunit alpha, muscle-specific form	0.12	0.06	3	/	3	O
Q91V41	Ras-related protein Rab-14	0.11	0.18	2	/	2	O
P62141	Serine/threonine-protein phosphatase PP1-beta catalytic subunit	0.11	0.03	8	/	5	O
O70492	Sorting nexin-3	0.11	0.02	3	/	5	O
Q9D3D9	ATP synthase subunit delta, mitochondrial	0.11	0.03	2	/	4	O
Q61316	Heat shock 70 kDa protein 4	0.11	0.03	8	/	16	O
P19096	Fatty acid synthase	0.11	0.03	41	/	60	O
Q80UW2	F-box only protein 2	0.11	0.03	8	/	9	O
P63085	Mitogen-activated protein kinase 1	0.11	0.05	2	/	2	O
Q9QZE5	Coatomer subunit gamma	0.11	0.02	2	/	2	O
P42125	3,2-trans-enoyl-CoA isomerase, mitochondrial	0.11	0.03	2	/	5	O
P17182	Alpha-enolase	0.11	0.03	26	/	20	O
P05213	Tubulin alpha-1B chain	0.10	0.06	27	/	18	O
B1ATE2	Ring finger protein 213 (Fragment)	0.10	0.07	2	/	4	O
P62737	Actin, aortic smooth muscle	0.10	0.04	19	/	20	O
Q9CZC8	Secernin-1	0.10	0.01	2	/	4	O
P61082	NEDD8-conjugating enzyme Ubc12	0.09	0.14	2	/	2	O
Q9QXS1	Plectin-1	0.09	0.07	36	/	63	O
P62827	GTP-binding nuclear protein Ran	0.09	0.03	6	/	8	O
P80317	T-complex protein 1 subunit zeta	0.09	0.01	2	/	1	O
P68373	Tubulin alpha-1C chain	0.09	0.05	27	/	19	O
Q99K85	Phosphoserine aminotransferase	0.09	0.02	4	/	7	O
Q8CIE6	Coatomer subunit alpha	0.09	0.05	3	/	22	O
Q9DB79	Putative uncharacterized protein	0.09	0.02	4	/	3	O
A3QM89	Reticulon 1 (Fragment)	0.09	0.02	2	/	6	O
Q9EPQ7	StAR-related lipid transfer protein 5	0.08	0.01	2	/	2	O
P14131	40S ribosomal protein S16	0.08	0.02	3	/	2	O
Q9JKF1	Ras GTPase-activating-like protein IQGAP1	0.08	0.02	6	/	13	O
P35979	60S ribosomal protein L12	0.08	0.02	4	/	8	O
Q02053	Ubiquitin-like modifier-activating enzyme 1	0.08	0.02	3	/	18	O
Q3THE2	Myosin regulatory light chain MRLC2	0.08	0.05	4	/	5	O
Q9D6J6	NADH dehydrogenase [ubiquinone] flavoprotein 2, mitochondrial	0.08	0.02	2	/	3	O
P68369	Tubulin alpha-1A chain	0.08	0.04	25	/	20	O
P62715	Serine/threonine-protein phosphatase 2A catalytic subunit beta isoform	0.07	0.01	2	/	3	O
Q9WUL7	ADP-ribosylation factor-like protein 3	0.07	0.06	3	/	2	O
P08249	Malate dehydrogenase, mitochondrial	0.07	0.02	14	/	22	O
Q8CI94	Glycogen phosphorylase, brain form	0.07	0.03	10	/	15	O

