Electronic Supplementary Material (ESI) for Molecular BioSystems.

Supporting Information for

Competitive profiling of celastrol targets in human cervical cancer HeLa cells by quantitative chemical proteomics

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1. Supplementary Tables

Table S1. Quantitative **IA-yne** profiling of HeLa proteomes with celastrol pretreatment.

Accession	Description	Coverage	PSMs	Unique Peptides	TMT *in vitro*	TMT *in situ*
Q9H9A6	Leucine-rich repeat-containing protein 40 OS=Homo sapiens GN=LRRC40 PE=1 SV=1	6.31	2	2	0.08	0.36
O75533	Splicing factor 3B subunit 1 OS=Homo sapiens GN=SF3B1 PE=1 SV=3	2.61	2	2	0.12	0.38
Q93008	Probable ubiquitin carboxyl-terminal hydrolase FAF-X OS=Homo sapiens GN=USP9X PE=1 SV=3	1.95	4	4	0.12	0.69
Q9NVI1	Fanconi anemia group I protein OS=Homo sapiens GN=FANCI PE=1 SV=4	3.01	3	3	0.13	0.36
O75643	U5 small nuclear ribonucleoprotein 200 kDa helicase OS=Homo sapiens GN=SNRNP200 PE=1 SV=2	2.25	3	3	0.13	0.64
Q96P70	Importin-9 OS=Homo sapiens GN=IPO9 PE=1 SV=3	5.19	6	3	0.13	0.86
Q5T4S7	E3 ubiquitin-protein ligase UBR4 OS=Homo sapiens GN=UBR4 PE=1 SV=1	4.48	18	15	0.15	0.68
P02730	Band 3 anion transport protein OS=Homo sapiens GN=SLC4A1 PE=1 SV=3	1.98	2	2	0.15	0.47
P30085	UMP-CMP kinase OS=Homo sapiens GN=CMPK1 PE=1 SV=3	8.67	2	1	0.17	0.43
Q9UHD1	Cysteine and histidine-rich domain-containing protein 1 OS=Homo sapiens GN=CHORDC1 PE=1 SV=2	36.75	7	7	0.17	0.36
Q9UL46	Proteasome activator complex subunit 2 OS=Homo sapiens GN=PSME2 PE=1 SV=4	34.73	10	5	0.17	0.38
P35998	26S protease regulatory subunit 7 OS=Homo sapiens GN=PSMC2 PE=1 SV=3	18.71	6	6	0.17	0.71
P38117	Electron transfer flavoprotein subunit beta OS=Homo sapiens GN=ETFB PE=1 SV=3	8.63	2	2	0.17	0.99
Q9UNM6	26S proteasome non-ATPase regulatory subunit 13 OS=Homo sapiens GN=PSMD13 PE=1 SV=2	3.99	2	1	0.18	0.46
Q7Z6Z7	E3 ubiquitin-protein ligase HUWE1 OS=Homo sapiens GN=HUWE1 PE=1 SV=3	9.60	30	27	0.18	0.67
Q7L2H7	Eukaryotic translation initiation factor 3 subunit M OS=Homo sapiens GN=EIF3M PE=1 SV=1	6.95	2	2	0.18	0.82
P32929	Cystathionine gamma-lyase OS=Homo sapiens GN=CTH PE=1 SV=3	10.37	3	3	0.18	0.73
Q9H2U2	Inorganic pyrophosphatase 2, mitochondrial OS=Homo sapiens GN=PPA2 PE=1 SV=2	6.59	2	1	0.19	0.95
O43747	AP-1 complex subunit gamma-1 OS=Homo sapiens GN=AP1G1 PE=1 SV=5	5.47	3	3	0.19	0.86
Q10567	AP-1 complex subunit beta-1 OS=Homo sapiens GN=AP1B1 PE=1 SV=2	15.91	12	4	0.20	0.77
P33176	Kinesin-1 heavy chain OS=Homo sapiens GN=KIF5B PE=1 SV=1	2.60	2	2	0.20	0.65
Q5VYK3	Proteasome-associated protein ECM29 homolog OS=Homo sapiens GN=ECM29 PE=1 SV=2	9.32	16	14	0.20	0.66
A0AVT1	Ubiquitin-like modifier-activating enzyme 6 OS=Homo sapiens GN=UBA6 PE=1 SV=1	3.23	3	3	0.22	0.51
P39023	60S ribosomal protein L3 OS=Homo sapiens GN=RPL3 PE=1 SV=2	14.89	9	7	0.22	0.88
Q9NSE4	Isoleucine--tRNA ligase, mitochondrial OS=Homo sapiens GN=IARS2 PE=1 SV=2	3.66	3	3	0.25	0.78
P52701	DNA mismatch repair protein Msh6 OS=Homo sapiens GN=MSH6 PE=1 SV=2	3.82	4	4	0.25	0.48
O43592	Exportin-T OS=Homo sapiens GN=XPOT PE=1 SV=2	10.81	8	7	0.25	0.71
P07237	Protein disulfide-isomerase OS=Homo sapiens GN=P4HB PE=1 SV=3	22.05	8	8	0.25	0.57
Q13200	26S proteasome non-ATPase regulatory subunit 2 OS=Homo sapiens GN=PSMD2 PE=1 SV=3	24.89	22	15	0.26	0.69
P61981	14-3-3 protein gamma OS=Homo sapiens GN=YWHAG PE=1 SV=2	19.84	7	3	0.27	0.92
O60763	General vesicular transport factor p115 OS=Homo sapiens GN=USO1 PE=1 SV=2	9.67	6	6	0.27	0.36
P10809	60 kDa heat shock protein, mitochondrial OS=Homo sapiens GN=HSPD1 PE=1 SV=2	71.38	79	33	0.27	0.68
O43776	Asparagine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=NARS PE=1 SV=1	8.21	3	3	0.27	0.75
P10599	Thioredoxin OS=Homo sapiens GN=TXN PE=1 SV=3	65.71	15	7	0.27	0.71
Q08211	ATP-dependent RNA helicase A OS=Homo sapiens GN=DHX9 PE=1 SV=4	3.15	3	3	0.29	0.55
P60228	Eukaryotic translation initiation factor 3 subunit E OS=Homo sapiens GN=EIF3E PE=1 SV=1	5.39	2	2	0.29	0.66
P53985	Monocarboxylate transporter 1 OS=Homo sapiens GN=SLC16A1 PE=1 SV=3	13.20	5	5	0.29	0.67
Q9Y262	Eukaryotic translation initiation factor 3 subunit L OS=Homo sapiens GN=EIF3L PE=1 SV=1	5.14	2	2	0.29	0.71

Q9H3U1	Protein unc-45 homolog A OS=Homo sapiens GN=UNC45A PE=1 SV=1	4.98	3	3	0.30	0.22
P49189	4-trimethylaminobutyraldehyde dehydrogenase OS=Homo sapiens GN=ALDH9A1 PE=1 SV=3	15.59	5	5	0.30	0.51
P30101	Protein disulfide-isomerase A3 OS=Homo sapiens GN=PDIA3 PE=1 SV=4	22.77	12	10	0.31	0.63
Q92973	Transportin-1 OS=Homo sapiens GN=TNPO1 PE=1 SV=2	35.97	30	19	0.31	1.01
P15121	Aldose reductase OS=Homo sapiens GN=AKR1B1 PE=1 SV=3	56.01	25	11	0.33	0.73
Q15084	Protein disulfide-isomerase A6 OS=Homo sapiens GN=PDIA6 PE=1 SV=1	12.95	4	4	0.33	0.64
P00390	Glutathione reductase, mitochondrial OS=Homo sapiens GN=GSR PE=1 SV=2	5.75	2	2	0.33	0.62
O15355	Protein phosphatase 1G OS=Homo sapiens GN=PPM1G PE=1 SV=1	7.69	3	3	0.33	0.45
P46940	Ras GTPase-activating-like protein IQGAP1 OS=Homo sapiens GN=IQGAP1 PE=1 SV=1	17.86	23	19	0.33	0.63
P68036	Ubiquitin-conjugating enzyme E2 L3 OS=Homo sapiens GN=UBE2L3 PE=1 SV=1	28.57	4	3	0.33	0.91
Q9Y570	Protein phosphatase methylesterase 1 OS=Homo sapiens GN=PPME1 PE=1 SV=3	5.18	2	2	0.33	0.66
Q9BPX3	Condensin complex subunit 3 OS=Homo sapiens GN=NCAPG PE=1 SV=1	2.56	2	2	0.33	0.67
P49915	GMP synthase [glutamine-hydrolyzing] OS=Homo sapiens GN=GMPS PE=1 SV=1	18.33	11	10	0.33	0.70
Q05639	Elongation factor 1-alpha 2 OS=Homo sapiens GN=EEF1A2 PE=1 SV=1	35.85	30	2	0.34	0.68
P42704	Leucine-rich PPR motif-containing protein, mitochondrial OS=Homo sapiens GN=LRPPRC PE=1 SV=3	40.46	60	41	0.35	0.72
P26640	Valine--tRNA ligase OS=Homo sapiens GN=VARS PE=1 SV=4	26.74	29	23	0.36	0.64
Q00610	Clathrin heavy chain 1 OS=Homo sapiens GN=CLTC PE=1 SV=5	38.51	72	43	0.36	0.96
O43143	Pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15 OS=Homo sapiens GN=DHX15 PE=1 SV=2	9.18	6	5	0.36	0.69
P07741	Adenine phosphoribosyltransferase OS=Homo sapiens GN=APRT PE=1 SV=2	18.33	2	2	0.36	0.70
Q04917	14-3-3 protein eta OS=Homo sapiens GN=YWHAH PE=1 SV=4	18.29	6	2	0.36	0.98
P13804	Electron transfer flavoprotein subunit alpha, mitochondrial OS=Homo sapiens GN=ETFA PE=1 SV=1	8.71	2	2	0.36	0.75
P68104	Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 PE=1 SV=1	65.80	67	12	0.37	0.62
Q16543	Hsp90 co-chaperone Cdc37 OS=Homo sapiens GN=CDC37 PE=1 SV=1	5.56	5	2	0.37	0.59
Q14974	Importin subunit beta-1 OS=Homo sapiens GN=KPNB1 PE=1 SV=2	25.11	21	17	0.38	0.36
Q15008	26S proteasome non-ATPase regulatory subunit 6 OS=Homo sapiens GN=PSMD6 PE=1 SV=1	12.85	4	4	0.38	0.48
P00338	L-lactate dehydrogenase A chain OS=Homo sapiens GN=LDHA PE=1 SV=2	64.76	70	20	0.38	0.64
P13639	Elongation factor 2 OS=Homo sapiens GN=EEF2 PE=1 SV=4	62.24	93	42	0.39	0.78
P78347	General transcription factor II-I OS=Homo sapiens GN=GTF2I PE=1 SV=2	4.51	2	2	0.39	0.38
O95757	Heat shock 70 kDa protein 4L OS=Homo sapiens GN=HSPA4L PE=1 SV=3	8.10	7	1	0.39	0.71
P53618	Coatomer subunit beta OS=Homo sapiens GN=COPB1 PE=1 SV=3	23.92	26	16	0.39	0.84
P05388	60S acidic ribosomal protein P0 OS=Homo sapiens GN=RPLP0 PE=1 SV=1	34.07	11	9	0.39	0.49
Q9UBB4	Ataxin-10 OS=Homo sapiens GN=ATXN10 PE=1 SV=1	5.68	3	2	0.40	1.01
Q14204	Cytoplasmic dynein 1 heavy chain 1 OS=Homo sapiens GN=DYNC1H1 PE=1 SV=5	24.77	104	83	0.40	0.99
P00492	Hypoxanthine-guanine phosphoribosyltransferase OS=Homo sapiens GN=HPRT1 PE=1 SV=2	10.55	2	2	0.42	0.92
P07355	Annexin A2 OS=Homo sapiens GN=ANXA2 PE=1 SV=2	62.54	45	22	0.42	0.72
Q92616	eIF-2-alpha kinase activator GCN1 OS=Homo sapiens GN=GCN1 PE=1 SV=6	26.62	67	55	0.43	0.60
P04406	Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens GN=GAPDH PE=1 SV=3	58.81	47	18	0.43	1.13
P62829	60S ribosomal protein L23 OS=Homo sapiens GN=RPL23 PE=1 SV=1	37.14	4	4	0.44	0.86
P00558	Phosphoglycerate kinase 1 OS=Homo sapiens GN=PGK1 PE=1 SV=3	58.51	32	19	0.44	0.68
P78417	Glutathione S-transferase omega-1 OS=Homo sapiens GN=GSTO1 PE=1 SV=2 - [GSTO1_HUMAN]	56.44	11	3	0.44	0.69
P23921	Ribonucleoside-diphosphate reductase large subunit OS=Homo sapiens GN=RRM1 PE=1 SV=1	19.82	13	11	0.44	0.70
P63151	Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B OS=Homo sapiens GN=PPP2R2A PE=1 SV=1	16.55	9	6	0.44	0.70
Q16881	Thioredoxin reductase 1, cytoplasmic OS=Homo sapiens GN=TXNRD1 PE=1 SV=3	16.49	8	6	0.44	0.71

