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# Sorbin and SH3 Domain-Containing Protein 2 Is Released From Infarcted Heart in the Very Early Phase: Proteomic Analysis of Cardiac Tissues From Patients

Yu Kakimoto, MD; Shinji Ito, PhD; Hitoshi Abiru, BS; Hirokazu Kotani, MD, PhD; Munetaka Ozeki, PhD; Keiji Tamaki, MD, PhD; Tatsuaki Tsuruyama, MD, PhD

**Background**—Few proteomic studies have examined human cardiac tissue following acute lethal infarction. Here, we applied a novel proteomic approach to formalin-fixed, paraffin-embedded human tissue and aimed to reveal the molecular changes in the very early phase of acute myocardial infarction.

**Methods and Results**—Heart tissue samples were collected from 5 patients who died within 7 hours of myocardial infarction and from 5 age- and sex-matched control cases. Infarcted and control myocardia were histopathologically diagnosed and captured using laser microdissection. Proteins were extracted using an originally established method and analyzed using liquid chromatography–tandem mass spectrometry. The label-free quantification demonstrated that the levels of 21 proteins differed significantly between patients and controls. In addition to known biomarkers, the sarcoplasmic protein sorbin and SH3 domain-containing protein 2 (SORBS2) was greatly reduced in infarcted myocardia. Immunohistochemical analysis of cardiac tissues confirmed the decrease, and Western blot analysis showed a significant increase in serum sorbin and SH3 domain-containing protein 2 in acute myocardial infarction patients (n=10) compared with control cases (n=11).

**Conclusions**—Our advanced comprehensive analysis using patient tissues and serums indicated that sarcoplasmic sorbin and SH3 domain-containing protein 2 is released from damaged cardiac tissue into the bloodstream upon lethal acute myocardial infarction. The proteomic strategy presented here is based on precise microscopic findings and is quite useful for candidate biomarker discovery using human tissue samples stored in depositories. (*J Am Heart Assoc.* 2013;2:e000565 doi: 10.1161/JAHA.113.000565)

**Key Words:** myocardial infarction • proteomics • SORBS2 • tissue

Many animal experiments have been performed to date to elucidate the mechanism of cardiac ischemic injury,<sup>1,2</sup> and these studies have enhanced our understanding of cardiac remodeling following hypoxic stress. Clinical studies using samples from admitted patients have also been conducted to discover diagnostic or prognostic biomarkers for

acute myocardial infarction (AMI).<sup>3,4</sup> Some cardiac proteins are in practical use for early diagnosis of AMI, including troponins<sup>5</sup> and heart-type fatty acid-binding protein (H-FABP).<sup>6</sup> However, ischemic heart failure is still a major cause of sudden death,<sup>7–9</sup> and lethal AMI occurring before hospitalization has not been sufficiently investigated.

It is often difficult to define the ischemic lesion at autopsy because sudden death results in few anatomical changes to the heart. Microscopic alterations appear within 30 minutes after infarction, whereas macroscopic changes appear >4 hours later.<sup>10–12</sup> Although some AMI model experiments have attempted to determine the molecular profile alterations associated with short-term ischemia, elucidation of the acute proteomic changes is challenging if tissues are collected macroscopically.<sup>13,14</sup>

Formalin fixation and paraffin embedding are essential steps for accurate microscopic tissue sampling. Formaldehyde cross-links the side chains of amino acids, which stabilizes cellular morphology and prevents decomposition.<sup>15,16</sup> However, intermolecular bridging is considered

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Accompanying Tables S1 through S3 are available at <http://jaha.ahajournals.org/content/2/6/e000565/suppl/DC1>

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problematic for extracting biomolecules for proteomic research. Recently, commercial kits enabling efficient protein extraction from formalin-fixed and paraffin-embedded (FFPE) samples have emerged.<sup>17–19</sup> We also developed an original method to reduce the interference associated with formalin fixation and thus to provide sufficient mass spectrum intensity from human FFPE tissues.<sup>20</sup> In this study, we microdissected the ischemic lesions from FFPE heart tissue and applied the modified extraction procedure. Subsequent analysis of the protein samples using label-free mass spectrometry resulted in identification of 21 proteins displaying differential expression in AMI. This research is the first attempt to discern the proteomic changes occurring in the very early phase of infarction using microscopically dissected myocardia from FFPE human heart tissue.

## Methods

### Patients

Heart tissues and blood samples were obtained from forensic autopsies performed at the Kyoto University Graduate School of Medicine between February 2010 and November 2012. The clinical histories and autopsy findings were retrospectively reviewed, and the stored samples were analyzed for the present study under anonymity. This project was approved by the Ethics Committee of Medicine at Kyoto University.

AMI was diagnosed on the basis of clinical episode and autopsy findings<sup>21</sup>: (1) patients died within 7 hours of the onset of symptoms without any angioplasty or thrombolytic therapy; (2) serum was positive for H-FABP, as determined using a commercial ELISA kit (Rapicheck; DS Pharm Biomedical, Osaka, Japan)<sup>22</sup>; and (3) contraction bands or wavy fibers were observed in the free wall of the left ventricle on histopathology. Control cases were selected using the following criteria: (1) serum was negative for H-FABP, as determined by Rapicheck ELISA; (2) no pathological features of myocardial infarction, cardiomyopathy, myocarditis, or congenital heart abnormalities were observed; and (3) coronary atherosclerosis was not obvious.

For cardiac proteomic analysis, we selected 5 AMI patients and 5 age- and sex-matched control cases. For serum immunoblotting, we collected blood from 10 AMI patients and 11 controls.

### Heart Tissue and Serum Samples

Hearts were immediately fixed in 10% buffered formalin after removal from the body at autopsy. After fixation, the free wall of each left ventricle was embedded in paraffin. The blocks were continuously cut into 4- $\mu$ m sections for microscopic observation and 5- $\mu$ m sections for proteomic analysis. For

accurate diagnosis, 4- $\mu$ m specimens were stained with hematoxylin and eosin and phosphotungstic acid–hematoxylin. Patient serum was stored at  $-40^{\circ}\text{C}$  until further analysis.

### Histopathology

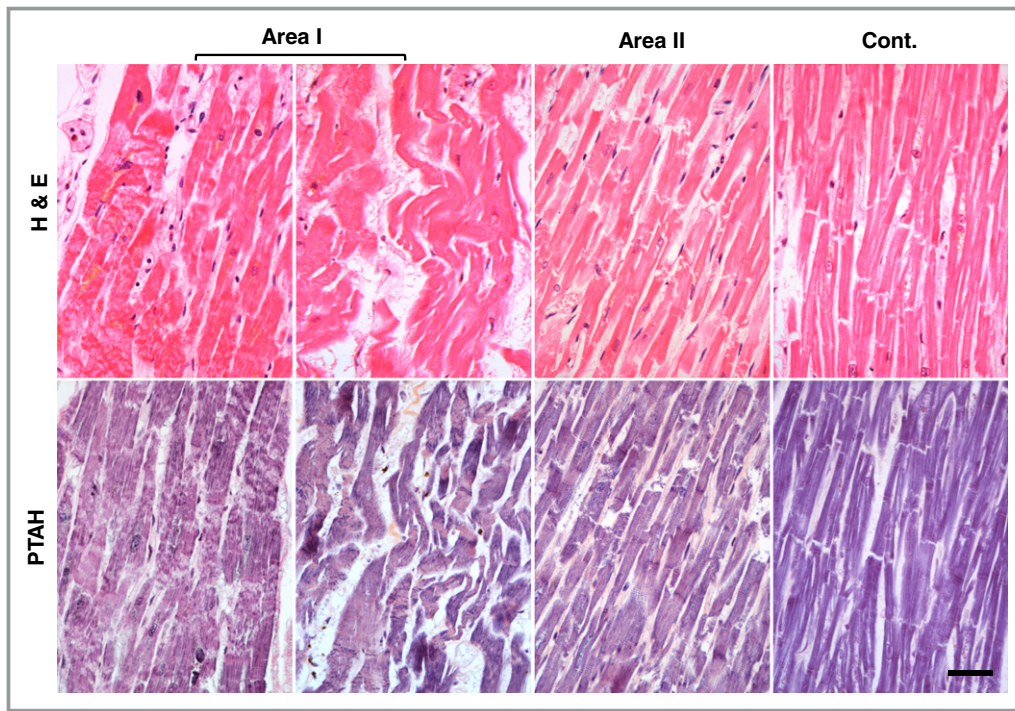
Longitudinal sections of myocardia were observed microscopically, where the cardiac linear structure is more evident than in cross-sectioned muscle fibers.<sup>23</sup> Prominent neutrophilic infiltration was not sampled because it occurs  $>12$  hours after infarction.<sup>10–12</sup> In each ischemic area of the left ventricle in AMI hearts, we defined 2 regions: area I contained distinctive contraction bands or wavy fibers, and area II showed other minor irregular patterns, such as fragmented myocytes. The free wall of the left ventricle was also sampled from each control case Figure 1.

### Laser Capture Microdissection

Serial sections of diagnostic slides were mounted on Frame Slides (Micro Dissect GmbH, Herborn, Germany) and stained with Mayer's hematoxylin. Stained slides were air-dried. Laser capture microdissection was performed using an LMD 6500 (Leica Microsystems, Wetzlar, Germany) instrument to capture microscopically defined areas. Cardiac tissues of 10 mm<sup>2</sup> in total were collected into a 500- $\mu$ L cap from each sampling. Large capillaries and areas of fibrosis were excluded. A flowchart of the subsequent proteomic approach is shown in Figure 2.

### Protein Extraction

After dissection, cardiac proteins were extracted using a previously described method, with modifications.<sup>20</sup> Acetonitrile (CH<sub>3</sub>CN) and dithiothreitol were purchased from Nacalai Tesque (Kyoto, Japan). Ammonium bicarbonate (NH<sub>4</sub>HCO<sub>3</sub>) and trifluoroacetic acid were purchased from Sigma-Aldrich (St. Louis, MO). Each microdissected sample was suspended in 20  $\mu$ L of 0.1 mol/L NH<sub>4</sub>HCO<sub>3</sub> containing 30% (v/v) CH<sub>3</sub>CN and centrifuged at 10 000g for 1 minute. Tubes were heated at 95°C for 90 minutes with shaking every 20 minutes to avoid condensation of the buffer in the cap. After retrieval, the samples were centrifuged at 10 000g for 1 minute, cooled on ice, and then 1  $\mu$ L of a 1  $\mu$ g/ $\mu$ L trypsin (Sequencing Grade Modified Trypsin; Promega, Madison, WI) solution was added to each tube for protein digestion. The samples were incubated at 37°C overnight. Protein content was estimated using the bicinchoninic acid method (Micro BCA Assay; Termo Scientific, Cramlington, UK) with bovine albumin as the standard. Next, 10 mmol/L dithiothreitol was added to each tissue digest, and the tube was heated at 95°C for 5 minutes to deactivate the trypsin. After drying, samples were



**Figure 1.** Hematoxylin and eosin (H&E) and phosphotungstic acid–hematoxylin (PTAH) staining of cardiac tissues. Two sampling areas were microscopically selected from the left ventricular free wall of each infarcted heart: area I and area II. Area I contains distinctive contraction bands (left) and wavy fibers (right). Area II is surrounded by area I and shows minor irregularities such as fragmented myocardia. From each control, cardiac tissue was taken from the left ventricular free wall. Magnification  $\times 400$ . Scale bar=50  $\mu\text{m}$ .

resuspended in 0.1% trifluoroacetic acid with 2%  $\text{CH}_3\text{CN}$ , resulting in a final protein concentration of 0.2  $\mu\text{g}/\mu\text{L}$ . The proteins extracted from 3 histopathological types (area I, area II, and control) were used directly in the subsequent proteomic analysis (15 samples in total).

### Peptide Separation and Mass Spectrometry

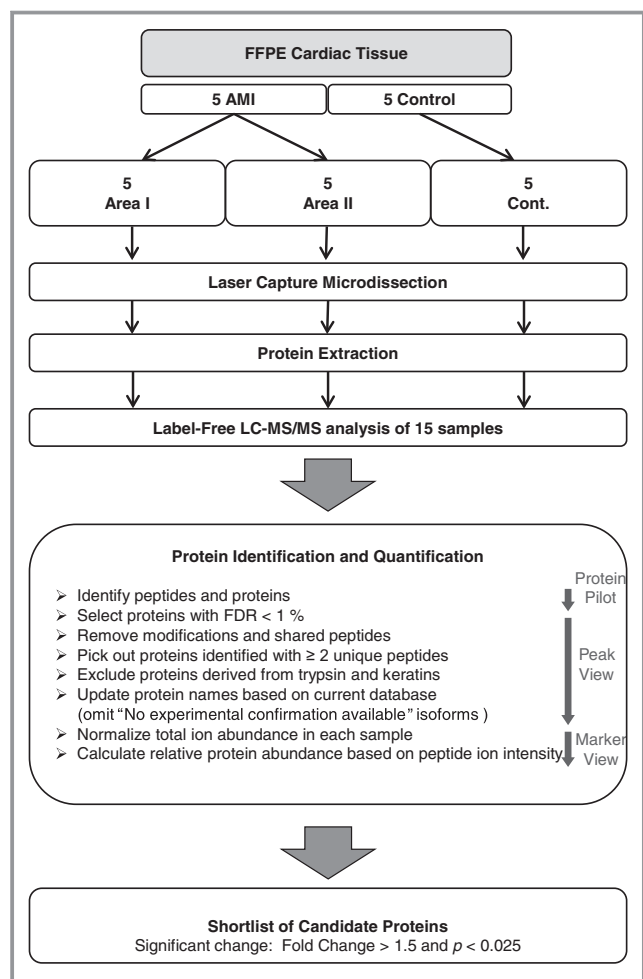
All liquid chromatography (LC) solvents were LC-mass spectrometry (MS) grade and purchased from Wako Pure Chemical Industries, Ltd (Osaka, Japan). A 5- $\mu\text{L}$  aliquot of each trypsinized sample was separated using nanoflow reverse-phase LC (NanoLC-Ultra System; Eksigent, Dublin, CA) with a cHiP-based platform (cHiPLC-Nanoflex System; Eksigent, Dublin, CA) using the trap-and-elute method. An aliquot of each sample (5  $\mu\text{L}$ ) was automatically injected onto a trap column (Nano cHiPLC Trap column, 200  $\mu\text{m}\times 0.5\text{ mm}$ ; ChromXP C18-CL, 3  $\mu\text{m}$ , 120  $\text{\AA}$ ; Eksigent, Dublin, CA) and washed for 10 minutes using 0.1% formic acid as the loading solvent. The trap column was then switched online with the analytical column (Nano cHiPLC column, 75  $\mu\text{m}\times 15\text{ cm}$ ; ChromXP C18-CL, 3  $\mu\text{m}$ , 120  $\text{\AA}$ ; Eksigent, Dublin, CA), and peptides were eluted with the following binary gradient: initial composition 2% solvent B (98% solvent A), then changed from 2% solvent B to 40% solvent B over 125 minutes, from 60% solvent B to 90% solvent B over 1 minutes, maintained at 90% solvent B for 5 minutes, then

switch back to the initial composition [2% solvent B]). Solvent A consisted of 2%  $\text{CH}_3\text{CN}$  and 0.1% formic acid, and solvent B consisted of 80%  $\text{CH}_3\text{CN}$  and 0.1% formic acid. The column flow rate was set to 300 nL/min. Eluted peptides were analyzed using a quadrupole-time-of-flight hybrid mass spectrometer (Triple TOF 5600 system; AB SCIEX, Framingham, MA) equipped with an electrospray ionization source optimized for nanoflow (NanoSpray, AB SCIEX). The ion spray voltage floating was +2.3 kV, and the interface heater temperature (IHT) was set at 150°C. The MS was carried out in a data-dependent acquisition method, in which the 10 most abundant ions detected in each 0.25-second time-of-flight mass spectrometer survey scan were automatically subjected to MS/MS scans for an accumulation time of 100 ms. Time-of-flight mass spectrometer scans were performed over the  $m/z$  range of 400 to 1250 with 50-mDa tolerance, excluding former target ions for 10 seconds. Tandem MS (MS/MS) scans were performed with a collision energy of 35 kV with UNIT-resolution in the  $m/z$  range of 100 to 1600 with 50-mDa tolerance, excluding former target ions for 10 seconds.

### Identification and Quantification of Peptides/Proteins

Peptides and proteins were identified using the Paragon algorithm provided with Protein Pilot 4.5 beta (AB SCIEX) and





**Figure 2.** Flow diagram of proteomic analysis. AMI indicates acute myocardial infarction; FDR, false discovery rate; FFPE, formalin-fixed, paraffin-embedded; LC-MS/MS, liquid chromatography–tandem mass spectrometry.

using the combined database of Uniprot-Swissprot (version 2010-6, *Homo sapiens*) and sequences for known contaminants (AB SCIEX). False discovery rate (FDR) analysis was performed after peptide/protein identification using Proteomic System Performance Evaluation Pipeline (PSPEP) software (AB SCIEX). The results of FDR analyses for each sample (ie, number of peptides/proteins with the global FDR from Fit [ $<1\%$ ] and local FDR [ $<5\%$ ]) are described in the Results section).

Label-free quantification of peptides was performed using the Protein Quantitation 1.0 MicroApp (PQMA), which is part of Peak View 1.1.1 (AB SCIEX). First, liquid chromatography–tandem mass spectrometry (LC-MS/MS) data sets for all samples (15 samples) were analyzed at the same time using Protein Pilot 4.5 beta to produce a single group file that included the entire list of identified peptides/proteins throughout the samples and conditions. Second, the template group file was imported to the Peak View 1.1.1 platform using PQMA to construct the list of peaks for all detected unique peptides

(template peptides/proteins list). Third, individual LC-MS/MS data sets (wiff files) were imported to the Peak View 1.1.1 platform and analyzed by PQMA to quantitate each peptide/protein appearing in the template peptide/protein list. The results of PQMA were exported to Marker View 1.2.1 (AB SCIEX).

Peptides with a confidence  $>0.95$  were selected for exportation. Shared peptides, peptides for keratins, trypsins, bovine serum albumin, and decoy sequences generated for FDR (reversed sequences) were not exported. Ambiguous proteins identified on the basis of only 1 peptide were excluded. The current status of each protein was referred to the UniProt database website. "No experimental confirmation available" isoforms were also omitted from our list.

Protein abundance was calculated with Marker View 1.2.1 from the sum of the peak areas of detected peptides that originated from the same protein. Each abundance value was normalized against the total area sum of the individual sample. The reliability of the protein identification was validated by analyzing 3 replicates of each sample by LC-MS/MS and repeating postseparation software analysis. The analytical replication of the representative samples yielded basically the same results. The deviation of the number of detected proteins and peptides with a reliability of  $>99\%$  (ie, with a global FDR score from Fit of  $>1\%$ ) was in the range of  $\pm 0.62\%$  and  $\pm 1.79\%$ , respectively.

## Immunohistochemistry

Deparaffinized and rehydrated FFPE heart sections were subjected to antigen retrieval with Proteinase K (Dako, Glostrup, Denmark) at room temperature for 10 minutes and then heated in 10 mmol/L sodium citrate buffer at  $120^{\circ}\text{C}$  for 20 minutes. Blocking was performed with 1% bovine serum albumin and 0.1% cold-water fish gelatin at room temperature for 30 minutes. Specimens were immunostained with rabbit polyclonal antibody against sorbin and SH3 domain-containing protein 2 (SORBS2; 2.5  $\mu\text{g}/\text{mL}$ ; Abcam, Cambridge, UK) at  $4^{\circ}\text{C}$  overnight. EnVision G|2 System/AP, Rabbit/Mouse (Dako) was used for detection. We selected permanent red as the chromogen instead of 3,3'-diaminobenzidine because cardiac myocytes in subjects older than middle-aged contain abundant lipofuscin, a brown pigment easily confused with 3,3'-diaminobenzidine. Counterstaining was performed with Mayer's hematoxylin. Negative controls were stained using normal rabbit serum (ImmunoBioScience, Mukilteo, WA) instead of the primary antibody.

## Western Blot Analyses

Ten microliters of serum was collected from each subject. Albumin and gamma globulin were removed using an Albumin/IgG Removal kit (Thermo Scientific) because serum

analysis is complicated by high concentrations of these proteins, which can constitute >70% of total serum protein. After albumin and gamma globulin removal, the protein concentration was estimated using the bicinchoninic acid method (BCA Assay; Thermo Scientific). Dried protein (40 µg) was dissolved in sample buffer containing 1% SDS and 10% 2-mercaptoethanol and subjected to SDS-PAGE on a 4% to 15% TGX gel (Bio-Rad, Hercules, CA). After electrophoresis, proteins were transferred onto a polyvinylidene difluoride membrane (Bio-Rad). The membrane was incubated with anti-SORBS2 (2.5 µg/mL; Abcam) and rabbit polyclonal antibody against transferrin (1.0 µg/mL; Abcam). Immunoreactive bands were visualized using a chemiluminescence substrate (Thermo Scientific), and images were captured using a LAS-4000 mini (Fujifilm, Tokyo, Japan). Densitometric image analysis was performed using Image J software (<http://rsb.info.nih.gov/ij/>). Each densitometric level of SORBS2 was normalized against that of transferrin.<sup>24</sup>

## Statistical Analysis

The nonparametric, Mann–Whitney *U* test was used for comparison of the patients' ages, cardiac MS intensities, and serum immunoblotting densities. In this analysis, we set the significance level  $\alpha$  to 0.05. In cardiac MS screening, as double comparisons were performed (area I versus control and area II versus control) for each protein, we considered  $P < 0.025$  ( $0.05/2$ ) as significant after Bonferroni's correction. Briefly, fold-change values  $> 1.5$  and  $P < 0.025$  were considered significant in heart tissue screening, and  $P < 0.05$  was considered significant for patient age and serum immunoblotting. All calculations were performed using R statistical software (version 3.0.1; <http://www.r-project.org/>).

## Results

### Patient Characteristics

For MS screening of the cardiac tissue, tissues from 5 AMI patients (mean age  $\pm$  SD,  $59 \pm 12$  years) and 5 controls ( $57 \pm 14$  years) were examined. For serum immunoblotting verification, samples from 10 AMI patients ( $60 \pm 13$  years) and 11 controls ( $60 \pm 17$  years) were examined (Table 1). No significant age difference was observed among AMI patients and controls, both in the screening and in the validation analysis ( $P = 0.84$  and  $P = 1.00$ , respectively). All cases enrolled in this study are of Asian origin.

### Protein Identification and Quantification

LC-MS was performed on 10 tissue samples (5 from area I and 5 from area II) collected from 5 AMI patients and on 5 tissue

samples collected from 5 control subjects (Figure 2). From 243 551 spectra, 10 396 peptides and 734 proteins were identified, with a false-discovery rate of  $< 1\%$  (Table 2). All proteins identified in this study are listed in Table S1. With stringent filtration criteria (Figure 2), we selected 4564 peptides (Table S2) and 485 proteins (Table S3) for label-free quantification.

The distribution of all 485 proteins is illustrated in a volcano plot (Figure 3). The intensity levels of 21 proteins differed significantly between AMI patients and control subjects. The levels of 12 proteins were higher and of 9 proteins were lower in AMI tissue. The identity and primary intra- or extracellular localization of these proteins according to Gene Ontology (<http://www.geneontology.org/>) analysis are listed in Table 3, which shows that 7 proteins localized in the cytoplasm, 6 in mitochondria, 1 in the nucleus, and 7 in the extramycocardial space. We focused on the sarcoplasmic proteins like troponin T and H-FABP, which are traditional AMI biomarkers.<sup>25,26</sup>

## Immunohistochemistry

SORBS2 was observed in uniform alignment along the Z-band in the myocardial cytoskeleton and was prominent in the intercalated disk in control heart tissue (Figure 4A). In contraction bands in area I (Figure 4B), the regularity of the Z-band collapsed, and blurry immunostaining was observed in accordance with morphological changes, whereas the staining of the intercalated disk was maintained as a dense line. In wavy fibers in area I (Figure 4C), some myocytes showed an unstained cytoplasm, and adjacent myocardial cytoplasm was weakly stained with anti-SORBS2. In irregular myocytes in area II (Figure 4D), immunostaining signals clearly disappeared from the Z-lines, and some of the stained intercalated disks appeared ruptured, with loss of tight adherence between myocytes. Rupture of the intercalated disk was rare in area I (Figure 4B and 4C). In general, myocardial staining of SORBS2 was lower in AMI tissue than in control tissue.

## Serum Analyses

All 10 AMI cases in this study showed a positive level of serum H-FABP by a commercial ELISA kit, and 11 control cases showed a negative level (Figure 5A). Although individual differences were observed in serum Western blotting against SORBS2 (Figure 5B), the densitometric level of SORBS2 was significantly higher in AMI patients than in controls (Figure 5C). The level of SORBS2 in serum was 2.8-fold higher in AMI patients ( $P = 0.020$ ).

## Discussion

This study examined cases of sudden death occurring within 7 hours after myocardial infarction. Analysis of FFPE patient

**Table 1.** Patient Characteristics

Cause of Death	Sex	Age (y)	PMI (day)	Heart (g)	Coronary Findings at Autopsy	Cardioversion
<b>AMI Patients</b>						
AMI*	M	54	1.7	432	Thrombus in LCX	+
AMI*	M	40	1.3	454	Thrombus in LAD	+
AMI*	M	61	1.5	360	–	+
AMI*	M	62	0.9	389	Thrombus in LAD	+
AMI*	F	78	0.4	314	–	+
AMI	M	48	1.2	476	Plaque erosion in LAD	+
AMI	M	65	3.3	418	–	–
AMI	M	57	1.4	441	–	+
AMI	F	83	2.0	395	–	+
AMI	M	48	1.4	456	Plaque erosion in LAD	+
<b>Control Subjects</b>						
Drowning*	M	61	1.7	433	–	+
Hypothermia*	M	61	3.0	380	–	–
Pancreatic cancer*	F	80	2.8	266	–	–
Drowning*	M	39	1.8	283	–	–
Blood loss*	M	45	1.3	370	–	+
Blood loss	M	73	2.5	378	–	–
Asphyxia	M	41	1.5	446	–	–
Hypothermia	F	88	2.7	403	–	–
SAH	F	69	1.2	285	–	+
SAH	M	64	2.5	387	–	+
Drowning	F	35	1.2	228	–	+

Serums of all 21 patients listed here were used for Western blotting. AMI indicates acute myocardial infarction; F, female; LAD, left anterior descending artery; LCX, left circumflex artery; M, male; MS, mass spectrometry; PMI, postmortem interval; SAH, subarachnoid hemorrhage.

\*Heart tissues of 10 patients were used for MS analysis.

tissue using a novel proteomic approach identified 485 proteins and revealed that the levels of 21 proteins differed between AMI and control tissues (Table 3).

### Known Sarcoplasmic Proteins

Some sarcoplasmic proteins have been reported as deviation components that are released from myocardia when the heart is severely damaged. H-FABP was established as an early biomarker because it leaks from cardiac cells following ischemic injury.<sup>26,27</sup> Compared with troponin T or myoglobin, H-FABP is distinctively useful for diagnosis of ischemic injury within the first 4 hours of symptom appearance.<sup>6,28</sup> In our research, we examined AMI patients whose serum was positive for H-FABP by Rapicheck ELISA. Subsequent proteomic analysis confirmed a lower level of H-FABP in heart tissue of AMI patients than that of control subjects.

Myomesin is a modular protein that cross-links the thick filaments in the M-band of striated muscle.<sup>29</sup> It has been

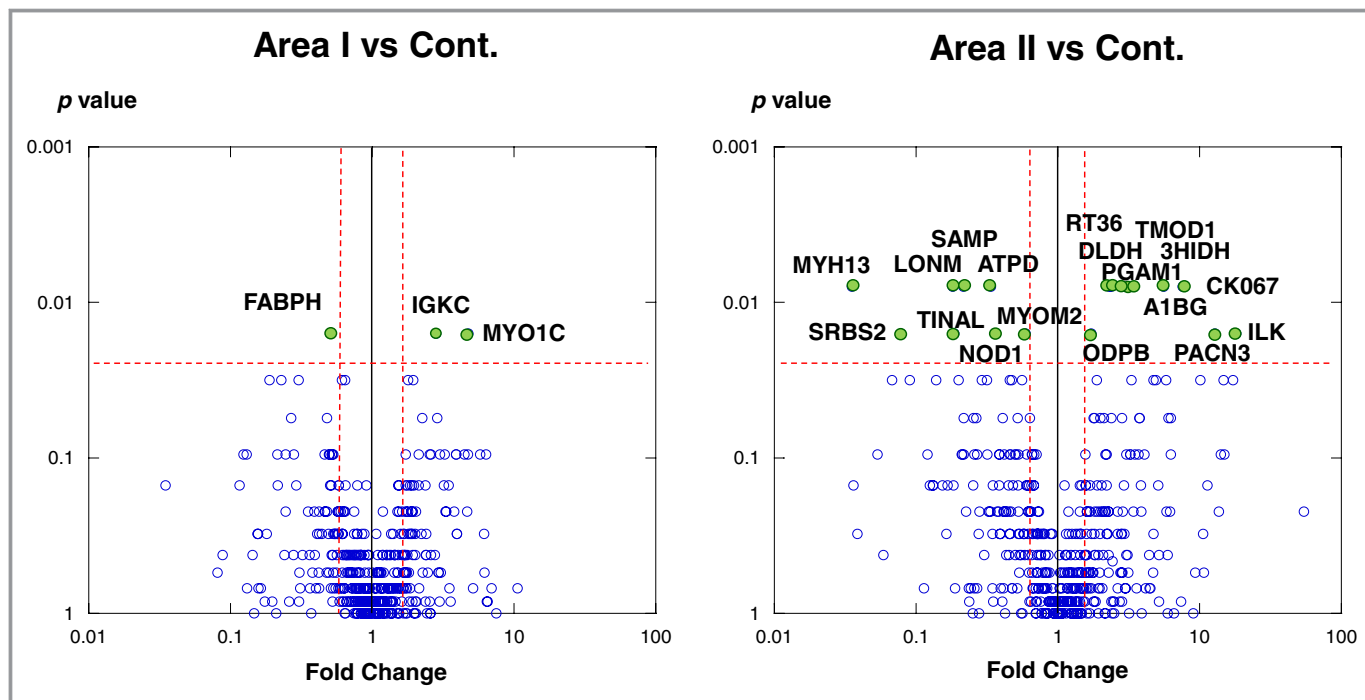
reported that myomesin levels decrease on acute ischemia<sup>30</sup> and in chronic heart failure.<sup>31</sup> The reduction in myomesin expression detected at the proteomic level in this study

**Table 2.** Summary of FFPE Cardiac MS Analysis

Data Level	FDR	ID Yield
Protein	1%	734
	5%	833
	10%	913
Peptide	1%	10 396
	5%	13 006
	10%	14 536
Spectral	1%	243 551
	5%	281 051
	10%	296 651

FDR indicates false discovery rate; FFPE, formalin-fixed, paraffin-embedded; MS, mass spectrometry.





**Figure 3.** Differential levels of protein in acute myocardial infarction (AMI) and control tissues. Protein expression was compared between area I and control (left) and area II and control (right). Each point represents an individual protein. Vertical line represents 1.5-fold change, and horizontal line denotes  $P=0.025$  (Mann–Whitney  $U$  test followed by Bonferroni’s correction). The most prominent proteins ( $P<0.025$  and negative fold-change  $<-1.5$  or  $1.5 <$ positive fold-change) are labeled with their UniProt entry name. 3HIDH indicates 3-hydroxyisobutyrate dehydrogenase; A1BG, alpha-1B-glycoprotein; ATPD ATP synthase subunit delta; DLDH, dihydrolipoyl dehydrogenase; FABPH, fatty acid-binding protein, heart (H-FABP); IGKC, Ig kappa chain C region; ILK, integrin-linked protein kinase; LONM, Lon protease homologue; MYH13, myosin heavy-chain 13; MYO1C, myosin 1; MYOM2, myomesin-2; ODPB, pyruvate dehydrogenase E1 component subunit beta; PACN3, protein kinase C and casein kinase substrate in neurons protein 3; PGAM1, phosphoglycerate mutase 1; SAMP, serum amyloid P-component; SRBS2, sorbin and SH3 domain-containing protein 2 (SORBS2); TINAL, tubulointerstitial nephritis antigen-like; TMOD1, tropomodulin-1.

agrees with previous reports. Levels of some other known biomarkers, such as cardiac myosin-binding protein C<sup>32,33</sup> and cardiac troponin I<sup>34,35</sup> were also shown to decrease in AMI tissue (Table S3), but these proteins were not listed in Table 2 because of the strict limits used regarding detection: ( $\geq 2$  peptides), probability ( $P<0.025$  in the Mann–Whitney  $U$  test followed by Bonferroni’s correction), and  $\pm 1.5$ -fold change.

### Sarcoplasmic SORBS2

SORBS2 is an adapter protein that functions in cytoskeletal organization, cell adhesion, and signaling pathways.<sup>36</sup> Northern blot analyses showed that the highest levels of SORBS2 occur in the heart, where it is expressed at much higher levels than in other tissues, and that very little is detected in skeletal muscle.<sup>37</sup> In cultured cardiomyocytes, SORBS2 is observed in the Z-band and intercalated disk.<sup>38</sup> The Z-band is a septal segment of striated muscle at the end of the sarcomere, and  $\alpha$ -actinin is the major component. The intercalated disk is a specialized type of Z-band found at the junctions of cardio-

myocytes. Although SORBS2 is also observed at focal adhesions in fibroblasts and tight junctions in epithelial cells,<sup>39</sup> immunohistochemical visualization in human heart tissue or proteomic analyses of changes in SORBS2 in AMI patients have not been reported to date.

Using an advanced proteomic method, in this study we first demonstrated high expression of SORBS2 in human heart tissue and a significant decrease in SORBS2 level on lethal cardiac infarction. Immunohistochemical analyses also showed remarkable alterations in SORBS2 localization in AMI cardiac tissue. Alignment of SORBS2 at the Z-lines in the sarcoplasm disappeared upon AMI, and the dense deposits of SORBS2 were stripped from the intercalated disks in area II. Although MS analysis did not indicate a significant reduction in SORBS2 level in area I, immunohistochemical signals decreased in the cytoplasm of contraction bands and wavy fibers. In contrast, Western blot analysis showed a significant increase in SORBS2 level in the serum of AMI patients. These results indicate SORBS2 is released from the heart into the bloodstream upon severe ischemic heart injury.

**Table 3.** Cardiac Proteins Detected Differentially in the Very Early Phase of AMI

UniProt Accession	Protein Name	Cellular Component	Area I vs Control		Area II vs Control	
			Fold-Change	P Value	Fold-Change	P Value
P05413_FABPH	Fatty acid-binding protein, heart (H-FABP)	Cytoplasm	-2.0	0.016	-1.4	0.310
O94875_SRBS2	Sorbin and SH3 domain-containing protein 2 (SORBS2)	Cytoplasm	-1.2	0.690	-12.8	0.016
P54296_MYOM2	Myomesin-2	Cytoplasm	-1.1	0.690	-1.7	0.016
Q9UKX3_MYH13	Myosin heavy-chain 13	Cytoplasm	1.1	0.548	-28.3	0.008
P18669_PGAM1	Phosphoglycerate mutase 1	Cytoplasm	1.6	0.841	2.9	0.008
Q9UKS6_PACN3	Protein kinase C and casein kinase substrate in neurons protein 3	Cytoplasm	2.6	0.095	12.8	0.016
Q13418_ILK	Integrin-linked protein kinase	Cytoplasm	2.1	0.690	18.2	0.016
P11177_ODPB	Pyruvate dehydrogenase E1 component subunit beta	Mitochondrion	1.2	0.690	1.7	0.016
P09622_DLDH	Dihydrolipoyl dehydrogenase	Mitochondrion	1.3	1.000	2.4	0.008
P31937_3HIDH	3-hydroxyisobutyrate dehydrogenase	Mitochondrion	2.0	0.310	3.4	0.008
P82909_RT36	28S ribosomal protein S36, mitochondrial	Mitochondrion	1.7	0.421	2.3	0.008
P30049_ATPD	ATP synthase subunit delta	Mitochondrion	1.1	0.690	-3.0	0.008
P36776_LONM	Lon protease homologue	Mitochondrion	-4.4	0.032	-5.5	0.008
O00159_MYO1C	Nuclear myosin 1 (NM1)	Nucleus	4.8	0.016	2.5	1.000
P28289_TMOD1	Tropomodulin-1	Erythrocyte cytoplasm	1.7	0.548	3.2	0.008
Q9H7C9_CK067	Mth938 domain-containing protein	Adipocyte cytoplasm	4.0	0.310	7.6	0.008
P02743_SAMP	Serum amyloid P-component	Extracellular space	-1.1	0.151	-4.6	0.008
P04217_A1BG	Alpha-1B-glycoprotein	Extracellular space	2.6	0.421	5.6	0.008
P14543_NID1	Nidogen-1	Extracellular space	-1.6	0.222	-2.7	0.016
Q9GZM7_TINAL	Tubulointerstitial nephritis antigen-like	Extracellular space	-2.2	0.222	-5.3	0.016
P01834_IGKC	Ig kappa chain C region	Extracellular space	2.8	0.016	2.2	0.095

Difference >1.5-fold change and  $P < 0.025$  (Mann-Whitney  $U$  test followed by Bonferroni's correction) was considered significant. Fold-change values indicate higher (+) and lower (-) intensity levels in AMI samples compared with controls. AMI indicates acute myocardial infarction.

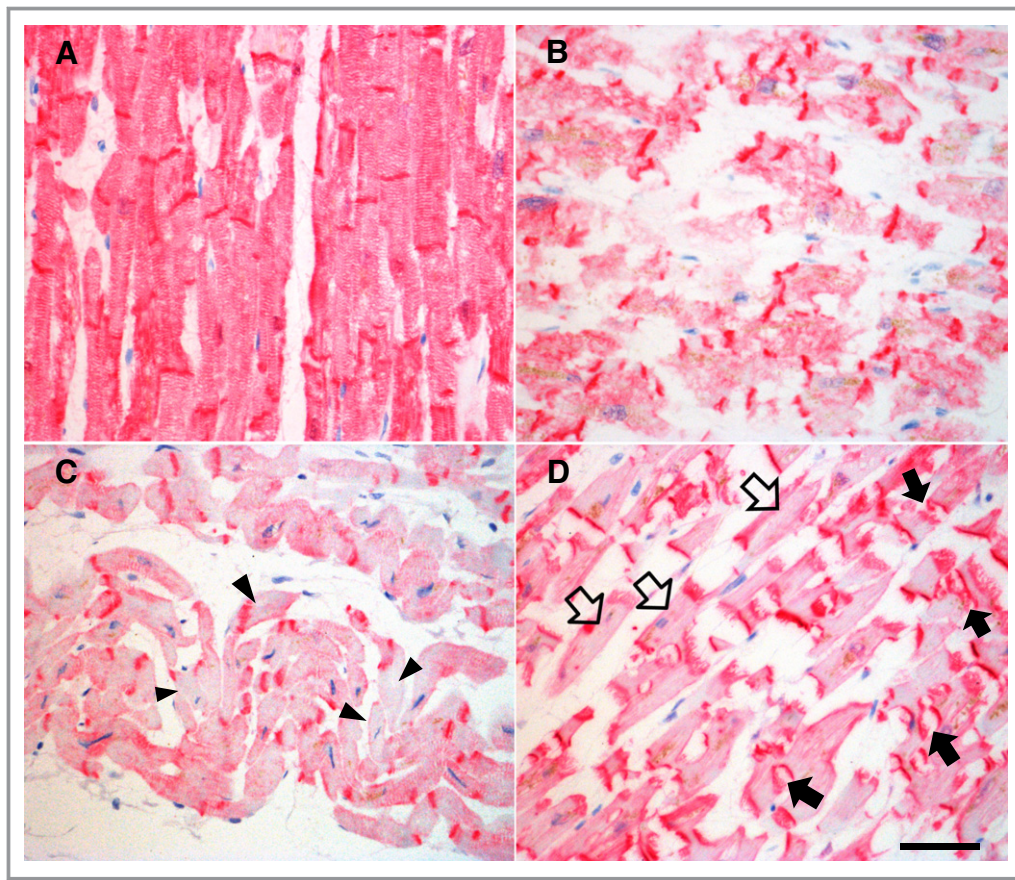
The structural features of the Z-band also suggest SORBS2 rapidly leaks from the myocardia soon after infarction. At the Z-band, the extracellular space invaginates into the sarcolemma and forms a transverse tubular system. SORBS2 is supposed to link the T-tubule membrane to the Z-band and contributes to signal transduction in response to extracellular stimuli.<sup>38</sup> Such linkage to the sarcolemmic membrane may facilitate speedy release of SORBS2 upon severe cardiac ischemia.

SORBS2 also functions as a docking site for other Z-band proteins, such as  $\alpha$ -actinin and Abl family kinases.<sup>40</sup> On a dramatic decrease in the level of SORBS2 in cardiac myocytes, cytoskeletal organization and cell signaling pathways become disconnected, and ultimately the ventricular muscle becomes in danger of losing its contractile function as a syncytial organ. The decrease in SORBS2 level in the myocardium itself possibly causes cardiac contractile deficiency. The typically high level of SORBS2 in the heart under normal conditions and the remarkable decrease on infarction imply that the degree of increase in the serum level of

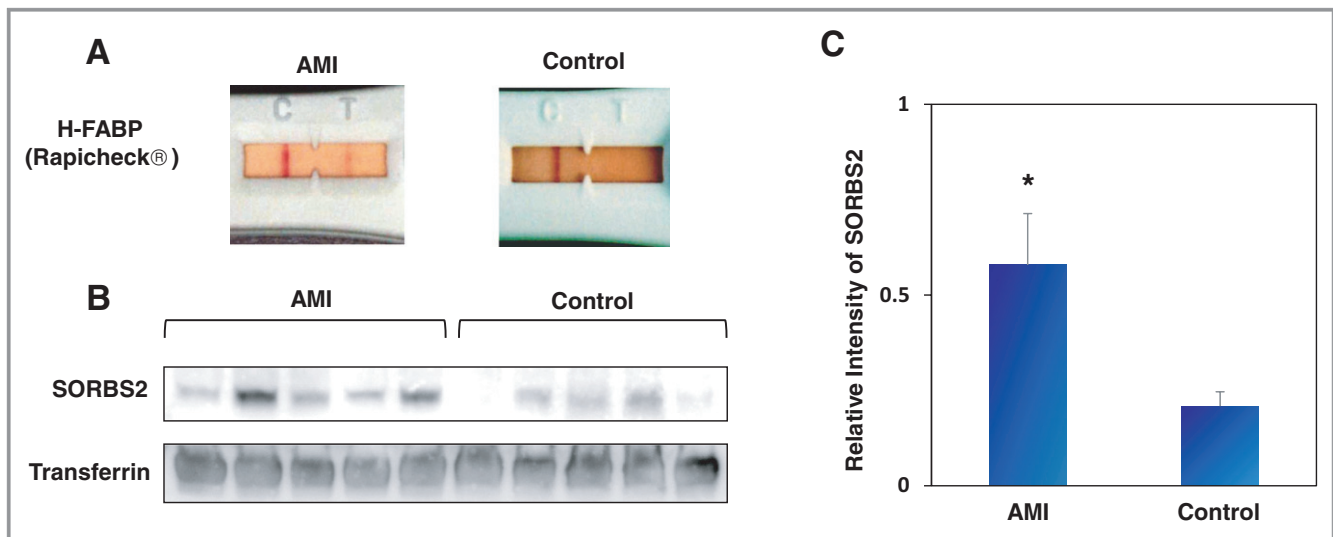
SORBS2 is strongly correlated with the severity of ischemic heart damage.

### Other Proteins

In the present proteomic survey, many metabolic proteins were also detected at different levels in the heart tissue of AMI patients and control subjects. Pyruvate dehydrogenase E1 component subunit beta is an element of the pyruvate dehydrogenase complex, which catalyzes the oxidative decarboxylation of pyruvate to form acetyl CoA.<sup>41</sup> This reaction constitutes the bridge between anaerobic and aerobic energy metabolism. An increase in pyruvate dehydrogenase E1 component subunit beta indicates increased energy demand and acceleration of glycolysis in myocytes. Dihydrolipoyl dehydrogenase is also an essential element of the pyruvate dehydrogenase complex (E3 component) and other mitochondrial multienzyme complexes, such as alpha-ketoglutarate dehydrogenase, branched-chain alpha-ketoacid dehydrogenase, and the glycine cleavage system.<sup>42,43</sup> Dihydrolipoyl



**Figure 4.** Immunostaining of SORBS2 in human heart tissues. A, SORBS2 regularly localizes along the Z-line in the myocardial cytoplasm and is densely expressed in the intercalated disk in control heart tissue. B, In AMI tissue, the alignment of SORBS2 in the Z-bands is disordered at the contraction bands in area I. C, Some wavy fibers show low staining in the Z-lines (arrowheads) in area I. D, Sarcomeric arrays of SORBS2 disappear from cardiac myocytes (open arrows) in area II. Some intercalated disks appear to have burst (arrows). Magnification  $\times 400$ . Scale bar=50  $\mu\text{m}$ . AMI indicates acute myocardial infarction; SORBS2, sorbin and SH3 domain-containing protein 2.



**Figure 5.** Serum analyses. A, Representative serum ELISA against H-FABP. In the commercial ELISA kit, “C” denotes positive control and “T” denotes true positive. AMI cases showed positive results, and control cases showed negative results. B, Representative Western blots against SORBS2 and transferrin. For each lane, 40  $\mu\text{g}$  of serum protein was applied C, Relative intensity level of SORBS2 normalized to that of transferrin. AMI cases (n=10) and controls (n=11) were compared. Each bar represents mean $\pm$ SEM. \* $P < 0.05$  (Mann–Whitney *U* test). AMI indicates acute myocardial infarction; H-FABP, fatty acid-binding protein, heart; SEM, standard error of the mean; SORBS2, sorbin and SH3 domain-containing protein 2.



dehydrogenase generates ATP from major energy substrates. 3-Hydroxyisobutyrate dehydrogenase catalyzes degradation of the glucogenic amino acid valine to produce the metabolic intermediate succinyl-CoA<sup>44,45</sup> and is involved in satisfying increasing energy demand. Overexpression of 28S ribosomal protein S36 (RT36) delays cell-cycle progression, thereby lowering energy consumption.<sup>46</sup> In the early stage of AMI, area II showed a significant decline in 28S ribosomal protein S36 level, which may be a response to severe stress.

## Study Limitations

First, most of the patients involved in this study experienced chemical or electrical cardioversion at the hospital. Such emergency treatments may damage cardiac muscle. We cannot deny the possibility that our observations were not only based on ischemic injury but also treatment-related damage. Second, 2 isoforms of SORBS2 were identified in our research (Table S2). MS analysis indicated a large amount of isoform 3 and a significant decrease in infarcted tissue. Although a small amount of isoform 2 was also detected, this isoform was excluded from the selected protein list because it was found to be a “no experimental confirmation available” isoform at the time of data processing (Figure 2).

## Conclusions

A novel method for extracting proteins from FFPE tissue enabled the proteomic analysis of human cardiac tissue obtained from cases of sudden death due to AMI. Label-free LC-MS accompanied by precise microscopic sampling revealed in vivo proteomic alterations corresponding with histopathological findings. Among the significant proteomic changes observed, the level of SORBS2 was found to be markedly lower in AMI tissue compared with control tissue and was detected at strikingly high levels in the serum of AMI patients. These observations suggest that SORBS2 is released from cardiac myocytes on acute lethal infarction. Although further clinical research using AMI serum is necessary for clarification of the usefulness of SORBS2 in the early diagnosis, this sarcoplasmic protein could be contributing to the assessment of ischemic severity on cardiac tissue.

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## Disclosures

None.

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**Supplemental Table I. Proteins identified with FDR < 1 %**

UniProt Accession	Protein Name	%Cov	%Cov(50)	%Cov(95)	Peptides(95%)
Q8WZ42-8 TITIN_HUMAN	Isoform Cardiac novex-1 of Titin	44.55	28.39	25.59	873
P12883 MYH7_HUMAN	Myosin-7	87.60	82.02	80.67	1782
cont 000141	spt P00761  Trypsin precursor (EC 3.4.21.4) [Sus scrofa (contaminant)]	97.40	97.40	89.18	593
P68133 ACTS_HUMAN	Actin, alpha skeletal muscle	94.96	94.69	91.51	497
Q14315-2 FLNC_HUMAN	Isoform 2 of Filamin-C	57.17	43.46	41.34	127
P35609 ACTN2_HUMAN	Alpha-actinin-2	81.32	76.62	75.84	168
P02768 ALBU_HUMAN	Serum albumin	89.66	87.19	81.77	205
Q14896 MYPC3_HUMAN	Myosin-binding protein C, cardiac-type	67.95	59.31	56.25	157
P09493 TPM1_HUMAN	Tropomyosin alpha-1 chain	97.18	94.37	94.37	222
P17661 DESM_HUMAN	Desmin	89.36	76.60	74.26	96
P54296 MYOM2_HUMAN	Myomesin-2	59.73	43.21	40.20	72
P02452 CO1A1_HUMAN	Collagen alpha-1(I) chain	71.17	51.37	50.89	246
P69905 HBA_HUMAN	Hemoglobin subunit alpha	88.73	88.03	87.32	143
P12111-2 CO6A3_HUMAN	Isoform 2 of Collagen alpha-3(VI) chain	43.89	23.19	20.97	60
P25705 ATPA_HUMAN	ATP synthase subunit alpha, mitochondrial	64.92	57.87	54.97	80
P02461 CO3A1_HUMAN	Collagen alpha-1(III) chain	60.78	44.13	43.11	224
P68871 HBB_HUMAN	Hemoglobin subunit beta	100.00	99.32	96.60	183
P10916 MLRV_HUMAN	Myosin regulatory light chain 2, ventricular/cardiac muscle isoform	94.58	94.58	94.58	126
P08590 MYL3_HUMAN	Myosin light chain 3	92.31	87.69	87.69	176
P06576 ATPB_HUMAN	ATP synthase subunit beta, mitochondrial	71.08	66.54	65.60	111
O75112 LDB3_HUMAN	LIM domain-binding protein 3	64.92	54.75	53.37	66
Q13813-3 SPTA2_HUMAN	Isoform 3 of Spectrin alpha chain, brain	51.71	25.49	23.00	50
P06732 KCRM_HUMAN	Creatine kinase M-type	83.99	72.70	70.87	81
P08123 CO1A2_HUMAN	Collagen alpha-2(I) chain	66.69	41.43	38.73	117
P98160 PGBM_HUMAN	Basement membrane-specific heparan sulfate proteoglycan core protein	32.43	16.92	14.71	53
Q99798 ACON_HUMAN	Aconitate hydratase, mitochondrial	58.08	54.87	47.82	48
P52179-2 MYOM1_HUMAN	Isoform 2 of Myomesin-1	53.12	32.98	29.89	48
Q15149-3 PLEC1_HUMAN	Isoform 3 of Plectin-1	54.60	17.99	12.43	50
P18206-2 VINC_HUMAN	Isoform Vinculin of Vinculin	61.35	36.96	33.40	48
P45379 TNNT2_HUMAN	Troponin T, cardiac muscle	67.45	47.99	47.65	79
P15924 DESP_HUMAN	Desmoplakin	52.49	18.67	15.05	47
P02144 MYG_HUMAN	Myoglobin	87.01	81.17	77.92	86

P04075 ALDOA_HUMAN	Fructose-bisphosphate aldolase A	78.02	73.08	71.15	52
P02787 TRFE_HUMAN	Serotransferrin	61.32	45.27	44.56	38
P04264 K2C1_HUMAN	Keratin, type II cytoskeletal 1	52.95	41.93	41.93	43
P16615-2 AT2A2_HUMAN	Isoform HK2 of Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	51.45	34.50	31.09	40
P14618-2 KPYM_HUMAN	Isoform M1 of Pyruvate kinase isozymes M1/M2	66.48	49.53	45.20	29
P48735 IDHP_HUMAN	Isocitrate dehydrogenase [NADP], mitochondrial	64.16	52.43	49.78	38
P04406 G3P_HUMAN	Glyceraldehyde-3-phosphate dehydrogenase	74.63	65.97	63.28	72
P00505 AATM_HUMAN	Aspartate aminotransferase, mitochondrial	68.14	53.72	53.72	40
P49748-2 ACADV_HUMAN	Isoform 2 of Very long-chain specific acyl-CoA dehydrogenase, mitochondrial	45.81	42.18	41.39	31
P02511 CRYAB_HUMAN	Alpha-crystallin B chain	85.71	85.71	85.14	45
P02545-2 LMNA_HUMAN	Isoform Lamin C of Lamin-A/C	66.08	43.71	39.34	27
O94875-3 SRBS2_HUMAN	Isoform 3 of Sorbin and SH3 domain-containing protein 2	62.48	40.31	40.31	28
P17540 KCRS_HUMAN	Creatine kinase S-type, mitochondrial	63.25	60.86	54.65	53
Q13423 NNTM_HUMAN	NAD(P) transhydrogenase, mitochondrial	39.78	26.98	22.74	34
P11142 HSP7C_HUMAN	Heat shock cognate 71 kDa protein	48.61	34.83	33.59	41
P22695 QCR2_HUMAN	Cytochrome b-c1 complex subunit 2, mitochondrial	58.50	51.66	49.23	33
Q02218 ODO1_HUMAN	2-oxoglutarate dehydrogenase, mitochondrial	42.62	29.03	25.71	30
Q5VTT5 MYOM3_HUMAN	Myomesin-3	41.41	24.01	20.88	23
P19367-4 HXK1_HUMAN	Isoform TD of Hexokinase-1	41.77	25.08	23.54	21
P31930 QCR1_HUMAN	Cytochrome b-c1 complex subunit 1, mitochondrial	53.13	51.04	51.04	30
P55268 LAMB2_HUMAN	Laminin subunit beta-2	38.21	16.63	12.35	21
P13645 K1C10_HUMAN	Keratin, type I cytoskeletal 10	52.40	42.47	41.95	25
P14923 PLAK_HUMAN	Junction plakoglobin	49.80	38.66	35.17	20
P28331 NDUS1_HUMAN	NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	51.44	41.13	34.39	26
P63261 ACTG_HUMAN	Actin, cytoplasmic 2	84.27	79.73	77.60	323
P40926 MDHM_HUMAN	Malate dehydrogenase, mitochondrial	64.79	57.40	53.55	30
P40939 ECHA_HUMAN	Trifunctional enzyme subunit alpha, mitochondrial	47.31	36.70	30.54	31
P35527 K1C9_HUMAN	Keratin, type I cytoskeletal 9	57.30	49.92	41.89	28
P08670 VIME_HUMAN	Vimentin	74.89	58.15	54.29	42
P40925 MDHC_HUMAN	Malate dehydrogenase, cytoplasmic	59.88	50.60	48.20	37
Q01082-3 SPTB2_HUMAN	Isoform 2 of Spectrin beta chain, brain 1	39.58	13.87	10.77	22
P12235 ADT1_HUMAN	ADP/ATP translocase 1	74.50	62.08	62.08	28
P19429 TNNI3_HUMAN	Troponin I, cardiac muscle	67.62	57.14	50.95	58
P08572 CO4A2_HUMAN	Collagen alpha-2(IV) chain	42.82	19.80	16.82	44
P11532-4 DMD_HUMAN	Isoform Dystrophin-3 of Dystrophin	34.65	11.72	8.73	30
P05413 FABPH_HUMAN	Fatty acid-binding protein, heart	94.74	93.98	93.98	46
P11216 PYGB_HUMAN	Glycogen phosphorylase, brain form	53.02	29.54	24.32	18

P00558 PGK1_HUMAN	Phosphoglycerate kinase 1	68.11	51.80	45.56	22
Q99959-2 PKP2_HUMAN	Isoform A of Plakophilin-2	54.60	24.37	23.06	17
P68371 TBB2C_HUMAN	Tubulin beta-2C chain	60.67	54.83	51.01	32
P08238 HS90B_HUMAN	Heat shock protein HSP 90-beta	47.65	27.21	26.93	19
P24752 THIL_HUMAN	Acetyl-CoA acetyltransferase, mitochondrial	56.44	39.34	39.34	23
P01857 IGHG1_HUMAN	Ig gamma-1 chain C region	60.91	59.09	57.88	34
O76041 NEBL_HUMAN	Nebulette	56.90	22.19	19.53	22
P55084 ECHB_HUMAN	Trifunctional enzyme subunit beta, mitochondrial	48.73	35.65	32.70	21
P17174 AATC_HUMAN	Aspartate aminotransferase, cytoplasmic	63.20	54.00	50.61	23
P09622 DLDH_HUMAN	Dihydrolipoyl dehydrogenase, mitochondrial	49.51	31.63	31.63	22
O75390 CISY_HUMAN	Citrate synthase, mitochondrial	43.13	28.54	28.54	18
P07195 LDHB_HUMAN	L-lactate dehydrogenase B chain	50.30	45.51	39.82	35
P06396-2 GELS_HUMAN	Isoform Cytoplasmic of Gelsolin	43.78	28.59	27.36	18
P13929 ENOB_HUMAN	Beta-enolase	61.06	53.00	50.69	21
Q9UKX2 MYH2_HUMAN	Myosin-2	63.11	39.10	31.12	430
P01024 CO3_HUMAN	Complement C3	34.82	16.90	14.43	21
P35555 FBN1_HUMAN	Fibrillin-1	26.12	9.23	7.45	22
P04792 HSPB1_HUMAN	Heat shock protein beta-1	94.63	83.90	80.00	31
P08559 ODPA_HUMAN	Pyruvate dehydrogenase E1 component subunit alpha, somatic form,	52.56	35.64	35.38	19
P11047 LAMC1_HUMAN	Laminin subunit gamma-1	42.64	15.91	12.37	19
P60174 TPIS_HUMAN	Triosephosphate isomerase	81.12	66.67	62.25	25
P08107 HSP71_HUMAN	Heat shock 70 kDa protein 1A/1B	45.09	31.67	31.67	31
P11177 ODPB_HUMAN	Pyruvate dehydrogenase E1 component subunit beta, mitochondrial	58.22	44.29	44.29	26
P11021 GRP78_HUMAN	78 kDa glucose-regulated protein	48.17	27.68	27.68	28
P24043 LAMA2_HUMAN	Laminin subunit alpha-2	29.18	10.06	7.85	21
Q9NPC6 MYOZ2_HUMAN	Myozenin-2	54.92	49.62	46.59	21
Q14112-2 NID2_HUMAN	Isoform 2 of Nidogen-2	24.02	13.42	13.42	17
P08237 K6PF_HUMAN	6-phosphofructokinase, muscle type	30.26	22.69	18.85	16
P55072 TERA_HUMAN	Transitional endoplasmic reticulum ATPase	53.10	26.05	22.83	15
Q96HC4 PDLI5_HUMAN	PDZ and LIM domain protein 5	43.79	30.87	26.17	15
Q71U36 TBA1A_HUMAN	Tubulin alpha-1A chain	44.57	40.80	37.69	15
P31040 DHSA_HUMAN	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial	42.32	24.40	21.99	15
P20674 COX5A_HUMAN	Cytochrome c oxidase subunit 5A, mitochondrial	83.33	59.33	58.67	19
P12110 CO6A2_HUMAN	Collagen alpha-2(VI) chain	43.28	16.00	15.51	15
P12829 MYL4_HUMAN	Myosin light chain 4	83.25	63.96	58.38	52
P12109 CO6A1_HUMAN	Collagen alpha-1(VI) chain	38.81	18.87	16.15	21
P42765 THIM_HUMAN	3-ketoacyl-CoA thiolase, mitochondrial	50.13	41.56	39.29	14

P14543-2 NID1_HUMAN	Isoform 2 of Nidogen-1	31.96	16.70	13.11	13
Q9BX66-11 SRBS1_HUMAN	Isoform 11 of Sorbin and SH3 domain-containing protein 1	36.33	16.03	15.40	16
Q16891-2 IMMT_HUMAN	Isoform 2 of Mitochondrial inner membrane protein	48.06	23.29	18.74	14
P13533 MYH6_HUMAN	Myosin-6	79.47	71.02	64.78	1212
P02675 FIBB_HUMAN	Fibrinogen beta chain	43.79	29.53	27.70	13
P49411 EFTU_HUMAN	Elongation factor Tu, mitochondrial	57.52	31.19	29.20	12
P48047 ATPO_HUMAN	ATP synthase subunit O, mitochondrial	78.87	63.85	44.13	17
P01009 A1AT_HUMAN	Alpha-1-antitrypsin	61.48	36.60	29.67	15
P38646 GRP75_HUMAN	Stress-70 protein, mitochondrial	47.72	23.71	23.71	16
P12277 KCRB_HUMAN	Creatine kinase B-type	63.78	59.06	53.28	41
P09972 ALDOC_HUMAN	Fructose-bisphosphate aldolase C	60.71	48.63	45.88	21
P49821 NDUV1_HUMAN	NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial	41.59	29.53	21.12	11
O15061-2 SYNEM_HUMAN	Isoform Beta of Synemin	46.37	13.25	11.73	14
P08133 ANXA6_HUMAN	Annexin A6	46.51	21.69	19.47	12
P21980 TGM2_HUMAN	Protein-glutamine gamma-glutamyltransferase 2	33.48	21.11	19.94	13
Q86TD4 SRCA_HUMAN	Sarcalumenin	30.47	18.56	14.81	15
P10809 CH60_HUMAN	60 kDa heat shock protein, mitochondrial	48.34	25.13	24.61	10
P06744 G6PI_HUMAN	Glucose-6-phosphate isomerase	43.01	26.70	23.12	11
P35579 MYH9_HUMAN	Myosin-9	38.72	10.66	9.34	20
P05091 ALDH2_HUMAN	Aldehyde dehydrogenase, mitochondrial	45.84	28.05	28.05	13
Q16698 DECR_HUMAN	2,4-dienoyl-CoA reductase, mitochondrial	58.81	34.93	32.54	19
P36871 PGM1_HUMAN	Phosphoglucomutase-1	37.72	25.80	21.53	10
P19022 CADH2_HUMAN	Cadherin-2	29.36	19.43	16.67	13
P63316 TNNC1_HUMAN	Troponin C, slow skeletal and cardiac muscles	64.60	58.39	50.31	24
P01876 IGHA1_HUMAN	Ig alpha-1 chain C region	45.04	38.24	38.24	13
O95831 AIFM1_HUMAN	Apoptosis-inducing factor 1, mitochondrial	54.32	25.45	22.51	10
Q9H987 SYP2L_HUMAN	Synaptopodin 2-like protein	36.13	15.66	15.66	11
P38117-2 ETFB_HUMAN	Isoform 2 of Electron transfer flavoprotein subunit beta	37.86	30.92	27.75	10
P23327 SRCH_HUMAN	Sarcoplasmic reticulum histidine-rich calcium-binding protein	20.89	17.31	17.31	9
P07355-2 ANXA2_HUMAN	Isoform 2 of Annexin A2	41.74	28.85	24.37	9
P33121-2 ACSL1_HUMAN	Isoform 2 of Long-chain-fatty-acid--CoA ligase 1	36.63	23.84	18.75	13
P15259 PGAM2_HUMAN	Phosphoglycerate mutase 2	49.01	35.97	35.97	11
P00367 DHE3_HUMAN	Glutamate dehydrogenase 1, mitochondrial	46.42	27.96	19.53	11
Q96I99 SUCB2_HUMAN	Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial	49.31	26.39	22.92	11
P55290 CAD13_HUMAN	Cadherin-13	31.28	16.41	16.41	15
P11310 ACADM_HUMAN	Medium-chain specific acyl-CoA dehydrogenase, mitochondrial	44.89	24.70	24.70	11
O75746 CMC1_HUMAN	Calcium-binding mitochondrial carrier protein Aralar1	47.49	18.73	17.40	11

P01023 A2MG_HUMAN	Alpha-2-macroglobulin	26.12	9.50	8.96	12
P02679 FIBG_HUMAN	Fibrinogen gamma chain	34.00	24.28	20.31	9
Q562R1 ACTBL_HUMAN	Beta-actin-like protein 2	66.76	52.39	51.60	134
P32119 PRDX2_HUMAN	Peroxiredoxin-2	45.45	38.38	38.38	14
Q16555 DPYL2_HUMAN	Dihydropyrimidinase-related protein 2	45.28	18.01	18.01	8
P00403 COX2_HUMAN	Cytochrome c oxidase subunit 2	37.89	37.89	37.89	10
Q16795 NDUA9_HUMAN	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial	39.52	26.53	23.08	10
P02790 HEMO_HUMAN	Hemopexin	37.23	25.11	23.59	9
P00738 HPT_HUMAN	Haptoglobin	42.12	28.08	26.11	10
Q6NZI2 PTRF_HUMAN	Polymerase I and transcript release factor	40.26	24.36	23.33	11
P07108 ACBP_HUMAN	Acyl-CoA-binding protein	81.61	65.52	65.52	12
Q14894 CRYM_HUMAN	Mu-crystallin homolog	44.90	34.39	34.39	12
P07954 FUMH_HUMAN	Fumarate hydratase, mitochondrial	42.94	28.63	24.12	11
P30041 PRDX6_HUMAN	Peroxiredoxin-6	69.64	54.02	50.89	10
P55809 SCOT1_HUMAN	Succinyl-CoA:3-ketoacid-coenzyme A transferase 1, mitochondrial	42.88	25.96	24.04	12
Q13011 ECH1_HUMAN	Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial	54.27	34.45	32.62	14
P62258 1433E_HUMAN	14-3-3 protein epsilon	54.12	34.12	30.98	10
P13804 ETFA_HUMAN	Electron transfer flavoprotein subunit alpha, mitochondrial	42.94	33.93	31.83	8
P67936 TPM4_HUMAN	Tropomyosin alpha-4 chain	80.65	59.27	51.21	41
P13637 AT1A3_HUMAN	Sodium/potassium-transporting ATPase subunit alpha-3	32.77	13.92	10.37	9
P30086 PEBP1_HUMAN	Phosphatidylethanolamine-binding protein 1	70.05	63.64	59.36	9
P02462 CO4A1_HUMAN	Collagen alpha-1(IV) chain	42.36	9.47	7.49	14
P26038 MOES_HUMAN	Moesin	44.02	15.77	14.38	8
Q05639 EF1A2_HUMAN	Elongation factor 1-alpha 2	32.40	22.03	22.03	11
P63267 ACTH_HUMAN	Actin, gamma-enteric smooth muscle	86.97	86.70	85.90	470
Q9UKX3 MYH13_HUMAN	Myosin-13	61.71	32.20	26.68	286
P36957 ODO2_HUMAN	Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial	34.00	19.87	16.11	9
P10412 H14_HUMAN	Histone H1.4	24.66	24.66	24.66	13
P11217 PYGM_HUMAN	Glycogen phosphorylase, muscle form	38.00	22.57	16.51	14
Q702N8 XIRP1_HUMAN	Xin actin-binding repeat-containing protein 1	30.55	9.60	6.89	11
P62937 PPIA_HUMAN	Peptidyl-prolyl cis-trans isomerase A	63.03	44.24	44.24	9
P07339 CATD_HUMAN	Cathepsin D	35.68	24.27	19.66	8
Q01813 K6PP_HUMAN	6-phosphofructokinase type C	34.69	17.98	13.01	9
P00568 KAD1_HUMAN	Adenylate kinase isoenzyme 1	67.01	45.88	45.88	7
P49753 ACOT2_HUMAN	Acyl-coenzyme A thioesterase 2, mitochondrial	37.06	25.88	19.46	9
P13073 COX41_HUMAN	Cytochrome c oxidase subunit 4 isoform 1, mitochondrial	46.75	31.95	31.95	13



Q06830 PRDX1_HUMAN	Peroxisredoxin-1	51.26	43.22	39.20	10
Q15124 PGM5_HUMAN	Phosphoglucomutase-like protein 5	34.39	13.76	13.76	7
P13647 K2C5_HUMAN	Keratin, type II cytoskeletal 5	39.49	24.41	20.17	12
P47985 UCRI_HUMAN	Cytochrome b-c1 complex subunit Rieske, mitochondrial	37.23	29.93	29.56	8
P36542 ATPG_HUMAN	ATP synthase subunit gamma, mitochondrial	42.95	27.85	21.48	9
Q8NHM4 TRY6_HUMAN	Putative trypsin-6	50.61	50.20	39.68	54
Q16836-2 HCDH_HUMAN	Isoform 2 of Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial	69.74	33.85	27.69	11
P19404 NDUV2_HUMAN	NADH dehydrogenase [ubiquinone] flavoprotein 2, mitochondrial	53.01	37.75	37.75	8
cont 000137	spt P00760  Cationic trypsin precursor (EC 3.4.21.4) (Beta-trypsin) (Fragment) [Bos taurus (contaminant)]	60.08	39.51	39.09	41
Q9H223 EHD4_HUMAN	EH domain-containing protein 4	38.08	15.71	14.05	7
P02533 K1C14_HUMAN	Keratin, type I cytoskeletal 14	44.49	26.06	19.92	9
P07237 PDIA1_HUMAN	Protein disulfide-isomerase	33.66	15.94	13.98	8
Q9Y4G6 TLN2_HUMAN	Talin-2	33.48	5.82	4.13	9
P13535 MYH8_HUMAN	Myosin-8	62.42	39.13	28.45	343
P42126 D3D2_HUMAN	3,2-trans-enoyl-CoA isomerase, mitochondrial	42.38	26.16	21.85	9
P10515 ODP2_HUMAN	Dihydropyridyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial	32.46	12.21	10.97	7
P28289 TMOD1_HUMAN	Tropomodulin-1	52.37	21.45	21.45	6
P31937 3HIDH_HUMAN	3-hydroxyisobutyrate dehydrogenase, mitochondrial	47.92	27.08	23.21	9
Q99497 PARK7_HUMAN	Protein DJ-1	51.32	42.33	34.92	7
P62805 H4_HUMAN	Histone H4	60.19	42.72	42.72	9
Q99878 H2A1J_HUMAN	Histone H2A type 1-J	57.03	35.94	35.94	6
P09382 LEG1_HUMAN	Galectin-1	65.93	57.04	57.04	6
P01834 IGKC_HUMAN	Ig kappa chain C region	80.19	80.19	80.19	27
P27824 CALX_HUMAN	Calnexin	28.55	15.71	14.53	7
O14958 CASQ2_HUMAN	Calsequestrin-2	28.82	13.78	13.78	6
P02671-2 FIBA_HUMAN	Isoform Alpha of Fibrinogen alpha chain	38.51	19.72	17.24	9
P21796 VDAC1_HUMAN	Voltage-dependent anion-selective channel protein 1	43.11	22.61	22.61	8
P35221 CTNA1_HUMAN	Catenin alpha-1	39.96	14.35	9.38	7
P22626 ROA2_HUMAN	Heterogeneous nuclear ribonucleoproteins A2/B1	40.51	19.55	19.55	6
Q6YN16 HSDL2_HUMAN	Hydroxysteroid dehydrogenase-like protein 2	45.22	23.21	22.97	8
Q99623 PHB2_HUMAN	Prohibitin-2	49.83	28.09	28.09	7
P13807 GYS1_HUMAN	Glycogen [starch] synthase, muscle	32.16	10.45	9.09	6
P30044 PRDX5_HUMAN	Peroxisredoxin-5, mitochondrial	77.57	46.73	36.45	6
P35908 K22E_HUMAN	Keratin, type II cytoskeletal 2 epidermal	45.07	25.04	16.28	13
Q16134 ETFD_HUMAN	Electron transfer flavoprotein-ubiquinone oxidoreductase, mitochondrial	28.36	17.99	13.94	8

P04179 SODM_HUMAN	Superoxide dismutase [Mn], mitochondrial	40.99	36.49	34.68	11
O96000 NDUBA_HUMAN	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 10	48.26	41.28	36.63	6
P22061 PIMT_HUMAN	Protein-L-isoaspartate(D-aspartate) O-methyltransferase	47.14	39.65	35.24	7
P00450 CERU_HUMAN	Ceruloplasmin	19.62	9.58	8.26	8
P69892 HBG2_HUMAN	Hemoglobin subunit gamma-2	72.79	72.79	66.67	25
O75306 NDUS2_HUMAN	NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial	46.22	18.57	17.28	9
P14927 QCR7_HUMAN	Cytochrome b-c1 complex subunit 7	64.86	43.24	34.23	7
P27338 AOFB_HUMAN	Amine oxidase [flavin-containing] B	44.23	15.19	13.65	6
Q14BN4-4 SLMAP_HUMAN	Isoform 4 of Sarcolemmal membrane-associated protein	40.04	17.04	10.40	5
Q9P2R7-2 SUCB1_HUMAN	Isoform 2 of Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial	43.08	16.78	11.56	5
P02647 APOA1_HUMAN	Apolipoprotein A-I	47.57	28.84	21.72	7
P35222 CTNB1_HUMAN	Catenin beta-1	28.17	17.93	17.93	12
P00915 CAH1_HUMAN	Carbonic anhydrase 1	43.68	34.10	30.65	5
O75947 ATP5H_HUMAN	ATP synthase subunit d, mitochondrial	89.44	40.37	39.75	8
P55786 PSA_HUMAN	Puromycin-sensitive aminopeptidase	21.22	8.27	6.42	5
Q9UBY9 HSPB7_HUMAN	Heat shock protein beta-7	59.41	53.53	38.82	5
O75489 NDUS3_HUMAN	NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial	48.86	24.24	24.24	6
P00387 NB5R3_HUMAN	NADH-cytochrome b5 reductase 3	33.22	24.25	19.27	5
Q9Y623 MYH4_HUMAN	Myosin-4	62.25	35.17	28.42	386
P01859 IGHG2_HUMAN	Ig gamma-2 chain C region	53.37	45.71	36.50	23
P45880-1 VDAC2_HUMAN	Isoform 1 of Voltage-dependent anion-selective channel protein 2	37.54	18.77	18.77	8
P08758 ANXA5_HUMAN	Annexin A5	25.31	16.88	16.88	5
P07737 PROF1_HUMAN	Profilin-1	57.14	45.71	45.71	6
P82909 RT36_HUMAN	28S ribosomal protein S36, mitochondrial	56.31	51.46	51.46	5
P09211 GSTP1_HUMAN	Glutathione S-transferase P	50.00	32.38	32.38	7
O14639-4 ABLM1_HUMAN	Isoform 4 of Actin-binding LIM protein 1	53.37	12.72	12.72	6
O14558 HSPB6_HUMAN	Heat shock protein beta-6	48.75	38.75	38.12	6
P04040 CATA_HUMAN	Catalase	29.79	16.89	12.52	5
P00338 LDHA_HUMAN	L-lactate dehydrogenase A chain	40.96	25.30	21.69	10
P30049 ATPD_HUMAN	ATP synthase subunit delta, mitochondrial	52.98	31.55	25.00	9
P02743 SAMP_HUMAN	Serum amyloid P-component	34.08	29.60	29.60	6
Q9UHQ9 NB5R1_HUMAN	NADH-cytochrome b5 reductase 1	35.74	17.70	15.08	5
P61978 HNRPK_HUMAN	Heterogeneous nuclear ribonucleoprotein K	40.60	17.28	14.04	6
P30048 PRDX3_HUMAN	Thioredoxin-dependent peroxide reductase, mitochondrial	41.02	27.73	25.00	8
P35232 PHB_HUMAN	Prohibitin	50.74	20.59	20.59	5
P30101 PDIA3_HUMAN	Protein disulfide-isomerase A3	34.46	17.23	10.89	5
P06733 ENOA_HUMAN	Alpha-enolase	52.53	38.25	32.03	12

Q09666 AHNK_HUMAN	Neuroblast differentiation-associated protein AHNAK	44.01	19.93	16.06	22
P10606 COX5B_HUMAN	Cytochrome c oxidase subunit 5B, mitochondrial	61.24	39.53	39.53	12
Q9NZN4 EHD2_HUMAN	EH domain-containing protein 2	32.23	13.26	11.60	6
P04004 VTNC_HUMAN	Vitronectin	29.50	10.04	10.04	5
P24539 AT5F1_HUMAN	ATP synthase subunit b, mitochondrial	42.58	30.08	21.48	5
Q8NI60-3 ADCK3_HUMAN	Isoform 3 of Chaperone activity of bc1 complex-like, mitochondrial	22.35	10.76	10.76	5
Q99877 H2B1N_HUMAN	Histone H2B type 1-N	64.29	47.62	35.71	9
P30042 ES1_HUMAN	ES1 protein homolog, mitochondrial	45.90	26.87	26.87	5
Q00325 MPCP_HUMAN	Phosphate carrier protein, mitochondrial	36.46	14.36	14.36	8
P07900 HS90A_HUMAN	Heat shock protein HSP 90-alpha	37.43	25.14	22.81	16
Q9UIJ7 KAD3_HUMAN	GTP:AMP phosphotransferase mitochondrial	39.21	29.96	21.15	4
Q9Y6M9 NDUB9_HUMAN	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 9	56.42	39.66	34.64	7
Q02252 MMSA_HUMAN	Methylmalonate-semialdehyde dehydrogenase [acylating], mitochondrial	25.98	9.35	9.35	5
Q5VST9-6 OBSCN_HUMAN	Isoform 5 of Obscurin	19.46	1.65	0.93	7
P50395 GDIB_HUMAN	Rab GDP dissociation inhibitor beta	28.54	15.06	13.03	5
P06753 TPM3_HUMAN	Tropomyosin alpha-3 chain	88.73	71.48	62.32	98
A7E2Y1 MYH7B_HUMAN	Myosin-7B	51.78	17.57	13.03	131
Q03252 LMNB2_HUMAN	Lamin-B2	37.33	8.50	7.17	4
P11055 MYH3_HUMAN	Myosin-3	61.55	36.24	26.19	358
P63104 1433Z_HUMAN	14-3-3 protein zeta/delta	40.41	28.57	28.57	8
Q16586 SGCA_HUMAN	Alpha-sarcoglycan	21.45	16.28	13.18	4
P07951 TPM2_HUMAN	Tropomyosin beta chain	89.79	69.37	52.82	88
P02042 HBD_HUMAN	Hemoglobin subunit delta	89.12	88.44	84.35	90
Q8NDY3 ARHL1_HUMAN	[Protein ADP-ribosylarginine] hydrolase-like protein 1	41.81	12.99	12.99	4
Q16775 GLO2_HUMAN	Hydroxyacylglutathione hydrolase, mitochondrial	22.73	11.69	11.69	4
P78417 GSTO1_HUMAN	Glutathione S-transferase omega-1	40.66	19.09	19.09	4
P18859 ATP5J_HUMAN	ATP synthase-coupling factor 6, mitochondrial	69.44	44.44	44.44	6
O75915 PRAF3_HUMAN	PRA1 family protein 3	37.77	20.74	20.74	6
P99999 CYC_HUMAN	Cytochrome c	57.14	38.10	38.10	6
P47755 CAZA2_HUMAN	F-actin-capping protein subunit alpha-2	20.98	20.63	20.63	4
P30043 BLVRB_HUMAN	Flavin reductase	31.55	22.33	22.33	5
P08865 RSSA_HUMAN	40S ribosomal protein SA	26.78	15.59	15.59	4
P61604 CH10_HUMAN	10 kDa heat shock protein, mitochondrial	66.67	42.16	42.16	5
Q02978 M2OM_HUMAN	Mitochondrial 2-oxoglutarate/malate carrier protein	49.68	21.97	12.74	4
P84243 H33_HUMAN	Histone H3.3	63.24	42.65	42.65	9
Q02338 BDH_HUMAN	D-beta-hydroxybutyrate dehydrogenase, mitochondrial	41.11	13.99	11.08	5
Q16082 HSPB2_HUMAN	Heat shock protein beta-2	68.68	46.70	41.21	5

P26373 RL13_HUMAN	60S ribosomal protein L13	45.97	24.17	24.17	5
P07919 QCR6_HUMAN	Cytochrome b-c1 complex subunit 6, mitochondrial	52.75	50.55	50.55	4
P13489 RINI_HUMAN	Ribonuclease inhibitor	34.06	14.75	13.02	5
O43678 NDUA2_HUMAN	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 2	57.58	48.48	48.48	5
Q9Y2Q3 GSTK1_HUMAN	Glutathione S-transferase kappa 1	35.40	24.78	24.78	4
O00151 PDLI1_HUMAN	PDZ and LIM domain protein 1	58.97	17.33	17.33	5
Q9Y4W6 AFG32_HUMAN	AFG3-like protein 2	25.72	10.04	4.77	4
Q9Y490 TLN1_HUMAN	Talin-1	23.02	4.17	3.23	7
P12814 ACTN1_HUMAN	Alpha-actinin-1	55.04	32.40	26.79	40
P30038 AL4A1_HUMAN	Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial	24.51	8.53	8.53	4
P50213 IDH3A_HUMAN	Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial	39.62	16.67	12.30	5
P61981 1433G_HUMAN	14-3-3 protein gamma	36.03	24.29	24.29	7
P00441 SODC_HUMAN	Superoxide dismutase [Cu-Zn]	53.25	53.25	44.81	4
P50461 CSR3_HUMAN	Cysteine and glycine-rich protein 3	68.56	42.27	42.27	8
P30084 ECHM_HUMAN	Enoyl-CoA hydratase, mitochondrial	43.10	21.38	18.28	6
O43181 NDUS4_HUMAN	NADH dehydrogenase [ubiquinone] iron-sulfur protein 4, mitochondrial	36.57	19.43	19.43	4
P50995 ANX11_HUMAN	Annexin A11	33.27	10.10	8.71	4
Q14192 FHL2_HUMAN	Four and a half LIM domains protein 2	36.56	14.34	14.34	5
Q13554 KCC2B_HUMAN	Calcium/calmodulin-dependent protein kinase type II subunit beta	27.56	11.14	10.09	6
P30153 2AAA_HUMAN	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha	26.32	10.36	9.00	4
P10644 KAP0_HUMAN	cAMP-dependent protein kinase type I-alpha regulatory subunit	35.17	14.17	14.17	7
Q9HBL0 TENS1_HUMAN	Tensin-1	20.63	4.50	4.09	6
O95299 NDUAA_HUMAN	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10,	36.90	21.13	12.39	5
P14854 CX6B1_HUMAN	Cytochrome c oxidase subunit 6B1	68.60	59.30	37.21	5
P13639 EF2_HUMAN	Elongation factor 2	31.24	10.26	5.83	4
P16219 ACADS_HUMAN	Short-chain specific acyl-CoA dehydrogenase, mitochondrial	32.28	14.08	8.25	3
Q92523 CPT1B_HUMAN	Carnitine O-palmitoyltransferase 1, muscle isoform	32.51	8.29	5.44	3
P62988 UBIQ_HUMAN	Ubiquitin	64.47	44.74	44.74	4
P51884 LUM_HUMAN	Lumican	28.40	11.83	8.58	3
Q9GZM7 TINAL_HUMAN	Tubulointerstitial nephritis antigen-like	28.91	14.13	8.78	3
P39059 COFA1_HUMAN	Collagen alpha-1(XV) chain	9.01	6.48	5.69	11
P27144 KAD4_HUMAN	Adenylate kinase isoenzyme 4, mitochondrial	38.12	21.52	16.59	3
Q08380 LG3BP_HUMAN	Galectin-3-binding protein	24.79	9.57	6.67	3
Q9NX63 CHCH3_HUMAN	Coiled-coil-helix-coiled-coil-helix domain-containing protein 3, mitochondrial	45.81	15.42	14.98	3
Q07021 C1QBP_HUMAN	Complement component 1 Q subcomponent-binding protein, mitochondrial	17.73	12.06	12.06	5
P0CG05 LAC2_HUMAN	Ig lambda-2 chain C regions	69.81	44.34	44.34	8
P12429 ANXA3_HUMAN	Annexin A3	46.75	13.62	11.46	4

Q13228 SBP1_HUMAN	Selenium-binding protein 1	38.98	21.61	13.35	5
P21912 DHSB_HUMAN	Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial	53.57	18.57	11.43	3
Q15084 PDIA6_HUMAN	Protein disulfide-isomerase A6	28.86	12.73	9.77	3
P49189 AL9A1_HUMAN	4-trimethylaminobutyraldehyde dehydrogenase	30.16	10.12	7.69	3
O60237 MYPT2_HUMAN	Protein phosphatase 1 regulatory subunit 12B	38.09	6.41	4.07	3
Q9P0J0 NDUAD_HUMAN	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 13	60.42	23.61	23.61	5
O95168 NDUB4_HUMAN	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 4	36.43	30.23	30.23	3
P07437 TBB5_HUMAN	Tubulin beta chain	57.88	51.13	45.05	28
P18669 PGAM1_HUMAN	Phosphoglycerate mutase 1	52.36	48.43	48.43	11
P23297 S10A1_HUMAN	Protein S100-A1	48.94	48.94	48.94	6
Q9BZL4 PP12C_HUMAN	Protein phosphatase 1 regulatory subunit 12C	38.62	6.14	6.14	4
P50895 BCAM_HUMAN	Basal cell adhesion molecule	32.32	5.73	5.73	3
P29692-2 EF1D_HUMAN	Isoform 2 of Elongation factor 1-delta	25.66	5.10	5.10	3
Q13642-1 FHL1_HUMAN	Isoform SLIM1 of Four and a half LIM domains protein 1	41.43	13.57	13.57	4
P23528 COF1_HUMAN	Cofilin-1	53.61	25.90	25.90	3
P56134-2 ATPK_HUMAN	Isoform 2 of ATP synthase subunit f, mitochondrial	37.50	37.50	37.50	4
P02766 TTHY_HUMAN	Transthyretin	31.97	31.97	31.97	3
Q92629-3 SGCD_HUMAN	Isoform 3 of Delta-sarcoglycan	48.44	13.67	13.67	3
P35573-3 GDE_HUMAN	Isoform 6 of Glycogen debranching enzyme	22.63	3.83	3.30	4
P15121 ALDR_HUMAN	Aldose reductase	31.01	20.25	11.71	5
P05026 AT1B1_HUMAN	Sodium/potassium-transporting ATPase subunit beta-1	36.30	15.51	10.89	3
O75521 PECI_HUMAN	Peroxisomal 3,2-trans-enoyl-CoA isomerase	16.75	9.90	9.90	3
P23368 MAOM_HUMAN	NAD-dependent malic enzyme, mitochondrial	27.74	5.65	5.65	3
Q9UI47 CTNA3_HUMAN	Catenin alpha-3	29.05	14.53	8.27	5
P62158 CALM_HUMAN	Calmodulin	55.03	35.57	35.57	7
P62269 RS18_HUMAN	40S ribosomal protein S18	34.87	26.32	26.32	4
P47756 CAPZB_HUMAN	F-actin-capping protein subunit beta	37.55	15.16	11.55	3
Q9NUB1-2 ACS2L_HUMAN	Isoform 2 of Acetyl-coenzyme A synthetase 2-like, mitochondrial	21.69	6.55	4.95	3
O75208 COQ9_HUMAN	Ubiquinone biosynthesis protein COQ9, mitochondrial	55.35	25.16	22.33	4
P04843 RPN1_HUMAN	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	28.17	7.91	7.91	4
O75323 NIPS2_HUMAN	Protein NipSnap homolog 2	38.81	20.28	20.28	5
P50502 F10A1_HUMAN	Hsc70-interacting protein	38.75	14.09	9.49	3
P00751 CFAB_HUMAN	Complement factor B	17.67	5.37	3.93	3
P08574 CY1_HUMAN	Cytochrome c1, heme protein, mitochondrial	28.62	15.69	13.54	6
P29218 IMPA1_HUMAN	Inositol monophosphatase 1	23.47	11.19	11.19	3
Q7Z3D6-5 CN159_HUMAN	Isoform 5 of UPF0317 protein C14orf159, mitochondrial	34.04	8.87	8.87	5
P19105 ML12A_HUMAN	Myosin regulatory light chain 12A	67.84	35.09	35.09	6



Q9H7C9 CK067_HUMAN	UPF0366 protein C11orf67	55.74	41.80	41.80	4
P02763 A1AG1_HUMAN	Alpha-1-acid glycoprotein 1	17.41	17.41	17.41	3
P35237 SPB6_HUMAN	Serpin B6	35.90	13.83	10.37	3
P02794 FRIH_HUMAN	Ferritin heavy chain	60.11	30.60	18.58	4
P05165 PCCA_HUMAN	Propionyl-CoA carboxylase alpha chain, mitochondrial	32.01	7.54	5.12	3
Q8WZ42-6 TITIN_HUMAN	Isoform Small cardiac novex-3 of Titin	33.65	18.59	16.90	93
Q96CN7 ISOC1_HUMAN	Isochorismatase domain-containing protein 1	20.13	13.42	13.42	3
P39019 RS19_HUMAN	40S ribosomal protein S19	47.59	27.59	21.38	3
O75367 H2AY_HUMAN	Core histone macro-H2A.1	33.87	11.56	10.75	3
Q8N335 GPD1L_HUMAN	Glycerol-3-phosphate dehydrogenase 1-like protein	37.89	7.69	7.69	3
P07942 LAMB1_HUMAN	Laminin subunit beta-1	21.56	6.77	3.92	6
P51970 NDUA8_HUMAN	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 8	24.42	18.60	18.60	3
P42704 LPPRC_HUMAN	Leucine-rich PPR motif-containing protein, mitochondrial	24.25	5.74	3.01	4
Q71UI9 H2AV_HUMAN	Histone H2A.V	39.06	36.72	36.72	5
P48681 NEST_HUMAN	Nestin	23.32	5.24	3.02	4
P09493-5 TPM1_HUMAN	Isoform 5 of Tropomyosin alpha-1 chain	90.61	73.47	73.47	99
P53597 SUCA_HUMAN	Succinyl-CoA ligase [GDP-forming] subunit alpha, mitochondrial	15.03	11.56	7.23	2
Q9UBQ7 GRHPR_HUMAN	Glyoxylate reductase/hydroxypyruvate reductase	25.30	16.16	10.37	2
O15273 TELT_HUMAN	Telethonin	34.13	22.16	17.37	3
P60981 DEST_HUMAN	Destrin	30.91	19.39	13.94	2
P02760 AMBP_HUMAN	Protein AMBP	23.86	10.80	10.80	4
O00330 ODPX_HUMAN	Pyruvate dehydrogenase protein X component, mitochondrial	32.73	10.58	8.18	3
O75251 NDUS7_HUMAN	NADH dehydrogenase [ubiquinone] iron-sulfur protein 7, mitochondrial	30.52	22.07	15.02	3
O75112-2 LDB3_HUMAN	Isoform 2 of LIM domain-binding protein 3	56.56	50.73	48.62	50
P14625 ENPL_HUMAN	Endoplasmin	24.91	9.47	4.48	3
P56556 NDUA6_HUMAN	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 6	55.84	20.78	15.58	5
P07858 CATB_HUMAN	Cathepsin B	15.34	7.96	5.60	2
Q13418 ILK_HUMAN	Integrin-linked protein kinase	34.07	7.30	4.43	2
Q9UI09 NDUAC_HUMAN	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 12	58.62	33.10	33.10	5
P05023-2 AT1A1_HUMAN	Isoform Short of Sodium/potassium-transporting ATPase subunit alpha-1	26.58	13.80	11.45	6
Q96Q06 PLIN4_HUMAN	Perilipin-4	26.16	3.39	3.02	3
P51149 RAB7A_HUMAN	Ras-related protein Rab-7a	37.68	17.87	11.59	2
Q9NZ45 CISD1_HUMAN	CDGSH iron sulfur domain-containing protein 1	34.26	25.93	25.93	2
Q96HC4-2 PDLI5_HUMAN	Isoform 2 of PDZ and LIM domain protein 5	77.35	64.53	59.83	14
P07951-3 TPM2_HUMAN	Isoform non-muscle of Tropomyosin beta chain	85.08	58.47	38.71	46
Q07020 RL18_HUMAN	60S ribosomal protein L18	34.04	13.83	13.83	2
Q13683-9 ITA7_HUMAN	Isoform Alpha-7X2DB of Integrin alpha-7	22.88	5.69	2.38	2

P13861 KAP2_HUMAN	cAMP-dependent protein kinase type II-alpha regulatory subunit	39.11	6.44	6.44	2
P01871 IGHM_HUMAN	Ig mu chain C region	26.99	6.19	6.19	2
O00217 NDUS8_HUMAN	NADH dehydrogenase [ubiquinone] iron-sulfur protein 8, mitochondrial	33.33	10.95	10.95	2
Q9NY65 TBA8_HUMAN	Tubulin alpha-8 chain	29.62	20.94	20.49	8
Q14203 DCTN1_HUMAN	Dynactin subunit 1	26.53	1.72	1.72	2
Q8NB12 SMYD1_HUMAN	SET and MYND domain-containing protein 1	23.47	5.51	5.51	2
O00483 NDUA4_HUMAN	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 4	56.79	27.16	27.16	2
Q96RQ3 MCCA_HUMAN	Methylcrotonoyl-CoA carboxylase subunit alpha, mitochondrial	13.52	6.07	4.00	2
Q00059 TFAM_HUMAN	Transcription factor A, mitochondrial	52.44	8.54	8.54	2
P18124 RL7_HUMAN	60S ribosomal protein L7	37.90	13.31	8.47	2
O75131 CPNE3_HUMAN	Copine-3	22.72	3.35	3.35	2
P28161 GSTM2_HUMAN	Glutathione S-transferase Mu 2	41.28	11.47	11.47	2
O75347 TBCA_HUMAN	Tubulin-specific chaperone A	67.59	17.59	17.59	2
P04208 LV106_HUMAN	Ig lambda chain V-I region WAH	59.63	40.37	27.52	2
P23083 HV103_HUMAN	Ig heavy chain V-I region V35	52.14	24.79	24.79	3
Q9UBR2 CATZ_HUMAN	Cathepsin Z	18.48	7.26	7.26	2
P84077 ARF1_HUMAN	ADP-ribosylation factor 1	24.31	9.94	9.94	2
P61088 UBE2N_HUMAN	Ubiquitin-conjugating enzyme E2 N	34.21	13.82	13.82	2
P14174 MIF_HUMAN	Macrophage migration inhibitory factor	27.83	18.26	17.39	3
P04632 CPNS1_HUMAN	Calpain small subunit 1	18.66	10.45	10.45	2
O43488 ARK72_HUMAN	Aflatoxin B1 aldehyde reductase member 2	18.11	10.58	6.41	2
Q16718 NDUA5_HUMAN	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5	48.28	21.55	21.55	2
P84157 MXRA7_HUMAN	Matrix-remodeling-associated protein 7	26.47	14.71	14.71	2
P24310 CX7A1_HUMAN	Cytochrome c oxidase subunit 7A1, mitochondrial	46.84	29.11	29.11	3
P01766 HV305_HUMAN	Ig heavy chain V-III region BRO	37.50	25.00	25.00	3
O95182 NDUA7_HUMAN	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 7	41.59	23.89	23.89	3
P35268 RL22_HUMAN	60S ribosomal protein L22	21.88	18.75	18.75	2
P06703 S10A6_HUMAN	Protein S100-A6	43.33	16.67	16.67	2
O75380 NDUS6_HUMAN	NADH dehydrogenase [ubiquinone] iron-sulfur protein 6, mitochondrial	31.45	21.77	21.77	2
P14406 CX7A2_HUMAN	Cytochrome c oxidase subunit 7A2, mitochondrial	27.71	27.71	27.71	2
Q13424 SNTA1_HUMAN	Alpha-1-syntrophin	29.50	7.13	5.54	2
O15230 LAMA5_HUMAN	Laminin subunit alpha-5	16.21	1.60	1.22	4
P10768 ESTD_HUMAN	S-formylglutathione hydrolase	13.12	9.57	9.57	2
O43920 NDUS5_HUMAN	NADH dehydrogenase [ubiquinone] iron-sulfur protein 5	17.92	17.92	17.92	3
P05556-2 ITB1_HUMAN	Isoform Beta-1B of Integrin beta-1	15.97	3.80	3.80	3
P02751-10 FINC_HUMAN	Isoform 10 of Fibronectin	15.53	3.72	2.39	4
P19823 ITIH2_HUMAN	Inter-alpha-trypsin inhibitor heavy chain H2	17.55	4.02	2.85	2

Q9UKS6 PACN3_HUMAN	Protein kinase C and casein kinase substrate in neurons protein 3	36.79	6.13	6.13	2
Q7Z4W1 DCXR_HUMAN	L-xylulose reductase	36.48	7.38	7.38	2
P15090 FABP4_HUMAN	Fatty acid-binding protein, adipocyte	51.52	22.73	15.91	3
P07585 PGS2_HUMAN	Decorin	26.74	6.68	6.68	2
O75438-2 NDUB1_HUMAN	Isoform 2 of NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 1	34.29	18.10	18.10	2
Q9HCC0-2 MCCB_HUMAN	Isoform 2 of Methylcrotonoyl-CoA carboxylase beta chain, mitochondrial	21.71	8.19	6.09	3
P00918 CAH2_HUMAN	Carbonic anhydrase 2	21.15	7.31	7.31	2
P24298 ALAT1_HUMAN	Alanine aminotransferase 1	14.72	4.23	4.23	2
P16671 CD36_HUMAN	Platelet glycoprotein 4	12.29	5.93	5.93	3
O95298 NDUC2_HUMAN	NADH dehydrogenase [ubiquinone] 1 subunit C2	36.97	22.69	22.69	3
P15088 CBPA3_HUMAN	Mast cell carboxypeptidase A	18.71	4.32	4.32	2
P15311 EZRI_HUMAN	Ezrin	39.42	10.41	6.83	4
P01781 HV320_HUMAN	Ig heavy chain V-III region GAL	56.90	31.03	17.24	2
Q08257 QOR_HUMAN	Quinone oxidoreductase	39.51	6.08	6.08	2
P18136 KV313_HUMAN	Ig kappa chain V-III region HIC	37.98	33.33	33.33	3
Q14974 IMB1_HUMAN	Importin subunit beta-1	12.56	2.74	2.74	2
P0C0L5 CO4B_HUMAN	Complement C4-B	23.05	7.63	5.05	6
P23396 RS3_HUMAN	40S ribosomal protein S3	30.04	9.05	9.05	2
Q8IWX7-2 UN45B_HUMAN	Isoform 2 of Protein unc-45 homolog B	33.41	4.59	4.00	4
Q04760 LGUL_HUMAN	Lactoylglutathione lyase	40.76	17.39	13.04	3
P36578 RL4_HUMAN	60S ribosomal protein L4	24.36	7.96	4.68	2
Q07507 DERM_HUMAN	Dermatopontin	19.90	9.45	9.45	2
P68366 TBA4A_HUMAN	Tubulin alpha-4A chain	42.63	36.16	33.48	12
P17931 LEG3_HUMAN	Galectin-3	38.40	21.60	21.60	5
P23246 SFPQ_HUMAN	Splicing factor, proline- and glutamine-rich	41.58	8.06	4.39	2
P35998 PRS7_HUMAN	26S protease regulatory subunit 7	36.95	5.08	5.08	2
Q9UJY1 HSPB8_HUMAN	Heat shock protein beta-8	12.24	9.18	9.18	2
Q9UMS6 SYNP2_HUMAN	Synaptopodin-2	13.27	1.74	1.74	2
O95292 VAPB_HUMAN	Vesicle-associated membrane protein-associated protein B/C	34.98	9.88	9.88	2
P45954 ACDSB_HUMAN	Short/branched chain specific acyl-CoA dehydrogenase, mitochondrial	9.26	4.40	4.40	2
P49419 AL7A1_HUMAN	Alpha-aminoadipic semialdehyde dehydrogenase	25.97	4.27	4.27	2
P60660 MYL6_HUMAN	Myosin light polypeptide 6	47.68	34.44	24.50	34
Q00610-2 CLH1_HUMAN	Isoform 2 of Clathrin heavy chain 1	22.27	3.60	1.40	2
P30046 DOPD_HUMAN	D-dopachrome decarboxylase	50.85	30.51	21.19	2
Q99714 HCD2_HUMAN	3-hydroxyacyl-CoA dehydrogenase type-2	39.85	7.66	7.66	2
P31150 GDIA_HUMAN	Rab GDP dissociation inhibitor alpha	26.85	9.62	7.61	3
P37802 TAGL2_HUMAN	Transgelin-2	28.14	11.56	11.56	2

P04899 GNAI2_HUMAN	Guanine nucleotide-binding protein G(i) subunit alpha-2	28.17	6.20	6.20	2
P09669 COX6C_HUMAN	Cytochrome c oxidase subunit 6C	38.67	36.00	36.00	3
P43155-3 CACP_HUMAN	Isoform 3 of Carnitine O-acetyltransferase	25.74	10.48	5.51	2
P04217 A1BG_HUMAN	Alpha-1B-glycoprotein	21.01	8.08	6.46	2
O75964 ATP5L_HUMAN	ATP synthase subunit g, mitochondrial	37.86	37.86	27.18	2
P46976 GLYG_HUMAN	Glycogenin-1	9.71	9.71	6.86	2
P23526 SAHH_HUMAN	Adenosylhomocysteinase	21.06	9.26	6.71	2
P35613 BASI_HUMAN	Basigin	17.66	9.61	7.01	3
P01011 AACT_HUMAN	Alpha-1-antichymotrypsin	10.87	6.38	6.38	3
P07099 HYEP_HUMAN	Epoxide hydrolase 1	21.76	7.03	7.03	2
P52565 GDIR1_HUMAN	Rho GDP-dissociation inhibitor 1	27.45	12.25	12.25	2
P43034 LIS1_HUMAN	Platelet-activating factor acetylhydrolase IB subunit alpha	37.32	4.63	4.63	2
Q92736 RYSR2_HUMAN	Ryanodine receptor 2	18.53	2.56	1.63	7
P05166 PCCB_HUMAN	Propionyl-CoA carboxylase beta chain, mitochondrial	34.32	7.42	5.57	2
P62857 RS28_HUMAN	40S ribosomal protein S28	40.58	30.43	30.43	2
P05155 IC1_HUMAN	Plasma protease C1 inhibitor	15.40	8.20	6.20	2
Q15848 ADIPO_HUMAN	Adiponectin	24.59	12.30	12.30	2
Q04446 GLGB_HUMAN	1,4-alpha-glucan-branching enzyme	22.51	5.84	3.70	2
Q9BYX7 ACTBM_HUMAN	Putative beta-actin-like protein 3	74.67	44.00	33.07	85
P62424 RL7A_HUMAN	60S ribosomal protein L7a	36.84	19.17	14.29	3
P22352 GPX3_HUMAN	Glutathione peroxidase 3	24.78	22.57	5.31	1
Q9BQ69 MACD1_HUMAN	MACRO domain-containing protein 1	30.15	10.15	6.46	2
P11182 ODB2_HUMAN	Lipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex, mitochondrial	18.67	4.77	4.77	2
P62277 RS13_HUMAN	40S ribosomal protein S13	21.19	11.26	11.26	2
O60313 OPA1_HUMAN	Dynamin-like 120 kDa protein, mitochondrial	23.23	2.19	2.19	2
Q99832 TCPH_HUMAN	T-complex protein 1 subunit eta	27.44	6.63	1.29	1
P12694 ODBA_HUMAN	2-oxoisovalerate dehydrogenase subunit alpha, mitochondrial	39.55	4.49	4.49	2
P13798 ACPH_HUMAN	Acylamino-acid-releasing enzyme	20.90	3.42	3.42	2
P36776 LONM_HUMAN	Lon protease homolog, mitochondrial	18.25	3.44	2.19	2
O60220 TIM8A_HUMAN	Mitochondrial import inner membrane translocase subunit Tim8 A	53.61	22.68	22.68	2
Q9BR39 JPH2_HUMAN	Junctophilin-2	21.55	5.46	2.87	1
P21397 AOFA_HUMAN	Amine oxidase [flavin-containing] A	21.06	7.78	4.17	2
P0CAP1-11 GCOM1_HUMAN	Isoform Gcom1 of GRINL1A complex locus protein 1	32.55	5.82	2.36	1
P20618 PSB1_HUMAN	Proteasome subunit beta type-1	24.07	9.54	5.81	1
Q13326 SGCG_HUMAN	Gamma-sarcoglycan	22.34	9.28	6.53	1
Q99426 TBCB_HUMAN	Tubulin-folding cofactor B	18.44	8.20	3.69	1

Q14624-2 ITIH4_HUMAN	Isoform 2 of Inter-alpha-trypsin inhibitor heavy chain H4	16.85	3.28	1.31	1
P10599 THIO_HUMAN	Thioredoxin	39.05	20.95	12.38	1
P02774 VTDB_HUMAN	Vitamin D-binding protein	18.35	5.27	2.11	1
P01008 ANT3_HUMAN	Antithrombin-III	18.75	7.76	2.59	1
P55795 HNRH2_HUMAN	Heterogeneous nuclear ribonucleoprotein H2	28.95	7.35	3.79	1
Q9Y6K1 DNM3A_HUMAN	DNA (cytosine-5)-methyltransferase 3A	34.21	3.51	1.43	1
O00159-3 MYO1C_HUMAN	Isoform NM1 of Myosin-Ic	31.03	3.16	2.20	2
P00747 PLMN_HUMAN	Plasminogen	24.69	2.22	1.36	1
P26678 PPLA_HUMAN	Cardiac phospholamban	40.38	38.46	38.46	3
O43676 NDUB3_HUMAN	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 3	18.37	18.37	11.22	1
O95169 NDUB8_HUMAN	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 8, mitochondrial	50.54	11.29	6.45	1
Q13404-2 UB2V1_HUMAN	Isoform UEV-1A of Ubiquitin-conjugating enzyme E2 variant 1	45.88	17.06	5.88	1
P42356-2 PI4KA_HUMAN	Isoform PI4K97 of Phosphatidylinositol 4-kinase alpha	19.44	2.58	1.29	1
P27797 CALR_HUMAN	Calreticulin	22.78	6.48	3.12	1
P68104 EF1A1_HUMAN	Elongation factor 1-alpha 1	30.09	19.48	16.67	6
Q16762 THTR_HUMAN	Thiosulfate sulfurtransferase	37.37	20.54	10.44	2
P51649 SSDH_HUMAN	Succinate-semialdehyde dehydrogenase, mitochondrial	21.87	5.42	1.87	1
Q15327 ANKR1_HUMAN	Ankyrin repeat domain-containing protein 1	22.88	6.90	6.90	2
P52272-2 HNRPM_HUMAN	Isoform M1-M2 of Heterogeneous nuclear ribonucleoprotein M	42.55	6.22	4.49	2
P14314 GLU2B_HUMAN	Glucosidase 2 subunit beta	16.10	3.98	3.98	2
Q9BV79 MECR_HUMAN	Trans-2-enoyl-CoA reductase, mitochondrial	17.43	6.70	6.70	2
Q16851 UGPA_HUMAN	UTP--glucose-1-phosphate uridylyltransferase	32.09	2.36	2.36	1
P20339 RAB5A_HUMAN	Ras-related protein Rab-5A	28.37	15.35	5.58	1
Q13561 DCTN2_HUMAN	Dynactin subunit 2	21.20	4.49	4.49	2
P62753 RS6_HUMAN	40S ribosomal protein S6	29.32	8.03	4.82	1
Q92841-4 DDX17_HUMAN	Isoform 4 of Probable ATP-dependent RNA helicase DDX17	32.10	1.65	1.65	1
P62263 RS14_HUMAN	40S ribosomal protein S14	36.42	8.61	8.61	1
O75083-3 WDR1_HUMAN	Isoform 2 of WD repeat-containing protein 1	6.65	2.15	2.15	1
P35580 MYH10_HUMAN	Myosin-10	31.02	4.61	3.54	10
P07996 TSP1_HUMAN	Thrombospondin-1	14.70	1.03	1.03	1
O00410 IPO5_HUMAN	Importin-5	13.04	1.64	0.64	1
P15880 RS2_HUMAN	40S ribosomal protein S2	40.27	3.75	3.75	1
Q9UN36-3 NDRG2_HUMAN	Isoform 3 of Protein NDRG2	29.17	5.83	5.83	2
P26440 IVD_HUMAN	Isovaleryl-CoA dehydrogenase, mitochondrial	17.73	2.36	2.36	1
O00748 EST2_HUMAN	Carboxylesterase 2	16.99	1.79	1.79	1
P63220 RS21_HUMAN	40S ribosomal protein S21	63.86	12.05	12.05	1
Q03135 CAV1_HUMAN	Caveolin-1	23.03	7.86	7.86	1



O14949 QCR8_HUMAN	Cytochrome b-c1 complex subunit 8	30.49	15.85	15.85	1
P46776 RL27A_HUMAN	60S ribosomal protein L27a	20.27	7.43	7.43	1
cont 000143	pdb 1FNI_A  A Chain A, Crystal Structure Of Porcine Beta Trypsin With 0.01% Polydocanol [Sus scrofa (contaminant)]	100.00	100.00	92.38	596
P68032 ACTC_HUMAN	Actin, alpha cardiac muscle 1	95.23	94.96	91.51	517
P12882 MYH1_HUMAN	Myosin-1	65.50	37.80	30.27	444
P09493-6 TPM1_HUMAN	Isoform TPM1kappa of Tropomyosin alpha-1 chain	96.48	83.45	83.45	136
P14618 KPYM_HUMAN	Pyruvate kinase isozymes M1/M2	72.69	52.35	48.02	29
P01861 IGHG4_HUMAN	Ig gamma-4 chain C region	51.07	36.39	35.17	22
P69891 HGB1_HUMAN	Hemoglobin subunit gamma-1	73.47	72.79	66.67	25
P01877 IGHA2_HUMAN	Ig alpha-2 chain C region	36.47	29.41	29.41	9
P09104 ENOG_HUMAN	Gamma-enolase	43.78	22.12	19.82	7
A6NL28 TPM3L_HUMAN	Putative tropomyosin alpha-3 chain-like protein	65.02	20.18	15.70	21
P31946 1433B_HUMAN	14-3-3 protein beta/alpha	40.65	16.67	16.67	5
P0CG06 LAC3_HUMAN	Ig lambda-3 chain C regions	66.98	44.34	44.34	9
P27348 1433T_HUMAN	14-3-3 protein theta	42.45	13.06	13.06	4
P01743 HV102_HUMAN	Ig heavy chain V-I region HG3	40.17	19.66	19.66	2
P05198 IF2A_HUMAN	Eukaryotic translation initiation factor 2 subunit 1	22.22	3.81	3.81	1
RRRRRP15924 DESP_HUMAN	REVERSED Desmoplakin	36.05	1.67	0.73	2
Q3V6T2 GRDN_HUMAN	Girdin	25.82	0.53	0.37	1
A2RUR9-3 C144A_HUMAN	Isoform 3 of Coiled-coil domain-containing protein 144A	32.15	2.25	0.61	1
Q86TC9 MYPN_HUMAN	Myopalladin	18.86	2.04	2.04	2
Q9NVE7 PANK4_HUMAN	Pantothenate kinase 4	26.39	1.81	1.81	1
Q8WXF1 PSPC1_HUMAN	Paraspeckle component 1	30.40	4.97	2.10	1
Q13200 PSMD2_HUMAN	26S proteasome non-ATPase regulatory subunit 2	19.49	2.20	1.65	1
O76031 CLPX_HUMAN	ATP-dependent Clp protease ATP-binding subunit clpX-like, mitochondrial	21.01	1.58	1.58	1
Q14254 FLOT2_HUMAN	Flotillin-2	30.61	2.57	2.57	1
Q9NR28 DBLOH_HUMAN	Diablo homolog, mitochondrial	30.54	4.18	4.18	2
Q9NQC3 RTN4_HUMAN	Reticulon-4	12.08	1.09	1.09	1
P49590 SYHM_HUMAN	Probable histidyl-tRNA synthetase, mitochondrial	23.32	1.98	1.98	1
P31939 PUR9_HUMAN	Bifunctional purine biosynthesis protein PURH	18.24	2.53	2.53	1
Q9Y6C2 EMIL1_HUMAN	EMILIN-1	11.42	1.28	1.28	1
Q9UL25 RAB21_HUMAN	Ras-related protein Rab-21	37.33	4.44	4.44	1
Q9H2U2 IPYR2_HUMAN	Inorganic pyrophosphatase 2, mitochondrial	32.04	6.89	3.59	1
P51687 SUOX_HUMAN	Sulfite oxidase, mitochondrial	17.98	1.83	1.83	1
P28838 AMPL_HUMAN	Cytosol aminopeptidase	18.11	2.31	2.31	1
P25686 DNJB2_HUMAN	DnaJ homolog subfamily B member 2	28.09	3.09	3.09	1

Q8NBN7 RDH13_HUMAN	Retinol dehydrogenase 13	16.01	3.93	3.93	1
Q86WU2 LDHD_HUMAN	Probable D-lactate dehydrogenase, mitochondrial	21.30	5.92	2.96	1
Q14103-4 HNRPD_HUMAN	Isoform p37 of Heterogeneous nuclear ribonucleoprotein D0	37.63	4.88	4.88	1
P61247 RS3A_HUMAN	40S ribosomal protein S3a	31.06	3.03	3.03	1
P13716 HEM2_HUMAN	Delta-aminolevulinic acid dehydratase	23.03	5.76	5.76	1
P02748 CO9_HUMAN	Complement component C9	15.03	2.15	2.15	1
P52943 CRIP2_HUMAN	Cysteine-rich protein 2	35.58	6.73	6.73	1
P23381 SYWC_HUMAN	Tryptophanyl-tRNA synthetase, cytoplasmic	18.26	3.40	3.40	1
P19827 ITIH1_HUMAN	Inter-alpha-trypsin inhibitor heavy chain H1	8.12	1.32	1.32	1
P60866 RS20_HUMAN	40S ribosomal protein S20	47.06	9.24	9.24	1
P49257 LMAN1_HUMAN	Protein ERGIC-53	10.39	3.92	2.16	1
P29966 MARCS_HUMAN	Myristoylated alanine-rich C-kinase substrate	24.40	8.43	5.72	1
O76062 ERG24_HUMAN	Delta(14)-sterol reductase	15.79	3.11	3.11	1
O14773 TPP1_HUMAN	Tripeptidyl-peptidase 1	10.30	3.91	2.49	1
Q9Y3D6 FIS1_HUMAN	Mitochondrial fission 1 protein	44.74	8.55	8.55	1
Q9HCP6 HHATL_HUMAN	Protein-cysteine N-palmitoyltransferase HHAT-like protein	12.70	2.38	2.38	1
Q13510 ASAH1_HUMAN	Acid ceramidase	12.91	2.79	2.79	1
P62140 PP1B_HUMAN	Serine/threonine-protein phosphatase PP1-beta catalytic subunit	17.13	3.06	3.06	1
P53041 PPP5_HUMAN	Serine/threonine-protein phosphatase 5	12.42	2.60	2.60	1
P25789 PSA4_HUMAN	Proteasome subunit alpha type-4	20.31	3.45	3.45	1
P25311 ZA2G_HUMAN	Zinc-alpha-2-glycoprotein	22.82	3.36	3.36	1
P05387 RLA2_HUMAN	60S acidic ribosomal protein P2	63.48	10.43	10.43	1
A6NDG6 PGP_HUMAN	Phosphoglycolate phosphatase	21.50	4.05	4.05	1
Q92506 DHB8_HUMAN	Estradiol 17-beta-dehydrogenase 8	21.07	4.60	4.60	1
Q13765 NACA_HUMAN	Nascent polypeptide-associated complex subunit alpha	17.67	6.05	6.05	1
P83731 RL24_HUMAN	60S ribosomal protein L24	29.30	8.28	8.28	2
P21266 GSTM3_HUMAN	Glutathione S-transferase Mu 3	24.89	5.33	5.33	2
Q9BWH2 FUND2_HUMAN	FUN14 domain-containing protein 2	18.52	6.35	6.35	1
Q53GG5-2 PDLI3_HUMAN	Isoform ALP-H of PDZ and LIM domain protein 3	18.99	4.75	4.75	1
P62829 RL23_HUMAN	60S ribosomal protein L23	27.14	10.71	10.71	1
P47914 RL29_HUMAN	60S ribosomal protein L29	27.67	9.43	9.43	1
P28072 PSB6_HUMAN	Proteasome subunit beta type-6	28.87	4.60	4.60	1
P24666 PPAC_HUMAN	Low molecular weight phosphotyrosine protein phosphatase	28.48	5.70	5.70	1
P10301 RRAS_HUMAN	Ras-related protein R-Ras	29.36	7.34	7.34	1
P08294 SODE_HUMAN	Extracellular superoxide dismutase [Cu-Zn]	27.08	5.42	5.42	1
P02792 FRIL_HUMAN	Ferritin light chain	21.71	8.57	8.57	2
P01772 HV311_HUMAN	Ig heavy chain V-III region KOL	22.22	12.70	12.70	1

P01591 IGJ_HUMAN	Immunoglobulin J chain	22.01	7.55	7.55	1
O95563 BR44_HUMAN	Brain protein 44	33.86	6.30	6.30	1
O75431 MTX2_HUMAN	Metaxin-2	11.41	3.42	3.42	1
Q9Y6B6 SAR1B_HUMAN	GTP-binding protein SAR1b	12.12	5.56	5.56	1
Q9UM22 EPDR1_HUMAN	Mammalian ependymin-related protein 1	10.71	4.91	4.91	1
Q9NPJ3 ACO13_HUMAN	Acyl-coenzyme A thioesterase 13	27.14	8.57	8.57	1
Q9BVC6 TM109_HUMAN	Transmembrane protein 109	12.35	4.94	4.94	1
Q9BUR5 APOO_HUMAN	Apolipoprotein O	16.16	5.56	5.56	1
Q99584 S10AD_HUMAN	Protein S100-A13	27.55	11.22	11.22	1
Q6UXV4 APOOL_HUMAN	Apolipoprotein O-like	10.82	4.48	4.48	1
P56385 ATP5I_HUMAN	ATP synthase subunit e, mitochondrial	37.68	14.49	14.49	1
P00846 ATP6_HUMAN	ATP synthase subunit a	11.06	4.43	4.43	2
P81605 DCD_HUMAN	Dermcidin	20.00	10.00	10.00	1
P62861 RS30_HUMAN	40S ribosomal protein S30	35.59	16.95	16.95	1
P01703 LV105_HUMAN	Ig lambda chain V-I region NEWM	27.18	16.50	16.50	1
O00168 PLM_HUMAN	Phospholemman	25.00	13.04	13.04	1
P35754 GLRX1_HUMAN	Glutaredoxin-1	10.38	10.38	10.38	1
Q8WUD1 RAB2B_HUMAN	Ras-related protein Rab-2B	46.30	6.02	6.02	1
Q9HAT2 SIAE_HUMAN	Sialate O-acetyltransferase	21.41	2.29	2.29	1
P07305 H10_HUMAN	Histone H1.0	35.57	6.70	6.70	1
O95674 CDS2_HUMAN	Phosphatidate cytidyltransferase 2	15.51	4.27	4.27	1
O43852 CALU_HUMAN	Calumenin	23.81	6.35	3.49	1
Q9Y277 VDAC3_HUMAN	Voltage-dependent anion-selective channel protein 3	27.56	8.13	8.13	2
P51659 DHB4_HUMAN	Peroxisomal multifunctional enzyme type 2	21.47	1.63	1.63	1
Q9ULA0 DNPEP_HUMAN	Aspartyl aminopeptidase	20.63	2.53	2.53	1
Q9NXA8 SIRT5_HUMAN	NAD-dependent deacetylase sirtuin-5	23.55	5.16	5.16	1
Q9Y696 CLIC4_HUMAN	Chloride intracellular channel protein 4	20.55	4.35	4.35	1
Q8N4Q1 MIA40_HUMAN	Mitochondrial intermembrane space import and assembly protein 40	24.65	12.68	12.68	1
P51452 DUS3_HUMAN	Dual specificity protein phosphatase 3	12.43	6.49	6.49	1
P22392 NDKB_HUMAN	Nucleoside diphosphate kinase B	46.05	19.74	6.58	1
Q9Y4J8-4 DTNA_HUMAN	Isoform Dystrobrevin-beta of Dystrobrevin alpha	29.28	7.76	2.65	1
Q9Y2P4 S27A6_HUMAN	Long-chain fatty acid transport protein 6	20.52	2.75	1.78	1
P19338 NUCL_HUMAN	Nucleolin	28.17	1.69	1.69	1
P00734 THRB_HUMAN	Prothrombin	27.33	1.93	1.93	1
P01019 ANGT_HUMAN	Angiotensinogen	17.32	2.68	2.68	1
Q15119 PDK2_HUMAN	[Pyruvate dehydrogenase [lipoamide]] kinase isozyme 2, mitochondrial	16.46	3.19	3.19	1
Q16363 LAMA4_HUMAN	Laminin subunit alpha-4	19.97	1.65	1.65	3

RRRRRQ5VV42-2 CDKAL_HUMAN	REVERSED Isoform 2 of CDK5 regulatory subunit-associated protein 1-like 1	16.39	3.28	3.28	1
P63173 RL38_HUMAN	60S ribosomal protein L38	17.14	17.14	17.14	1
O00429-4 DNM1L_HUMAN	Isoform DLP1b of Dynamin-1-like protein	28.76	6.30	2.72	2
Q9BZQ8 NIBAN_HUMAN	Protein Niban	11.31	2.37	1.51	1
Q32MK0 MYLK3_HUMAN	Putative myosin light chain kinase 3	26.62	1.34	1.34	1
O94875-2 SRBS2_HUMAN	Isoform ArgBP2a of Sorbin and SH3 domain-containing protein 2	59.31	38.14	38.14	26
P19652 A1AG2_HUMAN	Alpha-1-acid glycoprotein 2	14.93	8.96	8.96	2
Q14847 LASP1_HUMAN	LIM and SH3 domain protein 1	34.87	8.81	4.98	1
Q9UHV9 PFD2_HUMAN	Prefoldin subunit 2	37.66	9.09	9.09	1
Q99578 RIT2_HUMAN	GTP-binding protein Rit2	24.88	5.07	5.07	1
P31948 STIP1_HUMAN	Stress-induced-phosphoprotein 1	38.67	4.60	2.95	2
Q16629 SFRS7_HUMAN	Splicing factor, arginine/serine-rich 7	61.34	9.66	9.66	2
P10909-2 CLUS_HUMAN	Isoform 2 of Clusterin	31.74	3.79	3.79	2
P55822 SH3BG_HUMAN	SH3 domain-binding glutamic acid-rich protein	22.59	8.79	4.60	1
Q96KP4 CNDP2_HUMAN	Cytosolic non-specific dipeptidase	22.95	6.53	4.21	2
Q9UGV6 HMGLX_HUMAN	Putative high mobility group protein 1-like 10	40.28	6.16	6.16	1
P62851 RS25_HUMAN	40S ribosomal protein S25	39.20	8.00	8.00	1
Q9HBL7 CI046_HUMAN	Transmembrane protein C9orf46	29.25	14.29	7.48	1
P61457 PHS_HUMAN	Pterin-4-alpha-carbinolamine dehydratase	31.73	17.31	9.62	1
Q9BRL6 SFR2B_HUMAN	Splicing factor, arginine/serine-rich 2B	41.13	2.84	2.84	1
P41222 PTGDS_HUMAN	Prostaglandin-H2 D-isomerase	19.47	8.42	8.42	1
Q9Y6C9 MTCH2_HUMAN	Mitochondrial carrier homolog 2	10.89	2.97	2.97	1
P11586 C1TC_HUMAN	C-1-tetrahydrofolate synthase, cytoplasmic	19.57	2.35	2.35	2
O95817 BAG3_HUMAN	BAG family molecular chaperone regulator 3	28.70	2.26	2.26	1
P50991 TCPD_HUMAN	T-complex protein 1 subunit delta	22.08	3.90	2.41	1
P26641 EF1G_HUMAN	Elongation factor 1-gamma	33.87	5.95	5.95	2
Q9UL01 DSE_HUMAN	Dermatan-sulfate epimerase	14.20	0.94	0.94	1
Q8N142-2 PURA1_HUMAN	Isoform 2 of Adenylosuccinate synthetase isozyme 1	18.60	2.40	2.40	1
O43837 IDH3B_HUMAN	Isocitrate dehydrogenase [NAD] subunit beta, mitochondrial	39.74	9.35	9.35	3
Q15582 BGH3_HUMAN	Transforming growth factor-beta-induced protein ig-h3	19.33	4.83	3.51	2
P53985 MOT1_HUMAN	Monocarboxylate transporter 1	4.20	2.40	2.40	1
Q9Y512 SAM50_HUMAN	Sorting and assembly machinery component 50 homolog	30.28	2.35	2.35	1
Q9UHG3 PCYOX_HUMAN	Prenylcysteine oxidase 1	14.26	3.96	2.18	1
P04433 KV309_HUMAN	Ig kappa chain V-III region VG (Fragment)	25.22	7.83	7.83	1
Q8NCW5 AIBP_HUMAN	Apolipoprotein A-I-binding protein	20.83	6.94	4.17	1
P54920 SNAA_HUMAN	Alpha-soluble NSF attachment protein	24.41	3.39	3.39	1
P50990 TCPQ_HUMAN	T-complex protein 1 subunit theta	15.33	1.82	1.82	1

P56181 NDUV3_HUMAN	NADH dehydrogenase [ubiquinone] flavoprotein 3, mitochondrial	48.15	14.81	14.81	1
P61353 RL27_HUMAN	60S ribosomal protein L27	20.59	6.62	6.62	1
Q96CX2 KCD12_HUMAN	BTB/POZ domain-containing protein KCTD12	23.38	8.31	4.61	1
P17980 PRS6A_HUMAN	26S protease regulatory subunit 6A	14.12	2.28	2.28	1
O60763 USO1_HUMAN	General vesicular transport factor p115	13.41	1.98	1.04	1
Q9GZT3 SLIRP_HUMAN	SRA stem-loop-interacting RNA-binding protein, mitochondrial	39.45	16.51	10.09	1
P01621 KV303_HUMAN	Ig kappa chain V-III region NG9 (Fragment)	33.00	27.00	27.00	2
P21810 PGS1_HUMAN	Biglycan	24.46	2.45	2.45	1
RRRRRQ15382 RHEB_HUMAN	REVERSED GTP-binding protein Rheb	18.48	3.80	3.80	1
P27816-2 MAP4_HUMAN	Isoform 2 of Microtubule-associated protein 4	31.15	2.35	2.35	2
Q16563 SYPL1_HUMAN	Synaptophysin-like protein 1	15.44	4.25	4.25	1
P17612 KAPCA_HUMAN	cAMP-dependent protein kinase catalytic subunit alpha	26.78	5.13	2.56	1
P62249 RS16_HUMAN	40S ribosomal protein S16	36.99	7.53	7.53	1
Q14525 KT33B_HUMAN	Keratin, type I cuticular Ha3-II	42.08	4.21	4.21	2
P02788 TRFL_HUMAN	Lactotransferrin	30.14	3.24	1.83	1
P62750 RL23A_HUMAN	60S ribosomal protein L23a	13.46	13.46	13.46	2
Q969G5 PRDBP_HUMAN	Protein kinase C delta-binding protein	27.59	10.73	5.36	1
P40429 RL13A_HUMAN	60S ribosomal protein L13a	34.48	3.94	3.94	1
Q99807 COQ7_HUMAN	Ubiquinone biosynthesis protein COQ7 homolog	32.72	5.07	5.07	1
Q14240 IF4A2_HUMAN	Eukaryotic initiation factor 4A-II	24.08	4.18	4.18	2
P22830 HEMH_HUMAN	Ferrochelatase, mitochondrial	17.26	3.55	3.55	1
P14621 ACYP2_HUMAN	Acylphosphatase-2	32.32	9.09	9.09	1
O95865 DDAH2_HUMAN	N(G),N(G)-dimethylarginine dimethylaminohydrolase 2	14.74	3.51	3.51	1
Q08499-7 PDE4D_HUMAN	Isoform PDE4DN3 of cAMP-specific 3',5'-cyclic phosphodiesterase 4D	29.30	3.72	3.72	1
Q9UKU7 ACAD8_HUMAN	Isobutyryl-CoA dehydrogenase, mitochondrial	27.47	6.51	6.51	2
Q9Y230 RUVB2_HUMAN	RuvB-like 2	20.30	3.46	2.38	1
P05141 ADT2_HUMAN	ADP/ATP translocase 2	60.07	34.90	34.90	18
RRRRRO95461-2 LARGE_HUMAN	REVERSED Isoform 2 of Glycosyltransferase-like protein LARGE1	12.78	1.14	1.14	1
Q02878 RL6_HUMAN	60S ribosomal protein L6	12.50	3.13	3.13	1
Q9NUI1-2 DECR2_HUMAN	Isoform 2 of Peroxisomal 2,4-dienoyl-CoA reductase	40.28	3.79	3.79	1
Q9UPU7-2 TBD2B_HUMAN	Isoform 2 of TBC1 domain family member 2B	26.81	0.77	0.77	1
RRRRRQ9H400 LIME1_HUMAN	REVERSED Lck-interacting transmembrane adapter 1	17.29	2.71	2.71	1
O43399-4 TPD54_HUMAN	Isoform 4 of Tumor protein D54	57.50	4.50	4.50	1
P54652 HSP72_HUMAN	Heat shock-related 70 kDa protein 2	46.95	15.81	15.81	25
Q9GZT9 EGLN1_HUMAN	Egl nine homolog 1	33.57	2.58	2.58	1
P56381 ATP5E_HUMAN	ATP synthase subunit epsilon, mitochondrial	68.63	15.69	15.69	1
Q9H1E5 TMX4_HUMAN	Thioredoxin-related transmembrane protein 4	24.36	3.44	3.44	1

P41250 SYG_HUMAN	Glycyl-tRNA synthetase	18.81	1.08	1.08	1
P00325 ADH1B_HUMAN	Alcohol dehydrogenase 1B	19.47	3.47	2.13	1
Q9H7Z7 PGES2_HUMAN	Prostaglandin E synthase 2	37.14	3.71	3.71	1
P25325 THTM_HUMAN	3-mercaptopyruvate sulfurtransferase	25.93	3.70	3.70	1

% Cov (Coverage) is the percentage of matching amino acids from identified peptides having confidence greater than 0 divided by the total number of amino acids in the sequence.

%Cov(50) and %Cov(95) are the same definition but with the peptide confidence greater than or equal to 50 % and 95 % respectively.

Peptides (95%) is the number of distinct peptides having at least 95% confidence. Multiple modified and cleaved states of the same underlying peptide sequence are considered distinct peptides because they have different molecular formulas. Multiple spectra of the same peptide, due to replicate acquisition or different charge states, only count once.

Supplemental Table II. Peptides used for label-free quantification (before normalization)

UniProt Accession	Peptide sequence	m/z	Ret.Time	Area I No 1	Area I No 2	Area I No 3	Area I No 4	Area I No 5	Area II No 1	Area II No 2	Area II No 3	Area II No 4	Area II No 5	Control No 1	Control No 2	Control No 3	Control No 4	Control No 5
Q8WZ42-8 TITIN	VRAENAAGISEPSR	486.25	52.43	6.05E+02	2.16E+03	1.48E+04	7.59E+03	4.11E+04	1.65E+04	4.28E+02	9.08E+02	1.54E+02	5.73E+02	1.15E+04	5.95E+03	2.74E+04	3.09E+02	8.12E+02
Q8WZ42-8 TITIN	AENAAGISEPSR	601.29	52.74	4.93E+04	8.90E+04	1.10E+05	1.06E+05	6.28E+05	1.79E+03	1.52E+05	2.20E+05	6.41E+05	5.32E+05	2.92E+05	1.36E+05	9.23E+04	4.31E+02	2.07E+05
Q8WZ42-8 TITIN	VLDKPGPPASVK	403.24	55.2	1.64E+03	6.90E+03	1.15E+03	4.67E+02	3.70E+02	1.89E+03	4.61E+02	4.10E+02	9.05E+04	8.25E+04	4.47E+03	2.28E+03	3.31E+02	4.59E+04	2.59E+03
Q8WZ42-8 TITIN	LTSGEAPGIR	500.77	55.58	2.09E+04	1.26E+03	7.53E+03	4.71E+04	2.94E+04	2.67E+03	1.70E+04	3.22E+03	2.97E+04	1.70E+02	3.22E+04	1.54E+04	5.81E+03	3.40E+02	2.77E+04
Q8WZ42-8 TITIN	VGASDPSDSSDPQIAK	787.35	55.74	1.84E+05	6.67E+05	8.25E+03	7.80E+05	1.51E+05	2.56E+05	3.65E+04	3.88E+04	1.57E+05	2.00E+02	5.50E+05	5.74E+05	4.79E+05	2.49E+05	2.04E+05
Q8WZ42-8 TITIN	EESSESSEGTVEEVATVK	834.88	55.76	5.61E+02	1.12E+04	2.65E+02	2.22E+04	1.29E+03	2.34E+04	3.11E+02	1.45E+02	3.46E+02	1.54E+02	2.92E+04	3.55E+03	7.72E+02	2.43E+02	4.67E+02
Q8WZ42-8 TITIN	GVASAVVSEDEK	531.28	55.87	2.30E+04	3.02E+02	5.08E+02	2.67E+04	5.45E+02	3.47E+04	3.51E+02	4.95E+02	1.86E+03	6.01E+03	2.96E+04	1.07E+03	3.98E+03	8.74E+03	1.73E+02
Q8WZ42-8 TITIN	VCAQNQVGIGR	572.80	56.28	8.45E+04	4.76E+02	1.10E+03	1.85E+04	1.43E+03	6.46E+02	4.67E+03	2.08E+03	1.05E+04	1.63E+03	2.88E+04	1.15E+04	2.00E+03	4.56E+03	1.96E+02
Q8WZ42-8 TITIN	KGEDEVVTSSHLAVHK	434.73	56.77	3.99E+02	4.65E+02	1.32E+03	2.38E+03	4.38E+02	3.21E+03	1.13E+03	1.28E+03	2.08E+03	9.45E+03	1.76E+03	7.91E+02	1.27E+03	3.57E+03	2.06E+03
Q8WZ42-8 TITIN	YEITAANSSGTTK	671.83	56.8	2.86E+03	8.85E+03	1.43E+03	4.90E+02	4.96E+02	2.86E+03	3.84E+02	9.79E+02	5.76E+04	5.29E+02	2.13E+03	6.44E+02	2.10E+03	3.22E+04	3.49E+03
Q8WZ42-8 TITIN	AVVQEEISQK	565.81	57.15	3.38E+03	1.83E+02	3.28E+02	3.25E+03	1.23E+03	1.32E+03	8.33E+02	5.48E+02	9.03E+03	2.64E+04	1.04E+04	2.95E+03	1.19E+03	1.58E+03	4.50E+03
Q8WZ42-8 TITIN	VEAEPAEVTER	615.30	57.16	2.70E+03	3.14E+03	3.89E+03	6.15E+03	9.92E+03	7.39E+02	9.31E+02	6.14E+03	2.57E+02	4.38E+03	2.60E+04	1.24E+03	3.57E+03	2.84E+02	1.79E+03
Q8WZ42-8 TITIN	SRQPAEEYEDDTER	607.94	57.16	1.47E+05	3.09E+04	4.38E+02	9.84E+04	2.38E+04	2.98E+03	1.03E+03	7.17E+02	4.97E+03	2.52E+03	1.13E+05	9.34E+03	5.35E+02	5.28E+03	1.77E+03
Q8WZ42-8 TITIN	ISGSPK	415.73	57.36	4.78E+05	2.64E+05	8.98E+03	7.37E+04	5.37E+03	1.89E+04	3.67E+03	4.43E+03	1.38E+05	3.92E+05	4.20E+05	2.22E+04	8.42E+03	3.23E+04	3.52E+05
Q8WZ42-8 TITIN	IDVTPVGSK	458.26	57.61	1.24E+04	4.20E+04	4.41E+03	5.39E+04	2.00E+04	1.35E+04	4.24E+02	1.14E+03	4.19E+03	4.75E+02	4.91E+04	2.12E+04	3.19E+03	2.63E+03	6.14E+04
Q8WZ42-8 TITIN	VEAMGMSSEAK	570.26	57.73	9.80E+03	1.03E+03	2.02E+03	1.67E+04	7.64E+04	3.70E+03	2.73E+03	6.38E+02	4.80E+02	7.84E+02	3.09E+04	2.53E+04	9.01E+02	3.56E+03	4.33E+03
Q8WZ42-8 TITIN	VAEVPQPPGK	511.29	57.94	5.37E+03	3.71E+03	1.58E+04	1.19E+04	1.19E+05	8.52E+04	1.93E+04	3.95E+04	1.07E+04	7.89E+03	1.18E+05	5.89E+03	2.07E+04	9.67E+03	4.65E+03
Q8WZ42-8 TITIN	VVIDNVGTK	472.77	58.25	2.74E+03	2.73E+03	1.56E+03	1.29E+03	3.47E+03	1.78E+03	8.05E+02	2.57E+02	3.37E+03	4.36E+04	3.09E+03	3.27E+03	1.22E+03	9.53E+03	2.40E+03
Q8WZ42-8 TITIN	NAMGSASATIR	539.77	58.25	2.59E+04	8.21E+03	4.79E+03	5.66E+03	1.08E+03	3.71E+03	1.02E+04	1.36E+04	6.78E+03	4.51E+04	6.67E+03	1.23E+03	1.76E+03	5.42E+03	2.84E+03
Q8WZ42-8 TITIN	PSEPSEPTITK	593.30	58.62	1.52E+04	2.89E+04	1.43E+04	1.50E+04	2.05E+04	1.85E+04	7.42E+04	9.28E+04	8.38E+02	2.05E+02	1.72E+04	2.72E+04	1.85E+04	1.17E+03	2.16E+04
Q8WZ42-8 TITIN	IPAVVTGR	406.75	59.77	2.79E+02	1.58E+02	5.40E+04	1.75E+02	8.26E+04	5.14E+02	8.90E+04	1.17E+04	2.47E+02	4.61E+02	3.32E+02	8.60E+02	6.53E+04	2.82E+02	1.81E+03
Q8WZ42-8 TITIN	AVDPIDAPK	463.25	59.85	2.82E+04	2.46E+04	1.15E+03	7.82E+03	1.86E+03	8.30E+02	2.71E+03	7.89E+02	6.03E+03	8.27E+04	3.64E+04	6.93E+03	6.71E+02	1.80E+04	4.57E+04
Q8WZ42-8 TITIN	AGSSPPSKPTEYVTAR	549.95	60.59	2.09E+05	1.84E+05	9.36E+03	2.98E+05	1.55E+05	2.82E+05	2.78E+03	1.70E+03	1.68E+03	2.82E+03	2.43E+05	2.11E+05	2.65E+03	1.58E+03	2.87E+05
Q8WZ42-8 TITIN	VLAEENLAGPGKPSK	460.93	60.95	1.30E+05	1.43E+05	1.10E+04	2.31E+05	1.02E+04	8.66E+03	7.82E+03	4.33E+03	3.58E+02	4.84E+02	3.70E+05	2.43E+05	1.62E+04	1.65E+02	2.85E+05
Q8WZ42-8 TITIN	IGTGPPTESKPVIAK	498.96	61.16	1.10E+05	6.23E+04	1.21E+02	1.33E+05	3.31E+03	3.16E+03	5.48E+02	5.36E+02	1.46E+03	4.08E+02	1.04E+05	3.57E+03	1.39E+03	1.70E+03	1.15E+05
Q8WZ42-8 TITIN	DSGDYTITAENSSGSK	816.35	61.62	1.19E+05	5.56E+04	2.11E+03	1.30E+05	3.14E+03	1.01E+04	6.24E+03	1.17E+03	5.18E+02	6.57E+02	1.40E+04	7.07E+04	3.50E+03	9.69E+02	6.95E+04
Q8WZ42-8 TITIN	GEDEVVTSSHLAVHK	536.61	61.67	3.08E+03	7.56E+04	4.09E+03	1.08E+05	8.94E+04	7.54E+03	3.48E+03	1.27E+03	2.66E+03	2.96E+02	7.61E+04	7.44E+04	3.97E+03	3.68E+02	9.66E+04
Q8WZ42-8 TITIN	VGVGPTIETK	500.79	61.74	3.87E+04	4.25E+04	8.23E+03	6.34E+04	1.08E+05	6.31E+03	3.18E+03	8.70E+03	3.73E+04	2.67E+04	8.15E+04	6.02E+04	1.21E+04	5.75E+03	2.84E+02
Q8WZ42-8 TITIN	YLDATPVTK	504.27	61.91	1.32E+03	1.05E+04	1.50E+03	1.39E+04	2.01E+03	3.13E+03	1.94E+02	1.56E+03	3.25E+02	1.50E+04	7.13E+04	2.47E+02	1.42E+03	2.48E+04	2.43E+03
Q8WZ42-8 TITIN	YVITATNSCGSK	622.30	62	2.67E+03	1.09E+03	3.31E+03	4.45E+02	9.52E+02	4.20E+03	4.98E+03	6.98E+03	2.99E+04	3.72E+04	2.30E+03	1.34E+03	7.94E+04	2.36E+04	1.65E+03
Q8WZ42-8 TITIN	IADASDEGWKR	448.89	62.11	1.06E+03	1.30E+04	1.36E+03	2.12E+03	6.86E+02	3.73E+03	1.24E+03	1.35E+03	4.90E+04	4.44E+04	2.87E+03	7.73E+03	1.29E+03	5.79E+03	2.14E+03
Q8WZ42-8 TITIN	SMTVYEGESAR	615.27	62.41	1.53E+02	1.73E+04	6.81E+03	5.88E+04	1.36E+05	5.82E+03	7.53E+03	2.46E+03	1.00E+03	5.73E+02	1.40E+05	4.79E+04	2.32E+03	4.43E+02	1.09E+03
Q8WZ42-8 TITIN	YEIVADGR	461.73	62.53	1.57E+03	6.90E+03	6.80E+03	1.31E+03	2.93E+04	7.87E+03	2.81E+03	6.11E+03	7.20E+03	1.53E+04	1.07E+03	1.72E+03	3.37E+03	7.15E+03	6.26E+03
Q8WZ42-8 TITIN	NAAGAIKPSDSTGPITAK	595.98	62.62	4.56E+04	4.65E+04	4.63E+03	8.29E+04	4.70E+04	2.54E+03	2.33E+03	5.30E+03	1.12E+04	9.65E+03	7.53E+04	2.02E+04	1.60E+03	5.15E+03	2.61E+03
Q8WZ42-8 TITIN	PSTYHIPTK	555.28	62.88	7.89E+03	7.23E+03	6.07E+03	2.24E+04	3.50E+04	6.19E+03	1.11E+04	2.30E+03	9.88E+03	9.90E+02	3.58E+04	1.23E+04	3.03E+04	2.83E+03	2.20E+03
Q8WZ42-8 TITIN	YGRPPVGPVK	431.26	62.96	1.28E+03	4.29E+03	3.05E+04	1.39E+04	3.88E+03	1.29E+04	2.64E+03	2.75E+03	7.88E+02	4.68E+03	1.99E+03	4.97E+03	7.47E+02	3.23E+03	2.18E+03
Q8WZ42-8 TITIN	PPGKPEVIDVTK	427.24	63.21	3.76E+04	2.89E+03	3.41E+03	2.91E+03	2.12E+02	4.94E+03	4.58E+02	4.49E+03	4.19E+02	1.22E+02	4.55E+04	2.40E+02	7.11E+03	5.37E+02	4.27E+04
Q8WZ42-8 TITIN	VTNDNLLSR	516.27	63.3	2.83E+04	1.15E+03	2.44E+03	2.41E+03	9.78E+03	8.84E+03	2.88E+03	1.05E+03	6.88E+03	5.77E+04	2.78E+03	7.10E+02	6.32E+03	4.41E+03	2.60E+04
Q8WZ42-8 TITIN	AAEVPAPIR	462.27	63.4	6.77E+03	1.29E+04	4.26E+03	1.26E+03	5.00E+02	2.65E+03	4.05E+02	7.38E+03	3.35E+04	2.39E+04	1.02E+04	1.23E+03	4.38E+03	1.12E+04	3.76E+04
Q8WZ42-8 TITIN	TAVEKDEITLK	416.23	63.41	1.15E+03	2.56E+02	3.47E+03	1.96E+03	1.09E+04	2.41E+02	1.05E+03	6.23E+02	4.94E+04	5.99E+03	4.94E+03	3.01E+03	3.41E+02	3.04E+04	7.13E+02
Q8WZ42-8 TITIN	LKENTENYFR	438.56	63.88	4.49E+03	9.13E+03	1.56E+04	1.97E+04	5.48E+03	2.62E+03	3.02E+03	1.32E+04	3.37E+04	3.24E+04	2.81E+04	1.19E+04	3.34E+03	1.46E+04	2.69E+03
Q8WZ42-8 TITIN	SDVPIQAPH	482.25	64.03	1.10E+05	1.14E+05	5.43E+03	2.11E+05	6.48E+04	1.87E+04	9.00E+04	8.46E+04	6.96E+03	8.77E+03	2.51E+05	9.37E+02	2.61E+02	2.83E+03	1.48E+05
Q8WZ42-8 TITIN	SVEVMETETAR	626.30	64.15	1.19E+04	1.71E+04	1.09E+04	6.29E+03	2.52E+03	6.37E+03	3.56E+02	7.71E+02	6.50E+02	1.45E+02	3.16E+04	5.94E+03	2.21E+03	1.16E+03	7.41E+03
Q8WZ42-8 TITIN	DGEEIVPSPK	535.77	64.18	7.51E+02	8.99E+02	3.67E+03	1.37E+04	4.21E+03	1.96E+04	5.09E+03	6.04E+03	5.20E+02	2.19E+03	6.05E+03	2.17E+04	3.69E+04	3.42E+02	2.67E+02
Q8WZ42-8 TITIN	ITNYVVER	497.27	64.33	3.28E+03	3.24E+04	4.75E+04	7.22E+04	5.57E+04	2.68E+04	3.82E+04	1.78E+04	1.12E+03	9.25E+02	8.65E+04	6.65E+04	5.34E+04	8.14E+02	3.53E+02
Q8WZ42-8 TITIN	AGGPGEPAEVPGTVK	683.35	64.49	3.23E+04	5.06E+04	4.26E+03	2.86E+04	5.40E+04	1.42E+03	4.85E+04	3.92E+03	2.64E+02	1.09E+03	2.77E+04	1.94E+04	4.46E+03	7.26E+02	5.41E+04
Q8WZ42-8 TITIN	YTLTVENNSGSK	656.82	64.82	4.08E+04	4.70E+04	1.70E+04	7.82E+04	5.69E+04	9.12E+03	4.26E+03	1.11E+04	3.55E+03	3.41E+03	8.99E+04	7.22E+03	4.47E+03	7.57E+03	8.61E+04
Q8WZ42-8 TITIN	GRPAPEVTWK	621.33	64.87	2.91E+02	3.09E+04	1.09E+04	7.29E+03	4.83E+04	2.81E+04	5.38E+04	2.75E+04	1.15E+03	3.59E+02	5.73E+04	3.87E+04	8.54E+03	1.98E+03	2.06E+03
Q8WZ42-8 TITIN	LGSATASINVK	530.81	64.91	1.18E+05	2.44E+04	4.49E+02	1.27E+04	1.82E+04	1.56E+04	6.07E								



Q8WZ42-8 TITIN	EAHVLYKPAVSTK	688.89	65.89	1.18E+04	8.10E+04	3.35E+02	2.92E+03	1.57E+03	4.69E+02	1.28E+03	1.61E+03	5.35E+02	4.83E+02	1.30E+05	4.19E+03	2.73E+02	8.57E+03	1.18E+05
Q8WZ42-8 TITIN	AVPEAPTVPK	553.32	65.95	2.74E+03	1.02E+03	1.74E+03	5.68E+02	6.20E+02	4.52E+02	6.45E+03	2.63E+02	1.98E+05	2.15E+05	6.54E+02	7.26E+02	1.10E+03	8.23E+04	5.63E+03
Q8WZ42-8 TITIN	ITVDDVTR	459.75	66.13	3.48E+02	5.49E+03	3.33E+03	2.16E+03	4.60E+03	5.16E+02	1.01E+05	6.17E+02	5.51E+05	5.15E+05	1.20E+04	2.33E+05	1.64E+02	4.31E+05	7.49E+02
Q8WZ42-8 TITIN	DGIEIEER	480.74	66.26	9.37E+03	3.85E+04	1.82E+03	4.26E+03	1.79E+04	1.02E+05	5.84E+04	8.12E+02	1.24E+04	3.40E+03	1.41E+05	1.05E+05	9.34E+02	2.64E+03	9.55E+04
Q8WZ42-8 TITIN	VLAENLAGPGK	534.80	66.44	1.39E+02	3.96E+04	1.86E+03	2.23E+04	3.11E+04	8.92E+03	3.78E+04	1.10E+04	2.06E+03	7.13E+02	1.49E+05	2.15E+04	2.32E+04	7.50E+02	4.19E+04
Q8WZ42-8 TITIN	YCVVVENSTGSR	657.31	66.54	1.72E+03	7.30E+03	1.21E+04	3.32E+04	5.50E+03	2.46E+04	5.09E+02	1.84E+04	7.00E+02	1.71E+02	1.58E+04	8.69E+03	6.86E+03	5.69E+02	1.29E+03
Q8WZ42-8 TITIN	VFAENETGLSRPR	492.59	66.76	1.28E+03	5.73E+05	5.74E+05	7.82E+05	7.35E+05	7.84E+05	3.36E+05	4.51E+05	1.21E+04	3.10E+02	1.13E+03	3.46E+05	4.27E+05	6.08E+03	7.87E+05
Q8WZ42-8 TITIN	AADPIDPPGPPAK	623.33	66.95	1.44E+03	1.60E+05	2.40E+05	2.25E+05	6.27E+03	4.14E+05	1.34E+05	2.01E+05	2.49E+05	2.83E+04	4.63E+03	1.42E+05	1.26E+05	2.86E+05	2.19E+05
Q8WZ42-8 TITIN	IQEAEGGLIK	529.30	66.99	4.00E+02	1.14E+03	1.86E+03	1.47E+03	3.83E+02	1.15E+03	1.88E+03	6.66E+02	1.68E+05	1.77E+05	1.58E+03	1.10E+03	4.95E+02	1.54E+04	5.88E+03
Q8WZ42-8 TITIN	DEVELPR	429.23	67.2	3.22E+02	6.39E+03	5.96E+04	7.28E+03	8.19E+03	1.18E+05	9.22E+04	2.08E+05	3.84E+02	1.37E+03	5.70E+03	6.32E+03	1.95E+05	1.54E+03	8.20E+02
Q8WZ42-8 TITIN	IPAVVTGRPVPTK	667.91	67.34	1.59E+02	1.55E+04	9.53E+02	1.37E+04	4.67E+04	3.16E+02	3.32E+04	1.09E+03	1.46E+02	2.73E+02	4.49E+02	2.61E+04	2.77E+03	1.58E+03	9.95E+02
Q8WZ42-8 TITIN	NDHISAHLEVPK	453.91	67.38	8.52E+04	7.24E+03	7.37E+02	1.30E+03	7.88E+03	2.76E+03	1.34E+03	2.71E+03	7.20E+04	1.05E+05	4.08E+03	8.59E+02	8.40E+02	1.90E+04	1.58E+03
Q8WZ42-8 TITIN	VSAVNIVGQ GK	536.31	67.48	5.78E+04	1.03E+05	9.48E+02	1.09E+04	6.58E+02	9.44E+03	2.67E+03	1.90E+03	2.62E+03	4.22E+03	2.43E+05	1.26E+05	2.49E+04	8.88E+02	1.22E+05
Q8WZ42-8 TITIN	NFPSHTVYVR	407.21	67.62	4.43E+03	9.06E+02	5.90E+02	1.35E+04	5.13E+04	1.95E+03	1.12E+04	6.62E+04	2.15E+04	1.60E+04	8.43E+03	4.04E+04	1.93E+03	1.47E+04	7.83E+03
Q8WZ42-8 TITIN	ITNYIVEK	490.28	67.66	2.40E+04	6.96E+04	3.86E+03	1.91E+03	7.53E+03	6.41E+03	1.01E+03	2.32E+02	1.91E+04	4.52E+04	7.73E+04	6.33E+03	1.05E+04	1.36E+03	1.31E+05
Q8WZ42-8 TITIN	VTGYIER	500.76	67.7	4.22E+02	1.17E+03	6.35E+04	1.07E+04	3.15E+03	9.40E+04	3.80E+02	1.74E+05	4.25E+02	1.27E+02	1.05E+04	3.57E+03	2.05E+05	7.20E+02	1.66E+03
Q8WZ42-8 TITIN	NGEEVPFDNR	588.77	67.73	9.31E+02	6.10E+02	5.77E+04	2.19E+03	6.04E+02	9.01E+04	1.65E+04	3.10E+04	3.97E+02	5.75E+02	2.01E+02	4.54E+02	4.02E+03	4.34E+02	3.22E+02
Q8WZ42-8 TITIN	PPGRPEAIVTR	435.93	67.78	1.01E+05	1.48E+05	9.73E+03	1.22E+05	6.84E+04	1.17E+03	6.88E+04	1.34E+05	6.48E+04	8.85E+04	1.17E+05	1.12E+05	1.21E+05	1.50E+05	6.33E+04
Q8WZ42-8 TITIN	TYALNAAGVSK	547.80	67.79	1.61E+03	5.47E+06	1.14E+07	3.92E+06	6.24E+05	4.34E+06	4.55E+06	5.57E+06	3.26E+02	2.39E+03	3.84E+06	3.65E+06	2.73E+06	1.20E+03	5.24E+06
Q8WZ42-8 TITIN	IGYSDDPSDVPDK	646.80	67.86	1.33E+05	5.39E+04	4.84E+03	1.20E+05	1.68E+04	2.72E+04	8.13E+02	6.82E+03	1.83E+03	2.12E+02	1.08E+05	3.37E+04	4.92E+03	9.75E+03	1.50E+05
Q8WZ42-8 TITIN	PLAESVIAP	480.27	67.86	3.46E+02	8.40E+04	3.64E+02	4.73E+02	2.49E+05	3.45E+05	1.02E+03	2.48E+03	1.03E+03	3.59E+02	2.56E+05	1.28E+05	1.65E+05	1.48E+03	1.39E+05
Q8WZ42-8 TITIN	EPGQPEVTNITR	654.85	68.21	1.05E+05	1.05E+03	1.31E+03	3.23E+03	1.15E+04	1.71E+03	3.80E+02	1.52E+03	1.51E+02	4.73E+02	9.89E+04	4.53E+03	6.73E+02	5.14E+02	6.75E+04
Q8WZ42-8 TITIN	RPVDDGGSEITGYHVER	629.64	68.23	8.66E+04	5.27E+03	1.00E+04	2.09E+03	5.76E+03	1.57E+03	9.64E+03	5.78E+02	9.05E+02	1.95E+02	4.00E+03	1.30E+04	3.22E+02	4.72E+02	5.53E+03
Q8WZ42-8 TITIN	PPGRPEAIVITR	435.93	68.38	1.12E+05	3.04E+03	2.73E+03	7.61E+03	2.44E+03	9.23E+02	8.78E+02	6.38E+02	6.50E+04	8.85E+04	2.82E+03	1.39E+03	5.52E+03	1.50E+05	1.06E+05
Q8WZ42-8 TITIN	EPSYTPGPPSAPR	678.33	68.38	2.37E+05	5.06E+04	2.25E+04	1.82E+05	1.96E+05	1.48E+04	9.77E+02	9.77E+03	1.72E+04	4.55E+03	1.89E+05	1.73E+05	2.27E+04	4.63E+03	2.98E+05
Q8WZ42-8 TITIN	IADASPDEGWK	594.78	68.43	2.13E+05	7.12E+03	3.86E+03	1.44E+04	2.10E+04	8.10E+03	6.04E+02	7.22E+02	5.12E+03	1.30E+02	2.11E+05	8.42E+03	2.37E+03	9.54E+03	2.17E+05
Q8WZ42-8 TITIN	ITGYIVER	475.77	68.76	4.45E+02	3.09E+04	4.49E+04	4.49E+04	5.68E+05	3.26E+04	2.23E+05	4.82E+05	1.30E+03	7.94E+02	1.86E+04	2.48E+02	1.09E+05	2.44E+03	2.02E+05
Q8WZ42-8 TITIN	SDSGPYPLTAR	582.29	68.85	1.10E+05	6.54E+02	1.72E+04	2.61E+03	1.38E+04	1.44E+03	4.97E+02	1.48E+04	4.56E+03	1.05E+03	3.19E+03	1.10E+05	9.46E+02	2.47E+03	3.01E+05
Q8WZ42-8 TITIN	NEEAIFDSSK	570.26	68.99	1.15E+04	4.66E+04	4.23E+03	8.30E+03	8.23E+04	2.09E+03	4.30E+04	2.76E+03	7.07E+03	2.80E+04	3.58E+04	4.11E+03	2.04E+04	6.40E+03	2.79E+04
Q8WZ42-8 TITIN	PPGKPEVINITR	440.93	69.06	1.55E+03	1.19E+04	5.73E+02	5.46E+04	6.42E+04	4.68E+03	5.00E+03	2.68E+03	1.33E+03	1.65E+03	3.36E+03	4.72E+04	1.60E+04	9.28E+02	2.76E+02
Q8WZ42-8 TITIN	VMDVPGPPK	470.25	69.14	5.02E+04	2.26E+04	2.52E+03	2.90E+04	4.88E+04	8.48E+03	3.68E+04	8.11E+04	2.57E+03	2.19E+03	1.88E+04	3.50E+04	1.68E+04	6.15E+03	3.14E+04
Q8WZ42-8 TITIN	IVGYSIEK	454.76	69.15	4.14E+02	4.44E+03	1.10E+03	1.65E+03	2.44E+04	2.55E+03	2.25E+03	8.26E+02	1.55E+03	9.55E+04	8.47E+02	8.62E+03	1.64E+04	3.72E+02	1.31E+03
Q8WZ42-8 TITIN	VLVLDKPGPPR	595.87	69.29	2.96E+03	1.39E+04	8.54E+02	3.44E+04	4.35E+04	6.23E+03	1.06E+04	2.33E+03	3.91E+02	2.12E+02	2.79E+04	6.26E+04	4.60E+03	4.87E+02	3.47E+04
Q8WZ42-8 TITIN	VGGDPIP NVK	498.27	69.33	8.24E+03	2.65E+04	1.38E+04	3.65E+04	1.90E+04	9.48E+03	1.75E+04	7.03E+03	3.00E+02	4.60E+03	2.11E+03	1.18E+04	2.04E+04	6.19E+02	2.04E+04
Q8WZ42-8 TITIN	DIENQTVLK	530.29	69.4	6.93E+02	3.21E+03	6.00E+05	7.44E+03	1.31E+03	1.22E+05	7.19E+05	8.52E+05	1.28E+05	1.18E+05	4.43E+03	2.07E+03	3.33E+03	4.40E+04	9.76E+03
Q8WZ42-8 TITIN	EEGSPYWSR	555.75	69.69	1.02E+04	4.03E+04	4.64E+03	2.00E+05	1.81E+05	4.89E+03	1.25E+05	8.22E+02	1.62E+04	2.18E+03	4.53E+03	1.30E+05	3.14E+04	1.46E+04	9.02E+02
Q8WZ42-8 TITIN	SATVLTPTGTTVTR	652.37	69.79	6.72E+03	8.32E+04	4.53E+03	1.75E+05	1.25E+03	5.10E+03	1.17E+03	3.21E+03	5.89E+02	9.44E+02	8.59E+04	2.04E+03	2.40E+03	1.01E+03	1.73E+04
Q8WZ42-8 TITIN	NLAVTDIK	437.25	69.87	2.03E+03	2.82E+03	4.36E+04	2.35E+03	4.26E+03	3.07E+03	4.35E+03	6.68E+04	1.70E+03	3.60E+03	1.39E+04	6.33E+02	2.13E+03	6.53E+02	2.42E+03
Q8WZ42-8 TITIN	GLEEGKEYQFR	452.56	69.97	1.60E+03	2.12E+03	9.94E+02	1.81E+03	5.59E+04	2.13E+02	1.54E+03	4.48E+02	1.58E+03	1.22E+03	1.32E+03	3.11E+03	5.85E+03	1.12E+03	2.38E+03
Q8WZ42-8 TITIN	VSAENQFGISK	590.31	70.1	1.07E+05	5.36E+04	4.33E+03	1.91E+04	2.09E+04	6.03E+03	1.18E+04	2.95E+04	2.27E+04	1.15E+03	8.81E+04	4.47E+03	4.44E+03	2.00E+03	6.21E+04
Q8WZ42-8 TITIN	TIDVPISGRPAK	450.93	70.12	2.53E+02	3.02E+04	1.26E+03	6.58E+04	8.29E+04	1.96E+03	7.98E+03	6.84E+03	7.57E+03	6.42E+03	3.56E+02	1.12E+05	5.27E+03	4.09E+04	2.90E+03
Q8WZ42-8 TITIN	MEVTGLEEGK	546.77	70.29	7.44E+02	1.47E+05	7.62E+04	2.12E+05	1.24E+05	1.96E+05	1.37E+05	3.16E+03	3.20E+03	2.43E+03	1.88E+03	1.51E+05	1.05E+05	1.84E+03	1.89E+05
Q8WZ42-8 TITIN	VLDPRPGPEGLK	458.93	70.42	6.41E+03	3.04E+05	4.43E+03	5.81E+05	3.69E+05	3.86E+05	2.76E+04	4.23E+03	2.01E+03	6.69E+02	3.62E+03	3.75E+05	2.37E+05	8.44E+02	4.98E+05
Q8WZ42-8 TITIN	VFAENETGLSR	611.81	70.44	5.07E+05	5.06E+05	1.76E+04	6.79E+05	4.13E+03	1.30E+04	7.02E+02	2.12E+04	4.50E+02	1.83E+03	5.31E+05	3.60E+03	5.60E+03	1.24E+03	4.57E+05
Q8WZ42-8 TITIN	VGIDNVVR	436.25	70.5	2.03E+03	2.11E+05	1.25E+05	3.54E+05	4.31E+05	2.09E+05	4.24E+05	2.12E+05	1.86E+05	3.47E+04	1.47E+03	2.41E+05	3.16E+05	3.09E+04	3.68E+05
Q8WZ42-8 TITIN	TLTATNPGGFAK	589.31	70.59	1.12E+03	1.75E+04	2.58E+04	1.10E+04	2.25E+02	3.74E+04	4.14E+03	1.34E+03	6.79E+02	1.22E+04	2.28E+04	4.79E+03	1.87E+04	1.14E+03	2.65E+04
Q8WZ42-8 TITIN	GVGEPVQASPIK	677.37	70.66	4.02E+04	1.49E+03	1.56E+02	1.36E+03	7.74E+02	2.42E+02	1.12E+03	1.18E+03	1.16E+03	6.89E+02	4.98E+03	5.83E+02	1.88E+02	1.50E+03	1.36E+04
Q8WZ42-8 TITIN	VTGEPVETDNPVEAR	835.40	71.02	4.08E+05	3.27E+05	2.91E+03	4.85E+05	3.70E+05	5.39E+03	1.56E+03	3.33E+03	1.05E+03	6.71E+02	4.73E+05	3.39E+05	3.32E+03	1.14E+03	4.64E+05
Q8WZ42-8 TITIN	VEPITEPEVESK	678.85	71.02	3.46E+05	3.38E+05	4.55E+03	3.83E+05	4.30E+03	6.14E+03	5.65E+02	8.61E+02	2.82E+02	2.15E+02	4.42E+05	3.60E+05	2.40E+05	1.38E+03	3.29E+05
Q8WZ42-8 TITIN	DYVVYDTR	515.75	71.08	1.18E+05	2.95E+04	9.61E+02	4.13E+03	8.16E+02	7.57E+02	7.14E+02	2.09E+02	3.						

Q8WZ42-8 TITIN	EDEELLR	452.22	72.47	1.12E+04	1.23E+04	3.55E+03	7.06E+02	2.27E+04	1.50E+04	4.90E+03	6.70E+03	7.36E+03	2.77E+03	3.73E+03	2.12E+04	1.20E+03	4.14E+03	7.42E+02
Q8WZ42-8 TITIN	YYGAVGSTLR	543.78	72.59	3.18E+03	1.05E+04	7.30E+03	5.31E+02	5.70E+04	1.19E+05	2.21E+04	1.66E+03	1.75E+03	3.33E+02	2.47E+03	6.10E+04	2.79E+04	2.23E+03	2.84E+03
Q8WZ42-8 TITIN	LEDAGEVQLTAK	637.34	72.8	2.75E+04	1.39E+03	1.09E+04	6.85E+03	2.78E+04	1.18E+04	9.25E+03	7.16E+03	5.29E+02	7.58E+02	2.34E+04	2.49E+03	9.96E+02	1.06E+03	5.98E+04
Q8WZ42-8 TITIN	HDSVSLTWTDPKK	505.27	72.89	3.44E+03	1.58E+03	2.57E+03	7.96E+03	7.29E+04	1.61E+03	2.14E+03	8.08E+02	1.27E+05	9.74E+03	2.26E+03	4.68E+04	9.02E+03	9.07E+04	2.81E+03
Q8WZ42-8 TITIN	FECELSR	442.20	73.1	6.56E+03	1.11E+04	7.03E+03	1.64E+04	9.55E+04	1.85E+04	5.36E+03	2.51E+04	6.21E+03	4.71E+02	4.85E+04	3.24E+04	1.93E+04	1.59E+03	4.74E+04
Q8WZ42-8 TITIN	RPDYDGGSPNLSYHVER	654.64	73.11	7.56E+04	2.11E+03	7.28E+02	5.83E+03	1.33E+03	2.64E+03	1.73E+03	1.61E+03	1.75E+04	1.31E+04	2.08E+04	6.09E+02	9.52E+02	2.42E+03	2.57E+04
Q8WZ42-8 TITIN	SLEVTNIAK	487.78	73.32	6.88E+03	3.20E+03	5.68E+03	1.57E+04	1.02E+04	2.46E+03	3.31E+03	2.96E+03	2.43E+05	1.89E+05	6.05E+02	8.02E+03	1.74E+03	1.24E+05	2.51E+03
Q8WZ42-8 TITIN	SLSLQYSAK	498.77	73.32	2.30E+02	7.47E+02	7.18E+02	1.15E+03	5.81E+02	9.98E+02	3.30E+03	9.98E+02	1.49E+05	1.37E+05	3.60E+03	1.94E+03	2.66E+03	1.35E+04	2.52E+03
Q8WZ42-8 TITIN	VFAENQAGLS DPR	702.35	73.51	4.85E+04	3.27E+05	2.01E+03	5.32E+05	3.21E+05	1.77E+04	3.82E+02	5.58E+02	1.20E+04	8.07E+03	4.67E+03	4.97E+03	5.33E+03	5.47E+03	2.71E+05
Q8WZ42-8 TITIN	SPFEKPGAPGKPTITAVTK	482.27	73.53	2.44E+03	1.91E+04	6.31E+03	5.70E+04	7.95E+04	2.93E+03	1.03E+03	2.15E+04	1.00E+04	3.39E+04	6.60E+04	6.15E+02	2.23E+04	2.88E+04	5.89E+04
Q8WZ42-8 TITIN	TITGLTENQEYK	698.85	73.68	1.18E+04	1.88E+04	1.42E+02	7.23E+04	8.80E+02	4.17E+02	3.30E+02	6.27E+02	4.08E+03	9.36E+02	5.68E+04	8.96E+03	7.11E+03	1.25E+03	5.69E+04
Q8WZ42-8 TITIN	VSGIPPTLK	504.81	73.73	1.23E+03	1.45E+05	4.76E+04	9.27E+04	7.92E+04	4.19E+04	1.82E+04	1.83E+04	1.37E+03	1.96E+03	6.83E+02	2.24E+04	4.52E+04	2.07E+03	1.92E+03
Q8WZ42-8 TITIN	YEILTEGR	490.76	73.89	3.13E+04	3.26E+04	3.17E+05	3.73E+05	3.78E+05	3.90E+05	3.68E+05	3.09E+03	5.30E+03	1.26E+03	9.19E+03	5.95E+05	3.93E+05	8.91E+02	1.42E+04
Q8WZ42-8 TITIN	YILTVENSSGSK	649.34	73.94	1.86E+03	4.34E+03	3.94E+04	1.38E+05	9.31E+04	1.23E+05	6.57E+04	2.32E+04	3.76E+04	1.22E+05	1.30E+03	1.10E+05	6.59E+04	6.24E+03	2.82E+03
Q8WZ42-8 TITIN	APEIIDVSSK	529.79	74.05	4.17E+03	3.83E+03	1.20E+05	8.67E+04	1.49E+05	1.49E+05	6.03E+04	1.65E+03	2.44E+03	2.98E+03	4.36E+03	1.23E+05	3.77E+03	5.84E+03	3.10E+03
Q8WZ42-8 TITIN	PVDDGGSEITGYHVER	577.26	74.08	5.07E+04	2.06E+02	7.84E+02	1.66E+03	3.23E+03	2.53E+03	8.02E+02	3.79E+02	1.82E+03	1.09E+03	3.07E+04	2.32E+02	2.67E+02	2.28E+03	4.01E+03
Q8WZ42-8 TITIN	LTTGSEYQFR	601.30	74.17	5.27E+02	9.92E+04	2.72E+03	7.52E+04	1.15E+04	1.33E+05	6.06E+03	2.35E+03	7.14E+02	1.22E+04	1.31E+04	6.63E+04	4.73E+04	5.96E+03	7.05E+03
Q8WZ42-8 TITIN	YNLTLENNSGSK	670.33	74.2	1.66E+05	7.89E+03	8.36E+02	4.99E+02	3.14E+03	1.14E+03	8.33E+02	1.28E+03	2.03E+03	1.16E+03	4.54E+04	1.07E+03	3.28E+02	6.22E+03	1.97E+05
Q8WZ42-8 TITIN	ITNYIIEK	497.28	74.24	3.11E+03	5.97E+04	4.50E+03	9.66E+04	1.38E+05	1.18E+05	8.54E+04	1.11E+03	3.80E+03	1.79E+03	3.04E+03	2.54E+04	8.13E+04	2.40E+04	8.11E+03
Q8WZ42-8 TITIN	GRPEPDITWTK	433.90	74.48	1.08E+03	2.84E+05	1.71E+05	3.08E+05	3.13E+04	2.58E+05	1.27E+05	3.89E+04	9.97E+02	2.48E+03	1.85E+03	3.08E+05	2.38E+04	4.42E+02	3.53E+02
Q8WZ42-8 TITIN	ITNYIEK	497.28	74.5	2.59E+03	7.38E+04	6.15E+02	9.89E+04	1.46E+05	1.24E+05	3.08E+03	6.71E+03	1.73E+04	5.33E+03	8.02E+02	7.76E+04	8.34E+04	4.01E+04	1.16E+05
Q8WZ42-8 TITIN	ASQTPGPVVDLK	606.33	74.6	3.70E+05	2.02E+03	6.80E+03	1.03E+04	9.59E+03	3.17E+04	9.54E+03	1.02E+04	2.20E+02	4.12E+02	3.79E+05	2.12E+03	5.58E+02	2.60E+03	7.92E+03
Q8WZ42-8 TITIN	NAVGVSLPR	456.77	74.62	1.23E+05	5.12E+03	6.25E+04	2.64E+04	6.66E+04	3.72E+04	1.57E+04	4.69E+03	5.43E+03	1.54E+04	4.11E+05	2.00E+04	4.74E+03	2.64E+04	5.64E+05
Q8WZ42-8 TITIN	TIDVPISGR	479.27	74.67	4.51E+05	6.96E+05	2.72E+03	3.38E+03	2.37E+04	9.56E+03	6.00E+02	4.38E+03	2.93E+03	7.43E+02	5.05E+05	9.44E+02	1.80E+04	4.98E+03	5.31E+05
Q8WZ42-8 TITIN	GRPTPEITWSR	433.90	74.69	1.09E+03	2.79E+05	1.88E+04	3.13E+05	1.76E+05	2.59E+05	9.78E+03	2.52E+03	7.41E+02	1.57E+03	1.53E+04	3.09E+05	2.39E+04	4.95E+02	3.01E+05
Q8WZ42-8 TITIN	VVIQDPYR	495.27	74.71	1.71E+03	1.12E+05	5.51E+04	3.68E+05	3.06E+05	6.51E+05	3.73E+04	6.41E+04	2.43E+03	5.19E+02	3.24E+05	6.23E+04	6.10E+03	1.38E+05	3.84E+05
Q8WZ42-8 TITIN	HIAIAWKPEK	430.58	74.72	1.43E+02	1.05E+04	1.33E+04	1.23E+05	2.30E+04	1.02E+05	4.12E+04	3.87E+02	2.01E+02	7.52E+02	1.36E+03	3.39E+04	4.10E+03	1.33E+03	3.18E+04
Q8WZ42-8 TITIN	LSDISTVVGK	509.79	74.84	2.18E+03	5.08E+04	9.19E+03	1.02E+05	4.06E+03	1.05E+05	1.25E+03	4.68E+03	1.63E+04	3.48E+02	1.52E+03	5.30E+02	3.53E+04	5.94E+03	9.94E+04
Q8WZ42-8 TITIN	ITGYVIEAQR	575.32	74.92	4.27E+02	1.88E+05	3.92E+03	2.77E+05	1.82E+05	2.49E+05	1.10E+05	3.31E+04	1.52E+04	1.62E+02	3.80E+03	1.41E+05	2.21E+02	5.21E+03	3.88E+03
Q8WZ42-8 TITIN	SWSTVTTECSK	614.78	74.98	8.74E+04	5.19E+03	3.49E+03	2.08E+02	9.23E+02	5.27E+03	1.99E+03	2.67E+02	5.15E+03	3.12E+03	8.61E+04	1.51E+04	5.78E+02	2.00E+04	3.16E+03
Q8WZ42-8 TITIN	IEFGQAR	467.26	75.02	6.94E+02	2.94E+03	5.58E+03	1.48E+03	1.16E+03	1.11E+05	8.97E+02	2.27E+03	3.36E+05	2.55E+05	1.82E+03	6.95E+02	1.61E+03	1.27E+05	1.42E+03
Q8WZ42-8 TITIN	DTWGVVSSGSSK	605.30	75.14	4.57E+03	5.69E+03	4.51E+04	1.86E+03	1.08E+04	5.33E+04	1.13E+04	1.17E+04	3.92E+04	1.81E+04	2.55E+03	2.26E+03	1.11E+03	1.98E+04	1.12E+04
Q8WZ42-8 TITIN	TEAYAVSFK	551.77	75.3	3.52E+02	1.69E+05	2.25E+04	2.81E+05	1.78E+05	6.98E+04	8.21E+03	1.08E+04	3.30E+02	1.16E+03	2.76E+05	7.24E+04	1.45E+05	1.30E+04	2.22E+05
Q8WZ42-8 TITIN	LDPDTEKVR	415.55	75.35	1.68E+03	2.43E+03	6.90E+02	5.80E+02	1.02E+03	3.97E+03	1.72E+03	8.23E+02	7.92E+04	4.55E+04	8.98E+02	8.44E+02	2.24E+03	5.80E+03	1.54E+03
Q8WZ42-8 TITIN	STGLTEGLEEHR	746.36	75.59	1.31E+05	4.03E+03	8.78E+02	6.34E+02	4.61E+03	1.23E+04	5.08E+03	5.52E+03	1.50E+03	5.20E+02	1.51E+05	1.12E+04	2.59E+03	1.85E+03	6.07E+03
Q8WZ42-8 TITIN	EPVNP GPPTVVK	665.87	75.64	1.77E+05	1.65E+04	4.77E+02	4.27E+04	1.47E+04	3.26E+03	7.86E+03	2.17E+03	4.10E+03	8.45E+03	6.54E+04	2.07E+04	4.41E+04	4.51E+03	1.04E+05
Q8WZ42-8 TITIN	VGDEAWIK	459.24	75.65	4.07E+03	2.30E+03	2.36E+04	1.14E+05	1.63E+05	1.97E+05	1.41E+05	3.69E+03	2.26E+03	5.07E+02	8.89E+02	7.30E+04	6.43E+02	1.80E+03	9.18E+03
Q8WZ42-8 TITIN	PPGTPEPIMVK	583.32	75.67	7.01E+05	7.19E+04	1.63E+04	1.31E+05	8.47E+04	2.40E+03	2.15E+04	2.16E+04	1.01E+06	1.04E+06	8.14E+03	6.95E+04	5.87E+04	1.21E+06	6.59E+04
Q8WZ42-8 TITIN	VTGLTENS DYQYR	773.36	75.76	5.91E+04	5.72E+02	3.54E+04	1.14E+04	5.96E+02	5.95E+02	4.87E+03	1.00E+04	2.83E+02	1.17E+03	3.64E+04	1.12E+03	1.16E+03	4.91E+03	6.22E+03
Q8WZ42-8 TITIN	TAPEYYAPEVH	638.80	75.79	3.94E+02	4.08E+04	2.71E+03	1.58E+04	2.01E+04	6.65E+03	2.56E+03	1.91E+05	4.61E+03	3.22E+03	6.48E+02	3.44E+04	4.13E+03	2.21E+03	3.71E+04
Q8WZ42-8 TITIN	NAAGNFSEPSDSSGAIAR	926.43	75.84	9.55E+04	1.43E+04	6.33E+03	1.84E+05	1.31E+05	6.94E+02	1.83E+03	2.78E+03	2.15E+03	2.54E+03	1.38E+05	9.59E+03	9.10E+04	1.44E+03	1.14E+05
Q8WZ42-8 TITIN	AWVSVTNNCNR	632.30	76.02	3.74E+04	7.40E+02	9.45E+02	1.73E+04	1.04E+03	4.21E+02	1.01E+03	4.79E+02	3.56E+04	4.26E+04	1.41E+04	1.97E+03	1.63E+03	9.08E+03	3.09E+03
Q8WZ42-8 TITIN	VTLVDVTR	451.77	76.19	4.48E+02	1.07E+06	3.09E+04	1.25E+06	9.53E+05	1.25E+06	8.54E+05	7.33E+03	1.95E+02	3.15E+02	4.20E+03	1.18E+06	1.09E+06	6.50E+02	4.78E+03
Q8WZ42-8 TITIN	VSAENQFGISKPLK	506.61	76.27	3.43E+03	1.65E+04	9.42E+04	1.18E+05	9.13E+04	4.17E+04	8.07E+04	1.58E+02	6.20E+03	5.23E+02	1.53E+04	7.78E+04	1.50E+04	2.81E+04	3.02E+04
Q8WZ42-8 TITIN	IIGYVVER	474.78	76.29	5.03E+05	2.29E+05	3.04E+05	2.13E+05	4.18E+05	2.47E+05	3.54E+05	7.24E+03	3.91E+02	1.24E+03	5.67E+05	5.31E+05	1.96E+05	4.95E+02	3.53E+05
Q8WZ42-8 TITIN	VIDVPGPVR	476.28	76.52	7.77E+02	5.92E+05	5.01E+05	6.98E+05	2.07E+05	6.29E+05	3.60E+05	3.48E+04	1.70E+03	2.43E+02	3.11E+03	6.14E+05	1.80E+03	2.90E+03	6.75E+05
Q8WZ42-8 TITIN	STAELYLTK	563.80	76.83	3.57E+03	1.74E+03	3.86E+03	1.31E+05	1.34E+04	9.79E+04	2.61E+04	4.27E+03	3.12E+04	2.75E+04	1.46E+04	5.84E+04	1.64E+03	1.74E+04	1.35E+03
Q8WZ42-8 TITIN	VSAENIVGIGKPSK	466.94	76.95	8.18E+04	4.02E+03	2.26E+03	1.33E+04	9.64E+03	1.83E+04	9.89E+03	1.85E+03	4.22E+02	3.04E+03	3.02E+05	3.90E+03	1.07E+05	1.51E+03	3.07E+03
Q8WZ42-8 TITIN	IGVGKPSAATPFVK	457.94	77	1.25E+03	6.74E+04	1.92E+03	7.88E+04	1.08E+05	3.66E+03	6.23E+04	1.39E+03	5.64E+03	2.39E+03	4.84E+02	1.09E+05	2.21E+02	9.16E+02	1.08E+05
Q8WZ42-8 TITIN	LHEGMEYTFR	428.20	77.07	2.30E+03	3.59E+04	2.13E+04	1.07E+04	5.12E+04	1.26E+04	2.76E+03	7.78E+02	8.						

