Electronic Supplementary Material (ESI) for Chemical Communications.

Supporting information

A cell-permeable Ub-Dha probe for profiling E1-E2-E3 enzymes in live cells

Qiong Xia‡[a], Xianbin Meng‡[b], Yu Wang*[a], Rujing Yuan[a], Pincheng Li[a], Liwen Liu[a] and Yi-Ming Li*[a]

a. *School of Food and Biological Engineering, Engineering Research Center of Bio-process, Ministry of Education, Hefei University of Technology, Hefei 230009, China.*

b. *MOE Key Laboratory of Bioinformatics, School of Life Sciences, Tsinghua University, Beijing, 100084, China*

Email: ymli@hfut.edu.cn; wangyuch@mail.ustc.edu.cn

List of contents

1. General information

a. Materials

All reagents were used directly from commercial suppliers was essentially as described[1,2]. 2-Cl-(Trt)-Cl resin was purchased from Tianjin Nankai HECHENG S&T Co., Ltd (Tianjing, China). Fmoc-amino acids were purchased from GL Biochem (Shanghai, China). tris (2-carboxyethyl) phosphine (TCEP) and guanidine hydrochloride (Gn-HCl) were purchased from Adamas-beta (Shanghai, China). 5, 5'-dithion-bis-2-nitrbenzoic acid (DTNB), 4-Dimethylaminoazobenzene-4'-carboxylic acid (DABCYL), Rhodamine B (RhoB) were purchased from J&K Scientific (Beijing). NH_2NH_2-HCl and 2-Mercaptoethanol were purchased from Energy Chemical. Acetonitrile (CH_3CN, HPLC grade), trifluoroacetic acid (TFA, HPLC grade) and phenylsilane were purchased from J. T. Baker. O-methylhydroxylamine, α, α-di-bromo-adipyl(bis)amide and Acetylacetone were purchased from Sinopharm Chemical Reagent Co. Ltd.

b. RP-HPLC, FPLC and LC-MSMS

SHIMADZU Prominence HPLC (LC-20AT with SPD-20A) was used for analysis and purification. Analytical Welch XB-C18 column (4.6 × 250 mm, 5 μm, 120 Å, 1.0 mL/min) was used for analysis. Semi-preparative Welch XB-C18 (250 ×10 mm, 5 μm, 120 Å, flow rate 4.0 ml/min.) was used for purification. Analysis and purification were monitored at 214 and 254 nm. For RP-HPLC, buffer A contained 0.08% TFA in CH_3CN and buffer B contained 0.1% TFA in H_2O.

ESI mass spectrometry (ESI-MS) was performed using LC/MS-2020 system (Shimadzu). The Time of Flight Mass Spectrometer (Agilent 6210) was used for high resolution ESI-MS measurements.

c. SDS-PAGE, Immunoblotting and Antibodies

For SDS-PAGE analysis, protein samples were loaded onto a 4-20% gradient gel in Tris-MES buffer. Electrophoresis was performed at 90 V for 5 min and then at 120 V for 60 min. All proteins gel images were captured on ChemDocXRS+ (Bio-Rad). For immunoblotting analysis, protein samples were transferred to polyvinylidene fluoride membrane (PVDF, Bio-Rad) at 300 mA for 90 min. 3% (m/v) BSA solution was added to TBS buffer (20 mM Tris-HCl, 137 mM NaCl, pH 7.6) and incubated with PVDF at 37°C for 3 hours. Anti-biotin antibody or anti-Ubch7 antibody in TBS buffer was then incubated with PVDF at 37 °C for 2 h. PVDF was washed twice with TBST (20 mM Tris-HCl, 137 mM NaCl, 0.1% Tween-20, pH 7.6), then goat anti-rabbit IgG coupled with horseradish peroxidase (HRP) was added and incubated at 37°C for 2 hours. Protein detection was performed using chemiluminescent solution (ECL, Sangon Biotech).

Anti-Biotin antibody (ab1227) and Anti-Ubch7 (ab108936) were purchased from Abcam. The secondary goat anti rabbit IgG (HRP) antibody (D111018) was purchased from Sangon Biotech.

2. Supplementary chemically synthesized methods

a. General procedure for solid phase peptide synthesis

Preparation of 2-Cl-(Trt)-NHNH2 resin

0.595 g (0.25 mmol) of 2-Cl-(Trt)-Cl resin (0.42 mmol/g) was swelled with DMF for 30min. 10 ml of 5% (v/v) hydrazinium hydroxide solution was added to the resin and reacted at 37 °C for 30 min and repeated once. Then 10 ml of 5% (v/v) MeOH solution was added to the resin and reacted at 35 °C for 10 min and repeated once. The resin could be used directly for the next coupling step. Notably, the 2-Cl-(Trt)-$NHNH_2$ resin should be prepared before use due to its instability.

The protocol for Fmoc-based solid-phase peptide synthesis was essentially as described (The details for chemical protein synthesis were described in Page 4 in SI)[1]. It should be noted that we used two dipeptide analogues (pseudoproline dipeptide Leu56-Ser57 and dimethoxybenzyl Asp52-Gly53) to improve the synthesis efficiency. Peptides were cleaved from the support for 3 hours in a standard cleavage TFA cocktail (TFA: phenol: H_2O: thioanisole: 1,2-ethanedithiol EDT= 82.5:5:5:5:2.5, 2-3 mL per 100 mg resin). Remove the TFA and add ice ether to give crude peptide.

b. General steps of cR10-S-S-Ub (1-75)-C

The **12** was synthesized using hydrazine-loaded 2-Cl trityl resin by microwave-assisted peptide synthesis. cR10-S-S-TNB (5 eq.) was dissolved in 300 µl ligation buffer (6 M Gn-HCl, 0.2 M Na_2HPO_4, pH 7), and 700 µl **12** (1 mmol, dissolved in ligation buffer, 1 eq.) was slowly added to the above reaction. The pH was then adjusted to 7 and stirred at 37 ºC for 2 hours. The reaction was separated by semi-preparative HPLC (C18 column) using a gradient of 20-70% B over 40 min to give **13**. And then, 1 mg **13** (1 µmol, 1 eq.) was dissolved in 150 µl ligation buffer (6 M Gn-HCl, 0.2 M NaH_2PO_4, pH 3.0) and cooled to -15 °C. Then, 1.4 µl of 0.5 M $NaNO_2$ (7 eq.) was added to the reaction and was stirred at -15 °C for 20 min to convert the peptide hydrazide to acyl azide. Then, 10 eq. Cys was dissolved in 10 µl buffer (6 M Gn-HCl, 0.2 M Na2HPO4, pH 7.0), the pH was adjusted to to 8.0, and stirred at room temperature for 30 min. The reaction was analyzed by analytical HPLC (C4 column) using a 20-70% gradient B over 30 min.

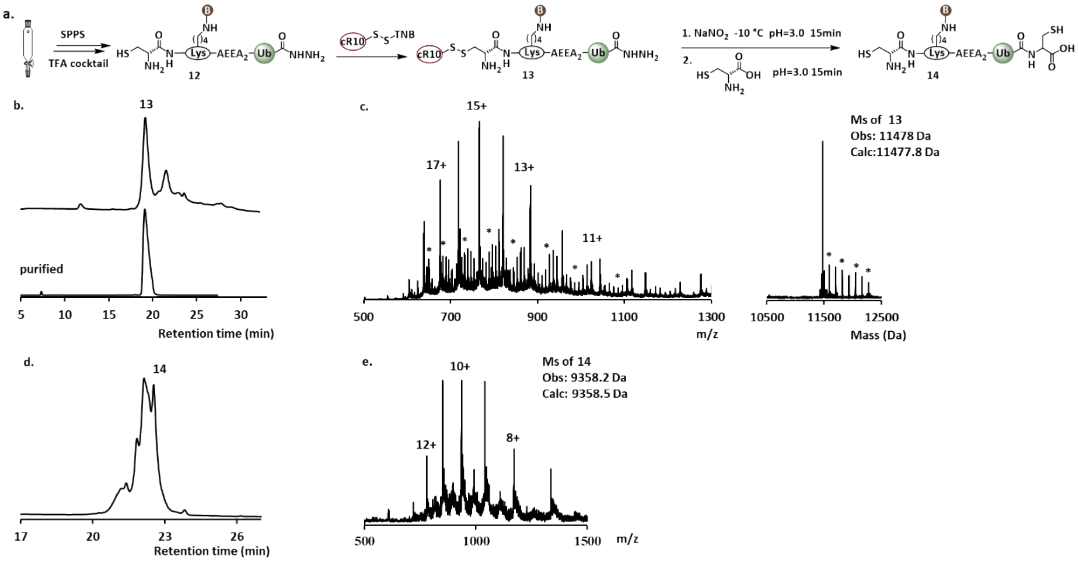

Figure S1. (a) Chemical synthesis of **cR10-UB (1-75)-C.** (b) Analytical HPLC chromatogram (λ=214 nm) of crude and purified **13**. (c) Analytical HPLC chromatogram (λ=214 nm) of purified and deconvoluted mass of **13**. '*' represents TFA adducts. (d) Analytical HPLC chromatogram (λ=214 nm) of 14. The molecular weight of peak 2 was 2212 Da lower than the theoretical value (Figure S1e), which demonstrated that the removal of cR10 from the N-terminus of cR10-Ub.

c. General steps of C-terminal peptide hydrazides

C-terminal peptide hydrazide (100 mg) was dissolved in ligation buffer (6 M Gn-HCl, 0.2 M Na_2HPO_4, pH 2.3), acetyl acetone (10 eq.) was added and the pH was adjusted to 2.3, stirred at room temperature for 3 hours. Then 2-mercaptoethanol (100 eq.) and TCEP (5 mg/ml) were added to the reaction and the pH adjusted to 8.1, stirred at room temperature for 3 hours. The reaction was separated by semi-preparative HPLC (C18 column) using a gradient of 20-70% B over 40 min (Figure 1a, 1c.).

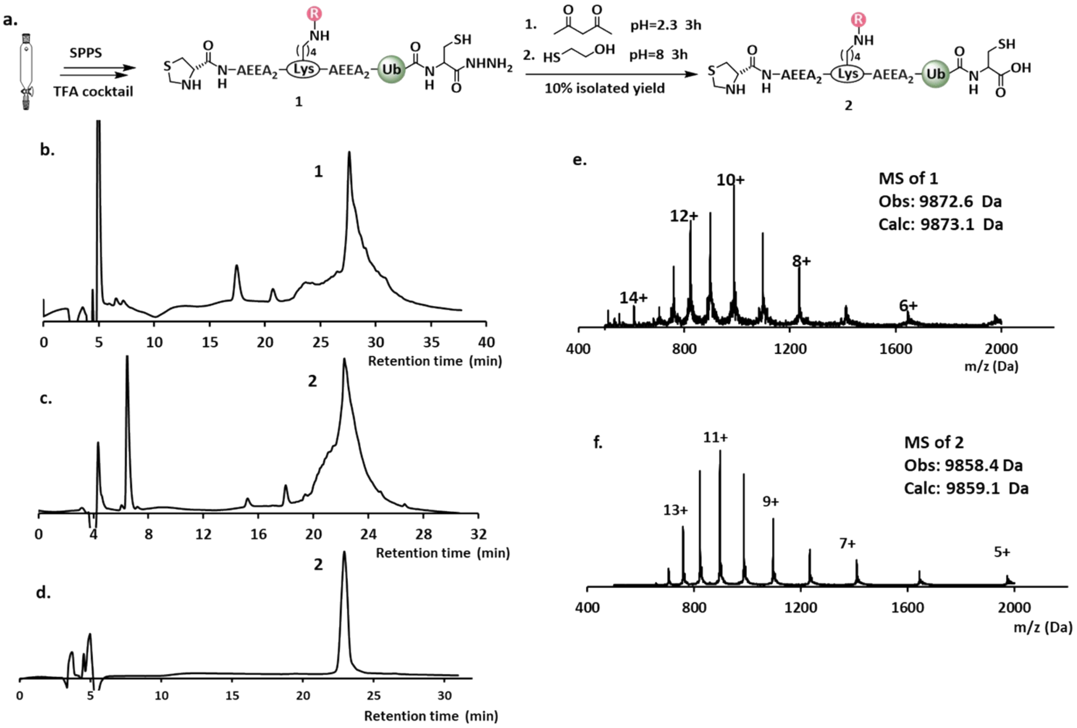

Figure S2. Chemical synthesis of peptide **2**. (a) Synthetic route for **2**. (b) Analytical HPLC chromatogram (λ=214 nm) of crude peptide **1.** (c) Analytical HPLC chromatogram (λ=214 nm) of crude peptide **2.** (d) Analytical HPLC chromatogram (λ=214 nm) of purified peptide **2.** (e) ESI-MS analysis of peptide **1.** (f) ESI-MS analysis of peptide **2.**

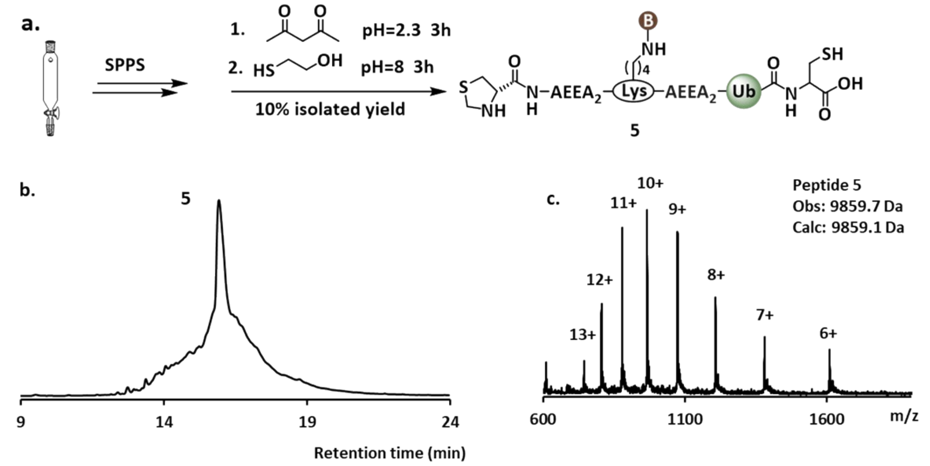

Figure S3. Chemical synthesis of peptide **5**. (a) Synthetic route for **5**. (b) Analytical HPLC chromatogram (λ=214 nm) of crude peptide **5.** (c) ESI-MS analysis of peptide **5.**

d. General steps of convert Cys to DHA

The protocol for conversion of convert Cys to DHA was essentially as described[1]. Briefly, the peptide **2** or **5** (1 mmol, 1 eq.) was dissolved in 1 ml ligation buffer (6 M Gn-HCl, 0.1 M Na_2HPO_4, pH 9). 15.3 mg α, α"-di-bromo-adipyl(bis)amide (50 eq.) was dissolved in 20 µl DMF and the pH was adjusted to 8.5, stirred at 37 ºC for 2 hours. The reaction was separated by semi-preparative HPLC (C18 column) using a gradient of 20-70% B over 40 min.

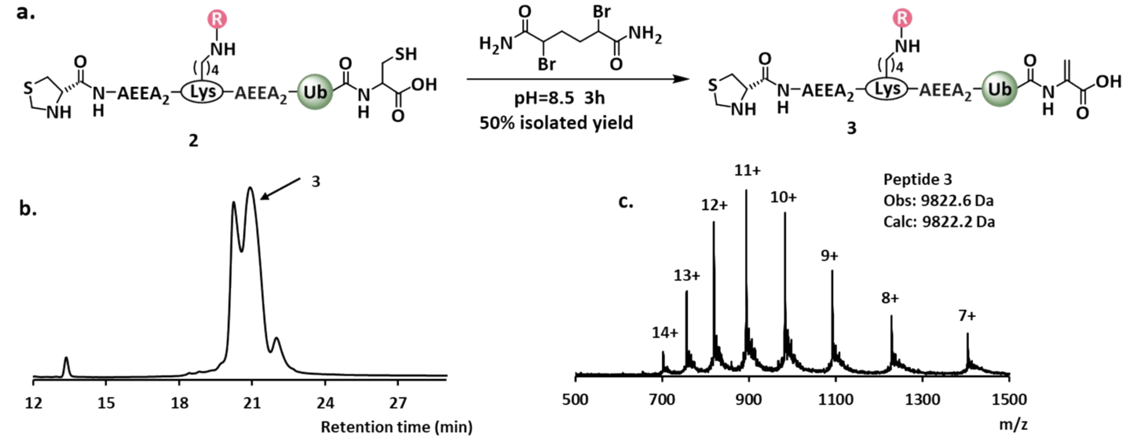

Figure S4. Chemical synthesis of peptide **3**. (a) Synthetic route for **3**. (b) Analytical HPLC chromatogram (λ=214 nm) of crude peptide **3.** (c)ESI-MS analysis of peptide **3.**

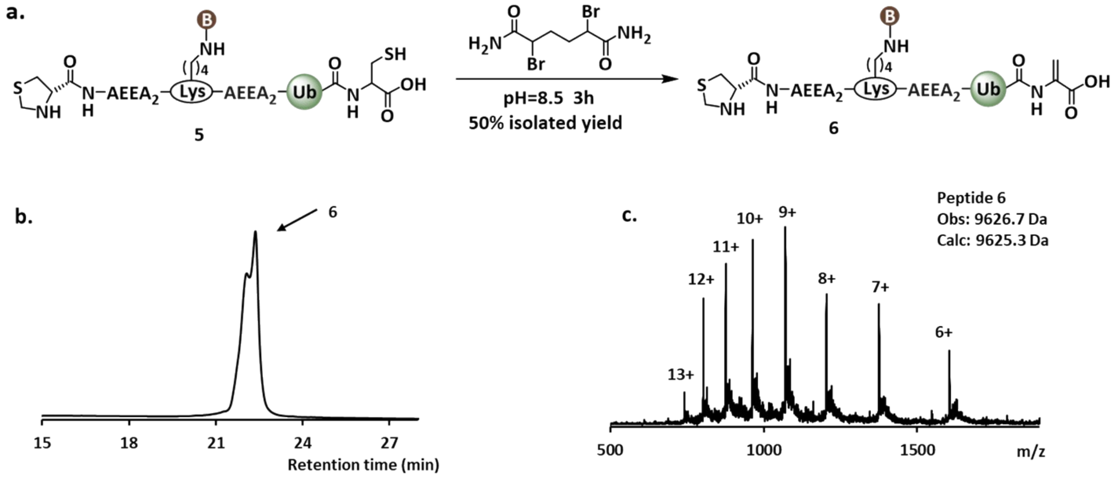

Figure S5. Chemical synthesis of peptide **6**. (a) Synthetic route for **6**. (b) Analytical HPLC chromatogram (λ=214 nm) of crude peptide **6.** (c)ESI-MS analysis of peptide **6.**

e. General steps of convert THZ to Cys

Briefly, the peptide **3** or **6** (1 mmol, 1 eq.) was dissolved in 1 ml buffer (6 M Gn-HCl, 0.2 M Na_2HPO_4, 0.2 M $MeONH_2$, pH 7), pH adjusted to 3.8 and stirred at 37 ºC for 2 hours. The reaction was separated by semi-preparative HPLC (C18 column) using a 20-70% gradient B over 40 min.

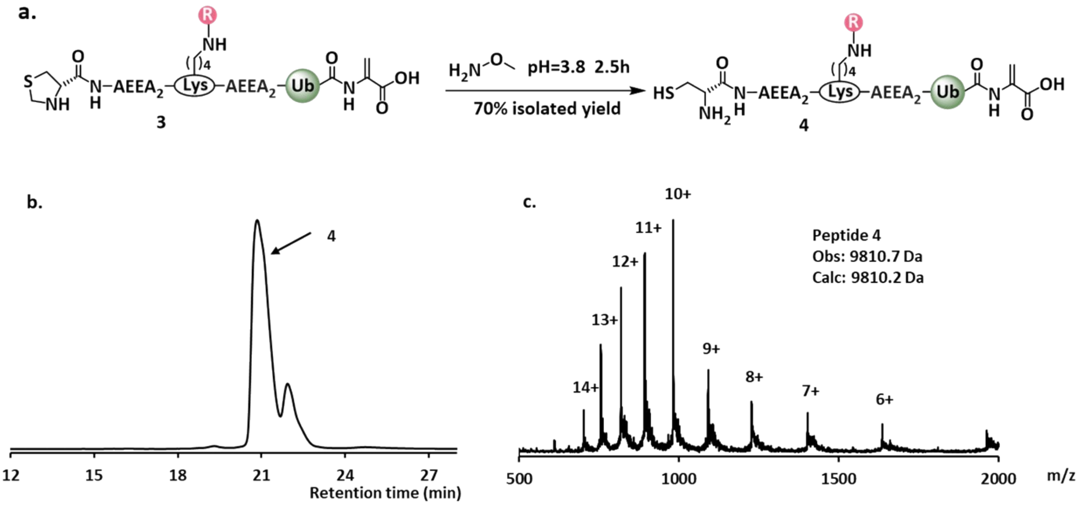

Figure S6. Chemical synthesis of peptide **4**. (a) Synthetic route for **4**. (b) Analytical HPLC chromatogram (λ=214 nm) of crude peptide **4.** (c) ESI-MS analysis of peptide **4.**

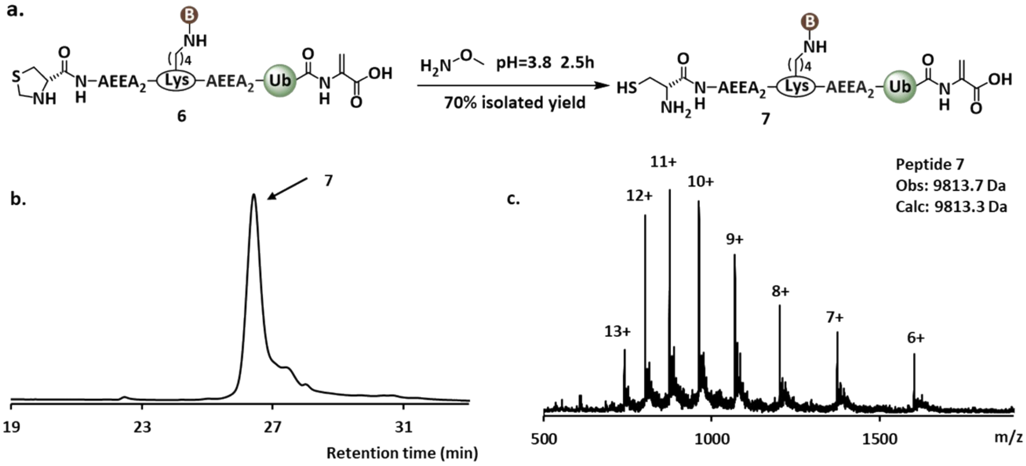

Figure S7. Chemical synthesis of peptide **7**. (a) Synthetic route for **7**. (b) Analytical HPLC chromatogram (λ=214 nm) of crude peptide **7.** (c) ESI-MS analysis of peptide **7.**

f. General steps of cR10-S-S-TNB or cR10D-S-S-TNB

The details for the preparation of cR10-S-S-TNB and cR10D-S-S-TNB were described in the Angew. Chem. Int. Ed. 2021, 60, 7333– 7343[3].

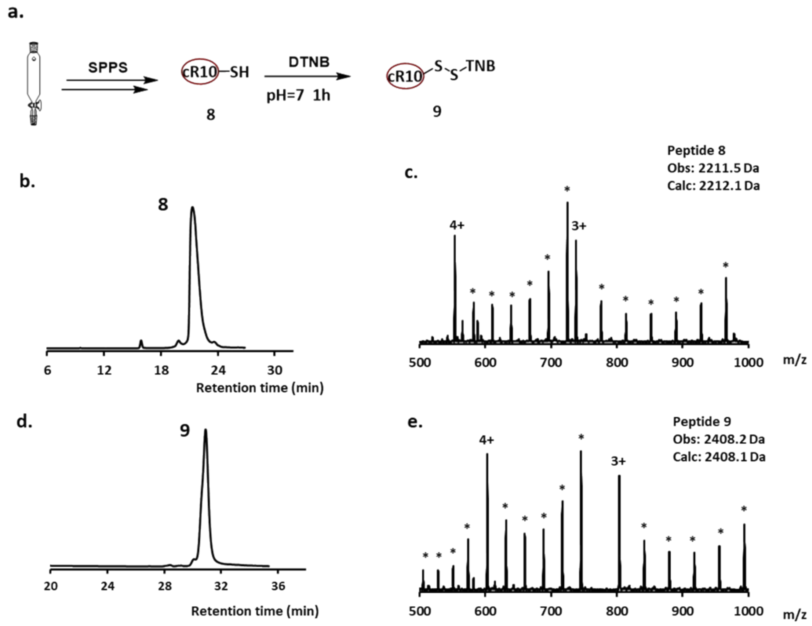

Figure S8. Chemical synthesis of peptide **9 (cR10-S-S-TNB)**. (a) Synthetic route for **9**. (b) Analytical HPLC chromatogram (λ=214 nm) of crude peptide **9.** (c) ESI-MS analysis of peptide **9.** (d) Analytical HPLC chromatogram (λ=214 nm) of crude peptide **9.** (e) ESI-MS analysis of peptide **7.** '*' represents TFA adducts.

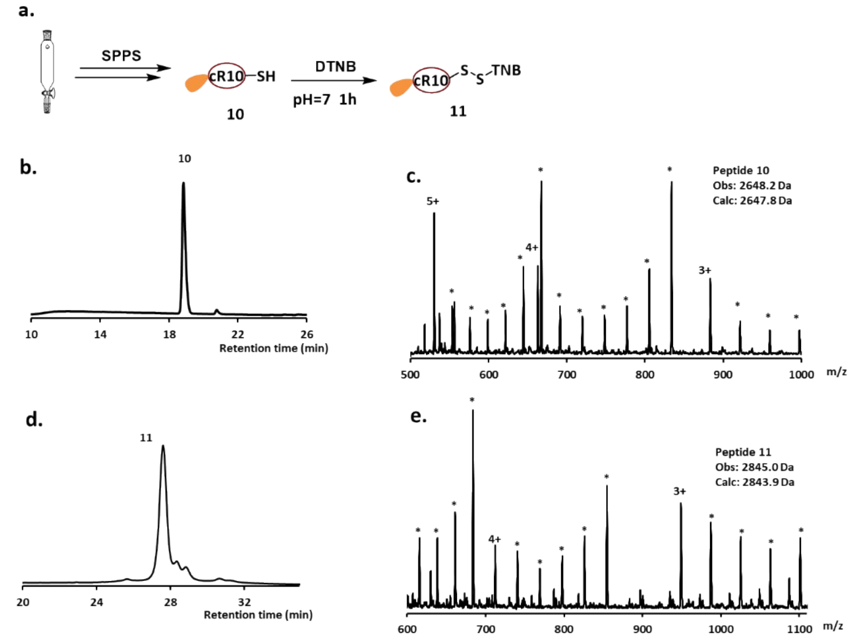

Figure S9. Chemical synthesis of peptide **11 (cR10D-S-S-TNB)**. (a) Synthetic route for **11**. (b) Analytical HPLC chromatogram (λ=214 nm) of crude peptide **11.** (c) ESI-MS analysis of peptide **6.** (d) Analytical HPLC chromatogram (λ=214 nm) of crude peptide **11.** (e) ESI-MS analysis of peptide **7.** '*' represents TFA adducts.

g. Synthesis of cR10D-S-S-K(Rhob)-Ub-(1-75)-Dha (probe 1)

The synthesis protocol was as described the above. Briefly, **11** (5 eq.) was dissolved in 300 µl ligation buffer (6 M Gn-HCl, 0.2 M Na_2HPO_4, pH 7), and 700 µl **4** (1 mmol, dissolved in ligation buffer, 1 eq.) was slowly added to the above reaction. The pH was adjusted to 7 and stirred at 37 ºC for 2 hours. The reaction was separated by semi-preparative HPLC (C18 column) using a gradient of 20-70% B over 40 min (Figure 1a, 1d.).

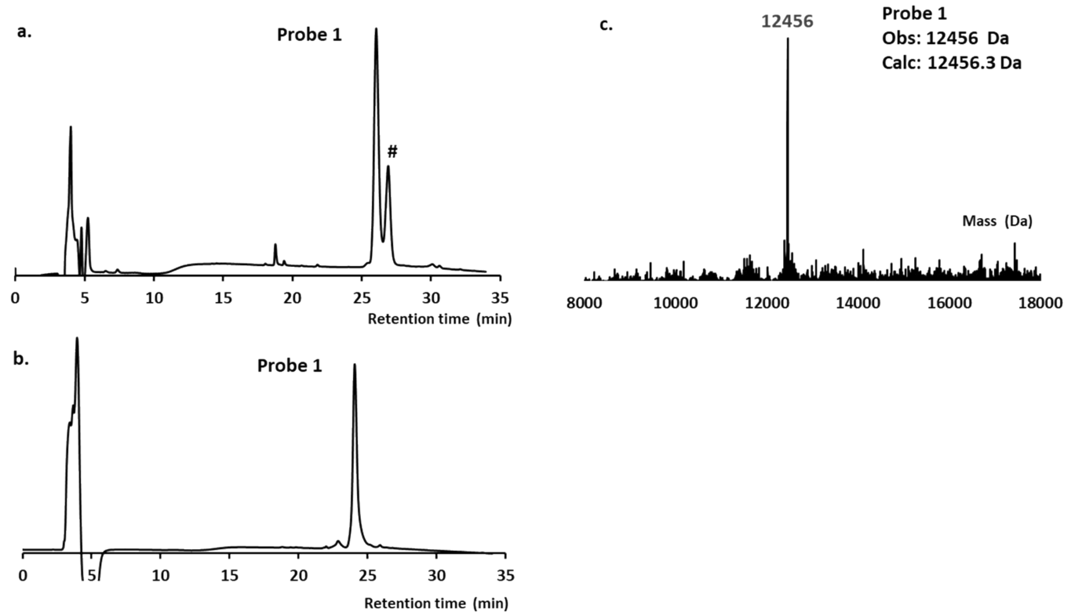

Figure S10. (a) Analytical HPLC chromatogram (λ=214 nm) of crude **Probe 1**. (b) Analytical HPLC chromatogram (λ=214 nm) of purified **Probe 1**. (c) Deconvoluted mass of **Probe 1.** ("#" represents peptide 4 dimer.)

h. Synthesis of cR10D-S-S-K(Biotin)-Ub-(1-75)-Dha (probe 2)

Like above, 11 (5 eq.) was dissolved in 300 µl ligation buffer (6 M Gn-HCl, 0.2 M Na_2HPO_4, pH 7), and 700 µl **7** (1 mmol, dissolved in ligation buffer, 1 eq.) was slowly dripped to the above reaction. The pH was adjusted to 7 and stirred at 37 ºC for 2 hours. The reaction was separated by semi-preparative HPLC (C18 column) using a gradient of 20-70% B over 40 min (Figure 3a, 3b.).

