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Abstract: Nanoparticle (NP)–protein interactions in complex samples have not yet been clearly understood. Nevertheless, several studies demonstrated that NP’s physicochemical features significantly impact on the protein corona composition. Taking advantage of the NP potential to harvest different subsets of proteins, we assessed for the first time the capacity of three kinds of superparamagnetic NPs to highlight the erythrocyte minor proteome. Using both qualitative and quantitative proteomics approaches, nano-liquid chromatography–tandem mass spectrometry allowed the identification of 893 different proteins, confirming the reproducible capacity of NPs to increase the number of identified proteins, through a reduction of the sample concentration range and the capture of specific proteins on the three different surfaces. These NP-specific protein signatures revealed significant differences in their isoelectric point and molecular weight. Moreover, this NP strategy offered a deeper access to the erythrocyte proteome highlighting several signaling pathways implicated in important erythrocyte functions. The automated potentiality, the reproducibility, and the low-consuming sample demonstrate the strong compatibility of our strategy for large-scale clinical studies and may become a standardized sample preparation in future erythrocyte-associated proteomics studies.

Keywords: nanoparticles, red blood cells, mass spectrometry, quantitative proteomics, protein corona, minor proteome

Introduction

With the emergence of nanotechnology, the engineering of “smart” nanoparticles (NPs) has opened up a host of possibilities in medicine and biology.^{1–3} Nevertheless, once injected in blood circulation, the fate of these NPs must be anticipated to prevent an NP-associated toxicity.^{4,5} When an NP is introduced into a biological fluid, it is well recognized that proteins immediately cover its surface, resulting in the formation of a protein “corona”, which will rapidly evolve according to the concentration and the affinity of proteins for the NP.^{6,7} Since the last decade, several studies used different analytical methods⁸ and focused on the performance of NPs in the presence of complex protein mixtures^{9–11} to demonstrate the complexity of these NP–protein interactions.^{12,13} First, the “nano-dimension” of these particles endows them with properties completely different from those of bulk materials with the same compositions. Moreover, NPs have a very large surface-to-volume ratio, so that even small amount of particles presents large surface areas available for protein binding. Finally, the physicochemical properties of NPs such as their size, their surface charge, or their chemical functionalization would determine their protein corona composition,^{11,14–17} which may more influence the biological response of the body.^{18,19} This capacity of NPs to concentrate

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at their surface different subsets of proteins according to their physicochemical properties may be useful in proteomics to improve protein detection and identification, and detect potential disease-associated species.^{20–22} In fact, despite the constant technological advances in mass spectrometry (MS) and sample fractionation methods, the limited dynamic range of current mass spectrometers hinders the entire proteome coverage of biological fluids in which the protein concentration range spans more than ten orders of magnitude.^{23,24} Thus, the low-abundant protein compartment where disease-associated biomarkers are thought to reside is still unattainable. Various nanomaterial-associated strategies^{25–28} have been integrated in MS in order to detect disease-associated biomarkers, and have been found extremely useful to improve protein enrichment and sample preparation, particularly NP-associated technology.^{29–31}

Finding biomarker for disease detection, stratification, as well as therapeutic monitoring is a biomedical priority. Erythrocytes or red blood cells (RBCs) are a paradigmatic situation for clinical proteomics and also a major circulating compartment to individualize biomarkers.^{32,33} RBCs circulate all over the body and deliver oxygen to most organs. They are crucial micro-organisms able to capture and provide remote biomolecular information at the periphery. They are also involved in hematological malignancies^{34,35} for which relevant biomarkers are still missing. Because of the presence of hemoglobin (Hb), which represents 98% of the total RBC soluble protein content and masks the 2% of biologically interesting low-abundant proteins, it is difficult to investigate the deep RBC proteome in clinical and large-scale studies. Although technical advances in RBC sample preparation and fractionation have greatly contributed to reduce the protein concentration range, allowing to increase the number of identified proteins by tandem MS (MS/MS),^{36,37} these approaches are time-consuming and require intensive fractionation on gel and large volumes of sample to be really efficient, thus limiting the clinical translation of such technologies for high-throughput large-scale studies. Until now, the capacity of NPs for protein enrichment in complex protein mixture has never been assessed with RBC proteins.

In the present work, the potential capacity of three kinds of NPs to capture RBC proteins was determined by a qualitative and quantitative proteomics analysis. Based on a fast experimental protocol that required low volume of RBC lysates, and without any fractionation step, nano-liquid chromatography (LC)–MS/MS analysis of the different NP-treated samples revealed 893 different proteins, demonstrating the interest of our nanoproteomics approach to analyze

the RBC proteome in a large-scale context. We used label-free quantification³⁸ to confirm the reproducibility and the influence of the NP surface on protein capture, highlighting subsets of proteins specific to each kind of NPs. Through this work, we demonstrated for the first time the interest of chemically modified NPs in sample preparation for RBC proteomics studies.

Methods

Magnetic NPs

Superparamagnetic NPs of 100 nm in aqueous suspension were obtained from Chemicell GmbH (Berlin, Germany). Three different kinds of NPs grafted with different matrices and functional groups were used in our study, fluidMAG-OS (OS-NP), fluidMAG-PAA (PAA-NP), and fluidMAG-Q (Q-NP) (Table 1). They have a multi-domain core allowing a fast and easy magnetic isolation by an external magnet (MagnetoPURE, Chemicell GmbH). More detailed features are available at <http://www.chemicell.com/>.

The size and zeta potential of the magnetic NPs were determined with a Malvern Zetasizer NanoZS. NPs were diluted in phosphate-buffered saline (PBS; pH 7.3) before measurement, and the measurement was conducted at 25°C using 0.5 mg/mL NP concentrations.

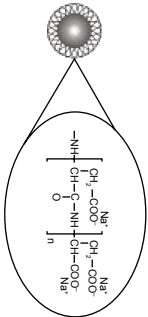
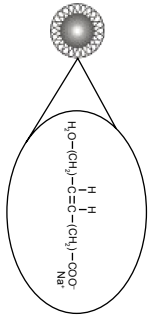
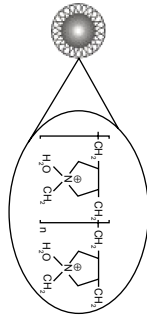
RBC preparation and lysis

Blood samples were collected from five healthy consenting donors, three men and two women aged 44–62 years (mean 55.4 ± 7.7 years) by venipuncture in ethylenediaminetetraacetic acid vacutainer tubes. RBC lysis was performed according to the protocol previously published by Roux-Dalvai et al.³⁷ Briefly, samples were firstly centrifuged at $1,000 \times g$ at +4°C for 10 minutes to eliminate plasma and buffy coat. To further eliminate leukocytes, a ficoll gradient separation was performed. After removal of the monolayer containing mononuclear cells, erythrocytes were carefully collected, avoiding top RBC layer and polynuclear cells collected in the pellet. Erythrocytes were then washed three times with PBS + PMSF (154 mM NaCl, 10 mM phosphate buffer, pH 7.4 containing 0.1 mM PMSF). At each step, along with supernatant, the upper RBC layer was removed.

The lysis of RBC was operated by hypotonic shock. Red cells were diluted to a 1:3 ratio with lysis buffer (5 mM phosphate buffer, pH 7.4 containing 1 mM ethylenediaminetetraacetic acid, and 0.5 mM PMSF) containing protease inhibitor and left in ice for 30 minutes. After freezing, red cells were thawed at 37°C. The procedure of freezing/

Table 1 NP properties

	FluidMAG-PAA	FluidMAG-OS	FluidMAG-Q
Matrix	Aspartic acid	Oleic acid	PolyDADMAC
Functional group	Sodium carboxylate	Sodium carboxylate	Quaternary amine group
Diameter (nm)	112.4	107.7	106.9
PDI	0.11	0.12	0.19
Zeta potential (mV)	-37	-26	+41.0

Notes: The manufacturer provides information about the matrix and the functional group. The mean diameter, the PDI, and the zeta potential have been determined with a Malvern Zetasizer NanoZS. NPs were diluted in PBS (pH 7.3) before measurement, and the measurement was conducted at 25°C using 0.5 mg/mL NP concentrations.

Abbreviations: NP, nanoparticle; PDI, polydispersity index; PBS, phosphate-buffered saline; PolyDADMAC, polydiallyldimethylammonium chloride.

thawing was repeated twice for each sample. At the end of the lysis step, after a centrifugation at 36,000× *g* for 10 minutes at +4°C, the clear supernatants were collected, pooled, and stored at -80°C until use.

RBC proteins–NPs incubation

Five hundred micrograms of each kind of NPs were individually incubated in two replicates for 45 minutes with 200 µL of hemolysate containing 1 mg of total protein. Then, NPs were attracted to one side of the vial by an external magnet, and supernatant was removed. NPs were washed three times in 500 µL PBS. Finally, NP-associated proteins were desorbed using 40 µL of 8 M urea –2% CHAPS, and the protein concentrations were determined by a Bradford protein assay (Bio-Rad Laboratories, Hercules, CA, USA).

Analysis of RBC lysate fractions by SDS-PAGE

Each sample was mixed with Laemmli buffer (4% sodium dodecyl sulfate [SDS], 20% glycerol, 10% 2-mercaptoethanol, 0.004% bromophenol blue, 0.125 M Tris-HCl). The mixture was heated in boiling water for 5 minutes and loaded on a precast 4%–15% polyacrylamide gel. Staining and destaining were performed with Coomassie blue and 30% ethanol/7% acetic acid in water, respectively.

LC–MS/MS analysis of RBC proteins

The [Supplementary materials](#) provide a detailed description of LC–MS/MS identification.

Briefly, 10 µg of each duplicated eluate and crude RBC lysate were separately diluted in Laemmli buffer and stacked in one band after a short and low-voltage electrophoretic migration on SDS-polyacrylamide gel electrophoresis (SDS-PAGE) gel. The stacking bands were cut, proteins were in-gel digested by trypsin, and resulting peptides were extracted from the gel and analyzed by nano-LC–MS/MS using an ultimate 3000 system (Dionex, Amsterdam, the Netherlands) coupled to an LTQ-Orbitrap Velos mass spectrometer (Thermo Scientific, Bremen, Germany). The LTQ-Orbitrap was operated in data-dependent acquisition mode with the Xcalibur software. Survey scan MS spectra were acquired in the Orbitrap in the 300–2,000 *m/z* range with the resolution set to a value of 60,000. The five most intense ions per survey were selected for collision-induced dissociation fragmentation, and the resulting fragments were analyzed in the linear trap quadrupole (LTQ).

Database search and data analysis

The Mascot Daemon software (version 2.3.0, Matrix Science, London, UK) was used to perform database searches against *Homo sapiens* entries in Uniprot protein database. The mass tolerances in MS and MS/MS were set to 5 ppm and 0.6 Da, respectively, and the instrument setting was specified as “ESI-Trap”. Mascot results were parsed with the in-house-developed software Mascot File parsing and Quantification (MFPaQ) v4.0.0 software (<http://mfpaq.sourceforge.net/>), and protein hits were automatically validated if they satisfied one of the following criteria: identification with at least one top-ranking peptide with a Mascot score of more than

39 (P -value <0.001) or at least two top-ranking peptides each with a Mascot score of more than 22 (P -value <0.05). When several proteins matched exactly the same set of peptides, only one member of the protein group was reported in the final list. To evaluate the false-positive rate in these experiments, all the initial database searches were performed using the “decoy” option of Mascot. Mascot results were parsed with the in-house-developed software MFPaQ v4.0.0 (<http://mfpaq.sourceforge.net/>), and protein hits were automatically validated.

Label-free quantification

Quantification of proteins was performed using the label-free module implemented in the MFPaQ v4.0.0 software (<http://mfpaq.sourceforge.net/>). For each sample, the software uses the validated identification results and extracted ion chromatogram (XIC) of the identified peptides in the corresponding raw nano-LC–MS files based on their experimentally measured retention time and monoisotopic m/z values. Quantification of peptide ions was performed based on calculated XIC area values. To compare the abundance profile of one protein in different samples, a protein abundance index (PAI) was calculated for each protein in the different NP samples. PAI was defined as the average of XIC area values for three intense reference tryptic peptides identified for this protein. If only one or two peptides were used to identify the protein, the protein-related PAI was calculated based on the XIC area value of these peptides. As the three different kinds of NPs were experimentally duplicated, six PAI values were obtained for each protein; the highest PAI value was normalized to 1, and the five other PAI values were thus comprised between 0 and 1. Normalized PAIs were submitted to software R for protein hierarchical clustering.³⁹

Results

Magnetic NPs

In this study, we investigated the capacity of three different kinds of 100 nm NPs for protein capture in RBC lysates through the protein identification and quantification of their respective eluted corona. This size of NPs offers a high surface-to-volume ratio and facilitates the NP collection by an external magnet. The main difference between these NPs concerns their surface charge and/or functional group. First, according to dynamic light scattering and zeta potential measurements, the respective NPs were homogeneous in size and monodispersed. Q-NPs displayed a positive charge, and PAA-NPs and OS-NPs both displayed a negative charge (Table 1).

SDS-PAGE analysis

As particles fulfilled critical quality criteria, 500 μg of each kind of NPs, developing 280 cm^2 surface area, were separately incubated in duplicates for 45 minutes with 200 μL of RBC lysates (ie, 1 mg of proteins), followed by extensive washing to remove all unbound proteins. First, the Bradford assays revealed $19 \pm 1 \mu\text{g}$ of proteins eluted from the surface of each kind of NPs, which represented 2% of the initial protein input. Prior to deeper characterization of each NP corona, the same quantity of proteins was loaded on an SDS-PAGE gel (Figure 1) to obtain a protein profile of each condition. For the three types of NPs, SDS-PAGE analysis of the eluted protein corona revealed a pattern obviously different from nontreated sample. Interestingly, the high-abundant Hb was considerably reduced, and the protein profiles of NP-treated samples revealed a great enrichment between 20 kDa and

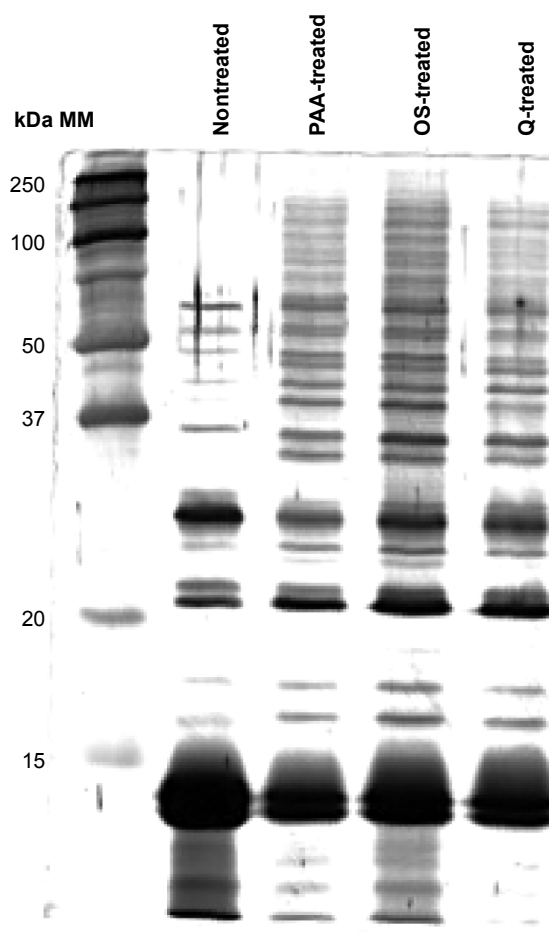


Figure 1 SDS-PAGE of nontreated and NP-treated RBC lysates.

Notes: The same quantity of proteins was loaded on gel for the different tracks. We can see the diminution of hemoglobin proportion in NP-treated samples for which we can distinct two bands corresponding to alpha and beta hemoglobin subunits (around 14 kDa).

Abbreviations: SDS-PAGE, sodium dodecyl sulfate-polyacrylamide gel electrophoresis; NP, nanoparticle; RBC, red blood cell; MM, molecular markers.

250 kDa with the appearance of numerous bands, which were not detected in the control condition.

Protein identification by nano-LC–MS/MS

To better estimate the protein enrichment offered by the NP treatment, a deeper characterization of each NP corona was performed by nano-LC–MS/MS protein identification. Figure 2A sums up the results obtained for each duplicated sample and gives an insight of the harvesting capacity for each condition. The different protein lists are detailed in the [Supplementary materials](#). The two replicates of the crude RBC lysate revealed 108 different proteins, whereas two of the NPs-eluted coronae significantly highlighted more species ($P=0.009$, Mann–Whitney test), from 525 to 576 different species according to the type of NPs (Figure 2A).

Altogether, 909 different proteins were identified from our RBC samples of which 893 were present in the list of NP-treated samples (Figure 2B). Among these 893 proteins, 801 were exclusively identified from NP-eluted coronae, and 92 were shared with crude RBC lysate. A focus on the three NP samples revealed a relatively similar number of identified proteins varying from 525 for OS- and Q-NPs to 576 for PAA-NPs, the three kinds of NPs only sharing 193 proteins (Figure 2C).

Effect of NP treatment on nano-LC–MS/MS analytical coverage

The nano-LC–MS/MS analysis showed that the NP treatment of the sample greatly enhanced the number of identified proteins; this must result from a better MS/MS sampling of

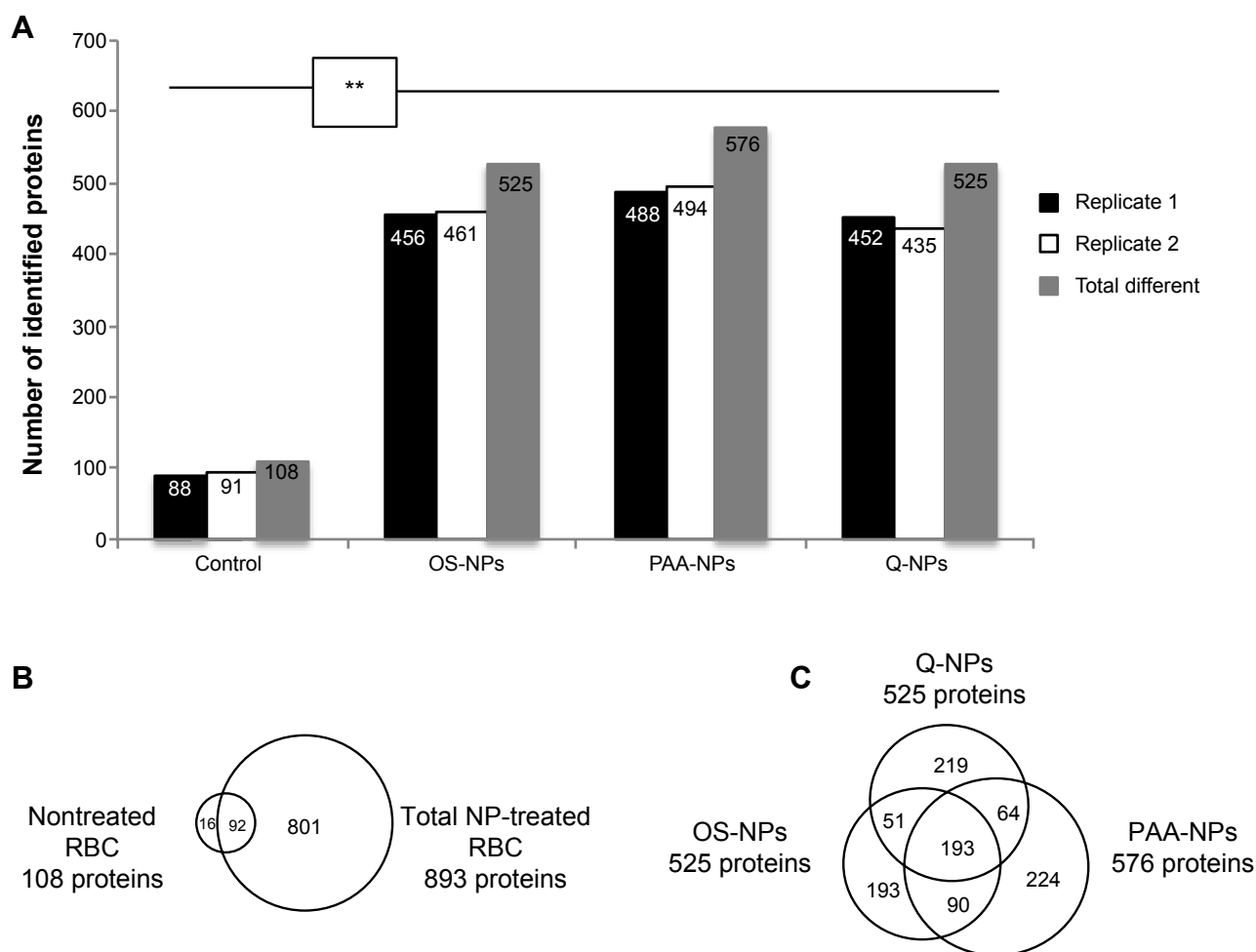


Figure 2 Protein identification results and NP comparison.

Notes: (A) Graphical representation of the number of identified proteins by nano-LC–MS/MS in each replicate, in nontreated and NP-treated RBC lysates. “Total different” columns represent the total number of identified proteins in each condition after merging both replicates. (B and C) Venn diagrams representing the extent of overlap of proteins identified by LC–MS/MS analysis. (B) Comparison made between the nontreated RBC extract (108 proteins) and all NP-treated samples (894 proteins). (C) Comparison among the three NP-treated samples (PAA-NP, 576 proteins; OS-NP, 525 proteins; Q-NP, 525 proteins). The number of identified proteins in NP samples is significantly higher than in nontreated samples (Mann–Whitney test $P=0.009$).

Abbreviations: LC–MS/MS, liquid chromatography–tandem mass spectrometry; NP, nanoparticle; RBC, red blood cell.

the detected ions. To illustrate that effect, we compared the 20 most abundant identified proteins (ie, the 20 proteins with the higher MS/MS queries) in nontreated and NP-treated RBCs (Table 2 and [Supplementary materials](#)). Interestingly, according to the sample treatment, the 20 most abundant proteins were not strictly the same. In fact, only Hb-related subunits and spectrin chains, the two major constituents of RBCs, were shared by all conditions. Nevertheless, the rank and thus the relative abundance of these proteins were different. For example, Hb subunit beta and spectrin alpha chain that were respectively the first and the 20th most abundant protein in nontreated sample occupied the 5th and the 1st rank, respectively, in OS-NP sample. And carbonic anhydrase 1 that appeared just after the Hb-related subunits, as the 12th most abundant protein in nontreated RBC, only occupied the 70th rank in OS-NP sample. These results demonstrate that NP treatment modified the relative protein concentration in RBC sample. This modification of the protein abundance rank was also different according to the kind of NPs, suggesting the differential affinity of the NP surface for RBC proteins. Moreover, we also observed that the number of MS/MS queries assigned to these 20 most abundant proteins was greatly lower in NP-treated condition than in control. In control, 94% of the total MS/MS queries that were generated during the run were assigned to these 20 proteins, of which 91% to the Hb-related subunits. In the NP-treated sample, the 20 most abundant proteins only generated 42%–45% of the total MS/MS queries, of which 20%–29% were assigned to Hb-related subunits, according to the kind of NPs. This observation revealed that NP treatment greatly decreased the proportion of abundant proteins. Finally, for each kind of NPs, we showed that 90%–95% of the 20 most abundant proteins are the same between replicates. We also observed that the 20 most abundant proteins as well as Hb-related subunits generated the same part of MS/MS queries between replicates ([Supplementary materials](#)). These results confirmed the reproducibility of capture of each kind of NPs for these 20 most abundant proteins.

To determine whether NP treatment increased the proportion of low-abundant proteins in RBC samples, the MS/MS queries, the peptide number, and the sequence coverage of ten low-abundant proteins in nontreated sample (ie, proteins with low MS/MS queries) were determined in OS-NPs sample (Table 3). In nontreated sample, these ten low-abundant proteins generated from one to three MS/MS queries, with a low coverage of each protein sequence (from 1.4% to 17.1%). They represented 0.1% of the total MS/MS queries generated by the sample. In OS-NP samples, the same proteins

generated from five to 63 MS/MS queries, allowing a greater coverage of the protein sequence (from 11.9% to 79.6%) through the detection and identification of different peptides for each protein. These ten proteins represented 2% of the total MS/MS queries generated by the NP-treated sample. This enhanced detection of low-abundant proteins was also observed in Q- and PAA-NPs ([Supplementary materials](#)). These observations clearly demonstrated that NP treatment also increased the proportion of low-abundant proteins.

Qualitative and quantitative reproducibility in protein harvesting

Although NP-treated samples allowed a great increase in protein identification, providing access to low-abundant proteins, it was important to confirm the reproducibility of NPs for RBC protein harvesting. First, in a qualitative approach, we compared the MS spectra of each replicate and observed that the MS signal of 90%–94% of identified peptides was present in both replicates per type of NPs, thus confirming the qualitative reproducibility of NPs for protein harvesting (Figure 3A). Then, to assess the quantitative reproducibility of NP-strategy, we used the MFPaQ software,⁴⁰ which was designed to parse and validate protein identifications from Mascot result files and quantify the identified proteins. The quantification module of MFPaQ v4.0.0 was upgraded so that it could handle label-free quantification as described by Mouton-Barbosa et al.⁴¹ More information is available in the [Supplementary materials](#). Briefly, a PAI was calculated for all identified proteins. To assess the quantitative reproducibility of each type of NPs for protein harvesting, the PAI ratio of all identified proteins was determined in duplicates ([Supplementary materials](#)). As shown in Figure 3B, quantitative reproducibility of NPs was found to be good between the duplicates. In fact, the majority of quantified proteins on each kind of NPs revealed a PAI ratio close to the expected value of 1 ([Supplementary materials](#)).

Differential capture of proteins by the NP surface

As the protein capture by NPs was qualitatively and quantitatively reproducible, we aimed to determine if there was an NP-dependent protein harvesting. Based on these quantification results, we normalized the PAIs obtained for each protein in each sample and submitted them to hierarchical clustering with the software R. According to the PAI values of each protein in each condition, the clustering revealed ten differentially quantified protein groups ([Supplementary materials](#)). Among them, groups 4, 5, and 8 revealed 68, 100,

Table 2 List of the 20 most abundant proteins (decreasing from 1 to 20) identified from NPs corona and crude RBC extract

Total MS/MS number	MW	pI	Description	#total MS/MS	%total MS/MS	Rank	%total MS/MS	#total MS/MS	Description	pI	MW	Total MS/MS number
Control RBC												
18,796	16,102	6.75	Hemoglobin subunit beta	2,654	14.1	1	4.4	795	Hemoglobin subunit beta OS	6.75	16,102	18,096
	16,101	7.86	Beta-globin	2,424	12.9	2	4.4	788	Spectrin, beta, erythrocytic	5.15	247,271	
	11,534	5.9	Beta globin (fragment)	1,921	10.2	3	4.3	787	Spectrin beta chain, erythrocyte	5.15	247,171	
	11,496	6.17	Hemoglobin beta (fragment)	1,731	9.2	4	4.2	759	Spectrin alpha chain, erythrocyte	4.95	281,039	
	15,305	8.72	Hemoglobin subunit alpha	1,563	8.3	5	3.3	590	Hemoglobin beta (fragment)	6.17	11,496	
	11,532	5.46	Hemoglobin beta (fragment)	1,499	8.0	6	3.1	568	Hemoglobin subunit alpha	8.72	15,305	
	10,979	6.17	Hbbm fused globin protein (fragment)	1,480	7.9	7	3.1	555	Hemoglobin beta (fragment)	5.46	11,532	
	16,159	7.85	Delta globin	1,429	7.6	8	2.7	495	Hbbm fused globin protein (fragment)	6.17	10,979	
	8,386	6.63	Hemoglobin alpha 2 (fragment)	1,242	6.6	9	2.4	443	Delta globin	7.85	16,159	
	4,263	4.96	Truncated beta globin	968	5.2	10	2.0	358	Solute carrier family 4, anion exchanger, member 1	5.1	102,150	
	16,187	6.64	Hemoglobin subunit gamma-I	242	1.3	11	1.8	330	Transitional endoplasmic reticulum ATPase	5.14	89,950	
	28,909	6.59	Carbonic anhydrase I	113	0.6	12	1.5	272	Proteasome subunit alpha type-6	6.34	27,838	
	59,947	6.9	Catalase	103	0.5	13	1.4	245	Acylamino-acid-releasing enzyme	5.29	82,142	
	247,171	5.15	Spectrin beta chain, erythrocyte	84	0.4	14	1.3	239	Clathrin heavy chain I	5.48	193,260	
	102,150	5.1	Solute carrier family 4, anion exchanger, member 1	72	0.4	15	1.3	236	Hemoglobin subunit gamma-I	6.64	16,187	
	32,325	6.45	Purine nucleoside phosphorylase	59	0.3	16	1.3	228	Myosin-9	5.5	227,646	
	22,049	5.66	Peroxiredoxin-2	57	0.3	17	0.9	171	Delta-aminolevulinic acid dehydratase	6.32	36,728	
	25,133	6	Peroxiredoxin-6	54	0.3	18	0.8	152	Ankyrin-1	5.65	207,334	
	29,285	6.87	Carbonic anhydrase 2	50	0.3	19	0.8	140	Importin-5	4.83	125,032	
	281,039	4.95	Spectrin alpha chain, erythrocyte	49	0.3	20	0.8	136	E3 ubiquitin-protein ligase UBR4	5.7	580,547	
			The 20 most abundant proteins	94.7			45.8		The 20 most abundant proteins			
			Related to hemoglobin (among the 20 most abundant)	91.3			20.3		Related to hemoglobin (among the 20 most abundant)			
OS-NPs												
13,101	281,039	4.95	Spectrin alpha chain erythrocyte	659	5.0	1	4.3	779	Hemoglobin subunit beta	6.75	16,102	18,073
	247,171	5.15	Spectrin beta chain erythrocyte	468	3.6	2	3.8	688	Beta globin (fragment)	5.9	11,534	
	247,271	5.15	Spectrin beta, erythrocyte	465	3.5	3	3.6	656	Beta-globin	7.86	16,101	
	102,150	5.1	Solute carrier family 4, anion exchanger, member 1	459	3.5	4	3.3	596	Hemoglobin beta (fragment)	6.17	11,496	
	16,102	6.75	Hemoglobin subunit beta	428	3.3	5	3.1	565	Hemoglobin beta (fragment)	5.46	11,532	
	11,532	5.46	Hemoglobin beta (fragment)	351	2.7	6	2.7	484	Hemoglobin subunit alpha	8.72	15,305	

(Continued)

Table 2 (Continued)

Total MS/MS number	MW	pI	Description	#total MS/MS	%/total MS/MS	Rank	%/total MS/MS	#total MS/MS	Description	pI	MW	Total MS/MS number
14,069	6.46		Hemoglobin beta subunit variant (fragment)!	333	2.5	7	2.6	475	Hb β m fused globin protein (fragment)	6.17	10,979	
11,496	6.17		Hemoglobin beta (fragment)!	331	2.5	8	2.4	442	Delta globin	7.85	16,159	
16,159	7.85		Delta globin	283	2.2	9	2.0	363	Spectrin beta chain, erythrocyte	5.15	247,171	
15,305	8.72		Hemoglobin subunit alpha	272	2.1	10	2.0	360	Spectrin, beta, erythrocytic	5.15	247,271	
16,187	6.64		Hemoglobin subunit gamma-1	212	1.6	11	1.6	286	Ankyrin-1	5.65	207,334	
16,173	6.64		Hemoglobin subunit gamma-2	212	1.6	12	1.5	263	Spectrin alpha chain, erythrocyte	4.95	281,039	
8,386	6.63		Hemoglobin alpha 2 (fragment)	199	1.5	13	1.3	230	Truncated beta globin	4.96	4,263	
207,334	5.65		Ankyrin-1	196	1.5	14	1.2	217	Uncharacterized protein	7.04	98,190	
580,547	5.7		E3 ubiquitin-protein ligase UBR4	133	1.0	15	1.2	212	Hemoglobin subunit gamma-1	6.64	16,187	
271,766	5.77		Talin-1	126	1.0	16	1.2	210	Hemoglobin subunit gamma-2	6.64	16,173	
57,794	6.01		T-complex protein 1 subunit beta	100	0.8	17	1.1	200	E3 ubiquitin-protein ligase UBR4	5.7	580,547	
82,465	5.49		Calpain-1 catalytic subunit	86	0.7	18	1.1	191	Solute carrier family 4, anion exchanger, member 1	5.1	102,150	
100,877	5.08		26S proteasome non-ATPase regulatory subunit 2	84	0.6	19	1.0	178	T-complex protein 1 subunit gamma	6.1	61,066	
51,296	5.49		RuvB-like 2	84	0.6	20	0.9	162	T-complex protein 1 subunit beta	6.01	57,794	
			The 20 most abundant proteins	41.8	41.8				The 20 most abundant proteins			
			Related to hemoglobin (among the 20 most abundant)	20.0	29.5				Related to hemoglobin (among the 20 most abundant)			

Notes: Information about protein description, MW, pI, number, and proportion of MS/MS queries are provided. The % MS/MS has been normalized to the total MS/MS queries per run. Bold proteins are hemoglobin-related subunits or fragments.

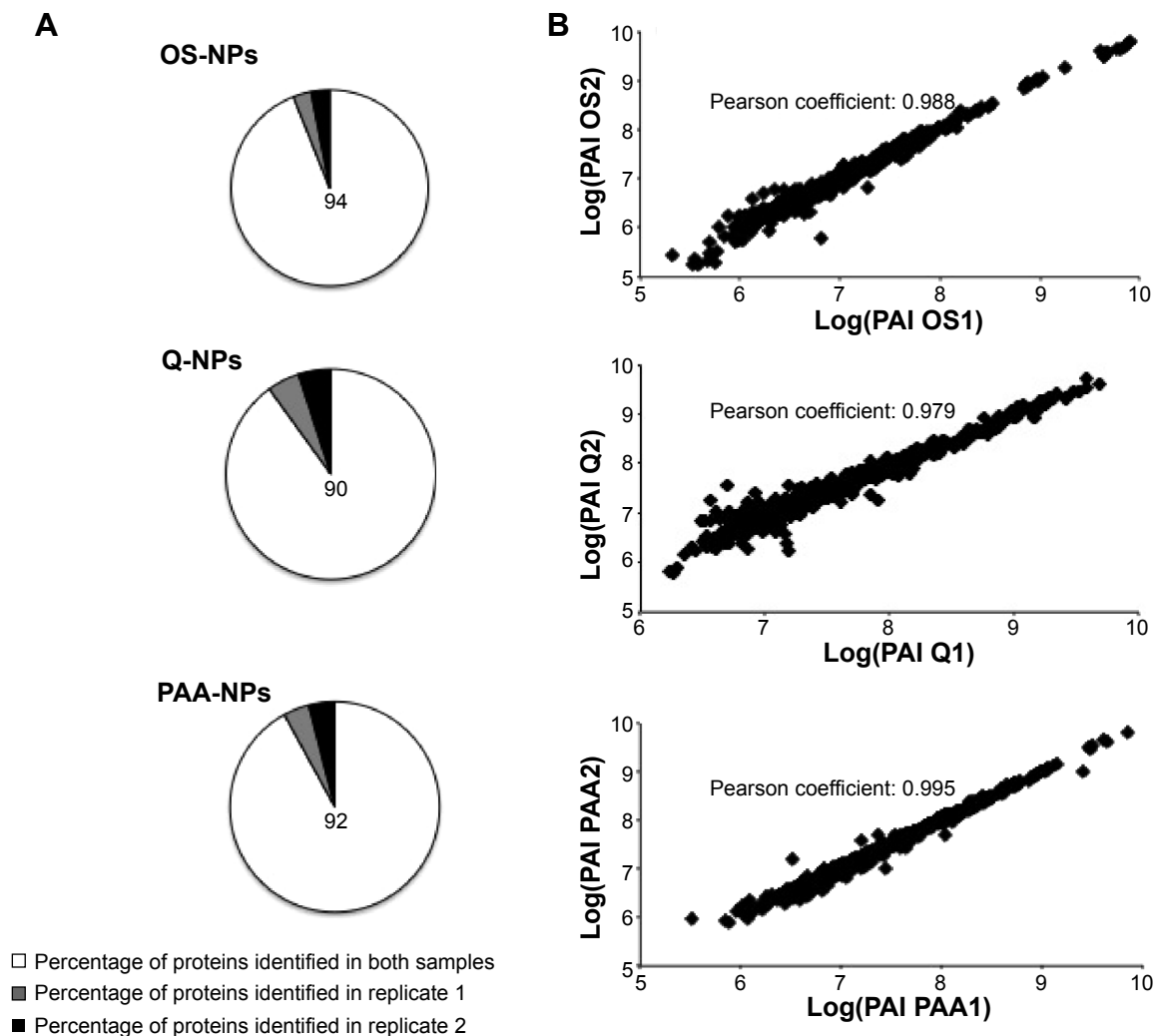
Abbreviations: NPs, nanoparticles; RBC, red blood cell; MS/MS, tandem mass spectrometry; MW, molecular weight; pI, isoelectric point.

Table 3 Comparison between nontreated and OS-NPs-treated RBC, of the ten less abundant proteins identified in nontreated RBC

Control RBC			Description	OS-NPs		
MS/MS queries	Peptide number	Sequence coverage (%)		Sequence coverage (%)	Peptide number	MS/MS queries
1	1	3.4	Calpain small subunit I	60.8	12	63
2	2	3.4	Heat shock protein HSP 90-alpha	26	17	30
2	2	2	T-complex protein I subunit theta	48.5	28	63
2	1	5.2	Proteasome subunit alpha type-7	42.9	8	13
2	2	5	Transkelolase	11.9	5	11
2	2	17.1	Ubiquitin-conjugating enzyme E2 N	79.6	10	28
2	1	1.4	Plastin-2	18	9	19
2	2	14.1	Hemoglobin subunit theta-I	17.6	2	5
3	2	13.2	Proteasome subunit alpha type-2	41.5	6	11
3	2	9.5	Proteasome subunit beta type-5	27.4	7	12

Notes: The total number of MS/MS queries, the number of different identified peptides, and the protein sequence coverage inform about the enrichment of these ten proteins in NP sample.

Abbreviations: RBC, red blood cell; NPs, nanoparticles; MS/MS, tandem mass spectrometry.

**Figure 3** Qualitative and quantitative reproducibility for NPs.

Notes: (A) Qualitative and (B) Quantitative reproducibility for protein harvesting in each kind of NPs over replicates. (A) Pie chart representing the part of MS signals detected in both replicate (white), in replicate 1 (gray), or in replicate 2 (black). (B) Correlation of log(PAI) values for all quantified proteins between replicates in NP-treated samples.

Abbreviations: NPs, nanoparticles; MS, mass spectrometry; PAI, protein abundance index.

and 136 different proteins that specifically constituted the respective corona of Q-, OS-, and PAA-NPs (Figure 4A). To deeply characterize this protein capture specificity, we compared the molecular weight (MW) and the isoelectric point (pI) of proteins in these three groups. PAA-specific proteins revealed significantly higher MWs than OS-NPs (Figure 4B and [Supplementary materials](#)). In fact, the median protein MW in PAA-group was 50,547 Da; it was only 33,667 Da in OS-group. Regarding the pI, the three protein groups showed significant differences (Figure 4C and [Supplementary materials](#)). The positively charged Q-NPs revealed 90% of specific proteins that were negatively charged at pH 7.4 (ie, with a pI <7.4), whereas negatively charged OS- and PAA-NPs harvested less than 70% of specific protein with pI <7.4, confirming previous reports that suggested NP surface charge would influence the protein corona.

Functional analysis of RBC proteins

As NPs considerably increased the number of identified proteins in RBC samples and as the different surfaces harvested different subproteomes, we were interested in determining the functional pathways that were significantly represented by NP-harvested proteins in comparison with nontreated sample. In this aim, we submitted our data set to Ingenuity Pathway Analysis software⁴² (Ingenuity Systems, Redwood City, CA, USA) to perform the functional characterization of the RBC proteome and identify the main molecular pathways and networks. This automatic annotation tool uses a knowledge database and assigns proteins to functional classes or specific canonical pathways (CPs) related to various biological processes.

According to the functional analysis, the 893 proteins identified from the three different kinds of NPs had been associated to 140 different and significantly represented CPs and revealed 98 species related to hematological diseases; the 109 proteins from the crude extract only highlighted 40 different CPs and 31 proteins previously described in hematological diseases.

The ten more significant CPs for crude RBC lysate (Figure 5A) were related to the cellular origin and known functions of RBC. Most of them involved protein and nucleic acid degradation, anaerobic glycolysis, and response to oxidative stress. Although these ten CPs were not the most significant in NP-treated lysates, they were more represented in these samples than crude extract. Figure 5A shows the ratio of proteins identified in these ten CPs for crude and NP-treated RBC extracts. This ratio matches to the number of proteins from our data set that maps to the pathway divided by the total number of proteins referenced in this pathway

by the software. We noticed in all CPs that these ratios were higher for the NP-treated samples, intending that NP increased the identification of proteins related to these CPs. On the other hand, when we considered NPs as the reference sample (Figure 5B), the ten more significant CPs were related to cellular assembly and organization of cytoskeleton, which play an important role in RBC. These pathways that are related to important RBC functions were almost absent from the set of proteins identified in the crude RBC sample, illustrating the impact of the enrichment following protein harvesting using NP technology.

Discussion

Although the behavior of NPs in the presence of complex protein mixture is still far from being completely understood, several studies have demonstrated that the physicochemical features of NPs greatly influenced the composition of their protein corona. In 2008, Lundqvist et al¹⁴ demonstrated, in plasma, qualitative differences in the protein corona of different types of NPs, according to the surface properties and the size of NPs. In 2012, Capriotti et al¹¹ demonstrated that charge density on cationic liposomes influenced both qualitative and quantitative plasma protein capture. Recently, Tenzer et al¹⁵ performed both qualitative and quantitative proteomics to demonstrate that the NP size significantly determined the protein corona. Interestingly, they also demonstrated that the relative proportion of plasma proteins was modified on NP surface compared to their proportion in control plasma. These results suggest that different kinds of NPs may harvest different subproteomes and modify the range of protein concentration in complex samples. As these two properties may be helpful in proteomics approaches to increase the proteome coverage of a biological sample, we assessed for the first time the ability of chemically modified NPs to increase protein identification in RBC samples. The challenge with RBC sample is to decrease the concentration of Hb, which represents 98% of the total protein concentration. NPs provide great advantages for ex vivo experiments; their functionalized surfaces, their nanometer size, and their great surface-to-volume ratio endow them with unique physicochemical properties making them very attractive for protein harvesting.

In this study, we used three kinds of 100 nm superparamagnetic NPs that strongly differ in their surface chemistry. The magnetic properties of these NPs considerably facilitated their handling during washing and elution steps through the use of an external magnet. We selected a strong anion exchanger (Q-NP), a strong cation exchanger (PAA-NP), and a hydrophobic (OS-NP) surface to increase

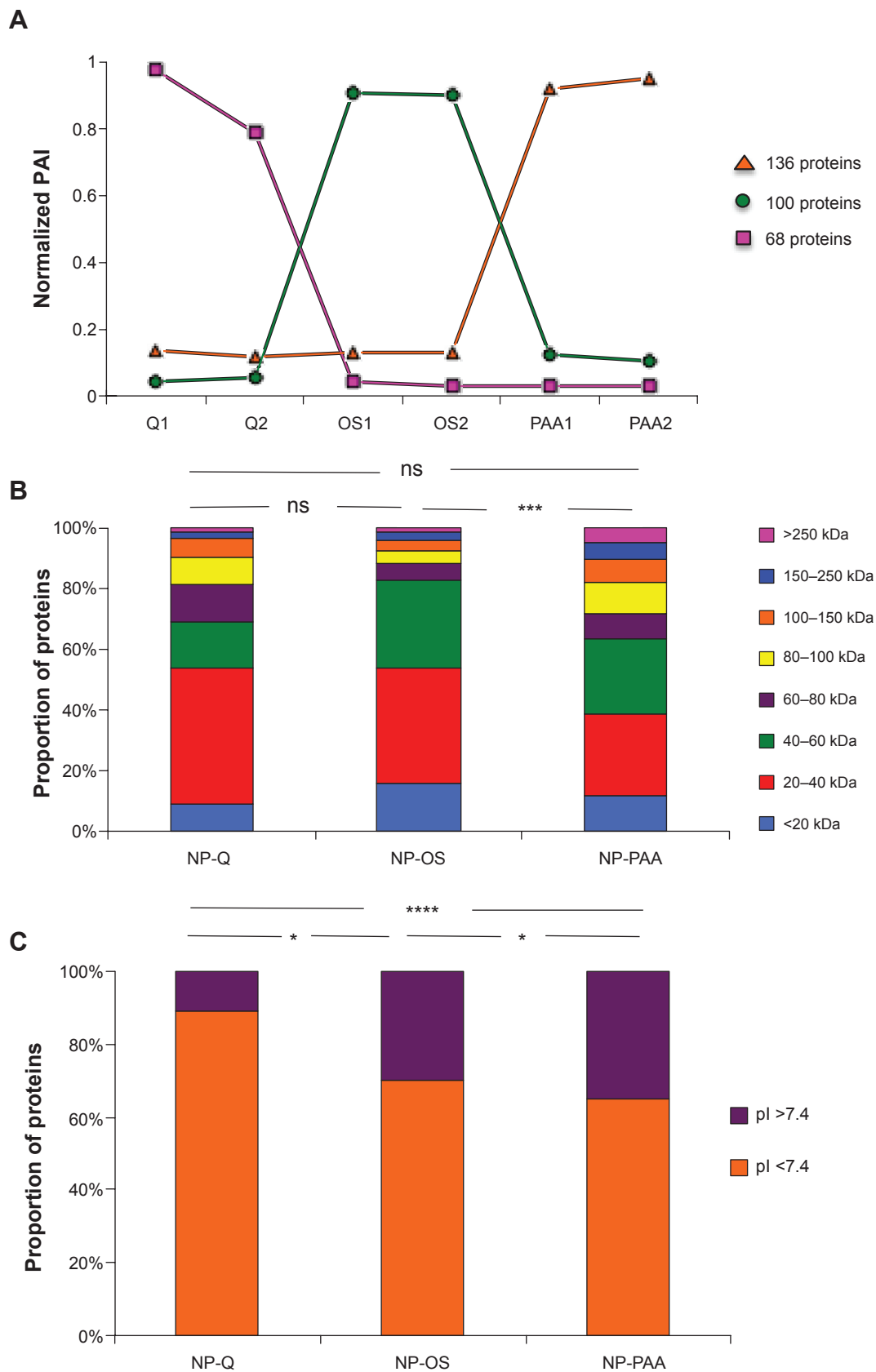


Figure 4 Characterization and comparison of protein groups specific to NP surface by quantitative mass spectrometry.

Notes: (A) Graphical representation of the mean normalized PAI value of three protein groups (obtained by hierarchical clustering) specific to NP surface. Here, 136, 100, and 68 proteins are preferentially captured by PAA-NPs, OS-NPs, and Q-NPs, respectively. Histogram representing (B) the MW and (C) the pI of these specific proteins for each NP surface. * $P < 0.05$; *** $P < 0.001$; **** $P < 0.0001$.

Abbreviations: NP, nanoparticle; PAI, protein abundance index; MW, molecular weight; pI, isoelectric point; ns, non significant.

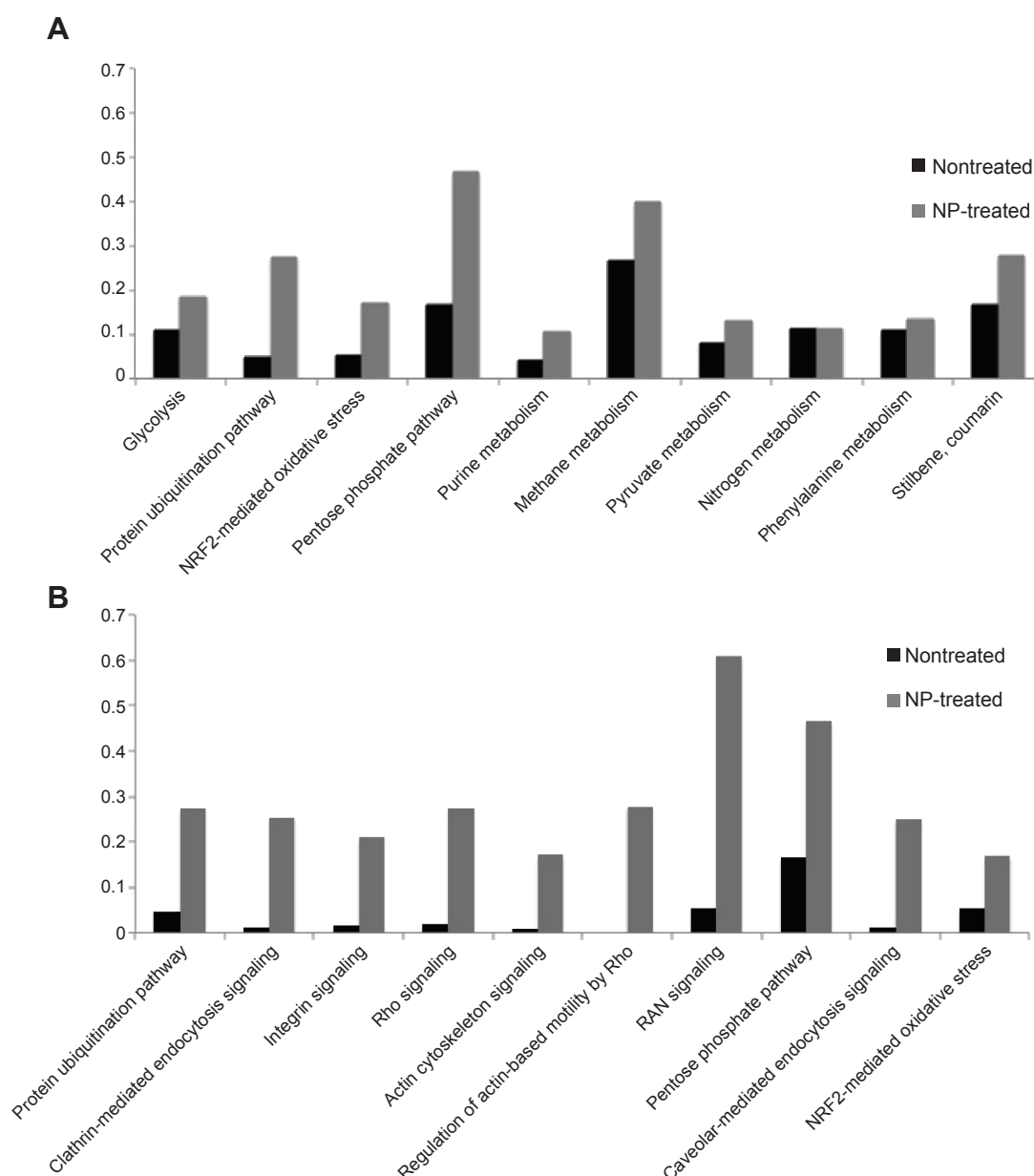


Figure 5 Functional annotation of RBC proteins identified by nano-LC-MS/MS.

Notes: Top ten of significant CPs for (A) untreated and (B) NP-treated RBC extract. For each CP, the bars show the ratio between the number of identified proteins classified in that pathway and the total number of proteins referenced in this pathway by the software for untreated (black bar) and treated RBC extract (gray bar).

Abbreviations: RBC, red blood cell; LC-MS/MS, liquid chromatography–tandem mass spectrometry; CPs, canonical pathways; NP, nanoparticle.

the probability to harvest different subsets of proteins. After the incubation of NPs with RBC protein extract, the nano-LC-MS/MS analysis of each eluted corona enabled the identification of more than 500 proteins, increasing by 400% the number of identified species compared to a control extract of RBC (108 proteins). Actually, synergic effects occurring at the NP surface can explain this improvement in protein identification. First, the proportion of high-abundant proteins is decreased on NP surface. Moreover, as observed by Tenzer et al³⁵ the abundance rank of proteins (estimated

by the number of MS/MS queries) was different between NP-treated and untreated sample. These results confirm that NPs modify the range of protein concentration at their surface. Interestingly, the 20 most abundant proteins harvested by NPs were also different according to the NP chemical functionalization ([Supplementary materials](#)). This observation confirms that the affinity of each protein may be different according to the NP properties, influencing the protein concentration on the NP surface. The second effect concerns the increase of low-abundant proteins on NPs.

In fact, we observed that low-abundant proteins identified in nontreated sample were present in higher abundance on NPs. Here also, the higher affinity of several low-abundant proteins for the different kinds of chemical functionalization allowed their accumulation on the NP surfaces. Thus, through the respective decrease of high-abundant proteins and increase of low-abundant proteins, NP treatment greatly reduces the range of concentration in the sample, making detectable more peptides by the MS instruments. Moreover, because RBC proteins have different affinities for the three kinds of NPs, distinct subproteomes were harvested on each surface, and we finally identified a total of 893 different proteins from these three types of NPs. Among these 893 identified proteins, label-free quantification allowed us to determine which were NP-specific protein signatures. Focusing on the MW and the pI, we found significant differences between these three NP-specific protein groups. While the positively charged Q-NP revealed 90% specific proteins with $pI < 7.4$ (ie, negatively charged at pH 7.4), the negatively charged OS and PAA-NPs bound less than 35% of specific proteins with $pI > 7.4$. We also observed that PAA-NPs harvested specific proteins with higher MW than the ones harvested by OS-NPs. According to these results, we confirmed that properties such as surface charge or chemical functionalization impact on NP–protein interaction.

Although the complexity of the NP–protein interactions is far to be understood, an NP-associated sample preparation of RBC samples in clinical proteomics appears obvious. During its 4-month life span, RBC travels along the entire blood stream to deliver oxygen to most organs. As a major circulating compartment, it is considered as a crucial micro-organite able to contain biomarkers associated both to hematological and non-hematological disorders.³³ In the aim to detect protein modifications in pathological context, the access to the RBC proteome is a major issue to identify potential therapeutic targets. Although technical advances in RBC sample preparation and fractionation have greatly contributed to a better proteome coverage in RBC samples, they remain both time- and sample-consuming and thus incompatible with large-scale clinical studies. We demonstrated that our NP treatment is a very reproducible strategy that specifically allowed the access to the RBC minor proteome. Thus, signaling pathways highlighted in nontreated sample and implicated in important RBC functions such as oxygen transport, glycolysis, and protection against oxidative stress were more represented by NP treatment, offering the possibility to better understand mechanisms responsible for dysfunctions of these key

functional pathways. Moreover, NP treatment specifically highlighted RhoA, Rac, and Cdc42 signaling that have essential functions in morphology and deformability regulations of the erythrocyte cytoskeleton.^{43,44} The maintenance of normal deformability is crucial to permit RBC to enter into narrow capillaries, and dysfunctions of these pathways have been associated with hemolytic anemia. Access to such mandatory pathways for erythrocyte functions would greatly improve investigations on erythrocyte disorders. This access to the minor RBC proteome could also provide precious information for non-hematological disorders. For instance, the specific identification by NP treatment of alpha-synuclein and DJ-1,⁴⁵ two major proteins associated to Parkinson's disease,^{46,47} may open the way to new proteomics analysis of RBCs in this disease.^{48,49}

Finally, one great advantage of our approach, in comparison with immuno-depletion³⁶ or ProteoMiner,³⁷ concerns its efficiency from low volume of sample (200 μ L of RBC containing 1 mg of protein). In their study, Ringrose et al³⁶ and Roux-Dalvai et al³⁷ both performed on-gel fractionation after immuno-depletion or ProteoMiner, and identified 700 and 1,578 different proteins from 200 mg and 5.7 g of starting material, respectively. We would certainly identify more proteins if we had combined such fractionation to NP treatment. Although getting high quantity of RBC proteins is not a limiting factor, as 50 mL of total blood could be easily obtained, the possibility to work on low volumes is more compatible with clinical-automated facilities. And the magnetic feature of NPs allowed us to easily automate all the experimental protocol. Villanueva et al⁵⁰ have already described this kind of platform and demonstrated the reproducibility of NPs for protein harvesting, suggesting the ability to simultaneously process hundreds of samples in reproducible and clinically adapted conditions.

Conclusion

For the first time, we took advantage of the complexity of the NP–protein interactions to increase the proteome coverage in RBC lysates, via the capture of complementary subproteomes on different kinds of NPs. Through a qualitative and quantitative proteomics approach, we confirmed the impact of the NP surface functionalization and charge on protein capture, both demonstrating the reduction of the sample concentration range on the NPs and the specificity of capture for each surface. These synergic effects opened a window on the RBC minor proteome, which is a major issue to identify biomarkers associated to hematological and/or non-hematological disorders.

Disclosure

The authors report no conflicts of interest in this work.

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Supplementary data index

Suppl data 1: Detailed protocol of nano-lc-ms/ms identification and label free quantification.

Suppl. data 2: Non-redundant lists of the proteins identified in red blood cell (RBC) lysate with or without NP treatment.

Sheet 1 ("All 909 proteins"): This list was created by merging the different protein lists obtained after analysis of each sample (untreated RBC lysate or elution fractions from 3 different NPs).

Sheet 2 ("Non-treated"), Sheet 3 ("Q-Treated"), Sheet 4 ("OS-Treated), Sheet 5 ("PAA-Treated) display individual lists of the proteins identified from each condition.

In all these lists, the information detailed below is given:

AC/ID: accession number in Uniprot database. For more clarity, if several proteins match the same set of peptides, only one member of the protein group is indicated in these concise lists.

MW: molecular weight

pI: Isoelectric point

Description: gene name and protein description

Fractions: sample(s) where the protein has been identified.

The letters correspond to the samples (**GR_C1/2**: 'non-treated' replicate 1/2, **GR_Q1/2**: Q-treated replicate 1/2, **GR_OS 1/2**: OS-treated replicate 1/2, **GR_PAA 1/2**: PAA-treated replicate 1/2).

score: Mascot protein score in this sample

#Sequences: number of unique sequence identified in the sample giving the Mascot score

#Peptides: number of peptides unique regarding sequence and possible modification

Coverage (%): protein sequence coverage

#MS/MS: number of MSMS queries

Suppl. data 3: Non-redundant lists of the proteins identified and quantified according to the NP-treatment of red blood cell (RBC) lysate.

Non-redundant list of identified and quantified proteins for 2 replicate samples and for each type of NPs. Quantification was performed using the label-free module implemented in the MFPaQ software. For each sample, the software uses the validated identification results and extracted ion chromatogram of the identified peptides in the corresponding raw nano-LC-MS files based on their experimentally measured retention time (RT) and monoisotopic m/z values.

AC/ID: accession number in Uniprot database. Details of protein groups can be viewed in the column called "other AC's".

MW: molecular weight

pI: Isoelectric point

Description: gene name and protein description

#QPep: number of peptides quantified for the 2 replicates

PAI (Protein Abundance Index): to compute this index for a given protein, an intensity comparison of its peptides is first performed across the different replicates. The three

peptides exhibiting the highest intensities are selected and used as references to compute the PAI of this protein in the different replicates. Then, in each condition the PAI is defined as the average of the intensities of these three reference peptides.

Log PAI : this value was used to generate the correlation graphs of the fig.3B

Suppl. data 4: Hierarchical clustering of all proteins identified and quantified from NP-treatment and Non-redundant list of proteins preferentially harvested by one type of NPs.

To obtain these lists, the PAI obtained in each NP-sample for each protein were normalized by its highest value providing value between 0 and 1.

Normalized PAI were submitted to software R for protein hierarchical clustering.

Sheet 1 Graphical representation of the 10 different groups of proteins obtained by the hierarchical clustering. The table provides the average of the normalized PAI of each group of proteins for each type of NPs and for each replicate.

Sheet, 2, 3, 4 highlights the 68, 100, 136 proteins preferentially captured by Q, OS or PAA-NPs. The normalized PAI of each protein for each sample is given. The last line gives the average of the normalized PAI of these proteins for each condition.

Suppl. data 5: Isoelectric point (pI) and molecular weight (MW) of NP specific protein signatures.

Suppl data 6: Box plot representing (A) the isoelectric point and (B) the molecular weight of each NP-specific protein signatures.

Suppl data 7: List of the 20 most abundant proteins (decreasing from 1 to 20) identified from all conditions. Information about protein description, molecular weight (MW), isoelectric point (pI), number and proportion of MS/MS queries are provided. the % MS/MS has been normalized to the total MS/MS queries per run. Bold proteins are hemoglobin-related subunits or fragments.

Supplemental Data 1:

Detailed protocol of nano-lc-ms/ms
identification and label free
quantification.

LC-MS/MS analysis of RBC proteins

10 µg of each eluate and crude RBC lysate were diluted in Laemli buffer and stacked in one band after a short and low voltage electrophoretic migration on SDS PAGE gel. The stacking band was cut and washed in 100 mM ammonium bicarbonate, reduction and alkylation of cysteines were performed by mixing the gel pieces in 10 mM DTT for 35 min at 56 °C followed by 55 mM iodoacetamide for 30 min at room temperature in the dark. Additional cycles of washes was then performed and proteins were digested by incubating the band gel with 0.6 µg of modified sequencing grade trypsin (Promega) in 50 mM ammonium bicarbonate overnight at 37°C. The resulting peptides were extracted from the gel by three steps: a first incubation in 50 mM ammonium bicarbonate for 15 min at 37 °C and two incubations in 10 % formic acid, acetonitrile (1:1) for 15 min at 37 °C. The three collected extractions were pooled with the initial supernatant, dried in a SpeedVac, and resuspended with 14 µl of 5 % acetonitrile, 0.05 % trifluoroacetic acid.

The peptide mixtures were analyzed by nano-LC-MS/MS using an ultimate3000 system (Dionex, Amsterdam, The Netherlands) coupled to an LTQ-Orbitrap Velos mass spectrometer (Thermo Scientific, Bremen, Germany). 5 µl of each sample were loaded on a C₁₈ precolumn (300 µm inner diameter X 5 mm; Dionex) at 20 µl/min in 5 % acetonitrile, 0.05 % trifluoroacetic acid. After 5 min of desalting, the precolumn was switched on line with the analytical C₁₈ column (75 µm inner diameter X 15 cm; PepMap C₁₈, Dionex) equilibrated in 95 % solvent A (5 % acetonitrile, 0.2% formic acid) and 5 % solvent B (80 % acetonitrile, 0.2 % formic acid). Peptides were eluted using a 5-50% gradient of solvent B during 80 min at a 300 nl /min flow rate. The LTQ-Orbitrap was operated in data-dependent acquisition mode with the Xcalibur software. Survey scan MS spectra (m/z mass range 300-2000) were acquired in the Orbitrap with the resolution set to a value of 60,000 at m/z 400 (AGC target value of 1x10⁶ charges). The five most intense ions per survey with a charge state greater than one were selected for CID fragmentation, and the resulting fragments were analyzed in the

linear trap (LTQ). Collision energy was set to 35% for MS/MS. Dynamic exclusion was used within 60 s to prevent repetitive selection of the same peptide.

Database Search and Data Analysis

The Mascot Daemon software (version 2.3.0, Matrix Science, London, UK) was used to perform database searches in batch mode with all the raw files acquired on sample. To automatically extract peak lists from Xcalibur raw files, the ExtractMSN macro provided with Xcalibur (version 2.0 SR2, Thermo Fisher Scientific) was used through the Mascot Daemon Interface. The following parameters were set for creation of the peak lists: parent ions in the mass range 400-4500, no grouping of MS/MS scans, and threshold at 1000. A peak list was created for each sample analyzed, and individual Mascot searches were performed. Data were searched against homo sapiens entries in Uniprot protein database (release 2010_09 - Sep 21, 2010; 1215533 sequences). Carbamidomethylation of cysteines was set as a fixed modification and oxidation of methionine and protein amino-terminal acetylation were set as variable modifications for all Mascot searches. Specificity of trypsin digestion was set for cleavage after K and R and one missed trypsin cleavage site was allowed. The mass tolerances in MS and MS/MS were set to 5 ppm and 0.6 Da respectively, and the instrument setting was specified as "ESI-Trap". Mascot results were parsed with the in-house developed software MFPaQ v4.0.0 software (<http://mfpaq.sourceforge.net/>), and protein hits were automatically validated if they satisfied one of the following criteria: identification with at least one top ranking peptide with a Mascot score of more than 39 (p-value < 0.001) or at least two top ranking peptides each with a Mascot score of more than 22 (p-value < 0.05). When several proteins matched exactly the same set of peptides, only one member of the protein group was reported in the final list. To evaluate the false positive rate in these experiments, all the initial database searches were performed using the "decoy" option of Mascot.

Label-free Quantification

Quantification of proteins was performed using the label-free module implemented in the MFPaQ v4.0.0 software (<http://mfpaq.sourceforge.net>). For each sample, the software uses the validated identification results and extracted ion chromatogram (XIC) of the identified peptides in the corresponding raw nano-LC-MS files based on their experimentally measured retention time (RT) and monoisotopic m/z values. Only top ranking peptides with a Mascot score higher than the identity threshold at $p = 0.05$ (i.e Mascot score = 22) were selected for quantification. Peptide ions identified in all the samples to be compared were used to build a retention time matrix in order to align LC-MS runs. If some peptide ions were sequenced by MS/MS and validated only in some of the samples to be compared, their XIC signal was extracted in the nanoLC-MS raw file of the other samples using a predicted RT value calculated from this alignment matrix by a linear interpolation method. Quantification of peptide ions was performed based on calculated XIC areas values. To perform normalization of a group of comparable runs, the software computed XIC area ratios for all the extracted signals between a reference run and all the other runs of the group, and used the median of the ratios as a normalization factor. In order to perform protein relative quantification in different samples, a Protein Abundance Index was calculated, defined as the average of XIC area values for at most three intense reference tryptic peptides identified for this protein (the three peptides exhibiting the highest intensities across the different samples were selected as reference peptides, and these same three peptides were used to compute the PAI of the protein in each sample; if only one or two peptides were identified and quantified in the case of low-abundant proteins, the PAI was calculated based on their XIC area values). To compare the relative selectivity in protein harvesting, of each kind of NPs, the PAI obtained in each NP-sample for each protein were Standardized by its highest value. Standardized PAI were submitted to software R for protein hierarchical clustering (20).

Supplemental Data 2:

Non-redundant lists of the proteins identified in red blood cell (RBC) lysate with or without NP treatment.

Supplemental Data 2

Sheet 1

All 909 proteins

P2195	PR58_HUMAN	4293.12	7.11	26S protease regulatory subunit 8 OS=Homo sapiens GN=PR58M1 PE=1 SV=1	GR: C1	1383.14	18	15	44.6	38	67	GR: Q2	817.69	20	19	53.2	36	51.7	50	49.9	46	GR: PAK1	1633.92	33	27	62.1	74	
P2196	FLJ22_HUMAN	4733.81	5.19	FtsH-2 OS=Homo sapiens GN=FLJ22_H1 PE=1 SV=1	GR: C1	1588.19	13	15	44.9	56	62	GR: Q2	1000.86	20	22	56.5	47	56.7	50	49.7	46	GR: PAK1	315.97	12	12	38.4	20	16
P2197	ACTC_HUMAN	4233.81	5.26	Actin, alpha isoform, muscle 1 OS=Homo sapiens GN=ACTC1 PE=1 SV=1	GR: C1	603.88	13	15	31.1	32.4	62	GR: Q2	1243.43	20	21	32.5	46	32.4	50	45.8	45	GR: PAK1	478.46	18	14	36.2	18	14
P2198	DEOC_HUMAN	3543.59	9.08	Putative deoxyribose-phosphate adenosine OS=Homo sapiens GN=DEOCB4 PE=1 SV=2	GR: C1	1871.59	17	17	58.2	68	68	GR: Q2	142.71	20	19	68.6	73	16.4	50	47.0	46	GR: PAK1	51.24	6	4	18.4	7.0	4
P2199	CNS5_HUMAN	3726.8	6.1	COP9 apiculate complex subunit 5 OS=Homo sapiens GN=COP9B1 PE=1 SV=4	GR: C1	1121.89	17	15	55.2	46	49	GR: Q2	844.38	19	16	50.5	58	50.5	58	46	46	GR: PAK1	738	18	16	51.8	34	16
P2200	GNVBS3_HUMAN	4292.19	5.71	HSP70D7 OS=Homo sapiens PE=2 SV=1	GR: C1	1132.46	18	16	58.1	50	50	GR: Q2	1186.12	19	19	56.2	23	19	56.2	23	19	GR: PAK1	139.91	25	21	66.5	56	69
P2201	PRF2_HUMAN	4602.27	5.71	26S protease regulatory subunit 7 OS=Homo sapiens GN=PRF2B1 PE=1 SV=3	GR: C1	562.82	19	19	48	51	50	GR: Q2	1168.12	20	20	51.3	55	51.3	55	49	47	GR: PAK1	986.87	27	24	56.1	68	68
P2202	AZRY2_HUMAN	2585.31	6.33	DnaJ (Hsp40) homolog, subfamily C, member 13 OS=Homo sapiens GN=AZRY2B1 PE=1 SV=1	GR: C1	431.7	5	5	21	5	5	GR: Q2	172.15	19	15	17.2	15	17.2	22	21	17	GR: PAK1	1045.23	29	29	65.3	61	63
P2203	O15028	4237.38	5.42	26S protease non-ATPase regulatory subunit 6 OS=Homo sapiens GN=O15028B1 PE=1 SV=1	GR: C1	1040.15	22	21	54.5	47	47	GR: Q2	1449	25	24	10.8	63	10.8	63	43	43	GR: PAK1	1382.07	31	28	62.9	59	59
AP273	AA273_HUMAN	4377.6	5.11	AP2-2 OS=Homo sapiens GN=AA273B1 PE=1 SV=3	GR: C1	1522.93	23	22	59.1	67	67	GR: Q2	1093.7	23	6	5.4	54	5.4	10	10	23	GR: PAK1	119.94	29	34	43.3	61	61
P2204	AA273_HUMAN	1059.61	6.69	AP2-complex subunit alpha 1 OS=Homo sapiens GN=AA273A1 PE=1 SV=3	GR: C1	1466.96	27	22	43.3	66	66	GR: Q2	1110.82	29	26	46.3	60	24.7	34	34	23	GR: PAK1	996.44	36	34	43.3	61	61
P2205	AA273_HUMAN	6665.51	9.32	Semaphorin-3 protein, putative class 2A, 63 kDa regulatory subunit A, alpha isoform OS=Homo sapiens GN=AA273B1 PE=1 SV=3	GR: C1	1466.96	27	22	43.3	66	66	GR: Q2	1110.82	29	26	46.3	60	24.7	34	34	23	GR: PAK1	996.44	36	34	43.3	61	61
P2206	PRF1_HUMAN	3870.46	8.29	Protein arginase-2 OS=Homo sapiens GN=PRF1B1 PE=1 SV=2	GR: C1	1532.82	19	15	61.1	62	62	GR: Q2	1414.02	21	17	12.8	56	35.7	45	35.7	45	GR: PAK1	1151.11	13	13	29.5	19	16
P2207	PRF1_HUMAN	3870.46	8.29	Protein arginase-2 OS=Homo sapiens GN=PRF1B1 PE=1 SV=2	GR: C1	1532.82	19	15	61.1	62	62	GR: Q2	1414.02	21	17	12.8	56	35.7	45	35.7	45	GR: PAK1	1151.11	13	13	29.5	19	16
P2208	STAU1_HUMAN	14263.56	5.01	Ubiquitin-conjugating enzyme E2 O OS=Homo sapiens GN=STAU1 PE=1 SV=3	GR: C1	1845.57	13	15	10.4	7	7	GR: Q2	1243.43	20	21	32.5	46	32.4	50	45.8	45	GR: PAK1	478.46	18	14	36.2	18	14
P2209	STAU1_HUMAN	14263.56	5.01	Ubiquitin-conjugating enzyme E2 O OS=Homo sapiens GN=STAU1 PE=1 SV=3	GR: C1	1845.57	13	15	10.4	7	7	GR: Q2	1243.43	20	21	32.5	46	32.4	50	45.8	45	GR: PAK1	478.46	18	14	36.2	18	14
P2210	ACTN1_HUMAN	10534.64	5.22	Alpha-actinin-1 OS=Homo sapiens GN=ACTN1 PE=1 SV=2	GR: C1	1510.59	24	23	46.7	49	49	GR: Q2	1425.19	30	30	30	46	57	56	57	56	GR: PAK1	42.71	14	4	5.4	40	40
P2211	PRF1_HUMAN	3870.46	8.29	Protein arginase-2 OS=Homo sapiens GN=PRF1B1 PE=1 SV=2	GR: C1	1532.82	19	15	61.1	62	62	GR: Q2	1414.02	21	17	12.8	56	35.7	45	35.7	45	GR: PAK1	1151.11	13	13	29.5	19	16
P2212	PRF1_HUMAN	3870.46	8.29	Protein arginase-2 OS=Homo sapiens GN=PRF1B1 PE=1 SV=2	GR: C1	1532.82	19	15	61.1	62	62	GR: Q2	1414.02	21	17	12.8	56	35.7	45	35.7	45	GR: PAK1	1151.11	13	13	29.5	19	16
P2213	PRF1_HUMAN	3870.46	8.29	Protein arginase-2 OS=Homo sapiens GN=PRF1B1 PE=1 SV=2	GR: C1	1532.82	19	15	61.1	62	62	GR: Q2	1414.02	21	17	12.8	56	35.7	45	35.7	45	GR: PAK1	1151.11	13	13	29.5	19	16
P2214	PRF1_HUMAN	3870.46	8.29	Protein arginase-2 OS=Homo sapiens GN=PRF1B1 PE=1 SV=2	GR: C1	1532.82	19	15	61.1	62	62	GR: Q2	1414.02	21	17	12.8	56	35.7	45	35.7	45	GR: PAK1	1151.11	13	13	29.5	19	16
P2215	PRF1_HUMAN	3870.46	8.29	Protein arginase-2 OS=Homo sapiens GN=PRF1B1 PE=1 SV=2	GR: C1	1532.82	19	15	61.1	62	62	GR: Q2	1414.02	21	17	12.8	56	35.7	45	35.7	45	GR: PAK1	1151.11	13	13	29.5	19	16
P2216	PRF1_HUMAN	3870.46	8.29	Protein arginase-2 OS=Homo sapiens GN=PRF1B1 PE=1 SV=2	GR: C1	1532.82	19	15	61.1	62	62	GR: Q2	1414.02	21	17	12.8	56	35.7	45	35.7	45	GR: PAK1	1151.11	13	13	29.5	19	16
P2217	PRF1_HUMAN	3870.46	8.29	Protein arginase-2 OS=Homo sapiens GN=PRF1B1 PE=1 SV=2	GR: C1	1532.82	19	15	61.1	62	62	GR: Q2	1414.02	21	17	12.8	56	35.7	45	35.7	45	GR: PAK1	1151.11	13	13	29.5	19	16
P2218	PRF1_HUMAN	3870.46	8.29	Protein arginase-2 OS=Homo sapiens GN=PRF1B1 PE=1 SV=2	GR: C1	1532.82	19	15	61.1	62	62	GR: Q2	1414.02	21	17	12.8	56	35.7	45	35.7	45	GR: PAK1	1151.11	13	13	29.5	19	16
P2219	PRF1_HUMAN	3870.46	8.29	Protein arginase-2 OS=Homo sapiens GN=PRF1B1 PE=1 SV=2	GR: C1	1532.82	19	15	61.1	62	62	GR: Q2	1414.02	21	17	12.8	56	35.7	45	35.7	45	GR: PAK1	1151.11	13	13	29.5	19	16
P2220	PRF1_HUMAN	3870.46	8.29	Protein arginase-2 OS=Homo sapiens GN=PRF1B1 PE=1 SV=2	GR: C1	1532.82	19	15	61.1	62	62	GR: Q2	1414.02	21	17	12.8	56	35.7	45	35.7	45	GR: PAK1	1151.11	13	13	29.5	19	16
P2221	PRF1_HUMAN	3870.46	8.29	Protein arginase-2 OS=Homo sapiens GN=PRF1B1 PE=1 SV=2	GR: C1	1532.82	19	15	61.1	62	62	GR: Q2	1414.02	21	17	12.8	56	35.7	45	35.7	45	GR: PAK1	1151.11	13	13	29.5	19	16
P2222	PRF1_HUMAN	3870.46	8.29	Protein arginase-2 OS=Homo sapiens GN=PRF1B1 PE=1 SV=2	GR: C1	1532.82	19	15	61.1	62	62	GR: Q2	1414.02	21	17	12.8	56	35.7	45	35.7	45	GR: PAK1	1151.11	13	13	29.5	19	16
P2223	PRF1_HUMAN	3870.46	8.29	Protein arginase-2 OS=Homo sapiens GN=PRF1B1 PE=1 SV=2	GR: C1	1532.82	19	15	61.1	62	62	GR: Q2	1414.02	21	17	12.8	56	35.7	45	35.7	45	GR: PAK1	1151.11	13	13	29.5	19	16
P2224	PRF1_HUMAN	3870.46	8.29	Protein arginase-2 OS=Homo sapiens GN=PRF1B1 PE=1 SV=2	GR: C1	1532.82	19	15	61.1	62	62	GR: Q2	1414.02	21	17	12.8	56	35.7	45	35.7	45	GR: PAK1	1151.11	13	13	29.5	19	16
P2225	PRF1_HUMAN	3870.46	8.29	Protein arginase-2 OS=Homo sapiens GN=PRF1B1 PE=1 SV=2	GR: C1	1532.82	19	15	61.1	62	62	GR: Q2	1414.02	21	17	12.8	56	35.7	45	35.7	45	GR: PAK1	1151.11	13	13	29.5	19	16
P2226	PRF1_HUMAN	3870.46	8.29	Protein arginase-2 OS=Homo sapiens GN=PRF1B1 PE=1 SV=2	GR: C1	1532.82	19	15	61.1	62	62	GR: Q2	1414.02	21	17	12.8	56	35.7	45	35.7	45	GR: PAK1	1151.11	13	13	29.5	19	16
P2227	PRF1_HUMAN	3870.46	8.29	Protein arginase-2 OS=Homo sapiens GN=PRF1B1 PE=1 SV=2	GR: C1	1532.82	19	15	61.1	62	62	GR: Q2	1414.02	21	17	12.8	56	35.7	45	35.7	45	GR: PAK1	1151.11	13	13	29.5	19	16
P2228	PRF1_HUMAN	3870.46	8.29	Protein arginase-2 OS=Homo sapiens GN=PRF1B1 PE=1 SV=2	GR: C1	1532.82	19	15	61.1	62	62	GR: Q2	1414.02	21	17	12.8	56	35.7	45	35.7	45	GR: PAK1	1151.11	13	13	29.5	19	16
P2229	PRF1_HUMAN	3870.46	8.29	Protein arginase-2 OS=Homo sapiens GN=PRF1B1 PE=1 SV=2	GR: C1	1532.82	19	15	61.1	62	62	GR: Q2	1414.02	21	17	12.8	56	35.7	45	35.7	45	GR: PAK1	1151.11	13	13	29.5	19	16
P2230	PRF1_HUMAN	3870.46	8.29	Protein arginase-2 OS=Homo sapiens GN=PRF1B1 PE=1 SV=2	GR: C1	1532.82	19	15	61.1	62	62	GR: Q2	1414.02	21	17	12.8	56	35.7	45	35.7	45	GR: PAK1	1151.11	13	13	29.5	19	16
P2231	PRF1_HUMAN	3870.46	8.29	Protein arginase-2 OS=Homo sapiens GN=PRF1B1 PE=1 SV=2	GR: C1	1532.82	19	15	61.1	62	62	GR: Q2	1414.02	21	17	12.8	56	35.7	45	35.7	45	GR: PAK1	1151.11	13	13	29.5	19	16
P2232	PRF1_HUMAN	3870.46	8.29	Protein arginase-2 OS=Homo sapiens GN=PRF1B1 PE=1 SV=2	GR: C1	1532.82	19	15	61.1	62	62	GR: Q2	1414.02	21	17	12.8	56	35.7	45	35.7	45	GR: PAK1	1151.11	13	13	29.5	19	16
P2233	PRF1_HUMAN	3870.46	8.29	Protein arginase-2 OS=Homo sapiens GN=PRF1B1 PE=1 SV=2	GR: C1	1532.82	19	15	61.1	62	62	GR: Q2	1414.02	21	17	12.8	56	35.7	45	35.7	45	GR: PAK1	1151.11	13	13	29.5	19	16
P2234	PRF1_HUMAN	3870.46	8.29	Protein arginase-2 OS=Homo sapiens GN=PRF1B1 PE=1 SV=2	GR: C1	1532.82	19	15	61.1	62	62	GR: Q2	1414.02	21	17	12.8	56	35.7	45	35.7	45	GR: PAK1	1151.11	13	13	29.5	19	16
P2235	PRF1_HUMAN	3870.46	8.29	Protein arginase-2 OS=Homo sapiens GN=PRF1B1 PE=1 SV=2	GR: C1	1532.82	19	15	61.1	62	62	GR: Q2	1414.02	21	17	12.8	56	35.7	45	35.7	45	GR: PAK1	1151.11	13	13	29.5	19	16
P2236	PRF1_HUMAN	3870.46	8.29	Protein arginase-2 OS=Homo sapiens GN=PRF1B1 PE=1 SV=2	GR: C1	1532.82	19	15	61.1	62	62	GR: Q2	1414.02	21	17	12.8	56	35.7	45	35.7	45	GR: PAK1	1151.11	13	13	29.5	19	16
P2237	PRF1_HUMAN	3870.46	8.29	Protein arginase-2 OS=Homo sapiens GN=PRF1B1 PE=1 SV=2	GR: C1	1532.82	19	15	61.1	62	62	GR: Q2	1414.02	21	17	12.8	56	35.7	45	35.7	45	GR: PAK1	1151.11	13	13	29.5	19	16
P2238	PRF1_HUMAN	3870.46	8.29	Protein arginase-2 OS=Homo sapiens GN=PRF1B1 PE=1 SV=2	GR: C1	1532.82	19	15	61.1	62	62	GR: Q2	1414.02	21	17	12.8	56	35.7	45	35.7	45	GR: PAK1	1151.11					

