

Extended Data

Extended Materials Methods

Cell culture; hormone and inhibitor treatment

T47DM cells were used for all experiments unless otherwise stated. For hormone induction experiments, cells were grown in RPMI medium without Phenol Red, supplemented with 10% dextran-coated charcoal-treated FBS (DCC/FBS) after 24 h in serum-free conditions; cells were incubated with R5020 (10 nM) or vehicle (ethanol) as described (Vicent et al. 2011). For hormone induction experiments in MCF7 cells a similar procedure was performed; cells were grown in DMEM medium without Phenol Red, supplemented with 10% dextran-coated charcoal-treated FBS (DCC/FBS) after 24 h in serum-free conditions; cells were incubated with Estradiol (10 nM) or vehicle (ethanol). PARG and PARP inhibition were carried out via incubating cells with 5uM TA (tannic acid) or 10uM 3AB (3-amino-benzamide) respectively 1 hour prior to hormone treatment. All transfections were performed using Lipofectamine²⁰⁰⁰ (Invitrogen) according to manufacturers instructions.

PAR-capture ELISA

Hormone and or inhibitor treatments were carried out as described, and sample preparation was carried out as follows: At the required time point, cells were washed twice with ice-cold PBS and scraped in lysis buffer (0.4 M NaCl, 1% Triton X-100) plus protease inhibitors. Cell suspensions were then incubated for 30 min on ice with periodic vortexing. The disrupted cell suspension was centrifuged at 10,000g for 10 min at 4°C, and the supernatant was recovered, snap-frozen, and stored at 80°C until required. Ninety-six-well black-walled plates were incubated with 2 ng/mL anti-PAR monoclonal antibody (Trevigen) in 50 mM sodium carbonate (pH 7.6) overnight at 4°C. The plates were washed once with PBS and blocked with blocking solution (5% semiskimmed milk powder, 0.1% Tween 20, 25 mM Tris at pH 7.4, 150 mM NaCl) for 1 h at room temperature. The plate was then washed four times in PBS and 0.1% Tween 20. One-hundred microliters of each sample (20 mg of total protein) or a PAR standard was applied and incubated for 1.5 h at room temperature. The plate was washed four times with PBS and 0.1% Tween 20 and incubated with anti-PAR rabbit

polyclonal antibody (Trevigen) for 1.5 h at room temperature. The plate was washed four times with PBS and 0.1% Tween 20 and incubated with anti-rabbit HRP conjugate secondary antibody (5% semiskimmed dried milk) for 1.5 h at room temperature. The plate was washed six times with PBS and 0.1% Tween 20, and PAR was identified via incubation with TACs Sapphire (Trevigen) for 10 min in the dark. The reaction was terminated with 5% phosphoric acid, and the absorbance at 450 nm and 520 nm was recorded.

NAD depletion assay

T47D^M cells were either left untreated or treated with the inhibitor indicated prior to R5020 addition as described. NAD concentration was determined as described (Wright et al 2012). At $T = t$, cells were washed with ice-cold PBS and incubated in 0.5 M PCA for 20 min on ice. An equal volume of KOH (1 M)/K₂HPO₄ (0.33 M) (pH 7.0) was added, and the samples were vortexed and incubated for 20 min on ice. Samples were spun at 10,000 rpm for 2 min at 4°C, and the supernatant was stored at -20°C. The quantification of NAD was carried out as follows: Samples were added to an equal volume of reaction buffer (200 mM Bicine at pH 7.8, 1 mg/mL BSA, 1M EtOH, 10mMEDTA at pH 8.0, 4mM phenazine). One tenth of the reaction volume of alcohol dehydrogenase was added and incubated for 30 min at 30°C. The reaction was terminated with a 0.33 sample volume of 12 mM iodoacetate, and the absorbance at 570 nm was measured.

Modelling and evaluation of the phosphorylated and unphosphorylated T45 NUDIX5 homodimer. In order to mimic the phosphorylation in T45 of NUDIX5 homodimer, we modeled the mutant form T45D with MODELLER (Fischer et al 2003). The dimer structure of NUDIX5 was taken from the crystal 2DSC (Zhong et al 2006) deposited in the Protein Data Bank (Berman et al 2000) and used as template for modeling. We used MODELLER to generate, by simulated annealing and distance restraints, two sets of 500 conformations of the native and T45D mutant form of NUDIX5 homodimer. These sets respectively mimicked the homodimer interaction of the phosphorylated and non-phosphorylated forms of NUDIX5.

The comparison of the homodimer interaction, phosphorylated and non-phosphorylated, was performed using the docking score potential of ZRANK (Pierce et al 2007). We calculated the distribution of the scores of docking of both sets.

Chromatin Immunoprecipitation (ChIP) in cultured cells. ChIP assays were performed as described (Vicent et al 2009) using the H2A specific antibody (Cell Signaling Technologies), or the H1 antibody (AE4 abcam). Quantification of chromatin immunoprecipitation was performed by qRT-PCR and the fold enrichment of target sequences in the immunoprecipitated (IP) compared to input (I) fractions were calculated using the comparative Ct method with ($2^{\text{Ct(IP)}-\text{Ct(Ref)}}$). Values were corrected by the human b-globin gene and referred as relative abundance over time zero. Primers sequences are available on request

RNA interference experiments. All siRNAs were transfected into the T47D^M cells using Lipofectamine 2000 (Invitrogen) as described (Vicent et al 2009). siRNA are sequences available on request.

RNA extraction and RT-PCR. Total RNA was prepared and cDNA generated as previously described (Wright et al. 2012). Quantification of gene products was performed by qRT-PCR. Each value calculated using the standard curve method was corrected by the human GAPDH and expressed as relative RNA abundance over time zero. Primer sequences are available on request.

Protein Extract Preparation, western blotting/Co-immunoprecipitation assay. Cells were prepared as previously described (Wright et al 2012), briefly cells were lysed (1% NP40, 150mM NaCl, 50mM Tris-HCl) and following total protein quantification, 2mg of cell extracts were incubated with protein G/A agarose beads previously coupled with 5µg of the corresponding antibodies or an unspecific control antibody as described (Vicent et al. 2009). Inputs and immunoprecipitated material was analyzed by western blot using; PARP1 (Cell Signalling technologies), PARG (Abcam ab169639), PAR (trevigen) and NUDIX5 (abcam) specific antibodies.

Immunofluorescence. T47D^M or MCF7 cells were grown on coverslips treated with hormone for the desired length of time as described in previous sections prior to fixation using 4% paraformaldehyde in PBS for 15 min and permeabilized with PBS

0.2% Triton X-100 at room temperature. Coverslips were blocked with 5% skim-milk for 1 h at room temperature and incubated 2 hours with primary antibodies diluted in PBS 1% skim-milk at 1/500 PAR monoclonal and or polyonal (trevigen), 1/1000 (PARP1 (Cell Signalling technologies), or 1/500 anti-phospho Serine 118 ER, anti-luciferase (Sigma L0159). After washes with PBS Tween 20 0.05%, samples were incubated with secondary antibodies (AlexaFluor 555 anti-rabbit and AlexaFluor 488 anti-mouse, Invitrogen-Molecular Probes) for 1 h at room temperature. After washes with PBS Tween 0.05% and DNA staining with DAPI, samples were mounted with mowiol. Images were acquire with a Leica TCS SP5 CFS confocal microscope.

Microarray Design and Procedure. The levels of NUDIX5 were reduced in T47D^M cells using siRNA as described or the activity of PARP and PARG were inhibited by treating T47D^M cells with either treated with 3AB or TA respectively. As a control, T47D^M cells were treated with solvent (EtOH alone) prior to R5020 induction for 0 or 6 hours as described above. Total RNA was prepared and cDNA generated as described. Independently generated biological replicates hybridised against the human whole genome 44K expression platform (Agilent). Significantly induced, or repressed genes were considered as those with a log₂ fold of ≥ 1.5 and ≤ -1.5 respectively and a q value of ≤ 5.00 .

Site directed mutagenesis and detection of Myc-NUDIX5 phosphomimetic constructs for expression in mammalian cells. Site-directed mutagenesis was carried out on the wild-type human PARP1 fused to Myc (pCMV-Myc NUDT5; genescript) as directed in the Quick Change mutagenesis kit. The mutagenic primers were as follows 5'-3'; T45D Fw; TGTACGTTTCACTGATTCCCAATCTCTAGTTTTACCAGTAGGATCC, T47D Rv; GGATCCTACTGGTAAACTAGAGATTGGGAATCAGTGAAACGTACA. Following the mutagenesis procedure, mutations were confirmed by sequencing. Myc-wtNUDIX5 or Myc-NUDIX5-Thr/Asp mutant plasmids were transfected into T47D^M cells using Lipofectamine 2000 (Invitrogen) as described. 48 hours later, cells were treated with hormone, cell proliferation, and gene or protein expression determined as described above.

Cell proliferation assay

T47D^M / MCF7 cells transfected with control, NUDIX5 siRNAs or treated with the inhibitors 3AB/tannic acid as described above. Cells (1×10^4) were plated in a 96-well plate in the presence or absence of R5020 (T47D^M) or estradiol (MCF7). The cell proliferation ELISA BrdU Colorimetric assay (Roche) was performed according to the manufacturer's instructions. The experiments were performed in triplicate.

Purification of Recombinant NUDT5 in vitro

Recombinant NUDIX5 was produced using 1-step Human high yield in vitro mammalian translation (IVT) system (Thermo Scientific). Briefly, IVT reactions containing (HeLa cell lysate, accessory proteins, reaction mix, 4ug NUDIX5 DNA (pANT7 GST-NUDT5 (DNASU, plasmid depository)) in 100ul was dialysed for 16 hours at 30°C according to manufacturers instructions. Recombinant NUDIX5 was then purified from the total reaction using GST beads (as described Wright et al 2012).

DNA damage; Cell Survival Assay

MCF7 cells were transfected with control, NUDIX5 siRNAs or treated with the inhibitors 3AB/tannic acid as described above. Cells were then plated in a 100mm plates at varying concentrations and subjected to DNA damage (H₂O₂) at varying concentrations (0.1, 0.2, 0.5mM). The medium was replaced every 3 days and the resultant surviving colonies stained using crystal violet solution (0.5% crystal violet, 10% methanol). Data is represented as a percentage surviving fraction compared to control (undamaged).

PAR Mass Spec Peptide Enrichment analysis

T47D cells were treated with hormone or ethanol for 30 minutes and the resultant lysates were immunoprecipitated using anti-PAR antibody. Immunoprecipitated peptides were digested with trypsin and 1ug of each sample were analyzed by LCMSMS using a MEDI_CID method in the LTQ Orbitrap XL. To avoid carry over, samples were injected in increasing amount and BSA controls were included both in the digestion

and LCMSMS analysis for quality control. Samples were searched against SwissProt_Human (January 2013) using an internal version of the search algorithm Mascot (<http://www.matrixscience.com/>). Data analysis was performed with Proteome Discoverer v1.3. Peptides have been filtered based on the FDR (False Discovery rate) for peptides with FDR better (lower) than 5%. Protein Discoverer gives an approximate estimation of protein amount with the parameter “Area” which is the average peak area of the 3 top peptides for a given protein. Immunoprecipitation was performed in two independent experiments for both control and hormone treated samples and the relative fold change compared to control was determined using the average area for the two experiments.

Real time ATP visualisation using ATeam probes following hormone

T47D cells were transfected with either Nuclear (Nuc) / Mitochondrial (Mito) or Cytoplasmic (Cyto) targeted A-team constructs in 35mm diameter cell culture plates using lipofectamine 2000 (Roche, following manufacturers instructions). 24 hours prior to hormone treatment cells were serum starved (RPMI 0% FCS, minus phenol red). For each individual experiment, 4 fields of view were selected containing between 2-5 cells/view. R5020 was added directly at the microscope prior to YFP and CFP emission detection at 1 minute intervals for the length of time required at selected FOV. For analysis; multiple regions of interest (ROI) of equal size were selected from each individual cell imaged and the ratio for each region of interest (ROI) was calculated following background subtraction according to protocol detailed in Kardash *et al.*, 2011. Results are represented as the mean +/-SEM of multiple ROIs.

ATP visualisation using Bioluminescence Imaging

T47D or MCF7 cells were seeded in RPMI or DMEM media respectively, as described above in black walled 96 well plates, were transfected using lipofectamine 2000 (Invitrogen, as described above) with the luciferase constructs (Nuc/Cyto/Mito-luciferase) as required, at a concentration of 50ng DNA/well. 24 hours prior to imaging the cells were starved with 0% FCS. R5020 or 17-estradiol were added as

described above for the length of time prior to the addition of 100ul of D-luciferin (1mg/ml, Sigma). The relative amounts of ATP were then visualised and quantitated using bioluminescence imaging IVIS system (Xenogen Corp).

Solexa ChIP-seq analysis

DNA was subjected to deep sequencing using the Solexa genome analyzer (Illumina Hi-Seq 2000). Single-ended sequences were trimmed to 50 bp and mapped to the human genome assembly hg19 using Bowtie (<http://bowtie-bio.sourceforge.net>), an ultrafast short-read mapping program (Langmead et al. 2009), keeping only tags that mapped uniquely and with no more than two mismatches.

Peak detection and annotation analysis

The integrated software Macs (Zhang et al. 2008) was used to detect peaks that were enriched from background reads. The algorithm was applied by using the sliding window method to count the reads using the “nomodel” option, shift size set to 75, tag size set to 50, and a P-value threshold of 1×10^{-3} settings for transcription factors and chromatin remodelers; BPTF, HP1y, PARP1, CDK2, CTCF, PR, and PolIII to identify differential binding between the two conditions by treating the T0 of the samples as the control. In the case of histone modifications, the algorithm was applied using “nomodel,” “nolambda,” and a P-value threshold of 1×10^{-3} . In order to perform the average profiles, we used R programming language for plotting the mapped read signals over the regions of interest. All of the genome-wide annotations and statistics of protein–DNA interaction patterns from ChIP-seq data were performed with the standalone application CEAS (Cis-regulatory Element Annotation System). In the case of the ChIP-seq PR data, the signals of treated and untreated samples were compared using Poisson analysis (P-value < 0.001) (Ballare et al. 2013).

GO Biological Process and Pathway Analysis

GO biological process and pathway analysis was performed using MSigDB Collections database v4 gene set enrichment analysis online tools using a significance cut off value of $p < 0.05$.

Extended References

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Extended Tables

Extended Table 1: Peptide Enrichment Before and after Hormone following ADPR enrichment. Table lists accession number; description, and the peptide enrichment score for 2 independent experiments (A, B; hormone treated T30 and C, D Control T0) as described in methods above), results are represented as a $\log_2(\text{ratio})$ Hormone (T30)/Control (T0).

Extended Table 2: PAR Mass Spec Functional Groups. Table lists accession number; description, and the peptide ratio (hormone/control) for functionally related groups of proteins; histones, kinases, phosphatase and enzymes involved in NAD, ADPR metabolism and ATP synthesis.

Extended Table 3: GO Biological Function Analysis Control (T0) PAR Mass Spec. Significant ($p < 0.05$) GO biological processes enriched using proteins identified in control (T0) PAR mass spec analysis.

Extended Table 4: GO Biological Function Analysis Control (T30) PAR Mass Spec. Significant ($p < 0.05$) GO biological processes enriched using proteins identified in control (T30) PAR mass spec analysis.

Extended Table 5: GO Biological Function Analysis for Genes Dependent on Nudix5. Significant ($p < 0.05$) GO biological processes enriched using genes identified as Nudix5 dependent (Figure 4A).

Extended Table 6: GO Biological Function Analysis for Genes Independent on Nudix5. Significant ($p < 0.05$) GO biological processes enriched using genes identified as Nudix5 independent (Figure 4A).

Extended Table 7: Pathway Analysis (KEGG/REACTOME for Genes Dependent or Independent on Nudix5. Significant ($p < 0.05$) pathways enriched using genes identified as Nudix5 dependent or independent (Figure 4A).

Extended Table 1

Accession	Description	Area				log (area)				Hormone	Control	Hormone/Control
		Hormone_1	Hormone_2	Control 1	Control 2	Hormone_1	Hormone_2	Control 1	Control 2			
		A3: Area	B3: Area	C3: Area	D3: Area	A3: Area	B3: Area	C3: Area	D3: Area			
P5385	ATP synthase subunit e, mitochondrial OS=Homo sapiens GN=ATP5E PE=1 Sv=2 - [ATP5E_HUMAN]	1.9797	2.2697	7.296	7.356	7.326	7.323	7.323	7.323	4	4.326	
C9Y92	Uncharacterized protein OS=Homo sapiens GN=HNRPL PE=4 Sv=1 - [C9Y92_HUMAN]	2.1037	2.1037			7.323	7.094	7.323	7.323	4	4.323	
Q12738	Skeletal alpha-2 casein, desialylated OS=Homo sapiens GN=HDHL PE=1 Sv=2 - [N]	1.6567	1.2417			7.336	7.094	7.336	7.211	4	4.215	
P04792	Heat shock protein beta-1 OS=Homo sapiens GN=HSPB1 PE=1 Sv=2 - [HSPB1_HUMAN]	1.3729	1.1097			7.140	7.140	7.140	7.140	3	4.140	
U01561	Acyl carrier protein, mitochondrial OS=Homo sapiens GN=NDUFA1 PE=1 Sv=3 - [ACPM_HUMAN]	1.2087	1.4127			7.082	7.150	7.082	7.116	3	4.116	
E9FE4	Uncharacterized protein OS=Homo sapiens GN=DLAT PE=3 Sv=1 - [E9FE4_HUMAN]	1.3897	1.0437			7.143	7.018	7.143	7.080	3	4.080	
D6A32	Uncharacterized protein OS=Homo sapiens GN=MAP1B PE=4 Sv=2 - [D6A32_HUMAN]	1.1927	1.1927			7.076	7.076	7.076	7.076	3	4.076	
Q9D9F5	Isomorf 5 of Serine RNA effector nucleoside diphosphate kinase OS=Homo sapiens GN=SRRT_HUMAN	3.5427	5.4305			7.503	7.045	7.503	7.345	3	4.345	
P5CYG9	Uncharacterized protein OS=Homo sapiens GN=AP2B1 PE=4 Sv=1 - [P5CYG9_HUMAN]	1.3077	9.3276			7.116	6.972	7.116	7.044	3	4.044	
Q9UN52	COP3 signalosome complex subunit 3 OS=Homo sapiens GN=COP3 PE=1 Sv=3 - [C3N3_HUMAN]	1.2097	8.4486			7.082	6.927	7.082	7.005	3	4.005	
A3K11	Exosome component 2 (Fragment) OS=Homo sapiens GN=EXOSC2 PE=4 Sv=1 - [A3K11_HUMAN]	9.3186	6.9369			6.969	6.969	6.969	6.969	3	3.969	
E9FK3	Uncharacterized protein OS=Homo sapiens GN=CPNE3 PE=4 Sv=1 - [E9FK3_HUMAN]	1.2367	6.3856			7.090	6.822	7.090	6.956	3	3.956	
E9K28	Protein In-7 homolog C OS=Homo sapiens GN=LIN7C PE=1 Sv=1 - [LIN7C_HUMAN]	1.1017	7.9566			7.001	6.900	7.001	6.945	3	3.945	
Q9NUP9	Palmitoyl transferase 1 OS=Homo sapiens GN=PPT1 PE=1 Sv=1 - [PPT1_HUMAN]	1.1547	6.3336			7.062	6.802	7.062	6.932	3	3.932	
P50897	Uncharacterized protein OS=Homo sapiens GN=C12orf10 PE=4 Sv=1 - [F6VR8_HUMAN]	7.9666	6.901			6.901	6.901	6.901	6.901	3	3.901	
R6A22	Outamer protein complex, subunit beta 2 (beta prime), isoform CRA_D OS=Homo sapiens GN=COPB2 PE=2	1.3227	4.0375			7.121	6.606	7.121	6.864	3	3.864	
Q12554	Proteinase isozyme chaperone OS=Homo sapiens GN=HSPD2 PE=2 Sv=2 - [HSPD2_HUMAN]	1.3037	5.9965			7.087	6.817	7.087	6.819	3	3.819	
Q16851-2	Isomorf 2 of UTP-glucose-1-phosphate uridylyltransferase OS=Homo sapiens GN=UGP2 - [UGPA_HUMAN]	1.2097	3.2826			6.984	6.516	6.984	6.750	3	3.750	
F5H170	Uncharacterized protein OS=Homo sapiens GN=DNAAF4 PE=4 Sv=1 - [F5H170_HUMAN]	5.54556				6.744		6.744	6.744	3	3.744	
Q92799-3	Isomorf 3 of Symplekin OS=Homo sapiens GN=SYMVK - [SYMVK_HUMAN]	5.45556				6.737		6.737	6.737	3	3.737	
O95182	NADH dehydrogenase [ubiquinone] L1 alpha subcomplex subunit 7 OS=Homo sapiens GN=NDUFA7 PE=1 Sv=	7.8465	2.8176			6.895	6.450	6.895	6.672	3	3.672	
Q9D9F5-5	Isomorf 5 of Protein transferase OS=Homo sapiens GN=SEC31A - [SEC31A_HUMAN]	7.5405	1.7096			6.877	6.233	6.877	6.521	3	3.521	
R4GLG2	Uncharacterized protein OS=Homo sapiens GN=ZC3H1A PE=2 Sv=1 - [R4GLG2_HUMAN]	3.31156	5.34165	11.4465	6.521	5.728	5.059	6.521	5.393	1	1.127	
Q31ZD1	Uncharacterized protein OS=Homo sapiens GN=ARPC3 PE=4 Sv=1 - [Q31ZD1_HUMAN]	5.0336				7.700		7.700	7.700	0.998		
Q99497	Protein DJ-1 OS=Homo sapiens GN=PAK7 PE=1 Sv=2 - [PAK7_HUMAN]	5.2398	3.3898	5.50767	6.14987	8.719	8.530	7.741	7.789	8.625	7.765	
Q9NUP9-2	Isomorf 2 of Protein kinase C and cAMP kinase substrate OS=Homo sapiens GN=PKCBL1 - [NM1T1_HUMAN]	1.4682	6.41116	1.41556	7.164	6.807	6.507	7.164	6.985	6.151	6.834	
Q9P10	NADH dehydrogenase [ubiquinone] L1 alpha subcomplex subunit 3 OS=Homo sapiens GN=NDUFA3 PE=1 S	1.3857	1.21527			7.142	7.085	7.142	7.085	6.329	6.249	
Q9C836	Scavenger mRNA-decapping enzyme Dcp5 OS=Homo sapiens GN=DPCS PE=1 Sv=2 - [DPCS_HUMAN]	1.3037	2.4776			7.115	6.394	7.115	6.394	0.721		
Q31B13	Uncharacterized protein OS=Homo sapiens GN=PSPH PE=4 Sv=1 - [Q31B13_HUMAN]	9.83556	6.4035	6.9931	6.943	5.806	6.797	6.993	6.502	6.017	6.056	
Q8WMM7-6	Isomorf 6 of Ataxin-2-like protein OS=Homo sapiens GN=ATXN2 - [ATXN2_HUMAN]	2.79567	7.91226	2.8546	3.7856	7.448	6.898	7.448	6.578	1.772	1.512	
P07355	Isomorf 5 of OS=Homo sapiens GN=ANKK2 PE=1 Sv=1 - [ANKK2_HUMAN]	1.21347	9.73165	4.0255	7.549	7.337	6.898	7.443	6.898	6.791	6.652	
P36871	Phosphoglucomutase-1 OS=Homo sapiens GN=PGM1 PE=1 Sv=3 - [PGM1_HUMAN]	1.8277	4.4256	1.5336	6.3416	7.198	6.974	6.185	6.802	6.086	6.404	
P90V0	Uncharacterized protein OS=Homo sapiens GN=CPTH PE=3 Sv=1 - [E9PDV0_HUMAN]	1.5767	7.5226	3.2205	7.261	6.889	6.508	7.075	6.508	0.567		
F5H8D7	Uncharacterized protein OS=Homo sapiens GN=XRCCL1 PE=4 Sv=1 - [F5H8D7_HUMAN]	5.2446	1.4666			6.720	6.166	6.720	6.166	0.553		
Q8M1F7	Nuclear pore complex protein NuP93 OS=Homo sapiens GN=NUP93 PE=1 Sv=2 - [NUP93_HUMAN]	1.9437		3.7626	7.128	7.128	7.710	6.856	6.575	7.128	6.575	
Q31E0	Uncharacterized protein OS=Homo sapiens GN=HNF1A - [Q31E0_HUMAN]	1.6988	7.1276			7.028	6.710	7.028	7.369	6.823	6.546	
F5H3H2	Uncharacterized protein OS=Homo sapiens GN=PKL PE=4 Sv=1 - [F5H3H2_HUMAN]	2.0077		5.7326	7.303	7.303	7.140	6.856	6.788	6.788	6.544	
Q92922	SWI/SNF complex subunit SMARCC1 OS=Homo sapiens GN=SMARCC1 PE=1 Sv=3 - [SMRCC1_HUMAN]	2.6967	7.9605	6.3576	7.431	6.901	6.527	7.431	6.930	7.166	6.639	
Q6K537	4.1G isoform OS=Homo sapiens GN=EPH4L1 PE=2 Sv=1 - [Q6K537_HUMAN]	1.8617	8.7186	3.9836	3.6976	6.940	6.600	6.940	6.584	7.105	6.584	
Q8R8W7-2	Isomorf 2 of Cdk5 cyclin dependent kinase 2 OS=Homo sapiens GN=CDK5 - [CDK5_HUMAN]	1.3397	9.2706	3.3566	7.127	6.967	6.526	6.789	7.047	6.526	6.521	
P20492	Isomorf 2 of salivary T alpha-untilated sequence 1 OS=Homo sapiens GN=STAF1 PE=1 Sv=2 - [STAF1_HUMAN]	1.7526	1.8937	1.73465	6.761	6.748	6.239	6.748	6.239	6.629	6.372	
Q9Y650	Cytoskeletal dynein 1 light intermediate chain 1 OS=Homo sapiens GN=DNVLC1L1 PE=1 Sv=3 - [DC11L1_HUMAN]	1.2827	7.3756	1.4576	3.7076	6.868	6.163	6.868	6.868	6.386	6.502	
Q9YK70	Protein CDV3 homolog OS=Homo sapiens GN=CDV3 PE=1 Sv=1 - [CDV3_HUMAN]	6.6567	2.2917	6.6886	1.9707	7.823	7.360	6.886	6.795	5.920	5.801	
Q9C677	Coiled-coil domain-containing protein 12A OS=Homo sapiens GN=CCDC124 PE=1 Sv=1 - [CC124_HUMAN]	1.9077	3.3246	1.1247	6.126	7.280	6.522	7.051	7.280	6.786	6.494	
P30419-2	Isomorf 2 of Glyoxalase II N-tetradecanoyltransferase 1 OS=Homo sapiens GN=NMT1 - [NMT1_HUMAN]	1.45457	1.6087	2.62126	1.91067	7.162	7.206	6.418	6.963	7.184	6.691	
A6M8N	Adrenomedullin OS=Homo sapiens GN=ADM - [ADM_HUMAN]	3.1867	1.4383	1.9246	7.244	7.244	7.244	7.244	7.244	6.716	6.662	
R4D31	Uncharacterized protein OS=Homo sapiens GN=NDP51 PE=2 Sv=1 - [R4D31_HUMAN]	1.7367	7.3476	4.2866	3.2746	7.240	6.865	6.632	6.515	7.053	6.574	
AM8UN4	Uncharacterized protein OS=Homo sapiens GN=ATP6V1 PE=2 Sv=1 - [AM8UN4_HUMAN]	7.5445	5.0765	2.1986	6.884	6.741	6.342	6.812	6.342	0.470		
AM6M8	ARD1 homolog A, N-acetyltransferase (S. cerevisiae), isoform CRA_D OS=Homo sapiens GN=NAO1 PE=4 Sv	2.8077	6.9636	4.1836	5.51226	7.458	6.843	6.621	6.741	7.150	6.681	
B1A49	Tubulin tyrosine ligase-like family, member 12 OS=Homo sapiens GN=TLTL2 PE=1 Sv=1 - [B1A49_HUMAN]	1.3297	4.1356			7.123	6.655	7.123	6.655	0.469		
Q9LCA2	Uncharacterized protein OS=Homo sapiens GN=GNAN3 - [Q9LCA2_HUMAN]	2.3557	2.5257	2.1947	7.402	7.402	7.341	7.371	7.371	6.224	6.224	
P35659	Protein DEK OS=Homo sapiens GN=DEK PE=1 Sv=1 - [DEK_HUMAN]	2.2867	1.5017	4.8965	6.2765	7.359	7.176	6.690	6.942	2.668	2.668	
Q9YK8	28S ribosomal protein S26, mitochondrial OS=Homo sapiens GN=MRPS26 PE=1 Sv=1 - [MRPS26_HUMAN]	7.2426	2.0866	6.860	6.860	6.319	6.517	6.860	6.418	4.452	4.452	
Q41396	Thioredoxin-like protein 1 OS=Homo sapiens GN=TXNL1 PE=1 Sv=3 - [TXNL1_HUMAN]	1.8137	6.8006	5.37116	7.258	6.928	6.730	7.258	6.817	6.441	6.441	
Q12347-3	Isomorf 3 of Serine/arginine-rich splicing factor 6 OS=Homo sapiens GN=SRSF6 - [SRSF6_HUMAN]	5.6317	1.9007	1.8326	8.4496	7.751	7.279	7.205	6.927	7.515	7.077	
P11413	Glucocorticoid-inducible protein 1 OS=Homo sapiens GN=IGFBP1 PE=1 Sv=1 - [IGFBP1_HUMAN]	1.8927	6.6565	1.73465	7.277	7.277	7.091	7.277	7.091	6.844	6.844	
AMZ71	Uncharacterized protein OS=Homo sapiens GN=COX7A2 PE=4 Sv=1 - [AMZ71_HUMAN]	3.9567	2.9517	9.6326	1.5777	7.556	7.470	6.984	7.198	7.513	7.091	
Q9N06	Uncharacterized protein OS=Homo sapiens GN=BZWI PE=4 Sv=1 - [Q9N06_HUMAN]	6.0906	6.0795	2.0446	6.959	6.959	6.784	6.310	6.959	6.422	6.422	
P86821-2	Isomorf 2 of U1 small nuclear ribonucleoprotein 70 kDa OS=Homo sapiens GN=SNRP70 - [RU17_HUMAN]	2.6217		1.0467	8.7295	6.339	6.077	7.607	7.019	7.419	7.019	
E9P54	Uncharacterized protein OS=Homo sapiens GN=SRP8 PE=4 Sv=1 - [E9P54_HUMAN]	1.18356		8.7295	6.339	6.339	6.949	6.339	5.941	6.339	5.941	
P5580-2	Isomorf 2 of protein domain superfamily 1 OS=Homo sapiens GN=VDAC2 - [VDAC2_HUMAN]	8.45567	4.01667			7.927	7.804	7.927	7.804	6.902	6.902	
P12181	V-type proton ATPase subunit B, brain isoform OS=Homo sapiens GN=ATP9B1 PE=1 Sv=3 - [VAT9B_HUM]	1.9297	9.3285	5.9136	3.9256	7.111	6.970	7.111	6.954	7.041	6.655	
Q43488	Atlatrin B1 aldehyde reductase member 2 OS=Homo sapiens GN=ARKR2 PE=1 Sv=3 - [ARKR2_HUMAN]	7.9427	7.7356	3.2336	7.9556	7.888	6.889	6.510	6.903	7.088	6.888	
P19523	Spermidine synthase OS=Homo sapiens GN=SRM PE=1 Sv=1 - [SPEM_HUMAN]	1.9357	1.2077	5.3585	6.167	7.082	6.729	7.082	6.905	0.381		
Q11428	Splicing factor 3A subunit 2 OS=Homo sapiens GN=SF3A2 PE=1 Sv=2 - [SF3A2_HUMAN]	3.3267	1.5217	9.1216	6.9916	7.522	7.182	6.960	6.966	7.352	6.973	
P5128	TROV2 protein, member 1 OS=Homo sapiens GN=TROV2 PE=1 Sv=1 - [TROV2_HUMAN]	1.7767	1.2307	6.9095	6.749	7.249	7.091	7.249	7.171	7.171	6.968	
Q9Y558	Translin-associated protein 1 OS=Homo sapiens GN=TSNAX PE=1 Sv=1 - [TSNAX_HUMAN]	1.8947	4.5195	1.4347	7.277	7.277	6.655	7.156	7.277	6.906	6.372	
Q15056-2	Isomorf 2 of Eukaryotic translation initiation factor 4H OS=Homo sapiens GN=EIF4H - [IF4H_HUMAN]	6.7147	7.1887	3.1977	2.7357	7.827	7.505	7.437	7.842	7.471	7.371	
P61405	Histone H4 OS=Homo sapiens GN=HIST1H4 PE=1 Sv=2 - [H4_HUMAN]	3.8107	2.6047	1.3657	1.3227	7.581	7.416	7.135	7.121	7.498	7.128	
BM1453	Transcriptional coactivator CoA2 OS=Homo sapiens GN=RBM14RBM1 fusion PE=2 Sv=1 - [BM1453_HUMAN]	1.4447	5.0286	4.9806	2.7306	7.159	6.701	6.697	6.436	6.930	6.527	
Q01721	Uncharacterized protein OS=Homo sapiens GN=CCND1 PE=1 Sv=1 - [CCND1_HUMAN]	1.2528	1.1945	1.3228	8.416	8.416	8.416	8.416	8.416	8.416	8.416	
F8W25	Uncharacterized protein OS=Homo sapiens GN=DNM1L PE=3 Sv=1 - [F8W25_HUMAN]	1.1837	1.6407	8.1346	6.8705	7.339	7.215	6.910	6.938	7.277	6.924	
Q01081	Splicing factor U2AF 35 kDa subunit OS=Homo sapiens GN=U2AF1 PE=1 Sv=3 - [U2AF1_HUMAN]	2.5007	1.6057	4.4836	6.9626	7.182	7.017	6.652	6.844	7.099	6.748	
E9PC19	Uncharacterized protein OS=Homo sapiens GN=PDPS PE=3 Sv=1 - [E9PC19_HUMAN]	4.7517	4.5407	2.0277	7.687	7.687	7.316	6.767	7.316	6.351	6.351	
Q9N4R5	Sialic acid synthase											