Q8WZ42-8 TITIN	HSITLGWGK	499.77	78.01	6.37E+04	2.66E+03	3.48E+03	1.25E+03	2.09E+02	1.09E+03	6.22E+03	6.78E+03	3.63E+03	2.20E+03	8.04E+02	7.51E+03	6.83E+03	5.13E+03	2.58E+03
Q8WZ42-8 TITIN	YTLTLENSSGTK	657.33	78.09	3.06E+04	1.79E+03	7.60E+02	9.07E+03	7.09E+03	4.78E+03	4.13E+03	3.03E+03	4.66E+02	1.33E+03	7.68E+04	4.25E+03	1.03E+04	5.88E+02	1.76E+04
Q8WZ42-8 TITIN	TWSTVTPEVK	574.30	78.35	8.98E+03	2.20E+03	7.67E+02	9.53E+02	1.83E+05	6.25E+03	5.37E+03	6.38E+02	1.04E+03	9.07E+03	2.57E+05	8.80E+03	2.72E+04	8.91E+03	3.05E+05
Q8WZ42-8 TITIN	EDELLRPVTTTQH	834.41	78.46	5.56E+04	3.33E+04	4.20E+04	1.78E+04	8.53E+02	3.85E+04	6.98E+03	4.97E+03	1.75E+02	2.85E+02	6.17E+03	7.60E+03	9.74E+02	1.24E+03	3.79E+03
Q8WZ42-8 TITIN	HLNEGNQYLFR	464.23	78.68	1.35E+05	8.63E+02	1.85E+03	2.03E+03	4.13E+04	1.27E+03	1.03E+04	2.59E+03	8.94E+04	5.61E+02	1.88E+04	1.13E+03	4.25E+03	2.03E+04	1.74E+03
Q8WZ42-8 TITIN	SWQVISEK	488.76	78.69	2.18E+04	9.61E+03	2.54E+03	1.20E+03	3.42E+04	1.75E+03	1.59E+03	1.38E+03	1.44E+05	1.43E+05	4.44E+04	1.14E+04	2.29E+04	1.06E+05	1.14E+03
Q8WZ42-8 TITIN	HSISLAWTK	521.79	78.74	1.58E+03	3.84E+03	6.19E+02	9.97E+02	4.03E+04	1.47E+03	1.22E+03	1.80E+03	2.64E+03	4.72E+03	5.92E+04	1.17E+03	9.81E+03	3.69E+03	2.04E+04
Q8WZ42-8 TITIN	VLDTPGPPQDLK	640.35	78.88	1.32E+05	7.05E+03	8.03E+03	7.81E+03	4.09E+03	3.61E+03	7.11E+02	9.98E+02	1.07E+04	1.23E+04	5.27E+04	1.45E+05	3.48E+04	6.03E+02	1.48E+05
Q8WZ42-8 TITIN	WSIVAESK	460.25	79.14	1.91E+03	4.05E+04	2.34E+03	2.44E+03	5.13E+04	7.75E+04	8.58E+02	3.31E+03	3.60E+03	6.66E+03	6.74E+02	7.66E+02	3.57E+04	1.74E+04	8.35E+04
Q8WZ42-8 TITIN	VPGPPGTPQVAVTK	724.91	79.19	6.04E+04	1.06E+04	3.33E+03	4.90E+04	5.82E+04	6.75E+03	1.23E+04	2.54E+03	5.19E+02	1.20E+03	2.26E+04	5.70E+03	1.65E+04	1.00E+03	9.90E+04
Q8WZ42-8 TITIN	VVGYYIER	474.78	79.22	1.24E+03	1.66E+03	5.11E+02	7.50E+02	5.04E+02	1.08E+03	8.69E+02	7.48E+02	3.83E+05	2.92E+05	8.16E+03	1.24E+04	6.06E+02	3.90E+05	1.12E+03
Q8WZ42-8 TITIN	IDGYITSYR	544.27	79.27	4.75E+03	4.40E+04	1.86E+03	4.91E+04	2.82E+04	6.56E+04	2.41E+03	3.67E+02	1.64E+03	4.33E+03	3.56E+03	1.71E+05	8.67E+02	3.54E+02	9.72E+02
Q8WZ42-8 TITIN	VSGLTEGHEYEFR	508.58	79.29	4.46E+02	3.22E+05	2.49E+03	4.86E+05	2.19E+05	3.74E+05	1.59E+05	8.79E+03	3.95E+03	1.82E+03	1.16E+03	2.66E+05	2.01E+05	4.07E+03	8.58E+02
Q8WZ42-8 TITIN	DTLPEDTGYYR	665.30	79.32	3.97E+03	2.86E+05	1.88E+03	4.71E+05	2.16E+05	1.64E+05	5.09E+02	5.45E+03	1.66E+04	3.49E+03	2.25E+04	2.67E+05	1.81E+05	1.20E+03	2.27E+04
Q8WZ42-8 TITIN	MPYDVPEPR	552.26	79.5	1.51E+03	5.56E+05	2.58E+05	7.26E+05	5.09E+05	6.16E+05	4.60E+05	4.10E+03	6.16E+03	3.70E+03	1.06E+04	6.35E+05	9.69E+04	2.40E+04	8.50E+03
Q8WZ42-8 TITIN	SDVPIQAPHFK	413.56	80.36	3.97E+02	1.01E+04	1.12E+04	1.07E+04	1.20E+05	5.70E+03	6.36E+03	1.81E+04	7.14E+02	1.43E+03	4.18E+03	9.81E+03	5.19E+03	1.92E+03	1.48E+05
Q8WZ42-8 TITIN	TLEGMGAVHALR	418.89	80.53	1.33E+05	5.55E+03	8.31E+02	5.76E+03	1.35E+03	6.18E+03	1.06E+03	6.11E+03	3.19E+03	5.55E+02	1.84E+05	2.05E+03	1.05E+05	2.51E+03	5.98E+03
Q8WZ42-8 TITIN	EGTGPIFIK	481.27	80.62	7.59E+02	2.26E+05	1.74E+05	2.26E+05	2.22E+05	3.58E+05	1.56E+05	3.88E+05	2.89E+03	1.91E+03	5.38E+04	2.10E+05	1.79E+05	7.95E+02	1.66E+03
Q8WZ42-8 TITIN	TYIPVMSGENK	619.81	80.8	1.10E+03	1.49E+05	6.69E+02	2.67E+05	1.70E+05	2.82E+05	4.12E+03	2.32E+03	4.60E+02	9.21E+02	9.17E+03	1.52E+05	2.70E+03	5.20E+03	3.76E+03
Q8WZ42-8 TITIN	VGGGEYIELK	532.78	80.87	2.79E+05	8.81E+04	5.84E+04	3.61E+05	4.06E+05	4.96E+04	1.93E+04	2.63E+04	1.17E+03	3.23E+02	1.82E+04	2.75E+04	9.92E+04	1.58E+03	3.89E+05
Q8WZ42-8 TITIN	TPVQEEVIEVK	635.85	81.06	1.69E+05	8.78E+02	4.73E+02	4.25E+03	9.87E+02	1.23E+03	2.32E+03	1.46E+03	2.53E+03	9.22E+03	1.93E+04	5.15E+02	7.22E+04	9.04E+02	3.12E+03
Q8WZ42-8 TITIN	LIPPSFTK	451.77	81.12	1.56E+04	1.13E+04	2.23E+04	5.11E+04	2.49E+04	2.14E+04	1.31E+04	1.71E+04	1.06E+03	3.94E+02	1.83E+05	1.84E+04	5.07E+04	4.35E+03	1.82E+05
Q8WZ42-8 TITIN	VYAENIVGVGK	574.82	81.16	2.23E+05	5.41E+03	6.28E+04	2.30E+05	4.66E+04	7.40E+04	6.03E+04	6.35E+04	1.84E+04	7.56E+04	2.57E+05	5.46E+03	1.92E+05	1.49E+04	2.97E+05
Q8WZ42-8 TITIN	TADQDLVVDVGK	630.33	81.42	4.47E+04	3.57E+04	1.98E+04	2.16E+03	1.24E+03	1.76E+03	3.10E+02	1.35E+04	1.34E+03	1.38E+04	3.98E+04	5.17E+03	8.06E+03	2.76E+03	2.62E+03
Q8WZ42-8 TITIN	VYAENIAGIGK	567.81	81.49	1.81E+05	2.57E+03	8.73E+03	7.46E+02	2.32E+02	1.92E+03	4.74E+03	1.05E+03	1.47E+03	6.50E+02	1.98E+05	2.87E+03	3.86E+03	4.44E+04	2.39E+05
Q8WZ42-8 TITIN	AAGVGPASLPSDPATAR	769.40	81.55	9.31E+02	8.68E+04	5.97E+04	2.46E+03	1.91E+02	9.07E+04	8.45E+02	4.64E+03	7.57E+03	4.56E+03	1.95E+03	4.63E+04	2.07E+03	9.82E+02	7.45E+03
Q8WZ42-8 TITIN	GVEFNVPR	459.25	81.69	5.85E+02	3.29E+05	2.26E+02	3.58E+05	2.00E+05	2.18E+05	3.35E+03	1.63E+04	9.64E+02	2.54E+04	1.58E+03	2.69E+05	2.35E+03	5.63E+02	1.90E+03
Q8WZ42-8 TITIN	TAHDPIPPGPPPIPR	517.94	81.73	4.89E+05	2.81E+04	1.81E+04	5.31E+05	1.70E+04	1.06E+03	3.11E+03	2.67E+02	8.73E+03	7.26E+03	4.81E+05	1.92E+04	2.04E+05	3.27E+04	5.08E+03
Q8WZ42-8 TITIN	YGVSGSDQTLTIK	684.85	81.74	1.21E+05	1.84E+03	3.13E+03	1.73E+05	1.22E+04	7.16E+02	1.17E+03	1.09E+03	1.57E+03	2.95E+03	1.62E+05	7.43E+03	5.00E+04	3.26E+03	1.69E+05
Q8WZ42-8 TITIN	VTGLTEDHEYEFR	532.58	81.77	1.19E+03	2.52E+05	3.42E+03	1.03E+03	2.65E+03	4.32E+05	6.52E+03	3.00E+03	9.18E+02	3.12E+02	6.32E+02	2.90E+05	7.04E+02	1.11E+03	1.90E+03
Q8WZ42-8 TITIN	YEDLETSAELR	663.31	81.88	2.27E+04	7.78E+02	1.55E+04	9.56E+03	6.92E+03	2.12E+03	4.64E+02	8.36E+03	1.10E+05	9.86E+04	1.50E+04	1.86E+03	1.74E+03	2.88E+04	2.03E+03
Q8WZ42-8 TITIN	VLEPISGKPLPK	421.93	81.88	2.11E+05	6.90E+02	2.85E+03	8.08E+03	6.62E+03	8.46E+02	3.42E+02	4.11E+03	1.64E+02	1.34E+03	5.39E+04	1.89E+03	9.45E+04	5.49E+02	1.06E+04
Q8WZ42-8 TITIN	TLEEEVTVVK	573.82	82.13	3.89E+05	1.42E+04	5.09E+03	1.59E+04	2.18E+04	7.06E+03	8.11E+02	2.83E+03	7.69E+02	1.40E+03	5.42E+05	2.53E+03	3.42E+05	1.45E+03	1.31E+04
Q8WZ42-8 TITIN	YQEGIFVR	506.27	82.19	5.01E+05	4.21E+05	6.97E+03	7.92E+03	8.89E+02	1.26E+03	2.33E+04	4.58E+03	4.86E+06	3.36E+06	4.66E+05	6.47E+03	8.93E+05	2.02E+06	1.54E+04
Q8WZ42-8 TITIN	ITGYVVEMQTK	634.83	82.53	7.06E+04	7.52E+03	6.87E+03	4.17E+04	1.90E+03	2.17E+03	4.59E+03	4.00E+03	1.37E+03	1.40E+03	7.72E+04	1.19E+04	2.43E+03	9.61E+02	2.33E+04
Q8WZ42-8 TITIN	LINGNEYQFR	627.32	82.75	1.13E+05	1.03E+03	1.80E+03	2.92E+03	5.94E+03	2.75E+03	2.86E+03	1.68E+03	4.36E+03	1.58E+04	9.57E+04	1.81E+03	6.09E+03	7.24E+02	1.32E+03
Q8WZ42-8 TITIN	SSVLSLWVGK	475.75	82.92	1.02E+05	5.18E+03	9.58E+03	1.19E+05	9.09E+02	2.47E+03	2.91E+03	2.26E+03	1.08E+05	3.32E+03	1.12E+05	4.70E+03	1.02E+05	1.95E+04	8.59E+04
Q8WZ42-8 TITIN	IDGGQYILR	517.78	82.93	6.95E+03	2.17E+05	8.86E+03	3.00E+05	2.90E+05	2.82E+05	9.59E+02	2.49E+03	2.21E+05	1.75E+05	8.87E+02	2.56E+05	1.43E+05	2.37E+05	3.21E+05
Q8WZ42-8 TITIN	VIGLPGPK	442.26	83.03	9.83E+02	2.01E+04	1.44E+03	2.53E+03	3.22E+02	2.40E+04	2.25E+04	9.59E+03	7.61E+04	6.02E+04	1.08E+03	2.54E+03	1.87E+03	9.04E+02	6.86E+04
Q8WZ42-8 TITIN	SLAVPIVAK	449.29	83.06	3.47E+03	8.80E+05	1.59E+04	1.14E+06	8.14E+05	8.97E+05	1.38E+04	8.94E+03	2.76E+02	5.05E+02	7.97E+03	9.09E+05	3.87E+03	1.66E+03	1.02E+06
Q8WZ42-8 TITIN	LTEGNEYVFR	614.30	83.11	2.95E+02	1.93E+04	3.11E+02	3.53E+05	1.05E+05	4.41E+03	9.05E+02	2.27E+03	2.29E+02	2.58E+03	6.24E+02	9.31E+03	1.45E+05	6.68E+02	2.78E+05
Q8WZ42-8 TITIN	VSAENENEGTTPSEITVVAR	687.00	83.12	1.40E+05	5.60E+03	9.69E+02	1.84E+05	1.70E+03	9.18E+02	8.38E+02	1.65E+03	6.00E+02	3.86E+02	1.31E+05	4.50E+02	8.39E+04	1.50E+03	1.37E+05
Q8WZ42-8 TITIN	SSVLSLWSR	504.76	83.22	5.90E+02	8.64E+04	3.99E+04	1.64E+05	6.22E+04	1.38E+05	1.82E+04	1.56E+04	1.92E+04	6.22E+04	1.53E+04	3.42E+04	1.89E+04	1.62E+04	2.06E+03
Q8WZ42-8 TITIN	VGEAFALTGR	510.78	83.4	1.61E+03	3.12E+04	1.53E+04	2.66E+04	2.37E+04	1.49E+04	2.56E+04	9.74E+02	9.13E+02	1.17E+03	4.34E+05	2.11E+04	2.82E+04	1.60E+03	2.19E+04
Q8WZ42-8 TITIN	VLWSKPDITDLR	665.36	83.47	4.57E+03	2.93E+03	8.68E+03	4.37E+02	1.33E+03	6.25E+03	4.80E+04	7.46E+04	3.94E+02	3.71E+02	5.84E+03	9.28E+04	1.07E+03	3.11E+03	1.20E+03
Q8WZ42-8 TITIN	TWVLATDR	481.25	83.52	1.19E+04	4.67E+05	1.17E+04	6.45E+04	1.40E+05	2.49E+04	1.42E+04	6.51E+03	7.78E+03	4.11E+02	1.39E+04	8.69E+04	1.44E+05	2.44E+04	2.99E+05
Q8WZ42-8 TITIN	VPLIEGNEYR	623.82	83.53	6.01E+05	2.87E+03	2.83E+04	7.76E+05	2.07E+04	1.52E+03	1.12E+03	2.30E+03	7.91E+02	8.14E+03	5.98E+05	6.61E+03	2.56E+05	7.22E+02	6.91E+05
Q8WZ42-8 TITIN	EDLQKPVLDLK	649.37	83.53	6.50E+04	8.63E+03	1.19E+03	3.35E+04	1.85E+04	7.06E+02	2.13E+03	6.29E+02	1.98E+03	2.19E+03	4.46E+04	7.96E+03	2.65E+03	1.15E+03	2.25E+03
Q8WZ42-8 TITIN	HDSVSLTWTDPK	693.34	83.6	7.32E+04	1.73E+05	1.15E+05	8.38E+04	1.67E+04	3.68E+03	1.07E+05	2.73E+04	2.11E+03	1.30E+04	5.12E+04	1.45E+05	7.42E+04	1.20E+03	6.13E+04
Q8WZ42-8 TITIN	QENATVQGLIQGK	628.85	83.6	1.31E+05	1.60E+03	1.17E+04	1.48E+04	9.50E+03	4.37E+03	1.87E+03	1.24E+03							

Q8WZ42-8 TITIN	EQSVLEFR	504.26	85.28	4.09E+04	1.20E+03	1.49E+04	4.63E+03	1.64E+05	2.82E+05	3.55E+03	1.70E+03	1.47E+03	3.05E+03	6.82E+02	1.04E+03	3.02E+03	1.29E+03	3.11E+05
Q8WZ42-8 TITIN	FILNVQSKPTAEVK	525.30	85.34	3.90E+03	4.01E+03	1.44E+03	9.39E+02	3.62E+03	1.60E+03	1.77E+05	1.81E+05	4.18E+02	2.80E+03	2.33E+03	1.33E+03	1.99E+03	3.30E+02	1.05E+03
Q8WZ42-8 TITIN	NAADSVSEPESTGPIIVK	634.32	85.34	2.31E+03	8.01E+02	4.18E+03	7.64E+04	6.04E+03	7.46E+02	2.23E+03	9.34E+03	2.24E+03	2.26E+03	1.84E+04	2.53E+03	4.33E+04	8.75E+03	7.85E+04
Q8WZ42-8 TITIN	PPGTPDYIDVTR	665.84	85.36	2.25E+03	7.61E+04	1.36E+05	1.74E+04	4.18E+03	5.31E+04	2.88E+04	1.14E+03	3.18E+02	1.17E+04	1.18E+04	8.20E+04	4.79E+04	2.73E+03	2.69E+04
Q8WZ42-8 TITIN	DPCDPPGQPEVTNITR	869.91	85.51	8.30E+04	2.76E+03	6.49E+02	3.63E+04	8.62E+04	2.68E+03	2.71E+02	6.41E+02	8.92E+02	6.59E+02	7.50E+04	5.44E+03	6.42E+03	3.58E+03	9.12E+04
Q8WZ42-8 TITIN	LLEGHEYVFR	421.56	85.61	1.35E+03	7.02E+03	5.17E+02	2.77E+04	1.76E+04	1.44E+04	4.65E+03	3.64E+03	1.01E+03	5.23E+02	2.19E+05	5.84E+03	1.21E+05	6.33E+02	9.10E+03
Q8WZ42-8 TITIN	LSQDDLEIVRPAR	504.61	85.62	2.29E+05	2.47E+03	1.29E+03	3.65E+05	2.32E+05	9.10E+02	7.69E+02	3.97E+02	1.44E+03	1.22E+03	3.31E+05	1.27E+04	8.60E+04	1.04E+03	4.08E+05
Q8WZ42-8 TITIN	LSQTEPVTLIK	614.86	85.84	9.58E+04	5.18E+02	1.12E+03	3.35E+03	1.29E+03	1.10E+04	5.10E+02	6.98E+02	5.92E+03	4.87E+02	8.41E+04	2.78E+03	6.12E+03	2.55E+03	5.98E+03
Q8WZ42-8 TITIN	AEGFINLK	446.25	85.89	1.03E+04	4.19E+04	5.46E+03	1.19E+05	1.77E+05	1.96E+05	8.75E+04	9.59E+02	8.27E+02	8.23E+02	1.88E+03	9.51E+04	1.47E+03	5.98E+02	1.52E+05
Q8WZ42-8 TITIN	DPCDPPGRPEAIVTR	579.30	85.96	2.08E+05	5.57E+03	1.89E+04	3.53E+05	2.62E+05	8.71E+04	5.44E+02	1.28E+03	8.74E+03	5.30E+03	3.82E+05	2.90E+05	1.11E+05	8.08E+03	2.11E+05
Q8WZ42-8 TITIN	DPCDPPGRPEAIVTR	579.30	85.96	2.08E+05	5.57E+03	1.89E+04	3.53E+05	2.62E+05	8.71E+04	5.44E+02	1.28E+03	8.74E+03	5.30E+03	3.82E+05	2.90E+05	1.11E+05	8.08E+03	2.11E+05
Q8WZ42-8 TITIN	VEEGVVPDKEYVLR	544.96	86.05	9.19E+02	6.07E+06	2.06E+04	1.34E+07	9.61E+06	9.54E+06	2.06E+04	6.16E+03	2.55E+04	9.57E+02	6.92E+06	9.72E+06	4.76E+06	1.40E+04	1.21E+07
Q8WZ42-8 TITIN	VLDPRPGPEGPVQVTGVTS	721.39	86.06	9.13E+04	9.77E+02	3.42E+03	7.47E+04	1.85E+03	2.59E+03	1.65E+03	5.78E+02	2.18E+03	1.11E+03	9.84E+04	3.29E+03	3.37E+04	2.29E+03	4.90E+04
Q8WZ42-8 TITIN	DSLRPDHGLYMIK	515.60	86.12	9.68E+04	7.74E+03	7.60E+03	2.89E+05	1.60E+04	7.41E+02	8.03E+02	4.98E+03	6.94E+03	6.58E+02	1.42E+05	3.90E+04	2.74E+05	1.50E+03	1.20E+05
Q8WZ42-8 TITIN	DLNMVVSAAAR	538.28	86.26	9.36E+02	7.32E+02	7.26E+04	9.17E+02	2.72E+03	2.44E+03	3.63E+03	1.11E+05	2.88E+03	1.91E+03	6.52E+02	8.70E+03	6.44E+03	1.47E+03	1.08E+03
Q8WZ42-8 TITIN	STDFATLSVK	578.30	86.28	3.43E+03	2.52E+04	4.92E+03	7.00E+04	6.76E+04	2.06E+04	2.10E+03	4.62E+03	2.04E+03	4.50E+03	1.83E+03	4.89E+04	3.64E+03	2.84E+03	2.72E+03
Q8WZ42-8 TITIN	ASEASRPIMAQNPDAPGRPEVTDVTR	716.87	86.44	6.15E+02	1.18E+04	1.33E+03	1.04E+05	6.35E+04	1.90E+04	5.96E+02	9.38E+03	1.65E+04	4.91E+04	5.03E+04	2.06E+04	2.23E+05	1.25E+04	1.09E+05
Q8WZ42-8 TITIN	IEAEPIQFTK	588.32	86.69	8.55E+04	2.36E+04	4.53E+05	2.36E+05	5.24E+03	6.16E+02	1.29E+03	5.45E+06	2.63E+04	2.41E+03	1.76E+05	1.76E+04	1.25E+05	6.27E+02	1.45E+05
Q8WZ42-8 TITIN	MPVDPPGKPEVIDVTK	574.64	86.8	1.46E+05	2.60E+04	1.86E+04	3.10E+05	1.70E+05	7.14E+04	2.67E+03	3.85E+03	4.39E+03	7.28E+02	2.60E+05	1.80E+04	9.55E+04	1.68E+03	1.46E+05
Q8WZ42-8 TITIN	LFTVGIR	403.25	86.9	8.65E+03	1.51E+03	3.85E+03	1.03E+03	5.15E+05	2.78E+03	5.29E+02	1.87E+03	2.41E+05	6.78E+02	4.61E+03	6.87E+02	5.25E+03	1.32E+05	3.06E+03
Q8WZ42-8 TITIN	LVRPLHSVEVMEETAR	656.35	87.01	6.58E+02	1.07E+04	8.92E+03	2.69E+04	5.60E+04	5.02E+04	6.52E+04	2.48E+03	1.36E+03	1.61E+03	4.31E+02	2.10E+04	6.61E+04	6.37E+03	1.28E+05
Q8WZ42-8 TITIN	AVPVPTVSWHK	407.56	87.05	2.92E+04	1.13E+03	2.76E+02	7.86E+04	2.87E+03	9.84E+03	5.87E+02	1.02E+03	1.62E+03	2.51E+03	1.89E+05	7.38E+02	6.07E+04	3.40E+02	7.46E+04
Q8WZ42-8 TITIN	QLGVPVIAR	476.80	87.08	4.88E+05	1.01E+03	4.58E+03	5.48E+05	3.22E+03	4.28E+03	6.06E+03	7.57E+03	3.45E+03	3.22E+03	8.36E+05	6.96E+03	5.78E+05	7.72E+02	9.20E+05
Q8WZ42-8 TITIN	AGVGEHADVPGPPIVEEK	606.32	87.16	2.58E+05	1.70E+04	1.04E+03	3.92E+05	1.98E+05	1.77E+04	7.94E+02	1.18E+03	1.08E+04	1.30E+03	3.03E+05	7.14E+03	1.42E+05	2.13E+03	3.42E+05
Q8WZ42-8 TITIN	NSMTVVWSR	540.27	87.21	3.72E+04	2.82E+03	1.46E+04	8.91E+02	3.37E+03	2.57E+03	1.42E+03	3.33E+03	2.75E+04	4.18E+04	4.43E+04	8.44E+02	5.09E+03	2.88E+04	7.80E+04
Q8WZ42-8 TITIN	VEVEAVNITQEPR	742.39	87.34	5.61E+02	9.63E+02	5.05E+02	4.54E+03	7.61E+02	4.94E+02	7.12E+02	1.42E+04	4.16E+04	4.47E+04	1.90E+04	1.01E+03	1.76E+03	5.69E+04	7.47E+02
Q8WZ42-8 TITIN	LIEGIR	407.26	87.42	4.59E+03	1.29E+04	1.47E+03	7.13E+03	4.75E+03	5.70E+03	2.42E+03	9.60E+02	2.16E+02	2.70E+02	3.22E+05	7.59E+03	3.59E+05	2.47E+02	3.79E+05
Q8WZ42-8 TITIN	FTCEIQSAPNVR	682.83	87.44	6.24E+03	6.04E+03	9.56E+02	4.83E+04	9.13E+03	1.40E+03	4.00E+04	6.20E+03	1.43E+04	3.83E+04	3.72E+04	2.44E+03	5.21E+03	1.67E+04	5.00E+04
Q8WZ42-8 TITIN	VLDTPGPPQNLAVK	724.91	87.46	1.66E+05	1.94E+03	2.34E+03	1.67E+05	2.98E+03	7.77E+02	3.99E+02	5.81E+02	1.24E+02	8.26E+02	7.52E+04	2.04E+03	1.62E+04	9.13E+02	1.80E+05
Q8WZ42-8 TITIN	YTVTDLQAGEEYK	758.87	87.51	6.28E+02	2.12E+03	1.39E+03	1.31E+05	7.29E+03	9.31E+02	1.31E+04	5.68E+04	2.66E+03	4.07E+03	1.41E+05	3.45E+02	2.84E+04	9.09E+03	1.10E+05
Q8WZ42-8 TITIN	ATGLQEGTEYEFR	750.86	87.67	1.83E+05	3.21E+02	1.57E+03	2.27E+05	1.43E+03	1.37E+03	2.01E+03	1.92E+03	2.46E+04	3.80E+03	1.40E+05	1.12E+04	5.45E+04	3.79E+04	1.71E+05
Q8WZ42-8 TITIN	QLSVPIAK	477.80	87.77	5.50E+05	2.47E+03	1.48E+03	3.49E+05	2.38E+03	5.44E+02	8.55E+02	3.88E+03	1.41E+04	8.31E+03	1.10E+05	9.39E+02	1.92E+05	4.30E+04	2.76E+05
Q8WZ42-8 TITIN	LIPNGQYEFR	618.82	87.83	9.76E+02	5.72E+04	2.57E+04	9.54E+02	4.97E+02	6.42E+04	1.98E+03	1.09E+04	7.09E+02	6.67E+03	1.32E+03	7.25E+04	2.86E+03	4.23E+03	4.90E+03
Q8WZ42-8 TITIN	SELDFMASK	478.73	87.91	2.13E+03	2.89E+05	1.29E+04	4.11E+05	2.28E+05	1.12E+05	2.99E+03	2.59E+03	3.27E+02	2.40E+03	7.01E+02	1.19E+04	9.98E+02	2.21E+03	2.84E+05
Q8WZ42-8 TITIN	NVYSLEIR	497.27	87.96	1.05E+03	1.26E+05	2.95E+03	2.05E+05	8.87E+04	1.77E+05	2.23E+05	6.78E+04	3.90E+04	1.51E+05	2.40E+03	1.35E+05	1.23E+05	4.94E+04	2.06E+05
Q8WZ42-8 TITIN	DAHRPGWLPVSESVTR	602.98	88	3.14E+03	5.65E+02	4.67E+02	3.20E+02	2.03E+03	7.43E+02	2.87E+02	4.01E+04	9.35E+02	4.52E+02	1.59E+05	5.47E+02	7.03E+04	1.08E+03	8.32E+03
Q8WZ42-8 TITIN	AGSDLVLDAAVGGKPEPK	575.31	88.04	9.36E+06	1.56E+04	2.47E+03	1.19E+07	2.04E+05	2.82E+03	2.34E+03	3.02E+04	1.59E+05	8.27E+04	9.51E+04	1.25E+05	1.65E+04	4.04E+04	1.15E+04
Q8WZ42-8 TITIN	LRPGSGGKPPDEAPFTYQL	572.55	88.06	1.90E+03	1.42E+03	7.12E+02	1.12E+05	1.45E+04	1.43E+03	3.54E+03	1.39E+03	2.14E+03	1.12E+03	9.62E+04	7.46E+02	4.76E+02	7.39E+02	8.25E+04
Q8WZ42-8 TITIN	LIEGLVVK	435.79	88.07	6.77E+02	2.62E+03	1.11E+03	2.23E+03	1.50E+03	2.75E+03	1.10E+03	1.60E+03	1.18E+05	1.61E+05	2.61E+03	7.07E+02	2.59E+03	1.06E+05	6.48E+02
Q8WZ42-8 TITIN	AEDPVFLPSPPSKPK	536.96	88.38	7.43E+04	2.54E+03	1.10E+04	2.01E+04	5.84E+02	9.35E+02	3.09E+03	2.68E+03	3.47E+03	1.33E+03	6.70E+04	5.30E+02	8.79E+04	9.21E+03	2.81E+04
Q8WZ42-8 TITIN	NPFVVPDAPK	542.29	88.48	2.21E+05	4.67E+03	8.42E+03	4.27E+05	4.64E+04	1.37E+04	2.00E+03	2.28E+03	3.64E+03	2.93E+03	2.75E+05	1.18E+04	1.54E+05	1.75E+04	3.86E+05
Q8WZ42-8 TITIN	VTGLQEGSTYEFR	743.86	88.69	1.76E+05	4.70E+03	1.29E+04	2.51E+05	5.40E+03	3.79E+03	1.19E+03	1.45E+03	3.71E+03	5.09E+02	1.89E+05	4.83E+03	9.27E+04	2.10E+03	2.04E+05
Q8WZ42-8 TITIN	EYTLTHLPQGAEYR	559.95	89.12	1.56E+04	7.64E+03	3.99E+03	4.04E+05	3.78E+03	1.89E+04	2.40E+04	1.71E+04	3.22E+02	3.40E+03	2.43E+05	2.60E+03	8.30E+04	4.14E+02	2.65E+05
Q8WZ42-8 TITIN	VKAENEIGEPSLPSRPVVAK	573.33	89.15	2.08E+03	5.25E+04	6.64E+03	3.13E+03	1.01E+05	1.02E+05	3.42E+04	3.29E+04	6.41E+02	2.83E+04	7.23E+04	4.15E+04	1.01E+03	4.06E+04	3.26E+02
Q8WZ42-8 TITIN	DLVYTLR	440.25	89.26	1.04E+04	1.10E+03	6.39E+02	1.76E+03	8.84E+02	1.53E+03	2.90E+02	4.16E+03	2.42E+05	1.99E+05	6.44E+03	1.94E+03	7.06E+02	2.05E+05	4.60E+02
Q8WZ42-8 TITIN	LEADVSGRPPPTMEWSK	633.98	89.27	1.51E+03	5.30E+04	2.11E+04	1.81E+05	1.14E+05	1.22E+04	1.60E+04	3.97E+03	6.05E+02	5.27E+02	1.29E+05	2.30E+04	1.10E+05	3.58E+02	1.57E+05
Q8WZ42-8 TITIN	IDLVSAMK	438.74	89.38	1.56E+05	5.16E+03	4.70E+03	1.29E+04	1.22E+04	3.38E+04	3.52E+04	8.41E+03	2.51E+03	6.99E+02	1.21E+04	4.10E+04	2.08E+03	3.36E+03	1.03E+03
Q8WZ42-8 TITIN	YRPGSEPLDSEPETAR	817.39	89.4	2.19E+05	1.90E+03	6.98E+03	2.87E+05	1.33E+05	2.80E+04	7.16E+02	2.41E+03	1.80E+04	2.92E+02	2.27E+05	1.86E+03	7.70E+04	7.90E+02	2.30E+05
Q8WZ42-8 TITIN	AEWEEVTNTAVEK	753.36	89.5	2.00E+03	1.58E+03	2.00E+03	1.11E+05	5.85E+04	2.95E+03	6.75E+03	3.52E+03	1.34E+03	8.75E+02	1.16E+05	4.25E+03	2.97E+04	8.60E+02	1.28E+05
Q8WZ42-8 TITIN	IVHYVVEALEK	650.37	89.53	7.85E+02	8.15E+04	2.79E+04	2.90E+03	1										

Q8WZ42-8 TITIN	NAAHEDGGIYSLTVENPAG	710.34	90.1	1.52E+03	1.25E+04	9.15E+04	7.30E+04	1.22E+04	5.67E+03	5.15E+04	8.85E+03	3.98E+04	4.99E+04	1.12E+03	1.32E+05	1.19E+04	6.22E+04	6.60E+04
Q8WZ42-8 TITIN	INTSAFELNER	647.33	90.16	1.03E+05	7.72E+03	1.02E+04	3.23E+04	4.47E+03	8.04E+02	1.96E+04	2.98E+03	3.05E+03	1.23E+03	1.11E+05	1.25E+04	6.37E+04	5.86E+02	1.77E+05
Q8WZ42-8 TITIN	PIMAQNPVDAPGRPEVTDV TR	755.06	90.17	4.36E+03	1.08E+03	2.18E+03	7.69E+04	9.57E+03	1.90E+03	2.06E+02	1.28E+03	2.44E+03	4.14E+02	1.64E+04	2.09E+03	1.49E+04	9.21E+02	1.11E+04
Q8WZ42-8 TITIN	IADFSTNLVNK	611.33	90.19	7.73E+03	6.25E+03	6.02E+03	3.64E+05	1.15E+03	1.57E+04	1.30E+03	1.36E+03	7.34E+02	2.88E+03	2.79E+05	6.02E+03	9.48E+04	2.08E+03	3.43E+05
Q8WZ42-8 TITIN	ETVTAVTVQDLR	666.36	90.42	4.66E+05	2.34E+03	1.67E+03	7.36E+05	9.82E+05	5.59E+03	2.78E+03	3.35E+03	2.09E+04	3.58E+02	4.93E+05	6.45E+05	3.44E+05	7.74E+03	7.89E+05
Q8WZ42-8 TITIN	VTAVNEYGPGVPTDVPK	871.95	90.45	6.58E+04	2.81E+02	1.25E+03	3.88E+03	1.10E+03	8.09E+02	5.11E+02	4.24E+03	8.71E+02	8.36E+02	8.58E+03	1.13E+03	1.09E+04	4.81E+03	6.98E+02
Q8WZ42-8 TITIN	GDSGTYYDLVLENK	705.84	90.48	7.01E+02	5.74E+05	7.04E+05	2.55E+03	2.76E+03	8.79E+05	1.14E+05	2.95E+05	6.90E+02	3.04E+03	1.87E+03	5.59E+03	2.20E+03	3.97E+03	1.92E+03
Q8WZ42-8 TITIN	VIIIDKPGPPTGPIK	515.65	90.53	1.91E+03	3.63E+02	2.98E+02	1.24E+03	2.21E+03	8.81E+02	2.28E+03	5.80E+02	1.35E+05	7.71E+04	8.22E+02	8.20E+02	1.41E+03	6.77E+04	2.13E+02
Q8WZ42-8 TITIN	VTGLTEGNEYEFH	748.34	90.65	6.68E+04	1.31E+03	1.25E+03	8.26E+02	5.85E+02	7.63E+02	2.23E+03	5.73E+02	7.19E+02	9.83E+02	7.79E+03	1.12E+03	8.03E+02	8.55E+02	1.69E+03
Q8WZ42-8 TITIN	LLEGNEYTFR	621.31	90.68	1.12E+03	1.03E+03	9.92E+02	2.62E+05	8.35E+03	2.08E+03	1.64E+03	5.04E+03	2.19E+04	4.30E+04	2.13E+05	3.81E+03	1.68E+05	2.62E+03	8.24E+03
Q8WZ42-8 TITIN	LSQDDLEIVR	594.32	90.75	2.04E+05	1.32E+04	5.87E+03	3.62E+03	3.69E+03	1.22E+03	3.63E+03	3.34E+03	1.31E+04	9.28E+03	2.41E+03	2.48E+04	1.15E+04	2.30E+04	2.30E+03
Q8WZ42-8 TITIN	VTGLIENHDYEFR	531.59	90.91	2.02E+05	9.19E+04	3.39E+04	5.29E+03	5.65E+03	2.88E+04	4.02E+04	1.33E+04	5.65E+02	1.77E+03	3.98E+03	7.22E+03	3.02E+03	2.36E+03	2.89E+03
Q8WZ42-8 TITIN	VVDFLTEENK	597.31	90.91	1.39E+03	1.44E+05	1.26E+03	2.02E+05	3.48E+04	1.61E+05	2.13E+03	4.17E+04	5.93E+03	2.67E+03	1.14E+05	1.20E+03	6.45E+03	1.26E+03	7.47E+04
Q8WZ42-8 TITIN	VLDTPSPPVNLK	640.37	90.93	5.27E+04	3.09E+03	3.35E+03	5.84E+02	1.97E+03	5.73E+02	1.70E+03	3.61E+03	2.78E+03	3.30E+02	6.04E+04	1.44E+04	3.23E+04	2.12E+03	2.20E+05
Q8WZ42-8 TITIN	VNVVEATSTVVLH	700.36	90.98	4.28E+02	1.35E+04	1.46E+04	2.41E+05	4.22E+03	2.79E+04	1.04E+03	2.35E+03	1.70E+04	6.16E+02	1.37E+05	2.46E+03	4.20E+04	1.03E+04	3.32E+03
Q8WZ42-8 TITIN	DENVIVPEEIK	642.84	91.01	1.09E+03	1.95E+03	8.33E+02	4.71E+05	4.30E+03	7.83E+03	4.20E+03	3.10E+03	6.42E+02	8.45E+02	3.08E+05	3.31E+03	1.34E+05	1.20E+03	3.36E+05
Q8WZ42-8 TITIN	SSITLGWSK	489.77	91.06	4.85E+04	4.16E+03	6.22E+03	6.15E+02	3.30E+03	1.44E+03	2.20E+03	4.24E+02	3.82E+04	5.04E+04	2.70E+04	1.45E+03	6.70E+03	1.66E+03	3.06E+03
Q8WZ42-8 TITIN	VSAVNCAGQGEPIEMNEPV QAK	757.70	91.07	8.79E+02	1.87E+04	1.20E+04	5.09E+02	2.84E+03	5.36E+04	9.47E+02	1.23E+03	9.14E+02	6.45E+02	7.02E+02	5.09E+03	1.64E+03	1.01E+03	4.67E+02
Q8WZ42-8 TITIN	VLGVPVIAK	448.30	91.09	7.94E+05	1.69E+03	3.67E+03	5.29E+03	4.70E+03	4.34E+03	2.23E+03	2.51E+02	4.06E+03	3.15E+02	9.58E+05	4.70E+03	7.75E+05	9.99E+02	1.01E+04
Q8WZ42-8 TITIN	GKPFPEVAWTK	630.34	91.09	1.12E+05	7.78E+02	6.16E+02	1.58E+03	3.84E+02	8.29E+03	2.70E+02	6.21E+02	2.04E+04	1.81E+04	1.56E+04	1.41E+03	1.81E+04	5.74E+03	2.47E+03
Q8WZ42-8 TITIN	EAFSSVVIK	497.28	91.13	4.78E+03	4.73E+03	7.55E+02	4.43E+05	3.58E+05	3.32E+05	4.93E+03	9.34E+04	1.28E+04	7.80E+03	2.64E+03	2.58E+04	1.24E+04	1.90E+03	4.39E+05
Q8WZ42-8 TITIN	VPGPPGTPVVTLSSR	732.41	91.24	2.79E+03	7.53E+03	6.77E+03	6.90E+05	3.46E+05	1.90E+04	9.62E+03	6.83E+03	5.27E+02	6.91E+02	4.77E+05	1.85E+04	2.50E+05	1.18E+03	2.30E+05
Q8WZ42-8 TITIN	STITLDWKEPR	673.36	91.26	1.56E+03	1.35E+04	4.37E+04	5.22E+02	3.04E+04	9.58E+03	5.80E+04	2.39E+04	1.44E+03	1.41E+03	1.12E+03	9.82E+03	6.41E+02	3.34E+03	2.82E+04
Q8WZ42-8 TITIN	VPDAPDQPIVTEVTK	804.93	91.27	1.96E+05	2.88E+03	5.44E+03	4.32E+05	4.26E+04	7.20E+03	1.73E+03	1.01E+04	7.91E+02	2.70E+02	3.43E+05	1.59E+04	5.37E+04	2.12E+03	3.81E+05
Q8WZ42-8 TITIN	NAAGVFSEPESTGAITAR	932.96	91.47	3.09E+03	3.20E+03	4.58E+02	2.02E+05	1.48E+05	1.77E+03	3.02E+02	8.79E+02	3.17E+03	3.13E+02	1.36E+05	7.91E+03	1.32E+05	2.19E+03	2.02E+05
Q8WZ42-8 TITIN	TPSPDYDFYRPR	559.60	91.59	2.55E+03	5.13E+03	1.82E+04	1.68E+05	1.52E+05	7.65E+03	6.21E+03	4.52E+03	1.41E+03	2.30E+03	4.34E+03	7.06E+03	6.69E+04	1.17E+03	1.94E+05
Q8WZ42-8 TITIN	YGVGEPELESEPVVAK	787.41	91.63	3.88E+04	1.07E+04	5.95E+02	3.39E+04	1.82E+05	2.19E+03	2.27E+03	1.49E+04	2.48E+03	1.75E+03	1.27E+05	4.38E+03	1.30E+05	7.29E+02	1.37E+04
Q8WZ42-8 TITIN	VLDTPGPPVNVTVK	718.41	91.68	1.37E+03	1.23E+04	1.45E+04	5.20E+04	2.61E+04	3.46E+04	1.01E+04	3.85E+04	2.90E+03	4.96E+02	4.63E+04	6.23E+03	3.82E+04	1.73E+02	2.39E+04
Q8WZ42-8 TITIN	IDVTPVGSKLEIR	476.27	91.71	4.20E+03	1.65E+03	8.16E+03	6.97E+03	1.35E+04	1.49E+04	8.78E+04	5.11E+03	1.28E+03	2.04E+03	9.66E+04	5.75E+03	1.25E+05	1.11E+03	3.85E+03
Q8WZ42-8 TITIN	FGISEPLTSPK	588.32	91.75	5.96E+05	3.06E+04	1.51E+04	9.43E+05	2.11E+04	2.28E+04	3.76E+04	2.54E+03	5.06E+02	7.53E+02	6.91E+02	9.24E+03	5.65E+05	7.75E+03	8.07E+05
Q8WZ42-8 TITIN	VMAENEYGIGEPTEPTEPV	1097.52	91.75	4.43E+04	9.09E+02	2.81E+03	2.27E+03	2.55E+02	4.56E+02	9.81E+02	2.33E+03	6.66E+02	5.22E+02	9.29E+02	2.55E+03	1.26E+03	6.20E+02	4.71E+03
Q8WZ42-8 TITIN	VFAENEYGIGDPGETR	877.41	91.96	2.33E+05	4.12E+03	3.35E+03	4.17E+05	2.11E+05	1.72E+03	6.92E+03	1.47E+03	6.57E+02	2.05E+03	2.70E+05	8.22E+03	2.20E+05	1.57E+03	3.02E+05
Q8WZ42-8 TITIN	VTGYLIEMQK	591.31	92.11	1.59E+03	1.01E+05	7.85E+03	7.48E+03	3.77E+04	1.35E+03	7.60E+03	3.62E+03	1.17E+04	2.97E+03	1.35E+05	2.11E+05	1.29E+04	2.33E+03	8.59E+03
Q8WZ42-8 TITIN	AAWYTIDSR	541.77	92.21	2.74E+03	1.02E+03	9.36E+03	2.00E+05	5.87E+04	2.28E+03	1.57E+03	1.98E+03	1.70E+04	3.50E+03	9.71E+02	7.28E+02	9.49E+04	1.92E+04	2.15E+05
Q8WZ42-8 TITIN	SPPHFELSSLR	423.89	92.22	6.34E+02	5.87E+02	5.68E+03	2.60E+04	2.34E+03	4.34E+03	8.52E+02	6.51E+02	3.75E+02	3.28E+02	3.26E+05	7.37E+03	1.77E+05	8.95E+02	1.50E+04
Q8WZ42-8 TITIN	LLEKPPDIPDSR	460.59	92.25	8.84E+03	6.87E+03	1.52E+03	1.24E+05	6.32E+02	1.94E+03	2.74E+02	8.36E+02	1.53E+03	8.72E+02	2.33E+04	1.48E+04	1.65E+04	1.44E+03	5.96E+04
Q8WZ42-8 TITIN	FPLALEEK	473.77	92.41	4.10E+05	1.42E+05	1.64E+04	2.48E+05	6.15E+04	1.77E+04	3.09E+05	3.11E+03	2.75E+03	1.03E+03	1.77E+05	6.20E+04	3.49E+05	6.40E+02	3.00E+05
Q8WZ42-8 TITIN	YGPVPESEPIVAR	785.42	92.59	3.76E+03	2.28E+03	4.71E+03	3.93E+05	9.55E+03	4.31E+03	3.90E+03	1.32E+03	1.30E+04	4.02E+03	3.11E+05	7.88E+03	2.73E+05	7.11E+03	3.32E+05
Q8WZ42-8 TITIN	AYTLEEEAVSVQR	747.87	92.94	1.69E+03	1.10E+03	6.98E+02	6.17E+03	2.59E+03	3.35E+03	2.90E+02	2.84E+03	8.28E+02	8.58E+02	5.49E+04	2.50E+03	1.30E+03	7.48E+03	5.30E+03
Q8WZ42-8 TITIN	SNGGSPIQGYIIEK	731.88	93.16	9.92E+03	1.14E+03	7.54E+02	4.31E+03	3.67E+02	1.02E+03	1.56E+03	1.18E+03	1.20E+03	1.78E+03	8.88E+04	2.10E+03	1.20E+04	2.40E+03	2.73E+02
Q8WZ42-8 TITIN	SVFPELTR	474.76	93.4	4.40E+05	5.97E+04	8.83E+04	5.51E+04	1.46E+05	1.36E+05	2.95E+04	4.86E+04	2.75E+04	4.05E+03	8.26E+04	2.37E+04	4.31E+04	6.97E+04	7.56E+04
Q8WZ42-8 TITIN	DPIEPPGPPTNFR	718.86	93.42	4.17E+04	3.64E+03	5.68E+03	4.12E+04	1.95E+05	5.97E+04	2.32E+03	1.05E+03	1.22E+03	2.86E+03	6.14E+04	8.80E+03	1.79E+04	5.05E+03	5.49E+04
Q8WZ42-8 TITIN	ADSSSILIIK	523.81	93.5	5.52E+03	1.67E+04	4.43E+03	8.62E+04	3.99E+04	2.76E+02	2.73E+03	1.72E+03	3.66E+02	8.42E+02	7.63E+03	1.40E+03	9.34E+04	3.11E+03	8.27E+04
Q8WZ42-8 TITIN	FVMTIENPAGK	603.81	93.52	1.96E+05	6.09E+02	3.62E+03	2.26E+04	5.88E+03	2.07E+02	5.03E+03	1.32E+03	2.35E+03	2.54E+03	1.33E+05	3.53E+03	4.40E+04	1.89E+03	9.15E+04
Q8WZ42-8 TITIN	DPCDPPGTPEPIMVK	798.38	93.64	2.42E+04	7.08E+02	4.20E+03	3.12E+04	2.45E+04	4.54E+02	8.94E+03	1.34E+04	1.37E+03	2.49E+03	2.52E+04	9.71E+03	8.92E+03	2.59E+03	4.28E+04
Q8WZ42-8 TITIN	LLEGNEYVFR	620.30	93.65	1.04E+04	1.09E+05	1.35E+04	3.01E+04	1.43E+03	8.45E+02	3.47E+05	1.27E+05	1.03E+03	5.36E+03	3.46E+03	2.98E+05	2.80E+03	2.76E+03	1.41E+04
Q8WZ42-8 TITIN	SDGGSPITGYMYMER	766.84	93.69	7.01E+02	5.19E+03	8.03E+02	1.23E+03	3.64E+03	6.59E+03	6.08E+03	1.98E+03	7.34E+04	6.93E+04	5.43E+02	6.83E+04	5.71E+02	7.56E+04	8.04E+03
Q8WZ42-8 TITIN	LVVEELPVR	527.32	93.95	5.24E+05	9.92E+02	1.10E+03	1.29E+04	1.90E+03	6.12E+03	6.32E+02	2.55E+02	8.98E+03	1.93E+03	7.07E+05	4.64E+03	6.36E+05	8.45E+03	3.73E+04
Q8WZ42-8 TITIN	DSMVVTWAR	532.76	94.06	1.23E+05	1.80E+05	1.37E+03	1.32E+05	4.52E+04	1.50E+04	7.72E+03	2.24E+03	7.56E+02	1.35E+03	1.74E+04	1.53E+05	6.70E+03	3.45E+03	2.18E+05
Q8WZ42-8 TITIN	EDEELLRPVTTTQHLSEYK	763.39	94.11	2.18E+03	1.35E+03	3.41E+03	1.14E+05											



Q8WZ42-8 TITIN	VFAENLAGLSK	574.82	94.81	7.20E+03	4.83E+04	4.94E+03	3.63E+05	5.02E+04	2.90E+03	1.04E+05	1.44E+04	7.63E+04	2.79E+04	2.75E+05	2.93E+05	2.25E+05	1.28E+05	2.08E+05
Q8WZ42-8 TITIN	AIGVSEPSEISENVVAK	864.95	94.81	3.64E+02	2.96E+03	9.51E+02	1.32E+05	1.93E+03	2.67E+03	3.63E+03	4.83E+03	1.69E+03	6.37E+02	9.78E+04	4.30E+03	6.89E+03	2.24E+02	8.35E+04
Q8WZ42-8 TITIN	NSLLWVK	430.26	94.94	1.56E+03	1.28E+04	2.25E+04	1.85E+04	1.33E+05	3.05E+04	8.37E+03	4.04E+03	6.46E+02	2.42E+02	2.19E+03	1.76E+04	3.68E+03	7.23E+02	1.71E+05
Q8WZ42-8 TITIN	NSILWVK	430.26	94.94	1.56E+03	1.28E+04	2.25E+04	1.85E+04	1.33E+05	3.05E+04	8.37E+03	4.04E+03	6.46E+02	2.42E+02	2.19E+03	1.76E+04	3.68E+03	7.23E+02	1.71E+05
Q8WZ42-8 TITIN	VLD R PGPPEGPVVISGVTAE	706.39	95.07	1.68E+06	1.52E+05	1.45E+05	6.31E+04	3.90E+04	4.76E+04	3.55E+04	1.59E+04	9.50E+03	2.71E+04	1.88E+04	2.78E+05	1.71E+04	1.61E+04	8.73E+04
Q8WZ42-8 TITIN	VQNL LPDHEYQFR	553.61	95.54	8.57E+02	8.78E+02	2.36E+04	2.87E+04	1.50E+05	9.89E+03	3.45E+04	2.69E+04	1.16E+03	5.61E+02	3.05E+03	1.86E+03	2.75E+04	1.18E+03	2.10E+05
Q8WZ42-8 TITIN	DPIAPPGPPFPK	616.84	95.59	6.49E+04	5.79E+04	7.58E+03	2.33E+05	1.80E+05	3.44E+03	3.06E+03	2.23E+03	1.46E+03	1.20E+03	2.03E+05	4.15E+04	8.35E+04	2.69E+03	7.63E+04
Q8WZ42-8 TITIN	VSGENEFVGVIPAETK	817.41	95.67	2.38E+03	1.71E+03	5.06E+02	2.10E+05	1.28E+05	2.92E+02	2.73E+03	5.75E+04	1.58E+03	2.71E+03	1.54E+05	1.71E+03	1.53E+04	1.26E+03	1.90E+05
Q8WZ42-8 TITIN	EPGPPGTPFATAISK	735.39	95.69	8.90E+04	2.26E+03	6.77E+02	1.20E+05	1.21E+04	4.75E+03	1.36E+04	5.81E+02	7.71E+03	1.98E+03	1.02E+04	1.58E+03	1.66E+04	1.35E+03	3.24E+04
Q8WZ42-8 TITIN	NGILWQTVSK	573.32	95.75	4.23E+03	1.95E+05	1.68E+05	1.96E+04	1.69E+05	5.22E+05	4.15E+04	8.80E+02	2.06E+03	1.43E+03	7.25E+03	5.81E+04	2.56E+03	2.53E+02	6.69E+04
Q8WZ42-8 TITIN	DSGAYTLTATNPGGFAK	835.91	95.77	1.09E+05	1.56E+03	1.12E+03	1.40E+05	5.75E+02	2.03E+03	1.21E+03	2.00E+03	3.10E+04	1.29E+03	1.07E+05	7.33E+03	7.23E+03	1.83E+03	1.78E+05
Q8WZ42-8 TITIN	DTIVVNAGETFR	661.34	95.8	8.47E+02	1.80E+03	9.74E+02	1.06E+04	1.01E+03	8.19E+03	6.67E+03	1.25E+04	8.68E+03	4.38E+03	4.12E+03	3.30E+03	2.08E+04	2.80E+04	4.74E+04
Q8WZ42-8 TITIN	ELSDAPAFISQPR	715.87	95.84	1.19E+05	2.37E+04	1.22E+04	1.12E+05	1.93E+04	2.75E+04	3.85E+04	1.42E+04	1.99E+04	5.48E+03	3.13E+05	7.31E+04	2.27E+04	1.23E+04	3.12E+05
Q8WZ42-8 TITIN	AENEIGIGEPSLPSRPVAK	688.38	95.96	4.06E+02	2.78E+02	6.60E+02	7.19E+04	1.14E+04	5.13E+03	2.40E+02	6.62E+03	2.93E+02	7.52E+02	5.02E+04	3.46E+03	1.09E+05	6.66E+02	5.46E+04
Q8WZ42-8 TITIN	DVWMPVTSASAK	646.32	96.04	2.30E+04	9.03E+03	2.46E+03	8.47E+03	3.71E+04	5.77E+03	7.54E+02	4.66E+03	2.79E+04	1.01E+04	9.17E+02	1.61E+04	4.01E+03	1.01E+05	1.69E+04
Q8WZ42-8 TITIN	EPITVPERPEDEVK	584.31	96.11	1.63E+03	9.26E+03	1.49E+03	1.91E+03	1.04E+04	2.99E+03	1.01E+03	7.41E+02	1.99E+05	1.66E+05	1.65E+03	1.77E+04	3.72E+03	2.90E+05	2.30E+03
Q8WZ42-8 TITIN	AWTPVTTYTVTR	647.84	96.28	7.35E+02	2.43E+04	1.77E+04	4.35E+04	1.49E+04	6.21E+04	1.29E+04	1.10E+04	4.95E+03	8.02E+02	2.54E+03	8.98E+03	4.78E+04	8.00E+02	3.27E+05
Q8WZ42-8 TITIN	GTQEITGDDRFELIK	574.63	96.72	9.51E+02	2.05E+03	3.24E+03	2.20E+04	3.19E+03	8.72E+03	2.73E+03	8.73E+03	9.29E+02	8.05E+02	4.01E+04	1.91E+03	2.51E+03	3.73E+03	5.51E+04
Q8WZ42-8 TITIN	VLGYVVEMQPK	631.84	96.72	2.95E+03	1.14E+04	7.30E+03	3.14E+05	1.88E+04	1.82E+04	1.24E+03	1.16E+03	1.36E+03	6.71E+02	2.07E+05	1.90E+02	2.87E+04	5.26E+03	3.35E+04
Q8WZ42-8 TITIN	VEIPVLGR	441.77	96.8	4.88E+03	7.56E+04	2.01E+05	1.76E+05	7.19E+04	2.89E+05	8.38E+04	1.41E+05	2.89E+04	1.02E+04	1.50E+04	2.04E+05	1.33E+04	2.25E+04	1.38E+05
Q8WZ42-8 TITIN	VSAENEIGIGDPSPPSKPVFA	747.06	96.84	3.67E+04	2.53E+03	1.21E+03	2.21E+05	4.60E+03	3.32E+02	1.01E+03	4.54E+02	1.11E+03	1.16E+03	8.28E+04	2.71E+03	2.08E+03	1.48E+03	1.22E+04
Q8WZ42-8 TITIN	GWSIVASDVTK	581.31	96.88	2.71E+03	1.88E+06	1.00E+06	1.05E+06	8.27E+06	1.21E+06	1.10E+07	1.20E+05	1.03E+04	3.47E+03	4.84E+05	4.15E+06	6.24E+05	4.26E+04	5.40E+05
Q8WZ42-8 TITIN	LTTGLE YQFR	614.32	97.15	1.11E+04	3.41E+04	5.98E+04	2.58E+05	1.24E+04	5.40E+03	2.11E+04	1.37E+05	5.56E+03	1.33E+04	4.15E+03	3.07E+04	4.42E+04	6.67E+02	1.51E+05
Q8WZ42-8 TITIN	ESLLSGIPEEQR	679.35	97.19	1.07E+03	5.71E+04	7.97E+02	1.43E+05	5.32E+04	1.60E+03	2.27E+03	3.04E+04	7.42E+02	8.84E+02	1.43E+05	2.20E+04	1.74E+04	1.26E+03	6.75E+04
Q8WZ42-8 TITIN	DSVNL TWEPASDGGSK	882.41	97.29	1.91E+03	1.44E+04	3.56E+03	8.65E+04	1.04E+04	1.96E+04	2.07E+03	2.47E+03	9.39E+02	1.05E+03	5.44E+04	1.92E+04	1.44E+04	5.19E+02	1.04E+04
Q8WZ42-8 TITIN	YGIGEPLESDSV VAK	782.40	97.31	9.08E+03	7.33E+03	1.47E+03	1.06E+05	2.48E+03	2.66E+03	1.81E+03	2.92E+03	3.07E+03	2.49E+03	5.98E+04	3.67E+03	4.09E+04	4.54E+03	2.56E+04
Q8WZ42-8 TITIN	YSLTLVNPAGEK	646.35	97.44	7.60E+04	3.39E+04	2.76E+04	2.71E+05	3.63E+03	7.76E+02	1.58E+05	1.05E+05	3.21E+03	9.96E+02	1.61E+05	4.25E+03	2.77E+04	1.98E+03	2.42E+04
Q8WZ42-8 TITIN	TIPSPPGIPEEVGTGK	789.92	97.68	8.74E+04	2.35E+04	4.48E+03	9.92E+03	3.16E+03	2.50E+03	6.89E+02	1.35E+03	2.89E+03	3.73E+02	4.45E+04	1.76E+03	1.27E+03	4.78E+03	2.31E+04
Q8WZ42-8 TITIN	VTGLYEGNTYEF R	774.87	98.12	3.31E+03	1.32E+04	1.36E+04	2.03E+05	1.34E+04	1.45E+04	5.28E+04	4.19E+04	3.70E+03	1.10E+03	1.18E+05	5.84E+03	4.60E+03	6.72E+03	1.08E+03
Q8WZ42-8 TITIN	DDVVAPDLDLK	600.31	98.15	2.32E+05	8.37E+03	2.71E+03	4.41E+05	1.92E+03	5.18E+03	1.09E+04	3.89E+03	5.69E+03	3.32E+02	2.66E+05	5.38E+03	2.30E+04	2.14E+03	5.57E+03
Q8WZ42-8 TITIN	VMAINLAGVGK	536.81	98.2	1.04E+04	2.04E+05	2.25E+04	7.92E+03	6.16E+04	1.83E+05	6.69E+04	1.39E+04	1.15E+03	2.45E+03	1.24E+04	7.33E+04	1.46E+04	1.21E+03	1.34E+03
Q8WZ42-8 TITIN	NTVTLTWNPPK	635.84	98.24	3.33E+04	3.68E+03	2.09E+04	2.95E+03	2.79E+04	2.38E+04	1.38E+03	8.62E+03	5.26E+03	6.77E+02	3.06E+04	2.50E+04	2.07E+03	1.47E+04	1.87E+03
Q8WZ42-8 TITIN	TGGSPITGYHLEFK	502.93	98.35	6.70E+02	9.84E+02	6.81E+03	8.44E+02	2.80E+04	7.06E+03	2.10E+03	1.20E+03	9.69E+03	6.62E+03	1.85E+05	1.43E+04	2.73E+03	1.92E+03	4.23E+03
Q8WZ42-8 TITIN	NAVGTISPPSQSSGI MTR	639.34	98.38	2.53E+04	6.26E+02	2.13E+03	9.11E+04	2.76E+02	8.37E+02	3.32E+02	2.10E+03	3.26E+03	5.93E+02	5.33E+04	2.57E+03	2.21E+02	1.13E+03	2.64E+04
Q8WZ42-8 TITIN	VAAENAAGVGEPSEPSV FY	684.00	98.58	1.90E+05	7.01E+02	9.49E+02	3.00E+05	6.61E+03	1.21E+03	4.89E+02	5.51E+03	8.81E+03	2.00E+03	2.29E+05	3.84E+03	7.91E+03	1.99E+02	1.35E+05
Q8WZ42-8 TITIN	EPGPPGTPFVTSISK	757.40	98.71	1.46E+04	1.22E+04	5.29E+03	5.99E+04	3.91E+04	3.08E+03	2.43E+03	1.29E+03	1.24E+05	5.27E+04	3.97E+04	3.95E+04	2.39E+04	4.03E+04	8.49E+04
Q8WZ42-8 TITIN	GGVEYLFR	470.75	98.9	6.85E+03	4.59E+05	7.89E+04	5.08E+05	6.27E+05	4.48E+05	2.82E+04	1.12E+04	7.60E+02	1.46E+03	1.34E+03	5.29E+05	1.92E+02	1.57E+03	4.54E+05
Q8WZ42-8 TITIN	VLD R PGPPEGLAVTEVTSE	731.06	98.97	5.82E+03	6.29E+02	1.18E+03	9.19E+04	1.14E+03	5.89E+02	1.53E+03	1.40E+03	9.46E+02	1.78E+02	9.39E+04	1.36E+03	1.20E+04	4.10E+02	3.25E+03
Q8WZ42-8 TITIN	LVPPSVELDVK	598.35	99.1	1.98E+03	1.13E+04	2.12E+03	1.72E+05	3.98E+02	4.76E+03	1.26E+03	1.99E+02	8.68E+02	1.08E+03	1.10E+03	1.25E+04	2.28E+04	4.84E+03	6.84E+04
Q8WZ42-8 TITIN	GTAIFACDI AK	555.28	99.15	5.03E+03	6.68E+04	3.66E+04	7.24E+04	5.34E+04	8.41E+04	3.73E+04	2.23E+04	1.32E+03	9.13E+02	1.01E+04	3.76E+04	4.42E+03	1.54E+04	9.73E+04
Q8WZ42-8 TITIN	VTAVNAAGNSEPSEASN FIS CR	742.02	99.22	7.04E+04	6.82E+03	1.83E+02	1.05E+05	9.73E+03	9.44E+02	5.81E+03	5.20E+03	7.29E+02	3.76E+02	7.82E+04	1.43E+03	7.05E+03	1.34E+03	4.21E+03
Q8WZ42-8 TITIN	LIQONEYIFR	626.84	99.24	9.43E+02	2.41E+03	1.33E+04	1.88E+05	3.13E+03	3.87E+03	4.64E+03	2.24E+03	3.47E+03	1.88E+03	8.68E+02	5.17E+03	3.39E+04	4.28E+03	9.86E+04
Q8WZ42-8 TITIN	STITLDWK	482.26	99.36	1.25E+03	5.83E+02	9.32E+02	5.92E+02	1.18E+04	5.29E+03	4.30E+02	5.92E+03	2.05E+05	2.57E+04	2.54E+03	9.18E+03	1.92E+05	9.07E+03	9.07E+03
Q8WZ42-8 TITIN	DVASAQWSPLSATSK	774.39	99.4	1.78E+05	5.55E+04	5.45E+03	1.68E+05	3.42E+04	1.49E+04	3.00E+05	1.32E+06	1.16E+03	5.13E+04	1.81E+05	6.20E+03	2.14E+04	2.49E+03	2.19E+03
Q8WZ42-8 TITIN	ALES DPIVAQYPYK	797.41	99.45	9.47E+04	2.71E+03	5.34E+02	9.39E+04	1.45E+03	2.10E+03	3.03E+03	1.64E+03	2.13E+03	5.79E+02	8.80E+04	1.27E+03	1.69E+03	1.48E+03	8.11E+03
Q8WZ42-8 TITIN	SSAVLAWLKP DHDGGS R	599.31	99.71	1.28E+03	5.33E+02	4.68E+04	4.16E+03	4.80E+03	8.99E+03	4.34E+03	2.36E+04	2.33E+04	2.27E+04	2.74E+02	5.04E+03	1.31E+03	1.23E+03	2.46E+03
Q8WZ42-8 TITIN	GEALLQTPDCEIK	708.86	99.8	8.22E+04	1.07E+03	1.88E+03	1.74E+04	1.36E+03	7.48E+02	3.62E+02	2.52E+03	2.00E+03	7.85E+03	2.04E+03	2.11E+03	8.38E+02	1.69E+04	1.23E+03
Q8WZ42-8 TITIN	VAAENMYGVGEPVQAS P I T AK	711.36	99.84	9.18E+02	2.41E+03	5.07E+03	1.27E+05	1.47E+04	1.37E+03	4.25E+02	2.27E+04	3.48E+02	1.43E+03	9.59E+04	7.81E+02	6.39E+02	4.36E+03	1.53E+05
Q8WZ42-8 TITIN	ATSYTITGLTENQEYK	909.94	99.99	2.93E+02	8.06E+02	3.00E+03	2.35E+02	1.54E+03	3.31E+03	8.70E+02	6.45E+02	1.35E+04	5.01E+04	7.06E+02	8.11E+02	1.03E+03	1.40E+04	1.14E+03
Q8WZ42-8 TITIN	DGGSPITNYIVEK	696.86	100.04	7.44E+04	1.02E+05	1.38E+04</												

Q8WZ42-8 TITIN	VLAENEIGGPCETTEPVK	1064.53	101.09	1.94E+03	1.20E+03	1.28E+04	2.13E+03	1.59E+03	2.74E+04	1.42E+04	9.99E+03	1.65E+02	2.53E+02	1.24E+02	7.75E+02	1.02E+03	1.67E+02	2.48E+03
Q8WZ42-8 TITIN	ILGYIVEYQK	613.34	101.23	1.13E+04	1.20E+04	1.27E+03	1.13E+04	2.61E+03	2.47E+03	9.29E+02	1.88E+03	4.99E+02	4.10E+03	1.73E+05	2.91E+02	1.55E+05	1.44E+03	3.14E+04
Q8WZ42-8 TITIN	ADAGIYTITLENK	704.87	101.23	1.14E+05	1.42E+04	1.25E+03	1.73E+04	1.77E+04	3.76E+03	5.64E+02	1.44E+03	2.97E+03	2.41E+03	1.03E+05	3.57E+03	4.53E+03	2.05E+03	2.28E+04
Q8WZ42-8 TITIN	YILTIENGVGEPK	716.89	101.59	9.25E+04	4.40E+03	5.88E+03	3.42E+05	4.33E+03	1.79E+03	1.54E+03	1.04E+03	1.01E+03	1.52E+03	2.61E+05	5.09E+03	2.85E+04	7.06E+02	1.28E+04
Q8WZ42-8 TITIN	VPEIKPAIPLPAPEPK	566.01	101.61	1.80E+05	2.08E+03	2.72E+02	1.09E+04	6.64E+02	3.96E+03	2.37E+03	4.80E+03	4.38E+02	1.22E+03	2.67E+05	1.24E+03	2.16E+03	4.22E+02	2.59E+03
Q8WZ42-8 TITIN	MTASEALQHPWLK	504.59	101.67	1.47E+03	1.40E+04	6.33E+03	3.68E+05	5.48E+03	2.55E+04	3.77E+02	3.73E+03	1.11E+03	1.07E+03	1.24E+05	3.34E+03	4.23E+04	5.79E+02	4.01E+05
Q8WZ42-8 TITIN	LIEGNEYIFR	627.33	101.69	2.32E+03	4.39E+03	3.26E+05	3.33E+04	2.12E+05	4.21E+05	9.56E+04	2.43E+03	3.64E+03	3.09E+03	7.76E+03	2.65E+05	6.22E+03	1.98E+03	1.30E+04
Q8WZ42-8 TITIN	VLAVNAAGESDPAHVPEPV LVK	738.07	101.74	4.02E+05	2.71E+03	3.94E+03	6.03E+05	1.02E+04	3.63E+03	5.44E+02	2.60E+03	6.12E+02	3.87E+02	5.02E+05	5.06E+05	1.78E+05	2.25E+02	5.04E+05
Q8WZ42-8 TITIN	VQILDKPGPPGGPIEFK	598.00	101.75	5.04E+04	1.17E+03	2.02E+03	7.41E+04	4.10E+03	5.89E+02	1.83E+02	1.87E+03	3.48E+03	5.14E+02	1.06E+05	1.34E+03	1.12E+04	1.76E+03	1.93E+02
Q8WZ42-8 TITIN	VTGLIEGSDYQFR	742.87	101.79	4.06E+02	2.75E+03	2.85E+04	2.81E+05	1.31E+03	2.04E+03	1.08E+04	6.74E+02	8.30E+02	3.20E+02	2.03E+05	1.38E+03	5.49E+03	1.39E+03	1.24E+04
Q8WZ42-8 TITIN	LTVIEPAWER	607.33	101.85	1.24E+05	6.68E+04	9.63E+03	7.94E+04	8.33E+05	1.70E+05	5.81E+03	3.24E+02	1.46E+04	1.79E+03	1.30E+05	2.49E+05	1.25E+04	1.65E+03	3.73E+05
Q8WZ42-8 TITIN	FDEVTAEAMTLK	677.83	101.96	6.49E+04	1.14E+03	2.51E+04	2.81E+04	3.77E+03	1.24E+04	1.06E+04	1.30E+04	7.48E+02	3.94E+02	1.15E+04	5.39E+02	4.94E+02	7.82E+03	2.45E+03
Q8WZ42-8 TITIN	AVNAIGVSEPSEISENVVAK	671.69	102.03	5.04E+04	6.10E+02	2.56E+03	7.07E+04	5.76E+02	1.35E+03	2.51E+03	7.17E+02	4.62E+03	1.74E+03	6.42E+04	6.47E+03	4.36E+03	1.58E+03	1.07E+04
Q8WZ42-8 TITIN	TAFVNVRLDSPSAPVNLTI	756.42	102.15	1.15E+04	1.66E+03	3.78E+03	7.67E+03	8.23E+03	8.75E+02	1.09E+03	1.01E+03	1.55E+03	1.20E+03	8.42E+04	6.35E+04	9.18E+04	6.90E+03	2.72E+02
Q8WZ42-8 TITIN	TVELDVADVPDPPR	761.89	102.23	7.65E+04	5.77E+04	2.26E+04	1.61E+05	1.04E+04	9.02E+04	1.35E+03	2.19E+04	1.83E+03	5.54E+03	4.70E+04	5.55E+04	1.58E+05	2.43E+02	6.34E+04
Q8WZ42-8 TITIN	VPPELPEKPAPEEVAPVPIPK	712.73	102.33	3.24E+02	1.26E+05	5.12E+04	5.73E+03	2.46E+05	7.70E+03	7.73E+03	7.78E+03	8.11E+02	9.87E+02	2.57E+03	8.25E+03	9.23E+02	2.76E+02	2.40E+05
Q8WZ42-8 TITIN	VLDSPSAPVNLTI	741.42	102.35	2.48E+03	7.16E+02	9.40E+02	2.50E+05	1.46E+04	8.61E+02	5.73E+02	2.14E+03	3.19E+04	5.23E+03	4.28E+05	3.96E+03	2.68E+05	1.17E+05	3.05E+03
Q8WZ42-8 TITIN	SITGYFLEK	529.28	102.61	7.77E+02	5.44E+03	1.55E+04	4.52E+03	1.80E+04	1.10E+05	1.51E+04	4.52E+03	1.34E+03	4.04E+02	1.77E+03	1.95E+02	1.42E+03	8.10E+02	1.10E+03
Q8WZ42-8 TITIN	NLFSVPGAPDKPTVSSVTR	658.02	102.75	2.64E+05	9.23E+03	4.37E+02	4.87E+05	8.23E+03	4.40E+03	1.03E+03	1.38E+03	6.47E+02	6.33E+02	3.43E+05	2.57E+03	1.13E+05	6.98E+02	1.81E+04
Q8WZ42-8 TITIN	IPFSGKPDVITWQK	571.65	102.78	7.23E+02	9.47E+03	6.57E+03	2.02E+03	5.76E+04	6.65E+04	1.06E+04	8.21E+03	1.58E+03	4.76E+02	3.84E+02	8.67E+03	3.21E+02	2.20E+03	1.96E+04
Q8WZ42-8 TITIN	VLDKPGPPAGPLEINGLTAE	706.39	102.78	1.07E+03	6.68E+03	2.80E+04	7.02E+02	2.17E+03	6.51E+03	2.22E+03	5.39E+05	8.72E+02	2.86E+02	9.13E+02	3.64E+03	1.01E+04	1.52E+03	6.59E+02
Q8WZ42-8 TITIN	KIPEPTKVPEIKPAIPLPAPEP K	623.12	102.8	3.68E+03	9.16E+02	2.00E+03	3.41E+03	8.22E+03	2.58E+03	1.77E+03	8.99E+03	3.97E+04	1.78E+03	2.92E+03	2.62E+04	2.36E+03	1.44E+04	1.24E+04
Q8WZ42-8 TITIN	EVTLDDISQIK	630.84	102.86	9.57E+02	3.93E+04	3.67E+04	5.96E+04	1.03E+05	1.37E+05	5.45E+02	6.79E+02	2.88E+04	6.43E+04	2.76E+03	1.16E+05	2.13E+04	6.15E+02	4.15E+04
Q8WZ42-8 TITIN	VLEADPYFTVK	641.34	102.88	7.24E+02	2.77E+04	2.59E+04	2.52E+05	1.68E+04	2.06E+05	5.63E+04	1.12E+05	1.99E+02	3.33E+03	9.83E+04	7.64E+03	6.68E+03	2.28E+03	4.82E+02
Q8WZ42-8 TITIN	LVSPDLQLDASVR	706.89	102.95	7.33E+04	4.92E+03	1.57E+03	1.31E+05	1.79E+03	4.79E+03	2.54E+05	2.50E+05	8.19E+02	1.55E+03	8.70E+04	2.60E+03	2.35E+03	6.09E+03	2.66E+02
Q8WZ42-8 TITIN	APEPISSKPVIVTGLQDITVS SDSVAK	909.49	103.05	1.36E+03	5.01E+03	8.70E+02	5.53E+04	1.37E+03	1.11E+03	6.52E+02	8.71E+02	4.15E+03	8.16E+03	3.40E+04	5.76E+02	1.11E+03	5.12E+03	1.01E+04
Q8WZ42-8 TITIN	VFAENLAGLSKSPSSDPIK	686.37	103.06	3.10E+03	1.29E+04	3.61E+03	1.25E+03	4.02E+02	7.94E+03	7.49E+03	1.56E+03	4.56E+04	4.67E+04	9.49E+02	1.89E+03	1.41E+03	3.30E+04	9.03E+03
Q8WZ42-8 TITIN	SSADLEWSPLK	665.34	103.23	1.32E+04	1.91E+04	7.29E+02	8.72E+04	6.00E+05	4.92E+03	2.60E+03	2.39E+03	8.07E+03	5.65E+03	1.36E+04	1.35E+04	4.05E+04	5.73E+03	4.14E+05
Q8WZ42-8 TITIN	VAGSQPITVAWYK	710.38	103.34	6.17E+03	5.74E+03	3.04E+03	7.40E+04	1.83E+03	2.70E+03	7.61E+02	2.67E+03	1.68E+05	1.57E+05	8.19E+04	2.88E+03	2.25E+04	1.04E+05	3.79E+03
Q8WZ42-8 TITIN	PGSPVGVSFDEVTK	763.40	103.36	2.46E+04	9.19E+03	3.15E+03	1.89E+04	2.64E+03	2.91E+03	5.71E+03	1.01E+03	1.24E+03	3.34E+03	2.16E+04	1.26E+03	5.75E+03	1.87E+03	8.38E+03
Q8WZ42-8 TITIN	VDVPFIFR	451.76	103.38	3.42E+04	4.94E+04	3.83E+03	8.52E+04	1.09E+04	2.74E+04	1.08E+03	2.19E+03	1.85E+03	1.24E+03	2.14E+05	1.00E+04	3.15E+05	3.89E+03	1.27E+05
Q8WZ42-8 TITIN	SAANLIVEEEDLR	729.87	103.49	3.79E+03	5.78E+02	7.75E+02	4.77E+05	4.17E+02	6.52E+03	1.48E+03	2.84E+02	2.06E+03	1.28E+03	4.33E+05	1.40E+04	1.73E+05	1.69E+03	1.09E+04
Q8WZ42-8 TITIN	DEGILTCISK	539.77	103.5	3.13E+03	1.77E+03	1.74E+03	7.29E+04	3.07E+03	5.04E+02	1.41E+03	4.65E+02	1.15E+04	9.67E+02	9.10E+03	7.70E+03	5.98E+03	2.28E+03	2.50E+04
Q8WZ42-8 TITIN	TVPSPTSLEITSVTK	828.96	103.55	2.17E+04	1.09E+03	7.43E+02	8.12E+04	6.01E+02	2.39E+03	1.20E+03	3.56E+02	3.35E+03	2.50E+03	4.99E+04	3.03E+04	1.22E+04	5.01E+02	2.13E+04
Q8WZ42-8 TITIN	YGVGEPLSVAIK	681.37	104.24	5.69E+04	3.65E+03	6.84E+03	2.01E+04	1.81E+02	9.87E+02	2.36E+03	3.59E+02	3.32E+03	1.49E+03	7.98E+04	2.61E+03	1.38E+03	1.17E+03	2.33E+02
Q8WZ42-8 TITIN	LTVTLHPPPTDSTLRPM	626.00	104.24	6.54E+04	9.34E+03	5.16E+03	8.21E+04	3.74E+02	2.19E+03	1.75E+03	3.38E+03	6.80E+02	1.24E+03	2.67E+04	3.51E+03	1.16E+03	4.30E+02	6.20E+02
Q8WZ42-8 TITIN	VNVEETATSTVLHIK	547.63	104.44	2.12E+05	1.73E+03	9.15E+03	9.02E+02	1.93E+03	9.44E+03	1.26E+03	1.11E+03	8.55E+02	1.08E+04	3.19E+05	6.35E+03	4.93E+03	2.12E+03	1.11E+04
Q8WZ42-8 TITIN	YEVLSQQPFTLDHAPR	634.32	104.57	6.88E+02	1.22E+03	1.60E+04	6.17E+03	5.09E+03	2.24E+04	5.22E+04	9.11E+04	6.07E+02	2.26E+03	1.79E+03	1.73E+04	3.01E+04	1.25E+03	5.80E+04
Q8WZ42-8 TITIN	FRVPDAPDQPIVTEVTK	638.01	104.67	2.85E+03	3.39E+03	3.57E+03	1.07E+03	1.71E+05	2.38E+03	5.80E+02	9.41E+03	4.98E+02	7.82E+02	7.32E+02	8.65E+04	2.27E+04	8.21E+02	3.50E+04
Q8WZ42-8 TITIN	STVSLIWAR	516.79	104.76	1.36E+03	7.57E+03	1.36E+05	6.32E+03	5.42E+03	2.50E+04	1.40E+05	4.55E+03	1.11E+03	1.36E+03	7.04E+03	2.04E+02	4.39E+03	1.69E+03	9.24E+03
Q8WZ42-8 TITIN	TTGLEEGVEYEFK	765.36	105.06	2.92E+03	1.10E+04	4.59E+04	7.80E+03	2.88E+03	2.89E+04	8.09E+03	2.28E+04	1.21E+04	3.17E+03	1.69E+03	2.75E+04	3.93E+04	3.16E+03	2.76E+04
Q8WZ42-8 TITIN	VLDTPGPVNLNR	647.38	105.34	5.97E+04	1.33E+03	4.33E+02	3.60E+03	8.66E+02	7.06E+02	4.35E+03	9.09E+03	1.28E+03	1.20E+02	4.44E+04	8.20E+02	4.22E+02	1.79E+03	7.12E+02
Q8WZ42-8 TITIN	VLDTPGPPGPITFK	719.90	105.34	2.45E+02	2.86E+05	4.15E+03	7.14E+02	1.05E+05	6.73E+03	9.35E+02	5.91E+03	7.24E+02	1.59E+03	3.23E+03	2.30E+05	1.78E+05	6.05E+02	3.26E+05
Q8WZ42-8 TITIN	TSVSLAWSVPEDEGGSK	874.93	105.91	1.30E+03	1.69E+04	2.04E+04	4.99E+04	9.32E+03	2.23E+04	3.28E+03	4.76E+03	4.82E+02	1.62E+03	1.61E+03	1.79E+04	1.67E+04	3.01E+02	1.10E+05
Q8WZ42-8 TITIN	NAFVTPGPPGPIEVTK	812.42	105.99	6.37E+03	9.23E+02	1.85E+04	1.79E+03	6.67E+02	2.78E+04	3.95E+04	3.62E+04	1.54E+04	3.34E+04	2.55E+03	1.30E+04	2.38E+03	1.73E+03	2.09E+03
Q8WZ42-8 TITIN	IEIPVIGR	448.78	106.15	2.60E+03	1.79E+03	4.37E+02	1.70E+03	1.69E+03	1.81E+02	7.83E+03	2.37E+03	1.60E+05	1.57E+05	5.15E+03	7.52E+02	1.23E+02	1.82E+05	4.71E+02
Q8WZ42-8 TITIN	TPILAINPIDR	611.86	106.73	7.10E+04	7.76E+02	1.21E+03	5.15E+03	8.35E+02	1.70E+03	1.05E+03	3.88E+02	1.25E+03	1.35E+03	8.09E+04	4.14E+03	1.14E+04	7.82E+02	7.42E+03
Q8WZ42-8 TITIN	AGSPFTIDVPISGRPAK	604.00	106.74	2.92E+03	2.03E+03	1.20E+03	6.86E+02	4.87E+02	2.46E+03	1.78E+04	9.77E+03	7.64E+04	5.51E+04	1.55E+03	1.75E+03	2.01E+03	5.50E+04	7.85E+02
Q8WZ42-8 TITIN	IVEPLKDIETMEK	515.61	106.76	1.01E+03	2.27E+03	5.39E+02	5.09E+02	5.42E+02	6.15E+02	8.73E+02	2.60E+03	8.11E+04	5.67E+04	6.72E+02	1.40E+03	5.32E+02	8.30E+04	1.58E+03

Q8WZ42-8 TITIN	VYAINAAGVGPASLPSDPA TAR	700.04	107.48	3.03E+03	7.43E+03	1.06E+04	2.08E+03	1.79E+05	7.99E+03	1.57E+03	2.07E+03	3.01E+02	1.03E+03	1.05E+03	2.90E+05	2.12E+05	2.23E+02	2.70E+05
Q8WZ42-8 TITIN	LEAPELDLDSLRK	543.29	107.48	4.28E+03	2.79E+03	2.18E+03	5.03E+03	7.52E+02	1.63E+03	1.51E+03	1.65E+03	3.10E+04	1.93E+04	5.86E+02	1.59E+03	5.64E+02	2.29E+04	4.23E+03
Q8WZ42-8 TITIN	TPILAINPIDRGPENLH	699.37	107.61	2.62E+03	2.19E+03	1.49E+03	8.39E+04	1.51E+04	1.13E+03	3.47E+03	6.31E+02	3.51E+02	1.06E+03	3.23E+04	5.68E+03	3.65E+03	5.81E+02	3.31E+04
Q8WZ42-8 TITIN	YGVGDPVFTEPAIAK	782.40	107.76	7.10E+02	3.79E+03	1.88E+04	1.56E+02	8.19E+04	2.50E+03	1.10E+03	7.38E+03	3.04E+02	5.80E+02	1.05E+03	6.20E+04	6.41E+04	1.77E+03	1.24E+05
Q8WZ42-8 TITIN	YISSLEILR	547.32	107.82	8.23E+02	2.08E+05	1.41E+04	4.46E+03	2.03E+05	2.58E+05	9.90E+02	2.11E+03	9.40E+02	3.53E+02	3.34E+03	2.75E+05	1.19E+03	5.09E+02	1.07E+03
Q8WZ42-8 TITIN	ITGYLLEMR	548.30	107.92	1.89E+03	1.15E+03	2.30E+05	5.65E+03	4.88E+03	4.93E+05	1.29E+03	2.60E+03	1.89E+05	1.74E+05	2.33E+03	2.52E+03	1.46E+03	2.32E+05	1.10E+03
Q8WZ42-8 TITIN	DAGEYTITATNPFGTK	843.41	108.02	2.93E+03	4.86E+03	4.23E+02	3.45E+03	8.57E+04	1.80E+04	3.74E+03	4.20E+02	9.17E+02	1.24E+03	1.78E+03	9.12E+04	7.85E+04	3.09E+03	1.03E+05
Q8WZ42-8 TITIN	TSLQEEMDSFSGSQK	837.37	108.08	4.03E+02	4.07E+03	2.10E+03	5.87E+02	1.67E+04	1.23E+03	1.46E+03	1.11E+03	5.33E+04	6.66E+04	4.04E+02	1.16E+03	2.16E+03	4.34E+03	7.02E+04
Q8WZ42-8 TITIN	VSGLDEGLMYEPLK	785.94	108.64	9.30E+02	2.60E+03	6.56E+03	2.42E+02	3.47E+02	8.29E+03	4.02E+02	8.36E+02	3.55E+02	1.10E+03	1.47E+02	5.46E+03	5.05E+03	4.80E+02	4.29E+04
Q8WZ42-8 TITIN	ILMPEQITIK	593.35	108.67	2.61E+03	5.80E+02	6.27E+03	7.58E+03	1.93E+04	1.43E+03	1.77E+03	3.76E+03	8.22E+04	1.76E+05	6.69E+02	2.49E+03	2.21E+03	7.14E+04	5.70E+03
Q8WZ42-8 TITIN	YFLTLENTAGVK	678.36	108.8	5.77E+02	2.60E+04	1.36E+03	1.10E+03	2.15E+04	4.05E+04	1.74E+03	2.48E+03	2.92E+03	5.93E+02	4.69E+03	1.93E+04	7.67E+03	6.70E+03	3.74E+04
Q8WZ42-8 TITIN	IEPLEVALGH	539.30	108.8	3.86E+02	3.65E+04	2.16E+04	3.26E+03	3.42E+03	1.97E+04	8.65E+03	6.80E+03	2.79E+02	8.20E+02	5.60E+03	3.32E+04	9.85E+03	1.64E+03	7.98E+04
Q8WZ42-8 TITIN	VDQLQEGCSYYFR	804.38	108.98	3.76E+04	4.39E+03	8.62E+03	1.27E+03	4.37E+03	1.87E+04	1.30E+03	6.44E+02	3.81E+02	1.98E+03	2.25E+04	1.40E+04	1.55E+03	7.41E+02	1.86E+04
Q8WZ42-8 TITIN	LLPGNEYIFR	611.33	109.03	4.98E+02	2.60E+05	3.44E+04	2.07E+03	2.63E+05	4.24E+05	2.39E+04	2.92E+04	1.26E+03	1.80E+03	7.54E+02	2.92E+05	1.27E+03	3.48E+03	5.83E+02
Q8WZ42-8 TITIN	VSLGDEGLMYEYR	766.36	109.08	1.49E+04	1.85E+04	1.11E+03	1.32E+04	4.92E+04	6.24E+03	3.87E+03	1.08E+04	1.50E+03	4.81E+02	1.30E+04	1.23E+05	1.02E+03	8.26E+02	1.27E+05
Q8WZ42-8 TITIN	HPFDVPDAPPPNIVDVR	661.34	109.2	2.66E+03	1.31E+05	5.72E+04	2.52E+03	7.77E+02	1.81E+05	5.03E+04	3.83E+03	2.39E+03	3.06E+02	6.00E+02	2.13E+04	8.94E+02	4.01E+03	9.42E+04
Q8WZ42-8 TITIN	SSGLTDGIAYEFR	708.34	109.26	1.21E+03	2.93E+04	7.66E+02	2.97E+03	8.06E+04	7.18E+03	1.22E+04	9.65E+03	1.72E+04	1.57E+03	1.73E+03	1.01E+05	1.98E+03	2.61E+03	1.30E+05
Q8WZ42-8 TITIN	ITQFVVPDLQTK	694.89	109.26	3.07E+02	7.69E+03	2.15E+03	9.95E+02	2.21E+05	9.57E+03	9.52E+03	2.61E+04	1.75E+03	8.38E+02	9.51E+02	1.53E+05	1.27E+04	9.65E+02	2.24E+05
Q8WZ42-8 TITIN	TVTGLVPDAEYQFR	798.41	109.27	1.78E+03	1.56E+05	3.05E+04	9.16E+02	4.51E+02	1.46E+05	4.57E+04	6.85E+04	1.24E+03	1.15E+03	1.19E+03	3.03E+03	1.83E+03	4.13E+02	4.61E+02
Q8WZ42-8 TITIN	ILIESANPLENAQDSAVR	666.35	109.28	7.32E+02	2.78E+03	1.42E+03	1.46E+03	1.28E+03	1.35E+03	5.95E+02	9.72E+02	4.68E+04	6.53E+04	3.58E+02	5.23E+03	1.33E+03	1.34E+03	1.11E+03
Q8WZ42-8 TITIN	VLPTIDLSTMPQK	721.90	109.29	3.85E+02	7.57E+02	5.46E+02	1.71E+03	2.93E+05	6.30E+03	2.04E+03	5.95E+04	1.12E+03	8.75E+02	7.61E+03	9.15E+04	2.97E+02	3.92E+02	3.20E+05
Q8WZ42-8 TITIN	VTSLMEGCDYQFR	774.85	109.3	8.92E+02	2.39E+04	6.82E+03	7.82E+02	1.03E+03	5.55E+04	1.27E+03	9.74E+03	1.44E+03	1.01E+03	3.38E+02	1.54E+03	6.85E+02	2.33E+03	1.14E+03
Q8WZ42-8 TITIN	AGEPVHIPADVTGLPMPK	610.33	109.44	4.28E+03	1.08E+03	2.63E+03	7.66E+03	1.27E+05	1.26E+03	7.14E+02	2.77E+03	1.15E+03	2.12E+03	1.20E+05	2.43E+05	4.50E+03	8.94E+02	2.54E+05
Q8WZ42-8 TITIN	TNLQFMGQAFK	642.33	109.63	8.56E+02	1.48E+04	1.76E+03	2.26E+03	3.47E+03	2.69E+04	1.43E+04	4.04E+03	4.57E+05	3.73E+05	1.75E+03	2.48E+03	4.25E+02	3.14E+05	9.87E+02
Q8WZ42-8 TITIN	IEPPEIELDADLRK	547.28	109.67	1.14E+03	1.59E+05	1.19E+05	2.94E+03	3.67E+03	8.79E+02	9.75E+04	1.02E+05	1.98E+03	1.90E+03	5.39E+02	3.45E+02	7.02E+02	2.69E+03	1.38E+03
Q8WZ42-8 TITIN	KIEPLEVALGHLAK	506.64	109.8	2.05E+02	8.23E+02	5.54E+02	2.06E+03	8.22E+04	1.42E+03	8.07E+02	3.46E+03	6.12E+02	3.74E+02	3.31E+02	1.20E+05	7.77E+02	1.53E+03	3.95E+04
Q8WZ42-8 TITIN	GMSEYSESAIEPVER	963.44	109.85	4.01E+04	7.17E+03	1.41E+04	4.45E+03	7.39E+04	1.25E+04	4.42E+03	1.78E+04	9.24E+02	4.72E+03	5.29E+03	1.12E+05	8.55E+04	4.14E+02	1.23E+05
Q8WZ42-8 TITIN	MLPPEIELDADLRK	547.30	109.98	3.93E+03	1.37E+05	8.58E+03	3.59E+02	1.23E+05	1.25E+05	5.47E+04	9.58E+04	7.38E+04	4.00E+04	9.98E+02	2.26E+05	1.95E+04	4.46E+02	4.22E+04
Q8WZ42-8 TITIN	IMAENAAGISAPSPFYK	1026.51	110.08	2.12E+02	3.68E+02	1.11E+03	4.52E+02	7.88E+02	6.89E+02	7.99E+02	6.69E+02	3.50E+04	3.46E+03	1.00E+03	1.02E+03	1.34E+03	1.60E+04	1.37E+03
Q8WZ42-8 TITIN	ECSAVLTVLEPAR	694.37	110.1	1.10E+04	6.66E+02	1.57E+04	3.32E+04	5.63E+03	1.14E+03	1.36E+03	7.73E+02	2.03E+03	1.37E+04	5.92E+04	3.98E+03	5.10E+03	7.16E+02	8.90E+03
Q8WZ42-8 TITIN	VLDTPGPVLNLRPTDITK	650.38	110.21	2.18E+05	3.29E+04	8.33E+03	3.43E+05	2.88E+05	6.24E+03	7.09E+03	8.77E+03	3.20E+04	2.44E+04	2.76E+05	2.56E+05	9.34E+03	2.81E+03	5.13E+03
Q8WZ42-8 TITIN	STDFDIFLR	551.26	110.34	7.61E+03	1.53E+03	2.00E+03	5.56E+03	9.43E+02	2.96E+03	1.17E+03	1.15E+03	2.91E+05	2.89E+05	4.07E+03	8.28E+03	2.43E+03	3.39E+05	1.97E+04
Q8WZ42-8 TITIN	VASIEIGPVSGQIMH	769.41	110.38	8.84E+04	2.68E+04	2.36E+03	7.85E+04	1.44E+05	1.12E+05	3.73E+03	2.97E+03	8.95E+02	2.50E+03	4.03E+04	7.98E+03	1.22E+03	4.32E+03	3.90E+04
Q8WZ42-8 TITIN	VLASNEYGIGLPAETTEPVK	1044.54	110.38	8.08E+02	1.22E+03	3.60E+02	2.72E+03	4.33E+02	7.11E+03	3.04E+02	3.86E+02	5.53E+02	1.09E+04	1.55E+03	1.96E+03	1.30E+03	1.11E+03	5.78E+02
Q8WZ42-8 TITIN	TTGLDEGLEFEFK	751.36	110.6	8.15E+04	6.09E+04	6.08E+02	2.67E+04	5.61E+03	2.16E+04	9.69E+02	6.72E+02	3.91E+04	7.86E+04	7.24E+04	2.27E+04	7.55E+04	1.43E+04	2.17E+04
Q8WZ42-8 TITIN	ICAINSEGVGEPATLPGSVV AQER	800.07	110.86	3.91E+04	1.29E+03	5.15E+02	7.97E+03	6.94E+03	1.47E+03	1.35E+03	1.31E+03	6.52E+04	1.94E+03	2.78E+04	1.02E+04	2.41E+03	4.69E+04	1.52E+04
Q8WZ42-8 TITIN	DLVIPPAFK	500.30	110.89	6.12E+03	3.33E+04	7.00E+04	1.26E+05	5.86E+04	3.08E+04	8.30E+04	1.31E+05	1.44E+02	2.05E+02	1.15E+04	1.97E+04	6.43E+04	6.97E+02	5.38E+04
Q8WZ42-8 TITIN	KGEVQEEEPFVPLTQR	667.02	110.92	3.20E+04	3.33E+02	1.46E+03	1.22E+05	2.12E+05	2.38E+03	3.17E+03	1.11E+03	5.15E+03	6.41E+03	1.32E+04	7.77E+04	2.64E+04	6.90E+02	1.49E+05
Q8WZ42-8 TITIN	VTAENEYGIGLPAQTADPIK	696.36	111.06	7.68E+03	6.50E+03	6.04E+03	5.04E+03	1.10E+03	5.70E+03	2.65E+05	1.52E+03	1.91E+04	4.21E+04	1.27E+04	5.17E+03	2.89E+03	2.56E+03	5.97E+03
Q8WZ42-8 TITIN	TPILAINPIDRGPENLHIA DK	631.59	111.14	5.66E+02	5.76E+02	1.66E+03	6.28E+02	1.04E+03	1.75E+03	1.38E+03	1.66E+03	7.22E+04	5.33E+03	3.91E+02	1.86E+03	1.03E+03	1.55E+04	2.25E+03
Q8WZ42-8 TITIN	TPLNPPPEPPNPPEVLDVTK	714.37	111.22	1.72E+03	4.25E+04	3.88E+02	1.99E+03	2.66E+03	2.73E+03	1.21E+05	2.19E+05	4.41E+04	1.14E+04	2.68E+03	8.52E+03	1.97E+03	8.36E+03	1.24E+03
Q8WZ42-8 TITIN	EREEPLFDIDSEMR	632.29	111.31	6.72E+02	1.56E+03	6.87E+02	8.72E+03	3.23E+04	8.61E+02	9.07E+02	4.25E+03	1.89E+03	6.39E+03	2.11E+03	5.12E+04	1.21E+04	1.37E+04	1.39E+04
Q8WZ42-8 TITIN	TIKPPPVEPEPTPIAAPVTVP VVGK	845.16	111.33	2.37E+03	3.55E+03	4.25E+02	2.44E+03	8.12E+04	4.74E+03	2.75E+03	4.00E+03	2.15E+04	1.63E+03	1.81E+05	1.28E+05	9.97E+04	3.28E+04	8.79E+04
Q8WZ42-8 TITIN	VLAENEYGIGLPAETAESV	1045.54	111.46	1.76E+04	7.58E+02	8.04E+02	4.34E+04	4.83E+03	1.96E+03	2.75E+03	5.08E+03	6.00E+02	2.86E+03	2.85E+04	6.31E+04	1.68E+03	5.51E+02	3.03E+04
Q8WZ42-8 TITIN	IYAMNSEGLGEPALVPGTP	1022.53	111.63	3.42E+03	6.00E+02	1.32E+03	2.68E+03	1.96E+04	6.45E+03	8.15E+02	6.00E+02	4.58E+02	7.78E+02	1.40E+03	5.11E+04	2.96E+04	1.38E+03	5.99E+04
Q8WZ42-8 TITIN	NPPFFDIR	503.26	111.73	1.37E+03	1.94E+03	2.90E+04	2.60E+03	1.81E+02	7.80E+03	5.84E+03	8.89E+03	2.29E+05	8.49E+04	2.64E+03	9.55E+03	1.47E+03	6.44E+04	9.92E+03
Q8WZ42-8 TITIN	LEADVHGKPLPTIEWLR	494.28	111.88	3.17E+04	4.09E+03	2.61E+03	2.40E+04	3.93E+04	1.17E+04	3.86E+03	3.85E+03	3.11E+04	1.75E+03	2.74E+04	1.51E+04	1.39E+04	8.48E+02	4.63E+03
Q8WZ42-8 TITIN	SDTGLYTITAVNNLGTASK	963.49	112.07	1.97E+03	2.30E+03	9.99E+02	1.11E+03	4.28E+03	3.57E+03	1.55E+03	2.35E+03	4.79E+04	8.54E+03	4.76E+02	8.22E+02	1.26E+03	1.97E+04	8.44E+02
Q8WZ42-8 TITIN	DDGGSPVINYIVEK	753.38	112.19	6.97E+02	6.59E+03	1.58E+03	1.18E+03	2.75E+03	3.29E+04	1.26E+04	2.84E+03	1.97E+04	5.76E+04	3.37E+03	7.81E+03	1.70E+03	1.97E+03	1.18E+0



Q8WZ42-8 TITIN	VTDVIEGTEVQFQVR	860.43	113.57	5.09E+05	1.35E+04	4.90E+05	6.64E+05	1.22E+03	2.54E+03	4.82E+02	1.73E+03	1.72E+03	1.36E+03	5.58E+05	2.56E+04	5.74E+03	4.58E+03	9.62E+02
Q8WZ42-8 TITIN	IDQLQEGCSYYFR	811.37	113.59	2.35E+03	2.00E+03	1.95E+03	2.11E+03	2.03E+03	1.29E+03	1.38E+03	3.04E+03	2.48E+03	6.38E+03	4.68E+03	2.32E+03	4.60E+02	2.97E+03	1.81E+03
Q8WZ42-8 TITIN	AQNLEEGIEYEFR	799.39	113.73	9.64E+03	3.79E+03	2.98E+04	5.87E+03	1.29E+04	8.54E+03	1.38E+03	2.85E+03	1.65E+03	8.54E+02	7.91E+02	2.77E+03	1.49E+03	5.32E+02	1.45E+04
Q8WZ42-8 TITIN	LAWTNVASEVQVTK	773.41	113.94	2.38E+03	2.36E+03	1.88E+03	8.69E+03	3.59E+02	3.94E+03	1.44E+03	4.82E+03	2.90E+04	6.38E+03	2.57E+02	3.05E+03	1.96E+03	1.06E+04	3.98E+03
Q8WZ42-8 TITIN	LVVSEPQSIR	661.86	114.23	1.93E+03	2.03E+04	7.64E+03	8.39E+03	1.04E+04	3.15E+04	2.07E+04	2.24E+04	1.47E+03	3.14E+04	1.21E+03	2.29E+03	1.41E+03	4.98E+03	4.92E+02
Q8WZ42-8 TITIN	EPLDDGGSVITNYVVER	931.96	114.37	8.06E+02	4.11E+03	9.33E+03	1.70E+03	8.92E+04	2.62E+04	1.23E+04	1.08E+04	1.07E+03	2.89E+03	6.28E+02	1.15E+05	5.95E+04	2.01E+04	1.08E+05
Q8WZ42-8 TITIN	IVPGVIGLMR	527.83	114.52	1.09E+03	1.32E+03	1.80E+03	3.76E+03	3.22E+02	4.74E+02	4.12E+02	6.87E+02	7.32E+05	6.08E+05	4.49E+03	6.06E+03	1.20E+03	7.54E+05	3.32E+03
Q8WZ42-8 TITIN	AGASFTMTVPFR	642.83	114.6	3.67E+03	1.67E+04	9.62E+03	5.34E+04	9.84E+03	1.19E+04	1.18E+04	8.54E+03	6.83E+03	2.67E+03	2.26E+03	6.85E+04	1.29E+04	6.29E+03	7.65E+03
Q8WZ42-8 TITIN	DLSLVVVTGLK	522.82	114.65	1.33E+04	8.89E+02	8.40E+03	7.82E+04	1.53E+03	1.11E+03	1.99E+03	1.62E+02	2.98E+03	3.51E+02	6.25E+04	1.68E+03	4.59E+03	3.70E+03	1.18E+04
Q8WZ42-8 TITIN	LAWALIEDK	529.80	114.67	4.68E+02	5.26E+03	2.07E+03	5.50E+03	3.12E+03	1.74E+03	1.60E+02	9.55E+02	5.31E+04	5.86E+04	6.19E+02	6.33E+02	6.17E+02	3.02E+04	3.36E+03
Q8WZ42-8 TITIN	IHAENLYGISDPLVSDSMK	697.02	114.73	4.72E+02	1.15E+03	2.64E+03	3.34E+02	8.41E+04	6.12E+03	3.56E+03	6.81E+02	2.34E+05	7.00E+03	1.12E+03	1.33E+05	1.71E+03	6.66E+04	1.24E+05
Q8WZ42-8 TITIN	IENLQEGCSYYFR	811.37	114.75	1.37E+03	2.26E+03	7.10E+02	2.18E+03	8.52E+02	5.80E+03	7.85E+02	5.53E+02	2.34E+04	1.99E+02	1.33E+03	1.68E+03	5.58E+03	2.02E+04	1.95E+03
Q8WZ42-8 TITIN	ATGLVEGLDYQFR	734.87	115.09	6.70E+02	1.54E+04	3.86E+02	2.46E+02	1.13E+05	4.83E+04	2.69E+03	5.16E+02	4.23E+02	4.60E+02	4.35E+03	1.58E+05	7.42E+04	3.72E+02	2.51E+05
Q8WZ42-8 TITIN	YGVSQPLVSSIIIVAK	780.95	115.12	6.93E+02	8.77E+03	9.33E+02	6.72E+02	1.99E+05	1.37E+04	8.87E+03	1.91E+03	1.89E+03	4.18E+02	6.17E+02	1.66E+05	8.36E+04	4.77E+02	1.90E+05
Q8WZ42-8 TITIN	AGSPFTIDVPISGR	708.88	115.12	1.10E+03	1.72E+03	6.48E+02	2.46E+03	9.17E+04	2.30E+03	2.16E+04	5.97E+03	4.27E+02	3.14E+02	3.02E+03	1.22E+05	1.49E+04	1.26E+03	5.24E+04
Q8WZ42-8 TITIN	YGVGEPPLNSAPVLMK	795.41	115.18	5.85E+02	2.09E+04	1.17E+04	1.73E+03	1.19E+03	2.12E+03	2.32E+03	1.06E+04	6.96E+04	1.77E+03	2.24E+03	8.38E+02	5.17E+02	4.85E+04	1.25E+03
Q8WZ42-8 TITIN	LIPGQEYIFR	618.34	115.33	2.35E+03	4.98E+03	5.36E+03	8.58E+02	7.98E+02	8.12E+02	8.14E+02	7.11E+02	2.55E+05	2.60E+05	2.44E+03	1.36E+03	1.99E+03	1.77E+05	9.16E+02
Q8WZ42-8 TITIN	VTEMLEYPDYELDER	951.43	115.54	4.90E+03	6.62E+03	7.11E+02	5.02E+03	1.24E+03	8.12E+02	6.59E+02	7.33E+02	2.73E+04	4.76E+03	1.07E+03	4.61E+02	1.37E+03	1.08E+04	1.53E+03
Q8WZ42-8 TITIN	IAVPITVITLGPSPKPK	577.70	115.84	4.72E+03	3.04E+03	1.60E+03	1.53E+02	3.09E+04	3.25E+03	2.75E+02	4.18E+02	2.13E+03	3.77E+02	2.83E+03	8.02E+04	2.92E+03	4.70E+03	5.47E+04
Q8WZ42-8 TITIN	VTNLQEGAIYYFR	787.40	116.02	6.56E+02	1.07E+03	1.89E+03	5.26E+02	4.35E+04	4.95E+02	9.11E+02	8.13E+02	7.86E+02	1.97E+04	1.18E+03	3.50E+04	9.24E+02	2.19E+03	5.09E+04
Q8WZ42-8 TITIN	PLDSDPVVAQIQY	722.87	116.38	1.08E+04	1.32E+03	4.46E+02	5.38E+04	4.81E+02	2.29E+03	8.54E+02	2.66E+03	2.88E+03	2.80E+02	1.44E+04	3.64E+03	1.22E+03	4.58E+02	1.87E+03
Q8WZ42-8 TITIN	LPYTTPGPPSTPWVTVNTR	695.37	116.67	1.36E+03	5.05E+03	1.07E+03	1.32E+03	4.19E+04	3.93E+03	1.76E+03	4.86E+03	1.36E+03	2.18E+03	1.35E+03	1.68E+04	5.14E+02	8.37E+03	3.24E+02
Q8WZ42-8 TITIN	LEAPELDLDELSELR	750.38	116.92	1.14E+03	1.81E+04	2.71E+03	1.49E+03	9.38E+04	4.23E+02	1.53E+03	2.54E+03	1.20E+04	1.24E+04	3.20E+03	1.10E+05	1.38E+04	5.53E+03	2.00E+05
Q8WZ42-8 TITIN	EQTMLPELDELRL	672.84	117.02	1.10E+04	6.29E+03	4.69E+03	2.23E+04	2.72E+04	1.66E+04	2.26E+04	4.69E+03	1.59E+03	2.95E+04	2.05E+03	1.16E+04	6.03E+04	3.45E+03	1.88E+05
Q8WZ42-8 TITIN	DEYEAPITVLDPTIK	852.44	117.09	1.22E+03	1.42E+03	5.97E+02	2.73E+03	2.22E+04	9.59E+02	3.54E+03	5.84E+02	1.63E+03	9.35E+02	1.18E+03	7.83E+03	2.10E+03	1.66E+03	4.66E+04
Q8WZ42-8 TITIN	PPENDGGVPISNYVEMR	658.32	117.22	9.08E+02	8.76E+04	2.20E+03	3.53E+02	7.73E+04	1.11E+03	1.01E+03	5.23E+03	3.26E+02	6.55E+03	2.69E+02	1.90E+05	3.57E+04	5.21E+03	4.78E+04
Q8WZ42-8 TITIN	VTGLTEGLEVEFR	757.38	117.41	2.17E+03	7.55E+04	1.98E+03	7.24E+02	1.11E+05	1.44E+03	7.00E+03	1.17E+04	2.17E+03	1.21E+03	5.88E+02	1.88E+05	1.63E+05	2.38E+05	1.62E+05
Q8WZ42-8 TITIN	YDVPGPPLNVITDVR	935.49	117.46	1.82E+02	2.58E+03	2.09E+03	8.09E+02	4.83E+03	2.17E+04	2.81E+03	3.20E+02	9.31E+02	9.10E+02	3.01E+03	5.35E+03	1.62E+02	1.21E+03	3.58E+04
Q8WZ42-8 TITIN	TISGLTTGAEYVFR	757.89	117.59	1.06E+03	1.37E+04	4.00E+03	7.76E+02	1.95E+04	1.33E+04	3.41E+04	7.74E+03	2.23E+03	1.17E+03	1.27E+03	1.37E+05	9.43E+04	9.10E+02	1.47E+05
Q8WZ42-8 TITIN	DDGSEITNYILEK	777.38	117.71	1.24E+03	1.74E+03	7.74E+02	6.06E+02	4.21E+03	4.94E+03	1.28E+03	1.40E+03	2.53E+04	1.99E+02	2.09E+04	1.91E+04	1.18E+03	5.51E+02	7.61E+02
Q8WZ42-8 TITIN	LSIPVPFR	464.78	117.92	6.00E+02	3.23E+02	1.17E+03	8.92E+02	2.75E+02	6.48E+02	6.79E+02	1.93E+02	1.39E+05	9.28E+03	1.40E+03	1.27E+02	1.35E+02	1.51E+05	1.24E+03
Q8WZ42-8 TITIN	DELAPPTLHLDFR	508.60	118.13	1.43E+02	3.80E+02	1.40E+03	2.31E+02	4.24E+04	3.63E+03	2.76E+03	1.20E+03	1.74E+02	3.75E+02	7.75E+02	5.12E+04	2.06E+03	7.99E+02	6.17E+04
Q8WZ42-8 TITIN	LTAPELDIDANFK	723.87	118.16	1.36E+03	4.02E+03	1.70E+03	1.29E+03	1.77E+03	8.30E+02	9.66E+02	7.54E+02	8.66E+02	3.39E+04	1.85E+03	5.53E+03	3.86E+02	4.98E+02	1.48E+03
Q8WZ42-8 TITIN	EGILMPPEPETQAVLSDTEK	739.04	118.23	4.63E+03	3.33E+03	3.21E+02	8.73E+05	6.70E+05	2.25E+04	2.52E+02	5.38E+03	5.41E+02	2.11E+04	6.78E+05	2.39E+05	1.25E+05	1.71E+03	6.11E+05
Q8WZ42-8 TITIN	WLEVINITK	558.33	118.37	2.35E+05	1.94E+04	1.31E+03	7.90E+04	1.96E+04	1.33E+04	1.88E+03	6.18E+03	4.90E+02	1.70E+03	2.32E+05	1.58E+04	1.79E+04	3.66E+03	1.02E+04
Q8WZ42-8 TITIN	IVNLTENAGYYFR	780.39	118.57	2.06E+03	4.72E+02	1.78E+03	2.19E+03	1.43E+03	1.27E+03	5.82E+02	8.61E+02	3.83E+04	8.64E+03	9.02E+02	1.03E+03	2.84E+02	2.86E+04	1.13E+03
Q8WZ42-8 TITIN	VTAVNEYGPGVPTDVPKPV	829.18	118.76	3.57E+03	5.39E+02	3.74E+03	1.82E+03	7.26E+03	1.32E+03	1.39E+03	7.16E+02	1.00E+03	4.94E+02	2.38E+04	8.22E+02	1.43E+04	7.21E+02	2.29E+04
Q8WZ42-8 TITIN	LNDPLSEPDPPR	771.37	118.79	9.30E+04	1.82E+03	3.41E+05	5.69E+04	2.63E+03	2.09E+03	1.03E+05	1.56E+03	3.38E+03	1.87E+03	5.70E+04	1.02E+03	1.20E+03	4.69E+02	7.28E+02
Q8WZ42-8 TITIN	VNDLAEGVPPYYFR	771.37	118.79	9.30E+04	1.82E+03	3.41E+05	5.69E+04	2.63E+03	2.09E+03	1.03E+05	1.56E+03	3.38E+03	1.87E+03	5.70E+04	1.02E+03	1.20E+03	4.69E+02	7.28E+02
Q8WZ42-8 TITIN	MVAQFPFGVPSEPK	767.39	118.81	1.05E+03	1.25E+03	1.31E+06	5.56E+02	8.14E+04	4.94E+03	5.61E+03	1.69E+03	3.49E+03	1.82E+03	2.18E+04	2.82E+04	9.35E+03	5.92E+02	5.28E+04
Q8WZ42-8 TITIN	AGEDVQVLIPFK	658.37	118.91	1.00E+04	7.26E+03	5.46E+03	3.16E+03	2.93E+05	2.13E+04	6.79E+03	4.93E+03	4.56E+03	2.14E+03	3.07E+03	2.36E+05	1.58E+05	7.17E+02	3.86E+05
Q8WZ42-8 TITIN	STVSLIWSAPAYDGGGSK	869.93	119.23	6.02E+02	2.63E+03	6.31E+02	1.83E+02	1.44E+03	2.03E+03	1.39E+03	1.08E+03	1.20E+04	1.66E+03	1.17E+03	5.34E+02	1.60E+03	2.96E+04	9.47E+02
Q8WZ42-8 TITIN	IINVAPSDSGVYSFEVQNPV	774.06	119.3	3.85E+03	7.41E+02	1.66E+03	2.42E+03	5.09E+03	3.06E+04	4.22E+02	3.58E+03	1.23E+03	2.46E+03	7.71E+02	2.49E+03	1.13E+03	8.82E+02	4.08E+02
Q8WZ42-8 TITIN	GK	774.06	119.3	3.85E+03	7.41E+02	1.66E+03	2.42E+03	5.09E+03	3.06E+04	4.22E+02	3.58E+03	1.23E+03	2.46E+03	7.71E+02	2.49E+03	1.13E+03	8.82E+02	4.08E+02
Q8WZ42-8 TITIN	VYAENAAGLSLPSETSPLIR	1044.55	119.37	3.03E+02	4.45E+03	1.19E+03	2.75E+02	3.32E+04	3.15E+02	1.44E+03	4.34E+03	7.25E+02	3.60E+02	7.06E+02	1.14E+05	2.27E+03	2.21E+02	1.02E+05
Q8WZ42-8 TITIN	TSFHVNTNLVPGNEYFR	682.00	119.76	2.08E+04	8.52E+02	1.03E+03	1.60E+03	8.55E+04	4.87E+03	3.80E+03	2.37E+02	3.71E+03	8.55E+04	7.63E+02	5.16E+04	7.79E+02	2.19E+03	1.18E+05
Q8WZ42-8 TITIN	VTVLDVPGPPGVEISNVSA	735.40	119.79	3.85E+02	3.24E+03	1.64E+04	1.10E+03	5.42E+04	3.22E+03	8.40E+02	6.48E+02	1.74E+03	1.08E+03	1.42E+03	2.62E+04	5.60E+03	1.84E+03	3.93E+04
Q8WZ42-8 TITIN	EK	735.40	119.79	3.85E+02	3.24E+03	1.64E+04	1.10E+03	5.42E+04	3.22E+03	8.40E+02	6.48E+02	1.74E+03	1.08E+03	1.42E+03	2.62E+04	5.60E+03	1.84E+03	3.93E+04
Q8WZ42-8 TITIN	SFTSLVFPNGVER	726.88	119.94	3.76E+03	3.58E+03	1.09E+03	1.72E+03	2.59E+04	4.92E+03	2.63E+03	1.45E+03	5.16E+02	5.58E+02	5.39E+03	1.51E+05	5.90E+02	3.12E+03	1.69E+05
Q8WZ42-8 TITIN	GLSDPVTIGPITVK																	

Q8WZ42-8 TITIN	VMAENEFVGVVPVETVDA VK	1045.54	121.96	4.43E+02	8.86E+02	5.00E+02	5.15E+03	8.78E+02	1.41E+03	2.52E+02	3.88E+02	3.92E+04	7.65E+03	1.04E+03	7.04E+02	2.40E+03	6.10E+04	1.72E+03
Q8WZ42-8 TITIN	LLERPPEFTLPLYNK	610.68	122.06	3.31E+04	6.04E+03	4.73E+02	4.15E+04	5.81E+03	1.06E+04	7.43E+02	3.77E+03	1.06E+03	9.76E+02	1.50E+05	1.18E+04	5.95E+03	1.06E+03	2.63E+04
Q8WZ42-8 TITIN	VSWRPPADDGGADILGY	894.93	122.16	2.58E+02	7.60E+04	1.89E+04	1.26E+03	2.90E+02	5.36E+04	3.76E+03	2.16E+04	1.82E+03	3.65E+02	1.12E+03	6.08E+03	9.09E+02	1.13E+03	1.59E+03
Q8WZ42-8 TITIN	IESYVIEMLK	612.83	122.31	1.50E+05	1.65E+03	7.09E+02	1.83E+05	2.21E+03	5.94E+03	3.62E+02	1.20E+03	1.81E+03	1.32E+03	1.75E+05	1.78E+03	7.84E+04	1.25E+03	2.18E+03
Q8WZ42-8 TITIN	GPPGPVEISNVSAEK	740.87	122.41	1.86E+03	4.43E+03	4.55E+03	3.09E+04	1.93E+03	1.26E+03	9.01E+02	1.29E+03	3.40E+03	6.98E+02	2.66E+02	1.91E+03	4.77E+03	3.46E+03	4.86E+02
Q8WZ42-8 TITIN	VSAVNEYGVGEPYEMPEPI VATEQPAPPR	1042.84	122.82	1.76E+04	1.92E+03	3.37E+02	4.40E+02	2.49E+03	1.61E+02	1.20E+03	1.69E+02	1.79E+03	1.13E+03	4.52E+04	1.74E+03	6.84E+03	9.35E+02	5.09E+04
Q8WZ42-8 TITIN	DPFDKPSQPGELEILSISK	700.70	122.89	1.11E+04	1.51E+05	7.18E+03	3.69E+02	4.50E+02	3.85E+04	5.40E+04	5.66E+04	4.96E+02	2.60E+04	3.45E+02	3.58E+02	2.83E+03	2.33E+03	5.18E+02
Q8WZ42-8 TITIN	LSDTSTLIGDAVELR	795.42	123.03	4.20E+04	5.48E+02	3.32E+02	2.88E+04	2.02E+03	2.57E+04	1.19E+03	1.02E+03	4.58E+03	3.80E+03	4.03E+04	2.94E+03	6.61E+02	3.40E+03	2.37E+03
Q8WZ42-8 TITIN	YSIENTDSSLLTIPQVTR	708.70	123.05	8.57E+04	5.57E+03	7.34E+02	9.98E+02	3.41E+02	4.31E+03	1.03E+03	4.36E+03	1.34E+03	2.75E+02	1.32E+05	4.41E+03	4.61E+04	2.43E+03	5.75E+04
Q8WZ42-8 TITIN	GEVQEEEPFVPLPTQR	935.98	123.13	9.57E+04	5.57E+03	1.33E+03	1.19E+05	2.61E+03	1.86E+03	1.02E+03	6.74E+03	2.66E+02	3.78E+02	5.26E+04	1.96E+03	2.35E+03	2.18E+02	2.80E+03
Q8WZ42-8 TITIN	LLPGLMEGQEYSFR	820.41	123.29	6.28E+04	3.50E+03	3.89E+03	7.68E+04	8.94E+02	1.78E+03	2.07E+03	2.55E+03	2.67E+03	6.60E+03	3.91E+04	9.54E+02	9.04E+03	8.58E+02	4.46E+03
Q8WZ42-8 TITIN	AENEAGVGHPSPTTEILSIE DPTSPSPPLDLHVTDAAGR	1008.75	123.4	8.04E+02	1.55E+04	8.57E+03	6.19E+02	4.38E+02	2.45E+04	3.53E+04	4.71E+04	4.10E+02	1.33E+02	1.81E+03	6.87E+02	1.23E+03	1.37E+03	2.00E+03
Q8WZ42-8 TITIN	IEPLEVALGHLAK	463.94	123.44	6.32E+04	2.82E+02	6.27E+03	9.40E+04	3.39E+03	6.03E+02	8.64E+02	2.31E+03	3.34E+02	7.97E+02	2.46E+05	3.08E+03	5.18E+04	1.26E+02	2.32E+03
Q8WZ42-8 TITIN	DLVIEPDVKPAFSSY	840.43	123.78	6.79E+04	1.17E+03	6.19E+03	8.23E+04	1.30E+03	8.83E+02	6.36E+02	2.09E+04	5.06E+03	4.96E+03	5.65E+04	1.50E+03	1.01E+03	4.83E+02	6.72E+04
Q8WZ42-8 TITIN	IEIPDLELADDLKK	537.97	123.8	5.70E+04	4.60E+03	2.03E+03	1.70E+03	2.70E+03	3.13E+02	1.07E+03	1.36E+03	2.93E+02	1.60E+04	9.60E+04	1.65E+03	5.27E+04	7.05E+02	6.90E+03
Q8WZ42-8 TITIN	VENLTEGAIYYFR	787.90	123.98	9.37E+04	1.68E+03	3.25E+03	1.11E+03	8.88E+02	1.88E+03	3.04E+02	2.73E+03	7.73E+02	2.69E+03	9.32E+04	7.49E+02	2.87E+03	4.13E+03	1.10E+03
Q8WZ42-8 TITIN	VAAENAIGQSDYTEIEDSVL AK	775.05	124.34	2.06E+05	2.09E+05	3.72E+03	5.86E+04	9.80E+03	4.29E+04	1.61E+02	2.04E+04	6.16E+02	1.71E+03	1.86E+05	1.43E+04	3.97E+04	4.41E+03	1.20E+05
Q8WZ42-8 TITIN	SIFLTDWPPK	602.32	124.34	6.57E+04	1.23E+05	3.17E+04	5.86E+04	1.79E+03	3.56E+05	7.03E+04	1.34E+05	9.11E+02	7.96E+03	4.23E+04	9.60E+03	7.70E+02	3.66E+03	2.16E+03
Q8WZ42-8 TITIN	DIRPSDITQITSTPTSSMLTIK	802.43	124.44	3.18E+04	7.57E+02	9.32E+02	2.40E+03	9.09E+04	2.23E+03	1.69E+03	2.06E+02	5.58E+03	2.18E+02	6.21E+04	2.50E+03	2.89E+03	1.31E+04	5.45E+04
Q8WZ42-8 TITIN	EILEPPEIDLDAASMR	864.43	124.86	1.17E+04	1.05E+03	1.17E+04	1.72E+04	8.22E+03	1.13E+04	1.23E+03	4.06E+02	4.66E+03	3.91E+02	9.98E+03	3.53E+03	1.06E+04	6.29E+03	1.43E+04
Q8WZ42-8 TITIN	YQGQFALESDPIVAQYPYK	726.02	125.22	4.68E+03	4.71E+03	7.98E+03	4.91E+03	2.68E+03	3.88E+02	1.43E+04	5.42E+03	4.63E+03	1.31E+04	3.43E+03	3.67E+03	1.52E+03	5.94E+03	8.96E+02
Q8WZ42-8 TITIN	LLFTAPEYYAPEVH	825.42	125.35	2.83E+03	3.23E+03	1.52E+04	8.98E+04	1.61E+04	7.29E+03	7.23E+03	2.90E+03	7.23E+03	1.08E+04	1.57E+04	1.33E+04	8.76E+03	1.54E+04	3.45E+03
Q8WZ42-8 TITIN	VADADYGGKPIPTIQWIK	653.03	125.67	1.34E+04	4.92E+02	3.51E+03	3.85E+02	3.26E+04	5.59E+03	6.48E+03	4.36E+02	7.15E+03	2.15E+03	2.14E+03	1.77E+04	1.43E+03	3.00E+03	1.98E+04
Q8WZ42-8 TITIN	DIEIKPSVELPFHTFNVK	705.05	125.82	2.42E+04	4.72E+03	3.95E+03	1.68E+04	8.88E+02	6.51E+03	4.56E+03	4.61E+03	5.75E+03	5.14E+03	6.81E+04	2.81E+03	2.59E+03	3.92E+03	1.96E+04
Q8WZ42-8 TITIN	EISIEAMDFVDR	712.84	125.95	8.06E+03	3.50E+03	7.33E+03	8.46E+04	7.46E+03	1.10E+04	3.08E+03	6.19E+03	1.46E+03	4.58E+03	8.94E+04	1.04E+04	7.78E+03	8.39E+03	5.14E+03
Q8WZ42-8 TITIN	VTGLVEGLEYPFR	755.90	126.18	1.02E+05	2.00E+03	3.04E+04	1.46E+05	1.22E+04	1.75E+03	3.33E+03	1.76E+04	7.47E+03	6.50E+03	1.11E+05	6.41E+03	6.49E+04	4.48E+03	1.58E+05
Q8WZ42-8 TITIN	TANSIFLTDWPPK	745.38	126.2	1.64E+04	6.77E+03	3.12E+04	7.50E+03	5.23E+04	5.04E+03	2.67E+03	1.46E+04	1.38E+04	5.88E+03	1.28E+04	9.49E+04	2.29E+04	1.55E+04	1.17E+05
Q8WZ42-8 TITIN	DTSTTTWQIVSATVAR	868.94	126.2	5.60E+04	7.88E+03	1.02E+04	7.06E+03	5.65E+03	1.04E+04	7.67E+03	2.01E+03	3.43E+03	1.85E+04	6.24E+04	1.72E+04	5.25E+03	9.30E+03	4.87E+03
Q8WZ42-8 TITIN	TLPQEATITTAISSSMVIK	707.38	126.25	1.08E+04	3.87E+04	5.62E+03	5.15E+03	1.40E+04	1.70E+04	2.79E+04	6.87E+04	6.22E+03	8.69E+03	7.77E+03	4.38E+04	1.25E+04	6.41E+03	8.90E+03
Q8WZ42-8 TITIN	DILIPPEGELDADLR	833.43	126.67	5.99E+03	5.74E+04	5.62E+04	1.36E+04	1.02E+04	3.69E+04	6.92E+03	4.18E+04	3.20E+03	2.82E+03	5.65E+03	1.69E+04	2.24E+03	4.52E+03	1.79E+03
Q8WZ42-8 TITIN	EVELLKPIEDVTIYEK	640.02	126.79	3.73E+02	1.95E+04	1.62E+03	1.54E+03	7.71E+03	7.07E+04	3.83E+03	5.87E+03	1.87E+03	5.04E+02	2.36E+03	5.26E+03	6.44E+03	2.73E+03	2.55E+03
Q8WZ42-8 TITIN	LEPELILDAN	612.33	126.96	1.12E+04	1.19E+05	1.42E+04	4.81E+04	6.66E+03	2.22E+05	1.15E+05	1.61E+05	6.45E+04	7.06E+03	4.65E+03	1.13E+04	2.56E+03	1.74E+05	4.45E+03
Q8WZ42-8 TITIN	VAEGVPTTQHLLPGLMEGQ EYSFR	887.11	127	1.01E+05	1.96E+03	1.89E+03	5.53E+02	1.07E+04	6.55E+03	3.77E+03	6.96E+02	8.34E+02	3.50E+03	1.48E+05	4.89E+03	2.56E+04	4.55E+03	1.44E+05
Q8WZ42-8 TITIN	EILGYWVEYR	664.34	127.09	2.36E+04	7.22E+03	1.62E+04	2.76E+04	1.03E+03	9.80E+03	4.01E+03	2.34E+04	1.73E+03	7.27E+04	1.67E+04	1.65E+02	5.42E+03	6.24E+02	1.58E+04
Q8WZ42-8 TITIN	DPFGPPDAPDKPIVEDVTSN SMLVK	890.11	127.36	3.05E+04	4.70E+03	5.69E+02	2.80E+03	2.45E+03	1.88E+02	3.93E+03	1.02E+04	8.01E+02	3.28E+02	1.79E+04	9.09E+03	1.35E+04	1.28E+04	6.11E+04
Q8WZ42-8 TITIN	LEPELILDANMAR	791.42	127.54	1.23E+04	1.16E+03	1.00E+04	2.04E+04	7.57E+03	7.19E+03	5.07E+03	8.87E+02	4.35E+03	4.38E+03	4.56E+04	7.89E+03	8.18E+03	4.76E+03	3.33E+04
Q8WZ42-8 TITIN	VTGLSEGCEYFFR	754.35	127.64	5.77E+04	7.55E+03	9.27E+03	3.41E+03	1.40E+04	2.87E+03	8.64E+03	3.13E+03	6.01E+03	5.33E+03	5.64E+04	1.11E+04	8.94E+03	1.35E+04	1.77E+04
Q8WZ42-8 TITIN	DLVIEPDVKPAFSSYSVQVG QDLK	878.79	127.88	3.83E+03	2.49E+03	7.38E+04	1.68E+03	3.07E+04	4.88E+03	8.43E+03	6.34E+03	3.34E+02	4.26E+03	2.95E+03	1.50E+04	1.84E+03	1.12E+03	4.60E+03
Q8WZ42-8 TITIN	SDTGTYYIIIEAVNVCGR	849.41	128.56	2.18E+03	1.99E+04	7.98E+03	7.68E+03	2.43E+04	1.17E+05	2.29E+03	2.82E+04	1.71E+04	1.30E+04	1.70E+02	7.60E+03	2.25E+04	3.25E+04	2.13E+04
Q8WZ42-8 TITIN	ISAINDAGVGEPVIPDVEI VER	788.42	128.89	1.56E+05	2.88E+03	4.99E+04	2.81E+03	1.90E+04	2.03E+04	8.67E+03	7.53E+03	1.65E+04	7.75E+03	1.62E+05	2.23E+04	1.44E+05	5.23E+03	1.73E+05
Q8WZ42-8 TITIN	FSCDTDGEPVPTVTWLR ANHVNVPECAFTVTDLVEG GK	961.95	128.97	5.07E+04	7.83E+03	3.21E+03	1.22E+03	4.75E+03	1.99E+03	1.10E+03	4.35E+02	3.21E+03	2.51E+03	3.90E+04	1.48E+04	4.44E+03	4.05E+03	1.77E+04
Q8WZ42-8 TITIN	VPDLLEGCQYEFR	784.87	129.61	5.34E+03	1.04E+04	3.58E+03	7.11E+03	3.93E+04	3.31E+03	2.39E+03	6.47E+03	4.94E+03	3.58E+03	9.85E+03	8.18E+04	2.37E+04	1.38E+04	1.28E+05
Q8WZ42-8 TITIN	ISGLVEGTMYYFR	768.38	129.77	3.52E+03	1.20E+04	1.50E+03	1.15E+04	5.24E+03	2.29E+03	2.08E+04	1.52E+04	1.38E+03	5.18E+03	1.90E+04	1.65E+04	4.32E+03	8.00E+03	1.30E+03
Q8WZ42-8 TITIN	NSATLAWLPLR	669.88	129.9	1.98E+05	1.32E+03	3.29E+03	1.87E+05	4.61E+03	1.43E+03	2.50E+03	1.35E+02	3.11E+03	9.67E+02	1.26E+05	6.79E+03	5.02E+03	3.69E+03	3.36E+04
Q8WZ42-8 TITIN	GDWVVALASVTK	624.33	130	1.83E+05	2.16E+03	4.52E+03	1.98E+05	2.00E+04	6.43E+03	7.00E+03	1.23E+04	1.12E+04	1.49E+04	1.75E+05	1.98E+04	9.76E+03	2.51E+04	6.96E+03
Q8WZ42-8 TITIN	SATLAWLPLR	612.86	130.23	1.62E+04	1.05E+03	2.30E+03	5.76E+04	1.40E+03	7.10E+03	4.86E+02	6.22E+02	1.50E+03	5.02E+04	6.22E+04	1.17E+04	4.59E+03	2.90E+03	7.96E+03
Q8WZ42-8 TITIN	DGGSPILGYIIR	695.37	130.28	1.68E+04	4.44E+03	1.08E+04	6.50E+03	1.32E+04	4.63E+02	3.00E+04	1.66E+04	3.91E+03	7.35E+03	5.14E+04	4.97E+03	2.15E+04	7.60E+02	4.06E+04
Q8WZ42-8 TITIN	GPAVEALDSEQEIAITFVK	952.48	130.59	7.56E+04	5.98E+03	1.88E+04	9.59E+03	2.03E+04	5.90E+03	1.01E+04	9.61E+04	5.09E+03	4.10E+03	1.16E+05	8.15E+03	6.78E+03	5.05E+03	1.11E+04
Q8WZ42-8 TITIN	DGGSPIIGYLIER	695.37	130.82	5.96E+03	2.23E+03	1.67E+04	4.04E+04	6.21E+04	6.94E+03	7.87E+02	1.18E+04	7.86E+03	7.69E+03	8.49				

Q8WZ42-8 TITIN	GTPPFSVSWFK	626.82	131.28	3.46E+04	1.08E+03	4.85E+03	1.74E+04	4.95E+03	8.84E+02	1.28E+03	1.23E+02	7.90E+03	6.73E+03	6.29E+04	6.71E+03	3.65E+03	9.28E+03	8.69E+03
Q8WZ42-8 TITIN	TAVNISPPSEPSDPVTLAENV VPPR	867.46	131.34	3.85E+03	9.26E+03	4.68E+03	1.92E+03	1.38E+04	7.24E+03	1.27E+04	2.52E+04	2.21E+03	1.99E+04	5.73E+03	1.16E+04	1.86E+03	4.45E+03	6.65E+03
Q8WZ42-8 TITIN	GSATLMWDAPLLDGGAR	865.93	131.57	3.73E+04	1.09E+04	4.40E+03	3.89E+03	6.32E+03	2.40E+04	4.33E+03	2.45E+04	1.23E+04	4.77E+03	3.93E+04	8.15E+03	3.86E+03	9.90E+03	1.83E+03
Q8WZ42-8 TITIN	INVTDSLTLTTLTSLIK	816.96	131.74	2.00E+04	7.85E+02	2.62E+03	3.46E+03	3.67E+03	5.33E+03	1.41E+03	5.81E+03	6.66E+02	6.34E+02	6.17E+04	4.27E+03	2.29E+04	1.55E+03	7.62E+04
Q8WZ42-8 TITIN	IPGPPETLQIFDVSR	834.95	132.13	1.17E+05	4.30E+03	8.14E+03	5.38E+03	7.10E+03	5.13E+03	1.65E+03	1.24E+04	2.13E+03	1.40E+03	1.68E+05	5.74E+03	2.44E+05	9.97E+02	3.78E+05
Q8WZ42-8 TITIN	AVNIAGIGEPGEVTDVIEMK	1021.53	132.49	4.03E+04	4.74E+03	2.42E+03	3.24E+03	6.06E+03	4.33E+02	6.41E+02	4.84E+03	7.90E+02	5.63E+03	5.47E+04	2.14E+03	2.71E+03	2.29E+03	6.60E+04
Q8WZ42-8 TITIN	FTLAVSPVDPGTPDYIDVT	1130.58	132.52	2.50E+04	1.12E+03	2.69E+03	2.83E+03	2.70E+03	2.76E+03	1.38E+03	1.53E+03	7.39E+02	3.22E+02	8.12E+03	5.86E+02	2.38E+03	1.32E+03	1.92E+04
Q8WZ42-8 TITIN	WEQFYVVMLPR	733.38	132.69	1.11E+05	2.84E+04	1.40E+04	8.21E+03	2.43E+04	2.82E+04	7.60E+02	2.05E+04	3.89E+03	5.60E+03	1.09E+05	6.82E+03	5.10E+04	6.78E+03	3.53E+03
Q8WZ42-8 TITIN	VEVFDVPGPVLDLKPVVTN	731.75	133.18	2.37E+05	1.02E+03	1.81E+03	5.18E+03	1.00E+04	3.80E+03	1.59E+03	2.55E+02	3.55E+03	4.68E+03	3.19E+05	5.48E+03	1.53E+05	2.83E+03	2.88E+05
Q8WZ42-8 TITIN	AENIVGLGLPDTTPIEQEK	747.39	133.34	5.84E+02	1.73E+04	8.66E+03	1.99E+04	6.68E+03	4.57E+03	6.92E+03	1.72E+04	1.76E+03	1.48E+04	3.53E+03	2.41E+04	8.14E+03	6.36E+02	9.20E+03
Q8WZ42-8 TITIN	DLIPNGEYFFR	685.84	133.4	1.40E+05	5.24E+03	2.91E+03	2.84E+03	6.74E+03	7.01E+03	4.56E+04	5.73E+03	6.54E+03	6.62E+03	1.62E+05	8.15E+03	7.27E+04	5.41E+03	1.51E+05
Q8WZ42-8 TITIN	DFTTTPGPPYALAVVDVTK	996.52	133.44	9.13E+03	1.82E+03	2.77E+03	7.11E+03	9.08E+03	1.42E+03	1.27E+03	2.63E+03	2.93E+03	5.72E+03	1.05E+04	1.49E+04	1.65E+04	5.23E+03	2.11E+04
Q8WZ42-8 TITIN	FSPSPPGKPVVTDITENAA TVSWTLPK	979.52	133.84	1.66E+04	9.61E+03	2.85E+03	4.62E+03	7.67E+03	5.10E+03	4.40E+03	6.17E+03	2.12E+03	1.71E+03	2.60E+04	5.76E+03	6.88E+03	2.91E+03	2.24E+04
Q8WZ42-8 TITIN	ELLLPVLK	519.35	134.63	3.54E+05	4.73E+03	6.03E+02	5.60E+05	9.54E+02	2.95E+03	3.18E+02	3.08E+03	2.78E+02	4.84E+02	4.40E+05	6.41E+03	2.04E+05	2.91E+02	1.09E+04
Q8WZ42-8 TITIN	NLCTLELFSVNR	704.87	134.73	1.73E+03	5.21E+03	7.13E+03	6.64E+03	1.40E+03	3.64E+03	7.73E+03	5.88E+03	2.57E+03	1.94E+04	1.79E+03	3.36E+04	2.87E+04	1.22E+04	6.58E+04
Q8WZ42-8 TITIN	FGIGSYLQSEVIECR	850.92	134.74	2.91E+03	1.68E+04	2.64E+03	1.38E+03	3.21E+04	2.41E+04	7.11E+03	1.12E+04	1.05E+04	3.21E+03	1.81E+03	3.57E+03	5.14E+03	4.17E+03	5.39E+03
Q8WZ42-8 TITIN	NAMPEDIAEYAVEIEGK	939.94	135.18	1.39E+03	1.27E+04	1.87E+04	9.34E+03	3.30E+03	2.60E+04	2.38E+03	1.91E+04	2.87E+03	3.70E+03	2.66E+04	4.05E+03	5.61E+03	9.01E+03	2.16E+04
Q8WZ42-8 TITIN	IEIPDLELADDLK	742.40	135.54	8.48E+03	6.06E+04	2.42E+05	1.15E+04	3.45E+04	5.53E+04	6.43E+05	3.80E+04	3.42E+05	9.67E+03	1.77E+04	1.04E+05	5.61E+05	9.91E+04	1.26E+04
Q8WZ42-8 TITIN	DTTTTVWDDVVSATVAR	861.44	135.82	6.35E+04	2.37E+05	1.19E+05	4.09E+04	1.28E+05	1.08E+05	4.20E+04	4.72E+04	1.31E+05	9.24E+04	8.89E+04	9.05E+04	1.02E+05	9.48E+04	5.86E+04
Q8WZ42-8 TITIN	ELPLIFITPLSDVK	792.96	136.08	1.87E+05	5.15E+04	1.49E+05	1.65E+05	2.64E+04	2.47E+05	1.90E+05	1.15E+05	2.81E+04	2.11E+04	1.79E+05	4.29E+04	9.17E+04	3.50E+04	1.16E+05
P02452 CO1A1	GPAGPQGR	418.72	31.38	3.17E+02	8.57E+02	2.18E+03	4.12E+02	1.65E+03	7.31E+02	2.55E+02	6.25E+02	3.25E+02	2.17E+02	1.28E+03	2.59E+02	5.12E+02	2.48E+03	5.38E+02
P12883 MYH7	EEQAEPDGTEADK	774.32	40.99	2.60E+03	2.42E+04	1.10E+03	1.09E+04	2.44E+04	2.94E+03	8.52E+02	2.40E+03	1.05E+05	4.00E+02	4.77E+03	8.53E+03	7.72E+02	2.14E+04	7.69E+04
P10916 MLRV	TIMDQNR	439.21	41.49	1.63E+04	1.76E+02	1.30E+03	2.04E+04	1.82E+03	1.77E+04	3.41E+03	3.46E+03	1.86E+03	1.68E+02	3.29E+04	1.43E+03	1.25E+03	1.09E+03	2.10E+04
Q14315-2 FLNC	SLTATGGNHVTAR	428.89	43.96	2.79E+02	1.96E+03	4.95E+02	1.68E+03	8.67E+03	8.52E+02	1.50E+02	1.46E+03	2.20E+03	1.89E+02	8.46E+03	1.31E+03	5.40E+02	4.34E+03	6.99E+03
P02461 CO3A1	GPVGPSGPPGK	475.26	44.28	9.14E+02	1.47E+03	9.27E+03	2.71E+02	2.21E+03	2.78E+02	5.27E+03	5.97E+03	2.39E+03	1.28E+02	1.86E+02	4.13E+03	8.31E+02	8.95E+02	8.95E+02
P02452 CO1A1	GESGSPGAGPTGAR	649.31	44.44	6.72E+03	7.96E+04	1.32E+05	2.11E+04	6.65E+03	3.34E+04	1.94E+03	6.29E+03	6.84E+03	4.78E+04	4.26E+04	7.62E+03	3.51E+04	8.41E+03	4.11E+04
P02768 ALBU	LDELRLDEGK	537.77	44.89	1.55E+03	1.73E+04	2.45E+05	5.09E+02	7.40E+04	4.05E+03	3.29E+05	8.13E+02	6.86E+04	6.76E+04	2.62E+04	7.83E+02	2.20E+05	3.65E+03	8.77E+03
P17661 DESM	VSDLTQAANK	523.78	45.39	1.46E+03	6.03E+03	1.29E+03	2.93E+03	1.74E+03	1.17E+04	6.90E+02	2.99E+02	1.55E+04	3.14E+04	1.14E+04	1.91E+03	5.84E+02	1.11E+03	4.46E+04
P08590 MYL3	LTEDEVEK	481.74	46.81	3.34E+04	1.97E+04	1.18E+04	9.48E+04	1.10E+04	9.74E+03	1.65E+04	9.72E+03	3.61E+04	4.84E+05	1.17E+05	1.10E+04	2.61E+04	1.76E+04	3.05E+04
Q14896 MYPC3	APARPAPDAPED	603.79	47.51	3.17E+02	1.68E+02	3.17E+02	1.90E+02	5.16E+02	1.52E+02	2.12E+04	1.51E+04	1.37E+02	5.43E+02	1.45E+02	2.71E+02	6.70E+02	3.83E+02	1.45E+02
P25705 ATPA	EPMQTGK	452.23	48.78	3.02E+03	1.65E+03	9.09E+04	1.77E+05	1.83E+05	3.94E+03	1.51E+05	1.40E+05	9.04E+03	2.65E+04	2.45E+03	3.54E+03	9.90E+04	1.24E+03	3.11E+03
Q14315-2 FLNC	GAGGQQLDVR	529.27	49.58	2.10E+04	4.77E+03	4.81E+02	1.34E+04	9.77E+02	4.64E+03	4.42E+03	3.91E+03	1.70E+04	1.90E+02	1.56E+04	1.39E+03	1.16E+03	1.57E+03	2.14E+04
P02768 ALBU	TCVADESAENCDK	692.77	50.74	1.53E+04	3.42E+04	3.66E+03	5.04E+04	1.46E+04	3.77E+04	2.38E+03	5.79E+03	2.21E+04	1.56E+02	2.04E+04	1.63E+04	1.44E+03	1.41E+04	7.91E+04
Q14315-2 FLNC	YADQEVPR	489.24	51.29	1.23E+04	6.62E+03	9.79E+02	1.78E+04	1.89E+04	2.08E+04	2.85E+02	2.21E+02	6.63E+02	2.41E+02	3.35E+04	1.62E+03	3.03E+02	5.15E+03	1.82E+04
P02768 ALBU	DDNPNLPR	470.73	51.34	8.97E+03	3.58E+02	1.20E+05	3.20E+05	2.80E+05	3.64E+05	1.54E+05	1.53E+05	2.56E+04	2.36E+02	4.69E+05	2.46E+04	1.78E+04	5.28E+02	2.29E+05
P35609 ACTN2	VLAVNGENER	586.31	51.52	1.26E+05	6.71E+04	1.37E+04	1.21E+05	2.01E+05	1.81E+05	5.78E+04	7.98E+04	1.74E+05	2.31E+02	1.87E+05	7.83E+04	1.17E+04	8.00E+04	1.54E+05
Q14896 MYPC3	APARPAPDAPEDTGD	740.34	51.65	6.37E+02	1.49E+03	8.38E+02	1.88E+03	3.99E+03	5.52E+02	1.30E+03	4.79E+02	3.31E+02	2.41E+02	2.16E+03	5.37E+04	8.98E+03	3.09E+02	1.90E+03
Q14896 MYPC3	ELVPDSR	408.22	51.65	2.21E+04	3.14E+04	3.06E+03	3.94E+04	3.66E+03	1.71E+04	2.88E+04	5.42E+03	1.83E+04	2.01E+02	4.14E+04	1.49E+04	1.73E+04	1.57E+04	5.33E+04
P12883 MYH7	LQTENGELSR	573.79	51.88	4.96E+05	2.63E+05	1.50E+04	5.29E+04	5.14E+03	3.21E+04	4.97E+03	7.06E+03	2.02E+05	6.45E+05	6.32E+05	1.69E+04	6.04E+03	1.42E+05	5.28E+05
P35609 ACTN2	ATLPEADGER	529.76	52.95	2.54E+04	8.98E+04	9.34E+03	5.83E+04	1.31E+05	8.36E+03	3.94E+04	1.32E+04	1.74E+05	1.94E+02	7.39E+04	9.28E+04	1.08E+05	8.97E+04	7.16E+04
Q14315-2 FLNC	IECDDKGDGSCDVR	504.54	53.59	4.35E+03	5.89E+03	1.32E+03	4.42E+03	1.26E+03	2.05E+03	2.80E+03	3.74E+03	2.54E+04	2.28E+04	1.62E+04	2.20E+03	9.38E+02	1.24E+04	1.37E+04
P02461 CO3A1	NGETGPQPPGPTGPGGDK	860.40	53.7	4.52E+02	4.08E+02	3.20E+04	1.52E+03	1.35E+03	1.18E+04	2.47E+03	3.10E+03	3.25E+02	6.29E+02	1.33E+04	5.00E+02	1.50E+03	1.69E+02	1.72E+03
P17661 DESM	AQYETIAAK	497.76	53.8	8.48E+04	3.89E+04	2.30E+04	9.16E+04	4.41E+03	1.37E+05	6.05E+03	3.10E+03	6.00E+04	1.22E+05	1.53E+05	5.56E+04	1.35E+04	4.63E+04	1.32E+05
P02768 ALBU	ETCFAEAGK	507.22	53.97	3.70E+03	1.94E+04	5.81E+03	1.00E+04	5.27E+03	1.15E+03	1.75E+02	3.25E+03	4.46E+03	1.64E+04	4.92E+03	4.65E+03	3.58E+03	1.99E+03	4.11E+03
P10916 MLRV	EMLTTQAER	539.76	54.13	6.74E+05	5.11E+05	1.55E+05	9.21E+05	9.06E+04	1.17E+06	5.82E+05	9.65E+03	6.91E+05	1.94E+02	1.03E+06	5.47E+05	5.67E+04	3.97E+05	9.26E+05
Q14896 MYPC3	VHSGTYQVTVR	416.22	54.37	1.57E+02	8.79E+03	4.15E+03	4.26E+04	2.62E+03	7.45E+03	2.53E+03	5.60E+02	4.36E+04	6.60E+02	2.45E+04	2.48E+04	1.72E+03	3.56E+04	3.21E+04
Q14896 MYPC3	KLEPAYQVSK	581.83	54.51	6.81E+03	1.97E+04	1.33E+03	1.62E+04	1.12E+04	1.86E+04	7.72E+03	2.59E+03	3.91E+04	2.11E+03	2.75E+04	1.25E+04	1.51E+03	2.11E+04	2.77E+04
P02768 ALBU	AEFAEVSK	440.72	54.56	9.31E+04	2.42E+04	1.30E+04	1.70E+04	9.40E+04	1.11E+05	1.04E+04	4.38E+03	6.25E+04	1.14E+03	9.68E+04	1.19E+04	2.94E+03	5.02E+04	5.29E+04
P08590 MYL3	EVEFDASK	462.72	54.6	3.46E+04	2.46E+05	1.95E+04	2.00E+04	2.87E+04	4.44E+05	4.56E+03	8.87E+03	3.65E+05	3.31E+05	3.93E+05	2.06E+05	1.40E+04	3.50E+05	4.66E+04
P08590 MYL3	AAPAPAPPE	459.24	54.86	3.83E+02	1.94E+02	1.50E+04	1.10E+03	3.98E+03	2.35E+02	3.69E+04	4.10E+04	1.5						

P08590 MYL3	AKAAPKAAPAPAPPPPERPK	522.79	56.02	3.95E+02	4.13E+02	1.16E+03	1.32E+03	2.03E+03	1.62E+02	1.99E+03	4.00E+04	1.93E+03	7.91E+02	8.52E+02	3.60E+02	2.86E+02	6.94E+02	8.34E+02
P06576 ATPB	IVGSEHYDVAR	623.31	56.05	4.98E+03	6.66E+04	1.73E+04	2.35E+04	2.96E+03	2.31E+03	2.64E+04	2.31E+04	2.65E+03	5.34E+02	8.03E+03	2.96E+04	1.88E+04	9.28E+02	1.60E+04
P12111-2 CO6A3	IASNSATAFR	519.28	56.31	1.86E+03	4.58E+03	6.80E+03	8.25E+03	2.68E+04	9.61E+03	2.51E+04	5.53E+03	2.42E+04	1.32E+03	1.57E+04	1.59E+03	2.84E+04	3.46E+03	2.20E+03
Q14896 MYPC3	YGLATEGTR	484.24	56.41	8.03E+04	1.12E+05	7.24E+03	1.62E+05	2.37E+05	2.53E+04	1.03E+04	1.00E+04	3.94E+04	8.60E+04	1.52E+05	1.87E+05	5.01E+03	4.01E+04	1.20E+05
P02452 CO1A1	DGEAGAQQPPGPAGPAGER	845.89	56.6	5.25E+02	2.20E+03	2.26E+04	6.93E+02	6.24E+03	1.36E+04	6.58E+03	4.08E+03	1.05E+03	1.92E+03	1.69E+03	1.65E+04	5.56E+03	4.18E+02	4.82E+02
P08590 MYL3	AAPKAAPAPAPPPPERPER	556.30	56.62	4.62E+04	5.15E+04	6.87E+03	9.98E+04	4.99E+03	3.47E+03	2.23E+03	8.33E+03	2.83E+05	1.96E+04	1.60E+05	9.15E+04	3.05E+03	2.15E+03	8.91E+04
Q14315-2 FLNC	LEPGGGAEAQAVR	627.82	56.63	1.15E+05	1.30E+05	7.50E+03	2.01E+04	1.14E+04	6.36E+03	6.14E+03	1.55E+04	1.71E+02	5.73E+02	8.53E+05	3.51E+05	6.98E+03	1.06E+03	2.86E+05
P08590 MYL3	PAPAPPPPERPK	461.58	56.73	1.12E+06	4.98E+05	8.54E+05	5.97E+05	9.64E+05	3.15E+05	8.05E+05	2.97E+05	9.75E+02	3.01E+02	1.17E+06	2.84E+05	4.28E+05	1.46E+02	6.11E+05
P08590 MYL3	PAPPPPERPK	607.83	56.8	2.00E+05	3.87E+05	1.84E+05	2.37E+05	7.51E+04	3.73E+04	5.97E+03	9.01E+03	3.23E+02	2.06E+03	3.73E+05	1.67E+05	8.36E+04	1.94E+02	2.40E+05
P08590 MYL3	APAPPPPERPK	643.35	56.92	3.34E+04	3.49E+04	1.19E+03	6.07E+04	1.65E+04	1.95E+03	2.25E+02	2.04E+02	3.03E+02	2.39E+02	2.48E+04	1.98E+04	4.88E+03	3.97E+02	3.88E+04
Q14315-2 FLNC	VGVTGCDPTR	567.26	56.99	1.41E+04	3.67E+04	7.47E+03	1.09E+05	8.47E+04	1.47E+05	6.75E+03	1.80E+03	3.26E+05	5.98E+02	4.76E+05	2.11E+05	3.86E+03	2.41E+02	1.74E+05
Q14315-2 FLNC	VHVQPAVDTSQVVK	446.25	57.38	8.81E+04	4.76E+04	1.42E+04	1.25E+05	1.01E+05	2.14E+04	6.24E+03	9.64E+02	9.95E+03	3.33E+02	3.72E+05	5.48E+04	1.02E+04	4.83E+03	1.50E+05
P17661 DESM	QVEVLTNQR	543.80	57.39	5.50E+02	1.37E+03	7.04E+03	4.89E+04	2.82E+05	1.37E+05	2.53E+04	7.82E+03	2.04E+03	1.37E+03	3.24E+03	1.18E+05	6.03E+04	1.55E+04	6.15E+02
P06576 ATPB	VLDGSAPIK	450.26	58.1	1.62E+05	1.38E+05	8.78E+03	2.31E+05	1.07E+04	1.22E+05	5.51E+03	4.50E+03	2.10E+05	2.81E+02	1.74E+02	1.64E+05	1.11E+04	1.17E+05	2.14E+05
P08590 MYL3	HVLATLGER	498.28	58.12	9.02E+05	9.66E+05	5.61E+03	8.64E+04	7.31E+03	1.21E+04	2.05E+04	2.84E+04	9.26E+04	1.34E+06	9.91E+04	4.40E+04	3.67E+04	1.26E+06	1.33E+04
P08590 MYL3	AAPAPAPPPPERPER	650.34	58.2	5.34E+05	9.36E+03	4.18E+03	9.44E+03	3.34E+03	2.61E+03	1.60E+03	3.17E+03	3.93E+05	4.34E+05	1.67E+03	5.55E+03	9.72E+03	4.20E+05	1.08E+06
P17661 DESM	DGEVVSEATQQQHE	778.84	58.82	7.62E+05	1.50E+04	2.94E+03	1.13E+05	2.71E+05	6.24E+05	6.98E+03	1.26E+04	1.22E+03	7.63E+02	4.53E+05	1.61E+04	5.98E+03	1.98E+03	8.61E+02
P35609 ACTN2	HAFAGAEQAETAANR	515.25	59.11	1.25E+04	7.54E+03	2.38E+02	4.13E+02	1.22E+04	7.04E+03	4.68E+02	4.89E+02	1.16E+04	4.50E+03	8.37E+03	3.46E+02	2.12E+03	1.14E+04	1.56E+03
P35609 ACTN2	AEDIVNTPKPDER	495.25	59.25	4.35E+03	8.83E+02	5.09E+02	8.95E+02	1.20E+03	3.60E+03	5.95E+02	8.76E+02	2.88E+04	1.54E+04	7.41E+02	1.72E+04	6.76E+03	1.05E+04	7.79E+02
P17661 DESM	DGEVVSEATQQQ	645.79	59.52	2.41E+04	3.18E+03	1.31E+04	4.52E+03	7.74E+03	2.84E+02	7.68E+03	1.82E+04	5.71E+02	2.28E+02	6.75E+02	1.33E+02	5.43E+02	1.59E+04	8.24E+03
P08590 MYL3	AAPAPAPPPPERPKE	551.96	59.75	5.00E+04	3.46E+03	6.78E+02	3.32E+03	8.87E+04	3.26E+02	7.99E+02	2.22E+02	7.14E+02	8.37E+02	1.57E+04	1.42E+02	3.03E+02	4.25E+02	1.71E+05
P17661 DESM	FASEASGYQDN	594.74	59.8	1.10E+05	3.02E+04	7.17E+02	9.23E+04	8.57E+02	1.65E+03	3.03E+02	8.89E+02	5.13E+02	7.58E+02	8.12E+04	3.51E+02	2.87E+02	4.02E+02	4.14E+04
P02768 ALBU	VTKCCTESLVNR	451.56	59.9	6.79E+03	6.15E+03	4.60E+03	2.55E+04	2.31E+05	2.34E+04	1.36E+05	1.21E+04	1.29E+05	2.14E+05	3.39E+04	6.10E+04	3.60E+03	2.99E+04	4.50E+04
P08590 MYL3	AAPAPAPPPPERPK	508.94	60.15	7.25E+02	4.39E+03	1.02E+04	1.33E+03	5.25E+02	1.48E+03	3.35E+02	9.45E+02	1.64E+04	4.66E+03	4.40E+03	3.89E+03	1.35E+03	2.72E+04	3.00E+03
P12883 MYH7	ANYAGADAPIEK	610.30	60.21	8.72E+04	1.25E+05	1.84E+04	1.24E+05	7.65E+02	2.94E+02	2.82E+02	1.09E+03	8.49E+04	6.76E+02	2.12E+05	1.08E+05	6.16E+03	2.16E+05	9.90E+04
Q14896 MYPC3	VGQHLQHDQSYDR	523.26	60.27	7.06E+04	1.03E+04	4.24E+03	2.08E+04	2.63E+03	3.50E+03	3.13E+03	2.30E+03	1.09E+05	1.51E+05	9.89E+03	2.08E+02	1.26E+04	4.94E+04	8.94E+03
P12883 MYH7	KLEDECSELKR	450.56	60.54	2.24E+04	7.01E+04	1.70E+04	4.74E+03	9.67E+04	2.21E+05	2.09E+04	5.92E+04	1.47E+06	3.78E+03	3.25E+05	6.31E+05	1.66E+04	6.50E+05	3.60E+05
P12111-2 CO6A3	VAVVQYSDR	518.77	60.54	2.10E+03	3.39E+02	2.03E+02	6.87E+02	6.08E+03	1.63E+02	5.38E+02	5.57E+02	1.50E+03	1.06E+05	7.95E+03	6.91E+02	7.01E+02	3.44E+04	1.33E+03
P54296 MYOM2	SYEESIDDER	621.76	60.66	9.81E+04	1.11E+05	3.95E+02	2.28E+05	2.97E+03	4.38E+03	1.13E+03	1.42E+02	7.80E+02	3.59E+02	2.00E+05	1.36E+05	1.24E+03	1.70E+03	2.37E+05
P35609 ACTN2	LMEEYER	485.22	60.78	1.21E+04	2.11E+04	3.92E+03	1.32E+04	3.43E+03	1.09E+04	9.00E+02	4.29E+02	5.04E+05	5.22E+05	9.38E+03	3.91E+03	7.91E+02	2.49E+05	3.14E+05
P17661 DESM	QEMMEYR	493.71	60.9	4.42E+04	4.87E+02	3.03E+03	3.01E+04	5.97E+04	5.29E+04	3.38E+04	8.23E+02	1.34E+03	3.80E+02	6.34E+04	1.10E+04	2.44E+03	5.74E+02	1.79E+02
P35609 ACTN2	HRPDLIDYSK	415.22	60.92	1.31E+05	5.72E+03	3.04E+02	7.40E+02	6.10E+03	1.52E+04	2.42E+02	5.40E+02	1.60E+02	1.37E+04	2.02E+05	8.05E+03	6.05E+02	8.92E+02	9.42E+02
P35609 ACTN2	FAGAEQAETAANR	668.32	62.05	8.82E+03	6.33E+02	6.01E+02	4.49E+03	3.79E+03	2.18E+04	8.93E+02	2.07E+04	9.36E+03	3.39E+02	9.55E+02	7.18E+02	1.22E+03	1.95E+03	1.61E+03
P12111-2 CO6A3	DQNVFVAQK	524.78	62.11	6.58E+02	6.38E+03	1.92E+04	3.66E+04	4.59E+02	2.41E+04	1.98E+02	5.32E+02	1.55E+04	3.48E+04	4.27E+04	3.22E+03	2.67E+02	1.04E+04	6.23E+03
P12883 MYH7	LFDNHLGK	472.25	62.28	2.13E+05	1.24E+04	6.48E+02	3.39E+04	1.82E+04	5.81E+03	5.21E+02	5.35E+03	6.06E+04	1.72E+05	1.89E+05	3.26E+03	1.23E+03	5.60E+03	1.80E+05
P54296 MYOM2	GQVSTNAVVVR	600.84	62.5	2.23E+04	4.09E+03	1.81E+03	1.32E+04	5.13E+03	1.39E+04	4.78E+02	2.15E+03	5.70E+02	2.03E+03	5.19E+03	1.61E+04	1.26E+03	4.49E+02	1.37E+04
Q14315-2 FLNC	TARPNTDNKDGTTIVR	468.75	62.52	4.21E+02	1.74E+03	1.44E+02	1.97E+04	6.58E+04	3.59E+02	4.05E+02	1.60E+03	1.12E+04	1.34E+04	3.10E+04	6.58E+04	8.84E+03	3.56E+03	4.93E+02
P02768 ALBU	LKECCEKPLLEK	478.26	62.56	2.61E+03	3.71E+03	2.28E+03	3.10E+03	4.55E+03	7.09E+02	1.07E+03	6.08E+02	2.73E+04	1.79E+05	3.68E+03	5.96E+03	3.45E+02	3.03E+03	1.69E+03
P02768 ALBU	EVDETYVPK	540.27	62.9	3.30E+02	4.89E+03	7.14E+04	5.96E+03	1.75E+05	2.00E+05	6.29E+04	4.71E+04	1.31E+05	2.00E+04	2.62E+04	1.92E+03	5.27E+04	6.23E+04	4.78E+03
P54296 MYOM2	IPDMAPPQAKPK	474.26	62.92	1.99E+03	3.73E+03	3.20E+03	2.77E+03	8.34E+04	3.37E+02	7.46E+02	3.88E+03	1.66E+04	3.86E+02	3.26E+02	6.86E+03	6.79E+02	1.10E+03	1.10E+04
P02768 ALBU	YICENQDSISSK	693.81	62.96	5.74E+05	3.07E+04	1.16E+04	1.50E+05	3.39E+05	2.73E+04	3.53E+03	1.05E+03	8.22E+02	4.61E+03	3.11E+05	4.19E+04	1.03E+03	1.63E+03	2.33E+03
P54296 MYOM2	LIPASASAAGQ	493.27	63	2.63E+02	2.22E+05	1.41E+05	5.53E+05	1.28E+04	1.16E+05	2.87E+03	1.49E+03	1.20E+03	1.28E+04	3.84E+03	1.83E+05	5.28E+02	1.10E+03	4.34E+02
P68871 HBB	DEVGGEALGR	551.28	63.08	2.85E+02	1.07E+03	1.81E+05	1.92E+05	1.64E+04	1.05E+04	1.88E+04	1.59E+05	1.51E+03	8.63E+02	3.00E+02	1.30E+03	5.38E+04	2.36E+02	6.37E+02
P12883 MYH7	IKELTYQTEEDR	508.92	63.11	4.39E+04	2.81E+04	2.59E+02	6.60E+04	1.91E+05	3.97E+02	1.13E+03	5.37E+04	4.10E+04	2.16E+03	1.07E+05	8.33E+02	2.54E+02	6.19E+04	1.39E+05
P17661 DESM	VSDLTQAANKNNDALR	577.30	63.16	5.59E+03	5.10E+03	7.64E+03	4.77E+04	4.11E+04	4.07E+04	4.73E+03	1.59E+04	3.43E+04	1.06E+03	6.00E+04	1.69E+04	1.33E+03	2.40E+04	9.97E+03
P06576 ATPB	VIGEPIDER	514.27	63.24	1.74E+02	2.90E+03	3.46E+04	7.08E+02	8.57E+02	2.13E+05	5.13E+04	2.42E+05	1.06E+03	3.86E+03	1.51E+04	8.25E+02	2.06E+05	4.40E+02	5.01E+02
Q14315-2 FLNC	HVSAYGPGLSHGMVNK	551.94	63.28	2.28E+04	1.88E+03	4.29E+03	5.95E+02	1.09E+03	4.19E+02	5.12E+02	9.93E+02	3.28E+03	1.01E+04	2.06E+03	4.54E+02	1.48E+03	4.75E+02	3.29E+02
P17661 DESM	ADVDAATLAR	501.76	63.45	7.81E+05	2.09E+04	7.15E+03	2.50E+04	1.36E+03	2.77E+04	1.81E+03	6.94E+04	5.10E+06	3.51E+06	4.32E+06	2.23E+04	5.76E+04	3.76E+06	9.28E+03
P02452 CO1A1	GFSGLDGAK	426.22	63.48	1.70E+04	3.00E+03	1.43E+03	3.44E+02	1.74E+03	6.90E+02	3.86E+02	9.03E+02	5.80E+03	2.53E+04	2.56E+03	1.81E+03	1.87E+03	1.30E+03	6.25E+02
P17661 DESM	TSGGAGGLGSLR	516.78	63.58	2.56E+05	1.61E+04	1.03E+04	3.22E+04	9.36E+03	1.16E+04	1.33E+02	1.53E+03	4.26E+05	3.65E+05	3.07E+04	2.61E+04	3.41E+03	1.69E+05	4.18E+05
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Q14315-2 FLNC	TDTYVTDNGDGTYP	789.34	65.39	4.58E+04	3.43E+04	8.62E+02	6.77E+04	2.86E+03	4.00E+03	8.25E+02	1.87E+03	6.24E+02	2.59E+02	6.12E+04	3.10E+03	2.05E+02	5.27E+03	1.93E+03
P08590 MYL3	AAPAPAPPEPERP	698.86	65.75	1.09E+04	9.94E+02	1.09E+04	2.12E+03	1.91E+03	8.27E+04	1.12E+04	1.08E+04	4.40E+02	9.76E+02	2.74E+02	4.61E+02	1.98E+03	7.82E+02	5.57E+02
P54296 MYOM2	SVVSGSGSWQR	531.77	65.93	2.97E+03	4.66E+02	1.30E+04	8.50E+02	5.45E+02	1.51E+03	9.94E+02	1.14E+04	1.30E+05	9.83E+04	3.03E+03	1.04E+03	8.02E+03	3.49E+04	7.52E+02
P12883 MYH7	QVQAEQDNLADAEER	858.40	66.02	3.79E+04	2.01E+03	3.77E+03	2.95E+03	8.88E+02	4.40E+02	1.33E+03	4.23E+02	8.99E+02	1.96E+02	1.75E+04	2.90E+03	2.10E+02	3.51E+04	1.16E+04
P35609 ACTN2	VIQSYNIR	496.78	66.08	1.48E+04	3.48E+03	7.98E+02	3.75E+03	5.95E+03	1.95E+03	1.45E+03	1.71E+03	6.53E+05	3.76E+05	5.17E+03	4.47E+03	1.35E+03	1.47E+05	8.17E+03
Q14315-2 FLNC	TGVEVGKPTHF	586.31	66.19	1.35E+04	1.91E+04	9.36E+02	2.94E+04	3.69E+03	1.34E+04	1.54E+04	5.97E+02	4.09E+02	3.49E+04	4.33E+04	1.51E+04	7.10E+02	7.35E+04	4.28E+03
P35609 ACTN2	AFAGAEQAETAANR	703.84	66.49	1.24E+05	1.07E+04	1.15E+03	8.67E+04	2.33E+02	1.93E+03	4.57E+02	7.32E+02	7.54E+02	5.92E+02	8.39E+04	2.08E+04	5.19E+03	1.37E+03	4.01E+02
P69905 HBA	ALSALSDLHAHK	421.57	66.63	1.20E+03	8.65E+03	4.67E+03	4.53E+04	1.06E+05	5.72E+04	2.35E+05	6.02E+03	1.02E+03	4.60E+02	1.77E+03	3.85E+03	2.38E+03	5.08E+03	1.75E+03
P02768 ALBU	ETYGEMADCCAK	660.75	66.77	5.35E+03	2.75E+04	8.12E+03	4.34E+04	3.23E+04	2.13E+04	1.89E+03	3.22E+03	1.81E+02	4.99E+02	3.91E+04	1.07E+04	7.35E+02	7.44E+02	6.23E+03
P06576 ATPB	LATDMGTMQER	626.79	66.82	3.14E+04	2.25E+03	4.48E+03	1.24E+03	3.57E+02	2.61E+02	7.29E+02	4.06E+02	3.46E+02	1.78E+02	2.08E+04	1.61E+03	3.47E+03	6.69E+02	3.34E+04
P17661 DESM	FANYIEK	442.73	66.84	2.18E+03	2.39E+03	2.13E+05	1.96E+03	4.55E+05	3.56E+05	4.37E+05	3.86E+05	4.31E+02	9.51E+03	2.38E+03	5.06E+02	2.93E+05	1.15E+03	2.79E+03
P69905 HBA	VDPVNFK	409.72	67.01	1.44E+06	1.80E+06	2.67E+04	1.87E+04	2.34E+05	4.79E+04	1.10E+05	1.04E+04	1.81E+06	2.06E+06	6.01E+04	4.76E+04	3.76E+04	1.88E+06	9.02E+05
P12883 MYH7	EKEMASMKEEFTR	539.26	67.15	3.24E+02	8.85E+02	1.20E+03	2.27E+04	4.28E+05	2.14E+03	2.32E+05	1.78E+03	3.44E+03	1.45E+04	1.21E+03	2.17E+05	1.08E+05	2.40E+04	7.14E+02
P35609 ACTN2	QYEHNIINYK	441.22	67.16	1.02E+04	7.22E+02	1.62E+03	1.49E+03	1.17E+03	9.67E+02	1.36E+03	4.34E+02	2.28E+05	3.23E+05	2.21E+03	9.12E+02	3.40E+02	8.11E+04	1.36E+04
Q14315-2 FLNC	VIDNGDGTFR	538.28	67.18	1.44E+04	6.77E+03	1.00E+05	2.02E+05	4.05E+04	6.49E+04	4.17E+04	2.58E+04	1.34E+05	6.05E+04	4.22E+03	1.29E+05	1.10E+05	5.65E+04	1.65E+04
P02768 ALBU	ADICLSEK	490.24	67.18	1.97E+03	7.83E+04	4.34E+04	6.01E+04	5.91E+04	5.63E+04	5.21E+04	5.21E+03	3.72E+03	3.88E+02	1.24E+05	2.48E+04	5.34E+04	1.29E+03	9.02E+02
P12883 MYH7	ELENELEAEQKR	744.37	67.28	8.87E+02	9.40E+04	1.76E+03	9.95E+03	2.09E+06	5.22E+03	1.47E+04	2.17E+04	7.13E+02	7.90E+02	2.28E+05	1.10E+06	6.37E+03	4.22E+02	4.00E+05
P54296 MYOM2	ASSQTSLGGTICR	640.82	67.38	8.38E+03	5.63E+04	1.22E+03	3.94E+04	1.08E+04	6.01E+03	4.60E+02	5.47E+02	1.60E+04	4.44E+02	1.42E+05	3.46E+03	7.00E+02	7.15E+03	8.44E+04
Q14315-2 FLNC	RDTVEVALEDK	637.83	67.82	1.69E+03	1.35E+04	2.71E+02	3.17E+04	1.19E+04	8.68E+02	8.50E+03	4.85E+02	2.98E+03	1.00E+04	4.05E+04	6.81E+03	1.10E+03	7.04E+03	4.10E+03
P54296 MYOM2	IPDMAPPQAK	598.30	67.84	2.45E+05	3.82E+03	1.54E+03	1.23E+04	5.35E+03	8.08E+03	1.25E+04	2.31E+03	1.26E+05	1.73E+04	5.29E+05	2.59E+03	6.34E+03	2.23E+05	3.49E+05
P69905 HBA	VGAHAGEYGAEALER	765.37	67.86	3.83E+06	2.94E+06	7.09E+04	3.21E+06	4.87E+06	5.63E+04	9.62E+04	1.13E+03	2.39E+03	5.25E+03	3.24E+06	3.13E+06	5.31E+03	1.94E+03	2.06E+06
Q14896 MYPC3	GGSSAALNGPTPGAPDD	757.34	68.3	1.05E+03	2.47E+03	5.96E+04	1.22E+03	3.83E+02	8.21E+02	2.23E+04	2.13E+04	1.25E+03	2.19E+03	1.35E+03	4.44E+03	2.80E+03	3.11E+02	3.14E+02
P12883 MYH7	AVIAAIGDR	443.26	68.58	1.25E+05	7.97E+03	5.15E+03	2.41E+03	6.01E+02	1.31E+03	3.62E+02	4.70E+02	1.27E+04	9.73E+04	4.73E+03	2.92E+03	1.43E+03	4.79E+04	8.71E+03
P12883 MYH7	VRELENELEAEQKR	581.64	68.7	3.54E+02	3.70E+03	7.73E+03	4.58E+03	1.32E+04	9.22E+03	2.33E+04	1.25E+03	6.81E+03	3.69E+02	1.49E+05	6.94E+03	6.07E+03	1.19E+03	8.30E+03
P06576 ATPB	PAVDPLDSTSR	579.30	68.82	2.17E+04	3.40E+03	1.20E+04	1.07E+03	1.24E+03	4.45E+03	4.70E+03	2.44E+04	2.44E+04	3.11E+03	1.59E+03	2.35E+03	4.92E+03	5.26E+03	1.40E+04
Q14896 MYPC3	NGLDLGEDAR	530.26	69.24	2.38E+04	2.48E+04	1.79E+03	7.98E+04	2.20E+05	2.38E+04	4.72E+04	1.03E+04	7.05E+02	2.28E+03	4.88E+05	2.66E+05	6.40E+02	1.40E+03	2.60E+05
P69905 HBA	AGEYGAEALER	583.28	69.29	9.56E+04	1.60E+04	1.46E+04	1.24E+05	9.76E+04	1.13E+04	1.08E+04	8.13E+03	2.72E+06	5.56E+06	9.76E+04	1.69E+04	5.46E+04	5.46E+06	1.01E+05
P25705 ATPA	ELIIGDR	408.23	69.34	1.02E+03	4.45E+05	3.75E+05	4.67E+04	8.84E+05	9.21E+05	8.95E+05	9.60E+03	1.07E+05	5.28E+04	9.65E+04	5.31E+05	5.92E+05	6.53E+04	4.29E+05
P35609 ACTN2	ISNRPAFMPSEGK	478.58	69.46	1.18E+06	6.21E+03	9.29E+03	4.40E+04	1.53E+06	2.34E+04	7.51E+03	1.29E+04	5.21E+02	9.15E+04	1.01E+06	1.79E+06	6.65E+04	6.43E+02	2.32E+06
Q14315-2 FLNC	AEIAFEDR	475.73	69.56	7.14E+03	2.74E+04	3.16E+04	6.66E+03	1.82E+04	1.32E+04	1.52E+04	3.10E+03	4.70E+05	2.93E+05	1.49E+04	8.28E+03	1.05E+04	8.58E+03	5.64E+04
Q14315-2 FLNC	YMPPEEGPYK	605.78	69.88	6.19E+04	7.77E+04	1.83E+05	3.85E+05	5.60E+04	1.36E+05	3.08E+04	1.45E+04	7.13E+02	4.98E+02	1.40E+04	2.82E+05	1.19E+05	1.81E+03	1.80E+03
Q14315-2 FLNC	FIFPHGVHSIDVK	531.28	70.17	6.33E+03	3.75E+04	2.39E+04	8.57E+04	4.06E+04	6.75E+04	2.33E+03	9.36E+03	9.71E+03	1.11E+03	2.62E+05	9.18E+03	1.03E+04	2.02E+04	9.89E+04
P06576 ATPB	SVFAGVHS	461.24	70.24	4.16E+03	4.44E+04	1.90E+04	2.12E+04	1.11E+05	1.11E+05	3.17E+05	2.54E+04	1.04E+03	5.64E+02	2.98E+04	5.50E+04	2.51E+04	5.91E+03	7.37E+04
P12111-2 CO6A3	VVESLDVQGDR	608.81	70.27	1.87E+05	2.46E+04	3.37E+04	4.18E+05	2.82E+05	3.38E+04	6.72E+03	1.69E+04	2.60E+03	8.24E+02	2.89E+05	1.88E+05	6.54E+03	6.98E+03	3.60E+05
P12883 MYH7	IEDEQALGSQLQKK	793.92	70.36	7.75E+02	9.08E+02	1.53E+03	3.27E+03	1.93E+05	4.17E+03	2.01E+03	6.07E+02	1.64E+02	8.36E+02	7.63E+04	4.24E+02	2.60E+03	4.34E+02	1.25E+05
P35609 ACTN2	SNRPAFMPSEGK	660.83	70.48	3.85E+04	3.98E+04	4.35E+04	5.02E+03	4.68E+02	1.34E+04	8.17E+03	7.04E+03	1.25E+04	3.44E+03	5.36E+05	8.53E+03	2.22E+04	4.88E+03	3.86E+05
Q14896 MYPC3	GGSDISASNKYGLATEGTR	628.64	70.61	5.43E+02	7.32E+03	9.88E+03	3.14E+03	1.19E+03	5.76E+03	9.51E+02	9.62E+03	2.37E+02	2.39E+02	2.23E+04	3.06E+03	1.56E+03	2.06E+03	5.36E+04
Q14315-2 FLNC	FNPQEMGPH	521.24	71.02	6.75E+05	1.46E+04	4.61E+03	5.80E+05	4.12E+04	7.68E+03	1.25E+04	2.97E+02	8.56E+02	5.37E+03	4.96E+05	1.80E+04	2.20E+04	1.78E+03	1.70E+05
P06576 ATPB	PNIQGEHYDVAR	486.24	71.03	3.82E+03	3.13E+03	1.22E+03	2.94E+04	3.02E+03	9.21E+03	1.78E+04	3.02E+03	2.06E+04	9.51E+04	1.39E+03	2.91E+04	8.25E+03	1.45E+04	1.14E+04
P02768 ALBU	TPTLVEVSR	501.28	71.08	4.63E+02	9.32E+04	1.20E+03	5.63E+04	6.91E+04	6.02E+03	2.14E+03	5.94E+04	4.46E+03	3.11E+04	5.25E+04	7.68E+04	1.58E+05	9.50E+03	7.47E+03
Q14896 MYPC3	QYGVTDLR	476.25	71.18	1.96E+05	1.52E+05	1.31E+04	1.16E+04	9.56E+03	1.20E+04	8.14E+03	2.06E+03	6.46E+02	1.32E+03	2.10E+05	4.59E+03	2.25E+03	1.59E+03	5.41E+04
P54296 MYOM2	AVGMSSENSQSDVIK	797.38	71.23	1.84E+04	4.97E+03	3.26E+02	2.68E+03	1.83E+04	9.59E+03	3.49E+03	8.86E+02	1.06E+03	1.90E+03	2.55E+04	6.32E+03	2.52E+03	4.95E+02	4.82E+03
P10916 MLRV	NLVHIITHGEEK	695.38	71.35	2.83E+03	3.86E+03	2.03E+04	1.31E+03	4.20E+03	2.89E+05	3.34E+03	9.64E+03	9.53E+04	2.46E+05	4.27E+05	1.02E+04	4.21E+03	2.01E+03	4.75E+03
P12111-2 CO6A3	TELQITINDPR	644.33	71.5	3.26E+05	2.05E+05	2.57E+04	4.55E+05	2.80E+05	3.28E+04	1.41E+04	1.18E+04	5.22E+03	5.61E+03	4.36E+05	1.90E+05	8.37E+03	2.78E+02	4.10E+05
P02768 ALBU	LVAASQAALG	450.76	71.78	6.69E+05	5.50E+05	1.50E+04	4.82E+05	2.33E+06	1.41E+04	3.19E+04	4.79E+04	6.06E+03	3.95E+03	1.25E+06	2.68E+04	8.14E+03	7.32E+02	7.61E+05
P25705 ATPA	ISVREPMQTGIK	453.59	71.91	5.73E+04	1.86E+04	6.05E+03	7.01E+04	2.24E+05	4.98E+03	1.54E+04	1.60E+04	2.67E+03	3.95E+02	2.46E+03	1.75E+04	1.22E+04	3.00E+03	2.50E+02
P08590 MYL3	LGQNPTQAEVLR	663.36	71.93	3.03E+04	1.24E+04	2.31E+03	1.08E+04	6.03E+03	2.09E+03	1.92E+03	8.04E+03	1.58E+05	4.28E+05	1.95E+04	4.88E+03	6.16E+03	1.50E+05	2.44E+04
P69905 HBA	VADALTNVAH	541.28	72.09	5.21E+06	1.73E+04	4.60E+03	1.91E+04	1.61E+06	2.39E+04	1.04E+04	1.07E+04	2.96E+03	1.33E+04	2.80E+06	1.46E+04	3.92E+02	2.90E+04	1.53E+06
P02768 ALBU	LCTVATLR	438.75	72.11	1.55E+04	2.58E+05	3.84E+04	2.02E+05	1.36E+05	2.26E+05	8.06E+04	9.76E+03	2.86E+04	2.18E+02	2.66E+04	8.84E+04	2.03E+05	1.07E+04	2.26E+04
P68871 HBB	LSTPDVVMGNPK	615.32	72.14	8.88E+03	3.11E+04	2.79E+03	1.02E+04	1.15E+03	4.17E+03	1.53E+04	8.35E+03	1.40E+04	6.62E+04	5.47E+02	1.81E+04	1.07E+04	2.34E+04	1.82E+03
P08590 MYL3	EGNGTVMGAELR	617.30	72.27	5														



P06576 ATPB	AHLDATTVLSR	592.33	73.13	2.21E+05	8.43E+03	5.07E+03	1.53E+04	5.73E+03	2.74E+04	1.28E+04	2.12E+03	1.63E+03	2.17E+02	1.26E+05	1.74E+04	2.03E+04	8.03E+02	3.23E+04
P17661 DESM	FASEASGYQDNAR	764.85	73.44	3.21E+06	2.14E+04	1.18E+04	2.97E+06	2.31E+06	2.36E+04	2.38E+04	4.96E+03	1.98E+04	4.92E+03	3.81E+06	3.33E+04	1.02E+06	6.16E+03	3.37E+06
P17661 DESM	LQEEIQLK	500.79	73.46	1.35E+02	8.20E+05	2.59E+04	2.24E+06	5.29E+05	3.76E+06	2.56E+05	1.29E+04	1.59E+04	6.04E+04	7.70E+02	7.45E+05	7.61E+05	2.12E+04	2.32E+06
P10916 MLRV	NLVHIITHGEEKD	502.26	73.6	3.49E+03	3.83E+03	3.33E+04	1.95E+03	9.65E+02	3.54E+03	3.15E+04	5.26E+03	1.88E+06	1.45E+06	5.48E+05	6.39E+04	7.68E+02	4.00E+04	5.60E+03
Q14315-2 FLNC	VYNVYTYTVK	543.79	73.76	3.40E+02	6.61E+03	1.32E+05	2.66E+03	9.38E+04	1.19E+05	7.02E+04	2.19E+03	3.77E+03	1.05E+04	7.15E+03	1.73E+05	4.24E+04	5.85E+03	1.48E+03
Q14896 MYPC3	AATTKEPVFIPR	443.91	73.84	2.46E+03	2.93E+02	1.70E+04	2.30E+04	4.12E+04	3.08E+04	7.10E+04	7.27E+03	3.77E+03	1.68E+04	1.26E+03	5.66E+04	3.03E+03	1.29E+03	7.42E+02
P02768 ALBU	AAFTTECCQAADK	629.26	73.84	1.20E+05	1.61E+04	9.42E+02	4.26E+04	2.44E+04	6.32E+03	2.63E+03	7.89E+03	4.59E+05	6.51E+05	8.98E+04	1.62E+04	9.45E+03	3.27E+05	8.84E+04
P10916 MLRV	IDKNDLR	437.24	73.99	1.92E+03	4.19E+02	6.36E+02	4.33E+02	1.29E+05	2.95E+04	2.16E+04	3.36E+02	4.05E+03	7.58E+02	2.46E+04	4.44E+04	4.50E+03	4.95E+03	7.04E+04
P54296 MYOM2	PSDTSEPVLEEAR	700.36	74.01	1.24E+05	1.54E+03	4.51E+02	1.29E+03	4.19E+02	5.68E+02	2.60E+03	1.77E+03	2.46E+03	5.01E+02	5.77E+04	8.36E+03	3.68E+02	7.43E+04	3.08E+04
P69905 HBA	VG AHAGEYGAEALE	687.32	74.15	5.84E+03	9.46E+02	2.15E+02	3.57E+03	5.37E+02	2.89E+04	6.46E+03	1.13E+03	1.63E+04	2.09E+03	2.77E+04	6.78E+02	2.94E+02	2.93E+03	6.05E+03
P69905 HBA	VG AHAGEYGAEAL	622.80	74.18	1.80E+03	2.88E+04	4.50E+04	8.61E+02	1.40E+05	3.55E+05	2.03E+04	7.13E+03	2.37E+04	2.20E+04	2.12E+03	2.39E+02	3.65E+04	4.19E+03	6.36E+03
Q14315-2 FLNC	ATIRPVFDPK	410.90	74.22	4.76E+03	6.62E+04	5.93E+03	2.02E+04	2.49E+03	6.66E+03	5.68E+03	9.03E+02	5.57E+04	2.55E+05	6.58E+03	4.99E+04	1.78E+04	9.25E+04	6.47E+03
P25705 ATPA	LELAQYR	446.75	74.32	1.22E+03	4.37E+05	2.78E+03	3.65E+05	1.08E+06	5.72E+02	2.46E+04	1.43E+03	1.04E+04	3.10E+04	8.68E+05	1.99E+04	7.91E+05	1.26E+03	6.59E+05
P12111-2 CO6A3	IAVAQYSDDDVK	604.81	74.36	2.03E+05	9.47E+02	1.63E+03	2.71E+05	1.01E+05	5.94E+03	3.07E+03	7.72E+03	1.60E+03	1.09E+03	2.17E+05	3.31E+03	1.98E+02	2.77E+03	2.29E+05
Q14896 MYPC3	IEDEGVYTVTVK	620.31	74.56	8.06E+05	7.83E+03	1.23E+04	1.86E+04	9.04E+03	4.36E+04	1.17E+03	1.16E+03	2.29E+03	3.77E+03	7.28E+05	3.11E+03	6.19E+04	2.48E+04	6.99E+05
P25705 ATPA	IYDDLSK	483.76	74.56	1.01E+04	5.07E+05	1.03E+04	3.07E+05	4.54E+04	2.58E+05	8.15E+04	4.08E+03	6.09E+02	1.03E+03	2.79E+02	1.53E+05	2.46E+05	1.27E+03	2.19E+05
P12111-2 CO6A3	ILAAESLPK	471.29	74.62	7.34E+02	1.02E+03	2.97E+02	1.08E+05	3.22E+02	1.42E+05	1.12E+03	4.15E+02	1.87E+03	5.18E+03	9.22E+02	5.70E+03	2.95E+02	3.28E+03	1.06E+03
P10916 MLRV	DGFIDKNDLR	596.80	74.69	3.54E+04	1.69E+03	1.39E+03	2.47E+03	9.31E+03	1.46E+04	8.06E+04	1.15E+05	4.00E+03	6.65E+02	8.30E+05	1.27E+04	1.54E+04	2.56E+04	1.11E+06
P12883 MYH7	ERLEAQTRPFDLK	534.96	74.9	3.12E+02	2.30E+04	9.41E+02	5.31E+04	1.52E+05	2.09E+04	1.73E+05	1.27E+04	9.09E+03	5.61E+04	1.41E+03	2.87E+05	1.88E+03	3.85E+02	8.87E+03
P12111-2 CO6A3	ALEFVAR	403.23	74.92	1.81E+02	1.05E+03	7.52E+04	5.96E+04	5.43E+05	4.19E+05	4.75E+05	1.66E+04	4.15E+03	2.15E+03	2.26E+03	1.49E+05	7.05E+04	1.22E+04	2.11E+05
P02768 ALBU	KYALVELVK	564.85	74.93	2.80E+02	1.94E+03	9.72E+03	1.69E+04	1.92E+05	6.94E+03	2.00E+05	8.96E+02	5.15E+02	5.97E+02	2.79E+02	6.49E+04	8.47E+02	3.58E+04	4.88E+04
Q14315-2 FLNC	QTAVSYVPK	514.28	75.17	1.18E+03	4.94E+03	5.81E+03	5.87E+05	2.90E+05	2.31E+04	7.77E+02	1.97E+03	2.03E+04	2.63E+02	6.32E+05	2.51E+03	3.51E+05	1.87E+04	5.45E+05
P08590 MYL3	TPEQIEEFK	560.78	75.3	1.77E+05	1.46E+03	9.75E+03	2.88E+04	8.74E+02	3.88E+03	1.17E+04	1.36E+04	1.82E+03	7.21E+03	1.25E+05	1.03E+03	1.55E+03	1.33E+03	1.15E+05
Q14315-2 FLNC	APSGNEEPCLLK	629.31	75.3	1.83E+04	1.74E+03	6.53E+03	1.78E+04	3.67E+03	4.45E+03	5.44E+03	4.64E+02	5.54E+02	2.34E+03	2.37E+05	4.84E+02	1.22E+03	2.48E+04	6.30E+04
Q14315-2 FLNC	HIGISFTPK	500.28	75.33	2.72E+03	1.68E+05	4.78E+03	3.03E+05	3.79E+05	3.71E+05	2.75E+05	7.14E+02	2.66E+03	7.17E+03	9.20E+02	4.77E+05	2.93E+05	1.84E+04	9.16E+02
P25705 ATPA	VVSQHQALLGTIR	474.61	75.36	3.14E+05	3.13E+03	4.63E+03	2.93E+03	2.01E+03	7.30E+03	1.93E+03	2.06E+03	7.84E+02	1.41E+03	1.40E+05	9.22E+02	2.58E+02	1.65E+03	5.74E+03
P12883 MYH7	IKELTYQTEEDRKNLLR	538.05	75.58	1.20E+03	5.26E+02	2.59E+03	1.63E+03	5.63E+04	9.46E+02	2.52E+02	4.32E+02	1.84E+03	2.41E+03	5.29E+02	3.15E+03	1.36E+03	1.20E+03	1.50E+05
P54296 MYOM2	VLCTPEGIR	494.27	75.59	2.45E+03	2.84E+05	3.08E+03	2.20E+05	2.24E+05	6.77E+04	1.87E+05	8.32E+03	1.22E+03	2.38E+03	1.22E+04	1.82E+05	7.27E+02	1.95E+03	2.99E+05
P54296 MYOM2	TSVVVQWDRPK	438.91	75.66	2.22E+03	1.22E+05	4.67E+03	2.37E+05	8.17E+04	4.34E+03	5.26E+03	9.97E+03	5.42E+02	5.91E+02	3.83E+03	3.31E+04	4.16E+04	1.67E+03	2.05E+05
P02768 ALBU	VEEPQNLK	535.29	75.74	1.23E+03	6.23E+04	5.40E+03	6.50E+04	4.72E+02	7.45E+04	1.45E+03	9.83E+04	1.31E+04	5.53E+02	3.23E+04	2.74E+03	1.79E+03	8.18E+02	4.92E+04
Q14315-2 FLNC	VVPVASLSDAR	614.83	76.13	5.13E+03	6.32E+03	5.35E+04	7.07E+02	1.68E+04	6.36E+04	3.51E+03	2.71E+03	1.56E+02	3.58E+02	1.02E+03	6.45E+02	5.28E+02	4.02E+03	3.45E+03
Q14315-2 FLNC	AGTNMMVMGVHGP	477.23	76.14	2.95E+02	1.65E+03	7.55E+04	4.15E+04	5.70E+04	3.83E+04	2.74E+04	8.15E+02	6.50E+02	4.43E+03	2.18E+04	5.00E+04	2.46E+03	2.53E+03	1.37E+04
P68871 HBB	VNDDEVGGEALGR	657.83	76.35	2.67E+06	2.32E+04	1.16E+04	2.25E+06	1.74E+06	6.66E+03	6.29E+03	1.35E+04	1.17E+06	1.31E+03	1.78E+06	3.30E+06	3.37E+05	1.27E+03	9.12E+05
P12883 MYH7	ISDLTEQLGSSGK	667.84	76.57	1.16E+05	4.41E+04	5.12E+05	2.15E+03	4.10E+03	1.31E+03	1.02E+03	3.92E+05	3.90E+04	5.13E+02	7.49E+03	1.07E+03	2.47E+03	2.14E+03	1.27E+03
P12883 MYH7	LEAQTRPFDLK	659.36	76.62	1.22E+06	2.51E+04	1.64E+04	6.88E+04	9.90E+03	1.90E+04	1.44E+04	3.05E+04	7.51E+02	4.85E+02	1.19E+06	3.33E+04	7.15E+05	1.48E+03	1.54E+04
Q14315-2 FLNC	DTVEVALEDK	559.78	76.77	1.54E+03	1.34E+04	2.97E+04	9.36E+04	7.23E+03	1.03E+04	1.79E+03	1.20E+04	1.67E+03	1.51E+04	1.73E+03	1.80E+03	6.30E+03	3.17E+03	5.16E+03
P12111-2 CO6A3	GFMYDRPLR	577.79	76.79	1.67E+03	9.22E+02	7.99E+04	2.08E+03	1.39E+03	6.21E+04	6.34E+04	3.44E+04	6.39E+03	6.74E+02	1.95E+03	1.07E+03	8.00E+02	3.25E+04	1.18E+03
P02768 ALBU	SLHTLFGDK	509.27	76.84	1.17E+05	3.28E+03	2.15E+03	1.02E+04	2.52E+04	2.77E+03	2.77E+03	2.54E+03	8.26E+02	1.55E+05	2.81E+05	5.63E+02	2.81E+03	6.60E+04	2.19E+03
P06576 ATPB	LVLEVAQH	454.76	76.93	5.39E+02	1.94E+03	2.04E+06	3.86E+06	1.62E+06	2.99E+06	1.69E+06	2.05E+06	2.31E+03	9.42E+04	1.40E+03	2.33E+06	5.38E+02	5.90E+02	2.45E+03
P02768 ALBU	FPKAEFAEVSK	418.22	77	5.24E+03	7.25E+03	6.23E+03	7.24E+04	7.54E+04	9.87E+04	1.90E+04	3.65E+03	4.51E+02	8.14E+02	3.40E+03	9.28E+04	2.82E+03	6.16E+03	9.40E+03
P10916 MLRV	EMLTTQAERFSK	720.86	77.04	6.99E+03	1.17E+03	2.91E+03	3.38E+03	1.50E+03	1.36E+03	2.20E+03	1.28E+03	6.48E+04	3.05E+05	1.48E+03	1.22E+03	5.29E+02	3.44E+04	2.35E+03
P02768 ALBU	LVAASQAAL	422.25	77.08	5.14E+05	1.19E+04	1.16E+03	7.55E+03	5.92E+02	6.34E+04	2.24E+04	3.73E+04	1.53E+03	7.62E+02	4.32E+05	3.21E+02	3.16E+03	2.85E+03	1.19E+04
P25705 ATPA	GYLDKLEPSK	575.31	77.11	5.94E+03	1.75E+04	4.27E+03	3.13E+04	8.22E+03	1.81E+04	5.71E+04	3.60E+03	5.33E+03	2.15E+04	1.40E+04	1.61E+04	7.85E+02	2.76E+03	6.41E+04
P54296 MYOM2	FLSELAH	408.72	77.11	4.25E+03	1.23E+02	1.50E+04	1.73E+05	6.17E+02	1.00E+05	9.51E+03	2.15E+03	9.83E+03	9.64E+03	4.04E+03	2.22E+04	1.65E+03	8.26E+02	2.66E+03
P12111-2 CO6A3	IIDELNVKPEGTR	742.41	77.24	2.24E+02	9.54E+03	9.73E+02	4.78E+03	2.21E+02	9.86E+03	4.39E+03	8.37E+02	3.49E+04	5.76E+04	1.76E+03	2.48E+03	2.70E+03	1.12E+04	5.56E+02
P69905 HBA	SPADK	517.27	77.27	2.56E+03	8.40E+04	7.19E+03	1.54E+05	9.92E+04	1.15E+05	8.62E+04	2.31E+03	2.15E+03	9.93E+03	2.41E+04	7.93E+04	6.09E+04	1.70E+03	6.25E+03
Q14315-2 FLNC	VAFAGAPITR	501.79	77.6	2.80E+05	2.01E+04	4.86E+03	1.23E+03	1.13E+03	8.08E+02	4.70E+03	1.17E+04	2.42E+03	4.20E+02	2.83E+05	1.10E+03	1.07E+04	8.18E+02	1.10E+04
Q14315-2 FLNC	LDVQFAGTAK	525.29	77.68	2.14E+05	3.45E+04	9.50E+03	1.31E+05	1.32E+05	7.70E+04	2.01E+04	5.45E+03	1.63E+03	9.98E+02	2.20E+05	3.94E+04	7.01E+04	9.04E+02	9.19E+04
P35609 ACTN2	DLGEAEFAR	504.24	77.68	2.78E+03	3.12E+05	8.66E+03	1.12E+05	3.23E+03	2.09E+04	6.32E+04	1.27E+04	2.38E+03	1.66E+03	7.42E+03	1.85E+05	1.15E+05	4.16E+03	1.23E+05
P08590 MYL3	AAPAPAPPEPERPKEVEFD ASK	608.31	77.71	2.28E+05	2.98E+03	6.10E+03	2.22E+05	7.35E+05	3.18E+04	6.52E+03	7.89E+03	1.57E+03	1.99E+03	2.53E+05	2.59E+04	2.10E+05	2.90E+03	5.01E+05
P68871 HBB	EFTPPVQ	409.21	77.81	1.85E														

Q14896 MYPC3	ITDAQPAFTGSYR	713.85	78.46	2.17E+05	5.64E+02	6.45E+02	8.13E+02	2.86E+02	1.36E+03	4.85E+02	3.24E+03	1.71E+04	1.01E+03	1.02E+05	1.78E+03	4.90E+02	2.44E+04	9.03E+03
Q14315-2 FLNC	GPGLSQAFVQK	594.82	78.91	2.32E+05	4.51E+03	9.50E+03	5.62E+04	3.99E+05	1.45E+03	1.62E+05	1.35E+03	3.23E+05	5.47E+05	4.42E+05	2.38E+05	1.54E+04	1.58E+05	3.13E+05
Q14315-2 FLNC	PAEFTIDAR	510.28	78.92	2.06E+05	1.49E+05	1.62E+04	2.70E+05	9.38E+05	4.00E+05	3.67E+04	1.21E+04	1.63E+03	4.58E+03	5.15E+05	5.44E+03	7.10E+05	1.93E+04	2.71E+05
Q14315-2 FLNC	TGVEVGKPTHFTVLTK	429.25	79.26	7.22E+04	3.86E+02	2.15E+04	4.79E+03	1.26E+03	1.23E+03	2.18E+03	1.02E+03	1.24E+04	1.96E+02	1.82E+03	5.67E+02	3.60E+04	2.66E+04	3.24E+03
P06576 ATPB	IPVGPETLGR	519.80	79.27	8.19E+06	6.26E+06	7.72E+02	4.34E+06	2.08E+06	1.71E+03	1.06E+04	4.91E+03	1.65E+04	1.31E+04	5.27E+06	7.41E+06	5.69E+06	6.51E+02	6.13E+06
P54296 MYOM2	AVNANGVGKPSDTSEPVLE EAR	737.39	79.47	2.20E+04	1.15E+03	2.34E+02	3.98E+03	4.23E+04	1.73E+02	2.33E+02	9.33E+02	8.22E+02	5.32E+03	4.88E+04	3.02E+02	2.18E+04	3.94E+02	1.32E+05
P08590 MYL3	ALGQNPTQAEVLR	698.88	79.64	9.45E+03	2.78E+03	4.41E+03	6.89E+03	5.20E+03	1.94E+03	2.52E+03	4.55E+03	4.04E+03	1.52E+03	1.56E+04	1.71E+04	4.36E+03	1.80E+03	2.34E+03
P35609 ACTN2	DYESASLTEVR	635.30	79.89	1.51E+06	3.93E+04	3.58E+03	2.15E+06	1.15E+06	8.81E+03	3.70E+03	4.59E+03	1.13E+03	9.27E+02	1.91E+06	5.93E+04	1.64E+06	2.42E+03	1.98E+06
P06576 ATPB	LDATTVLSR	488.28	79.95	1.09E+06	2.71E+05	1.14E+05	1.80E+05	7.52E+04	1.20E+04	8.15E+04	1.50E+03	4.79E+04	2.99E+04	5.26E+05	1.49E+05	1.23E+05	6.34E+04	5.82E+05
Q14896 MYPC3	LTVELADHDAEVK	720.37	80.01	1.93E+03	5.82E+03	5.51E+03	5.44E+03	1.05E+04	2.56E+04	1.57E+04	8.17E+02	6.50E+02	1.76E+04	5.17E+05	7.10E+03	2.11E+05	5.03E+03	5.73E+05
P12111-2 CO6A3	VGNALLEYVSR	554.29	80.14	6.77E+02	5.11E+03	8.07E+02	2.69E+04	5.66E+03	2.92E+04	2.48E+02	1.42E+03	5.85E+03	1.46E+04	7.07E+03	1.24E+04	9.41E+02	1.68E+03	9.75E+02
Q14896 MYPC3	PGITYEPPNYK	639.82	80.19	3.03E+05	4.00E+03	1.28E+03	9.25E+04	1.29E+03	6.91E+02	3.91E+03	4.42E+03	5.21E+02	2.89E+03	1.66E+05	1.03E+04	1.15E+04	1.52E+03	1.46E+05
P17661 DESM	EEAENNLAAFR	632.30	80.22	3.78E+06	1.45E+04	1.25E+04	3.62E+06	1.35E+06	5.50E+04	1.13E+04	2.21E+04	1.78E+03	1.68E+03	4.49E+06	3.43E+04	1.09E+06	1.41E+03	3.87E+06
P02768 ALBU	VHTECCHGDLLECADDR	639.26	80.42	3.35E+03	7.37E+03	8.28E+03	9.28E+02	1.23E+03	2.56E+04	6.46E+03	2.62E+03	5.04E+03	4.31E+03	2.49E+04	2.18E+04	2.59E+04	1.37E+04	4.34E+04
P12111-2 CO6A3	ALDTSEGVNQDTFGR	805.38	80.45	8.77E+04	1.76E+03	5.58E+03	1.15E+05	1.85E+02	7.54E+02	6.46E+02	3.37E+03	1.54E+03	1.38E+03	9.51E+04	3.73E+03	3.68E+04	1.20E+03	1.07E+05
Q14896 MYPC3	NPVGEDQVNLTVK	706.87	80.47	8.06E+05	9.32E+02	4.08E+03	1.54E+04	3.48E+04	1.35E+04	1.11E+05	1.44E+05	3.97E+04	1.84E+04	7.82E+05	3.61E+03	1.21E+05	2.05E+04	8.62E+05
P35609 ACTN2	VSDIAGAWQR	551.79	80.61	2.24E+05	1.64E+03	2.16E+03	2.60E+05	1.38E+03	1.79E+03	2.64E+02	7.68E+03	1.47E+03	7.22E+02	2.68E+05	7.11E+02	3.06E+03	8.00E+02	2.36E+05
Q14315-2 FLNC	YGGPQHIVGSPFK	693.86	80.7	6.68E+04	1.51E+03	2.97E+05	8.58E+02	2.94E+03	1.79E+03	2.22E+05	3.21E+05	1.15E+03	3.05E+03	1.14E+05	2.75E+03	1.26E+03	3.04E+02	2.99E+03
P10916 MLRV	DTFAALGR	425.72	80.85	4.56E+04	2.37E+03	3.68E+03	1.90E+03	1.06E+04	2.20E+04	1.86E+03	3.74E+03	1.61E+07	1.82E+07	1.10E+05	3.54E+03	4.85E+03	4.06E+04	1.35E+04
Q14896 MYPC3	VADVPDAPAAPK	596.83	80.88	2.59E+02	2.40E+06	4.42E+04	3.88E+06	2.04E+06	1.83E+04	1.17E+04	6.48E+03	1.04E+03	7.58E+02	2.81E+06	1.04E+05	1.66E+06	5.59E+04	2.97E+06
Q14315-2 FLNC	VIDVGEQAFSVNTR	753.39	80.93	6.00E+04	6.20E+02	1.62E+02	1.90E+04	6.47E+04	3.15E+03	2.10E+02	1.31E+04	3.24E+02	2.27E+03	1.46E+05	2.10E+04	4.40E+04	1.28E+04	9.42E+03
P12111-2 CO6A3	SQHPYVLTEDTLK	510.93	81.03	1.54E+03	6.25E+04	1.67E+04	3.55E+03	6.01E+02	1.15E+03	1.64E+04	1.41E+04	7.24E+04	1.14E+05	1.56E+03	1.96E+04	9.38E+02	1.04E+05	6.76E+02
P12111-2 CO6A3	SDDEVDPAVELK	716.33	81.29	1.18E+05	2.59E+03	3.75E+04	5.03E+03	8.23E+03	2.46E+04	6.94E+03	6.43E+03	3.20E+03	9.13E+02	1.37E+05	2.99E+03	5.70E+04	3.99E+02	1.81E+05
Q14896 MYPC3	EGQPLAGEEVSIR	692.86	81.8	1.79E+06	1.53E+05	1.26E+05	2.55E+06	1.64E+06	4.13E+04	1.23E+04	2.20E+05	3.71E+03	5.79E+02	1.91E+06	5.47E+04	7.99E+05	2.49E+02	2.10E+06
P35609 ACTN2	ELPPDQAQYCIK	702.84	81.88	1.69E+04	5.61E+03	2.02E+04	1.43E+05	3.55E+04	3.55E+04	4.88E+04	3.91E+04	4.16E+03	6.38E+03	6.29E+03	4.07E+03	2.17E+04	3.79E+02	1.92E+05
P25705 ATPA	VGLKAPGIIPR	560.86	81.94	3.39E+02	8.52E+02	1.36E+05	5.23E+02	9.86E+02	2.03E+03	1.11E+03	3.15E+04	3.22E+02	4.09E+02	5.55E+02	9.73E+02	1.18E+03	1.35E+03	2.15E+03
Q14315-2 FLNC	TVHVAFAGAPITR	447.26	81.97	1.92E+05	6.48E+04	1.38E+05	1.50E+04	3.30E+04	9.82E+04	1.98E+04	3.42E+04	2.57E+05	1.66E+03	1.96E+05	7.16E+04	1.43E+05	1.69E+03	1.29E+05
Q14315-2 FLNC	YTPATDGPYTVAVK	741.88	82.25	4.35E+02	1.73E+03	5.22E+02	7.17E+04	3.53E+03	1.72E+03	5.28E+02	6.10E+03	8.53E+02	1.37E+03	6.29E+04	1.40E+03	7.59E+03	2.31E+02	1.20E+04
Q14315-2 FLNC	TVHYTPATDGPYTVAVK	607.31	82.29	5.87E+03	1.18E+04	6.14E+02	3.31E+03	2.72E+03	5.06E+03	1.37E+04	4.16E+04	2.31E+05	4.64E+05	2.85E+03	1.29E+04	4.60E+03	1.42E+04	1.95E+03
P02768 ALBU	VSTPTLVEVSR	594.33	82.4	2.06E+03	4.73E+05	8.77E+03	2.75E+05	2.95E+04	1.35E+04	1.24E+05	1.41E+03	1.08E+03	7.25E+02	2.59E+04	1.51E+05	7.57E+02	1.62E+04	2.40E+05
P12883 MYH7	GKLTYYTQLEDLKR	565.31	82.49	1.95E+04	2.90E+03	2.23E+03	1.03E+03	2.56E+03	3.38E+03	1.50E+03	1.24E+03	1.42E+05	1.01E+05	3.38E+04	1.48E+04	1.93E+03	1.02E+05	3.31E+03
P35609 ACTN2	GITQEAMNEFR	676.82	82.69	2.64E+06	9.24E+03	1.71E+03	2.31E+06	2.31E+04	5.62E+04	2.06E+03	3.32E+04	9.59E+02	2.95E+02	2.69E+06	9.31E+03	3.03E+05	2.45E+03	2.50E+06
P02768 ALBU	YLYEIAR	464.25	82.7	9.05E+06	3.44E+03	1.20E+04	4.18E+04	1.82E+04	3.81E+04	2.08E+04	2.18E+03	1.13E+07	1.58E+07	1.26E+07	1.51E+03	1.96E+04	1.13E+07	6.87E+04
P68871 HBB	EFTPPVQAAAYQK	689.85	82.71	2.79E+06	1.05E+04	1.20E+04	5.23E+06	4.44E+06	8.57E+03	4.29E+03	1.53E+04	1.90E+03	2.39E+03	4.60E+06	8.30E+03	8.44E+04	8.39E+02	3.05E+06
Q14896 MYPC3	WLKDGVELTR	406.23	82.75	1.31E+04	3.11E+04	1.26E+03	2.87E+04	8.48E+03	3.55E+04	4.51E+03	1.88E+03	2.55E+03	3.43E+03	1.27E+04	1.85E+05	1.43E+04	2.21E+02	5.26E+03
P12883 MYH7	LQEAEEAVEAVN	651.31	82.86	5.51E+02	2.12E+03	5.32E+04	1.34E+03	1.79E+03	1.18E+05	1.49E+04	5.20E+03	1.26E+04	1.22E+03	3.78E+03	5.88E+02	9.09E+02	8.41E+03	8.66E+02
Q14896 MYPC3	EVGPADQGSYAVIAGSSK	868.43	82.94	3.70E+05	7.38E+02	4.20E+03	5.10E+05	2.88E+05	1.28E+04	6.98E+03	1.86E+03	1.98E+03	4.09E+03	1.61E+03	1.78E+05	2.50E+03	4.59E+05	4.59E+05
P10916 MLRV	EEIDEMIK	503.74	83.02	1.16E+03	2.30E+03	6.44E+02	1.87E+03	1.03E+04	5.38E+03	1.10E+03	6.29E+02	1.59E+05	1.43E+05	1.09E+03	4.38E+03	1.50E+03	1.95E+05	5.29E+02
P02768 ALBU	GDLLECADDR	553.74	83.05	3.74E+04	2.92E+03	1.69E+04	2.66E+03	2.30E+03	2.12E+03	4.07E+02	2.32E+03	4.97E+02	5.85E+02	2.28E+04	6.42E+02	2.40E+02	9.95E+02	4.87E+03
P25705 ATPA	VLSIGDGIAR	500.79	83.12	3.24E+06	3.15E+05	3.02E+05	3.94E+06	3.40E+06	2.38E+05	1.08E+05	2.91E+05	4.10E+04	3.12E+03	2.61E+06	3.06E+05	3.70E+06	2.80E+03	3.33E+06
P12111-2 CO6A3	NNLFTSSAGYR	615.30	83.16	3.50E+03	1.73E+03	2.15E+03	2.47E+05	1.20E+05	3.95E+03	3.43E+03	3.45E+03	3.62E+02	7.39E+02	1.80E+04	4.49E+03	1.32E+04	1.43E+03	2.73E+05
P08590 MYL3	VFDKEGNGTVMGAELR	574.96	83.27	2.42E+05	9.53E+03	1.96E+03	1.23E+04	4.27E+04	4.88E+03	4.32E+03	9.07E+02	4.34E+02	1.47E+03	4.00E+05	1.41E+04	4.63E+05	3.63E+03	5.41E+05
P69905 HBA	LASVSTVLTSK	553.33	83.31	1.39E+03	5.39E+05	2.61E+05	3.03E+02	2.84E+02	1.43E+05	9.76E+04	2.86E+03	4.45E+03	8.67E+03	2.07E+03	3.13E+05	9.40E+02	2.90E+03	9.01E+02
Q14315-2 FLNC	EVTTEFTVDAR	634.31	83.32	1.38E+04	1.33E+05	1.18E+04	3.24E+04	3.33E+04	7.11E+03	2.52E+03	2.50E+03	1.64E+04	4.65E+04	1.60E+04	1.04E+04	7.88E+03	5.50E+02	1.51E+04
P10916 MLRV	FEQTQIQEFK	649.31	83.33	1.86E+05	4.25E+02	9.14E+03	9.04E+03	1.07E+04	2.52E+03	6.12E+03	3.03E+02	2.31E+03	5.22E+04	1.93E+04	1.02E+05	1.39E+05	1.29E+03	2.43E+03
Q14896 MYPC3	SIFTVEGAEK	540.78	83.33	1.78E+06	1.56E+04	3.62E+04	7.03E+04	2.03E+04	1.18E+05	3.79E+03	4.03E+04	9.28E+05	1.24E+03	1.89E+06	1.49E+04	1.33E+04	8.67E+05	1.90E+06
P02768 ALBU	FQNALLVR	480.78	83.39	8.41E+02	1.95E+06	3.16E+06	3.20E+06	4.27E+06	3.77E+06	2.68E+06	5.84E+04	8.91E+03	1.91E+05	4.57E+02	1.85E+06	3.67E+02	8.13E+03	1.40E+03
P54296 MYOM2	VLDPEELER	550.28	83.47	1.21E+03	5.31E+05	7.05E+02	2.92E+05	3.72E+04	9.27E+04	1.10E+04	1.31E+04	7.15E+04	4.08E+04	2.75E+05	2.71E+04	2.20E+05	5.37E+04	4.15E+05
P06576 ATPB	MVGPIEEAVAK	572.31	83.56	1.16E+06	2.50E+03	1.41E+03	3.04E+04	5.78E+03	1.30E+04	4.31E+03	2.91E+03	7.56E+05	8.29E+02	2.78E+05	1.68E+03	3.49E+04	1.56E+06	1.10E+03
Q14896 MYPC3	PAPTIVWQK	520.30	83.58	1.30E+03	5.74E+03	3.82E+04	1.68E+03	2.85E+05	1.60E+03	3.15E+02	1.71E+04	3.17E+04	5.14E+04	4.03E+03	2.17E+04	8.88E+03	4.51E+03	7.20E+03