GRN01	GRN02	GRN03	GRN04	GRN05	GRN06	GRN07	GRN08	GRN09	GRN10	GRN11	GRN12	GRN13	GRN14	GRN15	GRN16	GRN17	GRN18	GRN19	GRN20	GRN21	GRN22	GRN23	GRN24	GRN25	GRN26	GRN27	GRN28	GRN29	GRN30	GRN31	GRN32	GRN33	GRN34	GRN35	GRN36	GRN37	GRN38	GRN39	GRN40	GRN41	GRN42	GRN43	GRN44	GRN45	GRN46	GRN47	GRN48	GRN49	GRN50	GRN51	GRN52	GRN53	GRN54	GRN55	GRN56	GRN57	GRN58	GRN59	GRN60	GRN61	GRN62	GRN63	GRN64	GRN65	GRN66	GRN67	GRN68	GRN69	GRN70	GRN71	GRN72	GRN73	GRN74	GRN75	GRN76	GRN77	GRN78	GRN79	GRN80	GRN81	GRN82	GRN83	GRN84	GRN85	GRN86	GRN87	GRN88	GRN89	GRN90	GRN91	GRN92	GRN93	GRN94	GRN95	GRN96	GRN97	GRN98	GRN99	GRN100	GRN101	GRN102	GRN103	GRN104	GRN105	GRN106	GRN107	GRN108	GRN109	GRN110	GRN111	GRN112	GRN113	GRN114	GRN115	GRN116	GRN117	GRN118	GRN119	GRN120	GRN121	GRN122	GRN123	GRN124	GRN125	GRN126	GRN127	GRN128	GRN129	GRN130	GRN131	GRN132	GRN133	GRN134	GRN135	GRN136	GRN137	GRN138	GRN139	GRN140	GRN141	GRN142	GRN143	GRN144	GRN145	GRN146	GRN147	GRN148	GRN149	GRN150	GRN151	GRN152	GRN153	GRN154	GRN155	GRN156	GRN157	GRN158	GRN159	GRN160	GRN161	GRN162	GRN163	GRN164	GRN165	GRN166	GRN167	GRN168	GRN169	GRN170	GRN171	GRN172	GRN173	GRN174	GRN175	GRN176	GRN177	GRN178	GRN179	GRN180	GRN181	GRN182	GRN183	GRN184	GRN185	GRN186	GRN187	GRN188	GRN189	GRN190	GRN191	GRN192	GRN193	GRN194	GRN195	GRN196	GRN197	GRN198	GRN199	GRN200	GRN201	GRN202	GRN203	GRN204	GRN205	GRN206	GRN207	GRN208	GRN209	GRN210	GRN211	GRN212	GRN213	GRN214	GRN215	GRN216	GRN217	GRN218	GRN219	GRN220	GRN221	GRN222	GRN223	GRN224	GRN225	GRN226	GRN227	GRN228	GRN229	GRN230	GRN231	GRN232	GRN233	GRN234	GRN235	GRN236	GRN237	GRN238	GRN239	GRN240	GRN241	GRN242	GRN243	GRN244	GRN245	GRN246	GRN247	GRN248	GRN249	GRN250	GRN251	GRN252	GRN253	GRN254	GRN255	GRN256	GRN257	GRN258	GRN259	GRN260	GRN261	GRN262	GRN263	GRN264	GRN265	GRN266	GRN267	GRN268	GRN269	GRN270	GRN271	GRN272	GRN273	GRN274	GRN275	GRN276	GRN277	GRN278	GRN279	GRN280	GRN281	GRN282	GRN283	GRN284	GRN285	GRN286	GRN287	GRN288	GRN289	GRN290	GRN291	GRN292	GRN293	GRN294	GRN295	GRN296	GRN297	GRN298	GRN299	GRN300	GRN301	GRN302	GRN303	GRN304	GRN305	GRN306	GRN307	GRN308	GRN309	GRN310	GRN311	GRN312	GRN313	GRN314	GRN315	GRN316	GRN317	GRN318	GRN319	GRN320	GRN321	GRN322	GRN323	GRN324	GRN325	GRN326	GRN327	GRN328	GRN329	GRN330	GRN331	GRN332	GRN333	GRN334	GRN335	GRN336	GRN337	GRN338	GRN339	GRN340	GRN341	GRN342	GRN343	GRN344	GRN345	GRN346	GRN347	GRN348	GRN349	GRN350	GRN351	GRN352	GRN353	GRN354	GRN355	GRN356	GRN357	GRN358	GRN359	GRN360	GRN361	GRN362	GRN363	GRN364	GRN365	GRN366	GRN367	GRN368	GRN369	GRN370	GRN371	GRN372	GRN373	GRN374	GRN375	GRN376	GRN377	GRN378	GRN379	GRN380	GRN381	GRN382	GRN383	GRN384	GRN385	GRN386	GRN387	GRN388	GRN389	GRN390	GRN391	GRN392	GRN393	GRN394	GRN395	GRN396	GRN397	GRN398	GRN399	GRN400	GRN401	GRN402	GRN403	GRN404	GRN405	GRN406	GRN407	GRN408	GRN409	GRN410	GRN411	GRN412	GRN413	GRN414	GRN415	GRN416	GRN417	GRN418	GRN419	GRN420	GRN421	GRN422	GRN423	GRN424	GRN425	GRN426	GRN427	GRN428	GRN429	GRN430	GRN431	GRN432	GRN433	GRN434	GRN435	GRN436	GRN437	GRN438	GRN439	GRN440	GRN441	GRN442	GRN443	GRN444	GRN445	GRN446	GRN447	GRN448	GRN449	GRN450	GRN451	GRN452	GRN453	GRN454	GRN455	GRN456	GRN457	GRN458	GRN459	GRN460	GRN461	GRN462	GRN463	GRN464	GRN465	GRN466	GRN467	GRN468	GRN469	GRN470	GRN471	GRN472	GRN473	GRN474	GRN475	GRN476	GRN477	GRN478	GRN479	GRN480	GRN481	GRN482	GRN483	GRN484	GRN485	GRN486	GRN487	GRN488	GRN489	GRN490	GRN491	GRN492	GRN493	GRN494	GRN495	GRN496	GRN497	GRN498	GRN499	GRN500	GRN501	GRN502	GRN503	GRN504	GRN505	GRN506	GRN507	GRN508	GRN509	GRN510	GRN511	GRN512	GRN513	GRN514	GRN515	GRN516	GRN517	GRN518	GRN519	GRN520	GRN521	GRN522	GRN523	GRN524	GRN525	GRN526	GRN527	GRN528	GRN529	GRN530	GRN531	GRN532	GRN533	GRN534	GRN535	GRN536	GRN537	GRN538	GRN539	GRN540	GRN541	GRN542	GRN543	GRN544	GRN545	GRN546	GRN547	GRN548	GRN549	GRN550	GRN551	GRN552	GRN553	GRN554	GRN555	GRN556	GRN557	GRN558	GRN559	GRN560	GRN561	GRN562	GRN563	GRN564	GRN565	GRN566	GRN567	GRN568	GRN569	GRN570	GRN571	GRN572	GRN573	GRN574	GRN575	GRN576	GRN577	GRN578	GRN579	GRN580	GRN581	GRN582	GRN583	GRN584	GRN585	GRN586	GRN587	GRN588	GRN589	GRN590	GRN591	GRN592	GRN593	GRN594	GRN595	GRN596	GRN597	GRN598	GRN599	GRN600	GRN601	GRN602	GRN603	GRN604	GRN605	GRN606	GRN607	GRN608	GRN609	GRN610	GRN611	GRN612	GRN613	GRN614	GRN615	GRN616	GRN617	GRN618	GRN619	GRN620	GRN621	GRN622	GRN623	GRN624	GRN625	GRN626	GRN627	GRN628	GRN629	GRN630	GRN631	GRN632	GRN633	GRN634	GRN635	GRN636	GRN637	GRN638	GRN639	GRN640	GRN641	GRN642	GRN643	GRN644	GRN645	GRN646	GRN647	GRN648	GRN649	GRN650	GRN651	GRN652	GRN653	GRN654	GRN655	GRN656	GRN657	GRN658	GRN659	GRN660	GRN661	GRN662	GRN663	GRN664	GRN665	GRN666	GRN667	GRN668	GRN669	GRN670	GRN671	GRN672	GRN673	GRN674	GRN675	GRN676	GRN677	GRN678	GRN679	GRN680	GRN681	GRN682	GRN683	GRN684	GRN685	GRN686	GRN687	GRN688	GRN689	GRN690	GRN691	GRN692	GRN693	GRN694	GRN695	GRN696	GRN697	GRN698	GRN699	GRN700	GRN701	GRN702	GRN703	GRN704	GRN705	GRN706	GRN707	GRN708	GRN709	GRN710	GRN711	GRN712	GRN713	GRN714	GRN715	GRN716	GRN717	GRN718	GRN719	GRN720	GRN721	GRN722	GRN723	GRN724	GRN725	GRN726	GRN727	GRN728	GRN729	GRN730	GRN731	GRN732	GRN733	GRN734	GRN735	GRN736	GRN737	GRN738	GRN739	GRN740	GRN741	GRN742	GRN743	GRN744	GRN745	GRN746	GRN747	GRN748	GRN749	GRN750	GRN751	GRN752	GRN753	GRN754	GRN755	GRN756	GRN757	GRN758	GRN759	GRN760	GRN761	GRN762	GRN763	GRN764	GRN765	GRN766	GRN767	GRN768	GRN769	GRN770	GRN771	GRN772	GRN773	GRN774	GRN775	GRN776	GRN777	GRN778	GRN779	GRN780	GRN781	GRN782	GRN783	GRN784	GRN785	GRN786	GRN787	GRN788	GRN789	GRN790	GRN791	GRN792	GRN793	GRN794	GRN795	GRN796	GRN797	GRN798	GRN799	GRN800	GRN801	GRN802	GRN803	GRN804	GRN805	GRN806	GRN807	GRN808	GRN809	GRN810	GRN811	GRN812	GRN813	GRN814	GRN815	GRN816	GRN817	GRN818	GRN819	GRN820	GRN821	GRN822	GRN823	GRN824	GRN825	GRN826	GRN827	GRN828	GRN829	GRN830	GRN831	GRN832	GRN833	GRN834	GRN835	GRN836	GRN837	GRN838	GRN839	GRN840	GRN841	GRN842	GRN843	GRN844	GRN845	GRN846	GRN847	GRN848	GRN849	GRN850	GRN851	GRN852	GRN853	GRN854	GRN855	GRN856	GRN857	GRN858	GRN859	GRN860	GRN861	GRN862	GRN863	GRN864	GRN865	GRN866	GRN867	GRN868	GRN869	GRN870	GRN871	GRN872	GRN873	GRN874	GRN875	GRN876	GRN877	GRN878	GRN879	GRN880	GRN881	GRN882	GRN883	GRN884	GRN885	GRN886	GRN887	GRN888	GRN889	GRN890	GRN891	GRN892	GRN893	GRN894	GRN895	GRN896	GRN897	GRN898	GRN899	GRN900	GRN901	GRN902	GRN903	GRN904	GRN905	GRN906	GRN907	GRN908	GRN909	GRN910	GRN911	GRN912	GRN913	GRN914	GRN915	GRN916	GRN917	GRN918	GRN919	GRN920	GRN921	GRN922	GRN923	GRN924	GRN925	GRN926	GRN927	GRN928	GRN929	GRN930	GRN931	GRN932	GRN933	GRN934	GRN935	GRN936	GRN937	GRN938	GRN939	GRN940	GRN941	GRN942	GRN943	GRN944	GRN945	GRN946	GRN947	GRN948	GRN949	GRN950	GRN951	GRN952	GRN953	GRN954	GRN955	GRN956	GRN957	GRN958	GRN959	GRN960	GRN961	GRN962	GRN963	GRN964	GRN965	GRN966	GRN967	GRN968	GRN969	GRN970	GRN971	GRN972	GRN973	GRN974	GRN975	GRN976	GRN977	GRN978	GRN979	GRN980	GRN981	GRN982	GRN983	GRN984	GRN985	GRN986	GRN987	GRN988	GRN989	GRN990	GRN991	GRN992	GRN993	GRN994	GRN995	GRN996	GRN997	GRN998	GRN999	GRN1000
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Q4378	SYN1c_HUMAN	6575.74	5.9	Assemblin-9/ENA synthase, cytoplasmic; OS=Homo sapiens GN=HNS9; PE=1 SV=1	GR_Q1	282.23	7	7	8.5	14	GR_Q2	235.65	8	8	11.2	14	GR_Q3	100.94	5	5	42.1	5	19.2	14	GR_PMA1	155.46	6	6	12.4	14	GR_PMA2	159.08	3	3	7.1	11				
P43034	UBR1c_HUMAN	4778.74	6.9	Protein-ubiquitin ligase; ubiquitin-protein ligase; OS=Homo sapiens GN=UBR1; PE=1 SV=1	GR_Q1	72.94	5	5	17	8	GR_Q2	103.24	6	6	17.9	8	GR_Q3	103.24	6	6	17.9	8	GR_Q4	103.24	6	6	17.9	8	GR_PMA1	188.80	6	6	12.4	14	GR_PMA2	193.08	3	3	7.1	11
Q43427	PCBP1c_HUMAN	2136.54	6.9	Acute basic-granule leukemia-associated protein; OS=Homo sapiens GN=PCBP1; PE=1 SV=1	GR_Q1	148.93	3	3	26.4	12	GR_Q2	214.60	5	5	39.3	10	GR_Q3	53.88	5	5	39.3	10	GR_Q4	53.88	5	5	39.3	10	GR_PMA1	64.29	3	3	11.5	14	GR_PMA2	104.29	2	2	2.3	6
Q43426	LOBP_HUMAN	1179.72	5.5	Lysyl-O-2-aryl aminopyridine; OS=Homo sapiens GN=LOBP; PE=1 SV=1	GR_Q1	148.93	3	3	26.4	12	GR_Q2	214.60	5	5	39.3	10	GR_Q3	53.88	5	5	39.3	10	GR_Q4	53.88	5	5	39.3	10	GR_PMA1	125.15	5	5	6.5	9	GR_PMA2	86.42	1	1	6.5	9
P21225	RAV2b_HUMAN	2071.59	4.2	Ras-related protein RAV2b; OS=Homo sapiens GN=RAV2b; PE=1 SV=1	GR_Q1	571.33	3	3	18.4	9	GR_Q2	53.88	5	5	39.3	10	GR_Q3	53.88	5	5	39.3	10	GR_Q4	53.88	5	5	39.3	10	GR_PMA1	210.4	1	1	6.5	9	GR_PMA2	57.9	1	1	6.5	9
P02779	FGF1c_HUMAN	5710.1	5.2	Fibroblast growth factor; OS=Homo sapiens GN=FGF1; PE=1 SV=3	GR_Q1	571.33	3	3	18.4	9	GR_Q2	53.88	5	5	39.3	10	GR_Q3	53.88	5	5	39.3	10	GR_Q4	53.88	5	5	39.3	10	GR_PMA1	306.82	7	7	6	17	GR_PMA2	54.23	1	1	6.5	9
Q00780	DHSD1c_HUMAN	3827.55	8.2	Steroid dehydrogenase; OS=Homo sapiens GN=DHSD1; PE=1 SV=1	GR_Q1	274.478	9.9	9.9	32.2	14	GR_Q2	168.59	2	2	11.1	6	GR_Q3	168.59	2	2	11.1	6	GR_Q4	168.59	2	2	11.1	6	GR_PMA1	104.99	5	5	10.9	9	GR_PMA2	46.82	1	1	2.1	6
Q13057	COX5c_HUMAN	6232.58	6.2	Blotulin toxin; cytochrome c oxidase; OS=Homo sapiens GN=COX5c; PE=1 SV=4	GR_Q1	141.73	5	4	10.8	11	GR_Q2	96.26	5	5	9.8	6	GR_Q3	100.94	5	5	16	14	GR_Q4	100.94	5	5	16	14	GR_PMA1	358.82	7	7	6	17	GR_PMA2	54.23	1	1	6.5	9
Q04848	PF2c_HUMAN	4096.96	6.2	Lactate dehydrogenase; OS=Homo sapiens GN=PF2c; PE=1 SV=2	GR_Q1	141.73	5	4	10.8	11	GR_Q2	96.26	5	5	9.8	6	GR_Q3	100.94	5	5	16	14	GR_Q4	100.94	5	5	16	14	GR_PMA1	358.82	7	7	6	17	GR_PMA2	54.23	1	1	6.5	9
P03176	KNH1c_HUMAN	4679.75	4.6	Secosteroid; OS=Homo sapiens GN=KNH1; PE=1 SV=1	GR_Q1	223.78	2	2	1	10	GR_Q2	168.59	2	2	11.1	6	GR_Q3	168.59	2	2	11.1	6	GR_Q4	168.59	2	2	11.1	6	GR_PMA1	104.99	5	5	10.9	9	GR_PMA2	46.82	1	1	2.1	6
Q12765	SCGN1c_HUMAN	4679.75	4.6	Secosteroid; OS=Homo sapiens GN=SCGN1; PE=1 SV=2	GR_Q1	223.78	2	2	1	10	GR_Q2	168.59	2	2	11.1	6	GR_Q3	168.59	2	2	11.1	6	GR_Q4	168.59	2	2	11.1	6	GR_PMA1	104.99	5	5	10.9	9	GR_PMA2	46.82	1	1	2.1	6
Q04848	PF2c_HUMAN	4096.96	6.2	Lactate dehydrogenase; OS=Homo sapiens GN=PF2c; PE=1 SV=2	GR_Q1	141.73	5	4	10.8	11	GR_Q2	96.26	5	5	9.8	6	GR_Q3	100.94	5	5	16	14	GR_Q4	100.94	5	5	16	14	GR_PMA1	358.82	7	7	6	17	GR_PMA2	54.23	1	1	6.5	9
Q13511	APC5c_HUMAN	1867.72	5.4	Actin-related protein 223 complex subunit 5; OS=Homo sapiens GN=APC5c; PE=1 SV=3	GR_Q1	168.32	6	6	17.8	13	GR_Q2	72.75	5	5	18.5	9	GR_Q3	174.48	3	3	14	8	GR_Q4	174.48	3	3	14	8	GR_PMA1	188.80	6	6	12.4	14	GR_PMA2	193.08	3	3	7.1	11
Q04426	STN1c_HUMAN	1741.36	7.3	Symplekin-1; OS=Homo sapiens GN=STN1; PE=1 SV=2	GR_Q1	168.32	6	6	17.8	13	GR_Q2	72.75	5	5	18.5	9	GR_Q3	174.48	3	3	14	8	GR_Q4	174.48	3	3	14	8	GR_PMA1	188.80	6	6	12.4	14	GR_PMA2	193.08	3	3	7.1	11
Q07620	GLRX3c_HUMAN	3793.34	5.3	Glutathione S-transferase; OS=Homo sapiens GN=GLRX3c; PE=1 SV=2	GR_Q1	272.8	8	8	31.3	13	GR_Q2	112.27	5	5	16.2	13	GR_Q3	174.48	3	3	14	8	GR_Q4	174.48	3	3	14	8	GR_PMA1	188.80	6	6	12.4	14	GR_PMA2	193.08	3	3	7.1	11
Q13404	UBRY1c_HUMAN	4659.37	7.1	Ubiquitin-conjugating enzyme E2 variant 1; OS=Homo sapiens GN=UBRY1; PE=1 SV=2	GR_Q1	64.35	5	5	15.9	8	GR_Q2	112.27	5	5	16.2	13	GR_Q3	174.48	3	3	14	8	GR_Q4	174.48	3	3	14	8	GR_PMA1	188.80	6	6	12.4	14	GR_PMA2	193.08	3	3	7.1	11
P13473	LAMP2c_HUMAN	4652.52	5.35	Lysosome-associated membrane glycoprotein 2; OS=Homo sapiens GN=LAMP2c; PE=1 SV=2	GR_Q1	68.89	1	1	5.5	2	GR_Q2	96.26	5	5	9.8	6	GR_Q3	100.94	5	5	16	14	GR_Q4	100.94	5	5	16	14	GR_PMA1	358.82	7	7	6	17	GR_PMA2	54.23	1	1	6.5	9
Q13820	CLU4Bc_HUMAN	10448.42	7.91	Clu-4B; OS=Homo sapiens GN=CLU4B; PE=1 SV=1	GR_Q1	68.89	1	1	5.5	2	GR_Q2	96.26	5	5	9.8	6	GR_Q3	100.94	5	5	16	14	GR_Q4	100.94	5	5	16	14	GR_PMA1	358.82	7	7	6	17	GR_PMA2	54.23	1	1	6.5	9
Q15181	IPR1c_HUMAN	33565.33	5.54	Inorganic pyrophosphatase; OS=Homo sapiens GN=IPR1c; PE=1 SV=2	GR_Q1	223.78	2	2	1	10	GR_Q2	168.59	2	2	11.1	6	GR_Q3	168.59	2	2	11.1	6	GR_Q4	168.59	2	2	11.1	6	GR_PMA1	104.99	5	5	10.9	9	GR_PMA2	46.82	1	1	2.1	6
Q04848	PF2c_HUMAN	4096.96	6.2	Lactate dehydrogenase; OS=Homo sapiens GN=PF2c; PE=1 SV=2	GR_Q1	141.73	5	4	10.8	11	GR_Q2	96.26	5	5	9.8	6	GR_Q3	100.94	5	5	16	14	GR_Q4	100.94	5	5	16	14	GR_PMA1	358.82	7	7	6	17	GR_PMA2	54.23	1	1	6.5	9
Q04848	PF2c_HUMAN	4096.96	6.2	Lactate dehydrogenase; OS=Homo sapiens GN=PF2c; PE=1 SV=2	GR_Q1	141.73	5	4	10.8	11	GR_Q2	96.26	5	5	9.8	6	GR_Q3	100.94	5	5	16	14	GR_Q4	100.94	5	5	16	14	GR_PMA1	358.82	7	7	6	17	GR_PMA2	54.23	1	1	6.5	9
Q04848	PF2c_HUMAN	4096.96	6.2	Lactate dehydrogenase; OS=Homo sapiens GN=PF2c; PE=1 SV=2	GR_Q1	141.73	5	4	10.8	11	GR_Q2	96.26	5	5	9.8	6	GR_Q3	100.94	5	5	16	14	GR_Q4	100.94	5	5	16	14	GR_PMA1	358.82	7	7	6	17	GR_PMA2	54.23	1	1	6.5	9
Q04848	PF2c_HUMAN	4096.96	6.2	Lactate dehydrogenase; OS=Homo sapiens GN=PF2c; PE=1 SV=2	GR_Q1	141.73	5	4	10.8	11	GR_Q2	96.26	5	5	9.8	6	GR_Q3	100.94	5	5	16	14	GR_Q4	100.94	5	5	16	14	GR_PMA1	358.82	7	7	6	17	GR_PMA2	54.23	1	1	6.5	9
Q04848	PF2c_HUMAN	4096.96	6.2	Lactate dehydrogenase; OS=Homo sapiens GN=PF2c; PE=1 SV=2	GR_Q1	141.73	5	4	10.8	11	GR_Q2	96.26	5	5	9.8	6	GR_Q3	100.94	5	5	16	14	GR_Q4	100.94	5	5	16	14	GR_PMA1	358.82	7	7	6	17	GR_PMA2	54.23	1	1	6.5	9
Q04848	PF2c_HUMAN	4096.96	6.2	Lactate dehydrogenase; OS=Homo sapiens GN=PF2c; PE=1 SV=2	GR_Q1	141.73	5	4	10.8	11	GR_Q2	96.26	5	5	9.8	6	GR_Q3	100.94	5	5	16	14	GR_Q4	100.94	5	5	16	14	GR_PMA1	358.82	7	7	6	17	GR_PMA2	54.23	1	1	6.5	9
Q04848	PF2c_HUMAN	4096.96	6.2	Lactate dehydrogenase; OS=Homo sapiens GN=PF2c; PE=1 SV=2	GR_Q1	141.73	5	4	10.8	11	GR_Q2	96.26	5	5	9.8	6	GR_Q3	100.94	5	5	16	14	GR_Q4	100.94	5	5	16	14	GR_PMA1	358.82	7	7	6	17	GR_PMA2	54.23	1	1	6.5	9
Q04848	PF2c_HUMAN	4096.96	6.2	Lactate dehydrogenase; OS=Homo sapiens GN=PF2c; PE=1 SV=2	GR_Q1	141.73	5	4	10.8	11	GR_Q2	96.26	5	5	9.8	6	GR_Q3	100.94	5	5	16	14	GR_Q4	100.94	5	5	16	14	GR_PMA1	358.82	7	7	6	17	GR_PMA2	54.23	1	1	6.5	9
Q04848	PF2c_HUMAN	4096.96	6.2	Lactate dehydrogenase; OS=Homo sapiens GN=PF2c; PE=1 SV=2	GR_Q1	141.73	5	4	10.8	11	GR_Q2	96.26	5	5	9.8	6	GR_Q3	100.94	5	5	16	14	GR_Q4	100.94	5	5	16	14	GR_PMA1	358.82	7	7	6	17	GR_PMA2	54.23	1	1	6.5	9
Q04848	PF2c_HUMAN	4096.96	6.2	Lactate dehydrogenase; OS=Homo sapiens GN=PF2c; PE=1 SV=2	GR_Q1	141.73	5	4	10.8	11	GR_Q2	96.26	5	5	9.8	6	GR_Q3	100.94	5	5	16	14	GR_Q4	100.94	5	5	16	14	GR_PMA1	358.82	7	7	6	17	GR_PMA2	54.23	1	1	6.5	9
Q04848	PF2c_HUMAN	4096.96	6.2	Lactate dehydrogenase; OS=Homo sapiens GN=PF2c; PE=1 SV=2	GR_Q1	141.73	5	4	10.8	11	GR_Q2	96.26	5	5	9.8	6	GR_Q3	100.94	5	5	16	14	GR_Q4	100.94	5	5	16	14	GR_PMA1	358.82	7	7	6	17	GR_PMA2	54.23	1	1	6.5	9
Q04848	PF2c_HUMAN	4096.96	6.2	Lactate dehydrogenase; OS=Homo sapiens GN=PF2c; PE=1 SV=2	GR_Q1	141.73	5	4	10.8	11	GR_Q2	96.26	5	5	9.8	6	GR_Q3	100.94	5	5	16	14	GR_Q4	100.94	5	5	16	14	GR_PMA1	358.82	7	7	6	17	GR_PMA2	54.23	1	1	6.5	9
Q04848	PF2c_HUMAN	4096.96	6.2	Lactate dehydrogenase; OS=Homo sapiens GN=PF2c; PE=1 SV=2	GR_Q1	141.73	5	4	10.8	11	GR_Q2	96.26	5	5	9.8	6	GR_Q3	100.94	5	5	16	14	GR_Q4	100.94	5	5	16	14	GR_PMA1	358.82	7	7	6	17	GR_PMA2	54.23	1	1	6.5	9
Q04848	PF2c_HUMAN	4096.96	6.2	Lactate dehydrogenase; OS=Homo sapiens GN=PF2c; PE=1 SV=2	GR_Q1	141.73	5	4	10.8	11	GR_Q2	96.26	5	5	9.8	6	GR_Q3	100.94	5	5	16	14	GR_Q4	100.94	5	5	16	14	GR_PMA1	358.82	7	7	6	17	GR_PMA2	54.23	1	1	6.5	9
Q04848	PF2c_HUMAN	4096.96	6.2	Lactate dehydrogenase; OS=Homo sapiens GN=PF2c; PE=1 SV=2	GR_Q1	141.73	5	4	10.8	11	GR_Q2	96.26	5	5	9.8	6	GR_Q3	100.94	5	5	16	14	GR_Q4	100.94	5	5	16	14	GR_PMA1	358.82	7	7	6	17	GR_PMA2	54.23	1	1	6.5	9
Q04848	PF2c_HUMAN	4096.96	6.2	Lactate dehydrogenase; OS=Homo sapiens GN=PF2c; PE=1 SV=2	GR_Q1	141.73	5	4	10.8	11	GR_Q2	96.26	5	5	9.8	6	GR_Q3	100.94	5	5	16	14	GR_Q4	100.94	5	5	16	14	GR_PMA1	358.82	7	7	6	17	GR_PMA2	54.23	1	1	6.5	9
Q04848	PF2c_HUMAN	4096.96	6.2	Lactate dehydrogenase; OS=Homo sapiens GN=PF2c; PE=1 SV=2	GR_Q1	141.73	5	4	10.8	11	GR_Q2																													

OS-1	OS-2	OS-3	OS-4	OS-5	OS-6	OS-7	OS-8	OS-9	OS-10	OS-11	OS-12	OS-13	OS-14	OS-15	OS-16	OS-17	OS-18	OS-19	OS-20	OS-21	OS-22	OS-23	OS-24	OS-25	OS-26	OS-27	OS-28	OS-29	OS-30	OS-31	OS-32	OS-33	OS-34	OS-35	OS-36	OS-37	OS-38	OS-39	OS-40	OS-41	OS-42	OS-43	OS-44	OS-45	OS-46	OS-47	OS-48	OS-49	OS-50	OS-51	OS-52	OS-53	OS-54	OS-55	OS-56	OS-57	OS-58	OS-59	OS-60	OS-61	OS-62	OS-63	OS-64	OS-65	OS-66	OS-67	OS-68	OS-69	OS-70	OS-71	OS-72	OS-73	OS-74	OS-75	OS-76	OS-77	OS-78	OS-79	OS-80	OS-81	OS-82	OS-83	OS-84	OS-85	OS-86	OS-87	OS-88	OS-89	OS-90	OS-91	OS-92	OS-93	OS-94	OS-95	OS-96	OS-97	OS-98	OS-99	OS-100	OS-101	OS-102	OS-103	OS-104	OS-105	OS-106	OS-107	OS-108	OS-109	OS-110	OS-111	OS-112	OS-113	OS-114	OS-115	OS-116	OS-117	OS-118	OS-119	OS-120	OS-121	OS-122	OS-123	OS-124	OS-125	OS-126	OS-127	OS-128	OS-129	OS-130	OS-131	OS-132	OS-133	OS-134	OS-135	OS-136	OS-137	OS-138	OS-139	OS-140	OS-141	OS-142	OS-143	OS-144	OS-145	OS-146	OS-147	OS-148	OS-149	OS-150	OS-151	OS-152	OS-153	OS-154	OS-155	OS-156	OS-157	OS-158	OS-159	OS-160	OS-161	OS-162	OS-163	OS-164	OS-165	OS-166	OS-167	OS-168	OS-169	OS-170	OS-171	OS-172	OS-173	OS-174	OS-175	OS-176	OS-177	OS-178	OS-179	OS-180	OS-181	OS-182	OS-183	OS-184	OS-185	OS-186	OS-187	OS-188	OS-189	OS-190	OS-191	OS-192	OS-193	OS-194	OS-195	OS-196	OS-197	OS-198	OS-199	OS-200	OS-201	OS-202	OS-203	OS-204	OS-205	OS-206	OS-207	OS-208	OS-209	OS-210	OS-211	OS-212	OS-213	OS-214	OS-215	OS-216	OS-217	OS-218	OS-219	OS-220	OS-221	OS-222	OS-223	OS-224	OS-225	OS-226	OS-227	OS-228	OS-229	OS-230	OS-231	OS-232	OS-233	OS-234	OS-235	OS-236	OS-237	OS-238	OS-239	OS-240	OS-241	OS-242	OS-243	OS-244	OS-245	OS-246	OS-247	OS-248	OS-249	OS-250	OS-251	OS-252	OS-253	OS-254	OS-255	OS-256	OS-257	OS-258	OS-259	OS-260	OS-261	OS-262	OS-263	OS-264	OS-265	OS-266	OS-267	OS-268	OS-269	OS-270	OS-271	OS-272	OS-273	OS-274	OS-275	OS-276	OS-277	OS-278	OS-279	OS-280	OS-281	OS-282	OS-283	OS-284	OS-285	OS-286	OS-287	OS-288	OS-289	OS-290	OS-291	OS-292	OS-293	OS-294	OS-295	OS-296	OS-297	OS-298	OS-299	OS-300	OS-301	OS-302	OS-303	OS-304	OS-305	OS-306	OS-307	OS-308	OS-309	OS-310	OS-311	OS-312	OS-313	OS-314	OS-315	OS-316	OS-317	OS-318	OS-319	OS-320	OS-321	OS-322	OS-323	OS-324	OS-325	OS-326	OS-327	OS-328	OS-329	OS-330	OS-331	OS-332	OS-333	OS-334	OS-335	OS-336	OS-337	OS-338	OS-339	OS-340	OS-341	OS-342	OS-343	OS-344	OS-345	OS-346	OS-347	OS-348	OS-349	OS-350	OS-351	OS-352	OS-353	OS-354	OS-355	OS-356	OS-357	OS-358	OS-359	OS-360	OS-361	OS-362	OS-363	OS-364	OS-365	OS-366	OS-367	OS-368	OS-369	OS-370	OS-371	OS-372	OS-373	OS-374	OS-375	OS-376	OS-377	OS-378	OS-379	OS-380	OS-381	OS-382	OS-383	OS-384	OS-385	OS-386	OS-387	OS-388	OS-389	OS-390	OS-391	OS-392	OS-393	OS-394	OS-395	OS-396	OS-397	OS-398	OS-399	OS-400	OS-401	OS-402	OS-403	OS-404	OS-405	OS-406	OS-407	OS-408	OS-409	OS-410	OS-411	OS-412	OS-413	OS-414	OS-415	OS-416	OS-417	OS-418	OS-419	OS-420
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BVDY9 BVDY9_HUMAN 35555.84 5.9 cDNA, FLJ1456, highly similar to Homo sapiens nucleolar protein serping 37C (VPS37C), mRNA
BVDY9 BVDY9_HUMAN 35555.84 5.9 cDNA, FLJ1456, highly similar to Homo sapiens nucleolar protein serping 37C (VPS37C), mRNA
BNDQ5 BNDQ5_HUMAN 30727.64 6.0 Uncharacterized protein OS=Homo sapiens GN=NDQ1 PE=2 SV=1
P816D5 DCD_HUMAN 11360.67 6.8 Dendrin OS=Homo sapiens GN=DCD PE=1 SV=2
O27281 INP2_HUMAN 113691.23 5.3 Inverted form-2 OS=Homo sapiens GN=INP2 PE=1 SV=2
BNDQ4 BNDQ4_HUMAN 17222.83 6.0 cDNA, FLJ42530, highly similar to Homo sapiens Olf-MF-ASB1 PE=1 SV=1
BNDQ2 BNDQ2_HUMAN 86594.63 6.2 cDNA, FLJ20878, highly similar to Homo sapiens Interferon-induced protein with histonepoxide
BNDQ3 BNDQ3_HUMAN 56586.86 7.2 repeat 5 (1/1) 5, mRNA OS=Homo sapiens PE=2 SV=1
O11318 FAD2_HUMAN 23422.93 5.6 Protein FAD2 OS=Homo sapiens GN=FAD2 PE=1 SV=1
BNDQ2 BNDQ2_HUMAN 117385.84 6.8 cDNA, FLJ45556, highly similar to MMS19-like protein OS=Homo sapiens PE=2 SV=1
O15166 TSP1_HUMAN 16970.53 4.35 Protein TSP1 OS=Homo sapiens GN=TSP1 PE=1 SV=1
O49P08 TAF12C_HUMAN 11556.67 9.87 Transcription factor TAF12C OS=Homo sapiens GN=TAF12C PE=1 SV=1
BNDQ6 BNDQ6_HUMAN 35329.47 5.14 Chromosome 22 open reading frame 25, isoform CRL, c OS=Homo sapiens GN=C22orf25 PE=2 SV=1
O56338 GPC1_HUMAN 29114.66 5.7 6-phosphogluconate-binding OS=Homo sapiens GN=GPC1 PE=1 SV=2

GR_Q1 62.89 1 2 3.7 2
GR_Q1 41.97 1 2 21.9 2
GR_Q1 53.41 1 1 9.1 1
GR_Q2 40.64 1 1 9.1 1
GR_Q2 79.54 1 1 6.5 1
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GR_Q1 42.72 1 1 2.8 1
GR_Q1 46.11 1 1 2.8 1
GR_Q1 39.85 1 1 10.8 1
GR_QS1 59.67 1 1 1.1 1
GR_QS1 63.06 1 1 7.8 1
GR_QS1 59.62 1 1 2.3 1
GR_QS1 46.35 1 1 5.3 1
GR_QS1 41.62 1 1 11.5 1
GR_QS2 63.16 1 1 8.9 1
GR_QS2 54.85 1 1 7.8 1
GR_QS2 54.85 1 1 2.3 1
GR_QS2 41.66 1 1 1.1 1

GR_PAI1 74.13 1 1 5.3 1
GR_PAI1 54.18 1 1 7.0 1
GR_PAI1 44 1 1 1.1 1

Supplemental Data 2

Sheet 2

Non-treated

AC	Description	Replicate_1	Score	Replicate_2	Score
P25325	3-mercaptopyruvate sulfurtransferase OS=Homo sapiens GN=MPST PE=1 SV=3			GR_C2	69.00
B4DQJ8	6-phosphogluconate dehydrogenase, decarboxylating OS=Homo sapiens GN=PGD PE=2 SV=1	GR_C1	203.06		
Q4LE36	ACLY variant protein (Fragment) OS=Homo sapiens GN=ACLY variant protein PE=2 SV=1	GR_C1	66.31	GR_C2	72.94
P13798	Acylamino-acid-releasing enzyme OS=Homo sapiens GN=APEH PE=1 SV=4	GR_C1	1405.15	GR_C2	1545.67
P23526	Adenosylhomocysteinase OS=Homo sapiens GN=AHCY PE=1 SV=4			GR_C2	81.09
P00568	Adenylate kinase isoenzyme 1 OS=Homo sapiens GN=AK1 PE=1 SV=3	GR_C1	140.08	GR_C2	126.07
P30566	Adenylosuccinate lyase OS=Homo sapiens GN=ADSL PE=1 SV=2	GR_C1	184.19	GR_C2	221.03
Q04828	Aldo-keto reductase family 1 member C1 OS=Homo sapiens GN=AKR1C1 PE=1 SV=1			GR_C2	42.80
P06733	Alpha-enolase OS=Homo sapiens GN=ENO1 PE=1 SV=2	GR_C1	65.1		
P16157	Ankyrin-1 OS=Homo sapiens GN=ANK1 PE=1 SV=3	GR_C1	322.17	GR_C2	257.74
P17174	Aspartate aminotransferase, cytoplasmic OS=Homo sapiens GN=GOT1 PE=1 SV=3			GR_C2	49.45
B3VL17	Beta globin (Fragment) OS=Homo sapiens PE=3 SV=1	GR_C1	42940.77	GR_C2	34352.62
C8C504	Beta-globin OS=Homo sapiens GN=HBB PE=3 SV=1	GR_C1	43951.21	GR_C2	35160.97
P53004	Biliverdin reductase A OS=Homo sapiens GN=BLVRA PE=1 SV=2			GR_C2	83.48
P07738	Bisphosphoglycerate mutase OS=Homo sapiens GN=BPGM PE=1 SV=2	GR_C1	566.78	GR_C2	510.10
P04632	Calpain small subunit 1 OS=Homo sapiens GN=CAPNS1 PE=1 SV=1	GR_C1	53.75	GR_C2	48.38
P07384	Calpain-1 catalytic subunit OS=Homo sapiens GN=CAPN1 PE=1 SV=1	GR_C1	126.79	GR_C2	139.47
P00915	Carbonic anhydrase 1 OS=Homo sapiens GN=CA1 PE=1 SV=2	GR_C1	2688.57	GR_C2	2957.43
P00918	Carbonic anhydrase 2 OS=Homo sapiens GN=CA2 PE=1 SV=2	GR_C1	822	GR_C2	739.80
P07451	Carbonic anhydrase 3 OS=Homo sapiens GN=CA3 PE=1 SV=3			GR_C2	50.99
P04040	Catalase OS=Homo sapiens GN=CAT PE=1 SV=3	GR_C1	1952.51	GR_C2	2147.76
P30046	D-dopachrome decarboxylase OS=Homo sapiens GN=DDT PE=1 SV=3	GR_C1	151.62		
A0N071	Delta globin OS=Homo sapiens GN=HBD PE=3 SV=1	GR_C1	19293.06	GR_C2	15434.45
P13716	Delta-aminolevulinic acid dehydratase OS=Homo sapiens GN=ALAD PE=1 SV=1	GR_C1	140.5	GR_C2	154.55
P09417	Dihydropteridine reductase OS=Homo sapiens GN=QDPR PE=1 SV=2			GR_C2	109.13
Q1VWM3	EPB41 protein (Fragment) OS=Homo sapiens GN=EPB41 PE=2 SV=1	GR_C1	42.42	GR_C2	38.18
Q4KKX0	EPB42 protein OS=Homo sapiens GN=EPB42 PE=2 SV=1	GR_C1	144.69	GR_C2	130.22
P27105	Erythrocyte band 7 integral membrane protein OS=Homo sapiens GN=STOM PE=1 SV=3	GR_C1	216.83	GR_C2	195.15
P30043	Flavin reductase OS=Homo sapiens GN=BLVRB PE=1 SV=3	GR_C1	956.79	GR_C2	861.11
P04075	Fructose-bisphosphate aldolase A OS=Homo sapiens GN=ALDOA PE=1 SV=2	GR_C1	105.39	GR_C2	94.85
P13630	GDP-L-fucose synthase OS=Homo sapiens GN=TSTA3 PE=1 SV=1			GR_C2	44.11
P48506	Glutamate--cysteine ligase catalytic subunit OS=Homo sapiens GN=GCLC PE=1 SV=2	GR_C1	129.38	GR_C2	155.26
P78417	Glutathione S-transferase omega-1 OS=Homo sapiens GN=GSTO1 PE=1 SV=2	GR_C1	272.75	GR_C2	245.48
P04406	Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens GN=GAPDH PE=1 SV=3	GR_C1	863.27	GR_C2	776.94
P62826	GTP-binding nuclear protein Ran OS=Homo sapiens GN=GAN PE=1 SV=3	GR_C1	328.23	GR_C2	361.05
Q14477	Hbbm fused globin protein (Fragment) OS=Homo sapiens GN=HBB PE=2 SV=1	GR_C1	31135.2	GR_C2	24908.15
P07900	Heat shock protein HSP 90-alpha OS=Homo sapiens GN=HSP90AA1 PE=1 SV=5	GR_C1	62.74	GR_C2	69.01
Q96T46	Hemoglobin alpha 2 (Fragment) OS=Homo sapiens GN=HBA2 PE=2 SV=1	GR_C1	8169.17	GR_C2	6535.34
Q6J127	Hemoglobin beta (Fragment) OS=Homo sapiens GN=HBB PE=2 SV=1	GR_C1	37605.19	GR_C2	30084.15
Q3LR79	Hemoglobin beta (Fragment) OS=Homo sapiens GN=HBB PE=2 SV=1	GR_C1	38341.55	GR_C2	30673.24
Q5XTR9	Hemoglobin delta-beta fusion protein (Fragment) OS=Homo sapiens GN=HBD/HBB PE=2 SV=1	GR_C1	230.36	GR_C2	207.32
P69905	Hemoglobin subunit alpha OS=Homo sapiens GN=HBA1 PE=1 SV=2	GR_C1	14737.41	GR_C2	11789.93
P68871	Hemoglobin subunit beta OS=Homo sapiens GN=HBB PE=1 SV=2	GR_C1	50872.59	GR_C2	40698.07
P68991	Hemoglobin subunit gamma-1 OS=Homo sapiens GN=HBG1 PE=1 SV=2	GR_C1	4385.7	GR_C2	4824.27
P09105	Hemoglobin subunit theta-1 OS=Homo sapiens GN=HBQ1 PE=1 SV=2			GR_C2	48.36
Q16775	Hydroxyacylglutathione hydrolase, mitochondrial OS=Homo sapiens GN=HAGH PE=1 SV=2	GR_C1	225.87		
P00492	Hypoxanthine-guanine phosphoribosyltransferase OS=Homo sapiens GN=HPRT1 PE=1 SV=2	GR_C1	277.5		
P07195	L-lactate dehydrogenase B chain OS=Homo sapiens GN=LDHB PE=1 SV=2	GR_C1	293.27	GR_C2	351.92
Q724W1	L-xylulose reductase OS=Homo sapiens GN=DCXR PE=1 SV=2	GR_C1	39.95		
Q04760	Lactoylglutathione lyase OS=Homo sapiens GN=GLO1 PE=1 SV=4			GR_C2	50.90
P24666	Low molecular weight phosphotyrosine protein phosphatase OS=Homo sapiens GN=ACPP1 PE=1 SV=3	GR_C1	97.61		
Q6PJ74	MSN protein (Fragment) OS=Homo sapiens GN=MSN PE=2 SV=1	GR_C1	157.63		
P22234	Multifunctional protein ADE2 OS=Homo sapiens GN=PAICS PE=1 SV=3	GR_C1	48.55	GR_C2	43.70
P58546	Myotrophin OS=Homo sapiens GN=MTPN PE=1 SV=2			GR_C2	53.79
Q6XQNE	Nicotinate phosphoribosyltransferase OS=Homo sapiens GN=NAPRT1 PE=1 SV=2	GR_C1	318.45	GR_C2	382.14
P15531	Nucleoside diphosphate kinase A OS=Homo sapiens GN=NDPK1 PE=1 SV=1	GR_C1	112.69	GR_C2	101.42
Q9NTK5	Ogg-like ATPase 1 OS=Homo sapiens GN=OLA1 PE=1 SV=2	GR_C1	195.86		
P62937	Peptidyl-prolyl cis-trans isomerase A OS=Homo sapiens GN=PP1A PE=1 SV=2	GR_C1	126.79		
Q06830	Peroxisomal protein OS=Homo sapiens GN=PRDX1 PE=1 SV=1	GR_C1	606.82	GR_C2	667.50
P32119	Peroxisomal protein OS=Homo sapiens GN=PRDX2 PE=1 SV=5	GR_C1	1233.37	GR_C2	1356.71
P30041	Peroxisomal protein OS=Homo sapiens GN=PRDX6 PE=1 SV=3	GR_C1	608.83	GR_C2	547.95
P30086	Phosphatidylethanolamine-binding protein 1 OS=Homo sapiens GN=PEBP1 PE=1 SV=3			GR_C2	123.36
P00558	Phosphoglycerate kinase 1 OS=Homo sapiens GN=PGK1 PE=1 SV=3	GR_C1	789.79	GR_C2	710.81
B4DJ26	Phosphoribosylformylglycinamide synthase (FGAR amidotransferase), isoform CRA_c OS=Homo sapiens GN=PFAS PE=2 SV=1			GR_C2	51.17
P13796	Plastin-2 OS=Homo sapiens GN=LCP1 PE=1 SV=6	GR_C1	71.16		
P68402	Platelet-activating factor acetylhydrolase IB subunit beta OS=Homo sapiens GN=PAFAH1B2 PE=1 SV=1	GR_C1	132.31		
Q15102	Platelet-activating factor acetylhydrolase IB subunit gamma OS=Homo sapiens GN=PAFAH1B3 PE=1 SV=1			GR_C2	63.29
Q06323	Proteasome activator complex subunit 1 OS=Homo sapiens GN=PSME1 PE=1 SV=1	GR_C1	46.96	GR_C2	42.26
P25787	Proteasome subunit alpha type-2 OS=Homo sapiens GN=PSMA2 PE=1 SV=2	GR_C1	48.41	GR_C2	53.25
P28066	Proteasome subunit alpha type-5 OS=Homo sapiens GN=PSMA5 PE=1 SV=3	GR_C1	133.13	GR_C2	146.44
P60900	Proteasome subunit alpha type-6 OS=Homo sapiens GN=PSMA6 PE=1 SV=1	GR_C1	48.44	GR_C2	38.75
Q14818	Proteasome subunit alpha type-7 OS=Homo sapiens GN=PSMA7 PE=1 SV=1	GR_C1	96.42	GR_C2	86.78
P49721	Proteasome subunit beta type-2 OS=Homo sapiens GN=PSMB2 PE=1 SV=1	GR_C1	67.38	GR_C2	60.64
P28074	Proteasome subunit beta type-5 OS=Homo sapiens GN=PSMB5 PE=1 SV=3	GR_C1	134.24	GR_C2	120.82
P28072	Proteasome subunit beta type-6 OS=Homo sapiens GN=PSMB6 PE=1 SV=4	GR_C1	98.72	GR_C2	118.46
Q5TDH0	Protein DDI1 homolog 2 OS=Homo sapiens GN=DDI2 PE=1 SV=1	GR_C1	82.31	GR_C2	98.77
P06703	Protein S100-A6 OS=Homo sapiens GN=S100A6 PE=1 SV=1			GR_C2	65.83
P05109	Protein S100-A8 OS=Homo sapiens GN=S100A8 PE=1 SV=1	GR_C1	35.61		
P21980	Protein-glutamine gamma-glutamyltransferase 2 OS=Homo sapiens GN=TGM2 PE=1 SV=2	GR_C1	255.52	GR_C2	281.07
P00491	Purine nucleoside phosphorylase OS=Homo sapiens GN=PNP PE=1 SV=2	GR_C1	1075.95	GR_C2	968.36
Q8WVW5	Putative uncharacterized protein (Fragment) OS=Homo sapiens PE=2 SV=1	GR_C1	161.38	GR_C2	177.52

P30613	Pyruvate kinase isozymes R/L OS=Homo sapiens GN=PKLR PE=1 SV=2	GR_C1	80.99		
P50395	Rab GDP dissociation inhibitor beta OS=Homo sapiens GN=GDI2 PE=1 SV=2	GR_C1	151.66	GR_C2	181.99
P00352	Retinal dehydrogenase 1 OS=Homo sapiens GN=ALDH1A1 PE=1 SV=2	GR_C1	114.14		
P49247	Ribose-5-phosphate isomerase OS=Homo sapiens GN=RPIA PE=1 SV=3	GR_C1	51		
P60891	Ribose-phosphate pyrophosphokinase 1 OS=Homo sapiens GN=PRPS1 PE=1 SV=2	GR_C1	98.73	GR_C2	88.86
P10768	S-formylglutathione hydrolase OS=Homo sapiens GN=ESD PE=1 SV=2			GR_C2	42.27
Q13228	Selenium-binding protein 1 OS=Homo sapiens GN=SELENBP1 PE=1 SV=2	GR_C1	799.67	GR_C2	719.70
Q15257	Serine/threonine-protein phosphatase 2A activator OS=Homo sapiens GN=PPP2R4 PE=1 SV=3			GR_C2	89.15
E2RVJ0	Solute carrier family 4, anion exchanger, member 1 OS=Homo sapiens GN=SLC4A1 PE=2 SV=1	GR_C1	1746.4	GR_C2	1397.12
P02549	Spectrin alpha chain, erythrocyte OS=Homo sapiens GN=SPTA1 PE=1 SV=5	GR_C1	610.25	GR_C2	488.20
P11277	Spectrin beta chain, erythrocyte OS=Homo sapiens GN=SPTB PE=1 SV=5	GR_C1	1210.47	GR_C2	968.38
P31948	Stress-induced-phosphoprotein 1 OS=Homo sapiens GN=STIP1 PE=1 SV=1	GR_C1	449.46	GR_C2	404.51
P00441	Superoxide dismutase [Cu-Zn] OS=Homo sapiens GN=SOD1 PE=1 SV=2			GR_C2	47.66
P50990	T-complex protein 1 subunit theta OS=Homo sapiens GN=CCT8 PE=1 SV=4	GR_C1	56.54	GR_C2	62.19
P10599	Thioredoxin OS=Homo sapiens GN=TXN PE=1 SV=3			GR_C2	113.71
P55072	Transitional endoplasmic reticulum ATPase OS=Homo sapiens GN=VCP PE=1 SV=4	GR_C1	581.24	GR_C2	464.99
P29401	Transketolase OS=Homo sapiens GN=TKT PE=1 SV=3	GR_C1	44	GR_C2	39.60
P60174	Triosephosphate isomerase OS=Homo sapiens GN=TP1 PE=1 SV=2			GR_C2	136.49
B3VL12	Truncated beta globin OS=Homo sapiens PE=3 SV=1	GR_C1	25683.24	GR_C2	20546.55
D0PNI1	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein zeta polypeptide OS=Homo sapiens GN=YWHAZ PE=3 SV=1	GR_C1	106.65	GR_C2	95.99
Q3MIH3	Ubiquitin A-52 residue ribosomal protein fusion product 1 OS=Homo sapiens GN=UBA52 PE=2 SV=1	GR_C1	561.51	GR_C2	505.36
B2RD79	Ubiquitin carboxyl-terminal hydrolase OS=Homo sapiens PE=2 SV=1	GR_C1	147.65	GR_C2	132.89
P61088	Ubiquitin-conjugating enzyme E2 N OS=Homo sapiens GN=UBE2N PE=1 SV=1	GR_C1	57.54	GR_C2	69.05
P22314	Ubiquitin-like modifier-activating enzyme 1 OS=Homo sapiens GN=UBA1 PE=1 SV=3	GR_C1	141.61		
Q0VAJ1	UGT1A4 protein OS=Homo sapiens GN=UGT1A4 PE=2 SV=1	GR_C1	85.87	GR_C2	77.28
E7ET08	Uncharacterized protein OS=Homo sapiens GN=HSPA8 PE=3 SV=1	GR_C1	194.22	GR_C2	174.80
C9JIM8	Uncharacterized protein OS=Homo sapiens GN=SLC2A1 PE=3 SV=1	GR_C1	249.02	GR_C2	298.82

Supplemental Data 2

Sheet 3

Q-Treated

AC	Description	Replicate 1	Score	Replicate 2	Score
P68871	Hemoglobin subunit beta OS=Homo sapiens GN=HBB PE=1 SV=2	GR_Q1	14996.26	GR_Q2	11385.61
Q6J1Z7	Hemoglobin beta (Fragment) OS=Homo sapiens GN=HBB PE=2 SV=1	GR_Q1	10771.86	GR_Q2	8401.99
P69905	Hemoglobin subunit alpha OS=Homo sapiens GN=HBA1 PE=1 SV=2	GR_Q1	5430.65	GR_Q2	4003.81
Q3LR79	Hemoglobin beta (Fragment) OS=Homo sapiens GN=HBB PE=2 SV=1	GR_Q1	13096.39	GR_Q2	9761.02
Q14477	Hbbm fused globin protein (Fragment) OS=Homo sapiens GN=HBB PE=2 SV=1	GR_Q1	7522.88	GR_Q2	6359.41
A0N071	Delta globin OS=Homo sapiens GN=HBD PE=3 SV=1	GR_Q1	5974.65	GR_Q2	6022.18
P02549	Spectrin alpha chain, erythrocyte OS=Homo sapiens GN=SPTA1 PE=1 SV=5	GR_Q1	18240.34	GR_Q2	19078.18
P11277	Spectrin beta chain, erythrocyte OS=Homo sapiens GN=SPTB PE=1 SV=5	GR_Q1	18376.29	GR_Q2	15341.22
E2RVJ0	Solute carrier family 4, anion exchanger, member 1 OS=Homo sapiens GN=SLC4A1 PE=2 SV=1	GR_Q1	7726.62	GR_Q2	5366.01
P55072	Transitional endoplasmic reticulum ATPase OS=Homo sapiens GN=VCP PE=1 SV=4	GR_Q1	7578.25	GR_Q2	7146
P16157	Ankyrin-1 OS=Homo sapiens GN=ANK1 PE=1 SV=3	GR_Q1	2936.72	GR_Q2	2612.36
P60900	Proteasome subunit alpha type-6 OS=Homo sapiens GN=PSMA6 PE=1 SV=1	GR_Q1	5246.43	GR_Q2	3096.78
P13798	Acylamino-acid-releasing enzyme OS=Homo sapiens GN=APEH PE=1 SV=4	GR_Q1	6594.6	GR_Q2	4554.51
P69891	Hemoglobin subunit gamma-1 OS=Homo sapiens GN=HBG1 PE=1 SV=2	GR_Q1	4238.18	GR_Q2	4452.53
P13716	Delta-aminolevulinic acid dehydratase OS=Homo sapiens GN=ALAD PE=1 SV=1	GR_Q1	2937.96	GR_Q2	3068.88
P07900	Heat shock protein HSP 90-alpha OS=Homo sapiens GN=HSP90AA1 PE=1 SV=5	GR_Q1	2650.82	GR_Q2	3021.94
P32119	Peroxiredoxin-2 OS=Homo sapiens GN=PRDX2 PE=1 SV=5	GR_Q1	840.88	GR_Q2	677.8
P50990	T-complex protein 1 subunit theta OS=Homo sapiens GN=CCT8 PE=1 SV=4	GR_Q1	2233.55	GR_Q2	2069.58
P00915	Carbonic anhydrase 1 OS=Homo sapiens GN=CA1 PE=1 SV=2	GR_Q1	1565.85	GR_Q2	1071.3
P07384	Calpain-1 catalytic subunit OS=Homo sapiens GN=CAPN1 PE=1 SV=1	GR_Q1	1496.93	GR_Q2	1287.28
P62826	GTP-binding nuclear protein Ran OS=Homo sapiens GN=GAN PE=1 SV=3	GR_Q1	191.32	GR_Q2	242.74
Q8WVW5	Putative uncharacterized protein (Fragment) OS=Homo sapiens PE=2 SV=1	GR_Q1	1414.3	GR_Q2	1405.49
P04040	Catalase OS=Homo sapiens GN=CAT PE=1 SV=3	GR_Q1	782.31	GR_Q2	433.7
Q4LE36	ACLY variant protein (Fragment) OS=Homo sapiens GN=ACLY variant protein PE=2 SV=1	GR_Q1	296.26	GR_Q2	124.01
P21980	Protein-glutamine gamma-glutamyltransferase 2 OS=Homo sapiens GN=TGM2 PE=1 SV=2	GR_Q1	2108.35	GR_Q2	1575.97
Q06830	Peroxiredoxin-1 OS=Homo sapiens GN=PRDX1 PE=1 SV=1	GR_Q1	228.75	GR_Q2	447.2
P28066	Proteasome subunit alpha type-5 OS=Homo sapiens GN=PSMA5 PE=1 SV=3	GR_Q1	1178.85	GR_Q2	2018.99
P25787	Proteasome subunit alpha type-2 OS=Homo sapiens GN=PSMA2 PE=1 SV=2	GR_Q1	1571.97	GR_Q2	1306.2
Q4KKX0	EPB42 protein OS=Homo sapiens GN=EPB42 PE=2 SV=1	GR_Q1	1629.98	GR_Q2	1114.55
P04632	Calpain small subunit 1 OS=Homo sapiens GN=CAPS1 PE=1 SV=1	GR_Q1	437.69	GR_Q2	215.96
O14818	Proteasome subunit alpha type-7 OS=Homo sapiens GN=PSMA7 PE=1 SV=1	GR_Q1	1234.11	GR_Q2	1085.63
P49721	Proteasome subunit beta type-2 OS=Homo sapiens GN=PSMB2 PE=1 SV=1	GR_Q1	1371.03	GR_Q2	1173.9
P00491	Purine nucleoside phosphorylase OS=Homo sapiens GN=PNP PE=1 SV=2	GR_Q1	402.59	GR_Q2	287.93
P27105	Erythrocyte band 7 integral membrane protein OS=Homo sapiens GN=STOM PE=1 SV=3	GR_Q1	1047.17	GR_Q2	1054.46
P28074	Proteasome subunit beta type-5 OS=Homo sapiens GN=PSMB5 PE=1 SV=3	GR_Q1	1444.39	GR_Q2	1823.8
P30041	Peroxiredoxin-6 OS=Homo sapiens GN=PRDX6 PE=1 SV=3	GR_Q1	441.73	GR_Q2	274.18
P00568	Adenylate kinase isoenzyme 1 OS=Homo sapiens GN=AK1 PE=1 SV=3	GR_Q1	106.02	GR_Q2	66.51
P60891	Ribose-phosphate pyrophosphokinase 1 OS=Homo sapiens GN=PRPS1 PE=1 SV=2	GR_Q1	274.85	GR_Q2	191.67
P00918	Carbonic anhydrase 2 OS=Homo sapiens GN=CA2 PE=1 SV=2	GR_Q1	299.22	GR_Q2	325.06
Q3MIH3	Ubiquitin A-52 residue ribosomal protein fusion product 1 OS=Homo sapiens GN=UBA52 PE=2 SV=1	GR_Q1	158.13	GR_Q2	161.15
Q1VWM3	EPB41 protein (Fragment) OS=Homo sapiens GN=EPB41 PE=2 SV=1	GR_Q1	946.83	GR_Q2	873.89
E7ET08	Uncharacterized protein OS=Homo sapiens GN=HSPA8 PE=3 SV=1	GR_Q1	511.64	GR_Q2	722.38
P22234	Multifunctional protein ADE2 OS=Homo sapiens GN=PAICS PE=1 SV=3	GR_Q1	36.48	GR_Q2	55.02
Q13228	Selenium-binding protein 1 OS=Homo sapiens GN=SELENBP1 PE=1 SV=2	GR_Q1	281.48	GR_Q2	273.86
Q06323	Proteasome activator complex subunit 1 OS=Homo sapiens GN=PSME1 PE=1 SV=1	GR_Q1	860.02	GR_Q2	555.2
P07738	Bisphosphoglycerate mutase OS=Homo sapiens GN=BPGM PE=1 SV=2	GR_Q1	69.03	GR_Q2	69.37
P04406	Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens GN=GAPDH PE=1 SV=3	GR_Q1	278.27	GR_Q2	425.34
D0PNI1	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein zeta polypeptide OS=Homo sapiens GN=YWHAZ PE=3 SV=1	GR_Q1	911.89	GR_Q2	573.56
P30043	Flavin reductase OS=Homo sapiens GN=BLVRB PE=1 SV=3	GR_Q1	582.43	GR_Q2	406.63
P78417	Glutathione S-transferase omega-1 OS=Homo sapiens GN=GSTO1 PE=1 SV=2	GR_Q1	112.98	GR_Q2	54.79
P15531	Nucleoside diphosphate kinase A OS=Homo sapiens GN=NME1 PE=1 SV=1	GR_Q1	461.76	GR_Q2	486.15
P28072	Proteasome subunit beta type-6 OS=Homo sapiens GN=PSMB6 PE=1 SV=4	GR_Q1	338.73	GR_Q2	1213.5
P30566	Adenylosuccinate lyase OS=Homo sapiens GN=ADSL PE=1 SV=2	GR_Q1	511.69	GR_Q2	217.55
Q5TDH0	Protein DD1 homolog 2 OS=Homo sapiens GN=DDI2 PE=1 SV=1	GR_Q1	43.96		
P48506	Glutamate--cysteine ligase catalytic subunit OS=Homo sapiens GN=GCLC PE=1 SV=2	GR_Q1	250.83	GR_Q2	205.99
P07195	L-lactate dehydrogenase B chain OS=Homo sapiens GN=LDHB PE=1 SV=2	GR_Q1	190.8	GR_Q2	250
P50395	Rab GDP dissociation inhibitor beta OS=Homo sapiens GN=GD12 PE=1 SV=2	GR_Q1	304.91	GR_Q2	381.86
P05109	Protein S100-A8 OS=Homo sapiens GN=S100A8 PE=1 SV=1	GR_Q1	98.47	GR_Q2	52.9
P49247	Ribose-5-phosphate isomerase OS=Homo sapiens GN=RPIA PE=1 SV=3	GR_Q1	146.6		
P00492	Hypoxanthine-guanine phosphoribosyltransferase OS=Homo sapiens GN=HPRT1 PE=1 SV=2	GR_Q1	326.63	GR_Q2	248.87
Q7Z4W1	L-xylulose reductase OS=Homo sapiens GN=DCXR PE=1 SV=2	GR_Q1	83.22		
Q9NTK5	Obg-like ATPase 1 OS=Homo sapiens GN=OLA1 PE=1 SV=2	GR_Q1	81.17	GR_Q2	85.34
P00352	Retinal dehydrogenase 1 OS=Homo sapiens GN=ALDH1A1 PE=1 SV=2	GR_Q1	134.19	GR_Q2	172.38
P22314	Ubiquitin-like modifier-activating enzyme 1 OS=Homo sapiens GN=UBA1 PE=1 SV=3	GR_Q1	134.15	GR_Q2	146.93
P24666	Low molecular weight phosphotyrosine protein phosphatase OS=Homo sapiens GN=ACPP1 PE=1 SV=3	GR_Q1	114.39	GR_Q2	195.45
P68402	Platelet-activating factor acetylhydrolase IB subunit beta OS=Homo sapiens GN=PAFAH1B2 PE=1 SV=1	GR_Q1	141.87	GR_Q2	72.88
P62937	Peptidyl-prolyl cis-trans isomerase A OS=Homo sapiens GN=PPIA PE=1 SV=2	GR_Q1	26.96		
Q15102	Platelet-activating factor acetylhydrolase IB subunit gamma OS=Homo sapiens GN=PAFAH1B3 PE=1 SV=1	GR_Q1	82.93		
P60174	Triosephosphate isomerase OS=Homo sapiens GN=TP1 PE=1 SV=2	GR_Q1	53.14		
P28RM7	Spectrin, beta, erythrocytic OS=Homo sapiens GN=SPTB PE=2 SV=1	GR_Q1	18491.68	GR_Q2	15224.1
P35579	Myosin-9 OS=Homo sapiens GN=MYH9 PE=1 SV=4	GR_Q1	5669.27	GR_Q2	5910.73
Q00610	Clathrin heavy chain 1 OS=Homo sapiens GN=CLTC PE=1 SV=5	GR_Q1	5208.03	GR_Q2	4956.03
Q5T4S7	E3 ubiquitin-protein ligase UBR4 OS=Homo sapiens GN=UBR4 PE=1 SV=1	GR_Q1	2090.06	GR_Q2	2391.26
P78371	T-complex protein 1 subunit beta OS=Homo sapiens GN=CCT2 PE=1 SV=4	GR_Q1	4234.48	GR_Q2	2984.98
P49368	T-complex protein 1 subunit gamma OS=Homo sapiens GN=CCT3 PE=1 SV=4	GR_Q1	1802.62	GR_Q2	1787.75
Q99832	T-complex protein 1 subunit eta OS=Homo sapiens GN=CCT7 PE=1 SV=2	GR_Q1	1989.81	GR_Q2	2313.05
O00410	Importin-5 OS=Homo sapiens GN=IPO5 PE=1 SV=4	GR_Q1	3029.41	GR_Q2	2279.45
Q13200	26S proteasome non-ATPase regulatory subunit 2 OS=Homo sapiens GN=PSMD2 PE=1 SV=3	GR_Q1	2350.07	GR_Q2	2175.1
Q93008	Probable ubiquitin carboxyl-terminal hydrolase FAF-X OS=Homo sapiens GN=USP9X PE=1 SV=3	GR_Q1	1645.65	GR_Q2	1685.99
Q86VP6	Cullin-associated NEDD8-dissociated protein 1 OS=Homo sapiens GN=CAND1 PE=1 SV=2	GR_Q1	1572.47	GR_Q2	1285.62
P29144	Tripeptidyl-peptidase 2 OS=Homo sapiens GN=TPP2 PE=1 SV=4	GR_Q1	2034.37	GR_Q2	1711.84

Q6VFAQ	Hemoglobin beta chain (Fragment) OS=Homo sapiens GN=HBB PE=2 SV=1	GR_Q1	475.15		
A8K2X8	cDNA FLJ78433, highly similar to Homo sapiens chaperonin containing TCP1, subunit 5 (epsilon) (CCT5), mRNA OS=Homo sapiens PE=2 SV=1	GR_Q1	2249.71	GR_Q2	1347.07
Q4LE45	MYH10 variant protein (Fragment) OS=Homo sapiens GN=MYH10 variant protein PE=2 SV=1	GR_Q1	2211.55	GR_Q2	2694.23
P14724	DNA damage-binding protein 1 OS=Homo sapiens GN=HSP90A1 PE=1 SV=1	GR_Q1	1160.72	GR_Q2	1858.5
P21333	Filamin-A OS=Homo sapiens GN=FLNA PE=1 SV=4	GR_Q1	439.16	GR_Q2	143.87
P50991	T-complex protein 1 subunit delta OS=Homo sapiens GN=CCT4 PE=1 SV=4	GR_Q1	1550.39	GR_Q2	1381.05
O14724	Beta-spectrin (Fragment) OS=Homo sapiens GN=HSP90A1 PE=2 SV=1	GR_Q1	3192.47	GR_Q2	1711.93
Q99460	26S proteasome non-ATPase regulatory subunit 1 OS=Homo sapiens GN=PSMD1 PE=1 SV=2	GR_Q1	2401.72	GR_Q2	1768.1
O00231	26S proteasome non-ATPase regulatory subunit 11 OS=Homo sapiens GN=PSMD11 PE=1 SV=3	GR_Q1	1096.63	GR_Q2	1119.92
B7Z815	Ubiquitin carboxyl-terminal hydrolase OS=Homo sapiens PE=2 SV=1	GR_Q1	1058.68	GR_Q2	1014.63
P08238	Heat shock protein HSP 90-beta OS=Homo sapiens GN=HSP90A1 PE=1 SV=4	GR_Q1	1936.26	GR_Q2	2131.06
P40227	T-complex protein 1 subunit zeta OS=Homo sapiens GN=CCT6A PE=1 SV=3	GR_Q1	2855.77	GR_Q2	1524.88
P62258	14-3-3 protein epsilon OS=Homo sapiens GN=YWHAE PE=1 SV=1	GR_Q1	2594.68	GR_Q2	2102.95
Q14974	Importin subunit beta-1 OS=Homo sapiens GN=KPNB1 PE=1 SV=2	GR_Q1	2436.29	GR_Q2	1622.37
Q14C86	GTPase-activating protein and VPS9 domain-containing protein 1 OS=Homo sapiens GN=GAPVD1 PE=1 SV=2	GR_Q1	868.23	GR_Q2	819.12
P17987	T-complex protein 1 subunit alpha OS=Homo sapiens GN=TCP1 PE=1 SV=1	GR_Q1	1687.1	GR_Q2	1982.84
P17858	6-phosphofructokinase, liver type OS=Homo sapiens GN=PFKL PE=1 SV=6	GR_Q1	620.82	GR_Q2	759.47
O60610	Protein diaphanous homolog 1 OS=Homo sapiens GN=DIAPH1 PE=1 SV=2	GR_Q1	1743.15	GR_Q2	1203.18
Q9Y230	RuvB-like 2 OS=Homo sapiens GN=RUVBL2 PE=1 SV=3	GR_Q1	1633.6	GR_Q2	1524.78
P49720	Proteasome subunit beta type-3 OS=Homo sapiens GN=PSMB3 PE=1 SV=2	GR_Q1	2004.71	GR_Q2	1564.45
Q0P512	Solute carrier family 2 (Facilitated glucose transporter), member 1 OS=Homo sapiens GN=SLC2A1 PE=2 SV=1	GR_Q1	593.98	GR_Q2	672.84
P12814	Alpha-actinin-1 OS=Homo sapiens GN=ACTN1 PE=1 SV=2	GR_Q1	2128.54	GR_Q2	1870.43
B3KNN7	cDNA FLJ30049 fis, clone ADRGL1000033, highly similar to 26S proteasome non-ATPase regulatory subunit 3 OS=Homo sapiens PE=2 SV=1	GR_Q1	353.29	GR_Q2	261.07
Q5XPI4	E3 ubiquitin-protein ligase RNF123 OS=Homo sapiens GN=RNF123 PE=1 SV=1	GR_Q1	175.87	GR_Q2	302.85
O95373	Importin-7 OS=Homo sapiens GN=IPO7 PE=1 SV=1	GR_Q1	950.7	GR_Q2	814.47
Q7Z627	E3 ubiquitin-protein ligase HUWE1 OS=Homo sapiens GN=HUWE1 PE=1 SV=3	GR_Q1	1164.71	GR_Q2	1430.91
P17980	26S protease regulatory subunit 6A OS=Homo sapiens GN=PSMC3 PE=1 SV=3	GR_Q1	2076.69	GR_Q2	980.43
P62195	26S protease regulatory subunit 8 OS=Homo sapiens GN=PSMC5 PE=1 SV=1	GR_Q1	1383.14	GR_Q2	817.69
Q14254	Flotillin-2 OS=Homo sapiens GN=LOT2 PE=1 SV=2	GR_Q1	1558.19	GR_Q2	1006.68
Q9Y265	RuvB-like 1 OS=Homo sapiens GN=RUVBL1 PE=1 SV=1	GR_Q1	2017.78	GR_Q2	1513.75
P68032	Actin, alpha cardiac muscle 1 OS=Homo sapiens GN=ACTC1 PE=1 SV=1	GR_Q1	693.68	GR_Q2	734.43
Q9Y315	Putative deoxyribose-phosphate aldolase OS=Homo sapiens GN=DERA PE=1 SV=2	GR_Q1	1871.59	GR_Q2	1421.71
P61163	Alpha-centractin OS=Homo sapiens GN=ACTR1A PE=1 SV=1	GR_Q1	1786.36	GR_Q2	1426.33
Q92905	COP9 signalosome complex subunit 5 OS=Homo sapiens GN=COPS5 PE=1 SV=4	GR_Q1	1121.89	GR_Q2	844.36
Q9Y6E3	HSPC027 OS=Homo sapiens PE=2 SV=1	GR_Q1	1132.48	GR_Q2	1185.12
Q9BT78	COP9 signalosome complex subunit 4 OS=Homo sapiens GN=COPS4 PE=1 SV=1	GR_Q1	1230.82	GR_Q2	1489.41
P35998	26S protease regulatory subunit 7 OS=Homo sapiens GN=PSMC2 PE=1 SV=3	GR_Q1	562.8	GR_Q2	694.33
A7E2Y5	DnaJ (Hsp40) homolog, subfamily C, member 13 OS=Homo sapiens GN=DNAJC13 PE=2 SV=1	GR_Q1	43.17		
E1P646	Adaptor-related protein complex 2, beta 1 subunit, isoform CRA_d OS=Homo sapiens GN=AP2B1 PE=4 SV=1	GR_Q1	789.34	GR_Q2	439.01
Q15008	26S proteasome non-ATPase regulatory subunit 6 OS=Homo sapiens GN=PSMD6 PE=1 SV=1	GR_Q1	1040.15	GR_Q2	1449
A8K781	cDNA FLJ75299, highly similar to Xenopus laevis proteasome (prosome, macropain) 26S subunit, ATPase 3, mRNA OS=Homo sapiens PE=2 SV=1	GR_Q1	1522.83	GR_Q2	1008.7
P30153	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform OS=Homo sapiens GN=PPP2R1A PE=1 SV=4	GR_Q1	1486.98	GR_Q2	1103.62
P20618	Proteasome subunit beta type-1 OS=Homo sapiens GN=PSMB1 PE=1 SV=2	GR_Q1	1532.62	GR_Q2	1419.02
P05164	Myeloperoxidase OS=Homo sapiens GN=MPO PE=1 SV=1	GR_Q1	672.43	GR_Q2	344.76
Q9C0C9	Ubiquitin-conjugating enzyme E2 O OS=Homo sapiens GN=UBE2O PE=1 SV=3	GR_Q1	186.57	GR_Q2	451.51
P37840	Alpha-synuclein OS=Homo sapiens GN=SNCA PE=1 SV=1	GR_Q1	229.57	GR_Q2	309.85
P28070	Proteasome subunit beta type-4 OS=Homo sapiens GN=PSMB4 PE=1 SV=4	GR_Q1	2731.63	GR_Q2	1498.39
O43707	Alpha-actinin-4 OS=Homo sapiens GN=ACTN4 PE=1 SV=2	GR_Q1	1510.59	GR_Q2	1457.19
O00232	26S proteasome non-ATPase regulatory subunit 12 OS=Homo sapiens GN=PSMD12 PE=1 SV=3	GR_Q1	863.43	GR_Q2	1032.29
EP9CQ3	Ubiquitin carboxyl-terminal hydrolase OS=Homo sapiens GN=USP15 PE=3 SV=2	GR_Q1	1541.25	GR_Q2	1211.13
O43681	ATPase ASNA1 OS=Homo sapiens GN=ASNA1 PE=1 SV=2	GR_Q1	915.91	GR_Q2	1322.86
Q13616	Cullin-1 OS=Homo sapiens GN=CUL1 PE=1 SV=2	GR_Q1	143.74	GR_Q2	339.37
B4DZV5	cDNA FLJ58820, highly similar to 55 kDa erythrocyte membrane protein (p55) OS=Homo sapiens PE=2 SV=1	GR_Q1	109.47		
O14744	Protein arginine N-methyltransferase 5 OS=Homo sapiens GN=PRMT5 PE=1 SV=4	GR_Q1	704.24	GR_Q2	725.45
Q2Q9H2	Glucose-6-phosphate 1-dehydrogenase (Fragment) OS=Homo sapiens GN=G6PD PE=2 SV=1	GR_Q1	160.49	GR_Q2	231.53
P25786	Proteasome subunit alpha type-1 OS=Homo sapiens GN=PSMA1 PE=1 SV=1	GR_Q1	745.62	GR_Q2	862.26
Q2TUW9	Lactoferrin OS=Homo sapiens PE=2 SV=1	GR_Q1	86.4	GR_Q2	233.13
P46459	Vesicle-fusing ATPase OS=Homo sapiens GN=NSF PE=1 SV=3	GR_Q1	1102.59	GR_Q2	460.88
Q709C8	Vacuolar protein sorting-associated protein 13C OS=Homo sapiens GN=VPS13C PE=1 SV=1	GR_Q1	673.26	GR_Q2	418.56
P62191	26S protease regulatory subunit 4 OS=Homo sapiens GN=PSMC1 PE=1 SV=1	GR_Q1	1050.19	GR_Q2	1036.1
P07237	Protein disulfide-isomerase OS=Homo sapiens GN=P4HB PE=1 SV=3	GR_Q1	576.54	GR_Q2	507.61
F222X4	Uncharacterized protein OS=Homo sapiens GN=XPO4 PE=4 SV=1	GR_Q1	630.99	GR_Q2	551.31
Q16401	26S proteasome non-ATPase regulatory subunit 5 OS=Homo sapiens GN=PSMD5 PE=1 SV=3	GR_Q1	738.6	GR_Q2	688.74
O00487	26S proteasome non-ATPase regulatory subunit 14 OS=Homo sapiens GN=PSMD14 PE=1 SV=1	GR_Q1	831.02	GR_Q2	845.91
Q08211	ATP-dependent RNA helicase A OS=Homo sapiens GN=DHX9 PE=1 SV=4	GR_Q1	66.85		
P68371	Tubulin beta-2C chain OS=Homo sapiens GN=TUBB2C PE=1 SV=1	GR_Q1	698.77	GR_Q2	377.08
Q32Q12	Nucleoside diphosphate kinase OS=Homo sapiens GN=NME1-NME2 PE=2 SV=1	GR_Q1	472.84	GR_Q2	565.03
Q9BT16	FLOT2 protein OS=Homo sapiens GN=FLOT2 PE=2 SV=1	GR_Q1	1292.33	GR_Q2	1225.28
Q9UL46	Proteasome activator complex subunit 2 OS=Homo sapiens GN=PSME2 PE=1 SV=4	GR_Q1	703.64	GR_Q2	575.64
Q4W4Y1	Dopamine receptor interacting protein 4 OS=Homo sapiens GN=DRIP4 PE=2 SV=1	GR_Q1	67.22		
P13098	COP9 signalosome complex subunit 1 OS=Homo sapiens GN=GPS1 PE=1 SV=4	GR_Q1	449.07	GR_Q2	607.23
O75955	Flotillin-1 OS=Homo sapiens GN=FLOT1 PE=1 SV=3	GR_Q1	1478.96	GR_Q2	1703.94
Q14203	Dynactin subunit 1 OS=Homo sapiens GN=DCTN1 PE=1 SV=3	GR_Q1	772.64	GR_Q2	766.25
P43686	26S protease regulatory subunit 6B OS=Homo sapiens GN=PSMC4 PE=1 SV=2	GR_Q1	484.44	GR_Q2	815.63
Q96P70	Importin-9 OS=Homo sapiens GN=IPO9 PE=1 SV=3	GR_Q1	1086.85	GR_Q2	815.01
P51665	26S proteasome non-ATPase regulatory subunit 7 OS=Homo sapiens GN=PSMD7 PE=1 SV=2	GR_Q1	841.59	GR_Q2	932.65
Q9UPU5	Ubiquitin carboxyl-terminal hydrolase 24 OS=Homo sapiens GN=USP24 PE=1 SV=3	GR_Q1	170.75	GR_Q2	185.05
P25789	Proteasome subunit alpha type-4 OS=Homo sapiens GN=PSMA4 PE=1 SV=1	GR_Q1	782.49	GR_Q2	623.51
P25788	Proteasome subunit alpha type-3 OS=Homo sapiens GN=PSMA3 PE=1 SV=2	GR_Q1	693.67	GR_Q2	817.14