P60903	Protein S100-A10 OS=Homo sapiens GN=S100A10 PE=1 SV=2	17.53	4	1	0.44	0.87
P14618	Pyruvate kinase PKM OS=Homo sapiens GN=PKM PE=1 SV=4	65.73	71	31	0.46	0.73
O95373	Importin-7 OS=Homo sapiens GN=IPO7 PE=1 SV=1	30.25	38	22	0.47	0.83
P08559	Pyruvate dehydrogenase E1 component subunit alpha, mitochondrial OS=Homo sapiens GN=PDHA1 PE=1 SV=3	13.59	4	4	0.47	0.65
P05023	Sodium/potassium-transporting ATPase subunit alpha-1 OS=Homo sapiens GN=ATP1A1 PE=1 SV=1	33.82	36	26	0.47	0.65
P60842	Eukaryotic initiation factor 4A-I OS=Homo sapiens GN=EIF4A1 PE=1 SV=1	21.92	9	6	0.47	0.92
Q99460	26S proteasome non-ATPase regulatory subunit 1 OS=Homo sapiens GN=PSMD1 PE=1 SV=2	8.08	6	5	0.48	0.66
Q99714	3-hydroxyacyl-CoA dehydrogenase type-2 OS=Homo sapiens GN=HSD17B10 PE=1 SV=3	41.76	12	7	0.48	1.05
Q16576	Histone-binding protein RBBP7 OS=Homo sapiens GN=RBBP7 PE=1 SV=1	19.53	6	6	0.48	0.93
Q9Y277	Voltage-dependent anion-selective channel protein 3 OS=Homo sapiens GN=VDAC3 PE=1 SV=1	21.91	6	4	0.48	1.03
P45974	Ubiquitin carboxyl-terminal hydrolase 5 OS=Homo sapiens GN=USP5 PE=1 SV=2	20.05	18	12	0.49	1.09
P13667	Protein disulfide-isomerase A4 OS=Homo sapiens GN=PDIA4 PE=1 SV=2	3.10	2	2	0.49	0.76
Q13889	General transcription factor IIH subunit 3 OS=Homo sapiens GN=GTF2H3 PE=1 SV=2	10.06	3	1	0.50	0.58
O14980	Exportin-1 OS=Homo sapiens GN=XPO1 PE=1 SV=1	28.57	38	24	0.52	0.66
P02765	Alpha-2-HS-glycoprotein OS=Homo sapiens GN=AHSG PE=1 SV=1	3.54	3	2	0.52	0.66
P62258	14-3-3 protein epsilon OS=Homo sapiens GN=YWHAE PE=1 SV=1	24.31	7	4	0.55	0.85
P30048	Thioredoxin-dependent peroxide reductase, mitochondrial OS=Homo sapiens GN=PRDX3 PE=1 SV=3	20.31	6	4	0.55	1.14
P56192	Methionine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=MARS PE=1 SV=2	20.56	17	12	0.57	0.69
O43169	Cytochrome b5 type B OS=Homo sapiens GN=CYB5B PE=1 SV=2	10.96	3	2	0.57	0.99
Q13428	Treacle protein OS=Homo sapiens GN=TCOF1 PE=1 SV=3	2.02	3	3	0.58	0.95
P49327	Fatty acid synthase OS=Homo sapiens GN=FASN PE=1 SV=3	39.43	119	73	0.60	0.87
O95881	Thioredoxin domain-containing protein 12 OS=Homo sapiens GN=TXNDC12 PE=1 SV=1	8.72	3	1	0.60	0.89
P32969	60S ribosomal protein L9 OS=Homo sapiens GN=RPL9 PE=1 SV=1	31.25	5	3	0.60	0.95
Q9BUF5	Tubulin beta-6 chain OS=Homo sapiens GN=TUBB6 PE=1 SV=1	22.20	30	3	0.61	0.83
P07814	Bifunctional glutamate/proline--tRNA ligase OS=Homo sapiens GN=EPRS PE=1 SV=5	32.80	46	36	0.62	0.88
Q7L1Q6	Basic leucine zipper and W2 domain-containing protein 1 OS=Homo sapiens GN=BZW1 PE=1 SV=1	21.00	6	5	0.63	0.87
Q9Y6C9	Mitochondrial carrier homolog 2 OS=Homo sapiens GN=MTCH2 PE=1 SV=1	7.59	2	2	0.63	0.96
Q9Y3U8	60S ribosomal protein L36 OS=Homo sapiens GN=RPL36 PE=1 SV=3	21.90	2	2	0.63	0.99
Q9Y490	Talin-1 OS=Homo sapiens GN=TLN1 PE=1 SV=3	14.76	28	23	0.64	1.01
P62851	40S ribosomal protein S25 OS=Homo sapiens GN=RPS25 PE=1 SV=1	15.20	2	2	0.64	0.95
P62753	40S ribosomal protein S6 OS=Homo sapiens GN=RPS6 PE=1 SV=1	13.65	5	3	0.64	0.85
P62826	GTP-binding nuclear protein Ran OS=Homo sapiens GN=RAN PE=1 SV=3	20.83	6	4	0.64	0.88
Q15436	Protein transport protein Sec23A OS=Homo sapiens GN=SEC23A PE=1 SV=2	3.53	2	1	0.64	1.12
Q8WUM4	Programmed cell death 6-interacting protein OS=Homo sapiens GN=PDCD6IP PE=1 SV=1	12.56	9	8	0.65	0.64
P23528	Cofilin-1 OS=Homo sapiens GN=CFL1 PE=1 SV=3	66.27	13	8	0.65	0.89
Q96FW1	Ubiquitin thioesterase OTUB1 OS=Homo sapiens GN=OTUB1 PE=1 SV=1 - [OTUB1_HUMAN]	53.88	6	5	0.67	0.78
Q9Y2V2	Calcium-regulated heat stable protein 1 OS=Homo sapiens GN=CARHSP1 PE=1 SV=2	10.88	3	1	0.67	0.78
P07437	Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=2	66.67	87	4	0.68	0.93
P48643	T-complex protein 1 subunit epsilon OS=Homo sapiens GN=CCT5 PE=1 SV=1	53.05	32	18	0.69	0.89
O00571	ATP-dependent RNA helicase DDX3X OS=Homo sapiens GN=DDX3X PE=1 SV=3	5.89	3	3	0.69	0.90
P08195	4F2 cell-surface antigen heavy chain OS=Homo sapiens GN=SLC3A2 PE=1 SV=3	35.40	48	22	0.70	0.84
P25789	Proteasome subunit alpha type-4 OS=Homo sapiens GN=PSMA4 PE=1 SV=1	21.46	3	3	0.70	1.18
P61927	60S ribosomal protein L37 OS=Homo sapiens GN=RPL37 PE=1 SV=2	22.68	4	3	0.70	1.02

P52788	Spermine synthase OS=Homo sapiens GN=SMS PE=1 SV=2	4.37	2	2	0.70	1.05
Q93009	Ubiquitin carboxyl-terminal hydrolase 7 OS=Homo sapiens GN=USP7 PE=1 SV=2	6.17	4	4	0.71	1.05
P30044	Peroxiredoxin-5, mitochondrial OS=Homo sapiens GN=PRDX5 PE=1 SV=4	10.28	3	2	0.71	1.12
O60841	Eukaryotic translation initiation factor 5B OS=Homo sapiens GN=EIF5B PE=1 SV=4	4.75	3	3	0.71	0.96
Q9BQE3	Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1	59.47	66	4	0.71	0.93
P07195	L-lactate dehydrogenase B chain OS=Homo sapiens GN=LDHB PE=1 SV=2	59.88	50	15	0.72	1.24
P34932	Heat shock 70 kDa protein 4 OS=Homo sapiens GN=HSPA4 PE=1 SV=4	42.38	39	23	0.72	1.17
Q02543	60S ribosomal protein L18a OS=Homo sapiens GN=RPL18A PE=1 SV=2	22.16	5	4	0.72	1.08
Q15185	Prostaglandin E synthase 3 OS=Homo sapiens GN=PTGES3 PE=1 SV=1	8.13	2	1	0.72	0.90
Q9BWH6	RNA polymerase II-associated protein 1 OS=Homo sapiens GN=RPAP1 PE=1 SV=3	1.01	3	1	0.73	1.44
P62280	40S ribosomal protein S11 OS=Homo sapiens GN=RPS11 PE=1 SV=3	20.89	4	4	0.73	0.85
Q9UBE0	SUMO-activating enzyme subunit 1 OS=Homo sapiens GN=SAE1 PE=1 SV=1	6.94	2	2	0.73	0.94
Q06830	Peroxiredoxin-1 OS=Homo sapiens GN=PRDX1 PE=1 SV=1	57.79	32	10	0.73	1.28
P63220	40S ribosomal protein S21 OS=Homo sapiens GN=RPS21 PE=1 SV=1	19.28	2	2	0.73	1.13
P50991	T-complex protein 1 subunit delta OS=Homo sapiens GN=CCT4 PE=1 SV=4	43.04	18	14	0.74	0.74
O00232	26S proteasome non-ATPase regulatory subunit 12 OS=Homo sapiens GN=PSMD12 PE=1 SV=3	9.87	5	3	0.74	0.86
P63104	14-3-3 protein zeta/delta OS=Homo sapiens GN=YWHAZ PE=1 SV=1	30.61	10	4	0.74	0.88
Q9HB71	Calcyclin-binding protein OS=Homo sapiens GN=CACYBP PE=1 SV=2	25.44	4	4	0.74	1.01
O76003	Glutaredoxin-3 OS=Homo sapiens GN=GLRX3 PE=1 SV=2	7.46	2	2	0.74	1.03
Q9BTW9	Tubulin-specific chaperone D OS=Homo sapiens GN=TBCD PE=1 SV=2	2.60	2	2	0.75	0.82
P40429	60S ribosomal protein L13a OS=Homo sapiens GN=RPL13A PE=1 SV=2	26.11	9	6	0.75	0.88
P62937	Peptidyl-prolyl cis-trans isomerase A OS=Homo sapiens GN=PPIA PE=1 SV=2	63.64	23	11	0.75	0.91
Q96A23	Copine-4 OS=Homo sapiens GN=CPNE4 PE=1 SV=1	4.31	2	1	0.75	0.96
P54819	Adenylate kinase 2, mitochondrial OS=Homo sapiens GN=AK2 PE=1 SV=2	16.74	4	3	0.75	1.05
Q13155	Aminoacyl tRNA synthase complex-interacting multifunctional protein 2 OS=Homo sapiens GN=AIMP2 PE=1 SV=2	6.88	3	2	0.76	0.81
Q06323	Proteasome activator complex subunit 1 OS=Homo sapiens GN=PSME1 PE=1 SV=1	22.49	4	4	0.76	0.81
Q14258	E3 ubiquitin/ISG15 ligase TRIM25 OS=Homo sapiens GN=TRIM25 PE=1 SV=2	4.13	2	2	0.78	0.89
P08134	Rho-related GTP-binding protein RhoC OS=Homo sapiens GN=RHOC PE=1 SV=1	26.94	4	3	0.78	1.01
B5ME19	Eukaryotic translation initiation factor 3 subunit C-like protein OS=Homo sapiens GN=EIF3CL PE=3 SV=1	2.63	2	2	0.78	1.14
Q6YN16	Hydroxysteroid dehydrogenase-like protein 2 OS=Homo sapiens GN=HSDL2 PE=1 SV=1	6.22	2	2	0.78	1.05
P39019	40S ribosomal protein S19 OS=Homo sapiens GN=RPS19 PE=1 SV=2	11.72	2	2	0.78	1.05
P57088	Transmembrane protein 33 OS=Homo sapiens GN=TMEM33 PE=1 SV=2	8.91	3	2	0.79	0.81
P27824	Calnexin OS=Homo sapiens GN=CANX PE=1 SV=2	22.30	13	10	0.79	0.82
P15531	Nucleoside diphosphate kinase A OS=Homo sapiens GN=NME1 PE=1 SV=1	43.42	8	2	0.79	0.89
P08237	ATP-dependent 6-phosphofructokinase, muscle type OS=Homo sapiens GN=PFKM PE=1 SV=2	9.49	5	4	0.79	0.89
P30041	Peroxiredoxin-6 OS=Homo sapiens GN=PRDX6 PE=1 SV=3	31.25	6	5	0.79	0.96
P09960	Leukotriene A-4 hydrolase OS=Homo sapiens GN=LTA4H PE=1 SV=2	9.49	6	5	0.79	1.09
Q5TFE4	5'-nucleotidase domain-containing protein 1 OS=Homo sapiens GN=NT5DC1 PE=1 SV=1	16.70	4	4	0.80	0.85
P51858	Hepatoma-derived growth factor OS=Homo sapiens GN=HDGF PE=1 SV=1	11.25	2	2	0.80	0.93
Q9Y2L1	Exosome complex exonuclease RRP44 OS=Homo sapiens GN=DIS3 PE=1 SV=2	6.05	3	3	0.80	1.02
P36952	Serpin B5 OS=Homo sapiens GN=SERPINB5 PE=1 SV=2	21.33	6	6	0.81	0.84
Q15645	Pachytene checkpoint protein 2 homolog OS=Homo sapiens GN=TRIP13 PE=1 SV=2	13.66	5	5	0.81	0.86
P63244	Receptor of activated protein C kinase 1 OS=Homo sapiens GN=RACK1 PE=1 SV=3	61.51	19	14	0.81	0.89