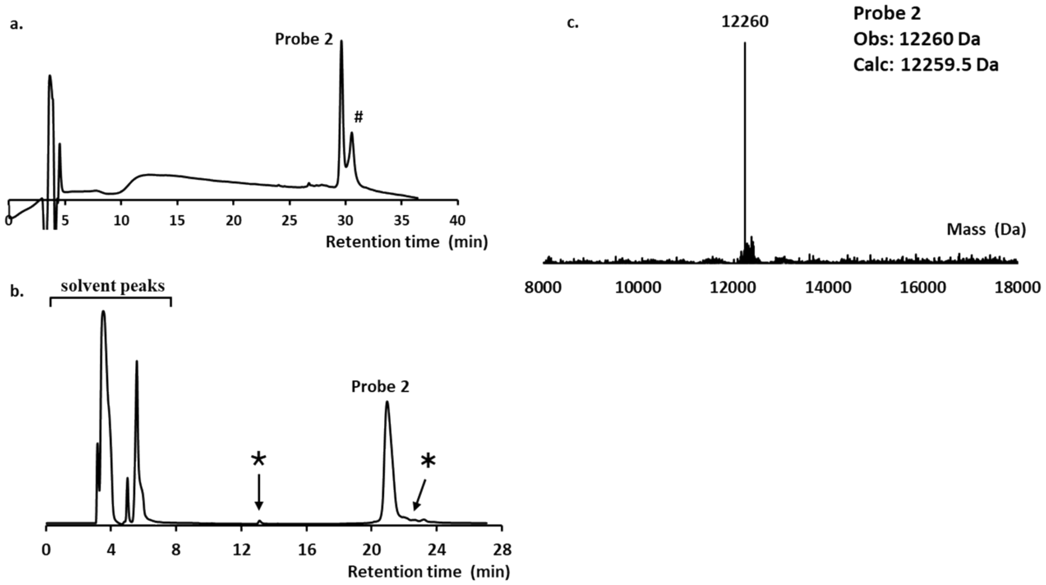

Figure S11. (a) Analytical HPLC chromatogram (λ=214 nm) of crude **Probe 2**. (b) Analytical HPLC chromatogram (λ=214 nm) of purified **Probe 2**. The additional peaks observed within 10 minutes of the retention time are the solvent peaks. '⋖' represents the 5, 5'-dithion-bis-2-nitrobenzoic acid (DTNB), '⤻' represents TFA adducts. (c) Deconvoluted mass of **Probe 2**. ("#" represents peptide **7** dimer.)

3. Probes refolding

Briefly, 1 mg probe was dissolved in 1 ml refolding buffer (6 M Gn-HCl, 0.2 M Na_2HPO_4, pH 7), then buffer exchanged into PBS buffer (2 mM KH_2PO_4, 10 mM Na_2HPO_4, 137 mM NaCl, 2.7 mM KCl, pH 7.4) for six times at 4 ºC (4 hours each time, 10% yield).

4. Labeling of E1/E2/E3 with probes in cells

Briefly, HeLa cells were treated with 5 μM **probe 2** for 4 h at 37 °C, then the probe was removed and cells were washed with cold PBS. Then 0.25% trypsin, 0.1% EDTA was added to cells and allowed to incubate for approximately 10 s at room temperature. Then trypsin solution was aspirated, and cells were incubated for 1min at 37 °C followed by harvest and washing with DPBS buffer. After that, cells were resuspended in RIPA Lysis Buffer (containing 1 mM iodoacetamide) supplemented with 1mM PMSF, and allowed to incubate on ice for 30 min and then centrifuged 11,000 rpm at 4 °C for 10 min to remove cell debris. Total protein concentration was determined using Bradford assay (Sangon Biotech). Prepared 100 μg cell lysates were used immediately for immunoblotting using an anti-Biotin antibody and anti-Ubch7 antibody.

5. Live-cell Imaging Confocal Microscopy

The protocols were essentially as described[1]. Briefly, HeLa cells were plated on sterile 35 mm glass-bottom dishes (biosharp BS-15-GJM) and allowed to adhere for 24 h at 37 °C and 5% CO_2 in DMEM (Gibco C11965500BT) supplemented with 10% FBS (Lonsera S711-001S), 100 units/mL penicillin and 0.1 mg/mL streptomycin (HyClone SV30010). Cells were then treated with PBS containing 5 μM **4** or **probe 1** for 1 h at 37°C and 5% CO_2. After 1 hour, the cells were washed three times with cold PBS and then stained with the dye Hoechst 33258 according to manufacturer's instructions for live-cell imaging. Cells were imaged with Argon laser (405 nm) and Argon laser (543nm) for visualizing Hoechst 33258 (blue nuclear staining), and RhoB (red emission) respectively with a Plan-Apochromat 100X/1.4 Oil DIC M27 objective on a Zeiss LSM 880 AxioObserver confocal laser scanning microscope. To enhance clarity and improve the visibility of the signal, the brightness/contrast parameters of the red channel images were adjusted using ImageJ. The parameters that were adjusted included the minimum value (0 increased to 22) and the maximum value (255 reduced to 162). Subsequently, the single channel images were merged using the image overlay tool (merge channels) of ImageJ software. All pictures with the same staining were adjusted using the same parameters.

Image analysis was performed on all images collected using FiJi software. Relative fluorescence intensities were determined by first identifying individual cells and the cytosolic compartment by applying a cell masking algorithm based on CT-DR staining. We use the FiJi software to open images of red fluorescence, with pre-processed segmentation performed using light as the signal area and dark as the background area. Then adjust the threshold, select the appropriate threshold algorithm. The average fluorescence intensity of the experimental group was calculated against the background of the parameter when the average fluorescence intensity of the control group was 0. The values presented are the averaged red fluorescence intensity (average red fluorescence intensity = total red fluorescence intensity of the area/the area)[4].

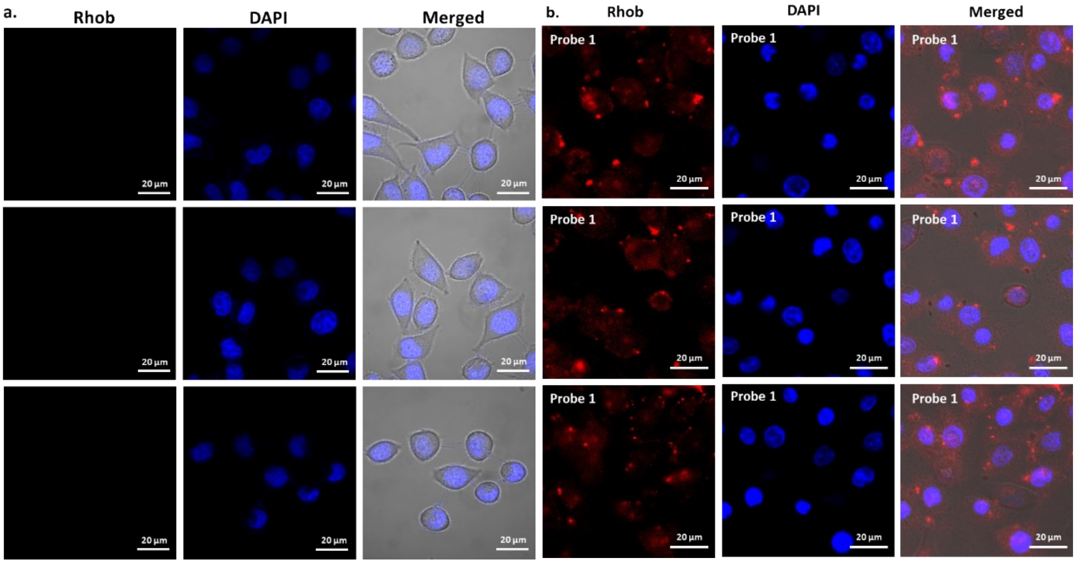

Figure S12. Representative images of delivery probes to live HeLa cells at 5 μM. a) Living-cell fluorescence imaging of HeLa cells treated with 5 μM **4**. (b) Living-cell fluorescence imaging of HeLa cells treated with 5 μM **probe 1**. Probes was visualized by TER fluorescence (red channel), Hoechst was used for nuclear staining (blue channel).

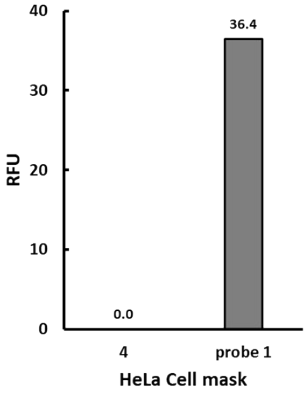

Figure S13. Quantification of cellular intensity in HeLa cells after treatment with 4 and Probe 1, relative to untreated cells.

6. MTT assay for evaluation of cell viability

Cell viability was assessed by 3-(4,5-dimethylthiazol-2-yl)-2,5-diphenyltetrazolium bromide (MTT) assay. Hela cells were inoculated into 96-well plates at 5000 cells per well and incubated with 100 µL of DMEM (containing 10% FBS) for 24 h. Five replicate wells were set up for each group, and 0.64% phenol was used as a positive control, untreated was used as a negative control. The cells were treated with 5 µM **probe 1** for 4 h to ensure the enough cellular uptake. After 4 h, the cells were washed three times with cold PBS, and re-incubated with fresh DMEM containing 10% FBS for 24 h. Then 20 µL of 5 mg/mL MTT solution was added. The cells were incubated for another 4 hours to reduce MTT to formazan crystals. The formazan product was then dissolved in dimethyl sulfoxide (DMSO) and quantified using a Bio-Rad 680 microplate reader at the absorbance of 490 nm[1].

7. Pulldown and Mass Spectrometry Analysis

Briefly, cell lysate generated from **probe 2** treated HeLa cells was incubated with streptavidin-agarose beads (Promega) at 4 °C for 2 hours. The beads were washed sequentially with 1 × binding buffer (25 mM Tris, 150 mM NaCl, 1 mM DTT, 0.5% v/v NP-40, pH 7.6), 2 × 0.5% SDS in PBS, 2 × 1 M NaCl in PBS, 2 × tris-buffered saline and 10 × 50 mM NH_4HCO_3 at pH 8.0. The samples were then analyzed by SDS-PAGE and LFQ mass spectrometry, with the protocol for processing the samples being essentially the same as described[1].

8. Mass Tables

Table S1. The three experiments figures of E1/E2/E3 enzymes.

C: Accession	C: Description	Abundance-1	Abundance-2	Abundance-3	Average
P22314	UBA1	1.2799E+08	1.6216E+08	2.2015E+08	1.7010E+08
A0AVT1	UBA6	2.2112E+09	1.9823E+07	5.4329E+06	7.4549E+08
P61077	UBE2D3	1.9855E+07	6.7643E+06	2.1380E+08	8.0140E+07
Q9H832	UBE2Z	1.1289E+07	1.1639E+07	1.1130E+07	1.1353E+07
Q15819	UBE2V2	2.1982E+07	8.3203E+06	1.5155E+07	1.5152E+07
Q712K3	UBE2R2	3.6734E+07	7.7191E+06	2.0547E+07	2.1666E+07
Q9C0C9	UBE2O	1.2483E+07	1.1590E+07	6.1506E+06	1.0075E+07
P61088	UBE2N	1.2456E+07	2.3905E+07	1.1195E+07	1.5852E+07
P68036	UBE2L3	1.3182E+07	2.2833E+07	1.7771E+07	1.7929E+07
P61086	UBE2K	1.6342E+07	3.8555E+06	9.2343E+07	3.7514E+07
P63279	UBE2I	1.3898E+07	2.3586E+07	9.0740E+06	1.5519E+07
P46934	NEDD4	7.3396E+07	6.7820E+07	1.0552E+08	8.2244E+07
Q7Z6Z7	HUWE1	3.0439E+07	6.4176E+06	2.3951E+07	2.0269E+07
Q05086	UBE3A	1.7060E+07	1.4141E+07	1.4715E+07	1.5305E+07
O75592	MYCBP2	7.8497E+06	7.8144E+06	9.6160E+06	8.4267E+06
Q8WU17	RNF139	2.2228E+07	1.7170E+07	2.2135E+07	2.0511E+07
Q5T4S7	UBR4	3.3247E+07	1.4512E+07	3.2930E+07	2.6896E+07
Q8IWV8	UBR2	2.3206E+07	1.4843E+07	7.6967E+06	1.5249E+07

Table S2: The following figure shows the cross-linking results of three experiments and the E1/ /E2/E3 enzymes were highlighted by yellow color.

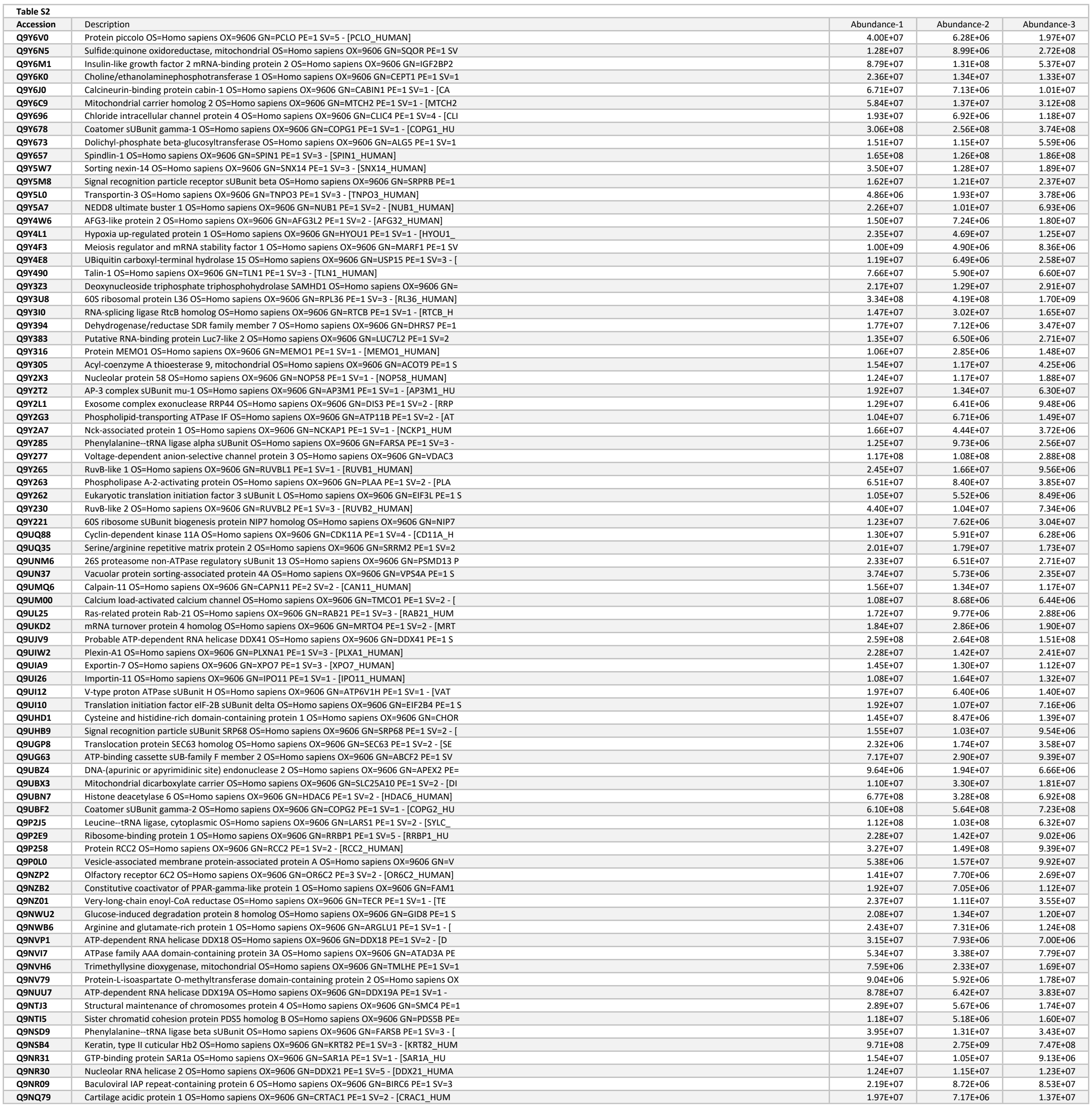

Table S2

Accession	Description	Abundance-1	Abundance-2	Abundance-3
Q9Y6V0	Protein piccolo OS=Homo sapiens OX=9606 GN=PCLO PE=1 SV=5 - [PCLO_HUMAN]	4.00E+07	6.28E+06	1.97E+07
Q9Y6N5	Sulfide:quinone oxidoreductase, mitochondrial OS=Homo sapiens OX=9606 GN=SQOR PE=1 SV	1.28E+07	8.99E+06	2.72E+08
Q9Y6M1	Insulin-like growth factor 2 mRNA-binding protein 2 OS=Homo sapiens OX=9606 GN=IGF2BP2	8.79E+07	1.31E+08	5.37E+07
Q9Y6K0	Choline/ethanolaminephosphotransferase 1 OS=Homo sapiens OX=9606 GN=CEPT1 PE=1 SV=1	2.36E+07	1.34E+07	1.33E+07
Q9Y6J0	Calcineurin-binding protein cabin-1 OS=Homo sapiens OX=9606 GN=CABIN1 PE=1 SV=1 - [CA	6.71E+07	7.13E+06	1.01E+07
Q9Y6C9	Mitochondrial carrier homolog 2 OS=Homo sapiens OX=9606 GN=MTCH2 PE=1 SV=1 - [MTCH2	5.84E+07	1.37E+07	3.12E+08
Q9Y696	Chloride intracellular channel protein 4 OS=Homo sapiens OX=9606 GN=CLIC4 PE=1 SV=4 - [CLI	1.93E+07	6.92E+06	1.18E+07
Q9Y678	Coatomer sUBunit gamma-1 OS=Homo sapiens OX=9606 GN=COPG1 PE=1 SV=1 - [COPG1_HU	3.06E+08	2.56E+08	3.74E+08
Q9Y673	Dolichyl-phosphate beta-glucosyltransferase OS=Homo sapiens OX=9606 GN=ALG5 PE=1 SV=1	1.51E+07	1.15E+07	5.59E+06
Q9Y657	Spindlin-1 OS=Homo sapiens OX=9606 GN=SPIN1 PE=1 SV=3 - [SPIN1_HUMAN]	1.65E+08	1.26E+08	1.86E+08
Q9Y5W7	Sorting nexin-14 OS=Homo sapiens OX=9606 GN=SNX14 PE=1 SV=3 - [SNX14_HUMAN]	3.50E+07	1.28E+07	1.89E+07
Q9Y5M8	Signal recognition particle receptor sUBunit beta OS=Homo sapiens OX=9606 GN=SRPRB PE=1	1.62E+07	1.21E+07	2.37E+07
Q9Y5L0	Transportin-3 OS=Homo sapiens OX=9606 GN=TNPO3 PE=1 SV=3 - [TNPO3_HUMAN]	4.86E+06	1.93E+07	3.78E+06
Q9Y5A7	NEDD8 ultimate buster 1 OS=Homo sapiens OX=9606 GN=NUB1 PE=1 SV=2 - [NUB1_HUMAN]	2.26E+07	1.01E+07	6.93E+06
Q9Y4W6	AFG3-like protein 2 OS=Homo sapiens OX=9606 GN=AFG3L2 PE=1 SV=2 - [AFG32_HUMAN]	1.50E+07	7.24E+06	1.80E+07
Q9Y4L1	Hypoxia up-regulated protein 1 OS=Homo sapiens OX=9606 GN=HYOU1 PE=1 SV=1 - [HYOU1_	2.35E+07	4.69E+07	1.25E+07
Q9Y4F3	Meiosis regulator and mRNA stability factor 1 OS=Homo sapiens OX=9606 GN=MARF1 PE=1 SV	1.00E+09	4.90E+06	8.36E+06
Q9Y4E8	UBiquitin carboxyl-terminal hydrolase 15 OS=Homo sapiens OX=9606 GN=USP15 PE=1 SV=3 - [	1.19E+07	6.49E+06	2.58E+07
Q9Y490	Talin-1 OS=Homo sapiens OX=9606 GN=TLN1 PE=1 SV=3 - [TLN1_HUMAN]	7.66E+07	5.90E+07	6.60E+07
Q9Y3Z3	Deoxynucleoside triphosphate triphosphohydrolase SAMHD1 OS=Homo sapiens OX=9606 GN=	2.17E+07	1.29E+07	2.91E+07
Q9Y3U8	60S ribosomal protein L36 OS=Homo sapiens OX=9606 GN=RPL36 PE=1 SV=3 - [RL36_HUMAN]	3.34E+08	4.19E+08	1.70E+09
Q9Y3I0	RNA-splicing ligase RtcB homolog OS=Homo sapiens OX=9606 GN=RTCB PE=1 SV=1 - [RTCB_H	1.47E+07	3.02E+07	1.65E+07
Q9Y394	Dehydrogenase/reductase SDR family member 7 OS=Homo sapiens OX=9606 GN=DHRS7 PE=1	1.77E+07	7.12E+06	3.47E+07
Q9Y383	Putative RNA-binding protein Luc7-like 2 OS=Homo sapiens OX=9606 GN=LUC7L2 PE=1 SV=2	1.35E+07	6.50E+06	2.71E+07
Q9Y316	Protein MEMO1 OS=Homo sapiens OX=9606 GN=MEMO1 PE=1 SV=1 - [MEMO1_HUMAN]	1.06E+07	2.85E+06	1.48E+07
Q9Y305	Acyl-coenzyme A thioesterase 9, mitochondrial OS=Homo sapiens OX=9606 GN=ACOT9 PE=1 S	1.54E+07	1.17E+07	4.25E+06
Q9Y2X3	Nucleolar protein 58 OS=Homo sapiens OX=9606 GN=NOP58 PE=1 SV=1 - [NOP58_HUMAN]	1.24E+07	1.17E+07	1.88E+07
Q9Y2T2	AP-3 complex sUBunit mu-1 OS=Homo sapiens OX=9606 GN=AP3M1 PE=1 SV=1 - [AP3M1_HU	1.92E+07	1.34E+07	6.30E+07
Q9Y2L1	Exosome complex exonuclease RRP44 OS=Homo sapiens OX=9606 GN=DIS3 PE=1 SV=2 - [RRP	1.29E+07	6.41E+06	9.48E+06
Q9Y2G3	Phospholipid-transporting ATPase IF OS=Homo sapiens OX=9606 GN=ATP11B PE=1 SV=2 - [AT	1.04E+07	6.71E+06	1.49E+07
Q9Y2A7	Nck-associated protein 1 OS=Homo sapiens OX=9606 GN=NCKAP1 PE=1 SV=1 - [NCKP1_HUM	1.66E+07	4.44E+07	3.72E+06
Q9Y285	Phenylalanine--tRNA ligase alpha sUBunit OS=Homo sapiens OX=9606 GN=FARSA PE=1 SV=3 -	1.25E+07	9.73E+06	2.56E+07
Q9Y277	Voltage-dependent anion-selective channel protein 3 OS=Homo sapiens OX=9606 GN=VDAC3	1.17E+08	1.08E+08	2.88E+08
Q9Y265	RuvB-like 1 OS=Homo sapiens OX=9606 GN=RUVBL1 PE=1 SV=1 - [RUVB1_HUMAN]	2.45E+07	1.66E+07	9.56E+06
Q9Y263	Phospholipase A-2-activating protein OS=Homo sapiens OX=9606 GN=PLAA PE=1 SV=2 - [PLA	6.51E+07	8.40E+07	3.85E+07
Q9Y262	Eukaryotic translation initiation factor 3 sUBunit L OS=Homo sapiens OX=9606 GN=EIF3L PE=1 S	1.05E+07	5.52E+06	8.49E+06
Q9Y230	RuvB-like 2 OS=Homo sapiens OX=9606 GN=RUVBL2 PE=1 SV=3 - [RUVB2_HUMAN]	4.40E+07	1.04E+07	7.34E+06
Q9Y221	60S ribosome sUBunit biogenesis protein NIP7 homolog OS=Homo sapiens OX=9606 GN=NIP7	1.23E+07	7.62E+06	3.04E+07
Q9UQ88	Cyclin-dependent kinase 11A OS=Homo sapiens OX=9606 GN=CDK11A PE=1 SV=4 - [CD11A_H	1.30E+07	5.91E+07	6.28E+06
Q9UQ35	Serine/arginine repetitive matrix protein 2 OS=Homo sapiens OX=9606 GN=SRRM2 PE=1 SV=2	2.01E+07	1.79E+07	1.73E+07
Q9UNM6	26S proteasome non-ATPase regulatory sUBunit 13 OS=Homo sapiens OX=9606 GN=PSMD13 P	2.33E+07	6.51E+07	2.71E+07
Q9UN37	Vacuolar protein sorting-associated protein 4A OS=Homo sapiens OX=9606 GN=VPS4A PE=1 S	3.74E+07	5.73E+06	2.35E+07
Q9UMQ6	Calpain-11 OS=Homo sapiens OX=9606 GN=CAPN11 PE=2 SV=2 - [CAN11_HUMAN]	1.56E+07	1.34E+07	1.17E+07
Q9UM00	Calcium load-activated calcium channel OS=Homo sapiens OX=9606 GN=TMCO1 PE=1 SV=2 - [	1.08E+07	8.68E+06	6.44E+06
Q9UL25	Ras-related protein Rab-21 OS=Homo sapiens OX=9606 GN=RAB21 PE=1 SV=3 - [RAB21_HUM	1.72E+07	9.77E+06	2.88E+06
Q9UKD2	mRNA turnover protein 4 homolog OS=Homo sapiens OX=9606 GN=MRTO4 PE=1 SV=2 - [MRT	1.84E+07	2.86E+06	1.90E+07
Q9UJV9	Probable ATP-dependent RNA helicase DDX41 OS=Homo sapiens OX=9606 GN=DDX41 PE=1 S	2.59E+08	2.64E+08	1.51E+08
Q9UIW2	Plexin-A1 OS=Homo sapiens OX=9606 GN=PLXNA1 PE=1 SV=3 - [PLXA1_HUMAN]	2.28E+07	1.42E+07	2.41E+07
Q9UIA9	Exportin-7 OS=Homo sapiens OX=9606 GN=XPO7 PE=1 SV=3 - [XPO7_HUMAN]	1.45E+07	1.30E+07	1.12E+07
Q9UI26	Importin-11 OS=Homo sapiens OX=9606 GN=IPO11 PE=1 SV=1 - [IPO11_HUMAN]	1.08E+07	1.64E+07	1.32E+07
Q9UI12	V-type proton ATPase sUBunit H OS=Homo sapiens OX=9606 GN=ATP6V1H PE=1 SV=1 - [VAT	1.97E+07	6.40E+06	1.40E+07
Q9UI10	Translation initiation factor eIF-2B sUBunit delta OS=Homo sapiens OX=9606 GN=EIF2B4 PE=1 S	1.92E+07	1.07E+07	7.16E+06
Q9UHD1	Cysteine and histidine-rich domain-containing protein 1 OS=Homo sapiens OX=9606 GN=CHOR	1.45E+07	8.47E+06	1.39E+07
Q9UHB9	Signal recognition particle sUBunit SRP68 OS=Homo sapiens OX=9606 GN=SRP68 PE=1 SV=2 - [	1.55E+07	1.03E+07	9.54E+06
Q9UGP8	Translocation protein SEC63 homolog OS=Homo sapiens OX=9606 GN=SEC63 PE=1 SV=2 - [SE	2.32E+06	1.74E+07	3.58E+07
Q9UG63	ATP-binding cassette sUB-family F member 2 OS=Homo sapiens OX=9606 GN=ABCF2 PE=1 SV	7.17E+07	2.90E+07	9.39E+07
Q9UBZ4	DNA-(apurinic or apyrimidinic site) endonuclease 2 OS=Homo sapiens OX=9606 GN=APEX2 PE=	9.64E+06	1.94E+07	6.66E+06
Q9UBX3	Mitochondrial dicarboxylate carrier OS=Homo sapiens OX=9606 GN=SLC25A10 PE=1 SV=2 - [DI	1.10E+07	3.30E+07	1.81E+07
Q9UBN7	Histone deacetylase 6 OS=Homo sapiens OX=9606 GN=HDAC6 PE=1 SV=2 - [HDAC6_HUMAN]	6.77E+08	3.28E+08	6.92E+08
Q9UBF2	Coatomer sUBunit gamma-2 OS=Homo sapiens OX=9606 GN=COPG2 PE=1 SV=1 - [COPG2_HU	6.10E+08	5.64E+08	7.23E+08
Q9P2J5	Leucine--tRNA ligase, cytoplasmic OS=Homo sapiens OX=9606 GN=LARS1 PE=1 SV=2 - [SYLC_	1.12E+08	1.03E+08	6.32E+07
Q9P2E9	Ribosome-binding protein 1 OS=Homo sapiens OX=9606 GN=RRBP1 PE=1 SV=5 - [RRBP1_HU	2.28E+07	1.42E+07	9.02E+06
Q9P258	Protein RCC2 OS=Homo sapiens OX=9606 GN=RCC2 PE=1 SV=2 - [RCC2_HUMAN]	3.27E+07	1.49E+08	9.39E+07
Q9P0L0	Vesicle-associated membrane protein-associated protein A OS=Homo sapiens OX=9606 GN=V	5.38E+06	1.57E+07	9.92E+07
Q9NZP2	Olfactory receptor 6C2 OS=Homo sapiens OX=9606 GN=OR6C2 PE=3 SV=2 - [OR6C2_HUMAN]	1.41E+07	7.70E+06	2.69E+07
Q9NZB2	Constitutive coactivator of PPAR-gamma-like protein 1 OS=Homo sapiens OX=9606 GN=FAM1	1.92E+07	7.05E+06	1.12E+07
Q9NZ01	Very-long-chain enoyl-CoA reductase OS=Homo sapiens OX=9606 GN=TECR PE=1 SV=1 - [TE	2.37E+07	1.11E+07	3.55E+07
Q9NWU2	Glucose-induced degradation protein 8 homolog OS=Homo sapiens OX=9606 GN=GID8 PE=1 S	2.08E+07	1.34E+07	1.20E+07
Q9NWB6	Arginine and glutamate-rich protein 1 OS=Homo sapiens OX=9606 GN=ARGLU1 PE=1 SV=1 - [	2.43E+07	7.31E+06	1.24E+08
Q9NVP1	ATP-dependent RNA helicase DDX18 OS=Homo sapiens OX=9606 GN=DDX18 PE=1 SV=2 - [D	3.15E+07	7.93E+06	7.00E+06
Q9NVI7	ATPase family AAA domain-containing protein 3A OS=Homo sapiens OX=9606 GN=ATAD3A PE	5.34E+07	3.38E+07	7.79E+07
Q9NVH6	Trimethyllysine dioxygenase, mitochondrial OS=Homo sapiens OX=9606 GN=TMLHE PE=1 SV=1	7.59E+06	2.33E+07	1.69E+07
Q9NV79	Protein-L-isoaspartate O-methyltransferase domain-containing protein 2 OS=Homo sapiens OX	9.04E+06	5.92E+06	1.78E+07
Q9NUU7	ATP-dependent RNA helicase DDX19A OS=Homo sapiens OX=9606 GN=DDX19A PE=1 SV=1 -	8.78E+07	6.42E+07	3.83E+07
Q9NTJ3	Structural maintenance of chromosomes protein 4 OS=Homo sapiens OX=9606 GN=SMC4 PE=1	2.89E+07	5.67E+06	1.74E+07
Q9NTI5	Sister chromatid cohesion protein PDS5 homolog B OS=Homo sapiens OX=9606 GN=PDS5B PE=	1.18E+07	5.18E+06	1.60E+07
Q9NSD9	Phenylalanine--tRNA ligase beta sUBunit OS=Homo sapiens OX=9606 GN=FARSB PE=1 SV=3 - [	3.95E+07	1.31E+07	3.43E+07
Q9NSB4	Keratin, type II cuticular Hb2 OS=Homo sapiens OX=9606 GN=KRT82 PE=1 SV=3 - [KRT82_HUM	9.71E+08	2.75E+09	7.47E+08
Q9NR31	GTP-binding protein SAR1a OS=Homo sapiens OX=9606 GN=SAR1A PE=1 SV=1 - [SAR1A_HU	1.54E+07	1.05E+07	9.13E+06
Q9NR30	Nucleolar RNA helicase 2 OS=Homo sapiens OX=9606 GN=DDX21 PE=1 SV=5 - [DDX21_HUMA	1.24E+07	1.15E+07	1.23E+07
Q9NR09	Baculoviral IAP repeat-containing protein 6 OS=Homo sapiens OX=9606 GN=BIRC6 PE=1 SV=3	2.19E+07	8.72E+06	8.53E+07
Q9NQ79	Cartilage acidic protein 1 OS=Homo sapiens OX=9606 GN=CRTAC1 PE=1 SV=2 - [CRAC1_HUM	1.97E+07	7.17E+06	1.37E+07

