

# SUPPLEMENTARY TABLES

## Acid sphingomyelinase deactivation post-ischemia promotes brain angiogenesis and remodeling by small extracellular vesicles

### Basic Research in Cardiology

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# Supplementary Table 1. Proteins significantly upregulated in sEVs released by hCMEC/D3 exposed to amitriptyline.

## Association according to KEGG pathway database:

Phagosome
Lysosome
Protein export
Antigen processing and presentation
Epstein-Barr virus infection
Viral myocarditis

Accession	Description	Protein name	Log <sub>2</sub> fold change	P-value
Q8NE71	ATP-binding cassette sub-family F member 1	ABCF1	1.12	0.00
P11310	Medium-chain specific acyl-CoA dehydrogenase, mitochondrial	ACADM	1.73	0.00
Q13443	Disintegrin and metalloproteinase domain-containing protein 9	ADAM9	1.38	0.00
Q13155	Aminoacyl tRNA synthase complex-interacting multifunctional protein 2	AIMP2	1.09	0.00
Q13740	CD166 antigen	ALCAM	1.20	0.00
P09972	Fructose-bisphosphate aldolase C	ALDOC	1.04	0.03
P15144	Aminopeptidase N	AN	1.10	0.00
Q9BX55	AP-1 complex subunit mu-1	AP1M1	1.06	0.00
Q92572	AP-3 complex subunit sigma-1	AP3S1	1.14	0.00
P05026	Sodium/potassium-transporting ATPase subunit beta-1	ATP1B1	1.00	0.00
P61769	Beta-2-microglobulin	B2M	1.21	0.00
Q05682	Caldesmon	CALD1	1.14	0.00
P27824	Calnexin	CANX	1.28	0.00
Q6NZ12	Caveolae-associated protein 1	CAVIN1	1.63	0.00
P45973	Chromobox protein homolog 5	CBX5	1.33	0.00
P16070	CD44 antigen	CD44	1.09	0.00
P15529	Membrane cofactor protein	CD46	1.28	0.00
P08174	Complement decay-accelerating factor	CD55	1.38	0.00
P48960	CD97 antigen	CD97	1.17	0.00
Q14008	Cytoskeleton-associated protein 5	CKAP5	1.11	0.00
Q6UVK1	Chondroitin sulfate proteoglycan 4	CSPG4	1.40	0.00
P07858	Cathepsin B	CTSB	1.06	0.00
P07339	Cathepsin D	CTSD	1.07	0.00
Q14247	Src substrate cortactin	CTTN	1.42	0.02
P17844	Probable ATP-dependent RNA helicase DDX5	DDX5	1.03	0.00
P31689	DnaJ homolog subfamily A member 1	DNAJA1	1.09	0.00
P23919	Thymidylate kinase	DTYMK	1.56	0.00
Q9BY44	Eukaryotic translation initiation factor 2A	EIF2A	1.23	0.00
P19525	Interferon-induced, double-stranded RNA-activated protein kinase	EIF2AK2	1.74	0.00
O75821	Eukaryotic translation initiation factor 3 subunit G	EIF3G	1.11	0.01
Q7L2H7	Eukaryotic translation initiation factor 3 subunit M	EIF3M	1.66	0.00
Q04637	Eukaryotic translation initiation factor 4 gamma 1	EIF4G1	1.05	0.00
P13804	Electron transfer flavoprotein subunit alpha, mitochondrial	ETFA	1.16	0.00
Q96A65	Exocyst complex component 4	EXOC4	2.02	0.00
Q13451	Peptidyl-prolyl cis-trans isomerase FKBP5	FKBP5	1.09	0.00
P35637	RNA-binding protein FUS	FUS	1.47	0.00
P51114	Fragile X mental retardation syndrome-related protein 1	FXR1	1.08	0.00
P60520	Gamma-aminobutyric acid receptor-associated protein-like 2	GABARAPL2	1.58	0.00
Q96RP9	Elongation factor G, mitochondrial	GFM1	1.06	0.00
P16278	Beta-galactosidase	GLB1	1.68	0.00
Q14344	Guanine nucleotide-binding protein subunit alpha-13	GNA13	2.20	0.00
P08236	Beta-glucuronidase	GUSB	1.98	0.00
P19367	Hexokinase-1	HK1	1.64	0.00
P01889	HLA class I histocompatibility antigen, B alpha chain	HLA-B	1.24	0.00
P10321	HLA class I histocompatibility antigen, C alpha chain	HLA-C	1.25	0.00
P51991	Heterogeneous nuclear ribonucleoprotein A3	HNRNPA3	1.63	0.00
P31943	Heterogeneous nuclear ribonucleoprotein H	HNRNPH1	1.08	0.00
P14866	Heterogeneous nuclear ribonucleoprotein L	HNRNPL	1.00	0.00
Q00839	Heterogeneous nuclear ribonucleoprotein U	HNRNPU	1.07	0.00
Q16666	Gamma-interferon-inducible protein 16	IFI16	1.38	0.00
Q9Y6M1	Insulin-like growth factor 2 mRNA-binding protein 2	IGF2BP2	1.29	0.00
P08648	Integrin alpha-5	ITGA5	1.38	0.00
P33176	Kinesin-1 heavy chain	KIF5B	1.19	0.00
P52292	Importin subunit alpha-1	KPNA2	1.39	0.00
P11279	Lysosome-associated membrane glycoprotein 1	LAMP1	1.24	0.00
Q9UHB6	LIM domain and actin-binding protein 1	LIMA1	1.38	0.00
Q8N1G4	Leucine-rich repeat-containing protein 47	LRRC47	1.11	0.01
P27816	Microtubule-associated protein 4	MAP4	1.32	0.00
P43243	Matrin-3	MATR3	1.73	0.00
P43121	Cell surface glycoprotein MUC18	MCAM	1.20	0.00
Q14566	DNA replication licensing factor MCM6	MCM6	1.26	0.00
Q95297	Myelin protein zero-like protein 1	MPZL1	1.15	0.00
P42285	Exosome RNA helicase MTR4	MTRX	1.61	0.00
P20591	Interferon-induced GTP-binding protein Mx1	MX1	1.37	0.00
Q92542	Nicestrin	NCSTN	1.72	0.00
P09874	Poly [ADP-ribose] polymerase 1	PARP1	1.06	0.00

Comparison of n=6 different samples/group obtained from 10 independent cell cultures.

## Supplementary Table 1. Proteins significantly upregulated in sEVs released by hCMEC/D3 exposed to amitriptyline.

Association according to KEGG pathway database:	
	Phagosome
	Lysosome
	Protein export
	Antigen processing and presentation
	Epstein-Barr virus infection
	Viral myocarditis

Accession	Description	Protein name	Log 2 fold change	P-value
O60664	Perilipin-3	PLIN3	1.04	0.00
P30876	DNA-directed RNA polymerase II subunit RPB2	POLR2B	1.15	0.00
Q06830	Peroxisome oxidoreductin-1	PRDX1	1.05	0.00
O75475	PC4 and SFRS1-interacting protein	PSIP1	1.57	0.00
P28066	Proteasome subunit alpha type-5	PSMA5	1.70	0.00
Q06323	Proteasome activator complex subunit 1	PSME1	1.39	0.00
Q9UKM9	RNA-binding protein Raly	RALY	1.06	0.00
Q14498	RNA-binding protein 39	RBM39	1.27	0.00
Q04206	Transcription factor p65	RELA	1.18	0.00
P13489	Ribonuclease inhibitor	RNH1	1.17	0.00
P27635	60S ribosomal protein L10	RPL10	1.00	0.00
P35268	60S ribosomal protein L22	RPL22	1.17	0.00
P36578	60S ribosomal protein L4	RPL4	1.11	0.00
P62841	40S ribosomal protein S15	RPS15	1.72	0.01
Q9P2E9	Ribosome-binding protein 1	RRBP1	1.10	0.00
Q14108	Lysosome membrane protein 2	SCARB2	1.48	0.00
P53985	Monocarboxylate transporter 1	SLC16A1	1.12	0.00
Q9H2H9	Sodium-coupled neutral amino acid transporter 1	SLC38A1	1.21	0.00
Q96QD8	Sodium-coupled neutral amino acid transporter 2	SLC38A2	1.07	0.00
Q15043	Zinc transporter ZIP14	SLC39A14	1.13	0.00
P08195	4F2 cell-surface antigen heavy chain	SLC3A2	1.45	0.00
P30825	High affinity cationic amino acid transporter 1	SLC7A1	1.08	0.02
Q01650	Large neutral amino acids transporter small subunit 1	SLC7A5	1.16	0.00
O60264	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	SMARCA5	1.03	0.00
Q8TAQ2	SWI/SNF complex subunit SMARCC2	SMARCC2	1.16	0.00
O95347	Structural maintenance of chromosomes protein 2	SMC2	1.76	0.00
Q9UQE7	Structural maintenance of chromosomes protein 3	SMC3	1.91	0.00
Q13501	Sequestosome-1	SQSTM1	3.70	0.00
P61011	Signal recognition particle 54 kDa protein	SRP54	1.15	0.00
Q9UHB9	Signal recognition particle subunit SRP68	SRP68	1.17	0.00
O76094	Signal recognition particle subunit SRP72	SRP72	1.09	0.00
P05455	Lupus La protein	SSB	1.00	0.00
O15400	Syntaxin-7	STX7	1.15	0.01
Q13428	Treacle protein	TCOF1	1.49	0.00
Q9Y5L0	Transportin-3	TNPO3	1.60	0.00
P06753	Tropomyosin alpha-3 chain	TPM3	1.09	0.01
Q13263	Transcription intermediary factor 1-beta	TRIM28	1.29	0.00
P49411	Elongation factor Tu, mitochondrial	TUFM	1.02	0.00
P26368	Splicing factor U2AF 65 kDa subunit	U2AF2	1.72	0.00
O94874	E3 UFM1-protein ligase 1	UFL1	1.08	0.00
Q16739	Ceramide glucosyltransferase	UGCG	1.11	0.03
Q08AM6	Protein VAC14 homolog	VAC14	1.24	0.00
Q15836	Vesicle-associated membrane protein 3	VAMP3	2.07	0.00
P08670	Vimentin	VIM	1.19	0.00
O75436	Vacuolar protein sorting-associated protein 26A	VPS26A	1.25	0.00

Comparison of n=6 different samples/group obtained from 10 independent cell cultures.

**Supplementary Table 2. Proteins significantly downregulated in sEVs released by hCMEC/D3 exposed to amitriptyline.**

<b>Association according to KEGG pathway database:</b>	
	Extracellular matrix - receptor interaction and focal adhesion

Accession	Description	Protein name	Log 2 fold change	P-value
P24821	Tenascin	TNC	-1.05	0.00
P02647	Apolipoprotein A-I	APOA1	-1.05	0.00
P08572	Collagen alpha-2(IV) chain	COL4A2	-1.06	0.00
O00622	CCN family member 1	CCN1	-1.13	0.00
Q96N76	Urocanate hydratase	UROC1	-1.29	0.01
P58107	Epiplakin	EPPK1	-1.31	0.01
P02788	Lactotransferrin	LTF	-1.34	0.00
O76074	cGMP-specific 3',5'-cyclic phosphodiesterase	PDE5A	-1.50	0.01
P26022	Pentraxin-related protein PTX3	PTX3	-2.28	0.00

Comparison of n=6 different samples/group obtained from 10 independent cell cultures.

### Supplementary Table 3. Differentially regulated protein networks identified by KEGG pathway database analysis.

Term ID	Term description	Observed gene count	Background gene count	Strength	False discovery rate	Matching proteins in the network
hsa04145	Phagosome	7	145	0.93	0.0014	VAMP3, CANX, ITGA5, LAMP1, STX7, HLA-C, HLA-B
hsa04142	Lysosome	8	123	1.06	0.00013	CTSD, SCARB2, GUSB, GLB1, AP3S1, LAMP1, CTSB, AP1M1
hsa03060	Protein export	3	23	1.36	0.0123	SRP68, SRP72, SRP54
hsa04612	Antigen processing and presentation	6	66	1.2	0.00027	CANX, CTSB, HLA-C, PSME1, HLA-B, B2M
hsa05169	Epstein-Barr virus infection	7	194	0.8	0.0061	EIF2AK2, HLA-C, POLR2B, RELA, CD44, HLA-B, VIM
hsa05416	Viral myocarditis	4	56	1.1	0.0123	CD55, HLA-C, HLA-B, EIF4G1

Term ID	Term description	Observed gene count	Background gene count	Strength	False discovery rate	Matching proteins in the network
hsa04512	ECM-receptor interaction	2	81	1.73	0.0125	TNC, COL4A2
hsa04510	Focal adhesion	2	197	1.34	0.0353	TNC, COL4A2

Comparison of n=6 different samples/group obtained from 10 independent cell cultures.

**Supplemental Table 4. List of all proteins identified by label free proteomics analysis.**

Accession	Description	Coverage [%]	# PSMs	# Unique Peptides	Antitriptyline 1	Antitriptyline 2	Antitriptyline 3	Antitriptyline 4	Antitriptyline 5	Antitriptyline 6	Vehicle 1	Vehicle 2	Vehicle 3	Vehicle 4	Vehicle 5	Vehicle 6	Average abundance	Average velocity	Ratio antitriptyline/vehicle	Log 2 fold change (antitriptyline/vehicle)	P-value
P8371	Tubulin beta-4B chain OS=Homo sapiens OX-9606 GN-TUBB4B PE=1 SV=1	81	5349	2	7.20E+05	1.58E+09	1.79E+09	1.67E+09	1.72E+09	1.81E+09	1.39E+09	1.39E+09	1.58E+09	1.43E+09	1.55E+09	1.68E+09	1.71E+09	1.71E+09	1.50E+09	1.14	0.00672027
Q71U36	Tubulin alpha-1A chain OS=Homo sapiens OX-9606 GN-TUBA1A PE=1 SV=1	77	3804	2	1.70E+05	8.77E+06	1.75E+07	1.02E+07	1.02E+07	1.08E+07	1.02E+07	1.36E+07	6.14E+06	1.58E+07	1.32E+07	1.14E+07	1.14E+07	1.14E+07	1.60E+07	0.98	0.927398077
Q9BOE3	Tubulin alpha-1C chain OS=Homo sapiens OX-9606 GN-TUBA1C PE=1 SV=1	73	3200	2	1.78E+05	1.89E+09	1.99E+09	1.71E+09	1.82E+09	1.88E+09	1.55E+09	1.60E+09	1.61E+09	1.62E+09	1.75E+09	1.55E+09	1.84E+09	1.84E+09	1.61E+09	1.14	0.000983406
Q7L7L0	Histone H2A type 3 OS=Homo sapiens OX-9606 GN-HIST3H2A PE=1 SV=3	64	2655	2	2.31E+05	2.19E+08	3.22E+08	2.42E+08	2.00E+08	1.76E+08	2.05E+08	2.78E+08	2.58E+08	3.62E+08	2.67E+08	1.64E+08	2.32E+08	2.32E+08	2.55E+08	0.91	0.505091271
P10412	Histone H1.4 OS=Homo sapiens OX-9606 GN-H1.4 PE=1 SV=2	39	706	2	1.89E+05	1.91E+09	1.70E+09	1.82E+09	1.81E+09	1.75E+09	1.60E+09	1.69E+09	1.70E+09	1.62E+09	1.60E+09	1.58E+09	1.81E+09	1.81E+09	1.63E+09	1.11	0.01966657
Q56281	Keratin type I cytoskeletal 6B OS=Homo sapiens OX-9606 GN-KRT6B PE=1 SV=5	32	706	2	1.89E+05	1.91E+09	1.70E+09	1.82E+09	1.81E+09	1.75E+09	1.60E+09	1.69E+09	1.70E+09	1.62E+09	1.60E+09	1.58E+09	1.81E+09	1.81E+09	1.63E+09	1.11	0.01966657
Q56281	Beta-actin-like protein 2 OS=Homo sapiens OX-9606 GN-ACTL2 PE=1 SV=2	32	1284	2	1.15E+05	4.90E+05	1.31E+06	3.10E+05	1.15E+05	1.15E+05	1.75E+05	1.05E+06	2.51E+05	1.75E+05	1.07E+06	7.88E+05	8.83E+05	8.83E+05	5.74E+05	0.62	0.32925262
Q13310	Polyadenylate-binding protein 4 OS=Homo sapiens OX-9606 GN-PABPC4 PE=1 SV=1	14	88	2	1.88E+06	2.49E+06	1.84E+06	2.07E+06	2.14E+06	1.65E+06	1.74E+06	1.85E+06	1.61E+06	1.73E+06	1.23E+06	1.49E+06	2.01E+06	2.01E+06	1.61E+06	1.25	0.023859109
P62820	Ras-related protein Rab-1A OS=Homo sapiens OX-9606 GN-RAB1A PE=1 SV=3	54	91	2	6.67E+06	8.09E+06	4.82E+06	5.06E+06	4.88E+06	4.99E+06	6.53E+06	4.64E+06	5.16E+06	4.89E+06	5.34E+06	5.75E+06	5.75E+06	5.75E+06	0.30	0.984813058	
P08754	Guanine nucleotide-binding protein (G) subunit alpha OS=Homo sapiens OX-9606 GN-GNAI3 PE=1 SV=3	21	120	2	1.66E+06	2.31E+06	2.28E+06	1.12E+06	1.23E+06	1.53E+06	1.67E+06	1.26E+06	1.62E+06	1.91E+06	1.11E+06	1.72E+06	1.72E+06	1.72E+06	1.03	0.34238845	
P62873	Guanine nucleotide-binding protein (G) subunit beta-1 OS=Homo sapiens OX-9606 GN-GNB1 PE=1 SV=3	21	174	2	7.07E+06	6.59E+06	6.89E+06	7.16E+06	7.33E+06	8.12E+06	7.13E+06	7.19E+06	6.71E+06	8.14E+06	6.80E+06	6.91E+06	7.19E+06	7.19E+06	7.03E+06	0.30	0.852075449
Q42919	Altoxin B1 subunit OS=Homo sapiens OX-9606 GN-AR7B2 PE=1 SV=3	15	34	2	1.43E+07	1.43E+07	1.29E+07	1.29E+07	1.29E+07	1.29E+07	1.29E+07	8.81E+06	7.29E+06	8.81E+06	7.29E+06	8.81E+06	7.29E+06	7.29E+06	8.81E+06	1.41	0.004861774
Q15836	Vesicle-associated membrane protein 3 OS=Homo sapiens OX-9606 GN-VAMP3 PE=1 SV=3	24	56	2	3.17E+06	4.53E+06	5.86E+06	6.42E+06	5.78E+06	8.20E+06	8.46E+06	8.62E+06	1.61E+06	7.29E+06	2.70E+06	5.66E+06	5.66E+06	5.66E+06	1.35E+06	4.19	0.000754519
P05148	Guanine nucleotide-binding protein (G) subunit alpha OS=Homo sapiens OX-9606 GN-GNAQ PE=1 SV=4	16	32	2	4.48E+06	6.55E+06	4.74E+06	4.71E+06	3.69E+06	4.47E+06	3.21E+06	3.17E+06	3.17E+06	2.29E+06	3.44E+06	4.77E+06	4.77E+06	4.77E+06	2.07	0.006232056	
P28482	Mtogen-activated protein kinase 1 OS=Homo sapiens OX-9606 GN-MAPK1 PE=1 SV=3	14	74	2	7.49E+06	7.48E+06	7.84E+06	8.75E+06	7.28E+06	7.87E+06	8.94E+06	8.37E+06	9.63E+06	8.19E+06	9.13E+06	8.29E+06	7.79E+06	7.79E+06	8.76E+06	0.89	0.10196294
Q16629	Serine/arginine-rich splicing factor 7 OS=Homo sapiens OX-9606 GN-SRSF7 PE=1 SV=1	16	72	2	1.47E+07	1.20E+07	8.62E+06	9.13E+06	9.02E+06	9.60E+06	9.31E+06	8.31E+06	4.70E+06	8.15E+06	6.44E+06	6.95E+06	1.05E+07	1.05E+07	7.31E+06	0.57	0.023709989
P09972	Fructose-bisphosphate aldolase C OS=Homo sapiens OX-9606 GN-ALDOCE PE=1 SV=2	17	54	2	2.39E+06	2.70E+06	2.37E+06	1.85E+06	1.80E+06	2.78E+06	3.10E+06	1.77E+06	6.09E+05	1.29E+06	1.48E+06	9.99E+05	2.58E+06	2.58E+06	1.26E+06	2.06	0.030700268
P31940	Succinate dehydrogenase [ubiquinol] flavoprotein subunit, mitochondrial OS=Homo sapiens OX-9606 GN-SDHA PE=1 SV=2	6	20	2	4.37E+06	2.70E+06	2.91E+06	2.87E+06	1.80E+06	3.67E+06	3.10E+06	1.77E+06	6.09E+05	1.29E+06	1.48E+06	9.99E+05	2.58E+06	2.58E+06	1.26E+06	2.06	0.030700268
Q43809	Cleavage and polyadenylation specificity factor subunit 5 OS=Homo sapiens OX-9606 GN-NLUDT21 PE=1 SV=1	21	14	2	1.71E+06	2.76E+06	2.91E+06	2.78E+06	2.99E+06	1.50E+06	1.40E+06	1.31E+06	1.98E+06	1.57E+06	8.67E+05	1.16E+06	2.44E+06	2.44E+06	1.38E+06	1.77	0.04094725
Q9NRV6	Phospholipid scramblase 3 OS=Homo sapiens OX-9606 GN-PLSCR3 PE=1 SV=2	11	25	2	6.49E+06	3.68E+06	5.38E+06	1.77E+06	3.85E+06	5.26E+06	2.48E+06	3.15E+06	5.13E+06	2.55E+06	4.17E+06	3.60E+06	4.40E+06	4.40E+06	3.51E+06	1.25	0.329367072
P58107	Epilipkin OS=Homo sapiens OX-9606 GN-EPPK1 PE=1 SV=3	5	34	2	1.11E+06	7.30E+05	1.05E+06	1.10E+06	1.03E+06	1.82E+06	5.03E+06	2.50E+06	2.12E+06	4.07E+06	3.17E+06	3.26E+06	1.22E+06	1.22E+06	3.02E+06	-1.31	0.00304223
Q01650	Large neutral amino acids transporter small subunit 1 OS=Homo sapiens OX-9606 GN-SLC7A5 PE=1 SV=2	6	34	2	5.84E+06	6.43E+06	7.64E+06	7.02E+06	6.73E+06	6.97E+06	3.22E+06	3.04E+06	3.40E+06	3.69E+06	2.48E+06	2.39E+06	6.77E+06	6.77E+06	3.04E+06	2.23	0.1665275E07
P28161	Neuro-S transmembrane 2 OS=Homo sapiens OX-9606 GN-NS2M2 PE=1 SV=2	13	54	2	2.88E+07	2.43E+07	2.29E+07	2.08E+07	2.16E+07	2.31E+07	4.14E+07	3.48E+07	3.19E+07	2.76E+07	3.23E+07	3.23E+07	2.36E+07	2.36E+07	3.34E+07	0.71	0.017663338
P48105	60S ribosomal protein L21 OS=Homo sapiens OX-9606 GN-RPL21 PE=1 SV=2	14	50	2	2.37E+06	2.98E+07	3.03E+07	2.95E+07	2.95E+07	3.97E+06	1.55E+07	1.71E+07	1.72E+07	1.68E+07	1.33E+07	1.13E+07	1.52E+07	1.52E+07	1.06	0.000232838	
Q13765	Nascent polypeptide-associated complex subunit alpha OS=Homo sapiens OX-9606 GN-NACA PE=1 SV=1	13	36	2	1.03E+07	1.14E+07	8.21E+06	1.21E+07	1.28E+07	1.03E+07	7.53E+06	7.70E+06	7.42E+06	7.13E+06	6.17E+06	5.83E+06	1.08E+07	1.08E+07	6.96E+06	1.56	0.001031881
Q15286	Ras-related protein Rab-35 OS=Homo sapiens OX-9606 GN-RAB35 PE=1 SV=1	23	63	2	1.62E+06	1.57E+06	2.59E+06	2.60E+06	2.68E+06	2.96E+06	1.20E+06	1.56E+06	1.57E+06	2.25E+06	1.60E+06	1.15E+06	2.34E+06	2.34E+06	1.56E+06	0.69	0.025175228
P21964	Catechol O-methyltransferase OS=Homo sapiens OX-9606 GN-COMT PE=1 SV=2	12	16	2	7.52E+05	5.21E+06	1.38E+06	3.17E+06	1.29E+06	5.96E+06	2.23E+06	8.44E+06	3.10E+06	5.18E+06	7.75E+06	6.81E+06	2.96E+06	2.96E+06	5.99E+06	0.53	0.084567892
P53999	Activated RNA polymerase II transcriptional coactivator p15 OS=Homo sapiens OX-9606 GN-SUB1 PE=1 SV=3	19	28	2	8.04E+06	6.16E+06	3.29E+06	6.73E+06	3.76E+06	6.25E+06	3.15E+06	6.27E+06	3.29E+06	1.57E+06	3.10E+06	4.00E+06	5.71E+06	5.71E+06	4.06E+06	1.40	0.49115204
Q14617	AP-3 complex subunit delta-3 OS=Homo sapiens OX-9606 GN-AP3D3 PE=1 SV=1	3	32	2	6.75E+06	7.81E+06	6.39E+06	4.07E+06	4.03E+06	6.35E+07	3.17E+06	4.50E+06	4.22E+06	3.47E+06	4.84E+06	3.47E+06	3.95E+06	3.95E+06	1.51	0.001005796	
Q16712	Glutathione S-transferase A3 OS=Homo sapiens OX-9606 GN-GSTA3 PE=1 SV=3	21	28	2	3.69E+07	4.85E+07	6.84E+07	4.07E+06	6.35E+07	6.47E+07	8.02E+07	8.02E+07	7.08E+07	8.02E+07	8.02E+07	8.02E+07	8.02E+07	8.02E+07	7.86E+07	0.76	0.124000400
P10301	Ras-related protein R-Ras OS=Homo sapiens OX-9606 GN-RRAS PE=1 SV=1	20	28	2	3.74E+06	4.33E+06	3.71E+06	4.14E+06	3.9E+06	4.97E+06	3.35E+06	2.13E+06	1.82E+06	2.75E+06	2.59E+06	1.56E+06	4.03E+06	4.03E+06	3.85E+06	0.77	0.000838833
Q08170	Serine/arginine-rich splicing factor 4 OS=Homo sapiens OX-9606 GN-SRSF4 PE=1 SV=2	11	75	2	2.55E+07	2.80E+07	3.10E+07	3.31E+07	3.72E+07	3.08E+07	2.53E+07	2.62E+07	2.83E+07	2.63E+07	2.41E+07	2.37E+07	3.09E+07	3.09E+07	2.57E+07	0.27	0.02241621
P13693	Transcriptionally-controlled tumor protein OS=Homo sapiens OX-9606 GN-TPT1 PE=1 SV=1	31	10	2	4.54E+06	3.91E+06	3.52E+06	4.06E+06	1.68E+06	4.73E+06	1.96E+06	3.99E+06	3.09E+06	2.22E+06	6.05E+06	5.26E+06	3.74E+06	3.74E+06	3.76E+06	0.99	0.980630094
Q9HC07	Transmembrane protein 165 OS=Homo sapiens OX-9606 GN-TMEM165 PE=1 SV=1	14	18	2	6.67E+06	7.12E+06	5.89E+06	7.69E+06	7.63E+06	6.85E+06	5.41E+06	5.87E+06	7.03E+06	5.82E+06	7.84E+06	3.76E+06	7.01E+06	7.01E+06	5.95E+06	1.18	0.139131248
Q9N8M4	Viscagin OS=Homo sapiens OX-9606 GN-VISN PE=1 SV=1	12	18	2	4.80E+06	3.85E+06	2.46E+06	3.53E+06	3.05E+06	3.05E+06	3.64E+06	4.95E+06	8.11E+06	1.64E+06	5.59E+06	2.76E+06	3.47E+06	3.47E+06	2.39E+06	0.54	0.003309177
P48055	LM and secretory cell antigen-like-containing domain protein OS=Homo sapiens OX-9606 GN-LMS1 PE=1 SV=4	14	50	2	1.11E+07	7.77E+06	9.95E+06	7.85E+06	1.02E+07	9.95E+06	1.16E+07	1.02E+07	1.02E+07	1.02E+07	1.02E+07	1.02E+07	1.02E+07	1.02E+07	0.72	0.022545847	
Q9BWD1	Acetyl-CoA acyltransferase, cytosolic OS=Homo sapiens OX-9606 GN-ACAT2 PE=1 SV=2	13	6	2	2.76E+06	2.23E+06	1.64E+06	2.47E+06	1.71E+06	2.31E+06	4.73E+06	2.91E+06	1.23E+06	1.69E+06	1.10E+06	9.05E+05	2.19E+06	2.19E+06	1.06	0.89511115	
P55809	Succinyl-CoA:3-ketoacid coenzyme A transferase 1, mitochondrial OS=Homo sapiens OX-9606 GN-OXCT1 PE=1 SV=1	9	10	2	3.56E+06	2.72E+06	2.61E+06	2.80E+06	2.33E+06	2.45E+06	2.57E+06	7.20E+05	1.48E+06	1.49E+06	2.42E+06	2.03E+06	3.04E+06	3.04E+06	1.78E+06	0.77	0.10120172
P11310	Medium-chain specific acyl-CoA dehydrogenase, mitochondrial OS=Homo sapiens OX-9606 GN-ACADM PE=1 SV=1	10	14	2	1																

Supplementary Table 4. List of all proteins identified by label free proteomics analysis.