P00588	Phosphoglycerate kinase 1 OS=Homo sapiens GN=PGK1 PE=1 SV=3 - [PGK1_HUMAN]	3.13388	2.32778	1.75388	8.496	8.367	8.244	8.095	8.431	8.169	0.262
C93850	Ribosomal protein L28, isoform CRA_c OS=Homo sapiens GN=RL28 PE=4 SV=1 - [C93850_HUMAN]	7.76227	8.86667	3.41117	3.99227	7.890	7.768	7.533	7.601	7.829	0.262
Q9Y3C5	Peptidyl-cis-trans isomerase Ia OS=Homo sapiens GN=PRPL1 PE=1 SV=1 - [PRPL1_HUMAN]	3.08887	6.81366	8.50766	7.08887	7.400	6.534	6.930	6.871	7.165	0.261
E7B9A1	Uncharacterized protein OS=Homo sapiens GN=PPRSP2 PE=4 SV=1 - [E7B9A1_HUMAN]	1.67687	6.80966	6.58166	7.224	6.935	6.818	6.700	6.818	6.818	0.261
P62851	40S ribosomal protein S25 OS=Homo sapiens GN=RS25 PE=1 SV=1 - [RS25_HUMAN]	7.65887	3.54477	2.77677	2.94177	7.884	7.550	7.468	7.469	7.717	0.261
P00403	Cytochrome c oxidase subunit 2 OS=Homo sapiens GN=MT-CO2 PE=1 SV=1 - [COX2_HUMAN]	4.69687	3.65077	2.31177	2.23877	6.732	7.562	7.364	7.350	7.617	0.260
FW9759	Uncharacterized protein OS=Homo sapiens GN=HANGAP1 PE=4 SV=1 - [FW9759_HUMAN]	2.11727	2.54957	7.80466	1.29977	7.677	7.189	6.892	7.114	7.263	0.260
E7CWF1	Uncharacterized protein OS=Homo sapiens GN=H1387 PE=4 SV=1 - [E7CWF1_HUMAN]	3.16687	3.16687	7.05877	3.16687	7.05877	7.05877	7.05877	7.174	8.037	0.260
E75S08	Uncharacterized protein OS=Homo sapiens GN=HM33 PE=4 SV=1 - [E75S08_HUMAN]	4.88387	2.92577	2.04877	1.90677	7.642	7.466	7.311	7.280	7.554	0.258
P52758	Ribonuclease UK114 OS=Homo sapiens GN=HRSP12 PE=1 SV=1 - [UK114_HUMAN]	1.86977	1.07377	6.23366	9.81766	7.272	7.031	6.195	6.992	7.151	0.258
P13584	General transcription factor IIIF subunit 2 OS=Homo sapiens GN=GTTF2F2 PE=1 SV=2 - [TF2F_HUMAN]	6.10226	1.01336	1.46236	1.29136	6.185	6.006	6.165	6.111	6.396	0.258
P04908	Histone H2A type 1-B/E OS=Homo sapiens GN=H2AHAB PE=1 SV=2 - [H2AHB_HUMAN]	1.07088	2.92887	5.09977	5.91077	8.030	7.964	7.707	7.772	7.997	0.257
P402W1	Uncharacterized protein OS=Homo sapiens GN=C21-1 PE=1 SV=1 - [C21-1_HUMAN]	1.57877	2.57877	4.93687	3.83887	6.596	6.596	6.596	6.596	6.596	0.257
Q07055	Cytoskeleton-associated protein 4 OS=Homo sapiens GN=CAP4 PE=1 SV=2 - [CAP4_HUMAN]	2.04587	1.27887	8.95866	8.97566	7.311	7.107	6.952	6.953	7.209	0.256
BR2277	Uncharacterized protein OS=Homo sapiens GN=HNI PE=4 SV=1 - [BR2277_HUMAN]	3.75177	2.92077	1.92577	1.75077	7.574	7.465	7.285	7.243	7.520	0.256
Q9Y262	Eukaryotic translation initiation factor 3 subunit L OS=Homo sapiens GN=EIF3L PE=1 SV=1 - [EIF3L_HUMAN]	1.56777	1.09577	5.11336	1.04077	7.195	7.039	6.709	7.017	7.117	0.254
P56537	Eukaryotic translation initiation factor 6 OS=Homo sapiens GN=EIF6 PE=1 SV=1 - [EIF6_HUMAN]	3.12127	1.66687	1.73577	1.74667	7.494	7.279	7.242	7.494	7.241	0.254
E7C8B9	Uncharacterized protein OS=Homo sapiens GN=H1387 PE=4 SV=1 - [E7C8B9_HUMAN]	7.88287	2.92577	2.04877	1.90677	7.642	7.466	7.311	7.280	7.554	0.254
B72608	Uncharacterized protein OS=Homo sapiens GN=FHL1 PE=2 SV=1 - [B72608_HUMAN]	3.22687	1.63977	1.24777	1.34777	7.509	7.215	7.096	7.129	7.362	0.249
P49736	DNA replication licensing factor MCM2 OS=Homo sapiens GN=MCM2 PE=1 SV=4 - [MCM2_HUMAN]	1.87177	1.84887	6.96466	1.57977	7.272	7.267	6.843	7.198	7.269	0.249
Q9Y220-2	Isom 2 of Suppressor of G2 allele of SKP1 homolog OS=Homo sapiens GN=SUGT1 - [SUGT1_HUMAN]	2.77887	1.36987	5.99366	1.27177	7.444	7.136	6.982	7.104	7.290	0.247
E7F948	Uncharacterized protein OS=Homo sapiens GN=HMC4 PE=3 SV=1 - [E7F948_HUMAN]	3.18177	2.80977	1.42277	2.01577	7.503	7.439	7.153	7.304	7.476	0.247
P62140	Serine/threonine-protein phosphatase P1 OS=Homo sapiens GN=PPP1CB PE=1 SV=3 - [PPP1CB_HUMAN]	1.57877	2.92887	5.09977	5.91077	8.030	7.964	7.707	7.772	7.997	0.247
E9PAQ6	Uncharacterized protein OS=Homo sapiens GN=CCT3 PE=3 SV=1 - [E9PAQ6_HUMAN]	1.30488	1.10088	5.18387	8.98687	8.115	8.041	7.715	7.954	8.078	0.244
Q9YHV9	Prefoldin subunit 2 OS=Homo sapiens GN=PF2D2 PE=1 SV=1 - [PF2D2_HUMAN]	3.07177	2.39277	2.92177	2.91177	7.844	7.487	7.379	7.464	7.665	0.244
Q81B3-2	Isom 2 of Serine/arginine methyltransferase protein 1 OS=Homo sapiens GN=SRRM1 - [SRRM1_HUMAN]	3.10387	1.27177	1.95466	1.30377	7.492	7.104	6.994	7.115	7.298	0.244
P68402	Platelet-activating factor acetylhydrolase IB subunit beta OS=Homo sapiens GN=PAFAH1B2 PE=1 SV=1 - [PAFAH1B2_HUMAN]	2.36127	2.30177	1.24867	1.43477	7.373	7.362	7.096	7.156	7.368	0.241
Q9Y2C3	Uncharacterized protein OS=Homo sapiens GN=H1387 PE=4 SV=1 - [Q9Y2C3_HUMAN]	7.88287	2.92577	2.04877	1.90677	7.642	7.466	7.311	7.280	7.554	0.241
P5974-2	Uncharacterized protein OS=Homo sapiens GN=H1387 PE=4 SV=1 - [P5974-2_HUMAN]	2.68977	2.35677	1.48777	1.40777	7.430	7.372	7.172	7.148	7.401	0.240
P61204	Cyclin-dependent kinase regulatory subunit 1 OS=Homo sapiens GN=CKS1B PE=1 SV=1 - [CKS1B_HUMAN]	1.13587	6.98566	6.98566	7.055	6.748	6.789	6.585	6.817	7.055	0.238
Q9Y6A4	Leucine-rich repeat-containing protein 59 OS=Homo sapiens GN=LRRCS9 PE=1 SV=1 - [LRRCS9_HUMAN]	3.58087	2.75387	1.82977	1.80177	7.514	7.440	7.262	7.255	7.497	0.238
P04941	Superoxide dismutase (Cu,Zn) OS=Homo sapiens GN=SOD1 PE=1 SV=2 - [SODC_HUMAN]	4.14687	2.97277	2.01177	2.04977	7.758	7.473	7.303	7.311	7.545	0.238
Q13438	Splectin-like protein 2 OS=Homo sapiens GN=SLPL2 PE=1 SV=1 - [SLPL2_HUMAN]	6.40877	2.92887	5.09977	5.91077	8.030	7.964	7.707	7.772	7.997	0.238
Q9Y348	Flap endonuclease 1 OS=Homo sapiens GN=FEN1 PE=1 SV=1 - [FEN1_HUMAN]	2.32987	1.56887	1.08477	1.13767	7.367	7.195	7.035	7.056	7.281	0.236
E9PL16	Uncharacterized protein OS=Homo sapiens GN=RL27A PE=3 SV=1 - [E9PL16_HUMAN]	1.94887	3.75177	3.40177	5.23477	7.961	7.758	7.522	7.719	7.860	0.236
Q9UNZ6-4	Isom 4 of NSF1-like cofactor p47 OS=Homo sapiens GN=NSF1LC - [NSF1LC_HUMAN]	1.85587	1.65587	1.10767	9.41566	7.288	7.219	7.044	6.974	7.244	0.235
Q9Y295	Developmentally-regulated GTP-binding protein 1 OS=Homo sapiens GN=DRG1 PE=1 SV=1 - [DRG1_HUMAN]	1.06477	6.98986	3.90866	9.03966	7.027	6.987	6.592	6.966	7.007	0.233
P02610	Protein SCG1 homolog, mitochondrial OS=Homo sapiens GN=SCG1 PE=1 SV=1 - [SCG1_HUMAN]	1.57877	1.00587	7.59666	6.93886	7.157	7.002	6.880	6.834	7.101	0.233
FH1E11	Uncharacterized protein OS=Homo sapiens GN=COPE PE=4 SV=1 - [FH1E11_HUMAN]	2.32127	2.02477	1.44067	1.11267	7.366	7.306	7.158	7.050	7.336	0.232
P13190	Cytochrome b-c1 complex subunit 1, mitochondrial OS=Homo sapiens GN=UQCRC1 PE=1 SV=3 - [UQCRC1_HUMAN]	3.12427	2.92377	1.96177	7.495	7.466	7.205	7.293	7.480	7.104	0.232
P48444	Cofactor subunit delta OS=Homo sapiens GN=ARCN1 PE=1 SV=1 - [COFD_HUMAN]	1.48687	6.49366	1.18227	6.477	7.172	6.808	7.073	7.172	6.941	0.231
Q9Y490	Talin-1 OS=Homo sapiens GN=TLN1 PE=1 SV=2 - [TLN1_HUMAN]	4.29277	3.46887	2.89887	1.78377	7.633	7.540	7.461	7.251	7.586	0.230
Q12323-2	Isom 2 of Gamma-glutamylcysteine synthetase OS=Homo sapiens GN=GGCT - [GGCT_HUMAN]	1.12987	5.97266	4.94666	5.97266	7.157	6.765	6.858	6.878	7.053	0.230
P36511	Coproporphyrinogen-III oxidase, mitochondrial OS=Homo sapiens GN=CPOX PE=1 SV=3 - [HEM6_HUMAN]	1.20447	1.40177	1.01887	1.06767	7.347	7.146	6.808	6.894	7.081	0.229
Q9YU35	Serine/arginine methyltransferase protein 2 OS=Homo sapiens GN=SRRM2 PE=1 SV=2 - [SRRM2_HUMAN]	2.22487	1.40177	1.01887	1.06767	7.347	7.146	6.808	6.894	7.081	0.229
P30050	60S ribosomal protein L12 OS=Homo sapiens GN=RL12 PE=1 SV=1 - [RL12_HUMAN]	1.26118	8.48387	5.02677	7.43977	8.101	7.929	7.701	7.871	8.015	0.228
FH5L24	Uncharacterized protein OS=Homo sapiens GN=HCT13 PE=5 SV=1 - [FH5L24_HUMAN]	2.16117	1.50887	1.06767	1.06767	7.336	7.178	7.028	7.256	7.708	0.228
P15105	Myosin Vb right chain 12A OS=Homo sapiens GN=MYL12A PE=1 SV=1 - [MYL12A_HUMAN]	6.40877	2.92887	5.09977	5.91077	8.030	7.964	7.707	7.772	7.997	0.228
P12956	X-ray repair cross-complementing protein 6 OS=Homo sapiens GN=XRCC6 PE=1 SV=2 - [XRCC6_HUMAN]	1.29688	6.73887	5.04177	5.67887	8.112	8.029	7.733	7.754	7.970	0.227
Q9M529	Phenylalanyl-tRNA synthetase beta chain OS=Homo sapiens GN=FA8B PE=1 SV=3 - [SYFB_HUMAN]	1.08727	3.31566	3.62266	7.036	6.533	6.533	6.533	6.533	6.533	0.226
C93853	Uncharacterized protein OS=Homo sapiens GN=RB7A PE=3 SV=1 - [C93853_HUMAN]	2.49587	2.00777	1.02167	1.76677	7.397	7.303	7.009	7.247	7.350	0.226
P33993	DNA replication licensing factor MCV7 OS=Homo sapiens GN=MCM7 PE=1 SV=4 - [MCM7_HUMAN]	2.00977	1.85767	9.24866	1.45377	7.303	7.269	6.966	7.162	7.286	0.226
Q9YU10-2	Isom 2 of Calcium gluconate-dependent protein kinase OS=Homo sapiens GN=CKII - [CKII_HUMAN]	1.97887	1.18888	6.28887	9.87887	7.858	7.858	7.858	7.858	7.858	0.226
P27816-6	Isom 6 of Microtubule-associated protein 4 OS=Homo sapiens GN=MAP4 - [MAP4_HUMAN]	3.97887	3.70677	2.33577	2.28367	7.600	7.569	7.368	7.359	7.584	0.226
014828-2	Isom 2 of Secretary carrier-associated membrane protein 3 OS=Homo sapiens GN=SCAMP3 - [SCAMP3_HUMAN]	1.02488	6.52666	7.02677	7.02677	8.246	6.931	6.687	6.847	6.847	0.221
P61163	Alpha-centractin OS=Homo sapiens GN=ACTR1A PE=1 SV=1 - [ACT1_HUMAN]	3.08987	2.15087	1.50667	1.59687	7.490	7.378	7.178	7.203	7.411	0.221
Q9Y531	Barrier-to-autointegration factor 3 OS=Homo sapiens GN=BAI3 PE=1 SV=1 - [BAI3_HUMAN]	1.24588	6.20587	6.43666	9.80587	8.095	7.852	7.807	7.704	7.976	0.221
FW9735	Uncharacterized protein OS=Homo sapiens GN=HAP11 PE=3 SV=1 - [HAP11_HUMAN]	1.57877	1.57877	9.82177	6.42666	7.828	7.828	7.828	7.828	7.828	0.221
P61204	ADP-ribosylation factor 3 OS=Homo sapiens GN=ARF3 PE=1 SV=2 - [ARF3_HUMAN]	4.90787	5.59477	2.23577	4.45767	7.691	7.478	7.349	7.649	7.719	0.220
P61203	60S ribosomal protein L38 OS=Homo sapiens GN=RL38 PE=1 SV=2 - [RL38_HUMAN]	1.36788	7.43587	5.80987	6.35387	8.136	8.081	7.764	8.004	7.804	0.220
Q9B8C2	Uridine-cytidine kinase 2 OS=Homo sapiens GN=UCK2 PE=1 SV=1 - [UCK2_HUMAN]	5.36066	3.23166	6.729	6.729	6.729	6.509	6.509	6.509	6.509	0.220
P12004	Proteasome activator complex subunit 1 OS=Homo sapiens GN=PA28C PE=1 SV=1 - [PACA_HUMAN]	1.50088	1.24388	7.72787	8.75887	8.178	8.095	7.848	7.943	7.915	0.220
Q9Y2E4	Soybean protein S (Fragment) OS=Homo sapiens GN=SN3S PE=2 SV=1 - [Q9Y2E4_HUMAN]	1.61277	1.11277	1.19577	5.64866	7.207	7.046	6.862	6.752	7.046	0.220
B4DD02	Uncharacterized protein OS=Homo sapiens GN=DHRF PE=2 SV=1 - [B4DD02_HUMAN]	3.83787	1.36787	1.37887	1.38587	7.584	7.136	7.139	7.142	7.360	0.219
P55072	Transitional endoplasmic reticulum ATPase OS=Homo sapiens GN=VCP PE=1 SV=4 - [TERA_HUMAN]	1.24788	6.56887	5.18887	5.79077	8.096	7.817	7.715	7.763	7.957	0.219
Q9B8D7	Carboxy-terminal nucleic acid-phosphatase OS=Homo sapiens GN=NTPCR PE=1 SV=1 - [NTPCR_HUMAN]	2.17987	1.57887	1.19787	1.05477	7.338	7.198	7.078	7.023	7.268	0.219
Q11105	Burkitt's lymphoma cell line OS=Homo sapiens GN=BM1 PE=1 SV=1 - [SET_HUMAN]	1.35488	3.65888	1.94688	1.65888	8.426	8.226	8.079	8.226	8.079	0.218
P13693	Transcriptionally-controlled tumor protein OS=Homo sapiens GN=TP73 PE=1 SV=1 - [TP73_HUMAN]	9.50487	4.73387	4.00387	4.63887	8.524	8.226	8.226	8.226	8.226	0.217
Q81U44	Leucine-rich repeat-containing protein 47 OS=Homo sapiens GN=LRRCA7 PE=1 SV=1 - [LRRCA7_HUMAN]	1.45987	1.91766	6.00066	8.23666	7.164	6.963	6.778	6.916	7.064	0.217
E7E7K1	Uncharacterized protein OS=Homo sapiens GN=SEPT7 PE=3 SV=1 - [E7E7K1_HUMAN]	3.27687	2.25477	1.75787	1.55387	7.515	7.353	7.245	7.191	7.434	0.217
P08579	U2 small nuclear ribonucleoprotein B OS=Homo sapiens GN=SNRBP2 PE=1 SV=1 - [RUB2_HUMAN]	1.77387	1.24587	7.50666	1.08887	7.249	7.095	6.927	7.172	6.956	0.216
Q33A25	RNA-binding protein 1 OS=Homo sapiens GN=RNBP1 PE=4 SV=1 - [RNBP1_HUMAN]	1.77387	1.24587	7.50666	1.08887	7.249	7.095	6.927	7.172	6.956	0.216
F5YQ02	Uncharacterized protein OS=Homo sapiens GN=TRM112 PE=4 SV=1 - [F5YQ02_HUMAN]	2.48287	2.29887	9.86566	1.21477	7.395	7.114	7.094	7.084	7.254	0.216
P55036	26S proteasome non-ATPase regulatory subunit 4 OS=Homo sapiens GN=PSMD4 PE=1 SV=1 - [PSMD4_HUMAN]	4.00117	1.20887	1.19387	1.51087	7.602	7.082	7.077	7.179	7.342	0.216
P61214	Small nuclear ribonucleoprotein Sm D1 OS=Homo sapiens GN=SNRPD1 PE=1 SV=1 - [SMDD1_HUMAN]	9.24187	1.07687	6.62787	3.73287	7.966	7.856	7.821	7.572	7.911	0.214
Q14240	Eukaryotic initiation factor 4A OS=Homo sapiens GN=EIF4A2 PE=1 SV=2 - [IF4A2_HUMAN]	2.42888	1.05988	9.86567	9.72687	8.385	8.025	7.994	7.988	8.205	0.214
Q33A07	Uncharacterized protein OS=Homo sapiens GN=H1387 PE=4 SV=1 - [Q33A07_HUMAN]	7.88288	2.92578	2.04878	1.90678	7.642	7.466	7.311	7.280	7.554	0.214
Q14157-4	Isom 4 of Ubiquitin-associated protein 2-like OS=H										