Q9NP72	Ras-related protein Rab-18 OS=Homo sapiens OX=9606 GN=RAB18 PE=1 SV=1 - [RAB18_HUM	1.03E+07	6.79E+06	6.44E+06
Q9NP55	BPI fold-containing family A member 1 OS=Homo sapiens OX=9606 GN=BPIFA1 PE=1 SV=1 - [B	2.89E+07	4.44E+06	1.79E+07
Q9HCC0	Methylcrotonoyl-CoA carboxylase beta chain, mitochondrial OS=Homo sapiens OX=9606 GN=M	5.92E+07	6.66E+07	8.51E+07
Q9HBG7	T-lymphocyte surface antigen Ly-9 OS=Homo sapiens OX=9606 GN=LY9 PE=1 SV=3 - [LY9_HU	4.57E+08	8.85E+06	2.20E+07
Q9HB07	MYG1 exonuclease OS=Homo sapiens OX=9606 GN=MYG1 PE=1 SV=3 - [MYG1_HUMAN]	1.60E+07	1.55E+07	1.85E+07
Q9HAV4	Exportin-5 OS=Homo sapiens OX=9606 GN=XPO5 PE=1 SV=1 - [XPO5_HUMAN]	1.94E+07	7.95E+06	3.71E+06
Q9H9J4	UBiquitin carboxyl-terminal hydrolase 42 OS=Homo sapiens OX=9606 GN=USP42 PE=1 SV=3 - [	5.00E+07	3.46E+07	1.06E+07
Q9H9C1	Spermatogenesis-defective protein 39 homolog OS=Homo sapiens OX=9606 GN=VIPAS39 PE=	3.88E+07	4.39E+06	1.57E+07
Q9H8Y8	Golgi reassembly-stacking protein 2 OS=Homo sapiens OX=9606 GN=GORASP2 PE=1 SV=3 - [	1.83E+07	2.63E+07	9.55E+06
Q9H832	UBiquitin-conjugating enzyme E2 Z OS=Homo sapiens OX=9606 GN=UBE2Z PE=1 SV=2 - [UBE2	1.13E+07	1.16E+07	1.11E+07
Q9H7D7	WD repeat-containing protein 26 OS=Homo sapiens OX=9606 GN=WDR26 PE=1 SV=3 - [WDR2	1.50E+07	2.55E+08	1.39E+07
Q9H6S0	3'-5' RNA helicase YTHDC2 OS=Homo sapiens OX=9606 GN=YTHDC2 PE=1 SV=2 - [YTDC2_HU	1.18E+07	4.26E+06	5.96E+06
Q9H4M9	EH domain-containing protein 1 OS=Homo sapiens OX=9606 GN=EHD1 PE=1 SV=2 - [EHD1_H	5.25E+07	1.95E+07	8.24E+06
Q9H4I3	TraB domain-containing protein OS=Homo sapiens OX=9606 GN=TRABD PE=1 SV=1 - [TRABD_	5.90E+07	9.25E+06	1.58E+07
Q9H4B4	Serine/threonine-protein kinase PLK3 OS=Homo sapiens OX=9606 GN=PLK3 PE=1 SV=2 - [PLK3	1.70E+07	6.93E+06	2.32E+09
Q9H2J7	Sodium-dependent neutral amino acid transporter B(0)AT2 OS=Homo sapiens OX=9606 GN=SL	6.02E+06	9.82E+06	1.13E+07
Q9H158	Protocadherin alpha-C1 OS=Homo sapiens OX=9606 GN=PCDHAC1 PE=2 SV=2 - [PCDC1_HUM	1.94E+07	8.51E+06	9.58E+06
Q9H0T7	Ras-related protein Rab-17 OS=Homo sapiens OX=9606 GN=RAB17 PE=1 SV=2 - [RAB17_HUM	1.95E+07	4.17E+06	8.21E+06
Q9H0A0	RNA cytidine acetyltransferase OS=Homo sapiens OX=9606 GN=NAT10 PE=1 SV=2 - [NAT10_H	1.51E+08	1.91E+07	1.50E+08
Q9H089	Large sUBunit GTPase 1 homolog OS=Homo sapiens OX=9606 GN=LSG1 PE=1 SV=2 - [LSG1_H	6.24E+06	1.15E+07	7.45E+06
Q9GZZ1	N-alpha-acetyltransferase 50 OS=Homo sapiens OX=9606 GN=NAA50 PE=1 SV=1 - [NAA50_H	1.42E+07	3.80E+06	8.21E+06
Q9C0C9	(E3-independent) E2 UBiquitin-conjugating enzyme OS=Homo sapiens OX=9606 GN=UBE2O PE	1.25E+07	1.16E+07	6.15E+06
Q9BZZ5	Apoptosis inhibitor 5 OS=Homo sapiens OX=9606 GN=API5 PE=1 SV=3 - [API5_HUMAN]	2.24E+07	6.78E+06	1.02E+07
Q9BXJ9	N-alpha-acetyltransferase 15, NatA auxiliary sUBunit OS=Homo sapiens OX=9606 GN=NAA15 P	2.72E+07	1.97E+07	2.51E+07
Q9BW92	Threonine--tRNA ligase, mitochondrial OS=Homo sapiens OX=9606 GN=TARS2 PE=1 SV=1 - [S	1.27E+07	1.46E+07	1.54E+07
Q9BVP2	Guanine nucleotide-binding protein-like 3 OS=Homo sapiens OX=9606 GN=GNL3 PE=1 SV=2 -	9.32E+08	1.78E+08	1.03E+09
Q9BUF5	TUBulin beta-6 chain OS=Homo sapiens OX=9606 GN=TUBB6 PE=1 SV=1 - [TBB6_HUMAN]	1.54E+09	1.06E+09	1.62E+09
Q9BTW9	TUBulin-specific chaperone D OS=Homo sapiens OX=9606 GN=TBCD PE=1 SV=2 - [TBCD_HUM	4.08E+07	1.02E+07	7.19E+06
Q9BT78	COP9 signalosome complex sUBunit 4 OS=Homo sapiens OX=9606 GN=COPS4 PE=1 SV=1 - [CS	2.37E+07	9.23E+06	1.16E+07
Q9BSJ8	Extended synaptotagmin-1 OS=Homo sapiens OX=9606 GN=ESYT1 PE=1 SV=1 - [ESYT1_HUM	1.52E+07	1.17E+07	6.58E+06
Q9BPX3	Condensin complex sUBunit 3 OS=Homo sapiens OX=9606 GN=NCAPG PE=1 SV=1 - [CND3_HU	1.51E+07	1.08E+07	1.62E+07
Q99873	Protein arginine N-methyltransferase 1 OS=Homo sapiens OX=9606 GN=PRMT1 PE=1 SV=3 - [A	1.91E+07	5.39E+06	9.09E+06
Q99848	Probable rRNA-processing protein EBP2 OS=Homo sapiens OX=9606 GN=EBNA1BP2 PE=1 SV=	4.40E+08	5.28E+08	9.87E+08
Q99832	T-complex protein 1 sUBunit eta OS=Homo sapiens OX=9606 GN=CCT7 PE=1 SV=2 - [TCPH_HU	3.24E+07	1.41E+07	3.93E+07
Q99829	Copine-1 OS=Homo sapiens OX=9606 GN=CPNE1 PE=1 SV=1 - [CPNE1_HUMAN]	9.06E+06	1.64E+07	2.12E+07
Q99729	Heterogeneous nuclear ribonucleoprotein A/B OS=Homo sapiens OX=9606 GN=HNRNPAB PE=1	5.27E+07	1.44E+07	7.84E+07
Q99714	3-hydroxyacyl-CoA dehydrogenase type-2 OS=Homo sapiens OX=9606 GN=HSD17B10 PE=1 S	2.24E+07	4.68E+06	1.02E+07
Q99615	DnaJ homolog sUBfamily C member 7 OS=Homo sapiens OX=9606 GN=DNAJC7 PE=1 SV=2 - [	2.26E+07	5.71E+06	3.06E+07
Q99613	Eukaryotic translation initiation factor 3 sUBunit C OS=Homo sapiens OX=9606 GN=EIF3C PE=1 S	1.90E+07	5.13E+06	1.06E+07
Q99460	26S proteasome non-ATPase regulatory sUBunit 1 OS=Homo sapiens OX=9606 GN=PSMD1 PE=	2.95E+07	5.17E+06	1.02E+07
Q96TA1	Protein Niban 2 OS=Homo sapiens OX=9606 GN=NIBAN2 PE=1 SV=3 - [NIBA2_HUMAN]	2.83E+07	1.23E+07	2.38E+07
Q96T68	Histone-lysine N-methyltransferase SETDB2 OS=Homo sapiens OX=9606 GN=SETDB2 PE=1 SV=	2.56E+07	7.14E+06	1.23E+07
Q96S94	Cyclin-L2 OS=Homo sapiens OX=9606 GN=CCNL2 PE=1 SV=1 - [CCNL2_HUMAN]	7.25E+06	1.49E+07	1.06E+07
Q96S82	UBiquitin-like protein 7 OS=Homo sapiens OX=9606 GN=UBL7 PE=1 SV=2 - [UBL7_HUMAN]	2.81E+07	1.18E+07	1.24E+07
Q96RQ3	Methylcrotonoyl-CoA carboxylase sUBunit alpha, mitochondrial OS=Homo sapiens OX=9606 GN	1.36E+10	1.29E+10	1.44E+10
Q96RP9	Elongation factor G, mitochondrial OS=Homo sapiens OX=9606 GN=GFM1 PE=1 SV=2 - [EFGM_	4.80E+07	5.03E+07	6.45E+06
Q96QK1	Vacuolar protein sorting-associated protein 35 OS=Homo sapiens OX=9606 GN=VPS35 PE=1 SV	8.23E+06	7.48E+07	9.71E+07
Q96QA5	Gasdermin-A OS=Homo sapiens OX=9606 GN=GSDMA PE=1 SV=4 - [GSDMA_HUMAN]	9.27E+06	6.51E+06	1.58E+07
Q96P70	Importin-9 OS=Homo sapiens OX=9606 GN=IPO9 PE=1 SV=3 - [IPO9_HUMAN]	9.20E+06	1.74E+07	1.01E+07
Q96P63	Serpin B12 OS=Homo sapiens OX=9606 GN=SERPINB12 PE=1 SV=1 - [SPB12_HUMAN]	2.33E+07	3.43E+07	4.18E+07
Q96P26	Cytosolic 5'-nucleotidase 1B OS=Homo sapiens OX=9606 GN=NT5C1B PE=2 SV=2 - [5NT1B_HU	2.05E+07	1.02E+07	7.17E+06
Q96N66	Lysophospholipid acyltransferase 7 OS=Homo sapiens OX=9606 GN=MBOAT7 PE=1 SV=2 - [MB	1.12E+07	7.79E+06	1.72E+07
Q96L92	Sorting nexin-27 OS=Homo sapiens OX=9606 GN=SNX27 PE=1 SV=2 - [SNX27_HUMAN]	1.79E+07	7.07E+06	8.17E+06
Q96KK5	Histone H2A type 1-H OS=Homo sapiens OX=9606 GN=H2AC12 PE=1 SV=3 - [H2A1H_HUMAN]	5.20E+07	2.52E+07	6.83E+07
Q96K76	UBiquitin carboxyl-terminal hydrolase 47 OS=Homo sapiens OX=9606 GN=USP47 PE=1 SV=3 - [	4.14E+07	1.45E+07	1.30E+07
Q96JN0	Ligand-dependent corepressor OS=Homo sapiens OX=9606 GN=LCOR PE=1 SV=2 - [LCOR_HU	1.23E+07	1.10E+07	1.51E+07
Q96JB3	Hypermethylated in cancer 2 protein OS=Homo sapiens OX=9606 GN=HIC2 PE=1 SV=2 - [HIC2_	2.17E+07	1.25E+07	1.39E+07
Q96I99	Succinate--CoA ligase [GDP-forming] sUBunit beta, mitochondrial OS=Homo sapiens OX=9606	3.24E+07	3.80E+07	1.57E+07
Q96HW7	Integrator complex sUBunit 4 OS=Homo sapiens OX=9606 GN=INTS4 PE=1 SV=2 - [INT4_HUM	2.92E+07	1.78E+07	1.39E+07
Q96HP0	Dedicator of cytokinesis protein 6 OS=Homo sapiens OX=9606 GN=DOCK6 PE=1 SV=3 - [DOCK	2.34E+07	2.16E+07	1.93E+07
Q96HE7	ERO1-like protein alpha OS=Homo sapiens OX=9606 GN=ERO1A PE=1 SV=2 - [ERO1A_HUMAN	1.22E+08	9.74E+07	8.67E+07
Q96GQ7	Probable ATP-dependent RNA helicase DDX27 OS=Homo sapiens OX=9606 GN=DDX27 PE=1 S	6.73E+07	3.89E+07	6.97E+06
Q96FX8	p53 apoptosis effector related to PMP-22 OS=Homo sapiens OX=9606 GN=PERP PE=1 SV=1 - [	1.36E+07	5.88E+06	3.26E+07
Q96FW1	UBiquitin thioesterase OTUB1 OS=Homo sapiens OX=9606 GN=OTUB1 PE=1 SV=2 - [OTUB1_HU	5.28E+07	3.95E+07	6.54E+07
Q96D46	60S ribosomal export protein NMD3 OS=Homo sapiens OX=9606 GN=NMD3 PE=1 SV=1 - [NM	1.73E+07	1.24E+07	1.58E+07
Q96CW1	AP-2 complex sUBunit mu OS=Homo sapiens OX=9606 GN=AP2M1 PE=1 SV=2 - [AP2M1_HUM	1.38E+07	5.85E+06	5.84E+06
Q96BM9	ADP-ribosylation factor-like protein 8A OS=Homo sapiens OX=9606 GN=ARL8A PE=1 SV=1 - [	1.87E+07	9.96E+06	1.48E+07
Q96AG4	Leucine-rich repeat-containing protein 59 OS=Homo sapiens OX=9606 GN=LRRC59 PE=1 SV=1	1.50E+07	2.09E+07	2.98E+07
Q96AC1	Fermitin family homolog 2 OS=Homo sapiens OX=9606 GN=FERMT2 PE=1 SV=1 - [FERM2_HUM	1.20E+07	9.55E+06	9.13E+06
Q969Y2	tRNA modification GTPase GTPBP3, mitochondrial OS=Homo sapiens OX=9606 GN=GTPBP3 PE=	1.94E+07	3.35E+08	1.19E+07
Q969X5	Endoplasmic reticulum-Golgi intermediate compartment protein 1 OS=Homo sapiens OX=9606	9.86E+06	8.40E+06	1.02E+07
Q969V3	Nicalin OS=Homo sapiens OX=9606 GN=NCLN PE=1 SV=2 - [NCLN_HUMAN]	1.38E+07	3.14E+06	1.04E+07
Q93009	UBiquitin carboxyl-terminal hydrolase 7 OS=Homo sapiens OX=9606 GN=USP7 PE=1 SV=2 - [UB	2.30E+07	1.48E+07	7.79E+06
Q93008	Probable UBiquitin carboxyl-terminal hydrolase FAF-X OS=Homo sapiens OX=9606 GN=USP9X	6.56E+06	7.11E+06	2.72E+07
Q92974	Rho guanine nucleotide exchange factor 2 OS=Homo sapiens OX=9606 GN=ARHGEF2 PE=1 SV	7.93E+06	1.14E+07	9.40E+06
Q92973	Transportin-1 OS=Homo sapiens OX=9606 GN=TNPO1 PE=1 SV=2 - [TNPO1_HUMAN]	1.64E+08	1.00E+08	1.00E+08
Q92945	Far upstream element-binding protein 2 OS=Homo sapiens OX=9606 GN=KHSRP PE=1 SV=4 - [	3.38E+07	8.51E+06	2.12E+07
Q92900	Regulator of nonsense transcripts 1 OS=Homo sapiens OX=9606 GN=UPF1 PE=1 SV=2 - [RENT1	1.76E+07	3.05E+07	2.74E+07
Q92841	Probable ATP-dependent RNA helicase DDX17 OS=Homo sapiens OX=9606 GN=DDX17 PE=1 S	3.82E+08	2.00E+08	2.54E+08
Q92621	Nuclear pore complex protein Nup205 OS=Homo sapiens OX=9606 GN=NUP205 PE=1 SV=3 - [	1.84E+07	1.10E+07	1.47E+07
Q92616	eIF-2-alpha kinase activator GCN1 OS=Homo sapiens OX=9606 GN=GCN1 PE=1 SV=7 - [GCN1_	4.83E+07	1.52E+07	1.19E+07
Q92598	Heat shock protein 105 kDa OS=Homo sapiens OX=9606 GN=HSPH1 PE=1 SV=1 - [HS105_HUM	1.90E+07	9.14E+06	6.33E+06
Q92597	Protein NDRG1 OS=Homo sapiens OX=9606 GN=NDRG1 PE=1 SV=1 - [NDRG1_HUMAN]	1.06E+07	1.54E+07	5.52E+06
Q92572	AP-3 complex sUBunit sigma-1 OS=Homo sapiens OX=9606 GN=AP3S1 PE=1 SV=1 - [AP3S1_H	1.37E+07	2.31E+07	7.03E+06
Q92526	T-complex protein 1 sUBunit zeta-2 OS=Homo sapiens OX=9606 GN=CCT6B PE=1 SV=5 - [TCP	1.66E+08	1.59E+08	2.17E+08
Q92499	ATP-dependent RNA helicase DDX1 OS=Homo sapiens OX=9606 GN=DDX1 PE=1 SV=2 - [DDX	1.58E+07	1.90E+07	6.83E+07
Q8WZ74	Cortactin-binding protein 2 OS=Homo sapiens OX=9606 GN=CTTNBP2 PE=1 SV=1 - [CTTB2_HU	1.61E+07	1.21E+07	4.27E+07
Q8WZ42	Titin OS=Homo sapiens OX=9606 GN=TTN PE=1 SV=4 - [TITIN_HUMAN]	9.89E+06	1.76E+07	9.88E+06
Q8WXH0	Nesprin-2 OS=Homo sapiens OX=9606 GN=SYNE2 PE=1 SV=3 - [SYNE2_HUMAN]	1.74E+07	2.17E+07	4.16E+06
Q8WVV9	Heterogeneous nuclear ribonucleoprotein L-like OS=Homo sapiens OX=9606 GN=HNRNPLL PE=	1.27E+07	1.12E+07	4.47E+06
Q8WVV4	Protein POF1B OS=Homo sapiens OX=9606 GN=POF1B PE=1 SV=3 - [POF1B_HUMAN]	5.55E+06	1.41E+07	9.58E+06
Q8WVM8	Sec1 family domain-containing protein 1 OS=Homo sapiens OX=9606 GN=SCFD1 PE=1 SV=4 - [	1.08E+07	2.23E+07	1.35E+07
Q8WUM4	Programmed cell death 6-interacting protein OS=Homo sapiens OX=9606 GN=PDCD6IP PE=1 S	1.00E+07	2.56E+07	4.09E+06
Q8WU17	E3 UBiquitin-protein ligase RNF139 OS=Homo sapiens OX=9606 GN=RNF139 PE=1 SV=1 - [RN1	2.22E+07	1.72E+07	2.21E+07
Q8TDN6	Ribosome biogenesis protein BRX1 homolog OS=Homo sapiens OX=9606 GN=BRIX1 PE=1 SV=	1.22E+08	1.10E+08	2.55E+08
Q8TD57	Dynein axonemal heavy chain 3 OS=Homo sapiens OX=9606 GN=DNAH3 PE=2 SV=1 - [DYH3_H	1.68E+07	5.62E+07	8.22E+06
Q8TCT9	Minor histocompatibility antigen H13 OS=Homo sapiens OX=9606 GN=HM13 PE=1 SV=1 - [HM	9.50E+06	2.48E+07	7.21E+06
Q8TBP6	Probable mitochondrial glutathione transporter SLC25A40 OS=Homo sapiens OX=9606 GN=SLC	2.80E+07	1.82E+07	1.69E+07
Q8NI35	InaD-like protein OS=Homo sapiens OX=9606 GN=PATJ PE=1 SV=3 - [INADL_HUMAN]	7.81E+06	8.74E+06	9.32E+06
Q8NHP1	Aflatoxin B1 aldehyde reductase member 4 OS=Homo sapiens OX=9606 GN=AKR7L PE=2 SV=7	1.30E+07	8.89E+06	1.71E+07
Q8NE86	Calcium uniporter protein, mitochondrial OS=Homo sapiens OX=9606 GN=MCU PE=1 SV=1 - [M	1.92E+07	4.88E+06	1.07E+07
Q8NE71	ATP-binding cassette sUB-family F member 1 OS=Homo sapiens OX=9606 GN=ABCF1 PE=1 SV	1.13E+08	9.29E+07	1.11E+08
Q8NCE2	MyotUBularin-related protein 14 OS=Homo sapiens OX=9606 GN=MTMR14 PE=1 SV=2 - [MTM	2.55E+07	2.02E+07	5.11E+06
Q8NC51	Plasminogen activator inhibitor 1 RNA-binding protein OS=Homo sapiens OX=9606 GN=SERBP1	1.68E+07	7.44E+06	8.36E+06
Q8NBU5	Outer mitochondrial transmembrane helix translocase OS=Homo sapiens OX=9606 GN=ATAD1	9.10E+06	5.44E+06	1.87E+07
Q8NBS9	Thioredoxin domain-containing protein 5 OS=Homo sapiens OX=9606 GN=TXNDC5 PE=1 SV=2	1.38E+07	1.05E+07	8.86E+06
Q8NBJ5	Procollagen galactosyltransferase 1 OS=Homo sapiens OX=9606 GN=COLGALT1 PE=1 SV=1 - [	1.37E+07	2.81E+07	3.90E+07
Q8N7X4	Melanoma-associated antigen B6 OS=Homo sapiens OX=9606 GN=MAGEB6 PE=1 SV=2 - [MA	2.66E+07	4.03E+07	2.25E+07
Q8N6G6	ADAMTS-like protein 1 OS=Homo sapiens OX=9606 GN=ADAMTSL1 PE=1 SV=4 - [ATL1_HUMA	1.99E+07	4.61E+06	2.28E+07
Q8N568	Serine/threonine-protein kinase DCLK2 OS=Homo sapiens OX=9606 GN=DCLK2 PE=1 SV=4 - [D	1.26E+07	4.93E+06	3.49E+07
Q8N2K0	Lysophosphatidylserine lipase ABHD12 OS=Homo sapiens OX=9606 GN=ABHD12 PE=1 SV=2 - [	1.37E+07	2.38E+07	1.54E+07
Q8N1W1	Rho guanine nucleotide exchange factor 28 OS=Homo sapiens OX=9606 GN=ARHGEF28 PE=1 S	1.14E+07	4.63E+06	1.83E+07
Q8N1N4	Keratin, type II cytoskeletal 78 OS=Homo sapiens OX=9606 GN=KRT78 PE=1 SV=2 - [K2C78_HU	1.05E+08	8.06E+07	3.67E+08
Q8N1F7	Nuclear pore complex protein Nup93 OS=Homo sapiens OX=9606 GN=NUP93 PE=1 SV=2 - [N	7.91E+06	1.13E+07	1.52E+07
Q8IZT6	Abnormal spindle-like microcephaly-associated protein OS=Homo sapiens OX=9606 GN=ASPM	1.39E+07	6.52E+06	5.09E+06
Q8IZ83	Aldehyde dehydrogenase family 16 member A1 OS=Homo sapiens OX=9606 GN=ALDH16A1 PE	1.55E+07	4.49E+06	1.89E+07
Q8IYS4	Dynein axonemal assembly factor 8 OS=Homo sapiens OX=9606 GN=DNAAF8 PE=1 SV=3 - [DA	2.84E+07	8.42E+06	7.88E+07
Q8IYD1	Eukaryotic peptide chain release factor GTP-binding sUBunit ERF3B OS=Homo sapiens OX=9606	1.01E+07	1.27E+07	1.25E+07
Q8IYB3	Serine/arginine repetitive matrix protein 1 OS=Homo sapiens OX=9606 GN=SRRM1 PE=1 SV=2	7.35E+06	4.02E+07	5.48E+06
Q8IY81	pre-rRNA 2'-O-ribose RNA methyltransferase FTSJ3 OS=Homo sapiens OX=9606 GN=FTSJ3 PE	8.50E+06	3.29E+07	2.01E+07
Q8IXI2	Mitochondrial Rho GTPase 1 OS=Homo sapiens OX=9606 GN=RHOT1 PE=1 SV=2 - [MIRO1_HU	1.00E+07	5.91E+06	3.21E+07
Q8IWV8	E3 UBiquitin-protein ligase UBR2 OS=Homo sapiens OX=9606 GN=UBR2 PE=1 SV=1 - [UBR2_HU	2.32E+07	1.48E+07	7.70E+06
Q8IW75	Serpin A12 OS=Homo sapiens OX=9606 GN=SERPINA12 PE=1 SV=1 - [SPA12_HUMAN]	1.20E+07	2.30E+07	6.08E+06
Q86YZ3	Hornerin OS=Homo sapiens OX=9606 GN=HRNR PE=1 SV=2 - [HORN_HUMAN]	1.43E+08	1.69E+08	2.02E+08
Q86Y56	Dynein axonemal assembly factor 5 OS=Homo sapiens OX=9606 GN=DNAAF5 PE=1 SV=4 - [DA	1.02E+07	1.40E+07	1.08E+07
Q86Y46	Keratin, type II cytoskeletal 73 OS=Homo sapiens OX=9606 GN=KRT73 PE=1 SV=1 - [K2C73_HU	1.43E+09	1.42E+09	1.09E+09
Q86X55	Histone-arginine methyltransferase CARM1 OS=Homo sapiens OX=9606 GN=CARM1 PE=1 SV=	7.80E+06	8.12E+06	1.30E+07
Q86WZ0	HEAT repeat-containing protein 4 OS=Homo sapiens OX=9606 GN=HEATR4 PE=2 SV=2 - [HEA	1.17E+07	3.17E+07	7.85E+06
Q86VP6	Cullin-associated NEDD8-dissociated protein 1 OS=Homo sapiens OX=9606 GN=CAND1 PE=1 S	2.10E+08	1.94E+08	2.43E+08