Accession	Description	Coverage [%]	iPSM	# Unique Peptides	Antitriptyline 1	Antitriptyline 2	Antitriptyline 3	Antitriptyline 4	Antitriptyline 5	Antitriptyline 6	Vehicle 1	Vehicle 2	Vehicle 3	Vehicle 4	Vehicle 5	Vehicle 6	Average antitriptyline	Average vehicle	Ratio antitriptyline/vehicle	Log 2 fold change (antitriptyline/vehicle)	P-value	
P08237	ATP-dependent 1-phosphofructokinase, muscle type OS=Homo sapiens OX=9606 GN=PFKM PE=1 SV=2	4	31	2	3.36E+07	3.55E+06	3.32E+06	3.58E+06	3.29E+06	2.64E+06	3.19E+06	3.14E+06	3.20E+06	3.29E+06	3.09E+06	2.54E+06	3.29E+06	3.29E+06	1.00	0.2480964	0.07	
P48888	Sulfotransferase 1E1 OS=Homo sapiens OX=9606 GN=SULT1E1 PE=1 SV=1	6	70	2	1.12E+07	1.10E+07	2.36E+07	2.45E+07	2.68E+07	1.84E+07	2.99E+07	4.45E+07	3.68E+07	2.97E+07	2.73E+07	1.92E+07	1.92E+07	3.27E+07	0.70	0.006451522	0.10	
Q92974	Rho guanine nucleotide exchange factor 2 OS=Homo sapiens OX=9606 GN=ARHGEF2 PE=1 SV=4	3	6	2	4.38E+05	1.83E+06	1.48E+06	9.46E+05	2.16E+06	1.24E+06	3.49E+05	6.85E+05	4.71E+05	3.60E+05	7.24E+05	1.37E+06	1.37E+06	6.38E+05	2.15	0.076597122	1.10	
O60664	Perilipin-3 OS=Homo sapiens OX=9606 GN=PLIN3 PE=1 SV=3	3	18	2	2.96E+06	2.74E+06	2.63E+06	3.40E+06	2.92E+06	2.30E+06	2.02E+06	1.29E+06	9.25E+05	1.41E+06	1.40E+06	1.20E+06	2.82E+06	1.37E+06	2.06	1.0	4.331E+05	0.5
P23468	Receptor-type tyrosine-protein phosphatase delta OS=Homo sapiens OX=9606 GN=PTPRD PE=1 SV=2	10	26	2	2.83E+06	2.39E+06	3.21E+06	2.65E+06	2.95E+06	1.93E+06	3.83E+06	3.17E+06	2.98E+06	3.22E+06	2.98E+06	2.66E+06	2.66E+06	3.27E+06	0.81	0.049632038	0.30	
P06866	Myosin protein-like protein 1 OS=Homo sapiens OX=9606 GN=MYO1B PE=1 SV=1	19	54	2	2.83E+06	2.47E+06	3.87E+06	3.45E+06	3.00E+06	2.00E+06	1.33E+06	1.76E+06	1.34E+06	1.33E+06	1.34E+06	1.37E+06	2.66E+06	1.37E+06	2.21	0.001098828	1.15	
P25272	Heterogeneous nuclear ribonucleoprotein M OS=Homo sapiens OX=9606 GN=HNRNPM PE=1 SV=3	3	34	2	1.83E+07	1.75E+07	1.57E+07	1.92E+07	1.64E+07	1.70E+07	1.28E+07	1.42E+07	1.47E+07	1.10E+07	1.11E+07	1.60E+07	1.73E+07	1.33E+07	1.31	0.037759562	0.90	
Q16836	Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial OS=Homo sapiens OX=9606 GN=HADH PE=1 SV=3	3	22	2	1.05E+07	1.20E+07	7.04E+06	8.88E+06	6.65E+06	7.03E+06	6.09E+06	5.54E+06	6.63E+06	3.48E+06	3.90E+06	3.82E+06	8.68E+06	4.41E+06	1.97	0.003213492	0.96	
P13489	Ribonucleic acid inhibitor OS=Homo sapiens OX=9606 GN=RNHI PE=1 SV=2	6	12	2	3.03E+06	3.61E+06	2.81E+06	3.12E+06	3.87E+06	2.69E+06	2.90E+06	1.65E+06	1.67E+06	1.90E+06	9.40E+05	1.42E+06	3.19E+06	1.42E+06	2.25	0.003485861	1.56	
Q14444	Capprin-1 OS=Homo sapiens OX=9606 GN=CAPRN1 PE=1 SV=2	5	8	2	2.74E+06	1.99E+06	3.38E+06	2.83E+06	3.38E+06	3.04E+06	9.42E+05	1.79E+06	2.11E+06	1.20E+06	1.91E+06	1.54E+06	2.89E+06	1.83E+06	1.56	0.003485861	1.56	
P06866	RNA-binding protein FUS OS=Homo sapiens OX=9606 GN=FUS PE=1 SV=1	19	54	2	5.74E+06	5.10E+06	4.98E+06	4.81E+06	4.08E+06	3.81E+06	4.87E+06	1.56E+06	1.70E+06	1.85E+06	1.78E+06	1.12E+06	4.72E+06	1.71E+06	2.76	4.2838E-05	0.47	
Q7R1V2	Glutathione S-transferase A5 OS=Homo sapiens OX=9606 GN=GSTA5 PE=1 SV=1	7	270	2	5.97E+07	5.78E+07	5.22E+07	5.68E+07	5.27E+07	4.54E+07	7.24E+07	6.94E+07	7.65E+07	8.07E+07	6.28E+07	4.92E+07	5.41E+07	6.85E+07	0.79	0.024471466	0.94	
Q8TBC4	NEDD8-activating enzyme E1 catalytic subunit OS=Homo sapiens OX=9606 GN=NEDD8 PE=1 SV=2	9	13	2	1.03E+06	1.03E+06	7.96E+05	3.26E+06	8.38E+05	2.29E+06	5.02E+05	1.76E+06	1.75E+06	3.05E+06	1.64E+06	1.33E+06	1.64E+06	1.51E+06	-0.12	0.831342966	0.34	
P61966	AP-1 complex subunit sigma-1A OS=Homo sapiens OX=9606 GN=AP1S1 PE=1 SV=1	15	5	2	3.88E+05	1.56E+06	2.77E+05	1.44E+06	8.54E+05	1.02E+06	3.29E+05	4.23E+05	3.67E+05	5.17E+05	5.50E+05	9.04E+05	5.35E+05	9.04E+05	1.69	0.245743931	0.76	
Q172E3	ATP-dependent RNA helicase DHX30 OS=Homo sapiens OX=9606 GN=DHX30 PE=1 SV=1	4	4	2	3.88E+05	1.56E+06	2.77E+05	1.44E+06	8.54E+05	1.02E+06	3.29E+05	4.23E+05	3.67E+05	5.17E+05	5.50E+05	9.04E+05	5.35E+05	9.04E+05	1.69	0.245743931	0.76	
Q14879	Interferon-induced protein with tetratricopeptide repeats 3 OS=Homo sapiens OX=9606 GN=IFIT3 PE=1 SV=1	4	4	2	1.43E+06	1.18E+06	1.58E+06	1.35E+06	2.08E+06	1.35E+06	1.96E+06	5.32E+06	1.49E+06	9.90E+06	1.57E+06	1.20E+06	1.37E+06	1.20E+06	1.04	0.082383824	2.06	
R40660	Ran GTPase-activating protein 1 OS=Homo sapiens OX=9606 GN=RANGAP1 PE=1 SV=1	2	4	2	2.40E+06	3.19E+06	2.89E+06	2.75E+06	1.33E+06	1.96E+06	6.28E+05	1.63E+06	1.49E+06	9.12E+05	9.50E+05	1.47E+06	1.20E+06	1.20E+06	1.97	0.001291444	1.07	
P32444	Reiteration domain 14 kDa subunit OS=Homo sapiens OX=9606 GN=RP34 PE=1 SV=1	30	13	2	4.84E+06	2.05E+06	1.42E+06	1.85E+06	1.62E+06	2.12E+06	2.84E+06	1.48E+06	1.58E+06	1.56E+06	1.36E+06	2.31E+06	1.78E+06	1.30	0.37361958	0.88		
P11233	Ras-related protein RaL OS=Homo sapiens OX=9606 GN=RALA PE=1 SV=1	19	8	2	1.40E+06	1.95E+06	2.30E+06	2.06E+06	1.39E+06	1.23E+06	1.34E+06	1.04E+06	7.84E+05	1.83E+06	6.05E+05	1.87E+06	1.12E+06	1.67	0.024126592	0.74		
P46783	40S ribosomal protein S10 OS=Homo sapiens OX=9606 GN=RPS10 PE=1 SV=1	15	58	2	1.40E+07	9.03E+06	5.81E+06	1.05E+07	6.21E+06	2.10E+07	1.30E+07	5.92E+06	6.69E+06	5.19E+06	5.44E+06	9.30E+06	6.69E+06	1.39	0.47	0.180156815	0.74	
Q75821	Eukaryotic translation initiation factor 3 subunit G OS=Homo sapiens OX=9606 GN=EIF3G PE=1 SV=2	13	6	2	1.42E+06	5.93E+05	1.07E+06	1.53E+06	1.20E+06	1.87E+06	7.54E+05	4.96E+05	6.39E+05	3.85E+05	6.48E+05	6.40E+05	1.28E+06	5.94E+05	2.16	0.10145098	0.81	
Q09439	Cationic 2 OS=Homo sapiens OX=9606 GN=CN2 PE=1 SV=4	13	25	2	7.21E+06	6.98E+06	6.20E+06	6.41E+06	6.43E+06	5.39E+06	3.22E+06	3.80E+06	3.37E+06	4.59E+06	4.59E+06	4.68E+06	1.42E+06	4.48E+06	1.42	0.02812715	1.42	
P22620	CAMP-dependent protein kinase catalytic subunit beta OS=Homo sapiens OX=9606 GN=PRKACB PE=1 SV=2	19	54	2	2.40E+06	2.58E+06	1.38E+06	1.91E+06	1.04E+06	1.31E+06	3.74E+06	3.37E+06	3.37E+06	2.01E+06	1.95E+06	2.70E+06	2.70E+06	2.70E+06	1.00	0.196465508	1.00	
P42167	Lamina-associated polypeptide 2, isoforms beta/gamma OS=Homo sapiens OX=9606 GN=LMP2 PE=1 SV=2	9	12	2	1.81E+06	4.74E+06	4.73E+06	5.04E+06	1.91E+06	1.74E+06	4.04E+06	4.56E+06	9.86E+05	4.55E+06	9.12E+05	3.37E+06	3.33E+06	3.07E+06	1.08	0.179534212	1.08	
P62847	40S ribosomal protein S24 OS=Homo sapiens OX=9606 GN=RPS24 PE=1 SV=1	20	53	2	1.47E+07	1.35E+07	1.13E+07	1.12E+07	1.10E+07	1.10E+07	8.79E+06	1.03E+07	4.09E+06	4.07E+06	6.75E+06	5.43E+06	1.15E+07	6.57E+06	0.12	0.005679177	0.81	
Q12805	EGF-containing fibronectin extracellular matrix protein 1 OS=Homo sapiens OX=9606 GN=EFEMP1 PE=1 SV=2	7	38	2	6.75E+06	5.72E+06	5.52E+06	5.18E+06	5.93E+06	5.62E+06	9.27E+06	7.99E+06	9.32E+06	7.23E+06	8.43E+06	7.68E+06	5.77E+06	8.39E+06	-0.54	0.00419633	0.25	
Q75436	Vacuolar protein sorting-associated protein 2beta OS=Homo sapiens OX=9606 GN=VPS26A PE=1 SV=2	9	7	2	2.20E+06	3.25E+06	2.25E+06	2.56E+06	2.50E+06	2.80E+06	1.72E+06	1.58E+06	1.91E+06	4.91E+05	1.57E+06	1.68E+06	1.18E+06	1.25	0.002179393	0.81		
Q09186	LIM domain and actin-binding protein OS=Homo sapiens OX=9606 GN=LIMA1 PE=1 SV=1	3	10	2	1.71E+06	3.05E+06	3.19E+06	3.09E+06	2.93E+06	2.67E+06	1.16E+06	1.16E+06	1.13E+06	8.99E+05	2.74E+06	1.05E+06	1.38E+06	1.38E+06	1.00	0.000447187	0.81	
Q15637	GTPase KRas OS=Homo sapiens OX=9606 GN=KRAS PE=1 SV=1	20	4	2	5.75E+06	5.75E+06	3.17E+06	3.74E+06	3.16E+06	6.91E+05	3.24E+06	5.89E+05	1.22E+06	2.25E+06	2.80E+06	3.38E+06	4.69E+06	3.66E+06	1.28	0.196465508	1.00	
Q9Y2V2	Calcium-regulated heat-stable protein 1 OS=Homo sapiens OX=9606 GN=CAHSP1 PE=1 SV=2	18	33	2	3.58E+06	5.70E+06	5.02E+06	6.87E+06	5.12E+06	4.47E+06	4.94E+06	5.38E+06	4.99E+06	3.25E+06	5.12E+06	4.48E+06	5.13E+06	4.69E+06	1.09	0.15481331	0.63	
P62306	Small nuclear ribonucleoprotein F OS=Homo sapiens OX=9606 GN=SNRPF PE=1 SV=1	24	28	2	6.90E+06	5.69E+06	4.66E+06	5.54E+06	4.52E+06	5.70E+06	4.06E+06	3.17E+06	4.53E+06	3.65E+06	2.24E+06	5.50E+06	3.62E+06	1.00	0.003112069	0.60		
Q35747	Serine/threonine-protein kinase OSR1 OS=Homo sapiens OX=9606 GN=OSR1 PE=1 SV=1	8	3	2	4.25E+06	4.57E+06	3.90E+06	1.91E+06	1.89E+06	1.48E+06	5.54E+06	1.79E+06	1.36E+06	5.28E+05	1.87E+06	1.78E+06	1.22E+06	1.46	0.66	0.282184988	0.55	
Q13414	Zinc finger Z-type and EF-hand domain containing protein OS=Homo sapiens OX=9606 GN=ZFP1 PE=1 SV=6	27	8	2	2.41E+06	3.90E+05	2.63E+06	1.91E+06	1.89E+06	1.48E+06	5.54E+06	1.79E+06	1.36E+06	5.28E+05	1.87E+06	1.78E+06	1.22E+06	1.46	0.66	0.282184988	0.55	
P23919	Thymidylate kinase OS=Homo sapiens OX=9606 GN=TYMK PE=1 SV=4	11	6	2	2.94E+06	4.06E+06	2.44E+06	3.19E+06	1.38E+06	2.23E+06	8.28E+05	9.57E+05	7.09E+05	1.12E+06	9.84E+05	2.71E+06	9.19E+05	2.95	1.56	0.004428635	0.68	
P55735	Protein SEC13 homolog OS=Homo sapiens OX=9606 GN=SEC13 PE=1 SV=3	7	25	2	5.31E+06	4.51E+06	5.39E+06	5.09E+06	5.09E+06	4.94E+06	3.58E+06	2.43E+06	3.88E+06	3.48E+06	3.24E+06	2.83E+06	5.20E+06	3.24E+06	1.68	5.55916E+05	0.56	
P61077	Ubiquitin-conjugating enzyme E2 D3 OS=Homo sapiens OX=9606 GN=UBE2D3 PE=1 SV=1	20	13	2	6.07E+06	7.24E+06	3.40E+06	6.96E+06	3.47E+06	4.51E+06	5.01E+06	5.01E+06	1.23E+06	1.97E+06	3.62E+06	2.70E+06	5.27E+06	2.95E+06	1.79	0.02630549	0.81	
Q04828	Aldo-keto reductase family 1 member C1 OS=Homo sapiens OX=9606 GN=AKR1C1 PE=1 SV=1	6	53	2	2.32E+07	2.60E+07	2.85E+07	3.19E+07	2.87E+07	2.68E+07	3.91E+07	4.12E+07	4.39E+07	4.28E+07	3.83E+07	3.38E+07	2.75E+07	3.98E+07	0.69	8.51919E+05	0.54	
Q10186	Nuclear transport factor 2 OS=Homo sapiens OX=9606 GN=NUP214 PE=1 SV=1	28	16	2	8.46E+06	7.74E+06	7.89E+06	1.19E+07	8.93E+06	1.19E+07	8.30E+06	8.68E+06	9.98E+06	9.89E+06	9.89E+06	8.86E+06	9.89E+06	1.08	0.000000000	0.81		
Q9JL86	Guanine nucleotide-binding protein (Gj)(Gs)(Go) subunit gamma-12 OS=Homo sapiens OX=9606 GN=GNNG12 PE=1 SV=3	32	24	2	4.59E+06	3.99E+06	3.58E+06	4.50E+06	3.75E+06	4.63E+06	2.32E+06	3.57E+06	3.32E+06	3.42E+06	2.77E+06	2.48E+06						