Q7Z3U7	Protein MON2 homolog OS=Homo sapiens GN=MON2 PE=1 SV=3	1.51	2	2	0.81	1.02
Q10471	Polypeptide N-acetylgalactosaminyltransferase 2 OS=Homo sapiens GN=GALNT2 PE=1 SV=1	5.95	4	3	0.81	1.04
P17987	T-complex protein 1 subunit alpha OS=Homo sapiens GN=TCP1 PE=1 SV=1	51.98	26	19	0.82	0.90
P50914	60S ribosomal protein L14 OS=Homo sapiens GN=RPL14 PE=1 SV=4	5.58	2	1	0.82	0.95
P27635	60S ribosomal protein L10 OS=Homo sapiens GN=RPL10 PE=1 SV=4	34.11	8	6	0.82	0.98
P61313	60S ribosomal protein L15 OS=Homo sapiens GN=RPL15 PE=1 SV=2	36.27	12	7	0.82	1.01
P23396	40S ribosomal protein S3 OS=Homo sapiens GN=RPS3 PE=1 SV=2	41.98	9	9	0.82	1.01
O14744	Protein arginine N-methyltransferase 5 OS=Homo sapiens GN=PRMT5 PE=1 SV=4	12.87	4	4	0.82	1.02
P17655	Calpain-2 catalytic subunit OS=Homo sapiens GN=CAPN2 PE=1 SV=6	7.43	4	4	0.82	1.05
O43252	Bifunctional 3'-phosphoadenosine 5'-phosphosulfate synthase 1 OS=Homo sapiens GN=PAPSS1 PE=1 SV=2	10.10	4	4	0.82	1.16
P26599	Polypyrimidine tract-binding protein 1 OS=Homo sapiens GN=PTBP1 PE=1 SV=1	10.73	4	4	0.83	0.82
P68371	Tubulin beta-4B chain OS=Homo sapiens GN=TUBB4B PE=1 SV=1	66.52	80	4	0.83	0.97
P62701	40S ribosomal protein S4, X isoform OS=Homo sapiens GN=RPS4X PE=1 SV=2	18.25	6	5	0.83	0.99
P12236	ADP/ATP translocase 3 OS=Homo sapiens GN=SLC25A6 PE=1 SV=4	37.92	15	3	0.83	1.02
P11310	Medium-chain specific acyl-CoA dehydrogenase, mitochondrial OS=Homo sapiens GN=ACADM PE=1 SV=1	28.50	14	8	0.83	1.03
P01023	Alpha-2-macroglobulin OS=Homo sapiens GN=A2M PE=1 SV=3	2.24	5	3	0.83	1.03
Q9Y371	Endophilin-B1 OS=Homo sapiens GN=SH3GLB1 PE=1 SV=1	6.30	3	2	0.83	1.06
P61247	40S ribosomal protein S3a OS=Homo sapiens GN=RPS3A PE=1 SV=2	31.06	9	8	0.83	1.14
P62736	Actin, aortic smooth muscle OS=Homo sapiens GN=ACTA2 PE=1 SV=1	26.79	39	1	0.83	1.14
P47756	F-actin-capping protein subunit beta OS=Homo sapiens GN=CAPZB PE=1 SV=4	25.99	4	4	0.83	1.17
Q9UGP8	Translocation protein SEC63 homolog OS=Homo sapiens GN=SEC63 PE=1 SV=2	4.21	2	2	0.84	0.96
Q15392	Delta(24)-sterol reductase OS=Homo sapiens GN=DHCR24 PE=1 SV=2	3.49	2	2	0.84	0.96
O60664	Perilipin-3 OS=Homo sapiens GN=PLIN3 PE=1 SV=3	6.22	4	2	0.84	0.98
P14625	Endoplasmin OS=Homo sapiens GN=HSP90B1 PE=1 SV=1	35.24	30	21	0.84	1.15
P61088	Ubiquitin-conjugating enzyme E2 N OS=Homo sapiens GN=UBE2N PE=1 SV=1	20.39	2	2	0.84	1.02
Q01518	Adenylyl cyclase-associated protein 1 OS=Homo sapiens GN=CAP1 PE=1 SV=5	16.63	7	6	0.84	1.26
P62266	40S ribosomal protein S23 OS=Homo sapiens GN=RPS23 PE=1 SV=3	23.78	4	3	0.85	0.96
P45880	Voltage-dependent anion-selective channel protein 2 OS=Homo sapiens GN=VDAC2 PE=1 SV=2	65.65	38	15	0.85	1.00
Q8TDB8	Solute carrier family 2, facilitated glucose transporter member 14 OS=Homo sapiens GN=SLC2A14 PE=2 SV=1	2.12	2	1	0.85	1.02
Q16851	UTP--glucose-1-phosphate uridylyltransferase OS=Homo sapiens GN=UGP2 PE=1 SV=5	5.12	2	2	0.85	1.07
P52789	Hexokinase-2 OS=Homo sapiens GN=HK2 PE=1 SV=2	8.83	6	6	0.85	1.13
P46063	ATP-dependent DNA helicase Q1 OS=Homo sapiens GN=RECQL PE=1 SV=3	13.56	8	8	0.86	0.87
P37802	Transgelin-2 OS=Homo sapiens GN=TAGLN2 PE=1 SV=3	15.58	4	3	0.86	0.97
Q86VP6	Cullin-associated NEDD8-dissociated protein 1 OS=Homo sapiens GN=CAND1 PE=1 SV=2	32.60	42	32	0.86	0.98
P68366	Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A PE=1 SV=1	59.60	61	5	0.86	0.98
P49368	T-complex protein 1 subunit gamma OS=Homo sapiens GN=CCT3 PE=1 SV=4	48.07	29	18	0.86	1.00
P07900	Heat shock protein HSP 90-alpha OS=Homo sapiens GN=HSP90AA1 PE=1 SV=5	46.31	56	18	0.86	1.22
O75390	Citrate synthase, mitochondrial OS=Homo sapiens GN=CS PE=1 SV=2	15.24	6	5	0.86	1.01
O14787	Transportin-2 OS=Homo sapiens GN=TNPO2 PE=1 SV=3	5.91	6	1	0.86	1.02
Q01813	ATP-dependent 6-phosphofructokinase, platelet type OS=Homo sapiens GN=PFKP PE=1 SV=2	8.93	6	5	0.86	1.03
P60709	Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1	54.13	69	7	0.86	1.04
O60488	Long-chain-fatty-acid--CoA ligase 4 OS=Homo sapiens GN=ACSL4 PE=1 SV=2	7.74	3	3	0.86	1.05
Q9Y3I0	tRNA-splicing ligase RtcB homolog OS=Homo sapiens GN=RTCB PE=1 SV=1	5.15	2	2	0.87	0.89

Q9BQB6	Vitamin K epoxide reductase complex subunit 1 OS=Homo sapiens GN=VKORC1 PE=1 SV=1	7.98	2	1	0.87	0.95
P13797	Plastin-3 OS=Homo sapiens GN=PLS3 PE=1 SV=4	36.35	29	19	0.87	0.96
P15880	40S ribosomal protein S2 OS=Homo sapiens GN=RPS2 PE=1 SV=2	36.86	12	10	0.87	0.96
P02786	Transferrin receptor protein 1 OS=Homo sapiens GN=TFRC PE=1 SV=2	33.16	29	21	0.87	0.98
P25705	ATP synthase subunit alpha, mitochondrial OS=Homo sapiens GN=ATP5A1 PE=1 SV=1	29.48	14	12	0.87	0.99
P15924	Desmoplakin OS=Homo sapiens GN=DSP PE=1 SV=3	3.10	5	5	0.87	1.01
O14929	Histone acetyltransferase type B catalytic subunit OS=Homo sapiens GN=HAT1 PE=1 SV=1	8.83	3	3	0.87	1.01
P14923	Junction plakoglobin OS=Homo sapiens GN=JUP PE=1 SV=3	3.62	2	2	0.87	0.93
P11177	Pyruvate dehydrogenase E1 component subunit beta, mitochondrial OS=Homo sapiens GN=PDHB PE=1 SV=3	7.52	2	2	0.88	1.16
P60900	Proteasome subunit alpha type-6 OS=Homo sapiens GN=PSMA6 PE=1 SV=1	8.54	2	2	0.88	1.18
P78371	T-complex protein 1 subunit beta OS=Homo sapiens GN=CCT2 PE=1 SV=4	42.24	18	15	0.88	0.91
P53621	Coatomer subunit alpha OS=Homo sapiens GN=COPA PE=1 SV=2	9.97	11	8	0.88	0.93
P36507	Dual specificity mitogen-activated protein kinase kinase 2 OS=Homo sapiens GN=MAP2K2 PE=1 SV=1	5.75	2	2	0.88	0.95
Q16181	Septin-7 OS=Homo sapiens GN=SEPT7 PE=1 SV=2	4.81	3	2	0.88	0.96
Q9BSJ8	Extended synaptotagmin-1 OS=Homo sapiens GN=ESYT1 PE=1 SV=1	3.89	3	3	0.88	0.86
P0CG39	POTE ankyrin domain family member J OS=Homo sapiens GN=POTEJ PE=3 SV=1	5.11	8	1	0.88	0.89
O96008	Mitochondrial import receptor subunit TOM40 homolog OS=Homo sapiens GN=TOMM40 PE=1 SV=1	6.09	2	2	0.88	1.10
P62979	Ubiquitin-40S ribosomal protein S27a OS=Homo sapiens GN=RPS27A PE=1 SV=2	16.03	2	2	0.89	0.98
P42677	40S ribosomal protein S27 OS=Homo sapiens GN=RPS27 PE=1 SV=3	25.00	4	2	0.89	0.98
P46782	40S ribosomal protein S5 OS=Homo sapiens GN=RPS5 PE=1 SV=4	22.06	6	4	0.89	0.98
P20810	Calpastatin OS=Homo sapiens GN=CAST PE=1 SV=4	8.33	4	4	0.89	0.99
Q06210	Glutamine--fructose-6-phosphate aminotransferase [isomerizing] 1 OS=Homo sapiens GN=GFPT1 PE=1 SV=3	25.04	15	12	0.89	1.09
P62913	60S ribosomal protein L11 OS=Homo sapiens GN=RPL11 PE=1 SV=2	19.66	5	4	0.89	1.11
Q00325	Phosphate carrier protein, mitochondrial OS=Homo sapiens GN=SLC25A3 PE=1 SV=2	17.13	7	5	0.89	1.19
P35573	Glycogen debranching enzyme OS=Homo sapiens GN=AGL PE=1 SV=3	4.57	6	6	0.90	1.13
Q02790	Peptidyl-prolyl cis-trans isomerase FKBP4 OS=Homo sapiens GN=FKBP4 PE=1 SV=3	6.75	2	2	0.90	1.26
O00116	Alkyldihydroxyacetonephosphate synthase, peroxisomal OS=Homo sapiens GN=AGPS PE=1 SV=1	5.93	3	2	0.90	1.15
P05386	60S acidic ribosomal protein P1 OS=Homo sapiens GN=RPLP1 PE=1 SV=1	14.04	2	1	0.90	0.96
P51148	Ras-related protein Rab-5C OS=Homo sapiens GN=RAB5C PE=1 SV=2	35.19	6	5	0.90	1.14
Q8TCT9	Minor histocompatibility antigen H13 OS=Homo sapiens GN=HM13 PE=1 SV=1	5.57	2	2	0.90	1.29
P04792	Heat shock protein beta-1 OS=Homo sapiens GN=HSPB1 PE=1 SV=2	49.76	8	7	0.90	1.12
Q9BQG0	Myb-binding protein 1A OS=Homo sapiens GN=MYBBP1A PE=1 SV=2	9.86	11	10	0.90	1.08
Q15365	Poly(rC)-binding protein 1 OS=Homo sapiens GN=PCBP1 PE=1 SV=2	45.22	18	6	0.90	1.08
Q562R1	Beta-actin-like protein 2 OS=Homo sapiens GN=ACTBL2 PE=1 SV=2	15.16	20	1	0.90	1.10
P31939	Bifunctional purine biosynthesis protein PURH OS=Homo sapiens GN=ATIC PE=1 SV=3	13.85	5	5	0.90	1.10
P12268	Inosine-5'-monophosphate dehydrogenase 2 OS=Homo sapiens GN=IMPDH2 PE=1 SV=2	15.18	5	4	0.90	1.11
Q04637	Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 PE=1 SV=4	8.88	12	11	0.90	1.13
P39748	Flap endonuclease 1 OS=Homo sapiens GN=FEN1 PE=1 SV=1	11.32	3	2	0.90	1.14
Q5JWF2	Guanine nucleotide-binding protein G(s) subunit alpha isoforms XLas OS=Homo sapiens GN=GNAS PE=1 SV=2	3.66	3	1	0.90	1.21
P61163	Alpha-centractin OS=Homo sapiens GN=ACTR1A PE=1 SV=1	17.55	5	4	0.91	1.13
P12277	Creatine kinase B-type OS=Homo sapiens GN=CKB PE=1 SV=1	14.17	7	4	0.91	0.94
Q9UHD8	Septin-9 OS=Homo sapiens GN=SEPT9 PE=1 SV=2	4.78	2	2	0.91	0.97
P26639	Threonine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=TARS PE=1 SV=3	30.71	27	18	0.91	0.99

