DPP9’s enzymatic activity and not its binding to CARD8 inhibits inflammasome activation

Andrew R. Griswold[1,2], Daniel P. Ball[3], Abir Bhattacharjee[3], Ashley J. Chui[4], Sahana D. Rao[4], Cornelius Y. Taabazuing[3], & Daniel A. Bachovchin[2,3,4] *

[1] Tri-Institutional MD-PhD Program, Memorial Sloan Kettering Cancer Center, Rockefeller University, Weill Cornell Medical College, New York, New York 10065, USA.

[2] Pharmacology Program, Weill Cornell Graduate School of Medical Sciences, Memorial Sloan Kettering Cancer Center, New York, New York 10065, USA.

[3] Chemical Biology Program, Memorial Sloan Kettering Cancer Center, New York, New York 10065, USA.

[4] Tri-Institutional PhD Program in Chemical Biology, Memorial Sloan Kettering Cancer Center, New York, New York 10065, USA.

*Corresponding Author, Daniel A. Bachovchin (bachovcd@mskcc.org)

TABLE OF CONTENTS

SUPPLEMENTAL FIGURES

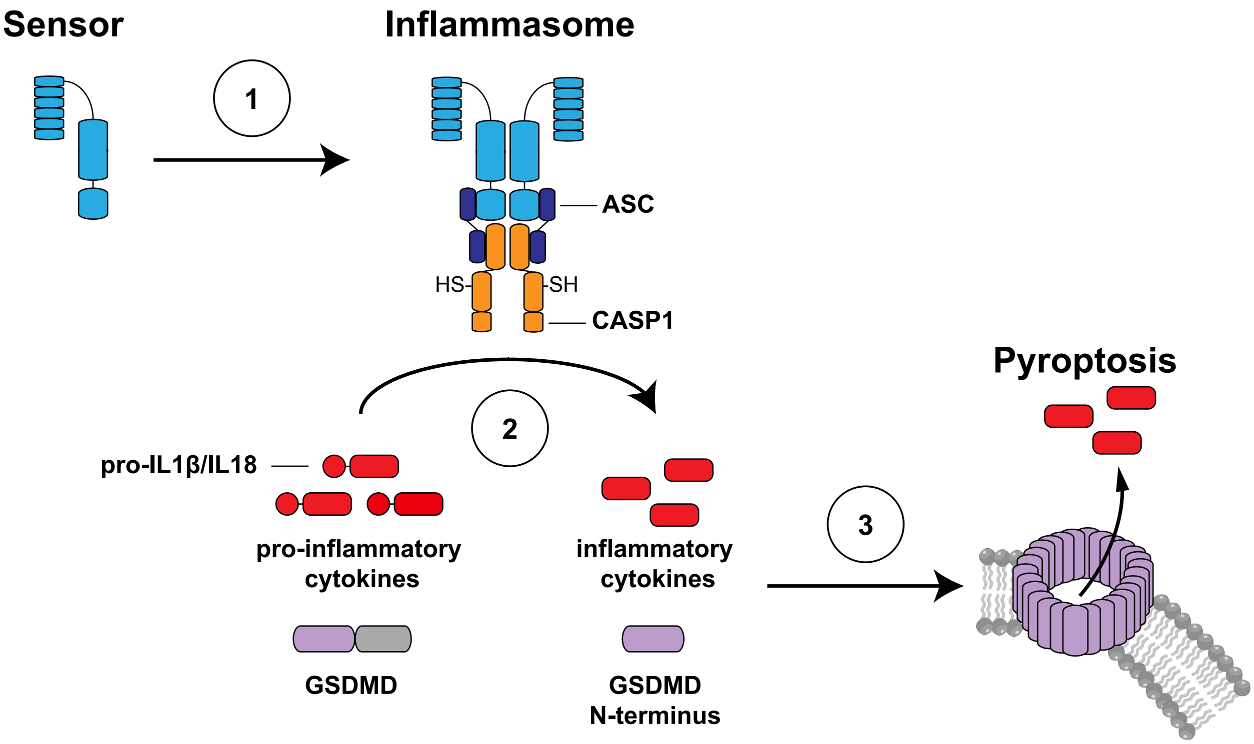


Figure S1. Inflammasome formation and activation. Graphical representation of the formation and downstream activity of inflammasomes. (1) Recognition of intracellular pathogenic structures or activities leads to formation of a multiprotein complex called an inflammasome, which recruits the cysteine protease caspase-1. (2) Active caspase-1 hydrolyzes pro-inflammatory cytokines and GSDMD. (3) The N-terminal fragment of GSDMD oligomerizes, forming a pore in the cell membrane that releases intracellular contents and triggers a lytic form of cell death called pyroptosis.

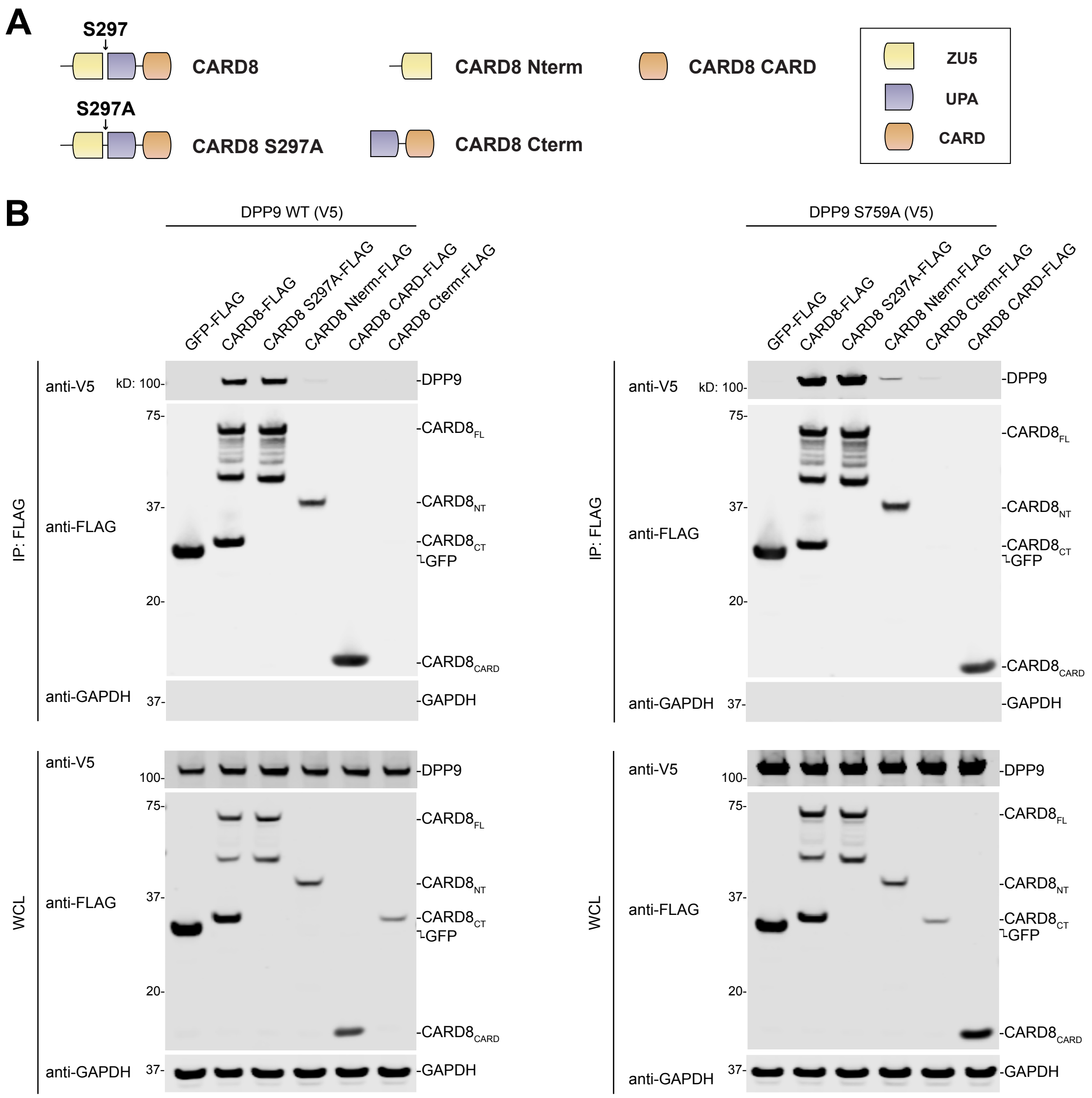


Figure S2. Full-length CARD8 binds to DPP9. (A) Graphical representation of CARD8 constructs tested. (B) HEK 293T cells were transiently transfected with constructs encoding the indicated V5-tagged DPP9 (2 μg) or FLAG-tagged proteins (2 μg). Lysates from these cells were mixed and subjected to anti-FLAG IPs. Immunoblots depict input whole cell lysate (WCL) and captured proteins (IP: FLAG).

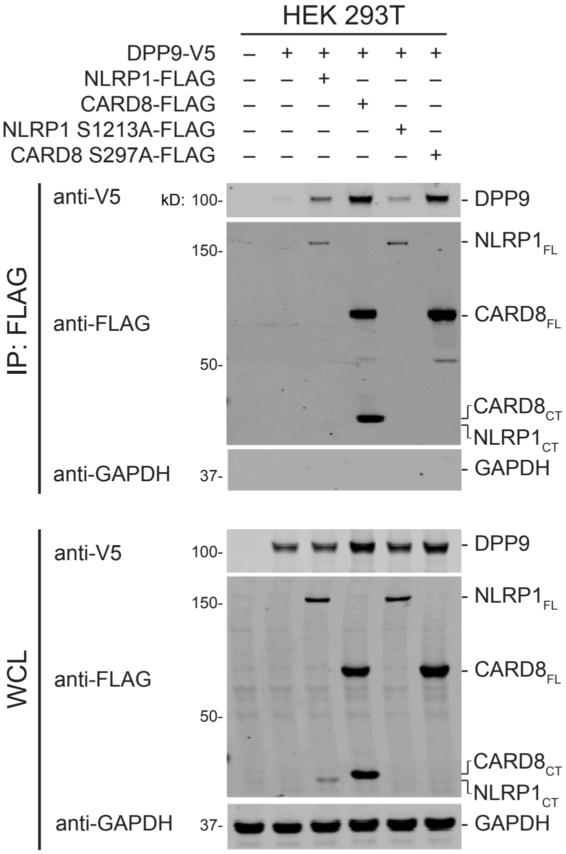


Figure S3. CARD8 autoproteolysis is not required for DPP9 binding. Anti-FLAG IPs of lysates from HEK 293T cells transiently transfected with constructs encoding V5-tagged DPP9 (0.5 μg) and the indicated FLAG-tagged protein (0.5 μg). Immunoblots depict input whole cell lysate (WCL) and captured proteins (IP: FLAG).

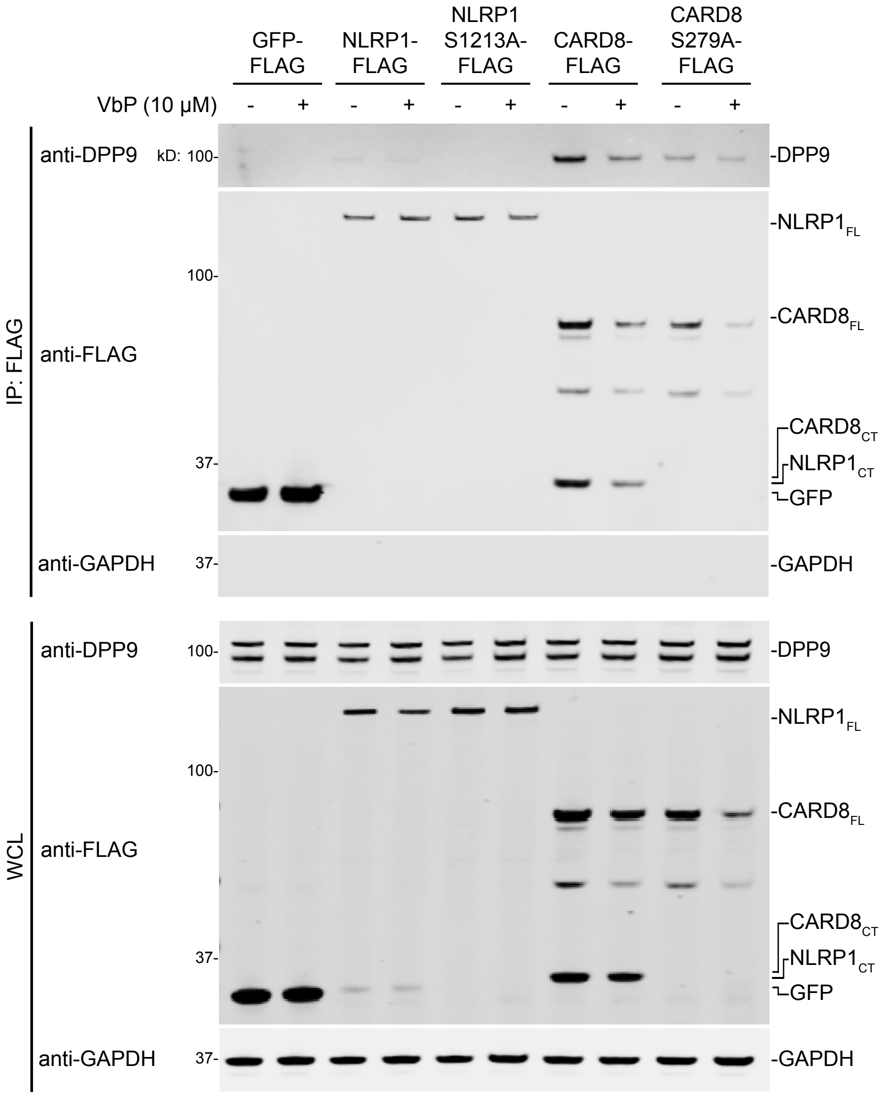


Figure S4. DPP8/9 inhibition in cells reduces CARD8 and NLRP1 protein levels. HEK 293T cells transiently transfected with constructs encoding the indicated FLAG-tagged protein (0.5 μg GFP, 0.5 μg CARD8, 2 μg NLRP1) were treated with DMSO or VbP (10 μM, 16 h) prior to FLAG IPs of lysates. Immunoblots depict input whole cell lysate (WCL) and captured proteins (IP: FLAG). The proteasome-mediated degradation of NLRP1 and CARD8 likely accounts for the lower levels of CARD8, NLRP1, and DPP9 in the FLAG IPs.

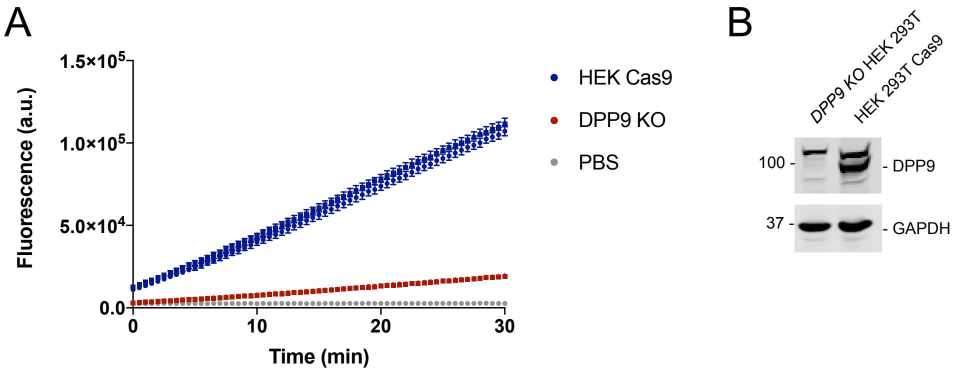


Figure S5. Confirmation of *DPP9* KO HEK 293T cells. (A) GP-AMC activity in lysates from Cas9-expressing (control) or *DPP9* KO HEK 293T cells. The data are the means ± SEM for three biological replicates. (B) Confirmation of *DPP9* knockout by immunoblotting.

BIOLOGICAL METHODS

Reagents and antibodies: Antibodies used include: V5 Rabbit polyclonal Ab (Abcam, Ab9116), DPP9 Rabbit polyclonal Ab (Abcam, Ab42080), CARD8 C-terminus Rabbit polyclonal Ab (Abcam, Ab24186), FLAG® M2 monoclonal Ab (Sigma, F3165), GAPDH Rabbit monoclonal Ab (Cell Signaling Tech, 14C10), human caspase-1 Rabbit polyclonal Ab (Cell Signaling Technology, #2225), IRDye 680 RD Streptavidin, (LI-COR 926-68079), IRDye 800CW anti-rabbit (LICOR, 925-32211), IRDye 800CW anti-mouse (LI-COR, 925-32210), IRDye 680CW anti-rabbit (LI-COR, 925-68073), IRDye 680CW anti-mouse (LI-COR, 925-68072). Other reagents used include: Val-boroPro (VbP)[1], 8J[2], Gly-Pro-AMC (VWR 100042-646), and TMTsixplex (Thermo, 90061).

Cell Culture. HEK 293T cells were purchased from ATCC. All HEK 293T cell lines were grown in Dulbecco's modified Eagle's medium (DMEM) with 10% fetal bovine serum (FBS). THP-1 (ATCC), *DPP8/9* KO THP-1[1], MV4:11 (ATCC) cells were grown in Roswell Park Memorial Institute medium (RPMI) with 10% FBS. All cells were grown at 37 °C in a 5% CO_2 incubator. Cell lines were regularly tested for mycoplasma using the MycoAlert™ Mycoplasma Detection Kit (Lonza).

Cloning. sgRNAs for DPP9 (GGCCAACATCGAGACAGGCG) were designed using the Broad Institute's web portal and cloned into the lentiGuide-Puro vector (Addgene no. 52963), as described previously.[1] Plasmids encoding CARD8[2], NLRP1 and mNLRP1B[3] were cloned as previously described and shuttled into modified pLEX_307 vectors (Addgene) with a C-terminal FLAG tag using Gateway technology (Thermo

Fisher Scientific). Plasmids for DPP4, DPP7, DPP8, and DPP9 were cloned as previously described[4] and shuttled into modified pLEX_307 vectors (Addgene) with a C-terminal V5 tag using Gateway technology (Thermo Fisher Scientific).

CRISPR/Cas9 gene editing. 5 x 10^5 HEK 293T cells stably expressing Cas9 generated previously,[5] were seeded in 6-well tissue culture dishes in 2 mL of media per well. The next day cells were transfected according to manufacturer's instructions (FuGENE HD, Promega) with sgRNA plasmid(s). After 48 h of transfection, cells were transferred to a 10 cm tissue culture dish and selected with puromycin (2 μg/mL) until untransfected control cells were all dead. Single cell clones were isolated by serial dilution and confirmed by Western blot.

GP-AMC assay. A solution of substrate (1 mM Gly-Pro-AMC) was prepared in DMSO. 19 µL of PBS or the indicated cell lysate was added to a 394-well, black, clear-bottom plate (Corning), followed by 1 μL of 1 mM substrate to initiate the reaction. Substrate cleavage was measured as increasing fluorescence signal recorded at ambient temperature every minute at 380-nm excitation and 460-nm emission wavelengths over a 30 min period.

FP-biotin enrichment of folded serine proteases. Cells pellets were lysed in Tris-Buffered Saline (TBS) with 0.5% NP-40 on ice for 20 min, and centrifuged at 20,000 x G for 10 min at 4 °C. Protein concentration of the soluble proteome was determined using the DC Protein Assay kit (Bio-Rad) and adjusted to 1 mg/mL. Lysates were reacted with the FP-PEG(n)-Biotin probe **1**, **2**, or **3** (10 μM) for 2 h at ambient temperature. Lysates were then separated from free probe by passage over a Sephadex G-25M column (GE Healthcare) with PBS (1.5 mL). 4 mL of TBS with 0.5% NP-40 was added (5.5 mL total volume), before the addition of 100 μL of high capacity NeutrAvidin-Agarose resin (Pierce). Samples were rotated end-over-end at 25 °C for 1 h. The samples were then washed with 3 × 10 mL PBS and eluted by resuspension in 100 μL of 2× sample loading dye and boiling at 95 °C for 10 min.

FLAG Immunoprecipitation. Cells pellets were lysed in Tris-Buffered Saline (TBS) with 0.5% NP-40 on ice for 20 min, and centrifuged at 20,000 x *g* for 10 min at 4 °C. Protein concentration of the soluble proteome was determined using the DC Protein Assay kit (Bio-Rad) and adjusted to 2 mg/mL. Lysates were incubated with 25 μL of anti-FLAG-M2 agarose resin (Sigma) overnight at 4 °C. After washing 3 x 1 mL with PBS, bound proteins were eluted by incubating resin with 50 μL of PBS with 150 ng/μL 3x-FLAG peptide for 1 h at 4 °C. An equal volume of 2x sample loading was added to the eluate and boiled. Immunoblots were developed with the Odyssey CLx imaging system (LI-COR) and band densities were quantified in Image Studio Ver 3.1(LI-COR).