**Supplemental Table 4. List of all proteins identified by label free proteomics analysis.**

Accession	Description	Coverage [%]	# PSMs	# Unique Peptides	Antitriptyline 1	Antitriptyline 2	Antitriptyline 3	Antitriptyline 4	Antitriptyline 5	Antitriptyline 6	Vehicle 1	Vehicle 2	Vehicle 3	Vehicle 4	Vehicle 5	Vehicle 6	Average antitriptyline	Average vehicle	Ratio antitriptyline/vehicle	Log 2 fold change (antitriptyline/vehicle)	P-value
Q86U2P	Kinectin OS=Homo sapiens OX-9606 GN-KTNI PE=1 SV=1	2	24	2	2.46E+06	2.63E+06	1.77E+06	1.98E+06	2.40E+06	2.08E+06	3.20E+06	3.46E+06	4.07E+06	2.85E+06	3.49E+06	2.99E+06	2.22E+06	3.34E+06	1.50	0.000622413	-0.59
P61101	Signal recognition particle 54 kDa protein OS=Homo sapiens OX-9606 GN-SRPA4 PE=1 SV=1	4	24	2	5.49E+06	5.85E+06	4.43E+06	4.41E+06	4.56E+06	3.88E+06	2.99E+06	3.16E+06	2.52E+06	1.93E+06	1.35E+06	8.93E+05	2.45E+06	2.14E+06	0.87	0.000338126	2.22
P27144	Adenylate kinase 4, mitochondrial OS=Homo sapiens OX-9606 GN-AK4 PE=1 SV=1	13	10	1	1.90E+06	1.78E+06	1.90E+06	1.74E+06	1.57E+06	8.20E+05	1.08E+06	8.41E+05	9.82E+05	1.13E+06	6.88E+05	1.78E+06	9.23E+05	1.78E+06	1.93	0.00256E+06	1.93
P07947	Tyrosine protein kinase Yes OS=Homo sapiens OX-9606 GN-YES1 PE=1 SV=3	4	61	2	2.61E+06	2.97E+06	1.83E+06	3.08E+06	1.80E+06	3.72E+06	2.46E+06	1.78E+06	1.78E+06	2.20E+06	2.29E+06	3.06E+06	2.67E+06	2.26E+06	0.24	0.002676934	0.24
P23538	DNA (cytosine-5)-methyltransferase 1 OS=Homo sapiens OX-9606 GN-DNMT1 PE=1 SV=2	2	5	2	9.01E+06	1.31E+07	9.21E+06	1.39E+07	1.16E+07	8.94E+06	1.14E+07	1.67E+07	1.03E+07	1.82E+07	9.95E+06	8.96E+06	1.10E+07	1.26E+07	0.89	0.04317191	-0.19
P07947	Promoted cell death protein 1 OS=Homo sapiens OX-9606 GN-PCD1 PE=1 SV=2	2	5	2	2.32E+06	7.40E+06	6.87E+06	7.32E+06	6.87E+06	6.48E+06	5.05E+06	5.62E+06	5.62E+06	7.03E+06	5.87E+06	5.28E+06	5.28E+06	5.28E+06	0.55	0.008957405	1.47
PR2750	60S ribosomal protein L23a OS=Homo sapiens OX-9606 GN-LRPL23A PE=1 SV=1	16	13	2	2.05E+06	3.20E+06	4.58E+06	3.61E+06	4.56E+06	3.52E+06	3.35E+06	2.07E+06	2.07E+06	2.55E+06	2.50E+06	2.39E+06	3.58E+06	2.74E+06	1.31	0.100649406	-0.18
P51610	Host cell factor 1 OS=Homo sapiens OX-9606 GN-HCFC1 PE=1 SV=2	1	6	2	5.52E+05	6.93E+05	7.11E+05	8.62E+05	1.00E+06	6.99E+05	3.41E+05	4.28E+05	4.96E+05	3.59E+05	3.59E+05	1.00E+06	7.53E+05	4.06E+05	0.89	0.001781073	1.85
Q14247	Src substrate cortactin OS=Homo sapiens OX-9606 GN-CTTN PE=1 SV=2	4	6	2	4.76E+05	2.40E+06	3.21E+06	3.12E+06	3.31E+06	2.73E+06	1.74E+06	1.74E+06	4.98E+05	5.49E+05	1.00E+06	2.54E+06	9.48E+05	1.68	0.016237802	2.68	
P23233	Glutathione peroxidase 3 OS=Homo sapiens OX-9606 GN-GPX3 PE=1 SV=2	8	393	2	1.95E+07	4.04E+07	4.12E+07	2.03E+07	2.56E+07	3.69E+07	3.53E+07	6.21E+07	3.54E+07	4.91E+07	4.96E+07	3.06E+07	4.47E+07	4.47E+07	0.67	0.02723575	-0.57
Q3UKJ3	Protein mono-ADP-ribosyltransferase PARP4 OS=Homo sapiens OX-9606 GN-PARP4 PE=1 SV=3	2	8	2	2.21E+06	2.90E+06	3.27E+06	1.90E+06	9.45E+05	2.16E+06	1.46E+06	1.95E+06	4.85E+05	1.21E+06	6.30E+05	2.22E+06	3.26E+06	1.14E+06	1.96	0.031716787	0.97
P08463	Ketohexokinase OS=Homo sapiens OX-9606 GN-KHK1 PE=1 SV=2	6	8	2	3.07E+06	2.94E+06	2.94E+06	2.94E+06	2.94E+06	2.22E+06	2.22E+06	2.70E+06	2.70E+06	3.12E+06	2.84E+06	2.70E+06	2.70E+06	2.70E+06	1.08	0.357277000	0.11
QJUDY4	DnaJ homolog subfamily B member 4 OS=Homo sapiens OX-9606 GN-DNAJB4 PE=1 SV=1	6	16	2	2.79E+06	4.11E+06	2.55E+06	3.76E+06	2.43E+06	3.97E+06	3.23E+06	2.79E+06	2.62E+06	2.55E+06	2.18E+06	2.82E+06	3.27E+06	2.70E+06	1.21	0.13621765	1.21
P61373	60S ribosomal protein L38 OS=Homo sapiens OX-9606 GN-LRPL38 PE=1 SV=2	33	24	2	6.91E+06	8.91E+06	1.10E+07	1.27E+07	1.11E+07	1.09E+07	6.86E+06	6.07E+06	9.12E+06	7.97E+06	8.14E+06	4.21E+06	1.03E+07	7.06E+06	0.54	0.10947836	0.54
Q9K6G9	N-terminal kinase-like protein OS=Homo sapiens OX-9606 GN-SCYL1 PE=1 SV=1	4	4	2	9.96E+05	1.25E+06	1.15E+06	1.06E+06	9.06E+05	9.96E+05	7.44E+05	7.87E+05	8.02E+05	8.32E+05	5.91E+05	1.06E+06	7.69E+05	1.43	0.001253744	1.43	
Q8NB95	Solute carrier family 43 member 3 OS=Homo sapiens OX-9606 GN-SLC43A3 PE=1 SV=2	5	18	2	5.74E+06	5.90E+06	5.41E+06	5.53E+06	5.29E+06	5.06E+06	4.20E+06	3.98E+06	3.67E+06	4.13E+06	3.34E+06	3.41E+06	5.42E+06	3.79E+06	0.52	1.18139E+05	0.52
P09595	Cadherin alpha-1 (VX) chain OS=Homo sapiens OX-9606 GN-COL15A1 PE=1 SV=2	1	34	2	1.13E+07	1.23E+07	8.66E+06	9.25E+06	9.67E+06	9.40E+06	1.42E+07	1.56E+07	1.13E+07	1.32E+07	1.14E+07	1.19E+07	1.01E+07	1.29E+07	-0.36	0.10770158	-0.36
R01180	Phosphatidylcholine-sterol acyltransferase OS=Homo sapiens OX-9606 GN-LCAT PE=1 SV=1	1	7	2	1.35E+07	1.52E+07	2.86E+07	1.52E+07	1.37E+07	1.39E+07	1.22E+07	2.54E+07	2.44E+07	1.63E+07	1.86E+07	1.67E+07	2.18E+07	2.18E+07	0.77	0.10581358	0.77
Q15046	Lysine-tRNA ligase OS=Homo sapiens OX-9606 GN-KARS1 PE=1 SV=1	5	3	2	2.99E+06	4.24E+06	5.18E+06	4.11E+06	3.27E+06	3.57E+06	3.99E+06	4.41E+06	4.29E+06	2.60E+06	9.07E+05	4.04E+06	3.29E+06	1.23	0.0275313	1.23	
Q8NB87	Prostaglandin reductase 2 OS=Homo sapiens OX-9606 GN-PTGR2 PE=1 SV=1	6	5	2	5.54E+05	4.93E+05	4.03E+05	3.07E+05	4.17E+05	1.29E+06	1.19E+06	1.19E+06	1.28E+07	5.07E+05	7.07E+05	4.35E+05	8.36E+05	0.52	0.028612787	0.52	
Q9BRLL6	Serine/arginine-rich splicing factor 8 OS=Homo sapiens OX-9606 GN-SRSF8 PE=1 SV=1	5	30	2	9.24E+06	1.16E+07	1.06E+07	1.15E+07	1.13E+07	9.80E+06	1.12E+07	1.15E+07	1.28E+07	1.07E+07	1.10E+07	1.10E+07	1.10E+07	1.10E+07	-0.14	0.001034611	-0.14
Q8NF17	Nuclear pore complex protein Nup93 OS=Homo sapiens OX-9606 GN-NUP93 PE=1 SV=2	2	24	2	2.36E+06	3.34E+06	1.81E+06	3.22E+06	3.51E+06	2.74E+06	1.09E+06	2.32E+06	2.73E+06	3.10E+06	2.76E+06	6.81E+05	2.83E+06	2.11E+06	0.42	0.176452279	0.42
Q13428	Tracleal protein OS=Homo sapiens OX-9606 GN-TCOF1 PE=1 SV=3	2	2	2	4.03E+06	3.83E+06	3.10E+06	3.14E+06	3.03E+06	6.02E+06	1.08E+06	1.18E+06	7.72E+05	1.52E+06	1.61E+06	1.49E+06	3.71E+06	1.49	0.00394E+06	1.49	
P55991	Actin-related protein 2/3 complex subunit 4 OS=Homo sapiens OX-9606 GN-ARPC4 PE=1 SV=3	16	16	2	6.43E+06	6.02E+06	7.43E+06	8.29E+06	6.43E+06	6.02E+06	9.65E+06	8.99E+06	6.65E+06	6.65E+06	5.87E+06	5.87E+06	7.45E+06	5.87E+06	0.03	0.009822100	0.03
Q8UKQ1	DCC-interacting protein 13a-Alpha OS=Homo sapiens OX-9606 GN-APPL1 PE=1 SV=1	4	11	2	1.28E+06	1.72E+06	1.73E+06	1.90E+06	1.90E+06	1.61E+06	1.45E+06	1.68E+06	1.68E+06	2.16E+06	1.69E+06	1.69E+06	1.69E+06	1.69E+06	0.06	0.775288131	0.06
Q02572	AP-3 complex subunit sigma-1 OS=Homo sapiens OX-9606 GN-AP3S1 PE=1 SV=1	12	17	2	3.86E+06	4.73E+06	2.72E+06	3.73E+06	3.31E+06	2.87E+06	1.14E+06	1.98E+06	2.44E+06	1.21E+06	1.64E+06	3.53E+06	1.61E+06	1.14	0.000531902	-1.14	
P19367	Hoxo kinase 1 OS=Homo sapiens OX-9606 GN-HK1 PE=1 SV=3	3	4	2	3.13E+06	2.81E+06	2.68E+06	2.41E+06	2.91E+06	3.17E+06	1.54E+06	5.78E+05	6.01E+05	7.90E+05	1.16E+06	2.85E+06	1.91E+06	1.64	0.341232E+05	1.64	
Q03722	Leukocyte surface antigen CD47 OS=Homo sapiens OX-9606 GN-CD47 PE=1 SV=1	5	48	2	9.50E+06	1.04E+07	1.48E+07	1.07E+07	1.34E+07	9.27E+06	8.13E+06	8.44E+06	8.77E+06	7.23E+06	7.80E+06	5.50E+06	1.13E+07	7.63E+06	0.57	0.001746523	0.57
Q07074	cAMP-specific 3'-5'-cyclic phosphodiesterase OS=Homo sapiens OX-9606 GN-PDE5A PE=1 SV=2	2	3	2	1.03E+06	1.03E+06	3.54E+06	4.80E+06	3.33E+06	2.10E+06	1.71E+06	1.71E+06	1.27E+06	1.12E+06	5.49E+05	1.55E+06	1.55E+06	1.55E+06	1.56	0.012534034	1.56
Q8LKM9	RNA-binding protein Rly1 OS=Homo sapiens OX-9606 GN-RALY1 PE=1 SV=1	6	15	2	7.09E+06	7.58E+06	8.06E+06	8.79E+06	8.26E+06	7.94E+06	4.93E+06	5.13E+06	2.10E+06	1.68E+06	4.87E+06	4.17E+06	7.95E+06	3.81E+06	0.28	0.000363003	-0.28
Q13451	Peptidyl-prolyl cis-trans isomerase FKBP5 OS=Homo sapiens OX-9606 GN-FKBP5 PE=1 SV=2	4	6	2	1.49E+06	1.10E+06	1.05E+06	1.35E+06	1.26E+06	1.59E+06	5.90E+05	5.41E+05	6.33E+05	1.25E+06	1.94E+06	7.44E+06	3.88E+06	5.88E+05	2.12	0.000654801	2.12
Q12846	Syntaxin 4 OS=Homo sapiens OX-9606 GN-STX4 PE=1 SV=2	7	16	2	2.94E+06	3.41E+06	3.81E+06	3.40E+06	3.31E+06	4.01E+06	2.67E+06	2.33E+06	2.33E+06	2.51E+06	1.94E+06	7.44E+06	3.28E+06	1.06	0.82510637	1.06	
Q9Y272	AP-3 complex subunit mu-1 OS=Homo sapiens OX-9606 GN-AP3M1 PE=1 SV=1	4	14	2	1.09E+06	9.78E+05	2.17E+06	1.73E+06	1.85E+06	2.01E+06	7.78E+05	1.34E+06	1.43E+06	6.88E+05	1.07E+06	9.94E+05	1.64E+06	1.05E+06	1.56	0.035494254	1.56
Q06278	Adhylin oxidase OS=Homo sapiens OX-9606 GN-AOX1 PE=1 SV=2	4	15	2	9.74E+05	1.28E+06	1.51E+06	1.18E+06	1.65E+06	1.63E+06	1.63E+06	2.22E+06	2.07E+06	2.52E+06	1.84E+06	1.84E+06	1.24E+06	2.08E+06	0.75	0.001151574	0.75
Q11619	Lysosomal protective protein OS=Homo sapiens OX-9606 GN-LP1 PE=1 SV=2	5	6	2	3.91E+06	5.76E+06	4.01E+06	3.69E+06	2.68E+06	1.03E+06	2.19E+06	2.38E+06	2.46E+06	2.56E+06	7.96E+05	7.39E+05	3.51E+06	1.85E+06	1.89	0.05396254	1.89
Q7L106	Basic leucine zipper and W2 domain-containing protein 1 OS=Homo sapiens OX-9606 GN-BZW1 PE=1 SV=1	5	21	2	6.16E+06	2.55E+06	6.23E+06	1.76E+06	6.88E+06	5.53E+06	1.66E+06	5.89E+06	1.66E+06	5.54E+06	4.38E+06	4.38E+06	4.21E+06	4.38E+06	0.92	0.166694136	0.92
Q15400	Syntaxin 7 OS=Homo sapiens OX-9606 GN-STX7 PE=1 SV=4	8	5	2	2.07E+06	2.04E+06	1.94E+06	1.88E+06	1.79E+06	5.45E+05	7.99E+05	8.03E+05	9.77E+05	8.08E+05	4.67E+05	1.71E+06	7.71E+05	2.21	0.100986842	2.21	
Q7L3L4	MOB kinase activator 1B OS=Homo sapiens OX-9606 GN-MOB1B PE=1 SV=3	9	28	2	1.80E+06	2.28E+06	1.99E+06	2.92E+06	2.35E+06	2.73E+06	2.53E+06	2.65E+06	2.71E+06	2.90E+06	3.58E+06	2.06E+06	2.31E+06	2.74E+06	0.84	0.158892327	-0.25
P55991	Protein kinase C and zeta1 kinase substrate protein 2 OS=Homo sapiens OX-9606 GN-PKCPSIN2 PE=1 SV=2	2	2	2	1.82E+06	2.46E+06	2.44E+06	1.94E+06	2.05E+06	1.32E+06	1.04E+06	1.06E+06	9.35E+05	1.03E+06	1.03E+06	1.03E+06	1.03E+06	1.03E+06	1.06	0.000378853	1.06
P53634	Dipeptidyl peptidase 1 OS=Homo sapiens																				

Supplemental Table 4. List of all proteins identified by label free proteomics analysis.

Accession	Description	Coverage [%]	IPSM	# Unique Peptides	Antitripitlyne 1	Antitripitlyne 2	Antitripitlyne 3	Antitripitlyne 4	Antitripitlyne 5	Antitripitlyne 6	Vehicle 1	Vehicle 2	Vehicle 3	Vehicle 4	Vehicle 5	Vehicle 6	Average antitripitlyne	Average vehicle	Ratio antitripitlyne/vehicle	Log 2 fold change (antitripitlyne/vehicle)	P-value
P63000	Ras-related C3 botulinum toxin substrate 1 OS=Homo sapiens OX=9606 GN=RAC1 PE=1 SV=1	32	167	3	1.79E+07	1.57E+07	2.01E+07	1.65E+07	2.04E+07	2.06E+07	1.59E+07	1.37E+07	1.34E+07	2.28E+07	1.93E+07	1.74E+07	1.85E+07	1.74E+07	1.02	0.42026623	0.27
P62841	40S ribosomal protein S15 OS=Homo sapiens OX=9606 GN=RPS15 PE=1 SV=2	47	26	3	3.27E+06	5.01E+06	8.01E+06	7.10E+06	1.06E+07	6.31E+06	1.46E+06	2.96E+06	1.61E+06	1.78E+06	1.79E+06	6.71E+06	2.01E+07	3.30	0.005324168	1.72	0.005324168
Q15404	Ras suppressor protein 1 OS=Homo sapiens OX=9606 GN=RSU1 PE=1 SV=3	18	24	3	7.41E+06	4.48E+06	4.98E+06	4.55E+06	5.36E+06	7.44E+06	1.04E+07	6.71E+06	5.89E+06	5.43E+06	6.33E+06	8.81E+06	5.70E+06	7.09E+06	0.80	0.20287752	0.80
P31949	Protein S100-A11 OS=Homo sapiens OX=9606 GN=S100A11 PE=1 SV=2	54	29	3	8.61E+06	1.14E+07	9.65E+06	1.50E+07	1.41E+07	1.15E+07	7.54E+06	6.68E+06	7.26E+06	6.10E+06	6.39E+06	5.01E+06	1.17E+07	6.50E+06	-0.31	0.026676145	1.80
P40495	Winged GTP-binding protein RhoG OS=Homo sapiens OX=9606 GN=RHOG PE=1 SV=1	24	33	3	4.73E+06	5.01E+06	3.07E+06	2.99E+06	3.57E+06	4.28E+06	3.83E+06	3.86E+06	3.58E+06	3.38E+06	2.18E+06	3.15E+06	3.94E+06	3.33E+06	1.18	0.119194838	0.24
Q92323	Cotomycin subunit 2 OS=Homo sapiens OX=9606 GN=COT2 PE=1 SV=1	9	9	3	2.43E+06	2.29E+06	2.29E+06	2.29E+06	2.29E+06	6.19E+06	3.19E+06	3.19E+06	3.19E+06	3.19E+06	3.19E+06	3.19E+06	3.19E+06	3.19E+06	2.38	0.001200033	0.25
Q92323	Rho repeat-containing protein 61 OS=Homo sapiens OX=9606 GN=WRD61 PE=1 SV=1	23	16	3	2.14E+06	5.11E+06	2.03E+06	4.60E+06	3.37E+06	6.92E+06	2.87E+06	1.57E+06	2.31E+06	1.58E+06	4.04E+06	2.78E+06	1.03E+06	2.53E+06	0.67	0.122966144	0.24
P15927	Replication protein A 32 kDa subunit OS=Homo sapiens OX=9606 GN=RP2 PE=1 SV=1	22	56	3	1.06E+07	9.71E+06	9.30E+06	1.04E+07	9.73E+06	1.28E+07	1.02E+07	9.23E+06	6.87E+06	9.28E+06	1.10E+07	5.91E+06	1.04E+07	8.76E+06	1.19	0.11767167	0.25
P62330	ADP-ribosylation factor 6 OS=Homo sapiens OX=9606 GN=ARF6 PE=1 SV=2	26	42	3	2.15E+06	1.06E+07	7.30E+06	4.05E+06	7.36E+06	4.72E+06	8.07E+06	9.68E+06	7.09E+06	4.89E+06	1.00E+07	8.31E+06	6.03E+06	8.1E+06	-0.43	0.18488461	0.43
Q87AQ2	SWI/SNF complex subunit SMARCC2 OS=Homo sapiens OX=9606 GN=SMARCC2 PE=1 SV=1	4	14	3	4.48E+06	4.92E+06	5.77E+06	7.20E+06	4.67E+06	5.94E+06	2.73E+06	2.63E+06	2.21E+06	2.82E+06	3.00E+06	2.74E+06	6.00E+06	2.89E+06	2.23	0.19691891	0.68
P21810	Blyssin OS=Homo sapiens OX=9606 GN=BLGN PE=1 SV=2	13	34	3	6.09E+06	5.35E+06	3.99E+06	5.36E+06	4.59E+06	6.28E+06	1.21E+07	5.59E+06	4.99E+06	8.88E+06	6.37E+06	7.98E+06	4.78E+06	7.88E+06	0.62	0.038928016	0.68
Q92323	Pol II RNA polymerase subunit 2 OS=Homo sapiens OX=9606 GN=POLR2B PE=1 SV=1	12	31	3	4.95E+06	4.79E+06	2.61E+06	2.61E+06	2.61E+06	3.12E+06	2.61E+06	2.61E+06	2.61E+06	2.61E+06	2.61E+06	2.61E+06	2.61E+06	2.61E+06	0.92	0.001200033	0.25
P42285	Exosome RNA helicase MTR4 OS=Homo sapiens OX=9606 GN=MTRX PE=1 SV=3	5	12	3	3.09E+06	3.37E+06	4.06E+06	4.75E+06	5.08E+06	3.52E+06	1.65E+06	1.33E+06	1.20E+06	1.65E+06	6.84E+05	3.98E+06	1.30E+06	1.61	0.000117013	1.00	0.000117013
P21291	Cysteine and glycine-rich protein 1 OS=Homo sapiens OX=9606 GN=CSR1 PE=1 SV=3	25	62	3	1.04E+07	9.40E+06	8.88E+06	7.95E+06	8.89E+06	9.35E+06	1.14E+07	9.83E+06	6.78E+06	9.81E+06	8.28E+06	8.63E+06	9.15E+06	9.01E+06	3.06	0.060538045	1.61
P17858	ATP-dependent 6-phosphofructokinase, liver type OS=Homo sapiens OX=9606 GN=PFKL PE=1 SV=6	9	49	3	1.82E+07	1.79E+07	1.92E+07	1.88E+07	1.73E+07	1.68E+07	2.21E+07	2.23E+07	2.23E+07	2.20E+07	1.92E+07	1.73E+07	1.80E+07	2.09E+07	0.86	0.020948453	0.86
P23270	CD70 antigen OS=Homo sapiens OX=9606 GN=CD70 PE=1 SV=2	20	30	3	1.86E+07	1.13E+07	1.19E+07	1.16E+07	1.21E+07	1.14E+07	1.12E+07	8.49E+06	6.30E+06	5.81E+06	8.42E+06	9.84E+06	1.28E+07	8.34E+06	0.62	0.01192165	0.62
P62330	Small nuclear ribonucleoprotein E OS=Homo sapiens OX=9606 GN=SNRPE PE=1 SV=1	52	155	3	2.05E+07	1.82E+07	1.41E+07	1.18E+07	1.39E+07	2.10E+07	1.32E+07	1.50E+07	1.21E+07	1.20E+07	1.17E+07	1.49E+07	1.66E+07	1.31E+07	1.26	0.029490098	0.94
P42895	Ethanol-converting enzyme 1 OS=Homo sapiens OX=9606 GN=ECE1 PE=1 SV=2	29	31	3	5.52E+06	6.39E+06	6.98E+06	5.27E+06	6.74E+06	6.57E+06	6.50E+06	1.77E+06	2.15E+06	4.78E+06	1.90E+06	3.39E+06	3.39E+06	3.39E+06	1.68	0.029490098	0.94
P08708	80S ribosomal protein S17 OS=Homo sapiens OX=9606 GN=RPS17 PE=1 SV=2	52	14	3	1.13E+07	1.01E+07	7.76E+06	8.73E+06	9.87E+06	2.10E+07	6.05E+06	4.98E+06	3.76E+06	4.95E+06	5.07E+06	5.15E+06	9.46E+06	5.07E+06	1.87	0.549057016	0.30
Q14828	Secretory carrier-associated membrane protein 3 OS=Homo sapiens OX=9606 GN=SCAMP3 PE=1 SV=3	16	26	3	9.22E+06	8.90E+06	6.67E+06	5.95E+06	5.74E+06	5.75E+06	6.17E+06	4.88E+06	3.37E+06	4.07E+06	3.78E+06	6.36E+05	7.05E+06	3.82E+06	1.85	0.009062845	0.86
Q98715	Collagen alpha-1(XII) chain OS=Homo sapiens OX=9606 GN=COL12A1 PE=1 SV=2	2	18	3	2.11E+06	2.87E+06	1.81E+06	1.95E+06	1.27E+06	1.85E+06	4.92E+06	1.88E+06	3.35E+06	4.07E+06	5.32E+06	4.21E+06	2.08E+06	4.0E+06	0.51	-0.97	0.010035328
P54578	Ubiquitin carboxyl-terminal hydrolase 14 OS=Homo sapiens OX=9606 GN=UHP14 PE=1 SV=3	11	13	3	8.00E+05	3.31E+06	4.02E+06	4.04E+06	4.04E+06	3.42E+06	4.46E+06	9.48E+05	2.06E+06	4.26E+06	3.44E+06	2.48E+06	3.41E+06	2.94E+06	1.14	0.567349191	1.14
Q13443	Disintegrin and metalloprotease domain-containing protein 9 OS=Homo sapiens OX=9606 GN=ADAM9 PE=1 SV=1	12	11	3	4.87E+06	3.13E+06	4.14E+06	4.21E+06	5.26E+06	5.45E+06	1.78E+06	2.37E+06	1.52E+06	2.39E+06	1.23E+06	1.62E+06	4.82E+06	1.85E+06	2.61	0.000866313	0.80
P48735	Isostrate dehydrogenase [NADP], mitochondrial OS=Homo sapiens OX=9606 GN=IDH2 PE=1 SV=2	11	13	3	8.07E+05	7.89E+05	6.83E+05	6.10E+05	7.08E+05	5.85E+05	6.74E+05	2.95E+06	3.15E+06	4.54E+06	3.15E+06	2.38E+06	3.76E+06	3.76E+06	1.74	0.001774218	1.74
Q93627	COP9 signalosome complex subunit 8 OS=Homo sapiens OX=9606 GN=COPS8 PE=1 SV=1	28	18	3	1.59E+06	1.82E+06	9.21E+05	9.16E+05	7.90E+05	1.01E+06	7.07E+05	6.01E+06	7.07E+05	6.01E+06	6.16E+05	5.87E+05	1.17E+06	6.62E+05	0.83	0.030582485	0.83
Q86Y82	Syntaxin-12 OS=Homo sapiens OX=9606 GN=STX12 PE=1 SV=1	15	46	3	7.71E+06	6.97E+06	8.61E+06	1.01E+07	8.83E+06	6.06E+06	5.94E+06	4.74E+06	6.24E+06	5.77E+06	4.26E+06	4.68E+06	8.05E+06	6.29E+05	1.52	0.603781413	1.52
Q12906	Interleukin enhancer-binding factor 3 OS=Homo sapiens OX=9606 GN=ILF3 PE=1 SV=3	8	14	3	4.27E+06	5.29E+06	6.83E+06	4.64E+06	5.31E+06	3.90E+06	2.77E+06	2.79E+06	2.01E+06	2.61E+06	2.40E+06	2.74E+06	5.04E+06	2.55E+06	1.97	0.001455152	1.97
P14923	Junctation plinkin OS=Homo sapiens OX=9606 GN=JUP PE=1 SV=1	10	39	3	3.99E+06	5.24E+06	2.88E+06	3.26E+06	5.90E+06	3.71E+06	1.97E+06	5.34E+06	1.43E+06	3.03E+06	2.72E+06	2.13E+06	4.16E+06	2.77E+06	0.58	0.089176842	0.58
P20748	Complement component C9 OS=Homo sapiens OX=9606 GN=C9 PE=1 SV=1	10	132	3	6.02E+06	6.17E+07	4.60E+07	5.40E+07	4.79E+07	4.82E+07	8.75E+07	6.38E+07	6.38E+07	6.38E+07	6.17E+07	6.05E+07	6.45E+07	6.45E+07	0.76	0.032326044	0.76
Q13428	Beta-2-syngrophin OS=Homo sapiens OX=9606 GN=SNTR2 PE=1 SV=1	18	18	3	4.64E+06	4.10E+06	4.50E+06	4.50E+06	3.46E+06	4.02E+06	3.82E+06	2.69E+06	4.82E+06	2.69E+06	4.82E+06	2.69E+06	2.84E+06	2.84E+06	0.59	0.049038988	0.59
P62318	Small nuclear ribonucleoprotein Sm D3 OS=Homo sapiens OX=9606 GN=SNRPD3 PE=1 SV=1	32	68	3	3.72E+07	3.71E+07	3.50E+07	3.16E+07	4.61E+07	5.02E+07	2.68E+07	2.82E+07	2.68E+07	2.99E+07	2.18E+07	6.23E+07	3.92E+07	2.60E+07	1.51	0.00469065	1.51
P12821	Angiotensin-converting enzyme OS=Homo sapiens OX=9606 GN=ACE PE=1 SV=1	2	20	3	9.35E+06	8.17E+06	4.80E+06	8.74E+06	7.11E+06	6.21E+06	1.96E+06	7.56E+06	6.54E+06	6.35E+06	7.71E+06	5.37E+06	7.40E+06	7.12E+06	0.36	0.000777776	0.36
P52788	Spermine synthase OS=Homo sapiens OX=9606 GN=SMS PE=1 SV=2	20	10	3	1.42E+06	1.07E+06	6.34E+05	1.06E+06	8.10E+05	1.64E+06	1.13E+06	5.48E+05	5.48E+05	5.48E+05	6.88E+05	6.52E+05	1.11E+06	8.49E+05	1.30	0.354421139	1.30
P56537	Eukaryotic translation initiation factor 6 OS=Homo sapiens OX=9606 GN=EIF6 PE=1 SV=1	22	20	3	1.09E+07	1.14E+07	7.61E+06	9.90E+06	8.97E+06	1.01E+07	8.15E+06	8.81E+06	8.57E+06	7.42E+06	8.71E+06	6.75E+06	9.82E+06	8.07E+06	1.22	0.027317347	1.22
P20748	3-mercaptopyruvate sulfurtransferase OS=Homo sapiens OX=9606 GN=CSPT1 PE=1 SV=3	21	33	3	3.85E+06	8.40E+06	2.51E+06	3.48E+06	3.86E+06	5.10E+06	5.29E+06	4.91E+06	2.40E+06	5.09E+06	1.45E+06	4.96E+06	4.64E+06	4.45E+06	1.04	0.841755611	1.04
P62070	Ras-related protein R-Ras2 OS=Homo sapiens OX=9606 GN=RRAS2 PE=1 SV=1	21	56	3	1.52E+07	1.58E+07	1.89E+07	1.71E+07	1.47E+07	1.48E+07	1.20E+07	1.18E+07	5.96E+06	1.33E+07	1.19E+07	8.65E+06	1.60E+07	1.06E+07	0.58	0.004012113	0.58
P28066	Proteasome subunit alpha type-5 OS=Homo sapiens OX=9606 GN=PSMA5 PE=1 SV=3	17	48	3	2.50E+07	2.49E+07	2.12E+07	2.53E+07	2.56E+07	7.09E+06	6.80E+06	7.02E+06	7.89E+06	6.72E+06	6.19E+06	5.17E+06	2.15E+07	6.63E+06	3.24	0.1700379693	3.24
P28062	Proteasome subunit beta type-8 OS=Homo sapiens OX=9606 GN=PSMB8 PE=1 SV=3	13	36	3	9.14E+06	7.92E+06	1.14E+07	1.03E+07	1.01E+07	9.85E+06	9.38E+06	8.91E+06	9.82E+06	8.68E+06	7.70E+06	9.77E+06	8.72E+06	1.16	0.104466351	1.16	
Q15366	Poly(O-C)-binding protein OS=Homo sapiens OX=9606 GN=PCBP2 PE=1 SV=1	1	38	3	1.36E+07	1.16E+07	9.14E+06	9.14E+06	8.63E+06	9.61E+06	9.56E+06	5.60E+									