Q86UP2	Kinectin OS=Homo sapiens OX=9606 GN=KTN1 PE=1 SV=1 - [KTN1_HUMAN]	1.29E+07	8.41E+06	1.49E+07
Q86TJ2	Transcriptional adapter 2-beta OS=Homo sapiens OX=9606 GN=TADA2B PE=1 SV=2 - [TAD2B_	1.53E+07	8.39E+06	3.24E+07
Q7Z7A1	Centriolin OS=Homo sapiens OX=9606 GN=CNTRL PE=1 SV=2 - [CNTRL_HUMAN]	2.71E+07	1.07E+07	2.23E+07
Q7Z794	Keratin, type II cytoskeletal 1b OS=Homo sapiens OX=9606 GN=KRT77 PE=1 SV=3 - [K2C1B_HU	1.21E+10	1.07E+10	1.12E+10
Q7Z6Z7	E3 UBiquitin-protein ligase HUWE1 OS=Homo sapiens OX=9606 GN=HUWE1 PE=1 SV=3 - [HU	3.04E+07	6.42E+06	2.40E+07
Q7Z5M8	Protein ABHD12B OS=Homo sapiens OX=9606 GN=ABHD12B PE=1 SV=1 - [AB12B_HUMAN]	1.25E+07	1.00E+07	8.81E+07
Q7RTS7	Keratin, type II cytoskeletal 74 OS=Homo sapiens OX=9606 GN=KRT74 PE=1 SV=2 - [K2C74_HU	1.43E+09	1.42E+09	1.09E+09
Q7L576	Cytoplasmic FMR1-interacting protein 1 OS=Homo sapiens OX=9606 GN=CYFIP1 PE=1 SV=1 - [	1.40E+07	1.44E+07	2.76E+07
Q7L523	Ras-related GTP-binding protein A OS=Homo sapiens OX=9606 GN=RRAGA PE=1 SV=1 - [RRA	4.11E+07	5.03E+07	5.12E+06
Q7L2H7	Eukaryotic translation initiation factor 3 sUBunit M OS=Homo sapiens OX=9606 GN=EIF3M PE=1	1.40E+07	1.09E+07	6.17E+06
Q7L1Q6	eIF5-mimic protein 2 OS=Homo sapiens OX=9606 GN=BZW1 PE=1 SV=1 - [5MP2_HUMAN]	1.11E+07	1.98E+07	2.60E+07
Q7L014	Probable ATP-dependent RNA helicase DDX46 OS=Homo sapiens OX=9606 GN=DDX46 PE=1 S	1.59E+07	2.87E+07	1.26E+07
Q7KZF4	Staphylococcal nuclease domain-containing protein 1 OS=Homo sapiens OX=9606 GN=SND1 P	1.46E+07	4.41E+06	2.27E+07
Q71U36	TUBulin alpha-1A chain OS=Homo sapiens OX=9606 GN=TUBA1A PE=1 SV=1 - [TBA1A_HUMA	3.56E+09	2.64E+09	4.75E+09
Q71DI3	Histone H3.2 OS=Homo sapiens OX=9606 GN=H3C13 PE=1 SV=3 - [H32_HUMAN]	3.34E+09	2.25E+09	8.67E+09
Q712K3	UBiquitin-conjugating enzyme E2 R2 OS=Homo sapiens OX=9606 GN=UBE2R2 PE=1 SV=1 - [UB	3.67E+07	7.72E+06	2.05E+07
Q6ZWH5	Serine/threonine-protein kinase Nek10 OS=Homo sapiens OX=9606 GN=NEK10 PE=1 SV=3 - [N	1.17E+07	1.48E+07	1.60E+07
Q6ZVX7	F-box only protein 50 OS=Homo sapiens OX=9606 GN=NCCRP1 PE=1 SV=1 - [FBX50_HUMAN]	7.94E+06	6.51E+06	6.52E+06
Q6ZMT4	Lysine-specific demethylase 7A OS=Homo sapiens OX=9606 GN=KDM7A PE=1 SV=2 - [KDM7A_	7.54E+06	2.14E+07	9.69E+07
Q6UWP8	Suprabasin OS=Homo sapiens OX=9606 GN=SBSN PE=1 SV=2 - [SBSN_HUMAN]	3.41E+07	1.78E+07	2.18E+07
Q6UB35	Monofunctional C1-tetrahydrofolate synthase, mitochondrial OS=Homo sapiens OX=9606 GN=	2.41E+08	3.04E+08	2.51E+08
Q6SA08	Testis-specific serine/threonine-protein kinase 4 OS=Homo sapiens OX=9606 GN=TSSK4 PE=1 S	1.06E+07	1.92E+07	1.10E+07
Q6QHF9	Peroxisomal N(1)-acetyl-spermine/spermidine oxidase OS=Homo sapiens OX=9606 GN=PAOX	6.88E+06	8.40E+06	1.10E+07
Q6PEZ8	Podocan-like protein 1 OS=Homo sapiens OX=9606 GN=PODNL1 PE=2 SV=2 - [PONL1_HUMA	8.47E+06	9.69E+06	5.72E+06
Q6P9B9	Integrator complex sUBunit 5 OS=Homo sapiens OX=9606 GN=INTS5 PE=1 SV=1 - [INT5_HUM	1.47E+07	8.03E+06	1.18E+07
Q6P3X3	Tetratricopeptide repeat protein 27 OS=Homo sapiens OX=9606 GN=TTC27 PE=1 SV=1 - [TTC2	7.80E+06	1.85E+07	3.24E+07
Q6P2Q9	Pre-mRNA-processing-splicing factor 8 OS=Homo sapiens OX=9606 GN=PRPF8 PE=1 SV=2 - [P	1.53E+07	5.80E+07	1.14E+07
Q6P1X5	Transcription initiation factor TFIID sUBunit 2 OS=Homo sapiens OX=9606 GN=TAF2 PE=1 SV=3	2.04E+08	2.82E+08	3.54E+08
Q6P1M0	Long-chain fatty acid transport protein 4 OS=Homo sapiens OX=9606 GN=SLC27A4 PE=1 SV=1	1.87E+07	2.94E+07	9.78E+06
Q6KB66	Keratin, type II cytoskeletal 80 OS=Homo sapiens OX=9606 GN=KRT80 PE=1 SV=2 - [K2C80_HU	2.33E+10	2.64E+10	2.39E+10
Q6IE37	Ovostatin homolog 1 OS=Homo sapiens OX=9606 GN=OVOS1 PE=2 SV=2 - [OVOS1_HUMAN]	1.28E+07	3.49E+06	7.63E+06
Q6DD88	Atlastin-3 OS=Homo sapiens OX=9606 GN=ATL3 PE=1 SV=1 - [ATLA3_HUMAN]	1.43E+07	2.52E+07	1.51E+07
Q68E01	Integrator complex sUBunit 3 OS=Homo sapiens OX=9606 GN=INTS3 PE=1 SV=1 - [INT3_HUM	1.36E+07	1.25E+07	1.21E+07
Q68CZ6	HAUS augmin-like complex sUBunit 3 OS=Homo sapiens OX=9606 GN=HAUS3 PE=1 SV=1 - [H	1.21E+07	6.23E+06	1.70E+07
Q5VWQ0	Lysine-specific demethylase 9 OS=Homo sapiens OX=9606 GN=RSBN1 PE=1 SV=2 - [RSBN1_HU	1.50E+07	1.45E+07	6.37E+07
Q5TEZ5	Uncharacterized protein C6orf163 OS=Homo sapiens OX=9606 GN=C6orf163 PE=4 SV=2 - [CF1	1.21E+07	1.25E+07	1.34E+07
Q5TEC6	Histone H3-7 OS=Homo sapiens OX=9606 GN=H3-7 PE=1 SV=1 - [H37_HUMAN]	6.62E+09	5.79E+09	7.38E+09
Q5TAA0	Tetratricopeptide repeat protein 22 OS=Homo sapiens OX=9606 GN=TTC22 PE=2 SV=1 - [TTC2	8.58E+06	5.83E+06	1.20E+07
Q5TA45	Integrator complex sUBunit 11 OS=Homo sapiens OX=9606 GN=INTS11 PE=1 SV=2 - [INT11_H	8.39E+06	9.68E+06	1.26E+07
Q5T9A4	ATPase family AAA domain-containing protein 3B OS=Homo sapiens OX=9606 GN=ATAD3B PE	7.71E+06	1.47E+07	2.20E+07
Q5T4S7	E3 UBiquitin-protein ligase UBR4 OS=Homo sapiens OX=9606 GN=UBR4 PE=1 SV=1 - [UBR4_HU	3.32E+07	1.45E+07	3.29E+07
Q5T160	Probable arginine--tRNA ligase, mitochondrial OS=Homo sapiens OX=9606 GN=RARS2 PE=1 S	7.95E+06	5.33E+07	1.22E+07
Q5SRE5	Nucleoporin NUP188 OS=Homo sapiens OX=9606 GN=NUP188 PE=1 SV=1 - [NU188_HUMAN]	9.95E+06	7.44E+06	1.54E+07
Q5K4L6	Solute carrier family 27 member 3 OS=Homo sapiens OX=9606 GN=SLC27A3 PE=1 SV=4 - [S27	5.44E+07	4.90E+07	1.97E+07
Q5JTH9	RRP12-like protein OS=Homo sapiens OX=9606 GN=RRP12 PE=1 SV=2 - [RRP12_HUMAN]	2.18E+07	2.18E+07	1.98E+07
Q5JRX3	Presequence protease, mitochondrial OS=Homo sapiens OX=9606 GN=PITRM1 PE=1 SV=3 - [P	1.59E+07	1.07E+07	1.01E+07
Q5D862	Filaggrin-2 OS=Homo sapiens OX=9606 GN=FLG2 PE=1 SV=1 - [FILA2_HUMAN]	2.36E+08	1.65E+08	2.86E+08
Q58FF8	Putative heat shock protein HSP 90-beta 2 OS=Homo sapiens OX=9606 GN=HSP90AB2P PE=1 S	4.07E+08	1.97E+08	2.15E+08
Q58FF3	Putative endoplasmin-like protein OS=Homo sapiens OX=9606 GN=HSP90B2P PE=5 SV=1 - [EN	9.27E+06	1.36E+08	3.63E+07
Q53GT1	Kelch-like protein 22 OS=Homo sapiens OX=9606 GN=KLHL22 PE=1 SV=2 - [KLH22_HUMAN]	5.11E+07	7.12E+07	4.11E+07
Q53EQ6	Tigger transposable element-derived protein 5 OS=Homo sapiens OX=9606 GN=TIGD5 PE=1 S	1.41E+09	5.66E+08	8.05E+06
Q4KMQ2	Anoctamin-6 OS=Homo sapiens OX=9606 GN=ANO6 PE=1 SV=2 - [ANO6_HUMAN]	1.84E+07	1.20E+07	2.48E+07
Q3ZCQ8	Mitochondrial import inner membrane translocase sUBunit TIM50 OS=Homo sapiens OX=9606 G	1.23E+07	8.17E+06	1.97E+07
Q3SY84	Keratin, type II cytoskeletal 71 OS=Homo sapiens OX=9606 GN=KRT71 PE=1 SV=3 - [K2C71_HU	1.43E+09	1.42E+09	1.09E+09
Q3SY69	Mitochondrial 10-formyltetrahydrofolate dehydrogenase OS=Homo sapiens OX=9606 GN=ALD	2.63E+08	3.51E+08	2.95E+08
Q3KQV9	UDP-N-acetylhexosamine pyrophosphorylase-like protein 1 OS=Homo sapiens OX=9606 GN=U	5.48E+07	2.89E+07	3.22E+07
Q3I5F7	Acyl-coenzyme A thioesterase 6 OS=Homo sapiens OX=9606 GN=ACOT6 PE=2 SV=2 - [ACOT6	8.54E+06	7.77E+06	9.31E+06
Q2TAY7	WD40 repeat-containing protein SMU1 OS=Homo sapiens OX=9606 GN=SMU1 PE=1 SV=2 - [S	1.43E+07	8.05E+06	1.90E+07
Q2M2I5	Keratin, type I cytoskeletal 24 OS=Homo sapiens OX=9606 GN=KRT24 PE=1 SV=1 - [K1C24_HU	1.33E+09	2.31E+09	2.84E+09
Q16822	Phosphoenolpyruvate carboxykinase [GTP], mitochondrial OS=Homo sapiens OX=9606 GN=PCK	3.59E+08	1.87E+08	1.49E+08
Q16658	Fascin OS=Homo sapiens OX=9606 GN=FSCN1 PE=1 SV=3 - [FSCN1_HUMAN]	4.13E+07	8.34E+07	3.54E+07
Q16630	Cleavage and polyadenylation specificity factor sUBunit 6 OS=Homo sapiens OX=9606 GN=CPSF	1.37E+07	7.95E+06	2.57E+07
Q16563	Synaptophysin-like protein 1 OS=Homo sapiens OX=9606 GN=SYPL1 PE=1 SV=1 - [SYPL1_HUM	1.02E+07	1.03E+07	1.05E+07
Q16555	Dihydropyrimidinase-related protein 2 OS=Homo sapiens OX=9606 GN=DPYSL2 PE=1 SV=1 - [	2.31E+07	4.19E+06	5.99E+06
Q16186	Proteasomal UBiquitin receptor ADRM1 OS=Homo sapiens OX=9606 GN=ADRM1 PE=1 SV=2 - [	2.05E+07	2.00E+07	2.42E+07
Q15819	UBiquitin-conjugating enzyme E2 variant 2 OS=Homo sapiens OX=9606 GN=UBE2V2 PE=1 SV=4	2.20E+07	8.32E+06	1.52E+07
Q15643	Thyroid receptor-interacting protein 11 OS=Homo sapiens OX=9606 GN=TRIP11 PE=1 SV=3 - [	2.27E+07	7.40E+06	9.54E+06
Q15517	Corneodesmosin OS=Homo sapiens OX=9606 GN=CDSN PE=1 SV=3 - [CDSN_HUMAN]	9.69E+06	2.82E+07	4.74E+06
Q15437	Protein transport protein Sec23B OS=Homo sapiens OX=9606 GN=SEC23B PE=1 SV=2 - [SC23B_	9.42E+06	1.64E+07	1.58E+07
Q15436	Protein transport protein Sec23A OS=Homo sapiens OX=9606 GN=SEC23A PE=1 SV=2 - [SC23A	1.55E+07	6.85E+06	8.49E+06
Q15418	Ribosomal protein S6 kinase alpha-1 OS=Homo sapiens OX=9606 GN=RPS6KA1 PE=1 SV=2 - [K	2.19E+07	1.45E+07	1.69E+07
Q15397	Pumilio homolog 3 OS=Homo sapiens OX=9606 GN=PUM3 PE=1 SV=3 - [PUM3_HUMAN]	8.05E+06	2.72E+07	5.35E+07
Q15393	Splicing factor 3B sUBunit 3 OS=Homo sapiens OX=9606 GN=SF3B3 PE=1 SV=4 - [SF3B3_HUMA	1.33E+07	1.26E+07	8.77E+06
Q15366	Poly(rC)-binding protein 2 OS=Homo sapiens OX=9606 GN=PCBP2 PE=1 SV=1 - [PCBP2_HUMA	5.83E+07	6.10E+06	5.13E+08
Q15365	Poly(rC)-binding protein 1 OS=Homo sapiens OX=9606 GN=PCBP1 PE=1 SV=2 - [PCBP1_HUMA	1.31E+08	1.37E+07	5.21E+08
Q15323	Keratin, type I cuticular Ha1 OS=Homo sapiens OX=9606 GN=KRT31 PE=1 SV=3 - [K1H1_HUMA	1.11E+09	4.52E+09	1.45E+09
Q15233	Non-POU domain-containing octamer-binding protein OS=Homo sapiens OX=9606 GN=NON	1.56E+07	1.28E+07	6.05E+06
Q15181	Inorganic pyrophosphatase OS=Homo sapiens OX=9606 GN=PPA1 PE=1 SV=2 - [IPYR_HUMAN]	1.01E+07	1.36E+07	8.27E+06
Q15149	Plectin OS=Homo sapiens OX=9606 GN=PLEC PE=1 SV=3 - [PLEC_HUMAN]	5.76E+06	4.51E+06	8.24E+06
Q15139	Serine/threonine-protein kinase D1 OS=Homo sapiens OX=9606 GN=PRKD1 PE=1 SV=2 - [KPCD	7.36E+06	1.12E+07	1.13E+07
Q15120	[Pyruvate dehydrogenase (acetyl-transferring)] kinase isozyme 3, mitochondrial OS=Homo sapien	1.25E+07	4.54E+06	4.76E+07
Q15102	Platelet-activating factor acetylhydrolase IB sUBunit alpha1 OS=Homo sapiens OX=9606 GN=PA	3.00E+07	7.54E+06	4.27E+07
Q15084	Protein disulfide-isomerase A6 OS=Homo sapiens OX=9606 GN=PDIA6 PE=1 SV=1 - [PDIA6_HU	1.14E+08	1.57E+08	3.44E+08
Q15075	Early endosome antigen 1 OS=Homo sapiens OX=9606 GN=EEA1 PE=1 SV=2 - [EEA1_HUMAN]	1.86E+07	7.65E+06	1.03E+07
Q15067	Peroxisomal acyl-coenzyme A oxidase 1 OS=Homo sapiens OX=9606 GN=ACOX1 PE=1 SV=3 -	1.08E+07	1.09E+07	1.20E+07
Q15029	116 kDa U5 small nuclear ribonucleoprotein component OS=Homo sapiens OX=9606 GN=EFTU	8.18E+06	9.67E+06	2.27E+07
Q15008	26S proteasome non-ATPase regulatory sUBunit 6 OS=Homo sapiens OX=9606 GN=PSMD6 PE=	3.42E+07	1.52E+07	7.19E+07
Q14980	Nuclear mitotic apparatus protein 1 OS=Homo sapiens OX=9606 GN=NUMA1 PE=1 SV=2 - [NU	2.26E+07	3.66E+07	1.28E+07
Q14974	Importin sUBunit beta-1 OS=Homo sapiens OX=9606 GN=KPNB1 PE=1 SV=2 - [IMB1_HUMAN]	1.34E+07	7.04E+07	1.40E+07
Q14807	Kinesin-like protein KIF22 OS=Homo sapiens OX=9606 GN=KIF22 PE=1 SV=5 - [KIF22_HUMAN]	1.29E+07	7.42E+06	1.08E+07
Q147U7	Single-pass membrane and coiled-coil domain-containing protein 1 OS=Homo sapiens OX=960	1.39E+07	4.93E+06	1.72E+07
Q14574	Desmocollin-3 OS=Homo sapiens OX=9606 GN=DSC3 PE=1 SV=3 - [DSC3_HUMAN]	1.45E+07	8.00E+06	2.07E+07
Q14573	Inositol 1,4,5-trisphosphate receptor type 3 OS=Homo sapiens OX=9606 GN=ITPR3 PE=1 SV=2	2.46E+07	9.32E+06	1.22E+07
Q14566	DNA replication licensing factor MCM6 OS=Homo sapiens OX=9606 GN=MCM6 PE=1 SV=1 - [M	4.60E+07	4.23E+07	8.49E+06
Q14525	Keratin, type I cuticular Ha3-II OS=Homo sapiens OX=9606 GN=KRT33B PE=1 SV=3 - [KT33B_HU	6.96E+08	4.52E+09	1.45E+09
Q14498	RNA-binding protein 39 OS=Homo sapiens OX=9606 GN=RBM39 PE=1 SV=2 - [RBM39_HUMA	1.71E+07	1.32E+07	1.08E+07
Q14331	Protein FRG1 OS=Homo sapiens OX=9606 GN=FRG1 PE=1 SV=1 - [FRG1_HUMAN]	2.19E+07	5.94E+06	3.44E+08
Q14315	Filamin-C OS=Homo sapiens OX=9606 GN=FLNC PE=1 SV=3 - [FLNC_HUMAN]	3.49E+07	2.36E+07	2.96E+07
Q14232	Translation initiation factor eIF-2B sUBunit alpha OS=Homo sapiens OX=9606 GN=EIF2B1 PE=1 S	1.77E+07	8.90E+06	1.62E+07
Q14204	Cytoplasmic dynein 1 heavy chain 1 OS=Homo sapiens OX=9606 GN=DYNC1H1 PE=1 SV=5 - [D	4.45E+07	3.24E+07	1.34E+07
Q14166	TUBulin--tyrosine ligase-like protein 12 OS=Homo sapiens OX=9606 GN=TTLL12 PE=1 SV=2 - [	6.27E+06	2.38E+07	2.58E+07
Q14152	Eukaryotic translation initiation factor 3 sUBunit A OS=Homo sapiens OX=9606 GN=EIF3A PE=1 S	8.39E+06	2.71E+06	2.01E+07
Q13885	TUBulin beta-2A chain OS=Homo sapiens OX=9606 GN=TUBB2A PE=1 SV=1 - [TBB2A_HUMAN]	1.74E+09	1.24E+09	2.39E+09
Q13838	Spliceosome RNA helicase DDX39B OS=Homo sapiens OX=9606 GN=DDX39B PE=1 SV=1 - [DX	9.21E+07	2.75E+06	1.83E+08
Q13637	Ras-related protein Rab-32 OS=Homo sapiens OX=9606 GN=RAB32 PE=1 SV=3 - [RAB32_HUM	3.66E+07	1.38E+07	7.97E+06
Q13619	Cullin-4A OS=Homo sapiens OX=9606 GN=CUL4A PE=1 SV=3 - [CUL4A_HUMAN]	1.16E+07	2.15E+07	2.26E+07
Q13595	Transformer-2 protein homolog alpha OS=Homo sapiens OX=9606 GN=TRA2A PE=1 SV=1 - [T	1.70E+07	9.60E+06	1.55E+07
Q13557	Calcium/calmodulin-dependent protein kinase type II sUBunit delta OS=Homo sapiens OX=9606	2.70E+07	1.83E+07	2.76E+07
Q13547	Histone deacetylase 1 OS=Homo sapiens OX=9606 GN=HDAC1 PE=1 SV=1 - [HDAC1_HUMAN]	1.93E+07	1.24E+07	1.21E+07
Q13523	Serine/threonine-protein kinase PRP4 homolog OS=Homo sapiens OX=9606 GN=PRPF4B PE=1	1.14E+08	1.34E+08	1.85E+08
Q13509	TUBulin beta-3 chain OS=Homo sapiens OX=9606 GN=TUBB3 PE=1 SV=2 - [TBB3_HUMAN]	1.74E+09	1.14E+09	1.96E+09
Q13459	Unconventional myosin-IXb OS=Homo sapiens OX=9606 GN=MYO9B PE=1 SV=3 - [MYO9B_HU	3.60E+07	8.47E+07	1.42E+08
Q13423	NAD(P) transhydrogenase, mitochondrial OS=Homo sapiens OX=9606 GN=NNT PE=1 SV=3 - [N	7.69E+06	1.18E+07	7.21E+06
Q13362	Serine/threonine-protein phosphatase 2A 56 kDa regulatory sUBunit gamma isoform OS=Homo	2.01E+07	2.12E+07	7.93E+06
Q13228	Methanethiol oxidase OS=Homo sapiens OX=9606 GN=SELENBP1 PE=1 SV=2 - [SBP1_HUMAN]	1.22E+08	1.08E+08	1.28E+08
Q13206	Probable ATP-dependent RNA helicase DDX10 OS=Homo sapiens OX=9606 GN=DDX10 PE=1 S	1.24E+07	9.02E+06	1.66E+07
Q13200	26S proteasome non-ATPase regulatory sUBunit 2 OS=Homo sapiens OX=9606 GN=PSMD2 PE=	3.24E+07	2.06E+07	7.91E+06
Q13185	Chromobox protein homolog 3 OS=Homo sapiens OX=9606 GN=CBX3 PE=1 SV=4 - [CBX3_HU	8.49E+06	6.13E+06	9.47E+06
Q13177	Serine/threonine-protein kinase PAK 2 OS=Homo sapiens OX=9606 GN=PAK2 PE=1 SV=3 - [PA	2.56E+07	7.12E+06	1.28E+07
Q13162	Peroxiredoxin-4 OS=Homo sapiens OX=9606 GN=PRDX4 PE=1 SV=1 - [PRDX4_HUMAN]	5.45E+08	4.42E+08	1.00E+09
Q13155	Aminoacyl tRNA synthase complex-interacting multifunctional protein 2 OS=Homo sapiens OX=	8.80E+07	6.21E+07	1.75E+07
Q13148	TAR DNA-binding protein 43 OS=Homo sapiens OX=9606 GN=TARDBP PE=1 SV=1 - [TADBP_H	2.57E+08	1.10E+07	1.17E+08
Q13131	5'-AMP-activated protein kinase catalytic sUBunit alpha-1 OS=Homo sapiens OX=9606 GN=PRK	3.01E+07	5.57E+06	5.08E+07
Q13107	UBiquitin carboxyl-terminal hydrolase 4 OS=Homo sapiens OX=9606 GN=USP4 PE=1 SV=3 - [UB	9.72E+06	1.11E+07	2.91E+07
Q13085	Acetyl-CoA carboxylase 1 OS=Homo sapiens OX=9606 GN=ACACA PE=1 SV=2 - [ACACA_HUM	5.15E+09	4.43E+09	3.30E+09
Q13045	Protein flightless-1 homolog OS=Homo sapiens OX=9606 GN=FLII PE=1 SV=2 - [FLII_HUMAN]	2.10E+07	1.98E+07	1.25E+07
Q12931	Heat shock protein 75 kDa, mitochondrial OS=Homo sapiens OX=9606 GN=TRAP1 PE=1 SV=3 -	6.98E+07	5.53E+07	5.85E+07
Q12906	Interleukin enhancer-binding factor 3 OS=Homo sapiens OX=9606 GN=ILF3 PE=1 SV=3 - [ILF3_	2.17E+07	1.24E+07	6.88E+06
Q12905	Interleukin enhancer-binding factor 2 OS=Homo sapiens OX=9606 GN=ILF2 PE=1 SV=2 - [ILF2_	4.84E+06	1.72E+07	1.64E+07