LDH cytotoxicity assays. Cells were seeded at 1 × 10^5 cells/well in 12-well tissue culture dishes in 1 mL of media per well. The following day cells were transiently transfected with a cocktail of CARD8 (0.05 μg), CASP1 (0.025 μg), GSDMD^{I105N} (0.05 μg) and GFP (0.875 μg) per well with FuGENE HD according to manufacturer's instructions (Promega). After 36 h, DMSO or VbP was added to the indicated samples, followed by an additional incubation of 6 h. Supernatants were analyzed for LDH activity using the Pierce LDH Cytotoxicity Assay Kit (Life Technologies) and lysates protein content was evaluated by immunoblotting.

FLAG Immunoprecipitation and tandem mass tag labeling for mass spectrometry. HEK 293T cells were seeded at 3 x 10^6 cells in 10 cm tissue culture dish in in 10 mL of media per dish. The following day cells were transiently transfected with 10 μg of either C-terminal FLAG tagged GFP (control) or CARD8 according to manufacturer's instructions (FuGENE HD, Promega). After 48 h, cells were treated with either DMSO or Val-boroPro (10 μM) for 24 h, at which point cells were harvested and lysed in 1 mL TBS containing 0.5% NP-40 per 10 cm dish on ice for 30 min. Lysates were then clarified at 20,000 x G for 10 min. The soluble fraction was retained, and protein concentrations were normalized by DC Assay (Bio-Rad). 100 μL of anti-FLAG-M2 agarose affinity gel (Sigma) was added to each lysate and samples were rotated end-over-end at 4°C overnight. After washing 3 x 1 mL with cold PBS, bound proteins were eluted with 200 μL of 3x FLAG tag peptide (Sigma) at a final concentration of 150 μg/mL for 1 hour at 4°C.

The eluted proteins were reduced with 10 mM dithiothreitol for 30 min at 56°C while shaking and then alkylated with 20 mM iodoacetamide for 30 min at ambient temperature, protected from light. Proteins were then precipitated by adding six volumes of pre-chilled acetone and incubated at –20 °C overnight. Samples were then centrifuged at 8000 x G for 10 min at 4 °C and then carefully inverted to decant acetone. Acetone-precipitated pellets were then resuspended with 100 μL of 50 mM triethylammonium bicarbonate

(TEAB) buffer per sample and total protein concentration was measured by DC assay. Proteins were then digested overnight at 37°C with 2.5 μg trypsin per 100 μg of sample.

TMTsixplex™ Isobaric Label Reagents (ThermoFisher Scientific), 0.8 mg per label, were equilibrated to room temperature, dissolved in 41 μL of dry acetonitrile and mixed by vortex briefly before use. 41 μL of each TMT label reagent was carefully added to each sample (126 & 127 = GFP; 128 & 129 = CARD8 DMSO; 130 & 131 = CARD8 VbP) and incubated at room temperature for 1 hour. 8 μL of 5% hydroxylamine was then added to each sample and incubated for 15 minutes to quench the labeling reaction. Samples were then combined in equal quantities, purified using the High pH Reversed-Phase Peptide Fractionation Kit (Pierce), and dried with a Genevac EZ-2 evaporator to give peptide pellets for tandem LC-MS/MS/MS analysis.

Tandem LC-MS/MS/MS. Mass spectrometry data was collected on an Orbitrap Fusion Lumos mass spectrometer coupled to an Easy-nLC 1200 (Thermo Fisher Scientific). Peptides were separated over a 220 min gradient of 0 to 50% acetonitrile in water with 0.1% formic acid at a flow rate of 300 nL/min on a 50 cm long PepMap RSLC C18 column (2 μm, 100Å, 75μ, x 50 cm). The full MS spectra were acquired in the Orbitrap at a resolution of 120,000. The 10 most intense MS1 ions were selected for MS2 analysis. The isolation width was set at 0.7 m/z and isolated precursors were fragmented by CID (35% CE). Following acquisition of each MS2 spectrum, a synchronous precursor selection (SPS) MS3 scan was collected on the top 10 most intense ions in the MS2 spectrum. The isolation width was set at 1.2 m/z and isolated precursors were fragmented using HCD. The mass spectrometry proteomics data have been deposited to the ProteomeXchange Consortium (http://proteomecentral.proteomexchange.org) via the PRIDE partner repository[6] with the dataset identifier PXD015047.

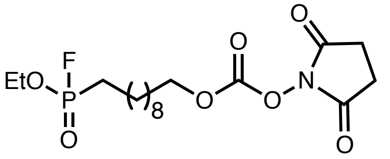
Proteomic Analysis. MS raw files were converted into MGF and processed using Proteome Discoverer version 2.2.0.388 (Thermo Scientific) by searching against the Uniprot human Database supplemented with GFP and common contaminant protein sequences and quantifying according to SPS MS3 reporter ions. Identification was based on CID spectra using SequestHT. Search criteria included: 20 ppm mass tolerance for MS spectra, 0.5 Da fragment mass tolerance for MS/MS spectra, a maximum of two allowed missed cleavages, static carbamidomethylation (+57.021 Da) of cysteine and TMTsixplex (+229.163 Da) of peptide N-terminus, dynamic modifications of methionine oxidation (+15.995 Da), N-terminal protein acetylation (+42.011 Da), asparagine or glutamine deamidation (+0.984 Da), and serine, tyrosine or tryptophan phosphorylation (+79.966 Da) and a false discovery rate of <0.01. Identified proteins and the TMT quantification are indicated in Table S1.

Statistical analysis. Two-sided Student's t tests were used for significance testing unless stated otherwise. P values less than 0.05 were considered to be significant. Graphs and error bars represent means ± SEM of independent biological experiments unless stated otherwise. The investigators were not blinded in all experiments. All statistical analysis was performed using GraphPad Prism 7.

SYNTHETIC METHODS AND COMPOUND CHARACTERIZATION

Materials and Methods: All non-aqueous reactions were carried out in oven- or flame-dried glassware under an atmosphere of nitrogen or argon. The reactions were magnetically stirred and monitored by analytical thin layer chromatography using pre-coated silica gel plates with F254 indicator from sigma-aldrich. All solvents used were HPLC grade and all other reagents were commercially purchased and used without further purification, unless stated otherwise. Biotin-PEG23-amine, biotin-PEG11-amine and biotin-PEG4-amine, used in the final step of the synthesis of the probes **1**, **2**, and **3**, were purchased from BroadPharm. NMR spectra was recorded on a Bruker UltraShield Plus 500 MHz Avance III (500 MHz ^{1}H and 125 MHz ^{13}C) spectrometer. Chemical shift values (∂) are reported in ppm relative to residual chloroform (∂ 7.26 ppm for ^{1}H; ∂ 77.23 ppm for ^{13}C). ^{1}H NMR spectra are reported as follows: ∂ (multiplicity, coupling constant, integration). High-resolution electrospray ionization (HRMS-ESI) mass spectra were obtained at the MSKCC analytical core facility on a Waters Micromass LCT Premier XE TOF LC-MS. Purity of the compounds were assayed using a Waters Acquity ultra-performance liquid chromatography (UPLC) system equipped with a SQ Detector and an ELS Detector. Gradient solvent consisted of 0.1% TFA and 5-95% acetonitrile in water over 8 min maintaining a constant flow rate of 0.30 ml/min.

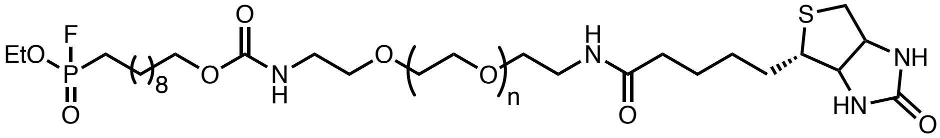
Experimental Details:



2,5-dioxopyrrolidin-1-yl (10-(ethoxyfluorophosphoryl)decyl) carbonate (4)

Compound **4** was synthesized following a previously reported literature procedure.[7]

^{1}H NMR (500 MHz, CDCl$_3$) ∂ 4.24 (t, *J* = 6.7 Hz, 2H), 4.22 – 4.14 (m, 2H), 2.77 (s, 4H), 1.86 – 1.77 (m, 2H), 1.71 – 1.64 (m, 2H), 1.63 – 1.53 (m, 2H), 1.37 – 1.30 (m, 4H), 1.30 (t, *J* = 14.2 Hz, 3H), 1.23 (bs, 8H); ^{13}C NMR (126 MHz, CDCl$_3$) ∂ 168.92, 151.64, 71.62, 63.08 (d, *J* = 7.1 Hz), 30.25 (d, *J* = 16.8 Hz), 29.27, 29.13, 29.00, 28.90, 28.35, 25.51, 25.40, 24.27 (dd, *J* = 143.0, 22.3 Hz), 21.91 (d, *J* = 5.2 Hz), 16.37 (d, *J* = 5.7 Hz); HRMS: m/z calcd. for $C_{17}H_{30}FNO_7P$ $[M+H]^+$ 410.1744, found: 410.1732.



n = 3,10, 22

FP-PEG(n)-Biotin (1 (n = 3), 2 (n = 10) and 3 (n = 22))

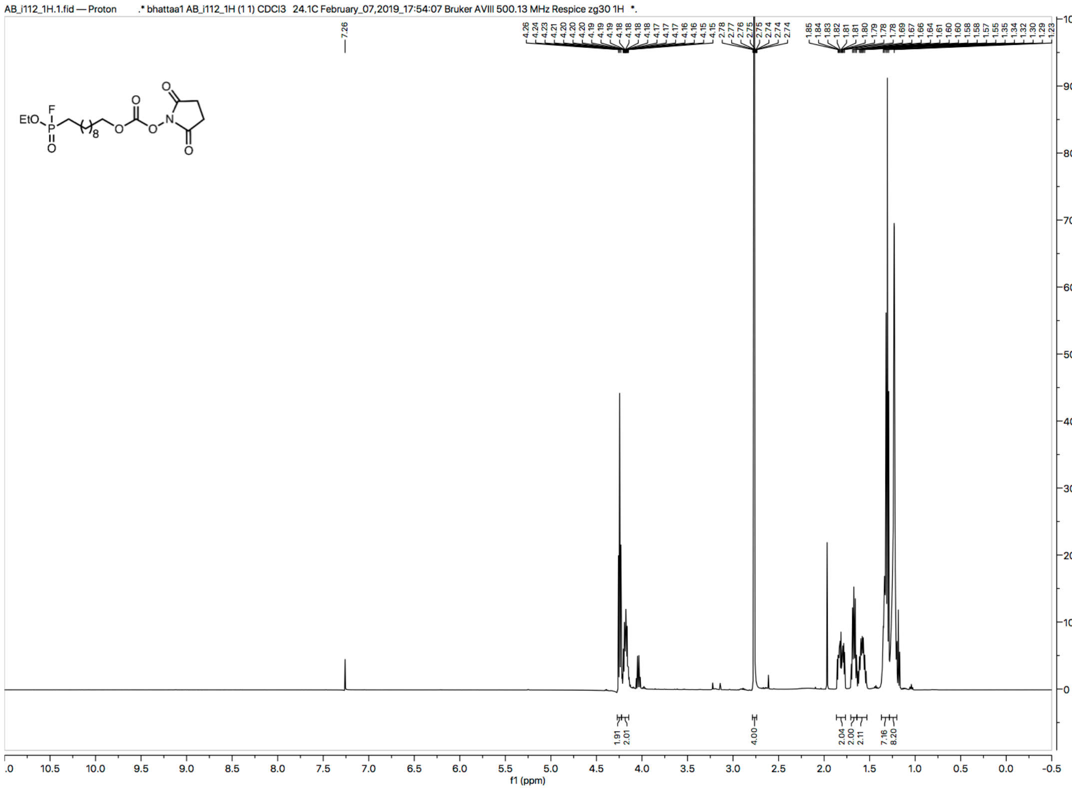
General Procedure: To a stirring solution of **4** (0.1 mmol, 1 equiv.) in MeOH (1 mL) was added the given NH$_2$-PEG(n)-biotin derivative (0.1 mmol, 1 equiv.) and allowed to react at ambient temperature until completion, as monitored by UPLC. The solution was then concentrated under reduced pressure and were used without any further purification.

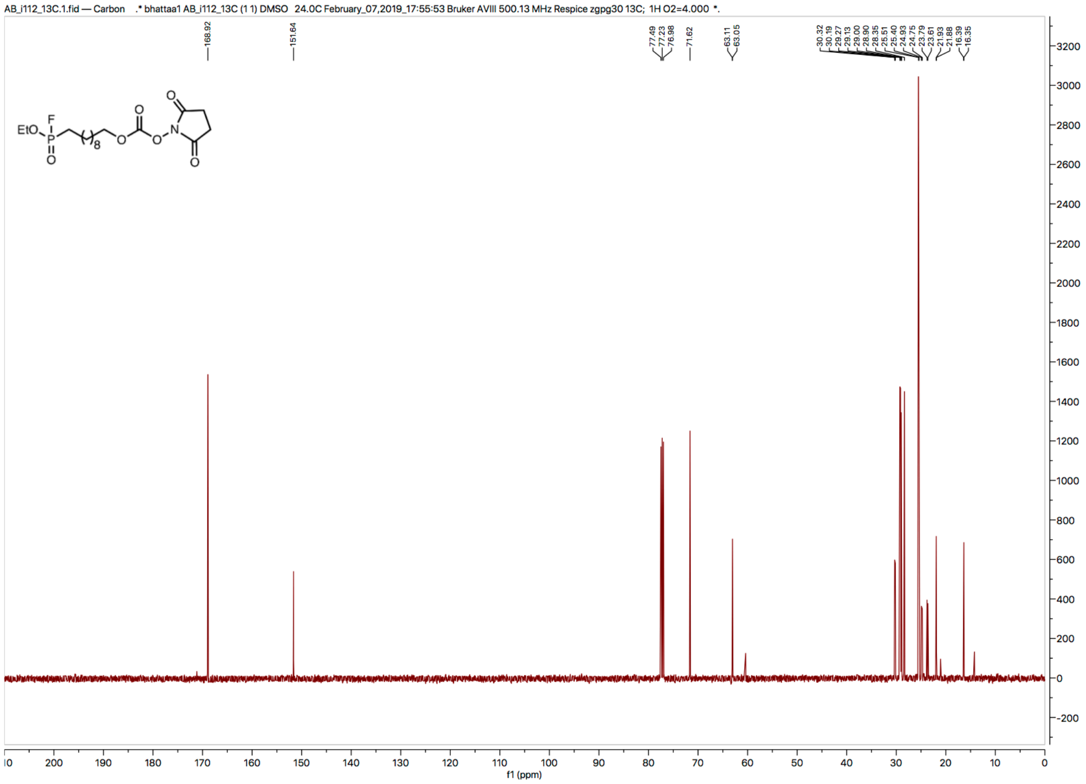
Purity of the FP-PEG(n)-biotin analogs was assessed by analytical UPLC followed by a HRMS-ESI acquisition.

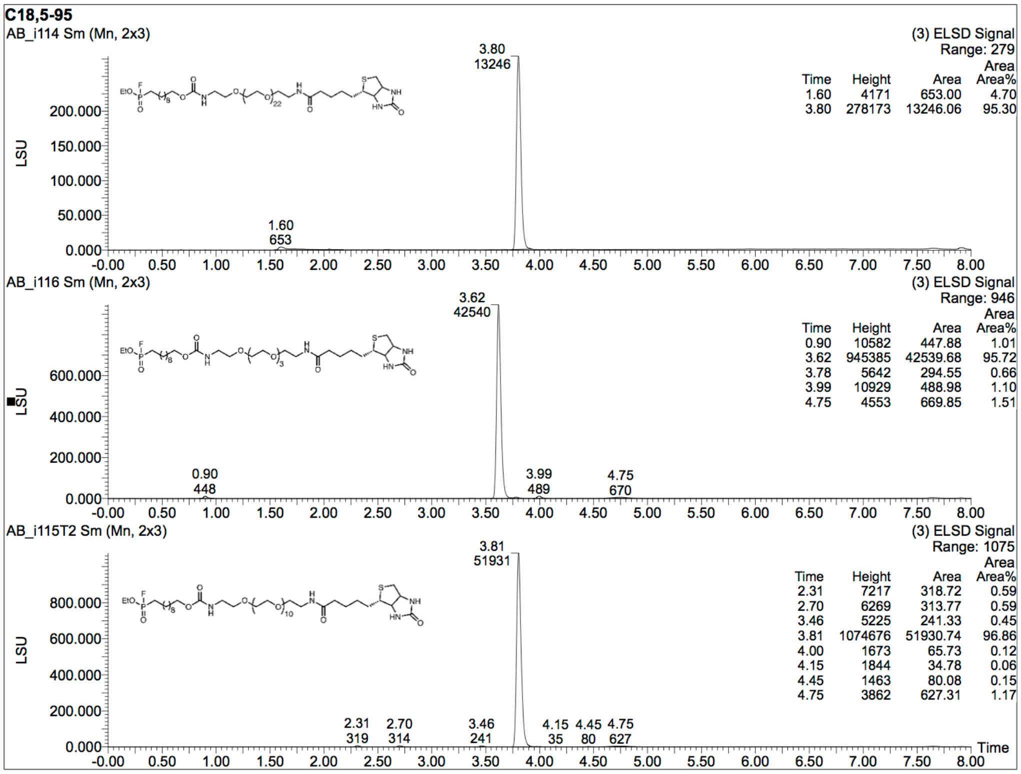
1: UPLC purity: 95.7% (t_R 3.62s); HRMS: m/z calcd for $C_{33}H_{63}N_4O_{10}FPS$ $[M+H]^+$ 757.3987, found: 757.3955.

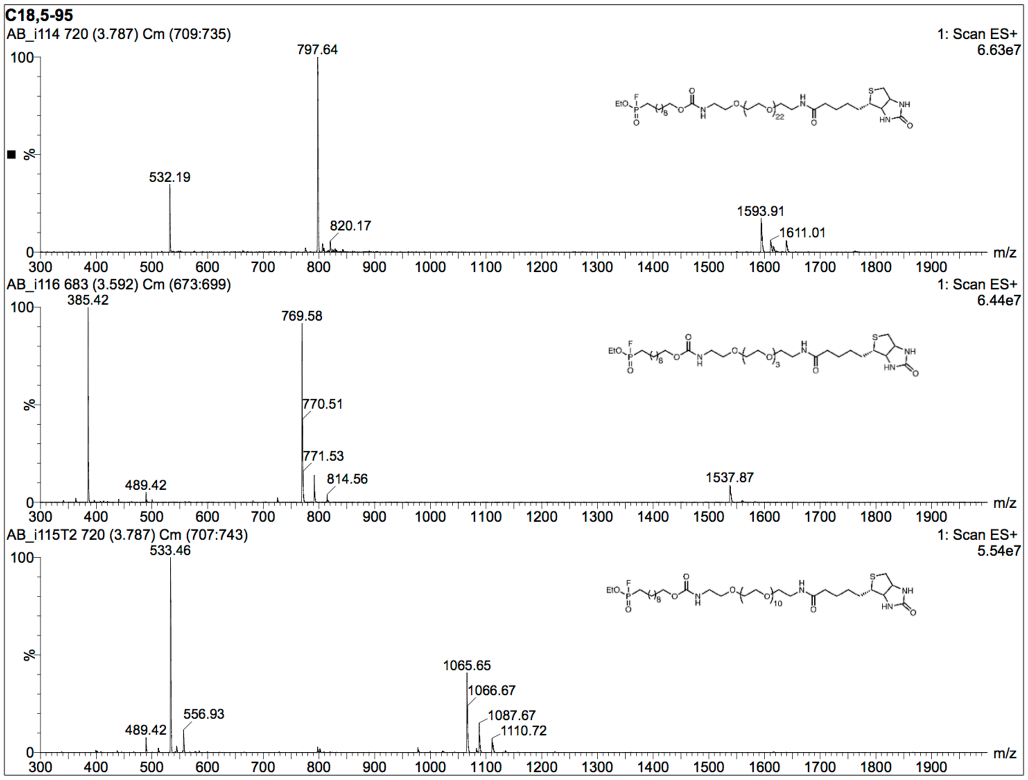
2: UPLC purity: 96.9% (t_R 3.81s); HRMS: m/z calcd for $C_{47}H_{90}N_4O_{17}FPSNa$ $[M+Na]^+$ 1087.5641, found: 1087.5629.

3: UPLC purity: 95.3% (t_R 3.80s); HRMS: m/z calcd for $C_{71}H_{138}N_4O_{29}FPSNa$ $[M+Na]^+$ 1615.8787, found: 1615.8834.