Q9Y371	Endophilin-B1 OS=Homo sapiens GN=SH3GLB1 PE=1 SV=1 - [SH3L1_HUMAN]	1.07027			6.95065	7.029	6.842	7.029	6.842	0.187
Q00425	Insulin-like growth factor 2 mRNA-binding protein 3 OS=Homo sapiens GN=IGFBP3 PE=2 SV=2 - [IF2B3_HUMAN]	5.94367	3.97567	3.23887	3.01067	7.767	7.599	7.513	7.479	0.187
EP92K4	Insulin-like growth factor 2 mRNA-binding protein 3 OS=Homo sapiens GN=IGFBP3 PE=2 SV=2 - [IF2B3_HUMAN]	5.94367	3.97567	3.23887	3.01067	7.767	7.599	7.513	7.479	0.187
B3KPW0	G-rich RNA sequence binding factor 1, isoform CRA_A OS=Homo sapiens GN=GRSF1 PE=2 SV=1 - [B3KPW0_HUMAN]	3.62367	3.19167	2.15567	2.26567	7.559	7.504	7.333	7.355	0.187
P39566	Dolichyl-diphosphoglycerate-3-phosphate glycoyltransferase 48 kDa subunit OS=Homo sapiens GN=DDO51	3.29967	3.60067	2.16867	2.32367	7.518	7.556	7.366	7.377	0.187
O95373	Importin-7 OS=Homo sapiens GN=IPOT7 PE=1 SV=1 - [IPOT_HUMAN]	1.97667	1.43067	1.14367	1.04967	7.296	7.155	7.058	7.021	0.186
959831-3	Isomorphin 3 of Agouti-signaling factor 1, mitochondrial OS=Homo sapiens GN=ADP1A1 - [ADP1A1_HUMAN]	6.67367	5.06767	3.76167	3.81767	7.824	7.705	7.575	7.582	0.186
P28666	Insulin-like growth factor 2 mRNA-binding protein 3 OS=Homo sapiens GN=IGFBP3 PE=2 SV=2 - [IF2B3_HUMAN]	5.94367	3.97567	3.23887	3.01067	7.767	7.599	7.513	7.479	0.186
P14174	Macrophage migration inhibitory factor OS=Homo sapiens GN=MIF PE=1 SV=4 - [MIF_HUMAN]	8.26267	6.28867	4.82367	4.94467	8.917	8.798	8.652	8.694	0.185
F22229	Phosphoglycerate mutase OS=Homo sapiens PE=3 SV=1 - [F2229_HUMAN]	3.31767	1.81467	1.62867	1.57967	8.521	8.259	8.198	8.390	0.185
P35527	Keratin, type 1 cytoskeletal 9 OS=Homo sapiens GN=KRT9 PE=1 SV=3 - [K1C9_HUMAN]	2.70367	2.13367	1.58567	1.59467	8.442	8.329	8.200	8.386	0.184
P08238	Heat shock protein 90 beta OS=Homo sapiens GN=HSP90B1 PE=1 SV=4 - [HSP90B_HUMAN]	7.61167	4.88267	3.87667	4.11367	8.883	8.689	8.588	8.614	0.184
P04264	Keratin, type 1 cytoskeletal 1 OS=Homo sapiens GN=KRT1 PE=1 SV=6 - [K1C1_HUMAN]	7.41967	5.21267	3.79567	4.37667	8.870	8.717	8.579	8.641	0.184
O95YR6	Ribophorin II OS=Homo sapiens GN=SRN2 PE=2 SV=1 - [Q95YR6_HUMAN]	2.95867	2.33367	1.58667	1.86867	7.471	7.368	7.200	7.419	0.184
Q91984	Sideroflexin-1 OS=Homo sapiens GN=SFN1 PE=1 SV=4 - [SFN1_HUMAN]	3.93367	1.68167	1.30267	2.18967	7.595	7.225	7.100	7.271	0.184
B40R31	Uncharacterized protein OS=Homo sapiens GN=DPYSL2 PE=2 SV=1 - [B40R31_HUMAN]	2.01667	1.46867	0.95766	1.33167	7.305	7.167	6.982	7.124	0.183
Q9UMU4	Programmed cell death 6-interacting protein OS=Homo sapiens GN=PCID6IP PE=1 SV=1 - [PC6IP_HUMAN]	2.43267	1.73667	1.34567	1.35167	7.384	7.240	7.129	7.131	0.182
P05623	Inhibitor of caspase OS=Homo sapiens GN=INHCA PE=1 SV=1 - [INHCA_HUMAN]	1.39167	0.92867	0.70367	0.88167	8.143	7.968	7.892	7.856	0.182
Q00041	Vaglin OS=Homo sapiens GN=HDLBP PE=1 SV=2 - [VGLN_HUMAN]	2.20367	1.91667	1.24267	1.49067	7.343	7.281	7.088	7.173	0.182
Q15102	Platelet-activating factor acetylhydrolase IB subunit gamma OS=Homo sapiens GN=PAFAH1B3 PE=1 SV=1 - [EP7EPD_HUMAN]	1.97767	1.27667	1.13167	0.90156	7.296	7.106	7.084	6.955	0.182
EP7EPD	Uncharacterized protein OS=Homo sapiens GN=ACAD9 PE=4 SV=1 - [EP7EPD_HUMAN]	7.45366	3.76156	4.70956	5.07156	6.872	6.867	6.673	6.670	0.181
O95777	N-alpha-acetyltransferase 28, Nac auxiliary subunit OS=Homo sapiens GN=NAASB PE=1 SV=3 - [NAASB_HUMAN]	1.62467	1.44767	1.07367	1.52266	7.211	7.160	7.031	6.979	0.181
Q96424	Protein LVRTC OS=Homo sapiens GN=LVRTC PE=1 SV=2 - [LVRTC_HUMAN]	1.80167	1.09567	0.72956	0.72566	7.040	6.957	7.148	6.967	0.180
P59897	Uncharacterized protein OS=Homo sapiens GN=TRAP1 PE=3 SV=1 - [F59897_HUMAN]	3.51567	2.43767	1.89767	1.97267	8.546	8.387	8.278	8.295	0.180
P38117	Electron transfer flavoprotein subunit beta OS=Homo sapiens GN=ETF3 PE=2 SV=3 - [ETF3_HUMAN]	4.52967	2.99967	2.43367	2.43967	7.656	7.477	7.386	7.567	0.180
B73236	ATPase, Na+/K+ transporting, alpha 1 polypeptide, isoform CRA_A OS=Homo sapiens GN=ATP1A1 PE=2 SV=2	3.90767	2.89067	1.84867	2.63767	7.592	7.455	7.267	7.421	0.179
P51021	Uncharacterized protein OS=Homo sapiens GN=CHP4 PE=4 SV=1 - [F51021_HUMAN]	6.48366	4.90266	3.50626	3.68166	6.812	6.956	6.704	6.642	0.179
P27921	Ribonuclease H1 OS=Homo sapiens GN=RNH1 PE=1 SV=1 - [RNH1_HUMAN]	1.94567	1.59567	1.49567	1.49567	7.982	7.862	7.642	7.642	0.179
Q80811	THO complex subunit 4 OS=Homo sapiens GN=THOC4 PE=1 SV=3 - [THOC4_HUMAN]	8.18467	7.46867	7.89567	7.41267	7.913	7.873	7.895	7.533	0.179
P08195-2	Isomorphin 2 of Agouti-signaling factor heavy chain OS=Homo sapiens GN=SLC3A2 - [AF2_HUMAN]	4.71467	2.76667	2.77067	2.77067	7.673	7.442	7.315	7.442	0.179
B72911	Uncharacterized protein OS=Homo sapiens GN=ACADM PE=2 SV=1 - [B72911_HUMAN]	3.35967	1.83767	1.17167	1.58067	7.526	7.264	7.199	7.395	0.178
P21333-2	Isomorphin 2 of Flavin-A OS=Homo sapiens GN=HNA - [HNA_HUMAN]	3.39367	2.52867	1.81367	2.08067	7.529	7.402	7.258	7.188	0.178
Q14658	Fibrinogen alpha 1 OS=Homo sapiens GN=FIB1A PE=1 SV=3 - [FIB1A_HUMAN]	4.93767	4.78267	3.68167	4.25867	7.926	7.813	7.652	7.518	0.178
P31040	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial OS=Homo sapiens GN=SDHA PE=	4.02967	3.62567	2.98867	2.16467	7.605	7.559	7.475	7.335	0.177
P06753	Isomorphin 2 of Topomoyasin alpha-3 chain OS=Homo sapiens GN=TPM3 - [TPM3_HUMAN]	2.68767	1.97067	1.12667	1.03867	8.429	8.276	8.051	8.203	0.176
Q15836	Vesicle-associated membrane protein 3 OS=Homo sapiens GN=VAMP3 PE=1 SV=3 - [VAMP3_HUMAN]	9.11766	3.70366	3.73366	4.01766	6.960	6.569	6.572	6.604	0.176
FRW40	Uncharacterized protein OS=Homo sapiens GN=ULIH4 PE=1 SV=1 - [FRW40_HUMAN]	3.03867	2.13267	1.56667	1.84067	7.482	7.329	7.195	7.265	0.176
Q31032	Uncharacterized protein OS=Homo sapiens GN=ULIH4 PE=1 SV=1 - [FRW40_HUMAN]	3.03867	2.13267	1.56667	1.84067	7.482	7.329	7.195	7.265	0.176
P14152	Isocoulyl-RNA synthetase, cytoplasmic OS=Homo sapiens GN=IARS PE=1 SV=2 - [SYIC_HUMAN]	6.19867	3.73267	3.29467	3.13767	6.572	6.572	6.572	6.572	0.175
P06493	Cyclin-dependent kinase 1 OS=Homo sapiens GN=CDK1 PE=1 SV=3 - [CDK1_HUMAN]	3.99967	2.72767	2.20167	2.21167	7.602	7.436	7.343	7.345	0.175
P15374	Ubiquitin carboxyl-terminal hydrolase isozyme L3 OS=Homo sapiens GN=UCHL3 PE=1 SV=1 - [UCHL3_HUMAN]	2.08267	1.31267	0.97466	1.27467	7.318	7.118	6.981	7.105	0.174
P25374	Uncharacterized protein OS=Homo sapiens GN=ULH3 PE=1 SV=1 - [UCHL3_HUMAN]	3.66267	2.54767	1.93567	2.15067	7.564	7.406	7.287	7.333	0.174
P24534	Elongation factor 1-beta OS=Homo sapiens GN=EF1B2 PE=1 SV=3 - [EF1B_HUMAN]	0.90867	0.63167	0.48367	0.51567	7.958	7.804	7.687	7.725	0.175
Q60814	Uncharacterized protein OS=Homo sapiens GN=EF1B2 PE=1 SV=3 - [EF1B_HUMAN]	0.90867	0.63167	0.48367	0.51567	7.958	7.804	7.687	7.725	0.175
P62191	26S proteasome regulatory subunit 4 OS=Homo sapiens GN=PSMC1 PE=1 SV=1 - [PR54_HUMAN]	2.79067	2.02367	1.67467	1.56367	7.446	7.321	7.224	7.194	0.174
Q9G273	SRA stem-loop-interacting RNA-binding protein, mitochondrial OS=Homo sapiens GN=SLIRP PE=1 SV=1 - [SI	3.03267	2.69567	1.79367	1.98867	7.481	7.401	7.254	7.383	0.174
P00568	Adenylate kinase isoenzyme 1 OS=Homo sapiens GN=AK1 PE=1 SV=3 - [KAD1_HUMAN]	1.30967	1.20567	0.92866	0.76366	7.117	7.081	6.968	6.883	0.174
Q15417	Calpain-3 OS=Homo sapiens GN=CAPN3 PE=1 SV=1 - [CAPN3_HUMAN]	2.74467	1.03567	0.84066	1.15167	7.438	7.015	6.926	7.180	0.173
P09429	Hsp90 molecular chaperone protein beta OS=Homo sapiens GN=HSP90B1 PE=1 SV=1 - [H90B_HUMAN]	2.80867	2.05367	1.48267	1.53167	8.262	8.138	8.023	8.180	0.173
P13101	X-ray repair cross-complementing protein 5 OS=Homo sapiens GN=XRCC5 PE=1 SV=3 - [XRCC5_HUMAN]	1.09067	0.71267	0.58067	0.60467	8.037	7.853	7.766	7.778	0.173
F5H6N3	Uncharacterized protein OS=Homo sapiens GN=CLTA PE=4 SV=1 - [F5H6N3_HUMAN]	2.87167	2.18367	1.46267	1.74567	7.458	7.339	7.287	7.399	0.172
P23246	Splicing factor, proline- and glutamine-rich OS=Homo sapiens GN=SFQ1 PE=2 SV=2 - [SFQO_HUMAN]	1.66167	1.18167	0.84467	1.00367	8.220	8.072	7.947	8.001	0.172
P05395	Rab GDP dissociation inhibitor beta OS=Homo sapiens GN=GDID PE=1 SV=2 - [GDIB_HUMAN]	5.86967	4.58467	3.39467	3.58567	7.769	7.661	7.554	7.715	0.172
P52442	ATP dependent protein 4A1 OS=Homo sapiens GN=ANP32 PE=1 SV=1 - [ATP4_HUMAN]	1.31867	1.08167	0.78967	0.82967	7.412	7.306	7.189	7.356	0.172
P54727	UV excision repair protein RAD23 homolog B OS=Homo sapiens GN=RAD23B PE=1 SV=1 - [RD23B_HUMAN]	2.61867	1.80867	1.32267	1.62267	7.418	7.257	7.121	7.210	0.172
P06733	Alpha-enolase OS=Homo sapiens GN=ENO1 PE=1 SV=2 - [ENO1_HUMAN]	1.41967	1.05467	0.84667	0.80126	9.152	9.023	8.928	8.904	0.172
F5M721	Uncharacterized protein OS=Homo sapiens GN=WP11 PE=4 SV=1 - [F5M721_HUMAN]	1.90267	1.37267	1.19667	1.62667	6.279	6.137	6.078	6.279	0.172
FRW40A	Ras-related protein Rab-18 OS=Homo sapiens GN=RAB18 PE=1 SV=1 - [RAB18_HUMAN]	3.17467	2.15667	1.72767	1.75367	7.532	7.334	7.248	7.248	0.172
PS0K92	Uncharacterized protein OS=Homo sapiens GN=HSP100 PE=1 SV=1 - [HSP100_HUMAN]	5.74767	4.56467	3.39267	3.53767	8.759	8.37667	8.548	8.705	0.172
Q01082	Spectrin beta chain, brain 1 OS=Homo sapiens GN=SPRTN1 PE=1 SV=2 - [SPTRB_HUMAN]	1.10467	0.66567	0.46766	0.39576	7.043	6.564	6.668	6.597	0.171
P05176	ATP synthase subunit beta, mitochondrial OS=Homo sapiens GN=ATP5B PE=1 SV=3 - [ATP5B_HUMAN]	4.04167	2.92667	2.26267	2.37967	8.606	8.466	8.355	8.366	0.171
B4E241	Splicing factor, arginine/serine-rich 3, isoform CRA_A OS=Homo sapiens GN=SRFS3 PE=2 SV=1 - [B4E241_HUMAN]	9.66067	6.29267	5.13967	5.99767	7.995	7.799	7.841	7.602	0.171
P11142	Heat shock cognate 71 kDa protein OS=Homo sapiens GN=HSPA70 PE=1 SV=1 - [HSPA70_HUMAN]	1.01767	0.92967	0.67067	0.68067	9.007	8.857	8.713	8.811	0.171
EP9495	Uncharacterized protein OS=Homo sapiens GN=ANP22 PE=1 SV=1 - [EP9495_HUMAN]	2.80867	2.05367	1.48267	1.53167	8.262	8.138	8.023	8.180	0.171
EP9C52	Uncharacterized protein OS=Homo sapiens GN=RBPP7 PE=4 SV=1 - [EP9C52_HUMAN]	6.69467	5.50967	4.04767	4.16667	7.826	7.741	7.607	7.619	0.170
P25705	ATP synthase subunit alpha, mitochondrial OS=Homo sapiens GN=ATP5A1 PE=1 SV=1 - [ATP5A_HUMAN]	2.65867	1.42667	1.07867	1.15067	8.425	8.154	8.070	8.289	0.170
B40D06	Uncharacterized protein OS=Homo sapiens GN=OBNI PE=2 SV=1 - [B40D06_HUMAN]	1.88067	1.03267	1.25067	1.25067	7.225	7.014	7.097	7.225	0.170
P15008	26S proteasome non-ATPase regulatory subunit 5 OS=Homo sapiens GN=PSMD5 PE=1 SV=1 - [PSMD5_HUMAN]	1.93367	1.39867	1.12667	1.27567	7.497	7.342	7.200	7.420	0.170
P39019	Eukaryotic initiation factor 4A1 OS=Homo sapiens GN=EIF4A3 PE=1 SV=4 - [IF4A3_HUMAN]	1.93367	1.58867	1.08767	1.63567	8.144	7.880	7.846	8.033	0.170
P50402	Emerin OS=Homo sapiens GN=EMD PE=1 SV=1 - [EMD_HUMAN]	2.10567	2.04967	1.34967	1.43267	7.313	7.312	7.130	7.156	0.169
Q85636	Glutaredoxin-related protein 5, mitochondrial OS=Homo sapiens GN=GLRX5 PE=1 SV=2 - [GLRX5_HUMAN]	1.25767	0.70866	0.60566	0.62856	7.085	6.851	6.928	6.968	0.169
P39019	40S ribosomal protein S19 OS=Homo sapiens GN=RPS19 PE=2 SV=1 - [RPS19_HUMAN]	1.91867	1.14467	0.80967	0.99967	8.283	8.059	8.016	7.987	0.169
Q9Y402	Uncharacterized protein OS=Homo sapiens GN=HSP90B1 PE=1 SV=1 - [H90B_HUMAN]	7.61167	4.88267	3.87667	4.11367	8.883	8.689	8.588	8.614	0.169
O14922-9	Isomorphin 9 of Histone acetyltransferase type 2 catalytic subunit OS=Homo sapiens GN=HAT1 - [HAT1_HUMAN]	2.07867	1.25967	0.94766	1.27267	7.318	7.100	6.967	7.210	0.168
P00491	Purine nucleoside phosphorylase OS=Homo sapiens GN=PNP PE=1 SV=2 - [PNP_HUMAN]	3.25267	1.82567	1.78067	1.53867	7.512	7.261	7.250	7.187	0.168
Q12904	Aminocyclase RNA synthase complex-interacting multifunctional protein 1 OS=Homo sapiens GN=AIMP1 PE=1	1.30967	1.57667	1.74067	1.28667	7.117	7.198	7.070	7.109	0.168
M99193	GMP synthase [glutamine-hydrolyzing] OS=Homo sapiens GN=GMPS PE=1 SV=1 - [GUA_HUMAN]	4.59467	4.20767	2.89567	3.12167	7.662	7.624	7.456	7.494	0.168
EP9235	Importin-7 OS=Homo sapiens GN=IPOT7 PE=1 SV=1 - [IPOT_HUMAN]	1.97667	1.43067	1.14367	1.04967	7.296	7.155	7.058	7.021	0.168
AK8766	Poly(RC) binding protein 2, isoform CRA_B OS=Homo sapiens GN=PCBP2 PE=2 SV=1 - [AK8766_HUMAN]	0.15867	0.66667	0.58667	0.67937	7.982	7.985	7.768	7.843	0.168
Q9Y230	RuvB-like 2 OS=Homo sapiens GN=RUVBL2 PE=1 SV=3 - [RUVBL2_HUMAN]	6.19767	4.38367	3.42667	3.66667	7.792	7.642	7.535	7.564	0.168
Q00299	Chloride intracellular channel protein 1 OS=Homo sapiens GN=CLIC1 PE=1 SV=4 - [CLIC1_HUMAN]	3.64667	5.00067	3.87667	3.82467	7.802	7.702	7.588	7.757	0.168
Q09017	14-3-3 protein eta OS=Homo sapiens GN=YWHAE PE=1 SV=4 - [1433F_HUMAN]	1.64267	1.03867	0.96467	0.84367	8.215	8.015	7.971	7.926	0.167
Q9Y283	Putative nuclear pore protein 2 OS=Homo sapiens GN=NP2 PE=1 SV=2 - [LCT2_HUMAN]	2.32367	1.							