# Supplemental Table 4. List of all proteins identified by label free proteomics analysis.

Accession	Description	Coverage [%]	iPSM#	# Unique Peptides	Antitrypticlyne 1	Antitrypticlyne 2	Antitrypticlyne 3	Antitrypticlyne 4	Antitrypticlyne 5	Antitrypticlyne 6	Vehicle 1	Vehicle 2	Vehicle 3	Vehicle 4	Vehicle 5	Vehicle 6	Average antitrypticlyne	Average vehicle	Ratio antitrypticlyne/vehicle	Log2 fold change (antitrypticlyne/vehicle)	P-value	
Q14117	Dihydropyrimidinase OS=Homo sapiens OX=9606 GN=DPVYS PE=1 SV=1	6	40	3	3.43E+06	4.63E+06	5.54E+06	6.17E+06	5.23E+06	4.08E+06	6.61E+06	6.97E+06	8.02E+06	8.69E+06	7.29E+06	5.87E+06	4.85E+06	7.24E+06	0.87	-0.58	0.00229304	
Q9NY12	H/ACA ribonucleoprotein complex subunit 1 OS=Homo sapiens OX=9606 GN=GAR1 PE=1 SV=1	16	30	3	4.55E+06	2.57E+06	3.93E+06	3.39E+06	3.79E+06	4.76E+06	2.37E+06	3.31E+06	2.52E+06	3.14E+06	2.82E+06	2.05E+06	3.97E+06	2.70E+06	1.47	0.56	0.008748343	
P49026	Malate dehydrogenase, mitochondrial OS=Homo sapiens OX=9606 GN=MDH2 PE=1 SV=3	3	25	3	2.25E+06	9.30E+05	1.23E+06	1.56E+06	1.31E+06	1.33E+06	3.56E+06	7.83E+05	1.54E+06	1.15E+06	1.55E+06	1.44E+06	1.72E+06	1.44E+06	0.84	-0.26	0.609708468	
P78344	Eukaryotic translation initiation factor 4 gamma 2 OS=Homo sapiens OX=9606 GN=EIF4G2 PE=1 SV=1	11	8	3	1.11E+06	8.26E+05	1.50E+06	1.72E+05	9.79E+05	1.68E+06	6.40E+05	1.89E+06	2.91E+05	1.18E+06	6.40E+05	1.14E+06	9.28E+05	1.14E+06	1.23	0.30	0.51971241	
P20042	Eukaryotic translation initiation factor 2 subunit 2 OS=Homo sapiens OX=9606 GN=EIF2S2 PE=1 SV=2	9	22	3	5.03E+06	4.03E+06	5.94E+06	7.06E+06	6.62E+06	5.32E+06	3.71E+06	3.81E+06	4.53E+06	3.86E+06	3.74E+06	3.78E+06	5.69E+06	3.91E+06	1.45	0.54	0.009558287	
P20042	ATPase, mitochondrial OS=Homo sapiens OX=9606 GN=ATP10 PE=1 SV=1	12	15	3	4.32E+06	2.14E+06	4.58E+06	4.26E+06	6.23E+06	4.32E+06	1.85E+06	1.11E+06	1.53E+06	4.33E+06	2.35E+06	3.93E+06	1.56E+06	2.97E+06	1.27	0.34	0.05671304	
P26196	Probable ATP-dependent RNA helicase DDX2 OS=Homo sapiens OX=9606 GN=DDX2 PE=1 SV=2	8	15	3	3.22E+06	3.14E+06	2.29E+06	3.33E+06	1.83E+06	2.45E+06	2.27E+06	1.09E+06	6.47E+05	1.86E+06	1.60E+06	1.90E+06	2.72E+06	1.44E+06	1.89	0.94	0.003851984	
Q9HC38	Glyoxalase domain-containing protein 4 OS=Homo sapiens OX=9606 GN=GLOD4 PE=1 SV=1	10	47	3	9.93E+06	1.02E+07	1.11E+07	9.27E+06	9.46E+06	1.08E+07	1.32E+07	1.28E+07	1.33E+07	1.19E+07	1.37E+07	1.05E+07	1.01E+07	1.26E+07	0.80	-0.32	0.002170711	
P30044	Peroxisome-anchored protein 1 OS=Homo sapiens OX=9606 GN=PRDX5 PE=1 SV=4	30	6	3	1.33E+06	6.28E+05	3.22E+06	2.47E+06	9.15E+05	3.91E+06				1.03E+06	2.48E+05	2.08E+06	6.37E+05	1.71	0.37	0.00873926		
Q13045	Protein flightless-1 homolog OS=Homo sapiens OX=9606 GN=FLII PE=1 SV=2	3	26	3	5.91E+06	3.77E+06	4.98E+06	5.44E+06	4.84E+06	2.18E+06	4.21E+06	3.45E+06	2.83E+06	4.22E+06	3.43E+06	2.74E+06	4.89E+06	3.48E+06	1.41	0.49	0.003001446	
Q94444	Cotasterone synthase OS=Homo sapiens OX=9606 GN=ACRNI PE=1 SV=1	10	30	3	4.5E+06	3.70E+06	3.39E+06	3.58E+06	3.03E+06	4.8E+06	2.09E+06	2.04E+06	2.15E+06	2.59E+06	1.30E+06	8.04E+05	3.29E+06	1.78E+06	1.95	0.89	0.002042845	
Q96039	60S ribosomal protein L24 OS=Homo sapiens OX=9606 GN=L24 PE=1 SV=1	16	52	3	2.29E+07	2.14E+07	2.16E+07	2.21E+07	2.15E+07	2.06E+07	1.48E+07	1.48E+07	1.39E+07	1.55E+07	1.39E+07	1.22E+07	1.34E+07	1.34E+07	1.66	0.17	0.562571061	
O00339	Matrin-2 OS=Homo sapiens OX=9606 GN=MATN2 PE=1 SV=4	5	13	3	3.03E+06				1.05E+06		4.13E+06	1.56E+06		3.02E+06	1.19E+06		2.04E+06	1.82E+06	0.82	-0.22	0.751689207	
Q9NQW7	Xaa-Pro aminopeptidase 1 OS=Homo sapiens OX=9606 GN=XPNPE1 PE=1 SV=3	5	32	3	5.13E+06	5.81E+06	3.12E+06	3.59E+06	3.14E+06	7.20E+06	8.32E+06	7.01E+06	6.54E+06	6.08E+06	5.48E+06	4.12E+06	6.77E+06	6.77E+06	-0.72	0.01427047	0.000424264	
P62851	40S ribosomal protein S25 OS=Homo sapiens OX=9606 GN=RPS25 PE=1 SV=1	22	93	3	5.64E+07	5.37E+07	6.71E+07	5.58E+07	7.96E+07	7.19E+07	4.00E+07	3.70E+07	4.91E+07	5.63E+07	4.21E+07	4.10E+07	6.41E+07	4.43E+07	1.45	0.53	0.004167895	
Q14847	LM and SH3 domain protein 1 OS=Homo sapiens OX=9606 GN=LASPI PE=1 SV=2	13	42	3	5.68E+06	6.65E+06	6.00E+06	5.56E+06	5.79E+06	5.48E+06	3.40E+06	3.40E+06	4.39E+06	5.69E+06	3.31E+06	2.42E+06	5.86E+06	3.77E+06	0.63	-0.004726468	0.000433346	
Q96039	Elongation factor 3, mitochondrial OS=Homo sapiens OX=9606 GN=EFM3 PE=1 SV=2	4	10	3	3.10E+06	2.99E+06	2.11E+06	2.58E+06	2.25E+06	2.17E+06	1.77E+06	8.56E+05	1.32E+06	1.15E+06	1.46E+06	7.14E+05	2.53E+06	1.21E+06	1.06	0.000433346	0.000433346	
Q9Y377	Endophilin B1 OS=Homo sapiens OX=9606 GN=SHCCLB1 PE=1 SV=1	4	10	3	1.53E+06	4.09E+06	4.09E+06	3.87E+06	3.40E+06	3.40E+06	3.63E+06	3.64E+06	3.52E+06	3.00E+06	2.84E+06	3.35E+06	3.35E+06	3.35E+06	1.00	0.00	0.985668439	
P49002	Cytosolic purine 5'-nucleotidase OS=Homo sapiens OX=9606 GN=N5C2 PE=1 SV=1	8	5	3	1.33E+06	5.91E+05	6.87E+05	6.10E+05	2.89E+05	6.17E+05	1.27E+06	1.08E+06	1.08E+06	1.47E+06	6.84E+05	8.30E+05	8.88E+05	8.88E+05	-0.07	-0.82136733	0.000433346	
P18885	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase gamma-2 OS=Homo sapiens OX=9606 GN=PLCG2 PE=1 SV=4	3	14	3	2.60E+06	2.35E+06	2.25E+06	1.75E+06	1.82E+06	2.63E+06	3.10E+06	3.38E+06	4.39E+06	3.84E+06	2.75E+06	2.64E+06	2.23E+06	3.36E+06	0.67	-0.59	0.00746715	
P05198	Eukaryotic translation initiation factor 2 subunit 1 OS=Homo sapiens OX=9606 GN=EIF2S1 PE=1 SV=3	9	62	3	1.57E+07	1.64E+07	1.48E+07	1.58E+07	1.60E+07	1.46E+07	1.58E+07	1.49E+07	1.55E+07	1.41E+07	1.16E+07	1.56E+07	1.56E+07	1.44E+07	0.11	-0.134565866	0.000433346	
P27701	CD82 double-strand break repair protein OS=Homo sapiens OX=9606 GN=CD82 PE=1 SV=1	15	18	3	3.48E+06	2.75E+06	4.50E+06	9.13E+06	4.64E+06	3.87E+06	2.62E+06	6.00E+06	8.98E+06	6.31E+06	4.27E+06	4.88E+06	4.95E+06	5.51E+06	0.90	-0.16	0.670793977	
P49659	Double-strand break repair protein NRE111 OS=Homo sapiens OX=9606 GN=NRE111 PE=1 SV=3	6	10	3	1.05E+06	1.15E+06	1.43E+06	1.08E+06	1.08E+06	1.10E+06	1.10E+06	1.10E+06	1.10E+06	1.10E+06	1.10E+06	1.10E+06	1.10E+06	1.10E+06	1.10E+06	0.64	0.015661392	0.000433346
P14324	Farnesyl pyrophosphate transferase OS=Homo sapiens OX=9606 GN=FPDS PE=1 SV=1	6	5	3	5.44E+06	6.80E+06	5.81E+06	5.70E+06	1.01E+06	1.44E+06	2.21E+06	1.65E+06	7.02E+05	1.65E+06	3.20E+06	5.94E+06	1.38E+06	1.24E+06	1.12	0.000433346	0.000433346	
Q6QNZ2	Cavolae-associated protein 1 OS=Homo sapiens OX=9606 GN=CAVIN1 PE=1 SV=1	8	26	3	5.89E+06	6.94E+06	8.46E+06	8.54E+06	8.49E+06	6.84E+06	3.24E+06	2.50E+06	2.18E+06	2.57E+06	2.25E+06	1.95E+06	6.73E+06	7.53E+06	3.09	0.63	2.60723E+05	
Q6O264	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5 OS=Homo sapiens OX=9606 GN=SMARCA5 PE=1 SV=1	3	17	3	4.11E+06	4.77E+06	3.77E+06	4.28E+06	3.75E+06	3.72E+06	1.78E+06	2.12E+06	1.49E+06	2.06E+06	2.28E+06	2.20E+06	4.07E+06	1.99E+06	1.03	1.03	3.27802E+05	
Q7S116	Rho-associated protein kinase 2 OS=Homo sapiens OX=9606 GN=ROCK2 PE=1 SV=4	3	7	3	7.20E+05	9.83E+05	1.19E+06	9.49E+05	4.24E+05	1.92E+06	2.33E+06	1.43E+06	1.82E+06	1.74E+06	1.54E+06	1.57E+06	1.03E+06	1.74E+06	0.59	-0.71	0.18981965	
Q15057	Arg-GAP with coiled-coil, ANK repeat and PH domain-containing protein 2 OS=Homo sapiens OX=9606 GN=ACAP2 PE=1 SV=3	6	23	3	3.98E+06	7.92E+06	1.13E+07	1.85E+07	1.19E+07	9.56E+06	9.70E+06	8.77E+06	7.41E+06	3.37E+06	3.39E+06	5.91E+06	1.05E+07	6.42E+06	0.75	-0.07	0.108354226	
P23831	Tryptophan-tRNA ligase, cytosolic OS=Homo sapiens OX=9606 GN=TWARS PE=1 SV=2	18	58	3	1.76E+06	1.76E+06	1.93E+06	1.43E+06	1.56E+06	1.27E+06	3.65E+06	1.43E+06	1.37E+06	6.82E+06	6.82E+06	4.70E+06	1.50E+06	1.50E+06	1.16	0.000433346	0.000433346	
Q95445	Apolipoprotein M OS=Homo sapiens OX=9606 GN=APOM1 PE=1 SV=2	18	58	3	4.67E+07	4.75E+07	4.75E+07	4.04E+07	4.82E+07	3.66E+07	6.34E+07	6.73E+07	5.99E+07	4.70E+07	4.70E+07	4.70E+07	4.70E+07	4.70E+07	0.84	0.004202983	0.000433346	
P10643	Complement component C7 OS=Homo sapiens OX=9606 GN=C7 PE=1 SV=2	2	66	3	2.89E+07	2.55E+07	1.75E+07	2.02E+07	1.89E+07	2.26E+07	3.47E+07	4.28E+07	2.49E+07	2.49E+07	2.22E+07	2.71E+07	2.22E+07	2.71E+07	0.32	-0.42	0.066148483	
Q10474	Protein arginine N-methyltransferase 5 OS=Homo sapiens OX=9606 GN=PRMT5 PE=1 SV=4	5	20	3	7.49E+06	1.01E+07	8.38E+06	8.59E+06	8.66E+06	5.17E+06	9.24E+06	2.00E+06	1.51E+06	1.03E+06	7.46E+06	1.82E+06	7.89E+06	5.21E+06	0.60	-0.20	2.01352765	
P06132	Uroporphyrinogen decarboxylase OS=Homo sapiens OX=9606 GN=UROD PE=1 SV=2	9	34	3	7.46E+06	6.25E+06	5.11E+06	3.84E+06	6.43E+06	2.66E+06	7.14E+06	7.85E+06	3.98E+06	6.87E+06	7.15E+06	5.76E+06	6.79E+06	6.79E+06	-0.24	-0.21858482	0.000433346	
P23229	Integrin alpha-8 OS=Homo sapiens OX=9606 GN=ITGA8 PE=1 SV=5	3	12	3	3.92E+05	6.07E+06	6.50E+06	7.27E+06	6.50E+06	1.11E+06	4.19E+06	6.23E+06	7.28E+06	5.38E+06	8.45E+06	6.61E+06	6.30E+06	1.05	0.07	0.17171384		
Q96039	Hemoglobin beta OS=Homo sapiens OX=9606 GN=HBGB PE=1 SV=3	5	47	3	3.92E+05	1.42E+06	2.18E+06	1.42E+06	1.42E+06	1.11E+06	4.19E+06	7.58E+06	6.23E+06	7.28E+06	5.38E+06	8.45E+06	6.61E+06	6.30E+06	1.05	0.07	0.17171384	
Q96039	Immunoglobulin superfamily member 8 OS=Homo sapiens OX=9606 GN=IGSF8 PE=1 SV=1	5	23	3	3.35E+06	2.72E+06	4.16E+06	4.29E+06	3.81E+06	2.21E+06	2.14E+06	2.03E+06	2.14E+06	2.16E+06	1.83E+06	3.66E+06	2.08E+06	1.76	0.82	0.000820177		
Q00059	Transcription factor A, mitochondrial OS=Homo sapiens OX=9606 GN=TFAM PE=1 SV=1	3	12	3	7.65E+06	8.65E+06	8.05E+06	9.73E+06	8.79E+06	7.88E+06	3.69E+06	7.24E+06	7.11E+06	6.92E+06	3.76E+06	6.09E+06	8.46E+06	5.80E+06	1.46	0.54	0.00907494	
P18077	60S ribosomal protein L35a OS=Homo sapiens OX=9606 GN=L35A PE=1 SV=2	22	73	3	1.62E+07	1.57E+07	1.60E+07	1.64E+07	1.63E+07	1.59E+07	1.46E+07	1.51E+07	1.59E+07	1.43E+07	1.35E+07	1.14E+07	1.64E+07	1.41E+07	0.21	-0.015389441	0.000433346	
Q9Y978	Bisphosphoglycerate kinase OS=Homo sapiens OX=9606 GN=AC02 PE=1 SV=2	4	14	3	1.55E+06	1.89E+06	2.20E+06	1.45E+06	1.65E+06	2.29E+06	1.48E+06	1.54E+06	2.02E+06									

**Supplemental Table 4. List of all proteins identified by label free proteomics analysis.**

Accession	Description	Coverage [%]	# PSMs	# Unique Peptides	Antitriptyline 1	Antitriptyline 2	Antitriptyline 3	Antitriptyline 4	Antitriptyline 5	Antitriptyline 6	Vehicle 1	Vehicle 2	Vehicle 3	Vehicle 4	Vehicle 5	Vehicle 6	Average antitriptyline	Average vehicle	Ratio antitriptyline/vehicle	Log 2 fold change (antitriptyline/vehicle)	P-value
Q9BXJ4	Complement C1q tumor necrosis factor-related protein 3 OS=Homo sapiens OX=9606 GN=C10TNF3 PE=1 Sv=1	13	74	4	2.71E+07	2.37E+07	2.01E+07	2.30E+07	2.01E+07	1.75E+07	3.27E+07	2.61E+07	2.44E+07	2.18E+07	1.86E+07	1.76E+07	2.19E+07	2.35E+07	1.07	-0.10	0.55721439
Q92542	Nicastrin OS=Homo sapiens OX=9606 GN=NCSTN PE=1 Sv=2	10	10	4	6.13E+06	4.68E+06	4.07E+06	4.39E+06	5.85E+06	5.45E+06	1.24E+06	1.39E+06	1.33E+06	2.15E+06	1.36E+06	1.84E+06	5.09E+06	3.50E+06	1.45	1.72	3.50612E-05
P00738	Hypatoglobulin OS=Homo sapiens OX=9606 GN=HP PE=1 Sv=1	10	91	4	3.01E+07	2.98E+07	2.57E+07	2.76E+07	2.37E+07	1.92E+07	3.19E+07	2.94E+07	2.66E+07	3.06E+07	2.07E+07	1.82E+07	2.60E+07	2.61E+07	1.00	0.00	0.98936982
Q13409	Cytoplasmic dynein 1 intermediate chain 2 OS=Homo sapiens OX=9606 GN=DYNC1I2 PE=1 Sv=3	12	12	4	3.06E+06	5.11E+06	3.45E+06	2.03E+06	2.03E+06	4.08E+06	1.14E+06	1.86E+06	1.60E+06	1.60E+06	3.79E+06	2.48E+06	3.29E+06	2.23E+06	1.48	0.56	0.13668438
P16070	CD44 antigen OS=Homo sapiens OX=9606 GN=CD44 PE=1 Sv=3	6	142	4	4.09E+07	4.02E+07	3.89E+07	4.50E+07	4.18E+07	4.84E+07	2.12E+07	2.21E+07	2.06E+07	2.06E+07	1.83E+07	1.65E+07	4.22E+07	1.99E+07	2.12	1.09	8.6851E-08
Q92542	Acyl-CoA oxidase 1 OS=Homo sapiens OX=9606 GN=ACO1 PE=1 Sv=1	54	54	4	1.95E+07	1.95E+07	1.95E+07	1.95E+07	1.95E+07	1.95E+07	1.95E+07	1.95E+07	1.95E+07	1.95E+07	1.95E+07	1.95E+07	1.95E+07	1.95E+07	1.00	0.00	1.00000000
P28022	Transmembrane protein PTX3 OS=Homo sapiens OX=9606 GN=PTX3 PE=1 Sv=3	14	28	4	1.67E+06	1.19E+06	1.48E+06	1.35E+06	1.65E+06	3.47E+06	9.21E+06	1.07E+06	5.79E+06	7.29E+06	7.29E+06	7.29E+06	1.64E+06	4.22E+06	0.21	-2.28	6.25913E-05
Q98005	Transmembrane 9 superfamily member 2 OS=Homo sapiens OX=9606 GN=TM9SF2 PE=1 Sv=1	9	48	4	8.56E+06	7.88E+06	8.28E+06	8.04E+06	7.52E+06	8.88E+06	6.05E+06	6.04E+06	4.48E+06	5.49E+06	5.60E+06	4.17E+06	8.14E+06	5.30E+06	1.54	0.62	7.88823E-05
Q00577	Transcriptional activator protein Pur-alpha OS=Homo sapiens OX=9606 GN=PURA PE=1 Sv=2	25	22	4	1.05E+07	1.09E+07	5.85E+06	5.95E+06	6.16E+06	7.87E+06	4.94E+06	8.84E+06	5.97E+06	5.55E+06	6.46E+06	5.28E+06	7.87E+06	5.00E+06	1.54	0.62	0.82657978
Q92522	Histone H1x OS=Homo sapiens OX=9606 GN=H1FX PE=1 Sv=1	16	114	4	5.90E+07	5.80E+07	5.83E+07	4.88E+07	4.63E+07	4.92E+07	4.97E+07	5.09E+07	4.75E+07	4.23E+07	4.02E+07	3.82E+07	5.23E+07	4.48E+07	1.17	0.22	0.29697859
Q13085	Acetyl-CoA carboxylase 1 OS=Homo sapiens OX=9606 GN=ACCAC1 PE=1 Sv=2	3	23	4	4.32E+06	5.51E+06	6.90E+06	5.10E+06	6.78E+06	4.51E+06	5.29E+06	5.87E+06	5.36E+06	6.02E+06	6.61E+06	5.10E+06	5.62E+06	4.50E+06	0.99	0.02	0.86745494
Q92542	Proteasome activator complex subunit 3 OS=Homo sapiens OX=9606 GN=PA3 PE=1 Sv=1	1	3	4	1.49E+07	1.49E+07	1.49E+07	1.49E+07	1.49E+07	1.49E+07	1.49E+07	1.49E+07	1.49E+07	1.49E+07	1.49E+07	1.49E+07	1.49E+07	1.49E+07	1.00	0.00	0.00000000
P06632	Calpain small subunit 1 OS=Homo sapiens OX=9606 GN=CAPNS1 PE=1 Sv=1	20	72	4	8.09E+06	6.43E+06	7.89E+06	7.54E+06	7.83E+06	7.12E+06	5.44E+06	4.11E+06	4.42E+06	5.24E+06	5.50E+06	4.33E+06	7.48E+06	4.84E+06	1.55	0.63	2.26971E-05
Q722W4	Zinc finger CCHC-type antiviral protein 1 OS=Homo sapiens OX=9606 GN=ZC3H4V1 PE=1 Sv=3	6	42	4	7.89E+06	8.72E+06	7.96E+06	9.03E+06	8.36E+06	3.96E+06	3.87E+06	4.57E+06	4.65E+06	4.58E+06	4.44E+06	8.22E+06	5.34E+06	0.95	2.32	2.322E-07	
Q8NE71	ATP-binding cassette sub-family F member 1 OS=Homo sapiens OX=9606 GN=ABCF1 PE=1 Sv=2	8	20	4	4.76E+06	3.93E+06	5.03E+06	6.96E+06	5.55E+06	5.82E+06	3.85E+06	1.87E+06	3.64E+06	3.15E+06	4.97E+06	1.70E+06	5.34E+06	2.45E+06	2.18	1.12	0.01916005
P28288	60S ribosomal protein L30 OS=Homo sapiens OX=9606 GN=RPL30 PE=1 Sv=2	51	62	4	1.83E+07	1.70E+07	1.40E+07	1.46E+07	1.72E+07	1.37E+07	1.37E+07	1.35E+07	8.98E+06	1.18E+07	1.13E+07	9.87E+06	1.60E+07	1.15E+07	1.39	0.47	0.01729187
Q92542	Signal transducer and activator of transcription 3 OS=Homo sapiens OX=9606 GN=STAT3 PE=1 Sv=2	4	34	4	4.89E+06	6.78E+06	5.04E+06	5.30E+06	5.42E+06	4.39E+06	5.28E+06	7.17E+06	5.89E+06	6.80E+06	5.99E+06	5.98E+06	5.30E+06	6.28E+06	0.84	0.04	0.33777029
Q92542	Ubiquitin thioesterase OTUB1 OS=Homo sapiens OX=9606 GN=OTUB1 PE=1 Sv=1	19	24	4	7.77E+06	7.05E+06	1.01E+07	7.77E+06	7.81E+06	7.74E+06	8.51E+06	9.36E+06	9.85E+06	7.94E+06	7.69E+06	7.05E+06	8.10E+06	8.75E+06	1.02	0.03	0.80251402
Q12905	Interleukin enhancer-binding factor 2 OS=Homo sapiens OX=9606 GN=ILF2 PE=1 Sv=1	15	42	4	9.74E+06	9.56E+06	5.10E+06	1.07E+07	7.77E+06	4.31E+06	1.26E+06	9.84E+06	9.95E+06	5.79E+06	1.09E+07	6.83E+06	9.81E+06	9.62E+06	1.02	0.02	0.87496593
Q75340	Programmed cell death protein 6 OS=Homo sapiens OX=9606 GN=PDCC6 PE=1 Sv=1	31	84	4	2.20E+07	2.25E+07	2.36E+07	1.97E+07	1.96E+07	1.77E+07	1.48E+07	1.55E+07	1.21E+07	1.40E+07	1.22E+07	2.05E+07	2.08E+07	1.48E+07	1.00	0.49	0.003738271
Q95834	Echinoderm microtubule-associated protein-like 2 OS=Homo sapiens OX=9606 GN=EML2 PE=1 Sv=1	9	36	4	7.87E+06	8.61E+06	7.93E+06	6.34E+06	5.89E+06	6.77E+06	1.04E+07	7.77E+06	7.49E+06	7.60E+06	7.94E+06	7.24E+06	8.53E+06	5.30E+06	0.85	-0.24	0.009156155
P28213	60S ribosomal protein L11 OS=Homo sapiens OX=9606 GN=RPL11 PE=1 Sv=2	31	82	4	1.72E+07	1.78E+07	1.51E+07	1.36E+07	1.66E+07	1.33E+07	1.57E+07	1.50E+07	1.37E+07	1.35E+07	1.75E+07	1.37E+07	1.56E+07	1.57E+07	1.00	0.91	0.21240929
Q92542	Mannose-1-phosphate guanylyltransferase beta OS=Homo sapiens OX=9606 GN=MGPPB PE=1 Sv=2	17	30	4	3.80E+06	4.75E+06	4.91E+06	3.60E+06	3.20E+06	3.75E+06	5.02E+06	5.78E+06	4.11E+06	6.92E+06	4.21E+06	3.37E+06	4.03E+06	4.80E+06	0.82	0.01	1.75644666
Q92542	GTP-binding protein SAR1a OS=Homo sapiens OX=9606 GN=SAR1A PE=1 Sv=1	1	3	4	1.45E+07	1.45E+07	1.45E+07	1.45E+07	1.45E+07	1.45E+07	1.45E+07	1.45E+07	1.45E+07	1.45E+07	1.45E+07	1.45E+07	1.45E+07	1.45E+07	1.00	0.00	0.00000000
Q14950	Myosin regulatory light chain 12B OS=Homo sapiens OX=9606 GN=MYL12B PE=1 Sv=2	29	65	4	2.18E+07	2.16E+07	2.18E+07	2.51E+07	2.14E+07	2.17E+07	2.15E+07	2.20E+07	2.21E+07	1.94E+07	1.84E+07	1.67E+07	2.22E+07	2.00E+07	1.11	0.15	0.68985072
P28072	Proteasome subunit beta type-6 OS=Homo sapiens OX=9606 GN=PSMB6 PE=1 Sv=4	29	74	4	2.83E+07	1.50E+07	1.33E+07	1.20E+07	1.37E+07	1.75E+07	2.40E+07	2.28E+07	2.46E+07	2.00E+07	1.76E+07	1.29E+07	1.55E+07	1.22E+07	0.37	-0.03	0.09320352
Q17866	KH domain-containing, RNA-binding, signal transduction-associated protein 1 OS=Homo sapiens OX=9606 GN=KHDRBS1 PE=1 Sv=1	12	30	4	5.23E+06	1.23E+07	1.18E+07	1.27E+07	1.02E+07	1.16E+07	8.84E+06	8.75E+06	8.21E+06	8.68E+06	6.70E+06	7.06E+06	5.18E+06	8.10E+06	1.46	0.58	2.42897E-05
Q92542	60S ribosomal protein L10 OS=Homo sapiens OX=9606 GN=RPL10 PE=1 Sv=2	11	45	4	1.23E+06	1.06E+06	5.19E+06	4.57E+06	4.57E+06	3.87E+06	9.21E+06	6.96E+06	7.72E+06	9.40E+06	6.51E+06	9.72E+06	5.61E+06	8.25E+06	0.68	-0.56	0.54828114
Q92542	Complement C3 subcomponent subunit B OS=Homo sapiens OX=9606 GN=C1QB PE=1 Sv=1	4	16	4	9.15E+06	9.34E+06	6.46E+06	6.56E+06	9.15E+06	9.43E+06	8.47E+06	9.36E+06	9.36E+06	1.72E+06	2.27E+06	4.98E+06	1.08E+07	1.08E+07	1.00	-0.73	0.00566008
Q13741	CD161 antigen OS=Homo sapiens OX=9606 GN=CD161 PE=1 Sv=3	11	39	4	2.82E+06	4.11E+06	2.82E+06	2.82E+06	2.82E+06	2.11E+06	2.11E+06	2.02E+06	2.02E+06	2.38E+06	2.38E+06	2.38E+06	3.00E+06	2.38E+06	1.20	0.00	0.00053732
Q92542	Phenylalanyl-tRNA ligase alpha subunit OS=Homo sapiens OX=9606 GN=FASEA PE=1 Sv=3	23	28	4	1.39E+07	1.68E+07	1.53E+07	1.57E+07	1.61E+07	1.53E+07	1.18E+07	1.20E+07	8.52E+06	1.25E+07	1.05E+07	1.06E+07	1.55E+07	1.10E+07	1.41	1.00	0.000155366
Q15427	Monocarboxylate transporter 4 OS=Homo sapiens OX=9606 GN=SLC16A3 PE=1 Sv=1	10	63	4	1.25E+07	1.30E+07	1.28E+07	1.58E+07	1.56E+07	1.05E+07	9.39E+06	7.77E+06	1.10E+07	1.04E+07	8.47E+06	5.79E+06	1.34E+07	8.81E+06	1.52	0.60	0.02350571
P22570	NADPH-dependent oxidoreductase, mitochondrial OS=Homo sapiens OX=9606 GN=FOXDR PE=1 Sv=3	12	50	4	1.21E+07	7.90E+06	1.19E+07	1.19E+07	1.21E+07	1.63E+06	1.07E+06	1.08E+07	1.08E+07	8.30E+06	8.77E+06	4.87E+06	1.04E+07	6.91E+06	0.21	0.33	0.33928786
P62244	40S ribosomal protein S15a OS=Homo sapiens OX=9606 GN=RPS15A PE=1 Sv=2	31	146	4	5.17E+07	5.71E+07	7.44E+07	7.29E+07	7.60E+07	6.92E+07	4.27E+07	4.70E+07	5.73E+07	5.67E+07	5.55E+07	4.01E+07	6.69E+07	5.01E+07	1.34	0.42	0.009914808
Q92542	DNA replication licensing factor OS=Homo sapiens OX=9606 GN=NLNKB PE=1 Sv=1	9	48	4	3.89E+06	3.09E+06	3.45E+06	3.92E+06	3.34E+06	3.12E+06	1.93E+06	1.93E+06	1.93E+06	1.93E+06	1.93E+06	1.93E+06	1.93E+06	1.93E+06	1.26	0.36	0.00336696
Q92542	Transmembrane 9 superfamily member 3 OS=Homo sapiens OX=9606 GN=TM9SF3 PE=1 Sv=1	4	28	4	5.08E+06	5.08E+06	6.56E+06	5.20E+06	6.47E+06	7.45E+06	4.77E+06	6.89E+06	4.83E+06	6.96E+06	5.14E+06	3.90E+06	6.01E+06	4.88E+06	1.23	0.60	0.09930230
P63151	Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B alpha isoform OS=Homo sapiens OX=9606 GN=PPP2R2A PE=1 Sv=1	13	34	4	4.89E+06	4.59E+06	7.21E+06	7.90E+06	6.68E+06	8.53E+06	5.94E+06	4.81E+06	7.54E+06	6.18E+06	5.85E+06	4.81E+06	6.63E+06	5.86E+06	1.10	0.18	0.343088155
P29401	Transketolase OS=Homo sapiens OX=9606 GN=TKT PE=1 Sv=3	9	52	4	5.87E+06	5.77E+06	7.08E+06	5.03E+06	5.63E+06	4.09E+06	6.79E+06	5.49E+06	6.14E+06	6.42E+06	6.29E+06	6.94E+06	5.30E+06	6.10E+06	1.03	0.07	0.796319818
Q15691	Microtubule-associated protein RP/EB family member 1 OS=Homo sapiens OX=9606 GN=MAPRE1 PE=1 Sv=3	26	40	4	9.57E+06	8.08E+06	9.56E+06	9.00E+06	9.62E+06	9.56E+06</											