AB_i112_1H.1.fid — Proton .* bhattaa1 AB_i112_1H (1 1) CDCl3 24.1C February_07,2019_17:54:07 Bruker AVIII 500.13 MHz Respice zg30 1H *.
7.26
4.26 4.24 4.23 4.21 4.20 4.20 4.20 4.19 4.19 4.19 4.18 4.18 4.18 4.18 4.17 4.17 4.17 4.16 4.16 4.15 4.15
2.78 2.77 2.76 2.75 2.75 2.74 2.74 2.74
1.85 1.84 1.83 1.82 1.81 1.81 1.80 1.79 1.78 1.78 1.69 1.67 1.66 1.64 1.61 1.60 1.60 1.58 1.58 1.57 1.55 1.35 1.34 1.32 1.30 1.29 1.23
1.91 2.01 4.00 2.04 2.00 2.11 7.16 8.20
EtO P F O 8 O O O N O O
f1 (ppm)


AB_i112_13C.1.fid — Carbon .* bhattaa1 AB_i112_13C (1 1) DMSO 24.0C February_07,2019_17:55:53 Bruker AVIII 500.13 MHz Respice zgpg30 13C; 1H O2=4.000 *.
168.92
151.64
77.49 77.23 76.98
71.62
63.11 63.05
30.32 30.19 29.27 29.13 29.00 28.90 28.35 25.51 25.40 24.93 24.75 23.79 23.61 21.93 21.88 16.39 16.35
EtO P F O 8 O O O N O O
f1 (ppm)


C18,5-95
AB_i114 Sm (Mn, 2x3)
(3) ELSD Signal
Range: 279
Time Height Area Area%
1.60 4171 653.00 4.70
3.80 278173 13246.06 95.30
3.80
13246
1.60
653
LSU
AB_i116 Sm (Mn, 2x3)
(3) ELSD Signal
Range: 946
Time Height Area Area%
0.90 10582 447.88 1.01
3.62 945385 42539.68 95.72
3.78 5642 294.55 0.66
3.99 10929 488.98 1.10
4.75 4553 669.85 1.51
3.62
42540
0.90
448
3.99
489
4.75
670
AB_i115T2 Sm (Mn, 2x3)
(3) ELSD Signal
Range: 1075
Time Height Area Area%
2.31 7217 318.72 0.59
2.70 6269 313.77 0.59
3.46 5225 241.33 0.45
3.81 1074676 51930.74 96.86
4.00 1673 65.73 0.12
4.15 1844 34.78 0.06
4.45 1463 80.08 0.15
4.75 3862 627.31 1.17
3.81
51931
2.31
319
2.70
314
3.46
241
4.15
35
4.45
80
4.75
627
Time
EtO
F
P
O
N
H
O
22
3
10
S
NH
HN
O


C18,5-95
AB_i114 720 (3.787) Cm (709:735)
1: Scan ES+
6.63e7
797.64
532.19
820.17
1593.91
1611.01
%
m/z
AB_i116 683 (3.592) Cm (673:699)
1: Scan ES+
6.44e7
385.42
769.58
770.51
771.53
814.56
489.42
1537.87
AB_i115T2 720 (3.787) Cm (707:743)
1: Scan ES+
5.54e7
533.46
556.93
489.42
1065.65
1066.67
1087.67
1110.72
EtO
F
P
O
N
H
22
3
10
S
NH
HN

MASS SPECTROMETRY DATA TABLES

Table S1. Mass spectrometry results from FLAG immunoprecipitation and tandem mass tag labeling of HEK 293T cells transiently transfected with constructs encoding for GFP-FLAG or CARD8-FLAG and treated with either DMSO or VbP. The TMT abundance based on SPS MS3 reporter ion quantification is indicated for each condition. The rows corresponding to CARD8 and DPP9 are highlighted.

Protein Accession and Description	TMT Abundance					
	GFP DMSO (1/2)	GFP DMSO (2/2)	CARD8 DMSO (1/2)	CARD8 DMSO (2/2)	CARD8 VbP (1/2)	CARD8 VbP (2/2)
Q13813-3: Isoform 3 of Spectrin alpha chain, non-erythrocytic 1 OS=Homo sapiens GN=SPTAN1	98.3	67.2	123.5	118.4	93.2	99.4
Q9Y2G2-5: Isoform 5 of Caspase recruitment domain-containing protein 8 OS=Homo sapiens OX=9606 GN=CARD8	2.2	1.6	143.6	174.4	129	149.2
P21333: Filamin-A OS=Homo sapiens GN=FLNA PE=1 SV=4	112.2	93.3	100.8	88.1	105.5	100.1
P35579: Myosin-9 OS=Homo sapiens GN=MYH9 PE=1 SV=4	194.8	276.1	32.9	32	34.6	29.6
B2ZZ89: Spectrin beta chain OS=Homo sapiens GN=SPTBN1 PE=2 SV=1	119.8	70.4	115.8	110.5	95.6	88
H6VRG1: Keratin 1 OS=Homo sapiens GN=KRT1 PE=3 SV=1	71.3	44.4	97.2	142.7	88.4	156
Q59EJ3: Heat shock 70kDa protein 1A variant (Fragment) OS=Homo sapiens PE=2 SV=1	23.3	18.3	149.5	147	125.4	136.5
P35580-4: Isoform 4 of Myosin-10 OS=Homo sapiens GN=MYH10	265.6	256	17.3	12.7	29.1	19.2
P35527: Keratin, type I cytoskeletal 9 OS=Homo sapiens GN=KRT9 PE=1 SV=3	106.3	40.1	102	130.8	78.4	142.4
P35908: Keratin, type II cytoskeletal 2 epidermal OS=Homo sapiens GN=KRT2 PE=1 SV=2	55.4	51.9	85.1	137.7	99.6	170.3
A0A140VK53: Testicular secretory protein Li 53 OS=Homo sapiens PE=2 SV=1	125.5	77.8	97.5	97.8	108.3	93.1
P13645: Keratin, type I cytoskeletal 10 OS=Homo sapiens GN=KRT10 PE=1 SV=6	62.2	46.7	84.5	139.1	99.2	168.3
Q08378: Golgin subfamily A member 3 OS=Homo sapiens GN=GOLGA3 PE=1 SV=2	204.6	157.9	66.7	45.2	64	61.6
P78527: DNA-dependent protein kinase catalytic subunit OS=Homo sapiens GN=PRKDC PE=1 SV=3	110.2	94	90.2	95.8	115.8	94
P10809: 60 kDa heat shock protein, mitochondrial OS=Homo sapiens GN=HSPD1 PE=1 SV=2	141.5	121.7	81.1	57.8	112.9	85
P07437: Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=2	42.4	35.8	85.1	147.8	178.1	110.8
J9R021: Eukaryotic translation initiation factor 3 subunit A OS=Homo sapiens GN=eIF3a PE=2 SV=1	208.5	256.3	33.7	23.1	41.7	36.6
V9HW22: Epididymis luminal protein 33 OS=Homo sapiens GN=HEL-S-72p PE=2 SV=1	52.3	40.9	130.7	138.3	121.3	116.6
P68363: Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1	44.4	39	103.5	142.8	145.9	124.4
P63261: Actin, cytoplasmic 2 OS=Homo sapiens GN=ACTG1 PE=1 SV=1	110.6	214.5	70	58.5	77.5	68.9
P68371: Tubulin beta-4B chain OS=Homo sapiens GN=TUBB4B PE=1 SV=1	50.5	40	98	138.5	159.6	113.5
P08238: Heat shock protein HSP 90-beta OS=Homo sapiens GN=HSP90AB1 PE=1 SV=4	119.6	125.6	91.8	85.9	90.2	86.9
A0A087WVQ6: Clathrin heavy chain OS=Homo sapiens GN=CLTC PE=1 SV=1	169.8	173.7	59.3	58.9	84.7	53.6
P07900-2: Isoform 2 of Heat shock protein HSP 90-alpha OS=Homo sapiens GN=HSP90AA1	104.9	149.3	91.8	69.5	90.5	94.1

D9ZGF8: Rho-associated protein kinase OS=Homo sapiens GN=ROCK1 PE=3 SV=1	162	121.4	86	63	90.5	76.9
P38646: Stress-70 protein, mitochondrial OS=Homo sapiens GN=HSPA9 PE=1 SV=2	63.3	65.3	124.9	126	105.9	114.6
B2RDD7: Protein arginine N-methyltransferase 5 OS=Homo sapiens PE=2 SV=1	82.4	134.9	98.8	92.3	98.3	93.3
P17987: T-complex protein 1 subunit alpha OS=Homo sapiens GN=TCP1 PE=1 SV=1	62.5	61.5	117.2	100.9	130.5	127.4
Q6P2Q9: Pre-mRNA-processing-splicing factor 8 OS=Homo sapiens GN=PRPF8 PE=1 SV=2	122.6	81.2	105.6	93.8	100.9	95.8
Q08211: ATP-dependent RNA helicase A OS=Homo sapiens GN=DHX9 PE=1 SV=4	176.4	144.2	67.3	48.3	96.5	67.3
Q4LE58: eIF4G1 variant protein (Fragment) OS=Homo sapiens GN=EIF4G1 variant protein PE=2 SV=1	232.9	165.6	53.6	38.8	63.1	46
P49327: Fatty acid synthase OS=Homo sapiens GN=FASN PE=1 SV=3	170	146.2	69.1	51.8	93.9	68.9
V9HW37: Epididymis secretory protein Li 69 OS=Homo sapiens GN=HEL-S-69 PE=1 SV=1	114.5	105.8	95.7	69.2	112.7	102.1
Q13885: Tubulin beta-2A chain OS=Homo sapiens GN=TUBB2A PE=1 SV=1	56.2	51.1	99.1	141.7	152.4	99.5
Q9BVA1: Tubulin beta-2B chain OS=Homo sapiens GN=TUBB2B PE=1 SV=1	63.2	56.5	91.3	143.8	158	87.3
P27708: CAD protein OS=Homo sapiens GN=CAD PE=1 SV=3	34.6	33.8	114.8	145.9	158.8	112.2
A0A024RDS1: Heat shock 105kDa/110kDa protein 1, isoform CRA_c OS=Homo sapiens GN=HSPH1 PE=3 SV=1	43	35.4	144.5	121.8	132.7	122.7
Q15393: Splicing factor 3B subunit 3 OS=Homo sapiens GN=SF3B3 PE=1 SV=4	121.6	96.9	109.6	86.6	96.9	88.4
O75643: U5 small nuclear ribonucleoprotein 200 kDa helicase OS=Homo sapiens GN=SNRNP200 PE=1 SV=2	127.5	105.2	94.2	76.8	109	87.2
V9HWB4: Epididymis secretory sperm binding protein Li 89n OS=Homo sapiens GN=HEL-S-89n PE=2 SV=1	72.7	131.1	101.9	100.5	93.5	100.5
V9HWB8: Pyruvate kinase OS=Homo sapiens GN=HEL-S-30 PE=1 SV=1	239.3	198.2	34.6	19	62	46.9
P17066: Heat shock 70 kDa protein 6 OS=Homo sapiens GN=HSPA6 PE=1 SV=2	1.6	1.7	145.5	154.5	152.7	144
P07814: Bifunctional glutamate/proline--tRNA ligase OS=Homo sapiens GN=EPRS PE=1 SV=5	143.9	108.9	91.6	57.4	115	83.2
E7EW20: Unconventional myosin-VI OS=Homo sapiens GN=MYO6 PE=1 SV=2	153.4	158.2	73.9	54.6	97.4	62.5
A0A024RAM4: Microtubule-associated protein 1B, isoform CRA_b OS=Homo sapiens GN=MAP1B PE=4 SV=1	67.8	67	128.5	115.5	101.7	119.6
P13639: Elongation factor 2 OS=Homo sapiens GN=EEF2 PE=1 SV=4	144.8	138.6	80.3	73.4	90.2	72.7
Q59H77: T-complex protein 1 subunit gamma (Fragment) OS=Homo sapiens PE=2 SV=1	78.8	66.6	110.5	86.4	144.2	113.4
P55884-2: Isoform 2 of Eukaryotic translation initiation factor 3 subunit B OS=Homo sapiens GN=EIF3B	251.3	195.6	42.3	28.2	47	35.5
O75533: Splicing factor 3B subunit 1 OS=Homo sapiens GN=SF3B1 PE=1 SV=3	162.7	119.1	89.4	59.7	92.9	76.2
P50990: T-complex protein 1 subunit theta OS=Homo sapiens GN=CCT8 PE=1 SV=4	86.7	72.4	126.1	93.8	107.6	113.4
P25205-2: Isoform 2 of DNA replication licensing factor MCM3 OS=Homo sapiens GN=MCM3	97.1	74.8	101.6	98.3	117.4	110.8
Q4LE36: ACLY variant protein (Fragment) OS=Homo sapiens GN=ACLY variant protein PE=2 SV=1	142.7	131.4	79.5	81.2	91	74.3
Q00839-2: Isoform Short of Heterogeneous nuclear ribonucleoprotein U OS=Homo sapiens GN=HNRNPU	227.7	156.7	53.5	28.8	73.7	59.5
P78371: T-complex protein 1 subunit beta OS=Homo sapiens GN=CCT2 PE=1 SV=4	86.2	72.5	120.9	91.7	107.2	121.5
Q53HV2: Chaperonin containing TCP1, subunit 7 (Eta) variant (Fragment) OS=Homo sapiens PE=2 SV=1	69	83.5	120	87.8	123.4	116.4
Q00839: Heterogeneous nuclear ribonucleoprotein U OS=Homo sapiens GN=HNRNPU PE=1 SV=6	166.3	162.1	71.7	48.7	92.6	58.6
E9KL35: Epididymis tissue sperm binding protein Li 3a OS=Homo sapiens PE=1 SV=1	215.1	206.3	45	29.8	62.6	41.1
V9HW80: Epididymis luminal protein 220 OS=Homo sapiens GN=HEL-S-70 PE=2 SV=1	146.9	134.3	78.8	43.7	95.4	100.9
Q86TI2-2: Isoform 2 of Dipeptidyl peptidase 9 OS=Homo sapiens GN=DPP9	4.1	5.8	153.5	155.2	131.2	150.2
P31689: DnaJ homolog subfamily A member 1 OS=Homo sapiens GN=DNAJA1 PE=1 SV=2	20.3	15.9	124.1	148.9	142.6	148.1
P19338: Nucleolin OS=Homo sapiens GN=NCL PE=1 SV=3	86.6	152.7	106.3	88.3	73.1	93.1

Q9P2R3-4: Isoform 4 of Rabankyrin-5 OS=Homo sapiens GN=ANKFY1	116	93.3	104.9	95.5	93.6	96.7
V9HWE1: Epididymis luminal protein 113 OS=Homo sapiens GN=HEL113 PE=2 SV=1	112.8	78.2	116.6	91.9	112.3	88.2
P50991: T-complex protein 1 subunit delta OS=Homo sapiens GN=CCT4 PE=1 SV=4	87.2	80.5	89.1	71.9	163.6	107.7
J3KTA4: Probable ATP-dependent RNA helicase DDX5 OS=Homo sapiens GN=DDX5 PE=1 SV=1	161.9	154.9	73.7	58.5	85.7	65.4
P52272: Heterogeneous nuclear ribonucleoprotein M OS=Homo sapiens GN=HNRNPM PE=1 SV=3	133	130.8	93.1	72.3	95.8	75
O43143: Pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15 OS=Homo sapiens GN=DHX15 PE=1 SV=2	135.3	102.2	94.1	80.4	104.5	83.5
Q15029: 116 kDa U5 small nuclear ribonucleoprotein component OS=Homo sapiens GN=EFTUD2 PE=1 SV=1	107.8	77.2	109.4	103.7	111.8	90
Q6NVC0: SLC25A5 protein (Fragment) OS=Homo sapiens GN=SLC25A5 PE=2 SV=1	27.3	29.9	132.7	132	149.2	128.9
A0A024R1N4: X-ray repair complementing defective repair in Chinese hamster cells 6 (Ku autoantigen, 70kDa), isoform CRA_a OS=Homo sapiens GN=XRCC6 PE=4 SV=1	176.3	152	65.9	51.5	85.5	68.7
G8JLB6: Heterogeneous nuclear ribonucleoprotein H OS=Homo sapiens GN=HNRNPH1 PE=1 SV=1	141.6	106.7	86.8	73.7	114.9	76.3
P09874: Poly [ADP-ribose] polymerase 1 OS=Homo sapiens GN=PARP1 PE=1 SV=4	212.5	189.7	55.1	29.6	63.6	49.5
Q59FF0: EBNA-2 co-activator variant (Fragment) OS=Homo sapiens PE=2 SV=1	184.4	145.1	84.9	46.3	71.3	68
Q13435: Splicing factor 3B subunit 2 OS=Homo sapiens GN=SF3B2 PE=1 SV=2	131.7	107.5	99.9	83.3	88.6	89.1
Q59G75: Isoleucyl-tRNA synthetase, cytoplasmic variant (Fragment) OS=Homo sapiens PE=2 SV=1	146.3	120.2	86.7	68	107.3	71.5
B2R9K8: cDNA, FLJ94440, highly similar to Homo sapiens chaperonin containing TCP1, subunit 6A (zeta 1)(CCT6A), mRNA OS=Homo sapiens PE=2 SV=1	84.7	84.9	108.6	80.2	116.4	125.1
B2R8Z8: cDNA, FLJ94136, highly similar to Homo sapiens synaptotagmin binding, cytoplasmic RNA interacting protein (SYNCRIP), mRNA OS=Homo sapiens PE=2 SV=1	156.9	127.7	88.2	58.8	92.4	76
Q59F66: DEAD box polypeptide 17 isoform p82 variant (Fragment) OS=Homo sapiens PE=2 SV=1	149.2	101.3	88.2	90.9	91.8	78.7
Q99460: 26S proteasome non-ATPase regulatory subunit 1 OS=Homo sapiens GN=PSMD1 PE=1 SV=2	130	103.1	62.6	131.7	109.7	63
P13647: Keratin, type II cytoskeletal 5 OS=Homo sapiens GN=KRT5 PE=1 SV=3	97.8	42.9	77.8	136.6	89.5	155.5
P11940: Polyadenylate-binding protein 1 OS=Homo sapiens GN=PABPC1 PE=1 SV=2	136.7	104.3	106.7	73.9	95.9	82.5
P05023: Sodium/potassium-transporting ATPase subunit alpha-1 OS=Homo sapiens GN=ATP1A1 PE=1 SV=1	164	150.5	61.8	70.4	83.9	69.4
P34932: Heat shock 70 kDa protein 4 OS=Homo sapiens GN=HSPA4 PE=1 SV=4	102.5	98.5	108.8	78.7	120.4	91.1
B2RCJ6: cDNA, FLJ96114, highly similar to Homo sapiens bromodomain and WD repeat domain containing 2 (BRWD2), mRNA OS=Homo sapiens PE=2 SV=1	29	26.9	124.8	140	154.5	124.8
B5BUB1: RuvB-like helicase (Fragment) OS=Homo sapiens GN=RUVBL1 PE=2 SV=1	71.8	59.9	106	107.1	139.7	115.5
O15371: Eukaryotic translation initiation factor 3 subunit D OS=Homo sapiens GN=EIF3D PE=1 SV=1	183.1	249.3	45.2	30	53.6	38.9
F4ZW66: NF110b OS=Homo sapiens PE=2 SV=1	180.7	128.8	74	52.9	98	65.6
B4E2A6: cDNA FLJ55508, highly similar to Sad1/unc-84-like protein 2 OS=Homo sapiens PE=2 SV=1	194.1	193.2	58.9	40.1	65.5	48.2
P49411: Elongation factor Tu, mitochondrial OS=Homo sapiens GN=TUFM PE=1 SV=2	97.9	119.9	90.1	81.4	116.3	94.4
V9HW26: ATP synthase subunit alpha OS=Homo sapiens GN=HEL-S-123m PE=2 SV=1	86.5	94.6	96.5	84.4	140.4	97.7
B2R853: cDNA, FLJ93744, highly similar to Homo sapiens keratin 6E (KRT6E), mRNA OS=Homo sapiens PE=2 SV=1	76.5	29	128	168.1	49.4	149
Q6P3W7: SCY1-like protein 2 OS=Homo sapiens GN=SCYL2 PE=1 SV=1	269.8	263.5	16.1	4	34.8	11.8
A8K3K1: cDNA FLJ78096, highly similar to Homo sapiens actin, alpha, cardiac muscle (ACTC), mRNA OS=Homo sapiens PE=2 SV=1	123.4	232.6	59.8	46.9	74.7	62.6
B0QY89: Eukaryotic translation initiation factor 3 subunit L OS=Homo sapiens GN=EIF3L PE=1 SV=1	235.8	236.8	32	20.6	43.8	31
Q16643-3: Isoform 3 of Drebrin OS=Homo sapiens GN=DBN1	139.1	237.1	61.4	53.7	53.9	54.8
Q59EI9: ADP,ATP carrier protein, liver isoform T2 variant (Fragment) OS=Homo sapiens PE=2 SV=1	41.9	28.4	123.2	112.3	161.4	132.9

