

SUPPLEMENTARY DATA

Assessment of electrophile damage in a human brain endothelial cell line utilizing a clickable alkyne analogue of 2-chlorohexadecanal

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LC-MS/MS and search parameter settings

Protein spots were excised from gels and tryptically digested according to the method by Shevchenko et al. [1]. Peptide extracts were dissolved in 0.1% formic acid and separated on a nano-HPLC system (Ultimate 3000™, LC Packings, Amsterdam, Netherlands). 70µl samples were injected and concentrated on the loading column (LC Packings C18 Pep-Map™, 5 µm, 100 Å, 300µm inner diameter x 1mm) for 5 min using 0.1% formic acid as isocratic solvent at a flow rate of 20 µl/min. The column was then switched into the nanoflow circuit, and the sample was loaded on the nanocolumn (LC-Packings C18 PepMap™, 75 µm inner diameter x 150 mm) at a flow rate of 300 nl/min and separated using the following gradient: solvent A: water, 0.3% formic acid, solvent B: acetonitrile/water 80/20 (v/v), 0.3% formic acid; 0 to 5 minutes: 4% B, after 40 minutes 55% B, then for 5 minutes 90% B and 47 minutes reequilibration at 4% B. The sample was ionized in a Finnigan nano-ESI source equipped with NanoSpray tips (PicoTip™ Emitter, New Objective, Woburn, MA, USA) and analysed in a Thermo-Finnigan LTQ linear iontrap mass-spectrometer (Thermo, San Jose, CA, USA). The MS/MS data were analyzed by searching the SwissProt public database with SpectrumMill Rev. 03.03.078 (Agilent, Darmstadt, GER) software (for more details see supplementary data). Acceptance parameters was a perotein score of more than 20 and individual peptide scores above 7.5

Chemicals

NH ₄ HCO ₃	Sigma A-6141
CaCl ₂ .2 H ₂ O	Merck 102382
Acetonitrile HPLC grade	Merck UN 1648
DTT	Sigma D-0632
IAA	Sigma I-1149
Modified Trypsin sequencing grade	Promega V5111

General MS/MS Search Parameters

Data Extraction

“Peak List Files” from RAW-data were created using the “Data Extractor” of the “Agilent - Spectrum Mill” Software (Rev. A. 03.03.084). The following settings were used:

N-terminus: Hydrogen
C-terminus : Free acid
Cys modification: Carbamidomethylation
Sequence tag length > 1
MH+: 400 – 4000 Da
Scan time: 0 – 70 min
Merge Scans +/- 0.1 sec, +/- 0.1 m/z
Find charge
Maximum z = 3
Minimum S/N : 3
Find ¹²C

MS/MS Search

The database used was the “homo sapiens” subset of the SwissProt database, downloaded on 13.3.2013 from <ftp://ftp.ncbi.nih.gov/blast/db/FASTA/>, containing 454402 entries.

Database searching was performed with the “MS/MS Search” feature of the “Agilent - Spectrum Mill” Software (Rev. 03.03.078) and the following settings were used:

Enzyme: Trypsin
N-terminus: Hydrogen
C-terminus : free acid
Allowed missed cleavages: 2
Cys modification: carbamidomethylation
Variable modifications: Oxidized (Met)
Pyro (N-term Glu)
Acrylamide (Cys)
Sequence tag length > 3

Minimum detected. Peaks: 4

Minimum matched peak intensity: 50%

Precursor mass tolerance: +/- 2.5 Da

Product mass tolerance: +/- 0.7 Da

Acceptance parameters:	minimum protein score:	20
	Individual peptide score:	>7.5
	SPI value :	> 75

[1] Shevchenko, A., Wilm, M., Vorm, O., Mann, M., Mass spectrometric sequencing of proteins silver-stained polyacrylamide gels. *Anal. Chem.* 1996, 68, 850-858.

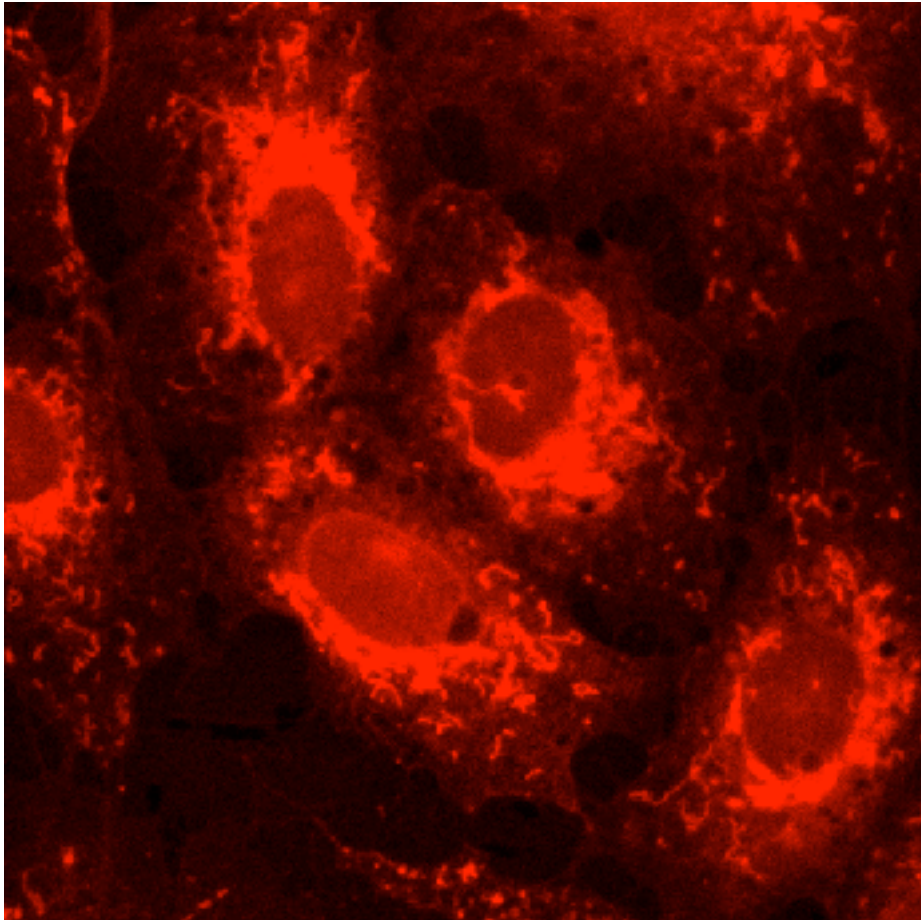


Fig. S1: Visualization of protein-2-CIHdyA-TAMRA adducts by confocal laser scanning microscopy in hCMEC/D3 cells

Cells grown on plastic chamber slides were incubated in the presence of 2-CIHdyA (25 μ M) for 30 min, fixed in methanol, permeabilized with Triton X-100, and subjected to click chemistry with N_3 -TAMRA. Cells were mounted in Moviol and analyzed by confocal laser scanning microscopy. For better visualization of cell borders, micrographs were overexposed by 50 %.

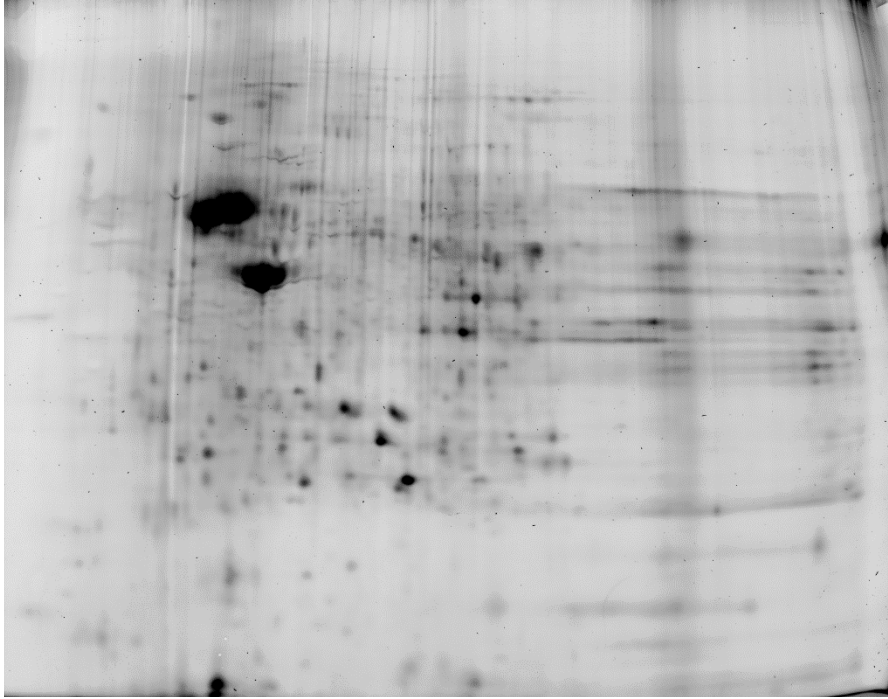


Fig. S2A: Grey scale image of a representative 2D gel utilized for separation of total hCMEC/D3 cell lysates

hCMEC/D3 cells plated in collagen-coated 10 cm culture dishes were grown to confluence and incubated in the presence of 50 μ M 2-ClHDyA for 30 min at 37°C. Subsequently, cells were washed with PBS and Schiff bases were reduced to stable amines. Cells were washed again, scraped in 300 μ l 'clicking buffer' and clicked with N₃-TAMRA. Separation in the first and second dimension was performed as described in Materials and Methods. Fluorescence imaging was performed on a Typhoon 9400 scanner. Fluorescent protein spots were picked, tryptically digested and identified by LC-MS/MS.

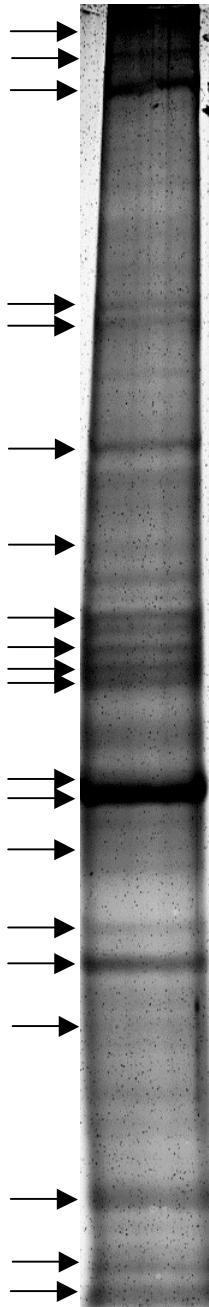


Fig. S2B: Grey scale image of a representative 1D gel utilized for membrane protein separation

hCMEC/D3 cells plated in collagen-coated 10 cm culture dishes were grown to confluence and incubated in the presence of 50 μ M 2-ClHDyA for 30 min at 37°C. Cells were washed with PBS and Schiff bases were reduced to stable amines. Cells were washed again, scraped in 300 μ l 'clicking buffer' and clicked with N₃-TAMRA. Separation was performed on self-cast 20 cm PA-SDS gels (12%). Fluorescence imaging was performed on a Typhoon 9400 scanner. Fluorescent bands indicated by arrows were picked, tryptically digested, and identified by LC-MS/MS.