P51610-2	Isoform 2 of Host cell factor 1 OS=Homo sapiens GN=HCF1 (-HCF1_HUMAN)	1.32777	8.54866	7.93566	7.08466	7.123	6.932	6.900	6.850	7.027	6.875	0.152
Q90888	Peptidyl-prolyl cis-trans isomerase FKBP3 OS=Homo sapiens GN=FKBP3 PE=1 SV=1 (-FKBP3_HUMAN)	7.27177	3.38877	3.99877	3.24877	7.862	7.555	7.602	7.510	7.708	7.556	0.152
Q91266	Nuclear ribonucleoproteins A1 OS=Homo sapiens GN=NUC1 PE=1 SV=1 (-NUC1_HUMAN)	6.85387	7.88277	3.53787	3.62387	7.823	7.508	7.537	7.559	7.702	7.555	0.152
P25196	Probable ATP-dependent RNA helicase DDX6 OS=Homo sapiens GN=DDX6 PE=1 SV=2 (-DDX6_HUMAN)	1.21267	1.21267	8.36766	8.71966	7.083	7.083	6.923	6.940	7.083	6.932	0.152
FS0794	Uncharacterized protein OS=Homo sapiens GN=OTUB1 PE=4 SV=1 (-FS0794_HUMAN)	3.58667	2.35477	1.78667	2.34977	7.585	7.372	7.252	7.371	7.463	7.311	0.152
Q9YSL4	Mitochondrial import inner membrane translocase subunit Timl3 OS=Homo sapiens GN=TIMM13L PE=1 SV=1	5.03577	5.09887	3.01277	4.24177	8.208	7.707	8.079	7.627	7.705	7.553	0.152
P27353	40S ribosomal protein S6 OS=Homo sapiens GN=RPS6 PE=1 SV=1 (-RPS6_HUMAN)	1.85858	1.27488	1.05788	1.11588	7.262	7.105	7.424	8.047	8.187	8.036	0.151
P27324	Cytochrome c-haem cytochrome c OS=Homo sapiens GN=CYTH PE=1 SV=1 (-CYTH_HUMAN)	7.08587	7.80887	7.80887	7.80887	7.808	7.808	7.808	7.808	7.808	7.808	0.151
B40X08	Uncharacterized protein OS=Homo sapiens GN=HUBP1 PE=2 SV=1 (-B40X08_HUMAN)	7.46787	5.49677	4.39067	4.66667	7.873	7.740	7.642	7.669	7.807	7.656	0.151
P51148	Ras-related protein Rab-5C OS=Homo sapiens GN=RAB5C PE=1 SV=2 (-RAB5C_HUMAN)	1.43467	1.63067	1.13667	1.02667	7.156	7.212	7.055	7.011	7.184	7.033	0.151
P13639	Elongation factor 2 OS=Homo sapiens GN=EEF2 PE=1 SV=4 (-EEF2_HUMAN)	2.73488	2.40088	1.79288	1.82788	8.437	8.380	8.253	8.262	8.408	8.258	0.151
P11714	Aspartate aminotransferase, cytoplasmic OS=Homo sapiens GN=PF1 PE=1 SV=3 (-PF1_HUMAN)	2.54667	2.00177	1.49277	1.70667	7.406	7.301	7.174	7.232	7.354	7.203	0.150
FS4688	Uncharacterized protein OS=Homo sapiens GN=HSPAL1 PE=1 SV=1 (-FS4688_HUMAN)	7.08887	2.20287	2.02887	2.02887	7.508	7.343	7.318	7.223	7.426	7.293	0.150
FS9408	Uncharacterized protein OS=Homo sapiens GN=SF3A1 PE=4 SV=1 (-FS9408_HUMAN)	1.74787	1.63277	1.15467	1.23767	7.242	7.213	7.062	7.092	7.228	7.077	0.150
Q15019	Septin-2 OS=Homo sapiens GN=SEPT2 PE=1 SV=1 (-SEPT2_HUMAN)	3.99667	2.95667	2.48467	2.38167	7.602	7.471	7.395	7.377	7.536	7.386	0.150
P35998	26S protease regulatory subunit 7 OS=Homo sapiens GN=PSMC2 PE=1 SV=3 (-PSMC2_HUMAN)	2.81267	2.26167	1.99867	1.59467	7.449	7.354	7.301	7.203	7.402	7.252	0.150
P50502	Hc70-interacting protein OS=Homo sapiens GN=HIT31 PE=1 SV=2 (-HIT31_HUMAN)	4.87767	6.10967	5.20867	2.86867	7.688	7.786	7.717	7.458	7.737	7.587	0.150
P60866	40S ribosomal protein S20 OS=Homo sapiens GN=RPS20 PE=1 SV=1 (-RPS20_HUMAN)	1.96867	7.98267	8.14467	8.14467	7.508	7.508	7.508	7.508	7.508	7.508	0.150
P07237	Protein disulfide-isomerase OS=Homo sapiens GN=PIH4 PE=1 SV=3 (-PIH4_HUMAN)	7.46187	3.29167	3.19767	3.87267	7.873	7.517	7.505	7.588	7.695	7.546	0.149
P62937	Peptidyl-prolyl cis-trans isomerase A OS=Homo sapiens GN=PP1A PE=1 SV=2 (-ATF31_HUMAN)	7.17688	6.01688	4.30488	5.05688	8.856	8.779	8.634	8.704	8.818	8.686	0.149
P24539	ATP synthase subunit b, mitochondrial OS=Homo sapiens GN=ATP5F1 PE=1 SV=2 (-ATP5F1_HUMAN)	3.31567	1.73467	1.47867	1.96567	7.521	7.239	7.169	7.293	7.380	7.231	0.149
Q9NR49	Nicotinamide phosphoribosyltransferase OS=Homo sapiens GN=NAAPT PE=1 SV=1 (-NAAPT_HUMAN)	2.59887	1.31887	1.13887	1.52167	7.415	7.120	7.056	7.182	7.267	7.119	0.149
P81017	Heat shock protein 70 OS=Homo sapiens GN=HSPA70 PE=1 SV=1 (-HSP70_HUMAN)	7.08887	2.59287	4.95887	4.95887	7.891	7.722	7.682	7.686	7.807	7.616	0.149
P73840-2	Isoform 2 of Alpha-synuclein OS=Homo sapiens GN=SNCA (-SYUA_HUMAN)	9.20066	5.58866	5.59066	6.35666	6.964	6.745	6.747	6.686	6.854	6.707	0.148
P46781	40S ribosomal protein S9 OS=Homo sapiens GN=RPS9 PE=1 SV=3 (-RPS9_HUMAN)	3.39267	1.87767	1.63067	1.98467	7.530	7.273	7.212	7.298	7.402	7.255	0.148
P43487	Ran-specific GTPase-activating protein OS=Homo sapiens GN=RANBP1 PE=1 SV=1 (-RANG_HUMAN)	1.44488	9.79167	7.96767	9.01767	8.159	8.991	7.901	7.955	8.075	7.928	0.147
Q9NRK4	14 kDa phosphate-dependent phosphatase OS=Homo sapiens GN=PH11 PE=1 SV=1 (-PH11_HUMAN)	5.81167	4.93467	3.74067	3.90067	7.764	7.693	7.573	7.591	7.729	7.582	0.147
B40W16	Isoform 1 of Histone-binding protein 1 OS=Homo sapiens GN=HBBP1 PE=1 SV=1 (-HBBP1_HUMAN)	1.59867	1.59867	1.59867	1.59867	7.908	7.908	7.908	7.908	7.908	7.908	0.147
P61106	Ras-related protein Rab-14 OS=Homo sapiens GN=RAB14 PE=1 SV=4 (-RAB14_HUMAN)	4.69787	2.19267	3.09867	1.69967	7.672	7.341	7.491	7.230	7.506	7.361	0.146
FW8181	60S ribosomal protein L6 OS=Homo sapiens GN=RPL6 PE=1 SV=1 (-RPL6_HUMAN)	1.49188	7.75367	7.23367	8.17867	8.173	8.889	7.913	8.031	8.361	8.148	0.146
Q3Z288	Uncharacterized protein OS=Homo sapiens GN=MTHFD1 PE=1 SV=1 (-G3Z288_HUMAN)	5.85667	5.85867	5.85867	5.85867	7.932	7.880	7.767	7.754	7.906	7.761	0.145
B40R70	Uncharacterized protein OS=Homo sapiens GN=PLUS PE=1 SV=1 (-B40R70_HUMAN)	8.29567	2.98867	2.94867	2.73567	7.724	7.471	7.467	7.437	7.597	7.452	0.145
Q14257	Reticulocalnexin-1 OS=Homo sapiens GN=RCN1 PE=1 SV=1 (-RCN1_HUMAN)	1.97867	1.97867	1.97867	1.97867	7.891	7.891	7.891	7.891	7.891	7.891	0.145
B72181	Tubulin beta-4B chain OS=Homo sapiens GN=TUBB4B PE=1 SV=1 (-TBB4B_HUMAN)	1.37989	1.10499	8.81688	8.86488	9.139	9.043	8.945	8.948	9.091	8.946	0.145
887355	Uncharacterized protein OS=Homo sapiens GN=ATP7A1 PE=2 SV=1 (-ATP7A1_HUMAN)	2.51367	1.71867	1.45667	1.52367	7.400	7.235	7.174	7.183	7.318	7.173	0.145
Q13011	Delta(3,5)-Delta(2,4)-dehydro-ATPase, mitochondrial OS=Homo sapiens GN=ECH1 PE=1 SV=2 (-ECH1_HUMAN)	1.93887	1.94267	1.36767	1.41967	7.287	7.288	7.136	7.152	7.288	7.144	0.144
Q9PH03	Integrin-linked kinase-associated serine/threonine phosphatase 2C OS=Homo sapiens GN=ILKAP PE=1 SV=1 (-ILKAP_HUMAN)	1.16167	7.81568	8.58467	6.84468	7.065	6.893	6.835	6.979	6.835	6.979	0.144
Q9YSL4	Uncharacterized protein OS=Homo sapiens GN=HSP101 PE=1 SV=1 (-HSP101_HUMAN)	7.08887	7.08887	7.08887	7.08887	7.088	7.088	7.088	7.088	7.088	7.088	0.144
Q04637-5	Isoform 5 of Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 (-IF4G1_HUMAN)	4.18187	2.82767	2.66867	2.29067	7.621	7.451	7.426	7.360	7.536	7.393	0.143
Q72784	DNAJC7 protein OS=Homo sapiens GN=DNAJC7 PE=2 SV=1 (-Q72784_HUMAN)	1.02767	7.12966	6.31866	5.99366	7.012	6.853	6.801	6.778	6.923	6.789	0.143
Q15181	Inorganic pyrophosphatase OS=Homo sapiens GN=PP1A PE=1 SV=2 (-PP1A_HUMAN)	1.29988	1.36888	1.11788	1.14188	8.255	8.136	8.048	8.057	8.196	8.052	0.143
Q9NR13-2	Isoform 2 of Structural maintenance of chromosomes protein 4 OS=Homo sapiens GN=SMC4 (-SMC4_HUMAN)	2.30967	1.93567	1.50667	1.48267	7.363	7.287	7.193	7.171	7.325	7.162	0.143
Q9YSL4	Uncharacterized protein OS=Homo sapiens GN=HSP90A PE=1 SV=1 (-HSP90A_HUMAN)	7.08887	7.08887	7.08887	7.08887	7.088	7.088	7.088	7.088	7.088	7.088	0.143
EP9LK3	Uncharacterized protein OS=Homo sapiens GN=NEPFS1 PE=1 SV=1 (-EP9LK3_HUMAN)	2.79187	1.82267	1.46767	1.79767	7.446	7.261	7.166	7.255	7.353	7.210	0.143
A6MKB8	Uncharacterized protein OS=Homo sapiens GN=RNPE4 PE=1 SV=1 (-A6MKB8_HUMAN)	2.51767	1.95767	1.62067	1.57867	7.401	7.292	7.198	7.346	7.204	7.042	0.143
P33136-2	Isoform 2 of Deoxyuridine 5'-triphosphate nucleodiphosphatase, mitochondrial OS=Homo sapiens GN=DUT (-DUT_HUMAN)	5.02967	2.58567	2.46667	2.74367	7.701	7.412	7.392	7.438	7.557	7.415	0.142
Q9YSL4	Isoform 1 of Cytoplasmic peroxisomal of Peroxisome-5, mitochondrial OS=Homo sapiens GN=PROX5 (-PROX5_HUMAN)	5.17667	4.80867	4.01067	4.16567	7.714	7.682	7.500	7.613	7.698	7.556	0.142
Q9YSL4	NADH dehydrogenase (ubiquinone) 1 alpha subunit assembly factor OS=Homo sapiens GN=NDUFA1 (-NDUFA1_HUMAN)	6.81867	8.47466	8.47466	8.47466	8.474	8.474	8.474	8.474	8.474	8.474	0.142
Q75369-6	Isoform 6 of Flavin-B OS=Homo sapiens GN=FNBB (-FNBB_HUMAN)	6.19367	1.57167	1.20767	1.09767	7.209	7.196	7.082	7.040	7.203	7.061	0.142
E7EQJ1	Uncharacterized protein OS=Homo sapiens GN=MSH2 PE=4 SV=1 (-E7EQJ1_HUMAN)	8.88366	5.09266	4.64866	5.06866	6.949	6.707	6.682	6.705	6.828	6.688	0.142
Q9YSL4	Vesicle-associated membrane protein-associated protein 8/C OS=Homo sapiens GN=VAMP8 PE=1 SV=3 (-VAMP8_HUMAN)	1.95467	6.61866	8.00666	7.65066	7.291	6.821	6.945	6.884	7.056	6.914	0.142
P22214	Ubiquitin-like modifier-activating enzyme 1 OS=Homo sapiens GN=UBM1 PE=1 SV=3 (-UBM1_HUMAN)	1.81688	1.33188	1.80668	1.25688	8.259	8.124	8.001	8.099	8.192	8.050	0.142
P53580	Uncharacterized protein OS=Homo sapiens GN=HSP101 PE=1 SV=1 (-HSP101_HUMAN)	7.08887	7.08887	7.08887	7.08887	7.088	7.088	7.088	7.088	7.088	7.088	0.142
P51659	Peroxisomal multifunctional enzyme type 2 OS=Homo sapiens GN=HSD17B4 PE=1 SV=3 (-HSD17B4_HUMAN)	2.11267	2.19967	1.46067	1.66467	7.325	7.342	7.164	7.221	7.334	7.193	0.141
P52272-2	Isoform 2 of Heterogeneous nuclear ribonucleoprotein M OS=Homo sapiens GN=HNRPM (-HNRPM_HUMAN)	1.42188	8.95167	8.02967	9.12167	8.152	7.993	7.905	7.960	8.073	7.932	0.141
Q00232	26S protease non-ATPase regulatory subunit 12 OS=Homo sapiens GN=PSMD12 PE=1 SV=3 (-PSMD12_HUMAN)	1.86567	1.28467	1.41867	8.271	7.214	7.089	7.152	7.271	7.130	7.100	0.140
P60338	Lactate dehydrogenase A chain OS=Homo sapiens GN=LDAH PE=1 SV=2 (-LDAH_HUMAN)	2.06688	1.46688	1.20788	1.31288	8.374	8.166	8.062	8.118	8.240	8.130	0.140
Q14737	Programmed cell death protein 1 OS=Homo sapiens GN=CD95 PE=1 SV=1 (-CD95_HUMAN)	1.90268	5.31967	4.11867	4.11867	7.728	7.311	7.288	7.311	7.423	7.311	0.140
Q9YSL4	Isoform 3 of Inorganic pyrophosphatase 2, mitochondrial OS=Homo sapiens GN=PPA2 (-PPA2_HUMAN)	3.74887	3.41867	2.21467	3.03067	7.573	7.534	7.345	7.482	7.554	7.413	0.140
Q10212-3	40S ribosomal protein S3a OS=Homo sapiens GN=RPS3A PE=1 SV=2 (-RPS3A_HUMAN)	1.05068	7.85467	6.87267	6.29067	8.021	7.895	7.837	7.799	7.958	7.818	0.140
P58546	Myotrophin OS=Homo sapiens GN=MTPN PE=1 SV=2 (-MTPN_HUMAN)	6.54467	4.85767	3.93067	4.27067	7.816	7.686	7.592	7.630	7.711	7.611	0.140
P51923	Methylenetetrahydrofolate synthetase, cytoplasmic OS=Homo sapiens GN=SHMT2 PE=1 SV=2 (-SHMT2_HUMAN)	3.36467	6.52567	6.29667	6.54667	7.505	7.527	7.367	7.391	7.528	7.391	0.140
P60228	Eukaryotic translation initiation factor 3 subunit E OS=Homo sapiens GN=EIF3E PE=1 SV=1 (-EIF3E_HUMAN)	2.20467	1.60667	1.110267	1.69167	7.652	7.042	7.042	7.042	7.538	7.169	0.140
B40407	ATP synthase subunit O, mitochondrial OS=Homo sapiens GN=ATP5O PE=1 SV=1 (-ATP5O_HUMAN)	4.10967	2.71267	2.68367	2.18967	7.614	7.433	7.429	7.340	7.524	7.384	0.139
Q9YSL4	PKAR2A protein OS=Homo sapiens GN=PKAR2A PE=2 SV=1 (-Q9YSL4_HUMAN)	1.57367	1.37667	1.06867	1.07067	7.197	7.139	7.029	7.029	7.168	7.029	0.139
Q7QZC4	Staphylococcal nuclease domain-containing protein 1 OS=Homo sapiens GN=SNDC1 PE=1 SV=1 (-SNDC1_HUMAN)	5.95167	3.89867	3.39767	3.57367	7.775	7.586	7.531	7.553	7.681	7.542	0.138
FW8706	Uncharacterized protein OS=Homo sapiens GN=HSP90A PE=1 SV=1 (-HSP90A_HUMAN)	7.08887	7.08887	7.08887	7.08887	7.088	7.088	7.088	7.088	7.088	7.088	0.138
EP9LH8	Uncharacterized protein OS=Homo sapiens GN=ESTR2 PE=1 SV=1 (-EP9LH8_HUMAN)	1.96267	7.74567	1.05767	1.27567	7.257	7.027	7.004	6.929	7.132	6.932	0.138
P62714	Serine/threonine phosphatase 2A catalytic subunit beta isoform OS=Homo sapiens GN=PPP2C PE=1 SV=1	2.18987	7.66466	1.02467	8.69066	7.340	6.884	7.010	6.939	7.112	6.975	0.138
FS40F5	Uncharacterized protein OS=Homo sapiens GN=ZC3H15 PE=1 SV=1 (-FS40F5_HUMAN)	1.09067	5.01366	7.90166	6.96666	7.037	6.978	6.898	6.843	7.008	6.870	0.138
PA9721	Proteasome subunit type 2 OS=Homo sapiens GN=PSMB2 PE=1 SV=1 (-PSMB2_HUMAN)	1.61067	1.42667	1.11067	1.10067	7.207	7.154	7.045	7.041	7.180	7.043	0.137
Q9YSL4	Glyoxal oxidase/hydroxypropyl-CoA lyase OS=Homo sapiens GN=HPOX PE=1 SV=1 (-HPOX_HUMAN)	6.17667	6.17667	6.17667	6.17667	6.176	6.176	6.176	6.176	6.176	6.176	0.137
P42771	Cylin-dependent kinase inhibitor 2A, isoforms 1/2/3 OS=Homo sapiens GN=CDKN2A PE=1 SV=1 (-CDKN2A_HUMAN)	2.4726										

Q8K55-2	Isomorf 2 of Histone-arginine methyltransferase CARM1 OS=Homo sapiens GN=CARM1 PE=1 SV=1 - [CARM1_HUMAN]	1.09957	1.63867	8.72268	1.18367	7.039	7.214	6.941	7.073	7.127	7.007	0.120
P22ZD0	Uncharacterized protein OS=Homo sapiens GN=USM02 PE=4 SV=1 - [P22ZD0_HUMAN]	1.89828	1.35588	9.48027	1.56088	8.279	8.132	7.977	8.193	8.205	8.085	0.120
P22ZD1	Uncharacterized protein OS=Homo sapiens GN=USM02 PE=5 SV=1 - [P22ZD1_HUMAN]	9.02867	8.83167	5.34567	5.66667	7.956	7.766	7.576	7.786	7.596	7.406	0.120
C9W390	Uncharacterized protein OS=Homo sapiens GN=PT1PFB PE=1 SV=1 - [C9W390_HUMAN]	2.02067	1.49167	1.19867	1.45267	7.305	7.174	7.078	7.162	7.239	7.120	0.119
B5M359	Replication protein A3, 14kDa, isoform CRA_A OS=Homo sapiens GN=RP3 PE=4 SV=1 - [B5M359_HUMAN]	6.92456	5.59667	9.39966	1.51567	6.984	7.408	7.160	7.196	7.077	7.019	0.119
P41250	Glycyl-RNA synthetase OS=Homo sapiens GN=GARS PE=1 SV=3 - [SYG_HUMAN]	4.51167	4.82567	3.57067	3.53167	7.654	7.683	7.553	7.548	7.669	7.550	0.119
P25205	DNA replication licensing factor PCNA3 OS=Homo sapiens GN=PCNA3 PE=1 SV=3 - [MCH3_HUMAN]	3.93867	3.01667	2.58167	2.66867	7.595	7.479	7.412	7.428	7.377	7.419	0.118
Q8P2Q9	Peptide 8 OS=Homo sapiens GN=PR8 PE=1 SV=1 - [PR8_HUMAN]	1.57667	1.52667	0.50866	1.54367	7.157	7.167	6.957	7.197	7.188	7.073	0.117
E7U949	Uncharacterized protein OS=Homo sapiens GN=CALDI PE=4 SV=1 - [E7U949_HUMAN]	1.84267	1.31467		1.18767	7.285	7.119		7.075	7.192	7.075	0.117
Q14974	Importin subunit beta-1 OS=Homo sapiens GN=KPMB1 PE=1 SV=1 - [IMB1_HUMAN]	7.73567	6.49467	5.33767	5.48667	7.888	7.812	7.727	7.739	7.850	7.733	0.117
Q9Y3F4	Serine-threonine kinase receptor-associated subunit OS=Homo sapiens GN=STRAP PE=1 SV=1 - [STRAP_HU]	3.27867	2.72767	2.16067	2.14667	7.616	7.436	7.334	7.408	7.476	7.359	0.117
Q92522	Histone H2A OS=Homo sapiens GN=H2AFY PE=1 SV=1 - [H2A_HUMAN]	4.09567	2.93067	2.73167	2.56667	7.712	7.467	7.436	7.409	7.540	7.423	0.117
Q12405	395-residional protein OS=Homo sapiens GN=ANP2A PE=1 SV=1 - [ANP2A_HUMAN]	1.43367	1.11667	9.00667	1.07667	7.157	7.067	6.916	7.032	7.112	6.995	0.117
Q60203	Amidophosphoribosyltransferase OS=Homo sapiens GN=PPAT PE=1 SV=1 - [PURL_HUMAN]	1.87367	1.34467	1.23367	1.19267	7.273	7.128	7.071	7.076	7.200	7.084	0.117
P16949	Stathin OS=Homo sapiens GN=STMN1 PE=1 SV=3 - [STMN1_HUMAN]	1.21068	0.93667	8.19567	8.24367	7.803	7.979	7.914	7.916	8.031	7.915	0.116
P32119	Peroxiredoxin-2 OS=Homo sapiens GN=PRDX2 PE=1 SV=5 - [PRDX2_HUMAN]	2.65118	1.88768	1.67668	1.74868	8.423	8.276	8.224	8.242	8.350	8.233	0.116
Q13347	Eukaryotic translation initiation factor 3 subunit 1 OS=Homo sapiens GN=EIF3 PE=1 SV=1 - [EIF31_HUMAN]	3.65267	2.56667	2.15567	2.55167	7.863	7.409	7.324	7.407	7.486	7.370	0.116
P1281-2	Isomorf 2 of Ubiquitin-conjugating enzyme E2 K OS=Homo sapiens GN=UBE2K - [UBE2K_HUMAN]	1.91766	1.83566	6.97766	6.08466	6.964	6.894	6.844	6.784	6.929	6.814	0.115
P49720	Prosome subunit beta type-3 OS=Homo sapiens GN=PSMB3 PE=1 SV=2 - [PSB3_HUMAN]	0.91767	1.90767	1.42267	2.30667	7.465	7.280	7.153	7.363	7.377	7.218	0.115
P26583	High mobility group protein B2 OS=Homo sapiens GN=HMGB2 PE=1 SV=2 - [HMGB2_HUMAN]	8.84267	5.84867	6.20367	4.92167	7.947	7.767	7.793	7.692	7.857	7.742	0.114
Q8QW06	Myeloma-overexpressed gene 2 protein OS=Homo sapiens GN=MYO2 PE=2 SV=3 - [MYO2_HUMAN]	1.68867	1.24467	1.06367	1.16567	7.227	7.095	7.027	7.068	7.161	7.047	0.114
P26281	40S ribosomal protein L16 OS=Homo sapiens GN=L16 PE=1 SV=1 - [RSL16_HUMAN]	3.89967	1.96867	1.09667	1.12967	8.254	8.529	8.093	8.154	8.238	8.124	0.114
Q9L416	Prosome activator complex subunit 2 OS=Homo sapiens GN=PSME2 PE=1 SV=4 - [PSME2_HUMAN]	1.30967	0.81366	7.48566	8.40966	7.117	6.910	6.874	6.925	7.014	6.899	0.114
P17812	CTP synthase 1 OS=Homo sapiens GN=CTSP PE=1 SV=2 - [PYR3_HUMAN]	2.49467	1.41867	1.55867	1.58767	7.469	7.152	7.107	7.201	7.310	7.197	0.114
Q9UM00	Ubiquitin-1 OS=Homo sapiens GN=UBQLN1 PE=1 SV=2 - [UBQLN_HUMAN]	2.12367	1.73667	1.54467	1.41467	7.327	7.239	7.189	7.150	7.283	7.170	0.114
Q9P9P9	Vacuolar protein sorting-associated protein VTA1 homolog OS=Homo sapiens GN=VTA1 PE=1 SV=1 - [VTA1_HUMAN]	2.48027	2.44567	1.81867	1.98067	7.395	7.388	7.259	7.297	7.391	7.278	0.113
Q12620	Alpha-9 protein OS=Homo sapiens GN=ALPHA9 PE=1 SV=1 - [ALPHA9_HUMAN]	1.18967			1.08967	7.086					6.924	0.113
P3080-2	Isomorf 2 of Profilin-2 OS=Homo sapiens GN=PFN2 - [PROF2_HUMAN]	2.14467	1.47367	1.30467	1.44267	7.331	7.168	7.115	7.159	7.250	7.137	0.113
Q98RA2	Isomorf 1 of Thib domain-containing protein 17 OS=Homo sapiens GN=TXND17 PE=1 SV=1 - [TXD17_HUMAN]	2.12367	1.05867	1.10567	1.21367	7.327	7.025	7.044	7.084	7.176	7.064	0.112
ES1899	Uncharacterized protein OS=Homo sapiens GN=RLP3 PE=3 SV=1 - [ESR19_HUMAN]	4.18567	4.73067	3.09267	3.82567	7.622	7.675	7.490	7.583	7.648	7.536	0.112
P62424	60S ribosomal protein L2a OS=Homo sapiens GN=RLP2A PE=1 SV=2 - [RL2A_HUMAN]	1.86868	1.12688	1.07868	1.16768	8.271	8.052	8.032	8.037	8.161	8.050	0.112
P49588	Nuclear autoantigenic sperm protein OS=Homo sapiens GN=NASP PE=1 SV=2 - [SYG2_HUMAN]	1.46467	1.03867	0.99267	1.05467	7.529	7.465	7.407	7.447	7.545	7.431	0.112
P78527	DNA-dependent protein kinase catalytic subunit OS=Homo sapiens GN=PRKDC PE=1 SV=3 - [PRKDC_HUMAN]	2.17967	2.00767	1.54267	1.70067	7.338	7.303	7.188	7.230	7.320	7.209	0.111
A03660-2	Isomorf 2 of Pleiotropic regulator 1 OS=Homo sapiens GN=PLRG1 - [PLRG1_HUMAN]	1.53866	2.31266		2.66866	6.711	6.364		6.426	6.537	6.426	0.111
P62495	Eukaryotic peptide chain release factor subunit 1 OS=Homo sapiens GN=EF1F PE=1 SV=3 - [ERF1_HUMAN]	3.61967	2.64567	2.26367	2.53667	7.559	7.422	7.355	7.404	7.491	7.379	0.111
P62701	40S ribosomal protein S4, isoform OS=Homo sapiens GN=PS4A PE=1 SV=2 - [RSM4_HUMAN]	8.98767	6.91867	6.17167	6.04267	7.954	7.840	7.790	7.781	7.897	7.778	0.111
P14868	Nucleoside diphosphate kinase type-1 OS=Homo sapiens GN=NDPK1 PE=1 SV=2 - [SVDC_HUMAN]	2.16467	1.62267	1.09667	1.12967	7.968	7.824	7.698	7.815	7.928	7.816	0.111
Q9P9P9	Dynein light chain roadblock-type 1 OS=Homo sapiens GN=DLNB1 PE=1 SV=3 - [DLNB1_HUMAN]	2.97167	3.00267	2.10467	2.54667	7.473	7.477	7.323	7.408	7.475	7.364	0.111
P51665	26S proteasome non-ATPase regulatory subunit 7 OS=Homo sapiens GN=PSMD7 PE=1 SV=2 - [PS07_HUMAN]	3.64567	3.04867	2.52967	2.64067	7.562	7.484	7.403	7.422	7.523	7.411	0.111
P08758	Anexin A5 OS=Homo sapiens GN=ANXA5 PE=1 SV=2 - [ANXA5_HUMAN]	1.04468	9.61767	7.54667	7.99767	7.819	7.983	7.878	7.903	8.001	7.890	0.110
C9A336	Uncharacterized protein OS=Homo sapiens GN=NP1B3 PE=3 SV=1 - [C9A336_HUMAN]	1.08667	1.00027	7.42166	8.13866	7.409	7.001	6.870	6.911	7.001	6.890	0.110
Q00231	26S proteasome core protein OS=Homo sapiens GN=PSMD1 PE=1 SV=3 - [PSD1_HU]	3.08667	2.71867	2.07667	2.46567	7.889	7.216	7.087	7.385	7.515	7.411	0.110
Q9Y333	Nucleosome assembly protein 1-like 4 OS=Homo sapiens GN=NAP1L4 PE=1 SV=1 - [NAP1L4_HUMAN]	5.09967	3.27067	3.10267	3.24167	7.708	7.514	7.492	7.511	7.611	7.501	0.110
Q9Y3C8	Ubiquitin-fold modifier-conjugating enzyme 1 OS=Homo sapiens GN=UFC1 PE=1 SV=3 - [UFC1_HUMAN]	6.10566	4.74366			6.878	6.676		6.786	6.877	6.766	0.110
B46086	Uncharacterized protein OS=Homo sapiens GN=IP05 PE=2 SV=1 - [B46086_HUMAN]	1.93567	2.70966	1.23567	6.82866	7.287	6.858	7.092	6.834	7.072	6.963	0.109
P49499-2	Isomorf 2 of Mannose-6-phosphate isomerase OS=Homo sapiens GN=MPI - [MPI_HUMAN]	1.49027	1.26967	1.24967	0.19866	7.174	7.103	7.059	6.964	7.139	7.029	0.109
Q124H2	Formylglyoxal lyase OS=Homo sapiens GN=SMI2 PE=1 SV=2 - [SMI2_HUMAN]	1.66267	5.42067		8.94967	7.626	7.734		7.447	7.447	7.445	0.109
B72566	Uncharacterized protein OS=Homo sapiens GN=UBA5 PE=2 SV=1 - [B72566_HUMAN]	1.77467	1.34867	1.34867	1.41567	7.240	7.130	7.151	7.249	7.140	7.140	0.109
P34932	Heat shock 70 kDa protein 4 OS=Homo sapiens GN=HSPM4 PE=1 SV=4 - [HSP74_HUMAN]	6.88567	5.75067	4.66167	5.15867	7.838	7.760	7.668	7.712	7.799	7.690	0.109
Q8H183	Mitotin, mitochondrial OS=Homo sapiens GN=NDUF42 PE=1 SV=1 - [MMIT_HUMAN]	1.08967	8.32166	8.31966	6.62466	7.037	6.920	6.920	6.821	6.979	6.871	0.108
P67936	Tropomyosin alpha-4 chain OS=Homo sapiens GN=TPMA PE=1 SV=3 - [TPMA_HUMAN]	1.38868	1.73867	9.19467	9.12867	8.142	8.690	7.964	7.865	8.076	7.980	0.108
Q9297-2	Isomorf 2 of Transcription factor 12 OS=Homo sapiens GN=TF12 PE=1 SV=1 - [TF12_HUMAN]	1.40367	1.09267	1.05267	1.10967	7.282	7.102	7.051	7.128	7.211	7.103	0.108
P49773	Histidine triad nucleotide-binding protein 1 OS=Homo sapiens GN=HNT1 PE=1 SV=2 - [HNT1_HUMAN]	7.30767	7.22267	5.56367	5.78067	7.864	7.859	7.745	7.762	7.861	7.754	0.108
A03852	Calumenin OS=Homo sapiens GN=CALU PE=1 SV=2 - [CALU_HUMAN]	3.20667	1.64567	1.80367	1.78467	7.506	7.216	7.256	7.251	7.361	7.254	0.107
Q90755	Serine/arginine-rich splicing factor 1 OS=Homo sapiens GN=SRSF1 PE=1 SV=2 - [SRSF1_HUMAN]	4.34367	3.37567	3.52167	2.54167	7.638	7.528	7.547	7.405	7.583	7.476	0.107
P61160	Actin-related protein 7 OS=Homo sapiens GN=ACTR7 PE=1 SV=1 - [ARP7_HUMAN]	2.26167	0.83066	0.36266	1.16567	7.354	6.919	6.926	7.134	7.137	7.030	0.107
P49331	Nucleoside diphosphate kinase type-1 OS=Homo sapiens GN=NDPK1 PE=1 SV=2 - [SVDC_HUMAN]	4.40367	2.82567	2.07667	2.46567	7.899	7.835	7.698	7.835	7.921	7.816	0.107
P78347-2	Isomorf 2 of General transcription factor II-H OS=Homo sapiens GN=GTIF2 - [GTIF2_HUMAN]	1.42067	1.49667	1.03867	1.25467	7.152	7.175	7.016	7.098	7.164	7.057	0.106
Q8H4V1	Membrane magnesium transporter 1 OS=Homo sapiens GN=MMGT1 PE=1 SV=1 - [MMGT1_HUMAN]	2.12367	1.74416	1.08667	7.32267	6.872	6.812	6.993	7.099	6.993	6.903	0.106
A03684-2	Isomorf 2 of Mitotic checkpoint protein BUB3 OS=Homo sapiens GN=BUB3 - [BUB3_HUMAN]	2.17467	1.66667	1.71167	1.51367	7.337	7.222	7.168	7.180	7.280	7.174	0.106
P15497	Keratin, type I cytoskeletal 5 OS=Homo sapiens GN=KIF1 PE=1 SV=2 - [RSM4_HUMAN]	1.04267	8.02867	8.02867	8.02867	8.018	7.905	7.805	7.906	7.961	7.856	0.106
P10768	Formylglyoxal lyase OS=Homo sapiens GN=SMI2 PE=1 SV=2 - [SMI2_HUMAN]	1.66267	3.70767	2.93367	3.64367	7.527	7.637	7.527	7.637	7.742	7.637	0.106
E7E983	Uncharacterized protein OS=Homo sapiens GN=RLP14 PE=4 SV=1 - [E7E983_HUMAN]	1.11568	1.61567	7.22167	5.86467	8.047	7.789	7.859	7.768	7.918	7.813	0.105
B4E2W0	Uncharacterized protein OS=Homo sapiens GN=HADHB PE=2 SV=1 - [B4E2W0_HUMAN]	1.23467	1.23867	9.70666	9.72966	7.091	7.093	6.988	7.092	6.988	6.988	0.105
P43686	26S proteasome regulatory subunit B6 OS=Homo sapiens GN=PSMC6 PE=1 SV=2 - [PRSB6_HUMAN]	4.23567	3.76167	3.06567	3.21367	7.627	7.575	7.486	7.507	7.601	7.497	0.104
P26441	Etrogens beta-1 OS=Homo sapiens GN=ESR1 PE=1 SV=1 - [ERBB1_HUMAN]	1.02667	1.51867	0.31567	0.31567	8.268	8.155	8.098	8.126	8.211	8.107	0.104
P62269	45S ribosomal protein L8 OS=Homo sapiens GN=RLP8 PE=1 SV=3 - [RSL8_HUMAN]	9.78667	5.58267	5.97567	6.05367	7.991	7.747	7.747	7.869	7.964	7.856	0.104
P09211	Glutathione S-transferase											