P06733: Alpha-enolase OS=Homo sapiens GN=ENO1 PE=1 SV=2	240.1	206.5	35.9	20.9	58.6	38.1
A0A024RBH2: Cytoskeleton-associated protein 4, isoform CRA_c OS=Homo sapiens GN=CKAP4 PE=4 SV=1	95.7	67.8	111	116	121.7	87.8
P60228: Eukaryotic translation initiation factor 3 subunit E OS=Homo sapiens GN=EIF3E PE=1 SV=1	222.7	218.3	35.8	33.2	44.4	45.7
P23396: 40S ribosomal protein S3 OS=Homo sapiens GN=RPS3 PE=1 SV=2	74.7	98.5	116.3	99.7	97.3	113.5
Q9NZI8: Insulin-like growth factor 2 mRNA-binding protein 1 OS=Homo sapiens GN=IGF2BP1 PE=1 SV=2	165.8	125.6	88.3	65.2	92.9	62.2
P02533: Keratin, type I cytoskeletal 14 OS=Homo sapiens GN=KRT14 PE=1 SV=4	112.6	34.9	81.5	129.9	76.8	164.3
A6NHR9: Structural maintenance of chromosomes flexible hinge domain-containing protein 1 OS=Homo sapiens GN=SMCHD1 PE=1 SV=2	217.8	152.6	55.2	48.8	76.7	49
A0A0S2Z3H3: Solute carrier family 25 member 4 isoform 1 (Fragment) OS=Homo sapiens GN=SLC25A4 PE=2 SV=1	43.2	29.6	118.7	123	159.6	125.9
P04075-2: Isoform 2 of Fructose-bisphosphate aldolase A OS=Homo sapiens GN=ALDOA	110	252.3	51.4	47.7	74.6	63.9
Q9Y230: RuvB-like 2 OS=Homo sapiens GN=RUVBL2 PE=1 SV=3	68	54.1	115.8	113	142.4	106.6
Q9NVI7-2: Isoform 2 of ATPase family AAA domain-containing protein 3A OS=Homo sapiens GN=ATAD3A	72.8	55.9	99.5	88.7	185.3	97.7
Q9BQA1: Methylosome protein 50 OS=Homo sapiens GN=WDR77 PE=1 SV=1	103.5	117.5	104.9	110.7	91.6	71.8
P14866: Heterogeneous nuclear ribonucleoprotein L OS=Homo sapiens GN=HNRNPL PE=1 SV=2	112	65.5	121.4	92.1	122.4	86.7
B3KS98: Eukaryotic translation initiation factor 3 subunit H OS=Homo sapiens GN=EIF3S3 PE=1 SV=1	174.7	261	35.7	33.8	49	45.7
Q9BQG0-2: Isoform 2 of Myb-binding protein 1A OS=Homo sapiens GN=MYBBP1A	180.5	120	71.5	66.5	92.7	68.9
O14654: Insulin receptor substrate 4 OS=Homo sapiens GN=IRS4 PE=1 SV=1	44.4	22.5	143.7	215.4	59.9	114.1
B2RBR9: cDNA, FLJ95650, highly similar to Homo sapiens karyopherin (importin) beta 1 (KPNB1), mRNA OS=Homo sapiens PE=2 SV=1	205.2	150.5	61.7	34.6	111.8	36.2
P62258: 14-3-3 protein epsilon OS=Homo sapiens GN=YWHAE PE=1 SV=1	145.5	158.3	83.5	66.6	65.7	80.5
O43390: Heterogeneous nuclear ribonucleoprotein R OS=Homo sapiens GN=HNRNPR PE=1 SV=1	120.9	83.1	99.4	109.6	102.1	85
A0A0A0MR66: RNA binding motif protein 10, isoform CRA_d OS=Homo sapiens GN=RBM10 PE=1 SV=1	168.8	131.2	74.6	70.2	79.1	76.1
P22626: Heterogeneous nuclear ribonucleoproteins A2/B1 OS=Homo sapiens GN=HNRNPA2B1 PE=1 SV=2	112.6	159.6	87.8	62.9	99.1	77.9
O43175: D-3-phosphoglycerate dehydrogenase OS=Homo sapiens GN=PHGDH PE=1 SV=4	125.1	140.3	80.5	75.4	89.2	89.5
P15880: 40S ribosomal protein S2 OS=Homo sapiens GN=RPS2 PE=1 SV=2	171.3	138.7	77.4	62.1	83.5	67.1
A8K521: DNA helicase OS=Homo sapiens PE=2 SV=1	97.8	72.9	90.3	98.8	134.7	105.4
P25789: Proteasome subunit alpha type-4 OS=Homo sapiens GN=PSMA4 PE=1 SV=1	139.2	184	69.7	48.5	92.6	66
P26641-2: Isoform 2 of Elongation factor 1-gamma OS=Homo sapiens GN=EEF1G	118.7	115.2	101.2	70.7	96	98.2
A0A0U1RRM4: Polypyrimidine tract-binding protein 1 OS=Homo sapiens GN=PTBP1 PE=1 SV=1	163.9	154.7	66.4	46.9	105.8	62.3
P61978-2: Isoform 2 of Heterogeneous nuclear ribonucleoprotein K OS=Homo sapiens GN=HNRNPK	186.7	125.4	74.8	37.7	99.5	76
A8K088: cDNA FLJ78614, highly similar to Homo sapiens eukaryotic translation initiation factor 4A, isoform 1 (EIF4A1), mRNA OS=Homo sapiens PE=2 SV=1	165.7	187.1	62.4	54	73.2	57.5
V9HWC7: Epididymis secretory sperm binding protein Li 128m OS=Homo sapiens GN=HEL-S-128m PE=2 SV=1	127.2	98.5	93.7	62.4	113.7	104.5
B5ME19: Eukaryotic translation initiation factor 3 subunit C-like protein OS=Homo sapiens GN=EIF3CL PE=3 SV=1	192.4	265.3	38.2	27.3	36.9	39.9
A8K9C4: Elongation factor 1-alpha OS=Homo sapiens PE=2 SV=1	102.7	105.2	91.2	81.1	128.3	91.5
Q7L2H7: Eukaryotic translation initiation factor 3 subunit M OS=Homo sapiens GN=EIF3M PE=1 SV=1	249	196.7	37.8	29.3	53	34.1
Q9NR30: Nucleolar RNA helicase 2 OS=Homo sapiens GN=DDX21 PE=1 SV=5	102.9	78.5	107.4	94.7	119.6	97
A8K0G3: AP complex subunit beta OS=Homo sapiens PE=2 SV=1	182.6	145.1	57.9	50.9	91.3	72.1

Q9BRS2: Serine/threonine-protein kinase RIO1 OS=Homo sapiens GN=RIOK1 PE=1 SV=2	228.9	196	35.3	31.3	67.9	40.6
P61978-3: Isoform 3 of Heterogeneous nuclear ribonucleoprotein K OS=Homo sapiens GN=HNRNPK	91.3	126.4	103.7	65.4	106.3	106.9
P04406: Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens GN=GAPDH PE=1 SV=3	134.5	190.2	64.3	59.1	82.8	69.2
Q92499: ATP-dependent RNA helicase DDX1 OS=Homo sapiens GN=DDX1 PE=1 SV=2	165.3	138.4	67.6	51.3	100.1	77.3
A0A0S2Z491: Nucleophosmin isoform 2 (Fragment) OS=Homo sapiens GN=NPM1 PE=2 SV=1	166	141.1	81.8	67.6	65.1	78.5
Q9Y4E8: Ubiquitin carboxyl-terminal hydrolase 15 OS=Homo sapiens GN=USP15 PE=1 SV=3	113.1	134.3	87.2	58	97.8	109.6
P62701: 40S ribosomal protein S4, X isoform OS=Homo sapiens GN=RPS4X PE=1 SV=2	126.4	145.7	79.7	69	110	69.1
V9HW31: ATP synthase subunit beta OS=Homo sapiens GN=HEL-S-271 PE=1 SV=1	180.6	195.4	60.1	48.4	68.9	46.5
O43707: Alpha-actinin-4 OS=Homo sapiens GN=ACTN4 PE=1 SV=2	251.5	156.6	55.7	38.4	53.4	44.3
A0A0D9SF53: ATP-dependent RNA helicase DDX3X OS=Homo sapiens GN=DDX3X PE=1 SV=1	124.9	89.9	96.8	97.4	107.4	83.6
Q9Y2H1: Serine/threonine-protein kinase 38-like OS=Homo sapiens GN=STK38L PE=1 SV=3	170.7	171.9	52.4	46.5	94.5	63.9
P54136: Arginine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=RARS PE=1 SV=2	117.2	104.4	99.6	90.1	96.6	92
Q59GY2: Ribosomal protein L4 variant (Fragment) OS=Homo sapiens PE=2 SV=1	125.7	114.2	99.9	82.2	99.3	78.7
E5KNY5: Leucine-rich PPR-motif containing OS=Homo sapiens GN=LRPPRC PE=4 SV=1	153.5	104.7	85.2	55.7	97.2	103.8
P14625: Endoplasmin OS=Homo sapiens GN=HSP90B1 PE=1 SV=1	224.8	196.7	36.7	36.4	62.9	42.5
A0A140VJW5: Testicular tissue protein Li 192 OS=Homo sapiens PE=2 SV=1	105.6	90.3	99	114.2	102.5	88.5
P13797: Plastin-3 OS=Homo sapiens GN=PLS3 PE=1 SV=4	142.2	123.8	81.3	91.9	82.2	78.6
Q16531: DNA damage-binding protein 1 OS=Homo sapiens GN=DDB1 PE=1 SV=1	116.5	89.9	81.6	108.6	100.3	103.1
Q13310-3: Isoform 3 of Polyadenylate-binding protein 4 OS=Homo sapiens GN=PABPC4	150.3	110.7	103.9	62.5	93.7	78.8
A8MXP9: Matrin-3 OS=Homo sapiens GN=MATR3 PE=1 SV=1	87.3	52.9	132.1	98	131.1	98.6
A0A140VK41: Testicular secretory protein Li 41 OS=Homo sapiens PE=2 SV=1	174.2	166.6	61.8	53.1	85.1	59.2
A0A024R1A3: Testicular secretory protein Li 63 OS=Homo sapiens GN=UBE1 PE=2 SV=1	258	222.6			74.3	45.1
Q59EG8: Proteasome 26S non-ATPase subunit 2 variant (Fragment) OS=Homo sapiens PE=2 SV=1	143.6	113	83.3	70.9	103.5	85.7
P13010: X-ray repair cross-complementing protein 5 OS=Homo sapiens GN=XRCC5 PE=1 SV=3	168.3	145.6	60.3	60.9	90.9	74.1
Q59FT7: Mitogen-activated protein kinase kinase kinase 7 interacting protein 1 isoform alpha variant (Fragment) OS=Homo sapiens PE=2 SV=1	168.5	134.3	76.1	51.3	85.9	84
B7ZM99: MTHFD1L protein OS=Homo sapiens GN=MTHFD1L PE=1 SV=1	186.5	141.4	60.2	44.6	96.7	70.6
O95831: Apoptosis-inducing factor 1, mitochondrial OS=Homo sapiens GN=AIFM1 PE=1 SV=1	141.2	102.9	88.4	76	104.9	86.6
B2R8R5: cDNA, FLJ94025, highly similar to Homo sapiens tripartite motif-containing 28 (TRIM28), mRNA OS=Homo sapiens PE=2 SV=1	119.6	99.3	101.7	88.2	105	86.3
Q53HU7: Eukaryotic translation initiation factor 3 subunit I (Fragment) OS=Homo sapiens PE=2 SV=1	154	223	67.2	44.9	57.8	53.2
Q09161: Nuclear cap-binding protein subunit 1 OS=Homo sapiens GN=NCBP1 PE=1 SV=1	152.4	119.5	60.7	66.7	123.5	77.2
A0A0C4DG89: Probable ATP-dependent RNA helicase DDX46 OS=Homo sapiens GN=DDX46 PE=1 SV=1	203.1	163.3	61.5	33.8	67.9	70.5
Q15057: Arf-GAP with coiled-coil, ANK repeat and PH domain-containing protein 2 OS=Homo sapiens GN=ACAP2 PE=1 SV=3	139.7	104.9	106.4	74.7	90.9	83.4
B4DRM3: cDNA FLJ54492, highly similar to Eukaryotic translation initiation factor 4B OS=Homo sapiens PE=2 SV=1	61.9	103.3	118.2	122.2	68	126.4
P60891: Ribose-phosphate pyrophosphokinase 1 OS=Homo sapiens GN=PRPS1 PE=1 SV=2	162.5	135.3	76	66.8	87.4	72
O95218-2: Isoform 2 of Zinc finger Ran-binding domain-containing protein 2 OS=Homo sapiens GN=ZRANB2	159.5	122.9	86.1	56.5	81.9	93.2

A0A140VJX1: Testicular tissue protein Li 198 OS=Homo sapiens PE=2 SV=1	228.7	166.8	45.7	21.3	94.2	43.3
Q6PKG0: La-related protein 1 OS=Homo sapiens GN=LARP1 PE=1 SV=2	208.2	183.8	52.5	49.3	83.3	23
A0A024RAZ7: Heterogeneous nuclear ribonucleoprotein A1, isoform CRA_b OS=Homo sapiens GN=HNRPA1 PE=4 SV=1	182.9	125.5	63	60	113.1	55.5
A8K984: Structural maintenance of chromosomes protein OS=Homo sapiens PE=2 SV=1	76.7	53.1	111.3	143.9	95.2	119.8
A0A024R6S1: DnaJ (Hsp40) homolog, subfamily A, member 2, isoform CRA_a OS=Homo sapiens GN=DNAJA2 PE=3 SV=1	25.7	22.5	135.8	147.3	115.3	153.4
Q5JR94: 40S ribosomal protein S8 OS=Homo sapiens GN=RPS8 PE=2 SV=1	214.2	172.8	57.9	37.1	65.4	52.5
Q9Y3F4-2: Isoform 2 of Serine-threonine kinase receptor-associated protein OS=Homo sapiens GN=STRAP	160.9	132.6	82.2	70.2	88.8	65.3
O60825: 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase 2 OS=Homo sapiens GN=PFKFB2 PE=1 SV=2	145	123	86.5	65	103	77.5
A0A024RD93: Phosphoribosylaminoimidazole carboxylase, phosphoribosylaminoimidazole succinocarboxamide synthetase, isoform CRA_c OS=Homo sapiens GN=PAICS PE=3 SV=1	177	127.1	89.6	48.4	82	75.9
A0A024RD18: Serine/threonine kinase 38, isoform CRA_a OS=Homo sapiens GN=STK38 PE=3 SV=1	167	160.5	75.3	46.9	74.8	75.4
Q99729-3: Isoform 3 of Heterogeneous nuclear ribonucleoprotein A/B OS=Homo sapiens GN=HNRNPAB	169.8	130.9	84.4	74.6	75.6	64.7
A2RUM7: Ribosomal protein L5 OS=Homo sapiens GN=RPL5 PE=2 SV=1	133	140	94.3	73.7	85.2	73.9
A0A0C4DG17: 40S ribosomal protein SA OS=Homo sapiens GN=RPSA PE=1 SV=1	276.4	200.1	24.9	29.1	45.2	24.4
P27348: 14-3-3 protein theta OS=Homo sapiens GN=YWHAQ PE=1 SV=1	179.6	141.4	74	62.7	82	60.4
P12268: Inosine-5'-monophosphate dehydrogenase 2 OS=Homo sapiens GN=IMPDH2 PE=1 SV=2	217.5	182.5	60.6	24.8	64.3	50.2
D3DQ70: SERPINE1 mRNA binding protein 1, isoform CRA_d OS=Homo sapiens GN=SERBP1 PE=4 SV=1	173.3	158.6	64.4	68.4	59.4	75.9
A0A140VK70: Testis secretory sperm-binding protein Li 197a OS=Homo sapiens PE=2 SV=1	146.5	118.3	89.5	55.5	105.8	84.4
O43242: 26S proteasome non-ATPase regulatory subunit 3 OS=Homo sapiens GN=PSMD3 PE=1 SV=2	148.2	118.1	75	64.5	98.3	96
P31153: S-adenosylmethionine synthase isoform type-2 OS=Homo sapiens GN=MAT2A PE=1 SV=1	105.8	76.1	93.4	92.2	106.9	125.5
A0A140VJY2: Testicular tissue protein Li 209 OS=Homo sapiens PE=2 SV=1	145.1	184.1	31.1	112.5	91.1	36.1
P23458: Tyrosine-protein kinase JAK1 OS=Homo sapiens GN=JAK1 PE=1 SV=2	198	136.8	54.6	71.5	86.7	52.4
Q05639: Elongation factor 1-alpha 2 OS=Homo sapiens GN=EEF1A2 PE=1 SV=1	125.7	107.5	110.3	45.9	126.6	84
P61247: 40S ribosomal protein S3a OS=Homo sapiens GN=RPS3A PE=1 SV=2	164.1	170.7	71.8	55.8	74	63.6
P15924: Desmoplakin OS=Homo sapiens GN=DSP PE=1 SV=3	113.8	55.1	98.4	101.3	79.7	151.7
O43719: HIV Tat-specific factor 1 OS=Homo sapiens GN=HTATSF1 PE=1 SV=1	166.6	120.7	77.2	57	79.3	99.3
P27824-2: Isoform 2 of Calnexin OS=Homo sapiens GN=CANX	212.2	156.5	57.1	36	79.4	58.7
V9HW63: Epididymis secretory sperm binding protein Li 97n OS=Homo sapiens GN=HEL-S-97n PE=2 SV=1	40.1	41.2	137.8	145.7	108.3	126.8
Q13428-4: Isoform 4 of Treacle protein OS=Homo sapiens GN=TCOF1	157.4	124.8	80.7	78.2	76.5	82.4
Q92945: Far upstream element-binding protein 2 OS=Homo sapiens GN=KHSRP PE=1 SV=4	168.5	148.5	60.7	80.5	71.3	70.5
B3KTJ9: cDNA FLJ38393 fis, clone FEBRA2007212 OS=Homo sapiens PE=2 SV=1	83.4	52.6	116.5	103.1	146.9	97.4
Q15459: Splicing factor 3A subunit 1 OS=Homo sapiens GN=SF3A1 PE=1 SV=1	201.1	175.9	45.7	49.1	74	54.1
Q92900: Regulator of nonsense transcripts 1 OS=Homo sapiens GN=UPF1 PE=1 SV=2	220.6	93.7	67.8	35.1	106.8	76
P62195: 26S proteasome regulatory subunit 8 OS=Homo sapiens GN=PSMC5 PE=1 SV=1	144.5	125.7	94.4	51.7	100.7	82.9
A0A024QZN9: Voltage-dependent anion channel 2, isoform CRA_a OS=Homo sapiens GN=VDAC2 PE=4 SV=1	146.7	92.9	91.3	85.9	109.4	73.8
Q9UHB6-4: Isoform 4 of LIM domain and actin-binding protein 1 OS=Homo sapiens GN=LIMA1	194.5	137.3	74.7	52.6	74	66.9
E9KL44: Epididymis tissue sperm binding protein Li 14m OS=Homo sapiens PE=2 SV=1	125.4	96.9	77.2	92.4	124.6	83.4