TABLE S1: 2-CIDyA-tagged proteins identified by LC-MS/MS after 2-D gel electrophoresis of total cell lysates

Protein name	UniProt accession number	Spot	Spectra	Distinct peptides	Distinct summed MS/MS search score	% AA coverage	Molecular mass (Da)	Molecular mass exper. (Da)	Cell lysate 1		Cell lysate 2	
									pi	pl exper.	pi	pl exper.
Myosin-9	P35579.4	365	35	13	222.06	8	226533.4	103702	5.50	5.10		
		865	80	22	390.80	12	226533.4	98336	5.50	5.25		
		923	45	15	242.00	9	226533.4	94877	5.50	5.15		
		791	167	34	605.53	18	226533.4	94840	5.50	5.25		
Vimentin	P08670.4	840	44	15	258.54	36	53651.9	55364	5.06	5.25		
		858	238	29	531.06	64	53651.9	53409	5.06	4.70		
		870	137	26	458.99	59	53651.9	54374	5.06	4.90		
		1664	364	38	633.46	67	53651.9	57759	5.06	4.90		
		1653	71	18	309.11	43	53651.9	56930	5.06	4.85		
		1285	34	12	198.39	27	53651.9	58287	5.06	5.20		
		1330	188	28	479.43	58	53651.9	57334	5.06	4.95		
		1344	513	32	570.04	65	53651.9	56401	5.06	4.70		
		1408	157	24	426.03	54	53651.9	53715	5.06	4.30		
		1509	37	14	226.47	31	53651.9	48819	5.06	4.65		
ATP synthase subunit beta, mitochondrial	P06576.3	840	9	7	111.58	18	56560.2	55364	5.26	5.25		
		858	10	6	107.33	16	56560.2	53409	5.26	4.70		
		870	385	25	521.47	72	56560.2	54374	5.26	4.90		
		1653	218	21	429.53	64	56560.2	56830	5.26	4.85		
		1330	234	22	454.09	70	56560.2	57334	5.26	4.95		
1344	77	17	325.11	63	56560.2	56401	5.26	4.70				
Putative elongation factor 1- alpha-like 3	Q5VTE0.1	938	212	14	275.33	50	50185.3	48078	9.15	9.90		
		1699	133	13	247.41	48	50185.3	52454	9.15	9.95		
		1700	196	14	265.92	50	50185.3	53294	9.15	8.50		
		1425	255	17	297.90	48	50185.3	51191	9.15	9.95		
1533	7	3	43.66	6	50185.3	46590	9.15	8.40				
Alpha-enolase	P06733.2	958	447	28	527.45	73	47169.2	47262	7.01	6.90		
		965	36	5	106.17	20	47169.2	47262	7.01	5.20		
		981	87	18	315.04	48	47169.2	45688	7.01	6.45		
		1012	16	9	128.84	21	47169.2	44188	7.01	6.95		
		1725	481	29	530.93	74	47169.2	50034	7.01	7.35		
		1733	108	18	335.51	55	47169.2	50034	7.01	6.55		
		1737	51	13	228.56	39	47169.2	52872	7.01	6.35		
		1767	413	28	517.39	73	47169.2	48501	7.01	6.95		
		1802	10	4	73.66	13	47169.2	47758	7.01	7.05		
		1427	250	24	451.61	70	47169.2	50384	7.01	6.65		
		1442	40	8	144.88	26	47169.2	51191	7.01	5.30		
		1448	27	11	185.34	30	47169.2	50384	7.01	6.10		
		1470	7	4	66.08	9	47169.2	49593	7.01	6.40		
1471	682	28	519.19	73	47169.2	48819	7.01	7.30				
1476	395	25	465.05	72	47169.2	48819	7.01	6.95				
1533	19	3	61.04	11	47169.2	46590	7.01	8.40				
Lupus La protein	P05456.2	958	51	17	279.17	46	46837.3	47262	6.68	6.90		
		981	89	22	353.36	51	46837.3	45688	6.68	6.45		
		1733	15	8	142.77	26	46837.3	50034	6.68	6.55		
		1767	6	4	79.89	13	46837.3	48501	6.68	6.95		
		1427	90	23	384.47	56	46837.3	50384	6.68	6.65		
		1442	16	6	108.22	19	46837.3	51191	6.68	5.90		
		1448	28	10	146.08	32	46837.3	50384	6.68	6.10		
1470	6	4	62.11	13	46837.3	49593	6.68	6.40				
1476	20	10	169.56	32	46837.3	48819	6.68	6.95				
Rab GDP dissociation inhibitor beta	P50395.2	958	20	10	145.85	27	50663.5	47262	6.11	6.90		
		1737	128	26	483.58	71	50663.5	52872	6.11	6.35		
		1427	116	24	427.78	71	50663.5	50384	6.11	6.65		
		1442	35	10	175.28	24	50663.5	51191	6.11	5.90		
		1448	98	24	397.97	65	50663.5	50384	6.11	6.10		
1470	124	26	418.65	75	50663.5	49593	6.11	6.40				
1476	12	5	78.97	14	50663.5	48819	6.11	6.95				
Eukaryotic initiation factor 4A-I	P60842.1	965	299	27	491.88	71	46154.2	47262	5.32	5.20		
		1763	211	24	447.33	68	46154.2	50034	5.32	5.25		
		1457	95	16	278.05	47	46154.2	51191	5.32	5.25		
		1555	67	15	287.72	47	46154.2	45179	5.32	5.25		
		1590	8	5	77.21	15	46154.2	44496	5.32	5.05		
1601	19	6	112.22	20	46154.2	44496	5.32	5.45				
Cartilage-associated protein	O75718.1	965	25	9	149.93	28	46562.1	47262	5.50	5.20		
		1763	4	3	37.90	5	46562.1	50034	5.50	5.25		
		1457	21	6	103.41	17	46562.1	51191	5.50	5.25		
Elongation factor 1-gamma	P26641.3	981	212	24	431.73	63	50119.1	45688	6.25	6.45		
		1733	222	21	396.56	60	50119.1	50034	6.25	6.55		
		1737	71	16	283.97	48	50119.1	52872	6.25	6.35		
		1427	355	28	522.64	78	50119.1	50384	6.25	6.65		
		1448	12	5	76.87	16	50119.1	50384	6.25	6.10		
1470	13	5	75.21	10	50119.1	49593	6.25	6.40				
Eukaryotic initiation factor 4A-III	P38919.4	981	56	15	222.15	39	46871.3	45688	6.30	6.45		
		1733	72	19	309.28	53	46871.3	50034	6.30	6.55		
		1767	83	17	280.15	53	46871.3	48501	6.30	6.95		
		1427	163	21	367.40	61	46871.3	50384	6.30	6.65		
Isocitrate dehydrogenase [NADP] cytoplasmic	O75874.2	1012	97	19	329.69	54	46659.6	44188	6.53	6.95		
		1802	77	20	340.08	60	46659.6	47758	6.53	7.05		
		1561	136	19	350.55	54	46659.6	45179	6.53	7.10		
Pyruvate dehydrogenase E1 component subunit alpha, cytosolic form mitochondrial	P08559.3	1012	15	8	125.92	23	43295.9	44188	8.35	6.95		
		1802	55	15	249.46	46	43295.9	47758	8.35	7.05		
		1561	18	4	61.07	9	43295.9	45179	8.35	7.10		
Plasminogen activator inhibitor 1	P05121.1	1012	11	3	45.59	10	45060.2	44188	6.67	6.95		
		1725	11	4	80.86	12	45060.2	50034	6.67	7.35		
		1767	37	11	189.34	40	45060.2	48501	6.67	6.95		
		1802	19	6	97.16	21	45060.2	47758	6.67	7.05		
1476	6	4	53.41	14	45060.2	48819	6.67	6.95				
Interleukin enhancer-binding factor 2	Q12905.2	1040	44	11	188.54	46	43062.4	41398	5.19	5.25		
		1853	8	6	100.80	22	43062.4	46671	5.19	5.35		
		1554	10	4	65.08	15	43062.4	45179	5.19	5.15		
		1555	61	10	176.45	36	43062.4	45179	5.19	5.25		
1801	8	4	68.40	14	43062.4	44496	5.19	5.45				