Q98X93	N-alpha-acetyltransferase 15, NAIA auxiliary subunit OS=Homo sapiens GN=NAI15 PE=1 SV=1 - [NAI15_HUMAN]	3.9196E	3.3636E	3.1286E	6.593	6.527	6.495	6.593	6.511	0.082
P93566	Adenylylsuccinate lyase OS=Homo sapiens GN=ADSL PE=1 SV=2 - [P93566_HUMAN]	2.3496E	1.1107E	1.1987E	7.371	7.168	7.045	7.130	7.087	0.082
Q14683	Structural maintenance of chromosomes protein 1A OS=Homo sapiens GN=SMC1A PE=1 SV=2 - [SMC1A_HUMAN]	5.1513E	4.7326E	4.1686E	6.712	6.675	6.603	6.620	6.656	0.082
EP9117	Uncharacterized protein OS=Homo sapiens GN=ATPS1 PE=4 SV=1 - [EP9117_HUMAN]	1.4178E	8.8175E	9.7596E	7.151	6.945	6.944	6.989	7.048	0.082
P10412	Histone H1.4 OS=Homo sapiens GN=HIST1H1E PE=1 SV=2 - [H14_HUMAN]	1.3077E	1.0466E	1.0258E	8.116	8.019	7.958	8.014	8.068	0.082
Q43776	Asparaginyl-tRNA synthetase, cytoplasmic OS=Homo sapiens GN=NARS PE=1 SV=1 - [SYNC_HUMAN]	2.2257E	2.0647E	1.7517E	8.027	7.317	7.243	7.256	7.331	0.249
G3JAL7	Puative uncharacterized protein LOC133819 OS=Homo sapiens GN=PRRC1 PE=4 SV=1 - [G3JAL7_HUMAN]	8.0506E	7.9626E	7.2006E	6.906	6.901	6.861	6.783	6.903	0.082
P54136	Agonyrin-like protein 2 OS=Homo sapiens GN=AGRYN2 PE=1 SV=2 - [AGRYN2_HUMAN]	2.2847E	1.4387E	1.4746E	7.248	7.248	7.248	7.248	7.248	0.082
P49755	Transmembrane emp24 domain-containing protein 10 OS=Homo sapiens GN=TMED10 PE=1 SV=2 - [TMED4_HUMAN]	2.0102E	1.5552E	1.4957E	7.303	7.192	7.162	7.175	7.247	0.079
Q15287-3	Isomorph 3 of RNA-binding protein with serine-rich domain 1 OS=Homo sapiens GN=RNPS1 - [RNPS1_HUMAN]	1.9217E	1.4127E	1.3047E	7.283	7.150	7.160	7.217	7.138	0.079
PE2854	40S ribosomal protein S26 OS=Homo sapiens GN=RS26 PE=1 SV=3 - [RS26_HUMAN]	9.0187E	5.5937E	5.9637E	5.8837E	7.955	7.748	7.770	7.851	0.079
AK1184	COP9 constitutive photomorphogenic homolog subunit 8 (Arabalopods), isoform CRA_b OS=Homo sapiens GN=40S	3.7887E	6.4416E	1.3047E	7.978	6.809	7.115	7.070	7.194	0.078
P21296	FACT complex subunit 3 OS=Homo sapiens GN=FACT3 PE=1 SV=1 - [FACT3_HUMAN]	1.3448E	1.0206E	1.1168E	8.234	8.018	8.046	8.048	8.125	0.078
P62826	GTP-binding nuclear protein Ran OS=Homo sapiens GN=NRAN PE=1 SV=3 - [RAN_HUMAN]	2.8977E	1.8148E	1.8898E	1.9448E	8.462	8.259	8.276	8.289	0.078
P00387-2	Isomorph 2 of NADH-cytochrome b5 reductase 3 OS=Homo sapiens GN=CYBR53 - [NBSR3_HUMAN]	1.9017E	2.7687E	2.0107E	7.279	7.442	7.262	7.263	7.360	0.078
Q9UK55	Huntingtin-interacting protein K OS=Homo sapiens GN=HYPK PE=1 SV=2 - [HYPK_HUMAN]	1.5107E	1.2927E	1.0287E	1.3277E	7.179	7.111	7.012	7.123	0.078
P40ZP5	Uncharacterized protein OS=Homo sapiens GN=DOB1 PE=1 SV=1 - [P40ZP5_HUMAN]	2.7347E	2.5787E	2.1717E	2.2907E	7.440	7.411	7.337	7.360	0.077
Q97893	FACT complex subunit 1 OS=Homo sapiens GN=FACT1 PE=1 SV=1 - [SPFH1_HUMAN]	1.2487E	2.2487E	1.9207E	7.257	7.502	7.253	7.202	7.304	0.077
P14618	Pyruvate kinase isozymes M1/M2 OS=Homo sapiens GN=PKM2 PE=1 SV=4 - [PKYM_HUMAN]	4.1798E	3.5248E	3.2268E	3.2208E	8.621	8.547	8.509	8.508	0.076
P53327-2	Isomorph 2 of Tumor protein D52 OS=Homo sapiens GN=TP52 - [TP52_HUMAN]	1.0107E	1.0107E	8.4775E	8.5296E	7.004	7.004	6.928	6.931	0.070
F2Z3AS	Uncharacterized protein OS=Homo sapiens GN=RLP3 PE=3 SV=1 - [F2Z3AS_HUMAN]	1.9988E	1.2448E	1.1838E	1.1938E	8.204	8.095	8.073	8.149	0.075
Q98988	UPF055 subunit C10orf10 OS=Homo sapiens GN=C10orf10 PE=1 SV=1 - [C5D10_HUMAN]	2.5917E	1.2807E	1.3017E	1.8137E	7.474	7.107	7.114	7.258	0.074
C531AS	Uncharacterized protein OS=Homo sapiens GN=C5orf101 PE=1 SV=1 - [C531AS_HUMAN]	1.9382E	2.2487E	2.8937E	2.8937E	7.266	7.266	7.266	7.266	0.074
Q864U2-2	Isomorph 2 of Polyadenylate-binding protein 2 OS=Homo sapiens GN=PABP1 - [PABR2_HUMAN]	3.4957E	4.1527E	2.7027E	1.3077E	7.533	7.162	7.432	7.116	0.074
P23528	Cofilin-1 OS=Homo sapiens GN=COF1 PE=1 SV=3 - [COF1_HUMAN]	4.5748E	4.1268E	3.6178E	3.7278E	8.660	8.616	8.558	8.571	0.073
PE2491	Ras-related protein Rab-11A OS=Homo sapiens GN=RAB11A PE=1 SV=3 - [RBI1A_HUMAN]	3.3397E	2.0727E	1.9917E	2.6377E	7.549	7.317	7.299	7.421	0.073
Q98929	Copine-1 OS=Homo sapiens GN=CPN1 PE=1 SV=1 - [CPN1_HUMAN]	1.2897E	9.9556E	9.8286E	9.1331E	7.110	6.998	6.992	6.970	0.073
Q91747	ADP-ribosyltransferase 1 OS=Homo sapiens GN=ART1 PE=1 SV=3 - [GGA2_HUMAN]	1.3945E	1.3945E	1.3945E	1.3945E	6.924	6.924	6.924	6.924	0.073
C53CE3	Ewing sarcoma breakpoint region 1, isoform CRA_e OS=Homo sapiens GN=EWSR1 PE=4 SV=1 - [CSG3E3_HUMAN]	1.6927E	1.7197E	1.1697E	1.7847E	7.229	7.235	7.068	7.251	0.072
Q00264	Membrane-associated progesterone receptor component 1 OS=Homo sapiens GN=PMR1 PE=1 SV=3 - [PMR1_HUMAN]	2.7997E	6.6557E	4.9227E	4.9477E	7.863	7.668	7.692	7.694	0.072
BT7403	Uncharacterized protein OS=Homo sapiens GN=GLD04 PE=2 SV=1 - [BT7403_HUMAN]	3.5567E	1.4037E	1.8937E	1.8937E	7.551	7.147	7.277	7.349	0.072
P60174	Trotophosphatase isomerase OS=Homo sapiens GN=TPPI PE=1 SV=2 - [TPPI_HUMAN]	6.1168E	3.2628E	3.6858E	3.8878E	8.786	8.513	8.566	8.590	0.072
P19445	40S ribosomal protein S23 OS=Homo sapiens GN=RS23 PE=1 SV=1 - [ACTC_HUMAN]	4.2288E	3.4288E	3.4288E	3.4288E	7.588	7.588	7.588	7.588	0.072
P49026	Malate dehydrogenase, mitochondrial OS=Homo sapiens GN=MDH2 PE=1 SV=3 - [MDHM_HUMAN]	3.9048E	3.2928E	3.0308E	3.0488E	8.592	8.517	8.482	8.484	0.072
P68032	Actin, alpha cardiac muscle 1 OS=Homo sapiens GN=ACTC1 PE=1 SV=1 - [ACTC_HUMAN]	8.9188E	7.8858E	7.3258E	7.6238E	8.992	8.897	8.865	8.882	0.071
PE6748-2	Isomorph 2 of Nucleohistomin OS=Homo sapiens GN=NPM1 - [NPM_HUMAN]	6.4978E	6.1248E	5.2218E	5.5028E	8.813	8.787	8.781	8.800	0.071
D684F8	Uncharacterized protein OS=Homo sapiens GN=HRNP PE=4 SV=1 - [D684F8_HUMAN]	1.7908E	1.1578E	1.2778E	1.1718E	8.253	8.063	8.106	8.069	0.071
Q15372	Uncharacterized protein OS=Homo sapiens GN=EIF3 PE=1 SV=1 - [EIF3H_HUMAN]	1.8567E	2.8797E	2.8797E	2.8797E	7.266	7.266	7.266	7.266	0.071
E7ER24	Uncharacterized protein OS=Homo sapiens GN=PMPCB PE=3 SV=1 - [E7ER24_HUMAN]	1.9177E	1.6567E	1.5667E	1.4677E	7.283	7.219	7.195	7.166	0.070
PE2266	40S ribosomal protein S23 OS=Homo sapiens GN=RS23 PE=1 SV=3 - [RS23_HUMAN]	6.6817E	5.2287E	4.7727E	5.3177E	7.825	7.718	7.679	7.772	0.070
Q973U8	60S ribosomal protein L36 OS=Homo sapiens GN=RLP36 PE=1 SV=3 - [RL36_HUMAN]	4.9257E	3.2357E	3.4067E	3.4237E	7.926	7.512	7.532	7.534	0.069
Q973U5	Ribosome maturation protein SBD5 OS=Homo sapiens GN=SBD5 PE=1 SV=4 - [SBD5_HUMAN]	6.6937E	1.5777E	1.4487E	1.2497E	7.198	7.161	7.097	7.198	0.069
Q92488-2	Isomorph 2 of Eukaryotic translation initiation factor 3 subunit 1 OS=Homo sapiens GN=EIF3 PE=1 SV=1 - [EIF3B_HUMAN]	1.9558E	1.0588E	8.5247E	8.9077E	8.040	8.023	7.931	7.995	0.068
P25398	40S ribosomal protein S12 OS=Homo sapiens GN=RS12 PE=1 SV=3 - [RS12_HUMAN]	1.0928E	2.1858E	1.8457E	1.9977E	7.343	7.339	7.266	7.279	0.068
Q51760	Splicing factor, arginine/serine-rich 11 (Fragment) OS=Homo sapiens GN=SF3B1 PE=2 SV=1 - [Q51760_HUMAN]	4.9907E	3.1807E	3.2717E	3.5467E	7.688	7.502	7.515	7.550	0.068
PE3501	Serine/threonine protein phosphatase 5 OS=Homo sapiens GN=PPP5C PE=1 SV=1 - [PPP5_HUMAN]	1.6007E	1.6007E	1.3817E	1.3567E	7.957	7.204	7.140	7.132	0.068
PE2906	Uncharacterized protein OS=Homo sapiens GN=RL1A PE=1 SV=2 - [RL1A_HUMAN]	0.0667E	7.0287E	6.7887E	6.7887E	7.987	7.849	7.849	7.849	0.068
Q9YQ44	Glutamate dehydrogenase OS=Homo sapiens GN=GLUD1 PE=3 SV=1 - [FGYQ44_HUMAN]	2.5688E	2.9357E	2.2267E	2.4787E	7.410	7.468	7.347	7.394	0.068
Q9Y3C4	TP53RK-binding protein OS=Homo sapiens GN=TP53RK PE=1 SV=1 - [TP53RK_HUMAN]	4.6955E	4.6276E	3.3396E	3.3396E	6.622	6.622	6.622	6.622	0.068
Q92958	Protein RC2/28 OS=Homo sapiens GN=RC2 PE=1 SV=2 - [RC2_HUMAN]	2.5177E	1.7787E	1.9527E	1.6827E	7.401	7.250	7.290	7.226	0.067
Q80XK5	DnaJ homology subfamily C member 9 OS=Homo sapiens GN=DNAJ9 PE=1 SV=1 - [DNJC9_HUMAN]	1.7487E	2.3807E	2.1587E	1.6827E	7.241	7.376	7.376	7.376	0.067
P11021	78 kDa glycosylated protein OS=Homo sapiens GN=HSPA5 PE=1 SV=1 - [GRP78_HUMAN]	1.3148E	1.1839E	1.1839E	1.1839E	8.348E	8.269	8.269	8.269	0.067
PE8708	40S ribosomal protein S17 OS=Homo sapiens GN=RS17 PE=1 SV=2 - [RS17_HUMAN]	1.5968E	7.9827E	7.2097E	1.3028E	8.203	7.902	7.858	8.115	0.067
Q80MS2-2	Isomorph 2 of Protein enabled homolog OS=Homo sapiens GN=ENAH - [ENAH_HUMAN]	1.7467E	1.1427E	1.4187E	1.0377E	7.242	7.058	7.152	7.016	0.066
B4DEK4	Uncharacterized protein OS=Homo sapiens GN=SNQ2 PE=2 SV=1 - [B4DEK4_HUMAN]	1.2717E	9.8446E	8.9596E	1.0747E	7.104	6.993	6.934	7.031	0.066
P26816	Proteasome subunit beta type-1 OS=Homo sapiens GN=PSMB1 PE=1 SV=2 - [PSB1_HUMAN]	2.9872E	2.6247E	2.4357E	2.3777E	7.475	7.199	7.386	7.376	0.066
Q14989	Euphorbia 1 OS=Homo sapiens GN=EUPL1 PE=1 SV=1 - [EUP1_HUMAN]	1.1767E	1.1767E	1.1767E	1.1767E	7.084	7.084	7.084	7.084	0.066
P58162	Phosphorylase OS=Homo sapiens GN=PYGL PE=3 SV=1 - [F58162_HUMAN]	1.9347E	2.6127E	1.8847E	1.9897E	7.286	7.417	7.275	7.299	0.066
Q15427	Splicing factor 3B subunit 4 OS=Homo sapiens GN=SF3B4 PE=1 SV=1 - [SF3B4_HUMAN]	1.2207E	1.0747E	1.1097E	8.7726E	7.086	7.031	7.059	7.052	0.065
P28074	Proteasome subunit beta type-5 OS=Homo sapiens GN=PSMB5 PE=1 SV=3 - [PSB5_HUMAN]	2.6997E	1.7637E	1.3687E	1.5987E	7.222	7.246	7.136	7.203	0.064
Q92957	Ras-related protein Rab-1A OS=Homo sapiens GN=RAB1A PE=1 SV=1 - [RAB1A_HUMAN]	1.5148E	1.0397E	1.1187E	1.2977E	7.573	7.380	7.491	7.406	0.064
P09561	U2 small nuclear ribonucleoprotein A OS=Homo sapiens GN=SNRPA1 PE=1 SV=2 - [RU2A_HUMAN]	2.9147E	2.3527E	1.9397E	2.5637E	7.465	7.269	7.299	7.364	0.064
Q972W6	39S ribosomal protein L46, mitochondrial OS=Homo sapiens GN=MRPL46 PE=1 SV=1 - [RM46_HUMAN]	1.7207E	1.2077E	1.2457E	1.2457E	7.236	7.082	7.095	7.159	0.063
P27797	Carectulin OS=Homo sapiens GN=CALR PE=1 SV=1 - [CALR_HUMAN]	1.6948E	1.2228E	1.2318E	1.2578E	8.229	8.087	8.090	8.158	0.063
D3Y718	Uncharacterized protein OS=Homo sapiens GN=RLP32 PE=4 SV=1 - [D3Y718_HUMAN]	1.1258E	7.6327E	8.7137E	7.8997E	8.051	7.883	7.940	7.869	0.063
P46777	60S ribosomal protein L5 OS=Homo sapiens GN=RLP5 PE=1 SV=1 - [R5_HUMAN]	8.1818E	8.2827E	8.5887E	8.1818E	8.140	8.140	8.140	8.140	0.063
Q80ND1	Acetyl-CoA acetyltransferase, cytosolic OS=Homo sapiens GN=ACAT2 PE=1 SV=2 - [THIC_HUMAN]	2.9067E	2.9817E	2.6217E	2.4867E	7.463	7.474	7.419	7.468	0.062
EP9E68	Uncharacterized protein OS=Homo sapiens GN=HSPAL PE=1 SV=1 - [EP9E68_HUMAN]	2.4057E	1.5947E	1.6147E	1.7887E	7.381	7.203	7.202	7.292	0.062
B3KW71	Quinoid dihydropteridine reductase, isoform CRA_e OS=Homo sapiens GN=QDR PE=2 SV=1 - [B3KW71_HUMAN]	8.0146E	7.1026E	6.8166E	6.8166E	6.904	6.808	6.854	6.904	0.062
Q91Q02	Proliferation-associated protein ZGA OS=Homo sapiens GN=PAGZA PE=1 SV=3 - [PAGZA_HUMAN]	9.1688E	1.1198E	8.5807E	9.0227E	7.962	6.899	6.934	7.965	0.061
P46249	Uncharacterized protein OS=Homo sapiens GN=SPR4 PE=1 SV=1 - [SPR4_HUMAN]	0.0007E	6.1887E	6.1887E	6.1887E	6.049	6.049	6.049	6.049	0.061
P46282	40S ribosomal protein S5 OS=Homo sapiens GN=RS5 PE=1 SV=4 - [RS5_HUMAN]	8.0077E	5.8987E	5.9617E	5.9297E	7.903	7.717	7.715	7.716	0.061
F8W7K3	Uncharacterized protein OS=Homo sapiens GN=SP1AN1 PE=4 SV=1 - [F8W7K3_HUMAN]	9.6806E	7.8496E	7.7056E	7.4056E	6.986	6.895	6.890	6.869	0.060
Q96A83	Isoschirimate domain-containing protein 2, mitochondrial OS=Homo sapiens GN=ISOC2 PE=1 SV=1 - [ISOC2_HUMAN]	1.2367E	1.1397E	1.0187E	1.0187E	7.052	7.056	7.008	7.092	0.060
B4D366	Proteasome (Prosome, macropain) 26S subunit, non-ATPase 13, isoform CRA_a OS=Homo sapiens GN=PSMI1	1.2657E	7.9426E	9.3446E	8.1686E	7.120	6.900	6.971	6.912	0.060
PE3313	Thymidine phosphorylase OS=Homo sapiens GN=TPP1 PE=1 SV=1 - [TPP1_HUMAN]	1.0387E								