Q12792	Twinfilin-1 OS=Homo sapiens OX=9606 GN=TWF1 PE=1 SV=3 - [TWF1_HUMAN]	1.27E+07	1.01E+07	7.62E+06
Q12768	WASH complex sUBunit 5 OS=Homo sapiens OX=9606 GN=WASHC5 PE=1 SV=1 - [WASC5_HU	2.00E+07	8.41E+06	1.67E+07
Q12765	Secernin-1 OS=Homo sapiens OX=9606 GN=SCRN1 PE=1 SV=2 - [SCRN1_HUMAN]	4.06E+09	1.91E+07	6.44E+06
Q09161	Nuclear cap-binding protein sUBunit 1 OS=Homo sapiens OX=9606 GN=NCBP1 PE=1 SV=1 - [N	7.49E+06	1.67E+07	5.61E+06
Q09028	Histone-binding protein RBBP4 OS=Homo sapiens OX=9606 GN=RBBP4 PE=1 SV=3 - [RBBP4_H	1.72E+07	1.33E+07	1.16E+07
Q08J23	RNA cytosine C(5)-methyltransferase NSUN2 OS=Homo sapiens OX=9606 GN=NSUN2 PE=1 SV	2.65E+07	3.43E+06	1.29E+07
Q08554	Desmocollin-1 OS=Homo sapiens OX=9606 GN=DSC1 PE=1 SV=2 - [DSC1_HUMAN]	2.46E+07	3.80E+07	7.43E+07
Q08211	ATP-dependent RNA helicase A OS=Homo sapiens OX=9606 GN=DHX9 PE=1 SV=4 - [DHX9_H	8.77E+07	5.61E+07	1.13E+08
Q08209	Protein phosphatase 3 catalytic sUBunit alpha OS=Homo sapiens OX=9606 GN=PPP3CA PE=1 SV	2.18E+07	1.65E+07	5.90E+06
Q08188	Protein-glutamine gamma-glutamyltransferase E OS=Homo sapiens OX=9606 GN=TGM3 PE=1	1.95E+07	1.02E+07	7.92E+06
Q07955	Serine/arginine-rich splicing factor 1 OS=Homo sapiens OX=9606 GN=SRSF1 PE=1 SV=2 - [SRSF	1.44E+07	9.66E+06	2.50E+07
Q07954	Prolow-density lipoprotein receptor-related protein 1 OS=Homo sapiens OX=9606 GN=LRP1 PE	2.54E+07	1.57E+07	9.80E+06
Q07020	60S ribosomal protein L18 OS=Homo sapiens OX=9606 GN=RPL18 PE=1 SV=2 - [RL18_HUMAN]	1.79E+07	4.50E+06	1.18E+08
Q06830	Peroxiredoxin-1 OS=Homo sapiens OX=9606 GN=PRDX1 PE=1 SV=1 - [PRDX1_HUMAN]	4.76E+08	5.55E+08	7.01E+08
Q06787	Synaptic functional regulator FMR1 OS=Homo sapiens OX=9606 GN=FMR1 PE=1 SV=1 - [FMR1_	2.13E+07	1.25E+07	2.46E+07
Q06330	Recombining binding protein suppressor of hairless OS=Homo sapiens OX=9606 GN=RBPJ PE=1	1.60E+07	1.02E+07	3.10E+07
Q06210	Glutamine--fructose-6-phosphate aminotransferase [isomerizing] 1 OS=Homo sapiens OX=960	4.47E+07	8.26E+06	1.31E+07
Q06124	Tyrosine-protein phosphatase non-receptor type 11 OS=Homo sapiens OX=9606 GN=PTPN11	1.16E+07	9.07E+06	5.53E+06
Q05655	Protein kinase C delta type OS=Homo sapiens OX=9606 GN=PRKCD PE=1 SV=2 - [KPCD_HUMA	1.21E+07	1.69E+07	8.17E+06
Q05086	UBiquitin-protein ligase E3A OS=Homo sapiens OX=9606 GN=UBE3A PE=1 SV=4 - [UBE3A_HU	1.71E+07	1.41E+07	1.47E+07
Q04917	14-3-3 protein eta OS=Homo sapiens OX=9606 GN=YWHAH PE=1 SV=4 - [1433F_HUMAN]	1.02E+08	1.10E+07	1.27E+07
Q04695	Keratin, type I cytoskeletal 17 OS=Homo sapiens OX=9606 GN=KRT17 PE=1 SV=2 - [K1C17_HU	1.66E+09	3.23E+09	3.05E+09
Q04446	1,4-alpha-glucan-branching enzyme OS=Homo sapiens OX=9606 GN=GBE1 PE=1 SV=3 - [GLG	4.41E+07	1.67E+07	1.10E+07
Q03519	Antigen peptide transporter 2 OS=Homo sapiens OX=9606 GN=TAP2 PE=1 SV=1 - [TAP2_HUM	3.51E+07	5.79E+06	9.03E+06
Q02978	Mitochondrial 2-oxoglutarate/malate carrier protein OS=Homo sapiens OX=9606 GN=SLC25A1	1.88E+07	3.04E+07	7.26E+06
Q02880	DNA topoisomerase 2-beta OS=Homo sapiens OX=9606 GN=TOP2B PE=1 SV=3 - [TOP2B_HUM	1.48E+07	1.05E+08	1.12E+08
Q02878	60S ribosomal protein L6 OS=Homo sapiens OX=9606 GN=RPL6 PE=1 SV=3 - [RL6_HUMAN]	6.10E+09	5.37E+09	6.66E+09
Q02809	Procollagen-lysine,2-oxoglutarate 5-dioxygenase 1 OS=Homo sapiens OX=9606 GN=PLOD1 PE	1.75E+07	1.07E+07	3.11E+07
Q02543	60S ribosomal protein L18a OS=Homo sapiens OX=9606 GN=RPL18A PE=1 SV=2 - [RL18A_HU	7.75E+08	1.04E+09	1.61E+09
Q02413	Desmoglein-1 OS=Homo sapiens OX=9606 GN=DSG1 PE=1 SV=2 - [DSG1_HUMAN]	1.03E+08	1.91E+08	1.56E+08
Q02218	2-oxoglutarate dehydrogenase complex component E1 OS=Homo sapiens OX=9606 GN=OGD	1.69E+07	7.88E+07	7.44E+07
Q01813	ATP-dependent 6-phosphofructokinase, platelet type OS=Homo sapiens OX=9606 GN=PFKP PE	2.70E+08	2.92E+08	2.07E+08
Q01469	Fatty acid-binding protein 5 OS=Homo sapiens OX=9606 GN=FABP5 PE=1 SV=3 - [FABP5_HUM	1.61E+07	9.70E+06	1.08E+07
Q01433	AMP deaminase 2 OS=Homo sapiens OX=9606 GN=AMPD2 PE=1 SV=2 - [AMPD2_HUMAN]	1.20E+07	9.61E+06	1.05E+07
Q01432	AMP deaminase 3 OS=Homo sapiens OX=9606 GN=AMPD3 PE=1 SV=1 - [AMPD3_HUMAN]	4.08E+07	3.12E+06	1.53E+07
Q00839	Heterogeneous nuclear ribonucleoprotein U OS=Homo sapiens OX=9606 GN=HNRNPU PE=1 SV	1.96E+08	2.56E+08	2.74E+08
Q00610	Clathrin heavy chain 1 OS=Homo sapiens OX=9606 GN=CLTC PE=1 SV=5 - [CLH1_HUMAN]	2.01E+08	2.36E+08	2.49E+08
Q00577	Transcriptional activator protein Pur-alpha OS=Homo sapiens OX=9606 GN=PURA PE=1 SV=2 -	2.74E+07	3.77E+06	1.18E+07
Q00341	Vigilin OS=Homo sapiens OX=9606 GN=HDLBP PE=1 SV=2 - [VIGLN_HUMAN]	3.06E+07	3.42E+07	6.97E+07
Q00325	Phosphate carrier protein, mitochondrial OS=Homo sapiens OX=9606 GN=SLC25A3 PE=1 SV=2	1.16E+07	1.77E+07	3.06E+08
Q00013	55 kDa erythrocyte membrane protein OS=Homo sapiens OX=9606 GN=MPP1 PE=1 SV=2 - [EM	3.84E+07	7.72E+06	9.66E+06
P84243	Histone H3.3 OS=Homo sapiens OX=9606 GN=H3-3B PE=1 SV=2 - [H33_HUMAN]	3.34E+09	3.23E+09	8.67E+09
P84103	Serine/arginine-rich splicing factor 3 OS=Homo sapiens OX=9606 GN=SRSF3 PE=1 SV=1 - [SRSF	1.64E+07	7.95E+06	1.44E+08
P84098	60S ribosomal protein L19 OS=Homo sapiens OX=9606 GN=RPL19 PE=1 SV=1 - [RL19_HUMAN]	2.73E+07	1.04E+07	2.57E+07
P84095	Rho-related GTP-binding protein RhoG OS=Homo sapiens OX=9606 GN=RHOG PE=1 SV=1 - [R	2.35E+07	2.61E+07	1.28E+07
P84022	Mothers against decapentaplegic homolog 3 OS=Homo sapiens OX=9606 GN=SMAD3 PE=1 SV	6.08E+06	1.38E+07	1.28E+07
P83881	60S ribosomal protein L36a OS=Homo sapiens OX=9606 GN=RPL36A PE=1 SV=2 - [RL36A_HU	2.04E+09	1.20E+09	2.01E+09
P83731	60S ribosomal protein L24 OS=Homo sapiens OX=9606 GN=RPL24 PE=1 SV=1 - [RL24_HUMAN]	2.20E+08	2.98E+08	3.49E+08
P81605	Dermcidin OS=Homo sapiens OX=9606 GN=DCD PE=1 SV=2 - [DCD_HUMAN]	6.96E+08	2.92E+08	4.86E+08
P80188	Neutrophil gelatinase-associated lipocalin OS=Homo sapiens OX=9606 GN=LCN2 PE=1 SV=2 - [	9.19E+06	9.14E+06	1.60E+07
P78386	Keratin, type II cuticular Hb5 OS=Homo sapiens OX=9606 GN=KRT85 PE=1 SV=1 - [KRT85_HUM	8.36E+08	2.85E+07	3.91E+08
P78371	T-complex protein 1 sUBunit beta OS=Homo sapiens OX=9606 GN=CCT2 PE=1 SV=4 - [TCPB_H	1.36E+07	4.11E+07	1.16E+07
P78362	SRSF protein kinase 2 OS=Homo sapiens OX=9606 GN=SRPK2 PE=1 SV=3 - [SRPK2_HUMAN]	5.65E+07	4.71E+07	6.26E+07
P78344	Eukaryotic translation initiation factor 4 gamma 2 OS=Homo sapiens OX=9606 GN=EIF4G2 PE=1	3.31E+07	7.66E+06	1.43E+07
P68402	Platelet-activating factor acetylhydrolase IB sUBunit alpha2 OS=Homo sapiens OX=9606 GN=PA	1.79E+07	2.05E+07	3.27E+07
P68371	TUBulin beta-4B chain OS=Homo sapiens OX=9606 GN=TUBB4B PE=1 SV=1 - [TBB4B_HUMAN]	2.23E+09	1.79E+09	2.60E+09
P68366	TUBulin alpha-4A chain OS=Homo sapiens OX=9606 GN=TUBA4A PE=1 SV=1 - [TBA4A_HUMA	3.08E+09	2.34E+09	4.33E+09
P68104	Elongation factor 1-alpha 1 OS=Homo sapiens OX=9606 GN=EEF1A1 PE=1 SV=1 - [EF1A1_HU	3.55E+09	4.14E+09	5.46E+09
P68036	UBiquitin-conjugating enzyme E2 L3 OS=Homo sapiens OX=9606 GN=UBE2L3 PE=1 SV=1 - [UB	1.32E+07	2.28E+07	1.78E+07
P68032	Actin, alpha cardiac muscle 1 OS=Homo sapiens OX=9606 GN=ACTC1 PE=1 SV=1 - [ACTC_HUM	1.88E+09	1.54E+09	3.05E+09
P63279	SUMO-conjugating enzyme UBC9 OS=Homo sapiens OX=9606 GN=UBE2I PE=1 SV=1 - [UBC9_	1.39E+07	2.36E+07	9.07E+06
P63244	Receptor of activated protein C kinase 1 OS=Homo sapiens OX=9606 GN=RACK1 PE=1 SV=3 - [	7.95E+08	6.57E+08	8.97E+08
P63241	Eukaryotic translation initiation factor 5A-1 OS=Homo sapiens OX=9606 GN=EIF5A PE=1 SV=2 -	2.48E+08	2.11E+08	1.79E+08
P63151	Serine/threonine-protein phosphatase 2A 55 kDa regulatory sUBunit B alpha isoform OS=Homo	3.13E+07	4.00E+07	2.35E+07
P63104	14-3-3 protein zeta/delta OS=Homo sapiens OX=9606 GN=YWHAZ PE=1 SV=1 - [1433Z_HUM	1.02E+08	4.58E+06	1.65E+07
P63010	AP-2 complex sUBunit beta OS=Homo sapiens OX=9606 GN=AP2B1 PE=1 SV=1 - [AP2B1_HUM	7.82E+07	4.41E+06	6.30E+06
P63000	Ras-related C3 botulinum toxin sUBstrate 1 OS=Homo sapiens OX=9606 GN=RAC1 PE=1 SV=1	1.54E+07	1.03E+07	7.74E+07
P62979	UBiquitin-40S ribosomal protein S27a OS=Homo sapiens OX=9606 GN=RPS27A PE=1 SV=2 - [R	1.41E+10	1.47E+10	2.89E+10
P62937	Peptidyl-prolyl cis-trans isomerase A OS=Homo sapiens OX=9606 GN=PPIA PE=1 SV=2 - [PPIA_	1.36E+07	9.19E+06	7.20E+06
P62917	60S ribosomal protein L8 OS=Homo sapiens OX=9606 GN=RPL8 PE=1 SV=2 - [RL8_HUMAN]	6.45E+08	7.60E+08	8.24E+08
P62913	60S ribosomal protein L11 OS=Homo sapiens OX=9606 GN=RPL11 PE=1 SV=2 - [RL11_HUMAN]	7.70E+08	7.80E+08	1.36E+09
P62910	60S ribosomal protein L32 OS=Homo sapiens OX=9606 GN=RPL32 PE=1 SV=2 - [RL32_HUMAN]	1.67E+08	1.68E+08	4.64E+08
P62888	60S ribosomal protein L30 OS=Homo sapiens OX=9606 GN=RPL30 PE=1 SV=2 - [RL30_HUMAN]	4.23E+07	4.78E+06	9.35E+07
P62873	Guanine nucleotide-binding protein G(I)/G(S)/G(T) sUBunit beta-1 OS=Homo sapiens OX=9606 G	2.03E+07	1.28E+07	2.73E+07
P62861	FAU UBiquitin-like and ribosomal protein S30 OS=Homo sapiens OX=9606 GN=FAU PE=1 SV=2	5.78E+06	1.40E+07	2.17E+07
P62854	40S ribosomal protein S26 OS=Homo sapiens OX=9606 GN=RPS26 PE=1 SV=3 - [RS26_HUMAN	1.58E+09	1.40E+09	2.17E+09
P62851	40S ribosomal protein S25 OS=Homo sapiens OX=9606 GN=RPS25 PE=1 SV=1 - [RS25_HUMAN	8.97E+08	8.73E+08	2.10E+09
P62847	40S ribosomal protein S24 OS=Homo sapiens OX=9606 GN=RPS24 PE=1 SV=1 - [RS24_HUMAN	1.18E+07	6.71E+06	1.78E+07
P62829	60S ribosomal protein L23 OS=Homo sapiens OX=9606 GN=RPL23 PE=1 SV=1 - [RL23_HUMAN]	1.62E+08	9.97E+07	2.08E+08
P62826	GTP-binding nuclear protein Ran OS=Homo sapiens OX=9606 GN=RAN PE=1 SV=3 - [RAN_HU	4.90E+08	5.13E+08	9.24E+08
P62820	Ras-related protein Rab-1A OS=Homo sapiens OX=9606 GN=RAB1A PE=1 SV=3 - [RAB1A_HU	2.78E+08	2.06E+08	3.99E+08
P62805	Histone H4 OS=Homo sapiens OX=9606 GN=H4-16 PE=1 SV=2 - [H4_HUMAN]	1.17E+07	1.37E+07	1.36E+07
P62753	40S ribosomal protein S6 OS=Homo sapiens OX=9606 GN=RPS6 PE=1 SV=1 - [RS6_HUMAN]	4.68E+07	1.17E+07	8.59E+07
P62750	60S ribosomal protein L23a OS=Homo sapiens OX=9606 GN=RPL23A PE=1 SV=1 - [RL23A_HU	3.87E+08	1.31E+07	6.28E+08
P62714	Serine/threonine-protein phosphatase 2A catalytic sUBunit beta isoform OS=Homo sapiens OX=	1.10E+08	9.65E+07	1.94E+08
P62701	40S ribosomal protein S4, X isoform OS=Homo sapiens OX=9606 GN=RPS4X PE=1 SV=2 - [RS4	7.61E+08	6.63E+08	1.07E+09
P62495	Eukaryotic peptide chain release factor sUBunit 1 OS=Homo sapiens OX=9606 GN=ETF1 PE=1 S	1.18E+07	1.60E+07	1.41E+07
P62424	60S ribosomal protein L7a OS=Homo sapiens OX=9606 GN=RPL7A PE=1 SV=2 - [RL7A_HUMAN	3.46E+08	1.81E+08	8.73E+08
P62333	26S proteasome regulatory sUBunit 10B OS=Homo sapiens OX=9606 GN=PSMC6 PE=1 SV=1 - [	1.93E+09	8.74E+06	5.91E+06
P62330	ADP-ribosylation factor 6 OS=Homo sapiens OX=9606 GN=ARF6 PE=1 SV=2 - [ARF6_HUMAN]	1.30E+07	2.64E+07	2.24E+07
P62280	40S ribosomal protein S11 OS=Homo sapiens OX=9606 GN=RPS11 PE=1 SV=3 - [RS11_HUMAN	1.60E+07	5.09E+06	3.09E+08
P62266	40S ribosomal protein S23 OS=Homo sapiens OX=9606 GN=RPS23 PE=1 SV=3 - [RS23_HUMAN	1.21E+09	9.95E+08	9.50E+08
P62263	40S ribosomal protein S14 OS=Homo sapiens OX=9606 GN=RPS14 PE=1 SV=3 - [RS14_HUMAN	2.82E+08	1.85E+08	5.57E+08
P62258	14-3-3 protein epsilon OS=Homo sapiens OX=9606 GN=YWHAE PE=1 SV=1 - [1433E_HUMAN]	1.02E+08	4.58E+06	1.31E+07
P62249	40S ribosomal protein S16 OS=Homo sapiens OX=9606 GN=RPS16 PE=1 SV=2 - [RS16_HUMAN	2.25E+08	2.08E+08	5.51E+08
P62244	40S ribosomal protein S15a OS=Homo sapiens OX=9606 GN=RPS15A PE=1 SV=2 - [RS15A_HU	9.04E+06	1.34E+07	8.88E+07
P62241	40S ribosomal protein S8 OS=Homo sapiens OX=9606 GN=RPS8 PE=1 SV=2 - [RS8_HUMAN]	3.19E+09	3.17E+09	6.32E+09
P61981	14-3-3 protein gamma OS=Homo sapiens OX=9606 GN=YWHAG PE=1 SV=2 - [1433G_HUMAN	1.02E+08	4.98E+06	1.44E+07
P61978	Heterogeneous nuclear ribonucleoprotein K OS=Homo sapiens OX=9606 GN=HNRNPK PE=1 SV	8.51E+07	7.88E+07	8.56E+07
P61960	UBiquitin-fold modifier 1 OS=Homo sapiens OX=9606 GN=UFM1 PE=1 SV=1 - [UFM1_HUMAN]	2.40E+07	2.78E+08	2.96E+08
P61956	Small UBiquitin-related modifier 2 OS=Homo sapiens OX=9606 GN=SUMO2 PE=1 SV=3 - [SUM	1.91E+07	2.24E+07	1.21E+07
P61927	60S ribosomal protein L37 OS=Homo sapiens OX=9606 GN=RPL37 PE=1 SV=2 - [RL37_HUMAN]	6.53E+08	4.16E+08	1.39E+07
P61626	Lysozyme C OS=Homo sapiens OX=9606 GN=LYZ PE=1 SV=1 - [LYSC_HUMAN]	1.51E+08	3.77E+07	1.42E+08
P61619	Protein transport protein Sec61 sUBunit alpha isoform 1 OS=Homo sapiens OX=9606 GN=SEC61	5.55E+07	6.76E+07	2.24E+07
P61586	Transforming protein RhoA OS=Homo sapiens OX=9606 GN=RHOA PE=1 SV=1 - [RHOA_HUMA	7.36E+06	1.22E+07	9.91E+06
P61513	60S ribosomal protein L37a OS=Homo sapiens OX=9606 GN=RPL37A PE=1 SV=2 - [RL37A_HU	4.28E+07	3.90E+07	2.20E+08
P61353	60S ribosomal protein L27 OS=Homo sapiens OX=9606 GN=RPL27 PE=1 SV=2 - [RL27_HUMAN]	2.65E+08	3.02E+08	3.78E+08
P61313	60S ribosomal protein L15 OS=Homo sapiens OX=9606 GN=RPL15 PE=1 SV=2 - [RL15_HUMAN]	2.18E+08	8.07E+07	2.48E+08
P61254	60S ribosomal protein L26 OS=Homo sapiens OX=9606 GN=RPL26 PE=1 SV=1 - [RL26_HUMAN]	2.61E+07	5.67E+06	2.25E+07
P61247	40S ribosomal protein S3a OS=Homo sapiens OX=9606 GN=RPS3A PE=1 SV=2 - [RS3A_HUMA	2.74E+08	1.76E+08	4.18E+08
P61221	ATP-binding cassette sUB-family E member 1 OS=Homo sapiens OX=9606 GN=ABCE1 PE=1 SV	1.29E+08	1.43E+08	1.16E+08
P61204	ADP-ribosylation factor 3 OS=Homo sapiens OX=9606 GN=ARF3 PE=1 SV=2 - [ARF3_HUMAN]	6.16E+08	6.04E+08	2.61E+08
P61163	Alpha-centractin OS=Homo sapiens OX=9606 GN=ACTR1A PE=1 SV=1 - [ACTZ_HUMAN]	8.64E+06	5.43E+06	1.14E+07
P61158	Actin-related protein 3 OS=Homo sapiens OX=9606 GN=ACTR3 PE=1 SV=3 - [ARP3_HUMAN]	6.35E+06	8.11E+06	2.35E+07
P61106	Ras-related protein Rab-14 OS=Homo sapiens OX=9606 GN=RAB14 PE=1 SV=4 - [RAB14_HUM	2.78E+08	2.35E+08	5.69E+08
P61088	UBiquitin-conjugating enzyme E2 N OS=Homo sapiens OX=9606 GN=UBE2N PE=1 SV=1 - [UBE	1.25E+07	2.39E+07	1.12E+07
P61086	UBiquitin-conjugating enzyme E2 K OS=Homo sapiens OX=9606 GN=UBE2K PE=1 SV=3 - [UBE2	1.63E+07	3.86E+06	9.23E+07
P61077	UBiquitin-conjugating enzyme E2 D3 OS=Homo sapiens OX=9606 GN=UBE2D3 PE=1 SV=1 - [U	1.99E+07	6.76E+06	2.14E+08
P61026	Ras-related protein Rab-10 OS=Homo sapiens OX=9606 GN=RAB10 PE=1 SV=1 - [RAB10_HUM	1.74E+08	2.35E+08	4.99E+08
P61019	Ras-related protein Rab-2A OS=Homo sapiens OX=9606 GN=RAB2A PE=1 SV=1 - [RAB2A_HU	2.01E+07	1.68E+07	3.81E+07
P61011	Signal recognition particle 54 kDa protein OS=Homo sapiens OX=9606 GN=SRP54 PE=1 SV=1 -	2.89E+07	2.04E+07	9.45E+06
P60953	Cell division control protein 42 homolog OS=Homo sapiens OX=9606 GN=CDC42 PE=1 SV=2 - [	4.00E+07	6.14E+06	7.54E+06
P60891	Ribose-phosphate pyrophosphokinase 1 OS=Homo sapiens OX=9606 GN=PRPS1 PE=1 SV=2 - [	7.71E+07	5.54E+07	8.70E+07
P60866	40S ribosomal protein S20 OS=Homo sapiens OX=9606 GN=RPS20 PE=1 SV=1 - [RS20_HUMAN	8.04E+07	8.16E+07	2.68E+08
P60842	Eukaryotic initiation factor 4A-I OS=Homo sapiens OX=9606 GN=EIF4A1 PE=1 SV=1 - [IF4A1_H	7.91E+08	9.43E+08	2.28E+09
P60709	Actin, cytoplasmic 1 OS=Homo sapiens OX=9606 GN=ACTB PE=1 SV=1 - [ACTB_HUMAN]	2.76E+09	2.62E+09	5.66E+09
P60228	Eukaryotic translation initiation factor 3 sUBunit E OS=Homo sapiens OX=9606 GN=EIF3E PE=1 S	1.47E+07	1.82E+07	8.79E+06
P60174	Triosephosphate isomerase OS=Homo sapiens OX=9606 GN=TPI1 PE=1 SV=4 - [TPIS_HUMAN]	2.00E+07	2.15E+07	1.79E+07
P59780	AP-3 complex sUBunit sigma-2 OS=Homo sapiens OX=9606 GN=AP3S2 PE=2 SV=1 - [AP3S2_H	1.27E+07	1.09E+07	6.13E+08