Poly(rC)-binding protein 2	Q15366.1	1097	16	6	103.41	23	38580.3	40742	6.33	6.65
		1164	16	5	75.41	15	38580.3	38269	6.33	6.50
		1951	13	4	62.18	12	38580.3	41706	6.33	6.85
		2180	10	5	85.80	16	38580.3	38244	6.33	6.25
		1665	22	6	101.46	20	38580.3	41282	6.33	6.65
1699	10	4	63.00	12	38580.3	39509	6.33	6.90		
1736	5	3	42.19	9	38580.3	37842	6.33	7.90		
1795	87	8	135.97	25	38580.3	36787	6.33	7.75		
Twinfilin-2	Q6IBS0.2	1153	60	11	204.02	44	39548.2	38269	6.37	6.80
		1951	33	9	159.33	36	39548.2	41706	6.37	6.85
		1665	31	7	125.09	31	39548.2	41282	6.37	6.65
		1699	37	10	184.54	47	39548.2	39509	6.37	6.90
Acetyl-CoA acetyltransferase, cytosolic	Q9BWD1.2	1153	94	11	197.62	44	41351.1	38269	6.47	6.80
		1164	53	10	183.27	49	41351.1	38269	6.47	6.50
		1951	51	9	171.35	41	41351.1	41706	6.47	6.85
		1665	63	11	180.24	44	41351.1	41282	6.47	6.65
		1699	97	12	227.73	51	41351.1	39509	6.47	6.90
1795	40	9	156.26	42	41351.1	36787	6.47	7.75		
Mitogen-activated protein kinase 1	P28482.3	1153	18	9	135.63	30	41389.9	38269	6.50	6.80
		1951	21	8	118.23	24	41389.9	41706	6.50	6.85
		1699	24	8	130.31	24	41389.9	39509	6.50	6.90
Sialic acid synthase	Q9NR45.2	1153	12	3	61.59	12	40307.8	38269	6.29	6.80
		1164	13	3	60.59	12	40307.8	38269	6.29	6.50
		1951	20	6	110.07	20	40307.8	41706	6.29	6.85
		1665	24	4	83.53	20	40307.8	41282	6.29	6.65
1699	25	4	85.01	20	40307.8	39509	6.29	6.90		
Eukaryotic translation initiation factor 3 subunit H	O15372.1	1164	42	9	147.79	30	39930.5	38269	6.09	6.50
		1951	27	7	124.08	24	39930.5	41706	6.09	6.85
		1603	11	3	44.81	7	39930.5	43826	6.09	6.60
		1665	95	17	273.34	52	39930.5	41282	6.09	6.65
Heterogeneous nuclear ribonucleoproteins A2/B1	P22626.2	1173	86	13	225.37	43	37429.9	39745	8.97	9.90
		2109	26	7	121.50	22	37429.9	37708	8.97	9.60
		2125	20	8	132.60	24	37429.9	35666	8.97	9.95
		2180	13	5	79.13	16	37429.9	38244	8.97	8.25
		2217	18	6	101.27	20	37429.9	36161	8.97	8.15
		2272	31	8	138.86	24	37429.9	34706	8.97	9.50
		1803	11	3	41.35	7	37429.9	35284	8.97	9.95
		1665	24	4	83.53	20	40307.8	41282	6.29	6.65
Glyceraldehyde-3-phosphate dehydrogenase	P04406.3	1173	50	9	149.92	36	36053.4	39745	8.57	9.90
		1205	18	7	103.04	28	36053.4	36023	8.57	8.20
		2109	230	18	339.09	64	36053.4	37708	8.57	9.60
		2125	33	8	151.47	36	36053.4	35666	8.57	9.95
2180	138	12	221.22	49	36053.4	38244	8.57	8.25		
1667	36	8	122.96	34	36053.4	40088	8.57	7.15		
Annexin A2	P07355.2	1205	84	17	292.01	55	38604.2	36023	7.58	8.20
		1209	14	6	97.75	21	38604.2	36023	7.58	7.25
		2135	39	12	183.56	43	38604.2	37182	7.58	6.75
		2177	55	12	204.57	43	38604.2	37182	7.58	6.45
		2180	228	21	396.10	60	38604.2	38244	7.58	8.25
		2185	25	9	144.53	31	38604.2	37182	7.58	6.60
		2215	183	23	403.61	69	38604.2	36161	7.58	7.35
		2217	287	24	458.15	71	38604.2	36161	7.58	8.15
		2220	142	22	394.18	67	38604.2	36161	7.58	7.75
		1687	345	26	492.05	72	38604.2	40088	7.58	7.15
		1736	202	23	421.79	69	38604.2	37842	7.58	7.90
		1743	50	14	240.60	47	38604.2	37842	7.58	6.70
		1746	122	21	358.04	67	38604.2	37309	7.58	7.35
		Transaldolase	P37837.2	1209	5	3	49.08	10	37540.3	36023
2135	27			9	141.23	27	37540.3	37182	6.36	6.75
2177	44			12	189.48	33	37540.3	37182	6.36	6.45
2185	32			10	160.38	28	37540.3	37182	6.36	6.60
1743	63			13	227.23	37	37540.3	37842	6.36	6.70
1746	8	5	71.99	17	37540.3	37309	6.36	7.35		
1806	12	5	79.79	14	37540.3	35775	6.36	5.45		
Guanine nucleotide-binding protein G(i)(G(s))/G(t) subunit	P62879.3	1226	38	6	103.35	21	37331.3	35494	5.60	5.40
		2182	84	13	232.12	48	37331.3	37182	5.60	5.45
		1806	126	12	233.37	48	37331.3	35775	5.60	5.45
60S acidic ribosomal protein P0	P05388.1	1226	20	6	90.66	22	34273.7	35494	5.72	5.40
		1250	3	3	52.02	15	34273.7	33984	5.72	6.65
		2177	37	10	180.93	43	34273.7	37182	5.72	6.45
		1743	3	3	53.73	9	34273.7	37842	5.72	6.70
		1806	21	10	157.89	37	34273.7	35775	5.72	5.45
Annexin A1	P04083.2	1250	270	23	436.83	70	38714.5	33984	6.57	6.65
		2177	88	20	362.05	66	38714.5	37182	6.57	6.45
		2185	255	23	441.88	70	38714.5	37182	6.57	6.60
		1687	72	18	315.53	59	38714.5	40088	6.57	7.15
		1743	274	24	456.06	72	38714.5	37842	6.57	6.70
1746	8	4	65.83	17	38714.5	37309	6.57	7.35		
PDZ and LIM domain protein 1	O00151.4	1250	76	13	243.74	59	36071.9	33984	6.56	6.65
		2135	163	19	355.25	79	36071.9	37182	6.56	6.75
		2185	49	11	185.07	48	36071.9	37182	6.56	6.60
		1743	66	14	231.56	60	36071.9	37842	6.56	6.70
		1746	4	3	39.98	11	36071.9	37309	6.56	7.35
F-actin-capping protein subunit beta	P47756.4	1350	17	8	124.53	38	31350.7	30057	5.36	5.55
		1407	9	3	47.14	12	31350.7	28391	5.36	5.40
		2422	208	16	310.44	59	31350.7	29332	5.36	5.50
		1876	28	7	105.27	25	31350.7	32122	5.36	5.65
Glutathione S-transferase omega-1	P78417.2	1446	70	11	164.64	42	27566.0	26586	6.24	5.80
		1493	41	9	134.57	36	27566.0	25140	6.24	6.15
		2516	10	3	45.70	12	27566.0	29697	6.24	5.25
		2556	43	8	119.11	33	27566.0	28625	6.24	5.80
		1982	10	4	55.70	17	27566.0	27662	6.24	5.85
		2053	52	9	133.96	36	27566.0	29530	6.24	5.85
2066	99	14	216.23	46	27566.0	26406	6.24	6.25		
Proteasome activator complex subunit 1	Q06323.1	1446	22	9	158.45	37	28723.3	26586	5.78	5.80
		2516	7	3	48.19	14	28723.3	29697	5.78	5.25
		2556	225	20	375.37	71	28723.3	28625	5.78	5.80
		2048	47	10	159.01	39	28723.3	25530	5.78	5.75
		2053	144	18	300.56	68	28723.3	25530	5.78	5.85
		2066	3	3	38.29	17	28723.3	26406	5.78	6.25
Heat shock protein beta-1	P04792.2	1502	115	15	267.31	85	22782.6	24353	5.98	6.05
		1512	16	5	75.56	25	22782.6	24353	5.98	5.30
		2712	172	14	258.80	84	22782.6	26363	5.98	6.10
		2752	21	7	102.18	35	22782.6	25488	5.98	6.60
		2093	72	11	195.66	66	22782.6	25816	5.98	6.60

		2130	196	15	276.45	85	22762.6	24707	5.98	6.10
		2192	10	3	41.37	17	22762.6	22746	5.98	6.40
Phosphoglycerate mutase 1	P18669.2	1521	33	8	134.19	46	28804.1	24227	6.68	7.10
		2626	60	8	141.49	43	28804.1	26363	6.68	6.60
		2662	229	18	329.33	79	28804.1	26666	6.68	7.15
		2053	13	4	76.78	23	28804.1	25816	6.68	6.60
		2129	186	13	238.62	50	28804.1	24707	6.68	7.20
		2130	8	3	47.85	16	28804.1	24707	6.68	6.10
Peroxiredoxin-6	P30041.3	1521	14	6	89.77	31	25035.1	24227	6.00	7.10
		2712	24	8	111.20	33	25035.1	26363	6.00	6.10
		2752	205	15	273.93	66	25035.1	25488	6.00	6.60
		2758	38	11	183.87	58	25035.1	25348	6.00	7.20
		2093	120	13	233.94	61	25035.1	25816	6.00	6.60
		2129	6	3	39.36	12	25035.1	24707	6.00	7.20
Rho GDP-dissociation inhibitor 1	P52565.3	1531	41	8	140.98	36	23207.2	23621	5.02	4.75
		2685	161	13	232.20	61	23207.2	25488	5.02	4.85
		2110	49	9	145.67	29	23207.2	25816	5.02	4.75
Lactoylglutathione lyase	Q04760.4	1531	13	5	69.91	26	20777.8	23621	5.12	4.75
		1574	56	10	177.65	51	20777.8	22306	5.12	4.75
		2854	11	4	52.68	16	20777.8	25070	5.12	4.50
		2110	36	8	129.11	42	20777.8	25816	5.12	4.75
		2169	79	8	143.96	32	20777.8	23666	5.12	4.70
Glutathione S-transferase P	P09211.2	1569	216	11	224.38	65	23356.0	22512	5.43	5.45
		1574	12	4	65.82	30	23356.0	22306	5.43	4.75
		2880	116	9	181.67	57	23356.0	23520	5.43	5.45
		2198	162	9	186.34	57	23356.0	22746	5.43	5.45
UMP-CMP kinase	P30085.3	1569	9	3	46.56	17	22222.5	22512	5.44	5.45
		2880	12	5	76.88	28	22222.5	23520	5.44	5.45
		2958	22	7	121.64	46	22222.5	22475	5.44	5.40
		2198	27	5	87.15	28	22222.5	22746	5.44	5.45
Proteasome subunit beta type-3	P49720.2	1802	40	5	99.96	35	22949.1	18597	6.14	6.20
		2910	31	6	112.87	38	22949.1	23520	6.14	6.30
		2192	51	6	113.17	38	22949.1	22746	6.14	6.40
Protein DJ-1	Q99497.2	1802	21	5	94.86	41	19891.2	18597	6.33	6.20
		2910	82	10	191.75	71	19891.2	23520	6.33	6.30
		2192	52	8	140.76	46	19891.2	22746	6.33	6.40
Galectin-1	P09382.2	2154	178	13	236.48	85	14715.8	16217	5.34	4.80
		3549	28	6	106.90	51	14715.8	15601	5.34	4.80
		2517	39	8	135.04	61	14715.8	15817	5.34	4.80
		2533	221	12	216.80	85	14715.8	15580	5.34	4.80
Major vault protein	Q14764.4	360	24	9	160.67	13	99327.3	103702	5.34	5.35
		776	211	37	670.88	53	99327.3	103795	5.34	5.35
POTE ankyrin domain family member F	A5A3E0.2	360	13	3	52.60	3	121445.3	103702	5.83	5.35
		776	4	2	35.03	2	121445.3	103702	5.83	5.35
Alanine-tRNA ligase, cytoplasmic	P49588.2	360	3	3	40.55	6	106811.0	103702	5.34	5.35
		776	98	26	476.39	38	106811.0	103702	5.34	5.35
Annexin A7	P20073.3	917	8	4	69.56	10	52739.5	48913	5.52	5.85
		1737	71	13	224.34	30	52739.5	52872	5.52	6.35
Eukaryotic translation initiation factor 2 subunit 3	P41091.3	938	13	3	49.71	7	51109.8	48078	8.66	9.90
		1700	9	4	56.97	12	51109.8	53294	8.66	8.50
Proliferation-associated protein 2G4	Q9UQ80.3	958	5	3	50.59	10	43787.1	47262	6.13	6.90
		981	153	23	412.85	69	43787.1	45888	6.13	6.45
		1767	15	7	117.84	24	43787.1	48501	6.13	6.95
Heterogeneous nuclear ribonucleoprotein F	P52597.3	965	132	15	270.15	53	45672.1	47262	5.38	5.20
		1763	29	8	136.48	30	45672.1	50034	5.38	5.25
Heterogeneous nuclear ribonucleoprotein A3	P51991.2	1173	65	10	169.08	30	39595.1	39745	9.09	9.90
		2109	6	3	48.46	13	39595.1	37708	9.09	9.60
L-lactate dehydrogenase A chain	P00338.2	1334	110	15	264.29	42	36688.9	31242	8.44	9.35
		2237	30	8	127.38	25	36688.9	33337	8.44	9.95
		2272	140	17	295.37	52	36688.9	34706	8.44	9.50
Prohibitin	P35232.1	1407	19	7	120.12	29	29804.2	28391	5.57	5.40
		2556	6	3	41.98	11	29804.2	28625	5.57	5.80
Chloride intracellular channel protein 1	O00299.4	1410	98	13	230.89	73	26922.9	28217	5.09	4.95
		2498	261	14	266.25	74	26922.9	30449	5.09	4.95
High mobility group protein B1	P09429.3	1521	21	5	92.63	29	24893.9	24227	5.61	7.10
		2626	21	7	103.41	25	24893.9	26363	5.61	6.60
		2662	29	6	101.46	30	24893.9	26666	5.61	7.15
Rho GDP-dissociation inhibitor 2	P52566.3	1531	12	4	57.34	29	22988.1	23621	5.10	4.75
		2685	14	4	66.86	29	22988.1	25488	5.10	4.85
Fibronectin	P02751.4	365	4	3	38.21	1	262625.9	103702	5.46	5.10
		852	13	5	85.58	2	262625.9	91468	5.46	4.90
Interferon-induced GTP-binding protein Mx1	P20591.4	642	12	3	36.53	4	75520.7	70659	5.60	5.40
		998	296	36	657.52	64	75520.7	79296	5.60	5.80
Tubulin beta-4B chain	P68371.1	858	433	24	472.19	73	49831.3	53409	4.79	4.70
		870	354	23	455.88	79	49831.3	54374	4.79	4.90
		1509	14	5	70.90	9	49831.3	48819	4.79	4.65
Tubulin alpha-1C chain	Q9BQE3.1	870	110	18	340.78	54	49895.6	54374	4.96	4.90
		873	33	11	189.88	39	49895.6	50647	4.96	5.35
		1427	9	5	74.40	14	49895.6	50384	4.96	6.65
		1442	12	4	71.79	11	49895.6	51191	4.96	5.90
		1448	15	7	122.43	20	49895.6	50384	4.96	6.10