Q14315-2 FLNC	HVSAYGPGLSHGMVKNKPA TFTIVTK	653.85	91.64	2.86E+03	3.81E+03	3.98E+03	3.67E+03	1.41E+04	9.80E+03	4.09E+03	2.80E+04	6.28E+02	1.14E+03	3.64E+02	1.43E+04	2.23E+03	1.03E+03	6.65E+03
P10916 MLRV	DTFAALGRVNVK	645.85	91.67	1.56E+02	6.57E+04	5.68E+03	7.39E+04	3.68E+04	4.67E+04	1.40E+04	4.47E+04	1.43E+05	1.37E+05	1.30E+04	4.53E+04	3.19E+03	1.61E+05	6.81E+04
P12111-2 CO6A3	QLGTVQQVISER	679.38	91.75	3.28E+05	8.50E+03	8.03E+03	7.37E+03	8.84E+03	3.40E+04	1.93E+04	3.35E+04	6.76E+02	2.04E+03	3.07E+05	1.49E+03	8.53E+04	1.95E+03	7.96E+03
P35609 ACTN2	NVNIQNFHTSWK	744.37	91.78	7.55E+02	1.02E+03	9.03E+02	1.38E+04	4.23E+03	3.15E+03	6.78E+03	5.88E+04	1.14E+03	3.62E+05	2.25E+05	3.42E+02	1.68E+04	1.33E+04	2.11E+04
P12883 MYH7	DVFPVDDKQEFVK	522.60	91.78	1.73E+06	3.97E+05	3.77E+05	2.64E+05	4.21E+04	6.91E+04	2.10E+05	2.97E+04	5.65E+04	4.94E+04	2.95E+06	1.08E+04	2.24E+05	1.69E+03	1.02E+04
P68871 HBB	VLVVCVLAH	427.25	92.05	2.37E+03	9.23E+04	4.15E+04	5.22E+04	1.11E+04	9.61E+04	3.60E+04	4.75E+03	7.15E+03	3.60E+02	8.59E+02	2.73E+04	3.41E+02	7.16E+03	1.81E+04
P12883 MYH7	ALQEAHQALDDLQAEED KVNTLTK	702.86	92.16	1.39E+03	2.46E+05	6.39E+04	6.07E+03	8.86E+04	1.70E+04	3.27E+04	1.37E+05	4.61E+03	1.75E+04	6.44E+04	2.91E+05	1.80E+04	1.42E+03	5.67E+04
P12111-2 CO6A3	VAVFFSNTPTR	619.83	92.27	1.61E+05	1.57E+04	4.79E+02	3.31E+04	1.77E+04	1.26E+04	1.07E+03	8.92E+03	5.67E+02	8.59E+02	2.54E+05	4.10E+03	1.71E+05	2.43E+03	4.54E+04
P25705 ATPA	GIRPAINVGLSVSR	480.29	92.27	7.46E+02	4.92E+06	2.16E+06	3.33E+04	1.21E+03	2.56E+06	1.07E+07	1.31E+07	8.38E+04	9.81E+03	2.13E+03	9.10E+06	2.26E+03	8.52E+04	9.22E+03
P25705 ATPA	HALIYDDLK	644.35	92.52	1.97E+02	1.79E+04	2.08E+04	1.63E+05	1.31E+05	3.32E+04	1.17E+03	1.12E+03	2.37E+03	2.84E+04	4.50E+05	2.45E+05	6.07E+05	1.36E+03	2.69E+05
Q14315-2 FLNC	SPFEVQVSPEAGVQK	801.41	92.59	3.16E+05	3.44E+03	3.37E+03	4.23E+03	3.96E+03	7.57E+02	2.53E+03	2.12E+03	3.60E+04	5.58E+02	4.86E+05	6.61E+03	1.16E+05	1.36E+03	3.85E+05
P25705 ATPA	QMSLLLR	430.75	92.65	6.87E+03	2.57E+04	7.05E+03	5.84E+03	2.18E+04	1.91E+04	1.28E+04	6.08E+03	6.85E+04	2.95E+03	1.40E+06	3.35E+04	9.11E+05	5.30E+04	2.09E+04
P25705 ATPA	VPVGEELLGR	534.80	92.81	7.58E+03	1.60E+03	1.31E+03	6.58E+02	6.98E+02	1.44E+03	6.60E+02	5.74E+03	1.78E+05	1.65E+05	1.88E+03	1.83E+03	2.82E+03	2.47E+05	1.63E+03
P12883 MYH7	PAAIPEGFIDSR	700.86	92.82	6.09E+03	1.84E+03	2.14E+03	2.30E+03	2.29E+03	1.03E+03	4.23E+03	1.24E+03	1.31E+04	8.05E+03	1.34E+05	8.31E+02	1.28E+04	6.39E+04	1.07E+04
P68871 HBB	GTFATLSELHCDK	711.34	92.87	6.74E+02	2.31E+03	1.69E+03	2.42E+03	1.68E+04	1.14E+04	7.23E+02	1.16E+03	1.30E+05	1.16E+05	5.69E+05	2.00E+03	1.64E+04	1.41E+04	1.26E+04
P68133 ACTS	DLYANNVM	470.22	92.87	2.65E+05	1.45E+03	7.05E+03	1.70E+04	7.37E+03	6.13E+03	8.72E+02	2.22E+03	3.26E+03	3.08E+03	2.38E+05	1.29E+03	1.55E+03	5.52E+03	2.19E+04
P12883 MYH7	LTGAIMHFGNMK	660.33	92.87	6.19E+05	4.24E+04	1.07E+03	6.02E+04	3.66E+04	7.79E+04	3.23E+04	1.57E+04	1.67E+03	3.01E+03	7.37E+05	2.26E+04	3.58E+02	5.83E+02	4.54E+04
Q14315-2 FLNC	LTVTSLQETGLK	645.37	92.89	7.72E+05	1.63E+03	6.93E+02	5.36E+03	1.42E+04	8.32E+02	1.77E+03	1.21E+03	7.08E+02	1.21E+03	7.39E+05	2.03E+03	1.57E+05	8.12E+02	4.83E+03
P35609 ACTN2	GYDLGEAEFAR	614.29	93.05	2.50E+02	3.43E+03	4.94E+04	2.47E+03	8.95E+02	7.67E+04	6.53E+03	2.37E+04	8.46E+02	3.91E+03	3.93E+03	2.21E+03	1.67E+03	1.53E+03	2.43E+03
P35609 ACTN2	SSALYGESDL	521.24	93.49	3.65E+05	1.56E+04	1.22E+04	3.43E+04	5.21E+03	5.54E+03	1.22E+03	2.46E+04	5.90E+03	1.42E+03	6.83E+05	2.12E+04	2.08E+04	5.21E+03	3.60E+05
Q14315-2 FLNC	DLAEDAPWK	522.75	93.68	3.61E+05	1.37E+04	3.87E+02	1.46E+04	4.91E+03	3.77E+03	1.78E+03	8.92E+02	1.63E+03	3.36E+03	2.27E+04	4.95E+03	1.62E+04	2.65E+03	6.25E+03
P68871 HBB	SAVTALWGK	466.76	93.87	4.40E+03	6.89E+06	2.08E+05	1.02E+07	2.33E+07	1.59E+07	2.87E+03	5.64E+04	8.30E+02	2.52E+03	1.62E+07	2.56E+05	9.09E+05	6.95E+03	9.87E+06
P02768 ALBU	AQYLQPCPFEDHVK	569.27	93.94	1.94E+03	5.38E+03	2.75E+03	2.58E+03	2.60E+03	1.21E+03	1.32E+04	2.04E+03	8.54E+03	5.06E+04	1.16E+03	3.87E+02	1.63E+03	5.45E+03	9.80E+02
Q14315-2 FLNC	VNQPASFAVQLNGAR	786.42	94.14	5.80E+04	3.11E+03	3.93E+03	3.75E+03	9.67E+02	2.50E+03	2.28E+03	5.87E+02	1.08E+05	9.83E+04	4.84E+04	1.32E+03	4.70E+02	1.17E+05	5.93E+03
P35609 ACTN2	MVSDIAGAWQR	617.30	94.31	1.65E+06	3.50E+04	1.35E+04	6.04E+04	1.23E+06	3.61E+04	2.38E+03	3.29E+02	2.53E+03	1.14E+03	1.50E+06	9.96E+03	3.27E+05	1.62E+03	1.43E+06
Q14896 MYPC3	YIFESIGAK	514.28	94.45	6.10E+02	8.60E+05	2.05E+04	1.27E+06	8.21E+05	1.05E+06	6.42E+05	6.56E+03	8.52E+04	1.27E+05	8.56E+02	9.37E+05	5.56E+05	2.49E+04	1.02E+06
P08590 MYL3	HVLATLGERLTEDEVEK	647.01	94.47	5.93E+03	2.05E+03	1.67E+03	9.02E+02	7.28E+03	1.06E+05	2.06E+03	1.50E+03	9.18E+03	2.70E+03	1.98E+03	2.82E+03	3.08E+04	2.08E+03	6.87E+02
P09493 TPM1	SKQLEDELVSLQK	758.91	94.48	4.47E+02	1.24E+03	2.01E+03	1.10E+03	3.67E+02	2.71E+03	3.52E+03	1.56E+04	6.56E+04	3.41E+04	5.24E+02	5.57E+02	1.55E+03	2.07E+04	1.07E+03
P35609 ACTN2	MLDAEDIVNTPKPKDER	614.97	94.56	1.52E+06	1.98E+04	5.43E+02	7.44E+05	1.23E+06	1.29E+04	9.45E+03	6.42E+03	2.42E+03	1.72E+03	1.86E+06	7.76E+03	4.89E+05	1.40E+03	1.84E+06
P54296 MYOM2	YAIQMMMEDK	628.79	94.61	1.58E+05	4.55E+02	1.44E+03	1.94E+03	4.61E+03	1.55E+04	2.85E+02	6.13E+02	5.35E+03	6.30E+02	1.30E+05	2.15E+03	1.90E+04	2.23E+03	1.75E+03
P68133 ACTS	NVMMSGTTMYPGIADR	835.39	94.66	2.78E+05	9.50E+02	2.64E+03	5.36E+04	2.81E+03	1.60E+03	1.07E+03	2.58E+03	1.62E+03	2.81E+03	2.77E+05	1.85E+03	1.87E+04	8.54E+02	1.87E+05
Q14315-2 FLNC	AFGPGLEGLVKNK	629.84	94.91	5.44E+05	9.85E+04	9.00E+04	5.37E+03	2.60E+05	1.55E+05	3.26E+05	4.52E+05	2.30E+03	2.94E+02	7.64E+05	1.64E+04	2.63E+05	3.45E+03	5.55E+05
P12883 MYH7	LTGAIMHFGN	530.77	94.91	1.91E+06	1.29E+04	2.56E+03	7.17E+03	6.19E+02	8.61E+03	1.53E+03	1.07E+03	1.55E+03	3.06E+03	1.16E+06	1.78E+03	1.85E+05	1.46E+03	1.57E+04
P17661 DESM	ELEDRFASEASGYQDNAR	724.34	94.95	2.80E+03	4.15E+03	5.45E+03	3.19E+03	9.68E+02	7.85E+04	6.89E+02	5.94E+02	4.83E+03	7.55E+03	1.83E+03	5.11E+03	1.39E+02	6.33E+03	1.05E+04
P69905 HBA	FLSFPTTK	470.76	94.97	6.45E+02	8.47E+05	7.49E+05	5.73E+02	1.36E+03	8.11E+05	6.23E+05	6.49E+03	1.39E+04	4.93E+03	1.65E+03	1.09E+06	4.51E+02	4.66E+03	7.40E+03
P17661 DESM	HQIQSYTCIDALK	550.27	95.24	3.95E+04	1.13E+03	3.22E+03	1.06E+04	6.95E+04	2.55E+03	6.61E+02	2.77E+03	1.62E+03	2.98E+03	1.83E+05	7.70E+03	6.06E+04	2.44E+03	7.55E+04
Q14315-2 FLNC	GAGTGGLGLAIEGPSEAK	792.91	95.28	2.64E+05	3.22E+03	4.93E+03	1.01E+05	3.96E+04	7.03E+03	3.00E+02	1.11E+03	5.92E+02	1.08E+03	6.19E+04	2.64E+04	1.37E+04	3.57E+03	2.54E+04
P06576 ATPB	IGLFGGAGVGK	488.28	95.29	1.59E+06	2.04E+03	1.82E+03	2.64E+03	1.29E+04	1.51E+03	1.42E+04	2.24E+04	2.17E+03	1.57E+03	1.27E+06	2.69E+03	1.48E+06	5.09E+03	1.42E+04
Q14896 MYPC3	VFSQNMVGFSDR	693.83	95.46	7.83E+02	1.88E+04	7.72E+03	7.26E+05	2.92E+05	2.45E+04	1.57E+04	2.13E+04	2.75E+03	6.34E+02	2.68E+05	1.80E+03	2.88E+05	1.45E+04	6.53E+05
P68133 ACTS	ANNVMSGTTMYPGIADR	927.93	95.61	1.43E+02	1.31E+02	3.86E+02	6.15E+04	1.27E+03	2.20E+02	5.71E+02	1.88E+03	1.27E+02	1.53E+03	8.21E+04	5.91E+03	5.39E+03	3.33E+03	2.28E+03
P12111-2 CO6A3	LLVLITGGK	457.31	95.87	5.47E+03	5.00E+02	7.62E+04	4.13E+02	4.54E+02	2.69E+02	2.42E+03	1.44E+04	5.84E+02	1.38E+02	7.58E+02	2.71E+03	2.43E+02	1.89E+02	1.99E+02
P12111-2 CO6A3	FDEHQSKPEILNLVK	599.66	96.24	8.81E+02	1.02E+04	6.38E+03	2.71E+03	5.32E+04	8.19E+04	2.78E+02	7.02E+02	1.04E+03	2.31E+03	1.23E+03	1.81E+04	1.26E+03	4.57E+02	1.13E+03
P68871 HBB	VNVDEVGGEAL	551.28	96.63	1.04E+05	1.51E+03	1.73E+03	2.75E+04	4.25E+03	1.68E+03	6.88E+03	3.81E+03	1.61E+04	4.50E+04	3.54E+04	1.27E+03	5.02E+03	2.61E+04	1.07E+04
P25705 ATPA	ILGADTSVDLEETGR	788.39	96.72	1.08E+04	4.58E+04	1.29E+04	1.76E+04	3.22E+03	6.16E+03	3.53E+03	3.16E+03	4.34E+05	1.50E+06	1.71E+03	1.54E+04	2.48E+04	4.65E+04	7.27E+02
P10916 MLRV	ADYVREMLTTQAER	561.61	96.74	6.19E+03	2.84E+03	9.85E+02	8.87E+02	1.74E+04	2.32E+04	9.19E+02	8.66E+02	4.04E+02	2.55E+02	1.13E+04	5.08E+03	7.76E+02	1.27E+03	2.73E+03
Q14896 MYPC3	LAPAPAPAEATGAPGEAPA PAAELGESAPSPK	965.16	96.97	4.04E+04	2.64E+03	4.56E+03	4.33E+03	8.58E+03	1.90E+03	1.10E+03	1.49E+03	3.83E+02	1.10E+03	7.11E+04	3.61E+03	8.72E+03	3.09E+02	8.14E+03
P12111-2 CO6A3	VAVVTYNNEVTTEIR	854.45	96.97	7.43E+03	2.73E+02	1.98E+03	4.32E+03	1.86E+03	1.24E+04	3.12E+03	3.00E+03	2.04E+05	7.84E+04	1.94E+03	6.74E+02	2.95E+02	2.33E+05	8.62E+03
P69905 HBA	VADALTNVAHVVD	648.33	96.99	1.95E+04	1.34E+04	1.97E+03	7.40E+04	6.48E+02	8.03E+03	1.09E+03	1.43E+03	7.98E+02	1.38E+03	6.82E+04	2.67E+04	1.16E+04	7.65E+02	1.02E+03
P12111-2 CO6A3	VEFLNAH	471.75	97.01	6.61E+03	4.76E+02	1.35E+03	1.54E+03	3.10E+03	1.40E+03	7.27E+02	1.20E+03	1.23E+05	2.84E+03	1.29E+05	1.02E+03	4.65E+02	8.02E+04	2.13E+03
Q14315-2 FLNC	VVNVAPPLDLK	626.37	97.11	1.89E+05	5.09E+03	1.70E+03	7.57E+04	1.94E+03	2.81E+03	2.49E+03	3.42E+03	6.31E+02	1.77E+03	2.04E+05	3.03E+02	5.86E+04	2	

P06576 ATPB	IMNVIGEPIDER	693.36	98.56	3.79E+06	1.18E+03	1.38E+03	2.91E+04	3.85E+04	2.12E+03	2.54E+03	4.87E+03	1.21E+04	2.25E+04	2.92E+06	4.85E+03	2.04E+04	1.90E+03	4.53E+04
Q14896 MYPC3	MIEGVVYEMR	613.80	98.61	9.00E+03	2.44E+04	3.71E+03	1.27E+04	7.34E+03	3.82E+02	2.12E+04	1.92E+03	7.84E+03	5.77E+04	5.72E+05	2.49E+04	5.47E+05	9.29E+03	5.15E+03
P02768 ALBU	VPQVSTPTLVEVSR	756.42	98.61	4.24E+03	2.00E+03	3.56E+03	8.30E+03	3.63E+03	8.64E+03	2.67E+03	2.57E+03	1.18E+07	1.58E+07	1.99E+03	1.54E+03	1.59E+03	1.04E+07	2.81E+03
P25705 ATPA	TGTAEMSSILEER	712.34	98.64	3.41E+06	4.23E+04	1.39E+04	4.55E+05	1.97E+05	1.62E+04	9.21E+02	1.68E+03	2.27E+03	5.18E+03	2.72E+06	3.71E+04	3.02E+04	2.05E+04	1.19E+04
P17661 DESM	ARVDVERDNLLDDLQR	643.00	98.81	2.17E+03	1.18E+04	4.29E+03	1.86E+04	3.93E+04	1.06E+05	3.69E+02	4.40E+02	2.69E+03	4.27E+02	1.75E+03	3.21E+03	9.52E+03	4.71E+02	1.71E+04
P68871 HBB	FGDLSTPDAVMGNPK	774.87	98.88	6.19E+04	1.53E+03	5.46E+02	1.09E+03	3.61E+04	4.58E+03	1.03E+03	7.62E+03	1.42E+03	2.27E+03	6.48E+02	1.44E+04	6.08E+02	4.64E+03	3.87E+02
Q14315-2 FLNC	LYAQDADGCPIDIK	761.37	99.02	8.41E+03	1.94E+03	2.78E+03	2.66E+04	1.15E+03	2.28E+03	5.65E+02	1.82E+03	3.18E+04	6.36E+05	3.22E+04	3.05E+03	1.53E+03	4.43E+05	1.21E+03
Q14315-2 FLNC	VEAAEIVEGEDSAY	741.35	99.09	4.64E+04	6.12E+02	1.55E+03	3.60E+03	1.96E+03	3.22E+03	1.30E+03	9.83E+02	7.73E+02	2.48E+03	3.81E+04	4.51E+03	6.19E+02	1.58E+03	2.88E+02
P35609 ACTN2	MLDAEDIVNTPK	673.34	99.22	2.33E+05	1.49E+03	6.35E+02	2.28E+05	2.05E+04	5.78E+02	9.34E+03	1.65E+04	7.04E+02	1.63E+03	2.59E+05	6.12E+02	4.54E+04	1.87E+03	2.58E+05
P54296 MYOM2	THFDVQFLEK	632.32	99.31	2.24E+04	2.16E+04	1.57E+03	6.97E+04	1.60E+03	5.51E+03	1.76E+03	7.47E+03	5.45E+03	7.91E+02	1.00E+04	1.34E+04	5.24E+03	5.31E+02	2.63E+04
P06576 ATPB	YMVGPIDEEAVAK	653.84	99.48	1.01E+03	2.90E+04	2.25E+04	1.63E+04	9.30E+03	1.22E+05	4.10E+03	1.80E+05	3.23E+03	1.83E+03	1.27E+04	1.78E+05	2.68E+03	2.60E+03	1.63E+04
P12111-2 CO6A3	SVEDAQDVSLALTQR	816.42	99.56	1.09E+04	2.71E+03	9.44E+03	1.09E+05	9.74E+02	9.67E+03	5.36E+03	2.34E+03	2.66E+03	1.90E+03	9.63E+04	5.30E+03	1.93E+03	6.97E+02	6.45E+03
P12111-2 CO6A3	GAQQPAGPAGPPGLIGEQGI SGPR	714.37	100.02	2.29E+03	6.40E+02	5.27E+03	2.71E+04	3.74E+03	1.16E+03	2.35E+03	8.56E+02	1.09E+03	4.02E+04	3.39E+03	1.13E+03	1.93E+03	1.19E+04	9.71E+02
P25705 ATPA	GIRPAINVGL	505.31	100.19	5.81E+02	5.10E+04	1.58E+03	4.00E+04	8.26E+03	1.36E+03	4.77E+02	1.36E+02	2.12E+02	6.58E+02	2.99E+02	7.00E+02	3.36E+04	4.61E+02	6.74E+04
Q14315-2 FLNC	WGDESVPGSPFK	653.31	100.19	2.25E+03	2.88E+02	6.95E+02	3.69E+04	4.59E+03	7.72E+02	2.37E+03	2.13E+03	1.31E+03	5.29E+02	3.61E+03	7.40E+03	2.03E+04	6.01E+02	3.97E+04
Q14896 MYPC3	LRLDVPISGD	542.80	100.2	4.34E+03	1.11E+04	4.52E+03	1.59E+04	5.71E+03	1.05E+04	1.60E+03	1.56E+03	2.92E+03	2.03E+03	1.03E+04	6.87E+04	4.73E+04	2.73E+03	3.95E+04
Q14896 MYPC3	PLEDQLVMVGQR	692.87	100.2	2.78E+05	8.38E+03	2.33E+04	3.90E+05	1.10E+04	7.05E+03	2.01E+03	2.60E+03	1.35E+03	8.05E+02	2.32E+05	7.52E+03	1.65E+04	1.54E+03	3.77E+04
Q14315-2 FLNC	VEAAEIVEGEDSAYSVR	912.44	100.22	1.03E+05	6.28E+03	1.42E+04	1.76E+05	1.76E+04	6.51E+03	3.11E+03	3.65E+03	5.90E+02	2.24E+02	1.55E+05	1.29E+04	8.60E+03	5.24E+03	1.52E+05
Q14896 MYPC3	SVEVAAGSPAVFEAETER	924.95	100.43	7.47E+05	2.30E+04	1.27E+04	3.46E+04	5.70E+03	3.93E+03	4.12E+03	1.03E+03	1.36E+03	1.29E+04	9.36E+05	5.44E+03	2.56E+03	1.26E+04	2.21E+04
Q14315-2 FLNC	TYVLFAGQNIER	673.87	100.43	2.84E+05	1.99E+05	3.82E+03	3.51E+05	1.90E+04	9.03E+03	8.13E+03	2.67E+03	1.16E+03	1.87E+02	3.77E+05	1.66E+04	2.38E+04	1.27E+03	1.20E+05
P69905 HBA	TYFPHFDLSHGSAQVK	611.97	100.49	2.85E+04	2.64E+03	4.61E+02	5.87E+04	3.70E+03	4.65E+03	1.86E+03	1.00E+04	1.78E+03	8.29E+02	3.03E+04	1.94E+03	8.62E+03	2.78E+03	2.65E+03
P25705 ATPA	EAYPGDVVFLHSR	518.59	100.6	3.85E+05	3.65E+03	3.81E+03	1.05E+04	1.18E+04	3.90E+03	1.81E+04	1.30E+04	9.23E+02	5.70E+03	5.17E+05	4.47E+03	2.23E+04	1.17E+03	5.22E+03
P12883 MYH7	LYTTQQLDLK	676.36	100.61	3.16E+06	2.94E+03	6.67E+02	2.54E+06	2.24E+03	5.16E+04	3.22E+03	2.78E+04	4.84E+03	1.38E+04	2.11E+06	2.38E+03	2.60E+02	3.98E+04	6.22E+04
P54296 MYOM2	GGVSDHSAFLFVR	464.57	100.63	2.69E+05	6.05E+03	5.02E+03	3.23E+03	1.33E+04	1.36E+04	4.13E+03	1.72E+03	1.06E+03	8.43E+02	3.06E+05	4.75E+03	8.13E+03	2.21E+02	1.26E+04
Q14315-2 FLNC	YWPTPEGEYAVH	724.83	100.75	7.46E+04	1.52E+03	1.16E+03	7.71E+03	1.73E+03	3.65E+02	2.80E+03	1.78E+03	3.23E+04	4.79E+04	7.06E+03	2.57E+03	1.69E+03	4.21E+03	4.68E+02
P35609 ACTN2	QLVPIRDQSLQEELAR	632.35	101.07	3.87E+02	2.38E+03	3.28E+04	5.05E+03	9.65E+05	2.87E+05	1.45E+05	3.08E+04	3.72E+03	2.64E+03	6.73E+03	5.00E+03	1.38E+03	9.48E+02	1.16E+05
P09493 TPM1	QLEDELVSLQK	651.35	101.07	1.93E+06	1.92E+04	6.55E+04	1.64E+06	5.48E+04	9.05E+04	2.50E+03	2.36E+03	1.63E+03	1.23E+03	1.60E+06	1.82E+04	1.40E+04	5.81E+03	4.75E+04
P35609 ACTN2	INLAMEIAEK	566.31	101.09	6.52E+02	4.40E+04	4.36E+03	6.78E+03	3.47E+03	1.78E+05	5.28E+03	3.97E+03	8.59E+02	1.47E+03	2.30E+04	2.46E+04	7.93E+03	1.05E+03	2.82E+04
P12883 MYH7	SPGVMDNPLVMHQLR	565.29	101.2	1.47E+04	5.33E+03	4.45E+03	8.83E+03	8.68E+03	9.59E+02	4.92E+03	1.48E+03	1.37E+03	1.17E+03	6.22E+04	3.15E+04	3.03E+04	6.55E+03	2.57E+03
Q14896 MYPC3	QGVLTLEIR	514.81	101.3	5.90E+02	2.60E+05	5.50E+03	3.82E+05	1.37E+04	3.80E+05	3.08E+05	4.12E+03	8.01E+02	9.36E+02	3.44E+05	1.92E+05	4.62E+04	2.12E+03	2.78E+05
Q14896 MYPC3	SVEVAAGSPAVFEAETERA GVK	735.38	101.37	4.49E+03	6.32E+02	8.49E+03	1.20E+04	2.51E+04	1.23E+03	2.30E+03	1.55E+03	1.16E+03	1.78E+03	1.39E+04	1.57E+04	4.82E+03	2.47E+03	1.84E+04
P68871 HBB	EFTPPVQAAY	561.78	101.43	1.68E+06	3.86E+03	1.30E+03	1.14E+06	2.10E+03	6.46E+03	6.46E+02	1.02E+03	1.92E+04	2.00E+03	9.52E+05	1.22E+04	1.34E+03	2.59E+02	1.56E+04
Q14315-2 FLNC	VHTPSGAVEECYVSELDS	722.33	101.51	5.36E+04	1.39E+03	1.85E+03	5.47E+04	1.18E+03	6.61E+02	1.08E+03	1.80E+03	1.67E+03	8.34E+02	7.12E+04	1.55E+03	2.67E+03	3.45E+03	9.24E+03
P06576 ATPB	IMNVIGEPIDERGPIK	594.32	101.54	3.37E+03	1.60E+03	1.40E+03	6.42E+03	6.93E+04	1.73E+03	1.01E+03	5.23E+02	1.83E+03	2.65E+04	4.13E+02	2.23E+04	2.97E+03	8.49E+02	1.01E+03
P02768 ALBU	LVNEVTEF	475.75	101.54	6.83E+05	1.63E+04	3.18E+03	1.80E+04	2.41E+03	2.00E+03	1.42E+03	4.41E+02	6.96E+02	2.15E+05	6.49E+05	9.28E+03	1.03E+04	7.44E+02	8.94E+03
P17661 DESM	VAELYEEELRELRR	602.32	101.73	3.54E+04	6.22E+04	3.16E+03	2.72E+03	4.10E+03	1.95E+05	1.88E+03	4.70E+03	6.39E+02	2.04E+03	1.42E+04	8.01E+03	9.46E+02	7.60E+02	2.45E+05
P12111-2 CO6A3	LQPVLQPLPSPGVGGK	793.97	101.74	1.92E+03	1.32E+03	3.26E+02	1.91E+05	5.48E+03	8.96E+02	1.43E+03	6.81E+02	7.56E+02	3.55E+02	1.37E+05	1.36E+03	7.05E+03	7.56E+02	4.56E+03
P12111-2 CO6A3	VVIHFTDGADGDLADLHR	488.50	101.82	2.06E+03	3.82E+02	2.32E+03	7.56E+04	1.41E+03	2.63E+03	1.41E+03	1.41E+03	2.31E+02	3.14E+03	7.13E+04	1.23E+03	2.69E+04	2.60E+02	5.38E+03
P12883 MYH7	FAVIAAIGDR	516.80	101.92	2.53E+05	4.29E+04	1.42E+03	7.20E+04	2.24E+03	3.72E+03	4.48E+02	1.91E+03	4.68E+04	5.35E+04	2.72E+05	5.60E+03	1.31E+05	1.67E+03	3.17E+03
P12883 MYH7	SPGVMDNPLVMH	648.81	102.21	2.75E+06	3.07E+04	6.24E+04	2.65E+06	1.00E+04	6.98E+04	9.05E+03	3.72E+03	3.80E+03	1.55E+03	1.94E+06	2.03E+04	2.45E+03	1.44E+03	8.61E+04
P54296 MYOM2	GLTTGEQYIFR	642.83	102.34	1.09E+04	7.29E+03	2.20E+03	2.27E+05	7.80E+03	7.58E+02	3.34E+02	1.80E+03	1.68E+04	1.77E+04	6.79E+04	5.92E+03	1.37E+05	8.85E+03	1.04E+04
P12883 MYH7	DVFPVDDKQEF	669.81	102.38	1.23E+05	7.86E+03	7.42E+02	2.92E+05	3.21E+03	8.73E+02	7.47E+02	1.29E+03	1.32E+03	4.88E+02	1.68E+05	1.85E+03	4.67E+04	6.69E+03	1.38E+04
P35609 ACTN2	TINEVETQILTR	708.89	102.4	1.70E+06	1.41E+04	1.19E+03	3.88E+03	2.53E+03	1.79E+04	7.24E+03	1.06E+03	2.69E+05	4.21E+05	2.22E+06	3.12E+04	3.11E+04	3.73E+03	3.85E+04
P06576 ATPB	PPILNALEVQGRETRLVLEV AQHLGESTVR	554.98	102.44	7.24E+02	7.18E+02	2.24E+03	6.94E+03	9.10E+02	5.39E+03	2.46E+05	3.12E+05	2.85E+03	3.12E+03	4.91E+02	6.31E+02	1.09E+03	5.35E+03	2.21E+03
P08590 MYL3	ALGQNPTQAEVLRVLGKPR	512.55	102.66	1.10E+04	4.95E+03	1.23E+03	2.49E+03	5.48E+04	8.30E+02	3.88E+03	5.00E+02	1.06E+03	1.72E+03	5.81E+03	1.60E+04	1.84E+03	6.37E+02	7.58E+04
P54296 MYOM2	YPVTGLFEGR	569.80	103.08	2.77E+05	3.98E+02	4.64E+03	2.65E+05	1.51E+04	2.35E+03	4.57E+02	1.27E+03	4.96E+03	4.14E+02	2.72E+05	1.21E+03	1.63E+03	2.66E+03	8.00E+03
Q14315-2 FLNC	NAGYVGLGLSIEGPSK	760.39	103.08	1.29E+05	7.88E+03	2.18E+03	1.94E+05	1.90E+03	3.00E+03	1.09E+03	1.86E+03	6.75E+02	3.77E+02	1.95E+05	3.59E+03	1.10E+03	6.91E+02	1.00E+03
P10916 MLRV	AAFPPDVTGNLDYK	754.37	103.15	3.94E+04	1.69E+03	6.81E+03	3.03E+04	8.89E+02	4.12E+03	2.98E+03	5.23E+03	1.59E+03	4.02E+02	5.64E+04	2.49E+03	4.08E+04	2.90E+03	3.38E+03
Q14315-2 FLNC	FGGEHIPNSPF	601.28	103.21	5.63E+03	2.33E+04	1.22E+04	4.55E+02	3.87E+04	3.05E+04	7.60E+02	6.12E+03	3.09E+02	5.86E+02	1.12E+04	1.49E+05	7.91E+02	1.68E+03	5.52E+04
P06576 ATPB	GLFGGAGVGK	431.75	103.26	3.81E+03	1.64E+05	1.78E+05	2.40E+05	1.42E+05	1.74E+05	2.70E+05	3.74E+05	5.44E+02						

Q14896 MYPC3	SVEVAAGSPAVF	567.29	104.08	9.43E+03	5.82E+02	3.03E+03	5.19E+04	3.34E+03	1.73E+03	1.02E+04	4.86E+04	8.20E+05	1.73E+05	2.70E+04	1.29E+03	4.16E+03	8.13E+05	1.35E+04
P10916 MLRV	SMFEQTQIQEFK	758.36	104.09	2.54E+06	9.69E+03	1.35E+03	1.83E+06	6.32E+02	7.62E+03	1.42E+03	7.97E+02	5.68E+02	1.70E+03	1.38E+06	5.72E+03	4.72E+02	1.19E+03	8.03E+03
P68133 ACTS	KDLYANNVMSGGTTMYPG IADR	792.05	104.59	5.81E+04	5.54E+02	2.68E+03	7.95E+04	1.39E+04	7.78E+02	3.24E+03	8.95E+02	2.70E+03	9.00E+02	2.45E+04	5.27E+03	2.99E+02	2.49E+03	4.47E+03
P10916 MLRV	EAFITMDQNRDGFIDK	633.97	104.61	1.94E+03	6.25E+03	3.26E+04	1.32E+03	9.43E+02	3.99E+03	1.40E+05	2.17E+05	9.19E+02	4.15E+03	1.82E+03	4.40E+03	5.52E+03	4.86E+02	3.81E+03
P12883 MYH7	QLDEKEALISQLTR	548.64	104.75	1.44E+05	2.22E+03	3.05E+03	2.08E+03	1.69E+04	1.80E+03	5.23E+03	5.18E+02	1.99E+03	1.10E+03	3.17E+05	6.58E+03	1.26E+04	4.90E+02	1.57E+04
P69905 HBA	TYFPHF	406.19	104.98	4.32E+03	1.97E+05	2.90E+03	1.86E+05	1.44E+04	5.94E+05	2.00E+03	9.65E+03	1.72E+05	2.23E+05	2.08E+03	7.64E+03	4.21E+02	1.78E+04	1.98E+05
P06576 ATPB	LVLEVAQHLGESTVR	825.96	105.18	5.21E+04	1.34E+04	6.63E+03	3.53E+03	1.21E+04	8.23E+03	3.27E+03	6.47E+03	6.97E+02	1.96E+03	3.19E+04	5.16E+03	4.50E+03	7.16E+02	5.77E+04
P54296 MYOM2	GQDVSILEIAGK	615.34	105.21	3.46E+05	9.83E+03	2.72E+03	2.53E+04	1.50E+03	5.86E+02	3.12E+04	6.80E+02	1.72E+03	3.68E+04	3.08E+05	1.35E+03	3.15E+03	1.25E+03	1.02E+03
P06576 ATPB	VVDLLAPYAK	544.82	105.21	1.25E+04	1.18E+06	1.12E+06	8.04E+02	1.09E+06	8.12E+05	5.76E+03	9.02E+03	3.46E+05	1.86E+05	9.21E+02	1.50E+06	1.92E+02	5.58E+05	1.36E+06
P25705 ATPA	ALIIYDDLSK	575.82	105.54	5.73E+02	8.54E+02	1.11E+05	2.01E+03	2.25E+02	1.55E+03	2.99E+04	4.21E+04	1.18E+04	5.15E+03	3.58E+02	2.64E+03	1.24E+03	6.77E+03	2.74E+03
P25705 ATPA	TSIAIDTIINQK	658.88	105.7	1.27E+06	1.51E+05	7.73E+03	1.37E+06	3.36E+04	1.83E+05	4.73E+03	2.15E+04	5.36E+03	1.05E+03	8.97E+05	4.36E+04	7.02E+04	1.18E+03	2.91E+04
P35609 ACTN2	WDKVKQLVPIRDQSLQEEL AR	636.35	105.72	4.52E+02	3.72E+03	6.43E+04	6.75E+02	2.55E+05	6.11E+03	6.56E+04	3.23E+04	7.49E+02	2.34E+03	2.10E+03	1.11E+03	1.17E+04	1.96E+03	5.22E+03
P17661 DESM	VDVERDNLLDDLQR	567.29	105.75	4.74E+03	2.48E+04	2.55E+04	2.38E+04	1.04E+05	4.91E+04	5.73E+04	3.14E+04	3.20E+04	1.38E+03	3.50E+04	8.09E+04	1.09E+04	2.10E+04	4.38E+04
P02768 ALBU	RHPDYSVLLLLR	490.27	105.77	6.68E+02	7.42E+02	8.87E+03	9.88E+02	8.47E+02	9.92E+02	9.88E+04	4.07E+04	6.49E+03	5.19E+03	9.19E+02	4.41E+03	9.17E+02	1.79E+04	1.35E+03
P06576 ATPB	SVEQEILVTGIK	658.37	105.88	1.13E+03	1.39E+05	1.02E+04	1.40E+03	5.59E+04	1.15E+05	2.51E+03	1.53E+03	5.31E+02	1.66E+03	2.82E+03	9.33E+04	9.24E+04	6.29E+03	1.13E+05
P69905 HBA	TYFPHFDLSH	421.87	106.03	4.35E+02	4.08E+03	7.25E+05	2.46E+04	2.90E+03	9.25E+02	3.89E+05	2.88E+05	1.61E+02	2.07E+02	2.06E+02	1.10E+03	1.98E+03	2.59E+03	6.42E+02
P54296 MYOM2	IAAVNLAGIGEPSDPSEHFK	684.69	106.09	9.39E+02	2.05E+03	1.12E+04	3.83E+02	1.64E+05	1.87E+04	3.56E+03	1.97E+03	1.86E+04	6.63E+03	1.83E+02	1.32E+05	1.18E+03	1.04E+04	2.04E+05
Q14315-2 FLNC	VPQLPITNFNR	649.86	106.13	8.73E+02	1.24E+05	6.16E+02	5.68E+05	2.31E+05	4.15E+03	2.57E+03	2.55E+03	1.46E+04	1.08E+03	4.51E+03	2.52E+05	2.48E+04	1.31E+04	5.34E+05
P69905 HBA	TYFPHFDLSHG	440.87	106.23	3.07E+02	4.08E+03	1.17E+05	1.82E+03	9.79E+02	3.73E+03	2.61E+05	1.29E+05	3.68E+02	2.36E+02	2.30E+02	1.90E+03	1.54E+03	2.49E+03	6.50E+02
P12883 MYH7	ILNPAAIPEGQFIDSRK	623.68	106.36	1.81E+03	2.81E+03	1.21E+04	1.00E+05	5.34E+03	2.20E+03	4.08E+05	1.64E+05	1.95E+03	1.86E+05	4.31E+03	8.05E+03	7.16E+03	6.30E+02	2.75E+04
P02768 ALBU	LVAASQAALGL	507.30	106.4	5.58E+06	3.97E+06	4.98E+06	2.84E+03	3.70E+06	5.71E+06	1.00E+05	4.51E+04	3.40E+03	9.85E+02	5.70E+06	3.07E+06	1.35E+06	4.86E+02	4.37E+06
P17661 DESM	RIESLNEEIAFLKK	563.99	106.74	6.84E+03	1.37E+03	1.08E+03	1.84E+05	3.36E+03	8.43E+02	5.17E+03	1.67E+03	9.75E+04	1.13E+05	1.15E+05	2.62E+03	2.02E+05	5.17E+04	2.00E+03
P17661 DESM	DNLLDDLQR	551.28	106.99	1.17E+05	8.82E+05	1.44E+06	7.32E+02	1.21E+06	3.53E+06	5.22E+03	1.00E+04	1.10E+04	1.08E+05	1.67E+03	1.33E+06	8.00E+05	1.67E+03	2.67E+06
P12111-2 CO6A3	SSIMAFAGNK	569.80	107.13	2.48E+03	2.35E+03	1.24E+04	2.51E+02	6.07E+04	3.64E+04	6.07E+03	6.25E+03	1.09E+04	2.39E+03	1.58E+03	2.48E+03	7.18E+02	6.22E+02	1.80E+03
Q14896 MYPC3	IAFQYGVTDLR	641.84	107.22	5.49E+02	8.15E+05	2.63E+04	8.29E+02	1.48E+06	1.89E+06	2.37E+04	3.26E+04	8.20E+02	1.73E+03	1.28E+03	1.20E+06	3.29E+03	7.67E+02	1.69E+06
Q14315-2 FLNC	ILPAPPDCCFDK	656.83	107.41	2.82E+02	1.83E+03	4.59E+03	1.36E+03	5.77E+03	1.43E+03	1.84E+03	1.48E+03	1.14E+05	1.04E+05	1.30E+03	3.10E+04	1.94E+05	5.42E+04	7.98E+04
P08590 MYL3	KDTGTIEDFVEGLR	543.93	107.44	3.70E+03	3.87E+03	1.38E+03	4.13E+02	4.07E+03	3.42E+03	1.94E+03	3.88E+03	1.38E+04	3.13E+03	1.57E+03	5.36E+04	1.40E+03	2.42E+04	5.52E+04
Q14896 MYPC3	PAPDAPEDTGDSEWVFDK	1045.95	107.65	1.12E+03	2.46E+03	6.60E+03	5.22E+02	4.86E+03	2.30E+04	2.29E+02	4.61E+02	4.10E+02	2.58E+02	3.15E+03	3.60E+03	8.01E+03	3.65E+02	9.15E+04
P10916 MLRV	FSKEEVDQMF	630.28	107.69	8.63E+02	5.25E+03	1.97E+03	1.06E+03	1.83E+03	6.53E+02	2.76E+03	5.87E+03	1.74E+04	2.00E+04	1.29E+03	1.34E+03	7.17E+03	4.76E+02	6.40E+03
Q14315-2 FLNC	GQHVPGPSFQF	600.79	107.76	4.76E+03	7.44E+03	3.46E+03	5.47E+04	6.12E+04	2.76E+04	6.83E+03	1.36E+04	7.02E+02	8.18E+02	1.84E+04	3.22E+04	1.17E+04	2.30E+02	5.83E+02
Q14896 MYPC3	GEAPAAELGESAPSPK	835.42	107.94	1.10E+04	4.55E+04	3.13E+04	1.47E+04	2.88E+03	5.37E+04	1.23E+04	1.83E+04	7.65E+02	1.38E+03	6.78E+02	5.48E+03	4.96E+03	1.60E+04	1.31E+03
P54296 MYOM2	HGLSEPSEITPIQAQDVTV VPSAPGR	924.81	108.1	5.80E+02	1.57E+03	1.57E+02	3.58E+02	6.12E+04	1.17E+03	1.08E+03	2.03E+03	9.47E+02	1.98E+02	3.18E+02	2.78E+04	1.96E+04	2.28E+02	9.62E+04
P25705 ATPA	GSDLDAATQQLLSR	737.88	108.24	6.04E+04	2.60E+02	2.96E+04	1.83E+04	5.50E+03	2.74E+04	4.73E+04	6.68E+02	4.86E+03	2.84E+02	3.03E+04	1.39E+02	2.09E+02	1.32E+03	4.96E+03
Q14315-2 FLNC	GQHVPGPSFQFTVGPLGEG GAHK	576.79	108.25	1.28E+03	3.23E+03	4.22E+03	4.42E+02	1.14E+05	1.09E+04	4.35E+03	1.79E+03	6.89E+02	1.08E+03	2.64E+03	6.52E+04	4.41E+02	3.89E+03	1.56E+05
P25705 ATPA	FENAFLSHVVSQH	505.59	108.29	7.20E+04	9.93E+03	6.28E+02	3.16E+03	7.20E+03	5.16E+03	2.45E+03	4.35E+03	2.03E+03	1.42E+03	4.15E+03	6.24E+03	4.10E+02	4.95E+03	1.82E+03
P02768 ALBU	VPQVSTPTLVEVSRNLGK	642.03	108.38	1.29E+03	2.03E+03	2.28E+04	4.38E+02	4.04E+03	8.10E+03	1.37E+05	2.19E+04	1.79E+03	1.74E+03	1.08E+03	2.09E+03	2.98E+03	3.40E+04	8.30E+02
P17661 DESM	VAELYEEELRELRL	550.29	108.49	8.79E+02	2.21E+04	1.89E+04	7.47E+02	8.02E+04	7.62E+03	3.58E+02	1.54E+03	6.18E+03	3.30E+03	4.30E+02	9.18E+02	6.89E+03	7.92E+03	1.21E+05
P25705 ATPA	SSILEERILGADTSVDLEETG	794.40	108.51	1.28E+03	2.29E+04	1.72E+04	3.13E+03	1.07E+05	9.52E+02	2.06E+05	3.87E+05	6.47E+03	2.87E+03	1.59E+03	1.94E+04	1.38E+03	6.89E+03	8.65E+02
Q14315-2 FLNC	GGLVGTAPAFSITDK	730.39	108.56	9.11E+02	8.55E+04	4.80E+02	2.08E+03	2.03E+05	4.87E+03	9.22E+04	3.05E+04	4.67E+02	1.03E+03	2.66E+02	2.10E+05	1.43E+03	6.51E+02	1.11E+05
P69905 HBA	VAHVDDMPNALSALSDDL HAHK	578.79	108.61	1.11E+03	6.68E+04	1.22E+04	4.83E+03	1.38E+03	1.18E+05	2.27E+04	1.77E+04	1.64E+03	2.42E+03	1.30E+04	9.78E+02	2.77E+02	1.34E+03	6.89E+02
Q14896 MYPC3	AHNMAGPGAPVTTTTEPVTV QEILQRPR	718.38	108.74	1.06E+03	3.94E+04	3.17E+04	1.20E+04	1.90E+05	1.53E+03	4.86E+03	2.70E+03	2.20E+02	2.29E+04	8.80E+03	7.71E+04	3.61E+04	2.04E+03	3.00E+05
P12883 MYH7	LCHPRVKVGNVEYVTKGQN VQQVIYATGALAK	845.96	108.84	1.02E+03	6.27E+03	2.99E+05	1.98E+05	1.63E+03	8.17E+04	1.61E+05	2.49E+05	9.42E+02	2.74E+02	9.48E+04	9.33E+03	1.15E+05	2.41E+03	2.85E+04
P08590 MYL3	IEFTPEQIEE	617.80	108.93	1.66E+04	5.00E+03	2.85E+03	4.34E+03	1.61E+04	7.33E+03	1.00E+04	8.78E+03	2.46E+03	2.02E+03	1.75E+03	4.08E+03	8.67E+03	1.33E+03	2.10E+05
Q14896 MYPC3	EPVFIPRPGITYEPPNYK	706.37	108.96	4.17E+03	2.16E+05	4.90E+05	4.12E+03	4.33E+05	7.87E+04	1.16E+05	8.33E+04	4.90E+03	3.02E+03	6.01E+02	1.88E+04	8.74E+03	2.95E+03	5.26E+04
Q14896 MYPC3	AEPMLAPAPAPAEATGAPG EAPAPAAELGESAPSPK	831.16	109.03	2.98E+03	1.63E+03	8.91E+02	1.52E+03	9.11E+04	1.43E+03	1.52E+03	1.70E+03	9.02E+02	6.04E+02	6.60E+03	1.13E+05	2.64E+04	6.97E+02	8.14E+04
P69905 HBA	VAHVDDMPNALSALSDDLH AHK	449.03	109.03	2.83E+04	2.55E+02	9.61E+02	1.56E+02	3.40E+02	4.27E+02	5.75E+02	2.37E+02	1.19E+03	1.60E+02	1.40E+03	3.40E+02	1.47E+03	2.60E+02	7.14E+02
P02768 ALBU	RPCFSALEVDETYVPK	618.64	109.16	1.27E+04	2.75E+04	2.20E+04	2.82E+06	4.13E+06	2.57E+06	3.86E+04	5.64E+04	1.95E+05	3.19E+05	3.61E+03	1.26E+06	4.19E+05	2.29E+03	2.73E+06
P10916 MLRV	PEETILNAFK	581.31	109.18	3.29E+02	7.26E+04	3.38E+03	4.48E+04	9.85E+04	3.41E+03	3.26E+03	1.97E+03	1.43E+04	9.47E+02	1.26E+04	8.35E+04	1.46E+03	3.56E+04	6.69E+04
P12883 MYH7	GQNVQQVIYATGALAK	830.95	109.31	1.25E+03	3.60E+03	1.77E+03	1.96E+03	1.24E+06	1.80E+04	1.04E+04	9.16E+03	5.99E+03	8.53E+02	2.98E+03	3.72E+05	1.54E+05	1.26E+04	1.78E+06
P25705 ATPA	LEPDNVGVVVFNGDK	801.41	109.55	3.85E+03	4.29E+03	4.23E+04	4.81E+04	1.98E+03	3									

P08590 MYL3	NKDTGTYEDFVEGLR	581.95	109.75	8.77E+03	1.40E+03	9.69E+02	1.87E+04	2.72E+05	8.72E+03	3.14E+03	7.89E+02	1.22E+04	1.44E+04	1.39E+04	4.11E+05	3.64E+03	7.53E+05	3.34E+05
P10916 MLRV	EAFITMDQNRDGFIDKNDL	600.29	109.9	1.33E+03	3.42E+03	4.49E+03	1.43E+04	3.64E+03	2.17E+03	1.47E+03	7.14E+02	1.19E+05	4.51E+03	1.57E+03	1.22E+05	5.79E+03	2.89E+04	7.74E+02
P02768 ALBU	TYETTLEKCCAAADPHECY	783.01	110.26	2.05E+03	1.37E+03	2.41E+03	1.56E+03	5.57E+02	1.82E+03	1.88E+03	2.04E+03	1.84E+03	2.79E+04	1.54E+03	1.25E+03	3.12E+03	1.70E+03	6.91E+03
P54296 MYOM2	SELAYEIFDK	607.80	110.71	2.88E+03	1.19E+03	1.34E+05	2.43E+03	3.51E+03	1.73E+03	6.23E+04	1.54E+05	4.88E+03	1.68E+03	2.97E+03	6.96E+02	1.39E+03	2.70E+03	3.42E+03
P06576 ATPB	PATTFAHLDAATTVLSRAI	627.67	111.05	3.85E+04	1.58E+04	1.97E+03	7.10E+04	1.56E+05	1.49E+03	1.47E+04	2.06E+04	1.28E+03	5.05E+02	2.97E+03	4.59E+04	6.73E+05	4.16E+02	7.03E+04
P69905 HBA	VDDMPNALSALSDLHAHK	484.24	111.46	2.18E+03	1.57E+05	1.27E+04	3.41E+03	1.13E+03	4.34E+05	1.52E+05	3.69E+03	1.39E+04	2.63E+03	3.39E+03	7.66E+02	4.20E+03	1.19E+03	1.72E+03
P12883 MYH7	LQEEISDLTEQLGSSGK	917.46	111.49	6.23E+02	7.46E+03	1.25E+04	1.36E+03	6.66E+04	1.36E+03	1.82E+04	7.65E+03	2.49E+03	1.84E+03	3.99E+03	1.51E+03	5.36E+03	1.01E+03	2.51E+04
P06576 ATPB	VLDSGAPIKIPVGPETLGR	640.37	111.49	8.25E+04	4.33E+02	2.88E+03	5.95E+04	1.93E+06	1.87E+03	1.70E+03	1.39E+04	4.60E+02	1.06E+03	4.51E+04	7.08E+05	2.72E+05	3.55E+02	2.83E+05
P35609 ACTN2	ASDKPYILAEELR	752.90	111.49	1.27E+03	6.58E+03	5.46E+02	1.81E+03	1.83E+03	1.01E+04	3.94E+03	5.10E+04	6.79E+03	5.01E+04	3.52E+03	9.28E+03	8.87E+02	1.58E+04	4.47E+03
P06576 ATPB	IDNIFRFTQAGSEVSALLGR	733.39	111.5	3.70E+03	8.89E+05	9.93E+03	1.05E+03	3.29E+02	1.73E+04	4.79E+05	6.48E+05	8.30E+02	7.25E+02	5.60E+02	3.00E+03	1.05E+03	1.30E+03	1.61E+03
Q14315-2 FLNC	DNGDGTYYTVSYLPDMSGR	974.42	111.52	1.85E+04	7.51E+03	1.90E+03	2.86E+03	3.01E+03	3.41E+03	4.32E+02	1.27E+03	1.33E+03	5.60E+02	4.87E+04	3.90E+03	2.56E+03	7.44E+02	3.54E+04
Q14896 MYPC3	FDCSNFNLTVH	648.79	111.76	3.67E+03	7.52E+03	9.75E+02	5.67E+04	3.53E+02	3.48E+03	8.16E+02	1.17E+03	5.06E+02	2.97E+02	3.20E+03	6.00E+03	5.12E+03	1.02E+03	8.26E+02
P12111-2 CO6A3	ALILVGLER	492.32	111.86	1.95E+03	1.93E+02	6.54E+02	1.51E+03	4.82E+02	3.42E+02	2.94E+02	5.65E+02	2.14E+05	3.70E+05	1.39E+03	3.81E+02	1.30E+03	1.88E+05	1.58E+03
P54296 MYOM2	VFLQAEHLSPDASYR	607.30	111.86	1.70E+03	2.23E+03	2.50E+03	5.04E+02	1.31E+03	6.36E+03	1.31E+03	5.71E+02	4.37E+04	2.58E+04	2.63E+03	9.04E+03	1.12E+03	1.72E+04	2.41E+03
P54296 MYOM2	WSDAVAALDPLDLRR	537.63	111.89	3.11E+03	1.48E+04	3.99E+03	1.57E+02	1.10E+03	1.03E+05	6.66E+04	2.79E+04	6.83E+02	1.18E+03	1.23E+03	5.00E+03	2.58E+02	2.42E+03	4.59E+02
P06576 ATPB	GPETLGRIMNVIGEPIDER	699.36	112	3.22E+03	6.20E+03	7.23E+03	2.67E+05	1.90E+06	1.00E+04	1.67E+03	1.22E+03	5.77E+02	2.09E+03	2.21E+04	1.53E+06	4.44E+05	1.73E+03	4.44E+05
P06576 ATPB	FTQAGSEVSALLGR	718.38	112.07	1.63E+06	2.79E+03	6.02E+03	1.34E+06	1.56E+06	2.46E+04	1.19E+04	4.83E+04	8.10E+02	2.74E+03	1.30E+06	6.40E+05	7.82E+05	1.77E+03	1.91E+06
Q14896 MYPC3	SPTDTILFIR	581.83	112.12	1.52E+03	2.44E+04	1.40E+04	1.68E+03	7.61E+02	4.84E+04	1.10E+05	7.43E+04	3.52E+02	3.23E+03	1.67E+03	2.90E+03	7.46E+03	9.85E+02	3.59E+03
Q14315-2 FLNC	GGLVGTAPPF	458.25	112.26	1.39E+05	4.38E+03	3.81E+03	9.47E+04	7.82E+03	1.69E+02	4.49E+03	5.72E+02	1.71E+03	2.73E+03	1.80E+05	6.67E+03	3.62E+03	4.24E+02	8.92E+03
P06576 ATPB	IPSAVGYQPTLATDMGTMQ	756.03	112.48	1.54E+03	3.57E+03	3.49E+03	8.77E+02	1.23E+06	4.02E+03	3.48E+03	8.03E+03	6.26E+02	3.00E+05	2.19E+03	2.06E+05	5.41E+04	5.62E+02	6.44E+05
P68871 HBB	VNVDEVGGEALGRL	714.37	112.52	4.29E+03	8.72E+02	1.62E+04	1.77E+03	1.00E+03	7.39E+04	1.46E+05	2.72E+04	2.69E+03	8.57E+02	1.01E+03	1.55E+03	1.40E+03	9.25E+02	1.14E+03
P08590 MYL3	IKIEFTPEQIEE	738.39	112.77	8.24E+03	8.56E+03	6.03E+02	3.62E+03	8.75E+04	6.22E+03	1.64E+03	3.32E+03	3.31E+06	2.68E+06	4.26E+04	2.00E+04	2.80E+05	4.43E+03	7.22E+04
P69905 HBA	MFLSFPTTK	536.28	112.78	1.98E+03	2.02E+07	3.58E+04	2.01E+07	2.38E+07	1.77E+07	2.78E+05	1.23E+07	7.38E+03	1.50E+04	2.19E+03	2.11E+07	4.41E+02	2.75E+04	8.44E+06
P35609 ACTN2	ILASDKPYILAEELR	577.66	112.81	4.27E+04	1.35E+04	2.69E+03	2.01E+04	1.67E+05	1.90E+02	6.42E+03	7.74E+03	2.88E+03	3.52E+02	3.13E+06	2.18E+04	2.11E+04	5.76E+03	3.16E+04
P17661 DESM	IESLNEEIAFLK	511.96	113.11	4.07E+02	1.05E+04	3.48E+03	8.96E+04	2.84E+05	4.91E+03	6.68E+03	5.85E+03	1.35E+03	9.47E+02	1.95E+05	1.18E+05	2.82E+03	2.13E+05	2.13E+05
P25705 ATPA	RTGAIVDVPVGEELLGR	594.34	113.13	1.80E+03	8.99E+03	9.96E+02	2.01E+03	8.66E+02	2.25E+04	2.05E+04	1.77E+03	1.28E+04	1.36E+03	7.80E+02	2.64E+02	6.37E+02	2.07E+04	1.74E+03
P17661 DESM	INLPIQTY	481.27	113.46	1.72E+03	1.95E+04	8.46E+04	1.79E+03	9.34E+02	5.22E+03	3.01E+04	1.84E+04	1.82E+03	1.55E+03	2.11E+03	1.37E+04	7.67E+02	1.68E+03	8.02E+02
P12111-2 CO6A3	QQSLETAMSFVAR	734.37	113.54	3.91E+03	8.72E+02	7.01E+03	3.43E+03	2.66E+04	4.55E+02	1.31E+03	1.18E+03	1.02E+03	1.61E+03	1.28E+04	2.03E+03	4.73E+02	8.13E+03	2.33E+04
Q14896 MYPC3	PIGLFVMR	466.77	113.78	2.90E+03	3.87E+02	1.18E+03	3.84E+02	2.67E+03	5.58E+02	1.43E+03	6.61E+02	1.73E+02	9.05E+02	1.08E+03	4.66E+04	1.20E+03	2.57E+03	2.88E+03
P35609 ACTN2	QFAAQANAIGPWIQNK	878.96	113.84	6.38E+02	2.29E+03	2.50E+03	5.67E+02	4.53E+03	5.58E+03	2.69E+03	5.58E+02	1.87E+05	1.12E+04	5.20E+03	8.44E+02	4.34E+03	6.45E+03	2.67E+03
P12111-2 CO6A3	VPQIAFVITGGK	731.89	114	2.20E+03	1.91E+04	5.72E+02	4.81E+03	1.26E+03	1.47E+05	1.57E+04	4.69E+04	2.28E+03	2.21E+03	6.09E+03	2.04E+03	1.45E+03	6.49E+03	3.62E+02
P02768 ALBU	HPDYSVVLRL	656.37	114.16	1.59E+03	5.47E+04	3.73E+04	3.14E+05	2.55E+05	1.38E+03	8.02E+04	7.38E+04	2.50E+03	1.67E+03	1.06E+04	2.25E+04	6.86E+02	2.06E+03	2.59E+04
Q14896 MYPC3	NSPTDTILFIR	638.85	114.24	3.55E+03	1.37E+06	2.08E+03	1.63E+06	1.21E+06	1.34E+04	1.61E+04	4.45E+03	5.29E+02	1.34E+03	2.09E+02	2.00E+06	1.04E+06	3.69E+02	1.32E+06
P54296 MYOM2	VYDDMILAMSR	657.31	114.42	5.40E+02	7.47E+03	1.32E+04	6.85E+03	1.48E+05	3.67E+04	8.60E+03	1.02E+04	5.27E+02	8.15E+02	1.18E+03	6.09E+04	5.68E+04	1.76E+04	1.69E+05
P17661 DESM	FLEQQNAALAAEVNRLK	639.02	114.61	5.37E+02	1.16E+03	2.20E+04	1.03E+03	2.81E+04	7.30E+04	8.86E+03	1.65E+04	7.35E+02	2.50E+02	1.05E+03	3.52E+02	3.52E+03	3.41E+02	1.74E+03
P25705 ATPA	EAYPGDVFYLH	655.81	114.63	2.08E+06	3.87E+04	9.93E+03	1.44E+03	2.94E+05	7.66E+03	1.20E+04	1.14E+04	1.34E+03	1.09E+03	4.18E+03	4.40E+05	4.45E+05	4.46E+02	9.53E+05
P02768 ALBU	TLFGDKLCTVATLR	513.28	114.73	2.55E+03	8.05E+03	7.24E+02	1.60E+04	9.40E+04	2.55E+03	2.72E+04	1.41E+04	7.44E+02	4.52E+03	2.83E+03	1.09E+05	2.09E+03	1.77E+03	8.80E+03
P02768 ALBU	EFNAETFTFH	621.78	114.75	1.43E+03	1.33E+03	2.45E+02	7.48E+02	3.70E+02	4.11E+03	1.72E+03	1.15E+03	2.46E+05	1.13E+04	1.52E+03	8.71E+02	1.12E+03	1.38E+05	1.80E+03
P69905 HBA	VADALTNVAHVDDMPN	876.92	114.78	8.37E+04	4.08E+03	3.25E+03	1.62E+03	7.53E+03	4.76E+03	1.71E+03	1.09E+03	4.38E+03	2.83E+03	9.52E+03	1.20E+04	6.67E+03	6.63E+02	3.98E+04
P12111-2 CO6A3	IGDLHPQIVNLLK	487.29	114.85	6.55E+02	1.85E+03	4.13E+02	5.41E+03	3.02E+02	1.24E+03	1.70E+03	2.75E+02	3.21E+04	9.25E+03	3.68E+03	2.52E+03	2.61E+03	4.36E+03	1.37E+03
P25705 ATPA	AIEEQVAVIYAGVR	759.42	115.13	2.79E+03	1.98E+03	1.90E+03	6.12E+03	1.15E+03	1.74E+03	3.90E+03	2.97E+03	9.54E+02	1.09E+03	5.75E+03	2.34E+04	2.81E+04	6.10E+02	1.14E+05
P08590 MYL3	TGTYEDFVEGLR	693.83	115.48	8.89E+02	1.03E+03	2.14E+03	2.86E+02	3.30E+04	9.48E+02	1.14E+03	1.21E+03	1.34E+03	2.26E+03	2.04E+03	5.72E+04	7.59E+04	2.54E+03	6.11E+04
P12111-2 CO6A3	VPQIAFVITGGK	615.37	115.53	1.81E+03	6.14E+04	1.62E+04	2.01E+03	7.13E+04	7.33E+04	9.51E+04	1.73E+05	3.98E+02	6.46E+02	4.61E+02	7.55E+03	1.50E+03	5.94E+03	6.55E+03
Q14315-2 FLNC	VDITYDGHVPVPGSPF	800.89	115.7	3.54E+04	1.70E+03	1.33E+03	3.68E+03	6.93E+02	1.57E+03	2.18E+03	1.14E+03	2.82E+03	2.50E+03	3.06E+04	9.29E+03	1.04E+04	3.50E+02	3.50E+03
P17661 DESM	RIESLNEEIAFLK	521.29	115.76	1.58E+03	6.33E+02	3.12E+02	2.91E+04	2.70E+05	1.15E+03	3.73E+03	1.11E+04	9.40E+02	1.62E+03	5.38E+03	5.83E+05	7.68E+03	2.34E+03	1.38E+05
P68871 HBB	GTFATLSELHCDKLHVDPE	633.06	116.02	1.33E+02	4.30E+02	2.48E+03	7.15E+02	1.92E+05	1.96E+04	5.11E+03	1.16E+03	4.86E+02	1.23E+03	2.98E+02	2.73E+04	1.88E+02	1.17E+03	4.05E+04
P12111-2 CO6A3	NFR	558.66	116.1	1.96E+03	4.63E+02	3.42E+03	6.31E+02	1.65E+05	8.32E+02	7.96E+02	2.40E+03	3.64E+02	2.39E+02	5.61E+02	9.48E+04	4.13E+02	5.05E+02	1.90E+05
Q14896 MYPC3	IEDGVQPQLVVLGGK	850.13	116.1	1.66E+02	2.17E+04	1.37E+03	8.27E+02	1.22E+02	5.78E+04	1.00E+03	5.47E+03	7.51E+02	6.28E+02	4.62E+02	1.10E+03	1.49E+02	2.31E+02	2.83E+02
P54296 MYOM2	MAGPGAPVTTTEPVTVQEI	560.27	116.22	1.03E+05	8.17E+02	1.04E+03	9.38E+04	4.24E+03	1.59E+03	6.31E+02	2.32E+03	1.70E+03	4.71E+02	1.02E+05	5.88E+02	1.60E+03	5.62E+02	1.65E+03
P17661 DESM	LQRPR	782.39	116.29	1.47E+03	1.81E+02	1.45E+03	7.41E+02	1.47E+04	2.34E+03	1.37E+03	6.12E+02	6.86E+04	1.45E+04					

P12883 MYH7	EAHQALDDLQAEEDKVN TLTKAKVKLEQQVDDLEGS LEQEK	951.48	117.12	9.58E+02	4.91E+02	5.34E+02	4.44E+03	1.02E+03	1.67E+03	1.91E+03	9.12E+03	2.48E+04	6.95E+02	1.27E+03	6.96E+03	1.72E+03	4.75E+04	2.78E+03
P12111-2 CO6A3	LLTPITTLTSEIQIK	843.49	117.15	2.12E+03	6.78E+02	5.21E+02	3.68E+03	2.32E+02	1.41E+03	9.69E+02	7.13E+02	6.97E+04	1.86E+04	7.73E+02	1.28E+03	1.53E+03	8.60E+03	5.02E+02
P02768 ALBU	SLHTLFGDKLCTVATLR	625.68	117.31	1.30E+03	9.19E+03	1.71E+04	1.14E+03	4.03E+05	2.54E+04	3.01E+04	5.24E+03	1.02E+03	6.32E+02	1.40E+04	1.08E+05	3.63E+02	1.53E+03	1.80E+05
P68133 ACTS	DLYANNVMSSGGTTMYPGI ADRMQKEITALAPSTMK	755.36	117.34	9.10E+02	4.42E+02	9.31E+02	3.66E+02	5.90E+04	8.80E+02	1.45E+06	1.06E+04	6.73E+02	1.16E+03	1.42E+05	1.88E+03	7.25E+03	1.50E+04	8.91E+04
P68133 ACTS	AGIHETTYNSIMKCDIDIRK DLYANNVMSSGGTTMYPGI	755.02	117.66	2.09E+03	1.44E+03	3.91E+03	5.93E+02	5.99E+04	1.85E+03	4.28E+02	4.98E+02	1.84E+04	5.25E+03	2.21E+05	1.03E+04	9.32E+03	2.09E+04	1.52E+05
P54296 MYOM2	GKDPLMYFIEK	670.85	117.71	2.18E+04	1.35E+03	3.08E+03	9.35E+03	1.84E+04	1.44E+04	1.80E+03	1.22E+03	1.34E+04	7.77E+02	7.41E+03	2.38E+04	5.16E+03	7.75E+02	4.77E+04
P35609 ACTN2	DGLGLCALIHR	584.32	117.74	3.73E+03	7.08E+03	1.58E+03	9.01E+02	8.00E+03	5.69E+02	5.47E+02	2.02E+03	2.55E+04	3.22E+04	2.04E+03	3.90E+02	7.01E+02	3.18E+04	1.25E+04
P54296 MYOM2	FLSELAHLEEDVH	769.88	117.85	6.16E+02	1.61E+04	2.68E+03	3.03E+03	2.14E+03	2.37E+04	8.65E+03	3.77E+03	2.55E+03	1.52E+03	2.38E+03	7.43E+03	1.28E+03	1.46E+03	8.76E+02
P08590 MYL3	LMAGQEDSNGCINYEAFVK	1044.98	118	6.26E+03	1.32E+02	1.39E+04	4.87E+03	1.04E+03	5.09E+03	1.33E+04	1.58E+02	6.62E+02	2.40E+04	4.93E+03	1.45E+03	9.69E+02	1.29E+03	1.85E+03
Q14315-2 FLNC	ILFAEAHIGPSPFK	509.62	118.13	5.86E+04	1.55E+02	4.80E+02	4.00E+02	1.28E+02	3.24E+02	3.62E+02	1.67E+02	5.46E+02	1.45E+03	4.20E+04	4.20E+03	1.69E+04	2.55E+02	3.41E+03
P68871 HBB	FESFGDLSTPDAVMGNPK	956.44	118.17	1.67E+05	1.66E+03	3.22E+03	3.92E+04	2.90E+04	5.53E+02	6.53E+02	1.30E+03	1.86E+04	2.39E+03	3.11E+03	6.01E+02	1.63E+03	2.55E+02	1.08E+04
Q14896 MYPC3	AHNMAGPGAPVTTEPVTV QEILQR	873.12	118.23	3.97E+03	1.63E+02	1.01E+03	1.60E+03	9.11E+02	1.69E+02	7.89E+02	2.64E+02	2.80E+04	4.76E+03	3.37E+03	1.50E+03	3.39E+03	1.63E+04	8.53E+02
P54296 MYOM2	DDVLYETETLPNLER	903.94	118.37	1.20E+02	3.06E+03	1.40E+03	1.23E+03	2.22E+04	1.38E+03	7.29E+02	1.22E+03	6.93E+03	7.79E+02	3.15E+03	1.49E+04	1.23E+04	2.81E+03	9.74E+04
Q14896 MYPC3	VGEPVNLLIPFQGKPR	588.68	118.53	1.33E+04	3.20E+02	3.41E+02	2.55E+04	3.84E+05	3.72E+03	1.94E+03	7.17E+02	5.01E+02	1.33E+02	3.85E+03	9.32E+04	5.12E+03	3.91E+02	1.89E+05
P69905 HBA	AVAHVDDMPNALSALSDDL HAH	546.77	118.65	5.93E+04	1.66E+03	1.41E+03	2.13E+04	2.18E+03	2.18E+03	5.41E+02	9.59E+02	1.25E+03	1.14E+03	1.13E+04	1.97E+03	1.02E+03	1.20E+03	2.18E+03
P17661 DESM	TNEKVELQELNDRFANYIE	818.42	118.89	3.14E+03	1.27E+04	7.03E+02	1.94E+03	1.16E+03	6.17E+04	2.16E+03	4.08E+03	5.67E+02	2.50E+03	5.94E+02	2.62E+03	1.52E+03	8.87E+02	9.28E+02
P08590 MYL3	EAFMLFDR	514.75	119.08	2.93E+03	2.67E+04	2.56E+03	1.37E+04	3.48E+02	5.20E+04	4.39E+04	1.85E+04	3.47E+06	2.50E+06	8.83E+03	1.22E+04	4.20E+03	3.50E+06	1.57E+03
P35609 ACTN2	LEGDHLQIQEALVFDNK	657.01	119.42	4.08E+03	3.17E+03	2.03E+03	8.55E+03	2.23E+05	5.62E+03	1.90E+03	3.40E+03	9.27E+02	4.96E+04	2.44E+03	6.12E+04	2.76E+02	4.50E+02	4.27E+05
Q14315-2 FLNC	SPFEVNVGMALGDANK	825.41	119.46	1.18E+03	8.01E+02	1.88E+03	7.49E+02	2.97E+04	1.59E+04	4.59E+03	1.54E+04	4.38E+02	4.39E+03	3.80E+02	6.73E+02	4.29E+03	4.08E+03	1.60E+03
P54296 MYOM2	GICELLIPK	493.29	119.56	3.26E+04	9.25E+03	2.14E+03	2.88E+04	1.62E+05	1.56E+04	1.37E+04	4.71E+03	2.19E+03	2.40E+03	5.58E+04	9.35E+03	1.58E+04	3.35E+03	2.79E+04
Q14315-2 FLNC	APLQVAVLGPTGVAEPVEV	668.05	119.71	3.36E+02	2.77E+03	3.02E+03	1.71E+03	2.16E+05	7.66E+02	8.17E+02	3.45E+03	6.91E+02	2.68E+03	4.04E+03	3.21E+05	1.35E+05	2.95E+03	2.86E+05
Q14315-2 FLNC	ITESDLSQLTASIR	767.41	119.84	1.45E+03	1.98E+06	3.07E+04	3.05E+03	3.45E+05	1.68E+06	8.23E+04	5.87E+03	6.91E+02	1.83E+03	9.78E+02	2.66E+05	2.64E+03	1.73E+03	1.19E+06
P08590 MYL3	IEFTPEQIEEFKE	819.90	120.01	2.10E+03	1.75E+03	1.41E+03	2.85E+03	9.37E+02	3.96E+02	1.35E+03	2.01E+03	2.52E+03	4.99E+04	1.34E+03	1.06E+03	9.83E+02	7.61E+02	8.19E+02
P54296 MYOM2	NYVVLWEPPTPR	779.41	120.41	2.82E+04	4.46E+03	8.33E+03	1.11E+04	3.49E+04	3.06E+04	9.45E+02	1.48E+03	7.78E+03	8.49E+02	6.62E+03	1.26E+05	2.48E+04	9.74E+02	1.24E+05
Q14896 MYPC3	IENMEDKATLVLVQVVDKPS PPQDLR	709.63	120.53	7.97E+03	6.86E+03	1.55E+03	9.76E+02	2.98E+04	3.11E+02	2.08E+03	1.31E+03	1.05E+03	6.12E+02	8.58E+03	6.27E+03	3.79E+03	7.87E+02	8.52E+03
P08590 MYL3	IKIEFTPEQIEEFK	584.31	120.59	8.94E+03	4.04E+03	4.55E+03	1.19E+04	5.82E+05	7.06E+02	5.71E+02	1.36E+03	2.55E+02	2.00E+04	1.74E+04	3.56E+05	8.11E+04	1.44E+03	2.39E+05
P12111-2 CO6A3	QSGVVPFIFQAK	660.86	120.75	2.33E+03	5.55E+03	4.97E+03	1.11E+04	1.48E+05	1.33E+03	8.89E+03	1.24E+03	1.56E+03	8.50E+03	1.13E+04	1.24E+04	4.22E+03	2.15E+04	1.12E+03
P12111-2 CO6A3	ALNLGYALDYAQR	734.38	120.82	5.31E+03	7.53E+03	3.40E+03	3.59E+02	5.61E+05	2.25E+04	2.38E+05	1.33E+05	1.20E+03	7.06E+04	4.04E+03	2.02E+04	1.77E+03	5.12E+02	5.26E+03
P08590 MYL3	IEFTPEQIEEFK	755.38	121.5	4.34E+04	2.63E+03	3.23E+03	8.53E+02	3.68E+03	1.67E+03	4.87E+02	1.32E+03	4.32E+06	6.57E+06	2.08E+03	1.45E+04	5.88E+03	2.79E+06	2.12E+04
P02768 ALBU	QNCLEFQLGEYK	800.87	121.53	7.20E+04	2.11E+03	1.18E+03	1.53E+04	9.40E+03	6.36E+03	2.99E+02	1.28E+03	1.46E+03	2.38E+02	3.33E+04	1.30E+03	2.64E+02	2.82E+03	2.92E+03
Q14315-2 FLNC	EAGDGVFECEYYPVVPGK	979.94	121.53	2.08E+04	6.25E+02	5.76E+02	1.91E+03	2.81E+03	5.47E+02	1.61E+03	9.65E+02	3.98E+03	1.35E+02	4.06E+04	5.12E+03	2.74E+03	5.27E+02	5.20E+03
P35609 ACTN2	SIEEIQSLITAH	670.85	121.54	1.74E+03	2.17E+05	2.00E+05	2.76E+03	4.04E+03	2.34E+05	2.73E+04	4.71E+04	4.98E+02	3.33E+02	1.20E+03	2.59E+03	3.16E+03	2.12E+03	1.81E+03
P17661 DESM	LQEEIQLKEEAENLAAFR	749.05	122.04	1.15E+03	1.15E+03	5.74E+02	1.28E+03	3.02E+03	3.05E+04	1.07E+03	1.03E+04	6.50E+04	1.94E+04	4.34E+03	3.72E+03	1.42E+03	9.51E+03	9.72E+02
P35609 ACTN2	QSFIDFMTR	572.78	122.13	2.31E+03	2.86E+04	4.66E+02	4.92E+03	6.75E+02	8.60E+04	2.20E+03	1.70E+03	2.54E+03	2.19E+03	1.77E+03	1.82E+03	3.24E+03	3.08E+03	5.37E+02
P02768 ALBU	PCFSALEVDETYVPK	849.41	122.26	1.95E+03	3.74E+03	1.96E+03	6.22E+02	7.83E+02	1.76E+03	4.85E+03	3.44E+03	1.14E+03	2.08E+04	1.65E+03	2.19E+03	2.15E+03	1.63E+03	1.75E+03
Q14315-2 FLNC	VTYCPTEPGTYIINIK	906.47	122.28	3.41E+02	7.79E+02	8.04E+02	4.06E+03	6.75E+02	7.13E+03	4.23E+02	7.03E+03	2.46E+03	3.10E+04	1.70E+03	1.33E+03	7.45E+02	4.69E+03	2.24E+03
P06576 ATPB	TREGNDLYHEMIESGVINL	773.39	122.43	7.08E+02	1.18E+03	6.28E+02	3.32E+03	7.84E+04	7.97E+02	5.37E+02	9.14E+02	1.02E+03	2.27E+03	3.28E+02	7.72E+02	1.51E+03	2.70E+03	6.22E+02
P68133 ACTS	DLYANNVMSSGGTTMYPGI ADR	749.35	122.54	9.01E+02	2.98E+03	2.08E+02	3.06E+03	5.57E+02	9.11E+02	1.54E+04	2.57E+02	9.20E+02	2.19E+03	1.31E+04	2.61E+03	1.71E+03	2.01E+03	4.81E+02
P06576 ATPB	AIAELGIYPAVD	616.33	122.61	8.29E+03	1.02E+04	1.61E+03	1.51E+03	1.26E+04	1.90E+04	2.66E+04	2.13E+04	3.80E+02	2.45E+03	8.44E+02	8.47E+04	6.91E+04	1.38E+03	1.10E+04
P08590 MYL3	DTGTYYEDFVEGLR	751.34	122.64	3.57E+05	2.30E+04	3.48E+04	1.39E+07	6.07E+03	4.76E+04	2.01E+04	4.39E+04	1.04E+03	1.25E+03	5.77E+04	2.32E+03	1.31E+04	6.58E+03	4.77E+03
Q14315-2 FLNC	DAGEGLLTVQILDPEGKPK	660.69	122.69	5.20E+04	3.24E+03	3.35E+03	1.56E+03	6.80E+02	6.92E+02	5.88E+03	2.07E+03	1.33E+03	1.40E+03	1.46E+05	9.55E+02	2.67E+03	2.35E+03	4.15E+02
Q14896 MYPC3	LDVPISGDPAPTIVWQK	918.50	122.87	5.97E+05	1.05E+04	1.33E+03	6.90E+02	8.28E+03	7.36E+03	4.21E+03	2.39E+03	5.24E+03	1.87E+03	6.00E+05	3.31E+03	3.13E+02	1.26E+03	1.67E+04
P35609 ACTN2	NNIDKLEGDHQLIQEALVF DNK	639.08	122.97	3.82E+03	2.08E+03	6.29E+02	8.33E+02	3.56E+04	1.38E+03	3.15E+02	1.78E+02	2.21E+02	1.49E+03	2.09E+03	1.10E+03	1.78E+03	1.36E+02	2.04E+03
P54296 MYOM2	YAVFDLMEGK	586.79	123.16	2.12E+05	7.31E+03	1.55E+04	2.94E+05	5.05E+03	3.09E+04	3.74E+03	2.46E+03	6.61E+03	1.31E+03	2.40E+05	1.56E+04	2.88E+03	3.26E+04	1.15E+04
P02768 ALBU	LGMFLYFYAR	631.82	123.18	2.22E+02	9.88E+04	2.97E+03	4.10E+03	1.41E+03	2.76E+04	7.13E+02	9.07E+03	5.70E+02	7.17E+02	1.22E+03	1.27E+03	1.00E+03	5.19E+02	8.18E+02
P54296 MYOM2	QSSSLVLIGDAFK	682.87	123.29	1.38E+05	1.52E+03	5.09E+02	1.97E+05	4										



Q14896 MYPC3	MAGPGAPVTTTEPVTVEI LQR	765.74	124.25	7.82E+03	5.07E+03	1.75E+03	3.20E+03	6.88E+02	6.47E+04	1.46E+03	1.86E+03	5.48E+02	9.41E+02	1.76E+03	3.43E+03	1.01E+03	7.04E+02	2.97E+02
P12111-2 CO6A3	SNDVFPEFYLK	679.83	124.37	4.75E+03	2.40E+04	1.67E+03	1.03E+04	7.72E+03	4.73E+04	7.30E+03	7.50E+02	3.31E+02	9.56E+03	4.18E+03	1.69E+03	4.61E+02	3.28E+03	3.08E+03
P54296 MYOM2	FSGGSPILGYLDK	758.89	124.39	1.14E+03	6.76E+03	3.23E+03	4.96E+02	4.29E+04	8.07E+02	3.29E+02	1.54E+03	8.05E+02	6.10E+03	2.55E+03	7.59E+04	3.83E+03	2.84E+03	2.47E+04
P10916 MLRV	DGFIDKNDLRDTFAALGR	675.35	124.49	1.37E+04	8.34E+03	1.12E+04	7.63E+03	2.41E+03	7.56E+04	4.61E+04	3.96E+03	1.35E+03	7.77E+02	4.56E+04	2.53E+04	6.08E+04	2.19E+03	4.18E+03
P35609 ACTN2	AGTQIENIEEDFRNLK	645.32	124.52	6.10E+03	6.89E+02	1.92E+03	6.21E+04	2.75E+03	1.16E+03	1.73E+02	1.27E+03	1.25E+03	8.14E+02	4.22E+04	7.80E+02	2.15E+03	9.91E+02	1.34E+03
Q14896 MYPC3	LRLDVPISGDPAPTIVWQK	702.40	124.54	2.02E+03	8.25E+02	5.98E+05	8.56E+02	6.60E+04	2.60E+03	5.15E+02	8.31E+02	6.17E+02	4.89E+02	3.40E+03	1.08E+04	2.27E+02	5.78E+02	1.72E+03
P10916 MLRV	TVFLTMFGEK	586.80	124.77	5.82E+05	3.82E+03	4.58E+03	2.87E+02	1.10E+04	1.45E+04	1.72E+03	5.26E+03	1.67E+03	7.44E+04	5.29E+02	2.44E+04	3.74E+05	9.11E+02	4.75E+05
P12883 MYH7	SPGVMDNPLVMHQLRCNG VLEGIR	659.59	124.85	1.38E+03	1.65E+03	7.58E+02	9.01E+02	2.90E+02	3.20E+04	6.48E+02	6.51E+02	6.55E+02	3.09E+02	6.48E+02	2.66E+02	9.93E+02	2.84E+02	3.18E+02
P12111-2 CO6A3	LVDYLDVGFDTTR	757.37	124.89	2.29E+03	1.94E+03	1.29E+03	4.28E+04	1.59E+03	7.21E+02	6.27E+02	1.23E+03	2.19E+05	1.95E+03	3.79E+04	2.94E+03	8.88E+03	2.45E+05	6.14E+02
Q14315-2 FLNC	AFGPGLEPTGCIVDKPAEFT IDAR	835.42	124.98	3.22E+04	3.76E+03	1.33E+03	2.82E+03	3.10E+04	6.46E+03	2.49E+02	1.95E+03	4.21E+03	1.78E+03	1.24E+05	4.38E+04	2.60E+04	6.43E+02	1.71E+04
P10916 MLRV	LKGADPEETILNAFK	549.30	125.32	1.38E+04	1.28E+03	3.80E+03	3.17E+04	5.20E+04	1.56E+03	2.28E+03	1.12E+03	5.47E+03	1.23E+03	9.51E+04	2.22E+04	1.22E+04	1.83E+04	7.38E+03
P25705 ATPA	TGAIVDVVPVGEELLGR	542.30	125.37	1.76E+05	1.98E+04	1.43E+03	3.41E+04	3.51E+05	7.62E+03	4.34E+04	5.23E+04	8.82E+02	3.00E+03	2.17E+05	1.98E+05	8.18E+04	4.50E+02	2.28E+05
Q14896 MYPC3	ALDFSEAPSFTQPLVNR	631.32	125.37	6.64E+03	1.95E+03	5.46E+03	7.58E+02	2.63E+03	1.90E+03	7.65E+02	7.76E+03	9.28E+02	3.04E+02	3.60E+04	6.10E+03	4.10E+03	1.84E+03	4.56E+04
P35609 ACTN2	REALERMEKLETIDQLHLE FAK	561.31	125.56	1.97E+04	6.99E+04	1.12E+04	1.05E+04	1.22E+05	3.24E+04	9.65E+04	2.64E+04	3.26E+04	7.90E+02	2.63E+03	4.36E+05	1.92E+05	4.28E+04	2.02E+04
P12111-2 CO6A3	DVVFLLDGSEGVR	703.37	125.67	2.73E+03	4.29E+05	2.54E+05	2.31E+04	1.60E+03	6.88E+05	1.08E+06	6.11E+05	4.46E+02	1.68E+03	1.84E+03	2.80E+03	1.12E+03	3.11E+03	1.81E+03
P12883 MYH7	DFELNAL	411.21	125.83	9.41E+03	1.86E+03	1.20E+03	6.90E+04	5.87E+02	8.32E+02	2.14E+02	2.52E+02	5.51E+02	5.48E+02	1.08E+04	1.86E+03	6.31E+02	8.28E+02	2.77E+02
Q14315-2 FLNC	SPFVVNVAPPLDLSK	791.94	126.33	2.09E+05	1.24E+04	1.18E+03	2.78E+03	2.23E+05	3.46E+04	3.71E+03	7.87E+02	2.45E+02	3.65E+03	3.47E+05	3.18E+05	1.04E+05	6.92E+02	2.50E+02
P12111-2 CO6A3	LSDAGITPLFLTR	702.40	126.56	1.38E+05	3.91E+02	1.04E+03	2.94E+05	3.17E+03	4.81E+02	1.01E+04	1.60E+03	5.27E+02	7.77E+03	1.74E+05	7.10E+02	2.82E+05	3.65E+03	4.63E+03
P10916 MLRV	VFSMFEQTQIQEFK	881.43	126.67	1.24E+04	3.54E+03	1.95E+03	5.37E+02	6.77E+02	2.90E+03	5.07E+02	1.31E+03	9.19E+02	8.93E+02	1.49E+04	1.08E+03	9.19E+02	1.31E+03	1.20E+04
P35609 ACTN2	GQGTVTFQSFIDFMTRETA DTDTAEQVIASFR	892.42	126.68	5.68E+04	3.73E+04	6.46E+03	3.06E+05	1.08E+05	6.49E+03	3.89E+02	3.86E+04	1.39E+03	9.65E+02	1.83E+05	4.20E+05	4.17E+05	4.94E+02	1.66E+05
P35609 ACTN2	ETADTDTAEQVIASFR	877.41	126.82	8.39E+05	3.20E+03	7.20E+03	7.84E+05	4.81E+04	2.09E+04	7.77E+03	1.00E+04	2.75E+03	1.06E+03	9.19E+05	2.08E+04	5.55E+04	3.07E+03	6.01E+04
Q14315-2 FLNC	VDITYDGHVPVPGSPFAVEG VLPPDSPK	930.81	127.15	7.72E+03	7.40E+02	6.57E+02	1.64E+03	3.15E+03	6.15E+03	4.95E+03	4.86E+03	4.13E+03	1.96E+02	8.82E+03	2.54E+03	1.50E+03	5.87E+02	4.61E+03
P12111-2 CO6A3	MKPLDGSALYTGSAALDFVR	681.02	127.2	8.41E+03	7.17E+02	1.33E+03	6.04E+02	1.11E+03	2.14E+03	5.23E+02	1.03E+03	3.79E+02	3.33E+02	5.77E+04	5.25E+02	7.90E+03	3.04E+03	1.17E+04
P35609 ACTN2	SIEEIQSLITAEHQFK	625.00	127.46	2.16E+05	9.50E+03	1.40E+03	3.65E+03	4.16E+03	2.01E+03	5.08E+02	1.70E+03	6.59E+03	5.34E+02	3.11E+05	6.06E+03	9.26E+04	4.62E+03	3.46E+05
P35609 ACTN2	LLETIDQLHLEFAK	557.31	127.64	6.77E+02	2.73E+03	1.27E+03	6.12E+02	5.95E+03	2.76E+03	1.34E+03	7.11E+02	5.81E+04	6.68E+05	1.31E+04	4.20E+03	2.07E+04	2.20E+04	1.27E+03
P54296 MYOM2	DTSLVMLWK	546.79	127.99	1.58E+03	3.23E+02	1.47E+02	4.39E+02	1.84E+02	1.29E+03	2.15E+03	7.70E+02	3.88E+04	1.30E+03	2.03E+03	4.16E+02	3.63E+02	4.87E+03	1.55E+03
Q14315-2 FLNC	GLSEGHTFQVAEFIVDTR	669.34	128.05	5.94E+03	2.59E+04	2.46E+03	8.73E+03	3.27E+02	9.21E+03	4.68E+02	2.58E+03	3.56E+02	1.52E+03	7.72E+04	2.47E+02	5.44E+02	8.23E+02	3.16E+04
P02768 ALBU	LVRPEVDVMCTAFHDNEET	784.69	128.23	2.65E+04	1.14E+03	6.19E+02	1.05E+03	7.64E+02	1.19E+03	9.06E+02	4.86E+02	1.78E+03	7.50E+03	2.79E+04	1.01E+03	1.44E+03	9.69E+02	1.91E+03
Q14896 MYPC3	EPPVLITRPLEDQLVMVGQ	764.09	128.36	8.97E+04	1.99E+04	4.20E+02	1.56E+03	8.33E+03	5.81E+03	9.04E+02	1.81E+03	2.49E+02	6.35E+02	1.57E+05	4.92E+03	1.19E+04	8.60E+02	1.25E+04
P54296 MYOM2	DPLMYFIEK	578.29	128.45	2.54E+03	2.96E+03	6.43E+02	6.05E+02	1.61E+03	7.62E+02	1.16E+03	1.63E+03	6.54E+03	4.79E+02	4.09E+03	3.73E+03	1.33E+03	4.55E+03	2.56E+04
P68871 HBB	SAVTALWGKVVNDEVGGE ALGR	743.39	128.71	3.93E+03	1.43E+03	1.88E+03	2.24E+03	3.32E+04	2.47E+02	6.18E+02	1.66E+03	3.85E+03	2.24E+03	3.30E+04	1.61E+03	1.88E+03	4.25E+03	8.06E+03
P69905 HBA	TYFPHFDL	520.25	128.72	1.25E+05	1.74E+03	4.69E+02	8.19E+04	3.49E+02	1.37E+03	1.07E+03	2.37E+03	9.42E+02	1.47E+03	2.53E+04	3.36E+03	3.65E+03	3.22E+02	1.18E+03
P35609 ACTN2	SGPGSVPGALDYAAF	704.84	128.85	4.98E+03	5.49E+02	8.64E+02	7.96E+04	1.15E+03	1.31E+03	5.08E+02	5.57E+02	3.24E+02	7.02E+02	6.27E+03	7.99E+02	3.91E+02	8.75E+02	1.62E+03
P02768 ALBU	LVNEVTEFAKTCVADESAAE NCDK	839.05	128.92	1.01E+03	2.61E+02	6.58E+02	1.20E+03	7.78E+02	1.06E+03	2.38E+02	5.41E+02	4.62E+02	8.17E+02	1.94E+04	1.70E+02	1.07E+03	5.43E+02	5.66E+02
P68871 HBB	YPWTQRFFESFGDLSTPDA VMGNPK	962.45	128.95	3.11E+04	1.24E+04	6.51E+02	3.10E+04	1.92E+03	1.32E+03	3.02E+02	3.21E+03	6.46E+02	4.62E+02	3.88E+04	3.74E+02	2.17E+03	1.15E+03	1.00E+04
P25705 ATPA	SLNLEPDNVGVVVFVGNPK	958.49	129.05	5.55E+04	1.04E+03	4.66E+02	1.24E+03	1.06E+03	8.49E+02	2.64E+02	1.88E+03	2.54E+03	4.27E+02	1.85E+04	6.79E+02	2.23E+03	5.28E+02	2.35E+03
P54296 MYOM2	FLSELAHLEEDVHLAR	627.00	129.07	8.00E+02	2.15E+03	1.49E+03	2.20E+05	3.09E+03	4.70E+03	9.48E+02	8.75E+02	1.07E+03	1.44E+03	1.94E+05	9.20E+03	1.93E+03	5.15E+02	2.89E+03
P17661 DESM	IESLNEEIAFLK	703.38	129.15	1.74E+03	2.90E+03	1.74E+03	1.18E+05	3.76E+03	3.28E+03	1.88E+03	5.09E+03	1.17E+06	6.98E+05	7.13E+04	3.16E+04	8.63E+02	1.01E+06	1.39E+03
P54296 MYOM2	APVYSGSSPVSGYFVDFR	967.97	129.54	5.01E+04	1.29E+03	3.18E+03	2.59E+02	2.34E+03	6.30E+02	3.94E+02	7.38E+02	6.37E+02	2.80E+02	4.41E+04	2.23E+04	5.80E+04	6.48E+02	7.38E+03
P35609 ACTN2	LNKDDPIGNINLAMEIAEK	700.03	129.61	5.32E+03	4.82E+03	1.87E+03	3.03E+03	3.20E+04	9.86E+03	9.71E+02	8.24E+02	2.77E+02	2.83E+03	3.23E+04	2.71E+03	4.00E+03	8.67E+02	1.28E+03
Q14315-2 FLNC	FNDEHIPDSPFVVPVSLSD DAR	843.07	130.2	1.67E+05	1.93E+03	7.86E+03	6.10E+02	3.67E+02	9.45E+02	7.75E+02	3.96E+02	3.86E+02	8.09E+02	1.26E+05	1.96E+03	4.15E+04	1.51E+03	3.27E+04
P54296 MYOM2	ATGIEMVMDR	618.31	130.21	2.09E+02	5.00E+02	1.60E+03	1.17E+03	2.26E+03	8.92E+02	3.36E+03	1.33E+03	2.22E+04	6.36E+02	6.82E+02	1.88E+03	1.08E+03	4.12E+04	8.17E+02
P25705 ATPA	FENAFLSHVVSQHALLGTI	789.76	130.32	2.83E+05	1.09E+03	5.89E+02	1.03E+03	5.62E+03	1.73E+03	1.77E+02	1.44E+03	3.38E+02	6.33E+02	1.59E+05	3.47E+03	7.40E+04	1.71E+03	2.59E+05
P02768 ALBU	VDFEFKPLVEEPQNLK	1023.05	130.51	2.98E+05	8.56E+02	4.97E+03	8.17E+02	6.61E+03	2.71E+02	1.56E+03	1.85E+03	3.20E+02	9.90E+02	2.60E+05	2.03E+03	2.39E+04	7.95E+02	2.58E+05
P12883 MYH7	EEQAEPDGTEEADKSAYLM GLNSADLLK	1008.81	130.61	5.44E+02	9.33E+02	2.72E+03	3.95E+02	2.11E+03	4.49E+02	5.74E+02	6.99E+02	1.64E+04	2.95E+03	1.39E+02	2.29E+02	4.40E+02	7.32E+03	1.28E+03
P54296 MYOM2	VSDAVAALDPLDLR	727.89	130.72	1.63E+04	2.86E+02	5.31E+02	5.30E+02	6.58E+02	5.21E+03	8.72E+02	6.68E+02	4.62E+02	6.09E+02	2.63E+04	1.35E+03	3.10E+04	4.17E+03	1.12E+03
P25705 ATPA	AQFGSDDLDAATQQLLSR	910.96	130.77	5.14E+04	5.85E+03	3.97E+02	2.90E+03	1.51E+03	2.81E+03	1.15E+03	4.88E+02	9.80E+02	4.76E+02	1.53E+04	7.68E+02	3.76E+03	1.46E+03	7.08E+03
Q14315-2 FLNC	IPGNWFQMVSAQER	831.91	130.82	2.55E+04	2.19E+03	6.44E+02	1.14E+03	6.14E+03	5.42E+02	1.34E+02	2.18E+03	1.17E+03	5.40E+02	5.81E+04	9.68E+02	3.32E+02	1.15E+03	1.27E+04

P02768 ALBU	LVRPEVDVMCTAFHDNEET FLK	649.07	131.13	2.87E+04	4.34E+02	1.74E+03	5.98E+02	1.14E+03	1.89E+03	1.92E+03	1.71E+03	5.39E+02	2.05E+03	2.25E+04	3.05E+03	2.42E+03	4.42E+03	2.73E+03
P06576 ATPB	AIAELGIYPAVDPLDSTSR	994.52	131.15	8.70E+05	1.56E+03	4.64E+03	8.57E+05	3.94E+04	4.51E+03	6.42E+03	6.77E+02	5.12E+02	5.94E+04	1.01E+04	1.92E+03	1.11E+04	2.74E+02	1.36E+04
P02768 ALBU	AVMDDFAAFVEK	671.82	131.23	1.76E+06	1.94E+03	2.65E+03	4.93E+02	2.49E+03	1.65E+03	1.65E+03	5.32E+03	7.06E+02	5.94E+02	1.66E+06	1.27E+04	2.84E+03	1.54E+03	4.36E+04
Q14315-2 FLNC	TFQVAEFIVDTR	713.37	131.31	9.28E+03	1.70E+03	4.75E+04	8.15E+04	1.10E+04	2.86E+03	5.18E+03	3.38E+03	3.56E+03	1.15E+03	1.09E+03	3.55E+03	6.16E+02	1.19E+03	1.44E+03
P12883 MYH7	LLSTLFANYAGADAPIEK	947.50	131.54	7.25E+05	5.42E+02	2.85E+03	2.31E+03	7.31E+03	1.03E+03	2.27E+03	1.70E+03	5.44E+02	3.49E+02	8.35E+05	1.11E+04	2.66E+05	1.36E+03	4.25E+03
Q14315-2 FLNC	GVAGVPAEFSIWTR	745.39	131.74	3.84E+05	3.11E+03	1.65E+03	2.65E+03	1.31E+03	3.53E+03	1.63E+03	9.77E+02	9.47E+02	4.89E+04	4.56E+05	3.38E+03	9.06E+04	2.30E+03	3.34E+03
P10916 MLRV	PEETILNAF	517.26	131.79	1.04E+04	4.60E+02	7.41E+02	8.68E+04	9.87E+02	3.58E+02	5.46E+02	7.21E+02	1.46E+03	1.41E+03	8.80E+02	1.87E+03	3.88E+03	1.53E+03	3.85E+03
Q14315-2 FLNC	VVTTYTPMAPGNYLIAIK	926.01	132.01	2.46E+04	2.41E+02	1.12E+03	1.35E+03	1.67E+03	2.89E+02	7.72E+02	2.42E+02	6.32E+02	1.63E+03	1.81E+04	1.50E+03	3.62E+02	4.45E+04	8.23E+02
Q14896 MYPC3	VGEPVNLIPFQ GK	755.93	132.1	4.00E+05	6.53E+02	1.83E+03	4.76E+03	5.81E+02	2.81E+03	9.59E+02	2.47E+02	3.43E+03	6.38E+02	1.39E+05	5.90E+03	1.84E+04	2.81E+03	3.62E+05
P68871 HBB	FFESFGDLSTPD	681.30	132.15	7.92E+02	1.27E+03	3.62E+03	1.38E+05	5.66E+02	1.69E+03	3.08E+02	8.00E+02	3.70E+02	7.09E+03	5.56E+03	2.39E+03	2.64E+02	7.29E+02	2.54E+02
P17661 DESM	ELQAQLQEQQVQVEMDMS KPD LTAALR	1033.86	132.24	1.13E+04	2.57E+02	2.80E+04	3.53E+02	3.26E+02	1.61E+03	4.82E+02	1.68E+03	5.59E+02	5.43E+02	4.17E+03	8.98E+02	1.78E+02	8.51E+02	3.59E+03
P69905 HBA	VDDMPNALSALSDLH VYAVNAIGMSRSPASQPF	799.38	132.33	1.01E+03	1.47E+04	3.92E+03	7.88E+02	3.92E+02	2.86E+04	1.15E+03	1.11E+03	6.42E+02	4.71E+02	2.09E+03	7.53E+02	8.96E+02	4.08E+02	3.23E+03
Q14896 MYPC3	MPIGPSEPTHLAVEDVSDT TVSLK	1148.57	132.37	6.38E+02	1.42E+03	1.75E+02	1.86E+02	1.22E+04	1.33E+03	6.40E+02	3.87E+03	5.38E+02	1.75E+03	3.23E+03	2.72E+04	1.00E+03	4.14E+02	2.17E+03
P06576 ATPB	GSITSVQAIYVPADDLTDP PATTFAH	920.13	132.44	3.68E+04	2.69E+02	2.31E+03	1.05E+03	1.26E+03	2.36E+02	1.44E+03	6.69E+02	1.60E+03	8.47E+02	1.12E+04	3.86E+02	4.13E+02	1.69E+03	5.28E+03
P06576 ATPB	EGNDLYHEMIESGVINLK	687.67	132.67	6.47E+05	3.21E+03	3.09E+03	5.95E+05	4.62E+03	5.49E+03	2.20E+04	8.93E+02	1.79E+03	8.33E+02	3.96E+05	2.14E+04	8.05E+04	5.85E+02	1.28E+04
P68871 HBB	FFESFGDLSTPDAVMGNPK	1029.98	132.67	1.43E+04	3.79E+02	4.43E+04	2.96E+06	3.27E+04	6.19E+02	9.18E+04	4.81E+03	1.16E+04	1.63E+04	1.18E+04	8.72E+03	9.28E+02	1.90E+04	5.73E+03
P12883 MYH7	MATDNADFVLTGFTSEEK	937.93	132.72	4.13E+04	1.55E+03	5.47E+02	1.51E+02	4.96E+02	1.71E+02	7.43E+02	8.75E+02	2.76E+02	8.51E+02	3.25E+04	1.60E+03	2.41E+03	9.11E+02	8.33E+04
P17661 DESM	INLPQTYALSALNFR	550.64	133.4	9.33E+04	1.76E+02	7.49E+02	3.63E+02	8.23E+02	3.48E+02	7.51E+02	3.94E+02	5.84E+02	4.21E+03	6.46E+04	1.79E+03	3.01E+03	4.00E+02	8.48E+04
Q14896 MYPC3	THCVVPELIIGNGYFR	661.01	133.56	5.24E+03	5.96E+02	7.44E+02	3.24E+03	1.46E+03	3.81E+02	6.57E+02	3.59E+02	4.11E+02	5.23E+03	2.25E+04	2.39E+03	5.36E+03	1.64E+03	1.89E+03
P10916 MLRV	DPEETILNAFK	638.82	133.61	1.63E+04	1.07E+03	1.02E+03	7.17E+02	2.16E+03	4.19E+03	1.72E+03	1.13E+03	6.56E+02	5.78E+02	1.65E+04	1.53E+03	1.22E+03	1.46E+03	8.23E+02
P69905 HBA	VADALTNVAHVDDMPNA	968.98	134.65	2.67E+05	2.47E+03	3.46E+03	1.61E+03	6.49E+03	1.14E+04	3.98E+03	1.91E+03	4.17E+03	2.39E+03	1.34E+05	6.63E+03	1.05E+04	2.09E+03	7.78E+04
P10916 MLRV	GADPEETILNAFK	702.85	134.71	5.24E+02	1.68E+04	3.79E+03	3.65E+03	1.82E+06	3.75E+06	1.04E+04	2.98E+04	5.60E+03	7.18E+02	4.39E+03	1.48E+06	8.89E+05	2.69E+03	3.81E+06
P02768 ALBU	EFNAETFTF	553.25	134.78	6.76E+03	8.55E+03	1.28E+04	1.02E+05	1.41E+04	3.67E+03	1.60E+03	1.28E+03	4.22E+03	2.21E+03	3.46E+03	2.91E+03	4.58E+03	2.97E+03	3.62E+03
P12883 MYH7	DQSPGKGTLEDQIIQANPAL EAFGNAK	938.14	134.95	1.11E+03	2.86E+03	3.55E+03	4.87E+03	1.37E+03	4.04E+04	1.18E+03	1.90E+03	8.08E+03	1.09E+03	7.30E+02	2.85E+03	7.47E+02	5.69E+03	3.90E+03
Q14896 MYPC3	LNFDLIQELSHEAR	562.29	135.01	2.24E+05	7.09E+03	9.09E+03	3.50E+03	3.43E+03	1.29E+04	3.49E+03	1.49E+04	2.12E+04	3.73E+04	3.59E+05	1.23E+04	6.38E+03	7.29E+03	1.72E+04
P12883 MYH7	ENKNLQEEISDLTEQLGSSG	773.38	135.17	6.21E+03	1.07E+04	5.00E+04	2.41E+04	1.96E+04	7.32E+03	2.77E+03	8.00E+03	4.45E+04	1.08E+04	2.33E+04	5.53E+04	1.18E+04	7.53E+04	1.88E+04
Q14315-2 FLNC	DAGEGLLTVQILDPEGK	877.96	135.26	4.40E+04	4.39E+03	1.75E+04	2.03E+03	6.35E+03	9.50E+03	7.51E+03	1.00E+04	2.79E+05	1.09E+05	2.19E+04	1.17E+04	1.73E+04	2.33E+05	3.16E+03
P35609 ACTN2	LEQAEEKGYEWWLLNEIR	707.36	135.4	1.66E+03	8.58E+03	7.50E+04	5.26E+03	5.88E+03	1.49E+04	1.24E+04	1.58E+04	1.40E+04	7.09E+03	1.81E+04	1.60E+04	9.13E+03	1.23E+05	1.65E+04
P69905 HBA	KVADALTNVAHVDDMPN ALSALSDLHAHK	781.90	135.41	2.06E+03	7.49E+03	6.47E+03	3.07E+03	4.55E+04	2.21E+04	3.66E+03	2.76E+04	7.48E+04	8.30E+03	2.98E+03	2.95E+04	6.48E+03	6.03E+04	5.58E+03
P12883 MYH7	NDLQLQVQAEQDNLADAE ER	767.04	135.42	6.54E+04	3.04E+03	6.83E+03	7.73E+03	4.09E+04	8.02E+04	1.61E+04	5.05E+03	2.10E+04	1.58E+04	7.61E+03	1.14E+05	9.53E+03	9.45E+04	1.96E+04
P02768 ALBU	RHPYFYAPELFFAK	633.67	135.45	7.74E+03	2.31E+03	5.49E+04	3.32E+03	1.96E+03	1.50E+04	2.58E+03	7.48E+03	2.01E+04	4.15E+04	4.14E+03	1.53E+04	5.55E+03	3.18E+04	1.20E+03
Q14896 MYPC3	KLEVYQSIADLMVGAK	588.99	135.46	6.24E+03	1.30E+03	4.43E+03	2.49E+02	3.66E+04	4.30E+03	3.58E+04	3.12E+04	5.46E+04	4.08E+03	6.64E+03	2.08E+04	2.30E+03	4.81E+03	3.26E+03
P69905 HBA	VADALTNVAHVDDMPNA LSALSDLHAHKLR	653.94	135.51	1.23E+04	1.88E+03	4.65E+03	2.32E+03	2.06E+04	8.22E+03	1.91E+04	1.77E+04	5.91E+03	1.41E+04	5.69E+03	2.09E+04	2.12E+03	1.03E+04	1.23E+03
P69905 HBA	FLASVSTVLTSK	626.86	135.56	7.38E+04	6.88E+04	2.80E+03	2.92E+04	9.76E+03	6.02E+04	1.03E+05	3.54E+04	1.51E+03	4.22E+04	5.19E+04	8.32E+04	9.18E+03	1.83E+04	1.74E+04
P06576 ATPB	KGSITSVQAIYVPADDLTDP APATTF AHL DATTVLSR	961.50	135.57	6.32E+04	3.30E+04	3.14E+04	2.61E+04	4.78E+04	9.06E+03	6.00E+04	1.30E+05	6.00E+04	3.48E+04	1.11E+04	1.55E+05	7.55E+03	1.18E+05	6.83E+04
P25705 ATPA	NVQAEEMVEFSSGLK	834.41	135.6	9.12E+04	1.82E+05	9.07E+04	1.25E+05	1.01E+05	2.04E+05	1.17E+05	2.74E+05	1.56E+05	8.97E+04	1.93E+05	1.62E+05	1.42E+05	1.42E+05	7.39E+04
P06576 ATPB	VALTGLTVAEYFR	720.40	135.66	4.00E+05	4.57E+04	4.92E+04	3.76E+05	8.55E+04	1.37E+05	2.15E+04	8.73E+04	5.80E+05	3.44E+05	3.30E+05	1.06E+05	6.60E+05	4.06E+05	7.78E+04
P08590 MYL3	IEFTPEQIEEFKEAF	928.95	135.69	4.97E+04	1.92E+04	1.12E+05	3.69E+04	1.14E+05	1.59E+05	6.63E+03	2.83E+04	2.10E+05	7.70E+04	1.04E+04	1.72E+05	9.45E+04	8.87E+04	1.25E+05
P02768 ALBU	EFNAETFTFHADICTLSEK	735.02	135.69	5.15E+04	1.46E+04	3.14E+04	4.82E+04	2.06E+04	8.10E+04	3.06E+04	1.79E+04	5.37E+04	3.93E+03	3.26E+04	2.69E+04	1.66E+04	1.08E+04	1.62E+04
P69905 HBA	VADALTNVAHVDDMPNA LSALSDLHAHK	749.88	135.74	5.95E+05	1.52E+05	2.42E+04	2.47E+05	6.02E+05	4.06E+05	3.45E+05	2.34E+05	2.53E+04	5.48E+04	4.46E+05	7.08E+04	3.70E+04	1.35E+05	2.52E+05
P17661 DESM	MALDVEIATYR	641.34	135.74	7.04E+04	8.58E+04	6.87E+04	8.80E+04	9.49E+04	5.72E+04	1.03E+05	9.70E+04	1.36E+05	1.05E+05	1.15E+05	9.07E+04	8.12E+04	3.81E+04	6.55E+04
P25705 ATPA	GMSLNLEPDNVGVVVF GN	1052.52	135.75	1.00E+05	7.50E+04	1.15E+05	9.70E+04	6.22E+04	1.17E+05	6.97E+04	8.86E+04	1.22E+05	4.10E+04	1.41E+05	1.61E+05	7.94E+04	1.26E+05	1.35E+05
Q14896 MYPC3	ISDSHEDTGILDFSSLLK	659.67	135.8	1.14E+05	1.90E+05	6.75E+03	2.68E+05	6.22E+04	2.19E+05	4.96E+04	9.40E+04	2.29E+04	1.29E+05	1.44E+05	2.59E+04	1.22E+05	2.37E+04	1.35E+05
Q14896 MYPC3	TMEWFTVLEHYR	537.93	135.81	2.89E+04	1.64E+04	1.25E+03	3.54E+04	5.25E+04	4.84E+04	6.85E+04	4.40E+04	1.76E+03	6.76E+03	3.70E+04	4.22E+04	7.35E+03	2.28E+03	5.35E+04
P35609 ACTN2	VEQIAAIAQELNELDYHDA VNVNDR	947.13	135.82	1.19E+05	6.01E+04	4.48E+04	6.66E+04	1.37E+05	1.55E+05	9.33E+04	5.03E+04	1.06E+04	1.25E+04	1.26E+05	6.54E+04	6.55E+04	3.34E+04	1.23E+05
P35609 ACTN2	DDPIGNINLAMEIAEK	871.94	135.83	3.66E+05	6.47E+04	2.46E+05	2.06E+05	2.83E+05	1.38E+05	1.96E+05	2.07E+05	1.74E+05	3.11E+05	2.52E+05	1.55E+05	4.41E+04	1.30E+05	1.07E+05
P02768 ALBU	HPYFYAPELFFAK	581.64	135.84	9.26E+04	4.94E+04	9.19E+04	5.13E+04	1.80E+05	1.48E+05	1.69E+05	4.22E+03	1.19E+05	1.99E+05	1.07E+05	7.44E+04	2.75E+04	5.10E+04	1.02E+04
P06576 ATPB	FLSQPFQVAEVFTGHMGK	675.01	135.85	1.48E+05	7.10E+04	2.44E+04	9.51E+04	3.07E+04	1.08E+05	2.99E+05	2.48E+05	3.24E+05	1.48E+05	1.17E+05	1.42E+04	7.25E+04	1.64E+04	1.45E+05



P69905 HBA	VADALTNVAHVDDMPNA LSALSDLHAH	717.85	135.85	2.18E+05	1.82E+05	5.27E+04	1.77E+05	1.69E+05	2.18E+05	6.05E+04	2.26E+05	2.52E+04	2.46E+05	2.58E+05	2.29E+04	8.71E+04	8.57E+04	1.68E+05
P12883 MYH7	MELQSALEEEAEASLEHEEG	744.01	135.85	2.10E+06	1.03E+06	1.05E+05	1.71E+06	1.39E+06	2.81E+06	8.50E+05	1.35E+06	1.33E+06	1.68E+06	2.55E+06	9.96E+04	4.67E+05	3.02E+04	2.19E+06
P25705 ATPA	LKEIVTNFLAGFEA	776.42	135.89	1.51E+05	1.77E+05	1.09E+05	9.64E+04	1.54E+05	8.80E+04	1.89E+05	1.00E+05	1.76E+05	1.21E+05	5.74E+04	1.46E+05	1.85E+05	3.83E+04	4.76E+04
P10916 MLRV	EEVDQMFAAFPDPVTGNLD YK	1193.55	135.9	6.05E+04	4.30E+04	3.14E+04	9.05E+04	1.05E+04	1.38E+05	3.75E+04	3.85E+04	1.01E+04	7.57E+04	9.26E+04	3.14E+04	2.43E+04	3.27E+04	1.42E+05
P10916 MLRV	AGGANSNVFSMFQEQIQE	1167.05	135.9	5.37E+04	5.99E+03	1.65E+04	6.22E+04	5.36E+04	8.98E+04	5.13E+04	3.75E+04	1.31E+04	6.76E+04	8.62E+04	2.40E+04	3.39E+04	1.03E+04	7.19E+04
P06576 ATPB	FLSQPFQVAEVFTGH	853.93	135.91	3.60E+05	2.69E+05	2.18E+05	2.64E+05	1.40E+05	3.36E+05	1.27E+05	9.01E+04	1.64E+05	2.34E+05	2.63E+05	6.75E+04	1.49E+05	1.89E+05	2.63E+05
P17661 DESM	TFGGAPGFPLGSPLSSPVFP	1044.55	135.93	4.00E+05	3.74E+05	5.19E+05	6.58E+05	3.64E+05	6.25E+05	3.81E+05	4.77E+05	4.28E+05	3.69E+05	5.54E+05	6.81E+05	3.93E+05	4.59E+05	3.86E+05
Q14896 MYPC3	LEAPAEEDVWEILR	835.43	135.93	5.29E+05	4.22E+05	1.50E+05	4.22E+05	1.64E+05	6.17E+05	8.29E+05	2.59E+05	8.79E+04	3.17E+05	4.62E+05	3.95E+05	1.57E+06	1.09E+05	3.64E+05
P35609 ACTN2	MPAYSGPGSVPGALDYAAF	935.95	135.93	2.19E+05	2.63E+05	8.21E+03	2.62E+05	1.22E+05	3.11E+05	1.32E+05	1.35E+05	1.78E+05	1.80E+05	2.82E+05	1.46E+05	1.18E+05	1.40E+05	2.17E+05
P54296 MYOM2	LIGGLPDPVVTIMEGK	771.42	135.94	2.61E+05	2.19E+05	9.82E+04	2.26E+05	4.17E+04	2.19E+05	2.82E+05	2.85E+05	4.42E+04	1.72E+05	1.43E+05	2.05E+05	2.04E+05	1.20E+05	1.88E+05
P12883 MYH7	IEDMAMLTFLHEPAVLYNL	783.41	135.94	9.17E+04	2.13E+05	3.20E+05	7.19E+04	2.44E+05	2.26E+05	1.05E+05	3.99E+05	2.59E+05	7.01E+04	1.92E+05	4.10E+05	6.01E+04	1.01E+05	1.22E+05
P08590 MYL3	IEFTPEQIEEFKEAFMLFDR	840.41	135.97	1.05E+05	1.89E+05	5.62E+04	8.01E+04	1.27E+05	1.68E+05	2.12E+05	1.48E+05	1.58E+05	7.23E+04	1.63E+05	2.17E+05	1.73E+04	2.03E+05	1.14E+05
P12883 MYH7	VIQYFAVIAAIGDR	768.43	136	2.65E+05	1.62E+05	2.50E+05	2.48E+05	9.48E+04	3.34E+05	4.18E+05	2.43E+05	3.76E+05	2.09E+05	2.22E+05	9.14E+04	2.94E+04	4.78E+05	2.76E+05
P08590 MYL3	MMDFFETFLPMLQHISK	656.65	136.03	2.19E+05	1.65E+05	2.17E+04	1.92E+05	6.75E+05	7.60E+05	3.77E+05	4.88E+05	4.48E+05	5.17E+05	5.97E+05	3.74E+05	7.45E+04	1.14E+04	4.90E+05
P02768 ALBU	DVFLGMFLYEYAR	812.40	136.04	5.42E+04	6.26E+04	1.05E+05	5.63E+04	7.34E+04	7.92E+04	8.30E+04	9.02E+04	1.44E+05	4.12E+04	3.67E+04	1.89E+05	2.16E+05	1.93E+05	2.27E+05
Q14315-2 FLNC	VEESTQVGGDPFPAVFGDF LGR	775.36	136.05	1.33E+05	1.34E+05	3.84E+04	1.22E+05	3.55E+04	1.19E+05	1.10E+05	1.81E+05	2.73E+04	1.34E+05	1.59E+05	1.51E+05	5.58E+04	5.08E+04	1.38E+05
P02768 ALBU	FYAPPELLFFAK	673.36	136.06	2.35E+05	2.75E+05	6.24E+04	1.22E+05	1.54E+05	2.12E+05	2.11E+05	1.76E+05	1.97E+05	1.76E+05	2.41E+05	1.40E+05	2.17E+04	8.14E+04	1.22E+05
P12883 MYH7	NLQEISDLTEQLGSSGK	974.48	136.06	7.71E+05	3.58E+05	2.87E+05	4.87E+05	6.01E+05	9.84E+05	3.60E+05	3.78E+05	5.45E+05	6.06E+05	8.80E+05	1.82E+04	3.56E+04	6.43E+04	6.12E+04
P10916 MLRV	EAPGPINFVTVF	596.30	136.07	1.66E+05	3.04E+05	1.52E+05	3.56E+05	6.37E+04	3.36E+05	5.52E+04	7.96E+04	1.41E+05	1.30E+05	2.77E+05	1.57E+05	1.80E+05	3.24E+04	2.11E+05
P10916 MLRV	GADPEETILNAF	638.81	136.08	3.94E+05	4.27E+05	4.55E+04	5.11E+05	1.62E+04	4.56E+05	7.62E+04	9.89E+04	4.95E+04	2.25E+05	4.56E+05	1.68E+05	1.68E+05	2.84E+04	3.29E+05
P12883 MYH7	MDADLSQLQTEVEEAVQEC	765.35	136.08	3.48E+05	7.05E+04	8.93E+03	1.49E+05	1.56E+05	4.53E+05	1.10E+05	1.08E+05	1.59E+05	2.18E+05	3.12E+05	1.41E+05	1.27E+04	3.85E+04	3.00E+05
P25705 ATPA	EVAFAQFGSDLAATQQL LSR	780.06	136.1	4.38E+04	2.63E+04	1.50E+04	2.42E+04	6.54E+04	4.42E+04	3.71E+04	7.35E+04	1.15E+04	3.80E+04	3.71E+04	1.83E+04	3.42E+04	3.80E+03	5.80E+04
P06576 ATPB	TVLIMELINNVAK	729.42	136.11	2.19E+05	1.51E+05	1.14E+05	1.24E+05	3.03E+05	1.80E+05	2.64E+05	2.02E+05	1.76E+04	1.60E+05	1.73E+05	1.71E+05	1.09E+05	1.43E+05	2.03E+05
P35609 ACTN2	VGWELLTTIAR	686.40	136.11	1.06E+05	1.02E+05	1.48E+04	1.20E+05	3.20E+05	2.02E+05	3.13E+05	3.63E+05	2.99E+05	1.55E+05	1.66E+05	3.54E+05	1.21E+05	3.05E+04	1.65E+05
P10916 MLRV	EAPGPINFVTFLTMFGEK	999.50	136.14	2.97E+04	9.46E+04	4.03E+04	2.52E+04	7.32E+04	5.75E+04	2.76E+04	8.66E+04	5.17E+04	1.38E+04	2.29E+04	8.28E+04	1.09E+04	6.75E+04	3.88E+04
P08590 MYL3	MMDFFETFLPMLQH	820.37	136.16	7.14E+05	3.46E+05	4.92E+05	7.34E+05	8.71E+04	6.65E+05	8.17E+04	1.35E+05	2.93E+04	3.07E+05	5.20E+05	2.05E+05	1.04E+05	2.14E+04	3.38E+05
P06576 ATPB	SLQDIIAILGMDDELSEEDK	707.02	136.17	6.20E+04	1.28E+04	2.73E+04	2.46E+04	9.88E+03	7.37E+03	5.94E+04	2.73E+04	5.85E+03	1.94E+04	5.07E+04	2.77E+04	6.04E+04	1.09E+04	1.15E+04
P35609 ACTN2	LASELLEWIR	615.35	136.18	5.31E+05	3.70E+05	3.83E+04	5.56E+04	5.01E+05	1.96E+05	1.12E+05	3.72E+04	6.87E+04	1.39E+04	5.73E+05	5.79E+04	6.20E+04	1.64E+04	4.53E+05
P02768 ALBU	DVFLGMF	828.37	136.2	5.01E+04	2.17E+05	5.18E+04	3.78E+05	8.69E+03	4.87E+05	1.68E+04	7.48E+04	2.22E+04	1.75E+04	2.82E+05	2.94E+04	1.27E+04	2.48E+04	2.23E+05
P25705 ATPA	EIVTNFLAGFEA	655.83	136.21	3.51E+05	2.97E+05	2.76E+05	2.76E+05	2.58E+05	4.12E+05	2.44E+05	3.50E+05	4.24E+05	2.50E+05	3.24E+05	4.11E+05	2.08E+05	3.15E+05	4.17E+05
P02768 ALBU	MPCAEDYLSVVLNQLCVLH EK	802.07	136.21	5.01E+04	2.30E+04	8.49E+04	2.76E+04	1.11E+05	6.72E+04	7.36E+04	8.09E+04	3.69E+03	5.85E+04	6.10E+04	6.08E+04	4.68E+03	1.82E+04	6.49E+04
P08590 MYL3	MMDFFETFLPM	631.27	136.23	1.74E+05	2.20E+04	1.09E+05	1.11E+04	2.24E+04	1.72E+04	1.25E+04	8.08E+03	2.84E+04	5.94E+04	6.68E+03	8.34E+04	7.43E+03	2.73E+04	9.88E+04
Q14896 MYPC3	LEAPAEEDVWEIL	757.38	136.24	3.61E+04	6.01E+04	1.36E+04	5.85E+04	1.14E+04	6.25E+04	2.11E+04	7.13E+04	2.17E+04	5.38E+03	5.66E+04	9.69E+04	6.77E+03	3.33E+04	5.88E+04
P02768 ALBU	HPYFYAPPELLFF	772.38	136.25	8.82E+04	9.80E+04	1.16E+04	8.05E+04	1.88E+05	1.86E+05	2.47E+05	2.12E+05	2.15E+05	1.06E+05	1.40E+05	1.85E+05	5.29E+04	2.30E+05	1.04E+05
Q14896 MYPC3	VGEPVNLIPF	599.35	136.38	3.12E+05	2.25E+05	1.42E+05	2.60E+05	7.70E+04	3.82E+05	9.53E+04	1.25E+05	1.68E+05	1.51E+05	2.55E+05	2.08E+04	1.18E+05	8.52E+03	2.21E+05
P02768 ALBU	FYAPPELLFF	573.80	136.72	1.32E+04	9.66E+04	9.70E+03	3.90E+04	1.34E+04	9.37E+04	2.10E+04	2.23E+04	2.36E+04	2.70E+04	6.43E+04	3.09E+03	2.03E+04	3.74E+04	3.95E+04
P02144 MYG	GHPETLEK	455.73	28.17	8.37E+02	8.53E+02	6.00E+02	5.95E+02	4.14E+02	3.40E+03	7.18E+02	3.03E+02	5.76E+02	6.61E+02	5.67E+02	9.07E+02	3.17E+02	3.63E+02	1.26E+03
P45379 TNNT2	AEEDEEEEEAK	654.26	34.94	3.83E+03	4.69E+02	2.76E+03	4.87E+03	8.93E+03	1.79E+03	2.76E+03	5.54E+03	3.58E+03	2.00E+02	5.90E+03	3.30E+03	2.66E+03	1.42E+03	8.30E+03
P02511 CRYAB	EKKPAVTAAPK	570.82	38.33	5.89E+03	2.35E+02	9.53E+02	2.03E+03	1.99E+04	1.84E+03	3.68E+03	6.03E+03	4.90E+03	1.55E+04	1.26E+04	1.14E+04	4.09E+03	5.90E+03	9.21E+03
P02144 MYG	GHHEAEIKPLAQSHATK	464.25	40.42	1.35E+02	2.53E+02	3.27E+02	8.89E+03	4.22E+03	1.66E+02	2.29E+02	1.63E+02	2.61E+02	1.83E+02	1.24E+02	1.42E+02	1.31E+02	3.90E+02	1.78E+02
P02144 MYG	GHHEAEIKPLAQSH	518.60	42.24	1.67E+02	1.48E+02	1.26E+02	7.20E+03	1.48E+03	2.41E+02	1.32E+02	2.12E+02	8.29E+02	9.05E+03	1.44E+02	1.32E+02	1.26E+02	2.52E+02	6.61E+03
P45379 TNNT2	EAEDGPMEEKPKP	482.88	42.85	3.14E+03	3.21E+03	1.03E+03	6.63E+03	1.98E+03	3.53E+03	9.97E+02	1.11E+03	1.46E+03	6.22E+03	2.82E+04	2.56E+03	4.45E+02	4.23E+03	8.24E+03
P02144 MYG	DMASNYK	414.68	42.85	5.05E+03	5.24E+02	8.62E+02	1.66E+03	4.75E+03	1.85E+03	9.00E+02	2.02E+03	1.00E+03	1.09E+04	1.46E+03	1.00E+03	7.00E+02	5.02E+02	8.09E+03
P45379 TNNT2	EAEDGPMEEKPKP	567.27	42.92	6.76E+02	6.17E+02	2.93E+02	2.36E+02	7.75E+02	7.93E+02	1.56E+02	2.77E+02	1.38E+03	7.79E+03	4.38E+02	8.84E+02	1.45E+03	2.68E+02	7.77E+02
P06732 KCRM	TDLNHNELK	542.27	43.15	6.74E+03	8.47E+02	3.48E+02	3.67E+03	1.54E+04	1.68E+04	6.36E+02	1.11E+03	7.46E+02	8.94E+03	3.49E+03	1.04E+03	2.84E+02	3.43E+02	2.33E+03
P08123 CO1A2	GPSGPQGIR	434.73	43.3	8.31E+02	1.58E+03	9.85E+02	1.73E+03	1.85E+03	1.26E+03	3.12E+03	6.80E+02	1.73E+03	7.49E+03	1.23E+03	2.03E+03	1.05E+03	9.08E+02	2.01E+03
P08123 CO1A2	GEAGAAGPAGPAGPR	618.31	46.45	1.23E+03	7.47E+04	6.60E+03	4.41E+04	1.68E+04	8.98E+03	3.67E+02	5.88E+02	2.18E+04	8.30E+04	1.65E+04	3.55E+03	5.94E+03	1.85E+04	3.47E+04
P45379 TNNT2	EEEAKEAEDGPMEEKPKP	571.27	46.54	3.50E+02	4.42E+02	3.14E+02	1.72E+02	5.70E+04	1.29E+03	2.74E+04	1.62E+04	4.96E+02	8.42E+02	6.89E+02	2.42E+03	6.59E+02	8.55E+02	4.02E+02
P04075 ALDOA	RLQSIGTENTENRR	601.64	47.58	1.29E+02	3.99E+02	2.31E+02	5.87E+02	1.42E+04	1.62E+02	7.37E+03	2.31E+02	4.81E+02	1.93E+02	1.83E+02	1.30E+02	1.64E+03	2.52E+02	1.23E+02
Q99798 ACON	DSSGQHVDVSPQSR	533.92	47.76	6.10E+04	2.82E+02	5.27E+02	1.29E+02	1.51E+05	5.61E+04	5.56E+03	1.91E+03	1.23E+02	6.04E+02	5.65E				

P04075 ALDOA	RLQSIGTENTENR	549.61	51.83	1.35E+05	4.93E+04	2.78E+03	1.68E+05	5.01E+05	6.17E+03	8.12E+03	7.40E+03	1.29E+03	1.93E+03	3.13E+05	9.48E+04	1.27E+05	1.53E+05	2.00E+05
P16615-2 AT2A2	DEMVATEQER	604.27	52.35	1.27E+04	8.94E+03	1.94E+03	1.73E+04	2.09E+03	3.10E+03	1.24E+03	8.86E+02	1.15E+03	2.01E+03	1.64E+04	8.44E+03	5.45E+02	3.04E+03	1.41E+04
P04075 ALDOA	YTPSQGAGAAASES	648.79	52.45	6.69E+02	9.73E+02	1.99E+03	7.02E+02	9.24E+02	3.32E+04	4.47E+02	1.53E+03	4.31E+03	8.03E+02	9.28E+02	6.47E+02	1.14E+03	1.88E+03	6.17E+02
P04075 ALDOA	LQSIGTENTENRR	549.61	52.56	2.12E+03	1.40E+03	5.76E+03	9.29E+03	1.26E+04	4.71E+03	6.45E+03	2.88E+03	6.76E+05	7.47E+05	5.14E+03	1.71E+03	3.46E+03	1.53E+05	5.25E+03
P02545-2 LMNA	SGAQASSTPLSPTR	680.35	53.36	1.27E+04	5.90E+03	7.88E+02	1.95E+04	5.51E+04	1.30E+04	1.34E+03	2.45E+03	3.77E+04	1.22E+02	2.53E+04	8.12E+03	3.23E+03	5.64E+03	2.15E+04
P02144 MYG	LFKGGHPETLEK	433.58	54.15	1.72E+04	6.55E+02	1.26E+03	1.49E+03	1.42E+03	7.75E+02	1.29E+03	1.17E+03	3.04E+03	4.09E+04	3.57E+03	3.27E+03	2.65E+03	2.07E+03	9.63E+02
Q15149-3 PLEC1	SYVDPSTDER	584.76	54.43	2.77E+03	5.00E+03	3.12E+03	1.16E+04	1.55E+04	1.26E+04	3.09E+03	3.80E+04	3.23E+02	5.01E+02	2.71E+04	1.03E+04	3.82E+03	2.61E+02	1.24E+03
P48735 IDHP	TIEAEEAHGTVTR	678.35	54.86	7.04E+04	6.57E+04	3.73E+03	8.54E+04	2.80E+05	1.45E+04	1.27E+04	3.04E+03	1.64E+03	5.37E+03	1.03E+05	1.27E+05	1.04E+05	1.87E+05	1.16E+05
P52179-2 MYOM1	QATSALQEEETSEK	775.37	55.32	1.07E+04	5.19E+03	1.69E+03	1.60E+04	2.81E+04	4.25E+03	7.21E+02	1.80E+03	3.50E+02	3.17E+03	3.98E+04	2.22E+02	2.15E+03	1.56E+03	1.77E+04
P16615-2 AT2A2	GAPEGVIDR	457.24	55.5	5.21E+03	6.72E+03	5.74E+03	5.10E+03	6.37E+03	2.02E+03	1.00E+03	2.09E+05	6.35E+03	3.27E+03	9.47E+03	1.56E+03	6.46E+03	4.69E+03	3.11E+04
P52179-2 MYOM1	DYVSTEDSPR	584.76	55.56	4.71E+04	2.66E+04	5.85E+02	1.27E+05	1.36E+05	1.80E+05	2.22E+03	8.27E+04	1.68E+03	3.81E+03	2.25E+05	3.41E+04	1.81E+02	1.68E+03	1.44E+05
P02144 MYG	VEADIPGH	419.21	55.64	1.22E+03	3.98E+04	2.93E+03	6.29E+03	8.27E+02	4.84E+03	7.55E+03	3.50E+03	1.38E+04	2.11E+03	1.21E+04	7.23E+03	4.09E+03	5.10E+03	2.60E+04
P02545-2 LMNA	ITESEEVVSR	574.79	55.95	1.80E+04	4.76E+04	6.07E+02	6.02E+04	1.91E+05	7.26E+04	3.92E+03	6.34E+02	1.38E+05	1.24E+05	1.23E+05	6.42E+04	2.60E+03	3.22E+04	5.13E+02
P48735 IDHP	ATDFVADR	447.72	56.43	5.50E+03	2.15E+03	7.46E+03	1.29E+04	9.77E+03	1.07E+03	4.60E+03	6.35E+03	3.87E+04	4.85E+04	1.46E+03	2.88E+03	6.57E+03	4.48E+03	1.38E+04
P04075 ALDOA	LQSIGTENTENR	745.86	56.56	4.80E+05	2.23E+05	2.60E+04	6.94E+05	1.63E+05	1.78E+06	2.44E+03	6.11E+02	3.70E+02	6.11E+02	9.70E+05	8.11E+04	2.36E+04	5.47E+02	5.89E+05
P16615-2 AT2A2	RIDEMVAEQER	492.91	56.75	5.51E+04	5.09E+04	5.15E+02	6.42E+04	4.21E+03	1.41E+05	2.36E+02	1.45E+03	6.16E+02	1.39E+05	1.34E+05	3.87E+04	3.94E+02	6.07E+04	9.90E+04
P02545-2 LMNA	LEAALGEAK	451.25	56.97	1.94E+02	9.92E+02	1.61E+04	7.84E+02	1.91E+05	1.69E+03	3.92E+05	2.87E+05	1.26E+04	2.54E+03	6.99E+02	3.23E+03	1.01E+05	3.77E+03	7.93E+02
P98160 PGBM	LSGSHSQGVAYPVR	486.59	57.13	1.49E+04	6.09E+02	2.86E+02	8.73E+03	8.14E+02	1.51E+03	1.44E+02	9.45E+02	6.27E+02	9.15E+02	4.29E+04	4.08E+02	2.79E+02	3.73E+02	3.79E+02
P98160 PGBM	GPSCQDCDTGYTR	701.77	57.28	4.84E+03	1.97E+04	1.45E+03	3.46E+04	2.19E+04	9.29E+03	1.00E+03	3.68E+03	2.26E+02	4.32E+02	6.52E+04	2.59E+04	2.16E+02	1.28E+02	5.19E+02
P08123 CO1A2	HGNRGETGSPGVPAGAV GPR	507.51	57.69	1.91E+04	3.09E+03	3.39E+02	4.55E+02	1.74E+02	8.06E+02	4.83E+02	3.75E+02	1.55E+03	6.78E+03	4.56E+02	5.10E+02	3.10E+02	1.18E+03	1.18E+03
P02545-2 LMNA	VAVEEVDEEGK	602.29	57.73	4.01E+04	6.54E+04	1.71E+02	1.11E+05	2.46E+05	1.37E+05	2.70E+03	9.23E+03	4.60E+02	3.27E+03	2.46E+05	8.32E+04	7.34E+02	4.93E+02	1.08E+05
P98160 PGBM	SIVPQGGSHSLR	413.23	57.99	1.11E+03	2.98E+03	6.58E+02	1.46E+04	1.20E+03	1.58E+02	1.16E+03	1.13E+04	5.58E+02	1.19E+03	2.84E+04	6.36E+03	3.97E+02	2.43E+03	1.79E+04
P45379 TNNT2	AEDEEEEEAKEAED	876.34	58	3.20E+02	1.68E+03	1.34E+02	6.13E+02	8.95E+03	1.58E+02	3.77E+03	4.76E+02	2.43E+02	2.78E+02	8.09E+02	3.72E+04	1.04E+03	2.51E+02	3.27E+02
Q13813-3 SPTA2	GSAHEVQR	442.21	58.03	1.91E+02	2.69E+02	6.37E+04	8.98E+02	6.11E+04	1.14E+03	9.31E+04	1.05E+05	1.01E+03	2.71E+02	5.76E+02	3.26E+02	5.45E+04	2.70E+04	4.27E+02
P02144 MYG	VEADIPGHGQE	576.27	58.29	2.87E+05	1.01E+05	2.35E+02	5.23E+03	9.76E+02	3.87E+03	8.17E+02	1.79E+03	5.54E+02	3.02E+02	8.05E+05	2.79E+03	1.89E+02	2.71E+03	1.07E+06
P02787 TRFE	LAQVPSHTVVAR	426.58	58.37	3.57E+02	6.23E+02	1.73E+03	7.34E+04	6.31E+04	7.66E+04	4.08E+03	5.60E+02	3.81E+02	1.37E+02	1.27E+05	3.07E+04	5.56E+02	1.42E+02	1.10E+03
Q13423 NNTM	TVAELEAEK	495.26	58.54	4.37E+03	6.06E+03	6.70E+02	2.84E+03	1.46E+02	2.26E+03	1.04E+03	4.88E+02	3.03E+04	3.35E+03	1.42E+04	6.60E+02	1.63E+03	4.32E+03	2.38E+04
P16615-2 AT2A2	TGDGVNDAPALK	579.29	58.72	4.01E+02	5.34E+03	1.71E+03	8.30E+03	2.26E+02	1.72E+04	9.21E+02	5.34E+02	7.21E+02	4.19E+02	5.19E+03	1.27E+03	3.22E+02	9.88E+02	1.17E+03
Q13813-3 SPTA2	SQLLGSHEVQR	442.24	58.79	3.71E+02	9.64E+02	1.87E+03	3.85E+02	3.95E+02	5.78E+02	7.93E+02	1.09E+03	1.97E+04	2.67E+04	2.97E+02	6.15E+02	4.37E+02	6.72E+03	7.34E+02
P15924 DESP	LLEAASVSSK	502.78	58.82	1.56E+03	2.02E+04	4.42E+02	4.27E+04	2.28E+04	3.50E+04	4.41E+02	4.72E+02	2.25E+04	5.13E+02	3.49E+04	6.49E+02	3.28E+02	8.70E+02	2.18E+04
P98160 PGBM	EQAWQRPDGQPATR	547.27	58.92	1.73E+04	4.94E+02	3.02E+03	1.01E+03	3.09E+02	4.12E+03	4.38E+02	1.86E+03	2.36E+03	3.89E+04	2.39E+02	1.89E+02	4.20E+02	2.54E+03	1.22E+04
P52179-2 MYOM1	NQVPINVHANPGK	463.25	58.94	1.25E+02	1.20E+04	1.87E+03	3.92E+04	2.63E+03	4.04E+02	8.92E+02	1.98E+03	3.75E+02	9.03E+02	1.08E+05	1.97E+04	6.81E+02	1.67E+02	6.48E+04
P02787 TRFE	EGTCPEAPTDECK	690.28	59.12	1.21E+02	1.86E+02	1.65E+02	3.06E+02	1.35E+02	5.25E+02	3.57E+02	1.68E+02	5.04E+02	1.53E+04	2.47E+02	3.22E+02	4.21E+02	4.30E+02	1.01E+03
P98160 PGBM	VTSYGGELR	491.25	59.26	1.22E+04	1.70E+04	1.34E+02	7.45E+02	1.71E+03	7.08E+02	1.52E+03	2.15E+03	1.21E+04	2.02E+04	3.04E+02	1.23E+03	1.16E+03	3.49E+03	1.02E+04
P22695 QCR2	AVAFQNPQTH	556.78	59.27	2.48E+02	1.30E+03	3.99E+02	2.24E+04	4.05E+03	1.27E+04	3.69E+03	5.32E+02	2.69E+03	1.75E+04	1.40E+04	1.02E+03	5.25E+02	1.08E+04	1.77E+03
P98160 PGBM	VPGSPTNLANR	563.30	59.46	2.47E+03	5.66E+04	2.98E+03	8.65E+04	1.83E+05	4.28E+03	3.67E+04	2.24E+04	7.54E+03	8.06E+03	1.29E+05	9.03E+04	1.81E+04	1.53E+03	1.10E+05
Q15149-3 PLEC1	DVAEVDTVR	502.26	59.62	1.95E+02	1.77E+03	1.74E+03	7.52E+02	5.22E+02	1.09E+03	1.94E+02	7.15E+02	3.09E+04	1.05E+03	2.80E+04	3.39E+02	1.67E+02	1.18E+03	1.70E+04
P45379 TNNT2	KKEEELVSLKDR	534.96	59.84	3.32E+02	1.28E+03	1.26E+03	5.97E+02	4.52E+02	5.15E+02	1.43E+05	2.49E+02	2.23E+05	5.07E+04	7.29E+02	7.32E+04	4.63E+02	6.73E+02	1.94E+03
Q15149-3 PLEC1	DTHDQLSEPSEVR	504.90	59.97	4.72E+04	2.86E+04	4.63E+02	4.88E+04	1.75E+03	4.02E+02	3.06E+03	2.85E+02	9.18E+02	3.01E+02	4.72E+04	2.32E+02	2.40E+03	1.40E+04	2.22E+04
Q13813-3 SPTA2	GEIDAHEDSFK	416.52	60.11	2.77E+02	3.21E+02	2.82E+02	1.09E+03	3.44E+02	4.74E+02	1.76E+03	5.37E+02	2.74E+04	3.41E+04	5.23E+02	2.00E+03	9.06E+02	2.00E+03	5.38E+02
Q15149-3 PLEC1	LVASMEEAR	503.26	60.16	4.83E+02	8.09E+02	1.36E+06	2.06E+06	2.84E+06	1.78E+06	3.37E+06	2.69E+06	2.08E+04	2.06E+04	2.29E+06	1.66E+06	1.94E+06	5.62E+02	1.97E+03
P52179-2 MYOM1	ASASSQQQASQHALSSEVS	716.01	60.43	2.97E+02	8.53E+03	1.20E+02	4.82E+04	5.32E+04	3.43E+02	2.18E+02	2.82E+02	7.48E+02	3.77E+02	5.65E+04	9.92E+03	2.32E+02	2.91E+02	1.43E+03
O75112 LDB3	SSLAEASDPGPPR	642.31	60.5	1.30E+05	1.84E+05	7.13E+02	4.14E+05	6.80E+02	4.23E+03	1.11E+03	1.04E+03	5.07E+05	1.20E+06	3.75E+03	2.91E+03	4.34E+02	2.56E+05	6.63E+04
P02545-2 LMNA	EGDLIAAQR	522.28	60.93	8.85E+02	1.87E+04	4.11E+04	2.94E+04	5.14E+04	2.68E+04	2.35E+03	4.75E+02	5.46E+02	3.47E+02	2.13E+03	9.74E+03	4.21E+04	5.62E+02	6.05E+02
P06732 KCRM	GYTLPPHCSR	565.78	60.98	1.17E+04	2.45E+03	6.66E+03	7.30E+03	9.04E+03	1.49E+03	4.72E+03	4.17E+02	1.29E+04	2.78E+04	1.14E+04	7.17E+03	1.55E+03	3.55E+04	8.50E+03
P52179-2 MYOM1	AYSSRSSAAHRRESEAFRRRA SASSQQASQHALSSEVSR	726.01	60.98	5.71E+03	1.10E+04	2.30E+02	1.94E+04	1.21E+02	4.02E+02	2.77E+02	9.92E+02	2.90E+02	3.87E+02	1.10E+04	1.58E+04	4.37E+02	8.01E+02	1.19E+04
P52179-2 MYOM1	SAVYTTQGSTAYSSR	739.35	61	3.26E+04	1.17E+04	7.96E+02	5.40E+04	8.24E+02	2.68E+03	4.80E+03	1.19E+03	3.11E+02	7.47E+02	5.00E+04	1.97E+04	1.41E+03	2.53E+02	4.10E+04
Q13813-3 SPTA2	LIQSHPESAEDLQEK	575.29	61.31	7.97E+04	1.15E+04	8.07E+02	5.95E+04	4.36E+04	1.96E+03	5.64E+02	2.65E+03	3.53E+03	5.14E+04	5.07E+04	2.97E+04	8.84E+02	4.36E+02	6.19E+04
P02545-2 LMNA	SLETENAGLR	545.28	61.38	2.99E+02	9.34E+03	3.51E+02	1.04E+03	1.43E+04	2.73E+02	3.50E+02	1.51E+03	4.44E+05	2.50E+05	1.13E+03	1.08E+03	7.01E+02	2.86E+05	4.14E+03
P98160 PGBM	TCESLGAGGYR	557.25	61.57	2.88E+02	4.07E+04	4.22E+03	1.47E+04	1.38E+04	3.40E+04	1.67E+03	8.22E+02	2.48E+04	3.65E+02	4.24E+04	3.06E+04	3.97E+04	8.	

Q02218 ODO1	SSPYPTDVAR	546.77	61.9	6.26E+03	6.13E+04	2.69E+03	1.33E+03	7.96E+02	2.82E+02	1.93E+04	1.03E+04	4.02E+05	2.66E+05	2.05E+03	5.21E+02	4.22E+03	4.44E+03	3.03E+03
P02511 CRYAB	HFSPEELK	493.75	62.01	1.52E+05	7.86E+04	5.85E+03	2.77E+04	9.63E+04	1.95E+05	2.52E+03	3.22E+03	8.94E+04	2.00E+05	3.26E+05	4.96E+04	3.17E+03	5.15E+04	1.27E+05
P98160 PGBM	LHHVSPADSGEYVCR	557.26	62.06	2.01E+02	1.46E+04	1.59E+03	7.32E+03	1.31E+03	6.36E+02	1.55E+03	2.20E+03	1.41E+04	2.76E+04	6.51E+04	3.34E+03	1.27E+03	1.74E+04	8.70E+04
O75112 LDB3	AHTAIASASTTAPASSPADS PR	688.00	62.23	1.36E+03	3.61E+04	2.44E+03	3.31E+04	4.34E+03	8.06E+02	1.60E+03	4.07E+02	1.14E+03	3.82E+02	2.83E+04	1.93E+04	1.57E+03	6.10E+02	4.90E+02
P16615-2 AT2A2	SMSVYCTPNKPSR	490.57	62.31	6.32E+02	5.26E+04	3.39E+03	8.89E+04	7.24E+04	8.21E+03	7.12E+02	7.82E+03	6.57E+02	4.13E+02	8.16E+04	3.39E+04	8.91E+02	6.59E+02	6.23E+02
O94875-3 SRBS2	LGEVTGSPSPPPR	647.34	62.34	1.01E+05	1.85E+05	2.32E+04	1.83E+05	8.57E+03	2.47E+04	4.19E+03	2.54E+03	2.72E+03	3.07E+03	1.40E+05	1.98E+05	2.61E+03	8.44E+03	1.07E+04
Q13813-3 SPTA2	HALLEADVAAHQDR	515.93	62.72	2.36E+02	5.39E+03	1.22E+03	9.86E+02	3.69E+02	4.26E+03	1.17E+03	4.75E+02	1.32E+03	8.82E+03	2.12E+04	3.32E+02	5.44E+02	1.82E+03	3.10E+04
O75112 LDB3	ASPGTPGTPELR	591.81	62.72	2.98E+05	4.20E+05	1.59E+03	3.46E+05	1.02E+05	4.60E+03	1.41E+03	1.09E+03	5.56E+02	8.52E+02	1.95E+05	1.37E+05	2.91E+03	7.76E+03	4.72E+05
P02511 CRYAB	VLGDVIEVHGKHEER	429.98	62.8	4.11E+02	1.40E+03	1.43E+02	2.39E+03	1.96E+02	1.16E+05	3.83E+02	1.59E+02	2.58E+03	1.05E+03	7.91E+04	1.86E+03	1.11E+03	1.14E+03	3.72E+03
Q02218 ODO1	VIPEDGPAQNPENVKR	611.99	62.87	3.43E+03	1.69E+03	6.41E+03	2.41E+03	1.43E+05	1.80E+03	3.19E+04	1.05E+04	1.33E+03	2.17E+02	4.93E+03	2.30E+04	3.54E+03	6.00E+02	1.43E+03
P04406 G3P	VGVNGFGR	403.22	63.11	8.99E+04	5.89E+04	1.21E+04	1.43E+05	2.18E+03	8.61E+03	1.23E+04	1.54E+04	6.78E+04	8.06E+02	1.05E+05	9.36E+03	1.40E+04	5.79E+02	8.04E+04
P02511 CRYAB	TIPITREEKPAVTAAPK	456.27	63.13	2.41E+02	2.14E+03	3.71E+05	2.08E+02	1.99E+02	2.67E+05	2.05E+04	5.43E+03	1.02E+03	7.90E+02	2.87E+03	7.76E+02	1.91E+05	6.11E+02	8.95E+02
P04406 G3P	QVVSDFNSDTH	668.30	63.38	3.26E+05	8.38E+04	3.25E+03	2.03E+05	1.96E+02	4.88E+03	1.16E+03	5.20E+02	1.06E+03	8.29E+02	1.35E+05	7.80E+02	7.90E+02	3.93E+02	1.35E+05
P02787 TRFE	EGTCPEAPTDECKPVK	568.59	63.4	4.65E+03	8.93E+02	1.40E+03	5.13E+02	1.48E+03	1.92E+03	1.33E+03	1.17E+03	5.26E+04	1.09E+05	3.39E+03	2.09E+02	3.95E+02	3.15E+04	1.87E+02
O75112 LDB3	TAIASASTTAPASSPADSPR	620.31	63.45	1.51E+04	5.37E+03	3.37E+04	1.30E+04	3.41E+03	1.03E+04	6.84E+03	4.88E+02	2.69E+03	6.07E+03	2.08E+04	1.06E+04	9.55E+02	8.85E+02	3.90E+02
Q99798 ACON	GHLDDPASQEIER	489.57	63.77	2.33E+05	9.64E+02	1.00E+03	3.37E+02	1.13E+03	4.54E+02	3.11E+02	3.92E+02	5.97E+03	4.82E+04	2.01E+04	1.17E+04	1.75E+02	2.84E+04	6.57E+04
P52179-2 MYOM1	VNTELPVK	450.26	63.79	2.08E+04	4.88E+03	8.17E+02	4.11E+02	8.30E+02	1.57E+03	2.81E+02	9.65E+02	1.07E+05	5.39E+04	5.08E+03	6.26E+02	2.82E+02	5.33E+03	2.03E+04
P48735 IDHP	GKLDGNQDLIR	614.83	63.81	1.78E+03	1.33E+03	6.96E+02	1.95E+03	2.72E+03	4.99E+02	3.33E+03	6.61E+03	7.80E+04	5.00E+04	2.35E+03	2.40E+02	5.43E+02	2.20E+04	6.49E+03
P98160 PGBM	SVADSGEYVCR	593.26	63.86	9.81E+03	2.56E+04	5.94E+03	2.64E+03	5.66E+03	7.00E+02	1.41E+03	2.00E+02	1.46E+04	3.47E+03	3.78E+04	1.36E+04	8.25E+02	1.65E+04	7.14E+03
P15924 DESP	QLQVEQESVK	601.32	64.43	1.22E+03	3.27E+02	7.92E+02	1.03E+03	1.90E+04	1.13E+04	2.23E+03	6.66E+03	8.20E+04	9.22E+04	1.08E+03	2.02E+03	1.21E+03	4.95E+04	4.58E+02
P02787 TRFE	KPVVEYANCHLAR	510.59	64.57	1.55E+05	3.43E+04	6.83E+03	5.24E+04	6.72E+03	1.19E+03	1.10E+04	2.58E+02	1.63E+05	1.67E+05	1.46E+02	2.15E+04	2.46E+03	4.62E+04	2.29E+03
Q15149-3 PLEC1	LTVDEAVR	451.75	64.59	3.34E+03	4.12E+04	7.35E+03	5.33E+03	6.03E+03	1.46E+04	9.01E+03	3.26E+04	2.31E+04	5.93E+04	1.44E+05	4.71E+04	1.63E+04	1.15E+04	5.41E+04
Q15149-3 PLEC1	SMVEEGTGLR	539.76	64.69	4.97E+02	2.69E+04	2.40E+03	4.70E+04	2.79E+04	1.52E+04	4.50E+02	1.53E+03	2.33E+03	8.26E+02	8.36E+04	5.98E+04	2.06E+03	5.07E+02	3.26E+04
Q13813-3 SPTA2	EPIVGSTDYGK	583.29	64.72	8.71E+02	1.06E+03	6.38E+03	1.00E+03	1.72E+03	6.32E+04	2.98E+02	7.82E+03	6.18E+02	5.77E+03	6.01E+02	3.46E+03	4.31E+03	9.64E+02	1.80E+03
P22695 QCR2	VIENLHAAAYR	419.56	64.82	2.33E+03	1.16E+05	1.90E+03	2.88E+05	7.78E+04	3.03E+05	2.45E+03	9.58E+03	2.34E+04	3.33E+03	2.06E+05	6.59E+04	1.57E+03	1.63E+04	2.88E+03
P45379 TNNT2	AEDEEEEEAKEAEDGPME ESKPKPR	598.47	64.87	1.54E+03	4.28E+03	4.69E+02	2.33E+03	2.42E+04	1.07E+03	3.33E+02	1.83E+03	3.70E+02	3.72E+02	4.63E+02	1.52E+04	7.23E+02	7.74E+02	7.55E+02
Q15149-3 PLEC1	LAEDEAFQR	539.76	64.95	7.37E+03	2.43E+04	5.67E+02	1.29E+04	1.43E+04	1.69E+04	5.75E+02	4.36E+03	2.74E+03	7.74E+02	6.83E+04	7.13E+03	1.13E+03	4.06E+03	3.31E+04
Q13813-3 SPTA2	MQHNLQEQIQAR	499.25	64.95	6.66E+04	1.03E+04	1.02E+03	1.84E+04	5.25E+03	2.22E+04	2.28E+03	3.47E+03	7.08E+02	7.86E+02	3.49E+04	8.85E+03	4.10E+03	4.73E+03	6.25E+04
P02144 MYG	IPGHGQEVLR	406.90	65.04	8.20E+02	3.76E+02	1.19E+05	3.36E+04	3.28E+02	2.10E+04	8.80E+04	1.39E+05	1.80E+03	1.52E+03	1.24E+03	1.70E+02	4.25E+04	8.20E+02	6.76E+02
Q02218 ODO1	AQSLVEAQPNVDK	699.86	65.18	1.66E+05	2.71E+04	8.55E+03	9.47E+04	1.38E+04	1.71E+03	1.02E+03	5.09E+03	2.92E+03	4.53E+03	7.28E+04	3.36E+03	3.40E+03	1.07E+04	9.36E+02
P18206-2 VINC	STLVEIQDSVK	559.81	65.18	1.67E+04	6.15E+04	1.23E+03	4.72E+03	1.95E+05	6.99E+03	1.33E+02	1.25E+02	3.80E+04	6.17E+02	3.05E+05	8.82E+04	1.55E+03	1.76E+03	1.81E+05
P02545-2 LMNA	EDLQELNDR	566.27	65.23	7.92E+04	9.28E+04	1.76E+03	1.45E+05	4.34E+04	3.01E+03	5.54E+04	6.04E+04	1.37E+03	6.92E+02	1.65E+05	4.31E+04	2.85E+03	3.84E+02	2.19E+02
P02545-2 LMNA	EAALSTALSEKR	425.90	65.9	5.13E+02	1.46E+03	5.04E+03	3.98E+03	6.45E+04	1.62E+04	2.94E+04	1.65E+04	5.61E+03	3.67E+03	3.73E+02	5.51E+03	3.03E+04	1.25E+03	2.50E+03
P02144 MYG	GKVEADIPGHGQEV	718.36	66.02	5.28E+04	5.93E+02	2.60E+03	2.14E+03	1.59E+03	1.26E+03	8.23E+03	1.77E+03	1.31E+04	1.62E+04	1.15E+03	5.78E+03	1.08E+03	5.13E+03	1.32E+05
P15924 DESP	LTYEIEDEKR	648.33	66.08	4.38E+03	3.06E+03	3.44E+03	7.54E+03	6.74E+03	1.58E+03	1.69E+03	1.32E+04	1.39E+03	2.29E+04	2.34E+04	8.47E+04	6.78E+02	8.73E+03	7.83E+03
P98160 PGBM	VGGHLRPGIVQSGGVVR	422.75	66.31	9.71E+02	2.96E+03	4.19E+02	4.25E+02	3.92E+03	2.14E+03	1.92E+03	1.40E+03	7.67E+03	3.68E+03	5.20E+04	1.11E+03	2.19E+03	1.69E+03	7.09E+04
Q13813-3 SPTA2	HQALQAEIAGHEPR	519.61	66.47	2.72E+04	2.38E+04	4.98E+03	1.60E+04	9.49E+02	1.81E+02	4.77E+02	9.84E+02	9.43E+03	3.69E+02	2.57E+04	2.03E+04	1.27E+04	1.70E+03	1.26E+04
P02144 MYG	GDFGADAQGAMNK	641.28	66.52	4.05E+05	1.15E+05	5.71E+03	4.23E+05	1.35E+05	1.21E+04	1.57E+03	6.67E+03	6.38E+02	1.33E+03	2.35E+05	5.89E+04	1.13E+03	6.50E+03	3.66E+05
Q13423 NNTM	AAALEQFK	439.24	66.54	3.39E+04	3.43E+02	3.33E+03	3.10E+02	6.26E+02	6.43E+02	4.15E+02	5.01E+02	2.50E+04	1.17E+04	2.58E+03	1.32E+03	2.96E+03	1.31E+04	8.18E+03
P18206-2 VINC	AVAGNISDPGLQK	635.34	66.64	3.23E+05	2.01E+05	1.60E+03	4.31E+05	3.28E+05	1.08E+04	1.88E+03	1.14E+04	2.08E+03	1.65E+03	4.09E+05	1.87E+05	4.69E+03	1.09E+03	4.19E+05
P48735 IDHP	LDGNQDLIR	522.28	66.77	3.34E+03	3.53E+04	6.00E+03	7.23E+03	2.40E+05	5.16E+03	1.50E+03	2.79E+04	4.73E+03	2.80E+03	2.35E+05	7.50E+04	1.46E+03	6.71E+02	2.58E+05
Q15149-3 PLEC1	GGELVYTDSEAR	648.81	66.77	2.51E+04	6.20E+04	1.55E+04	1.01E+05	2.76E+02	1.81E+04	5.59E+03	1.20E+04	4.88E+03	6.11E+03	9.03E+04	6.00E+04	1.19E+04	2.16E+04	7.83E+04
P15924 DESP	VVIVDPETNK	557.31	66.82	1.99E+04	8.69E+04	4.77E+02	1.12E+04	5.79E+03	3.24E+03	4.05E+03	2.32E+04	3.33E+02	5.02E+02	1.01E+05	1.04E+05	2.60E+03	4.70E+02	9.86E+04
P98160 PGBM	LRPGIVQSGGVVR	446.61	66.92	4.09E+04	4.15E+03	8.81E+03	6.30E+03	5.76E+03	1.14E+04	2.50E+03	5.05E+03	3.78E+02	5.64E+02	7.87E+04	6.53E+03	5.23E+03	1.71E+03	6.57E+04
P04406 G3P	VIPELNGK	435.26	66.93	7.57E+04	5.22E+03	1.90E+04	4.88E+03	6.75E+03	9.54E+03	4.10E+03	4.86E+03	1.40E+05	1.91E+05	1.84E+05	3.31E+03	5.51E+03	1.24E+05	1.93E+04
P98160 PGBM	RPEEVCGPTQFR	473.57	67.13	8.09E+02	1.02E+05	4.21E+03	1.72E+05	1.43E+05	8.24E+03	3.82E+03	4.48E+03	2.51E+03	4.45E+03	1.55E+05	9.43E+04	1.15E+03	3.13E+02	1.48E+05
Q15149-3 PLEC1	VPVDVAYQR	523.78	67.17	8.95E+04	1.65E+05	1.66E+04	2.67E+04	1.20E+04	9.98E+03	1.26E+04	1.05E+04	2.40E+04	5.63E+03	4.12E+05	2.75E+05	7.72E+03	9.30E+03	2.63E+05
Q15149-3 PLEC1	FPVTDVAVNK	495.77	67.41	2.39E+04	7.87E+04	7.51E+03	2.67E+04	8.93E+03	2.19E+04	3.86E+03	1.00E+03	1.30E+04	1.35E+04	1.71E+05	1.28E+04	7.63E+03	5.03E+03	7.90E+04
P48735 IDHP	FAQMLEK	433.73	67.62	8.95E+03	5.42E+02	5.69E+02	3.16E+03	3.43E+03	9.45E+02	1.40E+03	6.15E+02	8.08E+04	6.94E+04	1.35E+03	2.98E+03	3.20E+05	4.23E+04	8.39E+03
Q13813-3 SPTA2	GLVSSDELAK	509.77	68	5.53E+03	8.33E+03	1.14E+05	2.37E+03	2.40E+03	1.58E+05	7.23E+03	2.04E+05	8.84E+02	7.16E+03	1.24E+03	7.76E+03	1.91E+05	1.11E+03	4.76E

Q02218 ODO1	VIPEDGPAAQNPENVK	839.42	68.45	3.88E+04	1.21E+04	3.76E+03	3.42E+04	1.55E+04	9.43E+03	5.14E+03	8.48E+03	1.86E+03	2.36E+03	2.03E+04	1.22E+04	2.27E+03	1.71E+03	1.16E+05
P98160 PGBM	SAEPLALGR	457.26	68.65	3.57E+03	4.03E+05	1.56E+04	1.97E+05	8.81E+04	6.22E+04	8.12E+03	2.96E+04	1.90E+03	3.36E+03	6.94E+04	2.43E+05	3.72E+05	1.59E+02	9.06E+02
P02511 CRYAB	SSDGLTVNGPR	601.31	68.7	8.29E+02	2.01E+03	4.13E+04	3.77E+03	2.95E+03	9.04E+03	5.43E+03	4.77E+03	1.80E+03	5.52E+03	4.74E+04	5.30E+03	1.55E+03	7.41E+03	5.99E+02
Q99798 ACON	LDDPASQEIER	636.81	68.94	7.18E+04	1.33E+04	3.03E+04	1.59E+04	9.36E+03	1.92E+04	1.66E+04	1.41E+04	5.74E+03	1.27E+04	1.45E+03	1.46E+03	1.06E+03	3.82E+03	2.87E+02
P45379 TNNT2	DFDDIHR	459.21	69.69	2.81E+03	4.98E+05	6.19E+04	5.88E+05	4.22E+05	1.25E+05	3.51E+05	1.12E+05	4.20E+03	4.78E+03	2.06E+03	3.81E+05	3.37E+05	5.97E+02	3.10E+03
P45379 TNNT2	FDDIHR	401.69	69.74	1.27E+03	9.02E+04	9.33E+03	4.26E+05	1.87E+05	1.67E+04	1.84E+05	7.00E+03	4.04E+02	2.05E+02	1.77E+04	1.62E+05	8.37E+04	7.25E+02	1.75E+03
P45379 TNNT2	VDFDDIHR	508.74	69.76	3.00E+03	3.93E+06	5.54E+05	5.64E+06	2.36E+06	5.33E+05	4.92E+05	6.56E+05	5.52E+04	6.83E+03	2.69E+03	2.99E+06	2.23E+06	8.68E+02	1.01E+04
P15924 DESP	LSSEVEALR	502.28	70.01	2.61E+03	9.51E+04	1.65E+03	1.03E+04	4.70E+04	1.43E+04	4.90E+02	3.89E+03	5.51E+02	1.23E+03	2.48E+05	3.39E+03	4.59E+03	3.32E+03	2.28E+05
Q99798 ACON	GEFDPGQDTYQHPPK	572.59	70.01	3.21E+05	8.10E+02	1.19E+03	1.87E+05	2.44E+05	1.71E+03	8.22E+02	1.05E+03	5.36E+03	7.63E+03	1.53E+05	5.89E+03	1.28E+02	4.31E+03	1.21E+05
P98160 PGBM	FDQPDDFK	506.23	70.01	2.02E+04	4.97E+04	1.86E+04	2.11E+05	4.73E+04	8.79E+03	3.98E+03	4.38E+02	3.90E+04	7.53E+03	4.28E+03	2.53E+04	3.86E+04	2.77E+04	3.41E+03
P02545-2 LMNA	LQEKEDLQELNDR	543.94	70.04	4.11E+03	9.98E+03	3.59E+03	7.10E+03	5.70E+04	6.92E+03	1.37E+04	6.51E+02	7.15E+03	1.92E+03	8.72E+02	6.79E+03	1.18E+04	2.48E+03	1.54E+03
P08123 CO1A2	GETGSPGVPGAVGPR	781.90	70.24	7.44E+05	1.57E+06	5.25E+04	1.23E+06	5.25E+05	2.01E+04	9.92E+03	6.34E+03	1.50E+03	4.81E+03	5.51E+05	7.32E+05	1.07E+04	2.97E+02	1.37E+06
Q15149-3 PLEC1	AALAHSEEVTAQVAATK	595.31	70.32	3.77E+03	7.20E+03	3.32E+03	7.48E+03	8.18E+03	1.18E+04	3.59E+03	1.54E+04	1.36E+03	5.82E+03	7.25E+04	5.63E+04	3.39E+04	2.27E+03	8.90E+04
Q13423 NNTM	AVVLAANHFR	577.83	70.75	1.58E+03	8.28E+04	4.75E+03	6.32E+04	1.35E+05	5.93E+03	2.01E+04	8.02E+03	4.47E+04	9.10E+03	8.59E+02	1.05E+05	9.40E+04	3.31E+04	1.07E+05
P08123 CO1A2	APGPHGVPAGKHGNGRGE TGSPGVPGAVGPR	787.90	70.81	4.86E+02	2.53E+03	1.28E+05	1.75E+03	1.37E+05	4.42E+04	2.67E+05	3.27E+05	5.29E+02	4.69E+02	1.87E+04	1.54E+05	1.34E+03	1.75E+03	2.60E+02
Q5VTT5 MYOM3	ASELVVMGDHDAAR	490.91	70.82	1.14E+05	6.60E+03	1.67E+03	9.61E+03	1.09E+03	1.78E+03	2.74E+02	1.47E+03	1.87E+03	9.04E+02	9.54E+04	1.57E+04	4.26E+03	3.01E+03	1.36E+05
P04075 ALDOA	GILAADESTGSIKR	744.90	70.84	3.51E+04	1.69E+03	2.76E+02	1.54E+04	4.22E+03	2.25E+03	5.53E+02	2.02E+04	1.85E+03	3.45E+02	1.85E+04	9.03E+02	2.70E+03	2.24E+03	3.17E+04
Q99798 ACON	TFADPADYNK	571.26	70.85	3.34E+05	1.68E+03	3.38E+03	5.33E+03	3.81E+03	7.43E+03	8.73E+02	1.03E+03	5.37E+03	2.05E+03	7.19E+04	1.51E+03	2.35E+03	2.15E+03	5.76E+04
P02144 MYG	VEADIPGHGQEV	625.80	70.87	4.01E+06	1.12E+06	6.23E+03	2.13E+06	1.32E+06	1.44E+04	3.80E+03	8.85E+02	1.91E+03	1.29E+03	1.02E+06	2.28E+02	5.79E+03	2.71E+03	2.13E+06
P15924 DESP	LTVDSAIAR	473.27	71.06	1.06E+04	2.16E+05	8.48E+03	3.35E+05	2.19E+05	3.98E+05	1.32E+05	3.60E+03	1.01E+03	5.19E+03	1.91E+03	1.83E+05	2.35E+05	3.14E+03	1.45E+04
P06732 KCRM	YKPEEEYPDLK	749.36	71.15	2.21E+05	1.57E+03	8.12E+03	1.60E+04	2.14E+04	2.51E+04	1.03E+05	9.95E+04	1.12E+03	2.44E+03	7.69E+04	1.32E+03	7.08E+03	4.39E+02	6.63E+04
P02144 MYG	QSKHPGDFGADAQGAMNK	618.61	71.2	8.23E+04	2.59E+04	3.22E+02	9.89E+03	4.87E+04	1.84E+03	1.83E+03	2.72E+02	6.02E+02	1.44E+03	2.27E+04	2.58E+03	1.13E+03	2.47E+03	2.48E+04
Q02218 ODO1	NQGYDYVKPR	468.23	71.33	1.12E+05	1.31E+03	3.82E+03	3.54E+03	4.77E+02	1.32E+03	1.10E+03	8.24E+02	1.15E+03	6.66E+02	7.80E+03	5.37E+03	1.66E+03	3.21E+03	7.82E+04
P45379 TNNT2	EEEELVSLKDR	673.84	71.52	6.56E+03	3.54E+03	5.55E+03	8.78E+03	3.68E+04	1.68E+03	1.54E+04	2.30E+04	3.38E+02	3.02E+02	2.59E+03	1.74E+04	1.61E+04	5.07E+02	8.61E+02
P15924 DESP	DLKDEIVR	494.28	71.55	3.51E+02	8.33E+04	5.82E+04	7.97E+04	1.64E+05	1.85E+04	9.85E+03	6.11E+04	1.09E+03	2.88E+03	4.77E+04	1.01E+05	1.34E+05	8.27E+02	1.64E+05
Q13813-3 SPTA2	LQQSHPLSATQIQVK	559.98	71.71	6.74E+04	1.78E+03	9.33E+02	9.47E+02	5.20E+02	9.40E+02	4.65E+02	1.10E+03	4.76E+02	1.41E+02	7.18E+03	2.29E+02	1.21E+03	2.46E+02	5.63E+04
Q13813-3 SPTA2	DLTNVQNLQK	586.82	72.25	8.25E+04	1.56E+03	9.21E+03	2.96E+03	4.45E+03	2.39E+03	5.44E+03	6.03E+03	4.33E+02	9.14E+02	7.19E+04	1.38E+03	8.56E+02	1.12E+03	9.77E+04
P11142 HSP7C	RFDDAVVQSDMK	705.84	72.29	2.57E+04	4.69E+02	6.45E+02	6.66E+02	2.02E+04	7.03E+02	1.08E+03	1.40E+03	4.90E+02	6.99E+02	4.22E+02	2.22E+03	1.71E+03	6.21E+02	1.57E+03
P48735 IDHP	NTDESISGFAH	589.27	72.5	7.43E+04	5.83E+02	1.18E+03	5.09E+03	1.33E+04	1.38E+03	4.60E+03	3.01E+03	9.57E+02	2.54E+02	2.33E+04	1.21E+04	1.79E+03	4.63E+05	2.87E+04
Q5VTT5 MYOM3	VSPSPFGR	428.74	72.55	2.31E+02	6.54E+04	1.70E+03	7.50E+04	3.45E+05	1.33E+04	4.53E+05	6.15E+03	9.26E+02	2.37E+04	2.58E+05	2.59E+05	3.13E+05	9.39E+02	8.66E+02
P06732 KCRM	DKETPSGFTVD	598.29	72.58	3.35E+02	5.15E+03	2.29E+04	5.19E+03	2.63E+03	9.24E+03	1.63E+04	1.82E+03	1.25E+03	1.83E+04	3.53E+03	5.52E+03	1.45E+03	3.40E+04	1.85E+03
Q15149-3 PLEC1	VPLDVACAR	472.25	72.69	2.48E+03	1.27E+04	4.48E+03	8.90E+03	4.46E+04	4.68E+03	1.23E+04	6.54E+03	1.53E+03	1.68E+03	5.08E+04	3.71E+04	8.12E+03	8.38E+02	4.90E+03
Q5VTT5 MYOM3	SVSEAGVGESSAATEPIR	873.93	72.73	1.45E+05	6.70E+03	3.33E+03	2.24E+05	1.27E+05	9.13E+03	9.49E+02	1.59E+03	2.59E+02	5.28E+02	1.24E+05	2.67E+04	2.71E+04	3.07E+02	1.58E+05
P18206-2 VINC	ELTPQVVSAAAR	585.83	72.81	7.91E+02	3.89E+03	6.17E+05	2.70E+05	4.96E+05	4.88E+05	2.37E+05	2.15E+04	3.86E+03	3.29E+02	7.03E+03	8.40E+04	1.47E+04	4.53E+02	1.56E+03
P16615-2 AT2A2	TGTLTTNQMSVCR	706.34	72.88	3.44E+03	2.99E+03	3.58E+03	2.27E+04	5.02E+03	4.46E+04	5.07E+04	7.19E+02	3.86E+02	6.70E+03	2.60E+03	2.25E+03	9.03E+02	1.76E+03	2.00E+03
P15924 DESP	LTYEIEDEK	570.28	72.95	1.32E+03	5.54E+02	3.36E+03	3.09E+03	1.82E+03	1.22E+05	1.84E+03	1.02E+04	4.91E+04	5.45E+04	4.30E+03	6.02E+03	9.66E+03	6.35E+02	1.16E+03
P00505 AATM	PMYSNPPLNGAR	658.83	73.18	1.55E+04	1.93E+03	8.54E+02	5.51E+03	4.56E+03	2.05E+03	1.86E+03	1.17E+03	4.63E+02	6.46E+02	4.78E+03	1.12E+03	4.28E+03	4.57E+03	3.25E+03
Q13813-3 SPTA2	SADSGQALLAAGH	663.82	73.22	1.31E+03	6.70E+03	1.87E+04	2.48E+04	2.89E+03	1.45E+04	1.71E+03	3.76E+04	7.73E+03	1.74E+03	1.89E+03	2.68E+03	7.30E+03	1.53E+04	2.72E+03
P02545-2 LMNA	NIYSEELR	512.26	73.37	3.95E+03	1.55E+04	1.86E+04	8.83E+04	1.88E+05	1.13E+05	2.61E+05	1.39E+05	3.05E+03	1.32E+03	6.32E+03	5.80E+04	8.40E+03	6.83E+05	5.23E+03
P02545-2 LMNA	DLEDSTAR	459.73	73.39	6.36E+02	1.24E+05	2.26E+03	4.58E+05	3.46E+05	2.40E+05	1.66E+05	1.12E+04	1.37E+03	6.82E+02	6.30E+03	2.93E+05	2.61E+05	7.40E+02	3.60E+03
P02545-2 LMNA	EAALSTALSEK	560.30	73.44	3.94E+02	3.13E+05	3.27E+05	4.26E+05	3.35E+05	4.54E+05	1.98E+05	7.43E+03	7.59E+04	4.76E+04	4.17E+03	2.19E+05	7.19E+03	4.05E+04	1.69E+04
Q5VTT5 MYOM3	EQSTYVVLVR	547.79	73.54	2.82E+03	1.41E+04	9.72E+02	8.01E+02	2.37E+03	1.77E+03	2.80E+03	9.94E+02	1.01E+05	1.58E+05	1.16E+03	3.91E+02	5.69E+03	1.08E+05	2.47E+03
O75112 LDB3	ASPGTPGTPELRP	640.33	73.6	2.31E+05	2.92E+04	3.57E+04	9.29E+04	1.17E+04	3.73E+04	1.12E+04	2.14E+03	1.88E+05	1.09E+03	4.34E+04	3.23E+04	2.10E+04	1.86E+05	8.56E+04
P15924 DESP	YETEINIK	555.79	73.62	9.29E+02	2.14E+04	2.51E+04	7.99E+02	3.43E+02	6.75E+04	1.32E+03	1.60E+03	3.11E+02	9.23E+02	1.43E+03	4.67E+03	4.60E+03	1.04E+04	5.83E+02
P15924 DESP	YGDGIQLTR	511.77	73.77	6.95E+04	2.92E+04	3.40E+04	2.03E+03	1.23E+03	4.73E+04	5.65E+04	3.46E+04	9.50E+03	1.15E+03	6.41E+04	5.83E+04	1.91E+03	1.33E+06	6.55E+02
P48735 IDHP	VAKPVVEMDGDEMTR	559.60	74.01	1.26E+05	6.69E+03	1.39E+04	1.13E+04	1.95E+04	2.99E+03	2.26E+04	1.68E+05	7.35E+02	5.20E+02	5.90E+04	2.13E+04	7.53E+03	5.24E+02	5.70E+03
P02144 MYG	HPGDFGADAQGAMNKA	529.57	74.01	2.63E+04	3.20E+03	4.35E+02	1.55E+03	4.35E+03	3.87E+02	2.58E+02	5.88E+02	1.91E+03	1.54E+03	1.44E+03	3.28E+03	3.57E+02	1.73E+03	4.24E+03
P22695 QCR2	TISQATAAGDVIK	637.85	74.13	1.67E+05	1.39E+04	1.29E+03	7.95E+02	4.16E+02	7.75E+02	2.48E+03	6.24E+02	7.54E+03	1.24E+04	2.29E+03	5.22E+02	2.14E+02	8.05E+03	9.46E+02
P02511 CRYAB	LGDVIEVHGK	533.80	74.28	5.23E+02	3.68E+04	8.99E+03	1.21E+05	3.86E+04	1.03E+05	6.43E+03	1.54E+03	1.85E+03	1.74E+03	1.96E+03	1.06E+05	6.35E+04	8.29E+02	4.93E+02
Q13813-3 SPTA2	LFGAAEVQR	495.77	74.32	3.46E+03	1.55E+05	4.36E+04	2.36E+05	1.45E+05	2.35E+05	1.30E+04	4.42E+04	1.29E+03	3.00E+03	1.85E+05	6.41E+03	1.00E+05	2.81E+03	2.05E+05
P15924 DESP																		