Q10567	AP-1 complex subunit beta-1 OS=Homo sapiens GN=AP1B1 PE=1 SV=2	GR_Q1	824.3		
B0YJ88	Radixin OS=Homo sapiens GN=RD3X PE=2 SV=1	GR_Q1	158.35		
P42025	Beta-actin OS=Homo sapiens GN=ACTB PE=1 SV=1	GR_Q1	1096.35	GR_Q2	853.73
P48426	Phosphatidylinositol-5-phosphate 4-kinase type-2 alpha OS=Homo sapiens GN=PIP4K2A PE=1 SV=2	GR_Q1	589.46	GR_Q2	514.91
P61201	COP9 signalosome complex subunit 2 OS=Homo sapiens GN=COPS2 PE=1 SV=1	GR_Q1	664.98	GR_Q2	352.83
P68366	Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A PE=1 SV=1	GR_Q1	513.68		
Q61BT1	Proteasome subunit beta type OS=Homo sapiens GN=PSMB7 PE=2 SV=1	GR_Q1	876.18	GR_Q2	957.21
Q5VU58	Tropomyosin 3 OS=Homo sapiens GN=TPM3 PE=2 SV=1	GR_Q1	883.84	GR_Q2	768.51
Q5T447	E3 ubiquitin-protein ligase HECTD3 OS=Homo sapiens GN=HECTD3 PE=1 SV=1	GR_Q1	515.52	GR_Q2	525.17
P54920	Alpha-soluble NSF attachment protein OS=Homo sapiens GN=NAPA PE=1 SV=3	GR_Q1	200.08		
O43396	Thioredoxin-like protein 1 OS=Homo sapiens GN=TXNL1 PE=1 SV=3	GR_Q1	1006.6	GR_Q2	993.92
P31946	14-3-3 protein beta/alpha OS=Homo sapiens GN=YWHAB PE=1 SV=3	GR_Q1	702.61	GR_Q2	973.92
E9PBC8	Uncharacterized protein OS=Homo sapiens GN=PSMA7 PE=4 SV=1	GR_Q1	835.97	GR_Q2	841.59
P62333	26S proteasome regulatory subunit 10B OS=Homo sapiens GN=PSMC6 PE=1 SV=1	GR_Q1	628.61	GR_Q2	353.42
B2RDE1	cDNA, FLJ96568, highly similar to Homo sapiens tropomyosin 3 (TPM3), mRNA OS=Homo sapiens PE=2 SV=1	GR_Q1	867.87		
Q92973	Transportin-1 OS=Homo sapiens GN=TNPO1 PE=1 SV=2	GR_Q1	617.68	GR_Q2	583.47
Q15435	Protein phosphatase 1 regulatory subunit 7 OS=Homo sapiens GN=PPP1R7 PE=1 SV=1	GR_Q1	836.79	GR_Q2	569.65
P48556	26S proteasome non-ATPase regulatory subunit 8 OS=Homo sapiens GN=PSMD8 PE=1 SV=2	GR_Q1	562.96	GR_Q2	353.47
P84077	ADP-ribosylation factor 1 OS=Homo sapiens GN=ARF1 PE=1 SV=2	GR_Q1	540.05	GR_Q2	536.36
Q9GZP4	PITH domain-containing protein 1 OS=Homo sapiens GN=PITHD1 PE=1 SV=1	GR_Q1	537.52	GR_Q2	683.85
P61981	14-3-3 protein gamma OS=Homo sapiens GN=YWHAG PE=1 SV=2	GR_Q1	592.53	GR_Q2	857.38
B2R514	cDNA, FLJ92300, Homo sapiens COP9 subunit 6 (MOV34 homolog, 34 kD) (COPS6), mRNA OS=Homo sapiens	GR_Q1	664.16	GR_Q2	392.65
B2R8N1	cDNA, FLJ93976, highly similar to Homo sapiens COP9 homolog (COP9), mRNA OS=Homo sapiens PE=2 SV=1	GR_Q1	323.88	GR_Q2	248.41
Q2TU77	Aging-associated protein 2 OS=Homo sapiens GN=AAG2 PE=2 SV=1	GR_Q1	828.47	GR_Q2	529.28
P60842	Eukaryotic initiation factor 4A-I OS=Homo sapiens GN=EIF4A1 PE=1 SV=1	GR_Q1	421.76	GR_Q2	713.3
P02768	Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2	GR_Q1	456.95	GR_Q2	592.96
B7Z1K5	cDNA FLJ55956, highly similar to Tubulin alpha-6 chain OS=Homo sapiens PE=2 SV=1	GR_Q1	579.82		
P36959	GMP reductase 1 OS=Homo sapiens GN=GMPTX PE=1 SV=1	GR_Q1	190.31	GR_Q2	149.01
P08514	Integrin alpha-IIb OS=Homo sapiens GN=ITGA2B PE=1 SV=3	GR_Q1	232.2	GR_Q2	247.91
Q13618	Cullin-3 OS=Homo sapiens GN=CUL3 PE=1 SV=2	GR_Q1	157.85	GR_Q2	308.34
P27348	14-3-3 protein theta OS=Homo sapiens GN=YWHAQ PE=1 SV=1	GR_Q1	888.86	GR_Q2	930.34
B1AH89	Tubulin tyrosine ligase-like family, member 12 OS=Homo sapiens GN=TTLL12 PE=4 SV=1	GR_Q1	740.19	GR_Q2	404.13
P02647	Apolipoprotein A-I OS=Homo sapiens GN=APOA1 PE=1 SV=1	GR_Q1	421.33	GR_Q2	553.74
P52907	F-actin-capping protein subunit alpha-1 OS=Homo sapiens GN=CAPZA1 PE=1 SV=3	GR_Q1	328.87	GR_Q2	676.72
P14625	Endoplasmic reticulum chaperone protein OS=Homo sapiens GN=HSP90B1 PE=1 SV=1	GR_Q1	329.83	GR_Q2	378.23
P08311	Cathepsin G OS=Homo sapiens GN=CTSG PE=1 SV=2	GR_Q1	176.85	GR_Q2	117.68
P00387	NADH-cytochrome b5 reductase 3 OS=Homo sapiens GN=CYB5R3 PE=1 SV=3	GR_Q1	462.41	GR_Q2	237.94
Q96RL7	Vacuolar protein sorting-associated protein 13A OS=Homo sapiens GN=VPS13A PE=1 SV=2	GR_Q1	335.31	GR_Q2	157.06
P45974	Ubiquitin carboxyl-terminal hydrolase 5 OS=Homo sapiens GN=USP5 PE=1 SV=2	GR_Q1	502.75	GR_Q2	191.63
Q9Y4G6	Talin-2 OS=Homo sapiens GN=TLN2 PE=1 SV=4	GR_Q1	297.88	GR_Q2	163.1
B7Z596	cDNA FLJ55130, highly similar to Rattus norvegicus tropomyosin 1, alpha (Tpm1), transcript variant 8, mRNA OS=Homo sapiens PE=2 SV=1	GR_Q1	481.76	GR_Q2	428.01
B4DWW3	cDNA FLJ53229, highly similar to Importin alpha-7 subunit OS=Homo sapiens PE=2 SV=1	GR_Q1	628.41	GR_Q2	597.39
Q92688	Acidic leucine-rich nuclear phosphoprotein 32 family member B OS=Homo sapiens GN=ANP32B PE=1 SV=1	GR_Q1	965.88	GR_Q2	306.28
B1AKJ5	Nardilysin (N-arginine dihydrolase) OS=Homo sapiens GN=NRD1 PE=3 SV=1	GR_Q1	195.93	GR_Q2	274.42
B7Z763	Adenosine monophosphate deaminase (isoform E), isoform CRA_a OS=Homo sapiens GN=AMPD3 PE=2 SV=1	GR_Q1	112.79	GR_Q2	166
P19105	Myosin regulatory light chain 12A OS=Homo sapiens GN=MYL12A PE=1 SV=2	GR_Q1	295.67	GR_Q2	439.59
P52294	Importin subunit alpha-1 OS=Homo sapiens GN=KPNA1 PE=1 SV=3	GR_Q1	894.35	GR_Q2	749.23
Q13617	Cullin-2 OS=Homo sapiens GN=CUL2 PE=1 SV=2	GR_Q1	375.46	GR_Q2	262.34
B2R4M6	cDNA, FLJ92148, highly similar to Homo sapiens S100 calcium binding protein A9 (calgranulin B) (S100A9), mRNA OS=Homo sapiens PE=4 SV=1	GR_Q1	71.31	GR_Q2	66.21
P62495	Eukaryotic peptide chain release factor subunit 1 OS=Homo sapiens GN=ETRF1 PE=1 SV=3	GR_Q1	110.55		
B2R7T8	cDNA, FLJ93598, highly similar to Homo sapiens capping protein (actin filament) muscle Z-line, beta (CAPZB), mRNA OS=Homo sapiens PE=2 SV=1	GR_Q1	629.5	GR_Q2	480.94
Q9H0U4	Ras-related protein Rab-1B OS=Homo sapiens GN=RAB1B PE=1 SV=1	GR_Q1	170.69		
B4DH02	cDNA FLJ50510, highly similar to Heat shock 70 kDa protein 4 OS=Homo sapiens PE=2 SV=1	GR_Q1	742.53	GR_Q2	451.65
B4DLQ1	Uncharacterized protein OS=Homo sapiens GN=ALDH16A1 PE=2 SV=1	GR_Q1	896.22	GR_Q2	858.68
Q9P2R3	Ankyrin repeat and FYVE domain-containing protein 1 OS=Homo sapiens GN=ANKFY1 PE=1 SV=2	GR_Q1	384.93	GR_Q2	482.62
P80217	Interferon-induced 35 kDa protein OS=Homo sapiens GN=IFI35 PE=1 SV=5	GR_Q1	562.39	GR_Q2	100.19
P36915	Guanine nucleotide-binding protein-like 1 OS=Homo sapiens GN=GNL1 PE=1 SV=2	GR_Q1	345.75	GR_Q2	378.92
P30154	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform OS=Homo sapiens GN=PPP2R1B PE=1 SV=3	GR_Q1	562.99	GR_Q2	343.02
P67775	Serine/threonine-protein phosphatase 2A catalytic subunit alpha isoform OS=Homo sapiens GN=PPP2CA PE=1	GR_Q1	784.57	GR_Q2	827.7
A2A418	Gelsolin (Amyloidosis, Finnish type) OS=Homo sapiens GN=GSN PE=2 SV=1	GR_Q1	499.78	GR_Q2	465.33
Q9UN52	COP9 signalosome complex subunit 3 OS=Homo sapiens GN=COPS3 PE=1 SV=3	GR_Q1	582.98	GR_Q2	492.63
P35611	Alpha-adducin OS=Homo sapiens GN=ADD1 PE=1 SV=2	GR_Q1	389.65	GR_Q2	123.1
Q969U7	Proteasome assembly chaperone 2 OS=Homo sapiens GN=PSMG2 PE=1 SV=1	GR_Q1	77.05	GR_Q2	93.91
Q96QK1	Vacuolar protein sorting-associated protein 35 OS=Homo sapiens GN=VPS35 PE=1 SV=2	GR_Q1	293.12	GR_Q2	454.52
E9PM46	Ubiquitin carboxyl-terminal hydrolase OS=Homo sapiens GN=USP47 PE=3 SV=1	GR_Q1	342.52	GR_Q2	252.27
Q13561	Dynactin subunit 2 OS=Homo sapiens GN=DNCT2 PE=1 SV=4	GR_Q1	290.43	GR_Q2	199.19
Q5U5J2	CSNK2A1 protein OS=Homo sapiens GN=CSNK2A1 PE=1 SV=1	GR_Q1	528.4	GR_Q2	260
P27708	CAD protein OS=Homo sapiens GN=CAD PE=1 SV=3	GR_Q1	348.19	GR_Q2	63.93
P11021	78 kDa glucose-regulated protein OS=Homo sapiens GN=HSPA5 PE=1 SV=2	GR_Q1	384.93	GR_Q2	580.17
E7EX73	Uncharacterized protein OS=Homo sapiens GN=EIF4G1 PE=4 SV=1	GR_Q1	104.1	GR_Q2	105.36
P11215	Integrin alpha-M OS=Homo sapiens GN=ITGAM PE=1 SV=2	GR_Q1	226.72	GR_Q2	234.48
P35612	Beta-adducin OS=Homo sapiens GN=ADD2 PE=1 SV=3	GR_Q1	102.24	GR_Q2	171.99
P38606	V-type proton ATPase catalytic subunit A OS=Homo sapiens GN=ATP6V1A PE=1 SV=2	GR_Q1	344.46	GR_Q2	194.71
P62158	Calmodulin OS=Homo sapiens GN=CALM1 PE=1 SV=2	GR_Q1	643.74		
P26641	Elongation factor 1-gamma OS=Homo sapiens GN=EEF1G PE=1 SV=3	GR_Q1	586.74	GR_Q2	136.63
AK8K50	Heat shock 70kDa protein 1A OS=Homo sapiens GN=HSPA1A PE=2 SV=1	GR_Q1	211.32	GR_Q2	143.35
B3KQM6	cDNA FLJ90740 fis, clone PLACE1011045, highly similar to Autophagy-related protein 7 OS=Homo sapiens PE=2	GR_Q1	281.9	GR_Q2	138.69
P55036	26S proteasome non-ATPase regulatory subunit 4 OS=Homo sapiens GN=PSMD4 PE=1 SV=1	GR_Q1	317.74	GR_Q2	284.31
Q9BSL1	Ubiquitin-associated domain-containing protein 1 OS=Homo sapiens GN=UBAC1 PE=1 SV=1	GR_Q1	515.29	GR_Q2	607.51

Q95456	Proteasome assembly chaperone 1 OS=Homo sapiens GN=PSMG1 PE=1 SV=1	GR_Q1	57.25	GR_Q2	406.88
Q9UNZ2	NSFL1 cofactor p47 OS=Homo sapiens GN=NSFL1C PE=1 SV=2	GR_Q1	251.97	GR_Q2	278.24
O43149	Zinc finger ZZ-type and EF-hand domain-containing protein 1 OS=Homo sapiens GN=ZZEF1 PE=1 SV=6	GR_Q1	258.71	GR_Q2	220.46
Q99598	Translin-associated protein X OS=Homo sapiens GN=TSNAX PE=1 SV=1	GR_Q1	66.19	GR_Q2	204.83
Q15631	Translin OS=Homo sapiens GN=TSN PE=1 SV=1	GR_Q1	693.98	GR_Q2	346.78
B7Z507	cDNA FLJ51036, highly similar to Matrix metalloproteinase-9 (EC3.4.24.35) OS=Homo sapiens PE=2 SV=1	GR_Q1	140.11		
Q9BQA1	Methylosome protein 50 OS=Homo sapiens GN=WDR77 PE=1 SV=1	GR_Q1	634.36	GR_Q2	500.62
Q99733	Nucleosome assembly protein 1-like 4 OS=Homo sapiens GN=NAP1L4 PE=1 SV=1	GR_Q1	296.37	GR_Q2	385.44
P61224	Ras-related protein Rap-1b OS=Homo sapiens GN=RAP1B PE=1 SV=1	GR_Q1	497.33		
P12829	Myosin light chain 4 OS=Homo sapiens GN=MYL4 PE=1 SV=3	GR_Q1	467.16	GR_Q2	571.47
P62834	Ras-related protein Rap-1A OS=Homo sapiens GN=RAP1A PE=1 SV=1	GR_Q1	503.62	GR_Q2	387.99
B5MDH8	Uncharacterized protein OS=Homo sapiens GN=WDR91 PE=4 SV=2	GR_Q1	176.16	GR_Q2	79.06
P55209	Nucleosome assembly protein 1-like 1 OS=Homo sapiens GN=NAP1L1 PE=1 SV=1	GR_Q1	286.95	GR_Q2	266.12
Q15018	BRISC complex subunit Abro1 OS=Homo sapiens GN=FAM175B PE=1 SV=2	GR_Q1	110.82	GR_Q2	119.21
P23284	Peptidyl-prolyl cis-trans isomerase B OS=Homo sapiens GN=PPIB PE=1 SV=2	GR_Q1	154.77	GR_Q2	105.74
B4DM70	cDNA FLJ54451, highly similar to Stress-induced-phosphoprotein 1 OS=Homo sapiens PE=2 SV=1	GR_Q1	192.99		
DBMJ82	Kell blood group antigen OS=Homo sapiens GN=KEL PE=2 SV=1	GR_Q1	151.79	GR_Q2	110.83
B1AJY5	Proteasome (Prosome, macropain) 26S subunit, non-ATPase, 10 OS=Homo sapiens GN=PSMD10 PE=4 SV=1	GR_Q1	101.43	GR_Q2	131.77
P08246	Neutrophil elastase OS=Homo sapiens GN=ELANE PE=1 SV=1	GR_Q1	64.04		
O00629	Importin subunit alpha-4 OS=Homo sapiens GN=KPNA4 PE=1 SV=1	GR_Q1	513.79	GR_Q2	359.29
Q5U011	RAB11B, member RAS oncogene family OS=Homo sapiens PE=2 SV=1	GR_Q1	42.83	GR_Q2	72.72
P63208	S-phase kinase-associated protein 1 OS=Homo sapiens GN=SKP1 PE=1 SV=2	GR_Q1	237.95	GR_Q2	220.52
P27824	Calnexin OS=Homo sapiens GN=CANX PE=1 SV=2	GR_Q1	376.65	GR_Q2	165.59
Q8UII8	Cytokine receptor-like factor 3 OS=Homo sapiens GN=CRLF3 PE=1 SV=2	GR_Q1	273.34	GR_Q2	448.41
Q04917	14-3-3 protein eta OS=Homo sapiens GN=YWHAH PE=1 SV=4	GR_Q1	215.02	GR_Q2	301.99
Q9H8M7	Protein FAM188A OS=Homo sapiens GN=FAM188A PE=1 SV=1	GR_Q1	406.11	GR_Q2	116.25
Q9H9Q2	COP9 signalosome complex subunit 7b OS=Homo sapiens GN=COPS7B PE=1 SV=1	GR_Q1	433.76	GR_Q2	474.59
Q7Z351	Putative uncharacterized protein DKFZp686N02209 OS=Homo sapiens GN=DKFZp686N02209 PE=1 SV=1	GR_Q1	241.77		
O95747	Serine/threonine-protein kinase OSR1 OS=Homo sapiens GN=OSR1 PE=1 SV=1	GR_Q1	50.91	GR_Q2	115.73
P46060	Ran GTPase-activating protein 1 OS=Homo sapiens GN=RANGAP1 PE=1 SV=1	GR_Q1	139.21	GR_Q2	201.51
D3DRP5	Chromosome 9 open reading frame 19, isoform CRA_a (Fragment) OS=Homo sapiens GN=C9orf19 PE=4 SV=1	GR_Q1	157.16	GR_Q2	365.62
P02786	Transferrin receptor protein 1 OS=Homo sapiens GN=TFRC PE=1 SV=2	GR_Q1	182.8	GR_Q2	256.49
Q5JNW4	Proteasome subunit beta type OS=Homo sapiens GN=PSMB9 PE=2 SV=1	GR_Q1	331.2	GR_Q2	330.04
P60660	Myosin light polypeptide 6 OS=Homo sapiens GN=MYL6 PE=1 SV=2	GR_Q1	244.14	GR_Q2	304.58
B4DM76	cDNA FLJ57531, highly similar to DCN1-like protein 1 OS=Homo sapiens PE=2 SV=1	GR_Q1	287.63	GR_Q2	136.2
B4DWX5	cDNA FLJ55022, highly similar to F-box only protein 7 OS=Homo sapiens PE=2 SV=1	GR_Q1	374.12	GR_Q2	133.87
Q14697	Neutral alpha-glucosidase AB OS=Homo sapiens GN=GANAB PE=1 SV=3	GR_Q1	138.61	GR_Q2	96.14
Q9Y4G8	Rap guanine nucleotide exchange factor 2 OS=Homo sapiens GN=RAPGEF2 PE=1 SV=1	GR_Q1	62.14		
Q96NA2	Rab-interacting lysosomal protein OS=Homo sapiens GN=RILP PE=1 SV=1	GR_Q1	65.04		
Q9UPN7	Serine/threonine-protein phosphatase 6 regulatory subunit 1 OS=Homo sapiens GN=PPP6R1 PE=1 SV=5	GR_Q1	493.89	GR_Q2	266.83
O00743	Serine/threonine-protein phosphatase 6 catalytic subunit OS=Homo sapiens GN=PPP6C PE=1 SV=1	GR_Q1	414.7	GR_Q2	392.22
Q92539	Phosphatidate phosphatase LPIN2 OS=Homo sapiens GN=LPIN2 PE=1 SV=1	GR_Q1	89.44		
P30626	Sorcin OS=Homo sapiens GN=SRI PE=1 SV=1	GR_Q1	58.48	GR_Q2	95.98
Q13464	Rho-associated protein kinase 1 OS=Homo sapiens GN=ROCK1 PE=1 SV=1	GR_Q1	380.88	GR_Q2	93.25
Q13287	N-myc-interactor OS=Homo sapiens GN=NMI PE=1 SV=2	GR_Q1	196.17	GR_Q2	207.28
P24158	Myeloblastin OS=Homo sapiens GN=PRTN3 PE=1 SV=3	GR_Q1	45.6	GR_Q2	96.66
Q9Y570	Protein phosphatase methyltransferase 1 OS=Homo sapiens GN=PPME1 PE=1 SV=3	GR_Q1	141.56	GR_Q2	88.24
P47755	F-actin-capping protein subunit alpha-2 OS=Homo sapiens GN=CAPZA2 PE=1 SV=3	GR_Q1	256.53	GR_Q2	294.69
P62136	Serine/threonine-protein phosphatase PP1-alpha catalytic subunit OS=Homo sapiens GN=PPP1CA PE=1 SV=1	GR_Q1	387.49		
Q9NYU2	UDP-glucose:glycoprotein glucosyltransferase 1 OS=Homo sapiens GN=UGGT1 PE=1 SV=3	GR_Q1	211.77	GR_Q2	176.32
Q13564	NEDD8-activating enzyme E1 regulatory subunit OS=Homo sapiens GN=NAE1 PE=1 SV=1	GR_Q1	404.21	GR_Q2	313.61
Q14764	Major vault protein OS=Homo sapiens GN=MVP PE=1 SV=4	GR_Q1	335.36	GR_Q2	243.83
Q16512	Serine/threonine-protein kinase N1 OS=Homo sapiens GN=PKN1 PE=1 SV=2	GR_Q1	119.16	GR_Q2	106.73
Q96PU5	E3 ubiquitin-protein ligase NEDD4-like OS=Homo sapiens GN=NEDD4L PE=1 SV=2	GR_Q1	147.99	GR_Q2	71.43
F5GYF7	Uncharacterized protein OS=Homo sapiens GN=COP57A PE=4 SV=1	GR_Q1	305.84	GR_Q2	348.84
B4E1U9	cDNA FLJ54776, highly similar to Cell division control protein 42 homolog OS=Homo sapiens PE=2 SV=1	GR_Q1	160.41	GR_Q2	97.19
O43427	Acidic fibroblast growth factor intracellular-binding protein OS=Homo sapiens GN=FIBP PE=1 SV=3	GR_Q1	72.94	GR_Q2	126.22
Q8WW22	DnaJ homolog subfamily A member 4 OS=Homo sapiens GN=DNAJA4 PE=1 SV=1	GR_Q1	186.93	GR_Q2	219.58
P61225	Ras-related protein Rap-2b OS=Homo sapiens GN=RAP2B PE=1 SV=1	GR_Q1	571.33	GR_Q2	351.68
P33176	Kinesin-1 heavy chain OS=Homo sapiens GN=KIF5B PE=1 SV=1	GR_Q1	282.23	GR_Q2	235.65
P27797	Calreticulin OS=Homo sapiens GN=CALR PE=1 SV=1	GR_Q1	133.59	GR_Q2	197.02
Q12765	Secernin-1 OS=Homo sapiens GN=SCRN1 PE=1 SV=2	GR_Q1	281.11	GR_Q2	136.04
Q9BTE1	Dynactin subunit 5 OS=Homo sapiens GN=ECTN5 PE=1 SV=1	GR_Q1	55.58	GR_Q2	90.59
F5H2H8	Uncharacterized protein OS=Homo sapiens GN=SLC2A3 PE=3 SV=1	GR_Q1	101.27	GR_Q2	160.68
P17812	CTP synthase 1 OS=Homo sapiens GN=CTPS PE=1 SV=2	GR_Q1	141.73	GR_Q2	96.26
O95248	Myotubularin-related protein 5 OS=Homo sapiens GN=SBF1 PE=1 SV=3	GR_Q1	223.78		
B0U2C1	Proteasome (Prosome, macropain) subunit, beta type, 8 (Large multifunctional peptidase 7) OS=Homo sapiens GN=PSMB8 PE=4 SV=1	GR_Q1	174.79	GR_Q2	351.15
P13489	Ribonuclease inhibitor OS=Homo sapiens GN=RNH1 PE=1 SV=2	GR_Q1	318.59	GR_Q2	338.44
B4DUD6	cDNA FLJ54551, highly similar to Septin-7 OS=Homo sapiens PE=2 SV=1	GR_Q1	186.32		
O76003	Glutaredoxin-3 OS=Homo sapiens GN=GLRX3 PE=1 SV=2	GR_Q1	272.8	GR_Q2	72.76
Q92530	Proteasome inhibitor PI31 subunit OS=Homo sapiens GN=PSMF1 PE=1 SV=2	GR_Q1	64.35	GR_Q2	115.27
P08397	Porphyobilinogen deaminase OS=Homo sapiens GN=HMB5 PE=1 SV=2	GR_Q1	66.89		
B2RBP3	cDNA, FLJ95615, highly similar to Homo sapiens ubiquitin-activating enzyme E1C (UBA3 homolog, yeast)(UBE1C), mRNA OS=Homo sapiens PE=2 SV=1	GR_Q1	165.1	GR_Q2	263
A8K9T2	cDNA FLJ78744, highly similar to Homo sapiens WD repeat domain 23 (WDR23), transcript variant 1, mRNA OS=Homo sapiens PE=2 SV=1	GR_Q1	127.32	GR_Q2	267.77
Q9UHY1	Nuclear receptor-binding protein OS=Homo sapiens GN=NRBP1 PE=1 SV=1	GR_Q1	332.23	GR_Q2	226.12
P35813	Protein phosphatase 1A OS=Homo sapiens GN=PPM1A PE=1 SV=1	GR_Q1	169.54	GR_Q2	131.41
Q14152	Eukaryotic translation initiation factor 3 subunit A OS=Homo sapiens GN=EIF3A PE=1 SV=1	GR_Q1	130.22	GR_Q2	54.22
Q5H9R7	Serine/threonine-protein phosphatase 6 regulatory subunit 3 OS=Homo sapiens GN=PPP6R3 PE=1 SV=2	GR_Q1	93.82		
D3DWK4	Pyrroline-5-carboxylate reductase OS=Homo sapiens GN=PYRCL PE=3 SV=1	GR_Q1	115.85	GR_Q2	191.02

B2R7L2	cDNA, FLJ93494, highly similar to Homo sapiens annexin A7 (ANXA7), transcript variant 1, mRNA OS=Homo sapiens PE=2 SV=1	GR_Q1	112.32	GR_Q2	130.5
Q9BRP4	Proteasomal ATPase-associated factor 1 OS=Homo sapiens GN=PAAF1 PE=1 SV=2	GR_Q1	253.71	GR_Q2	240.19
B3KY95	cDNA FLJ16143 fis, clone BRAMY2038516, highly similar to Protein disulfide-isomerase A6 (EC 5.3.4.1) OS=Homo sapiens PE=2 SV=1	GR_Q1	211.2	GR_Q2	141.87
P62256	Ubiquitin-conjugating enzyme E2 H OS=Homo sapiens GN=UBE2H PE=1 SV=1	GR_Q1	138.78	GR_Q2	145.19
O75688	Protein phosphatase 1B OS=Homo sapiens GN=PPM1B PE=1 SV=1	GR_Q1	92.68		
B3KQT9	Uncharacterized protein OS=Homo sapiens GN=PDIA3 PE=2 SV=1	GR_Q1	265.28	GR_Q2	255.45
P11233	Ras-related protein Ral-A OS=Homo sapiens GN=RALA PE=1 SV=1	GR_Q1	203.47	GR_Q2	333.72
Q92882	Osteoclast-stimulating factor 1 OS=Homo sapiens GN=OSTF1 PE=1 SV=2	GR_Q1	148.15	GR_Q2	304.54
O15084	Serine/threonine-protein phosphatase 6 regulatory ankyrin repeat subunit A OS=Homo sapiens GN=ANKRD28 PE=1	GR_Q1	190.77	GR_Q2	193.56
Q16555	Dihydropyrimidinase-related protein 2 OS=Homo sapiens GN=DPYSL2 PE=1 SV=1	GR_Q1	161.23	GR_Q2	156.91
B3KU21	cDNA FLJ39092 fis, clone NT2RP7019835, highly similar to HEPATOMA-DERIVED GROWTH FACTOR OS=Homo sapiens PE=2 SV=1	GR_Q1	164.25	GR_Q2	115.19
B4DF68	cDNA FLJ55325, highly similar to Heat-shock protein 105 kDa OS=Homo sapiens PE=2 SV=1	GR_Q1	176.67	GR_Q2	87.36
P54105	Methylosome subunit pICln OS=Homo sapiens GN=CLNS1A PE=1 SV=1	GR_Q1	62.25	GR_Q2	57.31
Q96A72	Protein mago nashi homolog 2 OS=Homo sapiens GN=MAGOHB PE=1 SV=1	GR_Q1	269.18		
Q3ZT57	Ankyrin repeat domain 13, isoform CRA_b OS=Homo sapiens GN=ANKRD13 PE=2 SV=1	GR_Q1	40.65		
B4DNB9	cDNA FLJ53069, highly similar to AP-2 complex subunit mu-1 OS=Homo sapiens PE=2 SV=1	GR_Q1	36.98		
Q99816	Tumor susceptibility gene 101 protein OS=Homo sapiens GN=TSG101 PE=1 SV=2	GR_Q1	31.14		
Q61B22	Proteasome subunit beta type OS=Homo sapiens GN=PSMB10 PE=2 SV=1	GR_Q1	192.05	GR_Q2	245.68
B3KW16	cDNA FLJ41902 fis, clone PEBLM2004666, highly similar to WD repeat protein 81 OS=Homo sapiens PE=2 SV=1	GR_Q1	66.8		
B4DQH9	Uncharacterized protein OS=Homo sapiens GN=RANBP10 PE=2 SV=1	GR_Q1	119.19	GR_Q2	219.33
Q969T9	WW domain-binding protein 2 OS=Homo sapiens GN=WBP2 PE=1 SV=1	GR_Q1	44.03	GR_Q2	46.07
B2RDG9	cDNA, FLJ96603, highly similar to Homo sapiens actin-related protein 10 homolog (S. cerevisiae) (ACTR10), mRNA OS=Homo sapiens PE=2 SV=1	GR_Q1	81.67		
Q9H2M9	Rab3 GTPase-activating protein non-catalytic subunit OS=Homo sapiens GN=RAB3GAP2 PE=1 SV=1	GR_Q1	41.48		
B1APW5	ATPase, Ca++ transporting, plasma membrane 4 OS=Homo sapiens GN=ATP2B4 PE=2 SV=1	GR_Q1	97.2	GR_Q2	54.1
P55010	Eukaryotic translation initiation factor 5 OS=Homo sapiens GN=EIF5 PE=1 SV=2	GR_Q1	194.98	GR_Q2	184.9
P02792	Ferritin light chain OS=Homo sapiens GN=FTL PE=1 SV=2	GR_Q1	219.08	GR_Q2	145.61
BOUXA9	Casein kinase 2 beta polypeptide OS=Homo sapiens GN=CSNK2B PE=2 SV=1	GR_Q1	121.06	GR_Q2	128.89
B2RCM3	cDNA, FLJ96158, highly similar to Homo sapiens calpain 2, (mII) large subunit (CAPN2), mRNA OS=Homo sapiens PE=2 SV=1	GR_Q1	128.97	GR_Q2	75.82
Q9UJW0	Dynactin subunit 4 OS=Homo sapiens GN=DCTN4 PE=1 SV=1	GR_Q1	202.81	GR_Q2	49.68
O14523	C2 domain-containing protein 2-like OS=Homo sapiens GN=C2CD2L PE=1 SV=3	GR_Q1	214.49		
P62873	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1 OS=Homo sapiens GN=GNB1 PE=1 SV=3	GR_Q1	112.49	GR_Q2	70.19
Q9BT73	Proteasome assembly chaperone 3 OS=Homo sapiens GN=PSMG3 PE=1 SV=1	GR_Q1	128.8	GR_Q2	43.87
B4DT12	cDNA FLJ55654, highly similar to TBC1 domain family member 17 OS=Homo sapiens PE=2 SV=1	GR_Q1	231.87	GR_Q2	81.32
E9PAV3	Uncharacterized protein OS=Homo sapiens GN=NACA PE=4 SV=1	GR_Q1	129.87		
B7Z3E3	cDNA FLJ60267, highly similar to Homo sapiens reticulon 3 (RTN3), transcript variant 2, mRNA OS=Homo sapiens PE=2 SV=1	GR_Q1	54.16	GR_Q2	51.98
Q92614	Myosin-XVIIIa OS=Homo sapiens GN=MYO18A PE=1 SV=3	GR_Q1	50.02		
Q9ULH1	Arf-GAP with SH3 domain, ANK repeat and PH domain-containing protein 1 OS=Homo sapiens GN=ASAP1 PE=1	GR_Q1	248.25	GR_Q2	213.4
P63092	Guanine nucleotide-binding protein G(s) subunit alpha isoforms short OS=Homo sapiens GN=GNAS PE=1 SV=1	GR_Q1	114.68	GR_Q2	116.13
Q58WW2	DDB1- and CUL4-associated factor 6 OS=Homo sapiens GN=DCAF6 PE=1 SV=1	GR_Q1	71.54	GR_Q2	38.58
O76071	Probable cytosolic iron-sulfur protein assembly protein CIAO1 OS=Homo sapiens GN=CIAO1 PE=1 SV=1	GR_Q1	173.85	GR_Q2	198.94
P78318	Immunoglobulin-binding protein 1 OS=Homo sapiens GN=IGBP1 PE=1 SV=1	GR_Q1	213.27	GR_Q2	137.75
P46736	Lys-63-specific deubiquitinase BRCC36 OS=Homo sapiens GN=BRCC3 PE=1 SV=2	GR_Q1	77.37	GR_Q2	33.99
Q6FG59	CDC37 protein OS=Homo sapiens GN=CDC37 PE=2 SV=1	GR_Q1	54.07		
Q53HW2	Ribosomal protein P0 variant (Fragment) OS=Homo sapiens PE=2 SV=1	GR_Q1	214.89	GR_Q2	108.78
P53680	AP-2 complex subunit sigma OS=Homo sapiens GN=AP2S1 PE=1 SV=2	GR_Q1	83.51	GR_Q2	163.8
P22303	Acetylcholinesterase OS=Homo sapiens GN=ACHE PE=1 SV=1	GR_Q1	45.55	GR_Q2	47.9
Q9UNN5	FAS-associated factor 1 OS=Homo sapiens GN=FAF1 PE=1 SV=2	GR_Q1	101.26	GR_Q2	132.76
Q9NT62	Ubiquitin-like-conjugating enzyme ATG3 OS=Homo sapiens GN=ATG3 PE=1 SV=1	GR_Q1	132.37	GR_Q2	164.26
Q6N090	Putative uncharacterized protein DKFZp686G21220 (Fragment) OS=Homo sapiens GN=DKFZp686G21220 PE=1	GR_Q1	44.66	GR_Q2	115.29
Q9NXR7	BRCA1-A complex subunit BRE OS=Homo sapiens GN=BRE PE=1 SV=2	GR_Q1	136.74	GR_Q2	76.45
BOUZB3	Complement component 4A (Rodgers blood group) OS=Homo sapiens GN=C4A PE=4 SV=1	GR_Q1	265.01		
P35219	Carbonic anhydrase-related protein OS=Homo sapiens GN=CA8 PE=1 SV=3	GR_Q1	118.07		
B4DRN7	Uncharacterized protein OS=Homo sapiens GN=KIAA0528 PE=2 SV=1	GR_Q1	87.33		
B6KSH1	HCG1784554, isoform CRA_a OS=Homo sapiens GN=EIF3F PE=2 SV=1	GR_Q1	286	GR_Q2	174.82
Q6PIU2	Neutral cholesterol ester hydrolase 1 OS=Homo sapiens GN=NCEH1 PE=1 SV=3	GR_Q1	135.46	GR_Q2	49.72
E2QRC7	Uncharacterized protein OS=Homo sapiens GN=PSMG4 PE=4 SV=1	GR_Q1	166.7	GR_Q2	165.04
P62879	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2 OS=Homo sapiens GN=GNB2 PE=1 SV=3	GR_Q1	83.63		
Q6FH17	ARF6 protein OS=Homo sapiens GN=ARF6 PE=2 SV=1	GR_Q1	46.8	GR_Q2	49.38
Q0VF99	Oxysterol-binding protein OS=Homo sapiens GN=OSBP2 PE=2 SV=1	GR_Q1	54.71	GR_Q2	111.86
Q9BTY7	Protein FAM203A OS=Homo sapiens GN=FAM203A PE=1 SV=1	GR_Q1	43.44	GR_Q2	36.53
F5H6N3	Uncharacterized protein OS=Homo sapiens GN=CLTA PE=4 SV=1	GR_Q1	59.85	GR_Q2	127.64
Q99873	Protein arginine N-methyltransferase 1 OS=Homo sapiens GN=PRMT1 PE=1 SV=2	GR_Q1	52.51	GR_Q2	57.38
Q5TB20	Acidic (Leucine-rich) nuclear phosphoprotein 32 family, member E OS=Homo sapiens GN=ANP32E PE=2 SV=1	GR_Q1	183.13		
Q5HYL3	Putative uncharacterized protein DKFZp686H16220 OS=Homo sapiens GN=DKFZp686H16220 PE=1 SV=1	GR_Q1	110.77	GR_Q2	117.01
Q29694	MHC class I HLA-B antigen (Fragment) OS=Homo sapiens GN=HLA-B PE=2 SV=1	GR_Q1	123.64	GR_Q2	68.69
Q9NRY5	Protein FAM114A2 OS=Homo sapiens GN=FAM114A2 PE=1 SV=4	GR_Q1	100.62	GR_Q2	39.34
P02794	Ferritin heavy chain OS=Homo sapiens GN=FTH1 PE=1 SV=2	GR_Q1	170.82	GR_Q2	106.54
Q13576	Ras GTPase-activating-like protein IQGAP2 OS=Homo sapiens GN=IQGAP2 PE=1 SV=4	GR_Q1	63.27	GR_Q2	61.45
P11940	Polyadenylate-binding protein 1 OS=Homo sapiens GN=PABPC1 PE=1 SV=2	GR_Q1	104.8		
A6NN01	Histone H2A OS=Homo sapiens GN=H2AFV PE=3 SV=1	GR_Q1	36.78		
O43488	Aflatoxin B1 aldehyde reductase member 2 OS=Homo sapiens GN=AKR7A2 PE=1 SV=3	GR_Q1	207.44	GR_Q2	50.41
B4DUQ1	cDNA FLJ54552, highly similar to Heterogeneous nuclear ribonucleoprotein K OS=Homo sapiens PE=2 SV=1	GR_Q1	189.35	GR_Q2	181.45
Q9P0J7	E3 ubiquitin-protein ligase KCMF1 OS=Homo sapiens GN=KCMF1 PE=1 SV=2	GR_Q1	207.9	GR_Q2	88.67
Q13610	Periodic tryptophan protein 1 homolog OS=Homo sapiens GN=PWP1 PE=1 SV=1	GR_Q1	50.76	GR_Q2	59.68
B4DN59	cDNA FLJ52702, highly similar to Homo sapiens CD44 antigen (homing function and Indian blood group system) (CD44), transcript variant 4, mRNA OS=Homo sapiens PE=2 SV=1	GR_Q1	38.91		
P08754	Guanine nucleotide-binding protein G(k) subunit alpha OS=Homo sapiens GN=GNAI3 PE=1 SV=3	GR_Q1	121.7	GR_Q2	112.92

P07203	Glutathione peroxidase 1 OS=Homo sapiens GN=GPX1 PE=1 SV=4	GR_Q1	86.36	GR_Q2	103.68
P55957	BH3-interacting domain death agonist OS=Homo sapiens GN=BD PE=1 SV=1	GR_Q1	247.68	GR_Q2	66.05
P04899	Guanine nucleotide-binding protein G(i) subunit alpha-2 OS=Homo sapiens GN=GNAI2 PE=1 SV=3	GR_Q1	265.16		
Q15369	Transcription elongation factor B polypeptide 1 OS=Homo sapiens GN=TCEB1 PE=1 SV=1	GR_Q1	104.49		
P49354	Protein farnesyltransferase/geranylgeranyltransferase type-1 subunit alpha OS=Homo sapiens GN=FNTA PE=1	GR_Q1	95.32		
Q9H7G6	cDNA: FLJ20897 fis, clone ADKA03573 OS=Homo sapiens PE=2 SV=1	GR_Q1	53.71		
B0R0W4	Retinoblastoma binding protein 7 OS=Homo sapiens GN=RBBP7 PE=4 SV=1	GR_Q1	47.74		
D3DWY7	von Hippel-Lindau binding protein 1, isoform CRA_b OS=Homo sapiens GN=VBP1 PE=4 SV=1	GR_Q1	46.41		
B2R806	cDNA, FLJ93685, highly similar to Homo sapiens eukaryotic translation initiation factor 3, subunit 6 48kDa (EIF3S6), mRNA OS=Homo sapiens PE=2 SV=1	GR_Q1	40.07		
Q9Y244	Proteasome maturation protein OS=Homo sapiens GN=POMP PE=1 SV=1	GR_Q1	197.43		
E9PB22	Uncharacterized protein OS=Homo sapiens GN=CD47 PE=4 SV=1	GR_Q1	71.33	GR_Q2	39.35
Q8NBX0	Probable saccharopine dehydrogenase OS=Homo sapiens GN=SCCPDH PE=1 SV=1	GR_Q1	56.28	GR_Q2	93.65
P60520	Gamma-aminobutyric acid receptor-associated protein-like 2 OS=Homo sapiens GN=GABARAPL2 PE=1 SV=1	GR_Q1	84.24		
Q96PL5	Erythroid membrane-associated protein OS=Homo sapiens GN=ERMAP PE=1 SV=1	GR_Q1	68.21		
P61626	Lysozyme C OS=Homo sapiens GN=LYZ PE=1 SV=1	GR_Q1	67.91		
B8ZZW9	Uncharacterized protein OS=Homo sapiens GN=C7orf41 PE=4 SV=1	GR_Q1	88.74	GR_Q2	205.8
O43765	Small glutamine-rich tetratricopeptide repeat-containing protein alpha OS=Homo sapiens GN=SGTA PE=1 SV=1	GR_Q1	66.16	GR_Q2	43.38
P61586	Transforming protein RhoA OS=Homo sapiens GN=RHOA PE=1 SV=1	GR_Q1	122.73	GR_Q2	24.93
Q9C0B1	Alpha-ketoglutarate-dependent dioxygenase FTO OS=Homo sapiens GN=FTO PE=1 SV=3	GR_Q1	93.9		
P28676	Grancalcin OS=Homo sapiens GN=GCA PE=1 SV=2	GR_Q1	81.87		
Q9Y333	U6 snRNA-associated Sm-like protein LSM2 OS=Homo sapiens GN=LSM2 PE=1 SV=1	GR_Q1	66.15		
B4DM33	cDNA FLJ52068, highly similar to Microtubule-associated protein RP/EB family member 1 OS=Homo sapiens PE=2	GR_Q1	66.04		
F22ZV6	Uncharacterized protein OS=Homo sapiens GN=NAA38 PE=4 SV=1	GR_Q1	59.12		
Q9UBF2	Coatomer subunit gamma-2 OS=Homo sapiens GN=COPG2 PE=1 SV=1	GR_Q1	40		
B4DRF0	cDNA FLJ56418, highly similar to WD repeat protein 26 OS=Homo sapiens PE=2 SV=1	GR_Q1	59.21		
P08575	Receptor-type tyrosine-protein phosphatase C OS=Homo sapiens GN=PTPRC PE=1 SV=2	GR_Q1	74.53		
P36543	V-type proton ATPase subunit E 1 OS=Homo sapiens GN=ATP6V1E1 PE=1 SV=1	GR_Q1	72.59	GR_Q2	105.35
Q53F48	Heterogeneous nuclear ribonucleoprotein H3 isoform a variant (Fragment) OS=Homo sapiens PE=2 SV=1	GR_Q1	62.09		
Q59F14	Importin 4 variant (Fragment) OS=Homo sapiens PE=2 SV=1	GR_Q1	44.09		
O95273	Cyclin-D1-binding protein 1 OS=Homo sapiens GN=CCNDBP1 PE=1 SV=2	GR_Q1	42.88	GR_Q2	70.64
Q8IW70	Protein archaease OS=Homo sapiens GN=ZBTB80S PE=1 SV=2	GR_Q1	105	GR_Q2	196.81
Q99471	Prefoldin subunit 5 OS=Homo sapiens GN=PFDN5 PE=1 SV=2	GR_Q1	162.84	GR_Q2	108.49
O60888	Protein CutA OS=Homo sapiens GN=CUTA PE=1 SV=2	GR_Q1	73.55	GR_Q2	107.86
Q9H5X1	MIP18 family protein FAM96A OS=Homo sapiens GN=FAM96A PE=1 SV=1	GR_Q1	127.14	GR_Q2	79.03
Q9BPX3	Condensin complex subunit 3 OS=Homo sapiens GN=NCAPG PE=1 SV=1	GR_Q1	86.09	GR_Q2	62.94
B2R8A2	cDNA, FLJ93804, highly similar to Homo sapiens gp25L2 protein (HSGP25L2G), mRNA OS=Homo sapiens PE=2	GR_Q1	40.96	GR_Q2	51.39
B2LR44	RHD OS=Homo sapiens PE=2 SV=1	GR_Q1	70.24		
O60884	DnaJ homolog subfamily A member 2 OS=Homo sapiens GN=DNAJA2 PE=1 SV=1	GR_Q1	68.68		
Q9UNQ0	ATP-binding cassette sub-family G member 2 OS=Homo sapiens GN=ABCG2 PE=1 SV=3	GR_Q1	41.31		
P05386	60S acidic ribosomal protein P1 OS=Homo sapiens GN=RPLP1 PE=1 SV=1	GR_Q1	74.27		
A0PKJ4	NUP43 protein (Fragment) OS=Homo sapiens GN=NUP43 PE=2 SV=1	GR_Q1	95.78	GR_Q2	112.67
Q9H074	Polyadenylate-binding protein-interacting protein 1 OS=Homo sapiens GN=PAIP1 PE=1 SV=1	GR_Q1	112.47	GR_Q2	80.84
Q0VAS5	Histone H4 OS=Homo sapiens GN=HIST1H4H PE=2 SV=1	GR_Q1	55.21	GR_Q2	77.88
O94889	Kelch-like protein 18 OS=Homo sapiens GN=KLHL18 PE=2 SV=3	GR_Q1	73.56	GR_Q2	57.06
Q8N5K1	CDGSH iron-sulfur domain-containing protein 2 OS=Homo sapiens GN=CISD2 PE=1 SV=1	GR_Q1	48.63	GR_Q2	49.02
Q9U112	V-type proton ATPase subunit H OS=Homo sapiens GN=ATP6V1H PE=1 SV=1	GR_Q1	139.26		
Q09161	Nuclear cap-binding protein subunit 1 OS=Homo sapiens GN=NCBP1 PE=1 SV=1	GR_Q1	39.29		
Q9NWU2	Protein C22orf11 OS=Homo sapiens GN=C22orf11 PE=1 SV=1	GR_Q1	105.18	GR_Q2	55.13
P31153	S-adenosylmethionine synthase isoform type-2 OS=Homo sapiens GN=MAT2A PE=1 SV=1	GR_Q1	81.52	GR_Q2	73.98
O60925	Prefoldin subunit 1 OS=Homo sapiens GN=PFDN1 PE=1 SV=2	GR_Q1	86.41		
Q0VGL7	PPM1F protein OS=Homo sapiens GN=PPM1F PE=2 SV=1	GR_Q1	65.23		
B4DYD9	cDNA FLJ61465, highly similar to Homo sapiens vacuolar protein sorting 37C (VPS37C), mRNA OS=Homo sapiens PE=2 SV=1	GR_Q1	62.69		
B4DSC0	Uncharacterized protein OS=Homo sapiens GN=TNPO1 PE=2 SV=1	GR_Q1	41.37		
B1AQP2	Prefoldin subunit 2 OS=Homo sapiens GN=PFDN2 PE=2 SV=1	GR_Q1	53.41	GR_Q2	49.64
Q9P0S9	Transmembrane protein 14C OS=Homo sapiens GN=TMEM14C PE=1 SV=1	GR_Q1	47.89		
B0YJ28	Interleukin-18 OS=Homo sapiens GN=IL18 PE=3 SV=1	GR_Q1	42.37		
B7WNV6	Chromosome 22 open reading frame 25, isoform CRA_c OS=Homo sapiens GN=C22orf25 PE=2 SV=1	GR_Q1	40.11		
O95336	6-phosphogluconolactonase OS=Homo sapiens GN=PGLS PE=1 SV=2	GR_Q1	39.85		
B3VL12	Truncated beta globin OS=Homo sapiens PE=3 SV=1			GR_Q2	3541.13
P04075	Fructose-bisphosphate aldolase A OS=Homo sapiens GN=ALDOA PE=1 SV=2			GR_Q2	67.74
P10599	Thioredoxin OS=Homo sapiens GN=TXN PE=1 SV=3			GR_Q2	98.66
P00441	Superoxide dismutase [Cu-Zn] OS=Homo sapiens GN=SOD1 PE=1 SV=2			GR_Q2	121.88
P58546	Myotrophin OS=Homo sapiens GN=MTPN PE=1 SV=2			GR_Q2	82.31
O95782	AP-2 complex subunit alpha-1 OS=Homo sapiens GN=AP2A1 PE=1 SV=3			GR_Q2	84.37
P26038	Moesin OS=Homo sapiens GN=MSN PE=1 SV=3			GR_Q2	72.68
P68363	Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1			GR_Q2	397.65
Q96CW1	AP-2 complex subunit mu OS=Homo sapiens GN=AP2M1 PE=1 SV=2			GR_Q2	111.79
Q14240	Eukaryotic initiation factor 4A-II OS=Homo sapiens GN=EIF4A2 PE=1 SV=2			GR_Q2	733.09
P28289	Tropomodulin-1 OS=Homo sapiens GN=TMOD1 PE=1 SV=1			GR_Q2	53.17
Q9H479	Fructosamine-3-kinase OS=Homo sapiens GN=FN3K PE=1 SV=1			GR_Q2	58.41
B4DVY2	cDNA FLJ54184, highly similar to Tropomyosin alpha-4 chain OS=Homo sapiens PE=2 SV=1			GR_Q2	261.51
P21281	V-type proton ATPase subunit B, brain isoform OS=Homo sapiens GN=ATP6V1B2 PE=1 SV=3			GR_Q2	263.84
P51148	Ras-related protein Rab-5C OS=Homo sapiens GN=RAB5C PE=1 SV=2			GR_Q2	79.74
Q9NPQ8	Synembryon-A OS=Homo sapiens GN=RIC8A PE=1 SV=3			GR_Q2	137.53
Q4LE60	TNPO2 variant protein (Fragment) OS=Homo sapiens GN=TNPO2 variant protein PE=2 SV=1			GR_Q2	421.09
O75116	Rho-associated protein kinase 2 OS=Homo sapiens GN=ROCK2 PE=1 SV=4			GR_Q2	220.25
E7ETZ0	Uncharacterized protein OS=Homo sapiens GN=CALM1 PE=4 SV=1			GR_Q2	489.21
B4DMP4	cDNA FLJ53136, highly similar to Homo sapiens Vac14 homolog (VAC14), mRNA OS=Homo sapiens PE=2 SV=1			GR_Q2	48.16
P01871	Ig mu chain C region OS=Homo sapiens GN=IGHM PE=1 SV=3			GR_Q2	199.49
P63000	Ras-related C3 botulinum toxin substrate 1 OS=Homo sapiens GN=RAC1 PE=1 SV=1			GR_Q2	22.74
A8K008	cDNA FLJ78387 OS=Homo sapiens PE=2 SV=1			GR_Q2	182.28

P35613	Basigin OS=Homo sapiens GN=BSG PE=1 SV=2			GR_Q2	46.34
Q8TEA3	cDNA FLJ23738 fis, clone HEP15081, highly similar to PDZ domain-containing guanine nucleotide exchange factor I OS=Homo sapiens PE=2 SV=1			GR_Q2	60.98
P48507	Glutamate--cysteine ligase regulatory subunit OS=Homo sapiens GN=GCLM PE=1 SV=1			GR_Q2	108.04
P80188	Neutrophil gelatinase-associated lipocalin OS=Homo sapiens GN=LCN2 PE=1 SV=2			GR_Q2	56.64
O00505	Importin subunit alpha-3 OS=Homo sapiens GN=KPNA3 PE=1 SV=2			GR_Q2	289.45
P00390	Glutathione reductase, mitochondrial OS=Homo sapiens GN=GSR PE=1 SV=2			GR_Q2	54.38
P49327	Fatty acid synthase OS=Homo sapiens GN=FASN PE=1 SV=3			GR_Q2	82.69
Q2TAZ0	Autophagy-related protein 2 homolog A OS=Homo sapiens GN=ATG2A PE=1 SV=3			GR_Q2	197.73
Q5U0P9	Purine-rich element binding protein A OS=Homo sapiens PE=2 SV=1			GR_Q2	53.57
Q2YFE1	Integrin beta OS=Homo sapiens PE=2 SV=1			GR_Q2	37.69
B4E0R1	Integrin beta OS=Homo sapiens PE=2 SV=1			GR_Q2	46.24
P49913	Cathelicidin antimicrobial peptide OS=Homo sapiens GN=CAMP PE=1 SV=1			GR_Q2	95.52
P62140	Serine/threonine-protein phosphatase PP1-beta catalytic subunit OS=Homo sapiens GN=PPP1CB PE=1 SV=3			GR_Q2	163.61
Q6DD88	Atlastin-3 OS=Homo sapiens GN=ATL3 PE=1 SV=1			GR_Q2	90.68
Q9BTT0	Acidic leucine-rich nuclear phosphoprotein 32 family member E OS=Homo sapiens GN=ANP32E PE=1 SV=1			GR_Q2	262
F223H3	Uncharacterized protein OS=Homo sapiens GN=ANP32A PE=4 SV=2			GR_Q2	123.61
P09496	Clathrin light chain A OS=Homo sapiens GN=CLTA PE=1 SV=1			GR_Q2	73.77
Q8TEL1	FLJ00182 protein (Fragment) OS=Homo sapiens GN=FLJ00182 PE=2 SV=1			GR_Q2	108.87
Q9UBQ0	Vacuolar protein sorting-associated protein 29 OS=Homo sapiens GN=VPS29 PE=1 SV=1			GR_Q2	107.89
B4DPQ6	cDNA FLJ53636, highly similar to Septin-7 OS=Homo sapiens PE=2 SV=1			GR_Q2	87.61
Q59GZ0	KIAA0182 protein variant (Fragment) OS=Homo sapiens PE=2 SV=1			GR_Q2	64.31
Q6PJG0	Putative uncharacterized protein OS=Homo sapiens PE=1 SV=1			GR_Q2	134.65
P23528	Cofilin-1 OS=Homo sapiens GN=CFL1 PE=1 SV=3			GR_Q2	53.45
P04792	Heat shock protein beta-1 OS=Homo sapiens GN=HSPB1 PE=1 SV=2			GR_Q2	105.82
O14618	Copper chaperone for superoxide dismutase OS=Homo sapiens GN=CCS PE=1 SV=1			GR_Q2	153.12
E9PRT4	Uncharacterized protein OS=Homo sapiens GN=VPS26B PE=4 SV=1			GR_Q2	120.02
P02724	Glycophorin-A OS=Homo sapiens GN=GYPA PE=1 SV=2			GR_Q2	70.56
P30040	Endoplasmic reticulum resident protein 29 OS=Homo sapiens GN=ERP29 PE=1 SV=4			GR_Q2	131.43
C5MQH7	Programmed cell death 6 interacting protein OS=Homo sapiens GN=PDCC6IP PE=2 SV=1			GR_Q2	69.91
Q9UNW1	Multiple inositol polyphosphate phosphatase 1 OS=Homo sapiens GN=MINPP1 PE=1 SV=1			GR_Q2	61.09
P02787	Serotransferrin OS=Homo sapiens GN=TF PE=1 SV=3			GR_Q2	50.48
B3KSS1	cDNA FLJ36845 fis, clone ASTRO2013050, weakly similar to UBIQUITIN-ACTIVATING ENZYME E1 OS=Homo sapiens PE=2 SV=1			GR_Q2	36.88
Q9Y484	WD repeat domain phosphoinositide-interacting protein 4 OS=Homo sapiens GN=WDR45 PE=2 SV=1			GR_Q2	178.38
P07737	Profilin-1 OS=Homo sapiens GN=PFN1 PE=1 SV=2			GR_Q2	61.63
O43760	Synaptogyrin-2 OS=Homo sapiens GN=SYNGR2 PE=1 SV=1			GR_Q2	68.98
Q2YHU8	Rhesus blood group D antigen (Fragment) OS=Homo sapiens GN=RHD PE=2 SV=1			GR_Q2	71.47
B3KQ94	cDNA FLJ33161 fis, clone UTERU2000517, highly similar to Mitogen-activated protein kinase 10 (EC 2.7.11.24) OS=Homo sapiens PE=2 SV=1			GR_Q2	58.61
Q9BS26	Endoplasmic reticulum resident protein 44 OS=Homo sapiens GN=ERP44 PE=1 SV=1			GR_Q2	50.88
E0D851	Platelet glycoprotein Ib alpha OS=Homo sapiens GN=GP1BA PE=4 SV=1			GR_Q2	47.39
Q15843	NEDD8 OS=Homo sapiens GN=NEDD8 PE=1 SV=1			GR_Q2	45.05
Q02094	Ammonium transporter Rh type A OS=Homo sapiens GN=RHAG PE=1 SV=2			GR_Q2	83.33
Q9NZL9	Methionine adenosyltransferase 2 subunit beta OS=Homo sapiens GN=MAT2B PE=1 SV=1			GR_Q2	117.59
Q9BRX5	DNA replication complex GINS protein PSF3 OS=Homo sapiens GN=GINS3 PE=1 SV=1			GR_Q2	48.31
Q9Y5S9	RNA-binding protein 8A OS=Homo sapiens GN=RBM8A PE=1 SV=1			GR_Q2	87.81
P63151	Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B alpha isoform OS=Homo sapiens GN=PPP2R2A PE=1 SV=1			GR_Q2	79.87
P56537	Eukaryotic translation initiation factor 6 OS=Homo sapiens GN=EIF6 PE=1 SV=1			GR_Q2	45.73
Q15363	Transmembrane emp24 domain-containing protein 2 OS=Homo sapiens GN=TMED2 PE=1 SV=1			GR_Q2	79.54
Q15185	Prostaglandin E synthase 3 OS=Homo sapiens GN=PTGES3 PE=1 SV=1			GR_Q2	56.8

Supplemental Data 2

Sheet 4

OS-Treated

AC	Description	Replicate 1	Score	Replicate 2	Score
P68871	Hemoglobin subunit beta OS=Homo sapiens GN=HBB PE=1 SV=2	GR_OS1	7350.53	GR_OS2	5894.65
Q6J127	Hemoglobin beta (Fragment) OS=Homo sapiens GN=HBB PE=2 SV=1	GR_OS1	5528.57	GR_OS2	4324.83
P69905	Hemoglobin subunit alpha OS=Homo sapiens GN=HBA1 PE=1 SV=2	GR_OS1	2495.03	GR_OS2	2368.14
Q3LR79	Hemoglobin beta (Fragment) OS=Homo sapiens GN=HBB PE=2 SV=1	GR_OS1	6538.25	GR_OS2	5404.35
A0N071	Delta globin OS=Homo sapiens GN=HBD PE=3 SV=1	GR_OS1	4666.32	GR_OS2	3517.97
P02549	Spectrin alpha chain, erythrocyte OS=Homo sapiens GN=SPTA1 PE=1 SV=5	GR_OS1	13115.69	GR_OS2	13574.82
P11277	Spectrin beta chain, erythrocyte OS=Homo sapiens GN=SPTB PE=1 SV=5	GR_OS1	9548.97	GR_OS2	9680.48
E2RVJ0	Solute carrier family 4, anion exchanger, member 1 OS=Homo sapiens GN=SLC4A1 PE=2 SV=1	GR_OS1	5862.84	GR_OS2	5921.4
P55072	Transitional endoplasmic reticulum ATPase OS=Homo sapiens GN=VCP PE=1 SV=4	GR_OS1	887.67	GR_OS2	572.61
P16157	Ankyrin-1 OS=Homo sapiens GN=ANK1 PE=1 SV=3	GR_OS1	3144.26	GR_OS2	3439.09
P60900	Proteasome subunit alpha type-6 OS=Homo sapiens GN=PSMA6 PE=1 SV=1	GR_OS1	318.28	GR_OS2	255.31
P13798	Acylamino-acid-releasing enzyme OS=Homo sapiens GN=APEH PE=1 SV=4	GR_OS1	172.77		
P69891	Hemoglobin subunit gamma-1 OS=Homo sapiens GN=HBG1 PE=1 SV=2	GR_OS1	3856.72	GR_OS2	3104.49
P13716	Delta-aminolevulinic acid dehydratase OS=Homo sapiens GN=ALAD PE=1 SV=1	GR_OS1	147.27		
P07900	Heat shock protein HSP 90-alpha OS=Homo sapiens GN=HSP90AA1 PE=1 SV=5	GR_OS1	677.35	GR_OS2	881.23
P32119	Peroxisomal protein 2 OS=Homo sapiens GN=PRDX2 PE=1 SV=5	GR_OS1	448.13	GR_OS2	305.44
P50990	T-complex protein 1 subunit theta OS=Homo sapiens GN=CCT8 PE=1 SV=4	GR_OS1	1363.62	GR_OS2	1574.59
P00915	Carbonic anhydrase 1 OS=Homo sapiens GN=CA1 PE=1 SV=2	GR_OS1	1142.48	GR_OS2	957.65
P07384	Calpain-1 catalytic subunit OS=Homo sapiens GN=CAPN1 PE=1 SV=1	GR_OS1	1435.01	GR_OS2	1502.46
P62826	GTP-binding nuclear protein Ran OS=Homo sapiens GN=PPP60 PE=1 SV=3	GR_OS1	977.09	GR_OS2	986
Q8WVW5	Putative uncharacterized protein (Fragment) OS=Homo sapiens PE=2 SV=1	GR_OS1	1062.66	GR_OS2	1360.86
P04040	Catalase OS=Homo sapiens GN=CAT PE=1 SV=3	GR_OS1	170.28	GR_OS2	161.89
Q4LE36	ACYL variant protein (Fragment) OS=Homo sapiens GN=ACYL variant protein PE=2 SV=1	GR_OS1	296.68	GR_OS2	389.81
P21980	Protein-glutamine gamma-glutamyltransferase 2 OS=Homo sapiens GN=TGM2 PE=1 SV=2	GR_OS1	287.78	GR_OS2	261.58
Q06830	Peroxisomal protein 1 OS=Homo sapiens GN=PRDX1 PE=1 SV=1	GR_OS1	174.57	GR_OS2	143.47
P28066	Proteasome subunit alpha type-5 OS=Homo sapiens GN=PSMA5 PE=1 SV=3	GR_OS1	300.34	GR_OS2	444.43
P25787	Proteasome subunit alpha type-2 OS=Homo sapiens GN=PSMA2 PE=1 SV=2	GR_OS1	225.42	GR_OS2	137.93
Q4KKX0	EPB42 protein OS=Homo sapiens GN=EPB42 PE=2 SV=1	GR_OS1	512.52	GR_OS2	511.91
P04632	Calpain small subunit 1 OS=Homo sapiens GN=CAPNS1 PE=1 SV=1	GR_OS1	1775.88	GR_OS2	1967.88
O14818	Proteasome subunit alpha type-7 OS=Homo sapiens GN=PSMA7 PE=1 SV=1	GR_OS1	337.57	GR_OS2	245.44
P49721	Proteasome subunit beta type-2 OS=Homo sapiens GN=PSMB2 PE=1 SV=1	GR_OS1	105.99	GR_OS2	208.93
P00491	Purine nucleoside phosphorylase OS=Homo sapiens GN=PNP PE=1 SV=2	GR_OS1	115.59		
P27105	Erythrocyte band 7 integral membrane protein OS=Homo sapiens GN=STOM PE=1 SV=3	GR_OS1	706.33	GR_OS2	692.47
P28074	Proteasome subunit beta type-5 OS=Homo sapiens GN=PSMB5 PE=1 SV=3	GR_OS1	342.8	GR_OS2	260.61
P30041	Peroxisomal protein 6 OS=Homo sapiens GN=PRDX6 PE=1 SV=3	GR_OS1	507.25	GR_OS2	461.18
P00568	Adenylate kinase isoenzyme 1 OS=Homo sapiens GN=AK1 PE=1 SV=3	GR_OS1	875.31	GR_OS2	992.64
P60891	Ribose-phosphate pyrophosphokinase 1 OS=Homo sapiens GN=PRPS1 PE=1 SV=2	GR_OS1	238.46	GR_OS2	167.05
P00918	Carbonic anhydrase 2 OS=Homo sapiens GN=CA2 PE=1 SV=2	GR_OS1	232.25	GR_OS2	382.3
Q3MIH3	Ubiquitin A-52 residue ribosomal protein fusion product 1 OS=Homo sapiens GN=UBA52 PE=2 SV=1	GR_OS1	389.44	GR_OS2	468.26
Q1WWM3	EPB41 protein (Fragment) OS=Homo sapiens GN=EPB41 PE=2 SV=1	GR_OS1	529.52	GR_OS2	758.51
E7ET08	Uncharacterized protein OS=Homo sapiens GN=HSPA8 PE=3 SV=1	GR_OS1	651.9	GR_OS2	637.82
Q13228	Selenium-binding protein 1 OS=Homo sapiens GN=SELENBP1 PE=1 SV=2	GR_OS1	178.2	GR_OS2	140.58
Q06323	Proteasome activator complex subunit 1 OS=Homo sapiens GN=PSME1 PE=1 SV=1	GR_OS1	321.38	GR_OS2	293.94
P07738	Bisphosphoglycerate mutase OS=Homo sapiens GN=BPGM PE=1 SV=2	GR_OS1	53.25	GR_OS2	38.75
P04406	Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens GN=GAPDH PE=1 SV=3	GR_OS1	456.03	GR_OS2	467.66
D0PNI1	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein zeta polypeptide OS=Homo sapiens GN=YWHAZ PE=3 SV=1	GR_OS1	111.97	GR_OS2	103.41
P30043	Flavin reductase OS=Homo sapiens GN=BLVRB PE=1 SV=3	GR_OS1	692.56	GR_OS2	546.14
P28072	Proteasome subunit beta type-6 OS=Homo sapiens GN=PSMB6 PE=1 SV=4	GR_OS1	78.79	GR_OS2	88.79
Q5TDH0	Protein DDI1 homolog 2 OS=Homo sapiens GN=DDI2 PE=1 SV=1	GR_OS1	339.25	GR_OS2	704.34
P07195	L-lactate dehydrogenase B chain OS=Homo sapiens GN=LDHB PE=1 SV=2	GR_OS1	372.76	GR_OS2	276.52
P50395	Rab GDP dissociation inhibitor beta OS=Homo sapiens GN=GD12 PE=1 SV=2	GR_OS1	328.11	GR_OS2	230.41
P05109	Protein S100-A8 OS=Homo sapiens GN=S100A8 PE=1 SV=1	GR_OS1	60.48	GR_OS2	99.77
P49247	Ribose-5-phosphate isomerase OS=Homo sapiens GN=RPIA PE=1 SV=3	GR_OS1	34.78	GR_OS2	45.78
P00492	Hypoxanthine-guanine phosphoribosyltransferase OS=Homo sapiens GN=HPR1 PE=1 SV=2	GR_OS1	129.31	GR_OS2	58.45
Q9NTK5	Ogg-like ATPase 1 OS=Homo sapiens GN=OLA1 PE=1 SV=2	GR_OS1	200.11	GR_OS2	151.62
P00352	Retinal dehydrogenase 1 OS=Homo sapiens GN=ALDH1A1 PE=1 SV=2	GR_OS1	126.36	GR_OS2	124.75
P22314	Ubiquitin-like modifier-activating enzyme 1 OS=Homo sapiens GN=UBA1 PE=1 SV=3	GR_OS1	198.04	GR_OS2	218.08
P24666	Low molecular weight phosphotyrosine protein phosphatase OS=Homo sapiens GN=ACP1 PE=1 SV=3	GR_OS1	258.77	GR_OS2	107.71
P68402	Platelet-activating factor acetylhydrolase IB subunit beta OS=Homo sapiens GN=PAFAH1B2 PE=1 SV=1	GR_OS1	112.42	GR_OS2	63.93
Q15102	Platelet-activating factor acetylhydrolase IB subunit gamma OS=Homo sapiens GN=PAFAH1B3 PE=1 SV=1	GR_OS1	73.48	GR_OS2	108.95
B2RMN7	Spectrin, beta, erythrocytic OS=Homo sapiens GN=SPTB PE=2 SV=1	GR_OS1	9555.45	GR_OS2	9620.78
P35579	Myosin-9 OS=Homo sapiens GN=MYH9 PE=1 SV=4	GR_OS1	1231.49	GR_OS2	2004.18
Q00610	Clathrin heavy chain 1 OS=Homo sapiens GN=CLTC PE=1 SV=5	GR_OS1	567.09	GR_OS2	595.51
Q5T4S7	E3 ubiquitin-protein ligase UBR4 OS=Homo sapiens GN=UBR4 PE=1 SV=1	GR_OS1	1413.69	GR_OS2	1685.5
P78371	T-complex protein 1 subunit beta OS=Homo sapiens GN=CCT2 PE=1 SV=4	GR_OS1	2472.67	GR_OS2	2551.19
P49368	T-complex protein 1 subunit gamma OS=Homo sapiens GN=CCT3 PE=1 SV=4	GR_OS1	930.41		
Q99832	T-complex protein 1 subunit eta OS=Homo sapiens GN=CCT7 PE=1 SV=2	GR_OS1	1103.77	GR_OS2	1234.43
O00410	Importin-5 OS=Homo sapiens GN=IPO5 PE=1 SV=4	GR_OS1	736.79	GR_OS2	480.14
Q13200	26S proteasome non-ATPase regulatory subunit 2 OS=Homo sapiens GN=PSMD2 PE=1 SV=3	GR_OS1	1409.26	GR_OS2	1020.94
Q93008	Probable ubiquitin carboxyl-terminal hydrolase FAF-X OS=Homo sapiens GN=USP9X PE=1 SV=3	GR_OS1	633.93	GR_OS2	649.81
Q86VP6	Cullin-associated NEDD8-dissociated protein 1 OS=Homo sapiens GN=CAND1 PE=1 SV=2	GR_OS1	933.04	GR_OS2	647
A8K2X8	cDNA FLJ78433, highly similar to Homo sapiens chaperonin containing TCP1, subunit 5 (epsilon) (CCT5), mRNA OS=Homo sapiens PE=2 SV=1	GR_OS1	969.2	GR_OS2	752.82
Q4LE45	MYH10 variant protein (Fragment) OS=Homo sapiens GN=MYH10 variant protein PE=2 SV=1	GR_OS1	230.91	GR_OS2	495.61
Q16531	DNA damage-binding protein 1 OS=Homo sapiens GN=DDB1 PE=1 SV=1	GR_OS1	939.08	GR_OS2	1123.84
P21333	Filamin-A OS=Homo sapiens GN=FLNA PE=1 SV=4	GR_OS1	71.78	GR_OS2	198.9
P50991	T-complex protein 1 subunit delta OS=Homo sapiens GN=CCT4 PE=1 SV=4	GR_OS1	995.98	GR_OS2	805.29
O14724	Beta-spectrin (Fragment) OS=Homo sapiens GN=HSPTB1 PE=2 SV=1	GR_OS1	964.48	GR_OS2	903.62
Q99460	26S proteasome non-ATPase regulatory subunit 1 OS=Homo sapiens GN=PSMD1 PE=1 SV=2	GR_OS1	772.85	GR_OS2	952.84