P60174: Triosephosphate isomerase OS=Homo sapiens GN=TPI1 PE=1 SV=3	273	204.3	30.2	14.8	37.9	39.9
P17980: 26S proteasome regulatory subunit 6A OS=Homo sapiens GN=PSMC3 PE=1 SV=3	159.9	121.6	82.4	57.3	107.8	70.9
Q06830: Peroxiredoxin-1 OS=Homo sapiens GN=PRDX1 PE=1 SV=1	26	45.7	141.4	165.1	95.7	126.1
Q5H9N4: Putative uncharacterized protein DKFZp686L20222 OS=Homo sapiens GN=DKFZp686L20222 PE=3 SV=1	108.6	76.4	137.4	94.1	99	84.6
P23246: Splicing factor, proline- and glutamine-rich OS=Homo sapiens GN=SFPQ PE=1 SV=2	107.1	228.7	70.2	68	64	62
P30101: Protein disulfide-isomerase A3 OS=Homo sapiens GN=PDIA3 PE=1 SV=4	214.1	221.9	30.5	29.1	62.8	41.7
Q14240-2: Isoform 2 of Eukaryotic initiation factor 4A-II OS=Homo sapiens GN=EIF4A2	257.5	174.3	28.3	34.3	50.2	55.5
Q93009: Ubiquitin carboxyl-terminal hydrolase 7 OS=Homo sapiens GN=USP7 PE=1 SV=2	103.9	76.2	110.1	90.7	114.4	104.7
A0A024R4K3: Malate dehydrogenase OS=Homo sapiens GN=MDH2 PE=2 SV=1	216.8	185.1	55.7	27.8	51.4	63.1
Q15084-2: Isoform 2 of Protein disulfide-isomerase A6 OS=Homo sapiens GN=PDIA6	170.7	143.9	64	83.5	71	66.9
A0A024R201: Proteasome (Prosome, macropain) 26S subunit, non-ATPase, 13, isoform CRA_a OS=Homo sapiens GN=PSMD13 PE=4 SV=1	176.5	155.1	67	42	102.1	57.3
P31948-2: Isoform 2 of Stress-induced-phosphoprotein 1 OS=Homo sapiens GN=STIP1	166.1	156.1	54.7	73.8	73.1	76.2
P52907: F-actin-capping protein subunit alpha-1 OS=Homo sapiens GN=CAPZA1 PE=1 SV=3	112.8	81	117.8	98.6	97.5	92.2
A0A024RBS2: 60S acidic ribosomal protein P0 OS=Homo sapiens GN=RPLP0 PE=3 SV=1	93.5	159.8	89.7	66.8	106.3	83.9
Q16891: MICOS complex subunit MIC60 OS=Homo sapiens GN=IMMT PE=1 SV=1	74.9	60.8	124.9	109.9	125.3	104.2
A0A087WUT6: Eukaryotic translation initiation factor 5B OS=Homo sapiens GN=EIF5B PE=1 SV=1	177.4	147.3	63.9	62.3	85	64.2
P53621-2: Isoform 2 of Coatomer subunit alpha OS=Homo sapiens GN=COPA	132.8	104.6	104.9	69.4	106	82.2
P49321: Nuclear autoantigenic sperm protein OS=Homo sapiens GN=NASP PE=1 SV=2	189.4	167.4	53.9	56.2	62.1	71
Q14566: DNA replication licensing factor MCM6 OS=Homo sapiens GN=MCM6 PE=1 SV=1	186.5	175	44		114.1	80.4
O00231-2: Isoform 2 of 26S proteasome non-ATPase regulatory subunit 11 OS=Homo sapiens GN=PSMD11	177.7	135.6	70.7	46.1	108	61.9
A0A024R7T3: Heterogeneous nuclear ribonucleoprotein F, isoform CRA_a OS=Homo sapiens GN=HNRPF PE=4 SV=1	164.7	124.7	75.6	55.2	105.7	74.2
A0A024R814: Ribosomal protein L7, isoform CRA_a OS=Homo sapiens GN=RPL7 PE=4 SV=1	150.9	130.1	95	66.6	82.2	75.2
B3KSH1: Eukaryotic translation initiation factor 3 subunit F OS=Homo sapiens GN=EIF3F PE=2 SV=1	281.9	197.5	30.1	19.8	37.2	33.6
P50454: Serpin H1 OS=Homo sapiens GN=SERPINH1 PE=1 SV=2	67.2	57.5	104.3	99.8	157	114.2
A0A0S2Z4A5: DNA helicase (Fragment) OS=Homo sapiens GN=MCM7 PE=2 SV=1	128.6	106.5	78.3	71.1	132.1	83.4
B3KXM2: Serine/threonine-protein phosphatase OS=Homo sapiens PE=2 SV=1	159.5	114.6	80.4	55.4	108.8	81.3
P09543: 2',3'-cyclic-nucleotide 3'-phosphodiesterase OS=Homo sapiens GN=CNP PE=1 SV=2	80.4	61.5	103	104.3	132.5	118.4
A8K651: cDNA FLJ75700, highly similar to Homo sapiens complement component 1, q subcomponent binding protein (C1QBP), nuclear gene encoding mitochondrial protein, mRNA OS=Homo sapiens PE=2 SV=1	156.7	146.7	66.2	71.5	81.3	77.7
Q13561-2: Isoform 2 of Dynactin subunit 2 OS=Homo sapiens GN=DCTN2	132.5	98.5	73.1	89.9	86.6	119.4
Q9P2E9: Ribosome-binding protein 1 OS=Homo sapiens GN=RRBP1 PE=1 SV=4	160.1	151.5	84.9	66.2	77.9	59.5
O15042: U2 snRNP-associated SURP motif-containing protein OS=Homo sapiens GN=U2SURP PE=1 SV=2	133.1	126.7	83.1	68.7	100.7	87.7
Q5U077: L-lactate dehydrogenase OS=Homo sapiens GN=LDHB PE=2 SV=1	148.9	293.5	34.4	23.8	52.5	46.8
X5DR09: General transcription factor IIi isoform A (Fragment) OS=Homo sapiens GN=GTF2I PE=2 SV=1	173.2	124	72.6	54.2	104.7	71.2
A0A0S2Z489: Proteasome (Prosome, macropain) 26S subunit, non-ATPase, 12, isoform CRA_a (Fragment) OS=Homo sapiens GN=PSMD12 PE=2 SV=1	183.7	167.7	53.8	40	110.6	44.2

V9HWD6: Epididymis secretory protein Li 1 OS=Homo sapiens GN=HEL-S-1 PE=2 SV=1	182.7	164.5	45.7	51.6	70.7	84.8
O00425: Insulin-like growth factor 2 mRNA-binding protein 3 OS=Homo sapiens GN=IGF2BP3 PE=1 SV=2	132.1	115.8	89.1	51	119.2	92.8
E9PRY8: Elongation factor 1-delta OS=Homo sapiens GN=EEF1D PE=1 SV=1	105.5	129.5	95.7	81.1	86.6	101.6
A8K9A4: cDNA FLJ75154, highly similar to Homo sapiens heterogeneous nuclear ribonucleoprotein C (C1/C2), mRNA OS=Homo sapiens PE=2 SV=1	107.2	84.4	125.4	85	100.4	97.6
P61981: 14-3-3 protein gamma OS=Homo sapiens GN=YWHAG PE=1 SV=2	117.5	87.3	98.9	91.9	84.8	119.7
Q15366-2: Isoform 2 of Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2	115.3	86.7	93.3	100.6	116.2	88
P39023: 60S ribosomal protein L3 OS=Homo sapiens GN=RPL3 PE=1 SV=2	108.9	91.4	111.5	104.8	78.7	104.7
Q53HB3: Proteasome 26S ATPase subunit 1 variant (Fragment) OS=Homo sapiens PE=1 SV=1	120.3	99.2	103.9	77.3	108.9	90.4
A8K7D9: Importin subunit alpha OS=Homo sapiens PE=2 SV=1	144.5	90	88.5	87.4	114.9	74.7
P22695: Cytochrome b-c1 complex subunit 2, mitochondrial OS=Homo sapiens GN=UQCRC2 PE=1 SV=3	80.9	70.4	113.7	95.1	124.4	115.5
P53618: Coatomer subunit beta OS=Homo sapiens GN=COPB1 PE=1 SV=3	129.2	113.9	88.6	69.3	113.5	85.6
A0A024R3W7: Eukaryotic translation elongation factor 1 beta 2, isoform CRA_a OS=Homo sapiens GN=EEF1B2 PE=3 SV=1	117.3	114.7	106.1	71.1	91.3	99.6
A0A024R1Q8: Ribosomal protein L23, isoform CRA_b OS=Homo sapiens GN=RPL23 PE=3 SV=1	38.8	27.2	156.8	137.8	109.8	129.6
P21796: Voltage-dependent anion-selective channel protein 1 OS=Homo sapiens GN=VDAC1 PE=1 SV=2	289.4	154.9	38.5		72.2	44.9
P26368: Splicing factor U2AF 65 kDa subunit OS=Homo sapiens GN=U2AF2 PE=1 SV=4	144.5	139.2	76.6	64.7	109.6	65.4
A2A3R6: 40S ribosomal protein S6 OS=Homo sapiens GN=RPS6 PE=2 SV=1	141.3	170.7	73	66.2	85.5	63.3
A0A024R7U6: DNA helicase OS=Homo sapiens GN=MCM4 PE=3 SV=1	192.5	163.3	52.6	41.6	79.6	70.3
A0A024R8S5: Protein disulfide-isomerase OS=Homo sapiens GN=P4HB PE=2 SV=1	231.7	152.1	47.2	47.1	58.2	63.7
P12004: Proliferating cell nuclear antigen OS=Homo sapiens GN=PCNA PE=1 SV=1	215.6	168.5	51.9	39.3	69.2	55.5
Q9BXP5: Serrate RNA effector molecule homolog OS=Homo sapiens GN=SRRT PE=1 SV=1	142.4	131.2	71	50.3	119	86.2
A0A024RDF6: Heterogeneous nuclear ribonucleoprotein D-like, isoform CRA_a OS=Homo sapiens GN=HNRPDL PE=4 SV=1	122.1	106	99.4	111	63.5	98
P62424: 60S ribosomal protein L7a OS=Homo sapiens GN=RPL7A PE=1 SV=2	100	172.7	94.4	67.5	85.5	79.9
O75822: Eukaryotic translation initiation factor 3 subunit J OS=Homo sapiens GN=EIF3J PE=1 SV=2	218.6	338.7	9.4	6.4	16.3	10.6
P28288: ATP-binding cassette sub-family D member 3 OS=Homo sapiens GN=ABCD3 PE=1 SV=1	35.6	28.9	126.6	147.3	141	120.6
B7Z8Z6: DNA helicase OS=Homo sapiens PE=2 SV=1	219.7	209	25.1	23	88.4	34.7
Q96AG4: Leucine-rich repeat-containing protein 59 OS=Homo sapiens GN=LRRC59 PE=1 SV=1	162.4	127.2	81.4	65	102.6	61.5
Q8WWY3: U4/U6 small nuclear ribonucleoprotein Prp31 OS=Homo sapiens GN=PRPF31 PE=1 SV=2	135.1	107	96.4	65.2	119.3	76.9
V9HW77: Epididymis luminal protein 211 OS=Homo sapiens GN=HEL-211 PE=2 SV=1	280.1	235.9	27.7		37	19.3
O75821: Eukaryotic translation initiation factor 3 subunit G OS=Homo sapiens GN=EIF3G PE=1 SV=2	262.2	189.3	41.2	15.4	50.5	41.4
Q99615: DnaJ homolog subfamily C member 7 OS=Homo sapiens GN=DNAJC7 PE=1 SV=2	43.4	35	135.3	110.7	162.5	113
Q9UBQ5: Eukaryotic translation initiation factor 3 subunit K OS=Homo sapiens GN=EIF3K PE=1 SV=1	289.2	216.8	21.4	15.4	34.4	22.8
Q14103: Heterogeneous nuclear ribonucleoprotein D0 OS=Homo sapiens GN=HNRNPD PE=1 SV=1	127.2	113.6	101.2	80.2	80.2	97.7
A0A024RBE7: Thymopoietin, isoform CRA_c OS=Homo sapiens GN=TMPO PE=4 SV=1	120.2	91.2	107.6	89	99.4	92.5
P07737: Profilin-1 OS=Homo sapiens GN=PFN1 PE=1 SV=2	166.1	255.3	34.6	32.2	61.9	49.9
A0A0A0MRA8: Band 4.1-like protein 3 OS=Homo sapiens GN=EPB41L3 PE=1 SV=1	136.6	171.3	68.1	57.7	98.8	67.5
P30153: Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform OS=Homo sapiens GN=PPP2R1A PE=1 SV=4	148.1	123.4	76.5	87	106.8	58.1

F4ZW62: NF45 OS=Homo sapiens PE=1 SV=1	27.4	172.2	112.5	91.5	96.2	100.3
P00338-3: Isoform 3 of L-lactate dehydrogenase A chain OS=Homo sapiens GN=LDHA	265.2	233.2	14.1	13.9	46.7	26.9
A8K7V1: cDNA FLJ78053, highly similar to Homo sapiens splicing factor 3a, subunit 3, 60kDa (SF3A3), mRNA OS=Homo sapiens PE=2 SV=1	210.9	188.4	40.2	29.7	72.6	58.1
P04843: Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1 OS=Homo sapiens GN=RPN1 PE=1 SV=1	182	135.4	75.1	74.5	75.3	57.7
P62979: Ubiquitin-40S ribosomal protein S27a OS=Homo sapiens GN=RPS27A PE=1 SV=2	46.8	36.5	144.6	130.3	126.3	115.6
P46783: 40S ribosomal protein S10 OS=Homo sapiens GN=RPS10 PE=1 SV=1	128.4	223.4	63.1	55.4	64.8	64.7
Q53SS8: Epididymis secretory protein Li 85 OS=Homo sapiens GN=PCBP1 PE=2 SV=1	88.6	67.8	95.7	134.3	124.8	88.8
A3R0T7: Liver histone H1e OS=Homo sapiens PE=2 SV=1	115.6	133.3	113.1	111.9	45.3	80.8
P36542: ATP synthase subunit gamma, mitochondrial OS=Homo sapiens GN=ATP5C1 PE=1 SV=1	68.5	53.3	126.6	111.6	134.6	105.5
J3QRS3: Myosin regulatory light chain 12A OS=Homo sapiens GN=MYL12A PE=1 SV=1	268.1	264	15.1	10.5	25.8	16.6
Q13283: Ras GTPase-activating protein-binding protein 1 OS=Homo sapiens GN=G3BP1 PE=1 SV=1	206.8	178.8	46.1		114.6	53.7
Q14247: Src substrate cortactin OS=Homo sapiens GN=CTTN PE=1 SV=2	164.4	146.2	66.6	70.4	73.9	78.4
V9HW88: Calreticulin, isoform CRA_b OS=Homo sapiens GN=HEL-S-99n PE=2 SV=1	251	194.1	33.2	10.3	57.7	53.7
A0A024R652: Methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 1, methenyltetrahydrofolate cyclohydrolase, formyltetrahydrofolate synthetase, isoform CRA_a OS=Homo sapiens GN=MTHFD1 PE=3 SV=1	177.8	148.1	59.2	54.2	93.9	66.8
Q9Y3I0: tRNA-splicing ligase RtcB homolog OS=Homo sapiens GN=RTCB PE=1 SV=1	131.5	88	96.2	104.9	100.3	79.1
P16402: Histone H1.3 OS=Homo sapiens GN=HIST1H1D PE=1 SV=2	128.6	142.9	100.2	85.8	68.7	73.7
J3KTL2: Serine/arginine-rich-splicing factor 1 OS=Homo sapiens GN=SRSF1 PE=1 SV=1	111	99.9	113.8	96.6	91.5	87.1
Q02978: Mitochondrial 2-oxoglutarate/malate carrier protein OS=Homo sapiens GN=SLC25A11 PE=1 SV=3	51.8	32.4	103.7	125.3	176.4	110.4
A8K401: Prohibitin, isoform CRA_a OS=Homo sapiens GN=PHB PE=2 SV=1	217.6	160.1	47.4	43.3	79.6	52
A8K7H3: cDNA FLJ77670, highly similar to Homo sapiens ribosomal protein S15a (RPS15A), mRNA OS=Homo sapiens PE=2 SV=1	138.8	194.8	69.3	46.3	90.2	60.6
B5BUB5: Autoantigen La (Fragment) OS=Homo sapiens GN=SSB PE=2 SV=1	183.2	150.3	68.6	48.7	84.2	65.1
Q9HBB3: 60S ribosomal protein L6 OS=Homo sapiens PE=2 SV=1	54.3	149.6	118.5	90	98	89.6
A0A087X2I1: 26S protease regulatory subunit 10B OS=Homo sapiens GN=PSMC6 PE=1 SV=1	178.5	115.7	71.8	48.5	97.3	88.2
P38159: RNA-binding motif protein, X chromosome OS=Homo sapiens GN=RBMX PE=1 SV=3	160.3	95.2	101	65.9	99.9	77.6
P62906: 60S ribosomal protein L10a OS=Homo sapiens GN=RPL10A PE=1 SV=2	96.5	131.9	107.5	79.7	98.5	86
P16403: Histone H1.2 OS=Homo sapiens GN=HIST1H1C PE=1 SV=2	36	96.7	133.5	147.8	69.4	116.6
Q99623: Prohibitin-2 OS=Homo sapiens GN=PHB2 PE=1 SV=2	145.4	111.3	68.1	95.4	104.5	75.3
E7EMB3: Calmodulin-2 OS=Homo sapiens GN=CALM2 PE=1 SV=1	165.7	121.3	93.9	93.5	58.2	67.4
A0A024QZ30: Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial OS=Homo sapiens GN=SDHA PE=3 SV=1	67.2	46.7	127.8	103.8	146.3	108.3
E9PFW3: AP-2 complex subunit mu OS=Homo sapiens GN=AP2M1 PE=1 SV=1	196.9	175.4	46.5	38.9	94	48.2
A0A0S2Z4Z6: Serine/arginine repetitive matrix 1 isoform 2 (Fragment) OS=Homo sapiens GN=SRRM1 PE=2 SV=1	148.3	120.2	100.2	67.8	84.1	79.4
A8K588: cDNA FLJ76823, highly similar to Homo sapiens splicing factor, arginine/serine-rich 6 (SFRS6), mRNA OS=Homo sapiens PE=2 SV=1	133.5	94.8	101.9	89.7	95.2	84.9
P25398: 40S ribosomal protein S12 OS=Homo sapiens GN=RPS12 PE=1 SV=3	171.1	163.8	63.3	72.2	65	64.6
P46060: Ran GTPase-activating protein 1 OS=Homo sapiens GN=RANGAP1 PE=1 SV=1	127.2	74.4	50.8	72.2	175.6	99.8

Q16576-2: Isoform 2 of Histone-binding protein RBBP7 OS=Homo sapiens GN=RBBP7	167.4	123.4	81.3	61.3	98.1	68.5
P62081: 40S ribosomal protein S7 OS=Homo sapiens GN=RPS7 PE=1 SV=1	165.8	221.6	55.2	38.8	70.9	47.7
P61221: ATP-binding cassette sub-family E member 1 OS=Homo sapiens GN=ABCE1 PE=1 SV=1	243.3	163.8	36.3	26.6	86.2	43.8
Q7L4Q3: Glutathione peroxidase OS=Homo sapiens GN=GPX1 PE=2 SV=1	5.6	5.1	153	160.6	117.3	158.4
A0A024R718: Pre-B-cell colony enhancing factor 1, isoform CRA_a OS=Homo sapiens GN=PBEF1 PE=4 SV=1	139.9	111.1	83.2	84.6	98.6	82.6
P29401-2: Isoform 2 of Transketolase OS=Homo sapiens GN=TKT	262.7	204.2	24.8	10.5	55.4	42.4
V9HWE9: Epididymis secretory protein Li 22 OS=Homo sapiens GN=HEL-S-22 PE=2 SV=1	253.3	258.3	21.7	15	32	19.6
A0A0S2Z410: Hydroxysteroid dehydrogenase 10 isoform 1 (Fragment) OS=Homo sapiens GN=HSD17B10 PE=2 SV=1	158.9	164.7	56.2	54.9	113.6	51.7
Q9NTJ3: Structural maintenance of chromosomes protein 4 OS=Homo sapiens GN=SMC4 PE=1 SV=2	85.8	82.2	138.4	85.3	113.9	94.4
Q16630-2: Isoform 2 of Cleavage and polyadenylation specificity factor subunit 6 OS=Homo sapiens GN=CPSF6	230.5	154	62.7	32.8	68.9	51.1
P43686: 26S proteasome regulatory subunit 6B OS=Homo sapiens GN=PSMC4 PE=1 SV=2	153.3	120.8	83.1	61.1	104.7	77
O95782: AP-2 complex subunit alpha-1 OS=Homo sapiens GN=AP2A1 PE=1 SV=3	165.2	141.5	72.4	55.1	81	84.7
P05387: 60S acidic ribosomal protein P2 OS=Homo sapiens GN=RPLP2 PE=1 SV=1	114	93.6	134	94	82.5	82
Q14683: Structural maintenance of chromosomes protein 1A OS=Homo sapiens GN=SMC1A PE=1 SV=2	51.6	39.1	104.2	127.5	138.9	138.7
A0A024RAI1: ARP3 actin-related protein 3 homolog (Yeast), isoform CRA_a OS=Homo sapiens GN=ACTR3 PE=3 SV=1	198.8	137.3	61.1	51.1	94.9	56.9
Q01804: OTU domain-containing protein 4 OS=Homo sapiens GN=OTUD4 PE=1 SV=4	154.8	105.9	73.1	68.4	100.8	96.8
E9PK25: Cofilin-1 OS=Homo sapiens GN=CFL1 PE=1 SV=1	96.8	70.7	98.1	110.5	119.6	104.4
B2RDE1: cDNA, FLJ96568, highly similar to Homo sapiens tropomyosin 3 (TPM3), mRNA OS=Homo sapiens PE=2 SV=1	107.7	119.8	109.2	127.1	56.3	79.8
P51398: 28S ribosomal protein S29, mitochondrial OS=Homo sapiens GN=DAP3 PE=1 SV=1	145.7	99.2	71.5	60.6	143.6	79.4
H7C2I1: Protein arginine N-methyltransferase 1 OS=Homo sapiens GN=PRMT1 PE=1 SV=1	147.5	175.6	69.2	48.4	95.1	64.3
B2RDY9: Adenylyl cyclase-associated protein OS=Homo sapiens PE=2 SV=1	154.1	195.9	44.8	43.1	91.9	70.3
P30048: Thioredoxin-dependent peroxide reductase, mitochondrial OS=Homo sapiens GN=PRDX3 PE=1 SV=3	117	87.2	98.3	113.5	86.1	97.9
Q9P035: Very-long-chain (3R)-3-hydroxyacyl-CoA dehydratase 3 OS=Homo sapiens GN=HACD3 PE=1 SV=2	67.5	44.9	127.3	132.5	118.4	109.4
A0A0K0K1K4: Proteasome subunit alpha type OS=Homo sapiens GN=HEL-S-276 PE=2 SV=1	170.2	161.2	62.9	47.4	94.1	64.1
Q8IX12: Cell division cycle and apoptosis regulator protein 1 OS=Homo sapiens GN=CCAR1 PE=1 SV=2	111.1	79.6	114.9	66.5	132.6	95.3
Q8NBS9: Thioredoxin domain-containing protein 5 OS=Homo sapiens GN=TXNDC5 PE=1 SV=2	56.5	44	112.2	149.9	123.8	113.6
P09661: U2 small nuclear ribonucleoprotein A' OS=Homo sapiens GN=SNRPA1 PE=1 SV=2	151.1	109.7	91.5	94.3	58.3	95.2
P57678: Gem-associated protein 4 OS=Homo sapiens GN=GEMIN4 PE=1 SV=2	95.7	73.3	121.8	91.3	111.7	106.4
B2RCM2: cDNA, FLJ96156, highly similar to Homo sapiens leucyl-tRNA synthetase (LARS), mRNA OS=Homo sapiens PE=2 SV=1	150.7	119.8	59.7	63.5	111.9	94.3
J3KQE5: GTP-binding nuclear protein Ran (Fragment) OS=Homo sapiens GN=RAN PE=1 SV=1	215.6	167.7	47.3	37.5	85.6	46.4
Q549M8: CLE7 OS=Homo sapiens GN=C14orf166 PE=2 SV=1	161	115.6	90.2	79	83.5	70.7
A0A024RAC5: Regulator of chromosome condensation 2, isoform CRA_a OS=Homo sapiens GN=RCC2 PE=4 SV=1	156.5	126.9	74.8	83.9	82.4	75.5
Q9UJS0-2: Isoform 2 of Calcium-binding mitochondrial carrier protein Aralar2 OS=Homo sapiens GN=SLC25A13	59.7	37.9	119.2	128.1	129.9	125.2
H0Y449: Nuclease-sensitive element-binding protein 1 (Fragment) OS=Homo sapiens GN=YBX1 PE=1 SV=1	45.2	170.8	113.9	91.8	88.4	89.8
P83731: 60S ribosomal protein L24 OS=Homo sapiens GN=RPL24 PE=1 SV=1	117.3	101.3	101.1	84.8	112.7	82.8
Q14257-2: Isoform 2 of Reticulocalbin-2 OS=Homo sapiens GN=RCN2	81.3	71.4	119.5	103.8	92.3	131.7