P26373	60S ribosomal protein L13 OS=Homo sapiens GN=RPL13 PE=1 SV=4	27.96	7	7	0.91	0.99
P08238	Heat shock protein HSP 90-beta OS=Homo sapiens GN=HSP90AB1 PE=1 SV=4	56.63	73	21	0.91	1.26
P18124	60S ribosomal protein L7 OS=Homo sapiens GN=RPL7 PE=1 SV=1	34.68	8	7	0.91	1.02
P22102	Trifunctional purine biosynthetic protein adenosine-3 OS=Homo sapiens GN=GART PE=1 SV=1	18.91	20	15	0.91	1.02
Q8TBC4	NEDD8-activating enzyme E1 catalytic subunit OS=Homo sapiens GN=UBA3 PE=1 SV=2	22.03	6	5	0.91	1.03
P18031	Tyrosine-protein phosphatase non-receptor type 1 OS=Homo sapiens GN=PTPN1 PE=1 SV=1	15.40	7	5	0.91	1.03
O75439	Mitochondrial-processing peptidase subunit beta OS=Homo sapiens GN=PMPCB PE=1 SV=2	7.16	2	2	0.91	1.05
P63167	Dynein light chain 1, cytoplasmic OS=Homo sapiens GN=DYNLL1 PE=1 SV=1	37.08	2	2	0.91	1.06
P31930	Cytochrome b-c1 complex subunit 1, mitochondrial OS=Homo sapiens GN=UQCRC1 PE=1 SV=3	10.63	6	3	0.91	1.07
P26641	Elongation factor 1-gamma OS=Homo sapiens GN=EEF1G PE=1 SV=3	34.10	25	12	0.91	1.09
P16615	Sarcoplasmic/endoplasmic reticulum calcium ATPase 2 OS=Homo sapiens GN=ATP2A2 PE=1 SV=1	22.84	21	18	0.91	1.12
Q15046	Lysine--tRNA ligase OS=Homo sapiens GN=KARS PE=1 SV=3	10.39	4	4	0.91	1.17
P08754	Guanine nucleotide-binding protein G(k) subunit alpha OS=Homo sapiens GN=GNAI3 PE=1 SV=3	22.88	7	5	0.92	0.77
Q96HE7	ERO1-like protein alpha OS=Homo sapiens GN=ERO1A PE=1 SV=2	8.12	4	3	0.92	0.96
O95202	LETM1 and EF-hand domain-containing protein 1, mitochondrial OS=Homo sapiens GN=LETM1 PE=1 SV=1	5.01	2	2	0.92	0.98
Q15021	Condensin complex subunit 1 OS=Homo sapiens GN=NCAPD2 PE=1 SV=3	15.13	14	14	0.92	0.98
Q9Y2H6	Fibronectin type-III domain-containing protein 3A OS=Homo sapiens GN=FNDC3A PE=1 SV=4	2.84	3	3	0.92	0.98
P49589	Cysteine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=CARS PE=1 SV=3	9.76	6	6	0.92	1.00
Q8NF37	Lysophosphatidylcholine acyltransferase 1 OS=Homo sapiens GN=LPCAT1 PE=1 SV=2	8.61	4	4	0.92	1.03
P17812	CTP synthase 1 OS=Homo sapiens GN=CTPS1 PE=1 SV=2	7.45	3	3	0.92	1.07
P43490	Nicotinamide phosphoribosyltransferase OS=Homo sapiens GN=NAMPT PE=1 SV=1	16.70	6	5	0.92	1.09
Q96QK1	Vacuolar protein sorting-associated protein 35 OS=Homo sapiens GN=VPS35 PE=1 SV=2	20.98	14	12	0.92	1.09
P04183	Thymidine kinase, cytosolic OS=Homo sapiens GN=TK1 PE=1 SV=2	7.69	2	1	0.92	1.14
P78527	DNA-dependent protein kinase catalytic subunit OS=Homo sapiens GN=PRKDC PE=1 SV=3	35.97	152	121	0.92	1.17
Q9HAV4	Exportin-5 OS=Homo sapiens GN=XPO5 PE=1 SV=1	17.61	17	16	0.92	1.17
P62879	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2 OS=Homo sapiens GN=GNB2 PE=1 SV=3	18.53	4	4	0.92	1.26
P22392	Nucleoside diphosphate kinase B OS=Homo sapiens GN=NME2 PE=1 SV=1	59.21	9	3	0.92	1.30
P27708	CAD protein OS=Homo sapiens GN=CAD PE=1 SV=3	6.38	11	8	0.93	0.76
P11766	Alcohol dehydrogenase class-3 OS=Homo sapiens GN=ADH5 PE=1 SV=4	20.32	5	4	0.93	0.91
O00410	Importin-5 OS=Homo sapiens GN=IPO5 PE=1 SV=4	39.02	42	30	0.93	1.00
Q13263	Transcription intermediary factor 1-beta OS=Homo sapiens GN=TRIM28 PE=1 SV=5	7.78	7	7	0.93	1.03
Q9NR31	GTP-binding protein SAR1a OS=Homo sapiens GN=SAR1A PE=1 SV=1	17.68	2	2	0.93	1.03
P42285	Superkiller viralicidic activity 2-like 2 OS=Homo sapiens GN=SKIV2L2 PE=1 SV=3	2.02	2	2	0.93	1.06
Q13085	Acetyl-CoA carboxylase 1 OS=Homo sapiens GN=ACACA PE=1 SV=2	8.53	12	12	0.93	1.17
P40261	Nicotinamide N-methyltransferase OS=Homo sapiens GN=NNMT PE=1 SV=1	16.29	2	2	0.93	1.12
P25398	40S ribosomal protein S12 OS=Homo sapiens GN=RPS12 PE=1 SV=3	19.70	2	2	0.93	1.12
Q9P258	Protein RCC2 OS=Homo sapiens GN=RCC2 PE=1 SV=2	22.41	12	10	0.93	1.13
Q687X5	Metalloreductase STEAP4 OS=Homo sapiens GN=STEAP4 PE=1 SV=1	27.89	14	8	0.93	1.14
Q92538	Golgi-specific brefeldin A-resistance guanine nucleotide exchange factor 1 OS=Homo sapiens GN=GBF1 PE=1 SV=2	1.61	2	2	0.93	1.20
P31946	14-3-3 protein beta/alpha OS=Homo sapiens GN=YWHAB PE=1 SV=3	17.89	6	1	0.94	0.93
P13861	cAMP-dependent protein kinase type II-alpha regulatory subunit OS=Homo sapiens GN=PRKAR2A PE=1 SV=2	9.65	3	3	0.94	0.93
Q9Y3F4	Serine-threonine kinase receptor-associated protein OS=Homo sapiens GN=STRAP PE=1 SV=1	14.00	4	4	0.94	0.95
Q9NQ88	Fructose-2,6-bisphosphatase TIGAR OS=Homo sapiens GN=TIGAR PE=1 SV=1	4.07	2	1	0.94	1.26

P41250	Glycine--tRNA ligase OS=Homo sapiens GN=GARS PE=1 SV=3	18.94	12	10	0.94	1.00
Q16658	Fascin OS=Homo sapiens GN=FSCN1 PE=1 SV=3	53.55	25	21	0.94	1.01
P40939	Trifunctional enzyme subunit alpha, mitochondrial OS=Homo sapiens GN=HADHA PE=1 SV=2	16.12	14	8	0.94	1.02
Q92499	ATP-dependent RNA helicase DDX1 OS=Homo sapiens GN=DDX1 PE=1 SV=2	3.65	2	2	0.94	1.06
P31040	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial OS=Homo sapiens GN=SDHA PE=1 SV=2	19.58	9	8	0.94	1.08
P40227	T-complex protein 1 subunit zeta OS=Homo sapiens GN=CCT6A PE=1 SV=3	33.33	18	13	0.94	1.09
O43175	D-3-phosphoglycerate dehydrogenase OS=Homo sapiens GN=PHGDH PE=1 SV=4	41.65	28	17	0.94	1.10
P83881	60S ribosomal protein L36a OS=Homo sapiens GN=RPL36A PE=1 SV=2	16.04	2	2	0.94	1.11
O60502	Protein O-GlcNAcase OS=Homo sapiens GN=MGEA5 PE=1 SV=2	4.48	2	2	0.94	1.17
Q16531	DNA damage-binding protein 1 OS=Homo sapiens GN=DDB1 PE=1 SV=1	10.44	12	12	0.94	1.18
P42765	3-ketoacyl-CoA thiolase, mitochondrial OS=Homo sapiens GN=ACAA2 PE=1 SV=2	28.97	6	6	0.94	1.15
O95292	Vesicle-associated membrane protein-associated protein B/C OS=Homo sapiens GN=VAPB PE=1 SV=3	18.11	4	2	0.95	0.97
P49748	Very long-chain specific acyl-CoA dehydrogenase, mitochondrial OS=Homo sapiens GN=ACADVL PE=1 SV=1	30.08	16	14	0.95	1.03
O75628	GTP-binding protein REM 1 OS=Homo sapiens GN=REM1 PE=1 SV=2	3.69	2	1	0.95	1.06
P49588	Alanine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=AARS PE=1 SV=2	41.01	34	28	0.95	1.09
Q9BXJ9	N-alpha-acetyltransferase 15, NatA auxiliary subunit OS=Homo sapiens GN=NAA15 PE=1 SV=1	6.93	7	6	0.95	1.13
O60701	UDP-glucose 6-dehydrogenase OS=Homo sapiens GN=UGDH PE=1 SV=1	9.72	3	3	0.95	1.14
Q15181	Inorganic pyrophosphatase OS=Homo sapiens GN=PPA1 PE=1 SV=2	38.41	9	6	0.95	1.14
P02768	Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2	7.06	12	4	0.95	1.27
Q9UIA9	Exportin-7 OS=Homo sapiens GN=XPO7 PE=1 SV=3	2.30	2	2	0.95	1.27
A5YKK6	CCR4-NOT transcription complex subunit 1 OS=Homo sapiens GN=CNOT1 PE=1 SV=2	0.84	2	2	0.95	0.85
Q9NTK5	Obg-like ATPase 1 OS=Homo sapiens GN=OLA1 PE=1 SV=2	8.84	3	3	0.96	0.81
Q9H2G2	STE20-like serine/threonine-protein kinase OS=Homo sapiens GN=SLK PE=1 SV=1	1.78	2	2	0.96	0.87
Q96N66	Lysophospholipid acyltransferase 7 OS=Homo sapiens GN=MBOAT7 PE=1 SV=2	7.20	2	2	0.96	0.91
Q92896	Golgi apparatus protein 1 OS=Homo sapiens GN=GLG1 PE=1 SV=2	6.62	5	5	0.96	0.92
P43246	DNA mismatch repair protein Msh2 OS=Homo sapiens GN=MSH2 PE=1 SV=1	8.46	8	6	0.96	0.93
Q07020	60S ribosomal protein L18 OS=Homo sapiens GN=RPL18 PE=1 SV=2	32.45	7	5	0.96	0.99
P22061	Protein-L-isoaspartate(D-aspartate) O-methyltransferase OS=Homo sapiens GN=PCMT1 PE=1 SV=4	15.86	4	2	0.96	1.03
P29401	Transketolase OS=Homo sapiens GN=TKT PE=1 SV=3	42.70	30	17	0.96	1.03
P50416	Carnitine O-palmitoyltransferase 1, liver isoform OS=Homo sapiens GN=CPT1A PE=1 SV=2	7.50	4	4	0.96	1.06
Q96QD8	Sodium-coupled neutral amino acid transporter 2 OS=Homo sapiens GN=SLC38A2 PE=1 SV=2	4.15	3	1	0.96	1.06
Q9P2J5	Leucine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=LARS PE=1 SV=2	15.22	12	12	0.96	1.08
P46777	60S ribosomal protein L5 OS=Homo sapiens GN=RPL5 PE=1 SV=3	17.51	4	4	0.96	1.08
P13489	Ribonuclease inhibitor OS=Homo sapiens GN=RNH1 PE=1 SV=2	17.79	8	7	0.96	1.17
P20020	Plasma membrane calcium-transporting ATPase 1 OS=Homo sapiens GN=ATP2B1 PE=1 SV=3	3.34	3	1	0.96	1.23
Q13838	Spliceosome RNA helicase DDX39B OS=Homo sapiens GN=DDX39B PE=1 SV=1	7.48	3	3	0.96	1.04
Q96HN2	Adenosylhomocysteinase 3 OS=Homo sapiens GN=AHCYL2 PE=1 SV=1	5.40	3	3	0.97	0.84
Q96TA1	Niban-like protein 1 OS=Homo sapiens GN=FAM129B PE=1 SV=3	10.46	7	7	0.97	0.86
O75534	Cold shock domain-containing protein E1 OS=Homo sapiens GN=CSDE1 PE=1 SV=2	7.14	4	4	0.97	0.86
P11142	Heat shock cognate 71 kDa protein OS=Homo sapiens GN=HSPA8 PE=1 SV=1	38.39	26	17	0.97	0.89
P49411	Elongation factor Tu, mitochondrial OS=Homo sapiens GN=TUFM PE=1 SV=2	32.74	11	11	0.97	0.92
Q02218	2-oxoglutarate dehydrogenase, mitochondrial OS=Homo sapiens GN=OGDH PE=1 SV=3	2.54	2	2	0.97	0.92
P35237	Serpin B6 OS=Homo sapiens GN=SERPINB6 PE=1 SV=3	30.59	9	8	0.97	0.92

