

Supplementary Materials

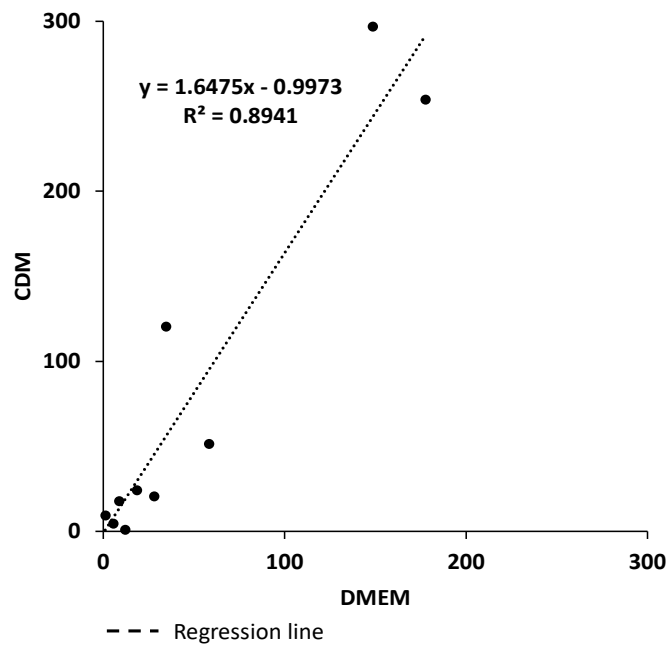


Figure S1. A scatter plot of the housekeeping genes' quantitative values. A scatter plot showing the correlation ($R^2 = 0.8941$) between the quantitative value of the CDM hADSCs and DMEM hADSCs: TFRC, YWHAZ, RPLP0, RPLP1, RPLP2, B2M, RPS18, PGK1, PPIA, and GAPDH ($n = 10$). The dotted line is the regression line. Each dot shows the abbreviated name of the protein. $n = 1$.

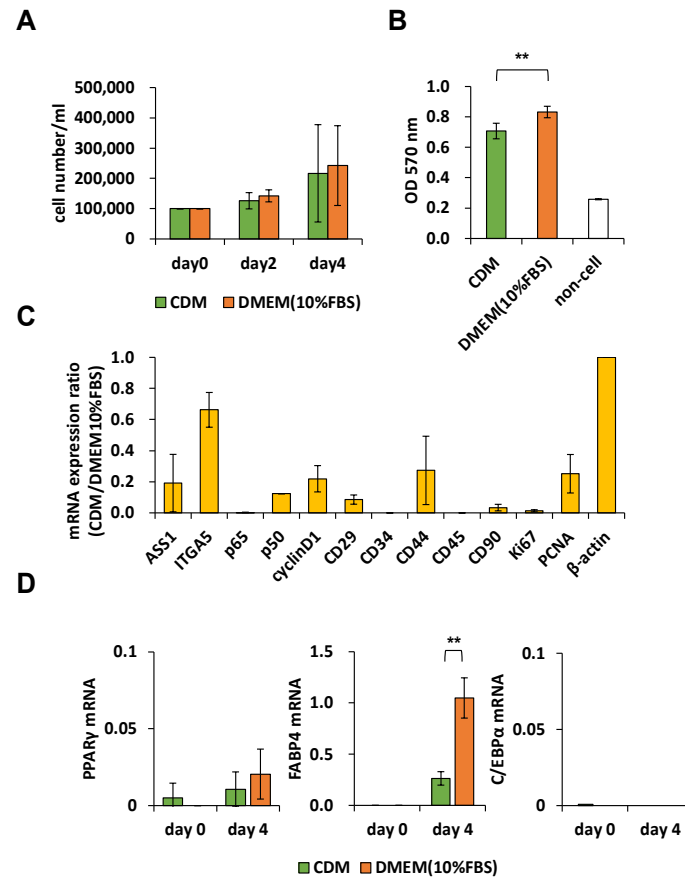


Figure S2. The evaluation of the cell growth ability, gene expression characteristics, and early adipocyte differentiation potential of hADSCs cultured in CDM or DMEM. Cell proliferation assays. hADSCs were counted after 2 and 4 days of culture in the CDM or DMEM (10% FBS). $n = 4$. Data are represented as the mean \pm S.D. (A). MTT cell count assays. hADSCs were analyzed after 4 days of culture in CDM or DMEM (10% FBS). Each measurement was obtained using a microplate reader. $n = 4$. Data are represented as the mean \pm S.D. ** $p < 0.01$ (B). The expression rate of various gene mRNAs expressed in ADSCs cultured in CDM was compared with that of ADSCs cultured in DMEM (10% FBS). cDNA was synthesized using ADSCs that had been cultured in both CDM and DMEM (10% FBS) for 48 h. The expression was calculated using the $\Delta\Delta C_t$ method. The expression of the target gene was corrected by the expression of the housekeeping gene (β -actin). Real time PCR was performed to detect factors related to the cell cycle, cell surface markers, and cell proliferation. The expression of various factors expressed by hADSCs cultured in DMEM (10% FBS) medium was defined as 1. The vertical axis shows the expression ratio of various factors expressed by hADSCs cultured in CDM. $n = 4$. Data are represented as the mean \pm S.D. (C). The expression of adipocyte differentiation marker gene mRNA on days 0 and 4 was shown by inducing the differentiation of ADSCs cultured in CDM or DMEM (10% FBS) into adipocytes. The expression was calculated using the $\Delta\Delta C_t$ method. When determining the expression of the target gene, the expression of the housekeeping gene (β -actin) was taken as 1. $n = 4$. Data are represented as the mean \pm S.D. ** $p < 0.01$ (D).

Table S1. Identification of endogenous proteins contained in hADSC cultured in medium, Chemically Defined.

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UniProt/EMBL/PROT ID	Description	Protein score ^a	Protein mass (kDa)	pI ^b	Num. of matches ^c	Num. of significant matches ^d	Num. of sequences ^e	Num. of significant sequences ^f	Num. of unique sequences ^g	Sequence coverage ^h	emPAI
ACTB1_HUMAN	Putative beta-actin-like protein 3	814	41889	5.31	240	84	5	5	1	0.18	0.64
ALBU_HUMAN	Serum albumin	5054	69221	5.22	1087	544	44	35	44	0.76	10.79
VIM2_HUMAN	Vimentin	5780	53815	5.06	1038	421	48	39	46	0.79	21.41
MYO9_HUMAN	Myosin-9	7160	226392	5.5	438	231	54	75	54	0.54	1.98
ENO4_HUMAN	Alpha-enolase	5608	47139	7.01	410	221	20	16	12	0.67	4.95
GDP_HUMAN	Glyceroldehyde-3-phosphate dehydrogenase	5249	36030	8.57	489	202	15	14	8	0.71	11.59
KPF1_HUMAN	Pyruvate kinase PKM	4800	57000	7.96	385	231	33	29	7	0.7	8.01
TBBA_HUMAN	Tubulin beta-2A chain	5170	49875	4.78	331	188	23	17	3	0.75	4.78
TBBB_HUMAN	Tubulin beta-8 chain	2182	48825	4.77	233	151	20	16	10	0.7	4.92
S10A_HUMAN	Protein S100-A6	4259	10173	5.33	140	104	7	4	7	0.39	6.25
FLNA_HUMAN	Filamin-A	3555	280564	5.7	359	190	79	47	75	0.52	1.11
FLNB_HUMAN	Filamin-B	796	277990	5.47	60	29	30	17	25	0.25	0.29
FLNC_HUMAN	Filamin-C	478	280841	5.65	41	15	25	13	22	0.18	0.21
HSPA_HUMAN	Heat shock protein HSP 90- α ha	3130	84607	4.84	343	197	35	25	21	0.65	3.19
ENPL_HUMAN	Endoplasmic	1990	92411	4.76	150	77	35	21	33	0.53	1.58
TRAP1_HUMAN	Heat shock protein 75 kDa, mitochondrial	765	80860	9.3	32	24	5	2	5	0.11	0.11
TLN1_HUMAN	Talin1	3355	269599	5.77	176	127	64	43	64	0.47	1.01
FAT2_HUMAN	Fatty acid synthase	3142	212254	6.01	188	120	63	45	46	0.43	1.12
EFZ2_HUMAN	Elongation factor 2	3095	95277	6.41	203	152	35	26	35	0.65	2.57
GSP1_HUMAN	78 kDa glucose-regulated protein	3083	72288	5.07	182	131	29	22	25	0.66	2.78
GPOT1_HUMAN	Stress70 protein, mitochondrial	5019	73835	5.97	37	26	16	11	16	0.36	0.97
HS1A2_HUMAN	Heat shock 70 kDa protein 1A	247	70059	5.48	25	15	7	6	5	0.22	0.43
LEI1_HUMAN	Gelsolin1	2041	47006	5.34	232	114	7	5	7	0.66	4.04
AMPH_HUMAN	Aminopeptidase N	3035	109471	5.31	129	96	30	22	30	0.42	1.6
COG4_HUMAN	CoG4p- α ha(3V) chain	2932	343457	6.26	164	122	55	39	55	0.35	0.63
GAP1_HUMAN	Adenyl cyclase-associated protein 1	2629	51880	5.24	148	92	18	11	4	0.49	1.42
IGGA1_HUMAN	Ras GTPase-activating-like protein IGAP1	2624	189134	6.08	131	97	43	35	43	0.44	1.27
PGAI_HUMAN	Protein disulfide-isomerase	2584	57081	4.76	227	96	26	14	26	0.61	1.78
ALDOA_HUMAN	Fructose-bisphosphate aldolase A	2576	39395	8.3	178	87	20	16	20	0.78	6.42
DYNC1_HUMAN	Cytoplasmic dynein 1 heavy chain 1	2523	532072	6.01	153	92	67	43	67	0.29	0.4
TBR1_HUMAN	Transcriptional endonuclease, reticulum A13type	1460	89268	5.14	111	66	24	13	13	0.55	2.54
UBA1_HUMAN	Ubiquitin- α ha modifier-activating enzyme 1	2362	117774	5.49	134	98	34	27	16	0.65	2.01
CANX_HUMAN	Calnexin-2 subunit, putative	2091	79945	4.87	95	76	24	21	23	0.59	2.53
ACTN1_HUMAN	Actinin-actinin-1	3032	102913	5.25	156	95	43	24	29	0.63	3.49
ACTN4_HUMAN	Actinin-actinin-4	1417	104788	5.27	114	70	23	20	19	0.52	1.41
COX4_HUMAN	CoG4p- α ha(3V) chain	10045	104642	5.26	100	67	25	17	17	0.45	1.16
SERP1_HUMAN	Serpin H1	1995	46411	8.75	167	114	23	21	23	0.65	6.2
GELS_HUMAN	Gelsolin	1555	85644	5.9	110	77	22	17	15	0.6	1.78
STAT1_HUMAN	Signal transducer and activator of transcription 1- α ha/beta	1909	87280	5.74	75	22	17	12	12	0.35	0.81
CHG1_HUMAN	60 kDa heat shock protein, mitochondrial	1873	61016	5.7	103	72	25	20	16	0.6	3.2
HSP_HUMAN	14-3-3 protein eta	175	28203	4.76	30	4	4	3	2	0.15	0.55
ANXA2_HUMAN	AnneXin A2	1778	36580	7.57	152	102	19	16	19	0.68	5.23
THO2_HUMAN	Thioredoxin	1685	11730	4.92	61	51	7	4	7	0.74	4.63
LDHA_HUMAN	L-lactate dehydrogenase A chain	1670	36665	5.44	156	82	19	15	12	0.79	4.68
LDHB_HUMAN	L-lactate dehydrogenase B chain	1369	36615	5.71	142	64	13	10	12	0.55	2.48
TYT1_HUMAN	Transketolase	1662	61835	7.58	68	67	22	16	22	0.64	2.67
PLG2_HUMAN	Fibrin	1634	531466	5.74	126	74	60	34	60	0.22	0.31
FBN1_HUMAN	Fibrillin-1	1631	262460	5.46	131	81	47	33	47	0.36	0.78
ACT1_HUMAN	ATP-kinase synthase	1857	120762	6.95	160	105	19	16	19	0.45	0.93
GSTP1_HUMAN	Glutathione S-transferase P	1561	23341	5.43	75	51	12	10	9	0.68	6.02
GOT1_HUMAN	Got1-1	1554	14891	6.22	163	99	10	9	7	0.6	6.37
PROT1_HUMAN	Protein-1	1514	15045	8.44	172	83	10	7	10	0.68	7.75
S10B_HUMAN	Protein S100-B1	1465	11733	6.56	92	73	5	5	5	0.65	21.41
IMD1_HUMAN	Importin subunit beta-1	1416	57103	4.68	81	57	24	24	24	0.54	1.91
PDIA3_HUMAN	Protein disulfide-isomerase A3	1376	56747	5.86	134	67	21	15	5	0.57	2.24
TSP1_HUMAN	Thrombospondin-1	1301	126300	4.71	131	69	27	18	27	0.32	0.97
ATP1_HUMAN	ATP synthase subunit beta, mitochondrial	1272	56525	5.26	116	62	26	24	6	0.78	5.33
TPS1_HUMAN	Troponin phosphatase isomerase	1247	30772	5.85	101	63	14	11	12	0.72	4.04
ANXA1_HUMAN	AnneXin A1	1235	36866	6.57	85	52	16	14	16	0.61	3.49
TAGL2_HUMAN	Transglutinin-2	1233	22377	8.41	91	61	15	11	15	0.74	8.1
EDHA_HUMAN	Trifunctional enzyme subunit α ha, mitochondrial	1215	82947	9.16	54	39	17	14	17	0.45	1.12
PGK1_HUMAN	Phosphoglycerate kinase 1	1192	44586	8.5	67	46	18	11	18	0.6	2.36
PRKDC_HUMAN	DNA-dependent protein kinase catalytic subunit	1180	468788	8.75	78	41	44	23	44	0.21	0.25
MYF1_HUMAN	Major myofibrin protein	1145	49266	5.34	61	45	21	17	45	0.53	1.14
PLIN2_HUMAN	Perilipin-2	868	47046	5.3	49	38	16	15	2	0.61	2.77
TOP1_HUMAN	T-complex protein 1 subunit beta	1110	57452	6.01	53	30	15	10	15	0.48	1.07
COX1_HUMAN	CoG4p- α ha(3V) chain	1106	130857	5.6	99	55	29	20	11	0.39	1.0
HYOU1_HUMAN	Hypoxia up-regulated protein 1	1077	111268	5.16	47	34	12	9	7	0.26	0.46
MARCKS_HUMAN	Myristic acid domain-rich C-kinase substrate	1071	31536	4.47	103	80	9	4	5	0.3	0.93
DPTL2_HUMAN	Dihydropyrimidinase-related protein 2	1058	62255	5.95	54	35	12	12	12	0.6	1.39
DPTL3_HUMAN	Dihydropyrimidinase-related protein 3	536	61924	6.04	29	18	12	6	10	0.45	0.5
WDR1_HUMAN	WD repeat-containing protein 1	1038	60152	6.17	59	29	18	12	18	0.59	1.27
GDI2_HUMAN	Ras GDP dissociation inhibitor beta	1030	50631	8.11	84	37	14	11	9	0.43	1.47
GDI1_HUMAN	Ras GDP dissociation inhibitor alpha	965	50550	5	45	22	11	6	6	0.37	0.64
FSCN1_HUMAN	Fascin	1025	54466	6.84	55	43	16	13	16	0.52	1.92
RPN2_HUMAN	Daltonyl- α -phosphogluconate- α -protein glycosyltransferase subunit 2	1016	69241	5.44	45	35	15	12	15	0.51	1.06
SGSH_HUMAN	Transforming growth factor-beta-induced protein α -3	1000	74634	7.62	52	35	14	7	14	0.45	0.57
ML12_HUMAN	Myosin regulatory light chain 12B	995	19767	4.71	49	26	11	8	6	0.93	4.3
MYL2_HUMAN	Myosin regulatory light polypeptide 9	350	18914	4.6	31	12	7	4	2	0.48	1.29
CATL1_HUMAN	Cathepsin B	977	57757	5.68	68	34	9	8	9	0.42	2
GARS_HUMAN	Glycine- α -RNA lyase	972	83113	6.61	59	34	16	11	10	0.54	0.93
TOP2_HUMAN	T-complex protein 1 subunit zeta	965	57888	6.23	45	34	13	13	13	0.47	1.21
ANXA5_HUMAN	AnneXin A5	964	55914	6.84	112	51	18	11	18	0.69	4.04
ATPA_HUMAN	ATP synthase subunit alpha, mitochondrial	947	59714	9.16	60	45	16	11	3	0.44	1.31
PRDX1_HUMAN	Peroxidase (peroxisomal)	938	25015	6	71	40	14	10	14	0.51	4.23
LPFR1_HUMAN	Leucine-rich PPR motif-containing protein, mitochondrial	925	187805	5.81	51	31	22	11	22	0.3	0.34
CATL2_HUMAN	Cathepsin K	916	36842	6.72	34	28	7	6	7	0.53	1.75
ARF1_HUMAN	ADP-ribosylation factor 4	575	20460	6.59	39	23	8	5	8	0.66	2.33
RN2_HUMAN	Ribonuclease inhibitor	898	49841	4.71	68	31	19	15	19	0.73	2.49
COPI1_HUMAN	Cotaxin subunit gamma-1	855	91655	5.32	51	25	22	15	22	0.45	1.07
PLT2_HUMAN	Plasmin-3	856	70766	5.41	52	38	19	15	19	0.57	1.42
PGAM1_HUMAN	Phosphoglycerate mutase 1	846	28786	6.67	102	45	12	7	12	0.66	2.17
PABP1_HUMAN	Poly(A)-binding protein 1	831	70726	5.31	27	17	8	4	8	0.21	0.34
GPI1_HUMAN	Glucose- α -phosphate isomerase	825	63107	6.43	54	37	16	7	16	0.55	0.81
EST1_HUMAN	S-60methylglutathione synthase	817	31442	6.54	34	22	12	7	12	0.73	1.52
PSMD1_HUMAN	26S proteasome non-ATPase regulatory subunit 2	809	100136	5.08	42	25	21	16	21	0.45	0.95
GNAH1_HUMAN	Neutral α -glucosidase AB	784	108807	5.74	70	40	28	17	28	0.57	0.95
NMT1_HUMAN	N-methyltransferase	782	29555	5.56	41	34	19	9	10	0.66	3.88
CATD_HUMAN	Cathepsin D	782	44524	6.1	64	37	13	9	13	0.54	1.55
OKAP1_HUMAN	Cytoskeleton-associated protein-4	788	65983	5.83	50	26	16	11	16	0.36	1.01

^aProtein score is calculated from the score of the peptide attributed to the protein.
^bpI is (Predicted) isoelectric point.
^cNumber of matches is spectrum number matched to protein¹.
^dNumber of significant matches is spectrum number that matches protein and exceeds the identification criteria.
^eNumber of sequences is number of peptides matched to protein².
^fNumber of significant sequences is number of peptides exceeding the identification criteria matched to proteins.
^gNumber of unique sequences is a unique³ number of peptides matched to proteins.
^hSequence coverage is the ratio of the total number of matched peptide residues to the total length of the protein.
ⁱExperimentally Modified Protein Abundance Index (http://www.matrixscience.com/help/quant_empai_help.html).

Table S1. Cont 1

UniProt/Swiss-Prot ID	Description	Protein score ^a	Protein mass (kDa)	pI ^a	Num. of matches ^a	Num. of significant matches ^a	Num. of sequences ^a	Num. of significant sequences ^a	Num. of unique sequences ^a	Sequence coverage ^a	emPAI
SAP1L1.HUMAN	Presenilin 6	774	581.4	5.9	35	24	17	12	12	0.61	1.37
EF1A1.HUMAN	Elongation factor 1-gamma	772	50.87	6.25	61	30	17	12	12	0.61	1.71
PRH4.HUMAN	Prd4-1/epsilon subunit alpha-1	770	60.84	5.99	30	24	18	12	12	0.36	0.98
LRP1.HUMAN	Protein-Low-density lipoprotein receptor-related protein 1	763	50427.6	5.16	76	40	37	21	17	0.19	0.62
TOP2A.HUMAN	Topoisomerase (DNA) subunit alpha	762	59.633	5.45	46	30	13	8	13	0.49	0.88
CPNS1.HUMAN	Oblastin subunit 1	755	28398	5.05	26	10	10	7	7	0.18	0.79
MOES1.HUMAN	Moesin	741	67.778	6.08	68	30	24	11	12	0.53	0.97
IFM2.HUMAN	Isolate dehydrogenase [NADP] cytoplasmic	733	48.620	6.33	68	30	13	8	12	0.55	0.97
PP2C.HUMAN	Farnesyltransferase [NADP]	735	24.42	6.83	32	24	8	8	8	0.47	1.17
HRP23.HUMAN	Heterogeneous nuclear ribonucleoprotein K	731	50.944	5.39	35	21	12	9	12	0.42	1.27
YIN1A.HUMAN	Yin1alpha	728	6.5	12332.2	5.2	26	30	12	12	0.36	0.72
PGC1A.HUMAN	Programmed cell death 1-interacting protein	727	55.963	6.13	38	20	12	5	12	0.24	0.61
PP2C.HUMAN	Protein phosphatase 2C isoenzyme B	715	23738	8.42	77	40	12	6	12	0.36	2.38
NOW1.HUMAN	Nucleoside diphosphate kinase B	714	71.62	6.52	65	25	25	12	12	0.37	0.87
NDPK1.HUMAN	Nucleoside diphosphate kinase A	706	17.128	5.83	86	23	9	7	5	0.78	5.83
NEP.HUMAN	Neuronal	706	65.440	6.54	44	22	12	12	12	0.43	0.83
SYO1.HUMAN	Isoenzyme-1 RNAase A6, cytoplasmic	700	144.008	5.82	69	38	27	14	27	0.37	0.55
UOCH1.HUMAN	UO-glucose 6-epimerase	696	54.989	6.73	40	27	19	14	17	0.61	1.89
6P0D.HUMAN	Emulphatorin, cytoplasmic, deacetylating	691	531.006	6.4	32	14	12	5	12	0.36	0.72
PGS1A.HUMAN	Protein disulfide-isomerase A6	689	60.911	4.95	50	33	13	12	11	0.56	2.08
GOIN1.HUMAN	gO1-2-4-like kinase activator (GDI)	682	29.972	7.29	40	20	10	10	10	0.12	0.15
OST4L.HUMAN	OSTF-1-like subunit of phosphatase-2	680	507.948	6.30	18	6	6	6	6	0.19	0.64
CD132.HUMAN	Cytosolic dymin 1 intermediate chain 2	679	71.412	5.08	30	25	10	4	4	0.2	0.94
2A4A.HUMAN	Serine threonine phosphatase 2A 65 kDa regulatory subunit A alpha isoform	678	65.627	6.07	30	13	10	12	12	0.36	1.07
ANKK1.HUMAN	Ankrrin 6	677	72.828	5.42	40	20	15	16	16	0.43	0.94
SPY1.HUMAN	Esperto-2	667	110.448	5.51	32	20	14	10	14	0.29	0.52
TOP2A.HUMAN	Topoisomerase (DNA) subunit alpha	667	60.296	5.8	17	18	10	10	10	0.36	0.96
GBF1.HUMAN	Guanine nucleotide-binding protein subunit beta-4	641	37.543	5.6	11	3	7	2	4	0.22	0.25
TOP2A.HUMAN	Topoisomerase (DNA) subunit alpha	639	59.239	5.8	22	14	16	16	16	0.48	1.17
SVEP1.HUMAN	Bifunctional diacylglycerol/phospho-inositol-3-OH kinase	631	170.483	7.02	60	37	24	11	24	0.31	0.51
SHJ1.HUMAN	Shal1-associated nuclear domain-containing protein 1	630	101.034	6.74	49	25	16	13	16	0.36	0.85
ALAI1.HUMAN	Artemin-like fibroblast growth factor 1	629	53.767	5.49	20	7	12	7	7	0.27	0.87
COH1A1.HUMAN	Coilin alpha-2/3 chain	627	129.035	6.08	50	30	10	16	16	0.24	0.38
HSP70.HUMAN	Heat shock 70 kDa protein	618	70.421	5.11	33	29	23	18	15	0.48	0.89
RBBP1.HUMAN	Reb-binding protein 1	614	12.821	5.09	17	22	18	17	17	0.18	0.28
CLIC1.HUMAN	Chloride intracellular channel protein 1	612	28.606	5.09	68	30	12	9	11	0.63	3
IPOL1.HUMAN	Importin-5	609	123.550	4.83	44	23	27	14	24	0.45	0.61
PIYU1.HUMAN	Glucose phosphorylase, brain form	602	98.935	6.4	31	16	8	13	12	0.28	0.40
TRFE1.HUMAN	Serine/threonine	600	7.914	6.81	42	19	15	8	8	0.32	0.54
RC3H1.HUMAN	Retinoid-inducible	594	37.470	4.74	27	17	10	8	8	0.45	0.74
SWO1.HUMAN	Tryptophan-5 RNAase, cytoplasmic	586	53.132	5.83	20	12	8	5	8	0.31	0.48
PGS1A.HUMAN	Protein disulfide-isomerase A6	584	72.887	4.96	13	16	19	2	16	0.38	0.86
TOP2A.HUMAN	Topoisomerase (DNA) subunit alpha	573	57.888	7.96	40	24	15	12	15	0.53	1.55
ANKK1.HUMAN	Neurokinin differentiation-associated protein ANKRR1	572	72.689	5.8	84	33	56	30	56	0.71	0.22
MTF1.HUMAN	Metformin-binding	563	60.7	5.63	20	1	2	2	2	0.23	0.35
SWO1.HUMAN	Serine-5 RNAase, cytoplasmic	556	58.740	6.55	30	25	8	6	6	0.33	0.64
ECM1.HUMAN	Erythrocyte hemoglobin	554	31.387	8.34	25	7	7	7	7	0.44	7
AT1A1.HUMAN	Sodium potassium-transporting ATPase subunit alpha-1	553	106.318	6.33	29	25	11	10	10	0.18	0.24
EIFK1.HUMAN	Eukaryotic translation initiation factor 3 subunit K	557	25.943	4.81	14	13	4	3	4	0.45	0.64
ITP1.HUMAN	Integrin beta-1	557	83.557	5.27	16	10	13	6	6	0.32	0.42
PSME2.HUMAN	Protein activator	554	27.084	5.54	28	16	6	6	6	0.4	1.47
COG2.HUMAN	Coilin alpha-2/3 chain	552	108.512	5.85	34	22	14	13	14	0.25	0.72
PAH1A1.HUMAN	Prd4-1/epsilon subunit alpha-1	548	61.911	5.27	48	25	18	11	11	0.36	0.95
UOCH1.HUMAN	UO-glucose 6-epimerase	547	17.7078	5.42	37	22	19	11	19	0.28	0.23
GAPDH.HUMAN	Glyceraldehyde-3-phosphate dehydrogenase	542	36.2	8.24	6	23	23	8	23	0.45	1.13
MDM1.HUMAN	Mad1 domain-containing protein	537	45.841	8.92	32	21	13	7	11	0.52	1.27
TH1A1.HUMAN	Acetyl-CoA acetyltransferase, cytosolic	533	33.224	6.47	20	19	7	6	7	0.47	1.02
ABP1.HUMAN	Actin-binding protein 2/2 complex subunit 2	532	34.111	5.27	48	25	11	11	11	0.26	0.31
DDX3X.HUMAN	ATP-dependent RNA helicase DDX3X	528	73.198	6.73	27	18	6	6	6	0.18	0.26
GAPDH.HUMAN	Glucose-6-phosphate dehydrogenase	524	39.919	6.39	35	21	12	8	12	0.43	0.76
CA1X.HUMAN	Calnexin	516	67.526	4.37	55	22	12	8	8	0.4	0.64
AP1.HUMAN	Adenosine phosphoribosyltransferase	515	10.955	5.78	13	11	4	4	4	0.49	1.21
SYA1A.HUMAN	Aluminum-3 RNAase, cytoplasmic	514	106.143	5.64	26	17	14	7	14	0.33	0.68
GA2.HUMAN	Guanine nucleotide-binding protein G12 subunit alpha-2	517	40.225	5.34	21	11	10	5	6	0.41	0.67
MYO1F.HUMAN	Myofibrin	510	23.461	5.84	81	29	28	15	28	0.36	0.33
PSMD1.HUMAN	26S proteasome non-ATPase regulatory subunit 1	505	105.769	5.25	31	16	24	8	24	0.33	0.49
SPTNL1.HUMAN	Spectrin alpha class, non-erythrocytic 1	496	24.844	5.22	37	22	19	19	19	0.16	0.14
PARK1.HUMAN	Proteinase nuclear acidic deubiquitinase 1	493	1.9176	6.33	13	8	6	6	6	0.72	3.27
ZYX.HUMAN	Zyxin	494	61.238	6.27	36	14	8	4	8	0.24	0.31
CAN1.HUMAN	Canalicular	490	61.838	5.49	30	17	13	9	13	0.41	0.50
HRP23.HUMAN	Heterogeneous nuclear ribonucleoprotein U	488	50.928	4.68	38	20	9	9	9	0.35	0.83
XRG1.HUMAN	X-ray repair cross-complementing protein 5	483	82.852	5.55	51	24	15	11	15	0.49	0.74
HRP23.HUMAN	Heterogeneous nuclear ribonucleoprotein U	479	56.381	5.89	29	19	11	8	10	0.54	1.76
EIF2.HUMAN	Elongation factor 1-beta	476	21.103	4.3	19	47	8	8	8	0.4	1.23
HRP23.HUMAN	Heterogeneous nuclear ribonucleoprotein U	476	22.168	5.98	55	32	9	7	9	0.71	2.56
CHOP1.HUMAN	Cytosolic non-specific lipoprotein	471	52.845	5.46	26	14	14	7	14	0.29	0.37
SC23A.HUMAN	Protein transport protein SC23A	469	86.015	6.44	28	15	14	7	14	0.41	0.84
GALL1.HUMAN	Galactin	389	37.084	4.47	45	18	14	10	14	0.8	2.07
DHES1.HUMAN	Dihydroxyacetone dehydrogenase 1, mitochondrial	461	61.359	7.48	20	10	9	4	9	0.23	0.3
TRPM1.HUMAN	Transient receptor potential subunit 1	460	28.504	4.87	38	20	12	6	6	0.34	0.19
SYO1.HUMAN	Serine-5 RNAase	451	140.887	6.3	20	12	12	12	12	0.31	0.21
LAMB1.HUMAN	Lamin subunit 1	454	197.909	4.83	33	25	18	8	11	0.14	0.21
EIF1.HUMAN	Elongation factor 1-beta	452	24.748	4.5	28	18	9	7	4	0.55	4.31
NEL1.HUMAN	Nucleosome protein 1	449	64.805	5.82	28	17	16	8	13	0.42	0.33
ALIL2.HUMAN	Alcohol dehydrogenase 1/2-formyltransferase dehydrogenase	449	101.681	6.13	19	13	13	5	9	0.21	0.23
PSB1.HUMAN	Proteinase subunit beta type-1	440	29.946	7.57	10	9	2	2	2	0.17	0.22
ABCT1.HUMAN	Adenosine nucleoside triphosphate 2/2 complex subunit 1B	438	40.923	4.39	15	15	9	9	9	0.26	0.68
NEL1.HUMAN	Nucleosome protein subunit beta-1	365	75.568	4.6	14	12	4	4	4	0.4	0.74
CPBP1.HUMAN	CPBP1 complex subunit beta-1	365	104.070	5.84	4	10	17	6	6	0.32	0.2
CPBP1.HUMAN	Poly(ADP-ribose) binding protein 2	249	38.556	6.33	42	19	9	5	5	0.43	0.72
ERL1.HUMAN	Erythrocyte membrane-anchoring receptor 3	166	25.010	8.87	10	7	3	3	2	0.22	0.74
LRP2.HUMAN	Low-density lipoprotein receptor 2	21829	9.96	2.1	15	15	15	15	15	0.53	0.55
CLIC1.HUMAN	Chloride intracellular channel protein 1	429	28.754	5.45	39	17	12	7	11	0.64	1.74
TOP2A.HUMAN	Topoisomerase (DNA) subunit alpha	611	60.495	5.1	14	15	15	15	15	0.54	0.74
SEPR.HUMAN	Protein disulfide-isomerase FAP	425	27.857	6.21	29	19	13	9	13	0.35	0.54
PSB1.HUMAN	Proteinase subunit beta type-1	421	29.955	7.72	15	9	5	3	5	0.36	0.53
UOCH1.HUMAN	UO-glucose 6-epimerase	423	14.008	5.43	26	25	9	9	9	0.45	2.4
MAP1B.HUMAN	Microtubule-associated protein 1B	407	27.048	4.73	29	16	17	11	17	0.15	0.19
SYO1.HUMAN	Serine-5 RNAase	407	17.374	5.72	15	9	9	9	9	0.3	0.24
SYO1.HUMAN	Serine-5 RNAase	406	27.548	5.72	15	9	9	9	9	0.48	0.24

^aProtein score is calculated from the score of the peptide attributed to the protein

^bpI is (Predicted) isoelectric point.

^cNumber of matches is spectrum number matched to protein⁴⁷⁾

^dNumber of significant matches is spectrum number that matches protein and exceeds the identification criteria.

^aNumber of sequences is number of peptides matched to protein.⁸²

^fNumber of significant sequences is number of peptides exceeding the identification

²Number of unique sequences is a unique⁴³ number of peptides matched to proteins.

^bSequence coverage is the ratio of the total number of matched peptide residues to the total length of the protein

¹Exponentially Modified Protein Abundance Index (http://www.matrixscience.com/help/quant_email_help.html)

Exponentially Modified Protein Abundance Index (http://www.matrixscience.com/help/quant_help.html).

Table S1, Cont.2.

UniProt/Swiss-Prot ID	Description	Protein score ¹	Protein mass (kDa)	pI ²	Num. of matches ¹	Num. of significant matches ¹	Num. of sequences ¹	Num. of significant sequences ¹	Num. of unique sequences ¹	Sequence coverage ³	emPAI ⁴
TOP2B2_HUMAN	Topoisomerase (beta) subunit theta	403	39583	5.42	26	13	12	7	12	0.34	0.63
FERM3_HUMAN	Fermitin family domain 2	400	77811	6.26	20	12	5	7	7	0.23	0.31
ADRH_HUMAN	Alcohol dehydrogenase class 3	399	39898	7.45	22	14	8	7	8	0.51	1.31
PLD5_HUMAN	Phospholipase 2-oxoglutarate 5-acyltransferase 1	396	83497	6.47	32	16	12	7	12	0.49	0.94
PLD2_HUMAN	Phospholipase 2-oxoglutarate 5-acyltransferase 2	262	84632	6.24	19	4	7	4	4	0.16	0.22
PLD3_HUMAN	Phospholipase 2-oxoglutarate 5-acyltransferase 3	231	84731	5.69	19	12	8	6	8	0.2	0.48
UAP1_HUMAN	UDP-glucose 4-epimerase pyrophosphatase	385	58732	5.92	27	11	10	5	10	0.31	0.63
PROX1_HUMAN	Peroxiredoxin-1	384	22096	6.27	57	25	13	6	10	0.75	2.07
PROX4_HUMAN	Peroxiredoxin-4	370	30521	5.98	29	14	12	6	10	0.65	1.26
PROX2_HUMAN	Peroxiredoxin-2	284	21878	5.66	18	12	5	5	4	0.78	1.57
PFKFB_HUMAN	ATP-dependent 6-phosphofructokinase, dimeric type	380	85542	7.5	28	20	14	12	13	0.41	0.8
PFKA_HUMAN	ATP-dependent 6-phosphofructokinase, liver type	325	84964	7.26	16	11	9	7	8	0.27	0.49
COPA_HUMAN	Cotinine subunit alpha	388	138258	7.7	42	19	24	11	24	0.35	0.4
VDAC1_HUMAN	Voltage-dependent anion-selective channel protein 1	385	30754	8.82	10	9	7	6	7	0.43	1.25
BZW1_HUMAN	Basic leucine zipper and W2 domain-containing protein 1	383	46013	5.75	24	15	11	6	11	0.38	0.88
VAT1_HUMAN	Synaptic vesicle membrane protein VAT-1 homolog	374	41893	5.88	40	18	14	9	14	0.54	1.45
PTBP1_HUMAN	Polypyrimidine tract-binding protein 1	374	57108	9.22	19	12	8	5	8	0.38	0.44
PSH1_HUMAN	Protein S-lysoxide 1	371	83241	5.05	36	21	13	7	13	0.41	0.57
YBX3_HUMAN	Y-box-binding protein 3	126	40066	9.77	8	5	5	3	3	0.23	0.37
COR1C2_HUMAN	Coronin-1C	370	53215	6.65	26	14	7	6	7	0.36	0.73
ROD3B_HUMAN	UV excision repair protein RAD23 homolog B	367	43145	4.79	17	13	7	6	7	0.33	0.78
ALDO_HUMAN	Aldehyde reductase	364	35830	6.51	23	13	7	3	7	0.5	0.42
PRH1_HUMAN	Protein phosphatase 1 regulatory subunit 7	364	41538	4.84	15	11	7	4	7	0.27	0.65
MKG1_HUMAN	Mitogen-activated protein kinase 1	364	41363	6.5	18	11	8	4	6	0.48	0.49
CALD1_HUMAN	Caldesmon	363	93175	5.82	26	12	8	5	8	0.17	0.25
MPT1_HUMAN	Protein phosphatase 1 regulatory subunit 12A	357	115211	5.31	10	6	4	1	4	0.06	0.04
CI13BP_HUMAN	Oxidomycin component 1 G subcomponent-binding protein, mitochondrial	357	31343	4.74	22	13	8	6	8	0.46	1.21
ORF1_HUMAN	Olfactin-1	357	33475	6.95	34	17	9	7	8	0.54	1.37
IPO12_HUMAN	Importin-7	356	118440	4.7	25	17	11	7	11	0.23	0.23
MYO1C_HUMAN	Unconventional myosin-1C	349	121606	9.46	26	13	14	7	14	0.23	0.27
GNIML1_HUMAN	Transmembrane glycoprotein NMB	342	63882	6.17	23	13	5	5	5	0.32	0.98
XRCO3_HUMAN	X-ray repair cross-complementing protein 6	342	69799	6.23	39	25	11	7	11	0.23	0.52
FUM1_HUMAN	Fumarate hydratase, mitochondrial	341	54602	8.85	21	12	8	6	8	0.33	0.84
PAPS3_HUMAN	Bifunctional 3'-phosphoadenosine 3'-phosphosulfate synthase 2	338	69457	6.18	20	12	6	9	2	0.42	0.18
CAVIN1_HUMAN	Caveolin-associated protein 1	336	43450	5.51	11	10	6	5	6	0.25	0.62
PSP1_HUMAN	Phosphatidylethanolamine-binding protein 1	335	21044	7.01	31	13	9	5	12	0.24	0.59
SCOR3_HUMAN	Lysosome membrane protein 2	334	54255	5	10	7	5	3	5	0.21	0.26
SC11A_HUMAN	Protein transport protein Sec23A	334	132931	6.43	23	14	13	8	13	0.22	0.29
XPO1_HUMAN	Exportin-1	333	123306	5.71	25	14	12	8	12	0.25	0.31
IF4G1_HUMAN	Eukaryotic translation initiation factor 4 gamma 1	331	175382	5.25	36	18	14	8	14	0.18	0.21
MBO1_HUMAN	Malate dehydrogenase, cytosolic	329	36403	6.91	41	18	11	8	11	0.6	1.79
POST1_HUMAN	Postnecin	328	83255	7.27	21	12	7	9	2	0.43	0.27
IF4A_HUMAN	Eukaryotic translation initiation factor 2 subunit 1	328	36089	5.02	12	10	6	5	6	0.38	1
LRRC1_HUMAN	Leucine-rich repeat-containing protein 59	326	34009	5.61	11	6	5	2	5	0.22	0.61
TAGLN_HUMAN	Transgelin	323	22596	8.87	39	18	10	5	10	0.6	1.49
GLYTH1_HUMAN	Serine hydroxymethyltransferase, mitochondrial	323	55958	8.76	14	11	6	4	6	0.27	0.36
DREL1_HUMAN	Drelin	323	71385	4.41	15	13	5	4	5	0.18	0.26
SEPT2_HUMAN	Septin-2	323	41461	6.15	20	14	10	7	9	0.51	1.02
RLR1_HUMAN	6S acidic ribosomal protein P0	321	34252	5.71	26	11	8	4	8	0.44	0.68
ERO1A_HUMAN	ERO-1-like protein alpha	320	54368	5.46	23	15	9	6	9	0.36	0.71
LAH1_HUMAN	Lupus La protein	315	46808	6.68	31	13	8	6	8	0.26	0.7
SAR1A_HUMAN	GTP-binding protein SAR1a	312	22353	6.21	12	8	4	3	4	0.17	0.74
ESYT1_HUMAN	Extended synaptotagmin-1	310	122780	5.57	24	14	14	7	14	0.24	0.27
AMEP1_HUMAN	Aminopeptidase B	307	72549	5.51	28	11	8	6	8	0.31	0.41
PAK2_HUMAN	Serine/threonine-protein kinase PAK 2	305	58005	5.68	13	10	5	4	5	0.24	0.63
IF4H_HUMAN	Eukaryotic translation initiation factor 4H	305	27368	6.67	20	14	4	2	4	0.38	0.55
CATL1_HUMAN	Cathepsin L1	305	31546	5.31	12	7	4	1	4	0.29	0.12
SOB1_HUMAN	Sinterin-1	304	35424	7.05	18	12	9	8	9	0.62	1.78
TMED4_HUMAN	Transmembrane emp24 domain-containing protein 10	303	24960	5.97	14	10	3	3	3	0.22	0.64
MOB1B_HUMAN	MOB1 domain activator 1B	303	25079	6.24	8	6	3	1	3	0.1	0.18
NADK2_HUMAN	Nucleoside-nucleotide pyrophosphorylase [carboxylating]	303	30826	5.81	18	11	4	4	4	0.45	1.24
GFPT1_HUMAN	Glutamine-nucleoside-diphosphate aminotransferase [isomerizing] 1	302	78756	6.66	22	16	14	11	12	0.36	0.79
GFPT2_HUMAN	Glutamine-nucleoside-diphosphate aminotransferase [isomerizing] 2	230	76882	7.03	14	11	9	7	7	0.46	0.98
NOO1_HUMAN	NAD(P)H dehydrogenase [ubiquinol]	297	30848	8.91	15	12	7	4	7	0.41	0.96
VBL1_HUMAN	Vagin	295	14388	6.43	22	10	13	7	2	0.17	0.23
ATPO1_HUMAN	ATP synthase subunit O, mitochondrial	295	23763	9.97	6	6	2	2	2	0.18	0.43
AREP1_HUMAN	ADP-ribosylation factor-like protein 6-interacting protein 1	292	23347	9.38	6	5	1	1	1	0.14	0.19
PROX3_HUMAN	Peroxiredoxin-3, mitochondrial	288	22073	6.93	23	10	8	6	8	0.57	2.07
ASPH1_HUMAN	Aspartyl (asparaginyl)beta-hydroxylase	288	85809	4.82	15	5	5	5	5	0.12	0.26
COR1L_HUMAN	Cotinine subunit beta	285	107074	5.72	37	18	17	10	17	0.32	0.48
LRX1A_HUMAN	Leukotriene A4 hydroxylase	283	66241	6.8	11	8	6	3	6	0.2	0.27
DICER1_HUMAN	2',5'-bisphosphate-3'-phosphate dependent endonuclease	282	36045	5.35	10	2	2	2	2	0.15	0.41
NEGR1_HUMAN	NAD(P)-cytochrome b5 reductase 2	281	34213	7.18	16	13	7	6	7	0.55	1.07
KOP1_HUMAN	Adenylate kinase 2, mitochondrial	281	26481	7.67	10	10	4	4	4	0.23	0.87
KOP2_HUMAN	Inhibitor of nuclear factor kappa-B kinase-interacting protein	279	39395	9.21	9	6	4	2	4	0.21	0.24
SHG1_HUMAN	Endoplasmic reticulum chaperone	277	41464	5.31	14	11	4	3	4	0.2	0.49
OSG1_HUMAN	Golgi apparatus protein 1	276	134464	6.52	29	8	13	5	13	0.18	0.17
SRC1_HUMAN	Src substrate cortactin	275	61549	5.24	13	7	7	4	7	0.24	0.31
FBX15_HUMAN	Putative F-box protein	274	64064	5.36	31	9	13	5	13	0.4	0.38
TNKS1_HUMAN	Thioredoxin domain-containing protein 5	273	47599	5.63	51	27	10	5	10	0.43	0.55
ECOR1_HUMAN	Trifunctional enzyme subunit beta, mitochondrial	273	51262	9.45	26	13	10	4	10	0.49	0.38
PTPR1_HUMAN	Protein-tyrosine phosphatase 1	272	35847	8.45	13	11	5	4	5	0.14	0.78
PORC1_HUMAN	Membrane-associated progesterone receptor component 1	271	21658	4.58	14	12	4	4	4	0.39	1.14
NOP1_HUMAN	NAD(P)+-cytochrome P450 reductase	269	76441	5.58	12	7	6	4	6	0.2	0.24
COPB2_HUMAN	Cotinine subunit beta'	268	102422	5.15	23	14	14	8	14	0.33	0.39
MYO1B_HUMAN	Unconventional myosin-b	265	131922	9.43	30	13	17	7	17	0.26	0.25
PARV1_HUMAN	Alphavirus	263	42217	5.89	5	5	2	2	2	0.08	0.22
USO1_HUMAN	General vesicular transport factor p15	263	107828	4.85	15	11	6	4	6	0.14	0.21
RLR1B_HUMAN	6S acidic ribosomal protein L3	263	46080	10.19	21	13	9	5	9	0.34	0.57
CAZA_HUMAN	F-actin-binding protein subunit alpha-1	263	32992	4.45	20	17	8	7	6	0.48	1.42
TMPO1_HUMAN	Transporter-2	125	101322	4.87	11	8	4	3	3	0.14	0.28
PUR1_HUMAN	Phosphoribosyltransferase, uridine synthase	260	144943	5.5	12	8	7	4	7	0.13	0.12
SOQR_HUMAN	Sulfide quinone oxidoreductase, mitochondrial	260	49929	9.18	14	12	7	6	7	0.22	0.65
ODO1_HUMAN	2-oxoglutarate dehydrogenase, mitochondrial	257	115861	6.14	12	10	5	3	5	0.1	0.11
USP14_HUMAN	Ubiquitin carboxyl-terminal hydrolase 14	256	56023	5.2	26	13	8	5	8	0.35	0.56
NP1L1_HUMAN	Nucleosome assembly protein 1-like 4	256	42797	4.8	15	9	7	4	7	0.36	0.47
BZW2_HUMAN	Basic leucine zipper and W2 domain-containing protein 2	256	46132	6.26	11	8	5	2	5	0.19	0.41
PSD1_HUMAN	26S proteasome non-ATPase regulatory subunit 13	254	42918	5.53	14	10	6	5	6	0.29	0.82
NEU1_HUMAN	Neuraminidase, mitochondrial	253	80600	6.21	24	8	4	3	4	0.13	0.23
EF3F_HUMAN	Eukaryotic translation initiation factor 3 subunit F	251	37540	5.24	13	10	4	4	4	0.29	0.74

¹Protein score is calculated from the score of the peptide attributed to the protein.

²pI is (Predicted) isoelectric point.

³Number of matches is spectrum number matched to protein¹.

⁴Number of significant matches is spectrum number that matches protein and exceeds the identification criteria.

⁵Number of sequences is number of peptides matched to protein².

⁶Number of significant sequences is number of peptides exceeding the identification criteria matched to proteins.

⁷Number of unique sequences is a unique⁶ number of peptides matched to proteins.

⁸Sequence coverage is the ratio of the total number of matched peptide residues to the total length of the protein.

⁹Exponentially Modified Protein Abundance Index (http://www.matrixscience.com/help/quant_empai_help.html).

Table S1, Cont.3.

UniProt/Swiss-Prot ID	Description	Protein score ¹	Protein mass (kDa)	pI ²	Num. of matches ¹	Num. of significant matches ¹	Num. of sequences ¹	Num. of significant sequences ¹	Num. of unique sequences ¹	Sequence coverage ³	emPAI ⁴
PI3L_HUMAN	Purification-sensitive antipeptidase	250	103211	5.49	18	10	8	4	8	0.18	0.18
LAHC1_HUMAN	Lamin subunit gamma-1	248	177489	5.01	18	11	14	8	14	0.18	0.24
PI3MDL_HUMAN	26S proteasome non-ATPase regulatory subunit 6	247	45502	5.45	10	8	4	2	4	0.17	0.2
PP4HL_HUMAN	Protein phosphatase 1 regulatory subunit 14B	246	15001	4.75	19	4	15	4	3	0.19	0.17
LGLL4_HUMAN	Lactoferrin-like	246	20764	5.12	13	9	4	3	4	0.17	0.81
PDIA5_HUMAN	Protein disulfide-isomerase A5	244	59558	8.08	10	3	4	1	4	0.22	0.07
RLS2_HUMAN	60S ribosomal protein L5	243	34541	8.73	27	9	8	3	8	0.42	0.44
COMT_HUMAN	Catechol O-methyltransferase	243	30018	5.26	17	12	7	5	7	0.41	1
GS1Y2_HUMAN	Citrate synthase, mitochondrial	242	91980	8.45	20	16	7	6	7	0.29	0.18
ETPL_HUMAN	Eukaryotic translation initiation factor 3 subunit O-like protein	241	105407	5.45	7	4	6	4	6	0.18	0.17
TM6SS1_HUMAN	Transmembrane 6 superfamily member 3	241	67843	6.83	7	8	2	1	2	0.06	0.06
PRPK_HUMAN	Phosphoinositide 3-kinase	240	21801	5.56	7	6	1	1	1	0.18	0.46
PEPD_HUMAN	Xaa-Pro dipeptidase	240	54513	5.84	10	8	5	5	5	0.24	0.47
COPE_HUMAN	Cotnamer subunit epsilon	238	34480	4.97	16	10	8	7	8	0.57	1.35
APES_HUMAN	Apoptosis inhibitor 5	237	58968	6.90	8	6	4	2	4	0.15	0.15
PROF2_HUMAN	Protein-2	237	15036	6.55	8	8	2	2	2	0.28	0.73
ROU1_HUMAN	Ras suppressor protein 1	236	31521	8.57	20	13	5	4	5	0.43	0.93
TOT1_HUMAN	Translationally controlled tumor protein	236	15383	4.84	12	8	6	5	6	0.44	1.87
CO1L1_HUMAN	Coactosin-like protein	233	15935	5.54	14	10	5	4	5	0.55	1.79
TM6SS2_HUMAN	Transmembrane 6 superfamily member 2	232	75725	7.23	11	10	3	3	3	0.12	0.22
ATLA32_HUMAN	Aldolase-3	231	60503	5.43	19	12	9	7	9	0.37	0.82
ORTAP_HUMAN	Ornithine-associated protein	230	46532	5.5	12	10	6	5	5	0.29	0.58
SCS5_HUMAN	Endoplasmic reticulum protein SCS5	86	50348	4.68	4	2	2	1	1	0.1	0.18
RON_HUMAN	Retinoblastoma	230	38866	4.86	15	9	6	3	6	0.38	0.38
VATB2_HUMAN	V-type proton ATPase subunit B, brain isoform	230	36465	5.57	14	7	10	5	10	0.43	0.45
RLA_HUMAN	60S ribosomal protein L8	230	37708	10.39	12	9	4	2	4	0.19	0.29
LMF2_HUMAN	Lease mutation factor 2	230	78647	10.1	15	6	5	4	5	0.14	0.23
BICA_HUMAN	Bikinin reductase A	230	33407	6.06	14	10	5	4	5	0.36	0.64
APEX1_HUMAN	DNA-(apurinic or apyrimidinic site) lyase	229	35532	6.33	15	11	5	4	5	0.28	0.8
LHO1_HUMAN	Lysoosomal acid base/cholesterol ester hydrolase	228	45300	8.42	9	7	5	4	5	0.28	0.44
RGRIP_HUMAN	Rab3 GTPase-activating protein non-catalytic subunit	228	155886	5.4	12	7	14	5	10	0.29	0.27
PGCS_HUMAN	Debar-1-oxopropyl-Co-carboxylate synthase	226	87248	6.66	43	11	10	5	10	0.29	0.27
SCRN1_HUMAN	Secernin-1	226	46353	4.68	18	13	6	6	6	0.29	0.57
HNRP1_HUMAN	Heterogeneous nuclear ribonucleoprotein F	225	45642	5.38	9	4	9	4	9	0.28	0.38
HNRPB_HUMAN	Heterogeneous nuclear ribonucleoprotein M	225	77464	8.84	16	9	6	3	6	0.17	0.24
HSP1_HUMAN	Heat-shock protein 1	224	21084	5.71	8	7	2	2	2	0.17	0.22
CD103_HUMAN	CD103 antigen	223	161587	5.59	17	11	10	6	10	0.15	0.2
COA1_HUMAN	CoA-pyruvate lyase (D) chain	220	138479	6.21	22	17	9	7	6	0.1	0.24
PGS6_HUMAN	26S proteasome non-ATPase regulatory subunit 14	217	34555	6.06	18	10	5	3	3	0.28	0.82
PP4GB_HUMAN	Lysoosomal protective protein	217	54431	6.16	11	8	7	4	4	0.27	0.36
ADP2_HUMAN	ADP-ATP translocase 2	192	32931	9.71	18	9	7	4	7	0.32	0.66
OUAL1_HUMAN	Osteocalcin ATPase 1	217	44715	7.64	12	8	5	3	3	0.3	0.6
RAB35_HUMAN	Rab-35-related protein Rab-35	194	23011	8.52	12	6	4	3	3	0.23	0.71
TSPD_HUMAN	Transducin protein	215	18816	6.43	13	6	3	3	3	0.48	0.82
KAP2_HUMAN	cAMP-dependent protein kinase type II- α regulatory subunit	212	45490	4.66	5	3	2	1	2	0.08	0.1
ANZB2_HUMAN	Acidic leucine-rich nuclear phosphoprotein 32 family member B	211	28770	3.84	6	6	3	3	2	0.27	0.54
ANZA_HUMAN	Acidic leucine-rich nuclear phosphoprotein 32 family member A	87	28568	3.89	5	2	2	2	2	0.2	0.34
SEPT3_HUMAN	Septin-3	211	65361	6.06	23	8	9	4	9	0.31	0.29
NRXN1_HUMAN	Narxin	211	131488	4.89	13	5	8	4	8	0.14	0.1
ETPL2_HUMAN	Elongation factor Tu, mitochondrial	210	45510	7.26	23	9	9	4	9	0.34	0.46
PUR2_HUMAN	Trifunctional purine biosynthetic protein adenosine-3	209	107699	6.26	13	6	9	4	9	0.23	0.17
QSO1_HUMAN	Rap1 GTPase-GDP dissociation inhibitor 1	209	66275	5.17	8	4	4	2	4	0.13	0.13
MP_HUMAN	Macrophage migration inhibitory factor	209	12468	7.74	46	18	3	3	3	0.36	1.67
DPP1_HUMAN	Dipeptidyl peptidase 3	209	82538	5.02	16	13	9	6	9	0.26	0.38
VATA_HUMAN	V-type proton ATPase catalytic subunit A	205	68260	5.95	16	7	8	6	6	0.34	0.36
FAAA_HUMAN	Fumarate hydratase	205	46344	6.46	12	8	6	3	6	0.35	0.31
HMS1_HUMAN	Hypoxanthine/Myo-inositol-Deoxy-thymine synthase, cytosolic	205	97257	5.22	24	9	9	6	9	0.38	0.66
FBP5_HUMAN	Peptide/Protein-cis-trans isomerase FKBP5	205	51180	5.7	9	6	5	3	5	0.21	0.68
IMA1_HUMAN	Importin subunit alpha-1	204	59991	4.89	20	10	8	5	7	0.35	0.63
ABDH4_HUMAN	Microsomal acid phosphatase, mitochondrial	203	33911	6.8	7	7	2	2	2	0.12	0.28
PRDX3_HUMAN	Thioredoxin-dependent peroxide reductase, mitochondrial	203	27675	7.67	9	8	4	3	4	0.42	0.57
SCFD1_HUMAN	Sac1 family domain-containing protein 1	203	72334	5.89	12	7	6	3	6	0.22	0.26
SNXA_HUMAN	Alphamethyl NEE attachment protein	203	33211	5.23	15	11	6	4	6	0.35	0.65
STAT2_HUMAN	Signal transducer and activator of transcription 2	203	97855	5.34	16	7	7	4	7	0.17	0.19
IMA2_HUMAN	Importin subunit alpha-2	202	59706	5.25	5	4	2	1	2	0.09	0.07
SCMR1_HUMAN	Sema100-related integrin-like receptor 1	201	25119	5.61	10	6	4	3	4	0.43	0.84
PI3MD4_HUMAN	26S proteasome non-ATPase regulatory subunit 4	200	40711	4.68	6	5	4	3	4	0.19	0.36
HPY_HUMAN	Hemoglobin	198	45177	6.13	18	11	6	3	6	0.24	0.32
RNDI1_HUMAN	RND domain-containing protein 1	198	27922	4.11	9	7	2	2	2	0.23	0.34
SET_HUMAN	Protein SET	198	33409	4.23	16	11	4	3	4	0.27	0.45
NDC80_HUMAN	Nuclear midline protein nDC80	198	38218	9.27	10	7	2	2	2	0.1	0.24
AKAP1_HUMAN	A-kinase anchor protein 2	198	84603	5.04	8	6	2	1	2	0.07	0.14
STPL_HUMAN	Stress-activated protein phosphatase 1	197	85598	6.4	24	5	8	4	8	0.27	0.31
FBP5_HUMAN	Peptide/Protein-cis-trans isomerase FKBP5	196	63044	4.91	9	6	5	3	5	0.18	0.22
DCIL1_HUMAN	Cytoskeletal dynamin 1 Ig-like intermediate chain 1	194	56544	6.01	11	7	3	3	3	0.11	0.25
ATPL_HUMAN	ATP synthase subunit g, mitochondrial	194	11421	9.65	6	3	4	1	4	0.48	0.43
SVK_HUMAN	Lysine-mRNA ligase	194	68005	5.84	17	8	8	4	8	0.3	0.36
PO2_HUMAN	Decorin	194	39722	8.75	4	3	2	2	2	0.12	0.23
VQCC2_HUMAN	Voltage-dependent anion-selective channel protein 2	193	31547	7.49	10	7	5	2	5	0.36	0.3
LMAN1_HUMAN	Protein ERGIC-53	193	57513	6.3	16	3	8	3	8	0.4	0.24
OTUB1_HUMAN	Ubiquitin thioesterase OTUB1	193	31264	4.95	14	7	8	5	8	0.61	0.94
GLUE2_HUMAN	Glucocorticoid 2 subunit beta	192	95388	4.33	17	13	5	4	5	0.2	0.42
NASP_HUMAN	Nuclear autoantigenic sperm protein	191	85188	4.26	17	8	6	4	6	0.19	0.22
TAF2_HUMAN	Tafiiin-2	190	39523	6.37	14	10	7	5	7	0.35	0.69
NP1L1_HUMAN	Nucleosome assembly protein 1-like 1	190	45346	4.36	24	14	7	5	7	0.39	0.58
MGST1_HUMAN	Microsomal glutathione S-transferase 1	188	17587	9.41	9	8	3	3	3	0.46	1.02
CTRH1_HUMAN	CoReceptor-like heparan sulfate-binding protein 1	188	26207	8.31	7	7	1	1	1	0.12	0.17
NPS1_HUMAN	Protein NpSnp homolog 1	187	33289	9.35	13	8	4	3	4	0.27	0.45
TRER_HUMAN	Transmembrane protein 126A	186	21513	9.26	5	5	1	1	1	0.11	0.21
DNKX_HUMAN	Transmembrane protein RNA helicase A	186	140869	6.41	15	7	7	3	7	0.12	0.09
IPYR1_HUMAN	Inorganic pyrophosphatase	185	32639	5.54	17	10	8	6	8	0.54	1.14
PCNA_HUMAN	Proliferating cell nuclear antigen	184	28760	4.57	11	8	7	5	7	0.56	1.06
DYN2_HUMAN	Dynamin-2	183	98063	7.04	5	4	2	1	2	0.87	0.04
COPI1_HUMAN	Copine-1	183	59022	5.52	16	12	5	4	5	0.24	0.42
HEXB_HUMAN	Hexameric hexosaminidase subunit beta	183	63071	6.26	13	7	6	3	6	0.19	0.22
PAI1_HUMAN	Plasminogen activator inhibitor 1	183	45031	6.88	8	5	6	3	6	0.29	0.32
BAFPI_HUMAN	Brain acid soluble protein 1	181	22480	4.64	54	15	7	6	7	0.54	2.58
ABRAL_HUMAN	Cortactin family protein ABRAL	180	9051	5.86	8	5	2	1	2	0.46	0.56
PRIO_HUMAN	Peptide/Protein-cis-trans isomerase C	180	22749	8.48	12	10	2	2	2	0.31	1.07
HNRI1_HUMAN	Heterogeneous nuclear ribonucleoprotein H	179	48188	5.89	9	7	4	3	4	0.18	0.29

¹Protein score is calculated from the score of the peptide attributed to the protein.

²pI is (Predicted) isoelectric point.

³Number of matches is spectrum number matched to protein¹.

⁴Number of significant matches is spectrum number that matches protein and exceeds the identification criteria.

⁵Number of sequences is number of peptides matched to protein¹.

⁶Number of significant sequences is number of peptides exceeding the identification criteria matched to proteins.

⁷Number of unique sequences is a unique⁷ number of peptides matched to proteins.

⁸Sequence coverage is the ratio of the total number of matched peptide residues to the total length of the protein.

⁹Exponentially Modified Protein Abundance Index (http://www.matrixscience.com/help/empai_help.html).

Table S1, Cont'd.