B4DJ30: cDNA FLJ61290, highly similar to Neutral alpha-glucosidase AB OS=Homo sapiens PE=2 SV=1	219.2	205	44.8	16.9	82.7	31.4
P25786-2: Isoform Long of Proteasome subunit alpha type-1 OS=Homo sapiens GN=PSMA1	176.6	136.2	84.8	57	75.5	69.9
Q05D08: PA2G4 protein (Fragment) OS=Homo sapiens GN=PA2G4 PE=2 SV=1	216.5	186.2	49.4	20.9	68.2	58.7
B4DLN1: cDNA FLJ60124, highly similar to Mitochondrial dicarboxylate carrier OS=Homo sapiens PE=2 SV=1	114.6	85.6	102.9	99.3	108.3	89.3
P46781: 40S ribosomal protein S9 OS=Homo sapiens GN=RPS9 PE=1 SV=3	171.3	170.5	70.2	52.1	80	55.8
P41091: Eukaryotic translation initiation factor 2 subunit 3 OS=Homo sapiens GN=EIF2S3 PE=1 SV=3	138.9	125.3	88.9	67.2	91.4	88.3
B3KM36: cDNA FLJ10153 fis, clone HEMBA1003417, highly similar to BAG family molecular chaperone regulator 2 OS=Homo sapiens PE=2 SV=1	18.2	14.9	137.3	165.8	136.2	127.6
A8K486: Peptidyl-prolyl cis-trans isomerase OS=Homo sapiens PE=2 SV=1	230.3	180	43	32.1	52.9	61.7
A0A0S2Z3L2: ATPase Ca++ transporting cardiac muscle slow twitch 2 isoform 1 (Fragment) OS=Homo sapiens GN=ATP2A2 PE=2 SV=1	155.9	105.3	65.8	65.9	107.7	99.3
Q9NYF8: Bcl-2-associated transcription factor 1 OS=Homo sapiens GN=BCLAF1 PE=1 SV=2	210.5	133.7	63.5	41.5	102.7	48
Q4VCS5: Angiomotin OS=Homo sapiens GN=AMOT PE=1 SV=1	129.4	84.2	98.2	92.4	97.8	98
P16989: Y-box-binding protein 3 OS=Homo sapiens GN=YBX3 PE=1 SV=4	143.4	126.6	77.1	92.7	100.4	59.8
P26196: Probable ATP-dependent RNA helicase DDX6 OS=Homo sapiens GN=DDX6 PE=1 SV=2	130.8	97.8	80.3	86.4	100.7	104.1
A0A0S2Z4Z9: Non-POU domain containing octamer-binding isoform 1 (Fragment) OS=Homo sapiens GN=NONO PE=2 SV=1	160	138.7	73.5	90.2	78	59.4
P11387: DNA topoisomerase 1 OS=Homo sapiens GN=TOP1 PE=1 SV=2	185.1	147.6	90.8	48.9	79.6	48
P62888: 60S ribosomal protein L30 OS=Homo sapiens GN=RPL30 PE=1 SV=2	153.6	182.2	72.1	54.6	77.9	59.6
Q15427: Splicing factor 3B subunit 4 OS=Homo sapiens GN=SF3B4 PE=1 SV=1	144.4	109.3	95.4	78	93.6	79.3
Q96EE3-1: Isoform B of Nucleoporin SEH1 OS=Homo sapiens GN=SEH1L	54.3	40.5	129.7	125.3	145.1	105.1
V9HW12: Epididymis secretory sperm binding protein Li 2a OS=Homo sapiens GN=HEL-S-2a PE=2 SV=1	53.8	38.7	144.5	160	84.2	118.9
Q53H12: Acylglycerol kinase, mitochondrial OS=Homo sapiens GN=AGK PE=1 SV=2	69.5	53.7	122	86.9	165.6	102.4
P30050: 60S ribosomal protein L12 OS=Homo sapiens GN=RPL12 PE=1 SV=1	61.7	154.1	91.2	73.1	125.8	94
P51991: Heterogeneous nuclear ribonucleoprotein A3 OS=Homo sapiens GN=HNRNPA3 PE=1 SV=2	147.9	117.2	68	54.8	142	70.1
P00492: Hypoxanthine-guanine phosphoribosyltransferase OS=Homo sapiens GN=HPRT1 PE=1 SV=2	173.5	115.9	101.6	65.7	86.2	57.1
Q7Z4V5-3: Isoform 3 of Hepatoma-derived growth factor-related protein 2 OS=Homo sapiens GN=HDGFL2	210.6	218.9	56.7	16.1	45.7	51.9
A8K3A8: cDNA FLJ75085, highly similar to Homo sapiens glutaminyl-tRNA synthetase (QARS), mRNA OS=Homo sapiens PE=2 SV=1	274.7	273.7		36.5	15.1	
H0Y368: Dolichol-phosphate mannosyltransferase subunit 1 (Fragment) OS=Homo sapiens GN=DPM1 PE=1 SV=1	33.9	24.3	132.4	140.7	152.5	116.2
A0A024R4Q8: Ribosomal protein S5, isoform CRA_a OS=Homo sapiens GN=RPS5 PE=3 SV=1	166	141	70.5	73.5	73.8	75.2
A8MUS3: 60S ribosomal protein L23a OS=Homo sapiens GN=RPL23A PE=1 SV=1	119.8	169.5	86.8	60.3	87.1	76.4
A0A087WV05: Uncharacterized protein OS=Homo sapiens PE=4 SV=1	172.8	148.9	47.3	72.8	73.3	84.9
Q5W0B1: RING finger protein 219 OS=Homo sapiens GN=RNF219 PE=1 SV=1	62.1	53.9	97.3	156.6	123.1	106.9
A8KAQ5: cDNA FLJ77404, highly similar to Homo sapiens small nuclear ribonucleoprotein 70kDa polypeptide (RNP antigen) (SNRP70), transcript variant 1, mRNA OS=Homo sapiens PE=2 SV=1	185	142.7	70.5	33.4	94.4	74
P55060: Exportin-2 OS=Homo sapiens GN=CSE1L PE=1 SV=3	174.9	139.8	64.8	73.3	83.8	63.4
P18621-3: Isoform 3 of 60S ribosomal protein L17 OS=Homo sapiens GN=RPL17	117	145.9	94.5	72.9	88.4	81.3
P06396: Gelsolin OS=Homo sapiens GN=GSN PE=1 SV=1	129.2	118.4	90.3	103.2	67.2	91.7

O15226-2: Isoform 2 of NF-kappa-B-repressing factor OS=Homo sapiens GN=NKRF	115.6	77.9	111.8	86.6	128.1	80.1
B7Z6Z4: Myosin light polypeptide 6 OS=Homo sapiens GN=MYL6 PE=1 SV=1	227.5	273		31	33.2	35.3
A0A024QYY3: Phosphoribosyl pyrophosphate synthetase-associated protein 2, isoform CRA_a OS=Homo sapiens GN=PRPSAP2 PE=4 SV=1	100	247.2	64.9	52.6	72	63.3
Q9UHX1: Poly(U)-binding-splicing factor PUF60 OS=Homo sapiens GN=PUF60 PE=1 SV=1	200.8	155.1	46.6	54.1	74.4	69.1
P62280: 40S ribosomal protein S11 OS=Homo sapiens GN=RPS11 PE=1 SV=3	120.1	142.2	94	68.6	95.6	79.3
Q16629: Serine/arginine-rich splicing factor 7 OS=Homo sapiens GN=SRSF7 PE=1 SV=1	172	103.1	100.5	64.8	84.4	75.1
J3QK89: Calcium homeostasis endoplasmic reticulum protein OS=Homo sapiens GN=CHERP PE=1 SV=1	147.8	119.5	75.4	66.1	100.5	90.7
P23381: Tryptophan--tRNA ligase, cytoplasmic OS=Homo sapiens GN=WARS PE=1 SV=2	136	148.6	91.8	50.4	95.5	77.7
O95292: Vesicle-associated membrane protein-associated protein B/C OS=Homo sapiens GN=VAPB PE=1 SV=3	43.7	31.7	131.8	134.6	147.1	111.1
P62316: Small nuclear ribonucleoprotein Sm D2 OS=Homo sapiens GN=SNRPD2 PE=1 SV=1	144.9	147.4	77.1	64.4	89	77.3
B3KSL5: cDNA FLJ36545 fis, clone TRACH2006670, highly similar to RNA-binding protein Luc7-like 2 OS=Homo sapiens PE=2 SV=1	159.3	170.6	68.6	61.5	74.9	65.1
J3QQ67: 60S ribosomal protein L18 (Fragment) OS=Homo sapiens GN=RPL18 PE=1 SV=1	151.7	119.3	83.5	77.5	98.8	69.3
Q53Z07: NPC-A-16 OS=Homo sapiens GN=RPL9 PE=2 SV=1	161.2	151.4	81.3	45.5	100.1	60.5
Q00325: Phosphate carrier protein, mitochondrial OS=Homo sapiens GN=SLC25A3 PE=1 SV=2	51.2	37.6	124.3	137.1	143.5	106.2
A6NEM2: Host cell factor 1 OS=Homo sapiens GN=HCFC1 PE=1 SV=2	41.9	43	135.5	120	162.9	96.8
A0A024RBB7: Nucleosome assembly protein 1-like 1, isoform CRA_a OS=Homo sapiens GN=NAP1L1 PE=3 SV=1	202.3	178.9	56.5	36.5	78.6	47.2
A0A024R8W0: DEAD (Asp-Glu-Ala-Asp) box polypeptide 48, isoform CRA_a OS=Homo sapiens GN=DDX48 PE=3 SV=1	179.7	187.1	67.4	27.2	76.3	62.3
P08708: 40S ribosomal protein S17 OS=Homo sapiens GN=RPS17 PE=1 SV=2	179.8	204	49	41.6	75.8	49.7
Q09028: Histone-binding protein RBBP4 OS=Homo sapiens GN=RBBP4 PE=1 SV=3	167.1	128.1	58.4	51	116.6	78.8
P61163: Alpha-centractin OS=Homo sapiens GN=ACTR1A PE=1 SV=1	37.3	88	125.7	121.5	99.8	127.7
P13995: Bifunctional methylenetetrahydrofolate dehydrogenase/cyclohydrolase, mitochondrial OS=Homo sapiens GN=MTHFD2 PE=1 SV=2	40.4	28.8	123.5	136.5	125.2	145.6
Q59F99: Staufen isoform b variant (Fragment) OS=Homo sapiens PE=2 SV=1	96.9	78.6	116.2	103.6	95.6	109.1
Q658Y4: Protein FAM91A1 OS=Homo sapiens GN=FAM91A1 PE=1 SV=3	17.1	11.8	141.8	112.9	170.2	146.2
P15170-3: Isoform 3 of Eukaryotic peptide chain release factor GTP-binding subunit ERF3A OS=Homo sapiens GN=GSPT1	111.5	106.8	98.7	85.3	97	100.8
A0A024R713: Dihydrolipoyl dehydrogenase OS=Homo sapiens GN=DLD PE=3 SV=1	129.5	155.9	75	71.1	67.9	100.6
F6WQW2: Ran-specific GTPase-activating protein OS=Homo sapiens GN=RANBP1 PE=1 SV=1	166.2	87	98.7	60.4	94.6	93
A8K7N0: cDNA FLJ75556, highly similar to Homo sapiens ribosomal protein L14, mRNA OS=Homo sapiens PE=2 SV=1	150.7	113.3	89.9	69.1	96.8	80.3
B4DWA6: cDNA FLJ60094, highly similar to F-actin capping protein subunit beta OS=Homo sapiens PE=2 SV=1	125.5	91	115.1	85.1	88.3	95
Q13442: 28 kDa heat- and acid-stable phosphoprotein OS=Homo sapiens GN=PDAP1 PE=1 SV=1	242	350.1			8	
Q9UNE7: E3 ubiquitin-protein ligase CHIP OS=Homo sapiens GN=STUB1 PE=1 SV=2	39.2	22.8	142.1	122.8	127.7	145.4
A8K492: cDNA FLJ76789, highly similar to Homo sapiens methionine-tRNA synthetase (MARS), mRNA OS=Homo sapiens PE=2 SV=1	140.6	107.4	93.6	70.3	109.1	79.1
Q8TA92: Similar to AFG3 ATPase family gene 3-like 2 (Yeast) (Fragment) OS=Homo sapiens PE=2 SV=1	51.1	50.5	125.3	106.3	135.5	131.3
Q9UKV3: Apoptotic chromatin condensation inducer in the nucleus OS=Homo sapiens GN=ACIN1 PE=1 SV=2	258.8	138.4	79.5		79.1	44.2
O75947: ATP synthase subunit d, mitochondrial OS=Homo sapiens GN=ATP5H PE=1 SV=3	164.6	132.5	58	93.2	96.3	55.5
D9HTE9: Plasma membrane citrate carrier OS=Homo sapiens GN=SLC25A1 PE=2 SV=1	25.7	19.3	159.7	178.5	79.4	137.4

Q13838-2: Isoform 2 of Spliceosome RNA helicase DDX39B OS=Homo sapiens GN=DDX39B	186.1	140.6	69	48.5	92.6	63.1
P62847-4: Isoform 4 of 40S ribosomal protein S24 OS=Homo sapiens GN=RPS24	173.9	198.5	63	45.9	58.8	59.9
P08559-4: Isoform 4 of Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial OS=Homo sapiens GN=PDHA1	196.2	135.4	72.8	53.3	73.7	68.5
A0A024R8D2: Solute carrier family 27 (Fatty acid transporter), member 4, isoform CRA_a OS=Homo sapiens GN=SLC27A4 PE=4 SV=1	37.4	22.3	133.3	112	154.7	140.2
Q5SRQ6: Casein kinase II subunit beta OS=Homo sapiens GN=CSNK2B PE=1 SV=2	93.2	84.5	84.3	169.9	78.2	89.8
E9PB61: THO complex subunit 4 OS=Homo sapiens GN=ALYREF PE=1 SV=1	213.9	158.8	57.1	55.8	56.9	57.5
P25685: DnaJ homolog subfamily B member 1 OS=Homo sapiens GN=DNAJB1 PE=1 SV=4	40	34.5	136.4	119.2	157.8	112.1
P26373: 60S ribosomal protein L13 OS=Homo sapiens GN=RPL13 PE=1 SV=4	139.1	104.2	112	86.5	67.9	90.4
A8K517: Ribosomal protein S23, isoform CRA_a OS=Homo sapiens GN=RPS23 PE=2 SV=1	44.9	162.4	101.7	87.4	116.4	87.2
Q5HYL6: Putative uncharacterized protein DKFZp686E1899 OS=Homo sapiens GN=DKFZp686E1899 PE=2 SV=1	114.7	97.7	122.5	89.6	88.7	86.7
P54886: Delta-1-pyrroline-5-carboxylate synthase OS=Homo sapiens GN=ALDH18A1 PE=1 SV=2	187.3	152.8	32.8	52.9	130.1	44.2
A0A024R4E5: High density lipoprotein binding protein (Vigilin), isoform CRA_a OS=Homo sapiens GN=HDLBP PE=1 SV=1	162.1	142.6	61.5	69.2	93.7	70.9
Q13242: Serine/arginine-rich splicing factor 9 OS=Homo sapiens GN=SRSF9 PE=1 SV=1	170.3	144.6	79.2	51.7	84.5	69.7
Q5TDE9: Chromosome 1 open reading frame 57, isoform CRA_d OS=Homo sapiens GN=C1orf57 PE=2 SV=1	45.4	42.3	125.1	98.9	174	114.4
P08579: U2 small nuclear ribonucleoprotein B'' OS=Homo sapiens GN=SNRPB2 PE=1 SV=1	205.4	152.1	59.6	47.3	73.5	62.1
Q9BS26: Endoplasmic reticulum resident protein 44 OS=Homo sapiens GN=ERP44 PE=1 SV=1	61.7	51.4	115.6	131	127.5	112.8
P35659: Protein DEK OS=Homo sapiens GN=DEK PE=1 SV=1	247	185.6	34.5		90.5	42.5
E9PAV3: Nascent polypeptide-associated complex subunit alpha, muscle-specific form OS=Homo sapiens GN=NACA PE=1 SV=1	158.8	129.2	77.4	79.3	80.9	74.4
B3KP90: cDNA FLJ31447 fis, clone NT2NE2000913, highly similar to Protein phosphatase 2C isoform beta (EC 3.1.3.16) OS=Homo sapiens PE=2 SV=1	124.9	108.4	102.1	64	101.3	99.3
P62249: 40S ribosomal protein S16 OS=Homo sapiens GN=RPS16 PE=1 SV=2	128.1	163.3	88	71.4	78.6	70.6
P27635: 60S ribosomal protein L10 OS=Homo sapiens GN=RPL10 PE=1 SV=4	66.2	120.4	125.2	92.7	88.2	107.3
V9HW43: Epididymis secretory protein Li 102 OS=Homo sapiens GN=HEL-S-102 PE=2 SV=1	12.6	9.1	177	162.2	120.4	118.7
B2RDP6: cDNA, FLJ96709, highly similar to Homo sapiens glutamate rich WD repeat protein GRWD (GRWD), mRNA OS=Homo sapiens PE=2 SV=1	72.6	68.5	122.6	150.6	85.3	100.4
O43852-3: Isoform 3 of Calumenin OS=Homo sapiens GN=CALU	133.1	107.6	96.2	82	80.2	100.8
Q59GW6: Acetyl-CoA acetyltransferase, cytosolic variant (Fragment) OS=Homo sapiens PE=2 SV=1	59.1	46	130.3	115.7	135.5	113.5
P12532: Creatine kinase U-type, mitochondrial OS=Homo sapiens GN=CKMT1A PE=1 SV=1	249.8	231.5	22.2	18.3	38.2	39.9
Q59HH3: Trifunctional purine biosynthetic protein adenosine-3 (Fragment) OS=Homo sapiens PE=2 SV=1	124	116.9	118.7	75.6	80	84.7
A0A158RFU6: RAB7, member RAS oncogene family, isoform CRA_a OS=Homo sapiens GN=RAB7A PE=2 SV=1	249	187	44.6		62.1	57.2
Q9ULV4-3: Isoform 3 of Coronin-1C OS=Homo sapiens GN=CORO1C	57.3	41.6	118.6	127.2	131.6	123.7
Q32Q12: Nucleoside diphosphate kinase OS=Homo sapiens GN=NME1-NME2 PE=1 SV=1	210.5	169.2	50.2	52	66.7	51.4
Q9Y657: Spindlin-1 OS=Homo sapiens GN=SPIN1 PE=1 SV=3	165.6	150	64.7	51.6	105.1	63
O75832: 26S proteasome non-ATPase regulatory subunit 10 OS=Homo sapiens GN=PSMD10 PE=1 SV=1	195.7	134.2	51.4	36.9	117.5	64.3
Q53G35: Phosphoglycerate mutase (Fragment) OS=Homo sapiens PE=2 SV=1	264.5	196.8	34.1	22.3	40.8	41.4
P61604: 10 kDa heat shock protein, mitochondrial OS=Homo sapiens GN=HSPE1 PE=1 SV=2	261.9	215.4	25.5	13.9	45.5	37.8