P61224	Ras-related protein Rap-1b OS=Homo sapiens GN=RAP1B PE=1 SV=1	24.46	3	3	0.97	0.96
O75131	Copine-3 OS=Homo sapiens GN=CPNE3 PE=1 SV=1	7.26	3	2	0.97	1.00
P35580	Myosin-10 OS=Homo sapiens GN=MYH10 PE=1 SV=3	7.44	15	1	0.97	1.04
P55809	Succinyl-CoA:3-ketoacid coenzyme A transferase 1, mitochondrial OS=Homo sapiens GN=OXCT1 PE=1 SV=1	18.65	6	6	0.97	1.03
Q96KB5	Lymphokine-activated killer T-cell-originated protein kinase OS=Homo sapiens GN=PBK PE=1 SV=3	6.83	3	2	0.97	0.87
Q9P035	Very-long-chain (3R)-3-hydroxyacyl-CoA dehydratase 3 OS=Homo sapiens GN=HACD3 PE=1 SV=2	5.25	2	2	0.98	0.78
P16070	CD44 antigen OS=Homo sapiens GN=CD44 PE=1 SV=3	8.49	11	6	0.98	0.83
Q00341	Vigilin OS=Homo sapiens GN=HDLBP PE=1 SV=2	4.50	3	3	0.98	0.85
Q02878	60S ribosomal protein L6 OS=Homo sapiens GN=RPL6 PE=1 SV=3	43.75	15	12	0.98	1.15
Q8TEX9	Importin-4 OS=Homo sapiens GN=IPO4 PE=1 SV=2	2.04	2	2	0.98	1.08
Q9H9B4	Sideroflexin-1 OS=Homo sapiens GN=SFXN1 PE=1 SV=4	7.76	2	2	0.98	1.28
P0DMV9	Heat shock 70 kDa protein 1B OS=Homo sapiens GN=HSPA1B PE=1 SV=1	29.17	16	9	0.98	1.34
P15170	Eukaryotic peptide chain release factor GTP-binding subunit ERF3A OS=Homo sapiens GN=GSPT1 PE=1 SV=1	22.04	10	8	0.98	0.90
Q92598	Heat shock protein 105 kDa OS=Homo sapiens GN=HSPH1 PE=1 SV=1	35.20	27	19	0.98	0.94
P30520	Adenylosuccinate synthetase isozyme 2 OS=Homo sapiens GN=ADSS PE=1 SV=3	14.47	4	4	0.98	0.97
Q9ULV4	Coronin-1C OS=Homo sapiens GN=CORO1C PE=1 SV=1	6.12	3	2	0.98	1.05
P62136	Serine/threonine-protein phosphatase PP1-alpha catalytic subunit OS=Homo sapiens GN=PPP1CA PE=1 SV=1	8.48	2	2	0.98	1.11
Q15067	Peroxisomal acyl-coenzyme A oxidase 1 OS=Homo sapiens GN=ACOX1 PE=1 SV=3	5.91	2	2	0.98	0.85
P55060	Exportin-2 OS=Homo sapiens GN=CSE1L PE=1 SV=3	35.53	36	25	0.99	1.04
O95340	Bifunctional 3'-phosphoadenosine 5'-phosphosulfate synthase 2 OS=Homo sapiens GN=PAPSS2 PE=1 SV=2	18.24	8	8	0.99	1.12
Q9BQ52	Zinc phosphodiesterase ELAC protein 2 OS=Homo sapiens GN=ELAC2 PE=1 SV=2	6.90	4	4	0.99	0.86
Q63HN8	E3 ubiquitin-protein ligase RNF213 OS=Homo sapiens GN=RNF213 PE=1 SV=3	1.06	4	4	0.99	0.87
P13010	X-ray repair cross-complementing protein 5 OS=Homo sapiens GN=XRCC5 PE=1 SV=3	19.81	12	9	0.99	0.87
Q7L576	Cytoplasmic FMR1-interacting protein 1 OS=Homo sapiens GN=CYFIP1 PE=1 SV=1	2.95	3	3	0.99	0.88
P17858	ATP-dependent 6-phosphofructokinase, liver type OS=Homo sapiens GN=PFKL PE=1 SV=6	5.26	3	2	0.99	0.88
Q9Y6E2	Basic leucine zipper and W2 domain-containing protein 2 OS=Homo sapiens GN=BZW2 PE=1 SV=1	15.27	7	5	0.99	0.89
P11021	78 kDa glucose-regulated protein OS=Homo sapiens GN=HSPA5 PE=1 SV=2	24.16	14	11	0.99	1.26
P36578	60S ribosomal protein L4 OS=Homo sapiens GN=RPL4 PE=1 SV=5	30.21	21	13	0.99	0.91
P31947	14-3-3 protein sigma OS=Homo sapiens GN=SFN PE=1 SV=1	20.97	6	2	0.99	0.92
P36871	Phosphoglucomutase-1 OS=Homo sapiens GN=PGM1 PE=1 SV=3	38.26	17	15	0.99	1.03
P21964	Catechol O-methyltransferase OS=Homo sapiens GN=COMT PE=1 SV=2	11.44	2	2	0.99	1.02
P67775	Serine/threonine-protein phosphatase 2A catalytic subunit alpha isoform OS=Homo sapiens GN=PPP2CA PE=1 SV=1	20.39	5	5	0.99	1.09
P60891	Ribose-phosphate pyrophosphokinase 1 OS=Homo sapiens GN=PRPS1 PE=1 SV=2	16.98	4	4	0.99	0.87
Q99798	Aconitate hydratase, mitochondrial OS=Homo sapiens GN=ACO2 PE=1 SV=2	4.10	2	2	0.99	0.95
Q16822	Phosphoenolpyruvate carboxykinase [GTP], mitochondrial OS=Homo sapiens GN=PCK2 PE=1 SV=3	3.13	2	2	0.99	1.05
Q9Y5L0	Transportin-3 OS=Homo sapiens GN=TNPO3 PE=1 SV=3	4.77	4	3	1.00	0.77
Q08J23	tRNA (cytosine(34)-C(5))-methyltransferase OS=Homo sapiens GN=NSUN2 PE=1 SV=2	31.03	19	17	1.00	0.78
Q9NZ01	Very-long-chain enoyl-CoA reductase OS=Homo sapiens GN=TECR PE=1 SV=1	5.52	2	2	1.00	1.15
P47897	Glutamine--tRNA ligase OS=Homo sapiens GN=QARS PE=1 SV=1	4.90	2	2	1.00	1.16
Q99832	T-complex protein 1 subunit eta OS=Homo sapiens GN=CCT7 PE=1 SV=2	53.22	29	21	1.00	0.96
Q9C0B1	Alpha-ketoglutarate-dependent dioxygenase FTO OS=Homo sapiens GN=FTO PE=1 SV=3	13.47	5	5	1.00	0.86
Q07065	Cytoskeleton-associated protein 4 OS=Homo sapiens GN=CKAP4 PE=1 SV=2	5.65	3	3	1.00	0.87
P49207	60S ribosomal protein L34 OS=Homo sapiens GN=RPL34 PE=1 SV=3	35.90	5	5	1.00	0.88

O95671	N-acetylserotonin O-methyltransferase-like protein OS=Homo sapiens GN=ASMTL PE=1 SV=3	3.06	2	2	1.00	0.88
Q09666	Neuroblast differentiation-associated protein AHNAK OS=Homo sapiens GN=AHNAK PE=1 SV=2	4.40	5	4	1.00	0.89
O00159	Unconventional myosin-Ic OS=Homo sapiens GN=MYO1C PE=1 SV=4	8.47	8	6	1.00	0.99
P30153	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A OS=Homo sapiens GN=PPP2R1A PE=1 SV=4	30.56	18	10	1.00	1.12
P55786	Puromycin-sensitive aminopeptidase OS=Homo sapiens GN=NPEPPS PE=1 SV=2	16.32	15	11	1.00	0.92
P11586	C-1-tetrahydrofolate synthase, cytoplasmic OS=Homo sapiens GN=MTHFD1 PE=1 SV=3	12.73	8	8	1.00	0.92
Q96RS6	NudC domain-containing protein 1 OS=Homo sapiens GN=NUDCD1 PE=1 SV=2	5.49	2	2	1.00	0.93
Q9H4A4	Aminopeptidase B OS=Homo sapiens GN=RNPEP PE=1 SV=2	11.08	6	6	1.00	1.15
P84098	60S ribosomal protein L19 OS=Homo sapiens GN=RPL19 PE=1 SV=1	22.45	9	5	1.00	0.95
Q92945	Far upstream element-binding protein 2 OS=Homo sapiens GN=KHSRP PE=1 SV=4	20.82	11	10	1.00	0.97
P54886	Delta-1-pyrroline-5-carboxylate synthase OS=Homo sapiens GN=ALDH18A1 PE=1 SV=2	5.66	4	4	1.00	1.08
P26038	Moesin OS=Homo sapiens GN=MSN PE=1 SV=3	8.67	5	4	1.00	1.24
O14880	Microsomal glutathione S-transferase 3 OS=Homo sapiens GN=MGST3 PE=1 SV=1	38.82	5	4	1.00	1.18
Q14203	Dynactin subunit 1 OS=Homo sapiens GN=DCTN1 PE=1 SV=3	2.90	3	3	1.00	1.12
P62906	60S ribosomal protein L10a OS=Homo sapiens GN=RPL10A PE=1 SV=2	17.05	3	3	1.00	0.84
P18669	Phosphoglycerate mutase 1 OS=Homo sapiens GN=PGAM1 PE=1 SV=2	8.27	3	2	1.00	0.62
Q14566	DNA replication licensing factor MCM6 OS=Homo sapiens GN=MCM6 PE=1 SV=1	2.68	2	2	1.00	1.10
Q16222	UDP-N-acetylhexosamine pyrophosphorylase OS=Homo sapiens GN=UAP1 PE=1 SV=3	5.36	2	2	1.00	0.91
P31949	Protein S100-A11 OS=Homo sapiens GN=S100A11 PE=1 SV=2	34.29	3	3	1.01	0.77
P31327	Carbamoyl-phosphate synthase [ammonia], mitochondrial OS=Homo sapiens GN=CPS1 PE=1 SV=2	33.53	56	37	1.01	0.80
P41252	Isoleucine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=IARS PE=1 SV=2	13.31	14	12	1.01	0.87
Q9P289	Serine/threonine-protein kinase 26 OS=Homo sapiens GN=STK26 PE=1 SV=2	6.97	2	2	1.01	0.88
Q8NC51	Plasminogen activator inhibitor 1 RNA-binding protein OS=Homo sapiens GN=SERBP1 PE=1 SV=2	13.73	5	4	1.01	0.88
P50990	T-complex protein 1 subunit theta OS=Homo sapiens GN=CCT8 PE=1 SV=4	46.17	31	24	1.01	0.89
O60610	Protein diaphanous homolog 1 OS=Homo sapiens GN=DIAPH1 PE=1 SV=2	4.32	4	4	1.01	0.90
Q16719	Kynureninase OS=Homo sapiens GN=KYNU PE=1 SV=1	17.20	6	6	1.01	0.91
P62917	60S ribosomal protein L8 OS=Homo sapiens GN=RPL8 PE=1 SV=2	18.29	3	3	1.01	0.91
P27797	Calreticulin OS=Homo sapiens GN=CALR PE=1 SV=1	17.51	5	5	1.01	0.91
P46977	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase STT3A OS=Homo sapiens GN=STT3A PE=1 SV=2	6.24	3	3	1.01	0.92
P52888	Thimet oligopeptidase OS=Homo sapiens GN=THOP1 PE=1 SV=2	3.63	2	2	1.01	0.92
P35606	Coatomer subunit beta' OS=Homo sapiens GN=COPB2 PE=1 SV=2	6.18	4	4	1.01	0.98
P32119	Peroxiredoxin-2 OS=Homo sapiens GN=PRDX2 PE=1 SV=5	44.95	9	5	1.01	1.44
O75874	Isocitrate dehydrogenase [NADP] cytoplasmic OS=Homo sapiens GN=IDH1 PE=1 SV=2	22.95	9	8	1.01	1.01
Q9Y617	Phosphoserine aminotransferase OS=Homo sapiens GN=PSAT1 PE=1 SV=2	8.11	3	3	1.01	1.08
Q9NYU2	UDP-glucose:glycoprotein glucosyltransferase 1 OS=Homo sapiens GN=UGGT1 PE=1 SV=3	2.57	3	2	1.01	0.89
Q16186	Proteasomal ubiquitin receptor ADRM1 OS=Homo sapiens GN=ADRM1 PE=1 SV=2	2.70	2	1	1.01	1.00
P61978	Heterogeneous nuclear ribonucleoprotein K OS=Homo sapiens GN=HNRNPK PE=1 SV=1	27.43	15	11	1.01	1.12
P20839	Inosine-5'-monophosphate dehydrogenase 1 OS=Homo sapiens GN=IMPDH1 PE=1 SV=2	3.89	2	1	1.01	0.95
Q9UI26	Importin-11 OS=Homo sapiens GN=IPO11 PE=1 SV=1	5.64	3	3	1.01	0.89
P02042	Hemoglobin subunit delta OS=Homo sapiens GN=HBD PE=1 SV=2	6.80	2	1	1.02	0.70
Q15393	Splicing factor 3B subunit 3 OS=Homo sapiens GN=SF3B3 PE=1 SV=4	1.81	2	2	1.02	0.80
Q9Y678	Coatomer subunit gamma-1 OS=Homo sapiens GN=COPG1 PE=1 SV=1	32.95	25	20	1.02	0.84
P50454	Serpin H1 OS=Homo sapiens GN=SERPINH1 PE=1 SV=2	33.97	12	9	1.02	0.85