Supplemental Table 4. List of all proteins identified by label free proteomics analysis.

Accession	Description	Coverage [%]	# PSMs	# Unique Peptides	Antitryptic1	Antitryptic2	Antitryptic3	Antitryptic4	Antitryptic5	Antitryptic6	Vehicle 1	Vehicle 2	Vehicle 3	Vehicle 4	Vehicle 5	Vehicle 6	Average antitryptic	Average vehicle	Ratio antitryptic/vehicle	Log 2 fold change (antitryptic/vehicle)	P-value	
P01834	Immunoglobulin kappa constant OS=Homo sapiens OX=9066 GN=IGKC PE=1 Sv=1	79	15	5	1.02E+06						4.22E+06	2.56E+05			3.65E+05	1.98E+07	1.02E+06		6.18E+06	0.16	-2.80	
Q9Y240	C-type lectin domain family 11 member A OS=Homo sapiens OX=9066 GN=CLEC11A PE=1 Sv=1	15	261	5	9.65E+07	8.48E+07	8.38E+07	8.63E+07	7.80E+07	7.39E+07	1.29E+08	1.10E+08	9.88E+07	1.02E+08	1.08E+07	8.28E+07	8.39E+07	1.02E+08	0.82	0.02138225	-0.20	
Q02750	Dual specificity mitogen-activated protein kinase kinase 1 OS=Homo sapiens OX=9066 GN=MAP2K1 PE=1 Sv=2	34	66	5	1.61E+07	1.69E+07	1.90E+07	2.26E+07	1.75E+07	1.75E+07	1.37E+07	1.63E+07	1.32E+07	1.86E+07	1.39E+07	1.52E+07	1.83E+07	1.52E+07	1.20	0.04360231	0.27	
P13804	Electron transfer flavoprotein subunit alpha, mitochondrial OS=Homo sapiens OX=9066 GN=ETFA PE=1 Sv=1	27	42	5	7.63E+06	7.46E+06	1.04E+07	1.03E+07	7.46E+06	1.14E+07	6.07E+06	3.16E+06	5.17E+06	2.99E+06	3.78E+06	3.32E+06	9.11E+06	4.08E+06	2.23	0.000918344	1.20	
P30613	Pyruvate kinase PKLR OS=Homo sapiens OX=9066 GN=PKLR PE=1 Sv=2	13	196	5	1.42E+07	1.59E+07	1.16E+07	1.16E+07	1.07E+07	1.16E+07	1.79E+07	1.98E+07	1.49E+07	1.55E+07	1.35E+07	1.17E+07	1.26E+07	1.55E+07	0.81	0.073344758	-0.30	
P25290	Beta-5-oxoprolactone oxidoreductase OS=Homo sapiens OX=9066 GN=CBPZ1 PE=1 Sv=3	13	96	5	2.29E+07	2.22E+07	2.44E+07	2.44E+07	2.44E+07	2.44E+07	2.44E+07	2.44E+07	2.44E+07	2.44E+07	2.44E+07	2.44E+07	2.44E+07	2.44E+07	1.37	0.02327575	0.45	
P16278	Beta-galactosidase OS=Homo sapiens OX=9066 GN=GLB1 PE=1 Sv=2	13	36	5	1.31E+07	1.24E+07	1.05E+07	1.05E+07	1.05E+07	1.05E+07	1.05E+07	1.05E+07	1.05E+07	1.05E+07	1.05E+07	1.05E+07	1.05E+07	1.05E+07	1.05E+07	1.05E+07	1.05E+07	1.05E+07
P17844	Probable ATP-dependent RNA helicase DDX5 OS=Homo sapiens OX=9066 GN=DDX5 PE=1 Sv=1	20	105	5	9.90E+06	1.16E+07	1.05E+07	1.02E+07	1.08E+07	8.26E+06	5.33E+06	6.22E+06	4.79E+06	5.40E+06	4.52E+06	3.79E+06	1.02E+07	5.01E+06	2.04	0.167936	1.03	
O00487	26S proteasome non-ATPase regulatory subunit 14 OS=Homo sapiens OX=9066 GN=PSMD14 PE=1 Sv=1	36	63	5	1.92E+07	2.30E+07	2.31E+07	1.72E+07	1.42E+07	1.42E+07	1.16E+07	1.92E+07	9.12E+06	7.35E+06	8.91E+06	9.83E+06	1.91E+07	1.10E+07	1.00	0.00485815	1.00	
P06858	Liponin lipase OS=Homo sapiens OX=9066 GN=LPL PE=1 Sv=1	19	52	5	1.08E+07	9.72E+06	6.17E+06	1.01E+07	1.10E+07	5.17E+07	1.53E+07	1.41E+07	1.34E+07	1.14E+07	1.25E+07	9.60E+06	1.35E+07	0.71	0.00172828	-0.24		
Q04375	D-3-phosphoglycerate dehydrogenase OS=Homo sapiens OX=9066 GN=PHGDH PE=1 Sv=4	15	112	5	4.05E+07	4.23E+07	3.45E+07	4.36E+07	3.18E+07	3.62E+07	5.10E+07	5.20E+07	4.43E+07	4.19E+07	4.34E+07	3.80E+07	3.82E+07	4.52E+07	0.84	0.00386253	-0.49	
P20073	Chord nuclear protein 4 OS=Homo sapiens OX=9066 GN=NCU4 PE=1 Sv=4	35	62	5	1.92E+07	1.79E+07	1.91E+07	1.91E+07	1.91E+07	1.91E+07	1.91E+07	1.91E+07	1.91E+07	1.91E+07	1.91E+07	1.91E+07	1.91E+07	1.91E+07	1.91E+07	1.91E+07	1.91E+07	1.91E+07
P30050	60S ribosomal protein L12 OS=Homo sapiens OX=9066 GN=RPL12 PE=1 Sv=1	45	142	5	3.88E+07	4.15E+07	3.07E+07	2.72E+07	3.13E+07	3.34E+07	3.38E+07	4.05E+07	2.90E+07	3.08E+07	2.72E+07	2.65E+07	3.38E+07	3.13E+07	1.08	0.1430112375	1.08	
P21926	CD9 antigen OS=Homo sapiens OX=9066 GN=CD9 PE=1 Sv=4	21	179	5	1.01E+08	9.41E+07	9.44E+07	1.09E+08	9.57E+07	9.34E+07	7.32E+07	7.22E+07	7.22E+07	6.42E+07	6.12E+07	6.42E+07	9.79E+07	6.86E+07	0.51	8.4871E-06	1.43	
Q9Y4K0	Lysyl oxidase homolog 2 OS=Homo sapiens OX=9066 GN=LOXL2 PE=1 Sv=1	11	40	5	5.42E+06	6.29E+06	5.30E+06	5.92E+06	5.19E+06	4.71E+06	1.15E+07	1.16E+07	1.16E+07	9.89E+06	9.13E+06	8.83E+06	5.47E+06	1.04E+07	0.52	0.69966E-05	0.52	
Q9YK40	cAMP-dependent protein kinase type I-alpha regulatory subunit OS=Homo sapiens OX=9066 GN=PRKAR1A PE=1 Sv=1	22	82	5	1.23E+07	1.12E+07	9.75E+06	1.27E+07	1.40E+07	1.13E+07	1.28E+07	1.24E+07	7.55E+06	7.83E+06	1.24E+07	1.08E+07	1.19E+07	1.06E+07	0.16	0.29772265	-0.16	
Q14786	Neuropilin-1 OS=Homo sapiens OX=9066 GN=NP1 PE=1 Sv=3	11	52	5	1.34E+07	1.46E+07	1.25E+07	1.41E+07	1.16E+07	1.04E+07	1.05E+07	9.38E+06	7.56E+06	9.75E+06	7.60E+06	7.86E+06	1.29E+07	8.79E+06	1.45	0.000612827	1.45	
P22234	Multifunctional protein ADE2 OS=Homo sapiens OX=9066 GN=PAICS PE=1 Sv=3	21	24	5	6.12E+06	1.36E+07	5.07E+06	6.12E+06	6.12E+06	6.12E+06	5.79E+06	6.46E+06	3.37E+06	3.42E+06	5.30E+06	5.72E+06	9.77E+06	5.01E+06	0.86	0.015273477	0.86	
O00151	PDZ and LIM domain protein 1 OS=Homo sapiens OX=9066 GN=PDLIM1 PE=1 Sv=4	21	24	5	1.27E+07	1.09E+07	7.60E+06	9.94E+06	1.03E+07	1.01E+07	6.99E+06	7.05E+06	4.52E+06	5.86E+06	5.37E+06	5.54E+06	1.03E+07	5.89E+06	1.74	0.000500038	1.74	
P20618	Proteasome subunit beta type-1 OS=Homo sapiens OX=9066 GN=PSMB1 PE=1 Sv=2	32	76	5	2.01E+07	2.03E+07	2.04E+07	2.10E+07	2.19E+07	2.31E+07	2.31E+07	2.23E+07	2.30E+07	2.37E+07	2.03E+07	1.79E+07	2.11E+07	2.17E+07	0.97	0.59856577	-0.34	
P27361	Mitogen-activated protein kinase 3 OS=Homo sapiens OX=9066 GN=MAPK3 PE=1 Sv=4	25	76	5	2.81E+07	2.60E+07	1.81E+07	2.44E+07	2.22E+07	1.88E+07	2.18E+07	1.80E+07	2.00E+07	1.77E+07	1.60E+07	2.34E+07	2.07E+07	1.25	0.020872159	1.25		
P11279	Lysosome-associated membrane glycoprotein 1 OS=Homo sapiens OX=9066 GN=LAMP1 PE=1 Sv=3	12	126	5	6.23E+07	5.77E+07	5.88E+07	5.94E+07	5.62E+07	5.30E+07	2.02E+07	3.26E+07	3.07E+07	1.82E+07	1.81E+07	2.63E+07	3.17E+07	2.44E+07	1.24	5.57772E-06	1.24	
P00119	Ras-related protein Rab-2A OS=Homo sapiens OX=9066 GN=RAB2A PE=1 Sv=1	32	80	5	1.40E+07	1.21E+07	1.52E+07	1.34E+07	1.47E+07	1.05E+07	1.27E+07	1.06E+07	1.12E+07	9.47E+06	1.09E+07	8.69E+06	1.41E+07	1.06E+07	1.32	0.00085458	1.32	
P52239	Importin subunit alpha-1 OS=Homo sapiens OX=9066 GN=IMP2 PE=1 Sv=1	25	40	5	1.92E+07	1.83E+07	1.92E+07	1.92E+07	1.92E+07	1.92E+07	1.92E+07	1.92E+07	1.92E+07	1.92E+07	1.92E+07	1.92E+07	1.92E+07	1.92E+07	1.92E+07	1.92E+07	1.92E+07	1.92E+07
Q6V017	Protocadherin Fat 4 OS=Homo sapiens OX=9066 GN=GFAT4 PE=1 Sv=2	2	26	5	4.67E+06	3.73E+06	4.64E+06	3.10E+06	4.70E+06	3.50E+06	7.24E+06	7.46E+06	6.02E+06	5.83E+06	6.19E+06	7.14E+06	4.06E+06	6.65E+06	0.61	0.187968E-05	0.61	
Q15435	Protein phosphatase 1 regulatory subunit 7 OS=Homo sapiens OX=9066 GN=PPP1R7 PE=1 Sv=1	19	90	5	1.10E+07	1.48E+07	1.20E+07	1.47E+07	1.17E+07	1.27E+07	1.37E+07	8.95E+06	1.34E+07	1.67E+07	1.18E+07	1.20E+07	1.23E+07	1.28E+07	-0.76	0.734981671	-0.76	
P35268	60S ribosomal protein L22 OS=Homo sapiens OX=9066 GN=RPL22 PE=1 Sv=2	49	64	5	1.51E+07	4.93E+07	1.75E+07	1.75E+07	1.75E+07	1.41E+07	1.97E+07	1.82E+07	1.83E+07	1.59E+07	1.78E+07	1.53E+07	1.47E+07	1.75E+07	1.00	0.070062315	1.00	
P09900	Proteasome subunit alpha type-B OS=Homo sapiens OX=9066 GN=PSMA6 PE=1 Sv=1	25	115	5	4.05E+07	4.58E+07	4.04E+07	5.14E+07	4.14E+07	3.38E+07	4.23E+07	4.77E+07	4.93E+07	5.82E+07	4.23E+07	3.27E+07	4.03E+07	4.59E+07	-0.19	1.374809E-09	-0.19	
Q08927	Glyoxylate reductase/hydroxypyruvate reductase OS=Homo sapiens OX=9066 GN=GRHPR PE=1 Sv=1	26	66	5	8.34E+06	9.21E+06	9.21E+06	1.15E+07	8.29E+06	1.10E+07	9.32E+06	9.63E+06	9.32E+06	9.63E+06	9.63E+06	9.65E+06	9.76E+06	1.01E+07	-0.06	0.626018192	-0.06	
P61223	Ras-related protein Rap-2b OS=Homo sapiens OX=9066 GN=RAP2B PE=1 Sv=1	6	26	5	3.82E+06	1.73E+07	1.89E+07	1.89E+07	1.89E+07	1.89E+07	1.89E+07	1.89E+07	1.89E+07	1.89E+07	1.89E+07	1.89E+07	1.89E+07	1.89E+07	1.89E+07	1.18	0.021366336	1.18
Q00666	Neuroblast differentiation-associated protein AHNAK OS=Homo sapiens OX=9066 GN=AHNAK PE=1 Sv=2	3	27	5	8.34E+06	5.61E+06	8.92E+06	9.47E+06	6.91E+06	1.13E+07	7.25E+06	8.82E+06	7.20E+06	8.20E+06	5.65E+06	6.66E+06	7.68E+06	7.63E+06	1.01	0.069113912	1.01	
Q9BR76	Coronin-1B OS=Homo sapiens OX=9066 GN=CORO1B PE=1 Sv=1	14	66	5	2.03E+07	1.75E+07	1.75E+07	1.75E+07	1.75E+07	1.41E+07	1.97E+07	1.82E+07	1.83E+07	1.59E+07	1.78E+07	1.53E+07	1.47E+07	1.75E+07	1.00	0.007062315	1.00	
P47756	F-actin-capping protein subunit beta OS=Homo sapiens OX=9066 GN=CAPZB PE=1 Sv=4	26	50	5	1.51E+07	1.50E+07	1.34E+07	1.26E+07	1.19E+07	1.39E+07	9.57E+06	1.16E+07	1.03E+07	9.71E+06	7.71E+06	7.58E+06	1.36E+07	9.41E+06	0.53	0.000481615	0.53	
Q9XK55	AP-1 complex subunit mu-1 OS=Homo sapiens OX=9066 GN=AP1M1 PE=1 Sv=3	18	61	5	1.28E+07	1.29E+07	1.50E+07	1.40E+07	1.33E+07	1.23E+07	7.88E+06	7.54E+06	5.41E+06	6.79E+06	5.27E+06	5.69E+06	1.34E+07	6.43E+06	2.08	0.5590849E-06	2.08	
P00119	Importin subunit alpha-1 OS=Homo sapiens OX=9066 GN=IMP2 PE=1 Sv=1	25	40	5	1.92E+07	1.83E+07	1.92E+07	1.92E+07	1.92E+07	1.92E+07	1.92E+07	1.92E+07	1.92E+07	1.92E+07	1.92E+07	1.92E+07	1.92E+07	1.92E+07	1.92E+07	1.92E+07	1.92E+07	
P13204	Proliferating cell nuclear antigen OS=Homo sapiens OX=9066 GN=PCNA PE=1 Sv=1	25	40	5	6.83E+06	1.22E+07	1.50E+07	1.40E+07	1.50E+07	1.31E+07	5.89E+06	1.09E+07	6.54E+06	1.22E+07	9.93E+06	1.08E+07	1.27E+07	9.38E+06	1.36	0.0477290312	1.36	
P07686	Beta-hexosaminidase subunit beta OS=Homo sapiens OX=9066 GN=HEXB PE=1 Sv=3	15	17	5	5.18E+06	3.34E+06	4.16E+06	2.34E+06	1.69E+06	1.77E+06	6.27E+05	1.76E+06	6.21E+05	1.22E+06	8.90E+05	1.85E+06	2.46E+06	1.16E+06	0.11	0.1154984E-06	0.11	
Q96KP4	Cytosolic non-specific dipeptidase OS=Homo sapiens OX=9066 GN=CNDP2 PE=1 Sv=2	19	91	5	1.56E+07	2.93E+07	2.37E+07	1.67E+07	1.82E+07	1.73E+07	2.43E+07	2.42E+07	1.88E+07	2.53E+07	1.68E+07	1.98E+07	2.11E+07	1.98E+07	-0.09	0.643617171	-0.09	
P04062	Lysosomal acid glucosylceramidase OS=Homo sapiens OX=9066 GN=GBA PE=1 Sv=1	15	42	5	7.62E+06	6.78E+06	7.85E+06	5.84E+06	6.87E+06	6.11E+06	5.90E+06	5.59E+06	4.51E+06									