		1457	12	6	101.60	20	49895.6	51191	4.96	5.25
		1513	4	3	43.23	9	49895.6	48060	4.96	4.95
RuvB-like 2	Q9Y230.3	873	36	9	160.49	24	51156.8	50647	5.49	5.35
		1410	30	11	190.88	26	51156.8	52856	5.49	5.75
Spliceosome RNA helicase DDX39B	Q13838.1	873	26	9	137.07	24	48991.6	50647	5.44	5.35
		1410	83	16	293.46	46	48991.6	52856	5.44	5.75
Actin-like protein 6A	O96019.1	873	3	3	54.55	10	47461.3	50647	5.40	5.35
		1457	13	7	114.13	21	47461.3	51191	5.40	5.25
		1561	16	5	91.79	15	47461.3	45179	5.40	7.10
26S protease regulatory subunit 7	P35998.3	917	80	23	370.95	59	48634.1	48913	5.71	5.85
		1442	164	25	445.93	65	48634.1	51191	5.71	5.90
		1448	24	8	133.92	21	48634.1	50384	5.71	6.10
Heterogeneous nuclear ribonucleoprotein H	P31943.4	917	15	6	91.55	17	49229.7	48913	5.89	5.85
		1380	192	18	317.45	58	49229.7	53715	5.89	6.05
		1408	12	3	57.79	13	49229.7	53715	5.89	4.30
		1442	19	7	117.78	21	49229.7	51191	5.89	5.90
		1448	68	12	204.99	40	49229.7	50384	5.89	6.10
Actin-related protein 3B	Q9P1U1.1	917	23	5	79.41	15	47608.0	48913	5.61	5.85
		1442	19	4	63.54	12	47608.0	51191	5.61	5.90
HLA class I histocompatibility antigen, A-11 alpha chain	P13746.1	1058	17	5	88.05	23	40937.0	42071	5.77	5.40
		1077	23	9	152.15	34	40937.0	41398	5.77	5.95
		1601	13	6	99.08	26	40937.0	44496	5.77	5.45
Adenosine kinase	P55263.2	1097	55	12	215.75	38	40545.7	40742	6.23	6.65
		1603	28	7	114.16	18	40545.7	43826	6.23	6.60
HLA class I histocompatibility antigen, A-2 alpha chain	P01892.1	1097	31	9	163.19	38	40922.1	40742	6.50	6.65
		1603	42	13	218.92	44	40922.1	43826	6.50	6.60
Septin-2	Q15019.1	1097	23	9	147.44	31	41487.7	40742	6.15	6.65
		1603	188	19	331.72	65	41487.7	43826	6.15	6.60
		1665	16	6	96.32	22	41487.7	41282	6.15	6.65
Mitotic checkpoint protein BUB3	O43684.1	1153	25	6	97.97	20	37155.0	38269	6.37	6.80
		1665	12	5	83.36	18	37155.0	41282	6.37	6.65
		1699	11	5	77.12	18	37155.0	39509	6.37	6.90
		1795	46	9	155.28	32	37155.0	36767	6.37	7.75
Mannose-1-phosphate 4-epimerase	Q9Y5P6.2	1153	13	4	53.96	12	39834.7	38269	6.16	6.80
		1795	15	4	62.88	12	39834.7	36767	6.16	7.75
RNA-binding protein 4	Q9BWF3.1	1153	5	3	48.11	6	40314.1	38269	6.61	6.80
		1665	3	3	43.23	7	40314.1	41282	6.61	6.65
		1699	6	3	45.39	7	40314.1	39509	6.61	6.90
		1795	7	4	68.33	15	40314.1	36767	6.61	7.75
Heterogeneous nuclear ribonucleoprotein A/B	Q99729.2	1153	6	3	45.26	7	36225.0	38269	8.21	6.80
		1209	24	7	116.62	20	36225.0	36023	8.21	7.25
		1699	39	10	164.12	20	36225.0	39509	8.21	6.90
		1746	33	7	118.37	19	36225.0	37309	8.21	7.35
Ubiquitin-like domain-containing CTD phosphatase 1	Q8WVY7.2	1164	7	3	38.94	8	36804.8	38269	6.07	6.50
		1665	14	5	65.91	15	36804.8	41282	6.07	6.65
Methionine adenosyltransferase 2 subunit beta	Q9NZL9.1	1205	4	3	43.96	13	37552.0	36023	6.90	8.20
		1736	29	7	122.21	28	37552.0	37842	6.90	7.90
		1746	13	4	75.05	17	37552.0	37309	6.90	7.35
Heterogeneous nuclear ribonucleoprotein H3	P31942.2	1250	9	5	74.18	15	36926.7	33984	6.37	6.65
		1743	9	4	68.33	13	36926.7	37842	6.37	6.70
		1746	11	5	71.44	15	36926.7	37309	6.37	7.35
Ester hydrolase C11	Q9H0W9.1	1250	5	3	51.23	12	35117.6	33984	6.23	6.65
		1743	4	3	52.27	12	35117.6	37842	6.23	6.70
Annexin A3	P12429.3	1350	110	16	279.46	60	36375.5	30057	5.63	5.55
		1876	240	21	369.15	63	36375.5	32122	5.63	5.65
Tropomyosin alpha-3 chain	P06753.1	1376	89	10	172.62	22	32818.9	29671	4.68	4.30
		1912	131	15	256.97	36	32818.9	31706	4.68	4.25
14-3-3 protein epsilon	P62258.1	1376	28	9	160.85	39	29174.1	29671	4.63	4.30
		1387	242	18	336.54	71	29174.1	29294	4.63	4.15
		1912	46	10	173.79	40	29174.1	31706	4.63	4.25
Enolase-phosphatase E1	Q9UHY7.1	1387	6	3	58.27	20	28932.8	29294	4.66	4.15
		1912	7	3	53.50	16	28932.8	31706	4.66	4.25
6-phosphogluconolactonase	O95336.2	1502	9	5	71.28	26	27547.0	24353	5.70	6.05
		2053	18	8	121.40	38	27547.0	25530	5.70	5.85
Protein S100-A6	P06703.1	2154	56	3	48.63	46	10179.8	16217	5.32	4.80
		2533	32	2	34.60	16	10179.8	15580	5.32	4.80
Alpha-actinin-4	O43707.2	865	456	55	1033.53	72	104854.6	98336	5.27	5.25
		791	421	57	1069.74	74	104854.6	94840	5.27	5.25
Elongation factor 2	P13639.4	877	243	36	643.31	48	95338.7	96589	6.41	7.25
		807	357	47	819.01	56	95338.7	94840	6.41	7.30
60 kDa heat shock protein, mitochondrial	P10809.2	1354	184	33	615.01	70	61055.0	59677	5.70	5.25
		1360	212	34	640.98	69	61055.0	59677	5.70	5.25
		1266	40	10	180.43	23	61055.0	63360	5.70	5.50
		1285	3	3	50.97	6	61055.0	58267	5.70	5.20
T-complex protein 1 subunit theta	P50990.4	1354	12	5	78.20	9	59620.9	59677	5.42	5.25
		1266	261	30	562.27	63	59620.9	63360	5.42	5.50
T-complex protein 1 subunit epsilon	P48643.1	1354	7	4	62.89	6	59671.4	59677	5.45	5.25
		1266	191	29	515.78	56	59671.4	63360	5.45	5.50
T-complex protein 1 subunit beta	P78371.4	1554	16	10	165.64	30	57488.5	59677	6.01	6.45