Q5VTT5 MYOM3	VGTSWQTVNNKPIQGTR	672.35	74.99	4.59E+03	1.51E+04	5.42E+02	2.30E+02	1.39E+03	7.31E+02	3.94E+02	7.20E+02	5.52E+02	2.78E+03	6.53E+04	2.52E+03	1.49E+03	9.41E+02	7.95E+04
P02144 MYG	HPGDFGADAQGAM	637.27	75.05	8.11E+05	3.34E+05	1.23E+04	5.28E+05	4.76E+03	1.00E+04	4.52E+03	6.43E+03	3.93E+02	3.18E+03	3.55E+05	1.30E+04	5.37E+04	9.66E+03	4.70E+05
P11142 HSP7C	EIAEAYLGK	497.27	75.1	7.93E+03	1.20E+03	2.33E+05	7.73E+02	1.85E+05	4.14E+03	9.08E+04	1.87E+05	3.06E+04	1.54E+03	9.99E+03	1.62E+05	7.00E+02	3.06E+04	8.59E+02
P02511 CRYAB	VLGDVIEVHGK	583.33	75.12	9.15E+05	1.32E+04	1.35E+05	1.24E+05	1.48E+04	1.23E+05	1.69E+04	3.16E+04	1.20E+06	7.41E+02	1.59E+06	1.09E+04	5.83E+03	1.25E+03	1.53E+06
Q13813-3 SPTA2	LIQNNHYAMEDVATR	592.29	75.15	8.18E+04	2.38E+03	1.85E+04	1.31E+03	6.24E+02	5.51E+04	1.05E+03	1.49E+03	4.00E+02	3.88E+03	3.71E+04	8.94E+02	8.54E+02	4.61E+03	5.99E+02
Q13813-3 SPTA2	SLQQLAEER	537.28	75.51	1.12E+04	2.97E+02	1.28E+05	1.28E+03	2.32E+05	3.05E+05	9.72E+04	2.21E+04	2.70E+04	2.77E+04	4.04E+04	9.99E+04	1.98E+04	8.33E+04	1.96E+03
P52179-2 MYOM1	PSDLAGPVVAETR	656.35	75.58	2.25E+03	1.05E+03	2.47E+04	4.72E+03	1.67E+03	2.84E+04	5.84E+03	1.22E+04	1.31E+03	9.42E+03	7.10E+02	3.10E+04	3.10E+03	2.15E+03	3.77E+02
P16615-2 AT2A2	KAEIGIAMSGTAVAK	501.95	75.6	7.08E+04	3.20E+03	5.32E+02	9.77E+03	2.35E+03	1.11E+03	5.97E+02	1.54E+04	3.54E+04	4.18E+03	4.42E+03	3.42E+03	1.47E+03	9.98E+03	5.11E+03
Q13423 NNTM	IGYTDLPSR	511.27	75.64	3.16E+05	3.03E+05	3.03E+05	3.56E+05	1.17E+05	2.90E+04	2.17E+03	1.30E+05	3.49E+05	4.15E+05	1.29E+03	2.05E+05	4.85E+03	3.85E+05	2.64E+05
P16615-2 AT2A2	WGSNELPAEEGK	658.81	75.71	5.69E+04	4.93E+04	1.19E+03	1.42E+03	1.35E+03	5.16E+03	9.00E+02	2.59E+02	1.49E+03	2.13E+03	1.90E+04	5.36E+04	1.41E+02	1.99E+04	2.72E+03
P52179-2 MYOM1	MAALES�K	431.74	75.86	3.17E+03	8.55E+03	1.42E+03	2.66E+03	8.33E+02	3.74E+03	3.04E+03	1.60E+03	8.89E+04	4.15E+04	2.51E+03	2.63E+03	1.29E+03	8.34E+03	5.26E+02
P02787 TRFE	KPVDEYKDCHLAQVPSHTV VAR	499.26	75.92	1.49E+03	2.44E+03	5.68E+05	9.65E+04	1.56E+05	4.24E+03	2.00E+04	4.96E+03	8.33E+02	3.09E+03	6.48E+02	1.59E+04	3.07E+03	1.33E+03	5.35E+03
P04406 G3P	GILGYTEH	445.22	76.09	4.24E+03	5.60E+03	5.43E+05	1.34E+06	2.90E+05	1.98E+06	1.56E+05	2.15E+03	7.19E+02	9.55E+02	1.69E+03	1.82E+05	3.75E+02	2.42E+04	7.33E+05
P02787 TRFE	DGAGDVAFVK	489.75	76.11	3.20E+02	1.61E+04	4.63E+04	8.57E+04	7.60E+04	1.96E+04	9.02E+04	9.21E+03	7.28E+02	2.26E+02	2.36E+04	6.57E+04	3.51E+04	7.22E+03	7.17E+04
P04406 G3P	VIISAPSAD	436.74	76.44	4.75E+02	8.18E+04	3.89E+02	7.07E+03	4.77E+03	1.67E+03	3.06E+03	8.44E+03	7.20E+03	5.31E+02	3.94E+03	1.68E+05	1.58E+05	1.63E+04	7.45E+02
P02144 MYG	GLSDGEWQ	446.19	76.55	1.22E+05	6.33E+02	3.49E+03	7.93E+03	1.15E+04	1.29E+04	5.07E+03	1.05E+03	5.16E+02	4.39E+02	8.31E+04	2.43E+03	1.20E+03	1.58E+02	7.66E+04
P48735 IDHP	VCVETVESGAMTK	677.32	76.64	2.07E+05	6.75E+03	1.03E+03	1.09E+04	7.81E+03	3.45E+03	4.11E+02	7.67E+02	2.14E+04	1.21E+04	1.10E+05	8.98E+03	5.62E+03	4.08E+03	1.97E+05
P16615-2 AT2A2	TITGSTYAPIGEVHK	525.28	76.76	4.65E+04	1.43E+05	3.77E+04	5.39E+04	8.19E+04	8.32E+04	5.19E+04	6.88E+03	1.75E+03	2.35E+03	2.15E+03	2.20E+05	1.38E+03	9.30E+02	1.17E+03
Q15149-3 PLEC1	LAAEQELIR	521.80	76.77	1.48E+03	9.63E+02	3.15E+02	1.50E+05	9.98E+04	1.52E+05	6.18E+04	2.46E+03	9.95E+04	1.06E+05	5.48E+03	8.01E+04	1.80E+04	7.49E+03	3.61E+03
P45379 TNNT2	QQXEINVLRL	430.91	76.81	1.00E+04	3.66E+02	2.96E+03	4.38E+03	1.18E+03	6.12E+04	6.90E+03	2.41E+03	1.22E+03	1.60E+04	7.08E+02	2.84E+04	1.73E+03	1.73E+02	7.19E+02
P15924 DESP	LEEELEGMR	553.27	76.81	1.11E+05	2.84E+03	3.08E+02	1.27E+03	3.08E+03	6.24E+04	1.62E+05	1.83E+05	1.52E+05	3.55E+02	7.66E+04	3.38E+03	6.79E+02	2.51E+03	1.50E+03
Q13813-3 SPTA2	DLTGVQNLRL	508.28	76.88	2.71E+05	4.45E+02	3.05E+03	3.24E+04	1.66E+05	9.54E+04	2.42E+04	5.81E+03	1.91E+03	5.33E+03	2.78E+05	1.99E+04	2.95E+04	9.95E+02	1.56E+05
P04075 ALDOA	QLLLTADDR	522.79	76.97	3.47E+04	1.21E+06	3.09E+05	1.91E+06	2.04E+06	2.83E+06	1.74E+06	3.41E+05	2.50E+03	4.61E+02	1.23E+03	8.96E+05	7.46E+05	1.20E+05	1.84E+06
Q02218 ODO1	IGGQESALPLR	570.82	77.03	4.84E+04	6.51E+03	7.78E+02	2.81E+04	3.58E+03	1.21E+04	5.89E+03	3.29E+02	2.08E+03	2.70E+02	1.03E+05	5.65E+03	2.65E+04	2.78E+02	1.47E+05
P15924 DESP	LQSLTENLTK	573.82	77.07	1.26E+05	4.82E+04	3.88E+03	1.74E+04	2.36E+03	4.47E+03	3.63E+02	6.47E+03	9.12E+02	1.09E+03	1.47E+03	5.93E+02	6.52E+02	1.16E+03	1.26E+05
Q15149-3 PLEC1	EQLQLLEEQRH	474.92	77.09	6.92E+02	4.32E+03	2.56E+04	9.96E+03	3.12E+04	6.68E+04	4.26E+02	2.81E+03	1.43E+04	1.71E+04	8.31E+02	4.31E+03	1.45E+04	1.99E+03	2.10E+03
Q13813-3 SPTA2	LIQEQHPPEELIK	535.95	77.19	1.76E+03	1.68E+03	1.76E+04	3.85E+03	2.13E+03	5.89E+04	2.06E+04	1.55E+03	8.98E+03	1.51E+04	2.77E+03	4.87E+02	5.33E+03	2.05E+04	2.02E+02
P98160 PGBM	IAHVELADAGQYR	481.58	77.25	1.10E+04	2.95E+03	4.43E+03	4.55E+03	1.58E+05	6.90E+03	6.16E+03	4.06E+03	1.36E+05	7.48E+04	1.65E+05	1.36E+05	9.08E+04	3.95E+04	2.06E+05
P48735 IDHP	PVVEMDGDDEMTR	689.80	77.38	1.77E+05	2.45E+03	1.01E+03	1.89E+04	4.58E+03	3.37E+02	2.28E+03	1.89E+03	1.23E+03	1.00E+03	5.81E+04	3.98E+03	2.42E+03	1.04E+03	7.25E+04
P16615-2 AT2A2	EFDELNPSAQR	653.31	77.43	7.05E+05	1.03E+03	1.89E+03	1.06E+04	2.13E+05	1.57E+04	9.08E+03	4.68E+03	1.40E+04	9.78E+03	4.54E+05	9.17E+03	1.55E+04	1.15E+03	5.17E+05
Q15149-3 PLEC1	GLLSAEVAR	458.26	77.45	1.75E+04	7.76E+02	3.73E+03	2.70E+03	1.08E+03	2.48E+03	1.08E+03	1.33E+03	1.13E+05	1.85E+04	2.75E+04	4.28E+04	3.09E+04	8.69E+04	3.84E+03
P18206-2 VINC	QVATALQNLQTK	657.87	77.63	2.52E+05	5.95E+02	1.17E+03	1.17E+04	1.02E+04	8.62E+03	8.62E+02	8.68E+02	1.05E+04	2.12E+05	2.56E+05	4.55E+03	3.27E+03	1.99E+03	2.40E+05
P18206-2 VINC	WIDNPTVDDR	615.79	77.7	1.16E+03	5.07E+03	4.39E+03	5.70E+04	4.03E+04	4.43E+03	9.89E+02	2.73E+03	1.67E+03	2.28E+03	7.89E+04	3.49E+03	4.15E+04	5.64E+02	8.42E+04
Q15149-3 PLEC1	GGAEGELQALR	550.79	78.08	4.97E+03	1.81E+04	3.19E+03	4.53E+03	6.00E+04	1.47E+03	3.16E+03	1.43E+03	8.76E+02	7.90E+02	6.10E+03	7.30E+04	3.60E+04	3.54E+03	7.56E+04
Q13813-3 SPTA2	IDGITIQAR	493.77	78.14	3.42E+04	5.23E+05	1.29E+05	2.60E+05	7.13E+04	4.54E+03	1.53E+05	3.48E+05	2.85E+02	2.91E+03	3.87E+04	3.44E+05	4.61E+05	1.75E+04	7.78E+04
P18206-2 VINC	TISPMVMDAK	546.77	78.19	4.45E+03	1.07E+05	1.53E+04	6.83E+04	1.28E+03	2.75E+04	1.72E+05	6.71E+03	9.58E+03	3.65E+03	1.35E+03	2.40E+05	7.31E+02	5.15E+02	3.87E+02
P06732 KCRM	FEEILTR	454.25	78.26	7.76E+06	6.80E+06	7.51E+06	1.24E+07	7.05E+06	7.25E+06	5.90E+06	9.11E+04	8.88E+03	1.98E+03	6.70E+06	9.25E+06	5.20E+06	7.39E+03	1.06E+07
P52179-2 MYOM1	EDEGLYTR	548.27	78.32	3.03E+03	1.70E+05	7.85E+03	1.47E+05	1.21E+03	5.97E+03	1.48E+05	1.69E+03	6.65E+03	2.03E+03	9.61E+02	2.08E+05	5.55E+02	2.28E+03	3.09E+03
P18206-2 VINC	MLVAGATSIAR	545.31	78.36	2.16E+05	1.05E+04	1.43E+03	1.74E+04	1.27E+05	3.51E+03	1.55E+04	4.04E+03	9.08E+02	3.17E+03	2.78E+05	1.83E+03	1.62E+04	2.50E+04	5.30E+04
P98160 PGBM	NELLHFER	529.27	78.38	6.26E+02	6.04E+03	1.11E+04	1.56E+05	1.23E+05	1.37E+04	6.67E+03	1.50E+03	5.59E+03	1.37E+03	4.21E+03	2.16E+03	1.25E+03	4.18E+03	1.49E+05
P04075 ALDOA	ADDGRFPQVIK	448.24	78.4	1.42E+03	3.58E+04	5.55E+03	1.04E+06	3.16E+05	4.74E+05	2.85E+04	2.43E+03	7.06E+02	2.05E+03	3.58E+05	1.28E+04	9.05E+03	1.96E+03	7.65E+05
P45379 TNNT2	EEEEVSLK	538.28	78.49	2.14E+03	1.03E+06	9.31E+02	1.78E+06	2.61E+03	2.02E+06	2.70E+05	2.89E+04	6.18E+04	7.14E+02	6.84E+02	4.93E+05	4.57E+03	1.25E+05	1.82E+06
P04075 ALDOA	GILAADESTGSIK	666.85	78.56	3.05E+04	4.05E+04	2.60E+03	8.73E+04	2.87E+03	2.33E+03	5.12E+04	3.38E+03	7.15E+03	2.53E+06	8.35E+04	1.31E+03	2.08E+04	1.53E+06	3.63E+04
P11142 HSP7C	FDDAVVQSDMK	627.79	78.64	3.08E+05	3.56E+03	1.58E+03	2.96E+05	1.18E+05	3.18E+02	3.77E+03	2.04E+03	6.73E+02	6.18E+02	2.91E+05	2.43E+03	1.62E+04	7.07E+02	1.78E+04
P02545-2 LMNA	NSNLVGAAHEELQSR	584.99	78.78	5.16E+03	1.19E+06	8.62E+05	8.84E+05	1.02E+06	1.70E+05	8.40E+05	1.16E+06	1.53E+03	5.40E+02	3.86E+02	1.06E+06	5.79E+03	6.31E+02	5.65E+05
Q13813-3 SPTA2	SSEIEAFAFR	577.76	78.85	2.09E+05	2.08E+05	1.23E+04	6.09E+05	1.61E+05	1.02E+05	1.10E+05	5.21E+04	3.40E+02	1.00E+03	1.27E+05	1.60E+05	1.01E+05	1.51E+03	3.36E+05
Q5VTT5 MYOM3	IGALSATPLK	485.80	78.92	1.37E+05	1.04E+04	8.20E+03	6.58E+03	1.68E+05	6.42E+03	4.52E+03	3.93E+04	7.52E+02	7.21E+02	1.40E+05	6.26E+03	1.18E+05	1.60E+02	1.80E+02
P04075 ALDOA	YTPSQAGAAASESL	705.33	78.93	1.24E+04	2.69E+04	6.14E+03	5.94E+03	7.07E+03	8.36E+04	8.46E+03	6.89E+03	9.61E+02	2.87E+03	2.37E+04	1.34E+03	1.83E+03	7.64E+02	1.28E+04
P18206-2 VINC	NPNGQAAYEHFETMK	579.60	79	5.26E+02	5.19E+02	1.52E+03	8.08E+02	4.95E+03	1.28E+05	6.37E+03	3.22E+03	4.66E+02	2.04E+02	9.78E+02	5.02E+02	5.47E+02	7.65E+02	2.74E+03
P00505 AATM	QWLQEVK	465.76	79.15	1.43E+05	1.43E+03	1.68E+03	2.09E+03	1.71E+03	9.87E+03	1.10E+05	1.30E+03	3.99E+02	2.62E+02	2.73E+05	3.29E+04	5.01E+04	1.19E+03	3.92E+03
P04																		



P15924 DESP	ISITEGIER	509.28	80.5	1.31E+03	1.34E+04	3.45E+05	3.44E+05	1.76E+05	3.15E+05	1.64E+05	8.89E+03	1.72E+03	3.53E+03	2.25E+05	2.23E+05	2.90E+03	9.58E+02	2.56E+05
Q13423 NNTM	MATQASTLYSNNITK	821.91	80.75	1.59E+05	1.87E+03	6.05E+03	6.10E+04	5.61E+03	6.44E+02	3.02E+02	4.74E+03	8.49E+02	1.58E+03	9.05E+04	2.71E+03	3.35E+04	2.33E+03	8.13E+02
P00505 AATM	DDNGKPYVLPVSR	487.26	80.79	3.35E+05	3.10E+03	3.10E+04	7.30E+03	8.03E+03	6.87E+03	1.08E+04	1.07E+03	1.03E+03	1.27E+03	3.65E+05	7.57E+03	4.72E+04	4.87E+02	1.11E+03
Q5VTT5 MYOM3	YTLEIAAGK	483.27	80.84	5.27E+02	4.57E+04	2.93E+03	1.24E+05	9.60E+03	7.84E+04	1.04E+04	4.36E+03	1.03E+03	5.10E+03	8.27E+02	9.67E+04	3.22E+04	6.57E+03	3.91E+04
P02144 MYG	DMASNYKEL	535.74	80.94	9.94E+04	1.35E+03	2.06E+04	6.10E+03	3.71E+03	8.78E+03	9.53E+03	1.80E+03	2.98E+02	1.88E+03	7.51E+03	9.21E+02	1.80E+03	4.94E+02	6.21E+03
P02787 TRFE	HSTIFENLANK	637.33	80.96	9.47E+04	1.28E+03	1.04E+03	1.00E+05	6.11E+04	8.69E+03	3.02E+03	1.12E+04	1.04E+05	2.13E+05	1.78E+05	6.52E+03	2.35E+04	7.25E+03	8.32E+04
P00505 AATM	MNLGVGAYR	490.75	81.01	2.91E+03	5.25E+05	3.79E+04	8.51E+05	8.39E+05	1.09E+06	2.26E+04	1.04E+04	2.79E+03	1.54E+03	5.25E+03	4.88E+05	1.46E+05	1.13E+03	6.68E+05
P98160 PGBM	LYQASPADSGEYVCR	829.88	81.22	2.52E+04	1.05E+03	3.60E+03	2.61E+04	1.09E+04	5.55E+03	1.41E+03	1.10E+03	2.40E+05	3.77E+04	3.81E+04	2.78E+02	3.12E+03	1.47E+05	6.48E+04
P00505 AATM	IGASFLQR	446.26	81.26	2.62E+02	1.38E+06	9.50E+04	1.78E+06	2.15E+06	1.53E+06	1.71E+06	1.54E+05	1.06E+03	5.61E+02	2.05E+03	1.72E+06	1.18E+06	9.32E+02	1.76E+06
P16615-2 AT2A2	NAENAIEALK	536.78	81.26	4.22E+05	2.39E+05	1.55E+03	4.27E+05	3.88E+05	5.21E+05	2.21E+04	8.04E+04	7.02E+02	9.70E+02	3.44E+03	2.09E+05	6.13E+02	3.15E+03	5.10E+05
P02545-2 LMNA	VAVEEVDEEGKFVR	535.94	81.32	6.49E+03	7.04E+02	4.58E+02	1.92E+03	1.29E+05	1.54E+03	2.09E+03	9.55E+02	1.46E+03	3.00E+03	5.22E+03	7.60E+02	9.20E+03	3.87E+03	1.59E+03
Q13813-3 SPTA2	EELYQNLTR	583.30	81.32	7.84E+02	2.71E+04	6.98E+03	9.61E+04	3.21E+03	2.31E+03	1.01E+03	1.81E+04	1.20E+04	3.67E+03	8.60E+04	3.34E+04	2.52E+04	1.55E+04	7.55E+04
Q13813-3 SPTA2	DEDSAEALLK	545.77	81.36	8.56E+02	6.82E+04	1.67E+03	1.25E+05	2.73E+04	1.18E+05	8.89E+02	3.09E+04	1.18E+04	3.39E+02	6.62E+02	2.33E+04	2.23E+03	9.91E+02	4.91E+04
P18206-2 VINC	SFLDSGYR	472.73	81.47	8.17E+02	1.62E+05	1.28E+04	2.70E+05	1.49E+05	3.03E+05	8.48E+03	4.87E+03	1.17E+03	6.06E+02	5.40E+02	1.96E+05	4.75E+02	5.07E+03	2.25E+05
Q13423 NNTM	APMVNPTLVGH	568.30	81.57	6.91E+04	5.83E+04	3.02E+04	1.31E+03	1.56E+03	6.09E+04	5.78E+04	2.79E+04	5.01E+04	1.89E+03	5.67E+04	3.54E+04	5.98E+02	6.78E+03	8.21E+04
P02787 TRFE	YLGEYVK	500.75	81.59	9.67E+03	3.55E+05	4.50E+05	2.12E+03	3.49E+02	6.46E+05	2.91E+05	1.53E+03	9.06E+02	5.80E+02	3.55E+03	2.37E+05	4.17E+02	5.23E+03	7.39E+02
P98160 PGBM	SIEYSPQLEDAGSR	776.37	82	1.17E+05	7.06E+02	3.29E+03	1.35E+05	7.25E+03	9.64E+02	1.26E+03	4.67E+02	1.25E+04	5.94E+03	4.53E+04	1.43E+03	1.15E+04	6.93E+02	1.13E+05
P52179-2 MYOM1	VSEPVAALDPAEK	663.35	82.08	1.21E+03	6.05E+05	7.09E+02	7.96E+05	3.07E+04	2.88E+04	7.48E+03	8.94E+02	7.21E+03	4.93E+03	5.90E+05	7.73E+03	4.04E+05	3.02E+03	5.89E+05
P18206-2 VINC	ETVQTTEQILK	702.86	82.1	2.20E+05	1.91E+04	1.30E+04	2.43E+05	1.48E+04	4.53E+03	3.69E+02	6.82E+03	6.32E+02	3.15E+02	2.10E+05	3.76E+03	3.40E+03	5.06E+02	2.43E+05
P48735 IDHP	SCFYAIQK	544.27	82.11	5.06E+04	4.05E+03	4.89E+04	3.90E+03	9.77E+03	2.61E+03	3.09E+03	9.70E+03	4.53E+04	2.28E+04	1.74E+04	1.83E+03	5.96E+03	2.54E+03	4.35E+03
P11142 HSP7C	SQHIDIVLVGGSTR	494.61	82.18	3.35E+05	2.72E+03	4.90E+04	4.89E+03	2.05E+04	1.03E+04	5.93E+03	3.29E+02	8.74E+02	3.13E+05	5.22E+03	1.04E+04	3.03E+03	7.12E+03	5.22E+03
P18206-2 VINC	LLAVAATAPPDAPNR	738.91	82.23	3.27E+05	5.85E+03	1.04E+04	4.16E+05	9.40E+03	8.97E+03	1.18E+03	3.37E+03	4.26E+03	1.14E+03	4.30E+05	1.13E+04	7.16E+04	1.30E+03	2.94E+05
Q13423 NNTM	IYPAQNPELLNK	700.38	82.29	1.45E+05	3.02E+03	6.84E+02	2.01E+05	1.02E+05	3.63E+03	3.30E+03	1.07E+04	8.61E+03	5.04E+04	7.76E+03	2.41E+05	5.57E+03	1.30E+04	1.29E+05
P45379 TNNT2	KVLAIDLHNLNEDQLR	555.31	82.32	3.33E+03	1.32E+03	1.02E+03	6.62E+03	3.75E+05	8.21E+04	8.62E+03	2.87E+03	8.74E+03	7.98E+04	2.65E+03	1.03E+05	1.20E+04	3.90E+03	7.92E+03
P45379 TNNT2	IPDGERVDFDDIHR	421.71	82.35	2.90E+04	7.03E+02	4.13E+03	1.63E+04	4.45E+05	8.64E+03	3.87E+04	3.92E+04	9.20E+03	1.14E+03	1.45E+02	4.83E+04	6.93E+02	2.46E+04	1.21E+04
P06732 KCRM	FDPIISDR	481.75	82.37	7.97E+02	4.26E+02	4.72E+03	4.40E+03	7.98E+04	9.12E+02	1.10E+03	6.57E+04	1.16E+04	2.10E+03	4.60E+02	2.90E+03	3.01E+03	8.52E+02	1.36E+05
P16615-2 AT2A2	LDFEGEQLSK	583.29	82.67	3.20E+04	6.93E+02	2.32E+03	4.28E+03	5.84E+02	2.19E+03	3.21E+03	5.48E+02	5.91E+04	5.98E+04	1.11E+04	6.47E+02	6.04E+02	3.46E+02	2.48E+04
Q5VTT5 MYOM3	VSDLHEGHFYEFR	545.93	82.68	2.41E+03	3.13E+03	3.62E+03	7.77E+04	4.49E+04	6.43E+04	4.50E+03	9.43E+02	2.21E+03	2.01E+02	2.90E+03	5.78E+03	2.44E+02	1.33E+02	7.27E+04
P18206-2 VINC	IPTISTQLK	500.79	82.7	2.35E+03	4.25E+06	3.01E+05	3.95E+06	3.40E+06	3.06E+06	3.56E+06	2.91E+05	4.11E+04	3.09E+03	2.68E+06	4.38E+06	3.71E+06	2.75E+04	3.34E+06
Q99798 ACON	LEAPDADELPK	599.30	82.71	9.41E+05	3.00E+03	2.82E+03	2.21E+06	1.35E+06	2.23E+03	3.66E+03	1.09E+03	2.80E+03	3.05E+03	1.27E+06	8.89E+05	8.18E+05	1.51E+03	1.44E+06
P22695 QCR2	YEDFSNLGTTH	642.28	82.83	3.41E+03	7.12E+04	6.69E+03	7.80E+03	3.01E+03	1.08E+05	7.33E+03	4.17E+03	8.02E+02	1.98E+02	5.76E+02	3.18E+04	3.73E+03	2.01E+03	9.01E+03
P52179-2 MYOM1	VNYIFNEK	513.77	82.92	1.06E+05	5.61E+03	3.21E+02	2.76E+03	2.43E+02	2.68E+03	6.65E+02	7.82E+02	7.46E+02	7.02E+02	1.33E+05	3.03E+03	2.95E+04	8.18E+03	4.25E+03
Q15149-3 PLEC1	DSELGSVR	488.26	82.96	8.68E+03	9.07E+04	5.28E+03	1.65E+05	6.29E+04	6.45E+04	1.91E+03	2.28E+03	8.13E+04	6.40E+02	8.33E+03	1.61E+05	1.05E+05	8.27E+04	1.34E+05
P04406 G3P	VVDLMAHMASKE	665.83	83	5.06E+02	2.98E+04	1.04E+05	8.61E+03	1.54E+03	2.58E+04	1.93E+05	6.60E+03	1.98E+05	1.09E+05	1.29E+03	1.07E+04	4.61E+02	1.31E+05	5.31E+03
Q13423 NNTM	GITHIGYTDLPSR	477.25	83.22	1.83E+03	3.17E+03	1.04E+04	1.51E+04	3.20E+05	7.21E+02	1.29E+05	2.27E+04	8.26E+04	1.23E+03	2.04E+05	8.31E+03	1.13E+05	3.90E+03	4.58E+05
P15924 DESP	GIVDSITGQR	523.28	83.34	7.82E+03	1.43E+05	1.47E+04	2.43E+05	1.74E+05	2.58E+05	9.73E+04	1.64E+03	4.06E+04	5.90E+02	2.28E+03	1.27E+05	9.72E+04	3.85E+04	1.20E+03
P04075 ALDOA	AIMENANVLAR	601.32	83.58	2.33E+05	2.19E+03	2.66E+02	1.33E+04	2.40E+04	1.27E+03	1.10E+03	2.47E+03	1.86E+05	3.21E+02	1.51E+05	5.63E+02	4.15E+02	4.77E+05	5.63E+03
Q5VTT5 MYOM3	EDEGLVMVR	556.26	83.66	5.92E+04	4.15E+03	9.96E+03	1.86E+03	3.45E+03	1.08E+03	1.57E+03	8.27E+03	4.66E+02	1.40E+03	4.73E+04	3.32E+03	7.65E+02	8.99E+02	1.11E+03
P06732 KCRM	LNKPEEYDLSK	575.62	83.68	1.39E+06	1.69E+03	1.26E+04	2.19E+04	4.07E+03	1.90E+04	1.36E+03	1.23E+04	1.05E+03	5.89E+02	6.75E+05	1.00E+04	2.45E+05	7.95E+02	1.46E+04
P52179-2 MYOM1	EGVSYVFR	478.75	83.74	5.25E+02	1.34E+05	2.77E+04	8.29E+04	3.56E+05	4.10E+04	8.52E+03	1.66E+05	7.30E+05	2.07E+05	1.82E+05	1.90E+05	1.97E+05	4.03E+05	2.49E+05
P04075 ALDOA	PYQYPALTPEQK	717.87	83.91	1.27E+05	1.88E+04	2.98E+03	1.15E+04	9.20E+03	7.77E+03	3.89E+03	8.26E+02	2.43E+03	1.81E+04	1.66E+04	1.63E+04	1.27E+04	1.38E+03	5.99E+04
P15924 DESP	LGIYEAMK	462.75	83.93	8.60E+04	4.17E+03	1.83E+03	5.26E+03	1.28E+03	1.76E+03	3.29E+03	7.59E+03	2.15E+05	2.02E+05	1.15E+05	1.91E+04	5.97E+04	1.36E+05	5.50E+03
Q13423 NNTM	FFTGGQITAAGK	570.80	83.97	2.68E+05	2.35E+05	6.33E+02	1.37E+05	3.85E+05	2.99E+03	5.39E+05	2.61E+04	1.04E+03	1.38E+03	1.26E+05	2.38E+05	8.88E+04	7.46E+02	9.18E+04
Q5VTT5 MYOM3	TEIAFLQTHR	405.89	84.25	9.69E+02	1.07E+05	3.06E+03	1.62E+05	2.04E+03	1.35E+05	1.39E+05	1.09E+03	6.70E+02	6.12E+02	4.19E+03	1.56E+05	7.14E+02	2.15E+02	2.52E+03
Q99798 ACON	ATIERDGYAQILR	502.61	84.26	1.05E+04	8.08E+02	7.02E+02	2.69E+03	2.64E+04	1.47E+04	9.07E+04	2.08E+03	1.32E+03	2.85E+03	1.13E+04	5.28E+04	2.76E+03	1.26E+03	1.19E+03
Q02218 ODO1	KPLIIFTPK	528.84	84.42	3.52E+02	1.03E+05	1.36E+04	9.11E+04	2.72E+03	1.22E+05	1.78E+05	2.07E+03	3.79E+02	3.81E+02	1.90E+03	8.98E+04	1.60E+03	9.28E+02	6.30E+02
P45379 TNNT2	VLAIDLHNLNEDQLREK	598.33	84.44	3.27E+02	2.56E+04	1.10E+04	2.30E+04	3.13E+03	7.72E+04	3.30E+03	2.11E+03	9.81E+04	9.35E+04	1.77E+03	1.40E+04	2.97E+03	4.33E+04	6.82E+03
P02511 CRYAB	RPFPPHSPSR	458.91	84.67	1.93E+04	1.10E+03	1.03E+03	8.47E+02	9.65E+03	5.32E+03	2.83E+03	1.81E+04	1.13E+06	9.62E+03	5.17E+04	2.18E+03	3.17E+04	1.33E+06	3.53E+03
P18206-2 VINC	MLVNSMNTVK	618.33	84.74	1.47E+03	2.89E+03	1.06E+03	7.29E+03	9.68E+04	2.95E+03	5.59E+04	2.48E+04	2.17E+04	2.12E+04	1.45E+03	4.61E+03	6.84E+02	2.38E+03	7.66E+04
P15924 DESP	QLQNIQATSR	636.35	84.96	4.12E+03	2.09E+03	5.16E+03	7.84E+02	2.63E+03	7.99E+02	6.38E+02	1.80E+03	6.49E+04	1.07E+05	5.15E+03	5.41E+02	5.83E+03	3.72E+04	3.80E+03
Q99798 ACON	FNPETDYLTGTDGKK	562.61	85.11</															

Q15149-3 PLEC1	AQAEAQQPTFDALR	773.39	85.81	1.93E+03	2.85E+05	1.28E+04	8.55E+04	1.29E+04	1.61E+04	1.90E+05	3.49E+05	9.99E+03	3.19E+04	2.12E+03	3.15E+05	1.13E+03	2.90E+03	3.57E+04
P06732 KCRM	GQSIDDMPAQK	651.82	85.81	4.61E+04	5.53E+05	2.46E+02	1.80E+06	6.17E+05	6.87E+05	2.51E+03	4.22E+03	4.07E+02	2.61E+03	3.02E+04	3.25E+05	3.56E+04	6.50E+03	1.35E+05
P15924 DESP	LPVDIAYK	459.77	85.83	1.65E+04	7.53E+03	4.18E+03	3.10E+05	9.74E+03	4.09E+03	2.61E+04	8.62E+03	2.57E+03	3.79E+03	2.44E+05	2.35E+04	9.60E+04	1.91E+05	7.69E+04
P16615-2 AT2A2	AEIGIAMGSGTAVAK	688.36	86.16	7.00E+04	3.35E+04	7.38E+02	2.22E+05	1.96E+04	1.85E+04	3.72E+03	2.42E+03	5.67E+03	3.41E+03	4.39E+04	6.55E+03	1.53E+04	3.01E+05	5.46E+04
Q99798 ACON	LTGSLGWSSPK	610.32	86.4	3.40E+05	3.94E+03	7.81E+02	3.02E+03	7.47E+02	1.23E+03	1.33E+03	1.15E+03	1.56E+03	9.14E+03	1.06E+04	3.88E+03	7.81E+03	3.78E+02	5.31E+03
Q02218 ODO1	FEEFLQR	484.75	86.42	3.94E+05	9.86E+04	1.53E+03	5.50E+04	5.17E+04	1.46E+04	1.35E+04	1.53E+03	3.13E+03	8.20E+02	2.76E+05	1.04E+04	2.02E+05	2.45E+02	6.07E+04
Q99798 ACON	IVYGHLDDEPASQEIER	614.64	86.49	1.19E+06	1.26E+03	1.26E+04	1.03E+06	1.41E+06	4.79E+04	4.49E+03	4.60E+03	1.57E+03	4.81E+02	8.04E+05	4.32E+04	2.29E+05	1.92E+03	1.06E+06
P98160 PGBM	TPSGLYLGTCTER	648.82	86.64	7.07E+04	1.33E+04	6.78E+02	8.03E+03	1.06E+04	1.33E+04	8.60E+02	3.16E+03	2.33E+03	6.87E+02	7.37E+04	7.46E+03	5.39E+04	1.64E+03	9.30E+04
P02144 MYG	ADIPGHGQEVLR	702.88	86.68	1.26E+05	1.04E+03	3.18E+03	3.36E+04	5.36E+02	3.49E+03	4.85E+02	1.38E+03	1.44E+04	7.50E+03	9.76E+04	1.49E+04	8.35E+04	1.11E+03	3.87E+03
P02545-2 LMNA	TALINSTGEEVAMR	746.38	86.75	2.65E+02	1.58E+03	2.19E+03	1.76E+05	1.74E+04	1.26E+04	2.52E+03	7.12E+03	3.87E+03	2.64E+03	1.18E+05	5.07E+03	1.57E+05	1.84E+03	1.33E+05
Q5VTT5 MYOM3	VGFGNDWER	540.25	86.87	6.08E+02	1.40E+03	6.01E+03	2.17E+05	1.95E+04	2.69E+03	9.05E+02	9.81E+02	2.25E+03	1.42E+03	1.95E+05	2.45E+03	1.23E+05	8.13E+02	2.12E+05
P02144 MYG	VEADIPGHGQEVLR	544.96	86.87	8.87E+06	1.62E+04	3.36E+03	6.05E+04	3.21E+04	2.68E+04	2.04E+03	1.49E+03	1.57E+03	2.36E+03	6.85E+06	1.79E+04	6.68E+04	5.79E+02	1.21E+07
P06732 KCRM	VLTLLEYKK	553.84	87.04	1.25E+02	3.78E+04	1.02E+04	6.54E+04	1.09E+05	8.92E+04	3.72E+04	1.72E+03	1.14E+03	5.06E+02	1.95E+03	5.50E+03	4.35E+02	5.13E+02	1.00E+05
P98160 PGBM	LVSEDPINDGEWHR	556.26	87.09	7.81E+02	2.54E+03	3.85E+03	4.97E+04	9.58E+02	3.78E+03	5.38E+02	1.26E+05	7.13E+02	1.65E+03	1.53E+04	2.34E+03	2.80E+04	1.97E+03	6.04E+04
P98160 PGBM	LGTVPQFPR	507.78	87.16	7.65E+03	7.27E+04	9.35E+03	2.69E+04	1.00E+04	8.96E+04	8.19E+03	2.42E+03	1.00E+05	3.37E+04	3.41E+03	6.02E+03	2.81E+03	1.73E+04	7.86E+03
P02545-2 LMNA	SNEDQSMGNWQIK	768.84	87.24	2.06E+03	9.31E+03	4.26E+04	7.59E+02	9.78E+02	6.99E+04	1.34E+04	4.67E+03	1.70E+02	1.32E+03	2.55E+03	6.17E+03	6.12E+02	9.30E+02	1.49E+03
P02787 TRFE	SVIPSDGSPVACVK	679.85	87.28	9.44E+04	1.55E+03	2.29E+04	3.08E+05	2.83E+05	2.81E+04	6.26E+03	4.46E+03	1.60E+03	2.19E+03	2.50E+05	1.81E+05	1.04E+05	1.29E+04	1.35E+05
P15924 DESP	NATILELR	465.27	87.32	1.22E+03	5.77E+04	2.30E+03	1.81E+05	3.79E+04	2.10E+05	8.96E+03	3.23E+04	5.37E+03	2.90E+03	4.24E+03	8.00E+03	3.76E+03	4.92E+03	6.74E+03
P15924 DESP	TGSQYDIQDAIDK	727.34	87.4	1.22E+03	3.17E+03	1.48E+03	5.04E+04	3.06E+04	1.42E+04	9.47E+04	5.52E+03	2.06E+03	7.24E+02	3.66E+04	1.69E+04	1.34E+04	9.62E+02	1.13E+05
P52179-2 MYOM1	MGIGFPSR	432.72	87.42	3.18E+03	5.10E+03	5.72E+03	8.36E+03	7.16E+02	1.50E+04	1.27E+04	1.02E+04	2.84E+05	2.78E+05	3.26E+03	1.63E+04	8.67E+02	3.33E+05	1.06E+04
Q15149-3 PLEC1	NLVDNITGQR	565.30	87.72	5.54E+04	4.74E+04	7.11E+04	6.13E+03	4.13E+02	3.79E+04	1.16E+05	6.82E+04	2.79E+03	2.50E+03	8.59E+04	7.05E+04	3.23E+03	2.62E+03	7.59E+02
P00505 AATM	VGADTMVCK	478.24	87.81	2.46E+05	1.98E+05	7.18E+02	1.91E+05	4.11E+05	1.47E+05	5.79E+02	1.47E+04	4.59E+02	3.75E+03	1.18E+03	3.15E+03	6.14E+02	6.78E+02	2.11E+05
P18206-2 VINC	ALASQLQDSLK	587.31	88.07	2.76E+06	1.80E+04	7.51E+03	3.51E+06	1.04E+07	9.56E+03	4.16E+04	8.75E+04	3.53E+03	2.92E+03	4.59E+06	8.34E+04	5.03E+06	1.03E+03	3.59E+06
P45379 TNNT2	YEINVLK	453.75	88.18	7.56E+06	4.46E+04	1.50E+04	1.32E+05	6.26E+04	1.55E+05	3.27E+03	2.55E+03	1.23E+03	4.21E+02	6.98E+06	6.18E+04	2.12E+04	1.40E+03	1.15E+05
P18206-2 VINC	SLLDASEEAIKK	435.24	88.32	6.41E+04	1.15E+03	2.48E+03	1.79E+03	1.74E+03	1.01E+03	5.13E+03	6.57E+02	9.05E+04	7.62E+04	5.46E+04	2.46E+03	1.92E+03	4.13E+04	1.03E+03
P17540 KCRS	ITQGQVDEHYVLLSR	593.96	88.33	1.59E+06	1.10E+04	1.59E+04	1.53E+06	1.67E+04	1.38E+05	6.19E+03	2.21E+03	1.10E+03	9.24E+02	1.03E+06	8.78E+02	1.55E+05	1.03E+03	6.73E+04
P02511 CRYAB	VLGDVIEVH	490.77	88.51	1.83E+03	1.35E+06	1.48E+06	1.95E+06	1.35E+05	1.55E+06	2.21E+05	1.02E+04	1.36E+03	1.11E+03	3.72E+03	6.19E+05	5.93E+02	6.19E+02	7.31E+02
P04406 G3P	VSVVDLTCR	496.26	88.64	3.44E+04	9.25E+05	4.52E+05	6.39E+04	2.18E+05	1.12E+06	8.34E+03	2.00E+04	6.01E+03	1.09E+03	7.74E+04	3.67E+05	4.55E+04	6.30E+03	6.51E+04
P02787 TRFE	EFQLFSSPHGK	638.82	88.7	4.90E+04	1.35E+03	8.95E+02	6.03E+04	9.22E+04	9.75E+03	1.98E+03	4.53E+03	8.99E+03	2.94E+03	2.42E+03	7.02E+03	2.67E+03	9.83E+02	8.26E+02
Q15149-3 PLEC1	AQVEQELTLR	644.35	88.7	2.79E+04	8.65E+02	4.47E+03	1.41E+04	4.51E+03	6.15E+03	4.75E+02	8.91E+02	2.84E+04	4.21E+03	1.63E+03	1.63E+03	1.42E+03	8.04E+04	1.22E+04
Q99798 ACON	SQFTITPGSEQIR	732.38	88.74	8.48E+05	9.42E+04	5.82E+04	6.32E+05	1.62E+04	2.39E+03	3.74E+03	1.10E+03	1.00E+03	1.75E+03	4.33E+05	3.05E+03	1.02E+05	1.34E+03	6.11E+05
Q13423 NNTM	TTVLAMDQVPR	615.83	88.97	3.98E+05	1.24E+03	1.83E+03	3.79E+05	1.66E+04	1.10E+04	2.72E+03	1.89E+03	8.32E+02	1.89E+03	2.95E+05	2.27E+03	1.05E+05	1.07E+03	4.12E+05
Q15149-3 PLEC1	EGLTSIEEVTCK	603.31	89.07	6.74E+04	3.36E+03	5.96E+02	1.73E+03	1.17E+03	1.41E+03	9.48E+03	3.27E+03	8.36E+03	1.32E+05	1.13E+03	3.29E+03	3.24E+03	4.98E+04	5.94E+02
P15924 DESP	LNDLQATEQR	694.36	89.28	4.04E+04	3.23E+04	6.49E+03	1.42E+03	9.20E+02	7.66E+03	1.36E+03	1.29E+04	1.15E+04	3.00E+04	8.29E+03	1.05E+03	1.55E+03	2.49E+04	1.49E+03
P98160 PGBM	GSIQVDGEELVSGR	723.36	89.44	2.00E+03	8.57E+02	3.55E+03	2.27E+04	2.33E+03	1.58E+03	1.22E+03	7.56E+02	1.32E+02	7.44E+02	2.95E+03	2.18E+02	3.99E+04	2.69E+03	1.29E+04
Q99798 ACON	DGYAQILR	468.25	89.45	7.70E+05	6.36E+03	1.71E+03	6.75E+05	8.89E+02	9.88E+02	6.60E+02	7.08E+03	1.40E+03	3.58E+03	4.12E+05	4.35E+02	2.94E+05	1.04E+03	5.06E+05
P02144 MYG	VEADIPGHGQEVLR	682.35	89.55	7.48E+06	5.35E+03	3.04E+03	3.63E+06	3.21E+06	1.44E+04	3.85E+03	8.18E+03	1.99E+03	1.70E+03	3.10E+06	3.61E+04	3.83E+05	6.95E+02	4.71E+06
Q13423 NNTM	VEASDLVVK	536.81	89.76	2.75E+05	1.04E+04	8.06E+02	1.14E+04	9.54E+03	2.50E+04	1.24E+03	5.41E+02	2.00E+03	8.98E+03	3.05E+05	2.28E+04	1.21E+04	3.48E+03	1.14E+04
P00505 AATM	IAAALNTPDLRK	465.95	89.79	1.17E+03	2.80E+03	2.82E+03	3.32E+03	4.06E+03	6.49E+02	4.88E+03	2.38E+03	1.11E+05	5.75E+04	1.64E+03	2.45E+03	7.46E+03	5.23E+04	1.36E+03
P52179-2 MYOM1	FDVSFGR	414.21	89.89	1.07E+04	1.76E+05	4.52E+02	2.88E+05	2.92E+03	8.53E+03	4.66E+02	3.62E+02	5.86E+03	4.26E+02	1.07E+04	1.51E+03	9.56E+04	1.25E+03	1.59E+05
Q15149-3 PLEC1	TPVEVPVGGFK	565.31	89.91	9.86E+02	3.93E+03	2.28E+04	8.74E+04	2.05E+03	1.09E+03	1.78E+03	8.74E+03	2.52E+03	4.98E+03	7.07E+04	3.16E+03	5.92E+04	8.83E+03	2.24E+02
P04075 ALDOA	IVAPGKGLADESTGSIK	633.36	89.91	4.93E+04	4.38E+02	5.04E+04	1.34E+03	6.01E+02	6.66E+04	1.65E+04	3.63E+02	8.86E+03	1.87E+03	1.38E+03	2.31E+03	9.50E+02	1.01E+03	1.92E+03
Q15149-3 PLEC1	WQAVLAQTDVDR	643.84	90.18	3.54E+03	2.64E+04	4.63E+04	5.51E+04	4.65E+04	1.15E+05	2.71E+04	1.67E+03	1.15E+03	1.01E+03	1.21E+03	2.44E+04	1.44E+03	2.31E+03	5.00E+04
P02787 TRFE	IECVSAETTEDCIAK	806.36	90.28	7.20E+03	3.25E+03	1.05E+04	1.05E+03	3.82E+02	3.22E+03	1.04E+03	1.36E+04	3.11E+04	4.51E+04	5.60E+02	2.04E+03	6.60E+02	4.04E+03	3.80E+02
P98160 PGBM	LPQVSPADSGEYVCR	810.89	90.35	1.41E+03	1.29E+04	9.42E+04	3.65E+02	3.62E+03	4.37E+04	6.35E+04	1.53E+04	8.14E+03	1.07E+03	6.57E+02	1.10E+04	1.21E+03	5.68E+03	2.04E+03
P22695 QCR2	SMAASGNLGHPTF	645.30	90.42	4.93E+04	1.83E+03	1.00E+04	3.46E+03	3.61E+02	5.65E+02	3.26E+03	1.53E+03	5.71E+03	2.72E+02	9.23E+02	7.88E+03	5.36E+02	9.84E+03	3.40E+03
P22695 QCR2	ATAAGDVIKAAYNQVKIA QGNLSNTDVQAAK	806.42	90.53	2.39E+02	7.14E+03	1.06E+05	5.12E+03	1.38E+04	5.33E+04	2.50E+05	3.59E+04	2.29E+05	9.56E+04	4.97E+02	3.01E+03	1.23E+03	2.45E+04	6.76E+03
P18206-2 VINC	LANVMMGPYR	576.29	90.55	1.87E+05	2.77E+03	5.95E+02	4.72E+03	1.13E+03	3.14E+03	6.23E+03	4.56E+04	5.14E+04	1.51E+04	2.12E+05	7.56E+02	4.12E+04	1.81E+03	2.40E+02
Q15149-3 PLEC1	MGIVGPEFK	489.26	90.58	4.09E+03	1.09E+05	9.61E+03	8.33E+04	7.80E+04	1.24E+05	5.55E+03	4.39E+03	4.43E+03	3.63E+03	1.05E+03	1.34E+04	3.21E+03	4.83E+03	8.80E+04
P02545-2 LMNA	LADALQELR	514.79	90.6	3.88E+05	1.59E+04	3.79E+04	1.38E+03	1.15E+03	1.29E+04	3.61E+02	1.57E+04	3.89E+05	3.33E+05	1.21E+05	2.38E+03	6.31E+04	2.84E+05	9.46E+04



P11142 HSP7C	NQVAMNPTNTVFDK	825.40	91.96	1.91E+05	3.95E+03	9.71E+02	1.08E+04	3.05E+04	2.59E+03	2.57E+02	5.39E+03	2.03E+03	1.51E+03	2.18E+05	7.55E+03	5.96E+03	9.76E+02	4.31E+03
P17540 KCRS	LFPPSADYPDLRK	506.94	92.02	2.58E+02	8.20E+03	2.96E+04	7.60E+03	4.22E+04	2.13E+04	1.35E+04	4.03E+03	8.64E+03	5.89E+02	1.89E+04	3.51E+04	9.46E+03	4.40E+02	1.63E+04
P18206-2 VINC	MTGLVDEAIDTK	646.82	92.04	6.23E+02	1.80E+04	2.57E+04	1.58E+04	4.41E+03	1.30E+04	1.11E+04	9.00E+03	2.23E+03	5.06E+04	2.84E+05	1.78E+04	2.31E+05	1.61E+04	2.39E+05
O75112 LDB3	DPALDTNGSLVAPSPPEAR	665.33	92.12	1.63E+04	1.36E+05	1.84E+05	1.88E+03	4.15E+03	5.43E+05	1.50E+05	2.49E+05	1.55E+04	1.45E+04	6.12E+03	6.22E+02	8.68E+02	1.22E+04	2.88E+03
P98160 PGBM	AGFFGDAMK	472.22	92.13	8.09E+02	2.05E+03	9.27E+04	2.92E+03	1.55E+02	8.56E+02	1.28E+04	9.74E+02	7.07E+02	5.35E+02	1.48E+03	6.75E+04	6.30E+03	1.31E+03	9.44E+02
O94875-3 SRBS2	SSILQHERPPPLPTTPVPR	580.82	92.54	5.89E+03	4.66E+03	9.96E+02	9.16E+04	1.33E+05	3.46E+03	1.33E+03	1.24E+03	2.99E+03	8.11E+03	1.37E+05	1.46E+03	3.35E+04	3.45E+03	1.91E+05
P02511 CRYAB	YLRPPSFLR	574.83	92.66	4.56E+03	1.49E+05	3.55E+05	3.66E+05	7.51E+04	6.74E+04	1.82E+05	5.98E+02	6.09E+02	7.56E+02	6.63E+03	2.81E+05	4.95E+02	6.63E+02	6.11E+04
P15924 DESP	LVFDGLR	410.24	92.66	5.26E+03	1.14E+03	1.13E+05	5.13E+03	6.33E+03	3.97E+03	2.53E+04	1.66E+04	9.16E+02	1.30E+03	1.33E+03	7.47E+04	1.31E+04	5.00E+03	3.61E+03
P02511 CRYAB	YLRPPSF	440.24	92.71	1.25E+04	1.23E+03	2.33E+03	1.73E+03	2.37E+02	9.02E+02	1.20E+03	2.51E+04	5.64E+02	5.15E+02	3.42E+04	2.98E+03	5.56E+04	6.43E+03	8.84E+03
P45379 TNNT2	AIDHLNEDQLR	662.34	92.71	8.76E+02	6.17E+02	2.01E+04	5.69E+03	8.33E+03	4.58E+02	6.11E+03	4.68E+03	6.94E+02	2.40E+03	1.64E+05	2.71E+03	7.96E+02	2.61E+03	5.20E+03
Q99798 ACON	FNPETDYLTTGTDGK	779.36	92.84	5.48E+05	1.33E+03	7.25E+02	4.11E+04	6.78E+03	7.91E+02	1.11E+03	4.51E+03	2.78E+03	1.07E+03	2.51E+05	4.96E+03	2.90E+04	1.32E+03	3.08E+04
P17540 KCRS	VPPPLPQFGK	540.31	92.92	1.29E+06	1.54E+05	6.23E+03	5.59E+05	4.01E+05	1.35E+03	6.01E+03	1.70E+04	9.84E+05	2.17E+03	5.69E+05	1.33E+04	1.36E+05	9.62E+04	1.81E+05
P45379 TNNT2	VLAIDLHNLNEDQLR	512.61	93.02	4.01E+06	2.20E+03	1.23E+03	9.99E+04	2.64E+04	1.82E+03	9.27E+02	1.51E+03	8.11E+05	1.50E+03	4.13E+06	2.29E+03	6.73E+05	9.87E+05	1.58E+04
P00505 AATM	EFSIYMTK	509.75	93.09	2.61E+03	1.18E+04	1.70E+05	1.45E+03	6.58E+04	2.16E+05	1.20E+05	1.40E+03	3.15E+04	2.80E+02	1.27E+05	3.70E+04	5.46E+04	6.17E+04	8.91E+04
P22695 QCR2	ATAAPAGAPPQDLEFTK	955.49	93.1	7.76E+04	3.94E+03	3.87E+03	2.77E+04	4.56E+04	8.01E+03	3.43E+03	6.13E+02	5.52E+03	4.27E+03	3.74E+04	1.05E+03	2.90E+03	1.75E+03	7.21E+04
P11142 HSP7C	MVNHFIAEFK	618.31	93.22	6.09E+04	1.13E+03	1.37E+05	3.02E+03	2.84E+03	6.08E+05	4.09E+03	1.30E+03	1.93E+03	1.02E+04	1.95E+03	1.85E+03	2.27E+03	3.31E+03	7.89E+02
Q15149-3 PLEC1	ELIPTEEALR	585.82	93.3	1.07E+05	4.03E+04	4.53E+03	1.33E+05	9.21E+04	3.99E+04	9.78E+04	1.49E+03	2.24E+03	6.29E+02	8.75E+02	3.00E+04	5.87E+03	8.79E+03	2.06E+04
P98160 PGBM	AAGVPSATITWR	615.34	93.4	1.80E+04	6.05E+03	1.22E+03	7.40E+03	1.65E+05	6.12E+03	3.29E+04	1.07E+05	1.12E+03	2.49E+03	1.15E+05	3.75E+03	1.35E+05	2.08E+03	2.32E+04
Q13813-3 SPTA2	ITALDEFATK	554.80	93.69	6.77E+02	1.24E+05	2.18E+03	2.54E+05	7.57E+04	4.94E+03	2.59E+03	6.59E+03	1.24E+03	1.29E+03	1.31E+03	1.84E+03	5.22E+03	3.20E+03	1.93E+05
P02787 TRFE	ASYLDCIR	470.73	93.73	3.31E+05	6.97E+02	1.38E+03	3.70E+03	1.94E+03	3.81E+02	2.51E+03	1.61E+03	1.08E+03	8.54E+02	5.81E+04	6.61E+03	6.08E+03	7.44E+02	1.21E+03
P04406 G3P	GALNQIIPASTGAAK	706.40	93.83	2.12E+05	1.02E+06	4.99E+03	1.23E+06	1.85E+06	4.03E+06	1.09E+06	1.39E+06	1.28E+03	5.88E+02	1.91E+05	1.07E+06	6.14E+03	2.12E+03	8.65E+05
Q02218 ODO1	NTNAGAPPGTAYQSPLPLS	671.00	93.91	1.21E+06	2.71E+04	1.59E+04	5.64E+05	1.57E+03	7.36E+02	7.74E+03	1.63E+04	5.41E+02	7.04E+02	1.49E+06	4.63E+03	5.54E+05	3.18E+03	5.08E+05
P15924 DESP	FLSEMLK	434.23	94.2	5.32E+03	9.18E+03	1.10E+03	8.04E+03	3.25E+04	3.80E+04	1.86E+02	1.47E+03	1.26E+05	1.34E+05	7.57E+02	4.08E+03	3.09E+03	1.09E+05	1.59E+03
P48735 IDHP	DQTDQVTTIDSALATQK	924.95	94.21	2.35E+04	5.47E+03	5.55E+03	4.07E+04	1.05E+04	1.65E+04	1.91E+03	3.47E+02	2.83E+03	4.35E+03	1.34E+04	5.88E+03	9.41E+02	4.77E+03	6.41E+04
P16615-2 AT2A2	EEMHLEDSANFIK	781.86	94.22	3.96E+02	5.84E+04	8.20E+02	4.67E+02	7.59E+02	7.83E+04	1.68E+03	1.79E+03	7.72E+03	2.26E+04	1.00E+03	2.77E+04	6.53E+02	1.13E+04	1.79E+03
Q15149-3 PLEC1	LEQLFQDEVAK	660.35	94.38	2.72E+04	1.17E+05	9.00E+02	6.89E+04	1.72E+05	2.64E+05	1.00E+05	2.84E+03	2.51E+02	1.78E+05	7.07E+04	1.83E+05	1.23E+03	9.80E+02	3.56E+04
P02787 TRFE	EGYYGYTGAFR	642.29	94.41	2.96E+05	1.03E+04	2.73E+02	1.06E+05	3.15E+04	8.04E+03	5.23E+02	1.37E+03	1.49E+03	3.11E+03	2.59E+05	1.17E+04	8.30E+04	3.93E+02	1.48E+05
Q02218 ODO1	VVNAPIFHVN	555.30	94.57	3.21E+05	6.51E+03	2.13E+03	2.29E+03	8.84E+02	1.11E+03	8.72E+04	1.17E+03	2.35E+04	3.61E+04	2.35E+05	1.58E+03	1.16E+05	1.19E+05	7.51E+02
P02787 TRFE	STIFENLANK	568.80	95.17	3.83E+03	1.05E+05	2.18E+03	1.74E+05	1.05E+03	1.29E+05	1.31E+05	2.10E+03	1.44E+03	2.05E+03	2.42E+03	5.03E+04	1.57E+03	4.66E+03	1.51E+03
P02511 CRYAB	FSVNLVDK	461.25	95.36	8.91E+04	6.68E+02	4.08E+03	3.13E+03	2.48E+03	1.28E+04	1.26E+04	2.92E+03	6.89E+05	7.96E+05	1.19E+05	1.84E+03	3.16E+03	7.06E+05	5.23E+04
P00505 AATM	ILIRPMVSNPLNGAR	604.67	95.4	5.98E+02	4.26E+03	7.48E+03	8.47E+02	9.53E+04	2.26E+04	2.37E+03	2.50E+03	1.53E+03	8.61E+02	6.37E+02	9.84E+03	6.82E+02	1.69E+03	3.96E+04
P48735 IDHP	SSGFFVWACK	521.24	95.64	9.03E+04	1.28E+03	1.27E+04	9.71E+02	9.16E+02	2.77E+03	2.46E+03	1.19E+03	1.03E+04	6.43E+02	1.32E+04	2.05E+03	1.48E+03	1.82E+04	2.93E+03
P98160 PGBM	LEGDTLIIPR	563.83	95.89	1.06E+03	3.79E+03	9.28E+02	1.56E+05	1.36E+05	1.04E+04	2.40E+03	2.70E+02	1.04E+04	6.69E+03	3.77E+05	2.28E+03	2.67E+05	2.56E+03	3.43E+05
P00505 AATM	ASAELALGENSEVLK	765.90	96.03	6.99E+04	1.52E+04	3.41E+03	1.93E+04	2.00E+04	1.55E+04	3.92E+02	8.31E+03	1.45E+03	1.35E+03	7.57E+04	2.47E+04	2.10E+04	1.42E+03	3.38E+04
P18206-2 VINC	SLLDASEEAIK	588.31	96.25	5.32E+03	7.32E+03	1.99E+03	8.97E+04	8.13E+03	2.22E+03	2.94E+03	1.75E+03	2.72E+04	3.21E+03	2.82E+05	2.62E+04	2.34E+04	3.84E+04	6.16E+03
O75112 LDB3	PSAFSSLAEASD	591.27	96.45	4.99E+03	3.02E+04	9.14E+03	8.98E+03	3.14E+03	2.84E+03	2.92E+03	1.37E+03	1.28E+03	6.88E+02	1.37E+04	4.48E+04	2.83E+04	1.57E+03	3.90E+04
P52179-2 MYOM1	DADAEIEGAPAAPLDVK	841.42	96.64	2.00E+04	5.43E+03	4.08E+03	2.64E+04	2.06E+03	1.46E+03	6.54E+02	1.33E+03	5.29E+02	8.23E+02	1.04E+03	8.44E+02	3.28E+03	1.84E+03	8.96E+02
P16615-2 AT2A2	IGIFGQDEDVTSK	704.85	96.82	2.91E+03	6.58E+04	4.13E+04	6.33E+05	4.47E+05	2.78E+04	2.42E+04	5.85E+03	1.01E+03	2.55E+03	4.66E+05	2.94E+04	1.42E+05	2.01E+03	6.28E+05
Q13813-3 SPTA2	DVEDEETWIR	646.29	96.93	9.56E+04	9.11E+02	5.12E+02	4.40E+04	1.24E+03	2.76E+03	9.85E+02	1.76E+03	7.78E+02	5.01E+02	4.40E+04	1.03E+03	4.99E+02	1.17E+04	4.26E+02
P18206-2 VINC	MSAEINEIIR	588.32	97.01	1.48E+04	4.03E+05	4.48E+05	7.26E+03	6.38E+04	1.38E+05	1.34E+05	6.79E+02	2.53E+04	1.36E+05	1.22E+04	7.57E+03	5.64E+03	1.71E+05	5.08E+02
P06732 KCRM	VLTCPNSLGTGLR	665.86	97.06	1.78E+03	4.22E+04	4.10E+02	2.02E+05	1.33E+03	2.32E+04	4.82E+03	2.17E+03	2.32E+03	8.49E+02	2.77E+05	1.09E+04	1.30E+05	2.05E+03	2.19E+04
O75112 LDB3	ASPGTPGTPELRPTF	764.39	97.15	2.98E+04	1.35E+03	1.29E+03	1.74E+05	1.66E+03	1.82E+03	7.82E+02	3.19E+03	2.56E+03	3.59E+02	2.13E+04	1.15E+04	4.08E+04	3.62E+02	4.60E+03
Q15149-3 PLEC1	GFFDPNTHENLTYR	570.94	97.23	8.76E+03	7.13E+03	3.86E+03	3.41E+02	3.13E+03	5.58E+04	2.12E+03	4.15E+03	2.45E+03	1.37E+03	2.69E+02	2.60E+03	9.25E+02	9.48E+02	3.60E+02
P52179-2 MYOM1	GHEGIMYFVEK	655.31	97.33	1.31E+03	2.62E+04	2.01E+03	1.97E+04	3.40E+04	2.70E+04	6.29E+03	9.28E+02	7.25E+02	2.87E+03	1.29E+03	1.83E+04	7.05E+03	3.60E+03	1.23E+04
P18206-2 VINC	TNLLQVCER	538.28	97.45	3.10E+02	2.02E+05	5.45E+03	2.01E+03	1.06E+05	1.29E+05	9.57E+02	1.76E+03	8.76E+04	8.08E+04	1.51E+05	7.03E+04	7.39E+02	5.16E+04	8.04E+04
P02787 TRFE	SASDLTWDNLK	625.31	97.82	2.47E+05	8.80E+03	1.35E+03	2.12E+04	1.50E+03	4.82E+02	1.87E+03	4.53E+03	4.38E+04	3.95E+03	1.84E+05	1.95E+03	4.47E+03	8.48E+04	2.10E+04
P15924 DESP	IEVLEELR	565.31	97.98	1.23E+04	3.76E+03	2.56E+03	2.86E+05	4.99E+03	2.31E+03	1.10E+03	9.14E+02	3.02E+03	3.44E+03	3.68E+03	2.57E+03	1.40E+05	4.28E+03	2.55E+05
Q99798 ACON	VAEKEGWPLDIR	471.59	98.2	4.82E+02	1.39E+03	4.36E+02	1.78E+03	2.95E+04	8.35E+03	2.12E+03	5.99E+03	7.23E+02	1.49E+03	4.33E+02	3.16E+03	2.43E+03	6.16E+03	3.14E+03
P98160 PGBM	LLQVTPADSGEYVCR	825.91	98.38	7.16E+04	8.11E+02	2.30E+03	8.23E+04	9.24E+02	2.28E+03	8.01E+03	3.42E+04	2.25E+03	1.33E+03	9.31E+04	3.23E+03	5.51E+03	9.42E+02	3.44E+03
P15924 DESP	GLVGIEFK	431.76	98.48	1.53E+03	1.20E+04	1.17E+04	9.87E+04	3.93E+04	3.33E+04	1.76E+03	2.29E+03	3.68E+03	6.94E+02	1.55E+05	7.77E+04	1.23E+04	6.67E+03	1.04E+05
Q0																		

P52179-2 MYOM1	HFQPEIQWYR	468.57	99.97	7.45E+02	1.93E+03	2.04E+02	6.35E+03	1.43E+03	3.69E+03	3.39E+02	3.16E+02	2.73E+02	1.30E+03	3.35E+04	1.25E+03	5.08E+02	3.04E+02	1.85E+03
Q13813-3 SPTA2	DVTGAEALLER	587.31	100.04	1.83E+05	4.78E+02	3.39E+03	3.69E+05	8.81E+03	2.91E+04	2.56E+04	4.23E+03	1.99E+05	2.17E+03	2.05E+05	4.17E+03	2.88E+03	2.58E+03	4.98E+03
P16615-2 AT2A2	MNVFDTELK	548.77	100.07	6.50E+02	9.31E+03	2.04E+04	3.80E+05	1.11E+04	2.29E+04	3.49E+03	1.48E+03	4.47E+03	5.31E+02	2.41E+03	2.45E+03	4.93E+04	5.83E+03	2.55E+05
P04406 G3P	LTGMAF	639.32	100.12	1.77E+03	8.13E+03	1.55E+03	3.72E+03	1.84E+03	2.50E+03	1.05E+04	1.86E+03	3.89E+03	3.68E+03	3.82E+04	5.91E+02	2.73E+04	4.32E+03	1.28E+04
P22695 QCR2	QVAEQFLNMR	618.31	100.16	3.59E+05	2.04E+03	3.46E+03	1.45E+03	2.32E+03	1.36E+03	5.19E+03	7.99E+03	2.25E+03	5.61E+02	1.92E+05	3.14E+03	6.49E+03	6.65E+03	1.37E+02
P04406 G3P	VIISAPSADAPM	586.30	100.22	4.21E+03	2.82E+05	1.18E+05	1.98E+03	2.93E+04	2.09E+05	6.94E+04	1.71E+05	1.09E+03	3.23E+03	4.70E+03	1.70E+03	9.00E+04	7.07E+02	1.12E+03
Q5VT5 MYOM3	GPPATLPPPAQVQAFR	823.95	100.42	1.44E+05	2.52E+03	7.49E+03	1.15E+04	8.71E+03	4.65E+03	2.54E+03	2.79E+03	5.32E+02	8.02E+02	6.93E+04	4.22E+03	3.14E+03	1.10E+03	4.37E+04
P98160 PGBM	HPTPLALGFHTVTLLR	478.28	100.49	6.47E+02	2.10E+03	7.97E+02	4.51E+02	2.07E+04	2.12E+03	2.01E+03	8.31E+04	2.44E+02	4.22E+02	1.47E+03	5.28E+03	9.24E+02	1.02E+04	9.71E+02
P48735 IDHP	NILGGTVFR	488.78	100.56	8.77E+02	1.66E+06	4.04E+04	1.83E+06	2.24E+06	2.37E+06	2.63E+04	9.23E+03	8.33E+03	1.51E+03	1.18E+06	6.70E+04	1.01E+06	7.40E+03	2.17E+06
P22695 QCR2	AVAFQNPQTHVIENLHAAA YR	588.31	100.76	8.81E+03	2.21E+03	1.96E+03	1.29E+05	3.64E+05	3.82E+03	4.38E+03	1.22E+04	2.90E+05	1.18E+05	2.60E+04	2.37E+03	2.92E+02	4.06E+05	1.93E+05
P22695 QCR2	LLNVTTAPEFR	630.85	100.77	6.81E+02	5.68E+04	8.37E+04	3.68E+04	7.41E+04	1.06E+05	3.39E+03	1.40E+03	5.69E+03	5.27E+03	1.24E+03	2.67E+03	2.64E+04	6.98E+03	9.41E+03
Q99798 ACON	WVIGDENYEGSSR	834.39	100.79	1.96E+05	3.66E+03	1.13E+03	1.58E+05	2.61E+04	7.22E+03	2.20E+03	4.23E+02	1.17E+03	2.86E+03	8.72E+04	2.07E+04	3.32E+03	9.04E+02	3.33E+04
P15924 DESP	NNYDEEISLK	669.33	100.83	1.37E+04	1.18E+04	5.32E+03	3.14E+04	1.02E+04	4.56E+04	1.26E+04	3.87E+04	2.01E+03	5.12E+04	4.90E+03	9.86E+03	2.48E+03	1.30E+03	1.02E+05
P98160 PGBM	LPAVEPTDQAQYLCR	852.42	100.87	1.06E+05	9.72E+03	7.98E+02	1.13E+05	3.15E+03	1.48E+03	3.77E+03	8.97E+02	1.22E+03	5.14E+02	1.32E+05	1.68E+03	4.39E+03	2.27E+03	1.33E+03
P48735 IDHP	LVPGWTKPITIGR	479.96	101.13	4.92E+05	5.29E+03	2.21E+03	1.30E+04	4.07E+03	1.08E+04	3.94E+03	7.37E+03	1.11E+04	5.13E+03	1.73E+05	2.23E+03	1.69E+03	1.81E+04	1.02E+04
P06732 KCRM	RGTGGVDTAAVGSVFDVS NADR	718.34	101.15	6.67E+02	1.94E+05	7.74E+04	1.50E+03	5.59E+05	1.26E+05	6.14E+05	2.62E+04	2.40E+02	2.02E+03	9.51E+02	3.99E+05	7.50E+02	1.26E+02	1.48E+05
Q99798 ACON	FRLEAPDADELPK	500.93	101.15	6.18E+02	5.09E+03	2.09E+03	9.31E+03	2.04E+04	1.27E+04	3.65E+03	1.02E+03	1.84E+05	8.78E+03	1.37E+04	9.31E+03	3.59E+03	4.16E+04	5.74E+03
P04075 ALDOA	ALSDHHIYLEGTLKPN	641.01	101.26	7.89E+04	1.43E+04	2.54E+03	3.97E+03	3.50E+03	2.97E+03	3.21E+04	9.20E+03	1.67E+02	9.87E+02	2.19E+03	1.33E+03	8.52E+02	1.36E+03	5.79E+03
P00505 AATM	FQVTVQTSIGTGALR	725.41	101.3	6.13E+05	8.90E+04	9.06E+03	7.57E+05	3.05E+04	1.82E+04	5.77E+04	1.24E+04	1.49E+03	6.40E+02	5.02E+05	1.06E+05	3.60E+04	3.15E+02	4.67E+04
Q15149-3 PLEC1	SQVMDEATALQLR	731.37	101.36	3.12E+04	1.73E+03	3.92E+02	1.18E+04	1.20E+03	3.13E+03	1.63E+03	3.22E+03	2.64E+03	6.95E+02	2.88E+04	6.34E+03	1.68E+04	1.53E+03	4.35E+03
P22695 QCR2	RWEVADLQPQLK	494.94	101.44	2.34E+02	3.35E+03	1.26E+03	5.87E+02	1.12E+05	5.77E+03	3.75E+03	9.31E+03	2.19E+02	9.25E+02	4.87E+02	1.16E+04	1.39E+04	4.08E+02	8.67E+03
P98160 PGBM	MASVGLSDIAMDTTVTHAT SHGR	590.29	101.46	6.28E+04	9.62E+02	9.70E+03	6.94E+03	3.28E+03	2.52E+04	9.40E+02	2.52E+03	5.34E+03	1.56E+03	9.56E+04	4.43E+03	1.80E+03	2.24E+03	1.95E+04
Q99798 ACON	VGLIGSCTNSSYEDMGR	894.90	101.48	6.70E+04	1.36E+03	3.96E+03	7.62E+04	4.54E+03	4.90E+03	2.19E+03	2.35E+03	2.12E+03	2.03E+02	2.84E+04	6.82E+03	6.81E+02	4.45E+02	4.98E+03
P04075 ALDOA	GVPPLAGTNGETTTQGLDG LSER	758.05	101.54	1.81E+05	1.12E+03	2.38E+03	1.97E+05	6.54E+03	2.93E+03	1.90E+03	1.94E+03	1.98E+03	6.30E+02	1.48E+05	1.02E+03	1.07E+03	7.73E+02	6.22E+03
Q13813-3 SPTA2	SADESGQALLAAGHYASDE VR	716.34	101.92	8.36E+02	2.04E+03	3.80E+04	4.68E+03	6.09E+03	3.46E+04	8.13E+02	9.82E+03	4.46E+02	4.49E+02	4.34E+03	1.90E+04	2.36E+04	1.23E+04	1.21E+04
Q5VT5 MYOM3	TEIPFDLGK	567.29	101.96	1.67E+04	2.21E+04	9.27E+04	1.99E+02	5.79E+04	2.98E+05	8.67E+05	7.14E+03	9.53E+02	1.31E+03	3.66E+03	1.03E+05	4.14E+04	2.06E+03	1.64E+05
P04406 G3P	IISNASCTTNCLAPLAK	860.44	102.1	4.68E+05	3.95E+03	2.58E+03	4.62E+05	1.09E+04	2.33E+04	2.11E+03	1.66E+03	1.21E+03	2.71E+02	2.87E+05	6.54E+02	1.22E+04	4.48E+03	4.29E+04
Q15149-3 PLEC1	LQEAGILSAEELQR	778.92	102.19	6.74E+04	4.12E+03	1.66E+03	5.81E+03	1.15E+03	1.61E+03	4.79E+03	1.39E+03	1.34E+03	2.57E+02	8.09E+04	1.54E+03	6.83E+03	3.30E+03	4.17E+03
P00505 AATM	IAAAIILNTPDLR	634.37	102.5	2.45E+06	1.45E+04	2.17E+03	3.44E+04	6.74E+03	4.15E+03	2.48E+03	1.50E+03	3.63E+04	2.81E+04	1.95E+06	1.64E+04	1.17E+04	3.28E+03	1.11E+04
Q13423 NNTM	AQYPIADLVK	559.31	102.51	2.56E+03	7.14E+04	4.92E+03	2.65E+04	1.32E+04	4.38E+04	1.72E+04	6.40E+03	7.39E+04	2.36E+04	1.04E+05	2.00E+04	4.83E+04	1.56E+05	5.80E+04
Q13423 NNTM	DDDFDFGTMGH	571.22	102.61	1.45E+03	9.75E+03	1.07E+04	1.20E+05	8.94E+03	4.34E+03	2.50E+04	4.75E+02	4.24E+02	6.12E+02	7.91E+04	1.98E+04	3.26E+03	2.30E+03	9.79E+03
P18206-2 VINC	MLGQMTDQVADLR	739.36	102.7	3.16E+02	7.82E+02	4.45E+02	1.13E+05	1.17E+04	2.32E+03	1.16E+03	2.73E+03	1.78E+03	1.73E+03	1.74E+05	1.12E+03	3.28E+04	2.77E+03	9.18E+03
P48735 IDHP	TTDFLDTIK	527.28	102.74	2.42E+05	1.36E+03	2.43E+04	9.87E+02	2.82E+02	7.00E+02	5.95E+03	3.81E+02	4.39E+02	1.34E+03	1.82E+05	2.12E+03	1.35E+04	2.70E+04	1.39E+04
O75112 LDB3	ASPGTPTGPELRPTFSPAFSR	725.04	102.82	1.76E+05	3.36E+03	6.57E+03	1.22E+06	1.19E+03	7.59E+02	1.49E+03	5.93E+02	4.77E+03	1.14E+03	4.45E+05	1.05E+04	3.36E+05	8.14E+02	6.61E+03
Q13423 NNTM	SLGAEPLEVDLK	635.85	102.9	4.39E+05	4.66E+03	1.96E+03	2.48E+05	5.93E+03	4.58E+03	2.83E+03	1.25E+03	1.90E+05	7.06E+04	3.05E+05	1.19E+04	3.23E+03	2.01E+05	5.28E+03
Q02218 ODO1	LVEDHLAVQSLIR	498.29	103.13	3.20E+03	3.92E+02	9.15E+03	6.74E+02	2.21E+03	5.44E+03	2.84E+02	7.39E+02	1.77E+03	5.73E+02	1.42E+05	3.66E+03	1.45E+03	2.53E+03	1.04E+04
P17540 KCRS	DKPVSPLLTCAGMAR	520.28	103.25	2.13E+04	3.08E+03	1.23E+04	8.74E+03	1.00E+04	1.29E+04	2.05E+03	1.84E+03	1.42E+04	8.29E+03	1.58E+04	1.89E+03	1.04E+03	4.57E+03	2.65E+04
P98160 PGBM	AGLSSGFIGCVR	583.80	103.25	1.45E+03	8.02E+03	8.23E+03	3.06E+04	9.57E+04	2.91E+03	4.06E+03	4.45E+03	3.83E+02	5.62E+02	2.25E+03	2.29E+04	1.22E+05	1.05E+03	2.73E+05
Q15149-3 PLEC1	QEQALLEEIER	679.35	103.38	1.18E+03	1.56E+03	5.25E+03	7.83E+02	1.42E+05	7.44E+03	7.21E+03	1.31E+03	3.65E+03	1.98E+03	5.25E+03	2.32E+03	2.14E+03	7.55E+02	4.01E+05
Q99798 ACON	INGPFTDLAHPVAEVGK	621.33	103.51	5.69E+05	2.79E+04	3.24E+03	2.24E+05	3.82E+04	3.16E+03	9.91E+03	3.54E+02	1.20E+03	3.57E+02	1.79E+05	1.70E+03	5.51E+03	4.74E+03	8.97E+03
P52179-2 MYOM1	LNEDHLLHAPEFIIKPR	511.28	103.56	9.89E+02	7.02E+04	5.67E+03	5.08E+04	3.23E+04	3.64E+03	1.65E+02	1.99E+04	9.66E+03	1.44E+04	2.83E+04	1.77E+04	1.95E+04	2.15E+03	2.16E+04
P18206-2 VINC	LLAVAATAPPDAPNREEV DER	794.41	103.6	2.63E+03	2.82E+03	1.08E+03	1.82E+03	2.70E+02	2.80E+03	9.38E+02	3.58E+03	1.27E+05	2.89E+04	1.65E+03	3.08E+03	9.77E+02	6.53E+04	1.48E+03
P00505 AATM	IPEQSVLLLH	574.84	103.66	2.70E+05	1.76E+03	9.62E+02	2.33E+04	2.61E+03	1.01E+03	5.95E+02	6.37E+02	1.17E+04	1.06E+04	2.09E+05	1.27E+03	2.28E+03	3.64E+03	3.09E+03
P98160 PGBM	SPVISIDPPSSTVQQGDASF	763.39	103.72	1.15E+04	2.16E+03	6.86E+03	1.44E+03	7.99E+02	2.80E+04	1.45E+03	8.80E+02	5.11E+03	6.32E+03	1.14E+04	5.79E+03	2.16E+04	4.05E+03	3.43E+03
P15924 DESP	SMVEDITGLR	560.79	103.83	1.22E+03	2.24E+05	1.12E+04	9.20E+02	7.70E+04	2.20E+03	1.20E+03	9.62E+02	2.44E+03	2.33E+03	5.90E+02	2.20E+05	4.15E+03	2.16E+03	1.56E+05
Q02218 ODO1	SSFDEMLPGTHFQR	551.26	104.24	1.77E+05	2.33E+04	3.44E+04	3.89E+04	3.44E+04	1.95E+04	2.81E+04	4.79E+02	6.55E+03	1.38E+05	1.52E+05	8.93E+04	3.75E+02	3.97E+04	5.00E+04
P52179-2 MYOM1	FPVTGLIEGR	544.81	104.29	5.12E+05	4.81E+03	2.25E+03	1.07E+03	4.74E+03	1.73E+03	5.15E+05	1.10E+03	6.96E+02	8.77E+02	3.82E+05	1.54E+03	1.82E+04	2.09E+03	4.34E+03
P52179-2 MYOM1	IGGAEITGYVNYR	788.40	104.54	4.21E+04	1.36E+04	6.64E+03	8.77E+03	2.70E+03	1.41E+05	5.36E+02	6.78E+03	1.82E+03	2.52E+03	2.87E+03	1.92E+03	3.21E+03	2.66E+03	2.57E+03
P11142 HSP7C	NSLESYAFNMK	652.30	104.56	2.80E+03	7.91E+03	4.26E+02	5.12E+02	1.20E+05	9.12E+04	1.18E+03	6.14E+02	3.13E+02	2.55E+03	1.15E+03	2.79E+04	5.28E+02	3.30E+04	1.09E+05
Q13423 NNTM	VALSPAGVQNLVK	648.39	104.59	7.77E+05	8.76E+03	5.45E+02	6.62E+05	1.36E+03	1.24E+03	7.99E+02								

Q5VTT5 MYOM3	FAVLBLEK	467.77	104.78	7.12E+02	1.20E+03	1.52E+02	3.24E+03	1.89E+02	3.34E+03	4.15E+03	3.13E+03	1.82E+05	1.62E+05	8.66E+02	3.90E+02	1.60E+03	1.78E+05	8.97E+02
P04406 G3P	LTGMAFRVPTANVSVVDLT CR	752.39	105.01	1.87E+03	2.63E+03	2.19E+04	2.66E+05	1.14E+04	3.37E+03	2.21E+02	4.49E+02	1.67E+03	6.26E+02	1.06E+05	5.42E+02	3.55E+03	7.87E+02	1.92E+03
P04406 G3P	VPTANVSVVDLTCR	737.39	105.06	1.33E+06	3.66E+04	1.52E+04	1.33E+06	3.84E+04	4.76E+04	7.74E+03	7.86E+03	9.65E+02	5.65E+03	1.15E+06	2.34E+04	1.61E+04	1.51E+03	6.57E+04
P02787 TRFE	FDEFFSEGCAPGSK	760.82	105.11	1.89E+05	1.75E+03	9.00E+03	2.51E+05	6.33E+03	8.30E+02	2.23E+04	8.47E+03	2.43E+02	7.84E+02	1.90E+05	4.08E+02	2.19E+03	7.40E+02	1.40E+04
P22695 QCR2	YEDFSNLGTTLLR	555.95	105.13	1.17E+03	2.21E+05	6.28E+03	1.47E+03	5.06E+05	3.26E+05	3.42E+04	1.27E+04	7.32E+02	8.37E+03	4.55E+02	3.19E+05	1.44E+03	1.88E+03	4.93E+05
O75112 LDB3	ASPGTPGTPELRPTFSPAFSR	757.39	105.16	1.14E+03	1.67E+05	2.23E+05	3.63E+03	1.20E+03	1.78E+05	2.15E+03	7.66E+02	2.82E+03	1.61E+03	2.47E+03	1.09E+03	2.33E+03	1.32E+03	1.29E+05
P16615-2 AT2A2	VDQSILTGESVSVIK	787.93	105.21	1.49E+03	5.13E+05	5.24E+03	1.71E+02	3.66E+05	7.63E+05	1.13E+04	1.25E+04	5.73E+02	1.75E+03	1.86E+03	3.26E+05	1.70E+05	2.47E+03	5.67E+05
P02545-2 LMNA	IDSLSAQLSQLQK	715.90	105.24	4.43E+03	7.29E+04	1.23E+04	8.09E+03	1.56E+05	1.95E+05	1.45E+04	3.26E+04	2.31E+03	1.35E+03	2.34E+03	7.49E+04	3.32E+03	3.96E+03	1.33E+05
P45379 TNNT2	SFMPNLVPPK	565.31	105.24	2.19E+03	2.56E+06	8.18E+05	5.19E+06	2.86E+06	4.37E+06	3.09E+06	5.26E+05	1.25E+04	5.37E+04	2.33E+03	4.40E+06	1.36E+06	1.07E+06	4.55E+06
P02144 MYG	DMASNYKELGFQG	730.33	105.34	1.90E+05	2.88E+03	5.06E+03	1.13E+05	1.80E+03	7.36E+03	2.25E+03	5.23E+03	5.73E+02	4.79E+02	5.09E+03	1.04E+04	1.48E+03	7.23E+02	1.26E+04
Q13813-3 SPTA2	DLAALGDKVNSLGETAER	620.31	105.34	1.58E+03	1.23E+03	6.45E+02	3.47E+04	8.54E+02	1.34E+04	1.25E+05	2.47E+03	1.30E+05	4.54E+03	1.69E+03	5.56E+03	2.20E+03	2.78E+03	4.33E+04
P17540 KCRS	TLDQCIQTGVNDPBGHPFIK	695.01	105.42	2.22E+03	8.47E+02	9.15E+02	1.68E+03	1.51E+03	2.81E+03	1.37E+05	8.72E+03	5.04E+02	2.28E+03	8.78E+02	6.66E+02	4.08E+03	1.71E+03	1.02E+03
P52179-2 MYOM1	ATLTFSHLNKEDEGLYTIR	552.79	105.47	5.08E+03	4.91E+03	1.90E+03	1.01E+04	5.29E+02	3.69E+03	2.97E+03	7.41E+02	3.44E+04	8.44E+03	3.10E+03	1.63E+03	2.94E+03	4.87E+04	5.98E+03
P00505 AATM	ISVAGVTSSNVGYLAH	787.91	105.57	5.93E+05	7.76E+03	3.69E+03	6.87E+05	6.23E+03	1.60E+04	4.55E+02	6.79E+02	4.33E+02	2.82E+02	4.31E+05	2.24E+04	8.53E+03	9.57E+03	2.91E+04
P00505 AATM	IPEQSVLLLHACAHNPTGV DPR	592.56	105.6	1.63E+03	3.91E+03	3.51E+03	4.04E+02	2.57E+03	6.98E+04	5.08E+03	1.55E+04	1.63E+03	5.18E+03	3.83E+02	1.86E+03	1.70E+03	1.60E+03	5.50E+02
Q15149-3 PLEC1	SIQEELQQLR	622.33	105.65	1.05E+04	3.82E+02	5.83E+02	1.36E+03	3.15E+03	2.14E+03	6.05E+02	3.02E+03	6.82E+03	5.05E+03	3.15E+04	1.07E+04	1.50E+03	1.88E+02	3.39E+03
P22695 QCR2	NALANPLYCPDYR	755.36	105.75	1.63E+05	2.53E+03	4.57E+03	1.97E+04	4.20E+02	5.13E+02	4.71E+03	2.47E+03	1.45E+03	1.14E+03	1.24E+05	3.95E+03	1.65E+03	1.43E+03	1.81E+03
P17540 KCRS	LFPPSADYPDLR	695.85	105.75	2.23E+04	1.54E+05	5.58E+04	3.16E+04	1.37E+05	1.45E+05	1.90E+04	3.35E+04	2.54E+04	1.36E+03	2.36E+03	1.18E+05	1.79E+04	6.37E+03	1.03E+05
Q13813-3 SPTA2	ADVVESWYGEK	616.81	105.77	6.13E+04	1.03E+04	1.18E+04	2.86E+03	2.59E+03	4.18E+02	3.26E+03	6.23E+02	8.54E+02	3.92E+04	1.02E+05	5.49E+03	2.07E+03	1.97E+03	3.81E+03
P06732 KCRM	VLTLLEYK	489.80	105.91	6.11E+04	7.71E+03	8.23E+03	1.25E+04	7.94E+03	2.98E+03	4.84E+03	5.92E+03	2.83E+06	3.67E+06	4.78E+04	1.88E+04	7.42E+03	2.47E+06	9.66E+03
P04075 ALDOA	IYLEGTLKPN	630.86	105.98	1.35E+03	2.85E+03	1.05E+04	1.01E+03	5.21E+02	2.83E+04	3.00E+03	9.86E+02	6.85E+03	1.70E+03	1.82E+03	1.28E+03	1.02E+03	2.69E+03	1.15E+03
P48735 IDHP	DLAGCIHGLSNVK	442.90	106.34	1.36E+03	3.80E+04	1.52E+03	6.59E+02	1.76E+05	1.34E+05	4.75E+03	7.23E+02	1.86E+02	3.42E+02	2.99E+02	5.16E+03	2.58E+02	2.64E+02	8.07E+04
P98160 PGBM	SPAYTLVWTR	597.32	106.42	1.71E+03	1.24E+05	1.24E+04	1.54E+03	8.42E+04	1.96E+05	1.20E+04	1.44E+03	8.22E+02	1.21E+03	4.38E+02	1.65E+05	2.39E+03	6.28E+03	5.88E+02
Q02218 ODO1	SSENGVDYVIMGMPHR	597.95	106.44	7.20E+04	8.74E+02	2.19E+03	1.06E+03	1.11E+03	1.35E+03	6.73E+02	7.02E+02	4.41E+03	3.46E+03	3.93E+03	5.70E+02	2.72E+02	4.86E+03	1.01E+03
P04075 ALDOA	IGEHTPSALAIMENAN	834.41	106.49	1.03E+03	2.70E+02	2.18E+03	9.28E+02	6.41E+02	6.95E+04	3.82E+02	3.23E+02	9.41E+02	3.29E+02	1.33E+03	6.23E+02	9.31E+02	9.20E+02	1.09E+03
Q15149-3 PLEC1	VLALPEPSAAPTLR	766.45	106.73	1.41E+02	1.00E+05	4.40E+03	4.74E+02	6.05E+04	3.91E+03	3.10E+03	1.03E+04	1.49E+03	3.02E+03	1.84E+03	8.88E+04	1.18E+05	8.51E+03	1.06E+05
P04406 G3P	SSTFDAGAGIALNDHFVK	617.31	106.85	4.37E+03	4.78E+03	5.75E+03	6.94E+04	9.04E+02	2.27E+03	1.65E+03	1.95E+03	2.91E+04	1.72E+04	1.86E+04	8.78E+03	1.39E+03	2.89E+04	1.70E+04
P45379 TNNT2	ALSNMMHF	475.71	106.85	1.09E+03	7.26E+02	1.71E+03	1.40E+05	1.99E+02	1.46E+03	9.58E+02	1.21E+03	6.96E+02	3.09E+02	1.14E+03	2.36E+03	8.13E+03	1.14E+03	7.78E+03
Q13813-3 SPTA2	GVIDMGNSLIER	652.34	107.01	1.54E+04	5.21E+04	6.23E+04	1.64E+03	7.37E+04	3.74E+03	2.74E+04	1.79E+04	1.45E+04	1.51E+04	3.57E+03	6.55E+04	1.01E+03	3.86E+04	9.86E+04
P16615-2 AT2A2	EFTLEFSR	514.76	107.15	2.26E+03	3.46E+02	6.38E+03	3.76E+02	9.65E+02	2.59E+03	4.07E+04	2.67E+04	1.82E+05	3.44E+05	5.97E+02	6.41E+02	3.33E+03	2.68E+05	3.62E+03
Q15149-3 PLEC1	LLFNDVQTLK	595.84	107.23	7.02E+03	3.81E+03	8.18E+03	3.25E+02	5.25E+04	1.12E+05	8.01E+03	1.89E+03	9.64E+02	4.34E+02	1.83E+03	1.86E+03	1.42E+03	6.63E+03	7.43E+02
P02787 TRFE	EFQLFSSPH	546.26	107.4	1.46E+05	1.41E+03	3.48E+03	2.70E+04	3.34E+03	1.48E+03	1.49E+03	1.10E+03	1.26E+03	1.71E+03	6.26E+04	7.73E+03	3.42E+03	1.29E+03	8.83E+03
P52179-2 MYOM1	WVQTLWSGER	631.32	107.48	2.49E+03	1.71E+04	5.88E+03	3.22E+03	1.56E+03	2.94E+04	3.99E+03	1.00E+04	1.90E+04	3.83E+04	1.85E+03	7.52E+02	8.03E+02	5.47E+03	1.53E+03
Q13423 NNTM	APMVNPTLGVHEADLLK	602.33	107.53	3.19E+03	1.22E+04	3.92E+02	2.97E+03	4.30E+05	1.88E+03	1.42E+03	2.75E+03	7.06E+03	9.56E+03	6.49E+02	5.36E+05	1.62E+05	1.73E+03	3.33E+05
P22695 QCR2	MALIGLGVSHPVLK	478.95	107.66	2.05E+02	1.30E+04	7.07E+03	7.79E+02	3.83E+05	1.33E+04	1.37E+04	5.29E+03	1.43E+02	5.03E+02	4.53E+02	3.32E+05	3.14E+02	6.56E+02	1.39E+05
P17540 KCRS	ADLFDVPIK	509.28	108.12	9.00E+04	5.78E+03	3.46E+03	1.07E+04	7.01E+03	7.52E+03	7.56E+02	1.17E+03	1.74E+03	6.98E+02	9.66E+04	1.03E+03	2.59E+03	3.40E+03	2.38E+03
P15924 DESP	IEPHTGLLLLSVQK	516.64	108.16	1.86E+02	4.09E+02	1.49E+02	1.03E+03	1.45E+03	2.42E+02	2.06E+03	4.10E+02	2.37E+04	4.85E+04	2.71E+02	5.63E+02	1.07E+03	1.38E+04	6.45E+02
P48735 IDHP	YFDLGLPNR	547.78	108.25	1.93E+03	4.22E+05	5.53E+03	1.40E+03	5.25E+05	1.04E+06	6.22E+02	7.44E+02	4.03E+02	1.61E+03	1.42E+03	5.09E+05	2.54E+03	1.39E+03	9.53E+05
P04075 ALDOA	FSHEEIAMATVTALR	559.29	108.3	5.77E+02	7.45E+04	1.44E+04	3.72E+02	4.72E+05	1.49E+05	7.55E+03	4.35E+04	1.78E+03	6.14E+02	1.10E+03	3.99E+05	2.08E+05	2.02E+03	4.23E+05
Q15149-3 PLEC1	SSIAGLLK	451.29	108.67	2.52E+03	1.58E+04	2.87E+03	3.03E+03	6.80E+03	4.28E+04	5.19E+02	1.63E+03	1.96E+03	2.49E+02	2.42E+02	5.88E+04	5.77E+02	5.75E+02	8.73E+03
P22695 QCR2	LGHTPFVDEL	564.29	108.73	7.23E+02	5.83E+04	3.14E+03	2.04E+05	1.39E+03	1.93E+05	3.64E+03	4.01E+03	8.95E+03	2.98E+02	7.11E+04	1.08E+04	5.77E+04	8.12E+02	4.02E+04
P04406 G3P	VPTANVSVVDLTCRLEKPA	535.80	108.85	6.49E+04	2.02E+04	1.65E+03	4.13E+03	1.15E+04	1.92E+04	1.40E+03	1.66E+03	2.59E+04	1.88E+04	8.88E+02	3.52E+04	2.82E+04	1.06E+04	4.62E+03
P11142 HSP7C	DAGTIAGLNVLR	600.34	108.87	5.56E+02	6.02E+05	1.22E+03	7.79E+02	5.83E+05	2.92E+04	9.60E+03	8.46E+02	1.54E+04	1.30E+04	9.14E+02	7.25E+05	5.13E+05	1.88E+04	7.41E+05
P98160 PGBM	GSVYIGGAPDVATLTGGR	845.96	109.09	2.78E+04	2.27E+05	1.71E+05	2.01E+05	1.31E+04	6.91E+04	6.45E+03	2.49E+05	1.56E+03	4.38E+02	9.50E+04	9.79E+03	4.75E+03	4.99E+02	9.95E+04
P06732 KCRM	TVDDVIQTGVNDPBGHPF	905.93	109.12	6.23E+03	2.02E+05	9.61E+03	1.22E+03	4.78E+02	5.32E+05	2.25E+03	1.46E+04	5.04E+03	2.21E+03	2.37E+03	1.02E+03	1.86E+02	1.90E+03	1.65E+03
P15924 DESP	AITGFDDPFSGK	627.80	109.36	1.64E+03	5.50E+02	2.26E+03	5.40E+02	5.59E+04	2.54E+03	2.40E+03	2.13E+02	3.87E+03	1.43E+04	5.53E+03	2.14E+04	3.75E+04	3.44E+03	1.40E+05
P98160 PGBM	MASVGLSDIAMDTTVTHAT SH	715.67	109.45	3.49E+04	1.22E+04	2.13E+03	1.48E+04	2.49E+03	2.23E+03	4.34E+03	3.70E+02	1.45E+04	8.56E+02	2.65E+04	1.20E+03	7.52E+02	5.44E+03	2.42E+03
Q15149-3 PLEC1	THYSELTLTSQYIK	595.64	109.54	9.65E+02	3.17E+04	1.68E+05	5.58E+02	1.49E+03	5.49E+04	7.99E+04	1.14E+05	8.51E+02	7.16E+02	1.56E+03	3.24E+03	8.64E+02	3.06E+03	8.92E+04
Q99798 ACON	SHFEPNEYIHYDLLEK	678.66	109.72	1.37E+05	5.40E+02	8.82E+03	1.85E+03	1.17E+03	1.84E+03	1.19E+04	2.32E+03	1.91E+03	9.58E+02	1.47E+03	4.24E+03	2.80E+03	1.06E+03	2.84E+03
P22695 QCR2	VTSEELHYFVQNHFTSAR	542.02	110.03	1.77E+02	5.12E+02	1.25E+03	6.44E+02	4.21E+02	1.35E+03	1.								

P02787 TRFE	LAPNNLKPVVAEFYGSK	616.34	110.47	1.21E+05	1.29E+03	8.57E+02	3.27E+03	2.88E+03	4.57E+03	1.67E+02	1.87E+03	5.35E+02	1.07E+03	7.60E+04	1.43E+04	2.07E+03	2.55E+03	1.34E+03
P18206-2 VINC	MALLMAEMSR	576.78	110.5	9.40E+02	2.41E+04	2.86E+03	9.54E+02	2.94E+05	1.13E+04	5.89E+03	1.00E+04	4.12E+03	8.67E+04	8.39E+02	3.62E+05	1.46E+03	3.78E+04	1.29E+05
P11142 HSP7C	TVTNAVVTVPAYFNDSQR	661.34	110.5	2.87E+04	9.27E+03	1.65E+03	1.45E+05	2.08E+04	8.88E+04	1.49E+04	1.19E+04	7.53E+02	9.15E+02	1.33E+05	3.72E+04	7.59E+04	5.65E+03	1.83E+05
Q15149-3 PLEC1	LLDAQLATGGIVDPR	769.93	110.6	4.85E+04	2.47E+03	9.67E+02	2.22E+03	9.19E+02	2.07E+03	1.07E+03	1.09E+04	3.03E+04	4.97E+04	3.89E+04	5.90E+02	1.47E+03	1.59E+04	2.22E+03
P52179-2 MYOM1	TPVTGYFVDLK	620.33	110.62	2.75E+04	7.68E+03	1.08E+03	8.81E+02	4.76E+05	3.27E+04	2.84E+03	6.34E+04	8.53E+03	3.62E+02	1.97E+04	3.92E+05	1.91E+05	1.40E+03	5.03E+05
P22695 QCR2	WEVADLQPQLK	663.85	111.3	2.55E+03	3.74E+04	5.70E+04	5.84E+03	2.73E+02	6.18E+04	8.19E+04	1.10E+05	9.47E+03	1.84E+03	1.52E+03	6.49E+02	2.63E+03	1.03E+04	2.90E+03
P02545-2 LMNA	DLEALLNSK	501.78	111.66	1.87E+03	5.97E+03	6.35E+03	1.52E+03	2.40E+04	4.10E+03	6.43E+02	1.96E+03	8.14E+03	1.06E+05	5.17E+02	2.97E+04	1.92E+04	9.95E+03	2.79E+04
Q13423 NNTM	ILVGGGVAGLASAGAAK	762.96	111.71	1.31E+03	1.26E+04	1.94E+03	2.55E+04	4.10E+04	5.27E+03	5.49E+03	3.21E+04	3.87E+02	4.54E+02	2.96E+02	2.52E+04	1.55E+04	6.33E+02	7.69E+03
O75112 LDB3	QYNNPIGLYSAETLR	869.94	111.71	2.28E+03	1.48E+04	6.21E+03	2.02E+03	1.34E+03	3.34E+04	1.06E+03	2.23E+03	7.74E+02	1.10E+03	3.68E+02	3.80E+03	1.96E+03	3.49E+02	1.10E+03
Q13813-3 SPTA2	EANELQQWINEK	751.37	112.01	8.34E+03	1.14E+03	1.34E+04	2.69E+03	1.78E+04	3.40E+03	1.80E+03	5.45E+02	8.34E+03	6.27E+02	1.01E+04	2.12E+03	1.70E+03	5.94E+03	1.27E+04
P52179-2 MYOM1	GLTDSLLLLDDYSSK	807.40	112.31	3.69E+04	2.48E+03	8.01E+02	1.07E+04	2.06E+03	4.99E+02	1.23E+04	1.34E+03	4.97E+02	2.58E+03	1.32E+04	9.67E+02	5.34E+02	6.28E+02	8.35E+02
P06732 KCRM	ELFDPIISR	602.81	112.48	1.30E+04	5.79E+04	2.47E+04	3.29E+03	3.27E+06	6.66E+06	2.45E+04	3.91E+04	1.37E+03	4.56E+02	3.37E+03	3.24E+06	1.60E+06	4.16E+02	5.38E+06
P02511 CRYAB	DAIHPWIR	629.34	112.94	3.24E+05	2.96E+04	1.61E+03	1.88E+05	6.81E+04	3.81E+04	3.69E+03	1.41E+04	1.61E+03	6.70E+02	2.73E+05	5.23E+04	2.58E+04	2.16E+03	1.75E+04
P22695 QCR2	AASGNLGHPTPFVDEL	764.37	113.19	7.79E+03	6.55E+02	8.86E+02	2.03E+04	2.56E+03	3.23E+03	1.91E+03	4.16E+03	1.97E+03	2.35E+03	3.28E+04	1.15E+04	9.84E+03	1.67E+03	3.59E+03
P16615-2 AT2A2	VGEATETALCLVEK	782.40	113.78	1.54E+03	2.23E+04	1.99E+03	1.74E+05	9.43E+04	7.49E+04	9.56E+02	1.40E+03	3.96E+02	3.86E+03	1.21E+05	6.89E+04	2.30E+04	3.56E+03	8.32E+04
Q13813-3 SPTA2	EANEVISLWK	560.30	113.83	7.59E+02	1.30E+04	8.53E+02	3.10E+03	3.78E+03	3.88E+04	1.22E+03	2.01E+03	1.58E+03	1.19E+03	2.82E+03	8.90E+03	1.38E+03	1.16E+03	2.75E+03
Q13423 NNTM	EANSIIITPGYGLCAA	860.95	114.07	9.08E+04	4.31E+04	6.78E+04	7.74E+04	2.37E+03	8.47E+04	2.17E+03	1.28E+04	3.39E+03	2.25E+03	6.32E+04	7.95E+03	3.60E+04	4.73E+03	1.93E+03
P52179-2 MYOM1	AASAYDYGSSHGLTDSLL LDDYSSK	908.42	114.25	2.94E+03	1.84E+04	8.00E+02	8.83E+03	2.34E+03	5.03E+04	4.32E+02	7.10E+02	1.06E+03	1.67E+03	2.52E+03	1.07E+03	3.40E+03	1.95E+03	1.94E+02
P17540 KCRS	RGTGGVDTAAVADVYDISN IDR	755.71	114.29	2.27E+03	3.53E+03	3.93E+03	5.23E+02	2.27E+03	5.02E+03	5.95E+04	1.82E+03	9.76E+03	2.56E+03	2.16E+03	7.08E+03	2.25E+03	1.11E+04	1.58E+03
Q13423 NNTM	DDDFDGTMGHVIR	503.90	114.31	2.03E+03	2.29E+02	4.35E+02	6.92E+02	8.74E+02	2.25E+02	1.79E+03	1.20E+04	6.64E+04	1.95E+02	1.60E+03	5.80E+02	1.51E+03	2.93E+04	4.22E+03
P98160 PGBM	YELGSLAVLR	589.33	114.52	2.04E+03	1.15E+03	3.08E+03	1.75E+05	4.09E+03	1.96E+03	1.71E+02	6.32E+02	1.25E+05	1.38E+04	4.96E+02	5.51E+04	3.07E+04	1.29E+05	4.23E+04
P15924 DESP	TMIQSPSGVILQEADVHA	708.37	114.52	2.69E+03	6.11E+03	8.56E+03	8.72E+02	3.58E+02	5.93E+04	3.93E+04	3.72E+04	7.14E+03	3.17E+03	1.80E+03	8.39E+03	3.13E+03	3.34E+03	1.87E+03
P52179-2 MYOM1	VLGGLPDVVTIQEGK	762.93	114.52	1.24E+03	8.39E+03	5.29E+03	1.46E+03	2.69E+05	1.76E+04	4.07E+03	6.45E+03	2.89E+03	2.25E+03	3.62E+02	2.33E+05	1.43E+05	3.01E+03	3.74E+05
Q15149-3 PLEC1	SLVPAAELESR	642.86	114.62	8.48E+02	8.09E+04	2.95E+04	1.14E+03	1.52E+03	1.81E+05	5.72E+04	1.82E+05	3.17E+02	6.74E+02	9.87E+02	1.27E+03	4.27E+02	1.84E+03	1.63E+02
P15924 DESP	ITNLTQQLEQASIVK	843.48	114.76	7.22E+04	1.78E+03	1.65E+03	1.87E+03	1.77E+04	8.90E+03	1.04E+03	1.63E+02	4.51E+02	2.74E+03	1.56E+03	3.92E+04	7.70E+03	9.69E+02	6.06E+04
P02787 TRFE	DQYELLCLDNTR	741.85	115	2.13E+03	1.08E+04	1.56E+04	1.09E+03	1.21E+05	1.16E+04	4.03E+03	6.20E+03	4.63E+02	1.80E+03	5.96E+02	4.67E+04	2.16E+04	2.34E+03	6.88E+04
P45379 TNNT2	ALSNMMHFGGY	614.27	115.08	7.23E+04	2.25E+04	6.27E+03	1.99E+05	1.70E+03	1.38E+03	8.24E+02	1.13E+03	2.96E+03	8.91E+02	7.71E+04	2.77E+03	1.08E+04	7.93E+02	5.14E+03
Q99798 ACON	EDIANLADEFK	632.81	115.25	1.41E+03	7.17E+03	1.84E+03	2.36E+03	7.64E+05	3.47E+03	2.55E+03	1.50E+04	3.07E+03	1.38E+03	2.86E+05	4.28E+05	2.25E+05	9.32E+02	7.20E+05
P45379 TNNT2	SFMPNLVPPKIPDGER	599.99	115.33	4.04E+04	5.58E+02	1.52E+03	3.49E+04	3.73E+04	4.70E+03	3.82E+02	7.75E+04	1.43E+04	5.79E+04	3.13E+04	4.82E+03	1.13E+04	3.79E+03	4.97E+04
Q13813-3 SPTA2	DLSSVQTLTK	602.83	115.71	1.11E+04	6.10E+03	2.28E+04	3.80E+04	2.63E+03	1.72E+03	1.19E+03	5.99E+03	9.27E+04	4.55E+02	1.57E+03	8.88E+03	2.27E+03	3.55E+04	2.35E+04
P52179-2 MYOM1	DAGYIEVILK	560.82	116.14	5.91E+04	2.24E+03	6.05E+03	2.51E+04	4.76E+03	1.06E+03	7.65E+02	5.63E+03	9.47E+02	8.80E+02	5.67E+04	3.74E+03	1.77E+03	1.74E+03	2.14E+03
P22695 QCR2	SMAASGNLGHPTPFVDEL	873.41	116.15	4.45E+03	3.14E+03	9.67E+02	1.74E+03	9.73E+03	2.59E+03	1.56E+03	9.48E+02	2.22E+03	1.12E+03	2.65E+03	4.62E+04	9.41E+03	7.05E+02	5.02E+03
P48735 IDHP	LILPHVDIQLK	430.27	116.41	1.01E+03	7.37E+03	6.14E+03	3.45E+02	9.80E+04	1.21E+04	7.29E+03	5.90E+03	4.32E+02	4.53E+02	1.38E+03	5.99E+04	1.12E+05	1.13E+03	1.05E+05
Q02218 ODO1	VFHLPTTF	531.78	117.28	7.06E+03	3.15E+03	6.44E+02	4.77E+03	6.66E+03	1.97E+03	5.85E+02	3.50E+03	1.77E+02	7.53E+02	2.76E+03	2.17E+04	1.23E+04	2.94E+03	4.50E+04
P02787 TRFE	DYELLCLDGR	649.31	117.54	8.42E+04	2.40E+03	9.37E+03	1.62E+03	2.26E+04	1.71E+03	4.22E+04	1.58E+03	3.79E+03	1.08E+03	3.05E+04	2.06E+04	2.35E+04	1.51E+04	1.16E+04
Q02218 ODO1	LGFYGLDESDDK	736.35	117.56	5.00E+02	8.36E+04	9.74E+03	4.06E+03	8.07E+04	7.46E+04	4.71E+03	8.28E+04	3.70E+03	5.04E+03	5.60E+02	9.81E+04	6.20E+03	1.40E+03	1.13E+05
Q99798 ACON	LQLLEPFDK	551.81	117.58	2.45E+03	1.10E+03	3.16E+03	3.28E+03	2.41E+04	3.14E+03	5.96E+04	2.22E+04	4.44E+05	6.15E+05	2.72E+02	6.98E+02	1.24E+03	2.26E+05	2.71E+04
P17540 KCRS	REVENVAITALEGLK	547.98	117.64	2.32E+03	1.20E+04	2.65E+03	1.89E+03	4.21E+05	1.15E+04	1.19E+03	1.03E+04	2.92E+03	1.85E+03	2.06E+03	3.10E+05	2.33E+03	1.21E+04	1.94E+05
P04406 G3P	VIISAPSADAPMFVMGVNH EK	738.37	118.09	1.17E+06	3.20E+03	3.09E+03	3.44E+05	6.96E+05	2.02E+04	5.63E+04	1.49E+04	2.86E+03	9.99E+04	2.86E+03	5.47E+05	6.20E+03	8.11E+02	7.46E+05
P22695 QCR2	VAESAVAGSAEANAFSVLQ	653.32	118.15	2.39E+04	2.67E+03	4.08E+05	1.77E+04	2.54E+04	7.37E+02	6.92E+03	7.79E+03	5.62E+03	5.35E+03	1.83E+03	1.45E+03	1.77E+03	6.09E+02	4.22E+02
P04406 G3P	VIISAPSADAPMFVMGVNH EKYDNSLK	734.12	118.18	4.13E+02	1.65E+03	5.49E+02	2.95E+02	1.41E+04	7.54E+02	5.68E+02	1.50E+03	1.24E+02	1.02E+03	2.68E+02	2.48E+03	4.71E+02	6.28E+02	1.85E+04
P52179-2 MYOM1	FHAGASTMPLSFGVTPYGY ASR	773.38	118.34	6.43E+02	1.51E+03	3.70E+03	2.54E+03	1.57E+03	2.46E+04	1.07E+04	2.17E+04	6.77E+03	2.94E+03	2.54E+03	9.89E+02	2.39E+03	8.43E+03	2.77E+03
O75112 LDB3	ASPGTPGTPELRPTFSPAF	965.49	118.4	4.98E+02	1.47E+03	9.17E+03	1.14E+03	1.14E+04	6.75E+02	2.82E+03	5.73E+02	3.49E+02	7.86E+02	3.41E+03	4.16E+04	5.36E+02	6.38E+02	1.49E+04
Q13423 NNTM	SLANVILGGYGTSTAGGK	883.96	118.44	2.74E+03	4.22E+02	1.88E+02	6.61E+03	3.74E+03	9.54E+02	5.14E+02	3.47E+03	7.18E+02	3.27E+04	2.25E+03	6.81E+03	1.95E+03	5.08E+02	2.31E+04
P16615-2 AT2A2	NYLEPAILE	531.28	118.5	3.39E+02	1.35E+03	1.20E+05	2.90E+03	3.44E+03	7.19E+02	1.33E+05	2.15E+03	1.42E+03	4.75E+03	4.39E+02	5.09E+02	1.72E+03	1.21E+03	7.42E+02
Q5VTT5 MYOM3	GLPDVATIMEDK	644.83	118.58	1.94E+03	5.00E+04	2.64E+04	1.06E+04	9.57E+03	4.49E+04	4.94E+04	3.05E+04	3.23E+02	3.45E+03	1.61E+03	1.54E+04	1.31E+03	1.07E+03	3.85E+03
P06732 KCRM	LSVEALNSLTGEFKGK	564.98	118.81	2.59E+03	1.92E+03	3.62E+03	4.59E+02	1.89E+03	5.77E+04	4.48E+03	3.77E+02	3.05E+03	1.82E+03	1.09E+03	1.09E+03	3.62E+02	2.86E+03	1.32E+04
P16615-2 AT2A2	NAENAIEALKEYEPEMGK	679.33	119.35	7.55E+03	2.36E+03	8.67E+03	1.86E+03	6.05E+04	5.97E+03	1.21E+04	4.50E+02	1.22E+04	8.19E+03	2.54E+03	4.39E+04	7.67E+03	4.11E+02	1.76E+04
P17540 KCRS	GYTLQCIQTGVDPNGHPFI	768.38	120.2	3.78E+04	1.18E+03	4.64E+03	1.07E+03	1.60E+03	6.58E+02	1.65E+03	3.24E+03	7.57E+02	7.73E+02	3.18E+04	1.76E+04	1.29E+03	5.98E+02	8.95E+04
Q15149-3 PLEC1	SPVPASELLASGVLSR	783.95	120.36	9.90E+02	5.47E+03	9.15E+02	4.26E+03	1.15E+05	7.64E+03</									

P48735 IDHP	GRPTSTNPIASIF	680.87	121.15	1.06E+05	1.14E+03	1.94E+03	9.56E+03	4.18E+02	1.21E+03	1.27E+03	2.28E+03	2.61E+03	6.23E+02	3.78E+04	8.44E+02	5.59E+03	2.97E+03	2.33E+03
Q13813-3 SPTA2	DLASVQALLR	543.32	121.22	1.61E+04	2.73E+03	9.61E+02	4.86E+04	7.54E+04	1.42E+04	4.06E+03	2.33E+03	1.71E+03	3.45E+03	4.89E+02	4.33E+04	6.00E+04	2.30E+04	6.97E+04
P18206-2 VINC	VDQLTAQLADLAAR	742.91	121.28	1.32E+05	5.99E+02	2.56E+03	1.19E+05	4.20E+04	3.11E+03	4.40E+04	1.75E+02	8.92E+02	1.69E+03	1.59E+05	4.75E+02	1.33E+03	8.33E+02	9.21E+03
Q5VTT5 MYOM3	SVIGSGTWEAISSESPVR	931.47	121.63	6.61E+04	1.05E+03	9.34E+02	2.10E+03	6.03E+03	1.63E+03	5.33E+02	1.41E+03	6.39E+02	1.48E+03	4.24E+04	5.20E+03	3.13E+03	5.72E+02	9.75E+03
P02511 CRYAB	APSWFDTGLSEMR	748.84	121.65	6.96E+04	9.91E+02	2.49E+03	4.35E+03	2.81E+03	4.11E+03	1.70E+03	1.40E+03	1.59E+03	1.60E+03	1.27E+05	6.42E+03	1.19E+03	7.31E+02	8.84E+03
P02144 MYG	GLSDGEWQL	502.74	121.65	1.26E+04	4.16E+03	1.53E+03	6.54E+03	1.27E+04	7.90E+03	2.26E+02	1.52E+03	5.94E+03	1.07E+03	9.03E+03	2.33E+03	1.66E+03	4.08E+02	1.92E+05
P06732 KCRM	LGYYVLTCPNLTGLR	832.44	121.87	3.15E+02	2.94E+03	3.05E+03	6.62E+04	2.18E+03	9.09E+02	5.32E+02	1.15E+03	3.68E+02	3.31E+02	2.40E+03	4.89E+02	9.84E+02	5.89E+02	9.82E+02
P16615-2 AT2A2	SLPSVETLGCTSVICSDK	919.95	121.95	3.71E+03	1.91E+03	1.67E+03	1.80E+04	2.09E+02	1.37E+03	8.14E+02	1.09E+03	1.17E+03	3.01E+02	7.89E+03	6.61E+03	4.98E+03	8.14E+02	9.71E+02
P02787 TRFE	MYLGYEYVTAIR	739.87	122.04	1.31E+03	1.31E+04	1.40E+04	3.09E+03	3.91E+04	1.22E+04	1.12E+04	1.17E+03	1.83E+03	3.66E+03	2.35E+03	5.75E+03	9.61E+03	5.58E+02	9.79E+03
P06732 KCRM	LGSSEVEQVQLVVDGK	893.48	122.26	3.70E+04	9.58E+03	2.73E+03	3.68E+04	1.58E+03	6.81E+03	5.84E+02	5.56E+02	1.60E+03	1.02E+03	2.87E+04	1.06E+04	2.46E+04	2.68E+03	1.56E+04
O75112 LDB3	ASPGTPTPELRPTFSPAFSR	960.73	122.42	1.60E+03	1.62E+04	3.43E+02	6.61E+02	1.29E+03	2.48E+04	1.32E+03	2.42E+03	2.70E+02	2.35E+02	1.25E+03	2.68E+03	1.36E+03	1.34E+03	3.52E+02
P98160 PGBM	PSAFSSLAESDPGPPR	706.02	122.45	9.98E+02	2.03E+03	3.40E+05	3.31E+02	8.01E+02	1.18E+03	2.70E+04	8.56E+02	6.40E+02	7.84E+02	4.62E+02	1.67E+03	2.66E+02	2.84E+03	2.38E+03
P04406 G3P	VISSGSVASYVTSPQGFQFR	882.40	122.51	4.08E+05	1.35E+03	4.19E+03	2.88E+05	4.86E+03	2.43E+03	4.39E+02	1.13E+03	2.43E+03	1.73E+02	3.81E+05	6.68E+03	1.10E+03	4.06E+04	5.75E+04
P17540 KCRS	LISWYDNEFGYSNR	558.61	122.82	1.01E+05	2.91E+04	6.76E+04	2.29E+04	1.89E+04	1.08E+04	2.66E+03	1.42E+04	1.65E+02	8.26E+02	1.44E+05	1.55E+03	6.43E+03	9.72E+02	1.57E+04
P04075 ALDOA	TFLIWINEEDHTR	551.81	122.96	4.04E+04	2.90E+04	1.11E+04	8.49E+04	4.03E+03	4.48E+04	3.26E+03	6.57E+03	1.54E+03	1.42E+03	3.89E+04	5.81E+03	9.75E+03	9.44E+02	1.34E+04
P98160 PGBM	TVPPAVTGITF	613.82	123	3.39E+03	8.01E+03	8.48E+02	5.94E+02	1.88E+04	9.93E+03	2.34E+02	4.17E+02	6.74E+02	7.39E+02	2.76E+04	6.95E+03	1.48E+04	9.44E+02	4.35E+04
P15924 DESP	HLISTHFAPGDFQGFALVNP	683.01	123.03	2.96E+04	1.18E+04	2.21E+03	1.12E+03	3.61E+03	1.23E+04	8.43E+02	4.28E+03	1.85E+03	3.06E+02	4.03E+04	1.77E+03	4.39E+03	2.20E+03	1.41E+04
Q99798 ACON	QR	735.86	123.29	7.27E+04	4.39E+05	6.52E+05	1.06E+04	9.34E+02	1.22E+06	2.69E+04	2.03E+04	1.56E+03	5.86E+02	1.73E+04	7.16E+03	3.86E+02	4.74E+02	2.35E+03
P45379 TNNT2	TFNETQIEWFR	607.98	123.57	1.95E+04	1.12E+03	2.21E+03	2.29E+04	2.24E+03	1.30E+03	1.55E+03	3.48E+02	2.13E+04	3.10E+02	4.24E+04	6.39E+02	1.60E+03	2.07E+04	1.57E+03
P98160 PGBM	AKELWQSIYNLEAEK	951.47	123.57	1.76E+04	2.30E+03	9.24E+02	1.07E+03	1.40E+03	1.18E+03	9.95E+02	1.81E+02	4.58E+02	9.74E+03	7.80E+03	5.72E+03	2.47E+02	7.86E+02	1.95E+04
P22695 QCR2	LYIFQASPADAGQYVCR	802.93	123.78	1.01E+05	5.54E+03	9.27E+02	1.80E+03	1.23E+03	1.62E+03	4.18E+02	8.82E+02	2.86E+02	9.99E+02	6.05E+04	2.22E+03	3.69E+03	2.59E+02	5.16E+04
Q15149-3 PLEC1	GLVIASLENYSPVSR	514.95	124.04	1.11E+03	2.04E+02	7.85E+02	1.01E+03	1.93E+02	7.62E+02	1.77E+02	2.86E+02	3.35E+03	2.94E+04	1.61E+02	4.84E+02	1.93E+02	4.11E+03	6.47E+02
P48735 IDHP	LGPHLPLEVAYQR	474.29	124.04	1.62E+04	7.18E+02	1.80E+03	3.25E+03	4.03E+02	4.98E+02	2.32E+03	8.14E+02	2.83E+05	1.59E+04	3.65E+02	4.66E+02	3.63E+03	2.28E+05	1.85E+03
P02511 CRYAB	IIWQFIK	664.81	124.06	1.07E+03	1.89E+04	3.35E+03	1.52E+03	1.25E+03	8.16E+04	3.27E+04	3.19E+04	9.72E+02	1.40E+03	3.15E+03	5.75E+02	3.87E+02	1.10E+03	1.21E+03
P11142 HSP7C	SWFDTGLSEMR	808.90	124.34	1.72E+04	2.94E+02	1.06E+03	1.51E+05	1.49E+03	3.16E+02	1.54E+03	2.20E+03	3.02E+02	1.16E+03	9.97E+04	1.07E+04	2.63E+03	4.07E+02	1.94E+04
Q13423 NNTM	SFYPEEVSSMVLTK	962.49	124.44	1.23E+04	7.84E+03	4.61E+03	1.21E+03	1.61E+04	1.05E+04	6.99E+02	2.43E+03	1.45E+03	5.57E+02	1.83E+03	1.09E+05	9.84E+04	1.31E+03	6.47E+04
P02511 CRYAB	SLGVGYAAVDNPIFYKPN	570.26	124.5	1.69E+05	3.66E+02	1.93E+03	1.27E+05	3.53E+03	5.37E+03	2.82E+03	7.21E+02	4.76E+02	9.52E+02	1.76E+04	8.32E+02	5.12E+03	5.92E+02	9.82E+03
Q13813-3 SPTA2	LFDQFFGEH	556.84	124.6	7.89E+04	2.63E+02	4.55E+02	5.64E+03	1.28E+03	2.88E+02	1.33E+02	3.79E+02	6.50E+02	1.76E+02	3.87E+04	1.38E+03	8.63E+02	8.47E+02	1.31E+04
P06732 KCRM	DLIGVQNLK	822.41	124.74	1.77E+04	1.22E+05	1.61E+03	4.59E+05	1.44E+04	1.74E+05	8.97E+02	9.50E+03	5.96E+02	2.63E+02	1.95E+05	1.23E+05	4.35E+04	4.33E+03	4.62E+05
P15924 DESP	SFLVWVNEEDHLR	667.83	124.9	1.38E+04	7.93E+03	2.28E+02	3.54E+04	2.67E+03	1.51E+03	1.45E+03	1.11E+03	8.11E+02	9.27E+02	7.95E+03	4.22E+02	4.38E+02	9.72E+02	2.13E+03
P17540 KCRS	SVEEVASEIQPF	1055.01	124.96	1.65E+05	5.13E+03	5.97E+03	2.05E+03	3.46E+05	3.82E+03	3.86E+03	5.48E+03	1.42E+03	3.72E+03	5.01E+04	3.60E+04	1.60E+04	3.85E+02	1.14E+05
Q02218 ODO1	GTGGVDTAADVYDISNDR	792.76	124.98	1.28E+03	1.41E+04	2.92E+03	2.09E+02	2.74E+03	2.55E+04	2.38E+03	3.59E+04	5.81E+02	2.12E+02	5.57E+02	9.88E+02	1.25E+03	2.49E+03	1.35E+03
P98160 PGBM	NITLSLVANPSHLEAADPVV	700.91	125.2	4.34E+02	4.22E+02	8.44E+02	6.57E+02	4.12E+02	7.51E+02	3.21E+02	7.64E+02	5.62E+04	4.21E+02	5.90E+02	1.01E+03	7.26E+02	3.21E+04	7.73E+02
P02144 MYG	MGK	450.94	125.42	5.43E+03	3.72E+03	2.80E+03	7.70E+03	1.23E+04	1.19E+04	6.57E+03	1.10E+03	4.33E+02	3.35E+02	1.64E+06	4.48E+04	1.45E+04	2.71E+02	3.39E+03
Q99798 ACON	IPGDQVVSVVFIK	530.28	125.82	3.38E+03	1.81E+03	1.28E+03	8.01E+03	6.31E+02	8.50E+02	1.21E+03	5.71E+02	1.60E+03	1.43E+03	1.84E+04	8.01E+02	1.34E+03	4.83E+02	5.58E+03
P17540 KCRS	HGATVLTALGGILK	905.45	126.65	6.19E+02	7.67E+02	1.71E+03	2.23E+03	2.94E+02	2.96E+03	2.65E+03	7.04E+02	2.85E+04	5.43E+03	2.58E+03	1.03E+04	4.82E+02	5.61E+02	2.87E+03
Q15149-3 PLEC1	LQLEFPDKWDGK	667.89	126.9	5.71E+02	1.29E+03	1.51E+04	3.43E+02	4.57E+04	2.25E+03	2.70E+03	3.29E+02	5.59E+02	3.73E+02	3.96E+02	3.55E+04	8.55E+02	5.44E+02	6.53E+02
P18206-2 VINC	VTPNGYTLQCIQTGVNDP	874.93	127.02	4.58E+04	1.05E+03	6.97E+02	1.70E+03	2.41E+03	1.06E+03	6.62E+02	1.05E+03	4.62E+02	2.20E+03	5.27E+02	1.22E+03	2.44E+03	5.41E+02	1.91E+04
P04406 G3P	GHPFIK	659.84	127.17	4.25E+02	8.68E+02	4.13E+03	2.60E+03	1.17E+04	1.19E+03	8.67E+02	8.43E+02	4.83E+02	1.10E+03	1.00E+03	1.99E+04	3.92E+04	5.55E+02	1.55E+04
P15924 DESP	DEETGLCLLPLK	665.84	127.19	8.10E+02	4.54E+03	9.81E+02	3.40E+02	1.93E+02	2.15E+04	1.28E+03	1.02E+04	6.68E+02	6.07E+03	2.53E+03	1.22E+03	1.05E+03	2.59E+03	2.90E+02
P16615-2 AT2A2	AKDIVPGDIVEIAVGDKVPA	598.34	127.27	6.36E+02	3.84E+02	2.18E+03	1.70E+03	1.31E+03	4.28E+02	9.11E+03	1.14E+03	1.33E+03	2.97E+03	9.33E+02	3.00E+03	8.11E+02	1.65E+03	4.20E+02
P48735 IDHP	DIR	622.85	127.74	9.53E+05	4.49E+03	6.41E+02	3.26E+02	3.14E+03	2.82E+04	1.40E+03	1.05E+03	4.33E+02	8.60E+02	4.02E+05	6.70E+03	1.56E+03	5.62E+02	2.36E+04
P04075 ALDOA	LIDDMVAQVLK	703.04	127.74	4.84E+05	1.58E+03	3.18E+04	8.69E+05	7.84E+03	1.32E+04	4.82E+03	6.58E+03	1.83E+03	4.29E+02	7.08E+05	9.67E+03	7.52E+03	1.10E+03	1.42E+04
Q15149-3 PLEC1	IGEHTPSALAIMENANVLAR	827.43	127.84	3.57E+03	8.89E+03	1.45E+03	4.31E+04	1.09E+03	7.41E+03	6.06E+02	1.47E+03	2.02E+02	1.47E+03	2.07E+04	3.81E+02	2.09E+03	7.90E+02	1.17E+04
P00505 AATM	DPYTGQSVSLFQALK	588.82	128.04	8.42E+02	1.12E+03	6.45E+02	1.06E+03	8.51E+04	8.33E+02	2.90E+02	8.84E+02	1.00E+03	1.28E+03	1.62E+03	3.24E+03	1.55E+03	1.48E+03	7.82E+02
P17540 KCRS	ISVAGVTSSNVGYLAHAIH	627.77	128.25	8.21E+05	7.66E+03	1.98E+03	4.48E+05	1.88E+04	1.75E+04	9.68E+02	2.55E+03	6.19E+02	5.62E+02	4.66E+05	1.20E+04	2.11E+03	2.25E+02	3.48E+04
Q13813-3 SPTA2	QVTK	976.47	128.43	3.27E+04	1.41E+03	1.83E+03	7.45E+02	1.23E+03	1.95E+03	1.16E+03	1.65E+03	6.12E+02	2.17E+02	2.24E+04	1.51E+03	7.20E+02	3.64E+03	2.09E+03
P15924 DESP	GWEFMWNER	583.30	128.96	7.92E+03	1.24E+03	1.96E+03	1.08E+03	7.97E+02	1.34E+03	2.03E+03	1.21E+03	2.19E+03	2.39E+03	3.83E+02	7.24E+03	8.68E+02	3.44E+02	1.03E+04
Q5VTT5 MYOM3	ITISTDAFEDTVTIPSPPTNV	971.50	129.24	1.46E+03	2.48E+03	1.67E+03	8.76E+02	1.21E+03	4.20E+03	1.91E+03	5.47E+02	2.24E+04	2.15E+02	1.57E+03	1.84E+03	6.00E+02	3.55E+02	2.89E+02
P02545-2 LMNA	HASEIR	947.46	129.4	7.45E+02	1.34E+04	8.79E+03	5.02E+02	1.27E+02	1.58E+04	5.92E+03	2.72E+03	4.70E+03	8.17E+					



P02511 CRYAB	APSWFDTGLSEMRLEK	622.97	129.86	8.37E+02	1.42E+03	6.58E+02	9.72E+02	1.93E+03	6.87E+04	5.09E+02	3.72E+03	1.62E+03	3.33E+02	1.41E+03	3.38E+02	3.58E+02	7.72E+02	4.08E+02
Q13813-3 SPTA2	AQLADSFHLQQFFR	569.96	130.68	1.81E+03	9.47E+03	7.06E+02	3.62E+03	3.96E+03	4.52E+04	1.89E+03	2.67E+03	3.95E+02	2.62E+03	1.88E+03	4.23E+03	1.79E+03	6.61E+03	1.44E+03
Q13813-3 SPTA2	DLTSWVTEMK	605.30	130.83	5.98E+03	1.58E+04	1.37E+04	7.99E+03	7.18E+02	1.10E+04	8.66E+03	1.52E+04	9.51E+03	5.28E+04	8.52E+03	5.83E+03	1.12E+04	8.93E+03	1.01E+04
Q13813-3 SPTA2	VEDLFLTFAK	591.82	130.9	1.65E+04	2.56E+03	4.57E+03	1.14E+03	3.93E+03	2.54E+03	2.49E+03	2.20E+03	3.01E+03	1.25E+03	9.80E+03	3.23E+03	1.01E+03	4.49E+03	1.77E+03
P04075 ALDOA	LKPWALTF	488.29	130.95	3.22E+04	2.68E+02	1.40E+03	4.56E+04	2.78E+02	1.66E+03	7.64E+02	1.01E+03	3.30E+02	1.04E+03	1.47E+04	1.36E+03	9.33E+02	2.68E+03	9.40E+02
Q13813-3 SPTA2	EAIVTSEELGQDLEHVEVL	789.41	131	2.08E+04	7.69E+03	9.43E+03	2.39E+05	8.30E+03	1.16E+03	1.22E+04	1.98E+03	7.28E+03	1.49E+04	3.49E+04	6.62E+03	1.88E+04	4.82E+03	2.39E+04
Q5VTT5 MYOM3	FQWFFQR	529.76	131.01	3.90E+02	4.71E+03	6.08E+03	1.18E+03	5.54E+03	3.93E+03	3.68E+03	4.24E+03	4.93E+02	9.78E+02	2.20E+02	6.75E+02	2.83E+02	7.62E+02	4.57E+04
P06732 KCRM	DKETPSGFTVDDVIQTGVD NPGHPF	891.42	131.28	5.32E+04	2.53E+03	5.90E+03	9.71E+03	8.09E+03	6.88E+03	5.79E+03	7.30E+03	1.12E+04	4.07E+03	4.67E+04	8.98E+03	4.26E+03	5.79E+03	2.91E+04
P04406 G3P	VIIAPSADAPMFVMGVNH	978.49	131.34	3.22E+04	9.76E+03	1.05E+04	3.43E+03	2.47E+03	3.56E+03	8.25E+03	3.73E+03	9.06E+03	5.82E+03	1.42E+04	7.96E+03	1.95E+03	1.02E+04	4.94E+03
P06732 KCRM	AGHPFMWNQHLGYVLTCP SNLGTGLR	718.11	131.49	2.55E+03	1.43E+03	5.07E+03	6.09E+02	5.00E+03	2.49E+04	1.82E+04	4.55E+03	1.34E+03	4.33E+03	1.56E+03	8.44E+03	3.96E+03	4.38E+03	1.49E+03
P48735 IDHP	LNEHFLNTDFLDTIK	641.00	131.56	2.64E+05	6.65E+03	5.11E+03	4.63E+03	3.84E+03	1.20E+04	2.68E+03	2.35E+03	1.31E+04	2.25E+03	1.69E+05	8.21E+03	2.50E+03	5.26E+03	2.45E+05
P18206-2 VINC	MQEAMTQEVSDVFSDTTTP	786.70	131.73	3.40E+04	4.53E+03	3.27E+03	6.76E+02	2.26E+03	1.21E+04	7.11E+03	6.01E+03	5.11E+03	1.80E+03	4.37E+04	8.11E+03	1.40E+04	4.98E+03	7.15E+03
Q02218 ODO1	VFHLPTTFIGGQESALPLR	728.73	131.74	8.05E+04	1.20E+04	2.51E+03	1.81E+03	6.47E+03	6.23E+03	4.39E+03	4.60E+02	6.77E+03	1.84E+03	6.70E+04	1.53E+04	1.17E+04	3.31E+03	8.71E+04
P17540 KCRS	EVENVAITALEGLK	743.41	132.13	2.27E+04	1.11E+03	1.19E+04	2.42E+06	4.71E+03	4.47E+03	8.06E+03	9.80E+03	5.32E+03	3.06E+03	3.19E+04	3.47E+03	7.45E+03	1.10E+04	5.85E+04
Q13813-3 SPTA2	EAFNTEKGDLSLDSVEALI	765.38	132.19	1.28E+04	1.40E+04	5.41E+04	9.69E+03	2.40E+04	4.91E+04	9.33E+03	2.03E+04	4.74E+03	2.87E+04	1.91E+04	2.85E+04	4.04E+03	2.44E+04	7.96E+03
P52179-2 MYOM1	FALFDLAEQK	555.79	132.26	2.72E+05	9.54E+03	1.05E+03	2.55E+02	1.21E+04	1.22E+04	4.73E+03	6.01E+03	1.56E+03	4.34E+02	3.67E+05	4.65E+03	1.38E+04	4.71E+03	3.24E+03
P16615-2 AT2A2	TVEEVLGHFGVNESTGLSL EQVK	825.09	132.35	4.63E+03	4.11E+03	3.79E+03	3.39E+03	2.71E+04	3.79E+04	3.08E+03	8.44E+03	4.25E+03	2.40E+03	2.99E+03	2.09E+04	2.53E+03	4.53E+03	4.80E+02
Q99798 ACON	AKDINQEVYNFLATAGAK	651.67	132.63	7.67E+03	3.18E+03	3.08E+03	3.42E+04	6.93E+04	2.89E+04	3.19E+02	2.36E+04	8.97E+02	2.77E+03	8.26E+03	9.32E+03	1.12E+04	2.97E+03	9.45E+02
Q99798 ACON	GHLDNISNLLIGAINIENG	740.40	132.72	2.17E+05	1.97E+04	6.75E+03	3.41E+03	3.78E+03	9.97E+03	8.06E+03	6.38E+03	1.65E+05	2.16E+04	1.16E+05	4.06E+03	1.96E+04	3.36E+05	2.26E+04
Q5VTT5 MYOM3	DCLILTWAPPSDTR	794.39	132.93	1.70E+04	7.89E+02	3.87E+04	1.17E+04	4.59E+04	6.89E+03	5.53E+04	2.58E+04	4.52E+04	3.90E+03	8.29E+03	1.20E+04	1.39E+05	3.97E+03	1.51E+05
Q99798 ACON	DLEDLQILIK	600.35	132.96	1.96E+05	1.79E+03	8.49E+03	4.31E+03	1.66E+04	1.04E+04	1.36E+03	6.31E+03	6.31E+03	1.20E+03	8.73E+04	1.02E+04	5.13E+04	8.24E+03	2.48E+05
P45379 TNNT2	ELWQSIYNLEAEK	811.91	133.03	1.59E+06	6.98E+03	4.06E+03	3.60E+03	1.23E+04	1.66E+04	5.04E+03	1.02E+04	8.00E+03	9.98E+03	1.44E+06	3.77E+03	5.59E+04	2.70E+03	1.35E+04
P04406 G3P	LVINGNPITIFQER	807.45	133.06	2.76E+04	1.50E+03	7.89E+03	8.43E+05	1.81E+03	1.58E+03	2.67E+02	1.11E+04	4.41E+02	1.93E+03	1.50E+04	4.07E+03	1.16E+04	5.95E+02	5.85E+03
Q13813-3 SPTA2	ELPTAFDYVEFTR	794.39	133.13	1.04E+05	2.81E+03	1.06E+04	2.16E+04	4.63E+04	1.48E+04	1.48E+04	3.49E+04	2.49E+03	2.29E+03	1.29E+05	1.32E+04	1.39E+05	3.93E+03	6.76E+03
P52179-2 MYOM1	ENLPSDYMVPIFSGR	862.92	133.23	4.61E+04	2.91E+03	1.06E+04	2.47E+03	7.15E+03	1.08E+04	4.72E+03	3.94E+03	1.96E+03	4.02E+03	9.18E+04	5.54E+03	9.66E+03	3.04E+03	4.41E+04
Q15149-3 PLEC1	ESADPLGAWLQDAR	764.87	133.33	4.53E+04	4.48E+03	6.93E+03	9.53E+03	2.58E+03	6.43E+03	8.65E+03	6.67E+03	7.96E+03	2.12E+03	6.48E+04	1.25E+04	3.34E+03	5.20E+03	1.04E+04
P04406 G3P	VIIAPSADAPMFV	709.37	133.39	5.48E+03	9.20E+04	1.14E+04	8.91E+03	4.58E+03	8.90E+03	1.40E+04	1.27E+04	4.18E+04	5.88E+03	3.72E+03	1.15E+04	2.75E+03	3.75E+04	1.31E+04
P02144 MYG	TVLTALGGILK	543.35	133.41	7.04E+04	1.40E+03	3.63E+02	6.62E+02	2.52E+03	1.85E+03	3.03E+02	6.87E+02	2.57E+02	4.50E+02	4.09E+04	3.64E+03	4.73E+04	6.29E+02	2.21E+03
P18206-2 VINC	VAMANIQQMLVAGATSIA	681.37	133.53	6.87E+03	7.62E+03	3.45E+03	1.29E+03	1.55E+05	4.50E+04	6.27E+03	2.52E+04	5.61E+03	8.36E+03	3.30E+03	1.44E+05	7.82E+03	5.18E+03	1.84E+05
P98160 PGBM	QPDFISFGLVGGPEFR	641.33	133.65	1.07E+04	3.69E+03	1.11E+04	4.20E+03	2.79E+02	3.95E+03	7.94E+03	2.38E+03	1.17E+05	2.23E+04	9.79E+03	1.16E+04	5.18E+04	8.86E+03	
P04075 ALDOA	VNPCIGGVILFHETLYQK	677.70	133.89	5.06E+03	4.00E+03	3.46E+03	2.70E+03	1.42E+04	2.38E+04	3.45E+03	8.30E+03	2.56E+03	1.34E+03	2.46E+03	9.84E+03	6.45E+03	2.35E+03	1.25E+04
P18206-2 VINC	TIESILEPVAQQISH	832.95	133.97	5.50E+03	5.84E+03	9.01E+03	5.36E+04	1.25E+04	7.64E+02	7.99E+03	1.52E+04	3.17E+03	1.02E+04	2.36E+04	1.45E+04	1.30E+04	3.72E+03	7.71E+03
P48735 IDHP	FLNTTDFLDTIK	714.37	134.03	5.86E+03	1.00E+04	9.04E+03	3.76E+03	2.28E+04	2.78E+04	5.14E+03	5.56E+03	2.12E+04	6.17E+03	3.66E+03	1.03E+05	6.66E+04	3.33E+03	1.45E+05
P15924 DESP	SVEEVASEIQPFLR	802.42	134.2	2.58E+04	1.47E+04	9.74E+03	8.23E+03	7.55E+04	1.84E+05	1.43E+04	3.28E+04	1.16E+03	2.12E+03	6.19E+04	1.12E+04	3.08E+04	4.11E+03	8.18E+04
P06732 KCRM	LSVEALNSLTGEFK	754.40	134.43	2.18E+03	1.01E+04	5.79E+03	1.38E+03	4.24E+05	1.58E+05	1.37E+04	3.46E+05	1.63E+04	9.36E+02	1.12E+04	1.67E+05	2.21E+03	1.75E+04	3.93E+02
Q99798 ACON	AFVTSPEIVTAL	624.35	134.44	4.09E+04	2.76E+04	6.33E+03	7.84E+03	4.94E+03	1.99E+04	7.50E+03	1.78E+04	4.07E+03	2.73E+03	1.54E+04	1.05E+04	9.32E+03	3.99E+03	1.47E+04
P15924 DESP	QPVTVTELVDGILR	813.96	134.46	2.35E+03	8.66E+03	1.56E+04	3.21E+03	4.36E+03	4.75E+04	4.24E+03	1.33E+04	2.95E+03	1.01E+04	8.73E+02	3.24E+03	2.19E+03	6.55E+03	1.24E+03
P17540 KCRS	GLSLPPACTRAERREVENV AITALEGLK	749.41	134.53	2.29E+03	2.03E+04	8.00E+03	4.00E+03	8.54E+05	1.87E+05	6.23E+03	1.21E+06	2.11E+04	1.67E+04	4.50E+03	6.70E+05	1.28E+03	1.55E+04	1.39E+03
P52179-2 MYOM1	NTGIEMFMEK	656.82	134.63	1.23E+05	2.34E+03	7.42E+03	3.05E+03	6.28E+03	6.63E+03	2.79E+03	3.77E+03	4.36E+03	3.49E+03	1.39E+05	3.85E+03	8.06E+04	2.33E+03	4.67E+03
P48735 IDHP	FAQMLEKVCVETVESGAM	734.36	134.89	7.33E+02	6.33E+03	2.53E+04	6.43E+03	3.89E+04	2.42E+04	7.60E+03	3.29E+03	3.89E+04	2.59E+03	5.38E+03	1.72E+04	6.21E+03	2.79E+04	1.72E+03
P00505 AATM	NLDKEYLPIGGLAEFCK	637.33	134.92	8.91E+02	5.46E+03	1.55E+04	7.67E+03	4.61E+04	1.35E+04	2.09E+04	7.05E+03	2.25E+04	4.35E+03	8.02E+03	8.86E+03	2.57E+03	5.78E+03	2.62E+02
Q02218 ODO1	SWDIFFR	485.74	134.99	1.28E+05	1.32E+03	9.24E+02	9.12E+04	1.52E+03	6.93E+03	4.48E+02	2.22E+03	5.12E+02	3.81E+02	9.90E+04	1.82E+03	1.88E+03	2.78E+02	1.25E+03
Q13813-3 SPTA2	DVDEIEAWISEK	717.35	135.13	2.58E+03	4.57E+04	1.88E+04	5.81E+03	9.73E+04	7.17E+04	2.06E+04	1.70E+05	3.64E+04	7.22E+03	1.90E+04	2.54E+04	4.09E+03	7.05E+03	1.61E+04
Q99798 ACON	QGLLPLTFADPADYNK	881.95	135.21	6.97E+03	5.75E+03	5.86E+03	8.74E+03	1.21E+05	1.35E+05	1.83E+02	1.50E+04	3.40E+03	1.52E+05	5.14E+03	8.80E+03	2.37E+03	2.08E+03	1.85E+03
P04406 G3P	VIHDNFGIVEGLMTTVH	627.99	135.35	6.60E+05	1.94E+04	6.39E+03	4.21E+05	9.52E+03	1.56E+04	3.47E+03	1.68E+04	1.13E+04	1.54E+03	4.81E+05	1.29E+04	8.02E+04	3.60E+04	1.17E+04
P52179-2 MYOM1	AAIAPSPPCDITCLESFR	663.34	135.42	4.73E+03	6.99E+04	2.63E+04	2.35E+04	8.12E+04	2.13E+04	2.50E+04	4.38E+04	1.68E+04	4.16E+04	2.68E+04	7.14E+04	4.63E+03	1.03E+05	9.52E+03
P22695 QCR2	LPNGLVIASLENYSPVSR	965.02	135.67	6.39E+04	5.59E+04	2.81E+04	6.63E+04	7.20E+04	5.62E+04	6.46E+04	8.16E+04	6.91E+04	4.83E+04	6.22E+04	4.54E+04	3.70E+04	6.94E+04	4.82E+04
P02787 TRFE	TAGWNIPMGLLYNK	789.41	135.74	3.07E+05	4.98E+04	2.20E+05	6.28E+04	2.66E+05	1.34E+05	1.66E+05	9.86E+04	1.47E+05	2.24E+05	3.02E+05	1.62E+05	1.05E+05	1.88E+05	2.46E+05
Q5VTT5 MYOM3	STFGPSVEFTSVLKPVFAR	690.37	135.81	1.84E+05	1.38E+05	6.22E+04	1.80E+05	1.79E+05	2.56E+05	3.33E+05	2.86E+05	3.25E+04	1.88E+05	1.39E+05	2.34E+05	1.42E+05	8.19E+04	1.30E+05
P00505 AATM	EYLPIGGLAEFCK	720.38	135.84	1.73E+05	3.42E+04	1.56E+05	1.02E+05	1.25										



P45379 TNNT2	DLNELQALIEAH	683.35	135.95	5.40E+05	2.35E+05	2.30E+05	4.00E+05	5.59E+04	4.16E+05	1.22E+05	1.10E+05	5.88E+04	3.70E+04	3.07E+05	1.30E+05	1.21E+05	5.25E+04	1.66E+05
P45379 TNNT2	DLNELQALIEAHFENR	637.99	135.98	2.36E+05	1.10E+05	2.99E+03	1.68E+05	3.07E+05	4.66E+05	1.76E+05	1.48E+05	2.28E+05	2.55E+05	3.36E+05	1.73E+05	6.99E+04	1.32E+05	4.81E+05
Q99798 ACON	DINQEVYNFLATAGAK	877.44	135.98	2.84E+05	1.81E+05	1.87E+05	7.92E+04	2.04E+05	3.12E+05	2.58E+05	1.58E+05	1.59E+05	1.42E+05	2.06E+05	7.31E+04	4.34E+04	2.85E+04	2.05E+05
P02787 TRFE	SAGWNIPIGLLYCDLPEPR	1057.54	136.02	6.30E+04	5.76E+04	4.51E+04	6.84E+04	1.08E+05	7.43E+04	5.66E+04	6.15E+04	1.05E+04	6.81E+04	7.95E+04	8.41E+04	1.68E+04	3.12E+04	5.41E+04
P48735 IDHP	DIFQEIFDK	577.79	136.03	1.14E+05	6.14E+04	4.15E+04	5.64E+04	1.09E+04	9.81E+04	1.92E+04	8.17E+04	1.85E+04	8.40E+04	8.92E+04	1.08E+05	1.63E+04	5.71E+04	1.21E+05
P17540 KCRS	TVGMVAGDEESYEVFADLF DPVIK	878.09	136.07	2.76E+04	2.97E+04	4.46E+04	1.33E+04	2.19E+04	1.29E+04	1.40E+04	1.27E+04	3.28E+04	3.01E+04	4.09E+04	8.41E+04	1.27E+04	3.07E+04	4.11E+04
P04075 ALDOA	TVPPAVTGITFL	608.35	136.07	2.16E+05	2.21E+05	4.68E+04	1.21E+05	8.97E+04	1.46E+05	1.50E+05	4.08E+04	1.97E+04	1.18E+05	1.21E+05	1.42E+05	5.58E+04	1.89E+04	8.48E+04
Q02218 ODO1	IEQLSPFPFDLLK	830.47	136.26	2.06E+04	5.06E+04	3.73E+03	4.10E+04	1.39E+04	7.69E+04	9.16E+04	1.02E+05	5.82E+03	7.00E+04	7.72E+04	1.04E+05	4.34E+04	6.56E+04	1.25E+05
P02511 CRYAB	IPADVPLTITSSSLSDGVL VNGPR	875.46	137.89	3.18E+03	7.46E+03	1.54E+03	5.75E+03	4.91E+03	1.47E+03	8.49E+02	1.35E+04	2.06E+03	2.32E+03	1.52E+03	4.53E+03	5.09E+03	4.88E+02	1.14E+03
P60174 TPIS	TATPQQAQEVHEK	489.58	39.61	1.11E+03	1.38E+02	1.87E+02	5.26E+02	2.05E+03	1.46E+03	1.03E+03	4.86E+02	1.21E+02	5.06E+02	3.00E+03	3.96E+02	3.58E+02	2.95E+02	3.82E+02
O75390 CISY	AYAQGISR	433.23	46.48	8.69E+02	2.20E+03	9.85E+02	1.01E+03	1.62E+03	8.66E+02	1.43E+03	1.96E+03	1.35E+03	1.50E+04	1.97E+03	1.35E+03	2.17E+02	1.57E+03	1.72E+03
P09622 DLDH	ADGGTQVIDTK	552.78	47.52	7.47E+02	8.09E+04	3.30E+03	6.57E+03	6.39E+03	4.02E+03	3.81E+03	9.71E+04	4.56E+04	3.55E+04	4.10E+04	7.13E+04	7.64E+03	6.64E+04	2.98E+04
P14923 PLAK	HPEAEMAQNSVR	456.88	47.6	4.39E+02	2.03E+02	2.29E+02	2.20E+03	1.51E+03	4.06E+03	4.84E+02	1.20E+02	2.21E+03	4.97E+04	3.83E+03	7.99E+02	2.88E+02	1.50E+03	1.82E+03
P13929 ENOB	IEEALGDK	437.73	47.88	7.69E+02	4.62E+02	1.52E+04	9.37E+03	1.38E+04	2.08E+04	1.29E+04	2.07E+03	2.23E+04	3.13E+03	1.67E+04	1.67E+04	8.50E+03	2.48E+04	2.35E+02
P08238 HS90B	IEDVGSDEEDDSGK	747.81	49.71	2.32E+03	9.23E+02	1.03E+03	3.75E+03	4.16E+03	8.85E+03	2.72E+02	9.29E+02	5.09E+02	2.07E+03	1.61E+04	3.39E+02	5.75E+02	1.07E+03	5.06E+03
P08670 VIME	QVDVNASLAR	544.77	49.71	1.09E+04	3.25E+02	3.22E+03	8.77E+03	6.84E+03	1.01E+04	1.25E+03	2.24E+03	1.13E+03	7.65E+02	7.83E+02	1.13E+03	2.10E+03	2.66E+02	2.12E+02
P55084 ECHB	LVMAAANR	423.23	50.18	2.06E+03	2.95E+02	3.15E+03	6.73E+03	2.18E+04	6.01E+03	8.16E+03	1.45E+03	8.71E+03	1.49E+02	2.29E+02	6.83E+03	3.28E+03	4.67E+03	1.84E+02
P31930 QCR1	FTGSEIR	405.21	51.07	1.73E+04	1.42E+04	3.58E+03	2.18E+04	3.51E+03	6.05E+03	2.16E+03	1.87E+03	1.15E+04	6.05E+02	1.13E+04	7.97E+03	1.52E+03	1.73E+04	1.21E+04
P55072 TERA	LAGESENLR	538.27	51.63	4.78E+03	6.30E+03	3.97E+03	8.57E+03	3.81E+02	1.23E+03	2.63E+03	4.78E+03	6.33E+02	1.63E+02	9.90E+03	4.26E+03	1.96E+03	1.43E+03	9.98E+03
P14923 PLAK	HVAAGTQQPYTDGVR	533.93	51.88	5.85E+03	3.11E+03	1.94E+03	2.89E+03	2.60E+04	1.78E+04	2.50E+03	2.59E+03	8.98E+02	3.45E+02	1.93E+04	9.21E+03	5.02E+03	9.95E+02	9.33E+03
P40926 MDHM	IQEAGTEVVK	537.29	52.33	9.24E+04	5.72E+04	7.39E+02	8.84E+04	1.23E+05	7.12E+03	9.59E+02	9.00E+03	1.48E+05	1.26E+05	6.82E+04	4.99E+04	3.11E+02	4.66E+04	9.44E+04
Q01082-3 SPTB2	LVSDGNINSDR	595.29	53.62	3.00E+02	3.44E+02	5.20E+02	2.29E+03	1.35E+02	1.86E+03	2.45E+02	8.37E+02	3.17E+03	5.14E+03	2.83E+03	1.59E+02	3.13E+02	2.85E+04	1.49E+02
P19367-4 HXX1	LVPDSDVR	450.74	53.92	1.88E+02	2.02E+03	3.84E+02	9.84E+03	1.63E+03	6.16E+02	1.93E+02	4.87E+02	3.17E+03	3.39E+04	1.79E+03	1.57E+03	3.28E+02	3.19E+02	1.06E+03
Q99959-2 PKP2	EAGPSVAVDSSGR	616.30	54.78	1.33E+04	7.62E+03	3.31E+03	5.65E+04	8.46E+04	8.21E+04	6.73E+03	1.35E+04	8.50E+03	2.83E+04	1.50E+05	5.02E+04	9.54E+02	5.77E+04	4.07E+04
P35555 FBN1	AGYQSTLTR	498.76	55.45	9.01E+02	1.07E+04	1.06E+03	8.23E+02	1.69E+02	4.15E+02	1.45E+03	6.63E+02	9.73E+02	1.73E+04	5.36E+02	1.98E+02	2.43E+03	7.19E+02	8.99E+03
P01024 CO3	QELSEAEQATR	631.30	55.76	4.37E+03	7.04E+02	4.24E+02	6.75E+02	6.37E+02	2.01E+03	2.06E+02	1.78E+03	2.27E+03	2.66E+04	1.59E+03	8.72E+02	2.23E+02	7.62E+03	2.33E+02
P14923 PLAK	TMQNTSDLDTAR	676.81	55.89	5.84E+03	3.85E+03	7.83E+02	6.87E+03	1.45E+03	2.20E+03	8.46E+02	3.83E+02	1.02E+03	3.72E+02	2.29E+04	6.15E+03	4.93E+02	3.92E+02	1.46E+03
P40939 ECHA	ILQEGVDPK	499.78	56.08	2.94E+04	2.10E+04	8.31E+02	3.07E+04	9.48E+04	2.27E+03	7.42E+02	2.97E+03	7.73E+04	4.08E+02	3.59E+04	1.83E+04	7.67E+02	1.06E+04	3.07E+04
P06396-2 GELS	PALPAGTEDTAK	585.80	56.49	1.56E+04	1.19E+04	4.05E+03	4.47E+04	1.48E+03	3.64E+03	5.70E+03	2.53E+04	5.13E+02	6.45E+04	7.52E+04	9.10E+03	6.84E+03	5.86E+02	2.84E+02
P07195 LDHB	IVADKEDYSVTANSK	504.26	56.49	1.29E+05	2.28E+04	3.51E+02	5.11E+04	7.80E+03	8.01E+02	4.94E+03	9.51E+02	2.67E+05	2.98E+05	5.91E+04	5.69E+04	1.82E+03	2.27E+05	6.93E+04
P40925 MDHC	LGVTANDVK	458.76	56.89	4.70E+03	4.96E+02	1.22E+04	1.84E+04	1.49E+03	7.90E+04	1.89E+04	2.28E+04	1.76E+02	4.47E+04	5.05E+04	8.81E+03	2.51E+04	1.87E+04	3.97E+04
P08559 ODPA	YHGHSMSDPGVSUR	531.57	57.01	2.01E+02	1.62E+03	2.05E+03	7.93E+02	5.56E+02	3.30E+04	8.60E+02	1.98E+02	7.17E+04	5.06E+04	1.04E+04	8.72E+02	3.43E+02	2.81E+04	2.20E+03
P11532-4 DMD	VDAAQMPQEAQK	658.32	57.04	1.04E+04	6.59E+03	1.06E+03	8.62E+03	2.90E+03	3.73E+03	1.28E+02	4.62E+02	7.89E+02	2.04E+02	8.23E+03	1.23E+03	1.74E+02	2.95E+02	5.78E+03
P60174 TPIS	SNVSDAVAQSTR	617.80	57.45	8.81E+04	5.18E+04	1.39E+03	1.90E+05	2.53E+05	9.72E+03	1.68E+03	7.40E+03	1.29E+03	1.99E+04	3.29E+05	5.46E+04	1.36E+04	7.07E+03	1.69E+05
P08559 ODPA	YGMGTSVER	500.23	58.33	1.61E+04	2.15E+04	1.22E+03	1.12E+04	9.86E+03	2.88E+03	6.57E+03	1.25E+03	1.55E+05	9.39E+04	1.80E+04	3.12E+03	2.03E+03	8.26E+04	3.44E+04
P11532-4 DMD	TAALQSATPVER	622.33	58.84	1.58E+02	6.41E+03	4.05E+02	9.71E+03	5.38E+03	3.17E+03	1.12E+03	5.77E+03	1.72E+02	2.56E+02	4.42E+04	1.07E+04	3.79E+03	4.88E+02	1.52E+02
O76041 NEBL	HATAISDPPELKR	478.93	58.91	9.75E+02	7.13E+02	4.88E+02	9.03E+02	6.64E+02	1.83E+02	5.73E+02	2.85E+02	3.31E+04	2.09E+04	3.43E+02	1.65E+02	1.06E+03	1.03E+04	5.47E+02
P07195 LDHB	LKDDEVAQLK	579.82	58.92	2.51E+03	4.82E+03	8.24E+02	6.27E+04	3.17E+04	5.06E+04	1.32E+02	7.24E+02	2.51E+03	9.83E+04	5.47E+04	5.77E+03	1.65E+02	2.87E+03	2.16E+03
P31930 QCR1	LCTSATESEVAR	633.80	59.14	6.85E+04	8.33E+04	3.04E+04	5.66E+04	6.87E+04	1.17E+05	5.28E+03	1.35E+04	1.86E+03	6.30E+03	1.01E+05	6.18E+04	6.56E+03	3.36E+02	6.85E+03
P06396-2 GELS	DSQEEETEALTSK	555.93	59.5	3.59E+02	4.71E+02	2.18E+02	9.51E+02	4.34E+02	6.49E+02	8.29E+02	3.44E+02	2.91E+04	1.87E+03	1.23E+03	1.31E+03	2.96E+02	1.42E+04	4.30E+02
P13929 ENOB	TAIQAAGYPDK	567.79	59.64	2.92E+04	2.09E+04	1.85E+03	8.54E+04	1.31E+05	8.57E+04	1.39E+03	5.03E+02	2.04E+03	3.58E+02	1.59E+05	1.82E+04	3.17E+02	4.95E+02	5.54E+04
P40926 MDHM	TPGVAADLSH	484.25	60.15	1.73E+02	3.27E+02	1.26E+04	5.20E+02	1.55E+03	2.95E+03	1.84E+04	2.21E+04	3.97E+02	7.96E+02	7.16E+02	1.40E+03	3.37E+04	7.20E+02	3.24E+02
P24043 LAMA2	LVEHVPQPVR	410.90	60.26	7.60E+04	6.17E+04	2.92E+03	1.24E+05	8.90E+04	1.86E+03	1.21E+03	6.48E+02	9.25E+02	3.78E+02	1.43E+05	3.64E+03	1.43E+03	1.27E+02	1.18E+05
P24043 LAMA2	VSVSSGGDCIR	540.26	60.46	1.85E+04	5.95E+04	8.06E+03	6.38E+04	5.50E+03	5.66E+02	5.75E+02	6.99E+02	4.68E+02	4.48E+03	6.08E+04	3.92E+04	3.33E+03	4.71E+03	7.40E+04
P11047 LAMC1	EVVCTNCPTGTTGK	705.32	60.56	2.14E+04	2.81E+04	7.39E+03	4.72E+04	2.95E+03	1.09E+04	2.60E+03	3.93E+03	1.99E+02	5.00E+02	5.67E+04	3.82E+04	3.83E+03	5.97E+02	1.24E+03
P35555 FBN1	YQCACNPGYHSTPDR	571.24	61.48	3.17E+03	4.35E+03	2.45E+03	7.58E+03	1.82E+02	2.90E+03	3.71E+02	1.63E+03	4.25E+04	2.60E+04	5.60E+02	9.86E+02	2.61E+02	9.70E+03	4.75E+03
P24752 THIL	GQPDVVVKEDEEYKR	597.63	61.49	8.00E+02	2.06E+03	6.36E+02	1.85E+03	1.07E+05	1.53E+04	2.03E+04	2.83E+03	3.72E+02	8.41E+02	8.29E+02	7.58E+03	1.47E+03	7.94E+02	8.51E+02
P17174 AATC	VGNLTVVGK	443.77	61.64	2.21E+02	8.32E+02	2.81E+03	3.42E+04	2.63E+04	2.57E+04	1.47E+03	5.46E+03	4.58E+02	6.49E+02	1.06E+03	2.27E+04	1.16E+03	3.57E+02	1.17E+03
P06396-2 GELS	HVVPNEVVVQR	425.91	61.79	4.44E+02	6.46E+04	2.81E+03	1.09E+05	5.19E+03	3.94E+03	3.40E+03	5.33E+03	2.53E+02	4.53E+02	1.50E+05	9.06E+04	3.12E+03	1.40E+02	9.73E+04
P08559 ODPA	SMSDPGVSUR	549.75	61.84	2.11E+03	3.51E+03	3.36E+04	2.72E+03	3.20E+02	8.55E+02	2.90E+04	5.78E+04	4.18E+02	2.94E+03	5.25E+03	1.02E+03	4.48E+04	1.08E+03	2.31E+03
P24043 LAMA2	VNVEGIH																	

Q01082-3 SPTB2	VLDNAIETEK	566.30	63.16	5.92E+02	6.60E+03	1.60E+04	2.77E+03	1.18E+04	6.54E+03	2.49E+04	3.80E+03	6.72E+02	6.26E+02	4.08E+04	2.63E+03	3.73E+03	5.22E+02	2.20E+03
P11532-4 DMD	QLLEQPQAEAK	627.84	63.5	3.34E+03	1.76E+03	1.58E+03	2.47E+04	4.12E+04	2.78E+03	3.73E+02	1.03E+04	1.46E+04	2.46E+04	5.09E+04	2.54E+02	2.79E+02	1.43E+04	2.32E+03
P06396-2 GELS	TGAQELLR	444.25	63.73	2.03E+04	1.13E+04	2.91E+03	5.52E+03	3.65E+03	3.48E+03	1.39E+03	7.97E+02	8.19E+03	8.75E+03	2.04E+04	5.20E+02	2.39E+03	1.79E+04	3.20E+04
P01857 IGHG1	ALPAPIEK	419.76	63.94	2.06E+05	1.03E+04	1.63E+03	5.14E+03	1.27E+04	1.02E+04	2.15E+03	2.74E+02	9.02E+04	3.92E+05	9.99E+03	7.99E+03	2.53E+03	6.36E+04	9.76E+03
O75390 NEBL	HATAISDPPELK	426.89	64.15	5.92E+03	4.44E+03	1.92E+03	3.78E+03	2.33E+03	7.66E+03	3.58E+03	8.42E+02	2.06E+03	1.42E+03	7.48E+04	5.73E+03	2.15E+03	3.94E+02	3.98E+04
O76041 NEBL	GMQAGTDTLEMQHAK	539.92	64.41	2.57E+03	2.81E+04	1.80E+04	7.50E+04	2.76E+03	1.46E+04	2.16E+03	2.11E+03	3.90E+03	3.62E+02	6.12E+04	1.98E+04	1.35E+03	1.96E+03	6.60E+03
P08237 K6PF	IGLIQGNR	435.76	64.41	5.88E+03	7.14E+03	1.04E+03	3.52E+03	3.39E+02	9.34E+02	6.63E+02	2.23E+03	3.13E+03	3.07E+04	4.17E+03	9.12E+02	2.58E+03	3.21E+03	4.42E+03
P04792 HSPB1	QLSSGVSEIR	538.29	64.51	1.27E+05	1.31E+05	9.65E+03	2.86E+05	3.40E+05	8.99E+03	5.14E+03	5.44E+03	1.52E+03	1.41E+04	2.71E+05	2.41E+05	1.33E+04	4.42E+03	1.57E+05
P07195 LDHB	IVADKDYSVTAN	648.32	64.52	4.97E+03	1.29E+04	5.22E+02	8.20E+03	3.94E+03	1.12E+04	2.72E+02	4.77E+02	4.52E+04	5.22E+04	3.60E+04	3.11E+03	4.64E+03	1.74E+04	8.43E+03
P08572 CO4A2	IAVQPGTVGPQGR	640.36	64.56	4.13E+05	1.68E+05	1.10E+04	4.99E+05	3.75E+05	1.59E+03	7.03E+03	3.33E+03	5.13E+02	4.16E+02	3.96E+05	1.71E+05	1.51E+03	3.23E+03	4.74E+05
P55268 LAMB2	SLAASTAETAGSAQGR	803.89	64.62	5.62E+02	3.62E+02	2.55E+04	1.36E+02	3.56E+02	4.84E+04	3.90E+03	3.25E+03	1.11E+03	1.59E+03	8.95E+02	5.71E+02	2.74E+02	1.39E+02	6.35E+02
P08670 VIME	DGQVINETSQHDDLE	612.94	64.62	6.30E+04	3.41E+03	7.70E+02	1.74E+03	2.12E+03	3.77E+03	2.93E+03	2.12E+03	1.50E+03	1.76E+03	2.12E+04	1.34E+03	1.91E+03	8.33E+02	6.85E+04
O75390 CISY	TDHQFTELTR	416.54	64.66	1.54E+03	1.49E+04	4.45E+03	2.93E+03	1.16E+03	1.72E+04	2.53E+02	2.21E+04	3.69E+03	3.00E+02	1.26E+04	1.11E+03	3.45E+04	3.27E+03	4.83E+03
P19429 TNNI3	VDKVDEERYDIEAK	570.28	64.87	4.08E+02	4.95E+02	1.37E+02	1.77E+03	7.13E+05	1.68E+04	1.01E+04	8.92E+02	2.12E+03	6.12E+02	5.14E+04	1.69E+05	6.53E+02	8.36E+02	1.08E+05
P11532-4 DMD	DQAANLMANR	552.28	65.05	7.17E+03	1.16E+05	6.12E+04	6.53E+04	4.62E+04	1.26E+03	1.32E+05	3.57E+04	2.08E+04	1.70E+04	6.03E+04	3.78E+05	2.35E+05	1.20E+05	5.90E+03
P35555 FBN1	ISPDLCGR	430.72	65.08	6.39E+03	5.62E+03	1.28E+04	3.25E+04	4.66E+03	5.35E+03	1.03E+04	3.69E+03	2.55E+04	5.74E+04	4.97E+03	2.10E+04	5.46E+03	8.82E+03	3.10E+03
Q01082-3 SPTB2	VAVVNIQIAR	485.29	65.31	5.47E+02	2.54E+04	1.70E+03	1.99E+03	1.30E+05	1.32E+03	6.55E+03	3.69E+03	5.02E+03	1.37E+03	9.51E+04	5.01E+04	3.37E+03	1.29E+03	7.13E+04
Q01082-3 SPTB2	AFEDEMSEGR	521.22	65.36	1.64E+04	6.68E+03	3.40E+03	1.36E+03	4.34E+03	1.42E+03	1.72E+03	2.77E+03	6.44E+04	7.09E+04	3.17E+03	2.47E+03	1.94E+03	5.51E+04	4.61E+03
P24752 THIL	EVVIVSATR	487.29	65.46	8.77E+02	1.56E+03	1.15E+06	1.97E+06	6.79E+06	3.84E+06	1.74E+06	1.21E+06	5.30E+05	4.67E+05	1.22E+03	1.22E+03	1.85E+06	4.22E+05	9.11E+02
Q9NPC6 MYOZ2	AELPDYR	432.22	65.61	1.11E+05	1.30E+05	2.04E+04	1.14E+04	4.80E+05	2.20E+04	1.79E+05	8.66E+03	8.78E+04	1.40E+05	5.31E+05	7.48E+04	4.82E+03	8.69E+04	2.32E+05
P09622 DLDH	GIEMSEVR	460.73	65.64	4.89E+03	1.05E+04	9.81E+02	9.32E+03	2.33E+02	1.17E+04	4.76E+03	2.59E+03	1.08E+05	8.96E+04	3.58E+03	1.28E+04	5.24E+02	6.62E+04	2.54E+05
P08237 K6PF	MQQGSPTPFDR	660.81	66	7.47E+03	1.03E+04	1.11E+03	1.76E+04	4.15E+03	7.09E+02	1.52E+03	1.35E+03	3.94E+04	1.45E+05	1.77E+04	1.36E+03	9.98E+02	2.51E+04	2.21E+04
P08107 HSP71	ATAGDTHLGGEDFDNR	559.25	66.06	1.49E+05	7.63E+04	1.83E+04	1.47E+05	1.53E+05	1.73E+04	5.38E+04	9.49E+03	2.31E+03	2.67E+04	2.10E+05	9.75E+04	1.16E+04	7.25E+03	1.79E+05
P11021 GRP78	LTPEEIER	493.76	66.1	5.72E+03	1.99E+03	1.68E+04	8.34E+03	4.24E+03	1.06E+04	3.50E+04	4.40E+04	4.62E+05	3.91E+05	3.98E+03	4.07E+02	1.07E+04	3.48E+05	3.01E+03
P05413 FABPH	SIVTLDGGK	445.25	66.21	1.93E+04	4.85E+04	1.74E+04	2.22E+04	1.14E+04	1.54E+04	3.99E+04	2.26E+04	4.86E+04	6.57E+04	1.50E+05	9.23E+04	2.83E+04	1.09E+04	2.06E+05
Q99959-2 PKP2	IQEQQVQTLAR	657.36	66.24	1.52E+05	4.61E+04	3.79E+03	1.65E+05	1.20E+05	6.16E+03	1.70E+03	3.75E+03	8.54E+03	4.08E+02	2.11E+05	5.44E+04	4.60E+03	5.97E+03	1.43E+05
P14923 PLAK	GIMEDEACGR	605.25	66.41	3.35E+03	1.92E+04	2.70E+03	1.02E+04	2.97E+04	1.81E+03	1.04E+03	3.95E+03	7.03E+02	3.20E+03	4.02E+04	1.98E+04	1.10E+03	6.98E+02	3.90E+04
P08238 HS90B	EQVANSAFVER	625.31	66.47	8.88E+03	3.81E+04	1.13E+03	7.72E+04	4.42E+04	2.29E+03	2.37E+03	3.74E+03	2.90E+04	2.45E+04	1.08E+05	1.70E+04	8.82E+03	1.30E+04	1.38E+04
P11532-4 DMD	YQETMSAIR	549.77	66.53	3.93E+03	1.17E+04	1.14E+04	3.48E+04	8.82E+03	2.42E+03	1.69E+04	3.07E+03	3.16E+04	4.43E+04	4.37E+03	4.81E+03	4.15E+03	1.83E+04	4.13E+03
P40925 MDHC	GEFVTTVQQR	582.80	66.62	4.85E+05	9.06E+03	2.50E+03	1.49E+04	6.63E+03	4.16E+03	5.86E+04	1.02E+03	1.79E+06	1.65E+06	1.21E+04	7.91E+03	4.11E+03	7.56E+05	1.09E+06
P00558 PGK1	LGRPDGVMPDK	427.89	66.69	7.87E+04	4.26E+04	3.33E+03	2.63E+04	2.50E+03	4.60E+03	1.74E+02	3.51E+03	1.52E+03	2.27E+03	1.76E+04	2.33E+03	3.97E+03	2.53E+04	2.12E+04
Q96HC4 PDLI5	SPSWQRPNQVPSTGR	585.30	66.92	7.04E+04	8.53E+03	1.87E+03	4.38E+04	6.97E+04	1.03E+04	1.02E+04	1.45E+03	1.53E+03	9.14E+03	3.22E+04	1.77E+04	1.18E+04	6.54E+02	3.48E+03
Q9NPC6 MYOZ2	EVHGNVDGMDLGR	495.89	67.05	1.59E+03	4.38E+04	1.34E+04	9.00E+04	1.79E+03	2.36E+04	1.60E+04	1.00E+04	1.07E+03	7.91E+02	8.12E+04	5.67E+03	1.01E+04	1.28E+03	9.19E+04
P08670 VIME	LQDEIQNMK	559.78	67.09	6.58E+03	1.57E+04	3.47E+03	3.98E+03	6.24E+02	3.42E+02	1.61E+03	1.03E+04	5.96E+04	1.58E+05	1.09E+04	1.75E+03	5.69E+03	4.26E+04	1.32E+03
P08572 CO4A2	GLDGYQGPDPGR	616.30	67.15	1.21E+05	1.01E+04	1.26E+03	5.42E+04	8.02E+03	9.09E+03	7.13E+02	2.04E+03	8.04E+04	1.21E+05	2.47E+04	4.87E+03	1.66E+04	6.15E+03	1.70E+05
P55084 ECHB	NVVVVDGVR	478.78	67.16	2.70E+04	4.93E+04	6.91E+02	2.71E+03	9.74E+03	7.33E+02	2.68E+03	1.23E+04	1.29E+05	8.89E+04	6.21E+04	2.85E+02	8.08E+03	9.61E+04	4.05E+04
P24043 LAMA2	TGFGGVSCDR	499.72	67.21	3.74E+04	5.52E+02	2.54E+03	4.32E+03	7.37E+04	2.33E+04	9.23E+04	7.55E+04	3.61E+04	1.04E+05	1.98E+04	1.34E+03	1.67E+04	1.93E+04	3.10E+03
P09622 DLDH	VCHAGTLESAFR	489.91	67.35	3.95E+02	8.14E+04	3.37E+03	3.37E+04	2.45E+03	4.18E+04	7.74E+03	1.17E+03	3.03E+02	4.98E+02	1.18E+03	6.72E+04	1.89E+04	4.82E+02	9.87E+04
O75390 CISY	VVPGYGHAVLR	584.33	67.38	1.11E+03	1.27E+05	2.01E+03	1.66E+05	6.27E+05	3.05E+03	8.59E+02	9.77E+02	4.90E+03	4.72E+02	2.43E+05	2.56E+05	4.60E+03	1.81E+03	2.94E+05
Q99959-2 PKP2	LEISPDSSPER	615.30	67.48	9.51E+03	1.37E+05	1.99E+03	2.56E+05	1.18E+03	9.31E+04	4.82E+03	1.17E+04	8.70E+02	1.06E+03	1.94E+05	1.25E+04	6.94E+03	1.10E+03	1.05E+05
P11216 PYGB	VEDVEALDR	523.27	67.52	1.13E+05	8.37E+03	6.78E+03	3.06E+03	7.78E+04	4.18E+04	4.81E+04	1.06E+03	9.15E+05	5.06E+05	2.08E+04	2.87E+04	1.41E+04	9.48E+05	3.27E+05
P08670 VIME	FANYIDK	435.72	67.58	7.38E+02	6.25E+02	3.21E+03	9.94E+02	1.26E+03	4.86E+02	5.32E+03	6.81E+03	4.05E+04	3.62E+04	4.55E+02	7.46E+02	8.24E+03	1.69E+04	1.92E+03
P55268 LAMB2	GPLGDQYQTVK	603.31	67.61	4.35E+03	1.23E+03	1.19E+04	3.36E+03	8.08E+03	3.59E+04	1.18E+03	4.75E+02	2.12E+04	5.53E+03	8.14E+04	5.85E+02	1.53E+04	1.60E+03	5.86E+04
P04792 HSPB1	DGVVEITGK	459.25	67.85	1.90E+02	1.53E+03	1.09E+03	8.97E+02	2.12E+04	4.07E+04	3.75E+04	3.81E+04	4.03E+03	9.88E+03	3.74E+03	2.08E+03	1.26E+05	3.87E+03	5.32E+03
P01024 CO3	AAVYHHFISDGVR	491.25	67.97	4.61E+02	2.27E+03	1.41E+04	1.14E+03	1.78E+03	5.50E+03	9.60E+03	1.48E+03	1.84E+04	4.94E+04	7.65E+03	3.38E+03	1.58E+03	1.18E+04	6.73E+03
P55268 LAMB2	AAQLDGLER	522.28	68.01	1.52E+03	3.50E+05	3.35E+04	5.21E+05	4.28E+05	2.23E+04	3.69E+05	3.61E+03	4.40E+04	7.47E+02	3.63E+05	4.42E+05	1.61E+04	1.35E+03	9.74E+03
P13929 ENOB	GNPTVEVDLHTAK	690.86	68.13	2.73E+05	1.84E+05	5.99E+03	2.37E+04	4.30E+04	4.50E+04	6.96E+03	5.09E+03	2.53E+03	8.52E+03	2.97E+05	2.20E+05	1.54E+04	1.80E+03	3.76E+05
O75390 CISY	PGYGHAVLR	485.27	68.17	7.68E+03	8.75E+02	2.34E+03	1.80E+02	9.03E+02	3.36E+02	1.50E+03	2.26E+03	3.38E+05	2.21E+05	3.07E+03	6.65E+03	1.38E+03	1.95E+05	4.84E+03
P11532-4 DMD	EEAEQVLGQAR	615.31	68.31	4.29E+03	9.04E+03	1.75E+03	1.33E+03	4.74E+04	1.48E+03	1.61E+03	1.93E+03	3.84E+04	9.73E+04	7.86E+04	6.03E+03	1.03E+03	8.42E+04	7.82E+04
P11532-4 DMD	LASLEPR	441.75	68.38	9.77E+03	5.89E+03	5.50E+03	1.13E+04	1.68E+04	3.71E+03	4.94E+02	6.02E+03	2.57E+02	4.26E+02	4.05E+04	1.72E+04	1.02E+04	1.85E+02	7.77E+03
P05413 FABPH	THSTFKNTEISFK	513.93	68.61	1.														