# Supplementary Table 4. List of all proteins identified by label free proteomics analysis.

Accession	Description	Coverage [%]	# PSMs	# Unique Peptides	Antitriptyline 1	Antitriptyline 2	Antitriptyline 3	Antitriptyline 4	Antitriptyline 5	Antitriptyline 6	Antitriptyline 7	Antitriptyline 8	Antitriptyline 9	Antitriptyline 10	Antitriptyline 11	Antitriptyline 12	Average antitriptyline	Average vehicle	Ratio antitriptyline/vehicle	Log <sub>2</sub> fold change (antitriptyline/vehicle)	P-value
P0851	Heterogeneous nuclear ribonucleoprotein A1 OS=Homo sapiens OX=9606 GN=HNRNP1A1 PE=1 SV=5	23	98	6	1.76E+07	2.55E+07	1.97E+07	2.18E+07	1.83E+07	2.23E+07	1.45E+07	1.45E+07	1.12E+07	1.13E+07	1.17E+07	9.34E+06	2.09E+07	1.21E+07	1.73	0.000206591	
P07858	Cathepsin B OS=Homo sapiens OX=9606 GN=CTSB PE=1 SV=3	24	92	6	2.81E+07	2.12E+07	2.62E+07	2.42E+07	2.70E+07	1.45E+07	1.37E+07	1.13E+07	1.15E+07	1.21E+07	1.06E+07	2.56E+07	4.06E38E+06	1.23E+07	2.08	4.00E38E+06	
Q12904	Amoacyl tRNA synthase complex-interacting multifunctional protein 1 OS=Homo sapiens OX=9606 GN=AMP1 PE=1 SV=2	25	72	6	2.07E+07	1.88E+07	1.56E+07	1.89E+07	1.63E+07	1.80E+07	9.11E+06	8.70E+06	8.62E+06	9.56E+06	1.06E+07	7.70E+06	1.77E+07	9.05E+06	1.96	2.65149E+06	
Q15555	Microtubule-associated protein RP/EB family member 2 OS=Homo sapiens OX=9606 GN=MAPRE2 PE=1 SV=1	25	123	6	1.68E+07	1.75E+07	1.89E+07	1.87E+07	1.58E+07	1.65E+07	2.30E+07	2.80E+07	2.61E+07	1.98E+07	1.81E+07	2.10E+07	1.79E+07	2.27E+07	1.09	0.0257944	
Q39714	3-hydroxyacyl-CoA dehydrogenase type 2 OS=Homo sapiens OX=9606 GN=HSD17B10 PE=1 SV=3	24	66	6	1.70E+07	1.70E+07	1.99E+07	1.21E+07	1.21E+07	1.87E+07	1.41E+07	1.19E+07	1.03E+07	8.00E+06	1.03E+07	1.01E+07	1.57E+07	1.98E+07	1.46	0.011127501	
P08403	Nucleolar protein 58 OS=Homo sapiens OX=9606 GN=N58 PE=1 SV=1	24	96	6	1.85E+07	1.45E+07	1.91E+07	1.86E+07	2.05E+07	1.67E+07	1.55E+07	5.23E+06	5.23E+06	1.33E+06	9.70E+06	1.46E+06	1.33E+06	9.72E+06	1.73	0.000713073	
P30419	Glycylpeptide N-tetraacyltransferase 1 OS=Homo sapiens OX=9606 GN=NTM1 PE=1 SV=2	23	92	6	3.09E+07	2.94E+07	2.74E+07	2.53E+07	2.73E+07	2.67E+07	2.32E+07	1.97E+07	2.32E+07	2.30E+07	1.94E+07	1.70E+07	1.57E+07	2.10E+07	1.33	0.0045387	
P01857	Immunoglobulin heavy constant gamma 1 OS=Homo sapiens OX=9606 GN=IGHG1 PE=1 SV=1	38	33	6	1.12E+07	1.57E+07	2.12E+07	2.34E+07	2.25E+07	2.19E+07	3.45E+07	1.78E+07	2.08E+07	1.98E+07	2.03E+07	1.07E+08	1.93E+07	3.88E+07	0.53	0.280131754	
P18669	Phosphoglycerate mutase 1 OS=Homo sapiens OX=9606 GN=PGAM1 PE=1 SV=2	37	125	6	4.05E+07	3.85E+07	2.86E+07	3.69E+07	3.00E+07	3.15E+07	3.95E+07	3.70E+07	2.89E+07	3.37E+07	3.36E+07	3.18E+07	3.43E+07	3.41E+07	1.01	0.92093334	
P04745	Alpha-1-antitrypsin 1 OS=Homo sapiens OX=9606 GN=AMY1A PE=1 SV=2	12	304	6	1.38E+08	1.43E+08	1.24E+08	1.37E+08	1.25E+08	1.64E+08	1.49E+08	1.39E+08	1.58E+08	1.24E+08	1.33E+08	1.31E+08	1.44E+08	1.44E+08	0.91	1.003320306	
P31146	Coronin-1A OS=Homo sapiens OX=9606 GN=CORO1A PE=1 SV=4	26	133	6	2.96E+07	2.32E+07	2.21E+07	2.74E+07	2.44E+07	2.36E+07	3.64E+07	3.98E+07	2.85E+07	3.05E+07	2.62E+07	3.04E+07	2.44E+07	3.20E+07	-0.19	0.013136093	
P21131	Basigin OS=Homo sapiens OX=9606 GN=BSG PE=1 SV=2	21	131	6	1.93E+07	1.85E+07	1.82E+07	1.76E+07	1.86E+07	2.05E+07	1.67E+07	1.55E+07	1.35E+07	1.37E+07	1.41E+07	1.41E+07	2.24E+07	2.93E+07	1.88	8.5245E+06	
P08243	Asparagine synthetase [glutamine-hydrolyzing] OS=Homo sapiens OX=9606 GN=ASNS PE=1 SV=4	18	52	6	9.54E+06	7.80E+06	9.53E+06	1.03E+07	6.90E+06	7.59E+06	6.53E+06	7.28E+06	6.34E+06	7.09E+06	6.78E+06	6.90E+06	8.61E+06	6.81E+06	1.26	0.02148764	
Q60749	Zeranolxin-2 OS=Homo sapiens OX=9606 GN=SNX2 PE=1 SV=2	20	131	6	2.13E+07	2.37E+07	2.27E+07	2.30E+07	2.12E+07	1.97E+07	2.25E+07	2.10E+07	2.05E+07	2.18E+07	1.57E+07	2.05E+07	2.19E+07	2.07E+07	0.34	0.34619375	
Q30399	Homogentisate 1,2-dioxygenase OS=Homo sapiens OX=9606 GN=HGD PE=1 SV=4	19	158	6	1.75E+07	1.93E+07	2.31E+07	1.62E+07	2.53E+07	1.65E+07	2.50E+07	2.58E+07	2.19E+07	2.40E+07	2.30E+07	1.98E+07	1.97E+07	2.32E+07	0.85	0.077537453	
P27635	60S ribosomal protein L10 OS=Homo sapiens OX=9606 GN=RPL10 PE=1 SV=2	31	101	6	5.33E+07	4.82E+07	4.88E+07	5.54E+07	4.78E+07	4.54E+07	2.62E+07	2.77E+07	3.15E+07	2.17E+07	1.91E+07	4.98E+07	2.48E+07	1.20	1.34317E+06		
P09103	Serine/arginine-rich splicing factor 3 OS=Homo sapiens OX=9606 GN=SRSF3 PE=1 SV=1	41	152	6	4.95E+07	4.40E+07	3.66E+07	4.11E+07	4.37E+07	3.71E+07	3.21E+07	2.95E+07	2.70E+07	3.03E+07	2.61E+07	2.32E+07	4.20E+07	2.80E+07	1.50	0.000270887	
Q12124	Eukaryotic translation initiation factor 3 subunit 1 OS=Homo sapiens OX=9606 GN=EIF3M1 PE=1 SV=1	24	28	6	9.52E+06	8.40E+06	8.40E+06	8.57E+06	9.56E+06	1.45E+06	5.44E+06	3.76E+06	2.18E+06	1.39E+06	2.54E+06	6.50E+06	2.50E+06	3.16E+06	0.98	0.002022277	
P31689	DnaI homolog subfamily A member 1 OS=Homo sapiens OX=9606 GN=DNAI1A PE=1 SV=2	23	55	6	1.21E+07	1.75E+07	1.47E+07	1.60E+07	1.73E+07	1.65E+07	6.92E+06	7.20E+06	7.66E+06	8.71E+06	6.53E+06	7.15E+06	1.57E+07	7.36E+06	2.13	5.20254E+05	
Q16394	Exostasin-1 OS=Homo sapiens OX=9606 GN=EXT1 PE=1 SV=2	11	116	6	1.95E+07	1.89E+07	1.44E+07	1.38E+07	1.18E+07	1.75E+07	2.58E+07	2.82E+07	1.96E+07	1.61E+07	2.11E+07	2.37E+07	1.60E+07	2.24E+07	-0.49	0.016203370	
P49721	Proteasome subunit beta type 2 OS=Homo sapiens OX=9606 GN=PSMB2 PE=1 SV=1	46	75	6	2.10E+07	2.27E+07	1.97E+07	1.81E+07	2.01E+07	2.06E+07	2.28E+07	1.84E+07	1.55E+07	2.10E+07	1.58E+07	1.99E+07	1.90E+07	1.90E+07	0.71	0.54208023	
Q3UL46	Proteasome activator complex subunit 2 OS=Homo sapiens OX=9606 GN=PSME2 PE=1 SV=1	36	28	6	7.37E+07	4.87E+07	4.62E+07	7.52E+07	6.49E+07	5.52E+07	4.52E+07	6.37E+07	2.78E+07	3.65E+07	4.86E+07	3.40E+07	6.06E+07	3.82E+07	1.59	0.006812268	
P27229	E-pyrophosphatase dehydrogenase, decarboxylating OS=Homo sapiens OX=9606 GN=PGD PE=1 SV=3	20	120	6	4.99E+07	5.13E+07	5.08E+07	5.75E+07	5.49E+07	4.98E+07	6.52E+07	6.71E+07	6.06E+07	5.83E+07	5.44E+07	5.24E+07	6.66E+07	6.66E+07	-0.35	0.010082499	
P30566	Adenylyltransferase OS=Homo sapiens OX=9606 GN=ADSL PE=1 SV=2	24	71	6	2.08E+07	2.34E+07	2.28E+07	2.28E+07	2.08E+07	2.24E+07	1.99E+07	1.82E+07	1.71E+07	2.04E+07	2.24E+07	2.34E+07	2.34E+07	2.34E+07	-0.02	0.845027107	
Q15459	Splicing factor 3A subunit 1 OS=Homo sapiens OX=9606 GN=SF3A1 PE=1 SV=1	14	57	6	8.78E+06	5.91E+06	7.94E+06	6.98E+06	6.81E+06	7.93E+06	4.34E+06	4.82E+06	6.06E+06	3.75E+06	4.32E+06	1.34E+06	7.39E+06	4.10E+06	1.80	0.002164005	
P15559	NAD(P)H dehydrogenase [quinone] 1 OS=Homo sapiens OX=9606 GN=NQO1 PE=1 SV=1	31	35	6	2.66E+07	2.97E+07	3.93E+07	4.00E+07	3.68E+07	3.27E+07	2.74E+07	2.49E+07	3.00E+07	1.98E+07	1.69E+07	1.64E+07	3.42E+07	2.26E+07	1.51	0.6500479335	
Q3UJH8	Septin-9 OS=Homo sapiens OX=9606 GN=SEPT9 PE=1 SV=1	13	62	6	1.83E+07	2.21E+07	1.99E+07	2.03E+07	1.79E+07	1.80E+07	2.03E+07	1.54E+07	1.66E+07	1.70E+07	1.53E+07	1.27E+07	1.94E+07	1.62E+07	1.20	0.027414774	
Q99536	Synaptic vesicle membrane protein VAT1 L homolog OS=Homo sapiens OX=9606 GN=VAT1 PE=1 SV=2	30	65	6	1.42E+07	1.51E+07	1.92E+07	1.47E+07	1.36E+07	1.78E+07	2.50E+07	4.09E+07	1.78E+07	1.68E+07	1.40E+07	1.57E+07	1.48E+07	1.07	0.1503314891		
Q29499	ATP-dependent RNA helicase 8 OS=Homo sapiens OX=9606 GN=DDX1 PE=1 SV=2	26	129	6	7.75E+06	7.82E+06	8.00E+06	8.70E+06	9.60E+06	7.80E+06	6.82E+06	6.82E+06	6.82E+06	6.70E+06	7.25E+06	6.84E+06	8.84E+06	8.84E+06	1.26	0.001545781	
P08173	Complement decay-accelerating factor 3 OS=Homo sapiens OX=9606 GN=CD35 PE=1 SV=4	20	76	6	2.20E+07	1.70E+07	1.98E+07	1.80E+07	2.24E+07	1.89E+07	1.89E+07	1.89E+07	1.89E+07	1.89E+07	1.89E+07	1.89E+07	2.21E+07	2.15E+07	0.25	2.1711E+05	
Q1MKD3	Heterogeneous nuclear ribonucleoprotein L-like protein 2 OS=Homo sapiens OX=9606 GN=HNRNPUL2 PE=1 SV=1	11	66	6	2.15E+07	2.07E+07	2.43E+07	1.80E+07	2.26E+07	2.01E+07	1.82E+07	1.71E+07	2.28E+07	2.01E+07	1.56E+07	1.21E+07	1.90E+07	1.11	0.145669718		
P46776	60S ribosomal protein L27a OS=Homo sapiens OX=9606 GN=RPL27A PE=1 SV=1	31	117	6	4.46E+07	4.34E+07	4.90E+07	4.07E+07	3.82E+07	3.96E+07	3.00E+07	2.88E+07	2.53E+07	2.32E+07	2.60E+07	2.12E+07	4.25E+07	2.57E+07	1.67	1.6369E+05	
Q27243	Serine protease HTRA1 OS=Homo sapiens OX=9606 GN=HTRA1 PE=1 SV=2	15	66	6	5.77E+06	1.22E+07	9.57E+06	1.20E+07	1.01E+07	1.15E+07	1.78E+07	2.12E+07	1.54E+07	1.47E+07	1.74E+07	1.85E+07	1.03E+07	1.75E+07	-0.72	0.000459262	
P25786	Proteasome subunit alpha type 1 OS=Homo sapiens OX=9606 GN=PSMA1 PE=1 SV=1	22	127	6	4.76E+07	4.74E+07	4.43E+07	3.88E+07	4.41E+07	3.70E+07	3.91E+07	4.90E+07	4.45E+07	4.22E+07	3.83E+07	3.15E+07	4.02E+07	4.08E+07	1.06	0.442280152	
P49411	Alpha-amylase 2 OS=Homo sapiens OX=9606 GN=AMY2A PE=1 SV=1	17	42	6	1.54E+07	1.47E+07	1.43E+07	1.23E+07	1.25E+07	1.23E+07	1.39E+07	1.39E+07	1.39E+07	1.39E+07	1.39E+07	1.39E+07	1.38E+07	1.21E+07	1.41	0.027389154	
Q29598	Head shock protein 105 kDa OS=Homo sapiens OX=9606 GN=HSPH1 PE=1 SV=5	9	58	6	1.54E+07	1.46E+07	1.24E+07	1.23E+07	1.27E+07	1.18E+07	1.24E+07	1.98E+06	9.11E+06	1.10E+07	6.78E+06	6.71E+06	1.32E+07	9.48E+06	1.39	0.48062372	
Q43684	Mitotic checkpoint protein BUB3 OS=Homo sapiens OX=9606 GN=BUB3 PE=1 SV=1	21	87	6	1.86E+07	2.10E+07	2.21E+07	2.12E+07	2.19E+07	1.88E+07	1.61E+07	1.75E+07	1.66E+07	1.65E+07	1.53E+07	1.36E+07	2.06E+07	1.59E+07	1.29	0.00247396	
P49736	DNA replication licensing factor MCM2 OS=Homo sapiens OX=9606 GN=MCM2 PE=1 SV=4	9	56	6	1.31E+07	1.43E+07	1.69E+07	1.33E+07	1.16E+07	1.38E+07	9.81E+06	9.82E+06	8.69E+06	8.93E+06	9.03E+06	7.76E+06	1.46E+07	9.01E+06	0.67	0.707947E+05	
Q9H44	Aminopeptidase B OS=Homo sapiens OX=9606 GN=RNPEP1 PE=1 SV=2	12	40	6	1.39E+07	1.29E+07	1.26E+07	1.36E+07	1.25E+07	1.35E+07	8.93E+06	1.15E+07	4.36E+06	3.67E+06	4.94E+06	6.92E+06	1.32E+07	6.71E+06	1.96	0.029919677	
Q9NVA2	Septin-11 OS=Homo sapiens OX=9606 GN=SEPT11 PE=1 SV=3	21	129	6	3.29E+07	3.33E+07	2.63E+07	2.76E+07	2.24E+07	2.42E+07	2.91E+07	2.87E+07	1.98E+07								

Supplemental Table 4. List of all proteins identified by label free proteomics analysis.

Accession	Description	Coverage [%]	# PSMs	# Unique Peptides	Antitriptingylne 1	Antitriptingylne 2	Antitriptingylne 3	Antitriptingylne 4	Antitriptingylne 5	Antitriptingylne 6	Vehicle 1	Vehicle 2	Vehicle 3	Vehicle 4	Vehicle 5	Vehicle 6	Average antitriptingylne	Average vehicle	Ratio antitriptingylne/vehicle	Log 2 fold change (antitriptingylne/vehicle)	P-value
P00736	Complement C1r subcomponent OS=Homo sapiens OX=9606 GN=C1R PE=1 SV=2	14	43	7	5.75E+06	3.35E+06	3.62E+06	6.35E+06	5.03E+06	5.67E+06	8.39E+06	7.63E+06	9.83E+06	7.21E+06	6.70E+06	3.00E+07	4.96E+06	1.16E+07	-1.23	0.13191979	
Q9NR30	Nuclear RNA helicase 2 OS=Homo sapiens OX=9606 GN=DDX21 PE=1 SV=5	14	64	7	8.58E+06	9.13E+06	8.47E+06	7.28E+06	6.59E+06	7.70E+06	6.80E+06	4.86E+06	3.92E+06	5.67E+06	5.53E+06	7.98E+06	6.0790562	5.75E+06	1.39	0.47	0.00790562
P32969	60S ribosomal protein L9 OS=Homo sapiens OX=9606 GN=RPL9 PE=1 SV=1	59	59	7	5.53E+07	2.64E+07	1.97E+07	1.74E+07	1.70E+07	2.45E+07	1.12E+07	2.33E+07	1.45E+07	1.46E+07	2.19E+07	1.63E+07	2.00E+07	1.70E+07	1.18	0.24	0.26951843
Q06830	Peroxiredoxin-1 OS=Homo sapiens OX=9606 GN=PRDX1 PE=1 SV=1	34	142	7	5.53E+07	5.20E+07	6.12E+07	4.76E+07	4.75E+07	4.87E+07	2.41E+07	2.74E+07	2.49E+07	2.41E+07	2.85E+07	1.68E+07	5.04E+07	2.43E+07	2.07	1.05	4.18809E-07
U15230	Laminin subunit alpha-5 OS=Homo sapiens OX=9606 GN=LAMA5 PE=1 SV=8	3	46	7	1.13E+07	5.89E+06	8.21E+06	8.33E+06	1.06E+07	8.31E+06	1.20E+07	9.05E+06	7.92E+06	9.33E+06	6.67E+06	6.30E+06	8.76E+06	8.87E+06	0.99	0.020395658	
P14543	Myosin-4 OS=Homo sapiens OX=9606 GN=MYO4 PE=1 SV=2	8	82	7	1.93E+07	1.15E+07	1.24E+07	1.43E+07	1.19E+07	1.43E+07	1.24E+07	1.24E+07	1.24E+07	1.24E+07	1.24E+07	1.24E+07	1.24E+07	1.24E+07	1.07E+07	0.59	0.003029207
P16133	60S ribosomal protein L15 OS=Homo sapiens OX=9606 GN=RPL15 PE=1 SV=1	31	137	7	7.63E+07	7.21E+07	7.68E+07	7.45E+07	6.81E+07	6.44E+07	4.58E+07	4.50E+07	4.35E+07	4.63E+07	3.94E+07	3.56E+07	7.05E+07	4.26E+07	1.67	0.73	8.53724E-07
Q16666	Gamma-interferon-inducible protein 16 OS=Homo sapiens OX=9606 GN=IFI16 PE=1 SV=3	10	73	7	1.92E+07	1.85E+07	1.95E+07	2.25E+07	2.14E+07	2.00E+07	9.15E+06	7.06E+06	8.27E+06	8.06E+06	8.27E+06	5.68E+06	2.02E+07	7.75E+06	1.60	1.38	3.29898E-08
O75475	PC4 and SFRS1-interacting protein OS=Homo sapiens OX=9606 GN=PSIP1 PE=1 SV=1	17	65	7	1.43E+07	1.48E+07	1.44E+07	1.50E+07	1.34E+07	1.39E+07	5.63E+06	5.20E+06	4.91E+06	4.04E+06	3.67E+06	5.50E+06	1.43E+07	1.50E+06	2.96	1.57	2.0519E-09
P30101	Protein disulfide-isomerase A3 OS=Homo sapiens OX=9606 GN=PIPD3 PE=1 SV=4	14	124	7	2.40E+07	2.43E+07	2.41E+07	2.47E+07	2.78E+07	2.38E+07	2.85E+07	2.99E+07	2.83E+07	2.85E+07	2.52E+07	2.30E+07	2.51E+07	2.71E+07	0.93	0.11	1.186769308
P30241	Pantoic acidase OS=Homo sapiens OX=9606 GN=PAO PE=1 SV=1	10	71	7	1.92E+07	1.63E+07	1.63E+07	1.51E+07	1.69E+07	1.19E+07	1.59E+07	1.69E+07	1.69E+07	1.69E+07	1.69E+07	1.69E+07	1.69E+07	1.69E+07	1.72E+07	0.17	0.00362193
P33748	Flap endonuclease 1 OS=Homo sapiens OX=9606 GN=FEN1 PE=1 SV=1	17	94	7	9.95E+07	1.00E+08	9.81E+07	1.04E+08	8.75E+07	9.39E+07	8.25E+07	8.12E+07	8.73E+07	8.85E+07	7.82E+07	6.97E+07	9.72E+07	8.12E+07	1.20	0.26	0.01466215
O94776	Mastitis-associated protein MT42 OS=Homo sapiens OX=9606 GN=MTA2 PE=1 SV=1	12	28	7	1.29E+07	1.30E+07	1.22E+07	1.42E+07	1.08E+07	1.16E+07	9.80E+06	6.46E+06	6.68E+06	6.76E+06	5.13E+06	5.52E+06	1.26E+07	7.16E+06	0.82	0.00020020	
Q9NZ94	EH domain-containing protein 2 OS=Homo sapiens OX=9606 GN=EH2 PE=1 SV=2	18	132	7	1.28E+07	1.28E+07	1.26E+07	1.39E+07	1.23E+07	1.43E+07	1.46E+07	1.23E+07	1.21E+07	1.24E+07	1.17E+07	1.05E+07	1.34E+07	1.23E+07	1.10	0.13	0.191221272
Q9Y223	Bifunctional UDP-N-acetylglucosamine 2-epimerase/N-acetylmannosamine kinase OS=Homo sapiens OX=9606 GN=GNE PE=1 SV=1	12	68	7	1.48E+07	1.41E+07	1.11E+07	1.18E+07	1.22E+07	1.03E+07	1.41E+07	1.44E+07	1.24E+07	1.38E+07	1.17E+07	9.75E+06	1.21E+07	1.27E+07	0.95	0.07	0.533882523
P22708	CAD protein OS=Homo sapiens OX=9606 GN=CAD PE=1 SV=1	37	708	7	7.57E+06	3.99E+06	1.19E+07	1.31E+07	1.09E+07	1.13E+07	7.77E+06	8.09E+06	8.37E+06	6.71E+06	6.07E+06	7.63E+06	1.08E+07	7.77E+06	1.39	0.00091683	
O13414	Pro-mRNase L1 OS=Homo sapiens OX=9606 GN=PMR1 PE=1 SV=1	10	245	7	1.04E+07	1.34E+07	1.34E+07	1.71E+07	1.24E+07	1.24E+07	1.20E+07	1.27E+07	1.30E+07	1.19E+07	1.12E+07	1.75E+06	1.34E+07	1.13E+07	0.24	0.11	1.17469E-08
Q9Y247	Nck-associated protein 1 OS=Homo sapiens OX=9606 GN=NCKAP1 PE=1 SV=1	6	83	7	1.05E+07	1.16E+07	1.62E+06	1.18E+07	1.02E+06	8.33E+06	8.68E+06	7.82E+06	1.04E+07	9.92E+06	6.87E+06	6.63E+06	9.92E+06	6.63E+06	0.25	0.01	1.24273246
P38117	Electron transfer flavoprotein subunit beta OS=Homo sapiens OX=9606 GN=ETFb PE=1 SV=3	35	40	7	1.80E+07	1.83E+07	1.52E+07	1.77E+07	1.66E+07	1.85E+07	9.78E+06	9.01E+06	1.17E+07	1.12E+07	8.02E+06	6.54E+06	1.74E+07	9.38E+06	0.79	0.91	1.90347E-05
P62081	40S ribosomal protein S7 OS=Homo sapiens OX=9606 GN=RPS7 PE=1 SV=1	46	60	7	2.19E+07	1.64E+07	1.60E+07	1.38E+07	1.41E+07	1.62E+07	1.08E+07	1.12E+07	8.22E+06	8.43E+06	9.74E+06	8.86E+06	1.64E+07	9.55E+06	1.82	0.89	0.0123388
P49304	Platelet-activating factor acetylhydrolase II subunit alpha OS=Homo sapiens OX=9606 GN=PAFAH1B1 PE=1 SV=2	21	46	7	2.44E+07	2.48E+07	2.75E+07	2.65E+07	3.13E+07	2.50E+07	1.79E+07	1.93E+07	1.91E+07	1.68E+07	1.66E+07	1.29E+07	2.76E+07	1.77E+07	1.50	0.58	0.00117847
P60709	Actin, cytoplasmic 1 OS=Homo sapiens OX=9606 GN=ACTB PE=1 SV=1	83	4523	7	2.96E+09	2.75E+09	2.75E+09	2.73E+09	2.74E+09	2.87E+09	2.40E+09	2.21E+09	2.45E+09	2.43E+09	2.43E+09	2.29E+09	2.65E+09	2.65E+09	0.23	0.00	1.2377E-05
P30241	Keratin, type I cytoskeletal 14 OS=Homo sapiens OX=9606 GN=KRT14 PE=1 SV=4	45	534	7	5.53E+07	6.75E+07	4.52E+07	6.82E+07	6.82E+07	6.82E+07	6.82E+07	6.82E+07	6.82E+07	6.82E+07	6.82E+07	6.82E+07	6.82E+07	6.82E+07	3.31E+07	0.22	0.00537448
P27348	14-3-3 protein theta OS=Homo sapiens OX=9606 GN=YYHQA PE=1 SV=1	42	159	8	4.20E+07	4.31E+07	5.30E+07	4.45E+07	4.81E+07	4.45E+07	4.50E+07	4.42E+07	4.62E+07	4.66E+07	4.69E+07	3.25E+07	4.59E+07	4.36E+07	1.05	0.07	0.428267914
P01023	Alpha-2-macroglobulin OS=Homo sapiens OX=9606 GN=A2M PE=1 SV=3	9	2864	8	9.99E+09	9.99E+09	1.19E+10	1.07E+10	1.12E+10	1.06E+10	9.80E+09	8.98E+09	1.09E+10	1.00E+10	1.13E+10	9.11E+09	1.07E+10	1.00E+10	1.10	0.10	1.80898824
O94973	AP-2 complex subunit alpha-2 OS=Homo sapiens OX=9606 GN=AP2A2 PE=1 SV=2	25	100	8	2.86E+07	3.25E+07	3.30E+07	3.31E+07	3.49E+07	3.88E+07	1.85E+07	2.06E+07	2.26E+07	1.49E+07	3.09E+07	1.96E+07	3.35E+07	2.12E+07	1.58	0.69	0.01271791
P62937	Pexidy-prolyl cis-trans isomerase A OS=Homo sapiens OX=9606 GN=PP1A PE=1 SV=2	67	305	8	1.42E+08	1.43E+08	9.47E+07	9.63E+07	8.57E+07	1.16E+08	1.91E+08	1.44E+08	9.83E+07	1.02E+08	1.18E+08	1.20E+08	1.13E+08	1.29E+08	0.88	0.11	0.377781509
Q16161	Septin-7 OS=Homo sapiens OX=9606 GN=SEPT7 PE=1 SV=1	16	198	8	6.72E+07	6.45E+07	4.02E+07	3.99E+07	3.80E+07	3.69E+07	2.30E+07	2.39E+07	2.60E+07	2.60E+07	3.24E+07	3.18E+07	4.12E+07	3.85E+07	1.23	0.30	0.00391985
Q9NQD3	Retculin-1 OS=Homo sapiens OX=9606 GN=RTN4 PE=1 SV=1	13	331	8	4.75E+07	4.10E+07	4.48E+07	4.48E+07	4.48E+07	4.48E+07	4.48E+07	4.48E+07	4.48E+07	4.48E+07	4.48E+07	4.48E+07	4.48E+07	4.48E+07	1.06	0.11	0.27203232
P61074	Triosephosphate isomerase OS=Homo sapiens OX=9606 GN=TFPI PE=1 SV=3	40	213	8	6.28E+07	4.64E+07	4.64E+07	4.85E+07	4.24E+07	4.63E+07	6.22E+07	4.86E+07	4.31E+07	4.26E+07	4.40E+07	3.95E+07	4.93E+07	4.65E+07	1.06	0.88	0.567813307
Q16401	26S proteasome non-ATPase regulatory subunit 5 OS=Homo sapiens OX=9606 GN=PSMD5 PE=1 SV=3	21	104	8	1.96E+07	1.58E+07	1.48E+07	1.93E+07	1.32E+07	1.60E+07	1.49E+07	1.26E+07	9.54E+06	7.63E+06	9.71E+06	1.13E+07	1.64E+07	1.09E+07	0.59	0.59	0.00392316
P22626	Heterogeneous nuclear ribonucleoproteins A2/B1 OS=Homo sapiens OX=9606 GN=HNRNP2B1 PE=1 SV=2	27	122	8	3.88E+07	3.97E+07	3.34E+07	3.71E+07	3.07E+07	3.67E+07	2.36E+07	2.36E+07	2.04E+07	2.11E+07	2.04E+07	1.85E+07	3.61E+07	2.13E+07	1.70	0.71	1.4672E-07
P67775	Serine/threonine-protein phosphatase 2A catalytic subunit alpha isoform OS=Homo sapiens OX=9606 GN=PPP2CA PE=1 SV=1	44	140	8	5.45E+07	5.15E+07	4.01E+07	3.96E+07	4.75E+07	5.46E+07	5.02E+07	4.70E+07	3.50E+07	2.99E+07	3.59E+07	3.58E+07	4.80E+07	3.90E+07	1.23	0.30	0.060716714
P30241	Pro-mRNase L1 OS=Homo sapiens OX=9606 GN=PMR1 PE=1 SV=1	10	245	7	1.04E+07	1.34E+07	1.34E+07	1.71E+07	1.24E+07	1.24E+07	1.20E+07	1.27E+07	1.30E+07	1.19E+07	1.12E+07	1.75E+06	1.34E+07	1.13E+07	0.24	0.11	1.17469E-08
Q93063	Exostosin-2 OS=Homo sapiens OX=9606 GN=EXT2 PE=1 SV=1	17	106	8	1.48E+07	1.64E+07	1.52E+07	1.61E+07	1.31E+07	1.67E+07	5.85E+06	2.63E+07	2.37E+07	2.21E+07	2.28E+07	2.55E+07	1.54E+07	2.58E+07	0.74	0.30	0.67022E-05
P18823	Inter-alpha-trypsin inhibitor heavy chain H2 OS=Homo sapiens OX=9606 GN=IH2H2 PE=1 SV=2	9	416	8	2.90E+08	3.31E+08	3.31E+08	3.32E+08	3.85E+08	2.87E+08	4.20E+08	4.60E+08	5.65E+08	4.51E+08	5.07E+08	3.40E+08	3.26E+08	4.57E+08	0.71	0.49	0.00655964
P08582	Melanotransferin OS=Homo sapiens OX=9606 GN=MELTF PE=1 SV=2	18	115	8	2.63E+07	2.31E+07	2.64E+07	2.30E+07	2.08E+07	2.10E+07	1.47E+07	1.13E+07	1.31E+07	1.27E+07	1.18E+07	8.00E+06	2.34E+07	1.19E+07	0.98	0.99	7.58315E-06
P17980	26S proteasome regulatory subunit 6A OS=Homo sapiens OX=9606 GN=PSMC3 PE=1 SV=3	22	141	8	3.58E+07	3.22E+07	3.17E+07	2.99E+07	2.39E+07	3.26E+07	2.60E+07	2.33E+07	1.82E+07	1.38E+07	1.86E+07	1.65E+07	3.10E+07	1.97E+07	1.57	0.69	0.00888322
P10108	Anthraxin III OS=Homo sapiens OX=9606 GN=SERPNC1 PE=1 SV=1	21	738	8	5.84E+08	6.21E+08	7.02E+08	6.40E+08	6.61E+08	5.92E+08	7.41E+08	8.87E+08</									

Supplementary Table 4. List of all proteins identified by label free proteomics analysis.