P04075	Fructose-bisphosphate aldolase A OS=Homo sapiens GN=ALDOA PE=1 SV=2	54.40	32	18	1.02	0.87
P40763	Signal transducer and activator of transcription 3 OS=Homo sapiens GN=STAT3 PE=1 SV=2	14.42	10	8	1.02	0.89
Q13162	Peroxiredoxin-4 OS=Homo sapiens GN=PRDX4 PE=1 SV=1	6.64	3	1	1.02	0.93
P53396	ATP-citrate synthase OS=Homo sapiens GN=ACLY PE=1 SV=3	24.34	28	21	1.02	0.93
P16083	Ribosyldihydronicotinamide dehydrogenase [quinone] OS=Homo sapiens GN=NQO2 PE=1 SV=5	15.58	3	2	1.02	0.94
P51114	Fragile X mental retardation syndrome-related protein 1 OS=Homo sapiens GN=FXR1 PE=1 SV=3	4.35	2	2	1.02	1.21
P15311	Ezrin OS=Homo sapiens GN=EZR PE=1 SV=4	4.10	2	1	1.02	0.98
Q9NZJ7	Mitochondrial carrier homolog 1 OS=Homo sapiens GN=MTCH1 PE=1 SV=1	7.97	2	2	1.02	1.02
Q9Y263	Phospholipase A-2-activating protein OS=Homo sapiens GN=PLAA PE=1 SV=2	6.04	3	3	1.03	0.80
O00429	Dynamin-1-like protein OS=Homo sapiens GN=DNM1L PE=1 SV=2	16.58	6	6	1.03	0.86
Q15165	Serum paraoxonase/arylesterase 2 OS=Homo sapiens GN=PON2 PE=1 SV=3	22.88	3	3	1.03	0.87
P60174	Triosephosphate isomerase OS=Homo sapiens GN=TPI1 PE=1 SV=3	53.15	14	10	1.03	0.91
P35232	Prohibitin OS=Homo sapiens GN=PHB PE=1 SV=1	11.76	3	2	1.03	1.03
P61158	Actin-related protein 3 OS=Homo sapiens GN=ACTR3 PE=1 SV=3	26.79	10	8	1.03	0.93
P30050	60S ribosomal protein L12 OS=Homo sapiens GN=RPL12 PE=1 SV=1	28.48	6	4	1.03	1.12
P00966	Argininosuccinate synthase OS=Homo sapiens GN=ASS1 PE=1 SV=2	22.09	6	6	1.03	0.91
P63241	Eukaryotic translation initiation factor 5A-1 OS=Homo sapiens GN=EIF5A PE=1 SV=2	51.30	6	5	1.03	1.12
P08174	Complement decay-accelerating factor OS=Homo sapiens GN=CD55 PE=1 SV=4	9.97	4	4	1.03	0.90
O00764	Pyridoxal kinase OS=Homo sapiens GN=PDXK PE=1 SV=1	17.31	3	3	1.03	1.03
O15372	Eukaryotic translation initiation factor 3 subunit H OS=Homo sapiens GN=EIF3H PE=1 SV=1	9.66	2	2	1.03	0.98
P62244	40S ribosomal protein S15a OS=Homo sapiens GN=RPS15A PE=1 SV=2	23.08	3	3	1.04	0.80
P05141	ADP/ATP translocase 2 OS=Homo sapiens GN=SLC25A5 PE=1 SV=7	29.19	14	2	1.04	0.81
Q86Y56	Dynein assembly factor 5, axonemal OS=Homo sapiens GN=DNAAF5 PE=1 SV=4	4.68	3	3	1.04	0.84
P11498	Pyruvate carboxylase, mitochondrial OS=Homo sapiens GN=PC PE=1 SV=2	17.74	14	13	1.04	0.90
O15067	Phosphoribosylformylglycinamidine synthase OS=Homo sapiens GN=PFAS PE=1 SV=4	10.69	12	10	1.04	0.95
Q99615	DnaJ homolog subfamily C member 7 OS=Homo sapiens GN=DNAJC7 PE=1 SV=2	4.66	2	2	1.04	0.96
P12004	Proliferating cell nuclear antigen OS=Homo sapiens GN=PCNA PE=1 SV=1	22.99	5	5	1.04	1.12
Q13011	Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial OS=Homo sapiens GN=ECH1 PE=1 SV=2	6.71	2	1	1.04	1.01
P46781	40S ribosomal protein S9 OS=Homo sapiens GN=RPS9 PE=1 SV=3	18.04	4	4	1.05	0.81
P25205	DNA replication licensing factor MCM3 OS=Homo sapiens GN=MCM3 PE=1 SV=3	6.93	5	5	1.05	0.83
Q86X76	Nitrilase homolog 1 OS=Homo sapiens GN=NIT1 PE=1 SV=2	7.95	2	2	1.05	0.83
O60506	Heterogeneous nuclear ribonucleoprotein Q OS=Homo sapiens GN=SYNCRIP PE=1 SV=2	4.01	2	2	1.05	1.19
P21333	Filamin-A OS=Homo sapiens GN=FLNA PE=1 SV=4	40.76	109	74	1.05	1.01
Q15437	Protein transport protein Sec23B OS=Homo sapiens GN=SEC23B PE=1 SV=2	3.52	2	1	1.05	1.14
P09382	Galectin-1 OS=Homo sapiens GN=LGALS1 PE=1 SV=2	26.67	2	2	1.05	1.26
O00299	Chloride intracellular channel protein 1 OS=Homo sapiens GN=CLIC1 PE=1 SV=4	32.78	9	6	1.05	0.98
P25787	Proteasome subunit alpha type-2 OS=Homo sapiens GN=PSMA2 PE=1 SV=2	17.09	3	2	1.05	1.02
Q12931	Heat shock protein 75 kDa, mitochondrial OS=Homo sapiens GN=TRAP1 PE=1 SV=3	11.51	6	3	1.05	1.22
P11940	Polyadenylate-binding protein 1 OS=Homo sapiens GN=PABPC1 PE=1 SV=2	15.88	12	3	1.05	1.10
Q9UBQ5	Eukaryotic translation initiation factor 3 subunit K OS=Homo sapiens GN=EIF3K PE=1 SV=1	14.68	3	3	1.05	0.93
P23526	Adenosylhomocysteinase OS=Homo sapiens GN=AHCY PE=1 SV=4	20.60	8	7	1.06	0.83
O75694	Nuclear pore complex protein Nup155 OS=Homo sapiens GN=NUP155 PE=1 SV=1	4.60	7	4	1.06	0.84
P18621	60S ribosomal protein L17 OS=Homo sapiens GN=RPL17 PE=1 SV=3	36.41	7	7	1.06	0.87

P22234	Multifunctional protein ADE2 OS=Homo sapiens GN=PAICS PE=1 SV=3	38.59	21	13	1.06	0.88
Q15366	Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2 PE=1 SV=1	36.16	14	5	1.06	0.88
Q13310	Polyadenylate-binding protein 4 OS=Homo sapiens GN=PABPC4 PE=1 SV=1	12.73	10	1	1.06	0.89
P23634	Plasma membrane calcium-transporting ATPase 4 OS=Homo sapiens GN=ATP2B4 PE=1 SV=2	3.38	3	1	1.06	0.89
Q99873	Protein arginine N-methyltransferase 1 OS=Homo sapiens GN=PRMT1 PE=1 SV=2	17.73	5	5	1.06	0.90
Q9BTE3	Mini-chromosome maintenance complex-binding protein OS=Homo sapiens GN=MCMBP PE=1 SV=2	4.83	3	3	1.06	0.90
Q7KZF4	Staphylococcal nuclease domain-containing protein 1 OS=Homo sapiens GN=SND1 PE=1 SV=1	9.34	7	7	1.06	0.93
P40926	Malate dehydrogenase, mitochondrial OS=Homo sapiens GN=MDH2 PE=1 SV=3	45.56	15	12	1.06	1.37
Q14152	Eukaryotic translation initiation factor 3 subunit A OS=Homo sapiens GN=EIF3A PE=1 SV=1	6.37	7	7	1.06	1.07
P62191	26S protease regulatory subunit 4 OS=Homo sapiens GN=PSMC1 PE=1 SV=1	10.00	4	3	1.06	0.89
P06744	Glucose-6-phosphate isomerase OS=Homo sapiens GN=GPI PE=1 SV=4	5.38	4	2	1.06	1.12
Q13620	Cullin-4B OS=Homo sapiens GN=CUL4B PE=1 SV=4	5.15	3	3	1.06	1.04
O75915	PRA1 family protein 3 OS=Homo sapiens GN=ARL6IP5 PE=1 SV=1	15.96	2	2	1.06	0.99
Q07866	Kinesin light chain 1 OS=Homo sapiens GN=KLC1 PE=1 SV=2	1.57	2	1	1.06	0.95
Q01650	Large neutral amino acids transporter small subunit 1 OS=Homo sapiens GN=SLC7A5 PE=1 SV=2	12.62	10	5	1.07	0.75
P83731	60S ribosomal protein L24 OS=Homo sapiens GN=RPL24 PE=1 SV=1	19.11	5	4	1.07	0.80
P30154	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A OS=Homo sapiens GN=PPP2R1B PE=1 SV=3	10.48	6	1	1.07	0.84
P62424	60S ribosomal protein L7a OS=Homo sapiens GN=RPL7A PE=1 SV=2	25.19	6	6	1.07	0.87
P62249	40S ribosomal protein S16 OS=Homo sapiens GN=RPS16 PE=1 SV=2	34.25	6	5	1.07	0.89
P05165	Propionyl-CoA carboxylase alpha chain, mitochondrial OS=Homo sapiens GN=PCCA PE=1 SV=4	3.02	2	1	1.07	0.93
Q9Y6D6	Brefeldin A-inhibited guanine nucleotide-exchange protein 1 OS=Homo sapiens GN=ARFGEF1 PE=1 SV=2	1.57	2	2	1.07	1.05
Q14697	Neutral alpha-glucosidase AB OS=Homo sapiens GN=GANAB PE=1 SV=3	14.62	10	10	1.07	1.09
P63010	AP-2 complex subunit beta OS=Homo sapiens GN=AP2B1 PE=1 SV=1	10.14	9	1	1.07	1.26
P16435	NADPH--cytochrome P450 reductase OS=Homo sapiens GN=POR PE=1 SV=2	13.15	8	7	1.07	1.02
P00505	Aspartate aminotransferase, mitochondrial OS=Homo sapiens GN=GOT2 PE=1 SV=3	13.72	5	5	1.07	0.88
P52209	6-phosphogluconate dehydrogenase, decarboxylating OS=Homo sapiens GN=PGD PE=1 SV=3	8.28	3	2	1.07	1.05
Q7L2E3	Putative ATP-dependent RNA helicase DHX30 OS=Homo sapiens GN=DHX30 PE=1 SV=1	2.51	2	2	1.07	0.93
Q9H845	Acyl-CoA dehydrogenase family member 9, mitochondrial OS=Homo sapiens GN=ACAD9 PE=1 SV=1	6.12	3	3	1.07	1.18
P48147	Prolyl endopeptidase OS=Homo sapiens GN=PREP PE=1 SV=2	7.61	5	4	1.08	0.78
P35613	Basigin OS=Homo sapiens GN=BSG PE=1 SV=2	7.27	2	2	1.08	0.78
O00469	Procollagen-lysine,2-oxoglutarate 5-dioxygenase 2 OS=Homo sapiens GN=PLOD2 PE=1 SV=2	8.96	5	5	1.08	1.20
O75947	ATP synthase subunit d, mitochondrial OS=Homo sapiens GN=ATP5H PE=1 SV=3	37.27	4	4	1.08	1.12
Q00839	Heterogeneous nuclear ribonucleoprotein U OS=Homo sapiens GN=HNRNPU PE=1 SV=6	16.36	16	12	1.08	1.15
Q9P0L0	Vesicle-associated membrane protein-associated protein A OS=Homo sapiens GN=VAPA PE=1 SV=3	18.47	4	2	1.08	0.87
P60660	Myosin light polypeptide 6 OS=Homo sapiens GN=MYL6 PE=1 SV=2	19.21	3	2	1.08	0.89
P06733	Alpha-enolase OS=Homo sapiens GN=ENO1 PE=1 SV=2	52.76	27	16	1.08	1.26
O75369	Filamin-B OS=Homo sapiens GN=FLNB PE=1 SV=2	23.71	54	37	1.08	1.12
O75153	Clustered mitochondria protein homolog OS=Homo sapiens GN=CLUH PE=1 SV=2	8.48	7	7	1.08	0.96
Q14166	Tubulin--tyrosine ligase-like protein 12 OS=Homo sapiens GN=TTLL12 PE=1 SV=2	3.11	2	2	1.08	1.00
P42695	Condensin-2 complex subunit D3 OS=Homo sapiens GN=NCAPD3 PE=1 SV=2	1.94	2	2	1.08	1.09
P08865	40S ribosomal protein SA OS=Homo sapiens GN=RPSA PE=1 SV=4	27.80	7	5	1.08	1.06
O00592	Podocalyxin OS=Homo sapiens GN=PODXL PE=1 SV=2	3.94	2	2	1.08	1.13
P47914	60S ribosomal protein L29 OS=Homo sapiens GN=RPL29 PE=1 SV=2	14.47	3	2	1.08	1.15