		1303	144	24	445.24	66	57488.5	58287	6.01	6.60
4-trimethylaminobutylaldehyde dehydrogenase	P49189.3	1623	7	3	47.42	7	53802.2	54586	5.69	5.90
		1380	7	3	48.38	6	53802.2	53715	5.69	6.05
		1410	36	13	232.51	35	53802.2	52856	5.69	5.75
Trifunctional enzyme subunit beta, mitochondrial	P55084.3	1700	5	3	39.69	6	51294.8	53294	9.44	8.50
		1425	31	10	159.35	20	51294.8	51191	9.44	9.95
6-phosphogluconate dehydrogenase, decarboxylating	P52208.3	1725	9	4	68.46	11	53140.3	50034	6.80	7.35
		1471	4	3	42.96	6	53140.3	48819	6.80	7.30
Elongation factor Tu, mitochondrial	P49411.2	1767	39	12	188.60	31	49541.8	48501	7.26	6.95
		1802	63	15	250.94	40	49541.8	47758	7.26	7.05
		1561	57	13	204.93	34	49541.8	45179	7.26	7.10
Phosphoglycerate kinase 1	P00558.3	1869	127	22	395.45	65	44615.0	46671	8.30	8.30
		1533	159	21	375.34	59	44615.0	46590	8.30	8.40
Protein CYR61	O0622.1	1869	10	5	83.93	17	42026.9	46671	8.63	8.30
		1533	48	13	214.40	43	42026.9	46590	8.63	8.40
Cytosolic acyl coenzyme A thioester hydrolase	O00154.3	1951	14	6	110.29	20	41796.3	41706	8.85	6.85
		1561	25	8	145.82	27	41796.3	45179	8.85	7.10
		1699	11	6	100.75	21	41796.3	39509	8.85	6.90
Fructose-bisphosphate aldolase A	P04075.2	1964	122	16	290.95	59	39420.2	43277	8.30	9.50
		1736	7	4	50.90	12	39420.2	37842	8.30	7.90
		1795	38	9	160.86	30	39420.2	36767	8.30	7.75
Heterogeneous nuclear ribonucleoprotein A1	P09651.5	2125	25	7	118.68	24	38746.8	35666	9.17	9.95
		2272	7	4	64.71	14	38746.8	34706	9.17	9.50
		1803	156	15	271.26	43	38746.8	35284	9.17	9.95
Heterogeneous nuclear ribonucleoprotein A0	Q13151.1	2125	4	3	56.71	18	30840.8	35666	9.34	9.95
		1803	17	5	85.63	23	30840.8	35284	9.34	9.95
Glyoxylate reductase/hydroxypyruvate reductase	Q9UBQ7.1	2135	13	3	54.41	13	35668.5	37182	7.01	6.75
		2185	4	3	51.19	13	35668.5	37182	7.01	6.60
		1743	32	8	146.01	31	35668.5	37842	7.01	6.70
		1746	25	6	103.11	20	35668.5	37309	7.01	7.35
Serine/threonine-protein phosphatase PP1-gamma catalytic subunit	P36873.1	2177	65	12	219.95	43	36984.0	37182	6.12	6.45
		1743	7	5	71.05	18	36984.0	37842	6.12	6.70
Malate dehydrogenase, mitochondrial	P40926.3	2177	10	7	118.32	25	35503.5	37182	8.92	6.45
		2180	33	10	191.56	40	35503.5	38244	8.92	8.25
		1803	9	5	90.29	16	35503.5	35284	8.92	9.95
Pyruvate dehydrogenase E1 component subunit beta, mitochondrial	P11177.3	2182	59	12	202.31	44	39233.6	37182	6.21	5.45
		1806	91	14	253.78	52	39233.6	35775	6.21	5.45
F-actin-capping protein subunit alpha-1	P52907.3	2182	80	10	191.46	56	32922.9	37182	5.45	5.45
		1806	121	12	230.87	59	32922.9	35775	5.45	5.45
L-lactate dehydrogenase B chain	P07195.2	2182	9	4	59.17	13	36638.7	37182	5.71	5.45
		2235	178	19	357.45	67	36638.7	32469	5.71	5.65
		1806	35	9	160.14	34	36638.7	35775	5.71	5.45
		1876	49	10	169.08	34	36638.7	32122	5.71	5.65
UDP-glucose 4-epimerase	Q14376.2	2185	15	5	86.43	18	38281.9	37182	6.26	6.60
		1743	34	9	152.00	35	38281.9	37842	6.26	6.70
Aflatoxin B1 aldehyde reductase member 2	O43488.3	2185	4	4	60.24	14	39589.2	37182	6.71	6.60
		1743	12	5	77.21	17	39589.2	37842	6.71	6.70
Malate dehydrogenase, cytoplasmic	P40925.4	2215	8	3	45.60	9	36426.3	36161	6.91	7.35
		2217	22	6	98.11	20	36426.3	36161	6.91	8.15
		2220	5	3	41.04	10	36426.3	36161	6.91	7.75
		1687	5	4	57.61	13	36426.3	40088	6.91	7.15
Inorganic pyrophosphatase	Q15181.2	2235	44	12	211.68	59	32660.2	32469	5.54	5.65
		1876	3	3	44.92	18	32660.2	32122	5.54	5.65
Annexin A5	P08758.2	2330	193	21	375.51	73	35936.9	33337	4.94	4.70
		1866	392	22	408.54	74	35936.9	32979	4.94	4.70
		1876	15	3	51.80	15	35936.9	32122	4.94	5.65
		1879	202	19	341.98	70	35936.9	31706	4.94	4.55
Elongation factor 1-delta	P29692.5	2330	4	4	67.46	17	31122.0	33337	4.90	4.70
		1787	76	11	207.98	56	31122.0	35775	4.90	4.50
		1879	3	3	26.13	16	31122.0	31706	4.90	4.55
Costomer subunit epsilon	Q14579.3	2330	6	3	47.95	12	34482.2	33337	4.98	4.70
		1866	89	13	244.52	63	34482.2	32979	4.98	4.70
		1879	15	6	103.00	25	34482.2	31706	4.98	4.55
Endoplasmic reticulum resident protein 29	P30040.4	2660	86	12	216.15	54	28993.6	28281	6.77	6.25
		2053	15	4	67.15	18	28993.6	25530	6.77	5.85
		2129	12	4	70.70	16	28993.6	24707	6.77	7.20
Calpain small subunit 1	P04632.1	2685	119	12	208.04	67	28315.9	25488	5.05	4.85
		2110	187	12	219.51	69	28315.9	25816	5.05	4.75
UPF0568 protein C14	Q9Y224.1	2752	115	14	256.37	64	28068.2	25488	6.19	6.60
		2093	33	7	127.70	33	28068.2	25816	6.19	6.60
Hypoxanthine-guanine phosphoribosyltransferase	P00492.2	2752	88	12	233.31	76	24579.5	25488	6.21	6.60
		2093	46	7	138.71	40	24579.5	25816	6.21	6.60
Thioredoxin-dependent peroxide reductase, mitochondrial	P30048.3	2880	14	6	99.76	24	27692.8	23520	7.67	5.45
		2910	32	5	91.91	21	27692.8	23520	7.67	6.30
		2192	29	5	87.85	19	27692.8	22746	7.67	6.40

TABLE S2: 2-CIDyA-tagged proteins identified by LC-MS/MS after 1-D SDS-PAGE of enriched membrane fractions

Protein name	UniProt accession number	Spot	Spectra	Distinct peptides	Distinct summed MS/MS search score	% AA coverage	Molecular mass (Da)	Molecular mass exper. (Da)	pI	Membrane fraction				
										Membrane fraction 1	Membrane fraction 2	Membrane fraction 3		
Myosin-9	P35579.4	1	398	70	1214.76	43	226533.4	914650	5.50					
		2	1683	107	2011.10	54	226533.4	400760	5.50					
		4	378	66	1157.98	43	226533.4	94950	5.50					
		1	32	15	254.80	11	226533.4	914650	5.80					
		2	198	67	1048.30	42	226533.4	400760	5.80					
		3	1133	120	2196.93	57	226533.4	264190	5.80					
		4	66	30	445.19	18	226533.4	94950	5.80					
		1	231	63	1035.85	38	226533.4	914650	5.80					
		2	209	57	909.08	34	226533.4	400760	5.80					
		3	910	102	1914.32	52	226533.4	264190	5.80					
		4	46	17	270.09	10	226533.4	94950	5.80					
		Neuroblast differentiation-associated protein AHNAK	Q09666.2	1	139	24	355.54	4	629104.8	914650	5.80			
2	92			29	436.77	6	629104.8	400760	5.80					
2	198			70	1054.75	15	629104.8	400760	5.80					
POTE ankyrin domain family member F	A5A3E0.2	1	23	4	68.00	4	121445.5	914650	5.83					
		2	5	4	62.32	4	121445.3	400760	5.83					
		2	6	3	49.67	3	121445.3	400760	5.83					
Fibronectin	P02751.4	4	38	12	163.92	6	262625.9	94950	5.46					
		2	40	18	274.33	10	262625.9	400760	5.46					
		2	65	22	351.90	13	262625.9	400760	5.46					
Integrin beta-1	P05556.2	5	29	8	120.64	11	88415.9	86920	5.27					
		4	41	14	211.43	22	88415.9	94950	5.27					
		4	38	11	175.95	20	88415.9	94950	5.27					
		5	25	11	160.71	16	88415.9	86920	5.27					
		6	432	28	534.37	47	72333.3	68990	5.07					
78 kDa glucose-regulated protein P11021.2	P11021.2	6	208	29	510.72	48	72333.3	68990	5.07					
		6	253	35	632.20	50	72333.3	68990	5.07					
		6	290	29	494.97	53	75520.7	68990	5.60					
Interferon-induced GTP-binding protein Mx1	P20591.4	6	142	30	477.23	56	75520.7	68990	5.60					
		6	221	34	594.56	59	75520.7	68990	5.60					
		6	114	21	335.79	40	72932.8	68990	4.96					
Protein disulfide-isomerase A4	P13667.2	6	27	10	152.85	19	72932.8	68990	4.96					
		6	52	17	235.16	30	72932.8	68990	4.96					
		6	69	15	231.26	25	67820.4	68990	6.07					
Moesin	P26038.3	6	36	17	233.01	32	67820.4	68990	6.07					
		6	31	9	136.60	17	67820.4	68990	6.07					
		6	83	12	167.97	24	65401.8	68990	9.05					
Septin-9	Q9UHD8.2	6	34	11	165.36	26	65401.8	68990	9.05					
		6	33	11	168.67	22	65401.8	68990	9.05					
		6	34	9	130.82	14	73243.8	68990	6.73					
ATP-dependent RNA helicase DDX3X	O00571.3	6	15	7	109.53	12	73243.8	68990	6.73					
		6	26	13	195.74	22	73243.8	68990	6.73					
		8	288	38	651.07	69	53651.9	52900	5.06					
Vimentin	P08670.4	10	39	15	235.16	34	53651.9	49970	5.06					
		11	16	8	108.47	17	53651.9	48820	5.06					
		8	354	39	684.76	72	53651.9	52900	5.06					
		9	26	11	169.24	25	53651.9	51180	5.06					
		10	42	18	283.12	41	53651.9	49970	5.06					
		11	24	11	177.01	24	53651.9	48820	5.06					
		8	327	41	693.41	72	53651.9	52900	5.06					
		10	39	13	208.92	29	53651.9	49970	5.06					
		11	19	9	132.69	20	53651.9	48820	5.06					
		Protein disulfide-isomerase A3	P30101.4	8	98	20	352.14	49	56762.7	52900	5.99			
				8	67	18	307.66	46	56762.7	52900	5.99			
				8	204	26	457.47	60	56762.7	52900	5.99			
Tubulin beta-4B chain	P68371.1	8	32	11	192.63	34	49831.3	52900	4.79					
		9	128	16	300.92	47	49831.3	51180	4.79					
		10	69	15	275.67	44	49831.3	49970	4.79					
		11	57	13	224.36	37	49831.3	48820	4.79					
		9	41	12	199.43	43	49831.3	51180	4.79					
		10	90	18	312.40	53	49831.3	49970	4.79					
		11	84	17	297.35	55	49831.3	48820	4.79					
		8	58	13	222.68	39	49831.3	52900	4.79					
		9	124	17	298.12	55	49831.3	51180	4.79					
		10	73	14	222.58	40	49831.3	49970	4.79					
		Polypyrimidine tract-binding protein 1	P26599.1	8	30	8	141.32	30	57221.6	52900	9.22			
8	28			6	105.16	19	57221.6	52900	9.22					
8	45			6	108.53	21	57221.6	52900	9.22					
Brain acid soluble protein 1	P80723.2	8	24	7	111.02	57	22693.5	52900	4.64					
		8	22	6	108.25	51	22693.5	52900	4.64					
		8	19	5	95.10	37	22693.5	52900	4.64					
Dihydropyridyl dehydrogenase, mitochondrial	P09622.2	8	9	4	77.75	11	54177.6	52900	7.95					
		8	7	4	65.65	10	54177.6	52900	7.95					
		8	12	6	101.01	14	54177.6	52900	7.95					
Tubulin alpha-1C chain	Q9BQE3.1	9	38	9	147.61	29	49895.6	51180	4.96					
		10	63	13	234.10	42	49895.6	49970	4.96					
		11	90	16	267.54	51	49895.6	48820	4.96					
		10	68	14	258.00	43	49895.6	49970	4.96					
		11	123	19	344.34	60	49895.6	48820	4.96					
		9	75	11	205.97	36	49895.6	51180	4.96					
		10	96	14	253.72	46	49895.6	49970	4.96					