Accession	Description	Coverage [%]	IPSM46	# Unique Peptides	Antitryptic1	Antitryptic2	Antitryptic3	Antitryptic4	Antitryptic5	Antitryptic6	Vehicle 1	Vehicle 2	Vehicle 3	Vehicle 4	Vehicle 5	Vehicle 6	Average antitryptic1	Average vehicle	Ratio antitryptic1/vehicle	Log2 fold change (antitryptic1/vehicle)	P-value
Q9NSD9	Pharyngalysine-rRNA ligase beta subunit OS=Homo sapiens OX=9606 GN=FRSFB PE=1 SV=3	18	72	9	1.68E+07	1.59E+07	1.80E+07	2.25E+07	1.52E+07	2.04E+07	1.42E+07	1.35E+07	1.15E+07	1.41E+07	1.30E+07	1.37E+07	1.81E+07	1.34E+07	1.35	0.4	0.008214467
Q04637	Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens OX=9606 GN=EIF4G1 PE=1 SV=4	8	76	9	2.43E+07	2.43E+07	2.50E+07	2.50E+07	2.11E+07	1.08E+07	1.20E+07	1.09E+07	1.02E+07	1.07E+07	1.07E+07	9.81E+06	2.33E+07	1.13E+07	1.05	4.1	4.192E-08
Q07955	Serine/arginine-rich splicing factor 1 OS=Homo sapiens OX=9606 GN=SRSF1 PE=1 SV=2	3	68	9	1.62E+07	1.55E+07	1.62E+07	1.71E+07	1.48E+07	1.57E+07	1.52E+07	1.58E+07	1.45E+07	1.40E+07	1.29E+07	1.32E+07	1.59E+07	1.43E+07	1.12	0.16	0.016194833
Q9YV69	Cytosolic dynein 1 light intermediate chain 1 OS=Homo sapiens OX=9606 GN=DYNC1L1 PE=1 SV=3	22	47	9	8.72E+07	8.2E+07	8.82E+07	8.81E+07	9.80E+07	8.93E+07	9.47E+07	1.11E+08	9.29E+07	1.12E+08	9.19E+07	7.83E+07	8.89E+07	9.68E+07	0.92	-0.12	0.205672623
P04439	HLA class I histocompatibility antigen, A alpha chain OS=Homo sapiens OX=9606 GN=HLA-A PE=1 SV=2	52	728	10	3.40E+08	3.67E+08	3.35E+08	3.67E+08	3.49E+08	3.25E+08	2.03E+08	2.21E+08	1.95E+08	2.14E+08	1.88E+08	1.74E+08	3.52E+08	1.99E+08	1.77	0.62	2.0783E-08
P53103	14-3-3 protein zeta/delta OS=Homo sapiens OX=9606 GN=PPP1R12 PE=1 SV=2	20	216	10	3.85E+07	3.85E+07	3.85E+07	3.85E+07	3.85E+07	4.43E+07	3.85E+07	4.39E+07	3.85E+07	4.39E+07	3.85E+07	4.16E+07	4.33E+07	3.85E+07	1.07	0.08	0.326398307
Q04307	Alfa-actinin-4 OS=Homo sapiens OX=9606 GN=ACTN1 PE=1 SV=2	23	198	10	2.85E+07	2.46E+07	1.98E+07	2.32E+07	2.10E+07	2.21E+07	2.46E+07	2.07E+07	1.94E+07	1.82E+07	1.75E+07	1.69E+07	2.29E+07	1.95E+07	0.82	2.0	0.063512393
Q16181	Septin-7 OS=Homo sapiens OX=9606 GN=SEPTIN7 PE=1 SV=2	29	139	10	3.77E+07	2.80E+07	3.42E+07	3.22E+07	3.11E+07	3.62E+07	3.98E+07	3.01E+07	3.23E+07	2.72E+07	2.72E+07	2.99E+07	3.32E+07	3.11E+07	1.07	0.10	0.398713546
Q75533	Splicing factor 3B subunit 1 OS=Homo sapiens OX=9606 GN=SF3B1 PE=1 SV=3	14	121	10	2.24E+07	2.11E+07	2.33E+07	2.28E+07	2.29E+07	2.54E+07	1.99E+07	1.88E+07	1.24E+07	1.35E+07	1.72E+07	1.36E+07	2.30E+07	1.57E+07	0.43	0.001566099	
O15371	Eukaryotic translation initiation factor 3 subunit 3 OS=Homo sapiens OX=9606 GN=EIF3D PE=1 SV=1	28	105	10	2.09E+07	1.66E+07	2.64E+07	1.69E+07	2.56E+07	2.82E+07	9.59E+06	9.56E+06	1.41E+07	7.48E+06	1.49E+07	1.42E+07	2.25E+07	1.16E+07	0.95	0.001958966	
P41091	Eukaryotic translation initiation factor 2 subunit 3 OS=Homo sapiens OX=9606 GN=EIF2S3 PE=1 SV=3	37	128	10	3.39E+07	3.87E+07	3.39E+07	3.80E+07	3.54E+07	3.75E+07	2.79E+07	2.89E+07	2.38E+07	2.64E+07	2.73E+07	2.59E+07	3.62E+07	2.66E+07	1.36	0.44	7.93919E-06
Q9BLU2	Cell surface glycoprotein MUC1 OS=Homo sapiens OX=9606 GN=MUC1 PE=1 SV=2	24	106	10	2.78E+07	2.78E+07	3.18E+07	2.78E+07	2.78E+07	2.78E+07	2.78E+07	2.78E+07	2.78E+07	2.78E+07	2.78E+07	2.78E+07	2.78E+07	2.78E+07	2.20	0.00	1.33E+07
Q9B2U2	Heterogeneous nuclear ribonucleoprotein U-like protein 1 OS=Homo sapiens OX=9606 GN=HNRNPUL1 PE=1 SV=2	22	73	10	2.09E+07	1.55E+07	1.95E+07	2.32E+07	2.42E+07	2.04E+07	1.75E+07	1.09E+07	1.04E+07	1.24E+07	9.57E+06	8.70E+06	2.06E+07	1.16E+07	1.78	0.83	0.000525162
Q02878	60S ribosomal protein L6 OS=Homo sapiens OX=9606 GN=RPL6 PE=1 SV=3	42	185	10	9.32E+07	9.0E+07	7.39E+07	6.28E+07	7.31E+07	6.57E+07	5.74E+07	5.36E+07	4.93E+07	4.22E+07	4.92E+07	3.67E+07	7.66E+07	4.81E+07	0.67	0.001378615	
P26599	Poly(rimidine) tract-binding protein 1 OS=Homo sapiens OX=9606 GN=PTBP1 PE=1 SV=1	28	126	10	3.28E+07	3.04E+07	2.67E+07	3.01E+07	2.80E+07	3.16E+07	2.33E+07	2.15E+07	1.77E+07	1.83E+07	1.80E+07	1.38E+07	2.99E+07	1.88E+07	0.7	7.6072E-05	
PE1978	Heterogeneous nuclear ribonucleoprotein K OS=Homo sapiens OX=9606 GN=HNRNP K PE=1 SV=1	28	161	10	7.59E+07	8.44E+07	7.77E+07	7.31E+07	7.04E+07	7.33E+07	4.64E+07	5.21E+07	4.07E+07	4.36E+07	4.11E+07	3.97E+07	4.46E+07	4.40E+07	1.72	0.79	4.3559E-07
Q16631	DNA damage-binding protein 1 OS=Homo sapiens OX=9606 GN=DDIT3 PE=1 SV=1	14	105	10	3.41E+07	3.71E+07	2.40E+07	2.46E+07	2.52E+07	2.33E+07	2.37E+07	2.19E+07	1.60E+07	1.73E+07	1.79E+07	1.74E+07	2.81E+07	1.90E+07	1.46	0.56	0.01134477
P14865	Heterogeneous nuclear ribonucleoprotein 1 OS=Homo sapiens OX=9606 GN=HNRNP L1 PE=1 SV=2	26	78	10	2.48E+07	2.29E+07	1.98E+07	1.98E+07	1.99E+07	1.99E+07	1.99E+07	1.99E+07	1.22E+07	1.21E+07	1.14E+07	6.79E+06	2.22E+07	1.11E+07	2.00	0.67	3.65452E-05
O00571	ATP-dependent RNA helicase DDX3X OS=Homo sapiens OX=9606 GN=DDX3X PE=1 SV=3	20	96	10	2.64E+07	2.56E+07	2.61E+07	2.49E+07	1.99E+07	2.53E+07	2.81E+07	1.92E+07	1.55E+07	1.28E+07	1.63E+07	1.14E+07	2.48E+07	1.55E+07	1.59	0.67	0.000212078
P22087	RNA 2'-O-methyltransferase fibrillarin OS=Homo sapiens OX=9606 GN=FBL PE=1 SV=2	41	127	10	3.48E+07	3.73E+07	3.76E+07	3.30E+07	3.77E+07	3.88E+07	2.55E+07	2.71E+07	2.09E+07	2.20E+07	1.90E+07	2.09E+07	3.65E+07	2.26E+07	1.62	0.69	5.82681E-06
P53618	Coatomer subunit beta OS=Homo sapiens OX=9606 GN=COPB1 PE=1 SV=3	17	90	10	2.82E+07	3.15E+07	3.62E+07	2.66E+07	4.54E+07	3.74E+07	1.98E+07	2.07E+07	2.41E+07	1.85E+07	1.99E+07	1.61E+07	3.42E+07	2.05E+07	1.73	0.79	0.002403435
Q15582	Transforming growth factor-beta-induced protein in hi OS=Homo sapiens OX=9606 GN=TGFB1 PE=1 SV=1	19	94	10	1.63E+07	1.66E+07	2.40E+07	2.19E+07	2.22E+07	2.39E+07	3.79E+07	2.42E+07	3.34E+07	3.04E+07	3.88E+07	3.80E+07	2.08E+07	3.38E+07	0.62	0.00131446	
Q9N7K3	Obg-like ATPase 1 OS=Homo sapiens OX=9606 GN=OLA1 PE=1 SV=2	18	93	10	3.21E+07	3.01E+07	2.74E+07	2.57E+07	2.70E+07	3.58E+07	3.67E+07	3.37E+07	3.18E+07	2.90E+07	3.38E+07	3.90E+07	2.89E+07	3.02E+07	-0.09	-0.07	0.000000000
Q09845	FACT complex subunit SRB1 OS=Homo sapiens OX=9606 GN=SRB1 PE=1 SV=1	28	146	10	3.89E+07	3.89E+07	2.07E+07	2.07E+07	2.07E+07	2.07E+07	2.07E+07	2.07E+07	2.07E+07	2.07E+07	2.07E+07	2.07E+07	2.07E+07	2.07E+07	1.89	0.59	0.50391E-05
Q92616	WIP-2 alpha kinase activator GCN1 OS=Homo sapiens OX=9606 GN=GCN1 PE=1 SV=6	6	45	10	3.90E+07	3.54E+07	3.28E+07	2.19E+07	3.93E+07	3.02E+07	3.42E+07	3.87E+07	3.93E+07	2.11E+07	3.84E+07	3.88E+07	3.22E+07	3.17E+07	1.01	0.02	0.919279436
Q16610	Extracellular matrix protein 1 OS=Homo sapiens OX=9606 GN=ECM1 PE=1 SV=2	28	28	10	4.92E+06	4.40E+06	1.29E+06	3.02E+06	1.36E+06	3.21E+06	1.45E+06	4.69E+06	6.20E+06	1.45E+06	5.83E+06	5.81E+06	3.03E+06	1.62E+07	-2.42	0.10	1.31775E97
P27994	Transcriptin protein A 70 kDa DNA-binding subunit OS=Homo sapiens OX=9606 GN=RNAP1 PE=1 SV=2	24	94	10	3.02E+07	3.12E+07	2.30E+07	2.59E+07	2.36E+07	3.01E+07	2.28E+07	2.38E+07	1.84E+07	1.73E+07	1.66E+07	1.52E+07	2.77E+07	1.91E+07	1.44	0.53	0.003868654
Q92849	40S ribosomal protein S16 OS=Homo sapiens OX=9606 GN=RPS16 PE=1 SV=2	49	420	10	1.68E+08	1.79E+08	1.57E+08	1.58E+08	1.52E+08	1.47E+08	1.23E+08	1.27E+08	1.02E+08	1.06E+08	1.14E+08	1.03E+08	1.60E+08	1.12E+08	0.50	0.00	1.45359E-05
P42100	Nicotinamide phosphoribosyltransferase OS=Homo sapiens OX=9606 GN=NAMPT PE=1 SV=1	30	77	10	2.65E+07	2.65E+07	2.70E+07	2.76E+07	2.76E+07	2.76E+07	2.44E+07	2.02E+07	1.90E+07	2.02E+07	2.24E+07	1.59E+07	2.89E+07	2.02E+07	1.53	0.29	0.001868868
P35573	Glycogen debranching enzyme OS=Homo sapiens OX=9606 GN=GBL PE=1 SV=1	9	139	10	8.87E+07	2.82E+07	2.23E+07	2.07E+07	1.97E+07	2.48E+07	3.69E+07	3.59E+07	2.96E+07	3.66E+07	3.66E+07	3.66E+07	4.31E+07	3.08E+07	0.75	0.00	0.197953663
O60763	General vesicular transport factor p115 OS=Homo sapiens OX=9606 GN=USO3 PE=1 SV=1	11	94	10	2.97E+07	9.47E+07	1.34E+08	1.54E+08	1.55E+08	1.21E+08	1.33E+08	1.22E+08	1.88E+08	1.68E+08	1.38E+08	1.19E+08	1.25E+08	1.45E+08	0.86	-0.21	0.244434148
P22102	Trifunctional purine biosynthetic protein adenosine-3 OS=Homo sapiens OX=9606 GN=GART PE=1 SV=1	16	60	10	2.28E+07	2.67E+07	2.14E+07	2.88E+07	2.37E+07	2.06E+07	1.44E+07	1.62E+07	1.36E+07	1.55E+07	1.19E+07	1.07E+07	2.40E+07	1.37E+07	0.80	0.00	0.000120978
O00429	Dynamitin-1 like protein OS=Homo sapiens OX=9606 GN=DNM1L PE=1 SV=2	19	81	10	1.56E+07	2.01E+07	1.72E+07	1.49E+07	1.72E+07	1.56E+07	1.48E+07	1.78E+07	1.41E+07	1.88E+07	1.30E+07	1.68E+07	1.55E+07	1.57E+07	1.08	0.11	0.316199479
P20774	Mimcain OS=Homo sapiens OX=9606 GN=OGN PE=1 SV=1	27	295	10	1.03E+08	9.22E+07	9.30E+07	1.29E+08	1.11E+08	9.77E+07	1.46E+08	1.28E+08	1.27E+08	1.42E+08	1.29E+08	1.17E+08	1.04E+08	1.32E+08	-0.35	0.00	0.001925452
P19105	Vinculin OS=Homo sapiens OX=9606 GN=VCL PE=1 SV=1	22	84	10	2.79E+07	2.79E+07	2.19E+07	2.19E+07	2.19E+07	2.79E+07	3.10E+07	2.94E+07	3.45E+07	3.17E+07	3.14E+07	3.55E+07	3.14E+07	3.45E+07	0.22	0.00	0.139781974
Q9LUN7	Sorting nexin-6 OS=Homo sapiens OX=9606 GN=SNX6 PE=1 SV=1	22	64	10	1.76E+07	2.24E+07	2.11E+07	2.02E+07	1.92E+07	1.82E+07	1.57E+07	1.89E+07	1.78E+07	1.45E+07	1.79E+07	1.78E+07	1.99E+07	1.71E+07	1.16	0.22	0.018173079
P08779	Keratin, type I cytoskeletal 16 OS=Homo sapiens OX=9606 GN=KRT16 PE=1 SV=4	53	480	10	1.66E+08	7.54E+07	4.25E+07	5.44E+07	4.59E+07	1.39E+08	9.02E+07	1.66E+08	8.20E+07	9.51E+07	5.68E+07	3.56E+07	8.72E+07	7.59E+07	1.15	0.20	0.715868387
P06748	Nucleophosmin OS=Homo sapiens OX=9606 GN=NPM1 PE=1 SV=2	38	225	10	1.21E+08	1.30E+08	1.53E+08	1.42E+08	1.36E+08	1.55E+08	2.00E+07	8.84E+07	9.02E+07	6.97E+07	7.51E+07	7.11E+07	1.39E+08	8.08E+07	0.79	0.83	8.36565E-06
P16401	Histone H1.5 OS=Homo sapiens OX=9606 GN=H1-5 PE=1 SV=3	36	739	10	8.61E+08	8.83E+08	8.83E+08	8.83E+08	8.83E+08	8.12E+08	7										