Q9BW60	Elongation of very long chain fatty acids protein 1 OS=Homo sapiens GN=ELOVL1 PE=1 SV=1	4.30	2	1	1.08	1.22
P09622	Dihydrolipoyl dehydrogenase, mitochondrial OS=Homo sapiens GN=DLD PE=1 SV=2	16.50	8	7	1.08	1.13
P14314	Glucosidase 2 subunit beta OS=Homo sapiens GN=PRKCSH PE=1 SV=2	4.17	2	2	1.09	0.83
P60953	Cell division control protein 42 homolog OS=Homo sapiens GN=CDC42 PE=1 SV=2	14.66	2	2	1.09	0.86
P08758	Annexin A5 OS=Homo sapiens GN=ANXA5 PE=1 SV=2	11.56	3	3	1.09	0.87
O94925	Glutaminase kidney isoform, mitochondrial OS=Homo sapiens GN=GLS PE=1 SV=1	11.36	6	6	1.09	0.88
P05556	Integrin beta-1 OS=Homo sapiens GN=ITGB1 PE=1 SV=2	19.80	13	12	1.09	0.89
O95347	Structural maintenance of chromosomes protein 2 OS=Homo sapiens GN=SMC2 PE=1 SV=2	8.19	8	8	1.09	0.90
P22314	Ubiquitin-like modifier-activating enzyme 1 OS=Homo sapiens GN=UBA1 PE=1 SV=3	45.46	50	33	1.09	0.93
P34897	Serine hydroxymethyltransferase, mitochondrial OS=Homo sapiens GN=SHMT2 PE=1 SV=3	25.20	13	11	1.09	0.93
P21399	Cytoplasmic aconitate hydratase OS=Homo sapiens GN=ACO1 PE=1 SV=3	4.61	3	3	1.09	1.03
Q9Y266	Nuclear migration protein nudC OS=Homo sapiens GN=NUDC PE=1 SV=1	12.39	4	4	1.09	0.92
O15427	Monocarboxylate transporter 4 OS=Homo sapiens GN=SLC16A3 PE=1 SV=1	7.31	3	3	1.10	0.81
Q09161	Nuclear cap-binding protein subunit 1 OS=Homo sapiens GN=NCBP1 PE=1 SV=1	7.72	4	4	1.10	0.85
P49321	Nuclear autoantigenic sperm protein OS=Homo sapiens GN=NASP PE=1 SV=2	4.06	4	2	1.10	0.86
Q8NE71	ATP-binding cassette sub-family F member 1 OS=Homo sapiens GN=ABCF1 PE=1 SV=2	3.20	2	2	1.10	0.87
O94979	Protein transport protein Sec31A OS=Homo sapiens GN=SEC31A PE=1 SV=3	3.03	4	2	1.10	0.91
P11717	Cation-independent mannose-6-phosphate receptor OS=Homo sapiens GN=IGF2R PE=1 SV=3	3.01	6	5	1.10	0.94
P25788	Proteasome subunit alpha type-3 OS=Homo sapiens GN=PSMA3 PE=1 SV=2	4.71	2	1	1.10	0.95
P21796	Voltage-dependent anion-selective channel protein 1 OS=Homo sapiens GN=VDAC1 PE=1 SV=2	18.73	5	3	1.10	0.99
O15260	Surfeit locus protein 4 OS=Homo sapiens GN=SURF4 PE=1 SV=3	10.78	3	2	1.11	0.77
P11413	Glucose-6-phosphate 1-dehydrogenase OS=Homo sapiens GN=G6PD PE=1 SV=4	16.31	7	6	1.11	0.84
P62820	Ras-related protein Rab-1A OS=Homo sapiens GN=RAB1A PE=1 SV=3	42.44	9	5	1.11	0.85
Q9P2E9	Ribosome-binding protein 1 OS=Homo sapiens GN=RRBP1 PE=1 SV=4	2.70	2	2	1.11	0.87
P61026	Ras-related protein Rab-10 OS=Homo sapiens GN=RAB10 PE=1 SV=1	16.50	3	1	1.11	0.89
P52732	Kinesin-like protein KIF11 OS=Homo sapiens GN=KIF11 PE=1 SV=2	2.18	2	2	1.11	0.89
P35579	Myosin-9 OS=Homo sapiens GN=MYH9 PE=1 SV=4	41.84	92	56	1.11	0.90
P54577	Tyrosine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=YARS PE=1 SV=4	3.60	2	2	1.11	1.07
Q8NBN3	Transmembrane protein 87A OS=Homo sapiens GN=TMEM87A PE=1 SV=3	3.42	2	2	1.11	0.98
P50502	Hsc70-interacting protein OS=Homo sapiens GN=ST13 PE=1 SV=2	7.05	2	2	1.11	1.09
Q8NBI5	Solute carrier family 43 member 3 OS=Homo sapiens GN=SLC43A3 PE=1 SV=2	3.46	2	2	1.11	1.03
O15131	Importin subunit alpha-6 OS=Homo sapiens GN=KPNA5 PE=1 SV=2	6.53	2	2	1.11	1.33
Q9Y265	RuvB-like 1 OS=Homo sapiens GN=RUVBL1 PE=1 SV=1	6.58	2	2	1.11	1.25
P23381	Tryptophan--tRNA ligase, cytoplasmic OS=Homo sapiens GN=WARS PE=1 SV=2	4.88	2	2	1.11	0.86
P60981	Destrin OS=Homo sapiens GN=DSTN PE=1 SV=3	35.15	7	4	1.11	0.85
Q9NZM1	Myoferlin OS=Homo sapiens GN=MYOF PE=1 SV=1	20.43	30	28	1.12	0.90
P43304	Glycerol-3-phosphate dehydrogenase, mitochondrial OS=Homo sapiens GN=GPD2 PE=1 SV=3	4.26	2	2	1.12	0.96
Q14643	Inositol 1,4,5-trisphosphate receptor type 1 OS=Homo sapiens GN=ITPR1 PE=1 SV=3	2.03	5	4	1.12	0.96
Q9Y383	Putative RNA-binding protein Luc7-like 2 OS=Homo sapiens GN=LUC7L2 PE=1 SV=2	14.03	5	5	1.12	0.97
P31948	Stress-induced-phosphoprotein 1 OS=Homo sapiens GN=STIP1 PE=1 SV=1	7.18	3	3	1.12	0.98
P19338	Nucleolin OS=Homo sapiens GN=NCL PE=1 SV=3	7.89	3	3	1.12	1.00
O94855	Protein transport protein Sec24D OS=Homo sapiens GN=SEC24D PE=1 SV=2	3.20	3	3	1.12	1.02
Q9UGI8	Testin OS=Homo sapiens GN=TES PE=1 SV=1	7.84	3	2	1.12	1.08

P49257	Protein ERGIC-53 OS=Homo sapiens GN=LMAN1 PE=1 SV=2	5.10	3	3	1.12	1.07
P36776	Lon protease homolog, mitochondrial OS=Homo sapiens GN=LONP1 PE=1 SV=2	20.33	14	10	1.12	0.82
P07737	Profilin-1 OS=Homo sapiens GN=PFN1 PE=1 SV=2	55.71	9	6	1.13	1.19
Q8NCW5	NAD(P)H-hydrate epimerase OS=Homo sapiens GN=APOA1BP PE=1 SV=2	12.85	2	2	1.13	1.03
Q9HCC0	Methylcrotonoyl-CoA carboxylase beta chain, mitochondrial OS=Homo sapiens GN=MCCC2 PE=1 SV=1	4.09	2	2	1.13	1.07
O75223	Gamma-glutamylcyclotransferase OS=Homo sapiens GN=GGCT PE=1 SV=1	9.04	2	2	1.14	0.86
Q9UDY8	Mucosa-associated lymphoid tissue lymphoma translocation protein 1 OS=Homo sapiens GN=MALT1 PE=1 SV=1	3.16	2	2	1.14	0.87
P06753	Tropomyosin alpha-3 chain OS=Homo sapiens GN=TPM3 PE=1 SV=2	14.74	4	4	1.14	0.90
Q96CS3	FAS-associated factor 2 OS=Homo sapiens GN=FAF2 PE=1 SV=2	4.27	2	2	1.14	0.91
O60547	GDP-mannose 4,6 dehydratase OS=Homo sapiens GN=GMDS PE=1 SV=1	25.54	7	7	1.14	0.97
P46779	60S ribosomal protein L28 OS=Homo sapiens GN=RPL28 PE=1 SV=3	27.01	7	4	1.14	1.03
P38606	V-type proton ATPase catalytic subunit A OS=Homo sapiens GN=ATP6V1A PE=1 SV=2	4.21	3	2	1.15	0.88
P55072	Transitional endoplasmic reticulum ATPase OS=Homo sapiens GN=VCP PE=1 SV=4	40.94	31	21	1.15	0.91
P49419	Alpha-aminoadipic semialdehyde dehydrogenase OS=Homo sapiens GN=ALDH7A1 PE=1 SV=5	19.29	9	7	1.15	1.13
P24752	Acetyl-CoA acetyltransferase, mitochondrial OS=Homo sapiens GN=ACAT1 PE=1 SV=1	11.24	3	3	1.15	1.14
Q12965	Unconventional myosin-Ie OS=Homo sapiens GN=MYO1E PE=1 SV=2	2.35	2	2	1.15	1.02
P04083	Annexin A1 OS=Homo sapiens GN=ANXA1 PE=1 SV=2	41.33	12	11	1.16	1.28
P04843	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1 OS=Homo sapiens GN=RPN1 PE=1 SV=1	27.84	13	12	1.16	0.89
P50395	Rab GDP dissociation inhibitor beta OS=Homo sapiens GN=GDI2 PE=1 SV=2	20.00	7	6	1.16	0.92
Q92841	Probable ATP-dependent RNA helicase DDX17 OS=Homo sapiens GN=DDX17 PE=1 SV=2	3.43	2	2	1.16	0.99
Q96KA5	Cleft lip and palate transmembrane protein 1-like protein OS=Homo sapiens GN=CLPTM1L PE=1 SV=1	6.51	3	3	1.16	1.02
Q92597	Protein NDRG1 OS=Homo sapiens GN=NDRG1 PE=1 SV=1	12.94	3	3	1.16	1.33
P62241	40S ribosomal protein S8 OS=Homo sapiens GN=RPS8 PE=1 SV=2	25.96	4	4	1.17	0.88
P07954	Fumarate hydratase, mitochondrial OS=Homo sapiens GN=FH PE=1 SV=3	22.94	8	8	1.17	1.17
P11279	Lysosome-associated membrane glycoprotein 1 OS=Homo sapiens GN=LAMP1 PE=1 SV=3	4.80	2	2	1.17	0.97
Q29RF7	Sister chromatid cohesion protein PDS5 homolog A OS=Homo sapiens GN=PDS5A PE=1 SV=1	4.49	5	5	1.18	0.83
P62910	60S ribosomal protein L32 OS=Homo sapiens GN=RPL32 PE=1 SV=2	25.19	6	5	1.18	0.85
P38646	Stress-70 protein, mitochondrial OS=Homo sapiens GN=HSPA9 PE=1 SV=2	49.78	39	27	1.18	0.92
Q6XQN6	Nicotinate phosphoribosyltransferase OS=Homo sapiens GN=NAPRT PE=1 SV=2	15.99	5	5	1.18	1.10
Q13148	TAR DNA-binding protein 43 OS=Homo sapiens GN=TARDBP PE=1 SV=1	5.07	2	2	1.19	0.87
P55209	Nucleosome assembly protein 1-like 1 OS=Homo sapiens GN=NAP1L1 PE=1 SV=1	5.37	3	2	1.19	0.92
P31153	S-adenosylmethionine synthase isoform type-2 OS=Homo sapiens GN=MAT2A PE=1 SV=1	5.82	3	3	1.21	1.15

Table S2. Competitive proteomic results of previously reported celastrol targets.