Q00231	26S proteasome non-ATPase regulatory subunit 11 OS=Homo sapiens GN=PSMD11 PE=1 SV=3	GR_OS1	903.35	GR_OS2	920.72
B7Z815	Ubiquitin carboxyl-terminal hydrolase OS=Homo sapiens PE=2 SV=1	GR_OS1	80.05	GR_OS2	62.64
P08238	Heat shock protein HSP 90-beta OS=Homo sapiens GN=HSP90AB1 PE=1 SV=4	GR_OS1	638.22	GR_OS2	612.54
P40227	T-complex protein 1 subunit zeta OS=Homo sapiens GN=CCT6A PE=1 SV=3	GR_OS1	1096.34	GR_OS2	1230.48
P62258	14-3-3 protein epsilon OS=Homo sapiens GN=YWHAE PE=1 SV=1	GR_OS1	172.14	GR_OS2	103.08
Q14974	Importin subunit beta-1 OS=Homo sapiens GN=KPNB1 PE=1 SV=2	GR_OS1	1015.11	GR_OS2	841.54
Q14C86	GTPase-activating protein and VPS9 domain-containing protein 1 OS=Homo sapiens GN=GAPVD1 PE=1 SV=2	GR_OS1	444.46	GR_OS2	507
P17987	T-complex protein 1 subunit alpha OS=Homo sapiens GN=TCP1 PE=1 SV=1	GR_OS1	1163.58	GR_OS2	1076.19
P17858	6-phosphofructokinase, liver type OS=Homo sapiens GN=PFKL PE=1 SV=6	GR_OS1	736.79	GR_OS2	618.3
O60610	Protein diaphanous homolog 1 OS=Homo sapiens GN=DIAPH1 PE=1 SV=2	GR_OS1	938.01	GR_OS2	565.16
Q9Y230	RuvB-like 2 OS=Homo sapiens GN=RUVBL2 PE=1 SV=3	GR_OS1	1915.08	GR_OS2	1886.79
P49720	Proteasome subunit beta type-3 OS=Homo sapiens GN=PSMB3 PE=1 SV=2	GR_OS1	439.07	GR_OS2	359.21
Q0P512	Solute carrier family 2 (Facilitated glucose transporter), member 1 OS=Homo sapiens GN=SLC2A1 PE=2 SV=1	GR_OS1	1356.78	GR_OS2	1353.89
Q5XP14	E3 ubiquitin-protein ligase RNF123 OS=Homo sapiens GN=RNF123 PE=1 SV=1	GR_OS1	689.02	GR_OS2	664.55
O95373	Importin-7 OS=Homo sapiens GN=IPO7 PE=1 SV=1	GR_OS1	447.97	GR_OS2	260.11
Q7Z627	E3 ubiquitin-protein ligase HUWE1 OS=Homo sapiens GN=HUWE1 PE=1 SV=3	GR_OS1	827.01	GR_OS2	680.02
P17980	26S protease regulatory subunit 6A OS=Homo sapiens GN=PSMC3 PE=1 SV=3	GR_OS1	1083.01	GR_OS2	1363.53
P62195	26S protease regulatory subunit 8 OS=Homo sapiens GN=PSMC5 PE=1 SV=1	GR_OS1	1237.52	GR_OS2	1048.55
Q14254	Flotillin-2 OS=Homo sapiens GN=FLT2 PE=1 SV=2	GR_OS1	1249.52	GR_OS2	1421.61
Q9Y265	RuvB-like 1 OS=Homo sapiens GN=RUVBL1 PE=1 SV=1	GR_OS1	1349.63	GR_OS2	1412.3
P68032	Actin, alpha cardiac muscle 1 OS=Homo sapiens GN=ACTC1 PE=1 SV=1	GR_OS1	441.07	GR_OS2	588.36
Q9Y315	Putative deoxyribose-phosphate aldolase OS=Homo sapiens GN=DERA PE=1 SV=2	GR_OS1	140.91	GR_OS2	167.12
P61163	Alpha-centractin OS=Homo sapiens GN=ACTR1A PE=1 SV=1	GR_OS1	148.72	GR_OS2	116.8
Q92905	COP9 signalosome complex subunit 5 OS=Homo sapiens GN=COPS5 PE=1 SV=4	GR_OS1	766.72	GR_OS2	823.44
Q9Y6E3	HSPC027 OS=Homo sapiens PE=2 SV=1	GR_OS1	999.46	GR_OS2	1190.41
Q9B778	COP9 signalosome complex subunit 4 OS=Homo sapiens GN=COPS4 PE=1 SV=1	GR_OS1	1046.11	GR_OS2	1011.97
P35998	26S protease regulatory subunit 7 OS=Homo sapiens GN=PSMC2 PE=1 SV=3	GR_OS1	753.83	GR_OS2	643.17
A7E2Y5	DnaJ (Hsp40) homolog, subfamily C, member 13 OS=Homo sapiens GN=DNAJC13 PE=2 SV=1	GR_OS1	172.15	GR_OS2	242.67
E1P646	Adaptor-related protein complex 2, beta 1 subunit, isoform CRA_d OS=Homo sapiens GN=AP2B1 PE=4 SV=1	GR_OS1	263.05	GR_OS2	458.07
Q15008	26S proteasome non-ATPase regulatory subunit 6 OS=Homo sapiens GN=PSMD6 PE=1 SV=1	GR_OS1	1103.2	GR_OS2	917.94
A8K781	cDNA FLJ75299, highly similar to Xenopus laevis proteasome (prosome, macropain) 26S subunit, ATPase 3, mRNA OS=Homo sapiens PE=2 SV=1	GR_OS1	1088.4	GR_OS2	1282.14
P20618	Proteasome subunit beta type-1 OS=Homo sapiens GN=PSMB1 PE=1 SV=2	GR_OS1	261.36	GR_OS2	162.46
P05164	Myeloperoxidase OS=Homo sapiens GN=MPO PE=1 SV=1	GR_OS1	827.81	GR_OS2	504.07
Q9C0C9	Ubiquitin-conjugating enzyme E2 O OS=Homo sapiens GN=UBE2O PE=1 SV=3	GR_OS1	633.24	GR_OS2	397.44
P37840	Alpha-synuclein OS=Homo sapiens GN=SNCA PE=1 SV=1	GR_OS1	1548.45	GR_OS2	1594.94
P28070	Proteasome subunit beta type-4 OS=Homo sapiens GN=PSMB4 PE=1 SV=4	GR_OS1	50.91	GR_OS2	145.7
O00232	26S proteasome non-ATPase regulatory subunit 12 OS=Homo sapiens GN=PSMD12 PE=1 SV=3	GR_OS1	660.19	GR_OS2	679.62
E9PCQ3	Ubiquitin carboxyl-terminal hydrolase OS=Homo sapiens GN=USP15 PE=3 SV=2	GR_OS1	157.89	GR_OS2	188.65
O43681	ATPase ASNA1 OS=Homo sapiens GN=ASNA1 PE=1 SV=2	GR_OS1	95.69	GR_OS2	108.5
Q13616	Cullin-1 OS=Homo sapiens GN=CUL1 PE=1 SV=2	GR_OS1	295.29	GR_OS2	306.44
B4DZV5	cDNA FLJ58820, highly similar to 55 kDa erythrocyte membrane protein (p55) OS=Homo sapiens PE=2 SV=1	GR_OS1	337.83	GR_OS2	462.64
Q2Q9H2	Glucose-6-phosphate 1-dehydrogenase (Fragment) OS=Homo sapiens GN=G6PD PE=2 SV=1	GR_OS1	307.71	GR_OS2	328.6
P25786	Proteasome subunit alpha type-1 OS=Homo sapiens GN=PSMA1 PE=1 SV=1	GR_OS1	63	GR_OS2	73.39
Q2TUW9	Lactoferrin OS=Homo sapiens PE=2 SV=1	GR_OS1	839.77	GR_OS2	626.98
P46459	Vesicle-fusing ATPase OS=Homo sapiens GN=NSF PE=1 SV=3	GR_OS1	565.92	GR_OS2	709.82
Q709C8	Vacuolar protein sorting-associated protein 13C OS=Homo sapiens GN=VPS13C PE=1 SV=1	GR_OS1	56.71	GR_OS2	142.82
P62191	26S protease regulatory subunit 4 OS=Homo sapiens GN=PSMC1 PE=1 SV=1	GR_OS1	437.25	GR_OS2	472.74
P07237	Protein disulfide-isomerase OS=Homo sapiens GN=P4HB PE=1 SV=3	GR_OS1	125.49	GR_OS2	128.82
F2Z2X4	Uncharacterized protein OS=Homo sapiens GN=XPO4 PE=4 SV=1	GR_OS1	137.96	GR_OS2	106.58
Q16401	26S proteasome non-ATPase regulatory subunit 5 OS=Homo sapiens GN=PSMD5 PE=1 SV=3	GR_OS1	1143.19	GR_OS2	966.28
O00487	26S proteasome non-ATPase regulatory subunit 14 OS=Homo sapiens GN=PSMD14 PE=1 SV=1	GR_OS1	811.52	GR_OS2	789.75
Q08211	ATP-dependent RNA helicase A OS=Homo sapiens GN=DHX9 PE=1 SV=4	GR_OS1	163.64	GR_OS2	114.28
P68371	Tubulin beta-2C chain OS=Homo sapiens GN=TUBB2C PE=1 SV=1	GR_OS1	891.67	GR_OS2	1040.99
Q9UL46	Proteasome activator complex subunit 2 OS=Homo sapiens GN=PSME2 PE=1 SV=4	GR_OS1	345.08	GR_OS2	273.06
Q4W4Y1	Dopamine receptor interacting protein 4 OS=Homo sapiens GN=DRIP4 PE=2 SV=1	GR_OS1	811.31	GR_OS2	630.43
Q13098	COP9 signalosome complex subunit 1 OS=Homo sapiens GN=GPS1 PE=1 SV=4	GR_OS1	231.67	GR_OS2	259.61
Q75955	Flotillin-1 OS=Homo sapiens GN=FLT1 PE=1 SV=3	GR_OS1	636.67	GR_OS2	1096.32
Q14203	Dynactin subunit 1 OS=Homo sapiens GN=DCTN1 PE=1 SV=3	GR_OS1	44.26	GR_OS2	72.37
P43686	26S protease regulatory subunit 6B OS=Homo sapiens GN=PSMC4 PE=1 SV=2	GR_OS1	642.38	GR_OS2	666.04
Q96P70	Importin-9 OS=Homo sapiens GN=IPO9 PE=1 SV=3	GR_OS1	459.67	GR_OS2	218.7
P51665	26S proteasome non-ATPase regulatory subunit 7 OS=Homo sapiens GN=PSMD7 PE=1 SV=2	GR_OS1	242.59	GR_OS2	202.06
Q9UPU5	Ubiquitin carboxyl-terminal hydrolase 24 OS=Homo sapiens GN=USP24 PE=1 SV=3	GR_OS1	79.78	GR_OS2	117.25
P25789	Proteasome subunit alpha type-4 OS=Homo sapiens GN=PSMA4 PE=1 SV=1	GR_OS1	143.52	GR_OS2	92.29
P25788	Proteasome subunit alpha type-3 OS=Homo sapiens GN=PSMA3 PE=1 SV=2	GR_OS1	166.44	GR_OS2	102.99
Q10567	AP-1 complex subunit beta-1 OS=Homo sapiens GN=AP1B1 PE=1 SV=2	GR_OS1	159	GR_OS2	270.21
P48426	Phosphatidylinositol-5-phosphate 4-kinase type-2 alpha OS=Homo sapiens GN=PIP4K2A PE=1 SV=2	GR_OS1	278.55	GR_OS2	338.99
P61201	COP9 signalosome complex subunit 2 OS=Homo sapiens GN=COPS2 PE=1 SV=1	GR_OS1	161.32	GR_OS2	125.54
P68366	Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A PE=1 SV=1	GR_OS1	372.31	GR_OS2	549.28
Q5T447	E3 ubiquitin-protein ligase HECTD3 OS=Homo sapiens GN=HECTD3 PE=1 SV=1	GR_OS1	90.59	GR_OS2	90.87
P54920	Alpha-soluble NSF attachment protein OS=Homo sapiens GN=NAPA PE=1 SV=3	GR_OS1	712.34	GR_OS2	819.91
O43396	Thioredoxin-like protein 1 OS=Homo sapiens GN=TXNL1 PE=1 SV=3	GR_OS1	44.94	GR_OS2	87.1
P62333	26S protease regulatory subunit 10B OS=Homo sapiens GN=PSMC6 PE=1 SV=1	GR_OS1	495.84	GR_OS2	559.69
B2RDE1	cDNA, FLJ96568, highly similar to Homo sapiens tropomyosin 3 (TPM3), mRNA OS=Homo sapiens PE=2 SV=1	GR_OS1	279.54	GR_OS2	244.48
Q92973	Transporin-1 OS=Homo sapiens GN=TNPO1 PE=1 SV=2	GR_OS1	493.12	GR_OS2	146.62
Q15435	Protein phosphatase 1 regulatory subunit 7 OS=Homo sapiens GN=PPP1R7 PE=1 SV=1	GR_OS1	169.89	GR_OS2	83.68

P48556	26S proteasome non-ATPase regulatory subunit 8 OS=Homo sapiens GN=PSMD8 PE=1 SV=2	GR_OS1	339.22	GR_OS2	356.87
P84077	ADP-ribosylation factor 1 OS=Homo sapiens GN=ARF1 PE=1 SV=2	GR_OS1	1004.16	GR_OS2	896.71
Q9GZP4	PITH domain-containing protein 1 OS=Homo sapiens GN=PITHD1 PE=1 SV=1	GR_OS1	113.48	GR_OS2	108.44
B2R514	cDNA, FLJ92300, Homo sapiens COP9 subunit 6 (MOV34 homolog, 34 kD) (COPS6), mRNA OS=Homo sapiens PE=2 SV=1	GR_OS1	291.33	GR_OS2	266.46
B2R8N1	cDNA, FLJ93976, highly similar to Homo sapiens COP9 homolog (COP9), mRNA OS=Homo sapiens PE=2 SV=1	GR_OS1	346.5	GR_OS2	364.35
Q2TU77	Aging-associated protein 2 OS=Homo sapiens GN=AAG2 PE=2 SV=1	GR_OS1	720.1	GR_OS2	537.45
P60842	Eukaryotic initiation factor 4A-I OS=Homo sapiens GN=EIF4A1 PE=1 SV=1	GR_OS1	235.31	GR_OS2	130.84
P02768	Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2	GR_OS1	345.47	GR_OS2	249.72
P36959	GMP reductase 1 OS=Homo sapiens GN=GMPR PE=1 SV=1	GR_OS1	68.11	GR_OS2	102.87
P08514	Integrin alpha-IIb OS=Homo sapiens GN=ITGA2B PE=1 SV=3	GR_OS1	938.98	GR_OS2	1020.83
Q13618	Cullin-3 OS=Homo sapiens GN=CUL3 PE=1 SV=2	GR_OS1	371.43	GR_OS2	292.63
P02647	Apolipoprotein A-I OS=Homo sapiens GN=APOA1 PE=1 SV=1	GR_OS1	298.29	GR_OS2	304.48
P52907	F-actin-capping protein subunit alpha-1 OS=Homo sapiens GN=CAPZA1 PE=1 SV=3	GR_OS1	67.47		
P08311	Cathepsin G OS=Homo sapiens GN=CTSG PE=1 SV=2	GR_OS1	222.15	GR_OS2	243.31
P45974	Ubiquitin carboxyl-terminal hydrolase 5 OS=Homo sapiens GN=USP5 PE=1 SV=2	GR_OS1	496.78	GR_OS2	432.56
Q9Y4G6	Talin-2 OS=Homo sapiens GN=TLN2 PE=1 SV=4	GR_OS1	457.1	GR_OS2	310.33
B7Z596	cDNA FLJ55130, highly similar to Rattus norvegicus tropomyosin 1, alpha (Tpm1), transcript variant 8, mRNA OS=Homo sapiens PE=2 SV=1	GR_OS1	305.93	GR_OS2	288.73
B4DWX3	cDNA FLJ53229, highly similar to Importin alpha-7 subunit OS=Homo sapiens PE=2 SV=1	GR_OS1	82.19	GR_OS2	139.72
P19105	Myosin regulatory light chain 12A OS=Homo sapiens GN=MYL12A PE=1 SV=2	GR_OS1	145.47	GR_OS2	155.86
P52294	Importin subunit alpha-1 OS=Homo sapiens GN=KPNA1 PE=1 SV=3	GR_OS1	182.11	GR_OS2	146.84
B2R4M6	cDNA, FLJ92148, highly similar to Homo sapiens S100 calcium binding protein A9 (calgranulin B) (S100A9), mRNA OS=Homo sapiens PE=4 SV=1	GR_OS1	122.47	GR_OS2	112.9
P62495	Eukaryotic peptide chain release factor subunit 1 OS=Homo sapiens GN=ETF1 PE=1 SV=3	GR_OS1	106.07	GR_OS2	122.08
B2R7T8	cDNA, FLJ93598, highly similar to Homo sapiens capping protein (actin filament) muscle Z-line, beta (CAPZB), mRNA OS=Homo sapiens PE=2 SV=1	GR_OS1	262.71	GR_OS2	254.8
Q9H0U4	Ras-related protein Rab-1B OS=Homo sapiens GN=RAB1B PE=1 SV=1	GR_OS1	555.36	GR_OS2	510.25
B4DH02	cDNA FLJ50510, highly similar to Heat shock 70 kDa protein 4 OS=Homo sapiens PE=2 SV=1	GR_OS1	440.87	GR_OS2	303.64
B4DLQ1	Uncharacterized protein OS=Homo sapiens GN=ALDH16A1 PE=2 SV=1	GR_OS1	255.25	GR_OS2	198.46
Q9P2R3	Ankyrin repeat and FYVE domain-containing protein 1 OS=Homo sapiens GN=ANKFY1 PE=1 SV=2	GR_OS1	387.88	GR_OS2	424.85
P30154	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform OS=Homo sapiens GN=PPP2R1B PE=1 SV=3	GR_OS1	539.25	GR_OS2	403.62
Q9UNSD	COP9 signalosome complex subunit 3 OS=Homo sapiens GN=COPS3 PE=1 SV=3	GR_OS1	368.63	GR_OS2	531.22
P35611	Alpha-adducin OS=Homo sapiens GN=ADD1 PE=1 SV=2	GR_OS1	349.79	GR_OS2	339.03
Q969U7	Proteasome assembly chaperone 2 OS=Homo sapiens GN=PSMG2 PE=1 SV=1	GR_OS1	50.48	GR_OS2	53.99
Q96QK1	Vacuolar protein sorting-associated protein 35 OS=Homo sapiens GN=VPS35 PE=1 SV=2	GR_OS1	61.66		
P13561	Dynactin subunit 2 OS=Homo sapiens GN=DCTN2 PE=1 SV=4	GR_OS1	624.44	GR_OS2	499.82
P27708	CAD protein OS=Homo sapiens GN=CAD PE=1 SV=3	GR_OS1	273.72	GR_OS2	146.67
P11021	78 kDa glucose-regulated protein OS=Homo sapiens GN=HSPA5 PE=1 SV=2	GR_OS1	294.34	GR_OS2	278.68
P11215	Integrin alpha-M OS=Homo sapiens GN=ITGAM PE=1 SV=2	GR_OS1	311.71	GR_OS2	352.96
P35612	Beta-adducin OS=Homo sapiens GN=ADD2 PE=1 SV=3	GR_OS1	384.84	GR_OS2	327.34
P38606	V-type proton ATPase catalytic subunit A OS=Homo sapiens GN=ATP6V1A PE=1 SV=2	GR_OS1	61.54		
A8K50	Heat shock 70kDa protein 1A OS=Homo sapiens GN=HSPA1A PE=2 SV=1	GR_OS1	436	GR_OS2	228.85
P55036	26S proteasome non-ATPase regulatory subunit 4 OS=Homo sapiens GN=PSMD4 PE=1 SV=1	GR_OS1	143.97	GR_OS2	200.2
Q9BSL1	Ubiquitin-associated domain-containing protein 1 OS=Homo sapiens GN=UBAC1 PE=1 SV=1	GR_OS1	399.44	GR_OS2	404.51
O43149	Zinc finger ZZ-type and EF-hand domain-containing protein 1 OS=Homo sapiens GN=ZZEF1 PE=1 SV=6	GR_OS1	78.59	GR_OS2	117.53
Q99598	Translin-associated protein X OS=Homo sapiens GN=TSNAX PE=1 SV=1	GR_OS1	84.64		
B7Z507	cDNA FLJ51036, highly similar to Matrix metalloproteinase-9 (EC3.4.24.35) OS=Homo sapiens PE=2 SV=1	GR_OS1	106.93	GR_OS2	114.07
Q99733	Nucleosome assembly protein 1-like 4 OS=Homo sapiens GN=NAP1L4 PE=1 SV=1	GR_OS1	58.46	GR_OS2	59.43
P12829	Myosin light chain 4 OS=Homo sapiens GN=MYL4 PE=1 SV=3	GR_OS1	306.36	GR_OS2	334.52
P62834	Ras-related protein Rap-1A OS=Homo sapiens GN=RAP1A PE=1 SV=1	GR_OS1	109.22	GR_OS2	249.56
B5MDH8	Uncharacterized protein OS=Homo sapiens GN=WDR91 PE=4 SV=2	GR_OS1	78.15	GR_OS2	121.66
D8MJ82	Kell blood group antigen OS=Homo sapiens GN=KEL PE=2 SV=1	GR_OS1	121.68		
B1AJY5	Proteasome (Prosome, macropain) 26S subunit, non-ATPase, 10 OS=Homo sapiens GN=PSMD10 PE=4 SV=1	GR_OS1	165.99	GR_OS2	310.51
P08246	Neutrophil elastase OS=Homo sapiens GN=ELANE PE=1 SV=1	GR_OS1	59.81	GR_OS2	51.68
O00629	Importin subunit alpha-4 OS=Homo sapiens GN=KPNA4 PE=1 SV=1	GR_OS1	143.74	GR_OS2	175.41
Q5U011	RAB11B, member RAS oncogene family OS=Homo sapiens PE=2 SV=1	GR_OS1	448.22	GR_OS2	429.74
P63208	S-phase kinase-associated protein 1 OS=Homo sapiens GN=SKP1 PE=1 SV=2	GR_OS1	224.44	GR_OS2	405.91
P27824	Calnexin OS=Homo sapiens GN=CANX PE=1 SV=2	GR_OS1	189.9	GR_OS2	115.76
Q9H9Q2	COP9 signalosome complex subunit 7b OS=Homo sapiens GN=COPS7B PE=1 SV=1	GR_OS1	332.1	GR_OS2	434.56
Q95747	Serine/threonine-protein kinase OSR1 OS=Homo sapiens GN=OSR1 PE=1 SV=1	GR_OS1	411.75	GR_OS2	398.01
P46060	Ran GTPase-activating protein 1 OS=Homo sapiens GN=RANGAP1 PE=1 SV=1	GR_OS1	186.39	GR_OS2	222.38
D3DRP5	Chromosome 9 open reading frame 19, isoform CRA_a (Fragment) OS=Homo sapiens GN=C9orf19 PE=4 SV=1	GR_OS1	290.88	GR_OS2	133.16
P02786	Transferrin receptor protein 1 OS=Homo sapiens GN=TFRC PE=1 SV=2	GR_OS1	250.11	GR_OS2	320.88
B4DM76	cDNA FLJ57531, highly similar to DCN1-like protein 1 OS=Homo sapiens PE=2 SV=1	GR_OS1	40.01		
B4DWX5	cDNA FLJ55022, highly similar to F-box only protein 7 OS=Homo sapiens PE=2 SV=1	GR_OS1	72.67	GR_OS2	42.97
Q14697	Neutral alpha-glucosidase AB OS=Homo sapiens GN=GANAB PE=1 SV=3	GR_OS1	60.09	GR_OS2	68.14
Q96NA2	Rab-interacting lysosomal protein OS=Homo sapiens GN=RILP PE=1 SV=1	GR_OS1	201.9	GR_OS2	147.25
Q9UPN7	Serine/threonine-protein phosphatase 6 regulatory subunit 1 OS=Homo sapiens GN=PPP6R1 PE=1 SV=5	GR_OS1	94.69	GR_OS2	197.45
Q92539	Phosphatidate phosphatase LPIN2 OS=Homo sapiens GN=LPIN2 PE=1 SV=1	GR_OS1	42.75	GR_OS2	57.09
P30626	Sorcin OS=Homo sapiens GN=SRI PE=1 SV=1	GR_OS1	113.22	GR_OS2	100.81
P24158	Myeloblastin OS=Homo sapiens GN=PRTN3 PE=1 SV=3	GR_OS1	281.75	GR_OS2	215.47
Q9Y570	Protein phosphatase methylesterase 1 OS=Homo sapiens GN=PPME1 PE=1 SV=3	GR_OS1	211.19	GR_OS2	173.92
P47755	F-actin-capping protein subunit alpha-2 OS=Homo sapiens GN=CAPZA2 PE=1 SV=3	GR_OS1	136.04	GR_OS2	152.25
Q9NYU2	UDP-glucose:glycoprotein glucosyltransferase 1 OS=Homo sapiens GN=UGGT1 PE=1 SV=3	GR_OS1	75.56	GR_OS2	77.56
Q13564	NEDD8-activating enzyme E1 regulatory subunit OS=Homo sapiens GN=NAE1 PE=1 SV=1	GR_OS1	75.79	GR_OS2	64.21
F5GYF7	Uncharacterized protein OS=Homo sapiens GN=COP57A PE=4 SV=1	GR_OS1	263.44	GR_OS2	357.7

B4E1U9	cDNA FLJ54776, highly similar to Cell division control protein 42 homolog OS=Homo sapiens PE=2 SV=1	GR_OS1	147.67	GR_OS2	119.73
P61225	Ras-related protein Rap-2b OS=Homo sapiens GN=RAP2B PE=1 SV=1	GR_OS1	160.39	GR_OS2	265.34
P33176	Kinesin-1 heavy chain OS=Homo sapiens GN=KIF5B PE=1 SV=1	GR_OS1	262.51	GR_OS2	193.1
P27797	Calreticulin OS=Homo sapiens GN=CALR PE=1 SV=1	GR_OS1	135.98		
F5H2H8	Uncharacterized protein OS=Homo sapiens GN=SLC2A3 PE=3 SV=1	GR_OS1	77.39	GR_OS2	82.45
P17812	CTP synthase 1 OS=Homo sapiens GN=CTPS PE=1 SV=2	GR_OS1	217.33	GR_OS2	231.33
P13489	Ribonuclease inhibitor OS=Homo sapiens GN=RNH1 PE=1 SV=2	GR_OS1	377.22	GR_OS2	452.8
O76003	Glutaredoxin-3 OS=Homo sapiens GN=GLRX3 PE=1 SV=2	GR_OS1	117.48	GR_OS2	202.52
Q92530	Proteasome inhibitor PI31 subunit OS=Homo sapiens GN=PSMF1 PE=1 SV=2	GR_OS1	69.04	GR_OS2	75.52
P08397	Porphobilinogen deaminase OS=Homo sapiens GN=HMBS PE=1 SV=2	GR_OS1	164.32	GR_OS2	218.71
B2RBP3	cDNA, FLJ95615, highly similar to Homo sapiens ubiquitin-activating enzyme E1C (UBA3 homolog, yeast)(UBE1C), mRNA OS=Homo sapiens PE=2 SV=1	GR_OS1	80.97	GR_OS2	55.12
D3DWK4	Pyroline-5-carboxylate reductase OS=Homo sapiens GN=PYCRL PE=3 SV=1	GR_OS1	231.48	GR_OS2	265.09
B2R7L2	cDNA, FLJ93494, highly similar to Homo sapiens annexin A7 (ANXA7), transcript variant 1, mRNA OS=Homo sapiens PE=2 SV=1	GR_OS1	138.32	GR_OS2	171.62
Q9BRP4	Proteasomal ATPase-associated factor 1 OS=Homo sapiens GN=PAAF1 PE=1 SV=2	GR_OS1	161.43	GR_OS2	211.8
B3KY95	cDNA FLJ16143 fis, clone BRAMY2038516, highly similar to Protein disulfide-isomerase A6 (EC 5.3.4.1) OS=Homo sapiens PE=2 SV=1	GR_OS1	230.46	GR_OS2	208.2
O75688	Protein phosphatase 1B OS=Homo sapiens GN=PPM1B PE=1 SV=1	GR_OS1	175.67	GR_OS2	100.34
B3KW16	cDNA FLJ41902 fis, clone PEBLM2004666, highly similar to WD repeat protein 81 OS=Homo sapiens PE=2 SV=1	GR_OS1	255	GR_OS2	228.09
B1APW5	ATPase, Ca++ transporting, plasma membrane 4 OS=Homo sapiens GN=ATP2B4 PE=2 SV=1	GR_OS1	131.91	GR_OS2	296.15
O14523	C2 domain-containing protein 2-like OS=Homo sapiens GN=C2CD2L PE=1 SV=3	GR_OS1	119.43	GR_OS2	110.9
B4DT12	cDNA FLJ55654, highly similar to TBC1 domain family member 17 OS=Homo sapiens PE=2 SV=1	GR_OS1	40.09	GR_OS2	48.83
E9PAV3	Uncharacterized protein OS=Homo sapiens GN=NACA PE=4 SV=1	GR_OS1	73.63	GR_OS2	115.05
B7Z3E3	cDNA FLJ60267, highly similar to Homo sapiens reticulon 3 (RTN3), transcript variant 2, mRNA OS=Homo sapiens PE=2 SV=1	GR_OS1	57.37	GR_OS2	129.3
Q53HW2	Ribosomal protein P0 variant (Fragment) OS=Homo sapiens PE=2 SV=1	GR_OS1	97.31	GR_OS2	101.26
P22303	Acetylcholinesterase OS=Homo sapiens GN=ACHE PE=1 SV=1	GR_OS1	149.24	GR_OS2	169.33
Q9NT62	Ubiquitin-like-conjugating enzyme ATG3 OS=Homo sapiens GN=ATG3 PE=1 SV=1	GR_OS1	52.98		
Q6PIU2	Neutral cholesterol ester hydrolase 1 OS=Homo sapiens GN=NCEH1 PE=1 SV=3	GR_OS1	200.6	GR_OS2	151.91
Q0VF99	Oxysterol-binding protein OS=Homo sapiens GN=OSBP2 PE=2 SV=1	GR_OS1	60.01	GR_OS2	113.05
Q9BTY7	Protein FAM203A OS=Homo sapiens GN=FAM203A PE=1 SV=1	GR_OS1	56.74		
Q9NRY5	Protein FAM114A2 OS=Homo sapiens GN=FAM114A2 PE=1 SV=4	GR_OS1	78.22	GR_OS2	62.91
B4DUQ1	cDNA FLJ54552, highly similar to Heterogeneous nuclear ribonucleoprotein K OS=Homo sapiens PE=2 SV=1	GR_OS1	68.34	GR_OS2	174.31
Q9P0J7	E3 ubiquitin-protein ligase KCMF1 OS=Homo sapiens GN=KCMF1 PE=1 SV=2	GR_OS1	219.36	GR_OS2	195.8
B4DN59	cDNA FLJ52702, highly similar to Homo sapiens CD44 antigen (homing function and Indian blood group system) (CD44), transcript variant 4, mRNA OS=Homo sapiens PE=2 SV=1	GR_OS1	56.1	GR_OS2	96.14
P08754	Guanine nucleotide-binding protein G(k) subunit alpha OS=Homo sapiens GN=GNAI3 PE=1 SV=3	GR_OS1	77.21	GR_OS2	79.47
Q96PL5	Erythroid membrane-associated protein OS=Homo sapiens GN=ERMAP PE=1 SV=1	GR_OS1	69.3	GR_OS2	129.88
P16126	Lysozyme C OS=Homo sapiens GN=LYZ PE=1 SV=1	GR_OS1	142.9		
P36543	V-type proton ATPase subunit E 1 OS=Homo sapiens GN=ATP6V1E1 PE=1 SV=1	GR_OS1	48.44		
Q53F48	Heterogeneous nuclear ribonucleoprotein H3 isoform a variant (Fragment) OS=Homo sapiens PE=2 SV=1	GR_OS1	42.59	GR_OS2	49.77
O95273	Cyclin-D1-binding protein 1 OS=Homo sapiens GN=CCNDBP1 PE=1 SV=2	GR_OS1	38.6		
P05386	60S acidic ribosomal protein P1 OS=Homo sapiens GN=RPLP1 PE=1 SV=1	GR_OS1	71.81		
Q9NWU2	Protein C20orf11 OS=Homo sapiens GN=C20orf11 PE=1 SV=1	GR_OS1	54	GR_OS2	73.45
B1AQP2	Prefoldin subunit 2 OS=Homo sapiens GN=PFDN2 PE=2 SV=1	GR_OS1	63.05	GR_OS2	54.95
P04075	Fructose-bisphosphate aldolase A OS=Homo sapiens GN=ALDOA PE=1 SV=2	GR_OS1	709.34	GR_OS2	720.5
P10599	Thioredoxin OS=Homo sapiens GN=TXN PE=1 SV=3	GR_OS1	148.09	GR_OS2	100.26
O95782	AP-2 complex subunit alpha-1 OS=Homo sapiens GN=AP2A1 PE=1 SV=3	GR_OS1	541.44	GR_OS2	468.09
P68363	Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1	GR_OS1	611.15	GR_OS2	684.64
P28289	Tropomodulin-1 OS=Homo sapiens GN=TMOD1 PE=1 SV=1	GR_OS1	346.56	GR_OS2	525.15
Q9H479	Fructosamine-3-kinase OS=Homo sapiens GN=FN3K PE=1 SV=1	GR_OS1	49.91		
P51148	Ras-related protein Rab-5C OS=Homo sapiens GN=RAB5C PE=1 SV=2	GR_OS1	552.9	GR_OS2	472.76
Q9NPQ8	Synembryn-A OS=Homo sapiens GN=RIC8A PE=1 SV=3	GR_OS1	602.11	GR_OS2	449.17
B4DMP4	cDNA FLJ53136, highly similar to Homo sapiens Vac14 homolog (VAC14), mRNA OS=Homo sapiens PE=2 SV=1	GR_OS1	40.9		
P63000	Ras-related C3 botulinum toxin substrate 1 OS=Homo sapiens GN=RAC1 PE=1 SV=1	GR_OS1	46.04		
P35613	Basigin OS=Homo sapiens GN=BSG PE=1 SV=2	GR_OS1	190.28	GR_OS2	331.79
P48507	Glutamate-cysteine ligase regulatory subunit OS=Homo sapiens GN=GCLM PE=1 SV=1	GR_OS1	251.22	GR_OS2	299.83
P49327	Fatty acid synthase OS=Homo sapiens GN=FASN PE=1 SV=3	GR_OS1	205.5	GR_OS2	172.11
Q2TAZ0	Autophagy-related protein 2 homolog A OS=Homo sapiens GN=ATG2A PE=1 SV=3	GR_OS1	78.86		
Q5U0P9	Purine-rich element binding protein A OS=Homo sapiens PE=2 SV=1	GR_OS1	40.76	GR_OS2	71.06
Q2YFE1	Integrin beta OS=Homo sapiens PE=2 SV=1	GR_OS1	51.04	GR_OS2	96.92
B4E0R1	Integrin beta OS=Homo sapiens PE=2 SV=1	GR_OS1	87.36	GR_OS2	51.99
Q6DD88	Atlastin-3 OS=Homo sapiens GN=ATL3 PE=1 SV=1	GR_OS1	99.04	GR_OS2	126.84
P23528	Cofilin-1 OS=Homo sapiens GN=CFL1 PE=1 SV=3	GR_OS1	41.61	GR_OS2	102.38
P04792	Heat shock protein beta-1 OS=Homo sapiens GN=HSPB1 PE=1 SV=2	GR_OS1	54.87		
O14618	Copper chaperone for superoxide dismutase OS=Homo sapiens GN=CCS PE=1 SV=1	GR_OS1	60.46		
P07737	Profilin-1 OS=Homo sapiens GN=PFN1 PE=1 SV=2	GR_OS1	108.04	GR_OS2	68.58
Q96T46	Hemoglobin alpha 2 (Fragment) OS=Homo sapiens GN=HBA2 PE=2 SV=1	GR_OS1	1150.39	GR_OS2	1313.78
P29401	Transketolase OS=Homo sapiens GN=TKT PE=1 SV=3	GR_OS1	272.4	GR_OS2	211.9
B2RD79	Ubiquitin carboxyl-terminal hydrolase OS=Homo sapiens PE=2 SV=1	GR_OS1	205.5	GR_OS2	199.54
P00558	Phosphoglycerate kinase 1 OS=Homo sapiens GN=PGK1 PE=1 SV=3	GR_OS1	55.94		
P31948	Stress-induced-phosphoprotein 1 OS=Homo sapiens GN=STIP1 PE=1 SV=1	GR_OS1	163.42	GR_OS2	296.92
P61088	Ubiquitin-conjugating enzyme E2 N OS=Homo sapiens GN=UBE2N PE=1 SV=1	GR_OS1	364.44	GR_OS2	313.27
Q6XQN6	Nicotinate phosphoribosyltransferase OS=Homo sapiens GN=NAPRT1 PE=1 SV=2	GR_OS1	516.92	GR_OS2	319.18
P13796	Plastin-2 OS=Homo sapiens GN=LCP1 PE=1 SV=6	GR_OS1	241.57	GR_OS2	174.78
Q6PJT4	MSN protein (Fragment) OS=Homo sapiens GN=MSN PE=2 SV=1	GR_OS1	242.93		
P06733	Alpha-enolase OS=Homo sapiens GN=ENO1 PE=1 SV=2	GR_OS1	42.64	GR_OS2	81.74

Q16775	Hydroxyacylglutathione hydrolase, mitochondrial OS=Homo sapiens GN=HAGH PE=1 SV=2	GR_OS1	131.24	GR_OS2	140.3
P53004	Biliverdin reductase A OS=Homo sapiens GN=BLVRA PE=1 SV=2	GR_OS1	185.16	GR_OS2	177.33
P09105	Hemoglobin subunit theta-1 OS=Homo sapiens GN=HBQ1 PE=1 SV=2	GR_OS1	56.6	GR_OS2	64.22
Q9UK54	Hemoglobin beta subunit variant (Fragment) OS=Homo sapiens GN=HBB PE=2 SV=1	GR_OS1	5586.26	GR_OS2	4416.95
P69892	Hemoglobin subunit gamma-2 OS=Homo sapiens GN=HBG2 PE=1 SV=2	GR_OS1	3861.21	GR_OS2	3177.9
E9PEQ4	Uncharacterized protein OS=Homo sapiens GN=DNM2 PE=3 SV=1	GR_OS1	173.09	GR_OS2	255.33
Q9Y490	Talin-1 OS=Homo sapiens GN=TLN1 PE=1 SV=3	GR_OS1	2791.72	GR_OS2	2512.48
P08237	6-phosphofructokinase, muscle type OS=Homo sapiens GN=PFBK PE=1 SV=2	GR_OS1	159.98	GR_OS2	220.8
E7ESC6	Uncharacterized protein OS=Homo sapiens GN=XPO7 PE=4 SV=1	GR_OS1	858.96	GR_OS2	713.71
P55060	Exportin-2 OS=Homo sapiens GN=CSE1L PE=1 SV=3	GR_OS1	821.2	GR_OS2	836.12
F5H2F4	Uncharacterized protein OS=Homo sapiens GN=MTHFD1 PE=3 SV=1	GR_OS1	240.16	GR_OS2	333.15
P54577	Tyrosyl-tRNA synthetase, cytoplasmic OS=Homo sapiens GN=YARS PE=1 SV=4	GR_OS1	46.18	GR_OS2	56.54
Q86UX7	Fermitin family homolog 3 OS=Homo sapiens GN=FERMT3 PE=1 SV=1	GR_OS1	389.91	GR_OS2	358.46
Q14558	Phosphoribosyl pyrophosphate synthase-associated protein 1 OS=Homo sapiens GN=PRPSAP1 PE=1 SV=2	GR_OS1	196.08	GR_OS2	323.18
Q5VYK3	Proteasome-associated protein ECM29 homolog OS=Homo sapiens GN=ECM29 PE=1 SV=2	GR_OS1	527.69	GR_OS2	548.48
O60664	Perilipin-3 OS=Homo sapiens GN=PLIN3 PE=1 SV=3	GR_OS1	792.07	GR_OS2	879.53
P17213	Bactericidal permeability-increasing protein OS=Homo sapiens GN=BPI PE=1 SV=4	GR_OS1	67.54	GR_OS2	76.59
Q3LXA3	Bifunctional ATP-dependent dihydroxyacetone kinase/FAD-AMP lyase (cyclizing) OS=Homo sapiens GN=DAK PE=1 SV=2	GR_OS1	783.08	GR_OS2	720.41
Q01813	6-phosphofructokinase type C OS=Homo sapiens GN=PFBK PE=1 SV=2	GR_OS1	285.09		
Q99536	Synaptic vesicle membrane protein VAT-1 homolog OS=Homo sapiens GN=VAT1 PE=1 SV=2	GR_OS1	534.35	GR_OS2	484.11
P30740	Leukocyte elastase inhibitor OS=Homo sapiens GN=SERPINB1 PE=1 SV=1	GR_OS1	267.12		
Q6FGX3	RAB6A protein OS=Homo sapiens GN=RAB6A PE=2 SV=1	GR_OS1	466.26	GR_OS2	388.03
P41091	Eukaryotic translation initiation factor 2 subunit 3 OS=Homo sapiens GN=EIF2S3 PE=1 SV=3	GR_OS1	46.2	GR_OS2	59.78
F5H3X9	Uncharacterized protein OS=Homo sapiens GN=PPP2R1A PE=4 SV=1	GR_OS1	607.7	GR_OS2	434.93
P68104	Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 PE=1 SV=1	GR_OS1	94.83	GR_OS2	196.31
Q9NRW1	Ras-related protein Rab-6B OS=Homo sapiens GN=RAB6B PE=1 SV=1	GR_OS1	483.32	GR_OS2	447.19
Q9NRV9	Heme-binding protein 1 OS=Homo sapiens GN=HEBP1 PE=1 SV=1	GR_OS1	448	GR_OS2	499.89
Q9NR46	Endophilin-B2 OS=Homo sapiens GN=SH3GLB2 PE=1 SV=1	GR_OS1	222.04	GR_OS2	275.27
Q9H4M9	EH domain-containing protein 1 OS=Homo sapiens GN=EHD1 PE=1 SV=2	GR_OS1	101.54		
Q96F85	CB1 cannabinoid receptor-interacting protein 1 OS=Homo sapiens GN=CNRIP1 PE=1 SV=1	GR_OS1	94.86	GR_OS2	202.88
P61086	Ubiquitin-conjugating enzyme E2 K OS=Homo sapiens GN=UBE2K PE=1 SV=3	GR_OS1	404.92	GR_OS2	185.95
Q8WVM8	Sec1 family domain-containing protein 1 OS=Homo sapiens GN=SCFD1 PE=1 SV=4	GR_OS1	345.86	GR_OS2	403.22
Q96IJ6	Mannose-1-phosphate guanylttransferase alpha OS=Homo sapiens GN=GMPPA PE=1 SV=1	GR_OS1	495.74	GR_OS2	293.1
P14868	Aspartyl-tRNA synthetase, cytoplasmic OS=Homo sapiens GN=DARS PE=1 SV=2	GR_OS1	337.08	GR_OS2	326.66
P07954	Fumarate hydratase, mitochondrial OS=Homo sapiens GN=FH PE=1 SV=3	GR_OS1	314.64	GR_OS2	473.33
P68036	Ubiquitin-conjugating enzyme E2 L3 OS=Homo sapiens GN=UBE2L3 PE=1 SV=1	GR_OS1	143.79	GR_OS2	201.92
P28838	Cytosol aminopeptidase OS=Homo sapiens GN=LAP3 PE=1 SV=3	GR_OS1	264.36	GR_OS2	253.38
O14980	Exportin-1 OS=Homo sapiens GN=XPO1 PE=1 SV=1	GR_OS1	255.76	GR_OS2	245.1
P61106	Ras-related protein Rab-14 OS=Homo sapiens GN=RAB14 PE=1 SV=4	GR_OS1	219.28	GR_OS2	303.76
B4DPM7	cDNA FLJ55739, highly similar to 26S proteasome non-ATPase regulatory subunit 3 OS=Homo sapiens PE=2 SV=1	GR_OS1	341.39		
P23743	Diacylglycerol kinase alpha OS=Homo sapiens GN=DGKA PE=1 SV=3	GR_OS1	431.55	GR_OS2	287.03
P51812	Ribosomal protein S6 kinase alpha-3 OS=Homo sapiens GN=RPS6KA3 PE=1 SV=1	GR_OS1	165.53	GR_OS2	120.64
P43490	Nicotinamide phosphoribosyltransferase OS=Homo sapiens GN=NAMPT PE=1 SV=1	GR_OS1	81.2	GR_OS2	172.64
P22061	Protein-L-isoaspartate (D-aspartate) O-methyltransferase OS=Homo sapiens GN=PCMT1 PE=1 SV=4	GR_OS1	409.44	GR_OS2	439.49
B2R9U2	cDNA, FLJ94557, highly similar to Homo sapiens FK506 binding protein 4, 59kDa (FKBP4), mRNA OS=Homo sapiens PE=2 SV=1	GR_OS1	217.5	GR_OS2	349.63
Q6IBG5	MYL6 protein OS=Homo sapiens GN=MYL6 PE=2 SV=1	GR_OS1	339.83	GR_OS2	317.31
C3PTT6	Pancreatic adenocarcinoma upregulated factor OS=Homo sapiens GN=PAUF PE=2 SV=1	GR_OS1	453.76		
P07996	Thrombospondin-1 OS=Homo sapiens GN=THBS1 PE=1 SV=2	GR_OS1	307.9	GR_OS2	318.33
P61020	Ras-related protein Rab-5B OS=Homo sapiens GN=RAB5B PE=1 SV=1	GR_OS1	445.05	GR_OS2	345.33
Q15276	Rab GTPase-binding effector protein 1 OS=Homo sapiens GN=RABEP1 PE=1 SV=2	GR_OS1	123.08	GR_OS2	158.85
B7ZW70	LOC727761 protein OS=Homo sapiens GN=LOC727761 PE=2 SV=1	GR_OS1	268.64	GR_OS2	232.9
Q13492	Phosphatidylinositol-binding clathrin assembly protein OS=Homo sapiens GN=PICALM PE=1 SV=2	GR_OS1	99.99	GR_OS2	98.97
Q16563	Synaptophysin-like protein 1 OS=Homo sapiens GN=SYPL1 PE=1 SV=1	GR_OS1	58.21	GR_OS2	98.36
O94903	Proline synthase co-transcribed bacterial homolog protein OS=Homo sapiens GN=PROSC PE=1 SV=1	GR_OS1	97.16	GR_OS2	155.38
P04921	Glycophorin-C OS=Homo sapiens GN=GYPC PE=1 SV=1	GR_OS1	822.88	GR_OS2	681.8
P61006	Ras-related protein Rab-8A OS=Homo sapiens GN=RAB8A PE=1 SV=1	GR_OS1	280.83	GR_OS2	214.48
P54136	Arginyl-tRNA synthetase, cytoplasmic OS=Homo sapiens GN=RARS PE=1 SV=2	GR_OS1	66.05	GR_OS2	83.26
B3KSY4	HCG1787779, isoform CRA_b OS=Homo sapiens GN=COR07 PE=2 SV=1	GR_OS1	254.33	GR_OS2	312.32
B4DJA5	Uncharacterized protein OS=Homo sapiens GN=RAB5A PE=2 SV=1	GR_OS1	283.56	GR_OS2	219.17
Q16851	UTP--glucose-1-phosphate uridylyltransferase OS=Homo sapiens GN=UGP2 PE=1 SV=5	GR_OS1	172.76	GR_OS2	185.36
B0UX83	HLA-B associated transcript 3 OS=Homo sapiens GN=BAT3 PE=4 SV=1	GR_OS1	385.84	GR_OS2	336.85
Q00796	Sorbitol dehydrogenase OS=Homo sapiens GN=SORD PE=1 SV=4	GR_OS1	100.94	GR_OS2	111.44
Q13057	Bifunctional coenzyme A synthase OS=Homo sapiens GN=COASY PE=1 SV=4	GR_OS1	332.97	GR_OS2	308.69
Q16543	Hsp90 co-chaperone Cdc37 OS=Homo sapiens GN=CDC37 PE=1 SV=1	GR_OS1	430.75	GR_OS2	358.83
Q9HAB8	Phosphopantothenate--cysteine ligase OS=Homo sapiens GN=PPCS PE=1 SV=2	GR_OS1	169.01	GR_OS2	135.59
B7Z5E3	L-lactate dehydrogenase OS=Homo sapiens GN=LDHA PE=2 SV=1	GR_OS1	96.87		
B9A6M6	TBC1 domain family, member 24 OS=Homo sapiens GN=TBC1D24 PE=2 SV=1	GR_OS1	58.82	GR_OS2	45.52
Q13404	Ubiquitin-conjugating enzyme E2 variant 1 OS=Homo sapiens GN=UBE2V1 PE=1 SV=2	GR_OS1	68.71	GR_OS2	89.9
P13473	Lysosome-associated membrane glycoprotein 2 OS=Homo sapiens GN=LAMP2 PE=1 SV=2	GR_OS1	208.17		
O60763	General vesicular transport factor p115 OS=Homo sapiens GN=USO1 PE=1 SV=2	GR_OS1	256.49	GR_OS2	288.38
Q07960	Rho GTPase-activating protein 1 OS=Homo sapiens GN=ARHGAP1 PE=1 SV=1	GR_OS1	128.26	GR_OS2	197.57
P51692	Signal transducer and activator of transcription 5B OS=Homo sapiens GN=STAT5B PE=1 SV=2	GR_OS1	84.74	GR_OS2	121.39
O94919	Endonuclease domain-containing 1 protein OS=Homo sapiens GN=ENDOD1 PE=1 SV=2	GR_OS1	124.62	GR_OS2	283.54
P25685	DnaJ homolog subfamily B member 1 OS=Homo sapiens GN=DNAJB1 PE=1 SV=4	GR_OS1	186.85	GR_OS2	86.06
Q6B0K9	Hemoglobin subunit mu OS=Homo sapiens GN=HBM PE=2 SV=1	GR_OS1	408.62	GR_OS2	91.13
B4DV64	cDNA FLJ61420, highly similar to Homo sapiens olfactomedin 4 (OLFM4), mRNA OS=Homo sapiens PE=2 SV=1	GR_OS1	204.49	GR_OS2	160

Q13201	Multimerin-1 OS=Homo sapiens GN=MMRN1 PE=1 SV=3	GR_OS1	59.16	GR_OS2	101.16
O14964	Hepatocyte growth factor-regulated tyrosine kinase substrate OS=Homo sapiens GN=HGS PE=1 SV=1	GR_OS1	138.84	GR_OS2	102.17
Q14773	Inter cellular adhesion molecule 4 OS=Homo sapiens GN=ICAM4 PE=2 SV=1	GR_OS1	186.65	GR_OS2	217.62
F5GXS3	Uncharacterized protein OS=Homo sapiens GN=RHD PE=4 SV=1	GR_OS1	66.82	GR_OS2	168.84
P50895	Basal cell adhesion molecule OS=Homo sapiens GN=BCAM PE=1 SV=2	GR_OS1	96.5	GR_OS2	137.99
Q9BXD5	N-acetylneuraminase lyase OS=Homo sapiens GN=NPL PE=2 SV=1	GR_OS1	65.37	GR_OS2	94.5
Q9NP58	ATP-binding cassette sub-family B member 6, mitochondrial OS=Homo sapiens GN=ABCB6 PE=1 SV=1	GR_OS1	168.85	GR_OS2	356.98
Q15365	Poly(rC)-binding protein 1 OS=Homo sapiens GN=PCBP1 PE=1 SV=2	GR_OS1	232.72	GR_OS2	186.21
Q99497	Protein DJ-1 OS=Homo sapiens GN= PARK7 PE=1 SV=2	GR_OS1	120.74	GR_OS2	141.24
O15439	Multidrug resistance-associated protein 4 OS=Homo sapiens GN=ABCC4 PE=1 SV=3	GR_OS1	87.56	GR_OS2	151.93
Q04323	UBX domain-containing protein 1 OS=Homo sapiens GN=UBXN1 PE=1 SV=2	GR_OS1	134.57	GR_OS2	120.92
P38919	Eukaryotic initiation factor 4A-III OS=Homo sapiens GN=EIF4A3 PE=1 SV=4	GR_OS1	89.6		
P09972	Fructose-bisphosphate aldolase C OS=Homo sapiens GN=ALDOC PE=1 SV=2	GR_OS1	277.69	GR_OS2	287.07
P01009	Alpha-1-antitrypsin OS=Homo sapiens GN=SERPINA1 PE=1 SV=3	GR_OS1	203.12	GR_OS2	200.65
B4DL P6	Serine/threonine-protein phosphatase OS=Homo sapiens PE=2 SV=1	GR_OS1	83.61	GR_OS2	139.22
Q6PCE3	Glucose 1,6-bisphosphate synthase OS=Homo sapiens GN=PGM2L1 PE=1 SV=3	GR_OS1	71.61	GR_OS2	83.92
E7EQ55	Uncharacterized protein OS=Homo sapiens GN=UCLH5 PE=4 SV=1	GR_OS1	59.82	GR_OS2	73.54
Q9Y371	Endophilin-B1 OS=Homo sapiens GN=SH3GLB1 PE=1 SV=1	GR_OS1	77.73	GR_OS2	60.16
O15400	Syntaxin-7 OS=Homo sapiens GN=STX7 PE=1 SV=4	GR_OS1	259.37	GR_OS2	241.33
Q2YDC2	HCG1985580, isoform CRA_f OS=Homo sapiens GN=PDCD6 PE=2 SV=1	GR_OS1	95.89	GR_OS2	119.2
O95816	BAG family molecular chaperone regulator 2 OS=Homo sapiens GN=BAG2 PE=1 SV=1	GR_OS1	83.98	GR_OS2	116.12
Q96IU4	Abhydrolase domain-containing protein 14B OS=Homo sapiens GN=ABHD14B PE=1 SV=1	GR_OS1	138.65	GR_OS2	102.03
B4E2N0	Uncharacterized protein OS=Homo sapiens GN=LZIC PE=2 SV=1	GR_OS1	44.31	GR_OS2	101.22
A2RRF3	EPS15L1 protein OS=Homo sapiens GN=EPS15L1 PE=2 SV=1	GR_OS1	53.91	GR_OS2	93.77
P02671	Fibrinogen alpha chain OS=Homo sapiens GN=FGA PE=1 SV=2	GR_OS1	52.08	GR_OS2	55.59
P18577	Blood group Rh(CE) polypeptide OS=Homo sapiens GN=RHCE PE=1 SV=2	GR_OS1	227.68	GR_OS2	341.37
Q53E29	Mitogen-activated protein kinase kinase 3 isoform B variant (Fragment) OS=Homo sapiens PE=2 SV=1	GR_OS1	72.99	GR_OS2	66.01
Q9UN37	Vacuolar protein sorting-associated protein 4A OS=Homo sapiens GN=VPS4A PE=1 SV=1	GR_OS1	39.32		
P26447	Protein S100-A4 OS=Homo sapiens GN=S100A4 PE=1 SV=1	GR_OS1	46.11	GR_OS2	49.44
Q08495	Dematin OS=Homo sapiens GN=EPB49 PE=1 SV=3	GR_OS1	127.12	GR_OS2	169.05
P16152	Carbonyl reductase [NADPH] 1 OS=Homo sapiens GN=CBR1 PE=1 SV=3	GR_OS1	167.59	GR_OS2	152.41
P14314	Glucosidase 2 subunit beta OS=Homo sapiens GN=PRKCSH PE=1 SV=2	GR_OS1	73.9	GR_OS2	50.24
Q9GZS3	WD repeat-containing protein 61 OS=Homo sapiens GN=WDR61 PE=1 SV=1	GR_OS1	169.49	GR_OS2	193.99
O00154	Cytosolic acyl coenzyme A thioester hydrolase OS=Homo sapiens GN=ACOT7 PE=1 SV=3	GR_OS1	121.44	GR_OS2	132.53
P35754	Glutaredoxin-1 OS=Homo sapiens GN=GLRX PE=1 SV=2	GR_OS1	172.44	GR_OS2	90.23
P10909	Clusterin OS=Homo sapiens GN=CLU PE=1 SV=1	GR_OS1	141.63	GR_OS2	65.73
P00813	Adenosine deaminase OS=Homo sapiens GN=ADA PE=1 SV=3	GR_OS1	38.37	GR_OS2	49.99
Q9HAV0	Guanine nucleotide-binding protein subunit beta-4 OS=Homo sapiens GN=GNB4 PE=1 SV=3	GR_OS1	107.61		
F5H157	Uncharacterized protein OS=Homo sapiens GN=RAB35 PE=3 SV=1	GR_OS1	100.4		
Q6IPX4	RPS16 protein OS=Homo sapiens GN=RPS16 PE=2 SV=1	GR_OS1	71.73		
P40925	Malate dehydrogenase, cytoplasmic OS=Homo sapiens GN=MDH1 PE=1 SV=4	GR_OS1	52.99		
Q6PGP7	Tetratricopeptide repeat protein 37 OS=Homo sapiens GN=TTC37 PE=1 SV=1	GR_OS1	46.29	GR_OS2	153.08
A4D2J0	SNARE protein Ykt6 OS=Homo sapiens GN=YKT6 PE=2 SV=1	GR_OS1	119.78	GR_OS2	101.16
P12273	Prolactin-inducible protein OS=Homo sapiens GN=PIP PE=1 SV=1	GR_OS1	119.83		
B7ZBJ4	Calcium binding protein 39-like OS=Homo sapiens GN=CAB39L PE=4 SV=1	GR_OS1	61.26		
P06727	Apolipoprotein A-IV OS=Homo sapiens GN=APOA4 PE=1 SV=3	GR_OS1	51.29		
P30453	HLA class I histocompatibility antigen, A-34 alpha chain OS=Homo sapiens GN=HLA-A PE=1 SV=1	GR_OS1	49.02		
Q9UBQ7	Glyoxylate reductase/hydroxypyruvate reductase OS=Homo sapiens GN=GRHPR PE=1 SV=1	GR_OS1	62.09	GR_OS2	98.12
C9JRV9	Uncharacterized protein OS=Homo sapiens GN=UBA5 PE=4 SV=1	GR_OS1	47.3	GR_OS2	39.87
C9IZ76	Uncharacterized protein OS=Homo sapiens GN=PPP2R4 PE=4 SV=1	GR_OS1	107.67		
Q5D862	Filaggrin-2 OS=Homo sapiens GN=FLG2 PE=1 SV=1	GR_OS1	79.95		
C3W811	ADP-ribosyltransferase 4 (Dombrock blood group) (Fragment) OS=Homo sapiens GN=ART4 PE=4 SV=1	GR_OS1	71.1		
Q6JSD8	Aquaporin 1 splice variant 2 (Fragment) OS=Homo sapiens GN=AQP1 PE=2 SV=1	GR_OS1	129.6		
Q9Y3E0	Vesicle transport protein GOT1B OS=Homo sapiens GN=GOLT1B PE=1 SV=1	GR_OS1	174.86	GR_OS2	106.47
B4DME9	Uncharacterized protein OS=Homo sapiens GN=KLC4 PE=2 SV=1	GR_OS1	50.08		
P62837	Ubiquitin-conjugating enzyme E2 D2 OS=Homo sapiens GN=UBE2D2 PE=1 SV=1	GR_OS1	40.05	GR_OS2	81.07
Q9BVJ7	Dual specificity protein phosphatase 23 OS=Homo sapiens GN=DUSP23 PE=1 SV=1	GR_OS1	100.15	GR_OS2	56.51
Q8WYNO	Cysteine protease ATG4A OS=Homo sapiens GN=ATG4A PE=1 SV=1	GR_OS1	100.29	GR_OS2	49.24
P56545	C-terminal-binding protein 2 OS=Homo sapiens GN=CTBP2 PE=1 SV=1	GR_OS1	68.29	GR_OS2	45.04
O43665	Regulator of G-protein signaling 10 OS=Homo sapiens GN=RGS10 PE=1 SV=2	GR_OS1	38.36	GR_OS2	31.12
D3DP13	Fibrinogen beta chain, isoform CRA_e OS=Homo sapiens GN=FGB PE=4 SV=1	GR_OS1	53.51		
Q0Z7S6	Carcinoembryonic antigen-related cell adhesion molecule 8 OS=Homo sapiens GN=CEACAM8 PE=2 SV=1	GR_OS1	52.65		
P07741	Adenine phosphoribosyltransferase OS=Homo sapiens GN=APRT PE=1 SV=2	GR_OS1	46.67		
B4DNB8	Uncharacterized protein OS=Homo sapiens GN=DCAF6 PE=2 SV=1	GR_OS1	26.77		
O00299	Chloride intracellular channel protein 1 OS=Homo sapiens GN=CLIC1 PE=1 SV=4	GR_OS1	67.36	GR_OS2	56.7
Q96BN8	Protein FAM105B OS=Homo sapiens GN=FAM105B PE=1 SV=3	GR_OS1	57.58	GR_OS2	59.23
O15173	Membrane-associated progesterone receptor component 2 OS=Homo sapiens GN=PGRMC2 PE=1 SV=1	GR_OS1	53.34	GR_OS2	57.57
O15067	Phosphoribosylformylglycinamide synthase OS=Homo sapiens GN=PFAS PE=1 SV=4	GR_OS1	69.49		
B3KUB8	cDNA FLJ39539 fis, clone PUAEN2008228, highly similar to Platelet glycoprotein 4 OS=Homo sapiens PE=2 SV=1	GR_OS1	63.57		
O43592	Exportin-T OS=Homo sapiens GN=XPOT PE=1 SV=2	GR_OS1	48.4		
P20645	Cation-dependent mannose-6-phosphate receptor OS=Homo sapiens GN=M6PR PE=1 SV=1	GR_OS1	41.22		
Q9UI26	Importin-11 OS=Homo sapiens GN=IPO11 PE=1 SV=1	GR_OS1	57.09		
Q1MW40	Responsive to centrifugal force and shear stress gene 1 OS=Homo sapiens GN=RECS1 PE=2 SV=1	GR_OS1	59.53	GR_OS2	122.47
P01040	Cystatin-A OS=Homo sapiens GN=CSTA PE=1 SV=1	GR_OS1	53.21	GR_OS2	46.49
O43515	Mutant erythrocyte membrane glycoprotein Rh50 OS=Homo sapiens GN=Rh50 PE=2 SV=1	GR_OS1	61.73		
B4DVH6	cDNA FLJ57611, moderately similar to WD repeat domain phosphoinositide-interacting protein 4 OS=Homo sapiens PE=2 SV=1	GR_OS1	57.36		
P01833	Polymeric immunoglobulin receptor OS=Homo sapiens GN=PIGR PE=1 SV=4	GR_OS1	39.49		
Q27J81	Inverted formin-2 OS=Homo sapiens GN=INF2 PE=1 SV=2	GR_OS1	59.67		

B2R5X9	cDNA, FLJ92678, highly similar to Homo sapiens interferon-induced protein with tetratricopeptide repeats 5 (IFIT5), mRNA OS=Homo sapiens PE=2 SV=1	GR_OS1	59.62	GR_OS2	54.85
Q9NVZ3	Adaptin ear-binding coat-associated protein 2 OS=Homo sapiens GN=NECAP2 PE=1 SV=1	GR_OS1	46.33	GR_OS2	51.1
Q13158	Protein FADD OS=Homo sapiens GN=FADD PE=1 SV=1	GR_OS1	41.62		
P78417	Glutathione S-transferase omega-1 OS=Homo sapiens GN=GSTO1 PE=1 SV=2			GR_OS2	53.16
P29144	Tripeptidyl-peptidase 2 OS=Homo sapiens GN=TPP2 PE=1 SV=4			GR_OS2	82.01
B3KNN7	cDNA FLJ30049 fis, clone ADRGL1000033, highly similar to 26S proteasome non-ATPase regulatory subunit 3 OS=Homo sapiens PE=2 SV=1			GR_OS2	287.57
P14625	Endoplasmin OS=Homo sapiens GN=HSP90B1 PE=1 SV=1			GR_OS2	195.85
Q96RL7	Vacuolar protein sorting-associated protein 13A OS=Homo sapiens GN=VPS13A PE=1 SV=2			GR_OS2	113.97
Q9BQA1	Methylosome protein 50 OS=Homo sapiens GN=WDR77 PE=1 SV=1			GR_OS2	72.8
Q13464	Rho-associated protein kinase 1 OS=Homo sapiens GN=ROCK1 PE=1 SV=1			GR_OS2	78.87
B3KQT9	Uncharacterized protein OS=Homo sapiens GN=PDIA3 PE=2 SV=1			GR_OS2	50.8
Q9UNN5	FAS-associated factor 1 OS=Homo sapiens GN=FAF1 PE=1 SV=2			GR_OS2	41.15
P62879	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2 OS=Homo sapiens GN=GNB2 PE=1 SV=3			GR_OS2	95.79
Q29694	MHC class I HLA-B antigen (Fragment) OS=Homo sapiens GN=HLA-B PE=2 SV=1			GR_OS2	118.45
Q59F14	Importin 4 variant (Fragment) OS=Homo sapiens PE=2 SV=1			GR_OS2	42.56
P26038	Moesin OS=Homo sapiens GN=MSN PE=1 SV=3			GR_OS2	272.03
P49913	Cathelicidin antimicrobial peptide OS=Homo sapiens GN=CAMP PE=1 SV=1			GR_OS2	62.85
Q02094	Ammonium transporter Rh type A OS=Homo sapiens GN=RHAG PE=1 SV=2			GR_OS2	40.96
B4DQJ8	6-phosphogluconate dehydrogenase, decarboxylating OS=Homo sapiens GN=PGD PE=2 SV=1			GR_OS2	45.71
Q15257	Serine/threonine-protein phosphatase 2A activator OS=Homo sapiens GN=PPP2R4 PE=1 SV=3			GR_OS2	74.63
Q2TU64	PIG48 OS=Homo sapiens PE=2 SV=1			GR_OS2	633.78
B4E3A8	Uncharacterized protein OS=Homo sapiens GN=SERPINB1 PE=2 SV=1			GR_OS2	246.57
Q5JP53	Tubulin beta polypeptide OS=Homo sapiens GN=TUBB PE=3 SV=1			GR_OS2	570.69
O95630	STAM-binding protein OS=Homo sapiens GN=STAMPB PE=1 SV=1			GR_OS2	61.64
P61158	Actin-related protein 3 OS=Homo sapiens GN=ACTR3 PE=1 SV=3			GR_OS2	42.72
A8K8L7	Calcium binding protein 39, isoform CRA_a OS=Homo sapiens GN=CAB39 PE=2 SV=1			GR_OS2	98.68
P18206	Vinculin OS=Homo sapiens GN=VCL PE=1 SV=4			GR_OS2	118.89
D7RX09	Desmoplakin la OS=Homo sapiens PE=2 SV=1			GR_OS2	75.04
P43034	Platelet-activating factor acetylhydrolase IB subunit alpha OS=Homo sapiens GN=PAFAH1B1 PE=1 SV=2			GR_OS2	42.69
P02679	Fibrinogen gamma chain OS=Homo sapiens GN=FGG PE=1 SV=3			GR_OS2	89.59
O15511	Actin-related protein 2/3 complex subunit 5 OS=Homo sapiens GN=ARPC5 PE=1 SV=3			GR_OS2	40.11
O75935	Dynactin subunit 3 OS=Homo sapiens GN=DCTN3 PE=1 SV=1			GR_OS2	116.02
O43150	Arf-GAP with SH3 domain, ANK repeat and PH domain-containing protein 2 OS=Homo sapiens GN=ASAP2 PE=1 SV=3			GR_OS2	71.65
C77TP28	Blood group kell-cellano system OS=Homo sapiens GN=KEL PE=4 SV=1			GR_OS2	146.76
P05198	Eukaryotic translation initiation factor 2 subunit 1 OS=Homo sapiens GN=EIF2S1 PE=1 SV=3			GR_OS2	64.25
Q92508	Protein PIEZO1 OS=Homo sapiens GN=FAM38A PE=1 SV=4			GR_OS2	51.55
P02675	Fibrinogen beta chain OS=Homo sapiens GN=FGB PE=1 SV=2			GR_OS2	122.99
O00442	RNA 3'-terminal phosphate cyclase OS=Homo sapiens GN=RTCD1 PE=1 SV=1			GR_OS2	72.25
P61081	NEDD8-conjugating enzyme Ubc12 OS=Homo sapiens GN=UBE2M PE=1 SV=1			GR_OS2	54.91
B4DGX3	Phosphoribosylaminoimidazole-succinocarboxamide synthase OS=Homo sapiens PE=2 SV=1			GR_OS2	40.89
Q6ZMU0	Delta-aminolevulinic acid dehydratase OS=Homo sapiens PE=2 SV=1			GR_OS2	66.59
B4DFL8	cDNA FLJ59865, highly similar to WW domain-binding protein 2 OS=Homo sapiens PE=2 SV=1			GR_OS2	104.22
B2RB13	cDNA, FLJ95253, highly similar to Homo sapiens acyl-CoA synthetase long-chain family member 6(ACSL6), mRNA OS=Homo sapiens PE=2 SV=1			GR_OS2	67.62
P11172	Uridine 5'-monophosphate synthase OS=Homo sapiens GN=UMPS PE=1 SV=1			GR_OS2	84.48
Q9BS40	Latexin OS=Homo sapiens GN=LXN PE=1 SV=2			GR_OS2	36.94
Q9HDC9	Adipocyte plasma membrane-associated protein OS=Homo sapiens GN=APMAP PE=1 SV=2			GR_OS2	49.11
B2CS11	MHC class I antigen (Fragment) OS=Homo sapiens GN=HLA-B PE=3 SV=1			GR_OS2	133.73
O94905	Erlin-2 OS=Homo sapiens GN=ERLIN2 PE=1 SV=1			GR_OS2	71.77
Q53TN4	Cytochrome b reductase 1 OS=Homo sapiens GN=CYBRD1 PE=1 SV=1			GR_OS2	62.38
P29972	Aquaporin-1 OS=Homo sapiens GN=AQP1 PE=1 SV=3			GR_OS2	165.76
P30044	Peroxisomal protein 5, mitochondrial OS=Homo sapiens GN=PRDX5 PE=1 SV=4			GR_OS2	95.76
Q9Y6M5	Zinc transporter 1 OS=Homo sapiens GN=SLC30A1 PE=1 SV=3			GR_OS2	71.99
P36507	Dual specificity mitogen-activated protein kinase kinase 2 OS=Homo sapiens GN=MAP2K2 PE=1 SV=1			GR_OS2	42.79
Q59HE5	Cysteine-tRNA ligase isoform b variant (Fragment) OS=Homo sapiens PE=2 SV=1			GR_OS2	42.3
Q04656	Copper-transporting ATPase 1 OS=Homo sapiens GN=ATP7A PE=1 SV=3			GR_OS2	30.11
Q02413	Desmoglein-1 OS=Homo sapiens GN=DSG1 PE=1 SV=2			GR_OS2	103.06
P20160	Azurocidin OS=Homo sapiens GN=AZU1 PE=1 SV=3			GR_OS2	70.07
P05090	Apolipoprotein D OS=Homo sapiens GN=APOD PE=1 SV=1			GR_OS2	67.33
P51571	Translocon-associated protein subunit delta OS=Homo sapiens GN=SSR4 PE=1 SV=1			GR_OS2	61.68
B7Z3V1	cDNA FLJ60077, highly similar to Sodium/potassium-transporting ATPase alpha-1 chain (EC 3.6.3.9) (Fragment) OS=Homo sapiens PE=2 SV=1			GR_OS2	53.55
B0AZU0	cDNA, FLJ79530, highly similar to Homo sapiens O-acyltransferase (membrane bound) domain containing 2 (OACT2), mRNA OS=Homo sapiens PE=2 SV=1			GR_OS2	51.75
E7ET43	Uncharacterized protein OS=Homo sapiens GN=CEACAM1 PE=4 SV=2			GR_OS2	45.78
B2RAM2	cDNA, FLJ94999, highly similar to Homo sapiens calpain 7 (CAPN7), mRNA OS=Homo sapiens PE=2 SV=1			GR_OS2	43.71
F5H399	Uncharacterized protein OS=Homo sapiens GN=RAB2A PE=3 SV=1			GR_OS2	39.47
P01112	GTPase HRas OS=Homo sapiens GN=HRAS PE=1 SV=1			GR_OS2	54.47
Q3SYB4	SERPINB12 protein OS=Homo sapiens GN=SERPINB12 PE=2 SV=1			GR_OS2	42.57
Q96AP7	Endothelial cell-selective adhesion molecule OS=Homo sapiens GN=ESAM PE=1 SV=1			GR_OS2	40.96
B4DDV4	cDNA FLJ52530, highly similar to Tumor protein D54 OS=Homo sapiens PE=2 SV=1			GR_OS2	63.16
B4DQX2	cDNA FLJ55586, highly similar to MMS19-like protein OS=Homo sapiens PE=2 SV=1			GR_OS2	41.66

Supplemental Data 2

Sheet 5

PAA-Treated

AC	Description	Replicate 1	Score	Replicate 2	Score
P68871	Hemoglobin subunit beta OS=Homo sapiens GN=HBB PE=1 SV=2	GR_PAA1	13059.23	GR_PAA2	13628.57
Q6J127	Hemoglobin beta (Fragment) OS=Homo sapiens GN=HBB PE=2 SV=1	GR_PAA1	9911.17	GR_PAA2	10329.67
P69905	Hemoglobin subunit alpha OS=Homo sapiens GN=HBA1 PE=1 SV=2	GR_PAA1	3941.28	GR_PAA2	4490.78
Q3LR79	Hemoglobin beta (Fragment) OS=Homo sapiens GN=HBB PE=2 SV=1	GR_PAA1	11589.07	GR_PAA2	11552.47
A0N071	Delta globin OS=Homo sapiens GN=HBD PE=3 SV=1	GR_PAA1	6320.51	GR_PAA2	6215.63
P02549	Spectrin alpha chain, erythrocyte OS=Homo sapiens GN=SPTA1 PE=1 SV=5	GR_PAA1	5712.3	GR_PAA2	5066.94
P11277	Spectrin beta chain, erythrocyte OS=Homo sapiens GN=SPTB PE=1 SV=5	GR_PAA1	7828.43	GR_PAA2	7636.08
E2RVJ0	Solute carrier family 4, anion exchanger, member 1 OS=Homo sapiens GN=SLC4A1 PE=2 SV=1	GR_PAA1	3155.26	GR_PAA2	3021.19
P55072	Transitional endoplasmic reticulum ATPase OS=Homo sapiens GN=VCP PE=1 SV=4	GR_PAA1	2336.26	GR_PAA2	2045.72
P16157	Ankyrin-1 OS=Homo sapiens GN=ANK1 PE=1 SV=3	GR_PAA1	5348.03	GR_PAA2	5476.76
P60900	Proteasome subunit alpha type-6 OS=Homo sapiens GN=PSMA6 PE=1 SV=1	GR_PAA1	624.32	GR_PAA2	744.23
P69891	Hemoglobin subunit gamma-1 OS=Homo sapiens GN=HBG1 PE=1 SV=2	GR_PAA1	3938	GR_PAA2	3611.27
P07900	Heat shock protein HSP 90-alpha OS=Homo sapiens GN=HSP90AA1 PE=1 SV=5	GR_PAA1	728.98	GR_PAA2	845.97
P32119	Peroxisomal protein 2 OS=Homo sapiens GN=PRDX2 PE=1 SV=5	GR_PAA1	1719.38	GR_PAA2	1684.33
P50990	T-complex protein 1 subunit theta OS=Homo sapiens GN=CCT8 PE=1 SV=4	GR_PAA1	2062.32	GR_PAA2	2974.47
P00915	Carbonic anhydrase 1 OS=Homo sapiens GN=CA1 PE=1 SV=2	GR_PAA1	945.13	GR_PAA2	854.61
P07384	Calpain-1 catalytic subunit OS=Homo sapiens GN=CAPN1 PE=1 SV=1	GR_PAA1	1417.89	GR_PAA2	1720.41
P62826	GTP-binding nuclear protein Ran OS=Homo sapiens GN=RAN PE=1 SV=3	GR_PAA1	1428.18	GR_PAA2	1192.2
Q8WVW5	Putative uncharacterized protein (Fragment) OS=Homo sapiens PE=2 SV=1	GR_PAA1	1070.64	GR_PAA2	995.41
P04040	Catalase OS=Homo sapiens GN=CAT PE=1 SV=3	GR_PAA1	213.94	GR_PAA2	258.41
Q4LE36	ACLY variant protein (Fragment) OS=Homo sapiens GN=ACLY variant protein PE=2 SV=1	GR_PAA1	1495.02	GR_PAA2	2020.56
P21980	Protein-glutamine gamma-glutamyltransferase 2 OS=Homo sapiens GN=TGM2 PE=1 SV=2	GR_PAA1	118.51	GR_PAA2	79.98
Q06830	Peroxisomal protein 1 OS=Homo sapiens GN=PRDX1 PE=1 SV=1	GR_PAA1	1339.37	GR_PAA2	1571.91
P28066	Proteasome subunit alpha type-5 OS=Homo sapiens GN=PSMA5 PE=1 SV=3	GR_PAA1	724.98	GR_PAA2	1013.04
P25787	Proteasome subunit alpha type-2 OS=Homo sapiens GN=PSMA2 PE=1 SV=2	GR_PAA1	845.66	GR_PAA2	747.63
Q4KKX0	EPB42 protein OS=Homo sapiens GN=EPB42 PE=2 SV=1	GR_PAA1	985.95	GR_PAA2	1137.39
P04632	Calpain small subunit 1 OS=Homo sapiens GN=CAPNS1 PE=1 SV=1	GR_PAA1	832.86	GR_PAA2	803.11
O14818	Proteasome subunit alpha type-7 OS=Homo sapiens GN=PSMA7 PE=1 SV=1	GR_PAA1	417.5	GR_PAA2	329.14
P49721	Proteasome subunit beta type-2 OS=Homo sapiens GN=PSMB2 PE=1 SV=1	GR_PAA1	735.86	GR_PAA2	531.37
P27105	Erythrocyte band 7 integral membrane protein OS=Homo sapiens GN=STOM PE=1 SV=3	GR_PAA1	905.71	GR_PAA2	1246.85
P28074	Proteasome subunit beta type-5 OS=Homo sapiens GN=PSMB5 PE=1 SV=3	GR_PAA1	954.45	GR_PAA2	1186.98
P30041	Peroxisomal protein 6 OS=Homo sapiens GN=PRDX6 PE=1 SV=3	GR_PAA1	362.55	GR_PAA2	416.59
P00568	Adenylate kinase isoenzyme 1 OS=Homo sapiens GN=AK1 PE=1 SV=3	GR_PAA1	179.54	GR_PAA2	223.2
P60891	Ribose-phosphate pyrophosphokinase 1 OS=Homo sapiens GN=PRPS1 PE=1 SV=2	GR_PAA1	811.09	GR_PAA2	1008.76
P00918	Carbonic anhydrase 2 OS=Homo sapiens GN=CA2 PE=1 SV=2	GR_PAA1	306.46	GR_PAA2	280.78
Q3MIH3	Ubiquitin A-52 residue ribosomal protein fusion product 1 OS=Homo sapiens GN=UBA52 PE=2 SV=1	GR_PAA1	335.86	GR_PAA2	368.81
Q1WWM3	EPB41 protein (Fragment) OS=Homo sapiens GN=EPB41 PE=2 SV=1	GR_PAA1	129.71	GR_PAA2	84.69
E7ET08	Uncharacterized protein OS=Homo sapiens GN=HSPA8 PE=3 SV=1	GR_PAA1	637.42	GR_PAA2	867.36
Q13228	Selenium-binding protein 1 OS=Homo sapiens GN=SELENBP1 PE=1 SV=2	GR_PAA1	206.43	GR_PAA2	213.96
Q06323	Proteasome activator complex subunit 1 OS=Homo sapiens GN=PSME1 PE=1 SV=1	GR_PAA1	327.73	GR_PAA2	351.67
P07738	Bisphosphoglycerate mutase OS=Homo sapiens GN=BPGM PE=1 SV=2	GR_PAA1	271.74	GR_PAA2	275.5
P04406	Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens GN=GAPDH PE=1 SV=3	GR_PAA1	683.45	GR_PAA2	607.14
P30043	Flavin reductase OS=Homo sapiens GN=BLVRB PE=1 SV=3	GR_PAA1	348.95	GR_PAA2	619.71
P28072	Proteasome subunit beta type-6 OS=Homo sapiens GN=PSMB6 PE=1 SV=4	GR_PAA1	249.54	GR_PAA2	279.53
Q5TDH0	Protein DD11 homolog 2 OS=Homo sapiens GN=DD12 PE=1 SV=1	GR_PAA1	87.47		
P07195	L-lactate dehydrogenase B chain OS=Homo sapiens GN=LDHB PE=1 SV=2	GR_PAA1	403.06	GR_PAA2	465.69
P50395	Rab GDP dissociation inhibitor beta OS=Homo sapiens GN=GDI2 PE=1 SV=2	GR_PAA1	34.24	GR_PAA2	38.91
P05109	Protein S100-A8 OS=Homo sapiens GN=S100A8 PE=1 SV=1	GR_PAA1	255.96	GR_PAA2	200.3
P00492	Hypoxanthine-guanine phosphoribosyltransferase OS=Homo sapiens GN=HPRT1 PE=1 SV=2	GR_PAA1	164.28	GR_PAA2	146.17
Q9NKT5	Ogg-like ATPase 1 OS=Homo sapiens GN=OLA1 PE=1 SV=2	GR_PAA1	287.58	GR_PAA2	247.41
P00352	Retinal dehydrogenase 1 OS=Homo sapiens GN=ALDH1A1 PE=1 SV=2	GR_PAA1	43.59	GR_PAA2	67.26
P22314	Ubiquitin-like modifier-activating enzyme 1 OS=Homo sapiens GN=UBA1 PE=1 SV=3	GR_PAA1	61.94		
P24666	Low molecular weight phosphotyrosine protein phosphatase OS=Homo sapiens GN=ACP1 PE=1 SV=3	GR_PAA1	308.3	GR_PAA2	385.31
P68402	Platelet-activating factor acetylhydrolase IB subunit beta OS=Homo sapiens GN=PAFAH1B2 PE=1 SV=1	GR_PAA1	121.48	GR_PAA2	195.21
B2RMN7	Spectrin, beta, erythrocytic OS=Homo sapiens GN=SPTB PE=2 SV=1	GR_PAA1	7726.47	GR_PAA2	7591.1
P35579	Myosin-9 OS=Homo sapiens GN=MYH9 PE=1 SV=4	GR_PAA1	1238.52	GR_PAA2	1388.15
Q00610	Clathrin heavy chain 1 OS=Homo sapiens GN=CLTC PE=1 SV=5	GR_PAA1	141.57	GR_PAA2	187.42
Q5T4S7	E3 ubiquitin-protein ligase UBR4 OS=Homo sapiens GN=UBR4 PE=1 SV=1	GR_PAA1	3698.35	GR_PAA2	3665.73
P78371	T-complex protein 1 subunit beta OS=Homo sapiens GN=CCT2 PE=1 SV=4	GR_PAA1	4338.61	GR_PAA2	5535.42
P49368	T-complex protein 1 subunit gamma OS=Homo sapiens GN=CCT3 PE=1 SV=4	GR_PAA1	4279.09	GR_PAA2	3954.98
Q99832	T-complex protein 1 subunit eta OS=Homo sapiens GN=CCT7 PE=1 SV=2	GR_PAA1	2811.16	GR_PAA2	3720.19
O00410	Importin-5 OS=Homo sapiens GN=IPO5 PE=1 SV=4	GR_PAA1	1161.68	GR_PAA2	1282.24
Q13200	26S proteasome non-ATPase regulatory subunit 2 OS=Homo sapiens GN=PSMD2 PE=1 SV=3	GR_PAA1	1363.16	GR_PAA2	1197.92
Q93008	Probable ubiquitin carboxyl-terminal hydrolase FAF-X OS=Homo sapiens GN=USP9X PE=1 SV=3	GR_PAA1	779.47	GR_PAA2	875.06
Q86VP6	Cullin-associated NEDD8-dissociated protein 1 OS=Homo sapiens GN=CAND1 PE=1 SV=2	GR_PAA1	2165.11	GR_PAA2	1874.23
A8K2X8	cDNA FLJ78433, highly similar to Homo sapiens chaperonin containing TCP1, subunit 5 (epsilon) (CCT5), mRNA OS=Homo sapiens PE=2 SV=1	GR_PAA1	1575.79	GR_PAA2	1656.2
Q4LE45	MYH10 variant protein (Fragment) OS=Homo sapiens GN=MYH10 variant protein PE=2 SV=1	GR_PAA1	416.63	GR_PAA2	539.81
Q16531	DNA damage-binding protein 1 OS=Homo sapiens GN=DDB1 PE=1 SV=1	GR_PAA1	926.58	GR_PAA2	894.26
P21333	Filamin-A OS=Homo sapiens GN=FLNA PE=1 SV=4	GR_PAA1	2004.31	GR_PAA2	1994
P50991	T-complex protein 1 subunit delta OS=Homo sapiens GN=CCT4 PE=1 SV=4	GR_PAA1	2255.13	GR_PAA2	2560.83
O14724	Beta-spectrin (Fragment) OS=Homo sapiens GN=HSPTB1 PE=2 SV=1	GR_PAA1	884.17	GR_PAA2	875.2
Q99460	26S proteasome non-ATPase regulatory subunit 1 OS=Homo sapiens GN=PSMD1 PE=1 SV=2	GR_PAA1	2484.64	GR_PAA2	2015.18
O00231	26S proteasome non-ATPase regulatory subunit 11 OS=Homo sapiens GN=PSMD11 PE=1 SV=3	GR_PAA1	2008.42	GR_PAA2	1411.12
B7Z815	Ubiquitin carboxyl-terminal hydrolase OS=Homo sapiens PE=2 SV=1	GR_PAA1	94.97	GR_PAA2	118.55
P40227	T-complex protein 1 subunit zeta OS=Homo sapiens GN=CCT6A PE=1 SV=3	GR_PAA1	1862.25	GR_PAA2	1803.15
Q14974	Importin subunit beta-1 OS=Homo sapiens GN=KPNA1 PE=1 SV=2	GR_PAA1	281.21	GR_PAA2	356.58