UniProt/Swiss-Prot ID	Description	Protein score ^a	Protein mass (kDa)	pI ^b	Num. of matches ^c	Num. of significant matches ^d	Num. of sequences ^e	Num. of significant sequences ^f	Num. of unique sequences ^g	Sequence coverage ^h	emPAI ⁱ
TF1B2_HUMAN	Transcription intermediary factor 1-beta	176	88492	5.52	10	7	6	4	6	0.17	0.27
SCOT1_HUMAN	Succinyl-CoA:cholesterol coenzyme A transferase 1, mitochondrial	175	56122	7.14	10	8	6	5	6	0.29	0.45
HEXA_HUMAN	Beta-hexosaminidase subunit alpha	175	60664	5.04	9	6	5	4	4	0.21	0.32
GLRX1_HUMAN	Glutaredoxin-1	174	17149	8.33	12	6	2	2	2	0.47	1.82
AATC2_HUMAN	Aspartate aminotransferase, cytoplasmic	174	46219	6.52	13	5	4	2	4	0.16	0.2
TRP1_HUMAN	Transferin receptor protein 1	173	84810	6.18	27	15	8	4	8	0.2	0.22
ALIB1_HUMAN	Aldehyde dehydrogenase 5, mitochondrial	173	57170	6.38	20	13	5	3	5	0.19	0.44
AMP1_HUMAN	Cytosolic aminopeptidase	172	56131	8.03	17	10	6	10	6	0.38	0.56
PIRFG1_HUMAN	CTP synthase 1	172	66848	6.02	8	8	3	3	3	0.13	0.26
MOGS_HUMAN	Mannose-6-phosphogalactose 4-epimerase	172	91861	8.37	21	11	9	6	9	0.24	0.51
HMOX3_HUMAN	Heme oxygenase 2	171	36010	5.31	5	3	4	2	4	0.25	0.26
ORLH1_HUMAN	Oligonucleotide, mitochondrial	171	29516	6.41	6	5	2	1	2	0.2	0.17
DDX35L_HUMAN	Probable ATP-dependent RNA helicase DDX58	167	166531	6.03	6	4	4	2	4	0.11	0.08
PIB2L_HUMAN	Prohibitin-2	166	33276	8.23	13	8	7	4	7	0.39	0.85
PGM1_HUMAN	Phosphoglucomutase-1	166	81411	6.3	8	6	5	3	5	0.19	0.23
DNAA2_HUMAN	DnaJ homolog subfamily A member 2	165	45717	6.06	11	7	4	2	4	0.24	0.2
ACSL3_HUMAN	Long-chain-fatty-acyl-CoA ligase 3	165	60368	8.65	18	9	9	5	9	0.2	0.3
DKC2L_HUMAN	DbaH24-like steroid reductase	165	60062	8.42	20	9	9	4	9	0.38	0.22
TMO3L_HUMAN	Protein disulfide-isomerase TMO3	165	51839	4.8	6	4	4	2	4	0.21	0.17
ETFA_HUMAN	Electron transfer flavoprotein subunit alpha, mitochondrial	165	29558	8.62	9	6	4	2	4	0.26	0.27
ZASU2_HUMAN	Serine/threonine-protein phosphatase 2A 58 kDa regulatory subunit delta isoform	163	89947	8.24	4	3	3	2	3	0.1	0.13
ECM1_HUMAN	DbaH23-like delta2 A'-domain-CoA isomerase, mitochondrial	163	35782	8.16	13	8	4	2	4	0.19	0.26
RND1L_HUMAN	Rhs-GTPase-activating protein 1	162	58404	5.85	21	15	8	6	8	0.36	0.84
POP_HUMAN	Lysosomal Pro-X carboxypeptidase	162	55764	6.75	7	4	2	2	2	0.1	0.16
QSOX1_HUMAN	Rhs-GDP-association inhibitor 1	161	23192	5.02	25	12	8	5	8	0.51	1.44
CSRP1_HUMAN	Cysteine and glycine-rich protein 1	161	20554	8.9	9	6	6	4	6	0.42	1.23
PURH1_HUMAN	Bifunctional purine biosynthesis protein PURH	160	64575	6.27	17	7	11	4	11	0.36	0.29
COPZ2_HUMAN	Catenin subunit zeta-2	159	23533	5.08	7	6	3	3	3	0.25	0.69
UBP2L_HUMAN	Ubiquitin carboxyl-terminal hydrolase 5	158	95725	4.91	14	8	8	5	8	0.2	0.24
SUST2_HUMAN	Suspectosome-1	158	47657	5.1	9	6	3	3	3	0.3	0.3
NLTP_HUMAN	Non-specific lipid transfer protein	157	58556	6.44	5	3	1	1	3	0.07	0.07
CATC2_HUMAN	Deacetylase 2	157	51820	6.54	10	8	6	4	6	0.36	0.38
AMM1_HUMAN	Protein arginine N-methyltransferase 1	157	41468	5.24	7	7	3	3	3	0.35	0.35
MP2K2_HUMAN	Dual specificity mitogen-activated protein kinase kinase 2	157	44396	6.12	5	5	2	2	1	0.12	0.21
MP2K1_HUMAN	Dual specificity mitogen-activated protein kinase kinase 1	150	43411	6.18	8	6	4	2	3	0.28	0.21
HCDL1_HUMAN	3-hydroxyacyl-CoA dehydrogenase type-2	156	29606	7.86	8	5	3	2	3	0.2	0.85
LAMP1_HUMAN	Lysosome-associated membrane glycoprotein 1	156	44854	9	15	6	4	2	4	0.14	0.2
Serpin H4	Serpin H4	156	46820	6.29	12	6	5	3	5	0.12	0.21
GT2S1_HUMAN	Proteasome activator complex subunit 1	155	71590	6.85	20	8	9	5	9	0.27	0.34
MAOX1_HUMAN	NAD(P)-dependent malic enzyme	155	64109	5.79	5	4	4	4	4	0.19	0.3
ERFPL1_HUMAN	Endoplasmic reticulum resident protein 29	155	28675	6.77	16	6	6	3	6	0.38	1.04
DDX1_HUMAN	ATP-dependent RNA helicase DDX1	154	82380	6.81	13	5	7	4	7	0.18	0.22
ACSL3L_HUMAN	Long-chain-fatty-acyl-CoA ligase 1	153	77693	8.81	6	4	5	3	5	0.16	0.17
DCN1L_HUMAN	Dancin subunit 1	152	141807	5.81	16	8	9	5	9	0.4	0.13
DDCP1_HUMAN	Unoporphyrinogen decarboxylase	152	40761	5.77	16	7	8	3	8	0.5	0.36
TRP1L_HUMAN	Tryptophanase 1	151	61210	6.01	11	6	4	3	4	0.07	0.07
MXK3L_HUMAN	Mitogen-activated protein kinase 3	149	43108	6.28	11	6	7	4	5	0.39	0.47
IMA3_HUMAN	Importin subunit alpha-3	116	57851	4.8	15	4	8	3	6	0.35	0.24
GRAL1_HUMAN	Glucuronate 6-phosphatase N-acetyltransferase	149	20736	6.17	8	6	4	1	4	0.42	0.81
GEH6_HUMAN	Glutathione synthetase	148	52352	5.67	8	5	7	5	7	0.25	0.49
ATP5B_HUMAN	ATP synthase subunit c, mitochondrial	148	18480	5.21	8	5	3	2	3	0.24	0.56
CRPT1_HUMAN	Protein carboxy homology 2	148	29539	4.81	8	4	5	4	5	0.45	1.22
NOMD1_HUMAN	Nodal modulator 1	148	134239	5.54	18	7	10	5	10	0.19	0.17
IFAE1_HUMAN	Eukaryotic translation initiation factor 4E	147	25062	5.79	12	6	4	3	4	0.33	0.64
DNAB3_HUMAN	DnaJ homolog subfamily B member 4	146	37783	8.65	8	5	6	3	6	0.37	0.39
NNO1_HUMAN	Non-POU domain-containing octamer-binding protein	145	54187	8.01	10	3	2	1	2	0.11	0.08
TOMT1_HUMAN	Mitochondrial import receptor subunit TOMT1	145	67412	6.75	7	5	4	1	4	0.16	0.13
TENA1_HUMAN	Tenascin	145	240700	4.79	11	5	7	2	7	0.09	0.04
SAH8_HUMAN	Adenosine homocysteine lyase	144	47865	5.92	23	10	7	4	7	0.2	0.42
FUBP2_HUMAN	Far upstream element-binding protein 2	144	73070	6.55	10	6	8	4	8	0.24	0.26
CTND1_HUMAN	Catenin delta-1	144	108103	5.86	5	5	2	2	2	0.06	0.08
PLBL2_HUMAN	Putative phospholipase B-like 2	144	65430	6.34	16	6	4	3	4	0.2	0.29
PURB1_HUMAN	Multifunctional protein ADE2	144	47048	6.95	13	4	9	3	9	0.46	0.3
LMNB1_HUMAN	LIM and nuclear coat (LINC)-like domain-containing protein 1	143	37226	8.63	8	7	5	4	5	0.32	0.39
MRPL1_HUMAN	Chloramphenicol resistance-Ser345phosphate receptor	143	20972	5.07	4	4	2	1	2	0.16	0.49
STYLC1_HUMAN	Tyrosine-tyrosine kinase, cytoplasmic	143	59106	6.81	16	9	5	4	5	0.15	0.33
SECT1_HUMAN	Protein SECT1 homolog	142	35516	5.22	8	7	4	2	4	0.26	0.42
RPE1_HUMAN	Ribulose-1,5-bisphosphate 3-epimerase	142	24811	5.33	5	5	1	1	1	0.16	0.29
PSMD1_HUMAN	26S proteasome non-ATPase regulatory subunit 3	141	69839	8.47	15	6	8	4	8	0.25	0.31
DDX8_HUMAN	Probable ATP-dependent RNA helicase DDX8	140	54382	8.85	11	8	5	4	5	0.37	0.36
GORK1_HUMAN	Quinone oxidoreductase PIG3	140	35514	6.67	5	3	4	2	4	0.2	0.26
SFRB1_HUMAN	Serin B8	138	42739	5.41	3	3	1	1	1	0.06	0.1
PIG3L_HUMAN	Phosphatidylethanolamine-binding electron assembly protein	138	70710	7.7	8	4	4	1	4	0.22	0.13
SOX1L_HUMAN	N-terminal kinase-like protein	138	89575	5.94	4	3	3	2	3	0.11	0.1
EPTR1_HUMAN	Eukaryotic translation initiation factor 3 subunit 1	137	36476	5.38	9	6	7	4	7	0.38	0.77
KHS1_HUMAN	Kinesin-1 heavy chain	137	109817	6.12	13	5	10	3	10	0.22	0.12
SVMC2_HUMAN	Methionine-mRNA ligase, cytoplasmic	136	101052	5.82	9	2	4	1	4	0.11	0.04
STC2_HUMAN	Glutamine-mRNA ligase	136	87142	6.71	16	7	6	3	6	0.19	0.15
UFL1_HUMAN	E3 UFM1-protein ligase 1	135	89540	6.35	7	4	3	2	3	0.09	0.1
SFRP5_HUMAN	Signal receptor-type particle receptor subunit beta	135	29884	9.17	3	3	2	2	2	0.13	0.22
ROBO1_HUMAN	60 kDa 55-kDa Rho-GDP-binding protein	135	60631	8.27	9	7	5	3	5	0.19	0.23
EHDL1_HUMAN	EH domain-containing protein 1	135	61137	6.33	13	3	5	1	4	0.16	0.07
DNB1_HUMAN	Peroxisomal multifunctional enzyme type 2	135	79636	8.86	14	6	8	4	8	0.26	0.23
PSB1_HUMAN	Proteasome subunit beta type-1	134	26472	8.27	11	5	6	3	6	0.4	0.87
PTTG1_HUMAN	Putative tumor-transforming gene 1 protein-interacting protein	133	20510	8.14	4	4	1	1	1	0.1	0.22
AP2A1_HUMAN	AP-2 complex subunit delta-1	133	107478	6.82	33	8	11	6	9	0.23	0.26
AP2A2_HUMAN	AP-2 complex subunit delta-2	83	103895	6.53	10	4	6	3	4	0.15	0.13
EPH4_HUMAN	Endoplasmic reticulum resident protein 44	132	46841	5.09	7	7	2	2	2	0.11	0.19
CIT1_HUMAN	Cit-1-tetrahydrofolate synthase, cytoplasmic	132	101495	6.89	27	10	13	7	7	0.28	0.23
SOD1_HUMAN	Superoxide dismutase [Cu-Zn]	132	15928	5.7	14	5	4	3	4	0.54	1.17
IMA5_HUMAN	Importin subunit alpha-5	132	60184	4.84	7	5	3	2	3	0.14	0.23
GLRX3_HUMAN	Glutaredoxin-3	132	37408	5.31	16	7	6	3	6	0.3	0.4
SIAS1_HUMAN	Sulfate acid synthase	130	40281	8.29	17	8	8	4	8	0.48	0.51
TRIL1_HUMAN	Tril-1 membrane glycoprotein	130	17923	8.86	2	1	2	1	2	0.15	0.26
DCN2L_HUMAN	Dancin subunit 3	130	21106	5.37	8	4	2	2	2	0.31	0.48
SCMD1_HUMAN	Calcium-binding mitochondrial carrier protein SCMD1	130	33232	6	7	5	4	2	4	0.22	0.17
PHL2_HUMAN	Four and a half LIM domain protein 2	129	32171	7.8	6	2	6	2	6	0.37	0.29
MAP4_HUMAN	Microtubule-associated protein 4	129	120930	5.32	25	7	11	3	11	0.18	0.11
TM6SF_HUMAN	Fruitease-2-like phosphatase TM6SF	128	30042	7.6	6	5	4	3	4	0.24	0.31
ENPP1_HUMAN	Ectonucleotide pyrophosphatase/phosphodiesterase family member 1	128	104857	6.76	11	7	6	3	6	0.12	0.13

^aProtein score is calculated from the score of the peptide attributed to the protein.^bpI is (Predicted) isoelectric point.^cNumber of matches is spectrum number matched to protein¹.^dNumber of significant matches is spectrum number that matches protein and exceeds the identification criteria.^eNumber of sequences is number of peptides matched to protein¹.^fNumber of significant sequences is number of peptides exceeding the identification criteria matched to proteins.^gNumber of unique sequences is a unique¹ number of peptides matched to proteins.^hSequence coverage is the ratio of the total number of matched peptide residues to the total length of the protein.ⁱExponentially Modified Protein Abundance Index (http://www.matrixscience.com/help/empai_help.html).

Table S1, Cont.5.

UniProt/Swiss-Prot ID	Description	Protein score ^a	Protein mass (kDa)	pI ^b	Num. of matches ^c	Num. of significant matches ^c	Num. of sequences ^c	Num. of significant sequences ^c	Num. of unique sequences ^c	Sequence coverage ^d	emPAI
NADP7_HUMAN	Nicotinamide phosphoribosyltransferase	128	35487	8.89	5	5	4	4	5	0.22	0.48
AT2A2_HUMAN	Sarcosine ⁺ /retinoidic retinolic acid-ATPase 2	128	114083	5.23	15	5	10	4	2	0.18	0.2
GOPR5_HUMAN	GdpG resident protein GOPR5	126	60556	5.02	6	3	5	3	5	0.2	0.23
COR1_HUMAN	Carbonic dehydratase (NADPH) 1	126	20356	6.55	5	5	4	3	5	0.2	0.51
SPBB3_HUMAN	Serpin B6	126	42594	5.18	9	4	4	4	4	0.17	0.48
MIC2J_HUMAN	C-type histamine receptor 2	125	16658	5.54	15	8	9	5	9	0.16	0.13
RLT21_HUMAN	60S ribosomal protein L27-4like 1	125	14558	5.27	5	5	5	1	1	0.2	0.32
1C12_HUMAN	HLA class I histocompatibility antigen, Cw-12 alpha chain	125	40860	5.91	11	6	5	4	3	0.27	0.5
NAC24_HUMAN	Nucleic acid polymerase-associated confinder subunit alpha-2	101	22509	4.68	7	5	1	1	1	0.05	0.16
SYN2_HUMAN	Aspartate ⁺ -tRNA ligase, cytosolic	123	62902	5.9	12	7	6	3	6	0.22	0.32
ESY72_HUMAN	Extended synaptotagmin-2	123	102284	9.33	5	3	3	1	3	0.07	0.04
OPD7L_HUMAN	Glutamate peptide synthetase-4like protein	122	42397	5.84	10	7	4	3	4	0.23	0.34
VKOR1_HUMAN	Vitamin K epoxide reductase complex subunit 1	122	18223	9.53	7	5	2	2	2	0.19	0.57
IASPP_HUMAN	Rib-associated inhibitor	121	89036	6.37	4	4	1	1	1	0.03	0.05
TOM1_HUMAN	Target of Mitochondrial protein 1	120	53785	4.99	6	6	5	3	3	0.28	0.36
NOO2_HUMAN	Ribosylhydronicotinamide dehydrogenase [autone]	120	25802	5.88	4	4	1	1	1	0.09	0.17
FLU2_HUMAN	Protein (ligand-1) homolog	120	144659	5.75	18	6	12	4	12	0.22	0.16
MT1_HUMAN	Interferon-induced GTP-binding protein Mt1	119	75473	5.8	10	6	5	3	5	0.18	0.25
LPXN_HUMAN	Leupaxin	119	43304	5.82	11	7	2	2	2	0.11	0.21
FABP4_HUMAN	Protein FABP4	119	55366	6.15	6	5	1	1	1	0.05	0.08
CAT2_HUMAN	Cathepsin 2	118	33848	6.7	3	3	2	2	2	0.12	0.28
IMDH2_HUMAN	Inosine-3'-monophosphate dehydrogenase 2	118	55770	6.44	13	6	8	5	8	0.34	0.45
PAFSL_HUMAN	Bifunctional 2'-phosphogluconate 5'-phosphoglucate synthase 1	118	70788	6.4	6	2	4	2	4	0.16	0.13
HSPB9_HUMAN	Heat shock protein beta-9	118	17125	5.95	6	2	3	1	3	0.39	0.27
MBP12_HUMAN	Myelin-binding protein 1A	117	148762	9.34	6	4	7	3	7	0.09	0.09
KAT1_HUMAN	Kynurenine ⁺ -pyridoxate transaminase 3	117	51388	6.4	6	4	3	2	3	0.18	0.18
ACBP_HUMAN	Acyl-CoA-binding protein	117	10038	6.12	11	2	3	2	3	0.51	1.25
NAH13_HUMAN	Nucleoside triphosphatase 15, NaH auxiliary subunit	117	101208	7.23	10	4	6	3	6	0.14	0.13
GOLP3_HUMAN	Golgi phosphoprotein 3	116	33790	6.05	8	4	4	2	4	0.23	0.28
PML_HUMAN	Protein PML	116	97489	5.88	15	5	8	2	8	0.19	0.09
FABP9_HUMAN	Fatty acid-binding protein, heart	115	14848	6.29	17	6	8	3	8	0.21	0.26
RTFAT2_HUMAN	RNA transcription, translation and transport factor protein	114	28051	6.19	6	4	3	3	3	0.21	0.58
ERD2_HUMAN	ERF domain-containing protein 2	114	61123	6.63	15	8	6	4	6	0.24	0.31
ASAH1_HUMAN	Acid ceramidase	113	44631	7.52	4	2	4	2	4	0.22	0.21
CY12_HUMAN	Cytochrome c1, heme protein, mitochondrial	113	35399	9.15	10	6	4	3	4	0.2	0.42
TSD1_HUMAN	Thioredoxin domain-containing protein 17	113	13932	5.4	7	5	5	3	5	0.42	0.4
GALK1_HUMAN	Galactokinase	113	42246	6.04	13	7	3	2	3	0.23	0.22
PPT1_HUMAN	CAD protein	113	242929	6.02	24	6	12	5	12	0.13	0.09
RLT22_HUMAN	60S ribosomal protein L28	112	17741	11.68	9	5	2	2	2	0.08	0.08
AFM1_HUMAN	Apoptosis-inducing factor 1, mitochondrial	112	66859	9.04	3	3	3	3	3	0.11	0.21
ANKK1_HUMAN	Ankrrin-1	110	57706	5.52	6	5	3	2	3	0.2	0.17
CUL4B_HUMAN	Cul4B-4B	112	103916	7.01	3	2	3	2	3	0.05	0.08
SC24D_HUMAN	Protein transport protein Sc24D	111	112936	6.91	13	5	10	4	9	0.22	0.16
AMPK1_HUMAN	Adenosine triphosphatase complex-interacting multifunctional protein 2	111	35236	6.45	13	7	7	5	7	0.53	0.6
DNPH1_HUMAN	2'-deoxyadenoside 5'-phosphate N-hydrolase 1	111	19097	4.97	5	3	2	2	2	0.29	0.81
SC24A_HUMAN	Protein transport protein Sc24A	110	119674	7.58	3	3	1	1	1	0.03	0.03
HNPL1_HUMAN	Heterogeneous nuclear (nonribosomal) protein U-like protein 1	110	96878	6.49	9	5	2	1	4	0.08	0.04
S10A12_HUMAN	Protein S100-A16	109	11784	6.28	6	4	2	1	2	0.29	0.41
ONE2_HUMAN	Onecortin-2	109	62042	6.16	16	5	6	3	6	0.16	0.22
ANM5_HUMAN	Protein arginine N-methyltransferase 5	109	72838	5.88	17	11	5	4	5	0.21	0.26
LYZAP2_HUMAN	Acyl-protein thioesterase 2	108	24721	6.75	8	5	2	1	2	0.22	0.18
NUP160_HUMAN	Nuclear pore complex protein Nup160	108	182017	9.31	9	3	6	2	6	0.05	0.1
CDB1_HUMAN	CDB1 antigen	108	25792	5.09	6	3	2	2	2	0.18	0.38
ADPF1_HUMAN	ADP-ribosylation factor 6	108	20069	5.24	10	7	5	3	5	0.46	0.55
HCOX1_HUMAN	Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial	107	34272	8.88	10	5	4	2	4	0.25	0.27
MESD_HUMAN	LRP chaperone MESD	107	26080	7.8	7	5	4	3	4	0.3	0.61
SERD2_HUMAN	Phosphoserine aminotransferase	107	40397	7.56	17	4	8	3	8	0.46	0.36
SVAP1_HUMAN	Synapse-associated protein 1	106	39809	4.45	4	4	1	1	1	0.1	0.23
MACP1_HUMAN	Microtubule-actin crosslinking factor 1, isoforms 1/2/3/5	106	83787	5.28	50	4	28	3	28	0.08	0.02
GLT1K1_HUMAN	Glutathione S-transferase kappa 1	105	25480	8.5	10	4	5	4	5	0.38	0.91
SYO2C_HUMAN	Aspartate ⁺ -tRNA ligase, cytoplasmic	105	57100	6.11	7	3	6	2	6	0.24	0.18
GPI1_HUMAN	Glycosyl-transferase protein	105	67889	5.97	10	5	6	3	6	0.18	0.2
ACAD9_HUMAN	Acyl-CoA dehydrogenase family member 9, mitochondrial	104	68717	6.16	5	4	3	2	3	0.12	0.2
LTH1_HUMAN	E3 ubiquitin-protein ligase lathrin	104	200423	5.89	6	3	6	2	6	0.06	0.04
INF2_HUMAN	Inverted formin-2	104	135540	5.26	13	4	9	4	9	0.17	0.13
ALTA1_HUMAN	Alpha-aminoadipic semialdehyde dehydrogenase	104	58450	6.21	7	6	7	6	7	0.27	0.53
BNH1_HUMAN	Myo basic domain-interacting protein 1	103	84658	4.97	2	2	1	1	1	0.03	0.07
TBCD1_HUMAN	TBC1 domain family member 4	102	146471	6.57	7	2	6	1	6	0.1	0.03
SPSY1_HUMAN	Serpin synthesis	101	41242	4.87	10	6	7	4	7	0.43	0.5
IPD4_HUMAN	Importin-4	101	118440	4.88	9	5	6	3	6	0.13	0.11
DOCK7_HUMAN	Dedicator of cytokinesis protein 7	101	242407	6.34	12	6	7	4	7	0.08	0.07
MPPL1_HUMAN	Mitochondrial processing peptidase subunit alpha	101	58216	6.45	8	6	2	2	2	0.08	0.15
SBB2_HUMAN	Adenosine 2'-phosphate 5'-phosphoglucate transporter 1	101	47484	9.32	2	1	2	1	2	0.07	0.09
SSBP2_HUMAN	Single-strand DNA-binding protein, mitochondrial	100	17249	9.59	6	2	4	2	4	0.41	0.81
RLT23_HUMAN	60S ribosomal protein L13	100	24247	11.65	15	5	4	2	4	0.19	0.41
QPN2_HUMAN	Qpnrad1	100	63026	6.43	14	4	5	3	5	0.09	0.22
PEX14_HUMAN	Peroxisomal membrane protein PEX14	100	41212	4.89	3	3	1	1	1	0.1	0.11
PSD1_HUMAN	26S proteasome non-ATPase regulatory subunit 12	100	52371	7.53	11	3	7	3	7	0.23	0.17
USMD2_HUMAN	Up-regulated during skeletal muscle growth protein 5	100	6452	9.78	4	2	1	1	1	0.26	0.85
OTD1_HUMAN	D-mannosyl-CoA deacylase	98	23409	8.35	11	3	4	2	4	0.26	0.42
OSGPF_HUMAN	Prokaryotic RNA N-methyltransferase (transacetylase) transferase	98	36403	5.94	4	2	3	1	3	0.23	0.12
CDB3_HUMAN	CDB3 antigen	98	25619	8.14	37	13	3	2	3	0.21	0.82
ECMD2_HUMAN	Proteinase-associated protein, ECMD2 homolog	98	204160	6.74	16	4	13	2	13	0.19	0.04
TRF1_HUMAN	Acetyl-CoA acyltransferase, mitochondrial	98	45171	8.88	4	4	2	2	2	0.12	0.2
IVD2_HUMAN	Isovaleryl-CoA dehydrogenase, mitochondrial	97	46280	8.45	5	2	3	2	3	0.18	0.2
OA12_HUMAN	Oxidative amino transferase, mitochondrial	97	48204	6.57	5	5	7	4	7	0.22	0.54
HPRT1_HUMAN	Hypoxanthine ⁺ -guanine phosphoribosyltransferase	96	24564	6.21	3	3	2	2	2	0.28	0.4
MI0B2_HUMAN	Unconventional myosin-bb	96	24249	8.91	9	2	7	1	7	0.06	0.02
EBF3A_HUMAN	Eukaryotic translation initiation factor 3 subunit A	95	166468	6.38	6	3	5	1	5	0.06	0.03
APOL2_HUMAN	Apolipoprotein L2	95	37069	6.28	6	4	2	2	2	0.17	0.4
ROV1B_HUMAN	RuvB-like 4	94	50196	6.02	6	1	6	1	6	0.1	0.08
ACM1_HUMAN	Phosphoenolpyruvate carboxylase mutase	94	58114	5.84	15	7	5	3	5	0.25	0.23
ACON1_HUMAN	Aconitate hydratase, mitochondrial	94	85372	7.26	10	4	4	2	4	0.12	0.1
TADP1_HUMAN	TAR DNA-binding protein 43	94	44711	5.85	6	4	5	4	5	0.29	0.45
ANFY1_HUMAN	Rabanyl-5	93	128318	5.7	18	9	8	2	8	0.15	0.07
P2H2_HUMAN	Prd-3-hydroxylase 3	93	81786	5.93	6	4	6	2	6	0.16	0.17
SEL1L_HUMAN	Selenoprotein N	93	65773	5.92	2	2	2	2	2	0.09	0.14
IFU1_HUMAN	Eukaryotic translation initiation factor 6	93	26582	4.56	12	6	6	4	6	0.58	1.18
ERD3_HUMAN	Prokaryotic arginyltransferase protein 28	92	13554	8.86	2	2	2	1	2	0.09	0.29
SYO1C_HUMAN	Aspartate ⁺ -tRNA ligase, cytoplasmic	92	134379	6.95	11	6	6	4	6	0.14	0.13

^aProtein score is calculated from the score of the peptide attributed to the protein.

^bpI is (Predicted) isoelectric point.

^cNumber of matches is spectrum number matched to protein¹.

^cNumber of significant matches is spectrum number that matches protein and exceeds the identification criteria.

^cNumber of sequences is number of peptides matched to protein¹.

^cNumber of significant sequences is number of peptides exceeding the identification criteria matched to proteins.

^cNumber of unique sequences is a unique¹ number of peptides matched to proteins.

^cSequence coverage is the ratio of the total number of matched peptide residues to the total length of the protein.

^dExponentially Modified Protein Abundance Index (http://www.matrixscience.com/help/quant_help.html).

Table S1, Cont'd.

UniProt/Swiss-Prot ID	Description	Protein score ^a	Protein mass (kDa)	pI ^b	Num. of matches ^c	Num. of significant matches ^d	Num. of sequences ^e	Num. of significant sequences ^f	Num. of unique sequences ^g	Sequence coverage ^h	emPAI
ISG15_HUMAN	Ubiquitin-like protein- ISG15	92	17676	8.84	4	2	4	2	4	0.36	0.38
USP44_HUMAN	Ubiquitin-like modifier-activating enzyme 6	92	117395	5.16	12	3	8	1	8	0.17	0.16
IPYR2_HUMAN	Inorganic pyrophosphatase 2, mitochondrial	92	37896	7.07	5	3	4	2	4	0.2	0.25
VPTG2_HUMAN	Vascular cell adhesion-associated protein 12C	92	423124	6.38	12	4	10	2	10	0.07	0.03
TYPH3_HUMAN	Thymidine phosphorylase	92	49924	5.36	8	5	3	2	3	0.13	0.18
ARX44_HUMAN	Armenin A4	91	35660	5.84	6	3	3	2	3	0.16	0.26
PRKSF_HUMAN	PRKAT family protein 3	91	21600	5.77	7	4	4	2	4	0.16	0.21
GBF1_HUMAN	Gdp-specific brefeldin A-resistance guanine nucleotide exchange factor 1	91	206315	5.48	27	5	11	5	10	0.13	0.13
ZAB1_HUMAN	Serine/threonine-protein phosphatase ZA 55 kDa regulatory subunit B alpha isoform	91	51659	5.82	5	2	4	1	4	0.11	0.08
CCO4L_HUMAN	Collagen alpha1(VII) chain	90	332941	5.38	11	1	6	1	6	0.03	0.01
PGFRB_HUMAN	Platelet-derived growth factor receptor beta	90	123889	4.88	9	4	3	2	3	0.06	0.07
RST5_HUMAN	Aldehyde reductase 13.14-oxidase	90	66777	6.54	3	3	1	1	1	0.06	0.12
SYR2_HUMAN	Arginine-tRNA ligase, cytoplasmic	90	75331	6.26	10	5	8	4	8	0.17	0.25
OKSP1_HUMAN	CDK3 regulatory subunit-associated protein 3	90	36885	4.68	6	5	3	3	3	0.09	0.25
ABD1_HUMAN	Monoclonal Ab-derived AbBD12	90	45008	8.87	6	3	4	2	2	0.23	0.2
EIF3_HUMAN	Eukaryotic translation initiation factor 3 subunit H	89	39905	6.09	19	6	8	3	8	0.35	0.37
AKT2_HUMAN	RAC-beta serine/threonine-protein kinase	89	55720	5.98	4	2	3	1	3	0.11	0.08
ARPD_HUMAN	Actin-related protein 10	89	46177	7.07	4	4	3	3	3	0.21	0.31
PP4R1_HUMAN	Serine/threonine-protein phosphatase 4 regulatory subunit 1	89	106938	4.64	4	2	3	1	3	0.08	0.04
HDF_HUMAN	Hepatosarcoma-derived growth factor	89	28772	4.7	6	2	3	2	3	0.26	0.36
CYB5_HUMAN	Cytochrome b5	88	15321	4.88	2	2	1	1	1	0.28	0.71
CUT1_HUMAN	Protein CUT1	88	19104	5.42	6	6	2	2	2	0.25	0.54
NDP9_HUMAN	Protein NDP9D	88	60794	4.61	7	4	3	2	3	0.15	0.23
GHC1_HUMAN	Mitochondrial glutamate carrier 1	87	34448	9.42	9	2	6	1	6	0.37	0.27
MAGM_HUMAN	NAD-dependent male enzyme, mitochondrial	87	65492	7.53	4	2	3	1	3	0.1	0.07
QCR2_HUMAN	Cytochrome bcr1 complex subunit 2, mitochondrial	87	48413	6.74	7	2	4	1	4	0.14	0.09
MAGD1_HUMAN	Melanoma-associated antigen D1	87	86107	5.84	5	2	4	1	4	0.12	0.05
RTM4_HUMAN	Retinoblastoma	87	128651	4.43	2	2	2	2	2	0.04	0.07
KLC1_HUMAN	Kinesin light chain 1	87	65269	5.87	8	3	5	2	5	0.12	0.14
LRG4_HUMAN	Leucine-rich repeat-containing protein 47	86	63434	5.95	8	4	2	1	2	0.1	0.07
OTPF1_HUMAN	Cytosolic FMR1-interacting protein 1	86	146088	6.46	11	5	8	1	8	0.15	0.09
AERP_HUMAN	Adenosine enhancer-binding protein 1	85	130847	5.05	3	1	2	1	2	0.03	0.03
ACQD2_HUMAN	Very long-chain specific acyl-CoA dehydrogenase, mitochondrial	85	70458	8.92	2	1	2	1	2	0.03	0.03
ABCD3_HUMAN	ATP-binding cassette sub-family D member 3	84	75428	9.41	5	1	2	1	2	0.04	0.06
GLSK_HUMAN	Glutathione S-transferase, mitochondrial	84	73414	7.85	8	5	4	3	4	0.12	0.19
TAF1_HUMAN	Taf11	83	40236	6.48	9	4	4	2	4	0.28	0.51
CD98_HUMAN	CD98 antigen	83	18836	4.58	3	2	2	1	2	0.39	0.24
SAP1_HUMAN	G-protein-coupled receptor 47	83	20523	5.17	13	4	3	2	3	0.2	0.48
TRPL2_HUMAN	Tumor necrosis factor alpha-induced protein B-like protein 3	83	32938	8.75	2	1	2	1	2	0.07	0.14
SC24C_HUMAN	Protein transport protein Scs24C	82	118249	6.71	6	3	4	1	3	0.09	0.07
NBE2_HUMAN	Serine/threonine-protein kinase Nbe2	82	39363	8.26	5	3	4	2	4	0.21	0.12
ATPS_HUMAN	ATP synthase-coupling factor 6, mitochondrial	82	12580	9.52	4	2	2	1	2	0.32	0.38
FUBP1_HUMAN	Far upstream element-binding protein 1	82	67518	7.18	8	3	7	3	7	0.2	0.2
GETT1_HUMAN	Glu-tartrate S-transferase, thiamin-B	82	27480	5.89	5	3	1	1	1	0.21	0.16
GETM2_HUMAN	Glu-tartrate S-transferase Mu 3	82	26542	5.37	3	3	1	1	1	0.07	0.17
ATO1_HUMAN	Copper transport protein ATO1	82	7587	6.71	2	1	1	1	1	0.23	0.16
GLB1L_HUMAN	1,4-galactose-4-epimerase	81	88423	5.87	25	12	8	3	8	0.29	0.17
COG3_HUMAN	Hsp60 co-chaperone Cdg37	81	44440	5.17	6	5	3	3	3	0.16	0.32
STTQ_HUMAN	Threonine-DNA ligase, cytoplasmic	81	93362	6.23	13	5	8	3	8	0.18	0.22
NDU5_HUMAN	ADP-sugar pyrophosphatase	81	24312	4.87	4	3	3	2	3	0.18	0.4
LZC_HUMAN	Protein LZC	81	21481	4.88	5	3	1	1	1	0.15	0.21
COL1_HUMAN	Collagen	81	76526	4.98	6	4	2	1	2	0.06	0.12
GALT2_HUMAN	Polypeptide N-acetylglucosaminyltransferase 2	79	64891	8.63	5	2	5	2	5	0.14	0.14
CDV2_HUMAN	Protein CDV2 homolog	81	27318	6.08	4	2	3	1	3	0.23	0.16
NSD4_HUMAN	Steroid-4-alpha-oxo-3-beta-hydrogenase, decarboxylating	80	41974	8.16	6	1	1	1	1	0.29	0.1
SFO1_HUMAN	Sekine factor 1	80	68286	9.07	6	4	3	1	3	0.1	0.06
ARFG1_HUMAN	ADP-nucleosylation factor GTPase-activating protein-1	80	44440	5.46	4	2	4	2	4	0.18	0.21
THM1_HUMAN	3-ketopropyl-CoA thiolase, mitochondrial	80	41898	6.32	5	3	4	3	4	0.28	0.35
QCR1_HUMAN	Cytochrome bcr1 complex subunit 1, mitochondrial	80	52612	5.84	15	2	4	2	4	0.15	0.17
LSM1_HUMAN	U6 snRNP-associated Sm-B-like protein Lsm1	80	9122	9.81	1	1	1	1	1	0.33	0.56
LSMA1_HUMAN	LSM domain and actin-binding protein 1	80	85173	6.41	4	1	3	1	3	0.08	0.05
SAMH1_HUMAN	Deoxyribose triphosphate triphosphohydrolase SAMH1	80	72155	6.69	4	2	4	2	4	0.11	0.12
USAF2_HUMAN	Sekine factor UFAP 65 kDa subunit	80	53467	9.19	4	3	3	2	3	0.1	0.17
OPTN_HUMAN	Optineurin	80	65880	5.17	1	1	1	1	1	0.03	0.07
ARE1_HUMAN	ADP-nucleosylation factor-B-like protein 3	79	29443	6.74	6	1	3	1	3	0.36	0.22
MMP2_HUMAN	72 kDa type IV collagenase	79	73835	5.28	6	3	3	2	3	0.13	0.18
BD2_HUMAN	BHD-interacting domain death agonist	79	21981	5.27	7	4	3	2	3	0.29	0.46
LMAN1_HUMAN	Vascular integrin alpha-5 membrane protein VPS6	78	40203	6.46	10	5	4	4	4	0.28	0.51
NU133_HUMAN	Nuclear pore complex protein Nup133	78	128888	4.97	5	3	4	2	4	0.06	0.07
POX_HUMAN	Peroxidase	78	35060	5.76	9	3	7	2	7	0.49	0.27
GRPR2_HUMAN	Quercetin reductase/hydroxyprocate reductase	78	35648	7.01	9	6	4	3	4	0.27	0.42
URE22_HUMAN	Ubiquitin-conjugating enzyme E2 Z	78	38186	5.37	2	2	1	1	1	0.06	0.11
AKA12_HUMAN	Armeninase protein 12	78	191367	4.37	18	6	9	4	9	0.13	0.09
TPB1_HUMAN	Trophoblast glycoprotein	77	46003	6.35	7	3	2	2	2	0.09	0.2
GRPE2_HUMAN	GDI/EPGL endoplasmic functional protein	77	88638	6.84	15	4	3	7	7	0.18	0.15
DOAP1_HUMAN	Protein diaphanous homolog 1	77	141258	5.31	16	4	10	3	10	0.17	0.09
PCYT1A_HUMAN	Onion-epiophosphate cyclitoltransferase A	77	41705	6.82	6	1	3	1	3	0.13	0.1
FDTA_HUMAN	Serine synthase	77	48004	6.1	9	2	6	2	6	0.23	0.19
CUL2_HUMAN	Cul2-1	77	86927	6.45	5	3	2	1	2	0.1	0.05
LARP1_HUMAN	Leu-related protein 1	77	124334	8.91	5	4	3	2	3	0.24	0.07
IFITAX_HUMAN	Eukaryotic translation initiation factor 1A, X-chromosomal	76	16450	5.07	4	3	1	1	1	0.1	0.38
AASS_HUMAN	Aldehyde-aminooxidase semialdehyde synthase, mitochondrial	76	102066	6.18	6	3	5	2	5	0.11	0.09
PAG2_HUMAN	Proliferator-associated protein 2G4	76	43759	6.13	5	2	4	1	4	0.21	0.21
EXOC1_HUMAN	Exocyst complex component 5	76	86790	5.8	3	2	1	2	1	0.08	0.1
TRD2_HUMAN	E3 ubiquitin/ISG15 ligase TRD2	76	70928	8.44	8	4	3	1	3	0.08	0.12
EPF2_HUMAN	Eukaryotic translation initiation factor 3 subunit 2	76	29045	4.72	1	1	1	1	1	0.05	0.15
GMPPR_HUMAN	Mannose-1-phosphate guanylyltransferase beta	75	39809	6.16	5	2	4	2	4	0.24	0.23
HEMO_HUMAN	Hemoglobin	76	51643	6.55	18	7	7	3	7	0.21	0.38
ABR8_HUMAN	Protein ABD14B	75	22532	5.84	3	3	3	3	3	0.2	0.14
SPEF_HUMAN	Spermidine synthase	75	33803	5.3	10	6	6	3	6	0.5	0.44
PLAP_HUMAN	Phospholipase A2-activating protein	75	87101	5.88	9	3	5	1	5	0.12	0.05
ETPL_HUMAN	Electron transfer flavoprotein subunit beta	75	27126	8.24	1	1	1	1	1	0.07	0.16
COR1B_HUMAN	Coronin-1B	67	54200	5.81	17	3	5	3	5	0.18	0.26
ORBL_HUMAN	Orb1/Orb1-related protein 1	75	28020	6.71	6	2	3	1	3	0.21	0.16
GDN_HUMAN	Gdn-derived protein	75	43974	9.35	2	2	1	1	1	0.07	0.1
NO13_HUMAN	Nuclein	74	62935	6.4	8	5	3	2	3	0.12	0.14
NR11_HUMAN	Hesiderin triad nucleotide-binding protein 1	74	13783	6.43	16	4	3	2	3	0.6	0.81
MRAT_HUMAN	Matrix-remodelling-associated protein 7	74	21452	6.24	2	2	1	1	1	0.14	0.21
FAPD5_HUMAN	Fatty acid-binding protein, epidermal	74	15155	6.8	15	3	3	3	3	0.24	0.31
TBCD_HUMAN	Tubulin-binding cofactor D	74	27308	5.08	6	1	3	1	3	0.19	0.16

^aProtein score is calculated from the score of the peptide attributed to the protein.

^bpI is (Predicted) isoelectric point.

^cNumber of matches is spectrum number matched to protein¹¹.

^dNumber of significant matches is spectrum number that matches protein and exceeds the identification criteria.

^eNumber of sequences is number of peptides matched to protein¹².

^fNumber of significant sequences is number of peptides exceeding the identification criteria matched to proteins.

^gNumber of unique sequences is a unique¹³ number of peptides matched to proteins.

^hSequence coverage is the ratio of the total number of matched peptide residues to the total length of the protein.

ⁱExponentially Modified Protein Abundance Index (http://www.matrixscience.com/help/quant_help.html).

Table S1, Cont'd.

UniProt/Swiss-Prot ID	Description	Protein score ^a	Protein mass (kDa)	pI ^b	Num. of matches ^c	Num. of significant matches ^d	Num. of sequences ^e	Num. of significant sequences ^f	Num. of unique sequences ^g	Sequence coverage ^h	emPAI ⁱ
COR2L2_HUMAN	GDPN ligandosome complex subunit B	74	23211	5.25	7	4	4	2	4	0.49	0.21
KCTD12_HUMAN	BTB/POZ domain-containing protein KCTD12	74	58679	5.51	9	4	4	2	4	0.23	0.26
TPD52L2_HUMAN	Tumor protein D54	73	22224	5.26	7	3	3	2	3	0.33	0.75
C24A_HUMAN	C24 antigen	73	61467	5.13	2	2	2	2	2	0.04	0.11
RFA2L2_HUMAN	Radical protein A 32 kDa subunit	72	29228	5.75	6	2	4	1	4	0.31	0.15
TTIP2L_HUMAN	Tricarboxylate transport protein, mitochondrial	72	33951	9.91	9	3	4	2	4	0.22	0.28
CHM8L_HUMAN	Charged multivesicular body protein 4b	72	24935	4.26	2	2	2	2	2	0.19	0.29
COX6A1_HUMAN	Co-ligand subunit (VI) chain	72	183447	4.54	18	2	10	2	10	0.14	0.05
SPTC2L_HUMAN	Serine polyketide oxidoreductase 2	72	62864	7.29	3	1	1	1	1	0.13	0.67
HGS_HUMAN	Hepatocyte growth factor-regulated tyrosine kinase substrate	72	86138	5.84	7	4	3	2	3	0.08	0.7
VASP_HUMAN	Vasodilator-stimulated phosphoprotein	72	39805	8.05	5	2	4	2	4	0.14	0.23
IFM1_HUMAN	Interferon-induced transmembrane protein 3	72	14622	6.49	2	2	2	2	2	0.38	0.75
SYOC_HUMAN	Cysteine-mRNA ligase, cytoplasmic	72	85419	6.31	7	3	4	1	4	0.13	0.95
SPR3L_HUMAN	Protein spastin homolog 1	72	56594	6.19	3	2	1	2	2	0.06	0.98
QALX_HUMAN	QAP synthase [Lysine-methyltransferase]	71	76887	8.42	3	2	3	2	3	0.13	0.12
VATL_HUMAN	V-type proton ATPase 16 kDa proteolipid subunit	71	15725	7.88	3	3	1	1	1	0.2	0.3
YDZAL_HUMAN	Histone H2A type 2-A	71	14087	10.9	3	3	1	1	1	0.22	0.24
LMNA_HUMAN	Protein A-C	71	74085	6.57	10	3	6	2	6	0.15	0.12
OKAP5_HUMAN	Osteoklaster-associated protein 5	71	22352	7.85	6	2	6	2	6	0.05	0.64
ABR7L2_HUMAN	Aldehyde B1 aldehyde reductase member 2	71	29564	6.7	5	3	2	2	2	0.14	0.23
ACPH_HUMAN	Acyl-CoA oxidase	70	81173	5.29	9	3	6	3	6	0.17	0.17
MMS1L_HUMAN	MMS1 nucleotide excision repair protein homolog	70	113217	5.82	5	2	4	1	4	0.07	0.84
RPB1L_HUMAN	DNA-directed RNA polymerase II subunit RPB1 l-rs1	70	13080	6.28	5	4	1	1	1	0.26	0.88
TMOD3_HUMAN	Tropomodulin-3	70	38570	5.86	10	6	3	2	3	0.24	0.37
UCBL1_HUMAN	Putative cytochrome b-c1 complex subunit Rbx1a-Ba protein 1	70	30786	9.04	1	1	1	1	1	0.07	0.14
SCRB1_HUMAN	Scavenger receptor class B member 1	70	60838	8.55	9	2	5	1	5	0.28	0.27
RPL1L_HUMAN	Dolichyl-4-phosphoUDP-glucosyltransferase subunit 1	70	68527	5.86	27	11	10	4	10	0.29	0.28
MGAT1_HUMAN	Alcohol 1-mannosyl-2-oxo-3-oxo-4-oxo-5-oxo-6-oxo-7-oxo-8-oxo-9-oxo-10-oxo-11-oxo-12-oxo-13-oxo-14-oxo-15-oxo-16-oxo-17-oxo-18-oxo-19-oxo-20-oxo-21-oxo-22-oxo-23-oxo-24-oxo-25-oxo-26-oxo-27-oxo-28-oxo-29-oxo-30-oxo-31-oxo-32-oxo-33-oxo-34-oxo-35-oxo-36-oxo-37-oxo-38-oxo-39-oxo-40-oxo-41-oxo-42-oxo-43-oxo-44-oxo-45-oxo-46-oxo-47-oxo-48-oxo-49-oxo-50-oxo-51-oxo-52-oxo-53-oxo-54-oxo-55-oxo-56-oxo-57-oxo-58-oxo-59-oxo-60-oxo-61-oxo-62-oxo-63-oxo-64-oxo-65-oxo-66-oxo-67-oxo-68-oxo-69-oxo-70-oxo-71-oxo-72-oxo-73-oxo-74-oxo-75-oxo-76-oxo-77-oxo-78-oxo-79-oxo-80-oxo-81-oxo-82-oxo-83-oxo-84-oxo-85-oxo-86-oxo-87-oxo-88-oxo-89-oxo-90-oxo-91-oxo-92-oxo-93-oxo-94-oxo-95-oxo-96-oxo-97-oxo-98-oxo-99-oxo-100-oxo-101-oxo-102-oxo-103-oxo-104-oxo-105-oxo-106-oxo-107-oxo-108-oxo-109-oxo-110-oxo-111-oxo-112-oxo-113-oxo-114-oxo-115-oxo-116-oxo-117-oxo-118-oxo-119-oxo-120-oxo-121-oxo-122-oxo-123-oxo-124-oxo-125-oxo-126-oxo-127-oxo-128-oxo-129-oxo-130-oxo-131-oxo-132-oxo-133-oxo-134-oxo-135-oxo-136-oxo-137-oxo-138-oxo-139-oxo-140-oxo-141-oxo-142-oxo-143-oxo-144-oxo-145-oxo-146-oxo-147-oxo-148-oxo-149-oxo-150-oxo-151-oxo-152-oxo-153-oxo-154-oxo-155-oxo-156-oxo-157-oxo-158-oxo-159-oxo-160-oxo-161-oxo-162-oxo-163-oxo-164-oxo-165-oxo-166-oxo-167-oxo-168-oxo-169-oxo-170-oxo-171-oxo-172-oxo-173-oxo-174-oxo-175-oxo-176-oxo-177-oxo-178-oxo-179-oxo-180-oxo-181-oxo-182-oxo-183-oxo-184-oxo-185-oxo-186-oxo-187-oxo-188-oxo-189-oxo-190-oxo-191-oxo-192-oxo-193-oxo-194-oxo-195-oxo-196-oxo-197-oxo-198-oxo-199-oxo-200-oxo-201-oxo-202-oxo-203-oxo-204-oxo-205-oxo-206-oxo-207-oxo-208-oxo-209-oxo-210-oxo-211-oxo-212-oxo-213-oxo-214-oxo-215-oxo-216-oxo-217-oxo-218-oxo-219-oxo-220-oxo-221-oxo-222-oxo-223-oxo-224-oxo-225-oxo-226-oxo-227-oxo-228-oxo-229-oxo-230-oxo-231-oxo-232-oxo-233-oxo-234-oxo-235-oxo-236-oxo-237-oxo-238-oxo-239-oxo-240-oxo-241-oxo-242-oxo-243-oxo-244-oxo-245-oxo-246-oxo-247-oxo-248-oxo-249-oxo-250-oxo-251-oxo-252-oxo-253-oxo-254-oxo-255-oxo-256-oxo-257-oxo-258-oxo-259-oxo-260-oxo-261-oxo-262-oxo-263-oxo-264-oxo-265-oxo-266-oxo-267-oxo-268-oxo-269-oxo-270-oxo-271-oxo-272-oxo-273-oxo-274-oxo-275-oxo-276-oxo-277-oxo-278-oxo-279-oxo-280-oxo-281-oxo-282-oxo-283-oxo-284-oxo-285-oxo-286-oxo-287-oxo-288-oxo-289-oxo-290-oxo-291-oxo-292-oxo-293-oxo-294-oxo-295-oxo-296-oxo-297-oxo-298-oxo-299-oxo-300-oxo-301-oxo-302-oxo-303-oxo-304-oxo-305-oxo-306-oxo-307-oxo-308-oxo-309-oxo-310-oxo-311-oxo-312-oxo-313-oxo-314-oxo-315-oxo-316-oxo-317-oxo-318-oxo-319-oxo-320-oxo-321-oxo-322-oxo-323-oxo-324-oxo-325-oxo-326-oxo-327-oxo-328-oxo-329-oxo-330-oxo-331-oxo-332-oxo-333-oxo-334-oxo-335-oxo-336-oxo-337-oxo-338-oxo-339-oxo-340-oxo-341-oxo-342-oxo-343-oxo-344-oxo-345-oxo-346-oxo-347-oxo-348-oxo-349-oxo-350-oxo-351-oxo-352-oxo-353-oxo-354-oxo-355-oxo-356-oxo-357-oxo-358-oxo-359-oxo-360-oxo-361-oxo-362-oxo-363-oxo-364-oxo-365-oxo-366-oxo-367-oxo-368-oxo-369-oxo-370-oxo-371-oxo-372-oxo-373-oxo-374-oxo-375-oxo-376-oxo-377-oxo-378-oxo-379-oxo-380-oxo-381-oxo-382-oxo-383-oxo-384-oxo-385-oxo-386-oxo-387-oxo-388-oxo-389-oxo-390-oxo-391-oxo-392-oxo-393-oxo-394-oxo-395-oxo-396-oxo-397-oxo-398-oxo-399-oxo-400-oxo-401-oxo-402-oxo-403-oxo-404-oxo-405-oxo-406-oxo-407-oxo-408-oxo-409-oxo-410-oxo-411-oxo-412-oxo-413-oxo-414-oxo-415-oxo-416-oxo-417-oxo-418-oxo-419-oxo-420-oxo-421-oxo-422-oxo-423-oxo-424-oxo-425-oxo-426-oxo-427-oxo-428-oxo-429-oxo-430-oxo-431-oxo-432-oxo-433-oxo-434-oxo-435-oxo-436-oxo-437-oxo-438-oxo-439-oxo-440-oxo-441-oxo-442-oxo-443-oxo-444-oxo-445-oxo-446-oxo-447-oxo-448-oxo-449-oxo-450-oxo-451-oxo-452-oxo-453-oxo-454-oxo-455-oxo-456-oxo-457-oxo-458-oxo-459-oxo-460-oxo-461-oxo-462-oxo-463-oxo-464-oxo-465-oxo-466-oxo-467-oxo-468-oxo-469-oxo-470-oxo-471-oxo-472-oxo-473-oxo-474-oxo-475-oxo-476-oxo-477-oxo-478-oxo-479-oxo-480-oxo-481-oxo-482-oxo-483-oxo-484-oxo-485-oxo-486-oxo-487-oxo-488-oxo-489-oxo-490-oxo-491-oxo-492-oxo-493-oxo-494-oxo-495-oxo-496-oxo-497-oxo-498-oxo-499-oxo-500-oxo-501-oxo-502-oxo-503-oxo-504-oxo-505-oxo-506-oxo-507-oxo-508-oxo-509-oxo-510-oxo-511-oxo-512-oxo-513-oxo-514-oxo-515-oxo-516-oxo-517-oxo-518-oxo-519-oxo-520-oxo-521-oxo-522-oxo-523-oxo-524-oxo-525-oxo-526-oxo-527-oxo-528-oxo-529-oxo-530-oxo-531-oxo-532-oxo-533-oxo-534-oxo-535-oxo-536-oxo-537-oxo-538-oxo-539-oxo-540-oxo-541-oxo-542-oxo-543-oxo-544-oxo-545-oxo-546-oxo-547-oxo-548-oxo-549-oxo-550-oxo-551-oxo-552-oxo-553-oxo-554-oxo-555-oxo-556-oxo-557-oxo-558-oxo-559-oxo-560-oxo-561-oxo-562-oxo-563-oxo-564-oxo-565-oxo-566-oxo-567-oxo-568-oxo-569-oxo-570-oxo-571-oxo-572-oxo-573-oxo-574-oxo-575-oxo-576-oxo-577-oxo-578-oxo-579-oxo-580-oxo-581-oxo-582-oxo-583-oxo-584-oxo-585-oxo-586-oxo-587-oxo-588-oxo-589-oxo-590-oxo-591-oxo-592-oxo-593-oxo-594-oxo-595-oxo-596-oxo-597-oxo-598-oxo-599-oxo-600-oxo-601-oxo-602-oxo-603-oxo-604-oxo-605-oxo-606-oxo-607-oxo-608-oxo-609-oxo-610-oxo-611-oxo-612-oxo-613-oxo-614-oxo-615-oxo-616-oxo-617-oxo-618-oxo-619-oxo-620-oxo-621-oxo-622-oxo-623-oxo-624-oxo-625-oxo-626-oxo-627-oxo-628-oxo-629-oxo-630-oxo-631-oxo-632-oxo-633-oxo-634-oxo-635-oxo-636-oxo-637-oxo-638-oxo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Table S1. Cont 8.

UniProt/Swiss-Prot ID	Description	Protein score ^a	Protein mass (kDa)	pI ^a	Num. of matches ^a	Num. of significant matches ^a	Num. of sequences ^a	Num. of significant sequences ^a	Num. of unique sequences ^a	Sequence coverage ^b	emPA ^c
PGRK2.HUMAN	Membrane-associated progesterone receptor component 2	55	55	5.18	1	1	1	1	1	0.08	0.16
SPRHR.HUMAN	Spermatocyte reduction	55	28031	8.24	1	1	1	1	1	0.08	0.16
THYTX.HUMAN	Transferrin	55	15877	5.52	2	2	2	2	2	0.15	0.23
HS105.HUMAN	Heart shock protein 105 kDa	55	96804	5.28	11	1	8	1	8	0.15	0.52
LASPT2.HUMAN	LM and SH2 domain protein 1	55	29868	6.61	10	3	4	3	4	0.21	0.24
RM12.HUMAN	35S ribosomal protein L12, mitochondrial	55	91335	9.04	1	1	1	1	1	0.31	0.23
STX7.HUMAN	Syntaxin-7	55	28797	5.41	3	2	2	2	2	0.19	0.15
MTGDF.HUMAN	Myelin-derived growth factor	55	19193	6.2	4	2	2	2	2	0.12	0.25
JOSL2.HUMAN	Joslyn-2	55	20743	6.9	1	1	1	1	1	0.11	0.21
TS101.HUMAN	Tumor susceptibility gene 101 protein	54	43916	6.06	6	1	4	1	4	0.24	0.61
FA2H.HUMAN	Oxidation of fatty acids 2	54	54716	7.12	2	1	1	1	1	0.07	0.09
QO2R.HUMAN	Quinone oxidoreductase	54	35185	8.56	8	4	6	4	6	0.34	0.6
DCR1L.HUMAN	Dicerin-1	54	28382	8.54	1	1	1	1	1	0.08	0.15
CO5B.HUMAN	CO5B decarboxylase	54	14168	6.02	2	1	1	1	1	0.19	0.23
LAMP1.HUMAN	Lysosomal-associated membrane decarboxylase 2	54	44932	5.35	1	1	1	1	1	0.04	0.1
RDH12.HUMAN	Retinol dehydrogenase 14	54	35841	6.02	3	2	2	2	2	0.11	0.12
HMPL.HUMAN	Hemerythrin nuclear ribonucleoprotein L	54	44092	8.46	4	3	2	3	3	0.18	0.14
IFR1.HUMAN	Interferon- γ inducible protein 16	54	88199	9.31	5	1	3	1	3	0.08	0.05
MMP1.HUMAN	Matrix metalloproteinase 1	54	65852	7.63	6	1	3	1	3	0.08	0.07
PFM1.HUMAN	Protein phosphatase 1F	54	48900	4.99	3	2	2	2	2	0.13	0.19
TL2.HUMAN	Translocin beta-like protein 2	53	28876	8.52	1	1	1	1	1	0.03	0.09
OSIP1.HUMAN	Osteocalcin-related beta-stalk protein 1	53	8411	15.82	2	2	2	2	2	0.24	0.22
DC2.HUMAN	D-lysine decarboxylase β -like protein	53	14186	5.89	7	5	3	2	3	0.52	0.78
APPL1.HUMAN	Apoptosis	53	41713	8.24	6	5	3	2	3	0.1	0.22
NOL4.HUMAN	NADH-dependent oxidoreductase chain 4	53	51547	9.4	1	1	1	1	1	0.03	0.08
DOX1.HUMAN	Dolichol kinase	53	59229	8.87	5	2	4	1	4	0.12	0.07
SWP1.HUMAN	Switch-associated protein 70	53	68804	5.88	10	4	15	8	15	0.08	0.14
JUP1.HUMAN	Junctional microtubule associated homolog 1	52	16005	5.47	1	1	1	1	1	0.12	0.29
SHK1.HUMAN	SH2 domain-containing kinase-binding protein 1	52	70882	8.24	5	2	4	1	4	0.12	0.08
PGM3.HUMAN	Basement membrane-specific heparan sulfate proteoglycan core protein	51	46532	6.06	1	1	8	1	8	0.04	0.04
MSMO1.HUMAN	Methylmalonate decarboxylase 1	51	14127	11.05	1	1	1	1	1	0.22	0.34
TRIA1.HUMAN	Tripartite motif-containing protein 47	51	35183	6.75	15	3	18	3	18	0.15	0.18
SOAT1.HUMAN	Protein transport protein SCA1A	51	23373	5.4	10	2	7	1	7	0.08	0.02
SOAT1.HUMAN	Stearoyl-CoA transferase 1	51	64492	8.08	12	4	18	2	18	0.08	0.02
BDH2.HUMAN	3-hydroxybutyrate dehydrogenase type 2	51	26707	7.56	2	2	1	1	1	0.09	0.17
ADRO2.HUMAN	NADH-dependent oxidoreductase, mitochondrial	51	53863	8.72	2	2	2	2	2	0.1	0.06
CSN1.HUMAN	COPII signalosome complex subunit 1	51	55501	6.3	3	1	3	1	3	0.15	0.19
APB3.HUMAN	APB3 complex subunit beta-1	51	21244	5.76	13	5	9	3	9	0.14	0.11
ULAI.HUMAN	NEDD8-activating enzyme E1 regulatory subunit	50	62029	4.9	4	2	4	2	4	0.09	0.09
MG13.HUMAN	MG13 complex subunit MG13	50	13079	9.44	2	2	2	2	2	0.44	0.88
TOPBP1.HUMAN	Activated R1A protein kinase 2 transcriptional coactivator p15	50	14388	9.6	2	1	2	1	2	0.31	0.23
ACTN1.HUMAN	Aspirin acetyltransferase, mitochondrial	50	47487	8.14	1	1	3	1	3	0.1	0.3
VASN.HUMAN	Vasoin	50	71688	7.16	2	2	1	1	1	0.06	0.06
QPL1.HUMAN	Quaternone peroxidase 1	50	22075	6.15	10	4	4	4	4	0.45	0.4
RECQ1.HUMAN	ATP-dependent DNA helicase Q1	50	73410	8.12	3	1	3	1	3	0.1	0.06
HWE1.HUMAN	ES ubiquitin-protein ligase HWE1	50	48189	5.1	14	3	8	2	8	0.05	0.05
HYEP.HUMAN	Exonin hyaluronate 1	50	52815	6.27	3	1	3	1	3	0.15	0.19
PTPA.HUMAN	Serine/threonine-protein phosphatase 2A activator	50	40641	5.63	5	2	2	2	2	0.18	0.23
TBD1.HUMAN	Tubulin-specific chaperone D1	50	12315	5.8	2	2	2	2	2	0.17	0.07
ALG1.HUMAN	Oncofetal glycoprotein beta-bisectin-mannosyltransferase	49	52484	6.81	2	2	2	2	2	0.11	0.17
NPT2.HUMAN	Endoplasmic reticulum protein 2	49	16559	7.56	3	1	3	1	3	0.37	0.48
PMH1.HUMAN	Purine nucleoside phosphorylase	49	32097	6.95	8	3	4	3	4	0.31	0.07
LSMT.HUMAN	USP on RNA-associated Ser-His protein LSm7	49	11595	5.1	6	3	3	3	3	0.52	0.29
EMT1.HUMAN	Extracellular matrix protein 1	49	60835	8.25	3	1	3	1	3	0.07	0.07
LMNB1.HUMAN	Lamin A	49	46379	6.07	1	1	2	1	2	0.07	0.09
TC13.HUMAN	Tail-binding protein 3	49	13726	8.04	3	1	3	1	2	0.28	0.35
PGM5L.HUMAN	24S proteasome non-ATPase regulatory subunit B	49	35887	5.73	1	1	1	1	1	0.04	0.1
CBX3.HUMAN	Chromatin-associated protein homolog 3	49	20798	5.23	4	2	2	2	2	0.25	0.49
BCAT2.HUMAN	Branched-chain amino-acid aminotransferase, mitochondrial	49	24926	8.88	4	3	2	1	2	0.15	0.41
PAB1.HUMAN	Protein-binding domain 1	49	11843	7.88	8	6	7	6	7	0.97	0.97
4F2.HUMAN	4F2 cell-surface antigen heavy chain	49	47952	4.89	5	2	3	2	3	0.09	0.13
SRD5.HUMAN	Ribosome maturation protein SRD5	49	28746	8.61	2	1	2	1	2	0.22	0.18
YF1B.HUMAN	Protein YF1B	48	34143	9.21	3	3	1	1	1	0.08	0.13
GREL2.HUMAN	Ureapylase with GCG-like domain protein 2	48	38166	4.5	2	2	1	1	1	0.04	0.11
NCA.HUMAN	Nucleoside	48	76362	5.67	2	1	4	1	4	0.04	0.07
KOY1.HUMAN	UMP-CMP kinase	48	22208	5.44	3	2	2	1	2	0.17	0.21
MAT1A.HUMAN	Methionine-associated protein 1A	47	30528	4.85	14	3	9	3	9	0.06	0.04
EMC1.HUMAN	ER membrane protein complex subunit 1	47	11489	7.28	1	1	1	1	1	0.13	0.1
PTCH1.HUMAN	Protocadherin cell-surface protein	47	129551	6.37	3	1	2	1	2	0.02	0.03
HMS1.HUMAN	Minor histone-complex associated protein 3	47	11462	6.01	2	2	2	2	2	0.23	0.2
SSR1.HUMAN	Transferase-associated protein subunit delta	47	18897	5.76	9	2	2	2	2	0.18	0.54
CHMP1.HUMAN	Charged multivesicular body protein 3	47	23907	5.1	1	1	1	1	1	0.14	0.18
DRH1.HUMAN	Dehydrogenase reductase SDR family member 7	47	38274	8.59	1	1	1	1	1	0.27	0.4
RT8.HUMAN	28S ribosomal protein S6, mitochondrial	47	14218	9.3	3	2	1	1	1	0.19	0.23
AT10L.HUMAN	Atto-180 protein family 1 member C1	47	36765	6.32	6	3	3	3	3	0.23	0.4
ITPA.VJ.HUMAN	Interferon alpha-1	47	115884	5.45	6	2	6	2	6	0.11	0.07
DPF2.HUMAN	Dipeptidyl peptidase 2	47	54307	5.81	4	1	2	1	2	0.19	0.08
APMA1.HUMAN	Adipocyte plasma membrane-associated protein	47	66451	5.82	2	2	2	2	2	0.18	0.2
VAC1.HUMAN	Protein VAC1 homolog	47	87917	5.76	6	1	4	1	4	0.12	0.05
ACQ1.HUMAN	Cytochrome associated cytochrome	46	88337	8.23	7	2	3	1	3	0.07	0.04
AT10L.HUMAN	ATP10-like protein 10	46	91293	6.1	5	2	3	1	3	0.13	0.1
PTCH1.HUMAN	Protocadherin cell-surface protein	46	29377	6.8	3	2	1	1	1	0.14	0.03
KSR1.HUMAN	NR4A1 inhibitor beta	46	37748	6.7	1	1	1	1	1	0.12	0.06
RM2.HUMAN	35S ribosomal protein L28, mitochondrial	46	30108	8.34	2	2	2	2	2	0.11	0.32
DNCL1.HUMAN	DNA-Like protein 1	46	30035	5.18	1	1	1	1	1	0.16	0.15
OPT1A.HUMAN	Carbamate Oxidoreductase/transferase 1, liver isoform	46	88211	8.85	6	3	12	3	12	0.09	0.09
THOP1.HUMAN	Thimet oligopeptidase	46	78789	5.72	8	2	7	2	7	0.18	0.11
BACH1.HUMAN	Cysteine acid coenzyme A thioester hydrolase	46	47169	8.85	6	2	7	2	7	0.13	0.1
NRHP1.HUMAN	Nuclear receptor-binding protein	46	96807	5.02	3	2	2	2	2	0.09	0.15
PRPO.HUMAN	Pyridoxal-5-phosphate oxidase	45	29969	6.62	2	1	1	1	1	0.07	0.15
NUD5.HUMAN	Nuclear pore complex protein Nup205	45	22716	6.81	5	5	5	5	5	0.05	0.05
IFR1.HUMAN	Interferon growth factor receptor subunit 15-like 1	45	84197	4.93	3	3	3	3	3	0.08	0.05
SPB1.HUMAN	Skin fibroblast protein 38 subunit 1	45	145738	6.65	6	3	3	3	3	0.05	0.03
EPD3.HUMAN	Enzyme P granules protein 5 homolog	45	29293	5.99	6	5	5	5	5	0.04	0.03
PXN.HUMAN	Peroxidase homolog	45	15710	6.79	5	3	4	3	4	0.06	0.08
MYO1B.HUMAN	ES ubiquitin-protein ligase MYO1B	44	50919	6.63	2	2	1	1	1	0.06	0.01
CSN1.HUMAN	COPII signalosome complex subunit 7a	44	40258	8.33	2	2	1	1	1	0.11	0.19
DNCL1.HUMAN	Dicerin subunit 2	44	32024	5.1	3	1	3	1	3	0.17	0.1
RM2.HUMAN	Residual of microtubule dynamics protein 3	44	52086	5.02	2	2	2	2	2	0.12	0.1

*Protein score is calculated from the score of the peptide attributed to the protein

^bpI is (Predicted) isoelectric point.