P00558 PGK1	AHSSMVG VNL P Q K	684.36	69.67	1.53E+04	1.34E+03	6.26E+02	2.41E+03	1.93E+03	6.18E+02	9.97E+02	1.40E+03	1.43E+03	8.83E+02	6.83E+04	7.61E+02	3.73E+02	2.22E+02	7.92E+04
P07195 LDHB	IVVVV TAG V R	457.29	69.71	1.35E+03	2.97E+05	2.50E+04	1.09E+05	1.52E+06	9.40E+04	5.28E+04	3.73E+04	3.84E+03	1.57E+03	3.53E+05	1.14E+06	5.56E+05	1.06E+03	3.59E+05
P55084 ECHB	LEQDEYALR	568.78	69.94	1.94E+05	2.52E+03	5.66E+03	2.81E+04	8.09E+03	2.62E+03	6.79E+02	1.25E+03	6.27E+05	1.61E+03	4.81E+05	7.29E+02	3.47E+02	8.00E+02	3.04E+04
P24752 THIL	MGNVLQGGEGQAPTR	757.87	70	2.79E+05	2.85E+03	7.84E+02	5.51E+03	8.34E+02	5.80E+02	1.94E+03	6.16E+03	5.99E+02	6.69E+02	7.39E+04	8.97E+02	1.90E+02	2.55E+02	3.89E+04
P17174 AATC	INVSGLTTK	466.77	70.12	1.12E+04	3.27E+04	5.43E+03	9.67E+03	1.18E+04	9.24E+03	1.19E+05	5.73E+03	3.81E+03	5.47E+02	2.13E+05	1.01E+05	2.16E+04	1.48E+03	9.44E+04
P31930 QCR1	IAEVDASVVR	529.80	70.18	1.63E+06	1.81E+06	1.68E+04	1.93E+06	1.94E+06	2.01E+04	7.02E+04	2.55E+04	4.69E+02	9.01E+02	1.18E+06	1.99E+06	1.27E+06	1.98E+05	1.72E+06
P08670 VIME	FADLSEAA NR	547.27	70.29	6.32E+05	2.36E+05	5.00E+03	6.26E+05	4.05E+05	1.53E+04	3.37E+02	2.06E+03	6.03E+02	2.42E+03	2.89E+05	1.24E+05	3.51E+03	7.82E+02	6.56E+05
P28331 NDUS1	VGMQIPR	400.73	70.63	6.96E+02	4.87E+03	1.56E+03	9.39E+03	1.99E+04	8.62E+03	2.58E+04	2.75E+04	1.66E+05	1.27E+04	5.66E+03	2.46E+03	5.95E+02	6.60E+03	1.33E+05
P63261 ACTG	GYSFTTTAER	566.77	70.69	7.83E+05	7.29E+05	2.82E+04	9.81E+05	6.39E+05	4.47E+04	2.15E+04	5.68E+03	4.44E+02	1.58E+03	9.99E+05	4.57E+04	4.24E+04	2.07E+03	9.92E+05
Q99959-2 PKP2	YSQNIYQNR	649.83	70.76	5.82E+04	1.22E+03	1.68E+03	7.44E+03	4.32E+03	1.17E+03	1.04E+03	1.13E+03	1.46E+03	2.44E+03	5.12E+04	6.34E+02	6.14E+02	1.74E+03	4.36E+04
P11532-4 DMD	QITVDSEIR	530.79	70.9	4.94E+03	3.74E+04	4.24E+03	6.29E+04	4.74E+04	8.07E+04	2.69E+04	6.15E+02	8.14E+04	5.36E+03	2.54E+03	3.63E+04	6.27E+03	2.36E+05	7.16E+04
P40926 MDHM	VNV P V I G G H A G K	574.33	71.05	9.37E+04	2.08E+03	1.34E+03	1.22E+03	1.18E+05	1.25E+03	1.27E+03	2.86E+03	4.32E+04	5.88E+04	1.01E+05	3.09E+03	4.30E+02	2.40E+04	1.29E+05
P55268 LAMB2	AGNSLAASTAEETAGSAQG	616.96	71.07	5.31E+04	6.03E+02	9.41E+02	7.32E+04	3.46E+03	1.20E+03	1.32E+03	1.05E+03	8.67E+02	1.62E+03	6.35E+04	7.10E+02	1.07E+03	8.86E+02	7.75E+04
P28331 NDUS1	VVLGSSALQR	515.30	71.31	4.42E+04	7.13E+03	2.12E+03	7.21E+03	4.07E+02	2.17E+02	1.42E+03	1.68E+03	2.96E+02	1.40E+03	5.02E+04	2.66E+03	9.20E+02	4.35E+02	6.05E+04
P11047 LAMC1	DNVEGFNCER	591.75	71.8	3.34E+02	2.81E+03	4.35E+03	1.17E+03	4.63E+02	1.26E+04	9.65E+02	2.07E+02	1.84E+04	3.72E+04	4.28E+02	1.97E+02	3.48E+03	1.07E+04	2.10E+03
O76041 NEBL	GTAISDPPELK	564.29	71.85	5.96E+05	7.20E+05	2.75E+05	4.10E+05	1.25E+03	9.94E+05	1.01E+05	1.01E+04	6.59E+02	9.56E+02	5.28E+03	1.96E+05	3.87E+04	1.09E+03	3.48E+03
P05413 FABPH	QVASMTKPTTIEEK	516.29	72.01	7.41E+05	5.98E+04	4.51E+03	9.43E+04	8.82E+03	3.32E+03	3.85E+03	6.47E+02	2.67E+04	6.18E+03	5.48E+05	4.61E+04	5.07E+04	6.81E+02	1.88E+04
P11177 ODPB	VVSPWNSEDAK	616.30	72.08	8.14E+02	8.01E+04	8.49E+02	2.59E+05	1.73E+05	1.11E+04	1.66E+05	6.56E+03	1.15E+04	4.28E+04	1.92E+03	1.25E+05	3.83E+03	4.13E+03	2.25E+03
P08107 HSP71	GGSGSGPTIEEVD	602.77	72.13	1.20E+03	8.13E+04	5.69E+03	1.77E+05	6.28E+03	5.10E+03	8.48E+03	1.51E+03	5.70E+02	8.25E+02	3.37E+03	6.26E+04	3.83E+03	2.90E+03	1.89E+03
P08559 ODPA	SSDPPFEVR	517.25	72.13	3.09E+03	7.97E+03	7.09E+03	1.89E+04	2.10E+03	4.55E+04	7.68E+04	2.45E+03	8.50E+02	3.52E+03	6.41E+04	3.34E+04	5.09E+03	7.71E+02	5.63E+04
P40939 ECHA	DTSASVAVGLK	559.80	72.18	2.83E+02	1.09E+05	1.35E+03	1.24E+05	1.15E+05	2.21E+03	5.89E+03	1.44E+03	5.58E+02	2.19E+02	1.58E+04	9.10E+04	1.76E+04	1.72E+03	6.47E+02
P28331 NDUS1	VAVTPPGLAR	490.80	72.21	9.74E+02	2.00E+05	2.36E+05	3.27E+05	4.35E+05	1.23E+05	3.16E+05	1.21E+06	2.22E+02	1.07E+03	1.44E+03	7.00E+05	1.68E+05	5.78E+02	1.31E+05
P31930 QCR1	MVLAAGGVEH	527.77	72.27	3.45E+04	4.18E+04	5.44E+03	1.72E+04	2.93E+03	2.58E+04	4.47E+03	4.56E+03	5.69E+03	2.60E+03	9.63E+03	1.15E+04	5.12E+04	5.28E+03	1.88E+04
P24752 THIL	LNVTPLAR	442.27	72.48	1.32E+03	1.90E+05	2.30E+02	2.05E+05	2.35E+05	5.69E+03	2.67E+05	1.60E+03	5.90E+04	3.71E+04	1.67E+03	2.00E+05	4.06E+05	8.52E+03	2.59E+03
P17174 AATC	ITWSNPPAQGAR	649.34	72.63	3.14E+05	4.41E+04	1.48E+03	2.35E+05	5.51E+04	1.90E+04	5.13E+03	4.59E+03	3.77E+02	3.34E+03	3.07E+05	3.82E+03	1.10E+04	4.91E+02	4.93E+05
P11047 LAMC1	EAQQALGSAADATEAK	816.40	72.68	1.09E+05	2.10E+03	1.03E+03	3.58E+04	2.96E+04	1.01E+03	1.84E+03	4.09E+03	1.23E+03	1.10E+03	9.25E+04	8.59E+02	1.11E+03	7.15E+02	9.67E+04
P24043 LAMA2	EGNDALDEANR	623.29	72.68	4.74E+02	5.83E+03	5.70E+03	7.99E+03	1.25E+05	5.09E+04	2.36E+04	7.08E+02	7.30E+03	1.45E+04	2.07E+03	2.35E+04	6.47E+02	2.23E+03	1.46E+03
P55268 LAMB2	DLLQAAQDK	501.27	72.75	3.91E+04	1.81E+03	1.99E+04	2.20E+03	1.75E+05	9.19E+02	9.72E+04	2.24E+04	4.11E+04	4.07E+03	2.05E+05	3.17E+04	3.19E+03	3.46E+04	1.41E+05
P60174 TPIS	TGEISPGMIK	516.77	72.8	1.14E+03	5.08E+03	3.85E+03	1.51E+04	1.78E+04	2.96E+04	1.10E+04	1.78E+03	7.92E+02	1.12E+03	3.08E+04	4.36E+04	1.05E+04	1.41E+03	2.12E+04
P24752 THIL	MLEIDPQK	487.25	72.89	1.15E+03	1.49E+03	6.34E+03	3.71E+03	2.65E+05	5.36E+03	1.85E+03	8.77E+02	4.91E+03	2.35E+03	8.23E+04	1.61E+03	2.33E+03	4.92E+04	9.45E+04
P31930 QCR1	SLLTYGR	405.23	73.12	3.85E+03	3.72E+04	4.38E+02	1.42E+04	3.95E+05	5.44E+03	3.95E+05	2.37E+03	4.93E+04	4.49E+04	9.82E+02	1.14E+05	1.56E+05	4.05E+05	1.12E+03
P35555 FBN1	GEDIDVECEK	620.25	73.16	7.87E+04	1.11E+04	1.18E+04	1.10E+04	9.28E+02	5.05E+02	6.76E+03	1.68E+03	6.39E+02	2.68E+02	8.89E+03	1.18E+03	2.96E+02	6.05E+02	5.90E+03
P19429 TNNI3	NICIDLSGMEGRK	645.83	73.27	7.09E+03	8.82E+02	1.00E+05	1.23E+04	5.41E+04	2.95E+04	7.83E+04	3.19E+03	3.79E+04	2.77E+03	5.76E+03	4.32E+04	4.95E+03	8.48E+04	3.34E+03
O75390 CISY	HLPNDPMFK	549.77	73.47	6.53E+04	2.22E+03	2.33E+03	2.39E+03	6.90E+03	5.04E+02	8.97E+02	2.90E+03	2.07E+05	1.29E+05	1.26E+03	5.70E+02	9.14E+02	8.71E+04	1.99E+03
P11532-4 DMD	EGPYTVDAIQK	610.81	73.53	5.36E+04	3.31E+04	3.22E+04	2.07E+04	1.09E+03	2.27E+04	8.79E+02	6.83E+02	8.10E+03	1.21E+04	2.39E+04	1.13E+04	5.23E+04	7.17E+03	1.41E+04
P40939 ECHA	DATLTALDR	488.26	73.64	4.00E+03	3.12E+05	1.32E+03	3.70E+05	5.11E+05	2.36E+05	3.06E+05	1.31E+03	7.76E+03	1.66E+04	1.75E+03	2.53E+05	3.92E+05	3.12E+04	8.36E+03
P60174 TPIS	IYGGSVTGATCK	635.33	73.68	9.02E+03	1.96E+02	3.92E+03	1.38E+05	4.60E+03	5.07E+03	4.14E+02	1.21E+03	6.47E+03	1.95E+03	2.89E+05	1.12E+04	9.09E+02	1.37E+03	2.42E+05
P24752 THIL	DGLTDSVYNK	512.75	73.85	1.32E+05	1.24E+05	1.34E+04	1.98E+05	3.59E+04	3.00E+04	2.36E+04	8.21E+03	4.23E+04	3.26E+04	1.06E+05	2.68E+04	5.12E+03	3.05E+04	1.40E+05
P19367-4 HXX1	FLSESMSGK	512.77	73.91	8.78E+04	6.16E+02	5.03E+03	6.62E+03	3.65E+04	7.02E+04	4.09E+04	1.26E+03	1.95E+05	9.38E+04	9.13E+04	6.59E+04	2.72E+03	2.13E+05	2.62E+04
P19367-4 HXX1	TTVGVDGSLYK	570.30	74.12	2.29E+03	4.39E+04	9.26E+03	1.19E+05	5.99E+04	1.98E+04	2.06E+04	2.32E+04	1.34E+03	2.51E+03	7.32E+03	3.31E+04	1.31E+05	8.83E+02	8.34E+03
Q01082-3 SPTB2	LESEHPDQAQAILSR	565.29	74.2	1.81E+04	4.61E+03	1.40E+04	1.45E+03	3.85E+02	2.01E+03	6.17E+02	9.75E+04	2.36E+03	1.55E+03	2.56E+04	1.68E+04	7.26E+03	6.36E+03	1.52E+04
Q99959-2 PKP2	AALLVPPR	418.77	74.43	5.88E+03	3.49E+03	2.67E+03	1.31E+04	1.16E+04	9.98E+03	1.07E+04	1.04E+04	4.10E+04	1.22E+04	2.65E+04	1.22E+04	3.73E+04	5.86E+04	1.55E+04
P55268 LAMB2	LQELEGTYEENER	805.37	74.56	6.73E+04	1.98E+03	1.12E+04	1.00E+04	3.04E+04	1.35E+04	5.17E+03	5.93E+02	1.22E+03	2.77E+03	4.54E+04	1.79E+03	5.67E+03	1.88E+02	5.51E+04
P31930 QCR1	EVESMG AHLNAYSTR	555.59	74.61	1.32E+03	4.01E+04	1.60E+04	1.01E+05	2.10E+05	1.91E+04	3.43E+04	4.94E+04	3.34E+03	1.71E+03	1.56E+03	5.98E+04	1.30E+03	1.88E+03	2.86E+03
P24043 LAMA2	IDDL S Q E I K	530.78	74.82	2.63E+04	4.38E+03	7.71E+04	1.91E+04	1.50E+03	8.49E+04	4.72E+02	1.20E+04	1.61E+04	2.65E+03	2.41E+04	6.86E+03	6.11E+03	2.60E+04	1.96E+04
P11532-4 DMD	SPFPSQHLEAPEDK	527.92	74.88	6.88E+04	5.71E+02	5.61E+02	3.66E+02	2.44E+03	1.63E+03	3.25E+02	8.06E+02	4.13E+03	4.44E+03	8.50E+04	5.20E+02	3.04E+03	6.37E+03	2.64E+03
P09622 DLDH	EANLAASFGK	504.26	75.03	4.07E+03	1.44E+05	1.52E+04	3.25E+05	6.58E+05	2.55E+05	4.12E+05	2.40E+04	2.77E+03	7.87E+02	4.54E+05	3.19E+05	3.53E+05	6.65E+03	5.05E+02
P11532-4 DMD	LSGLQPQIER	570.82	75.08	1.10E+05	9.64E+03	1.38E+04	5.26E+03	1.78E+03	1.12E+03	1.33E+03	1.12E+03	5.52E+02	4.71E+02	1.14E+05	2.84E+02	8.86E+02	1.24E+03	2.19E+03
P13929 ENOB	GNPTVEVDLH	540.77	75.1	1.49E+05	4.23E+04	7.82E+04	3.99E+04	1.37E+04	7.53E+03	3.75E+04	2.18E+03	4.06E+03	3.50E+03	8.46E+04	1.87E+04	8.41E+03	1.70E+04	8.49E+02
P68371 TBB2C	INVYNEATGGK	664.83	75.43	3.43E+05	4.38E+02	4.78E+04	7.88E+04	1.23E+03	2.24E+05	6.61E+04	3.59E+02	2.60E+03	1.99E+03	3.21E+05	1.78E+03	5.71E+04	2.30E+03	2.65E+05
P19367-4 HXX1	FLSQIESDR	547.78	75.62	1.43E+														

P08572 CO4A2	ATPFIECNGGR	582.78	76.43	6.34E+02	1.90E+03	2.08E+05	1.09E+05	6.43E+02	1.63E+05	3.40E+04	1.41E+03	3.24E+03	6.19E+03	7.19E+02	4.09E+04	1.21E+03	1.33E+03	3.20E+03
P11047 LAMC1	NTIETGNLAEQAR	773.38	76.66	1.46E+05	6.96E+03	4.19E+03	1.44E+05	1.22E+04	1.70E+04	1.56E+04	4.20E+03	1.71E+03	1.68E+03	8.65E+04	2.14E+05	6.13E+03	1.73E+03	1.14E+05
P11532-4 DMD	VLQEDLEQEVR	743.38	76.74	2.60E+04	1.60E+04	5.94E+03	1.49E+04	2.69E+02	4.98E+03	3.32E+04	1.76E+04	2.47E+03	4.87E+03	5.77E+04	1.27E+04	1.34E+04	7.90E+02	1.12E+04
P11532-4 DMD	LLEQSIQSAQETEK	802.41	76.88	1.24E+03	2.70E+03	4.11E+02	1.22E+02	3.87E+02	3.19E+03	2.50E+03	1.08E+03	1.09E+04	2.90E+04	1.63E+03	3.68E+03	1.06E+04	3.32E+03	7.67E+02
P11532-4 DMD	ILADLEENR	601.31	76.88	1.20E+05	4.15E+03	3.76E+03	5.95E+03	2.29E+03	2.86E+03	1.48E+03	3.22E+03	8.93E+04	9.43E+04	1.60E+05	1.43E+03	3.14E+05	6.87E+04	2.02E+04
P55084 ECHB	AMIVEAYPK	511.27	77.05	4.00E+05	1.36E+03	4.11E+04	1.35E+04	3.69E+04	1.55E+03	6.17E+02	7.75E+04	1.11E+05	1.32E+05	4.15E+05	1.59E+03	2.32E+03	1.13E+05	1.75E+04
P19367-4 HXX1	GAAMVTAVAYR	555.29	77.1	1.03E+05	1.63E+03	4.10E+03	3.27E+03	6.61E+03	1.71E+03	3.95E+03	4.02E+03	8.11E+02	1.17E+03	1.12E+05	1.77E+03	4.98E+03	5.43E+03	2.32E+03
Q01082-3 SPTB2	LEDLEVIQHR	417.90	77.15	1.66E+03	3.47E+04	2.68E+02	8.90E+04	9.62E+02	1.06E+04	6.86E+02	2.78E+03	4.53E+03	1.85E+03	2.80E+02	1.45E+04	1.33E+03	1.21E+03	3.46E+02
P55084 ECHB	DLMPHDLAR	534.27	77.23	2.14E+05	6.76E+04	2.19E+03	5.55E+04	8.91E+04	5.70E+03	2.46E+03	2.09E+03	6.83E+04	2.26E+03	4.33E+04	7.84E+03	5.65E+04	1.89E+05	6.58E+04
P24752 THIL	LEDLIVK	415.25	77.23	6.61E+02	2.24E+03	2.08E+04	2.36E+05	3.87E+05	2.53E+05	2.32E+05	6.20E+04	9.17E+03	8.79E+02	2.85E+03	1.72E+05	2.98E+05	5.04E+03	2.09E+03
P09622 DLDH	FPFAANSR	455.23	77.37	5.88E+02	9.49E+03	4.59E+04	4.31E+05	4.04E+02	2.61E+05	1.56E+05	3.18E+05	3.78E+05	1.67E+05	1.71E+03	3.63E+03	6.95E+02	4.13E+04	1.95E+04
P55268 LAMB2	ALAEGGSILSR	537.30	77.41	2.47E+05	1.25E+04	1.00E+03	2.80E+04	6.46E+03	2.65E+04	9.33E+03	1.96E+04	5.10E+04	8.44E+04	3.45E+05	6.27E+03	3.64E+05	3.16E+03	2.66E+04
P19429 TNNI3	IDALSGMEGR	524.76	77.45	9.21E+02	1.01E+05	2.41E+03	1.27E+05	5.09E+03	2.69E+03	4.54E+04	8.85E+02	1.15E+03	2.97E+03	2.51E+03	6.44E+04	2.95E+03	4.25E+02	5.96E+04
P08107 HSP71	FGDPVVQSDMK	611.79	77.46	1.74E+05	1.52E+03	3.79E+04	2.77E+03	1.08E+03	1.73E+03	1.63E+03	4.21E+04	1.05E+04	3.17E+05	2.06E+05	7.66E+04	8.34E+02	4.54E+04	3.09E+03
P28331 NDUS1	NRLLEVSPNLVR	475.93	77.48	6.02E+02	2.77E+03	8.94E+02	1.07E+04	2.90E+05	4.93E+03	1.70E+05	2.05E+03	3.34E+03	5.91E+02	4.60E+03	1.30E+05	5.46E+03	4.83E+02	1.30E+04
P17174 AATC	VFGLYNER	506.75	77.48	3.93E+03	3.67E+03	2.37E+04	1.61E+04	3.19E+03	1.18E+05	1.39E+03	1.43E+04	5.25E+02	8.00E+04	1.93E+03	8.16E+04	2.66E+03	1.88E+05	6.22E+03
P17174 AATC	HIYLLPSGR	528.30	77.86	3.05E+03	4.30E+03	3.49E+03	2.84E+03	1.48E+04	6.22E+03	1.04E+03	1.26E+03	7.49E+02	2.34E+03	3.08E+05	2.92E+03	9.16E+03	1.65E+04	2.00E+04
P09622 DLDH	IDVSIEAASGGK	573.80	77.9	1.75E+04	9.37E+03	1.78E+04	2.45E+04	3.22E+04	1.18E+04	5.55E+03	2.86E+03	1.94E+03	1.97E+03	2.88E+04	1.38E+04	6.48E+03	7.31E+03	4.87E+04
P05413 FABPH	LGVEFDETTADDRK	532.59	78.01	1.95E+04	3.23E+04	9.37E+03	7.01E+04	3.19E+04	2.79E+03	9.99E+03	5.07E+03	2.57E+05	1.98E+05	7.00E+03	1.65E+05	1.60E+04	2.67E+05	2.78E+04
P40925 MDHC	EVGVYEAALK	504.27	78.2	6.26E+03	1.02E+04	4.00E+05	8.66E+05	4.04E+02	9.11E+05	2.68E+03	1.09E+04	1.43E+03	2.20E+03	3.77E+03	1.94E+05	1.39E+03	4.98E+02	9.45E+02
P55084 ECHB	AALTGLLHR	476.29	78.51	4.62E+06	6.88E+06	5.00E+06	2.71E+05	1.80E+06	3.98E+06	6.78E+05	1.34E+04	1.50E+04	1.92E+04	2.12E+03	3.04E+06	5.59E+06	2.84E+02	2.30E+03
P08670 VIME	TYSLSALRPSTSR	499.27	78.61	8.94E+04	3.91E+04	1.33E+03	1.91E+05	1.77E+05	8.43E+03	3.53E+04	2.95E+02	3.37E+03	7.64E+03	1.48E+04	5.25E+04	6.06E+03	1.77E+04	2.43E+05
P55084 ECHB	VGLPPEK	426.76	78.71	1.08E+03	3.08E+05	1.79E+05	7.07E+05	6.32E+02	4.19E+05	3.28E+04	9.96E+05	2.63E+02	1.40E+04	9.11E+02	2.99E+05	1.07E+03	1.53E+03	6.39E+03
P00558 PGK1	ALMDEVVK	452.74	79.04	1.81E+03	7.26E+05	3.81E+03	9.99E+03	5.98E+05	1.37E+04	6.21E+05	4.94E+04	4.03E+02	4.75E+02	3.68E+02	7.87E+05	4.79E+05	4.68E+03	6.79E+05
P05413 FABPH	WDGQETTLVR	602.80	79.1	6.38E+03	2.88E+05	5.73E+04	4.34E+05	2.39E+05	1.76E+05	4.50E+04	1.23E+05	4.14E+04	2.04E+05	1.10E+04	4.62E+05	2.29E+03	1.92E+04	7.25E+05
P08670 VIME	SLYASSPGGVYATR	714.86	79.15	4.02E+05	4.76E+03	5.27E+03	9.81E+04	5.44E+04	1.88E+04	1.96E+03	8.97E+03	6.30E+02	2.12E+03	2.26E+05	1.02E+04	1.48E+05	2.73E+03	1.45E+05
P40939 ECHA	SEVSSDEDIQR	706.32	79.25	1.39E+04	8.68E+04	1.22E+04	8.09E+04	2.23E+04	1.09E+04	1.02E+04	3.99E+03	4.41E+02	3.74E+02	7.79E+04	3.66E+04	1.78E+04	1.26E+04	1.83E+04
P40925 MDHC	DVIATDKEDVAFK	725.87	79.32	6.01E+04	1.20E+04	5.54E+04	2.04E+05	1.40E+05	2.46E+04	6.60E+03	3.38E+04	2.51E+03	4.28E+02	1.51E+05	1.70E+05	1.17E+05	6.83E+03	1.71E+05
P19429 TNNI3	AELQDLR	474.23	79.38	9.51E+04	2.70E+03	6.38E+03	6.06E+02	2.43E+03	3.64E+02	4.42E+02	9.45E+02	1.65E+03	4.41E+03	7.49E+04	2.07E+03	4.48E+03	2.90E+03	7.41E+03
P24752 THIL	NEQDAYAINSCTR	772.85	79.43	1.06E+05	3.05E+03	1.14E+03	5.52E+03	8.15E+03	4.29E+02	7.55E+02	8.87E+02	1.02E+04	4.93E+03	1.86E+04	4.50E+03	2.03E+03	5.22E+02	7.52E+03
P17174 AATC	VGGVQSLGGTGALR	636.36	79.44	1.49E+06	6.03E+03	9.42E+03	3.02E+04	1.40E+04	1.24E+04	5.51E+03	1.02E+03	3.53E+03	1.17E+03	2.11E+06	1.83E+06	1.18E+06	1.10E+04	2.41E+06
P55268 LAMB2	DTEQTLVQVQR	755.36	79.78	1.41E+03	2.53E+03	7.29E+02	1.10E+03	2.00E+03	3.83E+03	4.70E+03	1.02E+04	1.63E+04	4.06E+04	7.87E+02	3.68E+03	5.99E+03	5.94E+03	2.60E+03
O76041 NEBL	ATTLVTPEMER	667.33	79.86	3.29E+03	1.33E+05	4.84E+02	2.34E+04	3.59E+03	9.76E+02	3.68E+03	1.23E+03	5.81E+02	5.21E+02	1.53E+03	1.13E+05	1.14E+05	1.11E+03	5.87E+03
P28331 NDUS1	KPMVVLGSSALQR	462.60	79.86	2.29E+03	7.71E+04	2.90E+03	1.64E+05	2.28E+05	8.90E+04	1.65E+05	9.34E+03	2.99E+02	1.36E+03	1.33E+03	9.09E+04	3.82E+03	2.04E+02	3.16E+03
Q99959-2 PKP2	DLNLTGGIQR	529.80	80.01	1.23E+05	1.03E+04	5.27E+03	3.02E+05	3.28E+04	1.01E+04	1.13E+04	1.52E+04	1.20E+04	2.39E+04	2.83E+05	5.39E+04	5.33E+04	4.30E+03	2.14E+05
P19367-4 HXX1	AEMELGLR	459.74	80.08	3.07E+02	1.34E+05	7.76E+03	2.91E+03	1.51E+05	2.10E+04	1.14E+05	2.12E+04	5.42E+04	3.63E+04	8.68E+04	1.54E+05	8.04E+02	3.13E+03	1.54E+05
P40939 ECHA	FVDLYGAQK	520.77	80.25	4.72E+05	3.28E+03	6.76E+02	6.41E+03	6.41E+05	2.20E+03	1.11E+03	3.03E+03	7.35E+03	6.94E+02	4.41E+05	1.97E+04	5.95E+04	2.68E+03	5.06E+05
P08107 HSP71	LNVHFVEEFKR	473.26	80.33	1.11E+03	2.55E+03	2.98E+04	2.43E+03	5.06E+04	4.52E+02	3.33E+04	3.30E+04	5.27E+03	1.25E+04	2.49E+03	7.18E+04	8.72E+02	9.44E+02	2.72E+03
P19367-4 HXX1	FNTSDVSAIEK	605.80	80.36	1.54E+03	3.92E+03	5.37E+02	1.46E+05	8.01E+02	2.85E+02	7.29E+03	4.23E+03	1.38E+03	1.25E+03	1.55E+05	7.82E+04	3.29E+04	2.98E+03	1.31E+05
P11532-4 DMD	DSTQWLEAK	539.26	80.39	5.65E+03	1.49E+03	1.19E+03	1.62E+03	2.25E+03	2.81E+04	6.26E+03	2.07E+03	3.98E+03	7.62E+02	4.33E+03	7.45E+02	5.06E+03	1.84E+03	1.22E+03
P05413 FABPH	NGDILTLK	437.26	80.66	5.33E+03	3.91E+04	9.78E+03	3.13E+03	4.02E+03	2.95E+03	8.29E+02	1.13E+03	2.34E+05	2.12E+05	1.98E+03	7.52E+02	3.05E+03	2.15E+05	1.71E+04
P60174 TPIS	HVFGESDELIGQK	486.91	80.68	2.28E+05	1.78E+03	2.49E+03	2.94E+03	1.89E+03	4.48E+02	8.90E+02	1.69E+03	2.18E+03	1.32E+03	2.06E+05	3.75E+03	2.67E+03	7.96E+02	1.80E+03
P08670 VIME	EEAENTLQSF	662.31	80.88	5.57E+05	2.27E+05	8.56E+02	7.53E+04	3.92E+03	3.67E+02	4.07E+03	4.16E+02	2.71E+03	9.87E+02	2.88E+05	3.17E+05	1.17E+05	6.38E+03	4.64E+05
Q01082-3 SPTB2	IVSSSDVGHDEYSTQSLVK	684.34	81.25	1.42E+03	4.39E+02	2.41E+03	6.03E+04	1.96E+04	1.54E+05	2.31E+04	1.41E+03	9.56E+02	2.12E+03	5.48E+04	2.55E+04	4.14E+04	2.03E+03	4.13E+04
P28331 NDUS1	LEEVSPLVR	578.32	81.26	4.80E+05	5.56E+03	3.98E+03	1.86E+04	2.07E+03	1.65E+03	1.02E+03	2.84E+04	4.64E+02	2.67E+03	3.04E+05	8.20E+02	1.86E+04	9.47E+02	1.35E+04
P19367-4 HXX1	ITPELLTR	471.79	81.31	4.69E+05	4.88E+05	3.79E+02	8.03E+02	6.25E+04	5.63E+04	3.60E+04	2.92E+03	8.99E+02	7.07E+02	5.85E+05	9.80E+03	5.75E+05	1.83E+02	5.24E+04
P00558 PGK1	ALESPERPF	523.27	81.35	8.17E+03	1.18E+05	9.39E+02	7.52E+04	3.23E+03	5.08E+02	1.67E+03	6.69E+03	4.77E+03	3.93E+04	5.56E+03	3.42E+03	5.19E+04	5.75E+02	6.20E+04
P11047 LAMC1	DIEEIMK	439.22	81.45	4.60E+03	1.05E+04	1.43E+05	3.85E+03	2.10E+03	1.07E+04	2.98E+03	1.25E+05	8.64E+02	2.08E+03	1.34E+03	6.14E+03	4.44E+02	1.53E+04	1.05E+03
Q01082-3 SPTB2	VLVLSQDYGK	561.31	81.55	1.16E+03	6.25E+02	5.10E+03	1.45E+04	1.65E+03	2.87E+03	9.10E+02	8.98E+03	5.54E+02	2.27E+03	3.96E+04	4.21E+02	1.63E+04	1.34E+03	6.40E+04
P35555 FBN1	GFYKPDVK	540.81	81.6	1.25E+05	2.04E+03	2.68E+02	1.01E+03	7.96E+02	1.02E+03	1.73E+03	1.49E+05	3.43E+03	7.66E+02	8.43E+04	3.31E+02	6.37E+02	3.54E+04	6.82E+03
P17174 AATC	LALGDDSPALK	550.30	81.72	9.99E+05														

Q71U36 TBA1A	DVNAAIATIK	508.29	82.96	5.81E+03	1.43E+05	2.22E+04	2.80E+05	2.05E+05	3.86E+05	3.80E+04	3.45E+03	4.83E+04	1.19E+03	2.29E+05	1.92E+05	3.49E+04	3.03E+03	2.97E+05
P40926 MDHM	VNVVPVIGGH	446.26	83.02	5.91E+05	5.65E+03	1.34E+04	1.08E+03	3.11E+03	3.02E+03	8.73E+04	1.23E+04	2.22E+06	1.71E+06	2.47E+05	6.02E+03	4.19E+04	1.54E+06	5.18E+05
O76041 NEBL	GMQVSTDTLDVQR	725.35	83.22	1.55E+05	6.84E+02	4.42E+02	1.34E+05	4.39E+03	2.21E+03	1.96E+03	2.64E+03	5.31E+02	1.55E+03	1.24E+05	5.88E+03	2.18E+04	1.38E+03	1.38E+05
P40939 ECHA	FGELVMTK	462.75	83.25	1.56E+05	9.38E+04	1.22E+04	1.54E+03	2.02E+04	1.36E+05	4.90E+04	6.42E+03	3.52E+03	1.53E+03	1.88E+05	6.54E+04	9.40E+04	2.90E+03	9.45E+05
P11177 ODPB	ILEDNSIPQVK	628.35	83.35	4.06E+05	3.65E+04	1.03E+04	1.32E+04	1.36E+04	1.81E+04	1.48E+04	1.72E+03	1.44E+03	2.39E+04	3.15E+04	3.04E+04	4.25E+03	1.60E+03	1.09E+04
P14923 PLAK	LLNDEDPVVVTK	671.37	83.42	1.49E+04	1.06E+04	4.65E+03	1.51E+05	7.45E+02	7.92E+02	3.33E+02	8.49E+02	1.80E+03	7.38E+02	1.25E+05	1.17E+03	3.76E+04	4.19E+03	1.41E+05
P01024 CO3	GYTQQLAFR	542.28	83.74	9.22E+03	9.77E+02	1.17E+03	1.33E+03	1.38E+03	2.94E+03	4.28E+02	1.93E+03	8.15E+02	1.24E+05	9.41E+03	3.76E+02	8.97E+02	3.88E+04	2.90E+03
P08559 ODPA	SKSDPIMLLK	566.32	83.8	1.80E+03	1.06E+03	1.54E+03	9.25E+02	1.64E+04	2.84E+04	7.09E+04	1.09E+03	3.25E+03	5.56E+02	9.54E+02	7.05E+04	4.99E+02	6.44E+02	1.78E+03
P14923 PLAK	LAEPSQLLK	499.80	83.8	1.02E+03	1.53E+05	6.45E+03	3.59E+05	1.82E+05	4.68E+05	3.06E+04	8.69E+02	9.61E+02	6.77E+02	2.04E+02	1.20E+05	8.72E+02	2.55E+03	5.01E+03
P11216 PYGB	FSAFLEK	421.23	83.98	2.55E+04	9.68E+02	1.52E+03	2.62E+03	7.19E+02	1.61E+03	4.32E+03	3.11E+03	4.24E+03	8.71E+02	9.22E+04	2.62E+03	6.72E+04	5.67E+03	1.05E+03
P40926 MDHM	ANTFVAELK	496.77	84.02	7.86E+05	4.53E+03	1.67E+03	2.56E+04	3.16E+03	1.68E+04	2.99E+03	5.74E+03	8.02E+02	5.56E+02	7.79E+05	2.93E+03	1.55E+04	1.38E+03	2.31E+04
P11532-4 DMD	QAPIGGDFPAVQK	664.35	84.02	6.89E+03	2.08E+03	2.90E+03	1.38E+04	1.23E+04	5.53E+04	1.26E+03	5.83E+04	1.40E+03	3.05E+03	4.82E+03	1.22E+03	1.98E+03	2.77E+05	2.29E+03
P31930 QCR1	EVESMG AHLNAY	660.80	84.04	1.49E+05	8.65E+02	2.68E+03	4.90E+03	1.18E+03	2.25E+03	9.20E+02	1.23E+03	1.90E+02	2.30E+03	8.85E+04	4.02E+03	2.71E+04	1.06E+03	5.95E+04
P08572 CO4A2	AHNQDLGLAGSCLAR	508.91	84.09	1.60E+05	4.30E+03	1.44E+03	5.44E+04	1.81E+04	7.39E+03	1.71E+03	9.27E+02	4.51E+02	7.12E+02	1.41E+05	1.03E+03	3.92E+04	7.60E+02	1.88E+05
P19429 TNNI3	NIDALSGMEGR	581.78	84.55	2.77E+06	2.81E+06	1.06E+05	5.30E+06	4.96E+05	1.03E+05	4.57E+04	2.51E+04	5.82E+02	4.90E+03	3.04E+06	8.39E+03	4.48E+05	4.99E+02	2.59E+06
Q01082-3 SPTB2	ETASELLMR	525.27	84.6	4.40E+05	1.94E+05	1.67E+04	2.02E+05	1.53E+04	1.87E+05	6.37E+04	1.75E+03	1.61E+04	1.59E+03	2.27E+05	8.28E+04	3.43E+05	4.40E+03	3.46E+05
P11177 ODPB	DAINQGMDEELERDEK	631.28	84.74	7.01E+02	3.51E+03	5.71E+03	1.22E+03	8.84E+04	7.95E+02	8.60E+02	4.72E+02	1.17E+03	9.00E+02	7.49E+02	9.60E+03	1.84E+03	1.96E+03	8.62E+02
P55268 LAMB2	DALLEALK	436.76	84.82	9.62E+02	5.94E+05	5.54E+03	6.39E+05	3.86E+05	6.24E+05	3.19E+05	5.92E+03	4.23E+02	1.32E+04	3.37E+03	1.54E+05	1.72E+04	6.05E+02	1.68E+04
P55084 ECHB	DFMYVSQDPK	615.28	85.05	2.71E+05	5.93E+03	1.15E+03	1.17E+03	6.71E+03	4.72E+02	5.07E+02	1.15E+04	3.24E+03	1.38E+03	2.23E+05	6.96E+03	5.28E+02	3.01E+03	4.23E+03
O75390 CISY	GFSIPECQK	504.74	85.33	1.69E+05	3.84E+03	1.75E+03	1.39E+04	5.73E+03	1.45E+03	2.90E+04	7.49E+03	5.93E+03	2.06E+02	1.54E+05	4.65E+02	2.78E+04	2.97E+03	1.04E+05
P40926 MDHM	AGQATLMSMAYAGAR	727.85	85.54	3.24E+05	2.00E+04	5.67E+03	1.21E+05	4.71E+04	1.38E+04	1.70E+03	5.34E+03	1.67E+04	3.53E+03	1.55E+05	1.90E+04	2.21E+05	1.99E+04	3.44E+05
P01857 IGHG1	EPQSVYTLPPSRDELTK	624.99	85.59	2.21E+03	4.65E+02	1.21E+03	1.39E+03	1.39E+05	1.25E+03	7.91E+04	1.58E+05	2.64E+03	3.04E+03	7.89E+02	8.82E+03	7.47E+02	1.16E+03	8.49E+02
O75390 CISY	SAAVTALNSES NFAR	769.38	85.87	5.15E+04	2.20E+04	2.92E+03	5.44E+03	9.46E+02	1.18E+03	1.21E+03	6.56E+02	2.01E+03	5.93E+02	1.01E+04	5.42E+03	9.27E+02	2.44E+03	1.38E+03
P05413 FABPH	LVDSKNFDDYMK	492.23	86.37	1.42E+03	1.63E+03	1.78E+04	3.31E+02	1.17E+03	1.17E+05	9.53E+02	2.19E+04	9.07E+03	5.56E+03	1.18E+03	1.02E+03	1.97E+03	1.19E+04	1.59E+04
P08107 HSP71	AQIHDLVLVGGSTR	489.28	86.39	2.06E+05	2.66E+04	2.07E+03	3.40E+04	1.83E+03	1.01E+04	5.82E+02	1.63E+03	2.37E+04	5.72E+03	2.07E+05	6.38E+03	2.55E+04	3.22E+03	3.31E+03
P08237 K6PF	NVLGHMQQGGSPFPDR	614.30	86.45	1.39E+05	2.54E+03	4.49E+03	1.69E+04	1.02E+05	2.07E+04	3.98E+04	2.55E+05	5.46E+03	5.88E+03	2.17E+05	1.50E+04	2.84E+03	3.62E+03	3.22E+05
P31930 QCR1	QGTPLAQAVEGPS NVR	876.95	86.55	1.55E+05	2.70E+03	1.44E+03	6.73E+04	3.36E+02	2.38E+03	8.69E+03	4.57E+04	3.97E+03	2.80E+02	3.37E+04	9.11E+02	4.40E+03	5.79E+03	4.81E+03
P07195 LDHB	LIAPVAEE EATVPNNK	565.64	86.8	3.25E+05	3.19E+04	1.83E+04	4.36E+05	1.64E+04	7.20E+03	5.65E+04	7.29E+02	3.12E+03	3.65E+02	2.84E+05	1.00E+05	1.71E+05	2.30E+03	3.97E+05
P07195 LDHB	EEEATVPNNK	565.77	86.85	1.16E+05	3.04E+04	6.51E+02	3.52E+05	4.01E+03	3.66E+03	1.63E+03	8.54E+03	3.55E+03	2.82E+03	7.63E+04	3.55E+03	1.18E+04	3.17E+03	6.12E+04
P31930 QCR1	DDALPFAH	443.21	86.88	1.51E+03	4.31E+05	7.33E+02	3.98E+05	3.68E+05	2.72E+05	2.73E+03	1.30E+03	2.61E+03	3.98E+03	1.23E+03	2.44E+05	2.38E+04	4.73E+03	3.63E+02
O75390 CISY	ALGFPLERPK	564.33	86.89	4.93E+03	3.43E+05	1.99E+03	2.83E+05	4.14E+05	1.86E+04	5.16E+04	9.49E+02	1.57E+03	8.78E+02	6.03E+03	5.35E+02	1.68E+04	7.79E+02	3.17E+05
Q99959-2 PKP2	AHLTVGQAAAGSGNLLTE	641.67	86.9	2.06E+03	1.51E+03	2.57E+03	9.32E+04	3.37E+03	6.57E+03	4.49E+02	1.71E+03	6.74E+02	5.22E+03	1.18E+05	1.77E+03	2.39E+04	1.09E+03	1.09E+05
P14923 PLAK	LVQLLVK	406.78	86.9	4.38E+04	3.68E+03	8.02E+02	2.90E+03	1.39E+03	1.44E+03	1.30E+03	7.77E+02	4.42E+03	6.10E+03	1.00E+05	8.75E+02	3.40E+04	8.75E+02	6.16E+03
P63261 ACTG	VAPEEHPVLLTEAPLNPKA NR	575.31	86.92	2.95E+05	6.81E+06	9.30E+06	1.19E+07	9.15E+06	8.40E+06	1.29E+05	1.08E+05	1.24E+04	4.92E+03	3.15E+05	4.94E+06	3.64E+04	2.20E+04	2.26E+05
P28331 NDUS1	VVAACAMPVMK	560.29	86.94	5.51E+02	3.95E+02	2.52E+03	2.13E+04	2.67E+03	1.57E+03	2.40E+03	2.49E+03	2.02E+04	4.00E+04	2.47E+03	9.68E+04	1.55E+04	3.91E+04	7.50E+04
P40925 MDHC	NVIIWGNHSSTQYPDVNHA	570.79	86.98	7.36E+04	1.17E+03	1.99E+03	9.22E+02	2.00E+04	5.40E+03	5.29E+03	1.22E+03	1.80E+03	2.20E+03	4.70E+02	2.90E+02	8.30E+02	5.23E+03	3.03E+03
P55084 ECHB	LMLDLNK	423.74	87.13	5.67E+03	1.42E+05	8.40E+02	1.27E+05	1.61E+05	1.13E+04	5.92E+03	7.33E+03	6.54E+04	2.49E+05	4.54E+03	1.04E+05	1.13E+03	2.24E+04	1.73E+05
P01024 CO3	ISLPSLK	443.77	87.38	3.07E+03	2.20E+02	1.69E+05	9.70E+02	1.17E+03	1.66E+03	1.68E+05	7.66E+03	1.72E+03	5.02E+03	3.61E+03	3.26E+03	3.48E+03	1.40E+03	4.03E+03
Q01082-3 SPTB2	IDDIFER	454.23	87.39	2.18E+05	4.78E+03	9.81E+02	1.95E+04	9.18E+03	1.24E+02	9.70E+02	1.13E+03	2.72E+03	1.71E+03	2.28E+05	2.30E+03	2.44E+05	1.91E+03	2.50E+05
P11177 ODPB	DAINQGMDEELER	760.34	87.72	1.44E+04	6.12E+03	4.26E+02	2.53E+05	4.26E+03	3.73E+03	4.52E+03	3.47E+03	1.62E+03	5.46E+02	1.73E+05	5.30E+02	4.51E+04	1.13E+03	2.65E+05
P07195 LDHB	GSLFLQTPK	495.78	87.87	6.18E+03	3.64E+03	1.03E+03	1.83E+03	1.27E+03	1.74E+03	1.28E+03	2.86E+02	1.06E+03	3.08E+02	1.14E+05	1.57E+03	7.63E+03	7.73E+02	1.48E+03
P31930 QCR1	LSSPLASGAVANK	607.85	87.87	4.02E+02	1.95E+04	1.78E+04	2.72E+04	9.77E+02	2.23E+04	2.56E+03	9.02E+03	1.10E+05	3.21E+05	5.22E+02	2.95E+02	9.08E+02	4.44E+04	1.25E+03
P17174 AATC	IGADFLAR	431.74	87.91	1.73E+03	1.94E+06	2.24E+04	3.20E+06	1.69E+06	2.13E+06	2.96E+04	1.66E+03	2.77E+05	3.57E+05	2.35E+03	1.23E+05	1.75E+06	5.19E+06	2.59E+06
P00558 PGK1	VDFNVPK	475.24	88.09	3.23E+03	7.39E+04	1.46E+04	4.21E+05	5.51E+04	1.81E+04	6.13E+03	1.68E+05	7.55E+02	1.29E+03	2.01E+05	1.38E+04	7.86E+03	7.50E+02	2.13E+05
P08670 VIME	LGDLYEEEMR	627.79	88.15	6.42E+04	3.65E+03	6.78E+03	1.65E+05	8.28E+03	3.34E+02	4.61E+03	4.23E+03	5.07E+04	7.98E+02	3.37E+05	3.13E+04	2.97E+05	3.07E+03	3.78E+05
P05413 FABPH	LGVFEDETTADDR	734.33	88.33	3.16E+05	1.52E+05	2.02E+04	1.03E+06	1.06E+05	4.57E+04	2.62E+04	5.81E+04	2.11E+02	2.05E+03	1.05E+06	3.47E+05	9.90E+05	2.27E+04	2.25E+05
P28331 NDUS1	VAGMLQSFQGK	583.30	88.33	1.03E+04	2.13E+05	1.77E+03	2.27E+05	4.81E+04	2.96E+05	1.39E+03	5.30E+03	3.39E+02	7.56E+02	7.18E+04	9.28E+04	1.27E+04	3.59E+04	2.00E+05
O76041 NEBL	EPAVIGRPDFEHAVEASK	651.33	88.34	6.70E+02	2.77E+03	1.89E+03	6.61E+04	3.04E+04	1.73E+03	1.61E+03	1.21E+03	9.85E+02	2.91E+02	5.00E+04	1.98E+03	7.44E+03	2.40E+03	2.74E+04
P19367-4 HXX1	GAALITAVGVR	514.32	88.38	1.43E+05	1.95E+03	1.57E+06	1.26E+03	1.87E+03	4.18E+02	6.58E+05	1.03E+06	2.21E+04	2.26E+04	1.47E+05	3.13E+03	1.30E+05	9.76E+03	2.28E+04
P55072 TERA	GDDLSTAILK	516.78	88.65	1.82E+03	6.99E+02	1.44E+03	1.57E+05	8.86E+02	4.34E+02	2.93E+04	3.21E+03	4.56E+04	2.63E+03	1.09E+05	5.23E+02	2.71E+04	1.27E+04	1.05E+05
P11532-4 DMD	VGNILQLGSK	514.81	88.69															



P08237 K6PF	SFEQISANITK	619.32	89.89	5.21E+04	3.15E+03	1.39E+03	2.55E+03	3.18E+03	1.91E+03	3.96E+03	4.48E+02	7.02E+03	5.17E+04	1.11E+03	9.56E+02	8.42E+03	4.97E+04	6.14E+03
P24752 THIL	LGSIAIQGAIEK	600.35	90.01	1.35E+05	5.19E+03	3.23E+03	2.97E+04	6.25E+04	3.86E+04	1.24E+02	1.77E+03	3.85E+04	2.10E+04	1.81E+05	1.13E+04	7.87E+04	1.66E+04	5.92E+04
P24752 THIL	EAYMGNVLQGGEGQAPTR	939.44	90.07	7.60E+04	1.77E+03	9.04E+02	4.29E+02	6.96E+03	6.34E+02	3.90E+02	7.95E+02	3.79E+02	2.28E+02	6.77E+02	1.89E+03	1.46E+03	2.36E+02	1.03E+04
P11532-4 DMD	SLEGSDDAVLLQR	701.36	90.15	6.49E+03	6.65E+04	9.74E+04	2.25E+04	1.15E+03	1.37E+05	2.29E+04	1.55E+04	2.20E+03	4.84E+02	6.59E+03	2.94E+04	9.57E+03	8.82E+02	8.62E+03
P01024 CO3	FISLGEACK	484.25	90.18	4.64E+03	1.25E+04	1.95E+03	2.15E+04	2.39E+04	2.53E+02	3.25E+02	3.02E+03	5.10E+04	1.07E+05	1.81E+03	2.00E+03	8.97E+03	1.29E+04	1.16E+04
P13929 ENOB	IEEALGDKAIFAGR	497.27	90.2	6.34E+04	8.24E+02	8.56E+04	1.10E+03	1.78E+04	3.61E+04	8.84E+03	1.98E+05	7.69E+04	1.11E+04	5.49E+03	7.45E+03	2.05E+03	4.23E+04	2.03E+03
P35555 FBN1	LETCFLR	441.23	90.34	1.52E+05	1.42E+04	7.87E+03	1.36E+04	7.34E+03	2.12E+03	1.37E+04	1.30E+04	4.83E+02	1.08E+03	1.39E+05	2.92E+04	1.54E+05	1.44E+03	2.16E+05
P12235 ADT1	QLFLGGVDR	502.78	90.49	2.29E+03	8.06E+05	2.97E+04	1.01E+06	1.70E+06	1.13E+06	1.40E+05	1.67E+04	3.56E+03	4.34E+03	9.71E+05	4.73E+05	3.98E+05	4.37E+02	1.57E+06
P00558 PGK1	SLEPVAVELK	542.82	90.53	2.42E+03	1.34E+05	1.09E+05	4.32E+03	1.29E+04	1.51E+05	8.50E+04	1.19E+04	3.38E+03	3.76E+03	1.24E+03	1.04E+05	1.93E+03	7.93E+03	4.03E+03
P40925 MDHC	NVVIWGNH	476.75	90.58	1.68E+05	1.41E+03	4.89E+02	4.12E+03	2.28E+03	1.54E+03	1.90E+03	7.04E+02	1.43E+04	1.63E+02	8.98E+04	8.72E+02	1.50E+04	2.23E+04	1.92E+03
P12235 ADT1	AAFYGVYDTAK	603.30	90.75	1.15E+05	1.39E+04	1.13E+03	4.17E+04	2.27E+04	1.03E+03	1.54E+03	3.48E+03	1.35E+03	6.66E+02	1.06E+05	5.61E+02	4.61E+04	1.96E+03	3.28E+03
Q01082-3 SPTB2	LLEVLSGER	508.29	90.78	5.17E+04	2.10E+05	1.63E+03	1.36E+04	1.62E+05	9.54E+05	7.48E+04	2.89E+04	1.68E+04	1.52E+03	1.87E+03	1.08E+05	2.53E+03	2.37E+03	5.88E+02
P08559 ODPA	IYSSDPPFEVR	655.32	90.83	1.03E+05	2.43E+03	1.12E+04	5.08E+03	7.56E+02	2.03E+03	2.45E+03	7.19E+02	8.18E+03	7.29E+04	3.87E+04	2.12E+03	2.47E+03	6.54E+03	1.36E+04
P11532-4 DMD	NLSTLEDLNTR	638.33	90.93	9.86E+04	1.84E+04	1.94E+03	7.43E+04	8.29E+03	1.55E+04	2.96E+04	1.10E+03	4.70E+03	4.80E+03	3.08E+04	2.43E+04	6.79E+04	2.08E+03	2.82E+04
P01857 IGHG1	STSGGTAALGLVK	632.83	91.01	1.00E+06	1.03E+04	2.70E+03	2.13E+04	2.77E+04	1.28E+04	1.13E+04	6.46E+03	5.98E+03	2.66E+03	2.31E+05	3.04E+04	1.72E+04	1.23E+04	8.34E+03
O76041 NEBL	VPVFEDIK	473.76	91.09	3.68E+03	1.82E+06	1.44E+06	1.63E+05	7.89E+04	1.70E+05	1.15E+06	3.29E+05	1.27E+05	2.50E+03	7.05E+02	1.58E+06	2.76E+03	2.04E+05	1.42E+05
O76041 NEBL	QNQLAATLASNVK	679.37	91.4	7.47E+02	8.44E+03	3.66E+02	3.97E+05	3.26E+05	2.87E+04	4.56E+03	2.78E+04	1.35E+03	6.76E+02	3.08E+05	7.60E+03	2.39E+04	4.20E+03	3.52E+05
P09622 DLDH	AIGDVVAGPMLAHK	460.26	91.45	4.75E+04	9.87E+02	8.91E+03	8.03E+02	1.63E+03	1.01E+04	3.86E+03	1.81E+04	2.16E+04	2.92E+04	5.20E+03	9.93E+02	9.17E+02	2.65E+04	1.80E+03
P40939 ECHA	TLQEVTLQSQAQR	815.92	91.52	2.85E+04	6.53E+03	1.61E+03	5.48E+03	2.26E+04	1.16E+03	2.69E+03	6.64E+03	1.65E+03	2.76E+02	7.66E+04	3.89E+03	3.04E+03	1.41E+03	1.45E+04
P08237 K6PF	SGSHTVAVMNVGAPAAGM NAAVR	723.36	91.6	1.74E+03	6.54E+02	2.84E+04	4.72E+03	1.11E+04	3.79E+03	3.42E+04	2.06E+04	1.70E+03	2.92E+03	5.41E+04	1.20E+04	2.70E+04	3.02E+03	4.92E+03
P19367-4 HXK1	LALLQVR	406.77	91.65	1.42E+03	8.72E+04	4.12E+03	1.21E+05	1.52E+05	1.88E+05	1.28E+03	2.55E+03	2.56E+02	3.01E+02	2.20E+02	1.07E+05	1.46E+02	7.19E+02	1.65E+05
P55268 LAMB2	IQNVVTSFAPQR	679.88	91.68	2.21E+05	6.11E+03	8.67E+03	3.16E+05	2.41E+04	4.72E+03	3.01E+04	7.93E+03	1.41E+03	6.12E+02	2.04E+05	6.76E+03	6.08E+04	4.68E+03	2.48E+05
O76041 NEBL	GRPSLILDTPAMR	476.27	91.75	1.57E+05	1.52E+03	5.25E+04	7.98E+03	8.80E+03	5.66E+03	9.67E+04	1.87E+03	1.14E+03	1.81E+03	9.11E+04	6.78E+03	1.13E+05	3.02E+03	7.14E+03
P04792 HSPB1	RVPFSLLR	494.31	91.81	3.49E+03	4.73E+03	2.24E+05	1.28E+04	5.67E+02	1.51E+03	3.70E+04	1.03E+04	3.04E+03	3.21E+03	1.77E+04	6.50E+03	2.36E+03	4.94E+03	2.49E+03
P35555 FBN1	NTPEYEELCP	675.80	91.86	1.57E+05	7.10E+03	7.20E+02	1.50E+05	9.05E+03	3.74E+03	2.56E+03	8.71E+02	1.59E+03	6.03E+02	1.63E+05	1.46E+03	1.26E+05	6.50E+02	2.07E+04
P08238 HS90B	HLEINPDHPIVETLR	594.99	92.04	3.29E+03	1.67E+03	4.40E+02	7.48E+03	1.88E+03	1.24E+03	5.76E+02	1.08E+03	5.16E+03	1.77E+03	1.07E+05	1.09E+04	4.89E+03	3.65E+03	2.12E+03
P12235 ADT1	VSYFPDVT	542.28	92.14	7.86E+04	8.95E+03	3.21E+03	1.34E+05	7.74E+04	9.30E+02	3.68E+03	2.52E+03	3.15E+03	2.44E+03	5.65E+03	1.68E+05	1.64E+04	8.81E+03	1.64E+05
P55268 LAMB2	AETVQAALAEAQR	708.36	92.16	7.41E+03	9.66E+02	2.38E+03	8.21E+03	9.72E+03	3.15E+03	1.30E+03	1.42E+03	3.10E+04	1.19E+04	9.58E+04	1.67E+03	6.37E+03	7.61E+04	4.33E+03
P55072 TERA	EVDIGIPDATGR	621.82	92.19	1.48E+05	1.89E+03	2.40E+03	2.54E+03	3.90E+03	2.24E+03	2.49E+04	7.00E+04	5.38E+03	1.13E+05	1.48E+04	6.38E+02	1.57E+05	1.22E+05	3.60E+03
P24043 LAMA2	GTYFDGTGFAK	582.27	92.24	5.04E+03	3.10E+03	4.02E+03	4.09E+02	7.02E+04	7.15E+03	1.03E+04	2.39E+03	3.90E+04	5.20E+04	1.08E+03	2.18E+04	1.10E+03	1.19E+05	5.05E+03
P55072 TERA	WALSQSNPALR	665.35	92.27	4.94E+04	8.29E+04	7.24E+04	5.49E+02	3.73E+03	4.21E+04	8.55E+04	5.04E+05	2.53E+03	1.13E+03	1.86E+03	4.83E+03	6.31E+02	2.16E+03	1.71E+03
Q9NPC6 MYOZ2	SPPNPDNAPGYSGPLK	862.43	92.27	6.14E+05	1.57E+03	4.39E+03	3.16E+05	1.89E+05	1.57E+04	4.34E+02	2.65E+03	6.44E+02	9.10E+02	4.39E+05	8.67E+03	9.62E+03	2.22E+03	4.86E+05
Q01082-3 SPTB2	LEMNLGLQK	523.27	92.32	1.50E+05	1.68E+03	5.18E+03	2.50E+04	9.20E+03	3.24E+03	2.32E+03	1.70E+03	5.93E+03	6.25E+02	1.32E+05	2.28E+04	2.64E+02	2.22E+04	1.73E+04
P40939 ECHA	VIGMHYFSPVDK	464.91	92.45	5.92E+02	2.80E+03	2.73E+03	9.06E+04	1.93E+05	5.75E+02	2.03E+03	1.93E+03	2.22E+03	9.79E+02	5.79E+02	5.15E+02	7.30E+02	2.32E+03	1.28E+05
P40925 MDHC	VIVVGNPANTNCLTASK	850.95	92.52	1.99E+03	5.83E+02	1.49E+03	6.93E+03	9.68E+03	5.49E+03	2.12E+03	7.58E+02	1.33E+02	5.89E+02	7.11E+04	1.58E+02	8.66E+03	1.67E+02	1.44E+03
P11216 PYGB	HLDHVAALFPGDVDR	554.62	92.53	2.07E+04	4.89E+02	4.98E+03	1.95E+04	2.60E+03	2.47E+04	7.83E+02	6.22E+02	3.48E+03	4.75E+03	2.14E+03	1.09E+03	5.41E+04	8.36E+03	2.42E+03
P01024 CO3	IPIEDGSGEVLSR	735.89	92.57	4.77E+03	1.75E+04	7.34E+03	2.74E+03	9.53E+03	2.88E+04	3.07E+03	1.37E+03	1.29E+04	1.07E+05	4.38E+04	8.24E+03	9.44E+03	1.58E+04	8.66E+04
P35555 FBN1	YEDEECTLPIAGR	748.34	92.79	1.31E+04	2.19E+03	3.61E+03	9.84E+03	1.42E+03	4.46E+03	8.31E+02	4.12E+03	8.64E+02	2.90E+03	1.43E+05	5.12E+03	1.02E+05	1.64E+03	7.12E+03
P00558 PGK1	VSHVSTGGGASLELLEGK	580.98	92.8	1.18E+05	2.67E+03	1.01E+03	9.09E+03	2.39E+03	2.83E+03	2.40E+03	3.85E+03	1.89E+03	3.47E+03	6.31E+03	1.01E+04	6.78E+03	5.53E+02	9.34E+03
Q99959-2 PKP2	LEVAELNGVPR	598.83	92.94	6.95E+04	8.98E+02	8.33E+02	6.66E+03	5.21E+02	9.35E+02	5.32E+02	3.88E+02	9.50E+02	6.24E+02	1.16E+05	1.10E+03	3.12E+04	1.89E+03	3.84E+03
P55268 LAMB2	YSEIEPSTEGEVIYR	886.42	93.04	5.43E+04	1.59E+03	3.73E+03	5.51E+04	2.27E+04	1.56E+03	5.82E+03	2.55E+03	1.34E+03	1.68E+02	5.91E+04	7.53E+02	5.86E+04	9.36E+02	1.06E+04
P28331 NDUS1	TSWEDALS	532.75	93.05	4.94E+02	1.87E+05	2.64E+04	3.86E+03	4.82E+04	1.08E+05	1.36E+04	8.22E+04	1.77E+03	4.60E+02	5.18E+03	1.20E+03	2.19E+03	6.14E+02	6.57E+02
O76041 NEBL	DLESIIK	409.24	93.19	3.20E+03	2.33E+03	3.68E+02	2.81E+04	6.19E+03	2.87E+03	3.46E+02	6.01E+04	6.34E+02	1.28E+03	1.94E+03	1.69E+03	1.11E+03	1.05E+03	1.28E+05
P01857 IGHG1	GPSVFLAPSSK	593.83	93.25	1.84E+06	4.19E+03	1.59E+03	1.55E+04	5.98E+04	8.11E+03	8.90E+03	5.79E+03	1.67E+03	1.38E+03	4.71E+05	9.98E+02	2.14E+05	1.36E+03	2.41E+04
P19367-4 HXK1	AAQLCGAGMAAVVDK	702.85	93.37	3.52E+04	1.68E+03	1.05E+03	5.96E+03	1.15E+04	9.73E+03	1.05E+04	1.05E+04	9.51E+03	4.19E+02	2.58E+04	1.71E+03	1.00E+04	1.00E+04	1.92E+04
P05413 FABPH	LILTLTH	405.76	93.54	7.05E+04	6.06E+03	2.19E+03	1.72E+03	3.45E+02	1.23E+03	3.46E+02	1.34E+02	6.35E+02	2.28E+02	1.02E+05	1.06E+03	9.14E+03	3.52E+02	5.73E+03
Q9NPC6 MYOZ2	VATPFGGFEK	526.77	93.59	1.58E+03	8.40E+05	9.38E+03	1.20E+06	2.62E+05	1.58E+04	4.99E+05	3.59E+02	1.93E+04	7.85E+03	1.04E+04	2.38E+06	8.30E+02	4.41E+03	1.11E+06
P00558 PGK1	VNDAFGTAHR	545.76	93.62	3.65E+03	4.18E+05	2.99E+05	1.87E+05	1.13E+05	2.46E+05	1.17E+04	5.81E+03	6.50E+02	9.16E+03	5.94E+02	2.54E+05	5.58E+02	9.78E+02	2.49E+05
P11216 PYGB	DFYELEPEK	585.27	93.64	8.29E+04	2.08E+03	5.42E+02	3.97E+03	4.76E+03	2.57E+03	2.39E+02	1.36E+04	7.01E+04	2.86E+04	3.57E+04	1.97E+03	8.92E+02	6.55E+04	1.63E+04
O76041 NEBL	GFTPVVDDPVTER	716.36	93.73	1.72E+05	7.59E+03	1.25E+03	1.05E+05	4.53E+04	2.76E+03	1.73E+04	2.38E+03	1.44E+04	1.36E+03	3.74E+04	1.23E+04	4.56E+04	2.16E+03	6.37E+04
P11047 LAMC1	AFDITYVR	492.76	94.0															



P00558 PGK1	LGDVYVNDAFGTAHR	817.90	94.66	2.16E+03	9.01E+02	1.33E+05	1.10E+05	3.85E+03	1.37E+05	5.03E+04	3.60E+04	1.33E+04	2.26E+03	5.89E+04	8.20E+02	1.44E+04	5.20E+03	1.12E+04
P24752 THIL	VNINGGAVSLGHPIGMSG	636.34	94.69	8.18E+04	1.26E+04	1.44E+04	1.78E+04	1.16E+03	2.19E+04	2.07E+03	2.43E+03	2.62E+03	1.51E+03	7.95E+02	8.10E+04	4.51E+02	2.99E+03	1.00E+04
P08107 HSP71	NQVALNPQNTVFDPAK	829.93	94.84	1.62E+04	1.08E+04	1.08E+04	2.58E+04	4.33E+04	1.46E+04	6.23E+03	4.51E+02	1.15E+03	8.18E+02	1.20E+05	1.60E+03	1.43E+04	4.20E+02	1.63E+05
P35555 FBN1	GFIPNIR	408.74	94.89	4.35E+04	7.25E+02	7.25E+02	8.21E+02	5.67E+02	4.06E+02	2.44E+02	6.58E+02	1.73E+03	2.62E+02	1.42E+05	2.10E+03	3.60E+04	4.37E+02	6.57E+03
P06396-2 GELS	AGALNSNDAFVFLK	660.35	95.04	2.36E+05	1.60E+03	2.72E+03	4.28E+03	3.15E+02	1.53E+03	5.97E+03	1.20E+03	2.44E+04	3.01E+04	2.74E+05	2.09E+03	1.51E+05	7.68E+04	2.12E+05
P08559 ODPA	MVNSNLASVEELK	717.37	95.11	2.37E+05	1.29E+03	3.13E+03	2.04E+05	1.76E+04	1.17E+03	5.40E+03	3.99E+03	6.26E+04	7.24E+04	7.49E+04	6.09E+03	5.70E+04	1.78E+04	5.79E+04
P55072 TERA	GILLYGPPGTGK	586.84	95.74	8.37E+02	5.54E+02	7.80E+02	8.67E+02	3.25E+03	2.72E+03	7.21E+02	1.20E+03	8.33E+02	1.33E+03	1.74E+05	1.43E+03	8.17E+04	1.64E+03	6.86E+03
P06396-2 GELS	VPFDDAATLHTSTAMAAQHG MDDDGTTGQK	719.08	95.82	5.75E+02	1.26E+03	3.51E+02	2.13E+03	4.18E+04	1.87E+03	9.30E+02	1.21E+03	2.33E+02	7.48E+02	2.24E+03	2.29E+03	4.16E+02	3.09E+03	1.19E+04
P19429 TNNI3	NITEIADLTQK	623.34	95.89	1.33E+05	1.94E+06	1.06E+04	4.34E+06	3.26E+06	7.59E+03	9.38E+02	4.54E+03	1.13E+03	9.39E+02	1.40E+06	1.10E+06	1.29E+06	9.76E+03	4.64E+06
P28331 NDUS1	DFYMTDSISR	617.77	96.56	8.49E+04	6.37E+03	4.75E+03	1.46E+05	4.84E+03	2.06E+04	3.61E+03	1.64E+03	5.86E+02	1.80E+03	6.63E+04	4.30E+03	6.26E+03	1.10E+03	1.68E+04
P63261 ACTG	VAPEEHPVLLTEAPLNPK	652.03	96.8	4.31E+03	2.34E+04	1.78E+04	2.16E+06	1.20E+03	2.47E+04	1.22E+04	3.85E+02	1.22E+04	1.39E+03	2.07E+06	1.84E+04	8.13E+05	1.38E+03	1.99E+06
P08559 ODPA	GDFIPGLR	437.74	96.81	9.71E+04	9.35E+04	1.07E+03	3.25E+05	6.17E+05	2.40E+02	2.06E+04	2.19E+03	1.29E+05	2.53E+03	4.03E+05	4.79E+03	4.78E+05	2.60E+05	1.10E+04
P08559 ODPA	LEEGPPVTTVLTR	706.39	96.82	1.59E+04	1.56E+03	6.91E+03	9.15E+04	3.62E+03	1.56E+04	4.18E+03	2.22E+03	6.12E+04	1.61E+05	7.98E+03	7.01E+02	4.94E+03	1.72E+05	9.37E+02
P11021 GRP78	VTHAVVTVPAFYFNDAGR	629.99	97.28	4.77E+03	6.04E+03	8.61E+03	3.05E+03	5.07E+03	5.29E+04	4.49E+03	5.94E+03	2.83E+03	7.90E+02	9.39E+02	6.10E+03	2.81E+03	2.61E+03	5.16E+03
P11216 PYGB	GLAGLGDVAEVR	578.82	97.72	1.78E+03	1.44E+04	1.34E+03	4.67E+05	2.16E+04	5.24E+03	3.73E+04	3.19E+04	5.63E+02	1.44E+03	4.00E+05	2.34E+04	3.73E+05	5.18E+03	3.02E+04
P08572 CO4A2	SLLYFEGQEK	607.31	97.77	6.39E+04	1.50E+04	7.72E+04	4.51E+04	2.08E+04	4.78E+03	7.16E+04	3.04E+04	1.56E+03	3.18E+03	3.57E+04	1.35E+04	4.82E+03	7.19E+02	3.52E+04
O75390 CISY	ALGFPLER	451.76	97.98	1.80E+03	1.21E+06	7.27E+04	4.49E+05	1.59E+05	1.71E+05	1.30E+04	1.20E+03	2.14E+03	7.75E+02	1.54E+03	8.64E+05	7.44E+05	5.19E+02	8.21E+05
P11177 ODPB	EGVECEVINMR	639.80	98	4.88E+03	4.58E+03	4.96E+02	3.04E+03	1.18E+03	2.64E+03	1.25E+03	7.10E+02	7.31E+04	4.70E+04	7.41E+02	2.23E+03	2.87E+03	5.64E+04	1.08E+03
P07195 LDHB	SADTLWDIQR	588.80	98.2	2.06E+06	3.46E+04	2.40E+04	1.98E+06	7.91E+03	2.25E+04	1.45E+05	2.12E+03	2.16E+03	2.36E+03	1.76E+06	1.94E+04	7.01E+03	1.54E+03	2.13E+06
Q01082-3 SPTB2	SQNVTDSSLSAEAIR	889.45	98.44	7.99E+03	1.01E+03	1.57E+03	4.06E+04	1.49E+03	4.91E+03	1.57E+03	1.38E+04	2.55E+03	2.51E+03	3.52E+04	7.49E+02	8.25E+03	1.00E+04	5.10E+03
P28331 NDUS1	GWNILTNSKE	581.31	98.44	7.81E+03	1.47E+03	5.33E+03	3.09E+04	4.83E+03	1.88E+04	1.21E+03	8.66E+03	3.76E+05	3.62E+05	3.59E+04	9.57E+03	3.19E+03	6.67E+05	1.97E+04
P08238 HS90B	YHTSQSGDEMTSLSEYVSR	726.32	98.53	3.22E+02	1.55E+03	8.89E+03	2.13E+03	2.01E+04	5.46E+04	1.70E+03	1.07E+03	2.24E+03	1.52E+03	1.44E+03	9.45E+02	1.34E+03	2.67E+03	1.21E+03
P08237 K6PF	VLVVDHGFEGFLAK	461.93	98.54	3.47E+03	1.60E+03	2.58E+03	1.24E+03	5.79E+03	4.27E+03	4.72E+03	1.10E+04	1.30E+05	1.00E+05	5.27E+02	4.16E+03	2.87E+02	1.43E+05	2.26E+03
P35555 FBN1	GFQLDLR	424.73	98.65	5.81E+03	2.70E+03	2.25E+03	1.24E+03	3.51E+03	2.50E+03	2.28E+03	3.24E+03	1.33E+05	2.32E+05	2.26E+03	8.99E+02	1.33E+03	1.11E+05	2.26E+03
P55072 TERA	YEMFAQTLQQR	751.36	98.68	4.34E+04	1.10E+03	1.22E+03	1.18E+03	2.82E+02	1.41E+03	7.17E+02	8.39E+02	2.80E+02	4.60E+03	4.83E+03	1.04E+03	7.17E+02	6.92E+03	1.29E+03
P63261 ACTG	TVLSGGTMYPGIADR	819.91	98.69	1.04E+05	1.49E+04	1.54E+04	1.08E+05	6.81E+02	2.82E+02	1.29E+03	1.61E+03	3.42E+02	6.66E+02	8.45E+04	1.14E+04	4.19E+02	2.53E+03	3.09E+03
P19429 TNNI3	TLLLQIAK	450.30	98.78	1.40E+06	3.32E+03	8.91E+03	3.94E+03	5.67E+04	1.18E+04	8.73E+03	1.76E+03	1.42E+02	5.36E+02	1.44E+06	1.06E+04	1.58E+04	6.19E+02	4.90E+04
Q99959-2 PKP2	AVSMLEADHMLPSR	519.59	98.79	2.12E+03	6.75E+03	4.74E+03	2.15E+05	4.78E+03	1.60E+03	2.22E+05	2.83E+05	6.36E+04	6.01E+04	2.08E+05	8.86E+04	5.27E+04	2.95E+04	2.83E+04
P63261 ACTG	GIVTNWDDMEK	654.30	98.94	2.53E+04	2.32E+04	5.58E+02	7.85E+03	8.60E+03	2.26E+05	2.96E+02	9.79E+03	4.62E+02	2.72E+03	3.22E+04	1.02E+04	2.10E+03	4.65E+03	2.25E+03
P11021 GRP78	ITPSYVAFTPEGER	783.38	99.1	2.70E+03	6.50E+05	1.03E+06	2.88E+04	1.51E+04	2.27E+05	1.19E+05	2.33E+05	1.71E+04	1.96E+05	1.51E+04	2.80E+03	1.07E+04	2.44E+04	2.50E+02
P55072 TERA	EMVELPLR	493.77	99.11	1.52E+05	6.20E+04	5.11E+03	1.72E+04	2.66E+03	6.48E+02	3.57E+03	1.28E+03	1.90E+03	1.19E+04	1.03E+05	3.68E+04	3.37E+03	1.92E+04	6.83E+02
P31930 QCR1	NALVSHLDGTTVCEDIGR	666.33	99.12	3.30E+03	5.56E+03	1.81E+03	4.06E+04	1.08E+04	1.04E+04	8.94E+02	2.51E+04	6.63E+03	2.97E+03	2.10E+04	4.09E+03	2.33E+03	1.87E+04	1.81E+04
P00558 PGK1	DVLFLK	734.44	99.2	4.44E+02	4.89E+04	2.36E+03	1.70E+05	1.43E+04	7.41E+04	2.33E+03	1.83E+03	3.12E+02	4.46E+02	3.15E+02	3.74E+04	9.03E+03	1.78E+02	4.59E+04
Q99959-2 PKP2	TSSVPEYVYNLH	704.84	99.33	2.88E+03	1.30E+04	3.95E+03	1.17E+05	3.02E+03	3.67E+02	1.92E+03	1.91E+04	6.09E+03	1.02E+04	3.80E+03	1.31E+03	1.58E+03	1.58E+04	4.75E+04
P05413 FABPH	SLGVGF	579.31	99.37	1.21E+04	2.70E+03	3.61E+03	2.08E+04	2.40E+03	1.03E+03	1.54E+03	4.11E+04	2.42E+05	3.61E+05	1.14E+04	6.27E+03	1.53E+03	3.92E+05	2.32E+03
P07195 LDHB	MVVESAYEVK	634.33	99.52	1.95E+05	4.38E+03	1.61E+03	1.52E+05	1.59E+03	8.30E+03	3.59E+03	6.19E+04	6.10E+02	9.43E+02	1.51E+05	3.08E+03	8.67E+03	1.25E+03	3.04E+03
P12235 ADT1	EFHGLDCCI	411.21	99.63	2.84E+02	8.16E+03	7.98E+02	8.43E+03	1.21E+04	1.86E+03	1.03E+03	2.63E+03	1.17E+03	7.67E+03	1.32E+05	1.29E+04	3.33E+03	3.07E+02	8.86E+03
P55268 LAMB2	GSCYPLATGDLLVGR	704.85	99.76	5.32E+04	1.22E+04	4.44E+04	2.13E+03	1.85E+04	2.75E+04	3.29E+03	5.61E+04	2.58E+03	2.23E+03	2.59E+04	6.51E+03	2.28E+03	2.12E+03	3.32E+03
P07195 LDHB	LIAPVAEEEEATVPN	726.88	99.85	8.44E+02	1.72E+03	4.67E+02	1.36E+03	1.66E+03	4.60E+02	2.55E+03	9.83E+03	1.80E+03	1.27E+03	1.91E+02	5.06E+02	2.22E+04	1.60E+03	9.32E+04
P08559 ODPA	SDPIMLLK	458.76	99.95	9.19E+03	2.57E+05	8.77E+03	2.58E+05	3.38E+05	3.42E+05	2.58E+03	4.72E+03	2.19E+02	6.76E+02	1.94E+03	4.10E+05	1.31E+05	4.61E+02	3.79E+05
Q9NPC6 MYOZ2	YTFENFQYQSR	741.84	99.99	2.76E+02	1.01E+03	2.61E+03	2.81E+04	2.14E+02	4.47E+02	1.02E+03	5.77E+02	7.14E+04	1.69E+05	7.38E+04	1.09E+04	1.33E+03	1.32E+03	2.94E+03
P00558 PGK1	VSTGGGASLELLEK	709.38	100.06	4.83E+03	1.25E+03	1.60E+05	4.62E+03	3.11E+03	2.73E+05	2.89E+04	7.57E+04	1.57E+04	2.02E+03	2.38E+03	3.17E+03	9.47E+02	4.32E+04	2.05E+03
P08559 ODPA	EILAEITGR	501.28	100.1	2.16E+03	8.88E+03	3.69E+04	3.84E+05	2.51E+03	6.23E+05	3.35E+02	1.44E+03	1.51E+03	2.63E+02	4.14E+02	3.99E+04	7.56E+05	5.17E+02	6.99E+05
O75390 CISY	MLGYTDHQFTLTR	571.28	100.24	2.33E+03	1.34E+04	3.49E+03	2.44E+04	1.18E+04	6.62E+03	3.73E+03	3.85E+03	5.39E+03	1.65E+03	2.30E+03	4.62E+03	1.30E+03	7.89E+02	2.71E+04
P08237 K6PF	DLQANVEHLVQK	697.37	100.43	2.40E+05	3.32E+04	6.78E+03	2.53E+05	3.73E+04	1.94E+04	7.31E+02	2.06E+03	2.76E+03	2.18E+02	2.11E+05	2.53E+03	2.37E+04	1.70E+03	1.58E+04
P06396-2 GELS	EPGLQIWR	499.77	100.51	2.34E+05	3.68E+03	2.20E+02	1.37E+04	1.53E+04	6.70E+02	1.52E+03	1.57E+03	1.24E+04	1.73E+04	2.72E+05	8.57E+03	4.54E+03	5.00E+03	9.62E+02
P28331 NDUS1	FASEIAGVDDLGTTR	804.90	100.66	2.03E+05	7.24E+02	4.69E+03	2.81E+05	2.70E+03	6.40E+03	8.80E+02	3.49E+03	9.05E+03	1.94E+03	1.70E+05	5.41E+03	4.89E+03	3.40E+03	1.44E+04
P60174 TPIS	FFVGGNWK	477.75	100.7	3.53E+05	4.33E+03	6.12E+03	1.17E+04	1.72E+04	5.49E+03	5.85E+03	1.07E+03	2.49E+03	1.55E+03	4.01E+05	2.52E+04	1.63E+04	2.53E+03	4.63E+03
P11047 LAMC1	LNTFGDEVFNDPK	748.36	100.71	1.85E+04	1.01E+04	1.96E+04	2.08E+03	6.45E+03	6.84E+04	5.83E+02	1.30E+03	2.35E+02	2.62E+02	4.62E+02	1.01E+03	5.18E+02	6.40E+02	2.42E+02
P55268 LAMB2	LGIVQGIVGAR	541.84	100.92	1.75E+05	5.57E+02	1.12E+03	3.72E+03	4.96E+02	3.43E+02	2.11E+03	5.09E+02	3.06E+03	1.71E+03	1.97E+05	4.16E+02	1.43E+03	4.58E+02	4.18E+03
P2404																		

P11047 LAMC1	SAGYLDDVTLASAR	719.86	102.1	1.87E+05	1.16E+03	4.21E+03	1.17E+04	4.50E+03	7.14E+02	4.73E+02	2.28E+04	1.23E+03	2.07E+03	2.54E+05	1.47E+04	3.10E+03	3.38E+03	4.01E+03
P09622 DLDH	ALTGGIAHLFK	564.33	102.14	1.51E+05	1.70E+04	4.01E+03	2.16E+03	9.36E+04	1.26E+04	3.95E+04	1.00E+03	1.68E+03	2.25E+03	5.79E+02	1.63E+05	8.37E+02	1.13E+03	1.92E+03
P31930 QCR1	ADLTEYLSATHYK	720.85	102.22	4.40E+05	3.01E+02	5.42E+03	2.25E+03	6.87E+02	1.15E+03	2.66E+03	9.93E+02	5.90E+02	1.73E+03	2.32E+05	1.53E+03	2.82E+03	3.15E+02	7.75E+03
P04792 HSPB1	VPFSLLR	416.26	102.38	1.51E+05	4.05E+05	6.95E+04	9.18E+05	3.59E+04	5.11E+04	5.89E+04	3.91E+04	4.93E+02	8.92E+02	4.30E+02	2.26E+06	7.00E+05	9.68E+02	1.10E+06
Q01082-3 SPTB2	QALQDRTLALYK	632.35	102.47	3.99E+03	2.22E+03	4.38E+03	3.29E+04	1.48E+04	4.54E+04	9.29E+03	8.32E+03	1.29E+03	6.69E+03	2.76E+04	6.28E+03	1.76E+03	1.43E+03	7.51E+03
P11532-4 DMD	NILSEFQR	503.77	102.51	1.43E+03	1.61E+03	1.22E+03	7.11E+04	9.73E+02	2.17E+03	2.04E+03	2.29E+03	9.46E+02	8.77E+02	6.51E+03	5.12E+03	3.62E+04	4.52E+03	7.16E+04
O76041 NEBL	PSLILDTPAMR	607.33	102.54	8.09E+04	1.23E+04	1.10E+03	9.31E+03	2.16E+03	9.39E+02	4.99E+02	2.09E+04	6.28E+02	2.90E+03	3.13E+05	1.22E+04	1.30E+04	5.11E+03	2.86E+04
P55084 ECHB	TPFLLSGTSYK	607.33	102.57	8.10E+04	1.24E+04	1.11E+03	9.34E+03	2.15E+03	9.37E+02	4.98E+02	2.09E+04	6.27E+02	2.90E+03	3.13E+05	1.23E+04	1.30E+04	5.12E+03	2.86E+04
P28331 NDUS1	FEAPLFNAR	532.78	102.85	7.05E+03	1.99E+03	1.39E+03	4.58E+02	8.46E+03	6.28E+02	2.05E+03	1.05E+03	5.58E+05	1.31E+03	2.98E+03	7.48E+03	4.91E+02	4.52E+05	6.62E+02
P40926 MDHM	LTLYDIAH	473.26	103.2	2.39E+03	1.71E+05	4.12E+03	1.26E+03	1.17E+04	2.38E+03	1.20E+03	1.28E+03	3.27E+05	2.64E+05	2.03E+03	5.52E+04	3.86E+03	1.19E+05	1.08E+05
P08670 VIME	DNLAEDIMR	538.75	103.3	2.84E+02	8.79E+03	5.61E+03	2.70E+05	7.17E+03	1.11E+04	1.75E+04	3.52E+03	2.99E+03	1.51E+03	1.03E+03	1.23E+04	1.15E+05	4.88E+02	2.62E+05
P13929 ENOB	FMIELDGTEENK	648.81	103.56	2.03E+04	1.56E+03	6.38E+03	3.41E+03	1.58E+03	8.46E+02	1.65E+03	2.98E+02	6.08E+05	8.21E+05	2.56E+04	6.80E+03	3.27E+02	3.15E+05	3.95E+03
P11216 PYGB	ARPEYMLPVHfyGR	579.28	103.6	4.98E+03	4.13E+04	1.70E+03	5.32E+04	4.92E+05	2.44E+03	2.58E+06	2.03E+06	2.54E+03	1.85E+03	2.04E+04	2.14E+05	2.14E+04	1.78E+03	4.21E+04
Q96HC4 PDLI5	GPFLVALGK	451.28	103.99	7.71E+02	7.66E+02	2.42E+05	4.20E+02	3.37E+02	9.51E+02	2.56E+05	3.33E+05	2.78E+02	7.73E+02	2.26E+02	6.05E+02	2.30E+03	1.41E+03	1.21E+03
P01024 CO3	QPSSAAFAFVK	576.81	104.04	3.34E+02	1.79E+03	1.32E+03	1.93E+03	6.29E+03	1.26E+03	4.18E+03	1.82E+03	1.10E+05	1.70E+05	2.49E+02	1.37E+03	5.07E+02	7.63E+04	1.61E+03
Q9NPC6 MYOZ2	FKVPDFE	441.22	104.06	7.17E+02	4.22E+03	3.76E+03	7.74E+04	4.90E+03	1.08E+03	1.94E+03	9.28E+03	5.65E+02	2.15E+03	7.62E+03	4.11E+03	5.79E+04	2.31E+03	8.29E+03
P11021 GRP78	AVVTVPAYFNDAQR	775.90	104.26	7.53E+02	1.81E+04	1.29E+04	1.77E+04	7.62E+02	6.14E+04	6.76E+02	4.20E+03	8.92E+02	4.19E+02	1.35E+04	7.73E+03	1.17E+03	4.64E+03	3.85E+04
P40926 MDHM	GCDVVVIPAGVPR	641.35	104.39	1.50E+05	2.45E+03	3.85E+02	6.64E+04	5.03E+03	4.76E+02	1.22E+03	1.52E+03	8.44E+04	9.40E+04	7.97E+03	3.19E+03	1.24E+03	1.81E+04	8.73E+03
P60174 TPIS	VTNGAFTGEISPGMIK	811.42	104.71	4.78E+04	3.15E+03	2.60E+03	1.24E+04	1.17E+03	1.08E+03	1.14E+04	6.94E+02	1.32E+03	1.45E+03	5.10E+03	1.17E+03	3.87E+03	9.09E+02	1.07E+03
P11021 GRP78	NELESYAYSILK	658.82	104.78	1.86E+03	6.63E+02	9.88E+02	1.13E+03	2.46E+03	2.64E+02	1.99E+03	1.69E+03	3.84E+04	8.88E+04	2.27E+03	2.31E+03	7.23E+02	5.16E+04	5.67E+02
P06396-2 GELS	EPANLEMSLFGGK	429.56	104.85	1.23E+03	2.92E+04	9.34E+02	2.63E+03	6.63E+03	6.06E+04	7.27E+02	1.42E+03	4.94E+02	1.64E+03	2.33E+02	7.74E+04	1.29E+03	4.37E+03	6.51E+04
P24752 THIL	FGNEVPVTVTVK	701.90	105.16	7.58E+02	3.66E+05	7.92E+03	1.14E+04	6.15E+05	2.73E+04	1.09E+04	9.44E+03	3.91E+02	5.33E+02	5.08E+03	2.85E+05	1.95E+05	1.26E+03	3.95E+05
P08107 HSP71	NALESYAFNMK	644.30	105.34	1.98E+03	3.78E+03	1.24E+05	1.07E+03	1.37E+03	7.35E+02	1.55E+05	2.62E+05	2.24E+03	3.27E+03	1.64E+03	2.88E+03	2.65E+03	1.63E+04	3.87E+03
P60174 TPIS	VPADTEVVCAPPTAY	766.87	105.34	8.95E+04	4.66E+03	5.99E+02	3.85E+04	2.04E+03	1.55E+03	2.19E+02	1.74E+03	5.45E+02	9.45E+02	6.04E+04	5.34E+03	9.37E+03	1.62E+03	4.91E+04
Q9NPC6 MYOZ2	DIMLEELSH	543.76	105.49	1.41E+03	1.60E+03	2.12E+05	2.40E+03	3.60E+03	6.30E+02	5.86E+03	2.17E+03	5.25E+03	1.52E+03	1.20E+02	5.86E+03	2.09E+03	2.34E+03	2.49E+03
P01024 CO3	TVMVNIENPEGIPVK	820.44	105.67	8.56E+02	4.85E+02	2.35E+03	2.32E+03	4.72E+04	3.35E+03	3.10E+02	5.40E+02	1.03E+03	4.73E+02	3.76E+03	5.05E+03	1.27E+03	1.31E+03	1.91E+03
P12235 ADT1	FLAGGVAAAVSK	603.33	105.77	4.71E+05	7.42E+03	2.45E+03	9.54E+05	6.02E+04	1.61E+04	2.08E+03	9.62E+02	9.81E+02	8.90E+02	3.88E+05	5.61E+03	2.52E+03	3.45E+03	2.74E+04
P05413 FABPH	LIDGKLLTLTHGTAVCTR	504.29	106.09	1.02E+03	8.11E+04	1.36E+04	2.01E+03	1.22E+04	3.35E+04	6.54E+04	1.41E+05	2.04E+03	1.04E+03	1.69E+03	5.18E+04	1.34E+03	2.19E+03	1.70E+04
P01857 IGHG1	TLMISRTPEVTCVVVDVSH EDPEVK	695.35	106.31	5.68E+02	9.94E+04	2.48E+04	1.96E+03	3.67E+05	4.84E+05	1.49E+04	1.58E+04	1.05E+03	2.33E+03	2.27E+03	1.40E+04	9.92E+02	5.31E+03	3.15E+04
P28331 NDUS1	ILQDIASGSHFPSQVLK	614.00	106.59	3.88E+04	1.29E+04	1.53E+04	8.51E+03	7.11E+03	1.24E+04	4.49E+04	5.86E+04	4.11E+04	3.45E+04	1.08E+03	2.33E+03	1.52E+03	3.19E+06	1.36E+03
P01857 IGHG1	TPEVTCVVVDVSHEDPEVK	694.67	106.6	1.43E+03	5.84E+04	1.41E+04	3.86E+04	1.03E+06	1.18E+05	4.98E+04	1.09E+04	1.09E+03	2.56E+03	5.57E+04	3.11E+04	1.34E+04	1.81E+03	1.38E+05
P14923 PLAK	SAIVHLINYGDAELATR	677.02	107.49	9.89E+02	2.94E+03	6.96E+03	5.66E+03	5.87E+04	1.03E+05	1.69E+03	7.78E+02	2.57E+03	3.53E+03	1.14E+03	1.29E+03	1.25E+03	5.23E+02	6.73E+04
P55072 TERA	AIANECQANFISIK	761.39	107.52	1.66E+03	1.69E+03	2.41E+03	6.01E+03	2.51E+03	1.78E+03	4.32E+02	1.33E+03	6.85E+03	2.99E+04	5.07E+02	2.99E+04	5.13E+04	1.65E+03	1.86E+03
P55072 TERA	LGDVISIQPCPDVK	742.40	107.57	7.55E+02	5.64E+03	1.02E+04	5.18E+03	5.16E+02	4.33E+03	9.62E+02	2.22E+03	6.41E+03	1.12E+04	1.82E+03	2.80E+03	6.33E+02	1.16E+03	2.17E+03
P08670 VIME	ETNLDSLPLVDTH	727.36	107.61	3.36E+03	9.85E+03	7.86E+04	3.97E+03	2.27E+03	1.64E+04	8.83E+04	1.36E+03	7.38E+02	9.08E+02	5.39E+02	1.42E+03	1.07E+03	4.15E+04	4.16E+02
P08237 K6PF	IFANTPDSGCVLGMR	790.88	107.73	1.46E+03	2.31E+03	1.98E+03	2.85E+03	6.04E+04	1.90E+04	8.22E+03	2.07E+04	1.50E+03	8.87E+02	9.80E+02	7.20E+04	2.09E+03	1.92E+03	1.04E+05
P09622 DLDH	NETLGGTCLNVGCIIPSK	853.42	107.74	1.33E+03	8.91E+03	1.43E+03	1.14E+03	5.60E+02	3.34E+04	2.42E+03	2.64E+03	3.29E+03	8.60E+02	8.97E+02	7.40E+02	1.45E+03	7.06E+02	5.21E+02
P00558 PGK1	IQLINMLDK	601.33	107.8	2.89E+04	2.24E+03	1.83E+03	1.29E+04	3.46E+03	4.39E+03	4.36E+04	1.57E+03	2.28E+03	3.46E+04	6.97E+04	1.47E+05	1.11E+05	1.73E+04	1.04E+05
P31930 QCR1	DVVFNyLH	503.75	107.84	7.62E+02	1.08E+05	1.49E+04	1.48E+03	2.29E+04	8.35E+04	2.31E+04	5.35E+04	5.71E+02	3.58E+03	4.02E+02	2.41E+04	1.32E+02	4.12E+02	1.50E+03
P08238 HS90B	TLTLVDGTIGMTK	675.37	107.91	2.75E+02	1.46E+04	1.05E+03	6.07E+03	1.15E+05	1.06E+03	5.82E+02	4.38E+03	1.35E+03	1.23E+05	1.79E+03	9.39E+04	3.30E+03	8.42E+05	1.94E+05
P63261 ACTG	TVPIYEGYALPH	680.35	107.95	2.10E+03	1.01E+05	3.04E+05	2.56E+03	6.61E+03	4.08E+05	1.54E+03	1.46E+04	2.73E+02	2.55E+03	4.54E+02	1.59E+04	2.44E+04	1.72E+03	6.20E+03
P14923 PLAK	TLVTONSGVEALIH	741.40	107.96	9.41E+02	5.10E+03	9.43E+02	3.82E+02	5.10E+02	2.21E+03	7.95E+03	1.99E+03	1.29E+04	3.50E+04	1.23E+03	1.35E+03	2.50E+03	5.84E+03	1.74E+03
P11021 GRP78	SDIDEIVLVGGSTR	730.39	108.03	1.14E+03	6.57E+03	9.01E+04	1.98E+03	6.31E+03	9.40E+04	6.64E+04	1.57E+05	2.01E+04	1.52E+03	1.63E+03	5.76E+03	5.61E+03	1.38E+04	3.08E+02
P55072 TERA	VINQILTEMDGMSTK	840.40	108.23	8.57E+04	7.90E+03	4.48E+02	9.16E+03	1.37E+04	2.11E+04	1.71E+03	1.54E+03	6.22E+02	1.24E+03	9.41E+02	1.49E+03	9.43E+02	1.60E+03	4.90E+02
P40925 MDHC	ELTEEKESAFEF	729.84	108.49	2.38E+03	3.74E+03	2.10E+03	1.16E+03	8.02E+02	1.11E+03	3.19E+03	3.56E+03	4.13E+04	7.05E+03	2.58E+02	2.71E+03	2.20E+02	8.13E+02	1.36E+03
P14923 PLAK	NLALCPANHAPLQEAAVIP	700.04	108.6	1.54E+04	1.65E+04	1.89E+03	3.31E+05	1.53E+04	1.66E+04	2.03E+03	7.62E+03	8.12E+03	2.05E+03	5.29E+03	7.23E+03	2.54E+03	2.85E+03	2.54E+04
P13929 ENOB	AVENINSTLGPALLQK	834.47	108.62	8.20E+02	1.59E+04	3.97E+02	7.31E+03	4.12E+02	1.31E+03	1.18E+03	5.34E+03	3.86E+02	1.69E+02	3.22E+03	3.32E+03	8.60E+02	1.80E+02	6.63E+04
Q71U36 TBA1A	VDLEPTVIDEVR	692.87	108.62	2.21E+03	3.12E+03	2.83E+03	1.50E+03	2.27E+03	2.79E+03	1.59E+02	4.19E+03	1.21E+04	2.83E+04	1.10E+03	1.35E+03	1.58E+03	3.66E+02	2.59E+03
P11021 GRP78	INNEPTAAAIAyGLDKR	606.00	108.64	1.53E+04	5.52E+03	4.31E+03	2.44E+03	1.59E+05	1.04E+03	8.19E+03	1.93E+03	3.15E+03	3.96E+02	1.37E+03	1.38E+05	2.70E+04	7.24E+02	1.34E+04
P13929 ENOB	MILPVGASSFK	575.32	108.64	4.57E+02	1.08E+03	2.00E+03	4.51E+02	4.78E+03	2.40E+03	4.51E+02	1.49E+03	1.71E+05	1.78E+05	7.64E+03	3.97E+03	9.84E+02		

P11177 ODPB	DIIFAIK	410.25	109.7	3.76E+03	1.78E+03	1.25E+03	6.37E+02	8.49E+02	1.13E+03	3.37E+02	1.12E+03	1.35E+05	1.36E+05	4.71E+03	1.04E+03	3.74E+02	8.02E+04	1.24E+03
P28331 NDUS1	IASQVAALDLGYKPGVEAIR	691.06	109.75	3.03E+03	2.49E+03	3.38E+03	1.86E+05	1.63E+05	1.73E+03	7.15E+02	1.52E+03	1.29E+03	2.57E+03	6.37E+02	1.09E+05	1.03E+05	1.56E+03	1.58E+05
P08238 HS90B	ALLFIPR	415.27	110.06	1.01E+03	2.28E+03	3.61E+02	1.83E+02	2.13E+02	7.01E+02	1.91E+02	1.39E+02	1.24E+05	1.48E+05	6.47E+02	2.60E+03	5.57E+02	2.49E+05	1.86E+03
P40939 ECHA	AMTIPFVR	467.76	110.15	3.47E+03	1.29E+03	8.57E+02	7.84E+02	1.82E+03	7.63E+02	4.53E+02	2.81E+03	2.56E+04	2.59E+04	5.89E+02	5.21E+03	6.72E+03	8.87E+03	5.36E+02
Q99959-2 PKP2	ENYLTAGLTVGQVR	760.92	110.31	2.00E+05	2.67E+03	2.93E+03	6.43E+04	1.70E+04	4.32E+03	2.35E+03	2.63E+03	5.11E+02	8.16E+02	1.65E+05	5.96E+04	3.28E+04	3.92E+02	6.42E+03
P08237 K6PF	LPLMECVQVTK	630.84	110.44	2.73E+03	3.01E+03	4.00E+03	1.50E+03	2.90E+03	2.49E+03	6.94E+02	1.59E+03	1.69E+04	2.30E+04	1.79E+03	3.00E+03	1.93E+03	4.33E+04	8.47E+02
P04792 HSPB1	GPSWDPFR	481.23	110.57	2.30E+03	1.49E+03	3.78E+03	1.90E+03	1.30E+03	3.78E+03	7.50E+02	1.26E+03	7.06E+05	8.92E+05	1.49E+03	2.39E+03	2.40E+03	4.98E+05	1.36E+03
P31930 QCR1	MVLAAGGVEHQQLDLA QK	698.04	110.93	1.89E+04	5.88E+03	5.61E+02	5.78E+02	5.35E+03	1.05E+05	4.45E+04	1.84E+04	8.58E+02	4.28E+03	3.80E+02	2.59E+04	1.22E+04	8.58E+02	5.51E+02
P11216 PYGB	VIPAADLSQQISTAGTEASG TGNMK	816.41	110.96	2.49E+03	1.96E+03	3.77E+03	8.27E+03	3.93E+03	1.16E+03	3.57E+03	1.08E+03	3.87E+04	2.16E+04	2.70E+03	5.18E+03	9.85E+02	1.37E+03	1.87E+03
P04792 HSPB1	LSSGVSEIRHTADRWRVSL DVPNHFAPDELTVK	605.32	111.02	1.29E+05	4.88E+03	1.98E+03	2.44E+05	1.11E+05	8.09E+03	2.09E+03	2.90E+03	6.16E+02	9.38E+03	1.34E+05	4.27E+05	1.56E+04	2.57E+03	5.39E+04
P04792 HSPB1	VSLDVNHFAPDELTVK	595.31	111.05	2.07E+05	3.83E+03	2.91E+03	4.33E+05	4.87E+05	4.61E+03	1.59E+03	1.23E+04	1.03E+03	8.80E+04	5.26E+05	6.74E+05	1.28E+04	1.34E+05	9.76E+04
P24752 THIL	VNINGGAVSLGHPIGM	768.40	111.1	1.82E+03	4.33E+03	1.82E+03	3.84E+03	2.97E+03	2.42E+03	6.08E+02	6.12E+03	1.22E+03	4.37E+04	1.62E+03	1.37E+03	3.07E+03	2.64E+04	1.93E+03
P01024 CO3	VPVAVQGEDTVQSLTQGD GVAK	733.39	111.11	5.31E+03	8.90E+05	5.91E+05	4.15E+03	1.60E+04	1.12E+04	4.82E+05	1.50E+03	1.65E+04	9.11E+02	1.32E+03	3.65E+04	1.81E+03	3.24E+03	4.89E+02
P06396-2 GELS	DPDQTDGLGLSYLSSH	852.89	111.25	5.94E+03	6.09E+02	5.21E+02	2.63E+04	9.14E+02	1.26E+03	6.05E+02	8.70E+02	5.06E+02	9.51E+02	1.11E+04	3.20E+02	3.48E+02	3.44E+02	6.34E+02
P04792 HSPB1	EITIPVTFESR	646.35	111.31	2.96E+03	1.15E+03	1.68E+03	8.91E+03	2.22E+03	2.02E+03	1.00E+03	5.32E+02	9.01E+03	1.02E+03	3.87E+02	5.35E+04	4.71E+04	9.95E+03	4.99E+04
P08238 HS90B	APFDLFENK	540.77	111.56	1.79E+03	6.67E+03	4.01E+03	1.56E+03	7.42E+04	6.56E+03	4.84E+03	2.34E+03	2.54E+03	1.43E+03	4.53E+03	7.98E+04	3.29E+02	2.67E+03	7.90E+04
P68371 TBB2C	AVLVDLEPGTMDSVR	801.41	111.9	3.92E+05	1.17E+04	9.59E+02	4.33E+05	2.38E+05	2.03E+03	9.67E+03	5.46E+03	1.03E+03	1.08E+04	5.19E+05	4.57E+05	1.66E+05	2.14E+03	5.64E+04
P11532-4 DMD	LLVEELPLR	541.33	112.08	4.18E+02	2.44E+03	4.80E+03	6.70E+04	7.46E+04	2.77E+03	7.39E+02	3.26E+03	1.15E+03	2.36E+02	5.79E+02	1.04E+05	7.33E+03	4.41E+02	1.25E+05
P01024 CO3	VELLHNPACSLATTK	581.98	112.34	3.27E+03	4.75E+03	7.21E+03	2.38E+03	2.86E+02	1.66E+04	7.07E+03	3.14E+03	4.34E+04	3.79E+04	1.50E+03	3.62E+03	2.03E+03	3.90E+04	5.24E+02
P08237 K6PF	ALVFPVAELK	607.86	112.63	4.63E+02	7.72E+03	4.80E+03	6.94E+05	3.22E+05	1.17E+04	6.67E+03	1.35E+04	1.27E+02	2.27E+03	1.97E+03	4.05E+05	2.50E+05	4.33E+02	6.89E+05
P08559 ODPA	VDGMDILCVR	560.78	112.75	1.37E+05	6.28E+03	8.82E+04	2.04E+05	2.61E+03	8.72E+02	1.30E+05	1.10E+05	1.50E+03	1.98E+03	1.72E+05	1.77E+03	1.38E+04	1.09E+03	1.99E+04
Q96HC4 PDLI5	ILGEVINALK	535.33	113.36	4.74E+04	7.39E+02	2.49E+02	1.07E+04	5.43E+02	9.53E+02	4.01E+02	5.60E+02	8.68E+03	2.56E+03	6.88E+04	3.98E+03	3.96E+02	9.05E+03	5.86E+03
P08107 HSP71	LLQDFFNGR	555.29	113.65	1.89E+03	8.32E+04	2.04E+03	6.37E+02	8.39E+04	1.47E+05	1.06E+04	4.19E+04	1.11E+05	2.17E+05	1.47E+04	3.25E+03	1.15E+03	9.15E+04	1.58E+03
P40939 ECHA	FGGQNPPELLTQMVS	789.40	113.73	1.34E+03	1.58E+03	5.29E+03	5.51E+02	4.19E+05	6.68E+03	2.33E+03	1.18E+03	8.57E+02	4.62E+03	1.54E+03	8.29E+04	2.56E+04	4.84E+03	2.77E+05
O75390 CISY	GLVYETSVLDPDEGIR	881.95	113.93	2.27E+03	1.86E+04	5.72E+03	2.53E+03	4.66E+05	6.18E+03	8.38E+03	2.10E+04	4.54E+03	4.46E+02	3.20E+02	4.89E+05	3.64E+05	3.16E+03	4.97E+05
P24043 LAMA2	TPYNILSSPDYVGVTK	877.45	114.24	4.26E+03	1.85E+03	1.61E+03	4.22E+03	3.66E+03	1.12E+03	1.23E+03	3.31E+03	4.12E+04	3.76E+03	9.24E+02	1.37E+03	5.81E+02	2.65E+04	3.80E+03
P55268 LAMB2	SLADVDAILAR	572.32	114.34	3.21E+03	9.65E+03	6.03E+03	1.09E+03	1.50E+05	2.40E+04	4.19E+03	4.81E+05	5.32E+05	3.16E+05	2.58E+03	2.05E+05	2.81E+05	4.79E+05	1.93E+05
P07195 LDHB	FIIPIQIVK	479.31	114.52	1.68E+03	4.34E+05	6.48E+03	4.30E+02	1.91E+02	9.99E+05	3.29E+05	3.30E+05	7.90E+02	1.22E+02	3.90E+02	1.65E+03	3.36E+02	1.34E+02	1.66E+03
P09622 DLDH	IYAIGDVVAGPMLAHK	552.31	114.73	2.00E+04	2.68E+05	6.31E+03	2.32E+03	8.22E+02	3.94E+05	5.09E+04	1.50E+05	3.60E+02	6.38E+02	6.63E+03	9.58E+03	7.52E+03	1.47E+03	2.94E+03
P14923 PLAK	VSVELTNLSFK	618.84	114.82	6.68E+03	3.27E+03	1.54E+03	1.84E+04	1.81E+03	1.10E+03	3.78E+03	4.17E+03	4.26E+04	1.71E+05	5.74E+03	7.65E+03	8.23E+03	7.21E+04	2.98E+03
P07195 LDHB	GEMMDLQHGSFLQTPK	644.65	115.06	1.58E+03	7.59E+04	1.63E+03	3.73E+04	1.65E+03	2.17E+05	7.13E+04	9.34E+04	2.38E+03	1.18E+03	2.38E+03	1.03E+04	4.25E+03	8.91E+02	7.88E+03
P13929 ENOB	ILENNEALELLK	699.89	115.07	1.46E+03	1.06E+05	3.34E+03	8.92E+02	1.23E+03	4.84E+05	7.19E+04	1.73E+04	6.92E+02	2.30E+03	6.06E+02	1.98E+03	1.21E+03	3.10E+03	6.91E+02
P11047 LAMC1	SQECYFDPELYR	775.34	115.28	1.15E+03	1.13E+03	4.88E+02	1.02E+03	3.15E+02	6.35E+02	1.14E+03	9.87E+02	2.17E+04	9.49E+03	5.28E+02	8.51E+02	8.74E+02	1.39E+04	9.29E+02
P24752 THIL	QATVLAGAGLPSTCTINK	942.52	115.36	1.31E+02	8.40E+03	5.93E+02	6.32E+02	3.27E+04	1.63E+02	1.20E+03	1.00E+02	2.38E+03	1.36E+03	8.31E+02	5.73E+03	7.41E+02	2.16E+02	1.38E+04
P04792 HSPB1	LAVSNEITIPVTFESR	953.50	115.38	2.56E+02	2.26E+03	4.31E+03	1.34E+03	2.02E+05	5.83E+03	2.31E+03	1.29E+03	7.10E+02	4.35E+02	1.19E+03	2.25E+05	3.61E+03	2.07E+04	4.34E+05
P06396-2 GELS	QTQVSVLPEGGETPLFK	915.49	115.43	5.80E+02	1.38E+03	5.86E+02	8.22E+02	2.78E+04	2.14E+03	9.00E+02	7.33E+02	1.26E+03	1.34E+04	3.36E+02	7.05E+03	6.55E+03	5.41E+02	3.78E+04
P40925 MDHC	FVEGLPINDFSR	697.36	115.76	5.14E+03	1.89E+04	6.82E+03	3.02E+03	1.09E+06	1.16E+04	2.46E+03	2.95E+03	1.04E+03	2.25E+03	1.04E+05	1.26E+06	6.75E+05	2.47E+03	2.06E+06
P06396-2 GELS	VHVSEEGTEPEAMLQVLGP	717.03	116.08	3.13E+03	4.74E+04	1.19E+03	8.27E+04	1.71E+03	4.23E+04	1.47E+03	1.38E+03	8.99E+02	1.03E+03	3.69E+03	5.44E+03	3.29E+03	1.85E+03	1.19E+04
P08237 K6PF	IMEIVDAITTTAQSHQR	638.33	116.13	2.90E+03	1.04E+04	2.28E+04	3.18E+03	6.27E+04	3.11E+02	4.50E+02	2.06E+04	5.17E+03	4.80E+02	1.48E+02	3.81E+04	7.18E+03	1.59E+03	1.70E+03
P04792 HSPB1	LFDQAFGLPR	582.31	116.13	3.07E+03	1.93E+03	5.92E+03	5.36E+03	2.98E+05	1.90E+06	3.94E+03	5.63E+03	6.29E+03	7.51E+03	1.01E+03	3.88E+05	3.89E+05	1.63E+03	1.17E+06
P55072 TERA	LIVDEAINEDNSVVLSQPK	724.05	116.15	4.01E+02	1.14E+03	3.36E+03	1.02E+03	2.79E+03	6.06E+04	2.48E+03	1.03E+04	1.84E+02	6.33E+02	1.19E+03	9.14E+02	3.33E+03	7.74E+02	8.09E+02
P08572 CO4A2	SVSIGYLLVK	539.83	116.2	1.26E+05	7.77E+03	2.34E+03	1.63E+05	5.68E+03	2.36E+03	4.10E+03	6.01E+03	8.52E+02	6.54E+02	1.37E+05	8.97E+03	1.05E+05	1.58E+03	1.28E+03
P11216 PYGB	DYFFALAHTVR	670.35	116.25	1.79E+05	8.22E+02	4.27E+03	5.66E+04	7.45E+04	2.25E+04	4.39E+03	1.91E+04	7.86E+02	1.51E+03	3.65E+04	4.12E+03	1.37E+04	4.46E+02	1.29E+05
P12235 ADT1	GADIMYTGTVDCWR	794.35	116.26	2.30E+03	3.01E+02	3.22E+03	6.14E+02	4.80E+04	2.85E+04	2.42E+03	1.01E+04	4.43E+02	1.11E+03	8.95E+02	8.85E+03	2.61E+02	1.80E+03	3.70E+04
P55072 TERA	DVDLEFLAK	525.28	116.37	6.16E+04	2.79E+03	1.67E+04	7.85E+04	2.87E+03	8.52E+03	4.75E+02	4.84E+03	8.16E+02	3.71E+02	3.71E+04	8.90E+03	1.91E+04	6.00E+02	5.56E+04
P28331 NDUS1	HGDVGAPIADVILPGAAYT	698.70	116.38	7.21E+02	2.88E+04	1.16E+04	1.88E+03	2.06E+03	3.87E+04	8.28E+03	2.04E+04	2.04E+03	4.90E+02	1.13E+03	1.29E+03	8.97E+02	3.14E+03	1.23E+03
P08559 ODPA	GPILMELQTYR	660.85	116.41	7.63E+02	2.35E+03	4.07E+03	2.63E+03	4.24E+05	7.61E+03	8.31E+03	5.86E+02	3.49E+03	9.49E+02	1.47E+03	2.39E+05	2.77E+04	2.93E+03	5.78E+04
P14923 PLAK	ALMGSPQLVAAVVR	706.40	116.41	1.14E+03	2.89E+03	3.59E+03	9.98E+02	1.31E+04	2.51E+04	8.75E+03	1.24E+04	1.84E+03	3.28E+02	1.11E+03	2.51E+04	2.68E+03	1.11E+03	7.26E+04
P11177 ODPB	DFLPIGK	451.77	117.04	3.13E+03	1.20E+02	1.42E+03	2.52E+03	2.60E+03	1.58E+03	9.55E+03	5.71E+03	3.54E+05	3.08E+05	4.91E+02	5.26E+03	1.03E+03	2.63E+05	2.77E+03
P01024 CO3	AGDFLEANYMNLQR	821.39	117.11	3.12E+03	1.43E+03	1.02E+03	1.69E+03	3.59E+04	1.77E+03	1.06E+03	9.86E+02	2.67E+03	1.72E+03					

O75390 CISY	DIYWNTLNSGR	669.32	118.1	1.55E+04	7.47E+02	4.79E+03	9.55E+03	9.50E+02	3.96E+03	4.78E+02	1.99E+03	9.14E+02	2.07E+04	5.78E+03	1.06E+03	1.02E+03	5.57E+04	1.32E+03
P01024 CO3	SGIPIVTPSYQHFTK	596.66	118.26	2.62E+04	7.79E+03	5.31E+04	1.31E+05	1.31E+04	1.01E+03	2.39E+03	1.62E+03	6.15E+04	3.04E+03	2.16E+04	9.76E+04	6.45E+04	4.65E+04	3.26E+04
P11047 LAMC1	QDIAVISDSYFPR	756.39	118.59	1.94E+03	1.67E+06	1.36E+04	7.05E+03	8.34E+05	7.52E+03	8.89E+03	3.00E+03	1.05E+06	1.05E+04	2.22E+06	8.34E+05	6.63E+05	5.18E+05	2.18E+06
P08670 VIME	KVESLQEEIAFLK	511.96	118.62	1.54E+03	2.93E+02	5.14E+02	1.66E+03	2.64E+05	1.96E+03	3.72E+02	4.22E+02	5.57E+04	4.20E+03	2.44E+02	1.33E+03	1.39E+03	4.42E+04	5.35E+02
P55268 LAMB2	AMDYDLLLR	555.29	118.64	7.34E+02	1.28E+03	2.44E+03	5.48E+03	1.12E+04	1.02E+03	7.60E+03	6.43E+02	5.85E+04	3.03E+03	2.28E+03	6.21E+04	2.10E+03	2.88E+04	4.58E+02
P55268 LAMB2	VLDPAIPIPDYSSR	820.44	118.66	5.25E+03	1.25E+04	2.74E+03	6.26E+02	1.32E+04	8.44E+03	4.79E+02	2.31E+03	1.29E+03	1.28E+03	7.42E+02	8.34E+03	5.60E+03	2.89E+04	1.93E+04
P40926 MDHM	VDFPQDQLTALTGR	780.90	118.86	2.21E+04	1.49E+04	2.70E+04	1.16E+04	2.81E+04	3.90E+04	2.20E+03	8.69E+03	1.69E+03	2.43E+03	7.57E+03	8.07E+03	1.16E+04	7.86E+02	3.34E+04
P24043 LAMA2	QFGLTTSIPFR	633.85	119.02	7.87E+02	4.40E+03	2.07E+03	1.43E+03	5.35E+04	1.25E+03	5.38E+02	6.12E+03	5.24E+02	9.09E+02	1.66E+04	1.43E+04	1.06E+03	3.73E+03	3.81E+04
P40926 MDHM	GYLGPEQLPDKL	716.36	119.11	2.72E+03	7.21E+02	3.38E+03	8.48E+03	3.66E+03	2.13E+03	5.61E+02	2.93E+02	2.54E+04	5.67E+03	6.70E+02	5.71E+02	1.51E+03	1.52E+03	5.86E+02
P08670 VIME	EMEENFAVEAANYQDTIGR	729.66	119.26	5.97E+02	1.14E+03	8.73E+02	5.43E+03	6.46E+02	2.54E+03	1.91E+03	2.83E+02	5.71E+03	4.79E+04	1.02E+03	1.35E+03	2.96E+02	3.49E+03	1.01E+03
P11047 LAMC1	DGFFGNPLAPNPADK	780.39	119.31	2.11E+03	1.04E+04	3.24E+03	6.83E+02	1.23E+03	8.11E+03	1.46E+03	4.93E+02	4.61E+04	1.16E+03	8.46E+02	4.70E+03	8.77E+03	1.01E+04	1.67E+03
P08559 ODPA	LPCIFICENNR	661.33	119.45	9.87E+04	2.01E+03	3.33E+03	2.30E+03	2.13E+04	2.98E+04	1.95E+04	5.28E+03	1.43E+03	7.97E+02	2.64E+03	2.14E+04	3.90E+02	2.34E+03	1.60E+04
P14923 PLAK	NEGATATYAAAVLFR	742.38	119.47	9.98E+04	3.47E+04	1.54E+03	7.73E+04	6.15E+02	2.59E+03	4.31E+03	2.71E+03	8.90E+03	2.71E+03	1.28E+05	2.17E+03	1.51E+03	2.55E+03	6.08E+03
P19367-4 HXK1	MVSGMYLGELVR	677.85	119.59	3.01E+02	1.39E+04	4.92E+03	3.30E+02	1.59E+04	7.33E+03	4.09E+04	4.47E+04	1.91E+03	3.90E+02	1.10E+03	1.37E+03	8.72E+02	3.46E+02	3.72E+03
P24043 LAMA2	SLGLICDGCVPVGTGPR	854.92	119.77	1.28E+03	6.23E+02	1.00E+04	2.34E+03	1.50E+03	1.26E+03	5.60E+03	4.84E+02	2.86E+02	1.81E+03	1.21E+03	1.66E+03	9.50E+02	1.30E+04	3.74E+03
P63261 ACTG	TVPIYEGYALPHAILR	605.00	119.87	1.25E+03	6.68E+03	4.78E+02	1.51E+03	5.67E+04	9.60E+02	4.10E+03	2.28E+03	2.09E+03	1.23E+03	1.59E+03	5.03E+03	7.15E+02	1.12E+03	2.79E+03
P11021 GRP78	AKFEELNMDLFR	504.92	120.12	1.50E+02	1.85E+03	1.47E+03	2.83E+02	4.24E+04	7.60E+03	1.91E+03	8.51E+03	5.47E+02	1.06E+03	4.44E+02	1.52E+03	3.78E+02	4.72E+02	3.19E+02
P24043 LAMA2	VDDAWDLLR	551.78	120.27	1.24E+02	1.74E+03	3.18E+03	3.43E+03	4.39E+04	5.08E+03	2.95E+02	2.14E+03	2.77E+03	3.42E+03	2.28E+03	4.89E+03	8.83E+03	2.45E+03	5.33E+04
P40926 MDHM	TIPLISQCTPK	657.38	120.29	1.37E+05	7.04E+02	5.43E+02	1.38E+05	7.55E+03	2.76E+03	1.05E+03	3.46E+03	2.64E+05	3.31E+03	1.95E+04	7.58E+03	7.62E+03	5.28E+04	1.06E+04
P40925 MDHC	ELTEEKESAFEFLS	829.89	120.8	6.91E+03	4.04E+03	1.05E+03	4.22E+02	1.57E+04	1.93E+03	1.77E+03	2.99E+02	5.83E+02	3.65E+02	2.78E+03	5.67E+03	3.96E+02	6.53E+02	6.53E+03
P19367-4 HXK1	MISGMYLGIVR	684.85	121.02	2.01E+03	2.43E+04	4.27E+02	1.99E+03	1.50E+03	1.10E+04	4.51E+03	8.04E+03	3.28E+03	8.44E+02	6.35E+02	1.35E+04	1.21E+03	2.28E+02	1.28E+03
P28331 NDUS1	VSDTDLCTEEVFPFAGAGT DLR	766.36	121.07	1.84E+03	2.32E+03	8.53E+03	3.51E+02	6.41E+02	4.41E+03	1.02E+04	1.91E+04	1.29E+04	3.48E+03	8.32E+02	2.28E+03	1.37E+03	7.13E+03	1.57E+03
P68371 TBB2C	FWEVISDEHGIDPTGTYHG DSDLQLER	779.86	121.35	1.85E+06	4.04E+05	9.44E+03	1.75E+03	4.21E+03	1.90E+06	1.35E+04	8.46E+05	3.71E+02	4.21E+02	6.88E+02	3.95E+03	5.56E+02	5.61E+02	9.88E+03
P17174 AATC	NTPVYVSSPTWENHNAVFS AAGFK	875.09	121.39	2.03E+03	6.08E+02	2.43E+02	7.03E+04	4.02E+03	4.15E+03	2.78E+02	1.35E+03	1.09E+03	6.50E+02	1.54E+03	1.79E+03	1.76E+03	6.14E+02	1.22E+02
O75390 CISY	SQLSAAVTALNSESNFAR	933.47	121.44	1.39E+04	8.72E+02	2.49E+03	3.80E+04	9.80E+02	8.54E+02	2.46E+03	2.54E+03	2.29E+03	3.97E+02	1.59E+03	1.44E+03	2.42E+03	1.13E+03	1.36E+03
P04792 HSPB1	LTVEAPMPKLATQSNEITIP VTFESR	959.50	121.55	7.03E+02	3.00E+03	1.94E+03	2.04E+03	1.14E+05	5.76E+03	1.38E+03	1.62E+03	2.23E+03	4.74E+03	3.62E+03	2.68E+04	8.42E+03	2.46E+03	4.40E+04
P11216 PYGB	DYFFALAH	492.24	121.59	6.19E+04	1.54E+03	1.35E+03	7.09E+04	1.86E+03	1.66E+03	3.13E+02	5.88E+02	3.31E+02	1.18E+03	5.92E+04	2.33E+03	7.55E+02	2.72E+03	7.94E+02
P11532-4 DMD	IFLTEQPLEGLEK	758.91	121.76	3.84E+04	9.67E+02	7.70E+02	6.20E+04	3.11E+02	1.01E+03	1.53E+02	3.13E+02	5.58E+02	3.73E+02	7.57E+04	1.06E+03	3.42E+03	1.60E+03	4.74E+03
P11177 ODPB	TIRPMDMETIEASVMK	617.98	122.08	3.70E+04	6.21E+02	2.65E+02	1.89E+05	1.55E+04	4.56E+02	6.59E+02	3.01E+02	6.11E+02	1.86E+02	1.53E+05	7.39E+03	1.05E+05	1.39E+03	3.67E+03
P01024 CO3	SNLDEDIHAENIVSR	908.95	122.09	7.15E+03	1.04E+04	2.66E+03	2.20E+03	4.03E+04	7.99E+03	1.55E+02	4.39E+03	3.16E+02	1.07E+03	1.04E+03	6.64E+03	5.72E+02	8.12E+02	9.60E+03
P24043 LAMA2	IYFGGLPTLR	568.83	122.46	3.77E+04	9.79E+02	1.92E+03	1.68E+05	7.81E+02	1.10E+03	3.35E+02	3.88E+03	5.12E+02	1.03E+03	1.12E+05	3.35E+03	9.02E+02	6.90E+02	6.46E+02
P00558 PGK1	ITLPVDFVTADK	659.87	122.87	5.38E+05	7.92E+03	3.22E+02	5.99E+05	8.27E+02	3.43E+03	3.86E+02	5.03E+03	3.63E+02	1.50E+04	4.20E+05	1.22E+03	8.70E+03	1.75E+03	1.10E+04
Q01082-3 SPTB2	LTTLELLEVR	593.84	123.29	4.09E+05	2.24E+03	6.55E+03	3.70E+05	2.65E+03	6.91E+02	1.43E+03	6.39E+03	4.49E+02	3.59E+02	4.32E+05	7.95E+03	1.58E+04	4.14E+03	1.65E+04
Q71U36 TBA1A	EIIDLVLR	543.31	123.65	2.67E+05	3.01E+04	1.20E+04	1.99E+05	1.89E+03	2.97E+04	1.80E+04	4.59E+04	5.60E+03	6.00E+03	2.35E+05	2.31E+03	1.43E+04	3.16E+02	6.37E+03
Q9NPC6 MYOZ2	FMSFVNPLSGR	627.82	123.65	1.88E+05	1.81E+03	2.09E+03	1.43E+05	1.58E+03	5.37E+02	4.17E+03	9.37E+02	8.71E+02	1.99E+03	2.13E+05	3.70E+03	1.35E+04	5.58E+03	5.40E+03
P40925 MDHC	SLLYSIGNGSVFGK	721.39	123.71	5.34E+04	1.54E+03	8.49E+02	1.65E+03	4.15E+02	5.62E+02	1.58E+03	1.02E+03	2.17E+03	2.37E+03	2.06E+04	1.14E+03	3.39E+03	6.40E+03	1.35E+03
P08559 ODPA	MVNSNLASVEELKEIDVEV	758.39	123.99	3.10E+03	3.85E+03	1.66E+03	2.27E+03	2.92E+03	8.70E+03	1.24E+03	1.41E+04	2.04E+03	9.07E+02	1.25E+04	9.12E+02	2.78E+03	1.51E+03	1.07E+03
P40926 MDHM	LTLYDIAHTPGVAADLSH	632.00	124.16	2.60E+05	1.52E+05	7.81E+03	1.96E+05	9.80E+02	2.59E+04	4.91E+03	1.04E+05	9.89E+02	1.35E+03	1.10E+05	5.03E+03	2.75E+04	7.34E+04	6.17E+03
P00558 PGK1	ITLPVDFVTADKFDENAK	675.02	124.25	7.18E+02	2.06E+03	2.45E+03	1.44E+03	7.86E+02	2.55E+04	3.38E+03	2.03E+03	2.38E+02	1.99E+03	4.65E+03	1.70E+03	1.59E+03	6.42E+02	1.63E+03
P00558 PGK1	VLNNMEIGTSLFDEEGAK	656.32	124.29	5.08E+04	1.15E+03	3.14E+02	3.59E+04	3.80E+02	3.14E+03	3.70E+02	6.00E+02	1.37E+03	5.90E+02	2.18E+04	1.49E+03	7.17E+03	1.57E+03	3.09E+04
P01024 CO3	TELRPGETLNVNFLLR	624.68	124.49	1.37E+04	3.54E+02	1.25E+02	2.29E+03	4.88E+04	2.07E+02	1.00E+03	4.77E+02	5.00E+02	3.34E+02	2.35E+03	5.89E+02	3.78E+03	3.24E+02	1.00E+04
Q71U36 TBA1A	TIGGGDDSFNTFFSETGAGK	1004.45	124.49	8.51E+04	1.61E+03	2.59E+03	8.48E+04	2.34E+03	2.16E+04	6.53E+02	2.84E+03	1.81E+02	1.45E+03	8.26E+04	5.24E+02	6.69E+03	7.66E+02	8.83E+04
Q9NPC6 MYOZ2	DIMLEELSHLSNR	778.89	124.55	1.78E+05	5.88E+03	6.87E+02	2.85E+05	3.46E+03	1.92E+03	9.78E+02	8.76E+02	4.61E+03	6.39E+02	2.49E+05	2.28E+04	1.48E+04	9.64E+02	5.21E+04
Q01082-3 SPTB2	FMELLEPLNER	695.85	124.57	5.69E+03	2.33E+04	4.46E+02	8.21E+03	2.01E+03	7.95E+04	3.54E+04	3.74E+04	1.58E+03	1.57E+03	4.29E+03	2.04E+03	4.51E+03	1.24E+03	1.22E+03
P40925 MDHC	EVGVYEALKDDSWLK	876.45	124.67	8.11E+03	3.64E+02	4.62E+02	4.43E+04	2.16E+03	3.06E+03	2.16E+03	5.61E+02	5.01E+03	3.27E+03	4.44E+04	9.45E+02	6.52E+02	1.15E+03	3.86E+03
P12235 ADT1	IPKEQGFLSFWR	503.27	125.02	4.86E+02	5.83E+02	5.26E+02	1.79E+03	2.29E+04	9.17E+02	9.07E+02	1.06E+03	1.67E+03	2.55E+02	4.31E+03	2.18E+03	4.08E+02	8.09E+02	2.08E+04
P55084 ECHB	AMSDWFAENYMGR	846.84	125.06	8.75E+04	7.97E+02	7.29E+02	1.19E+03	1.17E+03	3.00E+02	2.13E+03	3.31E+02	3.26E+02	3.73E+02	4.99E+04	1.23E+03	9.16E+02	1.45E+03	1.88E+04
P08237 K6PF	IMEIVDAITTAQSH	815.41	125.25	4.23E+04	2.39E+03	4.31E+03	5.95E+03	1.92E+03	1.59E+04	7.63E+02	2.03E+04	5.87E+02	1.14E+03	9.95E+03	2.58E+03	3.36E+03	2.99E+04	6.99E+02
P08670 VIME	ILLAELEQLK	585.36	126.25	4.73E+05	4.43E+04	1.65E+02	3.98E+05	7.54E+03	3.48E+04	2.04E+04	5.77E+04	4.39E+02	7.02E+02	2.92E+05	1.33E+05	1.77E+05	3.18E+02	6.59E+03
P08107 HSP71	FEELCSDLFR	629.79	126.31	4.04E+04	1.63E+03	1.99E+03	4.89E+04	3.05E+03	1.41E+03	1.30E+03	7.03E+03	3.6						

P19429 TNNI3	ISADAMMQAL	525.75	127.11	2.43E+05	2.84E+03	4.41E+03	2.07E+05	1.22E+03	6.83E+03	1.68E+03	1.59E+02	4.97E+02	5.08E+03	3.65E+03	2.47E+03	1.27E+03	4.50E+02	3.71E+03
P11532-4 DMD	RPQLEELITAAQNLK	575.33	127.13	2.97E+04	1.54E+04	8.31E+03	2.37E+04	8.42E+03	3.84E+03	2.04E+03	1.07E+04	2.11E+03	1.89E+03	2.28E+04	3.31E+03	1.92E+04	3.21E+03	5.03E+03
P55084 ECHB	TPFLLSGTSYKDLMPHDLA	566.29	127.52	8.93E+03	5.84E+03	6.24E+03	2.97E+03	1.55E+04	1.09E+04	3.33E+03	3.51E+04	4.02E+03	6.14E+03	1.01E+04	9.04E+03	4.99E+02	3.44E+03	1.34E+04
P60174 TPIS	QSLGELIGTLNAAK	707.90	127.66	1.71E+05	2.87E+03	2.25E+03	1.94E+05	5.27E+03	3.91E+03	2.86E+03	4.45E+03	1.66E+03	3.07E+03	1.79E+04	3.04E+03	2.25E+04	1.04E+04	6.07E+03
P11216 PYGB	IGEEFLTDLSQLKK	540.97	127.71	1.05E+03	1.88E+03	1.22E+03	1.92E+03	4.45E+02	7.29E+02	1.19E+03	1.93E+03	3.82E+04	2.14E+03	4.87E+02	7.59E+02	2.48E+02	7.34E+02	1.08E+03
P11021 GRP78	DNHLLGTFDLTGIPPAPR	645.34	127.95	1.98E+04	1.79E+04	3.39E+04	2.11E+04	6.01E+03	2.57E+04	3.59E+03	1.21E+04	7.32E+03	1.53E+04	1.86E+03	7.78E+04	1.64E+04	1.10E+04	1.34E+04
P55072 TERA	NVFIIGATNRPDHDPAILRP	630.36	127.99	1.54E+03	8.98E+03	7.18E+03	5.37E+03	7.76E+04	5.57E+03	5.43E+02	7.56E+03	7.19E+03	3.42E+03	3.40E+03	1.27E+04	4.91E+03	5.15E+03	6.63E+03
P40926 MDHM	IFGVTTLDIVR	617.36	128.23	1.54E+04	1.42E+04	1.70E+03	6.97E+05	4.43E+03	2.53E+03	9.68E+03	4.81E+03	2.99E+03	5.34E+03	5.78E+05	6.66E+03	5.25E+03	3.18E+03	6.98E+03
P19367-4 HXK1	IDEAILITWTK	651.87	128.34	8.44E+03	6.86E+02	9.81E+02	2.79E+03	4.05E+03	7.78E+03	3.32E+03	4.31E+03	8.85E+03	2.53E+04	2.77E+03	8.18E+03	2.27E+03	7.27E+03	2.07E+03
P00558 PGK1	TGQATVASGIPAGWMGLD CGPESSK	807.38	128.44	3.20E+04	1.56E+03	2.66E+03	9.07E+03	5.49E+03	1.58E+04	4.77E+03	1.25E+03	4.59E+03	9.69E+03	3.09E+04	1.86E+04	6.34E+03	5.60E+02	1.83E+04
P24043 LAMA2	VSFLWDVGSVGR	689.86	128.76	7.05E+03	8.19E+03	3.68E+03	2.12E+04	1.53E+04	4.37E+03	4.71E+03	1.81E+04	3.11E+03	1.70E+03	1.88E+04	2.93E+04	4.28E+04	7.00E+03	3.89E+04
P08670 VIME	VESLQEEIAFLK	703.38	128.87	7.51E+02	1.50E+03	3.90E+03	1.42E+05	3.27E+03	1.28E+04	6.89E+03	6.26E+03	1.20E+02	1.23E+06	8.74E+02	2.07E+04	1.41E+04	1.46E+03	4.00E+03
P40939 ECHA	MQLLEIITTEK	659.87	128.92	9.22E+04	3.42E+03	2.47E+04	4.18E+03	3.34E+03	8.07E+03	5.58E+02	7.38E+03	1.83E+03	6.39E+03	4.67E+04	4.26E+04	7.60E+03	8.62E+03	1.53E+04
P01024 CO3	SSLSVPYVIVPLK	701.42	128.96	5.34E+03	4.04E+03	7.09E+02	1.07E+03	1.36E+03	1.10E+03	2.99E+02	1.11E+03	3.45E+02	6.22E+04	1.14E+03	3.24E+03	2.61E+02	1.19E+03	2.51E+03
P40925 MDHC	ESAFEFLSS	508.73	129.49	2.47E+03	3.52E+02	5.18E+02	2.61E+04	7.79E+02	6.86E+02	4.91E+02	1.03E+03	7.22E+02	3.48E+02	3.15E+03	1.64E+02	2.81E+02	1.73E+02	7.68E+02
P60174 TPIS	ALAEGLGVIACIGEK	722.39	129.54	2.20E+04	2.91E+03	8.31E+03	3.91E+03	6.19E+03	2.37E+03	2.03E+04	7.77E+03	6.78E+03	3.88E+03	4.78E+04	3.53E+04	1.56E+04	8.61E+03	1.29E+04
P63261 ACTG	VALDFEQEMATAASSSSLE	705.34	129.7	1.60E+04	6.12E+03	7.13E+02	1.21E+02	4.91E+03	1.00E+04	2.59E+03	6.83E+03	2.85E+03	1.05E+04	1.91E+04	5.41E+03	1.36E+04	5.86E+03	2.37E+03
P60174 TPIS	VAHALAEGLGVIACIGEK	584.32	129.74	2.67E+04	7.53E+03	2.04E+03	1.40E+04	1.23E+04	2.71E+03	5.45E+03	2.11E+03	1.38E+03	9.50E+03	3.44E+04	2.57E+03	5.85E+03	1.86E+03	3.90E+03
P00558 PGK1	ALESPERPFLAILGGAK	590.34	129.85	2.48E+05	6.87E+03	2.14E+03	3.48E+05	2.04E+03	4.77E+03	6.21E+03	6.15E+03	4.96E+03	8.85E+03	1.56E+05	3.60E+03	1.96E+05	5.32E+03	7.59E+03
Q01082-3 SPTB2	EVDDLEQWIAER	751.86	129.85	5.94E+04	7.42E+03	6.32E+03	1.28E+04	2.65E+03	8.05E+03	3.59E+03	6.94E+03	7.73E+03	3.21E+04	5.19E+03	2.48E+03	6.12E+03	2.48E+03	8.02E+03
P31930 QCR1	NNGAGYFLEHLAFK	790.90	130.01	8.54E+03	2.81E+03	5.79E+03	7.34E+03	1.97E+04	4.47E+03	3.78E+03	1.20E+04	8.38E+03	1.79E+04	5.66E+03	3.78E+03	9.23E+03	1.06E+04	6.04E+03
P01857 IGHG1	TTPPVLSDSGSFFLYSK	937.46	130.08	1.17E+05	1.84E+03	2.16E+03	1.36E+04	1.43E+03	1.61E+04	6.04E+03	1.68E+04	9.88E+03	2.00E+03	2.03E+04	1.59E+04	2.18E+03	1.30E+04	1.98E+04
P11216 PYGB	VAIQLNDTHPALSIPELMR	706.72	130.1	5.87E+04	4.59E+03	5.21E+03	1.21E+04	3.71E+04	2.51E+03	1.52E+04	6.32E+02	3.84E+03	9.53E+03	6.23E+04	5.61E+03	1.30E+04	8.20E+03	1.72E+04
P55084 ECHB	AQDEGLLSDVVPFK	759.40	130.2	1.67E+05	2.85E+04	6.07E+03	2.94E+02	5.24E+04	2.22E+03	5.86E+03	5.18E+04	1.38E+04	2.04E+02	1.67E+05	1.20E+04	3.53E+04	9.04E+03	1.96E+04
Q01082-3 SPTB2	DVEDEILWVGER	730.36	130.38	1.81E+04	1.53E+04	7.76E+03	6.87E+03	5.32E+03	7.60E+03	1.50E+04	9.64E+03	1.13E+03	7.25E+03	7.59E+04	2.54E+04	1.18E+04	2.48E+04	5.80E+03
P40926 MDHM	LTLYDIAHTPGVAADLSHIE TK	592.07	130.41	4.29E+05	3.49E+03	3.67E+03	2.83E+03	3.10E+03	6.60E+02	6.17E+02	7.97E+02	6.61E+02	2.28E+03	3.01E+05	1.23E+03	1.24E+05	3.77E+03	4.23E+05
P55268 LAMB2	QLDALLEALK	557.33	130.56	2.93E+03	8.58E+03	6.17E+03	4.11E+04	1.37E+03	8.45E+03	7.57E+03	1.09E+04	2.91E+02	5.13E+03	7.19E+04	3.30E+03	3.71E+03	2.78E+03	1.08E+04
P24043 LAMA2	IQDMSGWYLTDLPGR	876.42	130.79	1.73E+04	9.66E+03	2.49E+03	5.53E+03	3.74E+04	1.34E+04	1.57E+04	1.83E+04	3.81E+03	9.29E+03	2.00E+04	9.68E+03	1.24E+04	7.08E+03	8.27E+03
Q9NPC6 MYOZ2	FKVPDFEL	497.77	130.95	1.22E+03	1.55E+03	1.06E+03	6.79E+04	3.36E+04	1.36E+03	4.70E+02	5.47E+02	1.27E+02	2.18E+02	6.27E+02	3.83E+03	8.07E+02	1.33E+02	4.28E+02
P28331 NDUS1	VALIGSPVDLTYTYDHLGD SPK	787.74	130.97	7.85E+04	5.11E+03	2.40E+03	1.16E+03	4.77E+03	2.12E+03	1.77E+03	7.80E+03	9.23E+03	2.16E+03	3.34E+04	6.55E+03	8.41E+03	4.63E+03	1.24E+04
P40939 ECHA	MGLVDQLVEPLGPKPPE ER	758.74	131.05	1.14E+05	2.70E+03	9.18E+02	6.51E+03	2.01E+03	1.07E+03	2.40E+03	6.11E+03	4.72E+03	9.97E+02	9.46E+04	2.16E+03	1.06E+04	2.60E+03	7.35E+04
P60174 TPIS	VVLAYEPVWAIGTGK	801.95	131.23	4.48E+05	4.37E+03	3.54E+03	4.43E+03	6.13E+03	3.56E+03	2.35E+03	3.51E+03	1.09E+04	2.45E+03	4.10E+05	3.08E+03	5.18E+03	5.03E+03	4.71E+03
P40939 ECHA	LTAYAMTIPFVR	691.88	131.48	1.46E+03	5.66E+03	4.08E+03	1.28E+03	4.75E+04	4.64E+03	3.23E+03	4.11E+03	2.62E+03	4.78E+03	4.71E+03	1.04E+04	5.29E+03	3.83E+03	1.94E+03
P31930 QCR1	YIYDQCPAVAGYGPQLPD YNR	882.42	131.49	2.24E+04	4.71E+03	6.75E+03	1.73E+04	6.22E+03	2.68E+03	1.51E+04	1.70E+04	5.31E+04	9.67E+03	9.44E+03	8.03E+03	9.79E+03	1.28E+04	1.28E+04
P00558 PGK1	VLPQVDALSNI	549.31	131.59	7.74E+05	8.80E+03	2.90E+04	3.67E+03	1.76E+04	1.74E+04	4.47E+05	2.28E+05	1.81E+03	3.38E+02	6.80E+05	8.64E+03	3.29E+05	2.50E+03	6.16E+05
P19367-4 HXK1	GDFIALDLGSSFR	727.87	131.72	5.57E+04	6.34E+04	3.49E+03	8.36E+03	2.93E+03	1.86E+04	3.31E+03	1.37E+04	8.27E+03	1.62E+03	7.34E+04	1.15E+04	5.97E+03	1.17E+04	1.09E+04
P60174 TPIS	VPADTEVVCAPPTAYIDFA	712.35	132.03	1.59E+05	3.26E+04	2.58E+03	5.15E+03	9.29E+03	6.94E+04	7.39E+03	1.28E+04	1.53E+04	5.14E+03	1.72E+05	2.37E+04	7.11E+04	1.30E+04	2.26E+05
P11021 GRP78	FEELNMDLFR	657.31	132.05	1.39E+05	1.60E+04	5.16E+03	2.32E+03	3.71E+04	1.90E+03	1.78E+03	1.19E+04	1.80E+03	3.05E+03	8.32E+04	4.52E+04	9.30E+03	1.04E+04	1.77E+04
P06396-2 GELS	AQPVQVAEGSEPDGFWEAL GGK	758.04	132.17	2.97E+03	1.88E+04	3.39E+03	3.57E+03	4.46E+03	2.39E+04	5.09E+03	6.13E+03	6.72E+03	6.44E+03	4.08E+03	1.14E+04	2.20E+03	1.17E+04	6.10E+03
P11047 LAMC1	LSAEDLVLEGAGLR	721.90	132.33	2.03E+05	9.47E+03	2.33E+03	2.08E+03	1.44E+04	2.90E+04	2.13E+02	2.09E+04	4.50E+03	1.01E+03	2.57E+05	7.35E+02	3.09E+05	2.00E+04	2.81E+05
P40925 MDHC	ELTEEKESAFEFSSA	908.93	132.5	4.33E+03	8.92E+03	4.67E+03	7.03E+03	2.78E+03	3.04E+03	7.29E+03	1.79E+03	1.90E+04	4.68E+03	2.96E+03	4.24E+03	4.51E+03	7.74E+04	3.06E+03
P11532-4 DMD	SPAQILISLESEER	786.41	132.61	1.02E+04	4.59E+03	8.97E+03	3.12E+03	2.19E+04	1.87E+03	1.90E+03	4.07E+03	1.94E+04	4.80E+03	2.75E+04	7.25E+03	5.70E+03	3.69E+04	1.87E+04
P40926 MDHM	SQETECTYFSTPLLLGK	958.97	132.74	8.64E+04	6.37E+03	1.73E+03	1.18E+03	8.92E+02	5.06E+03	2.40E+03	6.17E+03	1.50E+04	2.08E+03	3.29E+04	4.67E+03	5.34E+03	2.33E+03	1.28E+04
P11177 ODPB	VLLGEEVAQYDGAYK	901.46	133.01	2.20E+04	7.70E+03	4.06E+04	3.75E+03	5.89E+03	2.41E+03	4.58E+03	1.68E+04	6.04E+03	3.41E+03	3.59E+04	5.58E+03	6.13E+03	7.01E+03	2.00E+04
P11216 PYGB	IVNGWQVEEADDWLR	915.45	133.03	7.74E+03	1.41E+04	6.00E+03	3.91E+03	1.70E+04	7.93E+03	1.22E+04	1.03E+04	1.88E+03	3.51E+03	1.47E+04	2.33E+04	1.13E+04	5.95E+03	2.31E+04
P11021 GRP78	TFAPEEISAMVLTk	768.90	133.11	4.54E+04	4.28E+03	3.32E+03	3.44E+03	3.15E+03	9.73E+03	1.75E+03	7.15E+03	4.55E+03	1.92E+03	9.37E+04	5.13E+03	4.60E+03	4.63E+03	7.47E+03
Q71U36 TBA1A	AVFVDLEPTVIDEVR	851.46	133.28	3.07E+05	8.42E+03	2.61E+03	9.21E+03	3.30E+03	6.37E+03	9.97E+03	3.76E+03	6.57E+03	6.89E+03	2.83E+05	1.81E+04	1.95E+05	1.04E+04	1.78E+04
P55072 TERA	LDQLIYIPLPDEK	778.93	133.28	4.32E+04	8.36E+03	1.47E+03	6.09E+03	6.22E+03	1.07E+04	6.41E+03	9.17E+02	4.45E+03	2.77E+03	4.73E+04	5.61E+03	4.02E+04	4.51E+03	8.74E+03
P11532-4 DMD	SEAVLQSPFAIFR	797.41	133.43	1.29E+04	2.00E+04	5.36E+03	5.72E+04	1.38E+04	1.54E+04	1.35E+04	1.34E+04	8.33E+03	1.01E+04	4.84E+03	1.36E+04	3.44E+03	4.96E+03	2.65E+04
P11177 ODPB	TYYMSSGGLQPVPIVFR	914.48	133.53	9.57E+04	3.03E+03	7.83E+03	8.41E+03	5.09E+03	6.56E+03	4.60E+03	1.61E+04	7.00E+03	4.64E+03	6.93E+				



P01024 CO3	ILLQGTTPVAQMTEDAVDAE	719.70	134.58	8.54E+03	7.81E+03	9.95E+02	4.63E+03	8.77E+04	2.25E+04	8.01E+03	6.38E+03	1.24E+04	3.81E+03	7.37E+03	8.93E+03	1.95E+03	4.69E+03	4.31E+03
O76041 NEBL	GMQVSMDDIPDLR	737.88	134.64	6.70E+03	1.04E+04	6.72E+03	7.37E+04	8.54E+03	5.12E+04	5.34E+04	9.23E+03	4.73E+03	3.21E+03	2.17E+04	3.10E+04	4.05E+04	6.46E+03	5.81E+03
P01857 IGHG1	THTCPPCPAPELLGGPSVFL FPPKPK	683.36	134.71	4.00E+04	1.13E+04	3.59E+03	1.68E+04	5.03E+03	2.58E+04	3.23E+04	1.52E+04	4.21E+04	9.04E+03	3.98E+04	9.71E+03	1.36E+04	5.32E+04	3.02E+04
P40926 MDHM	FVFSLV DAMNGK	664.34	134.86	2.14E+05	1.11E+04	1.87E+04	8.88E+03	1.48E+04	3.31E+03	2.34E+03	1.25E+04	1.24E+04	1.83E+04	4.37E+04	1.12E+04	6.92E+04	2.49E+03	7.14E+03
P31930 QCR1	HLGGIPWTYAEDA VPTLTP	766.38	134.93	2.02E+04	7.47E+03	2.47E+04	2.33E+03	2.18E+04	5.15E+04	3.42E+03	3.59E+04	2.03E+04	2.15E+04	7.83E+03	1.69E+04	2.36E+03	6.84E+03	1.55E+03
P68371 TBB2C	ALTVPELTQQMFDAK	846.44	135.17	1.80E+04	9.20E+03	2.44E+04	1.81E+04	7.75E+04	9.48E+03	1.53E+04	9.11E+03	1.47E+04	3.31E+03	1.16E+05	1.48E+04	1.55E+04	1.26E+04	2.92E+04
P11216 PYGB	LLPLVSEDEVFIR	700.91	135.19	3.27E+03	4.22E+03	9.01E+04	6.15E+03	7.88E+03	1.78E+03	4.84E+03	4.69E+03	3.44E+03	6.17E+03	1.53E+03	1.41E+03	1.07E+03	1.42E+03	3.18E+03
P19367-4 HXK1	LSDETLDIMTR	703.86	135.21	9.31E+05	8.81E+04	7.99E+03	4.97E+05	4.96E+04	1.18E+05	6.42E+03	4.25E+04	2.36E+04	4.49E+03	9.44E+05	3.95E+04	2.62E+05	9.21E+03	7.81E+04
P05413 FABPH	SLGVGFATR	454.25	135.43	8.35E+04	3.00E+04	8.47E+03	2.17E+04	1.59E+04	5.60E+04	2.16E+04	3.12E+04	1.72E+03	7.91E+03	7.79E+04	1.64E+04	3.37E+04	2.19E+04	3.00E+04
O75390 CISY	DILADLIPK	499.30	135.57	3.84E+03	4.50E+05	9.64E+02	7.46E+02	8.06E+04	4.02E+05	2.90E+03	5.28E+04	9.71E+02	4.23E+02	2.01E+03	1.52E+05	1.25E+05	4.50E+04	1.74E+05
P14923 PLAK	EAADAIDAEGASAPLMELL HSR	756.38	135.61	7.11E+04	1.28E+05	1.82E+05	1.30E+05	1.73E+05	9.55E+04	8.95E+03	3.36E+04	1.89E+05	1.02E+05	6.84E+04	2.03E+05	1.41E+05	2.26E+05	4.01E+04
P11047 LAMC1	DTLQEANDILNNLK	800.91	135.62	1.10E+05	1.22E+04	4.12E+04	7.10E+04	4.11E+04	1.01E+05	4.86E+04	4.84E+04	7.06E+04	9.95E+04	1.26E+04	7.92E+04	1.01E+05	4.00E+04	1.39E+05
P17174 AATC	APPSVFAEVPQAQPVLVFK	675.38	135.67	6.94E+04	3.49E+04	3.90E+04	7.23E+04	1.16E+05	1.43E+05	4.70E+04	4.68E+04	1.23E+05	9.79E+04	1.88E+04	9.87E+04	3.67E+04	4.75E+04	1.08E+05
P13929 ENOB	HIADLAGNPDLLPVPFNV INGGSHAGNK	756.40	135.71	1.06E+05	1.93E+05	1.17E+05	1.30E+05	1.92E+05	1.14E+05	1.13E+05	1.74E+04	1.77E+05	7.89E+04	2.26E+05	1.86E+05	1.38E+05	4.71E+04	1.58E+05
P11177 ODPB	IMEGPAFNFLDAPAVR	874.44	135.72	1.57E+06	9.54E+05	8.53E+05	1.18E+06	6.66E+05	2.21E+06	6.01E+05	6.77E+05	7.89E+05	1.01E+06	1.51E+06	3.15E+05	3.58E+05	4.77E+05	1.50E+06
P12235 ADT1	EQGFLSFWR	585.29	135.74	3.05E+05	1.28E+04	7.72E+04	1.53E+05	7.59E+04	2.73E+04	5.15E+03	1.47E+03	1.24E+05	2.65E+05	2.11E+05	2.10E+04	4.04E+03	4.32E+04	4.45E+05
P40939 ECHA	TVLGTPEVLLGALPGAGGT	669.71	135.75	9.23E+04	1.05E+05	1.56E+04	8.83E+04	1.39E+05	1.08E+05	1.49E+05	1.32E+05	1.49E+05	1.15E+05	7.99E+04	1.09E+05	1.08E+05	1.25E+04	9.07E+04
P09622 DLDH	NLGLEELGIEDPR	784.42	135.8	1.62E+05	1.46E+05	4.97E+04	1.85E+05	6.00E+04	1.39E+05	1.60E+05	1.25E+05	2.44E+05	2.05E+05	1.83E+04	3.71E+05	1.43E+05	7.20E+04	2.74E+05
P28331 NDUS1	GLLTYTSWEDALSR	806.39	135.84	1.59E+05	1.34E+05	9.33E+04	1.08E+05	1.30E+05	1.47E+05	1.04E+05	8.38E+04	6.32E+04	2.09E+04	9.23E+04	2.23E+05	1.38E+05	1.05E+05	1.85E+05
P55268 LAMB2	VLVLEMFSGGDAAALER	889.46	135.84	1.12E+05	2.70E+05	2.08E+05	3.82E+05	3.46E+04	1.75E+05	1.62E+05	1.89E+05	3.20E+05	2.91E+05	3.08E+05	5.68E+05	4.85E+04	5.12E+04	1.67E+05
P17174 AATC	IVASTLSNPPELFEWTGNVK	745.38	135.85	1.92E+05	1.36E+05	8.07E+04	1.66E+05	1.17E+05	2.89E+05	1.54E+05	1.65E+05	1.32E+05	4.67E+04	3.92E+05	2.88E+05	1.15E+05	2.20E+05	2.83E+05
Q9NPC6 MYOZ2	VPDFELLLLTDP	764.42	135.86	9.63E+04	3.50E+04	7.65E+04	9.77E+04	4.88E+04	1.28E+05	6.01E+04	4.51E+04	6.81E+04	4.45E+04	8.88E+04	1.81E+05	7.19E+04	2.27E+05	3.34E+04
P31930 QCR1	DVVFNYLHATAF	698.86	135.88	1.23E+05	2.34E+05	7.66E+04	8.60E+04	6.16E+04	1.27E+05	3.60E+04	3.25E+04	9.77E+04	4.92E+04	1.74E+05	1.04E+05	6.78E+04	6.32E+04	9.02E+04
P09622 DLDH	IPNIYAIGDVVAGPMLAHK	660.36	135.89	2.04E+05	1.87E+05	4.35E+04	1.15E+05	3.27E+04	1.65E+05	1.14E+05	1.42E+05	2.58E+05	3.58E+04	1.17E+05	4.02E+04	2.53E+04	9.65E+04	1.36E+05
P24752 THIL	TPIGSFLGSLLLPATK	851.49	135.94	1.85E+04	4.05E+04	1.05E+05	3.27E+04	1.74E+05	8.07E+04	2.59E+04	1.50E+05	1.25E+05	7.45E+04	2.33E+04	1.10E+05	7.61E+04	9.35E+04	1.11E+04
P40925 MDHC	ESAFEFLLSSA	544.25	135.94	2.47E+04	1.54E+05	3.39E+04	1.77E+05	8.08E+03	5.49E+04	1.48E+04	9.88E+03	1.97E+04	6.35E+04	2.98E+04	1.04E+04	3.55E+04	3.11E+04	7.06E+04
P40925 MDHC	DLDVAILVGSMPR	693.37	135.95	1.84E+05	1.19E+05	4.06E+04	1.48E+05	1.81E+05	1.73E+05	2.11E+05	2.30E+05	2.03E+05	4.15E+04	1.24E+05	1.04E+05	9.31E+04	2.62E+05	1.33E+05
P40939 ECHA	TIEYLEEVAITFAK	813.94	136	1.00E+05	9.53E+04	8.20E+04	9.25E+04	1.85E+05	1.08E+05	2.19E+05	2.24E+05	2.28E+05	2.39E+04	8.73E+04	1.64E+05	1.24E+05	1.16E+05	1.41E+05
P04792 HSPB1	LPEEWSQWLGGSSWPGYV	745.03	136.01	6.80E+05	3.74E+05	1.03E+04	6.63E+04	4.23E+04	9.18E+04	4.81E+04	3.22E+05	3.52E+04	4.53E+04	6.30E+05	3.59E+04	1.05E+04	3.30E+04	3.20E+04
P17174 AATC	FLFPFFDSAYQGFASGNLER	771.38	136.01	1.04E+05	1.12E+05	3.86E+04	3.89E+04	2.29E+04	1.36E+05	1.16E+05	1.17E+05	1.72E+04	1.47E+04	2.01E+05	1.58E+05	7.52E+04	2.15E+04	1.27E+05
P07195 LDHB	SLADELALVDVLEDK	815.43	136.03	3.00E+05	3.95E+05	2.47E+05	2.73E+05	3.18E+05	3.28E+05	2.52E+05	1.93E+05	3.28E+04	2.83E+05	3.02E+05	5.02E+04	2.52E+05	3.37E+05	3.32E+05
P40939 ECHA	DLNSDMDSILASLK	761.40	136.07	2.13E+04	1.69E+05	2.93E+04	7.78E+04	5.08E+04	1.92E+05	3.97E+05	2.13E+05	3.04E+04	2.64E+05	2.02E+05	7.65E+04	1.23E+05	6.34E+04	1.37E+05
P40939 ECHA	MVGVPAAALDMMMLTGR	781.40	136.08	2.26E+05	1.92E+05	5.31E+04	2.00E+05	3.39E+05	2.55E+05	3.18E+05	3.50E+05	2.40E+05	3.44E+05	2.14E+05	2.62E+05	1.36E+05	4.93E+04	2.15E+05
P40939 ECHA	ADMVIEAVFEDLSLK	840.43	136.25	4.66E+04	7.77E+04	1.70E+04	4.40E+04	7.46E+04	1.73E+05	3.33E+04	2.71E+04	8.85E+04	6.33E+04	1.09E+05	8.61E+03	1.26E+04	2.75E+04	1.80E+04
P19429 TNNI3	ISADAMMQALLGA	646.33	136.36	1.98E+04	3.24E+04	1.02E+04	2.46E+04	2.92E+04	1.16E+05	3.56E+04	5.69E+04	6.48E+04	1.30E+04	6.96E+04	6.24E+03	4.57E+03	8.55E+04	1.01E+05
P19429 TNNI3	ISADAMMQALLGAR	724.37	136.6	9.26E+03	7.54E+03	2.21E+04	4.70E+03	1.08E+04	9.22E+03	9.09E+03	9.71E+03	9.57E+02	4.90E+03	6.42E+04	2.62E+04	1.93E+04	1.72E+04	3.68E+04
Q562R1 ACTBL	DCYVGDQAQSKR	456.21	44.49	2.28E+02	2.27E+02	2.68E+02	2.08E+02	2.16E+02	1.75E+02	1.26E+02	2.46E+02	2.37E+02	5.12E+02	1.59E+02	1.62E+02	1.74E+02	1.84E+02	4.23E+02
P47985 UCRI	ESLSGQAVR	473.75	45.88	5.07E+03	5.33E+03	6.85E+02	7.72E+03	6.98E+03	1.15E+04	4.97E+03	2.55E+03	2.06E+02	2.19E+02	9.73E+03	2.38E+03	4.27E+02	4.18E+03	9.31E+03
Q9BX66-11 SRBS	VGEQDSAPTQEKPTSPGK	619.31	46.26	1.45E+04	8.57E+03	3.71E+03	2.00E+04	1.73E+04	4.42E+04	1.46E+03	1.22E+04	7.05E+02	1.35E+02	3.16E+04	6.34E+03	1.78E+02	3.41E+03	2.43E+04
P23327 SRCH	DEEDEDVSTER	726.78	49.24	1.59E+04	1.77E+04	6.62E+02	4.33E+04	2.87E+04	6.78E+04	1.33E+03	1.75E+03	3.85E+04	1.98E+02	1.07E+05	1.39E+04	4.69E+02	1.59E+02	5.80E+04
P10809 CH60	VGGTSDVEVNEK	617.30	49.37	1.32E+04	5.43E+03	1.10E+04	1.96E+04	4.61E+04	2.35E+03	5.94E+03	3.86E+03	3.98E+04	1.89E+02	2.79E+04	1.55E+04	4.50E+03	2.28E+04	2.59E+04
P23327 SRCH	SHEEDDNDDDVSTEYGH QAHR	643.50	50.92	1.54E+02	1.93E+02	2.28E+02	1.24E+03	5.83E+03	1.61E+04	2.67E+02	6.38E+02	5.69E+02	1.33E+02	3.40E+02	1.94E+02	1.73E+02	2.26E+02	1.10E+04
P36871 PGM1	LSGTGSAGATIR	545.79	51.04	3.77E+02	4.06E+02	6.98E+03	8.47E+02	7.20E+03	3.98E+03	2.22E+03	2.70E+03	5.61E+02	2.67E+02	3.07E+02	6.78E+02	4.99E+03	3.46E+02	2.40E+02
P20674 COX5A	SHGSQETDEEFDAR	536.56	51.73	1.40E+04	4.08E+03	5.71E+02	2.16E+03	4.05E+03	1.76E+04	2.65E+02	1.23E+03	1.95E+04	1.22E+03	1.08E+04	4.28E+02	2.08E+03	1.26E+03	1.06E+04
P02790 HEMO	VAEGETKPPDPVTER	548.27	52.12	6.71E+04	4.74E+04	1.65E+03	6.97E+04	1.92E+03	9.64E+04	4.17E+03	2.20E+03	4.07E+03	2.13E+02	1.01E+05	2.25E+04	2.33E+03	3.61E+03	4.12E+04
P01009 A1AT	FLENEDR	461.72	52.15	4.16E+03	2.79E+03	1.73E+03	2.71E+03	9.81E+03	1.41E+03	5.74E+02	6.82E+03	2.07E+03	2.50E+04	3.99E+03	1.50E+03	2.93E+03	3.77E+03	1.95E+03
P02462 CO4A1	HSQTIDDPQCPGSGTK	538.58	52.49	5.40E+02	1.09E+03	2.34E+03	1.90E+03	1.15E+03	8.01E+02	1.12E+03	4.66E+03	1.29E+03	3.91E+04	2.14E+03	2.35E+03	1.27E+03	1.02E+04	1.39E+03
P12829 MYL4	HVLATLGEK	484.28	53.27	4.41E+02	7.83E+02	8.07E+03	4.01E+04	3.85E+02	1.66E+02	1.22E+04	1.21E+04	2.69E+02	3.57E+02	5.73E+02	5.83E+02	2.62E+03	9.57E+02	1.29E+03
Q9H987 SYP2L	TPPPVAPKPPSR	415.24	53.29	2.89E+03	4.56E+04	3.69E+03	3.76E+04	4.72E+03	6.85E+03	1.64E+03	2.23E+02	1.10E+03	1.85E+02	7.85E+04	9.72E+04	2.14E+04	1.11E+05	6.20E+03
P36871 PGM1	TQAYQDQKPGTSGLR	550.61	53.36	1.79E+04	4.64E+03	1.88E+03	1.92E+04	3.67E+04	1.80E+03	2.06E+03	4.92E+03	1.45E+04						



P49821 NDUV1	HFRPELEER	404.88	54.43	1.75E+02	2.34E+02	1.34E+04	2.57E+04	1.31E+04	1.27E+02	1.16E+04	1.10E+04	3.40E+02	2.99E+02	6.24E+02	4.67E+03	1.82E+04	2.76E+02	1.48E+02
P38117-2 ETFB	TALAMGADR	453.23	54.82	4.76E+04	1.44E+04	4.08E+03	5.53E+04	6.46E+03	4.15E+03	2.68E+03	1.37E+04	8.81E+03	8.73E+03	3.76E+04	5.63E+04	3.99E+03	9.20E+03	6.24E+04
P23327 SRCH	SHEEDNDDDVSTEYGH	693.58	54.99	1.53E+04	7.95E+02	1.23E+03	2.46E+03	3.19E+02	7.07E+02	1.82E+02	3.08E+02	1.98E+02	5.81E+02	4.15E+03	5.02E+02	1.59E+02	2.01E+02	3.64E+03
P35579 MYH9	QLEEAEEEAQR	666.31	55.33	6.89E+02	2.07E+03	2.12E+05	7.03E+02	7.58E+02	1.70E+05	3.62E+04	7.42E+04	1.99E+03	1.32E+04	1.45E+03	3.37E+03	1.60E+05	2.20E+03	7.79E+02
P13073 COX41	DHPLPEVAH	507.75	56.28	3.17E+04	4.66E+04	6.67E+03	4.41E+04	1.93E+03	9.69E+03	4.46E+03	8.27E+03	2.32E+04	2.40E+03	4.25E+03	1.49E+04	1.76E+03	1.82E+04	3.02E+04
P02790 HEMO	GNVAEGETKPPDPVTER	605.29	56.51	8.18E+04	2.09E+04	5.79E+03	6.29E+04	1.25E+04	5.22E+03	4.61E+03	1.39E+03	6.19E+02	1.63E+03	6.60E+04	1.48E+04	7.03E+03	1.73E+03	1.25E+02
P55290 CAD13	INENTGSVSVTR	638.83	56.56	5.13E+04	5.46E+04	3.64E+03	1.11E+05	1.59E+04	4.62E+03	4.36E+03	7.34E+03	3.71E+02	1.03E+03	1.31E+05	6.43E+04	5.31E+03	1.97E+03	1.61E+03
P31040 DHSA	NTVVATGGYGR	547.78	56.59	1.04E+03	5.58E+03	2.57E+03	5.28E+03	1.26E+04	8.32E+02	8.52E+03	1.27E+02	5.19E+04	3.19E+04	2.66E+03	4.19E+03	1.65E+03	1.96E+03	4.25E+03
P00568 KAD1	EVQQGEFEER	625.79	56.68	8.03E+02	3.46E+02	4.18E+05	2.23E+02	1.89E+05	7.22E+05	6.36E+05	8.17E+05	2.51E+02	1.06E+03	5.25E+02	1.14E+05	1.24E+06	5.46E+02	7.70E+02
P21980 TGM2	LAEKEETGMAMR	455.89	56.69	1.25E+03	2.46E+03	7.32E+03	4.91E+03	1.99E+03	6.11E+03	4.18E+04	8.05E+03	6.65E+04	5.50E+04	6.10E+03	4.46E+03	2.58E+04	3.62E+04	1.08E+04
P49411 EFTU	KYEEIDNAPEER	498.24	57.08	2.70E+03	8.41E+03	3.34E+03	9.05E+02	2.02E+02	2.86E+03	2.83E+02	2.76E+02	1.29E+03	2.00E+04	1.35E+02	2.94E+03	2.00E+02	3.30E+02	8.81E+03
O15061-2 SYNEM	TQEAGALGVSDR	602.31	57.29	4.33E+02	3.48E+03	4.23E+04	5.11E+02	7.74E+02	6.22E+04	8.13E+04	1.14E+05	2.37E+04	1.60E+04	4.39E+02	2.67E+04	9.10E+04	3.44E+03	1.97E+03
P07108 ACBP	QATVGDINTER	602.30	57.49	4.99E+02	4.45E+04	1.82E+03	6.55E+04	1.46E+05	8.95E+04	1.32E+05	3.23E+02	5.48E+02	2.87E+04	1.45E+05	4.22E+04	8.78E+02	1.98E+03	7.24E+02
P13804 ETFA	GTSFDAAATSGGSASSEK	815.86	57.71	4.49E+04	3.37E+04	1.90E+03	7.62E+04	5.68E+04	8.73E+03	6.50E+03	1.01E+04	6.48E+02	1.58E+02	4.25E+04	3.45E+04	2.51E+03	1.01E+03	7.48E+02
Q86TD4 SRCA	EETEDANEAPLR	751.84	58.44	2.52E+04	3.66E+03	1.40E+04	2.84E+04	2.94E+04	6.94E+04	4.89E+04	5.46E+04	6.50E+02	2.68E+03	1.57E+04	4.25E+02	2.24E+03	2.17E+03	1.10E+04
P13073 COX41	DHPLPEVAHVK	414.56	58.51	1.20E+05	7.08E+04	5.37E+03	1.44E+05	4.30E+05	1.09E+05	3.23E+05	4.97E+03	4.71E+05	7.04E+02	1.10E+05	9.32E+04	7.48E+02	6.78E+04	1.55E+05
P31040 DHSA	TSTGDGTAMITR	605.79	58.86	7.74E+03	4.13E+03	3.90E+02	2.56E+02	5.12E+02	3.44E+02	3.91E+03	1.16E+03	2.44E+04	2.53E+04	1.80E+04	6.51E+03	1.55E+02	7.19E+03	1.54E+04
P55809 SCOT1	QHEADADLINAGK	461.23	58.89	5.15E+02	3.74E+02	1.15E+03	2.88E+02	1.54E+04	5.88E+02	2.57E+03	3.61E+02	7.91E+02	2.24E+02	5.73E+02	4.88E+02	2.23E+03	5.29E+02	6.95E+02
P14543-2 NID1	EHILGAAGATDPQR	479.25	59.31	4.47E+02	6.74E+02	2.87E+03	3.92E+02	1.79E+03	3.02E+02	2.99E+02	5.41E+04	1.30E+03	4.91E+02	1.25E+04	2.38E+03	2.73E+02	6.26E+02	1.67E+04
P30086 PEBP1	LYEQLSGK	469.25	59.43	2.20E+02	7.96E+03	1.04E+03	2.25E+04	1.10E+04	7.41E+03	1.95E+03	2.83E+02	1.40E+04	5.02E+03	1.95E+04	3.62E+03	5.82E+02	4.35E+02	1.92E+04
P19022 CADH2	IVSQAPSTSPN	599.31	59.54	1.69E+05	1.29E+05	1.87E+03	2.23E+05	3.22E+04	6.63E+04	5.06E+02	1.31E+03	1.63E+03	1.99E+03	8.17E+04	1.16E+05	8.99E+04	4.50E+03	1.34E+05
P08133 ANXA6	SEISGDLAR	474.25	59.74	5.59E+02	5.97E+02	7.63E+02	8.97E+02	9.01E+02	1.19E+03	1.06E+03	4.88E+03	2.46E+03	1.36E+04	4.85E+02	1.70E+03	4.80E+03	2.99E+02	1.44E+03
P07237 PDIA1	YKPESEELTAER	484.57	59.74	2.23E+02	3.27E+04	6.37E+02	5.21E+04	1.22E+03	1.07E+03	6.22E+02	4.56E+02	5.42E+02	2.41E+02	8.37E+04	3.71E+04	1.32E+02	3.98E+02	5.32E+04
P38646 GRP75	QAASSLQQASLK	616.34	59.84	7.91E+02	8.14E+02	3.35E+03	8.00E+02	1.54E+03	2.41E+03	7.71E+02	3.47E+02	3.36E+04	1.73E+04	5.80E+02	4.60E+02	1.87E+02	2.04E+02	1.34E+02
P63316 TNNC1	AAVEQLTTEEQKN	680.34	59.84	1.69E+03	8.36E+02	9.28E+02	3.16E+02	8.24E+02	6.48E+02	6.03E+02	1.35E+03	1.48E+04	2.72E+03	9.80E+03	1.75E+03	2.42E+02	6.18E+03	1.37E+04
P14543-2 NID1	EYTVTEPER	562.27	59.87	3.39E+02	2.81E+04	2.04E+03	3.67E+04	1.10E+03	5.41E+03	1.03E+03	3.22E+02	2.70E+03	1.82E+02	5.05E+04	1.62E+04	4.15E+02	4.40E+02	4.08E+04
P02675 FIBB	QFGFNVATNTDGK	654.81	59.88	2.49E+02	3.55E+02	3.25E+03	2.98E+02	3.09E+04	2.80E+02	1.00E+04	3.68E+02	2.89E+03	7.90E+03	3.46E+03	5.16E+02	1.34E+03	3.58E+02	3.80E+02
Q9BX66-11 SRBS	LSDLNTPESR	630.81	60.08	6.85E+03	1.39E+04	4.61E+02	3.78E+04	6.21E+03	1.90E+03	1.83E+03	4.69E+02	4.93E+03	8.74E+02	2.92E+04	1.77E+04	4.20E+02	2.01E+03	1.04E+04
P12109 CO6A1	VAVVQYSGTGQQRPER	592.31	60.08	2.63E+05	7.49E+04	1.86E+05	3.22E+05	3.83E+05	3.33E+05	1.24E+05	2.91E+02	3.87E+02	2.54E+02	2.52E+05	1.09E+05	1.70E+03	6.93E+04	3.56E+05
P09972 ALDOC	LSQIGVENTEENRR	548.95	60.11	2.51E+02	6.11E+02	7.99E+04	4.10E+02	2.74E+04	2.78E+03	4.76E+03	6.35E+03	5.84E+04	1.04E+05	4.35E+02	1.76E+02	1.48E+04	8.36E+02	1.52E+03
P00403 COX2	LLDVDNR	422.73	60.36	1.43E+05	8.85E+04	5.40E+02	1.34E+05	5.18E+03	1.30E+05	5.76E+03	2.33E+03	1.60E+05	1.37E+05	8.67E+04	6.00E+03	4.35E+03	4.96E+04	1.41E+05
Q6NZI2 PTRF	EGVELGEGERPEED	787.83	60.4	4.46E+02	1.77E+02	1.46E+04	3.59E+02	2.07E+02	1.01E+03	5.18E+03	1.15E+03	8.33E+02	1.36E+03	1.55E+02	3.35E+02	8.70E+03	7.76E+02	4.62E+02
P01023 A2MG	LHVHVEPHTETVR	515.94	60.7	5.92E+02	1.25E+03	1.70E+03	9.12E+02	5.53E+02	8.33E+02	6.70E+02	9.23E+02	5.66E+02	8.10E+04	2.11E+02	9.53E+02	2.38E+02	1.97E+04	5.48E+02
Q9H987 SYP2L	LADEGPVQSPSPH	667.32	60.7	6.46E+03	4.08E+03	1.16E+04	2.49E+03	1.31E+02	4.58E+02	2.54E+02	3.59E+02	1.86E+04	3.06E+02	6.65E+03	7.66E+03	3.37E+02	6.16E+04	4.54E+03
P12829 MYL4	KEAAKPAPAPAPAPAPAP APEAPK	604.09	60.85	1.47E+03	5.88E+02	2.37E+02	3.12E+04	9.94E+02	2.47E+02	1.44E+02	5.84E+02	6.15E+02	8.00E+02	3.11E+03	1.11E+03	2.39E+02	1.51E+02	2.61E+02
P63316 TNNC1	AAVEQLTTEEQK	623.32	61.24	6.20E+05	4.24E+03	5.89E+02	1.23E+04	2.73E+04	2.57E+04	3.05E+04	1.32E+04	1.14E+06	1.49E+06	4.29E+04	1.24E+03	1.80E+03	3.70E+05	2.42E+04
P42765 THIM	ITAHLVHELK	594.84	61.29	1.91E+02	2.62E+02	1.69E+03	3.91E+02	1.24E+04	4.88E+02	3.11E+02	1.83E+04	2.47E+02	1.05E+03	1.96E+02	3.35E+02	6.73E+03	4.61E+02	4.30E+02
Q9BX66-11 SRBS	ITAGVIPTHHQFITNER	472.25	61.65	1.78E+05	1.34E+03	3.55E+03	1.84E+05	3.16E+04	2.14E+05	7.64E+03	2.07E+03	3.33E+02	4.05E+02	7.83E+02	2.55E+04	2.56E+03	1.10E+03	4.08E+02
Q702N8 XIRP1	EQHLQVSVQVAGER	526.61	61.67	9.36E+04	3.81E+03	4.91E+02	2.37E+04	2.10E+02	2.88E+02	6.01E+03	8.79E+03	8.09E+02	4.78E+02	4.78E+04	3.95E+02	2.40E+03	1.00E+03	1.93E+04
P07355-2 ANXA2	TNQLQEINR	622.81	61.72	3.57E+03	1.90E+02	3.61E+02	1.02E+04	5.00E+04	1.81E+02	1.30E+03	8.88E+02	1.92E+04	9.37E+03	3.17E+04	6.42E+02	1.63E+03	1.24E+03	6.28E+03
P49411 EFTU	YEEIDNAPEER	682.80	61.99	9.04E+04	2.88E+04	4.21E+02	4.06E+04	5.57E+04	2.04E+03	8.13E+02	7.24E+02	6.05E+02	3.75E+02	6.43E+04	2.81E+04	1.45E+02	4.23E+02	3.92E+02
P07237 PDIA1	TVIDYNGER	533.76	62.03	2.77E+02	1.44E+02	3.13E+02	6.95E+02	5.03E+03	1.85E+04	1.76E+02	3.76E+02	5.49E+03	3.04E+02	6.82E+02	1.50E+02	1.19E+04	2.66E+03	3.24E+02
P00367 DHE3	IIAEGANGPTTPEADK	792.40	62.03	1.02E+05	1.02E+05	4.08E+04	9.45E+04	1.88E+04	2.32E+03	7.75E+02	2.41E+02	9.01E+02	1.51E+02	8.11E+04	4.85E+04	4.81E+02	1.12E+03	1.85E+02
Q9H987 SYP2L	LRPEAPAPGGAPEPPSAR	608.98	62.21	3.35E+04	1.04E+04	4.86E+03	3.12E+04	9.14E+02	7.88E+02	3.97E+02	1.17E+03	2.74E+03	2.51E+02	1.13E+04	1.85E+03	3.21E+02	1.64E+03	6.94E+02
P02462 CO4A1	AHQDLGTAGSCLR	462.56	62.28	6.96E+04	3.67E+04	7.28E+03	9.16E+04	1.47E+05	1.92E+04	2.49E+03	8.98E+03	1.17E+05	5.18E+02	2.12E+05	5.75E+04	3.59E+03	6.96E+02	1.40E+05
P13073 COX41	ESFAEMNR	492.22	62.39	1.17E+03	3.13E+02	9.23E+03	4.99E+03	3.20E+03	1.02E+04	2.17E+03	1.22E+03	2.27E+03	3.75E+04	2.20E+03	2.99E+02	1.71E+03	8.58E+02	1.16E+03
P01023 A2MG	YGAAATFTR	443.73	62.41	2.69E+02	1.46E+03	2.66E+03	1.10E+03	1.72E+04	5.98E+02	3.26E+04	3.15E+03	1.52E+04	3.10E+04	6.90E+02	1.28E+03	3.01E+03	1.26E+03	6.44E+02
Q9Y4G6 TLN2	SLSVDPGAPNAK	578.30	62.46	3.38E+02	7.99E+03	5.30E+02	7.77E+02	7.13E+03	3.66E+04	2.33E+04	2.77E+02	1.66E+03	4.18E+04	3.03E+02	1.58E+04	4.92E+02	2.84E+04	1.33E+04
P31937 3HIDH	MDAPVSGGVGAAR	594.30	62.5	1.12E+04	2.76E+03	1.27E+04	3.86E+02	3.83E+02	5.11E+02	4.50E+04	1.76E+03	5.78E+03	8.40E+02	3.13E+02	3.17E+03	7.28E+02	8.04E+02	9.84E+02
P38117-2 ETFB	VETTEDLVAK	552.79	62.67	7.23E+04	7.87E+04	1.55E+02	1.26E+05	2.81E+04	3.08E+03	3.13E+03	1.32E+03	4.76E+05	1.72E+03	2.21E+05	1.59E+05	1.56E+03	2.30E+05	1.79E+05
P14543-2																		

P21980 TGM2	TVEGAGLTEEQK	629.32	63.64	3.59E+04	1.99E+03	5.02E+03	7.26E+02	6.79E+03	3.50E+02	1.46E+03	2.99E+03	2.34E+03	5.11E+02	1.07E+05	1.30E+03	7.24E+03	4.60E+02	6.63E+04
P05091 ALDH2	TIEEVVGR	451.75	63.7	2.27E+02	2.25E+02	1.14E+04	1.23E+04	6.46E+04	4.21E+03	2.22E+04	6.79E+04	1.07E+04	9.11E+02	6.51E+02	3.02E+02	1.06E+05	2.11E+02	1.10E+03
P36871 PGM1	QEATLVVGGDGR	601.32	63.73	3.96E+04	2.49E+04	1.73E+03	3.01E+03	1.05E+05	3.30E+03	6.85E+03	9.03E+02	3.08E+02	2.66E+03	8.56E+04	7.04E+03	5.44E+02	2.56E+02	7.10E+04
P00403 COX2	LNQTTFTATR	576.80	63.77	4.71E+02	1.23E+03	2.83E+04	5.97E+04	7.39E+04	7.92E+04	6.48E+03	3.44E+02	1.95E+02	4.80E+02	6.41E+04	2.36E+04	2.32E+03	1.72E+03	9.52E+02
P42126 D3D2	DTLENTIGHR	578.29	63.79	4.27E+02	6.43E+03	5.22E+03	3.14E+04	1.30E+05	1.78E+04	8.80E+04	6.78E+02	5.49E+02	1.18E+03	4.50E+04	1.71E+03	3.86E+04	2.62E+02	2.80E+03
Q9Y4G6 TLN2	LLVSGAASPDK	579.82	63.81	5.17E+02	3.41E+03	2.91E+02	2.11E+03	7.99E+02	3.56E+02	6.30E+02	5.77E+02	1.83E+04	3.13E+04	1.44E+03	2.82E+03	5.75E+02	1.86E+04	2.73E+02
O15061-2 SYNEMEEYGIQAEER		612.29	64.2	2.42E+03	2.55E+04	9.70E+03	2.50E+04	8.69E+03	2.65E+04	5.21E+02	2.24E+04	2.28E+03	6.08E+04	2.96E+04	1.29E+03	1.36E+03	6.20E+03	2.14E+04
P26038 MOES	TANDMIHAENMR	468.21	64.3	2.64E+04	1.53E+04	3.58E+02	3.93E+04	1.80E+03	2.26E+04	3.21E+02	3.04E+03	8.45E+03	5.08E+02	4.81E+04	1.53E+04	3.43E+03	2.11E+02	3.31E+04
O95831 AIFM1	AALSASEGEEVPODK	765.87	64.38	1.08E+05	4.76E+04	2.13E+03	8.81E+04	1.02E+04	3.12E+03	2.79E+03	1.98E+03	4.61E+03	6.26E+03	5.70E+04	3.99E+04	1.59E+03	5.05E+02	2.66E+03
P26038 MOES	ISQLEMAR	474.25	64.38	1.94E+05	2.03E+02	1.03E+05	3.03E+05	4.82E+04	2.35E+05	7.21E+04	2.64E+03	3.39E+03	1.36E+02	9.67E+02	1.48E+04	8.07E+04	1.08E+03	5.92E+02
P07355-2 ANXA2	TPAQYDASELK	611.80	64.44	5.55E+03	2.68E+03	6.13E+04	4.86E+02	8.26E+04	7.80E+04	2.60E+04	3.72E+04	9.03E+03	6.95E+03	4.17E+03	1.24E+03	1.29E+04	1.33E+04	4.42E+04
P47985 UCRI	LEVLDSTK	452.75	64.57	3.69E+04	4.93E+04	5.27E+03	3.49E+03	2.31E+03	6.72E+03	1.45E+04	4.92E+03	5.10E+04	6.83E+03	4.84E+04	2.06E+04	7.44E+03	2.97E+04	5.27E+04
Q16891-2 IMMT	SEFEQNLSEK	605.78	64.59	4.55E+03	1.87E+04	2.63E+03	3.28E+03	6.17E+03	1.07E+04	8.57E+03	7.87E+02	1.39E+05	1.56E+05	1.83E+05	4.30E+02	2.22E+02	1.35E+03	8.61E+04
P42765 THIM	ARPQTTLEQLQK	471.60	64.66	3.62E+02	1.94E+04	5.13E+02	8.73E+04	4.31E+04	1.14E+04	1.41E+02	7.27E+03	3.73E+02	2.22E+02	8.96E+04	3.06E+03	2.44E+03	6.05E+02	5.30E+04
P02675 FIBB	AHYGGFTVQNEANK	512.58	64.82	1.41E+02	4.20E+02	3.45E+02	2.01E+04	6.81E+04	4.30E+04	5.42E+03	7.80E+02	8.96E+03	1.67E+04	5.09E+02	7.53E+03	8.27E+02	1.39E+04	5.55E+02
P07355-2 ANXA2	AYTNFDAER	543.74	65.05	1.73E+02	2.35E+04	1.04E+03	7.28E+04	5.58E+04	3.76E+03	1.02E+03	4.61E+02	4.92E+02	1.92E+02	8.27E+04	2.12E+04	2.78E+03	5.22E+02	9.63E+04
P09972 ALDOC	LSQIGVENTEENR	744.87	65.13	1.27E+05	4.87E+04	4.34E+02	1.34E+05	4.85E+03	5.44E+03	2.05E+03	3.06E+03	6.95E+02	3.24E+03	1.08E+05	1.73E+04	9.02E+02	1.37E+03	5.63E+03
P23327 SRCH	EEDEEVS AELGHQAPSHR	673.97	65.21	2.63E+04	2.04E+04	3.66E+02	2.11E+04	1.56E+03	4.35E+02	2.07E+02	1.65E+03	1.96E+03	8.63E+02	7.16E+04	4.29E+04	4.65E+02	1.55E+03	3.45E+04
P08133 ANXA6	DAISGIGTDEK	553.28	65.23	1.51E+04	1.52E+04	1.80E+03	1.20E+04	1.46E+04	2.85E+03	1.65E+04	2.23E+04	1.33E+05	8.32E+04	9.70E+03	2.63E+03	2.64E+04	4.54E+04	4.67E+04
P26038 MOES	AQMVQEDLEK	595.79	65.26	6.16E+02	1.64E+02	4.36E+03	9.62E+03	5.67E+03	1.90E+03	1.31E+03	1.77E+03	1.95E+04	5.16E+04	7.28E+02	1.85E+02	4.92E+02	7.06E+02	9.91E+02
Q01813 K6PP	LPDDQIPK	463.25	65.26	3.72E+02	1.28E+04	8.47E+02	2.19E+03	6.17E+03	6.35E+03	1.26E+04	1.84E+04	1.45E+03	1.80E+04	7.70E+02	7.59E+03	1.08E+03	6.67E+02	1.71E+04
Q16891-2 IMMT	GVYSEETLR	527.26	65.26	8.54E+02	7.21E+04	4.00E+03	9.84E+04	1.92E+05	4.24E+02	1.15E+04	5.33E+03	6.11E+02	1.67E+03	1.90E+05	1.11E+05	1.57E+03	1.97E+02	9.83E+04
Q9H987 SYP2L	PEAPAPGGAPEPPSAR	533.27	65.31	3.35E+04	5.87E+03	7.61E+02	3.81E+04	4.99E+03	1.88E+03	7.47E+02	1.27E+03	1.24E+04	8.77E+04	2.55E+04	9.29E+03	3.19E+03	2.58E+04	6.13E+03
Q14894 CRYM	FADTVQGEVR	561.28	65.94	1.04E+05	2.01E+04	4.25E+03	1.83E+05	2.62E+04	8.19E+03	6.10E+02	3.20E+03	3.55E+03	5.57E+04	1.40E+05	1.39E+05	1.89E+03	6.72E+05	1.80E+05
P12829 MYL4	EAAKPAPAPAPAPAPAPA PEAPK	762.42	65.96	6.14E+04	1.48E+04	3.09E+03	2.96E+05	3.07E+03	2.03E+03	6.16E+02	3.02E+02	3.27E+02	2.95E+02	1.38E+05	1.23E+04	1.87E+03	2.09E+02	1.91E+02
P05091 ALDH2	VIQVAAGSSNLK	593.84	65.99	7.38E+02	4.65E+03	7.79E+03	1.79E+03	1.60E+04	1.13E+03	3.52E+03	1.02E+04	4.20E+03	2.98E+03	1.30E+05	7.70E+04	9.75E+03	6.42E+02	3.12E+04
Q702N8 XIRP1	VEIPSGQVSR	536.29	66	4.66E+02	1.61E+05	4.00E+02	5.29E+04	6.51E+03	3.39E+04	2.47E+04	1.19E+04	3.59E+03	1.97E+04	5.57E+05	2.97E+05	5.79E+03	1.13E+04	2.97E+05
P31937 3HIDH	DLGLAQDSATSTK	653.83	66.11	1.13E+05	6.39E+04	9.61E+04	6.99E+04	9.90E+04	3.43E+05	2.66E+04	4.19E+04	2.13E+02	1.76E+03	6.97E+04	2.77E+04	1.07E+04	4.18E+03	9.46E+04
Q9Y4G6 TLN2	QALIAPGDAER	570.80	66.23	4.50E+03	2.41E+03	3.50E+02	6.12E+02	1.61E+02	8.06E+02	1.03E+04	1.09E+03	3.98E+04	5.18E+04	8.20E+02	1.04E+03	6.60E+02	3.69E+04	1.01E+04
P14543-2 NID1	ASLHGGEPTTIR	451.25	66.39	5.73E+02	1.41E+05	1.46E+04	1.65E+04	5.66E+02	5.20E+03	1.38E+03	1.06E+03	1.37E+03	6.44E+02	2.08E+05	1.00E+05	5.57E+03	8.64E+02	1.86E+05
P14543-2 NID1	EDLSPSITQR	573.30	66.59	7.61E+02	8.06E+03	1.97E+04	2.06E+04	4.62E+02	4.88E+04	1.03E+04	6.32E+02	9.44E+02	3.26E+02	6.35E+04	4.60E+03	2.20E+04	6.68E+02	3.15E+03
P02675 FIBB	PAPPPISGGYR	584.81	66.59	8.01E+04	2.07E+03	4.24E+03	2.26E+04	5.05E+03	3.74E+03	1.45E+03	1.14E+04	3.02E+02	5.84E+03	3.02E+04	3.15E+03	6.65E+02	7.68E+02	5.37E+03
Q99497 PARK7	VEKDGLILTSR	410.91	67.27	7.17E+03	1.50E+04	5.66E+03	8.39E+03	4.26E+03	2.34E+03	4.02E+03	1.85E+03	9.69E+04	8.19E+04	1.55E+04	7.74E+03	8.05E+03	1.09E+05	4.33E+03
P35579 MYH9	KEEELQAALAR	419.90	67.37	3.91E+03	4.76E+02	1.20E+04	1.04E+03	2.83E+04	3.25E+04	1.03E+04	2.01E+03	6.00E+02	6.31E+02	1.93E+03	2.43E+03	2.10E+03	7.39E+02	1.16E+03
P00367 DHE3	TAAAYVNAIEK	540.29	67.42	1.07E+04	1.14E+04	4.57E+03	3.76E+03	3.99E+02	5.64E+03	3.45E+04	3.28E+04	9.38E+02	2.38E+03	6.33E+03	1.08E+04	4.60E+04	1.18E+03	8.71E+02
P00738 HPT	TEGDGVYTLNNEK	720.34	67.48	7.46E+04	9.87E+03	1.98E+03	1.44E+04	4.44E+03	1.69E+04	2.32E+03	5.08E+02	4.94E+02	5.65E+04	4.75E+04	7.32E+03	1.15E+03	1.89E+04	3.76E+03
P13533 MYH6	TLEDQANEYR	619.79	67.53	7.07E+04	3.33E+04	6.75E+03	2.00E+04	1.20E+04	1.47E+04	8.64E+03	2.08E+03	5.84E+02	2.53E+03	1.11E+04	8.30E+03	1.01E+04	2.17E+03	1.25E+05
P32119 PRDX2	ATAVVDGAFK	489.77	67.53	1.46E+03	2.15E+04	5.69E+03	4.41E+03	3.32E+03	6.18E+03	4.43E+03	2.02E+03	2.44E+03	6.89E+03	5.85E+04	4.81E+03	7.35E+03	1.54E+03	5.99E+04
P00738 HPT	TEGDGVYTLNDK	656.31	67.64	5.04E+04	4.20E+04	4.23E+04	4.23E+04	6.50E+04	9.59E+04	4.49E+04	1.57E+04	6.79E+02	1.66E+03	3.07E+04	9.04E+03	2.99E+04	1.74E+03	1.16E+04
P10412 H14	PAAPAAPAP	769.40	67.71	1.01E+05	9.54E+04	1.16E+05	2.20E+03	7.82E+02	1.91E+05	7.57E+04	5.25E+04	1.01E+03	2.28E+02	3.40E+03	7.16E+03	5.28E+04	4.85E+02	2.99E+03
P01876 IGHA1	TPLTATLSK	466.28	67.84	1.30E+03	9.23E+03	9.24E+03	9.52E+03	8.06E+04	1.15E+04	9.52E+03	2.42E+03	1.43E+03	1.20E+02	3.50E+04	2.08E+04	8.90E+03	1.75E+03	2.88E+04
P31040 DHSA	HTLSYVDVGTGK	638.83	67.86	5.43E+03	1.03E+05	1.36E+03	6.24E+03	1.99E+04	4.96E+03	3.02E+02	3.47E+02	2.17E+04	5.17E+03	9.59E+04	9.34E+04	5.81E+02	1.67E+04	9.17E+04
P21980 TGM2	NEFGEIQGDK	568.76	67.89	8.39E+03	8.34E+03	4.69E+02	7.15E+03	6.45E+03	5.01E+02	3.80E+02	1.31E+03	2.16E+03	8.36E+03	6.50E+04	1.92E+03	7.04E+03	2.46E+04	3.05E+04
P13533 MYH6	SLNDFTTQR	541.27	67.92	1.09E+04	5.73E+02	9.00E+02	2.66E+04	6.05E+02	8.46E+04	2.45E+05	5.89E+03	1.62E+03	9.44E+02	2.25E+03	3.00E+03	9.01E+03	6.96E+02	4.65E+02
P02679 FIBG	VAQLEAQCQEPCK	723.84	68.06	4.27E+04	3.15E+03	3.32E+03	7.37E+03	1.14E+04	2.55E+03	2.08E+03	1.34E+03	1.73E+03	6.32E+02	2.30E+04	3.78E+03	6.09E+02	6.17E+02	5.52E+03
P10412 H14	ALAAAGYDVEK	554.29	68.08	6.03E+05	3.50E+05	8.00E+03	1.03E+06	6.29E+05	5.23E+04	1.67E+04	3.60E+03	9.99E+02	5.04E+02	7.74E+05	2.54E+05	4.15E+03	1.76E+03	8.43E+05
Q05639 EF1A2	VETGILRPG	471.27	68.12	7.37E+03	3.78E+02	2.34E+04	8.27E+03	1.29E+02	3.50E+04	1.90E+03	1.07E+05	5.66E+04	4.82E+04	8.45E+03	5.96E+02	1.11E+03	3.21E+04	8.82E+03
O15061-2 SYNEMSGEFHAEPTVIEK		481.91	68.45	5.41E+03	5.35E+03	3.02E+03	2.00E+03	6.49E+04	2.15E+02	2.42E+02	2.52E+03	3.24E+02	7.13E+03	5.76E+04	8.67E+04	1.56E+04	6.86E+04	1.87E+03
P49753 ACOT2	AHAMAQVDAWK	614.30	68.62	2.86E+03	2.26E+03	1.19E+03	3.12E+02	1.37E+03	3.30E+03	1.74E+03	3.00E+03	8.99E+02	3.36E+04	2.17E+03	4.20E+02	1.88E+03	1.06E+05	2.12E+04
P62258 1433E	YLAEFATGNDRK	462.23	68.95	6.73E+02	2.13E+03	1.75E+03	4.79E+03	6.86E+04	1.35E+04	2.56E+04	1.68E+03	2.17E+04	7.17E+03	9.81E+02	3.28E+04	5.05E+03	1.81E+04	5.77E+03
P42765 THIM																		

P67936 TPM4	IQALQQADEAEDR	807.89	69.89	3.08E+04	4.80E+03	4.97E+03	5.18E+03	2.72E+03	2.13E+02	4.06E+03	1.87E+03	1.38E+03	8.71E+02	1.93E+04	4.12E+02	4.94E+02	1.88E+02	1.81E+04
Q16698 DECR	LDPTGTFEK	504.26	69.98	1.37E+06	1.26E+06	5.92E+03	1.50E+06	1.34E+06	7.86E+04	2.81E+03	6.93E+03	1.35E+03	2.20E+03	9.44E+05	1.34E+06	6.87E+04	1.32E+03	1.36E+06
P02675 FIBB	YGGFTVQNEANK	664.32	70.06	8.34E+04	3.84E+03	1.29E+03	3.06E+03	9.84E+02	3.74E+03	2.54E+03	1.01E+03	3.07E+04	3.91E+04	1.41E+04	7.78E+02	1.13E+03	2.62E+04	1.58E+04
P55809 SCOT1	STGCDFAVSPK	556.26	70.3	4.56E+04	5.60E+04	1.81E+03	2.47E+04	1.56E+05	1.34E+04	6.66E+04	3.23E+03	1.11E+03	3.62E+03	1.69E+04	4.88E+04	9.08E+04	3.65E+02	6.55E+04
P26038 MOES	ALTSELANAR	523.29	70.32	1.01E+04	8.90E+04	5.55E+03	1.60E+05	1.49E+05	1.75E+05	3.10E+03	1.76E+03	4.71E+03	8.00E+03	2.78E+04	6.19E+04	9.53E+04	2.69E+04	6.13E+03
P32119 PRDX2	RLSEYGVVLK	590.32	70.33	3.17E+04	4.57E+04	2.61E+03	2.20E+04	8.81E+04	2.77E+04	7.62E+04	1.84E+03	1.32E+04	8.97E+03	2.38E+04	8.76E+04	4.22E+04	1.63E+04	2.12E+04
P02462 CO4A1	GQDLGTAGSCLR	589.30	70.37	1.25E+04	1.12E+04	3.86E+04	9.12E+03	1.15E+04	3.89E+03	7.63E+03	1.61E+04	1.52E+03	7.72E+03	8.99E+03	1.48E+04	1.07E+04	6.88E+03	4.06E+03
P31040 DHSA	IDEYDYKPIQGGQK	604.63	70.37	1.42E+05	1.31E+03	1.06E+03	4.95E+03	6.65E+03	7.78E+03	5.39E+03	1.91E+03	9.05E+03	1.59E+03	5.52E+04	8.56E+03	2.40E+02	2.06E+03	3.63E+04
P62258 I433E	EAAENSLVAYK	597.80	70.44	2.38E+05	2.06E+05	4.45E+03	8.43E+03	1.77E+04	3.82E+03	3.60E+03	7.92E+03	1.43E+03	6.83E+03	3.78E+05	8.95E+03	1.97E+04	1.99E+03	1.22E+05
P20674 COX5A	LNDFASTVR	511.77	70.5	7.51E+03	3.29E+05	8.10E+04	7.03E+05	3.99E+05	1.32E+04	1.65E+05	1.52E+05	6.33E+02	6.34E+02	6.59E+05	4.02E+05	3.53E+05	7.46E+02	5.00E+05
Q702N8 XIRP1	KEELVSGELPR	419.57	70.6	1.52E+04	1.36E+04	1.81E+03	2.98E+04	7.79E+03	1.25E+04	1.92E+03	8.09E+03	6.73E+03	1.99E+03	3.10E+03	6.36E+04	7.10E+03	4.60E+03	3.21E+03
P01023 A2MG	LPPNVVEESAR	605.82	70.61	4.03E+04	1.04E+04	3.62E+03	3.32E+04	4.55E+04	3.99E+03	1.01E+04	4.11E+03	8.62E+03	1.47E+03	1.35E+04	2.57E+04	1.18E+04	2.44E+04	2.39E+04
P05091 ALDH2	TEQGPQVDETQFK	753.86	70.69	4.57E+04	3.10E+03	1.39E+03	3.35E+04	1.05E+05	4.79E+02	3.51E+02	4.89E+02	1.81E+03	1.44E+03	7.16E+04	3.99E+02	9.94E+02	1.81E+03	4.30E+04
P08133 ANXA6	STPEYFAER	550.26	70.89	8.69E+02	3.04E+04	1.97E+04	2.16E+04	7.18E+04	5.35E+04	3.90E+04	3.83E+03	1.61E+03	5.14E+02	7.45E+02	6.03E+04	8.01E+04	6.47E+02	2.12E+03
P23327 SRCH	EEDEEVSAELGH	672.29	70.93	3.19E+05	1.98E+05	2.44E+03	2.94E+05	3.46E+03	3.81E+02	2.75E+03	3.61E+02	1.27E+05	2.63E+04	1.90E+05	1.10E+04	6.82E+03	3.22E+04	1.71E+05
P62258 I433E	YDEMVESMK	566.24	71.04	2.19E+03	1.50E+05	8.41E+03	1.37E+05	9.68E+04	1.57E+05	1.13E+05	8.44E+02	3.11E+02	5.40E+03	1.48E+04	2.05E+05	1.66E+05	2.36E+03	4.26E+03
P12829 MYL4	PAPAPAPAPAPAPEAP K	629.34	71.04	1.33E+05	3.66E+04	5.53E+03	5.82E+05	2.59E+03	1.13E+04	3.45E+02	1.11E+04	5.27E+03	1.12E+03	1.42E+05	3.04E+04	2.26E+04	4.10E+03	1.52E+05
P13073 COX41	FKESFAEMNR	420.20	71.15	1.27E+03	2.00E+04	1.39E+04	1.99E+04	1.96E+05	1.36E+04	1.44E+04	6.86E+03	1.28E+03	1.57E+04	5.54E+03	6.10E+04	8.01E+03	2.61E+03	2.29E+04
P38646 GRP75	QAVTNPNNTFYATK	784.89	71.25	1.30E+05	3.90E+03	3.97E+02	3.80E+03	1.38E+05	3.46E+03	1.49E+03	6.69E+03	2.39E+03	2.58E+03	8.39E+04	3.50E+02	1.93E+03	1.08E+03	1.04E+05
P31040 DHSA	GEGGILNSQGER	665.34	71.38	3.71E+05	2.92E+04	3.71E+03	1.70E+03	2.96E+03	7.18E+03	8.83E+03	4.44E+03	5.75E+02	2.08E+03	2.72E+05	8.38E+03	3.01E+03	6.24E+03	3.73E+05
Q9BX66-11 SRBS	LSSLDPVSER	595.31	71.59	1.89E+04	2.62E+04	1.87E+05	2.46E+05	1.34E+04	1.87E+05	2.00E+04	1.01E+04	1.64E+04	1.49E+04	1.19E+04	3.96E+04	6.37E+04	6.56E+04	2.14E+04
P12829 MYL4	ESNGTVMGAELR	632.30	71.67	7.86E+04	2.73E+06	2.49E+06	1.31E+06	1.13E+05	2.63E+05	4.36E+05	3.84E+04	5.52E+02	7.54E+02	2.65E+05	1.68E+06	2.43E+06	4.90E+02	1.50E+05
P10809 CH60	IPAMTIK	422.75	71.98	2.73E+03	5.69E+04	8.22E+03	2.96E+03	9.64E+02	2.53E+03	1.17E+05	1.97E+04	5.46E+02	9.06E+03	9.36E+02	3.22E+04	6.53E+04	1.47E+03	8.62E+03
P23327 SRCH	SDEEDFQDEYK	702.78	72.16	6.95E+04	1.03E+03	1.41E+03	3.41E+03	1.81E+02	1.82E+03	5.27E+02	1.17E+03	1.37E+03	6.94E+02	6.12E+04	5.94E+02	5.34E+02	6.19E+02	5.15E+04
P38117-2 ETFB	LGPLQVAR	427.27	72.31	1.37E+03	2.60E+05	2.25E+03	2.45E+04	8.71E+05	1.60E+04	1.31E+04	2.32E+04	1.43E+03	9.25E+02	5.57E+05	3.65E+05	1.91E+04	1.11E+03	3.42E+05
Q9H223 EHD4	ADQVDTQQLMR	652.82	72.35	1.19E+03	1.45E+03	7.14E+03	7.70E+02	6.48E+02	3.24E+04	1.59E+03	2.65E+03	1.54E+05	1.81E+05	2.87E+03	1.57E+03	1.40E+03	1.06E+03	1.34E+03
P11310 ACADM	TRPVVAAGAVGLAQR	489.29	72.39	1.72E+03	3.54E+03	1.07E+03	3.13E+03	5.68E+05	6.93E+03	1.28E+03	7.60E+03	8.97E+02	6.75E+02	2.78E+05	2.07E+04	1.07E+03	2.23E+03	4.57E+05
P49753 ACOT2	GETLPPVGVNR	569.82	72.56	8.26E+04	7.23E+03	1.09E+03	1.28E+04	1.65E+04	7.94E+03	8.32E+02	3.07E+03	1.13E+03	2.35E+04	4.12E+04	7.12E+03	4.70E+02	2.13E+03	5.66E+04
P12110 CO6A2	DIASPHELYR	651.33	72.56	5.19E+03	1.15E+04	3.77E+03	7.27E+03	1.88E+05	7.54E+03	1.30E+03	4.04E+03	2.30E+06	7.78E+05	2.50E+05	2.42E+03	2.94E+03	1.43E+04	2.86E+05
Q16795 NDUA9	FIHVSHLNANIK	464.93	72.62	4.95E+04	1.19E+03	1.42E+03	4.42E+04	1.06E+05	8.54E+02	5.04E+04	1.81E+03	8.81E+02	2.61E+02	8.01E+02	2.92E+04	1.13E+03	1.91E+02	1.27E+03
P38117-2 ETFB	GIHVEVPPAEAER	468.58	72.7	1.93E+05	3.25E+04	1.80E+04	1.61E+04	1.02E+04	1.51E+04	3.42E+04	1.89E+04	9.13E+02	2.93E+04	1.85E+05	4.43E+04	7.33E+03	6.15E+04	2.47E+04
P19022 CADH2	TFYGEVPENR	606.29	72.92	1.85E+03	6.36E+03	3.58E+04	1.79E+03	1.96E+03	4.65E+04	2.82E+04	4.20E+04	2.62E+02	1.75E+03	3.27E+03	3.58E+03	1.63E+03	6.87E+02	3.38E+03
P30041 PRDX6	DINAYNCEPTEK	763.33	72.97	4.72E+04	3.85E+03	1.25E+03	3.04E+04	2.67E+03	1.24E+03	1.19E+03	2.21E+03	9.67E+03	2.40E+03	2.60E+04	2.47E+02	2.96E+03	4.79E+04	3.64E+04
Q06830 PRDX1	ATAVMPDGQFK	582.79	72.99	8.33E+02	1.45E+04	5.06E+03	1.98E+03	3.60E+03	8.85E+02	1.93E+03	4.76E+02	8.05E+03	9.94E+02	1.46E+03	2.67E+03	1.58E+04	1.66E+03	4.26E+03
O15061-2 SYNEM	LCAQEAELR	552.28	73.01	3.25E+03	6.64E+03	6.57E+02	4.02E+03	1.69E+03	1.06E+03	3.39E+03	2.81E+03	6.34E+04	6.55E+04	1.87E+04	1.48E+03	2.29E+03	7.00E+04	6.27E+03
P05091 ALDH2	VVGNPFDSK	481.75	73.05	1.88E+03	4.07E+03	2.30E+03	1.33E+03	1.64E+05	3.36E+03	3.05E+04	1.22E+03	6.67E+02	4.99E+02	1.53E+04	2.25E+04	1.21E+03	5.51E+03	6.04E+03
P00367 DHE3	YSTDVSVDEVK	621.30	73.21	1.11E+05	3.18E+03	2.57E+02	1.84E+03	2.98E+04	8.05E+02	1.16E+04	1.68E+03	7.14E+02	4.46E+02	2.92E+04	4.55E+03	1.09E+03	2.96E+03	8.18E+04
P07954 FUMH	AAAEVNDYGLDPK	745.86	73.87	2.26E+05	1.81E+03	2.36E+03	4.62E+03	3.71E+03	1.42E+03	2.25E+03	5.21E+02	7.48E+03	3.88E+02	1.17E+05	3.46E+03	1.90E+03	4.35E+02	1.61E+05
Q702N8 XIRP1	EQIVGGDVQGYR	660.83	73.92	1.11E+05	1.97E+04	1.18E+03	7.79E+03	2.41E+03	1.02E+03	1.57E+03	1.68E+03	1.56E+03	4.64E+03	4.45E+04	9.97E+03	7.21E+03	1.99E+03	2.77E+04
P02679 FIBG	YLQEIYNSNNQK	757.37	73.96	7.03E+04	4.46E+04	5.06E+02	2.02E+04	9.83E+04	3.24E+03	1.30E+03	1.92E+05	5.75E+02	3.88E+03	1.28E+04	1.22E+05	3.24E+04	2.15E+03	4.00E+04
P10412 H14	KASGPPVSELITK	442.92	73.97	5.58E+03	5.11E+03	5.11E+03	1.65E+03	1.13E+05	1.13E+04	9.61E+03	9.67E+03	8.99E+02	2.25E+02	5.86E+03	2.59E+04	4.56E+03	9.31E+02	1.55E+04
P55290 CAD13	DLHPNTDPFK	592.29	74.03	1.13E+04	6.46E+03	1.72E+04	7.93E+02	3.36E+03	1.06E+05	1.76E+04	4.05E+03	1.82E+03	2.25E+04	2.39E+03	1.39E+04	7.96E+02	9.21E+02	9.06E+02
P05091 ALDH2	LADLIER	415.24	74.17	2.01E+03	3.22E+03	1.59E+03	1.48E+03	2.03E+03	5.78E+02	3.43E+03	9.67E+03	1.13E+05	3.39E+05	1.49E+03	2.39E+03	2.56E+03	2.35E+04	8.06E+03
P49821 NDUV1	GGAGFPTGLK	452.75	74.17	1.58E+03	1.44E+04	4.28E+03	3.23E+04	1.93E+05	1.39E+04	2.47E+05	3.31E+05	8.69E+02	1.59E+03	1.78E+04	7.66E+04	8.45E+04	8.39E+02	3.65E+03
Q6NZI2 PTRF	SFTPDHVYVAR	431.22	74.38	3.05E+04	2.64E+03	1.91E+03	5.90E+04	5.92E+02	3.29E+02	1.33E+03	8.41E+02	1.27E+05	1.51E+05	3.72E+03	1.47E+03	3.91E+02	8.31E+04	9.22E+02
P01876 IGHA1	SVTWSSESGQVTAR	732.86	74.42	4.88E+04	4.81E+03	5.35E+02	2.69E+03	8.89E+02	2.77E+02	4.85E+03	7.01E+02	5.12E+02	1.46E+03	1.20E+04	6.81E+02	1.59E+03	7.39E+02	1.11E+03
Q702N8 XIRP1	EAASSVDVQALR	623.33	74.46	1.46E+04	3.02E+04	1.45E+03	8.90E+04	7.07E+04	1.31E+05	2.01E+02	5.19E+04	1.01E+03	1.20E+03	4.15E+04	2.14E+04	1.75E+04	3.27E+03	1.13E+05
P11217 PYGM	MSLVEEGAVK	531.78	74.49	2.85E+02	3.92E+04	1.37E+04	3.08E+04	7.77E+03	5.14E+04	1.62E+04	4.10E+04	1.58E+04	7.69E+02	6.96E+04	9.48E+04	3.20E+04	3.32E+03	1.82E+04
P31040 DHSA	AGEESVMNLDK	596.78	74.57	1.57E+05	8.35E+02	2.14E+03	2.34E+03	8.52E+03	2.14E+02	4.57E+03	5.09E+02	2.43E+04	1.88E+03	1.84E+05	1.03E+04	7.15E+02	1.83E+03	4.96E+04
Q96199 SUCB2	DPNVVQQLAK	520.79	74.62	1.42E+05	1.12E+03	1.85E+04	6.15E+03	5.65E+03	2.03E+04	4.75E+03	1.08E+04	2.28E+03	1.45E+03	1.40E+05	1.37E+03	4.42E+02	3.09E+03	1.18E+04
P49821 NDUV1	EAYEAGLIGK																	