Reference	*Description*	*Accession*	*TMT in vitro*	*TMT in situ*
6	Heat shock protein HSP 90-beta	P08238	0.91	1.26
7	Hsp90 co-chaperone Cdc37	Q16543	**0.37**	**0.59**
8	Prostaglandin E synthase 3 (p23)	Q15185	0.72	0.90
9	Inhibitor of nuclear factor kappa-B kinase beta	O14920	Undetected	Undetected
10	Proteasomes **(#)**	N/A	N/A	N/A
11	Peroxiredoxin-1	Q06830	0.73	1.28
14	Annexin A2	P07355	**0.42**	**0.72**
14	Elongation factor 1-alpha 1	P68104	**0.37**	**0.62**
14	Tubulin beta chain	P07437	0.68	0.93

(#): multiple proteasome subunits were identified as below:

Accession	*Description*	*TMT in vitro*	*TMT in situ*
Q9UNM6	26S proteasome non-ATPase regulatory subunit 13	**0.18**	**0.46**
Q15008	26S proteasome non-ATPase regulatory subunit 6	**0.38**	**0.48**
Q99460	26S proteasome non-ATPase regulatory subunit 1	**0.48**	**0.66**
Q13200	26S proteasome non-ATPase regulatory subunit 2	**0.26**	**0.69**
P35998	26S protease regulatory subunit 7	**0.17**	**0.71**

2. Supplementary Figures

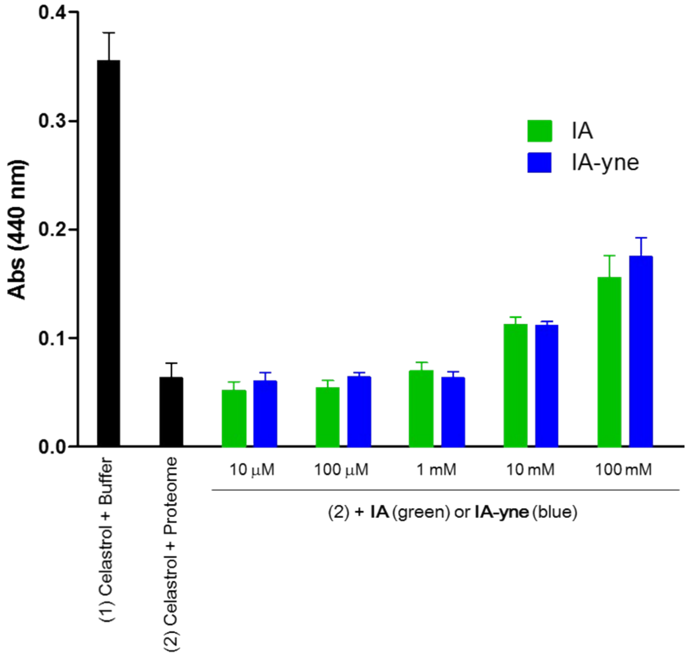
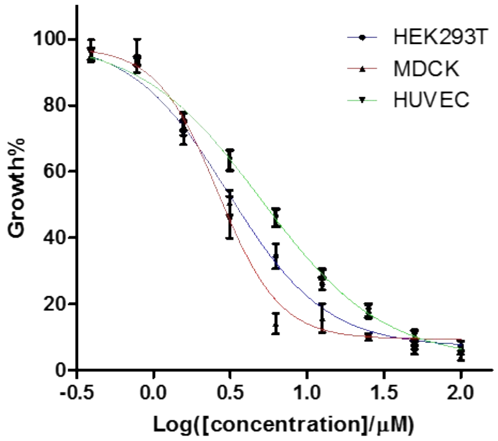


Figure S1. Low concentrations (less than 1 mM) of iodoacetamide (**IA**) and **IA-yne** did not effect on celastrol-proteins interaction. 100 M of celastrol (10 mM stock in DMSO) was incubated with HeLa cell lysates (1.0 mg/mL) suspended in lysis buffer (50 mM HEPES pH 7.4, 150 mM NaCl, 0.1% Triton X-100, 3.0 mM $MgCl_2$, 1.0 mM EDTA and complete protease inhibitor (Roche)) and equal volume of lysis buffer for 30 minutes at room temperature in triplicate. Celastrol-treated proteomes were added with increasing concentrations of iodoacetamide and incubate for 1 hour at room temperature. The amount of free celastrol was determined by absorbance at 440 nm.



	GI$_{50}$/μM
HEK293T	2.65 ± 0.11
HUVEC	4.54 ± 0.13
MDCK	2.41 ± 0.09

Figure S2. Proliferation inhibitory effect of celastrol towards HEK293T, MDCK and HUVEC cell lines.

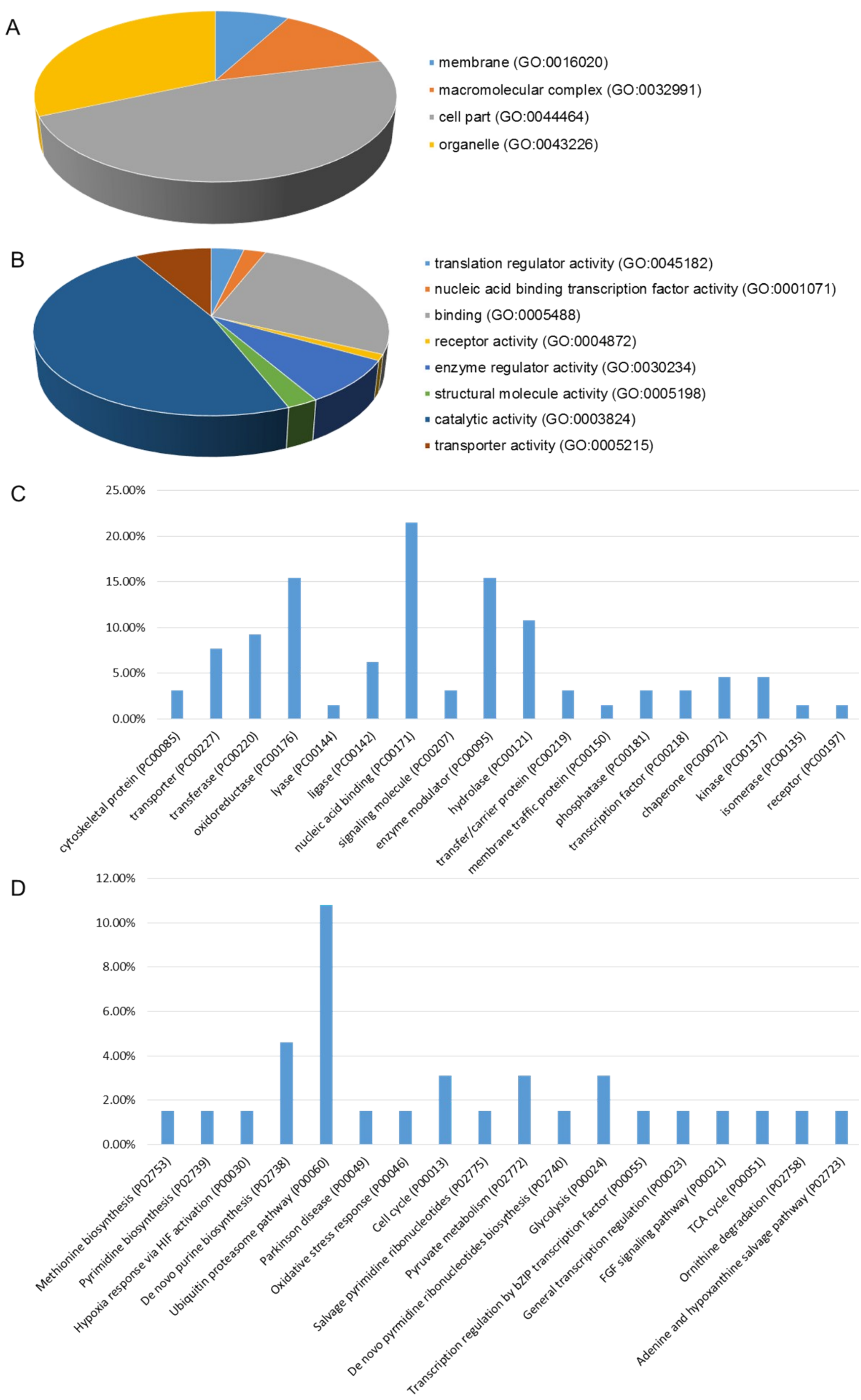


Figure S3. Gene Ontology (GO) PANTHER bioinformatics analysis of (A) cellular component; (B) molecular function; (C) protein class; (D) pathways of 66 celastrol targets.

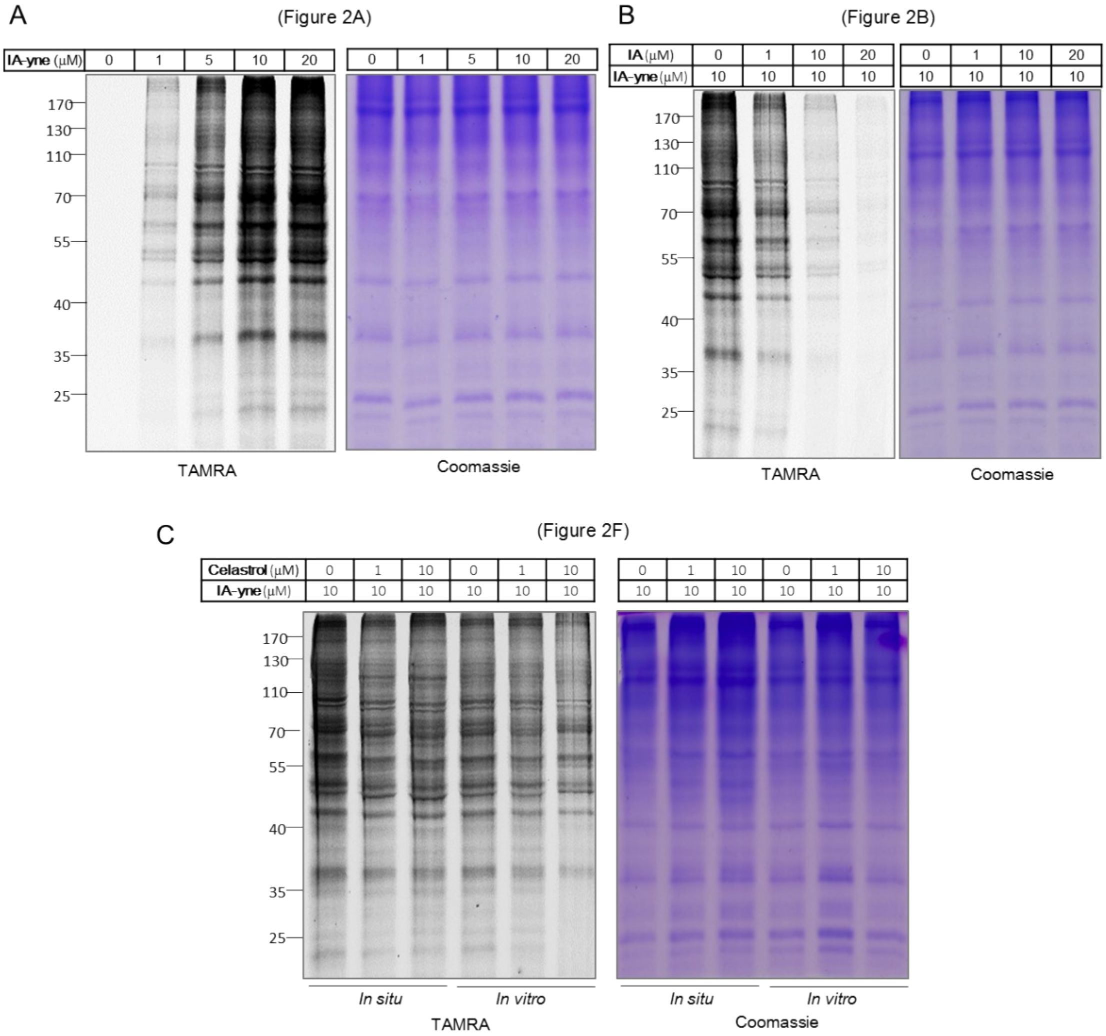


Figure S4. Full coomassie blue stained gel imaging of (A) **Figure** 2A; (B) **Figure** 2B; (C) **Figure** 2F.