P31153	S-adenosylmethionine synthase isoform type-2 OS=Homo sapiens GN=MAT2A PE=1 SV=1 - [METK2_HUMAN]	2.37027	2.16127	2.00127	2.32327	7.375	7.335	7.301	7.366	7.355	7.334	0.021
E7ERW8	Uncharacterized protein OS=Homo sapiens GN=DDIAP1 PE=1 SV=1 - [E7ERW8_HUMAN]	4.61926	3.97826	3.86726	4.12226	6.685	6.577	6.587	6.615	6.621	6.601	0.020
940397	Uncharacterized protein OS=Homo sapiens GN=SNRPD3 PE=2 SV=1 - [940397_HUMAN]	1.17038	7.93273	9.93027	8.50727	8.026	7.897	7.920	7.967	7.967	7.967	0.016
P11977	Plastin-3 OS=Homo sapiens GN=PLS3 PE=1 SV=4 - [PLS3_HUMAN]	4.44727	5.30727	4.73927	4.56727	7.648	7.725	7.676	7.680	7.686	7.688	0.019
Q9MJU7	ATP-dependent RNA helicase DDX19A OS=Homo sapiens GN=DDX19A PE=1 SV=1 - [DDX19A_HUMAN]	1.73727	1.92527	1.75627	1.82727	7.240	7.284	7.251	7.262	7.243	7.243	0.019
Q98252	Endoplasmic reticulum resident protein 44 OS=Homo sapiens GN=ERP44 PE=1 SV=1 - [ERP44_HUMAN]	8.06126	8.19426	8.19426	7.28126	6.906	6.913	6.862	6.906	6.888	6.888	0.019
Q9H4N9	SNRPC protein OS=Homo sapiens GN=SNRPG PE=4 SV=1 - [Q9H4N9_HUMAN]	4.33927	4.87527	4.51427	4.39427	7.637	7.688	7.655	7.643	7.663	7.644	0.014
C530K3	Uncharacterized protein OS=Homo sapiens GN=OR8K3 PE=1 SV=1 - [OR8K3_HUMAN]	3.49528	3.49528	2.64328	3.49528	6.307	6.307	6.422	6.459	6.459	6.451	0.014
E9PQ08	Uncharacterized protein OS=Homo sapiens GN=SLUGL2 PE=4 SV=1 - [E9PQ08_HUMAN]	7.59726	6.46226	5.99826	5.98626	6.881	6.670	6.673	6.755	6.753	6.763	0.012
Q9UM54	Pre-mRNA-processing factor 19 OS=Homo sapiens GN=PRPF19 PE=1 SV=1 - [PRPF19_HUMAN]	2.70227	4.50127	3.30827	3.30827	7.432	7.653	7.422	7.520	7.543	7.531	0.012
B4DFL2	Isochorate dehydrogenase [NADP] OS=Homo sapiens GN=IDH2 PE=2 SV=1 - [B4DFL2_HUMAN]	5.38226	6.97326	4.80826	4.03727	6.731	6.990	6.682	7.016	6.860	6.849	0.012
P20E08	Moesin OS=Homo sapiens GN=MSN PE=1 SV=3 - [MOES_HUMAN]	5.27627	3.80727	4.20026	4.41327	7.722	7.580	7.635	7.646	7.651	7.640	0.011
P32341	Radioligand nuclear receptor OS=Homo sapiens GN=RXRB PE=1 SV=1 - [RXRB_HUMAN]	5.27627	4.41326	4.69226	4.69226	7.722	7.580	7.635	7.646	7.651	7.640	0.011
P19338	Nucleolin OS=Homo sapiens GN=NCL PE=1 SV=3 - [NCL_HUMAN]	4.38228	3.31328	3.70228	3.45628	8.642	8.520	8.568	8.573	8.581	8.571	0.010
B7W099	Target of myb1 (Chicken) OS=Homo sapiens GN=TOM1 PE=4 SV=2 - [B7W099_HUMAN]	3.53526	3.22326	3.71026	3.71026	6.548	6.508	6.569	6.548	6.539	6.530	0.010
Q92161	Translational activator GCN1 OS=Homo sapiens GN=GCN1L1 PE=1 SV=6 - [GCN1L1_HUMAN]	1.06427	6.77326	6.65826	1.03727	7.027	6.831	6.823	7.016	6.929	6.920	0.009
E7EQ23	Uncharacterized protein OS=Homo sapiens GN=CSPT1 PE=4 SV=1 - [E7EQ23_HUMAN]	1.16627	1.12727	1.26127	1.53427	7.067	7.238	7.101	7.186	7.152	7.143	0.009
Q9H444	Charged multimeric body protein 4 OS=Homo sapiens GN=CM4B PE=1 SV=1 - [CM4B_HUMAN]	1.51227	8.41326	1.60927	1.60927	7.180	6.925	7.035	7.047	7.052	7.043	0.009
Q94837	Single-stranded DNA-binding protein, mitochondrial OS=Homo sapiens GN=SSBP1 PE=1 SV=1 - [SSBP_HUM]	1.07928	8.30827	9.18827	9.38727	8.033	7.920	7.963	7.973	7.976	7.968	0.008
P98179	Putative RNA-binding protein 3 OS=Homo sapiens GN=RBM3 PE=1 SV=1 - [RBM3_HUMAN]	4.09027	2.23427	2.94727	2.98627	7.612	7.349	7.487	7.475	7.480	7.472	0.008
Q00571	ATP-dependent RNA helicase DDX3X OS=Homo sapiens GN=DDX3X PE=1 SV=3 - [DDX3X_HUMAN]	2.31027	2.62527	2.34627	2.51827	7.364	7.423	7.370	7.401	7.394	7.386	0.008
Q9QK98	Uncharacterized protein OS=Homo sapiens GN=SRP8 PE=2 SV=1 - [Q9QK98_HUMAN]	1.13717	1.27527	1.17127	1.98326	7.137	7.105	7.235	6.993	7.121	7.114	0.008
B7Z206	Uncharacterized protein OS=Homo sapiens GN=ROSL PE=2 SV=1 - [ROSL_HUMAN]	2.01527	1.71217	1.90227	1.76127	7.304	7.236	7.279	7.246	7.270	7.263	0.008
P37837	Transaldolase OS=Homo sapiens GN=TALDO1 PE=1 SV=2 - [TALDO_HUMAN]	3.68727	1.46227	2.52327	2.07627	7.567	7.165	7.402	7.317	7.366	7.360	0.006
B4C288	Uncharacterized protein OS=Homo sapiens GN=FAF2 PE=2 SV=1 - [B4C288_HUMAN]	1.12227	1.06426	1.35627	1.35627	7.050	6.957	7.132	7.050	7.045	7.005	0.006
O95881	Thioredoxin domain-containing protein 12 OS=Homo sapiens GN=TXNDC12 PE=1 SV=1 - [TXNDC12_HUMAN]	1.39527	1.34327	1.35327	1.35327	7.145	7.128	7.131	7.136	7.131	7.131	0.005
Q9NYU2-2	Isoform 2 of UDP-glucosyltransferase 1 OS=Homo sapiens GN=UGT1 - [UGGT1_HUMAN]	9.91276	9.91276	8.53326	9.73526	7.044	6.965	6.931	6.989	6.965	6.960	0.004
Q9Y19-2	Isoform 2 of UDP-glucosyltransferase 1 OS=Homo sapiens GN=UGT1 - [UGGT1_HUMAN]	1.10727	3.80727	4.23527	4.23527	7.145	7.031	7.043	7.033	7.030	7.030	0.004
EPG121	Uncharacterized protein OS=Homo sapiens GN=TSN PE=4 SV=1 - [EPG121_HUMAN]	8.12526	8.91426	5.55626	1.28627	6.910	6.950	6.745	7.109	6.930	6.927	0.003
Q14152	Eukaryotic translation initiation factor 3 subunit A OS=Homo sapiens GN=EIF3A PE=1 SV=1 - [EIF3A_HUMAN]	2.45827	3.00627	2.82327	2.58727	7.391	7.481	7.451	7.413	7.434	7.432	0.002
Q00325-2	Isoform 2 of Phosphate carrier protein, mitochondrial OS=Homo sapiens GN=SLC25A3 - [MPCP_HUMAN]	4.01327	2.60227	2.57727	4.01427	7.603	7.415	7.411	7.604	7.509	7.507	0.002
Q94760-2	Isoform 2 of Lactoylglutathione lyase OS=Homo sapiens GN=GLI1 - [GLI1_HUMAN]	1.17028	5.24927	5.70727	1.06928	8.008	7.720	7.756	8.029	7.894	7.893	0.001
Q12964-2	Isoform 2 of Histone acetyltransferase OS=Homo sapiens GN=HAT2 - [HAT2_HUMAN]	6.90627	4.94727	4.66427	4.66427	7.844	7.607	7.542	7.627	7.623	7.623	0.001
Q9H44-2	Isoform 2 of Eukaryotic translation initiation factor 2A OS=Homo sapiens GN=EIF2A - [EIF2A_HUMAN]	5.30126	5.63726	4.99526	4.99526	6.724	6.724	6.751	6.699	6.724	6.725	-0.001
Q14252	Bifunctional 3'-phosphoadenosine 5'-phosphosulfate synthase 1 OS=Homo sapiens GN=PAPS1 PE=1 SV=2 - [PAPS1_HUMAN]	1.06927	3.75526	8.95926	9.18926	7.029	6.867	6.944	6.963	6.948	6.949	-0.001
PE6780	Casein kinase II subunit beta OS=Homo sapiens GN=CSNK2B PE=1 SV=1 - [CSK2B_HUMAN]	1.11627	1.39127	1.12927	1.38227	7.048	7.143	7.053	7.140	7.095	7.097	-0.001
Q60227-7	Isoform 7 of C-Jun-amino-terminal kinase-interacting protein OS=Homo sapiens GN=SPAG3 - [JIP4_HUMAN]	2.53726	2.49626	2.49626	2.43126	6.309	6.397	6.398	6.398	6.398	6.398	-0.003
B7Z206	Uncharacterized protein OS=Homo sapiens GN=ROSL PE=2 SV=1 - [ROSL_HUMAN]	2.01527	1.71217	1.90227	1.76127	7.304	7.236	7.279	7.246	7.270	7.263	0.002
P06506-3	Isoform 3 of Heterogeneous nuclear ribonucleoprotein Q OS=Homo sapiens GN=SYNCRIP - [HNRQP_HUMAN]	6.05727	3.81627	4.40727	4.36227	7.782	7.582	7.644	7.729	7.682	7.687	-0.005
P10599	Thioredoxin OS=Homo sapiens GN=TXN PE=1 SV=3 - [THIO_HUMAN]	3.81127	2.37727	2.51327	3.68727	7.781	7.376	7.400	7.567	7.479	7.483	-0.005
Q9F811	Anarasin OS=Homo sapiens GN=CIAP1N1 PE=1 SV=2 - [CFN1_HUMAN]	1.49327	1.11627	1.34527	1.26827	7.174	7.048	7.129	7.103	7.111	7.116	-0.005
P61758	Uncharacterized protein OS=Homo sapiens GN=VBP1 PE=1 SV=3 - [P61758_HUMAN]	2.66927	1.99227	2.25327	2.41527	7.426	7.299	7.363	7.363	7.368	7.368	-0.005
P04181	Quinoline aminotransferase OS=Homo sapiens GN=QSOX1 PE=1 SV=1 - [QAT_HUMAN]	3.46927	3.46927	3.46927	3.46927	7.510	7.540	7.582	7.641	7.652	7.652	-0.004
P63999	Activated RNA polymerase II transcriptional coactivator p15 OS=Homo sapiens GN=SUB1 PE=1 SV=3 - [TCF4_HUMAN]	3.34027	1.31718	7.14427	6.57527	7.524	8.137	7.854	7.818	7.830	7.836	-0.006
D68FH4	Uncharacterized protein OS=Homo sapiens GN=CYSB8 PE=1 SV=1 - [D68FH4_HUMAN]	3.36727	3.27927	3.27927	3.47727	7.527	7.516	7.541	7.528	7.528	7.528	-0.006
FRW906	Adenylosuccinate synthase OS=Homo sapiens GN=ADSS PE=3 SV=1 - [FRW906_HUMAN]	1.42827	1.42827	1.44027	1.46227	7.155	7.159	7.165	7.155	7.167	7.167	-0.007
D15116	US snRNP-associated Sm-like protein LSm1 OS=Homo sapiens GN=LSM1 PE=1 SV=1 - [LSM1_HUMAN]	4.73726	6.73726	6.73726	6.16926	6.681	6.883	6.790	6.782	6.792	6.790	-0.008
P10666	Uncharacterized protein OS=Homo sapiens GN=ROSL PE=2 SV=1 - [ROSL_HUMAN]	2.01527	1.71217	1.90227	1.76127	7.304	7.236	7.279	7.246	7.270	7.263	-0.008
Q13867	Bleomycin hydrolase OS=Homo sapiens GN=BLHM PE=1 SV=1 - [BLHM_HUMAN]	1.62327	1.12427	1.52327	1.25427	7.210	7.051	7.183	7.098	7.131	7.141	-0.010
P62312	US snRNP-associated Sm-like protein Lsm6 OS=Homo sapiens GN=LSM6 PE=1 SV=1 - [LSM6_HUMAN]	6.12526	5.26626	5.65626	5.26626	6.787	6.721	6.765	6.754	6.765	6.765	-0.011
B4DM74	Uncharacterized protein OS=Homo sapiens GN=RLP18A PE=2 SV=1 - [B4DM74_HUMAN]	1.77327	1.19327	1.52527	1.46027	7.249	7.077	7.183	7.164	7.163	7.174	-0.011
Q9NR05	Ubiquitin-1 OS=Homo sapiens GN=UBQ1L1 PE=1 SV=2 - [UBQL1_HUMAN]	8.43926	1.50227	1.11227	1.20727	6.926	7.177	7.046	7.062	7.052	7.064	-0.013
P52787	Uncharacterized protein OS=Homo sapiens GN=USO1 PE=1 SV=1 - [USO1_HUMAN]	4.59627	3.89627	3.89627	3.89627	6.592	6.592	6.592	6.592	6.592	6.592	-0.014
AK8318	Uncharacterized protein OS=Homo sapiens GN=PRKCSH PE=2 SV=1 - [AK8318_HUMAN]	4.89127	3.84927	4.63627	4.34427	7.689	7.585	7.666	7.638	7.637	7.652	-0.015
Q3KW3	Uncharacterized protein OS=Homo sapiens GN=HARS PE=4 SV=1 - [Q3KW3_HUMAN]	1.37827	1.44827	1.45027	1.47227	7.139	7.161	7.168	7.150	7.168	7.168	-0.015
A2A8K4	RD RNA binding protein OS=Homo sapiens GN=RDBP PE=4 SV=1 - [A2A8K4_HUMAN]	6.63526	2.26226	4.00126	4.16226	6.822	6.355	6.604	6.608	6.588	6.604	-0.016
US snRNP-associated Sm-like protein LSm3 OS=Homo sapiens GN=LSM3 PE=1 SV=1 - [LSM3_HUMAN]	1.1.63526	1.79227	1.79227	1.67527	7.152	7.253	7.213	7.224	7.203	7.219	7.219	-0.016
P5C276	Uncharacterized protein OS=Homo sapiens GN=USO1 PE=1 SV=1 - [USO1_HUMAN]	6.16526	3.49627	4.89126	4.16226	6.842	6.782	6.830	6.842	6.842	6.842	-0.016
Q9WVC2	40S ribosomal protein S21 OS=Homo sapiens GN=RPS21 PE=2 SV=1 - [Q9WVC2_HUMAN]	9.43827	8.09127	9.01127	9.15227	7.975	7.908	7.955	7.962	7.941	7.958	-0.017
P62277	40S ribosomal protein S13 OS=Homo sapiens GN=RPS13 PE=1 SV=2 - [RPS13_HUMAN]	7.23827	6.11627	6.65127	7.27727	7.865	7.768	7.823	7.862	7.826	7.842	-0.017
Q75354-2	Isoform 2 of Cold shock domain-containing protein E1 OS=Homo sapiens GN=CSD1 - [CSD1_HUMAN]	1.07727	5.43326	8.75026	7.24226	7.032	6.735	6.940	6.860	6.884	6.901	-0.017
P46537	Glossary synthase OS=Homo sapiens GN=GLS PE=1 SV=1 - [GLS_HUMAN]	6.94726	6.94726	6.94726	6.94726	6.842	6.842	6.842	6.842	6.842	6.842	-0.018
D6R206	Uncharacterized protein OS=Homo sapiens GN=WDRL PE=1 SV=1 - [D6R206_HUMAN]	6.05926	6.05926	4.93326	8.13126	6.842	6.782	6.830	6.842	6.842	6.842	-0.019
P08779	Keratin, type I cytoskeletal 16 OS=Homo sapiens GN=KRT16 PE=1 SV=4 - [KIC16_HUMAN]	6.87127	5.21527	6.73727	6.29327	7.837	7.717	7.797	7.799	7.777	7.798	-0.021
Q00211	ATP-dependent RNA helicase A OS=Homo sapiens GN=DHX9 PE=1 SV=4 - [DHX9_HUMAN]	1.94327	1.30027	1.41827	1.29427	7.288	7.115	7.152	7.295	7.202	7.223	-0.022
Q9H451-2	Isoform 2 of Serine/threonine-protein phosphatase PGAMS, mitochondrial OS=Homo sapiens GN=PGAMS - [P	5.54726	2.74926	2.75026	5.83226	6.559	6.439	6.441	6.968	6.744	6.766	-0.022
P05236	60S ribosomal protein L23 OS=Homo sapiens GN=L23 PE=1 SV=1 - [RLA23_HUMAN]	3.61928	3.61928	3.61928	3.61928	8.744	8.439	8.441	8.622	8.499	8.521	-0.022
Q9H460-2	Isoform 2 of 26S proteasome non-ATPase regulatory subunit 1 OS=Homo sapiens GN=PSMD1 - [PSMD1_HUMAN]	4.96276	5.92626	5.85626	1.19027	6.087	6.981	6.933	7.075	7.098	7.098	-0.022
Q9HDC9-2	Isoform 2 of Adipocyte plasma membrane-associated protein OS=Homo sapiens GN=APMAP - [APMAP_HUM]	1.42627	1.54227	1.18427	2.07327	7.154	7.188	7.073	7.317	7.171	7.195	-0.024
Q92598-2	Isoform 2 of Heat shock protein 105 kDa OS=Homo sapiens GN=HSPH1 - [HSPH1_HUMAN]	1.78027	2.39127	2.11927	2.25627	7.250	7.379	7.326	7.353	7.314	7.340	-0.025
G3V4F7	Uncharacterized protein OS=Homo sapiens GN=SRPF PE=4 SV=1 - [G3V4F7_HUMAN]	6.55326	6.03626	8.49326	7.89026	6.816	6.956	6.929	6.897	6.886	6.913	-0.027
P64243	Histone H3.3 OS=Homo sapiens GN=H3.3 PE=1 SV=1 - [H3.3_HUMAN]	1.09327	1.09327	1.09327	1.09327	6.963	6.963	6.963	6.963	6.963	6.963	-0.027
FRW906	Uncharacterized protein OS=Homo sapiens GN=CTSD PE=3 SV=1 - [FRW906_HUMAN]	1.28827	1.69327	1.69327	1.74527	7.157	7.229	7.151	7.242	7.197	7.198	-0