			11	119	16	291.94	48	49895.6	48820	4.96
Polymerase I and transcript release factor	Q6NZI2.1		9	31	8	147.21	24	43476.3	51180	5.51
			8	13	4	69.32	12	43476.3	52900	5.51
			8	35	7	128.91	18	43476.3	52900	5.51
			9	15	5	82.12	15	43476.3	51180	5.51
Dihydrolipoylysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial	P36957.4		10	24	8	132.25	20	48755.6	49970	9.10
			10	22	7	122.44	18	48755.6	49970	9.10
			9	9	3	55.77	10	48755.6	51180	9.10
			10	20	6	90.50	16	48755.6	49970	9.10
Heterogeneous nuclear ribonucleoprotein H	P31943.4		10	5	3	48.38	8	49229.7	49970	5.89
			11	7	4	63.22	11	49229.7	48820	5.89
			10	15	6	102.83	17	49229.7	49970	5.89
			11	10	6	92.50	17	49229.7	48820	5.89
			10	31	8	123.23	23	49229.7	49970	5.89
			11	4	3	40.43	8	49229.7	48820	5.89
PDZ and LIM domain protein 7	Q9NR12.1		10	7	3	39.40	7	49845.0	49970	8.76
			10	6	3	37.82	7	49845.0	49970	8.76
			9	6	3	40.53	7	49845.0	51180	8.76
RuvB-like 1	Q9Y265.1		11	4	4	62.15	10	50228.3	48820	6.02
			10	6	4	57.95	13	50228.3	49970	6.02
			10	26	9	154.27	28	50228.3	49970	6.02
Rho GTPase-activating protein 1	Q07960.1		11	8	3	58.85	10	50436.0	48820	5.85
			10	6	3	59.11	10	50436.0	49970	5.85
			11	11	6	93.88	21	50436.0	48820	5.85
			10	9	5	76.82	17	50436.0	49970	5.85
			11	12	6	87.33	19	50436.0	48820	5.85
Protein disulfide-isomerase A6	Q15084.1		11	6	3	53.12	10	48121.6	48820	4.95
			11	27	8	145.11	26	48121.6	48820	4.95
			11	47	10	186.18	31	48121.6	48820	4.95
Cytochrome b-c1 complex subunit 2, mitochondrial	P22695.3		12	44	9	162.49	27	48443.2	43860	8.74
			12	39	10	187.40	29	48443.2	43860	8.74
			12	53	11	201.10	32	48443.2	43860	8.74
HLA class I histocompatibility antigen, A-11 alpha chain	P13746.1		12	13	6	102.16	22	40937.0	43860	5.77
			13	15	8	125.42	29	40937.0	42830	5.77
			13	21	9	146.68	30	40937.0	42830	5.77
			13	42	11	197.70	41	40937.0	42830	5.77
Interleukin enhancer-binding factor 2	Q12905.2		12	9	5	85.87	18	43062.4	43860	5.19
			13	5	3	51.70	8	43062.4	42830	5.19
			12	8	5	79.40	18	43062.4	43860	5.19
			13	11	6	104.59	24	43062.4	42830	5.19
			12	16	6	99.00	21	43062.4	43860	5.19
			13	9	5	81.84	16	43062.4	42830	5.19
Endoplasmic reticulum resident protein 44	Q9BS26.1		12	17	5	66.29	12	46971.4	43860	5.09
			12	14	3	44.10	8	46971.4	43860	5.09
			12	12	3	46.50	8	46971.4	43860	5.09
Guanine nucleotide-binding protein subunit alpha-11	P29992.2		14	10	5	61.32	18	42123.6	37370	5.51
			14	23	8	121.69	27	42123.6	37370	5.51
			14	43	13	200.61	43	42123.6	37370	5.51
Glyceraldehyde-3-phosphate dehydrogenase	P04406.3		15	52	12	183.30	47	36053.4	35120	8.57
			15	117	15	259.28	54	36053.4	35120	8.57
			15	131	16	256.32	59	36053.4	35120	8.57
Annexin A2	P07355.2		15	25	10	165.00	39	38604.2	35120	7.58
			16	275	28	530.89	72	38604.2	33810	7.58
			15	43	12	181.16	43	38604.2	35120	7.58
			16	319	26	487.14	70	38604.2	33810	7.58
			15	80	15	248.43	58	38604.2	35120	7.58
			16	310	24	450.39	71	38604.2	33810	7.58
Annexin A1	P04063.2		15	20	8	130.64	30	38714.5	35120	6.57
			15	44	16	256.35	58	38714.5	35120	6.57
			15	65	18	286.99	63	38714.5	35120	6.57
Fructose-bisphosphate aldolase A	P04075.2		15	16	6	103.40	21	39420.2	35120	8.30
			14	15	5	84.87	20	39420.2	37370	8.30
			15	23	8	117.51	31	39420.2	35120	8.30
			14	7	3	42.45	10	39420.2	37370	8.30
			15	28	8	134.30	33	39420.2	35120	8.30
Heterogeneous nuclear ribonucleoproteins A2/B1	P22626.2		15	14	5	70.56	16	37429.9	35120	8.97
			15	27	10	145.91	31	37429.9	35120	8.97
			16	15	5	80.89	17	37429.9	33810	8.97
			14	5	3	39.56	10	37429.9	37370	8.97
			15	39	9	138.51	28	37429.9	35120	8.97
			16	44	8	120.54	24	37429.9	33810	8.97
Apolipoprotein L2	Q9BQE5.1		15	10	3	51.38	9	37092.5	35120	6.28
			15	12	3	56.88	9	37092.5	35120	6.28
			15	21	6	113.64	22	37092.5	35120	6.28
RNA-binding protein Raly	Q9UKM9.1		15	5	3	48.70	9	32463.3	35120	9.20
			15	6	3	51.29	9	32463.3	35120	9.20
			15	12	5	79.93	15	32463.3	35120	9.20
60S acidic ribosomal protein P0	P05388.1		16	28	6	115.22	24	34273.7	33810	5.72
			16	51	9	149.54	32	34273.7	33810	5.72
			16	34	8	129.94	30	34273.7	33810	5.72
60S ribosomal protein L6	Q02878.3		16	26	7	111.81	25	32728.1	33810	10.59
			16	55	11	178.20	37	32728.1	33810	10.59
			16	99	13	233.35	44	32728.1	33810	10.59
Syntaxin-12	Q86Y82.1		16	7	3	47.00	13	31642.1	33810	5.46
			16	13	5	70.78	23	31642.1	33810	5.46
			16	22	5	89.22	23	31642.1	33810	5.46