Q9NQ92: Coordinator of PRMT5 and differentiation stimulator OS=Homo sapiens GN=COPRS PE=1 SV=3	89.6	90.1	120.9	119.3	79.2	101
Q15008-4: Isoform 4 of 26S proteasome non-ATPase regulatory subunit 6 OS=Homo sapiens GN=PSMD6	161.9	137.8	68.4	40.8	99.9	91.1
Q07666: KH domain-containing, RNA-binding, signal transduction-associated protein 1 OS=Homo sapiens GN=KHDRBS1 PE=1 SV=1	159.2	95.1	88.6	78.1	108.5	70.5
P42677: 40S ribosomal protein S27 OS=Homo sapiens GN=RPS27 PE=1 SV=3	32.5	32.1	124.9	154.3	161.8	94.3
P62263: 40S ribosomal protein S14 OS=Homo sapiens GN=RPS14 PE=1 SV=3	58.6	188	92.3	77.3	98.4	85.4
A8K9K6: cDNA FLJ76962, highly similar to Homo sapiens nucleolar protein 5A (56kDa with KKE/D repeat) (NOL5A), mRNA OS=Homo sapiens PE=2 SV=1	23.7	18.1	149	145.4	154.8	109
Q14498: RNA-binding protein 39 OS=Homo sapiens GN=RBM39 PE=1 SV=2	131.5	99.6	96.9	86.3	94.3	91.6
Q15181: Inorganic pyrophosphatase OS=Homo sapiens GN=PPA1 PE=1 SV=2	221.8	191.2	37.8	43.3	47.8	58
P42285: Superkiller viralicidic activity 2-like 2 OS=Homo sapiens GN=SKIV2L2 PE=1 SV=3	144.2	101.5	96.4	60.4	111.4	86.1
P23284: Peptidyl-prolyl cis-trans isomerase B OS=Homo sapiens GN=PPIB PE=1 SV=2	249.4	200.5	30.4	27	58.6	34.1
G3V5Z7: Proteasome subunit alpha type OS=Homo sapiens GN=PSMA6 PE=1 SV=1	178.1	165.6	53	38.8	85.1	79.3
A8K8U1: cDNA FLJ77762, highly similar to Homo sapiens cullin-associated and neddylation-dissociated 1 (CAND1), mRNA OS=Homo sapiens PE=2 SV=1	188.5	191.7	24	53.8	83.7	58.3
Q9Y512: Sorting and assembly machinery component 50 homolog OS=Homo sapiens GN=SAMM50 PE=1 SV=3	71.7	52.8	116.2	127.7	131.3	100.4
Q15717-2: Isoform 2 of ELAV-like protein 1 OS=Homo sapiens GN=ELAVL1	199.5	110.2	89.8	51.9	90.6	58
P49207: 60S ribosomal protein L34 OS=Homo sapiens GN=RPL34 PE=1 SV=3	153.1	145.5	77.2	59.9	100.6	63.7
O43318: Mitogen-activated protein kinase kinase kinase 7 OS=Homo sapiens GN=MAP3K7 PE=1 SV=1	134.5	119.7	95.3	44.1	104.3	102.2
Q53R19: Arp2/3 complex 34 kDa subunit OS=Homo sapiens GN=ARPC2 PE=2 SV=1	199.9	142.4	79.7	36.5	107.1	34.4
P20042: Eukaryotic translation initiation factor 2 subunit 2 OS=Homo sapiens GN=EIF2S2 PE=1 SV=2	123.4	105.5	116.8	110.1	63.1	81.1
B2RE46: cDNA, FLJ96923, highly similar to Homo sapiens ribophorin II (RPN2), mRNA OS=Homo sapiens PE=2 SV=1	175	126.8	65.8	73.5	78	80.9
Q8ND56: Protein LSM14 homolog A OS=Homo sapiens GN=LSM14A PE=1 SV=3	177.5	188.3	59	44	75.5	55.7
P35268: 60S ribosomal protein L22 OS=Homo sapiens GN=RPL22 PE=1 SV=2	221.8	162.3	33.3	31.2	71.7	79.7
Q14444: Caprin-1 OS=Homo sapiens GN=CAPRIN1 PE=1 SV=2	217.9	165.5	64.5	50.4	62.9	38.7
O14602: Eukaryotic translation initiation factor 1A, Y-chromosomal OS=Homo sapiens GN=EIF1AY PE=1 SV=4	330.4	254.6			8.8	6.1
Q13344: Fus-like protein (Fragment) OS=Homo sapiens PE=2 SV=1	250	197.5	41.7	20.1	48.6	42.2
A0A024RDJ3: H/ACA ribonucleoprotein complex subunit OS=Homo sapiens GN=NOLA1 PE=3 SV=1	175.6	131.6	88		116.7	88
P08574: Cytochrome c1, heme protein, mitochondrial OS=Homo sapiens GN=CYC1 PE=1 SV=3	42.7	29.7	150.2	149.1	105	123.3
H9ZYJ2: Thioredoxin OS=Homo sapiens GN=TXN PE=2 SV=1	105.7	81	108	131.3	81.9	92.1
P62851: 40S ribosomal protein S25 OS=Homo sapiens GN=RPS25 PE=1 SV=1	235.6	163	56.3	32.4	72.5	40.3
Q59G24: Activated RNA polymerase II transcription cofactor 4 variant (Fragment) OS=Homo sapiens PE=2 SV=1	295.3	234.4		24.7	29.2	16.3
P61204: ADP-ribosylation factor 3 OS=Homo sapiens GN=ARF3 PE=1 SV=2	250.2	156.5	28.7	46.3	84	34.3
Q04837: Single-stranded DNA-binding protein, mitochondrial OS=Homo sapiens GN=SSBP1 PE=1 SV=1	124.4	96.6	75.2	103.6	114.8	85.5
P62269: 40S ribosomal protein S18 OS=Homo sapiens GN=RPS18 PE=1 SV=3	108.2	173.7	81.8	67.8	88.8	79.9
Q9Y2W1: Thyroid hormone receptor-associated protein 3 OS=Homo sapiens GN=THRAP3 PE=1 SV=2	224.1	127.6	51.1	35.3	87.9	74.1
Q9P0L0-2: Isoform 2 of Vesicle-associated membrane protein-associated protein A OS=Homo sapiens GN=VAPA	38.3	30	137.1	138.9	138.5	117.2
B2R4C0: 60S ribosomal protein L18a OS=Homo sapiens PE=2 SV=1	28.3	162.9	118.7	96.9	97.8	95.4

H0YMV8: 40S ribosomal protein S27 OS=Homo sapiens GN=RPS27L PE=1 SV=1	33.9	29.6	133.9	215.5	94.2	92.9
O14617-5: Isoform 5 of AP-3 complex subunit delta-1 OS=Homo sapiens GN=AP3D1	111.1	90.9	106.4	65.4	116.7	109.4
P13073: Cytochrome c oxidase subunit 4 isoform 1, mitochondrial OS=Homo sapiens GN=COX4I1 PE=1 SV=1	254.9	214.1	24.4	24	55.5	27
P37802-2: Isoform 2 of Transgelin-2 OS=Homo sapiens GN=TAGLN2	291.3	197.2	21.5	25.4	40.2	24.4
Q6IAX2: RPL21 protein OS=Homo sapiens GN=RPL21 PE=2 SV=1	140.2	144.9	86.9	70.8	81.8	75.5
Q9UJZ1: Stomatin-like protein 2, mitochondrial OS=Homo sapiens GN=STOML2 PE=1 SV=1	52.5	45.1	106.5	174.2	73.3	148.4
Q8WVX7: Ribosomal protein S19 (Fragment) OS=Homo sapiens PE=2 SV=1	193	199.3	55.7	30.6	72.2	49.1
O94776: Metastasis-associated protein MTA2 OS=Homo sapiens GN=MTA2 PE=1 SV=1	196.8	122.2	85.4	52.1	101.7	41.8
I3L504: Eukaryotic translation initiation factor 5A-1 OS=Homo sapiens GN=EIF5A PE=1 SV=1	215.9	160.6	59.5	57.8	60.7	45.4
P62917: 60S ribosomal protein L8 OS=Homo sapiens GN=RPL8 PE=1 SV=2	139.6	121.9	100.7	84.3	85.9	67.6
Q8WUA2: Peptidyl-prolyl cis-trans isomerase-like 4 OS=Homo sapiens GN=PPIL4 PE=1 SV=1	123.6	91.2	103.2	49	123.7	109.4
Q9Y5M8: Signal recognition particle receptor subunit beta OS=Homo sapiens GN=SRPRB PE=1 SV=3	131.2	103.4	73.9	95.9	111.5	84.1
O94905: Erlin-2 OS=Homo sapiens GN=ERLIN2 PE=1 SV=1	90.7	68	142.1	106	104.6	88.7
Q8IYV2: DEAD (Asp-Glu-Ala-Asp) box polypeptide 20 OS=Homo sapiens GN=DDX20 PE=2 SV=1	94	74.4	111.7	102.6	119.4	97.9
O75534-4: Isoform 4 of Cold shock domain-containing protein E1 OS=Homo sapiens GN=CSDE1	121.4	93.9	109.7	95	90	90
A0A024R1U2: PHD finger protein 5A, isoform CRA_a OS=Homo sapiens GN=PHF5A PE=4 SV=1	95.1	74.4	110.1	153.2	77.1	90.1
B4DR52: Histone H2B OS=Homo sapiens PE=2 SV=1	149.8	147.1	78.6	62.1	103.6	58.8
A0A140VKA6: Testis secretory sperm-binding protein Li 233m OS=Homo sapiens PE=2 SV=1	218	175.4	52.3	32.2	69.9	52.1
P51572-2: Isoform 2 of B-cell receptor-associated protein 31 OS=Homo sapiens GN=BCAP31	254.3	192.3	44		65	44.4
P11177: Pyruvate dehydrogenase E1 component subunit beta, mitochondrial OS=Homo sapiens GN=PDHB PE=1 SV=3	216.4	156.5	45.4	53.3	78.2	50.2
M0QYS1: 60S ribosomal protein L13a (Fragment) OS=Homo sapiens GN=RPL13A PE=1 SV=2	128.9	177.7	92.6	62.6	71.4	66.7
Q96SB4-3: Isoform 1 of SRSF protein kinase 1 OS=Homo sapiens GN=SRPK1	195.4	132.9	73.5	74.5	63.6	60.1
P62277: 40S ribosomal protein S13 OS=Homo sapiens GN=RPS13 PE=1 SV=2	88.3	189.5	79.8	76.6	79.2	86.6
B4DT31: cDNA FLJ53425, highly similar to Far upstream element-binding protein 1 OS=Homo sapiens PE=2 SV=1	215.8	220.9	25	36.6	60.3	41.4
P62913: 60S ribosomal protein L11 OS=Homo sapiens GN=RPL11 PE=1 SV=2	76.9	63.1	117.6	121.1	116.6	104.7
Q9Y266: Nuclear migration protein nudC OS=Homo sapiens GN=NUDC PE=1 SV=1	164.5	147.5	48.6	52	88.1	99.4
B2R6F3: Splicing factor arginine/serine-rich 3 OS=Homo sapiens GN=SFRS3 PE=2 SV=1	71.5	114.5	95.2	155.6	99.2	63.9
Q5U5J2: CSNK2A1 protein OS=Homo sapiens GN=CSNK2A1 PE=1 SV=1	199.4	156.9	80.9		85.8	77
Q5HYG7: Putative uncharacterized protein DKFZp686M24262 OS=Homo sapiens GN=DKFZp686M24262 PE=2 SV=1	200.1	168.6	42.9	50.5	78.9	59.1
A0A024R056: Guanine nucleotide binding protein (G protein), beta polypeptide 1, isoform CRA_a OS=Homo sapiens GN=GNB1 PE=2 SV=1	173.7	129.8	47.4	52.1	127.6	69.3
B2R841: Serine/threonine-protein kinase PLK OS=Homo sapiens PE=2 SV=1	74.6	42.3	133.8	96.9	131.7	120.6
Q99497: Protein DJ-1 OS=Homo sapiens GN=PARK7 PE=1 SV=2	288.3	193.1		44.7	49.5	24.4
P34897: Serine hydroxymethyltransferase, mitochondrial OS=Homo sapiens GN=SHMT2 PE=1 SV=3	244.4	198.3	34.3		76.3	46.6
Q70IA6-3: Isoform 3 of MOB kinase activator 2 OS=Homo sapiens GN=MOB2	162.8	121.4	72.4	51.8	102.2	89.4
P06730-2: Isoform 2 of Eukaryotic translation initiation factor 4E OS=Homo sapiens GN=EIF4E	225	169.4	56.8	44.1	62.3	42.4
Q9Y5Q9: General transcription factor 3C polypeptide 3 OS=Homo sapiens GN=GTF3C3 PE=1 SV=1	56.7	59.8	134.7	124.3	124.5	99.9

B7Z4C8: 60S ribosomal protein L31 OS=Homo sapiens GN=RPL31 PE=1 SV=1	116.6	166.9	86.6	80.9	75	74
B2R4R9: HCG26477 OS=Homo sapiens GN=RPS28 PE=2 SV=1	172.7	153.3	69.6	99.8	45.9	58.7
Q9UBS4: DnaJ homolog subfamily B member 11 OS=Homo sapiens GN=DNAJB11 PE=1 SV=1	57.6	38.5	126	134.9	136.5	106.6
Q9UMS4: Pre-mRNA-processing factor 19 OS=Homo sapiens GN=PRPF19 PE=1 SV=1	175.4	122.9	74.9	67.4	93.4	66
A0A024R9Y7: Melanoma antigen family D, 2, isoform CRA_a OS=Homo sapiens GN=MAGED2 PE=4 SV=1	92.4	69.6	96.6	117.4	108.4	115.6
O95817: BAG family molecular chaperone regulator 3 OS=Homo sapiens GN=BAG3 PE=1 SV=3	19.1	16.7	152.3	150.1	111.4	150.4
Q53G26: DnaJ (Hsp40) homolog, subfamily A, member 3 variant (Fragment) OS=Homo sapiens GN=DNAJA3 PE=1 SV=1	27.7	29.1	128.4	117.1	162.7	134.9
P29966: Myristoylated alanine-rich C-kinase substrate OS=Homo sapiens GN=MARCKS PE=1 SV=4	261	197.3	35.2	36.1	44	26.4
P16949-2: Isoform 2 of Stathmin OS=Homo sapiens GN=STMN1	52.8	52.8	105.5	167	79.6	142.3
A0A024R6D8: Splicing factor, arginine/serine-rich 5, isoform CRA_a OS=Homo sapiens GN=SFRS5 PE=4 SV=1	123.4	87.9	117.2	84.3	94.5	92.7
P62805: Histone H4 OS=Homo sapiens GN=HIST1H4A PE=1 SV=2	183.1	115.6	86.6	41.3	89	84.4
P62314: Small nuclear ribonucleoprotein Sm D1 OS=Homo sapiens GN=SNRPD1 PE=1 SV=1	138.5	164.8	60	72.1	112.4	52.3
Q9Y277-2: Isoform 2 of Voltage-dependent anion-selective channel protein 3 OS=Homo sapiens GN=VDAC3	198.8	114.8	62.2	62.1	103.6	58.6
P46776: 60S ribosomal protein L27a OS=Homo sapiens GN=RPL27A PE=1 SV=2	17.2	141.5	128	123.9	80	109.4
B2RD14: Ubiquitin carboxyl-terminal hydrolase OS=Homo sapiens PE=2 SV=1	284.7	168.5	32.6	24.5	47.1	42.6
P18077: 60S ribosomal protein L35a OS=Homo sapiens GN=RPL35A PE=1 SV=2	148.9	139.2	95.9	62.2	87.7	66.2
P25788: Proteasome subunit alpha type-3 OS=Homo sapiens GN=PSMA3 PE=1 SV=2	168.4	166.8	67.8	57.9	79.2	59.9
P60866-2: Isoform 2 of 40S ribosomal protein S20 OS=Homo sapiens GN=RPS20	54.4	105.5	97.9	110.5	113	118.7
Q2NL82: Pre-rRNA-processing protein TSR1 homolog OS=Homo sapiens GN=TSR1 PE=1 SV=1	173.7	155.3	74.8	59.8	60.7	75.8
P07919: Cytochrome b-c1 complex subunit 6, mitochondrial OS=Homo sapiens GN=UQCRH PE=1 SV=2	23.2	27.3	139.5	189	90.9	130.1
Q9BUA3: Uncharacterized protein C11orf84 OS=Homo sapiens GN=C11orf84 PE=1 SV=3	194.6	147.1	58.1	49.1	65.3	85.7
P30837: Aldehyde dehydrogenase X, mitochondrial OS=Homo sapiens GN=ALDH1B1 PE=1 SV=3	183.8	205	47.5	35.5	83.9	44.3
A0A024R6D4: Enhancer of rudimentary homolog OS=Homo sapiens GN=ERH PE=3 SV=1	141	79.2	90.3	78.1	98.2	113.2
Q9Y3U8: 60S ribosomal protein L36 OS=Homo sapiens GN=RPL36 PE=1 SV=3	173.4	138.1	64.2	69.5	81.8	72.9
P84098: 60S ribosomal protein L19 OS=Homo sapiens GN=RPL19 PE=1 SV=1	95.8	110.9	102.2	91.5	65.3	134.4
Q8NCA5: Protein FAM98A OS=Homo sapiens GN=FAM98A PE=1 SV=1	29.1	28.3	145.7	208.6	63.6	124.6
O43290: U4/U6.U5 tri-snRNP-associated protein 1 OS=Homo sapiens GN=SART1 PE=1 SV=1	63.4	49.2	110.4	165.8	94.5	116.7
P62854: 40S ribosomal protein S26 OS=Homo sapiens GN=RPS26 PE=1 SV=3	148.9	174	73.6	65.7	79.4	58.4
D3DU92: RNA binding protein S1 OS=Homo sapiens GN=RNPS1 PE=1 SV=1	208.3	125.1	76.9	51.9	73.8	64.1
Q0VAB1: Translocase of inner mitochondrial membrane 50 homolog (S. cerevisiae) OS=Homo sapiens GN=TIMM50 PE=2 SV=1	147.5	100.3	117.4	59.4	121.9	53.6
P49721: Proteasome subunit beta type-2 OS=Homo sapiens GN=PSMB2 PE=1 SV=1	189.8	143	41.8	44.2	90.8	90.4
Q5JR05: Rho-related GTP-binding protein RhoC OS=Homo sapiens GN=RHOC PE=3 SV=1	279.3	197.2	27.5	35.3	60.7	
P08237-3: Isoform 3 of ATP-dependent 6-phosphofructokinase, muscle type OS=Homo sapiens GN=PFKM	83	62.5	102.7	96.8	139.6	115.4
P62304: Small nuclear ribonucleoprotein E OS=Homo sapiens GN=SNRPE PE=1 SV=1	174.1	161.8	50.3	45.6	88	80.2
O96019: Actin-like protein 6A OS=Homo sapiens GN=ACTL6A PE=1 SV=1	77.4	60	136.6	71.5	153.2	101.2