P57772	Selenocysteine-specific elongation factor OS=Homo sapiens OX=9606 GN=EEFSEC PE=1 SV=4 -	2.65E+07	6.74E+06	9.67E+06
P57088	Transmembrane protein 33 OS=Homo sapiens OX=9606 GN=TMEM33 PE=1 SV=2 - [TMM33_H	1.72E+07	5.89E+06	1.56E+07
P56962	Syntaxin-17 OS=Homo sapiens OX=9606 GN=STX17 PE=1 SV=2 - [STX17_HUMAN]	2.02E+07	8.06E+06	1.09E+07
P56537	Eukaryotic translation initiation factor 6 OS=Homo sapiens OX=9606 GN=EIF6 PE=1 SV=1 - [IF6_	1.57E+07	1.08E+07	7.36E+06
P56192	Methionine--tRNA ligase, cytoplasmic OS=Homo sapiens OX=9606 GN=MARS1 PE=1 SV=2 - [S	7.72E+06	9.04E+06	1.08E+07
P55884	Eukaryotic translation initiation factor 3 sUBunit B OS=Homo sapiens OX=9606 GN=EIF3B PE=1 S	1.47E+07	1.74E+07	7.81E+06
P55809	Succinyl-CoA:3-ketoacid coenzyme A transferase 1, mitochondrial OS=Homo sapiens OX=9606	1.23E+07	1.29E+07	1.49E+07
P55786	Puromycin-sensitive aminopeptidase OS=Homo sapiens OX=9606 GN=NPEPPS PE=1 SV=2 - [PS	1.74E+07	2.31E+07	8.66E+06
P55084	Trifunctional enzyme sUBunit beta, mitochondrial OS=Homo sapiens OX=9606 GN=HADHB PE=1	1.78E+07	5.62E+06	4.17E+08
P55072	Transitional endoplasmic reticulum ATPase OS=Homo sapiens OX=9606 GN=VCP PE=1 SV=4 - [	3.60E+07	1.23E+07	6.17E+06
P55060	Exportin-2 OS=Homo sapiens OX=9606 GN=CSE1L PE=1 SV=3 - [XPO2_HUMAN]	2.35E+07	4.42E+07	5.18E+07
P55039	Developmentally-regulated GTP-binding protein 2 OS=Homo sapiens OX=9606 GN=DRG2 PE=1	1.83E+07	1.84E+07	2.29E+08
P54886	Delta-1-pyrroline-5-carboxylate synthase OS=Homo sapiens OX=9606 GN=ALDH18A1 PE=1 SV	3.48E+08	4.68E+08	4.82E+08
P54652	Heat shock-related 70 kDa protein 2 OS=Homo sapiens OX=9606 GN=HSPA2 PE=1 SV=1 - [HSP	2.81E+08	3.13E+08	2.63E+08
P54578	UBiquitin carboxyl-terminal hydrolase 14 OS=Homo sapiens OX=9606 GN=USP14 PE=1 SV=3 - [	8.69E+06	1.19E+07	1.08E+07
P54577	Tyrosine--tRNA ligase, cytoplasmic OS=Homo sapiens OX=9606 GN=YARS1 PE=1 SV=4 - [SYYC	1.57E+07	1.09E+07	8.79E+07
P54136	Arginine--tRNA ligase, cytoplasmic OS=Homo sapiens OX=9606 GN=RARS1 PE=1 SV=2 - [SYRC	1.25E+08	1.57E+08	1.71E+08
P53992	Protein transport protein Sec24C OS=Homo sapiens OX=9606 GN=SEC24C PE=1 SV=3 - [SC24C	1.74E+07	9.27E+06	1.84E+07
P53621	Coatomer sUBunit alpha OS=Homo sapiens OX=9606 GN=COPA PE=1 SV=2 - [COPA_HUMAN]	1.69E+08	1.62E+08	1.99E+08
P53618	Coatomer sUBunit beta OS=Homo sapiens OX=9606 GN=COPB1 PE=1 SV=3 - [COPB_HUMAN]	3.45E+08	3.91E+08	3.91E+08
P53597	Succinate--CoA ligase [ADP/GDP-forming] sUBunit alpha, mitochondrial OS=Homo sapiens OX=	1.44E+07	1.92E+07	1.05E+07
P53396	ATP-citrate synthase OS=Homo sapiens OX=9606 GN=ACLY PE=1 SV=3 - [ACLY_HUMAN]	8.80E+06	1.20E+07	2.40E+07
P53007	Tricarboxylate transport protein, mitochondrial OS=Homo sapiens OX=9606 GN=SLC25A1 PE=1	2.27E+07	6.03E+06	7.23E+07
P53004	Biliverdin reductase A OS=Homo sapiens OX=9606 GN=BLVRA PE=1 SV=2 - [BIEA_HUMAN]	1.09E+07	6.87E+06	1.59E+07
P52948	Nuclear pore complex protein Nup98-Nup96 OS=Homo sapiens OX=9606 GN=NUP98 PE=1 SV	7.62E+06	8.91E+06	8.48E+06
P52789	Hexokinase-2 OS=Homo sapiens OX=9606 GN=HK2 PE=1 SV=2 - [HXK2_HUMAN]	1.06E+07	5.25E+06	7.63E+06
P52597	Heterogeneous nuclear ribonucleoprotein F OS=Homo sapiens OX=9606 GN=HNRNPF PE=1 SV	1.06E+08	1.05E+08	1.60E+08
P52272	Heterogeneous nuclear ribonucleoprotein M OS=Homo sapiens OX=9606 GN=HNRNPM PE=1 S	1.90E+08	1.26E+08	1.71E+08
P52209	6-phosphogluconate dehydrogenase, decarboxylating OS=Homo sapiens OX=9606 GN=PGD PE	3.22E+07	6.75E+07	5.41E+07
P51991	Heterogeneous nuclear ribonucleoprotein A3 OS=Homo sapiens OX=9606 GN=HNRNPA3 PE=1	2.38E+07	6.49E+06	6.09E+07
P51812	Ribosomal protein S6 kinase alpha-3 OS=Homo sapiens OX=9606 GN=RPS6KA3 PE=1 SV=1 - [K	5.52E+07	3.75E+06	5.81E+07
P51659	Peroxisomal multifunctional enzyme type 2 OS=Homo sapiens OX=9606 GN=HSD17B4 PE=1 SV	2.24E+07	1.10E+07	9.86E+06
P51571	Translocon-associated protein sUBunit delta OS=Homo sapiens OX=9606 GN=SSR4 PE=1 SV=1	8.42E+06	1.01E+07	8.08E+06
P51570	Galactokinase OS=Homo sapiens OX=9606 GN=GALK1 PE=1 SV=1 - [GALK1_HUMAN]	1.63E+08	1.49E+08	6.14E+08
P51532	Transcription activator BRG1 OS=Homo sapiens OX=9606 GN=SMARCA4 PE=1 SV=2 - [SMCA4_	1.54E+07	1.22E+07	6.96E+06
P51149	Ras-related protein Rab-7a OS=Homo sapiens OX=9606 GN=RAB7A PE=1 SV=1 - [RAB7A_HU	2.53E+07	1.10E+07	8.53E+07
P51148	Ras-related protein Rab-5C OS=Homo sapiens OX=9606 GN=RAB5C PE=1 SV=2 - [RAB5C_HU	9.16E+06	7.12E+06	5.49E+07
P51114	Fragile X mental retardation syndrome-related protein 1 OS=Homo sapiens OX=9606 GN=FXR1	8.50E+06	1.27E+07	3.73E+06
P50995	Annexin A11 OS=Homo sapiens OX=9606 GN=ANXA11 PE=1 SV=1 - [ANX11_HUMAN]	2.23E+07	6.99E+06	8.50E+06
P50991	T-complex protein 1 sUBunit delta OS=Homo sapiens OX=9606 GN=CCT4 PE=1 SV=4 - [TCPD_	1.78E+08	2.12E+08	2.43E+08
P50990	T-complex protein 1 sUBunit theta OS=Homo sapiens OX=9606 GN=CCT8 PE=1 SV=4 - [TCPQ_	5.80E+07	7.32E+07	6.92E+07
P50914	60S ribosomal protein L14 OS=Homo sapiens OX=9606 GN=RPL14 PE=1 SV=4 - [RL14_HUMAN]	2.76E+09	2.51E+09	2.57E+09
P50570	Dynamin-2 OS=Homo sapiens OX=9606 GN=DNM2 PE=1 SV=2 - [DYN2_HUMAN]	7.83E+06	1.17E+07	1.48E+07
P50454	Serpin H1 OS=Homo sapiens OX=9606 GN=SERPINH1 PE=1 SV=2 - [SERPH_HUMAN]	7.94E+08	9.03E+08	1.47E+09
P50452	Serpin B8 OS=Homo sapiens OX=9606 GN=SERPINB8 PE=1 SV=2 - [SPB8_HUMAN]	1.59E+07	1.35E+07	1.25E+07
P50416	Carnitine O-palmitoyltransferase 1, liver isoform OS=Homo sapiens OX=9606 GN=CPT1A PE=1 S	1.16E+07	1.59E+07	1.69E+07
P50213	Isocitrate dehydrogenase [NAD] sUBunit alpha, mitochondrial OS=Homo sapiens OX=9606 GN=I	1.52E+07	3.73E+07	2.21E+08
P49915	GMP synthase [glutamine-hydrolyzing] OS=Homo sapiens OX=9606 GN=GMPS PE=1 SV=1 - [G	3.15E+07	8.05E+06	8.87E+06
P49748	Very long-chain specific acyl-CoA dehydrogenase, mitochondrial OS=Homo sapiens OX=9606 G	3.05E+07	4.97E+06	8.07E+06
P49736	DNA replication licensing factor MCM2 OS=Homo sapiens OX=9606 GN=MCM2 PE=1 SV=4 - [M	4.54E+06	3.09E+06	1.46E+07
P49593	Protein phosphatase 1F OS=Homo sapiens OX=9606 GN=PPM1F PE=1 SV=3 - [PPM1F_HUMAN]	1.57E+07	9.39E+06	1.08E+07
P49591	Serine--tRNA ligase, cytoplasmic OS=Homo sapiens OX=9606 GN=SARS1 PE=1 SV=3 - [SYSC_H	1.49E+07	1.76E+07	1.27E+07
P49588	Alanine--tRNA ligase, cytoplasmic OS=Homo sapiens OX=9606 GN=AARS1 PE=1 SV=2 - [SYAC	1.68E+07	8.60E+07	7.21E+07
P49411	Elongation factor Tu, mitochondrial OS=Homo sapiens OX=9606 GN=TUFM PE=1 SV=2 - [EFTU_	1.29E+08	1.38E+08	3.43E+08
P49368	T-complex protein 1 sUBunit gamma OS=Homo sapiens OX=9606 GN=CCT3 PE=1 SV=4 - [TCP	3.80E+08	3.70E+08	3.64E+08
P49327	Fatty acid synthase OS=Homo sapiens OX=9606 GN=FASN PE=1 SV=3 - [FAS_HUMAN]	8.17E+07	5.28E+07	4.53E+07
P49207	60S ribosomal protein L34 OS=Homo sapiens OX=9606 GN=RPL34 PE=1 SV=3 - [RL34_HUMAN]	1.62E+08	7.61E+07	8.00E+08
P49189	4-trimethylaminobutyraldehyde dehydrogenase OS=Homo sapiens OX=9606 GN=ALDH9A1 PE	1.74E+07	6.63E+06	1.00E+07
P48735	Isocitrate dehydrogenase [NADP], mitochondrial OS=Homo sapiens OX=9606 GN=IDH2 PE=1 SV	3.06E+08	2.14E+08	7.65E+08
P48668	Keratin, type II cytoskeletal 6C OS=Homo sapiens OX=9606 GN=KRT6C PE=1 SV=3 - [K2C6C_HU	4.25E+09	4.55E+09	4.22E+09
P48643	T-complex protein 1 sUBunit epsilon OS=Homo sapiens OX=9606 GN=CCT5 PE=1 SV=1 - [TCPE	7.22E+07	5.98E+07	1.44E+08
P48594	Serpin B4 OS=Homo sapiens OX=9606 GN=SERPINB4 PE=1 SV=2 - [SPB4_HUMAN]	1.46E+07	9.92E+06	1.11E+07
P48444	Coatomer sUBunit delta OS=Homo sapiens OX=9606 GN=ARCN1 PE=1 SV=1 - [COPD_HUMAN]	3.28E+07	5.65E+06	8.95E+06
P48147	Prolyl endopeptidase OS=Homo sapiens OX=9606 GN=PREP PE=1 SV=2 - [PPCE_HUMAN]	1.05E+07	2.25E+07	1.17E+07
P48047	ATP synthase sUBunit O, mitochondrial OS=Homo sapiens OX=9606 GN=ATP5PO PE=1 SV=1 - [	2.90E+07	7.40E+06	2.25E+07
P47914	60S ribosomal protein L29 OS=Homo sapiens OX=9606 GN=RPL29 PE=1 SV=2 - [RL29_HUMAN]	1.45E+07	7.86E+06	7.17E+06
P47756	F-actin-capping protein sUBunit beta OS=Homo sapiens OX=9606 GN=CAPZB PE=1 SV=4 - [CA	9.61E+06	9.71E+06	1.07E+07
P47755	F-actin-capping protein sUBunit alpha-2 OS=Homo sapiens OX=9606 GN=CAPZA2 PE=1 SV=3	1.81E+07	6.46E+06	2.98E+07
P46977	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase sUBunit STT3A OS=Homo sapie	2.07E+07	5.73E+06	1.92E+07
P46940	Ras GTPase-activating-like protein IQGAP1 OS=Homo sapiens OX=9606 GN=IQGAP1 PE=1 SV=	1.71E+08	1.90E+08	1.64E+08
P46934	E3 UBiquitin-protein ligase NEDD4 OS=Homo sapiens OX=9606 GN=NEDD4 PE=1 SV=4 - [NED	7.34E+07	6.78E+07	1.06E+08
P46821	MicrotUBule-associated protein 1B OS=Homo sapiens OX=9606 GN=MAP1B PE=1 SV=2 - [MAP	9.97E+06	3.66E+06	1.89E+07
P46782	40S ribosomal protein S5 OS=Homo sapiens OX=9606 GN=RPS5 PE=1 SV=4 - [RS5_HUMAN]	1.83E+07	1.06E+07	1.24E+07
P46781	40S ribosomal protein S9 OS=Homo sapiens OX=9606 GN=RPS9 PE=1 SV=3 - [RS9_HUMAN]	2.16E+07	1.41E+07	6.46E+07
P46779	60S ribosomal protein L28 OS=Homo sapiens OX=9606 GN=RPL28 PE=1 SV=3 - [RL28_HUMAN]	1.05E+08	8.70E+07	2.15E+08
P46778	60S ribosomal protein L21 OS=Homo sapiens OX=9606 GN=RPL21 PE=1 SV=2 - [RL21_HUMAN]	1.07E+07	7.00E+06	2.88E+08
P46777	60S ribosomal protein L5 OS=Homo sapiens OX=9606 GN=RPL5 PE=1 SV=3 - [RL5_HUMAN]	1.54E+08	8.55E+06	1.51E+08
P46776	60S ribosomal protein L27a OS=Homo sapiens OX=9606 GN=RPL27A PE=1 SV=2 - [RL27A_HU	8.60E+08	3.13E+08	1.24E+09
P46459	Vesicle-fusing ATPase OS=Homo sapiens OX=9606 GN=NSF PE=1 SV=3 - [NSF_HUMAN]	2.47E+07	1.52E+07	1.83E+07
P45974	UBiquitin carboxyl-terminal hydrolase 5 OS=Homo sapiens OX=9606 GN=USP5 PE=1 SV=2 - [UB	1.39E+07	9.16E+06	1.36E+07
P45954	Short/branched chain specific acyl-CoA dehydrogenase, mitochondrial OS=Homo sapiens OX=9	7.40E+06	2.24E+07	1.31E+08
P45880	Voltage-dependent anion-selective channel protein 2 OS=Homo sapiens OX=9606 GN=VDAC2	2.36E+08	2.98E+08	5.70E+08
P43490	Nicotinamide phosphoribosyltransferase OS=Homo sapiens OX=9606 GN=NAMPT PE=1 SV=1 -	6.42E+07	6.31E+07	5.90E+07
P43304	Glycerol-3-phosphate dehydrogenase, mitochondrial OS=Homo sapiens OX=9606 GN=GPD2 PE	9.77E+06	9.53E+06	1.24E+07
P42766	60S ribosomal protein L35 OS=Homo sapiens OX=9606 GN=RPL35 PE=1 SV=2 - [RL35_HUMAN]	1.32E+07	1.00E+07	2.50E+08
P42765	3-ketoacyl-CoA thiolase, mitochondrial OS=Homo sapiens OX=9606 GN=ACAA2 PE=1 SV=2 - [	1.80E+07	6.99E+06	4.13E+07
P42704	Leucine-rich PPR motif-containing protein, mitochondrial OS=Homo sapiens OX=9606 GN=LRPP	3.19E+07	3.73E+06	1.09E+07
P42568	Protein AF-9 OS=Homo sapiens OX=9606 GN=MLLT3 PE=1 SV=2 - [AF9_HUMAN]	2.34E+07	4.76E+06	1.25E+07
P42357	Histidine ammonia-lyase OS=Homo sapiens OX=9606 GN=HAL PE=1 SV=1 - [HUTH_HUMAN]	7.89E+06	6.19E+06	1.05E+07
P41252	Isoleucine--tRNA ligase, cytoplasmic OS=Homo sapiens OX=9606 GN=IARS1 PE=1 SV=2 - [SYIC	1.34E+08	9.27E+07	9.69E+07
P41250	Glycine--tRNA ligase OS=Homo sapiens OX=9606 GN=GARS1 PE=1 SV=3 - [GARS_HUMAN]	2.56E+08	1.47E+08	2.31E+08
P41091	Eukaryotic translation initiation factor 2 sUBunit 3 OS=Homo sapiens OX=9606 GN=EIF2S3 PE=1	2.24E+07	1.79E+07	2.83E+07
P40939	Trifunctional enzyme sUBunit alpha, mitochondrial OS=Homo sapiens OX=9606 GN=HADHA PE=	1.77E+08	1.33E+08	1.23E+08
P40763	Signal transducer and activator of transcription 3 OS=Homo sapiens OX=9606 GN=STAT3 PE=1	6.09E+06	1.12E+07	1.08E+07
P40616	ADP-ribosylation factor-like protein 1 OS=Homo sapiens OX=9606 GN=ARL1 PE=1 SV=1 - [ARL	1.16E+07	1.70E+07	1.01E+08
P40429	60S ribosomal protein L13a OS=Homo sapiens OX=9606 GN=RPL13A PE=1 SV=2 - [RL13A_HU	2.26E+07	9.17E+06	7.66E+06
P40227	T-complex protein 1 sUBunit zeta OS=Homo sapiens OX=9606 GN=CCT6A PE=1 SV=3 - [TCPZ_	2.03E+08	1.64E+08	1.98E+08
P39023	60S ribosomal protein L3 OS=Homo sapiens OX=9606 GN=RPL3 PE=1 SV=2 - [RL3_HUMAN]	2.54E+08	2.78E+08	6.16E+08
P38919	Eukaryotic initiation factor 4A-III OS=Homo sapiens OX=9606 GN=EIF4A3 PE=1 SV=4 - [IF4A3_H	4.36E+08	7.45E+06	7.85E+07
P38646	Stress-70 protein, mitochondrial OS=Homo sapiens OX=9606 GN=HSPA9 PE=1 SV=2 - [GRP75_	1.77E+09	1.78E+09	1.79E+09
P38606	V-type proton ATPase catalytic sUBunit A OS=Homo sapiens OX=9606 GN=ATP6V1A PE=1 SV=	1.67E+07	1.10E+07	6.63E+06
P38117	Electron transfer flavoprotein sUBunit beta OS=Homo sapiens OX=9606 GN=ETFB PE=1 SV=3 - [	4.49E+07	7.44E+06	1.52E+07
P37802	Transgelin-2 OS=Homo sapiens OX=9606 GN=TAGLN2 PE=1 SV=3 - [TAGL2_HUMAN]	3.12E+07	1.28E+07	8.69E+06
P37235	Hippocalcin-like protein 1 OS=Homo sapiens OX=9606 GN=HPCAL1 PE=1 SV=3 - [HPCL1_HUM	2.46E+07	3.57E+07	1.12E+07
P36915	Guanine nucleotide-binding protein-like 1 OS=Homo sapiens OX=9606 GN=GNL1 PE=1 SV=2 -	1.33E+07	7.15E+06	9.15E+06
P36873	Serine/threonine-protein phosphatase PP1-gamma catalytic sUBunit OS=Homo sapiens OX=960	1.51E+07	1.34E+07	1.25E+07
P36776	Lon protease homolog, mitochondrial OS=Homo sapiens OX=9606 GN=LONP1 PE=1 SV=2 - [L	4.13E+08	4.62E+08	4.08E+08
P36578	60S ribosomal protein L4 OS=Homo sapiens OX=9606 GN=RPL4 PE=1 SV=5 - [RL4_HUMAN]	2.30E+08	2.14E+08	5.23E+08
P36542	ATP synthase sUBunit gamma, mitochondrial OS=Homo sapiens OX=9606 GN=ATP5F1C PE=1 S	1.30E+08	9.21E+06	2.59E+08
P36405	ADP-ribosylation factor-like protein 3 OS=Homo sapiens OX=9606 GN=ARL3 PE=1 SV=2 - [ARL	1.02E+07	2.09E+07	1.17E+07
P35998	26S proteasome regulatory sUBunit 7 OS=Homo sapiens OX=9606 GN=PSMC2 PE=1 SV=3 - [PR	1.16E+07	1.26E+07	1.77E+07
P35908	Keratin, type II cytoskeletal 2 epidermal OS=Homo sapiens OX=9606 GN=KRT2 PE=1 SV=2 - [K2	1.24E+10	1.08E+10	1.16E+10
P35900	Keratin, type I cytoskeletal 20 OS=Homo sapiens OX=9606 GN=KRT20 PE=1 SV=1 - [K1C20_HU	1.66E+09	6.57E+08	1.34E+09
P35712	Transcription factor SOX-6 OS=Homo sapiens OX=9606 GN=SOX6 PE=1 SV=3 - [SOX6_HUMAN	9.41E+08	9.08E+06	1.59E+07
P35610	Sterol O-acyltransferase 1 OS=Homo sapiens OX=9606 GN=SOAT1 PE=1 SV=3 - [SOAT1_HUMA	3.79E+07	7.44E+06	2.48E+07
P35606	Coatomer sUBunit beta' OS=Homo sapiens OX=9606 GN=COPB2 PE=1 SV=2 - [COPB2_HUMAN]	1.34E+07	8.99E+06	8.58E+06
P35580	Myosin-10 OS=Homo sapiens OX=9606 GN=MYH10 PE=1 SV=3 - [MYH10_HUMAN]	7.53E+06	1.04E+08	1.90E+08
P35579	Myosin-9 OS=Homo sapiens OX=9606 GN=MYH9 PE=1 SV=4 - [MYH9_HUMAN]	1.58E+08	2.02E+08	7.10E+07
P35527	Keratin, type I cytoskeletal 9 OS=Homo sapiens OX=9606 GN=KRT9 PE=1 SV=3 - [K1C9_HUMAN	1.07E+10	1.24E+10	1.04E+10
P35408	Prostaglandin E2 receptor EP4 sUBtype OS=Homo sapiens OX=9606 GN=PTGER4 PE=1 SV=1 - [	2.67E+07	1.49E+07	6.59E+06
P35232	Prohibitin 1 OS=Homo sapiens OX=9606 GN=PHB1 PE=1 SV=1 - [PHB1_HUMAN]	4.87E+07	8.79E+06	1.27E+08
P35030	Trypsin-3 OS=Homo sapiens OX=9606 GN=PRSS3 PE=1 SV=2 - [TRY3_HUMAN]	3.15E+08	2.64E+08	1.47E+07
P34932	Heat shock 70 kDa protein 4 OS=Homo sapiens OX=9606 GN=HSPA4 PE=1 SV=4 - [HSP74_HU	8.78E+06	8.90E+06	7.50E+06
P34931	Heat shock 70 kDa protein 1-like OS=Homo sapiens OX=9606 GN=HSPA1L PE=1 SV=2 - [HS71L	3.18E+08	2.49E+08	2.48E+08
P34897	Serine hydroxymethyltransferase, mitochondrial OS=Homo sapiens OX=9606 GN=SHMT2 PE=1 S	2.02E+08	9.53E+07	1.72E+08
P33993	DNA replication licensing factor MCM7 OS=Homo sapiens OX=9606 GN=MCM7 PE=1 SV=4 - [M	2.11E+07	3.40E+07	1.99E+07
P33991	DNA replication licensing factor MCM4 OS=Homo sapiens OX=9606 GN=MCM4 PE=1 SV=5 - [M	6.69E+06	1.20E+07	3.92E+07
P33947	ER lumen protein-retaining receptor 2 OS=Homo sapiens OX=9606 GN=KDELR2 PE=1 SV=1 - [E	6.88E+07	7.92E+07	2.40E+07
P33176	Kinesin-1 heavy chain OS=Homo sapiens OX=9606 GN=KIF5B PE=1 SV=1 - [KINH_HUMAN]	2.81E+07	1.90E+07	1.49E+07