Voltage-dependent anion-selective channel protein 1	P21796.2	17	66	15	264.46	76	30772.7	31820	8.62
		17	54	9	159.43	48	30772.7	31820	8.62
		16	7	4	56.76	22	30772.7	33810	8.62
		17	67	13	220.79	68	30772.7	31820	8.62
Prohibitin-2	Q99623.2	17	52	12	212.93	44	33296.5	31820	9.83
		17	58	14	226.69	53	33296.5	31820	9.83
		16	8	4	59.25	14	33296.5	33810	9.83
		17	47	12	195.83	44	33296.5	31820	9.83
Leucine-rich repeat-containing protein 59	Q96AG4.1	17	41	9	154.70	34	34930.6	31820	9.61
		17	43	8	144.70	34	34930.6	31820	9.61
		17	57	11	183.94	39	34930.6	31820	9.61
Malate dehydrogenase, mitochondrial	P40926.3	17	11	9	153.06	34	35503.5	31820	8.92
		16	6	3	52.57	13	35503.5	33810	8.92
		16	58	11	195.08	44	35503.5	33810	8.92
NADH-cytochrome b5 reductase 3	P00387.3	17	26	8	137.64	30	34235.1	31820	7.18
		17	36	7	114.20	23	34235.1	31820	7.18
		17	27	7	120.45	23	34235.1	31820	7.18
Voltage-dependent anion-selective channel protein 2	P45880.2	17	19	6	104.33	27	31566.7	31820	7.50
		17	27	8	128.69	39	31566.7	31820	7.50
		16	8	3	39.44	13	31566.7	33810	7.50
		17	29	8	132.31	39	31566.7	31820	7.50
ATP synthase subunit gamma, mitochondrial	P36542.1	17	19	5	85.50	18	32996.2	31820	9.23
		17	47	9	144.05	31	32996.2	31820	9.23
		17	79	10	163.22	41	32996.2	31820	9.23
ER membrane protein complex subunit 2	Q15006.1	17	13	4	55.04	12	34833.7	31820	6.15
		17	13	5	72.45	16	34833.7	31820	6.15
		17	12	5	78.06	17	34833.7	31820	6.15
Annexin A3	P12429.3	17	4	3	45.16	9	36375.5	31820	5.63
		17	5	4	41.69	10	36375.5	31820	5.63
		17	15	7	89.00	24	36375.5	31820	5.63
40S ribosomal protein S8	P62241.2	18	58	9	151.40	45	24205.3	25790	10.32
		18	64	11	189.96	58	24205.3	25790	10.32
		18	10	4	53.37	21	24205.3	25790	10.32
Membrane-associated progesterone receptor component 2	O15173.1	18	31	7	114.07	35	23818.6	25790	4.76
		18	36	9	133.56	34	23818.6	25790	4.76
		18	9	3	53.98	18	23818.6	25790	4.76
60S ribosomal protein L13	P26373.4	18	35	6	90.21	27	24261.6	25790	11.62
		18	41	6	97.03	24	24261.6	25790	11.62
		18	28	6	94.77	24	24261.6	25790	11.62
Vesicle-trafficking protein SEC22b	O75396.4	19	34	6	117.50	34	24593.5	24780	6.44
		19	62	10	180.40	47	24593.5	24780	6.44
		19	36	7	134.51	43	24593.5	24780	6.44
Ras-related protein Rab-6A	P20340.3	19	17	7	104.28	34	23592.9	24780	5.42
		19	41	10	169.89	53	23592.9	24780	5.42
		19	28	9	140.37	48	23592.9	24780	5.42
Ras-related protein Rab-11B	Q15907.4	19	21	6	97.09	27	24488.6	24780	5.65
		19	62	10	183.50	52	24488.6	24780	5.65
		19	74	11	204.72	56	24488.6	24780	5.65
60S ribosomal protein L14	P50914.4	19	19	5	90.46	24	23432.0	24780	10.94
		19	36	6	107.11	30	23432.0	24780	10.94
		19	16	4	72.03	22	23432.0	24780	10.94
Ras-related protein Rab-7a	P51149.1	19	5	3	57.13	18	23489.9	24780	6.39
		19	29	8	144.52	46	23489.9	24780	6.39
		20	12	6	109.42	37	23489.9	24350	6.39
		19	62	13	241.42	66	23489.9	24780	6.39
		20	14	4	68.55	26	23489.9	24350	6.39
Thioredoxin-dependent peroxide reductase, mitochondrial	P30048.3	19	7	3	49.81	14	27692.8	24780	7.67
		19	22	5	88.45	21	27692.8	24780	7.67
		19	30	6	105.36	24	27692.8	24780	7.67
ATP synthase subunit O, mitochondrial	P48047.1	20	30	9	168.57	49	23277.4	24350	9.97
		20	69	11	200.19	66	23277.4	24350	9.97
		20	42	8	154.12	49	23277.4	24350	9.97
Peroxisome protein 1	Q06830.1	20	25	7	124.26	37	22110.5	24350	8.27
		20	60	11	183.00	47	22110.5	24350	8.27
		20	27	7	101.68	33	22110.5	24350	8.27
GTP-binding protein SAR1a	Q9NR31.1	20	10	3	47.82	15	22366.9	24350	6.22
		20	10	4	70.96	27	22366.9	24350	6.22
		19	9	4	66.38	27	22366.9	24780	6.22
ELAV-like protein 1	Q15717.2	17	18	7	115.40	25	36092.1	31820	9.23
		17	9	4	61.66	15	36092.1	31820	9.23
Heat shock protein beta-1	P04792.2	18	54	13	198.91	63	22782.6	25790	5.98
		18	87	15	260.66	85	22782.6	25790	5.98
B-cell receptor-associated protein 31	P51572.3	18	27	8	133.50	27	27991.8	25790	8.44
		18	41	9	152.29	30	27991.8	25790	8.44

Proteasome subunit alpha type-7	O14818.1	18	8	5	79.62	23	27887.0	25790	8.60
		18	16	6	109.75	34	27887.0	25790	8.60
Ras-related protein Raj-A	P11233.1	18	16	4	74.46	22	23566.9	25790	6.66
		18	25	5	99.26	34	23566.9	25790	6.66
Electron transfer flavoprotein subunit beta	P38117.3	18	8	5	64.82	23	27843.8	25790	8.25
		18	9	7	94.92	30	27843.8	25790	8.25
Ras-related protein Rab-5B	P61020.1	18	9	4	64.11	26	23706.9	25790	8.29
		18	8	4	66.87	20	23706.9	25790	8.29
Calpain small subunit 1	P04632.1	18	5	4	61.01	14	28315.9	25790	5.05
		18	11	6	95.20	25	28315.9	25790	5.05
60S ribosomal protein L7	P18124.1	18	14	4	58.72	14	29225.9	25790	10.66
		18	32	9	131.26	43	29225.9	25790	10.66
3-hydroxyacyl-CoA dehydrogenase type-2	Q99714.3	19	70	14	260.26	78	26923.2	24780	7.65
		19	52	12	222.66	72	26923.2	24780	7.65
Transgelin	Q01995.4	20	23	9	122.37	50	22611.0	24350	8.87
		20	34	12	178.75	69	22611.0	24350	8.87
Thymidylate kinase	P23919.4	20	15	4	70.30	19	23819.5	24350	8.40
		20	7	4	61.90	18	23819.5	24350	8.40
Ras-related protein Rab-1B	Q9H0U4.1	20	16	5	68.43	28	22171.3	24350	5.55
		20	23	5	75.97	28	22171.3	24350	5.55
Sodium/potassium-transporting ATPase subunit alpha-1	P05023.1	1	16	8	131.14	10	112896.8	914650	5.33
		1	28	9	148.64	11	112896.8	914650	5.33
Alpha-actinin-4	O43707.2	5	79	21	337.56	27	104854.6	86920	5.27
		5	86	30	455.31	39	104854.6	86920	5.27
Dihydropyrimidinase-related protein 2	Q16555.1	7	23	8	126.01	18	62294.0	58910	5.95
		7	27	9	142.53	22	62294.0	58910	5.95
Glucosylceramidase	P04062.3	7	9	4	51.73	7	59716.6	58910	7.29
		7	4	3	36.64	5	59716.6	58910	7.29
Paraspeckle component 1	Q8WXF1.1	7	5	3	40.51	6	58743.9	58910	6.26
		7	8	4	62.28	7	58743.9	58910	6.26
Calreticulin	P27797.1	8	5	3	43.32	13	48141.8	52900	4.29
		8	13	6	93.84	19	48141.8	52900	4.29
Annexin A11	P50995.1	9	19	8	135.08	18	54390.0	51180	7.53
		9	33	13	208.33	27	54390.0	51180	7.53
Cytosol aminopeptidase	P28838.3	9	6	4	52.29	8	56166.7	51180	8.03
		9	23	8	111.53	19	56166.7	51180	8.03
Inosine 5'-monophosphate dehydrogenase 2	P12268.2	9	7	3	47.98	7	55805.3	51180	6.44
		8	6	5	68.17	14	55805.3	52900	6.44
HLA class I histocompatibility antigen, B-40 alpha chain	Q04826.1	14	30	9	157.98	32	40505.4	37370	6.09
		12	21	8	145.40	26	40505.4	43860	6.09
L-lactate dehydrogenase A chain	P00338.2	17	6	3	51.76	10	36688.9	31820	8.44
		17	11	7	92.76	25	36688.9	31820	8.44
GTP:AMP phosphotransferase, mitochondrial	Q9UJ7.4	18	4	3	47.39	15	25565.5	25790	9.15
		18	12	5	87.69	25	25565.5	25790	9.15
Cytochrome b-c1 complex subunit Rieske, mitochondrial	P47985.2	19	21	7	98.86	24	29668.1	24780	8.55
		19	16	6	82.65	21	29668.1	25790	8.55
60S ribosomal protein L9	P32969.1	20	13	3	42.20	18	21863.5	24350	9.96
		19	24	6	98.31	37	21863.5	24780	9.96
Major vault protein	Q14764.4	4	19	12	183.14	16	99327.3	94950	5.34
		4	14	7	104.73	13	99327.3	94950	5.34
Tubulin beta-2B chain	Q9BVA1.1	8	12	5	90.12	16	49953.4	52900	4.78
		11	58	14	228.79	39	49953.4	48820	4.78
RNA-binding motif protein, X chromosome	P38159.3	13	10	5	62.80	16	42332.0	42830	10.06
		13	21	5	75.09	13	42332.0	42830	10.06
HLA class I histocompatibility antigen, A-69 alpha chain	P10316.2	14	48	12	207.62	43	40977.1	37370	6.42
		14	36	11	190.88	43	40977.1	37370	6.42
Guanine nucleotide-binding protein G(i) subunit alpha-2	P04899.3	14	22	9	157.24	37	40451.1	37370	5.34
		14	29	7	111.59	24	40451.1	37370	5.34
Inhibitor of nuclear factor kappa-B kinase-interacting protein	Q70UQ0.1	14	5	4	68.20	11	39309.2	37370	9.21
		14	6	3	51.09	8	39309.2	37370	9.21
Poly(rC)-binding protein 2	Q15366.1	15	9	4	57.09	13	38580.3	35120	6.33
		15	16	5	75.45	16	38580.3	35120	6.33
Replication factor C subunit 4	P35249.2	15	6	5	53.86	17	39682.0	35120	8.26
		15	11	4	56.82	14	39682.0	35120	8.26
Eukaryotic translation initiation factor 2 subunit 1	P05198.3	15	6	3	37.46	8	36112.4	35120	5.02
		15	11	4	50.80	12	36112.4	35120	5.02
ATP synthase subunit b, mitochondrial	P24539.2	19	27	8	131.52	36	28908.8	24780	9.37
		19	77	11	209.03	50	28908.8	24780	9.37
Transmembrane emp24 domain-containing protein 9	Q9BVK6.2	19	17	5	84.20	22	27277.5	24780	7.81