# Supplementary Table 4. List of all proteins identified by label free proteomics analysis.

Accession	Description	Coverage [%]	# PSMs	# Unique Peptides	Antitriptyline 1	Antitriptyline 2	Antitriptyline 3	Antitriptyline 4	Antitriptyline 5	Antitriptyline 6	Vehicle 1	Vehicle 2	Vehicle 3	Vehicle 4	Vehicle 5	Vehicle 6	Average antitriptyline	Average vehicle	Ratio antitriptyline/vehicle	Log 2 fold change (antitriptyline/vehicle)	P-value
Q9Y30	RNA-splicing ligase RtcB homolog OS=Homo sapiens OX=9606 GN=RTCB PE=1 SV=1	39	174	13	4.43E+07	4.57E+07	4.55E+07	4.29E+07	3.63E+07	4.20E+07	3.60E+07	3.78E+07	3.16E+07	2.88E+07	3.30E+07	2.99E+07	4.28E+07	4.28E+07	1.00	0.000582775	0.39
O00622	CCN family member 1 OS=Homo sapiens OX=9606 GN=CCN1 PE=1 SV=1	36	309	13	6.61E+07	5.16E+07	5.93E+07	6.32E+07	6.69E+07	6.31E+07	1.39E+08	1.39E+08	1.38E+08	1.49E+08	1.14E+08	1.28E+08	6.17E+07	1.35E+08	0.46	1.28282E-06	-1.13
O95373	Importin-7 OS=Homo sapiens OX=9606 GN=IPO7 PE=1 SV=1	17	108	13	2.98E+07	3.47E+07	2.87E+07	2.90E+07	3.48E+07	3.36E+07	2.41E+07	1.89E+07	2.26E+07	1.96E+07	2.61E+07	2.17E+07	3.18E+07	2.22E+07	1.43	0.001494878	0.52
O00231	26S proteasome non-ATPase regulatory subunit 11 OS=Homo sapiens OX=9606 GN=PSMD11 PE=1 SV=3	44	282	13	5.86E+07	5.65E+07	5.48E+07	5.72E+07	5.47E+07	5.32E+07	2.87E+07	4.10E+07	3.80E+07	3.92E+07	3.78E+07	3.19E+07	5.55E+07	4.44E+07	1.25	0.017186633	0.25
Q15033	Peromysc-Homo sapiens OX=9606 GN=POSTN PE=1 SV=2	19	144	13	3.81E+07	3.22E+07	3.30E+07	2.89E+07	2.73E+07	3.27E+07	5.11E+07	4.86E+07	3.23E+07	3.92E+07	4.29E+07	3.78E+07	3.19E+07	4.20E+07	0.76	0.153545311	-0.40
P05768	60S ribosomal non-ATPase regulatory subunit 10A OS=Homo sapiens OX=9606 GN=PSMD10 PE=1 SV=2	21	166	13	3.79E+07	3.49E+07	3.50E+07	3.49E+07	3.49E+07	3.49E+07	4.78E+07	4.78E+07	4.78E+07	4.78E+07	4.78E+07	4.78E+07	4.78E+07	4.78E+07	1.00	0.000219193	0.51
P55786	Purothionin-sensitive aminopeptidase OS=Homo sapiens OX=9606 GN=NPPEPS PE=1 SV=2	19	148	13	3.87E+07	4.96E+07	3.77E+07	4.32E+07	3.72E+07	4.45E+07	4.48E+07	4.57E+07	4.64E+07	4.05E+07	4.73E+07	3.96E+07	4.22E+07	4.40E+07	-0.40	0.430260256	-0.40
P12429	Annexin A3 OS=Homo sapiens OX=9606 GN=ANXA3 PE=1 SV=3	44	233	13	7.70E+07	7.38E+07	6.16E+07	6.67E+07	7.53E+07	6.37E+07	6.64E+07	6.68E+07	6.38E+07	5.80E+07	5.76E+07	4.89E+07	6.97E+07	6.03E+07	1.16	0.21035041928	0.21
Q9Y230	RuvB-like 2 OS=Homo sapiens OX=9606 GN=RUVBL2 PE=1 SV=3	30	152	13	4.60E+07	4.63E+07	4.38E+07	4.80E+07	4.80E+07	4.38E+07	3.20E+07	2.90E+07	3.15E+07	2.89E+07	2.48E+07	4.64E+07	2.97E+07	1.16	0.6478941E+07	0.64	
Q8BLX7	Fermitin family homolog 3 OS=Homo sapiens OX=9606 GN=FERMT3 PE=1 SV=1	22	216	13	5.85E+07	6.21E+07	5.95E+07	6.33E+07	5.82E+07	5.49E+07	4.80E+07	7.88E+07	7.89E+07	7.94E+07	7.93E+07	7.97E+07	5.91E+07	7.98E+07	1.00	5.14872E-07	0.74
P06228	Eukaryotic translation initiation factor 3 subunit E OS=Homo sapiens OX=9606 GN=EIF3E PE=1 SV=1	35	209	13	5.87E+07	6.31E+07	6.35E+07	6.71E+07	6.77E+07	5.83E+07	8.41E+07	8.88E+07	4.52E+07	4.42E+07	4.50E+07	4.00E+07	6.31E+07	4.32E+07	1.46	0.61537E-06	1.46
Q14974	Importin subunit beta-1 OS=Homo sapiens OX=9606 GN=KPN1B1 PE=1 SV=2	24	168	13	4.81E+07	4.32E+07	4.32E+07	4.32E+07	4.32E+07	2.81E+07	2.81E+07	2.81E+07	2.81E+07	2.81E+07	2.81E+07	2.81E+07	2.81E+07	2.81E+07	1.00	7.01917E-06	0.48
P39023	60S ribosomal protein L3 OS=Homo sapiens OX=9606 GN=RPL3 PE=1 SV=2	43	274	14	1.15E+08	1.15E+08	1.16E+08	1.11E+08	1.11E+08	1.11E+08	1.11E+08	1.11E+08	1.11E+08	1.11E+08	1.11E+08	1.11E+08	1.11E+08	1.11E+08	1.00	1.36959E-06	0.56
P11021	Endoplasmic reticulum chaperone BiP OS=Homo sapiens OX=9606 GN=HSPA5 PE=1 SV=2	31	323	14	4.66E+07	4.68E+07	4.07E+07	3.68E+07	3.89E+07	3.58E+07	4.08E+07	3.79E+07	2.87E+07	3.07E+07	2.97E+07	3.20E+07	4.09E+07	3.33E+07	1.23	0.021029202	0.30
P06493	Cyclin-dependent kinase 1 OS=Homo sapiens OX=9606 GN=CDK1 PE=1 SV=3	56	238	14	8.99E+07	9.42E+07	8.03E+07	8.18E+07	9.00E+07	8.91E+07	4.63E+07	5.46E+07	4.57E+07	4.38E+07	5.08E+07	4.92E+07	8.75E+07	4.84E+07	1.81	1.3434E-07	0.85
P02753	60S ribosomal protein S1 OS=Homo sapiens OX=9606 GN=PSO1 PE=1 SV=1	40	305	14	1.64E+07	1.61E+08	1.31E+08	1.36E+08	1.22E+08	1.37E+08	7.79E+07	9.17E+07	6.42E+07	3.97E+07	6.74E+07	6.11E+07	1.38E+08	7.37E+07	1.88	1.80894E-06	1.88
P50960	Exportin-2 OS=Homo sapiens OX=9606 GN=OSE1L PE=1 SV=1	22	168	14	4.81E+07	4.32E+07	4.32E+07	4.32E+07	4.32E+07	5.06E+07	4.75E+07	3.39E+07	3.00E+07	3.48E+07	3.39E+07	2.71E+07	4.70E+07	3.22E+07	1.54	3.9912E-07	0.46
P20591	Interferon-induced GTP-binding protein M1 OS=Homo sapiens OX=9606 GN=MX1 PE=1 SV=4	32	182	14	6.06E+07	5.34E+07	5.73E+07	5.24E+07	4.74E+07	5.23E+07	2.31E+07	2.32E+07	2.02E+07	1.88E+07	1.76E+07	2.21E+07	5.39E+07	2.08E+07	2.59	0.1142E+07	1.97
P46777	60S ribosomal protein L5 OS=Homo sapiens OX=9606 GN=RPL5 PE=1 SV=3	47	322	14	1.86E+08	1.61E+08	1.38E+08	1.51E+08	1.49E+08	1.48E+08	1.31E+08	1.11E+08	0.96E+08	1.02E+08	0.94E+08	0.82E+08	1.56E+08	1.00E+08	1.52	4.83677E-05	1.44
Q9H223	EH domain-containing protein 4 OS=Homo sapiens OX=9606 GN=EHD4 PE=1 SV=1	42	198	14	5.51E+07	5.49E+07	4.75E+07	4.87E+07	4.77E+07	4.95E+07	1.39E+07	4.00E+07	3.70E+07	3.09E+07	3.21E+07	3.49E+07	5.05E+07	3.57E+07	1.45	0.623792E-05	0.60
P38606	N-type protein tyrosine kinase catalytic subunit A OS=Homo sapiens OX=9606 GN=PTP61A PE=1 SV=2	38	145	14	3.11E+07	3.34E+07	3.46E+07	3.17E+07	2.93E+07	3.07E+07	3.43E+07	3.31E+07	3.03E+07	2.71E+07	3.14E+07	2.87E+07	3.18E+07	3.06E+07	1.00	0.423305356	0.86
Q02026	Peroxidase homolog OS=Homo sapiens OX=9606 GN=PXND1 PE=1 SV=2	15	126	14	6.81E+07	1.84E+07	1.57E+07	1.02E+07	1.69E+07	1.84E+07	3.97E+07	2.93E+07	2.76E+07	2.46E+07	3.10E+07	2.61E+07	1.67E+07	2.91E+07	-0.80	0.016569565	-0.80
O00413	Importin-5 OS=Homo sapiens OX=9606 GN=IPO5 PE=1 SV=1	12	136	14	3.61E+07	3.60E+07	3.72E+07	3.72E+07	3.72E+07	2.81E+07	2.81E+07	2.81E+07	2.81E+07	2.81E+07	2.81E+07	2.81E+07	2.81E+07	2.81E+07	1.00	0.002178917	0.47
P14625	Endoplasmic reticulum OS=Homo sapiens OX=9606 GN=HSP90B1 PE=1 SV=1	22	317	14	4.28E+07	4.22E+07	3.45E+07	4.00E+07	3.74E+07	3.51E+07	4.55E+07	4.58E+07	4.23E+07	4.56E+07	4.30E+07	3.85E+07	3.87E+07	4.35E+07	0.89	1.02781294E-07	0.89
Q43854	EGF-like repeat and discoidin-like domain-containing protein 3 OS=Homo sapiens OX=9606 GN=EDIL3 PE=1 SV=1	15	185	14	8.84E+07	9.20E+07	7.83E+07	9.00E+07	7.63E+07	8.93E+07	1.09E+08	1.12E+08	1.09E+08	1.15E+08	9.30E+07	8.98E+07	8.50E+07	1.05E+08	-0.30	0.041098281	-0.30
P35998	26S proteasome regulatory subunit 7 OS=Homo sapiens OX=9606 GN=PSM22 PE=1 SV=3	42	161	14	4.70E+07	4.55E+07	3.77E+07	4.42E+07	3.87E+07	3.77E+07	3.38E+07	2.94E+07	3.15E+07	3.09E+07	2.28E+07	1.94E+07	4.18E+07	2.80E+07	1.55	0.000812550	1.55
Q55335	Heterochromatin protein 1-binding protein 3 OS=Homo sapiens OX=9606 GN=HP1B3 PE=1 SV=1	26	148	14	4.52E+07	4.14E+07	4.68E+07	4.68E+07	4.59E+07	4.16E+07	3.21E+07	3.06E+07	3.33E+07	3.32E+07	3.16E+07	2.17E+07	4.46E+07	3.04E+07	1.47	0.000125267	1.47
P06280	40S ribosomal protein S11 OS=Homo sapiens OX=9606 GN=PSO11 PE=1 SV=3	63	350	15	1.70E+08	1.69E+08	1.69E+08	1.71E+08	1.75E+08	1.52E+08	1.99E+08	1.24E+08	1.24E+08	1.24E+08	1.11E+08	0.98E+08	1.08E+08	1.18E+08	1.43	1.06456E-06	1.43
P11388	DNA topoisomerase 2-alpha OS=Homo sapiens OX=9606 GN=TOP2A PE=1 SV=3	12	94	14	2.05E+07	2.18E+07	2.21E+07	2.14E+07	2.14E+07	1.91E+07	1.93E+07	1.37E+07	1.72E+07	1.63E+07	1.03E+07	8.15E+06	1.08E+07	1.54E+07	0.51	0.006878621	0.51
P07942	Laminin subunit beta-1 OS=Homo sapiens OX=9606 GN=LAMB1 PE=1 SV=2	10	133	14	2.07E+07	2.07E+07	2.27E+07	2.58E+07	2.45E+07	2.63E+07	3.64E+07	3.49E+07	3.43E+07	3.24E+07	3.62E+07	2.67E+07	2.47E+07	3.26E+07	0.76	0.001423994	0.76
P62826	GTP-binding nuclear protein Ran OS=Homo sapiens OX=9606 GN=RRN PE=1 SV=3	49	719	15	4.54E+08	5.14E+08	4.04E+08	4.17E+08	4.32E+08	4.24E+08	3.87E+08	4.25E+08	4.09E+08	4.25E+08	3.54E+08	3.14E+08	4.41E+08	3.74E+08	1.00	0.0168344	1.00
Q16555	Dihydropyrimidinase-related protein 2 OS=Homo sapiens OX=9606 GN=HGPS2 PE=1 SV=1	46	280	15	6.41E+07	6.79E+07	6.25E+07	5.95E+07	5.68E+07	6.28E+07	6.77E+07	7.12E+07	6.42E+07	6.42E+07	5.79E+07	5.96E+07	6.23E+07	6.52E+07	0.24	0.318854339	0.24
P62241	60S ribosomal protein S8 OS=Homo sapiens OX=9606 GN=PSO8 PE=1 SV=2	60	828	15	3.14E+08	3.23E+08	3.38E+08	3.12E+08	3.21E+08	3.45E+08	2.09E+08	2.20E+08	1.95E+08	2.02E+08	1.98E+08	1.75E+08	3.25E+08	2.00E+08	1.62	0.049199E-08	1.62
Q9Y242	60S ribosomal protein L7a OS=Homo sapiens OX=9606 GN=RPL7A PE=1 SV=1	36	167	15	3.14E+08	3.23E+08	3.38E+08	3.12E+08	3.21E+08	3.45E+08	2.09E+08	2.20E+08	1.95E+08	2.02E+08	1.98E+08	1.75E+08	3.25E+08	2.00E+08	1.62	0.049199E-08	1.62
Q9NMZ1	Myoferlin OS=Homo sapiens OX=9606 GN=MYOF PE=1 SV=1	11	174	14	4.47E+07	4.29E+07	3.99E+07	4.10E+07	3.92E+07	3.94E+07	3.04E+07	2.42E+07	2.81E+07	2.69E+07	2.43E+07	2.10E+07	4.10E+07	2.58E+07	1.59	0.772441E-06	1.59
Q9UHB9	Signal recognition particle subunit SRP68 OS=Homo sapiens OX=9606 GN=SRP68 PE=1 SV=2	32	198	15	4.23E+07	4.33E+07	3.87E+07	3.92E+07	3.53E+07	3.89E+07	2.15E+07	1.72E+07	1.62E+07	1.78E+07	1.78E+07	1.53E+07	3.96E+07	1.76E+07	2.24	1.787930E-08	2.24
O75955	Flotillin-1 OS=Homo sapiens OX=9606 GN=FLT1 PE=1 SV=3	38	175	15	3.40E+07	3.62E+07	3.73E+07	4.10E+07	4.21E+07	3.79E+07	5.26E+07	5.08E+07	5.08E+07	4.42E+07	4.42E+07	4.49E+07	3.81E+07	4.99E+07	-1.37	7.60348E-05	-1.37
O75891	Cytosolic 10-formyltetrahydrofolate dehydrogenase OS=Homo sapiens OX=9606 GN=ALDH1L1 PE=1 SV=2	19	425	15	1.97E+08	2.08E+08	1.74E+08	1.85E+08	1.70E+08	1.63E+08	2.51E+08	2.65E+08	2.09E+08	2.38E+08	2.15E+08	2.03E+08	1.83E+08	2.30E+08	0.80	0.00445169	0.80
P28786	Transferin receptor protein 1 OS=Homo sapiens OX=9606 GN=TFRC PE=1 SV=2	24	313	15	7.51E+07	7.97E+07															

**Supplementary Table 4. List of all proteins identified by label free proteomics analysis.**

Accession	Description	Coverage [%]	# PSMs	# Unique Peptides	Antitrypsine 1	Antitrypsine 2	Antitrypsine 3	Antitrypsine 4	Antitrypsine 5	Antitrypsine 6	Vehicle 1	Vehicle 2	Vehicle 3	Vehicle 4	Vehicle 5	Vehicle 6	Average antitrypsine	Average vehicle	Ratio antitrypsine/vehicle	Log 2 fold change (antitrypsine/vehicle)	P-value
Q8V6P6	Cullin-associated NEDD8-dissociated protein 1 OS=Homo sapiens OX=9606 GN=CAND1 PE=1 SV=2	24	316	21	9.30E+07	9.16E+07	8.84E+07	8.76E+07	8.37E+07	8.43E+07	9.53E+07	8.02E+07	6.96E+07	7.19E+07	6.46E+07	7.08E+07	8.78E+07	7.52E+07	1.17	0.03856109	
P35871	Phosphoglucomutase 1 OS=Homo sapiens OX=9606 GN=PGM1 PE=1 SV=2	50	249	21	1.18E+08	1.10E+08	1.18E+08	1.26E+08	1.25E+08	1.14E+08	1.57E+08	1.62E+08	1.49E+08	1.48E+08	1.37E+08	1.05E+08	1.07E+08	1.45E+08	0.82	-0.297021135	
P08473	Nephrilysin OS=Homo sapiens OX=9606 GN=NME PE=1 SV=2	40	278	21	7.90E+07	7.78E+07	8.97E+07	8.40E+07	9.29E+07	8.00E+07	6.14E+07	5.84E+07	7.07E+07	8.06E+07	5.84E+07	4.12E+07	8.54E+07	6.18E+07	1.38	0.005749762	
Q9P2J5	Leucine--rRNA ligase, cytoplasmic OS=Homo sapiens OX=9606 GN=LARS PE=1 SV=2	23	258	21	7.95E+07	7.32E+07	7.08E+07	6.19E+07	7.17E+07	6.54E+07	7.37E+07	4.23E+07	4.38E+07	4.18E+07	4.68E+07	3.68E+07	7.04E+07	4.34E+07	1.62	0.470058705	
Q57457	E3 ubiquitin-protein ligase UBR4 OS=Homo sapiens OX=9606 GN=UBR4 PE=1 SV=1	7	102	21	2.18E+07	1.92E+07	2.20E+07	2.17E+07	2.23E+07	2.09E+07	1.63E+07	1.05E+07	1.34E+07	1.19E+07	1.42E+07	1.15E+07	2.13E+07	1.30E+07	1.65	0.32881E-05	
Q92366	116 kDa US small nuclear ribonucleoprotein component OS=Homo sapiens OX=9606 GN=U2ED2 PE=1 SV=1	33	201	21	1.71E+08	1.81E+08	1.68E+08	1.47E+08	1.63E+08	1.63E+08	1.25E+08	1.34E+08	1.16E+08	1.21E+08	1.01E+08	1.62E+08	1.30E+08	1.62E+08	0.83	0.002092621	
Q15029	116 kDa US small nuclear ribonucleoprotein component OS=Homo sapiens OX=9606 GN=U2ED2 PE=1 SV=1	33	201	21	5.50E+07	5.46E+07	5.29E+07	5.45E+07	5.85E+07	5.42E+07	3.82E+07	3.65E+07	3.86E+07	3.87E+07	4.25E+07	3.41E+07	5.49E+07	3.81E+07	1.44	0.764209E-07	
P08238	Heat shock protein HSP 90-beta OS=Homo sapiens OX=9606 GN=HSP90AB1 PE=1 SV=4	52	1866	22	8.71E+08	9.37E+08	8.56E+08	8.81E+08	8.96E+08	8.14E+08	8.91E+08	9.15E+08	8.41E+08	8.06E+08	8.12E+08	7.02E+08	8.76E+08	8.28E+08	1.06	0.206432937	
P06737	Glycogen phosphorylase, liver form OS=Homo sapiens OX=9606 GN=PYGL PE=1 SV=4	40	787	22	2.48E+08	2.43E+08	2.23E+08	2.25E+08	2.25E+08	2.26E+08	2.52E+08	2.53E+08	2.43E+08	2.24E+08	2.33E+08	1.95E+08	2.31E+08	2.33E+08	0.99	-0.834485045	
P21399	Cytosolic acconitate hydratase OS=Homo sapiens OX=9606 GN=ACO1 PE=1 SV=2	34	668	22	2.47E+08	2.44E+08	2.31E+08	2.36E+08	2.15E+08	2.33E+08	8.52E+08	3.18E+08	2.68E+08	2.66E+08	2.61E+08	2.51E+08	3.18E+08	3.69E+08	0.86	0.264913113	
P05023	Sodium/potassium-transporting ATPase subunit alpha-1 OS=Homo sapiens OX=9606 GN=ATP1A1 PE=1 SV=1	26	335	22	1.31E+08	1.29E+08	1.21E+08	1.26E+08	1.24E+08	1.16E+08	1.02E+08	1.04E+08	9.44E+07	8.91E+07	8.88E+07	7.44E+07	1.24E+08	9.21E+07	1.35	0.000273934	
P35871	Cotaster subunit beta OS=Homo sapiens OX=9606 GN=CB2 PE=1 SV=2	39	231	22	6.22E+07	7.29E+07	5.98E+07	6.30E+07	6.16E+07	6.42E+07	3.66E+07	3.24E+07	3.89E+07	4.04E+07	3.17E+07	3.17E+07	5.04E+07	3.84E+07	1.78	0.05582706	
R04406	Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens OX=9606 GN=GAPDH PE=1 SV=3	82	4882	23	1.82E+09	1.71E+09	1.73E+09	1.64E+09	1.81E+09	1.91E+09	1.69E+09	1.72E+09	1.61E+09	1.60E+09	1.50E+09	1.55E+09	1.77E+09	1.63E+09	1.09	0.013562483	
P07900	Heat shock protein HSP 90-alpha OS=Homo sapiens OX=9606 GN=HSP90AA1 PE=1 SV=5	50	1956	23	3.02E+08	2.93E+08	3.25E+08	3.36E+08	3.11E+08	2.85E+08	3.04E+08	3.40E+08	3.59E+08	3.17E+08	3.37E+08	2.82E+08	3.09E+08	3.02E+08	1.00	0.322908266	
P08195	4F2 cell-surface antigen heavy chain OS=Homo sapiens OX=9606 GN=SLC3A2 PE=1 SV=3	40	505	23	2.10E+08	2.14E+08	1.84E+08	1.79E+08	1.76E+08	1.88E+08	8.27E+07	8.29E+07	5.68E+07	6.45E+07	7.38E+07	6.18E+07	1.92E+08	7.04E+07	2.73	1.18049E-07	
Q9Y5V9	FACT complex subunit SPT16 OS=Homo sapiens OX=9606 GN=SPT16H PE=1 SV=1	29	295	23	7.51E+07	8.30E+07	8.24E+07	8.02E+07	8.72E+07	7.82E+07	4.55E+07	3.80E+07	4.33E+07	3.79E+07	3.80E+07	3.57E+07	7.76E+07	3.97E+07	1.95	0.77842E-07	
Q15149	Plectin OS=Homo sapiens OX=9606 GN=PLEC PE=1 SV=3	7	143	23	3.00E+07	3.30E+07	3.08E+07	3.88E+07	3.33E+07	3.19E+07	2.19E+07	1.83E+07	2.27E+07	2.31E+07	2.02E+07	1.84E+07	3.30E+07	2.08E+07	1.59	0.285403E-08	
P11589	Alpha-enolase OS=Homo sapiens OX=9606 GN=ENO1 PE=1 SV=2	49	1037	24	5.36E+08	6.02E+08	4.65E+08	4.48E+08	4.48E+08	5.69E+08	6.82E+08	4.69E+08	5.25E+08	5.39E+08	5.18E+08	5.04E+08	5.04E+08	5.04E+08	0.92	0.256439E-08	
R48643	T-complex protein 1 subunit epsilon OS=Homo sapiens OX=9606 GN=CCT5 PE=1 SV=1	56	678	24	2.22E+08	2.23E+08	1.91E+08	2.00E+08	2.00E+08	2.06E+08	1.47E+08	1.56E+08	1.40E+08	1.28E+08	1.30E+08	1.09E+08	2.06E+08	1.35E+08	1.53	0.61124491E-05	
P50991	T-complex protein 1 subunit delta OS=Homo sapiens OX=9606 GN=CCT4 PE=1 SV=4	51	660	24	2.95E+08	2.90E+08	2.69E+08	2.72E+08	2.43E+08	2.83E+08	1.98E+08	1.90E+08	1.63E+08	1.81E+08	1.71E+08	1.57E+08	2.75E+08	1.77E+08	1.56	0.21589E-06	
P19338	Nucleolin OS=Homo sapiens OX=9606 GN=NCL PE=1 SV=3	33	322	24	9.01E+07	8.93E+07	9.76E+07	1.31E+08	9.84E+07	1.05E+08	6.56E+07	6.26E+07	6.58E+07	6.45E+07	6.44E+07	5.27E+07	1.02E+08	6.15E+07	0.64	0.000599336	
P08758	Annexin A5 OS=Homo sapiens OX=9606 GN=ANXA5 PE=1 SV=2	80	991	25	5.08E+08	4.55E+08	4.84E+08	4.77E+08	5.04E+08	4.41E+08	3.91E+08	3.55E+08	3.40E+08	3.38E+08	3.74E+08	2.94E+08	4.78E+08	3.49E+08	1.37	0.300974E-06	
P73371	T-complex protein 1 subunit beta OS=Homo sapiens OX=9606 GN=CCT2 PE=1 SV=4	61	555	25	2.83E+08	2.85E+08	2.43E+08	2.51E+08	2.35E+08	2.30E+08	1.92E+08	2.02E+08	1.80E+08	1.89E+08	1.84E+08	1.51E+08	2.55E+08	1.76E+08	1.44	0.000124793	
P11142	Heat shock cognate 71 kDa protein OS=Homo sapiens OX=9606 GN=HSP7AB PE=1 SV=1	38	2437	25	6.22E+07	6.92E+07	6.95E+07	1.01E+08	9.65E+07	9.54E+07	1.01E+08	9.02E+08	9.29E+08	9.72E+08	9.23E+08	9.23E+08	9.23E+08	9.23E+08	1.05	0.000234768	
P40227	T-complex protein 1 subunit zeta OS=Homo sapiens OX=9606 GN=CCT6A PE=1 SV=3	53	709	26	2.97E+08	2.95E+08	2.92E+08	3.03E+08	3.06E+08	2.83E+08	2.21E+08	2.17E+08	2.05E+08	1.92E+08	2.01E+08	1.77E+08	2.96E+08	2.02E+08	1.46	0.5516712E-06	
P13010	X-ray repair cross-complementing protein 5 OS=Homo sapiens OX=9606 GN=XRCC5 PE=1 SV=3	53	374	26	1.10E+08	1.14E+08	1.09E+08	1.01E+08	1.12E+08	1.13E+08	7.94E+07	8.32E+07	7.40E+07	7.05E+07	6.78E+07	6.29E+07	1.10E+08	7.30E+07	1.51	4.82714E-06	
P17987	T-complex protein 1 subunit alpha OS=Homo sapiens OX=9606 GN=TCP1 PE=1 SV=1	66	692	26	2.89E+08	3.16E+08	3.03E+08	2.56E+08	2.93E+08	2.80E+08	2.04E+08	2.37E+08	1.97E+08	2.10E+08	2.14E+08	1.72E+08	2.90E+08	2.05E+08	1.41	0.373317E-06	
Q8VUM4	Programmed cell death 6-interacting protein OS=Homo sapiens OX=9606 GN=PCDD6IP PE=1 SV=1	41	379	26	8.91E+07	9.65E+07	9.91E+07	9.75E+07	9.05E+07	9.14E+07	8.57E+07	7.93E+07	8.23E+07	8.04E+07	8.38E+07	7.47E+07	9.38E+07	8.10E+07	1.16	0.000202288	
Q14152	Eukaryotic translation initiation factor 3 subunit A OS=Homo sapiens OX=9606 GN=EIF3A PE=1 SV=1	21	374	26	1.17E+08	1.15E+08	1.11E+08	1.12E+08	8.94E+07	1.05E+08	6.75E+07	6.15E+07	6.26E+07	6.03E+07	5.66E+07	6.17E+07	1.09E+08	6.15E+07	1.76	0.32698E-05	
P0DMV9	Heat shock 70 kDa protein 1B OS=Homo sapiens OX=9606 GN=HSPA1B PE=1 SV=1	63	974	27	8.82E+07	8.87E+07	8.84E+07	8.95E+07	8.95E+07	6.63E+07	6.79E+07	6.89E+07	6.84E+07	6.84E+07	6.77E+07	6.77E+07	6.77E+07	6.77E+07	0.82	0.110239774	
P49368	T-complex protein 1 subunit gamma OS=Homo sapiens OX=9606 GN=CCT3 PE=1 SV=4	54	599	27	2.47E+08	2.40E+08	1.93E+08	1.83E+08	1.84E+08	1.15E+08	1.59E+08	1.58E+08	1.24E+08	1.40E+08	1.33E+08	1.34E+08	2.10E+08	1.41E+08	1.49	0.0008459	
P13193	Bifunctional purine biosynthesis protein PURH OS=Homo sapiens OX=9606 GN=ATIC PE=1 SV=3	57	530	27	1.55E+08	1.54E+08	1.45E+08	1.47E+08	1.55E+08	1.25E+08	1.82E+08	1.85E+08	1.57E+08	1.53E+08	1.56E+08	1.37E+08	1.48E+08	1.62E+08	0.57	0.151560445	
Q98932	T-complex protein 1 subunit eta OS=Homo sapiens OX=9606 GN=CCT7 PE=1 SV=4	61	772	28	3.51E+08	3.48E+08	3.08E+08	3.07E+08	3.34E+08	3.28E+08	2.33E+08	2.52E+08	2.20E+08	2.33E+08	2.34E+08	2.02E+08	3.29E+08	2.29E+08	1.44	0.2210E-06	
P05565	Integrin beta-1 OS=Homo sapiens OX=9606 GN=ITGB1 PE=1 SV=2	36	775	28	2.83E+08	3.06E+08	3.73E+08	3.77E+08	3.84E+08	3.64E+08	3.69E+08	2.76E+08	2.39E+08	2.89E+08	2.21E+08	2.18E+08	3.75E+08	2.42E+08	1.50	1.13194E-05	
P11589	C-1-naphtholase synthase, cytoplasmic OS=Homo sapiens OX=9606 GN=NMTHFD1 PE=1 SV=3	26	321	28	1.37E+08	1.45E+08	1.38E+08	1.32E+08	1.21E+08	1.23E+08	1.83E+08	1.82E+08	1.25E+08	1.35E+08	1.31E+08	1.29E+08	1.32E+08	1.32E+08	1.06	0.000267897	
P08074	Poly (ADP-ribose) polymerase 1 OS=Homo sapiens OX=9606 GN=PARP1 PE=1 SV=4	40	499	30	2.05E+08	1.95E+08	2.07E+08	2.09E+08	2.01E+08	1.95E+08	1.08E+08	1.04E+08	9.42E+07	9.77E+07	8.86E+07	8.98E+07	2.02E+08	9.70E+07	2.08	0.165545E-10	
P53621	Cotaster subunit alpha OS=Homo sapiens OX=9606 GN=COPA PE=1 SV=2	34	420	30	2.86E+08	2.80E+08	3.24E+08	4.11E+08	4.45E+08	3.24E+08	3.67E+08	3.78E+08	4.07E+08	6.55E+08	5.21E+08	3.01E+08	3.45E+08	4.23E+08	-0.29	0.148602083	
P41252	Isoleucine--rRNA ligase, cytoplasmic OS=Homo sapiens OX=9606 GN=IARS PE=1 SV=2	32	497	30	1.33E+08	1.45E+08	1.15E+08	1.29E+08	1.26E+08	1.26E+08	8.39E+07	7.54E+07	7.54E+07	7.08E+07	7.22E+07	7.20E+07	7.20E+07	7.48E+07	1.72	0.489517E-07	
P98160	Basement membrane-specific heparan sulfate proteoglycan core protein OS=Homo sapiens OX=9606 GN=HSPG2 PE=1 SV=1	10	269	30	9.29E+07	6.69E+07	5.83E+07	6.04E+07	5.34E+07	6.05E+07	9.00E+07	8.58E+07	5.08E+07	5.65E+07	5.69E+07	6.93E+07	6.54E+07	6.82E+07	-0.06	0.758444528	
Q8P2D9	Ple-mRNA-processing-splicing factor 8 OS=Homo sapiens OX=9606 GN=PRPF8 PE=1 SV=2	19	225	30	6.09E+07	5.59E+07	5.37E+07	4.86E+07													