Q6AWA4: Putative uncharacterized protein DKFZp686O0870 (Fragment) OS=Homo sapiens GN=DKFZp686O0870 PE=2 SV=1	111.6	89.4	215.3	126.1	39.5	18.1
A0A0U1RQC9: Cellular tumor antigen p53 OS=Homo sapiens GN=TP53 PE=1 SV=1	89.4	76.7	117.4	98	136.5	82
O75400: Pre-mRNA-processing factor 40 homolog A OS=Homo sapiens GN=PRPF40A PE=1 SV=2	116.4	69.3	86.1	96.1	123.6	108.4
A8K3Y5: cDNA FLJ78186 OS=Homo sapiens PE=2 SV=1	143.4	86.8	123.9	87	65.3	93.6
Q13151: Heterogeneous nuclear ribonucleoprotein A0 OS=Homo sapiens GN=HNRNPA0 PE=1 SV=1	173.1	124.5	52.8	78.2	87.7	83.7
Q96PK6: RNA-binding protein 14 OS=Homo sapiens GN=RBM14 PE=1 SV=2	80.2	70.3	126	88.3	147.7	87.4
A8K4W2: cDNA FLJ78635, highly similar to Homo sapiens ATP synthase, H+ transporting, mitochondrial F0 complex, subunit b, isoform 1 (ATP5F1), transcript variant 1, mRNA OS=Homo sapiens PE=2 SV=1	114.2	89.3	102.4	89.2	118.1	86.8
A0A024R394: Cysteine and histidine-rich domain (CHORD)-containing 1, isoform CRA_c OS=Homo sapiens GN=CHORDC1 PE=4 SV=1	151	127.4	64.9	69.4	111	76.3
V9HWC9: Superoxide dismutase [Cu-Zn] OS=Homo sapiens GN=HEL-S-44 PE=2 SV=1	313.8	195.9	15	19.4	28.9	26.8
A0A024R3D8: Acetyltransferase component of pyruvate dehydrogenase complex OS=Homo sapiens GN=DLAT PE=3 SV=1	74.2	35.2	160.3	79	71.9	179.3
Q05DF2: SF3A2 protein (Fragment) OS=Homo sapiens GN=SF3A2 PE=2 SV=1	216	164.7	61.9	20.9	76.8	59.8
P52298: Nuclear cap-binding protein subunit 2 OS=Homo sapiens GN=NCBP2 PE=1 SV=1	175.5	128.9	75.2	47.6	97.2	75.6
P49756: RNA-binding protein 25 OS=Homo sapiens GN=RBM25 PE=1 SV=3	115.6	83.6	87.6	80.3	144.3	88.6
K7ELC7: 60S ribosomal protein L27 (Fragment) OS=Homo sapiens GN=RPL27 PE=1 SV=1	164.2	136.7	69	69	90.3	70.8
Q9ULX6: A-kinase anchor protein 8-like OS=Homo sapiens GN=AKAP8L PE=1 SV=3	63.8	40.7	126.9	124.1	136.2	108.3
Q99700: Ataxin-2 OS=Homo sapiens GN=ATXN2 PE=1 SV=2	59.4	74.7	142.2	131.3	93.7	98.8
Q6FG99: RPLP1 protein OS=Homo sapiens GN=RPLP1 PE=2 SV=1	147.1	125	103.5	74.6	83.1	66.6
A0A024R6W2: Nudix (Nucleoside diphosphate linked moiety X)-type motif 21, isoform CRA_a OS=Homo sapiens GN=NUDT21 PE=4 SV=1	204.1	147.3	61	44.5	77.5	65.6
C1PHA2: Tyrosine-protein kinase receptor OS=Homo sapiens GN=KIF5B-ALK PE=2 SV=1	153.7	151.1	60.2	39.7	107.1	88.2
A0A0A0MTS2: Glucose-6-phosphate isomerase (Fragment) OS=Homo sapiens GN=GPI PE=1 SV=1	288.8	236			39.7	35.5
D9IAI1: Epididymis secretory protein Li 34 OS=Homo sapiens GN=PEBP1 PE=2 SV=1	338.8	245.8			15.5	
B2R6A5: cDNA, FLJ92862, highly similar to Homo sapiens solute carrier family 16 (monocarboxylic acid transporters), member 1 (SLC16A1), mRNA OS=Homo sapiens PE=2 SV=1	69.6	59.3	128.3	130.3	107.1	105.3
Q13573: SNW domain-containing protein 1 OS=Homo sapiens GN=SNW1 PE=1 SV=1	95.6	76	100.1	103	126.9	98.5
P11802: Cyclin-dependent kinase 4 OS=Homo sapiens GN=CDK4 PE=1 SV=2	51	40.7	122.5	141.3	134.9	109.6
P05198: Eukaryotic translation initiation factor 2 subunit 1 OS=Homo sapiens GN=EIF2S1 PE=1 SV=3	183.3	144.2	80.3	35.7	86.3	70.1
A0A0D9SGE8: PHD finger protein 6 OS=Homo sapiens GN=PHF6 PE=1 SV=1	112	89.1	110.1	121.7	70.8	96.5
B4DR61: Protein transport protein Sec61 subunit alpha isoform 1 OS=Homo sapiens GN=SEC61A1 PE=1 SV=1	48.9	43.8	125.6	145.2	123	113.6
Q9UN37: Vacuolar protein sorting-associated protein 4A OS=Homo sapiens GN=VPS4A PE=1 SV=1	42.9	39.7	115.2	132.3	163.9	106
Q9Y6Y0: Influenza virus NS1A-binding protein OS=Homo sapiens GN=IVNS1ABP PE=1 SV=3	184.3	128.9	107.7	51.5	65.7	61.9
P49458: Signal recognition particle 9 kDa protein OS=Homo sapiens GN=SRP9 PE=1 SV=2	150.4	123.6	84.4	102.7	73.3	65.6
Q59GX7: Stearoyl-CoA desaturase variant (Fragment) OS=Homo sapiens PE=2 SV=1	81.1	67.3	108.8	109.5	122	111.3
X6RAL5: Histone deacetylase complex subunit SAP18 OS=Homo sapiens GN=SAP18 PE=1 SV=1	215.4	130.2	76.2	35.1	79	64.1
E7ESZ7: NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10, mitochondrial OS=Homo sapiens GN=NDUFA10 PE=1 SV=1	117.8	82.3	99.8	82.2	127.3	90.5

A8K1K8: Chromosome 18 open reading frame 55, isoform CRA_b OS=Homo sapiens GN=C18orf55 PE=2 SV=1	31.7	15.9	156.3	116.5	131.5	148.1
B2R4V2: cDNA, FLJ92227, highly similar to Homo sapiens ribosomal protein L36a-like (RPL36AL), mRNA OS=Homo sapiens PE=2 SV=1	90.9	136.7	96.3	90.5	101.1	84.4
A0A024RCT9: High mobility group AT-hook 1, isoform CRA_b OS=Homo sapiens GN=HMGA1 PE=4 SV=1	184.7	115.3	71.4	98.3	58.4	71.9
O00483: Cytochrome c oxidase subunit NDUFA4 OS=Homo sapiens GN=NDUFA4 PE=1 SV=1	50.3	39.7	116	121.5	146.1	126.4
Q9NYK5-2: Isoform 2 of 39S ribosomal protein L39, mitochondrial OS=Homo sapiens GN=MRPL39	111.5	84.2	112.6	127	66.3	98.4
Q9BWJ5: Splicing factor 3B subunit 5 OS=Homo sapiens GN=SF3B5 PE=1 SV=1	161.6	108.4	88.2	91.2	76.8	73.7
Q5SRD1: Putative mitochondrial import inner membrane translocase subunit Tim23B OS=Homo sapiens GN=TIMM23B PE=5 SV=2	75.7	55.8	60.1	143.1	151	114.2
Q6P1L8: 39S ribosomal protein L14, mitochondrial OS=Homo sapiens GN=MRPL14 PE=1 SV=1	58.7	41.1	134.5	79.1	148	138.6
B4DPP6: cDNA FLJ54371, highly similar to Serum albumin OS=Homo sapiens PE=2 SV=1	44.8	30.2	137.8	184.4	94.5	108.3
A0A024R8P8: Ribosomal protein L38, isoform CRA_a OS=Homo sapiens GN=RPL38 PE=3 SV=1	44	35.5	150.2	117.8	110.7	141.8
Q0KKI6: Immunoblobulin light chain (Fragment) OS=Homo sapiens PE=1 SV=1	4.4	3.3	164.3	173.9	100.6	153.4
Q6IB11: PGRMC1 protein OS=Homo sapiens GN=PGRMC1 PE=2 SV=1	214.2	140.3	71.3	42.8	82.1	49.2
B3KSQ1: cDNA FLJ36768 fis, clone ADIPS1000064, highly similar to Synaptic glycoprotein SC2 OS=Homo sapiens PE=2 SV=1	52.7	49.3	135.6	136.3	101.8	124.3
P62318: Small nuclear ribonucleoprotein Sm D3 OS=Homo sapiens GN=SNRPD3 PE=1 SV=1	175.2	152.9	54.7	48.2	113.9	55
Q13642-4: Isoform 4 of Four and a half LIM domains protein 1 OS=Homo sapiens GN=FHL1	163	179.9	57.9	78.4	77.5	43.3
Q96HS1: Serine/threonine-protein phosphatase PGAM5, mitochondrial OS=Homo sapiens GN=PGAM5 PE=1 SV=2	73.4	58.4	129.5	85.7	143	109.9
Q5VV89: Microsomal glutathione S-transferase 3 OS=Homo sapiens GN=MGST3 PE=1 SV=1	44.1	37.8	128.7	148.5	93.5	147.5
A0A024R608: Ribosomal protein, large, P1, isoform CRA_a OS=Homo sapiens GN=RPLP1 PE=3 SV=1	146.2	102.8	103.4	77.3	83.5	86.8
Q6IPI1: 60S ribosomal protein L29 OS=Homo sapiens GN=RPL29 PE=2 SV=1	153.7	113.9	91.7	76.2	78.4	86.1
B2RDQ3: cDNA, FLJ96718, highly similar to Homo sapiens splicing factor, arginine/serine-rich 10 (transformer 2 homolog, Drosophila) (SFRS10), mRNA OS=Homo sapiens PE=2 SV=1	176.1	113.3	80.4	70.1	83.5	76.4
A0A0J9YX62: DnaJ homolog subfamily B member 6 OS=Homo sapiens GN=DNAJB6 PE=1 SV=1	43	34.7	142.6	146.1	126.5	107.1
A0A1W2PNV4: Uncharacterized protein OS=Homo sapiens PE=4 SV=1	159.5	120.1	97.9	64.8	87	70.6
P52294: Importin subunit alpha-5 OS=Homo sapiens GN=KPNA1 PE=1 SV=3	129	113.3	62.5	72.3	119.2	103.7
Q9BY44: Eukaryotic translation initiation factor 2A OS=Homo sapiens GN=EIF2A PE=1 SV=3	142	135.8	80.9	61.3	96.5	83.5
C9IZQ1: Translocon-associated protein subunit alpha OS=Homo sapiens GN=SSR1 PE=1 SV=1	90.8	56.9	115.1	126.4	113.8	97
Q9Y3D3: 28S ribosomal protein S16, mitochondrial OS=Homo sapiens GN=MRPS16 PE=1 SV=1	120.1	66.7	132.6	66.6	102.1	111.8
A0A024R866: Ribosomal protein L35, isoform CRA_a OS=Homo sapiens GN=RPL35 PE=3 SV=1	37.2	290.1	72.3	44.6	78.6	77.3
Q05519: Serine/arginine-rich splicing factor 11 OS=Homo sapiens GN=SRSF11 PE=1 SV=1	233.4	159.4	33.1	38.6	76.9	58.6
A8MU27: Small ubiquitin-related modifier 3 OS=Homo sapiens GN=SUMO3 PE=1 SV=1	288.4	200.2	31.7	29.8	49.9	
F8W727: 60S ribosomal protein L32 OS=Homo sapiens GN=RPL32 PE=1 SV=1		233.9	94.8	70.1	121.5	79.6
Q14978-2: Isoform Beta of Nucleolar and coiled-body phosphoprotein 1 OS=Homo sapiens GN=NOLC1	212.8	149.1	54.4	61.9	62.9	58.8
Q96GC5: 39S ribosomal protein L48, mitochondrial OS=Homo sapiens GN=MRPL48 PE=1 SV=2	163.2	129.8	65.3	51	83.8	106.9
Q13185: Chromobox protein homolog 3 OS=Homo sapiens GN=CBX3 PE=1 SV=4	126.3	96.9	94.4	92.8	93.3	96.2

A0A024R3W2: Translocase of outer mitochondrial membrane 20 homolog (Yeast), isoform CRA_a OS=Homo sapiens GN=TOMM20 PE=3 SV=1	78.3	51.6	101.3	125.3	125.2	118.4
Q709F0: Acyl-CoA dehydrogenase family member 11 OS=Homo sapiens GN=ACAD11 PE=1 SV=2	179.7	160	72.6	44.1	79.5	64.1
O75381: Peroxisomal membrane protein PEX14 OS=Homo sapiens GN=PEX14 PE=1 SV=1	64.7	44.2	121.6	115.2	134.9	119.3
V9HW09: Epididymis secretory sperm binding protein Li 91n OS=Homo sapiens GN=HEL-S-91n PE=2 SV=1	179.5	124.7	104.3	43.9	101.6	45.9
Q9UDW1: Cytochrome b-c1 complex subunit 9 OS=Homo sapiens GN=UQCR10 PE=1 SV=3	63.4	43.7	120.7	118.4	158.3	95.5
P82912: 28S ribosomal protein S11, mitochondrial OS=Homo sapiens GN=MRPS11 PE=1 SV=2	88.1	72.2	97.2	115.6	120.3	106.7
Q9Y5V3-2: Isoform 2 of Melanoma-associated antigen D1 OS=Homo sapiens GN=MAGED1	209.1	146.1	54.1	51.7	86.1	52.9
K7EM18: Eukaryotic translation initiation factor 1 OS=Homo sapiens GN=EIF1 PE=1 SV=1	309.5	244.1	24.2		22.2	
Q92522: Histone H1x OS=Homo sapiens GN=H1FX PE=1 SV=1	245.3	180.4	37.8	29.8	65.7	41
Q13330: Metastasis-associated protein MTA1 OS=Homo sapiens GN=MTA1 PE=1 SV=2	133.7	93	93.2	66.3	95.5	118.4
P00387-3: Isoform 3 of NADH-cytochrome b5 reductase 3 OS=Homo sapiens GN=CYB5R3	281.3	229.3			62	27.4
H7BY58: Protein-L-isoaspartate O-methyltransferase OS=Homo sapiens GN=PCMT1 PE=1 SV=1	149.7	122	94.3	55.8	91.3	86.8
A0A024RD03: Mitochondrial ribosomal protein S10, isoform CRA_a OS=Homo sapiens GN=MRPS10 PE=4 SV=1	119.5	97.1	109.8	80.4	113.9	79.3
P59998-3: Isoform 3 of Actin-related protein 2/3 complex subunit 4 OS=Homo sapiens GN=ARPC4	204.9	136.5	54.8	73.8	90.6	39.4
A8MWD9: Putative small nuclear ribonucleoprotein G-like protein 15 OS=Homo sapiens GN=SNRPGP15 PE=5 SV=2	166.1	161.2	74.5	53.9	82.4	61.8
E9PR30: 40S ribosomal protein S30 OS=Homo sapiens GN=FAU PE=1 SV=1		294.3	85.9	79.6	73.5	66.8
P60468: Protein transport protein Sec61 subunit beta OS=Homo sapiens GN=SEC61B PE=1 SV=2	71	55	107.8	124.2	144	98
A0A0S2Z404: Regulator of chromosome condensation 1 isoform 2 (Fragment) OS=Homo sapiens GN=RCC1 PE=2 SV=1	170.1	139.6	67.1	32.2	93.3	97.7
P61513: 60S ribosomal protein L37a OS=Homo sapiens GN=RPL37A PE=1 SV=2	212.6	154.1	62.6	17.2	94.7	58.8
B7Z8Q2: cDNA FLJ55606, highly similar to Alpha-2-HS-glycoprotein OS=Homo sapiens PE=2 SV=1	59.8	31.4	118.6	183.9	70.4	135.8
A0A024R3R5: Lamin B receptor, isoform CRA_a OS=Homo sapiens GN=LBR PE=4 SV=1	112.3	83.6	100.9	75.4	137.9	89.9
Q8WWC4: m-AAA protease-interacting protein 1, mitochondrial OS=Homo sapiens GN=MAIP1 PE=1 SV=1	52.5	43.6	124.9	126.8	153.7	98.5
Q6P2E9: Enhancer of mRNA-decapping protein 4 OS=Homo sapiens GN=EDC4 PE=1 SV=1	33	43.2	203.6	114.2	103.1	102.9
A0A0S2Z5M1: SEC63-like (S. cerevisiae) (Fragment) OS=Homo sapiens GN=SEC63 PE=2 SV=1	171.6	129.2	73.7	60.8	96.2	68.5
A0MNN4: CDW3/SMU1 OS=Homo sapiens GN=SMU1 PE=2 SV=1	210.9	120.3	81	39.4	73	75.4
O75937: DnaJ homolog subfamily C member 8 OS=Homo sapiens GN=DNAJC8 PE=1 SV=2	46.3	50.4	130.1	187	48.3	137.8
A8K6G9: cDNA FLJ76871, highly similar to Homo sapiens DEAH (Asp-Glu-Ala-His) box polypeptide 38 (DHX38), mRNA OS=Homo sapiens PE=2 SV=1	51.8	48.4	173	129.8	60.2	136.9
O75934: Pre-mRNA-splicing factor SPF27 OS=Homo sapiens GN=BCAS2 PE=1 SV=1	163.2	116.2	73.7	86.9	79.4	80.6
E7ER45: Maltase-glucoamylase, intestinal OS=Homo sapiens GN=MGAM PE=1 SV=2	15.6	23	98.2	266.6	75	121.7
P14174: Macrophage migration inhibitory factor OS=Homo sapiens GN=MIF PE=1 SV=4	277.7	203.2	23.6	24.9	45.2	25.4
O95073: Fibrinogen silencer-binding protein OS=Homo sapiens GN=FSBP PE=1 SV=1	160.5	119.5	94.4	37.9	125.7	62.1
Q6FGH5: RPS21 protein (Fragment) OS=Homo sapiens GN=RPS21 PE=2 SV=1	225.3	186.4	28.4	55.9	48.2	55.8
M0R1Y2: ER lumen protein-retaining receptor 1 (Fragment) OS=Homo sapiens GN=KDELR1 PE=1 SV=1	86.1	77.1	111.9	95	129.4	100.5
Q5SNV9-2: Isoform 2 of Uncharacterized protein C1orf167 OS=Homo sapiens GN=C1orf167	171.2	138.9	72.1	56.4	87.8	73.6
Q9BRL6: Serine/arginine-rich splicing factor 8 OS=Homo sapiens GN=SRSF8 PE=1 SV=1	119.5	95.7	120.6	105	65.6	93.7

B2RE40: cDNA, FLJ96911, highly similar to Homo sapiens nucleosomal binding protein 1 (NSBP1), mRNA OS=Homo sapiens PE=2 SV=1	215	151.5	57.1	41.1	72.6	62.7
A0A087X117: Nodal modulator 1 OS=Homo sapiens GN=NOMO1 PE=1 SV=1	88.5	67	99.6	112.4	135.3	97.3
Q9H2W6: 39S ribosomal protein L46, mitochondrial OS=Homo sapiens GN=MRPL46 PE=1 SV=1	164	130.2	92	40.2	90.3	83.3
A0A024RBF6: HCG26523, isoform CRA_a OS=Homo sapiens GN=hCG_26523 PE=4 SV=1	175.1	121.4	92.4	53.1	81.6	76.3
Q68DQ2: Very large A-kinase anchor protein OS=Homo sapiens GN=CRYBG3 PE=1 SV=3			103.2	182.1	153.5	161.2
C9JJ19: 28S ribosomal protein S34, mitochondrial OS=Homo sapiens GN=MRPS34 PE=1 SV=2	126.4	116.1	76.8	65.6	138.8	76.3
P56381: ATP synthase subunit epsilon, mitochondrial OS=Homo sapiens GN=ATP5E PE=1 SV=2	102.6	83.8	111.8	85.4	120.7	95.7

REFERENCES

[1] Okondo, M. C., Johnson, D. C., Sridharan, R., Go, E. B., Chui, A. J., Wang, M. S., Poplawski, S. E., Wu, W., Liu, Y., Lai, J. H., Sanford, D. G., Arciprete, M. O., Golub, T. R., Bachovchin, W. W., and Bachovchin, D. A. (2017) DPP8 and DPP9 inhibition induces pro-caspase-1-dependent monocyte and macrophage pyroptosis, *Nat. Chem. Biol. 13*, 46-53.

[2] Johnson, D. C., Taabazuing, C. Y., Okondo, M. C., Chui, A. J., Rao, S. D., Brown, F. C., Reed, C., Peguero, E., de Stanchina, E., Kentsis, A., and Bachovchin, D. A. (2018) DPP8/DPP9 inhibitor-induced pyroptosis for treatment of acute myeloid leukemia, *Nat. Med. 24*, 1151-1156.

[3] Okondo, M. C., Rao, S. D., Taabazuing, C. Y., Chui, A. J., Poplawski, S. E., Johnson, D. C., and Bachovchin, D. A. (2018) Inhibition of Dpp8/9 Activates the Nlrp1b Inflammasome, *Cell Chem Biol 25*, 262-267 e265.

[4] Bachovchin, D. A., Koblan, L. W., Wu, W., Liu, Y., Li, Y., Zhao, P., Woznica, I., Shu, Y., Lai, J. H., Poplawski, S. E., Kiritsy, C. P., Healey, S. E., DiMare, M., Sanford, D. G., Munford, R. S., Bachovchin, W. W., and Golub, T. R. (2014) A high-throughput, multiplexed assay for superfamily-wide profiling of enzyme activity, *Nat. Chem. Biol. 10*, 656-663.

[5] Chui, A. J., Okondo, M. C., Rao, S. D., Gai, K., Griswold, A. R., Johnson, D. C., Ball, D. P., Taabazuing, C. Y., Orth, E. L., Vittimberga, B. A., and Bachovchin, D. A. (2019) N-terminal degradation activates the NLRP1B inflammasome, *Science 364*, 82-85.

[6] Perez-Riverol, Y., Csordas, A., Bai, J., Bernal-Llinares, M., Hewapathirana, S., Kundu, D. J., Inuganti, A., Griss, J., Mayer, G., Eisenacher, M., Perez, E., Uszkoreit, J., Pfeuffer, J., Sachsenberg, T., Yilmaz, S., Tiwary, S., Cox, J., Audain, E., Walzer, M., Jarnuczak, A. F., Ternent, T., Brazma, A., and Vizcaino, J. A. (2019) The PRIDE database and related tools and resources in 2019: improving support for quantification data, *Nucleic Acids Res. 47*, D442-D450.

[7] Tully, S. E., and Cravatt, B. F. (2010) Activity-based probes that target functional subclasses of phospholipases in proteomes, *J Am Chem Soc 132*, 3264-3265.