Q14C86	GTPase-activating protein and VPS9 domain-containing protein 1 OS=Homo sapiens GN=GAPVD1 PE=1 SV=2	GR_PAA1	1290.7	GR_PAA2	1182.38
P17987	T-complex protein 1 subunit alpha OS=Homo sapiens GN=TCP1 PE=1 SV=1	GR_PAA1	1697.7	GR_PAA2	2095.12
P17858	6-phosphofructokinase, liver type OS=Homo sapiens GN=PFKL PE=1 SV=6	GR_PAA1	2088.96	GR_PAA2	2081.38
Q9Y230	RuvB-like 2 OS=Homo sapiens GN=RUVBL2 PE=1 SV=3	GR_PAA1	2124.71	GR_PAA2	1564.84
P49720	Proteasome subunit beta type-3 OS=Homo sapiens GN=PSMB3 PE=1 SV=2	GR_PAA1	1302.09	GR_PAA2	824.53
Q0P512	Solute carrier family 2 (Facilitated glucose transporter), member 1 OS=Homo sapiens GN=SLC2A1 PE=2 SV=1	GR_PAA1	588.34	GR_PAA2	627.16
Q5XPI4	E3 ubiquitin-protein ligase RNF123 OS=Homo sapiens GN=RNF123 PE=1 SV=1	GR_PAA1	1225.22	GR_PAA2	845.39
Q95373	Importin-7 OS=Homo sapiens GN=IPO7 PE=1 SV=1	GR_PAA1	1769.77	GR_PAA2	1521.64
Q7Z6Z7	E3 ubiquitin-protein ligase HUWE1 OS=Homo sapiens GN=HUWE1 PE=1 SV=3	GR_PAA1	1529.36	GR_PAA2	1182.27
P17980	26S protease regulatory subunit 6A OS=Homo sapiens GN=PSMC3 PE=1 SV=3	GR_PAA1	1354.68	GR_PAA2	1432.92
P62195	26S protease regulatory subunit 8 OS=Homo sapiens GN=PSMC5 PE=1 SV=1	GR_PAA1	1653.82	GR_PAA2	1601.18
Q14254	Flotillin-2 OS=Homo sapiens GN=LOT2 PE=1 SV=2	GR_PAA1	318.57	GR_PAA2	278.7
Q9Y265	RuvB-like 1 OS=Homo sapiens GN=RUVBL1 PE=1 SV=1	GR_PAA1	496.17	GR_PAA2	609.23
P68032	Actin, alpha cardiac muscle 1 OS=Homo sapiens GN=ACTC1 PE=1 SV=1	GR_PAA1	475.46	GR_PAA2	448.76
Q9Y315	Putative deoxyribose-phosphate aldolase OS=Homo sapiens GN=DERA PE=1 SV=2	GR_PAA1	51.24		
P61163	Alpha-centractin OS=Homo sapiens GN=ACTR1A PE=1 SV=1	GR_PAA1	711.58	GR_PAA2	982.85
Q92905	COP9 signalosome complex subunit 5 OS=Homo sapiens GN=COPS5 PE=1 SV=4	GR_PAA1	788	GR_PAA2	854.02
Q9Y6E3	HSPC027 OS=Homo sapiens PE=2 SV=1	GR_PAA1	1309.81	GR_PAA2	1575.25
Q9BT78	COP9 signalosome complex subunit 4 OS=Homo sapiens GN=COPS4 PE=1 SV=1	GR_PAA1	855.81	GR_PAA2	977.12
P35998	26S protease regulatory subunit 7 OS=Homo sapiens GN=PSMC2 PE=1 SV=3	GR_PAA1	995.87	GR_PAA2	602.02
A7E2Y5	DnaJ (Hsp40) homolog, subfamily C, member 13 OS=Homo sapiens GN=DNAJC13 PE=2 SV=1	GR_PAA1	1045.23	GR_PAA2	1134.92
E1P646	Adaptor-related protein complex 2, beta 1 subunit, isoform CRA_d OS=Homo sapiens GN=AP2B1 PE=4 SV=1	GR_PAA1	1104.69	GR_PAA2	994.14
Q15008	26S proteasome non-ATPase regulatory subunit 6 OS=Homo sapiens GN=PSMD6 PE=1 SV=1	GR_PAA1	1392.07	GR_PAA2	1075.12
A8K781	cDNA FLJ75299, highly similar to Xenopus laevis proteasome (prosome, macropain) 26S subunit, ATPase 3, mRNA OS=Homo sapiens PE=2 SV=1	GR_PAA1	1108.8		
P20618	Proteasome subunit beta type-1 OS=Homo sapiens GN=PSMB1 PE=1 SV=2	GR_PAA1	1059.87	GR_PAA2	795.05
P05164	Myeloperoxidase OS=Homo sapiens GN=MPO PE=1 SV=1	GR_PAA1	891.57	GR_PAA2	931.75
Q9C0C9	Ubiquitin-conjugating enzyme E2 O OS=Homo sapiens GN=UBE2O PE=1 SV=3	GR_PAA1	854.35	GR_PAA2	757.63
P37840	Alpha-synuclein OS=Homo sapiens GN=SNCA PE=1 SV=1	GR_PAA1	412.71	GR_PAA2	438.22
P28070	Proteasome subunit beta type-4 OS=Homo sapiens GN=PSMB4 PE=1 SV=4	GR_PAA1	1066.49	GR_PAA2	1319.41
O00232	26S proteasome non-ATPase regulatory subunit 12 OS=Homo sapiens GN=PSMD12 PE=1 SV=3	GR_PAA1	1080.35	GR_PAA2	1259.73
E9PCQ3	Ubiquitin carboxyl-terminal hydrolase OS=Homo sapiens GN=USP15 PE=3 SV=2	GR_PAA1	780.6	GR_PAA2	709
Q43681	ATPase ASNA1 OS=Homo sapiens GN=ASNA1 PE=1 SV=2	GR_PAA1	131.16	GR_PAA2	41.49
Q13616	Cullin-1 OS=Homo sapiens GN=CUL1 PE=1 SV=2	GR_PAA1	1053.12	GR_PAA2	986.48
B4DZV5	cDNA FLJ58820, highly similar to 55 kDa erythrocyte membrane protein (p55) OS=Homo sapiens PE=2 SV=1	GR_PAA1	720.83	GR_PAA2	586.1
Q2Q9H2	Glucose-6-phosphate 1-dehydrogenase (Fragment) OS=Homo sapiens GN=G6PD PE=2 SV=1	GR_PAA1	486.1	GR_PAA2	449.69
P25786	Proteasome subunit alpha type-1 OS=Homo sapiens GN=PSMA1 PE=1 SV=1	GR_PAA1	461.39	GR_PAA2	335.94
Q2TUW9	Lactoferrin OS=Homo sapiens PE=2 SV=1	GR_PAA1	1444.32	GR_PAA2	1580.79
P46459	Vesicle-fusing ATPase OS=Homo sapiens GN=NSF PE=1 SV=3	GR_PAA1	772.74	GR_PAA2	748.1
Q709C8	Vacuolar protein sorting-associated protein 13C OS=Homo sapiens GN=VPS13C PE=1 SV=1	GR_PAA1	795.54	GR_PAA2	698.76
P62191	26S protease regulatory subunit 4 OS=Homo sapiens GN=PSMC1 PE=1 SV=1	GR_PAA1	517.11	GR_PAA2	242.47
Q16401	26S proteasome non-ATPase regulatory subunit 5 OS=Homo sapiens GN=PSMD5 PE=1 SV=3	GR_PAA1	1110.69	GR_PAA2	929.16
O00487	26S proteasome non-ATPase regulatory subunit 14 OS=Homo sapiens GN=PSMD14 PE=1 SV=1	GR_PAA1	496.12	GR_PAA2	463.71
Q08211	ATP-dependent RNA helicase A OS=Homo sapiens GN=DHX9 PE=1 SV=4	GR_PAA1	634.98	GR_PAA2	901.42
P68371	Tubulin beta-2C chain OS=Homo sapiens GN=TUBB2C PE=1 SV=1	GR_PAA1	827.26	GR_PAA2	893.07
Q9UL46	Proteasome activator complex subunit 2 OS=Homo sapiens GN=PSME2 PE=1 SV=4	GR_PAA1	879.83	GR_PAA2	1216.96
Q4W4Y1	Dopamine receptor interacting protein 4 OS=Homo sapiens GN=DRIP4 PE=2 SV=1	GR_PAA1	117.23	GR_PAA2	37.47
Q13098	COP9 signalosome complex subunit 1 OS=Homo sapiens GN=GPS1 PE=1 SV=4	GR_PAA1	477.67	GR_PAA2	357.17
O75955	Flotillin-1 OS=Homo sapiens GN=LOT1 PE=1 SV=3	GR_PAA1	99.9	GR_PAA2	77
Q14203	Dynactin subunit 1 OS=Homo sapiens GN=DCTN1 PE=1 SV=3	GR_PAA1	149.71	GR_PAA2	39.36
P43686	26S protease regulatory subunit 6B OS=Homo sapiens GN=PSMC4 PE=1 SV=2	GR_PAA1	267.72	GR_PAA2	449.57
Q96P70	Importin-9 OS=Homo sapiens GN=IPO9 PE=1 SV=3	GR_PAA1	87.84	GR_PAA2	175.64
P51665	26S proteasome non-ATPase regulatory subunit 7 OS=Homo sapiens GN=PSMD7 PE=1 SV=2	GR_PAA1	226.26	GR_PAA2	155.7
Q9UPU5	Ubiquitin carboxyl-terminal hydrolase 24 OS=Homo sapiens GN=USP24 PE=1 SV=3	GR_PAA1	382.61	GR_PAA2	439.08
P25789	Proteasome subunit alpha type-4 OS=Homo sapiens GN=PSMA4 PE=1 SV=1	GR_PAA1	139.16	GR_PAA2	105.35
P25788	Proteasome subunit alpha type-3 OS=Homo sapiens GN=PSMA3 PE=1 SV=2	GR_PAA1	425.9	GR_PAA2	598.37
Q10567	AP-1 complex subunit beta-1 OS=Homo sapiens GN=AP1B1 PE=1 SV=2	GR_PAA1	703.47	GR_PAA2	537.02
P48426	Phosphatidylinositol-5-phosphate 4-kinase type-2 alpha OS=Homo sapiens GN=PIP4K2A PE=1 SV=2	GR_PAA1	1177.27	GR_PAA2	599.34
P61201	COP9 signalosome complex subunit 2 OS=Homo sapiens GN=COPS2 PE=1 SV=1	GR_PAA1	167.17	GR_PAA2	94.44
P68366	Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A PE=1 SV=1	GR_PAA1	457.62	GR_PAA2	689.96
Q5T447	E3 ubiquitin-protein ligase HECTD3 OS=Homo sapiens GN=HECTD3 PE=1 SV=1	GR_PAA1	256.23	GR_PAA2	91.73
P62333	26S protease regulatory subunit 10B OS=Homo sapiens GN=PSMC6 PE=1 SV=1	GR_PAA1	716.63	GR_PAA2	675.64
Q15435	Protein phosphatase 1 regulatory subunit 7 OS=Homo sapiens GN=PPP1R7 PE=1 SV=1	GR_PAA1	560.05	GR_PAA2	475.2
P48556	26S proteasome non-ATPase regulatory subunit 8 OS=Homo sapiens GN=PSMD8 PE=1 SV=2	GR_PAA1	266.94	GR_PAA2	626.81
P84077	ADP-ribosylation factor 1 OS=Homo sapiens GN=ARF1 PE=1 SV=2	GR_PAA1	713	GR_PAA2	616.75
Q9GZP4	PITH domain-containing protein 1 OS=Homo sapiens GN=PITHD1 PE=1 SV=1	GR_PAA1	63.61	GR_PAA2	104.68
B2R514	cDNA, FLJ92300, Homo sapiens COP9 subunit 6 (MOV34 homolog, 34 kD) (COPS6), mRNA OS=Homo sapiens PE=2 SV=1	GR_PAA1	376.73	GR_PAA2	394.22
B2R8N1	cDNA, FLJ93976, highly similar to Homo sapiens COP9 homolog (COP9), mRNA OS=Homo sapiens PE=2 SV=1	GR_PAA1	296.58	GR_PAA2	265.33
Q2TU77	Aging-associated protein 2 OS=Homo sapiens GN=AAG2 PE=2 SV=1	GR_PAA1	168.82	GR_PAA2	197.21
P60842	Eukaryotic initiation factor 4A-I OS=Homo sapiens GN=EIF4A1 PE=1 SV=1	GR_PAA1	305.83	GR_PAA2	168.9
P36959	GMP reductase 1 OS=Homo sapiens GN=GMPPR PE=1 SV=1	GR_PAA1	314.67	GR_PAA2	644.42
P08514	Integrin alpha-11b OS=Homo sapiens GN=ITGA2B PE=1 SV=3	GR_PAA1	251.64	GR_PAA2	262.03
Q13618	Cullin-3 OS=Homo sapiens GN=CUL3 PE=1 SV=2	GR_PAA1	223.72	GR_PAA2	217.25
P02647	Apolipoprotein A-I OS=Homo sapiens GN=APOA1 PE=1 SV=1	GR_PAA1	505.62	GR_PAA2	449.3

P52907	F-actin-capping protein subunit alpha-1 OS=Homo sapiens GN=CAPZA1 PE=1 SV=3	GR_PAA1	174.35	GR_PAA2	140.31
P08311	Cathepsin G OS=Homo sapiens GN=CTSG PE=1 SV=2	GR_PAA1	585.58	GR_PAA2	502.83
P45974	Ubiquitin carboxyl-terminal hydrolase 5 OS=Homo sapiens GN=USP5 PE=1 SV=2	GR_PAA1	48.23		
P19105	Myosin regulatory light chain 12A OS=Homo sapiens GN=MYL12A PE=1 SV=2	GR_PAA1	136.68	GR_PAA2	183.41
B2R4M6	cDNA, FLJ92148, highly similar to Homo sapiens S100 calcium binding protein A9 (calgranulin B) (S100A9), mRNA OS=Homo sapiens PE=4 SV=1	GR_PAA1	410.06	GR_PAA2	463.6
P62495	Eukaryotic peptide chain release factor subunit 1 OS=Homo sapiens GN=ETF1 PE=1 SV=3	GR_PAA1	288.09	GR_PAA2	449.05
B2R7T8	cDNA, FLJ93598, highly similar to Homo sapiens capping protein (actin filament) muscle Z-line, beta (CAPZB), mRNA OS=Homo sapiens PE=2 SV=1	GR_PAA1	320.92	GR_PAA2	375.27
Q9H0U4	Ras-related protein Rab-1B OS=Homo sapiens GN=RAB1B PE=1 SV=1	GR_PAA1	280.62	GR_PAA2	366.95
B4DH02	cDNA FLJ50510, highly similar to Heat shock 70 kDa protein 4 OS=Homo sapiens PE=2 SV=1	GR_PAA1	493.87	GR_PAA2	338.73
B4DLQ1	Uncharacterized protein OS=Homo sapiens GN=ALDH16A1 PE=2 SV=1	GR_PAA1	168.55	GR_PAA2	66.85
Q9UN52	COP9 signalosome complex subunit 3 OS=Homo sapiens GN=COPS3 PE=1 SV=3	GR_PAA1	626.94	GR_PAA2	454.3
P35611	Alpha-adducin OS=Homo sapiens GN=ADD1 PE=1 SV=2	GR_PAA1	475.02	GR_PAA2	383.31
Q969U7	Proteasome assembly chaperone 2 OS=Homo sapiens GN=PSMG2 PE=1 SV=1	GR_PAA1	192.76	GR_PAA2	86.19
Q13561	Dynactin subunit 2 OS=Homo sapiens GN=DCTN2 PE=1 SV=4	GR_PAA1	304.32	GR_PAA2	224.83
P27708	CAD protein OS=Homo sapiens GN=CAD PE=1 SV=3	GR_PAA1	219.74	GR_PAA2	146.36
P11021	78 kDa glucose-regulated protein OS=Homo sapiens GN=HSPA5 PE=1 SV=2	GR_PAA1	117.96		
P11215	Integrin alpha-M OS=Homo sapiens GN=ITGAM PE=1 SV=2	GR_PAA1	391.82	GR_PAA2	284.91
P35612	Beta-adducin OS=Homo sapiens GN=ADD2 PE=1 SV=3	GR_PAA1	281.12	GR_PAA2	266.07
P38606	V-type proton ATPase catalytic subunit A OS=Homo sapiens GN=ATP6V1A PE=1 SV=2	GR_PAA1	438.74	GR_PAA2	220.89
A8K510	Heat shock 70kDa protein 1A OS=Homo sapiens GN=HSPA1A PE=2 SV=1	GR_PAA1	232.64		
P55036	26S proteasome non-ATPase regulatory subunit 4 OS=Homo sapiens GN=PSMD4 PE=1 SV=1	GR_PAA1	583.12	GR_PAA2	430.6
O43149	Zinc finger ZZ-type and EF-hand domain-containing protein 1 OS=Homo sapiens GN=ZZEF1 PE=1 SV=6	GR_PAA1	53.27	GR_PAA2	56.1
Q99598	Translin-associated protein X OS=Homo sapiens GN=TSNAX PE=1 SV=1	GR_PAA1	118.28		
B7Z507	cDNA FLJ51036, highly similar to Matrix metalloproteinase-9 (EC3.4.24.35) OS=Homo sapiens PE=2 SV=1	GR_PAA1	319.4	GR_PAA2	399.24
P12829	Myosin light chain 4 OS=Homo sapiens GN=MYL4 PE=1 SV=3	GR_PAA1	491.54	GR_PAA2	548.44
P62834	Ras-related protein Rap-1A OS=Homo sapiens GN=RAP1A PE=1 SV=1	GR_PAA1	379.12	GR_PAA2	484.4
B5MDH8	Uncharacterized protein OS=Homo sapiens GN=WDR91 PE=4 SV=2	GR_PAA1	120.2	GR_PAA2	65.93
D8MJ82	Kell blood group antigen OS=Homo sapiens GN=KEL PE=2 SV=1	GR_PAA1	139.64	GR_PAA2	101.95
	Proteasome (Prosome, macropain) 26S subunit, non-ATPase, 10 OS=Homo sapiens GN=PSMD10 PE=4 SV=1	GR_PAA1	116.03	GR_PAA2	116.07
B1AJY5	Neutrophil elastase OS=Homo sapiens GN=ELANE PE=1 SV=1	GR_PAA1	87.19	GR_PAA2	143.36
P08246	Importin subunit alpha-4 OS=Homo sapiens GN=KPNA4 PE=1 SV=1	GR_PAA1	263.06	GR_PAA2	121.83
O00629	COP9 signalosome complex subunit 7b OS=Homo sapiens GN=COPS7B PE=1 SV=1	GR_PAA1	326.95	GR_PAA2	214.12
Q9H9Q2	Serine/threonine-protein kinase OSR1 OS=Homo sapiens GN=OSR1 PE=1 SV=1	GR_PAA1	215.79	GR_PAA2	179.36
O95747	Chromosome 9 open reading frame 19, isoform CRA_a (Fragment) OS=Homo sapiens GN=C9orf19 PE=4 SV=1	GR_PAA1	152.64	GR_PAA2	270.67
D3DRP5	Transferrin receptor protein 1 OS=Homo sapiens GN=TFRC PE=1 SV=2	GR_PAA1	192.91	GR_PAA2	242.3
P02786	cDNA FLJ57531, highly similar to DCN1-like protein 1 OS=Homo sapiens PE=2 SV=1	GR_PAA1	365.16	GR_PAA2	194.88
B4DM76	cDNA FLJ55022, highly similar to F-box only protein 7 OS=Homo sapiens PE=2 SV=1	GR_PAA1	172.67	GR_PAA2	149.63
B4DWX5	Neutral alpha-glucosidase AB OS=Homo sapiens GN=GANAB PE=1 SV=3	GR_PAA1	161.33	GR_PAA2	99.59
Q14697	Rab-interacting lysosomal protein OS=Homo sapiens GN=RILP PE=1 SV=1	GR_PAA1	65.87	GR_PAA2	50.21
Q96NA2	Phosphatidate phosphatase LPIN2 OS=Homo sapiens GN=LPIN2 PE=1 SV=1	GR_PAA1	56.28		
Q92539	Myeloblastin OS=Homo sapiens GN=PRTN3 PE=1 SV=3	GR_PAA1	264.93	GR_PAA2	198.59
P24158	Protein phosphatase methyltransferase 1 OS=Homo sapiens GN=PPME1 PE=1 SV=3	GR_PAA1	190.92	GR_PAA2	129.61
Q9Y570	UDP-glucose:glycoprotein glucosyltransferase 1 OS=Homo sapiens GN=UGGT1 PE=1 SV=3	GR_PAA1	46.59	GR_PAA2	48.69
Q9NYU2	Uncharacterized protein OS=Homo sapiens GN=COPS7A PE=4 SV=1	GR_PAA1	446.81	GR_PAA2	404.01
F5GYF7	cDNA FLJ54776, highly similar to Cell division control protein 42 homolog OS=Homo sapiens PE=2 SV=1	GR_PAA1	121.18	GR_PAA2	233.58
B4E1U9	Ras-related protein Rap-2b OS=Homo sapiens GN=RAP2B PE=1 SV=1	GR_PAA1	210.4	GR_PAA2	57.9
P61225	Uncharacterized protein OS=Homo sapiens GN=SLC2A3 PE=3 SV=1	GR_PAA1	127.19	GR_PAA2	147.47
F5H2H8	CTP synthase 1 OS=Homo sapiens GN=CTPS PE=1 SV=2	GR_PAA1	264.27	GR_PAA2	172.51
P17812	Ribonuclease inhibitor OS=Homo sapiens GN=RNH1 PE=1 SV=2	GR_PAA1	160.17	GR_PAA2	109.63
P13489	Proteasome inhibitor PI31 subunit OS=Homo sapiens GN=PSMF1 PE=1 SV=2	GR_PAA1	60.26	GR_PAA2	86.68
Q92530	Pyroline-5-carboxylate reductase OS=Homo sapiens GN=PYCRL PE=3 SV=1	GR_PAA1	156.46	GR_PAA2	180.67
D3DWK4	cDNA, FLJ93494, highly similar to Homo sapiens annexin A7 (ANXA7), transcript variant 1, mRNA OS=Homo sapiens PE=2 SV=1	GR_PAA1	68.43	GR_PAA2	169.97
B2R7L2	Proteasomal ATPase-associated factor 1 OS=Homo sapiens GN=PAAF1 PE=1 SV=2	GR_PAA1	129.75	GR_PAA2	111.47
Q9BRP4	cDNA FLJ16143 fis, clone BRAMY2038516, highly similar to Protein disulfide-isomerase A6 (EC 5.3.4.1) OS=Homo sapiens PE=2 SV=1	GR_PAA1	41.97	GR_PAA2	73.13
B3KY95	cDNA FLJ41902 fis, clone PEBLM2004666, highly similar to WD repeat protein 81 OS=Homo sapiens PE=2 SV=1	GR_PAA1	145.88	GR_PAA2	94.72
B3KW16	C2 domain-containing protein 2-like OS=Homo sapiens GN=C2CD2L PE=1 SV=3	GR_PAA1	69.03	GR_PAA2	215.58
O14523	Uncharacterized protein OS=Homo sapiens GN=NACA PE=4 SV=1	GR_PAA1	99.93	GR_PAA2	68.07
E9PAV3	cDNA FLJ60267, highly similar to Homo sapiens reticulon 3 (RTN3), transcript variant 2, mRNA OS=Homo sapiens PE=2 SV=1	GR_PAA1	57.14	GR_PAA2	54.12
B7Z3E3	Ribosomal protein P0 variant (Fragment) OS=Homo sapiens PE=2 SV=1	GR_PAA1	178.05	GR_PAA2	214.49
Q53HW2	Acetylcholinesterase OS=Homo sapiens GN=ACHE PE=1 SV=1	GR_PAA1	67.96		
P22303	Neutral cholesterol ester hydrolase 1 OS=Homo sapiens GN=NCEH1 PE=1 SV=3	GR_PAA1	103.69	GR_PAA2	194.77
Q6PIU2	cDNA FLJ54552, highly similar to Heterogeneous nuclear ribonucleoprotein K OS=Homo sapiens PE=2 SV=1	GR_PAA1	90.77	GR_PAA2	152.3
B4DUQ1	E3 ubiquitin-protein ligase KCMF1 OS=Homo sapiens GN=KCMF1 PE=1 SV=2	GR_PAA1	70.82	GR_PAA2	97.04
Q9P0J7	V-type proton ATPase subunit E 1 OS=Homo sapiens GN=ATP6V1E1 PE=1 SV=1	GR_PAA1	59.55		
P36543	Fructose-bisphosphate aldolase A OS=Homo sapiens GN=ALDOA PE=1 SV=2	GR_PAA1	67.73	GR_PAA2	68.96
P40475	AP-2 complex subunit alpha-1 OS=Homo sapiens GN=AP2A1 PE=1 SV=3	GR_PAA1	998.44	GR_PAA2	1046.14
Q95782	Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1	GR_PAA1	819.12	GR_PAA2	859.08
P68363	Tropomodulin-1 OS=Homo sapiens GN=TMOD1 PE=1 SV=1	GR_PAA1	357.03	GR_PAA2	545.85
P28289	Fructosamine-3-kinase OS=Homo sapiens GN=FN3K PE=1 SV=1	GR_PAA1	723.47	GR_PAA2	529.17
Q9H479	Ras-related protein Rab-5C OS=Homo sapiens GN=RAB5C PE=1 SV=2	GR_PAA1	275.02	GR_PAA2	133.06
P51148	Synembryn-A OS=Homo sapiens GN=RIC8A PE=1 SV=3	GR_PAA1	126.64	GR_PAA2	109.66
Q9NPQ8					

B4DMP4	cDNA FLJ53136, highly similar to Homo sapiens Vac14 homolog (VAC14), mRNA OS=Homo sapiens PE=2 SV=1	GR_PAA1	140.53	GR_PAA2	168.12
P63000	Ras-related C3 botulinum toxin substrate 1 OS=Homo sapiens GN=RAC1 PE=1 SV=1	GR_PAA1	339.02	GR_PAA2	190.7
P48507	Glutamate-cysteine ligase regulatory subunit OS=Homo sapiens GN=GCLM PE=1 SV=1	GR_PAA1	80.32	GR_PAA2	126.73
Q2TAZ0	Autophagy-related protein 2 homolog A OS=Homo sapiens GN=ATG2A PE=1 SV=3	GR_PAA1	133.26	GR_PAA2	171.42
Q5U0P9	Purine-rich element binding protein A OS=Homo sapiens PE=2 SV=1	GR_PAA1	99.26	GR_PAA2	88.07
P23528	Cofilin-1 OS=Homo sapiens GN=CFL1 PE=1 SV=3	GR_PAA1	151.78	GR_PAA2	57.42
P04792	Heat shock protein beta-1 OS=Homo sapiens GN=HSPB1 PE=1 SV=2	GR_PAA1	46.42	GR_PAA2	33.33
O14618	Copper chaperone for superoxide dismutase OS=Homo sapiens GN=CCS PE=1 SV=1	GR_PAA1	88.89		
P29401	Transketolase OS=Homo sapiens GN=TKT PE=1 SV=3	GR_PAA1	667.05	GR_PAA2	956.03
B2RD79	Ubiquitin carboxyl-terminal hydrolase OS=Homo sapiens PE=2 SV=1	GR_PAA1	1293.46	GR_PAA2	942.2
P00558	Phosphoglycerate kinase 1 OS=Homo sapiens GN=PGK1 PE=1 SV=3	GR_PAA1	212.5	GR_PAA2	370.12
P31948	Stress-induced-phosphoprotein 1 OS=Homo sapiens GN=STIP1 PE=1 SV=1	GR_PAA1	224.41	GR_PAA2	336.66
P61088	Ubiquitin-conjugating enzyme E2 N OS=Homo sapiens GN=UBE2N PE=1 SV=1	GR_PAA1	34.78		
Q6XQN6	Nicotinate phosphoribosyltransferase OS=Homo sapiens GN=NAPRT1 PE=1 SV=2	GR_PAA1	54.23		
P06733	Alpha-enolase OS=Homo sapiens GN=ENO1 PE=1 SV=2	GR_PAA1	277.64	GR_PAA2	252.68
P69892	Hemoglobin subunit gamma-2 OS=Homo sapiens GN=HBG2 PE=1 SV=2	GR_PAA1	3828	GR_PAA2	3758.77
E9PEQ4	Uncharacterized protein OS=Homo sapiens GN=DNM2 PE=3 SV=1	GR_PAA1	1629.83	GR_PAA2	2034.62
Q9Y490	Talin-1 OS=Homo sapiens GN=TLN1 PE=1 SV=3	GR_PAA1	1629.87	GR_PAA2	1521.26
P08237	6-phosphofructokinase, muscle type OS=Homo sapiens GN=PFKM PE=1 SV=2	GR_PAA1	922.48	GR_PAA2	1077.14
P55060	Exportin-2 OS=Homo sapiens GN=CSE1L PE=1 SV=3	GR_PAA1	52.93	GR_PAA2	58.96
F5H2F4	Uncharacterized protein OS=Homo sapiens GN=MTHFD1 PE=3 SV=1	GR_PAA1	939.14	GR_PAA2	861.82
P54577	Tyrosyl-tRNA synthetase, cytoplasmic OS=Homo sapiens GN=YARS PE=1 SV=4	GR_PAA1	614.9	GR_PAA2	307.56
Q86UX7	Fermitin family homolog 3 OS=Homo sapiens GN=FERMT3 PE=1 SV=1	GR_PAA1	810.03	GR_PAA2	842.73
Q14558	Phosphoribosyl pyrophosphate synthase-associated protein 1 OS=Homo sapiens GN=PRPSAP1 PE=1 SV=2	GR_PAA1	807.44	GR_PAA2	887.97
Q5VYK3	Proteasome-associated protein ECM29 homolog OS=Homo sapiens GN=ECM29 PE=1 SV=2	GR_PAA1	391.72	GR_PAA2	391.63
P17213	Bactericidal permeability-increasing protein OS=Homo sapiens GN=BPI PE=1 SV=4	GR_PAA1	464.81	GR_PAA2	353.42
Q01813	6-phosphofructokinase type C OS=Homo sapiens GN=PFKP PE=1 SV=2	GR_PAA1	908.37	GR_PAA2	640.69
Q99536	Synaptic vesicle membrane protein VAT-1 homolog OS=Homo sapiens GN=VAT1 PE=1 SV=2	GR_PAA1	479.23	GR_PAA2	452.55
P30740	Leukocyte elastase inhibitor OS=Homo sapiens GN=SERPINB1 PE=1 SV=1	GR_PAA1	549.4		
P41091	Eukaryotic translation initiation factor 2 subunit 3 OS=Homo sapiens GN=EIF2S3 PE=1 SV=3	GR_PAA1	564.35	GR_PAA2	739.12
P68104	Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 PE=1 SV=1	GR_PAA1	318.64	GR_PAA2	229.02
Q9NRW1	Ras-related protein Rab-6B OS=Homo sapiens GN=RAB6B PE=1 SV=1	GR_PAA1	158.77		
Q9NR46	Endophilin-B2 OS=Homo sapiens GN=SH3GLB2 PE=1 SV=1	GR_PAA1	42.37		
Q9H4M9	EH domain-containing protein 1 OS=Homo sapiens GN=EHD1 PE=1 SV=2	GR_PAA1	263.49	GR_PAA2	239.7
Q96F85	CB1 cannabinoid receptor-interacting protein 1 OS=Homo sapiens GN=CNRIP1 PE=1 SV=1	GR_PAA1	323.62	GR_PAA2	434.49
Q8WVM8	Sec1 family domain-containing protein 1 OS=Homo sapiens GN=SCFD1 PE=1 SV=4	GR_PAA1	65.28	GR_PAA2	87.44
Q96J06	Mannose-1-phosphate guanyltransferase alpha OS=Homo sapiens GN=GMPPA PE=1 SV=1	GR_PAA1	89.19	GR_PAA2	73.53
P14868	Aspartyl-tRNA synthetase, cytoplasmic OS=Homo sapiens GN=DARS PE=1 SV=2	GR_PAA1	377.14	GR_PAA2	394.07
P68036	Ubiquitin-conjugating enzyme E2 L3 OS=Homo sapiens GN=UBE2L3 PE=1 SV=1	GR_PAA1	268.77	GR_PAA2	338.67
P28838	Cytosol aminopeptidase OS=Homo sapiens GN=LAP3 PE=1 SV=3	GR_PAA1	115.36	GR_PAA2	30.77
O14980	Exportin-1 OS=Homo sapiens GN=XPO1 PE=1 SV=1	GR_PAA1	65.82		
P23743	Diacylglycerol kinase alpha OS=Homo sapiens GN=DGKA PE=1 SV=3	GR_PAA1	174.25	GR_PAA2	453.9
P51812	Ribosomal protein S6 kinase alpha-3 OS=Homo sapiens GN=RPS6KA3 PE=1 SV=1	GR_PAA1	295.38	GR_PAA2	255.12
P43490	Nicotinamide phosphoribosyltransferase OS=Homo sapiens GN=NAMPT PE=1 SV=1	GR_PAA1	533.69	GR_PAA2	432.81
P22061	Protein-L-isoaspartate(D-aspartate) O-methyltransferase OS=Homo sapiens GN=PCMT1 PE=1 SV=4	GR_PAA1	59.24	GR_PAA2	41.73
P07996	Thrombospondin-1 OS=Homo sapiens GN=THBS1 PE=1 SV=2	GR_PAA1	171.35	GR_PAA2	286.68
Q15276	Rab GTPase-binding effector protein 1 OS=Homo sapiens GN=RABEP1 PE=1 SV=2	GR_PAA1	75.12	GR_PAA2	53.73
B7ZW70	LOC727761 protein OS=Homo sapiens GN=LOC727761 PE=2 SV=1	GR_PAA1	159.98	GR_PAA2	48.97
Q13492	Phosphatidylinositol-binding clathrin assembly protein OS=Homo sapiens GN=PICALM PE=1 SV=2	GR_PAA1	419.8	GR_PAA2	438.39
O94903	Proline synthase co-transcribed bacterial homolog protein OS=Homo sapiens GN=PROSC PE=1 SV=1	GR_PAA1	268.87	GR_PAA2	347.21
P04921	Glycophorin-C OS=Homo sapiens GN=GYPC PE=1 SV=1	GR_PAA1	260.93	GR_PAA2	183.74
P61006	Ras-related protein Rab-8A OS=Homo sapiens GN=RAB8A PE=1 SV=1	GR_PAA1	110.77	GR_PAA2	158.27
P54136	Arginyl-tRNA synthetase, cytoplasmic OS=Homo sapiens GN=RARS PE=1 SV=2	GR_PAA1	199.17	GR_PAA2	124.71
Q00796	Sorbitol dehydrogenase OS=Homo sapiens GN=SORD PE=1 SV=4	GR_PAA1	104.59		
Q13057	Bifunctional coenzyme A synthase OS=Homo sapiens GN=COASY PE=1 SV=4	GR_PAA1	45.82		
B7Z5E3	L-lactate dehydrogenase OS=Homo sapiens GN=LDHA PE=2 SV=1	GR_PAA1	184.38	GR_PAA2	238.16
B9A6M6	TBC1 domain family, member 24 OS=Homo sapiens GN=TBC1D24 PE=2 SV=1	GR_PAA1	125.65	GR_PAA2	114.29
Q13404	Ubiquitin-conjugating enzyme E2 variant 1 OS=Homo sapiens GN=UBE2V1 PE=1 SV=2	GR_PAA1	53.24	GR_PAA2	83.14
O94919	Endonuclease domain-containing 1 protein OS=Homo sapiens GN=ENDOD1 PE=1 SV=2	GR_PAA1	226.2	GR_PAA2	201.94
P25685	DnaJ homolog subfamily B member 1 OS=Homo sapiens GN=DNAJB1 PE=1 SV=4	GR_PAA1	81.76	GR_PAA2	118.48
Q6B0K9	Hemoglobin subunit mu OS=Homo sapiens GN=HBM PE=2 SV=1	GR_PAA1	82.55	GR_PAA2	78.36
B4DV64	cDNA FLJ61420, highly similar to Homo sapiens olfactomedin 4 (OLFM4), mRNA OS=Homo sapiens PE=2 SV=1	GR_PAA1	200.33	GR_PAA2	69.4
Q13201	Multimerin-1 OS=Homo sapiens GN=MMRN1 PE=1 SV=3	GR_PAA1	69.29	GR_PAA2	46.11
Q9NP58	ATP-binding cassette sub-family B member 6, mitochondrial OS=Homo sapiens GN=ABCB6 PE=1 SV=1	GR_PAA1	121.24	GR_PAA2	177.93
Q15365	Poly(rC)-binding protein 1 OS=Homo sapiens GN=PCBP1 PE=1 SV=2	GR_PAA1	107.15	GR_PAA2	130.74
Q04323	UBX domain-containing protein 1 OS=Homo sapiens GN=UBXN1 PE=1 SV=2	GR_PAA1	142.12	GR_PAA2	55.45
P38919	Eukaryotic initiation factor 4A-III OS=Homo sapiens GN=EIF4A3 PE=1 SV=4	GR_PAA1	140.01		
O15400	Syntaxin-7 OS=Homo sapiens GN=STX7 PE=1 SV=4	GR_PAA1	82.23	GR_PAA2	57.47
P02671	Fibrinogen alpha chain OS=Homo sapiens GN=FGA PE=1 SV=2	GR_PAA1	53.13	GR_PAA2	127.7
P18577	Blood group Rh(CE) polypeptide OS=Homo sapiens GN=RHCE PE=1 SV=2	GR_PAA1	78.33	GR_PAA2	76.41
Q53E29	Mitogen-activated protein kinase kinase 3 isoform B variant (Fragment) OS=Homo sapiens PE=2 SV=1	GR_PAA1	166.06	GR_PAA2	66.79
Q9UN37	Vacuolar protein sorting-associated protein 4A OS=Homo sapiens GN=VPS4A PE=1 SV=1	GR_PAA1	113.04	GR_PAA2	52.69
P26447	Protein S100-A4 OS=Homo sapiens GN=S100A4 PE=1 SV=1	GR_PAA1	57.33	GR_PAA2	44.42
Q9GZS3	WD repeat-containing protein 61 OS=Homo sapiens GN=WDR61 PE=1 SV=1	GR_PAA1	87.14	GR_PAA2	42.87
Q6IPX4	RPS16 protein OS=Homo sapiens GN=RPS16 PE=2 SV=1	GR_PAA1	135.47	GR_PAA2	139.96
P40925	Malate dehydrogenase, cytoplasmic OS=Homo sapiens GN=MDH1 PE=1 SV=4	GR_PAA1	46.75	GR_PAA2	84.12
B4DME9	Uncharacterized protein OS=Homo sapiens GN=KLC4 PE=2 SV=1	GR_PAA1	53.6	GR_PAA2	84.71

O00299	Chloride intracellular channel protein 1 OS=Homo sapiens GN=CLIC1 PE=1 SV=4	GR_PAA1	47.86		
Q9UI26	Importin-11 OS=Homo sapiens GN=IPO11 PE=1 SV=1	GR_PAA1	53.28		
Q27J81	Inverted formin-2 OS=Homo sapiens GN=INF2 PE=1 SV=2	GR_PAA1	44		
P29144	Tripeptidyl-peptidase 2 OS=Homo sapiens GN=TPP2 PE=1 SV=4	GR_PAA1	141.17	GR_PAA2	65.25
B3KNN7	cDNA FLJ30049 fis, clone ADRGL1000033, highly similar to 26S proteasome non-ATPase regulatory subunit 3 OS=Homo sapiens PE=2 SV=1	GR_PAA1	1689.59	GR_PAA2	972.59
Q96RL7	Vacuolar protein sorting-associated protein 13A OS=Homo sapiens GN=VPS13A PE=1 SV=2	GR_PAA1	191.75	GR_PAA2	211.66
Q9BQA1	Methylosome protein 50 OS=Homo sapiens GN=WDR77 PE=1 SV=1	GR_PAA1	84.95	GR_PAA2	71.29
P62879	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2 OS=Homo sapiens GN=GNB2 PE=1 SV=3	GR_PAA1	125.76		
P26038	Moesin OS=Homo sapiens GN=MSN PE=1 SV=3	GR_PAA1	957.47	GR_PAA2	770.16
P49913	Cathelicidin antimicrobial peptide OS=Homo sapiens GN=CAMP PE=1 SV=1	GR_PAA1	89.18	GR_PAA2	47.81
B4DQJ8	6-phosphogluconate dehydrogenase, decarboxylating OS=Homo sapiens GN=PGD PE=2 SV=1	GR_PAA1	339.39	GR_PAA2	438.26
Q5JP53	Tubulin beta polypeptide OS=Homo sapiens GN=TUBB PE=3 SV=1	GR_PAA1	603.57	GR_PAA2	623.63
P61158	Actin-related protein 3 OS=Homo sapiens GN=ACTR3 PE=1 SV=3	GR_PAA1	435.65	GR_PAA2	399.88
A8K8L7	Calcium binding protein 39, isoform CRA_a OS=Homo sapiens GN=CAB39 PE=2 SV=1	GR_PAA1	216.85	GR_PAA2	314.31
P43034	Platelet-activating factor acetylhydrolase 1B subunit alpha OS=Homo sapiens GN=PAFAH1B1 PE=1 SV=2	GR_PAA1	186.89	GR_PAA2	132.64
P02679	Fibrinogen gamma chain OS=Homo sapiens GN=FGG PE=1 SV=3	GR_PAA1	356.92	GR_PAA2	54.23
O15511	Actin-related protein 2/3 complex subunit 5 OS=Homo sapiens GN=ARPC5 PE=1 SV=3	GR_PAA1	116.63	GR_PAA2	109.12
P05198	Eukaryotic translation initiation factor 2 subunit 1 OS=Homo sapiens GN=EIF2S1 PE=1 SV=3	GR_PAA1	101.85		
P02675	Fibrinogen beta chain OS=Homo sapiens GN=FGB PE=1 SV=2	GR_PAA1	195.22	GR_PAA2	118.7
O00442	RNA 3'-terminal phosphate cyclase OS=Homo sapiens GN=RTCD1 PE=1 SV=1	GR_PAA1	172.87	GR_PAA2	68.11
Q6ZMU0	Delta-aminolevulinic acid dehydratase OS=Homo sapiens PE=2 SV=1	GR_PAA1	49.82	GR_PAA2	50.98
P29972	Aquaporin-1 OS=Homo sapiens GN=AQP1 PE=1 SV=3	GR_PAA1	139.46		
Q14477	Hbbm fused globin protein (Fragment) OS=Homo sapiens GN=HBB PE=2 SV=1	GR_PAA1	6932.72	GR_PAA2	7658.35
P22234	Multifunctional protein ADE2 OS=Homo sapiens GN=PAICS PE=1 SV=3	GR_PAA1	642.49	GR_PAA2	706.92
P15531	Nucleoside diphosphate kinase A OS=Homo sapiens GN=NME1 PE=1 SV=1	GR_PAA1	422.62	GR_PAA2	557.41
P30566	Adenylosuccinate lyase OS=Homo sapiens GN=ADSL PE=1 SV=2	GR_PAA1	440.51	GR_PAA2	489.05
Q724W1	L-xylulose reductase OS=Homo sapiens GN=DCXR PE=1 SV=2	GR_PAA1	111.54	GR_PAA2	235.94
P30153	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform OS=Homo sapiens GN=PPP2R1A PE=1 SV=4	GR_PAA1	268.48	GR_PAA2	287.53
O14744	Protein arginine N-methyltransferase 5 OS=Homo sapiens GN=PRMT5 PE=1 SV=4	GR_PAA1	40.84	GR_PAA2	139.9
Q32Q12	Nucleoside diphosphate kinase OS=Homo sapiens GN=NME1-NME2 PE=2 SV=1	GR_PAA1	768.92	GR_PAA2	824.24
B0YJ88	Radixin OS=Homo sapiens GN=RDX PE=2 SV=1	GR_PAA1	506.5	GR_PAA2	512.2
P42025	Beta-centractin OS=Homo sapiens GN=ACTR1B PE=1 SV=1	GR_PAA1	417.87	GR_PAA2	724.55
Q6IBT1	Proteasome subunit beta type OS=Homo sapiens GN=PSMB7 PE=2 SV=1	GR_PAA1	119.11	GR_PAA2	347.85
P00387	NADH-cytochrome b5 reductase 3 OS=Homo sapiens GN=CYB5R3 PE=1 SV=3	GR_PAA1	585.08	GR_PAA2	492.74
B7Z763	Adenosine monophosphate deaminase (Isoform E), isoform CRA_a OS=Homo sapiens GN=AMPD3 PE=2 SV=1	GR_PAA1	382.1	GR_PAA2	443.13
P36915	Guanine nucleotide-binding protein-like 1 OS=Homo sapiens GN=GNL1 PE=1 SV=2	GR_PAA1	340.12	GR_PAA2	341.29
Q5U5J2	CSNK2A1 protein OS=Homo sapiens GN=CSNK2A1 PE=1 SV=1	GR_PAA1	66.49	GR_PAA2	176.74
P62158	Calmodulin OS=Homo sapiens GN=CALM1 PE=1 SV=2	GR_PAA1	138.01	GR_PAA2	85.58
P26641	Elongation factor 1-gamma OS=Homo sapiens GN=EEF1G PE=1 SV=3	GR_PAA1	56.55	GR_PAA2	81.74
Q95456	Proteasome assembly chaperone 1 OS=Homo sapiens GN=PSMG1 PE=1 SV=1	GR_PAA1	113.66	GR_PAA2	145.78
Q9UNZ2	NSFL1 cofactor p47 OS=Homo sapiens GN=NSFL1C PE=1 SV=2	GR_PAA1	295.51	GR_PAA2	326.15
P61224	Ras-related protein Rap-1b OS=Homo sapiens GN=RAP1B PE=1 SV=1	GR_PAA1	394.35	GR_PAA2	595.57
Q5JNW4	Proteasome subunit beta type OS=Homo sapiens GN=PSMB9 PE=2 SV=1	GR_PAA1	171.88	GR_PAA2	225.19
P60660	Myosin light polypeptide 6 OS=Homo sapiens GN=MYL6 PE=1 SV=2	GR_PAA1	217.8	GR_PAA2	210.87
Q9Y4G8	Rap guanine nucleotide exchange factor 2 OS=Homo sapiens GN=RAPGEF2 PE=1 SV=1	GR_PAA1	93.6	GR_PAA2	96.47
O00743	Serine/threonine-protein phosphatase 6 catalytic subunit OS=Homo sapiens GN=PPP6C PE=1 SV=1	GR_PAA1	62.98		
O43427	Acidic fibroblast growth factor intracellular-binding protein OS=Homo sapiens GN=FIBP PE=1 SV=3	GR_PAA1	64.29	GR_PAA2	104.28
Q8WW22	DnaJ homolog subfamily A member 4 OS=Homo sapiens GN=DNAJA4 PE=1 SV=1	GR_PAA1	51.79	GR_PAA2	76.98
B0U2C1	Proteasome (Prosome, macropain) subunit, beta type, 8 (Large multifunctional peptidase 7) OS=Homo sapiens GN=PSMB8 PE=4 SV=1	GR_PAA1	160.8	GR_PAA2	114.16
Q6IB22	Proteasome subunit beta type OS=Homo sapiens GN=PSMB10 PE=2 SV=1	GR_PAA1	114.67	GR_PAA2	532.69
B4DQH9	Uncharacterized protein OS=Homo sapiens GN=RANBP10 PE=2 SV=1	GR_PAA1	89.95	GR_PAA2	78.34
B2RDG9	cDNA, FLJ96603, highly similar to Homo sapiens actin-related protein 10 homolog (S. cerevisiae) (ACTR10), mRNA OS=Homo sapiens PE=2 SV=1	GR_PAA1	142.35		
Q9H2M9	Rab3 GTPase-activating protein non-catalytic subunit OS=Homo sapiens GN=RAB3GAP2 PE=1 SV=1	GR_PAA1	31.26		
Q9ULH1	Arf-GAP with SH3 domain, ANK repeat and PH domain-containing protein 1 OS=Homo sapiens GN=ASAP1 PE=1 SV=4	GR_PAA1	85.35	GR_PAA2	40.94
Q58WW2	DDB1- and CUL4-associated factor 6 OS=Homo sapiens GN=DCAF6 PE=1 SV=1	GR_PAA1	39.9		
P53680	AP-2 complex subunit sigma OS=Homo sapiens GN=AP2S1 PE=1 SV=2	GR_PAA1	142.73	GR_PAA2	115.8
B4DRN7	Uncharacterized protein OS=Homo sapiens GN=KIAA0528 PE=2 SV=1	GR_PAA1	66.64	GR_PAA2	243.08
B3KSH1	HCG1784554, isoform CRA_a OS=Homo sapiens GN=EIF3F PE=2 SV=1	GR_PAA1	167.07	GR_PAA2	218.15
E2QRC7	Uncharacterized protein OS=Homo sapiens GN=PSMG4 PE=4 SV=1	GR_PAA1	154.69	GR_PAA2	96.62
Q6FH17	ARF6 protein OS=Homo sapiens GN=ARF6 PE=2 SV=1	GR_PAA1	91.72		
Q5HYL3	Putative uncharacterized protein DKFZp686H16220 OS=Homo sapiens GN=DKFZp686H16220 PE=1 SV=1	GR_PAA1	81.85	GR_PAA2	88.07
O43488	Aflatoxin B1 aldehyde reductase member 2 OS=Homo sapiens GN=AKR7A2 PE=1 SV=3	GR_PAA1	59.1	GR_PAA2	42.36
Q13610	Periodic tryptophan protein 1 homolog OS=Homo sapiens GN=PWP1 PE=1 SV=1	GR_PAA1	63.27	GR_PAA2	79.18
P60520	Gamma-aminobutyric acid receptor-associated protein-like 2 OS=Homo sapiens GN=GABARAPL2 PE=1 SV=1	GR_PAA1	43.82		
B4DRF0	cDNA FLJ56418, highly similar to WD repeat protein 26 OS=Homo sapiens PE=2 SV=1	GR_PAA1	51.02	GR_PAA2	108.75
P08575	Receptor-type tyrosine-protein phosphatase C OS=Homo sapiens GN=PTPRC PE=1 SV=2	GR_PAA1	125.9	GR_PAA2	75.81
B3VL12	Truncated beta globin OS=Homo sapiens PE=3 SV=1	GR_PAA1	4312.48	GR_PAA2	4634.92
Q96CW1	AP-2 complex subunit mu OS=Homo sapiens GN=AP2M1 PE=1 SV=2	GR_PAA1	182.44	GR_PAA2	235.74
P12181	V-type proton ATPase subunit B, brain isoform OS=Homo sapiens GN=ATP6V1B2 PE=1 SV=3	GR_PAA1	437.78	GR_PAA2	541.92
O75116	Rho-associated protein kinase 2 OS=Homo sapiens GN=ROCK2 PE=1 SV=4	GR_PAA1	53.09		
A8K008	cDNA FLJ78387 OS=Homo sapiens PE=2 SV=1	GR_PAA1	126.1		
P80188	Neutrophil gelatinase-associated lipocalin OS=Homo sapiens GN=LCN2 PE=1 SV=2	GR_PAA1	185.91	GR_PAA2	252.79

P62140	Serine/threonine-protein phosphatase PP1-beta catalytic subunit OS=Homo sapiens GN=PPP1CB PE=1 SV=3	GR_PAA1	47.24		
Q6PJG0	Putative uncharacterized protein OS=Homo sapiens PE=1 SV=1	GR_PAA1	123.59	GR_PAA2	169.64
Q9Y484	WD repeat domain phosphoinositide-interacting protein 4 OS=Homo sapiens GN=WDR45 PE=2 SV=1	GR_PAA1	76.33	GR_PAA2	72.39
O43760	Synaptogyrin-2 OS=Homo sapiens GN=SYNGR2 PE=1 SV=1	GR_PAA1	49.34	GR_PAA2	47.16
C8C504	Beta-globin OS=Homo sapiens GN=HBB PE=3 SV=1	GR_PAA1	9595.38	GR_PAA2	10201.35
B3VL17	Beta globin (Fragment) OS=Homo sapiens PE=3 SV=1	GR_PAA1	12605.48	GR_PAA2	12832.6
P30613	Pyruvate kinase isozymes R/L OS=Homo sapiens GN=PKLR PE=1 SV=2	GR_PAA1	101.93	GR_PAA2	156.08
P48643	T-complex protein 1 subunit epsilon OS=Homo sapiens GN=CCT5 PE=1 SV=1	GR_PAA1	1590.27		
Q9UKV8	Protein argonaute-2 OS=Homo sapiens GN=EIF2C2 PE=1 SV=3	GR_PAA1	1121.11	GR_PAA2	1170.41
O60256	Phosphoribosyl pyrophosphate synthase-associated protein 2 OS=Homo sapiens GN=PRPSAP2 PE=1 SV=1	GR_PAA1	1146.28	GR_PAA2	1006.35
O94973	AP-2 complex subunit alpha-2 OS=Homo sapiens GN=AP2A2 PE=1 SV=2	GR_PAA1	594.78	GR_PAA2	622.19
B1ALA9	Phosphoribosyl pyrophosphate synthetase 1 OS=Homo sapiens GN=PRPS1 PE=3 SV=1	GR_PAA1	815.6		
D3DPJ2	Adenylyl cyclase-associated protein OS=Homo sapiens GN=CAP1 PE=3 SV=1	GR_PAA1	853.05	GR_PAA2	964.84
P23381	Tryptophanyl-tRNA synthetase, cytoplasmic OS=Homo sapiens GN=WARS PE=1 SV=2	GR_PAA1	710.53	GR_PAA2	861.52
P42858	Huntingtin OS=Homo sapiens GN=HTT PE=1 SV=2	GR_PAA1	201.51	GR_PAA2	326.04
P40114	Apolipoprotein B-100 OS=Homo sapiens GN=APOB PE=1 SV=2	GR_PAA1	170.57	GR_PAA2	141.68
P15311	Ezrin OS=Homo sapiens GN=EZR PE=1 SV=4	GR_PAA1	530.91	GR_PAA2	421.86
P48729	Casein kinase I isoform alpha OS=Homo sapiens GN=CSNK1A1 PE=1 SV=2	GR_PAA1	217.08	GR_PAA2	323.3
Q53FA7	Quinone oxidoreductase PIG3 OS=Homo sapiens GN=TP53I3 PE=1 SV=2	GR_PAA1	245.61	GR_PAA2	434.69
P61160	Actin-related protein 2 OS=Homo sapiens GN=ACTR2 PE=1 SV=1	GR_PAA1	568.61	GR_PAA2	367.14
P11908	Ribose-phosphate pyrophosphokinase 2 OS=Homo sapiens GN=PRPS2 PE=1 SV=2	GR_PAA1	782.38		
P63241	Eukaryotic translation initiation factor 5A-1 OS=Homo sapiens GN=EIF5A PE=1 SV=2	GR_PAA1	320.66	GR_PAA2	406.95
P49588	Alanyl-tRNA synthetase, cytoplasmic OS=Homo sapiens GN=AARS PE=1 SV=2	GR_PAA1	545.81	GR_PAA2	550.97
B4DKY1	Uncharacterized protein OS=Homo sapiens GN=CARS PE=2 SV=1	GR_PAA1	238.94	GR_PAA2	241.37
P13639	Elongation factor 2 OS=Homo sapiens GN=EEF2 PE=1 SV=4	GR_PAA1	204.4	GR_PAA2	408.7
P61221	ATP-binding cassette sub-family E member 1 OS=Homo sapiens GN=ABCE1 PE=1 SV=1	GR_PAA1	459.51	GR_PAA2	400.34
P24941	Cyclin-dependent kinase 2 OS=Homo sapiens GN=CDK2 PE=1 SV=2	GR_PAA1	250.59	GR_PAA2	305.56
Q8IUR7	Armadillo repeat-containing protein 8 OS=Homo sapiens GN=ARMC8 PE=1 SV=2	GR_PAA1	124.51	GR_PAA2	161.54
P31146	Coronin-1A OS=Homo sapiens GN=CORO1A PE=1 SV=4	GR_PAA1	262.36	GR_PAA2	342.35
P09543	2',3'-cyclic-nucleotide 3'-phosphodiesterase OS=Homo sapiens GN=CNP PE=1 SV=2	GR_PAA1	259.65	GR_PAA2	231.11
Q15404	Ras suppressor protein 1 OS=Homo sapiens GN=RSU1 PE=1 SV=3	GR_PAA1	149.82	GR_PAA2	137.48
O75083	WD repeat-containing protein 1 OS=Homo sapiens GN=WDR1 PE=1 SV=4	GR_PAA1	299.44		
O60488	Long-chain-fatty acid--CoA ligase 4 OS=Homo sapiens GN=ACSL4 PE=1 SV=2	GR_PAA1	382.49	GR_PAA2	489.8
F5H136	T-complex protein 1 subunit alpha OS=Homo sapiens GN=TCP1 PE=3 SV=1	GR_PAA1	513.85		
Q9H4B7	Tubulin beta-1 chain OS=Homo sapiens GN=TUBB1 PE=1 SV=1	GR_PAA1	220.84	GR_PAA2	245.17
O15143	Actin-related protein 2/3 complex subunit 1B OS=Homo sapiens GN=ARPC1B PE=1 SV=3	GR_PAA1	92.24		
Q15691	Microtubule-associated protein RP/EB family member 1 OS=Homo sapiens GN=MAPRE1 PE=1 SV=3	GR_PAA1	270.48	GR_PAA2	302.82
Q9ULC4	Malignant T cell-amplified sequence 1 OS=Homo sapiens GN=MCTS1 PE=1 SV=1	GR_PAA1	92.77	GR_PAA2	110.39
O43776	Asparaginyl-tRNA synthetase, cytoplasmic OS=Homo sapiens GN=NARS PE=1 SV=1	GR_PAA1	155.46	GR_PAA2	159.08
Q9UIQ6	Leucyl-cystinyl aminopeptidase OS=Homo sapiens GN=LNPEP PE=1 SV=3	GR_PAA1	123.15	GR_PAA2	86.42
Q9HD40	O-phosphoserine-tRNA(Sec) selenium transferase OS=Homo sapiens GN=SEPSECS PE=1 SV=2	GR_PAA1	291.17		
P59998	Actin-related protein 2/3 complex subunit 4 OS=Homo sapiens GN=ARPC4 PE=1 SV=3	GR_PAA1	158.6	GR_PAA2	177.12
O43426	Synaptojanin-1 OS=Homo sapiens GN=SYNJ1 PE=1 SV=2	GR_PAA1	57.36	GR_PAA2	100.79
Q13620	Cullin-4B OS=Homo sapiens GN=CUL4B PE=1 SV=4	GR_PAA1	109.14		
Q15181	Inorganic pyrophosphatase OS=Homo sapiens GN=PPA1 PE=1 SV=2	GR_PAA1	45.77		
P05089	Arginase-1 OS=Homo sapiens GN=ARG1 PE=1 SV=2	GR_PAA1	117.83	GR_PAA2	199.03
Q92747	Actin-related protein 2/3 complex subunit 1A OS=Homo sapiens GN=ARPC1A PE=1 SV=2	GR_PAA1	198.46	GR_PAA2	164.78
Q5TEG0	Novel enoyl-CoA hydratase/isomerase family protein (Fragment) OS=Homo sapiens GN=RP3-351K20.2-007 PE=2 SV=1	GR_PAA1	37.28	GR_PAA2	143.93
Q13418	Integrin-linked protein kinase OS=Homo sapiens GN=ILK PE=1 SV=2	GR_PAA1	61.83	GR_PAA2	98.94
Q15477	Helicase SKI2W OS=Homo sapiens GN=SKI2L PE=1 SV=3	GR_PAA1	67.4	GR_PAA2	84.97
Q13747	Alpha-1 antitrypsin (Fragment) OS=Homo sapiens PE=2 SV=1	GR_PAA1	57.98	GR_PAA2	37.6
Q0KKI6	Immunoglobulin light chain (Fragment) OS=Homo sapiens PE=2 SV=1	GR_PAA1	247.08		
B3KRM8	Translin, isoform CRA_b OS=Homo sapiens GN=TSN PE=2 SV=1	GR_PAA1	275.65	GR_PAA2	215.97
Q8N122	Regulatory-associated protein of mTOR OS=Homo sapiens GN=RPTOR PE=1 SV=1	GR_PAA1	62.61	GR_PAA2	72.62
B4DPJ2	cDNA FLJ51518, highly similar to Annexin A11 OS=Homo sapiens PE=2 SV=1	GR_PAA1	120.66	GR_PAA2	70.54
Q9BRG1	Vacuolar protein-sorting-associated protein 25 OS=Homo sapiens GN=VPS25 PE=1 SV=1	GR_PAA1	49.74	GR_PAA2	258.4
F5H6E2	Uncharacterized protein OS=Homo sapiens GN=MYO1C PE=4 SV=1	GR_PAA1	61.74		
B2R4D5	cDNA, FLJ92050, highly similar to Homo sapiens actin related protein 2/3 complex, subunit 3, 21kDa (ARPC3), mRNA OS=Homo sapiens PE=2 SV=1	GR_PAA1	111.94	GR_PAA2	203.84
B1AHM1	DEAD (Asp-Glu-Ala-Asp) box polypeptide 17 OS=Homo sapiens GN=DDX17 PE=3 SV=1	GR_PAA1	130.69	GR_PAA2	136.24
Q9Y450	HBS1-like protein OS=Homo sapiens GN=HBS1L PE=1 SV=1	GR_PAA1	91.29	GR_PAA2	73.36
Q05D08	PA2G4 protein (Fragment) OS=Homo sapiens GN=PA2G4 PE=2 SV=1	GR_PAA1	69.81	GR_PAA2	52.8
Q9BTE6	Alanyl-tRNA editing protein Aarsd1 OS=Homo sapiens GN=AARSD1 PE=1 SV=2	GR_PAA1	58.26	GR_PAA2	52.69
P17612	cAMP-dependent protein kinase catalytic subunit alpha OS=Homo sapiens GN=PRKACA PE=1 SV=2	GR_PAA1	72.52	GR_PAA2	47.43
P07814	Bifunctional aminoacyl-tRNA synthetase OS=Homo sapiens GN=EPRS PE=1 SV=5	GR_PAA1	130.56		
Q9Y678	Coatomer subunit gamma OS=Homo sapiens GN=COG P PE=1 SV=1	GR_PAA1	100.63	GR_PAA2	215.44
B2R491	Ribosomal protein S4, X-linked, isoform CRA_c OS=Homo sapiens GN=RPS4X PE=2 SV=1	GR_PAA1	96.55	GR_PAA2	153.3
P61026	Ras-related protein Rab-10 OS=Homo sapiens GN=RAB10 PE=1 SV=1	GR_PAA1	94.47	GR_PAA2	151.07
Q96T66	Nicotinamide mononucleotide adenylyltransferase 3 OS=Homo sapiens GN=NMNAT3 PE=1 SV=2	GR_PAA1	103.68	GR_PAA2	115.47
Q8N9N7	Leucine-rich repeat-containing protein 57 OS=Homo sapiens GN=LRRC57 PE=1 SV=1	GR_PAA1	128.39	GR_PAA2	99.64
B3KP20	cDNA FLJ30970 fis, clone HEART2000444, highly similar to Homo sapiens phospholysine phosphohistidine inorganic pyrophosphate phosphatase (LHPP), mRNA OS=Homo sapiens PE=2 SV=1	GR_PAA1	57.66	GR_PAA2	78.56
Q96TA1	Niban-like protein 1 OS=Homo sapiens GN=FAM129B PE=1 SV=2	GR_PAA1	148.12	GR_PAA2	41.48
B4DMY7	Mannose-6-phosphate utilization defect 1, isoform CRA_a OS=Homo sapiens GN=MPDU1 PE=2 SV=1	GR_PAA1	96.9	GR_PAA2	175.24
B011T1	MYO1F variant protein OS=Homo sapiens PE=2 SV=1	GR_PAA1	134.38	GR_PAA2	157.11
Q9Y613	FH1/FH2 domain-containing protein 1 OS=Homo sapiens GN=FHOD1 PE=1 SV=3	GR_PAA1	60.6	GR_PAA2	107.81
F5H715	Uncharacterized protein OS=Homo sapiens GN=AIDA PE=4 SV=1	GR_PAA1	53.83	GR_PAA2	42.79

B4DDW1	Uncharacterized protein OS=Homo sapiens GN=METTL7A PE=2 SV=1	GR_PAA1	122.59		
A0JP11	Phosphoinositide-3-kinase, regulatory subunit 4 OS=Homo sapiens GN=PIK3R4 PE=2 SV=1	GR_PAA1	46.64		
B4DHQ1	cDNA FLJ53452, highly similar to Histidyl-tRNA synthetase (EC 6.1.1.21) OS=Homo sapiens PE=2 SV=1	GR_PAA1	43.55		
Q15021	Condensin complex subunit 1 OS=Homo sapiens GN=NCAPD2 PE=1 SV=3	GR_PAA1	43.14		
O00233	26S proteasome non-ATPase regulatory subunit 9 OS=Homo sapiens GN=PSMD9 PE=1 SV=3	GR_PAA1	180.82	GR_PAA2	136.91
Q15366	Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2 PE=1 SV=1	GR_PAA1	109.7	GR_PAA2	124.03
P53621	Coatomer subunit alpha OS=Homo sapiens GN=COPA PE=1 SV=2	GR_PAA1	58.43	GR_PAA2	117.35
Q722W4	Zinc finger CCCH-type antiviral protein 1 OS=Homo sapiens GN=ZC3HAV1 PE=1 SV=3	GR_PAA1	58.27	GR_PAA2	114.21
Q15418	Ribosomal protein S6 kinase alpha-1 OS=Homo sapiens GN=RPS6KA1 PE=1 SV=2	GR_PAA1	85.66	GR_PAA2	110.16
Q0VGA5	SARS protein OS=Homo sapiens GN=SARS PE=2 SV=1	GR_PAA1	104.24	GR_PAA2	83
Q9NRF8	CTP synthase 2 OS=Homo sapiens GN=CTPS2 PE=1 SV=1	GR_PAA1	67.75	GR_PAA2	63.56
B0QZ18	Copine I OS=Homo sapiens GN=CPNE1 PE=4 SV=1	GR_PAA1	46.07	GR_PAA2	30.47
E9PCU1	Uncharacterized protein OS=Homo sapiens GN=PRUNE PE=4 SV=2	GR_PAA1	75.04		
E9PL45	Uncharacterized protein OS=Homo sapiens GN=RPS3 PE=4 SV=1	GR_PAA1	64.28		
O43747	AP-1 complex subunit gamma-1 OS=Homo sapiens GN=AP1G1 PE=1 SV=5	GR_PAA1	49.18		
Q15042	Rab3 GTPase-activating protein catalytic subunit OS=Homo sapiens GN=RAB3GAP1 PE=1 SV=3	GR_PAA1	45.06		
Q8N1G4	Leucine-rich repeat-containing protein 47 OS=Homo sapiens GN=LRRC47 PE=1 SV=1	GR_PAA1	39.84		
Q9Y4P8	WD repeat domain phosphoinositide-interacting protein 2 OS=Homo sapiens GN=WIP2 PE=1 SV=1	GR_PAA1	87.97	GR_PAA2	167.84
Q96AZ6	Interferon-stimulated gene 20 kDa protein OS=Homo sapiens GN=ISG20 PE=1 SV=2	GR_PAA1	120.1	GR_PAA2	125.08
B2RDW9	cDNA, FLJ96803, highly similar to Homo sapiens GTP binding protein 1 (GTPBP1), mRNA OS=Homo sapiens PE=2 SV=1	GR_PAA1	129.01	GR_PAA2	93.47
Q86VN1	Vacuolar protein-sorting-associated protein 36 OS=Homo sapiens GN=VPS36 PE=1 SV=1	GR_PAA1	34.21	GR_PAA2	71.07
P54619	5'-AMP-activated protein kinase subunit gamma-1 OS=Homo sapiens GN=PRKAG1 PE=1 SV=1	GR_PAA1	67	GR_PAA2	44.91
Q9H871	Protein RMD5 homolog A OS=Homo sapiens GN=RMND5A PE=1 SV=1	GR_PAA1	54.9		
Q9BPX5	Actin-related protein 2/3 complex subunit 5-like protein OS=Homo sapiens GN=ARPC5L PE=1 SV=1	GR_PAA1	101.2	GR_PAA2	103.56
P53990	IST1 homolog OS=Homo sapiens GN=KIAA0174 PE=1 SV=1	GR_PAA1	49.51	GR_PAA2	67.93
Q9NWX6	Probable tRNA(His) guanylyltransferase OS=Homo sapiens GN=THG1L PE=1 SV=2	GR_PAA1	32.31	GR_PAA2	58.67
P53618	Coatomer subunit beta OS=Homo sapiens GN=COPB1 PE=1 SV=3	GR_PAA1	64.79	GR_PAA2	47.98
Q6PIK3	HCG1995540, isoform CRA_b (Hcg2044074, isoform cra_d) OS=Homo sapiens GN=RAB4B PE=2 SV=1	GR_PAA1	106.18		
Q9NQC3	Reticulon-4 OS=Homo sapiens GN=RTN4 PE=1 SV=2	GR_PAA1	69.44		
Q9H9A6	Leucine-rich repeat-containing protein 40 OS=Homo sapiens GN=LRRC40 PE=1 SV=1	GR_PAA1	34.96		
A2RUM0	Poly (ADP-ribose) polymerase family, member 10 OS=Homo sapiens GN=PARP10 PE=2 SV=1	GR_PAA1	25.42		
F6U211	Uncharacterized protein OS=Homo sapiens GN=RPS10 PE=4 SV=1	GR_PAA1	49.21	GR_PAA2	73.35
Q06187	Tyrosine-protein kinase BTK OS=Homo sapiens GN=BTK PE=1 SV=3	GR_PAA1	60.15	GR_PAA2	50.15
B4E1Y5	cDNA FLJ50359, highly similar to Cytochrome b-245 heavy chain OS=Homo sapiens PE=4 SV=1	GR_PAA1	93.64		
Q9NS86	LanC-like protein 2 OS=Homo sapiens GN=LANCL2 PE=1 SV=1	GR_PAA1	66.29		
Q6ZW64	cDNA FLJ41552 fis, clone COLON2004478, highly similar to Protein Tro alpha1 H, myeloma OS=Homo sapiens PE=1 SV=1	GR_PAA1	66		
Q96GD0	Pyridoxal phosphate phosphatase OS=Homo sapiens GN=PDXP PE=1 SV=2	GR_PAA1	65.75		
Q5IRN2	DAZAP1/MEF2D fusion protein OS=Homo sapiens GN=DAZAP1/MEF2D fusion PE=2 SV=1	GR_PAA1	65.74		
Q9Y3C4	TP53RK-binding protein OS=Homo sapiens GN=TPRKB PE=1 SV=1	GR_PAA1	60.02		
Q9J320	Uncharacterized protein OS=Homo sapiens GN=ACSL6 PE=4 SV=1	GR_PAA1	48.94		
Q15370	Transcription elongation factor B polypeptide 2 OS=Homo sapiens GN=TCEB2 PE=1 SV=1	GR_PAA1	44		
B3KQV3	Uncharacterized protein OS=Homo sapiens GN=PIP4K2C PE=2 SV=1	GR_PAA1	74.13		
P81605	Dermcidin OS=Homo sapiens GN=DCLD PE=1 SV=2	GR_PAA1	54.18		
Q9Y285	Phenylalanyl-tRNA synthetase alpha chain OS=Homo sapiens GN=FARSA PE=1 SV=3	GR_PAA1	48.35		
P00491	Purine nucleoside phosphorylase OS=Homo sapiens GN=PNP PE=1 SV=2			GR_PAA2	40.46
Q15102	Platelet-activating factor acetylhydrolase 1B subunit gamma OS=Homo sapiens GN=PFAH1B3 PE=1 SV=1			GR_PAA2	58.45
O60610	Protein diaphanous homolog 1 OS=Homo sapiens GN=DIAPH1 PE=1 SV=2			GR_PAA2	95.81
P07237	Protein disulfide-isomerase OS=Homo sapiens GN=P4HB PE=1 SV=3			GR_PAA2	33.05
Q9P2R3	Ankyrin repeat and FYVE domain-containing protein 1 OS=Homo sapiens GN=ANKFY1 PE=1 SV=2			GR_PAA2	43
Q99733	Nucleosome assembly protein 1-like 4 OS=Homo sapiens GN=NAP1L4 PE=1 SV=1			GR_PAA2	60.73
P46060	Ran GTPase-activating protein 1 OS=Homo sapiens GN=RANGAP1 PE=1 SV=1			GR_PAA2	45.4
Q9UPN7	Serine/threonine-protein phosphatase 6 regulatory subunit 1 OS=Homo sapiens GN=PPP6R1 PE=1 SV=5			GR_PAA2	44.62
P47755	F-actin-capping protein subunit alpha-2 OS=Homo sapiens GN=CAPZA2 PE=1 SV=3			GR_PAA2	113.46
O76003	Glutaredoxin-3 OS=Homo sapiens GN=GLRX3 PE=1 SV=2			GR_PAA2	90.07
P08397	Porphobilinogen deaminase OS=Homo sapiens GN=HMBS PE=1 SV=2			GR_PAA2	48.33
B4DT12	cDNA FLJ55654, highly similar to TBC1 domain family member 17 OS=Homo sapiens PE=2 SV=1			GR_PAA2	71.94
P07737	Profilin-1 OS=Homo sapiens GN=PFN1 PE=1 SV=2			GR_PAA2	69.46
P61020	Ras-related protein Rab-5B OS=Homo sapiens GN=RAB5B PE=1 SV=1			GR_PAA2	177.12
Q16563	Synaptophysin-like protein 1 OS=Homo sapiens GN=SYPL1 PE=1 SV=1			GR_PAA2	41.75
B0UX83	HLA-B associated transcript 3 OS=Homo sapiens GN=BAT3 PE=4 SV=1			GR_PAA2	202.18
P13473	Lysosome-associated membrane glycoprotein 2 OS=Homo sapiens GN=LAMP2 PE=1 SV=2			GR_PAA2	62.72
Q99497	Protein DJ-1 OS=Homo sapiens GN=PARK7 PE=1 SV=2			GR_PAA2	77.04
O15439	Multidrug resistance-associated protein 4 OS=Homo sapiens GN=ABCC4 PE=1 SV=3			GR_PAA2	65.56
Q6JSD8	Aquaporin 1 splice variant 2 (Fragment) OS=Homo sapiens GN=AQP1 PE=2 SV=1			GR_PAA2	131.06
Q9Y3E0	Vesicle transport protein GOT1B OS=Homo sapiens GN=GOLT1B PE=1 SV=1			GR_PAA2	106.16
B4E3A8	Uncharacterized protein OS=Homo sapiens GN=SERPINB1 PE=2 SV=1			GR_PAA2	733.67
P18206	Vinculin OS=Homo sapiens GN=VCL PE=1 SV=4			GR_PAA2	63.3
B2RB13	cDNA, FLJ95253, highly similar to Homo sapiens acyl-CoA synthetase long-chain family member 6 (ACSL6), mRNA OS=Homo sapiens PE=2 SV=1			GR_PAA2	48.43
Q9HDC9	Adipocyte plasma membrane-associated protein OS=Homo sapiens GN=APMAP PE=1 SV=2			GR_PAA2	54.3
P62937	Peptidyl-prolyl cis-trans isomerase A OS=Homo sapiens GN=PP1A PE=1 SV=2			GR_PAA2	45.56
P60174	Triosephosphate isomerase OS=Homo sapiens GN=TP1I PE=1 SV=2			GR_PAA2	46.08
Q6VFG6	Hemoglobin beta chain (Fragment) OS=Homo sapiens GN=HBB PE=2 SV=1			GR_PAA2	333.68
Q72351	Putative uncharacterized protein DKFZp686N02209 OS=Homo sapiens GN=DKFZp686N02209 PE=1 SV=1			GR_PAA2	198.05
P62136	Serine/threonine-protein phosphatase PP1-alpha catalytic subunit OS=Homo sapiens GN=PPP1CA PE=1 SV=1			GR_PAA2	60.17
O95248	Myotubularin-related protein 5 OS=Homo sapiens GN=SBF1 PE=1 SV=3			GR_PAA2	149.65