P05091 ALDH2	VAFTGSTEIGR	569.30	75.21	1.73E+04	1.07E+05	2.52E+04	9.20E+04	2.33E+05	2.24E+04	5.17E+04	4.23E+03	7.14E+02	1.19E+03	8.53E+02	1.92E+05	1.41E+03	3.02E+03	1.82E+03
P13533 MYH6	ERLEAQTRPDIR	544.96	75.21	2.21E+03	1.01E+04	2.26E+03	3.13E+03	6.10E+02	4.56E+03	3.50E+04	3.12E+03	1.19E+03	4.77E+02	2.73E+03	1.30E+05	6.16E+02	1.77E+04	6.17E+02
P28289 TMOD1	ASNAMMNNNDLVR	725.33	75.4	4.20E+02	1.49E+03	1.18E+05	8.04E+02	1.75E+02	8.19E+04	5.97E+02	1.06E+05	5.93E+03	3.86E+04	5.27E+02	1.05E+03	1.65E+03	4.51E+02	9.41E+02
Q16555 DPYL2	VLSRPEEVEAEAVNR	566.63	75.46	2.47E+04	1.14E+03	7.53E+02	9.60E+02	4.74E+02	6.79E+02	3.89E+02	1.88E+03	1.28E+03	1.50E+03	9.75E+04	3.98E+02	2.19E+04	1.28E+03	6.73E+04
P01023 A2MG	SASNMAIVDVK	567.79	75.56	1.18E+04	1.92E+04	2.48E+04	3.57E+04	6.65E+04	1.75E+03	1.05E+04	1.94E+03	2.19E+05	4.00E+05	2.55E+03	3.07E+03	3.11E+03	1.35E+05	1.80E+04
P12109 CO6A1	LSIATDHTYR	430.57	75.62	6.37E+02	1.89E+03	9.50E+03	2.03E+05	8.44E+04	1.53E+04	4.22E+03	3.83E+03	1.44E+04	6.49E+02	2.10E+04	3.72E+04	1.46E+04	1.45E+03	1.40E+05
P31040 DHSA	TGHSLHTLYGR	452.25	75.69	4.08E+02	5.12E+04	1.95E+04	5.77E+04	9.64E+04	9.99E+02	2.19E+05	1.10E+04	5.22E+02	3.82E+02	1.00E+03	7.54E+04	1.12E+03	1.14E+03	8.26E+04
P10515 ODP2	PAPTPAATAS	442.23	75.97	7.48E+02	8.72E+04	1.63E+03	6.94E+04	1.46E+04	3.62E+04	2.59E+04	6.41E+02	1.27E+03	1.88E+03	1.59E+03	5.16E+04	3.15E+04	5.82E+03	4.80E+04
P02462 CO4A1	SLLYVQGNER	589.81	76.01	7.67E+02	8.47E+04	2.03E+04	1.03E+04	9.04E+03	2.07E+04	1.42E+04	3.35E+02	9.67E+02	2.11E+03	1.30E+05	8.47E+03	2.59E+04	1.52E+04	1.23E+05
P30041 PRDX6	VATPVDWK	458.25	76.02	1.43E+05	2.35E+03	4.56E+04	3.03E+04	1.66E+04	2.75E+04	1.06E+04	8.29E+03	1.13E+05	1.56E+05	1.70E+05	3.91E+03	1.69E+03	4.85E+04	5.10E+03
P38646 GRP75	DDIENMVK	482.23	76.11	5.23E+02	1.67E+03	6.59E+02	9.64E+04	6.53E+04	7.58E+04	5.49E+04	1.22E+04	1.22E+03	9.98E+03	5.42E+02	4.82E+04	1.68E+04	3.02E+04	6.45E+02
Q6NZI2 PTRF	VMIYQDEVK	562.79	76.33	1.97E+05	3.36E+04	9.70E+02	8.79E+03	1.02E+04	3.01E+03	1.77E+03	1.29E+03	5.91E+04	1.27E+04	1.94E+05	2.08E+04	1.12E+04	7.44E+04	1.96E+04
Q01813 K6PP	SFAGNLNTYK	557.78	76.33	2.03E+03	1.85E+03	3.20E+04	1.19E+03	3.72E+03	6.22E+04	3.13E+03	8.52E+02	3.58E+03	3.85E+03	7.60E+03	2.19E+03	1.19E+03	8.09E+02	6.50E+02
P01876 IGHA1	TFTCTAAYPESK	659.80	76.38	9.11E+02	1.49E+04	2.60E+04	2.37E+05	3.08E+05	2.84E+03	1.74E+03	2.14E+03	4.65E+02	5.11E+03	1.22E+03	4.36E+04	1.72E+03	1.30E+03	5.33E+04
P35579 MYH9	ALEQOQVEEMK	602.81	76.42	3.35E+03	2.12E+04	1.71E+03	7.35E+04	3.68E+04	1.78E+03	1.05E+06	6.37E+05	1.35E+05	1.00E+04	7.88E+03	1.01E+05	1.93E+04	2.70E+05	9.72E+04
P13637 AT1A3	VAEIPFNSTNK	610.32	76.67	1.31E+05	5.51E+03	3.46E+03	1.40E+04	1.30E+03	4.09E+04	4.02E+02	1.65E+05	1.24E+03	2.56E+03	1.91E+05	1.02E+03	6.71E+04	1.07E+05	3.43E+04
P49753 ACOT2	SFIPVER	424.24	76.76	1.33E+03	7.83E+02	6.35E+03	2.68E+05	2.73E+05	1.91E+05	1.85E+05	6.22E+04	3.71E+03	6.04E+04	4.71E+03	2.52E+05	1.04E+03	7.45E+03	2.05E+03
Q15124 PGM5	SMPTSMALDR	554.76	76.77	5.77E+03	1.40E+05	1.72E+04	1.54E+05	1.95E+05	1.31E+05	3.40E+04	1.02E+04	1.25E+03	1.09E+03	1.30E+03	5.43E+04	1.14E+04	1.26E+03	1.90E+05
P10809 CH60	NAGVEGSLIVEK	608.33	76.98	1.11E+04	1.52E+05	2.85E+05	5.48E+04	5.88E+05	2.75E+05	1.71E+05	5.29E+04	5.94E+02	1.03E+03	9.88E+02	6.37E+03	4.28E+03	3.08E+02	1.19E+03
Q13011 ECH1	VNLLYSR	432.75	77.09	3.02E+03	3.79E+03	4.50E+02	8.86E+02	1.50E+03	1.30E+03	2.19E+03	2.25E+03	2.67E+05	2.70E+03	1.17E+03	6.66E+02	6.44E+02	9.80E+04	2.71E+03
P13073 COX41	VNIQGLASK	513.80	77.2	1.52E+03	3.59E+05	8.12E+05	9.72E+05	9.55E+05	1.26E+06	3.80E+05	5.40E+05	1.10E+03	2.12E+03	3.80E+03	3.11E+05	5.87E+02	5.01E+02	9.71E+05
P36542 ATPG	LLIGVSSDR	480.28	77.22	2.91E+04	1.41E+05	1.02E+03	3.88E+02	1.10E+03	2.11E+03	1.42E+04	4.46E+02	9.10E+02	1.41E+03	3.23E+04	4.60E+03	1.54E+05	1.53E+04	1.12E+04
P36871 PGM1	YDYEEVEAEGANK	758.83	77.33	9.27E+04	2.08E+03	2.87E+03	1.47E+05	7.43E+04	2.61E+03	3.11E+03	4.79E+03	9.63E+02	4.80E+02	9.92E+04	3.02E+03	4.82E+03	2.74E+03	1.06E+05
P12110 CO6A2	IDSLSSEFK	448.74	77.33	6.30E+03	1.21E+04	2.70E+03	5.81E+03	1.28E+03	1.77E+04	5.95E+03	2.62E+03	1.92E+03	6.37E+02	1.75E+05	6.33E+03	1.01E+03	1.39E+03	9.74E+03
Q9UKX3 MYH13	STHPHFVRCLIPNETK	470.50	77.4	4.81E+04	5.49E+02	2.74E+02	1.20E+03	2.19E+03	8.68E+03	5.22E+02	2.21E+03	2.48E+02	8.13E+02	6.73E+03	1.31E+03	2.01E+03	1.47E+03	5.33E+02
Q702N8 XIRP1	GISLEEGARPDVSATR	553.29	77.48	1.05E+05	2.26E+04	1.38E+04	2.75E+04	4.82E+04	2.57E+03	4.39E+04	4.02E+04	1.47E+04	8.64E+03	4.13E+02	6.95E+04	1.31E+03	2.86E+04	3.28E+04
O95831 AIFM1	ISGLGLTPEQK	571.82	77.48	2.97E+05	3.07E+03	5.24E+05	1.39E+04	5.84E+03	1.35E+03	7.62E+03	3.98E+05	5.10E+02	1.24E+03	1.55E+02	2.33E+03	4.35E+02	1.10E+03	1.14E+03
P32119 PRDX2	LSEDYGVLK	512.27	77.56	1.32E+04	1.01E+06	1.12E+03	1.41E+06	3.21E+05	2.08E+04	2.75E+05	5.57E+03	1.71E+03	6.45E+03	1.71E+04	6.17E+05	1.58E+03	2.91E+04	9.75E+05
P67936 TPM4	YEEEEIKLLSDK	683.86	77.63	2.85E+05	6.11E+03	1.26E+04	1.13E+04	1.97E+04	1.73E+04	7.03E+03	3.70E+03	1.06E+03	1.00E+03	3.25E+05	1.07E+04	1.60E+05	1.51E+03	1.61E+04
P63316 TNNC1	AAVEQLTEEKNEFK	882.44	77.71	5.25E+02	1.06E+03	5.41E+02	2.05E+03	5.27E+05	7.49E+03	2.54E+03	7.54E+02	9.09E+02	7.26E+02	8.39E+04	4.38E+03	2.53E+04	5.60E+02	9.91E+03
Q9H987 SYP2L	GVQLFEQQR	552.79	77.76	2.17E+03	2.93E+04	2.55E+04	1.17E+05	4.11E+03	1.62E+05	1.89E+04	4.87E+02	1.00E+03	1.40E+03	1.29E+04	7.82E+04	3.58E+04	2.32E+03	8.36E+03
P55290 CAD13	VNSDGGGLVALR	550.80	77.85	8.34E+03	7.67E+03	1.15E+04	1.28E+04	5.74E+04	1.11E+03	3.78E+04	3.76E+03	9.15E+03	2.02E+03	1.96E+04	4.74E+04	2.76E+04	3.36E+04	8.24E+04
Q14894 CRYM	ELDDGLMK	496.73	78.22	1.80E+02	1.27E+05	2.05E+04	2.88E+05	3.05E+03	5.23E+04	8.18E+04	3.47E+04	7.13E+02	6.25E+02	1.61E+04	2.51E+05	1.11E+04	2.36E+03	4.36E+02
Q16836-2 HCDH	DTPGFIVNR	509.77	78.67	1.15E+03	1.65E+05	3.58E+03	2.62E+05	3.36E+05	1.00E+05	3.06E+05	2.26E+04	1.03E+03	3.58E+03	6.87E+02	2.33E+05	1.26E+03	3.12E+03	1.31E+05
P31040 DHSA	SMTLEIR	425.23	78.69	4.23E+04	9.87E+02	3.57E+03	7.32E+04	3.54E+03	1.20E+04	7.79E+02	8.66E+02	2.63E+03	2.06E+03	9.86E+04	1.28E+03	3.22E+04	1.17E+03	1.42E+03
P10515 ODP2	VFVSPLAK	430.77	78.7	7.38E+03	5.23E+04	1.28E+04	1.38E+05	3.15E+05	4.78E+03	2.35E+05	7.73E+03	4.77E+03	2.49E+04	5.13E+03	9.39E+04	3.44E+05	4.00E+02	1.43E+05
P01023 A2MG	VTAAPQSVCALR	608.33	78.96	1.83E+03	7.05E+02	1.11E+03	2.37E+03	1.29E+03	6.63E+02	2.19E+03	2.70E+03	1.41E+05	2.84E+05	4.20E+03	1.67E+03	1.44E+04	5.45E+04	1.36E+03
P01023 A2MG	SSGSLNNAIK	552.31	78.96	2.29E+04	6.68E+02	2.40E+03	8.31E+02	6.08E+02	1.96E+03	4.57E+02	5.98E+03	4.83E+03	7.23E+04	3.16E+03	3.71E+03	2.19E+03	7.54E+03	4.12E+03
P01009 A1AT	WERPFEVK	545.80	79.01	2.53E+03	2.63E+03	3.25E+04	3.20E+03	5.57E+03	1.09E+05	8.42E+04	1.09E+05	6.60E+04	2.08E+05	9.08E+03	1.57E+03	5.66E+02	4.42E+04	1.50E+04
P36957 ODO2	EAVTFLR	418.24	79.24	1.12E+03	2.44E+03	4.61E+02	1.98E+04	2.02E+05	2.92E+04	2.14E+05	7.25E+02	1.03E+04	1.82E+03	1.16E+03	1.02E+05	1.22E+03	8.00E+02	1.02E+03
P05091 ALDH2	ILGYINTGK	489.78	79.28	9.89E+02	5.01E+03	1.87E+03	1.05E+04	1.50E+03	1.55E+04	7.42E+02	7.72E+02	5.94E+04	1.56E+05	4.83E+03	1.45E+03	1.48E+03	2.83E+04	9.82E+02
P10809 CH60	VGLQVAVK	456.80	79.31	1.41E+05	1.93E+03	4.06E+02	1.11E+03	3.77E+03	2.70E+02	4.72E+03	5.90E+02	3.56E+02	4.38E+02	1.20E+05	1.19E+03	3.39E+03	2.46E+02	2.99E+03
P09972 ALDOC	ELSDIALR	458.76	79.37	2.70E+04	3.43E+05	4.44E+05	4.38E+05	3.58E+04	3.30E+05	2.14E+05	3.38E+05	1.51E+03	1.61E+03	3.18E+04	2.46E+05	8.44E+03	1.38E+04	2.16E+04
Q16698 DECR	AMLPPNSFQ GK	595.31	79.6	2.70E+04	3.93E+04	6.20E+03	4.68E+04	1.65E+04	4.08E+03	2.32E+03	1.17E+05	7.74E+05	1.30E+04	5.64E+03	1.01E+05	2.58E+04	4.90E+04	3.75E+03
P42765 THIM	TNVNGGAIALGHPLGGSGS	612.32	79.89	1.76E+05	2.50E+04	3.49E+03	1.51E+03	4.11E+03	1.83E+04	1.59E+04	1.49E+04	9.98E+02	5.96E+03	1.14E+05	4.26E+02	3.72E+04	4.08E+04	7.73E+03
P10412 H14	SGVSLAALK	423.26	80.05	1.68E+03	2.32E+04	3.82E+02	1.23E+04	5.16E+05	2.76E+03	3.13E+05	8.79E+03	6.38E+02	6.35E+02	3.31E+03	5.19E+04	1.66E+05	2.36E+03	1.21E+05
Q86TD4 SRCA	LIGIEVPHK	503.31	80.06	1.60E+03	1.98E+05	6.16E+03	3.49E+05	1.44E+05	3.18E+05	9.27E+04	8.53E+02	1.58E+03	2.63E+03	2.67E+03	6.23E+04	8.84E+02	2.66E+02	2.56E+05
P06744 G6PI	TFTTQETITNAETAK	828.41	80.06	5.65E+02	9.19E+03	1.05E+03	1.16E+05	8.94E+03	4.87E+03	4.11E+03	3.16E+03	1.72E+03	3.98E+02	8.86E+04	5.63E+03	2.46E+04	2.11E+03	1.30E+05
Q99497 PARK7	DGLILTSR	437.75	80.09	2.76E+04	1.42E+05	4.17E+03	1.38E+05	2.92E+03	8.26E+04	6.85E+04	7.26E+02	1.10E+03	8.92E+02	1.11E+03	1.08E+05	5.46E+04	1.99E+03	6.86E+02
P49753 ACOT2	GLAPEQPVTLR	590.84	80.38	4.40E+02	2.97E+05	4.97E+03	4.59E+05	3.49E+05	4.06E+05	4.23E+02	2.10E+03	5.11E+02	1.20E+03	3.34E+05	1.44E+05	5.97E+02	4.85E+02	5.27E+05
P02679 FIBG	YEASILTHDSSIR	497.92	80.4	9.55E+04	4.9													

P01023 A2MG	QTVSWAVTPK	558.80	81.38	2.48E+03	1.99E+03	1.17E+04	7.25E+02	5.37E+03	1.17E+04	2.12E+03	4.81E+03	5.68E+04	1.03E+05	3.03E+03	3.04E+04	2.10E+03	4.21E+04	7.91E+02
P42765 THIM	SLDLDISK	445.74	81.44	2.14E+03	6.79E+05	2.75E+04	7.82E+05	7.22E+05	6.12E+05	6.34E+05	1.99E+04	1.02E+03	4.43E+03	4.41E+03	6.36E+05	4.94E+03	2.96E+03	6.74E+05
P07954 FUMH	MNVNEVISNR	588.32	81.52	4.64E+04	3.89E+04	1.64E+05	3.93E+04	1.20E+04	2.32E+03	6.96E+04	6.68E+03	5.91E+06	7.08E+06	3.78E+04	3.10E+04	1.56E+04	5.06E+06	2.22E+05
P01023 A2MG	AIGYLNTRYQR	628.32	81.65	5.18E+02	5.38E+03	9.25E+02	4.62E+03	1.17E+05	1.42E+04	9.51E+02	2.13E+03	3.13E+04	4.24E+02	1.04E+05	9.10E+02	3.43E+04	1.57E+04	5.53E+02
P62258 1433E	YLAEFATGNDR	628.80	81.72	2.02E+05	1.54E+05	1.41E+05	9.76E+03	6.98E+02	3.41E+05	1.57E+04	4.03E+02	3.30E+03	1.20E+03	3.07E+05	2.00E+03	1.61E+05	7.24E+02	1.33E+04
P00367 DHE3	FTMELAK	420.23	82.19	1.02E+03	1.71E+04	3.87E+03	2.29E+04	6.82E+02	5.30E+02	3.23E+03	7.84E+03	4.88E+04	4.79E+04	1.12E+03	9.76E+03	4.36E+03	1.49E+05	1.48E+03
P38117-2 ETFB	EIDGGLETLR	551.79	82.2	2.01E+03	5.78E+05	2.38E+04	1.68E+05	1.52E+05	2.15E+05	4.86E+03	2.83E+03	1.68E+02	4.10E+02	1.23E+03	5.12E+05	5.12E+02	2.96E+03	2.59E+05
Q9H987 SYP2L	YVVEGTPGGLGPR	699.87	82.4	4.56E+04	1.11E+03	8.38E+03	2.11E+05	1.58E+05	2.76E+03	1.26E+03	8.17E+03	3.28E+03	5.34E+03	1.23E+05	4.13E+05	1.91E+04	9.44E+02	6.94E+04
P21980 TGM2	LVVNFESDK	525.78	82.63	1.62E+03	7.92E+03	1.62E+03	1.09E+05	3.22E+04	7.28E+02	3.22E+03	2.73E+03	6.34E+02	3.29E+04	6.60E+02	5.06E+03	2.44E+03	1.39E+03	8.97E+04
Q15124 PGM5	GLLTGSPQLK	507.30	82.68	1.83E+04	7.05E+03	3.54E+03	7.62E+04	1.21E+04	2.15E+04	6.41E+02	2.00E+03	2.39E+05	2.29E+04	4.69E+03	1.13E+03	9.59E+03	1.94E+05	8.48E+04
P09972 ALDOC	DNAGAAATEEFIK	633.31	82.71	1.58E+05	4.05E+03	1.15E+05	2.65E+04	7.39E+02	3.43E+03	5.70E+03	1.57E+03	8.35E+02	6.08E+02	1.51E+05	9.83E+02	2.06E+03	2.84E+03	5.63E+02
P12829 MYL4	VFDKESNGTVMGAELR	584.96	82.75	1.27E+03	1.03E+05	5.03E+03	1.93E+04	8.39E+04	3.29E+04	9.20E+03	7.25E+03	8.21E+02	5.54E+02	2.81E+03	3.45E+05	4.48E+02	1.18E+03	2.17E+04
P31040 DHSA	VTLEYRVIDK	444.92	82.85	1.65E+03	2.81E+03	2.56E+04	1.77E+05	2.85E+05	3.59E+03	2.16E+04	1.03E+04	1.23E+03	3.17E+02	2.38E+03	6.73E+03	1.15E+03	2.12E+03	1.19E+05
P07339 CATD	LSPEDYTLK	533.28	82.99	8.73E+03	8.18E+04	1.54E+05	3.23E+03	2.43E+05	1.97E+05	9.75E+04	9.49E+04	1.48E+03	1.92E+03	1.74E+04	4.82E+03	3.31E+03	1.27E+04	8.39E+02
Q16891-2 IMMT	GIEQAVQSHAVAEER	608.64	83.06	3.01E+02	2.07E+03	5.92E+02	8.07E+02	2.38E+05	1.71E+03	3.43E+03	1.57E+03	1.19E+03	7.21E+02	4.70E+03	9.47E+04	8.77E+02	1.80E+03	5.04E+02
P20674 COX5A	VIQELRPTLN	591.85	83.07	7.79E+05	3.80E+03	1.72E+03	9.61E+03	3.77E+02	2.69E+03	1.98E+03	2.05E+03	5.71E+02	6.92E+02	2.88E+05	1.48E+03	3.44E+03	2.42E+02	1.48E+04
P06744 G6PI	VFEGNRPTNSIVFTK	570.31	83.09	4.18E+03	3.04E+03	5.04E+03	3.45E+05	1.59E+05	2.37E+04	1.63E+03	3.65E+05	2.49E+02	6.02E+02	2.08E+05	3.33E+03	8.08E+04	1.82E+03	3.12E+05
P09972 ALDOC	DDNGVPFVR	509.75	83.16	3.80E+03	6.23E+02	1.22E+03	7.21E+02	9.79E+02	2.23E+04	6.63E+03	5.93E+02	5.97E+03	8.53E+04	5.02E+03	1.29E+03	3.19E+02	1.66E+04	2.84E+03
Q99878 H2A1J	IQAVLLPK	441.29	83.28	5.50E+05	6.12E+03	3.38E+03	1.05E+04	3.92E+04	1.55E+04	1.10E+05	8.24E+02	3.37E+02	1.78E+02	4.52E+05	4.85E+04	4.98E+03	2.38E+02	9.44E+03
P47985 UCRI	VPDFSEYR	506.74	83.44	2.29E+03	3.65E+05	3.59E+03	1.57E+03	5.94E+05	6.56E+03	3.52E+05	4.60E+02	4.48E+03	3.82E+03	4.19E+05	4.32E+05	5.24E+02	1.02E+03	3.22E+02
P49753 ACOT2	AATLILEPAGR	556.32	83.72	5.62E+03	1.31E+04	5.23E+03	4.34E+04	1.13E+05	1.23E+04	1.78E+03	8.23E+02	1.22E+03	1.19E+03	2.95E+04	1.38E+04	1.78E+02	1.19E+03	1.73E+05
P13637 AT1A3	DVAGDASESALLK	638.33	83.77	1.04E+05	5.31E+03	1.33E+03	1.85E+05	2.78E+04	7.01E+03	1.41E+03	2.66E+03	1.40E+06	2.26E+06	6.37E+04	3.48E+04	3.01E+04	6.45E+05	1.33E+05
P06744 G6PI	NLVTEDVMR	538.77	83.8	2.19E+03	7.29E+05	6.88E+05	9.23E+05	6.96E+05	8.34E+05	7.22E+05	2.30E+03	6.66E+04	1.75E+02	6.55E+05	8.73E+05	1.55E+03	1.56E+03	9.08E+02
P01023 A2MG	YDVENCLANK	584.78	83.95	4.93E+02	9.54E+03	3.63E+03	8.80E+04	1.08E+05	1.09E+03	3.13E+04	2.74E+03	5.90E+03	4.84E+02	1.74E+03	8.60E+05	9.81E+04	5.99E+02	3.03E+04
P12110 CO6A2	NLQGISSFR	511.27	83.99	3.44E+05	3.31E+05	3.96E+03	1.98E+04	1.55E+04	1.88E+05	1.06E+03	1.16E+03	2.90E+04	6.25E+02	3.20E+05	1.98E+05	1.04E+05	4.53E+05	3.99E+05
Q15124 PGM5	FNVANGGPAPDVVSDK	793.90	84.02	1.65E+03	3.64E+03	1.15E+04	5.69E+02	3.23E+03	3.83E+04	1.67E+03	5.22E+03	2.58E+02	4.47E+02	5.88E+02	9.36E+02	2.76E+03	4.55E+02	8.07E+02
P02675 FIBB	SILENLR	422.75	84.05	1.91E+03	1.07E+05	1.00E+04	1.71E+05	7.87E+05	3.03E+05	3.90E+05	1.42E+04	1.51E+03	8.93E+02	1.18E+03	1.89E+05	1.83E+03	1.91E+03	1.28E+03
Q14894 CRYM	LVTFYEDR	521.76	84.09	2.04E+05	2.69E+03	9.49E+03	2.25E+03	8.61E+02	2.63E+03	3.45E+03	1.68E+03	1.99E+03	2.27E+03	2.19E+05	1.78E+03	1.08E+05	1.02E+03	1.79E+03
P02679 FIBG	VELEDWNGR	559.27	84.09	2.45E+05	1.80E+03	1.74E+03	1.86E+03	4.08E+03	5.80E+02	1.64E+03	2.76E+03	1.19E+04	1.55E+03	1.55E+05	3.47E+04	5.47E+04	2.87E+03	2.60E+03
P07339 CATD	GPIPEVLK	426.76	84.3	5.39E+02	1.03E+04	4.26E+02	3.73E+04	2.41E+05	9.51E+02	2.72E+04	1.10E+03	8.96E+02	1.78E+03	8.04E+04	8.76E+04	1.80E+04	6.53E+03	1.90E+05
P11310 ACADM	GIVFEDVK	453.75	84.33	3.91E+05	6.54E+03	2.43E+03	1.28E+04	4.00E+03	3.62E+03	1.89E+04	9.93E+04	4.26E+02	2.46E+03	3.37E+05	8.43E+03	2.58E+05	1.00E+03	4.50E+05
P11217 PYGM	EIWGVPSR	536.77	84.39	8.08E+03	3.42E+04	2.36E+03	1.18E+05	1.38E+04	4.54E+03	8.76E+03	1.53E+03	2.35E+04	1.52E+03	1.35E+03	2.29E+03	1.09E+04	2.80E+04	1.56E+05
Q06830 PRDX1	TQADYGVLLK	554.30	84.6	1.03E+03	2.58E+05	2.35E+03	2.85E+05	3.42E+05	2.92E+04	2.12E+05	3.20E+04	2.24E+04	7.07E+03	4.11E+05	2.59E+05	1.78E+03	6.00E+03	3.11E+03
Q75746 CMC1	VSALNVLR	436.27	84.62	1.26E+04	1.15E+03	3.69E+03	3.45E+03	2.93E+03	1.32E+03	1.51E+03	1.63E+03	1.35E+05	9.99E+04	4.78E+02	9.25E+02	2.40E+03	1.04E+05	9.86E+02
P00738 HPT	SPVGVQPILNEH	645.35	84.66	1.37E+05	3.52E+03	8.09E+02	1.95E+03	1.08E+03	5.37E+03	2.30E+03	9.87E+03	7.79E+03	8.41E+03	1.36E+04	3.41E+03	9.61E+03	2.70E+04	8.53E+02
P62937 PIIA	HTGPGILSMAN	549.27	84.74	1.02E+05	1.75E+03	1.46E+03	1.71E+03	2.25E+04	1.87E+03	4.87E+03	1.39E+03	1.25E+04	3.59E+02	1.43E+04	2.83E+03	6.08E+03	2.33E+04	3.96E+04
P14543-2 NID1	YALSNSIGPVR	588.82	84.8	3.10E+02	8.41E+03	1.93E+03	1.10E+04	7.92E+04	6.68E+03	1.99E+03	2.92E+03	1.84E+03	2.99E+03	6.70E+02	1.10E+05	1.12E+03	2.29E+02	1.59E+03
Q86TD4 SRCA	FGQNFLEK	491.75	84.86	6.10E+02	7.82E+03	1.56E+05	3.12E+03	9.05E+02	1.11E+04	4.77E+03	1.64E+05	2.56E+03	5.83E+02	6.51E+02	9.09E+02	5.54E+03	3.08E+03	6.04E+03
P02679 FIBG	TSTADYAMFK	567.76	84.86	1.07E+03	2.91E+03	2.76E+05	1.51E+03	7.76E+02	3.78E+05	2.27E+05	1.74E+05	5.64E+04	2.63E+05	1.48E+03	6.98E+02	2.06E+02	8.05E+04	4.81E+02
P35579 MYH9	DELADEIANSSGK	674.81	85.06	7.06E+02	6.16E+02	7.40E+02	3.97E+03	5.45E+02	5.08E+02	1.66E+03	2.53E+04	1.89E+04	6.16E+04	1.49E+03	1.31E+03	2.69E+03	2.64E+04	8.40E+02
Q16795 NDUA9	FLNSFASMR	605.29	85.06	1.92E+03	1.50E+03	1.14E+04	3.24E+04	7.98E+04	2.63E+03	3.52E+05	2.66E+05	1.68E+03	7.24E+02	2.10E+03	8.41E+02	2.14E+03	1.81E+03	3.66E+03
Q16795 NDUA9	IPQAIAQLSK	534.82	85.12	1.00E+04	1.36E+05	2.03E+03	2.31E+05	1.58E+05	2.09E+03	2.49E+05	4.52E+03	5.14E+03	2.11E+03	5.63E+04	1.30E+05	1.01E+04	4.07E+03	7.21E+04
P49411 EFTU	ELAMPGEDLK	551.79	85.2	9.96E+02	7.05E+05	9.52E+02	9.53E+05	4.47E+05	3.42E+05	3.77E+03	1.10E+03	5.81E+05	4.37E+05	6.04E+05	4.19E+05	3.90E+05	2.99E+05	6.90E+05
P13533 MYH6	LQDAEEAVEAVNAK	743.87	85.28	6.64E+04	2.15E+03	1.10E+03	5.16E+04	1.72E+03	8.03E+03	1.32E+03	1.26E+03	9.01E+02	2.53E+02	3.94E+04	1.86E+03	2.99E+04	8.54E+02	9.52E+04
Q75746 CMC1	IADLPPANPDHIGGYR	569.30	85.3	9.70E+02	8.61E+03	2.85E+03	2.69E+04	2.32E+04	4.44E+03	1.33E+04	4.18E+04	2.64E+02	4.85E+03	1.50E+04	3.16E+04	1.50E+03	2.27E+03	1.32E+04
P02675 FIBB	EEAPSLRPAPPPISGGGYR	651.01	85.5	6.30E+04	1.59E+03	8.16E+02	3.41E+04	3.13E+03	5.09E+02	2.56E+03	4.50E+03	3.57E+02	4.04E+02	1.64E+04	5.27E+02	2.72E+03	2.02E+03	3.43E+03
P62805 H4	ISGLIYEETR	590.81	85.61	7.85E+05	1.41E+04	1.28E+04	1.10E+06	3.35E+04	7.90E+03	1.28E+04	9.12E+02	6.86E+02	1.29E+03	9.96E+05	3.02E+05	4.25E+05	2.63E+03	1.46E+04
Q16555 DPYL2	SLSGAQIDDNIPR	693.35	85.75	1.67E+04	1.83E+03	1.12E+03	9.99E+03	8.71E+03	9.72E+02	2.04E+03	2.04E+03	1.54E+04	3.46E+03	4.93E+02	2.17E+04	4.16E+03	2.03E+03	1.76E+04
Q9BX66-11 SRBS	LITPAPSSLPH	566.82	85.79	4.86E+02	3.89E+04	4.82E+04	6.20E+04	1.02E+04	1.15E+05	3.87E+03	4.75E+03	8.26E+04	3.02E+04	1.37E+04	2.05E+04	9.45E+04	2.04E+04	2.39E+04
Q702N8 XIRP1	EVFQALEAGK	546.30	85.83	2.48E+04	2.11E+05	8.24E+04	8.75E+04	1.49E+05	3.10E+05	2.49E+05	8.94E+04	1.97E+05	3.75E+04	7.43E+04	2.32E+05	5.14E+03	9.17E+04	1.75E+05
Q16698 DECR	FFSPLQK	433.74	86.09	8.70E+05														



O75746 CMC1	LATATFAGIENK	618.33	86.87	8.70E+03	1.19E+03	2.87E+03	2.16E+03	4.13E+03	9.86E+02	1.21E+03	5.79E+03	1.22E+04	1.04E+03	7.51E+04	3.49E+03	2.94E+04	6.60E+02	1.35E+05
Q16891-2 IMMT	LSEQELQFR	575.30	86.9	3.29E+05	2.42E+06	3.72E+06	3.86E+05	3.62E+06	2.87E+06	2.73E+06	5.55E+05	6.27E+03	3.14E+04	2.75E+05	2.76E+06	3.58E+04	2.99E+03	3.30E+05
P35579 MYH9	DVLLQVDDER	601.31	87	1.72E+03	1.52E+04	2.69E+04	1.39E+04	2.28E+03	1.02E+03	2.85E+04	3.46E+03	6.60E+02	4.25E+02	9.07E+02	3.36E+03	9.54E+02	5.69E+02	1.32E+03
Q9H223 EHD4	AGGADAVQTVTGGLR	686.86	87.11	6.57E+02	2.43E+04	1.45E+04	2.72E+03	2.29E+03	8.62E+04	1.00E+04	4.64E+03	2.17E+03	2.76E+02	1.63E+03	4.07E+04	4.96E+02	8.98E+02	3.62E+03
P10412 H14	ASGPPVSELITK	599.84	87.13	2.95E+05	1.68E+03	2.81E+05	1.67E+03	1.57E+05	7.04E+03	8.76E+02	6.60E+02	9.99E+04	5.15E+05	8.48E+05	1.05E+03	1.18E+05	1.23E+05	4.92E+05
Q16795 NDUA9	SFAFVGPSR	484.25	87.16	1.16E+04	2.77E+03	8.08E+02	6.78E+02	4.67E+03	9.67E+04	4.29E+04	1.89E+04	1.30E+03	1.87E+03	1.49E+04	2.11E+03	2.13E+03	2.87E+03	3.38E+03
P49821 NDUV1	IFTNLYGR	492.27	87.19	3.53E+05	4.85E+03	2.81E+02	9.03E+02	6.92E+02	4.07E+03	5.30E+04	2.38E+03	4.72E+04	1.63E+05	1.67E+05	1.51E+03	6.37E+02	1.33E+04	2.78E+05
Q6NZI2 PTRF	SFTPDHVY	532.76	87.2	6.17E+02	6.23E+03	9.06E+02	1.24E+05	2.22E+03	7.50E+02	9.85E+03	9.07E+02	5.23E+02	1.43E+03	7.00E+04	1.85E+03	2.32E+04	5.93E+02	5.92E+04
P38117-2 ETFB	LSVISVEDPPQR	670.36	87.23	5.79E+05	6.98E+02	3.09E+03	2.54E+05	8.46E+02	4.56E+03	6.42E+02	1.53E+03	1.15E+03	1.26E+03	3.18E+05	1.84E+03	8.40E+04	8.31E+02	4.36E+05
P38646 GRP75	TTPSVVAFTADGER	725.86	87.52	5.31E+02	3.31E+04	5.15E+04	1.91E+03	1.37E+05	1.66E+04	1.92E+03	3.35E+04	3.50E+02	9.29E+02	1.12E+03	1.40E+05	1.19E+03	4.91E+02	4.38E+03
P07237 PDIA1	ALLCLAVAAL	479.30	87.59	2.30E+05	1.49E+04	4.91E+02	1.96E+04	1.80E+03	8.17E+03	5.04E+02	1.27E+03	1.24E+03	1.65E+04	1.87E+05	6.57E+02	9.57E+04	6.82E+02	4.31E+04
P12109 CO6A1	IALVITDGR	479.30	87.59	2.30E+05	1.49E+04	4.91E+02	1.96E+04	1.80E+03	8.17E+03	5.04E+02	1.27E+03	1.24E+03	1.65E+04	1.87E+05	6.57E+02	9.57E+04	6.82E+02	4.31E+04
Q16891-2 IMMT	AVDEAADALLK	558.30	87.95	3.24E+05	9.98E+02	7.42E+02	2.18E+04	7.10E+03	2.37E+03	1.84E+04	7.33E+03	1.89E+03	2.06E+03	2.51E+05	7.94E+03	1.59E+05	8.31E+02	4.83E+03
P36871 PGM1	VDLGVLGK	400.75	87.95	1.18E+04	9.31E+03	1.15E+04	1.01E+04	1.15E+04	2.94E+03	1.67E+04	1.74E+03	2.70E+05	1.54E+05	4.91E+03	7.27E+03	2.44E+04	2.55E+05	1.42E+04
P48047 ATPO	VAAVSLNPYVK	580.84	87.97	7.94E+05	1.78E+04	1.04E+04	1.07E+06	9.39E+03	3.73E+03	6.81E+03	1.11E+03	1.32E+03	6.71E+02	6.18E+05	1.65E+04	3.88E+05	1.17E+03	8.68E+05
P36957 ODO2	TPAFAESVTEGDVR	739.86	88.1	4.81E+05	2.06E+04	1.20E+03	5.39E+05	1.07E+04	1.22E+03	2.76E+03	1.48E+04	1.70E+04	7.31E+03	3.82E+05	6.57E+02	3.73E+05	2.15E+04	5.00E+05
P55809 SCOT1	FYTDPVEAVK	584.80	88.2	1.48E+03	2.06E+03	3.90E+03	2.51E+03	8.15E+02	5.21E+03	1.10E+03	1.78E+03	8.40E+04	1.35E+05	1.59E+03	7.31E+02	1.63E+03	7.39E+04	4.31E+03
P48047 ATPO	LVRPPVQVY	535.82	88.48	2.63E+05	1.23E+04	4.06E+03	2.62E+05	5.97E+02	3.32E+03	3.09E+03	6.71E+03	1.20E+03	1.73E+03	1.51E+05	9.95E+02	9.46E+04	8.68E+02	5.90E+03
P10515 ODP2	DIDSFVPSK	504.26	88.54	1.40E+03	1.99E+03	1.75E+03	2.09E+03	1.73E+03	7.34E+02	3.14E+03	2.05E+03	8.24E+04	1.02E+05	1.30E+04	2.71E+03	9.48E+03	5.34E+04	1.28E+03
P42765 THIM	VLQSSSDAIYLAR	711.88	88.71	6.08E+02	1.53E+03	1.57E+03	1.45E+05	5.92E+03	4.26E+02	6.18E+02	1.71E+03	5.91E+02	2.67E+03	1.28E+05	2.22E+03	2.43E+04	3.20E+02	1.28E+03
Q14894 CRYM	SLGMAVEDTVAAK	646.33	88.98	1.37E+03	8.07E+03	5.19E+02	1.06E+05	7.17E+03	3.63E+04	4.75E+02	4.87E+04	2.97E+03	5.94E+02	3.68E+04	3.02E+04	3.38E+03	9.33E+03	5.11E+05
P01009 A1AT	TEEEDFHVDQVTTVK	631.29	88.98	2.03E+03	1.84E+03	2.88E+03	2.75E+03	1.16E+03	1.30E+03	1.74E+03	6.42E+02	1.80E+04	1.06E+05	1.05E+03	2.17E+03	2.68E+03	2.36E+04	6.99E+02
P09972 ALDOC	GILAADESVGSMK	674.84	89.09	1.37E+05	1.86E+03	1.23E+03	2.75E+05	1.45E+03	1.62E+03	1.47E+03	6.01E+04	8.36E+02	1.36E+03	1.68E+05	5.11E+03	1.16E+05	3.14E+02	1.26E+05
P13073 COX41	ASWSSLSMDEK	620.78	89.25	9.65E+03	5.65E+03	6.01E+03	3.29E+05	1.17E+04	8.53E+03	1.38E+03	1.07E+04	1.03E+03	2.77E+03	1.68E+05	1.39E+04	4.41E+04	3.15E+03	2.88E+05
Q01813 K6PP	DLQSNVEHLTEK	706.85	89.33	1.43E+03	1.49E+04	3.85E+02	6.69E+02	4.04E+04	5.18E+04	2.67E+03	1.04E+03	2.42E+03	8.49E+02	2.54E+03	8.29E+02	7.33E+02	4.88E+02	3.36E+03
P55290 CAD13	YEVSSPYFK	560.27	89.36	1.59E+03	1.95E+03	2.97E+03	8.07E+04	4.65E+03	7.53E+03	1.59E+03	8.79E+02	2.11E+03	1.17E+03	4.81E+04	2.64E+03	5.26E+04	5.78E+02	1.03E+05
P30086 PEBP1	NRPTSISWDGLDSGK	544.94	89.56	1.23E+05	8.00E+02	1.94E+03	2.43E+04	1.41E+03	1.60E+03	2.31E+03	3.74E+03	9.00E+03	3.84E+04	9.61E+03	4.12E+02	1.06E+03	6.09E+03	7.77E+03
Q16795 NDUA9	MGSQVPIPYR	582.31	89.82	1.27E+03	1.67E+05	1.31E+03	1.07E+05	1.36E+05	2.92E+03	2.58E+04	8.68E+04	5.42E+04	8.05E+04	7.20E+04	2.89E+03	1.03E+05	2.45E+04	1.51E+05
P11310 ACADM	IYQIYEGTSQIQR	799.91	89.86	2.44E+02	9.17E+02	4.24E+04	5.37E+04	8.43E+04	6.69E+02	7.71E+04	4.96E+03	1.85E+03	2.97E+03	4.96E+04	1.15E+03	8.05E+03	1.78E+03	1.02E+05
Q16698 DECR	VAFITGGGTGLGK	589.33	89.93	6.61E+05	4.73E+03	8.87E+02	2.34E+03	3.86E+03	2.79E+03	3.91E+03	6.26E+05	8.17E+02	6.06E+02	4.32E+05	1.35E+03	2.54E+05	9.75E+02	1.25E+04
P36957 ODO2	GIFDRPVAIGGK	615.35	89.94	1.01E+04	7.12E+04	2.34E+04	2.22E+04	8.24E+03	5.28E+04	2.87E+03	1.94E+03	3.15E+03	9.28E+02	1.02E+03	7.36E+04	6.06E+04	1.01E+03	3.88E+04
Q16555 DPYL2	MVIPGGIDVHTR	432.23	89.97	3.08E+03	1.34E+04	1.15E+03	4.67E+04	1.46E+05	2.77E+03	4.79E+04	3.05E+05	2.13E+04	6.72E+05	1.06E+04	5.23E+03	2.01E+03	2.66E+04	1.54E+05
P10809 CH60	LVQDVANNTNEEAGDGT	854.09	90.07	5.40E+04	5.07E+02	2.14E+02	1.60E+04	1.64E+03	5.24E+02	6.56E+02	9.90E+02	5.28E+02	7.19E+02	1.55E+03	5.29E+02	8.62E+02	3.27E+02	9.80E+02
P55809 SCOT1	MVSSYVGENAEFER	809.37	90.07	2.82E+03	3.41E+03	2.78E+02	5.72E+03	2.81E+03	5.96E+03	2.88E+02	3.24E+03	6.07E+04	4.81E+04	1.59E+03	1.24E+03	1.01E+04	1.07E+04	1.07E+03
Q14894 CRYM	LIYDSWSSGK	578.29	90.08	9.59E+02	1.30E+03	5.91E+02	4.51E+04	8.57E+03	5.78E+02	9.53E+03	7.07E+03	2.45E+03	1.37E+03	8.92E+03	9.24E+02	6.54E+03	5.07E+03	6.92E+04
O15061-2 SYNEM	EALGLEQLR	514.79	90.33	3.79E+05	5.43E+04	6.33E+02	1.07E+05	4.26E+05	1.81E+04	4.59E+02	5.55E+02	4.83E+05	1.92E+03	3.27E+05	1.92E+03	2.07E+05	3.49E+05	9.68E+04
P48047 ATPO	SFLSQGVLLK	553.81	90.42	3.01E+05	1.97E+05	3.10E+05	2.04E+04	4.40E+05	3.24E+05	1.67E+05	1.30E+04	5.75E+02	7.95E+02	1.87E+05	2.70E+05	5.67E+04	4.67E+02	2.86E+05
Q99878 H2A1J	NDEELNKLLGK	636.84	90.47	7.14E+02	4.95E+03	3.50E+03	1.68E+04	1.26E+05	1.49E+04	2.02E+03	6.02E+03	1.00E+03	5.99E+03	1.77E+03	4.48E+02	1.21E+03	4.06E+02	2.59E+04
P49821 NDUV1	LLEGCLVGGR	508.78	90.53	4.40E+02	1.86E+04	1.30E+03	1.18E+05	6.59E+04	7.47E+04	3.92E+03	1.65E+03	1.88E+03	2.81E+04	1.74E+04	3.15E+04	6.85E+03	2.66E+03	1.14E+05
Q16555 DPYL2	VFNLYPR	454.76	90.56	2.89E+03	3.51E+03	2.56E+05	5.78E+02	4.16E+02	3.22E+03	1.46E+02	7.72E+04	2.11E+05	1.72E+05	6.33E+03	5.31E+03	6.80E+02	1.19E+05	2.21E+03
Q13011 ECH1	YQETFNVIER	649.82	90.86	1.95E+05	1.96E+04	1.55E+04	2.25E+04	1.04E+04	1.67E+04	2.13E+03	7.65E+02	1.44E+03	2.69E+02	6.81E+04	1.39E+03	3.29E+04	2.67E+03	4.02E+04
Q6NZI2 PTRF	KLEVNEAELLR	657.37	91.16	1.07E+04	9.76E+03	5.59E+03	9.02E+02	5.76E+02	7.16E+02	8.52E+03	1.25E+03	7.73E+04	7.87E+04	4.78E+02	6.00E+02	6.27E+02	4.37E+04	1.34E+03
P55809 SCOT1	GMGGAMDLVSSAK	612.29	91.24	7.87E+02	4.67E+03	2.59E+03	4.51E+03	4.53E+03	1.77E+03	1.15E+03	1.68E+03	1.31E+03	1.76E+03	1.09E+05	9.84E+03	1.85E+04	2.09E+03	1.28E+03
P13637 AT1A3	IATLASGLEVGK	579.84	91.27	5.95E+04	7.09E+02	3.21E+02	7.20E+03	2.47E+03	9.45E+02	1.15E+03	4.62E+03	2.92E+03	1.74E+03	3.81E+03	1.60E+03	7.07E+02	9.77E+02	3.52E+03
Q16836-2 HCDH	TLSTIATSTDAASVVH	787.41	91.34	1.79E+05	1.34E+04	2.19E+03	3.32E+05	1.92E+05	3.00E+03	6.12E+03	6.56E+03	1.84E+03	9.70E+02	1.08E+05	4.39E+03	1.83E+05	2.51E+03	2.99E+05
Q99878 H2A1J	VTIAQGGVLPN	534.81	91.4	4.15E+05	1.64E+04	8.32E+03	3.83E+05	1.79E+04	3.16E+04	2.02E+04	4.43E+04	1.47E+03	1.24E+03	1.90E+05	4.89E+03	2.38E+05	1.60E+03	3.21E+05
P31040 DHSA	VPIKPNAGEESVMNLDK	646.67	91.41	3.55E+03	4.96E+03	3.17E+03	4.63E+04	4.99E+04	9.86E+03	1.04E+04	6.67E+03	3.42E+03	1.53E+03	3.38E+04	1.08E+04	1.12E+04	1.13E+03	7.95E+04
P35579 MYH9	ELQAQIAELK	571.81	91.52	1.75E+03	1.24E+04	2.96E+04	3.45E+03	7.45E+03	2.46E+03	1.21E+03	1.21E+03	2.92E+06	5.89E+03	1.20E+03	5.41E+03	1.33E+03	2.87E+06	8.55E+03
Q05639 EF1A2	SGDAIVEMVPGK	637.33	91.6	8.26E+04	3.24E+04	3.70E+03	5.04E+03	3.82E+03	5.00E+03	2.52E+03	5.13E+04	1.03E+04	8.85E+02	8.67E+04	8.33E+02	8.25E+03	6.05E+03	1.44E+03
P36542 ATPG	EVMLVGIGDK	530.79	91.71	4.46E+02	2.49E+05	1.62E+06	1.65E+05	2.02E+05	4.42E+04	2.38E+04	1.52E+06	9.91E+03	5.73E+03	1.58E+05	2.70E+05	2.57E+03	1.43E+04	1.99E+05
Q96199 SUCB2	INFDDNAEFR	6																



P63316 TNNC1	MLGQNPTPEELQE	743.35	92.42	2.50E+05	9.21E+03	2.19E+03	1.13E+05	4.38E+03	1.38E+03	8.94E+02	3.00E+03	5.86E+02	8.88E+02	5.99E+04	2.30E+04	1.14E+03	5.20E+03	2.71E+03
P48047 ATPO	LVRPPVQVYGIEGR	528.31	92.44	4.23E+04	1.15E+04	1.73E+05	1.17E+06	1.02E+06	5.96E+04	1.68E+04	1.33E+05	2.28E+03	8.30E+03	7.47E+05	1.15E+04	3.51E+05	1.24E+03	1.04E+06
P48047 ATPO	VAASVLNPNY	467.26	92.52	2.34E+05	3.07E+03	3.46E+06	6.41E+04	5.85E+03	1.61E+03	1.90E+06	3.65E+06	1.89E+03	2.12E+03	1.92E+05	1.35E+06	7.36E+03	4.32E+02	9.26E+03
P49411 EFTU	TVVTGIEMFHK	421.23	92.57	1.65E+03	5.41E+02	3.98E+03	1.22E+03	2.55E+04	1.13E+03	9.84E+02	1.74E+03	1.29E+03	4.26E+03	1.48E+05	1.15E+03	8.86E+04	8.02E+02	2.39E+04
P00403 COX2	MMITSQDVLH	587.78	92.58	5.74E+02	5.89E+03	1.81E+03	1.05E+05	2.42E+04	7.36E+03	1.03E+04	3.85E+02	1.16E+03	4.58E+02	2.34E+03	5.59E+03	1.54E+03	3.94E+02	7.21E+04
P20674 COX5A	NKPDIDAWELR	452.90	92.71	3.43E+03	2.51E+04	9.02E+02	4.36E+04	2.09E+04	8.78E+03	4.65E+02	7.04E+02	8.22E+02	4.45E+02	1.62E+05	8.64E+03	7.04E+04	5.08E+02	1.57E+04
P14543-2 NID1	QDLGSPEGIAVDHLGR	555.29	92.93	1.36E+03	6.00E+02	7.90E+03	2.58E+04	3.85E+04	4.88E+03	5.04E+02	2.52E+04	4.19E+03	3.78E+03	8.57E+04	2.56E+03	4.32E+04	1.26E+03	2.11E+04
P42126 D3D2	SLQMYLER	520.27	92.94	3.77E+04	7.04E+03	1.33E+03	2.50E+04	5.43E+04	7.28E+02	2.11E+03	5.92E+03	1.94E+04	7.52E+03	2.06E+05	1.20E+04	1.02E+05	1.17E+04	1.46E+04
P11217 PYGM	GLAGVENVTELK	615.34	92.97	6.00E+04	1.84E+05	1.96E+03	2.68E+05	5.63E+03	4.77E+03	1.62E+03	1.16E+03	1.72E+03	1.05E+04	8.96E+04	5.86E+04	2.00E+03	2.78E+03	1.97E+05
Q9BX66-11 SRBS	DISPEEIDLK	579.80	93.38	1.93E+03	1.55E+03	1.78E+03	4.30E+04	1.98E+04	8.83E+02	9.91E+02	9.74E+02	9.57E+02	6.79E+03	6.72E+03	1.24E+04	4.71E+04	6.32E+03	2.27E+04
Q16836-2 HCDH	FAAEHTIF	468.23	93.52	9.58E+04	8.89E+02	2.28E+03	9.17E+02	1.12E+03	2.82E+03	4.15E+02	3.63E+02	7.65E+02	1.40E+03	9.28E+02	8.95E+02	4.09E+03	4.17E+03	3.85E+03
P55809 SCOT1	LMPMQQIAN	523.26	93.52	2.81E+04	3.29E+03	7.87E+02	4.50E+03	2.94E+03	3.49E+03	2.39E+03	1.60E+04	2.33E+04	1.08E+05	6.47E+04	2.69E+03	1.57E+03	5.55E+04	2.17E+03
P01023 A2MG	VGFYESDVMGR	630.29	93.71	1.13E+03	2.79E+04	2.79E+04	2.36E+04	6.33E+04	3.92E+04	1.12E+04	2.21E+04	4.19E+03	1.04E+03	1.16E+04	9.51E+03	6.35E+03	1.04E+03	1.91E+04
P11310 ACADM	ENVLIGDGAGFK	610.32	93.85	1.19E+05	1.68E+03	1.46E+03	1.22E+04	6.71E+03	1.76E+03	6.94E+02	1.93E+03	8.79E+02	3.45E+03	1.56E+04	1.94E+03	1.43E+03	1.39E+03	2.82E+03
P19022 CADH2	GPFQELVLR	521.79	93.88	1.25E+05	2.21E+04	1.49E+03	8.46E+04	4.48E+04	5.34E+03	1.05E+03	2.14E+03	2.21E+03	8.21E+03	5.02E+04	1.04E+04	7.55E+04	1.52E+06	3.94E+04
P15259 PGAM2	ELKPTKPMQFLGDEETVR	530.28	93.98	2.79E+03	2.23E+03	1.40E+03	1.82E+05	7.36E+04	1.55E+03	3.75E+03	4.00E+03	2.09E+04	3.09E+03	7.98E+02	4.15E+03	1.14E+04	6.32E+04	
P38117-2 ETFB	LPAVVVTADLR	527.82	94.21	6.22E+05	5.40E+02	1.23E+03	3.00E+05	6.69E+03	1.44E+03	5.02E+03	4.67E+02	1.82E+03	1.66E+03	3.07E+05	1.43E+03	1.15E+05	1.04E+03	3.47E+03
P12110 CO6A2	VFAVVITDGR	538.81	94.45	8.04E+02	5.56E+03	1.52E+04	1.61E+05	1.49E+05	7.57E+03	9.29E+03	6.35E+03	2.28E+04	1.13E+05	6.42E+03	7.30E+03	2.25E+04	4.84E+04	1.14E+05
Q9Y4G6 TLN2	ALSDLISATK	509.79	94.69	4.69E+02	3.48E+03	3.82E+03	3.88E+04	3.80E+04	2.02E+03	1.42E+03	1.02E+03	2.84E+03	2.96E+03	3.31E+03	2.93E+03	8.71E+02	2.87E+04	4.38E+04
P00568 KAD1	IIFVVGPGSGK	565.83	94.71	1.57E+05	3.70E+03	8.87E+03	1.02E+04	2.71E+03	5.09E+02	2.35E+02	3.80E+03	2.33E+04	1.24E+03	1.12E+05	2.81E+03	8.53E+03	3.26E+04	8.63E+02
Q01813 K6PP	LLEEIATQMR	627.31	94.74	3.80E+03	2.24E+04	3.13E+03	9.55E+02	2.25E+03	1.66E+03	6.96E+03	1.25E+03	3.92E+04	9.15E+03	2.65E+03	1.15E+03	4.34E+03	1.16E+04	1.85E+03
P01009 A1AT	LQHLENELTHDIITK	601.99	94.89	8.93E+04	6.47E+03	1.96E+03	3.53E+03	2.25E+03	4.48E+03	5.30E+03	3.37E+03	3.60E+03	1.46E+05	4.16E+02	1.46E+03	1.75E+03	8.32E+02	1.88E+03
P08133 ANXA6	SLEDALSSDTSGHFR	541.25	95.01	6.63E+04	2.01E+03	1.71E+03	6.59E+03	4.74E+03	2.76E+03	4.72E+04	6.12E+04	3.30E+03	1.43E+03	7.98E+04	1.36E+03	4.81E+03	8.42E+02	1.29E+03
P42126 D3D2	VLVEPDAGAGVAVMK	728.40	95.06	2.86E+05	8.89E+03	1.98E+04	3.28E+05	4.07E+05	4.72E+03	1.42E+04	2.68E+03	1.41E+04	2.43E+04	1.49E+05	1.48E+04	8.31E+04	1.20E+03	2.99E+05
P36871 PGM1	ADNFEYSDPVDGSISR	886.39	95.14	6.80E+02	2.73E+03	6.31E+02	4.77E+04	5.51E+02	3.39E+03	2.91E+03	8.10E+03	1.96E+03	2.38E+03	4.27E+04	2.98E+03	2.93E+03	2.80E+03	3.17E+04
P49753 ACOT2	YRADTLGELDLER	517.27	95.45	1.08E+03	5.73E+03	3.27E+03	3.28E+03	6.04E+03	4.27E+03	1.40E+04	7.86E+03	2.94E+05	5.86E+04	3.29E+03	1.95E+03	1.88E+02	1.51E+05	4.32E+03
P49753 ACOT2	GPGVGLLQISK	499.30	95.74	2.07E+05	1.14E+03	1.48E+03	2.42E+03	9.01E+02	1.48E+03	2.43E+03	3.18E+03	2.66E+03	1.34E+03	1.62E+05	2.68E+03	7.78E+03	4.14E+03	7.99E+02
P30041 PRDX6	LSILYPATTGR	596.34	95.74	3.15E+03	2.48E+03	2.23E+04	1.49E+04	4.85E+03	2.24E+03	9.25E+02	1.82E+04	4.24E+03	1.57E+04	8.45E+03	1.30E+03	7.48E+03	1.11E+03	1.30E+03
P36542 ATPG	THSDQFLVAFK	646.83	95.87	9.77E+04	1.04E+04	2.62E+03	1.41E+03	1.97E+03	1.02E+04	8.70E+02	6.13E+03	3.16E+02	5.32E+03	1.03E+03	6.38E+03	1.37E+03	1.20E+03	2.12E+03
P12110 CO6A2	NFVINVVNR	537.81	95.97	3.43E+03	1.95E+04	5.78E+04	8.73E+04	2.42E+05	1.81E+04	9.62E+02	1.27E+03	3.95E+04	4.75E+04	8.80E+04	7.01E+04	8.70E+03	2.63E+04	1.22E+05
Q86TD4 SRCA	TIEGIVMAADSAR	667.34	96	1.60E+03	7.73E+03	1.18E+05	3.62E+03	8.89E+04	5.84E+04	1.57E+03	1.10E+04	1.56E+04	1.63E+04	9.57E+02	1.35E+03	1.62E+03	1.71E+04	2.00E+03
P07108 ACBP	PGMLDFTGK	483.24	96.29	1.74E+05	4.89E+02	8.23E+02	4.31E+02	2.41E+03	1.30E+03	1.32E+03	1.89E+03	3.06E+05	2.87E+05	1.23E+04	1.83E+03	1.49E+03	2.69E+05	1.92E+03
Q15124 PGM5	VPVYETPAGWR	637.84	96.4	4.06E+04	4.65E+03	1.50E+03	1.53E+03	6.38E+03	5.40E+02	2.27E+03	1.43E+03	3.47E+06	2.83E+06	3.55E+03	4.76E+03	1.11E+04	4.92E+06	5.27E+03
Q14894 CRYM	EAVLYVDSQEAALK	768.40	96.41	1.85E+03	1.90E+04	1.83E+04	1.09E+05	1.63E+04	7.08E+03	3.73E+05	4.64E+05	8.12E+03	1.26E+04	1.86E+04	2.40E+03	2.39E+04	2.43E+03	6.76E+03
P07355-2 ANXA2	DALNIETAIK	544.30	96.46	1.15E+03	4.14E+04	1.61E+03	1.16E+05	1.41E+05	7.00E+04	1.27E+04	6.69E+03	1.54E+04	4.81E+03	5.53E+02	1.33E+04	9.03E+03	5.27E+03	4.56E+04
Q75746 CMC1	LTLADIER	465.77	96.46	2.25E+04	4.80E+03	1.61E+04	2.65E+03	1.58E+03	1.46E+03	3.43E+03	9.76E+04	3.10E+05	2.84E+05	7.36E+02	3.14E+03	2.23E+03	2.44E+05	7.19E+03
Q562R1 ACTBL	VAPDEHPILLTEAPLNPK	652.03	96.52	4.33E+03	1.30E+06	1.77E+04	2.15E+06	1.75E+06	2.54E+04	5.64E+03	3.96E+03	4.34E+03	6.67E+02	2.81E+03	1.13E+06	8.12E+05	3.11E+02	1.98E+06
O15061-2 SYNEM	EVVYIGEDSTIAR	774.90	96.7	2.65E+03	1.63E+03	7.34E+03	3.32E+04	6.58E+02	4.31E+03	1.96E+02	1.21E+03	5.53E+02	2.26E+03	4.30E+04	3.13E+03	9.40E+03	8.03E+02	1.30E+04
P06744 G6PI	FLAQTEALMR	590.32	96.71	3.13E+04	3.00E+04	5.21E+03	6.77E+04	2.93E+04	2.52E+04	5.83E+02	1.85E+03	5.80E+04	1.68E+03	1.55E+03	1.69E+04	6.68E+03	2.25E+04	1.14E+04
P12277 KCRB	FPAEDEFDLSAHNNHMAK	543.25	96.85	8.96E+03	2.78E+02	2.01E+03	1.80E+03	3.52E+02	3.80E+03	1.90E+03	1.10E+03	1.99E+04	9.19E+03	3.11E+03	8.06E+02	2.62E+03	1.09E+04	4.59E+03
P07954 FUMH	AIEMLGELGSK	602.82	96.92	3.67E+03	7.26E+04	2.21E+04	5.22E+05	1.46E+05	1.93E+04	1.30E+04	5.03E+03	1.58E+04	4.09E+03	2.18E+05	1.99E+05	2.73E+05	1.70E+04	2.00E+04
P23327 SRCH	AEVGAPLSPDHSEEEEEEE GLEEDEPR	1046.44	96.97	5.78E+03	7.13E+03	9.21E+03	2.04E+02	1.22E+04	7.76E+03	5.36E+03	1.84E+04	1.21E+02	6.71E+02	3.44E+04	2.20E+03	1.42E+04	3.71E+02	8.37E+04
P07355-2 ANXA2	DIISDTSGDFR	613.29	97.14	6.13E+02	2.10E+03	2.77E+03	2.87E+05	3.36E+03	3.22E+03	2.38E+03	1.86E+03	3.38E+03	5.22E+03	1.35E+05	1.79E+03	5.80E+03	1.70E+03	1.45E+04
P11310 ACADM	EEIIPVAAEYDK	688.85	97.19	9.24E+03	1.94E+04	1.13E+03	3.87E+05	5.19E+03	2.95E+03	3.30E+03	2.30E+03	1.39E+03	8.89E+02	3.53E+05	3.06E+03	1.92E+05	2.32E+03	5.33E+05
Q06830 PRDX1	LVQAFQFTDK	598.82	97.2	4.56E+02	1.38E+04	1.92E+03	7.14E+04	1.75E+05	5.56E+03	8.35E+02	3.00E+03	3.71E+02	4.28E+02	1.26E+03	3.72E+04	1.01E+03	6.04E+03	1.78E+05
P02675 FIBB	IRPFPQ	452.75	97.23	6.34E+02	7.30E+03	6.70E+04	1.19E+03	1.88E+03	6.42E+04	5.32E+03	4.65E+04	4.72E+04	5.23E+05	1.98E+03	1.60E+04	2.65E+03	1.23E+04	4.18E+03
P36957 ODO2	GLVVPVIR	426.79	97.3	1.68E+03	4.16E+03	2.54E+03	6.54E+03	4.51E+03	8.89E+03	2.02E+03	2.93E+03	6.79E+05	5.87E+05	1.81E+03	1.99E+03	7.32E+03	6.72E+05	5.55E+03
P21980 TGM2	DLYLENPEIK	617.32	97.36	2.33E+03	1.62E+03	9.93E+03	1.94E+05	1.42E+05	1.91E+03	2.03E+04	2.55E+04	2.14E+04	6.80E+03	1.70E+05	1.43E+05	2.41E+04	1.60E+04	1.62E+05
Q75746 CMC1	LTVNDFVR	482.26	97.4	4.81E+03	2.64E+05	1.30E+04	4.03E+05	1.08E+05	2.87E+05	3.34E+03	8.17E+03	3.32E+03	8.22E+03	3.13E+04	2.75E+05	4.26E+04	6.38E+03	3.16E+05
P07237 PDIA1	LITLEEEMTK	603.82	97.43	1.52E+05	8.96E+04	1.02E+03	1.40E+04	9.90E+04	1.27E+05	2.26E+02	1.38E+03	2.56E+03	2.04E+03	2.56E+04	6.84E+04	1.57E+04	1.50E+03	3.06E+04
P36542 ATPG	TEEKPIFSLN	589.31																

P67936 TPM4	ERREKAEGDVAALNRRRIQL VEEELDRAQER	596.64	98.31	1.12E+03	2.97E+03	6.70E+02	7.14E+03	2.21E+03	3.18E+03	4.46E+02	6.97E+03	2.28E+03	2.58E+03	2.12E+03	1.03E+03	2.52E+05	4.00E+03	1.25E+03
P06744 G6PI	VWYVSNIDGTHIAK	534.95	98.41	1.50E+03	3.11E+03	2.38E+03	1.17E+05	1.38E+03	2.90E+03	5.96E+04	3.00E+04	5.50E+02	5.14E+03	1.18E+05	1.97E+04	1.70E+04	1.61E+03	4.02E+03
P12109 CO6A1	VPSYQALLR	523.80	98.41	2.66E+04	3.58E+04	1.72E+04	4.34E+05	4.62E+05	1.43E+04	4.69E+03	5.48E+03	3.69E+03	1.43E+03	1.35E+05	4.33E+03	2.57E+05	1.28E+03	1.66E+05
P09972 ALDOC	ALQASALNAWR	600.83	98.48	9.43E+04	1.31E+04	2.02E+03	8.99E+03	5.63E+03	1.24E+03	7.75E+02	7.14E+02	4.83E+03	2.09E+03	1.78E+05	4.63E+03	6.57E+03	1.09E+03	7.19E+03
P11310 ACADM	TGEYVPVPLIR	572.82	98.68	2.16E+05	1.73E+03	2.00E+03	3.05E+03	3.35E+03	5.46E+02	1.37E+03	4.56E+03	2.33E+04	3.00E+04	2.65E+05	4.26E+02	6.43E+03	7.53E+04	7.01E+02
Q13011 ECH1	MSMLQTQDLVK	647.33	98.8	2.14E+03	1.96E+03	1.48E+03	1.87E+03	3.81E+03	2.65E+04	2.10E+03	2.49E+03	3.41E+03	3.13E+03	1.35E+03	1.76E+03	9.38E+03	1.85E+03	4.50E+04
P48047 ATPO	LINLLAENGR	556.82	98.87	1.34E+03	1.60E+05	4.47E+03	1.04E+05	1.38E+03	1.58E+05	8.38E+02	6.59E+03	3.35E+02	1.69E+02	8.21E+02	9.14E+03	4.89E+02	1.11E+03	8.33E+04
P47985 UCRI	SGPFAPVLSATSR	645.35	98.97	2.21E+05	2.47E+03	5.53E+04	3.31E+05	5.94E+04	5.64E+05	5.04E+04	9.56E+04	1.37E+03	2.85E+03	2.37E+05	8.55E+04	2.26E+05	5.87E+02	2.36E+05
P49753 ACOT2	ADTLGELDLER	616.31	99.04	2.28E+05	2.41E+04	5.76E+03	4.52E+05	1.43E+04	1.35E+02	2.08E+03	3.56E+04	1.49E+03	2.70E+02	2.15E+05	2.39E+04	2.28E+04	2.07E+03	4.56E+05
P00367 DHE3	HGGTIPVPTAEFQDR	579.97	99.32	9.19E+04	1.97E+03	2.82E+03	3.21E+03	1.38E+03	7.14E+02	8.92E+04	3.00E+04	2.49E+04	3.46E+04	7.81E+03	6.28E+02	6.57E+02	7.13E+03	4.28E+02
P15259 PGAM2	YAGLKPGELPTCESLK	569.30	99.35	8.61E+02	8.90E+02	1.67E+03	4.96E+04	1.25E+03	2.40E+04	1.13E+04	4.77E+03	8.81E+02	9.77E+02	1.07E+05	8.24E+03	1.77E+04	1.65E+04	1.32E+03
P12277 KCRB	LEQQQAIDDLMPAQK	828.92	99.37	1.15E+03	4.89E+03	3.77E+03	5.27E+04	3.07E+03	1.80E+03	3.17E+03	7.93E+02	3.36E+02	3.98E+02	3.14E+03	2.07E+03	2.67E+03	2.13E+03	3.99E+04
Q05639 EF1A2	YYITIADPGRH	709.87	99.45	4.61E+03	3.05E+03	6.24E+02	6.56E+03	7.99E+03	7.74E+02	1.50E+03	6.52E+02	1.95E+04	7.67E+02	1.50E+04	8.96E+02	5.66E+02	2.64E+04	1.95E+04
P07954 FUMH	IYELAAGGTAVGTGLNTR	882.47	99.45	3.62E+02	6.60E+03	1.49E+04	6.24E+04	5.79E+03	3.54E+03	9.28E+02	2.64E+03	3.42E+03	1.29E+03	6.34E+04	7.55E+03	1.07E+04	2.48E+03	5.76E+03
Q13011 ECH1	MMADEALGSGLVSR	718.85	99.63	4.31E+05	3.53E+03	6.95E+02	3.96E+05	2.21E+03	4.26E+02	1.56E+02	1.42E+03	1.89E+03	8.65E+02	2.43E+05	3.54E+03	4.14E+03	6.27E+02	5.88E+03
P30041 PRDX6	DFTPVCTTELGR	669.82	99.68	1.98E+05	3.96E+02	1.10E+04	2.65E+05	1.15E+04	1.87E+04	1.96E+03	3.13E+03	1.57E+03	2.81E+03	2.34E+05	2.04E+03	2.55E+04	6.68E+03	8.93E+02
P12277 KCRB	LNPDLNQGDDLDPNYVLS SR	769.36	99.71	1.91E+06	4.97E+03	2.20E+03	2.16E+06	1.02E+04	2.24E+06	2.14E+02	2.15E+03	3.41E+05	3.16E+05	1.80E+06	3.12E+03	1.91E+05	4.66E+05	1.74E+06
P19404 NDUV2	NSDSILEAIQK	609.32	99.8	1.13E+05	2.05E+03	9.36E+02	1.17E+03	2.32E+04	1.08E+04	1.01E+05	1.55E+05	2.31E+03	2.77E+02	2.13E+03	1.66E+03	4.49E+03	8.74E+02	7.33E+02
P20674 COX5A	TLVITYDMVPEPK	696.86	100.22	7.07E+04	9.26E+04	3.46E+03	7.94E+04	9.68E+03	6.24E+04	1.38E+03	2.99E+03	1.51E+03	1.15E+03	4.41E+04	1.87E+04	7.48E+04	3.67E+04	1.41E+05
P13804 ETFA	AAVDAGFVPNDMQVGQTG	952.96	100.25	1.02E+05	1.26E+03	1.30E+03	7.69E+04	2.27E+03	7.34E+03	2.04E+02	2.33E+03	1.73E+03	1.30E+03	6.80E+04	6.37E+02	2.36E+03	2.92E+03	6.17E+03
P02675 FIBB	GGETSEMYLIQPDSSVKPY	753.03	100.36	1.34E+03	1.03E+04	2.39E+03	1.34E+03	6.96E+04	5.61E+03	1.10E+03	9.66E+02	7.73E+03	3.94E+03	8.26E+02	1.43E+04	2.58E+03	2.33E+03	8.09E+02
Q9H987 SYP2L	AATTLDEPIWR	636.83	100.39	6.46E+04	5.00E+03	3.40E+03	1.35E+03	1.80E+03	8.12E+03	9.25E+03	5.07E+02	1.52E+04	4.98E+03	2.08E+04	1.09E+03	1.59E+03	1.77E+04	4.79E+02
Q01813 K6PP	ELVVTQLGYDTR	697.37	100.4	2.40E+05	3.32E+04	6.78E+03	2.53E+05	3.73E+04	2.20E+04	7.31E+02	2.06E+03	2.76E+03	2.18E+02	2.30E+05	2.53E+03	2.37E+04	1.70E+03	2.05E+04
Q9H987 SYP2L	FQPGGGAPTAPSIFNR	857.43	100.43	3.06E+03	1.11E+03	2.61E+03	2.80E+03	1.51E+04	8.66E+03	3.91E+04	1.98E+04	1.43E+02	5.20E+02	2.84E+03	1.40E+03	5.51E+02	9.23E+02	1.52E+04
Q6N212 PTRF	LEVNEAELLR	593.33	100.53	2.97E+05	4.11E+03	3.04E+03	4.16E+03	1.43E+03	1.77E+03	1.40E+03	5.08E+02	5.63E+02	9.32E+02	2.50E+05	4.01E+03	8.72E+02	4.22E+03	2.85E+03
Q99497 PARK7	DMVICPDASLEDAK	737.86	100.58	1.05E+05	2.39E+03	4.93E+02	1.07E+05	2.54E+03	1.56E+03	3.17E+02	1.64E+03	2.49E+03	6.13E+03	1.09E+05	2.88E+03	9.58E+02	7.92E+02	5.88E+03
P48047 ATPO	LSNTQGVVSAF	561.79	100.64	1.71E+05	7.65E+05	3.13E+05	9.01E+04	3.81E+04	6.20E+05	1.19E+04	1.08E+03	1.62E+03	3.52E+03	7.71E+04	2.53E+05	8.06E+03	9.19E+03	1.62E+05
P07954 FUMH	IEYDTFGELK	607.80	100.69	4.22E+05	1.25E+03	1.92E+03	1.17E+04	6.98E+02	1.06E+04	3.53E+03	2.65E+04	2.00E+03	5.87E+02	2.59E+05	1.49E+03	2.55E+03	1.98E+03	3.60E+03
P02675 FIBB	TPCTVSCNIPVVSJK	752.88	100.81	7.60E+02	3.32E+03	4.94E+02	4.66E+03	1.88E+03	7.82E+02	1.79E+04	2.01E+03	2.58E+03	1.10E+05	2.33E+03	2.16E+03	1.69E+03	6.72E+03	3.84E+03
Q96199 SUCB2	VMVAEALDISR	602.33	101.07	2.51E+03	1.28E+05	2.61E+05	7.48E+04	2.56E+04	2.58E+05	8.41E+03	8.85E+03	6.98E+03	6.56E+02	1.47E+03	3.60E+04	6.39E+04	8.90E+02	9.26E+04
P42126 D3D2	AVQELWLR	507.79	101.08	7.53E+04	2.99E+04	1.31E+03	1.27E+03	1.29E+05	5.24E+03	1.09E+05	1.84E+05	5.48E+02	1.26E+05	8.17E+04	1.16E+05	7.03E+03	1.97E+03	9.05E+03
P15259 PGAM2	SFDIPPPMDEK	686.83	101.11	1.07E+05	2.28E+04	3.51E+03	3.99E+05	2.82E+04	2.49E+04	5.17E+03	4.74E+03	5.75E+02	1.48E+03	2.25E+05	1.10E+04	2.12E+04	5.77E+03	4.44E+04
P28289 TMOD1	LADLTGPIPK	569.35	101.12	3.70E+02	5.90E+04	8.98E+04	3.26E+02	2.36E+03	7.08E+04	8.16E+02	1.51E+03	2.96E+02	1.17E+03	2.89E+02	3.57E+02	4.05E+02	5.01E+02	2.67E+03
P19022 CADH2	LNGDFAQLNLK	616.83	101.17	1.54E+03	3.28E+04	1.41E+03	1.16E+04	1.06E+04	4.59E+04	2.01E+04	1.47E+04	2.25E+04	1.86E+04	3.02E+03	1.15E+04	1.41E+03	4.94E+02	3.34E+02
P05091 ALDH2	LGPALATGNVVVMK	685.40	101.48	2.48E+04	1.09E+03	1.59E+03	1.01E+04	6.41E+02	7.16E+02	1.66E+03	2.20E+03	5.86E+02	5.35E+02	8.68E+04	1.14E+03	4.19E+03	1.95E+03	2.84E+03
P31937 3HIDH	SPILLGSLAH	504.30	101.64	7.41E+02	1.73E+03	2.53E+05	2.52E+04	5.20E+04	1.22E+05	1.59E+03	1.29E+03	9.92E+02	1.25E+03	6.81E+02	2.44E+05	9.82E+02	4.08E+03	3.30E+04
Q15124 PGM5	FFSNLMDSGR	587.27	101.92	5.64E+04	7.05E+02	7.96E+02	1.06E+05	8.46E+02	3.38E+03	5.64E+03	4.45E+03	1.02E+03	1.11E+03	9.07E+04	1.72E+03	1.23E+03	1.16E+03	2.55E+03
P38646 GRP75	DAGQISGLNVLNR	621.84	102.03	3.26E+05	1.28E+04	9.31E+02	2.98E+05	2.53E+04	1.94E+03	3.56E+03	3.23E+02	1.02E+03	9.81E+02	2.43E+05	5.13E+03	6.29E+02	8.93E+02	2.07E+04
P12109 CO6A1	HLGVKVFSVAITPDHLEPR	527.79	102.1	2.85E+04	2.14E+04	5.88E+03	2.18E+05	4.47E+04	3.67E+03	9.60E+02	6.48E+02	1.34E+04	4.48E+03	7.05E+03	1.33E+04	1.12E+05	6.40E+04	2.10E+05
P13533 MYH6	PEGQFIDSRKGTCKLLSLDI DHNQYK	519.93	102.19	4.73E+04	1.97E+04	5.27E+03	1.11E+04	5.14E+03	2.57E+03	8.19E+03	1.39E+04	3.31E+05	1.74E+05	2.14E+05	4.21E+03	1.74E+03	2.91E+05	2.85E+03
P00568 KAD1	ATEPVIAFYEK	634.33	102.37	6.33E+03	3.66E+03	2.05E+03	8.43E+03	1.29E+03	5.91E+02	1.30E+03	6.42E+02	8.07E+04	1.31E+05	9.03E+03	2.76E+03	1.75E+03	2.19E+05	3.64E+03
P12109 CO6A1	VFSVAITPDHLEPR	527.62	102.38	2.12E+05	3.76E+03	8.36E+03	2.27E+05	5.24E+03	3.70E+03	2.01E+03	5.93E+03	3.42E+03	1.64E+03	1.63E+05	1.00E+03	5.26E+03	5.07E+02	5.90E+03
Q9UKX3 MYH13	LQVEEDKVNGLIKINAKLE QQTDDLEGSLEQEK	626.33	102.47	1.74E+04	1.74E+03	3.07E+03	8.79E+03	2.14E+03	1.42E+03	1.85E+03	3.06E+03	2.03E+03	7.21E+02	3.16E+03	8.63E+02	1.45E+03	3.72E+04	5.00E+03
Q9UKX3 MYH13	LEQQTDDLEGSLEQEK	621.30	102.49	9.98E+05	2.18E+04	9.57E+03	1.27E+06	7.88E+04	1.35E+04	6.21E+02	1.16E+03	4.59E+02	1.08E+03	1.52E+06	9.94E+04	1.76E+05	3.54E+02	6.82E+04
P21980 TGM2	TVEIPDPVEAGEEVK	806.41	102.56	2.14E+03	2.72E+04	2.14E+04	7.00E+03	1.20E+05	1.96E+05	6.93E+03	1.13E+04	9.48E+03	2.76E+03	2.90E+03	3.27E+04	5.29E+03	5.11E+02	3.73E+04
Q16698 DECR	IVINNAAGNFISPTER	858.46	102.65	2.76E+05	2.85E+03	4.42E+02	2.23E+05	4.68E+02	8.32E+02	9.08E+02	6.40E+02	8.57E+03	8.65E+02	9.12E+04	1.01E+03	5.77E+04	1.37E+02	3.05E+03
P01009 A1AT	SVLGQLGITK	508.31	102.66	2.09E+02	1.76E+03	8.05E+02	3.28E+05	1.45E+04	9.77E+03	2.13E+03	1.72E+03	2.02E+03	3.67E+03	2.23E+03	9.37E+03	2.42E+05	3.14E+03	3.18E+05
Q9BX66-11 SRBS	ASPSLSLPH	554.80	102.68	1.57E+03	2.17E+04	3.13E+04	1.40E+03	3.51E+02	8.61E+04	4.63E+03	4.38E+03	3.38E+03	4.44E+03	1.85E+04	9.35E+02	3.96E+03	8.72E+02	1.94E+03
P13533 MYH6	PNERKAPGVMDNPLVMHQ LR	575.29	102.96	1.18E+03	1.50E+06	1.99E+04	2.75E+03	3.82E+05	9.69E+03	1.75E+06	2.31E+06	1.09E+04	5.91E+03	4.16E+02	2.00E+06	1.46E+03	9.45E+03	3.90E+05
P07355-2 ANXA2	TDLEKDIISDTSGDFRK	647.33	103.03	2.52E+04	5.00E+02	8.51E+03	2.80E+03	1.50E+04	1.45E+03	2.26E+03	3.42E+03	1.86E+0						

P38117-2 ETFB	VDLVLLGK	428.78	103.48	3.11E+05	1.72E+03	2.38E+03	7.25E+03	4.11E+03	1.78E+03	4.42E+02	1.81E+03	6.90E+02	4.57E+02	2.45E+05	7.25E+03	1.58E+04	9.06E+02	8.42E+02
P00568 KAD1	GFLIDGYPR	519.27	103.5	2.86E+04	1.28E+04	2.03E+03	1.20E+05	1.73E+04	9.69E+03	1.48E+03	3.03E+03	1.23E+03	3.36E+03	1.78E+05	6.27E+04	1.99E+04	1.07E+04	4.06E+04
P19404 NDUV2	GPGFGVQAGL	451.75	103.52	6.03E+04	1.80E+04	5.24E+03	5.36E+04	9.43E+04	2.17E+03	1.40E+04	4.42E+03	2.51E+03	1.06E+04	5.85E+04	3.54E+04	6.13E+04	1.09E+03	1.60E+05
P62937 PPIA	FEDENFILK	577.79	103.62	4.69E+05	1.54E+04	8.36E+02	7.27E+05	2.40E+04	4.21E+04	3.16E+03	5.88E+04	9.68E+02	3.29E+02	4.86E+05	5.74E+04	1.71E+04	6.85E+02	1.43E+04
P32119 PRDX2	GLFIIDGK	431.75	103.65	1.79E+03	1.71E+05	3.54E+05	2.39E+05	3.17E+05	3.39E+05	2.83E+05	1.59E+04	2.17E+03	1.41E+03	5.82E+02	1.97E+05	1.23E+05	2.59E+02	1.79E+05
P09972 ALDOC	GVVPLAGTDGETTTQGLDG LSER	758.38	103.67	1.09E+06	2.50E+04	2.17E+04	6.76E+05	6.22E+04	9.21E+03	1.19E+03	4.62E+03	3.13E+02	2.05E+03	4.83E+05	1.67E+04	1.95E+04	1.82E+03	3.98E+05
P13533 MYH6	APGVMDNPLVMHQLR	559.96	103.7	6.60E+04	2.83E+05	1.80E+05	1.02E+04	3.92E+05	5.72E+03	2.90E+03	1.87E+03	6.19E+02	7.23E+04	3.19E+04	4.31E+05	2.19E+03	9.19E+02	1.72E+05
P00738 HPT	WMPICLPSKDYAEVGR	593.30	103.73	5.47E+03	2.22E+03	6.21E+02	6.92E+03	6.85E+03	2.34E+03	4.29E+04	1.43E+03	2.06E+03	7.94E+02	3.36E+03	2.93E+03	6.71E+03	5.25E+02	1.12E+03
P36871 PGM1	IALYETPTGWK	639.84	103.94	1.26E+05	2.18E+03	8.54E+02	3.14E+03	1.89E+03	1.13E+03	1.25E+03	5.13E+03	1.13E+03	4.07E+03	1.26E+05	1.58E+03	2.11E+03	1.29E+04	2.26E+03
Q86TD4 SRCA	ADNLATQMLMR	632.31	104.01	2.44E+03	6.39E+03	1.35E+04	1.89E+05	1.25E+04	2.12E+04	8.70E+03	1.36E+04	2.37E+03	1.72E+03	1.23E+05	4.38E+05	1.49E+05	1.22E+03	3.36E+05
P63316 TNNC1	GKSEELSDLFR	705.35	104.02	3.64E+05	4.84E+05	5.01E+05	1.03E+03	3.62E+04	6.17E+05	2.72E+03	6.69E+02	4.91E+04	2.40E+03	3.90E+05	1.54E+05	3.27E+05	1.21E+04	3.88E+05
Q86TD4 SRCA	TLMLNEDKPSDDYS AVLQR	732.36	104.04	1.29E+05	4.21E+02	3.54E+03	1.08E+05	5.77E+02	1.39E+03	9.06E+02	1.78E+03	4.56E+03	1.46E+04	1.53E+03	3.03E+03	3.18E+03	4.27E+03	2.72E+03
P12109 CO6A1	YLIVVTDGHPLEGYK	568.64	104.06	2.77E+02	3.76E+03	6.74E+03	6.50E+04	7.91E+02	1.62E+03	6.14E+03	5.79E+03	3.60E+02	8.92E+02	4.20E+04	2.93E+04	7.47E+03	2.95E+03	5.80E+03
O75746 CMC1	YMTPEDFVQR	643.30	104.13	9.36E+02	4.51E+03	1.45E+04	1.63E+03	8.32E+02	3.22E+02	8.93E+03	8.94E+02	2.75E+04	3.35E+04	1.57E+04	1.10E+03	9.76E+02	3.89E+03	3.46E+02
P01009 A1AT	VFSNGADLSPVTEEAPLK	917.46	104.22	1.01E+05	1.37E+03	4.21E+03	7.55E+04	2.62E+03	9.88E+02	1.01E+03	6.35E+02	3.26E+02	4.37E+02	2.00E+04	2.00E+03	7.49E+02	2.02E+03	1.85E+03
P30041 PRDX6	VVVFVFGPDK	504.28	104.29	4.95E+04	6.40E+03	9.40E+02	3.44E+03	1.21E+03	1.00E+04	5.50E+03	1.71E+04	2.35E+03	5.32E+03	1.54E+05	1.06E+03	8.00E+02	7.17E+03	9.32E+03
P01876 IGHA1	DASGVTFTWTPSSGK	770.87	104.37	1.92E+05	1.16E+03	6.91E+03	5.46E+05	9.35E+03	1.31E+03	2.07E+03	3.68E+03	8.98E+02	3.02E+02	2.08E+05	2.01E+03	5.06E+03	1.28E+03	6.27E+03
P38646 GRP75	VINEPTAAALAY	616.83	104.57	2.83E+04	1.55E+04	1.99E+03	1.19E+05	1.19E+04	3.22E+04	8.91E+03	4.42E+04	4.61E+03	4.48E+05	4.46E+04	4.85E+04	9.69E+03	1.87E+05	4.57E+03
O15061-2 SYNEM	YSWQDEIVQGTR	741.37	104.71	1.90E+04	1.41E+03	1.17E+03	1.15E+04	1.06E+03	1.46E+03	1.23E+03	2.08E+03	1.72E+03	9.27E+02	4.50E+03	5.06E+03	3.57E+04	1.29E+03	1.51E+04
P19022 CADH2	LSDPANWLK	522.28	104.88	8.67E+04	3.07E+02	8.89E+03	3.32E+03	8.91E+02	8.41E+02	4.42E+04	1.04E+05	6.27E+04	1.71E+04	1.11E+05	2.24E+03	2.45E+03	3.81E+04	4.11E+03
O15061-2 SYNEM	AALAEALLGR	457.28	104.88	5.58E+04	1.97E+03	4.50E+02	1.64E+03	2.41E+03	7.31E+03	3.05E+02	2.56E+03	7.58E+02	8.42E+02	1.95E+05	5.87E+03	9.06E+03	7.25E+02	3.63E+03
P55290 CAD13	TPHAEDMAELVIVGGK	556.28	104.9	4.41E+03	2.34E+05	1.36E+04	4.53E+02	4.47E+05	3.16E+05	5.84E+03	2.47E+04	3.30E+03	7.77E+02	5.54E+03	2.59E+05	3.48E+03	3.80E+03	5.31E+02
Q9H223 EHD4	EYQISAGDFPEVK	741.86	104.9	1.41E+03	8.91E+02	1.59E+04	2.96E+02	2.56E+02	3.93E+04	7.42E+03	2.71E+03	1.84E+03	3.29E+03	6.63E+02	5.56E+02	7.15E+02	2.13E+03	1.05E+03
Q9BX66-11 SRBS	TYIELLPAAEK	637.35	104.9	2.30E+04	5.70E+02	2.37E+04	7.08E+04	5.79E+03	3.87E+03	2.81E+03	1.27E+03	1.30E+03	1.54E+03	3.26E+04	1.45E+03	4.79E+03	9.30E+02	8.64E+03
P07108 ACBP	QATVGDINTERPGMLDFTG	717.36	104.95	6.51E+04	1.01E+05	8.44E+02	2.76E+04	1.90E+05	6.12E+03	2.19E+03	1.05E+03	1.61E+03	1.34E+03	1.60E+04	9.62E+04	2.78E+04	2.53E+03	1.80E+05
P19404 NDUV2	DTPENNDTPDFDTPENYKR	799.70	105.03	4.06E+02	8.17E+02	1.49E+03	1.24E+03	7.15E+04	2.39E+02	1.72E+03	1.16E+03	1.77E+03	6.84E+02	2.49E+02	2.22E+04	8.94E+02	1.26E+03	2.74E+03
P31937 3HIDH	MGAVFMDAPVSGGVGAAR	847.41	105.18	2.32E+03	2.18E+03	1.23E+03	5.05E+03	4.00E+03	2.24E+03	8.71E+04	9.46E+04	2.66E+05	2.61E+05	4.77E+02	7.50E+02	1.40E+03	5.18E+03	3.29E+03
P62805 H4	VFLENVIR	495.29	105.31	9.31E+05	4.98E+03	6.83E+04	2.65E+04	9.66E+03	4.72E+03	6.67E+03	1.03E+04	2.50E+03	6.39E+02	1.03E+06	2.38E+03	2.92E+03	6.80E+03	2.91E+04
P42126 D3D2	GVILTSRDPGVF	630.85	105.31	1.13E+05	1.97E+03	1.01E+03	2.02E+05	5.34E+02	3.20E+04	3.61E+03	2.94E+03	5.10E+04	6.95E+04	1.53E+05	1.06E+03	4.40E+03	1.83E+04	1.01E+04
P36957 ODO2	NVEAMNFADIER	704.83	105.52	6.69E+02	1.04E+05	2.63E+03	1.05E+03	3.98E+05	1.36E+04	1.79E+04	4.64E+03	6.29E+03	9.34E+02	6.68E+03	2.37E+05	6.37E+04	2.61E+03	2.28E+05
P36957 ODO2	VEGGTPLFLTR	595.33	105.57	3.86E+04	6.30E+05	3.12E+03	3.49E+03	7.96E+05	5.31E+05	5.11E+03	8.74E+03	7.33E+02	4.40E+04	3.68E+03	9.14E+05	4.94E+05	4.75E+03	3.18E+03
P02790 HEMO	VFPSPVDAAFR	610.81	105.62	6.82E+02	1.58E+05	7.21E+03	1.31E+04	2.98E+05	3.11E+05	2.51E+04	7.54E+03	4.99E+03	2.57E+03	4.10E+03	8.89E+04	4.89E+04	3.52E+03	1.23E+05
P49411 EFTU	ELLTEFGYK	550.29	105.64	1.43E+03	1.10E+05	3.30E+02	1.94E+04	1.02E+05	7.12E+04	2.81E+03	1.54E+04	1.65E+03	1.64E+03	7.02E+04	1.36E+05	1.72E+03	7.10E+03	2.87E+02
Q86TD4 SRCA	VTFVDTPGHIENR	730.89	105.65	5.48E+05	1.69E+04	5.16E+03	7.16E+05	1.94E+03	4.67E+03	1.89E+04	2.92E+04	5.67E+03	1.48E+03	5.28E+05	3.39E+04	2.68E+04	6.39E+02	1.04E+04
P35579 MYH9	GDLPFVVPR	500.28	105.69	4.77E+03	2.67E+02	1.86E+05	2.04E+03	2.47E+03	2.67E+02	3.50E+04	4.36E+04	7.34E+03	5.50E+03	3.01E+03	1.96E+03	1.58E+03	3.62E+02	1.60E+03
P01009 A1AT	GLFLSEGLK	482.28	105.73	4.63E+02	3.88E+02	1.19E+03	1.93E+04	6.19E+02	2.35E+03	1.12E+03	5.76E+02	2.72E+04	6.79E+04	2.13E+03	5.01E+03	1.54E+03	2.08E+04	3.47E+03
P13804 ETFA	VVPEMTEILK	579.82	105.9	6.79E+02	5.08E+05	2.65E+04	7.94E+03	6.72E+05	4.57E+05	3.85E+03	2.38E+04	1.18E+03	1.52E+03	9.83E+02	5.61E+05	1.60E+03	1.60E+05	5.42E+05
Q13011 ECH1	YCAQDAFFQVK	660.31	106.06	2.59E+04	7.39E+04	8.53E+04	6.00E+03	4.37E+03	1.78E+04	2.73E+03	1.73E+04	1.23E+03	1.26E+03	1.32E+03	3.67E+04	3.50E+02	6.91E+02	4.01E+04
P13533 MYH6	QLEEKEALISQLTR	553.31	106.06	7.43E+02	8.69E+05	2.48E+04	1.61E+03	1.02E+06	1.35E+06	8.46E+03	8.55E+03	1.28E+04	6.65E+03	3.50E+02	1.11E+06	8.74E+02	1.53E+04	1.08E+06
O75746 CMC1	FGLYLPK	419.25	106.08	4.90E+04	8.79E+03	1.75E+03	2.65E+03	3.29E+03	7.62E+03	8.44E+02	4.65E+02	5.86E+02	7.26E+02	1.65E+03	2.10E+03	1.03E+03	2.86E+02	9.86E+02
P26038 MOES	EDAVLEYLK	540.28	106.1	1.71E+03	7.41E+03	1.03E+05	3.99E+03	8.26E+02	7.76E+04	3.64E+04	5.18E+04	1.38E+03	3.45E+02	4.90E+02	5.52E+03	5.78E+03	3.54E+03	6.71E+02
Q16555 DPYL2	ILDGITGPEGH	611.33	106.13	5.60E+03	1.36E+04	1.56E+05	4.78E+04	1.09E+04	1.33E+05	1.52E+04	1.76E+04	2.11E+03	1.63E+03	8.09E+03	1.16E+03	7.77E+02	3.84E+03	6.76E+02
Q06830 PRDX1	GLFIIDDK	460.76	106.72	1.39E+04	1.01E+03	6.68E+02	1.20E+03	8.67E+03	9.03E+02	1.16E+03	6.59E+02	1.98E+05	2.15E+05	1.49E+03	2.99E+03	6.86E+02	1.77E+05	7.22E+02
P00403 COX2	VVLPPIEAPIR	553.85	106.99	2.76E+02	5.47E+06	3.68E+06	3.25E+02	5.61E+06	4.80E+06	4.84E+06	5.41E+04	1.48E+03	8.08E+02	4.96E+02	6.34E+06	1.08E+03	4.11E+02	4.98E+06
Q16891-2 IMMT	LSTDDLNSLIAHAHR	554.96	107.08	2.12E+03	1.01E+04	3.42E+03	1.04E+03	1.15E+03	1.88E+04	6.38E+03	4.74E+03	2.34E+04	4.01E+04	1.19E+03	1.55E+04	9.10E+02	1.61E+03	8.64E+04
P00367 DHE3	IIAEGANGPTTPEADKIFLER	748.06	107.2	4.44E+02	5.20E+02	1.18E+03	2.29E+03	1.33E+03	1.17E+03	2.33E+03	3.12E+02	2.58E+04	1.88E+04	2.56E+03	1.72E+02	3.96E+02	3.21E+04	3.84E+02
P12109 CO6A1	TAEYDVAYGESHLFR	586.61	107.3	1.72E+03	1.84E+05	5.16E+03	6.19E+02	2.51E+05	5.55E+05	5.51E+02	1.01E+03	1.02E+05	1.43E+05	1.42E+02	3.62E+05	1.11E+03	3.19E+04	1.32E+03
P12829 MYL4	NKEQGTYEDFVEGLR	595.62	107.38	3.44E+03	6.68E+02	2.06E+03	4.90E+02	1.38E+03	4.37E+03	5.41E+02	2.36E+03	1.20E+05	1.03E+04	8.46E+02	5.01E+02	8.47E+02	6.57E+03	5.99E+02
P02679 FIBG	IHLISTQSAIPY	671.87	107.42	1.53E+05	8.55E+03	1.02E+05	1.49E+04	7.72E+03	4.92E+04	8.56E+04	6.50E+04	3.48E+03	2.72E+02	4.57E+04	1.67E+04	8.39E+03	7.90E+02	1.34E+04
P62937 PPIA	EGMNIVEAMER	639.79	107.55	1.42E+03	2.74E+05	3.83E+03	4.46E+02	2.55E+05	4.27E+05	8.58E+03	2.04E+04	1.41E+03	1.36E+03	4.65E+02	3.02E+05	8.29E+02		

Q9Y4G6 TLN2	NVAQVAEDTVLQNR	778.40	108.49	1.22E+03	2.29E+04	1.79E+04	4.18E+02	6.98E+02	4.59E+04	8.69E+04	8.40E+04	3.28E+03	1.23E+04	2.44E+03	1.13E+03	9.13E+03	2.21E+03	5.30E+02
P07108 ACBP	TKPSDEEMLFYGH	556.27	109.08	7.80E+04	6.29E+03	1.54E+03	5.37E+03	9.53E+02	1.29E+04	1.26E+03	1.39E+03	2.38E+03	4.64E+02	1.32E+04	4.93E+03	8.77E+03	3.99E+02	2.82E+03
P14543-2 NID1	VLFDLTVNPR	651.86	109.23	1.90E+04	2.43E+05	1.46E+04	1.35E+04	1.24E+05	1.30E+04	3.79E+03	1.02E+03	1.14E+03	4.78E+03	1.46E+04	2.16E+05	2.99E+03	1.58E+03	2.53E+05
O95831 AIFM1	ELWFSDDPNVTK	725.85	109.32	1.40E+03	1.39E+04	1.47E+03	1.12E+03	9.95E+04	7.31E+02	8.60E+02	1.47E+04	1.52E+03	7.03E+02	2.84E+02	3.11E+04	2.52E+03	2.02E+03	3.50E+02
P31937 3HIDH	GSLLDSTIDPAVSK	801.93	109.44	3.84E+03	2.29E+03	1.70E+04	3.40E+04	4.47E+04	4.45E+03	2.03E+03	2.51E+03	1.81E+04	2.97E+04	1.29E+03	2.13E+04	1.35E+04	5.18E+03	5.00E+04
P02679 FIBG	IHLISTQSAIPYALR	561.31	109.49	1.63E+03	4.90E+04	6.01E+03	1.22E+03	2.08E+03	1.04E+04	1.27E+05	2.93E+03	2.40E+03	6.62E+02	1.12E+03	7.67E+02	5.54E+03	2.77E+03	8.46E+02
P00738 HPT	YVMLPVADQDQCIR	825.90	109.54	8.13E+03	3.10E+03	1.12E+03	9.47E+02	3.83E+03	2.50E+03	8.41E+02	6.47E+02	1.89E+03	5.64E+04	1.45E+03	6.01E+03	5.79E+03	7.06E+03	1.22E+03
Q9H223 EHD4	SISVIDSPGILSGEK	751.41	109.7	1.33E+03	2.59E+04	3.24E+04	1.53E+03	9.79E+02	8.80E+03	1.99E+03	8.81E+02	2.01E+04	1.15E+03	1.00E+03	1.89E+03	1.84E+03	2.59E+04	6.05E+03
P05091 ALDH2	AAFQLGSPWR	566.80	109.7	9.39E+04	7.82E+04	3.35E+04	1.43E+05	2.87E+05	6.51E+04	3.83E+03	6.35E+03	4.12E+03	1.17E+03	1.11E+05	2.06E+05	5.34E+03	4.34E+04	4.06E+03
Q9BX66-11 SRBS	FGDLLNIDDITAK	661.34	109.7	1.55E+04	3.35E+04	7.22E+03	1.65E+03	3.65E+03	6.36E+04	1.09E+04	1.70E+05	1.71E+03	3.77E+03	4.89E+03	1.84E+03	7.28E+02	1.34E+05	7.56E+04
P55809 SCOT1	GGHVDLTMLGAMQVSK	548.28	109.75	7.17E+03	6.31E+03	9.41E+03	1.71E+03	2.02E+03	3.46E+03	6.43E+04	5.85E+04	1.47E+03	3.93E+04	1.07E+03	1.07E+04	2.10E+03	8.35E+03	1.14E+03
P11310 ACADM	SLGQMPIIIAGNDQOK	856.95	109.77	4.46E+03	1.51E+03	3.09E+03	4.86E+03	1.85E+03	2.71E+03	4.25E+02	6.70E+02	1.54E+05	2.13E+05	9.80E+02	2.43E+03	1.87E+03	1.52E+05	1.37E+03
P38117-2 ETFB	IEVIKPGDLGVDLTSK	561.99	109.78	4.77E+03	4.49E+02	7.03E+02	2.60E+03	2.04E+05	2.98E+03	5.42E+03	7.13E+04	3.69E+03	1.11E+03	1.66E+03	1.70E+05	1.33E+05	1.86E+04	2.48E+05
P13533 MYH6	DPLNETVVVLYQK	745.40	109.8	2.37E+03	1.24E+04	1.42E+04	8.29E+02	3.48E+04	8.02E+04	3.92E+03	4.59E+03	8.63E+02	2.99E+03	4.15E+03	7.33E+04	1.00E+04	8.11E+02	1.06E+04
P20674 COX5A	ELGISTPEELGLDK	750.89	110.13	1.74E+03	3.67E+05	5.29E+04	2.53E+03	1.16E+03	3.46E+05	5.89E+04	6.81E+04	1.52E+03	2.70E+03	4.64E+03	4.16E+03	1.44E+03	2.03E+03	1.46E+03
P31040 DHSA	EPFVLPVTHYN	689.87	110.26	6.91E+04	3.99E+03	2.34E+03	1.77E+04	1.11E+03	9.08E+02	5.07E+02	6.34E+02	2.67E+02	1.25E+03	4.43E+04	2.52E+03	1.15E+04	4.34E+02	1.42E+03
P30086 PEBP1	LYTLVLTDPDAPSR	780.92	110.37	4.02E+03	3.45E+03	1.70E+03	1.06E+03	1.44E+05	2.34E+03	2.60E+02	5.93E+03	6.69E+02	4.69E+02	3.05E+03	1.78E+05	1.78E+05	2.29E+03	3.21E+05
Q96199 SUCB2	FFVADTANEALEAAKR	584.97	110.6	7.68E+02	7.04E+02	5.95E+02	4.95E+03	1.49E+04	4.06E+02	2.89E+03	1.31E+03	1.10E+03	3.98E+02	2.94E+02	4.32E+03	7.92E+03	4.48E+02	5.79E+02
P10809 CH60	EIGNIISDAMK	595.81	110.69	1.29E+04	5.13E+04	2.96E+03	3.53E+03	7.35E+03	6.26E+04	1.11E+03	1.60E+03	1.32E+03	1.11E+05	6.03E+03	1.99E+04	1.50E+04	5.55E+02	2.51E+03
P19404 NDUV2	FSCEPAGGLTSLTEPPK	867.43	110.7	8.87E+03	4.32E+03	8.12E+02	1.88E+04	4.87E+03	1.28E+03	1.02E+03	2.51E+03	3.81E+03	5.06E+02	7.78E+03	8.18E+02	1.66E+04	1.79E+03	3.69E+04
O15061-2 SYNEM	ENLLLEELR	629.32	110.7	5.46E+03	7.33E+03	9.91E+02	6.10E+02	1.76E+03	1.11E+04	1.78E+03	1.06E+04	1.17E+04	4.54E+04	2.81E+03	7.05E+02	2.48E+03	7.20E+03	6.59E+03
P12109 CO6A1	GLEQLLVGGSHLK	675.89	110.72	1.66E+03	2.04E+03	3.15E+03	2.75E+03	7.60E+04	3.18E+03	4.04E+02	4.12E+03	1.12E+03	5.11E+03	1.53E+03	4.10E+04	1.20E+04	4.30E+02	1.03E+05
P21980 TGM2	MDLLPLHMLHK	468.92	110.74	2.76E+03	2.61E+02	6.90E+02	2.62E+02	2.41E+03	5.78E+03	1.25E+03	2.75E+03	3.39E+04	3.47E+04	7.98E+02	4.49E+02	2.31E+02	6.21E+03	3.44E+02
P10515 ODP2	VPLPSLSPTMQAGTIAR	869.98	111.13	1.77E+05	2.34E+03	3.80E+03	1.36E+05	1.47E+05	1.15E+03	3.68E+03	1.21E+04	1.48E+03	3.98E+02	4.64E+04	7.95E+04	3.20E+03	9.12E+02	3.95E+04
P42765 THIM	TPFGAYGGLLK	562.31	111.26	3.54E+03	1.32E+03	4.62E+03	6.56E+03	3.83E+05	5.91E+03	1.17E+03	3.86E+03	1.25E+03	9.48E+02	7.16E+02	3.92E+05	9.89E+04	4.72E+03	3.57E+05
P63316 TNNC1	NADGYIDLDELK	683.33	111.42	3.33E+03	2.46E+04	5.18E+03	5.30E+03	5.96E+03	5.77E+03	1.46E+04	1.05E+03	1.46E+05	2.07E+05	4.72E+03	8.75E+02	4.74E+03	5.22E+04	1.74E+03
Q15124 PGM5	TIEEY AICPDLR	711.85	111.53	2.98E+03	2.76E+03	6.58E+02	1.02E+03	2.11E+03	2.67E+03	1.47E+03	6.88E+03	4.24E+03	7.31E+02	1.59E+03	2.30E+04	3.38E+03	1.27E+04	2.18E+04
Q01813 K6PP	NVIFQVVAELK	629.36	111.65	9.88E+02	3.96E+03	3.12E+04	1.67E+03	1.72E+03	9.24E+04	8.85E+03	7.29E+03	5.14E+04	6.55E+04	8.36E+02	1.38E+03	3.38E+03	3.50E+04	1.17E+03
Q9Y4G6 TLN2	VLAQATSDLVNAMR	744.90	111.66	2.70E+03	4.11E+03	2.32E+03	2.71E+04	4.33E+04	2.39E+02	9.76E+02	1.87E+03	7.97E+02	1.05E+03	3.46E+03	2.67E+03	2.35E+04	6.39E+02	1.62E+04
O95831 AIFM1	VEDTHIVAAVGLPEPVELA	702.05	111.68	2.24E+04	8.91E+03	7.02E+04	4.60E+03	3.31E+04	2.16E+02	2.65E+03	3.54E+04	7.21E+03	1.02E+03	2.19E+03	4.58E+03	4.56E+03	1.99E+03	2.39E+04
Q9H987 SYP2L	AQSAPPEAAVLPSPAPV ASPR	774.09	111.77	7.55E+03	1.72E+03	3.97E+03	3.12E+02	5.07E+03	7.66E+03	1.12E+03	4.56E+03	7.27E+02	4.79E+02	3.42E+04	1.10E+04	2.83E+03	4.06E+02	7.99E+03
P13073 COX41	SEDFSLPAYMDR	715.82	112.05	5.76E+05	1.72E+03	1.60E+03	9.92E+05	8.32E+05	1.89E+04	1.32E+04	1.15E+04	1.03E+04	1.75E+04	2.89E+03	5.40E+05	1.13E+05	2.39E+03	7.97E+05
P42765 THIM	AANDAGYFNDEMAPIEVK	977.95	112.18	2.71E+03	3.98E+03	2.16E+03	2.03E+03	2.34E+04	2.97E+03	5.66E+02	2.75E+03	2.19E+02	2.34E+03	8.85E+02	1.62E+04	2.75E+03	4.47E+03	5.08E+04
P12277 KCRB	VLTPELYAELR	652.37	112.33	9.77E+03	2.42E+03	2.29E+03	1.02E+06	3.70E+05	7.35E+03	4.40E+03	1.34E+04	3.07E+03	1.44E+03	2.55E+03	6.83E+05	3.88E+05	2.92E+03	2.87E+05
P62937 PPIA	VSFELFADKVPK	690.38	112.46	9.02E+02	2.05E+03	2.09E+03	2.03E+04	9.11E+04	8.27E+02	1.23E+03	1.60E+02	1.18E+03	3.38E+03	4.54E+02	3.95E+03	9.67E+03	3.51E+03	1.78E+04
Q9H987 SYP2L	FSTPAPQPTAEPLAPTVLAP	721.05	112.56	7.05E+03	6.93E+04	4.32E+03	5.58E+04	6.37E+03	1.55E+03	1.04E+03	4.11E+03	1.47E+03	9.69E+02	1.49E+04	7.53E+03	2.12E+04	1.92E+03	7.90E+03
Q16891-2 IMMT	LSTDDLNSLIAH	649.33	112.6	7.53E+02	8.37E+02	3.01E+03	1.82E+03	1.27E+03	1.07E+03	1.01E+03	4.28E+03	4.33E+03	1.38E+04	2.32E+02	2.09E+03	1.35E+03	1.32E+03	2.02E+03
P62937 PPIA	SIYGKFEDEFILK	611.31	112.69	1.08E+03	3.10E+03	1.49E+04	3.17E+03	4.21E+04	1.67E+04	6.60E+02	6.81E+03	1.23E+03	1.96E+03	1.17E+03	8.37E+03	6.50E+03	2.06E+03	1.56E+04
P19022 CADH2	SAAPHPGDIGDFINEGLK	613.31	112.99	1.56E+03	1.25E+04	1.41E+03	1.89E+05	1.75E+05	4.53E+03	1.13E+03	6.03E+03	3.64E+02	1.04E+03	6.62E+02	9.01E+04	5.29E+04	1.29E+04	2.66E+04
P38646 GRP75	VINEPTAAALAYGLDK	823.44	113.06	1.66E+03	8.28E+02	6.25E+02	7.29E+04	1.28E+05	2.05E+02	7.27E+02	4.12E+03	5.85E+02	1.35E+03	1.73E+03	9.55E+04	3.73E+04	1.36E+04	6.98E+04
O15061-2 SYNEM	VVKPLDVPAPSLEGDLGST HWK	587.07	113.17	1.42E+04	5.14E+02	2.75E+02	3.57E+03	5.08E+02	7.86E+02	3.26E+02	1.32E+03	1.90E+02	5.13E+02	2.49E+04	1.11E+03	3.78E+03	5.48E+02	1.67E+03
P55290 CAD13	SIVVSPILIPENQR	782.95	113.24	6.59E+02	3.53E+02	4.05E+03	4.24E+02	1.23E+05	5.52E+03	4.01E+03	2.53E+03	7.36E+02	8.07E+02	5.62E+02	8.46E+04	6.09E+04	4.45E+02	1.73E+05
P02790 HEMO	SGAQATWTELPWPHEK	613.30	113.29	1.70E+05	1.82E+03	1.33E+05	1.29E+05	4.07E+04	1.40E+03	4.73E+03	3.05E+02	3.74E+02	1.80E+03	1.97E+05	1.58E+03	9.03E+02	8.77E+02	4.48E+03
P08133 ANXA6	SELDMLDIR	546.27	113.29	7.53E+02	2.88E+03	8.73E+03	3.14E+03	1.35E+03	1.60E+04	2.68E+03	2.73E+02	1.00E+05	3.39E+03	1.89E+03	4.19E+03	9.54E+02	9.05E+04	1.49E+03
P13637 AT1A3	GVGHISEGNETVEDIAR	915.46	113.32	1.47E+03	1.63E+03	3.50E+03	1.14E+03	4.73E+03	3.80E+03	7.56E+03	9.45E+03	3.12E+02	1.97E+03	1.80E+03	3.53E+04	3.07E+04	7.10E+02	7.00E+04
Q9Y4G6 TLN2	NLATSLAELR	544.31	113.34	5.98E+04	3.17E+05	2.79E+05	2.86E+03	5.44E+02	2.51E+05	3.86E+05	1.18E+05	4.89E+04	2.07E+04	6.01E+04	1.22E+03	1.30E+03	7.42E+04	4.81E+02
P14543-2 NID1	NIFWTDNSLDR	690.83	113.42	1.28E+02	7.04E+02	4.23E+02	2.38E+03	6.98E+02	1.14E+03	5.93E+02	2.09E+03	5.34E+04	1.07E+04	1.67E+03	2.32E+04	1.23E+03	8.27E+04	5.45E+03
P48047 ATPO	TDPSILGGMIVR	629.84	113.83	1.55E+04	1.54E+04	1.94E+03	1.92E+03	5.99E+05	3.15E+03	7.08E+03	1.48E+04	3.70E+03	1.11E+04	2.22E+03	7.92E+05	4.56E+05	4.13E+02	4.52E+05
Q16836-2 HCDH	TFESLVDFSK	586.80	113.85	1.59E+03	1.71E+04	5.74E+03	2.65E+03	3.94E+05	2.43E+04	5.31E+03	1.14E+04	1.38E+03	1.34E+03	2.80E+05	2.94E+05	2.52E+05	1.47E+03	4.28E+05
Q6NZI2 PTRF	QAEMEGAVQSIQGELSK	902.94	113.9	1.82E+05	1.00E+04	5.65E+03	1.56E+04	2.76E+05	6.85E+03	3.02E+03	7.23E+03							

Q16836-2 HCDH	TVVLVDQTEDILAK	772.43	115.08	3.97E+04	1.66E+03	1.09E+03	2.23E+04	7.37E+03	7.82E+02	6.68E+02	2.84E+03	3.27E+03	1.35E+03	1.94E+04	3.85E+03	4.89E+02	1.01E+04	7.58E+03
Q96199 SUCB2	FFVADTANEALEAAK	798.90	115.25	4.15E+02	7.88E+03	2.76E+03	1.56E+03	9.76E+04	3.05E+03	2.14E+03	3.90E+03	1.89E+03	3.30E+03	1.72E+03	7.49E+04	2.02E+04	7.18E+02	1.11E+05
P08133 ANXA6	DAFVAIVQSVK	588.82	115.62	2.40E+03	2.30E+03	4.95E+04	2.20E+03	4.68E+02	1.59E+05	5.05E+04	4.78E+04	1.59E+03	5.06E+03	1.45E+02	9.56E+02	3.37E+03	1.91E+03	4.86E+02
Q13011 ECH1	NQSLVNELAFTAR	731.88	115.63	1.73E+03	9.00E+02	1.03E+04	3.57E+03	9.79E+02	2.34E+03	8.04E+03	1.14E+04	5.21E+02	9.32E+02	1.59E+03	3.74E+03	2.25E+03	4.02E+04	3.41E+03
P47985 UCRI	EIEQEAAVELSQLR	807.41	115.79	1.14E+03	8.09E+02	1.01E+03	1.31E+03	1.14E+03	9.12E+03	5.01E+04	3.90E+04	4.47E+02	1.29E+03	8.78E+02	4.08E+02	9.66E+02	8.58E+02	1.73E+03
P12109 CO6A1	LLLFSDGNSQGATPAAIEK	966.51	115.79	4.25E+02	2.58E+03	4.70E+02	1.33E+04	9.42E+03	1.52E+03	1.73E+03	1.28E+03	2.79E+02	3.81E+04	1.21E+04	1.00E+04	3.86E+03	1.17E+03	4.29E+03
P49821 NDUV1	GDARPAEIDSLWEISK	596.30	116.05	7.86E+03	3.67E+03	2.28E+04	1.67E+03	1.64E+03	2.74E+02	1.29E+04	2.22E+04	2.05E+04	1.99E+03	1.20E+03	4.10E+03	2.08E+03	4.39E+03	6.45E+03
P42765 THIM	DFTATDLSEFAAK	708.34	116.15	1.61E+03	1.49E+04	6.79E+03	8.68E+02	1.57E+05	4.24E+03	3.52E+02	9.34E+03	1.27E+03	1.19E+03	3.91E+02	1.55E+05	1.08E+05	2.64E+02	2.07E+05
P12829 MYL4	IDFTADQIEEFK	728.36	116.28	8.04E+04	2.81E+04	2.36E+04	2.89E+05	5.68E+04	2.35E+04	1.13E+03	1.85E+04	5.66E+02	3.88E+02	2.80E+05	1.17E+05	2.41E+04	1.00E+03	3.34E+05
P12110 CO6A2	YGGHLFSDQVEVFSPPGSD	732.03	116.34	4.62E+04	7.31E+02	5.67E+04	6.81E+04	4.95E+03	2.14E+03	3.13E+04	2.77E+03	4.89E+02	1.37E+03	1.24E+05	1.33E+03	1.09E+05	9.88E+02	7.30E+03
P62937 PIIA	VSEFLFADK	528.27	116.34	5.11E+02	6.17E+02	7.62E+02	2.48E+02	6.31E+02	5.78E+02	1.87E+03	2.76E+03	1.35E+03	3.65E+05	5.73E+03	1.14E+03	2.73E+03	2.44E+05	3.33E+03
P62805 H4	TVTAMDVVYALKR	489.61	116.38	3.94E+02	8.45E+02	7.05E+03	5.63E+02	1.01E+03	4.12E+02	6.62E+04	3.64E+04	2.66E+02	3.59E+02	1.97E+02	3.72E+02	7.09E+02	2.62E+02	3.25E+02
P30041 PRDX6	LPFPIIDDR	543.30	116.43	5.15E+05	5.03E+03	1.67E+03	3.31E+04	2.67E+04	1.11E+03	5.11E+02	1.52E+04	5.68E+05	1.09E+03	6.89E+05	5.98E+04	3.67E+04	1.43E+06	3.68E+04
P20674 COX5A	GINTLVTYDMVPEPK	838.93	116.53	4.96E+04	1.04E+04	1.64E+05	1.68E+03	4.98E+05	1.36E+05	4.26E+04	1.32E+05	2.44E+04	3.78E+03	1.32E+04	4.15E+05	1.60E+05	2.19E+03	5.35E+05
P31937 3HIDH	SPILLGSLAHQIYR	523.30	116.66	6.26E+03	3.47E+03	9.91E+03	1.13E+03	8.84E+02	2.48E+03	6.68E+04	1.81E+04	2.20E+03	1.90E+03	1.56E+03	4.10E+02	1.27E+03	4.53E+02	1.00E+03
Q562R1 ACTBL	IWYHTFYNELR	514.59	116.68	1.38E+03	1.37E+03	6.61E+02	3.78E+02	8.51E+02	1.05E+03	2.32E+03	1.25E+03	5.32E+04	3.47E+02	4.75E+02	4.29E+03	2.31E+02	7.62E+03	6.08E+03
Q96199 SUCB2	EQIDIFEGIK	596.32	117.09	4.89E+02	5.49E+04	1.49E+05	3.01E+03	2.97E+04	3.51E+04	7.24E+04	1.34E+05	9.82E+02	3.45E+03	2.71E+02	5.03E+04	8.61E+03	2.83E+04	8.35E+04
P00403 COX2	SWAVPTLGLK	536.31	117.25	2.69E+03	2.76E+04	6.99E+03	4.66E+03	3.06E+03	2.01E+05	2.04E+04	8.22E+03	1.02E+03	3.37E+03	5.35E+03	1.69E+03	6.51E+02	1.24E+03	1.06E+03
Q9H223 EHD4	YLLEQDFPGMR	684.83	117.32	2.00E+03	3.65E+02	7.08E+02	1.49E+03	3.83E+04	1.77E+03	2.53E+03	6.07E+02	1.74E+03	1.20E+03	4.69E+03	8.39E+03	1.31E+03	1.93E+03	3.08E+04
P00403 COX2	ILYMTDEVNDPSLTIK	926.47	117.32	2.06E+03	1.52E+04	7.26E+05	1.01E+03	3.49E+04	6.23E+02	1.39E+03	2.62E+03	1.65E+03	6.57E+02	1.15E+03	2.74E+03	2.58E+03	1.87E+03	4.85E+04
P00738 HPT	DIAPTLTLYVGK	645.87	117.57	1.78E+03	1.55E+04	2.01E+03	4.66E+03	1.23E+04	9.27E+03	5.07E+03	6.36E+03	9.00E+02	4.58E+04	3.50E+03	1.65E+04	2.99E+03	1.87E+04	8.52E+03
P13533 MYH6	ILNPVAIPEGFIDSR	586.66	117.99	1.80E+03	1.42E+04	7.58E+03	2.50E+03	4.51E+05	1.70E+04	1.92E+04	1.08E+04	3.18E+03	1.68E+03	2.01E+05	2.38E+05	2.79E+05	2.04E+03	5.93E+05
O95831 AIFM1	TGGLEIDSDFGGFR	735.85	118.02	3.32E+03	3.87E+03	2.73E+03	1.44E+03	1.10E+05	1.05E+04	1.84E+04	7.48E+03	9.37E+02	1.76E+04	6.92E+03	1.58E+05	1.98E+04	9.87E+02	9.32E+04
P10515 ODP2	ISVNDFIK	524.81	118.05	7.92E+04	3.83E+03	4.96E+02	7.27E+04	2.97E+04	6.22E+03	1.56E+04	3.78E+04	8.51E+02	4.07E+02	5.62E+04	1.48E+04	7.04E+03	2.61E+02	3.06E+04
P12829 MYL4	EQGTYYEDFVEGLR	771.86	118.1	1.25E+03	6.52E+03	7.96E+02	5.59E+02	1.07E+05	5.73E+03	6.12E+03	1.81E+03	1.38E+05	1.02E+03	7.12E+02	7.06E+04	3.76E+03	1.30E+04	1.16E+05
P01023 A2MG	QGIPIFFGQVR	574.81	118.25	2.21E+04	5.54E+04	4.84E+03	2.32E+03	1.30E+05	1.79E+04	4.79E+03	5.89E+03	2.43E+02	4.68E+02	3.73E+02	1.83E+04	1.97E+03	6.27E+02	2.09E+03
P19022 CADH2	IDPVNGQITIAVLDLDR	862.98	118.31	8.61E+02	2.02E+03	5.16E+03	1.56E+03	3.81E+04	8.63E+03	4.21E+02	1.60E+03	3.82E+03	6.76E+02	5.99E+02	4.90E+03	3.78E+04	1.50E+02	4.01E+04
P01023 A2MG	TEHPFTVEEFVLPK	558.29	118.34	1.08E+03	1.87E+03	1.65E+04	7.24E+03	3.47E+03	2.69E+03	4.14E+04	7.61E+03	2.47E+03	2.69E+04	2.51E+04	1.91E+05	1.41E+04	1.28E+04	1.91E+03
P38646 GRP75	VEAVNMAEGIIHDTETK	619.64	118.35	6.44E+03	7.98E+03	3.87E+02	1.30E+04	8.48E+04	4.75E+03	2.02E+03	9.93E+03	3.52E+03	2.48E+03	5.45E+03	1.46E+05	1.39E+04	8.90E+03	1.68E+05
P30041 PRDX6	DGDSVMVLPTIPEEEAK	915.45	118.45	1.73E+04	1.36E+03	1.95E+03	6.88E+04	2.24E+04	5.96E+03	2.31E+03	2.85E+03	3.15E+02	4.84E+02	2.26E+04	1.06E+04	3.03E+03	4.47E+02	1.69E+04
P08133 ANXA6	DLEADIIGDTSGHFQK	582.62	118.51	3.19E+03	2.10E+04	5.72E+03	7.22E+03	1.48E+04	5.78E+03	3.26E+03	8.07E+03	4.59E+02	3.26E+02	5.84E+03	3.98E+03	2.64E+03	4.97E+02	9.19E+02
Q6NZI2 PTRF	IIGAVDQIQLTQAQLEER	675.70	118.57	2.58E+03	1.14E+03	2.83E+03	1.19E+03	7.91E+02	3.01E+02	8.20E+03	8.80E+03	5.58E+04	4.09E+03	1.53E+02	3.03E+02	1.18E+03	7.94E+03	9.40E+02
P35579 MYH9	DLGVELEALK	558.79	118.95	8.14E+03	3.37E+03	2.15E+03	1.54E+03	7.75E+02	3.30E+03	6.01E+02	6.01E+03	5.77E+04	1.41E+05	1.52E+03	3.52E+03	1.10E+04	1.10E+05	3.35E+03
P12110 CO6A2	DYDSLAPQGGFFDR	765.85	119.08	6.38E+03	1.39E+03	2.61E+03	1.25E+03	3.98E+02	2.00E+03	5.53E+02	1.61E+02	4.74E+04	1.75E+03	1.93E+02	7.74E+03	1.27E+03	1.18E+04	1.05E+03
P12277 KCRB	TDLNPDNLQGGDDLDPNY VLSSR	840.06	119.3	3.76E+03	1.51E+03	1.69E+03	2.74E+02	1.76E+04	3.22E+03	4.25E+02	2.12E+03	9.66E+02	1.27E+03	1.45E+03	3.47E+03	2.30E+03	2.55E+03	4.12E+04
P23327 SRCH	FTIIPNPLDR	593.34	119.69	7.45E+02	2.28E+03	1.63E+04	1.74E+03	3.42E+05	6.88E+05	6.26E+03	1.15E+04	7.31E+03	2.32E+04	7.65E+02	3.10E+05	2.03E+03	2.63E+04	5.07E+05
P38646 GRP75	SDIGEVILVGGMTR	723.39	119.94	4.47E+02	8.23E+03	8.73E+02	4.66E+02	5.01E+03	5.47E+02	4.49E+03	9.45E+02	2.26E+03	7.61E+02	6.94E+02	1.30E+05	2.72E+03	1.56E+03	1.82E+04
P07339 CATD	FQDILGMAYPR	620.31	120.51	5.48E+02	1.52E+04	9.61E+03	1.84E+03	4.75E+04	6.51E+04	3.61E+04	5.68E+04	1.84E+03	8.67E+04	8.17E+03	3.26E+03	2.50E+03	6.36E+03	5.13E+03
P62937 PIIA	IIPGFMCQGGDFTR	771.37	120.59	2.79E+04	1.15E+03	2.76E+03	6.17E+04	1.45E+03	7.64E+02	8.41E+02	2.83E+02	4.90E+04	2.12E+04	9.47E+04	5.43E+03	4.53E+03	5.74E+04	2.50E+03
Q06830 PRDX1	QGGGLGPMNIPLVSDPK	811.93	120.77	6.10E+02	1.24E+03	4.07E+02	3.08E+02	1.61E+03	2.41E+03	3.64E+03	4.55E+03	8.12E+02	2.62E+04	3.13E+03	6.57E+03	2.38E+04	2.47E+03	3.49E+02
P36957 ODO2	LGFM SAFVK	500.27	121.02	7.71E+03	4.17E+03	2.23E+03	6.24E+02	1.04E+05	1.29E+03	9.84E+03	2.02E+03	6.23E+03	6.27E+04	8.55E+02	8.58E+04	4.28E+03	2.44E+03	1.07E+03
P42765 THIM	KDGTVTAGNASGVADGAG AVIIASEDAVK	882.12	121.12	4.87E+02	5.47E+02	6.10E+02	2.70E+02	1.78E+04	3.28E+02	1.90E+03	4.31E+02	8.10E+02	6.49E+02	1.94E+03	2.53E+03	1.31E+03	1.20E+03	5.94E+03
P07954 FUMH	VAAALTGLPFVTAPNK	749.93	121.41	3.17E+02	6.93E+02	1.00E+03	5.90E+02	1.70E+05	3.97E+02	2.63E+03	2.59E+03	1.14E+03	2.20E+02	2.11E+03	7.50E+04	5.56E+04	1.12E+03	1.47E+05
P49411 EFTU	LLDAVDTYIPVPAR	771.93	121.6	2.22E+05	3.37E+03	3.19E+02	2.83E+03	2.82E+04	2.71E+03	8.34E+02	1.13E+03	9.65E+02	6.73E+02	1.79E+05	7.37E+03	5.14E+03	3.80E+02	1.58E+04
Q99497 PARK7	GAEEMETVIVDVMR	838.41	121.63	1.58E+05	1.06E+04	3.81E+03	1.41E+03	1.72E+04	1.62E+04	6.40E+03	8.06E+03	6.23E+03	1.21E+03	2.06E+05	2.45E+04	6.54E+03	1.32E+03	2.12E+05
P06744 G6PI	DASTNGLINFIK	646.84	121.87	1.01E+04	1.36E+03	2.11E+03	6.70E+04	2.47E+03	3.67E+02	9.63E+02	2.65E+03	2.90E+03	1.54E+03	2.89E+04	1.60E+03	3.40E+03	1.02E+04	6.57E+03
P01009 A1AT	LAEF AF	697.35	122	2.19E+03	3.00E+05	8.30E+03	1.13E+04	8.64E+04	2.22E+05	9.81E+03	5.28E+03	1.15E+05	1.42E+03	1.25E+03	5.58E+04	2.31E+05	1.56E+05	1.90E+05
P00367 DHE3	FGIFPGIDVPAPDMSTGER	958.47	122.03	5.35E+02	4.41E+02	1.02E+03	7.40E+02	1.85E+02	3.91E+03	5.66E+03	1.00E+03	3.48E+04	3.18E+03	3.57E+03	2.47E+03	9.13E+02	2.03E+04	1.03E+03
P49821 NDUV1	PAEIDSLWEISK	694.36	122.08	1.27E+05	4.39E+04	6.76E+03	1.45E+05	3.78E+03	5.97E+02	3.22E+04	2.17E+04	2.24E+04	4.49E+02	6.25E+04	4.06E+03	3.37E+02	3.43E+02	7.81E+02
P31040 DHSA	EPIPVLPTVHYNMGGIPTNY	780.74	122.09	2.06E+03	8.08E+02	2.70E+03	1.12E+03	1.63E+04	6.36E+02	6.84E+03	7.39E+02	5.81E+02	1					



O75746 CMC1	GLIPQLIGVAPEK	667.91	123.19	3.14E+04	1.61E+03	7.09E+02	6.54E+03	4.57E+02	1.43E+03	7.89E+02	7.24E+02	7.19E+02	1.37E+03	2.92E+04	1.08E+03	1.48E+03	3.34E+02	8.14E+03
Q9BX66-11 SRBS	NPVDYMDLPLFSSSPSR	906.42	123.2	2.30E+03	2.80E+03	3.17E+03	2.14E+03	4.50E+03	5.22E+03	2.17E+03	1.83E+03	2.44E+03	6.15E+03	6.87E+02	4.03E+03	9.45E+03	8.32E+03	4.86E+03
O95831 AIFM1	VLIVSEDPPELPMRPLSK	728.40	123.24	1.04E+05	4.58E+03	2.18E+03	6.39E+03	4.96E+02	1.66E+03	1.88E+03	8.05E+02	8.21E+02	1.29E+02	7.18E+04	5.19E+02	3.29E+04	4.76E+02	3.53E+02
P12277 KCRB	DLFDPIEDR	616.81	123.34	2.96E+05	1.42E+04	2.28E+03	2.21E+05	6.94E+03	5.27E+02	5.70E+02	2.43E+03	4.50E+02	1.43E+03	4.31E+05	2.60E+04	9.90E+03	2.02E+03	2.13E+02
P12277 KCRB	TFLVWVNEEDHLR	553.28	123.44	9.11E+03	6.40E+03	4.51E+02	1.39E+04	2.15E+03	1.07E+04	1.47E+04	1.55E+04	5.18E+04	1.32E+04	3.33E+04	3.47E+02	1.36E+03	1.08E+03	3.22E+03
P14543-2 NID1	MVYWTDDITEPSIGR	834.41	123.47	2.72E+03	1.01E+04	3.58E+03	6.13E+03	1.86E+02	1.14E+04	1.65E+03	8.07E+02	2.26E+03	1.27E+03	4.14E+03	3.72E+03	7.79E+03	7.79E+03	4.57E+03
O75746 CMC1	YEGFFGLYR	576.28	123.49	6.47E+02	4.42E+03	2.52E+03	1.21E+03	4.49E+04	9.69E+02	6.37E+02	2.26E+03	1.12E+03	3.07E+03	2.49E+02	2.87E+04	2.83E+03	3.46E+03	1.06E+04
P08133 ANXA6	EAILDIITSR	565.82	123.52	1.48E+05	1.06E+04	3.52E+02	1.71E+05	4.81E+03	1.16E+03	2.75E+03	2.41E+03	8.23E+02	1.99E+03	1.23E+05	2.66E+03	7.84E+04	2.16E+03	1.49E+05
P36542 ATPG	IYGLGSLALYEK	663.87	123.55	3.12E+05	8.80E+02	1.55E+03	3.58E+05	2.21E+04	2.04E+03	8.97E+02	1.33E+03	8.44E+02	1.14E+04	2.42E+05	1.40E+04	5.84E+03	5.39E+02	3.03E+04
P55809 SCOT1	YGLANWVWIPGK	682.84	123.57	1.08E+05	2.16E+03	1.73E+03	1.07E+04	3.63E+04	3.68E+03	2.48E+03	5.46E+03	3.89E+02	3.31E+02	1.24E+05	1.24E+03	1.54E+03	3.78E+03	4.88E+04
P07237 PDIA1	EADDIVNWLK	601.81	123.68	4.86E+04	2.07E+03	2.22E+03	3.63E+04	3.58E+04	1.91E+03	5.67E+02	4.32E+02	3.49E+03	8.34E+02	6.78E+04	8.65E+03	4.42E+03	1.85E+03	4.27E+03
Q9Y4G6 TLN2	TLAGAVSDLLK	543.82	123.73	6.58E+04	4.71E+03	4.54E+02	1.15E+05	1.15E+03	2.01E+04	4.79E+03	4.79E+03	4.68E+03	2.40E+02	1.45E+05	4.80E+03	8.37E+02	1.99E+03	5.38E+03
P11217 PYGM	QVIEQLSSGFFSPK	783.91	123.78	5.83E+04	5.89E+02	2.08E+03	8.18E+03	5.30E+02	5.58E+03	2.78E+03	2.56E+03	2.77E+03	1.65E+03	8.93E+04	1.87E+03	6.73E+02	1.20E+03	2.49E+04
P35579 MYH9	IMGIPEEQMGLLR	808.41	123.78	1.95E+04	2.40E+03	3.08E+03	8.59E+03	1.45E+03	2.51E+03	2.85E+03	2.23E+03	4.66E+02	1.55E+04	1.92E+04	2.63E+02	8.25E+03	1.76E+03	3.47E+03
Q13011 ECH1	VIGNQSLVNELAFTAR	866.47	123.8	5.76E+04	8.34E+02	6.33E+02	3.00E+02	9.25E+03	2.11E+03	3.29E+03	7.71E+03	6.97E+02	1.73E+03	7.34E+04	6.29E+03	1.36E+04	4.48E+02	1.60E+04
P49753 ACOT2	TPLAVELEVLDGHDPPDGR	677.34	124.14	1.09E+05	1.00E+03	2.30E+03	3.06E+04	1.32E+03	6.59E+02	5.71E+02	5.88E+02	1.40E+03	1.70E+03	1.22E+04	3.96E+03	5.69E+03	2.54E+04	4.43E+03
P02462 CO4A1	SFWLATIER	561.80	124.17	2.18E+03	1.36E+03	1.97E+03	4.85E+03	2.01E+03	1.24E+03	1.02E+03	3.15E+02	1.53E+03	3.64E+03	3.32E+03	3.22E+03	4.33E+04	8.73E+02	9.95E+03
P06744 G6PI	IEPELDGSAQVTSHDASTNG LINFIK	919.46	124.21	1.23E+04	2.39E+05	1.31E+05	7.47E+03	1.35E+04	8.52E+02	5.70E+04	3.26E+04	3.48E+03	1.05E+03	3.01E+03	6.58E+05	4.52E+05	2.63E+04	8.01E+04
P19404 NDUV2	AAAVLPVLDLAQR	668.90	124.52	4.05E+05	1.85E+02	2.93E+02	5.20E+05	7.31E+03	1.54E+03	1.00E+03	2.05E+03	9.33E+02	9.85E+02	2.82E+05	7.46E+03	9.65E+03	4.19E+02	7.24E+03
P12277 KCRB	LAVEALSSLDGDLAGR	793.92	124.55	1.14E+04	1.06E+03	7.74E+02	1.83E+05	2.24E+04	9.67E+02	5.95E+02	3.35E+03	2.50E+02	9.88E+02	1.33E+05	2.17E+04	8.69E+03	1.10E+03	3.70E+03
P20674 COX5A	ELGISTPEELGLDKV	800.43	124.6	1.49E+03	1.83E+03	1.78E+03	4.51E+04	5.04E+02	2.86E+03	6.52E+02	2.65E+04	3.12E+05	1.47E+04	3.35E+03	2.92E+03	3.14E+03	1.23E+05	1.97E+03
P13804 ETFA	LLYDLADQLHAAVGASR	604.99	124.65	8.52E+02	8.90E+02	1.72E+03	6.90E+04	2.07E+04	6.03E+02	1.66E+03	2.56E+03	1.03E+03	7.90E+02	5.98E+04	9.71E+03	9.03E+02	1.40E+03	4.79E+03
P49821 NDUV1	GPDWILGEIK	564.31	124.98	2.55E+05	9.09E+02	5.26E+03	2.36E+05	1.43E+03	8.49E+02	1.30E+03	2.40E+02	1.54E+03	3.73E+02	2.05E+05	1.14E+04	1.52E+04	8.73E+03	2.76E+04
P13804 ETFA	ASSTSPVEISEWLDQK	888.93	125.2	1.22E+03	9.25E+02	1.67E+03	9.24E+04	3.46E+03	5.15E+02	1.60E+03	4.67E+02	2.30E+03	2.11E+03	1.01E+05	6.98E+03	1.93E+03	5.86E+02	2.52E+03
P14543-2 NID1	ALEGLQYPFAVTSYGK	872.46	125.31	1.65E+03	3.54E+03	2.02E+03	7.88E+02	4.51E+02	2.37E+04	2.10E+03	4.39E+03	4.82E+02	4.17E+03	1.90E+03	1.04E+03	7.31E+02	7.94E+03	3.56E+03
P21980 TGM2	SWIGSVDILR	573.32	125.54	4.87E+04	1.03E+03	1.01E+03	1.39E+04	3.28E+03	2.93E+02	3.31E+02	1.33E+03	1.27E+03	5.29E+02	4.56E+03	1.53E+03	1.60E+03	7.16E+02	3.56E+02
P31937 3HIDH	TPVGFILGNMGNPMAK	852.43	125.67	3.58E+03	2.86E+03	4.46E+03	5.71E+03	4.84E+04	7.10E+02	4.33E+02	8.18E+02	1.27E+03	2.94E+03	5.88E+02	1.39E+04	3.00E+03	6.67E+02	8.13E+03
Q16836-2 HCDH	FAAEHTIFASNTSSLQITSIA NATTR	918.13	125.77	1.87E+03	6.14E+02	7.23E+02	1.02E+03	1.45E+03	4.71E+02	1.08E+03	6.61E+03	2.25E+04	8.03E+03	5.92E+02	8.69E+03	1.09E+03	3.16E+03	2.12E+02
P38646 GRP75	SLGIETLGGVFTK	661.37	126.27	5.27E+03	2.63E+02	1.83E+03	2.24E+03	1.54E+04	7.92E+02	1.30E+03	1.89E+03	1.74E+03	1.09E+03	3.42E+03	2.40E+02	1.12E+04	2.56E+03	1.15E+04
Q16891-2 IMMT	ELDSITPEVLPGWK	792.43	126.36	6.92E+04	5.03E+03	2.77E+02	4.42E+02	4.17E+04	1.58E+04	1.47E+03	1.31E+03	1.55E+03	3.74E+03	1.69E+05	9.71E+04	5.14E+04	1.35E+03	7.46E+04
Q99497 PARK7	EGPYDVVVLPGGNLAGQN LSESAAVK	862.11	126.38	8.81E+03	2.82E+02	4.43E+02	3.50E+02	9.20E+02	4.60E+02	2.87E+02	6.53E+02	1.50E+02	5.72E+02	2.30E+04	9.81E+02	4.34E+02	5.92E+02	3.94E+04
P10809 CH60	ISSIQSIVPALEIANAHR	640.36	126.51	5.00E+04	1.58E+04	1.29E+03	2.21E+03	2.27E+04	1.78E+02	3.59E+03	2.19E+04	2.80E+02	9.95E+02	4.56E+03	3.02E+04	1.12E+04	6.86E+03	8.53E+03
P05091 ALDH2	TIPIDGDFFSYTR	766.38	126.64	6.01E+02	2.04E+03	1.33E+03	1.03E+05	1.06E+03	2.10E+03	7.16E+03	6.56E+03	2.50E+02	3.40E+04	8.96E+02	8.44E+02	1.12E+03	9.90E+02	1.88E+03
P21980 TGM2	ALLVEPVINSY	609.34	126.96	2.81E+03	1.47E+04	1.81E+03	5.95E+04	1.76E+05	1.46E+03	6.25E+02	1.09E+04	6.41E+02	4.31E+02	7.24E+03	2.46E+04	4.76E+02	8.17E+02	8.04E+02
P13637 AT1A3	EAFQNAYLELGGGLGER	883.94	127.37	6.75E+03	7.43E+02	2.37E+03	2.32E+03	2.08E+02	1.96E+03	4.36E+02	9.97E+02	1.05E+03	3.11E+03	1.39E+03	2.10E+03	4.80E+02	5.65E+03	5.64E+03
P62805 H4	TVTAMDVVYALK	655.85	127.41	3.37E+05	1.71E+03	1.07E+05	3.40E+05	1.92E+04	1.01E+04	5.92E+03	3.28E+03	2.73E+03	8.04E+03	4.00E+05	2.72E+03	2.40E+04	7.90E+03	1.18E+04
O95831 AIFM1	ALGTEVIQLFPEK	722.90	127.54	2.71E+04	1.03E+03	9.04E+03	2.26E+03	5.26E+04	1.58E+03	4.49E+02	3.79E+03	3.87E+03	4.09E+02	4.86E+04	2.12E+05	6.89E+04	5.18E+02	1.34E+05
O95831 AIFM1	ILPEYLSNWTMEK	812.41	127.58	2.33E+02	2.51E+04	6.45E+03	2.16E+03	5.95E+02	5.11E+04	7.92E+02	8.04E+04	5.38E+04	5.84E+03	4.31E+03	1.28E+03	1.09E+03	1.02E+05	4.12E+02
P12110 CO6A2	DVTVTAIGIGDMFHEK	578.29	127.63	9.34E+02	2.08E+03	1.25E+03	1.26E+03	2.86E+02	1.29E+04	1.11E+04	2.50E+03	5.24E+02	3.96E+04	1.93E+03	2.46E+03	8.07E+02	1.42E+03	3.32E+03
Q01813 K6PP	IIEVVDAIMTTAQSHQR	638.00	127.75	2.08E+03	4.47E+02	1.25E+03	7.64E+02	4.47E+04	6.67E+02	1.73E+03	3.63E+02	4.36E+02	5.99E+02	2.41E+02	1.11E+03	2.87E+03	5.72E+02	2.02E+03
Q9BX66-11 SRBS	SVLEGGDIPLQGLSGLK	841.97	127.79	3.86E+04	2.00E+03	4.98E+02	2.80E+02	6.66E+02	1.30E+03	7.41E+02	4.22E+02	2.27E+02	3.53E+02	8.40E+04	1.99E+03	2.95E+03	5.89E+02	4.32E+04
P55809 SCOT1	AGGAGVPAFYTPTGYGTLV QEGGSPK	865.78	127.82	3.90E+04	1.78E+04	1.28E+04	3.95E+02	1.30E+04	1.95E+05	3.42E+03	7.00E+03	4.42E+02	1.82E+02	6.68E+04	7.13E+04	9.78E+03	4.08E+02	6.78E+04
P26038 MOES	TQEQLALEMAELTAR	852.43	127.84	8.16E+03	2.96E+03	3.96E+02	1.29E+04	2.18E+03	3.60E+03	4.92E+03	2.43E+03	9.80E+02	1.55E+04	2.43E+03	1.23E+03	7.76E+02	7.12E+02	5.52E+03
P19022 CADH2	FAIQTDPNSENDGLVTVVKPI DFETNR	964.16	128.05	1.83E+04	2.34E+03	8.41E+02	3.89E+02	2.82E+03	1.20E+03	3.28E+03	2.32E+03	6.50E+02	4.73E+02	4.33E+04	4.18E+02	8.98E+03	4.37E+02	4.81E+04
P20674 COX5A	PTLNELGISTPEELGLDK	963.51	128.19	3.06E+02	4.65E+03	1.54E+03	2.53E+02	3.11E+03	2.06E+04	1.44E+03	2.72E+02	3.75E+02	1.86E+02	1.25E+03	4.11E+03	8.34E+02	1.08E+03	1.81E+03
P00403 COX2	LLDVDNRVVLPIEAPIR	644.71	128.51	4.80E+02	1.90E+02	1.40E+03	3.01E+02	2.21E+04	1.63E+03	1.49E+02	9.35E+02	8.56E+02	1.93E+02	3.16E+03	5.42E+02	4.61E+02	1.54E+03	3.91E+02
P19022 CADH2	AFDLPLSPVTIK	650.88	128.59	3.97E+04	7.07E+02	1.76E+03	7.53E+03	9.06E+02	1.13E+03	7.01E+02	3.58E+02	1.43E+03	6.62E+02	5.16E+04	2.95E+02	1.06E+03	7.50E+02	4.00E+03
Q86TD4 SRCA	YQLYTGAEPPTSEFTVLMH GPK	824.07	128.64	6.07E+03	1.13E+03	5.94E+02	1.26E+03	2.12E+02	3.94E+02	9.90E+02	4.83E+02	1.52E+03	3.09E+02	3.20E+04	1.16E+03	6.28E+02	2.19E+02	5.25E+03
P01009 A1AT	LSSWVLLMK	538.81	128.7	1.42E+03	8.05E+02	6.92E+03	2.22E+02	2.56E+02	1.27E+03	1.79E+03	1.32E+03	2.51E+02	4.01E+04	6.78E+02	6.87E+02	3.78E+02	5.09E+02	8.27E+02
P28289 TMOD1	VEMIEVSMLEK	654.33	129.14	1.07E+03	5.72E+03	1.15E+03	3.33E+03	3.48										



P10515 ODP2	YLEKPITMLL	610.85	129.55	2.08E+04	1.37E+03	6.62E+02	7.25E+03	9.57E+02	1.36E+03	1.04E+03	2.60E+02	6.22E+02	8.43E+02	6.14E+02	8.13E+03	7.57E+04	1.87E+02	4.01E+03
P01009 A1AT	LAFAFSLYR	608.82	129.63	4.72E+02	3.65E+02	1.52E+03	1.03E+03	8.59E+02	1.33E+03	9.80E+02	1.72E+03	1.93E+04	1.41E+02	2.87E+03	1.62E+03	1.68E+03	1.39E+04	2.62E+03
P11217 PYGM	IGEDFISDLQLRK	550.29	130.12	2.83E+03	1.45E+03	4.00E+03	2.03E+03	5.54E+02	2.99E+02	3.17E+04	4.49E+04	1.99E+04	1.42E+03	1.71E+03	1.58E+03	7.14E+03	9.74E+03	4.42E+02
Q96199 SUCB2	ILNNSGLPITSAIDLEDAAK	1028.05	130.28	1.17E+04	1.06E+03	4.87E+02	8.03E+02	1.12E+03	5.91E+02	4.95E+02	2.96E+02	1.15E+03	1.47E+02	2.75E+04	3.42E+02	9.51E+02	1.57E+03	4.41E+03
P28289 TMOD1	TLNVESNFISGAGILR	845.96	130.33	1.93E+04	1.78E+03	1.44E+03	6.88E+02	1.66E+03	4.80E+03	1.11E+03	6.79E+02	8.92E+02	1.01E+03	8.82E+03	2.53E+03	5.30E+02	4.42E+02	2.75E+03
P07355-2 ANXA2	SYSPYDMLESIR	730.84	130.63	6.08E+02	4.44E+03	6.05E+02	5.20E+02	1.52E+04	7.07E+04	2.92E+03	4.49E+02	4.18E+02	1.63E+02	1.11E+03	1.91E+03	6.13E+02	3.07E+02	8.32E+02
P48047 ATPO	LSNTQGVVSAFSTMMSVHR	684.67	130.74	6.96E+04	1.39E+03	1.06E+03	1.87E+03	5.48E+02	2.17E+03	6.22E+02	2.32E+03	9.73E+02	1.02E+03	4.79E+04	3.30E+02	4.04E+04	3.46E+03	1.72E+03
Q16555 DPYL2	IAVGSDADLVWDPDSVK	950.49	130.88	5.24E+02	7.98E+02	5.27E+03	3.33E+02	2.52E+03	2.79E+03	1.05E+03	1.17E+03	5.32E+02	4.21E+04	4.22E+03	3.73E+03	1.73E+03	7.22E+02	5.11E+03
P36871 PGM1	SIFDFSALK	514.28	131.07	1.30E+03	9.21E+02	1.45E+03	6.28E+03	1.18E+03	2.63E+03	7.20E+02	3.29E+02	9.88E+04	2.84E+04	3.13E+03	1.90E+03	8.81E+02	9.13E+04	1.16E+04
P11217 PYGM	VAIQLNDTHPSLAPELMR	706.72	131.15	2.49E+02	1.85E+03	5.25E+02	9.67E+02	1.17E+03	2.48E+02	2.72E+02	1.97E+03	1.07E+04	8.18E+02	9.79E+02	9.28E+02	1.92E+03	2.18E+04	1.04E+03
Q702N8 XIRP1	ELQGLLNQVQALEK	791.94	131.19	2.46E+04	1.23E+03	5.29E+03	2.09E+03	2.42E+03	7.68E+02	5.12E+02	2.60E+03	7.39E+02	2.80E+03	4.97E+03	1.09E+03	1.86E+03	3.08E+02	9.58E+02
P42765 THIM	DGTVTAGNASGVADGAGA VIIASEDAVK	839.41	131.2	2.49E+03	1.33E+04	3.04E+03	2.57E+03	6.33E+03	2.70E+03	1.23E+03	6.62E+02	5.82E+02	2.47E+03	7.32E+02	1.10E+03	4.06E+02	4.22E+02	1.53E+03
Q16836-2 HCDH	FAGLHFFNPVPMK	535.29	131.29	1.79E+05	7.54E+02	2.69E+02	1.52E+03	4.91E+02	4.60E+02	7.46E+02	1.17E+03	4.19E+02	2.52E+02	1.28E+05	9.42E+02	5.06E+02	2.45E+02	1.30E+03
P06744 G6PI	MIPCDFLIPVQTQHPPIR	670.02	131.36	2.95E+04	1.08E+03	2.11E+03	6.21E+03	4.50E+03	1.42E+03	5.97E+02	5.41E+02	1.48E+03	1.31E+03	1.63E+04	4.12E+03	2.10E+03	6.19E+02	2.03E+04
Q95831 AIFM1	APSHVFPLLIGGGTAAFAAA	675.37	131.37	3.04E+03	3.20E+02	8.65E+02	2.38E+03	6.05E+04	2.15E+03	8.82E+02	1.72E+03	2.48E+03	6.45E+02	2.00E+03	2.68E+04	1.00E+03	9.08E+02	9.99E+03
P55290 CAD13	DIQGSQDIFK	632.33	131.62	1.70E+05	5.86E+03	1.08E+03	2.07E+05	7.57E+02	5.22E+04	5.24E+02	1.38E+04	4.73E+02	2.92E+03	7.15E+03	4.28E+03	1.23E+03	3.81E+03	3.42E+03
P07237 PDIA1	ILEFFGLK	483.79	131.8	2.75E+04	9.20E+02	3.81E+02	2.40E+02	1.18E+03	4.19E+02	6.15E+02	7.05E+02	2.88E+02	2.94E+02	3.84E+04	1.21E+03	9.65E+02	2.37E+02	9.83E+02
P07954 FUMH	THIQDAVPLTLGQEFSGYV QQVK	849.43	132.13	3.14E+03	3.02E+03	5.28E+04	1.15E+04	2.23E+04	2.00E+03	3.57E+03	2.85E+03	1.42E+04	7.88E+03	2.64E+04	1.96E+04	3.54E+03	2.03E+04	5.87E+04
Q14894 CRYM	GYLGVMPAYSAEDALTT	979.48	132.13	2.05E+04	6.61E+03	1.07E+04	4.59E+03	2.80E+03	6.57E+03	2.18E+02	6.67E+03	6.99E+02	7.12E+03	2.19E+04	1.24E+04	1.79E+04	1.74E+04	4.07E+04
P30041 PRDX6	PGLLLLGDVAPNFEANTTV GR	700.02	132.37	2.24E+04	5.80E+03	1.25E+04	6.73E+03	3.59E+03	3.20E+03	3.75E+03	8.67E+02	1.80E+03	2.88E+04	8.43E+03	1.19E+04	5.13E+03	9.82E+03	2.81E+03
Q01813 K6PP	MLAIYDGFDFGFAK	724.37	132.44	1.18E+05	1.12E+04	1.14E+04	9.04E+03	2.49E+04	2.67E+04	4.03E+04	2.58E+03	2.39E+03	6.45E+03	1.42E+05	1.66E+04	3.00E+04	9.27E+03	5.66E+03
Q16698 DECR	DPDMVQNTVSELIK	794.90	132.72	1.97E+05	1.62E+04	5.89E+03	8.15E+03	1.35E+04	4.35E+03	8.99E+03	6.67E+03	2.35E+04	3.39E+03	1.02E+05	9.96E+04	9.23E+03	1.60E+04	1.48E+05
P05091 ALDH2	TFVQEDIYDEFVER	895.42	133.13	2.15E+04	2.62E+04	9.07E+03	3.30E+03	1.07E+04	3.59E+03	1.15E+04	1.49E+04	2.32E+03	5.16E+03	1.35E+04	3.57E+03	1.05E+04	7.56E+02	1.80E+04
P11217 PYGM	LLSFVDDEAFIR	712.87	133.23	3.23E+04	1.50E+05	3.52E+03	4.64E+03	6.44E+03	3.40E+05	4.12E+03	1.14E+04	8.86E+03	8.67E+03	7.10E+04	6.16E+03	3.40E+04	7.99E+03	8.67E+04
P13533 MYH6	NRILYGDFRQRYRILNPVAI PEGQFIDSR	876.97	133.32	2.95E+05	1.10E+04	3.06E+03	6.11E+03	1.56E+06	7.43E+03	4.08E+03	2.08E+04	5.00E+03	4.43E+04	6.08E+05	6.49E+05	3.15E+05	8.28E+03	4.88E+05
P11310 ACADM	AFTGFIVEADTPGIQIGR	946.48	133.41	1.80E+04	1.13E+04	4.42E+03	3.19E+04	3.64E+03	6.37E+03	3.99E+03	1.45E+04	1.98E+03	2.39E+03	7.43E+03	9.14E+03	3.63E+03	3.00E+03	9.85E+03
Q96199 SUCB2	ETYLAILMDR	612.82	133.51	8.64E+03	6.31E+03	3.88E+02	3.41E+03	3.25E+04	2.00E+03	2.13E+03	2.58E+03	4.03E+03	3.28E+03	1.21E+03	2.48E+04	2.83E+03	1.33E+03	4.42E+03
P07339 CATD	AIGAVPLIQGEYMIPCEK	966.50	133.53	3.42E+04	3.53E+03	4.56E+04	2.29E+03	4.20E+03	4.85E+03	1.39E+04	2.22E+03	1.33E+05	5.05E+03	9.40E+03	3.46E+03	5.43E+03	1.24E+04	1.77E+04
Q16795 NDUA9	NDFEDVVFVK	630.30	133.56	1.62E+04	4.82E+04	5.27E+03	1.72E+03	3.82E+03	4.51E+04	3.28E+03	6.48E+04	8.93E+03	1.71E+03	1.10E+04	7.17E+03	6.77E+03	1.21E+04	1.73E+03
P20674 COX5A	WVTYFNKPIDAWELR	685.01	133.82	1.70E+03	1.29E+04	4.58E+03	3.29E+03	4.70E+03	7.60E+04	3.70E+03	3.17E+03	2.73E+04	1.58E+03	4.86E+03	1.00E+04	4.04E+03	5.88E+04	1.96E+03
O75746 CMC1	IAPLAEGALPYNLAELQR	647.03	133.84	2.42E+04	4.48E+03	7.13E+03	7.16E+02	3.73E+03	3.09E+03	7.63E+03	2.55E+03	1.60E+03	1.65E+03	2.65E+04	3.67E+03	3.07E+03	2.25E+03	4.05E+04
P10809 CH60	TLNDELEIEGGMK	752.88	133.94	3.61E+04	6.14E+03	1.71E+04	3.84E+03	7.19E+03	5.89E+03	1.39E+04	1.83E+04	3.22E+03	8.56E+03	5.54E+04	6.65E+03	2.63E+04	2.67E+03	7.76E+04
P38646 GRP75	AQFEGIVTDLIR	681.37	134.1	2.23E+05	4.01E+03	3.21E+03	1.92E+03	1.94E+04	8.53E+03	1.59E+03	5.56E+03	1.52E+04	6.82E+03	1.62E+05	1.02E+04	1.00E+05	2.15E+04	1.33E+04
O75746 CMC1	DLGIFGLYK	513.29	134.1	2.20E+03	6.51E+03	7.87E+02	4.09E+03	8.57E+02	2.10E+03	6.46E+03	1.39E+03	3.86E+03	6.74E+03	2.16E+03	3.79E+03	1.50E+03	3.24E+04	1.92E+03
P13804 ETFA	LEVAPISDIIAIK	691.42	134.2	3.51E+05	2.70E+03	7.42E+02	1.43E+02	4.90E+03	5.61E+03	1.72E+03	3.53E+03	1.18E+03	4.23E+03	2.75E+05	7.04E+03	6.60E+04	1.51E+03	1.92E+05
Q16891-2 IMMT	GMSVSDLADKLDLSTDDLNSL IAHAHR	667.34	134.81	3.93E+03	7.36E+03	1.41E+03	5.57E+03	3.11E+04	3.65E+03	1.37E+04	3.31E+03	5.88E+03	3.63E+02	4.42E+04	8.55E+03	4.95E+03	1.39E+04	7.06E+02
P42126 D3D2	DADVQNFSVFSISK	735.37	135.05	5.17E+03	6.45E+04	2.04E+04	1.13E+04	5.54E+03	6.56E+04	1.06E+04	5.63E+04	8.52E+03	1.32E+04	2.65E+04	6.92E+03	1.62E+04	9.43E+03	7.38E+03
Q05639 EF1A2	VETGILRPGMVVTFAPVNIT TEVK	857.81	135.18	5.11E+03	3.93E+04	1.70E+03	1.99E+04	1.10E+03	8.81E+04	2.97E+03	6.67E+04	2.06E+03	2.33E+03	6.81E+03	2.28E+03	1.16E+03	6.67E+03	1.17E+04
Q9BX66-11 SRBS	HFIPADYLESTEEFIR	656.32	135.27	6.43E+04	8.31E+03	5.99E+04	1.18E+04	1.42E+04	4.27E+03	5.47E+03	1.26E+04	1.13E+04	4.18E+03	5.55E+04	3.92E+03	6.79E+03	1.01E+04	5.45E+03
P02790 HEMO	EVGTPHGIIILDSVDAAFICP GSSR	814.41	135.3	2.58E+04	1.32E+04	1.62E+04	5.21E+03	2.33E+03	2.28E+04	6.90E+03	6.58E+03	1.12E+05	1.28E+05	2.33E+04	1.28E+05	2.27E+04	4.68E+03	2.17E+04
Q16795 NDUA9	FGPIPLGSLGWK	636.36	135.32	4.01E+02	1.60E+04	5.94E+04	6.41E+03	1.99E+05	1.83E+05	1.36E+05	1.41E+05	1.01E+04	4.82E+03	5.60E+03	1.13E+05	2.33E+03	6.32E+03	2.32E+03
P00568 KAD1	IGQPTLLLYVDAGPETMTQ	735.05	135.41	1.78E+04	3.36E+04	2.10E+03	9.32E+03	2.45E+05	7.58E+03	9.60E+03	9.92E+03	7.42E+03	3.17E+05	4.56E+03	3.60E+04	6.47E+04	5.11E+04	2.04E+03
Q16698 DECR	EQWDTIEELIR	716.36	135.54	2.92E+05	1.15E+05	9.67E+04	2.85E+05	8.96E+04	2.71E+05	2.01E+05	6.89E+04	2.62E+05	2.83E+05	5.36E+04	7.59E+04	1.80E+05	2.88E+05	8.70E+03
P20674 COX5A	VIQELRPTLNELGISTPEELG LDK	888.82	135.56	1.25E+05	3.35E+03	3.05E+05	5.04E+03	5.27E+04	8.45E+03	9.72E+03	2.28E+04	5.75E+04	1.54E+05	9.15E+04	6.71E+04	1.82E+04	7.42E+04	1.49E+05
P09972 ALDOC	TPSALAIENANVLAR	826.97	135.77	1.32E+04	1.09E+04	5.93E+04	1.35E+04	9.94E+04	1.20E+05	2.11E+04	2.26E+04	9.71E+04	8.55E+04	1.14E+05	9.12E+04	6.78E+04	7.35E+04	7.46E+04
P08133 ANXA6	GLGTDEDTIIDITHR	590.31	135.82	1.14E+05	1.37E+04	7.26E+04	1.01E+05	1.28E+05	3.81E+04	2.01E+05	1.73E+05	1.17E+05	8.33E+04	5.82E+04	1.47E+05	8.00E+04	1.68E+05	4.58E+04
P09972 ALDOC	YTPPEIAMATVTALR	833.43	135.82	2.23E+05	4.92E+05	1.17E+05	1.74E+05	6.93E+04	2.54E+05	1.44E+05	1.69E+05	1.46E+05	9.58E+04	2.24E+05	7.93E+04	1.23E+05	1.23E+05	2.12E+05
P49411 EFTU	DLEKPFLLPVEAVYSVPGR	710.39	135.86	3.55E+05	1.24E+05	5.43E+04	2.94E+05	6.68E+04	6.06E+04	1.04E+05	6.13E+04	2.15E+05	3.91E+04	2.39E+05	1.15E+05	1.74E+05	4.35E+04	1.49E+05
Q16836-2 HCDH	LLVPYLMEAIR	659.38	135.92	1.10E+06	9.91E+05	1.45E+05	4.53E+05	1.65E+05	1.03E+06	1.48E+04	7.69E+04	1.19E+05	1.60E+05	3.78E+05	1.01E+05	2.11E+05	7.13E+04	2.04E+05
P63316 TNNC1	IDYDEFLEFMK	725.33	135.92	2.90E+05	2.95E+04	2.11E+												

P00403 COX2	MLPPLFLEPGDLR	749.41	135.97	1.00E+05	2.49E+05	4.02E+04	1.59E+05	1.80E+05	1.30E+05	2.04E+05	1.80E+05	2.33E+05	1.20E+05	1.69E+05	2.06E+04	1.08E+05	4.04E+04	1.36E+05
P13533 MYH6	NLQEEISDLTEQLGEGGK	654.32	135.97	1.98E+05	2.37E+05	2.86E+04	2.49E+05	1.73E+05	2.45E+05	2.69E+05	2.47E+05	8.15E+04	2.53E+05	2.22E+05	5.79E+04	1.45E+05	5.17E+04	2.16E+05
P01009 A1AT	ITPNLAEFAP	561.80	136	2.93E+04	1.50E+04	2.49E+04	2.17E+04	1.11E+05	3.58E+04	4.81E+04	8.78E+03	7.48E+04	1.17E+05	2.29E+04	4.77E+04	5.11E+04	1.92E+04	2.75E+04
P28289 TMOD1	DLDEDEILGALTEEELR	980.48	136.03	1.40E+05	1.61E+05	1.05E+04	1.82E+05	1.57E+04	1.58E+05	1.88E+05	2.10E+05	1.56E+05	1.57E+05	2.27E+05	4.65E+04	2.33E+04	4.59E+04	2.13E+05
P32119 PRDX2	EGGLGPLNIPLLDVTR	867.99	136.06	1.54E+05	1.49E+05	1.62E+05	1.94E+05	7.36E+04	2.07E+05	1.01E+05	7.52E+04	1.88E+04	1.51E+05	2.09E+05	4.62E+04	1.02E+05	2.45E+04	1.81E+05
P48047 ATPO	FSPLTTNLLAENGR	937.01	136.06	2.98E+05	1.93E+05	1.21E+04	1.64E+05	1.45E+05	2.66E+05	1.20E+05	8.98E+04	1.70E+04	1.55E+04	1.16E+05	1.45E+05	1.10E+04	1.12E+05	1.43E+05
Q13011 ECH1	VFPDKEVMLDAAALAAEI SSK	773.41	136.1	9.26E+04	1.60E+05	1.04E+04	5.00E+04	3.68E+04	1.32E+05	3.04E+05	1.56E+05	1.32E+04	1.32E+05	4.64E+04	1.21E+05	1.97E+05	1.35E+05	5.73E+04
P31040 DHSA	LGANSLLDLVVFGFR	737.42	136.11	7.46E+04	5.71E+04	1.22E+05	4.33E+04	6.37E+04	1.19E+05	8.69E+04	1.00E+05	2.30E+04	4.50E+04	8.02E+04	1.46E+05	4.02E+04	9.59E+04	4.11E+04
P00568 KAD1	GQLVPLETVLDMLR	792.45	136.12	5.13E+04	9.83E+04	4.32E+04	1.29E+05	1.53E+04	1.91E+05	1.60E+05	1.29E+05	3.94E+04	2.81E+04	1.33E+05	5.66E+04	1.50E+04	6.25E+04	1.38E+05
P12829 MYL4	MLDFETFLPILQH	802.41	136.25	8.89E+04	8.03E+04	1.94E+04	7.46E+04	1.71E+05	1.30E+05	1.11E+05	3.84E+04	2.96E+04	2.51E+04	1.14E+05	1.23E+05	5.05E+04	2.87E+04	9.68E+03
P00403 COX2	IFEMGPVFTL	577.30	136.37	1.25E+05	1.93E+05	3.19E+04	1.82E+05	1.61E+05	3.25E+05	8.47E+04	1.02E+05	1.60E+05	1.47E+05	1.58E+05	1.86E+05	7.95E+04	1.35E+05	2.17E+05
P10809 CH60	ALMLQGVDLLADAVAVTM GPK	705.05	136.41	1.42E+04	1.88E+03	1.08E+04	5.96E+03	2.34E+04	1.53E+04	2.50E+04	5.77E+03	2.73E+04	1.12E+04	1.25E+04	1.89E+03	5.64E+03	1.77E+04	7.41E+03
Q09666 AHNK	KLEGDIK	401.74	34.12	2.07E+02	1.27E+02	4.02E+02	1.49E+03	6.33E+03	1.34E+02	1.83E+02	1.65E+02	1.50E+03	3.65E+03	1.51E+02	5.06E+02	9.34E+02	2.24E+03	4.17E+03
Q09666 AHNK	KIEGDLC	401.74	34.12	2.07E+02	1.27E+02	4.02E+02	1.49E+03	6.33E+03	1.34E+02	1.83E+02	1.65E+02	1.50E+03	3.65E+03	1.51E+02	5.06E+02	9.34E+02	2.24E+03	4.17E+03
P14854 CX6B1	AEGTFPGK	403.70	43.72	2.29E+03	3.42E+03	1.26E+03	3.77E+03	1.32E+03	2.40E+03	6.83E+02	2.18E+03	6.40E+03	1.15E+03	2.88E+03	3.17E+03	1.90E+03	1.69E+03	3.31E+03
O14558 HSPB6	VVGEHVEVHAR	411.22	44.45	1.60E+02	2.68E+02	5.19E+02	9.10E+02	2.60E+03	1.99E+02	6.00E+02	2.98E+03	5.29E+03	2.23E+02	5.67E+03	1.73E+04	1.44E+03	4.44E+03	3.54E+03
Q5VST9-6 OBSCN	AEGAPASPPSTGTR	649.82	47.89	5.12E+02	1.60E+03	2.12E+03	6.57E+03	1.65E+04	4.68E+03	9.44E+03	4.08E+02	5.35E+03	1.12E+03	1.99E+04	3.31E+03	6.55E+02	2.83E+03	2.04E+03
P02671-2 FIBA	GGSTSYGTGSETESPR	786.84	49.11	8.97E+03	6.42E+02	1.83E+02	4.07E+03	5.83E+04	9.76E+03	1.28E+03	3.74E+03	1.37E+04	2.49E+02	1.16E+04	6.85E+02	4.83E+02	3.62E+03	2.01E+03
O75947 ATP5H	YTAQVDAEEK	577.27	49.52	2.47E+04	6.71E+03	3.24E+02	2.64E+04	2.94E+04	2.95E+04	6.04E+02	6.75E+02	3.08E+02	2.40E+04	2.03E+04	5.72E+03	2.06E+02	1.28E+04	3.24E+04
Q99623 PHB2	IVAQEGEAEEK	608.31	49.73	1.03E+04	2.10E+03	1.05E+03	1.23E+04	3.39E+04	1.33E+03	1.11E+03	1.15E+03	2.96E+04	1.88E+04	1.19E+04	6.59E+03	2.41E+02	9.28E+03	1.47E+04
P50461 CSRP3	ALDSTTVAAH	493.25	50.03	5.57E+03	6.62E+03	1.12E+03	9.44E+03	6.82E+02	8.87E+02	1.34E+02	3.18E+02	6.84E+03	1.61E+02	1.98E+04	6.58E+03	7.11E+02	4.90E+03	4.61E+03
P50461 CSRP3	SLESTNVTDK	547.27	50.14	2.72E+04	3.45E+03	2.38E+03	2.35E+04	3.47E+03	3.27E+04	2.94E+02	5.58E+02	2.67E+04	1.39E+02	5.40E+04	1.29E+04	1.62E+03	1.70E+04	2.47E+04
P24539 AT5F1	LAQLEEAK	451.25	52.19	1.42E+04	5.05E+03	8.10E+02	8.64E+03	6.54E+03	1.31E+04	1.52E+03	1.76E+03	1.16E+04	5.86E+02	2.22E+04	5.48E+03	5.80E+03	4.42E+03	1.03E+04
Q9BZL4 PP12C	SQESSTLEGGPSAR	703.33	52.49	1.29E+02	3.72E+03	5.92E+02	3.17E+03	5.85E+02	5.98E+02	2.03E+03	5.31E+02	4.82E+03	1.22E+04	6.13E+02	2.95E+03	1.14E+04	2.20E+03	4.87E+02
Q9Y490 TLN1	ADAEGESDLENSR	696.80	53	2.43E+03	2.12E+03	9.61E+02	1.59E+03	9.17E+03	1.77E+02	3.12E+02	6.76E+02	2.93E+03	3.59E+02	1.61E+04	7.17E+02	5.72E+02	3.14E+02	1.06E+03
P82909 RT36	SAGLPSHSSVISQHSK	541.28	53.02	3.72E+02	2.92E+02	1.86E+02	4.78E+02	8.37E+03	3.88E+03	6.68E+02	9.41E+02	7.73E+02	5.25E+02	1.53E+03	1.26E+03	1.40E+04	1.47E+02	3.30E+02
Q9BZL4 PP12C	VPGVENSDDSPAQR	678.33	53.26	3.68E+03	2.95E+03	6.95E+03	1.48E+03	6.04E+02	5.56E+02	1.36E+02	2.26E+02	1.93E+02	2.53E+02	1.24E+04	2.08E+03	1.78E+02	1.93E+02	3.77E+03
Q13554 KCC2B	ESSDSANTTIEDEDAK	856.36	53.31	1.72E+03	2.06E+03	1.02E+03	5.10E+03	5.16E+02	5.36E+02	6.54E+02	4.17E+03	1.74E+02	3.44E+02	8.56E+03	6.81E+02	1.81E+02	1.38E+02	4.37E+03
P27824 CALX	SDAEEDGGTVSQEEDR	926.87	53.67	8.87E+03	3.71E+03	1.75E+02	7.49E+03	1.75E+03	4.48E+02	3.38E+02	4.15E+02	2.32E+02	1.36E+02	8.80E+03	1.54E+03	2.04E+03	6.96E+02	1.54E+02
P30042 ES1	GVEVTVGHEQEEGGK	518.92	53.69	6.73E+02	3.64E+03	3.97E+02	2.71E+04	2.77E+03	2.44E+03	1.16E+03	1.97E+03	6.77E+02	2.49E+02	2.78E+04	5.07E+03	7.50E+02	3.83E+02	3.88E+04
Q09666 AHNK	ADLDVSGPK	451.24	54.76	4.93E+03	1.78E+03	1.06E+03	6.83E+03	6.39E+03	1.45E+04	8.43E+02	1.02E+04	6.20E+03	5.01E+03	2.82E+03	8.11E+02	3.51E+02	6.35E+03	3.71E+03
Q09666 AHNK	ADIDVSGPK	451.24	54.76	4.93E+03	1.78E+03	1.06E+03	6.83E+03	6.39E+03	1.45E+04	8.43E+02	1.02E+04	6.20E+03	5.01E+03	2.82E+03	8.11E+02	3.51E+02	6.35E+03	3.71E+03
Q09666 AHNK	ADVDISGPK	451.24	54.99	8.36E+02	8.08E+03	5.03E+03	8.37E+03	1.74E+04	7.71E+03	2.66E+03	9.21E+03	3.89E+03	4.49E+02	4.77E+03	1.92E+02	1.30E+03	1.65E+03	7.79E+03
Q5VST9-6 OBSCN	AAPGLTANKPPAAAAAR	492.95	55.35	3.09E+03	4.78E+03	2.39E+03	1.61E+04	4.19E+04	1.18E+03	3.23E+03	1.41E+03	2.62E+03	6.66E+02	4.49E+04	2.29E+04	9.64E+02	3.26E+03	1.75E+03
O60237 MYPT2	LESGGSNPTTSDSYGDR	871.88	55.45	1.93E+04	5.16E+03	1.49E+02	2.27E+04	4.43E+03	2.89E+04	5.88E+02	3.51E+02	1.97E+03	2.88E+02	1.56E+04	2.84E+03	6.07E+02	2.07E+03	9.21E+02
P26373 RL13	STESLQANVQR	616.81	56.15	2.36E+03	4.73E+03	1.26E+03	1.96E+02	2.72E+02	1.71E+03	7.82E+02	3.01E+03	8.06E+03	2.04E+04	1.46E+03	7.03E+02	1.94E+03	4.62E+03	1.50E+03
P35573-3 GDE	SPSHQSVVAVSR	501.94	56.64	1.57E+03	1.64E+03	2.65E+03	1.83E+03	3.31E+04	5.23E+02	5.58E+04	2.40E+04	4.58E+02	1.36E+03	2.43E+03	2.42E+04	1.10E+04	1.27E+03	2.12E+03
P00441 SODC	HVGD LGNVTADK	613.31	56.87	2.74E+03	3.61E+03	9.71E+03	5.90E+04	3.99E+03	4.77E+03	5.82E+03	1.46E+03	1.24E+02	2.08E+03	4.68E+04	2.28E+04	1.71E+03	9.67E+03	2.92E+04
P22061 PIMT	SGGASHSELIHNL	493.26	57.57	3.86E+03	3.58E+02	3.35E+03	1.88E+03	1.71E+04	1.25E+04	3.28E+04	8.90E+03	8.74E+03	3.10E+04	4.36E+02	2.31E+04	7.99E+03	2.55E+03	2.91E+03
P84243 H33	YRPGTVALR	516.80	57.63	7.19E+04	4.25E+04	6.47E+04	1.19E+05	5.67E+04	1.41E+05	6.77E+04	4.98E+03	1.28E+03	1.58E+03	1.18E+05	4.22E+04	5.02E+04	3.93E+03	1.77E+02
P00338 LDHA	VTLTSEEAR	567.79	58.07	5.21E+04	3.78E+04	1.30E+04	6.72E+04	1.02E+05	6.07E+03	2.05E+03	1.16E+04	4.82E+02	5.43E+02	4.97E+04	5.53E+04	4.73E+03	9.85E+02	5.68E+04
Q9HBL0 TENS1	VATTPGSPSLGR	571.81	58.17	1.29E+03	1.70E+03	4.80E+03	4.31E+04	2.02E+04	4.21E+04	4.24E+04	3.70E+04	1.57E+02	1.81E+03	8.57E+03	1.71E+04	1.17E+04	2.66E+02	3.36E+03
P99999 CYC	TGQAPGYSYTAANK	714.84	58.25	6.03E+04	2.44E+04	3.70E+03	6.26E+04	1.22E+05	6.62E+03	1.80E+03	1.30E+03	5.29E+02	8.55E+02	1.54E+05	7.15E+03	9.84E+02	1.66E+02	6.92E+02
P02671-2 FIBA	NPSSAGSWNSGSSGPGSTG	655.29	58.67	3.37E+04	6.46E+03	1.03E+04	1.04E+04	5.47E+04	4.53E+03	4.83E+03	5.59E+03	3.89E+03	5.66E+02	2.95E+04	9.72E+03	1.11E+03	9.06E+02	1.43E+03
Q15084 PDIA6	GESPVDYDGGGR	576.27	58.84	6.94E+03	3.99E+03	9.32E+02	2.62E+03	1.47E+03	1.08E+04	7.22E+03	1.78E+03	1.60E+05	2.48E+05	4.14E+03	4.81E+03	1.31E+03	2.15E+04	5.97E+03
P50461 CSRP3	ALDSTTVAHESE	665.81	59.7	1.44E+04	2.71E+03	1.79E+03	4.56E+03	6.92E+02	1.49E+03	3.58E+02	1.01E+04	1.33E+02	9.25E+02	7.62E+03	2.50E+03	3.44E+03	1.73E+03	1.51E+03
Q03252 LMNB2	AGGPATPLSPTR	562.81	59.72	7.73E+02	4.20E+02	6.76E+03	1.18E+04	6.09E+03	2.85E+03	3.34E+04	5.57E+04	3.56E+04	3.70E+04	6.56E+03	2.24E+03	6.62E+03	1.15E+04	2.60E+03
Q16775 GLO2	TVQQHAGETDPVTTMR	590.95	60.46	3.07E+03	1.50E+04	1.00E+04	3.36E+04	4.35E+04	1.72E+03	2.07E+02	1.30E+03	9.40E+03	1.39E+04	4.93E+04	1.83E+04	2.43E+03	1.10E+04	4.87E+04
Q6YN16 HSDL2	SGAVEETFR	498.24	60.47	5.75E+02	2.21E+02	6.65E+02	1.91E+03	1.00E+03	4.15E+02	2.31E+03	3.48E+03	3.02E+03	3.09E+04	5.19E+03	2.58E+03	5.90E+03	1.81E+03	8.25E+03
P82909 RT36	SAGLPSHSSVISQH	469.57	60.54	2.81E+03	5.13E+04	5.66E+04	1.16E+05	2.08E+04	1.29E+05	3.62E+04	3.79E+03	1.37E+04	1.18E+03	4.72E+04	4.11E+04	3.40E+03	1	

Q9UBY9 HSPB7	ALPAQDPPMEK	598.80	62.31	1.08E+05	4.87E+04	1.12E+03	1.21E+05	7.88E+04	2.51E+05	6.36E+03	1.15E+03	5.84E+03	1.53E+03	2.79E+05	2.97E+04	1.74E+03	1.05E+03	3.68E+02
P63104 1433Z	SVTEQGAELSNEER	774.86	62.46	1.30E+05	6.78E+04	1.68E+03	1.23E+05	9.88E+04	1.95E+03	5.46E+02	7.05E+02	7.47E+02	9.90E+02	1.27E+05	5.66E+04	5.05E+02	1.12E+03	1.20E+05
P30084 ECHM	AFAAGADIK	432.23	62.47	1.37E+04	4.00E+02	7.23E+02	1.56E+03	1.44E+03	3.42E+02	1.78E+03	3.66E+02	1.83E+03	3.33E+02	1.28E+03	1.73E+03	3.73E+02	1.19E+03	8.23E+02
P30101 PDIA3	QAGPASVPLR	498.28	62.61	1.51E+03	8.44E+02	1.37E+03	7.03E+02	9.00E+02	8.45E+02	4.70E+02	7.85E+02	9.54E+02	2.79E+04	4.61E+02	2.06E+03	1.16E+03	2.04E+03	6.95E+02
Q08380 LG3BP	ASHEEVEGLVEK	442.89	62.8	2.39E+04	3.29E+04	1.10E+03	1.91E+04	3.44E+03	1.76E+04	1.85E+04	7.63E+02	7.57E+02	3.47E+02	1.12E+05	4.41E+03	5.10E+02	3.83E+02	5.94E+04
O14639-4 ABLM1	STSQGSINSVPVYSR	741.86	62.93	3.50E+04	5.68E+03	1.22E+03	4.10E+04	9.73E+02	1.44E+03	4.11E+02	1.61E+02	5.32E+02	1.61E+02	3.57E+04	6.27E+03	1.39E+03	5.28E+02	6.76E+02
Q6YN16 HSDL2	DEQQISAAVEK	609.30	62.93	6.38E+04	3.43E+04	4.99E+02	1.85E+02	1.28E+05	3.26E+03	5.29E+02	1.57E+03	1.60E+03	4.51E+02	7.03E+04	2.31E+04	5.03E+02	6.28E+02	1.04E+05
P50395 GDIB	IPGSPPEMGR	564.28	62.98	2.89E+04	2.98E+03	3.32E+02	1.07E+04	1.35E+04	1.11E+03	1.16E+03	2.45E+05	1.07E+04	3.43E+04	2.04E+04	6.07E+02	4.83E+02	2.55E+03	1.22E+04
P04179 SODM	HHAAYVNNLNVTTEK	580.29	62.98	2.74E+02	8.09E+04	2.36E+04	7.38E+04	4.77E+05	1.23E+05	4.43E+05	4.37E+05	6.16E+02	2.41E+02	2.39E+04	8.29E+02	5.34E+04	6.29E+05	4.02E+02
Q16134 ETFD	GIATNDVGIQK	558.30	62.98	1.50E+04	2.09E+03	1.01E+03	1.65E+04	5.28E+04	2.10E+04	1.35E+03	1.75E+03	5.71E+02	3.43E+02	4.20E+04	9.64E+02	8.31E+02	1.70E+05	2.05E+04
Q9NX63 CHCH3	LSENVDR	473.25	63.06	3.32E+04	3.05E+04	3.25E+02	5.70E+04	4.99E+04	6.16E+03	1.20E+05	1.13E+05	1.28E+05	2.36E+03	1.23E+05	3.84E+04	4.56E+04	3.89E+04	4.75E+02
P30049 ATPD	IEANEALVK	493.78	63.19	5.01E+04	1.45E+05	3.43E+03	3.27E+05	1.52E+04	7.04E+02	1.55E+04	4.45E+02	3.82E+03	6.20E+03	9.87E+04	1.54E+05	3.40E+03	1.42E+05	9.35E+04
Q03252 LMNB2	ELEEAMAGER	567.76	63.24	9.27E+02	1.69E+04	1.76E+03	1.80E+02	1.71E+02	1.39E+03	6.20E+02	5.68E+04	2.49E+03	5.73E+02	3.96E+04	1.34E+04	5.24E+02	1.02E+03	2.11E+04
P30153 2AAA	MAGDPVANVR	515.26	63.37	6.50E+03	5.85E+04	1.47E+04	4.04E+04	2.68E+05	4.92E+04	2.34E+05	1.40E+05	7.59E+03	4.17E+04	2.06E+03	1.33E+05	4.39E+03	2.92E+04	5.10E+04
P61981 1433G	YLAEVATGEK	540.78	63.5	2.67E+04	5.07E+04	5.23E+02	8.87E+04	1.64E+05	1.35E+05	3.81E+02	4.72E+03	9.33E+04	2.42E+04	2.82E+05	4.34E+04	8.52E+02	4.05E+04	4.67E+04
P06733 ENOA	IGAENVYHNLK	572.31	63.66	8.73E+03	1.46E+04	2.34E+03	1.43E+04	8.23E+03	3.28E+02	8.22E+02	2.15E+02	3.00E+02	1.23E+03	7.03E+04	3.37E+04	1.35E+03	3.65E+03	3.87E+04
P82909 RT36	DNPKNVSEALR	447.24	63.92	4.48E+02	5.96E+02	2.20E+03	4.35E+02	5.35E+02	3.40E+02	7.42E+02	2.14E+04	6.74E+04	1.10E+05	3.33E+03	1.08E+03	1.21E+03	2.76E+04	2.26E+03
P00450 CERU	VNKDDEEFIESNK	522.92	63.92	1.95E+02	2.56E+03	5.78E+02	6.80E+02	1.20E+04	4.90E+02	3.83E+02	7.62E+02	1.92E+03	3.98E+04	1.41E+03	6.75E+03	5.22E+02	1.42E+03	2.32E+03
P63104 1433Z	YLAEVAAGDDK	576.28	63.99	1.73E+04	1.78E+04	1.41E+03	3.73E+03	9.56E+03	1.39E+04	5.59E+03	1.79E+02	5.16E+04	1.48E+03	7.75E+04	1.64E+03	5.87E+02	7.23E+03	6.11E+04
P09382 LEG1	FNAHGDAANTIVCNSK	530.92	64.11	9.14E+02	9.07E+03	5.58E+03	3.19E+03	1.94E+03	8.90E+02	7.75E+02	3.10E+03	3.68E+03	1.45E+03	5.69E+04	1.39E+03	1.55E+02	5.53E+03	6.97E+04
P30101 PDIA3	LAPEYEAATAA	596.30	64.12	7.44E+04	8.49E+04	5.70E+04	7.43E+03	1.08E+05	9.51E+04	5.82E+04	4.71E+04	1.30E+04	7.42E+02	1.75E+05	9.56E+04	4.69E+04	1.41E+03	1.07E+05
O14639-4 ABLM1	SSGREEDDEELLR	512.24	64.29	2.73E+02	8.04E+02	1.39E+07	7.88E+03	1.23E+03	1.55E+03	6.53E+03	2.09E+06	3.90E+04	3.41E+02	6.19E+02	1.23E+03	1.39E+07	3.63E+04	4.14E+03
P10606 COX5B	LVPQQLAH	453.26	64.38	2.55E+04	1.65E+04	5.61E+02	4.80E+03	2.27E+04	6.58E+03	5.14E+03	2.22E+03	1.02E+06	8.31E+05	1.13E+04	8.99E+03	1.69E+03	2.09E+05	2.17E+04
P30101 PDIA3	SEPIPESNDGPVK	684.83	64.48	2.24E+03	5.33E+02	5.06E+04	1.39E+05	1.03E+05	1.96E+05	1.87E+04	3.61E+04	3.80E+04	5.17E+04	4.63E+02	6.67E+02	4.08E+04	2.42E+04	1.10E+03
P61978 HNRPK	IDEPLEGSEDR	630.29	64.51	8.12E+04	9.53E+04	3.50E+02	1.19E+05	9.99E+04	2.07E+03	1.82E+03	7.59E+02	2.57E+03	3.90E+02	6.49E+04	9.21E+04	2.87E+02	7.12E+02	9.18E+04
Q6YN16 HSDL2	DSLSDDVVK	489.24	64.64	3.06E+02	1.24E+04	2.45E+03	2.30E+04	6.24E+04	3.02E+04	3.74E+03	2.54E+04	5.93E+02	8.72E+03	8.22E+02	6.59E+02	9.96E+03	6.11E+02	3.64E+04
Q9HBL0 TENS1	AIASPGSPSLGR	556.81	64.72	1.45E+03	2.77E+03	7.33E+03	5.50E+04	1.12E+03	7.51E+03	2.54E+03	7.91E+02	3.74E+02	8.04E+02	1.05E+03	6.67E+03	4.70E+02	5.79E+02	2.94E+03
Q02338 BDH	ALTATTPYTR	547.79	65.36	9.21E+02	4.70E+02	1.73E+03	3.30E+02	5.58E+03	1.42E+03	2.34E+03	5.08E+02	1.02E+04	3.29E+04	1.09E+03	5.54E+02	2.46E+04	2.59E+04	6.50E+02
P01859 IGHG2	GLPAPIEK	412.75	65.41	1.80E+05	1.00E+03	2.96E+03	2.94E+02	6.05E+03	1.87E+03	8.77E+02	8.09E+02	6.22E+04	2.89E+05	1.43E+03	1.59E+03	2.12E+02	4.12E+04	4.55E+03
P61978 HNRPK	RPAEDMEEQAFK	527.24	65.56	4.39E+03	8.14E+02	3.05E+03	5.33E+03	9.88E+03	3.21E+04	4.63E+03	1.84E+04	1.24E+03	8.46E+02	1.01E+03	7.06E+02	1.07E+03	5.31E+04	2.01E+04
P50895 BCAM	SPPYQLDSQGR	624.31	65.59	3.52E+02	4.57E+03	2.78E+03	1.41E+03	4.90E+02	1.11E+04	1.17E+03	1.00E+03	7.13E+03	1.36E+04	7.53E+02	3.27E+02	2.26E+02	1.48E+03	1.59E+03
P62988 UBIQ	TLSDYNIQK	541.28	65.86	1.41E+05	5.81E+04	1.65E+05	1.93E+04	6.64E+05	2.08E+05	1.34E+05	8.32E+04	2.03E+04	3.22E+04	6.29E+05	1.26E+05	6.72E+03	1.19E+04	2.96E+05
P04040 CATA	FSTVAGESGADTVR	742.35	65.89	4.16E+04	6.27E+04	2.04E+02	7.15E+03	3.44E+02	5.76E+02	3.89E+02	2.87E+02	1.04E+03	1.04E+03	2.61E+04	1.60E+04	4.37E+02	5.02E+02	1.94E+04
Q14192 FHL2	NSLVDKPFPAK	595.33	66.04	4.51E+02	2.01E+04	1.54E+03	1.50E+04	2.64E+03	1.05E+03	2.32E+03	4.71E+02	4.01E+02	2.82E+03	8.50E+04	3.54E+04	2.19E+03	1.36E+03	4.26E+04
O43181 NDUS4	EDAVSFAEK	498.24	66.1	1.87E+03	1.26E+03	7.44E+02	8.43E+02	1.15E+03	1.08E+03	1.44E+03	3.48E+03	4.95E+04	3.40E+04	3.50E+04	4.43E+02	5.52E+03	8.15E+03	6.13E+02
P30038 AL4A1	AIEAALAAAR	443.26	66.18	3.24E+02	8.59E+02	1.16E+04	1.07E+03	8.77E+02	5.08E+02	1.17E+03	1.10E+04	5.58E+04	3.16E+04	4.97E+02	2.29E+03	5.47E+04	2.78E+04	1.18E+03
P22061 PIMT	VQLVVGDR	471.77	66.28	3.09E+02	2.09E+03	6.15E+03	1.43E+04	1.57E+05	9.25E+04	4.09E+04	1.16E+05	3.19E+04	2.25E+04	1.32E+05	2.08E+03	9.11E+02	5.57E+02	1.27E+03
Q16586 SGCA	SHDAEEVLPSTPASR	532.59	66.29	1.40E+04	4.71E+04	9.76E+02	7.80E+04	7.02E+02	2.10E+03	2.61E+02	2.49E+02	1.15E+03	1.12E+03	5.82E+04	8.38E+03	6.55E+02	6.17E+02	7.23E+04
P07919 QCR6	LELCDER	439.21	66.33	8.42E+02	1.69E+03	3.09E+02	4.37E+03	3.71E+02	5.61E+02	2.00E+03	1.10E+03	5.87E+04	6.48E+04	1.02E+03	4.18E+03	8.53E+02	4.32E+03	1.82E+03
P04004 VTNC	RVDTVDPYPR	438.90	66.43	4.13E+03	5.13E+02	2.10E+02	1.59E+03	1.34E+04	6.19E+02	3.34E+02	5.46E+02	4.87E+03	2.17E+04	3.14E+02	8.14E+02	1.45E+03	2.63E+03	2.68E+03
Q9Y4W6 AFG32	GAILTGPPGTGK	534.80	66.44	6.43E+02	4.33E+04	5.77E+03	2.32E+04	3.11E+04	1.01E+04	3.78E+04	1.14E+04	2.06E+03	7.13E+02	1.49E+05	2.15E+04	2.32E+04	7.50E+02	4.19E+04
Q5VST9-6 OBSCN	FLQEDVGTR	532.77	66.49	1.96E+03	2.87E+04	4.17E+03	3.86E+03	1.47E+04	1.39E+04	2.30E+04	1.33E+04	2.18E+02	3.85E+02	8.28E+04	3.34E+04	3.13E+04	1.02E+03	5.48E+04
Q16134 ETFD	GAPLNTPTVEDR	635.34	66.54	3.26E+05	2.04E+05	2.33E+03	4.16E+05	3.20E+05	9.19E+03	7.18E+02	7.82E+03	5.94E+02	1.34E+02	4.04E+05	1.89E+05	4.29E+03	5.55E+02	4.05E+05
P27824 CALX	AEDEILNR	544.77	66.59	4.33E+05	7.68E+05	7.46E+05	8.58E+05	2.62E+05	7.52E+05	5.87E+05	2.06E+05	4.06E+04	8.67E+04	6.70E+05	5.45E+05	1.22E+04	2.53E+04	9.65E+05
P05026 AT1B1	AYGENIGYSEK	615.79	66.61	4.17E+03	2.84E+03	1.44E+03	3.28E+02	7.21E+02	3.76E+03	8.71E+02	6.87E+03	2.21E+04	6.99E+04	1.14E+03	1.77E+03	5.09E+02	1.79E+04	1.23E+04
Q13642-1 FHL1	AIVAGDQNVYK	653.84	66.77	2.96E+05	1.09E+04	9.88E+02	3.30E+05	1.34E+05	3.51E+04	1.27E+03	1.00E+04	6.01E+04	6.24E+04	4.96E+05	1.05E+05	7.85E+02	2.54E+04	3.30E+05
Q14BN4-4 SLMAI	ELENQVGSJK	558.80	67.13	4.58E+04	4.11E+04	3.19E+03	2.00E+04	6.61E+02	2.19E+03	1.49E+03	1.03E+04	9.20E+02	7.93E+02	8.88E+04	3.22E+04	1.28E+04	1.13E+03	1.48E+02
P05026 AT1B1	TEISFRPNDPK	652.33	67.18	2.65E+02	8.26E+02	9.28E+04	4.40E+02	1.18E+03	1.61E+03	6.06E+03	3.88E+03	2.98E+04	4.30E+04	2.77E+03	1.39E+03	2.96E+03	6.87E+03	4.32E+02
O60237 MYPT2	LYESALTENQK	648.32	67.59	9.32E+02	4.75E+04	1.59E+03	7.30E+04	7.71E+03	4.85E+04	1.06E+04	1.23E+03	9.24E+02	7.35E+02	5.47E+04	2.83E+04	2.21E+04	5.20E+02	5.77E+04
P04040 CATA	FNTANDDNVTQVR	747.35	67.64	8.36E+02	1.60E+03	1.38E+03	7.89E+02	3.88E+02	4.61E+02	1.37E+03	2.99E+02	5.35E+03	2.16E+04	1.39E+03	9.49E+02	8.02E+02	7.86E+03	8.86E+02
P30049 ATPD	AQAELVGTADATR	716.36	67.76															

O96000 NDUBA	EVEQFTQVAK	589.81	68.92	3.35E+03	3.24E+03	6.92E+03	7.64E+04	7.28E+04	7.28E+04	2.29E+04	5.24E+04	7.08E+02	6.10E+03	3.74E+03	3.26E+04	1.89E+04	1.63E+03	1.78E+04
P23297 S10A1	DVDAVDKVMK	560.27	68.93	9.17E+03	1.13E+04	3.41E+03	3.06E+04	1.63E+04	3.16E+03	5.70E+03	8.25E+02	3.33E+04	1.36E+04	6.84E+03	7.20E+03	6.71E+03	1.34E+04	8.36E+03
O96000 NDUBA	YQDLGAYSSAR	615.79	68.94	1.18E+05	1.16E+04	7.39E+02	9.23E+04	5.69E+03	3.99E+03	6.88E+02	5.57E+02	1.40E+03	2.58E+03	4.05E+04	1.86E+04	2.03E+03	3.20E+02	8.84E+04
P45880-1 VDAC2	NNFAVGYR	470.73	68.98	3.01E+03	4.70E+03	9.05E+03	5.27E+03	1.14E+03	4.74E+03	8.77E+02	3.88E+02	1.30E+05	1.12E+05	1.98E+03	1.91E+04	3.93E+03	1.04E+04	8.03E+03
Q5VST9-6 OBSCN	ALDDLSAEER	559.77	69.15	2.11E+04	2.91E+03	7.76E+02	1.22E+03	3.16E+03	1.18E+03	6.70E+02	1.20E+03	5.02E+02	1.01E+03	1.09E+04	1.05E+04	1.87E+03	2.61E+03	3.42E+04
Q00325 MPCP	IQTQPGYANTLR	681.36	69.7	1.35E+06	1.01E+04	8.45E+02	3.21E+05	7.66E+05	1.49E+04	1.62E+03	3.72E+02	6.03E+03	3.43E+02	6.23E+05	1.61E+03	4.35E+02	8.61E+03	8.73E+05
P02671-2 FIBA	MELERPGGNEITR	501.25	69.87	6.57E+03	5.11E+03	4.89E+03	3.32E+04	2.45E+05	3.20E+03	5.84E+02	3.55E+03	8.83E+02	6.46E+03	3.91E+04	4.69E+04	8.87E+02	2.23E+03	1.66E+04
P00450 CERU	DDEEFIESNK	613.26	70.18	1.98E+04	3.77E+03	1.44E+03	1.92E+03	1.32E+03	3.36E+03	1.69E+03	5.90E+02	2.66E+02	4.79E+03	1.91E+03	2.16E+03	5.17E+03	1.03E+03	2.02E+03
Q92523 CPT1B	ILDDPSPQPGEK	761.37	70.44	3.19E+04	6.94E+03	2.52E+03	2.93E+04	6.80E+03	1.11E+03	1.76E+03	6.43E+02	3.30E+03	1.10E+03	5.72E+04	5.67E+03	1.69E+04	6.38E+03	5.34E+04
Q16082 HSPB2	SVPHAHPATAEYEFANPSR	521.24	70.62	3.32E+03	2.43E+05	5.77E+04	5.78E+05	9.00E+04	7.40E+05	7.86E+03	2.95E+04	2.04E+03	4.58E+03	2.15E+05	9.42E+04	1.34E+05	4.70E+02	1.69E+05
P02671-2 FIBA	EVDLKDYEDQK	755.36	70.74	3.08E+03	6.26E+03	2.24E+03	7.33E+03	2.95E+04	1.46E+04	1.41E+03	2.57E+03	7.81E+02	6.52E+02	1.17E+04	3.15E+03	2.48E+03	6.07E+02	4.18E+03
Q16586 SGCA	SPHHPGFLYGSATPEDR	623.30	70.75	2.37E+04	7.15E+03	1.09E+04	9.08E+02	3.78E+03	1.33E+04	1.70E+03	2.33E+03	5.81E+03	1.16E+04	3.26E+03	2.06E+03	3.40E+03	1.59E+03	2.02E+03
P02743 SAMP	IVLGQEQDSYGGK	697.35	70.75	2.56E+05	3.16E+04	6.31E+03	2.90E+04	8.76E+03	3.66E+03	1.03E+04	7.83E+03	7.11E+03	8.98E+03	1.00E+05	1.40E+05	1.69E+04	8.93E+04	1.76E+05
Q9Y490 TLN1	ALSTDPAAPNLK	599.33	70.78	6.50E+04	1.81E+03	5.29E+02	3.33E+03	8.03E+03	5.72E+02	3.17E+02	3.35E+03	5.76E+04	8.50E+04	7.38E+04	1.42E+04	4.59E+03	1.60E+04	4.44E+04
P02647 APOA1	THLAPYSDEL	434.56	70.8	3.37E+05	1.12E+06	5.03E+02	1.16E+06	3.36E+06	1.13E+06	3.43E+06	1.87E+04	1.89E+03	1.34E+03	1.31E+04	2.13E+06	6.73E+05	3.71E+03	1.17E+06
P14927 QCR7	DDTIYEDVDK	671.29	70.89	6.05E+05	5.53E+05	5.46E+03	7.16E+05	1.88E+04	1.95E+04	8.26E+03	6.13E+02	7.18E+03	9.27E+03	4.24E+05	5.29E+05	8.33E+03	1.27E+04	5.39E+05
O14639-4 ABLM1	EEDDEELLR	574.26	71.03	4.07E+03	1.71E+05	1.69E+04	2.30E+05	1.74E+04	2.03E+05	3.86E+04	3.00E+03	6.22E+02	1.24E+03	1.25E+03	6.76E+04	7.17E+04	2.69E+03	1.45E+03
P22626 ROA2	GGNFGFGDSR	507.23	71.15	1.09E+04	4.11E+03	5.95E+02	3.52E+03	4.44E+04	1.88E+04	8.58E+02	8.55E+02	2.13E+04	2.19E+04	4.27E+04	3.76E+03	4.16E+03	6.05E+03	1.03E+04
Q9UIJ7 KAD3	TLPQAEALDR	557.30	71.22	1.07E+04	5.77E+05	8.04E+03	4.27E+05	5.01E+05	3.15E+05	4.22E+05	6.43E+03	5.14E+02	1.14E+03	1.07E+04	5.26E+05	3.30E+05	1.09E+03	6.81E+03
P30153 2AAA	FSNLASDEQDSVR	734.34	71.36	5.50E+03	1.07E+03	1.42E+03	6.12E+02	2.46E+03	2.28E+04	1.21E+03	1.61E+02	7.85E+03	1.02E+04	1.73E+03	2.07E+03	2.69E+03	1.85E+04	1.24E+03
P04040 CATA	LSQEDPDYGR	646.82	71.49	3.33E+02	8.98E+02	3.39E+04	1.84E+03	1.54E+03	4.57E+04	1.46E+04	1.44E+04	2.29E+04	5.25E+04	7.64E+02	9.37E+04	2.17E+04	3.85E+03	1.83E+03
P04004 VTNC	VDTVDPYPR	580.30	71.59	4.94E+04	8.22E+04	4.69E+03	3.26E+04	2.71E+04	5.14E+04	1.50E+04	3.14E+04	8.23E+04	1.73E+03	9.75E+04	2.32E+04	4.10E+04	9.47E+04	5.88E+04
Q9UHQ9 NB5R1	EDLEELQAR	551.77	71.7	1.78E+03	7.42E+04	2.24E+03	1.51E+05	1.25E+05	7.92E+03	1.38E+03	5.52E+03	1.13E+03	7.97E+03	1.91E+03	1.73E+05	9.42E+04	1.12E+04	1.35E+03
P82909 RT36	VVQVVKPHTPLIR	495.98	71.73	1.87E+03	3.79E+03	1.33E+03	5.75E+04	6.84E+04	4.74E+03	3.36E+03	3.78E+02	6.44E+02	2.15E+02	2.66E+03	1.44E+04	1.60E+04	1.25E+03	6.17E+04
Q16775 GLO2	EAAIVDPVQPQK	647.85	71.93	4.52E+04	4.45E+03	2.05E+03	7.76E+03	1.19E+04	3.78E+03	1.22E+03	4.02E+02	3.87E+02	4.51E+02	7.35E+04	5.66E+02	5.41E+03	1.18E+03	3.53E+04
P07900 HS90A	ELISNSSDALDK	646.34	72.06	2.34E+05	2.64E+04	6.68E+03	2.24E+04	2.39E+04	9.59E+03	1.86E+04	1.01E+03	6.19E+03	6.13E+03	3.31E+05	3.45E+04	2.01E+04	7.34E+02	2.90E+05
Q99877 H2B1N	KESYSVYVYK	633.32	72.35	3.15E+04	2.65E+03	1.06E+03	1.12E+03	1.82E+03	3.40E+03	1.98E+03	2.73E+04	8.21E+04	7.44E+04	2.62E+04	2.11E+03	4.40E+02	3.62E+04	9.17E+03
P02743 SAMP	QGYFVEAQPK	583.79	72.48	2.38E+05	2.30E+03	9.84E+03	1.40E+03	1.38E+04	1.42E+04	2.76E+02	6.90E+03	3.26E+03	1.54E+02	3.43E+04	2.12E+03	2.47E+02	4.16E+02	9.17E+03
P84243 H33	STELLIR	416.25	72.59	1.19E+04	6.63E+04	9.44E+03	1.94E+04	2.51E+05	4.36E+04	2.93E+04	1.75E+04	8.06E+04	5.40E+02	4.66E+04	6.50E+04	1.99E+04	1.14E+05	7.25E+05
P04040 CATA	ADVLTTGAGNPVGDK	707.86	72.63	4.97E+04	1.45E+02	2.47E+03	2.12E+03	2.48E+03	6.26E+02	1.32E+03	4.26E+03	1.61E+03	3.21E+03	5.01E+04	1.66E+04	3.99E+03	1.48E+03	8.35E+02
Q9NZN4 EHD2	VVGTPEVLR	485.29	73.07	4.65E+03	3.36E+03	4.79E+03	2.05E+03	2.40E+03	1.81E+03	5.37E+03	7.35E+03	1.75E+04	8.70E+04	1.94E+03	5.78E+03	2.83E+03	2.73E+04	3.32E+03
P21796 VDAC1	VTQSNFAVGYK	607.31	73.23	3.59E+05	9.79E+02	3.87E+03	7.84E+03	2.09E+04	2.16E+03	3.84E+03	6.70E+03	2.40E+03	2.42E+02	1.78E+05	8.86E+03	2.68E+03	1.52E+02	8.73E+04
P04179 SODM	DFGSFDK	408.18	73.52	7.20E+03	2.60E+03	7.50E+02	3.45E+03	2.69E+03	1.53E+03	3.76E+03	9.78E+03	1.16E+05	1.00E+05	1.82E+02	3.92E+03	2.12E+03	2.05E+04	1.01E+03
P10606 COX5B	ASGGGVPTDEEQATGLER	887.42	73.53	1.10E+05	6.24E+03	1.47E+03	1.15E+05	1.45E+04	2.40E+04	3.52E+03	6.63E+03	2.44E+02	2.01E+03	7.40E+04	2.88E+03	9.93E+02	1.89E+03	6.75E+04
Q6YN16 HSDL2	VESTGAVPEFK	582.30	73.66	4.81E+03	7.59E+03	7.40E+04	2.08E+05	6.21E+04	7.68E+04	7.78E+04	2.38E+04	8.61E+03	7.62E+03	7.39E+03	4.80E+04	9.78E+03	5.65E+03	2.64E+04
Q02252 MMSA	AEMDAAIASCK	555.26	73.68	3.41E+03	1.42E+04	1.03E+03	1.33E+04	3.01E+04	4.31E+02	5.85E+03	7.88E+02	1.45E+03	4.91E+02	4.06E+03	1.63E+03	1.92E+04	8.98E+02	1.03E+04
P14927 QCR7	LPENLYNDR	567.28	73.97	1.31E+03	4.49E+05	1.31E+05	1.38E+06	5.18E+05	1.24E+06	2.79E+05	6.30E+05	7.33E+03	2.63E+03	2.78E+03	4.64E+05	6.05E+04	9.09E+03	6.47E+02
P50213 IDH3A	APIQWEER	514.76	73.98	2.69E+03	3.53E+04	7.21E+04	8.04E+03	2.23E+05	1.72E+04	9.04E+04	1.13E+05	8.05E+03	1.68E+04	1.20E+05	6.43E+04	2.95E+03	1.84E+04	8.97E+04
P10606 COX5B	EDPNLVPSISNKR	734.89	74.38	4.76E+03	2.73E+03	2.07E+03	1.67E+04	1.62E+05	7.07E+03	1.13E+04	3.03E+03	3.64E+03	2.05E+02	5.93E+03	7.78E+03	6.53E+02	2.56E+02	1.21E+04
P07437 TBB5	ISVYYNEATGGK	651.32	74.41	5.65E+03	5.46E+04	9.14E+03	1.22E+05	6.73E+04	1.93E+05	1.30E+04	1.11E+04	3.52E+03	5.85E+03	2.72E+03	8.65E+04	2.72E+04	2.11E+03	4.17E+02
O14558 HSPB6	HFSPEEIAVK	578.80	74.58	1.52E+03	8.87E+05	5.35E+05	3.02E+05	1.35E+04	3.56E+04	2.29E+05	2.71E+05	1.06E+03	1.47E+03	4.68E+05	8.64E+03	1.73E+05	5.12E+03	3.36E+05
Q6YN16 HSDL2	TAAEEIEAVGGK	587.80	74.7	1.26E+05	5.68E+03	2.60E+03	5.73E+02	5.72E+02	1.01E+03	2.30E+03	3.48E+02	1.63E+03	5.56E+02	9.18E+04	1.42E+03	5.92E+03	8.34E+02	4.50E+03
Q09666 AHNK	GDVDVSLPK	465.25	74.72	1.30E+05	3.29E+05	3.10E+05	3.31E+05	1.73E+05	3.38E+05	1.34E+05	8.71E+03	1.34E+05	1.95E+03	6.77E+03	2.28E+05	3.39E+04	1.18E+05	3.77E+03
P35222 CTNB1	LLNDEDQVVVNK	693.37	74.76	5.44E+04	3.30E+04	4.80E+03	2.28E+05	1.40E+05	1.19E+05	4.91E+03	1.83E+04	4.46E+03	2.09E+03	2.43E+04	3.41E+04	1.85E+03	6.23E+02	4.35E+04
Q16586 SGCA	VPLPIEGR	440.77	74.84	7.98E+02	2.60E+02	1.38E+04	2.98E+05	2.92E+05	3.27E+05	2.05E+05	6.12E+04	3.39E+03	8.49E+02	1.76E+02	2.64E+05	2.82E+05	1.29E+04	5.22E+02
P35221 CTNA1	IAEQVASFQEEK	689.85	74.9	7.07E+04	5.54E+03	6.63E+02	8.84E+03	8.59E+03	1.20E+04	2.40E+03	4.46E+02	2.64E+03	1.59E+03	6.45E+04	4.36E+03	2.49E+03	9.08E+03	8.10E+03
Q14192 FHL2	YISFEER	472.23	74.97	1.39E+03	5.67E+04	2.73E+05	5.51E+05	1.02E+06	8.05E+05	5.40E+05	3.46E+04	1.26E+03	1.32E+03	8.30E+04	4.64E+05	1.20E+04	5.98E+03	5.45E+04
O75947 ATP5H	SWNETLTSR	547.27	75.1	1.34E+03	1.76E+05	2.75E+04	6.45E+05	6.15E+05	7.65E+05	3.58E+05	8.07E+04	1.92E+04	4.44E+03	1.93E+03	3.24E+05	7.26E+04	5.03E+03	1.50E+03
P22626 ROA2	GGGGNFGPGGNSNFR	689.32	75.12	1.49E+05	1.40E+05	2.12E+03	1.08E+04	2.68E+03	1.68E+04	9.34E+02	6.57E+02	3.56E+04	2.20E+04	1.50E+05	4.18E+03	4.50E+03	2.19E+03	7.64E+04
Q9NZN4 EHD2	LEGHLPANLPR	425.24	75.15	3.71E+03	3.14E+05	1.35E+03	4.22E+05	4.09E+05	3.82E+05	2.11E+03	4.59E+04	8.00E+03	4.29E+03	5.84E+03	2.70E+05	4.26E+05	6.61E+03	3.47E+05
P04179 SODM	GELLEAIKR	514.																