^cNumber of matches is spectrum number matched to protein.⁴⁷

^aNumber of matches is spectrum number matched to protein⁴¹.

^dNumber of significant matches is spectrum number that matches p

^aNumber of sequences is number of peptides matched to protein^{#2}.

[†]Number of significant sequences is number of peptides exceeding the identification

³Number of unique sequences is a unique⁶³ number of peptides matched to proteins.

^bSequence coverage is the ratio of the total number of matched peptide residues to the total length of the protein.

¹Exponentially Modified Protein Abundance Index (http://www.mstrixscience.com/help/quant_empi_help.html)

Table S1. Cont 9

Protein score is calculated from the score of the peptide attributed to the protein.

$|\text{pI}|$ is (Predicted) isoelectric point.

Number of matches is spectrum number matched to protein¹⁶.

Number of significant matches is spectrum number that matches protein and exceeds the identification criteria.

Number of sequences is number of peptides matched to protein¹⁶.

Number of significant sequences is number of peptides exceeding the identification criteria matched to proteins.

Number of unique sequences is a unique¹⁶ number of peptides matched to proteins.

Sequence coverage is the ratio of the total number of matched peptide residues to the total length of the protein.

50% sequence coverage means that at least 50% of the amino acid residues in the protein are covered by at least one peptide.

Table S1, Cont 16.

UniProt/Swiss-Prot ID	Description	Protein score ^a	Protein mass (kDa)	pI ^b	Num. of matches ^c	Num. of significant matches ^d	Num. of sequences ^e	Num. of significant sequences ^f	Num. of unique sequences ^g	Sequence coverage ^h	emPAI
XPC_HUMAN	Exportin-5	35	136222	5.56	8	2	3	1	3	0.85	0.08
QDR_HUMAN	Quarantine reductase, mitochondrial	35	96221	8.14	7	2	4	2	4	0.16	0.16
HMOX1_HUMAN	Heme oxygenase 1	35	32788	7.88	5	1	3	1	3	0.19	0.14
ASPS_HUMAN	Asparagine synthetase [glutamine-hydrolyzing]	35	64229	6.39	4	1	4	1	4	0.19	0.07
SPART_HUMAN	Spartin	35	72788	5.66	3	2	2	2	2	0.11	0.12
PONZ_HUMAN	Serum peroxanase/ arylsterase 2	35	39372	5.33	3	1	2	1	2	0.19	0.11
QLRF_HUMAN	Glucosylated lysosomal membrane protein	35	43636	6.1	2	1	1	1	1	0.05	0.1
TDJ_HUMAN	Transport and Golgi organization protein 1 homolog	35	213570	4.76	5	2	3	1	3	0.04	0.02
EPF2_HUMAN	Eukaryotic translation initiation factor 2A	34	84949	5.8	2	2	1	1	1	0.04	0.07
TMED3_HUMAN	Transmembrane emp24 domain-containing protein 3	34	24761	5.4	1	1	1	1	1	0.13	0.18
EXOC2_HUMAN	Exocyst complex component 2	34	104000	6.46	10	1	6	1	6	0.16	0.04
QLN_HUMAN	QlnA	34	68165	5.24	1	1	1	1	1	0.05	0.06
IFIT5_HUMAN	Interferon-induced protein with tetratricopeptide repeats 5	34	55812	7	4	1	4	1	4	0.21	0.08
RGS3_HUMAN	Synermyrin-A	34	59671	5.2	16	1	4	1	4	0.13	0.07
ERD1_HUMAN	Lecanoderm synthase	34	83255	6.16	2	1	1	1	1	0.02	0.05
DCPS_HUMAN	m7GpppX dephosphatase	34	38585	5.93	2	2	2	2	2	0.1	0.04
CTTM_HUMAN	Microtubule-associated GTP-actin-binding synthase, mitochondrial	34	105724	8.22	1	1	1	1	1	0.02	0.02
USP31_HUMAN	Probable ubiquitin carboxyl-terminal hydrolase FAF-3	34	292584	5.22	18	1	11	1	11	0.08	0.01
TRXR1_HUMAN	Thioredoxin reductase 1, cytosolic	33	70862	7.16	5	2	4	2	4	0.12	0.13
DPPI_HUMAN	Dibasic-hydrophobic mannosyltransferase subunit 1	33	29616	9.57	7	1	4	1	4	0.24	0.15
NSF1C_HUMAN	NSF1 cofactor p47	33	40548	4.89	3	1	2	1	2	0.11	0.11
RML2_HUMAN	35S ribosomal protein L54, mitochondrial	33	15809	9.6	1	1	1	1	1	0.19	0.3
TRNL1_HUMAN	Thioredoxin-like protein 1	33	32231	4.84	4	2	3	2	3	0.21	0.28
SF3B4_HUMAN	Splicing factor 3B subunit 4	33	44357	8.54	2	1	2	1	2	0.11	0.1
GSBP_HUMAN	GSBP-interacting protein	33	15638	4.36	3	1	2	1	2	0.19	0.3
CONL2_HUMAN	Microtubule	33	27385	9.1	2	1	1	1	1	0.09	0.12
ODR8_HUMAN	2-oxoisovalerate dehydrogenase subunit beta, mitochondrial	33	43095	5.89	3	1	3	1	3	0.17	0.1
COMD2_HUMAN	COMD domain-containing protein 2	32	22721	6.24	5	2	3	1	3	0.24	0.2
UACA_HUMAN	Uveal autoantigen with collagen-coil domains and ankyrin repeats	32	162404	6.6	22	1	6	1	6	0.07	0.03
ROD2_HUMAN	E3 ubiquitin-protein ligase TRIM21	32	54135	5.88	5	1	5	1	5	0.17	0.08
COX4_HUMAN	Cytochrome oxidase 4	32	31708	6.51	6	2	3	2	3	0.28	0.13
VP37A_HUMAN	Vacuolar protein sorting-associated protein 37A	32	44287	5.37	1	1	1	1	1	0.1	0.1
ITGA2_HUMAN	Integrin alpha-2	32	128214	5.16	5	1	5	1	5	0.11	0.03
ACAT4_HUMAN	Acyloxyacyl-CoA transporter 1	32	60876	6.89	4	2	2	1	2	0.11	0.07
S3BA3_HUMAN	Zinc transporter ZIP9	32	32231	6.21	1	1	1	1	1	0.07	0.14
EXOC1_HUMAN	Exocyst complex component 1	32	83230	6.33	5	3	4	2	4	0.12	0.11
SSX2A1_HUMAN	Sukkle carrier family 52, riboflavin transporter, member 1	32	46287	5.9	2	2	1	1	1	0.05	0.09
RT1E_HUMAN	28S ribosomal protein S16, mitochondrial	32	15335	9.58	1	1	1	1	1	0.15	0.31
BGL1_HUMAN	Beta-mannosidase	32	76027	6.1	7	2	1	1	1	0.09	0.06
MDM1_HUMAN	Mitochondrial 2-oxoglutarate/malate carrier protein	32	34040	9.82	4	1	3	1	3	0.22	0.13
FBLN1_HUMAN	Fibulin-1	32	77162	5.07	6	4	4	2	4	0.12	0.18
KOM5_HUMAN	Lysine-specific demethylase 6B	32	176523	8.83	12	1	5	1	5	0.07	0.02
PSME4_HUMAN	Proteasome activator complex subunit 4	31	21199	6.45	4	1	3	1	3	0.03	0.02
ACAL_HUMAN	Alpha-galactosidase A	31	48725	5.35	3	2	1	1	1	0.06	0.08
EBP1_HUMAN	Enoamph-binding protein-like	31	23188	5.81	2	2	1	1	1	0.15	0.19
CD9_HUMAN	CD9 antigen	31	25398	6.8	3	2	2	1	2	0.27	0.18
POTD1_HUMAN	Prenylcysteine oxidase 1	31	56604	5.8	3	2	2	1	2	0.05	0.08
XPO4_HUMAN	Exportin-4	31	130058	4.85	9	2	7	2	7	0.13	0.07
SF3A2_HUMAN	Splicing factor 3A subunit 3	31	58512	6.27	2	1	2	1	2	0.1	0.07
CAB45_HUMAN	45 kDa calyx-binding protein	31	41780	4.76	5	2	2	1	2	0.14	0.1
CD72_HUMAN	CD72 antigen	31	57199	4.77	2	2	2	2	2	0.08	0.16
TXR4_HUMAN	Taxilin-expressed protein 284	31	24167	4.76	1	1	1	1	1	0.06	0.13
COAT1_HUMAN	CoA division cycle and apoptosis regulator protein 1	31	132738	5.57	7	1	4	1	4	0.06	0.03
KDEL1_HUMAN	KDEL motif-containing protein 1	31	58005	7.59	1	1	1	1	1	0.03	0.07
EDL4_HUMAN	Endoplasmic reticulum chaperone	31	70552	6.14	8	2	6	1	6	0.13	0.06
FUCO2_HUMAN	Tissue alpha-L-fucosidase	31	53655	6.27	1	1	1	1	1	0.08	0.08
AFAM1_HUMAN	Adrenomedullin	31	69024	5.84	5	2	3	2	3	0.12	0.06
PPPT1_HUMAN	Serine/threonine-protein phosphatase 6 regulatory subunit 1	31	96664	4.45	4	2	2	1	2	0.05	0.04
GT027_HUMAN	UPF0807 protein G20orf7	30	19279	6.34	2	1	2	1	2	0.16	0.24
RGD1_HUMAN	Immunoglobulin GTPase family G protein	30	62478	4.81	3	2	1	1	1	0.05	0.07
YIF1A_HUMAN	Protein YIF1A	30	31891	8.88	3	2	3	2	3	0.19	0.3
CARM1_HUMAN	Histone H3-lysine methyltransferase CARM1	30	63511	6.25	6	3	4	2	4	0.17	0.21
KIF1_HUMAN	Kinesin-13-like motor domain containing coiled-coil stalk	30	45266	8.3	2	1	2	1	2	0.14	0.1
NAV1_HUMAN	Neuron navigator 1	30	202347	8.2	9	2	6	1	6	0.07	0.04
CASP8_HUMAN	Caspase-8	30	46351	5.73	1	1	1	1	1	0.06	0.09
GORS2_HUMAN	Golgi reassembly-stacking protein 2	30	47116	4.73	2	1	2	1	2	0.08	0.09
NPS1_HUMAN	Protein Nip5 homolog 2	30	33721	9.42	3	1	2	1	2	0.15	0.13
SARK1_HUMAN	Sarcolysosomal lysosomal hydrolase-like protein 1	30	58913	6.48	6	1	6	1	6	0.25	0.07
GSN3_HUMAN	COP9 signalosome complex subunit 3	30	47842	6.19	9	1	8	1	8	0.44	0.09
GSN2_HUMAN	Glutamate-cysteine ligase regulatory subunit	30	30708	5.89	1	1	1	1	1	0.11	0.14
MAP1F_HUMAN	Microtubule-associated protein 1F	29	112162	6.92	3	1	3	1	3	0.05	0.04
PGP1_HUMAN	Prostaglandin G/H synthase 1	29	68642	6.81	2	2	2	2	2	0.09	0.13
MOT4_HUMAN	Microtubule motor transporter 4	29	49437	8.23	4	2	2	1	2	0.03	0.09
NAGK_HUMAN	N-acetyl-D-glucosamine kinase	29	37352	5.81	9	1	3	1	3	0.15	0.12
NUCB2_HUMAN	Nucleobindin-2	29	50164	5.03	3	2	2	1	2	0.08	0.09
RGR1_HUMAN	Receptor-interacting serine/threonine-protein kinase 2	29	61156	6.83	2	1	2	1	2	0.09	0.07
LMO7_HUMAN	LM domain only protein 7	29	192578	8.24	10	1	5	1	5	0.05	0.02
AKAD1_HUMAN	AKR1A1-related oxidoreductase	29	24730	6.85	2	1	1	1	1	0.17	0.18
POXOD1_HUMAN	Purkinje cell-specific oxidoreductase domain-containing protein 2	29	51772	5.65	5	2	5	2	5	0.26	0.15
DHS2A_HUMAN	Deoxyribonuclease-2-delta	29	39558	8.3	4	2	2	1	2	0.15	0.23
LEO3_HUMAN	Galactose-3-epimerase	29	26106	6.57	5	1	4	1	4	0.22	0.17
PPH1_HUMAN	Peptidyl-prolyl cis-trans isomerase F, mitochondrial	28	22028	9.48	2	2	2	2	2	0.27	0.46
DH102_HUMAN	Dynamin heavy chain 10, axonemal	28	514512	5.84	13	1	10	1	10	0.06	0.01
LEP1_HUMAN	Lipin-1	28	113952	5.4	8	1	7	1	7	0.13	0.04
MALD1_HUMAN	MARVEL domain-containing protein 1	28	18902	9.89	2	1	1	1	1	0.17	0.24
EDL3_HUMAN	EDL-like repeat and discoidin-like domain-containing protein 3	28	53708	7.88	2	1	2	1	2	0.11	0.08
ADBP1_HUMAN	Adenosine diphosphate synthase complex-interacting multifunctional protein 1	28	34331	6.81	3	2	3	2	3	0.17	0.27
SNX5_HUMAN	Sorting nexin-5	28	46787	6.21	1	1	1	1	1	0.05	0.09
MA1A2_HUMAN	Mannosyl-6-phosphate isomerase 1, 2-alpha-mannosidase IB	28	72857	7.17	2	1	1	1	1	0.03	0.06
FKBP4_HUMAN	Peptidyl-prolyl cis-trans isomerase FKBP4	28	51772	5.35	7	1	5	1	5	0.15	0.08
PSMD4_HUMAN	Proteasome assembly chaperone 4	28	13768	6.94	1	1	1	1	1	0.13	0.35
USOL1_HUMAN	Ubiquitin-1	28	62478	5.02	4	1	3	1	3	0.16	0.07
XPO7_HUMAN	Exportin-7	28	198883	5.24	2	1	2	1	2	0.05	0.04
HGB1_HUMAN	Oxygen-dependent coproporphyrinogen-III oxidase, mitochondrial	28	50120	6.59	4	1	3	1	3	0.2	0.09
NET2_HUMAN	Osmoglycin NET2	28	30588	6.82	6	1	3	1	3	0.23	0.14
EMP1_HUMAN	Endoplasmic membrane protein 3	27	18417	8.16	1	1	1	1	1	0.21	0.25
WASO1_HUMAN	WASH complex subunit S	27	134031	6.54	5	2	4	1	4	0.05	0.06
NU155_HUMAN	Nuclear pore complex protein Nup155	27	155100	5.78	8	1	4	1	4	0.09	0.03
USP2L_HUMAN	Ubiquitin-associated protein 2-Bie	27	114485	6.81	3	1	3	1	3	0.05	0.04
WAC1A_HUMAN	WASH complex subunit 2A	27	147085	4.89	3	1	3	1	3	0.04	0.03

^aProtein score is calculated from the score of the peptide attributed to the protein.

^bpI is (Predicted) isoelectric point.

^cNumber of matches is spectrum number matched to protein¹¹.

^dNumber of significant matches is spectrum number that matches protein and exceeds the identification criteria.

^eNumber of sequences is number of peptides matched to protein¹¹.

^fNumber of significant sequences is number of peptides exceeding the identification criteria matched to proteins.

^gNumber of unique sequences is a unique¹¹ number of peptides matched to proteins.

^hSequence coverage is the ratio of the total number of matched peptide residues to the total length of the protein.

ⁱExponentially Modified Protein Abundance Index (http://www.matrixscience.com/help/quant_Lemaps_help.html).

Table S1, Cont 11.

UniProt/Swiss-Prot ID	Description	Protein score ¹	Protein mass (kDa)	pI ²	Num. of matches ³	Num. of significant matches ⁴	Num. of sequences ⁵	Num. of significant sequences ⁶	Num. of unique sequences ⁷	Sequence coverage ⁸	emPAI ⁹
SIRM1_HUMAN	Serine/arginine repetitive matrix protein 1	27	102274	11.34	6	2	3	1	3	0.09	0.09
CSF2_HUMAN	CSF2 antigen	27	91809	6.5	2	1	2	1	2	0.07	0.05
SORCS4_HUMAN	Sorcs4	27	21662	5.32	5	1	3	1	3	0.22	0.21
MTXN4_HUMAN	Methylthioester-1-phosphate isomerase	27	39125	5.89	2	1	2	1	2	0.21	0.11
GPIH_HUMAN	GPI-anchored transmembrane	27	45223	5.76	2	1	1	1	1	0.07	0.1
NUP88_HUMAN	Nuclear pore complex protein Nup88	27	83489	5.47	3	1	2	1	2	0.06	0.05
GDP_HUMAN	Gammaglutamylhydrolase	27	35841	6.67	1	1	1	1	1	0.08	0.12
ANX11_HUMAN	Annexin A11	27	54355	7.53	2	1	2	1	2	0.07	0.08
IFIT1_HUMAN	Exonuclease translation initiation factor 2 subunit 2	27	38384	5.6	3	1	3	1	3	0.15	0.11
IFIT1_HUMAN	Interferon-induced protein with tetranucleotide repeats 1	27	53325	6.75	3	1	3	1	3	0.13	0.08
RRAGD_HUMAN	Rac-related GTP-binding protein G	27	44196	4.94	1	1	1	1	1	0.06	0.1
NRSF_HUMAN	Nuclear receptor-binding factor 2	27	32358	5.61	1	1	1	1	1	0.3	0.14
TARA_HUMAN	TRIO and F-actin-binding protein	26	261217	8.86	10	1	7	1	7	0.05	0.02
GCSH_HUMAN	Glycine cleavage system H protein, mitochondrial	26	18873	4.91	3	1	2	1	2	0.29	0.24
CHD1_HUMAN	Chromatin domain-containing protein 1	26	44812	8.74	6	2	4	2	4	0.26	0.2
NEX3_HUMAN	Serine/threonine-protein kinase Nsk3	26	107100	5.51	8	2	6	1	6	0.13	0.04
ENAH_HUMAN	Protein enabled homolog	26	66470	6.51	14	2	3	1	3	0.08	0.13
PABP1_HUMAN	Pab1 (ADP-ribosyl) polymerase 1	26	113012	8.96	5	1	3	1	3	0.09	0.04
ODRP_HUMAN	Pyruvate dehydrogenase E1 component subunit beta, mitochondrial	26	38208	6.2	12	3	3	2	3	0.21	0.24
LONM_HUMAN	Lon protease homolog, mitochondrial	26	106422	6.01	10	2	5	1	5	0.16	0.04
FABR8_HUMAN	Protein FABR8	26	37167	5.86	2	1	2	1	2	0.09	0.12
UBQ1L_HUMAN	Ubiquitin-conjugating enzyme E2 G1	26	19497	5.21	2	1	2	1	2	0.35	0.23
COX2_HUMAN	Cytochrome c oxidase subunit 2	26	23548	4.67	8	1	3	1	3	0.3	0.16
KDM1A_HUMAN	Lysine-specific histone demethylase 1A	26	92845	6.11	5	2	4	1	4	0.12	0.05
ACCSB_HUMAN	Short-branched chain specific acyl-CoA dehydrogenase, mitochondrial	26	74455	6.33	2	1	2	1	2	0.09	0.09
TT1L2_HUMAN	Tubulin-tyrosine lyase-like protein 12	26	74356	5.33	3	1	2	1	2	0.06	0.06
PIRPA_HUMAN	Pir-1 RNA-processing-aiding factor 8	26	273427	8.95	7	1	5	1	5	0.04	0.02
UMPF_HUMAN	Uridine 5'-monophosphate synthase	25	57189	6.61	1	1	1	1	1	0.07	0.08
BGN_HUMAN	Bergen	25	73553	5.13	2	1	2	1	2	0.05	0.06
SCFD2_HUMAN	Sec1 family domain-containing protein 2	25	70579	6.21	4	1	3	1	3	0.12	0.06
SMO1_HUMAN	Small nuclear ribonucleoprotein Sm D3	25	13907	10.33	1	1	1	1	1	0.17	0.34
LYPL1_HUMAN	Lysophospholipase-like protein 1	25	26299	7.71	3	1	2	1	2	0.21	0.17
BET1L_HUMAN	BET1-like protein	25	12380	7.88	3	1	3	1	3	0.47	0.39
SNR1_HUMAN	Vacuolar-sorting protein SNR1	24	28846	6.2	1	1	1	1	1	0.14	0.15
SNAG_HUMAN	Gammaglutamyl NSF attachment protein	24	34724	5.3	4	1	4	1	4	0.24	0.13
TPRGL_HUMAN	Tumor protein p27-regulated gene 1-like protein	24	30183	6.85	4	1	4	1	4	0.19	0.15
KPRA_HUMAN	Phosphoribosyl pyrophosphate synthase-associated protein 1	24	39369	6.73	2	1	2	1	2	0.09	0.11
LANC1_HUMAN	LonC-like protein 1	24	45254	7.86	3	1	2	1	2	0.16	0.1
DESU1_HUMAN	Desmodulin isopeptidase 1	24	18251	4.66	1	1	1	1	1	0.15	0.25
ABHD8_HUMAN	Protein ABHD11	24	34668	9.3	5	1	2	1	2	0.16	0.13
ORL1_HUMAN	Or-like protein	24	33756	6.26	2	1	2	1	2	0.11	0.13
CCORL_HUMAN	Coumarin-oligomer domain-containing protein 90	23	108106	9.72	11	2	5	1	5	0.09	0.04
DNREP1_HUMAN	Aspartyl aminopeptidase	23	52395	7.03	4	1	2	1	2	0.08	0.08
PAPR4_HUMAN	Pab1 (ADP-ribosyl) polymerase 4	23	192472	5.43	11	1	7	1	7	0.07	0.02
ERD1_HUMAN	Squalene monooxygenase	23	63882	8.8	3	1	2	1	2	0.06	0.07
PLCG1_HUMAN	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase gamma-1	23	148438	5.73	5	1	4	1	4	0.06	0.03
ELP1_HUMAN	Elongator complex protein 5	23	110158	6.61	2	2	2	1	2	0.03	0.03
INT3_HUMAN	Integrator complex subunit 3	23	117994	5.53	5	1	4	1	4	0.1	0.04
USP7_HUMAN	Ubiquitin carboxyl-terminal hydrolase 7	23	126220	5.33	6	2	5	1	5	0.11	0.03
YPS2_HUMAN	Protein YPS2	23	38223	5.47	1	1	1	1	1	0.07	0.22
CSPP2_HUMAN	Variation core protein	23	372590	4.43	5	1	3	1	3	0.02	0.01
TRPF_HUMAN	Thyroid receptor-interacting protein 6	23	90255	7.19	3	1	1	1	1	0.09	0.09
TTG1_HUMAN	Tetratricopeptide repeat protein 1	23	23505	4.78	2	1	2	1	2	0.2	0.13
RANL_HUMAN	Ran-specific GTPase-activating protein	23	23286	5.19	5	1	2	1	2	0.15	0.19
COMD1_HUMAN	COMD domain-containing protein 5	22	24555	6.52	2	1	1	1	1	0.18	0.18
MA2B2_HUMAN	Epididymis-specific alpha-mannosidase	22	113988	6.74	2	1	2	1	2	0.05	0.04
PDS2_HUMAN	GPI transmembrane component PDS2	22	61617	6.05	2	1	1	1	1	0.05	0.07
MAREL_HUMAN	Microtubule-associated protein RP/EB family member 3	22	31962	5.35	2	1	1	1	1	0.09	0.14
HEAT1_HUMAN	HEAT repeat-containing protein 1	22	242215	6.11	7	1	6	1	6	0.05	0.02
VPS16_HUMAN	Vacuolar protein sorting-associated protein 16 homolog	22	94634	6.32	2	1	2	1	2	0.05	0.05
VMP1_HUMAN	Vacuole membrane protein 1	22	46208	6.47	3	1	1	1	1	0.07	0.09
TBCD3_HUMAN	TBC1 domain family member 23	22	78272	5.23	2	1	1	1	1	0.04	0.05
PSJ1_HUMAN	PDZ and LIM domain protein 1	22	36048	6.56	7	1	7	1	7	0.14	0.12
GRB2_HUMAN	Growth factor receptor-bound protein 2	22	25190	5.89	2	1	1	1	1	0.13	0.18
PAK1_HUMAN	Pak1b	21	64464	5.8	6	1	5	1	5	0.2	0.07
WFS1_HUMAN	Wfs1 protein	21	100227	6.34	2	1	2	1	2	0.03	0.04
CEP41_HUMAN	Centrosomal protein of 41 kDa	21	41343	8.46	2	1	2	1	2	0.14	0.11
QLTP_HUMAN	Glycylserine transfer protein	21	23324	6.9	3	1	2	1	2	0.29	0.19
VPS53_HUMAN	Vacuolar protein sorting-associated protein 53 homolog	21	78602	5.74	3	1	3	1	3	0.14	0.05
ACADM_HUMAN	Medium-chain specific acyl-CoA dehydrogenase, mitochondrial	20	46559	6.61	5	1	2	1	2	0.1	0.09
CHS6B_HUMAN	Cytochrome c oxidase subunit (b)	20	10186	6.54	7	1	6	1	6	0.45	0.49
RM44_HUMAN	38S ribosomal protein L44, mitochondrial	20	37512	6.84	1	1	1	1	1	0.12	0.12
SNR3_HUMAN	Sorting reagent	20	66550	5.4	3	1	3	1	3	0.13	0.06
PTPRR_HUMAN	Serine/threonine-protein phosphatase 6 regulatory subunit 2	20	104676	6.74	4	1	4	1	4	0.11	0.04
ORL3_HUMAN	Orlike receptor-like factor 3	19	49735	5.01	3	1	2	1	2	0.13	0.09
MG10_HUMAN	MCO5 complex subunit MG10	19	8802	6.69	3	1	1	1	1	0.41	0.58
SYDM_HUMAN	Aspartate-tRNA ligase, mitochondrial	19	73516	8.19	4	3	1	1	1	0.04	0.06
NUT14_HUMAN	Nuclear pore complex protein Nup14	19	213488	7.15	1	1	1	1	1	0.02	0.02
GRM1_HUMAN	GRAM domain-containing protein 1A	19	89520	6.26	2	1	1	1	1	0.05	0.05
EP3B1_HUMAN	Epidermal growth factor receptor kinase substrate 8	19	91824	7.1	3	1	3	1	3	0.08	0.05
CPN1_HUMAN	Anion-exchange	19	33561	5.44	4	1	4	1	4	0.17	0.13
MGST1_HUMAN	Microsomal glutathione S-transferase 3	19	16596	9.46	3	2	1	1	1	0.18	0.26
RAV1_HUMAN	Ribonucleoprotein PTP-binding 1	19	63837	8.79	4	1	2	1	2	0.11	0.07
MOP1_HUMAN	Malik-related tyrosine phosphatase 1	19	55016	7.53	2	1	2	1	2	0.09	0.09
GOSR2_HUMAN	Gq12 SNAP receptor complex member 2	19	24760	7.85	1	1	1	1	1	0.09	0.18
VPS33_HUMAN	Vacuolar protein sorting-associated protein 33A	19	67568	6.5	6	1	3	1	3	0.13	0.06
MCM2_HUMAN	DNA replication licensing factor-MCM2	18	101832	5.24	5	1	4	1	4	0.09	0.04
CYBP_HUMAN	Calyculin-binding protein	18	26194	8.28	3	1	2	1	2	0.19	0.17
EMC10_HUMAN	ERM membrane protein complex subunit 10	18	17330	5.78	1	1	1	1	1	0.14	0.16
DHX15_HUMAN	Pir-1 RNA-binding factor ATP-dependent RNA helicase DHX15	18	98375	7.12	5	1	4	1	4	0.13	0.05
PAPR9_HUMAN	Pab1 (ADP-ribosyl) polymerase 9	18	98281	6.12	2	1	2	1	2	0.04	0.04
SLH47_HUMAN	Sodium/hydrogen exchanger 7	18	80580	5.97	1	1	1	1	1	0.03	0.05
SELO_HUMAN	Selenoprotein O	18	73444	5.69	2	1	2	1	2	0.08	0.06
NCOX1_HUMAN	Neurochordin	17	78814	5.34	7	1	6	1	6	0.13	0.05
PGLT1_HUMAN	Protein O-methylglucuronidase 1	17	46159	6.91	1	1	1	1	1	0.08	0.09
CUJ_HUMAN	Clustered mitochondria protein homolog	17	146577	5.75	5	1	5	1	5	0.09	0.03
DDH1D_HUMAN	Dc2-hydroxyglutarate dehydrogenase, mitochondrial	16	56380	8.21	2	1	1	1	1	0.05	0.08
DSR4C_HUMAN	Dual-specific RNA-dependent adenosine deaminase	15	13581	8.86	4	1	4	1	4	0.06	0.03
PHAGE_HUMAN	Bisphosphoglycerate mutase	14	29897	6.1	1	1	1	1	1	0.12	0.15
EXOS4_HUMAN	Exosome complex component MTR3	14	28218	6.06	2	1	1	1	1	0.13	0.16

¹Protein score is calculated from the score of the peptide attributed to the protein.

²pI is (Predicted) isoelectric point.

³Number of matches is spectrum number matched to protein¹.

⁴Number of significant matches is spectrum number that matches protein and exceeds the identification criteria.

⁵Number of sequences is number of peptides matched to protein².

⁶Number of significant sequences is number of peptides exceeding the identification criteria matched to proteins.

⁷Number of unique sequences is a unique³ number of peptides matched to proteins.

⁸Sequence coverage is the ratio of the total number of matched peptide residues to the total length of the protein.

⁹Exponentially Modified Protein Abundance Index (http://www.ma.biology.mcgill.ca/help/quant_help.html).

Table S2. Identification of endogenous proteins contained in hADSC cultured in medium, DMEM/10% FBS.

UniProt/MSS-PROT ID	Description	Protein score ^a	Protein mass (kDa)	pI ^b	Num. of matches ^c	Num. of significant matches ^d	Num. of sequences ^e	Num. of significant sequences ^f	Num. of unique sequences ^g	Sequence coverage ^h	empPAF
MYH9_HUMAN	Myosin-9	7632	226392	5.5	539	301	139	91	119	8.69	6.6
MYH10_HUMAN	Myosin-10	1255	228938	5.44	96	47	50	26	32	0.33	0.67
MYH14_HUMAN	Myosin-14	294	227132	5.52	33	14	19	7	12	0.11	0.14
FLNA_HUMAN	Filamin-A	6172	280564	5.7	620	309	114	85	105	0.63	3.2
FLNB_HUMAN	Filamin-B	2286	299541	5.85	194	123	66	41	20	0.52	1.44
FLNC_HUMAN	Filamin-C	1082	277890	5.47	95	49	59	32	49	0.41	0.64
VIME_HUMAN	Vimentin	6140	53619	5.06	804	380	61	50	15	0.89	132.88
TUB1_HUMAN	Tubulin	2604	20559	5.71	225	145	63	60	26	0.59	1.93
TUB2_HUMAN	Tubulin-2	161	271443	5.4	20	9	16	5	9	0.1	0.08
LDHA_HUMAN	L-lactate dehydrogenase A chain	3474	36865	8.44	248	158	22	15	15	0.8	6.7
LDHB_HUMAN	L-lactate dehydrogenase B chain	760	36815	5.21	81	40	15	11	13	0.6	3.37
ACTN1_HUMAN	Alpha-actinin-1	3222	102993	5.25	246	141	50	36	10	0.71	4.73
ACTN2_HUMAN	Alpha-actinin-2	1980	104768	5.27	185	94	46	31	28	0.67	2.59
ENO4_HUMAN	Alpha-enolase	3169	47139	7.01	182	103	27	19	17	0.74	7.32
ENO3_HUMAN	Gamma-enolase	510	47239	4.91	29	14	7	5	2	0.25	0.7
GDP_HUMAN	Glyceroldehyde-3-phosphate dehydrogenase	2932	36300	6.57	224	103	19	14	9	0.77	13.13
KPF10_HUMAN	Pyruvate kinase PKM	2871	57900	7.96	221	147	39	33	6	0.78	16.79
TBB2A_HUMAN	Tubulin beta-2A chain	2307	49875	4.79	222	132	28	23	5	0.81	14.77
TBB2B_HUMAN	Tubulin beta-2B chain	1150	49925	4.77	130	60	28	20	13	0.92	7.08
ALDOA_HUMAN	Fructose-bisphosphate aldolase A	2982	39395	8.3	184	96	25	16	25	0.8	11.58
PFIC2_HUMAN	Phenyl	2184	531468	5.24	181	92	36	70	25	0.26	0.56
FINC_HUMAN	Fibronectin	1999	262480	5.46	154	93	60	40	60	0.45	0.86
CODA2_HUMAN	Codan alpha-2(VI) chain	1888	343437	6.26	100	73	55	40	55	0.21	0.67
IQGAP1_HUMAN	Ras GTPase-activating protein (GAP)	1827	180124	6.08	116	73	53	36	53	0.29	1.43
GRP78_HUMAN	78 kDa glucose-regulated protein	1815	72288	5.67	169	102	33	25	28	0.69	3.76
HSP17A_HUMAN	Heat shock 70 kDa protein 1A	315	70309	5.68	37	17	20	11	16	0.56	0.92
DYRK1_HUMAN	Cytosolic kinase 1 heavy chain 1	1743	532072	6.01	135	80	84	53	64	0.3	0.92
EPZ_HUMAN	Elongation factor 2	1628	95277	6.41	118	70	42	26	42	0.62	2.73
UBA1_HUMAN	Ubiquitin-like modifier-activating enzyme 1	1601	117374	5.69	96	65	26	61	20	0.61	2.01
GSTP1_HUMAN	Glutathione S-transferase P	1593	23341	5.43	74	57	15	13	15	0.92	16.03
PDAT1_HUMAN	Protein disulfide-isomerase	1552	57081	4.76	160	77	32	18	32	0.61	3.01
LEIF1_HUMAN	LEIF-1 protein, alpha	214	28201	4.76	22	9	11	5	9	0.32	1.06
TUBA1C_HUMAN	Tubulin alpha-1C chain	1127	49863	4.96	131	71	25	22	1	0.75	7.79
SEPT9_HUMAN	Septin-9	1461	46417	8.75	93	62	24	21	62	0.54	5.58
WDH1_HUMAN	WD repeat-containing protein 1	1454	68152	6.37	63	46	23	18	23	0.68	2.11
EMF_HUMAN	Endomembrin	1433	92411	4.76	126	68	42	28	12	0.55	2.88
TBR1_HUMAN	Transcriptional endoplasmic reticulum ATPase	1363	89266	5.14	60	26	58	26	58	0.35	3.08
ANKK_HUMAN	Neuroblast differentiation-associated protein ANKAK	1329	62699	5.8	244	85	135	57	135	0.33	0.46
CO1A1_HUMAN	Codan alpha-1(I) chain	1314	13857	5.6	165	78	40	30	12	0.53	1.55
QARS_HUMAN	Cysteine-tRNA ligase	1311	83119	6.61	81	48	30	20	30	0.61	2.18
GKAP4_HUMAN	Cytoskeleton-associated protein 4	1302	65983	5.83	99	44	28	16	28	0.58	1.93
ANKA2_HUMAN	Annexin A2	1284	28550	7.27	167	86	29	25	29	0.79	8.56
MAP1B_HUMAN	Microtubulin-associated protein 1B	1251	270468	4.73	87	57	51	37	51	0.36	0.68
VDAC1_HUMAN	Voltage-dependent anion-selective channel protein 1	1245	30754	8.62	47	34	16	12	16	0.76	4.77
LRP1_HUMAN	Protein-tyrosine phosphatase receptor-related protein 1	1218	104278	5.16	63	48	37	30	47	0.23	0.53
ANKA5_HUMAN	Annexin A5	1182	35914	4.94	103	54	22	24	12	0.74	6.89
PDAT2_HUMAN	Protein disulfide-isomerase A3	1177	56747	5.88	93	53	27	18	3	0.69	3.04
VINC_HUMAN	Vinculin	1153	123722	5.5	89	51	38	21	38	0.45	1.1
DPFV2_HUMAN	Dihydropyrimidinase-related protein 2	1146	62255	5.95	77	48	25	17	21	0.71	2.82
DPFV1_HUMAN	Dihydropyrimidinase-related protein 3	541	61824	6.04	29	21	17	11	14	0.67	1.4
OHMT_HUMAN	60 kDa heat shock protein, mitochondrial	1100	61016	5.7	48	36	20	16	20	0.52	2.2
PAHA1_HUMAN	ProHsp44-hydrolyase subunit alpha-1	1084	61011	5.7	51	32	19	14	19	0.52	1.6
PGP1_HUMAN	Phosphoglycerate kinase 1	1076	44586	8.3	75	40	23	15	5	0.68	2.45
HYOU1_HUMAN	Hypoxia-upregulated protein 1	1070	111266	5.16	52	35	20	13	20	0.38	0.69
MYO1_HUMAN	Major myosin protein	1051	99586	5.34	56	40	23	14	23	0.46	0.8
ATPA_HUMAN	ATP synthase subunit alpha, mitochondrial	1048	59174	9.16	55	27	21	13	21	0.54	1.85
TOPB_HUMAN	T-complex protein 1 subunit beta	1046	57452	6.01	46	34	22	17	22	0.62	2.43
CO1A2_HUMAN	Codan alpha-2(VII) chain	1038	129235	9.98	71	41	32	20	32	0.45	0.91
CODA1_HUMAN	Codan alpha-1(XII) chain	1034	332941	5.38	73	40	47	23	47	0.26	0.74
RIBL_HUMAN	Ribonuclease inhibitor	1004	49941	4.71	53	36	19	15	19	0.61	2.49
MOES_HUMAN	Myosin	967	97778	6.08	77	38	29	17	38	0.56	2.03
TSP1_HUMAN	Thrombospondin-1	958	129300	4.71	98	54	19	29	29	0.35	0.79
ADCK1_HUMAN	Adenylate cyclase-associated protein 1	831	51889	8.24	79	37	20	12	5	0.56	2.68
ACLY_HUMAN	ATP-citrate lyase	933	125762	6.85	68	39	34	22	34	0.49	1.22
MARCKS_HUMAN	Myristoylated alanine-rich C-kinase substrate	928	31836	4.67	116	69	5	5	5	0.35	1.2
CODA3_HUMAN	Codan alpha-1(VI) chain	903	108462	5.26	45	37	16	21	16	0.37	0.85
LMY2_HUMAN	LLM domain only protein 7	894	192576	8.34	56	29	27	16	27	0.27	0.45
CAH2_HUMAN	Calnexin-2 catalytic subunit	881	79945	4.87	58	34	26	16	20	0.54	1.7
LEI1_HUMAN	Calnexin-1	877	14706	5.24	129	50	11	11	11	0.87	6.06
CALD1_HUMAN	Caldesmon	871	93175	5.82	90	39	22	13	22	0.3	0.79
FSN1_HUMAN	Fusin	854	54896	6.24	44	28	17	13	17	0.56	1.92
CODP1_HUMAN	Coatomer subunit gamma-1	846	97655	5.22	42	23	23	13	23	0.5	0.74
CODP2_HUMAN	Coatomer subunit gamma-2	151	97560	5.56	10	5	7	3	5	0.12	0.14
STAT1_HUMAN	Signal transducer and activator of transcription 1--alpha/beta	845	87280	5.74	41	27	21	14	21	0.4	0.96
TRXR1_HUMAN	Thioredoxin reductase 1, cytosolic	842	70862	7.16	37	27	20	15	20	0.49	1.57
SVAC1_HUMAN	Alarmin--tRNA ligase, cytosolic	833	106743	5.24	48	35	26	20	26	0.47	1.19
COTL1_HUMAN	Cotlin-1	832	18691	8.22	52	34	11	9	9	0.57	6.37
SEDA_HUMAN	D--phenylglyoxylate dehydrogenase	831	58614	6.29	40	34	19	16	3	0.58	2.77
GLIS1_HUMAN	Glis1	816	85844	5.9	57	39	19	14	19	0.52	1.18
PROT1_HUMAN	Profilin-1	808	15045	8.44	88	48	13	8	13	0.44	16.75
TAGL_HUMAN	Transgelin	804	22598	8.87	131	47	18	14	18	0.95	21.18
CAT1_HUMAN	Cathepsin D	799	44524	6.1	57	35	18	12	18	0.6	3.07
TPM1_HUMAN	Tropomyosin alpha-1 chain	789	28504	4.87	87	44	18	10	10	0.54	3.27
TPM2_HUMAN	Tropomyosin alpha-2 chain	222	23689	4.89	85	22	21	11	12	0.46	3.05
TRT1_HUMAN	Trentholectin	783	87835	7.58	55	36	21	16	21	0.55	1.85
TOPP_HUMAN	T-complex protein 1 subunit alpha	761	59329	7.55	44	29	20	16	20	0.58	2.08
QANAS_HUMAN	Neutral alpha-glucosidase A5	740	108007	5.74	63	36	32	19	32	0.6	1.38
SYWC_HUMAN	Trypsinogen--tRNA ligase, cytosolic	760	53132	5.83	43	27	19	15	2	0.82	2.5
ANKA1_HUMAN	Annexin A1	759	38890	6.57	95	31	18	12	18	0.65	2.62
PEBP1_HUMAN	Phenylaldehyde ammonia--binding protein 1	754	21044	7.01	24	17	7	6	7	0.62	2.23
AMPK1_HUMAN	Adenosine phosphatase	741	109471	5.31	66	39	34	20	34	0.49	1.07
ANKA3_HUMAN	Annexin A3	739	75828	5.42	89	38	40	20	40	0.68	2.01
SPBL1_HUMAN	Serpin B6	737	42594	5.18	30	22	16	11	16	0.55	1.93
GDB1_HUMAN	Rab GDP dissociation inhibitor beta	733	50831	6.11	53	30	23	14	17	0.71	2.44
GDB2_HUMAN	Rab GDP dissociation inhibitor alpha	286	50550	5	31	22	15	14	9	0.58	2.17
PFKAP_HUMAN	ATP-dependent 6-phosphofructokinase, placental type	733	85542	7.5	48	28	27	16	23	0.59	1.18
PFKAL_HUMAN	ATP-dependent 6-phosphofructokinase, liver type	264	84844	7.26	15	8	9	5	8	0.21	0.28
ECDA_HUMAN	Trifunctional enzyme subunit alpha, mitochondrial	733	82947	9.16	38	26	17	12	17	0.4	0.93
SHD1_HUMAN	Staphylococcal nuclease domain-containing protein 1	730	101934	6.74	52	33	30	18	30	0.44	1.09
SEPT2_HUMAN	Septin-2	729	41461	6.15	36	29	14	12	13	0.57	2.68

^aProtein score is calculated from the score of the peptide attributed to the protein.
^bpI is (Predicted) isoelectric point.
^cNumber of matches is spectrum number matched to protein¹.
^dNumber of significant matches is spectrum number that matches protein and exceeds the identification criteria.
^eNumber of sequences is number of peptides matched to protein¹.
^fNumber of significant sequences is number of peptides exceeding the identification criteria matched to proteins.
^gNumber of unique sequences is a unique¹ number of peptides matched to proteins.
^hSequence coverage is the ratio of the total number of matched peptide residues to the total length of the protein.
ⁱExponentially Modified Protein Abundance Index (http://www.matrixscience.com/help/quant_empai_help.html).

Table S2, Cont 1.

UniProt/Swiss-Prot ID	Description	Protein score ^a	Protein mass (kDa)	pI ^b	Num. of matches ^c	Num. of significant matches ^d	Num. of sequences ^e	Num. of significant sequences ^f	Num. of unique sequences ^g	Sequence coverage ^h	emPAI ⁱ	
STP2L_HUMAN	Bifunctional glutamate-proline-4-irRNA ligase	725	170483	7.02	58	32	35	20	35	0.39	0.63	
FAS_HUMAN	Fatty acid synthase	716	273254	6.91	67	40	42	25	42	0.31	0.47	
TOP2Z_HUMAN	T-complex protein 1 subunit zeta	712	57888	6.23	39	27	22	15	22	0.65	1.94	
MYOF_HUMAN	Myofibrin	708	234581	5.84	78	39	51	26	51	0.37	0.88	
TPIS_HUMAN	Troponin phosphatase isomerase	705	30772	5.85	64	39	16	12	11	0.77	4.77	
CTNA1_HUMAN	Catenin alpha-1	691	100009	5.95	24	19	21	13	19	0.38	0.72	
SEPR_HUMAN	Profilin endoprotease FAP	690	87657	6.21	46	22	26	19	26	0.46	1.47	
CPNS1_HUMAN	Capsin small subunit 1	682	28298	5.05	27	11	20	14	11	4	0.79	4.79
ATP1E_HUMAN	ATP synthase subunit beta, mitochondrial	681	95525	5.26	59	40	27	22	8	0.78	3.81	
CAVIN1_HUMAN	Caveolin-associated protein 1	670	63450	5.51	26	19	9	5	9	0.32	0.78	
ML125_HUMAN	Myosin regulatory light chain 12B	658	19767	4.71	38	11	27	13	11	1	0.84	11.19
ML12A_HUMAN	Myosin regulatory light chain 12A	640	19781	4.67	37	27	13	11	1	0.84	11.19	
UGPA_HUMAN	UDP-glucose-1-phosphate uridylyltransferase	630	56905	8.16	44	28	18	15	4	0.6	2	
PLN2_HUMAN	Parvalbumin-3	620	47046	5.3	32	23	16	11	3	0.59	1.85	
PTBP1_HUMAN	Polypyrimidine tract-binding protein 1	620	57186	5.22	25	18	9	7	9	0.32	0.67	
PSMD1_HUMAN	26S proteasome non-ATPase regulatory subunit 1	611	105769	5.25	33	24	18	14	18	0.34	0.74	
MAP4_HUMAN	Microtubule-associated protein 4	611	120930	5.32	66	22	22	10	22	0.36	0.46	
TRIO_HUMAN	Threosulin	649	17350	4.82	39	27	8	5	8	0.78	4.63	
CHN2_HUMAN	Calnexin-2	640	36391	5.89	50	30	14	8	13	0.51	1.79	
CHN2_HUMAN	Calnexin-2	640	36376	5.95	44	27	11	9	10	0.6	2.4	
IMB1_HUMAN	Importin subunit beta-1	631	97108	4.88	48	28	25	18	25	0.52	1.08	
IPO3_HUMAN	Importin-5	616	123550	4.83	60	36	38	26	38	0.55	1.41	
TEN1_HUMAN	Tenascin	611	240700	4.79	45	30	29	18	29	0.59	0.37	
TAGL2_HUMAN	Transgelin-2	597	22377	8.41	65	30	15	10	15	0.84	8.94	
PRDX4_HUMAN	Peroxisomal-4	589	25019	6	38	20	14	8	14	0.76	2.76	
COPR1_HUMAN	Coatomer subunit beta	583	107074	5.72	33	20	22	14	22	0.38	0.73	
SVYQ1_HUMAN	Isochucine-irRNA ligase, cytosolic	578	144406	5.82	53	29	17	28	28	0.37	0.64	
SPTN1_HUMAN	Spectrin alpha chain, non-erythrocytic 1	578	294384	5.22	50	17	29	12	29	0.35	0.19	
COPR1_HUMAN	Coatomer subunit alpha	571	138258	7.7	40	26	21	15	21	0.26	0.57	
PDIA4_HUMAN	Protein disulfide-isomerase A6	570	48091	4.85	30	21	11	9	11	0.48	1.59	
QBXL_HUMAN	Quanine nucleotide-binding protein subunit beta-4	567	17543	5.6	11	5	7	4	3	0.39	0.66	
P4HA2_HUMAN	Profilin 4-hydroxylase subunit alpha-2	560	60864	5.49	44	29	20	12	20	0.47	1.28	
SCG1A_HUMAN	Protein transport protein SCG1A	555	123931	6.43	35	19	19	10	19	0.31	0.37	
UGCG_HUMAN	UDP-glucose 4-epimerase glucosyltransferase 1	550	170703	5.92	41	27	25	17	25	0.37	0.53	
PPR1_HUMAN	Peptidyl-prolyl isomerase B	545	23728	9.42	60	25	17	6	17	0.64	3.02	
PGAM1_HUMAN	Phosphoglycerate mutase 1	535	28788	6.67	47	28	11	8	11	0.45	3.22	
CLIC4_HUMAN	Chloride intracellular channel protein 4	531	28754	5.45	43	25	14	8	13	0.72	2.66	
CORP2_HUMAN	Coatomer subunit beta-2	528	102422	5.15	42	26	24	17	24	0.46	1.08	
FRS1_HUMAN	Peptidyl-prolyl isomerase FKBP10	524	64024	5.96	39	23	20	11	20	0.43	1.05	
EFI1Q_HUMAN	Elongation factor 1-gamma	523	50067	6.25	41	24	19	12	19	0.55	1.95	
TOP2L_HUMAN	T-complex protein 1 subunit epsilon	520	59633	5.45	34	25	16	12	16	0.54	1.86	
VAT1_HUMAN	Synaptic vesicle membrane protein VAMP-1 homolog	510	41953	5.88	36	24	16	10	16	0.59	2.44	
VGLL1_HUMAN	Vagin	500	141368	6.43	44	20	25	13	3	0.32	0.47	
GPPT1_HUMAN	T-complex protein 1 subunit delta	503	60206	5.8	31	19	19	12	7	0.58	1.29	
GPPT1_HUMAN	Glutamine--fructose-5-phosphate aminotransferase [isomerizing] 1	501	78758	6.66	28	18	22	13	18	0.51	0.89	
GPPT2_HUMAN	Glutamine--fructose-5-phosphate aminotransferase [isomerizing] 2	467	76882	7.03	12	5	9	3	5	0.21	0.18	
RSP1_HUMAN	Ribosome-binding protein 1	465	152381	6.69	52	24	20	12	24	0.34	0.26	
HSPB1_HUMAN	Heat shock protein beta-1	469	22768	5.88	54	38	13	8	13	0.86	8.57	
ZAKA_HUMAN	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform	467	65267	5	23	14	15	10	15	0.42	0.9	
MGM1_HUMAN	Malic dehydrogenase, mitochondrial	466	35481	8.92	31	17	12	7	12	0.48	1.27	
VAT1_HUMAN	V-type proton ATPase catalytic subunit A	465	68260	5.35	35	25	18	12	18	0.46	1.08	
GP2D_HUMAN	Glucose-6-phosphate 1-dehydrogenase	464	56219	6.29	26	26	19	12	18	0.57	1.88	
PRDX2_HUMAN	Peroxisomal-2, mitochondrial	463	22072	8.93	26	16	10	6	10	0.66	2.67	
RPN2_HUMAN	Dolichyl-diphosphoglycerate--protein glucosyltransferase subunit 2	463	69241	5.44	30	22	17	14	17	0.55	1.33	
PSMD2_HUMAN	26S proteasome non-ATPase regulatory subunit 2	475	100126	5.66	37	22	19	12	19	0.41	0.72	
SVOC_HUMAN	Cysteine-irRNA ligase, cytosolic	475	85419	6.31	23	13	15	7	15	0.34	0.41	
S10AB_HUMAN	Protein S100-A11	473	11733	6.96	42	17	6	5	6	0.74	21.41	
PARK1_HUMAN	Protein nuclear acid dehydrogenase DJ-1	468	18878	6.33	32	19	9	6	9	0.72	3.77	
PLDGG_HUMAN	Protein kinase-2-oxoglutarate 5-dehydrogenase 3	467	84731	5.89	28	21	11	9	11	0.26	0.72	
PLDGG_HUMAN	Protein kinase-2-oxoglutarate 5-dehydrogenase 2	468	84632	6.24	31	13	19	9	19	0.36	0.54	
PLDGG_HUMAN	Protein kinase-2-oxoglutarate 5-dehydrogenase 1	467	84497	6.47	26	17	17	9	17	0.35	0.57	
HSP74_HUMAN	Heat shock 70 kDa protein 4	466	94271	5.11	37	24	23	15	23	0.43	0.95	
HSP105_HUMAN	Heat shock protein 105 kDa	466	96004	5.28	16	4	14	3	14	0.25	0.14	
UGDH_HUMAN	UDP-glucose 6-dehydrogenase	463	54899	6.73	35	26	19	16	19	0.68	2.37	
NEP_HUMAN	Neprilysin	460	85460	5.54	35	18	21	11	21	0.4	0.71	
GPT1_HUMAN	Glucose-6-phosphate isomerase	447	63107	6.43	30	16	14	8	14	0.44	0.94	
STIP1_HUMAN	Stress-induced-phosphoprotein 1	446	62598	6.4	22	14	12	7	12	0.33	0.59	
NMT1_HUMAN	Nucleoside 5-methyltransferase	439	28555	5.56	36	17	11	6	11	0.66	1.32	
ADH2_HUMAN	Alcohol dehydrogenase class-2	438	38986	7.45	18	13	8	5	8	0.39	0.69	
BQCH1_HUMAN	Transforming growth factor-beta-induced protein ig-h3	437	74634	7.62	26	13	15	7	15	0.37	0.48	
CORP1_HUMAN	Cysteine and glycine-rich protein 1	430	29554	6.9	30	19	9	7	9	0.37	2.07	
CALU_HUMAN	Calnexin	428	37084	4.47	50	18	18	9	18	0.52	1.74	
HRP23_HUMAN	Heterogeneous nuclear ribonucleoprotein U	428	95228	5.76	29	19	16	10	16	0.34	0.66	
PSBB_HUMAN	Proteasome subunit beta type-5	423	28462	6.43	15	12	6	5	6	0.38	1.07	
TOP2L_HUMAN	T-complex protein 1 subunit gamma	422	60495	6.3	28	13	15	8	15	0.42	0.74	
GPPIIP_HUMAN	Glucose-6-phosphate dehydrogenase	420	35846	7.01	9	7	4	3	4	0.28	0.42	
AT2_HUMAN	AT2 cell surface antigen heavy chain	417	67952	4.89	25	16	15	10	15	0.37	0.85	
OST4L_HUMAN	Dolichyl-diphosphoglycerate--protein glucosyltransferase 48 kDa subunit	416	50769	6.09	19	13	9	6	9	0.4	0.78	
DREL1_HUMAN	Drelin	415	71285	4.41	19	15	15	9	15	0.29	0.51	
AP1B1_HUMAN	AP-1 complex subunit beta-1	230	104570	4.94	22	8	16	7	11	0.28	0.32	
PGCRL_HUMAN	Programmed cell death 6-interacting protein	405	95963	6.13	32	18	19	10	8	0.36	0.89	
PCN1_HUMAN	Profilin 2-hydroxylase 1	405	83341	5.05	34	17	18	9	18	0.45	0.65	
TMED4_HUMAN	Transmembrane emp24 domain-containing protein 10	404	24860	6.97	14	9	6	4	6	0.38	0.94	
SVLQ_HUMAN	Serpin-irRNA ligase, cytosolic	403	58740	6.25	27	16	16	7	16	0.42	0.64	
CALX_HUMAN	Calnexin	403	67526	4.47	33	19	13	8	13	0.32	0.87	
COS1A1_HUMAN	Collagen alpha-1(V) chain	403	183447	4.94	18	13	12	8	12	0.14	0.2	
NBL1_HUMAN	Nbl-1-like protein 1	402	84085	5.22	24	22	15	13	15	0.32	0.91	
AT1A2_HUMAN	Adiponectin-2	401	65503	5.43	32	10	19	15	10	0.51	1.14	
GCN1_HUMAN	eIF-2-alpha kinase activator GCN1	399	292372	7.29	40	22	22	14	22	0.15	0.22	
CLIC7_HUMAN	Chloride intracellular channel protein 1	399	26906	5.09	44	22	14	9	13	0.69	3	
TL1B1_HUMAN	Tax1-binding protein 3	398	13728	8.04	13	11	5	4	5	0.85	2.28	
PLS1_HUMAN	Plasmin-3	395	70766	5.41	45	24	29	20	5	0.63	2.25	
FEN1L_HUMAN	Fen1-like family homolog 2	393	77811	6.26	26	19	15	10	15	0.39	1.01	
NBSR1_HUMAN	NADH-cytochrome b5 reductase 3	389	34213	7.18	24	14	13	8	13	0.62	1.64	
IDH2_HUMAN	Isocitrate dehydrogenase (NADP) cytosolic	387	46630	6.53	34	21	16	9	16	0.56	1.44	
ARF1_HUMAN	ADP-ribosylation factor 4	384	25498	6.59	33	15	13	7	9	0.63	3.07	
PPCE_HUMAN	Profilin endoprotease	380	86648	5.53	18	11	12	7	12	0.33	0.44	
TOP2L_HUMAN	T-complex protein 1 subunit delta	377	57888	7.06	32	20	19	13	19	0.58	1.55	
ITAV_HUMAN	Integrin alpha-V	375	115984	5.45	29	18	18	12	18	0.3	0.54	
SPTB1_HUMAN	Spectrin-beta chain, non-erythrocytic 1	372	274439	5.39	34	13	22	9	22	0.17	0.17	

^aProtein score is calculated from the score of the peptide attributed to the protein.

^bpI is (Predicted) isoelectric point.

^cNumber of matches is spectrum number matched to protein¹⁰.

^dNumber of significant matches is spectrum number that matches protein and exceeds the identification criteria.

^eNumber of sequences is number of peptides matched to protein¹⁰.

^fNumber of significant sequences is number of peptides exceeding the identification criteria matched to proteins.

^gNumber of unique sequences is a unique¹⁰ number of peptides matched to proteins.

^hSequence coverage is the ratio of the total number of matched peptide residues to the total length of the protein.

ⁱExponentially Modified Protein Abundance Index (http://www.matrixscience.com/help/quant_help.html).

Table S2, Cont.2.