P32969	60S ribosomal protein L9 OS=Homo sapiens OX=9606 GN=RPL9P9 PE=1 SV=1 - [RL9_HUMAN]	3.50E+08	3.07E+08	2.66E+08
P32119	Peroxiredoxin-2 OS=Homo sapiens OX=9606 GN=PRDX2 PE=1 SV=5 - [PRDX2_HUMAN]	4.08E+07	8.94E+06	1.16E+08
P31948	Stress-induced-phosphoprotein 1 OS=Homo sapiens OX=9606 GN=STIP1 PE=1 SV=1 - [STIP1_	5.19E+07	7.14E+06	1.15E+07
P31946	14-3-3 protein beta/alpha OS=Homo sapiens OX=9606 GN=YWHAB PE=1 SV=3 - [1433B_HUM	1.02E+08	1.54E+07	1.86E+07
P31944	Caspase-14 OS=Homo sapiens OX=9606 GN=CASP14 PE=1 SV=2 - [CASPE_HUMAN]	1.11E+07	4.23E+06	1.57E+07
P31943	Heterogeneous nuclear ribonucleoprotein H OS=Homo sapiens OX=9606 GN=HNRNPH1 PE=1 S	2.15E+08	1.66E+08	2.23E+08
P31930	Cytochrome b-c1 complex sUBunit 1, mitochondrial OS=Homo sapiens OX=9606 GN=UQCRC1 P	2.01E+07	1.14E+07	8.19E+06
P31689	DnaJ homolog sUBfamily A member 1 OS=Homo sapiens OX=9606 GN=DNAJA1 PE=1 SV=2 - [	1.08E+07	6.37E+06	1.42E+07
P31323	cAMP-dependent protein kinase type II-beta regulatory sUBunit OS=Homo sapiens OX=9606 G	1.62E+07	2.94E+07	1.11E+07
P31151	Protein S100-A7 OS=Homo sapiens OX=9606 GN=S100A7 PE=1 SV=4 - [S10A7_HUMAN]	9.56E+06	8.44E+06	1.59E+07
P31040	Succinate dehydrogenase [UBiquinone] flavoprotein sUBunit, mitochondrial OS=Homo sapiens O	1.58E+07	1.52E+07	9.86E+06
P31025	Lipocalin-1 OS=Homo sapiens OX=9606 GN=LCN1 PE=1 SV=1 - [LCN1_HUMAN]	7.64E+06	9.96E+06	1.65E+08
P30989	Neurotensin receptor type 1 OS=Homo sapiens OX=9606 GN=NTSR1 PE=1 SV=2 - [NTR1_HUM	1.77E+07	8.12E+06	9.21E+06
P30837	Aldehyde dehydrogenase X, mitochondrial OS=Homo sapiens OX=9606 GN=ALDH1B1 PE=1 SV	8.68E+06	1.32E+07	6.87E+06
P30153	Serine/threonine-protein phosphatase 2A 65 kDa regulatory sUBunit A alpha isoform OS=Homo	4.48E+07	5.79E+07	1.62E+07
P30101	Protein disulfide-isomerase A3 OS=Homo sapiens OX=9606 GN=PDIA3 PE=1 SV=4 - [PDIA3_HU	9.63E+06	1.58E+07	7.15E+06
P30085	UMP-CMP kinase OS=Homo sapiens OX=9606 GN=CMPK1 PE=1 SV=3 - [KCY_HUMAN]	2.48E+07	1.13E+07	1.32E+07
P30050	60S ribosomal protein L12 OS=Homo sapiens OX=9606 GN=RPL12 PE=1 SV=1 - [RL12_HUMAN]	6.92E+07	8.55E+06	2.45E+08
P30041	Peroxiredoxin-6 OS=Homo sapiens OX=9606 GN=PRDX6 PE=1 SV=3 - [PRDX6_HUMAN]	1.16E+08	1.02E+08	8.33E+07
P29508	Serpin B3 OS=Homo sapiens OX=9606 GN=SERPINB3 PE=1 SV=2 - [SPB3_HUMAN]	6.21E+07	6.22E+06	1.45E+08
P29144	Tripeptidyl-peptidase 2 OS=Homo sapiens OX=9606 GN=TPP2 PE=1 SV=4 - [TPP2_HUMAN]	2.56E+07	8.20E+06	4.11E+06
P28838	Cytosol aminopeptidase OS=Homo sapiens OX=9606 GN=LAP3 PE=1 SV=3 - [AMPL_HUMAN]	2.02E+07	5.18E+07	4.47E+07
P28482	Mitogen-activated protein kinase 1 OS=Homo sapiens OX=9606 GN=MAPK1 PE=1 SV=3 - [MK0	1.47E+07	7.62E+06	1.10E+07
P28330	Long-chain specific acyl-CoA dehydrogenase, mitochondrial OS=Homo sapiens OX=9606 GN=A	1.34E+07	6.07E+06	1.14E+08
P28161	Glutathione S-transferase Mu 2 OS=Homo sapiens OX=9606 GN=GSTM2 PE=1 SV=2 - [GSTM2_	1.64E+07	1.03E+07	2.03E+07
P27816	MicrotUBule-associated protein 4 OS=Homo sapiens OX=9606 GN=MAP4 PE=1 SV=3 - [MAP4_	4.25E+07	2.69E+06	1.57E+07
P27708	CAD protein OS=Homo sapiens OX=9606 GN=CAD PE=1 SV=3 - [PYR1_HUMAN]	2.74E+08	1.86E+08	2.44E+08
P27635	60S ribosomal protein L10 OS=Homo sapiens OX=9606 GN=RPL10 PE=1 SV=5 - [RL10_HUMAN]	6.03E+08	5.84E+08	7.85E+08
P27348	14-3-3 protein theta OS=Homo sapiens OX=9606 GN=YWHAQ PE=1 SV=1 - [1433T_HUMAN]	1.02E+08	1.19E+07	1.11E+07
P26641	Elongation factor 1-gamma OS=Homo sapiens OX=9606 GN=EEF1G PE=1 SV=3 - [EF1G_HUMA	4.71E+07	6.78E+07	1.66E+08
P26640	Valine--tRNA ligase OS=Homo sapiens OX=9606 GN=VARS1 PE=1 SV=4 - [SYVC_HUMAN]	1.38E+07	9.35E+06	1.12E+08
P26639	Threonine--tRNA ligase 1, cytoplasmic OS=Homo sapiens OX=9606 GN=TARS1 PE=1 SV=3 - [S	2.17E+07	1.06E+07	6.08E+07
P26599	Polypyrimidine tract-binding protein 1 OS=Homo sapiens OX=9606 GN=PTBP1 PE=1 SV=1 - [PT	4.45E+07	5.87E+07	6.78E+07
P26373	60S ribosomal protein L13 OS=Homo sapiens OX=9606 GN=RPL13 PE=1 SV=4 - [RL13_HUMAN]	3.63E+07	8.79E+06	9.52E+07
P26368	Splicing factor U2AF 65 kDa sUBunit OS=Homo sapiens OX=9606 GN=U2AF2 PE=1 SV=4 - [U2A	2.29E+08	6.45E+06	2.11E+07
P26196	Probable ATP-dependent RNA helicase DDX6 OS=Homo sapiens OX=9606 GN=DDX6 PE=1 SV=	2.77E+07	1.55E+07	1.04E+07
P26038	Moesin OS=Homo sapiens OX=9606 GN=MSN PE=1 SV=3 - [MOES_HUMAN]	5.82E+06	6.05E+06	1.08E+07
P25705	ATP synthase sUBunit alpha, mitochondrial OS=Homo sapiens OX=9606 GN=ATP5F1A PE=1 SV=	1.40E+09	1.30E+09	1.29E+09
P25311	Zinc-alpha-2-glycoprotein OS=Homo sapiens OX=9606 GN=AZGP1 PE=1 SV=2 - [ZA2G_HUMA	1.86E+07	5.62E+06	6.27E+06
P25205	DNA replication licensing factor MCM3 OS=Homo sapiens OX=9606 GN=MCM3 PE=1 SV=3 - [M	1.40E+07	1.03E+07	1.18E+07
P25103	SUBstance-P receptor OS=Homo sapiens OX=9606 GN=TACR1 PE=1 SV=1 - [NK1R_HUMAN]	1.63E+07	1.16E+07	7.43E+08
P24666	Low molecular weight phosphotyrosine protein phosphatase OS=Homo sapiens OX=9606 GN=A	1.78E+07	8.90E+06	8.92E+07
P24539	ATP synthase F(0) complex sUBunit B1, mitochondrial OS=Homo sapiens OX=9606 GN=ATP5PB P	3.62E+07	4.67E+06	7.61E+06
P24390	ER lumen protein-retaining receptor 1 OS=Homo sapiens OX=9606 GN=KDELR1 PE=1 SV=1 - [E	1.55E+07	8.98E+06	2.44E+07
P24298	Alanine aminotransferase 1 OS=Homo sapiens OX=9606 GN=GPT PE=1 SV=3 - [ALAT1_HUMAN]	1.23E+07	4.87E+06	1.42E+07
P23528	Cofilin-1 OS=Homo sapiens OX=9606 GN=CFL1 PE=1 SV=3 - [COF1_HUMAN]	4.72E+08	5.85E+08	6.39E+08
P23526	Adenosylhomocysteinase OS=Homo sapiens OX=9606 GN=AHCY PE=1 SV=4 - [SAHH_HUMAN]	3.05E+07	2.61E+07	1.11E+07
P23396	40S ribosomal protein S3 OS=Homo sapiens OX=9606 GN=RPS3 PE=1 SV=2 - [RS3_HUMAN]	7.95E+08	8.39E+08	1.25E+09
P23381	Tryptophan--tRNA ligase, cytoplasmic OS=Homo sapiens OX=9606 GN=WARS1 PE=1 SV=2 - [	2.25E+07	7.37E+06	7.25E+06
P23284	Peptidyl-prolyl cis-trans isomerase B OS=Homo sapiens OX=9606 GN=PPIB PE=1 SV=2 - [PPIB_	9.01E+06	1.09E+07	1.50E+07
P23246	Splicing factor, proline- and glutamine-rich OS=Homo sapiens OX=9606 GN=SFPQ PE=1 SV=2 -	1.98E+07	8.81E+06	9.07E+06
P22735	Protein-glutamine gamma-glutamyltransferase K OS=Homo sapiens OX=9606 GN=TGM1 PE=1	2.76E+07	6.60E+06	6.71E+06
P22694	cAMP-dependent protein kinase catalytic sUBunit beta OS=Homo sapiens OX=9606 GN=PRKAC	1.31E+07	5.27E+07	1.84E+07
P22626	Heterogeneous nuclear ribonucleoproteins A2/B1 OS=Homo sapiens OX=9606 GN=HNRNPA2B1	1.39E+07	5.16E+06	5.49E+06
P22314	UBiquitin-like modifier-activating enzyme 1 OS=Homo sapiens OX=9606 GN=UBA1 PE=1 SV=3	1.28E+08	1.62E+08	2.20E+08
P22234	Bifunctional phosphoribosylaminoimidazole carboxylase/phosphoribosylaminoimidazole succinoc	8.45E+06	9.03E+06	3.50E+07
P22102	Trifunctional purine biosynthetic protein adenosine-3 OS=Homo sapiens OX=9606 GN=GART PE	3.16E+07	1.49E+07	7.49E+07
P22087	rRNA 2'-O-methyltransferase fibrillarin OS=Homo sapiens OX=9606 GN=FBL PE=1 SV=2 - [FBRL	1.22E+08	3.14E+06	2.59E+08
P21796	Voltage-dependent anion-selective channel protein 1 OS=Homo sapiens OX=9606 GN=VDAC1	8.16E+06	1.08E+08	6.88E+07
P21399	Cytoplasmic aconitate hydratase OS=Homo sapiens OX=9606 GN=ACO1 PE=1 SV=3 - [ACOHC_	3.94E+07	5.28E+06	1.06E+07
P21333	Filamin-A OS=Homo sapiens OX=9606 GN=FLNA PE=1 SV=4 - [FLNA_HUMAN]	1.86E+07	5.57E+07	2.77E+07
P21283	V-type proton ATPase sUBunit C 1 OS=Homo sapiens OX=9606 GN=ATP6V1C1 PE=1 SV=4 - [V	1.20E+07	7.83E+06	9.11E+06
P21281	V-type proton ATPase sUBunit B, brain isoform OS=Homo sapiens OX=9606 GN=ATP6V1B2 PE=	1.30E+07	3.06E+06	1.52E+07
P20936	Ras GTPase-activating protein 1 OS=Homo sapiens OX=9606 GN=RASA1 PE=1 SV=1 - [RASA1_	8.69E+06	4.86E+06	2.08E+07
P20930	Filaggrin OS=Homo sapiens OX=9606 GN=FLG PE=1 SV=3 - [FILA_HUMAN]	1.31E+07	2.24E+07	2.42E+06
P20929	Nebulin OS=Homo sapiens OX=9606 GN=NEB PE=1 SV=5 - [NEBU_HUMAN]	4.66E+06	1.04E+07	1.47E+07
P20073	Annexin A7 OS=Homo sapiens OX=9606 GN=ANXA7 PE=1 SV=3 - [ANXA7_HUMAN]	1.42E+07	3.70E+06	2.17E+07
P19784	Casein kinase II sUBunit alpha' OS=Homo sapiens OX=9606 GN=CSNK2A2 PE=1 SV=1 - [CSK22_	1.74E+07	1.25E+07	1.26E+07
P19623	Spermidine synthase OS=Homo sapiens OX=9606 GN=SRM PE=1 SV=1 - [SPEE_HUMAN]	2.32E+07	6.94E+06	6.70E+07
P19367	Hexokinase-1 OS=Homo sapiens OX=9606 GN=HK1 PE=1 SV=3 - [HXK1_HUMAN]	1.02E+07	1.16E+07	7.17E+06
P19338	Nucleolin OS=Homo sapiens OX=9606 GN=NCL PE=1 SV=3 - [NUCL_HUMAN]	1.23E+07	5.73E+06	6.94E+06
P18754	Regulator of chromosome condensation OS=Homo sapiens OX=9606 GN=RCC1 PE=1 SV=1 - [R	8.57E+06	1.37E+07	7.26E+06
P18621	60S ribosomal protein L17 OS=Homo sapiens OX=9606 GN=RPL17 PE=1 SV=3 - [RL17_HUMAN]	5.33E+08	4.60E+08	8.07E+08
P18583	Protein SON OS=Homo sapiens OX=9606 GN=SON PE=1 SV=4 - [SON_HUMAN]	2.80E+07	2.37E+07	7.73E+07
P18206	Vinculin OS=Homo sapiens OX=9606 GN=VCL PE=1 SV=4 - [VINC_HUMAN]	1.55E+07	4.99E+06	6.04E+06
P18124	60S ribosomal protein L7 OS=Homo sapiens OX=9606 GN=RPL7 PE=1 SV=1 - [RL7_HUMAN]	2.74E+08	4.83E+07	8.91E+07
P18085	ADP-ribosylation factor 4 OS=Homo sapiens OX=9606 GN=ARF4 PE=1 SV=3 - [ARF4_HUMAN]	3.85E+08	7.31E+08	2.67E+08
P18077	60S ribosomal protein L35a OS=Homo sapiens OX=9606 GN=RPL35A PE=1 SV=2 - [RL35A_HU	6.01E+07	6.20E+07	8.16E+07
P17987	T-complex protein 1 sUBunit alpha OS=Homo sapiens OX=9606 GN=TCP1 PE=1 SV=1 - [TCPA_	5.82E+08	6.23E+08	5.95E+08
P17931	Galectin-3 OS=Homo sapiens OX=9606 GN=LGALS3 PE=1 SV=5 - [LEG3_HUMAN]	2.44E+07	1.49E+07	2.46E+07
P17858	ATP-dependent 6-phosphofructokinase, liver type OS=Homo sapiens OX=9606 GN=PFKL PE=1	3.67E+08	4.11E+08	4.45E+08
P17844	Probable ATP-dependent RNA helicase DDX5 OS=Homo sapiens OX=9606 GN=DDX5 PE=1 SV=	3.71E+08	3.00E+08	2.68E+08
P17812	CTP synthase 1 OS=Homo sapiens OX=9606 GN=CTPS1 PE=1 SV=2 - [PYRG1_HUMAN]	1.48E+08	1.59E+08	1.90E+08
P17655	Calpain-2 catalytic sUBunit OS=Homo sapiens OX=9606 GN=CAPN2 PE=1 SV=6 - [CAN2_HUMA	1.62E+07	7.15E+06	6.03E+06
P17152	Transmembrane protein 11, mitochondrial OS=Homo sapiens OX=9606 GN=TMEM11 PE=1 SV=	3.09E+07	4.07E+06	9.38E+07
P16615	Sarcoplasmic/endoplasmic reticulum calcium ATPase 2 OS=Homo sapiens OX=9606 GN=ATP2A	1.05E+08	6.81E+07	4.48E+07
P16435	NADPH--cytochrome P450 reductase OS=Homo sapiens OX=9606 GN=POR PE=1 SV=2 - [NCP	1.41E+07	6.84E+06	3.48E+07
P16219	Short-chain specific acyl-CoA dehydrogenase, mitochondrial OS=Homo sapiens OX=9606 GN=	3.03E+07	3.93E+06	1.27E+08
P15924	Desmoplakin OS=Homo sapiens OX=9606 GN=DSP PE=1 SV=3 - [DESP_HUMAN]	3.48E+07	5.61E+07	3.52E+07
P15880	40S ribosomal protein S2 OS=Homo sapiens OX=9606 GN=RPS2 PE=1 SV=2 - [RS2_HUMAN]	1.22E+08	1.60E+08	3.89E+08
P15374	UBiquitin carboxyl-terminal hydrolase isozyme L3 OS=Homo sapiens OX=9606 GN=UCHL3 PE=1	2.40E+07	6.52E+06	2.81E+07
P15170	Eukaryotic peptide chain release factor GTP-binding sUBunit ERF3A OS=Homo sapiens OX=9606	2.19E+07	3.85E+06	1.60E+07
P15121	Aldo-keto reductase family 1 member B1 OS=Homo sapiens OX=9606 GN=AKR1B1 PE=1 SV=3	2.47E+07	3.42E+07	1.48E+07
P14923	Junction plakoglobin OS=Homo sapiens OX=9606 GN=JUP PE=1 SV=3 - [PLAK_HUMAN]	1.52E+08	1.06E+08	6.01E+07
P14868	Aspartate--tRNA ligase, cytoplasmic OS=Homo sapiens OX=9606 GN=DARS1 PE=1 SV=2 - [SY	1.93E+08	1.61E+08	1.68E+08
P14866	Heterogeneous nuclear ribonucleoprotein L OS=Homo sapiens OX=9606 GN=HNRNPL PE=1 SV	1.16E+07	3.04E+07	4.26E+07
P14735	Insulin-degrading enzyme OS=Homo sapiens OX=9606 GN=IDE PE=1 SV=4 - [IDE_HUMAN]	1.17E+07	8.21E+06	1.35E+07
P14625	Endoplasmin OS=Homo sapiens OX=9606 GN=HSP90B1 PE=1 SV=1 - [ENPL_HUMAN]	4.72E+08	3.95E+08	4.13E+08
P14618	Pyruvate kinase PKM OS=Homo sapiens OX=9606 GN=PKM PE=1 SV=4 - [KPYM_HUMAN]	1.04E+09	1.08E+09	1.17E+09
P14324	Farnesyl pyrophosphate synthase OS=Homo sapiens OX=9606 GN=FDPS PE=1 SV=4 - [FPPS_HU	1.11E+07	6.81E+06	1.01E+07
P13929	Beta-enolase OS=Homo sapiens OX=9606 GN=ENO3 PE=1 SV=5 - [ENOB_HUMAN]	8.90E+08	1.03E+09	1.94E+09
P13807	Glycogen [starch] synthase, muscle OS=Homo sapiens OX=9606 GN=GYS1 PE=1 SV=2 - [GYS1_H	1.87E+08	1.81E+08	2.34E+08
P13804	Electron transfer flavoprotein sUBunit alpha, mitochondrial OS=Homo sapiens OX=9606 GN=ETF	1.96E+08	1.29E+07	1.22E+07
P13797	Plastin-3 OS=Homo sapiens OX=9606 GN=PLS3 PE=1 SV=4 - [PLST_HUMAN]	1.42E+07	7.06E+06	2.29E+07
P13747	HLA class I histocompatibility antigen, alpha chain E OS=Homo sapiens OX=9606 GN=HLA-E PE	2.27E+08	2.35E+08	3.41E+08
P13674	Prolyl 4-hydroxylase sUBunit alpha-1 OS=Homo sapiens OX=9606 GN=P4HA1 PE=1 SV=2 - [P4	1.55E+07	7.83E+06	1.44E+07
P13667	Protein disulfide-isomerase A4 OS=Homo sapiens OX=9606 GN=PDIA4 PE=1 SV=2 - [PDIA4_HU	1.23E+07	9.55E+06	7.21E+06
P13647	Keratin, type II cytoskeletal 5 OS=Homo sapiens OX=9606 GN=KRT5 PE=1 SV=3 - [K2C5_HUMA	3.96E+09	4.49E+09	4.21E+09
P13646	Keratin, type I cytoskeletal 13 OS=Homo sapiens OX=9606 GN=KRT13 PE=1 SV=4 - [K1C13_HU	2.32E+09	3.34E+09	2.70E+09
P13645	Keratin, type I cytoskeletal 10 OS=Homo sapiens OX=9606 GN=KRT10 PE=1 SV=6 - [K1C10_HU	8.90E+09	1.11E+10	8.94E+09
P13639	Elongation factor 2 OS=Homo sapiens OX=9606 GN=EEF2 PE=1 SV=4 - [EF2_HUMAN]	1.24E+08	1.10E+08	1.88E+08
P12955	Xaa-Pro dipeptidase OS=Homo sapiens OX=9606 GN=PEPD PE=1 SV=3 - [PEPD_HUMAN]	1.81E+07	1.18E+07	1.66E+07
P12814	Alpha-actinin-1 OS=Homo sapiens OX=9606 GN=ACTN1 PE=1 SV=2 - [ACTN1_HUMAN]	1.64E+07	6.63E+07	4.21E+07
P12273	Prolactin-inducible protein OS=Homo sapiens OX=9606 GN=PIP PE=1 SV=1 - [PIP_HUMAN]	2.52E+08	7.34E+07	3.04E+08
P12236	ADP/ATP translocase 3 OS=Homo sapiens OX=9606 GN=SLC25A6 PE=1 SV=4 - [ADT3_HUMAN]	1.33E+09	1.22E+09	2.11E+09
P12235	ADP/ATP translocase 1 OS=Homo sapiens OX=9606 GN=SLC25A4 PE=1 SV=4 - [ADT1_HUMAN]	1.33E+09	1.20E+09	1.95E+09
P12004	Proliferating cell nuclear antigen OS=Homo sapiens OX=9606 GN=PCNA PE=1 SV=1 - [PCNA_H	3.72E+07	9.88E+06	1.27E+07
P11586	C-1-tetrahydrofolate synthase, cytoplasmic OS=Homo sapiens OX=9606 GN=MTHFD1 PE=1 SV	1.03E+07	8.02E+06	2.51E+07
P11498	Pyruvate carboxylase, mitochondrial OS=Homo sapiens OX=9606 GN=PC PE=1 SV=2 - [PYC_HU	4.98E+10	5.65E+10	5.26E+10
P11413	Glucose-6-phosphate 1-dehydrogenase OS=Homo sapiens OX=9606 GN=G6PD PE=1 SV=4 - [	1.91E+07	1.11E+07	3.25E+07
P11387	DNA topoisomerase 1 OS=Homo sapiens OX=9606 GN=TOP1 PE=1 SV=2 - [TOP1_HUMAN]	1.25E+09	8.98E+08	1.07E+09
P11310	Medium-chain specific acyl-CoA dehydrogenase, mitochondrial OS=Homo sapiens OX=9606 GN	2.36E+08	2.16E+08	1.41E+08
P11216	Glycogen phosphorylase, brain form OS=Homo sapiens OX=9606 GN=PYGB PE=1 SV=5 - [PYGB	7.76E+07	1.01E+07	9.65E+07
P11177	Pyruvate dehydrogenase E1 component sUBunit beta, mitochondrial OS=Homo sapiens OX=960	1.37E+07	1.21E+07	4.03E+06
P11172	Uridine 5'-monophosphate synthase OS=Homo sapiens OX=9606 GN=UMPS PE=1 SV=1 - [UMP	4.07E+07	8.13E+06	9.65E+06
P11166	Solute carrier family 2, facilitated glucose transporter member 1 OS=Homo sapiens OX=9606 GN	7.49E+07	6.96E+07	5.01E+07
P11142	Heat shock cognate 71 kDa protein OS=Homo sapiens OX=9606 GN=HSPA8 PE=1 SV=1 - [HSP7	2.81E+08	3.13E+08	2.68E+08
P11021	Endoplasmic reticulum chaperone BiP OS=Homo sapiens OX=9606 GN=HSPA5 PE=1 SV=2 - [BIP	3.75E+08	4.23E+08	3.74E+08
P10809	60 kDa heat shock protein, mitochondrial OS=Homo sapiens OX=9606 GN=HSPD1 PE=1 SV=2 -	2.82E+08	3.81E+08	3.03E+08

P10768	S-formylglutathione hydrolase OS=Homo sapiens OX=9606 GN=ESD PE=1 SV=2 - [ESTD_HUMA	1.47E+07	7.56E+06	2.09E+07
P10696	Alkaline phosphatase, germ cell type OS=Homo sapiens OX=9606 GN=ALPG PE=1 SV=4 - [PPBN	1.08E+07	3.96E+06	1.83E+08
P10412	Histone H1.4 OS=Homo sapiens OX=9606 GN=H1-4 PE=1 SV=2 - [H14_HUMAN]	1.49E+08	1.58E+08	2.06E+08
P0DMV8	Heat shock 70 kDa protein 1A OS=Homo sapiens OX=9606 GN=HSPA1A PE=1 SV=1 - [HS71A_H	3.18E+08	2.49E+08	1.20E+08
P0C0L4	Complement C4-A OS=Homo sapiens OX=9606 GN=C4A PE=1 SV=2 - [CO4A_HUMAN]	1.45E+07	2.05E+07	1.11E+07
P09884	DNA polymerase alpha catalytic sUBunit OS=Homo sapiens OX=9606 GN=POLA1 PE=1 SV=2 - [	2.09E+07	5.18E+06	1.71E+07
P09874	Poly [ADP-ribose] polymerase 1 OS=Homo sapiens OX=9606 GN=PARP1 PE=1 SV=4 - [PARP1_	1.36E+07	3.40E+07	1.17E+07
P09622	Dihydrolipoyl dehydrogenase, mitochondrial OS=Homo sapiens OX=9606 GN=DLD PE=1 SV=2 -	9.07E+06	2.53E+07	3.38E+07
P09471	Guanine nucleotide-binding protein G(o) sUBunit alpha OS=Homo sapiens OX=9606 GN=GNAO	1.64E+08	1.68E+08	2.51E+08
P09104	Gamma-enolase OS=Homo sapiens OX=9606 GN=ENO2 PE=1 SV=3 - [ENOG_HUMAN]	8.70E+08	1.15E+09	2.03E+09
P08865	40S ribosomal protein SA OS=Homo sapiens OX=9606 GN=RPSA PE=1 SV=4 - [RSSA_HUMAN]	1.07E+08	9.38E+07	3.50E+08
P08779	Keratin, type I cytoskeletal 16 OS=Homo sapiens OX=9606 GN=KRT16 PE=1 SV=4 - [K1C16_HU	2.56E+09	4.02E+09	3.27E+09
P08754	Guanine nucleotide-binding protein G(i) sUBunit alpha-3 OS=Homo sapiens OX=9606 GN=GNAI	1.19E+08	1.68E+08	1.77E+08
P08708	40S ribosomal protein S17 OS=Homo sapiens OX=9606 GN=RPS17 PE=1 SV=2 - [RS17_HUMAN	6.39E+07	2.62E+07	2.41E+08
P08670	Vimentin OS=Homo sapiens OX=9606 GN=VIM PE=1 SV=4 - [VIME_HUMAN]	5.80E+07	5.75E+07	3.99E+08
P08559	Pyruvate dehydrogenase E1 component sUBunit alpha, somatic form, mitochondrial OS=Homo s	3.05E+08	9.17E+06	2.30E+08
P08243	Asparagine synthetase [glutamine-hydrolyzing] OS=Homo sapiens OX=9606 GN=ASNS PE=1 SV	1.79E+08	2.28E+08	1.77E+08
P08240	Signal recognition particle receptor sUBunit alpha OS=Homo sapiens OX=9606 GN=SRPRA PE=1	1.48E+07	7.67E+06	6.77E+06
P08238	Heat shock protein HSP 90-beta OS=Homo sapiens OX=9606 GN=HSP90AB1 PE=1 SV=4 - [HS9	4.25E+08	4.53E+08	4.00E+08
P08237	ATP-dependent 6-phosphofructokinase, muscle type OS=Homo sapiens OX=9606 GN=PFKM PE	2.74E+08	2.16E+08	1.64E+08
P08134	Rho-related GTP-binding protein RhoC OS=Homo sapiens OX=9606 GN=RHOC PE=1 SV=1 - [R	2.25E+07	7.72E+06	1.29E+07
P08133	Annexin A6 OS=Homo sapiens OX=9606 GN=ANXA6 PE=1 SV=3 - [ANXA6_HUMAN]	1.32E+07	2.33E+07	6.50E+06
P07954	Fumarate hydratase, mitochondrial OS=Homo sapiens OX=9606 GN=FH PE=1 SV=3 - [FUMH_H	1.67E+07	5.27E+06	1.86E+07
P07900	Heat shock protein HSP 90-alpha OS=Homo sapiens OX=9606 GN=HSP90AA1 PE=1 SV=5 - [HS	3.05E+08	3.19E+08	2.34E+08
P07814	Bifunctional glutamate/proline--tRNA ligase OS=Homo sapiens OX=9606 GN=EPRS1 PE=1 SV=	1.46E+08	1.21E+08	1.01E+08
P07737	Profilin-1 OS=Homo sapiens OX=9606 GN=PFN1 PE=1 SV=2 - [PROF1_HUMAN]	5.39E+07	7.15E+06	1.72E+07
P07478	Trypsin-2 OS=Homo sapiens OX=9606 GN=PRSS2 PE=1 SV=1 - [TRY2_HUMAN]	4.21E+10	2.55E+10	3.49E+10
P07477	Serine protease 1 OS=Homo sapiens OX=9606 GN=PRSS1 PE=1 SV=1 - [TRY1_HUMAN]	2.12E+10	8.87E+09	1.76E+10
P07437	TUBulin beta chain OS=Homo sapiens OX=9606 GN=TUBB PE=1 SV=2 - [TBB5_HUMAN]	2.23E+09	1.81E+09	3.16E+09
P07384	Calpain-1 catalytic sUBunit OS=Homo sapiens OX=9606 GN=CAPN1 PE=1 SV=1 - [CAN1_HUMA	2.46E+07	9.04E+06	1.86E+07
P07355	Annexin A2 OS=Homo sapiens OX=9606 GN=ANXA2 PE=1 SV=2 - [ANXA2_HUMAN]	4.36E+08	3.49E+08	2.56E+08
P07339	Cathepsin D OS=Homo sapiens OX=9606 GN=CTSD PE=1 SV=1 - [CATD_HUMAN]	1.56E+07	1.12E+07	8.81E+06
P07305	Histone H1.0 OS=Homo sapiens OX=9606 GN=H1-0 PE=1 SV=3 - [H10_HUMAN]	4.00E+07	1.31E+07	2.10E+07
P07237	Protein disulfide-isomerase OS=Homo sapiens OX=9606 GN=P4HB PE=1 SV=3 - [PDIA1_HUMA	6.96E+06	7.23E+06	1.24E+07
P06858	Lipoprotein lipase OS=Homo sapiens OX=9606 GN=LPL PE=1 SV=1 - [LIPL_HUMAN]	7.06E+06	1.98E+07	9.27E+06
P06756	Integrin alpha-V OS=Homo sapiens OX=9606 GN=ITGAV PE=1 SV=2 - [ITAV_HUMAN]	9.38E+06	6.21E+06	1.10E+07
P06753	Tropomyosin alpha-3 chain OS=Homo sapiens OX=9606 GN=TPM3 PE=1 SV=2 - [TPM3_HUMA	1.46E+07	2.36E+07	8.01E+06
P06748	Nucleophosmin OS=Homo sapiens OX=9606 GN=NPM1 PE=1 SV=2 - [NPM_HUMAN]	1.64E+07	6.85E+07	2.40E+07
P06744	Glucose-6-phosphate isomerase OS=Homo sapiens OX=9606 GN=GPI PE=1 SV=4 - [G6PI_HUM	1.10E+07	1.22E+07	1.62E+07
P06737	Glycogen phosphorylase, liver form OS=Homo sapiens OX=9606 GN=PYGL PE=1 SV=4 - [PYGL_	5.67E+07	4.08E+06	1.44E+08
P06733	Alpha-enolase OS=Homo sapiens OX=9606 GN=ENO1 PE=1 SV=2 - [ENOA_HUMAN]	1.01E+09	1.33E+09	2.45E+09
P06730	Eukaryotic translation initiation factor 4E OS=Homo sapiens OX=9606 GN=EIF4E PE=1 SV=2 - [IF	2.67E+07	8.13E+06	1.80E+07
P06702	Protein S100-A9 OS=Homo sapiens OX=9606 GN=S100A9 PE=1 SV=1 - [S10A9_HUMAN]	2.53E+08	2.70E+08	2.01E+08
P06576	ATP synthase sUBunit beta, mitochondrial OS=Homo sapiens OX=9606 GN=ATP5F1B PE=1 SV=3	1.48E+07	5.34E+06	1.42E+07
P05388	60S acidic ribosomal protein P0 OS=Homo sapiens OX=9606 GN=RPLP0 PE=1 SV=1 - [RLA0_HU	2.98E+08	3.36E+08	4.36E+08
P05198	Eukaryotic translation initiation factor 2 sUBunit 1 OS=Homo sapiens OX=9606 GN=EIF2S1 PE=1	1.51E+07	1.41E+07	1.70E+07
P05166	Propionyl-CoA carboxylase beta chain, mitochondrial OS=Homo sapiens OX=9606 GN=PCCB PE	1.63E+08	1.97E+08	2.14E+08
P05165	Propionyl-CoA carboxylase alpha chain, mitochondrial OS=Homo sapiens OX=9606 GN=PCCA P	3.32E+09	2.95E+09	3.23E+09
P05141	ADP/ATP translocase 2 OS=Homo sapiens OX=9606 GN=SLC25A5 PE=1 SV=7 - [ADT2_HUMAN]	1.82E+09	1.73E+09	2.58E+09
P05109	Protein S100-A8 OS=Homo sapiens OX=9606 GN=S100A8 PE=1 SV=1 - [S10A8_HUMAN]	2.04E+08	1.70E+08	2.08E+08
P05091	Aldehyde dehydrogenase, mitochondrial OS=Homo sapiens OX=9606 GN=ALDH2 PE=1 SV=2 -	4.82E+08	3.78E+08	5.39E+08
P05089	Arginase-1 OS=Homo sapiens OX=9606 GN=ARG1 PE=1 SV=2 - [ARGI1_HUMAN]	3.02E+07	5.64E+06	1.94E+07
P05023	Sodium/potassium-transporting ATPase sUBunit alpha-1 OS=Homo sapiens OX=9606 GN=ATP1	1.98E+07	1.19E+07	2.62E+07
P04899	Guanine nucleotide-binding protein G(i) sUBunit alpha-2 OS=Homo sapiens OX=9606 GN=GNAI	1.64E+08	1.68E+08	2.18E+08
P04843	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase sUBunit 1 OS=Homo sapiens O	9.46E+07	7.69E+07	7.91E+07
P04792	Heat shock protein beta-1 OS=Homo sapiens OX=9606 GN=HSPB1 PE=1 SV=2 - [HSPB1_HUMA	2.04E+07	1.18E+07	1.24E+07
P04746	Pancreatic alpha-amylase OS=Homo sapiens OX=9606 GN=AMY2A PE=1 SV=2 - [AMYP_HUMA	1.38E+07	9.73E+06	8.38E+06
P04406	Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens OX=9606 GN=GAPDH PE=1 S	2.87E+09	2.79E+09	2.28E+09
P04280	Basic salivary proline-rich protein 1 OS=Homo sapiens OX=9606 GN=PRB1 PE=1 SV=3 - [PRP1_H	1.39E+07	9.03E+06	5.50E+06
P04264	Keratin, type II cytoskeletal 1 OS=Homo sapiens OX=9606 GN=KRT1 PE=1 SV=6 - [K2C1_HUMA	1.94E+10	2.06E+10	1.98E+10
P04259	Keratin, type II cytoskeletal 6B OS=Homo sapiens OX=9606 GN=KRT6B PE=1 SV=5 - [K2C6B_HU	8.47E+09	8.02E+09	7.71E+09
P04083	Annexin A1 OS=Homo sapiens OX=9606 GN=ANXA1 PE=1 SV=2 - [ANXA1_HUMAN]	1.42E+07	4.42E+06	2.53E+07
P04062	Lysosomal acid glucosylceramidase OS=Homo sapiens OX=9606 GN=GBA PE=1 SV=3 - [GLCM_	6.07E+06	1.22E+07	3.64E+06
P04040	Catalase OS=Homo sapiens OX=9606 GN=CAT PE=1 SV=3 - [CATA_HUMAN]	1.74E+07	2.31E+07	1.01E+07
P02771	Alpha-fetoprotein OS=Homo sapiens OX=9606 GN=AFP PE=1 SV=1 - [FETA_HUMAN]	9.45E+06	7.01E+06	5.32E+07
P02768	Albumin OS=Homo sapiens OX=9606 GN=ALB PE=1 SV=2 - [ALBU_HUMAN]	2.41E+11	2.68E+11	1.84E+11
P02545	Prelamin-A/C OS=Homo sapiens OX=9606 GN=LMNA PE=1 SV=1 - [LMNA_HUMAN]	6.67E+07	7.19E+07	5.89E+07
P02538	Keratin, type II cytoskeletal 6A OS=Homo sapiens OX=9606 GN=KRT6A PE=1 SV=3 - [K2C6A_HU	4.25E+09	4.55E+09	4.22E+09
P02533	Keratin, type I cytoskeletal 14 OS=Homo sapiens OX=9606 GN=KRT14 PE=1 SV=4 - [K1C14_HU	2.56E+09	4.02E+09	3.27E+09
P02452	Collagen alpha-1(I) chain OS=Homo sapiens OX=9606 GN=COL1A1 PE=1 SV=6 - [CO1A1_HUM	2.39E+07	5.79E+06	2.68E+07
P01876	Immunoglobulin heavy constant alpha 1 OS=Homo sapiens OX=9606 GN=IGHA1 PE=1 SV=2 - [I	2.61E+07	4.95E+07	4.70E+07
P01859	Immunoglobulin heavy constant gamma 2 OS=Homo sapiens OX=9606 GN=IGHG2 PE=1 SV=2	7.29E+06	8.23E+06	8.89E+06
P01857	Immunoglobulin heavy constant gamma 1 OS=Homo sapiens OX=9606 GN=IGHG1 PE=1 SV=1	1.46E+07	7.27E+06	8.96E+06
P01834	Immunoglobulin kappa constant OS=Homo sapiens OX=9606 GN=IGKC PE=1 SV=2 - [IGKC_HU	1.42E+07	4.74E+06	2.24E+07
P01833	Polymeric immunoglobulin receptor OS=Homo sapiens OX=9606 GN=PIGR PE=1 SV=4 - [PIGR_	3.90E+07	2.70E+07	4.05E+07
P01111	GTPase NRas OS=Homo sapiens OX=9606 GN=NRAS PE=1 SV=1 - [RASN_HUMAN]	1.29E+07	6.91E+06	1.33E+07
P01040	Cystatin-A OS=Homo sapiens OX=9606 GN=CSTA PE=1 SV=1 - [CYTA_HUMAN]	1.38E+08	1.14E+08	4.58E+07
P01036	Cystatin-S OS=Homo sapiens OX=9606 GN=CST4 PE=1 SV=3 - [CYTS_HUMAN]	1.34E+07	1.62E+07	1.23E+07
P01024	Complement C3 OS=Homo sapiens OX=9606 GN=C3 PE=1 SV=2 - [CO3_HUMAN]	3.91E+07	1.62E+07	2.69E+07
P01008	Antithrombin-III OS=Homo sapiens OX=9606 GN=SERPINC1 PE=1 SV=1 - [ANT3_HUMAN]	1.40E+07	1.02E+07	8.67E+07
P00966	Argininosuccinate synthase OS=Homo sapiens OX=9606 GN=ASS1 PE=1 SV=2 - [ASSY_HUMAN]	7.09E+07	2.18E+07	2.55E+08
P00558	Phosphoglycerate kinase 1 OS=Homo sapiens OX=9606 GN=PGK1 PE=1 SV=3 - [PGK1_HUMAN]	9.38E+07	9.12E+07	2.49E+08
P00505	Aspartate aminotransferase, mitochondrial OS=Homo sapiens OX=9606 GN=GOT2 PE=1 SV=3 -	1.76E+07	1.15E+07	1.59E+07
P00491	Purine nucleoside phosphorylase OS=Homo sapiens OX=9606 GN=PNP PE=1 SV=2 - [PNPH_HU	9.89E+06	1.31E+07	1.40E+07
P00390	Glutathione reductase, mitochondrial OS=Homo sapiens OX=9606 GN=GSR PE=1 SV=2 - [GSHR	1.56E+07	2.41E+07	1.90E+07
P00387	NADH-cytochrome b5 reductase 3 OS=Homo sapiens OX=9606 GN=CYB5R3 PE=1 SV=3 - [NB5	2.28E+07	1.06E+07	1.69E+07
P00367	Glutamate dehydrogenase 1, mitochondrial OS=Homo sapiens OX=9606 GN=GLUD1 PE=1 SV=2	1.49E+07	1.34E+07	9.52E+06
P00338	L-lactate dehydrogenase A chain OS=Homo sapiens OX=9606 GN=LDHA PE=1 SV=2 - [LDHA_H	2.06E+08	1.95E+08	2.31E+08
O96008	Mitochondrial import receptor sUBunit TOM40 homolog OS=Homo sapiens OX=9606 GN=TOM	8.41E+06	1.05E+07	1.97E+07
O95861	3'(2'),5'-bisphosphate nucleotidase 1 OS=Homo sapiens OX=9606 GN=BPNT1 PE=1 SV=1 - [BPN	5.35E+06	8.01E+06	1.67E+07
O95831	Apoptosis-inducing factor 1, mitochondrial OS=Homo sapiens OX=9606 GN=AIFM1 PE=1 SV=1	3.47E+07	7.30E+06	1.27E+07
O95782	AP-2 complex sUBunit alpha-1 OS=Homo sapiens OX=9606 GN=AP2A1 PE=1 SV=3 - [AP2A1_H	2.29E+07	1.29E+07	8.19E+07
O95747	Serine/threonine-protein kinase OSR1 OS=Homo sapiens OX=9606 GN=OXSR1 PE=1 SV=1 - [O	1.13E+07	8.41E+06	9.94E+06
O95478	Ribosome biogenesis protein NSA2 homolog OS=Homo sapiens OX=9606 GN=NSA2 PE=1 SV=	2.97E+08	2.67E+08	5.42E+08
O95477	Phospholipid-transporting ATPase ABCA1 OS=Homo sapiens OX=9606 GN=ABCA1 PE=1 SV=3	2.07E+07	4.94E+06	1.19E+07
O95470	Sphingosine-1-phosphate lyase 1 OS=Homo sapiens OX=9606 GN=SGPL1 PE=1 SV=3 - [SGPL1	4.37E+07	2.41E+06	1.28E+07
O95445	Apolipoprotein M OS=Homo sapiens OX=9606 GN=APOM PE=1 SV=2 - [APOM_HUMAN]	1.29E+07	6.07E+06	1.43E+07
O95433	Activator of 90 kDa heat shock protein ATPase homolog 1 OS=Homo sapiens OX=9606 GN=AH	2.74E+07	2.02E+07	4.63E+06
O95373	Importin-7 OS=Homo sapiens OX=9606 GN=IPO7 PE=1 SV=1 - [IPO7_HUMAN]	4.28E+07	7.23E+06	7.12E+07
O95197	Reticulon-3 OS=Homo sapiens OX=9606 GN=RTN3 PE=1 SV=2 - [RTN3_HUMAN]	7.99E+06	1.53E+07	6.33E+06
O95139	NADH dehydrogenase [UBiquinone] 1 beta sUBcomplex sUBunit 6 OS=Homo sapiens OX=9606	7.50E+06	8.63E+06	7.02E+06
O94979	Protein transport protein Sec31A OS=Homo sapiens OX=9606 GN=SEC31A PE=1 SV=3 - [SC31A	2.25E+07	8.44E+06	3.99E+06
O94973	AP-2 complex sUBunit alpha-2 OS=Homo sapiens OX=9606 GN=AP2A2 PE=1 SV=2 - [AP2A2_H	1.28E+07	4.74E+06	8.19E+07
O94925	Glutaminase kidney isoform, mitochondrial OS=Homo sapiens OX=9606 GN=GLS PE=1 SV=1 - [	1.54E+07	1.91E+07	5.35E+06
O94906	Pre-mRNA-processing factor 6 OS=Homo sapiens OX=9606 GN=PRPF6 PE=1 SV=1 - [PRP6_HU	7.71E+06	1.45E+07	7.50E+06
O94888	UBX domain-containing protein 7 OS=Homo sapiens OX=9606 GN=UBXN7 PE=1 SV=2 - [UBXN	9.44E+06	1.58E+07	1.19E+07
O94832	Unconventional myosin-Id OS=Homo sapiens OX=9606 GN=MYO1D PE=1 SV=2 - [MYO1D_HU	1.15E+07	2.53E+07	1.81E+07
O94826	Mitochondrial import receptor sUBunit TOM70 OS=Homo sapiens OX=9606 GN=TOMM70 PE=1	8.04E+06	1.00E+07	4.61E+07
O76094	Signal recognition particle sUBunit SRP72 OS=Homo sapiens OX=9606 GN=SRP72 PE=1 SV=3 - [	9.23E+07	8.97E+07	1.24E+08
O76013	Keratin, type I cuticular Ha6 OS=Homo sapiens OX=9606 GN=KRT36 PE=1 SV=1 - [KRT36_HUMA	2.46E+08	4.52E+09	2.79E+09
O76011	Keratin, type I cuticular Ha4 OS=Homo sapiens OX=9606 GN=KRT34 PE=1 SV=2 - [KRT34_HUMA	7.17E+08	7.03E+06	1.08E+08
O75874	Isocitrate dehydrogenase [NADP] cytoplasmic OS=Homo sapiens OX=9606 GN=IDH1 PE=1 SV=	2.06E+07	1.66E+07	1.07E+07
O75822	Eukaryotic translation initiation factor 3 sUBunit J OS=Homo sapiens OX=9606 GN=EIF3J PE=1 SV	1.20E+07	8.58E+06	1.11E+07
O75746	Calcium-binding mitochondrial carrier protein Aralar1 OS=Homo sapiens OX=9606 GN=SLC25A	9.81E+06	7.35E+07	5.76E+07
O75694	Nuclear pore complex protein Nup155 OS=Homo sapiens OX=9606 GN=NUP155 PE=1 SV=1 - [	1.97E+07	2.39E+06	3.75E+06
O75643	U5 small nuclear ribonucleoprotein 200 kDa helicase OS=Homo sapiens OX=9606 GN=SNRNP20	1.47E+07	7.58E+06	1.10E+07
O75635	Serpin B7 OS=Homo sapiens OX=9606 GN=SERPINB7 PE=1 SV=1 - [SPB7_HUMAN]	1.17E+07	1.81E+07	7.49E+06
O75592	E3 UBiquitin-protein ligase MYCBP2 OS=Homo sapiens OX=9606 GN=MYCBP2 PE=1 SV=4 - [MY	7.85E+06	7.81E+06	9.62E+06
O75534	Cold shock domain-containing protein E1 OS=Homo sapiens OX=9606 GN=CSDE1 PE=1 SV=2 -	3.13E+07	1.32E+07	1.58E+07
O75533	Splicing factor 3B sUBunit 1 OS=Homo sapiens OX=9606 GN=SF3B1 PE=1 SV=3 - [SF3B1_HUMA	1.72E+07	3.56E+07	2.80E+07
O75436	Vacuolar protein sorting-associated protein 26A OS=Homo sapiens OX=9606 GN=VPS26A PE=1	1.52E+07	1.54E+07	5.53E+06
O75390	Citrate synthase, mitochondrial OS=Homo sapiens OX=9606 GN=CS PE=1 SV=2 - [CISY_HUMAN	1.95E+08	7.83E+06	1.26E+08
O75369	Filamin-B OS=Homo sapiens OX=9606 GN=FLNB PE=1 SV=2 - [FLNB_HUMAN]	1.29E+07	2.05E+07	2.51E+07
O75366	Advillin OS=Homo sapiens OX=9606 GN=AVIL PE=1 SV=3 - [AVIL_HUMAN]	2.95E+07	1.26E+07	8.61E+07
O75352	Mannose-P-dolichol utilization defect 1 protein OS=Homo sapiens OX=9606 GN=MPDU1 PE=1	2.06E+07	6.07E+06	1.96E+07
O75165	DnaJ homolog sUBfamily C member 13 OS=Homo sapiens OX=9606 GN=DNAJC13 PE=1 SV=5 -	9.57E+06	7.50E+06	1.15E+07
O75131	Copine-3 OS=Homo sapiens OX=9606 GN=CPNE3 PE=1 SV=1 - [CPNE3_HUMAN]	9.52E+06	6.80E+06	1.67E+07
O60814	Histone H2B type 1-K OS=Homo sapiens OX=9606 GN=H2BC12 PE=1 SV=3 - [H2B1K_HUMAN]	2.01E+09	2.31E+09	3.11E+09
O60763	General vesicular transport factor p115 OS=Homo sapiens OX=9606 GN=USO1 PE=1 SV=2 - [US	1.50E+07	8.42E+06	3.03E+07