Q9NR30-2	Isoform 2 of Nucleolar RNA helicase 2 OS=Homo sapiens GN=DDX21 - [DDX21_HUMAN]	1.567E7	1.381E7	2.060E7	1.953E7	7.195	7.140	7.314	7.291	7.168	7.302	-0.135
P28072	Proteasome subunit beta type-6 OS=Homo sapiens GN=PSMB6 PE=1 SV=4 - [PSMB_HUMAN]	1.914E7	1.985E7	2.421E7	2.918E7	7.282	7.298	7.384	7.485	7.290	7.425	-0.135
F19494-3	Isoform 3 of heterogeneous nuclear ribonucleoprotein H5 OS=Homo sapiens GN=HNRNP15 - [HNRNP15_HUMAN]	2.207E7	1.649E7	2.558E7	2.656E7	7.344	7.217	7.408	7.424	7.261	7.416	-0.136
P22061	Protein-L-isoaspartate (D-aspartate) O-methyltransferase OS=Homo sapiens GN=PCMT1 PE=1 SV=4 - [PMTL_HUMAN]	5.063E7	8.588E7	1.004E8	8.163E7	7.704	7.934	8.002	7.912	7.819	7.957	-0.138
E9PFD4	Uncharacterized protein OS=Homo sapiens GN=BZV2 PE=4 SV=1 - [E9PFD4_HUMAN]	2.301E6	3.427E6	3.873E6	3.860E6	6.362	6.535	6.588	6.587	6.448	6.587	-0.139
P38159	Heterogeneous nuclear ribonucleoprotein G OS=Homo sapiens GN=HNRPG PE=1 SV=3 - [HNRPG_HUMAN]	3.030E7	2.019E7	3.432E7	3.382E7	7.481	7.305	7.536	7.529	7.393	7.532	-0.139
ABC264	Extracellular signal-regulated kinase 2 splice variant OS=Homo sapiens GN=HRK1 PE=2 SV=1 - [ABC264_HUMAN]	1.320E7	1.499E7	2.301E7	1.999E7	7.120	7.161	7.382	7.120	7.262	-0.141	-0.141
E9PFD2	Uncharacterized protein OS=Homo sapiens GN=HTSF1 PE=4 SV=2 - [E9PFD2_HUMAN]	1.293E7	6.956E6	1.251E7	1.370E7	7.112	6.842	7.101	6.977	7.137	7.137	-0.142
Q13442	28 kDa heat- and acid-stable phosphoprotein OS=Homo sapiens GN=PDAP1 PE=1 SV=1 - [HAP28_HUMAN]		5.828E6	8.355E6	7.852E6		6.766	6.922	6.885	6.766	6.908	-0.143
P23919	Thymidylate kinase OS=Homo sapiens GN=DTYMK PE=1 SV=4 - [KTHY_HUMAN]		4.015E6	5.260E6	5.987E6		6.604	6.721	6.777	6.604	6.749	-0.145
P40429	60S ribosomal protein L13a OS=Homo sapiens GN=RL13A PE=1 SV=2 - [RL13A_HUMAN]	7.175E7	4.387E7	8.294E7	7.427E7	7.856	7.642	7.919	7.871	7.749	7.895	-0.146
E5R054	Uncharacterized protein OS=Homo sapiens GN=PFN1 PE=4 SV=1 - [E5R054_HUMAN]		6.497E6	8.830E6	9.478E6		6.812	6.946	6.977	6.812	6.961	-0.149
P05511-3	Isoform 3 of heterogeneous nuclear ribonucleoprotein A1 OS=Homo sapiens GN=HNRNP1 - [RDA1_HUMAN]	1.517E8	1.345E8	2.095E8	2.941E8	8.196	8.129	8.321	8.310	8.162	8.316	-0.153
E9P773	dCTP pyrophosphatase 1 OS=Homo sapiens GN=DCTP1 PE=1 SV=1 - [DCTP1_HUMAN]	1.099E7	1.757E7	1.802E7	2.181E7	7.041	7.245	7.256	7.339	7.143	7.297	-0.154
Q98R12	39S ribosomal protein L45, mitochondrial OS=Homo sapiens GN=MRPL45 PE=1 SV=2 - [R45_HUMAN]		7.732E6	9.578E6	1.301E7		6.888	6.981	7.114	6.888	7.048	-0.160
O43390	Heterogeneous nuclear ribonucleoprotein R OS=Homo sapiens GN=HNRNP R PE=1 SV=1 - [HNRNP_R_HUMAN]	3.683E7	2.521E7	4.391E7	4.421E7	7.566	7.402	7.643	7.646	7.484	7.644	-0.160
Q3V4W0	Uncharacterized protein OS=Homo sapiens GN=HNRNP C PE=4 SV=1 - [Q3V4W0_HUMAN]	1.518E8	1.098E8	1.989E8	1.788E8	8.181	8.041	8.298	8.252	8.111	8.275	-0.164
Q15785	Mitochondrial import receptor subunit TOM34 OS=Homo sapiens GN=TMOM34 PE=1 SV=2 - [TMOM34_HUMAN]	1.186E7	1.499E6	6.409E6	6.124E6	7.074	6.175	6.807	6.787	6.625	6.797	-0.172
O94776	Metastasis-associated protein 2 OS=Homo sapiens GN=MTA2 PE=1 SV=1 - [MTA2_HUMAN]	4.493E6	3.313E6	5.799E6	6.653	6.520	6.760	6.586	6.760	6.586	6.760	-0.174
P62373	40S ribosomal protein S29 OS=Homo sapiens GN=RPS29 PE=1 SV=2 - [R29_HUMAN]	3.572E7	2.403E7	5.183E7	3.712E7	7.553	7.381	7.715	7.570	7.467	7.642	-0.175
Q97593-2	Isoform 2 of RNA-binding protein 8A OS=Homo sapiens GN=RBMA - [RBMA_HUMAN]	2.822E7	1.964E7	3.052E7	4.431E7	7.451	7.293	7.485	7.647	7.372	7.566	-0.194
Q00796	Scorbutol dehydrogenase OS=Homo sapiens GN=SORD PE=1 SV=4 - [DHSD_HUMAN]	8.868E6	4.228E6	1.083E7	8.538E6	6.948	6.626	7.034	6.932	6.787	6.983	-0.196
Q14566	DNA replication licensing factor MCM6 OS=Homo sapiens GN=MCM6 PE=1 SV=1 - [MCM6_HUMAN]		7.285E6	1.193E7	1.537E7		7.004	6.862	7.077	7.187	6.933	-0.198
Q97256	Coiled-coil domain-containing protein 72 OS=Homo sapiens GN=CCDC72 PE=1 SV=1 - [CCDC72_HUMAN]	1.654E6		2.775E6	2.467E6	6.219		6.443	6.392	6.219	6.418	-0.199
Q8W424-6	Isoform 6 of Titin OS=Homo sapiens GN=TTN - [TTIN_HUMAN]		1.730E7	2.958E7	7.238			7.238	7.441	7.238	7.441	-0.203
P49006	MARCKS-related protein OS=Homo sapiens GN=MARCKSL1 PE=1 SV=2 - [MRP_HUMAN]	6.066E6	5.676E6	7.730E6	1.180E7	6.783	6.754	6.888	7.072	6.768	6.980	-0.211
E5R201	Uncharacterized protein OS=Homo sapiens GN=PGM1 PE=4 SV=1 - [E5R201_HUMAN]		1.378E7	2.259E7	1.378E7		7.139	7.354	7.372	7.139	7.354	-0.215
Q97237	Peptidyl-prolyl cis-trans isomerase NIMA-interacting 4 OS=Homo sapiens GN=PIN4 PE=1 SV=1 - [PIN4_HUMAN]	1.148E7	6.748E7	4.622E7	7.060	7.829	7.665	7.449	7.669	7.445	7.667	-0.222
P22626	Heterogeneous nuclear ribonucleoproteins A2/B1 OS=Homo sapiens GN=HNRNP A2B1 PE=1 SV=2 - [RDA2_HUMAN]	2.561E8	2.096E8	3.858E8	3.877E8	8.408	8.321	8.586	8.589	8.365	8.587	-0.223
P62841	40S ribosomal protein S15 OS=Homo sapiens GN=RPS15 PE=1 SV=1 - [R15_HUMAN]	3.033E7	5.453E7	6.724E7	7.138E7	7.482	7.737	7.828	7.854	7.609	7.841	-0.231
O96019	Actin-like protein 6A OS=Homo sapiens GN=ACTL6A PE=1 SV=1 - [ACTL6A_HUMAN]	3.652E6	9.089E6	9.936E6	6.563	6.959	6.997	6.971	6.997	6.781	6.997	-0.237
Q72H49-2	Isoform 2 of HD domain-containing protein 2 OS=Homo sapiens GN=HDCC2 PE=1 SV=1 - [HDCC2_HUMAN]	5.995E6	6.885E6	9.874E6	1.421E7	6.770	6.825	6.994	7.152	6.798	7.073	-0.276
P26496	Mitochondrial ribosomal protein L27, isoform CRA_c OS=Homo sapiens GN=MRPL27 PE=4 SV=1 - [DGRANL27_HUMAN]	1.802E6	1.921E6	2.562E6	6.256	6.256	6.256	6.256	6.256	6.256	6.256	-0.277
E9PFD1	Uncharacterized protein OS=Homo sapiens GN=NUP155 PE=4 SV=1 - [E9PFD1_HUMAN]	6.800E6	3.516E6	6.493E6	6.800E6	6.546	6.546	6.812	6.838	6.546	6.825	-0.279
Q3V5D9	Uncharacterized protein OS=Homo sapiens GN=APEX1 PE=1 SV=1 - [G3V5D9_HUMAN]	1.802E6	6.386E6	1.503E7	1.051E7	6.834	6.804	7.177	7.022	6.819	7.099	-0.280
P63167	Dynein light chain 1, cytoplasmic OS=Homo sapiens GN=DNLL1 PE=1 SV=1 - [DYL1_HUMAN]	3.916E6	3.294E6	8.145E6	6.152E6	6.593	6.518	6.911	6.789	6.555	6.850	-0.295
Q96H79	Zinc finger CCH-type antiviral protein 2 OS=Homo sapiens GN=ZC3H1V1L PE=1 SV=2 - [ZCCH1V1L_HUMAN]	1.590E6		4.975E6	1.031E7	6.130		6.697	7.013	7.026	6.697	-0.307
P62877	E3 ubiquitin-protein ligase RBX1 OS=Homo sapiens GN=RBX1 PE=1 SV=1 - [RBX1_HUMAN]	1.802E6	6.909E6	1.802E6	7.345E6	6.034	6.839	7.012	6.834	6.837	6.866	-0.323
Q13409-6	Isoform 6 of Cytoplasmic dynein 1 intermediate chain 2 OS=Homo sapiens GN=DYNC12 - [DC12_HUMAN]	8.730E6	1.839E6	8.457E6	6.941	6.265	6.927	6.927	6.603	6.927	-0.324	
P47914	60S ribosomal protein L29 OS=Homo sapiens GN=RL29 PE=1 SV=2 - [R29_HUMAN]	6.107E7	3.912E7	1.319E8	9.069E7	7.786	8.120	7.958	7.689	8.039	-0.350	
Q7L2E3-3	Isoform 3 of Putative ATP-dependent RNA helicase DHX30 OS=Homo sapiens GN=DHX30 - [DHX30_HUMAN]	1.215E6	1.163E6	2.967E6	6.085	6.066	6.085	6.472	6.075	6.472	-0.397	
Q00578	Mitochondrial 2-oxoglutarate/malate carrier protein OS=Homo sapiens GN=SLC25A11 PE=1 SV=3 - [MCOM11_HUMAN]	1.256E7	9.137E6	2.835E7	7.099	6.961	7.453	7.454	7.030	7.453	-0.423	
R8KWC9	Uncharacterized protein OS=Homo sapiens GN=EM4 PE=4 SV=2 - [R8KWC9_HUMAN]	1.022E6	6.909E6	1.022E6	7.345E6	6.034	6.839	7.012	6.834	6.837	6.866	-0.429
D6R9P3	Uncharacterized protein OS=Homo sapiens GN=HNRNP AB PE=4 SV=1 - [D6R9P3_HUMAN]	7.647E7	4.505E7	4.347E7	7.356E8	7.884	7.654	7.638	8.867	7.669	8.252	-0.484
A6M660	Uncharacterized protein OS=Homo sapiens GN=CRY2 PE=1 SV=1 - [A6M660_HUMAN]	2.027E6	8.222E6	1.049E7	1.569E7	6.307	6.915	7.021	7.106	6.611	7.108	-0.487
P30049	ATP synthase subunit delta, mitochondrial OS=Homo sapiens GN=ATP5D PE=1 SV=2 - [ATPD_HUMAN]	6.386E6	5.704E6	1.840E7	1.984E7	6.805	6.756	7.265	7.297	6.781	7.281	-0.500
B4D1C4	Uncharacterized protein OS=Homo sapiens GN=LASP1 PE=2 SV=1 - [B4D1C4_HUMAN]	9.086E5	4.414E6	2.059E6	5.958	6.645	6.645	6.314	5.958	6.479	-0.521	
Q9KCD2-2	Isoform 2 of Methylcrotonyl-CoA carboxylase beta chain, mitochondrial OS=Homo sapiens GN=MCCC2 - [MCCC2_HUMAN]		2.115E6	7.942E6		6.325		6.894	6.325	6.894	-0.569	
C8K1M0	Glutathione reductase delta8-9 alternative splicing variant OS=Homo sapiens GN=GR PE=2 SV=1 - [C8K1M0_HUMAN]	1.194E7	1.079E6	1.335E7	7.077	6.033	7.126	6.655	7.126	-0.570	-0.570	
Q00752	Peptidyl-prolyl cis-trans isomerase D OS=Homo sapiens GN=PPID PE=1 SV=3 - [PPID_HUMAN]	1.464E6		5.538E6	6.165			6.743	6.165	6.743	-0.578	
P61081	NECD8-conjugating enzyme Ubc12 OS=Homo sapiens GN=UBE2M PE=1 SV=1 - [UBC12_HUMAN]	2.871E6	2.349E6	1.148E7	8.771E6	6.458	6.371	7.060	6.943	6.414	7.002	-0.584
P23288	NAD-dependent malic enzyme, mitochondrial OS=Homo sapiens GN=ME2 PE=1 SV=1 - [MCOM_HUMAN]	2.140E6		8.794E6	6.330	6.330	6.944	6.944	6.330	6.944	-0.617	
R8W855	Uncharacterized protein OS=Homo sapiens GN=EM4 PE=4 SV=2 - [R8W855_HUMAN]	2.422E6		1.038E7	1.056E7	6.384		7.012	6.384	7.018	-0.634	
P42765	3-ketoacyl-CoA thiolase, mitochondrial OS=Homo sapiens GN=ACA2A PE=1 SV=2 - [THIM_HUMAN]	8.778E5	1.446E7	1.017E7	5.943	6.905	7.160	7.008	6.424	7.084	-0.660	
Q9PDP3	Exosome complex component RRP41 OS=Homo sapiens GN=EXOSC4 PE=1 SV=3 - [EXOSC4_HUMAN]	9.767E5	8.951E6	5.979E6	5.990	6.952	6.748	5.990	6.850	6.850	-0.860	
Q98R16	Dihydropyrimidinase-related protein 5 OS=Homo sapiens GN=DHPYS5 PE=1 SV=1 - [DHPYS5_HUMAN]			9.063E5				5.957	3	5.957	-2.957	
P50203	Uncharacterized protein OS=Homo sapiens GN=DIABLO PE=4 SV=1 - [F50203_HUMAN]			1.437E6				6.158	3	6.158	-3.158	
Q9K6E7	Pentatricopeptide repeat-containing protein 3, mitochondrial OS=Homo sapiens GN=PTCD3 PE=1 SV=3 - [PTCD3_HUMAN]		1.106E6	4.073E6			6.044		6.010	3	6.327	-3.327
P49756	RNA-binding protein 25 OS=Homo sapiens GN=RBM25 PE=1 SV=3 - [RBM25_HUMAN]			2.279E6				6.358	3	6.358	-3.358	
B4DSY9	Uncharacterized protein OS=Homo sapiens GN=PRPF3 PE=2 SV=1 - [B4DSY9_HUMAN]		2.399E6				6.380		3	6.380	-3.380	
P55265-5	Isoform 5 of Double-stranded RNA-specific adenosine deaminase OS=Homo sapiens GN=ADAR - [DSRAD_HUMAN]		9.380E6	7.252E5			6.972	5.860	3	6.416	-3.416	
Q96L3	39S ribosomal protein L53, mitochondrial OS=Homo sapiens GN=MRPL53 PE=1 SV=1 - [R53_HUMAN]		3.231E6	2.945E6			6.509	6.469	3	6.469	-3.469	
P50X11	Uncharacterized protein OS=Homo sapiens GN=CDG PE=4 SV=1 - [F50X11_HUMAN]			1.915E6				6.505	3	6.505	-3.505	
E9P8T8	Uncharacterized protein OS=Homo sapiens GN=SUMF2 PE=4 SV=1 - [E9P8T8_HUMAN]		3.287E6	4.666E6			6.517	6.669	3	6.593	-3.593	
O75348	V-type proton ATPase subunit G 1 OS=Homo sapiens GN=ATP6V1G1 PE=1 SV=3 - [VATG1_HUMAN]		6.381E6	2.491E6			6.803	6.396	3	6.803	-3.603	
P55957	BH3-interacting domain death agonist OS=Homo sapiens GN=BIID PE=1 SV=1 - [BIID_HUMAN]		8.930E6	2.154E6			6.951	6.333	3	6.642	-3.642	
Q15006	Tetratricopeptide repeat protein 35 OS=Homo sapiens GN=TRC35 PE=1 SV=1 - [TRC35_HUMAN]		6.192E6	3.854E6			6.792	6.586	3	6.669	-3.669	
E5R8H0	Uncharacterized protein OS=Homo sapiens GN=HARP1 PE=4 SV=1 - [E5R8H0_HUMAN]			4.903E6			6.890	6.890	3	6.890	-3.890	
A6M4A2	Ubiquitin carboxyl-terminal hydrolase OS=Homo sapiens GN=USP14 PE=3 SV=1 - [A6M4A2_HUMAN]		3.656E6	7.134E6			6.563	6.853	3	6.708	-3.708	
E5RFP0	Uncharacterized protein OS=Homo sapiens GN=NUDC2 PE=4 SV=1 - [E5RFP0_HUMAN]		6.891E6	5.752E6			6.939	6.760	3	6.849	-3.849	
A6M1C4	Uncharacterized protein OS=Homo sapiens GN=ATXN10 PE=2 SV=4 - [A6M1C4_HUMAN]		9.533E6	5.399E6			6.979	6.732	3	6.856	-3.856	
Q974W6	ATG3-like protein 2 OS=Homo sapiens GN=ATG3L2 PE=1 SV=2 - [ATG3L2_HUMAN]		8.272E6	7.291E6			6.863	6.863	3	6.863	-3.863	
B7Z5P0	Nucleotide binding protein 2 (MnD homolog, E. coli), isoform CRA_d OS=Homo sapiens GN=NBP2 PE=2 SV=1 - [B7Z5P0_HUMAN]		8.827E6	7.129E6			6.946	6.853	3	6.899	-3.899	
Q9P961	Endophilin-A2 OS=Homo sapiens GN=SH3GL1 PE=1 SV=1 - [SH3G1_HUMAN]		6.103E6	1.038E7			6.786	7.016	3	6.901	-3.901	
P46976-3	Isoform GN-15 of Glycogenin-1 OS=Homo sapiens GN=GYGI - [GLYG_HUMAN]		6.495E6	1.005E7			6.813	7.002	3	6.907	-3.907	
Q9UJ12	ATPase inhibitor, mitochondrial OS=Homo sapiens GN=ATPIF1 PE=1 SV=1 - [ATPIF1_HUMAN]		8.615E6				6.935	3	6.935	-3.935		
Q96H24-3	Isoform 3 of Ran-binding protein 3 OS=Homo sapiens GN=RBND3 - [RBND3_HUMAN]		7.852E6	9.550E6			6.895	6.980	3	6.837	-3.937	
P50QW2	Uncharacterized protein OS=Homo sapiens GN=TF15 PE=4 SV=1 - [F50QW2_HUMAN]			8.944E6			6.952	6.952	3	6.852	-3.852	
E7EV06	Uncharacterized protein OS=Homo sapiens GN=SLC3A3R1 PE=4 SV=1 - [E7EV06_HUMAN]		8.828E6				6.992	3	6.992	-3.992		
Q1KMD3	Heterogeneous nuclear ribonucleoprotein U-like protein 2 OS=Homo sapiens GN=HNRNPUL2 PE=1 SV=1 - [HNRNPUL2_HUMAN]		1.231E7									

Extended Table 2

Histones, histone modifying proteins

Accession	Description	Identified Previously	Ratio H/C
P62805	Histone H4 OS=Homo sapiens GN=HIST1H4A PE=1 SV=2 - [H4_HUMAN]		0.370
P04908	Histone H2A type 1-B/E OS=Homo sapiens GN=HIST1H2AB PE=1 SV=2 - [H2A1B_HUMAN]		0.257
Q16777	Histone H2A type 2-C OS=Homo sapiens GN=HIST2H2AC PE=1 SV=4 - [H2A2C_HUMAN]		0.194
O60814	Histone H2B type 1-K OS=Homo sapiens GN=HIST1H2BK PE=1 SV=3 - [H2B1K_HUMAN]		0.174
O14929-2	Isoform B of Histone acetyltransferase type B catalytic subunit OS=Homo sapiens GN=HAT1 - [HAT1_HUMAN]		0.168
Q09028-3	Isoform 3 of Histone-binding protein RBBP4 OS=Homo sapiens GN=RBBP4 - [RBBP4_HUMAN]		0.143
Q86X55-2	Isoform 2 of Histone-arginine methyltransferase CARM1 OS=Homo sapiens GN=CARM1 - [CARM1_HUMAN]		0.120
Q92522	Histone H1x OS=Homo sapiens GN=H1FX PE=1 SV=1 - [H1X_HUMAN]		0.117
P16403	Histone H1.2 OS=Homo sapiens GN=HIST1H1C PE=1 SV=2 - [H12_HUMAN]		0.098
P10412	Histone H1.4 OS=Homo sapiens GN=HIST1H1E PE=1 SV=2 - [H14_HUMAN]		0.082
P84243	Histone H3.3 OS=Homo sapiens GN=H3F3A PE=1 SV=2 - [H33_HUMAN]		-0.027

ADP and ADP-ribose metabolism

Accession	Description	Identified Previously	Ratio H/C
O75874	Iso citrate dehydrogenase [NADP] cytoplasmic OS=Homo sapiens GN=IDH1 PE=1 SV=2 - [IDHC_HUMAN]		0.333
P53597	Succinyl-CoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial OS=Homo sapiens GN=SUCLG1 PE=1 SV=4 - [SUCA_HUMAN]		0.315
P30043	Flavin reductase (NADPH) OS=Homo sapiens GN=BLVRB PE=1 SV=3 - [BLVRB_HUMAN]		0.313
P09874	Poly [ADP-ribose] polymerase 1 OS=Homo sapiens GN=PARP1 PE=1 SV=4 - [PARP1_HUMAN]		0.280
P61204	ADP-ribosylation factor 3 OS=Homo sapiens GN=ARF3 PE=1 SV=2 - [ARF3_HUMAN]		0.220
P16152	Carbonyl reductase [NADPH] 1 OS=Homo sapiens GN=CBR1 PE=1 SV=3 - [CBR1_HUMAN]		0.197
P05141	ADP/ATP translocase 2 OS=Homo sapiens GN=SLC25A5 PE=1 SV=7 - [ADT2_HUMAN]		0.156
P12236	ADP/ATP translocase 3 OS=Homo sapiens GN=SLC25A6 PE=1 SV=4 - [ADT3_HUMAN]		0.126
Q9UJY4	ADP-ribosylation factor-binding protein GGA2 OS=Homo sapiens GN=GGA2 PE=1 SV=3 - [GGA2_HUMAN]		0.073
Q4DFL2	Iso citrate dehydrogenase [NADP] OS=Homo sapiens GN=IDH2 PE=2 SV=1 - [B4DFL2_HUMAN]		0.012
P11908	Ribose-phosphate pyrophosphokinase 2 OS=Homo sapiens GN=PRPS2 PE=1 SV=2 - [PRPS2_HUMAN]		0.157
P60891	Ribose-phosphate pyrophosphokinase 1 OS=Homo sapiens GN=PRPS1 PE=1 SV=2 - [PRPS1_HUMAN]		0.091
Q9UKK9	ADP-sugar pyrophosphatase OS=Homo sapiens GN=NUDT5 PE=1 SV=1 - [NUDT5_HUMAN]		0.366

ATP synthesis, metabolism

Accession	Description	Identified Previously	Ratio H/C
P56385	ATP synthase subunit e, mitochondrial OS=Homo sapiens GN=ATP5I PE=1 SV=2 - [ATP5I_HUMAN]		4.326
ABMUN4	Uncharacterized protein OS=Homo sapiens GN=ATP6V1E1 PE=2 SV=1 - [ABMUN4_HUMAN]		0.470
P21281	V-type proton ATPase subunit B, brain isoform OS=Homo sapiens GN=ATP6V1B2 PE=1 SV=3 - [VATB2_HUMAN]		0.386
Q9NVI7-2	Isoform 2 of ATPase family AAA domain-containing protein 3A OS=Homo sapiens GN=ATAD3A - [ATD3A_HUMAN]		0.283
P55072	Transitional endoplasmic reticulum ATPase OS=Homo sapiens GN=VCP PE=1 SV=4 - [TERA_HUMAN]		0.218
P55036	26S proteasome non-ATPase regulatory subunit 4 OS=Homo sapiens GN=PSMD4 PE=1 SV=1 - [PSMD4_HUMAN]		0.214
O95433	Activator of 90 kDa heat shock protein ATPase homolog 1 OS=Homo sapiens GN=AHS1 PE=1 SV=1 - [AHS1_HUMAN]		0.203
B1AJY5	Proteasome (Prosome, macropain) 26S subunit, non-ATPase, 10 OS=Homo sapiens GN=PSMD10 PE=4 SV=1 - [B1AJY5_HUMAN]		0.189
O00487	26S proteasome non-ATPase regulatory subunit 14 OS=Homo sapiens GN=PSMD14 PE=1 SV=1 - [PSDE_HUMAN]		0.188
B7Z3U6	ATPase, Na+/K+ transporting, alpha 1 polypeptide, isoform CRA_a OS=Homo sapiens GN=ATP1A1 PE=2 SV=1 - [B7Z3U6_HUMAN]		0.179
P36542	ATP synthase subunit gamma, mitochondrial OS=Homo sapiens GN=ATP5C1 PE=1 SV=1 - [ATPG_HUMAN]		0.172
P06576	ATP synthase subunit beta, mitochondrial OS=Homo sapiens GN=ATP5B PE=1 SV=3 - [ATPB_HUMAN]		0.171
P25705	ATP synthase subunit alpha, mitochondrial OS=Homo sapiens GN=ATP5A1 PE=1 SV=1 - [ATPA_HUMAN]		0.170
Q15008	26S proteasome non-ATPase regulatory subunit 6 OS=Homo sapiens GN=PSMD6 PE=1 SV=1 - [PSMD6_HUMAN]		0.170
C9J8H9	Uncharacterized protein OS=Homo sapiens GN=ATP5J2 PE=4 SV=1 - [C9J8H9_HUMAN]		0.162
Q13200	26S proteasome non-ATPase regulatory subunit 2 OS=Homo sapiens GN=PSMD2 PE=1 SV=3 - [PSMD2_HUMAN]		0.161
O75947-2	Isoform 2 of ATP synthase subunit d, mitochondrial OS=Homo sapiens GN=ATP5H - [ATPSH_HUMAN]		0.158
P05141	ADP/ATP translocase 2 OS=Homo sapiens GN=SLC25A5 PE=1 SV=7 - [ADT2_HUMAN]		0.156
P26196	Probable ATP-dependent RNA helicase DDX6 OS=Homo sapiens GN=DDX6 PE=1 SV=2 - [DDX6_HUMAN]		0.152
P24539	ATP synthase subunit b, mitochondrial OS=Homo sapiens GN=ATP5F1 PE=1 SV=2 - [AT5F1_HUMAN]		0.149
B7Z1R5	Uncharacterized protein OS=Homo sapiens GN=ATP6V1A PE=2 SV=1 - [B7Z1R5_HUMAN]		0.145
O00232	26S proteasome non-ATPase regulatory subunit 12 OS=Homo sapiens GN=PSMD12 PE=1 SV=3 - [PSD12_HUMAN]		0.140
P48047	ATP synthase subunit O, mitochondrial OS=Homo sapiens GN=ATP5O PE=1 SV=1 - [ATPO_HUMAN]		0.139
P12236	ADP/ATP translocase 3 OS=Homo sapiens GN=SLC25A6 PE=1 SV=4 - [ADT3_HUMAN]		0.126
P51665	26S proteasome non-ATPase regulatory subunit 7 OS=Homo sapiens GN=PSMD7 PE=1 SV=2 - [PSD7_HUMAN]		0.111
C9JA36	Uncharacterized protein OS=Homo sapiens GN=ATP1B3 PE=3 SV=1 - [C9JA36_HUMAN]		0.110
O00231	26S proteasome non-ATPase regulatory subunit 11 OS=Homo sapiens GN=PSMD11 PE=1 SV=3 - [PSD11_HUMAN]		0.110
Q9NTK5	Obg-like ATPase 1 OS=Homo sapiens GN=OLA1 PE=1 SV=2 - [OLA1_HUMAN]		0.103
Q92499	ATP-dependent RNA helicase DDX1 OS=Homo sapiens GN=DDX1 PE=1 SV=2 - [DDX1_HUMAN]		0.103
P17844	Probable ATP-dependent RNA helicase DDX5 OS=Homo sapiens GN=DDX5 PE=1 SV=1 - [DDX5_HUMAN]		0.087
E9PN17	Uncharacterized protein OS=Homo sapiens GN=ATP5L PE=4 SV=1 - [E9PN17_HUMAN]		0.082
B4DJ66	Proteasome (Prosome, macropain) 26S subunit, non-ATPase, 13, isoform CRA_d OS=Homo sapiens GN=PSMD13 PE=2 SV=1 - [B4DJ66_HUMAN]		0.060
P53396	ATP-citrate synthase OS=Homo sapiens GN=ACLY PE=1 SV=3 - [ACLY_HUMAN]		0.057
Q92841-4	Isoform 4 of Probable ATP-dependent RNA helicase DDX17 OS=Homo sapiens GN=DDX17 - [DDX17_HUMAN]		0.056
Q7L014	Probable ATP-dependent RNA helicase DDX46 OS=Homo sapiens GN=DDX46 PE=1 SV=2 - [DDX46_HUMAN]		0.040
Q9NUU7	ATP-dependent RNA helicase DDX19A OS=Homo sapiens GN=DDX19A PE=1 SV=1 - [DD19A_HUMAN]		0.019
O00571	ATP-dependent RNA helicase DDX3X OS=Homo sapiens GN=DDX3X PE=1 SV=3 - [DDX3X_HUMAN]		0.008
Q08211	ATP-dependent RNA helicase A OS=Homo sapiens GN=DHX9 PE=1 SV=4 - [DHX9_HUMAN]		-0.022
Q99460-2	Isoform 2 of 26S proteasome non-ATPase regulatory subunit 1 OS=Homo sapiens GN=PSMD1 - [PSMD1_HUMAN]		-0.023
P61221	ATP-binding cassette sub-family E member 1 OS=Homo sapiens GN=ABCE1 PE=1 SV=1 - [ABCE1_HUMAN]		-0.055
P18859	ATP synthase-coupling factor 6, mitochondrial OS=Homo sapiens GN=ATP5J PE=1 SV=1 - [ATP5J_HUMAN]		-0.059
Q7L2E3-3	Isoform 3 of Putative ATP-dependent RNA helicase DHX30 OS=Homo sapiens GN=DHX30 - [DHX30_HUMAN]		-0.397
P30049	ATP synthase subunit delta, mitochondrial OS=Homo sapiens GN=ATP5D PE=1 SV=2 - [ATPD_HUMAN]		-0.500
O75348	V-type proton ATPase subunit G 1 OS=Homo sapiens GN=ATP6V1G1 PE=1 SV=3 - [VATG1_HUMAN]		-3.600
Q9UII2	ATPase inhibitor, mitochondrial OS=Homo sapiens GN=ATPIF1 PE=1 SV=1 - [ATIF1_HUMAN]		-3.935

NAD metabolism

Accession	Description	Ratio H/C
Q95182	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 7 OS=Homo sapiens GN=NDUFA7 PE=1 SV=3 - [NDUA7_HUMAN]	3.672
Q9P0J0	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 13 OS=Homo sapiens GN=NDUFA13 PE=1 SV=3 - [NDUAD_HUMAN]	0.784
O75874	Isocitrate dehydrogenase [NADP] cytoplasmic OS=Homo sapiens GN=IDH1 PE=1 SV=2 - [IDHC_HUMAN]	0.333
P30043	Flavin reductase (NADPH) OS=Homo sapiens GN=BLVRB PE=1 SV=3 - [BLVRB_HUMAN]	0.313
P16152	Carbonyl reductase [NADPH] 1 OS=Homo sapiens GN=CBR1 PE=1 SV=3 - [CBR1_HUMAN]	0.197
Q9BU61	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex assembly factor 3 OS=Homo sapiens GN=NDUFAF3 PE=1 SV=1 - [NDUF3_HUMAN]	0.142
P50213	Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial OS=Homo sapiens GN=IDH3A PE=1 SV=1 - [IDH3A_HUMAN]	0.098
P00387-2	Isoform 2 of NADH-cytochrome b5 reductase 3 OS=Homo sapiens GN=CYB5R3 - [NB5R3_HUMAN]	0.078
B4DFL2	Isocitrate dehydrogenase [NADP] OS=Homo sapiens GN=IDH2 PE=2 SV=1 - [B4DFL2_HUMAN]	0.012
Q96II6	NADH dehydrogenase (Ubiquinone) 1 beta subcomplex, 10, 22kDa, isoform CRA_a OS=Homo sapiens GN=NDUFB10 PE=2 SV=1 - [Q96II6_HUMAN]	-0.053
P23368	NAD-dependent malic enzyme, mitochondrial OS=Homo sapiens GN=ME2 PE=1 SV=1 - [MAOM_HUMAN]	-0.614