UniProt/Swiss-Prot ID	Description	Protein score ¹	Protein mass (kDa)	pI ²	Num. of matches ³	Num. of significant matches ⁴	Num. of sequences ⁵	Num. of significant sequences ⁶	Num. of unique sequences ⁷	Sequence coverage ⁸	empAI ⁹
PF22L_HUMAN	Phosphoglucomutase, debranching	271	53.08	6.8	20	16	11	8	11	0.38	0.97
APF1A_HUMAN	AP-1 complex subunit delta-2	270	107476	6.53	37	19	23	12	18	0.39	0.6
APF2A_HUMAN	AP-2 complex subunit alpha-2	207	103885	6.53	21	8	13	5	8	0.24	0.22
OAT2_HUMAN	Omitron 2	270	43504	6.57	16	12	8	5	8	0.32	1.21
MMPI4_HUMAN	Matrix metalloproteinase-14	367	65852	7.63	38	12	10	5	10	0.2	0.37
HNRPF_HUMAN	Heterogeneous nuclear ribonucleoprotein F	366	45643	5.38	16	12	6	5	4	0.3	0.73
HNRH1_HUMAN	Heterogeneous nuclear ribonucleoprotein H	208	49198	5.85	18	9	10	7	6	0.28	0.61
HNRH2_HUMAN	Heterogeneous nuclear ribonucleoprotein H2	116	49232	5.89	11	6	9	6	8	0.38	0.66
AAT1_HUMAN	Aspartate aminotransferase, cytoplasmic	266	46219	6.52	22	12	12	7	12	0.53	0.88
DPE1_HUMAN	Dipeptidyl peptidase 4	365	80222	5.67	19	13	9	5	9	0.19	0.27
LAMC1_HUMAN	Laminin subunit gamma-1	363	177489	5.01	22	11	15	15	15	0.18	0.3
PGC4_HUMAN	Phosphatidylcholine-binding domain assembly protein	359	70710	7.7	16	11	8	6	8	0.24	0.51
SER2_HUMAN	Phosphoserine aminotransferase	357	40397	7.56	37	18	17	10	17	0.87	1.8
MDH2_HUMAN	Malate dehydrogenase, cytoplasmic	354	38403	6.91	21	13	9	5	9	0.55	0.77
LRSD1_HUMAN	Leucine-rich repeat-containing protein 58	353	36806	6.61	23	15	11	6	11	0.28	1.04
ERP29_HUMAN	Endoplasmic reticulum resident protein 29	350	28975	6.77	18	12	8	7	8	0.45	1.72
COPEL_HUMAN	Coatomer subunit epsilon	249	34460	4.97	18	15	8	7	8	0.44	1.23
RL3_HUMAN	RES domain protein L3	243	34341	9.73	19	10	8	4	8	0.4	0.82
VATB2_HUMAN	V-type proton ATPase subunit B, brain isoform	242	56465	5.57	25	16	11	9	11	0.41	0.94
RC3H3_HUMAN	Retinoid-binding-3	239	37470	4.14	16	10	6	5	2	0.35	0.94
FKBP9_HUMAN	Peptidyl-prolyl isomerase FKBP9	239	63044	4.91	20	15	8	6	8	0.22	0.59
YBX1_HUMAN	Y-box-binding protein 3	278	40066	9.77	11	6	5	2	3	0.23	0.23
DDX1_HUMAN	ATP-dependent RNA helicase DDX1	335	82360	6.81	23	13	14	7	14	0.32	0.43
AGM1_HUMAN	Phosphatidylcholine mutase	335	59814	5.84	19	12	13	8	13	0.4	0.75
LPFRP_HUMAN	Leucine-rich PPR motif-containing protein, mitochondrial	333	157805	5.81	25	14	16	8	16	0.22	0.24
PRDX4_HUMAN	Peroxiredoxin-4	277	30321	5.86	38	22	15	10	13	0.7	2.89
PRDX1_HUMAN	Peroxiredoxin-1	229	22098	8.27	53	22	20	11	17	0.88	6.8
PRDX2_HUMAN	Peroxiredoxin-2	165	21878	5.66	16	8	7	5	6	0.44	1.57
ESTL2_HUMAN	S-60methylthione hydrolase	324	31442	6.54	16	11	9	6	9	0.57	1.21
PALLD_HUMAN	Palladin	322	150470	6.67	36	17	20	9	20	0.24	0.28
PI3KB_HUMAN	Phosphoinositide 3-kinase, brain form	322	94635	6.4	26	14	19	10	15	0.33	0.64
PYLGL_HUMAN	Glycogen phosphorylase, liver form	308	97087	5.71	10	3	7	3	3	0.14	0.14
IFTA_HUMAN	Eukaryotic translation initiation factor 2, subunit 1	321	36089	6.02	20	15	10	7	10	0.47	1.24
QSOX1_HUMAN	QSOX superfamily protein 1	321	134464	6.52	38	12	18	6	18	0.28	0.21
DDX3X_HUMAN	ATP-dependent RNA helicase DDX3X	319	73198	6.73	15	11	10	7	10	0.25	0.49
IPOT1_HUMAN	Importin-7	318	118440	4.7	26	14	13	8	13	0.23	0.29
NUX2_HUMAN	Nucleolin	318	78588	4.8	23	13	11	6	11	0.21	0.39
ITB1_HUMAN	Integrin beta-5	316	88357	5.27	41	19	21	10	18	0.45	0.88
SYT1C_HUMAN	SNARE-binding RNA ligase	316	140387	7.53	19	14	12	6	12	0.6	1.2
CATB1_HUMAN	Oathesin-B	314	37797	5.88	33	12	21	7	12	0.42	1.41
RTN1_HUMAN	Reticulon-1	312	129851	4.43	19	10	7	4	7	0.14	0.17
SYT1C_HUMAN	Arginine-ADNA ligase, cytoplasmic	305	75331	6.26	24	11	17	6	17	0.25	0.56
SAP1_HUMAN	Proteasome	304	58074	5.06	46	17	17	7	17	0.5	0.81
FLK2_HUMAN	Four and a half LIM domain protein 2	304	32171	5.8	20	9	12	5	12	0.6	0.8
FBN1_HUMAN	Fibrillin-1	267	77162	5.07	23	6	12	3	7	0.19	0.24
DNCE2_HUMAN	Dynactin subunit 2	304	44204	5.1	9	8	4	4	4	0.15	0.46
ANKK4_HUMAN	Annexin A4	298	35860	5.84	20	13	11	5	7	0.36	0.7
COMT_HUMAN	Catechol O-methyltransferase	302	30018	5.26	20	13	10	6	10	0.53	1.29
NOMD1_HUMAN	Nodal modulator 1	302	134239	5.54	20	11	16	8	16	0.27	0.28
ECNM_HUMAN	Enoyl-CoA hydratase, mitochondrial	302	31387	6.34	11	9	7	6	7	0.42	1.21
EHOD_HUMAN	EH domain-containing protein-2	301	61123	6.03	22	14	14	10	14	0.38	0.98
IPYF_HUMAN	Isoarginine synthetase	301	35629	5.54	21	11	11	6	11	0.54	1.14
MYOTC_HUMAN	Unconventional myosin-c	300	121606	9.46	29	12	20	9	20	0.3	0.36
TOPC1_HUMAN	T-complex protein 1 subunit theta	299	59583	5.42	38	17	20	10	20	0.46	1.01
IMA1_HUMAN	Importin subunit delta-1	298	59591	4.85	13	7	11	5	6	0.28	0.42
PURH_HUMAN	Bifunctional purine biosynthesis protein PURH	287	64575	6.27	25	15	14	10	14	0.45	0.91
FKL1_HUMAN	Four and a half LIM domain protein 1	293	36239	9.25	17	12	7	6	7	0.32	0.99
RL2_HUMAN	RES domain protein L2	294	21850	9.86	26	17	8	6	8	0.62	2.75
LIMA1_HUMAN	LIM domain and actin-binding protein 1	293	85173	6.41	19	9	11	5	11	0.19	0.28
AMPL_HUMAN	Cytosolic aminopeptidase	293	85131	6.03	19	8	11	5	11	0.33	0.45
ALTAT1_HUMAN	Alpha-aminoadipic semialdehyde dehydrogenase	292	58450	8.21	15	10	10	7	10	0.35	0.85
TNMD3_HUMAN	Thrombospondin domain-containing protein 5	292	47599	5.63	40	17	13	9	13	0.43	1.2
TNRC1_HUMAN	Tumor necrosis factor receptor-associated protein 1	292	41324	6.47	13	10	8	6	8	0.51	1.24
STRAP_HUMAN	Serine-threonine kinase receptor-associated protein	289	38414	4.98	17	11	10	5	10	0.53	0.72
P85B_HUMAN	Proteinase subunit beta type-4	288	29185	5.72	11	7	6	7	7	0.47	1.34
DDX3_HUMAN	ATP-dependent RNA helicase A	283	140869	6.41	17	10	8	3	8	0.14	0.09
ALL1L_HUMAN	Mitochondrial 10-formyltetrahydrofolate dehydrogenase	281	101881	6.13	33	18	21	12	21	0.37	0.64
GLSK_HUMAN	Glyoxalase II, cytosolic	280	72414	7.85	29	10	14	5	14	0.32	0.33
APT1_HUMAN	Adenosine phosphoribosyltransferase	279	19595	5.78	7	5	4	4	4	0.53	1.31
SOCS1_HUMAN	Son-of-cells-1	279	32424	7.05	16	13	5	5	5	0.39	1.16
SCRN1_HUMAN	Secernin-1	274	46353	4.68	19	11	8	6	8	0.37	0.43
USO1_HUMAN	General vesicular transport factor p115	274	107828	4.85	28	19	13	10	13	0.23	0.47
ECHE_HUMAN	Trifunctional enzyme subunit beta, mitochondrial	273	51262	9.45	14	10	6	4	6	0.23	0.38
EDT1_HUMAN	Extended synaptotagmin-1	272	127180	5.57	23	14	10	6	10	0.18	0.23
ASNS_HUMAN	Asparagine synthetase [aspartate-hydrolyzing]	271	64329	6.39	28	12	8	7	8	0.51	0.88
IPYF_HUMAN	Isoarginine synthetase	270	68527	5.96	46	25	12	6	12	0.5	1.85
RD3B2_HUMAN	UV excision repair protein RAD32 homolog B	270	43145	4.79	12	11	6	5	6	0.31	0.78
COR6A2_HUMAN	Collagen alpha-2(VI) chain	269	108512	5.85	22	15	13	9	13	0.25	0.47
ORP5L_HUMAN	Optic atrophy 5, leucine-specific phosphatase	268	52645	5.66	16	10	11	6	11	0.43	0.61
MRC2_HUMAN	O-type mannose receptor 2	267	166368	5.54	26	15	15	9	15	0.23	0.25
XRCO2_HUMAN	X-ray repair cross-complementing protein 5	266	85652	5.95	27	16	18	11	18	0.45	0.74
RAB21_HUMAN	Ras-related protein RAB21	266	26643	6.22	9	7	4	3	4	0.36	0.59
NXP2_HUMAN	Protein NXP2	266	60704	4.61	12	9	9	6	9	0.26	0.51
IPYF_HUMAN	Eukaryotic translation initiation factor 2A-2	265	18782	5.38	10	9	6	4	6	0.42	2.35
TMX3_HUMAN	Protein disulfide-isomerase TMX3	265	51839	4.8	11	6	8	4	8	0.25	0.38
EF1B_HUMAN	Elongation factor 1-beta	263	24748	4.5	24	13	9	8	8	0.59	3.5
EF1D_HUMAN	Elongation factor 1-delta	151	31103	4.8	19	9	10	7	9	0.52	1.54
BASP1_HUMAN	Brain acid soluble protein 1	262	22680	4.64	41	15	7	5	7	0.54	1.99
P85B_HUMAN	Proteinase subunit beta type-6	261	25341	4.8	7	6	3	3	3	0.33	0.63
P85B_HUMAN	Proteinase activator complex subunit 2	261	27384	5.54	7	5	5	3	5	0.36	0.57
CANV_HUMAN	Calnexin catalytic subunit	260	81838	5.49	21	14	16	10	16	0.42	0.67
NDKA_HUMAN	Nucleoside diphosphate kinase B	259	17267	6.52	34	10	9	4	9	0.72	3.15
NDKA_HUMAN	Nucleoside diphosphate kinase A	90	17138	5.83	31	9	11	5	7	0.88	3.23
PSMD3_HUMAN	26S proteasome non-ATPase regulatory subunit 3	259	68939	8.47	19	14	10	7	10	0.23	0.61
ARHGAP1_HUMAN	Actin-related protein 2/3 complex subunit 1B	258	49923	6.69	25	13	6	4	6	0.41	1.04
ANX11_HUMAN	Annexin A11	255	54355	7.53	12	9	6	3	6	0.17	0.26
ITAH_HUMAN	Integrin alpha-5	255	114465	5.5	15	10	9	7	9	0.2	0.29
OSR1_HUMAN	Carbamoyl reductase (NADPH) 3	135	38931	5.82	11	7	5	3	2	0.27	0.5
ITB1_HUMAN	Integrin beta-5	248	87998	5.72	13	11	10	8	10	0.29	0.46
SCOR1_HUMAN	Lysosome membrane protein 2	245	54755	5	21	11	10	4	10	0.55	0.98

¹Protein score is calculated from the score of the peptide attributed to the protein.

²pI is (Predicted) isoelectric point.

³Number of matches is spectrum number matched to protein¹.

⁴Number of significant matches is spectrum number that matches protein and exceeds the identification criteria.

⁵Number of sequences is number of peptides matched to protein².

⁶Number of significant sequences is number of peptides exceeding the identification criteria matched to proteins.

⁷Number of unique sequences is a unique³ number of peptides matched to proteins.

⁸Sequence coverage is the ratio of the total number of matched peptide residues to the total length of the protein.

⁹Exponentially Modified Protein Abundance Index (http://www.matrixscience.com/help/quant_empai_help.html).

Table S2, Cont.3.

UniProt/Swiss-Prot ID	Description	Protein score ^a	Protein mass (kDa)	pI ^b	Num. of matches ^c	Num. of significant matches ^d	Num. of sequences ^e	Num. of significant sequences ^f	Num. of unique sequences ^g	Sequence coverage ^h	emPAI
PF3B2_HUMAN	Lysosomal protease protein	244	54431	6.18	8	8	5	5	5	0.17	0.26
C10B7_HUMAN	Complement component 1 G subcomponent-binding protein, mitochondrial	243	31343	4.74	15	9	7	7	7	0.47	0.74
HN1T1_HUMAN	Histidine triad nucleotide-binding protein 1	242	13793	6.43	13	9	4	3	4	0.47	2.28
EHD1_HUMAN	EH domain-containing protein 1	242	60559	6.35	19	9	10	5	10	0.33	0.23
PQM1_HUMAN	Phosphoglucomutase-1	241	61411	6.3	17	11	13	9	13	0.37	0.84
SRCO2_HUMAN	Src substrate cortactin	240	61549	5.24	13	8	9	5	9	0.22	0.4
PAT1_HUMAN	Flavinogen activator inhibitor 1	240	45031	6.68	12	8	6	6	6	0.36	0.91
NP1L1_HUMAN	Nucleosome assembly inhibitor 1-like 1	240	45346	4.36	18	11	8	6	7	0.47	0.73
CAPD2_HUMAN	Macrophage-capase protein	239	38474	5.82	23	14	9	6	9	0.45	1.13
ASPC2_HUMAN	Actinin-related protein 2/3 complex subunit 5	231	55770	6.44	12	8	5	3	5	0.25	0.65
NACAM2_HUMAN	Nascent polypeptide-associated complex subunit alpha, muscle-specific form	238	205295	9.6	13	8	7	5	7	0.04	0.11
NACAM1_HUMAN	Nascent polypeptide-associated complex subunit alpha	109	23209	4.68	3	2	1	1	1	0.07	0.19
LKHA4_HUMAN	Leukotriene A-4 hydrolase	237	69241	5.8	16	11	6	6	6	0.16	0.44
BCW1_HUMAN	Basic leucine zipper and WZ domain-containing protein 1	236	48013	5.75	13	8	9	5	8	0.35	0.54
PATD4_HUMAN	Profilin-like-associated protein 2d4	236	42759	6.12	11	5	6	3	6	0.32	0.33
DHE12_HUMAN	Very-long-chain 3-oxoacyl-CoA reductase	233	34302	9.24	12	7	6	4	6	0.38	0.62
GBH2_HUMAN	Glutathione synthetase	232	52332	5.87	10	8	5	4	5	0.37	0.37
MDH2_HUMAN	Malate+2-oxoglutarate dehydrogenase 2	231	55770	6.44	12	6	5	3	5	0.21	0.25
ASS2_HUMAN	Argininosuccinate synthase	230	46001	8.08	15	12	8	7	8	0.4	1.05
MKI1_HUMAN	Mitogen-activated protein kinase 1	230	41363	6.5	14	9	6	10	7	0.51	1.02
MKI2_HUMAN	Mitogen-activated protein kinase 3	91	43108	6.28	10	2	7	2	3	0.3	0.21
SEC12_HUMAN	Protein SEC13 homolog	230	35518	5.22	20	10	6	4	6	0.23	0.79
RISD1_HUMAN	Rho GTPase-activating protein 1	229	50404	5.85	32	11	14	6	14	0.44	0.64
UCHE1_HUMAN	Ubiquitin carboxyl-terminal hydrolase isozyme L1	229	24808	5.33	43	17	15	11	15	0.85	5.28
RTFAF_HUMAN	RNA transcription, translation and transport factor protein	222	28051	8.19	12	6	7	5	7	0.43	1.06
CSF1_HUMAN	Rap1 GTPase-GDP dissociation stimulator 1	222	66275	5.17	19	9	11	7	11	0.4	0.55
CGD41_HUMAN	Dolich-e-cad domain-containing protein 47	220	55838	4.76	13	8	5	2	5	0.2	0.16
AMPYL_HUMAN	Aminopeptidase B	219	72549	5.51	15	9	9	5	9	0.23	0.41
EIF3A_HUMAN	Eukaryotic translation initiation factor 3 subunit A	218	168468	6.38	21	11	12	5	12	0.14	0.13
RL1_HUMAN	6S ribosomal protein L1	218	46080	15.19	18	9	4	9	4	0.32	0.72
GRAG2_HUMAN	Quarner nucleotide-binding protein G0 subunit alpha-2	217	46425	5.34	28	12	12	6	12	0.44	0.85
GRAG1_HUMAN	Quarner nucleotide-binding protein G0 subunit alpha isoforms X1a	123	110956	4.91	9	5	4	4	3	0.06	0.16
SPD2_HUMAN	SH3 and PX domain-containing protein 2A	216	125213	9.01	11	7	5	3	5	0.08	0.11
GLYU2_HUMAN	Series hydroxymethyltransferase, mitochondrial	215	55958	8.76	12	5	7	2	7	0.21	0.45
TPD52_HUMAN	Tumor protein D54	214	22224	5.26	22	10	8	5	8	0.56	2.05
LMAN1_HUMAN	Protein EHD3-3	213	57513	6.3	11	6	5	3	5	0.15	0.34
EGU1_HUMAN	Endoplasmic reticulum	213	70533	6.14	21	11	11	9	11	0.3	0.7
THO2_HUMAN	3-hydroxyacyl-CoA thioester, peroxisomal	212	44264	8.76	11	9	6	4	6	0.33	0.46
CBSP_HUMAN	Calcium-binding, fibronectin-binding protein	212	18637	9.51	5	4	2	1	2	0.19	0.25
KIM1_HUMAN	Kinesin-1 heavy chain	212	108617	6.12	24	12	19	10	19	0.33	0.46
PDYK1_HUMAN	Pyridine kinase	211	35060	5.78	12	8	7	4	7	0.38	0.61
TCTP_HUMAN	Translationally-controlled tumor protein	211	19583	4.84	16	11	5	5	5	0.43	2.24
ALDH2_HUMAN	Aldehyde reductase	210	35830	6.51	17	8	10	5	10	0.54	0.78
CAL2A_HUMAN	E-cadherin-binding protein subunit alpha-1	210	32802	5.45	18	8	9	5	7	0.55	0.88
EIF3F_HUMAN	Eukaryotic translation initiation factor 3 subunit F	208	37540	5.24	8	5	6	4	6	0.28	0.66
OWH1_HUMAN	Ovalbumin-1	208	33130	5.14	12	9	5	3	5	0.35	0.46
DOTN1_HUMAN	Dominant subunit 1	207	141607	5.81	13	8	8	4	8	0.13	0.13
SAHR_HUMAN	Adenosine homocysteine	207	47685	5.92	17	7	10	5	10	0.29	0.55
ROTH_HUMAN	Reticulobulky-1	207	38866	4.86	17	8	9	5	9	0.27	0.28
SMYD1_HUMAN	S-methyltransferase	207	62327	6.58	13	7	9	4	9	0.33	0.3
PAPSS2_HUMAN	Paracetamol 2-phosphoadenosine 5-phosphosulfate synthase 2	206	69457	8.18	19	10	9	7	9	0.28	0.52
HTFA1_HUMAN	Serine protease HTFA1	206	51255	8.09	5	5	3	3	3	0.19	0.28
PHNPU_HUMAN	Purine nucleoside phosphorylase	205	32097	6.45	13	10	9	6	9	0.45	1.17
CDB1_HUMAN	CDB1 antigen	205	25792	5.09	8	6	3	3	3	0.25	0.62
PHS2_HUMAN	Prohibitin-2	205	32276	9.83	12	9	8	5	8	0.37	0.86
RLA2_HUMAN	6S acidic ribosomal protein P0	201	34252	5.71	20	11	11	8	11	0.56	1.97
TRD1_HUMAN	Thrombospondin domain-containing protein 17	201	12832	5.4	11	9	6	3	6	0.21	0.31
GSOT1_HUMAN	Glutathione S-transferase omega-1	201	27548	6.23	24	13	12	6	12	0.63	1.47
PDL1_HUMAN	PDZ and LIM domain protein 1	200	36049	6.56	15	9	8	5	8	0.43	1
ZYX_HUMAN	Zyxin	199	61298	6.22	24	11	12	6	12	0.4	0.72
SRPR1_HUMAN	Signal recognition particle receptor subunit alpha	199	69767	9.07	11	5	8	4	8	0.22	0.27
FKBP1_HUMAN	Peptidyl-farnesyl-oxo-trans isomerase FKBP1A	197	11943	7.88	11	9	4	4	4	0.49	2.89
MATP1_HUMAN	Mitochondrial-associated protein 1A	195	305298	4.85	18	8	14	5	14	0.1	0.07
HRPR1_HUMAN	Heterogeneous nuclear ribonucleoprotein M	195	77464	8.84	16	7	12	5	12	0.26	0.31
PDS4_HUMAN	Protein disulfide-isomerase A4	194	72887	4.86	16	8	13	6	13	0.27	0.49
GORO1_HUMAN	Quinone oxidoreductase PIG3	194	35514	6.87	8	6	5	4	5	0.24	0.8
OLA1_HUMAN	Ola-like A1Pase 1	193	44715	7.64	9	6	7	4	7	0.26	0.45
LMAN2_HUMAN	Vascular integrin-membrane protein VPS36	192	40203	6.46	12	5	7	3	7	0.31	0.36
PEPD2_HUMAN	Xaa-Pro dipeptidase	191	54513	5.64	9	5	7	5	7	0.28	0.47
CTHR1_HUMAN	Collagen triple helix repeat-containing protein 1	191	28207	8.31	16	8	7	4	7	0.48	0.88
EPD3_HUMAN	Eukaryotic translation initiation factor 3 subunit 1	191	36478	5.38	17	11	7	7	7	0.44	0.86
PCYO3_HUMAN	Prenyltransferase 3	190	56004	5.8	8	7	6	5	6	0.24	0.45
PSB1_HUMAN	Proteinase subunit beta type-7	190	28446	7.57	6	4	3	2	3	0.21	0.32
LPP1_HUMAN	Lipomycin-preferred partner	190	65704	7.18	9	6	7	5	7	0.28	0.46
ICL1_HUMAN	Calistatin	187	76526	4.88	10	8	7	6	7	0.2	0.39
TMBAL1_HUMAN	Transmembrane protein 43	186	44847	7.86	12	9	6	5	6	0.39	0.58
CDG31_HUMAN	Hsp80 co-chaperone Cdc37	186	44440	5.17	14	7	7	5	7	0.26	0.8
SNR3_HUMAN	Sorting nexin-3	185	66550	5.4	8	5	5	3	5	0.21	0.21
QDR1_HUMAN	Rho GTPase-dissociation inhibitor 1	185	23193	5.02	18	11	7	5	7	0.51	1.44
RABP2_HUMAN	Cellular retinoic acid-binding protein 2	185	15683	5.42	5	4	2	2	2	0.27	0.69
LAMP1_HUMAN	Lysosome-associated membrane glycoprotein 1	184	44854	9	12	7	6	3	6	0.12	0.32
MYO18_HUMAN	Unconventional myosin-Ib	182	131902	9.43	25	11	16	9	16	0.23	0.33
PDS2_HUMAN	Dolich-4-pyrophosphate-carboxylate synthase	181	67248	6.68	13	6	7	2	7	0.15	0.1
SYN1_HUMAN	Asparagine-GDNA lipase, cytosolic	179	62903	5.9	14	11	10	9	10	0.32	0.82
PRSS4_HUMAN	ZEB proteasome regulatory subunit 6A	179	49172	5.13	18	8	14	7	8	0.42	0.97
PUR1_HUMAN	Mitochondrial protein ADE2	177	47449	6.95	13	7	10	5	10	0.5	0.56
GLUT2_HUMAN	Glucose transporter 2 subunit beta	174	56053	5.2	11	4	8	3	8	0.27	0.25
GLUT1_HUMAN	Glucose transporter 1 subunit beta	172	59389	4.33	20	11	10	8	10	0.26	0.88
HSP90A_HUMAN	Heat shock protein beta-5	170	17125	5.85	14	8	8	5	8	0.86	2.32
PSD12_HUMAN	ZEB proteasome non-ATPase regulatory subunit 13	169	42918	5.53	11	6	7	3	7	0.29	0.34
GLCN_HUMAN	Glycosylkeratinase	169	58678	7.26	9	8	7	6	7	0.26	0.52
IFAG1_HUMAN	Eukaryotic translation initiation factor 4 gamma 1	166	175382	5.35	13	7	11	5	10	0.13	0.13
IFAG2_HUMAN	Eukaryotic translation initiation factor 4 gamma 2	38	178542	5.27	5	2	5	2	4	0.05	0.05
EPD1_HUMAN	Eukaryotic translation initiation factor 3 subunit D	165	63532	5.79	9	6	5	3	5	0.16	0.22
SDHA_HUMAN	Succinate dehydrogenase (ubiquinone), B-type, mitochondrial	165	72465	7.06	12	6	5	2	5	0.19	0.12
E4L1L_HUMAN	Band 4.1-like protein 3	164	120603	5.09	17	7	9	5	9	0.16	0.19
FAPB1_HUMAN	Fatty acid-binding protein, subdomain	163	15155	6.6	12	4	5	3	4	0.46	0.31
RALA_HUMAN	Ras-related protein RalA	163	23552	6.88	10	7	7	4	7	0.17	1.02
GBSL_HUMAN	Gamma-glutamyl-beta-alanine synthase-like protein	162	60548	6.2	7	4	4	3	4	0.18	0.23
AKA12_HUMAN	Acylase anchor protein 12	162	19197	4.37	11	5	9	3	9	0.09	0.07

^aProtein score is calculated from the score of the peptide attributed to the protein.

^bpI is (Predicted) isoelectric point.

^cNumber of matches is spectrum number matched to protein¹¹.

^dNumber of significant matches is spectrum number that matches protein and exceeds the identification criteria.

^eNumber of sequences is number of peptides matched to protein¹².

^fNumber of significant sequences is number of peptides exceeding the identification criteria matched to proteins.

^gNumber of unique sequences is a unique¹³ number of peptides matched to proteins.

^hSequence coverage is the ratio of the total number of matched peptide residues to the total length of the protein.

ⁱExponentially Modified Protein Abundance Index (http://www.matrixscience.com/help/quant_help.html).

Table S2. Cont'd.

UniProt/Swiss-Prot ID	Description	Protein score ^a	Protein mass (kDa)	pI ^b	Num. of matches ^c	Num. of significant matches ^d	Num. of sequences ^e	Num. of significant sequences ^f	Num. of unique sequences ^g	Sequence coverage ^h	emPAI ⁱ
DHRS1_HUMAN	Dehydrogenase/reductase SDR family member 7	116	39274	5.59	9	5	5	4	5	0.41	0.8
CEB1_HUMAN	Chromodomain protein homolog 3	115	20788	5.23	6	5	5	4	5	0.45	1.21
ITGA2_HUMAN	Integrin α IIb β	115	129214	5.16	13	6	12	6	12	0.19	0.21
NAAL1_HUMAN	Nucleoside diphosphate kinase 15, NaH auxiliary subunit	115	101208	7.23	11	5	7	3	7	0.14	0.13
LGL4_HUMAN	Lactoylglutathione lyase	115	20764	5.12	8	3	5	2	5	0.39	0.49
LAMP2_HUMAN	Lysosome-associated membrane glycoprotein 2	114	44932	5.25	6	5	3	3	3	0.89	0.32
PODOL_HUMAN	Progerin-related cell death protein 6	114	21855	5.16	5	3	3	2	3	0.26	0.46
LICD2_HUMAN	Lysosomal acid lipase (cholesterol) ester hydrolase	114	45390	6.42	1	1	1	1	1	0.05	0.1
PTTG1_HUMAN	Platylin tumor-transforming gene 1 protein-interacting protein	114	20310	5.14	3	3	1	1	1	0.21	0.27
PRRC1_HUMAN	Protein PRRC1	114	46672	5.56	4	3	2	2	2	0.87	0.2
F13A1_HUMAN	Actin-10-interacting protein	113	41305	5.18	11	5	6	3	6	0.21	0.35
ATPO_HUMAN	ATP synthase subunit delta, mitochondrial	113	17479	5.38	6	5	3	2	3	0.23	0.6
STX12_HUMAN	Syntaxin-12	113	31622	5.45	7	3	6	3	6	0.36	0.48
LACHN	Lipase La protease	113	46939	6.68	9	3	9	3	8	0.29	0.31
BCAT1_HUMAN	Branched-chain amino acid aminotransferase, cytosolic	112	42939	5.17	15	6	10	4	10	0.51	0.47
PDOL1_HUMAN	PDZ and LIM domain protein 5	112	63904	8.55	25	10	14	7	9	0.34	0.58
ROR1_HUMAN	Retinoid receptor	112	36554	4.26	14	5	9	5	6	0.38	0.76
PUR2_HUMAN	Trifunctional purine biosynthetic protein adenosine-3	112	107899	8.26	14	4	11	4	11	0.23	0.17
PIR1_HUMAN	CAD protein	112	242829	8.02	16	6	10	4	10	0.31	0.07
ATPO2_HUMAN	ATP synthase subunit O, mitochondrial	112	22253	9.97	10	4	5	2	5	0.27	0.43
HEBP2_HUMAN	Heme-binding protein 2	112	22861	4.58	3	2	3	2	3	0.24	0.43
DLB1_HUMAN	DnaJ homolog subfamily B member 11	111	40469	5.51	10	3	4	2	4	0.22	0.23
DNAA2_HUMAN	DnaJ homolog subfamily A member 2	111	45717	6.06	4	4	3	3	3	0.18	0.31
TNRC18_HUMAN	Tropomodulin-3	111	39570	5.08	6	4	5	3	5	0.22	0.37
AAT10_HUMAN	Aspartate aminotransferase, mitochondrial	111	47467	9.14	6	5	2	2	5	0.18	0.19
TADBP_HUMAN	TAR DNA-binding protein 43	111	44711	5.85	5	5	4	4	4	0.18	0.45
OGAD1_HUMAN	OGA domain-containing protein 1	111	27699	7.02	3	2	2	2	2	0.11	0.16
VATE1_HUMAN	V-type proton ATPase subunit E 1	110	26129	7.71	9	6	5	3	5	0.24	0.61
LIMS1_HUMAN	LIM and senescent cell antigen-like-containing domain protein 1	110	37226	8.43	6	5	3	3	3	0.15	0.4
PST1_HUMAN	PstA	109	30361	6.51	2	2	1	1	1	0.06	0.15
SGO2_HUMAN	Decatenation helicase	109	32051	9.24	2	2	2	2	2	0.11	0.3
DDIT3_HUMAN	Ddit3 subunit 3	109	21106	5.37	8	3	5	3	5	0.52	0.38
DORX_HUMAN	DORX domain-containing protein 1	109	35569	5.12	5	5	4	4	4	0.26	0.79
FURBP2_HUMAN	Far upstream element-binding protein 2	109	73070	6.65	17	4	14	3	14	0.32	0.19
PACRG_HUMAN	Protein kinase C δ and ϵ activator substrate in neurons protein 2	109	55704	5.08	8	5	5	3	5	0.17	0.16
TWFL1_HUMAN	Twist1-like-1	108	40258	6.48	6	6	3	3	3	0.14	0.26
RSU1_HUMAN	Ras suppressor protein 1	108	31521	8.37	13	8	8	5	8	0.84	0.93
WDR11_HUMAN	WD repeat-containing protein 11	108	13659	6.46	5	3	3	3	3	0.26	0.57
GNA1_HUMAN	Guanosine 6-phosphate N-acetyltransferase	107	20736	8.17	3	3	3	3	3	0.29	0.81
PRPF2_HUMAN	Prp-2	107	15026	4.59	8	6	3	3	3	0.38	0.71
GOLP3_HUMAN	Golgi phosphoprotein 3	107	33790	6.05	8	4	4	2	4	0.26	0.28
TOM2_HUMAN	Protein- γ -kluane gamma-kluantyltransferase 2	107	77280	5.11	15	5	10	4	10	0.31	0.24
CSNA1_HUMAN	Cytoskeleton cofilin subunit (BA), mitochondrial	107	12143	8.3	1	1	1	1	1	0.04	0.4
EIF3B_HUMAN	Eukaryotic translation initiation factor 3 subunit B	107	92424	4.89	18	7	11	4	9	0.25	0.2
BLVRD_HUMAN	Blood redoxin (NADPH)	107	22106	7.13	7	4	3	1	4	0.28	0.21
LYO1_HUMAN	Protein-lysine ϵ -oxidase	106	46915	6.36	7	2	4	2	4	0.16	0.19
CHMP5_HUMAN	Charged multivesicular body protein 5	106	24555	4.68	3	3	2	2	2	0.22	0.4
MCTD1_HUMAN	MED5 complex subunit MED1	105	5802	6.89	2	1	2	2	2	0.02	0.88
GOB2B_HUMAN	Gob2- β 2 domain-containing protein 80	104	108106	8.72	5	4	3	2	3	0.89	0.08
STOM_HUMAN	Erythrocyte band 7 integral membrane protein	104	31711	7.71	7	5	2	1	2	0.13	0.14
AKT1C_HUMAN	AKR-iso1 reductase family 1 member C1	104	36765	8.02	10	5	5	3	5	0.26	0.57
AKT1G_HUMAN	AKR-iso1 reductase family 1 member C3	104	36830	8.06	9	3	4	3	2	0.2	0.4
POKOR_HUMAN	Phosphatidylinositol carboxylase (GTP), mitochondrial	104	70865	7.57	13	7	9	4	8	0.28	0.27
MST1_HUMAN	Microsomal glutathione S-transferase 1	104	17587	9.41	6	3	3	2	3	0.25	1.02
EPH3_HUMAN	E-phosphatidylinositoltransferase	104	27530	8.57	9	3	6	2	6	0.21	0.35
PRRC3_HUMAN	DNA-dependent protein kinase catalytic subunit	103	468738	6.75	23	8	18	4	18	0.04	0.89
HNRPB_HUMAN	Heterogeneous nuclear ribonucleoprotein H3	101	38903	6.37	4	2	3	1	3	0.21	0.32
THREX1_HUMAN	Thioredoxin-DNA lyase, cytosolic	101	43302	6.23	21	8	13	4	13	0.21	0.22
TOP1_HUMAN	Topoisomerase I	101	66928	8.22	8	5	4	2	4	0.17	0.13
ARBP1_HUMAN	ADP-ribosylation factor-like protein 6-interacting protein 1	101	23347	8.38	4	4	1	1	1	0.14	0.19
TRMT1_HUMAN	Tyrosine-protein phosphatase non-receptor type 11	100	65393	8.87	11	5	7	4	7	0.23	0.28
TOM1B_HUMAN	Mitochondrial import receptor subunit TOM1B	100	67412	8.75	5	4	4	3	4	0.12	0.2
NPL1_HUMAN	Nucleosome assembly protein 1-like 4	100	42787	6.46	8	3	5	1	4	0.26	0.3
IFIA1_HUMAN	Eukaryotic translation initiation factor 1A, X-chromosomal	100	14650	5.07	3	3	1	1	1	0.1	0.38
SVPL1_HUMAN	Smad3 phosphorylation protein 1	99	28547	8.89	2	2	1	1	1	0.87	0.16
PP1F1_HUMAN	Protein phosphatase 1 regulatory subunit 7	99	41529	4.84	8	4	7	4	7	0.31	0.49
CRTPA_HUMAN	Cartilage-associated protein	99	46532	5.5	10	4	6	4	5	0.22	0.43
COPD1_HUMAN	Coupling subunit delta	98	27174	5.89	19	5	16	5	16	0.48	0.44
ECM21_HUMAN	Proteasome-associated protein (ECM2) homolog	98	204180	6.74	16	10	5	10	10	0.12	0.06
CTGF_HUMAN	Connective tissue growth factor	98	38065	6.43	16	6	10	4	10	0.43	0.55
ARF4_HUMAN	ADP-ribosylation factor 4	97	20089	9.04	11	4	7	2	6	0.58	0.51
DCN1_HUMAN	DCN1-like protein 1	96	30105	5.18	4	2	3	1	3	0.2	0.15
VAPAB_HUMAN	Vesicle-associated membrane protein-associated protein A	96	27875	8.8	10	4	7	2	7	0.4	0.35
CTSD1_HUMAN	Catenin delta-1	97	108133	5.68	20	7	13	4	13	0.24	0.21
UTRO1_HUMAN	Urographin	97	384220	8.2	10	4	7	1	7	0.84	0.01
ULA1_HUMAN	NECD-associated enzyme E1 regulatory subunit	97	60209	5.25	4	3	3	2	3	0.13	0.15
MCN2_HUMAN	Protein MCN2 homolog	97	190237	5.73	4	3	1	1	1	0.62	0.02
POAG_HUMAN	Phosphoglucomutase-2	94	68240	6.28	8	6	4	2	4	0.13	0.2
CHAPL_HUMAN	Chitinase-like-associated protein 5	97	25592	7.95	13	5	7	3	7	0.87	0.06
KLC1_HUMAN	Kinesin light chain 1	97	65269	5.87	10	3	7	3	7	0.2	0.21
ERP4_HUMAN	Endoplasmic reticulum resident protein 44	96	48941	5.09	9	4	6	2	6	0.16	0.19
FAAH_HUMAN	Fatty acid hydrolase	96	46244	8.46	3	2	1	2	2	0.12	0.86
GOPD1_HUMAN	Golgi resident protein GOPD1	96	60556	5.02	7	3	6	3	6	0.21	0.23
ANKK1_HUMAN	Ankrran K1	95	52766	5.52	8	4	5	3	5	0.14	0.77
CIT1C_HUMAN	Cit-1 tetrahydrofolate synthase, cytosolic	96	101495	8.89	15	7	12	6	12	0.21	0.28
SRP72_HUMAN	Signal recognition particle subunit SRP72	96	74560	8.31	13	7	8	4	8	0.25	0.25
OPH1_HUMAN	Golgi- β 1-phosphate mannose transferase subunit 1	95	25616	5.37	5	2	4	1	4	0.34	0.15
CRYAB_HUMAN	Alpha-crystallin B chain	95	20146	6.76	6	4	3	2	3	0.29	0.51
OTU1_HUMAN	High affinity cationic amino acid transporter 1	95	87584	5.29	10	6	4	2	4	0.1	0.18
PSA_HUMAN	Prostate-specific antigen	95	102311	5.49	16	4	13	3	13	0.21	0.13
OTUB1_HUMAN	Ubiquitin thioesterase OTUB1	95	31264	4.65	7	5	4	3	4	0.33	0.7
PIR1_HUMAN	GTP synthase 1	94	66446	6.02	10	6	6	3	6	0.17	0.21
ATP5F1_HUMAN	ATP synthase subunit f, mitochondrial	94	11421	8.65	9	5	3	2	3	0.5	1.03
DYN2_HUMAN	Dynamitin-2	94	80803	7.04	9	4	7	4	7	0.13	0.19
ORP1_HUMAN	Protein orp1 homolog 2	94	29639	6.81	10	4	6	3	6	0.45	0.82
ERL2_HUMAN	Efrin-2	93	37815	5.47	8	3	5	2	5	0.25	0.25
OPNMB_HUMAN	Transmembrane glycoprotein NMB	93	43882	6.17	4	2	2	1	2	0.95	0.07
LARP1_HUMAN	Lysine-rich protein 1	93	123434	8.91	5	3	4	2	4	0.96	0.07
DOC1L_HUMAN	Cytosolic dyx1c1 light intermediate chain 1	93	56544	6.01	3	2	2	1	2	0.1	0.08
ABMD_HUMAN	Protein adiponitrin-like transferase 5	93	72638	5.68	9	5	6	4	6	0.25	0.26

^aProtein score is calculated from the score of the peptide attributed to the protein.

^bpI is (Predicted) isoelectric point.

^cNumber of matches is spectrum number matched to protein¹.

^dNumber of significant matches is spectrum number that matches protein and exceeds the identification criteria.

^eNumber of sequences is number of peptides matched to protein².

^fNumber of significant sequences is number of peptides exceeding the identification criteria matched to proteins.

^gNumber of unique sequences is a unique³ number of peptides matched to proteins.

^hSequence coverage is the ratio of the total number of matched peptide residues to the total length of the protein.

ⁱExperimentally Modified Protein Abundance Index (http://www.matrixscience.com/help/quant_help.html).

Table S2, Cont'd.

UniProt/Swiss-Prot ID	Description	Protein score ^a	Protein mass (kDa)	pI ^b	Num. of matches ^c	Num. of significant matches ^d	Num. of sequences ^e	Num. of significant sequences ^f	Num. of unique sequences ^g	Sequence coverage ^h	emPAI ⁱ
CTP1_HUMAN	Cytidine FMN-interacting protein 1	93	145089	6.48	8	3	8	3	8	0.1	0.09
PAC2_HUMAN	Serine/threonine-protein kinase PAK 2	92	58008	5.59	7	4	4	3	4	0.13	0.24
PQD5_HUMAN	GPI transamidase component PQD-5	92	61617	6.05	3	3	2	2	2	0.09	0.15
IFJ2_HUMAN	Eukaryotic translation initiation factor 5	91	49182	5.41	8	3	3	2	3	0.16	0.16
ARMO3_HUMAN	Leu1 domain-containing protein ARMO3	91	91704	5.83	8	3	7	3	7	0.15	0.15
CD166_HUMAN	CD166 antigen	91	65061	5.52	9	5	5	4	5	0.2	0.29
IFB5_HUMAN	Eukaryotic translation initiation factor 2 subunit 2	91	38364	5.6	7	5	4	3	4	0.2	0.38
CRK_HUMAN	Adaptor molecule crk	91	33810	5.38	1	1	1	1	1	0.06	0.1
GRPL_HUMAN	Granulein	91	63000	6.43	6	3	4	2	4	0.11	0.22
SRRP3_HUMAN	Signal recognition particle 9 kDa protein	91	10105	7.77	2	2	1	1	1	0.12	0.48
UMPF_HUMAN	Uridine 5'-monophosphate synthase	90	52189	6.81	4	3	3	2	3	0.09	0.17
RGS2_HUMAN	G12A GTPase-1, no rhodopsin protein	90	60531	8.27	6	4	4	3	4	0.14	0.23
FRH_HUMAN	Ferritin heavy chain	90	21212	5.3	12	4	8	3	8	0.7	0.79
NRD91_HUMAN	Protein NRD91	90	42808	5.49	6	3	6	3	6	0.24	0.34
RL13_HUMAN	GSS domain protein L13	89	24247	11.45	11	4	6	2	6	0.27	0.41
HEXB_HUMAN	Beta-hexosaminidase subunit beta	89	63071	6.29	15	5	10	4	10	0.26	0.3
SGT2_HUMAN	Small glutamine-rich tetratricopeptide repeat-containing protein beta	89	33408	4.8	3	2	2	2	2	0.17	0.26
HNRL2_HUMAN	Heterogeneous nuclear ribonucleoprotein L2-like protein 2	88	85052	4.85	8	3	6	1	6	0.17	0.05
ERO1A_HUMAN	ERO1-like protein alpha	88	54358	5.48	6	2	6	2	4	0.24	0.17
STRA2_HUMAN	Indolecarbinol-5-O-methyltransferase	88	112179	6.78	6	3	5	2	5	0.12	0.06
MMS19_HUMAN	MMS19 nucleotide excision repair protein homolog	88	113217	5.92	5	2	5	2	5	0.11	0.08
PCNA_HUMAN	Proliferating cell nuclear antigen	87	28750	4.57	9	4	5	2	5	0.42	0.33
TOM1_HUMAN	Target of Mitochondrial protein 1	87	53785	4.59	10	3	6	2	6	0.29	0.17
PGC1L_HUMAN	Membrane-associated progesterone receptor component 1	87	21658	4.56	3	3	1	1	1	0.12	0.21
S10A6_HUMAN	Protein S100-A16	87	11784	6.38	7	2	4	2	4	0.53	1
COM1L_HUMAN	COM1 domain-containing protein 1	87	21165	5.85	2	2	2	2	2	0.15	0.48
HP1_HUMAN	Huntingtin-interacting protein 1	87	116148	5.2	11	3	5	1	5	0.11	0.04
XPOT_HUMAN	Exportin	86	123306	5.11	17	5	10	3	10	0.16	0.11
OPN1L1_HUMAN	Opn1-1	86	59022	5.52	5	4	3	3	3	0.11	0.24
KC1_HUMAN	UMP-CMP kinase	86	22208	5.44	8	6	5	4	5	0.3	1.1
GRB1_HUMAN	Guanine nucleotide-binding protein subunit alpha-11	86	42097	5.51	5	3	2	2	2	0.2	0.35
HEBP1_HUMAN	Heme-binding protein 1	86	21084	5.71	2	1	2	1	2	0.15	0.22
HEXA_HUMAN	Beta-hexosaminidase subunit alpha	85	68864	5.64	8	4	5	2	5	0.12	0.15
SCDH_HUMAN	Succinate dehydrogenase (SDH), mitochondrial	85	24735	8.35	6	2	3	2	3	0.25	0.4
EP150_HUMAN	Epidermal growth factor receptor substrate 15-kDa 1	84	94197	4.93	4	3	4	3	4	0.1	0.14
CA19A_HUMAN	Uncharacterized protein C10orf19	84	36324	5.6	6	5	2	2	2	0.15	0.26
SULF1_HUMAN	Extracellular sulfatase SULF1	83	100862	9.23	8	4	5	1	5	0.14	0.04
MAT2B_HUMAN	Methionine adenosyltransferase 2 subunit beta	83	37328	6.9	3	2	2	2	2	0.16	0.12
BRCA1_HUMAN	BRCA1	83	118460	6.88	5	3	4	1	4	0.06	0.07
TRF2_HUMAN	E3 ubiquitin/SCG15 ligase TRF2	82	70928	8.44	5	4	3	2	3	0.11	0.12
STAT3_HUMAN	Signal transducer and activator of transcription 3	82	88511	5.54	9	3	8	1	8	0.16	0.1
DBNL_HUMAN	Ordn-1-like protein	82	40178	5.02	9	3	6	3	6	0.18	0.3
TFPI1_HUMAN	Transcription intermediary factor 1-beta	82	88493	5.52	12	4	8	3	8	0.21	0.15
PSMD9_HUMAN	26S proteasome non-ATPase regulatory subunit 5	82	56160	5.35	3	3	3	2	3	0.1	0.25
GLB1L_HUMAN	1,4-alpha-glucosidase branching enzyme	82	80423	5.87	17	5	8	2	8	0.17	0.11
ITAT1_HUMAN	Integrin alpha-11	81	133386	6.24	15	2	11	2	11	0.15	0.06
RLB1_HUMAN	GSS domain protein L29	81	17141	11.66	16	5	2	1	2	0.17	0.26
STM2L2_HUMAN	Stomat-1-like protein 2, mitochondrial	81	38510	6.88	9	5	6	2	6	0.35	0.24
CSPT2_HUMAN	Vesicular core protein	81	372590	4.43	19	4	14	3	14	0.07	0.03
DTD1_HUMAN	D-aminooxy-L-histidine decarboxylase 1	80	23409	8.35	8	4	4	3	4	0.35	0.7
PROX3_HUMAN	Thioredoxin-dependent peroxide reductase, mitochondrial	80	27675	7.67	7	2	6	2	6	0.34	0.35
USMG3_HUMAN	Ubiquitin-regulated during skeletal muscle growth protein 3	80	6453	9.19	2	2	1	2	1	0.25	0.85
AIMP2_HUMAN	Aminoglycyl tRNA synthetase complex-interacting multifunctional protein 2	80	35326	8.45	11	5	5	3	5	0.3	0.42
PXN_HUMAN	Peroxidase homolog	80	165170	6.79	8	4	7	4	7	0.09	0.11
AMM1_HUMAN	Protein arginine N-methyltransferase 1	80	41488	5.24	6	4	6	4	6	0.25	0.48
EF1A_HUMAN	Elongation factor 1a, mitochondrial	79	49510	7.26	7	4	5	4	5	0.24	0.4
PST1_HUMAN	Pernicious anemia suppressor factor 19	79	32766	4.26	3	3	2	2	2	0.17	0.46
STX1_HUMAN	Syntaxin-7	79	29797	5.41	5	3	3	3	3	0.22	0.52
ZAB2_HUMAN	Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B alpha isoform	78	51659	5.82	8	3	6	2	6	0.25	0.18
ACAD9_HUMAN	New long-chain specific acyl-CoA dehydrogenase, mitochondrial	78	70345	8.97	8	5	8	5	8	0.23	0.35
RTGA_HUMAN	RNA 3'-terminal phosphate cyclase	76	39311	8.01	2	2	2	2	2	0.11	0.24
NUCB1_HUMAN	Nucleobindin-1	77	53846	5.15	10	3	8	3	8	0.22	0.28
MORF1_HUMAN	Multiple isoform polyporphosphate phosphatase 1	77	55016	7.93	2	1	3	1	3	0.11	0.08
PAPR4_HUMAN	Poly (ADP-ribose) polymerase 4	77	192472	5.43	2	2	2	2	2	0.03	0.04
MPV17_HUMAN	Protein MPV17	77	19720	9.54	2	2	1	1	1	0.13	0.23
TALDO2_HUMAN	Transaldolase	77	37516	6.36	8	5	7	4	7	0.24	0.58
FKBP3_HUMAN	Peptidyl-Hsp70 cis-trans isomerase FKBP3	76	25161	9.29	4	4	2	2	2	0.18	0.39
STC4_HUMAN	Serine/threonine-protein kinase 24	76	49277	5.49	4	2	3	2	3	0.12	0.18
CD63_HUMAN	CD63 antigen	76	25619	8.14	10	5	4	2	4	0.2	0.62
SHC1_HUMAN	Sorting nexin-1	76	46620	5.81	7	3	5	3	5	0.24	0.31
NOPR_HUMAN	NAD(P)+-cytochrome P450 reductase	76	76841	5.38	4	2	3	1	3	0.09	0.06
IVD_HUMAN	Isovaleryl-CoA dehydrogenase, mitochondrial	76	46290	8.45	2	1	2	1	2	0.09	0.09
QSOX1_HUMAN	Glutathione S-transferase kappa 1	76	25480	8.5	8	6	5	5	5	0.42	1.25
S12AL_HUMAN	Sickle cell carrier family 12 member 4	76	120572	6.02	4	2	3	1	3	0.05	0.04
UBAL2_HUMAN	Ubiquitin-like modifier-activating enzyme 6	75	117895	5.76	8	5	6	3	6	0.09	0.11
SERC1_HUMAN	Serine incorporator 1	75	50461	5.59	2	1	2	1	2	0.06	0.09
ASAH1_HUMAN	Acid ceramidase	74	44631	7.52	5	2	4	2	4	0.23	0.21
KAD1_HUMAN	Adipocyte kinase isoenzyme 1	74	21621	8.73	8	3	4	2	4	0.34	0.46
VAT1L_HUMAN	V-type proton ATPase 16 kDa proteolipid subunit	74	15725	7.88	1	1	1	1	1	0.2	0.3
SVK_HUMAN	Lysine-epsilon-lysine ligase	73	68005	5.94	7	6	5	4	5	0.16	0.28
RRA5_HUMAN	Rham-1-like protein RRA5	73	23468	6.43	9	4	7	3	7	0.57	0.7
JIP4_HUMAN	C-Jun-amino-terminal kinase-interacting protein 4	73	146115	5.05	8	2	6	2	6	0.1	0.06
TF2F_HUMAN	Twinfilin-2	73	39523	6.37	6	4	4	2	4	0.21	0.23
FAM8A_HUMAN	Protein FAM8A	73	55366	9.15	13	3	5	2	4	0.16	0.16
ILVBL_HUMAN	Acetabactate synthase-like protein	73	67825	8.43	12	6	7	4	7	0.24	0.28
ELAF2_HUMAN	Interferon-gamma-induced, double-stranded RNA-activated protein kinase	73	62558	8.58	1	1	1	1	1	0.02	0.02
DBST_HUMAN	DbpA homolog subfamily B member 12	72	41793	8.67	5	2	3	1	3	0.13	0.1
OSR1_HUMAN	Serine/threonine-protein kinase OSR1	72	57886	6.03	5	3	3	3	3	0.17	0.24
STG2_HUMAN	Glutamine-5-O-methyltransferase	72	67743	6.71	8	3	5	2	5	0.1	0.1
AAAT1_HUMAN	Neutral amino acid transporter B00	72	56562	5.34	3	3	3	3	3	0.11	0.25
GRG3_HUMAN	N-acetylglucosamine-6-sulfatase	72	62042	6.48	7	2	5	2	5	0.16	0.14
TBC2_HUMAN	Tubulin-specific chaperone E	72	59208	6.22	6	3	5	2	4	0.16	0.15
CARM1_HUMAN	Histone-arginine methyltransferase CARM1	72	65811	6.25	9	5	6	3	6	0.19	0.21
COX8B_HUMAN	Cytochrome c oxidase subunit 8B, mitochondrial	72	29467	6.89	2	2	1	1	1	0.09	0.15
NETJ1_HUMAN	Oncoap-1-related NET2	71	30589	6.82	6	4	4	3	4	0.29	0.5
AK1A1_HUMAN	Alcohol dehydrogenase [NAD(P)+]	71	36550	6.32	11	7	7	5	7	0.36	0.77
T12EA_HUMAN	Transmembrane protein 12EA	71	21513	9.36	4	2	3	1	3	0.36	0.21
RWD1_HUMAN	RWD domain-containing protein 1	71	27922	4.11	3	3	2	2	2	0.23	0.34
TRF_HUMAN	Transferin receptor protein 1	71	84818	6.18	12	6	8	4	8	0.19	0.22
BGLA_HUMAN	Beta-glactosidase	70	78027	6.1	9	4	8	4	8	0.14	0.18

^aProtein score is calculated from the score of the peptide attributed to the protein.

^bpI is (Predicted) isoelectric point.

^cNumber of matches is spectrum number matched to protein¹.

^dNumber of significant matches is spectrum number that matches protein and exceeds the identification criteria.

^eNumber of sequences is number of peptides matched to protein¹.

^fNumber of significant sequences is number of peptides exceeding the identification criteria matched to proteins.

^gNumber of unique sequences is a unique¹ number of peptides matched to proteins.

^hSequence coverage is the ratio of the total number of matched peptide residues to the total length of the protein.

ⁱExponentially Modified Protein Abundance Index (http://www.matrixscience.com/help/quant_help.html).

Table S2, Cont'd.

UniProt/Swiss- PROT ID	Description	Protein mass (kDa)	pI ^a	Num. of matches ^b	Num. of significant matches ^c	Num. of sequences ^d	Num. of significant sequences ^e	Num. of unique sequences ^f	Sequence coverage ^g	emPAI ^h
GSTF1_HUMAN	G-kinase stimulation factor subunit 2 (tau variant)	70	6.79	5	2	1	1	1	0.15	0.97
SAMEL2_HUMAN	Sorting and assembly machinery component 50 homolog	70	5.193	6.44	3	2	3	2	0.14	0.17
ASPL1_HUMAN	Aspartyl (neuraminid) sialinohydrolase	70	8.809	4.92	3	1	3	1	0.07	0.05
QTM2L_HUMAN	Glutathione S-transferase 3	70	2554.3	7	2	2	2	2	0.14	0.37
MPRL_HUMAN	Cation-independent mannose-6-phosphate receptor	70	274199	5.84	16	2	13	1	0.1	0.02
EEA1_HUMAN	Early endosome antigen 1	70	102367	5.55	14	4	13	4	0.17	0.11
ATB1L_HUMAN	Plasma membrane calcium-transporting ATPase 1	69	136868	5.73	8	3	6	2	0.09	0.06
ROA2L_HUMAN	Heterogeneous nuclear ribonucleoprotein A0	69	20822	8.34	4	2	4	2	0.25	0.31
LED2L_HUMAN	Gelsolin-2	69	26136	6.57	12	3	7	2	0.05	0.37
HRNPCL_HUMAN	Heterogeneous nuclear ribonucleoprotein D0	69	38410	7.82	10	6	4	3	0.13	0.38
EIF3H_HUMAN	Eukaryotic translation initiation factor 3 subunit H	69	39905	6.09	3	3	3	3	0.17	0.37
RAB1L1_HUMAN	Rab1-related protein Rab1-13	69	22100	8.27	5	1	4	1	0.28	0.2
MMF2_HUMAN	72 kDa type IV collagenase	68	73835	5.26	5	3	2	1	0.09	0.06
CUTL1_HUMAN	Protein Cutl1	68	19104	5.42	6	1	6	1	0.48	0.24
RAB21_HUMAN	Rab2-related protein Rab2-21	68	24202	8.11	5	1	4	1	0.28	0.19
XPO1_HUMAN	Exportin-1	68	10893	5.24	11	2	9	2	0.17	0.08
OPN2L_HUMAN	Opn2-related	68	60092	5.8	6	4	3	5	0.2	0.23
MYADM1_HUMAN	Myeloid-associated differentiation marker	68	35250	8.53	3	2	1	1	0.07	0.12
VAT1L_HUMAN	V-type proton ATPase subunit H	67	55847	6.07	7	2	7	2	0.29	0.16
NCO1_HUMAN	Neocytin	67	78292	5.87	6	3	4	1	0.1	0.05
OXFA2L_HUMAN	Oxidochrome c oxidase subunit FA2, mitochondrial	67	9390	8.75	3	1	2	1	0.45	0.53
IPOT1_HUMAN	Importin-8	67	115889	4.71	3	2	3	2	0.06	0.07
INF2_HUMAN	Inverted formin-2	67	135540	5.26	7	3	6	3	0.11	0.1
KOD12_HUMAN	BTB/POZ domain-containing protein KOD12	67	35679	5.51	4	2	4	2	0.25	0.26
BSOP1L_HUMAN	Radii GTPase-activating protein (neuraminidase) subunit	67	155886	5.4	9	3	9	3	0.13	0.08
KAT2L_HUMAN	Adenylate kinase 2, mitochondrial	67	26461	7.67	3	2	2	1	0.16	0.17
HUNE1_HUMAN	E3 ubiquitin-protein ligase HUNE1	67	481589	5.1	19	4	18	4	0.07	0.03
MPK3L_HUMAN	Dual specificity mitogen-activated protein kinase kinase 3	66	39293	7.05	2	4	1	4	0.21	0.11
PPIL4_HUMAN	Peptidyl-prolyl cis-trans isomerase-like 4	66	57189	5.83	3	2	2	2	0.11	0.16
VPS35L_HUMAN	Vacuolar protein sorting-associated protein 35	66	20735	5.97	3	2	2	2	0.28	0.49
NDUAA_HUMAN	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex subunit 10, mitochondrial	66	40725	8.67	4	3	3	3	0.16	0.36
DBLON_HUMAN	Dual homology, mitochondrial	66	27114	5.88	3	2	1	1	0.07	0.17
SECISL_HUMAN	Translation protein SECIS3 homolog	66	87842	5.21	6	4	3	2	0.29	0.21
TSPD_HUMAN	Transducator protein	66	18816	8.43	5	2	4	2	0.29	0.55
DLA1B_HUMAN	Dual homology subfamily B member 4	66	27182	6.85	9	4	5	1	0.23	0.38
PLXB2L_HUMAN	Plxin-82	65	204997	5.85	6	2	2	2	0.08	0.04
ACSL3L_HUMAN	Long-chain fatty-acyl-CoA ligase 3	65	80388	8.95	3	3	2	2	0.07	0.11
VADN1_HUMAN	Vannin	65	71688	7.18	1	1	1	1	0.02	1.08
PTGRL1_HUMAN	Prostaglandin reductase 1	65	35847	8.45	6	3	4	3	0.3	0.42
NACAGL_HUMAN	Alpha-N-acetylgalactosaminidase	65	48324	5.21	4	3	4	3	0.1	0.09
ARFG1_HUMAN	ADP-ribosylation factor GTPase-activating protein 1	65	44640	5.46	5	3	3	3	0.15	0.32
TMED7_HUMAN	Transmembrane emp24 domain-containing protein 7	65	25156	6.43	13	7	8	4	0.6	0.33
GRM4L_HUMAN	Glutamate receptor 4, mitochondrial	65	60062	7.57	2	2	2	2	0.1	0.13
LPB1_HUMAN	Linn-1-beta-1	64	113952	5.4	9	3	7	2	0.13	0.12
LTDORL_HUMAN	Regulator complex protein LAMTOR3	64	13614	6.73	4	2	3	2	0.54	0.82
TBCLL_HUMAN	Tubulin-binding collector 9	64	27058	5.08	4	3	3	3	0.35	0.25
FAM8B_HUMAN	Protein FAM8B	64	37167	5.96	3	2	3	2	0.17	0.25
IFTF1_HUMAN	Eukaryotic translation initiation factor 5B	64	128142	5.39	7	1	3	0	0.29	0.20
GBP1_HUMAN	Guanidylate-binding protein 1	64	67888	5.57	4	2	4	2	0.13	0.13
SP16L_HUMAN	FACT complex subunit SPT16	64	119338	5.5	6	3	4	1	0.07	0.04
SSBP1_HUMAN	Single-strand-DNA-binding protein, mitochondrial	64	17249	8.59	3	2	2	2	0.32	0.61
GSTF1L_HUMAN	Oxidoreductase-stimulating factor 1	64	23772	5.46	1	1	1	1	0.06	0.19
SGIP1_HUMAN	SGGP2-binding protein	63	111007	5.26	4	3	3	3	0.06	0.08
IFTT1_HUMAN	Intraflagellar transport protein 27 homolog	63	20467	5.28	2	1	2	1	0.21	0.22
PURB_HUMAN	Adenylsuccinate lyase	63	54854	6.89	11	4	6	3	0.25	0.25
LPL1_HUMAN	E3 UBR1-protein ligase 1	63	89540	6.35	7	3	6	2	0.17	0.1
RAVRI1_HUMAN	Ribonucleoprotein PTB-binding 1	63	83837	8.78	3	2	1	1	0.05	0.14
THL1_HUMAN	Acetyl-CoA acetyltransferase, mitochondrial	63	45171	6.98	2	1	1	1	0.04	0.1
DOL1L_HUMAN	Oxidation domain 1 lig1 intermediate chain 2	63	54086	5.97	6	2	5	2	0.14	0.17
SEM1A_HUMAN	Semaphorin-7A	63	74776	7.57	2	1	1	1	0.05	0.06
OPN2L_HUMAN	Gelsolin-2	63	63895	5.29	6	2	5	2	0.16	0.14
LMNA_HUMAN	Protein-A/C	63	74095	6.57	7	3	6	3	0.17	0.18
LMF2L_HUMAN	Lesch-Nyhan factor 2	63	79647	10.1	4	3	2	3	0.08	0.11
STAT2L_HUMAN	Signal transducer and activator of transcription 2	63	9785	5.34	6	2	5	1	0.09	0.04
RL1L_HUMAN	60S ribosomal protein L14	62	23417	10.94	11	5	6	3	0.28	0.7
CDP1_HUMAN	CDP antigen	62	25389	6.8	3	2	2	2	0.18	0.18
NSBA1L_HUMAN	Protein Nba1	62	103070	4.74	9	3	8	3	0.16	0.13
GORS1L_HUMAN	Gdp release- and -binding protein 2	62	47116	4.73	7	3	6	3	0.25	0.3
SEIL1_HUMAN	Protein seb1 homolog 1	62	8808	5.23	3	2	2	2	0.06	0.1
TIGAR_HUMAN	Fructose-2,6-bisphosphatase TIGAR	62	30043	7.6	5	3	3	3	0.24	0.32
MPPLA_HUMAN	Mitochondrial processing peptidase subunit alpha	61	58216	6.45	8	3	4	1	0.12	0.07
UBA1L_HUMAN	Ubiquitin-like modifier-activating enzyme 7	61	111624	5.64	2	1	1	1	0.03	0.04
AFD3J1_HUMAN	AF3 complex subunit delc-1	61	100078	8.89	10	2	8	2	0.11	0.07
TSP1L_HUMAN	Thrombospondin-1	61	139008	4.62	13	4	9	2	0.12	0.07
BTF3L_HUMAN	Transcription factor BTF3	61	22154	8.41	7	3	4	1	0.24	0.2
REL1_HUMAN	Len protease homolog, mitochondrial	61	106422	6.01	6	3	4	1	0.08	0.04
PRE1_HUMAN	Farnesyl beta-chase	61	20007	5.51	7	2	5	2	0.43	0.51
STAM1_HUMAN	Signal transducing adapter molecule 1	60	59142	4.7	6	1	4	1	0.14	0.07
BBFA_HUMAN	Bik-like protein 4	60	33407	6.06	7	2	5	2	0.24	0.28
SHNA_HUMAN	Alpha-subunit NSF attachment protein	60	33211	5.23	6	5	4	4	0.2	0.85
APMAP_HUMAN	Adipocyte plasma membrane-associated protein	60	44851	5.82	9	3	6	2	0.25	0.2
ACONL_HUMAN	Acetate hydratase, mitochondrial	60	65372	7.36	3	1	3	1	0.08	0.05
ARFG1_HUMAN	ADP-ribosylation factor GTPase-activating protein 3	60	58893	7.04	4	2	4	2	0.13	0.16
GGH2L_HUMAN	Gln:Glu-cysteine ligase regulatory subunit	60	30788	5.89	2	1	2	1	0.19	0.14
FOXC4L_HUMAN	Foxo4-related	60	19844	6.17	7	3	6	2	0.07	0.04
TTG2L_HUMAN	Tetratricopeptide repeat protein 37	60	175375	7.47	10	1	9	1	0.01	0.02
POSD1L_HUMAN	POS proteasome non-ATPase regulatory subunit 8	60	39507	6.73	9	2	7	2	0.23	0.23
PREP1_HUMAN	Presequence protease, mitochondrial	60	117338	6.45	9	1	8	1	0.13	0.04
CENT2_HUMAN	Centrin-2	60	10726	4.91	5	1	4	1	0.45	0.23
POSD1L_HUMAN	POS proteasome non-ATPase regulatory subunit 6	60	45002	5.45	4	2	4	2	0.14	0.2
ACAD9L_HUMAN	Medium-chain specific acyl-CoA dehydrogenase, mitochondrial	60	46559	8.61	3	2	2	2	0.13	0.09
PHOCOL_HUMAN	MDM-like protein phocin	60	26016	5.5	6	3	4	2	0.22	0.26
ECI1_HUMAN	Enoyl-CoA delta isomerase 1, mitochondrial	60	32785	8.8	5	2	3	2	0.23	0.29
APX1L_HUMAN	DNA-topoisomerase or apyrimidic site lyase	60	35522	8.33	7	1	6	1	0.26	0.12
OLP1L_HUMAN	OGG1-like domain-containing linker protein 1	59	162147	5.26	14	3	11	2	0.13	0.05
GREM1_HUMAN	Grem1-1	59	20683	8.53	3	3	2	2	0.17	0.49
PPD1L_HUMAN	Peptidyl-prolyl cis-trans isomerase D	59	40736	6.77	2	1	2	1	0.07	0.11
ATP1L_HUMAN	ATP synthase-coupling factor 6, mitochondrial	59	12580	5.2	3	2	2	2	0.40	0.81
WDFY1L_HUMAN	WD repeat and FYVE domain-containing protein 1	53	46293	6.99	2	2	2	2	0.13	0.2
NRP1_HUMAN	Neurexin-1	59	120369	5.58	2	1	2	1	0.04	0.04

^aProtein score is calculated from the score of the peptide attributed to the protein.