Q9NX63 CHCH3	VAEELALEQAK	600.83	75.97	4.45E+05	7.98E+03	4.70E+03	7.37E+03	5.22E+03	7.36E+03	3.03E+03	1.22E+03	3.77E+02	6.78E+02	4.48E+05	2.26E+03	5.90E+03	1.94E+03	4.50E+03
P51884 LUM	SLEDLQLTHNK	649.34	76.06	1.23E+04	6.48E+03	6.55E+03	5.21E+03	3.63E+03	7.23E+02	2.45E+03	1.72E+03	4.69E+03	3.80E+04	1.12E+04	4.54E+03	4.26E+02	1.26E+04	1.87E+03
Q5VST9-6 OBSCN	VEELGEASALR	587.31	76.14	1.65E+03	2.51E+05	1.76E+04	9.99E+04	3.11E+04	1.05E+03	1.05E+04	2.73E+04	4.93E+03	5.12E+03	2.40E+05	3.09E+05	1.19E+05	9.65E+02	6.36E+04
Q9UHQ9 NB5R1	VGDVVVEFR	460.75	76.32	3.48E+03	2.52E+05	9.92E+03	3.12E+05	4.07E+05	3.38E+05	3.61E+05	3.02E+04	7.24E+02	2.60E+03	3.19E+03	3.85E+05	5.92E+03	9.37E+02	5.18E+03
P35222 CTNB1	LAEPSQMLK	508.78	76.37	5.17E+04	6.47E+04	1.48E+03	1.30E+05	1.05E+05	1.78E+05	1.41E+03	1.58E+04	3.40E+02	7.74E+02	2.05E+05	5.61E+04	4.16E+04	2.35E+02	1.28E+05
P10644 KAP0	SENEEFVEVGR	647.80	76.5	1.02E+05	2.74E+03	7.59E+03	4.47E+02	3.48E+02	1.69E+03	1.50E+03	3.01E+03	2.67E+03	2.83E+03	1.26E+05	2.42E+03	9.02E+02	1.47E+03	6.94E+03
P18859 ATP5J	FEVIEKPQA	530.79	76.52	1.57E+06	3.90E+03	5.19E+03	7.91E+03	2.45E+04	5.00E+03	5.40E+04	1.93E+04	9.52E+03	4.17E+04	1.08E+06	7.76E+03	2.19E+05	2.74E+03	2.86E+04
P22626 ROA2	TLETVPLER	529.30	76.53	1.17E+03	5.72E+04	1.13E+05	3.91E+04	6.79E+04	7.69E+04	4.87E+04	9.37E+04	1.30E+04	8.12E+02	6.32E+02	7.70E+04	7.09E+03	5.52E+03	2.27E+03
P04179 SODM	INAQIMQLHH	402.21	76.55	3.34E+03	1.52E+04	7.91E+03	1.85E+05	5.68E+04	2.56E+04	9.12E+02	2.75E+05	2.23E+05	1.12E+05	5.48E+03	3.52E+04	4.63E+03	8.76E+05	1.31E+05
O43678 NDUA2	ALENVLSGK	465.77	76.57	5.65E+03	1.43E+05	2.17E+04	2.06E+05	3.09E+05	2.23E+05	2.70E+05	3.03E+04	2.07E+04	4.35E+04	4.02E+03	1.89E+05	4.25E+03	4.47E+03	1.19E+05
P00338 LDHA	LVIITAGAR	457.30	76.63	6.54E+02	8.60E+02	8.22E+03	1.62E+05	1.36E+05	1.91E+05	1.05E+05	8.86E+03	6.24E+03	3.76E+04	1.66E+03	1.15E+05	1.90E+03	1.03E+03	6.24E+02
P35221 CTNA1	LLSNTVMMPR	515.79	76.64	4.16E+04	2.62E+03	4.63E+03	5.44E+04	1.38E+05	1.45E+05	1.17E+05	5.19E+03	1.87E+03	1.07E+04	1.47E+04	2.74E+03	8.00E+02	2.03E+03	4.81E+02
Q99623 PHB2	LGLDYEER	497.75	76.78	1.22E+03	1.38E+03	2.11E+04	1.80E+03	5.10E+02	2.40E+03	5.96E+02	9.29E+02	3.83E+05	2.97E+02	3.63E+02	6.30E+03	7.61E+02	2.97E+05	1.07E+03
P35221 CTNA1	AIMAQLPQEQK	628.83	76.84	5.55E+04	1.42E+03	2.97E+03	1.55E+03	1.41E+03	8.39E+02	6.06E+02	2.31E+03	1.59E+04	2.19E+04	5.32E+04	1.55E+03	2.71E+03	5.18E+02	9.83E+02
O14639-4 ABLM1	TLSPTSAEGYQDVR	810.90	77.4	7.01E+04	5.02E+02	5.39E+02	3.04E+03	3.15E+03	2.39E+03	1.33E+03	6.63E+02	5.48E+03	1.10E+04	7.05E+04	4.21E+02	1.92E+03	2.79E+03	4.84E+03
P78417 GSTO1	HEVININLK	540.31	77.96	2.89E+04	1.46E+03	7.30E+03	6.31E+03	5.26E+03	3.72E+03	1.21E+03	4.16E+03	8.64E+02	1.90E+03	5.84E+04	1.61E+03	1.14E+03	7.35E+02	2.42E+03
P02647 APOA1	LSPLGEMMR	516.26	78.01	4.62E+05	3.45E+03	1.19E+03	1.42E+03	8.23E+03	2.06E+03	5.77E+02	5.41E+03	4.05E+06	2.91E+05	7.50E+05	2.34E+03	2.78E+03	2.62E+06	5.01E+03
P00915 CAH1	HDTSLKPISVSNPATAK	643.67	78.16	7.44E+02	1.20E+03	1.55E+03	3.43E+03	4.86E+03	1.81E+03	3.09E+02	1.20E+03	6.53E+02	4.93E+02	9.56E+04	1.15E+03	4.27E+03	1.63E+03	5.79E+03
P27338 AOFB	PVIYIDQTR	552.80	78.24	7.02E+04	1.21E+04	3.25E+03	2.28E+04	1.16E+04	6.08E+02	9.32E+03	1.16E+03	1.31E+03	1.41E+03	5.92E+04	3.24E+04	8.59E+03	1.34E+03	4.21E+04
P26373 RL13	TIGISVDPR	479.27	78.25	9.30E+04	7.57E+05	3.89E+03	7.01E+05	2.90E+05	1.10E+04	4.48E+05	8.07E+03	7.13E+04	8.53E+04	1.63E+05	5.11E+05	4.29E+05	9.91E+02	5.34E+05
P35573-3 GDE	IEEVVLEAR	529.30	78.32	1.46E+04	2.88E+04	1.80E+03	4.25E+04	1.33E+03	1.25E+04	2.63E+04	1.43E+03	4.62E+04	9.32E+03	2.99E+03	3.97E+04	2.87E+03	5.48E+04	9.85E+02
P39059 COFA1	AAGLLSTYR	476.27	78.46	7.08E+03	1.07E+05	1.75E+04	2.14E+04	3.18E+02	1.75E+04	3.63E+04	1.26E+03	8.52E+04	3.48E+04	2.14E+03	6.04E+04	6.23E+04	6.51E+04	6.19E+03
Q02252 MMSA	EGASILLDGR	515.78	78.63	2.71E+04	2.55E+04	1.36E+05	7.58E+03	4.04E+04	2.56E+04	8.41E+03	1.06E+05	7.72E+02	1.41E+05	3.88E+04	1.21E+04	3.60E+04	5.13E+02	1.81E+04
P30042 ES1	NLSTFAVDGK	526.27	78.63	3.08E+03	3.29E+03	5.98E+03	1.55E+03	6.66E+04	9.03E+02	1.73E+03	2.92E+03	4.81E+05	4.55E+03	2.10E+03	6.45E+03	6.83E+02	1.68E+04	2.76E+04
P04004 VTNC	IYISGMAPR	504.27	79.07	7.41E+05	1.17E+03	2.16E+04	5.30E+04	3.65E+04	4.18E+04	3.12E+04	1.16E+04	4.15E+02	1.79E+03	6.28E+05	1.84E+04	1.62E+05	6.15E+03	7.04E+04
P15121 ALDR	PEDPSLLEDPR	634.31	79.12	5.20E+04	2.47E+04	2.76E+04	2.65E+05	8.82E+04	3.92E+03	6.27E+03	2.89E+04	5.34E+02	5.29E+02	3.75E+04	7.59E+04	2.16E+04	6.28E+02	1.01E+05
P02042 HBD	EFTPQMQAAYQK	721.34	79.13	9.27E+04	1.27E+04	1.33E+03	2.62E+04	1.27E+04	6.46E+02	4.27E+03	2.10E+02	8.09E+02	2.95E+02	1.29E+05	1.95E+04	1.42E+03	1.20E+03	1.59E+04
P10644 KAP0	EDEISPPPNPVVK	759.40	79.38	2.89E+04	1.53E+04	5.47E+03	9.07E+02	2.06E+02	1.40E+04	1.87E+03	1.06E+03	1.16E+03	1.16E+03	1.43E+04	2.24E+03	7.86E+03	1.56E+03	6.33E+02
Q9Y6M9 NDUB9	IFPDSPGGTYSYER	713.34	79.42	1.16E+04	2.38E+04	3.07E+04	2.37E+04	2.52E+04	2.43E+04	1.59E+04	7.32E+03	1.33E+03	3.13E+03	3.63E+04	1.15E+05	6.43E+03	3.63E+02	5.69E+04
Q16134 ETFD	NLSIYDGPEQR	646.32	79.92	1.76E+03	2.08E+04	2.31E+05	5.20E+04	1.37E+05	9.72E+04	4.31E+04	3.63E+05	1.55E+03	7.98E+02	2.41E+03	1.81E+04	1.46E+03	8.43E+02	6.31E+04
Q9NX63 CHCH3	YSGAYGASVDEELK	788.36	80.19	3.03E+04	4.64E+02	3.27E+02	2.23E+03	9.38E+02	2.54E+03	1.49E+03	8.74E+02	1.81E+03	1.14E+03	4.92E+04	3.45E+04	3.40E+04	2.78E+03	5.46E+03
P35222 CTNB1	SPQMVAIVR	544.29	80.34	7.61E+03	5.45E+04	1.83E+03	8.58E+04	7.18E+04	5.00E+04	6.45E+04	1.03E+03	5.18E+03	5.36E+04	7.65E+02	1.53E+05	8.49E+02	5.47E+03	1.94E+03
P12814 ACTN1	GISQEQMNEFR	669.82	80.5	3.98E+04	2.88E+03	5.14E+03	1.97E+03	7.76E+02	1.61E+03	1.90E+04	1.42E+03	1.06E+03	1.24E+03	4.49E+04	8.81E+02	2.93E+03	5.55E+02	1.20E+03
O00151 PDLI1	SAMPFTASPASSTAR	791.88	80.52	2.52E+04	4.95E+02	1.07E+03	2.75E+03	2.27E+03	1.55E+03	1.17E+03	1.40E+03	3.91E+02	1.10E+03	7.22E+04	1.63E+03	5.72E+04	8.92E+02	5.42E+04
P23368 MAOM	IETQDIQALR	593.82	80.56	9.05E+04	1.71E+03	6.50E+04	3.48E+03	7.06E+02	1.07E+03	6.33E+03	8.77E+02	1.88E+03	1.03E+03	7.45E+04	2.16E+03	8.05E+02	1.44E+03	1.83E+03
P01834 IGKC	VYACEVTHQGLSSPVTK	606.97	80.68	2.49E+05	1.83E+03	1.59E+03	5.94E+04	1.24E+05	4.19E+03	1.13E+04	1.30E+04	2.65E+03	8.43E+02	1.14E+05	1.21E+04	2.19E+04	1.30E+03	1.67E+04
P30048 PRDX3	HLSVNDLPVGR	402.89	80.71	2.24E+05	3.77E+04	3.26E+04	2.32E+04	1.11E+04	1.12E+04	2.09E+04	5.03E+02	1.49E+03	2.68E+02	5.62E+03	1.83E+04	3.32E+03	1.18E+03	1.05E+04
P61981 I433G	NVTELNEPLSNEER	822.40	80.73	2.26E+05	1.82E+03	7.29E+02	7.28E+03	1.11E+03	1.11E+03	4.68E+02	1.23E+03	4.73E+03	5.83E+03	2.24E+05	4.25E+02	3.32E+04	4.26E+03	2.03E+03
P13489 RINI	ELTVSNNDINEAGVR	815.90	80.78	2.11E+03	8.48E+02	2.48E+03	1.49E+03	1.11E+03	5.32E+04	1.13E+03	9.21E+02	1.58E+03	4.34E+02	2.86E+02	1.09E+03	4.35E+02	8.07E+03	8.33E+02
O14558 HSPB6	HFSPEEIAVKV	628.34	80.83	5.94E+02	1.66E+05	1.15E+04	2.98E+05	9.63E+04	1.48E+05	1.72E+04	6.02E+03	4.07E+02	1.81E+03	1.20E+04	2.90E+05	2.76E+02	5.35E+04	2.20E+05
Q14192 FHL2	DDILCPDCGK	539.73	81.13	2.30E+02	9.52E+04	9.09E+03	1.05E+05	3.86E+04	2.73E+05	3.30E+04	1.09E+04	6.13E+02	1.05E+03	1.70E+03	1.53E+04	6.80E+04	3.85E+03	1.56E+05
P50895 BCAM	LVLAEAQVGDER	650.35	81.17	4.99E+03	3.45E+03	5.36E+03	1.80E+04	8.12E+03	1.75E+04	3.10E+03	9.53E+02	1.33E+03	2.00E+04	8.04E+03	2.51E+03	3.66E+03	1.68E+04	2.93E+04
Q9UBY9 HSPB7	SEPLAFPAR	494.27	81.45	1.07E+03	3.28E+05	1.96E+04	3.71E+05	5.96E+03	4.63E+03	1.73E+02	3.25E+03	4.44E+02	2.33E+03	1.87E+03	2.16E+05	9.16E+04	5.39E+03	1.59E+05
P30038 AL4A1	STGSIVGQQPFGGAR	731.37	81.52	2.25E+03	1.30E+04	3.52E+03	7.03E+04	4.85E+04	9.81E+04	2.86E+04	2.34E+04	1.18E+04	1.39E+04	5.57E+03	5.07E+03	1.25E+04	2.54E+04	1.77E+03
P13807 GYS1	TNNFNVTLK	590.31	81.55	1.17E+05	2.60E+04	3.41E+04	3.75E+04	3.87E+04	3.09E+05	1.55E+03	6.04E+02	8.62E+02	8.68E+04	1.54E+03	3.67E+04	7.06E+04	1.54E+06	1.08E+05
P01834 IGKC	SLSSTLTLSK	518.80	81.62	4.16E+05	2.31E+04	1.94E+04	1.12E+04	2.16E+03	7.79E+02	1.43E+02	1.53E+03	1.64E+05	5.95E+04	3.94E+04	7.55E+04	1.81E+04	1.94E+05	5.70E+03
O14958 CASQ2	LEVQAFER	496.26	81.67	6.70E+03	1.35E+04	3.47E+03	1.84E+05	5.17E+03	2.46E+05	1.86E+05	1.89E+03	6.02E+03	1.58E+03	1.28E+04	2.46E+05	3.24E+02	4.13E+03	3.39E+03
P02671-2 FIBA	ALTDMPQMR	531.76	81.8	1.49E+05	3.13E+03	7.26E+02	2.52E+03	2.49E+03	3.43E+03	1.34E+03	1.00E+03	1.41E+03	3.58E+03	3.82E+04	1.87E+03	1.53E+03	1.75E+03	1.56E+04
P21912 DHSB	QQYLQSIER	647.33	81.91	1.51E+05	3.36E+03	1.44E+03	4.61E+03	9.50E+02	1.31E+03	1.44E+03	1.94E+03	1.05E+04	6.21E+04	4.61E+04	2.84E+03	3.95E+03	9.45E+03	8.97E+04
P62988 UBIQ	ESTLHLVLR	534.31	82.02	4.33E+03	4.46E+02	5.20E+05	6.67E+05	4.57E+05	6.40E+05	3.62E+05	1.29E+04	3.29E+02	2.16E+03	1.40E+03	2.62E+05	1.76E+03	4.30E+03	6.32E+05
O43678 NDUA2	ALENVLSGKA	501.28	82.11	1.40E+03														



O14558 HSPB6	ASAPLPLGSAPGR	597.33	83.32	1.16E+06	1.14E+04	2.13E+04	1.04E+06	1.96E+04	2.15E+04	7.22E+04	4.74E+04	1.83E+03	4.18E+03	1.46E+06	1.28E+04	7.41E+05	4.30E+04	1.23E+06
Q9GZM7 TINAL	GVVSDHCYPFSGR	475.22	83.34	4.40E+03	2.04E+03	1.27E+03	7.51E+04	1.65E+03	2.53E+03	1.86E+04	2.76E+03	1.63E+03	3.36E+03	4.72E+04	6.05E+02	2.42E+04	2.60E+03	4.80E+04
Q9UHQ9 NB5R1	GPSGLLTYTGK	547.30	83.35	2.00E+05	3.62E+05	3.73E+05	9.07E+05	6.68E+05	1.20E+06	2.97E+05	4.55E+03	8.96E+02	6.55E+03	2.21E+05	3.24E+05	1.30E+05	6.94E+02	2.37E+05
P00387 NB5R3	GPSGLLVYQ GK	559.81	83.35	1.89E+05	1.52E+04	2.35E+03	4.95E+02	2.73E+03	3.33E+03	5.86E+03	1.38E+04	1.01E+03	9.98E+02	2.35E+05	3.91E+03	9.21E+03	3.95E+02	2.18E+05
P09211 GSTP1	ASCLYGQLPK	540.28	83.38	2.06E+05	6.87E+02	1.14E+05	1.59E+03	2.01E+04	1.95E+04	2.88E+03	1.01E+05	4.12E+02	7.61E+03	2.57E+05	1.48E+03	8.79E+02	3.94E+03	2.77E+03
P10606 COX5B	EDPNLVPSISNK	656.84	83.53	1.01E+06	9.97E+03	6.71E+02	2.30E+05	9.67E+03	1.20E+03	5.95E+03	1.76E+03	6.04E+02	1.17E+03	5.64E+05	5.29E+03	7.69E+03	3.14E+03	7.64E+05
Q03252 LMNB2	ALYESELADAR	619.31	83.82	1.71E+04	6.88E+02	2.71E+03	2.62E+04	4.63E+04	6.69E+02	1.86E+03	8.63E+02	7.36E+02	5.99E+02	4.36E+04	1.02E+03	7.21E+04	2.96E+03	5.91E+04
P55786 PSA	YAAVTQFEATDAR	721.84	83.91	6.98E+04	9.35E+03	9.30E+03	4.50E+03	1.32E+04	2.67E+04	1.19E+04	1.10E+03	3.62E+02	1.47E+02	4.31E+04	8.44E+04	1.51E+04	7.91E+02	1.12E+03
P02743 SAMP	DNELLVYK	497.27	83.97	3.83E+05	3.48E+04	3.25E+03	2.04E+05	7.30E+04	8.00E+03	1.24E+03	1.16E+04	9.76E+02	7.80E+03	4.00E+05	2.22E+03	1.18E+05	4.16E+03	1.19E+05
P06733 ENOA	LMIEMDG TENK	640.80	84.04	6.98E+04	1.02E+04	4.38E+03	5.00E+04	3.25E+04	1.28E+04	2.74E+04	3.21E+02	1.69E+02	1.07E+03	4.66E+04	3.76E+04	7.94E+03	6.33E+03	7.17E+04
Q99877 H2B1N	ESYSVYVYK	569.28	84.12	4.94E+03	7.53E+02	3.07E+03	1.52E+03	1.86E+03	1.37E+03	3.94E+02	5.23E+03	3.21E+04	1.10E+05	1.56E+04	1.76E+03	2.61E+04	6.13E+03	9.97E+02
P29692-2 EF1D	IASLEVENQSLR	679.87	84.13	4.75E+04	1.44E+03	2.70E+03	4.65E+02	6.70E+03	1.71E+02	1.56E+03	5.09E+03	8.24E+02	8.38E+02	5.66E+04	7.11E+03	3.50E+04	3.20E+03	6.39E+04
Q9NZN4 EHD2	ADMVETQQLMR	661.31	84.29	2.13E+04	8.52E+02	1.81E+03	5.16E+02	5.17E+03	1.32E+03	4.78E+02	3.92E+03	1.66E+03	1.15E+03	8.06E+02	1.92E+03	1.81E+03	1.80E+03	2.29E+03
P01834 IGKC	VYACEVTHQGL	610.29	84.32	7.09E+03	8.88E+02	1.72E+04	3.07E+03	6.82E+03	2.09E+03	1.38E+04	3.66E+04	2.80E+04	3.21E+04	4.04E+03	1.24E+04	8.90E+02	4.53E+03	7.56E+02
P13639 EF2	GVQYLNEIK	532.29	84.73	1.03E+05	3.11E+03	1.78E+03	3.37E+03	7.31E+02	4.66E+03	1.14E+03	3.78E+02	2.32E+04	1.22E+03	4.79E+04	2.90E+03	2.73E+04	2.48E+03	4.28E+04
P04179 SODM	GELLEAIK	436.76	84.82	9.62E+02	5.94E+05	5.54E+03	6.39E+05	3.82E+05	6.24E+05	3.19E+05	6.28E+02	3.06E+03	1.32E+04	3.37E+03	1.54E+05	1.72E+04	2.07E+03	1.60E+04
Q16134 ETFD	ALNEGGFQSIPK	630.83	84.83	1.23E+05	2.20E+03	1.58E+03	3.35E+03	1.38E+04	8.24E+02	1.41E+03	1.81E+03	9.89E+02	3.73E+03	1.32E+05	3.22E+03	4.24E+04	8.11E+03	7.67E+03
P02042 HBD	TAVNALWGK	480.27	84.95	2.76E+05	2.10E+05	1.46E+03	3.07E+05	3.88E+03	7.67E+02	1.44E+03	1.57E+03	1.99E+03	5.27E+02	6.46E+05	2.48E+03	1.63E+04	6.98E+02	1.85E+04
P08758 ANXA5	VLTEIIASR	501.30	85.03	1.53E+03	1.47E+04	3.26E+05	1.22E+06	2.05E+06	1.18E+04	2.86E+04	2.53E+04	3.07E+05	1.46E+05	2.07E+03	2.38E+04	1.53E+06	2.55E+05	1.92E+06
Q9UHQ9 NB5R1	MSQYLDL SK	542.77	85.15	6.96E+04	1.94E+03	1.84E+03	2.39E+03	3.32E+03	1.09E+04	3.60E+03	1.70E+04	2.27E+03	1.28E+03	5.58E+04	2.20E+04	4.13E+02	1.50E+03	8.63E+02
Q13228 SBP1	IYVV DVGSEPR	617.31	85.43	2.49E+03	7.25E+05	3.43E+05	4.05E+03	2.29E+04	6.90E+05	2.39E+04	1.88E+04	2.74E+03	1.65E+03	5.11E+03	3.98E+05	5.70E+02	1.61E+04	4.70E+02
Q9Y490 TLN1	AAMEPIVISAK	565.31	85.83	9.74E+03	3.68E+03	2.46E+04	2.08E+03	3.62E+03	5.97E+03	6.12E+02	1.32E+04	1.73E+03	9.28E+02	5.39E+04	1.61E+03	1.33E+04	4.25E+03	2.45E+03
P45880-1 VDAC2	YQLDPTASISAK	647.34	85.88	4.02E+05	1.56E+04	8.67E+03	4.40E+05	5.84E+03	4.04E+04	1.76E+03	7.65E+02	2.71E+03	1.05E+03	3.26E+05	1.42E+04	6.62E+04	6.62E+03	4.56E+05
P27144 KAD4	LMMSELENR	561.77	86.07	1.15E+05	4.10E+03	1.43E+03	6.72E+03	4.19E+03	3.52E+02	7.53E+02	2.84E+03	3.33E+04	1.55E+06	9.59E+03	1.10E+03	2.97E+03	9.54E+03	4.55E+03
Q9UIU7 KAD3	GVLETFSGTETNK	691.84	86.1	2.66E+03	1.47E+04	3.26E+03	3.72E+04	2.07E+04	1.13E+04	1.44E+03	7.55E+02	1.67E+03	8.36E+02	1.15E+04	6.29E+03	1.38E+03	7.36E+02	9.82E+02
P21912 DHSB	NEVDSTL TFR	591.30	86.1	5.58E+03	6.06E+03	1.20E+03	1.61E+05	8.05E+04	1.77E+03	3.26E+03	3.77E+04	1.60E+05	1.01E+05	1.03E+04	5.41E+04	1.53E+05	3.38E+05	1.36E+05
P12429 ANXA3	ALLTLADGR	465.27	86.28	3.88E+04	4.74E+04	8.12E+02	6.90E+04	1.69E+04	5.24E+04	1.57E+04	1.12E+04	8.61E+02	3.16E+03	9.68E+02	9.95E+03	1.35E+03	1.55E+03	7.71E+04
Q9UBV9 HSPB7	LAADGTVMNTFAHK	492.58	86.29	5.66E+04	6.02E+03	4.13E+03	5.41E+04	3.99E+04	5.65E+04	3.74E+03	2.62E+03	2.46E+03	1.24E+03	8.75E+04	1.88E+03	3.03E+04	1.60E+03	1.65E+04
O75947 ATP5H	AGLVDDFEK	497.25	86.57	9.45E+05	1.52E+04	1.48E+04	2.05E+05	2.70E+05	2.33E+04	1.29E+05	2.62E+03	3.49E+03	2.38E+03	4.77E+05	2.53E+04	5.04E+05	1.15E+03	6.40E+05
Q8NDY3 ARHL1	GLYQDLEDK	540.76	86.68	1.73E+05	1.69E+03	2.30E+03	6.40E+04	4.01E+04	1.07E+04	1.38E+03	1.14E+03	7.17E+02	2.22E+03	1.60E+05	4.36E+03	5.29E+03	1.07E+03	2.78E+04
P02647 APOA1	THLAPYSDEL	573.30	86.7	1.61E+05	2.55E+05	1.17E+03	5.41E+04	8.59E+03	2.73E+03	4.97E+03	9.58E+03	1.40E+04	1.58E+05	4.73E+05	4.52E+03	3.69E+05	1.78E+05	5.40E+04
Q09666 AHNK	GEGPDVDVNL PK	620.32	86.82	2.05E+05	3.03E+04	1.49E+03	2.42E+05	1.54E+05	8.10E+04	3.06E+02	2.19E+03	4.38E+04	7.63E+04	1.55E+05	2.53E+03	1.49E+05	2.15E+04	4.45E+04
P23528 COF1	YALYDATYETK	669.32	86.85	1.41E+05	3.61E+03	1.26E+04	1.70E+05	5.23E+03	2.34E+03	1.95E+03	5.00E+02	3.29E+03	6.50E+02	1.63E+05	3.27E+03	6.50E+04	4.43E+02	1.33E+05
Q09666 AHNK	AEGPEVDVNL PK	634.33	87	1.19E+05	3.39E+03	1.79E+04	1.26E+05	1.37E+04	1.59E+03	1.24E+05	1.09E+05	6.18E+04	5.29E+04	9.32E+04	4.78E+03	1.13E+04	4.20E+03	1.11E+05
P30043 BLVRB	NDSLPTVMSEGAR	739.35	87.03	5.58E+03	5.25E+02	2.87E+03	1.09E+05	1.65E+04	1.82E+03	1.59E+03	2.55E+03	4.11E+03	1.01E+03	8.61E+04	3.61E+02	4.14E+04	7.15E+02	8.63E+04
P27144 KAD4	SLLVPDHVITR	417.25	87.24	1.44E+03	1.18E+05	2.38E+03	1.72E+03	1.86E+05	1.53E+05	1.79E+04	1.88E+04	4.91E+03	1.67E+04	3.39E+02	1.66E+05	6.58E+02	6.55E+02	5.61E+03
P27338 AOFB	YVDLGGSYVGPTQNR	813.40	87.36	5.99E+04	6.01E+02	4.49E+03	4.98E+04	2.58E+03	4.22E+02	6.18E+03	9.99E+02	1.28E+02	3.17E+03	7.57E+03	1.33E+03	8.32E+03	1.38E+03	6.75E+04
P16219 ACADS	IAMQTLDMGR	568.28	87.66	2.25E+04	2.21E+03	5.29E+03	2.90E+04	1.23E+04	2.36E+03	2.80E+03	9.23E+02	2.41E+03	3.53E+03	1.90E+04	1.34E+03	3.77E+03	3.18E+03	6.22E+04
Q09666 AHNK	GEGPEVDVNL PK	627.32	87.82	3.07E+03	2.02E+04	2.49E+04	1.20E+04	2.67E+03	2.75E+03	2.86E+03	4.10E+05	6.32E+04	1.05E+05	9.96E+03	6.92E+02	3.39E+03	1.72E+04	1.18E+04
P18859 ATP5J	QTSGGPVDASSEYQELER	694.32	87.87	3.14E+03	3.57E+04	1.68E+03	1.15E+05	8.75E+04	2.77E+04	1.02E+03	6.99E+03	1.55E+03	1.88E+03	8.85E+04	1.36E+03	3.02E+04	3.75E+03	1.37E+05
Q92629-3 SGCD	VLGAEGTVFPK	559.32	87.96	3.86E+03	5.75E+03	1.44E+03	9.98E+04	9.28E+02	6.59E+02	7.84E+04	4.01E+04	5.49E+02	7.82E+02	1.65E+05	2.16E+03	1.31E+05	1.20E+04	1.33E+05
Q00325 MPCP	LPRPPPPEMPEL K	529.96	87.97	3.07E+04	1.02E+04	6.36E+02	8.20E+04	5.92E+04	3.29E+03	1.89E+03	4.66E+02	8.48E+02	1.89E+03	1.30E+05	4.94E+03	4.20E+04	4.47E+02	3.18E+05
P04179 SODM	INAQIMQLH	534.29	88.31	8.36E+04	3.57E+05	2.16E+05	3.47E+03	6.70E+04	4.28E+05	6.65E+05	7.88E+05	4.66E+04	8.22E+04	2.29E+03	2.17E+04	1.54E+03	4.69E+04	9.28E+04
P06733 ENOA	LAQANGWGMVSHR	509.26	88.38	4.79E+04	3.53E+03	3.13E+03	7.02E+02	1.54E+03	1.98E+03	2.40E+03	1.93E+03	7.62E+02	1.78E+03	3.89E+04	1.76E+03	1.33E+04	6.59E+03	1.30E+04
Q14BN4-4 SLMAI	DEILLLHQAAAK	661.38	88.48	1.80E+03	2.91E+02	1.81E+03	2.74E+03	8.25E+02	1.16E+03	1.26E+02	1.66E+03	2.53E+03	5.58E+02	8.22E+04	9.19E+02	1.48E+04	4.66E+02	6.28E+04
P49189 AL9A1	IGDPLLEDTR	564.80	88.53	1.34E+05	4.28E+03	3.94E+02	6.09E+02	1.10E+04	2.11E+03	2.14E+04	1.11E+05	8.18E+03	3.20E+04	1.72E+05	4.88E+03	1.02E+05	1.93E+03	5.27E+03
Q99623 PHB2	VLSRPNAQELPSMYQR	630.32	88.61	8.83E+02	5.75E+03	3.10E+04	3.04E+03	5.26E+02	4.96E+02	2.32E+04	5.32E+03	1.04E+05	3.26E+04	2.49E+02	2.00E+03	1.03E+03	9.65E+04	3.49E+03
P26373 RL13	VATWFNQPAR	595.31	88.82	2.60E+03	3.63E+03	1.46E+04	7.98E+04	3.80E+05	3.96E+04	2.17E+03	9.48E+03	7.21E+03	2.33E+04	3.81E+02	4.36E+05	8.87E+04	2.04E+03	1.38E+05
O95299 NDUAA	VVEDIEYLK	554.30	89.03	3.08E+03	3.82E+03	1.37E+04	2.11E+05	2.03E+05	5.23E+04	2.22E+04	9.53E+03	6.45E+02	1.98E+03	8.51E+02	2.13E+04	9.66E+04	1.38E+03	2.14E+05
Q13554 KCC2B	ISDILNSVR	508.79	89.13	9.91E+02	2.14E+04	3.58E+04	6.08E+04	4.46E+04	6.58E+04	1.59E+03	2.95E+04	1.05E+04	4.08E+03	3.17E+03	4.16E+02	6.41E+03	2.46E+04	5.01E+04
P62158 CALM	DSNGYISAAELR	633.31																



P50995 ANX11	LLISLSQGNR	550.82	90.53	8.20E+02	5.46E+02	9.31E+04	4.23E+03	8.66E+02	2.21E+03	1.69E+04	1.95E+04	2.77E+02	7.20E+02	1.34E+03	1.02E+03	6.19E+02	3.08E+02	2.84E+03
Q9Y623 MYH4	RDLEESTLQHEATAAALR	502.51	90.89	4.68E+02	5.02E+04	1.64E+03	3.09E+02	6.50E+02	4.31E+03	5.15E+03	4.60E+03	3.70E+02	1.48E+03	2.20E+02	3.62E+05	7.33E+02	1.44E+03	4.08E+02
Q02252 MMSA	TLADAEGDVFR	597.29	90.99	1.37E+03	1.08E+03	7.13E+02	1.18E+05	6.25E+03	1.44E+04	8.12E+03	1.04E+05	1.01E+03	8.71E+02	7.45E+04	1.52E+03	2.05E+04	7.37E+02	3.66E+04
P39059 COFA1	FTGSLQQLTVHPDPR	565.97	91.02	4.77E+04	2.47E+04	7.42E+03	4.76E+04	9.43E+02	8.20E+04	1.83E+03	5.00E+02	3.01E+03	3.33E+03	1.07E+03	1.15E+04	6.53E+02	2.19E+02	2.61E+03
P09211 GSTP1	MLLADQGSQSWK	638.82	91.09	9.63E+03	1.47E+03	8.78E+02	1.80E+03	9.62E+03	7.12E+03	1.63E+03	7.71E+03	1.92E+03	8.91E+02	1.16E+05	1.08E+04	1.99E+04	7.01E+02	2.17E+04
P14927 QCR7	DDTIYEDEDVKEAIR	604.28	91.22	9.44E+03	6.06E+02	1.60E+04	4.15E+02	2.16E+03	1.55E+03	3.37E+03	3.83E+03	9.29E+04	1.97E+04	5.83E+03	1.98E+03	1.71E+04	3.15E+04	2.12E+03
P30044 PRDX5	LLADPTGAFGK	545.30	91.29	7.15E+05	1.09E+04	1.30E+03	1.32E+06	8.32E+05	1.59E+05	3.99E+04	3.27E+03	9.81E+03	3.65E+03	7.72E+05	1.76E+04	5.26E+05	1.65E+03	9.32E+05
Q92629-3 SGCD	VLTQLITGPK	535.33	91.32	3.45E+03	3.21E+04	9.38E+03	1.91E+05	1.40E+05	1.56E+05	2.48E+03	1.43E+04	1.29E+03	8.47E+02	9.95E+02	1.44E+03	2.35E+03	1.92E+03	1.39E+05
P55786 PSA	VALSNMNVDR	616.32	91.39	1.06E+05	1.42E+05	5.16E+04	2.22E+05	7.07E+04	1.90E+05	9.98E+03	6.24E+04	2.65E+03	8.41E+02	1.11E+05	8.47E+04	2.12E+05	6.26E+03	1.14E+05
P35222 CTNB1	LVQLLVR	420.79	91.55	1.04E+03	3.99E+02	1.42E+03	6.08E+03	1.60E+02	7.00E+03	4.14E+03	4.17E+02	6.19E+04	7.22E+04	1.53E+02	8.73E+02	4.87E+02	2.14E+03	3.05E+02
P27824 CALX	TPELNLDQFHDK	486.24	91.65	8.36E+04	2.16E+03	2.73E+03	6.22E+03	1.13E+04	7.66E+03	1.59E+03	5.82E+03	2.20E+03	7.51E+02	4.78E+04	3.59E+03	6.32E+03	9.00E+02	3.33E+03
P13489 RINI	ELSLAGNELGDEGAR	765.87	91.68	6.16E+04	8.59E+02	6.63E+02	1.30E+04	7.34E+02	1.86E+03	9.54E+02	2.22E+03	1.42E+03	1.91E+03	4.24E+04	7.05E+03	3.00E+03	1.66E+03	1.12E+03
Q9Y6M9 NDUB9	QHPQPYIFPDSGGTSYER	726.01	91.87	8.97E+02	1.84E+03	2.06E+03	2.70E+03	4.02E+04	4.03E+02	5.39E+02	8.85E+02	7.88E+02	5.44E+02	1.62E+03	8.48E+02	8.41E+02	5.99E+02	1.01E+03
P35573-3 GDE	SGSLAVDNADPILK	700.37	92.32	3.13E+04	3.47E+03	2.09E+03	3.36E+03	1.20E+03	9.50E+02	8.14E+02	5.74E+03	1.83E+03	3.26E+04	6.06E+03	6.34E+02	5.99E+03	6.76E+02	2.43E+03
O75306 NDUS2	NITLNFPGQHPAAHGVL	486.26	92.53	8.18E+03	2.84E+03	2.82E+03	6.34E+03	1.15E+05	9.04E+02	5.23E+03	1.08E+04	2.65E+04	5.09E+03	5.34E+03	3.20E+03	2.04E+04	1.82E+03	3.78E+04
P15121 ALDR	EELFIVSK	482.77	92.56	9.79E+03	2.48E+03	1.52E+03	1.61E+03	2.20E+03	5.43E+02	4.02E+03	5.48E+03	9.16E+04	1.24E+05	3.19E+03	4.51E+03	9.92E+02	1.69E+05	2.11E+03
P35232 PHB	IFTSIGEDYDER	722.83	92.66	1.17E+03	9.98E+02	9.34E+02	6.87E+03	9.44E+02	7.97E+02	4.07E+02	1.31E+03	3.00E+03	1.31E+03	7.23E+04	3.69E+03	9.47E+04	7.24E+03	1.17E+04
O43181 NDUS4	NGWSYDIEER	634.79	92.68	2.61E+04	8.52E+02	3.04E+03	4.21E+03	4.56E+02	4.39E+03	1.19E+03	1.12E+04	1.16E+06	1.26E+06	1.05E+04	1.90E+03	6.57E+02	4.11E+05	2.38E+03
P04179 SODM	DFGSFDKFK	545.76	92.78	2.61E+03	1.80E+03	4.98E+03	2.72E+03	7.29E+04	4.87E+02	1.01E+03	1.35E+05	3.05E+02	2.40E+03	6.51E+02	7.63E+02	2.15E+03	8.07E+02	2.09E+04
P12429 ANXA3	GIGTDEFTLNR	611.81	92.86	2.32E+03	8.91E+02	1.46E+04	1.78E+04	4.61E+04	6.81E+03	6.32E+03	9.80E+02	8.59E+03	1.39E+03	6.18E+02	2.13E+04	2.34E+03	7.28E+02	5.82E+04
P39059 COFA1	TADTAVTGLASPLSTGK	795.42	92.87	3.73E+03	1.52E+03	8.93E+02	1.07E+03	3.48E+03	1.39E+03	1.94E+03	2.39E+03	1.13E+04	2.62E+03	6.16E+04	2.32E+03	3.82E+04	7.69E+03	4.43E+03
P00338 LDHA	SADTLWGIQK	559.80	92.94	3.01E+05	6.78E+02	3.43E+02	1.77E+04	4.11E+03	3.21E+03	4.84E+03	9.82E+02	8.60E+02	8.02E+02	7.47E+04	3.64E+03	1.35E+04	5.43E+03	1.86E+03
Q03252 LMNB2	GLESDVAELR	544.78	92.97	1.28E+04	2.26E+03	7.97E+04	6.34E+03	6.71E+03	9.22E+04	3.74E+04	5.04E+02	3.66E+03	1.12E+03	7.71E+04	8.27E+03	6.95E+04	6.64E+03	7.78E+02
O95299 NDUAA	LQSWLYSSR	570.29	93.05	1.03E+05	3.92E+04	3.34E+03	4.82E+03	1.87E+04	1.58E+03	2.35E+03	2.36E+03	3.92E+03	1.16E+03	6.92E+03	1.23E+03	4.59E+04	2.57E+04	6.93E+02
O75306 NDUS2	VLFGEITR	467.77	93.22	1.30E+03	1.66E+06	9.82E+05	1.27E+06	2.13E+06	2.03E+06	1.16E+06	7.66E+04	2.36E+04	3.02E+04	6.96E+04	3.09E+05	2.37E+05	9.12E+03	4.23E+05
P10606 COX5B	KGLDPYNVLAPK	657.87	93.34	9.04E+03	2.05E+03	2.19E+03	1.51E+03	2.72E+03	2.49E+03	5.31E+02	3.62E+02	1.95E+05	5.95E+04	1.06E+03	9.01E+02	1.14E+04	6.82E+04	4.07E+02
Q16082 HSPB2	TVDNLLEVSAR	608.83	93.42	2.00E+02	1.01E+03	2.38E+03	7.06E+03	2.42E+03	2.90E+03	4.44E+02	1.58E+04	6.58E+03	5.91E+03	1.13E+05	4.25E+02	3.76E+04	1.26E+03	1.58E+04
O75306 NDUS2	TSMESLIHFK	443.89	93.58	2.49E+04	4.09E+02	1.34E+03	7.47E+02	4.86E+02	3.19E+02	1.49E+03	7.90E+03	1.25E+05	1.95E+02	7.99E+02	1.67E+03	1.32E+03	8.47E+04	2.80E+02
P07737 PROF1	DSPSVWAAVPGK	607.32	93.68	2.27E+03	7.27E+02	6.08E+03	1.48E+04	2.05E+04	1.06E+04	1.35E+04	2.27E+03	5.19E+03	3.35E+03	1.82E+04	1.39E+04	1.96E+04	2.67E+03	1.47E+04
Q14192 FHL2	DNQNFVCVPEYK	730.30	93.9	1.11E+03	1.47E+04	6.68E+03	1.80E+03	1.30E+03	9.73E+04	2.91E+03	4.10E+02	4.23E+02	9.52E+02	1.92E+03	3.58E+02	2.15E+03	4.96E+02	1.95E+03
P99999 CYC	TGPNLHGLFGR	584.81	94.11	6.49E+05	8.88E+02	7.77E+03	1.40E+04	1.42E+04	4.06E+02	4.48E+03	6.45E+03	4.69E+02	3.18E+02	3.05E+05	6.92E+03	1.52E+05	3.08E+03	1.59E+04
P09211 GSTP1	TVVYFPVR	490.78	94.17	2.38E+03	7.11E+04	8.18E+03	2.72E+03	7.95E+02	1.95E+05	3.69E+04	1.76E+03	5.28E+03	5.44E+02	4.74E+02	4.04E+04	2.15E+03	2.12E+04	5.02E+02
Q99623 PHB2	STPAITLESPIK	589.31	94.31	4.64E+04	1.65E+04	2.38E+04	4.79E+03	2.33E+03	2.28E+04	3.37E+03	2.52E+04	2.98E+03	1.00E+04	7.38E+04	2.07E+03	1.44E+04	1.68E+03	2.60E+04
O00151 PDLI1	DFEQPLAISR	588.31	94.38	1.90E+05	1.00E+03	2.77E+04	2.13E+05	1.87E+03	1.83E+03	9.46E+04	1.55E+05	2.62E+04	1.81E+04	2.81E+05	2.02E+03	3.39E+02	9.01E+03	1.61E+03
P18859 ATP5J	FEDPKFEVIEKPOA	559.62	94.59	9.94E+02	2.99E+02	1.86E+03	1.87E+03	3.10E+05	9.71E+02	1.90E+04	3.18E+04	6.61E+02	2.19E+02	3.58E+03	3.76E+04	2.90E+03	2.63E+03	1.90E+04
P23368 MAOM	LFTPDVIR	480.78	94.9	1.16E+03	1.57E+05	7.51E+03	9.77E+04	3.82E+04	4.87E+03	1.23E+04	1.66E+03	2.12E+05	3.87E+05	4.36E+03	4.71E+03	1.47E+03	2.35E+06	5.81E+04
P21796 VDAC1	LTFDSSFSPTNGK	700.84	94.97	4.96E+04	4.76E+03	2.82E+03	1.53E+03	2.65E+03	2.87E+03	2.83E+04	5.08E+04	1.88E+03	8.28E+02	3.31E+03	8.43E+02	1.33E+03	2.75E+03	4.55E+02
Q9HBL0 TENS1	TPTQPLESFR	673.36	95	5.93E+02	3.81E+03	2.18E+03	1.02E+05	4.28E+03	1.92E+03	2.37E+04	9.01E+03	3.34E+03	3.45E+04	1.51E+03	4.29E+04	4.51E+02	6.03E+03	2.24E+02
O75306 NDUS2	GSGIQWDLR	516.27	95.1	1.57E+03	2.52E+05	1.68E+03	3.20E+05	2.56E+05	6.07E+03	1.89E+05	1.88E+03	1.80E+03	2.94E+03	1.39E+03	2.53E+05	1.01E+03	6.73E+03	3.24E+05
P00915 CAH1	SLLSNVEGDNAVPMQHNN RPTQPLK	690.60	95.22	1.95E+02	7.33E+02	3.87E+03	4.65E+02	1.10E+05	4.87E+02	4.86E+02	7.34E+02	7.10E+02	3.74E+02	7.73E+02	5.13E+03	1.37E+03	3.13E+02	6.64E+02
P27824 CALX	IPDPEAVKPDDWDEDAPAK	703.33	95.23	6.59E+03	5.27E+03	3.38E+03	1.51E+03	1.31E+03	3.05E+04	3.87E+03	5.30E+03	2.67E+03	2.66E+03	4.67E+03	2.78E+03	4.43E+03	8.99E+02	9.49E+02
P27338 AOFB	IMDLLGDR	466.75	95.34	6.25E+03	3.24E+03	1.81E+05	5.10E+03	8.58E+03	1.65E+04	1.64E+05	1.82E+05	2.34E+06	4.95E+06	3.70E+04	2.08E+03	1.20E+03	2.02E+06	1.45E+03
P00450 CERU	LISVDTEHSNIYLQNGPDR	724.36	95.42	4.89E+03	1.97E+03	5.41E+02	4.62E+03	4.05E+03	1.13E+04	8.30E+03	2.45E+03	4.24E+04	3.43E+04	1.71E+05	1.38E+03	7.95E+04	7.56E+04	3.81E+03
P00387 NB5R3	STPAITLESPIK	686.37	95.46	1.26E+05	1.84E+03	2.35E+03	6.17E+04	1.27E+03	1.62E+03	3.79E+03	5.67E+03	1.78E+03	2.69E+03	1.31E+05	8.52E+02	1.03E+05	9.99E+02	3.45E+03
P00915 CAH1	VLDALQAIK	485.80	95.52	4.92E+05	6.84E+03	1.64E+04	9.43E+03	9.84E+03	2.37E+04	6.45E+03	5.44E+03	2.89E+02	2.39E+02	3.98E+05	5.61E+03	2.40E+03	8.86E+02	3.95E+03
P00915 CAH1	LYPIANGNNQSPVDIK	871.96	95.52	4.29E+04	4.50E+03	1.11E+03	5.35E+03	2.33E+03	1.89E+03	4.67E+02	2.72E+03	2.01E+03	1.28E+02	2.09E+04	8.21E+02	3.02E+02	1.43E+03	7.74E+02
Q13554 KCC2B	VPDILSSVR	493.30	95.6	1.24E+03	2.60E+03	3.77E+03	1.04E+03	8.62E+03	2.95E+03	9.54E+04	5.96E+04	1.69E+03	1.36E+03	4.08E+02	1.12E+03	2.11E+03	2.38E+03	8.64E+03
P02743 SAMP	VEEYSLYIGR	578.80	95.69	2.30E+04	5.52E+03	4.02E+03	3.78E+03	2.63E+02	2.14E+03	3.82E+03	9.81E+03	1.37E+03	5.56E+02	4.20E+03	3.01E+03	1.04E+04	2.67E+03	1.74E+03
Q9UHQ9 NB5R1	GFTVADMIR	505.26	95.73	7.46E+03	8.06E+03	1.89E+03	1.38E+04	6.53E+03	1.72E+03	5.46E+03	4.31E+03	7.26E+04	6.11E+04	7.20E+03	8.28E+03	2.68E+03	6.34E+04	3.65E+03
P04004 VTNC	FEDGVLDPDYPR	711.84	95.8	6.23E+03	3.37E+03	3.25E+04	1.64E+03	1.97E+03	6.76E+03	9.11E+03	3.04E+04	2.35E+02	8.99E+03	1.57E+03	7.52E+03	7.80E+02	6.01E+02	1.87E+03
P12814 ACTN1	D																	

P13639 EF2	VFSGLVSTGLK	554.32	97.43	1.11E+03	2.43E+04	1.33E+03	1.07E+05	1.09E+03	5.00E+03	5.58E+02	3.62E+03	2.10E+03	2.48E+03	2.73E+02	3.22E+03	6.59E+04	2.13E+03	6.88E+04
P26373 RL13	LATQLTGPVMPVR	691.89	97.46	4.18E+03	4.31E+02	7.91E+02	2.57E+04	4.44E+02	6.02E+03	1.39E+03	2.36E+03	4.44E+02	9.03E+02	6.63E+04	4.87E+02	4.48E+04	4.47E+02	3.12E+02
Q9P0J0 NDUAD	LQIEDFEAR	560.78	97.61	1.92E+05	3.85E+04	1.93E+03	1.18E+03	9.72E+03	2.81E+04	6.03E+02	7.12E+02	2.29E+03	3.22E+03	1.06E+03	9.34E+03	3.14E+02	3.01E+03	1.50E+02
P11055 MYH3	IEEEEEIEAERATR	606.30	97.78	1.76E+03	6.43E+02	6.24E+02	5.68E+03	4.97E+03	5.55E+02	3.85E+02	2.77E+03	8.24E+04	3.08E+04	8.78E+02	2.83E+03	1.30E+03	1.08E+05	9.53E+02
Q13554 KCC2B	PDILSSVRR	521.80	97.79	1.48E+04	2.76E+03	1.46E+03	3.14E+04	7.57E+04	2.17E+04	2.42E+04	2.23E+04	5.16E+04	3.10E+04	1.21E+06	1.22E+03	7.95E+05	3.34E+05	2.83E+04
P35232 PHB	FDAGELITQR	575.30	98.1	1.55E+05	1.44E+03	1.83E+03	2.47E+03	3.03E+04	6.00E+02	9.17E+02	2.43E+03	2.17E+03	1.07E+03	1.12E+05	1.87E+03	1.13E+03	6.26E+03	1.30E+03
Q13642-1 FHL1	FVFHQEQVYCPDCAK	605.27	98.41	1.73E+03	1.62E+04	4.98E+02	1.03E+05	2.64E+03	4.37E+04	3.35E+02	5.79E+03	1.16E+03	1.53E+03	1.13E+05	1.39E+03	7.53E+03	5.33E+03	9.68E+02
P50995 ANX11	SETDLLDIR	531.28	98.59	1.87E+04	2.23E+04	4.51E+03	1.53E+05	3.88E+03	1.21E+04	1.19E+04	2.62E+04	1.04E+03	2.98E+03	3.33E+03	2.65E+03	7.65E+04	5.35E+02	1.01E+05
P51884 LUM	ISNIPDEYFK	613.31	98.63	6.08E+04	1.52E+03	4.20E+04	6.11E+04	2.63E+05	1.69E+05	2.31E+03	6.16E+02	3.59E+03	3.21E+04	1.01E+05	8.63E+02	1.33E+03	1.16E+04	1.63E+03
Q99877 H2B1N	LLLPGELAK	477.31	98.74	4.56E+06	5.20E+03	2.98E+04	7.40E+06	2.30E+04	3.53E+03	2.34E+04	2.12E+02	2.94E+02	4.09E+02	5.47E+06	1.92E+04	3.60E+06	5.79E+02	3.42E+04
Q00325 MPCP	GVAPLWMR	465.26	98.95	1.21E+03	1.91E+05	1.18E+03	3.62E+05	3.94E+05	4.05E+05	1.35E+05	1.53E+05	2.54E+04	4.03E+03	2.20E+02	1.74E+05	4.63E+03	1.09E+05	4.99E+05
Q09666 AHNK	FSMPGFK	407.20	98.95	9.21E+02	7.60E+04	4.44E+03	1.63E+05	7.22E+04	8.06E+03	1.90E+03	1.94E+03	9.85E+02	8.95E+02	6.18E+03	7.93E+04	8.59E+03	2.02E+02	1.54E+05
O75521 PECI	NAINTEMYHEIMR	541.26	99.07	4.11E+03	1.36E+04	1.05E+04	3.17E+04	6.24E+04	1.23E+03	3.46E+02	1.97E+03	1.71E+03	8.22E+02	1.18E+04	1.81E+04	1.25E+04	2.87E+03	1.72E+04
P02671-2 FIBA	MKPVPLVPGNFK	481.27	99.15	6.06E+02	2.59E+04	2.23E+04	1.88E+04	3.68E+04	8.32E+03	7.94E+03	1.92E+04	2.94E+05	1.17E+05	7.61E+02	4.29E+04	3.39E+04	1.43E+05	9.44E+03
P09382 LEG1	SFVLNLGK	439.26	99.15	1.75E+02	2.60E+05	4.96E+04	5.43E+05	4.62E+05	5.42E+05	2.47E+05	1.04E+03	4.71E+02	2.57E+03	5.66E+02	2.77E+05	1.00E+03	1.07E+03	4.56E+05
Q9Y6M9 NDUB9	EAEFEFYR	629.77	99.2	6.16E+02	1.35E+04	4.62E+03	8.20E+02	1.05E+05	1.20E+05	3.74E+03	5.29E+02	3.66E+03	4.37E+03	4.47E+02	2.79E+04	4.44E+02	6.07E+03	2.09E+03
P45880-1 VDAC2	VNNSSLIGVGYTQTLRPGV	701.72	99.32	3.62E+04	3.32E+02	6.50E+02	4.44E+03	6.46E+02	4.07E+02	2.20E+03	3.70E+02	1.28E+03	3.46E+02	3.85E+04	1.78E+03	1.65E+03	2.23E+02	3.43E+02
Q8NDY3 ARHL1	LEDLGAALYR	560.80	99.33	1.85E+05	1.65E+03	2.58E+03	3.79E+05	2.09E+04	5.90E+02	5.67E+02	1.92E+03	1.77E+03	1.12E+03	2.16E+05	5.55E+02	9.15E+03	5.95E+02	2.92E+03
P07900 HS90A	ALLFVPR	408.26	99.5	5.09E+02	1.48E+05	1.37E+04	2.77E+05	2.51E+05	2.78E+05	2.30E+03	7.49E+02	5.57E+02	7.30E+02	3.09E+02	4.79E+03	1.41E+02	1.81E+02	2.80E+05
P30153 2AAA	LAGGDWFTSR	555.28	99.5	4.86E+03	3.07E+04	9.25E+03	5.63E+04	3.43E+04	1.38E+05	1.25E+03	1.35E+03	5.09E+02	2.06E+03	7.12E+04	9.98E+04	4.01E+04	3.01E+03	6.38E+04
P35221 CTNA1	EELVAAVEDVR	615.32	99.84	5.28E+04	7.89E+02	1.29E+03	1.29E+04	1.37E+04	1.01E+03	5.83E+02	1.75E+03	1.66E+04	1.68E+04	5.87E+04	2.64E+03	2.55E+03	7.48E+03	6.24E+02
P12814 ACTN1	TINEVENQILTR	715.38	99.89	1.16E+05	3.20E+03	1.38E+03	1.07E+04	1.74E+03	9.24E+03	1.74E+03	1.06E+04	5.83E+02	2.48E+04	9.11E+04	4.39E+03	1.55E+03	1.56E+04	2.23E+03
P02766 TTHY	AADDTWEFPASGK	697.81	100.12	6.33E+04	1.61E+03	6.29E+02	3.72E+03	5.26E+03	1.93E+03	1.08E+03	5.17E+03	4.25E+02	1.71E+03	4.88E+04	1.68E+03	8.65E+02	4.17E+02	1.11E+04
Q9P0J0 NDUAD	ENLEEEAIIMK	659.83	100.2	1.37E+05	2.97E+03	1.26E+03	1.29E+05	6.86E+02	3.85E+03	4.08E+03	4.77E+02	1.53E+03	3.66E+04	9.35E+04	7.75E+03	1.05E+03	3.98E+04	1.11E+04
Q9HBL0 TENS1	LLSGFGLER	496.28	100.56	2.73E+03	1.39E+03	1.75E+03	7.28E+04	1.74E+04	6.89E+03	4.08E+02	5.30E+02	2.26E+03	2.71E+03	2.15E+03	5.73E+02	5.43E+04	2.86E+04	6.03E+04
P04004 VTNC	DWHGVPQVDAAMAGR	556.27	100.57	4.26E+04	3.79E+02	7.12E+02	3.62E+04	1.75E+04	8.04E+02	1.42E+03	1.29E+04	3.27E+04	2.32E+03	5.76E+04	5.03E+03	5.85E+03	1.33E+03	2.60E+02
O95168 NDUB4	GLIENPALLR	548.33	100.97	3.84E+05	1.13E+04	3.86E+03	3.34E+04	1.18E+04	2.20E+03	4.85E+02	2.40E+03	1.13E+04	1.84E+04	3.15E+05	2.13E+04	2.56E+05	1.63E+03	1.21E+04
P07900 HS90A	NPDDITNEEYGEFYK	917.40	101.05	5.01E+04	1.39E+03	2.57E+03	4.42E+04	2.00E+03	1.10E+03	4.40E+02	2.32E+03	1.29E+03	2.31E+03	3.67E+04	1.65E+03	1.35E+03	1.76E+03	4.46E+03
Q9BZL4 PP12C	FAERPALLELER	481.93	101.1	1.05E+03	4.16E+03	1.31E+04	2.76E+02	1.33E+03	7.38E+03	4.67E+03	4.19E+03	5.52E+03	2.26E+04	3.32E+02	5.14E+03	4.13E+02	1.82E+04	7.73E+02
Q13554 KCC2B	DLKPENLLASK	447.60	101.12	3.56E+02	9.58E+02	1.66E+04	7.77E+04	1.71E+03	2.25E+04	1.87E+04	1.22E+04	6.54E+02	7.56E+02	2.94E+02	1.50E+05	5.38E+04	1.60E+03	6.98E+04
O14958 CASQ2	AFEEAAEHFQPY	719.82	101.25	1.01E+03	4.06E+03	1.13E+03	1.55E+05	2.83E+03	1.03E+03	4.91E+02	1.83E+02	2.04E+03	1.76E+03	1.83E+05	3.70E+03	8.54E+03	9.56E+02	1.61E+04
P07737 PROF1	TLVLLMGK	437.78	101.27	4.82E+03	5.88E+02	9.78E+04	2.25E+03	3.70E+02	3.84E+03	9.44E+04	7.34E+03	1.27E+02	4.00E+02	2.69E+03	9.22E+02	3.25E+03	8.39E+02	1.31E+03
P49189 AL9A1	LLCGGDIYVPEDPK	752.87	101.33	2.63E+03	1.35E+04	2.12E+03	9.18E+02	3.81E+04	1.04E+04	1.44E+03	1.15E+03	9.78E+03	2.42E+04	4.21E+03	8.35E+03	3.89E+03	5.49E+03	5.09E+02
P30038 AL4A1	SADVESVVSGLTR	660.34	101.36	1.56E+04	2.42E+04	2.59E+04	2.78E+03	2.24E+04	7.55E+04	1.02E+04	1.00E+03	1.52E+05	1.45E+05	1.73E+03	1.10E+03	2.40E+03	3.64E+04	6.57E+02
P07900 HS90A	HLEINPDHSIITLR	596.32	101.38	1.47E+03	1.60E+03	2.61E+03	1.28E+03	5.86E+03	2.15E+03	5.46E+03	1.10E+03	4.28E+04	4.31E+04	5.90E+04	5.43E+03	2.20E+03	1.49E+04	2.26E+03
P07951 TPM2	TIDDLEDEVYAQK	769.86	101.41	2.55E+05	7.05E+02	7.73E+02	2.21E+05	8.81E+02	3.61E+03	1.19E+03	8.95E+02	8.74E+04	4.65E+05	1.82E+05	4.91E+03	8.72E+03	2.87E+04	5.44E+03
P08758 ANXA5	GTVTDFPGFDER	670.81	101.41	2.34E+05	7.30E+03	2.47E+04	2.00E+04	6.38E+03	3.24E+04	1.54E+04	3.65E+03	5.93E+02	8.71E+02	2.40E+05	6.57E+02	2.37E+03	4.32E+02	9.62E+03
Q6YN16 HSDL2	ALPCIVDVR	493.28	101.49	2.02E+03	3.89E+04	2.56E+04	2.28E+03	1.03E+05	9.58E+04	5.87E+03	1.04E+03	1.41E+03	8.02E+02	3.09E+03	4.11E+04	1.45E+03	2.45E+03	6.94E+04
P30044 PRDX5	FSMVVQDQIVK	611.83	101.56	1.88E+05	1.01E+03	1.40E+03	1.75E+04	6.40E+03	1.44E+03	1.17E+03	1.72E+03	5.08E+02	1.04E+03	1.13E+05	9.08E+03	3.53E+02	1.14E+03	1.05E+04
P18669 PGAM1	FSGWYDADLSPAGHEEAK	660.63	101.75	8.15E+04	1.61E+03	2.52E+02	5.70E+03	7.92E+02	1.70E+03	1.42E+03	8.58E+02	1.73E+02	8.41E+02	7.72E+03	9.19E+02	6.77E+02	2.34E+03	3.57E+02
P30043 BLVRB	PAHVVVGDVLQAADVDK	578.31	101.8	1.54E+04	1.82E+03	2.17E+03	1.23E+03	1.25E+04	4.76E+02	2.30E+04	1.13E+04	3.00E+03	4.46E+02	5.42E+03	2.05E+03	3.05E+04	2.27E+03	4.50E+04
Q9U147 CTNA3	TPEELEDVSDLEEEHEVR	719.00	101.85	3.89E+03	3.37E+03	7.16E+02	2.81E+04	9.43E+03	8.76E+03	1.59E+03	5.34E+02	2.96E+02	1.82E+03	2.86E+04	8.55E+02	1.55E+03	2.72E+03	5.18E+03
Q15084 PDIA6	GSTAPVGGGAFPTIVER	808.42	101.85	5.43E+04	9.41E+03	1.82E+03	4.47E+04	2.88E+03	3.51E+03	3.64E+03	4.40E+03	3.70E+02	1.44E+03	6.34E+04	3.18E+03	5.83E+03	2.60E+03	7.99E+03
P82909 RT36	LVSQEEMEFIQR	754.87	101.85	5.84E+04	2.90E+03	6.54E+04	5.48E+04	1.04E+03	2.02E+04	3.23E+04	4.98E+04	5.43E+02	5.39E+03	7.51E+04	5.07E+02	3.37E+03	8.68E+02	3.75E+04
P30084 ECHM	LFYSTFATDDR	668.31	101.93	4.42E+05	1.22E+03	1.96E+03	2.39E+03	9.72E+02	4.67E+02	3.78E+03	1.88E+05	1.40E+03	6.99E+03	5.09E+03	2.24E+03	1.73E+03	2.86E+03	2.06E+04
O14958 CASQ2	AFEEAAEHFQPYIK	560.61	101.98	5.01E+03	1.65E+03	1.86E+03	1.92E+04	1.01E+04	4.21E+03	6.30E+02	4.01E+02	2.64E+03	2.14E+03	1.15E+03	1.59E+04	8.83E+02	1.20E+03	1.20E+05
P50213 IDH3A	TPIAAGHPSMNLRLR	530.97	102.08	5.06E+03	4.39E+02	3.29E+02	3.88E+03	3.67E+02	1.13E+03	1.78E+03	5.06E+03	3.05E+03	3.56E+02	6.56E+04	2.09E+03	1.50E+03	2.04E+03	2.08E+03
P78417 GSTO1	EDPTVSALLTSEK	695.36	102.18	7.83E+04	1.40E+03	1.47E+03	1.37E+04	1.33E+03	1.09E+03	9.15E+02	1.30E+03	1.86E+03	4.99E+02	1.49E+05	2.99E+03	7.06E+03	2.99E+03	4.20E+03
O75489 NDUS3	ILTDYGFEGHPFR	517.92	102.18	2.23E+03	9.51E+04	2.03E+05	1.47E+03	3.18E+03	2.31E+05	2.40E+05	1.50E+05	3.16E+03	1.56E+04	1.14E+03	3.15E+05	1.48E+03	4.76E+02	7.87E+02
P55786 PSA	IDFVGLNDK	575.30	102.25	2.38E+04	3.46E+03	1.11E+06	8.50E+02	7.87E+02	4.73E+02	1.72E+06	2.27E+06	1.61E+04	1.86E+04	2.22E+03	1.61E+03	3.05E+03	6.17E+02	2.35E+0

Q9Y623 MYH4	DLEESTLQHEATAAALR	617.65	103.84	1.05E+04	4.49E+03	4.85E+06	5.68E+04	3.75E+03	4.27E+05	3.20E+06	5.74E+06	1.16E+03	6.91E+02	3.82E+03	3.40E+03	3.34E+03	8.63E+02	2.36E+03
Q9U147 CTNA3	DELTALEEVR	631.31	103.99	6.28E+03	8.64E+03	1.61E+04	1.13E+05	6.22E+03	6.30E+04	2.33E+03	2.74E+03	8.39E+04	1.31E+05	2.22E+04	1.56E+04	4.10E+03	1.13E+04	1.09E+05
Q09666 AHNK	VDVDVPDVNIEGPDAK	841.42	104.19	2.86E+03	2.61E+03	2.00E+03	1.59E+03	7.50E+02	4.72E+03	1.62E+03	1.41E+03	1.39E+03	3.79E+03	3.07E+03	2.86E+03	6.83E+03	3.20E+03	3.48E+04
P21796 VDAC1	GYGFLIK	427.74	104.22	1.78E+03	5.32E+02	1.06E+03	2.34E+02	8.79E+02	2.56E+02	6.80E+02	1.20E+03	8.94E+04	1.59E+05	1.70E+02	5.96E+02	4.23E+02	1.16E+04	4.27E+02
O75521 PECI	ATEMLIFGK	505.27	104.34	1.22E+05	2.65E+03	6.74E+02	1.01E+03	9.25E+02	2.66E+03	1.98E+03	2.12E+03	1.86E+03	5.53E+03	1.16E+04	7.34E+03	5.69E+03	2.21E+02	6.99E+03
P30049 ATPD	ASPTQVFFNGANVR	754.38	104.35	2.36E+03	1.32E+03	1.55E+03	5.85E+03	3.46E+03	1.31E+03	5.06E+04	4.37E+03	5.37E+04	2.20E+04	1.31E+04	1.49E+03	1.23E+03	1.91E+04	3.62E+02
P10606 COX5B	GLDPYNVLAPK	593.83	104.66	1.98E+06	8.54E+02	3.80E+02	8.11E+05	2.38E+02	1.19E+03	1.18E+03	2.28E+03	4.02E+03	1.55E+03	1.12E+06	1.14E+03	7.13E+02	6.16E+02	8.32E+02
O75306 NDUS2	LVMELSGEMVR	632.32	104.83	2.33E+03	2.81E+03	1.17E+05	3.81E+04	1.56E+04	3.51E+03	6.50E+04	7.60E+04	3.55E+02	5.32E+02	4.82E+03	6.53E+02	1.04E+03	3.66E+03	3.49E+03
P50995 ANX11	GTITDAPGFDPLR	680.35	105.23	1.43E+05	1.92E+03	2.03E+03	2.10E+05	8.04E+03	8.77E+03	7.13E+02	1.70E+03	1.99E+03	1.12E+03	1.62E+05	1.36E+04	1.34E+02	6.02E+03	1.76E+04
P27144 KAD4	IAQNFGLQHLSSGHFLR	482.01	105.68	4.70E+02	1.94E+02	2.93E+02	7.21E+02	1.61E+03	6.27E+02	3.01E+02	2.27E+02	2.93E+04	2.56E+04	5.51E+02	8.75E+02	1.79E+02	9.73E+03	4.89E+02
P30043 BLVRB	VVVGDLVQAADVDK	714.39	105.75	3.99E+03	1.74E+05	1.65E+04	2.55E+03	2.29E+03	5.39E+04	4.51E+04	1.44E+03	1.43E+03	1.16E+03	3.76E+03	7.82E+04	4.54E+02	4.42E+02	1.15E+03
Q13228 SBP1	GGPVQVLEDEELK	706.86	105.83	4.22E+02	1.16E+04	3.05E+04	9.25E+02	1.45E+04	4.29E+04	3.09E+03	5.76E+02	7.58E+04	8.84E+03	9.87E+02	1.19E+03	4.97E+03	6.72E+04	1.25E+04
Q09666 AHNK	ISMPDVDLHLK	423.23	105.85	1.75E+03	7.84E+02	2.77E+04	7.45E+02	4.71E+03	4.01E+04	1.94E+04	6.40E+03	1.69E+03	2.69E+02	2.60E+03	4.43E+02	1.35E+03	1.62E+03	6.40E+02
P00338 LDHA	FIIPNVVK	465.29	105.93	6.34E+02	7.60E+02	2.20E+03	6.46E+02	2.12E+03	8.11E+04	2.18E+03	1.65E+03	2.98E+02	3.92E+02	1.04E+03	8.55E+02	2.80E+02	3.90E+02	2.91E+02
P13807 GYS1	TQVELLEAPTALK	755.43	106.12	3.17E+02	4.33E+04	1.94E+04	3.91E+02	4.68E+04	5.77E+03	2.11E+03	1.58E+03	6.48E+02	2.51E+02	4.23E+02	8.89E+04	4.62E+02	3.88E+02	1.31E+05
P27338 AOFB	LLHDSGLNVVLEAR	545.31	106.15	4.12E+05	2.46E+04	1.21E+03	1.77E+04	4.74E+03	1.61E+04	2.49E+03	1.69E+03	1.27E+04	1.68E+04	2.67E+05	1.44E+03	1.19E+03	5.93E+03	1.23E+04
Q9Y4W6 AFG32	VGQISFDLPR	566.31	106.24	6.53E+05	3.14E+04	1.17E+03	1.96E+05	6.96E+04	3.18E+03	2.83E+03	3.14E+03	3.18E+03	1.81E+03	9.80E+05	9.74E+04	5.68E+04	1.42E+03	8.77E+04
Q13642-1 FHL1	QVIGTGSEFFPK	590.82	106.36	1.85E+03	3.26E+03	2.27E+03	5.78E+03	4.43E+03	2.64E+03	2.86E+03	2.01E+03	7.86E+04	1.12E+05	8.76E+02	8.42E+02	1.81E+03	3.11E+04	5.72E+02
P26373 RL13	GFSLEELR	475.75	106.48	2.66E+03	1.60E+03	1.87E+03	3.07E+03	1.22E+03	1.12E+03	1.12E+03	1.14E+03	8.00E+04	9.85E+04	1.95E+03	1.09E+03	1.99E+03	8.91E+04	2.47E+03
P18669 PGAM1	YADLTQDQLPSCESLK	906.42	106.49	3.73E+03	5.79E+03	1.22E+04	2.49E+03	1.99E+03	2.53E+04	8.62E+03	4.66E+03	1.37E+03	2.92E+03	4.93E+03	2.44E+03	3.78E+03	4.76E+02	4.50E+02
Q14BN4-4 SLMAI	EITSLQNSFQLR	718.38	106.49	4.18E+02	4.17E+02	5.05E+03	1.19E+04	1.90E+04	1.51E+04	4.52E+03	7.36E+02	1.79E+03	5.74E+02	9.32E+03	8.26E+02	4.99E+03	2.65E+02	9.07E+02
P22626 ROA2	IDTIEIITDR	594.83	106.56	1.91E+03	2.16E+03	8.10E+02	4.04E+03	2.08E+02	2.41E+03	6.56E+02	6.52E+02	8.17E+04	1.24E+05	4.21E+02	6.20E+02	4.86E+02	1.35E+05	2.03E+03
Q14BN4-4 SLMAI	DTDIASLQEELK	681.34	106.71	1.72E+03	6.50E+02	3.91E+03	2.34E+04	3.66E+02	7.83E+03	2.90E+03	4.39E+02	1.02E+04	3.97E+04	2.03E+04	1.38E+03	7.56E+02	2.00E+04	1.78E+03
Q13228 SBP1	NTGTEAPDYLATVDVDPK	953.46	106.79	1.03E+03	1.87E+03	1.95E+03	4.40E+02	2.50E+03	6.78E+02	9.21E+02	2.60E+03	1.66E+04	1.34E+04	2.04E+03	9.30E+02	3.74E+02	1.68E+03	6.06E+03
Q9Y490 TLN1	TMLESAGGLIQTAR	724.38	106.87	6.23E+02	1.37E+03	4.26E+02	5.12E+03	3.22E+03	1.49E+03	4.96E+03	1.91E+03	7.11E+03	2.76E+04	5.75E+02	1.83E+03	1.81E+03	2.21E+03	2.61E+03
P62158 CALM	EAFSLFDK	478.74	106.94	4.29E+03	5.47E+03	3.42E+03	1.96E+03	5.07E+03	1.20E+03	2.18E+03	1.35E+03	1.13E+05	1.80E+05	3.36E+03	5.23E+03	1.45E+03	6.80E+04	2.80E+03
P30048 PRDX3	DLSLDDFK	476.73	107	7.78E+03	6.08E+03	4.63E+02	4.75E+03	4.35E+02	8.37E+02	1.68E+03	4.24E+02	9.09E+04	1.01E+05	2.54E+02	1.56E+03	1.98E+03	5.56E+04	1.97E+03
P01834 IGKC	DSTYLSSTLTLSK	751.88	107	1.09E+04	1.18E+04	3.21E+04	4.93E+04	1.95E+04	6.14E+04	1.30E+03	5.05E+03	4.00E+02	5.18E+02	4.57E+04	1.39E+04	1.00E+04	1.55E+03	3.76E+04
P30044 PRDX5	THLPGFVEQAEALK	513.95	107.1	1.93E+02	6.83E+03	2.90E+03	6.63E+03	2.49E+03	4.34E+03	4.76E+03	1.51E+03	4.93E+04	8.75E+04	1.02E+04	3.49E+03	1.02E+03	5.04E+04	1.01E+04
P24539 AT5F1	LDYHISVQNMNR	502.91	107.12	8.12E+02	2.85E+03	1.01E+03	2.09E+03	4.09E+03	3.72E+02	2.81E+02	1.36E+03	9.77E+04	5.95E+04	1.17E+03	7.54E+02	3.16E+02	4.17E+04	1.23E+03
P16219 ACADS	LADMALALESAR	630.84	107.14	3.85E+03	6.20E+02	5.72E+04	2.52E+03	4.10E+03	1.90E+04	5.36E+04	4.56E+04	3.70E+04	7.84E+04	5.40E+02	6.74E+02	1.34E+03	9.05E+04	4.87E+02
P62988 UBIQ	TITLEVERPSDTIENVK	894.47	107.29	1.61E+03	3.54E+02	1.03E+04	7.23E+02	3.56E+05	1.22E+04	1.10E+04	7.05E+04	3.15E+02	1.63E+04	5.41E+05	3.86E+05	2.48E+05	7.60E+02	5.14E+05
Q9Y4W6 AFG32	DLFALAR	403.23	107.34	9.00E+04	1.92E+04	4.33E+03	3.88E+02	9.26E+04	2.81E+04	8.48E+02	7.29E+02	1.88E+03	1.06E+03	1.20E+05	8.16E+04	1.04E+04	8.31E+02	4.36E+03
P22061 PIMT	MGVIYVPLTDK	618.34	107.64	1.06E+03	5.92E+02	1.98E+04	2.54E+03	1.46E+03	5.09E+04	1.03E+04	1.42E+03	6.43E+03	2.15E+03	8.87E+02	9.93E+02	1.20E+03	2.09E+04	9.46E+02
Q02338 BDH	VVNISMLGR	538.30	107.67	5.98E+03	1.14E+03	1.20E+04	7.02E+02	3.33E+03	3.55E+04	3.68E+04	3.22E+04	1.34E+05	1.79E+05	2.46E+03	7.51E+02	2.16E+02	1.58E+05	1.65E+03
P47755 CAZA2	LLLNNNDNLLR	599.35	107.78	4.23E+02	1.79E+03	2.40E+03	9.06E+03	4.99E+02	2.10E+03	2.58E+03	8.31E+03	1.02E+05	1.27E+05	1.44E+03	8.08E+02	2.65E+02	2.59E+04	3.18E+03
P07900 HS90A	TLTIVDTGIGMTK	675.37	107.91	5.56E+03	1.47E+04	7.58E+02	1.94E+03	1.15E+05	4.31E+03	1.51E+03	4.38E+03	1.35E+03	1.23E+05	1.79E+03	9.39E+04	3.30E+03	8.42E+05	1.94E+05
P00441 SODC	LACGVIGIAQ	472.76	107.94	6.84E+02	1.40E+05	1.08E+04	3.72E+02	2.02E+05	1.54E+04	8.03E+03	1.03E+04	3.79E+03	1.44E+03	1.39E+03	1.70E+05	3.75E+04	5.90E+02	2.99E+05
Q6YN16 HSDL2	TAIHTAAMDMLGGPGIESQ	720.37	108.07	2.76E+03	6.98E+04	2.40E+04	2.38E+03	4.80E+03	5.15E+05	3.37E+03	2.24E+03	5.49E+02	2.17E+03	4.23E+03	3.43E+02	1.15E+03	9.21E+03	1.36E+03
P35222 CTNB1	HAVVNLINYQDDAELATR	681.34	108.11	1.96E+03	1.25E+04	2.68E+03	1.02E+03	4.37E+03	3.98E+04	2.58E+03	2.52E+03	4.89E+03	2.13E+04	1.24E+03	1.25E+04	2.00E+04	1.05E+03	1.50E+03
P11055 MYH3	DPLNETVVGLYQKSSNRLL AHLATFA	753.40	108.27	4.65E+02	4.00E+05	1.69E+03	1.02E+04	8.64E+02	3.82E+03	1.18E+04	1.79E+04	4.72E+03	2.28E+04	3.77E+04	1.48E+03	6.89E+03	3.51E+02	1.51E+03
P07737 PROF1	SSFYVNGTLGGQK	735.88	108.37	4.71E+04	2.70E+03	7.85E+02	5.48E+04	8.76E+02	7.89E+02	1.66E+03	2.16E+03	2.04E+02	4.21E+02	4.31E+04	2.14E+03	3.01E+03	2.06E+03	5.60E+03
Q09666 AHNK	VDVEVPDVSLEGPEGK	834.92	108.39	7.05E+03	9.03E+03	4.54E+03	2.86E+03	1.60E+04	2.89E+03	1.19E+04	6.98E+02	1.04E+03	1.29E+03	3.25E+02	2.72E+04	2.42E+04	2.39E+03	2.03E+04
O43678 NDUA2	AAAAASR	609.33	108.53	9.79E+04	1.31E+03	1.64E+04	8.52E+04	5.53E+03	3.46E+03	3.29E+04	7.22E+03	7.87E+03	4.96E+03	1.34E+05	6.12E+04	6.65E+02	5.47E+03	9.75E+03
O14558 HSPB6	APSVALPVAQVPTD	682.87	108.56	1.06E+04	3.48E+03	2.91E+04	1.22E+03	9.40E+02	9.48E+02	1.68E+04	1.55E+04	3.25E+03	2.71E+03	4.57E+03	1.01E+05	4.42E+04	2.12E+02	1.78E+03
P14854 CX6B1	GGDISVCEWYQR	706.82	108.57	2.28E+04	2.33E+03	1.74E+03	8.09E+03	7.26E+02	4.46E+02	1.81E+03	1.28E+03	7.65E+04	1.42E+05	2.32E+04	8.53E+02	2.25E+02	4.30E+04	2.63E+03
P99999 CYC	ADLIAYLK	453.77	108.64	5.20E+02	1.36E+02	5.93E+05	8.55E+02	2.25E+02	1.59E+02	5.92E+05	8.58E+05	1.55E+02	6.26E+02	2.59E+02	5.41E+02	8.85E+02	3.05E+02	6.65E+02
P04040 CATA	AFYVNVNNEEQR	741.37	108.7	6.07E+02	1.08E+04	2.06E+04	3.54E+03	3.79E+03	6.19E+03	3.82E+04	1.84E+04	1.24E+04	2.23E+04	6.04E+02	2.09E+03	1.19E+03	8.21E+03	2.23E+03
P50395 GDIB	DLGTESQIFISR	683.35	108.77	3.38E+03	1.31E+03	2.85E+04	1.78E+03	1.78E+03	1.38E+05	3.30E+03	2.02E+03	1.64E+04	3.70E+05	5.50E+02	3.50E+02	2.26E+03	5.50E+04	1.16E+03
P45880-1 VDAC2	GFGFLVK	412.74	109.03	3.32E+02	7.15E+02	7.32E+02	1.07E+03	3.22E+02	9.24E+02	3.22E+02	5.36E+02	9.20E+04	1.48E+05	1.20E+03	3.20E+02			

Q9UI47 CTNA3	VAHIVTGEMDSYEPGAYTE GVMR	838.06	109.46	1.87E+03	7.63E+02	1.50E+03	1.59E+03	6.47E+02	3.64E+02	2.47E+03	1.33E+03	1.22E+04	2.18E+03	1.69E+03	2.81E+02	1.17E+03	2.49E+04	3.19E+02
P13639 EF2	GHVFESQVAGTPMFVVK	654.66	109.7	6.83E+03	3.52E+03	2.06E+03	1.38E+03	1.07E+03	2.61E+03	2.50E+03	3.39E+03	3.12E+04	6.16E+04	3.41E+03	7.45E+02	4.02E+03	9.33E+03	4.94E+03
P45880-1 VDAC2	LTLSALVDGK	508.80	109.82	4.34E+03	1.36E+03	2.46E+02	3.81E+03	9.85E+02	7.05E+03	4.55E+02	9.55E+02	1.18E+04	7.59E+04	5.22E+03	2.52E+03	1.59E+03	4.01E+03	8.50E+02
P30049 ATPD	IEANEALVKALE	650.38	110.19	2.18E+05	3.29E+04	8.33E+03	3.43E+05	2.88E+05	6.24E+03	7.03E+03	8.77E+03	3.20E+04	2.44E+04	1.40E+03	2.49E+05	1.17E+05	2.81E+03	5.13E+03
P00441 SODC	GLTEGLHGFHVHEFGDNTA GCTSAGPHFNPLSR	693.33	110.23	1.51E+03	1.50E+03	2.54E+03	1.04E+04	5.10E+02	3.22E+03	2.20E+02	3.14E+04	2.37E+03	4.00E+03	1.75E+03	1.11E+03	1.71E+03	8.39E+03	1.15E+03
Q02978 M2OM	NVFNALIR	473.78	110.26	9.24E+02	3.62E+03	8.85E+03	4.01E+03	2.83E+03	3.63E+03	2.45E+04	1.09E+04	1.71E+05	1.62E+05	1.14E+04	6.37E+03	3.91E+03	1.15E+05	5.08E+03
P30048 PRDX3	IALLSDLTK	487.30	110.45	2.04E+04	8.53E+03	1.17E+03	2.46E+03	4.46E+04	2.54E+03	1.04E+04	4.73E+02	6.77E+02	9.21E+02	2.09E+04	4.25E+03	2.00E+03	2.76E+03	9.70E+03
P00387 NB5R3	STPAITLESFDIKYPLR	634.35	110.65	1.60E+04	4.68E+02	6.90E+03	8.75E+02	3.01E+04	8.61E+02	1.28E+03	1.78E+03	7.35E+03	4.16E+04	1.40E+04	4.41E+03	4.95E+02	1.58E+03	1.77E+03
O43181 NDUS4	LDITTLTGVPEEHK	555.97	110.75	1.91E+05	2.77E+03	5.80E+02	2.67E+05	2.56E+05	2.54E+03	8.98E+02	2.44E+03	8.32E+02	4.14E+02	1.74E+05	3.04E+05	1.68E+05	7.11E+03	2.21E+04
Q9Y623 MYH4	KQLDHEKSELQTSLEEAEA SLEHEEGK	619.30	111.01	4.25E+03	6.89E+02	6.16E+03	9.18E+03	1.22E+03	7.22E+03	2.66E+03	4.27E+03	1.38E+03	1.55E+06	6.22E+03	1.42E+03	4.52E+03	5.36E+05	1.81E+03
Q9Y2Q3 GSTK1	FLTAVNLEHPEMLEK	590.98	111.11	2.80E+04	2.53E+03	1.72E+03	1.91E+04	5.33E+04	2.41E+03	6.53E+02	2.20E+04	5.86E+03	6.47E+02	4.60E+03	1.11E+04	1.04E+03	3.09E+02	2.60E+04
Q09666 AHNK	VDIDVPDVNIEGPEGK	848.43	111.26	2.25E+04	2.93E+03	2.62E+03	4.32E+03	1.76E+04	2.89E+03	1.28E+03	6.40E+04	1.26E+03	2.35E+03	8.78E+03	1.09E+04	4.01E+03	7.38E+02	3.99E+04
Q09666 AHNK	VDIDVPDVNIEGPDAK	848.43	111.26	2.25E+04	2.93E+03	2.62E+03	4.32E+03	1.76E+04	2.89E+03	1.28E+03	6.40E+04	1.26E+03	2.35E+03	8.78E+03	1.09E+04	4.01E+03	7.38E+02	3.99E+04
P06733 ENOA	MILPVGAAFR	594.83	111.36	2.28E+05	2.81E+03	2.42E+03	4.62E+05	1.75E+04	1.20E+03	6.46E+02	1.78E+03	3.21E+04	5.67E+02	1.35E+05	1.10E+04	3.18E+04	2.66E+04	1.69E+04
Q09666 AHNK	VDVDIPDVNIEGPDAK	848.43	111.48	2.49E+04	4.18E+03	7.11E+02	5.73E+03	1.12E+04	1.09E+03	1.07E+03	1.20E+03	3.84E+03	2.36E+03	1.36E+04	1.19E+04	1.34E+04	3.88E+03	4.82E+04
Q9NZN4 EHD2	GYDFPAVLR	519.27	111.54	2.62E+03	4.16E+03	6.74E+03	6.35E+03	1.04E+03	5.26E+03	9.18E+02	1.22E+03	4.32E+04	1.33E+04	5.99E+02	2.20E+04	7.76E+03	3.34E+04	7.52E+03
P30042 ES1	GGAEVQIFAPDVPQMVID HTK	797.07	111.58	5.90E+02	1.46E+03	3.33E+03	3.90E+02	2.45E+04	1.89E+03	4.42E+03	2.59E+03	3.32E+03	9.84E+02	1.45E+03	6.07E+03	6.44E+02	6.75E+03	4.97E+03
P21796 VDAC1	WTEYGLTFTEK	687.83	111.66	2.85E+03	1.04E+03	7.83E+02	5.86E+04	2.55E+04	6.05E+03	8.61E+03	1.96E+03	1.89E+03	4.26E+02	3.14E+02	1.24E+04	2.77E+03	5.89E+02	3.65E+03
Q9Y623 MYH4	QTSLEEAESLEHEEGK	629.63	111.77	6.87E+02	2.29E+05	4.65E+03	5.98E+02	5.51E+02	8.70E+03	1.67E+04	5.24E+04	4.72E+03	8.11E+03	2.26E+02	1.60E+04	8.12E+03	1.80E+03	5.01E+02
O43181 NDUS4	LDITTLTGVPEEH	712.86	112.34	2.70E+04	1.18E+03	1.22E+03	9.51E+03	3.91E+02	5.83E+03	6.78E+03	1.44E+02	2.10E+04	1.36E+03	8.68E+03	1.51E+03	1.81E+03	7.26E+03	2.31E+03
Q9HBL0 TENS1	TPEEEPLNLEGLVAHR	602.31	112.35	2.26E+03	2.21E+02	3.28E+04	1.04E+04	5.19E+03	1.93E+03	5.13E+02	2.81E+03	5.07E+04	3.54E+03	1.02E+05	7.59E+03	1.27E+05	1.34E+04	8.84E+03
P35232 PHB	SLATAGDGLIELR	658.36	112.37	3.95E+03	2.53E+03	7.93E+02	1.58E+03	1.89E+03	2.63E+03	2.97E+03	9.42E+02	9.26E+04	2.03E+04	4.59E+03	2.45E+03	1.78E+03	4.69E+03	1.09E+03
O75489 NDUS3	SLVDLTAVDVPTTR	693.38	112.43	1.24E+05	4.29E+03	3.00E+03	2.55E+05	2.77E+05	2.48E+03	8.57E+02	3.90E+03	4.00E+03	1.83E+03	1.17E+04	3.26E+05	2.50E+05	2.27E+03	2.72E+05
P50461 CSRP3	GLQFQQSPK	950.46	112.44	6.35E+02	3.46E+03	3.39E+02	6.02E+02	1.43E+03	2.55E+04	1.03E+03	1.77E+03	8.41E+02	4.61E+03	7.80E+02	6.18E+02	1.98E+03	7.59E+02	8.41E+02
Q9Y2Q3 GSTK1	NEDITEPQSILAAAEK	864.94	112.52	3.67E+04	1.07E+03	2.81E+03	1.94E+04	1.19E+03	3.32E+02	5.78E+02	3.31E+03	2.67E+03	7.17E+02	3.09E+04	2.82E+03	5.96E+03	1.17E+03	5.56E+02
Q99623 PHB2	DLQMVNISR	594.82	112.67	1.92E+03	2.71E+03	1.71E+03	4.51E+03	3.59E+04	1.75E+03	1.51E+03	2.26E+03	1.53E+04	2.22E+04	4.06E+03	1.43E+02	3.57E+03	6.26E+04	4.02E+04
O96000 NDUBA	VDQEIINMQDR	737.37	112.77	1.18E+03	9.54E+03	6.87E+03	3.81E+03	4.17E+03	1.13E+05	2.39E+04	4.73E+04	7.51E+02	7.99E+03	1.10E+03	5.92E+03	9.92E+02	1.80E+04	7.45E+03
P00450 CERU	GAYPLSIEPIGVR	686.38	112.79	7.84E+02	1.50E+03	1.80E+03	4.86E+03	4.89E+04	9.15E+02	8.08E+02	5.68E+02	1.77E+03	5.47E+03	1.02E+03	3.19E+04	1.04E+04	4.85E+02	5.88E+03
P27338 AOFB	APLAAEWDNMTMK	768.35	112.97	1.49E+04	1.30E+03	7.73E+03	1.02E+04	2.67E+03	2.41E+03	5.31E+03	1.12E+04	1.02E+04	3.02E+03	1.59E+04	2.78E+03	2.80E+03	1.40E+03	4.72E+02
P51884 LUM	FNALQYLR	512.78	113.05	2.55E+03	8.83E+03	7.41E+03	6.56E+02	1.66E+03	1.38E+05	7.67E+04	8.46E+04	2.56E+03	2.35E+02	9.01E+02	3.62E+02	1.76E+03	5.59E+02	3.93E+02
P02671-2 FIBA	GLIDEVNDQFTNR	760.87	113.05	5.99E+02	6.47E+02	7.71E+03	2.21E+03	7.04E+02	4.83E+02	7.16E+04	2.36E+03	1.78E+03	5.45E+03	3.63E+03	2.35E+03	5.05E+02	4.82E+03	1.63E+04
P35573-3 GDE	SGGGYIVDPILR	673.36	113.25	1.25E+03	2.88E+03	2.41E+03	2.52E+02	8.84E+03	1.09E+03	3.05E+02	2.21E+03	3.29E+03	4.03E+02	3.16E+03	1.01E+03	1.70E+03	9.66E+02	2.18E+04
P12814 ACTN1	AGTQIENIEEDFRDGLK	645.65	113.69	1.21E+04	1.28E+04	1.73E+03	2.19E+03	1.38E+05	1.51E+04	2.48E+02	2.52E+03	8.07E+02	8.51E+02	5.56E+02	9.65E+02	1.28E+03	2.61E+03	4.62E+04
P27824 CALX	GLTSGWILSK	531.30	113.75	3.76E+04	1.43E+03	7.31E+03	5.99E+03	1.24E+03	9.12E+02	2.96E+02	5.91E+02	2.24E+03	4.27E+02	2.50E+04	2.73E+03	3.43E+03	7.63E+03	3.57E+03
P00450 CERU	ALYLQYTDETFR	760.38	113.79	2.90E+03	1.27E+03	1.43E+03	1.37E+04	5.84E+03	5.71E+02	1.23E+04	8.01E+03	3.01E+03	7.02E+04	6.52E+02	9.42E+02	4.71E+03	5.64E+03	8.55E+03
P14854 CX6B1	NCWQNYLDFHR	499.22	113.98	8.91E+02	1.82E+04	2.11E+03	4.33E+03	1.05E+03	7.37E+04	2.26E+04	1.20E+04	9.68E+03	1.30E+03	7.57E+02	1.09E+03	1.95E+03	8.42E+03	3.24E+03
P02647 APOA1	DYVSQFEFSALGK	700.85	114.04	3.01E+03	6.93E+02	1.81E+03	7.54E+03	6.51E+02	3.35E+03	1.08E+03	7.19E+02	1.19E+05	1.11E+04	1.05E+03	2.84E+03	5.22E+02	1.64E+05	2.36E+03
Q9UIJ7 KAD3	TVGIDDLTGEPLIQR	813.94	114.86	3.86E+03	2.72E+03	6.20E+04	4.74E+03	8.07E+02	2.33E+03	8.11E+04	6.73E+03	2.65E+03	1.35E+03	1.94E+03	3.52E+02	5.80E+03	1.94E+03	1.02E+03
P08758 ANXA5	FITIFGTR	477.77	115.03	5.92E+02	7.07E+02	1.59E+02	3.25E+02	1.68E+02	9.33E+02	1.82E+02	6.62E+02	5.82E+04	7.98E+04	3.68E+02	2.82E+03	7.26E+02	8.49E+04	5.57E+02
P13807 GYS1	LSDLLDWK	495.27	115.18	6.51E+04	1.56E+03	1.08E+03	4.81E+04	9.55E+02	2.63E+04	7.05E+03	1.02E+05	8.38E+02	1.06E+03	6.60E+04	2.60E+03	1.79E+03	2.64E+03	2.75E+03
P30084 ECHM	SLAMEMVLTGDR	661.83	115.48	2.10E+04	5.45E+03	5.21E+03	9.19E+03	2.01E+04	4.15E+03	7.10E+03	8.46E+03	6.52E+02	2.09E+03	1.08E+05	1.34E+04	1.41E+04	2.69E+03	5.53E+03
P22626 ROA2	GFGFVTFDDHDPVVK	565.93	115.48	6.21E+02	1.20E+03	1.05E+03	1.01E+03	1.41E+03	6.93E+02	4.83E+03	3.47E+02	4.26E+04	8.69E+02	2.77E+02	2.97E+03	2.92E+03	4.35E+04	7.29E+03
O00151 PDLI1	VTPPEGYEVVTVFPK	831.44	116.01	6.47E+04	7.07E+03	9.24E+02	1.67E+05	1.25E+04	7.51E+03	4.01E+03	2.99E+03	2.97E+02	3.11E+02	2.88E+05	1.39E+04	1.10E+04	1.40E+03	1.08E+04
O96000 NDUBA	TPVQPNPIVYMMK	759.40	116.16	6.26E+02	2.48E+03	4.75E+03	3.08E+03	3.85E+04	1.68E+03	4.53E+03	1.53E+04	6.09E+02	4.13E+02	3.18E+02	1.40E+05	1.42E+04	2.11E+03	1.16E+04
P04179 SODM	SIFWTNLSPNGGEPK	852.42	116.2	7.86E+04	1.84E+03	7.88E+03	2.58E+04	5.13E+02	2.90E+03	9.47E+02	2.44E+03	2.78E+02	3.42E+03	2.70E+03	1.14E+03	7.50E+02	7.71E+02	1.02E+03
Q9NZN4 EHD2	LNPFNGTFLNR	646.84	116.23	5.34E+02	9.86E+03	9.83E+04	4.77E+02	1.81E+03	3.53E+04	1.00E+03	1.09E+04	5.84E+02	2.51E+02	1.52E+03	1.23E+04	1.94E+03	3.29E+03	2.39E+03
P07900 HS90A	APFDLFENR	554.77	116.3	2.02E+03	5.54E+02	3.26E+03	1.54E+03	5.96E+02	1.65E+03	1.60E+03	2.59E+04	1.20E+05	5.73E+03	4.43E+03	7.49E+02	1.04E+03	1.03E+05	8.91E+02
P00387 NB5R3	DILLRPELELR	748.43	116.39	2.47E+03	1.33E+04	3.89E+03	1.27E+03	6.76E+04	3.65E+03	2.79E+03	1.04E+04	1.30E+03	4.66E+03	8.42E+02	8.44E+04	4.47E+03	8.12E+02	1.18E+05
P47755 CAZA2	EGAAHAFAQYNLDQFTPVK	703.02	116.39	6.83E+02	1.50E+03	4.47E+03	1.09E+03	2.64E+02	2.15E+02	6.19E+03	9.00E+02	3.22E+03	1.35E+04	1.04E+03	1.41E+03	7.94E+02	7.49E+02	2.56E+03
Q92523 CPT1B	YLESVRPLLDDEEYR	687.34	116.45	1.71E+04	8.75E+02	4.50E+03	1.06E+03	2.09E+03	1.40E+03	3.66E+04	1							

Q92629-3 SGCD	LEGDSEFLQPLYAK	805.41	116.95	4.65E+02	1.05E+04	2.13E+03	6.19E+03	3.11E+04	9.63E+03	3.12E+03	4.60E+03	2.64E+03	1.12E+03	4.04E+03	8.91E+04	1.89E+03	2.78E+02	3.94E+04
O75915 PRAF3	GIVLDALEQQEEGINR	892.46	116.97	1.09E+03	1.02E+04	3.17E+03	3.42E+02	6.16E+03	8.24E+03	3.10E+03	1.22E+03	6.37E+02	7.16E+02	1.88E+03	1.99E+03	6.73E+02	3.37E+02	6.71E+02
P30042 ES1	GGAEVQIFAPDVPQMH	848.41	117.12	6.08E+04	1.96E+03	4.27E+03	1.33E+04	5.15E+03	1.24E+03	1.74E+03	1.73E+03	1.74E+03	7.19E+02	1.42E+04	3.71E+03	7.75E+02	1.26E+04	1.06E+04
O95168 NDUB4	TLPETLDPAEYNISPETR	682.34	117.25	7.83E+03	9.74E+04	1.92E+05	2.65E+03	2.89E+03	3.79E+03	1.04E+03	1.09E+03	2.61E+03	6.79E+02	1.09E+03	2.62E+03	3.20E+03	3.86E+03	3.46E+02
Q13228 SBP1	LVLPSLISSR	542.84	117.36	1.84E+03	2.29E+03	7.00E+02	4.36E+03	3.19E+02	1.34E+02	2.22E+02	2.06E+03	2.05E+02	1.37E+05	2.66E+03	6.00E+02	7.15E+02	8.06E+04	4.24E+02
P07437 TBB5	AILVDLEPGTMDSVR	808.42	117.56	2.08E+05	8.88E+02	7.43E+03	4.60E+04	1.05E+05	8.85E+03	4.25E+03	1.54E+03	4.71E+02	1.24E+03	6.07E+04	8.60E+04	1.20E+04	1.22E+04	1.53E+05
P61604 CH10	FLPLFDR	454.26	117.61	3.31E+03	2.07E+03	1.61E+03	1.26E+03	6.50E+02	3.61E+03	1.35E+03	9.92E+02	4.11E+05	3.93E+05	3.17E+03	4.75E+03	6.93E+02	3.91E+05	3.81E+03
Q15084 PDIA6	LAAVDATVNQVLASR	764.43	118.1	1.02E+04	1.30E+03	2.30E+03	1.81E+03	3.84E+03	1.00E+04	2.05E+03	1.70E+03	3.30E+03	2.99E+04	5.60E+03	9.29E+02	1.35E+03	6.56E+02	2.56E+03
P30044 PRDX5	VGDAIPAVEVFEGEPGNK	914.46	118.22	9.74E+03	3.55E+03	5.22E+02	1.40E+04	1.04E+04	1.70E+03	2.25E+03	2.30E+03	7.36E+03	2.31E+03	2.23E+04	4.90E+04	2.78E+04	1.72E+04	1.38E+04
P35232 PHB	VLPSITTEILK	607.37	118.46	2.59E+03	4.12E+02	3.85E+02	2.77E+02	5.86E+02	2.42E+02	2.96E+02	4.68E+02	2.21E+05	1.48E+05	5.82E+02	1.19E+03	1.81E+02	1.84E+05	5.25E+02
P06733 ENOA	YISPDQLADLYK	713.87	118.55	1.84E+05	1.16E+03	8.01E+02	1.46E+05	6.11E+02	2.01E+03	6.47E+02	3.60E+04	7.42E+03	7.24E+02	4.98E+04	3.50E+03	4.52E+04	3.67E+03	6.90E+03
P27824 CALX	APVPTGEVYFADSFDR	885.92	118.56	5.87E+03	4.19E+03	2.00E+02	4.46E+03	4.52E+04	1.53E+04	3.51E+04	3.44E+03	7.39E+02	1.89E+03	2.03E+03	3.51E+04	1.03E+04	5.52E+03	9.07E+04
Q99623 PHB2	IGGVQDQDTILAEGLHFR	618.67	118.68	2.02E+03	1.29E+03	1.86E+03	5.93E+02	7.58E+04	1.66E+04	1.50E+03	4.71E+03	7.00E+02	3.16E+02	4.71E+02	3.30E+03	1.02E+03	1.76E+03	3.78E+04
Q99877 H2B1N	SFVNDIFER	563.78	118.72	8.18E+03	2.35E+03	1.24E+03	2.95E+03	6.98E+02	3.92E+03	1.44E+03	1.47E+03	6.40E+02	1.31E+05	4.86E+02	3.45E+03	2.34E+03	1.79E+03	1.80E+03
P02743 SAMP	ESVTDHVNLIPL	719.38	118.85	6.12E+02	1.54E+03	8.57E+02	3.02E+03	1.59E+03	3.65E+02	4.20E+03	1.00E+03	2.64E+03	1.66E+04	1.13E+02	1.76E+03	5.85E+02	6.37E+02	3.92E+02
O96000 NDUBA	AFDLIVDRPVTLVR	538.65	118.88	2.31E+02	2.17E+03	4.28E+02	5.49E+02	4.33E+04	4.24E+03	1.98E+03	7.42E+02	4.65E+02	4.19E+02	3.50E+02	3.40E+04	1.95E+03	1.61E+02	8.47E+04
P09211 GSTP1	PPYTVVYFPVR	669.37	118.93	1.17E+03	1.83E+04	7.01E+03	3.15E+03	1.33E+04	1.03E+05	4.30E+03	7.42E+02	8.65E+04	1.09E+04	1.27E+03	5.88E+03	8.42E+02	1.54E+05	1.08E+03
O43678 NDUA2	YAFGQETNVPLNFSADQV TR	791.05	119	2.86E+03	4.85E+03	9.10E+02	1.74E+03	7.81E+02	2.21E+04	8.57E+02	4.75E+03	4.92E+04	1.42E+03	4.16E+02	2.16E+03	1.83E+02	9.65E+03	5.80E+02
P61604 CH10	DYFLFR	430.72	119.33	1.58E+02	1.40E+02	1.41E+02	7.87E+02	3.34E+02	5.30E+02	2.85E+02	1.68E+02	3.34E+02	3.99E+04	1.53E+03	3.34E+03	3.82E+02	1.36E+03	2.48E+02
P61978 HNRPK	GSYGD LGGPIITQVTIPK	959.02	119.37	8.80E+02	1.11E+04	5.92E+03	3.39E+02	4.28E+03	4.14E+04	2.25E+03	4.40E+03	1.97E+03	2.18E+02	1.68E+03	2.20E+03	3.79E+02	9.23E+02	1.83E+03
P12429 ANXA3	SEIDLLDIR	537.29	119.52	1.26E+03	7.80E+03	1.78E+03	4.43E+03	6.71E+02	1.97E+03	5.15E+02	2.99E+03	3.46E+04	2.77E+03	2.66E+03	5.00E+03	7.59E+02	3.66E+04	1.82E+03
P39059 COFA1	AFLSSHLQDLSTIVR	562.98	119.77	5.35E+02	5.05E+02	2.63E+04	4.30E+02	4.28E+03	8.09E+02	1.05E+03	6.77E+02	2.96E+03	6.89E+03	1.33E+03	3.99E+02	2.37E+02	3.34E+02	7.78E+02
P78417 GSTO1	VPSLVGSFIR	537.82	119.8	1.88E+02	8.03E+02	2.21E+03	9.09E+02	1.16E+03	3.51E+02	3.43E+02	9.28E+02	3.55E+04	4.47E+02	1.26E+02	6.09E+02	3.90E+02	1.04E+05	1.74E+03
P08758 ANXA5	SEIDLFNIR	553.79	119.84	1.37E+03	2.85E+03	1.78E+05	3.73E+03	1.49E+03	4.91E+02	1.29E+05	1.40E+05	2.32E+04	4.96E+02	5.45E+03	3.45E+03	1.21E+03	3.69E+02	6.18E+03
O75521 PECI	STGFETLVVTSSEDGITK	892.45	120.23	1.43E+04	7.02E+03	7.61E+02	3.12E+03	1.31E+04	3.16E+03	1.96E+02	1.21E+03	5.45E+03	3.97E+03	2.56E+03	2.75E+03	5.26E+03	3.31E+03	2.02E+03
P63104 1433Z	GIVDQSQAYQEA FEISK	1021.00	120.24	2.24E+03	3.23E+03	5.44E+03	3.22E+03	1.05E+04	1.93E+04	2.98E+03	5.42E+03	2.45E+02	1.30E+03	4.87E+02	2.57E+03	1.47E+03	7.59E+02	1.42E+03
P61604 CH10	VVLDDKDYFLFR	510.61	120.28	4.01E+02	1.22E+04	1.00E+04	1.85E+03	1.03E+05	2.12E+04	1.34E+04	2.35E+04	1.21E+03	6.62E+02	1.12E+03	9.64E+04	1.01E+03	4.77E+02	3.93E+04
P09211 GSTP1	FQDGDLTLYQSNTILR	942.48	120.74	3.13E+02	7.52E+03	9.21E+03	6.39E+02	2.56E+03	2.88E+03	4.27E+04	5.40E+02	1.35E+03	8.69E+03	1.18E+03	2.53E+03	5.76E+02	1.17E+03	1.99E+03
P50395 GDIB	EIRPALELLEPIEQK	593.33	120.76	4.25E+05	1.14E+05	6.66E+03	4.84E+04	7.79E+03	4.21E+03	1.37E+04	5.73E+04	1.22E+03	2.00E+03	1.60E+04	8.04E+03	3.81E+04	7.34E+02	7.13E+04
P07919 QCR6	PEEEEEEEELVDPLTTVR	758.02	121.48	2.45E+03	1.39E+03	4.47E+02	1.93E+03	2.19E+03	1.03E+03	2.94E+03	2.26E+03	1.56E+03	2.15E+03	9.93E+02	3.93E+04	2.24E+04	9.23E+02	6.54E+03
O75947 ATP5H	YPYVPHQPIENL	778.88	121.68	1.52E+05	7.23E+03	7.17E+03	5.32E+04	1.68E+03	5.04E+03	2.52E+02	2.35E+03	2.51E+02	8.86E+02	9.39E+02	1.57E+04	2.39E+04	1.44E+03	1.70E+04
Q9U147 CTNA3	ELENLDYLAFK	677.85	121.93	3.49E+02	3.78E+03	8.36E+02	9.59E+02	8.93E+02	2.90E+04	7.96E+02	1.10E+04	3.21E+03	1.72E+04	1.63E+03	5.15E+03	3.75E+02	7.59E+03	9.58E+03
P50461 CSRP3	NFGPTGIGFGGLTQQVEK	925.47	122.01	4.40E+04	4.86E+02	1.60E+03	2.26E+05	6.56E+02	2.78E+03	4.63E+02	3.90E+02	1.51E+03	7.85E+02	3.86E+05	8.98E+03	1.98E+03	3.18E+02	3.78E+03
P50895 BCAM	VAYLDPLELSEK	717.38	122.02	1.53E+04	4.33E+03	1.34E+04	1.61E+03	2.99E+03	2.49E+04	3.42E+03	1.62E+04	5.79E+04	2.29E+03	5.35E+04	9.74E+04	2.74E+04	2.39E+04	4.86E+03
P30044 PRDX5	VNLAELFK	467.27	122.15	6.72E+02	1.55E+05	5.32E+03	2.71E+02	1.14E+03	2.47E+05	1.06E+05	1.17E+05	6.34E+03	1.98E+02	4.00E+02	2.54E+02	3.87E+02	5.53E+03	5.57E+02
P50213 IDH3A	IAEFAF	697.36	122.54	2.62E+05	3.91E+04	3.63E+04	2.50E+05	1.48E+04	8.01E+03	1.09E+04	1.26E+04	3.52E+02	1.20E+04	2.21E+05	2.31E+04	1.31E+04	2.15E+03	1.85E+05
Q09666 AHNK	ISMPDLDLNLK	629.84	122.57	3.96E+05	1.04E+04	3.74E+03	3.07E+05	4.96E+03	6.04E+04	4.33E+02	1.42E+04	9.36E+02	3.30E+02	1.63E+05	7.85E+03	5.89E+03	2.56E+03	1.58E+04
Q09666 AHNK	ISMPDLDLNLK	629.84	122.57	3.96E+05	1.04E+04	3.74E+03	3.07E+05	4.96E+03	6.04E+04	4.33E+02	1.42E+04	9.36E+02	3.30E+02	1.63E+05	7.85E+03	5.89E+03	2.56E+03	1.58E+04
P29692-2 EF1D	GVVQELQQAISK	650.37	122.69	2.67E+04	8.32E+03	3.72E+03	4.95E+03	6.93E+03	8.09E+02	2.61E+02	7.12E+03	1.41E+02	2.36E+03	4.68E+04	5.70E+03	1.24E+03	1.17E+03	4.34E+02
P21912 DHSB	YLGPAVLMQAYR	691.37	122.75	1.55E+04	3.11E+03	3.84E+02	7.19E+04	2.86E+03	5.34E+02	1.72E+03	3.62E+02	1.87E+03	7.72E+02	4.37E+04	4.56E+03	8.31E+02	4.68E+03	7.47E+03
Q9GZM7 TINAL	YWTAAANSWGPWGER	876.40	123.03	9.92E+03	1.26E+03	7.07E+02	1.28E+03	1.31E+02	1.84E+03	1.01E+03	4.68E+02	2.62E+02	3.70E+02	3.93E+04	1.22E+04	1.20E+04	5.08E+03	7.59E+03
O75915 PRAF3	AWDDFFPGSDR	656.78	123.16	1.28E+05	7.00E+03	4.91E+02	1.31E+05	5.15E+03	1.63E+04	2.44E+03	9.46E+02	2.18E+03	6.76E+02	1.41E+05	6.83E+02	8.11E+03	2.33E+03	4.82E+03
O75306 NDUS2	TYLQALPYFDR	693.85	123.28	1.76E+04	7.43E+04	6.69E+03	8.69E+03	4.91E+03	6.22E+04	8.09E+04	4.50E+02	3.06E+02	1.20E+03	1.85E+04	2.64E+03	1.33E+04	6.30E+02	2.21E+04
O95299 NDUAA	ITSAYLQDIENAYK	814.91	123.29	1.15E+05	2.11E+03	4.01E+03	3.90E+03	4.53E+03	1.42E+03	7.73E+02	1.11E+04	1.33E+03	3.40E+04	8.36E+04	6.88E+03	8.72E+03	2.63E+02	7.22E+03
P13489 RINI	LGDVGMAELCPGLHPSSR	651.33	123.4	1.49E+03	4.71E+03	1.78E+03	1.72E+03	1.76E+02	1.95E+04	1.60E+04	4.53E+03	1.71E+03	5.35E+02	3.49E+03	3.76E+02	4.88E+02	9.69E+03	1.50E+03
P21796 VDAC1	LTL SALLDGK	515.81	123.42	4.25E+04	8.97E+02	1.68E+02	5.85E+04	1.23E+03	2.25E+03	3.36E+03	2.15E+03	2.40E+03	1.29E+03	4.89E+04	1.38E+03	7.96E+02	3.07E+02	1.94E+03
P30049 ATPD	TFASPTQVFFNGANVR	878.44	123.47	4.95E+04	4.80E+03	6.60E+02	3.49E+03	8.18E+02	3.86E+03	4.78E+02	1.12E+03	4.97E+02	7.90E+02	3.34E+04	3.33E+03	9.96E+03	7.29E+02	1.66E+04
P35221 CTNA1	QIIVDPLSFSEER	766.90	123.7	1.82E+04	6.02E+03	3.88E+03	1.95E+03	5.62E+02	4.22E+03	1.06E+03	2.83E+03	1.26E+03	4.03E+04	5.22E+04	1.74E+03	7.37E+02	9.77E+02	5.19E+03
Q02338 BDH	FGVEAFSDCLR	622.29	123.82	2.35E+03	4.49E+02	1.48E+03	3.41E+03	5.00E+04	4.18E+03	1.18E+03	2.01E+03	4.78E+02	1.56E+03	5.81E+03	3.80E+03	5.73E+03	6.66E+03	2.21E+03
P30153 ZAAA	IGPILDNSTLQSEVKPILEK	732.08	124.16	3.10E+03	2.56E+03	1.26E+03	5.01E+04	3.93E+03	8.43E+02	1.04E+03	1.43E+03	6.43E+02	7.20E+02					



P09211 GSTP1	ALPGQLKPFETLLSQNQGG	709.39	125.42	9.66E+03	7.05E+02	3.05E+04	6.21E+04	1.06E+05	2.27E+03	6.34E+02	2.24E+03	5.77E+03	5.08E+03	4.16E+04	1.71E+04	2.06E+03	2.90E+03	7.44E+04
Q99623 PHB2	VLPSIVNEVLK	605.87	125.54	4.35E+04	2.86E+03	3.50E+02	2.73E+04	2.08E+05	1.38E+03	1.27E+03	2.42E+03	6.19E+02	3.03E+02	9.05E+03	1.19E+05	6.37E+04	1.68E+03	6.09E+04
P14927 QCR7	YEEENFYLEPY	748.32	125.92	9.61E+04	4.72E+02	2.31E+03	1.62E+03	1.69E+03	7.15E+02	1.11E+03	4.75E+03	1.72E+03	1.07E+03	2.59E+04	6.59E+03	1.12E+03	2.29E+03	9.01E+02
Q9UBY9 HSPB7	DFSPEDIIVTTSNNHIEVR	729.36	125.95	2.12E+04	1.91E+03	1.79E+03	4.90E+03	2.25E+03	6.48E+03	2.31E+03	3.21E+03	2.99E+03	1.39E+04	6.96E+04	1.63E+03	3.29E+03	1.45E+03	1.33E+04
P05026 AT1B1	SYEAYVLNIVR	663.86	125.98	8.19E+03	1.58E+04	3.84E+02	4.45E+04	1.63E+04	6.71E+03	4.90E+03	1.25E+03	8.17E+03	2.79E+03	4.38E+04	5.95E+03	3.56E+03	7.17E+03	6.05E+03
P15121 ALDR	MPILGLGTWK	558.32	126.18	3.00E+04	1.89E+02	1.86E+03	3.55E+04	1.81E+05	1.06E+04	2.91E+03	1.08E+03	1.87E+03	5.27E+02	1.60E+04	1.72E+05	4.04E+03	8.30E+02	1.45E+05
P30044 PRDX5	GVLFGVPGAFTPGCSK	768.90	126.31	8.42E+03	1.23E+02	2.59E+03	2.03E+03	1.26E+04	1.69E+03	1.57E+03	5.58E+03	3.56E+02	1.55E+03	1.22E+04	4.48E+03	2.61E+03	8.36E+02	2.10E+04
P35221 CTNA1	AHVLAASVEQATENFLEK	653.01	126.53	2.50E+02	4.20E+03	1.29E+03	7.44E+02	2.58E+03	1.44E+04	2.54E+02	6.60E+02	6.67E+03	7.69E+02	1.00E+03	7.13E+02	3.85E+02	2.60E+03	2.56E+02
Q08380 LG3BP	SDLAVPSELALLK	678.39	126.74	2.07E+04	1.70E+03	4.83E+02	4.59E+03	2.06E+03	9.52E+02	2.10E+02	1.95E+03	6.92E+03	1.46E+04	1.09E+05	1.58E+04	3.70E+03	3.42E+03	8.75E+02
Q9Y2Q3 GSTK1	MELLAHLLGEK	627.35	126.96	1.89E+03	4.21E+02	1.99E+04	9.35E+02	2.18E+02	4.83E+02	9.52E+04	1.24E+05	1.41E+03	1.68E+03	1.62E+03	4.59E+02	1.02E+03	1.15E+04	1.50E+02
P22061 PIMT	LILVGPAGGNQMLEQYDK	1022.03	127.01	2.18E+02	1.88E+05	1.41E+03	2.18E+04	5.54E+02	1.57E+05	4.72E+02	3.19E+02	2.44E+02	2.41E+02	6.61E+02	5.35E+02	2.92E+02	2.21E+02	4.25E+03
P30084 ECHM	AQFAQPEILIGTIPGAGGTQ	709.05	127.1	1.19E+05	2.54E+03	9.89E+02	2.36E+02	1.33E+04	3.46E+03	2.90E+03	1.20E+03	4.84E+02	6.94E+02	6.71E+04	1.27E+04	3.89E+03	2.12E+02	8.48E+04
P07919 QCR6	GDPEEEEEEEELVDPLTTV	815.37	127.58	6.05E+04	2.02E+02	1.33E+03	4.27E+02	6.15E+02	3.69E+03	8.10E+02	8.76E+02	6.24E+02	2.22E+03	3.62E+04	2.46E+03	6.03E+02	5.20E+02	5.31E+03
P13807 GYS1	GADVFLAALAR	581.32	127.63	3.38E+02	5.18E+02	1.93E+03	2.14E+03	3.44E+04	6.55E+02	2.40E+03	2.77E+03	4.20E+03	4.72E+02	9.13E+02	5.18E+04	4.31E+04	1.63E+04	3.19E+04
Q07021 C1QBP	AFVDFLSDEIKEER	566.62	127.94	1.04E+03	1.24E+03	1.95E+03	6.89E+03	1.21E+05	1.08E+03	9.18E+03	1.88E+04	1.72E+03	1.22E+03	3.33E+03	9.24E+04	1.98E+03	8.24E+02	1.22E+03
Q9P0J0 NDUAD	IALLPLLQAETDRR	536.99	128.03	7.24E+02	3.48E+04	3.67E+02	9.37E+02	1.15E+04	1.03E+04	2.58E+05	8.93E+04	2.24E+02	2.51E+02	2.70E+03	1.74E+03	1.84E+02	2.29E+02	9.62E+02
O75306 NDUS2	LDELEELLTNNR	729.88	128.25	1.10E+05	1.97E+03	2.12E+03	5.46E+03	3.57E+03	3.46E+03	1.07E+03	1.10E+03	1.83E+03	1.29E+03	3.91E+04	7.93E+03	8.46E+03	9.71E+02	1.97E+04
P02766 TTHY	TSESGELHGLTTEEEFVEGI	819.06	128.46	7.05E+03	5.01E+02	2.94E+03	1.37E+03	1.95E+02	2.31E+03	1.72E+03	3.50E+02	2.17E+02	2.03E+03	1.92E+04	4.12E+02	7.26E+02	7.83E+02	2.12E+03
Q00325 MPCP	FGFYEVFK	518.76	128.5	4.30E+02	1.36E+02	8.79E+02	3.44E+02	1.44E+03	5.19E+02	1.48E+03	2.89E+03	6.80E+04	2.68E+03	4.11E+02	8.91E+03	1.05E+03	3.14E+04	5.75E+02
P13807 GYS1	IADPSAYGIYILDR	783.91	128.55	5.71E+03	8.43E+02	9.45E+02	1.51E+03	1.04E+03	1.08E+03	2.52E+03	2.75E+03	2.32E+02	1.03E+03	3.77E+03	6.41E+03	5.66E+03	2.88E+02	1.46E+04
Q8NDY3 ARHL1	AAMLQGSVGDALGYR	747.39	129.07	3.32E+04	5.22E+02	9.55E+02	7.39E+02	3.12E+03	1.38E+03	5.71E+02	9.91E+02	1.67E+03	2.92E+04	7.89E+03	5.52E+03	1.24E+04	1.21E+03	1.19E+04
P30043 BLVRB	TVAGQDAVIVLLGTR	756.94	129.33	3.28E+04	1.79E+03	3.22E+02	2.24E+03	2.23E+03	3.56E+03	6.48E+02	1.05E+03	2.59E+03	1.66E+03	1.66E+04	6.32E+03	3.36E+02	1.32E+03	4.72E+03
O75489 NDUS3	DFPLSGYVELR	648.34	129.43	6.78E+02	1.17E+04	1.55E+03	1.37E+03	1.42E+04	2.99E+04	8.03E+03	1.65E+04	2.08E+03	3.45E+02	1.27E+03	3.06E+04	8.44E+03	7.37E+02	2.41E+03
O14958 CASQ2	LGFDEEGSLYILK	742.39	129.46	7.30E+04	8.12E+03	1.68E+03	3.07E+03	7.74E+02	6.85E+02	1.70E+03	1.04E+03	1.11E+03	1.79E+03	8.77E+04	1.38E+04	4.96E+04	8.23E+02	3.11E+04
P02647 APOA1	DLATVYVDVLK	618.35	129.97	1.80E+04	1.44E+03	8.64E+02	2.48E+03	4.96E+02	1.72E+03	1.76E+03	2.03E+03	4.12E+02	4.29E+03	8.35E+04	3.06E+03	2.80E+03	1.54E+03	7.83E+03
Q16082 HSPB2	VQAFLDVSHFTPDEVTVR	703.35	130.1	2.97E+03	4.83E+02	4.24E+02	2.26E+03	7.94E+03	7.38E+03	3.33E+02	4.15E+03	3.46E+05	1.17E+03	2.09E+03	2.04E+04	1.86E+03	1.37E+05	3.67E+02
P01859 IGHG2	FVSVLTVVHQDWLNGK	598.67	130.11	1.16E+05	7.38E+02	1.57E+02	8.70E+02	6.62E+03	4.20E+03	2.84E+03	4.86E+02	8.88E+02	4.96E+02	8.51E+03	7.13E+02	1.74E+02	1.07E+03	2.88E+02
P30048 PRDX3	MNIALLSDLTK	609.84	130.5	2.04E+04	4.79E+03	9.87E+03	3.41E+04	2.89E+03	2.72E+04	2.31E+03	2.88E+03	6.29E+03	1.70E+03	1.39E+04	1.20E+04	2.51E+04	9.39E+02	5.19E+03
Q13228 SBP1	EEIVYLPCIYR	699.36	130.7	3.62E+03	5.43E+03	3.88E+02	7.56E+02	6.41E+02	2.07E+03	1.87E+03	2.38E+03	8.57E+02	8.46E+03	5.64E+03	2.06E+03	6.40E+02	3.50E+03	1.42E+03
P30048 PRDX3	DYGVLLLEGSLALR	731.90	130.72	1.17E+05	4.59E+03	3.19E+03	4.39E+02	1.53E+03	5.08E+03	1.76E+03	3.17E+03	1.79E+03	1.19E+03	1.04E+05	2.92E+04	1.79E+04	9.45E+02	2.07E+05
O75947 ATP5H	LAALPENPAIDWAYYK	966.50	130.82	1.68E+04	8.51E+02	9.90E+02	7.91E+02	1.02E+04	4.63E+03	3.99E+02	2.47E+03	4.37E+03	1.68E+03	1.87E+04	2.23E+04	3.16E+04	3.50E+03	2.68E+05
P02042 HBD	FFSEFGDLSPPDAVMGNPK	1022.97	130.97	8.37E+04	2.42E+02	3.38E+03	3.45E+03	4.39E+03	7.83E+02	1.87E+03	4.11E+03	4.49E+02	3.72E+02	1.19E+05	1.17E+03	1.47E+03	1.48E+03	6.30E+03
Q16134 ETFD	IPVPILGPLMNNHGNIVR	738.74	131.05	2.17E+03	7.63E+02	4.00E+03	1.32E+03	5.37E+04	2.07E+03	3.05E+03	3.93E+03	1.14E+03	1.35E+03	2.38E+02	1.47E+04	4.07E+03	2.27E+03	5.68E+02
P47755 CAZA2	FIHAPPGEFNEVFNDVR	701.02	131.08	5.22E+04	8.86E+02	1.01E+03	3.08E+03	1.54E+03	8.86E+02	3.98E+02	3.10E+02	3.86E+02	1.35E+04	2.72E+04	9.38E+02	2.21E+03	1.01E+03	1.53E+03
P55786 PSA	LGLQNDLFLSLAR	673.87	131.15	3.39E+04	1.25E+03	5.00E+02	4.20E+02	7.21E+02	6.46E+02	2.73E+03	5.46E+02	4.83E+03	4.15E+03	3.73E+04	1.42E+04	2.88E+03	1.28E+04	2.30E+03
Q08380 LG3BP	ELSEALGQIFDSQR	796.90	131.28	2.13E+02	1.07E+03	2.11E+02	1.01E+03	5.08E+03	6.18E+02	8.26E+02	1.11E+03	3.97E+04	6.05E+02	4.31E+02	4.06E+02	1.51E+03	1.01E+04	1.37E+03
P00387 NB5R3	APEAWDYGQGFVNEEMIR	704.66	131.33	9.04E+03	3.06E+04	1.86E+03	1.97E+02	9.16E+04	2.01E+04	6.91E+04	3.77E+03	8.28E+02	9.82E+02	1.26E+04	1.22E+03	3.29E+02	1.78E+03	7.16E+03
P84243 H33	FQSAAGALQEASEAY	828.40	131.5	2.84E+02	2.08E+03	1.85E+04	2.93E+02	1.03E+03	2.12E+03	1.21E+03	4.97E+02	1.48E+03	4.90E+03	6.81E+02	5.89E+03	7.42E+02	1.54E+03	6.29E+02
P01834 IGKC	TVAAPSVFIFPPSDEQLK	973.51	131.56	9.74E+03	4.41E+05	1.84E+05	1.73E+04	2.91E+03	3.15E+05	5.40E+03	2.72E+03	2.01E+02	6.27E+02	8.84E+03	1.42E+04	9.19E+03	1.18E+03	1.91E+04
P35222 CTNB1	EAAEAIEAEGATAPLTELH SR	760.39	131.64	2.41E+03	4.60E+03	1.86E+03	1.10E+03	4.64E+02	4.15E+03	6.77E+02	1.38E+02	2.75E+03	2.45E+03	1.07E+04	1.74E+03	1.51E+04	4.31E+02	1.93E+02
P30048 PRDX3	GLFIIDPNGVIK	643.38	131.8	2.12E+05	9.87E+03	9.92E+02	9.19E+02	2.80E+03	4.23E+03	5.09E+03	9.81E+03	4.99E+02	5.54E+02	1.31E+05	3.86E+03	3.58E+03	2.51E+02	1.42E+04
P01859 IGHG2	TTPPMLDSDGSFFLYSK	953.45	131.86	6.56E+03	8.95E+02	1.15E+03	1.31E+03	1.23E+04	4.29E+04	9.65E+02	7.37E+03	1.00E+03	5.10E+02	9.03E+02	1.36E+03	8.91E+02	1.44E+03	8.46E+02
P23528 COF1	EILVGDVGTQVDDPYATFV	1083.55	131.98	4.67E+04	7.80E+03	2.09E+03	1.37E+03	2.70E+04	2.95E+02	3.99E+03	2.73E+03	3.03E+02	5.13E+02	1.04E+05	3.55E+05	9.68E+03	3.27E+02	3.87E+03
Q65YN16 HSDL2	SFTGNFVIDENILK	798.92	132.26	3.10E+04	5.91E+03	5.51E+02	2.49E+03	2.71E+03	9.90E+02	1.34E+03	2.32E+04	3.74E+02	1.69E+03	1.08E+04	1.66E+03	5.95E+03	4.42E+02	1.32E+04
O96000 NDUBA	DYKVDQEIINIMQDR	627.31	132.27	3.05E+03	2.65E+03	2.42E+02	1.69E+03	2.49E+04	7.41E+02	6.54E+02	4.61E+02	8.79E+02	5.40E+02	3.76E+02	1.42E+03	1.03E+03	7.13E+02	1.43E+03
P13639 EF2	EGIPALDNFLDK	666.35	132.71	2.13E+04	3.47E+03	4.48E+02	1.40E+03	3.52E+04	1.38E+03	1.47E+03	1.88E+03	1.44E+02	1.35E+03	1.60E+04	8.33E+03	4.56E+03	7.47E+02	1.23E+04
P07437 TBB5	ALTVPELTQQVFDAK	830.45	133.71	1.46E+05	2.11E+04	1.70E+03	1.07E+04	7.19E+03	1.48E+04	1.13E+03	6.91E+04	4.30E+02	5.81E+02	1.42E+05	2.22E+02	1.46E+04	1.45E+03	8.87E+02
Q07021 C1QBP	AFVDFLSDEIK	642.33	133.87	1.93E+05	4.64E+03	1.28E+03	1.19E+03	3.65E+03	1.65E+03	1.03E+03	8.79E+02	1.06E+04	7.21E+02	1.32E+05	1.61E+03	6.82E+03	1.80E+03	3.85E+03
P61978 HNRPK	IILDILISEPIK	670.90	133.95	2.53E+03	7.84E+02	2.94E+02	4.59E+02	3.00E+02	1.11E+03	6.04E+02	7.04E+02	1.52E+02	6.05E+02	5.28E+03	8.80E+02	1.81E+04	1.63E+03	1.23E+04
Q07021 C1QBP	VEEQPELTSTPNFVVEVIK	1144.09	134.07	5.83E+02	1.30E+03	3.38E+02	4.45E+02	2.10E+03	5.89E+02	9.07E+02								

P00915 CAH1	ADGLAVIGVLMK	593.84	135.49	1.34E+04	4.65E+04	1.09E+03	2.62E+04	1.86E+04	5.70E+04	3.45E+03	3.12E+04	1.34E+04	6.54E+03	2.35E+04	1.24E+04	1.36E+03	7.73E+03	8.38E+03
P07737 PROF1	TFVNITPAEVLVVGK	822.47	135.57	3.02E+03	4.20E+04	7.02E+03	1.79E+03	3.46E+04	7.66E+04	1.14E+04	2.27E+04	6.24E+04	1.22E+04	1.15E+03	2.35E+04	3.26E+03	3.47E+04	2.45E+04
P07919 QCR6	SHTEDCTEELFDLHAR	726.99	135.78	5.99E+04	4.33E+04	1.14E+04	4.19E+04	3.94E+04	4.70E+04	4.61E+04	5.49E+04	5.50E+04	5.60E+03	5.39E+04	8.31E+03	1.84E+04	1.48E+04	5.84E+04
P23297 S10A1	ELLQTELSGFLDAQK	846.44	135.9	2.62E+05	2.56E+05	2.27E+05	2.27E+05	2.60E+05	3.32E+05	8.27E+04	2.04E+05	3.32E+05	6.03E+04	1.79E+05	2.44E+05	1.89E+05	7.73E+04	2.46E+05
P08758 ANXA5	GLGTDEESILTLTSTR	852.94	135.91	5.64E+05	3.59E+05	1.25E+05	3.88E+05	2.86E+05	7.04E+05	1.41E+05	2.17E+05	1.18E+05	4.09E+05	5.80E+05	1.48E+05	1.19E+05	1.16E+05	3.44E+05
P01834 IGKC	SGTASVVCLLNNFYPR	870.94	135.93	2.94E+05	5.68E+04	1.29E+05	7.04E+04	1.88E+05	2.90E+05	1.41E+05	1.29E+05	2.36E+04	2.00E+05	1.08E+05	1.74E+05	4.07E+04	3.48E+04	6.87E+04
O14958 CASQ2	SDPDGYEFLEILK	763.38	135.95	2.22E+05	2.08E+05	4.48E+04	1.47E+05	2.89E+05	2.29E+05	2.23E+05	3.46E+05	2.13E+05	3.72E+04	2.40E+05	3.90E+04	2.65E+04	6.94E+04	2.04E+05
Q99877 H2B1N	AMGIMNSFVNDIFER	872.42	136.06	1.55E+05	7.47E+04	1.92E+04	1.42E+05	2.18E+05	2.81E+05	2.19E+05	1.51E+05	5.00E+04	3.58E+05	2.22E+05	2.92E+04	8.16E+04	1.31E+05	1.84E+05
P07951 TPM2	AISELDNALNDITSL	859.43	136.11	7.05E+04	2.45E+05	8.64E+04	3.20E+04	3.07E+05	1.07E+05	8.73E+04	4.30E+05	1.68E+04	1.24E+05	7.19E+04	3.44E+05	1.38E+04	9.65E+04	1.85E+05
Q9H7C9 CK067	ETGTEHSPGVQPADV	551.27	50.24	5.52E+03	3.38E+02	5.64E+02	1.38E+04	2.09E+04	2.83E+03	4.58E+02	2.67E+02	2.11E+04	2.89E+04	1.94E+04	3.10E+03	3.18E+02	2.34E+02	6.28E+03
P06703 S10A6	LQDAEIAR	458.25	52.15	8.22E+02	1.35E+04	4.80E+02	5.38E+03	8.29E+03	7.40E+02	5.95E+02	4.54E+02	2.90E+04	9.05E+03	2.81E+02	3.79E+04	5.39E+02	2.36E+04	1.41E+03
P42704 LPPRC	TVLDQQQTTPSR	636.83	53.72	5.47E+02	2.19E+02	4.33E+02	1.86E+02	2.63E+03	6.81E+02	8.39E+02	8.82E+02	1.52E+04	8.71E+02	1.57E+03	2.79E+02	2.85E+03	2.68E+03	3.64E+03
Q8WZ42-6 TITIN	DQQLQDQGESVR	701.83	54.21	6.23E+03	1.00E+03	8.27E+02	5.87E+03	7.79E+03	9.91E+02	9.01E+02	2.08E+03	2.52E+02	6.97E+02	1.52E+04	6.28E+02	1.16E+03	1.49E+02	7.27E+02
O15230 LAMA5	IAASATCGEEAPAR	673.82	55.89	1.99E+04	2.04E+04	6.20E+03	2.97E+04	2.10E+04	2.75E+03	6.37E+02	1.03E+04	1.02E+03	3.10E+02	3.45E+04	2.17E+04	2.81E+03	1.66E+03	1.01E+03
Q8WZ42-6 TITIN	VDHSAESIVQNPH	478.23	57.3	1.03E+03	1.82E+04	2.35E+03	8.69E+03	1.66E+03	1.83E+03	3.78E+03	3.23E+02	1.33E+04	3.66E+03	2.22E+04	5.94E+03	7.68E+03	2.90E+04	4.50E+03
P19823 TIH2	IYGNQDTSQK	677.33	57.94	5.96E+03	2.80E+03	3.61E+03	6.62E+02	1.22E+02	4.66E+03	6.03E+02	6.83E+02	2.24E+03	1.69E+04	8.48E+02	5.18E+02	2.26E+03	1.52E+03	2.09E+03
P07099 HYEP	VETSDEIHDHLHQR	427.70	57.98	9.61E+02	3.68E+02	2.14E+03	1.83E+04	1.43E+04	1.93E+04	6.61E+02	1.17E+03	8.99E+02	2.50E+03	1.06E+03	8.67E+03	1.08E+03	8.78E+02	5.84E+02
P51970 NDUA8	TDRPLPENPYHSR	527.93	58.1	1.66E+02	3.01E+03	2.45E+03	2.63E+04	3.71E+02	3.86E+04	3.16E+02	1.11E+03	6.20E+03	1.13E+04	2.62E+04	2.56E+03	1.67E+02	6.49E+03	4.47E+04
O43488 ARK72	MDAPASAAAVR	530.27	58.54	2.01E+04	2.14E+04	4.60E+03	2.50E+04	6.97E+03	4.76E+04	1.50E+04	1.14E+04	1.48E+04	3.43E+03	6.00E+04	1.96E+04	8.51E+03	8.85E+03	1.19E+04
O75380 NDUS6	VIACDGGGGALGHPK	451.23	58.56	9.06E+03	8.07E+03	4.51E+03	4.12E+03	4.38E+03	1.01E+04	2.16E+04	8.11E+03	9.23E+02	4.34E+02	2.77E+04	1.02E+04	2.68E+03	6.33E+03	4.43E+03
P00751 CFAB	LEDSVTYHCSR	437.20	59.02	2.44E+03	2.20E+03	5.66E+03	2.63E+03	5.06E+02	3.21E+03	5.80E+02	2.94E+03	2.01E+04	2.18E+04	2.69E+04	2.19E+03	3.33E+03	8.98E+03	6.02E+03
P24298 ALAT1	ANIGDAQAMGQR	616.29	59.09	2.77E+03	1.99E+03	3.41E+03	7.41E+03	6.98E+02	3.87E+02	1.05E+04	5.12E+03	2.46E+03	5.44E+02	4.35E+03	1.39E+03	1.46E+04	3.61E+02	4.61E+03
O95298 NDUC2	LHPEDFPEEDKK	495.24	59.35	8.25E+03	5.04E+03	1.87E+04	8.61E+03	2.03E+03	1.10E+04	1.91E+03	3.75E+02	5.04E+04	1.56E+04	2.91E+03	1.29E+03	1.11E+04	8.80E+02	2.18E+03
P23246 SFPQ	FGQGGAGPVGQGP	671.33	59.87	2.04E+04	7.63E+03	5.68E+03	2.90E+04	1.67E+04	3.38E+03	1.66E+03	9.12E+02	3.82E+03	7.78E+03	7.24E+03	8.30E+03	2.14E+03	2.63E+03	4.96E+03
O95298 NDUC2	FLPDEAR	424.22	60.02	1.30E+02	6.21E+02	3.32E+04	1.62E+03	6.81E+04	3.50E+04	6.17E+04	4.99E+04	1.03E+04	1.46E+02	3.72E+03	2.54E+04	3.93E+04	4.85E+02	1.14E+03
P09493-5 TPM1	SLQEQADAAEER	673.81	60.13	5.82E+03	8.85E+03	4.93E+02	1.15E+04	1.61E+03	7.59E+02	4.85E+02	2.41E+02	9.83E+02	1.96E+03	1.67E+04	4.41E+03	4.11E+03	2.16E+03	7.32E+02
P05165 PCCA	VTEDTSSVLR	553.79	60.28	4.75E+03	4.62E+03	2.79E+04	5.14E+03	1.06E+05	3.36E+04	8.71E+04	5.07E+03	1.11E+03	1.57E+03	2.60E+03	4.64E+03	4.78E+03	1.04E+03	4.17E+02
P61088 UBE2N	TNEAQAIETAR	602.30	60.36	7.17E+02	1.62E+03	1.11E+05	3.69E+03	1.20E+04	9.12E+03	2.25E+04	3.32E+03	4.12E+02	8.66E+02	2.79E+04	4.13E+03	4.83E+04	3.59E+03	4.58E+02
Q96HC4-2 PDL15	ASAAPKPEVPVQKP	505.96	60.73	6.40E+04	1.91E+03	5.40E+03	2.00E+03	1.34E+03	1.16E+04	2.07E+03	7.32E+02	2.31E+03	3.21E+03	1.61E+04	3.38E+03	8.18E+03	3.57E+03	4.29E+04
O00159-3 MYO1C	LGTDIEISPR	494.26	60.87	1.30E+04	1.64E+04	7.83E+03	3.35E+04	1.64E+04	2.43E+02	3.30E+04	1.57E+04	5.40E+02	1.03E+04	6.10E+04	1.53E+04	4.34E+04	1.10E+03	3.42E+04
P27816-2 MAP4	LATNTSAPDLK	565.80	61.19	2.77E+03	6.97E+02	2.87E+03	4.71E+03	4.35E+03	2.55E+03	3.94E+03	3.95E+03	5.93E+03	2.10E+04	7.98E+03	3.60E+03	5.80E+03	4.43E+04	2.48E+03
O00159-3 MYO1C	DQAVMISGESGAGK	674.82	61.26	4.59E+05	2.62E+05	2.52E+05	5.10E+05	1.56E+05	6.29E+05	4.94E+03	3.25E+04	1.29E+03	1.63E+02	3.18E+03	1.36E+05	2.73E+04	3.58E+02	1.21E+03
O95182 NDUA7	AVTPAPPIK	447.28	61.51	3.84E+03	1.64E+03	3.95E+03	8.26E+02	3.09E+03	1.13E+03	1.72E+02	5.98E+03	3.44E+04	4.37E+04	8.15E+02	1.80E+03	9.57E+03	3.52E+03	6.35E+02
Q9UBR2 CATZ	VGDYGSLSGR	505.75	61.54	2.16E+03	5.99E+03	4.66E+02	4.07E+03	5.91E+02	9.34E+02	4.85E+02	5.68E+03	6.84E+03	2.10E+04	1.92E+02	4.69E+02	1.37E+03	1.55E+04	4.56E+03
P09104 ENOG	IEEELGDEAR	580.78	61.67	2.25E+04	9.63E+04	6.53E+02	9.47E+02	7.75E+02	9.77E+02	6.83E+02	7.49E+02	3.57E+02	1.40E+04	2.08E+05	3.77E+02	2.62E+03	3.59E+05	1.33E+05
P04843 RPN1	GEDEEENNLEVR	716.82	61.77	1.38E+04	5.46E+03	2.70E+03	1.04E+03	4.47E+03	1.99E+03	1.27E+02	1.01E+03	2.08E+03	3.81E+02	6.26E+03	5.26E+03	4.07E+02	1.51E+03	1.44E+04
P04632 CPNS1	THYSNIEANESEEV	593.27	61.95	4.59E+02	3.63E+03	1.02E+04	5.93E+03	4.65E+02	2.53E+04	1.37E+04	5.50E+03	1.47E+03	1.80E+02	1.57E+03	1.40E+04	2.50E+04	3.09E+03	3.89E+03
P62269 RS18	AGELTEDEVER	624.29	61.99	4.26E+04	8.85E+04	1.18E+04	8.41E+04	4.53E+02	1.79E+03	4.58E+03	5.90E+03	4.70E+03	1.00E+04	1.07E+05	8.29E+04	1.55E+03	3.37E+04	7.41E+03
Q092736 RYR2	LTPSQEAMVDK	609.81	62.41	1.05E+04	2.10E+04	3.18E+04	2.30E+04	8.31E+04	7.29E+04	3.28E+04	1.26E+03	9.63E+03	4.02E+02	4.52E+04	1.73E+04	2.28E+04	6.23E+03	3.47E+02
O95182 NDUA7	ALVSGKPAESSAVAATEK	572.64	62.46	4.92E+02	2.86E+04	2.85E+03	3.60E+04	7.65E+04	2.60E+03	4.08E+03	6.98E+02	1.10E+03	1.79E+03	2.58E+04	5.78E+04	7.36E+03	8.13E+02	8.14E+02
P11586 C1TC	VVDVAYDEAK	583.29	62.55	1.05E+04	2.18E+03	8.72E+03	2.16E+04	1.38E+03	1.94E+04	9.05E+03	1.07E+04	1.15E+03	7.34E+02	7.54E+03	1.46E+03	1.65E+04	8.72E+02	1.12E+04
P48681 NEST	SLEEQDQETLR	674.33	62.58	2.15E+03	8.25E+02	1.65E+03	8.01E+03	2.79E+04	1.60E+03	3.61E+03	2.67E+02	2.10E+04	2.50E+04	1.97E+03	4.27E+04	1.77E+03	5.28E+03	9.44E+02
Q9UN36-3 NDRG	TASLTSAAASVDG	675.33	62.62	1.34E+03	5.33E+04	3.10E+02	4.36E+04	3.51E+03	6.98E+02	5.80E+02	1.08E+03	1.63E+02	3.09E+03	2.72E+04	5.44E+03	9.31E+02	1.24E+04	8.83E+02
Q13683-9 ITA7	VVDIDQADMOK	610.29	62.81	2.15E+03	8.51E+03	1.17E+05	3.79E+05	6.79E+03	2.59E+04	4.17E+05	1.22E+04	1.58E+03	1.36E+03	4.32E+03	2.83E+03	1.92E+04	1.05E+04	1.41E+04
P02794 FRIH	ELGDHVTNLR	577.30	62.88	3.99E+02	2.28E+04	2.15E+03	4.37E+04	4.04E+04	1.98E+05	3.57E+02	1.91E+03	3.53E+04	1.75E+02	3.45E+04	1.60E+02	5.27E+03	2.49E+04	1.82E+04
Q9UMS6 SYNP2	YVVDSDTVQAH	617.29	63.25	1.33E+04	4.78E+03	1.82E+04	2.23E+04	5.95E+02	3.96E+04	3.83E+02	1.92E+03	1.97E+03	4.27E+04	6.68E+02	1.53E+03	4.51E+03	2.68E+04	2.71E+02
Q9UJY1 HSPB8	FGVPAEGR	416.72	63.48	6.99E+02	7.47E+02	3.67E+02	2.98E+03	5.69E+02	1.63E+03	4.55E+02	1.87E+02	5.60E+04	3.47E+04	2.18E+03	4.61E+02	1.03E+03	2.85E+04	4.69E+03
P29218 JMPA1	LQVSQQEDITK	644.84	63.67	1.71E+04	4.30E+04	1.61E+03	1.16E+05	9.50E+04	4.21E+02	1.33E+03	1.05E+05	5.36E+04	2.40E+04	1.52E+05	6.08E+04	5.52E+04	5.91E+04	1.23E+05
Q15848 ADIPO	IFYNQNHVDGSGTK	591.27	64.16	1.71E+04	4.56E+02	2.09E+03	1.27E+04	2.61E+04	1.73E+04	1.14E+03	4.32E+02	3.99E+04	3.11E+04	9.63E+02	7.91E+02	4.33E+03	4.59E+04	9.13E+03
P36578 RL4	MINTDLR	475.24	64.2	3.37E+02	5.43E+02	1.45E+04	5.29E+02	6.37E+03	3.92E+04	1.72E+04	2.49E+02	4.84E+03	1.02E+04	6.84E+02	4.75E+02	2.70E+04	8.69E+02	

P50502 F10A1	QDPSVLHTEEMR	481.23	66.59	1.88E+04	3.06E+03	2.81E+03	4.88E+02	1.42E+03	4.85E+02	2.31E+03	1.44E+03	1.16E+05	1.85E+02	1.33E+03	1.05E+04	8.17E+02	1.30E+03	5.95E+04
P06703 S10A6	LMEDLDR	446.22	66.63	4.40E+03	1.21E+03	9.48E+02	2.83E+03	8.90E+02	7.51E+02	1.71E+03	9.49E+02	1.86E+05	3.33E+05	2.03E+03	8.99E+02	1.04E+03	7.39E+04	7.67E+03
Q92736 RYSR2	TVTITLGDGK	531.78	66.7	1.59E+03	2.84E+03	1.77E+05	1.64E+04	2.68E+03	2.86E+04	1.36E+05	9.62E+04	1.69E+03	5.25E+02	2.12E+03	3.80E+03	2.52E+05	4.15E+02	1.45E+03
P11182 ODB2	VEIMPPPKPK	411.57	66.71	2.41E+03	9.41E+03	3.55E+03	3.86E+04	5.89E+04	8.31E+03	2.50E+03	4.37E+04	6.42E+02	3.90E+03	9.92E+03	4.58E+04	9.41E+03	2.59E+02	1.99E+04
Q07507 DERM	GATTTFSAYER	570.29	66.72	7.47E+02	2.12E+03	1.50E+05	6.93E+02	3.38E+04	7.22E+02	9.64E+04	5.23E+04	2.02E+03	6.24E+02	3.77E+03	1.68E+03	5.62E+04	4.12E+03	9.68E+02
P07858 CATB	LPASFDAR	438.73	67.64	1.03E+03	1.58E+04	2.53E+03	5.26E+03	1.77E+03	2.49E+03	1.29E+04	2.61E+03	4.30E+02	9.41E+02	8.24E+04	2.92E+03	3.75E+03	7.75E+02	5.39E+04
Q8N335 GPD1L	LQGPQTSAEVYR	674.85	67.71	1.24E+04	1.47E+03	9.16E+02	1.68E+04	2.49E+03	4.04E+02	2.16E+03	1.03E+04	4.99E+03	2.62E+02	6.61E+04	3.24E+03	1.25E+03	2.23E+03	1.24E+03
P05166 PCCB	GHENVEAAQAEYIEK	563.27	67.78	8.20E+03	5.59E+03	2.22E+02	7.66E+03	5.44E+03	4.60E+02	7.94E+02	3.03E+03	8.62E+03	2.24E+03	6.78E+03	3.77E+03	2.70E+03	1.30E+04	1.20E+04
O75347 TBCA	DLEEAEEYK	563.25	67.79	6.11E+04	5.30E+04	1.53E+03	1.11E+04	8.70E+03	7.64E+02	1.85E+03	1.66E+02	6.09E+03	1.37E+03	7.42E+04	7.33E+04	5.69E+02	2.94E+04	3.77E+04
O75251 NDUS7	VYDQMPEPR	567.77	67.82	2.41E+03	1.85E+04	1.34E+04	1.26E+03	1.34E+03	3.11E+03	1.00E+03	1.37E+03	2.22E+04	1.49E+04	5.81E+02	2.91E+04	4.21E+03	1.98E+04	7.21E+02
Q9UI09 NDUAC	GLQQITGHGGLR	412.90	68.04	4.36E+02	7.43E+03	2.32E+03	5.55E+03	2.29E+03	1.07E+03	3.16E+03	1.93E+02	1.38E+03	7.97E+02	5.89E+04	2.15E+03	1.20E+03	4.65E+02	1.12E+05
P53597 SUCA	IAGLTAPPGR	476.78	68.32	9.50E+04	1.82E+05	2.76E+04	3.85E+04	5.52E+03	2.34E+04	3.87E+03	6.14E+03	3.14E+02	3.57E+02	1.18E+05	5.24E+04	1.97E+04	3.25E+02	1.06E+05
Q9UBQ7 GRHPR	ILDAAGANLK	493.29	68.63	8.37E+02	2.13E+03	1.30E+03	4.06E+03	1.54E+05	1.31E+03	1.81E+04	7.02E+02	4.08E+02	2.40E+03	1.61E+05	7.32E+04	1.24E+03	1.07E+03	1.06E+03
P01011 AACT	ADLSGITGAR	480.76	69.37	2.25E+03	6.75E+04	1.63E+03	1.52E+03	7.32E+03	2.30E+02	2.75E+03	1.88E+03	3.18E+05	4.79E+05	1.34E+04	7.51E+04	1.56E+03	1.68E+05	1.18E+04
P15090 FABP4	EVGVGFATR	468.25	69.83	1.59E+04	8.51E+04	4.01E+03	1.80E+04	2.37E+05	9.93E+04	1.53E+05	2.87E+04	1.77E+04	5.98E+03	2.00E+04	4.62E+04	5.43E+04	3.61E+04	3.11E+03
Q96KP4 CNDP2	TGQEIPVNVNR	556.81	69.96	1.54E+04	2.88E+02	6.18E+03	7.76E+03	4.36E+04	5.48E+03	3.01E+02	2.29E+04	5.50E+04	7.85E+03	4.75E+03	2.25E+03	3.18E+02	4.47E+04	2.12E+04
Q16629 SFRS7	VELSTGMPR	495.25	70.27	3.02E+03	4.37E+03	2.70E+04	2.05E+04	5.46E+03	2.02E+02	1.32E+03	1.43E+04	2.17E+04	6.95E+03	1.21E+04	1.90E+03	9.97E+03	8.59E+03	1.62E+04
O43837 IDH3B	GELASYDMR	521.24	70.27	2.37E+03	2.43E+03	2.23E+05	1.22E+04	3.63E+02	6.17E+05	8.30E+04	1.79E+05	1.14E+03	4.00E+03	2.24E+02	1.01E+05	1.10E+05	1.02E+03	6.55E+03
Q15848 ADIPO	GDIGETVPGAEGPR	706.34	70.44	3.55E+04	2.14E+03	6.62E+02	3.63E+02	9.93E+02	1.44E+03	3.72E+02	2.43E+03	1.08E+04	5.48E+03	1.08E+04	7.98E+02	5.62E+02	3.43E+04	3.17E+04
P07951-3 TPM2	RERAEADVASLNR	496.25	70.5	2.14E+03	8.15E+04	3.58E+04	7.43E+04	1.51E+05	7.58E+03	2.76E+04	4.96E+03	1.95E+03	2.47E+03	8.81E+03	1.81E+05	8.08E+04	1.09E+03	1.96E+04
P42704 LPPRC	LDSSAVLDTGK	553.29	70.68	1.11E+03	2.12E+04	4.66E+03	1.28E+04	2.51E+05	8.04E+02	5.90E+03	2.63E+03	2.04E+04	2.57E+04	1.51E+03	2.83E+03	3.25E+03	3.43E+04	1.58E+03
Q96KP4 CNDP2	MMEVAAADVK	532.75	70.87	7.69E+02	5.14E+02	4.71E+04	6.52E+04	5.71E+04	6.43E+04	4.63E+04	2.82E+03	6.81E+02	6.57E+02	4.79E+02	7.21E+04	5.45E+04	5.83E+02	6.67E+03
P62857 RS28	VEFMDDTSR	550.24	70.95	6.15E+02	1.86E+04	5.10E+04	5.45E+03	2.22E+04	9.82E+04	5.89E+04	7.57E+03	3.40E+03	2.26E+03	1.90E+03	2.38E+04	4.72E+04	2.36E+03	1.77E+03
Q96RQ3 MCCA	IIIEAPAPGIK	569.33	70.98	2.95E+03	8.64E+04	5.09E+03	7.34E+04	1.01E+05	4.05E+03	4.83E+04	9.83E+04	3.48E+03	3.30E+02	1.05E+04	3.27E+04	5.38E+04	6.04E+02	1.65E+02
P04899 GNAI2	YDEAASYIQSK	637.79	71	3.69E+04	3.69E+03	3.00E+03	1.76E+04	3.13E+03	4.03E+03	4.41E+02	1.34E+03	1.30E+03	5.00E+03	3.13E+04	1.46E+04	2.84E+03	2.48E+02	4.20E+04
O15230 LAMA5	GYAQMAPVQPR	609.31	71.26	4.80E+03	6.74E+02	1.94E+04	7.53E+03	1.75E+03	5.31E+03	2.53E+03	6.31E+03	1.33E+05	2.29E+05	6.78E+03	4.11E+04	7.28E+03	3.63E+04	1.30E+04
P13861 KAP2	APASVLPAAATPR	575.83	71.34	2.70E+03	2.82E+05	1.22E+03	1.47E+05	3.65E+05	2.89E+05	2.86E+05	1.08E+04	2.03E+02	2.40E+03	4.97E+04	2.88E+05	7.21E+04	1.57E+04	3.04E+04
P42704 LPPRC	IQEENVIPR	549.30	71.58	8.65E+04	1.49E+03	2.01E+04	1.52E+03	8.75E+02	9.52E+03	3.01E+04	7.82E+03	6.01E+03	1.21E+03	3.37E+04	3.62E+02	3.26E+03	4.09E+03	7.67E+03
P42704 LPPRC	GDVENIEVVQK	615.32	71.58	5.84E+04	1.85E+03	1.52E+04	8.95E+03	6.92E+03	5.03E+03	4.28E+03	6.62E+02	1.04E+05	1.08E+05	5.56E+03	9.30E+03	2.47E+03	6.87E+04	1.01E+05
P15088 CBPA3	IGTDVLSTR	481.27	71.74	2.36E+04	1.99E+03	1.13E+04	6.46E+04	8.29E+02	1.82E+04	5.54E+04	3.83E+03	1.82E+03	9.12E+02	3.50E+03	1.22E+03	6.74E+04	1.56E+03	2.08E+03
P09493-5 TPM1	ETAEADVASLNR	638.31	72.08	2.14E+03	1.28E+03	2.57E+03	1.87E+03	3.06E+02	4.16E+02	2.11E+03	1.32E+04	1.12E+04	3.05E+04	8.76E+02	7.57E+02	8.36E+02	3.65E+03	1.17E+03
Q13561 DCTN2	LTELETAVR	516.29	72.18	7.98E+05	4.07E+04	3.13E+02	9.62E+04	2.71E+02	5.61E+03	8.65E+03	1.42E+03	1.18E+04	5.94E+03	5.88E+04	5.57E+04	3.37E+03	9.44E+03	1.91E+04
P84077 ARF1	MLAEDELNR	488.74	72.26	2.03E+03	1.50E+05	4.14E+03	1.71E+05	1.07E+05	4.52E+03	1.25E+05	1.36E+03	9.18E+02	3.53E+03	6.77E+03	1.57E+05	2.09E+04	4.85E+03	2.45E+03
P60660 MYL6	EGNGTVMGAEIR	617.30	72.27	5.96E+06	1.14E+05	1.52E+04	2.24E+05	9.17E+04	2.60E+04	1.09E+04	2.30E+03	2.37E+06	4.02E+04	9.79E+06	2.75E+04	5.01E+03	3.84E+06	7.58E+06
P07951-3 TPM2	SLMASEEYSTK	687.81	72.85	6.29E+04	2.76E+03	3.57E+03	5.44E+02	1.00E+04	3.66E+03	2.12E+03	1.30E+05	1.04E+03	1.29E+02	9.98E+03	9.75E+02	1.04E+03	6.91E+02	1.08E+04
P60660 MYL6	ALGQNPTNAEVLK	677.87	73.06	1.23E+05	6.08E+02	1.36E+04	1.64E+03	1.03E+05	2.68E+03	4.68E+02	4.21E+03	1.29E+03	4.54E+02	8.75E+04	8.63E+02	1.56E+03	2.90E+03	8.53E+04
P10909-2 CLUS	IDSLENDR	537.77	73.11	2.31E+03	7.00E+03	3.03E+03	5.14E+02	2.44E+03	1.39E+03	3.19E+03	2.26E+04	8.11E+03	9.72E+03	5.16E+04	5.76E+03	1.58E+03	8.53E+03	2.62E+03
P49419 AL7A1	QASVADYEETVK	670.33	73.24	1.26E+03	5.43E+03	9.20E+04	1.43E+03	2.53E+03	1.76E+05	4.87E+04	4.10E+03	4.94E+03	4.25E+03	9.55E+02	2.94E+02	2.52E+03	2.85E+02	1.17E+03
P05165 PCCA	AMGQAVALAR	558.78	73.25	2.04E+03	1.84E+04	1.26E+06	7.57E+04	1.87E+04	2.73E+06	6.47E+05	2.02E+04	3.81E+03	4.88E+03	3.68E+04	1.34E+06	6.47E+03	2.18E+03	1.13E+05
Q71UI9 H2AV	GKAGKDSGK	452.75	73.61	2.27E+03	1.02E+03	1.18E+04	2.50E+03	7.51E+02	5.48E+02	1.24E+03	2.24E+05	5.77E+03	3.16E+03	3.74E+03	5.75E+02	8.60E+04	1.04E+04	4.69E+02
P43034 LIS1	EEFTSGGPLGQK	625.31	73.84	5.20E+03	5.01E+03	6.64E+04	6.03E+03	2.39E+03	6.45E+04	2.28E+04	2.17E+04	1.33E+04	1.00E+04	1.38E+04	5.66E+02	4.89E+03	3.71E+03	2.73E+03
P00751 CFAB	DISEVVTPR	508.27	74.08	2.59E+03	9.01E+03	8.48E+04	4.60E+03	6.24E+03	3.19E+04	3.58E+04	1.59E+03	1.01E+03	2.14E+04	3.69E+03	5.45E+03	3.45E+02	8.50E+03	1.29E+04
P09669 COX6C	AGIFQSVK	425.24	74.15	1.40E+05	4.37E+03	7.21E+03	5.22E+03	9.53E+03	6.89E+03	3.11E+05	2.41E+04	1.77E+03	5.13E+02	5.46E+03	5.24E+03	1.88E+03	2.78E+04	1.35E+03
Q00059 TFAM	SAYNVYVAER	586.29	74.41	6.11E+03	1.31E+04	6.76E+03	7.74E+04	1.06E+05	4.24E+04	5.94E+04	2.29E+03	1.56E+03	8.92E+02	1.11E+04	6.83E+04	2.13E+03	6.97E+03	1.29E+04
P17931 LEG3	VAVNDAHLLQYNHR	413.22	74.45	2.52E+03	3.58E+02	1.97E+03	1.70E+03	2.76E+04	5.81E+03	4.40E+02	2.71E+04	1.53E+03	2.01E+03	1.94E+04	5.24E+02	5.77E+03	1.70E+03	3.85E+04
Q81WX7-2 UN45B	AIDINSSDIK	538.28	74.57	5.29E+04	1.25E+04	7.60E+03	4.21E+04	1.49E+04	7.34E+02	2.73E+02	3.59E+03	9.07E+02	9.16E+02	1.37E+04	1.27E+04	3.15E+04	3.95E+03	6.32E+04
Q9H7C9 CK067	VPSSTVEYLK	561.81	74.77	4.02E+04	5.97E+03	2.18E+03	6.61E+03	5.46E+02	1.05E+04	1.31E+02	3.91E+02	1.08E+04	2.26E+03	1.87E+04	6.39E+03	1.12E+03	1.25E+04	6.78E+03
O75208 COQ9	YTDQGGEEEDYEESEQLQHR	857.68	74.93	2.25E+04	3.17E+02	8.42E+02	2.23E+03	1.52E+03	2.63E+02	1.80E+02	3.85E+02	8.05E+02	2.62E+02	1.58E+04	1.09E+03	1.29E+02	6.57E+02	1.62E+03
Q71UI9 H2AV	ATIAGGVIPH	496.78	75.08	6.16E+04	1.25E+05	1.02E+04	3.79E+04	2.26E+04	2.23E+05	2.39E+03	4.04E+03	4.99E+04	8.75E+03	1.40E+05	3.17E+04	2.15E+04	1.50E+04	4.30E+04
Q96Q06 PLIN4	EDTGLLATHTHGPEEAPR	598.63	75.28	3.69E+02	1.85E+04	6.20E+02	1.10E+05	2.75E+02	3.43E+03	1.08E+03	2.36E+03	4.12E+02	5.05E+02	1.17E+04	3.99E+04	1.33E+03	2.08E+02	2.16E+04
Q92736 RYSR2	LTEDVLADDR	573.78																

P04632 CPNS1	SMVAVMDSDTTGK	671.31	76.71	7.68E+04	7.18E+03	6.72E+03	1.39E+04	2.19E+04	1.22E+03	7.81E+03	1.24E+03	1.05E+03	2.27E+03	7.80E+04	2.59E+03	7.56E+03	1.67E+03	3.43E+04
P09669 COX6C	AYADFYR	453.21	76.79	7.80E+05	3.05E+04	1.70E+04	1.10E+04	7.25E+03	2.31E+04	1.43E+03	3.54E+03	1.24E+03	1.53E+03	5.38E+05	5.63E+03	1.53E+04	9.21E+02	2.16E+03
P18136 KV313	LLIYGASSR	490.28	76.9	6.55E+02	1.69E+04	1.26E+04	8.32E+04	3.02E+05	1.04E+05	1.24E+05	3.65E+02	4.33E+03	3.11E+03	8.55E+03	6.26E+04	1.88E+03	9.13E+02	5.93E+04
P62277 RS13	GLSQSALPYR	546.29	77.01	1.58E+05	5.03E+03	9.88E+04	1.18E+05	2.62E+04	2.36E+04	1.90E+05	5.41E+04	7.61E+04	4.06E+03	9.84E+04	5.73E+03	7.60E+04	2.16E+03	5.60E+03
Q9H7C9 CK067	EYNALVAQGVV	610.33	77.07	8.82E+02	1.49E+05	8.91E+04	2.42E+03	6.31E+02	2.59E+05	1.20E+05	9.34E+04	6.97E+02	3.01E+02	7.91E+02	6.75E+02	1.68E+03	6.87E+02	4.33E+04
P10768 ESTD	AFSGYLGTDSK	637.32	77.18	4.76E+04	1.23E+04	4.37E+03	2.98E+03	1.14E+03	9.50E+04	6.95E+03	7.17E+03	4.68E+04	3.33E+04	1.11E+04	1.45E+04	9.13E+03	4.06E+04	1.35E+04
P12694 ODBA	VMEAFEQAER	605.29	77.29	7.95E+02	8.32E+03	1.46E+04	1.37E+04	1.55E+03	5.16E+03	2.57E+03	1.12E+03	5.44E+04	4.94E+04	1.09E+03	2.54E+04	1.68E+03	9.63E+02	7.26E+03
P62269 RS18	YSQVLANGLDNK	661.34	77.29	1.28E+03	2.43E+03	2.76E+03	2.02E+04	1.41E+04	2.11E+03	1.01E+03	7.28E+02	2.76E+03	1.88E+04	2.98E+03	8.11E+03	8.82E+03	1.18E+03	9.87E+03
P31948 STIP1	ELIEQLR	450.76	77.94	4.94E+02	2.20E+05	1.56E+04	3.30E+05	4.13E+03	2.62E+05	1.54E+05	8.53E+03	1.65E+02	1.36E+03	2.43E+03	2.56E+05	2.59E+03	1.28E+03	2.84E+05
P02751-10 FINC	FTNIGPDTMR	576.28	77.96	1.00E+05	5.66E+03	1.18E+03	8.03E+02	5.80E+04	1.69E+03	2.31E+03	1.13E+03	6.87E+03	4.83E+02	1.51E+04	8.36E+02	5.09E+03	2.16E+03	1.14E+04
P13798 ACPH	ALDVSASDDEIAR	681.34	78	3.30E+03	7.57E+02	1.01E+03	4.51E+04	1.82E+04	1.23E+03	7.15E+02	1.23E+03	6.56E+02	3.87E+02	3.49E+03	2.24E+03	1.72E+04	3.19E+04	3.37E+04
Q16363 LAMA4	DVEVEDFQR	568.76	78.03	2.15E+03	5.72E+04	2.62E+03	3.67E+04	3.72E+04	7.61E+03	8.00E+04	1.53E+04	8.31E+02	2.79E+02	2.57E+02	1.01E+05	2.27E+04	5.85E+02	5.73E+04
P23526 SAHH	GISEETTTGVHNLKY	550.28	78.16	4.26E+04	3.16E+03	2.01E+03	7.99E+03	8.53E+03	1.93E+03	7.21E+03	2.99E+03	5.17E+03	7.17E+02	2.80E+04	1.34E+04	1.97E+04	7.76E+02	1.91E+04
P07942 LAMB1	AEMLLEEAK	517.27	78.41	2.55E+03	3.73E+02	4.65E+04	1.73E+03	1.34E+03	2.27E+05	6.12E+04	2.36E+04	1.64E+05	7.31E+04	1.77E+03	2.92E+03	2.34E+04	9.19E+04	1.12E+04
Q16363 LAMA4	LAALSIEEGK	515.79	78.49	7.65E+04	1.55E+04	2.78E+04	2.83E+04	2.05E+04	3.11E+04	1.87E+04	5.33E+04	5.17E+03	2.75E+04	5.90E+04	1.03E+04	4.35E+04	1.32E+03	5.00E+04
P18124 RL7	EVPAVPETLK	541.81	79.48	1.79E+03	7.74E+04	2.85E+02	1.03E+05	3.25E+04	4.07E+03	7.19E+02	1.23E+03	3.95E+02	2.16E+03	1.06E+03	5.09E+04	1.32E+04	1.44E+03	1.61E+04
Q15582 BGH3	ILGDPEALR	492.28	79.79	8.41E+02	2.26E+04	1.66E+05	3.30E+03	2.66E+04	1.72E+04	1.14E+05	6.05E+04	1.05E+04	2.22E+04	9.67E+02	1.58E+04	3.39E+03	1.44E+04	1.21E+03
P02794 FRIH	NVNQSLLELHK	432.24	79.86	1.53E+04	3.69E+03	1.52E+03	1.55E+03	9.28E+02	2.02E+03	9.69E+02	2.53E+06	4.75E+04	3.19E+04	4.68E+02	5.27E+03	2.83E+03	3.33E+03	4.13E+02
O60220 TIM8A	SKPVFSESLSD	598.30	79.9	1.06E+03	2.29E+05	1.16E+03	2.82E+05	1.79E+05	4.70E+02	1.49E+03	8.86E+03	2.28E+03	3.43E+02	3.49E+04	1.84E+05	1.10E+04	4.36E+03	2.97E+05
O95298 NDUC2	TYGEIFEK	493.75	79.97	4.31E+04	1.75E+03	9.27E+02	2.59E+03	4.52E+03	1.43E+03	3.75E+02	4.90E+03	5.62E+03	6.82E+02	2.52E+04	1.02E+04	6.27E+02	2.16E+04	6.07E+03
P07858 CATB	GLVSGGLYESH	559.78	80.04	5.60E+02	3.87E+04	4.69E+02	4.68E+04	1.85E+04	5.58E+03	1.25E+03	1.06E+03	8.39E+02	1.59E+03	1.34E+04	3.78E+03	4.13E+04	3.08E+03	5.68E+04
P62750 RL23A	LYDIDVAK	468.76	80.3	4.67E+03	1.34E+04	3.46E+04	1.92E+03	2.14E+04	3.00E+03	2.33E+04	1.08E+04	1.15E+03	1.16E+03	1.61E+03	1.21E+03	4.95E+02	1.98E+03	3.32E+03
O75131 CPNE3	SPLGEVAIR	471.27	80.42	6.35E+04	1.26E+05	2.93E+04	5.24E+04	1.38E+05	1.20E+05	1.21E+05	1.72E+03	1.77E+03	4.85E+03	2.43E+03	1.32E+05	1.04E+03	1.01E+03	1.19E+05
P01871 IGHM	YAATSQVLLPSK	639.36	80.43	1.22E+03	7.68E+03	1.99E+03	7.76E+03	5.40E+04	3.39E+02	1.86E+02	3.90E+02	2.42E+02	1.39E+03	2.51E+02	1.03E+04	9.43E+02	3.12E+02	4.74E+03
P17931 LEG3	GNDVAFHFNPR	425.21	80.59	4.22E+03	1.17E+05	4.44E+03	7.16E+04	2.27E+03	1.70E+05	8.11E+04	4.62E+02	1.44E+03	1.66E+03	1.76E+03	3.54E+03	5.80E+02	2.10E+03	1.66E+05
P35268 RL22	AGNLGGGVVTIER	621.84	81.08	5.24E+04	2.07E+03	1.25E+03	2.42E+03	1.43E+03	6.88E+02	1.81E+03	1.80E+03	3.12E+03	4.01E+02	5.99E+04	3.95E+03	3.51E+04	8.77E+02	4.15E+03
P62277 RS13	LILIESR	422.27	81.19	3.54E+04	9.76E+04	1.31E+03	1.76E+05	1.39E+05	1.36E+05	2.51E+04	9.87E+02	1.52E+03	6.58E+04	4.30E+04	1.24E+05	6.23E+04	2.52E+04	2.41E+05
O43837 IDH3B	AAAVPVEFQEH	599.30	81.29	3.17E+04	8.18E+03	1.09E+06	1.34E+03	3.67E+02	7.49E+05	2.74E+03	1.11E+06	2.09E+04	2.77E+04	1.27E+04	3.24E+03	1.38E+03	3.42E+04	2.18E+04
P0C0L5 CO4B	VDFTLSSER	527.26	81.62	9.20E+02	8.08E+02	1.10E+04	5.90E+02	1.80E+03	7.54E+02	4.76E+04	2.89E+03	1.98E+03	7.94E+02	1.69E+03	1.46E+03	1.26E+03	2.05E+04	2.63E+03
P11586 CITC	TPVPSDIDISR	600.31	81.89	2.91E+04	2.59E+05	1.03E+05	6.07E+04	1.61E+05	2.68E+05	5.11E+04	9.39E+04	6.78E+03	1.14E+03	5.24E+04	3.49E+04	2.57E+04	1.93E+04	4.07E+04
P09104 ENOG	DGKYDLDFK	550.77	81.95	2.41E+02	1.39E+04	5.98E+03	1.33E+04	7.21E+04	1.68E+04	1.21E+04	2.14E+02	4.78E+03	2.57E+03	6.53E+03	7.99E+04	1.86E+03	1.91E+04	2.90E+04
Q9UBR2 CATZ	NVDGVNYASITR	654.83	82.1	5.59E+02	1.49E+03	1.75E+03	4.70E+04	6.65E+02	3.86E+03	5.29E+02	6.59E+02	2.61E+04	4.93E+02	4.34E+02	5.38E+03	6.35E+04	3.07E+04	9.31E+04
P19105 ML12A	EAFNMVDQNR	619.29	82.36	5.67E+04	8.74E+02	1.22E+03	7.99E+03	6.29E+02	1.61E+03	8.06E+02	2.41E+03	1.51E+03	3.15E+03	5.12E+04	1.42E+03	1.69E+03	6.21E+02	9.78E+02
P52565 GDIR1	SIQEIQELDK	601.82	82.55	7.60E+02	1.81E+05	5.18E+03	1.60E+05	9.04E+02	2.37E+05	2.24E+04	7.15E+03	2.23E+04	1.56E+04	4.21E+04	7.02E+04	2.46E+05	2.44E+03	5.14E+04
Q9NZ45 CISD1	HNEETGDNVGLIHK	545.95	82.61	1.16E+05	1.32E+03	4.18E+03	1.29E+04	8.86E+03	1.79E+04	1.60E+03	1.06E+03	1.02E+03	7.09E+02	7.78E+04	1.82E+03	1.36E+04	2.98E+02	4.42E+03
P50502 F10A1	AIEINPDSAQPYK	723.37	82.9	5.28E+04	5.36E+03	3.99E+03	5.52E+03	2.86E+04	2.09E+03	1.90E+03	3.52E+02	4.72E+02	2.55E+02	2.35E+04	3.01E+02	6.58E+02	5.69E+02	7.23E+02
P15311 EZRI	IALLEEAR	457.77	83.01	6.91E+02	1.98E+05	6.22E+03	2.84E+05	1.54E+05	2.95E+05	1.39E+05	8.86E+03	1.63E+03	9.74E+02	5.63E+03	2.46E+05	6.75E+02	4.24E+03	2.54E+05
Q04760 LGUL	SLDFYTR	451.22	83.06	8.86E+02	1.68E+03	2.02E+03	2.20E+03	6.72E+03	1.90E+03	1.79E+03	4.26E+02	4.94E+04	7.87E+04	7.01E+02	2.27E+04	1.75E+03	7.54E+03	9.11E+02
P60660 MYL6	VFDLKEGNGTVMGAEIR	574.96	83.27	2.42E+05	9.53E+03	1.96E+03	1.19E+04	4.27E+04	3.19E+03	2.38E+03	7.45E+02	2.65E+02	1.47E+03	4.00E+05	1.41E+04	4.56E+05	1.34E+03	5.41E+05
Q9UKS6 PACN3	AQYEQTLAELHR	486.92	83.38	5.50E+04	5.00E+04	1.89E+04	1.35E+02	2.77E+02	1.18E+04	2.73E+04	3.51E+04	3.32E+04	1.37E+03	3.99E+04	5.25E+02	7.35E+02	4.22E+03	3.59E+03
P46976 GLYG	GALVLGSSSLK	472.79	83.68	2.86E+03	1.04E+03	3.69E+03	1.33E+03	5.93E+02	9.50E+02	3.71E+02	2.13E+03	1.49E+03	6.83E+02	9.11E+04	7.35E+02	2.48E+04	1.77E+03	1.41E+03
P37802 TAGL2	NVIGLQMGTR	601.82	83.87	2.64E+05	8.16E+03	1.31E+04	9.78E+03	7.11E+03	1.19E+05	1.14E+03	6.74E+03	9.92E+04	4.27E+04	1.21E+03	1.64E+03	1.02E+04	1.33E+04	2.40E+03
Q13561 DCTN2	YADLPGIAR	488.28	83.92	5.08E+04	2.84E+05	2.83E+05	6.39E+05	9.85E+05	1.05E+06	5.48E+05	2.03E+04	1.21E+04	5.40E+03	2.35E+04	3.16E+05	1.89E+03	6.62E+03	1.38E+03
Q9BQ69 MACD1	VDLSTSTDWK	576.29	84.27	1.28E+05	1.19E+04	2.68E+04	7.75E+03	3.69E+03	1.64E+03	9.49E+02	6.37E+04	1.14E+03	6.59E+02	1.66E+05	1.06E+05	2.98E+03	3.81E+02	2.44E+04
P43034 LIS1	AIADYLR	411.23	84.35	1.12E+04	8.42E+04	7.43E+03	1.33E+04	3.66E+02	7.91E+04	5.01E+04	2.96E+03	2.21E+04	2.96E+04	1.89E+04	7.79E+04	4.66E+04	5.96E+03	
O75323 NIPS2	SGPNIYELR	524.77	84.58	7.00E+05	1.14E+05	9.03E+02	8.66E+04	1.98E+04	8.15E+03	3.04E+04	4.69E+03	2.59E+03	1.92E+03	4.73E+05	2.05E+04	4.68E+05	2.29E+03	7.07E+05
Q08257 QOR	SDIAVPIPK	470.28	84.98	8.27E+04	9.12E+02	6.73E+02	3.61E+03	2.19E+03	1.79E+04	7.31E+02	1.44E+03	3.56E+03	6.75E+02	4.88E+04	4.11E+03	6.82E+03	5.96E+03	2.85E+03
O00330 ODPX	GIQEIADSVK	530.29	85.09	5.74E+02	5.19E+03	3.21E+03	2.28E+04	3.24E+04	1.66E+03	1.39E+04	3.32E+03	1.24E+04	3.81E+04	1.42E+04	4.11E+03	8.51E+03	3.49E+05	3.04E+04
P01011 AACT	EQLSLLDR	487.27	85.37	6.77E+03	2.18E+04	5.54E+03	8.71E+04	8.04E+04	1.30E+05	7.24E+03	8.71E+04	5.88E+02	9.59E+02	2.15E+03	4.44E+03	2.65E+03	1.19E+04	3.84E+04
Q9UMS6 SYNP2	VAEELILR	471.78	85.68	1.63E+04	1.36E+04	7.01E+02	2.85E+02	9.25E+02	6.64E+02	1.40E+03	2.27E+02	5.59E+03	2.93E+03	6.78E+02	5.92E+02	5.50E+02	1.39E+05	1.64E+03
Q96Q06 PLIN4	LGDLGPSFR	481.27	85.88	1.48E+03	5.66E+04	3.54E+03												