B4DUD6	cDNA FLJ54551, highly similar to Septin-7 OS=Homo sapiens PE=2 SV=1		GR_PAA2	108.51
P62256	Ubiquitin-conjugating enzyme E2 H OS=Homo sapiens GN=UBE2H PE=1 SV=1		GR_PAA2	73
Q969T9	WW domain-binding protein 2 OS=Homo sapiens GN=WBP2 PE=1 SV=1		GR_PAA2	53.28
P62873	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1 OS=Homo sapiens GN=GNB1 PE=1 SV=3		GR_PAA2	128.75
Q9BT73	Proteasome assembly chaperone 3 OS=Homo sapiens GN=PSMG3 PE=1 SV=1		GR_PAA2	78.89
Q92614	Myosin-XVIIIa OS=Homo sapiens GN=MYO18A PE=1 SV=3		GR_PAA2	52.31
P63092	Guanine nucleotide-binding protein G(s) subunit alpha isoforms short OS=Homo sapiens GN=GNAS PE=1 SV=1		GR_PAA2	26.95
Q9Y244	Proteasome maturation protein OS=Homo sapiens GN=POMP PE=1 SV=1		GR_PAA2	166.05
E9PB22	Uncharacterized protein OS=Homo sapiens GN=CD47 PE=4 SV=1		GR_PAA2	64.24
Q8NBX0	Probable saccharopine dehydrogenase OS=Homo sapiens GN=SCCPDH PE=1 SV=1		GR_PAA2	62.57
Q5XTR9	Hemoglobin delta-beta fusion protein (Fragment) OS=Homo sapiens GN=HBD/HBB PE=2 SV=1		GR_PAA2	94.99
B4DNA3	Adenylyl cyclase-associated protein OS=Homo sapiens PE=2 SV=1		GR_PAA2	855.21
Q6P5S8	IGK@ protein OS=Homo sapiens GN=IGK@ PE=1 SV=1		GR_PAA2	231.36
E7EUY0	Uncharacterized protein OS=Homo sapiens GN=PRKDC PE=4 SV=1		GR_PAA2	46.12
P42345	Serine/threonine-protein kinase mTOR OS=Homo sapiens GN=MTOR PE=1 SV=1		GR_PAA2	99.82
Q59E89	DnaJ (Hsp40) homolog, subfamily B, member 4 variant (Fragment) OS=Homo sapiens PE=2 SV=1		GR_PAA2	75.42
Q92835	Phosphatidylinositol-3,4,5-trisphosphate 5-phosphatase 1 OS=Homo sapiens GN=INPP5D PE=1 SV=2		GR_PAA2	101.56
Q5U025	ADP-ribosylation factor 6 OS=Homo sapiens PE=2 SV=1		GR_PAA2	150.15
B4DKI2	cDNA FLJ60282, highly similar to Sorbitol dehydrogenase (EC 1.1.1.14) OS=Homo sapiens PE=2 SV=1		GR_PAA2	130.04
O75874	Isocitrate dehydrogenase [NADP] cytoplasmic OS=Homo sapiens GN=IDH1 PE=1 SV=2		GR_PAA2	58.55
B2RCT6	cDNA, FLJ96276, highly similar to Homo sapiens G1 to S phase transition 1 (GSPT1), mRNA OS=Homo sapiens PE=2 SV=1		GR_PAA2	106.37
B2R680	cDNA, FLJ92827, highly similar to Homo sapiens signal transducer and activator of transcription 6, interleukin-4 induced (STAT6), mRNA OS=Homo sapiens PE=2 SV=1		GR_PAA2	83.21
O15144	Actin-related protein 2/3 complex subunit 2 OS=Homo sapiens GN=ARPC2 PE=1 SV=1		GR_PAA2	74.96
P23396	40S ribosomal protein S3 OS=Homo sapiens GN=RPS3 PE=1 SV=2		GR_PAA2	46.37
Q9BUL8	Programmed cell death protein 10 OS=Homo sapiens GN=PDCD10 PE=1 SV=1		GR_PAA2	162.7
Q5VW36	Uncharacterized protein KIAA1797 OS=Homo sapiens GN=KIAA1797 PE=1 SV=1		GR_PAA2	61.92
Q9H8W4	Pleckstrin homology domain-containing family F member 2 OS=Homo sapiens GN=PLEKHF2 PE=1 SV=1		GR_PAA2	46.64
B2RD40	cDNA, FLJ96442, highly similar to Homo sapiens copine II (CPNE2), mRNA OS=Homo sapiens PE=2 SV=1		GR_PAA2	45.61
B2RB57	cDNA, FLJ95321, highly similar to Homo sapiens ATG7 autophagy related 7 homolog (S. cerevisiae) (ATG7), mRNA OS=Homo sapiens PE=2 SV=1		GR_PAA2	89.68
B4DS71	cDNA FLJ57081, moderately similar to WD repeat protein 1 OS=Homo sapiens PE=2 SV=1		GR_PAA2	76.17
B0QYM8	Parvin, beta OS=Homo sapiens GN=PARVB PE=4 SV=1		GR_PAA2	57.56
D3DTH7	Myosin IC, isoform CRA_a OS=Homo sapiens GN=MYO1C PE=4 SV=1		GR_PAA2	55.43
Q13177	Serine/threonine-protein kinase PAK 2 OS=Homo sapiens GN=PAK2 PE=1 SV=3		GR_PAA2	42.32
B7Z8P7	cDNA FLJ59064, highly similar to UGA suppressor tRNA-associated protein OS=Homo sapiens PE=2 SV=1		GR_PAA2	87.36
P16989	DNA-binding protein A OS=Homo sapiens GN=CSDA PE=1 SV=4		GR_PAA2	68.37
P21283	V-type proton ATPase subunit C 1 OS=Homo sapiens GN=ATP6V1C1 PE=1 SV=4		GR_PAA2	57
Q86TP1	Protein prune homolog OS=Homo sapiens GN=PRUNE PE=1 SV=2		GR_PAA2	49.16
O43324	Eukaryotic translation elongation factor 1 epsilon-1 OS=Homo sapiens GN=EEF1E1 PE=1 SV=1		GR_PAA2	86.6
Q8NE71	ATP-binding cassette sub-family F member 1 OS=Homo sapiens GN=ABCF1 PE=1 SV=2		GR_PAA2	82.05
Q9Y2V2	Calcium-regulated heat stable protein 1 OS=Homo sapiens GN=CAHSP1 PE=1 SV=2		GR_PAA2	79.57
B7Z8F3	cDNA FLJ53587, highly similar to Surfeit locus protein 4 OS=Homo sapiens PE=2 SV=1		GR_PAA2	74.2
P80511	Protein S100-A12 OS=Homo sapiens GN=S100A12 PE=1 SV=2		GR_PAA2	58.07
P13224	Platelet glycoprotein Ib beta chain OS=Homo sapiens GN=GP1BB PE=1 SV=1		GR_PAA2	53.65
O75015	Low affinity immunoglobulin gamma Fc region receptor III-B OS=Homo sapiens GN=FCGR3B PE=1 SV=2		GR_PAA2	48.28
P17931	Galectin-3 OS=Homo sapiens GN=LGALS3 PE=1 SV=5		GR_PAA2	45.61
Q8WU76	Sec1 family domain-containing protein 2 OS=Homo sapiens GN=SCFD2 PE=1 SV=2		GR_PAA2	42.43
P55884	Eukaryotic translation initiation factor 3 subunit B OS=Homo sapiens GN=EIF3B PE=1 SV=3		GR_PAA2	42.43
O00560	Syntenin-1 OS=Homo sapiens GN=SDCBP PE=1 SV=1		GR_PAA2	40.19

Supplemental Data 3:

Non-redundant lists of the proteins
identified and quantified according to
the NP-treatment of red blood cell
(RBC) lysate

Supplemental Data 3

Sheet 1

The 20 most abundant proteins

Supplemental Data 3

Sheet 2

Feuil 1

Control RBC						Q-NPs						
Total MS/MS number	MW	pI	Description	#Total MS/MS	%total MS/MS	Rank	%total MS/MS	#Total MS/MS	Description	pI	MW	Total MS/MS number
18796	16102	6.75	Hemoglobin subunit beta	2654	14.1	1	4.4	795	Hemoglobin subunit beta OS	6.75	16102	18096
	16101	7.86	Beta-globin	2424	12.9	2	4.4	788	Spectrin, beta, erythrocytic	5.15	247271	
	11534	5.9	Beta globin (Fragment)	1921	10.2	3	4.3	787	Spectrin beta chain, erythrocyte	5.15	247171	
	11496	6.17	Hemoglobin beta (Fragment)	1731	9.2	4	4.2	759	Spectrin alpha chain, erythrocyte	4.95	281039	
	15305	8.72	Hemoglobin subunit alpha	1563	8.3	5	3.3	590	Hemoglobin beta (Fragment)	6.17	11496	
	11532	5.46	Hemoglobin beta (Fragment)	1499	8.0	6	3.1	568	Hemoglobin subunit alpha	8.72	15305	
	10979	6.17	Hbbm fused globin protein (Fragment)	1480	7.9	7	3.1	555	Hemoglobin beta (Fragment)	5.46	11532	
	16159	7.85	Delta globin	1429	7.6	8	2.7	495	Hbbm fused globin protein (Fragment)	6.17	10979	
	8386	6.63	Hemoglobin alpha 2 (Fragment)	1242	6.6	9	2.4	443	Delta globin	7.85	16159	
	4263	4.96	Truncated beta globin	968	5.2	10	2.0	358	Solute carrier family 4, anion exchanger, member 1	5.1	102150	
	16187	6.64	Hemoglobin subunit gamma-1	242	1.3	11	1.8	330	Transitional endoplasmic reticulum ATPase	5.14	89950	
	28909	6.59	Carbonic anhydrase 1	113	0.6	12	1.5	272	Proteasome subunit alpha type-6	6.34	27838	
	59947	6.9	Catalase	103	0.5	13	1.4	245	Acylamino-acid-releasing enzyme	5.29	82142	
	247171	5.15	Spectrin beta chain, erythrocyte	84	0.4	14	1.3	239	Clathrin heavy chain 1	5.48	193260	
	102150	5.1	Solute carrier family 4, anion exchanger, member 1	72	0.4	15	1.3	236	Hemoglobin subunit gamma-1	6.64	16187	
	32325	6.45	Purine nucleoside phosphorylase	59	0.3	16	1.3	228	Myosin-9	5.5	227646	
	22049	5.66	Peroxisredoxin-2	57	0.3	17	0.9	171	Delta-aminolevulinic acid dehydratase	6.32	36728	
	25133	6	Peroxisredoxin-6	54	0.3	18	0.8	152	Ankyrin-1	5.65	207334	
	29285	6.87	Carbonic anhydrase 2	50	0.3	19	0.8	140	Importin-5	4.83	125032	
	281039	4.95	Spectrin alpha chain, erythrocyte	49	0.3	20	0.8	136	E3 ubiquitin-protein ligase UBR4	5.7	580547	
The 20 most abundant proteins					94.7	The 20 most abundant proteins						
Related to Hemoglobin (among the 20 most abundant)					91.3	Related to Hemoglobin (among the 20 most abundant)						
						45.8						
						20.3						

OS-NPs						PAA-NPs						
Total MS/MS number	MW	pI	Description	#Total MS/MS	%total MS/MS	Rank	%total MS/MS	#Total MS/MS	Description	pI	MW	Total MS/MS number
13101	281039	4.95	Spectrin alpha chain, erythrocyte	659	5.0	1	4.3	779	Hemoglobin subunit beta	6.75	16102	18073
	247171	5.15	Spectrin beta chain, erythrocyte	468	3.6	2	3.8	688	Beta globin (Fragment)	5.9	11534	
	247271	5.15	Spectrin, beta, erythrocytic	465	3.5	3	3.6	656	Beta-globin	7.86	16101	
	102150	5.1	Solute carrier family 4, anion exchanger, member 1	459	3.5	4	3.3	596	Hemoglobin beta (Fragment)	6.17	11496	
	16102	6.75	Hemoglobin subunit beta	428	3.3	5	3.1	565	Hemoglobin beta (Fragment)	5.46	11532	
	11532	5.46	Hemoglobin beta (Fragment)	351	2.7	6	2.7	484	Hemoglobin subunit alpha	8.72	15305	
	14069	6.46	Hemoglobin beta subunit variant (Fragment)	333	2.5	7	2.6	475	Hbbm fused globin protein (Fragment)	6.17	10979	
	11496	6.17	Hemoglobin beta (Fragment)	331	2.5	8	2.4	442	Delta globin	7.85	16159	
	16159	7.85	Delta globin	283	2.2	9	2.0	363	Spectrin beta chain, erythrocyte	5.15	247171	
	15305	8.72	Hemoglobin subunit alpha	272	2.1	10	2.0	360	Spectrin, beta, erythrocytic	5.15	247271	
	16187	6.64	Hemoglobin subunit gamma-1	212	1.6	11	1.6	286	Ankyrin-1	5.65	207334	
	16173	6.64	Hemoglobin subunit gamma-2	212	1.6	12	1.5	263	Spectrin alpha chain, erythrocyte	4.95	281039	
	8386	6.63	Hemoglobin alpha 2 (Fragment)	199	1.5	13	1.3	230	Truncated beta globin	4.96	4263	
	207334	5.65	Ankyrin-1	196	1.5	14	1.2	217	Uncharacterized protein	7.04	98190	
	580547	5.7	E3 ubiquitin-protein ligase UBR4	133	1.0	15	1.2	212	Hemoglobin subunit gamma-1	6.64	16187	
	271766	5.77	Talin-1	126	1.0	16	1.2	210	Hemoglobin subunit gamma-2	6.64	16173	
	57794	6.01	T-complex protein 1 subunit beta	100	0.8	17	1.1	200	E3 ubiquitin-protein ligase UBR4	5.7	580547	
	82465	5.49	Calpain-1 catalytic subunit	86	0.7	18	1.1	191	Solute carrier family 4, anion exchanger, member 1	5.1	102150	
	100877	5.08	26S proteasome non-ATPase regulatory subunit 2	84	0.6	19	1.0	178	T-complex protein 1 subunit gamma	6.1	61066	
	51296	5.49	RuvB-like 2	84	0.6	20	0.9	162	T-complex protein 1 subunit beta	6.01	57794	
The 20 most abundant proteins					41.8	The 20 most abundant proteins						
Related to Hemoglobin (among the 20 most abundant)					20.0	Related to Hemoglobin (among the 20 most abundant)						
						41.8						
						29.5						

Supplemental Data 4

Hierarchical clustering of all proteins identified and quantified from NP-treatment and Non-redundant list of proteins preferentially harvested by one type of NPs.

Supplemental Data 4

Sheet 1

Feuil 1

Control RBC			Description	OS-NPs		
MS/MS queries	Peptide Number	Sequence coverage (%)		Sequence coverage (%)	Peptide Number	MS/MS queries
1	1	3.4	Calpain small subunit 1	60.8	12	63
2	2	3.4	Heat shock protein HSP 90-alpha	26	17	30
2	2	2	T-complex protein 1 subunit theta	48.5	28	63
2	1	5.2	Proteasome subunit alpha type-7	42.9	8	13
2	2	5	Transketolase	11.9	5	11
2	2	17.1	Ubiquitin-conjugating enzyme E2 N	79.6	10	28
2	1	1.4	Plastin-2	18	9	19
2	2	14.1	Hemoglobin subunit theta-1	17.6	2	5
3	2	13.2	Proteasome subunit alpha type-2	41.5	6	11
3	2	9.5	Proteasome subunit beta type-5	27.4	7	12

Control RBC			Description	Q-NPs		
MS/MS queries	Peptide Number	Sequence coverage (%)		Sequence coverage (%)	Peptide Number	MS/MS queries
1	1	3.4	Calpain small subunit 1	34.3	9	19
2	2	3.4	Heat shock protein HSP 90-alpha	45.1	41	153
2	2	2	T-complex protein 1 subunit theta	53.1	38	98
2	1	5.2	Proteasome subunit alpha type-7	57.1	14	54
3	2	13.2	Proteasome subunit alpha type-2	61.1	16	61
3	2	9.5	Proteasome subunit beta type-5	51	16	55
3	3	13.9	LMW phosphotyrosine protein phosphatase	28.5	4	6
4	3	13.7	Proteasome subunit alpha type-5	65.1	18	88
4	3	12.6	Ribose-phosphate pyrophosphokinase 1	22	6	15
4	2	5.1	Multifunctional protein ADE2	13.2	3	6

Control RBC			Description	PAA-NPs		
MS/MS queries	Peptide Number	Sequence coverage (%)		Sequence coverage (%)	Peptide Number	MS/MS queries
1	1	3.4	Calpain small subunit 1	64.2	17	38
1	1	4.9	L-xylulose reductase	31.6	6	14
2	2	3.4	Heat shock protein HSP 90-alpha	23.4	19	49
2	2	2	T-complex protein 1 subunit theta	50.2	37	123
2	1	5.2	Proteasome subunit alpha type-7	45	9	18
2	2	5	Transketolase	42.5	24	48
3	2	13.2	Proteasome subunit alpha type-2	64.5	17	43
3	2	9.5	Proteasome subunit beta type-5	47.9	15	34
3	3	13.9	LMW phosphotyrosine protein phosphatase	39.9	6	10
4	3	13.7	Proteasome subunit alpha type-5	46.9	14	52

Supplemental Data 5

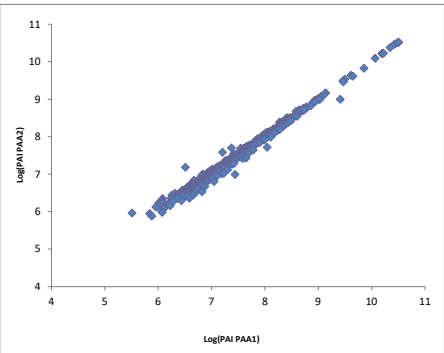
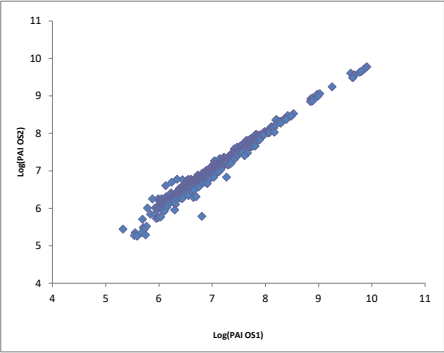
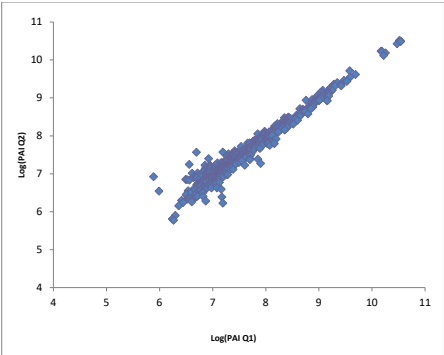
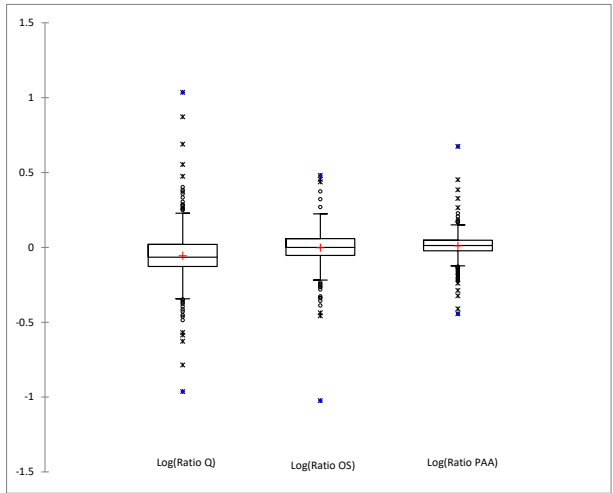
Isoelectric point (pI) and molecular weight (MW) of NP specific protein signatures.

Supplemental Data 5

Sheet 1

Box plot and summary

	GR-billes Q	GR-billes OS	GR-billes PAA	Replicats inj	Replicats gel
Minimum ratio	0.11	0.09	0.36	0.32	0.53
Maximum ratio	10.83	3.02	4.72	2.90	8.12
Mean ratio	0.96	1.03	1.04	0.99	1.09
Mean Log(ratio)	-0.056	-0.002	0.010	-0.010	0.020
Std dev Log(ratio)	0.170	0.117	0.082	0.060	0.090
Max Fold (100%)	10.835	10.564	4.721	3.170	8.120
99% fold distribution	4.255	2.429	2.114	1.530	2.260
95% fold distribution	2.153	1.637	1.424	1.350	1.590
75% fold distribution	1.492	1.299	1.174	1.130	1.160
Pearson correlation coefficient	0.979	0.988	0.995	ND	ND
Determination coefficient	0.959	0.976	0.991	0.988	0.971



Supplemental Data 5
Sheet 2

Quantified Proteins Q-treated

Log(PAI Q1)	Log(PAI Q2)
5.88622525	6.921040659
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6.85323945	7.225577235
6.49117568	6.848162359
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8.42618233	8.48851633
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Supplemental Data 5
Sheet 3

Quantified Proteins PAA-treated

AC	Other ACs	MW	pl	Description	#QPep	PAI PAA1	PAI PAA2	Log(PAI PAA1)	Log(PAI PAA2)	Ratio PAI
B4DHQ1		50547.7		5.16 cDNA FLJ5345:1 (3)		3.23E+06	1.53E+07	6.509548611	7.183569051	4.7208526
O60610	E9PEZ3, Q6UF	141942		5.31 Protein diaphan 2 (4)		3.24E+05	9.15E+05	5.510604045	5.961548516	2.82451881
B4DKY1		85022.9		6.61 Uncharacterizer 7 (12)		1.59E+07	3.86E+07	7.202368599	7.586159667	2.41986461
B4DDW1	Q9H8H3	20778.7		9.11 Uncharacterizer 1 (1)		2.35E+07	5.00E+07	7.371684899	7.698557724	2.1226228
B3KQV3	Q8TBX8, B4DY	30727.9		10 Uncharacterizer 1 (1)		1.21E+06	2.23E+06	6.08263749	6.347491923	1.84015511
Q8NE71	A2BF75, Q2L6I	96322.7		6.4 ATP-binding ca 1 (1)		1.02E+06	1.72E+06	6.009779695	6.236667552	1.68611758
E9PCU1		27035.8		5.24 Uncharacterizer 1 (1)		1.18E+06	1.89E+06	6.07041689	6.276042755	1.6055575
Q99733	B2R6J4, C9JZI	42968		4.6 Nucleosome as 1 (1)		1.80E+06	2.76E+06	6.255727646	6.44029075	1.52954798
Q15477	Q96BC0	138637		5.72 Helicase SKI2W 2 (5)		2.06E+06	3.06E+06	6.313565928	6.486136896	1.48789049
Q86TP1		50795.1		5.28 Protein prune h 2 (2)		8.98E+05	1.33E+06	5.953256027	6.124780545	1.48430968
O75116		161939		5.75 Rho-associated 1 (1)		4.63E+06	6.84E+06	6.665496557	6.834882672	1.47701911
B4DMY7		17266.2		8.85 Mannose-P-dol 2 (2)		6.78E+06	1.00E+07	6.831064062	7.000394785	1.47683074
Q5VW36		202111		6.17 Uncharacterizer 4 (5)		1.10E+06	1.62E+06	6.040621303	6.209927157	1.47674617
P13489		51765.8		4.71 Ribonuclease ir 3 (3)		3.48E+07	4.91E+07	7.54095619	7.691012737	1.41272148
B0V218	O75955, Q6IB5	23443		7.7 Flotillin 1 (Fragr 2 (4)		6.86E+06	9.68E+06	6.836477595	6.986049658	1.41114637
O95248	A6PVG8	210294		6.46 Myotubularin-re 1 (2)		1.24E+06	1.74E+06	6.092139756	6.241043159	1.40897538
Q9P2R3	B3KPZ0, F5H7I	129915		5.7 Ankyrin repeat :2 (3)		1.24E+06	1.73E+06	6.091748257	6.237346167	1.39829212
O76003		37693.3		5.31 Glutaredoxin-3 1 (1)		6.44E+06	8.98E+06	6.808646563	6.953491924	1.39587125
B2RD27	P51665	37045.5		6.29 cDNA, FLJ96425 (6)		2.55E+07	3.44E+07	7.406579836	7.536722466	1.34940598
Q9Y613	B4DVN5	127328		6.01 FH1/FH2 doma 2 (2)		2.84E+06	3.76E+06	6.453030233	6.575097549	1.32454683
P17931	Q86TY5, Q6FG	26193.1		8.57 Galectin-3 OS= 1 (1)		1.73E+06	2.29E+06	6.238097476	6.359503307	1.32253091
B0QYM8	A6NG58, Q9HE	37571.8		5.43 Parvin, beta OS2 (3)		4.00E+06	5.28E+06	6.602220535	6.722326426	1.3185782
Q86VN1		44073.9		6.75 Vacuolar protei 2 (2)		9.47E+06	1.25E+07	6.976550617	7.096244046	1.3173265
Q9Y2V2		16110.1		8.41 Calcium-regula 1 (1)		1.03E+07	1.35E+07	7.014103748	7.131324102	1.30984635
Q15008	C9IZE4	45787.4		5.45 26S proteasom 28 (32)		1.88E+08	2.46E+08	8.274232517	8.390810102	1.30790917
O43427	Q53F51	42136.5		6.02 Acidic fibroblast 1 (4)		8.41E+06	1.09E+07	6.924738029	7.036546206	1.29362433
P42345		290759		6.73 Serine/threonin 2 (6)		3.65E+06	4.71E+06	6.562529573	6.672762327	1.28894016
Q06187	B2RAW1	76916.6		7.83 Tyrosine-protein 1 (1)		6.93E+05	8.88E+05	5.840548414	5.948506761	1.2822076
Q92747	Q53GB6	42112.9		8.46 Actin-related pr 2 (7)		1.79E+07	2.29E+07	7.25359611	7.3594313	1.27595451
P29144	Q5VZU9	139745		5.9 Tripeptidyl-pept 4 (7)		7.88E+06	1.00E+07	6.896615783	7.001048868	1.27184177
Q9UN37		49152.1		7.64 Vacuolar protei 2 (5)		8.01E+06	1.01E+07	6.903823453	7.005761486	1.2645559
P00915		28909.4		6.59 Carbonic anhyd 13 (13)		2.56E+08	3.23E+08	8.407597523	8.509029106	1.26308211
B4DRF0	Q9H7D7	52355.8		5.78 cDNA FLJ5641:3 (3)		4.16E+06	5.23E+06	6.618942727	6.718275899	1.25699391
O00231		47719.2		6.08 26S proteasom 32 (35)		3.81E+08	4.75E+08	8.58146911	8.677021038	1.24609722
B4E1U9		26910.6		7.52 cDNA FLJ5477:4 (5)		3.29E+07	4.10E+07	7.51699995	7.612274063	1.24530036
B4DPJ2		46025.5		8.76 cDNA FLJ5151:2 (3)		5.34E+06	6.63E+06	6.727536071	6.821494076	1.24153225
P07737	Q53Y44	15215.6		8.44 Profilin-1 OS=H 1 (1)		4.56E+06	5.65E+06	6.658645441	6.752223175	1.24044563
Q96GD0		32077.5		6.12 Pyridoxal phosp 2 (2)		3.46E+06	4.28E+06	6.539056577	6.631505336	1.23722521
P00568	Q6FGX9, Q5TG	21735.4		8.73 Adenylate kinas 6 (8)		3.93E+07	4.87E+07	7.594858999	7.687232752	1.23701154
Q6ZMU0		39595		7.59 Delta-aminolev 3 (5)		9.90E+06	1.22E+07	6.995609215	7.087114577	1.23454056
Q9H9A6		68720.3		6.04 Leucine-rich rep 2 (4)		2.64E+06	3.25E+06	6.421183889	6.512417224	1.23376753
Q13418	B7Z418	51899.1		8.3 Integrin-linked f 2 (3)		3.94E+06	4.85E+06	6.59531099	6.68617371	1.23271511
Q53EZ9		39665.1		7.05 Mitogen-activat 3 (6)		2.39E+06	2.94E+06	6.377731264	6.468400457	1.23216592
Q9Y3C4	A8K4V6, A9UK	19762.5		6.31 TP53RK-bindin 1 (1)		2.46E+06	3.03E+06	6.391492589	6.48104222	1.22899363
Q9Y3E0	F5H6U7	15415.4		10.36 Vesicle transpo 2 (2)		4.43E+06	5.44E+06	6.646300441	6.735477457	1.22793963
P61978	Q5T6W2, Q5TE	51229.5		5.39 Heterogeneous 1 (3)		9.09E+06	1.12E+07	6.958461584	7.04757911	1.22777144
P62937	A8K220, A8K4E	18229		7.68 Peptidyl-prolyl c 1 (3)		3.50E+06	4.29E+06	6.544252492	6.632734895	1.22597723
Q9H8W4		28464.1		8.55 Pleckstrin homc 2 (3)		4.46E+07	5.45E+07	7.649341668	7.736683613	1.22276203
P30613		62190.6		7.64 Pyruvate kinase 6 (8)		1.23E+07	1.50E+07	7.090238775	7.177250452	1.22183251
Q6B0K9		15722.2		6.12 Hemoglobin sul 2 (3)		2.44E+07	2.99E+07	7.388130849	7.475105979	1.2217297
Q9ULH1	B2RNV3	126390		6.95 Arf-GAP with SI 3 (3)		8.25E+06	9.99E+06	6.91634849	6.999656552	1.21145716
Q5QNY9	Q9BQA1	31595.4		4.75 WD repeat dom 2 (3)		1.00E+07	1.21E+07	7.001248319	7.084237911	1.21056912
P63241		17049.5		5.08 Eukaryotic trans 8 (9)		1.08E+08	1.31E+08	8.034454866	8.116952287	1.209198
Q9Y450	B7Z1K2	75938.8		6.17 HBS1-like prote 1 (2)		2.93E+06	3.53E+06	6.466195175	6.547724021	1.20650422
Q9HD40		56431.8		8.31 O-phosphosery 5 (9)		7.40E+06	8.92E+06	6.86920548	6.950297896	1.20529239
P53621		139797		7.7 Coatomer subu 4 (4)		5.11E+06	6.16E+06	6.708809126	6.78970568	1.20474894
A0JP11	B2RAJ6, Q995I	154373		6.81 Phosphoinositic 1 (1)		2.45E+06	2.95E+06	6.388946481	6.469597473	1.20406794
Q9Y244	D6MXU3	15836.1		5.01 Proteasome me 2 (2)		3.33E+06	4.01E+06	6.522831654	6.602652859	1.20176958
O43681		39223.6		4.81 ATPase ASNA12 (5)		9.30E+07	1.12E+08	7.968254802	8.047919555	1.20133672

Q4LE36		125389	8.24	ACLY variant p130 (38)	7.34E+07	8.81E+07	7.865542024	7.945190995	1.20129307
B4DIM0	E7ENH9	125970	8.4	cDNA FLJ5644:28 (32)	7.34E+07	8.81E+07	7.865542024	7.945190995	1.20129307
P18206		124292	5.5	Vinculin OS=Hc 1 (1)	3.13E+06	3.75E+06	6.495463751	6.574553634	1.19974758
Q5VYK3		205985	6.74	Proteasome-as: 12 (22)	6.76E+07	8.10E+07	7.829849167	7.908276873	1.1979197
O00629		58363.8	4.8	Importin subunit 2 (3)	9.53E+06	1.14E+07	6.978937623	7.057029567	1.19699392
Q93008		295515	5.52	Probable ubiquitin 25 (37)	2.68E+07	3.21E+07	7.428813665	7.506490205	1.19584954
P62136	E9PMD7, Q071	38229.1	5.94	Serine/threonine 1 (1)	8.09E+06	9.67E+06	6.907708527	6.985315302	1.19565745
P62140		37960.9	5.84	Serine/threonine 1 (2)	8.09E+06	9.67E+06	6.907708527	6.985315302	1.19565745
Q9BPX5		16930.8	6.15	Actin-related protein 3 (3)	1.39E+07	1.66E+07	7.143010978	7.220580725	1.19555551
Q1XBU6	P50502, B4E0L	28462.5	8.92	Aging-associate 5 (10)	1.07E+08	1.28E+08	8.030174157	8.107742584	1.19555188
Q13228		52927.8	5.93	Selenium-binding 5 (8)	2.02E+07	2.42E+07	7.305706888	7.383011921	1.19482701
B4DMP4	Q08AM6	81059.7	5.45	cDNA FLJ5313:10 (13)	1.01E+08	1.20E+08	8.00309502	8.079767187	1.19308715
O95373		120751	4.7	Importin-7 OS= 23 (31)	1.89E+08	2.25E+08	8.27573828	8.352128412	1.1923126
Q92835		134121	7.38	Phosphatidylinositol 2 (4)	4.43E+06	5.28E+06	6.646776286	6.722847884	1.19143841
P62195		45768.1	7.11	26S protease re 31 (34)	4.39E+08	5.22E+08	8.642387816	8.717943336	1.19002345
Q7Z2W4	C9J6P4, A8K9L	103135	8.72	Zinc finger CCC 1 (1)	1.30E+07	1.55E+07	7.114842756	7.189406206	1.18730815
P21980	B4DIT7	78420.1	5.11	Protein-glutaminase 4 (6)	1.70E+07	2.02E+07	7.231685399	7.305429355	1.18506987
O60256	B2R7R5	41298.5	7.08	Phosphoribosyl 18 (21)	8.78E+07	1.04E+08	7.943358975	8.016981038	1.18473731
O60488	Q5JWV8, Q8T7A	80220.2	8.66	Long-chain-fatty acid 8 (12)	2.61E+07	3.10E+07	7.417412191	7.490994486	1.18462882
Q9NPQ8		60184.7	5.2	Synembryon-A C3 (5)	5.82E+06	6.89E+06	6.76492912	6.838435202	1.18442096
P54136		76129.2	6.26	Arginyl-tRNA synthetase 6 (9)	9.38E+06	1.11E+07	6.972154073	7.045236075	1.18326495
B4DUD6		48135.8	8.86	cDNA FLJ5455:3 (3)	3.84E+06	4.54E+06	6.584315231	6.657201275	1.18273117
B2RDG9	Q9NZ32, Q05D	46817.5	7.54	cDNA, FLJ966C:2 (4)	9.58E+06	1.13E+07	6.98156452	7.053782514	1.18091325
P17858		85762.5	7.26	6-phosphofructokinase 27 (34)	2.06E+08	2.43E+08	8.313540284	8.385757812	1.18091198
P07814		172080	7.02	Bifunctional amino acid 3 (3)	1.99E+06	2.34E+06	6.298049292	6.369733666	1.17946314
O43426		174135	7.13	Synaptojanin-1 2 (7)	3.74E+06	4.40E+06	6.573128456	6.643831663	1.17680148
P23396		26842.5	9.68	40S ribosomal protein 1 (2)	6.02E+06	7.09E+06	6.779820265	6.850501465	1.17674185
O15143	A4D275	41721.7	8.69	Actin-related protein 2 (5)	1.79E+07	2.10E+07	7.252741917	7.32313433	1.17595963
Q5U025	P62330, Q6FGI	20312.5	9.04	ADP-ribosylation 1 (4)	8.09E+06	9.51E+06	6.908207113	6.978055904	1.17448856
Q6FH17		20213.5	8.81	ARF6 protein O 1 (2)	8.09E+06	9.51E+06	6.908207113	6.978055904	1.17448856
P02647		30758.9	5.56	Apolipoprotein 14 (17)	4.14E+07	4.86E+07	7.617194707	7.686611748	1.17332153
B4DLQ1	Q8IZ83	80836.5	7.55	Uncharacterized 2 (2)	1.83E+06	2.15E+06	6.263599007	6.332963455	1.17317945
B2RB57	E9PB95, C9JTI	79075.8	5.85	cDNA, FLJ9532:2 (2)	5.81E+06	6.81E+06	6.763907668	6.833142641	1.17282975
Q9NRF8		66320.1	6.45	CTP synthase 23 (4)	7.22E+06	8.47E+06	6.858775566	6.927755806	1.17214203
P62495		49228.4	5.51	Eukaryotic peptidase 9 (11)	3.40E+07	3.98E+07	7.531061548	7.600012462	1.17206289
Q8IUR7		76600.7	6.28	Armadillo repeat 6 (11)	1.01E+07	1.18E+07	7.003186036	7.072054847	1.17184133
Q709C8		424462	6.38	Vacuolar protein 20 (32)	1.41E+07	1.65E+07	7.147970619	7.216655359	1.17134476
Q96NA2		44344.7	5.47	Rab-interacting 3 (5)	8.22E+06	9.62E+06	6.914701107	6.983330655	1.17119591
P04792		22825.5	5.98	Heat shock protein 3 (4)	1.12E+07	1.31E+07	7.050484302	7.118018895	1.16824678
O43747	Q8IY97, B3KXV	92148.5	6.36	AP-1 complex subunit 2 (2)	2.96E+06	3.45E+06	6.470620209	6.537898546	1.16755766
E9PL45		18517.8	9.67	Uncharacterized 2 (3)	6.09E+06	7.10E+06	6.784321253	6.851295445	1.16674028
P07195	Q5U077	36900.3	5.71	L-lactate dehydrogenase 9 (11)	9.12E+07	1.06E+08	7.96003181	8.026507662	1.16540225
B2RCT6	Q7KZX8, A8K2	56319.5	5.45	cDNA, FLJ9627:1 (2)	9.14E+06	1.06E+07	6.960839489	7.027282995	1.16531546
P55036		40939.3	4.68	26S proteasome subunit 6 (8)	2.38E+08	2.78E+08	8.377127763	8.443557837	1.16527941
F6U211	Q59GE4, P467	19912.4	9.92	Uncharacterized 1 (1)	4.36E+06	5.08E+06	6.63960059	6.705727736	1.16445266
Q59E89		38816.7	8.79	DnaJ (Hsp40) homolog 2 (3)	9.06E+06	1.05E+07	6.95718731	7.02317236	1.16408596
P38919		47126.3	6.3	Eukaryotic initiation 2 (4)	8.16E+06	9.49E+06	6.911523768	6.977278474	1.1634687
A8K781		47577.6	5.11	cDNA FLJ7529:26 (28)	9.16E+07	1.07E+08	7.96199012	8.027727068	1.16342113
P17980		49457.6	5.13	26S proteasome re 26 (30)	9.16E+07	1.07E+08	7.96199012	8.027727068	1.16342113
P06733		47481.5	7.01	Alpha-enolase 6 (8)	1.96E+07	2.28E+07	7.293039627	7.357529943	1.16008635
Q6XQN6	C9J8U2, C9JCI	58112.2	5.51	Nicotinate phosphatase 2 (2)	3.64E+06	4.22E+06	6.561470034	6.625329131	1.15840146
O00299	Q5SRT3, Q53F	27247.9	5.09	Chloride intracellular 1 (2)	2.69E+06	3.12E+06	6.429833706	6.493527791	1.15796141
P30041		25133.2	6	Peroxiredoxin-6 8 (15)	5.14E+07	5.94E+07	7.710819083	7.774136056	1.15695635
P59998		19768.4	8.53	Actin-related protein 3 (4)	4.82E+07	5.58E+07	7.683073269	7.746258247	1.15660477
Q9NS86	B3KTN5, B4DV	51676.8	7.18	LanC-like protein 1 (1)	5.26E+06	6.08E+06	6.720954555	6.783939424	1.15607197
B7Z763		89970.1	6.37	Adenosine monophosphate 12 (17)	4.68E+07	5.40E+07	7.669833473	7.732485449	1.15518616
P25685	Q6FI51, B4DXE	38191.4	8.74	DnaJ homolog 4 (4)	1.60E+07	1.84E+07	7.203587991	7.265066446	1.1520689
Q96T66		28474.7	9.28	Nicotinamide monophosphate 3 (5)	1.34E+07	1.54E+07	7.128477854	7.187906256	1.14664347
P00492	Q6LET3	24791.7	6.21	Hypoxanthine-guanine phosphoribosyltransferase 6 (6)	1.31E+07	1.50E+07	7.115863602	7.174664378	1.14498758
Q9COC9		142631	5.01	Ubiquitin-conjugase 20 (27)	2.29E+08	2.61E+08	8.359628509	8.41709178	1.14146677

B7Z8F3		29551.4	8.86 cDNA FLJ5358 1 (2)	1.22E+06	1.39E+06	6.085880056	6.142968869	1.14048299
P30566	Q71UA4	55595.3	6.69 Adenylosuccina 3 (6)	1.22E+07	1.39E+07	7.087697476	7.14426075	1.13910373
B1AJY5	O75832, B1AJN	20432.3	5.37 Proteasome (Pr 4 (7)	2.33E+07	2.66E+07	7.367643384	7.424070931	1.13874779
A8K8L7	Q9Y376	40014.8	6.43 Calcium binding 5 (8)	2.54E+07	2.88E+07	7.405283889	7.460009555	1.13429408
Q8NBX0		47463.6	9.24 Probable sacch 2 (2)	4.87E+06	5.52E+06	6.687241966	6.741943257	1.13423042
F5H2F4		111342	8.66 Uncharacterize 14 (18)	4.90E+07	5.55E+07	7.690033939	7.744068125	1.13248951
P11586		102180	6.89 C-1-tetrahydrof 14 (17)	4.90E+07	5.55E+07	7.690033939	7.744068125	1.13248951
P22234		47790.4	6.95 Multifunctional j 18 (24)	1.18E+08	1.34E+08	8.073296721	8.126354327	1.12994578
Q92614		234168	5.95 Myosin-XVIIIa C 1 (4)	5.68E+06	6.41E+06	6.754117604	6.807065265	1.12965977
Q15435		41652.6	4.84 Protein phospho 11 (16)	5.18E+07	5.84E+07	7.713988408	7.766678671	1.12899044
Q13618	Q53S54	89443.7	8.68 Cullin-3 OS=Ho 6 (10)	1.20E+07	1.36E+07	7.080770019	7.133077572	1.12799598
Q9NTK5	D7EHM2	44943.4	7.64 Obg-like ATPas 4 (6)	1.14E+08	1.28E+08	8.05511102	8.106991911	1.12688835
Q14254		47433.8	5.19 Flotillin-2 OS=H 10 (14)	1.25E+07	1.41E+07	7.097996175	7.149401438	1.12565489
Q16531		128142	5.14 DNA damage-b 32 (41)	5.41E+07	6.08E+07	7.732959327	7.783619956	1.12372652
P08237		85983.7	8.23 6-phosphofruct 15 (22)	1.44E+08	1.61E+08	8.156926489	8.207540107	1.12360488
Q15021	B4E0B7, F5GZ	158508	6.19 Condensin com 2 (4)	3.01E+06	3.38E+06	6.479107064	6.529308753	1.12253965
P05388	Q53HW2	34422.9	5.71 60S acidic ribos 5 (6)	8.34E+06	9.36E+06	6.921245843	6.971256178	1.12204516
Q13747		22871	6.11 Alpha-1 antitryp 3 (7)	4.61E+06	5.16E+06	6.664103305	6.712821912	1.1187128
Q14558		39653.7	6.73 Phosphoribosyl 12 (15)	6.70E+07	7.50E+07	7.826190238	7.874817105	1.11847651
B3KSH1	O00303, B4DE1	39236	5.24 HCG1784554, i 3 (3)	4.46E+06	4.99E+06	6.649370386	6.697966482	1.11839726
P54619	Q8N7V9, B4DC	37726.8	6.42 5'-AMP-activate 3 (3)	7.74E+06	8.65E+06	6.888529689	6.936856608	1.11770429
P17213		54093.2	9.41 Bactericidal per 12 (17)	6.55E+07	7.32E+07	7.816062881	7.864288744	1.11744425
O15144	Q53R19	34425.5	6.84 Actin-related pr 2 (4)	2.01E+07	2.25E+07	7.303079432	7.351219633	1.11722386
Q86UX7		76475.2	6.52 Fermitin family 124 (26)	1.18E+08	1.31E+08	8.071560356	8.118864998	1.11507645
Q00796		38927.1	8.23 Sorbitol dehydr 4 (5)	1.79E+07	2.00E+07	7.253163217	7.300383203	1.11485911
P04114	C0JYY2	516651	6.58 Apolipoprotein I9 (21)	5.14E+06	5.72E+06	6.710612698	6.757630436	1.11434005
O00743		35805.7	5.43 Serine/threonin 1 (3)	7.21E+06	8.04E+06	6.858114732	6.905041087	1.11410559
Q9UPU5		297200	5.79 Ubiquitin carbo 22 (30)	2.47E+07	2.75E+07	7.392938768	7.439748375	1.11380614
B4DQJ8	P52209, A8K2Y	52352.5	7.12 6-phosphogluc 11 (12)	1.95E+07	2.17E+07	7.289622491	7.33601532	1.11273777
Q9BUL8		24685.8	7.79 Programmed ce 4 (4)	1.27E+07	1.41E+07	7.104465229	7.150235314	1.11114333
Q15042	A6H8Z3, C9J8C	111594	5.38 Rab3 GTPase-2 (3)	3.46E+06	3.84E+06	6.539018249	6.58472332	1.11097701
P49588		107485	5.34 Alanyl-tRNA sy 16 (18)	1.75E+07	1.94E+07	7.242009908	7.287430428	1.11024933
B3KY95	Q15084, B5MC	53655	5.35 cDNA FLJ1614 1 (1)	7.39E+06	8.19E+06	6.868525219	6.913311422	1.10862892
Q01813		86453.9	7.5 6-phosphofruct 9 (13)	1.22E+08	1.35E+08	8.085122151	8.129753493	1.10823367
Q96AZ6		20521.7	9.1 Interferon-stimu 1 (2)	1.08E+07	1.19E+07	7.032072114	7.076499275	1.10771277
Q9Y4P8	E7EVF6, B3KM	50175.1	6.04 WD repeat dom 3 (3)	1.19E+07	1.32E+07	7.076948123	7.12102921	1.10683042
P46459	B7Z5J7	83055.3	6.52 Vesicle-fusing f 23 (31)	9.13E+07	1.01E+08	7.960449392	8.004072578	1.10566404
Q13057		62632.1	6.51 Bifunctional coe 1 (1)	4.32E+06	4.78E+06	6.635680637	6.6791403	1.10524781
P68366	A8MUB1	50633.7	4.95 Tubulin alpha-4 8 (11)	9.65E+07	1.07E+08	7.984544151	8.027997612	1.10523203
B4DKI2		30314.6	8 cDNA FLJ6028 3 (4)	7.63E+06	8.43E+06	6.882531242	6.925593673	1.10423735
Q9UKV8		98400.4	9.32 Protein argonat 33 (37)	1.40E+08	1.54E+08	8.145184124	8.18813597	1.10395621
Q2TAZ0		214893	5.57 Autophagy-rela 4 (6)	5.76E+06	6.36E+06	6.760314754	6.803115562	1.10357234
Q9BT78		46524.8	5.57 COP9 signalos 22 (25)	2.07E+08	2.28E+08	8.315072695	8.357790922	1.10336252
Q0VGA5	Q53HA4, P4951	58883	6.05 SARS protein C 2 (4)	6.10E+06	6.73E+06	6.785302138	6.827911027	1.10308477
P63092	A6NI00	46092.1	5.59 Guanine nucleo 2 (2)	5.27E+06	5.81E+06	6.721701107	6.763978554	1.10224325
P11215	Q4VAK1	128410	6.88 Integrin alpha-N 10 (13)	1.45E+07	1.59E+07	7.160849995	7.20270356	1.10116796
C9JIG9		52109	7.64 Uncharacterize 4 (5)	4.18E+07	4.59E+07	7.621133357	7.661668966	1.0978313
Q7Z4W1		26181.7	8.33 L-xylulose redu 5 (6)	1.68E+07	1.84E+07	7.224420246	7.264606981	1.09694975
P48556		39871.9	9.73 26S proteasom 10 (15)	2.74E+08	3.00E+08	8.437570025	8.477190538	1.09552051
P25787		25996.3	6.92 Proteasome sul 14 (18)	2.97E+08	3.25E+08	8.472166053	8.5117032	1.09531024
P43490		55771.7	6.69 Nicotinamide pt 8 (10)	3.04E+07	3.32E+07	7.482539549	7.521768323	1.09453278
Q9P0J7		42603.2	5.41 E3 ubiquitin-prc 1 (1)	2.14E+07	2.34E+07	7.329811258	7.368879106	1.09412728
Q7Z6Z7	E9PD66, E7EV	485523	5.1 E3 ubiquitin-prc 28 (45)	4.69E+07	5.12E+07	7.670716251	7.709003436	1.09216231
Q14477		10978.6	6.17 Hbbm fused glo 8 (11)	2.71E+10	2.96E+10	10.43330227	10.4713917	1.0916651
Q6J1Z7		11495.9	6.17 Hemoglobin bel 12 (16)	2.71E+10	2.96E+10	10.43330227	10.4713917	1.0916651
P60900		27838	6.34 Proteasome sul 8 (9)	3.82E+08	4.17E+08	8.582432233	8.620193572	1.09084071
P68036	A8K4W8	18021.3	8.68 Ubiquitin-conju 4 (5)	8.95E+07	9.76E+07	7.951929685	7.989667452	1.09078151
Q99536		42121.5	5.88 Synaptic vesicle 11 (14)	4.46E+07	4.86E+07	7.648863688	7.686518451	1.09057306
Q32Q12		32906	8.7 Nucleoside dipt 15 (19)	3.91E+08	4.26E+08	8.592161543	8.629701957	1.09028595
P50990	Q53HU0	60152.7	5.42 T-complex prot 41 (44)	8.51E+08	9.26E+08	8.929756803	8.966660068	1.08868757

E2RVJ0	P02730	102150	5.1 Solute carrier fa 38 (47)	3.11E+09	3.39E+09	9.493442033	9.529923138	1.08762982
P21283	A8MQ60	44085	7.02 V-type proton A 1 (2)	3.07E+06	3.34E+06	6.487832606	6.52422984	1.08741979
Q10567		105482	4.94 AP-1 complex s 19 (22)	6.82E+07	7.41E+07	7.833928846	7.869725904	1.08591807
P22303	B7WPI6	68209.5	5.87 Acetylcholinestr 3 (5)	7.60E+06	8.24E+06	6.880598026	6.915862513	1.08458723
P48643		60089	5.45 T-complex prot 31 (39)	5.29E+08	5.74E+08	8.723296602	8.758557865	1.08457918
A8K2X8		60148	5.34 cDNA FLJ7843: 37 (44)	5.29E+08	5.74E+08	8.723296602	8.758557865	1.08457918
Q08211		142181	6.41 ATP-dependent 24 (35)	4.60E+07	4.98E+07	7.662957896	7.697296579	1.08227763
P07900		85005.8	4.94 Heat shock prot 14 (19)	2.07E+08	2.23E+08	8.315001465	8.348320726	1.07974017
Q96P70		116858	4.71 Importin-9 OS= 5 (8)	8.11E+06	8.76E+06	6.909189839	6.942423069	1.07952631
O43776		63757.8	5.9 Asparaginyl-TR 2 (2)	3.44E+06	3.71E+06	6.536145164	6.569296073	1.0793217
P60520	Q6FG91	13715.1	7.82 Gamma-aminot 1 (1)	9.33E+06	1.01E+07	6.969822967	7.002759224	1.07878837
Q14974	B2RBR9	98419.5	4.68 Importin subuni 8 (9)	1.00E+07	1.08E+07	7.001578971	7.034403342	1.07851049
B7Z8P7		53693.3	7.56 cDNA FLJ5906: 2 (3)	6.61E+06	7.12E+06	6.820067545	6.852631534	1.07786406
A0N071	P02042	16159.3	7.85 Delta globin OS 16 (17)	2.21E+10	2.37E+10	10.34342148	10.37554076	1.07676091
O94973		104807	6.53 AP-2 complex s 25 (30)	2.29E+08	2.46E+08	8.359648408	8.391279863	1.07555211
Q9BT73		13267.1	7.72 Proteasome as: 2 (2)	8.46E+06	9.10E+06	6.927271341	6.958863919	1.07545583
Q15404		31520.7	8.57 Ras suppressor 8 (13)	8.35E+07	8.98E+07	7.92184341	7.953265335	1.07503332
P02786	A8K6Q8	85274.1	6.18 Transferrin rece 3 (6)	9.50E+06	1.02E+07	6.977940702	7.009349932	1.0750019
P62333		44430.2	7.1 26S protease re 13 (17)	7.86E+07	8.45E+07	7.895303255	7.926701398	1.07497445
A7E2Y5	O75165	256572	6.31 DnaJ (Hsp40) h 28 (35)	3.40E+07	3.65E+07	7.531923639	7.562638267	1.07328393
O95456	B2RD51	33630.9	6.88 Proteasome as: 6 (7)	4.18E+07	4.48E+07	7.620999951	7.651280256	1.07221112
P62826	B5MDF5, A8K3	24578.7	7.01 GTP-binding nu 15 (18)	4.06E+09	4.35E+09	9.608657774	9.638908436	1.07213793
Q15365	Q53SS8	37987.1	6.66 Poly(rC)-binding 2 (2)	3.71E+07	3.98E+07	7.569579917	7.59936932	1.07099983
Q15181		33095.3	5.54 Inorganic pyrop 2 (5)	1.05E+07	1.12E+07	7.019187888	7.048969	1.07097939
B011T1	Q6ZNI9	125449	9.23 MYO1F variant 4 (5)	3.13E+06	3.35E+06	6.495922794	6.52544415	1.07033902
O15511		16367.3	5.47 Actin-related pr 2 (5)	6.18E+07	6.62E+07	7.791129684	7.820580225	1.0701645
P49368	Q5SZY0, B3KX	61065.5	6.1 T-complex prot 49 (53)	1.37E+09	1.47E+09	9.137819058	9.167057611	1.06964226
Q9ULC4		20769.9	8.98 Malignant T cell 4 (6)	4.46E+07	4.77E+07	7.649426434	7.678562701	1.06939037
P04406	E7EUT4	36201.5	8.57 Glyceraldehyde 10 (14)	1.42E+08	1.52E+08	8.152745064	8.181704979	1.06895621
P16157	E7EVE3, E7EV	207334	5.65 Ankyrin-1 OS=F 80 (97)	2.90E+09	3.10E+09	9.462247862	9.491028527	1.0685151
P69905	D1MGQ2	15305	8.72 Hemoglobin sul 16 (17)	1.16E+10	1.23E+10	10.06307418	10.09151814	1.06768702
P69891		16187.3	6.64 Hemoglobin sul 10 (12)	1.56E+10	1.66E+10	10.19222651	10.22031841	1.06682182
P69892	E7CYP2, D9YZ	16173.3	6.64 Hemoglobin sul 11 (13)	1.56E+10	1.66E+10	10.19213397	10.22014467	1.06662241
P48729	Q71TU5	39118	9.59 Casein kinase 1 11 (14)	6.10E+07	6.51E+07	7.785278881	7.813253275	1.06653324
B4DG22	P51812	80874.6	6.68 Uncharacterize 7 (14)	1.67E+07	1.78E+07	7.223172031	7.250994202	1.06615947
Q92530	Q5QPM7	29969.1	5.42 Proteasome inh 3 (5)	1.40E+07	1.49E+07	7.146274639	7.173510829	1.06472191
B3KRM8		21052.1	7.78 Translin, isoform 4 (4)	1.38E+07	1.47E+07	7.1397854	7.166557704	1.06358524
Q13098		56071.4	6.3 COP9 signalos 17 (22)	9.53E+07	1.01E+08	7.979049677	8.005569612	1.06296738
Q2F834	P19105, O1495	16438.7	4.41 Myosin regulat 4 (5)	3.83E+07	4.07E+07	7.58337036	7.609861532	1.06289698
Q27J81	C9JAR5	136851	5.26 Inverted formin- 1 (1)	1.08E+06	1.15E+06	6.033584166	6.059942595	1.06257215
P42025		42380.8	5.98 Beta-centractin 5 (8)	3.64E+07	3.87E+07	7.561072122	7.587376927	1.06244096
P35579	Q60FE2	227646	5.5 Myosin-9 OS=F 30 (40)	1.76E+08	1.87E+08	8.246702734	8.27189007	1.05971074
Q4W4Y1	Q8WUM4	96646.4	6.13 Dopamine rece 3 (8)	3.28E+06	3.47E+06	6.515767103	6.540607738	1.0588651
Q05DH1	O14818	26868.2	8.98 Proteasome sul 7 (10)	4.38E+07	4.64E+07	7.641791241	7.666518503	1.05858872
P05164		84784.2	9.19 Myeloperoxidas 22 (27)	1.82E+08	1.92E+08	8.259719712	8.284017808	1.05754315
P13639		96246.3	6.41 Elongation fact 9 (10)	1.95E+07	2.07E+07	7.290868243	7.31501864	1.05718355
Q14C86		166359	5.09 GTPase-activat 30 (37)	1.72E+08	1.82E+08	8.235526363	8.259343117	1.05637169
P00918		29284.9	6.87 Carbonic anhyd 8 (10)	2.08E+08	2.19E+08	8.317564784	8.34094871	1.05531941
O00410		125032	4.83 Importin-5 OS= 22 (28)	1.23E+08	1.29E+08	8.088958875	8.112230702	1.05504705
P50395	E7EU23, B4DL	51087.1	6.11 Rab GDP disso 2 (3)	3.37E+06	3.56E+06	6.528003962	6.551268776	1.05503001
P50570		98345.3	7.04 Dynamin-2 OS= 40 (49)	2.44E+08	2.57E+08	8.387185539	8.409848159	1.05356812
E9PEQ4		98190.3	7.04 Uncharacterize 39 (51)	2.44E+08	2.57E+08	8.387185539	8.409848159	1.05356812
P35612	B4DM17, Q05C	81259.6	5.67 Beta-adducin O 9 (12)	1.44E+08	1.51E+08	8.157471217	8.179997634	1.05323775
P40227	Q59ET3	58443.8	6.23 T-complex prot 29 (34)	5.95E+08	6.26E+08	8.774329261	8.796698971	1.05285778
P78371	B5BTY7	57794.3	6.01 T-complex prot 42 (53)	1.12E+09	1.18E+09	9.050883088	9.073172991	1.05266432
P21333	E9KL45, Q60FI	283301	5.7 Filamin-A OS=F 51 (65)	7.52E+07	7.92E+07	7.876426942	7.898578955	1.05233015
B4DH02	P34932, Q59GI	95156.6	5.11 cDNA FLJ5051: 7 (10)	3.43E+07	3.61E+07	7.534834149	7.556937361	1.05221191
P05089		34884.4	6.72 Arginase-1 OS= 3 (7)	8.95E+06	9.41E+06	6.951661601	6.9737381	1.05214719
Q969U7		29776.2	6.6 Proteasome as: 8 (12)	8.18E+07	8.60E+07	7.912771207	7.934683409	1.05174923
B0YJ88	A7YIJ8, P3524	68635.4	6.03 Radixin OS=Ho 9 (13)	2.12E+08	2.23E+08	8.326561875	8.348471497	1.05174298

P15311	Q6NUR7	69483.8	5.94 Ezrin OS=Homr 11 (15)	2.12E+08	2.23E+08	8.326561875	8.348471497	1.05174298
P26038		67891.8	6.08 Moesin OS=Ho 18 (23)	2.12E+08	2.23E+08	8.326561875	8.348471497	1.05174298
P26447		11948.8	5.85 Protein S100-A 2 (3)	1.08E+07	1.14E+07	7.035429516	7.056929744	1.05075201
P36543	Q53Y06, A8MU	26185.8	7.71 V-type proton A 1 (1)	2.69E+06	2.83E+06	6.430309229	6.451267902	1.04944256
B4DT12	Q9HA65, B9A6	69606.7	4.97 cDNA FLJ5565 1 (2)	3.04E+07	3.19E+07	7.48340352	7.504234175	1.04913326
P17987		60818.8	5.8 T-complex prot 32 (34)	9.57E+08	1.00E+09	8.980917198	9.001559609	1.04867861
Q9Y570		42687.4	5.67 Protein phospho 4 (4)	1.92E+07	2.01E+07	7.283204813	7.303571755	1.04801366
B4DRN7	F5H5R1	117550	5.6 Uncharacterizer 5 (7)	1.08E+07	1.13E+07	7.031812817	7.05198521	1.04754429
P50991	A8K3C3	58401	7.96 T-complex prot 27 (31)	1.30E+09	1.36E+09	9.11442955	9.134592688	1.04752196
P68871	D9YZU5	16102.3	6.75 Hemoglobin sul 19 (23)	3.16E+10	3.30E+10	10.49919639	10.51869661	1.04592421
B3VL17		11533.8	5.9 Beta globin (Fr 19 (22)	3.16E+10	3.30E+10	10.49919639	10.51869661	1.04592421
C8C504		16101.4	7.86 Beta-globin OS: 18 (21)	3.16E+10	3.30E+10	10.49919639	10.51869661	1.04592421
Q3LR79		11531.9	5.46 Hemoglobin bel 16 (18)	3.16E+10	3.30E+10	10.49919639	10.51869661	1.04592421
Q5TEG0	E9PEN7	24496.7	5.66 Novel enoyl-Co 4 (4)	1.21E+07	1.26E+07	7.081151604	7.100318444	1.04512164
Q9Y265	B5BUB1	50538.4	6.02 RuvB-like 1 OS 14 (17)	1.50E+08	1.56E+08	8.175190334	8.194139682	1.04459838
P14868		57499.2	6.11 Aspartyl-tRNA : 10 (13)	4.47E+07	4.67E+07	7.650167766	7.669073737	1.04449405
Q96IJ6		46604.2	6.73 Mannose-1-pho 2 (2)	5.94E+06	6.20E+06	6.773892633	6.792296667	1.04328757
P07237	E7EPA8	57479.8	4.76 Protein disulfide 2 (4)	1.48E+06	1.55E+06	6.171011946	6.189389238	1.04322333
B0QZ18	Q99829, Q59EI	60307.1	5.66 Copine I OS=Hr 4 (4)	6.59E+06	6.88E+06	6.819035764	6.837360392	1.04309684
P53990	A8K5S3, B4DH	39896.5	5.22 IST1 homolog C 3 (3)	8.82E+06	9.19E+06	6.945299335	6.963422044	1.04261197
Q96GG9	B4DM76	30333.1	5.18 DCN1-like prote 8 (8)	5.98E+07	6.23E+07	7.776789591	7.794776215	1.04228533
Q9BRP4		43132.4	5.92 Proteasomal A13 (3)	1.87E+07	1.95E+07	7.271995312	7.289773935	1.04178625
P62873	Q1RMY8, B2Rf	38151.3	5.6 Guanine nuclec 4 (4)	1.39E+07	1.44E+07	7.141648951	7.159379376	1.04167064
O94919		55722.5	5.55 Endonuclease c 5 (8)	2.86E+07	2.98E+07	7.456528074	7.474184805	1.0414939
Q86XM2		73849.2	5.82 ADD1 protein C 9 (12)	1.47E+08	1.53E+08	8.166496482	8.184126959	1.04143094
P00352	B4DDF8, B4DX	55454.2	6.3 Retinal dehydro 3 (3)	4.22E+06	4.39E+06	6.624963174	6.64247194	1.04113912
P00387	B7Z7L3	34440.8	7.18 NADH-cytochro 9 (11)	2.51E+07	2.61E+07	7.399428321	7.416834834	1.04089402
Q6PIU2	F5H7K4	46063.8	6.76 Neutral cholestr 3 (5)	9.40E+06	9.79E+06	6.973314233	6.990630169	1.04067695
P61221		68240.4	8.63 ATP-binding ca 6 (8)	1.75E+07	1.83E+07	7.244121146	7.261434737	1.04067133
P29401	Q53EM5	68519	7.58 Transketolase C 20 (24)	1.76E+08	1.83E+08	8.245438439	8.262339897	1.03968423
P62158	B2RDW0, Q9BI	16826.8	4.09 Calmodulin OS: 3 (4)	1.43E+07	1.49E+07	7.156328898	7.172801171	1.03865729
P61158	Q53QM2, Q59F	47797.2	5.61 Actin-related pr 7 (12)	5.01E+07	5.20E+07	7.699713141	7.716147424	1.03856643
P24941		34079.1	8.8 Cyclin-depende 6 (11)	2.25E+07	2.34E+07	7.352184558	7.368506633	1.03829814
Q99832	Q53HV2	59842.1	7.55 T-complex prot 37 (50)	9.08E+08	9.42E+08	8.957859726	8.974105379	1.03811545
B1ALA9		24467.6	7.62 Phosphoribosyl 8 (13)	7.78E+08	8.07E+08	8.890767225	8.907004925	1.03809643
B9A6M6	Q9ULP9	63985.4	7.14 TBC1 domain f: 4 (7)	3.97E+07	4.12E+07	7.599139275	7.615082398	1.03739255
P54577		59448.2	6.61 Tyrosyl-tRNA s: 15 (22)	3.83E+07	3.97E+07	7.58332652	7.599061531	1.03689555
P05109		10884.7	6.51 Protein S100-A: 6 (6)	4.10E+08	4.25E+08	8.613223298	8.628892387	1.03673817
B4E3A8		38774.7	6.22 Uncharacterizer 13 (13)	6.65E+07	6.90E+07	7.82295068	7.838618296	1.03673466
P30740		42828.7	5.9 Leukocyte elast 12 (13)	6.65E+07	6.90E+07	7.82295068	7.838618296	1.03673466
P63000	A4D2P0, A4D2	21835.4	8.77 Ras-related C3 6 (9)	1.12E+08	1.16E+08	8.049372885	8.06457695	1.03562867
P60891	Q53FW2, B2Rf	35325.1	6.51 Ribose-phospho: 13 (20)	9.92E+08	1.03E+09	8.996408221	9.011366248	1.03504213
P21281		56807	5.57 V-type proton A 10 (13)	3.65E+07	3.77E+07	7.562464759	7.575853326	1.03130843
P27105		31881.8	7.71 Erythrocyte ban 15 (18)	4.12E+08	4.25E+08	8.614974282	8.627998155	1.03044276
B2R514	E7EM64, Q7L5	33896.1	5.65 cDNA, FLJ923C 9 (12)	1.87E+08	1.93E+08	8.272540849	8.28518973	1.02955341
O94903		30609.7	7.09 Proline synthas f: 4 (7)	5.35E+07	5.50E+07	7.728252181	7.74062348	1.02889557
P24666	Q59EH3	18486.9	6.3 Low molecular v 6 (7)	2.95E+07	3.04E+07	7.470290646	7.482561558	1.02865777
P48426		46423.6	6.5 Phosphatidylinc 15 (17)	1.65E+08	1.70E+08	8.218469952	8.23028859	1.02758708
E7EUY0		470050	6.81 Uncharacterizer 1 (4)	1.60E+06	1.64E+06	6.20345501	6.215185524	1.0273786
P60842	A8K7F6	46352.6	5.32 Eukaryotic initia 5 (9)	1.73E+07	1.77E+07	7.237325326	7.248960055	1.02715203
P28289		40657.9	5.03 Tropomodulin-17 (11)	2.89E+07	2.96E+07	7.46063501	7.471673262	1.02574227
Q92905		37782.8	6.1 COP9 signalosr 17 (19)	1.49E+08	1.53E+08	8.173310968	8.184224627	1.02544804
B2RD79	P54578	56462.2	5.2 Ubiquitin carbo: 12 (17)	5.52E+08	5.66E+08	8.741793183	8.752598823	1.02519302
Q6ZW64		54313.6	6.07 cDNA FLJ4155: 1 (1)	4.84E+06	4.95E+06	6.684413904	6.694930831	1.02451171
Q4KKX0	P16452	70096.2	8.68 EPB42 protein t 26 (31)	2.89E+08	2.95E+08	8.460303646	8.470280962	1.02323955
P11413	A8K8D9	59675.2	6.39 Glucose-6-phos 24 (26)	1.00E+08	1.02E+08	8.000103921	8.00997547	1.02299038
P09543		47947.8	9.17 2',3'-cyclic-nucl 7 (11)	1.52E+07	1.55E+07	7.181847738	7.191645705	1.02281707
B3KNN7	F5H8K4	57310.7	8.49 cDNA FLJ3004: 35 (39)	2.04E+08	2.08E+08	8.308733186	8.318274316	1.02221237
Q9UL46	A8MZ76, C9JE	27555.4	5.54 Proteasome act 14 (16)	4.84E+08	4.94E+08	8.684409495	8.693932494	1.02216969
P28066	Q5U0A0	26565.3	4.74 Proteasome sul 11 (14)	4.62E+08	4.72E+08	8.664345802	8.673738335	1.02186267

Q16401	A8K4T6	56559.5	5.35 26S proteasom	21 (23)	1.89E+08	1.93E+08	8.275807172	8.285098301	1.0216241
B4DNA3		47319.4	8.4 Adenyl cyclas	17 (19)	9.76E+07	9.97E+07	7.989273357	7.998562209	1.02161874
O75083	Q59ER5, A8M	66836.1	6.17 WD repeat-cont	3 (7)	1.02E+07	1.04E+07	7.006739772	7.015899228	1.0213144
Q5JS54	C9J2F8, D6RB	13823	6.04 Proteasome as	3 (3)	4.17E+06	4.25E+06	6.619762596	6.628875407	1.02120471
F5H136		14580.6	4.72 T-complex prot	7 (8)	4.76E+08	4.86E+08	8.677987957	8.686955508	1.0208632
O00232		53269.7	7.53 26S proteasom	26 (32)	1.77E+08	1.81E+08	8.248530842	8.25714665	1.02003673
B4DQH9	Q6VN20	65071.6	6.47 Uncharacterize	4 (5)	9.10E+06	9.28E+06	6.958851874	6.967439278	1.01997001
P23743		83945.2	6.28 Diacylglycerol	k 10 (12)	3.21E+07	3.27E+07	7.506574878	7.515116769	1.01986313
B2R657	Q53HM8, B4DV	52891.8	5.38 cDNA, FLJ927	3 (5)	5.37E+06	5.48E+06	6.730150291	6.738440985	1.01927341
O00487		34725.6	6.06 26S proteasom	14 (19)	4.12E+08	4.20E+08	8.614733378	8.622996842	1.01920856
P41091		51647.4	8.66 Eukaryotic tran	14 (17)	1.00E+08	1.02E+08	8.002006036	8.010259701	1.01918651
Q5XPI4		149960	6.31 E3 ubiquitin-pro	34 (40)	7.60E+07	7.74E+07	7.880949781	7.889006023	1.01872331
P15531		17308.7	5.83 Nucleoside dipt	12 (14)	3.89E+08	3.96E+08	8.589464201	8.597283068	1.01816665
Q13616		90306.2	8.19 Cullin-1 OS=Ho	25 (33)	4.37E+07	4.44E+07	7.640114791	7.64756997	1.01731437
Q13492	B4DTM3	70881.1	7.7 Phosphatidylinc	5 (10)	2.95E+07	3.00E+07	7.47029162	7.477736479	1.0172902
Q5VSJ9		44244.6	9.85 Rh blood group	2 (2)	5.79E+07	5.89E+07	7.762872776	7.770237127	1.01710163
B3VL12		4263.24	4.96 Truncated beta	7 (8)	1.65E+10	1.68E+10	10.2184526	10.22578041	1.01701606
Q96TA1	Q5VVW7, Q4LI	83144.1	5.81 Niban-like prote	5 (6)	5.81E+06	5.91E+06	6.764402289	6.77160518	1.01672357
P11908		35146.1	6.15 Ribose-phosph	8 (10)	8.32E+08	8.46E+08	8.920274586	8.927394926	1.01653033
P28838		56530	8.03 Cytosol aminop	3 (4)	3.79E+06	3.84E+06	6.578282593	6.584701462	1.01488975
O95782		108561	6.63 AP-2 complex s	31 (39)	1.09E+09	1.11E+09	9.039340416	9.045594042	1.01450368
P05198	Q53XC0	36374.5	5.02 Eukaryotic tran	2 (3)	9.95E+06	1.01E+07	6.998035191	7.004151642	1.01418329
P68371	Q8IZ29, Q8N6	50255.2	4.79 Tubulin beta-2C	21 (25)	9.13E+07	9.26E+07	7.960470276	7.966390617	1.01372543
Q5JP53	P07437, B7ZAF	48135.1	4.7 Tubulin beta po	18 (22)	9.13E+07	9.26E+07	7.960470276	7.966390617	1.01372543
B2R491	Q96IR1, Q53H	29807.1	10.16 Ribosomal prot	2 (3)	8.36E+06	8.46E+06	6.922125294	6.927421351	1.01226928
P07996	Q59E99	133291	4.71 Thrombospondi	7 (11)	4.08E+07	4.12E+07	7.610146967	7.615386731	1.01213808
B3KUJ2	Q5JRR6	57489.8	5.94 cDNA FLJ4002	1 (1)	3.51E+06	3.55E+06	6.544914748	6.549919609	1.01159078
P17812		67332.3	6.02 CTP synthase	14 (7)	9.70E+06	9.81E+06	6.986876785	6.991583746	1.01089712
B4DZV5	Q5J7V5, Q000	49272.1	6.85 cDNA FLJ5882	18 (22)	1.11E+08	1.12E+08	8.046249201	8.050892622	1.01074924
O00178	B2RDW9	73035.3	8.6 GTP-binding pr	2 (3)	4.67E+06	4.71E+06	6.66957309	6.673473495	1.00902147
F5H715		32171.9	6.48 Uncharacterize	2 (3)	7.13E+06	7.19E+06	6.853019755	6.856912605	1.00900391
B4DV64	Q6UX06	42110.1	5.43 cDNA FLJ6142	3 (7)	1.35E+07	1.36E+07	7.129163032	7.132536752	1.00779853
B7Z815	Q93009, B7ZAJ	127272	5.45 Ubiquitin carbo	3 (9)	4.09E+06	4.12E+06	6.611515626	6.614716491	1.00739749
Q9Y6E3	Q53GN6	42872.2	5.71 HSPC027 OS=I	22 (26)	4.82E+08	4.85E+08	8.682925738	8.686117387	1.00737611
P30043		22219.5	7.13 Flavim reductas	9 (9)	5.58E+07	5.62E+07	7.746810789	7.749756596	1.00680603
Q9H871		44819.5	5.7 Protein RMD5 f	2 (3)	6.29E+06	6.33E+06	6.798890608	6.801660797	1.00639898
P62256	A4D1L6, Q7Z6I	20699.1	4.55 Ubiquitin-conju	2 (2)	1.07E+07	1.08E+07	7.029270217	7.031986431	1.00627391
P35998		49002.3	5.71 26S protease re	23 (28)	1.15E+08	1.15E+08	8.05993553	8.062131217	1.00506856
D8MJ82		83739.3	8.09 Kell blood group	6 (7)	1.91E+07	1.92E+07	7.281139401	7.282920442	1.00410942
Q99497		20049.6	6.33 Protein DJ-1 O	1 (2)	7.57E+05	7.60E+05	5.87921618	5.880891301	1.00386456
P36959		37850.9	6.6 GMP reductase	10 (15)	1.15E+08	1.15E+08	8.060223077	8.061587367	1.00314633
Q53FA7		35684.7	6.67 Quinone oxidor	11 (15)	1.03E+08	1.03E+08	8.012871376	8.013954938	1.00249811
Q13200	Q59EG8, F5GZ	100877	5.08 26S proteasom	25 (31)	2.10E+08	2.10E+08	8.322000206	8.323008617	1.00232465
Q1WWM3	C9JTS2, P1117	83617.8	5.52 EPB41 protein i	6 (9)	1.23E+08	1.23E+08	8.088862718	8.089586766	1.00166857
P08397	F5H345	39533.7	6.68 Porphobilinoge	1 (2)	4.90E+06	4.91E+06	6.690364501	6.690882697	1.0011939
P08514		114446	5.21 Integrin alpha-II	9 (10)	2.21E+07	2.21E+07	7.344009941	7.344106443	1.00022223
C9J3Z0		24127.4	6.89 Uncharacterize	1 (1)	4.90E+06	4.90E+06	6.689958688	6.689772023	0.99957028
B2RB13	Q9UKU0, B4DF	78714.1	6.98 cDNA, FLJ952	1 (4)	4.90E+06	4.90E+06	6.689958688	6.689772023	0.99957028
P60660	B7Z6Z4	17090.2	4.56 Myosin light pol	7 (8)	1.11E+08	1.11E+08	8.045597872	8.045111265	0.99888017
D6RCN7	Q9UI26, D6RJE	17116.1	6.41 Uncharacterize	1 (1)	1.30E+06	1.29E+06	6.112388676	6.111527177	0.99801829
P42858		351374	5.81 Huntingtin OS=	12 (24)	8.11E+06	8.09E+06	6.909053557	6.907870063	0.99727861
Q9Y484	C9JUS5, C9JB	40640.3	6.75 WD repeat dom	2 (3)	5.77E+06	5.75E+06	6.761275671	6.759816366	0.99664547
D3DTH7		99613.4	9.48 Myosin IC, isof	1 (2)	1.88E+06	1.88E+06	6.27531077	6.273564606	0.99598738
F5H6E2	B7Z3E5	119719	9.46 Uncharacterize	1 (2)	1.88E+06	1.88E+06	6.27531077	6.273564606	0.99598738
P07738	A4D1N9, B3KU	30157.6	6.1 Bisphosphoglyc	7 (11)	5.46E+07	5.43E+07	7.736875153	7.734943752	0.99556266
P35580	Q149N4	229827	5.44 Myosin-10 OS=	19 (25)	1.04E+08	1.03E+08	8.016874117	8.014835551	0.99531703
Q9Y678		98967	5.32 Coatomer subu	1 (4)	4.71E+06	4.68E+06	6.672645269	6.670537265	0.9951579
Q9BRG1		20848.6	5.97 Vacuolar protei	2 (3)	6.54E+06	6.50E+06	6.815562487	6.813030198	0.99418615
Q96F85		18750.6	7.72 CB1 cannabino	9 (11)	2.92E+08	2.91E+08	8.465971345	8.463253641	0.99376179
Q0P512	B3KVN0	54360.7	9.04 Solute carrier fe	13 (15)	8.55E+08	8.49E+08	8.931998304	8.929150015	0.99346303