O60762	Dolichol-phosphate mannosyltransferase sUBunit 1 OS=Homo sapiens OX=9606 GN=DPM1 PE=	9.25E+06	6.29E+06	5.75E+06
O60749	Sorting nexin-2 OS=Homo sapiens OX=9606 GN=SNX2 PE=1 SV=2 - [SNX2_HUMAN]	9.18E+06	1.62E+07	9.46E+06
O60701	UDP-glucose 6-dehydrogenase OS=Homo sapiens OX=9606 GN=UGDH PE=1 SV=1 - [UGDH_H	1.41E+08	1.01E+08	1.53E+08
O60568	Multifunctional procollagen lysine hydroxylase and glycosyltransferase LH3 OS=Homo sapiens OX	1.69E+07	1.40E+07	6.51E+06
O60502	Protein O-GlcNAcase OS=Homo sapiens OX=9606 GN=OGA PE=1 SV=2 - [OGA_HUMAN]	1.10E+07	9.28E+07	1.69E+07
O60313	Dynamin-like 120 kDa protein, mitochondrial OS=Homo sapiens OX=9606 GN=OPA1 PE=1 SV=3	8.62E+06	1.55E+07	1.39E+07
O60264	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin sUBfamily A memb	2.82E+07	1.37E+07	1.56E+07
O43865	S-adenosylhomocysteine hydrolase-like protein 1 OS=Homo sapiens OX=9606 GN=AHCYL1 PE	1.50E+07	1.32E+07	2.12E+07
O43837	Isocitrate dehydrogenase [NAD] sUBunit beta, mitochondrial OS=Homo sapiens OX=9606 GN=I	1.30E+07	1.93E+07	1.35E+08
O43813	Glutathione S-transferase LANCL1 OS=Homo sapiens OX=9606 GN=LANCL1 PE=1 SV=1 - [LAN	1.60E+07	1.48E+07	1.56E+08
O43790	Keratin, type II cuticular Hb6 OS=Homo sapiens OX=9606 GN=KRT86 PE=1 SV=1 - [KRT86_HUM	1.28E+09	2.85E+07	3.91E+08
O43776	Asparagine--tRNA ligase, cytoplasmic OS=Homo sapiens OX=9606 GN=NARS1 PE=1 SV=1 - [S	3.40E+08	2.85E+08	1.82E+08
O43772	Mitochondrial carnitine/acylcarnitine carrier protein OS=Homo sapiens OX=9606 GN=SLC25A20	2.47E+07	5.42E+06	2.88E+07
O43747	AP-1 complex sUBunit gamma-1 OS=Homo sapiens OX=9606 GN=AP1G1 PE=1 SV=5 - [AP1G1	8.80E+06	1.63E+07	2.28E+07
O43707	Alpha-actinin-4 OS=Homo sapiens OX=9606 GN=ACTN4 PE=1 SV=2 - [ACTN4_HUMAN]	1.46E+07	6.63E+07	4.48E+07
O43681	ATPase GET3 OS=Homo sapiens OX=9606 GN=GET3 PE=1 SV=2 - [GET3_HUMAN]	1.57E+07	9.59E+06	1.31E+07
O43670	BUB3-interacting and GLEBS motif-containing protein ZNF207 OS=Homo sapiens OX=9606 GN=	7.67E+07	2.92E+06	8.94E+07
O43639	Cytoplasmic protein NCK2 OS=Homo sapiens OX=9606 GN=NCK2 PE=1 SV=2 - [NCK2_HUMAN]	9.03E+07	1.50E+07	4.50E+06
O43592	Exportin-T OS=Homo sapiens OX=9606 GN=XPOT PE=1 SV=2 - [XPOT_HUMAN]	7.22E+07	9.96E+07	5.87E+07
O43402	ER membrane protein complex sUBunit 8 OS=Homo sapiens OX=9606 GN=EMC8 PE=1 SV=1 - [	3.36E+07	1.59E+07	7.49E+06
O43396	Thioredoxin-like protein 1 OS=Homo sapiens OX=9606 GN=TXNL1 PE=1 SV=3 - [TXNL1_HUMA	1.29E+07	8.77E+06	9.03E+06
O43242	26S proteasome non-ATPase regulatory sUBunit 3 OS=Homo sapiens OX=9606 GN=PSMD3 PE=	5.48E+07	6.18E+07	4.45E+07
O43175	D-3-phosphoglycerate dehydrogenase OS=Homo sapiens OX=9606 GN=PHGDH PE=1 SV=4 - [	1.24E+08	1.83E+08	1.78E+08
O43166	Signal-induced proliferation-associated 1-like protein 1 OS=Homo sapiens OX=9606 GN=SIPA1	2.59E+07	3.35E+07	1.40E+07
O43143	ATP-dependent RNA helicase DHX15 OS=Homo sapiens OX=9606 GN=DHX15 PE=1 SV=2 - [D	3.45E+08	4.00E+08	4.48E+08
O15371	Eukaryotic translation initiation factor 3 sUBunit D OS=Homo sapiens OX=9606 GN=EIF3D PE=1 S	1.00E+07	1.23E+07	1.46E+07
O15355	Protein phosphatase 1G OS=Homo sapiens OX=9606 GN=PPM1G PE=1 SV=1 - [PPM1G_HUMA	2.29E+07	1.75E+07	2.41E+07
O15260	Surfeit locus protein 4 OS=Homo sapiens OX=9606 GN=SURF4 PE=1 SV=3 - [SURF4_HUMAN]	2.12E+07	1.05E+07	1.91E+07
O15173	Membrane-associated progesterone receptor component 2 OS=Homo sapiens OX=9606 GN=P	1.26E+07	1.37E+07	1.56E+07
O15145	Actin-related protein 2/3 complex sUBunit 3 OS=Homo sapiens OX=9606 GN=ARPC3 PE=1 SV=	6.75E+06	1.20E+07	5.94E+06
O15067	Phosphoribosylformylglycinamidine synthase OS=Homo sapiens OX=9606 GN=PFAS PE=1 SV=4	1.15E+07	2.64E+07	6.84E+06
O15066	Kinesin-like protein KIF3B OS=Homo sapiens OX=9606 GN=KIF3B PE=1 SV=1 - [KIF3B_HUMAN]	3.54E+08	5.90E+06	1.43E+07
O14980	Exportin-1 OS=Homo sapiens OX=9606 GN=XPO1 PE=1 SV=1 - [XPO1_HUMAN]	2.18E+08	1.91E+08	2.49E+08
O14964	Hepatocyte growth factor-regulated tyrosine kinase sUBstrate OS=Homo sapiens OX=9606 GN=	9.21E+06	8.63E+06	1.04E+07
O14732	Inositol monophosphatase 2 OS=Homo sapiens OX=9606 GN=IMPA2 PE=1 SV=1 - [IMPA2_HU	2.14E+07	3.06E+07	9.54E+07
O14646	Chromodomain-helicase-DNA-binding protein 1 OS=Homo sapiens OX=9606 GN=CHD1 PE=1	2.72E+07	1.70E+07	1.69E+07
O14628	Zinc finger protein 195 OS=Homo sapiens OX=9606 GN=ZNF195 PE=1 SV=2 - [ZN195_HUMAN]	2.01E+07	5.24E+06	5.28E+06
O14617	AP-3 complex sUBunit delta-1 OS=Homo sapiens OX=9606 GN=AP3D1 PE=1 SV=1 - [AP3D1_H	2.39E+08	1.43E+08	1.43E+08
O14602	Eukaryotic translation initiation factor 1A, Y-chromosomal OS=Homo sapiens OX=9606 GN=EIF1	1.71E+07	4.03E+06	1.57E+08
O00763	Acetyl-CoA carboxylase 2 OS=Homo sapiens OX=9606 GN=ACACB PE=1 SV=3 - [ACACB_HUM	4.79E+09	3.71E+09	2.99E+09
O00712	Nuclear factor 1 B-type OS=Homo sapiens OX=9606 GN=NFIB PE=1 SV=2 - [NFIB_HUMAN]	1.24E+07	1.74E+07	1.21E+07
O00629	Importin sUBunit alpha-3 OS=Homo sapiens OX=9606 GN=KPNA4 PE=1 SV=1 - [IMA3_HUMAN]	2.20E+08	2.29E+08	2.18E+08
O00571	ATP-dependent RNA helicase DDX3X OS=Homo sapiens OX=9606 GN=DDX3X PE=1 SV=3 - [D	5.86E+08	4.48E+08	5.48E+08
O00567	Nucleolar protein 56 OS=Homo sapiens OX=9606 GN=NOP56 PE=1 SV=4 - [NOP56_HUMAN]	1.88E+07	5.17E+07	7.93E+07
O00534	von Willebrand factor A domain-containing protein 5A OS=Homo sapiens OX=9606 GN=VWA5	4.42E+07	8.10E+06	4.78E+07
O00505	Importin sUBunit alpha-4 OS=Homo sapiens OX=9606 GN=KPNA3 PE=1 SV=2 - [IMA4_HUMAN]	4.26E+08	2.09E+08	2.07E+08
O00487	26S proteasome non-ATPase regulatory sUBunit 14 OS=Homo sapiens OX=9606 GN=PSMD14 P	1.13E+07	1.99E+07	4.82E+08
O00469	Procollagen-lysine,2-oxoglutarate 5-dioxygenase 2 OS=Homo sapiens OX=9606 GN=PLOD2 PE	2.48E+07	1.84E+07	1.42E+07
O00458	Interferon-related developmental regulator 1 OS=Homo sapiens OX=9606 GN=IFRD1 PE=1 SV=	8.59E+06	8.76E+06	1.15E+07
O00425	Insulin-like growth factor 2 mRNA-binding protein 3 OS=Homo sapiens OX=9606 GN=IGF2BP3	7.03E+07	8.19E+07	6.89E+07
O00410	Importin-5 OS=Homo sapiens OX=9606 GN=IPO5 PE=1 SV=4 - [IPO5_HUMAN]	8.66E+06	2.66E+07	3.71E+07
O00303	Eukaryotic translation initiation factor 3 sUBunit F OS=Homo sapiens OX=9606 GN=EIF3F PE=1 S	1.82E+07	1.64E+07	1.16E+07
O00299	Chloride intracellular channel protein 1 OS=Homo sapiens OX=9606 GN=CLIC1 PE=1 SV=4 - [CLI	7.27E+06	4.57E+06	1.87E+07
O00264	Membrane-associated progesterone receptor component 1 OS=Homo sapiens OX=9606 GN=P	6.49E+06	8.58E+06	1.35E+07
O00232	26S proteasome non-ATPase regulatory sUBunit 12 OS=Homo sapiens OX=9606 GN=PSMD12 P	4.91E+06	1.68E+07	2.23E+07
O00231	26S proteasome non-ATPase regulatory sUBunit 11 OS=Homo sapiens OX=9606 GN=PSMD11 P	8.11E+06	9.02E+06	9.55E+06
O00203	AP-3 complex sUBunit beta-1 OS=Homo sapiens OX=9606 GN=AP3B1 PE=1 SV=3 - [AP3B1_HU	1.85E+07	2.96E+07	1.41E+07
O00178	GTP-binding protein 1 OS=Homo sapiens OX=9606 GN=GTPBP1 PE=1 SV=3 - [GTPB1_HUMAN]	5.84E+06	1.13E+07	9.54E+06
O00159	Unconventional myosin-Ic OS=Homo sapiens OX=9606 GN=MYO1C PE=1 SV=4 - [MYO1C_HUM	3.58E+07	6.76E+07	1.19E+08
O00154	Cytosolic acyl coenzyme A thioester hydrolase OS=Homo sapiens OX=9606 GN=ACOT7 PE=1 SV	9.80E+07	8.19E+07	8.83E+07
O00148	ATP-dependent RNA helicase DDX39A OS=Homo sapiens OX=9606 GN=DDX39A PE=1 SV=2 -	9.21E+07	2.13E+07	1.83E+08
O00116	Alkyldihydroxyacetonephosphate synthase, peroxisomal OS=Homo sapiens OX=9606 GN=AGPS	1.44E+07	8.71E+06	1.08E+07
B2RPK0	Putative high mobility group protein B1-like 1 OS=Homo sapiens OX=9606 GN=HMGB1P1 PE=5	9.05E+06	1.06E+07	5.66E+06
B0I1T2	Unconventional myosin-Ig OS=Homo sapiens OX=9606 GN=MYO1G PE=1 SV=2 - [MYO1G_HU	1.82E+07	1.51E+07	2.08E+07
A8MXE2	Beta-1,3-galactosyltransferase 9 OS=Homo sapiens OX=9606 GN=B3GALT9 PE=3 SV=2 - [B3GT	1.27E+07	1.11E+07	4.27E+06
A8MVW0	Protein FAM171A2 OS=Homo sapiens OX=9606 GN=FAM171A2 PE=1 SV=1 - [F1712_HUMAN]	2.37E+07	1.64E+07	9.37E+06
A8K2U0	Alpha-2-macroglobulin-like protein 1 OS=Homo sapiens OX=9606 GN=A2ML1 PE=1 SV=3 - [A	3.59E+07	8.33E+06	2.00E+07
A6NIZ1	Ras-related protein Rap-1b-like protein OS=Homo sapiens OX=9606 PE=2 SV=1 - [RP1BL_HUM	3.20E+07	7.98E+06	1.34E+07
A6NHR9	Structural maintenance of chromosomes flexible hinge domain-containing protein 1 OS=Homo s	1.43E+07	1.55E+07	1.02E+07
A0M8Q6	Immunoglobulin lambda constant 7 OS=Homo sapiens OX=9606 GN=IGLC7 PE=1 SV=3 - [IGLC	2.44E+07	9.04E+06	1.37E+07
A0JLT2	Mediator of RNA polymerase II transcription sUBunit 19 OS=Homo sapiens OX=9606 GN=MED1	1.29E+07	8.80E+06	2.14E+08
A0FGR8	Extended synaptotagmin-2 OS=Homo sapiens OX=9606 GN=ESYT2 PE=1 SV=1 - [ESYT2_HUM	2.83E+07	1.91E+07	1.86E+07
A0AVT1	UBiquitin-like modifier-activating enzyme 6 OS=Homo sapiens OX=9606 GN=UBA6 PE=1 SV=1	2.21E+09	1.98E+07	5.43E+06

9. Images for Western blot and SDS-Page

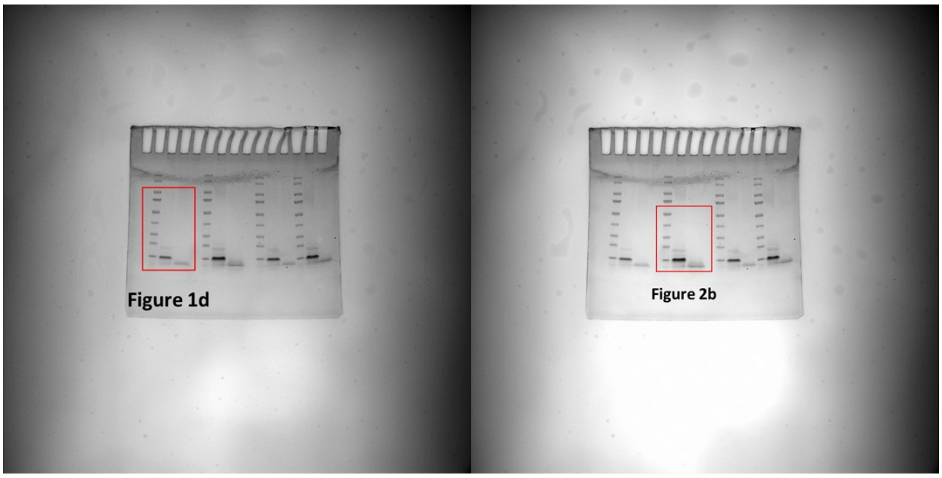

Figure S11. The raw images for electrophoresis data of Figure 1d and Figure 2b.

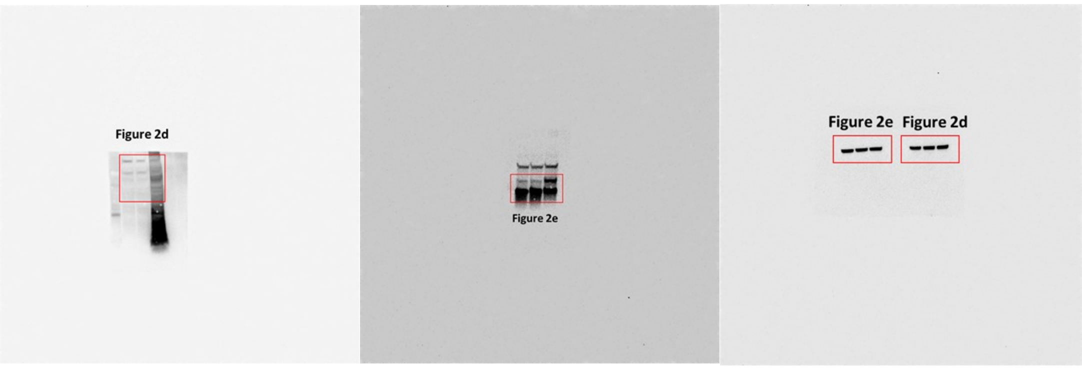

Figure S12. The raw images for Western blot of Figure 2d and 2e.

10. References

1. Y. Wang, J. Chen, X. Hua, X. Meng, H. Cai, R. Wang, J. Shi, H. Deng, L. Liu and Y. M. Li, *Angew. Chem. Int. Ed.*, 2022, **61**.

2. Y. Wang, C. Chen, X. Meng, J. Fan, M. Pan, J. Chen, H. Deng, S. Shi, L. Liu, Y. M. Li, *CCS Chem.*, 2020, **2**, 1157-1168.

3. S. Mandal, G. Mann, G. Satish and A. Brik, *Angew. Chem. Int. Ed.*, **2021**, 60, 7333-7343.

4. M. Chen, Z. Feng, X. Fan, J. Sun, W. Geng, T. Wu, J. Sheng, J. Qian and Z. Xu, *Nat Commun*, **2022**, 13, 6643.