^bIs (Predicted) isoelectric point.

^cNumber of matches is spectrum number matched to protein¹⁴.

^dNumber of significant matches is spectrum number that matches protein and exceeds the identification criteria.

^eNumber of sequences is number of peptides matched to protein¹².

^fNumber of significant sequences is number of peptides exceeding the identification criteria matched to proteins.

^gNumber of unique sequences is a unique number of peptides matched to proteins.

^hSequence coverage is the ratio of the total number of matched peptide residues to the total length of the protein.

ⁱExponentially Modified Protein Abundance Index (http://www.matrixscience.com/help/quant_empa_help.html).

Table S2. Cont'd.

UniProt/Swiss-Prot		Protein score ^a	Protein mass (kDa)	pI ^b	Num. of matches ^c	Num. of significant matches ^d	Num. of sequences ^e	Num. of significant sequences ^f	Num. of unique sequences ^g	Sequence coverage ^h	empPA ⁱ
PROT ID	Description										
TENM2_HUMAN	Tenascin-2	59	61.02	5.7	2	2	1	1	1	0.25	0.17
BP1_HUMAN	Insulin-like growth factor-binding protein 7	59	29111	8.25	9	3	5	3	5	0.29	0.53
ADG_HUMAN	Adenosine kinase	59	40520	6.24	5	2	4	2	4	0.22	0.23
DUS3_HUMAN	Dual specificity protein phosphatase 3	59	20465	2.16	2	1	2	1	2	0.1	0.22
REGO1_HUMAN	ATP-dependent DNA helicase G1	59	73410	9.12	14	4	8	2	8	0.27	0.12
ZAS2_HUMAN	Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit delta isoform	59	69947	5.24	3	2	2	1	2	0.06	0.06
TRB2_HUMAN	2-methylerythroid-specific thiolase, mitochondrial	58	41895	5.22	9	4	8	3	8	0.24	0.35
STX4_HUMAN	Syntaxin-4	58	34159	5.92	4	2	3	1	3	0.2	0.13
UBR5_HUMAN	Ubiquitin-conjugating enzyme E2 R2	58	27449	4.26	6	3	3	1	3	0.34	0.36
PSB2_HUMAN	Proteasome subunit beta type-2	58	22822	6.51	15	3	6	3	6	0.36	0.72
SGO1_HUMAN	Calsin-binding mitochondrial carrier protein SGMO-1	57	53320	6	5	2	5	2	5	0.21	0.17
DOTN_HUMAN	Dynactin subunit 4	57	52304	7.7	1	1	1	1	1	0.06	0.08
VMP1_HUMAN	Vacuole membrane protein 1	57	46208	6.47	2	2	1	1	1	0.07	0.09
AP1G1_HUMAN	AP-1 complex subunit gamma-1	57	97253	6.36	8	3	7	3	7	0.17	0.15
NPC1_HUMAN	Niemann-Pick C1 protein	57	142074	5.17	5	1	3	1	3	0.05	0.03
TMSB2_HUMAN	Transmembrane 8 superfamily member 2	57	75725	7.23	5	2	3	1	3	0.08	0.06
FKBP7_HUMAN	Peptidyl-prolyl isomerase FKBP7	57	28959	6.05	4	3	4	3	4	0.22	0.31
VASP_HUMAN	Vasodilator-stimulated phosphoprotein	56	38805	9.05	13	3	8	3	8	0.24	0.37
APBF_HUMAN	Apoptosis-inducing factor 1, mitochondrial	56	68559	9.04	3	1	3	1	3	0.09	0.06
COX1_HUMAN	Cytochrome c oxidase subunit 1	56	57003	6.19	3	3	2	2	2	0.06	0.16
HGG2_HUMAN	HGG1 domain family member 2A, mitochondrial	56	11521	10.21	3	3	1	1	1	0.2	0.42
NOL2_HUMAN	Nucleosent	56	45302	4.89	1	1	1	1	1	0.06	0.09
GSDE1_HUMAN	Odd shock domain-containing protein E1	56	88829	9.88	5	2	4	2	4	0.08	0.1
DORL2_HUMAN	Dorf-2	56	27549	6.73	2	2	1	1	1	0.13	0.18
COMD1_HUMAN	COMMD domain-containing protein 2	56	27231	6.24	7	2	3	1	3	0.31	0.44
EPCE2_HUMAN	Endoplasmic reticulum-Daql intermediate compartment protein 3	56	43194	5.68	4	2	2	1	2	0.09	0.1
QCRF_HUMAN	Cytochrome bmc1 complex subunit 6, mitochondrial	56	10722	4.29	2	1	1	1	1	0.2	0.46
MCFD2_HUMAN	Multiple coagulation factor deficiency protein 2	55	16380	4.21	1	1	1	1	1	0.16	0.28
RPL5_HUMAN	Rpl11 family-interacting protein 5	55	70372	9.28	4	3	3	2	3	0.1	0.13
NDC5_HUMAN	Nucleolin-5	55	50164	5.03	7	2	4	1	4	0.16	0.09
PLD3_HUMAN	Phospholipase D3	55	54871	6.02	5	1	4	1	4	0.21	0.05
TENM4_HUMAN	Tenascin-4	55	32092	6.7	5	2	4	1	4	0.13	0.17
CYBB2_HUMAN	Cytochrome b5 type B	54	16322	4.88	2	1	2	1	2	0.29	0.29
NPC2_HUMAN	Ecdysial secretory protein E1	54	16559	7.26	6	3	2	2	2	0.28	0.64
TRB2_HUMAN	Nucleosent TRB	54	287131	4.97	14	2	13	2	13	0.03	0.1
AFGA_HUMAN	Angiogenesis	54	53554	5.85	1	1	1	1	1	0.03	0.08
RAT1_HUMAN	RasGAP1	54	109973	5.67	8	1	5	1	5	0.08	0.04
XPO1_HUMAN	Exportin-1	54	123828	5.81	7	1	5	1	5	0.06	0.03
OSGEP_HUMAN	Proteinase RNA N6-adenosine threosylcarbamoyltransferase	54	36403	5.94	1	1	1	1	1	0.08	0.12
MCO4_HUMAN	Lactadherin	54	33005	6.47	11	3	9	3	9	0.41	0.34
AT131_HUMAN	Manganese-transporting ATPase 13A1	54	133870	8.46	12	1	6	1	6	0.07	0.03
NDC2_HUMAN	Nuclear magnetron protein nuc2	54	32219	5.27	4	2	4	2	4	0.15	0.21
TRXN1_HUMAN	Aldehyde dehydrogenase 1	54	61803	6.15	8	2	6	2	6	0.18	0.14
PRAF1_HUMAN	PRAF1 family protein 3	54	21600	9.77	2	1	2	1	2	0.14	0.21
TRF12_HUMAN	Multifunctional nucleoside diphosphate subunit TRM12-like protein	54	41980	5.71	3	1	3	1	3	0.21	0.33
SMTC_HUMAN	Cytosolic perox 5-methyltransferase	53	64429	5.75	6	4	5	4	5	0.19	0.29
NALB_HUMAN	NADH-thiamine oxidoreductase chain 4	53	51547	5.4	2	1	2	1	2	0.09	0.08
ABPL_HUMAN	Actin-related protein 2/3 complex subunit 5-like protein	53	18931	6.16	2	2	2	2	2	0.22	0.42
TTL12_HUMAN	Tubulin-tyrosine ligase-like protein 12	53	74356	5.23	4	3	4	3	4	0.15	0.18
ISOC2_HUMAN	Isocitronate dehydratase domain-containing protein 2	53	22223	7.87	6	2	5	2	5	0.46	0.45
PPPS_HUMAN	Farnesyl pyrophosphate synthase	53	48245	5.83	5	3	3	2	3	0.17	0.19
MCI1_HUMAN	MDC5 complex subunit MCI3	53	13079	9.44	4	2	2	2	2	0.44	0.66
SFO1_HUMAN	Sodium factor 1	53	65286	9.07	6	1	4	1	4	0.05	0.01
SAP2_HUMAN	Gardoside GMP activator	52	20829	5.17	3	2	2	2	2	0.18	0.48
USP9_HUMAN	Proteinase ubiquitin carboxyl-terminal hydrolase FAX-X	52	226094	5.52	15	3	14	3	14	0.12	0.04
PSB3_HUMAN	Core-binding factor subunit beta	52	27455	5.23	3	1	3	1	3	0.41	0.21
CUL5_HUMAN	Cul-5	52	90887	8.08	8	1	8	1	8	0.17	0.05
PLN2_HUMAN	Perlecan-2	52	40045	6.34	7	2	6	2	6	0.26	0.19
DPP3_HUMAN	Dipeptidyl peptidase 3	52	82538	5.02	9	2	8	2	8	0.23	0.11
MVD_HUMAN	Dihydrodipicolinate decarboxylase	52	43377	6.78	4	3	4	3	4	0.26	0.33
QNB1_HUMAN	Oligonucleotide, mitochondrial	52	28816	6.41	6	3	6	3	6	0.46	0.59
MLEC_HUMAN	Malecin	51	32214	5.27	2	1	1	1	1	0.08	0.14
TOP4_HUMAN	Activated RNA polymerase II transcriptional coactivator p15	51	14386	9.6	5	3	3	2	3	0.24	0.26
STOAC_HUMAN	Protein S100-A13	51	11464	5.91	10	3	5	1	5	0.39	0.43
UBR5_HUMAN	Ubiquitin-associated and E3S domain-containing protein B	51	72849	6.48	2	2	1	1	1	0.03	0.06
TBC1_HUMAN	Serine/threonine-protein kinase TBC1	51	63589	6.32	5	1	4	1	4	0.06	0.05
RRI1_HUMAN	Ribonucleoside-diphosphate reductase large subunit	51	90013	6.76	5	1	5	1	5	0.15	0.05
DHE2_HUMAN	Quinone dehydrogenase 1, mitochondrial	50	61359	7.69	8	2	6	2	6	0.21	0.15
STXB3_HUMAN	Syntaxin-6-like protein 3	50	67721	7.88	4	2	3	1	3	0.09	0.06
TMSB2_HUMAN	Transmembrane 8 superfamily member 3	50	67843	6.83	2	1	2	1	2	0.08	0.06
PTSG2_HUMAN	Prostaglandin G/H synthase	50	7091	9.56	2	2	1	1	1	0.16	0.27
DOK4_HUMAN	Doxylkinase kinase alpha	49	83577	6.28	5	2	4	1	4	0.09	0.05
CSB2_HUMAN	COP1 signalosome complex subunit 3	49	47842	6.19	6	2	6	2	6	0.27	0.19
FKBP4_HUMAN	Peptidyl-prolyl isomerase FKBP4	49	17772	5.35	8	2	4	2	4	0.17	0.24
ODD2_HUMAN	Dihydrodipicolinate decarboxylase component of 2-oxoglutarate dehydrogenase complex, mitochondrial	49	48724	9.11	3	1	3	1	3	0.11	0.09
POXA3_HUMAN	Protein disulfine-isomerase A3	49	95550	6.06	2	1	2	1	2	0.11	0.07
ADPQK_HUMAN	ADP-dependent glucokinase	49	54055	5.77	3	3	2	2	2	0.08	0.17
SAT2_HUMAN	Neutral amino acid transporter A	49	55888	5.88	4	3	2	2	2	0.1	0.18
COX2_HUMAN	Cytochrome c oxidase subunit 2	49	25456	4.67	5	3	2	1	2	0.13	0.38
NU155_HUMAN	Nuclear pore complex protein Nup155	49	155100	5.78	6	2	5	1	5	0.1	0.03
PAUK_HUMAN	Paikin	49	44464	5.8	8	2	6	2	6	0.24	0.14
SPN51_HUMAN	Protein spinter homolog 1	49	56594	6.19	3	2	3	2	3	0.13	0.16
RRI2_HUMAN	Ribonucleoside-diphosphate reductase subunit MD B	48	40710	4.89	1	1	1	1	1	0.07	0.11
TMSB2_HUMAN	Transmembrane 8 superfamily member 3	48	25885	4.71	1	1	1	1	1	0.12	0.17
ARPP1_HUMAN	Arp1	48	24927	5.57	2	2	1	1	1	0.12	0.18
LYPA_HUMAN	Acyl-coenzyme A thioesterase 1	48	24653	6.29	2	1	2	1	2	0.18	0.18
HEBO_HUMAN	3-hydroxybutyryl-CoA hydrolase, mitochondrial	48	43454	6.38	4	2	3	1	3	0.16	0.1
DHX15_HUMAN	Pra-mRNA-binding factor ATP-dependent RNA helicase DHX15	48	96875	7.12	5	3	4	2	4	0.09	0.1
MCRAL_HUMAN	Matrix remodeling-associated protein B	47	49101	6.75	1	1	1	1	1	0.04	0.05
LSM2_HUMAN	U6 snRNA-associated Sm-like protein LSM2	47	10828	6.04	2	1	2	1	2	0.41	0.45
QPE2_HUMAN	UPF0550 protein QPE2	47	108462	6.82	6	2	6	2	6	0.12	0.08
SYT2_HUMAN	Phospholipase-C/RNA lipase beta subunit	39	46074	5.64	8	3	4	3	4	0.15	0.21
QOZ_HUMAN	Quinone oxidoreductase	47	35185	8.66	2	1	2	1	2	0.12	0.13
MICAL1_HUMAN	[E=60]-monooxygenase MICAL1	47	117801	6	6	1	5	1	5	0.12	0.04
QPE2_HUMAN	QDH (GDP, endoplasmic reticulum protein	47	88836	6.84	6	1	4	1	4	0.08	0.05
DOX17_HUMAN	Proteinase ATP-dependent RNA helicase DOX17	47	80222	5.53	5	1	5	1	4	0.11	0.05
QPE2_HUMAN	E3 ubiquitin-protein ligase QPE2	47	34824	5.61	3	1	3	1	3	0.17	0.13
IAD1_HUMAN	HLA class I histocompatibility antigen, A-3 alpha chain	47	40815	5.66	5	2	5	2	5	0.25	0.23
QPE2_HUMAN	Cysteine-rich protein 2	47	27479	5.01	1	1	1	1	1	0.06	0.1
TYPH_HUMAN	Thymidine phosphorylase	46	49924	5.36	6	3	4	2	4	0.18	0.18

^aProtein score is calculated from the score of the peptide attributed to the protein.

^bpI is (Predicted) isoelectric point.

^cNumber of matches is spectrum number matched to protein¹.

^dNumber of significant matches is spectrum number that matches protein and exceeds the identification criteria.

^eNumber of sequences is number of peptides matched to protein¹.

^fNumber of significant sequences is number of peptides exceeding the identification criteria matched to proteins.

^gNumber of unique sequences is a unique⁶ number of peptides matched to proteins.

^hSequence coverage is the ratio of the total number of matched peptide residues to the total length of the protein.

ⁱExponentially Modified Protein Abundance Index (http://www.matrixscience.com/help/quant_empai_help.html).

Table S2. Cont'd.

UniProt/Swiss-Prot ID	Description	Protein score ^a	Protein mass (kDa)	pI ^b	Num. of matches ^c	Num. of significant matches ^d	Num. of sequences ^e	Num. of significant sequences ^f	Num. of unique sequences ^g	Sequence coverage ^h	emPAI ⁱ
ARHGAP2_HUMAN	Rho guanine nucleotide exchange factor 2	46	41476	6.8	1	1	1	1	1	0.04	0.04
VPS4A_HUMAN	Vacuolar protein sorting-associated protein 4A	46	40867	7.84	5	3	2	3	2	0.15	0.19
RS27L2_HUMAN	45S ribosomal protein S27-like	46	9471	9.57	2	1	2	1	2	0.3	0.53
EXOC5_HUMAN	Exosome complex component RRP46	46	29232	7.53	1	1	1	1	1	0.1	0.1
RBK1_HUMAN	Receptor-interacting serine/threonine-protein kinase 1	46	78883	5.92	4	1	3	1	3	0.08	0.06
SHV2L_HUMAN	Helicase SHV2	46	137688	5.72	4	1	3	1	3	0.35	0.93
IMM4L2_HUMAN	Immunin subunit alpha-5	46	60184	4.54	3	2	0.5	2	2	0.14	0.15
NRK2_HUMAN	Serine/threonine-protein kinase Nrsk2	46	34528	8.49	7	3	6	3	6	0.36	0.43
RPS7A_HUMAN	Ribosome-binding factor 2, mitochondrial	46	95545	6.08	2	1	2	1	2	0.06	0.05
AMRP_HUMAN	Alpha-2-macroglobulin receptor-associated protein	46	41441	8.73	5	3	3	2	3	0.12	0.22
MCL1_HUMAN	MCCO5 complex subunit MCL1	46	26139	8.48	6	1	2	1	2	0.09	0.17
YAP1_HUMAN	Transcriptional coactivator YAP1	45	54427	5	4	1	3	1	3	0.15	0.08
FKBP5_HUMAN	Peptidyl-prolyl cis-trans isomerase FKBP5	45	44534	4.78	8	3	4	1	4	0.21	0.1
RAV1B_HUMAN	Ram-specific GTPase-activating protein	45	23266	5.19	5	2	4	1	4	0.26	0.19
NSF1_HUMAN	NSF11 cofactor p47	45	40548	4.99	5	2	4	2	4	0.18	0.23
NUDC1_HUMAN	NuS2 domain-containing protein 1	45	66713	4.59	5	1	5	1	5	0.14	0.26
ACSD5_HUMAN	Short branched-chain specific acyl-CoA dehydrogenase, mitochondrial	45	47455	6.52	3	1	2	1	2	0.15	0.09
CI17_HUMAN	Monofunctional C1-tetrahydrofolate synthase, mitochondrial	45	105724	8.32	3	1	2	1	2	0.04	0.04
OSPF_HUMAN	OSPF glycoprotein	45	14168	6.02	6	2	3	2	3	0.49	0.76
WASCL_HUMAN	WASH complex subunit 4	45	136316	7.1	6	1	5	1	5	0.08	0.03
UPRAR_HUMAN	Urokinase plasminogen activator surface receptor	45	36993	6.2	5	2	4	1	4	0.3	0.12
RAB25_HUMAN	RAB25 GTP exchange factor	45	79321	6.42	8	2	6	1	6	0.17	0.05
PULB2_HUMAN	Putative phospholipase B-like 2	45	65430	6.34	5	2	3	2	3	0.08	0.14
LYR2C_HUMAN	Protein LYR2C	45	63799	9.33	5	3	3	3	3	0.15	0.22
TPBXL_HUMAN	Trophoblast glycoprotein	45	46003	6.35	3	1	2	1	2	0.06	0.09
PFMT1_HUMAN	Protein phosphatase 1F	44	49000	4.99	3	1	3	1	3	0.1	0.09
PKP11_HUMAN	Peptidyl-prolyl cis-trans isomerase FKBP11	44	22166	9.44	2	1	2	1	2	0.14	0.2
NPPE2_HUMAN	Nuclear pore glycoprotein p62	44	53222	5.21	2	1	2	1	2	0.08	0.08
CLP1L_HUMAN	Clp1L and clp1L2 transmembrane protein 1-like protein	44	22189	8.71	3	2	3	2	3	0.07	0.14
LOC12_HUMAN	Putative RRM-binding protein Loo-1-like 2	44	46468	10.02	4	1	4	1	4	0.19	0.09
SPRE_HUMAN	Sesquiterpene reductase	44	28031	8.24	1	1	1	1	1	0.08	0.16
CRP1L_HUMAN	CRP1 regulatory subunit-associated protein 3	44	96885	4.68	4	2	2	2	2	0.09	0.06
HM12L_HUMAN	Minor histocompatibility antigen H13	44	41462	6.01	3	1	2	1	2	0.13	0.11
DAD1_HUMAN	Dab1-like-3-oligodendrocyte-specific protein glycosyltransferase subunit DAD1	44	12489	6.52	2	2	1	1	1	0.11	0.28
RAB25L_HUMAN	Ram-2-like protein RAB25L	44	24762	4.85	7	1	6	1	6	0.13	0.16
PTPA_HUMAN	Serine/threonine-protein phosphatase 2A activator	44	40641	5.63	4	2	3	2	3	0.2	0.23
MAVS_HUMAN	Mitochondrial antiviral-signaling protein	44	22493	2.36	2	1	2	1	2	0.05	0.02
SOUB1_HUMAN	Signal peptide, GUS and EGF-like domain-containing protein 3	44	109210	7.85	4	2	3	1	3	0.06	0.04
EPHD2_HUMAN	EPH domain-containing protein D2	44	26880	5.15	2	1	2	1	2	0.12	0.17
SCDOL_HUMAN	Saccharosyl dehydrogenase-like oxidoreductase	44	47121	9.24	4	3	2	2	2	0.13	0.19
TM6SF4_HUMAN	Transmembrane 6 superfamily member 4	44	74470	6.1	7	1	5	1	5	0.16	0.06
NCHO_HUMAN	Non-TOU domain-containing octanone-binding protein	44	54197	6.01	5	1	4	1	4	0.21	0.05
ARK2_HUMAN	Alk100B B1 dehydro reductase member 2	43	39564	6.7	4	1	3	1	3	0.18	0.11
NLU2L_HUMAN	NADH-dependent oxidoreductase chain 5	43	66862	9.14	2	1	2	1	2	0.09	0.26
AMPD3_HUMAN	AMP deaminase 2	43	100264	6.46	3	1	2	1	2	0.04	0.04
IPYR2_HUMAN	Inorganic pyrophosphatase 2, mitochondrial	43	37896	7.07	2	1	2	1	2	0.14	0.12
TPP3L_HUMAN	Tumor necrosis factor alpha-induced protein 8	43	23969	7.74	4	1	3	1	3	0.2	0.2
MTX2_HUMAN	Metastin-2	43	29744	5.9	4	2	2	1	2	0.19	0.15
TMED2_HUMAN	Transmembrane emp24 domain-containing protein 3	43	24761	5.4	7	1	3	1	3	0.3	0.18
PTN2L_HUMAN	Tyrosine-protein phosphatase non-receptor type 23	43	176891	6.45	1	1	1	1	1	0.01	0.01
RAB35_HUMAN	Ram-3-like protein RAB35	43	23011	8.52	10	1	3	1	2	0.2	0.2
STFA2_HUMAN	Phenylalanine-tRNA ligase alpha subunit	43	57526	7.31	3	1	3	1	3	0.13	0.08
FAM101_HUMAN	Acyltransferase FAM101, mitochondrial	43	24827	6.96	3	3	2	2	2	0.25	0.39
RBP2L_HUMAN	E3 SUMO-protein ligase RBP2	43	35794	5.85	17	1	15	1	15	0.09	0.01
MEGAL_HUMAN	Lysosomal integral membrane protein 2	43	52750	9.17	4	1	3	1	3	0.09	0.08
RHO1_HUMAN	Rho GTPase-activating protein 17	43	95377	7.23	3	1	3	1	3	0.07	0.04
ASMTL_HUMAN	Proteinase-kinase O-methyltransferase	42	51140	5.48	3	1	3	1	3	0.13	0.08
CATL2_HUMAN	Cathepsin	42	95719	6.9	5	1	4	1	4	0.13	0.07
TB12L_HUMAN	182 kDa tubulin-sea-1-binding protein	42	181685	4.77	6	1	3	1	3	0.02	0.02
DCUP_HUMAN	Unconjugated deubiquitinase	42	40761	5.77	3	2	2	2	2	0.15	0.23
BDH2_HUMAN	3-hydroxybutyrate dehydrogenase type 2	42	26707	7.96	3	1	3	1	3	0.21	0.17
PLD1_HUMAN	Phospholipase C1	42	211371	6.8	5	1	4	1	4	0.04	0.02
HERL1_HUMAN	Heterogeneous nuclear ribonucleoprotein L-like	42	60045	7.83	2	2	2	2	2	0.08	0.15
HERC4_HUMAN	Probable E3 ubiquitin-protein ligase HERC4	41	118487	5.8	9	3	6	2	6	0.14	0.07
VPS2L_HUMAN	Vacuolar protein sorting-associated protein 51 homolog	41	95868	6.06	2	1	2	1	2	0.06	0.09
PHG1_HUMAN	Protein-4-oxalophorbonylamine dehydratase	41	11892	6.28	3	1	3	1	3	0.41	0.4
RECK_HUMAN	Reversion-inducing cysteine-rich protein with Kazal motifs	41	106388	6.35	9	1	7	1	7	0.17	0.04
CATL1_HUMAN	UPP087 protein C1orf123	41	18037	4.93	2	1	2	1	2	0.17	0.26
IMPA1_HUMAN	Invariant monophosphatase 1	41	30169	5.16	3	1	3	1	3	0.27	0.15
SH2C_HUMAN	Sorting nexin-2	41	98435	5.04	8	2	5	2	5	0.17	0.19
TF1_HUMAN	Tissue factor	41	33047	6.84	4	1	3	1	3	0.18	0.13
HP1_HUMAN	Hypoxanthine kinase factor 1-like inhibitor	41	40280	5.39	1	1	1	1	1	0.07	0.11
MTX2L_HUMAN	Sedolisin-dependent kinase sulfate isomerase type-2	41	49323	6.02	7	1	6	1	6	0.21	0.1
BAG3_HUMAN	BAG family molecular chaperone regulator 3	40	61557	6.46	3	2	3	2	3	0.13	0.15
UBE2Z_HUMAN	Ubiquitin-conjugating enzyme E2 Z	40	38186	5.37	2	1	2	1	2	0.11	0.11
ABHD14_HUMAN	Protein ABHD14B	40	22332	5.94	3	2	2	2	2	0.15	0.45
KAP2_HUMAN	cAMP-dependent protein kinase type II-Alpha regulatory subunit	40	45490	4.96	2	1	2	1	2	0.07	0.1
UBFD1_HUMAN	Ubiquitin domain-containing protein UBFD1	40	33551	5.55	4	2	3	1	3	0.17	0.13
OSBL2_HUMAN	Oxytocin-binding protein-related protein 8	40	101132	6.52	10	1	8	1	8	0.14	0.04
PAPPT1_HUMAN	TGDD-motif-like poly (ADP-ribose) polymerase	40	76178	6.19	69	1	3	1	3	0.28	0.26
ARMK2_HUMAN	Armadillo repeat-containing 2-related protein 2	40	65643	8.68	2	1	2	1	2	0.06	0.07
GLRX2_HUMAN	Glu-taraldehyde-3	40	37408	5.21	7	2	5	1	5	0.26	0.12
CHRP1_HUMAN	CR1 canonical receptor-interacting protein 1	40	18637	7.72	4	1	4	1	4	0.53	0.26
BR1_HUMAN	BFG-interacting domain death agonist	40	21981	5.27	4	3	2	1	2	0.25	0.21
SRPL2_HUMAN	Transcription-associated protein subunit delta	40	18897	5.76	4	2	2	2	2	0.18	0.12
CAT5_HUMAN	Citronellal epoxide sensor for mTORC1 subunit 2	40	36034	5.02	1	1	1	1	1	0.11	0.12
HOUH1_HUMAN	Pseudo-uridine-5'-phosphatase	40	25233	5.18	1	1	1	1	1	0.08	0.18
TOLIP_HUMAN	TGF-interacting protein	39	30262	5.69	3	1	3	1	3	0.18	0.15
GET2L_HUMAN	Glu-taraldehyde S-transferase Mu 2	39	29728	6	6	2	4	1	4	0.28	0.17
FIS1_HUMAN	Mitochondrial fusion 1 protein	39	16927	8.84	2	2	2	1	2	0.18	0.28
QSOX1_HUMAN	Olfactin subfamily A member 2	39	112017	5	7	1	5	1	5	0.09	0.04
LZIC_HUMAN	Protein LZIC	39	21481	4.88	3	1	2	1	2	0.26	0.21
AUP1_HUMAN	Ancient ubiquitin-like protein 1	39	32955	8.37	2	1	2	1	2	0.09	0.08
GPH1_HUMAN	Glucosamine-6-phosphate isomerase 1	39	32648	6.42	4	2	3	1	3	0.25	0.14
ANO12L_HUMAN	Anoctamin-10	39	76280	7.1	2	1	2	1	2	0.07	0.06
LAPTA_HUMAN	Lamin-associated polypeptide 2, isoform alpha	39	75446	7.56	3	3	3	3	3	0.17	0.05
MYLK_HUMAN	Myosin light chain kinase, smooth muscle	39	210583	5.85	10	1	8	1	8	0.09	0.22
CAT2_HUMAN	Cathepsin 2	39	33648	6.7	3	1	2	1	2	0.11	0.13
HDDC2_HUMAN	HD domain-containing protein 2	39	23376	5.33	3	2	2	2	2	0.21	0.19
HPH2L_HUMAN	Hypoxanthine-guanine phosphoribosyltransferase	39	24564	6.21	4	2	3	1	3	0.25	0.18

^aProtein score is calculated from the score of the peptide attributed to the protein.

^bpI is (Predicted) isoelectric point.

^cNumber of matches is spectrum number matched to protein^d.

^dNumber of significant matches is spectrum number that matches protein and exceeds the identification criteria.

^eNumber of sequences is number of peptides matched to protein^f.

^fNumber of significant sequences is number of peptides exceeding the identification criteria matched to proteins.

^gNumber of unique sequences is a unique^g number of peptides matched to proteins.

^hSequence coverage is the ratio of the total number of matched peptide residues to the total length of the protein.

ⁱExponentially Modified Protein Abundance Index (http://www.matrixscience.com/help/quant_empai_help.html).

Table S2. Cont 10.

UniProt/Swiss-Prot ID	Description	Protein score ^a	Protein mass (kDa)	pI ^b	Num. of matches ^c	Num. of significant matches ^d	Num. of sequences ^e	Num. of significant sequences ^f	Num. of unique sequences ^g	Sequence coverage ^h	emPAI
BMT1_HUMAN	Myo-inositol-dependent interacting protein 1	38	9500	10.07	3	1	2	1	2	0.01	0.01
GORL2_HUMAN	Cytoskeleton bcr1 complex subunit 8	38	9900	10.07	3	1	1	1	1	0.26	0.31
HEML2_HUMAN	Prothymosin domain	38	39306	6.68	4	1	3	1	3	0.15	0.11
NTSD1_HUMAN	S-trimethylcysteine domain-containing protein 1	38	51812	5.84	1	1	1	1	1	0.04	0.04
ATP1F_HUMAN	ATP synthase F0 subunit B1, mitochondrial	38	28890	9.37	3	1	3	1	3	0.14	0.15
CPPEF1_HUMAN	Serine/threonine-protein phosphatase CPPEF1	38	28528	5.16	2	1	2	1	2	0.12	0.12
RUVB1_HUMAN	RuvB-like 1	38	50196	6.02	3	2	3	2	3	0.12	0.18
CHG65_HUMAN	UPF0686 protein G1.1orf8	38	27338	5.28	4	2	2	1	2	0.16	0.16
SUMF5_HUMAN	Sulfatase-modifying factor 2	38	33822	7.28	1	1	1	1	1	0.03	0.13
PCYT2_HUMAN	Ethanolamine-phosphate cytidylyltransferase	38	43808	6.44	4	1	3	1	3	0.13	0.1
PNK2L_HUMAN	Phosphatidylethanol 3-kinase catalytic subunit 3	37	101405	6.37	4	1	4	1	4	0.06	0.04
CATL1_HUMAN	Cathepsin L1	38	37540	5.21	2	1	2	1	2	0.11	0.12
GGX_HUMAN	Glucagon debranching enzyme	38	174522	6.31	4	2	3	2	3	0.04	0.05
OPT1A_HUMAN	Geminin Chromatin/kinetochore 1, 1st isoform	37	88311	8.85	2	1	2	1	2	0.07	0.05
PAPS1_HUMAN	Bifunctional 5'-phosphoribosyltransferase 5'-phosphoribosyltransferase 1	37	70788	6.4	7	1	6	1	6	0.22	0.06
TRPG_HUMAN	Trapping protein particle complex subunit 8	37	16599	6.41	6	1	4	1	4	0.05	0.03
PLAG_HUMAN	Phospholipase A-2-converting protein	37	87101	5.86	3	1	3	1	3	0.09	0.05
CLCA4_HUMAN	Clathrin light chain A	37	27080	4.43	1	1	1	1	1	0.03	0.17
QBPR1_HUMAN	Menkesin polyisoprenyl transferase alpha	37	46262	6.13	2	2	1	1	1	0.04	0.05
CSPG1_HUMAN	Chondroitin sulfate proteoglycan 4	37	250382	5.27	4	1	4	1	4	0.04	0.02
SARH2_HUMAN	S-adenosylhomocysteine hydrolase-like protein 1	37	58913	8.49	7	3	6	2	6	0.17	0.15
SRRL2_HUMAN	Phosphoserine phosphatase	37	24992	5.53	2	1	2	1	2	0.12	0.18
GPC1_HUMAN	PDZ domain-containing protein GPC1	37	36027	5.9	2	1	2	1	2	0.08	0.12
SUGA_HUMAN	Succinate-CoA ligase (ADP/GDP-forming) subunit alpha, mitochondrial	36	36227	9.91	3	1	2	1	2	0.12	0.12
GBF1_HUMAN	Gdp-specific nucleotide A-arsenase guanine nucleotide exchange factor 1	36	206315	5.48	12	1	10	1	9	0.1	0.02
MOXA1_HUMAN	Maternal-zygotic-associated protein 7	36	21432	4.24	1	1	1	1	1	0.14	0.21
SOTD1_HUMAN	Sect1 family domain-containing protein 1	36	72344	5.89	8	5	6	1	6	0.17	0.33
K1C12_HUMAN	Keratin type I cytoskeletal 19	36	44079	5.04	1	1	1	1	1	0.06	0.1
ALG3_HUMAN	Galactose-4-epimerase	36	36322	9.34	1	1	1	1	1	0.05	0.13
OPA1_HUMAN	Dynamin-like 120 kDa protein, mitochondrial	36	11561	7.88	3	1	3	1	3	0.07	0.04
CHZ2_HUMAN	2'-5'-pyridine nucleotide 3'-phosphatase	36	47549	9.17	3	2	2	1	2	0.09	0.08
QLA4_HUMAN	GMP synthase [L-lysine-cysteine-binding]	36	74667	6.42	1	2	2	1	2	0.05	0.17
ANK13_HUMAN	Ankrrin A13	36	35393	5.67	3	1	2	1	2	0.09	0.12
LCAP_HUMAN	Leucyl-prolyl aminopeptidase	36	117374	5.5	4	1	3	1	3	0.04	0.04
CUL2_HUMAN	Cul-2	36	66927	6.45	3	1	3	1	3	0.09	0.05
SCAM1_HUMAN	Secretory carrier-associated membrane protein 1	35	37496	7.03	3	2	1	1	1	0.07	0.12
CDAL_HUMAN	Endonuclease	35	88027	5.18	2	2	2	1	2	0.05	0.11
UBAL3_HUMAN	NECD1-motif containing E1 catalytic subunit	35	51819	5.3	1	1	1	1	1	0.05	0.08
MOG1_HUMAN	Eukaryotic translation elongation factor 1 epsilon-1	35	19198	8.54	2	1	3	1	3	0.14	0.23
PTER_HUMAN	Phosphotransferase-related protein	35	38993	6.07	1	1	1	1	1	0.06	0.11
CHCH2_HUMAN	Cofactor coiled-coil coiled-coil helix domain-containing protein 2	35	15503	8.43	1	1	1	1	1	0.19	0.3
CBR1_HUMAN	CBR1 anion	35	18836	4.58	1	1	1	1	1	0.17	0.24
EPF3_HUMAN	Eukaryotic translation initiation factor 3 subunit J	35	28045	4.72	3	1	3	1	3	0.21	0.15
WTF1_HUMAN	Wntless	35	100227	8.24	3	1	3	1	3	0.06	0.04
TXD12_HUMAN	Threonine domain-containing protein 12	35	19194	5.24	2	1	2	1	2	0.31	0.24
ITD3_HUMAN	Inter-tubulin domain-containing protein 12	35	106397	6.14	9	1	7	1	7	0.14	0.04
ELARG_HUMAN	Elargin-5	34	13125	6.13	2	2	4	2	4	0.37	0.37
CHB1_HUMAN	Cytochrome b5 hemoproteinase homolog	34	28030	6.71	6	2	4	2	4	0.33	0.34
SOPR_HUMAN	Sulfate sulfonate oxidoreductase, mitochondrial	34	46929	9.18	4	2	3	2	3	0.11	0.09
E2B1_HUMAN	Translation initiation factor eIF-2B subunit alpha	34	33691	6.9	4	1	3	1	3	0.22	0.13
SPR2A_HUMAN	Signal peptide esterase-like 2A	34	58104	8.65	1	1	1	1	1	0.02	0.07
SRX1L_HUMAN	Serine racemase-1B	34	68551	5.44	2	1	2	1	2	0.07	0.06
REB2A_HUMAN	Rac-related protein Rab-22A	34	21841	8.32	2	1	2	1	2	0.15	0.21
UBP1L_HUMAN	Ubiquitin-conjugating enzyme E2 R1	34	26720	4.41	2	1	1	1	1	0.12	0.17
SOSTL1_HUMAN	Sost-like domain-containing protein 1	34	47557	5.1	6	2	8	2	8	0.38	0.19
ACBP_HUMAN	Arg-Arg-Arg-binding protein	34	10038	6.12	4	2	3	2	3	0.51	1.25
ERS1_HUMAN	ERp57-binding protein ERp57	34	68486	9.37	4	1	4	1	4	0.1	0.06
SARI1_HUMAN	GTP-binding protein SARI1b	34	22396	5.76	7	2	6	2	5	0.46	0.45
UBXK1_HUMAN	UBX domain-containing protein 4	34	96743	6.1	4	3	3	2	3	0.15	0.16
SPYK1_HUMAN	Sideroflexin-2	34	35481	9.28	6	1	4	1	4	0.24	0.12
MOST2_HUMAN	Microsomal diacylglycerol S-transferase 3	34	16906	9.46	6	4	2	2	2	0.32	1.1
TBR1L1_HUMAN	Thyroid receptor-interacting protein 13	33	22447	5.18	15	13	13	1	13	0.12	0.02
ATP1Q1_HUMAN	ATP synthase subunit gamma, mitochondrial	33	32975	9.23	3	1	3	1	3	0.17	0.13
SGT1_HUMAN	Protein SGT1 homolog	33	40998	5.07	3	1	3	1	3	0.15	0.11
BOLA2_HUMAN	Bola-like protein 2	33	10110	6.07	4	1	3	1	3	0.31	0.48
ORX1_HUMAN	Ox1-like protein	33	33756	6.26	3	1	1	1	1	0.06	0.13
STX17_HUMAN	Syntaxin 17	33	33383	6.14	3	1	2	1	2	0.15	0.13
PDZL2_HUMAN	PDZ and LIM domain protein 2	33	37436	9	2	2	1	1	1	0.06	0.12
APBL_HUMAN	Anchored protein B-100	33	515283	8.58	13	2	11	2	10	0.05	0.02
APOL2_HUMAN	Apolipoprotein L2	33	37698	6.29	2	1	2	1	2	0.12	0.12
SYMC1_HUMAN	Methionine-S-adenosyltransferase, cytosolic	33	101052	5.82	7	1	1	1	1	0.14	0.04
SRX1_HUMAN	Serine racemase-1	33	52868	7.07	1	1	1	1	1	0.03	0.08
CDRL1_HUMAN	Cerebellar degeneration-related protein 2-like	33	52978	5.7	2	1	2	1	2	0.08	0.08
HYEP_HUMAN	Exonin hydroxylase 1	33	53915	8.77	7	2	5	2	5	0.24	0.17
ILF3_HUMAN	Interleukin enhancer-binding factor 3	32	95278	8.86	3	2	3	2	3	0.07	0.04
TBCE1_HUMAN	Tubulin-specific chaperone cofactor E-like protein	32	48164	5.23	2	1	1	1	1	0.06	0.09
OCORL_HUMAN	Cofactor-like domain-containing protein 6	32	53556	6.07	9	2	4	1	4	0.16	0.08
MOGL_HUMAN	Mannosyl-glucosyltransferase	32	91861	8.97	5	2	5	2	5	0.14	0.1
CORR1_HUMAN	Coronin-1B	32	34200	5.81	6	2	5	2	5	0.26	0.17
WDR5L_HUMAN	WD repeat-containing protein 26	32	72078	5.74	2	1	2	1	2	0.06	0.04
TM165_HUMAN	Transmembrane protein 165	32	34683	6.54	1	1	1	1	1	0.06	0.13
DCT1_HUMAN	DnaJ homolog subfamily C member 10	32	91021	6.78	6	1	6	1	6	0.14	0.05
SRP98_HUMAN	Signal recognition particle subunit SRP98	32	70686	8.75	7	1	4	1	4	0.1	0.06
ACAD12_HUMAN	Acyl-CoA dehydrogenase family member 9, mitochondrial	32	68717	8.16	2	1	2	1	2	0.07	0.06
ACPL1_HUMAN	Acyl-CoA oxidase-like oxidizing enzyme	32	81173	5.29	5	1	5	1	5	0.17	0.05
GGK3L_HUMAN	Glucagon synthase kinase-3 beta	31	46715	8.88	3	2	2	1	2	0.13	0.09
APPL1_HUMAN	Apoptosis inhibitor 5	31	58968	6.99	2	1	2	1	2	0.08	0.07
ACOX2_HUMAN	Cytosolic acyl-CoA oxidase	31	98337	6.23	6	3	2	2	2	0.06	0.09
BDNF_HUMAN	Brain-derived neurotrophic factor	31	49132	6.26	6	1	5	1	4	0.23	0.08
END1L_HUMAN	Endonuclease domain-containing 1 protein	31	54981	5.55	3	1	2	1	2	0.12	0.08
PDCL1_HUMAN	Phosphatidylethanolamine-binding protein 3	31	27597	4.78	3	1	3	1	3	0.26	0.16
PDCL2_HUMAN	PTB-containing, coiled-coil and LIM1-interacting protein	31	28353	6.23	9	1	4	1	4	0.24	0.16
MALD1_HUMAN	MARVEL domain-containing protein 1	31	18902	9.69	1	1	1	1	1	0.17	0.24
KDEL2_HUMAN	KDEL motif-containing protein 2	31	58535	8.42	4	1	4	1	4	0.11	0.07
FUBP1_HUMAN	For upstream element-binding protein 1	31	67518	7.18	6	1	6	1	6	0.15	0.06
MOCS2_HUMAN	Molybdenum cofactor sulfurylase	31	88058	6.23	2	2	1	1	1	0.03	0.04
PTPE1_HUMAN	Protein-tyrosine phosphatase 2, mitochondrial	31	19181	8.85	3	1	2	1	2	0.16	0.24
PRD1_HUMAN	Protein-tyrosine phosphatase 1, mitochondrial	31	17317	5.93	2	1	2	1	2	0.31	0.27
SPD1_HUMAN	Serine palmitoyltransferase 1	31	52710	5.72	4	1	4	1	4	0.14	0.08
FUBP3_HUMAN	For upstream element-binding protein 3	31	61002	8.8	5	3	3	2	3	0.12	0.15

^aProtein score is calculated from the score of the peptide attributed to the protein.

^bpI is (Predicted) isoelectric point.

^cNumber of matches is spectrum number matched to protein^h.

^dNumber of significant matches is spectrum number that matches protein and exceeds the identification criteria.

^eNumber of sequences is number of peptides matched to protein^h.

^fNumber of significant sequences is number of peptides exceeding the identification criteria matched to proteins.

^gNumber of unique sequences is a unique^h number of peptides matched to proteins.

^hSequence coverage is the ratio of the total number of matched peptide residues to the total length of the protein.

ⁱExponentially Modified Protein Abundance Index (http://www.matrixscience.com/help/quant_empai_help.html).

Table S2, Cont 11.

UniProt/Swiss- PROT ID	Description	Protein score ^a	Protein mass (kDa)	pI ^b	Num, of matches ^c	Num, of significant matches ^d	Num, of sequences ^e	Num, of significant sequences ^f	Num, of unique sequences ^g	Sequence coverage ^h	empAI ⁱ
TIM23L1_HUMAN	Transmembrane protein 214	30	7160	5.25	4	1	1	1	1	0.1	0.2
DHBI1_HUMAN	Estradiol 17-β-Hydroxysteroid oxidase 11	30	32915	9.2	4	1	4	1	4	0.18	0.13
TIM23L2_HUMAN	Putative mitochondrial import inner membrane translocase subunit Tim23B	30	28030	9.47	2	1	2	1	2	0.21	0.16
TIM22_HUMAN	Translocase between the protein 2	30	48760	8.55	3	1	2	1	2	0.08	0.09
TXIP1_HUMAN	Tricarbaldehyde transport protein, mitochondrial	30	33991	9.91	8	2	4	1	4	0.2	0.28
PHB2_HUMAN	GTP-binding protein Phb2	30	20480	5.85	2	2	1	1	1	0.14	0.22
SCD16A_HUMAN	Protein transport protein SCD16A	30	23373	5.4	5	1	4	1	4	0.05	0.02
TBCD2_HUMAN	Tubulin-specific chaperone D	30	122515	5.8	2	1	1	1	1	0.02	0.03
NUE1A_HUMAN	Nuclear pore complex protein Nue1A	29	213468	7.55	4	1	3	1	3	0.02	0.02
QLIP1_HUMAN	Qlms pathogenesis-related protein 1	29	30346	8.8	1	1	1	1	1	0.09	0.15
DHRS1_HUMAN	Dehydrogenase 1, reductase SDR family member 1	29	33887	6.01	2	2	1	1	1	0.06	0.13
KPCA_HUMAN	Protein kinase C-α-like type 1	29	76700	6.61	3	1	3	1	3	0.1	0.06
RNAS2_HUMAN	Rna-related protein Rcras2	29	23385	5.74	4	1	3	1	3	0.25	0.19
MBRL1_HUMAN	Muscleblind-like protein 1	29	41780	5.16	2	1	2	1	2	0.13	0.1
ERAP1_HUMAN	Endoplasmic reticulum aminopeptidase 1	29	107168	6.02	4	1	3	1	3	0.08	0.04
ACOT1_HUMAN	Acyl-CoA:oxoacyl-Ac-Hydroxylase 13	29	14951	9.23	1	1	1	1	1	0.13	0.21
TREML1_HUMAN	Tumor necrosis factor-α-like-induced protein 3-like protein 3	29	35639	6.75	3	1	2	1	2	0.15	0.14
EMUL_HUMAN	Emerin	29	28978	5.29	3	2	3	2	3	0.24	0.33
LAMB1_HUMAN	Lamin B subunit beta-1	29	187069	4.83	15	2	11	2	11	0.15	0.04
ITMBP_HUMAN	Integral membrane protein 2B	29	30318	5	2	1	2	1	2	0.15	0.15
PURA_HUMAN	Phosphoribosylformylglycineamide synthase	29	144643	5.5	6	1	6	1	6	0.13	0.03
RAD2_HUMAN	RAD2 family molecule-chaperone regulator 2	29	23757	6.25	5	1	4	1	4	0.24	0.19
IAHL1_HUMAN	Isomyl acetate-hydroxylase esterase 1 homolog	29	27581	5.13	3	1	2	1	2	0.17	0.16
GCSF_HUMAN	G-CSF cleavage system H protein, mitochondrial	28	18873	4.81	2	1	2	1	2	0.29	0.24
MSL1_HUMAN	Mitochondrial lipase	28	32640	6.99	3	1	2	1	2	0.13	0.12
GOLPH_HUMAN	Gammaglutamyl hydrolase	28	35941	6.67	1	1	1	1	1	0.08	0.12
ARH1A_HUMAN	Arlylin repeat domain-containing protein 13A	28	17577	4.84	1	1	1	1	1	0.04	0.06
CSN8_HUMAN	COP9 signalosome complex subunit 8	28	23211	5.25	1	1	1	1	1	0.14	0.19
LPSX_HUMAN	Leucosin	28	43304	5.62	1	1	1	1	1	0.05	0.1
MACT1_HUMAN	Microtubule-actin cross-linking factor 1, isoform 1/2/3/5	28	83787	5.26	31	2	27	26	1	0.08	0.01
LMKD1_HUMAN	LM and cysteine-rich domain protein 1	28	40806	8.27	6	1	6	1	6	0.28	0.11
DPHVL1_HUMAN	2'-deoxyriboflavin 5'-phosphate 1-phosphatase 1	28	10097	4.67	3	3	3	3	3	0.26	0.21
DUC1_HUMAN	DnaJ homolog subfamily C member 11	28	63239	8.04	7	1	4	1	4	0.13	0.07
PTCD3_HUMAN	Pentatricopeptide repeat domain-containing protein 3, mitochondrial	28	78500	6	4	1	3	1	3	0.07	0.05
ZFYVL1_HUMAN	Zinc finger FYVE domain-containing protein 1	28	81729	7.29	1	1	1	1	1	0.17	0.24
COG2_HUMAN	Conserved oligomeric Golgi complex subunit 3	27	94038	5.39	2	1	2	1	2	0.07	0.05
KOL1A_HUMAN	Camptothecin	27	21712	6.12	2	2	2	2	2	0.12	0.48
EMAL1_HUMAN	Echinoderm microtubule-associated protein-like 4	27	10848	5.96	3	1	3	1	3	0.08	0.04
CSN1_HUMAN	COP9 signalosome complex subunit 1	27	55501	6.3	5	2	3	2	3	0.12	0.16
FADD_HUMAN	FAS-associated death domain protein	27	31935	5.48	3	1	4	1	4	0.12	0.19
MA3B1_HUMAN	Lysosomal alpha-mannosidase	27	113672	6.84	9	2	7	2	7	0.14	0.08
DOX33_HUMAN	Probable ATP-dependent RNA helicase DOX33	27	156331	6.23	7	1	6	1	6	0.11	0.04
SRR1_HUMAN	Signal recognition particle 14 kDa protein	27	14561	10.05	1	1	1	1	1	0.46	0.32
VP33A_HUMAN	Vacuolar protein sorting-associated protein 33A	27	67568	6.5	4	2	3	1	3	0.08	0.06
CLND2_HUMAN	Clatrin	26	47592	5.93	1	1	1	1	1	0.05	0.09
GMPR2_HUMAN	GMP reductase 2	26	37850	6.79	5	1	4	1	4	0.21	0.12
PUS2_HUMAN	Phosphatidyl seramitase 3	26	31626	6.22	2	1	2	1	2	0.19	0.14
POC2L_HUMAN	Protein POC2L C-terminal domain enhancer 1	26	17942	7.41	2	2	2	2	2	0.12	0.19
MUC12_HUMAN	Cell surface glycoprotein MUC12	26	71563	5.58	4	1	4	1	4	0.13	0.06
YELC1_HUMAN	Tyrosine phosphatase Yelc1	26	60763	6.22	5	1	4	1	4	0.12	0.07
HDA6L_HUMAN	Histone deacetylase 6	26	131338	5.14	1	1	1	1	1	0.02	0.03
PHM2_HUMAN	Phosphomannomutase 2	26	26064	6.35	4	1	2	1	2	0.1	0.16
DIST1_HUMAN	Dystonin	26	860127	5.14	30	2	27	2	27	0.07	0.01
GQR1_HUMAN	Oxycytochrome b-co1 complex subunit 1, mitochondrial	26	52612	5.94	6	1	5	1	5	0.19	0.08
DOX5_HUMAN	Probable ATP-dependent RNA helicase DOX5	26	69106	5.96	7	2	5	2	4	0.14	0.13
DAB2_HUMAN	Dab2-related protein 2	26	6230	5.34	3	1	2	1	2	0.08	0.05
HSD12L_HUMAN	Hydroxysteroid dehydrogenase-like protein 2	26	45386	6.07	7	1	6	1	6	0.26	0.1
TRITVL_HUMAN	Tryptic acid neutralizing factor protein 10-like protein	25	40280	5.86	1	1	1	1	1	0.07	0.11
F12R2_HUMAN	Protein FAM122B	25	26811	5.88	1	1	1	1	1	0.09	0.17
FBN1_HUMAN	Fibrillin-1	25	310022	4.81	23	1	18	1	18	0.13	0.01
PSPL1_HUMAN	Proteinase associated protein 1	25	55825	6.41	1	1	1	1	1	0.06	0.08
GOGB1_HUMAN	Golgi subunit B member 1	25	375700	4.96	25	1	21	1	21	0.1	0.01
APBDC1_HUMAN	DNA GTP-binding domain protein APBDC1-3C	25	23811	7.52	2	1	2	1	2	0.16	0.2
SDP2_HUMAN	Stronal cell-derived factor 2	25	23011	6.83	3	2	2	1	2	0.26	0.2
COA1A_HUMAN	Collagen alpha1(VI) chain	25	73317	9.62	4	1	3	1	3	0.11	0.06
DHRS4_HUMAN	Dehydrogenase 1, reductase SDR family member 4	25	38510	6.81	3	1	3	1	3	0.15	0.1
PCFR1_HUMAN	Phorbol-12-myristate-13-acetate receptor beta	25	123889	4.88	6	1	5	1	4	0.08	0.03
TAL1_HUMAN	Nucleosome TAD-1 isoform p40	25	42038	7.68	1	1	1	1	1	0.1	0.1
OPN1_HUMAN	Avian osteon	25	33561	5.44	1	1	1	1	1	0.09	0.13
ATOX1_HUMAN	Copper transport protein ATOX1	24	7397	6.71	7	1	4	1	4	0.66	0.71
MCAT_HUMAN	Mitochondrial carnitine acyltransferase carrier protein	24	35922	6.48	3	1	3	1	3	0.09	0.04
MPPL1_HUMAN	Mitochondrial processing peptidase subunit beta	24	54331	6.38	6	1	4	1	4	0.17	0.08
RAD2A_HUMAN	RAD2 family molecule-chaperone regulator 2	24	26071	6.1	7	1	6	1	6	0.24	0.11
EPPL2_HUMAN	Ectopic P granule protein 5 homolog	24	292293	5.09	5	1	5	1	5	0.04	0.01
GPTCL1_HUMAN	Glycyl-L-proline oxidoreductase-like protein	24	42897	9.84	1	1	1	1	1	0.09	0.1
ADAS1_HUMAN	Adipocyte triglyceride lipase protein, peroxisomal	24	12685	5.99	2	1	2	1	2	0.08	0.06
MAP1S_HUMAN	Microtubule-associated protein 1S	24	112142	6.92	3	1	2	1	2	0.03	0.04
ABCD3_HUMAN	ATP-binding cassette subfamily D member 3	24	74026	5.41	6	1	4	1	4	0.12	0.06
MPRE1_HUMAN	Menin phosphatase RhoGAP-like protein	24	16461	5.88	8	1	8	1	8	0.14	0.08
DOX1_HUMAN	Deoxyribose deaminase	24	20003	7.49	1	1	1	1	1	0.1	0.23
ACOT11_HUMAN	Acyl-CoA:oxoacyl-Ac-Hydroxylase 11	23	42648	6.9	2	1	2	1	2	0.2	0.2
AIMP1_HUMAN	Aminoacyl-tRNA synthase complex-interacting multifunctional protein 1	23	34331	6.81	7	1	6	1	6	0.37	0.13
BICO2_HUMAN	Protein bicoid/D homolog 2	23	94476	5.35	5	1	4	1	4	0.08	0.05
MTCH2_HUMAN	Mitochondrial carrier homolog 2	23	33309	8.25	2	1	2	1	2	0.1	0.13
MAOM1_HUMAN	NAD-dependent male enzyme, mitochondrial	23	65402	7.53	6	1	6	1	6	0.27	0.07
PGSV1_HUMAN	P53 proteasome non-ATPase regulatory subunit 10	23	24412	5.71	8	1	4	1	4	0.24	0.18
PCAT2_HUMAN	Lysophosphatidylcholine acyltransferase 2	23	60169	6.14	4	1	3	1	3	0.06	0.07
RUG2A_HUMAN	U2 small nuclear ribonucleoprotein A'	23	26396	8.27	1	1	1	1	1	0.1	0.16
LTOR1_HUMAN	Regulator complex protein-LAMTOR1	23	17754	5.01	5	1	4	1	4	0.48	0.26
CYR11_HUMAN	Protein CYR11	23	41998	8.64	6	1	5	1	5	0.19	0.1
DHX29_HUMAN	ATP-dependent RNA helicase DHX29	22	155138	6.3	7	1	6	1	6	0.08	0.03
DC_HUMAN	DnaJ-like-binding enzyme	22	117802	6.11	1	1	1	1	1	0.02	0.04
PGH1_HUMAN	Prostaglandin G/H synthase 1	22	68642	6.81	3	1	3	1	3	0.1	0.06
NRE2_HUMAN	NAD(P)+-hydroxylase	22	31054	5.66	1	1	1	1	1	0.14	0.14
LOBP2_HUMAN	Gulonic-3-β-oxidizing protein	22	65289	5.13	2	1	1	1	1	0.03	0.07
SLC10A_HUMAN	Solute carrier family 10 member 5	22	100890	6.54	3	1	3	1	3	0.09	0.04
ELMO2_HUMAN	ELMO domain-containing protein 2	22	34938	6.11	9	1	6	1	6	0.31	0.13
RAGP1_HUMAN	Ran GTPase-activating protein 1	22	63502	4.83	4	1	4	1	4	0.11	0.07
NCCH1_HUMAN	Neurofilament cation hydrolase 1	22	45779	6.76	2	1	1	1	1	0.07	0.1
EDC4_HUMAN	Enhancer of rRNA-decapping protein 4	21	151597	5.05	5	1	5	1	5	0.09	0.03

^aProtein score is calculated from the score of the peptide attributed to the protein.

^bpI is (Predicted) isoelectric point.

^cNumber of matches is spectrum number matched to protein¹.

^dNumber of significant matches is spectrum number that matches protein and exceeds the identification criteria.

^eNumber of sequences is number of peptides matched to protein¹.

^fNumber of significant sequences is number of peptides exceeding the identification criteria matched to proteins.

^gNumber of unique sequences is a unique⁶ number of peptides matched to proteins.

^hSequence coverage is the ratio of the total number of matched peptide residues to the total length of the protein.

ⁱExponentially Modified Protein Abundance Index (http://www.matrixscience.com/help/quant_help.html).

Table S2, Cont 12.

UniProt/Swiss-PROT ID	Description	Protein score ^a	Protein mass (kDa)	pI ^b	Num, of matches ^c	Num, of significant matches ^d	Num, of sequences ^e	Num, of significant sequences ^f	Num, of unique sequences ^g	Sequence coverage ^h	emPAI ⁱ
PRR1L1_HUMAN	Proteinase	21	97305	5.28	1	1	1	1	1	0.1	0.06
MANF_HUMAN	Mesencephalic astrocyte-derived neurotrophic factor	21	20687	8.93	5	1	2	1	2	0.16	0.22
SGSH_HUMAN	Sirt3-sirtuin	21	34755	8.86	2	1	2	1	2	0.11	0.13
YDF3_HUMAN	Protein YDF3	20	38223	5.47	1	1	1	1	1	0.08	0.11
UBPL2_HUMAN	Ubiquitin-associated protein 2-like	20	114465	6.61	9	1	5	1	5	0.1	0.04
TWIST1_HUMAN	Twist-related protein 1	19	69390	9.1	2	1	2	1	2	0.08	0.08
PAWR_HUMAN	PRK4 apoptosis W171 regulator protein	19	36545	5.35	1	1	1	1	1	0.05	0.12
MCU_HUMAN	Calcium uniporter protein, mitochondrial	19	39842	8.83	4	1	3	1	3	0.16	0.11
SSS4_HUMAN	Saltin carrier family 25 member 46	19	46145	6.97	3	1	1	1	1	0.06	0.08
HGI1A_HUMAN	HGI domain family member 1A, mitochondrial	19	10136	9.79	1	1	1	1	1	0.24	0.49
CRP2_HUMAN	Crotonylpeptide G	19	91855	5.79	1	1	1	1	1	0.027	0.08
FNCL2_HUMAN	Fibrinogen type II domain-containing protein 3B	19	32903	5.64	7	1	7	1	7	0.1	0.03
VTG1A_HUMAN	Vacuolar protein sorting-associated protein, VTI1 homolog	18	33858	5.87	5	1	3	1	3	0.16	0.13
MAES1_HUMAN	Measles virus-associated protein RP (EB) family member 3	17	31982	5.23	2	1	2	1	2	0.11	0.14
DNARE1_HUMAN	ATP-dependent RNA polymerase DNARE1	15	16668	7.88	1	1	1	1	1	0.03	0.03

Table S3. Identification of endogenous proteins (Biological Process: growth) in hADSC; group CDM & DMEM.