P08575	F5GXZ3, Q6PJ	148644	5.77 Receptor-type t 1 (1)	6.39E+06	6.35E+06	6.805704065	6.802632991	0.99295353
Q86VP6	A8K8U1	137999	5.52 Cullin-associate 33 (45)	3.23E+08	3.21E+08	8.509293562	8.505995266	0.99243416
P11142		71082.3	5.37 Heat shock cog 23 (27)	1.03E+08	1.02E+08	8.011629488	8.008215609	0.99217007
Q15418	E9PGT3, B7Z2	83069.9	7.68 Ribosomal prot 3 (5)	6.13E+06	6.08E+06	6.787553493	6.784105938	0.99209314
B2RDD7	B4DX49, O147	73347.9	5.88 cDNA, FLJ965E4 (5)	1.66E+07	1.64E+07	7.219239558	7.215639659	0.99174519
B4DWX5	A8K7F7, Q5TI8	46066.7	6.67 cDNA FLJ5502:4 (6)	3.65E+07	3.62E+07	7.562826976	7.559059447	0.99136246
F5GYF7	F5H248, A8K9#	23895.6	5.21 Uncharacterize 6 (8)	4.99E+07	4.95E+07	7.698333849	7.694315676	0.99079048
Q6VFAQ		4567.43	8.18 Hemoglobin bel 3 (4)	2.94E+09	2.91E+09	9.468137181	9.463613391	0.98963765
P26641	Q53YD7	50429.3	6.25 Elongation factr 4 (4)	1.74E+07	1.72E+07	7.241219254	7.2366694	0.98957826
P47755	A4D0V4, Q53G	33156.7	5.57 F-actin-capping 4 (4)	3.77E+07	3.72E+07	7.575778966	7.570434776	0.98776995
P08311		29161.2	11.19 Cathepsin G O:8 (8)	1.69E+08	1.67E+08	8.229156741	8.223677394	0.98746259
Q6IPX4	P62249	17267.1	10.97 RPS16 protein 1 (1)	9.11E+06	9.00E+06	6.959756325	6.954059219	0.9869676
B2RMN7		247271	5.15 Spectrin, beta, 120 (140)	5.18E+08	5.11E+08	8.714744677	8.708606025	0.98596466
P11277		247171	5.15 Spectrin beta cl 121 (141)	5.18E+08	5.11E+08	8.714744677	8.708606025	0.98596466
Q9UNS2		48412.2	6.19 COP9 signalos 6 (13)	1.33E+08	1.31E+08	8.125189789	8.118837291	0.98547929
P31146		51678.1	6.25 Coronin-1A OS 10 (11)	1.01E+08	9.92E+07	8.003059721	7.996434031	0.98485957
Q5UOP9		35003.5	6.29 Purine-rich elen 3 (5)	2.18E+07	2.15E+07	7.338517178	7.331877983	0.98482895
P02671	A8K3E4	95655.7	5.7 Fibrinogen alph 1 (3)	1.77E+07	1.74E+07	7.247357603	7.240712127	0.9848147
P55060	A3RLL6	111145	5.51 Exportin-2 OS= 3 (4)	4.81E+06	4.74E+06	6.682401761	6.675743393	0.98478547
P53680		17177.8	5.82 AP-2 complex s 5 (7)	1.12E+08	1.10E+08	8.047627211	8.040952081	0.98474746
O15400		29911.4	5.41 Syntaxin-7 OS=2 (2)	7.78E+06	7.67E+06	6.891224256	6.884515374	0.98467093
P27708		245167	6.02 CAD protein OS 5 (10)	8.92E+06	8.79E+06	6.950580241	6.943818938	0.98455209
P62879	Q6FHM2	38048.3	5.6 Guanine nuclec 4 (4)	1.29E+07	1.27E+07	7.110599177	7.103647035	0.98411955
P61163		42701	6.19 Alpha-centractin 11 (14)	1.25E+08	1.23E+08	8.095717491	8.088756921	0.98410045
B2RDW1	F5H2Z3, Q5U5	18295.6	9.68 Ribosomal prot 7 (8)	8.55E+08	8.40E+08	8.932016097	8.92433712	0.9824739
D3DWK4		30372.7	8.12 Pyrroline-5-carb 2 (2)	4.57E+07	4.48E+07	7.65954673	7.651205411	0.98097668
B0UX83	B4DZ12, B4E3'	119085	5.4 HLA-B associat 3 (3)	8.87E+06	8.70E+06	6.948122171	6.939574024	0.98050961
P25789		29750.3	7.57 Proteasome sul 4 (4)	3.29E+07	3.23E+07	7.517273802	7.508719995	0.98049683
O14523		76590.5	7.62 C2 domain-con 1 (2)	2.30E+06	2.25E+06	6.360821273	6.352258818	0.9804773
B7Z5J8	B7ZAC3, B7Z8-	58780.7	7.99 cDNA FLJ5613:2 (2)	5.82E+08	5.71E+08	8.765265483	8.756334917	0.9796466
F5H2H8	B7Z5A7	46553.2	6.36 Uncharacterize 2 (4)	5.82E+08	5.71E+08	8.765265483	8.756334917	0.9796466
B7ZW70		21165.1	8.87 LOC727761 prc 4 (9)	3.00E+07	2.94E+07	7.477632311	7.468455792	0.97909195
E1P646	A8K916, E1P64	106321	5.25 Adaptor-related 28 (33)	7.73E+07	7.56E+07	7.888138431	7.878485849	0.97801928
P17612	A8K8B9	40678	8.84 cAMP-depende 1 (3)	2.97E+06	2.90E+06	6.473118551	6.462821333	0.97656866
Q99627	Q53QS9	23268	5.25 COP9 signalos 8 (12)	1.21E+08	1.18E+08	8.081328743	8.070392839	0.97513354
P38606	B7Z1R5	68659.6	5.35 V-type proton A 7 (11)	1.90E+07	1.85E+07	7.278082404	7.266403258	0.97346615
Q7Z351		53502.9	8.74 Putative unchar 4 (6)	7.06E+07	6.87E+07	7.84909762	7.836653181	0.97175226
B4DR63	Q53HB3, Q53X	41255.2	4.9 Uncharacterize 9 (12)	1.48E+08	1.43E+08	8.169445057	8.156173381	0.96990305
P24158		28245.4	8.72 Myeloblastin O:4 (5)	1.18E+08	1.14E+08	8.071168013	8.057357821	0.96870113
Q99460	B2R6D0	106795	5.25 26S proteasom 32 (42)	3.13E+08	3.03E+08	8.495002649	8.481135144	0.9685733
Q9H4B7		50864.8	5.05 Tubulin beta-1 8 (10)	7.51E+07	7.27E+07	7.875382562	7.861472506	0.96847841
P02679	C9JEU5, C9JC	52106.1	5.37 Fibrinogen gam 6 (9)	1.31E+07	1.27E+07	7.117367217	7.103023661	0.96751219
P16989		40066	9.77 DNA-binding pr 1 (1)	1.18E+07	1.14E+07	7.072464124	7.058120292	0.96751157
P00558	A8K4W6	44985.3	8.3 Phosphoglycer 8 (12)	2.00E+07	1.93E+07	7.300881578	7.286438638	0.96729081
P23276		83683.3	8.09 Kell blood group 4 (7)	1.24E+07	1.19E+07	7.091928278	7.076763323	0.96568402
Q9NP58		94396.4	8.75 ATP-binding ca 2 (2)	7.32E+06	7.05E+06	6.864228376	6.848482421	0.96439299
P12829		21664.9	4.97 Myosin light ch 11 (11)	1.31E+08	1.27E+08	8.118851894	8.103027763	0.96421941
P30153	A8K3H8, B4DD	66065.2	5 Serine/threonin 6 (11)	1.69E+07	1.62E+07	7.227285859	7.210626793	0.96236747
Q8NEV1		45261	8.54 Casein kinase 1 3 (4)	1.36E+07	1.30E+07	7.132428501	7.115495737	0.96176116
Q6IB22	P40306	29203.2	8.26 Proteasome sul 2 (2)	9.33E+06	8.97E+06	6.969939503	6.953001153	0.96174879
P52907	A8K0T9	33073.4	5.45 F-actin-capping 4 (5)	6.77E+07	6.50E+07	7.830865247	7.813242478	0.96023434
O00560	B2R5Q7, B4DH	32595	7.05 Syntenin-1 OS= 1 (1)	6.73E+06	6.45E+06	6.82781938	6.809731274	0.95920602
Q9GZP4		24390.8	5.47 PITH domain-c 3 (3)	9.77E+06	9.36E+06	6.989696326	6.971285166	0.95849277
P28072	Q6IAT9	25569.5	4.8 Proteasome sul 5 (6)	3.77E+08	3.61E+08	8.576348359	8.557884295	0.95837602
B7Z5E3		40097	8.61 L-lactate dehyd 6 (7)	3.94E+07	3.77E+07	7.594965385	7.576476095	0.95832035
Q8N122		150653	6.43 Regulatory-ass 4 (6)	9.18E+06	8.79E+06	6.963051618	6.943778247	0.95659175
P49720		23218.6	6.14 Proteasome sul 13 (19)	5.39E+08	5.16E+08	8.731837456	8.71233544	0.95608826
P68363	B3KT06, B3KP:	50803.9	4.94 Tubulin alpha-1 9 (13)	1.04E+08	9.94E+07	8.017078905	7.997552467	0.95603449
P61224	B4DQI8	21039.7	5.65 Ras-related pro 7 (7)	5.42E+07	5.18E+07	7.734220264	7.714482051	0.95556842
P62834	A8KAH9, Q5UC	21315.8	6.38 Ras-related pro 7 (7)	5.42E+07	5.18E+07	7.734220264	7.714482051	0.95556842

P61225	Q5JQ44	20719.3	4.73 Ras-related pro 1 (1)	1.22E+07	1.16E+07	7.086267276	7.066069631	0.95455807
D3DPU2		51925.8	8.07 Adenyl cyclas 22 (25)	1.99E+08	1.90E+08	8.299269297	8.278897361	0.95417507
Q15366	Q59HD4, B4DX	38954.7	6.33 Poly(rC)-binding 2 (3)	2.26E+07	2.16E+07	7.354717987	7.3340427	0.95350882
P25786	Q53YE8	29822	6.15 Proteasome sul 10 (15)	3.06E+08	2.91E+08	8.485713659	8.464623284	0.95259791
O00442	A8K8K1	39824.6	8.01 RNA 3'-termina 3 (6)	1.62E+07	1.54E+07	7.21053543	7.188823777	0.95123615
P68104	Q5VTE0, Q53H	50451.2	9.1 Elongation fact 11 (15)	1.36E+08	1.29E+08	8.132604134	8.110797579	0.95102831
P51148		23695.9	8.64 Ras-related pro 5 (6)	2.55E+07	2.43E+07	7.40691781	7.384947739	0.95067031
O14724		23134	5.93 Beta-spectrin (F 12 (15)	1.63E+08	1.55E+08	8.212761884	8.190702756	0.95047538
P49721		22992.7	6.51 Proteasome sul 17 (18)	3.92E+08	3.72E+08	8.593247356	8.570569418	0.94912205
Q96CW1		49965.2	9.57 AP-2 complex s 12 (17)	2.62E+07	2.48E+07	7.417593996	7.394867902	0.94901681
B4DME9	C9JXT5, C9K0I	60003.2	5.81 Uncharacterize 1 (1)	4.46E+06	4.22E+06	6.648887545	6.625787932	0.94820095
Q14697		107263	5.74 Neutral alpha-g 6 (13)	1.23E+07	1.16E+07	7.088142316	7.064402546	0.94680432
Q9HDC9		46621.9	5.82 Adipocyte plas 1 (2)	1.11E+07	1.05E+07	7.044595091	7.020655461	0.94636871
B2R4M6	P06702	13258.6	5.71 cDNA, FLJ92148 (10)	2.32E+08	2.20E+08	8.365649894	8.341629478	0.94619268
P68402	Q6IBR6	25724.2	5.57 Platelet-activati 1 (1)	4.34E+06	4.10E+06	6.637179687	6.612953468	0.94574441
P32119	B4DF70	22049.3	5.66 Peroxiredoxin-2 11 (12)	7.12E+09	6.72E+09	9.852284246	9.827639434	0.94483329
Q9H0U4		22328.3	5.55 Ras-related pro 4 (6)	3.30E+07	3.12E+07	7.518907942	7.494259917	0.9448263
Q8WU76		75877.4	6.21 Sec1 family dor 1 (1)	1.28E+06	1.21E+06	6.10693	6.082104762	0.94444085
Q9GZS3		33730.8	5.16 WD repeat-conn 3 (4)	9.37E+06	8.84E+06	6.971659393	6.946685085	0.94411673
B3KW16	B7Z579, Q562E	81638.1	6.25 cDNA FLJ4190.4 (6)	1.06E+07	9.99E+06	7.024526569	6.999419085	0.94382726
P14780		79491.8	5.69 Matrix metallopro 9 (11)	2.80E+07	2.64E+07	7.446851931	7.421366698	0.94300667
B7Z507		72478.1	5.53 cDNA FLJ5103.8 (10)	2.80E+07	2.64E+07	7.446851931	7.421366698	0.94300667
Q8WW22	E9PDM9, F5H1	45453.3	7.52 DnaJ homolog : 1 (2)	1.15E+07	1.09E+07	7.061279043	7.035781933	0.94298089
Q5IRN2		49105.8	8.92 DAZAP1/MEF2 1 (1)	3.54E+06	3.33E+06	6.54902348	6.522869266	0.9415552
B0V0T3	Q5JNW4, P280	21042.4	4.8 Proteasome sul 3 (5)	1.66E+07	1.56E+07	7.219260405	7.19251132	0.9402664
Q06323	Q6IBM2	28876.1	5.78 Proteasome act 11 (13)	5.23E+07	4.92E+07	7.718893289	7.692023933	0.94000604
P23381		53473.7	5.83 Tryptophanyl-tR 20 (24)	7.16E+07	6.72E+07	7.854616123	7.827653077	0.93980327
P13224	F5H0F6	22274	9.67 Platelet glycopr 2 (2)	1.02E+07	9.54E+06	7.007083087	6.979689143	0.93887128
P61020		23920	8.29 Ras-related pro 3 (3)	2.30E+07	2.16E+07	7.360993376	7.333447697	0.93854331
Q6PJG0		24959.3	6.88 Putative unchar 1 (1)	1.63E+07	1.53E+07	7.21206301	7.183339779	0.93600198
Q0EFC6	E9PHP0	62553	9.22 HSR1 protein C6 (7)	1.56E+07	1.46E+07	7.192126377	7.162911188	0.9349423
Q9H9Q2		29888.5	5.83 COP9 signalos 6 (7)	3.03E+07	2.83E+07	7.481843729	7.452050544	0.93369883
Q9NYU2		177819	5.42 UDP-glucose:gl 1 (4)	3.80E+06	3.54E+06	6.57926751	6.54922259	0.93315778
Q8N9N7		27079.4	8.7 Leucine-rich rep 2 (3)	1.00E+07	9.31E+06	6.999984472	6.96908993	0.931334
P02675	Q32Q65	56576.5	8.54 Fibrinogen beta 4 (5)	1.98E+07	1.84E+07	7.296278335	7.264543192	0.92953309
Q06830		22324.4	8.27 Peroxiredoxin-1 19 (20)	4.44E+09	4.12E+09	9.647047824	9.614821651	0.92848272
P60709	Q8WVW5	42051.9	5.29 Actin, cytoplasm 24 (27)	1.06E+09	9.81E+08	9.023996675	8.991593684	0.92810478
P68032		42334	5.23 Actin, alpha car 16 (19)	7.22E+08	6.69E+08	8.858353378	8.825703532	0.92757739
Q16563	A4D0R1, A8K8	28888.8	8.69 Synaptophysin- 1 (1)	5.88E+07	5.44E+07	7.769495121	7.735518174	0.92474726
Q9H2M9	A6H8V0	157482	5.4 Rab3 GTPase-: 2 (5)	9.60E+06	8.84E+06	6.982315941	6.946576082	0.92100108
P04921		13801.7	4.69 Glycophorin-C 1 (3)	3.23E+07	2.97E+07	7.509109084	7.47322027	0.92068525
D3DUS9		31056.8	5.65 Triosephosphat 1 (1)	2.07E+08	1.90E+08	8.315505665	8.279474924	0.92038442
E9PAV3		205979	9.6 Uncharacterize 1 (3)	7.86E+06	7.23E+06	6.895506521	6.859416543	0.92025889
Q9H479		35377	7.13 Fructosamine-3 10 (12)	5.05E+07	4.64E+07	7.702926466	7.666560073	0.91967336
Q6P5S8		26041.9	5.94 IGK@ protein C3 (3)	4.79E+07	4.40E+07	7.680433722	7.643598923	0.91868198
Q0KKI6	Q8TCD0	24300.1	8.29 Immunobulbulir 3 (4)	4.79E+07	4.40E+07	7.680433722	7.643598923	0.91868198
P55884	B4DV79, B4DX	92823	4.89 Eukaryotic tran 1 (1)	3.38E+06	3.11E+06	6.52923302	6.492063368	0.91797393
P47756	B4DWA6, E7EC	31615.9	5.36 F-actin-capping 8 (9)	3.48E+07	3.19E+07	7.541750386	7.504052662	0.91685842
P31948	A8K690	63226.6	6.4 Stress-induced- 7 (10)	1.79E+07	1.64E+07	7.252399286	7.214555505	0.91655012
O43760	Q3KQZ2	25079.3	4.75 Synaptogyrin-2 2 (2)	1.26E+07	1.15E+07	7.100028822	7.061757423	0.91564811
Q15102		25832.3	6.33 Platelet-activati 1 (1)	5.82E+06	5.33E+06	6.765172913	6.72634772	0.91448126
P04040		59946.8	6.9 Catalase OS=H 10 (13)	1.64E+07	1.49E+07	7.21405453	7.174260242	0.91244293
P29972	B4DW35, B2R6	28736.1	6.95 Aquaporin-1 OS 1 (2)	1.94E+07	1.77E+07	7.28787425	7.247719739	0.91168643
Q99598	B1APC6	33205.8	6.1 Translin-associ 1 (2)	4.53E+06	4.13E+06	6.656430217	6.616258395	0.91165009
P40925	B7Z3I7, F5H09	36631.1	6.91 Malate dehydro 2 (5)	6.11E+06	5.55E+06	6.785991923	6.744159511	0.90817091
Q9Y4G8	B4DG82	168168	6.21 Rap guanine nu 4 (6)	1.18E+07	1.07E+07	7.070227812	7.027642171	0.90659717
Q9Y230		51295.6	5.49 RuvB-like 2 OS 29 (39)	2.65E+08	2.40E+08	8.422523275	8.379459815	0.90560026
Q13201	E7EPG1, B7Z7	139221	8.15 Multimerin-1 OS 2 (4)	6.38E+06	5.77E+06	6.805072695	6.761380621	0.90429041
P80188	B2ZDQ1	22744.8	9.02 Neutrophil gelat 6 (9)	3.29E+07	2.96E+07	7.516929966	7.471515464	0.90071106
Q00610		193260	5.48 Clathrin heavy c 11 (17)	3.19E+07	2.87E+07	7.503902503	7.458473436	0.90068086

Q9H4M9	B2R5U3	60645.7	6.35 EH domain-con 10 (17)	1.88E+07	1.69E+07	7.27344553	7.226965603	0.89850412
Q13404		16598.4	7.71 Ubiquitin-conjug 3 (3)	9.98E+06	8.96E+06	6.999275133	6.952400426	0.89768774
B2R4D5	B4DM63, O151	20735.4	8.78 cDNA, FLJ92053 (5)	1.54E+07	1.38E+07	7.187027425	7.139593129	0.89653181
Q04323	E9PJ81, E9PR	33419	5.23 UBX domain-cc 1 (2)	1.51E+07	1.35E+07	7.17798834	7.12959084	0.89454563
Q92539		100193	5.18 Phosphatidate 1 (3)	1.53E+07	1.36E+07	7.183650995	7.135005381	0.89403472
B4E1Y5	P04839	13292.9	9.6 cDNA FLJ50351 (1)	4.52E+06	4.03E+06	6.655177289	6.605690294	0.89230434
P61160		45017.3	6.3 Actin-related pr 12 (17)	4.58E+07	4.09E+07	7.660878481	7.611263322	0.89204105
Q5T447		98134.9	5.47 E3 ubiquitin-pro 3 (8)	5.12E+06	4.54E+06	6.708860849	6.657294884	0.88804308
B2R6N0	Q53HJ0, B4DIH	51868.2	5.37 cDNA, FLJ93026 (9)	1.11E+07	9.81E+06	7.043500298	6.991484113	0.88712295
P28074		28633.3	6.43 Proteasome sul 15 (16)	3.98E+08	3.53E+08	8.59947038	8.547356259	0.88692292
P61088		17184	6.13 Ubiquitin-conjug 2 (2)	5.91E+06	5.24E+06	6.771881296	6.719209383	0.88578452
Q9NRW1	B7Z337	23560.9	5.41 Ras-related pro 3 (4)	2.11E+07	1.87E+07	7.325038914	7.272280661	0.88560844
Q9NR46	F6RPD3, B7ZC	44174.7	5.72 Endophilin-B2 1 (4)	7.52E+06	6.65E+06	6.876318001	6.823062987	0.88459603
P20618	Q53FT8	26700.5	8.27 Proteasome sul 17 (18)	2.31E+08	2.05E+08	8.364458776	8.311137244	0.88446055
P28070		29242.5	5.72 Proteasome sul 12 (14)	2.66E+08	2.34E+08	8.424187685	8.369957497	0.88261197
Q08AL5	Q9Y4E8	110542	5 Ubiquitin carbox 18 (22)	7.96E+07	7.00E+07	7.901139596	7.845196466	0.87913763
P25788	Q6IB71	28643.2	5.19 Proteasome sul 8 (8)	1.20E+08	1.04E+08	8.077927702	8.018719015	0.87255199
Q6FHU0	P28062	30019.4	5.53 PSMB8 protein 3 (4)	1.79E+07	1.56E+07	7.252645941	7.192450495	0.87057172
P55072		89950	5.14 Transitional enc 33 (41)	1.65E+08	1.44E+08	8.218196471	8.157866076	0.87030124
P02788	B3VMW0, A8K	80013.6	8.5 Lactotransferrin 21 (21)	2.16E+08	1.88E+08	8.335110111	8.274398411	0.86953747
Q2TUW9		79812.4	8.51 Lactoferrin OS= 18 (18)	2.16E+08	1.88E+08	8.335110111	8.274398411	0.86953747
B3KP20		29488	6 cDNA FLJ30973 (5)	1.69E+07	1.47E+07	7.229155859	7.168215105	0.86907898
Q14203	E7EX90, E9PG	142348	5.61 Dynactin subun 2 (3)	5.70E+06	4.95E+06	6.756203453	6.694421445	0.86739715
Q9UPN7		97291	4.45 Serine/threonin 2 (3)	4.56E+06	3.95E+06	6.658778751	6.596258677	0.8659243
P07384		82465.4	5.49 Calpain-1 catal 33 (41)	3.05E+08	2.64E+08	8.484722357	8.421026227	0.86358257
Q58WW2		97258.7	5.14 DDB1- and CUL2 (3)	1.08E+07	9.29E+06	7.032740777	6.968013025	0.86153366
Q13620		104486	7.01 Cullin-4B OS= 2 (2)	3.74E+06	3.22E+06	6.572435826	6.507185982	0.86049858
P84077	P61204	20740.7	6.32 ADP-ribosylatio 14 (16)	1.44E+08	1.24E+08	8.159864994	8.094200349	0.85967709
O15439		150344	8.41 Multidrug resist 1 (2)	1.67E+06	1.44E+06	6.223249759	6.157498955	0.85950656
B4DI39	A8K5I0, F5H1D	67774.7	5.36 cDNA FLJ54325 (5)	4.73E+07	4.06E+07	7.674568209	7.608536126	0.85895007
Q8WVM8	Q53GW1	72676.2	5.89 Sec1 family dor 2 (6)	3.64E+06	3.13E+06	6.561519865	6.495358903	0.85869521
Q9Y490		271766	5.77 Talin-1 OS=Hor 31 (38)	2.92E+07	2.51E+07	7.465536653	7.399221281	0.85838996
B4E2S7		40186	5.39 Uncharacterizer 1 (1)	3.47E+06	2.97E+06	6.540086906	6.473305072	0.85746848
Q969T9	A6NG10, Q7Z5	28182.5	5.65 WW domain-bir 4 (4)	1.70E+07	1.45E+07	7.22940417	7.162607548	0.85743929
Q6IBT1	Q86U62, E9KL	30260.3	7.57 Proteasome sul 7 (7)	9.57E+07	8.20E+07	7.98075146	7.913950226	0.85743018
P43034		47178.4	6.97 Platelet-activati 4 (7)	2.47E+07	2.11E+07	7.391946994	7.325136992	0.85741287
P02549		281039	4.95 Spectrin alpha 107 (122)	1.01E+08	8.63E+07	8.004602171	7.936205312	0.85428571
Q5T4S7		580547	5.7 E3 ubiquitin-pro 82 (111)	1.44E+08	1.23E+08	8.15897459	8.090305582	0.85375054
Q96RL7		361872	5.94 Vacuolar protein 7 (16)	2.44E+07	2.07E+07	7.387422203	7.317016357	0.85034337
P23528	B4E112, E9PP	18718.7	8.22 Cofilin-1 OS=Hx 1 (1)	1.65E+07	1.40E+07	7.216266566	7.145532022	0.84969968
P48507	D3DT44	31049.9	5.69 Glutamate-cys 2 (2)	8.02E+06	6.79E+06	6.903917292	6.831657347	0.84672046
Q9UNZ2		40548.3	4.99 NSFL1 cofactor 5 (8)	2.26E+07	1.91E+07	7.354234984	7.281734523	0.84625167
Q9Y285	Q6IBR2, B4E3	57584.5	7.31 Phenylalanyl-tR 1 (1)	3.91E+06	3.31E+06	6.592407125	6.519768306	0.84598211
P04075		39851.5	8.3 Fructose-bisph 3 (4)	8.14E+06	6.88E+06	6.910452963	6.837688087	0.8457366
B3KSL2		78585.7	8.39 cDNA FLJ36531 (17)	1.51E+08	1.27E+08	8.178416458	8.105041997	0.84455034
B2RD40	Q719H8, Q96F	60430.2	5.64 cDNA, FLJ96441 (1)	1.35E+07	1.14E+07	7.13161825	7.056339495	0.84085526
Q15691	A2VCR0	30151.3	5.02 Microtubule-ass 8 (10)	5.01E+07	4.20E+07	7.699986292	7.623475085	0.83847244
P43686	A8K2M0	47450.6	5.09 26S protease re 11 (16)	3.46E+07	2.88E+07	7.539194744	7.459738812	0.83280643
O75015	Q9UPY7	26484.3	6.22 Low affinity imn 1 (2)	3.08E+06	2.55E+06	6.487990929	6.4069636	0.82979855
Q9NQC3	Q8IU44	130250	4.43 Reticulon-4 OS= 1 (1)	5.84E+06	4.82E+06	6.76629204	6.683260742	0.82597842
P04632		28468.8	5.05 Calpain small s 13 (18)	1.88E+08	1.55E+08	8.273914529	8.190867531	0.82594856
Q5HYL3		8101.05	6.81 Putative unchar 4 (4)	2.14E+07	1.76E+07	7.330909221	7.245572707	0.82160578
O00233		24837.6	6.46 26S proteasom 4 (5)	2.48E+07	2.03E+07	7.394999304	7.308259756	0.81895578
Q9NWX6		35150.6	8.11 Probable tRNA(2 (3)	1.42E+07	1.16E+07	7.153302763	7.064770044	0.81558134
A4D1P6		84204.1	6.15 WD repeat-cont 5 (7)	6.11E+06	4.96E+06	6.785983848	6.695260548	0.81147791
Q13177	A8K5M4	58291	5.69 Serine/threonin 1 (4)	6.61E+06	5.36E+06	6.820339034	6.729544515	0.81134484
Q15370	B7WPD3	13238.6	4.73 Transcription el 1 (2)	1.18E+06	9.58E+05	6.072679384	5.981298505	0.81025015
B2R680	A8K4S9, F5GZ	94850.5	5.84 cDNA, FLJ92822 (3)	4.71E+06	3.79E+06	6.673390179	6.579150691	0.80493444
P45974		96637.7	4.91 Ubiquitin carbox 3 (4)	4.84E+06	3.88E+06	6.684661581	6.588344055	0.80109215
Q59F66		81701	8.22 DEAD box poly 1 (6)	1.18E+07	9.40E+06	7.071565556	6.973348823	0.79759655

Q8N1G4		64004	8.55 Leucine-rich rep 2 (3)	3.69E+06	2.94E+06	6.566984493	6.468051067	0.79628141
Q13610	Q9BV37, Q53F	56363.3	4.6 Periodic tryptop 2 (2)	8.38E+06	6.57E+06	6.923118539	6.817850117	0.78475046
P53618		108214	5.72 Coatomer subu 1 (3)	5.00E+06	3.86E+06	6.699204176	6.586590658	0.77158981
O43149		335767	5.62 Zinc finger ZZ-t 3 (7)	9.08E+06	6.98E+06	6.958140077	6.844098996	0.76905769
Q13561	A8K8J9	44317.9	5.1 Dynactin subun 10 (11)	2.43E+07	1.86E+07	7.386223768	7.270436359	0.76597146
O14618	E9PP76, Q8NE	29535.6	5.32 Copper chapert 1 (1)	9.98E+06	7.63E+06	6.998940459	6.882384812	0.76461771
A8K008		52248	8.44 cDNA FLJ7838 5 (7)	1.27E+08	9.69E+07	8.10491976	7.986396898	0.76116207
B0QYT3	P46060, B4E0L	27122.1	5.07 Ran GTPase ac 1 (1)	6.68E+06	5.02E+06	6.82462239	6.700834454	0.75199
O43324	C9J1V9, D6RB	19855.4	8.54 Eukaryotic tran: 1 (1)	3.47E+06	2.57E+06	6.54006147	6.4106137	0.74225346
D3DRP5		38274.2	10.85 Chromosome 9 3 (4)	2.60E+07	1.93E+07	7.415555158	7.285743826	0.74163236
P37840	Q4W5L2, E7EF	14451.2	4.67 Alpha-synuclein 3 (4)	4.82E+07	3.56E+07	7.682720877	7.550915768	0.73823544
Q9UIQ6	B2RAK1	117787	5.5 Leucyl-cystinyl : 3 (6)	5.40E+06	3.96E+06	6.732494981	6.597619337	0.7330344
P08246		29127	9.71 Neutrophil elast 5 (5)	6.03E+07	4.41E+07	7.780447582	7.644658736	0.73149465
Q15276	F5GZU7, Q05B	99628.5	4.95 Rab GTPase-bi 1 (1)	2.71E+06	1.97E+06	6.433509405	6.293405509	0.72426267
Q9BTE6	B3KSP9, B4DI7	45793.4	6 Alanyl-tRNA ed 3 (5)	1.25E+07	9.01E+06	7.097327697	6.95493272	0.72045195
P11021		72402.5	5.07 78 kDa glucose 5 (5)	1.04E+07	7.34E+06	7.016767717	6.865698993	0.70620579
P61026		22754.7	8.59 Ras-related pro 3 (3)	4.11E+07	2.86E+07	7.613734726	7.457117464	0.69724071
P61006		23824.3	9.15 Ras-related pro 3 (4)	3.80E+07	2.62E+07	7.579980159	7.418260075	0.6890963
Q5TDH0		44950.7	4.95 Protein DDI1 hc 4 (5)	1.61E+07	1.08E+07	7.206577764	7.035025983	0.67367157
O95197	B7Z8W8, B7Z3	113169	4.85 Reticulon-3 OS: 1 (3)	1.99E+07	1.32E+07	7.298861323	7.11901016	0.66091991
P80511		10568.5	5.83 Protein S100-A 1 (1)	1.56E+07	1.03E+07	7.192966943	7.012073119	0.65933507
O43488		40019.9	6.7 Aflatoxin B1 ald 1 (1)	4.89E+06	3.20E+06	6.689642407	6.505019056	0.65369724
Q05D08		45578.7	9.08 PA2G4 protein 4 (7)	1.69E+07	1.06E+07	7.228428276	7.027169954	0.62913186
A2RUM0	B4E0C4, B3KY	110841	4.9 Poly (ADP-ribos 2 (2)	7.46E+06	4.68E+06	6.872496048	6.670085888	0.62746548
O75874	Q6FHQ6, Q567	46914.6	6.53 Isocitrate dehyd 2 (4)	4.53E+06	2.79E+06	6.656433024	6.445651901	0.61548699
P49913		19517.2	9.48 Cathelicidin ant 2 (2)	4.39E+07	2.67E+07	7.642789624	7.426704735	0.60801614
O14980		124447	5.71 Exportin-1 OS= 2 (5)	3.85E+06	2.29E+06	6.585606453	6.359747261	0.59448487
Q8NHP1		37340.3	6.27 Aflatoxin B1 ald 1 (2)	1.11E+07	6.37E+06	7.044273114	6.803968069	0.57503589
P22061	B7Z972	24791.6	6.7 Protein-L-isoas 2 (5)	6.59E+06	3.40E+06	6.818845479	6.531214317	0.5156664
E9PB22	Q08722	34351.4	6.82 Uncharacterizer 2 (3)	1.10E+08	5.19E+07	8.039627047	7.715239795	0.4738193
Q5XTR9		3938.9	5.28 Hemoglobin del 2 (2)	2.57E+09	1.00E+09	9.410736582	9.000099299	0.38847468
Q6PIK3		13641.9	9.26 HCG1995540, i 2 (2)	2.74E+07	9.85E+06	7.437653659	6.993225951	0.35939522

Supplemental Data 5

Sheet 4

Quantified Proteins OS-treated

AC	Other ACs	MW	pl	Description	#QPE	PAI OS1	PAI OS2	Log(PAI OS1)	Log(PAI OS2)	Ratio PAI
Q9NT62		36297.62	4.66	Ubiquitin-like-conjugating enzyme ATG3 OS=Homo sapiens GN=ATG3 PE=1 SV=1	1 (1)	1.34E+06	4.04E+06	6.125964932	6.606294133	3.022214753
OS9HE5		32451.41	5.33	Cysteine-RNA ligase isoform b variant (Fragment) OS=Homo sapiens PE=2 SV=1	1 (2)	1.73E+06	4.95E+06	6.239117896	6.69424664	2.851863717
O95197	B7Z3E3, F5H774, B7ZBW8	113168.66	4.85	Relicculin-3 OS=Homo sapiens GN=RTN3 PE=1 SV=2	1 (3)	2.19E+06	5.98E+06	6.33999837	6.776903016	2.734658993
Q02413		147022.25	4.9	Desmoglein-1 OS=Homo sapiens GN=DSG1 PE=1 SV=2	2 (2)	7.54E+05	1.78E+06	5.877641754	6.251119022	2.363073706
P00754	Q5TZK1	41076.48	5.5	Guanine nucleotide-binding protein (G <i>q</i>) subunit alpha OS=Homo sapiens GN=GNQA3 PE=1 SV=3	2 (2)	2.77E+06	5.81E+06	6.442668804	6.764178093	2.095569624
B4DVG3		31934.33	9.11	Phosphoribosylaminoimidazole-succinocarboxamide synthase OS=Homo sapiens PE=2 SV=1	2 (4)	9.69E+05	5.98E+05	5.986154902	6.254361916	1.85415349
D7RX09	P15924	281080.01	6.57	Desmoplakin la OS=Homo sapiens PE=2 SV=1	2 (5)	6.09E+05	1.02E+06	5.784439699	6.007974758	1.673150697
Q69BU7		29776.18	6.6	Proteasome assembly chaperone 2 OS=Homo sapiens GN=PSMG2 PE=1 SV=1	4 (6)	3.55E+06	5.90E+06	6.54977936	6.770603711	1.662740025
P29972	B4DW35, B2R6P2, B4E3E3, B4DPF5, B4DNW4, B4F4P6, B4DV2A	28736.14	6.95	Aquaporin-1 OS=Homo sapiens GN=AQP1 PE=1 SV=3	1 (2)	1.11E+07	1.83E+07	7.044838097	7.262361608	1.650150335
Q6JS08		15027.63	5.48	Aquaporin-1 splice variant 2 (Fragment) OS=Homo sapiens GN=AQP1 PE=2 SV=1	1 (2)	1.11E+07	1.83E+07	7.044838097	7.262361608	1.650150335
Q13464	D9ZGF8	159102.13	5.66	Rho-associated protein kinase 1 OS=Homo sapiens GN=ROCK1 PE=1 SV=1	2 (4)	9.86E+05	1.64E+06	5.998298354	6.214926699	1.646752554
C3JRV9		12758.33	5.46	Uncharacterized protein OS=Homo sapiens GN=UBA5 PE=4 SV=1	2 (3)	3.39E+06	5.55E+06	6.530669147	6.744331238	1.635543465
Q3SVB4	Q96P63	48814.33	5.25	SERPINB12 protein OS=Homo sapiens GN=SERPINB12 PE=2 SV=1	1 (1)	1.12E+06	1.80E+06	6.05100737	6.255374581	1.600911083
				cDNA, FLJ179530, highly similar to Homo sapiens O-acyltransferase (membrane bound) domain containing 2	2 (2)	1.11E+06	1.73E+06	6.04566778	6.236985408	1.553522789
BOAZU0	Q6ZW77	50192.26	7.95	(OACT2), mRNA OS=Homo sapiens PE=2 SV=1	4 (6)	3.59E+06	5.54E+06	6.554759147	6.743167305	1.543150053
P05106	B4DTY9	90193.61	5.09	Integrin beta-3 OS=Homo sapiens GN=ITGB3 PE=1 SV=2	6 (9)	1.39E+07	2.12E+07	7.143418158	7.327048462	1.526266261
Q9UN52		48412.23	6.19	COP9 signalosome complex subunit 3 OS=Homo sapiens GN=COP3 PE=1 SV=3	2 (3)	1.70E+06	2.98E+06	6.230212483	6.412225912	1.520594581
P02675	Q3Q365	56575.62	8.54	Fibrinogen beta chain OS=Homo sapiens GN=FGB PE=1 SV=2	4 (6)	3.93E+06	5.91E+06	6.593845203	6.77156365	1.505630649
Q9NP58		94396.37	8.75	ATP-binding cassette sub-family B member 6, mitochondrial OS=Homo sapiens GN=ABCB6 PE=1 SV=1	1 (1)	1.36E+06	2.01E+06	6.131942267	6.304128828	1.486574097
Q9HDC9	A2AZF9	46621.91	5.82	Adipocyte plasma membrane-associated protein OS=Homo sapiens GN=APMAP PE=1 SV=2	11 (13)	2.61E+07	3.85E+07	7.417379388	7.584972881	1.470935039
P35612	Q0SDK5	81259.6	5.67	Beta-adducin OS=Homo sapiens GN=ADD2 PE=1 SV=3	18 (19)	4.44E+07	6.52E+07	7.647812781	7.814153592	1.466699481
P54920		33687.45	5.23	Alpha-tubulin NSF attachment protein OS=Homo sapiens GN=NAPA PE=1 SV=3	16 (20)	1.81E+08	2.35E+08	8.206096679	8.367473762	1.450030332
P27185		31881.8	7.71	Cytochrome band 7 integral membrane protein OS=Homo sapiens GN=STOM PE=1 SV=3	10 (13)	2.86E+07	4.28E+07	7.470782321	7.63211119	1.449869351
P61014	Q5VTE0, Q6IP59, Q53HM9, Q6IP79, Q53H07, Q6IPN6	59451.24	9.1	Elongation factor 1-alpha OS=Homo sapiens GN=EEF1A1 PE=1 SV=1	3 (4)	4.02E+06	5.82E+06	6.604474185	6.764997693	1.447183186
B4DFL8	E7EX86	22871.39	9.11	cDNA FLJ59865, highly similar to WW domain-binding protein 2 OS=Homo sapiens GN=3.6.3.1	1 (1)	1.47E+06	2.12E+06	6.168264097	6.327217424	1.441960377
B7Z3V1		113791.04	5.21	OS=Homo sapiens PE=2 SV=1	3 (3)	4.20E+07	6.05E+07	7.623559236	7.781972236	1.440167479
F5GX33	Q5CCG7	53641.16	9.19	Uncharacterized protein OS=Homo sapiens GN=RHD PE=4 SV=1	3 (6)	3.18E+06	4.58E+06	5.502898614	6.66080787	1.438496289
P02679	Q3JEU5, Q3JC4C	52106.1	5.37	Fibrinogen gamma chain OS=Homo sapiens GN=FGG PE=1 SV=3	2 (3)	1.70E+06	2.98E+06	6.230212483	6.412225912	1.520594581
Q02094	EP9C36, Q9E298, Q9LH40, Q9LK70, Q9UHH2, F5H250, Q9LH09	44453.79	9.45	Blood group Rn(CE) polypeptide OS=Homo sapiens GN=RHCE PE=1 SV=2	5 (5)	4.34E+07	6.24E+07	7.637711876	7.795114423	1.436820676
P18577	Q9JUZ5, F5GXQ4, B5RHP0, D5L846, Q5SVJ9, Q9H248, Q9CJ07	45872.42		cDNA, FLJ94557, highly similar to Homo sapiens FK506 binding protein 4, 59kDa (FKBP4), mRNA OS=Homo sapiens PE=2 SV=1	5 (8)	3.55E+06	7.66E+06	6.728230293	6.884250609	1.432254897
B2R9J2		52087.19	5.35	sapiens PE=1 SV=1	18 (21)	6.69E+07	9.47E+07	7.825520819	7.976254698	1.414926581
Q92905		37782.8	6.1	COP9 signalosome complex subunit 5 OS=Homo sapiens GN=COP35 PE=1 SV=4	1 (1)	1.05E+06	1.48E+06	6.019276452	6.169430855	1.413039828
B4DVH6		145420.28	8.46	PE=2 SV=1	3 (4)	2.71E+06	3.80E+06	6.432253244	6.579279753	1.402899335
B4DLP6	P53041, Q9BPW0	55420.42	5.57	Serine/threonine-protein phosphatase OS=Homo sapiens PE=2 SV=1	1 (2)	1.64E+06	2.29E+06	6.213967871	6.359250932	1.397278773
B2RB13		78714.11	6.98	OS=Homo sapiens PE=2 SV=1	21 (24)	1.65E+07	2.30E+07	7.21665174	7.360984481	1.394224601
Q75955	Q53HQ0, Q5ST80	47553.7	7.08	Follitropin-1 OS=Homo sapiens GN=FLIT1 PE=1 SV=3	3 (4)	2.53E+06	3.52E+06	6.403251481	6.546529819	1.390843733
P10909	E7ET47	53031.22	5.89	Clusterin OS=Homo sapiens GN=CLU PE=1 SV=1	10 (11)	1.07E+07	1.47E+07	7.030924098	7.173894358	1.389857452
B4DPM7		58440.03	7.74	cDNA FLJ55739, highly similar to 26S proteasome non-ATPase regulatory subunit 3 OS=Homo sapiens PE=2 SV=1	1 (3)	2.39E+06	3.30E+06	6.378176323	6.517889899	1.379474179
AKK3E4		70182.97	8.23	rRNA OS=Homo sapiens PE=2 SV=1	12 (16)	6.51E+07	8.97E+07	7.813808926	7.952813796	1.377242212
Q6FGX3		23648.92	5.24	RAB6A protein OS=Homo sapiens GN=RAB6A PE=2 SV=1	14 (17)	1.06E+07	1.46E+07	6.55551339	6.765091556	1.375752203
B3KNN7	Q6BN0, B4DV84, Q43242, F5H8K4, Q96N86, Q8N9M2	57310.67	8.49	OS=Homo sapiens PE=2 SV=1	2 (2)	2.41E+06	3.32E+06	6.382140363	6.520637615	1.375616106
Q9BS40		25847.93	5.54	Latexin OS=Homo sapiens GN=LXN PE=1 SV=2	10 (12)	6.41E+07	8.81E+07	7.806764031	7.945200726	1.375424306
Q9NRW1		23560.92	5.41	Ras-related protein Rab-4B OS=Homo sapiens GN=RAB6B PE=1 SV=1	3 (3)	5.19E+07	7.05E+07	7.714816184	7.848396223	1.360128809
F5H157		21485.97	8.55	Uncharacterized protein OS=Homo sapiens GN=RAB35 PE=3 SV=1	23 (29)	4.38E+07	5.95E+07	6.61484716	6.774363815	1.357935365
Q14254		47433.81	5.19	Follitropin-2 OS=Homo sapiens GN=FLT2 PE=1 SV=2	6 (12)	1.88E+07	2.28E+07	7.225118711	7.357552063	1.35653427
P13948	AK8690	63226.64	6.4	Stress-induced-phosphoprotein 1 OS=Homo sapiens GN=STIP1 PE=1 SV=1	1 (1)	3.54E+06	4.80E+06	6.548588641	6.808965397	1.356356567
Q1MMW0	Q9JW19, C9JAP5, C9JWV9, B4DZN1, C3JEN3, C9JZ27, B4DU02, C9JYT2, Q969X1	3942.81	7.6	Responsive to centrifugal force and shear stress gene 1 OS=Homo sapiens GN=RECS1 PE=2 SV=1	7 (10)	3.42E+07	4.63E+07	7.533663612	7.665860665	1.355804445
P61106		24110.01	5.85	Ras-related protein Rab-14 OS=Homo sapiens GN=RAB14 PE=1 SV=4	6 (6)	5.43E+07	7.34E+07	7.734841064	7.865861417	1.352135929
P61006		23824.25	9.15	Ras-related protein Rab-8A OS=Homo sapiens GN=RAB8A PE=1 SV=1	4 (5)	3.02E+06	4.08E+06	6.480581783	6.610648137	1.349169001
B1APW5	Q68DH9, P23634, A7E2D8	130461.06	7.45	ATPase, Ca++ transporting, plasma membrane 4 OS=Homo sapiens GN=ATP2B4 PE=2 SV=1	3 (4)	3.03E+06	4.08E+06	6.480731526	6.610644313	1.348692016
P33176	Q5QJ44	110358.27	6.12	Kinesin-I heavy chain OS=Homo sapiens GN=KIF5B PE=1 SV=1	5 (9)	9.75E+06	1.29E+07	6.980146227	7.109307431	1.346360001
P61225	Q5QJ44	20719.29	4.73	Ras-related protein Rap-2b OS=Homo sapiens GN=RAP2B PE=1 SV=1	1 (1)	7.71E+06	1.05E+07	6.987295388	7.076767277	1.333128119
Q5TNT4	B4DW07	31734.76	8.89	Cytochrome b reductase 1 OS=Homo sapiens GN=CYBD1 PE=1 SV=1	6 (8)	2.66E+06	3.54E+06	6.424156455	6.54809096	1.332614996
Q6QD68	Q9JUU1, F5H6I7, B4DXC4	60959.59	5.43	Adipic-3 OS=Homo sapiens GN=ATL3 PE=1 SV=1	4 (5)	1.09E+07	1.45E+07	7.03641564	7.160801494	1.331637601
B4E1U9	P60953	26910.04	7.52	cDNA FLJ54776, highly similar to Ctl dival cation control protein 42 homolog OS=Homo sapiens PE=2 SV=1	14 (18)	6.57E+06	8.74E+06	6.817702701	6.914684172	1.330397657
Q13616		90306.24	8.19	Collin-1 OS=Homo sapiens GN=CLL1 PE=1 SV=2	34 (46)	1.58E+07	2.09E+07	7.199620828	7.320155916	1.319881944
P35579	Q6QFE2	227646.06	5.5	Myosin-9 OS=Homo sapiens GN=MYH9 PE=1 SV=4	4 (9)	9.38E+06	1.24E+07	6.9722770159	7.091799786	1.316829743
P21333	E9KL4S, Q6QFE6, Q5HY54, Q6QFE5	283300.9	5.7	Filamin-A OS=Homo sapiens GN=FLNA PE=1 SV=4	5 (12)	1.68E+06	1.79E+06	6.1332846	6.251902035	1.314066776
Q709C8		424461.61	6.38	Vacuolar protein-associated protein 13C OS=Homo sapiens GN=VPS13C PE=1 SV=1	2 (3)	1.08E+06	1.42E+06	6.0321928	6.150807643	1.314058932
				cDNA P56C0146 fs, clone PLACE1007202, highly similar to Protein disulfide-isomerase A3 (EC 5.3.4.1) OS=Homo sapiens PE=2 SV=1	2 (3)	2.11E+05	2.77E+05	5.323930341	5.442631389	1.313025939
B3KQT2	B3KQT9, P30101	55268	6.42	sapiens PE=2 SV=1	3 (5)	4.11E+06	5.17E+06	6.31385219	6.73020823	1.308648496
B1ANW7	Q549F0, Q9UNL5, AK8X95, F5G2D2	56305.43	5.02	Fas (TNFRSF6) associated factor 1 OS=Homo sapiens GN=FAF1 PE=4 SV=1	6 (7)	5.17E+06	6.76E+06	6.713525178	6.831011331	1.307964489
A4D2J0	B5BU81, O15498, Q9UE50	22574.47	6.44	SNARE protein Yk45 OS=Homo sapiens GN=YK46 PE=2 SV=1	8 (15)	3.49E+07	4.56E+07	7.542880432	7.658917589	1.306282645
P29401	B3K5K4, E7EP47, B4D3E1, Q53E5M, B4E022	68518.98	7.58	Transketolase OS=Homo sapiens GN=TKT PE=1 SV=3	4 (5)	1.81E+06	2.49E+06	6.368592967	6.685597268	1.307158348
Q95630		48616.77	5.89	STAM-binding protein OS=Homo sapiens GN=STAMBIP PE=1 SV=1	8 (15)	3.49E+07	4.56E+07	7.542880432	7.658917589	1.306282645
P35611	E7ENY0, Q86XM2, E7EV99, A2A3N8	81303.89	5.6	Alpha-adducin OS=Homo sapiens GN=ADD1 PE=1 SV=2	3 (5)	1.39E+06	1.81E+06	6.143112932	6.257905193	1.302543573
Q6RL7		361872.13	5.94	Vacuolar protein sorting-associated protein 13A OS=Homo sapiens GN=VPS13A PE=1 SV=2	9 (18)	4.97E+06	6.46E+06	6.696330306	6.810212693	1.299817524
Q4LE45		234731.74	5.46	MYH10 variant protein (Fragment) OS=Homo sapiens GN=MYH10 variant protein PE=2 SV=1	19 (22)	3.83E+07	4.98E+07	7.583262175	7.697137195	1.299795473
Q9COC9		142630.56	5.01	Ubiquitin-conjugating enzyme E2 O OS=Homo sapiens GN=UBE2O PE=1 SV=1	1 (2)	1.06E+06	1.37E+06	6.023480172	6.137338065	1.299744214
Q94905	ESRHW4	38043.54	5.47	Erlin-2 OS=Homo sapiens GN=ERLIN2 PE=1 SV=1	10 (12)	6.69E+07	8.60E+07	7.625671475	7.794277404	1.284120942
Q9H0U4		22328.29	5.55	Ras-related protein Rab-1B OS=Homo sapiens GN=RAP1B PE=1 SV=1	7 (9)	3.2E+06	4.19E+06	6.395381847	6.706236158	1.278952192
B1AJY5	Q75832, B1AJY7	20432.3	5.37	Proteasome (Prosome, multicatalytic) subunit non-ATPase, 10 OS=Homo sapiens GN=PSMD10 PE=4 SV=1	4 (5)	8.01E+06	1.02E+07	6.903854168	7.101005078	1.277014738
Q5JGJ9		35033.48	6.29	Purine-rich element binding protein A OS=Homo sapiens PE=2 SV=1	1 (1)	2.78E+06	3.38E+06	6.33886499	6.44535586	1.272308304
Q9NVZ3	F6SKR8, Q3F5E5, D6RAK6, B4DUJ7	28435.34	6.89	Adiponectin-binding cell-associated protein 2 OS=Homo sapiens GN=NECAP2 PE=1 SV=1	1 (4)	1.54E+06	2.52E+06	6.17425924	6.19756355	1.265698984
B4EDR1	Q6P7J5	80155.49	6.55	Integrin beta-4 OS=Homo sapiens PE=2 SV=1	4 (4)	1.42E+07	1.54E+07	7.085540444	7.186473632	1.261633429
Q16775	B4DT01	34240.49	8.35	Hydroxyacylglutathione hydrolase, mitochondrial OS=Homo sapiens GN=HAGH PE=1 SV=2	3 (4)	1.57E+07	1.97E+07	7.195605631	7.293404741	1.255236323
Q9HVA0		38								

Q10567 105482.41 4.94 AP-1 complex subunit beta-1 OS=Homo sapiens GN=AP1B1 PE=1 SV=2
P28289 40657.93 5.03 Tropomodulin-1 OS=Homo sapiens GN=TMOD1 PE=1 SV=1
Q0P512 54360.69 9.04 Solute carrier family 2 (Facilitated glucose transporter), member 1 OS=Homo sapiens GN=SLC2A1 PE=2 SV=1
P48556 39871.93 9.73 26S proteasome non-ATPase regulatory subunit 8 OS=Homo sapiens GN=PSMD8 PE=1 SV=2
P13786 70814.11 5.29 Plastin-2 OS=Homo sapiens GN=PLP1 PE=1 SV=4
P17213 54003.15 9.41 Bacterial permeability-increasing protein OS=Homo sapiens GN=BP1 PE=1 SV=4
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B7ZB4 23000.15 7.79 Calcium binding protein 39-like OS=Homo sapiens GN=CAB39L PE=4 SV=1
Q07960 50461.21 5.85 Rho GTPase-activating protein 1 OS=Homo sapiens GN=ARHGA1 PE=1 SV=1
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Q9H902 29888.51 5.83 COP9 signalosome complex subunit 7b OS=Homo sapiens GN=COPS7B PE=1 SV=1
Q9H4G4 17321.56 9.44 Golgi-associated plant pathogenesis-related protein 1 OS=Homo sapiens GN=GLIPR2 PE=1 SV=3
Q9GG09 30333.14 5.18 DCN1-like protein 1 OS=Homo sapiens GN=DCUN1D1 PE=1 SV=1
B2RMN7 247271.12 5.15 Spectrin, beta, erythrocytic OS=Homo sapiens GN=SPTB PE=2 SV=1
P11277 247171.05 5.15 Spectrin beta chain, erythrocyte OS=Homo sapiens GN=SPTB PE=1 SV=5
Q0YF99 102084.58 6.1 Oxygenated-binding protein OS=Homo sapiens GN=OSBP2 PE=2 SV=1
Q92508 28965.65 7.37 Protein PIEZO1 OS=Homo sapiens GN=FAH38A PE=1 SV=4
P11005 19838.51 4.67 Myosin regulatory light chain 12k OS=Homo sapiens GN=MYL12A PE=1 SV=2
P02549 281039.34 4.95 Spectrin alpha chain, erythrocyte OS=Homo sapiens GN=SPTA1 PE=1 SV=5
P38919 47126.29 6.3 Eukaryotic initiation factor 4A-III OS=Homo sapiens GN=EIF4A3 PE=1 SV=4
Q99460 106795.08 5.25 26S proteasome non-ATPase regulatory subunit 1 OS=Homo sapiens GN=PSMD1 PE=1 SV=2
O15439 150344 8.41 Multidrug resistance-associated protein 4 OS=Homo sapiens GN=ABCC4 PE=1 SV=3
Q04656 164752.19 5.85 Copper-transporting ATPase 1 OS=Homo sapiens GN=ATP7A PE=1 SV=3
O16543 44953.19 5.17 Hsp90 co-chaperone Cdc37 OS=Homo sapiens GN=CDC37 PE=1 SV=1
P00568 21735.35 8.73 Adenylate kinase isoenzyme 1 OS=Homo sapiens GN=AK1 PE=1 SV=3
P07954 54773.23 8.85 Fumarate hydratase, mitochondrial OS=Homo sapiens GN=FH1 PE=1 SV=3
B2R7L2 40536.8 6.25 saplins PE=2 SV=1
P18206 124292.03 5.5 Vinculin OS=Homo sapiens GN=VCL PE=1 SV=4
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Q9BRP4 43132.41 5.92 Proteasomal ATPase-associated factor 1 OS=Homo sapiens GN=PAAF1 PE=1 SV=2
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P50570 98345.29 7.04 Dyamin-2 OS=Homo sapiens GN=DNM2 PE=1 SV=2
B8JUK7 76475.22 6.52 Fermitin family homolog 3 OS=Homo sapiens GN=FERMT3 PE=1 SV=1
P14625 Q5CA05 52896.53 4.76 Endoplasmic OS=Homo sapiens GN=HSP90B1 PE=1 SV=1
P30041 25133.23 6.9 Peroxiredoxin-6 OS=Homo sapiens GN=PRDX6 PE=1 SV=3
Q96F85 18750.6 7.72 CB1 cannabinoid receptor-interacting protein 1 OS=Homo sapiens GN=CNIRP1 PE=1 SV=1
P17858 85762.46 7.26 6-phosphofructokinase, liver type OS=Homo sapiens GN=PFKL PE=1 SV=6
P27824 B4DGP8 67982.02 4.47 Calnexin OS=Homo sapiens GN=CANX PE=1 SV=2
Q13564 A6NFN4, B3KUP9, A8MU28, A6NCK0 60664.74 5.25 NEDD8-activating enzyme E1 regulatory subunit OS=Homo sapiens GN=NAE1 PE=1 SV=1
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EP9AV3 205979.15 9.6 Uncharacterized protein OS=Homo sapiens GN=NACA PE=4 SV=1
P09972 39830.39 6.41 Fructose-bisphosphate aldolase C OS=Homo sapiens GN=ALDOC PE=1 SV=2
Q973E0 F5H4U7 15415.41 10.36 Vesicle transport protein GOT1B OS=Homo sapiens GN=GOT1B PE=1 SV=1
O15563 A4D0R1, AK8865 29888.53 8.59 Synaptophysin-like protein 1 OS=Homo sapiens GN=SVPL1 PE=1 SV=1
P06237 Q6ZT11 85983.71 8.23 6-phosphofructokinase, muscle type OS=Homo sapiens GN=PFKM PE=1 SV=2
Q6LX06 57528.9 5.5 Olfactomedin-4 OS=Homo sapiens GN=OLFM4 PE=1 SV=1
Q14203 E7EX90, E9PGE1, E9FF55, Q6MZ23, A8MY36, A8MWX9, E7E9R0 124438.35 5.61 Dynactin subunit 1 OS=Homo sapiens GN=DCTN1 PE=1 SV=3
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P17987 60818.77 5.8 T-complex protein 1 subunit alpha OS=Homo sapiens GN=TC1P1 PE=1 SV=1
P36507 44681.16 6.12 Dual specificity mitogen-activated protein kinase kinase 2 OS=Homo sapiens GN=MAP2K2 PE=1 SV=1
B4DJAS P20339, Q6F144 22335.19 8.98 Uncharacterized protein OS=Homo sapiens GN=RA85A PE=2 SV=1
F5H399 18469.11 5.74 Uncharacterized protein OS=Homo sapiens GN=RA82A PE=3 SV=1
Q08495 45600.27 8.94 Dematin OS=Homo sapiens GN=EPB49 PE=1 SV=3
Q34490 55771.7 6.69 Nicotinamide phosphoribosyltransferase OS=Homo sapiens GN=NAMPT PE=1 SV=1
Arl-GAP with SH3 domain, ANK repeat and PH domain-containing protein 2 OS=Homo sapiens GN=ASAP2 PE=1 SV=3
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Q43223 E9PJ81, E9PRO7 33418.98 5.23 UBX domain-containing protein 1 OS=Homo sapiens GN=UBXN1 PE=1 SV=2
O15903 AK8Y79, AK8N7 146286.53 5.5 Phosphorylformylglyoxylamine synthase OS=Homo sapiens GN=PFAS PE=1 SV=4
P40327 275877.27 6.01 Fatty acid synthase OS=Homo sapiens GN=FSN PE=1 SV=3
P62826 B5DMF5, A8K3Z8 24578.68 7.01 GTP-binding nuclear protein Ran OS=Homo sapiens GN=NRN PE=1 SV=3
Q13098 B4DND6 56071.38 6.3 COP9 signalosome complex subunit 1 OS=Homo sapiens GN=GPS1 PE=1 SV=4
B2RD79 A6NJ2A, P54578 56462.19 5.2 Ubiquitin carboxyl-terminal hydrolase OS=Homo sapiens PE=2 SV=1
Q15257 Q5T949, B4DZF8, Q5T948 41097.61 5.63 Serine/threonine-protein phosphatase 2A activator OS=Homo sapiens GN=PPP2R4 PE=1 SV=3
P62195 45768.12 7.11 26S protease regulatory subunit 8 OS=Homo sapiens GN=PSMC5 PE=1 SV=1
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P00918 29284.94 6.87 Carbonic anhydrase 2 OS=Homo sapiens GN=CA2 PE=1 SV=2
Q02530 Q5QPW7 29969.08 5.42 Proteasome inhibitor P31 subunit OS=Homo sapiens GN=PSMF1 PE=1 SV=2
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B4DN59 36349.78 5.55 (CD44), transcript variant 4, mRNA OS=Homo sapiens PE=2 SV=1
cDNA FLJ16143 fs, clone BRAHMY238516, highly similar to Protein disulfide-isomerase A6 (EC 5.3.4.1) OS=Homo sapiens
B3KY95 B5MCO5 53655.01 5.35 saplins PE=2 SV=1
Q00232 53269.72 7.53 26S proteasome non-ATPase regulatory subunit 12 OS=Homo sapiens GN=PSMD12 PE=1 SV=3
B4DME9 Q9NSK0 60003.18 5.81 Uncharacterized protein OS=Homo sapiens GN=KLCA PE=2 SV=1
Q9BVJ7 16805.7 8.44 Dual specificity protein phosphatase 23 OS=Homo sapiens GN=DUSP23 PE=1 SV=1
P07195 Q5U077 36900.25 5.71 L-lactate dehydrogenase B chain OS=Homo sapiens GN=LHDB PE=1 SV=2
B3KSY4 B4DFF6, B3KUH7, B4DKU9, P57377 77412.32 5.04 HCG1787776, isoform CRA_b OS=Homo sapiens GN=COR07 PE=2 SV=1
Q94903 Q3DSW3, B3KMP6 30609.68 7.09 Profilin synthase co-transcribed bacterial homolog protein OS=Homo sapiens GN=PROSC PE=1 SV=2
B72507 P14H70 72478.09 5.53 cDNA FLJ51036, highly similar to Matrix metalloproteinase-9 (EC 3.4.24.35) OS=Homo sapiens PE=2 SV=1
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P36613 B4DNE1, B4DY23, Q5A451 42573.21 5.39 Basigin OS=Homo sapiens GN=BSG PE=1 SV=2
P51692 Q59H39 90322.77 5.71 Signal transducer and activator of transcription 5b OS=Homo sapiens GN=STAT5B PE=1 SV=2
P07384 82465.42 5.49 Calpain-1 catalytic subunit OS=Homo sapiens GN=CAPN1 PE=1 SV=1
B4DS00 Q9NWU2 17779.96 5.86 Uncharacterized protein OS=Homo sapiens GN=C2OR11 PE=2 SV=1
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P30626 B8MTM6, B4DKC2, C9JK06 21947.46 5.32 Sorcin OS=Homo sapiens GN=SRI PE=1 SV=1
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Q00487 34725.62 6.08 26S proteasome non-ATPase regulatory subunit 14 OS=Homo sapiens GN=PSMD14 PE=1 SV=1
P20160 27324.83 9.75 Azurocidin OS=Homo sapiens GN=AZU1 PE=1 SV=3
Q95373 120751.36 4.7 Interferon-7 OS=Homo sapiens GN=IFP1 PE=1 SV=1
P11021 72402.48 5.07 78 kDa glucose-regulated protein OS=Homo sapiens GN=GRP78 PE=1 SV=2
P22303 C9JG09, B7WP16, D6W5X8 68209.45 5.87 Acetylcholinesterase OS=Homo sapiens GN=AChE PE=1 SV=1
P43034 C9JLH8 47178.37 6.97 Platelet-activating factor acetylhydrolase IB subunit alpha OS=Homo sapiens GN=PAFAH1B1 PE=1 SV=2
P28838 56529.99 8.03 Cytosol aminopeptidase OS=Homo sapiens GN=LAP3 PE=1 SV=3
Q8WVV5 40819.36 5.78 Putative uncharacterized protein (Fragment) OS=Homo sapiens GN=CSP2 PE=2 SV=1
Q9NRV9 21197.56 5.71 Heme-binding protein 1 OS=Homo sapiens GN=HEBP1 PE=1 SV=1
P02647 30758.53 5.56 Apolipoprotein A-I OS=Homo sapiens GN=APOA1 PE=1 SV=1
P52907 A8K079 33073.39 5.45 F-actin-capping protein subunit alpha-1 OS=Homo sapiens GN=CAPZA1 PE=1 SV=3
P02786 A8K608 85274.1 6.18 Transferin receptor protein 1 OS=Homo sapiens GN=TFRC PE=1 SV=2
Q43149 333767.4 5.62 Zinc finger ZZ-type and EF-hand domain-containing protein 1 OS=Homo sapiens GN=ZEF1 PE=1 SV=6
Q9UBW8 30429.09 8.33 COP9 signalosome complex subunit 1 OS=Homo sapiens GN=COP9A PE=1 SV=1
Q8AL55 Q9Y4E8, E9PCQ3 5 Ubiquitin carboxyl-terminal hydrolase OS=Homo sapiens GN=UCLH5 PE=2 SV=1
cDNA FLJ78433, highly similar to Homo sapiens chaparotin containing TCP1, subunit 5 (epsilon) (CCT5), mRNA
A8K2X8 60147.97 5.34 OS=Homo sapiens PE=2 SV=1
Q8WYNO 46032.7 4.93 Cysteine protease ATGA4 OS=Homo sapiens GN=ATGA4 PE=1 SV=1
P45974 96637.68 9.25 Ubiquitin carboxyl-terminal hydrolase 5 OS=Homo sapiens GN=U5P26 PE=1 SV=2
B4DQX2 117385.94 6.03 cDNA FLJ55586, highly similar to MMS19-like protein OS=Homo sapiens PE=2 SV=1
O14618 Q8NEV0 29535.55 5.32 Copper chaperone for superoxide dismutase OS=Homo sapiens GN=CSC PE=1 SV=1
P04075 39851.48 8.3 Fructose-bisphosphate aldolase A OS=Homo sapiens GN=ALDOA PE=1 SV=2
Q13057 62632.08 6.51 Bifunctional coenzyme A synthase OS=Homo sapiens GN=COASY PE=1 SV=4
Q35HW2 34450.87 5.71 Ribosomal protein V0 variant (Fragment) OS=Homo sapiens PE=2 SV=1
Q9E536 42121.5 5.88 Synaptic vesicle membrane protein VAT-1 homolog OS=Homo sapiens GN=VAT1 PE=1 SV=2

4 (12) 5.96E+06 6.96E+06 6.77535274 6.842646377 1.167598793
12 (14) 1.51E+07 1.77E+07 7.179680668 7.24687029 1.167319181
11 (18) 9.40E+08 1.50E+09 8.97328118 9.040436446 1.167226843
9 (10) 4.92E+07 5.74E+07 7.692113075 7.58830689 1.166051813
5 (11) 4.27E+06 4.98E+06 6.63524816 6.697113046 1.165703847
2 (4) 1.31E+07 7.052468721 7.117763233 1.162124069
24 (27) 1.28E+08 1.49E+08 8.108096524 8.1731918 1.161703442
1 (2) 4.83E+06 5.61E+06 6.684206623 6.7491861 1.161345595
3 (7) 5.35E+06 6.20E+06 6.72798393 6.792729095 1.1607673
17 (26) 9.64E+07 1.12E+08 7.984128514 8.047742297 1.157747316
5 (6) 2.26E+07 2.62E+07 7.354664199 7.417935686 1.156835181
2 (3) 8.12E+06 9.38E+06 6.909364313 6.972325057 1.156007747
1 (1) 1.16E+06 1.34E+06 6.063904582 6.126830998 1.155916376
156 (171) 7.17E+08 8.28E+08 8.855730683 8.917907137 1.153922003
157 (172) 7.17E+08 8.28E+08 8.855730683 8.917907137 1.153922003
5 (6) 1.96E+06 2.26E+06 6.239180037 6.353941448 1.15382801
2 (3) 2.32E+06 2.67E+06 6.365722275 6.425896604 1.148614591
4 (5) 2.45E+07 2.81E+07 7.388387898 7.448107112 1.147411541
171 (216) 7.68E+08 8.80E+08 8.85231893 8.945483398 1.146440462
2 (3) 3.56E+06 4.08E+06 5.51843728 6.611014533 1.145963553
25 (29) 3.61E+07 4.14E+07 7.557884696 7.616998401 1.145812894
2 (5) 1.05E+06 1.20E+06 6.022319829 6.079682745 1.141203029
2 (2) 1.05E+06 1.20E+06 6.022863594 6.0789321 1.137914459
5 (7) 2.00E+07 2.27E+07 7.300237986 7.355994913 1.136990738
14 (18) 2.62E+08 2.98E+08 8.4910586 8.473534425 1.133518377
10 (12) 1.39E+07 1.58E+07 7.143438419 7.197681718 1.133034929
5 (9) 2.23E+07 2.52E+07 7.347505452 7.401738737 1.133008805
3 (4) 9.16E+05 1.04E+06 5.961858866 6.015037814 1.130261535
7 (9) 2.19E+07 2.47E+07 7.341125441 7.393526913 1.128239947
7 (10) 2.19E+07 2.47E+07 7.341125441 7.393526913 1.128239947
3 (4) 4.98E+06 5.62E+06 6.697591338 6.749878811 1.12794383
19 (24) 1.32E+08 1.48E+08 8.119416647 8.171404841 1.127166816
11 (16) 4.61E+06 5.19E+06 6.663930348 6.715524239 1.126143906
11 (14) 1.76E+07 1.98E+07 7.246458252 7.275050423 1.123649929
5 (9) 2.13E+06 2.39E+06 6.328214286 6.37853369 1.122818097
11 (14) 8.06E+07 9.00E+07 7.906474 7.95434669 1.116776304
3 (4) 6.57E+06 7.34E+06 6.817878671 6.865663357 1.116309688
16 (20) 2.95E+07 3.29E+07 7.469715618 7.51697941 1.114968998
3 (5) 9.22E+06 1.03E+07 6.964872389 7.01187918 1.11431196
1 (2) 2.28E+06 2.54E+06 6.358616843 6.405480601 1.111638957
4 (6) 3.65E+06 4.05E+06 6.561986217 6.607670641 1.11092419
7 (11) 1.90E+08 2.10E+08 8.277643429 8.323031599 1.101166633
1 (2) 2.60E+06 2.88E+06 6.414212948 6.459400747 1.10965455
3 (3) 5.44E+07 6.01E+07 7.735500312 7.778987256 1.105317288
2 (2) 2.26E+06 2.49E+06 6.354159569 6.397035315 1.09762782
1 (1) 2.76E+07 3.04E+07 7.44045727 7.48301664 1.102959002
7 (11) 2.13E+07 2.34E+07 7.327644521 7.369695093 1.102421321
4 (5) 4.94E+06 5.44E+06 6.93612927 6.73525315 1.100627153
2 (4) 4.15E+06 4.56E+06 6.617765549 6.659207477 1.100124731
2 (3) 3.92E+06 4.30E+06 6.592765555 6.633861633 1.099248288
23 (26) 9.73E+07 1.07E+08 9.988008667 8.02904455 1.099966262
2 (3) 4.01E+06 4.41E+06 6.603406001 6.643954343 1.097863488
5 (6) 5.17E+07 5.67E+07 7.713276886 7.753035555 1.09654553
1 (1) 1.86E+06 2.04E+06 6.269331124 6.289973212 1.095574934
3 (3) 6.79E+06 7.44E+06 6.83200351 6.871377556 1.095309231
2 (6) 2.88E+06 3.15E+06 6.45891116 6.498216402 1.09472552
2 (3) 1.72E+06 1.88E+06 6.235095873 6.274239519 1.094318261
4 (5) 5.08E+06 5.55E+06 6.705629773 6.744341237 1.093229805
2 (3) 1.38E+06 1.51E+06 6.441173349 6.479487736 1.091300633
3 (6) 2.09E+06 2.28E+06 6.320542989 6.358692118 1.091815181
10 (14) 1.05E+09 1.15E+09 9.02513931 9.05928739 1.090807863
7 (11) 1.28E+07 1.39E+07 7.105863275 7.142268838 1.08744005
6 (14) 1.42E+07 1.54E+07 7.152011793 7.188343021 1.087245535
2 (4) 1.49E+07 1.62E+07 7.174387613 7.210558535 1.086853285
20 (27) 5.23E+07 5.67E+07 7.718662798 7.753758738 1.084166392
4 (6) 6.10E+07 6.60E+07 7.785114644 7.819637347 1.082736315
3 (5) 7.74E+06 8.37E+06 6.888936835 6.922842781 1.081199772
20 (28) 9.73E+07 1.05E+08 7.988052148 8.02167829 1.080503411
16 (21) 1.86E+08 2.01E+08 8.269837642 8.303413643 1.080378669
2 (3) 2.25E+06 2.51E+06 6.365637007 6.39747617 1.079762808
6 (8) 1.69E+07 1.79E+07 7.192865461 7.225365741 1.07770595
6 (8) 8.13E+07 8.75E+07 9.09954464 7.942139927 1.07695212
3 (5) 8.02E+06 8.63E+06 6.904106083 6.936120372 1.075500622
2 (3) 2.21E+07 2.38E+07 7.345337052 7.376929771 1.075456178
4 (6) 5.65E+06 6.07E+06 6.752403555 6.783189551 1.073460321
22 (24) 2.98E+07 3.20E+07 7.474761597 7.504957545 1.072002868
1 (2) 2.64E+06 2.83E+06 6.422374088 6.452372309 1.071514916
3 (3) 4.33E+06 4.64E+06 6.636840825 6.666699712 1.0711712
6 (13) 2.51E+07 2.68E+07 7.399088478 7.42876111 1.070711907
5 (8) 5.67E+06 6.07E+06 6.75364919 6.782965554 1.06983392
2 (2) 3.08E+06 3.29E+06 6.46857169 5.516755062 1.067046566
3 (5) 5.25E+06 5.60E+06 6.720013552 6.74812111 1.066860282
14 (23) 1.65E+07 1.76E+07 7.216841773 7.244818755 1.066539591
5 (6) 1.71E+07 1.82E+07 7.23241901 7.260065999 1.06591874
4 (5) 4.40E+06 4.69E+06 6.64384744 6.671283942 1.065121614
34 (41) 1.53E+08 1.63E+08 8.185095837 8.212469344 1.065058069
1 (1) 1.53E+06 1.63E+06 6.183643917 6.210954753 1.064904926
6 (9) 1.68E+06 1.69E+06 6.791331478 6.818598266 1.064796925
3 (7) 3.75E+06 3.99E+06 6.574147803 6.601296754 1.064580853
6 (11) 6.38E+07 6.79E+07 7.804772332 7.831724163 1.064024998
14 (20) 1.12E+08 1.19E+08 8.049534692 8.076371575 1.06373441
2 (2) 6.53E+07 6.93E+07 7.814929676 7.840759986 1.061280806
11 (18) 1.85E+07 1.96E+07 7.62569384 7.29193299 1.060812444
7 (9) 5.85E+06 6.19E+06 6.766848546 6.791972445 1.05955961
4 (8) 7.13E+06 7.55E+06 8.652792064 6.877780854 1.059243945
1 (1) 2.38E+06 2.52E+06 6.376260431 6.40105091 1.058741359
7 (9) 8.47E+06 8.94E+06 6.927730055 6.951116733 1.055490902
21 (28) 8.93E+08 9.42E+08 9.950749462 8.974172173 1.055413661
12 (13) 7.86E+07 8.29E+07 7.895239386 7.918622178 1.055316654
6 (11) 1.14E+07 1.20E+07 7.056260728 7.078864038 1.053424245
3 (3) 1.38E+07 1.43E+07 7.13394883 7.156492853 1.053280454
7 (10) 4.53E+06 4.77E+06 6.656523213 6.678990701 1.052891957
4 (9) 6.13E+06 6.45E+06 6.787520175 6.809926395 1.051341409
6 (7) 1.45E+07 1.51E+07 7.161013608 7.180350414 1.047578993
7 (9) 4.81E+06 5.02E+06 6.681828893 6.700900305 1.044891368
26 (33) 6.98E+07 7.82526939 7.844087705 1.044283257
11 (1) 2.55E+07 2.66E+07 7.4066840911 7.42