P26039	Talin-1	0.07	0.02	37	/	49	O
P62908	40S ribosomal protein S3	0.07	0.03	9	/	11	O
P70349	Histidine triad nucleotide-binding protein 1	0.07	0.01	3	/	6	O
P28656	Nucleosome assembly protein 1-like 1	0.07	0.01	3	/	2	O
Q8VDM4	26S proteasome non-ATPase regulatory subunit 2	0.07	0.01	2	/	6	O
P57776	Elongation factor 1-delta	0.07	0.02	3	/	4	O
Q6GT24	Peroxiredoxin 6	0.07	0.02	38	/	37	O
P47199	Quinone oxidoreductase	0.06	0.01	2	/	3	O
Q9CWS0	N(G),N(G)-dimethylarginine dimethylaminohydrolase 1	0.06	0.02	6	/	17	O
Q9EQF6	Dihydropyrimidinase-related protein 5	0.06	0.03	2	/	4	O
P54071	Isocitrate dehydrogenase [NADP], mitochondrial	0.06	0.06	5	/	10	O
Q71LX4	Talin-2	0.06	0.02	5	/	19	O
Q8BTM8	Filamin-A	0.06	0.05	59	/	88	O
P17751	Triosephosphate isomerase	0.06	0.01	9	/	14	O
P63038	60 kDa heat shock protein, mitochondrial	0.06	0.02	5	/	10	O
Q9ERD7	Tubulin beta-3 chain	0.05	0.04	12	/	8	O
P80318	T-complex protein 1 subunit gamma	0.05	0.01	4	/	2	O
P29758	Ornithine aminotransferase, mitochondrial	0.05	0.03	4	/	3	O
Q9JHU4	Cytoplasmic dynein 1 heavy chain 1	0.05	0.02	68	/	76	O
P19157	Glutathione S-transferase P 1	0.05	0.02	5	/	7	O
Q9QUI0	Transforming protein RhoA	0.05	0.04	4	/	5	O
Q6ZWZ6	40S ribosomal protein S12	0.05	0.02	4	/	5	O
P46638	Ras-related protein Rab-11B	0.05	0.01	3	/	1	O
Q9R0P3	S-formylglutathione hydrolase	0.05	0.04	3	/	13	O
Q4FE56	Ubiquitin carboxyl-terminal hydrolase	0.05	0.01	3	/	15	O
Q9R0Q7	Prostaglandin E synthase 3	0.05	0.01	3	/	4	O
Q3UL78	Putative uncharacterized protein	0.05	0.02	5	/	4	O
Q3UBK2	Putative uncharacterized protein	0.05	0.02	3	/	7	O
A2AN08	E3 ubiquitin-protein ligase UBR4	0.05	0.01	3	/	5	O
P62821	Ras-related protein Rab-1A	0.04	0.01	3	/	2	O
P56480	ATP synthase subunit beta, mitochondrial	0.04	0.01	13	/	15	O
P50518	V-type proton ATPase subunit E 1	0.04	0.01	2	/	4	O
P99024	Tubulin beta-5 chain	0.04	0.01	22	/	22	O
P62835	Ras-related protein Rap-1A	0.04	0.01	3	/	4	O
Q9CRB6	Tubulin polymerization-promoting protein family member 3	0.04	0.01	5	/	8	O
P61750	ADP-ribosylation factor 4	0.04	0.01	3	/	5	O
P62270	40S ribosomal protein S18	0.04	0.01	2	/	2	O
P68372	Tubulin beta-2C chain	0.03	0.01	16	/	18	O
P25444	40S ribosomal protein S2	0.03	0.01	2	/	7	O

Q922F4	Tubulin beta-6 chain	0.03	0.01	12	/	4	O
Q9WTP7	GTP:AMP phosphotransferase mitochondrial	0.03	0.01	5	/	11	O
P26443	Glutamate dehydrogenase 1, mitochondrial	0.03	0.02	5	/	6	O
Q9WUA3	6-phosphofructokinase type C	0.03	0.02	3	/	4	O
Q7TMM9	Tubulin beta-2A chain	0.03	0.01	18	/	18	O
P10126	Elongation factor 1-alpha 1	0.03	0.01	6	/	4	O
P61027	Ras-related protein Rab-10	0.03	0.02	3	/	4	O
P62880	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2	0.03	0.02	7	/	6	O
Q6ZWN5	40S ribosomal protein S9	0.03	0.01	2	/	4	O
Q8C1X9	Anxa3 protein	0.03	0.01	15	/	23	O
P07356	Annexin A2	0.02	0.01	8	/	24	O
P62874	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1	0.02	0.01	4	/	5	O
O08638	Myosin-11	0.02	0.01	6	/	7	O
P97447	Four and a half LIM domains protein 1	0.02	0.01	2	/	11	O
Q8VDD5	Myosin-9	0.02	0.01	24	/	55	O
P35278	Ras-related protein Rab-5C	0.02	0.01	4	/	4	O
P63325	40S ribosomal protein S10	0.02	0.01	2	/	3	O
Q91V55	Putative uncharacterized protein	0.02	0.01	2	/	2	O
P16858	Glyceraldehyde-3-phosphate dehydrogenase	0.01	0.01	16	/	20	O
Q61879	Myosin-10	0.01	0.01	10	/	40	O
Q8VDN2	Sodium/potassium-transporting ATPase subunit alpha-1	0.01	0.01	2	/	8	O
Q9R0P5	Destrin	0.01	0.01	3	/	7	O
P48036	Annexin A5	0.01	0.01	12	/	21	O

Proteins are sorted in order of decreasing protein ratio.

¹Calculated from the intensity weighted average of individual peptide ratios. Ratio reflects the fold difference in protein abundance in ACM relative to cell lysates.

²Standard deviation of the protein ratio, calculated by error propagation derived from individual peptide ratios for ACM and cell lysates.

³Number of unique, quantified peptides used to calculate the protein ratio from ACM (*left*) and cell lysates (*right*) samples. A minimum of 2 unique, quantified peptides were required in at least ACM or cell lysates samples.

⁴Predicted protein subcellular localization. Primary sequence analysis was performed by Signal P 3.0 to distinguish N-terminal signal peptide-containing proteins from non-signal peptide-containing proteins, followed by TargetP to provide predicted subcellular localization. EM = Extracellular/Plasma membrane; EL=Endo/Lysosome; G = Golgi; M = Mitochondria; ER = Endoplasmic reticulum; O = Cytoplasm/Nucleus/Other