Table S3. Identification of endogenous proteins (Biological Process: growth) in hADSC; group CDM & DMEM.

UniProt/SWISS- Alternate ID	Biological Process growth	emPAI ^a	
		CDM	DMEM
VIM	skeletal muscle tissue regeneration	588.33	1108.52
TUBB6	seed trichome elongation	488.41	682.32
IQGAP1	neuron projection extension	101.79	191.57
VCL	axon extension	47.63	161.43
ANXA1	myoblast migration involved in skeletal muscle regeneration	51.36	88.25
MAP1B	axon extension	20.55	139.91
ATP5A1	growth	44.83	92.56
MYL9	cell elongation involved in imaginal disc-derived wing morphogenesis	40.16	92.56
PSAP	prostate gland growth	38.29	55.96
CLIC4	multicellular organism growth	19.61	71.03
GNAI2	multicellular organism growth	26.15	55.96
GNAS	developmental growth, multicellular organism growth	1.87	17.22
ITGB1	axon extension	24.28	55.96
MAPK1	endochondral bone growth	22.41	34.44
RAB10	pollen tube growth	15.88	64.57
ATP6V1A	imaginal disc growth	10.27	66.73
TNC	bud outgrowth involved in lung branching	5.60	75.34
ITGAV	cell growth	3.74	43.05
EIF4H	developmental growth	14.94	21.52
MTPN	cell growth, skeletal muscle tissue regeneration	18.68	10.76
POSTN	bone regeneration, neuron projection extension	14.01	23.68
SLC3A2	cell growth	1.87	43.05
PAK2	budding cell apical bud growth	12.14	10.76
SEC61A1	cell growth	14.94	10.76
CDC42	multicellular organism growth	10.27	17.22
CPNE1	neuron projection extension	12.14	10.76
GPX1	skeletal muscle tissue regeneration	3.74	12.91
PTK7	axis elongation	0.93	21.52
TRIM28	convergent extension involved in axis elongation	6.54	10.76
TMED2	multicellular organism growth	4.67	12.91
PRKAR1A	cardiac muscle cell proliferation	5.60	10.76

^aExponentially Modified Protein Abundance Index (http://www.matrixscience.com/help/quant_empai_help.html).

Table S4. Identification of endogenous proteins (Molecular Function: antioxidant activity) in hADSC; group CDM & DMEM.

Table S4. Identification of endogenous proteins (Molecular Function: antioxidant activity) in hADSC; group CDM & DMEM.

UniProt/SWISS- Alternate ID	Molecular Function antioxidant activity	emPAI ^a	
		CDM	DMEM
ALB	antioxidant activity	698.52	47.35
GSTP1	glutathione peroxidase activity	58.83	124.84
PRDX6	antioxidant activity, glutathione peroxidase activity, peroxidase activity, peroxiredoxin activity	48.56	64.57
PARK7	peroxiredoxin activity	30.82	51.66
PRDX1	peroxidase activity, peroxiredoxin activity, thioredoxin peroxidase activity	38.29	60.27
GSTO1	glutathione dehydrogenase (ascorbate) activity	26.15	30.13
PRDX4	antioxidant activity, peroxidase activity, peroxiredoxin activity, thioredoxin peroxidase activity	20.55	60.27
PRDX5	peroxidase activity, peroxynitrite reductase activity, thioredoxin peroxidase activity	14.01	49.51
TXNRD1	thioredoxin-disulfide reductase activity	2.80	66.73
PRDX2	antioxidant activity, peroxidase activity, peroxiredoxin activity, thioredoxin peroxidase activity	11.21	19.37
TXNDC17	peroxidase activity	5.60	21.52
GSTK1	glutathione peroxidase activity	6.54	15.07
PRDX3	peroxidase activity, peroxiredoxin activity, thioredoxin peroxidase activity	7.47	12.91
MGST1	glutathione peroxidase activity	8.40	10.76
GPX1	glutathione peroxidase activity	3.74	12.91
SOD1	superoxide dismutase activity	4.67	15.07

^aExponentially Modified Protein Abundance Index (http://www.matrixscience.com/help/quant_empai_help.html).

Table S5. Identification of endogenous proteins (Biological Process: immune system process) in hADSC; group CDM & DMEM.

UniProt/Swiss-Prot		Biological Process		empAI ²	
Accession ID		Immune system process		CDM	DMEM
TUBB8	natural killer cell mediated cytotoxicity			488.41	882.32
TUBB8	natural killer cell mediated cytotoxicity			384.44	388.89
TUBB8B	natural killer cell mediated cytotoxicity			388.89	388.89
MYH9	establishment of T cell polarity, leukocyte migration, monocyte differentiation, platelet formation			586.70	951.89
HSP90A1	IFN-gamma receptor signaling pathway involved in phagocytosis, toll-like receptor signaling pathway			439.85	454.16
HSP90A1	toll-like receptor signaling pathway			97.79	159.21
HSP90AA1	IFN-gamma receptor signaling pathway involved in phagocytosis			229.73	165.74
ACTN4	platelet formation			135.41	514.44
ACTN1	platelet formation			166.00	179.22
CLTC	antigen processing and presentation of exogenous peptide antigen via MHC class II			163.42	243.22
EEF2	hematopoietic progenitor cell differentiation			162.49	189.42
ANKK2	leukocyte development			116.73	271.25
LGALS1	T cell costimulation, plasma cell differentiation			118.68	180.81
PN1	leukocyte migration			97.12	281.64
DYNCH1H	antigen processing and presentation of exogenous peptide antigen via MHC class II			193.66	513.33
COL1A1	leukocyte migration			76.88	226.00
CAAR	antigen processing and presentation of peptide antigen via MHC class I, peptide antigen assembly with MHC class I protein complex			118.80	128.64
PCNA2	antigen processing and presentation of peptide antigen via MHC class I			84.98	142.88
THB1	immune response			82.18	148.82
MEK	leukocyte migration			68.03	139.91
HSPD1	B cell cytokine production, B cell proliferation, MyD88-dependent toll-like receptor signaling pathway, T cell activation, isotype switching to IgG isotypes			79.38	81.78
ARF4	antigen processing and presentation of exogenous peptide antigen via MHC class II			79.38	80.27
ARF1	antigen processing and presentation of exogenous peptide antigen via MHC class II			46.89	23.68
CTSD	antigen processing and presentation of exogenous peptide antigen via MHC class II			45.16	103.22
ANKK1	adaptive immune response, alpha-beta T cell differentiation, granulocyte chemotaxis, innate immune response, monocyte chemotaxis, neutrophil clearance, neutrophil homeostasis			91.36	98.29
COL1A2	leukocyte migration			39.82	116.39
STAT1	defense response to virus, interferon-gamma-mediated signaling pathway, type I interferon signaling pathway			56.97	64.07
IFNG	cellular response to interferon-gamma			21.75	73.18
CTSB	toll-like receptor signaling pathway			42.02	49.90
ACTR3	IFN-gamma receptor signaling pathway involved in phagocytosis			21.75	58.12
PRDC2	B cell lineage commitment, T cell differentiation in thymus, T cell lineage commitment, T cell receptor V(D)J recombination, V(D)J recombination, immunoglobulin V(D)J recombination, immunoglobulin production, pro-B cell differentiation, spleen development, thymus development			41.36	154.51
HSPA9	erythrocyte differentiation			25.95	68.81
CANX	antigen processing and presentation of exogenous peptide antigen via MHC class II, antigen processing and presentation of peptide antigen via MHC class I			38.82	83.01
DP1	erythrocyte homeostasis, humoral immune response			41.00	69.86
NRCC5	hematopoietic stem cell differentiation			34.05	43.05
PRDX1	erythrocyte homeostasis, natural killer cell mediated cytotoxicity			38.29	66.27
EPD1	erythrocyte maturation			24.28	60.27
PEMD2	T cell receptor signaling pathway, antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent, stimulatory C-type lectin receptor signaling pathway			26.16	56.12
PEMD1	T cell receptor signaling pathway, antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent, stimulatory C-type lectin receptor signaling pathway			24.28	66.27
ITGB1	B cell differentiation, leukocyte tethering or rolling			41.36	154.51
MAKP1	B cell receptor signaling pathway, IFN-gamma receptor signaling pathway involved in phagocytosis, T cell receptor signaling pathway, embryonic hematopoiesis, innate immune response, macrophage chemotaxis, microglia differentiation, monocyte chemotaxis, osteoclast development, thymus			22.41	24.44
MAKP3	IFN-gamma receptor signaling pathway involved in phagocytosis, thymus development			5.88	16.78
RAE15	antigen processing and presentation			15.88	24.44
RAE15	antigen processing and presentation			5.88	12.91
ACTR2	IFN-gamma receptor signaling pathway involved in phagocytosis			20.88	40.98
ARPC2	IFN-gamma receptor signaling pathway involved in phagocytosis			25.21	45.20
IRF	innate immune response, leukocyte migration			21.75	36.13
AP2A1	antigen processing and presentation of exogenous peptide antigen via MHC class II			11.21	66.73
AP2A2	antigen processing and presentation of exogenous peptide antigen via MHC class II			4.87	27.88
SEC11A	antigen processing and presentation of exogenous peptide antigen via MHC class I, antigen processing and presentation of peptide antigen via MHC class I			41.36	154.51
APF1B1	antigen processing and presentation of exogenous peptide antigen via MHC class II			20.88	62.42
DOOST	T cell activation			21.48	36.89
IRF7	hemopoiesis			26.16	37.88
DYNCH2	antigen processing and presentation of exogenous peptide antigen via MHC class II			26.16	23.68
IPD7	innate immune response			18.88	36.89
CTSK	toll-like receptor signaling pathway			26.16	12.91
SLC1	leukocyte migration			14.01	36.59
MYO1C	IFN-gamma receptor signaling pathway involved in phagocytosis			17.74	46.90
ACTR1A	antigen processing and presentation of exogenous peptide antigen via MHC class II			16.88	24.44
PSMA4	T cell receptor signaling pathway, antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent, stimulatory C-type lectin receptor signaling pathway			15.88	26.74
ARPC18	IFN-gamma receptor signaling pathway involved in phagocytosis			15.88	36.74
ICBP2	adaptive immune response, complement activation, classical pathway, innate immune response			15.88	25.62
RAE15C	antigen processing and presentation			5.34	43.88
POM3	hemopoiesis			8.34	36.59
DOXK1	innate immune response			18.88	29.88
PSME2	T cell receptor signaling pathway, antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent, stimulatory C-type lectin receptor signaling pathway			26.16	12.91
PCBP2	defense response to virus, innate immune response			26.21	34.44
PEMC4	T cell receptor signaling pathway, antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent, stimulatory C-type lectin receptor signaling pathway			15.07	25.62
ITGB1	antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent, stimulatory C-type lectin receptor signaling pathway			5.74	42.85
APF1B1	antigen processing and presentation of exogenous peptide antigen via MHC class II			16.88	23.68
PEMA7	T cell receptor signaling pathway, antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent, stimulatory C-type lectin receptor signaling pathway			14.94	19.27
PEMD1	T cell receptor signaling pathway, antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent, stimulatory C-type lectin receptor signaling pathway			15.07	25.62
CAPZ1	innate immune response			15.88	23.68
PSMA8	antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent, stimulatory C-type lectin receptor signaling pathway			11.21	23.68
RAE17A	antigen processing and presentation of exogenous peptide antigen via MHC class II			21.47	32.28
SLC3A2	leukocyte migration			1.97	43.05
PRKACA	stimulatory C-type lectin receptor signaling pathway			8.40	19.27
PRKACB	stimulatory C-type lectin receptor signaling pathway			15.07	15.07
PEMB2	T cell receptor signaling pathway, antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent, stimulatory C-type lectin receptor signaling pathway			15.07	15.07
SEC13	antigen processing and presentation of exogenous peptide antigen via MHC class II, antigen processing and presentation of peptide antigen via MHC class I			8.54	27.88
UREY1	T cell receptor signaling pathway, nucleotide-binding oligomerization domain containing signaling pathway, stimulatory C-type lectin receptor signaling pathway			6.34	23.68
PAF1A	T cell activation			19.27	21.82
ARPC4	IFN-gamma receptor signaling pathway involved in phagocytosis			19.27	17.22
DCN1	antigen processing and presentation of exogenous peptide antigen via MHC class II			9.34	23.68
SHMT2	response to type I interferon			21.27	21.82
PAK2	T cell costimulation, T cell receptor signaling pathway, stimulatory C-type lectin receptor signaling pathway			12.14	16.78
PEMC3	T cell receptor signaling pathway, antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent, stimulatory C-type lectin receptor signaling pathway			3.74	36.89
SEC14D	antigen processing and presentation of exogenous peptide antigen via MHC class II, antigen processing and presentation of peptide antigen via MHC class I			4.14	23.68
PSMA5	T cell receptor signaling pathway, antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent, stimulatory C-type lectin receptor signaling pathway			8.93	37.88
CD109	reticulocytosis			19.07	12.91
PEMD14	T cell receptor signaling pathway, antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent, stimulatory C-type lectin receptor signaling pathway			12.14	16.78
SEC1A1	response to interferon-gamma			14.94	16.78
ANCY	chronic inflammatory response to antigenic stimulus			12.14	19.27
PSMB8	T cell receptor signaling pathway, antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent, stimulatory C-type lectin receptor signaling pathway			6.54	27.88
PRCALM	hemopoiesis			5.88	23.68
APF1B1	antigen processing and presentation of exogenous peptide antigen via MHC class II			8.40	12.91
ARPC2	IFN-gamma receptor signaling pathway involved in phagocytosis			1.46	19.27
PPF1R14B	innate immune response			15.88	2.15
PSMA2	T cell receptor signaling pathway, antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent, stimulatory C-type lectin receptor signaling pathway			14.94	8.61
PSMA4	T cell receptor signaling pathway, antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent, stimulatory C-type lectin receptor signaling pathway			7.47	17.22
Exponentially Modified Protein Abundance Index (http://www.matrixscience.com/help/empai_help.html).					

UniProt/Swiss-Prot		Biological Process		empAI ²	
Accession ID		Immune system process		CDM	DMEM
PEMD12	T cell receptor signaling pathway, antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent, stimulatory C-type lectin receptor signaling pathway			15.07	12.91
PEMC2	T cell receptor signaling pathway, antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent, stimulatory C-type lectin receptor signaling pathway			7.47	25.68
CD042	IFN-gamma receptor signaling pathway involved in phagocytosis, T cell costimulation, dendritic cell migration, macrophage differentiation			19.27	17.22
DPN4	T cell activation, T cell costimulation			8.93	36.89
CAPZ2	innate immune response			7.47	36.13
PAFAH1B1	reticulocytosis development			9.34	12.91
IRF7	immune response			4.87	27.88
PSMC1	T cell receptor signaling pathway, antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent, stimulatory C-type lectin receptor signaling pathway			7.47	17.22
PEMB3	T cell receptor signaling pathway, antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent, stimulatory C-type lectin receptor signaling pathway			8.40	17.22
IRF17	erythrocyte homeostasis			8.40	19.27
URE2N	T cell receptor signaling pathway, nucleotide-binding oligomerization domain containing signaling pathway, stimulatory C-type lectin receptor signaling pathway			9.34	15.07
BYNCRIP	cellular response to interferon-gamma			3.74	17.22
IRFDC2	lymphocyte proliferation			7.47	19.27
SLC1	reticulocytosis differentiation			9.34	6.41
PEMB8	T cell receptor signaling pathway, antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent, stimulatory C-type lectin receptor signaling pathway			8.40	15.07
PEMD7	T cell receptor signaling pathway, antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent, stimulatory C-type lectin receptor signaling pathway			4.87	19.27
PPF1A	T cell activation			1.87	17.22
PEMB1	T cell receptor signaling pathway, antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent, stimulatory C-type lectin receptor signaling pathway			6.54	17.22
PEMB7	T cell receptor signaling pathway, antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent, stimulatory C-type lectin receptor signaling pathway			9.34	12.91
PEMC6	T cell receptor signaling pathway, antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent, stimulatory C-type lectin receptor signaling pathway			7.47	16.78
ITGB5	antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent, stimulatory C-type lectin receptor signaling pathway			3.74	23.68
OTUB1	adaptive immune response			6.54	12.91
IRF12	alpha-beta T cell differentiation			8.40	12.91
STAT2	defense response to virus, type I interferon signaling pathway			7.47	6.46
ENPP1	immune response			6.54	12.91
PRDX3	myeloid cell differentiation			7.47	12.91
PEMC4	T cell receptor signaling pathway, antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent, stimulatory C-type lectin receptor signaling pathway			4.87	15.07
BKPI	T cell receptor signaling pathway, stimulatory C-type lectin receptor signaling pathway			3.74	21.82
APF1B1	antigen processing and presentation, antigen processing and presentation, exogenous lipid antigen via MHC class II			4.87	12.91
CTP1	B cell proliferation, T cell proliferation			7.47	15.07
RAC1	IFN-gamma receptor signaling pathway involved in phagocytosis, T cell costimulation, mast cell chemotaxis			7.47	15.07
CTNNB1	cell differentiation, T cell differentiation in thymus, osteoclast differentiation, thymus development			9.93	21.82
PEMD11	T cell receptor signaling pathway, antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent, stimulatory C-type lectin receptor signaling pathway			3.74	15.07
PEMD12	T cell receptor signaling pathway, antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent, stimulatory C-type lectin receptor signaling pathway			3.74	12.91
TRIM28	innate immune response			6.54	16.78
DYLL1	antigen processing and presentation of exogenous peptide antigen via MHC class II			9.34	12.91
TRIM21	erythrocyte development			7.47	8.61
STOML2	CD4-positive, alpha-beta T cell activation, T cell receptor signaling pathway			3.74	12.91
PEMC5	T cell receptor signaling pathway, antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent, stimulatory C-type lectin receptor signaling pathway			7.47	6.46
DCN2	antigen processing and presentation of exogenous peptide antigen via MHC class II			1.87	21.82
PEME1	T cell receptor signaling pathway, antigen processing and presentation of exogenous antigen, antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent, stimulatory C-type lectin receptor signaling pathway			2.88	15.07
TRIOV2	immune system development			6.54	8.61
SCD1	reticulocytosis homeostasis, thymus development			4.87	15.07
LGALS3	endothelial chemotaxis, innate immune response, macrophage chemotaxis, monocyte chemotaxis, mononuclear cell migration, neutrophil chemotaxis			2.88	15.07
URE2D2	T cell receptor signaling pathway, TRF-dependent toll-like receptor signaling pathway, stimulatory C-type lectin receptor signaling pathway			8.40	4.31
ARPC1A	IFN-gamma receptor signaling pathway involved in phagocytosis			3.74	17.22
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Table S6. Identification of endogenous proteins (Biological Process: biological regulation) in hADSC; group CDM & DMEM.

UniProt/Swiss-Prot Accession ID	Biological Process biological regulation	enrPAP	
		CDM	DMEM
ACTA2	positive regulation of gene expression, regulation of blood pressure, vascular smooth muscle contraction	285.79	439.19
POTEE	retina homeostasis	245.54	200.79
SMO	SMAD protein signal transduction, negative regulation of neuron projection development, positive regulation of gene expression, positive regulation of glial cell proliferation, regulation of Schwann cell migration, regulation of axonogenesis	558.20	1109.55
MYH9	hemoglobin-mediated signaling pathway, negative regulation of actin filament polymerization, negative regulation of actin filament severing, platelet aggregation, positive regulation of protein processing in phagocytic vesicle, regulation of cell shape, regul	500.79	961.83
MYH10	regulation of cell shape	15.88	124.94
FLNA	adequate cytoskeleton-binding domain receptor signaling pathway, cytoskeletal sequestering of protein, negative regulation of apoptotic process, negative regulation of protein catabolic process, negative regulation of sequence-specific DNA binding transcri	521.19	824.68
HEP99AB1	ATP5-mediated unfolded protein response, ERBB2 signaling pathway, Fc-gamma receptor signaling pathway involved in phagocytosis, negative regulation of complement-dependent cytotoxicity, negative regulation of neuron apoptotic process, negative regulation o	439.93	452.18
HEP99B1	ATP5-mediated unfolded protein response, negative regulation of apoptotic process, regulation of phosphoenolpyruvate carboxykinase activity, sequestering of calcium ion, toll-like receptor signaling pathway	87.79	180.81
HEP99AB1	ERBB2 signaling pathway, Fc-gamma receptor signaling pathway involved in phagocytosis, positive regulation of cardiac muscle contraction, positive regulation of cell size, positive regulation of lamellipodium assembly, positive regulation of nitric oxide bi	200.79	165.74
ALB	hemolysis by symbol of host erythrocytes, maintenance of mitochondrion location, negative regulation of apoptotic process, negative regulation of programmed cell death, retina homeostasis	698.52	47.35
EEF1A1	calcium-mediated signaling, regulation of chaperone-mediated autophagy, regulation of transcription, DNA-templated	382.88	378.68
HEP99B1	ATP5-mediated unfolded protein response, ER overfold response, RE1-mediated unfolded protein response, PERK-mediated unfolded protein response, RNA interference, activation of signaling protein activity involved in unfolded protein response, endoplasmic r	503.80	589.94
HEP99A	maintenance of protein localization in endoplasmic reticulum, positive regulation of cell migration	132.61	247.86
HEP99A1	negative regulation of cell death, negative regulation of endoplasmic reticulum stress-induced intrinsic apoptotic signaling pathway, negative regulation of extrinsic apoptotic signaling pathway in absence of ligand, negative regulation of inclusion body a	15.88	61.84
HEP99A2	negative regulation of inclusion body assembly, positive regulation of calcium-transporting ATPase activity, positive regulation of cycle-dependent protein serine/threonine kinase activity involved in G2M transition of mitotic cell cycle, positive regulatio	19.81	38.99
TUBA1B	establishment or maintenance of cell polarity regulating cell shape	139.50	292.74
YWHAQ	negative regulation of ion transmembrane transport, negative regulation of transcription, DNA-templated, positive regulation of protein insertion into mitochondrial membrane involved in apoptotic signaling pathway, small GTPase mediated signal transduction	29.88	68.27
YWHAQ	negative regulation of protein kinase activity, negative regulation of protein serine/threonine kinase activity, positive regulation of protein insertion into mitochondrial membrane involved in apoptotic signaling pathway, regulation of neuron differentiation, regulation of signal transduction, regulation of synaptic plastic	38.82	47.35
YWHAQ2	hepatocellular carcinoma signal transduction, membrane repolarization during cardiac muscle cell action potential, negative regulation of cytoskeleton organization, negative regulation of cytoskeleton organization, negative regulation of cytoskeleton organization	42.98	51.68
YWHAH	glucocorticoid receptor signaling pathway, membrane depolarization during action potential, negative regulation of dendrite morphogenesis, positive regulation of protein insertion into mitochondrial membrane involved in apoptotic signaling pathway, positive	10.27	39.13
ENOF	negative regulation of cell growth, negative regulation of transcription, DNA-templated	284.94	273.38
ACTN4	MAPK cascade, filamentous cytoskeleton, cardiac conduction, cytoskeletal anchoring at plasma membrane, negative regulation of cellular component movement, negative regulation of heart rate, negative regulation of substrate adhesion-dependent cell spreading, peroxisome proliferator acti	136.41	914.44
ACTN1	negative regulation of cellular component movement, platelet aggregation, regulation of apoptotic process, regulation of nucleic acid-templated transcription	194.89	379.22
TLN1	RE1-mediated unfolded protein response, cytoskeletal anchoring at plasma membrane, platelet aggregation	131.67	374.82
TLN2	cytoskeletal anchoring at plasma membrane	7.47	25.69
CLTC	Wnt signaling pathway, planar cell polarity pathway, negative regulation of hyaluronan biosynthetic process, negative regulation of protein localization to plasma membrane, positive regulation of glucose import, regulation of mitotic spindle organization, si	163.42	243.23
CLTCL1	positive regulation of glucose import, signal transduction	20.59	30.13
PNB	cell redox homeostasis, positive regulation of viral entry into host cell, regulation of oxidative stress-induced intrinsic apoptotic signaling pathway	138.34	238.79
LDNA	positive regulation of apoptotic process	107.38	458.48
EEF2	positive regulation of cytoplasmic translation, positive regulation of translation	162.49	189.42
ALDOA	mitotic G2 DNA damage checkpoint, muscle cell cellular homeostasis, regulation of cell shape	116.73	272.20
PLEK	body fluid secretion, rheumatism, negative regulation of catalytic activity, negative regulation of low-density lipoprotein particle receptor catabolic process, negative regulation of receptor binding, negative regulation of receptor internalization, posi	103.19	279.92
ALX3	negative regulation of cell migration, negative regulation of epithelial cell proliferation, negative regulation of keratinocyte migration, negative regulation of keratinocyte proliferation, negative regulation of epithelium regeneration	92.19	282.12
LDALB1	T cell costimulation, cellular response to glucose stimulus, negative regulation of cell-substrate adhesion, negative regulation of neuron projection development, positive regulation of I-kappaB kinase/NF-kappaB signaling, positive regulation of dendritic cell differentiation, positive regulation of erythrocyte aggrega	118.80	180.81
PN1	cellular response to glucose stimulus, negative regulation of apoptotic process, negative regulation of transforming growth factor-beta secretion, positive regulation of axon extension, positive regulation of cell migration, positive regulation of chemotaxis, positive regulation o	97.29	251.68
COL4A3	positive regulation of endopeptidase activity, negative regulation of peptidase activity	126.07	180.81
COL1A1	blood coagulation, negative regulation of cell-substrate adhesion, platelet activation, positive regulation of canonical Wnt signaling pathway, positive regulation of cell migration, positive regulation of epithelial to mesenchymal transition, positive regulation of transcription, DNA-templated, regulation of immune respon	75.99	228.69
SCRNH1	negative regulation of endopeptidase activity	127.94	339.28
AKNAK	regulation of RNA splicing, regulation of voltage-gated calcium channel activity	93.38	459.48
IQGAP1	Aurp3 complex-mediated actin nucleation, ERK1 and ERK2 cascade, Ras protein signal transduction, activation of MAPK activity, epidermal growth factor receptor signaling pathway, fibroblast growth factor receptor signaling pathway, negative regulation of G	181.79	191.57
PASB	negative regulation of cellular metabolic process	130.74	36.88
PN1	Wnt signaling pathway, planar cell polarity pathway, negative regulation of actin filament polymerization, negative regulation of stress fiber assembly, positive regulation of ATPase activity, positive regulation of DNA metabolic process, positive regulatio	103.66	187.13
CALR	ATP5-mediated unfolded protein response, cell cycle arrest, cellular calcium ion homeostasis, glucocorticoid receptor signaling pathway, negative regulation of intracellular steroid hormone receptor signaling pathway, negative regulation of neuron differen	118.80	128.84
MARCKS	regulation of insulin secretion	88.72	178.85
ATP5B	negative regulation of cell adhesion involved in substrate-bound cell migration, regulation of intracellular pH	83.11	161.17
PDIA3	cell redox homeostasis, positive regulation of extrinsic apoptotic signaling pathway, protein retention in ER lumen, signal transduction	84.99	142.86
THBS1	activation of MAPK activity, cell cycle arrest, negative regulation of angiogenesis, negative regulation of antigen processing and presentation of peptide or polysaccharide antigen via MHC class II, negative regulation of blood vessel endothelial cell migration, negative regulation of GMP-mediated signaling, negative	82.18	148.82
CAP1	activation of cytoskeletal cytoskeleton, negative regulation of catalytic activity, signal transduction	127.94	124.84
VCP	activation of cytoskeleton endopeptidase activity involved in apoptotic process, endoplasmic reticulum unfolded protein response, positive regulation of ATP biosynthetic process, positive regulation of Lys63-specific deubiquitinase activity, positive regulation of mitochondrial membrane potential, positive regulatio	88.92	132.48
CRL1	Rho protein signaling, negative regulation of apoptotic process, positive regulation by host of viral process, regulation of dendritic spine morphogenesis	128.67	96.86
GSN	actin nucleation, barbed-end actin filament capping, negative regulation of viral entry into host cell, positive regulation of actin nucleation, positive regulation of cytoskeleton organization, negative regulation of sequestering of calcium ion, positive regulation of defense response to virus by	89.88	139.81
ANKK4	blood coagulation, homeostasis, negative regulation of apoptotic process, negative regulation of catalytic activity, negative regulation of coagulation, negative regulation of sequestering of calcium ion, positive regulation of defense response to virus by	79.87	189.28
MSN	actin filament anchoring, barbed-end actin filament capping, cytoskeletal anchoring at plasma membrane, negative regulation of ERK1 and ERK2 cascade, negative regulation of GTPase activity, negative regulation of T cell receptor signaling pathway, negative r	86.03	99.87
ZDR	cytoskeletal anchoring at plasma membrane, negative regulation of ERK1 and ERK2 cascade, negative regulation of T cell receptor signaling pathway, negative regulation of interleukin-2 secretion, negative regulation of p38MAPK cascade, positive regulation o	14.94	32.29
SDX	actin filament capping, barbed-end actin filament capping, negative regulation of GTPase activity, negative regulation of adherens junction organization, negative regulation of cell size, negative regulation of hemolysis, cell-cell adhesion, positive regulatio	12.14	65.43
ICL1	negative regulation of cell migration, platelet aggregation	47.83	161.43
HEPD1	MyD88-dependent toll-like receptor signaling pathway, activation of cytoskeleton endopeptidase activity involved in apoptotic process, negative regulation of apoptotic process, negative regulation of apoptotic process in bone marrow, negative regulation o	79.38	81.79
TAGLN2	negative regulation of transcription from RNA polymerase II promoter	65.11	89.81
ACLY	positive regulation of cellular metabolic process	70.97	105.47
SI048	positive regulation of fibroblast proliferation, signal transduction	181.79	12.91
SEPT1	negative regulation of ERK1 and ERK2 cascade, negative regulation of I-kappaB kinase/NF-kappaB signaling, negative regulation of JUN kinase activity, negative regulation of MAPK cascade, negative regulation of acute inflammatory response, negative regulation of apoptotic process, negative regulation of extrinsic	58.89	124.84
EPF4A1	negative regulation of RNA-directed 5'-5' RNA polymerase activity, negative regulation of exosty protein synthesis incorporation, negative regulation of telomerase insertion sequence binding, negative regulation of translation, nuclear-transcribed mRNA catabolic	79.97	85.10
EPF4A2	negative regulation of RNA-directed 5'-5' RNA polymerase activity, nuclear-transcribed mRNA poly(A) tail shortening, regulation of translational initiation	23.89	38.74
TK1	regulation of growth	70.94	80.99
ASFA	activation of phospholipase D activity, cellular copper ion homeostasis, epidermal growth factor receptor signaling pathway, long term synaptic depression, negative regulation of apoptotic process, positive regulation of ER to Golgi vesicle-mediated transp	79.38	89.27
ARF1	cellular copper ion homeostasis, long term synaptic depression, positive regulation of ER to Golgi vesicle-mediated transport, positive regulation of calcium ion-dependent exocytosis, positive regulation of catalytic activity, positive regulation of dendri	46.89	23.83
ARF3	small GTPase mediated signal transduction	40.16	17.22
ARF5	small GTPase mediated signal transduction	15.88	15.07
CAPN2	regulation of cytoskeleton organization	75.64	86.10
LRP1	negative regulation of Wnt signaling pathway, negative regulation of neuron apoptotic process, negative regulation of neuron projection development, negative regulation of platelet-derived growth factor receptor-beta signaling pathway, negative regulation	46.89	124.84
SI04A11	negative regulation of DNA replication, negative regulation of cell proliferation, regulation of cell proliferation, signal transduction	79.38	45.68
PGAM1	positive regulation of flagellated sperm motility, regulation of glycolytic process, regulation of pentose-phosphate shunt	60.79	73.18
PGAM4	positive regulation of flagellated sperm motility, regulation of pentose-phosphate shunt	32.69	15.87
HNR1	positive regulation of actin filament depolymerization, regulation of oligodendrocyte differentiation, regulation of ventricular cardiac muscle cell membrane repolarization	45.76	116.39
KPNE1	Ran protein signal transduction, modulation by virus of host process	89.77	79.84
ANKA1	O-protein coupled receptor signaling pathway, coupled to cyclic nucleotide second messenger, cell surface receptor signaling pathway, insulin secretion, negative regulation of T-helper 2 cell differentiation, negative regulation of apoptotic process, negative regulation of catalytic activity, negative regulation of exocy	81.38	88.25
EPFA	polyamine homeostasis, positive regulation of cell proliferation, positive regulation of translational elongation, positive regulation of translational termination	82.18	30.13
SEF2A	polyamine homeostasis, positive regulation of cell proliferation, positive regulation of translational elongation, positive regulation of translational termination	15.88	19.37
COL1A2	Rho protein signal transduction, blood coagulation, platelet activation, regulation of blood pressure, regulation of immune response, transforming growth factor beta receptor signaling pathway	58.82	116.39
MYOF	regulation of vascular endothelial growth factor receptor signaling pathway	37.05	111.93
PPB	positive regulation by host of viral genome replication, positive regulation of multicellular organism growth, protein stabilization, regulation of post-translational protein modification	48.49	77.48
STAT1	JAK-STAT cascade, activation of cytoskeleton endopeptidase activity involved in apoptotic process, interferon-gamma-mediated signaling pathway, negative regulation by virus of viral protein levels in host cell, negative regulation of I-kappaB kinase/NF-kappaB signaling, negative regulation of angiogenesis, negat	56.97	64.87
ANKA8	apoptotic signaling pathway, mitochondrial calcium ion homeostasis, regulation of muscle contraction	28.82	114.88
BAPI1B	induction of synaptic plasticity by chemical substance, negative regulation of intracellular transport, negative regulation of microtubule polymerization, positive regulatio	20.89	139.89
MYP	ERBB signaling pathway, negative regulation of protein autophosphorylation, negative regulation of protein tyrosine kinase activity, negative regulation of signaling	46.89	95.89
ATPSA1	lipid storage, negative regulation of endothelial cell proliferation, regulation of choline O-acetyltransferase activity	44.83	92.84
MYL3	myosin receptor signaling pathway, platelet aggregation, regulation of actin cytoskeleton organization, regulation of cell shape, regulation of muscle contraction, regulation of tube length, open tracheal system	46.76	92.88
MYL12B	regulation of cell shape	37.39	73.18
MYL12A	myosin receptor signaling pathway, platelet aggregation	31.76	73.18
JAR3	negative regulation of translational fidelity	45.76	89.28
TDR	activation of protein kinase B activity, cell redox homeostasis, negative regulation of hydrogen peroxide-induced cell death, negative regulation of protein export from nucleus, negative regulation of transcription from RNA polymerase II promoter, positive regulation of DNA binding, positive regulation of peptidyl-ase	51.38	73.84
RNH1	mRNA catabolic process, negative regulation of catalytic activity, regulation of angiogenesis	42.82	96.88
HEP9B1	intracellular signal transduction, negative regulation of apoptotic process, negative regulation of apoptotic signaling pathway, negative regulation of oxidative stress-induced intrinsic apoptotic signaling pathway, negative regulation of protein serine/threonine kinase activity, platelet aggregation, positive regulatio	42.82	94.71
CLC1	platelet aggregation, positive regulation of osteoblast differentiation, regulation of cell cycle, regulation of ion transmembrane transport, regulation of mitochondrial membrane potential, signal transduction	44.83	64.87
DPYSL2	positive regulation of glutamate secretion, regulation of axon extension, regulation of neuron differentiation, regulation of neuron projection development, signal transduction	42.82	129.15
BN01	gene silencing by RNA, regulation of transcription, DNA-templated	42.82	83.89
FLNB	cytoskeletal anchoring at plasma membrane, signal transduction	40.16	129.89
PRDX8	cell redox homeostasis	48.98	64.87
CC2	positive regulation of establishment of protein localization to telomere, positive regulation of protein localization to Cajal body, positive regulation of telomerase RNA localization to Cajal body, positive regulation of telomerase activity, positive regulat	34.55	89.25
PCN1	positive regulation of extracellular matrix disassembly, positive regulation of flagellum assembly, positive regulation of lamellipodium assembly, positive regulation of podosome assembly, regulation of actin cytoskeleton organization, regulation of microv	45.76	89.73

*Experimentally Modified Protein Abundance Index (http://www.matrixscience.com/help/quant_amp_help.htm).

Table S6. Cont 1

*Exponentially Modified Protein Abundance Index (http://www.matrixscience.com/help/quant_empai_help.html).

Table S8. Cont2

UniProt/Swiss-Prot Accession ID	Biological Process	log2(PAT)	
		CCM	DMEM
RP12A	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay	24.38	26.13
CTSK	bone resorption, positive regulation of protein targeting to mitochondrion, regulation of mitophagy, toll-like receptor signaling pathway	26.86	12.91
PRMT2	Wnt signaling pathway, integrin-mediated signaling pathway, regulation of cell shape, transforming growth factor beta receptor signaling pathway	13.07	49.91
DLG1	negative regulation of protein processing, negative regulation of transforming growth factor beta receptor signaling pathway, regulation of chondrocyte differentiation	14.91	26.89
MYO1C	Pc-gamma receptor signaling pathway involved in phagocytosis, positive regulation of actin filament polymerization, positive regulation of cell migration by vascular endothelial growth factor signaling pathway, positive	17.74	48.89
NR1E1	cellular response to glucose stimulus, negative regulation of cell proliferation, negative regulation of gene expression, negative regulation of myoblast substrate differentiation, positive regulation of DNA binding, positive regulation of epithelial cell proliferation, positive regulation of neuron projection development, negative regulation of transcription from RNA polymerase II promoter	16.98	26.99
PRDX3	cell redox homeostasis, negative regulation of apoptotic process, negative regulation of cytosolic-type endopeptidase activity involved in apoptotic process, negative regulation of endonuclease activity, negative regulation of transcription from RNA polymerase II promoter, positive regulation of collagen biosynthesis	14.91	49.91
RAP1B	Rap protein signal transduction, activation of MAPKK activity, cellular response to glucose stimulus, negative regulation of calcium ion-dependent exocytosis, negative regulation of collagen biosynthetic process, negative regulation of synaptic vesicle exocytosis, nerve	22.41	32.29
RAP1A	Rap protein signal transduction, activation of MAPKK activity, cellular response to glucose stimulus, negative regulation of collagen biosynthetic process, negative regulation of synaptic vesicle exocytosis, nerve growth factor signaling pathway, positive regulation of ERK1	16.91	25.91
IPF1EN1	MAPK cascade, SMAD protein import into nucleus, actin filament capping, common-partner SMAD protein phosphorylation, positive regulation of GTPase activity, positive regulation of interleukin-2 secretion, positive regulation of protein localization to plasma	14.94	39.74
RNMPF	negative regulation of blood pressure	26.86	21.52
APHCAP1	the protein signal transduction, positive regulation of GTPase activity, positive regulation of signal transduction, regulation of small GTPase mediated signal transduction, small GTPase mediated signal transduction	14.94	39.74
BPARC	negative regulation of angiogenesis, negative regulation of endothelial cell proliferation, positive regulation of endothelial cell migration, regulation of cell morphogenesis, regulation of cell proliferation, signal transduction	14.94	43.05
ATP1A1	cell communication by electrical coupling involved in cardiac conduction, cellular potassium ion homeostasis, cellular sodium ion homeostasis, membrane hyperpolarization, membrane repolarization during cardiac muscle cell action potential, negative regulation of transcription from RNA polymerase II promoter	28.21	17.22
APH2D2A	negative regulation of apoptotic process, negative regulation of angiogenesis, negative regulation of cell adhesion, positive regulation of GTPase activity, positive regulation of angiogenesis, regulation of Rho protein signal transduction, regulation of a	16.91	39.74
NAP1L1	positive regulation of cell proliferation	16.91	32.29
PTPRB	fibroblast growth factor receptor signaling pathway, negative regulation of mRNA splicing, via spliceosome, negative regulation of muscle cell differentiation, regulation of alternative mRNA splicing, via spliceosome	13.07	49.91
CCT3	positive regulation of protein localization to CagLI body, positive regulation of telomerase RNA localization to CagLI body, positive regulation of telomerase maintenance via telomerase, protein stabilization	16.91	39.74
ATP4VB2	insulin receptor signaling pathway, phagosome acidification, regulation of macroautophagy	11.21	49.91
VCAC2	negative regulation of intrinsic apoptotic signaling pathway, negative regulation of protein polymerization, regulation of antitumor transmembrane transport, regulation of neuron transport	6.54	58.12
PCBP1	positive regulation of transcription from RNA polymerase II promoter	26.86	49.91
RP33A	negative regulation of apoptotic process, nuclear-transcribed mRNA catabolic process, nonsense-mediated decay	6.54	43.05
TNMD1	cell redox homeostasis, signal transduction	2.89	68.73
ACM5	positive regulation of blood pressure	17.74	32.29
COMT	catecholamine metabolic process, negative regulation of dopamine metabolic process, negative regulation of renal sodium excretion, negative regulation of smooth muscle cell proliferation, neurotransmitter catabolic process, positive regulation of homocysteine metabolic process, regulation of sensory perception of pain	14.91	34.44
NME2	cellular response to glucose stimulus, integrin-mediated signaling pathway, negative regulation of apoptotic process, negative regulation of apoptotic process, negative regulation of cAMP biosynthetic process, positive regulation of epithelial cell proliferation, positive regulation of keratinocyte differentiation	48.76	26.89
PLD3	translocation	13.07	47.95
PSMA4	Pc-epithelial receptor signaling pathway, MAPK cascade, NIK/NF-kappaB signaling, T cell receptor signaling pathway, Wnt signaling pathway, planar cell polarity pathway, negative regulation of canonical Wnt signaling pathway, negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle, positive	15.88	39.74
SEIPINB8	negative regulation of endoplasmic reticulum stress	6.54	55.96
IL13RA4	active induction of host immune response by virus, negative regulation of mitochondrial outer membrane permeabilization involved in apoptotic signaling pathway, positive regulation of cell proliferation, regulation of insulin secretion	14.94	26.89
BLC5A4	negative regulation of mitochondrial outer membrane permeabilization involved in apoptotic signaling pathway, positive regulation of cell proliferation, regulation of insulin secretion	8.34	15.07
ARPC18	Arp2/3 complex mediated actin nucleation, Pc-gamma receptor signaling pathway involved in phagocytosis, epidermal receptor signaling pathway, regulation of actin filament polymerization	15.88	39.74
CSBP	blood coagulation, intrinsic pathway, cellular response to hypoxia, negative regulation of BDNF signaling pathway, negative regulation of FOS signaling pathway, negative regulation of defense response to virus, negative regulation of interferon-gamma production, negative regulation of interleukin-12	16.91	25.91
CSBP1	protein aggregation	6.88	47.95
DPY11	MEI-mediated ubiquitin-protein complex, circadian regulation of gene expression	15.88	47.95
SPR41	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay, nuclear-transcribed mRNA poly(A) tail shortening, positive regulation of neuron differentiation, regulation of mRNA stability, regulation of translation, regulation of translational initiation	21.48	17.22
RAB3C	blood coagulation, positive regulation of exocytosis, receptor internalization involved in canonical Wnt signaling pathway, regulation of autophagosome assembly, regulation of endocytosis, regulation of endosome size, regulation of filopodium assembly, regulation of transcription from RNA polymerase II promoter	9.34	43.05
C22B1	positive regulation of integrin-mediated signaling pathway, positive regulation of receptor internalization, regulation of potassium ion transport, regulation of vascular endothelial growth factor signaling pathway	26.86	12.91
ATP2A2	ER-chaperone signaling pathway, cellular calcium ion homeostasis, negative regulation of heart contraction, negative regulation of endoplasmic reticulum calcium ion concentration, positive regulation of fast	7.47	43.05
COR10C	activation of GTPase activity, negative regulation of epithelial cell migration, negative regulation of focal adhesion assembly, negative regulation of protein kinase activity by regulation of protein phosphorylation, negative regulation of substrate adhesion-dependent cell spreading, positive regulation of lamellipodium	14.94	25.91
NR1E3X	Wnt signaling pathway, extrinsic apoptotic signaling pathway via death domain receptors, intracellular signal transduction, intrinsic apoptotic signaling pathway, negative regulation of apoptotic process, negative regulation of cell growth, negative regulation of cytosolic-type endopeptidase activity involved in apoptotic	16.91	25.91
DBN1	maintenance of protein location in cell, regulation of dendrite development, regulation of neuronal synaptic plasticity	12.14	39.74
PAPB2	blood coagulation	14.91	32.29
PAS1	mitogen receptor signaling pathway, gene silencing by RNA, positive regulation of protein binding, positive regulation of transcription, DNA-templated, pre-miRNA export from nucleus, signal transduction, small GTPase mediated signal transduction	16.98	26.89
RP14	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay	9.34	39.74
TNBS4X	sequestration of actin monomers	17.74	17.22
TRIP10	positive regulation of kappaB transcription/NF-kappaB signaling, regulation of cell death, regulation of transcription, DNA-templated, signal transduction	16.91	34.44
PI1	homeostasis of number of cells within a tissue	14.91	32.29
LAMC1	positive regulation of epithelial cell proliferation	16.91	43.05
NCL	positive regulation of transcription from RNA polymerase II promoter, positive regulation of transcription of nuclear large RNA transcript from RNA polymerase II promoter	16.91	43.05
RP13	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay	9.34	39.74
RP2	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay, positive regulation of transference activity	15.88	23.88
TPN2	regulation of ATPase activity	16.91	43.05
COL3A1	integrin-mediated signaling pathway, negative regulation of immune response, negative regulation of neuron migration, platelet activation, positive regulation of Rho protein signal transduction, regulation of immune response, transforming growth factor beta receptor signaling pathway	17.74	17.22
PRKCSH	intracellular signal transduction	14.91	39.74
MR2	signal transduction	6.48	49.91
PSME2	Pc-epithelial receptor signaling pathway, MAPK cascade, NIK/NF-kappaB signaling, T cell receptor signaling pathway, Wnt signaling pathway, planar cell polarity pathway, negative regulation of canonical Wnt signaling pathway, negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle, positive	26.86	12.91
RP5	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay, regulation of translational fidelity	16.91	23.88
SCCBP	Rap protein signal transduction, epidermal receptor signaling pathway, negative regulation of proteasomal ubiquitin-dependent protein catabolic process, negative regulation of receptor internalization, positive regulation of JNK cascade, positive regulation of	14.94	26.89
YERK1	CRD-mediated mRNA stabilization, negative regulation of striated muscle cell differentiation, negative regulation of transcription from RNA polymerase II promoter, positive regulation of cell division, positive regulation of transcription from RNA polymerase	17.74	25.91
LAMR1	positive regulation of cell migration, positive regulation of epithelial cell proliferation	25.21	4.31
AKR1B1	CT-sterol hormone biosynthetic process, positive regulation of JAK-STAT cascade, positive regulation of smooth muscle cell proliferation, stress-activated protein kinase signaling cascade, tissue homeostasis	16.91	25.91
DPYB13	negative regulation of cell migration, negative regulation of neuron projection development, positive regulation of filopodium assembly, positive regulation of neuron projection development	26.86	84.57
IL5	regulation of respiratory gas exchange by neuroendocrine system process	6.54	39.74
CSBP2	negative regulation of defense response to virus, negative regulation of type I interferon production	25.21	14.44
RP5B	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay	7.47	34.44
PSBC4	Pc-epithelial receptor signaling pathway, MAPK cascade, NIK/NF-kappaB signaling, T cell receptor signaling pathway, Wnt signaling pathway, planar cell polarity pathway, negative regulation of canonical Wnt signaling pathway, negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle, positive	13.07	23.88
RP113	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay	16.91	19.37
RP5AX	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay, positive regulation of cell proliferation, positive regulation of translation	13.07	27.88
DP1	negative regulation of transcription from RNA polymerase II promoter, regulation of extracellular degradation, regulation of mRNA stability, regulation of protein catabolic process, regulation of protein export from nucleus	16.91	15.07
TGAP1	ERK1 and ERK2 cascade, endoplasmic A-mediated signaling pathway, entry of synaptobion into host cell by promotion of host phagocytosis, extrinsic apoptotic signaling pathway in absence of ligand, integrin-mediated signaling pathway, negative regulation of	5.74	49.91
EPF2	negative regulation of translational initiation, nuclear-transcribed mRNA catabolic process, nonsense-mediated decay	21.48	19.74
AP1B1	regulation of defense response to virus by virus	16.91	19.37
BZWI	regulation of transcription, DNA-templated	16.91	19.37
EMO2	blood coagulation, positive regulation of embryonic recycling, positive regulation of myoblast fusion	9.34	39.74
DPY23	activation of MAPK activity, negative regulation of gene expression, negative regulation of protein secretion, positive regulation of gene expression, regulation of endoplasmic reticulum stress-induced intrinsic apoptotic signaling pathway	11.21	26.89
EPF1	ERK-mediated unfolded protein response, negative regulation of guanylate cyclase exchange factor activity, negative regulation of translational initiation in response to stress, positive regulation of defense response to virus by host, positive regulation	16.91	34.44
SPB4	regulation of translational initiation	14.94	21.52
MAKRE1	negative regulation of microtubule binding, negative regulation of microtubule polymerization, positive regulation of cell migration, positive regulation of microtubule plus-end binding	26.86	12.91
PAPPC4	gene silencing by RNA, mRNA stabilization, negative regulation of nuclear-transcribed mRNA catabolic process, nonsense-mediated decay, negative regulation of nuclear-transcribed mRNA poly(A) tail shortening, nuclear-transcribed mRNA catab	17.74	25.91
PAPPC1	gene silencing by RNA, mRNA stabilization, negative regulation of nuclear-transcribed mRNA catabolic process, nonsense-mediated decay, nuclear-transcribed mRNA poly(A) tail shortening, positive	17.74	23.88
PRB47	Pc-epithelial receptor signaling pathway, MAPK cascade, NIK/NF-kappaB signaling, T cell receptor signaling pathway, Wnt signaling pathway, planar cell polarity pathway, negative regulation of canonical Wnt signaling pathway, negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle, positive	14.94	19.37
RP13	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay	14.94	27.88
YAK5	signal transduction	16.91	32.29
MDY1B4	mitogen metabolic process, estrogen metabolic process	6.54	27.88
ERD1A	cell redox homeostasis, endoplasmic reticulum unfolded protein response, intrinsic apoptotic signaling pathway in response to endoplasmic reticulum stress, release of sequestered calcium ion into cytosol	17.74	12.91
KPNA4	positive regulation of transcription from RNA polymerase II promoter	14.91	23.88
PRD13	Pc-epithelial receptor signaling pathway, MAPK cascade, NIK/NF-kappaB signaling, T cell receptor signaling pathway, Wnt signaling pathway, planar cell polarity pathway, negative regulation of canonical Wnt signaling pathway, negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle, positive	6.48	49.91
RSU1	positive regulation of GTPase activity, positive regulation of cell-substrate adhesion, signal transduction	13.07	23.88
TMD10	regulation of beta-amyloid formation	12.14	21.52
MTN1	negative regulation of integrin-mediated signaling pathway, positive regulation of cardiac muscle hypertrophy, positive regulation of macroautophagy, negative regulation of macromolecule biosynthetic process, positive regulation of protein metabolic process, regulation of barbed-end actin filament capping, regulation of	16.91	39.74
PCSTN	negative regulation of cell-substrate adhesion, negative regulation of substrate adhesion-dependent cell spreading, positive regulation of chemokine (C-C motif) ligand 2 secretion, positive regulation of smooth muscle cell migration, regulation of Notch signaling pathway, regulation of systemic arterial blood pressure	14.91	25.91
RAD23B	regulation of proteasomal ubiquitin-dependent protein catabolic process	12.14	23.88
TNPO1	regulation of mRNA stability	26.86	8.61
UREL3	positive regulation of protein targeting to mitochondrion, positive regulation of protein ubiquitination, positive regulation of ubiquitin-protein transference activity, regulation of transcription, DNA-templated	15.88	17.22
CARF2A	barbed-end actin filament capping, blood coagulation	15.88	23.88
SP1	regulation of translational initiation	6.54	39.74
BLOC	positive regulation of transcription elongation from RNA polymerase II promoter, regulation of transcription from RNA polymerase II promoter in response to hypoxia	9.34	25.91
KPFB	positive regulation of establishment of protein localization to plasma membrane, positive regulation of insulin secretion involved in cellular response to glucose stimulus, positive regulation of intracellular protein transport, positive regulation of poka	6.54	32.29
PSMA4	Pc-epithelial receptor signaling pathway, MAPK cascade, NIK/NF-kappaB signaling, T cell receptor signaling pathway, Wnt signaling pathway, planar cell polarity pathway, negative regulation of canonical Wnt signaling pathway, negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle, positive	11.21	23.88

*Experimentally Modified Protein Abundance Index (http://www.matrixscience.com/help/quant_ammal_help.htm).

Table S6. Cont 3.

^aExponentially Modified Protein Abundance Index (http://www.matrixscience.com/help/quant_empai_help.html).