P78371	B5BTY7	57794.26	6.01 T-complex protein 1 subunit beta OS=Homo sapiens GN=CT2 PE=1 SV=4	36 (42)	2.24E+08	2.31E+08	8.349884442	8.36436087	1.033894985
Q9V6M5		56290.43	6.02 Zinc transporter 1 OS=Homo sapiens GN=SLC30A1 PE=1 SV=3	1 (1)	2.41E+06	2.50E+06	6.382880734	6.397296161	1.033749772
Q1WWM3	P11171	83617.78	5.52 EPB41 protein (Fragment) OS=Homo sapiens GN=EPB41 PE=2 SV=1	15 (20)	5.56E+07	5.74E+07	7.744829743	7.759212294	1.033671522
000231	Q53F75	47719.15	6.08 26S proteasome non-ATPase regulatory subunit 11 OS=Homo sapiens GN=PSMD11 PE=1 SV=3	16 (26)	7.04E+07	7.27E+07	7.847456283	7.861620292	1.033151495
P61020		23919.99	8.29 Ras-related protein Rab-5B OS=Homo sapiens GN=RAB5B PE=1 SV=1	8 (9)	5.95E+07	6.15E+07	7.74672387	7.788769059	1.03299132
P14668	D3DP78	57499.18	6.11 Asparaginyl-tRNA synthetase, cytoplasmic OS=Homo sapiens GN=DARS PE=1 SV=2	9 (14)	9.71E+06	1.00E+07	6.576701598	7.00317488	1.03101668
Q9LUP5		297200.36	5.79 Ubiquitin carboxyl-terminal hydrolase 24 OS=Homo sapiens GN=USP24 PE=1 SV=3	3 (6)	2.98E+06	2.65E+06	6.41078571	6.42356331	1.029858651
B3KW16	B7Z579, B3KXU1, Q56ZET, E9PHG7	81638.08	6.25 cDNA FLJ141902.f1, clone PBLM2040666, highly similar to WD repeat protein 81 OS=Homo sapiens PE=2 SV=1	2 (2)	5.56E+06	5.72E+06	6.745219055	6.757165667	1.02788993
Q15276		99628.53	4.95 Rab GTPase-binding effector protein 1 OS=Homo sapiens GN=RABEP1 PE=1 SV=2	7 (11)	3.69E+06	3.69E+06	6.555588789	6.567307446	1.027350547
P11169	B7Z844, Q8TD88, F5H2H8, B7ZAC3, B7Z5A7, B7Z5J8, B7Z966 A4D181, D9IX63, B7ZBC3, D9IX67, E9PLT1, D9IX69, D9IX64, P16671, E7EU05	54345.43	6.84 Solute carrier family 2, facilitated glucose transporter member 3 OS=Homo sapiens GN=SLC2A3 PE=1 SV=1	3 (4)	7.59E+06	7.79E+06	6.880013363	6.89154843	1.026916346
B3KU88		53571.51	8.19 cDNA FLJ35839.f1, clone PUAEN200228, highly similar to Platelet glycoprotein 4 OS=Homo sapiens PE=2 SV=1	1 (3)	1.27E+06	1.30E+06	6.102829572	6.113829947	1.025652812
P54136		76129.16	6.26 Arginyl-tRNA synthetase, cytoplasmic OS=Homo sapiens GN=ARS PE=1 SV=2	2 (4)	2.17E+06	2.23E+06	6.337059463	6.347973341	1.025448557
B4D112	F5H1W7, Q9HA65, B9A6L8	69806.05	4.97 cDNA FLJ55654, highly similar to TBC1 domain family member 17 OS=Homo sapiens PE=2 SV=1	2 (2)	8.78E+06	9.00E+06	6.943736821	6.954004715	1.023924404
B4E3A8		38774.73	6.22 Uncharacterized protein OS=Homo sapiens GN=SERPNB1 PE=2 SV=1	8 (8)	7.06E+06	7.21E+06	6.848862996	6.858111654	1.021524195
P30740		42828.74	5.9 Leukocyte elastase inhibitor OS=Homo sapiens GN=SERPINB1 PE=1 SV=1	11 (13)	7.06E+06	7.21E+06	6.848862996	6.858111654	1.021524195
B2CS11	E3SWJ9, D3U401	32003.55	5.83 MHC class I antigen (Fragment) OS=Homo sapiens GN=HLA-B PE=3 SV=1	3 (4)	3.77E+06	3.85E+06	6.576553563	6.585231407	1.020182439
Q3MIH3	B6P287	15004.07	9.87 Ubiquitin A-52 residue ribosomal protein fusion product 1 OS=Homo sapiens GN=UBA52 PE=2 SV=1	6 (8)	9.65E+08	9.84E+08	8.984402781	8.993055627	1.02012372
Q99497		20049.55	6.33 Protein DJ-1 OS=Homo sapiens GN= PARK7 PE=1 SV=2	5 (7)	1.05E+07	1.07E+07	7.022287603	7.029828103	1.017514248
P40227	Q59ET3	58443.77	6.23 T-complex protein 1 subunit zeta OS=Homo sapiens GN=CT6A PE=1 SV=3	24 (30)	1.25E+08	1.28E+08	8.098516607	8.105987556	1.017351312
Q01813		86453.87	7.5 5-phosphoribosylamine type C OS=Homo sapiens GN=PFKP PE=1 SV=2	3 (6)	4.93E+06	5.01E+06	6.693085179	6.699962792	1.015962349
E2RVJ0	P02730	102149.58	5.1 Solute carrier family 4, anion exchanger, member 1 OS=Homo sapiens GN=SLC4A1 PE=2 SV=1	42 (50)	3.99E+09	4.05E+09	9.60067692	9.607220281	1.015180719
Q5F48		36599.16	6.8 Heterogeneous nuclear ribonucleoprotein H3 isoform a variant (Fragment) OS=Homo sapiens PE=2 SV=1	1 (1)	1.94E+06	1.96E+06	6.287095588	6.292818946	1.013265739
Q9VWM8	Q53GW1	72676.18	5.89 Sec1 family domain-containing protein 1 OS=Homo sapiens GN=SCFD1 PE=1 SV=4	11 (14)	1.49E+07	1.50E+07	7.17208553	7.176898653	1.011223132
B4DHO2	P34932	95156.57	5.11 cDNA FLJ50510, highly similar to Heat shock 70 kDa protein 4 OS=Homo sapiens PE=2 SV=1	10 (14)	8.79E+06	8.88E+06	6.943093141	6.948228811	1.010009993
000629		58563.84	4.8 Importin subunit alpha-4 OS=Homo sapiens GN=KPNA4 PE=1 SV=1	2 (3)	4.43E+06	4.47E+06	6.546652	6.560522625	1.008952278
P51148		23695.87	8.64 Ras-related protein Rab-5C OS=Homo sapiens GN=RAB5C PE=1 SV=2	11 (12)	7.06E+07	7.10E+07	7.84853021	7.851513858	1.006910425
Q29694		20433.83	5.06 MHC class I HLA-B antigen (Fragment) OS=Homo sapiens GN=HLA-B PE=2 SV=1	3 (4)	3.47E+06	3.49E+06	6.540121531	6.543098283	1.006877768
B7ZW70		21165.08	8.87 LOC727761 protein OS=Homo sapiens GN=LOC727761 PE=2 SV=1	3 (5)	1.03E+07	1.04E+07	7.012696558	7.015241777	1.005877779
Q9GZ53		33730.83	5.16 WD repeat-containing protein 61 OS=Homo sapiens GN=WD61 PE=1 SV=1	3 (4)	5.67E+06	5.70E+06	6.753542977	6.755518512	1.004559198
P22061		24791.64	6.7 Protein-L-aspartate(D-aspartate) O-methyltransferase OS=Homo sapiens GN=PCMT1 PE=1 SV=4	8 (12)	1.18E+07	1.18E+07	7.070335642	7.071956118	1.003738253
B2R8N1	Q966Z7, Q53Q59, E9PGT6	23239.96	5.25 cDNA, FLJ93976, highly similar to Homo sapiens COP9 homolog (COP9), mRNA OS=Homo sapiens PE=2 SV=1	7 (10)	8.35E+07	8.38E+07	7.921841186	7.923432377	1.003670573
P68366	ABMU81	50633.65	4.95 Tubulin alpha-4A chain OS=Homo sapiens GN=PTUB4A PE=1 SV=1	11 (13)	3.38E+07	3.39E+07	7.529027197	7.529805553	1.001793839
000154	B3KX12, B4DUJ0	42453.58	8.85 Cytosolic acyl coenzyme A thioester hydrolase OS=Homo sapiens GN=ACOT7 PE=1 SV=3	3 (3)	9.13E+06	9.14E+06	6.960419988	6.960781408	1.000832547
Q95816	B3KX46, B3KX59	25929.28	5.25 BAG family molecular chaperone regulator 2 OS=Homo sapiens GN=HABG2 PE=1 SV=1	3 (3)	5.04E+06	5.03E+06	6.70224687	6.701910157	0.999773308
Q27U77	B4EU06, P50502	41478.54	5.19 Aging-associated protein 2 OS=Homo sapiens GN=AAO2 PE=2 SV=1	9 (12)	3.37E+06	3.37E+06	6.528089817	6.527773045	0.999351683
Q6IBG5		13018.39	4.65 MYL5 protein OS=Homo sapiens GN=MYL5 PE=2 SV=1	6 (6)	1.75E+07	1.75E+07	7.243643347	7.243313197	0.999240091
P18152		30640.97	8.55 Carbonyl reductase [NADPH] 1 OS=Homo sapiens GN=CBR1 PE=1 SV=3	6 (6)	2.76E+06	2.76E+06	6.441620364	6.441007992	0.998590956
P36543	Q53Y06	26185.78	7.71 Y-type proton ATPase subunit E 1 OS=Homo sapiens GN=ATP6V1E1 PE=1 SV=1 cDNA FLJ36533.f1, clone TRACH2004428, highly similar to Lactotransferrin (EC 3.4.21.-) (Fragment) OS=Homo	1 (1)	6.94E+05	6.93E+05	5.841233475	5.840435906	0.998165216
B3KSL2		78585.67	8.39 sapiens FLJ36533.f1, clone TRACH2004428, highly similar to Lactotransferrin (EC 3.4.21.-) (Fragment) OS=Homo	13 (14)	1.72E+07	1.71E+07	7.23567565	7.234228319	0.996627295
P02788	B3VMW0, ABK494, E7ER44, E7EQB2, ABK9U8, B2MV13, B7ZAK2, B7ZAL5	80013.62	8.5 Lactotransferrin OS=Homo sapiens GN=LT PE=1 SV=6	13 (15)	1.72E+07	1.71E+07	7.23567565	7.234228319	0.996627295
B7Z6P1		38896.21	5.23 cDNA FLJ53662, highly similar to Actin, alpha skeletal muscle OS=Homo sapiens PE=2 SV=1	13 (20)	7.04E+08	7.01E+08	8.847671638	8.845934219	0.996007438
B4DWX5	ABK7F7, Q57T86, Q9Y311	46066.66	6.67 cDNA FLJ50510, highly similar to Foxo only protein 7 OS=Homo sapiens PE=2 SV=1	2 (3)	9.87E+05	9.83E+05	5.994318059	5.992495066	0.995809251
P78417	B2R893, Q5TA02, D3DRA3	27833.15	6.23 Glutathione S-transferase omega-1 OS=Homo sapiens GN=GSTO1 PE=1 SV=2	1 (2)	3.62E+06	3.61E+06	6.559195476	6.557259208	0.995551503
Q06323	Q6BM82	28876.08	5.78 Proteasome activator complex subunit 1 OS=Homo sapiens GN=PSME1 PE=1 SV=1	8 (9)	3.80E+07	3.78E+07	7.579411973	7.577411479	0.995404285
P52294	Q5BK22, Q3Y1Y4	60924.83	4.94 Importin subunit alpha-1 OS=Homo sapiens GN=KPNA1 PE=1 SV=3	2 (4)	5.40E+06	5.38E+06	6.732561202	6.730452096	0.995155377
Q9V490		271765.86	5.77 Talin-1 OS=Homo sapiens GN=TLN1 PE=1 SV=3	44 (66)	3.82E+07	3.80E+07	7.581636936	7.579292074	0.994615305
P56990	Q5SHU0	60152.72	5.42 Adapter-related protein complex 2, beta 1 subunit, isoform CNA_d OS=Homo sapiens GN=AP2B1 PE=4 SV=1	27 (34)	1.18E+08	1.18E+08	8.07363655	8.070916762	0.993738105
Q95273		40635.35	4.71 Cyclin-D1-binding protein 1 OS=Homo sapiens GN=CCNDPB1 PE=1 SV=2	2 (4)	1.36E+06	1.03E+06	6.018071371	6.014462631	0.991724951
P30453	B1PKZ1	41314.21	5.89 HLA class I histocompatibility antigen, A-34 alpha chain OS=Homo sapiens GN=HLA-A PE=1 SV=1	1 (2)	4.91E+06	4.91E+06	6.691367899	6.687878586	0.991561571
A2RRF3	Q9UBC2, B4DKA3, A5PKY0, A5PL29, ABK5P4	83310.73	4.92 EPS15L1 protein OS=Homo sapiens GN=EPS15L1 PE=2 SV=1	2 (3)	1.49E+06	1.47E+06	6.172447526	6.168509955	0.990953849
P07237	E7EP48	57479.82	4.76 Protein disulfide-isomerase OS=Homo sapiens GN=PIB4 PE=1 SV=3	3 (7)	2.92E+06	2.89E+06	6.466807818	6.460776346	0.987845733
P46459		83055.27	6.52 Vesicle-fusing ATPase OS=Homo sapiens GN=NSF PE=1 SV=3	21 (27)	5.53E+07	5.46E+07	7.742456931	7.736801454	0.987062025
Q2TA20		214893.14	5.57 Autophagy-related protein 2 homolog A OS=Homo sapiens GN=ATG2A PE=1 SV=3	1 (1)	1.63E+06	1.61E+06	6.122800826	6.206700554	0.986051795
P37840	Q4WL52, E7EPV7	14451.22	4.67 Alpha-synuclein OS=Homo sapiens GN=SNCA PE=1 SV=1	16 (16)	1.78E+09	1.76E+09	9.251304222	9.254189464	0.986018907
P43686	ABK2M0	47450.58	5.05 26S protease regulatory subunit 6B OS=Homo sapiens GN=PSMC4 PE=1 SV=2	13 (19)	2.35E+07	2.31E+07	7.371771128	7.363964592	0.982185378
Q16851	Q9KDK6, E7EUC7, B4DUP2	57075.78	8.16 UDP-glucose-1-phosphate uridylyltransferase OS=Homo sapiens GN=UGP2 PE=1 SV=5	6 (10)	1.07E+07	1.05E+07	7.031023447	7.022524623	0.980620919
P53004		33692.44	6.06 Bilevelidin reductase A OS=Homo sapiens GN=BLVRA PE=1 SV=2	4 (5)	5.11E+06	5.00E+06	6.708104318	6.699112385	0.979508179
E1P646	Q8QD00, ABK916, E1P647, ABK0G3, E1P648, P63010	106520.91	5.25 Adapter-related protein complex 2, beta 1 subunit, isoform CNA_d OS=Homo sapiens GN=AP2B1 PE=4 SV=1	14 (20)	1.59E+07	1.56E+07	7.240144445	7.152330433	0.979174248
P06733		47461.45	7.01 Alpha-enolase OS=Homo sapiens GN=ENO1 PE=1 SV=2	3 (4)	1.36E+06	1.36E+06	6.142690513	6.133308988	0.978814263
D6RC62	Q6PGP7	70172.51	6.26 Uncharacterized protein OS=Homo sapiens GN=TTCT3 PE=4 SV=1	1 (2)	2.54E+06	2.48E+06	6.405103521	6.395789917	0.978782995
B2RDE1	Q9VU59, Q5HYB6	29227.82	4.72 cDNA, FLJ95688, highly similar to Homo sapiens topomycin3 (TPM3), mRNA OS=Homo sapiens PE=2 SV=1	8 (12)	1.24E+07	1.21E+07	7.093447729	7.083575499	0.977524766
P05386	Q8QCA4, Q7Z612, Q6FG99	11620.73	4.26 G60 acidic ribosomal protein P1 OS=Homo sapiens GN=RPLP1 PE=1 SV=1	1 (1)	7.19E+06	7.02E+06	6.856689455	6.846190104	0.976114242
O75688	Q658R4, B3KP90	53179.58	4.95 Protein phosphatase 1B OS=Homo sapiens GN=PP1B PE=1 SV=1	4 (7)	4.47E+06	4.36E+06	6.65052112	6.639926608	0.975900381
P08397		39533.7	6.68 Porphobilinogen deaminase OS=Homo sapiens GN=HMB5 PE=1 SV=2	6 (8)	1.46E+07	1.42E+07	7.163463995	7.152608517	0.975314143
P55060		111144.58	5.51 Exportin-2 OS=Homo sapiens GN=CSE1L PE=1 SV=3	19 (30)	4.97E+07	4.84E+07	7.695922439	7.684913348	0.974692629
Q06U6		46604.21	6.73 Mannose-1-phosphate guanylyltransferase alpha OS=Homo sapiens GN=GMPPA PE=1 SV=1	6 (9)	7.06E+06	6.88E+06	6.848944581	6.837903935	0.974898392
P50991	ABK3C3	58400.95	7.96 T-complex protein 1 subunit delta OS=Homo sapiens GN=CTCA PE=1 SV=4	19 (20)	1.21E+08	1.18E+08	8.082071818	8.070862482	0.974519794
B4DM45		137476.66	5.3 cDNA FLJ56465, highly similar to Dynactin-1 OS=Homo sapiens GN=DNAAF1 PE=2 SV=1	1 (2)	5.25E+06	5.12E+06	6.702055077	6.709268406	0.974356079
P00915		28909.41	6.59 Carbonic anhydrase 1 OS=Homo sapiens GN=CA1 PE=1 SV=2	13 (13)	1.43E+08	1.39E+08	8.155871138	8.144249646	0.973696276
Q13200	Q9EQ68, Q53XQ4, F5G216	103077.07	5.08 26S proteasome non-ATPase regulatory subunit 2 OS=Homo sapiens GN=PSMD2 PE=1 SV=3	3 (36)	3.95E+07	3.82E+07	7.594893598	7.582211869	0.971336915
P04406	E7EUT4	56221.46	6.87 Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens GN=GAPDH PE=1 SV=3	8 (10)	1.06E+07	1.02E+07	7.024338822	7.010381922	0.970382823
P11215	Q4VAK1	128410.01	6.88 Integrin alpha-M OS=Homo sapiens GN=ITGAM PE=1 SV=2	7 (10)	1.49E+07	1.45E+07	7.137490805	7.160066261	0.969561711
P04921		13801.68	4.69 Glycophorin-C OS=Homo sapiens GN=GYPC PE=1 SV=1	3 (3)	9.38E+07	9.08E+07	9.72335189	9.758003299	0.967538176
Q96PL5		53198.84	8.75 Erythroid membrane-associated protein OS=Homo sapiens GN=ERMAP PE=1 SV=1	2 (2)	2.91E+06	2.82E+06	6.464197371	6.449822659	0.967442002
P68036	ABK4W8	18021.3	8.68 Ubiquitin-conjugating enzyme E2 L3 OS=Homo sapiens GN=UBE2L3 PE=1 SV=1 cDNA, FLJ92148, highly similar to Homo sapiens S100 calcium binding protein A9 (calgrulin B) (S100A9), mRNA	3 (4)	4.38E+07	4.24E+07	7.641789277	7.637355861	0.96731202
B2RM46	P06702	132558.56	5.71 OS=Homo sapiens PE=1 SV=1	3 (3)	6.70E+06	6.48E+06	6.825983662	6.811448125	0.96708459
Q9NVU2	ABKAK1	57119.39	5.42 UDP-glucose glycogen glucosyltransferase 1 OS=Homo sapiens GN=UGUT1 PE=1 SV=3	1 (1)	1.13E+06	1.09E+06	6.052193708	6.037570389	0.966889137</

P28070		29242.5	5.72	Proteasome subunit beta type-4 OS=Homo sapiens GN=PSMB4 PE=1 Sv=4	3 (4)	5.33E+06	5.00E+06	6.726762771	6.098612323	0.937237274
E7ET43		52320.15	5.61	Uncharacterized protein OS=Homo sapiens GN=CEACAM1 PE=4 Sv=2	1 (2)	1.13E+07	1.06E+07	7.054123454	7.257559624	0.936776894
P68363	B3KT06, Q53GA7, F5HSD3, B3KPS3, Q9BQE3	58083.86	4.94	Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 Sv=1	13 (15)	4.10E+07	3.83E+07	7.612792294	7.583325553	0.934400924
P27708		245167.34	6.02	CAD protein OS=Homo sapiens GN=CAD PE=1 Sv=3	4 (8)	5.49E+06	5.10E+06	6.739517636	6.770748089	0.929673501
Q95CK1	Q53FR4	52447.23	5.32	Nuclear protein sorting-associated protein 35 OS=Homo sapiens GN=VP53 PE=1 Sv=2	1 (3)	2.86E+06	2.38E+06	6.408051043	6.376045257	0.929609966
O95792		108551.16	6.63	AP-2 complex subunit alpha1 OS=Homo sapiens GN=AP2A1 PE=1 Sv=3	16 (21)	1.80E+07	1.67E+07	7.255244425	7.223108015	0.928674648
Q5TD40		44950.67	4.95	Protein DD1 homolog 2 OS=Homo sapiens GN=DD12 PE=1 Sv=1	6 (12)	6.17E+07	5.72E+07	7.79009792	7.757580839	0.927606996
P61978	Q5T6W5, Q5EC54, Q6B1N1, Q5T6W1, B4DUQ1, Q5T6W2, B4DFF1	51229.51	5.39	Heterogeneous nuclear ribonucleoprotein K OS=Homo sapiens GN=HNRNPK PE=1 Sv=1	1 (1)	5.87E+06	5.52E+06	6.775905252	6.724102247	0.925117711
P25685	Q6F151, B4DX52, Q6FHS4	38191.43	8.74	DnaJ homolog subfamily B member 1 OS=Homo sapiens GN=DNAJB1 PE=1 Sv=4	3 (5)	2.77E+06	2.56E+06	6.441971014	6.407952786	0.924668944
Q43681		39223.59	4.81	ATPase ASNA1 OS=Homo sapiens GN=ASNA1 PE=1 Sv=2	2 (4)	1.80E+07	1.66E+07	7.2545574	7.220557787	0.924656473
Q9P2R3		129914.7	5.7	Ankyrin repeat and FYVE domain-containing protein 1 OS=Homo sapiens GN=ANKFY1 PE=1 Sv=2	14 (19)	1.97E+07	1.82E+07	7.29542599	7.261018644	0.923831262
Q08211		142180.6	6.41	ATP-dependent RNA helicase A OS=Homo sapiens GN=DHX9 PE=1 Sv=4	4 (7)	2.11E+06	1.95E+06	6.323694978	6.289122952	0.923481019
B0UX83	P46379, B4DZ12, E7EMZ4	119084.78	5.4	HLA-B associated transcript 3 OS=Homo sapiens GN=BAT3 PE=4 Sv=1	7 (10)	1.09E+07	1.01E+07	7.0375931	7.00263922	0.922669406
B4E2N0		23967.37	5.05	Uncharacterized protein OS=Homo sapiens GN=L2C PE=2 Sv=1	2 (3)	4.43E+06	4.09E+06	6.64682332	6.611424146	0.921723831
C3W811		27688.86	8.9	ADP-ribosyltransferase 4 (Dombrock blood group) (Fragment) OS=Homo sapiens GN=ART4 PE=4 Sv=1	2 (3)	3.02E+06	2.79E+06	6.480430783	6.444947729	0.921545847
P27797	Q53G71	48282.89	7.13	Fructosamine-3-kinase OS=Homo sapiens GN=FN3K PE=1 Sv=1	1 (2)	5.07E+06	4.65E+06	6.70486776	6.667914495	0.918431424
Q9H479	B4DH12	35378.95	7.13	Fructosamine-3-kinase OS=Homo sapiens GN=FN3K PE=1 Sv=1	1 (2)	2.35E+06	2.15E+06	6.371232079	6.332397064	0.914461477
P62834	A8KAH9, Q5U0C3	21315.84	6.38	Ras-related protein Rap-1A OS=Homo sapiens GN=RAP1A PE=1 Sv=1	4 (7)	8.14E+06	7.43E+06	6.910789471	6.871209213	0.912892715
Q12YL5	B7Z296	28491.57	4.75	Tropomyosin 1 alpha variant 6 OS=Homo sapiens PE=2 Sv=1	8 (8)	1.16E+07	1.06E+07	7.065776754	7.02570074	0.911851226
Q02756	P31997	38415.2	6.95	Carcinoembryonic antigen-related cell adhesion molecule 8 OS=Homo sapiens GN=CEACAM8 PE=2 Sv=1	3 (3)	7.14E+06	6.50E+06	6.853461724	6.812759113	0.910536561
Q14C86		166359.05	5.09	GTPase-activating protein and VP50 domain-containing protein 1 OS=Homo sapiens GN=GAPVD1 PE=1 Sv=2	11 (15)	1.42E+07	1.29E+07	7.152244403	7.117126322	0.909456473
P28072	Q6IAT9	25569.53	4.8	Proteasome subunit beta type-6 OS=Homo sapiens GN=PSMB6 PE=1 Sv=4	3 (3)	1.11E+07	1.01E+07	7.045229779	7.003594195	0.908582602
P62258		29326.48	4.63	14-3-3 protein epsilon OS=Homo sapiens GN=VWHA E PE=1 Sv=1	5 (6)	1.10E+07	1.00E+07	7.043076932	7.001134288	0.907940433
P22314		118857.74	5.49	Ubiquitin-like modifier-activating enzyme 1 OS=Homo sapiens GN=UBA1 PE=1 Sv=3	7 (8)	7.62E+06	6.90E+06	6.88186091	6.838749559	0.905447905
B4DN88		103976.2	5.28	Uncharacterized protein OS=Homo sapiens GN=DCAF6 PE=2 Sv=1	2 (2)	3.88E+06	3.33E+06	6.565803826	6.521945067	0.903943404
Q72627	E7EVU8, E9PD66	485523.13	5.1	E3 ubiquitin-protein ligase HUWE1 OS=Homo sapiens GN=HUWE1 PE=1 Sv=3	14 (22)	1.99E+07	1.80E+07	7.292903497	7.255289968	0.903829414
P64077	P61284	20740.89	6.32	ADP-ribosylation factor 1 OS=Homo sapiens GN=ARF1 PE=1 Sv=2	17 (17)	1.13E+08	1.02E+08	8.052183196	8.007968176	0.903202186
B4DDV4	B4DPJ6, Q6B6E5, Q53GA0, Q5U0E0, Q6FGS1, Q43399, Q5JWU6	17222.83	6.01	cDNA FLJ52650, highly similar to Tumor protein D54 OS=Homo sapiens PE=2 Sv=1	2 (3)	4.33E+06	3.91E+06	6.636342922	6.591708078	0.902129499
Q13238		52027.84	5.93	Selenium-binding protein 1 OS=Homo sapiens GN=SELENBP1 PE=1 Sv=2	3 (6)	4.69E+06	4.28E+06	6.671461488	6.626655494	0.901739792
A7E2Y5	Q75165	265572.31	6.31	DnaJ (Hsp40) homolog, subfamily C, member 13 OS=Homo sapiens GN=DNAJ13 PE=2 Sv=1	6 (12)	3.05E+06	2.74E+06	6.484268529	6.438279686	0.899520691
Q2TU64		61110.48	5.98	GIP4 OS=Homo sapiens PE=2 Sv=1	13 (19)	1.18E+08	1.06E+08	8.072634116	8.026447296	0.899110728
P49368	Q5S2Y0, E9PAQ6, B3KX11	61065.53	6.1	T-complex protein 1 subunit gamma OS=Homo sapiens GN=CCT3 PE=1 Sv=4	16 (20)	1.18E+08	1.06E+08	8.072634116	8.026447296	0.899110728
B2RBP3	Q8TBC4	52473.6	5.3	mRNA OS=Homo sapiens PE=2 Sv=1	1 (3)	1.85E+06	1.66E+06	6.266487787	6.219974026	0.898434125
P26486		49226.24	5.51	Eukaryotic peptide chain release factor subunit 1 OS=Homo sapiens GN=ETRF1 PE=1 Sv=3	4 (5)	1.46E+07	1.31E+07	7.163738425	7.116984034	0.897364665
P05109		10884.67	6.51	Protein S100-A8 OS=Homo sapiens GN=S100A8 PE=1 Sv=1	2 (3)	1.57E+07	1.41E+07	7.195662032	7.148904739	0.895513389
Q16401	A8K7A6	56559.51	5.35	26S proteasome non-ATPase regulatory subunit 5 OS=Homo sapiens GN=PSMD5 PE=1 Sv=3	19 (24)	1.20E+08	1.07E+08	8.078516938	8.03016959	0.894648941
P02768	A6NB28, E7ESU5, F6KPQ5, Q5G689	71317.25	5.92	Serum albumin OS=Homo sapiens GN=ALB PE=1 Sv=2	9 (11)	1.32E+07	1.18E+07	7.211841186	7.073112402	0.893635271
Q6BIU4	B4DNR3, B4DQC4	22445.6	5.94	Athydiolase domain-containing protein 14B OS=Homo sapiens GN=ABHD14B PE=1 Sv=1	2 (4)	5.20E+06	4.65E+06	6.716333941	6.667393735	0.893428482
P62191	Q5JL38, Q6N3W6, Q5H3B3	49324.76	5.87	26S proteasome regulatory subunit 4 OS=Homo sapiens GN=PSMC1 PE=1 Sv=1	13 (13)	5.43E+07	4.85E+07	7.734837117	7.685364155	0.892333171
P21980		78420.1	5.11	Protein-glutamine gamma-glutamyltransferase 2 OS=Homo sapiens GN=TMGM2 PE=1 Sv=2	5 (9)	1.03E+07	9.19E+06	7.013676342	6.963341247	0.890563529
Q2VF42	A8K8D9, P11413	55187.98	6.91	Glucose-6-phosphate 1-dehydrogenase (Fragment) OS=Homo sapiens GN=G6PD PE=2 Sv=1	12 (16)	1.52E+07	1.35E+07	7.181550892	7.131170253	0.890470141
P00491	Q8N7G1	33225.24	6.45	Purine nucleoside phosphorylase OS=Homo sapiens GN=PNP PE=1 Sv=2	4 (4)	1.59E+06	1.42E+06	6.202234492	6.151540871	0.889828639
Q13561	F5H223, F5H257, Q53H88	44317.9	5.1	Dynactin subunit 2 OS=Homo sapiens GN=DCTN2 PE=1 Sv=4	3 (3)	7.08E+07	6.30E+07	8.849879545	7.999137281	0.889728979
P62333		44430.31	7.1	26S proteasome regulatory subunit 10B OS=Homo sapiens GN=PSMCOB PE=1 Sv=1	10 (16)	3.07E+07	2.73E+07	7.487668319	7.436873967	0.889622273
Q6CND6		58112.23	5.51	Nicotinate phosphoribosyltransferase OS=Homo sapiens GN=NAAPRT1 PE=1 Sv=2	7 (8)	2.54E+07	2.26E+07	7.405226959	7.354236993	0.889262613
Q43396	B2R960	32629.88	4.84	Thioredoxin-like protein 1 OS=Homo sapiens GN=TXNL1 PE=1 Sv=1	3 (3)	1.06E+07	9.44E+06	7.026556822	6.975058016	0.887975932
P56545	Q8Y44, Q5SOP8	49427.31	6.47	C-terminal-binding protein 2 OS=Homo sapiens GN=CTBP2 PE=1 Sv=1	1 (2)	2.63E+06	2.33E+06	6.420002027	6.367703583	0.88655025
P08311		29161.2	11.19	Cathepsin G OS=Homo sapiens GN=CTSG PE=1 Sv=2	3 (7)	8.82E+06	7.90E+06	6.950419345	6.897746119	0.885781843
F5H2F4		111341.81	8.66	Uncharacterized protein OS=Homo sapiens GN=MTFHD1 PE=3 Sv=1	9 (18)	9.36E+06	8.29E+06	6.971302502	6.918316287	0.885143706
P36959		37850.94	6.6	GMP reductase 1 OS=Homo sapiens GN=GMFR PE=1 Sv=1	4 (4)	4.27E+06	3.78E+06	6.630215898	6.577078179	0.884834975
Q9BXD5		35254.39	5.4	N-acetylneuraminatase lyase OS=Homo sapiens GN=NNPL PE=2 Sv=1	3 (10)	5.94E+06	5.25E+06	6.73554058	6.700246947	0.884088144
P68371	Q8N6N5, Q8I229	50255.17	4.79	Tubulin beta-2C chain OS=Homo sapiens GN=TUBB2C PE=1 Sv=1	20 (21)	4.15E+07	3.66E+07	7.615770634	7.563239884	0.882407619
Q5JP53	P07437, B7ZAF0, Q5SU16, Q5ST81	48135.14	4.7	Tubulin beta polypeptide OS=Homo sapiens GN=TUBB PE=3 Sv=1	14 (15)	4.15E+07	3.66E+07	7.615770634	7.563239884	0.882407619
Q14558		39653.74	6.73	Phosphoribosyl pyrophosphate synthase-associated protein 1 OS=Homo sapiens GN=PRPSAP1 PE=1 Sv=2	6 (7)	8.32E+06	7.33E+06	6.919990776	6.865259508	0.881594215
Q9Y315		35493.58	9.08	Putative deoxyribose-phosphate aldolase OS=Homo sapiens GN=DERA PE=1 Sv=2	2 (2)	2.15E+06	1.89E+06	6.332380891	6.277247446	0.880778224
P30044	A6NG06, B7ZLJ4	22300.63	8.93	Peroxiredoxin-5, mitochondrial OS=Homo sapiens GN=PRDX5 PE=1 Sv=4	1 (1)	2.47E+06	2.17E+06	6.392266658	6.336342162	0.879175351
P30154	B4DWW5	66798.72	4.84	GN=PP2R1B PE=1 Sv=3	9 (9)	9.25E+06	8.13E+06	6.966291894	6.910333414	0.879106579
Q60610	E9PEZ2, Q6JURC4	141941.8	5.31	Protein diaphanous homolog 1 OS=Homo sapiens GN=DIAPH1 PE=1 Sv=2	21 (26)	2.05E+07	1.80E+07	7.211251992	7.256004246	0.878709162
B4DQX2	P48426	40005.04	5.81	Uncharacterized protein OS=Homo sapiens GN=PIPKA2A PE=2 Sv=1	3 (7)	1.37E+07	1.20E+07	7.137729097	7.08021538	0.879564049
P60891	Q53FW2, B2R677	35325.12	6.51	Ribose-phosphate pyrophosphokinase 1 OS=Homo sapiens GN=PRPS1 PE=1 Sv=2	6 (7)	1.12E+07	9.77E+06	7.049071291	6.989918754	0.87266481
Q6PCE3		71365.84	6.81	Glucone 1,6-bisphosphate synthase OS=Homo sapiens GN=PFMD11 PE=1 Sv=1	4 (6)	7.11E+06	6.20E+06	6.851974291	6.792598827	0.872216979
Q00442	A8K8K1	39524.6	8.01	RNA 3-terminal phosphate cyclase OS=Homo sapiens GN=RTMCL1 PE=1 Sv=1	2 (4)	3.88E+06	3.39E+06	6.589203075	6.529776281	0.872119318
P06727		45371.47	5.38	Acidophorin A/V OS=Homo sapiens GN=APCA4 PE=1 Sv=3	2 (3)	4.67E+06	4.07E+06	6.668002624	6.609458086	0.870268433
Q14980		124446.52	5.71	Exonin 1 OS=Homo sapiens GN=XPO1 PE=1 Sv=1	9 (11)	1.72E+07	1.50E+07	7.235392624	7.175058483	0.870349383
P60842	A8K7F6	46352.64	5.32	Eukaryotic initiation factor 4A-1 OS=Homo sapiens GN=EIF4A1 PE=1 Sv=1	4 (8)	7.80E+06	6.78E+06	6.891834746	6.83108062	0.869452527
Q0UBQ7	Q5T9A5	36044.89	7.01	Glyoxylate reductase/hydroxypruvate reductase OS=Homo sapiens GN=GRHPR PE=1 Sv=1	2 (3)	2.34E+06	2.03E+06	6.368565289	6.307304932	0.868439639
Q43592	A8KA19	111147.77	5.24	Exonin-T OS=Homo sapiens GN=XPO7 PE=1 Sv=2	1 (1)	1.58E+06	1.37E+06	6.198156206	6.13590173	0.866454026
Q5T447		98134.86	5.47	E3 ubiquitin-protein ligase HECTD3 OS=Homo sapiens GN=HECTD3 PE=1 Sv=1	4 (7)	3.10E+06	2.68E+06	6.491370829	6.428792919	0.865808989
Q5VYK3		205985.07	6.74	Proteasome-associated protein ECM29 homolog OS=Homo sapiens GN=ECM29 PE=1 Sv=2	13 (16)	7.79E+07	6.75E+07	7.891702579	7.829104922	0.865769622
P28066	Q5U0A0	26565.27	4.74	Proteasome subunit alpha type-6 OS=Homo sapiens GN=PSMA5 PE=1 Sv=3	6 (7)	1.70E+07	1.47E+07	7.200292138	7.167633957	0.865648975
Q9NR46	B7ZC38	44174.69	5.72	Endophilin-B2 OS=Homo sapiens GN=SH3GLB2 PE=1 Sv=1	9 (15)	1.01E+07	8.74E+06	7.004385495	6.941421085	0.865038804
P23528	E9PS23, B4E112, E9PP50	18718.74	8.22	Cofilin-1 OS=Homo sapiens GN=CFIL1 PE=1 Sv=3	2 (2)	8.74E+06	7.56E+06	6.941629436	6.878617104	0.864943358
A8K510	P06107	70294.14	5.48	Heat shock 70kDa protein 1A OS=Homo sapiens GN=HSPA1A PE=2 Sv=1	1 (1)	1.88E+07	1.62E+07	7.274015246	7.210323781	0.86359185
P35998		49002.27	5.71	26S proteasome regulatory subunit 7 OS=Homo sapiens GN=PSMC2 PE=1 Sv=3	16 (23)	4.72E+07	4.08E+07	7.674276303	7.610312768	0.86305101
P49720		23218.96	6.14	Protein subunit beta type-3 OS=Homo sapiens GN=PSMB3 PE=1 Sv=2	1 (10)	1.31E+07	1.13E+07	7.116265485	7.051856196	0.86216564
				Bifunctional ATP-dependent dihydroacetone kinase/FAD-AMP lyase (cyclizing) OS=Homo sapiens GN=DAK PE=1 Sv=2	11 (15)	2.70E+07	2.33E+07	7.431829503	7.367230515	0.861789131
Q3LXA3	Q2L9C1	59252.16	7.12	Sv=2	3 (6)	1.49E+06	1.29E+06	6.17390077	6.109186928	0.861561252
B4DMP4										

Q92973		103771.34	4.83	Transportin-1 OS=Homo sapiens GN=TNPO1 PE=1 SV=2	5 (8)	8.50E+06	6.59E+06	6.929445794	6.819163978	0.775743569
Q14697	B4DJ30	107262.82	5.74	Neutral alpha-glucosidase AB OS=Homo sapiens GN=GANAB PE=1 SV=3	2 (8)	3.31E+06	2.57E+06	6.519984303	6.40959844	0.775557741
Q6B0K9		15722.2	6.12	Hemoglobin subunit mu OS=Homo sapiens GN=HBM PE=2 SV=1	3 (3)	6.26E+07	4.83E+07	7.796841377	7.683786615	0.770806269
P07738	A4D1N9, B3KUR3	30157.57	6.1	Bisphosphoglycerate mutase OS=Homo sapiens GN=HBPGM PE=1 SV=2	2 (3)	3.61E+06	2.76E+06	5.556960761	6.441031953	0.765722118
P61900		27837.98	6.34	Proteasome subunit alpha type-3 OS=Homo sapiens GN=PSMA6 PE=1 SV=1	5 (5)	9.20E+06	7.03E+06	6.963738765	6.847174187	0.764601986
B4DQ22	P51812, B4DK22, B7ZB17, F5GYC4	80274.6	6.88	Uncharacterized protein OS=Homo sapiens GN=RR68KA3 PE=2 SV=1	3 (5)	2.56E+06	1.95E+06	6.407546769	6.290705328	0.764114708
Q9GZP4		24390.83	5.47	PITH domain-containing protein 1 OS=Homo sapiens GN=PIITHD1 PE=1 SV=1	2 (2)	3.46E+06	2.64E+06	6.539546624	6.422100583	0.763051689
P35754		12053.29	8.33	Glutaredoxin-1 OS=Homo sapiens GN=GLRX PE=1 SV=2	2 (2)	8.37E+06	6.36E+06	6.922565288	6.80371951	0.760596325
B3KQ33	Q8TEX9, Q59FI4	120190.11	4.88	cDNA FLJ32715 fis, clone TEST2000784, highly similar to Importin-4 OS=Homo sapiens PE=2 SV=1	2 (2)	1.18E+06	8.91E+05	6.070089525	5.949648599	0.757807805
Q9NTK5	D7EHM2	44943.38	7.64	Obg-like ATPase 1 OS=Homo sapiens GN=OLA1 PE=1 SV=2	4 (5)	2.04E+07	1.53E+07	7.308830853	7.185344513	0.752512398
Q9UN37		49152.11	7.64	Vacuolar protein sorting-associated protein 4A OS=Homo sapiens GN=VPS4A PE=1 SV=1	3 (5)	2.50E+06	1.88E+06	6.397609249	6.273508417	0.751448407
P69905	D1MGQ2	15304.95	8.72	Hemoglobin subunit alpha OS=Homo sapiens GN=HBA1 PE=1 SV=2	15 (17)	4.73E+09	3.55E+09	9.674440125	9.549771476	0.750466557
B9A6M6	Q9ULP9	63985.35	7.14	TBC1 domain family, member 24 OS=Homo sapiens GN=TBC1D24 PE=2 SV=1	1 (1)	1.07E+07	8.05E+06	7.030955677	6.905965257	0.749910751
P68402	Q6IBR6	25724.19	5.57	Platelet-activating factor acetylhydrolase IB subunit beta OS=Homo sapiens GN=PAFAH1B2 PE=1 SV=1	1 (2)	1.39E+06	1.04E+06	6.142565383	6.016041581	0.747267677
P07741		19766.5	5.78	Adenine phosphoribosyltransferase OS=Homo sapiens GN=APRT PE=1 SV=2	1 (3)	5.08E+06	3.79E+06	6.705974655	6.578646268	0.745884552
Q8I283		86100.09	6.35	Adenylate dehydrogenase family 16 member A1 OS=Homo sapiens GN=ALDH16A1 PE=1 SV=2	3 (6)	2.90E+06	2.16E+06	6.462536134	6.334386925	0.744476153
P40721		22992.74	6.51	Proteasome subunit beta type-2 OS=Homo sapiens GN=PSMB2 PE=1 SV=1	4 (7)	1.21E+07	9.02E+06	7.083601771	6.955128207	0.743920346
F54X39		60020.92	5.48	Uncharacterized protein OS=Homo sapiens GN=PPP2R1A PE=4 SV=1	10 (17)	1.46E+07	1.08E+07	7.163245755	7.038603703	0.742263233
P68871	D9YZU5	16102.33	6.75	Hemoglobin subunit beta OS=Homo sapiens GN=HBB PE=1 SV=2	17 (18)	8.06E+09	5.96E+09	9.906412668	9.775197422	0.739238802
P04792		22825.51	5.98	Heat shock protein beta-1 OS=Homo sapiens GN=HSPB1 PE=1 SV=2	2 (5)	7.21E+06	5.31E+06	6.857963467	6.725102361	0.736442584
Q3LR79		11531.86	5.46	Hemoglobin beta (Fragment) OS=Homo sapiens GN=HBB PE=2 SV=1	12 (13)	7.51E+09	5.51E+09	9.875692815	9.7413645	0.733958805
A0N071	P02042	16159.33	7.85	Delta globin OS=Homo sapiens GN=HBD PE=3 SV=1	15 (16)	5.88E+09	4.29E+09	9.769096912	9.632395902	0.729959878
P25787	Q53GF5	25996.31	6.92	Proteasome subunit alpha type-2 OS=Homo sapiens GN=PSMA2 PE=1 SV=2	5 (6)	6.35E+06	4.63E+06	6.803102671	6.665585153	0.728588786
A4D1P6		84204.08	6.15	WD repeat-containing protein 91 OS=Homo sapiens GN=WDR91 PE=1 SV=2	3 (6)	1.96E+07	1.43E+07	7.29333361	7.155667931	0.728340266
P30043		22219.47	7.13	Flavin reductase OS=Homo sapiens GN=BLVRB PE=1 SV=3	10 (12)	1.47E+08	1.07E+08	1.168441195	8.030167455	0.727321222
Q9UK54		14069.22	6.46	Hemoglobin beta subunit variant (Fragment) OS=Homo sapiens GN=HBB PE=2 SV=1	13 (13)	6.88E+09	4.96E+09	9.837479825	9.695354985	0.720900024
P25788	Q6IB71	28643.17	5.19	Proteasome subunit alpha type-3 OS=Homo sapiens GN=PSMA6 PE=1 SV=2	4 (5)	1.12E+07	8.03E+06	7.050767151	6.904753061	0.714473146
Q8V9V6	A8K8U1	137999.3	5.52	Cullin-associated NEDD8-dissociated protein 1 OS=Homo sapiens GN=CAND1 PE=1 SV=2	23 (28)	6.42E+07	4.58E+07	7.807534331	7.661133794	0.713837672
Q6L1Z7		11495.89	6.17	Hemoglobin beta (Fragment) OS=Homo sapiens GN=HBB PE=2 SV=1	11 (12)	6.33E+09	4.51E+09	9.801249536	9.654361897	0.713037485
Q96P70		116858.1	4.71	Importin-9 OS=Homo sapiens GN=IPO9 PE=1 SV=3	8 (11)	1.32E+07	9.40E+06	7.120392987	6.973224526	0.712576572
P55072		89949.98	5.14	Transitional endoplasmic reticulum ATPase OS=Homo sapiens GN=VCP PE=1 SV=4	16 (22)	2.06E+07	1.47E+07	7.314252013	7.16685278	0.712198028
P01009	E9KL23	46878.08	5.37	Alpha-1-antitrypsin OS=Homo sapiens GN=SERPINA1 PE=1 SV=3	4 (5)	6.09E+06	4.32E+06	6.784427941	6.653534641	0.709458017
P69891		16187.33	6.64	Hemoglobin subunit gamma-1 OS=Homo sapiens GN=HBG1 PE=1 SV=2	9 (11)	4.36E+09	3.06E+09	9.639343421	9.485321834	0.701420433
P69892	D9YZU9, Q9UNL6, E7CYP2, D3GKDN	16173.32	6.64	Hemoglobin subunit gamma-2 OS=Homo sapiens GN=HBG2 PE=1 SV=2	9 (11)	4.36E+09	3.06E+09	9.639343421	9.485321834	0.701420433
P09105		15612.16	7.1	Hemoglobin subunit theta-1 OS=Homo sapiens GN=HBQ1 PE=1 SV=2	2 (2)	7.71E+06	5.39E+06	6.886903688	6.73169552	0.699501503
P00558	A8K4W6	44985.28	8.3	Phosphoglycerate kinase 1 OS=Homo sapiens GN=PGK1 PE=1 SV=3	3 (8)	2.28E+07	1.59E+07	7.357474491	7.201591387	0.698420369
B4DLT9	Q9UPN7	43406.97	4.74	Uncharacterized protein OS=Homo sapiens GN=PPP6R1 PE=2 SV=1	3 (3)	4.15E+06	2.85E+06	6.61815843	6.454349737	0.685790251
P25789		29750.29	7.57	Proteasome subunit alpha type-4 OS=Homo sapiens GN=PSMA4 PE=1 SV=1	3 (3)	4.66E+06	3.13E+06	6.668387797	6.495677138	0.671876329
Q0VGT5	Q9CDE2, F22ZX4	128609.32	4.98	Exportin 4 OS=Homo sapiens GN=XPO4 PE=2 SV=1	3 (3)	5.57E+06	3.73E+06	6.745744199	6.571692254	0.66980491
Q96NA2		44344.66	5.47	Rab-interacting lysosomal protein OS=Homo sapiens GN=RILP PE=1 SV=1	7 (9)	4.56E+06	3.05E+06	6.659046862	6.484503686	0.669047305
Q9BTY7	P0CB43	42558.83	4.73	Protein FAM203A OS=Homo sapiens GN=FAM203A PE=1 SV=1	3 (4)	2.73E+06	1.82E+06	6.436920475	6.260524532	0.666199125
Q6ZMU0		39594.96	7.59	Delta-aminolevulinic acid dehydratase OS=Homo sapiens PE=2 SV=1	3 (4)	7.41E+06	4.92E+06	6.869990623	6.691692987	0.663288342
P25786	Q53YE8	29821.97	6.15	Proteasome subunit alpha type-1 OS=Homo sapiens GN=PSMA1 PE=1 SV=1	3 (5)	8.55E+06	5.66E+06	6.931944928	6.75281049	0.662011544
Q5D862		249296.33	8.45	Filaggrin-2 OS=Homo sapiens GN=FLG2 PE=1 SV=1	1 (3)	1.26E+06	8.31E+05	6.101069603	5.91959797	0.658458439
P05164		84784.2	9.19	Myeloperoxidase OS=Homo sapiens GN=MPO PE=1 SV=1	17 (27)	4.59E+07	3.00E+07	7.661692532	7.477150305	0.653819355
Q96AP7		41435.68	9.42	Endothelial cell-selective adhesion molecule OS=Homo sapiens GN=ESAM PE=1 SV=1	1 (1)	3.56E+05	2.24E+05	5.551420092	5.349953111	0.628829661
Q15102		25832.28	6.33	Platelet-activating factor acetylhydrolase IB subunit gamma OS=Homo sapiens GN=PAFAH1B3 PE=1 SV=1	2 (2)	1.07E+07	6.69E+06	7.027585503	6.825426237	0.627828077
P68246		29127.02	9.71	Neutrophil elastase OS=Homo sapiens GN=ELANE PE=1 SV=1	2 (3)	4.05E+07	2.54E+07	7.607269676	7.404164919	0.626462736
Q70003		37693.34	5.31	Glutaredoxin-3 OS=Homo sapiens GN=GLRX3 PE=1 SV=2	1 (2)	2.04E+06	1.28E+06	6.310386212	6.106653774	0.62555797
Q9PJL7		42603.15	5.41	E3 ubiquitin-protein ligase KCMF1 OS=Homo sapiens GN=KCMF1 PE=1 SV=2	2 (2)	3.37E+06	2.19E+06	6.552453266	6.340755064	0.614188666
Q9LJ26		113489.14	5.14	Importin-11 OS=Homo sapiens GN=IPO11 PE=1 SV=1	1 (2)	5.03E+05	3.08E+05	5.701823679	5.485451523	0.607572129
B4DQJ8	P52209, A8K2Y9	52352.45	7.12	6-phosphogluconate dehydrogenase, decarboxylating OS=Homo sapiens GN=PGD PE=2 SV=1	1 (2)	8.88E+05	5.38E+05	5.948615907	5.73057505	0.605283929
B7Z5E3		40096.99	8.61	L-lactate dehydrogenase OS=Homo sapiens GN=LDAH PE=2 SV=1	1 (3)	9.74E+05	5.66E+05	5.988490093	5.752864455	0.581265253
Q27J81	C9JAR5	136851.23	5.26	Inverted formin-2 OS=Homo sapiens GN=INF2 PE=1 SV=2	1 (1)	5.85E+05	3.33E+05	5.766909564	5.521953576	0.568910523
P13716	B7Z3I9	36727.59	6.32	Delta-aminolevulinic acid dehydratase OS=Homo sapiens GN=ALAD PE=1 SV=1	4 (7)	8.10E+06	4.55E+06	6.90825831	6.67962168	0.561958
	B2R6J4, C9JZ17, F5HFY4, B7ZAK9, A8MXH2, C9J6D1, B7ZACT, A8MZ22, B4D505, B7ZB83	42967.95	4.6	Nucleosome assembly protein 1-like 4 OS=Homo sapiens GN=NAP1L4 PE=1 SV=1	1 (1)	1.07E+06	5.85E+05	6.030707226	5.767315098	0.545265315
Q99733	A8MZ22, B4D505, B7ZB83	39635.06	7.05	Dual specificity mitogen-activated protein kinase kinase 3 OS=Homo sapiens GN=MAP2K3 PE=1 SV=2	2 (4)	3.45E+05	1.87E+05	5.537307363	5.272280139	0.543216279
P46734	Q5Z6Z9	23492.93	5.48	Protein FADD OS=Homo sapiens GN=FADD PE=1 SV=1	1 (1)	5.26E+05	2.75E+05	5.721137638	5.439510894	0.522845358
Q13158	Q8LGG1, B4DD58	36531.11	6.91	Malate dehydrogenase, cytoplasmic OS=Homo sapiens GN=MDH1 PE=1 SV=4	1 (2)	4.75E+05	2.24E+05	5.676694524	5.349297736	0.470547221
P40925	F9H086	33205.76	6.1	Translin-associated protein X OS=Homo sapiens GN=TSNAX PE=1 SV=1	1 (2)	3.90E+05	1.79E+05	5.590531991	5.253100474	0.459799487
Q96598	B1AP06	24791.69	6.21	Hypoxanthine-guanine phosphoribosyltransferase OS=Homo sapiens GN=HPR1 PE=1 SV=2	1 (2)	1.97E+06	9.01E+05	6.294202569	5.954494356	0.457395394
P00492	Q8LET3	16846.9	8.26	Prolactin-inducible protein OS=Homo sapiens GN=PIP PE=1 SV=1	4 (4)	4.45E+06	1.95E+06	6.648082657	6.29012676	0.438575233
P12273		82141.98	5.29	Acylamino-acid-releasing enzyme OS=Homo sapiens GN=APEH PE=1 SV=4	3 (5)	4.99E+06	2.04E+06	6.69845171	6.31039686	0.409208975
P13798	C9JIF9	16982.46	9.38	Lysozyme C OS=Homo sapiens GN=LYZ PE=1 SV=1	1 (2)	1.86E+07	6.80E+06	7.269678656	6.832552016	0.365488199
P61626	B2R4C5	38679.63	6.23	Mutant erythrocyte membrane glycoprotein Rh50 OS=Homo sapiens GN=Rh50 PE=2 SV=1	2 (2)	5.61E+05	1.95E+05	5.748974342	5.291058393	0.348404737
Q43515		21553.01	6.74	Pancreatic adenocarcinoma upregulated factor OS=Homo sapiens GN=PAUF PE=2 SV=1	4 (5)	6.41E+06	6.06E+05	5.806584069	5.782736132	0.094656853
C3PTT6										

Supplemental Data 6

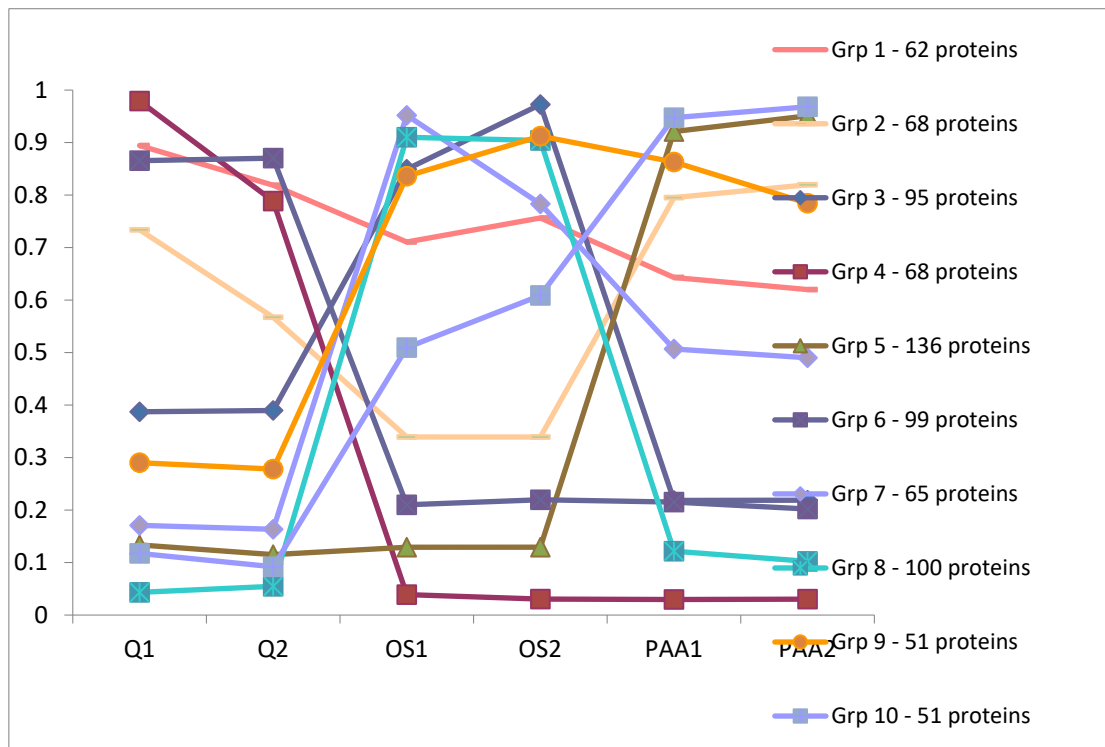
Box plot representing (A) the isoelectric point and (B) the molecular weight of each NP-specific protein signatures.

Supplemental Data 6

Sheet 1

Hierarchical Clustering

Q1	Q2	OS1	OS2	PAA1	PAA2	hclus,label
0.89437097	0.81882258	0.71064516	0.75641935	0.64306452	0.61998387	Grp 1 - 62 proteins
0.73380882	0.56729412	0.33919118	0.33908824	0.79517647	0.81966176	Grp 2 - 68 proteins
0.3872	0.38972632	0.84918947	0.97250526	0.21830526	0.2188	Grp 3 - 95 proteins
0.97908824	0.78857353	0.03894118	0.03042647	0.02966176	0.03029412	Grp 4 - 68 proteins
0.13360294	0.11509559	0.12920588	0.12925	0.92103676	0.95102941	Grp 5 - 136 proteins
0.86550505	0.87036364	0.2100202	0.21960606	0.21517172	0.2020202	Grp 6 - 99 proteins
0.17086154	0.16335385	0.95189231	0.78316923	0.50687692	0.49006154	Grp 7 - 65 proteins
0.04325	0.05473	0.91013	0.90402	0.12168	0.10222	Grp 8 - 100 proteins
0.29023529	0.27801961	0.83605882	0.91231373	0.863	0.78441176	Grp 9 - 51 proteins
0.11741176	0.09194118	0.5095098	0.60880392	0.94739216	0.9682549	Grp 10 - 51 proteins



Supplemental Data 6

Sheet 2

Specific Q

AC	Q1	Q2	OS1	OS2	PAA1	PAA2
P13716	1	0.848	0.021	0.011	0.003	0.004
P55072	1	0.909	0.024	0.017	0.038	0.04
P13798	1	0.857	0.01	0.004	0.001	0.013
Q05DH1	0.925	1	0.03	0.024	0.025	0.026
P14868	1	0	0.027	0.017	0.032	0.032
E9PBC8	0.902	1	0.031	0.024	0.027	0.028
P25788	1	1	0.036	0.026	0.113	0.096
Q04917	1	0.59	0.034	0.03	0.004	0.004
P21980	1	0.719	0.033	0.026	0.016	0.018
P62258	1	0.916	0.05	0.035	0.008	0.006
P25789	0.902	1	0.018	0.013	0.035	0.033
D0PN11	1	0.868	0.049	0.048	0.004	0.004
P27348	1	0.815	0.046	0.042	0.006	0.005
P61981	1	0.874	0.048	0.044	0.006	0.005
O43681	1	0.897	0.093	0.09	0.101	0.117
Q9UPU5	1	0.808	0.02	0.031	0.035	0.039
O43396	1	0.91	0.077	0.069	0.012	0.015
Q14974	1	0.606	0.231	0.214	0.014	0.013
Q9GZP4	1	0.793	0.025	0.019	0.018	0.023
P30153	1	0.523	0.095	0.071	0.052	0.053
P02768	1	0.264	0.126	0.111	0.009	0.055
F5H3X9	1	0.66	0.134	0.1	0.05	0.047
B2RDD7	1	0.804	0.02	0.009	0.072	0.071
Q5QNY9	1	0.809	0.064	0.057	0.048	0.058
P67775	1	0.807	0.025	0.02	0.014	0.02
P12814	1	0.702	0.019	0.012	0.003	0.006
P29144	0.908	1	0.067	0.064	0.05	0.036
B4DLQ1	1	0.975	0.095	0.094	0.077	0.025
Q9Y315	1	0.682	0.064	0.042	0.03	0.032
P30154	1	0.53	0.236	0.122	0.065	0.065
Q15631	1	0.849	0.017	0	0.141	0.156
Q4LE60	1	0.573	0.275	0.2	0.009	0.012
B7Z815	1	0.806	0.089	0.111	0.084	0.076
B1AH89	1	0.625	0.036	0.024	0.036	0.068
P54105	1	0.826	0.134	0	0	0
Q99733	0.798	1	0.06	0.048	0.023	0.032
Q9NXR7	1	0.495	0.042	0.032	0	0
P80217	1	0.965	0.085	0.061	0.043	0.044
Q9H5X1	0.911	1	0	0.079	0	0
Q99598	1	0.943	0.062	0.028	0.165	0.178
Q15018	1	0.852	0	0	0.104	0.083
Q9H074	1	0.863	0	0	0	0
B0YJ28	0.983	1	0	0	0	0
P31153	1	0.768	0	0	0	0
B8ZZW9	0.772	1	0	0	0.069	0
Q9BTE1	1	0.588	0	0	0	0.106
Q8IWT0	0.893	1	0	0	0	0
Q9H7G6	0.974	1	0	0	0	0
P58546	0.933	1	0	0	0.144	0
D3DWY7	1	0.731	0	0	0	0.2

F2Z2Y6	1	0.834	0	0	0	0
B4DYD9	1	0.781	0	0	0.231	0
Q9Y333	1	0.682	0	0	0	0
A0PJK4	1	0.72	0	0	0	0
B0R0W4	1	0.8	0	0	0	0
E9PRT4	1	0.978	0	0	0	0
Q9UBQ0	0.728	1	0	0	0	0
B3KQ94	1	0.858	0	0	0	0
P49354	1	0.497	0	0	0	0
Q3ZTS7	1	0.627	0	0	0	0
Q15363	1	0.795	0	0	0	0
B3KSS1	1	0.6	0	0	0	0
B0UZ83	1	0.399	0	0	0	0.116
Q9UBF2	1	0.671	0	0	0	0
P63151	1	0.875	0	0	0	0
O60884	0.949	1	0	0	0	0
Q0VGL7	1	0.832	0	0	0	0
Q9BRX5	1	0.624	0	0	0	0
Average	0.97908824	0.78857353	0.03894118	0.03042647	0.02966176	0.03029412

Supplemental Data 6

Sheet 3

Specific OS

AC	Q1	Q2	OS1	OS2	PAA1	PAA2
Q0P512	0.15	0.127	0.828	1	0.174	0.167
B2RDW1	0.065	0.065	0.981	1	0.215	0.199
Q13404	0.041	0.06	1	0.954	0.164	0.145
P04632	0.089	0.09	0.927	1	0.264	0.215
A8K781	0.054	0.039	1	0.113	0.085	0.096
B2LR44	0.065	0.067	0.639	1	0.144	0.144
Q2YHU8	0.074	0.09	0.693	1	0.186	0.181
P30043	0.072	0.075	1	0.727	0.118	0.106
P30041	0.108	0.091	0.878	1	0.16	0.178
P04075	0.06	0.028	0.966	1	0.019	0.02
P00568	0.023	0.228	0.883	1	0.033	0.042
P37840	0.003	0.003	1	0.986	0.008	0.006
F5H157	0.062	0.056	0.736	1	0.23	0.149
E7ESC6	0.107	0.11	1	0.805	0.053	0.028
Q6PIK3	0.068	0	0.728	1	0.135	0.047
Q9NRW1	0.044	0.016	0.727	1	0.088	0.078
Q9H0U4	0.045	0.028	0.779	1	0.165	0.116
P61026	0.053	0.037	0.74	1	0.174	0.116
P61106	0.081	0.111	0.738	1	0.131	0.058
P61006	0.048	0.061	0.74	1	0.154	0.097
P00558	0.153	0.053	1	0.699	0.237	0.218
Q13561	0.041	0.034	1	0.889	0.104	0.082
P00352	0.046	0.031	1	0.103	0.026	0.024
Q6XQN6	0.107	0.029	1	0.889	0.045	0.038
Q6B0K9	0.025	0.018	1	0.741	0.047	0.081
Q6FGX3	0.026	0.019	0.726	1	0.142	0.119
P51148	0.032	0.029	0.994	1	0.107	0.098
P61020	0.034	0.031	0.969	1	0.12	0.108
Q9NPQ8	0.144	0.074	1	0.796	0.12	0.139
O75340	0.194	0.09	1	0.839	0.037	0.051
P54920	0.031	0.019	0.691	1	0.016	0.026
Q2TAZ0	0.185	0.138	1	0.452	0.285	0.199
Q8WYN0	0.071	0.052	0.958	1	0.227	0.23
P48507	0.073	0.084	1	0.96	0.088	0.07
B4DJA5	0.032	0.041	0.912	1	0.109	0.136
P20160	0.024	0.036	0.943	1	0.318	0.26
Q5TDH0	0.029	0.023	1	0.944	0.089	0.057
Q4W4Y1	0.092	0.045	0.827	1	0.108	0.096
Q6FG59	0.066	0.025	0.834	1	0	0
P61088	0.005	0.008	1	0.948	0.013	0.012
O94919	0.044	0.067	0.803	1	0.287	0.216
P02724	0.049	0.077	1	0.819	0.033	0.047
P07737	0.176	0.178	1	0.506	0.196	0.238
B2R657	0.061	0.078	0.844	1	0.14	0.092
Q5U025	0.051	0.101	1	0.994	0.31	0.21
C5MQH7	0.095	0.086	0.781	1	0.191	0.186
Q9Y4G6	0.045	0.07	1	0.942	0.257	0.228
P61077	0.007	0.004	1	0.963	0.06	0.057
A5YM50	0.035	0.041	1	0.785	0.07	0.055
P31948	0.034	0.075	0.738	1	0.144	0.144

P01009	0.117	0.129	1	0.709	0.267	0.287
Q9BXD5	0.066	0.089	0.543	1	0.075	0.08
Q15102	0.059	0.064	1	0.628	0.165	0.104
P09105	0.081	0.071	1	0.699	0.134	0.132
C9JRV9	0.094	0	0.612	1	0.12	0.121
Q3LXA3	0.018	0.013	1	0.861	0.05	0.047
Q96IJ6	0.052	0.033	1	0.906	0.183	0.17
Q99497	0.041	0.082	0.983	1	0.134	0.126
A4D2J0	0.081	0.072	0.765	1	0.183	0.138
Q13057	0.013	0.011	0.966	1	0.063	0.055
Q15257	0.026	0.022	0.921	1	0	0.019
B3KSY4	0.076	0.04	0.908	1	0.148	0.128
P22061	0.032	0.081	1	0.996	0.151	0.081
Q15276	0.096	0.06	1	0.784	0.256	0.183
O15400	0.047	0.062	0.842	1	0.313	0.228
P35754	0.039	0.047	1	0.76	0.108	0.134
Q9NR46	0.027	0.022	1	0.931	0.203	0.197
P07741	0.041	0.115	1	0.746	0	0.226
Q07960	0	0	0.862	1	0.095	0.101
O95630	0	0	0.765	1	0.178	0
Q1MW40	0	0	0.738	1	0.16	0
Q8WVM8	0	0	1	0.952	0.087	0.07
P56545	0	0	1	0.886	0	0
P36507	0	0.059	0.911	1	0.156	0.197
P01833	0	0	1	0.787	0	0
Q13158	0	0	1	0.523	0.238	0
B4DDV4	0	0.075	1	0.902	0	0
Q16851	0	0	1	0.98	0.068	0.045
Q5D862	0	0.361	1	0.658	0.261	0
Q53TN4	0	0	0.75	1	0.094	0.07
O60664	0	0	1	0.954	0.023	0.016
B7Z3V1	0	0.112	0.694	1	0	0.414
P30044	0	0	1	0.879	0	0
Q96AP7	0	0	1	0.629	0	0
D6RCE2	0	0	1	0.978	0.19	0.251
P61081	0	0.026	1	0.787	0.009	0.051
F5H399	0	0	0.913	1	0	0
P06727	0	0	1	0.872	0	0
P10909	0	0.199	0.953	1	0.309	0.259
P05090	0	0	0.843	1	0	0
Q04656	0	0	0.879	1	0	0
Q96IU4	0	0	1	0.893	0.126	0.133
O15173	0	0.097	0.821	1	0.162	0.141
P04921	0	0	1	0.967	0.058	0.053
Q3SYB4	0	0	0.625	1	0.17	0
B4E2N0	0	0.026	1	0.921	0	0.032
B2R5X9	0	0	1	0.96	0.039	0
O00154	0	0	1	1	0.16	0.074
O15067	0	0.424	0.916	1	0.218	0
P01040	0	0.043	0.8	1	0.188	0.154

Average	0.04325	0.05473	0.91013	0.90402	0.12168	0.10222
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Supplemental Data 6

Sheet 4

Specific PAA

AC	Q1	Q2	OS1	OS2	PAA1	PAA2
P32119		0.266	0.21	0.09	0.099	1 0.913
Q06830		0.144	0.132	0.058	0.069	1 0.897
P49368		0.368	0.263	0.227	0.194	0.967 1
P50991		0.384	0.284	0.21	0.197	0.988 1
P16157		0.159	0.135	0.328	0.309	0.968 1
P17987		0.343	0.283	0.338	0.371	0.987 1
Q99832		0.33	0.284	0.233	0.283	0.999 1
P50570		1	0.104	0.069	0.058	0.796 0.822
F5H136		0.362	0.294	0.333	0.327	1 0.987
P62195		0.289	0.242	0.318	0.304	0.87 1
Q32Q12		0.324	0.378	0.016	0.018	0.949 1
P15531		0.339	0.436	0.019	0.018	1 0.984
Q9UKV8		0.703	0	0.012	0.024	0.945 1
Q9UL46		0.19	0.215	0.097	0.099	1 0.988
P55036		0.321	0.316	0.106	0.09	0.888 1
O95373		0.385	0.206	0.235	0.241	0.868 1
Q14C86		0.377	0.281	0.239	0.236	0.895 1
B4DMP4		0.357	0.341	0.06	0.056	0.854 1
P53680		0.325	0.391	0.201	0.19	1 0.952
A8K008		0.242	0.336	0.192	0.164	1 0.736
P08311		0.169	0.153	0.372	0.299	1 0.954
P23381		0.203	0.235	0.048	0.058	1 0.503
P60891		0.024	0.02	0.038	0.033	1 1
Q969U7		0.258	0.197	0.129	0.196	0.988 1
O95782		0.02	0.385	0.121	0.012	1 0.971
B1ALA9		0.026	0.02	0.044	0.039	0.997 1
O60256		0.198	0.139	0.066	0.07	0.873 1
Q7Z351		0.263	0.275	0.191	0.203	1 0.939
P36959		0.161	0.13	0.125	0.11	1 0.969
P11908		0.022	0.021	0.045	0.04	1 0.982
Q6P5S8		0.337	0.293	0.396	0.221	1 0.888
P35219		0.466	0.379	0	0	1 0.944
P00387		0.523	0.44	0.119	0.155	0.971 1
P63000		0.128	0.129	0.231	0.205	0.999 1
P05109		0.034	0.049	0.099	0.089	0.998 1
B4DPM7		0.068	0.062	0.166	0.229	1 0.988
P21281		0.377	0.445	0.149	0.122	1 0.997
P31146		0.132	0.014	0.018	0.017	1 0.952
Q96GG9		0.197	0.11	0.074	0.131	0.993 1
A6NN01		0.299	0.269	0.316	0.381	1 0.606
O60925		0.095	0.071	0	0.043	0.022 1
A0AUX0		0.212	0.173	0.05	0.028	0.896 1
O94973		0.043	0.027	0.195	0.185	0.962 1
B4DNA3		0.09	0.034	0.038	0.034	1 0.987
P15311		0.039	0.031	0.343	0.386	0.984 1
P07738		0.142	0.144	0.16	0.126	1 0.932
P63241		0.063	0.049	0.046	0.049	0.856 1
Q13616		0.164	0.139	0.221	0.278	1 0.983
Q15691		0.164	0.018	0.039	0.124	1 0.846
Q709C8		0.43	0.326	0.209	0.289	0.882 1

P30566	0.464	0.292	0.33	0.364	1	0.983
B2R4M6	0.026	0.052	0.097	0.094	1	0.914
P22234	0.041	0.035	0.077	0.078	0.955	1
Q96F85	0.018	0.008	0.076	0.084	1	0.96
Q13576	0.088	0.056	0.28	0.485	1	0.503
Q53FA7	0.134	0.198	0.374	0.204	0.827	1
P62937	0.34	0.303	0.314	0.339	0.899	1
Q9P0J7	0.206	0.14	0.562	0.345	1	0.541
A7E2Y5	0.12	0.077	0.143	0.11	0.964	1
Q15181	0.387	0.182	0.401	0.342	0.966	1
Q9H479	0.083	0.125	0.131	0.101	1	0.889
B2RD79	0.007	0.007	0.106	0.088	1	0.991
Q5H9R7	0.137	0.064	0.246	0	0.936	1
Q14558	0.047	0.056	0.344	0.318	0.925	1
B4DGX3	0.039	0.041	0.087	0.095	1	0.971
P43034	0.073	0.034	0	0	1	0.914
P29401	0.017	0.011	0.153	0.197	0.995	1
P80188	0.091	0.117	0.069	0.102	1	0.87
O60488	0.091	0.075	0.21	0.287	0.874	1
B2RCT6	0.264	0.15	0	0.193	0.888	1
B2R5N2	0.026	0.026	0.049	0.086	1	0.985
P55884	0.695	0.328	0	0	1	0.887
Q9BPX3	0.253	0.228	0	0	1	0.727
P42858	0.18	0.161	0.162	0	1	0.713
Q9NWX6	0.094	0.104	0.295	0.336	0.788	1
P61158	0.032	0.027	0.123	0.124	0.926	1
P04114	0.429	0.318	0	0	0.944	1
Q8IUR7	0.127	0.116	0.211	0.14	1	0.984
P53618	0.275	0.182	0	0	1	0.746
P42345	0.268	0.152	0	0	0.803	1
Q6IPX4	0.131	0.132	0.309	0.256	1	0.954
Q59F66	0.094	0.1	0.205	0.177	1	0.771
B7Z8P7	0.151	0	0	0	0.96	1
Q15404	0.008	0.006	0.059	0.061	0.963	1
D3DPU2	0.005	0.008	0.014	0.028	1	0.89
P54619	0.055	0.048	0	0	0.926	1
E9PCU1	0.119	0	0.285	0.098	0.645	1
B2R5N2	0	0.006	0.078	0.094	1	0.955
O43324	0	0	0	0	1	0.717
P21283	0	0	0	0.17	0.952	1
Q9NS86	0	0	0	0	0.895	1
P54577	0	0	0.15	0.166	0.998	1
B4DHQ1	0	0.754	0	0.428	0.219	1
Q0VGA5	0	0	0	0	0.938	1
B2R491	0	0.322	0.184	0	1	0.978
B4DPJ2	0	0	0	0	0.833	1
E9PL45	0	0	0.432	0	0.887	1
P49588	0	0	0.141	0.299	0.981	1
A0JP11	0	0.171	0	0	0.859	1
P13639	0	0	0.161	0.174	0.979	1
Q9NQC3	0	0	0	0	1	0.798

Q06187	0	0	0	0	0.807	1
O15143	0	0	0	0	0.88	1
B2R680	0	0	0	0	1	0.778
Q7Z2W4	0	0	0	0	0.872	1
P23396	0	0	0	0	0.879	1
Q8N1G4	0	0	0	0	1	0.77
E7EUY0	0	0	0	0	1	0.993
Q15418	0	0	0.469	0	1	0.959
P48729	0	0.043	0.312	0.231	0.97	1
Q8WU76	0	0	0	0	1	0.913
Q96BC0	0	0	0.37	0.266	0.695	1
Q9Y613	0	0	0.511	0	0.781	1
Q9Y2V2	0	0	0	0	0.79	1
B2RAM2	0	0	0	0.947	0	1
O43776	0	0	0	0	0.959	1
Q9Y450	0	0	0	0	0.858	1
D3DTH7	0	0	0	0	1	0.963
Q9Y678	0	0	0.31	0.273	1	0.962
Q92835	0	0	0	0.355	0.869	1
Q86VN1	0	0	0	0	0.786	1
Q59E99	0	0	0.323	0.276	1	0.978
P16989	0	0.1	0	0	1	0.935
F6U211	0	0	0	0	0.889	1
B3KPC7	0	0.113	0.258	0.291	0.866	1
O43426	0	0	0	0	0.879	1
B3KQV3	0	0	0	0	0.562	1
O15144	0	0	0.075	0.09	0.926	1
Q5IRN2	0	0	0	0	1	0.91
P07814	0	0	0	0	0.877	1
Q15021	0	0	0.028	0.034	0.922	1
O43747	0	0	0	0	0.886	1
B4DDW1	0	0.277	0.075	0.151	0.488	1
Q96T66	0	0	0.289	0.387	0.861	1
Q9Y285	0	0	0	0	1	0.818
Q13418	0	0	0.265	0.315	0.839	1
Average	0.133602941	0.115095588	0.129205882	0.12925	0.921036765	0.951029412

Supplemental Data 7

List of the 20 most abundant proteins
(decreasing from 1 to 20) identified
from all conditions.

Supplemental Data 7
Sheet 1

PL and MW Specific Proteins

Supplemental Data 8

Figure 1: Box plot representing (A) the isoelectric point and (B) the molecular weight of each NP-specific protein signatures.