Q9BV79 MECR	SLGAEHVITEEELR	528.28	87.03	8.37E+04	2.62E+03	3.88E+03	2.30E+03	5.68E+02	8.18E+02	3.81E+03	1.21E+03	5.62E+02	1.86E+03	1.51E+03	1.38E+03	4.18E+03	1.02E+03	4.54E+03
O60313 OPA1	GVEVDPSLIK	528.79	87.15	3.47E+04	7.81E+04	1.38E+03	1.29E+05	2.45E+05	1.03E+05	9.28E+03	1.49E+04	1.46E+03	1.08E+03	1.53E+03	4.55E+04	5.59E+04	1.17E+03	1.12E+05
O00483 NDUA4	FYSVNVVDYSK	611.29	87.86	8.21E+02	1.89E+03	1.54E+03	2.41E+05	2.07E+03	2.55E+03	1.61E+03	1.32E+04	3.12E+03	2.32E+02	2.01E+05	1.52E+03	6.60E+04	1.22E+03	3.47E+05
Q13424 SNTA1	TGLLELR	401.25	88.27	9.46E+04	3.35E+04	1.12E+03	1.28E+05	7.90E+04	1.59E+05	3.68E+03	6.64E+03	8.77E+02	2.31E+03	3.09E+03	2.09E+04	5.49E+03	7.23E+03	3.35E+03
Q14240 IF4A2	VFDMLNR	447.73	88.52	7.89E+02	2.82E+03	1.78E+03	1.53E+04	2.38E+03	3.71E+03	1.22E+03	2.92E+03	2.24E+03	5.91E+02	2.17E+03	6.72E+03	3.88E+04	6.67E+03	9.34E+04
P61088 UBE2N	LLAEPVPGIK	518.82	88.6	2.34E+02	7.48E+03	5.53E+02	2.51E+05	4.94E+04	8.98E+03	6.81E+02	8.72E+02	1.62E+03	5.00E+02	6.82E+02	5.39E+03	1.45E+05	1.73E+02	1.93E+05
O00217 NDUS8	YVNMQDPEMDMK	750.81	88.77	4.67E+04	3.01E+02	1.53E+03	3.89E+02	1.46E+02	2.59E+02	7.94E+02	2.72E+02	2.90E+02	3.34E+02	1.66E+02	5.09E+02	9.62E+02	4.06E+02	4.15E+03
P00918 CAH2	SADFTNFDPR	585.26	88.92	7.16E+04	6.72E+02	6.25E+03	1.77E+03	4.42E+02	7.71E+02	1.18E+03	2.32E+03	5.07E+02	5.99E+03	4.30E+04	2.22E+03	1.46E+03	5.89E+04	1.69E+03
P14314 GLU2B	ESLQQMAEVTR	646.32	89.05	7.93E+02	3.07E+03	9.71E+02	9.52E+04	2.44E+04	2.80E+04	1.56E+03	6.72E+04	1.61E+03	1.30E+03	2.64E+04	1.48E+04	3.45E+03	1.07E+04	2.67E+04
O75367 H2AY	AGVIFPVGR	458.27	89.48	3.13E+03	1.00E+05	4.22E+03	2.25E+05	1.82E+05	2.28E+05	1.05E+05	9.28E+02	1.03E+03	1.66E+03	1.39E+03	8.28E+04	8.37E+02	1.05E+03	1.98E+05
Q9UN36-3 NDRG:P	PEMILGH	796.40	89.7	2.85E+02	6.95E+02	3.62E+04	1.12E+03	3.09E+03	2.92E+02	7.63E+04	1.31E+04	7.00E+03	3.09E+03	1.61E+03	1.68E+03	9.08E+02	9.46E+03	1.27E+03
P17931 LEG3	IQVLVEPDHFK	442.24	89.93	9.14E+03	8.05E+03	1.13E+03	3.37E+05	2.59E+05	3.53E+05	2.69E+05	6.08E+03	2.65E+03	1.03E+03	7.14E+03	2.22E+04	2.41E+05	2.25E+03	2.49E+05
P62424 RL7A	AGVNTVTTLVENK	673.37	90.17	9.83E+02	9.66E+03	1.72E+03	7.69E+04	2.19E+04	4.80E+03	1.28E+03	5.68E+03	1.22E+03	1.05E+03	7.60E+02	7.53E+02	4.90E+04	2.17E+03	3.93E+04
Q15327 ANKR1	AIFDSLRL	411.23	90.42	2.22E+03	2.64E+03	3.29E+03	1.97E+04	4.09E+03	5.72E+02	1.70E+03	3.92E+03	3.73E+03	5.95E+02	1.06E+05	3.31E+04	2.67E+04	3.27E+03	2.56E+04
P49419 AL7A1	MIGGPILPSE	585.32	90.48	6.65E+03	1.01E+05	4.98E+02	7.58E+04	4.42E+02	5.67E+04	9.96E+04	4.70E+04	7.30E+05	1.45E+04	3.42E+03	7.45E+04	2.04E+03	9.65E+05	8.83E+04
P68366 TBA4A	VDNAAIAAIK	493.29	90.6	9.85E+04	3.66E+04	2.60E+03	1.47E+05	5.75E+04	4.98E+04	3.99E+04	4.89E+03	1.27E+03	7.84E+02	2.08E+05	1.80E+04	5.31E+04	1.44E+03	1.57E+05
Q04760 LGUL	IAWALSR	408.74	90.61	1.22E+03	6.48E+02	9.10E+02	2.81E+03	2.45E+02	4.42E+02	1.45E+03	3.05E+02	7.36E+04	7.56E+04	3.03E+02	2.29E+02	8.85E+02	5.67E+03	6.01E+02
P07942 LAMB1	DILAQSPAAEPLK	676.86	90.64	1.52E+03	3.73E+04	1.31E+04	2.18E+04	4.63E+05	1.07E+04	1.48E+04	5.83E+03	2.54E+03	1.42E+03	7.06E+04	5.48E+04	9.85E+03	2.69E+03	2.18E+05
P07942 LAMB1	FGYYGDALR	531.26	90.81	3.10E+03	1.08E+04	1.31E+04	2.71E+03	2.28E+04	6.61E+03	6.34E+04	1.79E+03	8.25E+02	2.12E+04	8.94E+04	4.52E+03	7.26E+03	1.51E+04	1.12E+04
P35268 RL22	ITVTSEVPFSK	604.33	91.14	8.18E+02	2.25E+03	1.48E+05	1.71E+03	2.29E+03	2.69E+05	4.90E+02	1.76E+05	6.23E+02	1.14E+03	3.65E+02	3.28E+03	3.38E+03	2.41E+03	1.05E+03
P04899 GNAI2	LLLLGAGESGK	529.32	91.27	6.40E+02	8.18E+04	7.14E+04	1.35E+05	4.85E+03	1.05E+05	7.45E+04	8.51E+04	3.03E+04	6.73E+02	7.15E+02	6.42E+03	6.02E+02	4.15E+04	1.05E+05
Q9BYX7 ACTBM	RVAPEEHPIILLTEAPLNPK	708.72	91.31	1.73E+02	1.31E+04	2.44E+03	1.26E+05	2.40E+05	9.37E+03	3.86E+03	6.27E+03	9.92E+02	3.15E+02	9.80E+02	5.62E+02	7.94E+02	1.59E+02	1.03E+05
O00429-4 DNM1L	LGHGVVNR	470.80	91.38	5.54E+02	3.93E+02	3.37E+03	5.93E+04	7.78E+02	5.72E+04	8.35E+03	2.89E+02	2.34E+03	1.14E+03	8.79E+02	3.12E+04	7.87E+02	6.95E+02	2.50E+02
Q13683-9 ITA7	AEELSFVAGAPR	623.82	91.63	6.92E+04	8.41E+03	2.93E+03	7.27E+02	1.04E+04	9.64E+04	2.04E+04	2.07E+03	1.94E+04	6.00E+02	1.06E+04	6.96E+04	2.29E+04	3.27E+02	1.44E+03
Q07507 DERM	YFESVLDR	514.76	91.76	4.23E+02	1.03E+04	2.31E+05	1.47E+04	7.91E+02	7.66E+03	7.32E+04	1.35E+04	2.00E+03	1.01E+03	1.34E+03	9.51E+03	7.92E+02	1.20E+03	9.42E+02
Q07020 RL18	TAVVVGTITDDVR	673.37	91.81	6.26E+02	1.52E+04	7.58E+03	6.57E+04	1.20E+05	2.19E+05	2.00E+04	1.55E+03	1.11E+04	3.29E+04	6.94E+03	3.58E+04	1.85E+04	1.02E+04	1.95E+05
Q9UJY1 HSPB8	LSSAWPGTLR	544.30	91.86	7.60E+04	7.56E+04	1.31E+04	7.51E+03	2.00E+04	1.11E+05	8.90E+03	7.17E+03	2.26E+03	2.00E+03	1.20E+05	8.09E+04	2.96E+04	3.96E+03	9.73E+03
P14625 ENPL	LSLNIDPDAK	543.29	91.88	2.97E+03	3.75E+03	2.69E+04	9.15E+03	1.82E+04	2.05E+04	5.97E+03	5.55E+03	1.62E+03	2.15E+03	7.15E+04	5.88E+03	1.40E+03	1.08E+03	2.13E+04
P29218 IMPA1	EIQVIPLQR	548.33	92	4.48E+02	3.55E+04	9.29E+04	6.93E+03	2.34E+02	1.17E+05	3.73E+03	1.62E+03	7.64E+02	1.20E+03	5.87E+02	3.62E+04	1.26E+03	1.85E+03	8.29E+03
P39019 RS19	VLQALEGLK	485.80	92.12	9.51E+04	5.69E+04	1.71E+03	5.57E+03	2.65E+02	7.04E+04	2.27E+03	4.50E+03	3.89E+02	8.23E+03	6.80E+04	5.78E+04	7.50E+03	7.65E+02	6.40E+03
P05023-2 AT1A1	SPDFTNENPLETR	760.36	92.15	1.06E+04	1.95E+04	1.09E+04	5.15E+02	9.09E+02	4.69E+04	4.43E+04	2.78E+03	5.43E+02	1.15E+03	1.35E+03	4.85E+03	2.15E+02	7.97E+03	1.49E+03
P05023-2 AT1A1	IVEIPFNSTNK	631.34	92.37	1.84E+04	4.88E+03	3.82E+03	1.01E+05	9.64E+03	4.29E+03	2.14E+04	1.05E+04	5.62E+03	2.90E+02	1.26E+05	3.62E+03	2.18E+04	5.06E+03	1.91E+04
Q9BYX7 ACTBM	VAPEEHPILLTEAPLNPK	656.69	92.66	2.07E+03	6.57E+05	8.75E+05	1.20E+05	8.71E+03	1.55E+04	7.81E+05	1.77E+05	3.52E+03	3.30E+02	1.37E+03	1.68E+05	8.94E+02	9.11E+03	4.59E+03
P24298 ALAT1	ALELEQELR	550.80	92.67	1.01E+03	1.02E+04	4.03E+03	7.82E+04	4.34E+04	7.18E+02	1.52E+03	3.60E+03	2.68E+03	7.54E+02	7.13E+02	1.40E+03	5.59E+03	8.74E+02	7.97E+04
P62750 RL23A	LAPDYDALDVANK	702.85	92.77	1.26E+04	3.40E+04	1.36E+04	8.85E+04	5.41E+05	3.22E+04	6.00E+03	8.93E+03	2.04E+03	1.39E+03	6.93E+04	4.11E+04	1.52E+04	1.02E+04	8.23E+03
P51149 RAB7A	DEFLIQASPR	588.30	93.12	1.14E+05	1.08E+03	9.93E+04	1.78E+03	2.19E+03	1.94E+05	2.65E+04	5.67E+04	7.12E+04	9.62E+04	3.06E+03	3.63E+03	2.49E+03	1.87E+05	2.19E+03
P23396 RS3	DEILPTTPISEQK	735.89	93.44	4.32E+03	6.82E+02	8.05E+02	5.71E+03	3.76E+03	5.23E+02	1.39E+03	1.38E+04	5.10E+04	3.19E+04	1.68E+04	8.39E+03	3.90E+03	8.08E+03	1.70E+03
P0C0L5 CO4B	VGDTLNLNLR	557.79	93.52	2.98E+03	7.89E+03	4.42E+03	3.06E+04	2.04E+05	4.05E+03	1.18E+03	8.64E+02	1.28E+04	1.61E+03	1.92E+04	1.40E+05	5.49E+04	4.06E+03	5.55E+04
P48681 NEST	GPPAPEVEELAR	716.87	93.62	1.03E+05	6.50E+03	3.19E+02	1.07E+05	4.40E+04	4.35E+03	7.18E+02	1.69E+03	3.33E+04	1.06E+04	4.03E+04	2.17E+04	2.10E+04	9.74E+02	3.63E+04
P07585 PGS2	VSPGAFTPLVK	558.32	93.99	1.82E+04	1.92E+03	1.01E+05	8.46E+02	1.22E+03	8.13E+03	2.12E+04	1.02E+04	2.35E+02	3.88E+02	4.80E+02	2.91E+03	2.17E+03	1.95E+03	1.52E+03
P68366 TBA4A	EIIDPVLDR	535.30	94.04	1.32E+03	1.10E+04	3.29E+02	7.74E+03	3.19E+04	2.30E+03	2.59E+03	4.46E+03	2.79E+05	2.93E+05	1.29E+03	5.30E+04	3.19E+03	3.42E+05	1.22E+03
O00217 NDUS8	EPATINYPFEK	654.83	94.22	1.08E+04	2.54E+04	3.69E+03	9.25E+04	1.35E+05	2.76E+03	2.69E+03	6.79E+03	1.43E+03	3.52E+03	1.36E+05	1.59E+04	1.95E+04	1.00E+03	1.62E+05
P12694 ODBA	GPGYGIMSIR	525.77	94.25	1.14E+04	3.60E+03	2.62E+04	2.58E+03	1.19E+04	1.69E+04	5.09E+04	3.18E+02	9.92E+02	2.27E+03	2.22E+03	6.80E+03	2.13E+03	1.87E+03	4.64E+03
P05556-2 ITB1	GEVFNELVGK	546.28	94.6	2.36E+04	6.66E+04	5.34E+03	2.94E+05	3.64E+04	6.18E+04	1.27E+03	7.06E+03	4.50E+03	8.01E+02	1.16E+05	5.11E+03	2.84E+04	1.02E+04	7.71E+04
P23083 HV103	MHWVRQAPQGLEWMGR	680.33	94.64	3.00E+03	6.07E+03	5.44E+04	6.78E+03	1.16E+03	4.57E+03	7.23E+03	1.08E+04	1.76E+04	5.92E+03	1.17E+03	7.11E+02	2.21E+03	2.96E+04	7.58E+03
P47756 CAPZB	LEVEANAFDQYR	784.87	94.97	3.06E+02	4.98E+03	2.59E+03	2.35E+03	4.47E+02	4.22E+04	3.83E+02	9.22E+03	1.78E+03	5.11E+02	1.27E+03	1.63E+03	1.59E+02	2.46E+03	1.24E+03
P23083 HV103	QAPGQGLEWMGR	665.32	95.29	1.73E+03	4.96E+03	3.90E+03	2.24E+03	1.04E+05	2.44E+03	1.67E+03	1.61E+04	8.11E+04	5.54E+04	7.11E+02	1.85E+03	7.91E+02	7.30E+04	2.26E+04
O75347 TBCA	LEAAYLDLQR	596.32	95.52	5.42E+04	5.17E+03	4.37E+03	3.45E+03	1.94E+03	4.80E+03	2.23E+03	7.85E+04	8.17E+04	4.99E+04	2.29E+03	8.92E+02	8.31E+02	2.66E+04	3.34E+02
P02760 AMB1	TVAACNLPIVR	578.83	95.77	1.55E+04	2.70E+03	5.02E+02	9.78E+02	5.69E+02	5.66E+03	2.93E+03	4.54E+02	2.49E+04	1.72E+04	8.59E+03	1.82E+03	6.87E+03	1.60E+04	1.68E+03
P29218 IMPA1	SLLVTELGSSR	581.33	95.84	1.07E+03	2.45E+03	4.76E+05	1.96E+03	2.52E+03	1.62E+03	9.11E+04	3.31E+05	6.56E+02	2.55E+03	7.43E+04	3.50E+03	5.61E+04	4.35E+02	1.95E+03
Q9NZ45 CISD1	IVHAFDMEDLGDK	497.24	97.31</															



O75323 NIPS2	EFLEFR	420.72	98.65	1.41E+03	2.98E+05	5.74E+03	3.54E+05	2.07E+05	1.40E+05	6.10E+03	5.22E+03	5.86E+02	4.81E+02	8.32E+02	2.94E+05	9.66E+02	1.64E+02	1.31E+05
O43920 NDUS5	WLTIQSGEQPYK	725.37	98.67	2.56E+03	1.34E+04	5.34E+03	2.79E+04	1.09E+04	1.27E+04	1.42E+04	9.82E+03	1.05E+04	4.73E+02	4.18E+03	1.10E+04	2.24E+03	9.33E+03	4.60E+04
Q9NY65 TBA8	ESIDLVLDR	530.29	98.87	2.25E+03	9.03E+03	1.55E+03	9.02E+04	9.63E+02	5.16E+03	9.81E+02	1.09E+05	4.48E+02	2.02E+03	1.11E+03	6.35E+04	1.31E+04	2.44E+03	1.05E+05
P28161 GSTM2	LLLEYTDSSYEK	795.39	99.01	2.49E+02	4.99E+02	2.17E+03	7.58E+02	2.65E+02	2.08E+03	1.16E+03	1.17E+03	3.18E+03	2.64E+02	2.55E+03	4.03E+03	4.40E+03	4.28E+03	1.72E+04
P23396 RS3	AELNEFLTR	546.79	99.22	4.13E+02	1.63E+03	3.01E+03	1.54E+03	1.53E+03	6.36E+02	2.40E+03	5.37E+03	3.17E+04	2.39E+02	1.63E+03	1.92E+03	1.45E+03	6.56E+04	2.41E+03
Q16762 THTR	FLGTEPEPDAVGLDSGHIR	670.33	99.3	5.67E+02	5.57E+04	7.83E+02	4.70E+04	1.49E+03	8.59E+02	8.86E+03	6.16E+02	2.62E+03	1.14E+03	9.92E+03	4.16E+04	5.59E+04	4.93E+03	1.37E+05
P19105 ML12A	FTDEEVDELYR	708.32	99.38	1.20E+03	3.81E+03	9.91E+02	1.15E+05	1.01E+04	1.20E+03	4.12E+02	2.72E+03	1.46E+03	1.82E+03	1.56E+05	1.77E+03	8.17E+03	1.02E+03	1.38E+04
Q71UI9 H2AV	GDEELDSLK	559.78	99.55	3.73E+03	6.91E+02	1.08E+03	3.25E+02	1.20E+03	3.78E+02	5.05E+03	1.08E+04	1.94E+05	2.23E+05	1.15E+03	8.59E+02	5.76E+02	1.53E+05	1.03E+03
P15090 FABP4	LVSSNFDDYMK	724.32	99.65	5.62E+04	2.36E+03	9.67E+02	4.13E+03	1.38E+03	4.26E+02	1.11E+03	1.02E+03	1.96E+04	4.59E+04	2.45E+03	9.49E+02	1.56E+03	1.86E+04	4.68E+03
P00918 CAH2	VVDVLSIK	494.29	99.77	5.17E+04	9.57E+04	2.80E+03	1.35E+04	9.82E+04	6.21E+04	6.82E+03	1.14E+03	7.24E+02	1.81E+03	1.42E+04	4.10E+04	1.07E+04	5.35E+02	4.00E+03
O75367 H2AY	SIAFFSIGSGR	546.29	99.79	2.34E+04	8.29E+02	7.90E+03	1.83E+03	3.85E+03	7.34E+03	3.52E+03	3.14E+03	1.95E+04	2.89E+04	5.82E+03	8.23E+03	3.84E+03	1.03E+04	6.86E+03
P14625 ENPL	GVVSDDDLPLNVSR	743.38	99.92	4.28E+04	4.94E+02	4.72E+03	1.11E+04	3.66E+03	3.32E+03	4.07E+03	8.64E+02	2.18E+04	2.56E+04	6.28E+04	3.51E+03	6.23E+02	8.71E+03	7.80E+02
Q9UI09 NDUAC	IQEWIPSTPYK	729.88	99.95	2.57E+03	4.26E+03	1.36E+03	2.07E+04	9.99E+03	3.46E+03	1.22E+03	3.00E+03	4.92E+02	1.09E+03	2.90E+04	1.38E+04	1.79E+04	1.73E+03	3.62E+04
O43488 ARK72	VASVLGTMEMGR	625.81	100.1	7.38E+03	2.12E+03	3.38E+02	5.68E+04	1.99E+03	4.59E+03	2.13E+03	4.58E+03	7.65E+03	1.89E+03	1.01E+03	9.47E+02	1.07E+04	1.65E+04	3.82E+03
P31948 STIP1	AAALEFLNR	502.78	100.14	5.28E+04	2.75E+03	9.22E+03	1.72E+04	8.53E+03	1.69E+04	1.55E+03	3.59E+03	1.70E+03	9.60E+02	2.20E+04	1.17E+04	2.82E+04	1.51E+03	3.63E+04
P56556 NDUA6	QATSTASTFVKPIFSR	580.98	100.25	8.99E+04	1.42E+03	3.62E+03	3.57E+04	7.63E+03	7.31E+02	3.34E+02	1.97E+03	1.86E+05	7.22E+03	1.74E+05	9.01E+02	2.56E+03	7.41E+04	1.97E+03
P05023-2 AT1A1	TSATWLALSR	553.30	100.41	5.11E+03	2.19E+03	2.39E+02	1.32E+03	1.88E+04	4.08E+04	1.43E+04	1.02E+04	2.79E+03	7.15E+02	1.52E+03	6.79E+03	1.23E+03	3.93E+03	3.44E+04
P35998 PRS7	FDEIDAIGGAR	582.29	100.92	2.62E+03	2.95E+05	2.24E+05	6.30E+03	4.85E+05	5.43E+05	2.66E+05	3.23E+05	2.12E+03	2.94E+04	6.52E+04	3.54E+05	1.14E+05	6.41E+04	5.05E+05
Q15327 ANKR1	TLLAHPVTLGEQQWK	574.32	101.03	5.01E+04	5.18E+04	8.43E+03	3.95E+03	7.05E+04	4.36E+04	1.30E+04	7.35E+03	8.95E+04	8.31E+02	2.97E+03	2.69E+03	2.00E+03	2.75E+03	4.55E+03
Q96HC4-2 PDL15	ASAAPKPEPVPVQKPTVTS VCSETSQELAEGQR	856.19	101.38	6.09E+04	2.66E+03	2.99E+03	3.69E+04	1.55E+03	4.45E+02	1.38E+02	1.67E+03	5.61E+02	7.62E+02	5.67E+04	3.41E+03	1.35E+03	1.83E+03	3.87E+03
Q8WZ42-6 TITIN	VFANVDIMPQEER	768.37	101.39	1.82E+04	6.31E+02	4.73E+03	9.14E+03	1.29E+03	3.65E+03	1.65E+02	1.04E+03	6.89E+05	3.18E+06	8.23E+03	2.67E+03	4.03E+02	3.22E+05	5.93E+03
P01011 AACT	EIGELYLPK	531.30	101.43	2.95E+04	1.18E+04	6.03E+04	4.51E+04	3.02E+05	5.15E+04	3.70E+05	3.39E+05	2.00E+04	2.56E+05	2.03E+03	1.00E+05	3.16E+04	4.05E+04	1.19E+04
P0COL5 CO4B	GHLFLQTDQPIYNPGQR	662.01	101.69	1.53E+03	1.46E+03	7.10E+02	2.96E+03	2.22E+03	3.80E+02	7.47E+03	3.24E+03	5.95E+03	6.13E+04	3.49E+02	1.38E+04	5.52E+03	3.50E+03	2.12E+03
Q8WZ42-6 TITIN	LSLLDTSSEISSR	704.37	101.69	2.88E+03	7.83E+02	2.80E+03	5.00E+03	6.86E+03	4.93E+04	1.93E+03	2.74E+03	3.77E+03	1.80E+03	3.05E+02	3.15E+03	4.00E+03	6.06E+02	5.92E+02
Q8N335 GPDIL	ALGITLIK	414.78	101.74	1.04E+03	2.28E+02	6.80E+02	4.18E+02	4.23E+02	2.08E+02	4.72E+02	1.63E+02	1.03E+04	8.44E+04	5.97E+02	2.72E+02	4.64E+02	7.66E+03	1.11E+03
Q81WX7-2 UN45B	IAAVSNPDIAFPGER	778.91	101.79	2.14E+03	1.87E+03	1.08E+03	7.86E+04	5.09E+03	7.58E+02	3.51E+02	3.41E+03	2.16E+03	2.72E+03	3.10E+04	4.82E+02	3.71E+04	3.32E+03	1.86E+03
P46976 GLYG	LVVLATPQVSDSMR	758.41	102.6	1.85E+04	3.04E+03	7.73E+02	1.95E+04	1.24E+03	1.35E+03	1.49E+03	1.37E+03	1.13E+04	1.64E+03	3.70E+04	7.16E+03	2.44E+04	2.24E+03	6.17E+03
P53597 SUCA	GGQTHLGLPVFNTVK	523.29	102.61	1.11E+03	2.01E+04	2.08E+04	1.44E+03	1.04E+05	1.33E+05	2.16E+04	3.02E+04	4.11E+02	1.12E+03	7.21E+03	3.82E+04	8.83E+02	3.48E+03	7.69E+04
P35613 BASI	SELHIENLNMEADPGQYR	706.00	103.03	3.93E+03	3.27E+03	3.53E+03	3.44E+04	4.44E+03	1.14E+03	6.29E+03	7.30E+03	1.99E+04	2.85E+04	2.57E+04	1.03E+04	1.27E+04	1.35E+05	1.66E+03
P04843 RPN1	TILPAAAQDVYYR	740.89	103.03	8.53E+03	1.82E+03	1.77E+04	2.56E+04	1.44E+03	2.74E+04	1.14E+03	9.77E+02	3.62E+03	2.48E+02	4.40E+03	1.05E+03	2.72E+03	2.54E+03	2.37E+04
P02760 AMBP	ETLLQDFR	511.27	103.13	1.16E+04	9.87E+04	2.32E+05	1.05E+03	6.37E+04	1.61E+05	2.33E+03	2.02E+03	5.62E+04	5.80E+04	3.93E+03	3.18E+04	8.46E+02	3.95E+04	1.88E+05
P14314 GLU2B	SLEDQVEMLR	610.31	103.18	7.82E+02	3.00E+04	8.56E+03	8.30E+02	1.83E+04	3.26E+03	8.40E+02	2.28E+03	1.70E+03	6.26E+02	4.45E+03	3.21E+04	2.53E+04	1.24E+03	1.94E+04
P14174 MIF	PMFIVNTNVPR	644.35	103.4	2.20E+04	1.89E+03	2.17E+03	4.84E+03	2.18E+04	1.60E+03	7.51E+02	1.00E+03	4.09E+02	1.01E+03	4.59E+03	2.44E+03	7.14E+02	1.30E+03	3.76E+03
P05556-2 ITB1	IGFGSFVEK	492.26	103.59	1.41E+04	4.87E+02	9.44E+02	2.66E+03	3.80E+03	9.81E+04	1.43E+05	1.24E+05	1.03E+05	1.50E+05	3.13E+03	2.06E+03	1.79E+03	1.18E+05	8.37E+03
P10909-2 CLUS	TLLSNLEEAK	559.31	103.76	1.12E+04	7.19E+02	7.75E+04	1.91E+04	2.40E+04	3.27E+03	6.32E+04	2.31E+04	1.18E+04	2.94E+04	1.21E+03	1.24E+05	3.05E+03	1.53E+04	5.48E+03
O15273 TELT	SPWLMMR	460.73	103.94	1.54E+03	7.68E+03	5.64E+04	1.52E+03	1.47E+05	3.70E+03	9.08E+04	1.89E+02	2.62E+02	2.55E+03	3.71E+02	5.26E+03	2.39E+04	2.64E+03	6.04E+04
O95292 VAPB	GPFTDVVTNLK	646.35	104.22	5.82E+04	4.68E+03	6.04E+02	4.74E+04	4.64E+02	4.45E+03	1.19E+03	9.80E+02	1.49E+05	2.14E+05	4.53E+04	1.64E+03	1.61E+04	1.83E+04	1.28E+04
P16671 CD36	ELLWGYR	468.75	104.85	9.63E+02	1.03E+05	7.28E+03	1.03E+03	6.33E+03	6.37E+03	4.18E+03	1.18E+03	1.16E+03	1.86E+03	7.93E+02	6.84E+04	4.11E+03	2.34E+03	1.37E+05
P02763 A1AG1	YVGGQEHFALLILR	584.99	105.15	5.45E+02	8.09E+02	1.96E+03	6.44E+02	9.75E+04	8.48E+02	2.11E+04	3.41E+03	6.91E+03	2.66E+03	3.69E+03	5.35E+03	6.78E+02	1.68E+03	8.15E+03
Q92736 RYS2	AFLDAAEDLEK	668.33	105.54	5.70E+04	3.79E+05	2.39E+05	6.90E+04	1.72E+03	8.03E+04	7.90E+03	1.82E+04	1.03E+04	3.11E+03	4.45E+02	1.57E+05	1.58E+03	3.99E+03	1.68E+03
P19105 ML12A	AMFDQSQIQEFK	736.35	105.57	4.56E+04	6.91E+03	3.14E+04	7.28E+02	6.27E+02	4.69E+03	5.94E+02	4.26E+02	8.52E+02	1.05E+04	4.41E+03	4.06E+03	2.25E+03	2.52E+03	8.60E+03
P35998 PRS7	ALDEGDIALLK	579.32	106.47	2.20E+04	1.35E+03	3.27E+03	8.67E+04	2.50E+04	4.77E+04	2.25E+03	2.37E+03	1.57E+04	2.96E+03	6.32E+04	7.51E+03	5.54E+02	2.29E+04	3.50E+02
P0COL5 CO4B	LTVAAPPSGGPGFLSIERPD SRPPR	644.35	106.64	7.34E+03	1.18E+05	1.74E+03	6.00E+02	1.17E+05	1.51E+05	8.62E+03	4.04E+03	2.15E+04	1.69E+04	4.19E+03	2.35E+05	6.50E+04	2.57E+03	1.57E+05
P18136 KV313	FSGSGSGTDFTLTISR	816.90	106.64	1.28E+04	7.65E+02	3.35E+02	2.46E+02	2.53E+03	3.82E+03	5.42E+02	1.67E+03	3.53E+03	1.09E+05	7.27E+03	3.76E+03	1.22E+03	1.95E+04	4.98E+02
P01781 HV320	NSLYLQMNLSR	669.84	106.7	7.51E+02	5.37E+02	2.84E+03	1.12E+04	4.66E+03	3.58E+02	7.73E+02	1.37E+03	5.06E+03	4.30E+04	4.24E+03	9.93E+03	1.07E+03	1.34E+03	1.24E+03
P35237 SPB6	LEESYDMESVLR	735.84	106.71	4.41E+04	2.72E+03	5.59E+02	8.45E+03	6.04E+02	4.90E+02	2.65E+03	2.73E+03	2.19E+03	6.97E+02	4.49E+04	1.23E+03	1.14E+03	9.50E+02	5.74E+02
Q96RQ3 MCCA	IPLSQEITLQGHAFEAR	680.36	107.03	6.50E+02	4.88E+03	3.09E+03	4.15E+02	3.04E+04	3.32E+03	6.47E+03	3.66E+03	1.86E+03	2.23E+03	7.96E+02	7.46E+03	3.97E+02	1.51E+03	5.43E+03
P0COL5 CO4B	GSFEPVGDVASK	670.33	107.16	2.43E+03	2.05E+03	2.12E+03	1.92E+03	1.64E+03	4.54E+03	2.38E+03	4.90E+02	5.64E+02	1.88E+04	1.74E+03	1.29E+03	3.68E+04	5.68E+02	3.12E+03
P19105 ML12A	GNFNIEFTR	630.84	107.26	5.17E+02	2.00E+03	5.71E+04	1.32E+03	6.84E+03	2.12E+04	5.38E+04	4.59E+04	3.18E+04	7.56E+04	5.57E+02	5.63E+03	9.77E+02	9.14E+04	3.46E+03
O75251 NDUS7	QSDVMIVAGTLTNK	738.89	107.38	1.44E+03	3.04E+03	2.79E+03	1.92E+03	3.38E+02	1.10E+03	4.71E+05	5.08E+05	7.13E+04	7.47E+04	1.39E+03	8.89E+03	9.44E+02	1.	

P09104 ENOG	GNPTVEVDLYTAK	703.86	108.42	1.04E+05	7.93E+02	5.48E+04	2.90E+04	3.41E+03	4.03E+03	2.14E+05	3.35E+05	1.88E+03	1.65E+03	3.00E+04	3.70E+03	1.69E+03	2.78E+03	1.15E+03
Q9UKS6 PACN3	SPDEVTLTSIVPTR	757.90	108.76	4.40E+03	2.03E+03	3.34E+02	6.70E+04	5.68E+03	8.76E+03	5.85E+03	8.59E+03	1.01E+05	3.40E+05	2.26E+04	8.01E+02	3.97E+02	1.47E+03	2.07E+04
Q9UKU7 ACAD8	AVIFEDCAVPVANR	752.38	108.83	2.75E+04	4.74E+04	1.09E+05	1.84E+03	1.28E+03	1.11E+05	7.71E+02	8.35E+02	1.81E+03	6.03E+04	2.55E+03	1.45E+03	5.41E+02	1.20E+03	1.96E+03
P07942 LAMB1	YSDIEPSTEGEVIFR	871.42	108.95	1.46E+03	7.79E+02	4.95E+02	7.21E+02	7.51E+02	7.43E+02	8.76E+02	2.93E+02	2.84E+04	4.33E+04	2.09E+03	1.05E+03	2.07E+03	3.24E+03	3.44E+03
P01781 HV320	GLEWVANIK	515.29	108.98	8.17E+04	1.67E+04	1.14E+03	2.19E+04	4.88E+03	2.62E+03	1.49E+03	1.40E+04	1.05E+04	2.91E+02	6.69E+04	1.90E+04	1.65E+04	2.55E+03	1.89E+04
P07942 LAMB1	IPSWTGAGFVR	595.82	109.21	2.83E+03	8.20E+05	3.31E+04	6.66E+04	1.97E+05	8.47E+05	3.46E+03	1.01E+03	9.23E+03	2.76E+03	3.62E+03	2.19E+05	9.09E+03	4.50E+03	3.61E+05
P51970 NDUA8	LGWVRPDLGELSK	490.61	109.57	7.94E+04	2.60E+03	5.00E+02	2.44E+03	1.98E+03	4.60E+02	2.30E+03	1.16E+03	2.24E+02	8.17E+02	2.46E+04	1.71E+03	6.93E+02	3.47E+03	3.68E+03
P31150 GDIA	FQLLEGPPESMGR	730.86	109.62	1.42E+04	1.46E+05	1.95E+04	8.65E+03	4.67E+04	1.10E+04	1.94E+05	1.60E+03	1.78E+03	1.28E+03	6.86E+02	2.38E+04	1.97E+02	1.42E+03	7.04E+03
P35237 SPB6	NLGMTDAFELGK	648.32	109.97	6.27E+02	2.30E+04	3.07E+03	3.12E+02	8.17E+02	6.92E+04	1.56E+03	5.23E+04	5.22E+02	1.63E+03	9.40E+02	1.98E+03	1.36E+03	8.26E+02	4.73E+02
P45954 ACDSB	GITSFLVDR	504.28	110.08	7.81E+03	1.90E+03	1.73E+03	1.87E+04	7.30E+02	3.90E+03	3.67E+02	1.62E+03	2.72E+04	3.12E+04	1.13E+04	6.56E+02	1.61E+03	2.99E+04	7.35E+03
Q14240 IF4A2	VLITDILLAR	557.84	110.12	1.17E+03	3.26E+04	7.22E+03	6.61E+02	2.63E+02	5.10E+02	4.84E+04	5.11E+04	3.72E+02	1.26E+03	7.91E+02	1.79E+02	3.26E+02	9.82E+02	2.00E+03
Q96CN7 ISOC1	GLGSTVQEIDLTVGK	758.91	110.21	5.28E+02	1.80E+03	1.22E+04	1.79E+03	2.21E+02	7.12E+03	1.16E+03	1.82E+03	5.25E+04	3.68E+04	8.44E+02	1.15E+03	3.38E+03	1.04E+04	1.67E+03
O75323 NIPS2	TVPLIQEMESR	651.84	110.23	3.95E+04	3.65E+04	8.26E+03	1.64E+04	9.11E+02	9.21E+04	1.46E+04	1.57E+04	1.32E+04	6.03E+04	3.08E+04	6.75E+03	3.89E+03	2.13E+04	2.16E+04
P08574 CY1	LFDFYFKPYPNSEAAR	638.99	110.23	1.22E+04	2.71E+03	1.24E+03	9.63E+03	3.86E+02	1.11E+03	2.26E+03	2.41E+03	3.99E+03	4.19E+04	4.25E+03	3.39E+03	3.81E+03	9.34E+02	1.81E+03
Q96Q06 PLIN4	DAVSSGVASVVDVAK	702.37	110.61	8.23E+03	2.93E+03	2.29E+04	1.29E+04	1.75E+03	3.10E+04	1.94E+03	1.04E+03	1.91E+04	2.33E+04	1.77E+04	1.76E+04	1.25E+04	2.14E+04	3.57E+03
Q9UKU7 ACAD8	IGSEGGFLIAVR	673.87	110.64	6.09E+03	1.15E+03	3.87E+03	7.56E+02	2.94E+03	3.80E+03	2.54E+02	8.35E+02	4.27E+03	2.50E+04	7.88E+03	1.79E+03	3.68E+03	1.43E+03	7.69E+03
Q96CN7 ISOC1	YFGDIISVGQR	627.83	110.65	1.40E+03	2.82E+03	2.41E+04	1.26E+04	6.39E+02	2.04E+03	3.10E+03	6.57E+02	7.47E+04	5.45E+04	1.42E+03	4.67E+02	7.71E+02	4.08E+04	1.40E+03
P19823 ITIH2	AEDHFSVIDFNQIR	602.29	110.69	4.19E+03	4.09E+02	3.21E+03	6.59E+03	3.17E+03	1.50E+04	3.39E+04	1.69E+03	5.76E+02	3.07E+04	5.55E+02	1.03E+03	3.83E+02	2.45E+03	8.42E+02
P28161 GSTM2	EDILENQFMDSR	748.84	110.75	2.22E+03	8.68E+02	2.49E+03	3.44E+03	2.03E+03	3.52E+03	1.35E+03	9.92E+02	4.48E+04	1.57E+04	3.72E+03	1.36E+03	1.17E+03	1.53E+04	1.31E+03
P43155-3 CACP	QPVVYSSPGVMLPK	807.95	110.77	3.98E+03	1.62E+03	5.27E+02	2.52E+02	3.56E+04	2.31E+03	1.77E+03	2.25E+03	2.75E+02	1.67E+03	2.35E+03	5.32E+03	3.04E+03	2.81E+02	9.22E+03
P15311 EZRI	QLLTLSSLSQAR	723.40	110.8	8.48E+02	1.77E+03	1.96E+03	3.79E+03	2.83E+02	9.93E+03	4.45E+02	7.08E+02	2.94E+04	2.51E+04	3.19E+03	8.75E+02	4.15E+03	4.33E+04	2.37E+03
P02763 A1AG1	TYMLAFDVNDEK	723.33	111.08	3.07E+03	5.85E+03	3.38E+03	7.39E+02	3.43E+04	8.69E+02	6.85E+02	1.93E+03	1.89E+03	2.18E+03	5.70E+02	1.24E+04	1.41E+03	1.63E+03	6.62E+03
P14174 MIF	LLCGLLAER	494.28	111.26	5.31E+03	7.85E+03	1.01E+04	1.62E+04	2.28E+04	1.07E+04	2.83E+04	5.15E+04	5.18E+02	2.06E+03	4.06E+03	8.04E+04	6.72E+03	2.34E+03	7.94E+04
P04843 RPN1	ALTSEIALLQSR	651.35	112.09	6.56E+04	7.50E+02	1.06E+04	1.03E+05	2.71E+03	1.09E+03	2.13E+03	1.47E+03	1.07E+04	8.44E+03	6.11E+04	2.10E+03	3.53E+03	1.42E+03	1.62E+03
Q00059 TFAM	SWEEQMIEVGR	682.32	112.12	2.81E+03	1.55E+04	1.85E+03	4.80E+02	1.59E+03	8.62E+03	3.59E+04	3.53E+04	4.15E+02	2.32E+04	4.51E+03	1.88E+03	1.13E+03	3.50E+03	2.05E+03
P51970 NDUA8	FYFWTK	446.22	113.03	5.81E+02	4.44E+02	2.01E+03	2.69E+02	1.41E+03	3.84E+02	2.48E+02	4.85E+02	4.37E+03	5.26E+04	7.83E+02	2.05E+02	2.41E+02	3.84E+03	3.10E+02
O75438-2 NDUB1	VNLLQIVR	477.81	113.09	1.98E+04	4.36E+03	4.60E+03	2.69E+02	4.62E+03	4.00E+03	1.51E+03	4.17E+03	2.26E+03	6.77E+04	6.77E+02	2.80E+03	7.68E+03	2.83E+04	1.31E+03
P52565 GDIR1	AEEYFLTPVEEAPK	875.93	113.16	3.52E+02	3.05E+03	1.87E+03	2.39E+04	2.88E+03	1.27E+03	1.10E+03	4.27E+02	3.53E+02	8.22E+02	6.32E+02	1.07E+05	1.96E+05	6.47E+02	1.97E+04
Q99714 HCD2	GGIVGMTLPIAR	592.85	113.18	2.28E+03	8.20E+03	1.67E+03	8.67E+02	1.93E+03	4.19E+04	5.18E+04	2.63E+04	1.97E+02	6.72E+02	3.36E+02	6.64E+02	1.40E+03	4.86E+02	6.63E+02
Q92736 RYR2	TVAGGLPGAGLFGPK	671.38	113.23	3.91E+04	7.63E+02	2.10E+02	7.35E+04	7.50E+03	4.14E+03	6.94E+03	4.82E+02	5.23E+03	1.47E+03	6.14E+04	9.41E+03	2.89E+03	1.74E+03	2.92E+03
P37802 TAGL2	TLMNLGGLAVAR	608.35	113.27	2.09E+05	4.32E+03	3.76E+03	1.03E+05	1.12E+05	1.69E+04	7.60E+03	2.51E+03	3.52E+03	8.27E+02	2.06E+05	1.04E+05	1.31E+04	8.75E+02	1.13E+05
P09669 COX6C	NYDVMMKDFEEMR	526.23	114.82	7.59E+02	1.32E+03	3.69E+02	2.32E+03	6.33E+04	7.09E+03	7.69E+02	2.78E+03	2.75E+02	2.63E+03	9.66E+02	6.55E+02	2.29E+03	5.81E+03	5.77E+03
Q08257 QOR	VDFVGGPEVLK	611.33	115.21	6.67E+02	1.51E+03	5.96E+03	1.09E+03	1.35E+04	4.58E+03	7.72E+02	2.82E+03	6.99E+04	1.15E+04	2.12E+03	3.88E+04	7.57E+03	1.86E+04	8.65E+03
P05556-2 ITB1	SLGTDLMNEMR	633.79	115.34	2.58E+04	5.03E+02	8.63E+02	2.78E+04	1.10E+04	4.12E+03	1.13E+04	1.79E+03	2.33E+03	1.76E+03	3.82E+03	7.33E+04	1.31E+04	1.16E+03	1.46E+05
O60220 TIM8A	FIDTSQFILNR	677.36	115.76	4.37E+04	6.88E+04	9.83E+03	2.11E+04	3.31E+04	3.56E+04	8.50E+02	1.60E+03	1.32E+03	3.04E+02	1.90E+04	2.39E+04	2.36E+03	2.27E+03	5.93E+04
P23526 SAHH	ALDIAENEMPGLMR	780.39	116.07	2.30E+04	1.26E+04	9.69E+03	2.10E+04	1.54E+04	1.39E+04	9.50E+03	1.16E+04	2.21E+03	9.99E+02	7.42E+02	1.43E+04	1.87E+03	2.17E+03	3.02E+04
P50502 F10A1	AIDLFTDAIK	553.81	116.84	1.18E+03	5.26E+04	7.52E+02	2.15E+03	4.44E+02	4.65E+04	6.95E+03	4.08E+03	1.91E+03	3.09E+02	7.35E+02	1.55E+03	4.82E+03	5.37E+02	2.35E+03
Q9BYX7 ACTBM	ELTDYLMK	506.75	117.07	5.86E+03	1.38E+04	1.86E+03	3.85E+03	4.19E+02	1.58E+03	6.85E+02	5.96E+02	1.29E+05	8.03E+04	1.57E+03	3.40E+03	1.32E+03	7.99E+04	1.90E+03
Q15582 BGH3	EGVYTVFAPTNEAFR	850.92	118.07	2.13E+03	3.79E+04	1.91E+03	3.27E+02	3.07E+02	9.43E+03	8.57E+02	1.23E+03	4.05E+02	3.04E+02	1.06E+03	2.76E+03	1.67E+03	3.58E+03	2.97E+03
P11182 ODB2	ILKEDILNYLEK	497.62	118.48	2.45E+03	6.84E+02	8.81E+02	1.34E+02	2.79E+04	7.06E+02	4.19E+02	4.36E+02	2.08E+03	1.45E+02	3.69E+02	1.44E+02	8.59E+02	1.55E+02	1.42E+03
P05165 PCCA	VVEEAPSIFLDAETR	838.42	118.69	7.83E+02	1.00E+03	2.33E+03	3.78E+03	1.89E+03	3.13E+03	7.26E+04	2.20E+02	2.68E+04	1.72E+03	3.54E+03	1.07E+03	3.49E+03	1.48E+03	6.15E+02
Q16762 THTR	TYEQVLENLESK	726.86	118.79	1.93E+03	1.37E+03	1.02E+05	4.28E+03	1.64E+03	9.19E+02	1.68E+03	7.53E+02	6.31E+02	1.59E+04	3.45E+03	2.62E+03	5.44E+02	2.84E+03	6.52E+02
P36578 RL4	NIPGITLLNVSK	634.88	118.89	1.55E+03	1.31E+03	2.54E+03	7.50E+02	4.62E+04	1.28E+03	1.34E+03	9.50E+02	1.34E+03	4.77E+02	1.68E+02	4.73E+04	5.73E+02	4.24E+02	3.78E+04
P62269 RS18	IPDWFLNR	530.78	118.9	1.06E+03	2.82E+03	2.88E+04	9.06E+02	1.84E+03	7.89E+04	1.05E+03	7.55E+04	2.35E+03	1.13E+04	1.81E+03	9.46E+02	2.66E+02	1.77E+04	9.50E+02
P08574 CY1	AANNALPPDLSYIVR	835.95	119	2.66E+04	4.55E+02	2.35E+03	1.59E+04	2.36E+03	4.34E+03	4.46E+03	2.81E+03	3.12E+02	9.54E+02	8.48E+03	5.36E+02	1.90E+03	1.51E+03	4.76E+03
P15088 CBPA3	FGLLPESR	533.29	119.57	1.04E+03	1.67E+03	1.31E+03	4.35E+03	2.10E+03	5.29E+02	8.64E+02	1.56E+03	1.49E+04	3.79E+05	1.11E+03	7.13E+02	6.77E+02	2.51E+03	2.03E+03
P84077 ARF1	DAVLLVFANK	545.32	119.6	1.21E+03	8.84E+02	3.40E+03	1.70E+03	4.22E+03	4.54E+03	1.32E+03	4.44E+03	2.34E+04	6.39E+03	7.41E+02	5.08E+03	5.00E+02	1.73E+04	4.94E+02
P05155 IC1	LEDMEQALSPSVFK	797.39	119.84	1.75E+03	1.99E+03	8.02E+02	2.19E+03	3.22E+03	5.69E+02	5.50E+03	8.67E+02	7.88E+02	1.03E+03	3.88E+03	1.14E+03	4.53E+03	3.63E+03	2.60E+02
Q13418 ILK	SAVVEMLIMR	574.81	119.95	2.39E+03	2.66E+02	2.55E+03	1.06E+03	2.21E+03	1.37E+03	3.82E+04	9.88E+03	4.84E+02	7.93E+04	6.02E+02	5.86E+02	6.81E+02	2.80E+03	6.04E+02
P35237 SPB6	IAELLSPGSVDPDLTR	784.44	120.82	3.80E+04	1.35E+02	4.00E+02	9.65E+04	5.54E+03	5.98E+02	8.39E+02	1.13E+03	2.94E+04	4.22E+03	1.00E+05	9.10E+02	8.73E+04	4.	

Q9Y277 VDAC3	LTLSALIDGK	515.81	123.42	4.25E+04	8.97E+02	1.68E+02	5.85E+04	1.23E+03	2.40E+03	2.55E+03	2.15E+03	2.40E+03	1.29E+03	4.89E+04	1.38E+03	7.96E+02	3.07E+02	1.94E+03
P62424 RL7A	VPPAINQFTQALDR	785.42	123.51	1.08E+04	3.51E+03	1.89E+03	7.60E+02	3.99E+03	1.65E+03	1.56E+03	1.50E+03	9.97E+03	2.27E+04	5.55E+03	9.00E+03	1.30E+03	6.69E+03	5.71E+03
P13861 KAP2	GSFGELALMYNTPR	778.38	123.55	1.87E+03	2.55E+03	6.36E+03	2.72E+04	6.45E+02	1.29E+04	8.01E+03	1.65E+04	2.37E+04	4.29E+03	1.08E+04	1.40E+04	3.20E+03	1.02E+04	1.07E+03
P48681 NEST	DNLAEELEGVAGR	686.84	123.58	1.06E+03	5.78E+03	5.92E+03	1.17E+03	2.25E+03	3.78E+03	2.52E+03	1.29E+03	5.12E+03	3.32E+04	3.77E+04	1.27E+03	9.94E+02	9.08E+02	3.36E+03
O75208 COQ9	MLIPYIEHWPR	485.59	123.67	1.28E+03	1.44E+04	4.52E+02	1.83E+02	1.65E+03	2.38E+03	1.26E+05	6.19E+04	5.51E+02	7.27E+02	1.16E+03	1.06E+03	2.73E+02	1.69E+02	1.36E+02
Q9UBQ7 GRHPR	IAAAGLDVTSPEPLPTNHPL LTLK	823.46	124.11	1.02E+04	1.59E+03	1.67E+03	1.43E+03	2.49E+03	2.11E+04	3.71E+03	2.68E+03	4.50E+02	7.58E+03	6.78E+03	6.61E+03	4.49E+02	4.35E+02	4.45E+03
P43155-3 CACP	LPVPPLQQSLDHLYLK	583.33	124.44	2.86E+04	1.07E+04	5.01E+03	6.60E+04	6.38E+04	6.84E+02	2.54E+03	8.88E+03	3.12E+03	4.55E+03	6.95E+02	1.79E+04	3.36E+03	2.39E+04	5.78E+04
Q9Y277 VDAC3	LTLDTIFVPNTGK	709.90	124.63	7.53E+02	1.48E+03	2.73E+03	2.91E+03	2.19E+02	6.06E+02	5.68E+02	1.96E+03	1.03E+03	2.37E+04	3.01E+02	7.46E+02	2.80E+03	7.49E+02	6.31E+02
Q9BV79 MECR	VVELKNLELAA	599.85	124.78	1.41E+03	1.92E+04	7.60E+02	2.30E+02	5.35E+02	1.51E+04	9.77E+04	1.52E+05	1.41E+03	1.01E+03	1.69E+03	1.29E+03	3.30E+03	9.17E+03	8.09E+02
P04217 A1BG	TPGAAANLELIFVGPQHAG NYR	766.07	124.85	8.31E+03	6.19E+03	4.68E+03	1.29E+03	1.93E+04	2.41E+03	2.07E+03	7.18E+03	7.02E+03	1.28E+03	4.34E+03	7.20E+03	1.13E+03	2.81E+03	2.83E+03
Q9NY65 TBA8	AVMIDLEPTVVDEVR	843.44	124.93	3.19E+03	8.45E+02	1.63E+04	8.38E+04	1.38E+03	3.97E+02	1.57E+03	7.51E+03	1.54E+04	3.94E+03	9.82E+04	1.33E+04	1.24E+03	5.26E+03	2.47E+03
Q07020 RL18	ILTFDQLALDSPK	730.90	125.01	1.93E+04	2.08E+02	1.32E+03	2.99E+03	1.57E+03	5.54E+02	1.37E+03	1.54E+03	2.28E+03	4.08E+02	4.83E+04	1.05E+03	8.27E+03	1.68E+03	1.60E+03
P39019 RS19	ELAPYDENWFYTR	852.39	125.18	1.22E+04	1.66E+02	2.54E+03	8.65E+02	2.21E+03	5.97E+02	8.73E+02	1.61E+03	5.36E+02	1.38E+03	2.23E+04	3.73E+02	4.25E+02	2.27E+03	2.73E+04
O75208 COQ9	ALSILMLPH	497.79	125.45	1.17E+05	1.74E+03	2.07E+02	1.22E+04	1.24E+04	4.43E+02	7.11E+02	2.04E+03	2.88E+02	1.83E+03	1.21E+04	5.22E+04	6.33E+03	1.56E+02	7.72E+03
P04843 RPN1	SEDLDDYGPPFR	656.31	125.63	2.22E+03	1.71E+03	2.57E+03	6.26E+03	3.65E+03	8.96E+03	4.89E+02	6.26E+02	1.41E+04	8.08E+03	8.60E+02	1.28E+03	2.72E+03	1.13E+04	4.69E+03
O15230 LAMA5	DLADLAAAYTALK	632.84	126.18	3.77E+03	1.49E+04	5.02E+03	1.75E+03	2.42E+03	2.49E+04	2.72E+04	5.00E+04	5.59E+02	4.03E+02	6.24E+02	2.19E+03	9.10E+02	7.11E+02	7.48E+02
P02751-10 FINC	GATYNIIVEALK	646.36	126.35	2.72E+04	1.23E+03	3.37E+02	9.67E+02	4.16E+02	2.74E+02	1.97E+03	7.04E+02	2.91E+02	1.93E+03	6.13E+03	8.06E+03	1.23E+04	1.48E+03	3.41E+02
P04217 A1BG	LETPDFQLFK	619.33	126.54	5.20E+02	2.48E+04	2.44E+04	1.21E+03	2.20E+03	2.73E+04	2.95E+04	1.10E+04	1.03E+04	6.06E+04	6.43E+02	4.13E+03	3.32E+02	9.74E+03	6.62E+02
O75131 CPNE3	DIVQFVPPFR	560.81	127.05	7.94E+03	1.94E+03	4.25E+03	1.13E+05	5.13E+03	2.58E+03	7.23E+02	1.11E+03	2.47E+02	1.40E+04	5.94E+04	1.82E+03	2.79E+03	2.55E+03	4.25E+03
P14406 CX7A2	LFQEDDEIPLYLK	811.92	127.17	1.55E+03	7.55E+02	2.03E+03	2.26E+03	3.10E+03	6.41E+02	3.40E+03	1.69E+03	7.13E+03	8.34E+03	2.67E+02	5.05E+03	3.14E+03	2.36E+03	5.96E+04
Q16718 NDUA5	ILDVLEEIPK	584.84	127.54	2.28E+05	2.26E+03	2.76E+03	2.41E+05	1.14E+04	2.95E+02	1.55E+03	6.16E+02	1.36E+02	1.29E+03	8.50E+04	3.67E+03	2.79E+03	1.78E+03	1.34E+04
P62857 RS28	EGDVLTLLESER	680.85	127.61	7.24E+04	1.54E+03	1.50E+03	1.07E+05	6.23E+03	2.64E+02	5.95E+03	1.59E+03	2.58E+03	2.81E+03	8.75E+04	2.38E+03	6.11E+03	1.81E+03	2.45E+03
P07099 HYEP	GGHFAAFEEPPELLAQDIR	667.34	127.92	1.03E+04	8.44E+02	8.03E+02	8.81E+03	3.61E+02	7.35E+03	3.51E+04	1.76E+04	9.25E+02	5.21E+03	1.10E+03	1.25E+03	2.62E+03	9.99E+03	6.30E+02
O15273 TELT	VLPLPIFTPAK	598.37	128.36	3.26E+03	3.83E+02	6.29E+02	3.92E+05	1.37E+03	6.74E+02	4.01E+02	2.14E+03	2.85E+02	4.16E+02	4.52E+05	8.78E+03	2.14E+03	2.88E+02	3.42E+03
P07585 PGS2	DFEPSLGPVPCPFR	732.35	128.55	2.51E+03	7.51E+02	5.87E+03	2.87E+03	4.88E+02	1.08E+03	1.50E+04	2.64E+03	7.78E+03	4.12E+03	6.77E+02	5.35E+02	6.95E+03	4.29E+02	8.98E+03
P13798 ACPH	TPLLLMLGQEDR	693.37	128.71	1.75E+05	4.76E+03	2.37E+04	3.36E+05	5.54E+03	2.74E+03	1.33E+04	4.15E+03	1.51E+03	3.98E+02	6.25E+05	6.32E+03	9.48E+04	1.44E+03	1.78E+04
Q16718 NDUA5	LWEPLVEEPPADQWK	918.96	128.9	4.88E+04	6.59E+02	2.21E+03	2.48E+03	3.95E+03	4.73E+02	5.73E+03	6.94E+03	3.57E+03	1.52E+03	7.51E+03	8.82E+03	2.76E+03	1.51E+02	1.36E+04
P36776 LONM	ILEFIAVSQLR	644.88	129.07	6.54E+02	1.33E+03	5.03E+03	6.77E+02	1.91E+04	2.17E+03	3.93E+03	2.77E+02	2.64E+02	4.36E+02	4.75E+02	4.40E+03	4.04E+02	1.74E+03	8.77E+02
Q13424 SNTA1	VKDELQALLAATSTAGSQD	720.39	129.54	1.83E+02	1.67E+03	7.49E+02	2.00E+03	2.84E+03	1.88E+03	3.19E+03	7.73E+02	6.60E+02	2.30E+02	3.28E+04	7.32E+02	2.07E+02	4.90E+02	2.10E+03
O60313 OPA1	TSVLEMIAQAR	609.83	130.02	9.18E+05	8.94E+03	6.27E+02	1.61E+06	1.12E+04	8.62E+03	1.13E+03	2.87E+03	2.53E+04	1.43E+03	1.41E+06	1.21E+04	2.41E+04	1.57E+04	1.74E+04
P0C0L5 CO4B	TTNIQGINLLFSSR	782.43	130.26	2.60E+02	4.55E+02	3.60E+02	1.01E+03	6.17E+02	8.98E+02	4.42E+02	1.16E+04	6.22E+02	1.64E+04	2.34E+03	4.41E+02	7.03E+02	6.06E+02	2.28E+02
P51149 RAB7A	EAINVEQAFQTIAR	795.42	130.69	2.69E+04	1.62E+02	9.86E+02	2.02E+03	4.16E+03	4.36E+03	4.01E+03	2.05E+03	1.85E+03	1.52E+03	8.81E+03	2.34E+03	3.21E+02	1.15E+03	3.85E+03
P05166 PCCB	LVPEDTIVPLESTK	827.47	130.97	7.74E+02	8.89E+02	2.54E+03	4.36E+02	4.28E+02	2.28E+02	1.80E+02	5.24E+02	2.45E+04	3.48E+02	1.64E+03	7.33E+02	2.34E+02	2.36E+04	2.86E+02
P02760 AMBP	VVAQGVGIPEDSIFTMADR	669.01	132.09	2.35E+04	1.09E+03	3.61E+03	6.04E+03	8.19E+03	3.91E+02	4.62E+03	2.37E+03	7.44E+02	1.44E+04	5.38E+03	2.16E+03	6.58E+03	5.67E+03	7.69E+03
Q96CN7 ISOC1	ILGIPVIVTEQYPK	785.46	132.43	1.98E+03	2.38E+02	3.07E+02	2.83E+04	4.49E+02	1.41E+02	3.47E+02	1.75E+02	4.73E+02	6.58E+02	4.42E+02	4.97E+02	4.23E+02	2.15E+02	4.34E+02
Q16629 SFRS7	NPPGFAFVEFEDPR	811.39	132.73	2.67E+03	6.89E+02	7.81E+02	1.64E+03	6.52E+02	2.95E+03	4.51E+03	3.79E+03	4.54E+03	1.40E+03	2.27E+03	3.05E+03	4.18E+03	3.66E+03	5.55E+02
O75323 NIPS2	SYQLRPGTMIEWGNYWAR	743.36	132.97	2.12E+05	3.23E+04	8.65E+02	4.84E+02	1.37E+04	1.45E+04	3.46E+04	1.38E+03	2.26E+04	5.44E+03	3.24E+05	8.32E+03	1.52E+05	2.14E+04	4.00E+03
P16671 CD36	SQVLQFFSSDICR	765.37	133.66	5.95E+04	1.17E+04	5.61E+03	5.64E+04	3.90E+03	3.57E+02	1.19E+03	1.40E+03	7.54E+03	7.27E+02	2.42E+04	6.42E+03	3.45E+03	8.74E+02	1.46E+04
Q13418 ILK	FDMIVPILEK	602.83	133.82	4.79E+02	2.05E+04	6.88E+02	5.16E+02	6.42E+02	2.34E+04	4.22E+03	2.31E+04	1.39E+03	1.61E+02	3.20E+02	1.65E+03	1.06E+03	2.33E+03	6.02E+02
P23246 SFPQ	LFVGNLPADITEFEFK	904.45	134.38	4.58E+02	5.96E+02	1.04E+03	3.28E+03	3.30E+03	1.60E+04	7.67E+03	9.41E+02	2.43E+03	1.87E+03	9.23E+02	1.50E+03	2.74E+03	7.21E+03	1.39E+03
Q16363 LAMA4	LTLSELDDIHK	630.36	134.46	1.06E+03	7.62E+03	2.41E+03	1.06E+03	3.97E+03	4.13E+04	4.78E+02	3.24E+03	3.95E+03	3.49E+02	9.77E+02	5.98E+02	8.21E+02	1.26E+04	4.37E+02
O00483 NDUA4	LALFNPVCWDR	724.86	135.34	9.50E+04	3.06E+04	2.72E+03	8.85E+02	1.05E+04	1.14E+05	1.05E+04	4.53E+04	2.80E+03	8.32E+03	5.05E+05	4.20E+04	9.07E+05	9.29E+03	1.92E+05
P68366 TBA4A	AVFVDLEPTVIDEIR	858.46	135.77	2.17E+05	2.67E+05	9.42E+04	3.47E+04	2.35E+05	2.18E+05	9.23E+04	3.01E+05	2.28E+05	1.42E+05	3.75E+04	2.29E+05	2.09E+05	1.67E+05	1.73E+05

**Supplemental Table III. Normalized intensity levels of 485 proteins**

UniProte Accession	Area I No 1	Area I No 2	Area I No 3	Area I No 4	Area I No 5	Area II No 1	Area II No 2	Area II No 3	Area II No 4	Area II No 5	Control No 1	Control No 2	Control No 3	Control No 4	Control No 5
Q8WZ42-8 TITIN	3.13E+07	4.76E+07	5.52E+07	5.59E+07	4.29E+07	4.50E+07	6.24E+07	6.68E+07	3.73E+07	2.75E+07	3.80E+07	5.59E+07	5.63E+07	3.18E+07	4.84E+07
P02452 CO1A1	8.82E+04	1.07E+05	3.65E+05	6.01E+04	3.06E+04	7.80E+04	5.17E+04	3.06E+04	2.40E+04	1.08E+05	3.31E+04	3.09E+04	1.23E+05	2.48E+04	6.11E+04
P12883 MYH7	2.38E+07	4.14E+06	5.48E+06	1.91E+07	8.35E+06	7.65E+06	8.51E+06	8.53E+06	2.96E+07	4.08E+07	2.36E+07	6.08E+06	1.18E+07	1.59E+07	1.85E+07
P10916 MLRV	1.00E+07	1.76E+06	2.36E+06	3.05E+06	6.67E+06	7.79E+06	3.30E+06	3.37E+06	2.98E+07	3.07E+07	1.02E+07	4.08E+06	5.19E+06	2.24E+06	1.46E+07
Q14315-2 FLNC	6.35E+06	5.14E+06	2.86E+06	5.11E+06	5.27E+06	5.54E+06	3.50E+06	3.93E+06	4.04E+06	4.42E+06	8.49E+06	7.06E+06	6.13E+06	3.09E+06	6.78E+06
P02461 CO3A1	9.05E+02	2.01E+03	7.42E+04	1.03E+03	2.63E+03	1.19E+04	1.31E+04	1.85E+04	4.08E+03	1.08E+03	8.04E+03	1.83E+03	7.88E+03	1.82E+03	6.95E+03
P02768 ALBU	2.49E+07	1.79E+07	1.95E+07	1.43E+07	1.89E+07	1.66E+07	1.30E+07	7.86E+06	4.04E+07	5.07E+07	2.83E+07	1.15E+07	1.04E+07	4.50E+07	1.45E+07
P17661 DESM	1.07E+07	2.86E+06	5.16E+06	1.01E+07	6.04E+06	9.98E+06	2.62E+06	2.81E+06	1.30E+07	7.98E+06	1.39E+07	4.59E+06	1.63E+07	1.05E+07	1.48E+07
P08590 MYL3	7.68E+06	3.50E+06	4.04E+06	9.70E+06	3.49E+06	2.99E+06	3.16E+06	2.85E+06	2.37E+07	2.28E+07	8.76E+06	3.27E+06	3.55E+06	2.47E+07	8.96E+06
Q14896 MYPC3	9.69E+06	9.27E+06	5.07E+06	9.57E+06	9.18E+06	6.45E+06	5.92E+06	3.38E+06	4.18E+06	2.15E+06	1.05E+07	7.47E+06	1.29E+07	4.32E+06	1.29E+07
P25705 ATPA	8.50E+06	8.66E+06	7.22E+06	8.97E+06	5.97E+06	5.18E+06	2.25E+07	3.09E+07	3.00E+06	3.75E+06	9.47E+06	1.27E+07	1.73E+07	2.25E+06	8.61E+06
P35609 ACTN2	1.84E+07	3.69E+06	2.23E+06	6.56E+06	9.02E+06	3.06E+06	3.02E+06	3.08E+06	8.27E+06	1.48E+07	1.65E+07	5.38E+06	8.23E+06	9.28E+06	1.04E+07
P12111-2 CO6A3	2.24E+06	1.14E+06	1.66E+06	2.50E+06	2.34E+06	2.27E+06	4.02E+06	2.86E+06	2.26E+06	2.38E+06	2.49E+06	1.01E+06	2.58E+06	2.42E+06	2.67E+06
P06576 ATPB	1.52E+07	1.14E+07	7.75E+06	1.04E+07	1.37E+07	6.72E+06	7.51E+06	1.04E+07	4.43E+06	3.10E+06	1.02E+07	1.71E+07	1.95E+07	5.96E+06	1.17E+07
P54296 MYOM2	2.10E+06	2.46E+06	1.48E+06	2.96E+06	1.72E+06	1.93E+06	1.62E+06	1.41E+06	1.16E+06	7.67E+05	2.78E+06	2.00E+06	2.11E+06	1.63E+06	3.08E+06
P68871 HBB	5.37E+06	7.98E+06	1.40E+06	1.28E+07	2.21E+07	1.65E+07	8.94E+05	1.04E+06	2.11E+06	4.53E+05	1.46E+07	3.89E+06	2.07E+06	3.69E+05	9.11E+06
P69905 HBA	8.95E+06	3.10E+07	4.33E+06	1.52E+07	2.43E+07	2.22E+07	6.27E+06	2.77E+07	7.48E+06	1.19E+07	4.76E+06	2.86E+07	1.11E+06	1.43E+07	9.64E+06
P68133 ACTS	4.01E+05	9.12E+03	3.41E+04	1.54E+05	1.21E+05	1.30E+04	2.49E+06	4.26E+04	4.50E+04	2.55E+04	6.41E+05	3.04E+04	1.01E+05	9.76E+04	3.01E+05
P09493 TPM1	1.28E+06	2.20E+04	1.21E+05	9.41E+05	4.08E+04	9.13E+04	1.02E+04	3.67E+04	1.01E+05	5.05E+04	9.57E+05	1.94E+04	2.18E+04	4.82E+04	3.17E+04
P02144 MYG	1.54E+07	2.19E+06	3.60E+05	4.23E+06	3.57E+06	1.77E+05	2.63E+05	4.00E+05	3.06E+05	1.56E+05	8.69E+06	3.61E+05	1.01E+06	2.10E+05	1.41E+07
P45379 TNNT2	9.38E+06	9.43E+06	3.38E+06	8.66E+06	5.51E+06	8.36E+06	8.80E+06	3.85E+06	2.86E+06	1.40E+06	8.33E+06	9.48E+06	7.15E+06	4.54E+06	4.86E+06
P02511 CRYAB	1.57E+06	2.20E+06	4.68E+06	1.86E+06	3.89E+05	3.10E+06	1.54E+06	4.36E+05	4.82E+06	1.95E+06	1.86E+06	1.29E+06	7.25E+05	4.16E+06	1.32E+06
P06732 KCRM	6.42E+06	1.01E+07	1.42E+07	8.71E+06	9.07E+06	1.74E+07	1.27E+07	3.60E+06	4.37E+06	5.36E+06	4.86E+06	1.43E+07	1.02E+07	4.72E+06	1.13E+07
P08123 CO1A2	5.07E+05	1.77E+06	3.39E+05	7.32E+05	5.03E+05	7.37E+04	4.77E+05	6.84E+05	4.07E+04	1.46E+05	3.51E+05	9.20E+05	2.70E+04	4.12E+04	9.17E+05
P04075 ALDOA	1.51E+06	2.15E+06	1.05E+06	3.08E+06	2.75E+06	5.71E+06	3.56E+06	1.12E+06	1.43E+06	5.00E+06	1.85E+06	1.76E+06	1.76E+06	4.56E+06	2.72E+06
Q99798 ACON	5.67E+06	1.65E+06	2.52E+06	3.71E+06	4.23E+06	2.65E+06	1.76E+06	2.15E+06	3.22E+06	2.66E+06	3.11E+06	1.85E+06	2.96E+06	1.62E+06	3.98E+06
P17540 KCRS	3.34E+06	7.19E+05	6.47E+05	3.01E+06	1.98E+06	7.94E+05	9.72E+05	2.78E+06	1.80E+06	1.23E+05	2.06E+06	1.54E+06	7.48E+05	4.45E+05	7.26E+05
P16615-2 AT2A2	1.37E+06	1.56E+06	1.07E+06	1.37E+06	1.42E+06	2.67E+06	9.15E+05	1.18E+06	9.17E+05	1.16E+06	1.17E+06	1.21E+06	9.84E+05	1.00E+06	1.98E+06
P02545-2 LMNA	1.14E+07	1.36E+07	3.62E+06	8.49E+06	5.02E+06	2.01E+06	9.63E+06	4.07E+06	1.94E+06	1.33E+06	5.27E+06	6.49E+06	1.31E+06	2.70E+06	7.96E+05
Q15149-3 PLEC1	6.62E+05	1.66E+06	3.53E+06	1.95E+06	3.03E+06	3.32E+06	7.21E+06	7.62E+06	1.40E+06	1.33E+06	2.63E+06	3.85E+06	3.62E+06	1.37E+06	1.07E+06
P48735 IDHP	2.01E+06	2.53E+06	4.82E+05	1.23E+06	2.75E+06	3.73E+06	2.53E+05	7.15E+05	1.03E+06	4.86E+05	1.73E+06	1.19E+06	2.38E+06	2.06E+06	3.03E+06
P52179-2 MYOM1	9.67E+05	1.76E+06	3.14E+05	1.18E+06	1.23E+06	9.03E+05	1.46E+06	1.02E+06	2.07E+06	1.10E+06	1.86E+06	1.45E+06	1.75E+06	2.03E+06	1.83E+06
P98160 PGBM	5.04E+05	1.71E+06	1.89E+06	1.35E+06	1.24E+06	1.04E+06	8.51E+05	1.56E+06	1.65E+06	5.23E+05	1.30E+06	1.61E+06	2.01E+06	1.02E+06	1.47E+06
Q13813-3 SPTA2	1.26E+06	1.66E+06	1.72E+06	1.63E+06	1.16E+06	1.74E+06	1.49E+06	2.47E+06	1.02E+06	6.08E+05	1.13E+06	1.18E+06	1.85E+06	7.80E+05	1.31E+06
P02787 TRFE	1.51E+06	7.42E+05	2.60E+06	9.84E+05	1.17E+06	1.17E+06	1.48E+06	6.25E+05	9.20E+05	1.32E+06	1.21E+06	1.06E+06	6.67E+05	9.57E+05	6.54E+05
Q13423 NNTM	2.01E+06	1.27E+06	1.04E+06	1.51E+06	1.34E+06	4.07E+05	1.53E+06	6.39E+05	1.44E+06	9.44E+05	1.34E+06	1.72E+06	1.32E+06	1.60E+06	1.54E+06
P15924 DESP	6.98E+05	1.64E+06	1.79E+06	1.51E+06	1.41E+06	2.84E+06	1.84E+06	1.67E+06	1.42E+06	1.22E+06	1.18E+06	1.71E+06	1.39E+06	3.73E+06	1.69E+06
P22695 QCR2	8.77E+05	7.35E+05	1.34E+06	6.13E+05	1.45E+06	1.24E+06	8.88E+05	6.63E+05	1.40E+06	6.69E+05	5.73E+05	1.03E+06	2.70E+05	1.09E+06	7.16E+05
O75112 LDB3	8.85E+05	1.13E+06	9.56E+05	1.79E+06	1.23E+05	8.28E+05	4.58E+05	5.63E+05	1.18E+06	1.83E+06	8.95E+05	3.65E+05	7.36E+05	9.29E+05	5.45E+05
P00505 AATM	4.00E+06	2.60E+06	1.12E+06	2.58E+06	2.93E+06	3.55E+06	4.03E+06	1.39E+06	4.65E+05	6.52E+05	2.87E+06	2.95E+06	2.41E+06	7.70E+05	2.39E+06
P18206-2 VINC	3.58E+06	6.23E+06	2.73E+06	5.85E+06	1.21E+07	4.95E+06	7.67E+06	1.31E+06	8.64E+05	1.10E+06	7.07E+06	6.57E+06	1.37E+07	9.38E+05	6.31E+06
Q02218 ODO1	2.13E+06	9.32E+05	3.81E+05	6.81E+05	7.04E+05	5.52E+05	9.14E+05	6.96E+05	9.89E+05	9.83E+05	1.89E+06	1.13E+06	1.53E+06	7.31E+05	1.21E+06

O94875-3 SRBS2	2.41E+05	2.22E+05	5.22E+04	2.19E+05	1.05E+05	3.05E+04	9.83E+03	1.23E+04	1.06E+04	1.65E+04	3.45E+05	2.28E+05	1.90E+05	2.66E+04	2.27E+05
P04406 G3P	3.28E+06	2.90E+06	2.77E+06	4.11E+06	2.62E+06	7.47E+06	3.54E+06	5.43E+06	8.34E+05	6.75E+05	1.92E+06	3.34E+06	8.09E+05	8.91E+05	2.14E+06
Q5VTT5 MYOM3	6.78E+05	5.71E+05	5.09E+05	7.32E+05	7.78E+05	9.36E+05	3.29E+06	8.97E+05	6.15E+05	8.02E+05	8.07E+05	1.06E+06	1.52E+06	7.30E+05	9.58E+05
P11142 HSP7C	6.48E+05	6.79E+05	7.66E+05	3.53E+05	8.14E+05	8.18E+05	2.26E+05	4.80E+05	7.94E+04	4.72E+04	6.39E+05	1.01E+06	8.80E+05	1.77E+05	7.06E+05
P60174 TPIS	1.12E+06	1.36E+05	1.74E+05	3.88E+05	3.76E+05	2.61E+05	3.14E+05	3.74E+05	2.03E+05	7.61E+04	1.38E+06	2.22E+05	3.78E+05	1.96E+05	5.30E+05
O75390 CISY	2.85E+05	2.37E+06	2.22E+05	5.77E+05	2.62E+06	6.22E+05	2.23E+05	2.95E+05	8.78E+05	5.63E+05	5.33E+05	1.84E+06	2.06E+06	7.33E+05	1.52E+06
P09622 DLDH	4.96E+05	2.17E+06	1.10E+06	6.57E+05	6.73E+05	1.59E+06	1.95E+06	2.74E+06	1.69E+06	1.38E+06	5.12E+05	1.11E+06	9.15E+05	7.83E+05	5.98E+05
P14923 PLAK	1.82E+05	4.16E+05	3.88E+05	6.31E+05	3.74E+05	7.26E+05	1.27E+05	1.48E+05	4.18E+05	5.40E+05	3.13E+05	4.18E+05	3.34E+05	5.86E+05	2.73E+05
P13929 ENOB	4.27E+05	6.07E+05	5.67E+05	1.73E+05	3.10E+05	7.81E+05	4.34E+05	5.10E+05	1.60E+06	1.58E+06	4.94E+05	4.99E+05	2.46E+05	1.22E+06	4.36E+05
P08238 HS90B	6.87E+04	9.90E+04	3.46E+04	7.75E+04	3.22E+05	8.02E+04	1.94E+04	6.72E+04	2.49E+05	4.34E+05	1.87E+05	2.46E+05	1.00E+05	2.03E+06	2.49E+05
P08670 VIME	1.70E+06	6.50E+05	2.24E+05	1.19E+06	5.70E+05	1.46E+05	3.32E+05	2.24E+05	3.44E+05	2.15E+06	9.99E+05	7.39E+05	1.32E+06	3.47E+05	1.51E+06
P55084 ECHB	4.52E+06	9.61E+06	1.19E+07	9.03E+05	3.71E+06	6.76E+06	1.41E+06	2.60E+06	1.59E+06	7.62E+05	1.50E+06	5.58E+06	8.05E+06	8.34E+05	1.97E+06
P31930 QCR1	2.88E+06	3.11E+06	5.20E+05	1.64E+06	2.33E+06	8.88E+05	1.38E+06	7.61E+05	1.32E+06	1.28E+06	1.70E+06	2.79E+06	2.72E+06	1.54E+06	1.30E+06
P55072 TERA	3.94E+05	2.06E+05	2.32E+05	1.72E+05	8.96E+04	1.60E+05	2.72E+05	1.25E+06	1.26E+05	2.62E+05	3.04E+05	1.15E+05	5.49E+05	3.31E+05	1.38E+05
P40926 MDHM	2.80E+06	5.35E+05	2.07E+05	1.39E+06	3.00E+05	1.35E+05	3.25E+05	4.69E+05	5.81E+06	3.30E+06	1.81E+06	2.03E+05	9.17E+05	4.41E+06	1.18E+06
Q01082-3 SPTB2	1.05E+06	6.31E+05	1.76E+05	5.68E+05	2.99E+05	1.46E+06	4.75E+05	7.67E+05	2.13E+05	1.84E+05	9.68E+05	4.36E+05	1.00E+06	3.39E+05	6.11E+05
P19367-4 H XK1	1.43E+06	1.28E+06	2.94E+06	6.84E+05	6.57E+05	7.40E+05	1.88E+06	2.54E+06	5.16E+05	3.30E+05	1.65E+06	8.73E+05	1.76E+06	5.89E+05	7.87E+05
Q99959-2 PKP2	5.59E+05	3.35E+05	2.74E+05	8.49E+05	3.40E+05	3.52E+05	4.89E+05	8.09E+05	4.51E+05	3.53E+05	1.17E+06	4.60E+05	3.88E+05	5.14E+05	5.37E+05
P35555 FBN1	4.11E+05	1.15E+05	9.49E+04	1.52E+05	8.19E+04	2.97E+04	8.72E+04	3.72E+05	3.48E+05	4.95E+05	4.19E+05	1.00E+05	6.34E+05	3.47E+05	1.90E+05
P01024 CO3	6.87E+04	1.03E+06	1.54E+06	1.08E+05	2.48E+05	1.07E+05	1.20E+06	8.46E+04	5.18E+05	1.20E+06	6.81E+04	1.91E+05	1.44E+05	4.98E+05	1.16E+05
P40939 ECHA	9.34E+05	1.47E+06	4.83E+05	8.06E+05	2.23E+06	1.23E+06	2.56E+06	2.13E+06	1.31E+06	1.25E+06	9.95E+05	1.29E+06	1.61E+06	6.71E+05	1.22E+06
P06396-2 GELS	3.68E+05	3.69E+05	5.10E+05	2.11E+05	2.30E+05	3.66E+05	1.67E+05	3.03E+05	1.45E+05	2.15E+05	5.03E+05	2.56E+05	3.08E+05	2.63E+05	3.27E+05
P07195 LDHB	2.30E+06	1.45E+06	6.36E+05	2.00E+06	1.87E+06	1.75E+06	1.59E+06	1.56E+06	5.56E+05	1.06E+06	2.21E+06	1.62E+06	1.47E+06	1.09E+06	2.60E+06
P40925 MDHC	8.34E+05	4.47E+05	1.07E+06	1.10E+06	1.18E+06	1.84E+06	7.96E+05	1.39E+06	3.16E+06	2.60E+06	4.87E+05	2.18E+06	1.38E+06	2.18E+06	2.72E+06
P08559 ODPA	4.86E+05	1.39E+06	4.39E+05	8.84E+05	1.09E+06	1.24E+06	8.25E+05	4.36E+05	7.57E+05	6.71E+05	4.89E+05	8.73E+05	2.14E+06	1.06E+06	8.82E+05
P11532-4 DMD	5.60E+05	1.32E+06	1.91E+06	3.91E+05	3.86E+05	1.14E+06	1.06E+06	4.60E+05	5.40E+05	5.41E+05	6.77E+05	1.37E+06	1.23E+06	1.64E+06	5.63E+05
O76041 NEBL	1.02E+06	3.36E+06	3.39E+06	1.31E+06	5.42E+05	1.58E+06	2.89E+06	9.92E+05	4.74E+05	1.15E+05	8.92E+05	2.37E+06	8.92E+05	7.55E+05	1.05E+06
P24043 LAMA2	1.59E+05	2.20E+05	3.34E+05	2.91E+05	8.98E+05	2.16E+05	1.02E+06	1.33E+06	3.23E+05	3.46E+05	2.90E+05	2.21E+05	2.91E+05	5.22E+05	3.06E+05
P11047 LAMC1	5.39E+05	1.91E+06	5.10E+05	3.08E+05	7.94E+05	4.24E+05	1.54E+05	5.75E+05	1.85E+06	2.75E+05	1.79E+06	1.27E+06	1.56E+06	1.24E+06	1.93E+06
P24752 THIL	5.77E+05	8.29E+05	2.38E+06	1.59E+06	6.47E+06	4.24E+06	3.97E+06	3.00E+06	1.27E+06	1.02E+06	3.12E+05	9.42E+05	4.10E+06	1.22E+06	5.24E+05
P17174 AATC	2.12E+06	3.16E+06	9.06E+05	3.07E+06	2.07E+06	4.11E+06	1.33E+06	1.35E+06	1.09E+06	1.22E+06	2.96E+06	3.38E+06	6.12E+06	1.13E+06	5.82E+06
P11021 GRP78	3.48E+05	8.30E+05	2.19E+06	9.28E+04	2.64E+05	5.27E+05	4.32E+05	1.04E+06	8.53E+05	1.01E+06	3.19E+05	4.13E+05	1.48E+05	8.94E+05	1.67E+05
P01857 IGHG1	2.13E+06	2.10E+05	9.31E+04	6.58E+04	1.22E+06	6.62E+05	3.47E+05	4.72E+05	2.32E+05	5.93E+05	4.96E+05	1.23E+05	3.70E+05	2.76E+05	1.71E+05
P08237 K6PF	3.31E+05	9.05E+04	1.51E+05	5.79E+05	4.54E+05	9.90E+04	1.74E+05	7.53E+05	3.21E+05	5.21E+05	3.11E+05	5.75E+05	4.62E+05	5.58E+05	7.65E+05
P04792 HSPB1	9.25E+05	1.08E+06	7.43E+05	1.18E+06	1.24E+06	2.18E+06	3.64E+05	9.28E+05	1.17E+06	1.55E+06	9.69E+05	4.51E+06	1.89E+06	1.32E+06	2.09E+06
P08572 CO4A2	5.86E+05	2.22E+05	5.41E+05	5.32E+05	3.16E+05	1.84E+05	2.02E+05	9.00E+04	1.31E+05	1.89E+05	4.39E+05	2.48E+05	2.36E+05	2.50E+04	5.68E+05
P55268 LAMB2	6.97E+05	1.50E+06	7.28E+05	1.35E+06	1.09E+06	1.01E+06	1.76E+06	1.72E+06	1.70E+06	1.13E+06	1.24E+06	1.67E+06	1.41E+06	1.32E+06	7.92E+05
P19429 TNNI3	3.42E+06	5.26E+06	4.91E+05	6.30E+06	3.42E+06	2.99E+05	4.04E+05	2.22E+05	1.83E+05	7.89E+04	3.93E+06	1.49E+06	2.50E+06	2.46E+05	4.95E+06
Q9NPC6 MYOZ2	7.92E+05	1.15E+06	6.29E+05	1.34E+06	7.64E+05	2.10E+05	1.30E+06	1.69E+05	4.55E+05	5.91E+05	1.01E+06	2.79E+06	2.65E+05	6.77E+05	1.32E+06
P08107 HSP71	4.06E+05	3.59E+05	4.38E+05	3.23E+05	4.57E+05	2.04E+05	4.75E+05	8.67E+05	2.45E+05	8.52E+05	6.04E+05	6.22E+05	1.01E+05	3.18E+05	5.07E+05
P05413 FABPH	8.46E+05	8.23E+05	3.91E+05	9.85E+05	3.52E+05	4.59E+05	4.25E+05	1.01E+06	1.35E+06	1.57E+06	1.17E+06	1.27E+06	1.59E+06	1.80E+06	8.63E+05
P00558 PGK1	1.27E+06	1.72E+06	1.38E+06	1.17E+06	6.26E+05	9.78E+05	2.24E+06	1.24E+06	3.25E+05	6.73E+05	1.04E+06	1.52E+06	1.81E+06	4.07E+05	1.44E+06
Q96HC4 PDLI5	7.85E+04	1.08E+04	4.39E+05	3.16E+04	5.21E+04	1.19E+04	4.53E+05	6.83E+05	1.57E+04	1.78E+04	6.05E+04	2.30E+04	2.03E+04	2.02E+04	6.87E+03
P11216 PYGB	3.76E+05	1.06E+05	2.35E+05	4.09E+05	5.48E+05	1.16E+05	4.60E+06	4.33E+06	1.72E+06	9.22E+05	4.61E+05	3.33E+05	8.05E+05	1.97E+06	3.89E+05
P28331 NDUS1	8.56E+05	9.62E+05	9.05E+05	9.02E+05	1.04E+06	8.70E+05	1.58E+06	3.32E+06	1.90E+06	7.13E+05	5.17E+05	1.54E+06	7.04E+05	8.23E+06	5.94E+05
P63261 ACTG	8.43E+05	8.28E+06	1.74E+07	8.75E+06	7.30E+06	8.93E+06	2.93E+05	3.06E+05	4.77E+04	3.81E+04	2.15E+06	5.21E+06	1.31E+06	8.23E+04	2.10E+06
P11177 ODPB	1.48E+06	1.19E+06	1.80E+06	1.19E+06	1.03E+06	2.21E+06	1.51E+06	1.79E+06	2.08E+06	2.26E+06	1.24E+06	6.58E+05	8.60E+05	1.64E+06	1.31E+06



P68371 TBB2C	1.72E+06	4.56E+05	1.49E+05	3.06E+05	2.37E+05	2.09E+06	1.78E+05	1.76E+06	2.80E+04	2.36E+04	5.72E+05	4.93E+05	3.35E+05	3.21E+04	2.35E+05
Q71U36 TBA1A	4.42E+05	2.00E+05	7.61E+04	3.31E+05	1.59E+05	4.37E+05	1.13E+05	1.23E+05	1.09E+05	6.25E+04	4.96E+05	2.21E+05	3.53E+05	2.71E+04	2.69E+05
P12235 ADT1	6.50E+05	9.41E+05	2.20E+05	1.35E+06	1.51E+06	1.18E+06	2.89E+05	8.72E+04	2.11E+05	4.05E+05	1.09E+06	7.18E+05	6.79E+05	1.25E+05	1.48E+06
Q562R1 ACTBL	3.93E+03	1.39E+06	3.36E+04	1.23E+06	1.29E+06	2.61E+04	1.37E+04	1.11E+04	8.68E+04	2.18E+03	2.06E+03	1.17E+06	1.14E+06	1.48E+04	1.29E+06
P47985 UCRI	2.02E+05	4.54E+05	1.19E+05	1.99E+05	4.92E+05	5.86E+05	8.04E+05	2.92E+05	8.69E+04	2.23E+04	4.96E+05	5.60E+05	3.32E+05	6.83E+04	1.98E+05
Q9BX66-11 SRBS1	2.45E+05	1.36E+06	7.20E+05	1.10E+06	2.46E+05	1.88E+06	7.02E+05	6.31E+05	2.04E+05	1.18E+05	1.78E+05	6.12E+05	1.38E+06	4.65E+05	6.53E+05
P23327 SRCH	4.31E+05	3.36E+05	3.17E+05	2.73E+05	3.15E+05	7.83E+05	6.37E+04	7.37E+04	2.68E+05	7.84E+04	3.96E+05	4.75E+05	9.39E+04	1.15E+05	6.13E+05
P10809 CH60	2.23E+05	3.51E+05	6.09E+05	7.07E+04	5.25E+05	3.58E+05	5.88E+05	2.63E+05	1.14E+05	2.04E+05	1.59E+05	1.34E+05	2.13E+05	1.04E+05	1.42E+05
P36871 PGM1	2.84E+05	5.15E+04	5.05E+04	1.37E+05	1.76E+05	2.17E+04	6.38E+04	6.13E+04	5.91E+05	2.93E+05	3.53E+05	3.33E+04	6.36E+04	6.76E+05	2.82E+05
P20674 COX5A	6.99E+05	9.17E+05	1.11E+06	5.15E+05	7.35E+05	6.80E+05	4.85E+05	8.40E+05	6.70E+05	2.58E+05	7.66E+05	9.64E+05	9.67E+05	5.47E+05	8.96E+05
P02790 HEMO	2.34E+05	2.66E+05	3.03E+05	1.68E+05	3.37E+05	4.68E+05	8.54E+04	5.49E+04	2.19E+05	3.57E+05	2.40E+05	2.78E+05	1.23E+05	6.42E+04	1.41E+05
P01009 A1AT	3.36E+05	6.08E+05	2.46E+05	3.89E+05	3.35E+05	6.38E+05	5.74E+05	6.93E+05	7.11E+05	1.19E+06	1.38E+05	3.68E+05	8.47E+05	6.03E+05	4.63E+05
P02462 CO4A1	5.67E+04	1.45E+05	1.27E+05	6.77E+04	1.26E+05	4.49E+04	4.49E+04	6.20E+04	1.84E+05	7.57E+04	2.13E+05	8.90E+04	1.19E+05	6.17E+04	1.81E+05
P12829 MYL4	7.39E+05	3.23E+06	4.61E+06	3.19E+06	4.02E+05	4.76E+05	9.84E+05	2.70E+05	4.71E+05	1.07E+05	1.46E+06	2.46E+06	3.55E+06	1.14E+05	1.34E+06
Q9H987 SYP2L	1.37E+05	1.97E+05	1.28E+05	2.87E+05	1.50E+05	1.98E+05	1.41E+05	8.57E+04	1.12E+05	1.54E+05	2.00E+05	6.51E+05	1.63E+05	4.99E+05	8.39E+04
P12110 CO6A2	4.82E+05	4.16E+05	2.67E+05	4.05E+05	5.52E+05	2.69E+05	1.07E+05	4.79E+04	3.70E+06	1.45E+06	7.30E+05	3.07E+05	4.54E+05	1.03E+06	8.13E+05
P21980 TGM2	7.26E+04	7.61E+04	1.05E+05	2.77E+05	3.88E+05	4.17E+05	1.57E+05	3.44E+05	2.09E+05	2.06E+05	2.80E+05	2.53E+05	1.22E+05	1.67E+05	3.10E+05
Q16891-2 IMMT	6.01E+05	2.72E+06	6.73E+06	3.06E+05	3.08E+06	2.89E+06	4.77E+06	1.23E+06	2.91E+05	3.65E+05	7.46E+05	3.20E+06	3.86E+05	5.71E+04	4.48E+05
P32119 PRDX2	1.34E+05	1.50E+06	1.44E+06	1.34E+06	8.76E+05	5.89E+05	1.59E+06	1.01E+06	5.78E+04	2.52E+05	1.87E+05	1.06E+06	7.46E+05	1.31E+05	9.23E+05
P49411 EFTU	8.51E+05	1.23E+06	2.40E+05	8.09E+05	7.61E+05	6.00E+05	6.57E+05	6.90E+05	1.74E+06	8.46E+05	1.14E+06	8.20E+05	1.17E+06	1.02E+06	8.12E+05
P30086 PEBP1	9.78E+04	1.82E+05	4.89E+04	4.14E+04	1.20E+05	1.77E+05	6.01E+05	4.87E+05	1.16E+05	7.58E+04	2.97E+04	1.98E+05	2.86E+05	2.55E+04	2.78E+05
P49821 NDUV1	5.41E+05	5.43E+05	1.64E+05	4.66E+05	2.33E+05	2.37E+05	8.81E+05	1.14E+06	1.51E+05	2.95E+05	3.02E+05	3.44E+05	4.73E+05	6.20E+04	5.02E+05
P38117-2 ETFB	1.21E+06	1.04E+06	1.00E+05	5.49E+05	9.48E+05	2.59E+05	1.18E+05	2.75E+05	7.43E+05	6.50E+04	1.12E+06	1.36E+06	5.33E+05	5.94E+05	1.01E+06
P35579 MYH9	3.01E+04	7.10E+04	8.92E+05	6.66E+04	1.19E+05	2.10E+05	2.35E+06	2.51E+06	5.45E+06	2.67E+06	3.17E+04	1.27E+05	2.94E+05	7.67E+06	7.98E+04
P13073 COX41	4.91E+05	5.41E+05	1.54E+06	1.44E+06	1.80E+06	1.40E+06	1.25E+06	1.19E+06	7.67E+05	1.12E+05	1.77E+05	1.07E+06	2.37E+05	1.74E+05	1.48E+06
P55290 CAD13	2.35E+05	3.34E+05	9.86E+04	2.45E+05	4.82E+05	4.84E+05	1.22E+05	1.18E+05	2.78E+04	4.59E+04	2.06E+05	4.92E+05	2.32E+05	8.36E+04	2.38E+05
P31040 DHSA	5.84E+05	2.88E+05	3.43E+05	2.56E+05	4.19E+05	1.67E+05	6.45E+05	2.88E+05	2.51E+05	1.73E+05	5.69E+05	3.97E+05	1.52E+05	2.53E+05	6.13E+05
P00568 KAD1	2.44E+05	1.65E+05	8.57E+05	1.60E+05	3.74E+05	9.15E+05	1.38E+06	1.97E+06	2.40E+05	6.90E+05	2.62E+05	2.84E+05	1.89E+06	7.16E+05	1.23E+05
O15061-2 SYNEM	3.55E+05	1.48E+05	1.62E+05	1.34E+05	4.11E+05	1.68E+05	1.59E+05	3.31E+05	8.86E+05	2.91E+05	4.99E+05	1.90E+05	5.49E+05	9.27E+05	1.15E+05
P07108 ACBP	3.21E+05	2.11E+05	2.73E+04	6.80E+04	2.54E+05	1.63E+05	2.42E+05	4.25E+04	5.39E+05	5.36E+05	2.16E+05	1.55E+05	5.70E+04	5.02E+05	1.24E+05
P13804 ETFA	3.75E+05	6.34E+05	6.88E+04	2.24E+05	5.67E+05	5.34E+05	1.12E+05	8.78E+04	1.32E+04	1.79E+04	3.78E+05	6.74E+05	1.34E+05	8.45E+04	5.03E+05
Q86TD4 SRCA	4.73E+05	2.62E+05	5.75E+05	8.07E+05	2.06E+05	4.75E+05	3.04E+05	5.66E+05	6.37E+04	5.79E+04	4.26E+05	5.77E+05	2.67E+05	5.62E+04	4.27E+05
P55809 SCOT1	1.55E+05	1.03E+05	6.19E+04	3.17E+04	1.72E+05	2.28E+05	2.45E+05	1.98E+05	2.61E+05	4.81E+05	2.31E+05	1.52E+05	1.93E+05	2.83E+05	1.26E+05
P14543-2 NID1	2.75E+04	4.80E+05	1.31E+05	7.99E+04	1.83E+05	1.18E+05	4.05E+04	1.89E+05	1.18E+05	6.00E+04	2.65E+05	4.95E+05	1.20E+05	2.06E+05	3.56E+05
P19022 CADH2	3.31E+05	2.25E+05	1.31E+05	3.06E+05	2.47E+05	1.80E+05	2.05E+05	3.82E+05	1.60E+05	8.78E+04	2.17E+05	2.55E+05	3.89E+05	2.90E+06	2.22E+05
P08133 ANXA6	2.33E+05	1.06E+05	2.91E+05	1.87E+05	1.79E+05	2.75E+05	6.19E+05	6.62E+05	6.49E+05	3.45E+05	1.68E+05	2.41E+05	3.95E+05	6.48E+05	1.64E+05
P07237 PDIA1	3.17E+05	1.66E+05	1.12E+04	9.01E+04	1.06E+05	1.54E+05	4.96E+03	1.64E+04	2.08E+04	3.04E+04	2.72E+05	1.21E+05	1.83E+05	1.47E+04	1.05E+05
P38646 GRP75	5.24E+05	9.67E+04	1.19E+05	3.55E+05	4.67E+05	1.46E+05	1.40E+05	2.46E+05	1.32E+05	7.13E+05	3.40E+05	6.44E+05	2.74E+05	4.89E+05	2.80E+05
P63316 TNNC1	1.15E+06	6.44E+05	1.34E+06	2.53E+05	6.06E+05	1.01E+06	2.80E+05	2.78E+05	2.30E+06	2.74E+06	5.35E+05	6.10E+05	1.26E+06	8.73E+05	9.89E+05
P02675 FIBB	2.71E+05	1.50E+05	1.68E+05	1.62E+05	7.19E+05	4.21E+05	7.43E+05	1.72E+05	1.57E+05	1.01E+06	8.72E+04	2.42E+05	2.81E+04	1.26E+05	2.54E+04
P12109 CO6A1	5.43E+05	3.71E+05	4.40E+05	8.72E+05	9.75E+05	9.23E+05	2.64E+05	6.32E+04	2.12E+05	3.06E+05	5.19E+05	6.56E+05	7.17E+05	3.17E+05	6.76E+05
P09972 ALDOC	1.32E+06	1.01E+06	1.52E+06	1.01E+06	2.29E+05	7.35E+05	6.82E+05	1.24E+06	4.77E+05	5.69E+05	9.74E+05	4.80E+05	5.03E+05	4.29E+05	5.59E+05
P00403 COX2	2.48E+05	6.49E+06	8.12E+06	3.72E+05	4.52E+06	5.56E+06	8.78E+06	7.85E+05	8.42E+05	5.85E+05	2.93E+05	6.79E+06	2.80E+05	4.22E+05	3.64E+06
Q6NZI2 PTRF	4.78E+05	7.26E+04	6.39E+04	1.23E+05	2.16E+05	1.44E+04	6.66E+04	4.48E+04	4.83E+05	4.33E+05	4.62E+05	3.82E+05	2.04E+05	3.96E+05	2.20E+05
P01023 A2MG	6.98E+04	1.46E+05	1.83E+05	1.15E+05	4.13E+05	9.45E+04	2.52E+05	1.31E+05	7.36E+05	1.43E+06	1.02E+05	1.18E+06	2.68E+05	5.74E+05	6.73E+04
P42765 THIM	3.79E+05	8.41E+05	1.20E+05	6.05E+05	1.49E+06	6.56E+05	1.14E+06	1.79E+05	4.27E+05	4.23E+04	5.90E+05	1.68E+06	4.37E+05	1.25E+06	1.31E+06
Q702N8 XIRP1	2.88E+05	4.98E+05	1.97E+05	1.85E+05	2.12E+05	4.82E+05	5.57E+05	4.38E+05	3.41E+05	1.11E+05	4.77E+05	7.17E+05	6.80E+04	2.61E+05	4.42E+05

P07355-2 ANXA2	2.53E+04	2.04E+05	1.48E+05	3.92E+05	4.05E+05	4.54E+05	3.17E+05	1.24E+05	8.94E+04	5.14E+04	1.55E+05	1.70E+05	1.49E+05	2.43E+05	2.82E+05
P00367 DHE3	2.20E+05	1.51E+05	1.08E+05	8.19E+04	4.25E+04	1.64E+04	2.53E+05	1.54E+05	3.44E+05	2.10E+05	8.24E+04	8.37E+04	8.06E+04	4.91E+05	5.92E+04
Q9Y4G6 TLN2	8.96E+04	3.93E+05	5.47E+05	1.08E+05	6.78E+04	3.50E+05	8.72E+05	4.31E+05	1.81E+05	2.32E+05	1.29E+05	3.34E+04	5.24E+04	3.48E+05	5.87E+04
P31937 3HIDH	9.31E+04	8.50E+04	7.09E+05	8.13E+04	1.84E+05	4.66E+05	3.89E+05	3.28E+05	3.52E+05	4.27E+05	4.46E+04	3.21E+05	4.43E+04	3.74E+04	1.24E+05
P36542 ATPG	3.43E+05	4.54E+05	2.95E+06	8.56E+05	5.80E+05	8.73E+04	2.96E+05	3.24E+06	8.41E+05	6.94E+05	8.47E+05	1.08E+06	4.08E+05	4.93E+05	1.53E+06
P10515 ODP2	1.90E+05	1.60E+05	3.95E+04	2.69E+05	4.61E+05	8.60E+04	4.87E+05	1.32E+05	1.43E+05	1.87E+05	7.38E+04	3.22E+05	6.61E+05	1.13E+05	1.74E+05
P05091 ALDH2	1.40E+05	3.21E+05	3.65E+05	4.16E+05	6.73E+05	1.51E+05	2.99E+05	3.09E+05	2.97E+05	7.78E+05	2.63E+05	8.41E+05	7.19E+05	2.01E+05	2.49E+05
P42126 D3D2	3.43E+05	1.27E+05	8.82E+04	3.45E+05	5.36E+05	1.23E+05	3.86E+05	5.14E+05	1.41E+05	3.44E+05	3.95E+05	1.57E+05	3.52E+05	7.79E+04	2.23E+05
P26038 MOES	1.60E+05	1.23E+05	3.88E+05	3.04E+05	1.53E+05	5.05E+05	2.01E+05	1.29E+05	5.76E+04	1.09E+05	4.81E+04	1.02E+05	2.61E+05	6.03E+04	3.06E+04
O95831 AIFM1	3.75E+05	1.16E+05	1.11E+06	7.04E+04	2.76E+05	7.09E+04	6.17E+04	1.11E+06	1.14E+05	4.83E+04	2.08E+05	4.91E+05	1.86E+05	2.01E+05	1.73E+05
Q01813 K6PP	2.44E+05	1.08E+05	1.56E+05	1.55E+05	1.60E+05	2.58E+05	1.31E+05	6.90E+04	1.56E+05	1.49E+05	2.77E+05	3.44E+04	9.41E+04	1.09E+05	3.41E+04
Q14894 CRYM	4.10E+05	1.99E+05	1.19E+05	8.47E+05	5.26E+04	1.12E+05	8.11E+05	1.17E+06	3.20E+04	1.15E+05	5.30E+05	4.77E+05	6.19E+05	1.29E+06	2.33E+05
Q99497 PARK7	2.20E+05	1.87E+05	2.86E+04	1.48E+05	2.12E+04	1.03E+05	1.40E+05	2.96E+04	1.64E+05	1.31E+05	2.16E+05	1.49E+05	1.04E+05	2.07E+05	1.89E+05
P00738 HPT	1.88E+05	6.91E+05	1.88E+05	5.28E+05	7.29E+05	1.23E+06	2.07E+06	8.97E+04	3.57E+04	2.45E+05	7.10E+04	6.39E+05	3.18E+05	1.38E+05	5.15E+04
P13533 MYH6	5.36E+05	3.25E+06	5.43E+05	2.84E+05	2.98E+06	1.80E+06	4.18E+06	5.42E+06	9.67E+05	8.29E+05	9.29E+05	4.88E+06	1.15E+06	1.09E+06	2.10E+06
P10412 H14	6.66E+05	5.10E+05	7.38E+05	6.03E+05	1.05E+06	2.58E+05	7.05E+05	1.53E+05	1.55E+05	7.37E+05	9.77E+05	3.51E+05	4.84E+05	2.33E+05	9.61E+05
P01876 IGHA1	1.61E+05	3.23E+04	7.68E+04	4.57E+05	2.95E+05	1.56E+04	3.08E+04	1.82E+04	4.97E+03	9.99E+03	1.53E+05	6.91E+04	2.42E+04	9.22E+03	5.83E+04
P02679 FIBG	4.77E+05	1.32E+05	1.19E+06	6.70E+04	9.31E+04	4.73E+05	7.68E+05	9.14E+05	1.18E+05	3.89E+05	1.81E+05	2.00E+05	1.65E+05	1.68E+05	4.81E+04
Q05639 EF1A2	6.79E+04	8.16E+04	8.33E+04	2.63E+04	1.05E+04	2.03E+05	9.70E+04	5.60E+05	1.36E+05	7.88E+04	7.40E+04	6.40E+03	2.84E+04	1.50E+05	2.75E+04
P49753 ACOT2	4.22E+05	3.78E+05	5.69E+04	7.31E+05	5.73E+05	6.14E+05	3.55E+05	2.42E+05	4.61E+05	2.60E+05	4.81E+05	4.64E+05	5.69E+04	5.46E+05	8.11E+05
P62258 1433E	2.99E+05	5.52E+05	2.84E+05	9.26E+04	1.39E+05	5.08E+05	2.80E+05	3.57E+04	3.34E+05	3.10E+04	4.23E+05	2.63E+05	5.05E+05	8.76E+04	9.56E+04
P48047 ATPO	1.72E+06	1.50E+06	7.76E+06	1.94E+06	1.95E+06	1.47E+06	3.87E+06	8.15E+06	9.33E+04	1.16E+05	1.44E+06	3.79E+06	2.04E+06	2.48E+05	2.44E+06
P67936 TPM4	2.17E+05	3.52E+04	9.50E+04	1.93E+05	2.12E+05	4.02E+04	2.51E+04	3.27E+04	1.74E+04	1.77E+04	2.09E+05	1.39E+04	5.87E+05	1.65E+04	3.47E+05
Q16698 DECR	3.35E+06	1.59E+06	2.31E+05	1.38E+06	1.10E+06	3.79E+05	3.96E+05	1.48E+06	1.76E+06	4.83E+05	1.76E+06	1.69E+06	1.73E+06	7.36E+05	1.34E+06
Q9H223 EHD4	3.89E+04	6.08E+04	1.36E+05	5.55E+03	3.60E+04	1.67E+05	4.29E+04	3.05E+04	2.75E+05	2.69E+05	3.75E+04	5.64E+04	1.98E+04	6.14E+04	2.83E+04
P11310 ACADM	5.04E+05	5.95E+04	1.08E+05	3.47E+05	5.02E+05	2.66E+04	2.11E+05	3.19E+05	2.78E+05	3.65E+05	8.27E+05	4.94E+04	7.19E+05	4.36E+05	1.06E+06
Q16795 NDUA9	1.02E+05	4.03E+05	1.55E+05	2.45E+05	5.09E+05	3.27E+05	1.48E+06	1.19E+06	1.25E+05	1.33E+05	9.83E+04	3.01E+05	1.80E+05	1.07E+05	1.54E+05
P30041 PRDX6	6.59E+05	2.97E+04	1.75E+05	2.60E+05	6.61E+04	6.85E+04	4.53E+04	1.38E+05	1.05E+06	3.04E+05	7.83E+05	9.36E+04	1.17E+05	2.82E+06	7.14E+04
Q06830 PRDX1	1.19E+04	3.30E+05	5.52E+04	2.64E+05	3.93E+05	4.59E+04	3.73E+05	9.80E+04	3.48E+05	3.61E+05	2.88E+05	3.21E+05	1.45E+05	3.56E+05	1.93E+05
P07954 FUMH	4.81E+05	1.34E+05	4.67E+05	3.75E+05	2.67E+05	3.98E+04	1.63E+05	9.76E+04	8.95E+06	1.01E+07	4.55E+05	3.49E+05	5.14E+05	9.28E+06	4.26E+05
P11217 PYGM	1.53E+05	4.85E+05	6.25E+04	2.92E+05	5.28E+04	4.07E+05	1.25E+05	2.36E+05	7.71E+05	8.73E+05	2.00E+05	2.01E+05	1.69E+05	8.46E+05	3.77E+05
Q96199 SUCB2	1.14E+05	3.16E+05	7.92E+05	1.12E+05	3.36E+05	3.29E+05	1.65E+05	3.37E+05	3.23E+04	2.00E+04	1.80E+05	2.99E+05	1.66E+05	7.02E+04	3.76E+05
P62805 H4	1.36E+06	6.60E+04	3.52E+05	8.90E+05	2.19E+05	2.65E+04	1.60E+05	1.12E+05	1.57E+04	1.62E+04	1.45E+06	4.60E+05	6.99E+05	3.72E+04	1.03E+05
P28289 TMOD1	1.33E+05	2.74E+05	4.42E+05	1.54E+05	3.51E+04	3.64E+05	3.27E+05	6.55E+05	2.55E+05	3.19E+05	1.65E+05	7.40E+04	3.95E+04	1.08E+05	2.16E+05
Q16555 DPYL2	3.71E+04	6.95E+04	9.71E+05	1.60E+05	1.49E+05	1.74E+05	1.45E+05	9.93E+05	3.85E+05	1.28E+06	9.91E+04	5.71E+04	2.00E+05	2.87E+05	2.30E+05
P13637 AT1A3	2.01E+05	2.61E+04	1.25E+05	2.56E+05	6.77E+04	8.55E+04	1.06E+05	3.86E+05	2.11E+06	3.24E+06	1.57E+05	1.07E+05	1.87E+05	1.39E+06	2.53E+05
Q15124 PGM5	8.59E+04	1.92E+05	6.43E+04	3.07E+05	1.68E+05	1.94E+05	8.15E+04	6.58E+04	5.59E+06	4.08E+06	6.22E+04	9.48E+04	2.82E+05	9.33E+06	3.18E+05
Q13011 ECH1	5.49E+05	2.85E+05	2.31E+05	2.80E+05	5.24E+04	2.00E+05	5.56E+05	3.87E+05	4.43E+05	2.34E+05	2.70E+05	1.84E+05	3.69E+05	5.14E+05	1.39E+05
Q9UKX3 MYH13	7.05E+05	2.59E+04	2.32E+04	7.33E+05	6.14E+04	2.31E+04	5.07E+03	1.31E+04	4.11E+03	3.74E+03	9.14E+05	1.05E+05	2.51E+05	7.10E+04	4.80E+04
Q16836-2 HCDH	1.06E+06	1.28E+06	2.90E+05	6.19E+05	8.10E+05	1.14E+06	5.69E+05	2.62E+05	2.25E+05	2.53E+05	5.47E+05	6.68E+05	9.14E+05	1.75E+05	7.00E+05
P36957 ODO2	3.59E+05	8.97E+05	6.40E+04	3.41E+05	1.13E+06	6.24E+05	4.32E+05	7.31E+04	1.09E+06	1.01E+06	2.37E+05	1.46E+06	1.41E+06	1.28E+06	5.07E+05
P06744 G6PI	1.02E+05	1.11E+06	1.51E+06	9.55E+05	6.76E+05	8.85E+05	1.44E+06	8.95E+05	2.03E+05	1.86E+04	6.86E+05	1.64E+06	8.28E+05	1.22E+05	3.70E+05
P07339 CATD	3.23E+04	7.22E+05	4.13E+05	6.42E+05	7.23E+05	6.56E+05	3.18E+05	3.48E+05	2.59E+05	1.41E+05	1.57E+05	6.87E+05	2.62E+05	2.68E+05	6.17E+05
Q99878 H2A1J	7.06E+05	5.83E+04	1.40E+05	2.79E+05	2.29E+05	1.82E+05	3.47E+05	2.52E+05	1.72E+05	2.66E+04	4.38E+05	7.66E+04	3.50E+05	3.64E+04	2.78E+05
O75746 CMC1	1.05E+05	3.32E+05	1.19E+05	2.62E+05	1.43E+05	3.04E+05	8.16E+04	3.33E+05	7.45E+05	6.35E+05	1.18E+05	3.65E+05	1.25E+05	7.27E+05	3.49E+05
P62937 PPIA	4.00E+05	3.22E+05	5.15E+04	5.22E+05	3.24E+05	4.84E+05	3.81E+04	1.96E+05	1.97E+05	6.95E+05	3.61E+05	3.95E+05	8.84E+04	6.19E+05	3.05E+05
P15259 PGAM2	7.33E+04	2.79E+04	1.18E+04	3.63E+05	7.61E+04	1.22E+05	3.06E+04	2.71E+04	8.20E+03	3.34E+04	2.00E+05	2.06E+04	6.02E+04	6.12E+04	7.10E+04

P12277 KCRB	1.49E+06	1.05E+05	3.07E+04	2.10E+06	3.32E+05	2.22E+06	4.75E+04	9.56E+04	6.29E+05	4.92E+05	1.44E+06	7.98E+05	8.57E+05	8.92E+05	1.55E+06
P19404 NDUV2	3.91E+05	3.77E+04	2.57E+04	4.40E+05	1.57E+05	2.82E+04	2.42E+05	3.40E+05	1.88E+04	2.03E+04	2.78E+05	1.10E+05	1.51E+05	1.13E+04	1.41E+05
Q09666 AHNK	8.89E+05	5.79E+05	7.58E+05	9.05E+05	4.10E+05	6.37E+05	5.28E+05	1.53E+06	5.08E+05	3.83E+05	3.92E+05	4.26E+05	4.24E+05	3.63E+05	3.69E+05
P14854 CX6B1	3.69E+04	9.14E+04	1.12E+04	1.59E+04	1.52E+05	9.55E+04	1.76E+05	7.15E+04	1.42E+05	2.07E+05	2.86E+04	1.97E+05	9.09E+04	9.70E+04	1.91E+04
O14558 HSPB6	7.75E+05	1.15E+06	1.07E+06	9.43E+05	9.82E+04	2.02E+05	5.69E+05	6.98E+05	1.78E+04	1.48E+04	1.17E+06	4.43E+05	1.34E+06	1.93E+05	1.16E+06
Q5VST9-6 OBSCN	2.97E+04	3.19E+05	9.40E+04	7.84E+04	8.05E+04	2.49E+04	1.02E+05	1.78E+05	2.77E+05	1.08E+05	2.42E+05	4.06E+05	2.37E+05	3.10E+05	1.10E+05
P02671-2 FIBA	1.34E+05	5.16E+04	8.71E+04	4.52E+04	3.16E+05	4.34E+04	1.51E+05	7.76E+04	4.76E+05	1.92E+05	8.03E+04	1.11E+05	5.72E+04	2.85E+05	4.27E+04
O75947 ATP5H	7.56E+05	2.20E+05	9.12E+04	5.35E+05	6.84E+05	8.10E+05	8.28E+05	1.81E+05	4.15E+04	4.77E+04	3.66E+05	4.05E+05	8.85E+05	4.35E+04	6.25E+05
Q99623 PHB2	7.04E+04	3.50E+04	1.45E+05	3.12E+04	2.64E+05	4.58E+04	5.53E+04	8.57E+04	8.05E+05	1.21E+05	5.97E+04	1.44E+05	1.18E+05	8.55E+05	1.20E+05
P50461 CSRP3	1.01E+05	2.99E+04	5.24E+04	1.85E+05	1.76E+04	7.35E+04	1.97E+04	4.21E+04	5.59E+04	1.21E+04	3.88E+05	5.25E+04	2.42E+04	4.57E+04	7.72E+04
P24539 AT5F1	1.10E+04	2.54E+04	6.25E+05	1.55E+04	4.37E+05	4.05E+05	1.06E+06	3.31E+04	1.70E+05	1.01E+05	1.96E+04	6.61E+05	1.15E+04	1.12E+05	1.58E+04
Q9BZL4 PP12C	3.22E+03	1.16E+04	3.72E+04	2.83E+03	1.86E+03	8.36E+03	1.16E+04	1.01E+04	1.58E+04	5.00E+04	8.00E+03	1.05E+04	1.67E+04	3.75E+04	3.28E+03
Q9Y490 TLN1	8.39E+04	2.32E+04	5.55E+04	3.48E+04	3.04E+04	1.02E+04	1.95E+04	4.52E+04	1.58E+05	5.49E+05	1.24E+05	2.82E+04	4.41E+04	8.08E+04	4.61E+04
P82909 RT36	4.23E+04	6.31E+04	2.26E+05	1.32E+05	7.33E+04	1.55E+05	1.24E+05	1.56E+05	1.25E+05	1.67E+05	7.75E+04	6.02E+04	5.30E+04	5.73E+04	6.82E+04
Q13554 KCC2B	1.48E+04	3.99E+04	2.84E+05	1.24E+05	9.69E+04	1.19E+05	2.66E+05	2.63E+05	9.76E+04	5.48E+04	7.45E+05	1.70E+05	1.26E+06	6.62E+05	1.26E+05
P27824 CALX	3.81E+05	8.42E+05	1.37E+06	5.08E+05	2.38E+05	7.90E+05	1.07E+06	4.53E+05	7.32E+04	1.32E+05	4.53E+05	6.10E+05	5.42E+04	7.44E+04	6.93E+05
P30042 ES1	5.15E+04	1.74E+04	3.08E+04	3.15E+04	1.23E+05	8.06E+03	1.67E+04	3.90E+04	7.34E+05	9.74E+03	6.60E+04	5.80E+04	2.09E+04	6.81E+04	9.11E+04
O60237 MYPT2	1.37E+04	5.68E+04	2.75E+04	5.51E+04	1.78E+04	1.20E+05	3.96E+04	7.51E+04	3.02E+04	7.87E+04	4.22E+04	3.31E+04	3.23E+04	3.30E+04	3.87E+04
P26373 RL13	6.95E+04	8.23E+05	4.03E+04	4.66E+05	4.97E+05	5.92E+04	7.70E+05	4.91E+04	2.51E+05	3.26E+05	1.39E+05	9.79E+05	7.93E+05	1.77E+05	4.40E+05
P35573-3 GDE	3.23E+04	3.94E+04	1.61E+04	2.76E+04	3.28E+04	1.48E+04	1.41E+05	6.82E+04	7.78E+04	6.23E+04	8.75E+03	6.75E+04	3.02E+04	1.05E+05	1.78E+04
P00441 SODC	9.13E+03	2.24E+05	1.54E+05	4.68E+04	1.63E+05	6.38E+04	2.57E+04	9.81E+04	1.07E+04	1.21E+04	3.14E+04	2.19E+05	5.91E+04	3.68E+04	2.16E+05
P22061 PIMT	7.14E+03	2.86E+05	1.29E+05	5.09E+04	1.56E+05	3.72E+05	2.69E+05	3.12E+05	7.85E+04	8.22E+04	8.26E+04	7.73E+04	7.31E+04	4.79E+04	8.45E+04
P84243 H33	5.63E+04	1.21E+05	1.68E+05	8.16E+04	2.80E+05	1.86E+05	2.86E+05	5.89E+04	1.27E+05	1.96E+04	9.94E+04	1.22E+05	9.97E+04	2.21E+05	4.78E+05
P00338 LDHA	2.37E+05	5.73E+04	5.38E+04	1.44E+05	1.82E+05	3.99E+05	2.01E+05	5.88E+04	1.70E+04	1.32E+05	7.72E+04	1.85E+05	3.20E+04	1.77E+04	4.21E+04
Q9HBL0 TENS1	5.51E+03	1.06E+04	8.78E+04	1.63E+05	3.56E+04	5.91E+04	1.18E+05	1.02E+05	8.53E+04	6.20E+04	6.88E+04	7.72E+04	2.71E+05	8.88E+04	4.93E+04
P99999 CYC	4.71E+05	2.61E+05	1.10E+06	1.73E+05	2.35E+05	2.39E+05	1.28E+06	1.78E+06	2.11E+03	1.98E+04	2.75E+05	9.42E+04	2.21E+05	8.81E+03	1.46E+05
Q15084 PDIA6	4.73E+04	1.58E+04	9.10E+03	2.83E+04	6.05E+03	2.38E+04	2.19E+04	1.60E+04	2.46E+05	3.99E+05	4.37E+04	9.21E+03	1.19E+04	4.51E+04	1.08E+04
Q03252 LMNB2	2.09E+04	2.17E+04	1.64E+05	2.56E+04	4.38E+04	9.51E+04	1.24E+05	2.32E+05	6.38E+04	5.60E+04	9.97E+04	2.57E+04	2.08E+05	4.02E+04	5.45E+04
Q16775 GLO2	7.85E+04	3.27E+04	2.51E+04	3.24E+04	4.32E+04	1.31E+04	3.46E+05	1.08E+04	1.79E+04	2.47E+04	1.17E+05	1.51E+05	1.29E+04	2.05E+05	5.68E+04
Q6YN16 HSDL2	1.53E+05	1.87E+05	2.34E+05	1.38E+05	2.69E+05	7.08E+05	1.65E+05	1.85E+05	2.67E+04	7.56E+04	1.16E+05	1.23E+05	5.68E+04	3.94E+04	1.72E+05
P07951 TPM2	2.65E+05	2.77E+05	1.60E+05	1.68E+05	2.59E+05	1.22E+05	1.55E+05	8.99E+05	1.57E+05	8.47E+05	1.81E+05	3.75E+05	4.69E+04	2.29E+05	1.84E+05
O95299 NDUAA	2.10E+05	8.23E+04	5.39E+04	1.75E+05	2.15E+05	5.80E+04	4.72E+04	6.21E+04	1.12E+04	5.54E+04	8.47E+04	6.80E+04	2.20E+05	5.20E+04	1.48E+05
P02766 TTHY	4.68E+04	3.01E+03	6.80E+03	3.29E+03	4.18E+03	4.64E+03	3.04E+04	3.75E+04	6.70E+04	5.36E+04	4.09E+04	6.84E+03	2.10E+04	5.19E+04	9.03E+03
P61978 HNRPK	9.04E+04	1.18E+05	1.93E+04	7.33E+04	1.11E+05	7.68E+04	2.71E+04	5.51E+04	1.32E+05	1.75E+05	5.85E+04	1.01E+05	3.29E+04	2.59E+05	8.46E+04
P01834 IGKC	1.22E+06	6.45E+05	7.46E+05	3.31E+05	6.77E+05	1.19E+06	3.08E+05	3.88E+05	3.35E+05	5.73E+05	2.71E+05	3.19E+05	1.42E+05	4.53E+05	9.84E+04
Q9UBY9 HSPB7	1.77E+05	4.32E+05	6.06E+04	4.83E+05	1.01E+05	3.27E+05	3.08E+04	3.94E+04	2.11E+04	2.85E+04	4.28E+05	3.77E+05	1.99E+05	1.91E+04	3.40E+05
P63104 1433Z	9.94E+04	9.53E+04	1.53E+04	7.46E+04	8.08E+04	3.44E+04	1.55E+04	1.29E+04	7.89E+04	5.37E+03	1.22E+05	6.27E+04	3.59E+03	1.66E+04	1.19E+05
P30084 ECHM	3.94E+05	1.03E+04	1.60E+04	7.69E+03	2.64E+04	8.25E+03	2.64E+04	4.04E+05	6.56E+03	1.44E+04	1.08E+05	3.10E+04	2.81E+04	1.26E+04	7.29E+04
P30101 PDIA3	6.34E+04	1.91E+05	2.19E+05	8.66E+04	1.59E+05	3.83E+05	1.43E+05	2.39E+05	3.42E+05	3.39E+05	1.36E+05	1.35E+05	1.29E+05	2.96E+05	7.20E+04
Q08380 LG3BP	2.97E+04	3.82E+04	3.22E+03	1.42E+04	7.82E+03	1.88E+04	3.31E+04	7.80E+03	7.12E+04	2.23E+04	1.33E+05	2.12E+04	7.99E+03	2.53E+04	4.02E+04
O14639-4 ABLM1	7.36E+04	1.91E+05	2.50E+07	1.67E+05	1.69E+04	2.77E+05	1.77E+05	4.27E+06	7.48E+04	2.03E+04	6.70E+04	1.69E+05	1.96E+07	7.88E+04	7.47E+03
P50395 GDIB	3.04E+05	1.77E+05	6.46E+04	3.52E+04	3.07E+04	1.88E+05	3.57E+04	7.28E+05	4.30E+04	5.81E+05	2.35E+04	1.03E+04	5.82E+04	1.07E+05	5.56E+04
P04179 SODM	1.28E+05	1.19E+06	4.94E+05	5.71E+05	1.18E+06	1.27E+06	2.91E+06	3.42E+06	8.36E+05	6.46E+05	2.95E+04	4.40E+05	1.81E+05	2.90E+06	2.50E+05
Q16134 ETFD	3.27E+05	2.57E+05	4.60E+05	2.91E+05	4.32E+05	1.49E+05	1.37E+05	9.50E+05	1.44E+04	2.10E+04	3.48E+05	2.91E+05	1.02E+05	4.39E+05	3.96E+05
Q9NX63 CHCH3	3.37E+05	4.18E+04	9.62E+03	3.83E+04	4.14E+04	1.57E+04	2.12E+05	2.34E+05	1.96E+05	5.96E+03	3.71E+05	7.75E+04	1.20E+05	7.93E+04	6.80E+03
P30049 ATPD	3.78E+05	4.39E+05	4.84E+04	4.02E+05	2.37E+05	1.86E+04	1.58E+05	5.30E+04	1.36E+05	7.68E+04	1.62E+05	4.48E+05	1.89E+05	3.04E+05	2.08E+05
P30153 2AAA	1.32E+04	9.96E+04	4.79E+04	8.48E+04	2.28E+05	2.06E+05	4.03E+05	2.92E+05	2.49E+04	7.80E+04	7.00E+04	2.46E+05	6.99E+04	9.31E+04	7.60E+04

P61981 I433G	1.68E+05	5.63E+04	2.25E+03	5.52E+04	1.23E+05	1.33E+05	1.44E+03	1.21E+04	1.47E+05	4.29E+04	3.02E+05	4.52E+04	4.77E+04	8.14E+04	3.18E+04
P06733 ENOA	3.60E+05	4.04E+04	2.71E+04	3.88E+05	4.49E+04	2.12E+04	5.90E+04	8.33E+04	1.42E+05	1.86E+05	2.04E+05	2.77E+05	2.11E+05	1.45E+05	1.06E+05
P00450 CERU	2.11E+04	1.97E+04	6.79E+04	2.26E+04	1.03E+05	5.65E+04	1.04E+05	7.28E+04	1.38E+05	3.94E+05	1.09E+05	6.15E+04	1.46E+05	1.93E+05	1.96E+04
P09382 LEG1	9.62E+03	3.09E+05	1.21E+05	6.10E+05	7.56E+05	5.50E+05	4.35E+05	2.35E+04	4.54E+04	3.29E+04	1.37E+05	2.98E+05	1.26E+05	4.57E+04	7.25E+05
P10606 COX5B	2.08E+06	4.11E+04	1.32E+04	6.78E+05	1.57E+05	4.16E+04	4.69E+04	3.32E+04	1.84E+06	1.28E+06	1.06E+06	2.78E+04	3.24E+04	5.14E+05	5.64E+05
Q02338 BDH	6.62E+03	3.50E+03	2.81E+04	5.75E+03	4.39E+04	4.25E+04	6.97E+04	7.13E+04	2.33E+05	3.79E+05	6.64E+03	5.81E+03	4.40E+04	6.10E+05	3.39E+03
P01859 IGHG2	2.00E+05	2.83E+03	7.67E+03	1.42E+03	1.84E+04	4.79E+04	7.94E+03	1.77E+04	9.64E+04	4.15E+05	6.48E+03	3.77E+03	1.79E+03	7.95E+04	5.39E+03
P50895 BCAM	1.37E+04	1.33E+04	3.87E+04	1.21E+04	8.56E+03	5.25E+04	1.30E+04	3.71E+04	9.96E+04	5.13E+04	3.72E+04	1.03E+05	4.38E+04	7.68E+04	2.33E+04
P62988 UBIQ	9.73E+04	4.43E+05	1.25E+06	3.95E+05	1.09E+06	8.43E+05	8.59E+05	2.11E+05	3.15E+04	7.24E+04	7.00E+05	7.98E+05	3.58E+05	3.09E+04	9.40E+05
P04040 CATA	6.17E+04	8.17E+04	1.05E+05	8.88E+03	6.31E+03	5.24E+04	9.48E+04	7.68E+04	6.50E+04	1.44E+05	4.72E+04	1.33E+05	3.93E+04	3.99E+04	1.64E+04
Q14192 FHL2	2.11E+03	2.00E+05	5.22E+05	3.87E+05	7.82E+05	1.15E+06	9.82E+05	9.46E+04	4.05E+03	8.77E+03	1.03E+05	5.31E+05	1.18E+05	2.13E+04	1.66E+05
O43181 NDUS4	1.63E+05	6.50E+03	1.01E+04	1.62E+05	1.91E+05	1.35E+04	1.75E+04	3.51E+04	1.85E+06	1.86E+06	1.36E+05	3.17E+05	2.47E+05	7.90E+05	1.79E+04
P30038 AL4A1	4.38E+04	8.67E+04	8.32E+04	4.96E+04	5.45E+04	2.02E+05	7.03E+04	7.61E+04	3.32E+05	2.73E+05	6.34E+03	1.07E+04	1.00E+05	1.65E+05	1.06E+04
Q16586 SGCA	2.55E+04	5.85E+04	4.62E+04	2.17E+05	2.19E+05	3.35E+05	3.51E+05	1.30E+05	1.56E+04	1.94E+04	3.68E+04	2.83E+05	4.01E+05	2.75E+04	4.88E+04
P07919 QCR6	8.19E+04	4.99E+04	2.42E+04	2.80E+04	3.14E+04	5.12E+04	8.80E+04	1.21E+05	1.74E+05	1.07E+05	5.50E+04	5.59E+04	5.92E+04	3.75E+04	4.70E+04
P04004 VTNC	5.59E+05	9.40E+04	1.07E+05	7.19E+04	7.13E+04	9.93E+04	9.68E+04	1.77E+05	1.81E+05	5.22E+04	4.69E+05	5.67E+04	2.95E+05	1.92E+05	8.73E+04
Q9Y4W6 AFG32	4.93E+05	1.24E+05	2.46E+04	1.80E+05	1.43E+05	4.27E+04	1.07E+05	5.58E+04	1.37E+04	1.04E+04	7.47E+05	2.13E+05	2.44E+05	5.71E+03	1.61E+05
P05026 AT1B1	8.36E+03	2.09E+04	1.70E+05	2.60E+04	1.34E+04	1.18E+04	2.01E+04	2.45E+04	9.02E+04	1.65E+05	2.85E+04	9.39E+03	9.84E+03	5.81E+04	1.23E+04
Q13642-1 FHL1	1.99E+05	3.26E+04	6.75E+03	2.52E+05	1.04E+05	7.98E+04	7.58E+03	3.64E+04	2.10E+05	2.51E+05	3.65E+05	1.10E+05	1.42E+04	1.13E+05	2.16E+05
Q14BN4-4 SLMAP	3.40E+04	4.76E+04	2.69E+04	3.94E+04	1.68E+04	2.74E+04	1.72E+04	3.13E+04	2.69E+04	6.36E+04	1.44E+05	3.70E+04	5.19E+04	4.75E+04	4.68E+04
P16219 ACADS	6.75E+04	5.14E+04	4.40E+05	2.65E+04	2.31E+04	3.24E+04	2.53E+05	2.04E+05	6.86E+04	1.32E+05	3.12E+04	1.41E+04	1.15E+04	2.59E+05	8.19E+04
P78417 GSTO1	1.14E+05	1.10E+05	8.24E+04	1.48E+05	8.00E+04	5.67E+04	3.61E+04	3.04E+04	5.88E+04	5.39E+03	2.47E+05	6.10E+04	4.18E+04	2.01E+05	6.13E+03
P07900 HS90A	2.47E+05	2.08E+05	5.41E+04	2.00E+05	2.95E+05	2.95E+05	5.31E+04	7.50E+04	2.59E+05	2.71E+05	2.60E+05	1.52E+05	4.04E+04	1.76E+06	5.49E+05
P08865 RSSA	1.87E+05	1.67E+05	3.20E+04	8.09E+04	6.44E+04	3.89E+03	3.54E+04	5.08E+05	8.82E+04	1.58E+05	2.24E+05	1.18E+05	1.22E+05	1.20E+05	9.40E+04
P14927 QCR7	4.80E+05	1.08E+06	2.89E+05	1.30E+06	4.20E+05	1.24E+06	5.05E+05	1.32E+06	2.30E+05	5.12E+04	3.49E+05	1.05E+06	1.30E+05	1.09E+05	3.77E+05
P50995 ANX11	1.58E+05	3.10E+04	1.80E+05	2.50E+05	6.44E+04	2.39E+04	5.15E+04	9.84E+04	6.51E+03	7.54E+03	1.07E+05	4.50E+04	1.10E+05	1.35E+04	7.99E+04
O96000 NDUBA	8.38E+04	3.40E+04	3.59E+04	1.02E+05	1.40E+05	1.93E+05	9.27E+04	2.38E+05	7.23E+03	2.58E+04	2.77E+04	2.40E+05	5.48E+04	4.18E+04	1.38E+05
P23297 S10A1	1.79E+05	2.87E+05	4.14E+05	1.48E+05	2.04E+05	3.28E+05	1.50E+05	4.18E+05	5.49E+05	1.06E+05	1.11E+05	2.59E+05	2.74E+05	1.65E+05	1.66E+05
P45880-1 VDAC2	2.95E+05	2.44E+04	3.48E+04	2.61E+05	6.60E+03	5.24E+04	9.52E+03	1.33E+04	3.58E+05	4.81E+05	2.23E+05	3.91E+04	1.05E+05	1.73E+05	3.04E+05
Q00325 MPCP	9.14E+05	2.27E+05	7.08E+03	4.42E+05	9.33E+05	4.18E+05	2.40E+05	3.20E+05	1.56E+05	1.32E+04	4.50E+05	2.44E+05	1.17E+05	2.72E+05	1.20E+06
Q92523 CPT1B	1.10E+05	1.70E+04	1.84E+04	2.25E+04	8.57E+03	5.37E+03	6.56E+04	2.30E+04	1.23E+05	5.92E+03	9.03E+04	6.33E+04	4.09E+04	3.89E+04	3.90E+04
Q16082 HSPB2	6.02E+03	2.68E+05	1.39E+05	3.84E+05	8.56E+04	7.38E+05	2.28E+04	1.08E+05	5.78E+05	8.95E+04	2.00E+05	1.52E+05	3.17E+05	2.63E+05	1.42E+05
P02743 SAMP	6.58E+05	8.48E+04	4.66E+04	1.41E+05	7.28E+04	2.91E+04	3.47E+04	7.97E+04	2.63E+04	6.82E+04	3.56E+05	1.54E+05	2.09E+05	1.83E+05	2.00E+05
P02647 APOA1	6.52E+05	1.48E+06	1.27E+04	7.09E+05	2.50E+06	1.12E+06	5.84E+06	7.68E+04	6.29E+06	6.67E+05	1.58E+06	2.22E+06	1.47E+06	5.41E+06	8.13E+05
P22626 ROA2	1.09E+05	2.20E+05	2.11E+05	3.36E+04	8.61E+04	1.13E+05	9.50E+04	1.96E+05	2.92E+05	2.42E+05	1.16E+05	9.13E+04	2.68E+04	3.50E+05	6.41E+04
Q9UIJ7 KAD3	1.19E+04	6.84E+05	4.13E+05	2.71E+05	4.07E+05	3.93E+05	9.47E+05	1.12E+05	8.57E+03	6.15E+03	1.50E+04	5.51E+05	4.76E+05	1.01E+04	7.72E+03
Q9UHQ9 NB5R1	1.87E+05	7.49E+05	6.99E+05	7.97E+05	8.94E+05	1.52E+06	1.13E+06	1.26E+05	1.17E+05	1.14E+05	1.73E+05	9.40E+05	3.26E+05	1.41E+05	1.62E+05
Q99877 H2B1N	3.16E+06	9.19E+04	9.76E+04	4.34E+06	1.81E+05	2.87E+05	4.17E+05	3.78E+05	2.48E+05	9.63E+05	3.42E+06	5.74E+04	5.19E+06	3.19E+05	1.50E+05
Q9NZN4 EHD2	6.22E+04	3.57E+05	2.08E+05	2.50E+05	3.12E+05	4.17E+05	1.83E+04	1.44E+05	1.21E+05	1.53E+05	4.11E+04	3.23E+05	6.16E+05	1.56E+05	2.37E+05
P21796 VDAC1	3.02E+05	8.80E+03	1.56E+04	7.29E+04	3.77E+04	1.33E+04	7.60E+04	1.28E+05	1.47E+05	2.31E+05	1.38E+05	2.48E+04	1.12E+04	2.81E+04	6.11E+04
Q02252 MMSA	2.54E+04	4.69E+06	4.28E+05	3.76E+06	4.54E+06	8.94E+04	2.24E+05	4.62E+05	5.97E+04	4.13E+05	2.98E+06	1.58E+05	1.96E+06	2.91E+05	2.75E+06
P50213 IDH3A	2.49E+05	2.59E+05	3.19E+05	1.95E+05	3.65E+05	4.86E+04	2.43E+05	8.52E+05	6.81E+04	5.79E+04	2.79E+05	3.16E+05	2.27E+05	4.90E+04	3.33E+05
P07437 TBB5	2.38E+05	8.22E+04	3.28E+04	1.03E+05	1.32E+05	2.12E+05	3.12E+04	1.67E+05	6.65E+03	1.09E+04	1.23E+05	1.78E+05	7.53E+04	2.87E+04	1.01E+05
P35222 CTNB1	8.17E+04	1.84E+05	1.09E+05	2.64E+05	1.53E+05	3.91E+05	1.35E+05	8.06E+04	2.75E+05	2.89E+05	1.57E+05	3.58E+05	1.56E+05	3.60E+04	1.21E+05
P35221 CTNA1	1.58E+05	2.21E+04	2.65E+04	4.62E+04	1.13E+05	1.73E+05	2.07E+05	5.91E+04	6.76E+04	1.31E+05	1.46E+05	1.42E+04	1.35E+04	4.13E+04	1.02E+04
P61604 CH10	3.52E+05	6.17E+04	1.26E+05	4.24E+04	9.25E+04	7.80E+04	1.93E+05	1.07E+05	6.37E+05	6.35E+05	1.91E+05	1.27E+05	3.96E+04	7.29E+05	1.16E+05
P15121 ALDR	6.40E+04	1.87E+05	6.79E+04	3.37E+05	3.42E+05	1.73E+04	4.07E+04	1.17E+05	2.51E+06	1.60E+06	3.65E+04	5.05E+05	1.71E+05	3.37E+05	2.90E+05

P51884 LUM	5.01E+04	1.81E+04	1.01E+05	3.85E+04	1.98E+05	3.01E+05	1.38E+05	1.77E+05	1.63E+04	1.00E+05	6.76E+04	5.95E+03	4.91E+03	4.51E+04	2.54E+03
P10644 KAP0	1.02E+05	2.81E+04	2.59E+04	1.74E+03	3.99E+03	2.07E+04	1.02E+04	1.18E+04	1.02E+04	7.59E+03	1.51E+05	2.02E+04	6.93E+04	6.91E+03	7.09E+03
P18859 ATP5J	1.12E+06	4.42E+04	1.79E+04	7.29E+04	3.20E+05	3.76E+04	1.27E+05	1.20E+05	1.81E+04	6.67E+04	7.42E+05	4.94E+04	3.64E+05	1.97E+04	1.65E+05
O43678 NDUA2	7.56E+04	2.94E+05	2.34E+06	1.90E+05	3.50E+05	1.24E+06	2.90E+06	3.30E+06	1.19E+05	7.67E+04	8.43E+04	2.71E+05	1.12E+04	4.47E+04	9.94E+04
P00915 CAH1	3.64E+05	6.41E+04	4.33E+04	2.58E+04	1.07E+05	8.31E+04	1.89E+04	8.42E+04	2.56E+04	1.11E+04	3.22E+05	2.59E+04	1.36E+04	2.18E+04	1.27E+04
P27338 AOFB	3.73E+05	4.49E+04	3.55E+05	6.07E+04	2.23E+04	3.53E+04	3.18E+05	4.02E+05	3.55E+06	7.10E+06	2.31E+05	4.13E+04	3.09E+04	3.69E+06	8.07E+04
P39059 COFA1	4.16E+04	1.46E+05	9.70E+04	4.09E+04	7.09E+03	1.03E+05	7.19E+04	4.63E+04	2.53E+05	7.12E+04	4.02E+04	7.98E+04	1.45E+05	2.53E+05	1.10E+04
P02042 HBD	6.40E+05	2.53E+05	7.22E+04	9.05E+05	6.40E+04	4.92E+04	5.67E+04	1.40E+04	2.10E+05	5.44E+04	1.10E+06	6.80E+04	1.03E+05	1.27E+05	3.74E+05
Q9Y6M9 NDUB9	8.70E+03	4.20E+04	6.73E+04	1.56E+04	1.26E+05	1.42E+05	3.42E+04	1.78E+04	8.68E+03	1.15E+04	2.29E+04	1.48E+05	1.08E+04	1.28E+04	3.91E+04
P12814 ACTN1	1.45E+05	2.44E+04	1.86E+04	2.48E+04	1.05E+05	2.93E+04	3.95E+04	3.95E+04	5.49E+04	8.77E+04	8.50E+04	2.22E+04	1.39E+04	6.64E+04	3.62E+04
O00151 PDLI1	1.85E+05	9.19E+03	5.34E+04	2.20E+05	1.23E+04	1.07E+04	1.69E+05	3.25E+05	4.03E+04	2.79E+04	3.84E+05	1.81E+04	9.60E+04	2.06E+04	4.34E+04
P23368 MAOM	6.09E+04	3.45E+05	1.37E+05	9.15E+04	6.59E+04	1.25E+04	6.09E+04	1.08E+05	3.23E+05	5.55E+05	4.72E+04	8.08E+04	3.63E+04	4.29E+06	3.97E+04
P30048 PRDX3	3.98E+05	7.68E+04	8.68E+04	3.79E+04	4.68E+04	5.00E+04	7.16E+04	3.52E+04	1.53E+05	1.50E+05	1.64E+05	7.13E+04	7.53E+04	1.12E+05	1.62E+05
P13489 RINI	4.38E+04	1.09E+04	1.12E+05	1.08E+04	4.75E+04	2.01E+05	4.47E+04	1.78E+04	7.62E+03	6.81E+03	2.82E+04	1.34E+05	5.92E+03	3.77E+04	3.65E+03
P13807 GYS1	1.34E+05	2.43E+05	1.08E+05	2.21E+05	2.53E+05	6.13E+05	3.17E+05	2.27E+05	1.15E+04	1.29E+05	4.47E+04	4.54E+05	1.71E+05	2.83E+06	1.89E+05
O14958 CASQ2	2.05E+05	4.40E+05	9.63E+04	4.60E+05	4.15E+05	4.86E+05	7.18E+05	7.14E+05	3.38E+05	6.54E+04	3.14E+05	3.32E+05	1.21E+05	1.48E+05	4.77E+05
P21912 DHSB	1.14E+05	1.34E+04	5.43E+03	1.37E+05	6.23E+04	3.55E+03	1.09E+04	8.15E+04	2.59E+05	2.33E+05	5.98E+04	6.35E+04	2.21E+05	6.41E+05	1.52E+05
P07737 PROF1	3.52E+06	1.59E+05	2.05E+05	2.06E+06	1.19E+06	2.64E+05	2.50E+06	8.86E+04	1.07E+05	2.74E+04	2.03E+06	1.41E+05	1.86E+05	7.57E+04	1.43E+06
Q9GZM7 TINAL	1.01E+04	5.52E+04	1.73E+04	7.36E+04	2.35E+04	5.52E+03	3.57E+04	1.25E+04	1.11E+04	7.53E+03	1.21E+05	6.56E+04	1.37E+05	1.83E+04	4.46E+04
P00387 NB5R3	2.26E+05	6.58E+04	3.12E+04	3.71E+04	1.43E+05	2.90E+04	1.41E+05	7.22E+04	1.84E+04	7.27E+04	2.35E+05	9.77E+04	1.65E+05	1.01E+04	2.27E+05
P09211 GSTP1	1.52E+05	1.07E+05	3.05E+05	4.14E+04	1.13E+05	3.23E+05	1.51E+05	2.34E+05	1.52E+05	4.82E+04	2.49E+05	8.07E+04	3.69E+04	3.35E+05	6.67E+04
P55786 PSA	1.55E+05	1.68E+05	2.11E+06	1.32E+05	6.35E+04	2.13E+05	2.96E+06	4.77E+06	3.84E+04	7.34E+04	1.16E+05	1.91E+05	3.26E+05	3.79E+04	7.83E+04
P29692-2 EF1D	4.92E+04	1.05E+04	1.15E+04	3.11E+03	1.01E+04	9.60E+02	3.10E+03	2.49E+04	1.45E+03	4.57E+03	6.18E+04	1.32E+04	5.08E+04	7.96E+03	4.19E+04
P13639 EF2	8.74E+04	3.69E+04	1.01E+04	6.52E+04	2.81E+04	1.34E+04	9.62E+03	1.89E+04	8.51E+04	9.52E+04	4.04E+04	1.57E+04	1.42E+05	2.67E+04	8.40E+04
P08758 ANXA5	5.31E+05	4.13E+05	1.18E+06	9.38E+05	1.73E+06	7.34E+05	5.33E+05	7.90E+05	7.61E+05	9.09E+05	4.95E+05	1.84E+05	2.32E+06	8.31E+05	1.49E+06
Q13228 SBP1	6.23E+03	8.01E+05	6.78E+05	6.05E+03	3.02E+04	7.21E+05	5.09E+04	1.94E+04	1.45E+05	2.42E+05	9.82E+03	4.15E+05	1.02E+04	3.08E+05	1.64E+04
P27144 KAD4	7.75E+04	1.31E+05	7.37E+03	5.27E+03	1.42E+05	1.51E+05	3.22E+04	4.45E+04	1.01E+05	2.28E+06	6.26E+03	1.74E+05	5.33E+03	3.63E+04	6.94E+03
P12429 ANXA3	2.80E+04	6.01E+04	3.08E+04	5.24E+04	4.70E+04	5.99E+04	3.83E+04	3.10E+04	6.62E+04	1.05E+04	2.54E+03	3.74E+04	6.23E+03	7.07E+04	8.93E+04
Q8NDY3 ARHL1	2.61E+05	7.65E+03	3.29E+04	2.56E+05	5.45E+04	2.07E+05	4.07E+04	1.03E+04	6.70E+03	4.69E+04	2.72E+05	1.45E+04	3.98E+04	1.11E+04	2.97E+04
P23528 COF1	1.24E+05	1.22E+04	2.64E+04	9.84E+04	2.38E+04	2.58E+03	1.01E+04	6.59E+03	5.40E+03	1.66E+03	1.59E+05	3.70E+05	1.04E+05	1.40E+03	8.93E+04
P30043 BLVRB	3.82E+04	1.91E+05	3.94E+04	6.61E+04	2.48E+04	5.85E+04	1.19E+05	3.34E+04	1.67E+04	6.11E+03	6.68E+04	8.96E+04	1.02E+05	8.65E+03	8.94E+04
Q92629-3 SGCD	5.15E+03	5.18E+04	2.33E+04	1.71E+05	1.27E+05	1.63E+05	1.42E+05	1.20E+05	6.74E+03	3.92E+03	1.02E+05	9.56E+04	1.89E+05	2.58E+04	2.03E+05
P49189 AL9A1	9.02E+04	1.91E+04	4.53E+03	8.78E+02	3.62E+04	1.22E+04	3.86E+04	2.28E+05	2.70E+04	8.03E+04	1.05E+05	1.36E+04	1.48E+05	1.35E+04	3.77E+03
P62158 CALM	1.16E+05	3.77E+04	9.58E+03	4.82E+04	3.58E+04	1.10E+05	4.93E+03	6.49E+03	1.97E+05	3.12E+05	3.74E+04	3.85E+04	3.85E+03	1.98E+05	4.83E+04
Q07021 C1QBP	1.31E+05	8.80E+03	1.56E+04	9.97E+03	9.36E+04	3.37E+03	1.99E+04	4.39E+04	2.04E+04	4.36E+03	1.19E+05	1.02E+05	8.55E+04	7.11E+03	1.27E+04
O95168 NDUB4	3.08E+05	1.18E+05	3.87E+05	2.51E+04	1.16E+04	6.00E+03	3.94E+04	1.67E+04	2.30E+04	2.98E+04	1.90E+05	2.97E+04	3.64E+05	1.54E+04	9.47E+03
Q9Y2Q3 GSTK1	1.06E+05	4.87E+03	4.49E+04	3.55E+04	4.61E+04	4.98E+03	1.64E+05	3.25E+05	2.39E+04	5.16E+04	2.27E+04	3.10E+04	2.02E+04	2.40E+04	2.27E+04
Q9Y623 MYH4	1.06E+04	3.05E+05	8.74E+06	3.85E+04	4.56E+03	4.38E+05	5.47E+06	1.18E+07	1.15E+04	2.23E+06	6.26E+03	3.95E+05	2.34E+04	9.82E+05	3.31E+03
P30044 PRDX5	6.11E+05	1.91E+05	2.52E+04	7.82E+05	6.39E+05	4.07E+05	2.64E+05	2.68E+05	1.11E+05	1.37E+05	5.56E+05	8.65E+04	7.82E+05	1.40E+05	6.44E+05
O75306 NDUS2	1.10E+05	2.14E+06	2.00E+06	9.47E+05	1.86E+06	2.07E+06	2.55E+06	4.47E+05	2.70E+05	5.92E+04	8.33E+04	5.97E+05	3.96E+05	1.96E+05	5.41E+05
P35232 PHB	1.08E+05	7.18E+03	8.04E+03	7.86E+03	2.69E+04	5.13E+03	2.24E+05	3.23E+05	5.17E+05	2.80E+05	1.14E+05	1.28E+04	1.38E+05	3.69E+05	1.04E+04
Q02978 M2OM	1.05E+03	7.34E+03	1.86E+04	2.82E+03	3.87E+03	9.66E+03	4.27E+04	2.43E+04	2.63E+05	2.32E+05	7.50E+03	7.35E+03	1.05E+04	2.21E+05	1.27E+04
Q9P0J0 NDUAD	2.18E+05	8.18E+04	6.40E+03	7.56E+04	1.62E+04	4.14E+04	4.46E+05	1.85E+05	6.07E+03	5.71E+04	5.81E+04	1.94E+04	2.17E+03	7.84E+04	7.96E+03
P11055 MYH3	2.56E+03	4.31E+05	1.15E+04	1.01E+04	3.57E+04	6.62E+03	2.62E+04	1.22E+05	1.44E+05	8.63E+04	2.62E+04	4.72E+03	1.65E+04	1.99E+05	3.39E+03
O75521 PECI	9.29E+04	2.49E+04	2.15E+04	2.06E+04	5.65E+04	6.90E+03	4.27E+03	1.08E+04	1.35E+04	1.47E+04	1.55E+04	2.90E+04	3.28E+04	1.17E+04	1.71E+04
P18669 PGAM1	5.70E+04	1.29E+04	2.52E+04	5.37E+03	1.39E+04	2.84E+04	3.79E+04	7.26E+04	2.77E+04	4.01E+04	8.35E+03	1.47E+04	9.45E+03	1.72E+04	2.10E+04
Q9UI47 CTNA3	8.21E+03	1.78E+04	3.44E+04	8.29E+04	1.27E+04	9.90E+04	1.22E+04	3.18E+04	1.50E+05	2.18E+05	3.23E+04	2.26E+04	1.01E+04	8.47E+04	8.09E+04



O75489 NDUS3	8.49E+04	1.27E+05	3.75E+05	1.49E+05	6.18E+05	2.62E+05	4.28E+05	3.61E+05	1.49E+04	2.96E+04	9.27E+03	1.10E+06	6.75E+05	7.68E+03	5.10E+05
P47755 CAZA2	3.53E+04	4.48E+03	1.42E+04	7.61E+03	1.70E+03	3.14E+03	1.56E+04	1.94E+04	1.58E+05	2.20E+05	1.77E+04	3.25E+03	4.58E+03	5.02E+04	4.74E+03
O75915 PRAF3	8.53E+04	1.84E+04	6.59E+03	7.56E+04	8.35E+03	2.40E+04	9.40E+03	4.43E+03	4.24E+03	1.99E+03	8.52E+04	2.76E+03	1.23E+04	4.85E+03	3.58E+03
Q9H7C9 CK067	3.09E+04	1.67E+05	1.65E+05	1.31E+04	1.63E+04	2.67E+05	2.05E+05	1.92E+05	4.89E+04	4.50E+04	2.32E+04	1.05E+04	4.36E+03	2.45E+04	3.68E+04
P06703 S10A6	3.46E+03	1.57E+04	2.57E+03	4.72E+03	6.78E+03	1.46E+03	3.91E+03	2.86E+03	3.22E+05	4.88E+05	1.38E+03	4.00E+04	2.22E+03	1.77E+05	5.91E+03
P42704 LPPRC	9.71E+04	2.65E+04	7.27E+04	1.35E+04	9.55E+03	1.57E+04	6.97E+04	2.45E+04	2.18E+05	1.94E+05	2.53E+04	1.32E+04	1.66E+04	2.00E+05	7.44E+04
Q8WZ42-6 TITIN	4.19E+04	3.09E+04	2.59E+04	3.07E+04	2.54E+04	7.71E+04	1.58E+04	1.35E+04	1.11E+06	4.62E+06	5.77E+04	3.70E+04	2.17E+04	6.50E+05	1.94E+04
O15230 LAMA5	1.94E+04	4.37E+04	5.62E+04	2.89E+04	1.89E+04	3.37E+04	5.26E+04	1.40E+05	2.04E+05	3.32E+05	8.40E+04	7.11E+04	2.18E+04	7.42E+04	1.37E+04
P19823 ITI2	6.72E+03	3.44E+03	1.23E+04	4.17E+03	2.43E+03	1.92E+04	5.85E+04	4.84E+03	4.23E+03	6.79E+04	8.38E+02	1.60E+03	3.69E+03	7.24E+03	1.91E+03
P07099 HYEP	7.47E+03	1.30E+03	5.30E+03	1.56E+04	1.08E+04	2.61E+04	6.06E+04	3.84E+04	2.74E+03	1.10E+04	1.29E+03	1.02E+04	5.18E+03	1.98E+04	7.91E+02
P51970 NDUA8	5.31E+04	6.50E+03	8.91E+03	1.67E+04	2.78E+03	3.86E+04	4.87E+03	5.61E+03	1.62E+04	9.23E+04	3.08E+04	4.62E+03	1.54E+03	2.51E+04	3.17E+04
O43488 ARK72	1.82E+04	2.53E+04	8.88E+03	4.70E+04	6.62E+03	5.11E+04	2.91E+04	3.25E+04	3.38E+04	7.60E+03	3.65E+04	2.12E+04	2.68E+04	4.61E+04	1.03E+04
O75380 NDUS6	3.56E+04	9.51E+03	8.50E+03	2.95E+03	3.89E+03	1.02E+04	3.86E+04	1.75E+04	1.86E+03	1.51E+03	1.71E+04	1.12E+04	4.59E+03	1.18E+04	5.47E+03
P00751 CFAB	4.67E+03	1.65E+04	1.83E+05	6.56E+03	5.37E+03	3.90E+04	6.61E+04	1.12E+04	1.18E+05	1.25E+05	4.23E+03	1.32E+04	6.27E+03	8.17E+04	1.74E+04
P24298 ALAT1	2.51E+03	1.30E+04	1.34E+04	4.93E+04	3.26E+04	1.08E+03	2.03E+04	1.78E+04	7.73E+03	1.85E+03	3.03E+03	2.88E+03	2.82E+04	2.25E+03	5.50E+04
O95298 NDUC2	3.41E+04	7.94E+03	9.51E+04	7.37E+03	5.51E+04	4.64E+04	1.09E+05	1.13E+05	9.97E+04	2.35E+04	1.90E+04	3.81E+04	7.14E+04	4.18E+04	6.12E+03
P23246 SFPQ	1.38E+04	8.83E+03	1.21E+04	1.86E+04	1.48E+04	1.90E+04	1.58E+04	3.78E+03	9.39E+03	1.38E+04	4.88E+03	1.01E+04	6.83E+03	1.79E+04	4.14E+03
P09493-5 TPM1	5.28E+03	1.09E+04	5.51E+03	7.70E+03	1.41E+03	1.15E+03	4.40E+03	2.75E+04	1.83E+04	4.64E+04	1.05E+04	5.32E+03	6.92E+03	1.06E+04	1.24E+03
P05165 PCCA	5.02E+03	2.57E+04	2.31E+06	4.86E+04	9.36E+04	2.71E+06	1.37E+06	5.19E+04	4.76E+04	1.17E+04	2.57E+04	1.38E+06	2.06E+04	8.55E+03	7.68E+04
P61088 UBE2N	6.30E+02	9.76E+03	2.01E+05	1.47E+05	4.53E+04	1.77E+04	3.93E+04	8.55E+03	3.05E+03	1.95E+03	1.71E+04	9.81E+03	2.71E+05	6.84E+03	1.26E+05
Q96HC4-2 PDLI5	8.28E+04	4.91E+03	1.51E+04	2.23E+04	2.13E+03	1.18E+04	3.75E+03	4.89E+03	4.32E+03	5.67E+03	4.35E+04	7.00E+03	1.33E+04	9.83E+03	3.05E+04
O00159-3 MYO1C	3.12E+05	2.98E+05	4.66E+05	3.13E+05	1.27E+05	6.16E+05	6.44E+04	9.84E+04	2.74E+03	1.50E+04	3.84E+04	1.56E+05	9.89E+04	2.65E+03	2.31E+04
P27816-2 MAP4	7.35E+03	9.07E+03	1.31E+04	2.14E+04	5.81E+03	6.67E+03	7.46E+03	1.07E+04	2.37E+04	6.05E+04	6.56E+04	5.75E+03	7.87E+04	8.84E+04	2.53E+04
O95182 NDUA7	2.87E+03	3.25E+04	1.22E+04	2.12E+04	5.88E+04	3.65E+03	7.22E+03	1.36E+04	5.33E+04	6.50E+04	1.59E+04	6.14E+04	2.37E+04	7.89E+03	9.44E+02
Q9UBR2 CATZ	1.80E+03	8.02E+03	3.98E+03	2.94E+04	9.28E+02	4.69E+03	1.72E+03	1.29E+04	4.95E+04	3.70E+04	3.74E+02	6.04E+03	9.08E+04	8.41E+04	6.36E+04
P09104 ENOG	8.37E+04	1.19E+05	1.10E+05	2.49E+04	5.63E+04	2.14E+04	3.85E+05	6.86E+05	1.05E+04	2.60E+04	1.46E+05	8.66E+04	8.63E+03	6.93E+05	1.06E+05
P04843 RPN1	5.98E+04	1.04E+04	6.02E+04	7.80E+04	9.06E+03	3.86E+04	6.60E+03	8.33E+03	4.58E+04	2.45E+04	4.34E+04	1.00E+04	1.31E+04	3.06E+04	2.89E+04
P04632 CPNS1	5.11E+04	1.16E+04	3.05E+04	1.14E+04	1.65E+04	2.60E+04	3.64E+04	1.37E+04	3.79E+03	3.50E+03	4.76E+04	1.71E+04	4.55E+04	8.66E+03	2.49E+04
P62269 RS18	1.02E+05	2.17E+05	8.06E+04	1.28E+05	1.06E+05	8.78E+04	3.46E+04	1.75E+05	2.13E+04	5.94E+04	2.22E+05	2.20E+05	1.93E+04	1.02E+05	8.34E+04
Q92736 RYS2	1.87E+05	5.66E+05	9.11E+05	1.08E+05	1.03E+05	2.10E+05	3.66E+05	3.53E+05	2.87E+05	4.10E+05	2.71E+05	2.03E+05	6.01E+05	2.62E+05	2.28E+04
P11586 C1TC	2.62E+04	2.80E+05	2.01E+05	4.73E+04	1.20E+05	2.81E+05	1.02E+05	2.13E+05	1.19E+04	2.67E+03	3.58E+04	3.75E+04	5.91E+04	3.67E+04	3.38E+04
P48681 NEST	7.07E+04	1.41E+04	1.42E+04	6.68E+04	5.48E+04	9.52E+03	1.16E+04	6.63E+03	8.93E+04	9.81E+04	2.75E+04	6.77E+04	3.33E+04	1.30E+04	2.64E+04
Q9UN36-3 NDRG2	1.08E+03	5.79E+04	6.56E+04	2.57E+04	4.87E+03	9.69E+02	1.31E+05	2.89E+04	1.08E+04	8.82E+03	1.72E+04	7.34E+03	2.57E+03	3.97E+04	1.40E+03
Q13683-9 ITA7	4.73E+04	1.82E+04	2.15E+05	2.18E+05	1.27E+04	1.20E+05	7.42E+05	2.90E+04	3.15E+04	2.79E+03	8.91E+03	7.47E+04	5.88E+04	2.51E+03	1.02E+04
P02794 FRIH	1.04E+04	2.84E+04	6.59E+03	2.60E+04	3.05E+04	1.96E+05	2.25E+03	5.17E+06	1.24E+05	4.58E+04	2.09E+04	5.61E+03	1.13E+04	5.14E+04	1.21E+04
Q9UMS6 SYNP2	1.96E+04	1.97E+04	3.40E+04	1.30E+04	1.12E+03	3.94E+04	3.02E+03	4.38E+03	1.14E+04	6.52E+04	8.04E+02	2.19E+03	7.09E+03	3.02E+05	1.25E+03
Q9UJY1 HSPB8	5.08E+04	8.19E+04	2.42E+04	6.03E+03	1.52E+04	1.10E+05	1.59E+04	1.50E+04	8.75E+04	5.24E+04	7.30E+04	8.39E+04	4.28E+04	5.90E+04	9.40E+03
P29218 IMPA1	1.23E+04	8.69E+04	1.03E+06	7.20E+04	7.22E+04	1.17E+05	1.63E+05	8.94E+05	8.27E+04	3.97E+04	1.36E+05	1.04E+05	1.57E+05	1.12E+05	8.69E+04
Q15848 ADIPO	3.49E+04	2.78E+03	4.94E+03	7.49E+03	2.00E+04	1.84E+04	2.57E+03	5.85E+03	7.61E+04	5.23E+04	7.01E+03	1.64E+03	6.85E+03	1.46E+05	2.66E+04
P36578 RL4	1.25E+03	1.99E+03	3.06E+04	7.35E+02	3.89E+04	3.96E+04	3.15E+04	2.45E+03	9.30E+03	1.52E+04	5.09E+02	4.92E+04	3.86E+04	2.35E+03	2.51E+04
Q9UI09 NDUAC	3.02E+04	5.43E+04	1.46E+04	6.67E+04	4.72E+04	2.78E+04	6.17E+04	1.18E+04	2.46E+04	3.15E+03	8.48E+04	4.48E+04	4.67E+04	5.02E+03	1.27E+05
P01871 IGHM	1.02E+03	8.49E+03	4.50E+03	4.58E+03	4.15E+04	2.41E+03	8.95E+02	3.56E+03	1.47E+04	4.80E+04	4.67E+02	1.34E+04	2.18E+03	4.85E+03	3.46E+03
O75112-2 LDB3	2.72E+05	1.06E+04	1.35E+03	8.93E+04	8.71E+04	1.95E+03	2.56E+03	4.34E+03	1.44E+03	4.35E+03	1.10E+05	6.34E+03	2.35E+03	9.17E+02	1.29E+05
P35613 BASI	3.17E+03	4.43E+03	7.22E+03	2.06E+04	3.45E+03	2.92E+03	1.13E+04	1.59E+04	2.12E+05	2.23E+05	1.60E+04	1.13E+04	1.86E+04	3.93E+05	1.53E+03
O43837 IDH3B	4.93E+04	1.27E+04	2.36E+06	8.06E+03	9.10E+02	1.34E+06	1.46E+05	2.62E+06	3.76E+04	5.39E+04	1.95E+04	1.09E+05	1.57E+05	7.31E+04	3.67E+04
P39019 RS19	9.60E+04	1.46E+05	1.98E+04	1.77E+04	1.10E+04	7.07E+04	1.05E+04	1.47E+04	4.40E+03	2.07E+04	1.19E+05	9.68E+04	1.17E+04	9.07E+03	7.21E+04
P60660 MYL6	4.19E+06	1.43E+05	1.13E+05	1.47E+05	1.78E+05	3.23E+04	3.97E+04	1.14E+05	3.65E+06	2.29E+05	6.14E+06	5.59E+04	6.95E+05	7.17E+06	5.35E+06

P50502 F10A1	4.82E+04	6.55E+04	1.36E+04	4.69E+03	2.25E+04	4.80E+04	1.89E+04	1.20E+04	1.78E+05	1.07E+03	1.53E+04	1.27E+04	8.81E+03	4.38E+03	4.08E+04
P11182 ODB2	3.22E+03	1.08E+04	7.96E+03	2.23E+04	6.41E+04	8.83E+03	4.96E+03	9.80E+03	4.08E+03	5.77E+03	6.15E+03	4.73E+04	1.44E+04	5.00E+03	1.39E+04
Q07507 DERM	7.75E+02	1.33E+04	6.84E+05	8.84E+03	2.56E+04	8.20E+03	2.88E+05	1.34E+05	6.03E+03	2.33E+03	3.05E+03	1.15E+04	7.97E+04	9.68E+03	1.24E+03
P07858 CATB	1.05E+03	5.84E+04	5.40E+03	2.99E+04	1.50E+04	7.91E+03	2.39E+04	7.50E+03	1.91E+03	3.62E+03	5.00E+04	6.91E+03	6.30E+04	7.01E+03	7.22E+04
Q8N335 GPD1L	9.14E+03	1.10E+05	2.16E+04	4.89E+04	6.12E+04	1.07E+05	6.02E+03	2.23E+04	5.73E+04	1.21E+05	7.12E+04	1.26E+05	1.35E+05	2.02E+04	5.19E+04
P05166 PCCB	5.95E+03	6.95E+03	4.97E+03	4.66E+03	4.34E+03	6.74E+02	1.65E+03	7.24E+03	4.97E+04	3.69E+03	5.03E+03	4.64E+03	4.11E+03	6.65E+04	8.01E+03
O75347 TBCA	7.63E+04	6.24E+04	1.06E+04	8.35E+03	7.86E+03	5.45E+03	6.93E+03	1.60E+05	1.32E+05	7.32E+04	4.57E+04	7.65E+04	1.96E+03	1.02E+05	2.48E+04
O75251 NDUS7	7.96E+05	3.12E+04	3.33E+04	2.57E+03	2.52E+03	1.55E+04	8.03E+05	1.04E+06	1.96E+05	2.42E+05	4.02E+03	4.58E+04	7.96E+03	7.02E+04	5.19E+03
P53597 SUCA	6.37E+04	2.17E+05	8.70E+04	2.30E+04	8.11E+04	1.54E+05	4.32E+04	7.41E+04	1.09E+03	2.11E+03	7.47E+04	9.34E+04	2.88E+04	6.92E+03	1.19E+05
Q9UBQ7 GRHPR	7.34E+03	4.00E+03	5.35E+03	3.16E+03	1.15E+05	2.20E+04	3.70E+04	6.89E+03	1.29E+03	1.43E+04	1.00E+05	8.23E+04	2.36E+03	2.73E+03	3.59E+03
P01011 AACT	2.55E+04	1.08E+05	1.21E+05	7.69E+04	2.88E+05	1.78E+05	6.45E+05	8.73E+05	5.09E+05	1.05E+06	1.05E+04	1.85E+05	5.01E+04	4.02E+05	4.05E+04
P15090 FABP4	4.78E+04	9.38E+04	8.95E+03	1.27E+04	1.76E+05	9.76E+04	2.61E+05	6.07E+04	5.62E+04	7.40E+04	1.34E+04	4.87E+04	7.82E+04	9.96E+04	5.08E+03
Q96KP4 CNDP2	1.07E+04	8.60E+02	9.58E+04	4.19E+04	7.44E+04	6.83E+04	7.91E+04	5.24E+04	8.36E+04	1.21E+04	3.12E+03	7.67E+04	7.67E+04	8.23E+04	1.82E+04
Q16629 SFRS7	3.77E+03	5.43E+03	4.99E+04	1.28E+04	4.51E+03	3.08E+03	9.89E+03	3.69E+04	3.94E+04	1.19E+04	8.58E+03	5.10E+03	1.98E+04	2.23E+04	1.09E+04
P07951-3 TPM2	4.31E+04	9.03E+04	7.08E+04	4.31E+04	1.19E+05	1.10E+04	5.04E+04	2.76E+05	4.50E+03	3.71E+03	1.12E+04	1.87E+05	1.15E+05	3.24E+03	1.98E+04
P62857 RS28	4.84E+04	2.16E+04	9.43E+04	6.46E+04	2.10E+04	9.64E+04	1.10E+05	1.87E+04	8.97E+03	7.24E+03	5.34E+04	2.70E+04	7.45E+04	7.58E+03	2.75E+03
Q96RQ3 MCCA	2.38E+03	9.79E+04	1.47E+04	4.24E+04	9.73E+04	7.22E+03	9.29E+04	2.08E+05	8.03E+03	3.65E+03	6.75E+03	4.14E+04	7.59E+04	3.85E+03	3.65E+03
P04899 GNAI2	2.49E+04	9.17E+04	1.34E+05	8.80E+04	3.81E+04	1.07E+05	1.27E+05	1.76E+05	4.75E+04	8.10E+03	1.91E+04	2.17E+04	4.81E+03	7.59E+04	9.57E+04
P13861 KAP2	3.03E+03	3.05E+05	1.36E+04	9.99E+04	2.70E+05	2.95E+05	4.99E+05	5.56E+04	3.59E+04	9.55E+03	3.61E+04	3.11E+05	1.05E+05	2.15E+04	2.05E+04
P15088 CBPA3	1.63E+04	3.92E+03	2.27E+04	3.97E+04	2.16E+03	1.84E+04	9.55E+04	1.10E+04	2.52E+04	5.42E+05	2.75E+03	1.99E+03	9.53E+04	7.39E+03	2.68E+03
Q13561 DCTN2	5.62E+05	3.49E+05	5.09E+05	4.23E+05	7.47E+05	1.03E+06	9.44E+05	4.43E+04	3.60E+04	1.62E+04	4.92E+04	3.83E+05	7.37E+03	1.73E+06	1.33E+04
P84077 ARF1	2.14E+03	1.62E+05	1.36E+04	9.92E+04	8.21E+04	8.87E+03	2.15E+05	1.18E+04	3.65E+04	1.42E+04	4.49E+03	1.67E+05	2.99E+04	4.02E+04	1.92E+03
P10909-2 CLUS	8.96E+03	8.28E+03	1.45E+05	1.13E+04	1.95E+04	4.56E+03	1.13E+05	9.32E+04	2.99E+04	5.58E+04	3.16E+04	1.34E+05	6.48E+03	4.33E+04	5.27E+03
P49419 AL7A1	5.24E+03	1.14E+05	1.66E+05	4.44E+04	2.20E+03	2.28E+05	2.52E+05	1.04E+05	1.10E+06	2.68E+04	2.61E+03	7.71E+04	6.39E+03	1.76E+06	5.83E+04
Q71UI9 H2AV	4.48E+04	1.36E+05	4.16E+04	2.34E+04	1.82E+04	2.19E+05	1.47E+04	4.86E+05	3.75E+05	3.35E+05	8.66E+04	3.42E+04	1.51E+05	3.25E+05	2.90E+04
P43034 LIS1	1.09E+04	9.57E+04	1.33E+05	1.11E+04	2.04E+03	1.41E+05	1.24E+05	5.04E+04	5.32E+04	5.65E+04	1.95E+04	8.09E+04	7.96E+03	9.15E+04	5.66E+03
P09669 COX6C	6.10E+05	3.88E+04	4.41E+04	1.06E+04	5.91E+04	3.63E+04	5.32E+05	6.21E+04	4.93E+03	6.68E+03	3.25E+05	1.19E+04	2.72E+04	6.28E+04	6.05E+03
Q00059 TFAM	5.91E+03	3.06E+04	1.55E+04	4.48E+04	7.92E+04	5.00E+04	1.62E+05	7.67E+04	2.97E+03	3.44E+04	9.31E+03	7.24E+04	4.56E+03	1.90E+04	9.72E+03
P17931 LEG3	1.57E+04	6.99E+05	3.00E+05	2.73E+05	5.05E+05	9.61E+05	1.45E+06	7.15E+04	9.53E+04	1.28E+04	1.77E+04	3.83E+05	4.01E+05	1.46E+04	5.88E+05
Q8IWX7-2 UN45B	3.64E+04	1.55E+04	1.56E+04	6.94E+04	1.47E+04	1.46E+03	1.06E+03	1.43E+04	4.60E+03	5.19E+03	2.67E+04	1.36E+04	9.59E+04	1.32E+04	4.24E+04
O75208 COQ9	9.36E+04	1.77E+04	2.70E+03	8.42E+03	1.15E+04	3.02E+03	2.16E+05	1.31E+05	2.47E+03	4.02E+03	1.74E+04	5.60E+04	9.42E+03	1.79E+03	6.17E+03
Q96Q06 PLIN4	6.68E+03	8.37E+04	4.87E+04	9.78E+04	7.65E+04	6.25E+04	1.05E+05	1.26E+04	5.79E+04	7.80E+04	1.92E+04	6.22E+04	2.33E+04	1.15E+05	1.87E+04
P45954 ACDSB	2.68E+04	8.04E+03	1.45E+04	2.49E+04	9.23E+03	5.99E+03	5.88E+04	1.14E+04	4.14E+04	4.54E+04	2.07E+04	2.82E+03	4.25E+03	5.55E+04	5.94E+03
O95292 VAPB	6.37E+04	1.25E+04	2.16E+03	3.31E+04	4.36E+03	8.72E+03	4.66E+03	8.00E+03	2.25E+05	3.08E+05	4.41E+04	9.23E+03	2.32E+04	3.44E+04	1.22E+04
P47756 CAPZB	9.50E+04	7.14E+04	2.92E+04	1.43E+05	1.29E+04	2.54E+05	2.27E+04	3.79E+04	2.00E+04	3.03E+04	6.93E+04	4.77E+04	5.55E+04	1.21E+04	1.67E+05
Q9BQ69 MACD1	8.51E+04	1.48E+04	5.53E+04	3.72E+04	5.04E+04	5.46E+04	1.39E+04	1.33E+05	3.69E+03	2.80E+03	1.02E+05	1.43E+05	4.87E+03	2.16E+03	2.22E+04
P16671 CD36	1.30E+05	1.43E+05	4.04E+04	3.66E+04	1.89E+04	2.86E+04	2.40E+04	2.36E+04	1.30E+05	2.14E+04	1.06E+05	1.20E+05	5.54E+04	3.19E+05	1.11E+05
P19105 ML12A	6.97E+04	1.12E+05	2.04E+05	1.47E+05	4.55E+04	1.07E+05	2.20E+05	1.06E+05	2.72E+05	3.64E+05	1.30E+05	1.46E+05	1.90E+04	3.54E+05	1.78E+04
P18136 KV313	8.90E+03	1.89E+04	2.33E+04	4.80E+04	2.25E+05	1.06E+05	2.11E+05	4.16E+03	1.18E+04	1.60E+05	9.45E+03	6.84E+04	4.34E+03	3.71E+04	3.89E+04
P62277 RS13	1.28E+05	1.10E+05	1.80E+05	1.69E+05	1.22E+05	1.57E+05	3.64E+05	1.12E+05	1.17E+05	9.98E+04	8.44E+04	1.34E+05	1.94E+05	4.99E+04	1.61E+05
P10768 ESTD	3.18E+04	1.97E+04	1.03E+04	2.72E+03	3.50E+03	9.54E+04	1.22E+04	2.07E+04	7.19E+04	6.60E+04	7.91E+03	1.56E+04	1.45E+04	7.86E+04	1.13E+04
P12694 ODBA	8.11E+03	1.28E+04	7.33E+04	9.38E+03	9.92E+03	2.16E+04	9.07E+04	2.93E+03	8.32E+04	7.37E+04	1.97E+03	3.32E+04	5.32E+03	5.16E+03	7.76E+03
P31948 STIP1	3.53E+04	2.39E+05	4.47E+04	2.00E+05	9.35E+03	2.73E+05	2.63E+05	2.47E+04	2.81E+03	3.31E+03	1.46E+04	2.76E+05	4.31E+04	5.08E+03	2.09E+05
P02751-10 FINC	1.96E+05	1.04E+05	8.64E+04	5.10E+03	4.71E+04	9.81E+04	5.85E+04	3.95E+04	1.61E+04	1.09E+04	4.86E+04	1.27E+04	2.62E+04	1.95E+04	8.55E+03
P13798 ACPH	1.18E+05	5.92E+03	4.45E+04	2.19E+05	1.75E+04	3.89E+03	2.38E+04	1.10E+04	3.25E+03	1.12E+03	3.76E+05	8.83E+03	1.57E+05	6.07E+04	3.36E+04
Q16363 LAMA4	5.28E+04	8.62E+04	5.90E+04	3.80E+04	4.55E+04	7.83E+04	1.68E+05	4.86E+04	1.50E+04	4.01E+04	3.60E+04	1.16E+05	9.38E+04	2.64E+04	7.02E+04
P23526 SAHH	4.35E+04	1.69E+04	2.10E+04	1.67E+04	1.77E+04	1.55E+04	2.84E+04	2.98E+04	1.11E+04	2.45E+03	1.72E+04	2.86E+04	3.02E+04	5.35E+03	3.21E+04

P07942 LAMB1	8.27E+03	9.38E+05	1.95E+05	5.46E+04	5.07E+05	1.12E+06	2.44E+05	7.27E+04	3.30E+05	2.06E+05	1.00E+05	2.92E+05	7.40E+04	2.42E+05	3.94E+05
P18124 RL7	1.39E+03	1.59E+05	1.54E+04	5.93E+04	2.45E+04	1.03E+05	4.71E+03	5.47E+03	3.53E+03	9.47E+03	9.92E+02	1.47E+05	1.92E+04	3.33E+03	1.06E+04
Q15582 BGH3	1.97E+03	6.49E+04	3.01E+05	2.08E+03	1.99E+04	2.61E+04	1.96E+05	1.26E+05	1.64E+04	3.21E+04	1.21E+03	1.92E+04	7.09E+03	3.28E+04	2.72E+03
O60220 TIM8A	2.97E+04	3.20E+05	1.98E+04	1.74E+05	1.57E+05	3.54E+04	3.97E+03	2.13E+04	5.40E+03	9.24E+02	3.22E+04	2.15E+05	1.87E+04	1.21E+04	2.32E+05
P62750 RL23A	1.14E+04	5.08E+04	8.68E+04	5.20E+04	4.15E+05	3.44E+04	4.98E+04	4.03E+04	4.80E+03	3.65E+03	4.24E+04	4.36E+04	2.19E+04	2.21E+04	7.53E+03
O75131 CPNE3	4.73E+04	1.37E+05	6.03E+04	9.49E+04	1.06E+05	1.20E+05	2.06E+05	5.77E+03	3.03E+03	2.70E+04	3.69E+04	1.38E+05	5.37E+03	6.47E+03	8.06E+04
P35268 RL22	3.53E+04	4.62E+03	2.68E+05	2.37E+03	2.75E+03	2.64E+05	3.90E+03	3.62E+05	5.62E+03	2.20E+03	3.60E+04	7.45E+03	5.39E+04	5.98E+03	3.39E+03
P0C0L5 CO4B	1.02E+04	1.41E+05	3.67E+04	2.16E+04	2.41E+05	1.59E+05	1.15E+05	4.72E+04	6.53E+04	1.65E+05	1.76E+04	4.04E+05	2.30E+05	5.80E+04	1.43E+05
P52565 GDIR1	7.37E+02	1.98E+05	1.27E+04	1.06E+05	2.79E+03	2.34E+05	3.99E+04	1.55E+04	3.40E+04	2.34E+04	2.55E+04	1.82E+05	6.19E+05	5.61E+03	4.63E+04
Q9NZ45 CISD1	7.76E+04	1.88E+03	1.12E+04	1.50E+04	8.46E+04	1.98E+04	6.02E+03	5.88E+03	1.83E+04	1.65E+04	8.59E+04	3.00E+03	2.15E+04	2.60E+04	3.18E+03
P15311 EZRI	1.02E+03	2.14E+05	1.47E+04	1.66E+05	1.14E+05	2.98E+05	2.36E+05	1.95E+04	4.67E+04	3.72E+04	5.27E+03	2.55E+05	6.75E+03	8.65E+04	1.67E+05
Q04760 LGUL	3.25E+04	5.89E+03	5.84E+03	3.35E+04	6.09E+03	6.40E+03	6.27E+03	4.84E+03	1.88E+05	2.24E+05	3.45E+04	2.61E+04	4.22E+03	2.50E+04	1.37E+03
Q9UKS6 PACN3	3.94E+04	5.58E+04	3.45E+04	3.86E+04	4.40E+03	2.01E+04	5.62E+04	8.90E+04	2.02E+05	4.88E+05	3.74E+04	1.37E+03	1.58E+03	1.04E+04	1.58E+04
P46976 GLYG	1.41E+04	4.38E+03	8.03E+03	1.20E+04	1.36E+03	2.26E+03	3.15E+03	7.15E+03	1.92E+04	3.32E+03	7.65E+04	8.14E+03	6.89E+04	7.29E+03	4.94E+03
P37802 TAGL2	3.13E+05	1.34E+04	3.03E+04	6.50E+04	8.80E+04	1.33E+05	1.48E+04	1.89E+04	1.54E+05	6.22E+04	1.24E+05	1.09E+05	3.27E+04	2.58E+04	7.52E+04
O75323 NIPS2	6.33E+05	5.20E+05	3.98E+04	2.64E+05	1.84E+05	2.55E+05	1.48E+05	6.90E+04	5.94E+04	9.79E+04	4.97E+05	3.44E+05	8.78E+05	8.38E+04	5.63E+05
Q08257 QOR	5.52E+04	2.60E+03	1.19E+04	2.71E+03	1.16E+04	2.20E+04	2.55E+03	8.68E+03	1.10E+05	1.73E+04	3.04E+04	4.43E+04	2.01E+04	4.46E+04	7.50E+03
O00330 ODPX	3.10E+03	1.90E+04	1.58E+04	1.58E+04	5.94E+04	6.69E+04	2.88E+04	1.15E+04	2.13E+04	5.67E+04	8.95E+03	2.94E+04	1.32E+04	6.43E+05	2.11E+04
Q99714 HCD2	1.06E+05	4.83E+04	2.23E+04	1.07E+04	1.41E+04	4.39E+04	9.47E+04	5.78E+04	5.41E+03	1.10E+04	5.08E+04	4.62E+03	1.88E+05	2.95E+03	1.38E+05
O43920 NDUS5	6.00E+03	2.37E+04	2.05E+04	1.84E+04	9.72E+03	1.37E+04	3.25E+04	2.34E+04	5.21E+05	5.70E+03	6.53E+03	1.42E+04	1.76E+04	4.05E+05	3.23E+04
O75438-2 NDUB1	1.51E+04	1.12E+04	1.60E+05	7.31E+04	2.84E+04	2.73E+04	4.70E+05	1.36E+04	6.39E+05	1.15E+06	8.09E+04	3.24E+05	2.34E+04	7.70E+06	1.26E+05
P62424 RL7A	8.10E+04	2.56E+04	8.18E+03	4.56E+04	2.93E+04	3.99E+04	6.06E+03	2.39E+04	1.13E+06	1.16E+06	4.40E+04	1.79E+04	7.25E+04	9.72E+05	1.14E+05
Q9BYX7 ACTBM	2.01E+05	8.04E+06	1.83E+07	7.21E+06	6.95E+06	8.25E+06	1.56E+06	6.14E+05	4.77E+05	1.48E+05	2.06E+05	5.28E+06	5.61E+04	1.30E+06	2.19E+05
Q9BV79 MECR	5.64E+04	2.34E+04	8.35E+03	1.45E+03	8.14E+02	1.56E+04	1.72E+05	3.13E+05	2.96E+03	4.10E+03	1.91E+03	2.75E+03	1.05E+04	1.85E+04	3.49E+03
O60313 OPA1	6.31E+05	9.33E+04	3.61E+03	9.97E+05	1.90E+05	1.10E+05	1.77E+04	3.63E+04	4.02E+04	3.57E+03	8.45E+05	5.95E+04	1.12E+05	3.08E+04	8.44E+04
O00483 NDUA4	6.35E+04	3.48E+04	7.66E+03	1.39E+05	9.28E+03	1.14E+05	2.05E+04	1.19E+05	8.90E+03	1.22E+04	4.21E+05	4.49E+04	1.36E+06	1.91E+04	3.51E+05
Q13424 SNTA1	6.28E+04	3.78E+04	3.37E+03	7.49E+04	6.05E+04	1.57E+05	1.17E+04	1.51E+04	2.31E+03	3.63E+03	2.14E+04	2.23E+04	7.97E+03	1.40E+04	3.55E+03
Q14240 IF4A2	1.30E+03	3.80E+04	1.62E+04	9.18E+03	1.96E+03	4.13E+03	8.42E+04	1.10E+05	3.93E+03	2.64E+03	1.77E+03	7.11E+03	5.48E+04	1.39E+04	6.22E+04
O00217 NDUS8	3.81E+04	2.76E+04	9.38E+03	5.34E+04	1.00E+05	2.96E+03	5.90E+03	1.44E+04	2.59E+03	5.50E+03	8.13E+04	1.69E+04	2.86E+04	2.56E+03	1.08E+05
P00918 CAH2	8.17E+04	1.03E+05	1.63E+04	8.78E+03	7.29E+04	6.16E+04	1.36E+04	7.06E+03	1.85E+03	1.11E+04	3.42E+04	4.46E+04	1.70E+04	1.08E+05	3.71E+03
P14314 GLU2B	1.04E+03	3.55E+04	1.71E+04	5.52E+04	3.16E+04	3.06E+04	4.07E+03	1.42E+05	4.97E+03	2.75E+03	1.85E+04	4.84E+04	4.02E+04	2.17E+04	3.01E+04
O75367 H2AY	1.81E+04	1.09E+05	2.23E+04	1.31E+05	1.39E+05	2.31E+05	1.85E+05	1.25E+04	3.41E+04	1.15E+05	4.94E+03	9.42E+04	9.13E+03	2.15E+04	1.34E+05
Q15327 ANKR1	3.47E+04	5.84E+04	2.11E+04	1.36E+04	5.51E+04	4.32E+04	2.49E+04	2.30E+04	1.40E+05	2.04E+03	6.50E+04	3.69E+04	4.02E+04	1.10E+04	1.96E+04
P68366 TBA4A	2.10E+05	3.38E+05	1.75E+05	1.09E+05	2.39E+05	2.64E+05	2.29E+05	6.34E+05	7.64E+05	6.22E+05	1.47E+05	3.09E+05	3.71E+05	9.29E+05	2.16E+05
O00429-4 DNM1L	7.53E+02	7.04E+03	1.08E+05	3.44E+04	1.84E+03	6.78E+04	1.51E+04	1.84E+04	5.54E+03	3.90E+04	6.31E+02	3.34E+04	2.09E+03	1.85E+03	4.55E+02
Q07020 RL18	1.32E+04	1.66E+04	1.60E+04	3.95E+04	9.01E+04	2.15E+05	3.63E+04	6.31E+03	2.01E+04	4.76E+04	3.30E+04	3.80E+04	3.75E+04	2.17E+04	1.28E+05
P14625 ENPL	3.03E+04	4.56E+03	5.68E+04	1.17E+04	1.62E+04	2.34E+04	1.70E+04	1.31E+04	3.52E+04	3.96E+04	8.02E+04	9.68E+03	2.83E+03	1.78E+04	1.44E+04
P05023-2 AT1A1	2.26E+04	2.85E+04	2.69E+04	5.92E+04	2.17E+04	9.00E+04	1.36E+05	4.80E+04	1.35E+04	3.08E+03	7.70E+04	1.57E+04	3.25E+04	3.09E+04	3.59E+04
P51149 RAB7A	9.33E+04	1.33E+03	1.80E+05	2.18E+03	4.69E+03	1.94E+05	5.18E+04	1.20E+05	1.10E+05	1.39E+05	7.09E+03	6.15E+03	3.93E+03	3.43E+05	3.94E+03
P23396 RS3	3.14E+03	2.48E+03	6.87E+03	4.17E+03	3.91E+03	1.14E+03	6.43E+03	3.91E+04	1.24E+05	4.58E+04	1.10E+04	1.06E+04	7.49E+03	1.34E+05	2.68E+03
P07585 PGS2	1.37E+04	2.87E+03	1.92E+05	2.14E+03	1.26E+03	9.02E+03	6.16E+04	2.62E+04	1.20E+04	6.43E+03	6.91E+02	3.55E+03	1.28E+04	4.32E+03	6.84E+03
P05556-2 ITB1	4.21E+04	7.25E+04	1.29E+04	1.86E+05	3.79E+04	1.61E+05	2.64E+05	2.71E+05	1.65E+05	2.17E+05	7.36E+04	8.30E+04	6.06E+04	2.35E+05	1.51E+05
P23083 HV103	3.14E+03	1.18E+04	1.05E+05	5.18E+03	7.75E+04	6.87E+03	1.51E+04	5.48E+04	1.48E+05	8.75E+04	1.12E+03	2.64E+03	4.19E+03	1.87E+05	1.97E+04
P02760 AMBP	3.35E+04	1.10E+05	4.24E+05	4.64E+03	5.35E+04	1.64E+05	1.68E+04	9.88E+03	1.23E+05	1.28E+05	1.07E+04	3.68E+04	2.00E+04	1.11E+05	1.28E+05
P14406 CX7A2	2.45E+03	5.36E+05	5.37E+05	6.65E+03	2.61E+03	3.65E+05	1.69E+04	3.03E+04	1.64E+05	8.11E+04	4.27E+02	2.10E+05	4.98E+03	1.71E+05	3.97E+04
P08574 CY1	2.86E+04	8.02E+03	1.87E+04	1.67E+04	1.51E+04	1.29E+04	2.36E+04	6.47E+04	3.58E+04	8.13E+04	1.32E+05	1.85E+04	2.22E+04	2.31E+04	1.15E+05
Q9NY65 TBA8	3.61E+03	1.06E+04	3.21E+04	1.00E+05	1.73E+03	5.44E+03	4.33E+03	2.37E+05	2.38E+04	8.51E+03	5.93E+04	7.93E+04	2.01E+04	1.40E+04	7.00E+04

P28161 GSTM2	1.63E+03	1.47E+03	8.38E+03	2.41E+03	3.46E+03	5.49E+03	4.26E+03	4.41E+03	7.21E+04	2.28E+04	3.74E+03	5.56E+03	7.80E+03	3.56E+04	1.20E+04
Q16762 THTR	1.65E+03	6.12E+04	1.85E+05	2.95E+04	2.32E+03	1.74E+03	1.79E+04	2.79E+03	4.88E+03	2.43E+04	7.99E+03	4.56E+04	7.90E+04	1.41E+04	9.00E+04
P56556 NDUA6	5.98E+04	2.11E+05	2.78E+04	2.11E+04	3.36E+04	7.88E+04	2.51E+04	7.84E+04	2.81E+05	1.09E+04	1.04E+05	2.32E+05	4.73E+03	1.38E+05	9.61E+04
P35998 PRS7	1.63E+04	3.17E+05	4.09E+05	5.35E+04	3.77E+05	5.78E+05	4.55E+05	6.65E+05	2.68E+04	4.62E+04	7.67E+04	3.73E+05	1.61E+05	1.58E+05	3.29E+05
P14174 MIF	1.81E+04	1.04E+04	2.21E+04	1.21E+04	3.30E+04	1.21E+04	4.94E+04	1.07E+05	1.39E+03	4.38E+03	5.17E+03	8.54E+04	1.04E+04	6.63E+03	5.42E+04
O15273 TELT	3.19E+03	8.65E+03	1.03E+05	2.26E+05	1.09E+05	4.28E+03	1.55E+05	4.75E+03	8.22E+02	4.23E+03	2.70E+05	1.45E+04	3.64E+04	5.32E+03	4.16E+04
P02763 A1AG1	2.40E+03	7.15E+03	9.60E+03	7.95E+02	9.73E+04	1.68E+03	3.70E+04	1.09E+04	1.32E+04	6.91E+03	2.55E+03	1.83E+04	2.92E+03	6.03E+03	9.63E+03
P01781 HV320	5.46E+04	1.85E+04	7.16E+03	1.91E+04	7.04E+03	2.92E+03	3.84E+03	3.13E+04	2.34E+04	6.18E+04	4.25E+04	2.98E+04	2.46E+04	7.08E+03	1.31E+04
P35237 SPB6	5.48E+04	2.78E+04	7.24E+03	6.06E+04	5.14E+03	6.88E+04	8.56E+03	1.14E+05	4.82E+04	9.35E+03	8.74E+04	4.24E+03	1.26E+05	8.34E+04	3.61E+03
P31150 GDIA	1.19E+04	1.59E+05	4.20E+04	6.92E+03	3.58E+04	1.16E+04	3.32E+05	3.82E+03	6.68E+03	2.03E+03	6.56E+02	2.54E+04	6.64E+03	5.94E+03	1.55E+04
P24310 CX7A1	1.97E+05	2.48E+06	7.43E+04	6.32E+03	1.36E+05	2.75E+06	3.90E+04	8.87E+04	1.81E+04	2.43E+04	1.01E+05	1.34E+05	9.51E+03	2.82E+04	2.91E+05
Q9UKU7 ACAD8	2.23E+04	5.20E+04	2.04E+05	1.50E+03	3.12E+03	1.12E+05	1.74E+03	3.41E+03	9.14E+03	1.22E+05	6.23E+03	3.34E+03	5.90E+03	4.78E+03	6.29E+03
Q96CN7 ISOC1	2.59E+03	5.21E+03	6.59E+04	2.45E+04	9.67E+02	9.11E+03	7.82E+03	5.41E+03	1.92E+05	1.31E+05	1.62E+03	2.18E+03	6.40E+03	9.37E+04	2.28E+03
P43155-3 CACP	2.16E+04	1.33E+04	9.95E+03	3.81E+04	7.35E+04	2.94E+03	7.32E+03	2.27E+04	5.10E+03	8.88E+03	1.82E+03	2.40E+04	8.95E+03	4.40E+04	4.37E+04
P05155 IC1	1.92E+03	3.60E+04	3.74E+03	2.31E+03	2.86E+03	6.24E+04	1.74E+05	1.11E+05	3.66E+03	2.88E+04	3.64E+03	3.17E+03	8.13E+03	1.01E+04	5.88E+02
Q13418 ILK	1.90E+03	2.23E+04	5.82E+03	9.06E+02	2.10E+03	2.43E+04	7.21E+04	6.73E+04	2.82E+03	1.14E+05	5.51E+02	2.30E+03	2.44E+03	9.32E+03	7.86E+02
P36776 LONM	1.50E+05	7.69E+03	1.62E+04	8.31E+02	2.97E+04	1.09E+04	3.50E+04	1.15E+04	6.76E+04	3.74E+04	1.78E+05	3.19E+05	2.23E+05	6.76E+04	1.09E+05
Q9Y277 VDAC3	2.87E+04	2.55E+03	5.21E+03	3.53E+04	1.07E+03	2.95E+03	5.28E+03	8.38E+03	5.16E+03	3.57E+04	2.94E+04	2.19E+03	5.04E+03	1.92E+03	1.68E+03
P04217 A1BG	5.85E+03	3.32E+04	5.23E+04	1.44E+03	1.59E+04	2.91E+04	5.35E+04	3.70E+04	2.60E+04	8.84E+04	2.98E+03	1.17E+04	2.04E+03	2.28E+04	2.28E+03
Q16718 NDUA5	1.83E+05	3.13E+03	8.95E+03	1.40E+05	1.14E+04	7.52E+02	1.23E+04	1.54E+04	5.57E+03	4.02E+03	5.52E+04	1.29E+04	7.76E+03	3.51E+03	1.76E+04