Table S8, Cont'd

UniProt/Swiss-Prot Accession ID	Biological Process Molecular regulation	enrPAP	
		CCM	OMIM
MAPK12	G-protein coupled receptor signaling pathway, positive regulation of cAMP biosynthetic process, positive regulation of protein kinase A signaling, regulation of protein kinase C signaling, signal transduction	7,427	12,911
EPF3	regulation of translational initiation	10,227	12,911
PKL2	androgen receptor signaling pathway, negative regulation of apoptotic process, negative regulation of transcription from RNA polymerase II promoter, negative regulation of transcription, DNA-templated, positive regulation of transcription, DNA-templated, regulation of transcription from RNA polymerase II promoter	3,174	23,688
SLA	negative regulation of MAP kinase activity, negative regulation of inflammatory response, negative regulation of interleukin-6 production, negative regulation of neuron death, negative regulation of protein homodimerization, positive regulation of muscle cell redox homeostasis, negative regulation of cardiac muscle hypertrophy, regulation of the force of heart contraction	7,427	12,911
GLRX3	cardio redox homeostasis, negative regulation of cardiac muscle hypertrophy, regulation of the force of heart contraction	10,227	12,911
SLC10P	CRD-mediated mRNA stabilization, negative regulation of translation, regulation of translation	3,174	23,688
SLC	cell cycle arrest, integrin-mediated signaling pathway, negative regulation of apoptotic process, negative regulation of cardiac muscle cell apoptotic process, negative regulation of neural precursor cell proliferation, negative regulation of neuron apoptotic process, negative regulation of protein kinase activity, negative regulation of apoptotic process, regulation of transcription from RNA polymerase II promoter	9,334	12,911
PCNA	DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest, mitotic telomere maintenance via semi-conservative replication, positive regulation of DNA repair, positive regulation of DNA replication, positive regulation of deoxyribonucleic acid, neg	9,334	12,911
POMK2	Fc-epsilon receptor signaling pathway, MAPK cascade, NIK/NF-kappaB signaling, T cell receptor signaling pathway, Wnt signaling pathway, planar cell polarity pathway, negative regulation of canonical Wnt signaling pathway, negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle, positive	7,427	12,911
POMK7	Fc-epsilon receptor signaling pathway, MAPK cascade, NIK/NF-kappaB signaling, T cell receptor signaling pathway, Wnt signaling pathway, planar cell polarity pathway, negative regulation of canonical Wnt signaling pathway, negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle, positive	4,837	12,911
RP118	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay	1,871	23,688
SLR4A	positive regulation of organelle organization	5,259	23,688
TFG	positive regulation of I-kappaB kinase/NF-kappaB signaling, signal transduction	3,174	23,688
TSPO	maintenance of protein location in mitochondrion, negative regulation of ATP metabolic process, negative regulation of glial cell proliferation, negative regulation of mitochondrion organization, negative regulation of mitophagy, negative regulation of rnr	8,334	12,911
SCSPN1	fibrolysis, negative regulation of cell adhesion mediated by integrin, negative regulation of extrinsic apoptotic signaling pathway via death domain receptors, negative regulation of extrinsic apoptotic signaling pathway via death domain	4,837	12,911
RP113	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay	6,407	12,911
PLN1	blood coagulation, fibrin clot formation, integrin-mediated signaling pathway, negative regulation of ERK1 and ERK2 cascade, negative regulation of cell adhesion, negative regulation of cell motility, negative regulation of protein phosphorylation, negative regulation of stem cell proliferation, negative regulation of sub	4,837	12,911
PP2CA	Fc-epsilon receptor signaling pathway, Wnt signaling pathway, calcium modulating pathway, calcitonin-RFAP1 signaling cascade, calcium-mediated signaling, cellular response to glucose stimulus, excitatory postsynaptic potential, modulation of synaptic transmission, negative regulation of chromatin binding, nega	9,334	12,911
CTPAP	negative regulation of post-translational protein modification, protein stabilization	6,407	12,911
CTNND1	Wnt signaling pathway, positive regulation of canonical Wnt signaling pathway, regulation of transcription, DNA-templated	4,837	12,911
DNAJB1	RET-mediated unfolded protein response, positive regulation of ATPase activity	6,407	12,911
MLN1	positive regulation of GTPase activity, positive regulation of intrinsic apoptotic signaling pathway, positive regulation of mitochondrial fusion, positive regulation of protein secretion, positive regulation of r	5,880	12,911
DT01	regulation of translational fidelity	6,407	12,911
IPM8B	negative regulation of G1/S transition of mitotic cell cycle, negative regulation of T cell proliferation, negative regulation of cell proliferation, negative regulation of cytokine production, negative regulation of neuron death, negative regulation of tumor necrosis factor production, positive regulation of ERK1 and ERK2 c	12,134	12,911
PEA18	DNA damage checkpoint, MAPK cascade, activation of MAPK activity, negative regulation of extrinsic apoptotic signaling pathway via death domain receptors, negative regulation of glucose input, positive regulation of extrinsic apoptotic signaling pathway via death domain	8,334	12,911
PRKX2	cell redox homeostasis, negative regulation of apoptotic process	11,211	12,911
PIMB1	Fc-epsilon receptor signaling pathway, MAPK cascade, NIK/NF-kappaB signaling, T cell receptor signaling pathway, Wnt signaling pathway, planar cell polarity pathway, negative regulation of canonical Wnt signaling pathway, negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle, positive	6,407	12,911
RTN4	negative regulation of axon extension, negative regulation of cell growth, regulation of apoptotic process, regulation of branching morphogenesis of a nerve, regulation of cell migration, regulation of nervous system development	10,227	12,911
SCND1	negative regulation of autophagosome assembly, regulation of ER to Golgi vesicle-mediated transport, regulation of protein transport	6,407	12,911
TGOD17	tumor necrosis factor-mediated signaling pathway	8,334	12,911
USP9	positive regulation of proteasomal ubiquitin-dependent protein catabolic process	11,211	12,911
RP15A	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay, positive regulation of cell cycle, positive regulation of cell proliferation	6,407	12,911
MC1B1	positive regulation of cell proliferation, regulation of growth, regulation of transcription, DNA-templated	9,334	12,911
PRKBT	Fc-epsilon receptor signaling pathway, MAPK cascade, NIK/NF-kappaB signaling, T cell receptor signaling pathway, Wnt signaling pathway, planar cell polarity pathway, negative regulation of canonical Wnt signaling pathway, negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle, positive	7,427	12,911
PMK2C	Fc-epsilon receptor signaling pathway, MAPK cascade, NIK/NF-kappaB signaling, T cell receptor signaling pathway, Wnt signaling pathway, planar cell polarity pathway, negative regulation of canonical Wnt signaling pathway, negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle, positive	7,427	12,911
RAE2A	positive regulation of acetylcholine, small GTPase mediated signal transduction	3,174	12,911
TG2B	integrin-mediated signaling pathway, transforming growth factor beta receptor signaling pathway	3,174	12,911
EPF6	gene silencing by RNA, miRNA mediated inhibition of translation, positive regulation of translation, regulation of fatty acid biosynthetic process, regulation of glycolytic process, regulation of megakaryocyte differentiation, regulation of reactive oxygen species metabolic process	7,427	12,911
PRF152A	positive regulation of ERK1 and ERK2 cascade, regulation of translational initiation	2,880	12,911
HL3GL1	positive regulation of catalytic activity, positive regulation of myosin-light-chain-phosphatase activity, positive regulation of transcription from RNA polymerase II promoter, regulation of cell adhesion, regulation of establishment of endothelial barrier, regulation of myosin-light-chain-phosphatase activity, regulation	11,211	12,911
AMP2	negative regulation of cell proliferation, positive regulation of neuron death, positive regulation of protein ubiquitination	6,407	12,911
CHP2	arrested receptor protein signaling pathway, negative regulation of gene expression, positive regulation of low-density lipoprotein particle receptor biosynthetic process, regulation of low-density lipoprotein particle clearance	6,407	12,911
CYC8	activation of cysteine-type endopeptidase activity involved in apoptotic process by cytochrome c, intrinsic apoptotic signaling pathway	12,134	12,911
OMD1B12	extragenic biosynthetic process, positive regulation of cell-substrate adhesion	4,837	12,911
NA2H1	negative regulation of insulin secretion	6,407	12,911
CABT	negative regulation of endopeptidase activity, negative regulation of peptidase activity, negative regulation of type II pancreatic cell apoptotic process	3,174	12,911
MPG05	positive regulation of apoptotic cell clearance, positive regulation of phagocytosis	4,837	12,911
NA-C4	regulation of transcription, DNA-templated	4,837	12,911
CTUB1	negative regulation of double-strand break repair, negative regulation of histone H2A K63-linked ubiquitination	6,407	12,911
OTSA	negative regulation of chaperone-mediated autophagy, positive regulation of cell activity, regulation of chaperone-mediated autophagy, regulation of protein stability	7,427	12,911
VASP	positive regulation of actin filament polymerization	3,174	12,911
DLD	cell redox homeostasis, regulation of acetyl-CoA biosynthetic process from pyruvate, regulation of membrane potential	4,837	12,911
KPN4A	modulation by virus of host process	8,334	12,911
RP122	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay	6,407	12,911
PLT11	BMK signaling pathway	9,334	12,911
STAT2	JAK-STAT cascade, regulation of mitochondrial fusion, regulation of protein phosphorylation, regulation of transcription from RNA polymerase II promoter, regulation of type I interferon-mediated signaling pathway, signal transduction, type I interferon signaling pathway	7,427	12,911
ADPR1	activation of cysteine-type endopeptidase activity, activation of store-operated calcium channel activity, positive regulation of calcium ion transport into cytosol, positive regulation of intracellular protein transport, positive regulation of cytoskeletal assembly	10,227	12,911
ACLB3	positive regulation of Golgi to plasma membrane protein transport, positive regulation of phosphatidylcholine biosynthetic process, positive regulation of acroline, very-low-density lipoprotein particle assembly	11,211	12,911
APXK1	cell redox homeostasis, negative regulation of nucleic acid metabolism, negative regulation of smooth muscle cell migration, positive regulation of DNA repair, positive regulation of G1/S transition of mitotic cell cycle, regulation of mRNA stability, regulation of transcription, DNA-templated, telomere main	12,134	12,911
APR8	negative regulation of dendrite development, negative regulation of receptor-mediated endocytosis, positive regulation of actin filament polymerization, positive regulation of establishment of protein localization to plasma membrane, regulation of Rac prot	8,334	12,911
DOB1	the signaling pathway, negative regulation of apoptotic process, positive regulation of protein complex stabilization, positive regulation by virus of viral protein levels in host cell, positive regulation of viral genome replication, positive regu	6,407	12,911
BFH9	regulation of translational initiation	9,334	12,911
CHP1	cellular phospholipid homeostasis, negative regulation of cell growth, negative regulation of fat cell differentiation, negative regulation of glucose input, negative regulation of glycogen biosynthetic process, negative regulation of insulin receptor si	8,334	12,911
P13	regulation of transcription, DNA-templated	7,427	12,911
REXA	BMAD protein signal transduction, lipid storage	6,407	12,911
LMA1	negative regulation of actin filament depolymerization	8,334	12,911
NAK1	blood coagulation, positive regulation of organelle organization	8,334	12,911
POR	negative regulation of cysteine-type endopeptidase activity involved in apoptotic process, negative regulation of lipase activity, positive regulation of cholesterol biosynthetic process, positive regulation of chondrocyte differentiation, positive regulation of smoothm	9,334	12,911
PCDML1	regulation of transcription, DNA-templated	3,174	12,911
PCD23	cell redox homeostasis, negative regulation of apoptotic process, negative regulation of cysteine-type endopeptidase activity involved in apoptotic process, negative regulation of kinase activity, positive regulation of NF-kappaB transcription factor activity, positive regulation of cell proliferation, regulation of m	7,427	12,911
PRN2	negative regulation of actin filament polymerization, negative regulation of epithelial cell migration, negative regulation of rRNA assembly, positive regulation of ATPase activity, positive regulation of actin filament polymerization, positive regula	7,427	12,911
PMK2C	Fc-epsilon receptor signaling pathway, MAPK cascade, NIK/NF-kappaB signaling, T cell receptor signaling pathway, Wnt signaling pathway, planar cell polarity pathway, negative regulation of canonical Wnt signaling pathway, negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle, positive	4,837	12,911
SEPT1	Fc-epsilon receptor signaling pathway, MAPK cascade, NIK/NF-kappaB signaling, T cell receptor signaling pathway, Wnt signaling pathway, planar cell polarity pathway, negative regulation of canonical Wnt signaling pathway, negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle, positive	7,427	12,911
WDR4	barbed-end actin filament capping, regulation of actin phosphorylation, regulation of actin monomers	6,407	12,911
TAB1BP3	iron protein signal transduction, Wnt signaling pathway, activation of GTPase activity, negative regulation of Wnt signaling pathway, negative regulation of cell proliferation, negative regulation of protein localization to cell surface, regulation of Wnt si	1,871	23,688
SEK2	free ubiquitin chain polymerization, intrinsic apoptotic signaling pathway in response to endoplasmic reticulum stress, positive regulation of poly(ADP-ribose) phosphorylation, positive regulation of type I interferon-mediated signaling pathway, regula	6,407	12,911
ATFVE1	insulin receptor signaling pathway, phagosome acidification, regulation of macrophage	6,407	12,911
APB1	blood coagulation, positive regulation of NF-kB cell differentiation	4,837	12,911
CDH1	activation of MAPK activity, cell surface receptor signaling pathway, positive regulation of 1-phosphotyrosine 4-kinase activity, positive regulation of B cell proliferation, positive regulation of cell proliferation, positive regulation of peptidyl-L-tyrosine phosphorylation, positive regulation of protein catabolic process	6,407	12,911
RP121	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay	4,837	12,911
PCOLCE	positive regulation of peptidase activity	9,334	12,911
BA1C1	Fc-epsilon receptor signaling pathway, Fc-gamma receptor signaling pathway involved in phagocytosis, G-protein coupled receptor signaling pathway, T cell costimulation, Wnt signaling pathway, planar cell polarity pathway, blood coagulation, bone resorption	7,427	12,911
GPX1	cell redox homeostasis, intrinsic apoptotic signaling pathway in response to oxidative stress, negative regulation of cysteine-type endopeptidase activity involved in apoptotic process, negative regulation of extrinsic apoptotic signaling pathway via death	3,174	12,911
RP118	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay	7,427	12,911
CTNND1	Wnt signaling pathway, calcium modulating signaling pathway, beta-catenin destruction complex disassembly, bone resorption, bundle of fil-Fc-epsilon receptor signaling pathway, negative regulation of cell communication, canonical Wnt signaling pathway, canonical Wnt signaling pathway involved in m	7,427	12,911
CARM1	DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest, intracellular ubiquitin receptor signaling pathway, negative regulation of dendrite development, negative regulation of protein binding, positive regulation of cell proliferation, posi	3,174	12,911
EPF4	muscle cell cellular homeostasis, positive regulation of actin filament depolymerization	24,238	23,688
DO18	arrested receptor protein signaling pathway, positive regulation of neuron differentiation, regulation of translation	7,427	12,911
CHP2	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay	6,407	12,911
IKNRP1	fibroblast growth factor receptor signaling pathway, regulation of RNA splicing	7,427	23,688
PRKX2	regulation of muscle contraction	4,837	12,911
LMN1	negative regulation of transcription, DNA-templated, positive regulation of GTPase activity, positive regulation of cell-substrate adhesion, positive regulation of focal adhesion assembly, positive regulation of gene expression, positive regulation of substrate adhesion-dependent cell spreading, regulation of epithelial	6,407	12,911
ME1	positive regulation of NADP metabolic process	3,174	12,911
PRKX2	Fc-epsilon receptor signaling pathway, MAPK cascade, NIK/NF-kappaB signaling, T cell receptor signaling pathway, Wnt signaling pathway, planar cell polarity pathway, negative regulation of canonical Wnt signaling pathway, negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle, positive	7,427	12,911
POMK12	Fc-epsilon receptor signaling pathway, MAPK cascade, NIK/NF-kappaB signaling, T cell receptor signaling pathway, Wnt signaling pathway, planar cell polarity pathway, negative regulation of canonical Wnt signaling pathway, negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle, positive	3,174	12,911
PTK7	canonical Wnt signaling pathway, planar cell polarity pathway involved in neural tube closure, positive regulation of neuron projection development, signal transduction	6,407	12,911
RP13A	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay	1,871	23,688
TGFB11	the signaling pathway, androgen receptor signaling pathway, negative regulation of cell proliferation, negative regulation of transforming growth factor beta receptor signaling pathway, positive regulation of epithelial to mesenchymal transition, positive regulation of transcription, DNA-templated, positive regulation	1,871	23,688

¹Exponentially Modified Protein Abundance Index (http://www.martinsciencia.com/help/quant_empir_help.htm)

Table S8, Cont'd

UniProt/Swiss-Prot Accession ID	Biological Process Molecular regulation	enrPAP	
		CCM	OMIM
TRIM2	Ras protein signal transduction, negative regulation of DNA demethylation, negative regulation of single stranded viral RNA replication via double stranded DNA intermediate, negative regulation of transcription from RNA polymerase II promoter, negative regulation of transcription, DNA-templated	6,541	19,176
PRK29	Wnt signaling pathway	6,541	19,176
TNFR1L1	negative regulation of phosphorylation, positive regulation of protein insertion into mitochondrial membrane involved in apoptotic signaling pathway, regulation of transcription, DNA-templated	5,880	12,911
BSR1	RET-mediated unfolded protein response, positive regulation of cell proliferation	4,837	12,911
ANCKY1	regulation of catalytic activity, regulation of cellular response to heat	6,407	12,911
DPF26	positive regulation of glucose	11,211	12,911
PC2	chromatin silencing at telomere, regulation of transcription, DNA-templated	7,427	12,911
RP119	cellular response to glucose stimulus, positive regulation of insulin secretion	1,871	23,688
DNAJA1	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay	6,407	12,911
ERH1	androgen receptor signaling pathway, negative regulation of JNK kinase activity, negative regulation of apoptotic process, negative regulation of establishment of protein localization to mitochondrion, negative regulation of ribosome stress-induced ntri	7,427	12,911
SDC1	positive regulation of Notch signaling pathway	10,227	12,911
NUTF2	phosphatidylinositol-mediated signaling, positive regulation of protein secretion, regulation of macrophage	6,407	12,911
RP114	negative regulation of vascular endothelial growth factor production, positive regulation of protein import into nucleus	3,174	12,911
RP112	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay	2,880	12,911
RP128	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay	6,407	12,911
PTGSR3	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay	6,407	12,911
TNFR2	regulation of cellular response to heat, signal transduction, telomere maintenance	3,174	12,911
TNFR3	negative regulation of GTPase activity, positive regulation of gene expression	4,837	12,911
TNFR4	erythrocyte development, pointed-end actin filament capping, positive regulation of mitotic cell cycle phase transition	7,427	12,911
DNAJA2	positive regulation of cell proliferation	7,427	12,911
RP1A3	modulation by virus of host process	7,427	12,911
TNFR2L2	T cell receptor signaling pathway, cellular calcium ion homeostasis, positive regulation of cardiomyocyte metabolic process, positive regulation of mitochondrial DNA replication, positive regulation of mitochondrial membrane potential	3,174	12,911
MAPK1	Wnt signaling pathway, positive regulation of Wnt signaling pathway, positive regulation of axon extension, regulation of epithelial cell migration, regulation of focal adhesion assembly, regulation of microtubule-based process	4,837	12,911
PRKX2	Fc-epsilon receptor signaling pathway, MAPK cascade, NIK/NF-kappaB signaling, T cell receptor signaling pathway, Wnt signaling pathway, planar cell polarity pathway, negative regulation of canonical Wnt signaling pathway, negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle, positive	7,427	12,911
AMP2B	activation of cysteine-type endopeptidase activity involved in apoptotic process, negative regulation of cell differentiation, positive regulation of protein export from nucleus	6,407	12,911
NTSE	negative regulation of inflammatory response	6,407	12,911
ADRC1C1	cholesterol homeostasis, progesterone metabolic process	6,407	12,911
PIMT1	DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest, cell surface receptor signaling pathway, negative regulation of megakaryocyte differentiation, positive regulation of erythrocyte differentiation, positive regulation of hemoglobin bios	6,407	12,911
DYTNCL1	positive regulation of mitotic cell cycle spindle assembly checkpoint	6,407	12,911
PUS2	regulation of nuclear acid-templated transcription	6,407	12,911
CHP2	G-protein coupled receptor signaling pathway, action potential, activation of phospholipase C activity, adenylate cyclase-activating G-protein coupled receptor signaling pathway, blood coagulation, entrainment of circadian clock, glutamate re	3,174	12,911
PRKX1A	activation of protein kinase A activity, blood coagulation, intracellular signal transduction, negative regulation of activated T cell proliferation, negative regulation of cAMP-dependent protein kinase activity, negative regulation of mitotic nuclear division, negative regulation of protein kinase activity, regulation of pro	6,407	12,911
NAK1	positive regulation of gene expression	6,407	12,911
ME30	Wnt signaling pathway	6,407	12,911
PIMB1	Fc-epsilon receptor signaling pathway, MAPK cascade, NIK/NF-kappaB signaling, T cell receptor signaling pathway, Wnt signaling pathway, planar cell polarity pathway, negative regulation of canonical Wnt signaling pathway, negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle, positive	2,880	12,911
TPH2B	regulation of apoptotic process	6,407	12,911
RP123A	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay	2,880	12,911
TRV2E	smoothed signaling pathway	6,407	12,911
BD01	activation of MAPK activity, cellular iron ion homeostasis, muscle cell cellular homeostasis, myofibril cellular homeostasis, negative regulation of cholesterol biosynthetic process, negative regulation of neuron apoptotic process, positive regulation of apoptotic process, positive regulation of catalytic activity, positive	4,837	12,911
SPR8B	RET-mediated unfolded protein response, small GTPase mediated signal transduction	2,880	12,911
TARD9P	3'-UTR-mediated mRNA stabilization, negative regulation by host of viral transcription, negative regulation of protein phosphorylation, positive regulation of insulin secretion, positive regulation of transcription from RNA polymerase II promoter, regula	6,407	12,911
AKR37	cellular calcium ion homeostasis, cellular water homeostasis, homeostasis, negative regulation of gene expression, regulation of cell shape	4,837	12,911
P2H1	negative regulation of cell proliferation	3,174	12,911
UBA2	positive regulation of catalytic activity	2,880	12,911
TNFR1	cell redox homeostasis	2,880	12,911
SLC3X	cell redox homeostasis, positive regulation of membrane potential, positive regulation of sodium ion transmembrane transporter activity	7,427	12,911
AMP2A	intracellular signal transduction, regulation of apoptotic process, regulation of mRNA stability, regulation of transcription, DNA-templated	2,880	12,911
EPF8	regulation of translational initiation	1,871	12,911
SLC3L3	negative regulation of T cell activation via T cell receptor contact with antigen bound to MHC molecules on antigen presenting cell, negative regulation of T cell receptor signaling pathway, negative regulation of endocytosis, negative regulation of extrinsic apoptotic signaling pathway, negative regulation of immunog	2,880	12,911
IFV10D	negative regulation of phosphatase activity	3,174	12,911
PARGA	regulation of cell shape	4,837	12,911
SEPTA	RET-mediated unfolded protein response	4,837	12,911
TMK3	cell redox homeostasis	3,174	12,911
STI3	negative regulation of protein folding	2,880	12,911
NDL2	protein retention in ER lumen	10,227	12,911
NDL3	3'-UTR-mediated mRNA stabilization, negative regulation of apoptotic process, negative regulation of intrinsic apoptotic signaling pathway in response to osmotic stress, negative regulation of necroptotic process, negative regulation of skeletal muscle tis	6,407	12,911
UBD2E2	Fc-epsilon receptor signaling pathway, T cell receptor signaling pathway, TRP-dependent toll-like receptor signaling pathway, regulation of transcription from RNA polymerase II promoter in response to hypoxia, stimulatory C-type lectin receptor signaling pathway	6,407	12,911
ADRC1A	Aryl2 complex-mediated actin nucleation, Fc-gamma receptor signaling pathway involved in phagocytosis, epsilon receptor signaling pathway, regulation of actin filament polymerization	3,174	12,911

¹Exponentially Modified Protein Abundance Index (http://www.martinsciencia.com/help/quant_empir_help.htm)

Table S7. Identification of endogenous proteins (Biological Process: metabolic process) in hADSC; group CDM & DMEM.

Table S7 Identification of endogenous proteins (Biological Process: metabolic process) in hADSC; group CDM & DMEM		Biological Process: metabolic process		UniProt	
Accession ID	Protein Name	Biological Process	UniProt	CDM	DMEM
MTF9	ATP metabolic process, membrane protein ectodomain proteolysis			380.72	361.88
FLNA	mRNA transcription from RNA polymerase II promoter			323.15	384.66
HEP9AAB1	chaperone-mediated autophagy, peptidyl-lysine phosphorylation, retrograde protein transport, ER to cytosol, ubiquitin-dependent ERAD pathway			425.85	454.18
HEP9AB1	retrograde protein transport, ER to cytosol, ubiquitin-dependent ERAD pathway			87.78	180.81
HEP9AAB1	chaperone-mediated autophagy, peptidyl-lysine phosphorylation			320.73	163.74
ALS	lipoprotein metabolic process			686.52	47.35
EEF1A1	transcription, DNA-templated, translation, translational elongation			382.83	376.83
HEP9A	ATP metabolic process, chaperone-mediated protein transport involved in chaperone-mediated autophagy, late endosomal microautophagy, mRNA processing, mRNA splicing, via spliceosome, protein targeting to lysosome involved in chaperone-mediated autophagy, proteolysis involved in cellular			361.59	359.58
HEP9A1A	ATP metabolic process			15.88	51.88
PKM	canonical glycolysis, glycolytic process, metabolic process, phosphorylation			285.10	434.80
TYRHA1	glucocorticoid catabolic process			69.27	361.32
ENO1	canonical glycolysis, gluconeogenesis, glycolytic process, transcription, DNA-templated			254.94	273.38
ENO2	canonical glycolysis, gluconeogenesis, glycolytic process			79.84	27.98
ACTA1	MAPK cascade			135.47	514.44
CLTC	receptor internalization			163.42	243.23
PAH8	lipoprotein biosynthetic process, peptidyl-proline hydroxylation, peptidyl-proline hydroxylation to 4-hydroxy-L-proline			138.34	236.78
LDHA	NAD metabolic process, carboxylate metabolic process, glycolytic process, lactate metabolic process, oxidation-reduction process, pyruvate metabolic process			167.29	459.48
EEF2	peptidyl-dihydramide biosynthetic process from peptidyl-histidine, translation, translational elongation			162.49	189.42
ALDOA	ATP biosynthetic process, canonical glycolysis, fructose 1,6-bisphosphate metabolic process, fructose metabolic process, gluconeogenesis, glycolytic process			119.19	279.82
ALDOA	canonical glycolysis, fructose 1,6-bisphosphate metabolic process, fructose metabolic process, gluconeogenesis, glycolytic process			17.74	75.34
PN1	peptide cross-linking			97.12	251.43
COL1A3	collagen catabolic process			128.87	180.81
COL1A1	collagen biosynthetic process, collagen catabolic process			75.88	226.89
BERPNNH1	collagen biosynthetic process, protein maturation			127.94	159.28
IQGAP1	ERK1 and ERK2 cascade			101.73	191.57
UBA1	cellular protein modification process, modification-dependent protein catabolic process, protein ubiquitination			161.66	163.88
FA3N	acetyl-CoA biosynthetic process, biosynthetic process, fatty acid biosynthetic process, lipid biosynthetic process, long-chain fatty-acyl-CoA biosynthetic process, oxidation-reduction process, pantothenate metabolic process			130.74	96.88
CALR	protein maturation by protein folding			119.80	120.54
ATP5B	ATP metabolic process, ER-associated metabolic catabolic process, NADH metabolic process, endoplasmic reticulum, autophagy, double-strand break repair, error-free translation synthesis, flavin adenosine dinucleotide catabolic process, proteasome-mediated ubiquitin-dependent p			107.12	181.52
PC1A3	oxidation-reduction process, proteolysis			84.98	142.68
THBS1	peptide cross-linking, protein O-linked fucosylation			82.18	148.52
VCP	ATP metabolic process, ER-associated metabolic catabolic process, NADH metabolic process, endoplasmic reticulum, autophagy, double-strand break repair, error-free translation synthesis, flavin adenosine dinucleotide catabolic process, proteasome-mediated ubiquitin-dependent p			82.18	148.52
ANPEP	protein catabolic process, proteolysis			100.88	96.88
OSN	amyloid fibril formation, cellular protein metabolic process			88.85	99.01
ANKK5	emphysema			16.97	109.28
MSN	receptor internalization			55.83	139.81
ER2	receptor internalization			14.94	32.29
HEP9C1	histone switching to ligand hydrolysis, protein maturation			75.29	16.29
ACLY	acetyl-CoA biosynthetic process, cholesterol biosynthetic process, cholate metabolic process, fatty acid biosynthetic process, lipid biosynthetic process, long-chain fatty-acyl-CoA biosynthetic process, oxaloacetate metabolic process			75.87	155.47
COL1A1	collagen catabolic process			75.84	81.79
DEPT1	glutathione derivative biosynthetic process, glutathione metabolic process, metabolic acid metabolic process, metabolic process, xenobiotic metabolic process			82.82	132.45
HEP9A1	RNA secondary structure unwinding, RNA splicing, mRNA 5' and processing, mRNA export from nucleus, mRNA splicing, via spliceosome, nuclear-transcribed mRNA catabolic process, nonsense-mediated decay, nuclear-transcribed mRNA poly(A) tail shortening, mRNA processing, selenocysteine metabolic process			75.97	38.74
EFNA2	RNA secondary structure unwinding, nuclear-transcribed mRNA poly(A) tail shortening, translation, translational initiation			29.88	38.74
TPH1	canonical glycolysis, gluconeogenesis, glycerolaldehyde-3-phosphate biosynthetic process, glycerolaldehyde-3-phosphate metabolic process, glycerolaldehyde-3-phosphate shunt			55.77	107.62
TKT	glycerolaldehyde-3-phosphate biosynthetic process, pentose-phosphate shunt, pentose-phosphate shunt, non-oxidative branch, xylulose biosynthetic process			75.84	83.85
ARF4	phosphatidylinositol biosynthetic process, protein ADP-ribosylation			75.38	89.27
ARF3	phosphatidylinositol biosynthetic process			46.89	23.85
ARF3	phosphatidylinositol biosynthetic process			46.16	17.52
CAPN2	protein autophagy, proteolysis involved in cellular protein catabolic process			75.84	86.18
LDHB	NAD metabolic process, carboxylate metabolic process, lactate metabolic process, oxidation-reduction process, pyruvate metabolic process			93.39	133.85
LRPI	lipoprotein metabolic process, retinol metabolic process			48.88	124.64
CAKAP4	cellular protein metabolic process			34.55	152.42
CAKAP4	carboxylate metabolic process			37.38	109.47
CAKAP4	carboxylate metabolic process			89.75	73.13
PGAM1	canonical glycolysis, gluconeogenesis, glycolytic process, respiratory burst			32.89	159.07
PGAM1	gluconeogenesis, glycolytic process			32.89	159.07
HEP9B1	apoptosis, DNA T-ageration			55.77	79.49
CTSD	autophagy, collagen catabolic process, protein catabolic process, proteolysis			45.16	103.52
ANKK1	DNA strand resection, peptide cross-linking			51.36	88.23
EPFA	mRNA export from nucleus, peptidyl-lysine modification to peptidyl-histidine, translation, translational translocation			82.18	39.13
EPFA2	peptidyl-lysine modification to peptidyl-histidine, translation, translational elongation, translational translocation			15.88	19.27
COL1A2	collagen catabolic process			30.82	118.39
PP1B	protein peptidyl-prolyl isomerization			45.49	77.49
STAT1	transcription, DNA-templated			55.97	64.57
ATP5A1	ATP metabolic process, ATP synthesis coupled proton transport, electron transport chain, lipid metabolic process, mitochondrial ATP synthesis coupled proton transport			44.83	82.88
ARS	histonecy-RNA aminoacylation, translation			45.78	89.25
TDO	glycerol ether metabolic process, nucleoside-containing small molecule interconversion, oxidation-reduction process, protein repair, sulfate assimilation, transcription, DNA-templated			91.38	79.84
RH1	mRNA catabolic process			42.02	96.88
CLC1	glutathione metabolic process			46.83	84.27
SPYB2	nucleoside-containing compound metabolic process			42.02	129.15
BNP1	RNA catabolic process, nucleic acid phosphodiester bond hydrolysis, transcription, DNA-templated			42.02	83.85
PF1D3	hydrogen peroxide catabolic process, lipid catabolic process, lipid metabolic process, oxidation-reduction process			46.88	84.27
EP1D3	glutathione metabolic process, translation, translational elongation			46.83	89.73
PAFA1	oxidation-reduction process, peptidyl-proline hydroxylation to 4-hydroxy-L-proline			32.89	83.85
PAFA1	cardiolipin acyl-chain remodeling, fatty acid beta-oxidation, fatty acid metabolic process, lipid metabolic process, oxidation-reduction process			42.98	89.73
UDPP	UDP-glucose metabolic process, UDP-glucuronate biosynthetic process, glucose 1-phosphate metabolic process, glycerol biosynthetic process			35.15	71.85
UDPP	2-oxoglutarate metabolic process, NADPH regeneration, glutathione metabolic process, glyoxylate cycle, succinate metabolic process, tricarballic acid cycle			35.29	64.57
EPF5	glutathione-RNA aminoacylation, poly-RNA aminoacylation, translation			37.75	73.18
PSAP	glycosylated metabolic process, lipid metabolic process, sphingolipid metabolic process			35.29	59.96
CT1B	collagen catabolic process, proteolysis involved in cellular protein catabolic process			42.02	45.89
PAFA2	oxidation-reduction process, peptidyl-proline hydroxylation			32.89	75.34
AARS	aminoacyl-RNA aminoacylation, RNA aminoacylation, RNA modification, translation			25.02	89.16
PRKDC	DNA recombination, T cell receptor V(D)J recombination, V(D)J recombination, cellular protein modification process, double-strand break repair, double-strand break repair via alternative nonhomologous end joining, immunoglobulin V(D)J recombination, peptidyl-serine phosphorylation, phospho			91.38	25.83
UCHL1	proteasome-mediated ubiquitin-dependent protein catabolic process, protein deubiquitination			25.85	53.81
NMT1	methyltransferase			32.89	62.42
RPN2	protein N-linked glycosylation via asparagine			38.42	45.81
MME	argininemia maturation, beta-amyloid metabolic process, creatinine metabolic process, proteolysis			37.75	62.42
BSBP1	translation			22.41	77.49
UDOH	UDP-glucose metabolic process, UDP-glucuronate biosynthetic process, carboxylate metabolic process, glycosaminoglycan biosynthetic process, oxidation-reduction process			25.85	64.57
TOPBP1	cellular protein metabolic process			39.22	36.89
PABK1	autophagy, enzyme active site formation via L-cysteine sulfenic acid, glutathione degradation, glycolate biosynthetic process, glyoxal catabolic process, glyoxal metabolic process, hydrogen peroxide metabolic process, lactate biosynthetic process, methylgly			39.82	91.46
FAP	proteolysis involved in cellular protein catabolic process			19.81	83.85
UDOT1	ER-associated metabolic protein catabolic process, UDP-glucylation, endoplasmic reticulum mannose trimming, protein N-linked glycosylation via asparagine			25.21	69.73
VAT1	oxidation-reduction process			25.15	69.73
GP1	aldehyde catabolic process, canonical glycolysis, carboxylate metabolic process, gluconeogenesis, glucose 6-phosphate metabolic process, glycolytic process, methylglyoxal biosynthetic process			41.09	45.89
PPKP	canonical glycolysis, fructose 1,6-bisphosphate metabolic process, fructose 6-phosphate metabolic process, glycolytic process through fructose-6-phosphate, phosphorylation			25.29	81.79
RPN1	protein N-linked glycosylation via asparagine, protein glycosylation			17.74	73.18
XRC5	DNA recombination, double-strand break repair, double-strand break repair via nonhomologous end joining, telomere maintenance, transcription, DNA-templated			34.55	43.89
PRDX1	hydrogen peroxide catabolic process, oxidation-reduction process, removal of superoxide radicals			35.29	69.27
SEPD	NADPH regeneration, carboxylate metabolic process, cholesterol biosynthetic process, glucose 6-phosphate metabolic process, glucose metabolic process, glutathione metabolic process, oxidation-reduction process, pentose biosynthetic process, pentose-phosphate shunt, pentose-ph			24.23	69.27
PEMD2	MAPK cascade, anaphase-promoting complex-dependent catabolic process, protein polyubiquitination			26.15	58.13

*Exponentially Modified Protein Abundance Index (http://www.mabscience.com/help/quant_empai_help.html)

Table S7. Cont 1

UniProt/Swiss-Prot ID	Biological Process	emPA ¹	CCM	DMEM
RPSA	endonucleolytic cleavage in ITS1 to separate SSU-rRNA from 5.8S rRNA and LSU-rRNA from trichotomic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA), endonucleolytic cleavage to generate mature 5' and 3' of SSU-rRNA from (SSU-rRNA, 5.8S rRNA, LSU-rRNA), nuclear-transcribed mRNA catabolic process, mRNA processing	51.66	81.86	81.86
CLIC4	glutathione metabolic process	71.03	64.57	64.57
LRPPRC	transcription, DNA-templated	34.44	103.52	103.52
NDH2	NADH metabolic process, carbohydrate metabolic process, gluconeogenesis, internal protein amino acid acetylation, malate metabolic process, oxaloacetate metabolic process, oxidation-reduction process, tricarboxylic acid cycle	56.13	72.16	72.16
COL12A1	collagen catabolic process	111.93	55.96	55.96
PSEN1	MAPK cascade, anaphase-promoting complex-dependent catabolic process, protein polyubiquitination	60.27	40.90	40.90
PP2D1A	RNA splicing, serine metabolic process, nuclear-transcribed mRNA catabolic process, nonsense-mediated decay, peptidyl-serine dephosphorylation	38.74	79.10	79.10
POD	D-glucose metabolic process, oxidation-reduction process, pentose biosynthetic process, pentose-phosphate shunt, pentose-phosphate shunt, oxidative branch	34.44	58.13	58.13
CAPN31	proteolysis	47.35	86.19	86.19
DNMT2	oxidation-reduction process	81.79	49.57	49.57
DNMT2	DNA methylation, GTP metabolic process, energy reserve metabolic process, genetic imprinting	55.96	60.27	60.27
GNA5	DNA methylation, energy reserve metabolic process, genetic imprinting	17.22	25.83	25.83
ITGB1	receptor internalization	55.96	53.81	53.81
MAPK1	DNA damage induced protein phosphorylation, ERK1 and ERK2 cascade, MAPK cascade in response to starvation, MAPK cascade involved in osmosensory signaling pathway, MAPK import into nucleus, arachidonic acid metabolic process, cytosine metabolic process, glycoaminoglycan biosynthetic	38.74	79.10	79.10
MAPK3	DNA damage induced protein phosphorylation, ERK1 and ERK2 cascade, arachidonic acid metabolic process, peptidyl-serine phosphorylation, peptidyl-tyrosine autophosphorylation, phosphorylation, transcription initiation from RNA polymerase I promoter, transcription, DNA-t	10.76	75.34	75.34
POCDBP	ubiquitin-independent protein catabolic process via the multivesicular body sorting pathway	45.20	64.57	64.57
NAK5	RNA aminoacylation for protein translation, translation, tryptophanyl-RNA aminoacylation	73.10	58.25	58.25
NDH1	NAD metabolic process, NADH metabolic process, carbohydrate metabolic process, carboxylic acid metabolic process, gluconeogenesis, malate metabolic process, oxaloacetate metabolic process, oxidation-reduction process, tricarboxylic acid cycle	32.29	62.42	62.42
PPP1CA	carbohydrate metabolic process, dephosphorylation, glycogen metabolic process, regulation of translational initiation by eIF2 alpha dephosphorylation	27.98	77.49	77.49
PPP1C2	glycogen metabolic process, protein dephosphorylation	25.83	36.59	36.59
RAB19	autophagosome assembly, autophagy, peptidyl-cysteine methylation	64.57	73.10	73.10
RAB1B	autophagy	27.98	38.74	38.74
RAB1A	autophagosome assembly, autophagy	32.29	10.76	10.76
SPTAN1	MAPK cascade	51.66	51.66	51.66
OCN1	translation	55.96	47.35	47.35
PHH1	collagen metabolic process, oxidation-reduction process, peptidyl-proline hydroxylation, protein hydroxylation	47.35	61.95	61.95
COL4A2	collagen catabolic process	38.74	61.95	61.95
MEF	carboxylic acid metabolic process, prostaglandin biosynthetic process	38.74	61.95	61.95
PLD1	cellular protein modification process, hydroxylysine biosynthetic process, oxidation-reduction process	43.90	40.90	40.90
AT7V1A	ATP metabolic process	60.27	58.13	58.13
YODAC1	macroautophagy	90.40	43.09	43.09
HDLBP	cholesterol metabolic process	68.89	38.59	38.59
PKBP12	protein-peptidyl-prolyl isomerization	60.27	60.27	60.27
HNRNPK	gene expression, mRNA processing, mRNA splicing, via spliceosome, protein sumoylation, transcription from RNA polymerase II promoter, transcription, DNA-templated	38.74	66.73	66.73
PT08	5-phosphoribose 1-diphosphate biosynthetic process, glycogen catabolic process, metabolic process	38.74	60.27	60.27
PT02	5-phosphoribose 1-diphosphate biosynthetic process, glycogen catabolic process	47.35	61.95	61.95
SARS	selenocysteine metabolic process, selenocysteinyl-RNA(Sec) biosynthetic process, seryl-RNA aminoacylation, tRNA processing, translation	43.09	51.66	51.66
PHGDH	L-serine biosynthetic process, cellular amino acid biosynthetic process, gamma-aminobutyric acid metabolic process, glutamine metabolic process, glycine metabolic process, oxidation-reduction process, serine family amino acid biosynthetic process, taurine metabolic process, threonine metabolic process	77.49	71.03	71.03
DRDC6	DNA ligase, DNA recombination, double-strand break repair via classical nonhomologous end joining, telomere maintenance, transcription, DNA-templated	38.74	61.95	61.95
SDT01	L-ascorbic acid metabolic process, glutathione derivative biosynthetic process, glutathione metabolic process, methylation, oxidation-reduction process, xenobiotic catabolic process	30.13	34.44	34.44
LMOT	protein ubiquitination	86.10	71.03	71.03
NPR1	DNA repair	27.98	60.27	60.27
SDOST	protein-N-linked glycosylation, protein-N-linked glycosylation via asparagine	36.59	38.74	38.74
CAND1	protein ubiquitination	38.74	47.35	47.35
ESD	formaldehyde catabolic process, glutathione derivative biosynthetic process	34.44	81.79	81.79
ESBP1	MAPK cascade	30.13	55.96	55.96
RPL9	cytoplasmic translation, nuclear-transcribed mRNA catabolic process, nonsense-mediated decay, rRNA processing, translation, translational initiation, viral transcription	49.51	17.22	17.22
RPB3	DNA repair, nuclear-transcribed mRNA catabolic process, nonsense-mediated decay, rRNA processing, transcription, DNA-templated, translation, translational initiation, viral transcription	51.66	55.96	55.96
PRAT1	L-serine biosynthetic process, cellular amino acid biosynthetic process, pyridoxine biosynthetic process	64.57	34.44	34.44
RPL12	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay, rRNA processing, translation, translational initiation, viral transcription	25.83	10.76	10.76
RPB7	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay, rRNA processing, translation, translational initiation, viral transcription	27.98	45.20	45.20
CAPN1	proteolysis, receptor catabolic process	36.59	73.10	73.10
PRDX4	4-hydroxyproline metabolic process, hsp90AB phosphorylation, oxidation-reduction process, protein maturation by protein folding, reactive oxygen species metabolic process	60.27	27.98	27.98
VARS	RNA aminoacylation for protein translation, translation, valyl-RNA aminoacylation	34.44	25.83	25.83
EEF2B2	translation, translational elongation	43.09	44.67	44.67
RPL7A	maturation of LSU-rRNA, nuclear-transcribed mRNA catabolic process, nonsense-mediated decay, rRNA processing, translation, translational initiation, viral transcription	30.13	12.91	12.91
CTBK	collagen catabolic process, proteolysis involved in cellular protein catabolic process	12.91	27.98	27.98
NBE1	UTP biosynthetic process, DNA metabolic process, GTP biosynthetic process, UTP biosynthetic process, nucleobase-containing small molecule interconversion, nucleoside diphosphate phosphorylation, phosphorylation, pyrimidine nucleotide metabolic process	36.59	32.29	32.29
PRDX3	NADPH oxidation, hydrogen peroxide catabolic process, oxidation-reduction process, reactive nitrogen species metabolic process	49.51	51.66	51.66
SPTBN1	MAPK cascade, common-partner SMAD protein phosphorylation	38.74	47.35	47.35
ALDH1L2	10-formyltetrahydrofolate catabolic process, biosynthetic process, folic acid metabolic process, metabolic process, one-carbon metabolic process, oxidation-reduction process	45.20	40.90	40.90
NUPF1	peptide catabolic process, proteolysis	21.52	45.20	45.20
ATP1A1	dephosphorylation	17.22	77.49	77.49
NAP1L1	DNA replication	32.29	55.96	55.96
PTBP1	MEI3-dependent viral translational initiation, alternative mRNA splicing, via spliceosome, gene expression, mRNA processing, mRNA splicing, via spliceosome	49.51	47.35	47.35
ATP6V1B2	ATP metabolic process	49.51	30.13	30.13
PCBP1	gene expression, mRNA splicing, via spliceosome, viral RNA genome replication	49.51	60.27	60.27
PLD3	cellular protein modification process, oxidation-reduction process	45.20	67.43	67.43
RPS3A	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay, rRNA processing, translation, translational initiation, viral transcription	43.09	66.73	66.73
TXNRD1	nucleobase-containing small molecule interconversion, oxidation-reduction process, selenium compound metabolic process	66.73	90.40	90.40
ACDH5	ethanol oxidation, formaldehyde catabolic process, oxidation-reduction process, peptidyl-cysteine S-nitrosylation, retinol metabolic process	32.29	66.73	66.73
COMT	catecholamine metabolic process, dopamine catabolic process, estrogen metabolic process, methylation, neurotransmitter catabolic process	34.44	27.98	27.98
NME2	GTP biosynthetic process, GTP biosynthetic process, UTP biosynthetic process, nucleobase-containing small molecule interconversion, nucleoside diphosphate phosphorylation, nucleoside triphosphate biosynthetic process, nucleotide metabolic process, peptidyl-histidine pho	36.59	38.74	38.74
PLD3	oxidation-reduction process	47.35	36.74	36.74
PSMA4	MAPK cascade, anaphase-promoting complex-dependent catabolic process, proteasome-mediated ubiquitin-dependent protein catabolic process, protein polyubiquitination, proteolysis involved in cellular protein catabolic process	38.74	8.61	8.61
C10BP	RNA splicing, blood coagulation, intrinsic pathway, complement activation, classical pathway, mRNA processing, transcription, DNA-templated	25.83	51.66	51.66
SPPT1	UDP-N-acetylglucosamine biosynthetic process, carboxylate derivative biosynthetic process, carbohydrate metabolic process, energy reserve metabolic process, fructose 6-phosphate metabolic process, glutamine metabolic process	22.60	45.20	45.20
SEI1	generation of precursor metabolites and energy, glycogen biosynthetic process	22.60	55.96	55.96
EFG1	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay, nuclear-transcribed mRNA poly(A) tail shortening, translation, translational initiation	17.22	75.34	75.34
RAB5C	receptor internalization involved in canonical Wnt signaling pathway, viral RNA genome replication	43.90	77.49	77.49
PCDH	UDP-N-acetylglucosamine biosynthetic process, carbohydrate metabolic process, gluconeogenesis metabolic process, glucose 1-phosphate metabolic process, protein-N-linked glycosylation, protein-O-linked glycosylation	36.59	32.29	32.29
CNDP2	glutathione biosynthetic process, peptide catabolic process, proteolysis, sulfur amino acid metabolic process	21.52	49.51	49.51
DOXK3	RNA secondary structure unwinding, transcription, DNA-templated, translational initiation	23.68	19.27	19.27
ECHE1	fatty acid-beta-oxidation, fatty acid metabolic process, lipid metabolic process	21.52	62.42	62.42
FDPS	cholesterol biosynthetic process, farnesyl diphosphate biosynthetic process, geranyl diphosphate biosynthetic process, isoprenoid biosynthetic process, lipid metabolic process, sterol biosynthetic process, sterol biosynthetic process	8.61	30.13	30.13
CYBER3	L-ascorbic acid metabolic process, cholesterol biosynthetic process, lipid metabolic process, oxidation-reduction process, steroid biosynthetic process, sterol biosynthetic process	48.96	86.10	86.10
PAH2B2	1'-phosphoadenosine 5'-phosphatidylate biosynthetic process, phosphorylation, sulfate assimilation	32.29	27.98	27.98
RAN	DNA metabolic process	25.83	43.09	43.09
RPL4	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay, rRNA processing, translation, translational initiation, viral transcription	38.74	38.74	38.74
MTFPE1	folic acid metabolic process, folic acid-containing compound biosynthetic process, folic acid-containing compound metabolic process, formate metabolic process, one-carbon metabolic process, oxidation-reduction process, tetrahydrofolate interconversion, tetrahydrofolate metabolic proce	19.27	38.74	38.74
HADHB	cardiolipin acyl-chain remodeling, fatty acid-beta-oxidation, fatty acid metabolic process, lipid metabolic process	27.98	49.51	49.51
EEF1D	mRNA transcription, transcription, DNA-templated, translation, translational elongation	34.44	51.66	51.66
PI	translate metabolic process, malate metabolic process, tricarboxylic acid cycle	32.29	23.68	23.68
RP41	diphosphate metabolic process, phosphate-containing compound metabolic process, RNA aminoacylation for protein translation	27.98	27.98	27.98
RPL5	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay, rRNA processing, translation, translational initiation, viral transcription	30.13	34.44	34.44
RPB2	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay, rRNA processing, translation, translational initiation, viral transcription	23.68	36.59	36.59
COL1A1	collagen catabolic process, peptide cross-linking	21.52	60.27	60.27
PRKCSH	N-glycan processing	30.13	34.44	34.44
MRCC2	collagen catabolic process	40.90	23.68	23.68
PMEE2	MAPK cascade, anaphase-promoting complex-dependent catabolic process, protein polyubiquitination	12.91	34.44	34.44

¹Exponentially Modified Protein Abundance Index (http://www.matrixscience.com/help/pquant_empa1_help.html).

Table S7. Cont'd

UniProt/Swiss-Prot Accession ID	Biological Process	enrichment p-value	enrichment q-value
ATC	de novo IMP biosynthetic process, cubitamine metabolic process, dithyrosine metabolic process, nucleoside metabolic process, purine ribonucleoside homopolymer biosynthetic process, ribonucleoside metabolic process, tetrahydrofolate biosynthetic process	19.27	24.59
RPB5	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay, RNA processing, translation, translational initiation, viral transcription	16.81	23.88
ACAT2	fatty acid beta-oxidation, lipid metabolic process, metabolic process	17.74	21.82
TS11	mRNA processing, mRNA splicing, via spliceosome, transcription from RNA polymerase I promoter	17.23	23.53
AKR1B1	C21 steroid hormone biosynthetic process, carbohydrate metabolic process, daunoside metabolic process, deoxorubicin metabolic process, fructose biosynthetic process, monosaccharide metabolic process, naphthene metabolic process, norepinephrine metabolic process, oxidation-reductase activity	16.81	25.83
QL5	cellular amino acid biosynthetic process, glutamate biosynthetic process, glutamine catabolic process	6.54	36.89
PCBP2	RNA-dependent viral translational initiation, gene expression, mRNA metabolic process, mRNA splicing, via spliceosome, proteasome-mediated ubiquitin-dependent protein catabolic process, viral RNA genome replication	16.87	27.98
RPB8	maturation of SSU-rRNA from trichloric RNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA), nuclear-transcribed mRNA catabolic process, nonsense-mediated decay, translation, translational initiation, viral transcription	14.94	27.88
SCN11	proteolysis	14.94	27.88
SDS	RNA-dependent viral translational initiation, RNA processing, histone mRNA metabolic process, RNA modification	16.88	12.91
PBM4	MAPK cascade, anaphase-promoting complex-dependent catabolic process, proteasome-mediated ubiquitin-dependent protein catabolic process, protein polyubiquitination, proteolysis, ubiquitin-dependent ERAD pathway	15.87	25.83
RPB15	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay, RNA processing, translation, translational initiation, viral transcription	16.88	19.37
RPB4	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay, RNA processing, translation, translational initiation, viral transcription	16.87	27.98
LAP1	UDP-N-acetylglucosamine biosynthetic process	14.91	17.22
ITD4V	ERK1 and ERK2 cascade	3.74	43.95
EPF2	formation of translation preinitiation complex, nuclear-transcribed mRNA catabolic process, nonsense-mediated decay, translation	21.48	16.78
SDN1	transcription, DNA-templated	16.81	19.37
EPF21	protein autophosphorylation, translation, translational initiation, xenophagy	19.27	34.44
EPF4	cytoplasmic translation, formation of translation preinitiation complex, translation	14.94	21.82
PABPC4	RNA catabolic process, mRNA polyadenylation, mRNA processing, mRNA splicing, via spliceosome, nuclear-transcribed mRNA catabolic process, nonsense-mediated decay, nuclear-transcribed mRNA poly(A) tail shortening, translation, translational initiation	17.74	23.53
PABPC1	mRNA polyadenylation, mRNA processing, mRNA splicing, via spliceosome, nuclear-transcribed mRNA catabolic process, nonsense-mediated decay, nuclear-transcribed mRNA poly(A) tail shortening, translational initiation	17.74	23.88
PBM7	MAPK cascade, anaphase-promoting complex-dependent catabolic process, proteasome-mediated ubiquitin-dependent protein catabolic process, protein polyubiquitination, proteolysis, proteolysis involved in cellular protein catabolic process, ubiquitin-dependent protein catabolic process	14.94	19.37
RP13	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay, RNA processing, translation, translational initiation, viral transcription	14.94	27.98
YARS	RNA aminoacylation for protein translation, translation, tyrosyl-tRNA aminoacylation, valyl-tRNA aminoacylation	19.27	32.29
HSD17B4	alpha-ketoglutarate metabolic process, androgen metabolic process, bile acid biosynthetic process, estrone metabolic process, fatty acid beta-oxidation, fatty acid beta-oxidation involving acyl-CoA oxidase, medium-chain fatty-acyl-CoA metabolic process, oxidation-reduction process, very long-chain fatty acid metabolism	6.54	32.29
SDC4	4-hydroxyproline metabolic process, cellular protein modification process, oxidation-reduction process, protein maturation by protein folding	17.74	12.91
PBM3	MAPK cascade, anaphase-promoting complex-dependent catabolic process, proteasome-mediated ubiquitin-dependent protein catabolic process, protein polyubiquitination, ubiquitin-dependent protein catabolic process	14.94	36.89
LAP3	protein metabolic process, proteolysis	11.21	27.98
MTN1	catecholamine metabolic process	16.88	16.78
ALDH1A1	L-proline biosynthetic process, cellular amino acid biosynthetic process, citrulline biosynthetic process, glutamate metabolic process, ornithine biosynthetic process, oxidation-reduction process, phosphorylation	13.87	21.82
RAO23B	global genome nucleotide-excision repair, nucleotide-excision repair, DNA damage recognition, nucleotide-excision repair, DNA duplex unwinding, nucleotide-excision repair, preincision complex assembly, proteasome-mediated ubiquitin-dependent protein catabolic process	12.14	23.88
NARS	carbamate biosynthetic process, homopolymer biosynthetic process	14.91	25.83
UBR3L3	cellular protein modification process, protein K11-linked ubiquitination, protein polyubiquitination, protein ubiquitination, transcription, DNA-templated, ubiquitin-dependent protein catabolic process	15.88	17.22
EPF3	formation of translation preinitiation complex, translation	6.54	36.13
BLCC	protein ubiquitination involved in ubiquitin-dependent protein catabolic process, transcription elongation from RNA polymerase II promoter, transcription from RNA polymerase II promoter, transcription, DNA-templated, ubiquitin-dependent protein catabolic process	14.91	25.83
LT4H	leukotriene biosynthetic process, leukotriene metabolic process, peptide catabolic process, proteolysis	6.40	27.98
PBM8	MAPK cascade, anaphase-promoting complex-dependent catabolic process, protein polyubiquitination, proteolysis involved in cellular protein catabolic process	11.21	23.88
RA7B1	supernumerary factor catabolic process, lipid catabolic process, lipid metabolic process, lipophagy	14.94	27.98
RPB10	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay, RNA processing, translation, translational initiation, viral transcription	14.94	16.78
STRAP	RNA splicing, mRNA processing, spliceosomal snRNP assembly	6.40	36.13
CBR1	cytochrome P-450 metabolic process, drug metabolic process, oxidation-reduction process, phytylquinone catabolic process, vitamin K metabolic process	4.87	36.74
CBR3	oxidation-reduction process, phytylquinone catabolic process	3.74	12.91
SLC3A2	carbohydrate metabolic process	1.87	43.95
ETP1	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay, protein methylation, translational termination	12.14	15.87
PSPF9	protein peptidyl-prolyl isomerization	6.80	36.89
GOI1	oxidation-reduction process	28.95	55.94
EPF23	formation of translation preinitiation complex, translation	4.87	36.74
PRKACA	lipopeptide metabolic process, mRNA processing, peptidyl-serine phosphorylation, peptidyl-threonine phosphorylation, phosphorylation, protein autophosphorylation	6.40	19.37
PRKACB	lipopeptide metabolic process, phosphorylation, protein phosphorylation	6.40	16.78
PBM2	MAPK cascade, anaphase-promoting complex-dependent catabolic process, proteasome-mediated ubiquitin-dependent protein catabolic process, protein polyubiquitination, proteolysis, proteolysis involved in cellular protein catabolic process	15.87	16.78
DRNR1A1	RNA splicing, gene expression, mRNA processing, mRNA splicing, via spliceosome	13.87	12.91
RARS	arginyl-tRNA aminoacylation, tRNA aminoacylation for protein translation, translation	6.54	36.89
TARS	tRNA aminoacylation for protein translation, tRNA aminoacylation, translation	6.54	27.98
UREY1	DNA double-strand break processing, double-strand break repair via nonhomologous end joining, error-free postreplicative DNA repair, global genome nucleotide-excision repair, postreplicative repair, protein K3-linked ubiquitination	6.54	19.37
UREY2	DNA double-strand break processing, double-strand break repair via nonhomologous end joining, error-free postreplicative DNA repair, global genome nucleotide-excision repair, protein K3-linked ubiquitination	6.54	27.98
RN11	purine ribonucleotide catabolic process, transcription, DNA-templated	7.47	19.37
ALDH1A1	carbamate biosynthetic process, cellular amino acid biosynthetic process, hormone metabolic process, neurotransmitter biosynthetic process, oxidation-reduction process	16.88	16.78
SLU11	cellular amino acid biosynthetic process, glutamate biosynthetic process, glutamate catabolic process, glutamine metabolic process, oxidation-reduction process, tricarboxylic acid metabolic process	16.88	4.31
DNK3	RNA processing, mRNA splicing, via spliceosome	6.40	27.88
EPF26	formation of translation preinitiation complex, translation	16.87	19.37
PUB1A	amyloid fibril formation, protein maturation by protein folding, protein peptidyl-prolyl isomerization	19.27	21.82
RPB8	cytoplasmic translation, nuclear-transcribed mRNA catabolic process, nonsense-mediated decay, RNA processing, translation, translational initiation, viral transcription	9.34	21.82
RP17	cytoplasmic translation, maturation of LSU-rRNA from trichloric RNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA), nuclear-transcribed mRNA catabolic process, nonsense-mediated decay, translation, translational initiation, viral transcription	7.47	17.22
NARS	histidyl-tRNA aminoacylation, mitochondrial translation	11.21	21.82
LARS	leucyl-tRNA aminoacylation, translation	6.40	25.83
NARS	asparaginyl-tRNA aminoacylation, tRNA aminoacylation for protein translation, translation	6.54	27.88
SRP14	protein deubiquitination, ubiquitin-dependent protein catabolic process	13.87	12.91
CARS	carbamyl-tRNA aminoacylation, translation	3.74	34.44
RP129	cytoplasmic translation, nuclear-transcribed mRNA catabolic process, nonsense-mediated decay, RNA processing, translation, translational initiation, viral transcription	7.47	27.98
PBM73	DNA-templated transcription, termination, covalent chromatin modification, histone H4 H3 methylation, methylation, peptidyl-arginine methylation, peptidyl-arginine methylation, to symmetrical dimethyl arginine, spliceosomal snRNP assembly, transcription, DNA-templated	12.14	12.91
DOX1	RNA secondary structure unwinding, double-strand break repair, mRNA processing, nucleic acid phosphodiester bond hydrolysis, spliceosomal complex assembly, RNA processing, RNA splicing, via endonucleolytic cleavage and ligation, transcription, DNA-templated	6.80	32.29
SDP17	cytoplasmic translational termination, nuclear-transcribed mRNA catabolic process, nonsense-mediated decay, protein methylation, translation	3.74	17.22
SHR2	L-serine biosynthetic process, folic acid metabolic process, glycine biosynthetic process from serine, one-carbon metabolic process, protein K3-linked deubiquitination, tetrahydrofolate interconversion, tetrahydrofolate metabolic process	19.27	21.82
LAMP1	autophagy	19.27	17.22
PAK2	MAPK cascade, histone H2B-H4 phosphorylation, peptidyl-serine phosphorylation, phosphorylation, protein autophosphorylation	12.14	16.78
PNL1	canonical glycolysis, carbohydrate metabolic process, fructose 1,6-bisphosphate metabolic process, fructose 6-phosphate metabolic process, glycolytic process, glycolytic process through fructose-6-phosphate, metabolic process, phosphorylation	13.87	23.88
PBM3	MAPK cascade, anaphase-promoting complex-dependent catabolic process, protein polyubiquitination, ubiquitin-dependent ERAD pathway	14.94	36.89
NPEP5	peptide catabolic process, protein polyubiquitination, proteolysis	13.87	12.91
SRH	polyamine biosynthetic process, spermidine biosynthetic process	7.47	27.98
QARS	glutamyl-tRNA aminoacylation, translation	11.21	16.78
SDHA	aerobic respiration, cellular respiration, mitochondrial electron transport, succinate to ubiquinone, oxidation-reduction process, respiratory electron transport chain, succinate metabolic process, tricarboxylic acid cycle	6.80	19.37
PAP5	glucose metabolic process, phosphatidylcholine biosynthetic process, triglyceride catabolic process	16.87	12.91
PBM45	MAPK cascade, RNA phosphodiester bond hydrolysis, anaphase-promoting complex-dependent catabolic process, proteasome-mediated ubiquitin-dependent protein catabolic process, protein polyubiquitination, proteolysis involved in cellular protein catabolic process	6.93	36.74
GO11	2-oxoglutarate metabolic process, aspartate biosynthetic process, aspartate catabolic process, biosynthetic process, cellular amino acid biosynthetic process, dicarboxylic acid metabolic process, gluconeogenesis, glutamate catabolic process to 2-oxoglutarate, glutamate catabolic process to aspartate, glutamate	4.87	32.29
OS	carbohydrate metabolic process, tricarboxylic acid cycle	17.74	4.31
COL1A1	collagen biosynthetic process, collagen catabolic process, integrin biosynthetic process	3.74	34.44
REXB	carbohydrate metabolic process, cellular protein metabolic process, chondroitin sulfate catabolic process, ganglioside catabolic process, glycosaminoglycan metabolic process, glycosphingolipid metabolic process, hyaluronan catabolic process, keratan sulfate catabolic process, oligosaccharide catabolic process	9.34	17.22
HNRNH8	alternative mRNA splicing, via spliceosome, gene expression, mRNA processing, mRNA splicing, via spliceosome	9.34	21.82
EPF8	translation, translational initiation	11.21	16.78
PAPF1B2	lipid catabolic process	14.91	12.91
PBM14	MAPK cascade, anaphase-promoting complex-dependent catabolic process, double-strand break repair via homologous recombination, double-strand break repair via nonhomologous end joining, proteasome-mediated ubiquitin-dependent protein catabolic process, protein K3-linked deubiquitination	12.14	16.78
RP13	cytoplasmic translation, nuclear-transcribed mRNA catabolic process, nonsense-mediated decay, RNA processing, translation, translational initiation, viral transcription	19.27	19.37
ANCY	S-adenosylhomocysteine catabolic process, S-adenosylmethionine cycle, homocysteine biosynthetic process, methylation, one-carbon metabolic process	12.14	19.37
SET	DNA replication	11.21	12.91
PBM88	MAPK cascade, anaphase-promoting complex-dependent catabolic process, protein polyubiquitination, proteolysis, proteolysis involved in cellular protein catabolic process	6.40	27.98
DNK2	2-oxoglutarate metabolic process, carbohydrate metabolic process, glyoxylate cycle, isocitrate metabolic process, oxidation-reduction process, tricarboxylic acid cycle	6.40	21.82
PICALM	positive regulation of aspartic-type endopeptidase activity involved in amyloid precursor protein catabolic process, receptor internalization	6.80	23.88
ALDH1A1	cellular amino acid metabolic process, choline catabolic process, glycine betaine biosynthetic process from choline, lysine catabolic process, metabolic process, oxidation-reduction process	16.88	16.13
ASNS	L-asparagine biosynthetic process, asparagine biosynthetic process, cellular amino acid biosynthetic process, glutamine metabolic process	6.93	36.89
QAT	L-proline biosynthetic process, arginine catabolic process to glutamate, arginine catabolic process to proline via ornithine, cellular amino acid biosynthetic process	4.87	36.13

*Experimentally Modified Protein Abundance Index (<http://www.matrixscience.com/help/help.html>).