		19	24	5	85.88	22	27277.5	24780	7.81
Ras-related protein R-Ras	P10301.1	19	12	4	71.66	24	23480.6	24780	6.44
		19	15	5	86.53	33	23480.6	24780	6.44
BAG family molecular chaperone regulator 2	O95816.1	19	11	5	71.22	23	23772.1	24780	6.25
		19	27	8	114.28	31	23772.1	24780	6.25
NADH dehydrogenase [ubiquinone] flavoprotein 2	P19404.2	19	9	4	61.64	24	27391.7	24780	8.21
		19	14	4	75.46	24	27391.7	24780	8.21
Proteasome subunit beta type-1	P20618.2	19	8	3	52.59	13	26489.5	24780	8.27
		19	11	4	70.07	19	26489.5	24780	8.27
Caveolin-1	Q03138.4	19	9	3	46.63	25	20471.7	24780	5.64
		20	16	6	88.89	41	20471.7	24350	5.64
		19	17	6	91.95	41	20471.7	24780	5.64
		20	20	8	111.23	46	20471.7	24350	5.64
Proteasome subunit alpha type-2	P25787.2	19	4	3	43.30	17	25898.7	24780	6.91
		19	27	6	99.48	41	25898.7	24780	6.91
Protein DJ-1	Q99497.2	19	4	2	31.63	18	19891.2	24780	6.33
		19	8	2	35.78	18	19891.2	24780	6.33
Ras-related protein Rap-1b-like protein	A6NIZ1.1	20	19	7	107.40	36	20925.0	24350	5.37
		20	16	6	81.18	39	20925.0	24350	5.37
Ras-related protein Rab-18	Q9NP72.1	20	9	6	104.42	34	22977.2	24350	5.11
		20	26	7	129.03	42	22977.2	24350	5.11
Superoxide dismutase [Mn], mitochondrial	P04179.2	20	16	6	89.29	33	24722.2	24350	8.34
		20	54	7	117.62	30	24722.2	24350	8.34
Ras-related protein Rab-2A	P61019.1	20	14	5	86.03	32	23545.7	24350	6.08
		20	17	6	97.18	38	23545.7	24350	6.08
28S ribosomal protein S23, mitochondrial	Q9Y3D9.2	20	11	5	82.34	32	21770.7	24350	8.94
		20	17	6	97.77	35	21770.7	24350	8.94
Rho-related GTP-binding protein RhoC	P08134.1	20	15	5	81.45	29	22006.5	24350	6.20
		19	4	3	49.01	18	22006.5	24780	6.20
		20	17	5	78.13	31	22006.5	24350	6.20
Transgelin-2	P37802.3	20	6	4	67.78	22	22391.6	24350	8.41
		20	11	4	65.62	20	22391.6	24350	8.41
NADH dehydrogenase [ubiquinone] 1 beta subcomplex	O96000.3	20	14	4	59.75	29	20776.8	24350	8.72
		19	7	3	49.50	20	20776.8	24780	8.72
		20	19	3	54.59	20	20776.8	24350	8.72
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex	Q9P032.1	20	10	4	57.43	22	20266.6	24350	8.85
		20	15	5	67.24	28	20266.6	24350	8.85
Peptidyl-prolyl cis-trans isomerase FKBP11	Q9NYL4.1	20	9	3	45.35	8	22180.5	24350	9.44
		20	9	3	46.62	14	22180.5	24350	9.44

TABLE S3: 2-CIHdYA-tagged proteins identified by LC-MS/MS after an azide-agarose pull-down

Pull-down 1
 Pull-down 2
 Pull-down 3

Protein name	UniProt accession number	Spectra	Distinct peptides	Distinct summed MS/MS search score	% AA coverage	Molecular mass (Da)	pI	GO - Cellular component*
Annexin A2	P07355.2	106	16	270.39	52	38604.2	7.58	PM, End, N, LM
		108	12	234.14	49	38604.2	7.58	
		74	9	170.1	33	38604.2	7.58	
Tubulin beta-4B chain	P68371.1	53	14	256.24	44	49831.3	4.79	Cyt, N
		42	12	210.86	34	49831.3	4.79	
		51	11	187.88	27	49831.3	4.79	
Transgelin-2	P37802.3	99	10	192.82	59	22391.6	8.41	EVE
		24	6	106.15	32	22391.6	8.41	
		42	7	123.13	43	22391.6	8.41	
Tubulin alpha-1C chain	Q9BQE3.1	53	10	183.10	30	49895.6	4.96	Cyt, N
		96	11	202.58	32	49895.6	4.96	
		44	9	169.46	29	49895.6	4.96	
Neuroblast differentiation-associated protein AHNAK	Q09666.2	29	10	156.13	1	629104.8	5.80	Cyt, N, PM, LM
		9	6	72.70	1	629104.8	5.80	
		4	3	37.90	0	629104.8	5.80	
Annexin A1	P04083.2	48	7	130.62	28	38714.5	6.57	Cyt, N, End, PM
		61	9	169.71	34	38714.5	6.57	
		44	10	177.33	36	38714.5	6.57	
Polymerase I and transcript release factor	Q6NZI2.1	26	6	118.21	20	43476.3	5.51	Cav, Cyt, N, Mito, PM, ER
		18	6	112.97	20	43476.3	5.51	
		38	7	132.46	21	43476.3	5.51	
Interferon-induced GTP-binding protein Mx1	P20591.4	28	4	67.07	9	75520.7	5.60	Cyt, ER, N
		24	5	80.71	11	75520.7	5.60	
		26	5	86.30	11	75520.7	5.60	
Lactoylglutathione lyase	Q04760.4	20	4	66.29	23	20777.8	5.12	Cyt
		20	3	56.41	20	20777.8	5.12	
		19	2	34.40	9	20777.8	5.12	
Annexin A3	P12429.3	12	3	53.85	11	36375.5	5.63	Cyt, PM
		11	3	48.07	11	36375.5	5.63	
		14	3	50.91	11	36375.5	5.63	
POTE ankyrin domain family member F	A5A3E0.2	13	3	53.22	3	121445.3	5.83	Cyt
		9	3	51.33	3	121445.3	5.83	
		11	3	38.38	3	121445.3	5.83	
Protein DJ-1	Q99497.2	20	3	49.44	25	19891.2	6.33	Cyt, N, Mito, PM

		22	3	52.44	28	19891.2	6.33	
		8	3	43.96	25	19891.2	6.33	
Alpha-actinin-4	O43707.2	5	3	46.95	3	104854.6	5.27	Cyt, C, J, N
		2	2	23.64	2	104854.6	5.27	
		3	2	31.70	2	104854.6	5.27	
Histone H3.1t	Q16695.3	20	3	38.41	16	15508.3	11.13	N
		28	3	39.53	16	15508.3	11.13	
		31	3	41.03	16	15508.3	11.13	
Protein S100-A11	P31949.2	25	2	37.37	23	11740.5	6.56	Cyt, N
		22	3	52.56	34	11740.5	6.56	
		29	4	65.01	42	11740.5	6.56	
Serum albumin	P02768.2	17	2	35.50	3	69367.1	5.92	EVE, N
		10	2	31.21	3	69367.1	5.92	
		20	2	33.37	3	69367.1	5.92	
Histone H2A type 3	Q7L7L0.3	12	3	39.25	26	14121.5	11.05	N
		16	3	46.54	26	14121.5	11.05	
		11	3	47.39	26	14121.5	11.05	
Protein S100-A6	P06703.1	16	2	34.53	16	10179.8	5.32	Cyt, N, PM
		14	2	33.25	16	10179.8	5.32	
		5	2	34.45	16	10179.8	5.32	
Glutathione S-transferase omega-1	P78417.2	11	2	34.49	9	27566.0	6.24	Cyt
		8	2	29.25	9	27566.0	6.24	
		7	2	32.15	9	27566.0	6.24	
Polyubiquitin-C	P0CG48.3	9	2	27.78	2	77039.0	7.16	Cyt, N, End, PM
		9	2	36.27	2	77039.0	7.16	
		5	2	34.76	2	77039.0	7.16	
Galectin-1	P09382.2	10	3	58.14	26	14715.8	5.34	Cyt
		7	2	35.84	17	14715.8	5.34	
		3	2	33.66	17	14715.8	5.34	
Perilipin-3	O60664.3	5	2	36.68	6	47075.2	5.30	Cyt, GA, End
		5	2	34.63	6	47075.2	5.30	
		4	2	31.41	6	47075.2	5.30	
Elongation factor 1-alpha 2	Q05639.1	11	2	32.66	4	50470.4	9.11	N
		8	3	46.27	7	50470.4	9.11	
Cofilin-1	P23528.3	2	1	20.77	12	18502.6	8.22	Cyt, N
		10	1	23.00	12	18502.6	8.22	
Brain acid soluble protein 1	P80723.2	9	2	36.76	18	22693.5	4.64	C, J, PM, Cyt, N
		9	2	35.66	15	22693.5	4.64	
Histone H1.5	P16401.3	4	3	46.52	10	22580.3	10.91	N
		13	3	45.84	16	22580.3	10.91	

Histone H1.3	P16402.2	4	2	38.45	10	22350.0	11.02	N
		7	2	32.66	10	22350.0	11.02	
Acetyl-CoA acetyltransferase, cytosolic	Q9BWD1.2	9	2	41.43	12	41351.1	6.47	Cyt, N
		9	4	67.77	22	41351.1	6.47	
Tumor protein D54	O43399.2	6	2	34.95	14	22237.8	5.26	Cyt
		7	3	48.98	21	22237.8	5.26	
Myosin-9	P35579.4	6	4	62.07	2	226533.4	5.50	Cyt, N, CJ, PM
		7	2	43.32	1	226533.4	5.50	
Fibronectin	P02751.4	7	2	40.53	1	262625.9	5.46	ER, GA, EVE
		4	3	45.92	1	262625.9	5.46	
Sodium/potassium-transporting ATPase subunit alpha-1	P05023.1	3	2	31.79	2	112896.8	5.33	PM, GA, ER
		3	3	29.96	3	112896.8	5.33	
Histone H2B type 1-M	Q99879.3	1	1	21.25	11	13989.3	10.31	N
		2	1	22.00	11	13989.3	10.31	

* Cyt. cytoplasm; PM, plasma membrane; N, nucleus; End, endosome; LM, lysosomal membrane; EVE, extravesicular exosome; Cav, ER, endoplasmic reticulum; CJ, cell junction; GA, Golgi apparatus

TABLE S4: Proteins identified by LC-MS/MS that unspecifically bound to azide-agarose during the pull-down assay

Protein name	UniProt accession number	Spectra	Distinct peptides	Distinct summed MS/MS search score	% AA coverage	Molecular mass (Da)	pI
Serum albumin	P02768.2	11	2	33.66	3	69367.1	5.92
		16	4	61.83	4	69367.1	5.92

Pull-down 1
Pull-down 3