Table S7. Cont 3

UniProt/Swiss-Prot ID	Biological Process	enrP47	enrP47
Accession ID	Biological regulation	CDM	OMEB
P0871	galactose catabolic process, gluconeogenesis, glycogen biosynthetic process, glycogen catabolic process, glycolytic process, organic substance metabolic process	6.54	27.83
P0872	transcription, DNA-templated	9.34	18.37
P08A2	MAPK cascade, anaphase-promoting complex-dependent catabolic process, proteasome-mediated ubiquitin-dependent protein catabolic process, protein polyubiquitination, proteolysis involved in cellular protein catabolic process	14.94	8.61
P08B4	MAPK cascade, anaphase-promoting complex-dependent catabolic process, proteasome-mediated ubiquitin-dependent protein catabolic process, protein polyubiquitination, proteolysis involved in cellular protein catabolic process	7.47	17.22
P08D13	MAPK cascade, anaphase-promoting complex-dependent catabolic process, proteasome-mediated ubiquitin-dependent protein catabolic process, protein polyubiquitination, ubiquitin-dependent protein catabolic process	13.07	12.91
P08C5	de novo IMP biosynthetic process, adenine biosynthetic process, purine ribonucleoside monophosphate biosynthetic process	8.40	21.82
C4LD	de novo IMP biosynthetic process, de novo pyrimidine nucleoside biosynthetic process, GTP biosynthetic process, arginine biosynthetic process, creatinine biosynthetic process, drug metabolic process, glutamine metabolic process, nitrogen compound metabolic process	8.40	21.82
RPL11	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay, rRNA processing, translation, translational initiation, viral transcription	8.40	18.37
UBR4	protein ubiquitination, protein ubiquitination involved in ubiquitin-dependent protein catabolic process	7.47	17.22
P08C2	MAPK cascade, anaphase-promoting complex-dependent catabolic process, protein polyubiquitination, ubiquitin-dependent ERAD pathway	9.34	18.37
APRT	AMP salvage, adenine metabolic process, adenine salvage, nucleoside metabolic process	10.27	16.76
CD-C42	protein ubiquitination, viral RNA genome replication	10.27	17.22
TUFR	mitochondrial translational elongation, translation, translational elongation	10.27	12.91
WMP14	collagen catabolic process, protein processing, proteolysis, zymogen activation	0.93	14.44
OLA1	ATP metabolic process	10.27	12.91
PYP2CA	RNA splicing, caramide metabolic process, nuclear-transcribed mRNA catabolic process, nonsense-mediated decay, protein dephosphorylation	4.87	13.91
RPL16	cytoplasmic translation, nuclear-transcribed mRNA catabolic process, nonsense-mediated decay, rRNA processing, translation, translational initiation, viral transcription	8.40	17.22
EH01	receptor recycling	5.80	27.86
INR0DRL3	oxidation-reduction process	10.27	8.40
DPN4	proteolysis	0.93	16.69
CD-C37	peptidyl-tyrosine phosphorylation	4.87	21.82
CPNE1	glycerophospholipid biosynthetic process, lipid metabolic process, proteolysis, transcription, DNA-templated	12.94	16.76
DPN3	proteolysis	14.91	6.48
KHSRP	RNA splicing, via transsplicing reactions, mRNA catabolic process, mRNA processing, transcription, DNA-templated	6.54	16.76
IBH9P	starkeyic acid metabolic process, glyoxylate metabolic process, oxidation-reduction process	7.47	17.22
WDRN7	gene expression, mRNA processing, mRNA splicing, via spliceosome	5.80	12.94
PAFAH1B1	lipid catabolic process, platelet activating factor metabolic process	9.34	12.91
PHB	DNA biosynthetic process, histone deacetylation	9.34	12.91
PNP	NAD biosynthesis via nicotinamide ribotide salvage pathway, inosine catabolic process, nicotinamide riboside catabolic process, purine nucleoside metabolic process, purine nucleotide catabolic process, purine-containing compound salvage, urate biosynthetic process	5.80	21.82
P08C3	MAPK cascade, anaphase-promoting complex-dependent catabolic process, protein polyubiquitination, transcription from RNA polymerase II promoter, ubiquitin-dependent ERAD pathway	7.47	17.22
P08B3	MAPK cascade, anaphase-promoting complex-dependent catabolic process, proteasome-mediated ubiquitin-dependent protein catabolic process, protein polyubiquitination, proteolysis involved in cellular protein catabolic process	8.40	17.22
P08B1	histidine metabolic process, oxidation-reduction process, prostaglandin metabolic process	10.27	16.76
RPL17	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay, rRNA processing, translation, translational initiation, viral transcription	8.40	18.37
KAR3	disubstituted triphosphatase biosynthetic process, tryptophan biosynthetic process, RNA processing, translation	10.27	12.91
RPL17	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay, rRNA processing, translation, translational initiation, viral transcription	10.27	12.91
EF3M	cytoplasmic translation initiation, formation of translation preinitiation complex, translation	6.54	17.22
EF3M	formation of translation preinitiation complex, translation, viral translational termination-reinitiation	6.54	16.76
CCSC47	ubiquitin-dependent ERAD pathway	5.80	12.91
UBE2N	DNA double-strand break processing, double-strand break repair via homologous recombination, double-strand break repair via nonhomologous end joining, global genome nucleotide excision repair, histone ubiquitination, postreplication repair, protein K63-linked ubiquitination, proteolysis	9.34	16.76
ALDH1	carbohydrate metabolic process, ethanol catabolic process, ethanol oxidation, oxidation-reduction process	13.07	4.31
SLURA	homeostatic process, oxidation-reduction process	11.21	6.48
EF3F	RES-dependent viral translational initiation, formation of translation preinitiation complex, protein deubiquitination, translation	10.27	12.91
PHL2	transcription, DNA-templated	3.74	23.88
SEA	carbohydrate metabolic process, ceramide biosynthetic process, glycosylceramide catabolic process, glycosphingolipid metabolic process, sphingine biosynthetic process	7.47	17.22
SLRX3	oxidation-reduction process	10.27	8.61
SYNCRP	RNA splicing, mRNA processing, mRNA splicing, via spliceosome	3.74	17.22
SLX	peptidyl-tyrosine phosphorylation, phosphorylation	12.94	16.76
IMPCH2	GMP biosynthetic process, GTP biosynthetic process, oxidation-reduction process, purine ribonucleoside monophosphate biosynthetic process	7.47	17.22
BL01	carbohydrate metabolic process, glutathione metabolic process, methylglyoxal metabolic process, pyruvate metabolic process	9.34	8.61
NC05	oligosaccharide metabolic process, protein N-linked glycosylation	12.94	16.76
QPR1	NAD biosynthetic process, NAD metabolic process, quinolate catabolic process	11.21	2.18
PCNA	DNA replication, error-free translesion synthesis, error-prone translesion synthesis, leading strand elongation, mismatch repair, mitotic telomere maintenance via semi-conservative replication, nucleotide-excision repair, DNA gap filling, nucleotide-excision repair, DNA incision, 5'-to-3' lesion	8.40	16.76
PRP7	proteolysis	4.87	23.88
P08B8	MAPK cascade, anaphase-promoting complex-dependent catabolic process, proteasome-mediated ubiquitin-dependent protein catabolic process, protein polyubiquitination, proteolysis involved in cellular protein catabolic process	8.40	16.76
P08D7	MAPK cascade, anaphase-promoting complex-dependent catabolic process, protein polyubiquitination	4.87	18.37
RPL18	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay, rRNA processing, translation, translational initiation, viral transcription	10.27	27.86
RPL9	mitochondrial translation, mitochondrial translational elongation, mitochondrial translation termination	6.54	17.22
SMS	methionine metabolic process, spermine biosynthetic process, spermine metabolic process	5.80	21.82
TSPD	heme biosynthetic process, steroid biosynthetic process, steroid metabolic process	9.34	8.61
RPL13	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay, rRNA processing, translation, translational initiation, viral transcription	8.40	17.22
ECM29	ubiquitin-dependent ERAD pathway	6.54	12.91
PLXN1	blood coagulation, fibrin clot formation	4.87	23.88
PYP2CA	dephosphorylation, protein dephosphorylation	1.87	17.22
CR1AP	peptidyl-proline hydroxylation to 3-hydroxy-L-proline	9.34	12.91
TNND1	transcription, DNA-templated	4.87	21.82
DT01	D-amino acid catabolic process, DNA replication, tRNA metabolic process	6.54	12.91
GN5	glycosaminoglycan metabolic process, keratan sulfate catabolic process, metabolic process	7.47	8.61
PCXK	phosphorylation, pyridoxal 5'-phosphate salvage, vitamin B6 metabolic process	3.74	19.37
SEA15	MAPK cascade	6.54	19.37
PRDX2	hydrogen peroxide catabolic process, oxidation-reduction process, removal of superoxide radicals	11.21	18.37
P08B1	MAPK cascade, anaphase-promoting complex-dependent catabolic process, proteasome-mediated ubiquitin-dependent protein catabolic process, protein polyubiquitination, proteolysis involved in cellular protein catabolic process	8.40	17.22
TNND17	oxidation-reduction process	5.80	21.82
USP5	protein K48-linked deubiquitination, proteolysis, ubiquitin-dependent protein catabolic process	11.21	8.61
RPL15A	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay, rRNA processing, translation, translational initiation, viral transcription	5.80	19.37
MCT51	RES-dependent translational initiation, formation of translation preinitiation complex, transcription, DNA-templated, translation	9.34	27.86
P08B7	MAPK cascade, anaphase-promoting complex-dependent catabolic process, proteasome-mediated ubiquitin-dependent protein catabolic process, protein polyubiquitination, proteolysis, proteolysis involved in cellular protein catabolic process	9.34	12.91
P08C3	MAPK cascade, anaphase-promoting complex-dependent catabolic process, proteasome-mediated ubiquitin-dependent protein catabolic process, protein catabolic process, protein polyubiquitination, ubiquitin-dependent ERAD pathway	7.47	16.76
PNC	protein deoxyribonucleic acid isomerization	10.27	8.61
EF6	maturation of 5.8S rRNA, maturation of 18S rRNA, translation, translational initiation	7.47	16.76
EF3A	RES-dependent viral translational initiation, formation of cytoplasmic translation initiation complex, formation of translation preinitiation complex, translation reinitiation, viral translational termination-reinitiation	2.80	26.13
PRP182A	protein dephosphorylation	5.80	16.76
AMP2	tRNA aminoacylation for protein translation, translation	8.40	12.91
CYC5	cellular respiration, mitochondrial electron transport, cytochrome c to oxygen, mitochondrial electron transport, ubiquinol to cytochrome c, oxidation-reduction process, protein dephosphorylation	12.94	4.31
SDH1212	nitrogen biosynthetic process, fatty acid biosynthetic process, lipid metabolic process, long-chain fatty acyl-CoA biosynthetic process, oxidation-reduction process, steroid biosynthetic process	4.87	17.22
GS5	cellular amino acid metabolic process, glutathione biosynthetic process	4.87	18.37
HA0H	fatty acid beta-oxidation, lipid metabolic process, oxidation-reduction process	5.80	16.76
WPI2	protein maturation	10.27	6.48
MP0E8	cellular protein metabolic process	4.87	17.22
NACA	transcription, DNA-templated	4.87	17.22
N4DK	N-acetylglucosamine metabolic process, N-acetylglucosamine metabolic process, N-acetylglucosamine catabolic process, UDP-N-acetylglucosamine biosynthetic process, carbohydrate phosphorylation, phosphorylation	1.87	11.63
OTUB1	DNA repair, protein K48-linked deubiquitination, protein deubiquitination	6.54	12.91
PEPD	cellular amino acid metabolic process, collagen catabolic process, proteolysis	7.47	16.76
CTSA	glycosphingolipid metabolic process, proteolysis involved in cellular protein catabolic process	7.47	16.76
DLD	2-oxoglutarate metabolic process, branched-chain amino acid catabolic process, dihydrofolate metabolic process, glycylglycine metabolic process, lipote metabolic process, lysine catabolic process, mitochondrial acetyl-CoA biosynthetic process from pyruvate, mitochondrial electron transport, NADH to ubiquinone	4.87	17.22
RPL22	cytoplasmic translation, nuclear-transcribed mRNA catabolic process, nonsense-mediated decay, rRNA processing, translation, translational initiation, viral transcription	8.40	12.91
ITAT2	transcription, DNA-templated	7.47	6.48
ALPH	activation of cysteine-type endopeptidase activity, oxidation-reduction process, peptidyl-amino acid modification	10.27	2.18
ACB3	fatty acid biosynthetic process, lipid metabolic process, long-chain fatty acid metabolic process, long-chain fatty acyl-CoA biosynthetic process, metabolic process	11.21	6.48
APRX1	DNA demethylation, DNA recombination, RNA phospholipid transfer, bond hydrolysis, endonucleolytic, base-excision repair, base-excision repair, base-free superphosphate removal, nucleic acid phosphodiester bond hydrolysis, oxidation-reduction process, telomere maintenance, transcription, DNA-templated	12.94	2.18
DCB1	UV-damage excision repair, global genome nucleotide-excision repair, histone H2A monoubiquitination, nucleotide-excision repair, DNA damage recognition, nucleotide-excision repair, DNA incision, 5'-to-3' lesion	4.87	17.22

*Exponentially Modified Protein Abundance Index (http://www.ma.utexas.edu/help/quant_enrP47_help.html)

Table S7. Cont'd

UniProt/Swiss-Prot Accession ID	Biological Process	GO	OMIM
GO	muscle biosynthetic process	4,877	15,871
EP3H	formation of translation preinitiation complex, translation, translational initiation	8,334	6,446
EPDP1	2'-phosphoadenosine 5'-phosphatidyltransferase metabolic process, generation of precursor metabolites and energy, nucleic acid phosphodiester bond hydrolysis, nucleoside triphosphate catabolic process, riboflavin metabolic process	8,334	12,831
PL2	transcription, DNA-templated	7,471	8,431
GO1K1	glutathione derivative biosynthetic process, glutathione metabolic process, oxidation-reduction process	8,334	15,871
HS017010	branched-chain amino acid catabolic process, lipid metabolic process, mitochondrial RNA methylation, mitochondrial RNA processing, oxidation-reduction process, RNA processing	7,471	15,774
SE2A	carbohydrate metabolic process, cholesterol sulfate catabolic process, glycoside catabolic process, glycosaminoglycan biosynthetic process, glycosaminoglycan metabolic process, glycosylating lipid metabolic process, hyaluronan catabolic process, keratan sulfate catabolic process	8,334	12,831
LMAA1	protein N-linked glycosylation via asparagine	8,446	12,831
PCR	carbinol metabolic process, cellular organophosphorus metabolic process, demethylation, fatty acid oxidation, flavonoid metabolic process, internal peptidyl-lysine acetylation, nitrate catabolic process, nitric oxide catabolic process, oxidation-reduction process, xenobiotic metabolic process	8,334	8,446
PCD2	hydrogen peroxide catabolic process, oxidation-reduction process, peptidyl-cysteine oxidation	7,471	12,831
PRP91	5-phosphoribose 1-diphosphate biosynthetic process, AMP biosynthetic process, cellular biosynthetic process, hypoxanthine biosynthetic process, nucleoside metabolic process, nucleoside biosynthetic process, phosphorylation, purine nucleobase metabolic process, pyrimidine nucleoside biosynthetic process, RNA processing	2,889	17,222
PSMD4	MAPK cascade, anaphase-promoting complex-dependent catabolic process, proteasome-mediated ubiquitin-dependent protein catabolic process, protein polyubiquitination, ubiquitin-dependent protein catabolic process	4,877	15,871
GAAT	de novo AMP biosynthetic process, biosynthetic process, glycine metabolic process, purine nucleobase biosynthetic process, purine ribonucleoside monophosphate biosynthetic process, ribonucleoside monophosphate biosynthetic process, tetrahydrofolate biosynthetic process	8,446	15,774
SKP1	DCF-dependent proteasomal ubiquitin-dependent protein catabolic process, histone H2A monoubiquitination, proteasome-mediated ubiquitin-dependent protein catabolic process, protein polyubiquitination, protein ubiquitination, stress-activated MAPK cascade, ubiquitin-dependent protein catabolic process	3,734	21,232
DARS	peptidyl-RNA aminoacylation, translation	2,889	22,846
US2K	proteasome-mediated ubiquitin-dependent protein catabolic process, protein K48-linked ubiquitination	7,471	12,831
CDB1	glutathione derivative biosynthetic process, glutathione metabolic process, oxidation-reduction process, xenobiotic metabolic process	8,446	15,774
PCP91	de novo CTP biosynthetic process, CTP biosynthetic process, glutamine metabolic process, nucleobase-containing small molecule interconversion, pyrimidine nucleoside biosynthetic process	7,471	12,831
PLB2	lipid catabolic process, lipid metabolic process	7,471	8,446
RPL21	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay, RNA processing, translation, translational initiation, viral transcription	4,877	15,871
PCOLCE	metabolism	8,334	4,231
APMAP	biosynthetic process	7,471	8,446
CPY1	glutathione metabolic process, hydrogen peroxide catabolic process, lipid metabolic process, lipoygenase pathway, oxidation-reduction process, protein oxidation, purine nucleoside catabolic process, triglyceride metabolic process	3,734	12,831
RPL19	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay, RNA processing, translation, translational initiation, viral transcription	7,471	15,774
ODDH	2-oxoglutarate metabolic process, NADH metabolic process, generation of precursor metabolites and energy, glycolytic process, glyoxylate metabolic process, lysine catabolic process, oxidation-reduction process, succinyl-CoA metabolic process, tricarboxylic acid cycle	8,334	4,231
TNINB1	proteasome-mediated ubiquitin-dependent protein catabolic process, transcription, DNA-templated	8,334	21,232
AKR1A1	D-glucuronate catabolic process, L-ascorbate acid biosynthetic process, aldehyde metabolic process, cellular aldehyde metabolic process, glucose metabolic process, glucuronate catabolic process to xylulose 5-phosphate, glutathione derivative biosynthetic process, oxidant separate biosynthetic process, branched-chain amino acid biosynthetic process, branched-chain amino acid catabolic process, lysine biosynthetic process, valine biosynthetic process	3,734	21,232
BCAT1	aspartate biosynthetic process, branched-chain amino acid biosynthetic process, branched-chain amino acid catabolic process, lysine biosynthetic process, valine biosynthetic process	2,889	21,232
CARM1	cellular lipid metabolic process, covalent chromatin modification, histone H3 R17 methylation, histone H3 R2 methylation, histone methylation, methylation, peptidyl-arginine methylation, to asymmetric dimethyl-arginine, transcription, DNA-templated	8,334	17,222
DDX8	RNA secondary structure remodeling, a noncatalytic nuclear-transcribed mRNA catabolic process involved in deadenylation-dependent decay	7,471	6,446
BRP4A	glycoprotein metabolic process	8,334	12,831
PAI	phenylalanine catabolic process, arginine catabolic process, aromatic amino acid family metabolic process, metabolic process, tyrosine catabolic process	8,446	4,231
JOHNPH1	gene expression, mRNA processing, mRNA splicing, via spliceosome	7,471	21,232
AK2	ADP biosynthetic process, AMP metabolic process, ATP metabolic process, nucleobase-containing compound metabolic process, nucleobase-containing small molecule interconversion, nucleotide phosphorylation, phosphorylation	8,334	8,446
MAP1	ADAP biosynthetic process, carboxylate metabolic process, metabolic process, oxidation-reduction process	3,734	15,871
PSMD11	MAPK cascade, anaphase-promoting complex-dependent catabolic process, proteasome-mediated ubiquitin-dependent protein catabolic process, protein polyubiquitination, ubiquitin-dependent protein catabolic process	3,734	15,871
PSMD12	MAPK cascade, anaphase-promoting complex-dependent catabolic process, protein polyubiquitination	3,734	12,831
PTK7	protein phosphorylation	8,334	21,232
RPL18A	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay, RNA processing, translation, translational initiation, viral transcription	1,877	17,222
TGPB10	transcription from RNA polymerase II promoter, ubiquitin-dependent SMAD protein catabolic process	1,877	23,846
TNRC2	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay, RNA processing, translation, translational initiation, viral transcription	1,877	15,871
TYNLL1	macrophage, transcription, DNA-templated	8,446	12,831
BAO2	protein metabolic process	8,446	8,446
DPY3X	covalent chromatin modification, histone H3-K4 methylation, transcription, DNA-templated	7,471	15,774
PCK2	NADH oxidation, gluconeogenesis, oxaloacetate metabolic process, pyruvate metabolic process	1,877	23,846
RPL19	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay, RNA processing, translation, translational initiation, viral transcription	4,877	15,871
LRDQ	heme biosynthetic process, heme metabolic process, protoporphyrinogen IX biosynthetic process	7,471	6,446
ERH	nucleobase-containing compound metabolic process, pyrimidine nucleoside metabolic process, pyrimidine nucleoside biosynthetic process	15,271	2,116
HEPD	carboxylate metabolic process, glucose metabolic process, oxidation-reduction process, pentose-phosphate shunt	8,334	2,116
ACSL	de novo AMP biosynthetic process, de novo AMP biosynthetic process, aerobic respiration, purine nucleoside metabolic process, purine ribonucleoside monophosphate biosynthetic process, ribonucleoside monophosphate biosynthetic process	2,889	17,222
RPL14	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay, RNA processing, translation, translational initiation, viral transcription	2,889	15,871
RPS12	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay, RNA processing, translation, translational initiation, viral transcription	8,334	23,846
RPS22	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay, RNA processing, translation, translational initiation, viral transcription	8,334	23,846
TALDO1	carbohydrate metabolic process, fructose 6-phosphate metabolic process, glyceraldehyde 3-phosphate metabolic process, pentose-phosphate shunt, non-oxidative branch, xylulose biosynthetic process	8,446	15,774
PTGDS	RNA-dependent DNA biosynthetic process, cyclooxygenase pathway, fatty acid biosynthetic process, fatty acid metabolic process, lipid metabolic process, prostaglandin biosynthetic process, prostaglandin metabolic process, telomere maintenance	3,734	17,222
ATP5D	ATP biosynthetic process, ATP synthesis coupled proton transport, mitochondrial ATP synthase coupled proton transport	1,877	12,831
DHRS7	oxidation-reduction process	3,734	15,871
STOML2	mitochondrial ATP synthase coupled proton transport, mitochondrial protein processing	3,734	12,831
PMCK	MAPK cascade, anaphase-promoting complex-dependent catabolic process, protein polyubiquitination, proteolysis	7,471	6,446
ATPPL	mitochondrial ATP synthase coupled proton transport	2,889	15,871
NTSE	AMP metabolic process, DNA metabolic process, adenosine biosynthetic process, dephosphorylation, nucleotide catabolic process, purine nucleoside catabolic process, pyrimidine nucleoside catabolic process	8,334	19,237
AKR1C1	bile acid metabolic process, bile alcohol metabolic process, bile alcohol metabolic process, oxidation-reduction process, pyruvate metabolic process, retinol metabolic process, xenobiotic metabolic process	4,877	12,831
PRMT1	histone H4 R3 methylation, methylation, peptidyl-arginine methylation, to asymmetric dimethyl-arginine	8,446	8,446
CBSL	cellular amino acid biosynthetic process, cysteine biosynthetic process, cysteine biosynthetic process from serine, cysteine biosynthetic process via cystathionine	7,471	12,831
PUS	mRNA splicing, via spliceosome	7,471	12,831
PSME1	MAPK cascade, anaphase-promoting complex-dependent catabolic process, protein polyubiquitination	2,889	15,871
TPD3D	ADAP metabolic process, oxidation-reduction process	2,889	15,871
MECQ	DNA recombination, DNA strand resection, double-strand break repair via homologous recombination	8,334	19,237
RPL12A	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay, RNA processing, translation, translational initiation, viral transcription	2,889	15,871
TNCOV2	transcription from RNA polymerase II promoter	8,446	8,446
SCD1	glutathione metabolic process, hydrogen peroxide biosynthetic process, oxidation-reduction process, removal of superoxide radicals, superoxide anion generation, superoxide metabolic process	4,877	15,871
TARDBP	RNA splicing, mRNA processing, transcription from RNA polymerase II promoter	8,446	15,774
US2K	cellular protein modification process, protein ubiquitination, protein ubiquitination involved in ubiquitin-dependent protein catabolic process, ubiquitin-dependent protein catabolic process	7,471	12,831
ANKK1	autophagy	4,877	12,831
P3H3	collagen metabolic process, oxidation-reduction process, peptidyl-proline hydroxylation	3,734	15,871
US2K	protein sumoylation	2,889	17,222
TNXL1	glycerol ether metabolic process, oxidation-reduction process, sulfate assimilation	2,889	15,871
ABHD10	cellular glucuronidation, glucuronide catabolic process	8,446	8,446
DLRX	nucleobase-containing small molecule interconversion, oxidation-reduction process, protein dephosphorylation	7,471	8,446
ANP2A	transcription, DNA-templated	2,889	15,871
DEC1	fatty acid beta-oxidation, lipid metabolic process, oxidation-reduction process	8,446	4,231
EP3H	MEK-dependent viral translational initiation, formation of translation preinitiation complex, translation, viral translational initiation-translation	1,877	15,871
OPT2	UDP-A-acetylglucosamine biosynthetic process, carboxylate derivative biosynthetic process, carbohydrate metabolic process, energy reserve metabolic process, fructose 6-phosphate metabolic process, glutamine metabolic process	11,271	15,774
LOXLS1	RNA splicing, mRNA processing	2,889	15,871
ACA44	alpha-ketoglutarate metabolic process, bile acid metabolic process, fatty acid beta-oxidation, fatty acid beta-oxidation using acyl-CoA oxidase, very long-chain fatty acid metabolic process	8,446	19,237
TNKS	peptidyl-cysteine oxidation	3,734	12,831
ACPI	peptidyl-tyrosine dephosphorylation	4,877	15,774
TNKS	transcription, DNA-templated	4,877	19,237
UBE2Q2	protein K48-linked ubiquitination, protein autoubiquitination, ubiquitin-dependent protein catabolic process	8,446	4,231
JOHNPH2	gene expression, mRNA splicing, via spliceosome	2,889	15,871

*Exponentially Modified Protein Abundance Index (http://www.matrixscience.com/help/quant_ompi_help.html).

Table S8. Identification of endogenous proteins (Biological Process: response to stimulus) in hADSC; group CDM & DMEM.

Table S8. Identification of endogenous proteins (Biological Process: response to stimulus) in hADSC; group CDM & DMEM			
UniProt/Swiss-Prot	Biological Process	anPA*	
Alternate ID	response to stimulus	CDM	DMEM
ACTA2	response to virus	286276	439.10
ITIH1	EMAP protein signal transduction, axon regeneration, cellular response to estradiol stimulus, cellular response to fibroblast growth factor stimulus, cellular response to oxidative stress, response to acrylamide, response to cocaine, response to estradiol	188.29	1189.85
TUBB8	axon guidance, natural killer cell mediated cytotoxicity	468.41	862.32
TUBB3	axon guidance	296.38	219.18
TUBB	natural killer cell mediated cytotoxicity	284.44	298.85
TUBB4B	natural killer cell mediated cytotoxicity	286.69	289.89
MYH9	aggregation involved in sorcap development, axon guidance, cardiac muscle hypertrophy in response to stress, chemotaxis, hypotonic response, integrin-mediated signaling pathway, plasma membrane repair, platelet aggregation, response to hydrogen peroxide, response to mechanical stimulus	280.70	801.88
ITIH2	axon guidance, plasma membrane repair	18.86	124.84
PLA2	adenosine cyclase-inhibiting G-protein coupled receptor signaling pathway, platelet aggregation, semaphorin-plexin signaling pathway, wound healing, spreading of cells	123.59	884.68
HSPP9A1	ATP-mediated unfolded protein response, ERBB2 signaling pathway, Fc-gamma receptor signaling pathway involved in phagocytosis, aggregation involved in sorcap development, cellular response to ATP, cellular response to drug, cellular response to interleukin-4, cellular response to	439.85	454.16
HSPP9B1	ATP-mediated unfolded protein response, cellular response to ATP, response to endoplasmic reticulum stress, response to hypoxia, response to stress, retrograde protein transport, ER to cytosol, toll-like receptor signaling pathway, ubiquitin-dependent ERAD pathway	57.75	180.91
HSPP9A1.1	ERBB2 signaling pathway, Fc-gamma receptor signaling pathway involved in phagocytosis, response to antibiotic, response to cocaine, response to cold, response to drug, response to estrogen, response to heat, response to salt stress, response to unfolded pro	129.75	163.74
ALB	cellular oxidant detoxification, cellular response to starvation	688.52	47.35
EPF1A1	calcium-mediated signaling, cellular response to epidermal growth factor stimulus	352.49	378.69
HSFA8	ATP-mediated unfolded protein response, ER involved response, RE1-mediated unfolded protein response, PERK-mediated unfolded protein response, activation of signaling protein activity involved in unfolded protein response, axon guidance, cellular heat acclimation, cellular res	303.80	899.84
HSFA1A	cellular heat acclimation, cellular response to heat, cellular response to oxidative stress	15.88	51.66
HSFA2	response to cold, response to heat, response to unfolded protein	19.81	36.59
TUBA1B	cellular response to interleukin-4, mechanosensory behavior, pigmenta	339.56	293.74
YWHAQ	small GTPase mediated signal transduction	28.89	69.27
YWHAB	cellular response to insulin stimulus	26.82	47.35
YWHAE	hippo signaling, intracellular signal transduction	42.96	81.65
YWHAH	glucocorticoid receptor signaling pathway	16.27	38.13
ENO1	response to virus	264.94	273.38
ACTN4	MAPK cascade, axon guidance, peroxisome proliferator activated receptor signaling pathway, platelet aggregation, response to hypoxia, retinoic acid receptor signaling pathway	158.41	514.44
ACTN1	platelet aggregation	184.89	370.22
TLN1	RE1-mediated unfolded protein response, platelet aggregation	151.87	374.42
CLTC	RET signaling pathway, plexin cell polarity pathway, aggregation involved in sorcap development, response to osmotic stress, signal transduction	163.40	244.22
CLTCL1	signal transduction	28.88	38.13
PNB	cellular response to hypoxia, response to endoplasmic reticulum stress, response to reactive oxygen species	136.34	236.78
L2DA	response to cAMP, response to drug, response to estrogen, response to glucose, response to hydrogen peroxide, response to hypoxia, response to nutrient, response to organic cyclic compound	137.29	453.45
EEF2	cellular response to brain-derived neurotrophic factor stimulus, cold acclimation, response to cytokinin, response to endoplasmic reticulum stress, response to estradiol, response to ethanol, response to folic acid, response to hydrogen peroxide, response to ischemia	162.49	189.42
ALDOA	mitotic G2 DNA damage checkpoint	110.19	279.82
ANKK3	response to thyroid hormone	116.73	271.26
PLEC	response to nutrient, wound healing	62.18	284.12
L2ALS1	cellular response to glucose stimulus, cellular response to organic cyclic compound, multicellular organismal response to stress, plasma cell differentiation, response to axon injury, response to drug, signal transduction	118.60	180.81
PN1	acute-phase response, cellular response to BMP stimulus, cellular response to angiotensin, cellular response to beta-amyloid, cellular response to glucose stimulus, cellular response to interleukin-1, cellular response to lipopolysaccharide, cellular respo	87.72	251.46
COL1A1	blood coagulation, cellular response to amino acid stimulus, cellular response to epidermal growth factor stimulus, cellular response to fibroblast growth factor stimulus, cellular response to fluoride, cellular response to mechanical stimulus, cellular response to retinoic acid, cellular response to transforming growth	76.59	229.69
SEPPORH1	response to unfolded protein	127.94	189.28
IQGAP1	ERK1 and ERK2 cascade, Ras protein signal transduction, cellular response to calcium ion, cellular response to epidermal growth factor stimulus, cellular response to fibroblast growth factor stimulus, cellular response to organic substance, cellular response	100.73	181.61
UBA1	cellular response to DNA damage stimulus	102.89	163.98
PASN	cellular response to interleukin-4	180.74	98.88
PTN1	RET signaling pathway, plexin cell polarity pathway, cellular response to growth factor stimulus	155.80	157.13
CALR	ATP-mediated unfolded protein response, cellular response to lithium ion, cellular response to organic substance, cellular senescence, glucocorticoid receptor signaling pathway, response to drug, response to estradiol, response to testosterone	116.80	120.94
PDIA3	response to endoplasmic reticulum stress, signal transduction	84.88	142.66
THSD1	behavioral response to pain, cellular response to growth factor stimulus, cellular response to heat, cellular response to tumor necrosis factor, chronic inflammatory response, immune response, response to calcium ion, response to drug, response to endoplasmic reticulum stress, response to glucose, response to	82.38	148.62
CAP1	signal transduction	98.99	120.94
VCP	ER-associated misfolded protein catalytic process, double-strand break repair, endoplasmic reticulum unfolded protein response, error-free translesion synthesis, retrograde protein transport, ER to cytosol, translesion synthesis, ubiquitin-dependent ERAD path	85.82	133.45
CTFL1	rho protein signal transduction, response to virus	128.81	94.86
SDN	arrested muscle atrophy	89.65	99.01
ANKK3	blood coagulation, positive regulation of macrophage in response to mitochondrial depolarization, response to organic substance, signal transduction, xenophagy	79.37	159.28
BBR1	cellular response to cAMP, cellular response to platelet derived growth factor stimulus, cellular response to testosterone stimulus, cellular response to thyroid hormone stimulus, phosphatidylinositol-mediated signaling, protein kinase A signaling, sphingosine-1-phosphate signaling pathway	87.72	129.81
IZR	axon guidance, cellular response to cAMP, phosphatidylinositol-mediated signaling, protein kinase A signaling, sphingosine-1-phosphate signaling pathway	14.94	52.29
RDX	cellular response to platelet-derived growth factor stimulus, cellular response to thyroid hormone stimulus, protein kinase A signaling	12.14	34.44
VCL	platelet aggregation	47.83	161.45
MYO1D1	B cell cytokine production, MyD88-dependent toll-like receptor signaling pathway, cellular response to heat, detection of misfolded protein, isotype switching to IgG1 response, response to ATP, response to activity, response to cocaine, response to cold, response to drug	79.38	81.79
COL6A1	cellular response to amino acid stimulus	78.64	81.79
HSR6A1	signal transduction	161.79	12.81
CD1P1	cellular oxidant detoxification, cellular response to cell-matrix adhesion, cellular response to epidermal growth factor stimulus, cellular response to glucocorticoid stimulus, cellular response to insulin stimulus, cellular response to lipopolysaccharide, response to L-ascorbic acid, response to amino acid, response to	88.83	124.84
EPFA1	cellular response to brain-derived neurotrophic factor stimulus, cellular response to salivatin ion, response to organic cyclic compound	79.37	86.16
ARF4	epidermal growth factor receptor signaling pathway, response to axon injury, small GTPase mediated signal transduction	79.38	69.27
ARF1	small GTPase mediated signal transduction	46.89	23.88
ARF3	small GTPase mediated signal transduction	46.16	17.22
ARF2	small GTPase mediated signal transduction	13.86	16.07
CAPK2	cellular response to amino acid stimulus, response to hypoxia	78.64	86.16
HSR6A1.1	protein kinase C-activating G-protein coupled receptor signaling pathway	46.89	124.84
HSR6A1.1	signal transduction	79.38	59.98
SPR1	Ras protein signal transduction	89.77	79.84
ANKK1	G-protein coupled receptor signaling pathway, coupled to cyclic nucleotide second messenger, adaptive immune response, cell surface receptor signaling pathway, cellular response to glucocorticoid stimulus, cellular response to hydrogen peroxide, granulocyte chemotaxis, inflammatory response, innate immune	51.36	83.25
COL1A2	rho protein signal transduction, blood coagulation, cellular response to amino acid stimulus, platelet activation, transforming growth factor beta receptor signaling pathway	26.82	118.39
MYOF	cellular response to heat, plasma membrane repair	27.26	113.93
STAT1	JAK-STAT cascade, cellular response to cytokine stimulus, cellular response to insulin stimulus, cellular response to interferon-beta, cellular response to organic cyclic compound, defense response to virus, interferon-gamma-mediated signaling pathway, response to cAMP, response to drug, response to hydroge	86.37	64.87
ANKK4	apoptotic signaling pathway	26.82	114.68
MAP1B	cellular response to growth factor stimulus, cellular response to peptide hormone stimulus, induction of synaptic plasticity by chemical substance, peripheral nervous system axon regeneration, response to axon injury, response to carbonylamine, response to drug, response to estradiol, response to inorganic subst	26.82	120.91
WUP	ERBB signaling pathway	46.89	98.88
MYL3	sphrin receptor signaling pathway, platelet aggregation	46.16	92.98
MYL1A	sphrin receptor signaling pathway, platelet aggregation	31.75	73.16
TN	response to radiation, response to reactive oxygen species, signal transduction	51.36	78.64
HSR1	cellular response to vascular endothelial growth factor stimulus, intracellular signal transduction, platelet aggregation, positive regulation of endothelial cell chemotaxis by VEGF-activated vascular endothelial growth factor receptor signaling pathway, response to unfolded protein, response to virus, vascular endot	42.82	94.71
CLC1	platelet aggregation, signal transduction	44.83	64.87
DYSL2	axon guidance, response to amphetamine, response to cocaine, response to drug, signal transduction	42.82	129.18
PLNB	cellular oxidant detoxification, response to reactive oxygen species	46.16	139.91
PEX18	cellular oxidant detoxification, response to reactive oxygen species	46.16	64.87
EPF1G	response to virus	44.83	68.73
MAHHA	response to drug, response to insulin	42.86	66.73
HYOU1	RE1-mediated unfolded protein response, cellular response to hypoxia, response to endoplasmic reticulum stress, response to ischemia	34.26	63.96
IDH1	response to organic cyclic compound, response to oxidative stress, response to steroid hormone	38.29	64.87
IPDS	cellular response to amino acid stimulus	31.75	163.32
IPDS	cellular response to interferon-gamma	31.75	113.16
PSAP	adenylyl cyclase-inhibiting G-protein coupled receptor signaling pathway, cellular response to organic substance	38.29	69.96
CTB8	cellular response to thyroid hormone stimulus, toll-like receptor signaling pathway	42.82	46.89
HSR4	response to unfolded protein	31.75	73.16
ACTR3	Fc-gamma receptor signaling pathway involved in phagocytosis, sphrin receptor signaling pathway	31.75	68.12
AAR5	cellular response to unfolded protein, endoplasmic reticulum unfolded protein response, response to amino acid	26.82	88.10
TNDC3	response to endoplasmic reticulum stress	36.49	49.57
PDIA8	RE1-mediated unfolded protein response, platelet aggregation, response to endoplasmic reticulum stress	37.26	69.27
PRKDC	cellular response to insulin stimulus, double-strand break repair, double-strand break repair via alternative nonhomologous end joining, intrinsic apoptotic signaling pathway in response to DNA damage, response to activity, response to gamma radiation, res	31.36	25.63
UCR1L	response to ischemia	28.89	63.91
PDIA8	peripheral nervous system axon regeneration, response to organic cyclic compound	28.96	63.91
HSR3	mitochondrial unfolded protein response	28.95	68.88
WMT	response to drug, response to organotin compound	32.69	62.45

*Exponentially Modified Protein Abundance Index (http://www.malacards.com/help/quant_empir_help.html).

Table S8. Cont 1.

UniProt/Swiss-Prot ID	Biological Process	enrP47
Alternate ID	Biological regulation	COM
RHNC	response to drug	34.42
RME	cellular response to UV-A, cellular response to cytokine stimulus	31.75
RHBP1	signal transduction	22.41
TOB1	response to stimulus	33.22
GNB2	G-protein coupled acetylcholine receptor signaling pathway, Ras protein signal transduction, Wnt signaling pathway, calcium modulating pathway, adenylyate cyclase-activating dopamine receptor signaling pathway, cellular response to catecholamine stimulus, cellular response to glucagon stimulus, cellular response to glucagon stimulus, signal transduction	28.21
GNB1	G-protein coupled acetylcholine receptor signaling pathway, Ras protein signal transduction, Wnt signaling pathway, calcium modulating pathway, adenylyate cyclase-activating dopamine receptor signaling pathway, cellular response to catecholamine stimulus, cellular response to glucagon stimulus, cellular response to glucagon stimulus, signal transduction	12.14
GNB4	cellular response to glucagon stimulus, signal transduction	38.82
PARK7	Ras protein signal transduction, cellular oxidant detoxification, cellular response to glyoxal, cellular response to hydrogen peroxide, cellular response to oxidative stress, cellular response to reactive oxygen species, detoxification of copper ion, detoxification of mercury	26.21
UGT1	ER-associated misfolded protein catabolic process, endoplasmic reticulum unfolded protein response	41.28
GP1	humoral immune response, response to cadmium ion, response to estradiol, response to immobilization stress, response to morphine, response to muscle stretch, response to progesterone, response to testosterone	28.88
CCT5	response to virus	34.95
XPCCS	cellular hyperosmotic salinity response, cellular response to DNA damage stimulus, cellular response to X-ray, cellular response to fatty acid, cellular response to gamma radiation, double-strand break repair via nonhomologous end joining, response to drug	35.28
PRDX1	adenylyate cyclase-activating dopamine receptor signaling pathway, platelet aggregation, response to drug	24.28
DEPO	cellular response to oxidative stress, response to ethanol, response to food, response to iron(II) ion, response to organic cyclic compound	26.15
PBMD2	Fc-epsilon receptor signaling pathway, MAPK cascade, NIK/NF-kappaB signaling, T cell receptor signaling pathway, Wnt signaling pathway, planar cell polarity pathway, stimulatory C-type lectin receptor signaling pathway, tumor necrosis factor-mediated signaling pathway	19.81
CLCA	cellular response to calcium ion	21.48
RAC1	cellular response to glucose stimulus, cellular response to growth factor stimulus	24.28
PBMD1	Fc-epsilon receptor signaling pathway, MAPK cascade, NIK/NF-kappaB signaling, T cell receptor signaling pathway, Wnt signaling pathway, planar cell polarity pathway, stimulatory C-type lectin receptor signaling pathway, tumor necrosis factor-mediated signaling pathway	19.81
PP2D1A	response to organic substance, second-messenger-mediated signaling	45.75
SDC2	signal transduction, small GTPase mediated signal transduction	26.15
GNAB2	G-protein coupled acetylcholine receptor signaling pathway, adaptation of signaling pathway by response to pheromone involved in conjugation with cellular fusion, adenosine receptor signaling pathway, adenylyate cyclase-activating G-protein coupled receptor signaling pathway, adenylyate cyclase-activating dopamine receptor signaling pathway, cellular response to catecholamine stimulus, cellular response to glucagon stimulus, cellular response to glucagon stimulus, signal transduction	1.97
ITGB1	cellular defense response, cellular response to low-density lipoprotein particle stimulus, integrin-mediated signaling pathway, transforming growth factor beta receptor signaling pathway, visual learning	22.41
MAPK1	B cell receptor signaling pathway, BMP signaling pathway, DNA damage induced protein phosphorylation, ERBB signaling pathway, ERK1 and ERK2 cascade, Fc-epsilon receptor signaling pathway, Fc-gamma receptor signaling pathway involved in phagocytosis, G-protein coupled receptor signal	8.80
MAPK2	BMP signaling pathway, DNA damage induced protein phosphorylation, ERK1 and ERK2 cascade, Fc-epsilon receptor signaling pathway, Fc-gamma receptor signaling pathway involved in phagocytosis, JAK-STAT cascade involved in growth hormone signaling pathway, MAPK import into nucleus, axon	30.82
PP1CA	beta-catenin destruction complex disassembly, enhancement of circadian clock by photoperiod, regulation of transcriptional inhibition by eIF2 alpha phosphorylation	26.21
PP1CB	entrainment of circadian clock by photoperiod	18.88
RAE1B	cellular response to insulin stimulus, cellular response to nerve growth factor stimulus, defense response to bacterium, fibroblast growth factor receptor signaling pathway, response to cadmium ion, small GTPase mediated signal transduction	8.80
RAE1C	cellular response to nerve growth factor stimulus, small GTPase mediated signal transduction	6.94
RAE1B	small GTPase mediated signal transduction	19.81
RAE1A	defense response to bacterium, small GTPase mediated signal transduction	19.81
IFTN1	MAPK cascade, axon guidance	29.88
ACTR2	Fc-gamma receptor signaling pathway involved in phagocytosis, ephrin receptor signaling pathway	29.21
ARPC2	Fc-gamma receptor signaling pathway involved in phagocytosis, ephrin receptor signaling pathway	18.88
CHN2	cellular response to mechanical stimulus	23.36
GCN1	cellular response to amino acid starvation, cellular response to leucine starvation, cellular response to stress, positive regulation of transcription from RNA polymerase II promoter in response to stress	28.82
COL4A2	response to glucose	31.75
MF	DNA damage response, signal transduction by p53 class mediator, cell surface receptor signaling pathway, inflammatory response, innate immune response, positive chemotaxis	19.81
VPB35	Wnt signaling pathway	22.41
PLD1	response to hypoxia	19.81
ATP13A	insulin receptor signaling pathway	8.40
VDAC1	behavioral fear response	11.21
AP2A1	Wnt signaling pathway, planar cell polarity pathway, ephrin receptor signaling pathway	4.81
AP2A2	Wnt signaling pathway, planar cell polarity pathway, ephrin receptor signaling pathway	26.21
RNRNPK	signal transduction	21.48
ZYX	integrin-mediated signaling pathway, signal transduction, transforming growth factor beta receptor signaling pathway	16.88
TNC	cellular response to prostaglandin D2 stimulus, cellular response to retinoic acid, cellular response to vitamin D, peripheral nervous system axon regeneration, response to ethanol, response to fibroblast growth factor, response to mechanical stimulus, response to wounding, wound healing	26.15
POD4	response to endoplasmic reticulum stress	16.81
SEC11A	IRE1-mediated unfolded protein response, response to calcium ion	22.41
IRCC5	cellular hyperosmotic salinity response, cellular response to X-ray, cellular response to gamma radiation, double-strand break repair via classical nonhomologous end joining	26.21
APB1	Wnt signaling pathway, planar cell polarity pathway, ephrin receptor signaling pathway	26.21
OST1	cellular oxidant detoxification, cellular response to arsenic-containing substance, positive regulation of skeletal muscle contraction by regulation of release of sequestered calcium ion, regulation of cardiac muscle contraction by regulation of the release of sequestered calcium ion, xenobiotic catabolic process	26.15
NPR1	Wnt signaling pathway, signal transduction by p53 class mediator resulting in cell cycle arrest, DNA repair, regulation of eIF2 alpha phosphorylation by dsRNA, signal transduction	58.88
DOB1	response to cytokine	21.48
PBP1	MAPK cascade	20.85
PRF3	DNA damage response, detection of DNA damage, DNA repair, cellular response to hydrogen peroxide, response to TNF agonist	16.88
PRF4	innate immune response, signal transduction	16.88
PRF5	I-kappaB phosphorylation, cellular oxidant detoxification	26.21
PRF6	Rho protein signal transduction, RhoGDI signaling pathway, Wnt signaling pathway, planar cell polarity pathway, apolipoprotein A1-mediated signaling pathway, ephrin receptor signaling pathway, negative chemotaxis, phosphatidylinositol-mediated signaling, platelet activation	21.48
RHOC	small GTPase mediated signal transduction, wound healing, spreading of cells	16.81
EEF1B2	response to ethanol	19.81
CTSK	beta-1a receptor signaling pathway	29.88
PERM2	Wnt signaling pathway, integrin-mediated signaling pathway, transforming growth factor beta receptor signaling pathway	13.87
MYO1C	Fc-gamma receptor signaling pathway involved in phagocytosis, positive regulation of cell migration by vascular endothelial growth factor signaling pathway	17.74
NBE1	cellular response to drug, cellular response to fatty acid, cellular response to glucose stimulus, response to arabin, response to cAMP, response to drug, response to testosterone	48.88
PRDX3	cellular oxidant detoxification, cellular response to reactive oxygen species, inflammatory response, response to oxidative stress	14.81
RAE1B	Rap protein signal transduction, cellular response to cAMP, cellular response to drug, cellular response to glucose stimulus, cellular response to gonadotropin-releasing hormone, cellular response to nerve growth factor stimulus, cellular response to organic cyclic compound, nerve growth factor signaling pathway, response to antipain	22.41
RAE1A	Rap protein signal transduction, cellular response to cAMP, cellular response to drug, cellular response to glucose stimulus, cellular response to nerve growth factor stimulus, cellular response to organic cyclic compound, nerve growth factor signaling pathway, response to antipain	16.81
IFTN1	MAPK cascade, SMAD protein import into nucleus, axon guidance, common-partner SMAD protein phosphorylation	14.81
ARHGAP1	Rho protein signal transduction, small GTPase mediated signal transduction	16.88
SPARC	cellular response to growth factor stimulus, response to L-ascorbic acid, response to cAMP, response to cadmium ion, response to calcium ion, response to cytokine, response to ethanol, response to glucocorticoid, response to gravity, response to lead ion, response to lipopolysaccharide, response to peptide hormone	14.81
ATP1A1	cellular response to mechanical stimulus, cellular response to steroid hormone stimulus, response to drug, response to glyoxal	26.21
ARHGAP1	semaphorin-plexin signaling pathway	16.81
PI3P1	RhoGDI signaling pathway	13.87
ATP13B2	insulin receptor signaling pathway	11.21
PLD2	cellular response to hormone stimulus, response to hypoxia	12.14
TNFRD1	cellular oxidant detoxification, response to reactive oxygen species, signal transduction	2.88
ACD5	response to lipopolysaccharide, response to retroviral stress, response to redox state	17.74
COMT	cellular response to phosphate starvation, response to drug, response to lipopolysaccharide, response to organic cyclic compound, response to pain	14.81
NBE2	cellular response to fatty acid, cellular response to glucose stimulus, cellular response to oxidative stress, integrin-mediated signaling pathway, response to growth hormone	45.75
PLD3	cellular response to hormone stimulus	13.87
PBMD4	Fc-epsilon receptor signaling pathway, MAPK cascade, NIK/NF-kappaB signaling, T cell receptor signaling pathway, Wnt signaling pathway, planar cell polarity pathway, stimulatory C-type lectin receptor signaling pathway, tumor necrosis factor-mediated signaling pathway	19.81
BERPBB	cellular response to osmotic stress	5.80
SLC24A4	active induction of host immune response by virus	14.81
ARPC1B	Fc-gamma receptor signaling pathway involved in phagocytosis, ephrin receptor signaling pathway, response to estrogen	16.88
C1QB	adaptive immune response, blood coagulation, intrinsic pathway, complement activation, classical pathway, innate immune response, phosphatidylinositol 3-kinase signaling	16.88
CSRP1	platelet aggregation	5.80
GFP11	IRE1-mediated unfolded protein response	16.88
EPF41	behavioral fear response	21.48
RAE1C	blood coagulation, receptor internalization involved in canonical Wnt signaling pathway, small GTPase mediated signal transduction	9.34
CD48	endosome to melanosome transport, pigment granule maturation	20.85
ATP2A2	ER-nucleus signaling pathway, cardiac muscle hypertrophy in response to stress, cellular response to oxidative stress, regulation of cardiac muscle contraction by calcium ion signaling, response to endoplasmic reticulum stress, response to peptide hormone	7.47
CDND1C	signal transduction	14.81
DOXKX	Wnt signaling pathway, cellular response to arsenic-containing substance, cellular response to osmotic stress, extrinsic apoptotic signaling pathway via death domain receptors, innate immune response, intracellular signal transduction, intrinsic apoptotic signaling pathway, response to virus	16.88
PAPEB2	blood coagulation	14.81
RAE1	androgen receptor signaling pathway, signal transduction, small GTPase mediated signal transduction	16.88
ITP1	response to stress	11.21
EPF1D	cellular response to ionizing radiation, signal transduction	19.81
COL1A1	cellular response to amino acid stimulus, integrin-mediated signaling pathway, platelet activation, response to cytokine, response to mechanical stimulus, response to radiation, transforming growth factor beta receptor signaling pathway	17.74
PRKCSH	intracellular signal transduction	14.81

*Exponentially Modified Protein Abundance Index (http://www.msystems.cmc.com/help/quant_enrP47_help.html).

Table 58. Cont.

*Exponentially Modified Protein Abundance Index (http://www.matrixscience.com/help/quant_empai_help.html)

Table S8. Cont 3

UniProt/Swiss-Prot ID	Biological Process	enrichment	enrichment
Alternate ID	biological regulation	CDM	DMEM
PCNA	DNA damage responses, detection of DNA damage, DNA damage responses, signal transduction by p53 class mediator resulting in cell cycle arrest, cellular response to UV, cellular response to hydrogen peroxide, error-free translation synthesis, error-prone translation synthesis, mismatch repair, nucle	9.34	19.78
PEMB8	Fc-epson receptor signaling pathway, MAPK cascade, NIK/NF-kappaB signaling, T cell receptor signaling pathway, Wnt signaling pathway, planar cell polarity pathway, stimulatory C-type lectin receptor signaling pathway, tumor necrosis factor-mediated signaling pathway	8.48	19.07
PSMD7	Fc-epson receptor signaling pathway, MAPK cascade, NIK/NF-kappaB signaling, T cell receptor signaling pathway, Wnt signaling pathway, planar cell polarity pathway, stimulatory C-type lectin receptor signaling pathway, tumor necrosis factor-mediated signaling pathway	4.87	19.37
TPO	signal transduction	3.74	19.22
TSPO	behavioral response to pain, cellular hypoxic response, cellular response to lipopolysaccharide, cellular response to zinc ion, peripheral nervous system axon regeneration, response to axon injury, response to drug, response to manganese ion, response to	9.34	18.61
SEPPIN1	cellular response to lipopolysaccharide, defense response to Gram-negative bacterium	4.87	21.82
SCN2D	ubiquitin-dependent ERAD pathway	6.54	19.91
FBLN1	blood coagulation, fibrin clot formation, integrin-mediated signaling pathway	4.87	23.68
PPP3R4	Fc-epson receptor signaling pathway, Wnt signaling pathway, calcium modulating pathway, calcineurin-NFAT signaling cascade, calcium-mediated signaling, cardiac muscle hypertrophy in response to stress, cellular response to drug, cellular response to glucose stimulus, excitatory postsynaptic potential, musc	1.87	17.22
COTL1	defense response to fungus	10.27	8.61
CTNND1	Wnt signaling pathway	4.87	21.82
DNAJB11	IRE1-mediated unfolded protein response	8.54	19.07
DNM1L	release of cytochrome c from mitochondria	6.54	17.22
GPNMB	positive chemotaxis	12.14	4.31
PEA3	DNA damage checkpoint, MAPK cascade, response to morphine	6.54	19.37
PRDX2	cellular response to oxidative stress, removal of superoxide radicals, response to oxidative stress, response to reactive oxygen species	11.24	19.37
PEMB1	Fc-epson receptor signaling pathway, MAPK cascade, NIK/NF-kappaB signaling, T cell receptor signaling pathway, Wnt signaling pathway, planar cell polarity pathway, stimulatory C-type lectin receptor signaling pathway, tumor necrosis factor-mediated signaling pathway	6.54	17.22
SCFD1	response to hypoxia, response to toxic substance	8.48	19.91
TANC217	cellular oxidant detoxification, tumor necrosis factor-mediated signaling pathway	6.54	21.82
RPPI5A	response to virus	6.54	19.37
MC1R1	cellular response to DNA damage stimulus	9.34	19.91
PSMD7	Fc-epson receptor signaling pathway, MAPK cascade, NIK/NF-kappaB signaling, T cell receptor signaling pathway, Wnt signaling pathway, planar cell polarity pathway, stimulatory C-type lectin receptor signaling pathway, tumor necrosis factor-mediated signaling pathway	9.34	19.91
PEMB8	Fc-epson receptor signaling pathway, MAPK cascade, NIK/NF-kappaB signaling, T cell receptor signaling pathway, Wnt signaling pathway, planar cell polarity pathway, stimulatory C-type lectin receptor signaling pathway, tumor necrosis factor-mediated signaling pathway, ubiquitin-dependent ERAD pathway	7.47	19.78
RAB2A	small GTPase mediated signal transduction	3.74	19.37
TGDS	integrin-mediated signaling pathway, transforming growth factor beta receptor signaling pathway	3.74	23.68
EPF8	response to insulin	7.47	19.78
PPP1R12A	cellular response to drug, signal transduction	8.54	19.07
SH2D1	signal transduction	11.24	4.31
CHP21	enzyme-linked receptor protein signaling pathway	8.54	19.07
CYC3	intrinsic apoptotic signaling pathway, response to reactive oxygen species	12.14	4.31
DNAM1	axon guidance	4.87	19.37
QDS	response to amino acid, response to cadmium ion, response to nutrient levels, response to oxidative stress, response to tumor necrosis factor, response to xenobiotic stimulus	4.87	19.37
NADH	response to activity, response to drug, response to hormone, response to insulin	8.54	19.07
DTYR1	DNA repair, adaptive immune response, cellular response to interleukin-1	6.54	19.91
VAPB	axon guidance	3.74	19.91
KPNA4	response to hydrogen peroxide	9.34	19.07
PSTL1	MAPK signaling pathway, response to starvation	9.34	19.78
STAT2	JAK-STAT cascade, defense response to virus, signal transduction, type I interferon signaling pathway	7.47	18.48
ASPM	cellular response to calcium ion, detection of calcium ion, regulation of cardiac muscle contraction by regulation of the release of sequestered calcium ion, response to ATP	10.27	2.15
ACSL3	response to nutrient, response to organic cyclic compound	11.24	8.48
APTX1	base excision repair, base-free sugar-phosphate removal, cellular response to DNA damage stimulus, cellular response to cAMP, cellular response to hydrogen peroxide, cellular response to organonitrogen compound, cellular response to peptide hormone stimulus, response to drug	12.14	1.15
APF8	small GTPase mediated signal transduction	6.54	19.07
DDI1	DNA damage responses, detection of DNA damage, UV damage excision repair, Wnt signaling pathway, global genome nucleotide excision repair, nucleotide excision repair, DNA damage recognition, nucleotide excision repair, DNA duplex unwinding, nucleotide excis	4.87	17.22
DNAJB4	response to heat, response to unfolded protein	6.54	19.91
ENPP1	cellular response to insulin stimulus, immune response	6.54	19.91
OSTK1	cellular oxidant detoxification	6.54	19.07
SECA	SMAD protein signal transduction	6.54	19.91
LXN1	blood coagulation	6.54	19.91
POR	cellular response to follicle-stimulating hormone stimulus, cellular response to gonadotropin stimulus, cellular response to peptide hormone stimulus, response to drug, response to nutrient, xenobiotic metabolic process	9.34	18.48
PCOLCE	response to hypoxia, response to oxidative stress	3.74	19.91
PRDX2	cellular oxidant detoxification, cellular response to oxidative stress, cellular response to reactive oxygen species, response to hydrogen peroxide, response to lipopolysaccharide, response to oxidative stress	7.47	19.91
PSMD4	Fc-epson receptor signaling pathway, MAPK cascade, NIK/NF-kappaB signaling, T cell receptor signaling pathway, Wnt signaling pathway, planar cell polarity pathway, stimulatory C-type lectin receptor signaling pathway, tumor necrosis factor-mediated signaling pathway	4.87	19.37
GAIT	response to biogenic substance, response to organic substance	6.54	19.78
SKP1	Fc-epson receptor signaling pathway, NIK/NF-kappaB signaling, T cell receptor signaling pathway, Wnt signaling pathway, stimulatory C-type lectin receptor signaling pathway, stress-activated MAPK cascade	3.74	21.82
TAX1BP3	Rho protein signal transduction, Wnt signaling pathway	1.87	23.68
IRF2K	cellular response to interferon beta, intrinsic apoptotic signaling pathway in response to endoplasmic reticulum stress	7.47	19.91
ATP4VE1	insulin receptor signaling pathway	6.54	19.91
AP1B1	blood coagulation	4.87	19.91
CDH1	cell surface receptor signaling pathway, cellular response to low-density lipoprotein particle stimulus	6.54	17.22
MSD1	cellular oxidant detoxification, cellular response to lipid hydroperoxide, response to drug, response to lipopolysaccharide, response to organonitrogen compound, xenobiotic metabolic process	8.48	19.78
CTP81	response to drug	7.47	19.91
RA11	Fc-epson receptor signaling pathway, Fc gamma receptor signaling pathway involved in phagocytosis, G-protein coupled receptor signaling pathway, Wnt signaling pathway, planar cell polarity pathway, axon guidance, blood coagulation, cellular response to mechanical stimulus, sphrin receptor signaling pathway	3.74	19.07
GPX1	UV protection, angiogenesis involved in wound healing, cellular oxidant detoxification, cellular response to oxidative stress, intrinsic apoptotic signaling pathway in response to oxidative stress, response to gamma radiation, response to hydrogen peroxide, response to hyd	3.74	19.91
CTNND1	Wnt signaling pathway, calcium modulating pathway, androgen receptor signaling pathway, beta-catenin destruction complex disassembly, canonical Wnt signaling pathway, canonical Wnt signaling pathway involved in midbrain dopaminergic neuron differentiation, canonical Wnt signaling pathway involved in regulat	6.54	21.82
CARM1	DNA damage responses, signal transduction by p53 class mediator resulting in cell cycle arrest, intracellular estrogen receptor signaling pathway, response to cAMP	6.54	19.91
SRP44	response to endoplasmic reticulum stress, response to unfolded protein	6.54	19.91
IRAK1	fibroblast growth factor receptor signaling pathway	7.47	23.68
LRPI1	cellular response to transforming growth factor beta stimulus	6.54	19.91
ME1	response to carbohydrate, response to hormone	3.74	17.22
PSMD11	Fc-epson receptor signaling pathway, MAPK cascade, NIK/NF-kappaB signaling, T cell receptor signaling pathway, Wnt signaling pathway, planar cell polarity pathway, stimulatory C-type lectin receptor signaling pathway, tumor necrosis factor-mediated signaling pathway	3.74	19.37
PSMD12	Fc-epson receptor signaling pathway, MAPK cascade, NIK/NF-kappaB signaling, T cell receptor signaling pathway, Wnt signaling pathway, planar cell polarity pathway, stimulatory C-type lectin receptor signaling pathway, tumor necrosis factor-mediated signaling pathway	3.74	19.91
PTK7	canonical Wnt signaling pathway, cellular response to retinoic acid, planar cell polarity pathway involved in neural tube closure, signal transduction, wound healing	6.54	21.82
TOPB101	Wnt signaling pathway, androgen receptor signaling pathway, response to heat, ubiquitin-dependent SMAD protein catabolic process	1.87	23.68
TRIM2	DNA damage, Ras protein signal transduction, innate immune response	6.54	19.78
VPS29	Wnt signaling pathway	6.54	19.91
SSR1	IRE1-mediated unfolded protein response	4.87	17.22
POK2	cellular response to glucose stimulus, cellular response to tumor necrosis factor, response to dexamethasone, response to lipopolysaccharide	1.87	23.68
DNAJA1	DNA damage responses, detection of DNA damage, androgen receptor signaling pathway, response to heat, response to unfolded protein	7.47	8.61
EXOC1	phosphatidylinositol-mediated signaling	9.34	2.15
ADSL	response to hypoxia, response to muscle activity, response to nutrient, response to starvation	2.86	17.22
PTGS1	signal transduction	3.74	17.22
DNAJA2	response to heat	7.47	8.61
BTBDL2	T cell receptor signaling pathway, stress-induced mitochondrial fusion	2.74	19.91
MACP1	Wnt signaling pathway, wound healing	4.87	19.91
PSMD8	Fc-epson receptor signaling pathway, MAPK cascade, NIK/NF-kappaB signaling, T cell receptor signaling pathway, Wnt signaling pathway, planar cell polarity pathway, stimulatory C-type lectin receptor signaling pathway, tumor necrosis factor-mediated signaling pathway	7.47	18.48
ARH1C1	cellular response to jasmonic acid stimulus, response to organophosphorus, xenobiotic metabolic process	4.87	19.91
PRMT1	DNA damage responses, signal transduction by p53 class mediator resulting in cell cycle arrest, cell surface receptor signaling pathway	6.54	8.61
ANKA1	response to calcium ion	6.54	21.82
PUS	cellular response to calcium ion	7.47	19.91
DNAD	G-protein coupled acetylcholine receptor signaling pathway, adenylyl cyclase-activating G-protein coupled receptor signaling pathway, blood coagulation, cellular response to pH, entrainment of circadian clock, glutamate receptor signaling pathway, phospholipase C-activating dopamine receptor signaling pathway	3.74	19.91
PRKAR1A	blood coagulation, cellular response to glucose stimulus, intracellular signal transduction	6.54	19.78
MEB3	Wnt signaling pathway	6.54	8.61
PSR1	Fc-epson receptor signaling pathway, MAPK cascade, NIK/NF-kappaB signaling, T cell receptor signaling pathway, Wnt signaling pathway, planar cell polarity pathway, stimulatory C-type lectin receptor signaling pathway, tumor necrosis factor-mediated signaling pathway	3.86	19.07
RECQL	double-strand break repair via homologous recombination	6.54	19.37
TRIOV2	response to UV, smoothed signaling pathway	6.54	8.61
SCD1	cellular response to ATP, cellular response to calcium ion, cellular response to oxidative stress, cellular response to potassium ion, removal of superoxide radicals, response to amphetamine, response to antibiotic, response to antipsychotic drug, response to axon injury, response to carbon monoxide, response	4.87	19.07
SRFBF2	response to drug	3.74	19.07
SRFBF8	IRE1-mediated unfolded protein response, small GTPase mediated signal transduction	2.86	19.07
TACR2P	response to endoplasmic reticulum stress	6.54	19.78
ANKA7	response to calcium ion, response to organic cyclic compound, response to salt stress	4.87	19.91

*Exponentially Modified Protein Abundance Index (http://www.matrixscience.com/help/quant_empai_help.html).

Table S8. Cont 4

UniProt/Swiss-Prot ID	Biological Process	enrichment	enrichment
Alternate ID	biological regulation	CDM	DMEM
TAK1L1	cellular response to oxidative stress	2.86	19.07
ANP32A	intracellular signal transduction	2.86	19.37
LGALB3	antibiotic chemotaxis, innate immune response, macrophage chemotaxis, monocyte chemotaxis, neutrophil chemotaxis, positive chemotaxis	2.86	19.07
PARVA	smooth muscle cell chemotaxis	4.87	19.78
SRPRK	IRE1-mediated unfolded protein response	4.87	19.91
TRK3	response to endoplasmic reticulum stress	3.74	19.91
YBX3	cellular hyperosmotic response, cellular response to tumor necrosis factor, response to cold	6.54	19.37
EBF2D2	Fc-epson receptor signaling pathway, T cell receptor signaling pathway, TNF-dependent toll-like receptor signaling pathway, regulation of transcription from RNA polymerase II promoter in response to hypoxia, stimulatory C-type lectin receptor signaling pathway	8.48	4.31
ADRC1A	Fc-gamma receptor signaling pathway involved in phagocytosis, sphrin receptor signaling pathway	3.74	17.22

*Exponentially Modified Protein Abundance Index (http://www.matrixscience.com/help/quant_empai_help.html).

Table S9. Primer sequences for quantitative real-time PCR.

Table S9. Primer sequences for quantitative real-time PCR.

Gens	Accession No.	Sequences (5'→ 3')	Length (bp)
human ASS1	NM_000050.4	Forward: CATCCTTTACCATGCTCATTTAGAC Reverse: ATTGTAGAGAGACAGTGGGGACTC	250
human ITGA5	NM_002205.4	Forward: CTGCTACCTCTCCACAGATAACTTC Reverse: GATCAGGTAAGTAAAGAT	229
human p65	XM_011545207.2	Forward: GGAGAAACGTAAAAGGACATATGAG Reverse: AAACCTCATCATAGTTGATGGTGCTC	193
human p50	NM_001165412.1	Forward: GAGCCAGAGTTTACATCTGATGATT Reverse: AAGGCATTATTAAGTATCCCAGAC	164
human cyclin D1	NM_053056.2	Forward: CCCC TTGATTAAACACACAGATAC Reverse: AGGTTGAGTACCCTAATTTTCCTTG	235
human CD29	NM_002211.3	Forward: CTGAAGACTATCCCATTGACCTCTA Reverse: GCTAATGTAAGGCATCACAGTCTTT	179
human CD34	NM_001025109.1	Forward: CCTGCTCTCTTGAATGATATAGCC Reverse: GAGACTAGAACTGAGCTGTTTGTC	227
human CD44	NM_000610.3	Forward: ACTAGTGTCAAGTGCCTCTTGTT Reverse: GCCTCTTTTTGGGAATATCTAGAAG	227
human CD45	NM_001267798.1	Forward: TTCTTAGGGTAACAGAGGAGGAAAT Reverse: ACAATACTTCTGTGTCCAGAAAGG	167
human CD90	NM_001311160.1	Forward: CAATCGGAGATCACTATGCTTTCT Reverse: ACTGCTTCATATACGTGAGACACAA	177
human Ki67	NM_001145966.1	Forward: AACACCTACAAAATGACTTCTCTGG Reverse: TAGTAGTGTGCTTCTGACCTCTT	204
human PCNA	NM_002592.2	Forward: CAAGTAATGTCGATAAAGAGGAGGA Reverse: TGGGAGCCAAGTAGTATTTTAAGTG	207
human PPAR γ	NM_001330615.1	Forward: AGCATTCTACTCCACATTACGAAG Reverse: CATGAGGCTTATTGTAGAGCTGAGT	169
human FABP4	NM_001442.2	Forward: AAGTCAAGAGCACCATAACCTTAGA Reverse: CCACAGAATGTTGTAGAGTTCAATG	217
human C/EBP α	NM_001285829.1	Forward: GTTTGTACTGTATGCCTTCAGCATT Reverse: AGAGTCTCATTTTGGCAAGTATCC	248
human β -actin	NM_001101	Forward: TGGCAGCCAGCACAATGAA Reverse: CTAAGTCATAGTCGCCTAGAAGCA	186