Kinases, Kinase regulatory proteins

Accession	Description	Ratio H/C
Q9UNF0-2	Isoform 2 of Protein kinase C and casein kinase substrate in neurons protein 2 OS=Homo sapiens GN=PACIN2 - [PACIN2_HUMAN]	0.834
P36507	Dual specificity mitogen-activated protein kinase kinase 2 OS=Homo sapiens GN=MAP2K2 PE=1 SV=1 - [MP2K2_HUMAN]	0.346
P22392-2	Isoform 3 of Nucleoside diphosphate kinase B OS=Homo sapiens GN=NME2 - [NDKB_HUMAN]	0.297
Q9H1E3	Nuclear ubiquitous casein and cyclin-dependent kinases substrate OS=Homo sapiens GN=NUCKS1 PE=1 SV=1 - [NUCKS_HUMAN]	0.285
P00558	Phosphoglycerate kinase 1 OS=Homo sapiens GN=PGK1 PE=1 SV=3 - [PGK1_HUMAN]	0.262
P61024	Cyclin-dependent kinases regulatory subunit 1 OS=Homo sapiens GN=CKS1B PE=1 SV=1 - [CKS1_HUMAN]	0.238
Q9BZK2	Uridine-cytidine kinase 2 OS=Homo sapiens GN=UCK2 PE=1 SV=1 - [UCK2_HUMAN]	0.220
Q16822	Phosphoenolpyruvate carboxykinase [GTP], mitochondrial OS=Homo sapiens GN=PCK2 PE=1 SV=3 - [PCKGM_HUMAN]	0.204
P06493	Cyclin-dependent kinase 1 OS=Homo sapiens GN=CDK1 PE=1 SV=3 - [CDK1_HUMAN]	0.175
P00568	Adenylate kinase isoenzyme 1 OS=Homo sapiens GN=AK1 PE=1 SV=3 - [KAD1_HUMAN]	0.174
P11908	Ribose-phosphate pyrophosphokinase 2 OS=Homo sapiens GN=PRPS2 PE=1 SV=2 - [PRPS2_HUMAN]	0.157
Q9H0C8	Integrin-linked kinase-associated serine/threonine phosphatase 2C OS=Homo sapiens GN=ILKAP PE=1 SV=1 - [ILKAP_HUMAN]	0.144
P42771	Cyclin-dependent kinase inhibitor 2A, isoforms 1/2/3 OS=Homo sapiens GN=CDKN2A PE=1 SV=2 - [CD2A1_HUMAN]	0.137
P12532	Creatine kinase U-type, mitochondrial OS=Homo sapiens GN=CKMT1A PE=1 SV=1 - [KCRU_HUMAN]	0.122
Q9Y3F4	Serine-threonine kinase receptor-associated protein OS=Homo sapiens GN=STRAP PE=1 SV=1 - [STRAP_HUMAN]	0.117
P78527	DNA-dependent protein kinase catalytic subunit OS=Homo sapiens GN=PRKDC PE=1 SV=3 - [PRKDC_HUMAN]	0.111
P60891	Ribose-phosphate pyrophosphokinase 1 OS=Homo sapiens GN=PRPS1 PE=1 SV=2 - [PRPS1_HUMAN]	0.091
P12277	Creatine kinase B-type OS=Homo sapiens GN=CKB PE=1 SV=1 - [KCRB_HUMAN]	0.087
P14618	Pyruvate kinase isozymes M1/M2 OS=Homo sapiens GN=PKM2 PE=1 SV=4 - [KPYM_HUMAN]	0.076
P67870	Casein kinase II subunit beta OS=Homo sapiens GN=CSNK2B PE=1 SV=1 - [CSK2B_HUMAN]	-0.001
O60271-7	Isoform 7 of C-Jun-amino-terminal kinase-interacting protein 4 OS=Homo sapiens GN=SPAG9 - [JIP4_HUMAN]	-0.003
A8CZ64	Extracellular signal-regulated kinase-2 splice variant OS=Homo sapiens GN=MAPK1 PE=2 SV=1 - [A8CZ64_HUMAN]	-0.141
P23919	Thymidylate kinase OS=Homo sapiens GN=DTYMK PE=1 SV=4 - [KTHY_HUMAN]	-0.145

Phosphatases

Accession	Description	Ratio H/C
P62140	Serine/threonine-protein phosphatase PP1-beta catalytic subunit OS=Homo sapiens GN=PPP1CB PE=1 SV=3 - [PP1B_HUMAN]	0.244
Q9BSD7	Cancer-related nucleoside-triphosphatase OS=Homo sapiens GN=NTPCR PE=1 SV=1 - [NTPCR_HUMAN]	0.218
P24666	Low molecular weight phosphotyrosine protein phosphatase OS=Homo sapiens GN=ACP1 PE=1 SV=3 - [PPAC_HUMAN]	0.204
F8VYE8	Serine/threonine-protein phosphatase OS=Homo sapiens GN=PPP1CC PE=3 SV=1 - [F8VYE8_HUMAN]	0.197
Q9NRX4	14 kDa phosphohistidine phosphatase OS=Homo sapiens GN=PHPT1 PE=1 SV=1 - [PHP14_HUMAN]	0.147
Q9H0C8	Integrin-linked kinase-associated serine/threonine phosphatase 2C OS=Homo sapiens GN=ILKAP PE=1 SV=1 - [ILKAP_HUMAN]	0.144
Q15181	Inorganic pyrophosphatase OS=Homo sapiens GN=PPA1 PE=1 SV=2 - [IPYR_HUMAN]	0.143
Q9H2U2-3	Isoform 3 of Inorganic pyrophosphatase 2, mitochondrial OS=Homo sapiens GN=PPA2 - [IPYR2_HUMAN]	0.140
P62714	Serine/threonine-protein phosphatase 2A catalytic subunit beta isoform OS=Homo sapiens GN=PPP2CB PE=1 SV=1 - [PP2AB_HUMAN]	0.138
Q96C90	Protein phosphatase 1 regulatory subunit 14B OS=Homo sapiens GN=PPP1R14B PE=1 SV=3 - [PP14B_HUMAN]	0.127
P53041	Serine/threonine-protein phosphatase 5 OS=Homo sapiens GN=PPP5C PE=1 SV=1 - [PPP5_HUMAN]	0.068
E9PMD7	Serine/threonine-protein phosphatase OS=Homo sapiens GN=PPP1CA PE=3 SV=1 - [E9PMD7_HUMAN]	0.058
O15355	Protein phosphatase 1G OS=Homo sapiens GN=PPM1G PE=1 SV=1 - [PPM1G_HUMAN]	0.052
Q96HS1-2	Isoform 2 of Serine/threonine-protein phosphatase PGAM5, mitochondrial OS=Homo sapiens GN=PGAM5 - [PGAM5_HUMAN]	-0.022
Q9H773	dCTP pyrophosphatase 1 OS=Homo sapiens GN=DCTPP1 PE=1 SV=1 - [DCTP1_HUMAN]	-0.154

Extended Table 3: PAR-Mass Spec GO Biological Process enrichment Control (T0) Proteins

Control Proteins GO Biological Process Enrichment	# Genes in Gene Set (K)	# Genes in Overlap (k)	k/K	p-value	FDR q-value
ORGANELLE_ORGANIZATION_AND_BIOGENESIS	473	8	0.0169	3.12E-06	2.58E-03
ONE_CARBON_COMPOUND_METABOLIC_PROCESS	26	3	0.1154	1.59E-05	6.58E-03
MITOCHONDRION_ORGANIZATION_AND_BIOGENESIS	48	3	0.0625	1.03E-04	2.83E-02
PROTEIN_TARGETING_TO_MITOCHONDRION	11	2	0.1818	1.88E-04	3.88E-02

Extended Table 4: PAR-Mass Spec GO Biological Process enrichment Hormone (T30) Proteins

Control Proteins GO Biological Process Enrichment	# Genes in Gene Set	# Genes in Overlap	k/K	p-value	FDR q-value
ESTABLISHMENT_OF_LOCALIZATION	870	50	0.0575	0.00E+00	0.00E+00
TRANSPORT	795	46	0.0579	0.00E+00	0.00E+00
BIOPOLYMER_METABOLIC_PROCESS	1684	104	0.0618	0.00E+00	0.00E+00
CELLULAR_PROTEIN_METABOLIC_PROCESS	1117	79	0.0707	0.00E+00	0.00E+00
CELLULAR_MACROMOLECULE_METABOLIC_PROCESS	1131	80	0.0707	0.00E+00	0.00E+00
RNA_METABOLIC_PROCESS	841	60	0.0713	0.00E+00	0.00E+00
PROTEIN_METABOLIC_PROCESS	1231	90	0.0731	0.00E+00	0.00E+00
NUCLEOBASENUCLEOSIDENUCLEOTIDE_AND_NUCLEIC_ACID_METABOLIC_PROCESS	1244	102	0.082	0.00E+00	0.00E+00
ORGANELLE_ORGANIZATION_AND_BIOGENESIS	473	40	0.0846	0.00E+00	0.00E+00
MACROMOLECULE_BIOSYNTHETIC_PROCESS	321	32	0.0997	0.00E+00	0.00E+00
BIOSYNTHETIC_PROCESS	470	49	0.1043	0.00E+00	0.00E+00
CELLULAR_COMPONENT_ASSEMBLY	298	33	0.1107	0.00E+00	0.00E+00
MACROMOLECULAR_COMPLEX_ASSEMBLY	280	33	0.1179	0.00E+00	0.00E+00
CATABOLIC_PROCESS	225	28	0.1244	0.00E+00	0.00E+00
CELLULAR_CATABOLIC_PROCESS	212	28	0.1321	0.00E+00	0.00E+00
CELLULAR_BIOSYNTHETIC_PROCESS	321	45	0.1402	0.00E+00	0.00E+00
RNA_PROCESSING	173	28	0.1618	0.00E+00	0.00E+00
TRANSLATION	180	31	0.1722	0.00E+00	0.00E+00
DNA_METABOLIC_PROCESS	257	27	0.1051	1.11E-16	4.82E-15
APOPTOSIS_GO	431	32	0.0742	2.33E-15	9.58E-14
PROGRAMMED_CELL_DEATH	432	32	0.0741	2.55E-15	9.58E-14
RNA_SPLICING	91	17	0.1868	2.55E-15	9.58E-14
ESTABLISHMENT_OF_CELLULAR_LOCALIZATION	353	29	0.0822	3.66E-15	1.31E-13
INTRACELLULAR_TRANSPORT	280	26	0.0929	5.44E-15	1.87E-13
MRNA_METABOLIC_PROCESS	84	16	0.1905	1.21E-14	3.98E-13
CELLULAR_LOCALIZATION	371	29	0.0782	1.32E-14	4.19E-13
PROTEIN_FOLDING	58	14	0.2414	1.63E-14	4.99E-13
MRNA_PROCESSING_GO_0006397	73	15	0.2055	2.49E-14	7.33E-13
REGULATION_OF_CELLULAR_METABOLIC_PROCESS	787	40	0.0508	2.35E-13	6.68E-12
CELL_DEVELOPMENT	577	34	0.0589	2.59E-13	7.13E-12
REGULATION_OF_METABOLIC_PROCESS	799	40	0.0501	3.79E-13	1.01E-11
CARBOXYLIC_ACID_METABOLIC_PROCESS	178	19	0.1067	2.14E-12	5.53E-11
ORGANIC_ACID_METABOLIC_PROCESS	180	19	0.1056	2.62E-12	6.55E-11
REGULATION_OF_APOPTOSIS	341	25	0.0733	3.66E-12	8.87E-11
REGULATION_OF_PROGRAMMED_CELL_DEATH	342	25	0.0731	3.90E-12	9.19E-11
TRANSCRIPTION	753	37	0.0491	5.09E-12	1.17E-10
REGULATION_OF_DEVELOPMENTAL_PROCESS	440	28	0.0636	5.59E-12	1.25E-10
RESPONSE_TO_STRESS	508	30	0.0591	6.34E-12	1.38E-10
NEGATIVE_REGULATION_OF_CELLULAR_PROCESS	646	32	0.0495	1.17E-10	2.46E-09
NEGATIVE_REGULATION_OF_APOPTOSIS	150	16	0.1067	1.19E-10	2.46E-09
NEGATIVE_REGULATION_OF_PROGRAMMED_CELL_DEATH	151	16	0.106	1.32E-10	2.65E-09
MACROMOLECULE_CATABOLIC_PROCESS	137	15	0.1095	3.13E-10	6.14E-09
NEGATIVE_REGULATION_OF_BIOLOGICAL_PROCESS	677	32	0.0473	3.76E-10	7.22E-09
ESTABLISHMENT_OF_PROTEIN_LOCALIZATION	190	17	0.0895	5.03E-10	9.42E-09
DNA_REPLICATION	102	13	0.1275	7.15E-10	1.31E-08
GENERATION_OF_PRECURSOR_METABOLITES_AND_ENERGY	123	14	0.1138	7.28E-10	1.31E-08
NEGATIVE_REGULATION_OF_DEVELOPMENTAL_PROCESS	197	17	0.0863	8.80E-10	1.54E-08
PROTEIN_RNA_COMPLEX_ASSEMBLY	67	11	0.1642	9.22E-10	1.59E-08
RIBONUCLEOPROTEIN_COMPLEX_BIOGENESIS_AND_ASSEMBLY	86	12	0.1395	1.11E-09	1.88E-08
NITROGEN_COMPOUND_METABOLIC_PROCESS	155	15	0.0968	1.78E-09	2.93E-08
MACROMOLECULE_LOCALIZATION	235	18	0.0766	1.92E-09	3.11E-08
PROTEIN_TRANSPORT	157	15	0.0955	2.12E-09	3.37E-08
CELLULAR_RESPIRATION	19	7	0.3684	2.39E-09	3.65E-08
TRNA_METABOLIC_PROCESS	19	7	0.3684	2.39E-09	3.65E-08
PROTEIN_LOCALIZATION	214	17	0.0794	3.12E-09	4.68E-08
PROTEIN_COMPLEX_ASSEMBLY	167	15	0.0898	4.97E-09	7.32E-08
REGULATION_OF_GENE_EXPRESSION	673	30	0.0446	5.14E-09	7.43E-08
TRANSCRIPTION_DNA_DEPENDENT	636	29	0.0456	5.63E-09	8.00E-08
RNA_BIOSYNTHETIC_PROCESS	638	29	0.0455	6.03E-09	8.43E-08
CELLULAR_COMPONENT_DISASSEMBLY	33	8	0.2424	7.18E-09	9.87E-08
AMINO_ACID_AND_DERIVATIVE_METABOLIC_PROCESS	101	12	0.1188	7.30E-09	9.87E-08
REGULATION_OF_CELLULAR_COMPONENT_ORGANIZATION_AND_BIOGENESIS	125	13	0.104	8.95E-09	1.19E-07
CELLULAR_LIPID_CATABOLIC_PROCESS	35	8	0.2286	1.19E-08	1.56E-07
SIGNAL_TRANSDUCTION	1634	50	0.0306	1.71E-08	2.21E-07
ALCOHOL_METABOLIC_PROCESS	88	11	0.125	1.80E-08	2.29E-07
ENERGY_DERIVATION_BY_OXIDATION_OF_ORGANIC_COMPOUNDS	37	8	0.2162	1.91E-08	2.39E-07
LIPID_CATABOLIC_PROCESS	38	8	0.2105	2.39E-08	2.94E-07
ANTI_APOPTOSIS	118	12	0.1017	4.29E-08	5.21E-07
REGULATION_OF_NUCLEOBASENUCLEOSIDENUCLEOTIDE_AND_NUCLEIC_ACID_METABOLIC_PROCESS	618	27	0.0437	4.53E-08	5.41E-07
INTRACELLULAR_PROTEIN_TRANSPORT	145	13	0.0897	5.36E-08	6.31E-07
ESTABLISHMENT_AND_OR_MAINTENANCE_OF_CHROMATIN_ARCHITECTURE	77	10	0.1299	5.54E-08	6.44E-07
AMINO_ACID_METABOLIC_PROCESS	78	10	0.1282	6.29E-08	7.20E-07
APOPTOTIC_PROGRAM	60	9	0.15	7.16E-08	8.09E-07
CHROMOSOME_ORGANIZATION_AND_BIOGENESIS	124	12	0.0968	7.47E-08	8.33E-07
DNA_REPAIR	125	12	0.096	8.17E-08	8.99E-07
CELLULAR_CARBOHYDRATE_METABOLIC_PROCESS	126	12	0.0952	8.93E-08	9.69E-07
CYTOSKELETON_ORGANIZATION_AND_BIOGENESIS	208	15	0.0721	9.45E-08	1.01E-06
CARBOHYDRATE_METABOLIC_PROCESS	180	14	0.0778	9.92E-08	1.05E-06
APOPTOTIC_NUCLEAR_CHANGES	19	6	0.3158	1.01E-07	1.05E-06
RESPONSE_TO_DNA_DAMAGE_STIMULUS	162	13	0.0802	1.97E-07	2.03E-06
POSITIVE_REGULATION_OF_BIOLOGICAL_PROCESS	709	28	0.0395	2.04E-07	2.08E-06
CELL_PROLIFERATION_GO_0008283	513	23	0.0448	2.86E-07	2.88E-06
AMINE_METABOLIC_PROCESS	141	12	0.0851	3.07E-07	3.05E-06
NUCLEOBASENUCLEOSIDE_AND_NUCLEOTIDE_METABOLIC_PROCESS	52	8	0.1538	3.14E-07	3.09E-06
BIOPOLYMER_CATABOLIC_PROCESS	117	11	0.094	3.50E-07	3.40E-06
DNA_CATABOLIC_PROCESS	23	6	0.2609	3.59E-07	3.44E-06
DNA_FRAGMENTATION_DURING_APOPTOSIS	13	5	0.3846	3.99E-07	3.78E-06
COFACTOR_METABOLIC_PROCESS	54	8	0.1481	4.25E-07	3.98E-06
REGULATION_OF_TRANSCRIPTION	566	24	0.0424	4.32E-07	4.00E-06
NITROGEN_COMPOUND_BIOSYNTHETIC_PROCESS	26	6	0.2308	7.92E-07	7.26E-06
RESPONSE_TO_CHEMICAL_STIMULUS	314	17	0.0541	8.06E-07	7.31E-06
AEROBIC_RESPIRATION	15	5	0.3333	9.11E-07	8.17E-06
NUCLEOTIDE_METABOLIC_PROCESS	42	7	0.1667	9.91E-07	8.79E-06
GLUCOSE_METABOLIC_PROCESS	28	6	0.2143	1.27E-06	1.11E-05
CELLULAR_LIPID_METABOLIC_PROCESS	255	15	0.0588	1.28E-06	1.11E-05
LIPID_METABOLIC_PROCESS	325	17	0.0523	1.29E-06	1.11E-05
RESPONSE_TO_OXIDATIVE_STRESS	46	7	0.1522	1.88E-06	1.60E-05
NUCLEAR_ORGANIZATION_AND_BIOGENESIS	30	6	0.2	1.96E-06	1.65E-05
RESPONSE_TO_ENDOGENOUS_STIMULUS	200	13	0.065	2.16E-06	1.80E-05
POSITIVE_REGULATION_OF_CELLULAR_PROCESS	668	25	0.0374	2.37E-06	1.96E-05

Extended Table 5

Gene Set Name	# Genes in Gene Set	# Genes in Overlap	p-value	FDR q-value
TRANSCRIPTION	753	62	0.00E+00	0.00E+00
SYSTEM_DEVELOPMENT	861	67	0.00E+00	0.00E+00
SIGNAL_TRANSDUCTION	1634	139	0.00E+00	0.00E+00
PROTEIN_METABOLIC_PROCESS	1231	82	0.00E+00	0.00E+00
NUCLEOBASENUCLEOSIDENUCLEOTIDE_AND_NUCLEIC_ACID_METABOLIC_PROCESS	1244	82	0.00E+00	0.00E+00
MULTICELLULAR_ORGANISMAL_DEVELOPMENT	1049	87	0.00E+00	0.00E+00
CELLULAR_PROTEIN_METABOLIC_PROCESS	1117	74	0.00E+00	0.00E+00
CELLULAR_MACROMOLECULE_METABOLIC_PROCESS	1131	76	0.00E+00	0.00E+00
CELL_SURFACE_RECEPTOR_LINKED_SIGNAL_TRANSDUCTION_GO_0007268	641	54	0.00E+00	0.00E+00
CELL_PROLIFERATION_GO_0008283	513	48	0.00E+00	0.00E+00
BIOPOLYMER_METABOLIC_PROCESS	1684	108	0.00E+00	0.00E+00
ANATOMICAL_STRUCTURE_DEVELOPMENT	1013	77	0.00E+00	0.00E+00
TRANSCRIPTION_DNA_DEPENDENT	636	52	1.11E-16	1.57E-14
REGULATION_OF_GENE_EXPRESSION	673	54	1.11E-16	1.57E-14
RNA_BIOSYNTHETIC_PROCESS	638	52	2.22E-16	2.97E-14
REGULATION_OF_CELLULAR_METABOLIC_PROCESS	787	58	3.33E-16	4.23E-14
RNA_METABOLIC_PROCESS	841	60	4.44E-16	5.37E-14
REGULATION_OF_METABOLIC_PROCESS	799	58	6.66E-16	7.69E-14
INTRACELLULAR_SIGNALING_CASCADE	667	52	1.11E-15	1.23E-13
REGULATION_OF_TRANSCRIPTION	566	46	1.15E-14	1.22E-12
ORGAN_DEVELOPMENT	571	45	6.73E-14	6.47E-12
REGULATION_OF_NUCLEOBASENUCLEOSIDENUCLEOTIDE_AND_NUCLEIC_ACID_METABOLIC_PROCESS	618	47	6.87E-14	6.47E-12
BIOPOLYMER_MODIFICATION	650	48	1.10E-13	1.00E-11
NEGATIVE_REGULATION_OF_BIOLOGICAL_PROCESS	677	49	1.29E-13	1.13E-11
ENZYME_LINKED_RECEPTOR_PROTEIN_SIGNALING_PATHWAY	140	22	2.76E-13	2.33E-11
ENZYME_REGULATOR_ACTIVITY	323	32	6.95E-13	5.70E-11
NEGATIVE_REGULATION_OF_CELLULAR_PROCESS	646	46	1.29E-12	1.02E-10
PROTEIN_MODIFICATION_PROCESS	631	45	2.15E-12	1.66E-10
RECEPTOR_ACTIVITY	583	43	2.22E-12	1.66E-10
CELL_CELL_SIGNALING	404	35	2.89E-12	2.10E-10
TRANSCRIPTION_FROM_RNA_POLYMERASE_II_PROMOTER	457	37	5.17E-12	3.55E-10
DNA_BINDING	602	42	2.34E-11	1.57E-09
REGULATION_OF_TRANSCRIPTION_DNA_DEPENDENT	461	36	2.79E-11	1.77E-09
PID_PDGFRTK_PATHWAY	129	19	3.69E-11	2.29E-09
POSITIVE_REGULATION_OF_CELLULAR_PROCESS	668	44	5.08E-11	2.94E-09
REGULATION_OF_RNA_METABOLIC_PROCESS	471	36	5.10E-11	2.94E-09
POST_TRANSLATIONAL_PROTEIN_MODIFICATION	476	36	6.85E-11	3.87E-09
POSITIVE_REGULATION_OF_BIOLOGICAL_PROCESS	709	45	1.02E-10	5.66E-09
GTPASE_REGULATOR_ACTIVITY	125	18	1.77E-10	9.54E-09
IMMUNE_RESPONSE	235	24	2.76E-10	1.46E-08
NERVOUS_SYSTEM_DEVELOPMENT	385	31	3.12E-10	1.62E-08
TRANSCRIPTION_FACTOR_ACTIVITY	354	29	7.77E-10	3.95E-08
REGULATION_OF_CELL_PROLIFERATION	308	26	3.09E-09	1.54E-07
IMMUNE_SYSTEM_PROCESS	332	27	3.47E-09	1.69E-07
RESPONSE_TO_VIRUS	50	11	6.30E-09	3.02E-07
ANATOMICAL_STRUCTURE_MORPHOGENESIS	376	28	1.23E-08	5.69E-07
RECEPTOR_BINDING	377	28	1.30E-08	5.81E-07
REGULATION_OF_SIGNAL_TRANSDUCTION	222	21	1.39E-08	6.08E-07
MULTI_ORGANISM_PROCESS	165	18	1.64E-08	7.06E-07
RESPONSE_TO_OTHER_ORGANISM	83	13	2.11E-08	8.81E-07
NUCLEOSIDE_TRIPHOSPHATASE_ACTIVITY	212	20	3.19E-08	1.29E-06
GUANYL_NUCLEOTIDE_EXCHANGE_FACTOR_ACTIVITY	46	10	3.50E-08	1.37E-06
PID_P53_DOWNSTREAM_PATHWAY	137	16	3.87E-08	1.49E-06
RESPONSE_TO_BIOTIC_STIMULUS	120	15	4.10E-08	1.55E-06
TISSUE_DEVELOPMENT	138	16	4.29E-08	1.60E-06
TRANSFERASE_ACTIVITY_TRANSFERRING_PHOSPHORUS_CONTAINING	424	29	4.38E-08	1.61E-06
TRANSFORMING_GROWTH_FACTOR_BETA_RECEPTOR_SIGNALING_PATHWAY	36	9	4.60E-08	1.67E-06
PID_ERBB1_DOWNSTREAM_PATHWAY	105	14	5.05E-08	1.81E-06
PYROPHOSPHATASE_ACTIVITY	226	20	9.23E-08	3.21E-06
PROTEIN_KINASE_CASCADE	293	23	9.39E-08	3.23E-06
HYDROLASE_ACTIVITY_ACTING_ON_ACID_ANHYDRIDES	228	20	1.07E-07	3.56E-06
SUBSTRATE_SPECIFIC_TRANSPORTER_ACTIVITY	392	27	1.10E-07	3.63E-06
CELL_DEVELOPMENT	577	34	1.16E-07	3.79E-06
RESPONSE_TO_STRESS	508	31	1.95E-07	6.20E-06
ESTABLISHMENT_OF_LOCALIZATION	870	43	3.57E-07	1.11E-05
DEFENSE_RESPONSE	270	21	3.91E-07	1.19E-05
TRANSMEMBRANE_RECEPTOR_ACTIVITY	418	27	3.94E-07	1.19E-05
PID_EPO_PATHWAY	34	8	4.34E-07	1.29E-05
KINASE_ACTIVITY	369	25	4.37E-07	1.29E-05
TRANSMEMBRANE_RECEPTOR_PROTEIN_SERINE_THREONINE_KINASE	47	9	5.41E-07	1.56E-05
PID_IL6_PATHWAY	47	9	5.41E-07	1.56E-05
REGULATION_OF_MOLECULAR_FUNCTION	324	23	5.59E-07	1.60E-05
TRANSPORT	795	40	5.83E-07	1.64E-05
MOLECULAR_ADAPTOR_ACTIVITY	49	9	7.86E-07	2.17E-05
PID_GMCSF_PATHWAY	37	8	8.72E-07	2.36E-05
ACTIN_FILAMENT_BASED_PROCESS	115	13	1.05E-06	2.78E-05
REGULATION_OF_DEVELOPMENTAL_PROCESS	440	27	1.06E-06	2.78E-05
RESPONSE_TO_CHEMICAL_STIMULUS	314	22	1.22E-06	3.16E-05
PID_SMAD2_3_NUCLEAR_PATHWAY	82	11	1.28E-06	3.28E-05
NEGATIVE_REGULATION_OF_CELL_PROLIFERATION	156	15	1.29E-06	3.28E-05

Extended Table 6

Gene Set Name	# Genes in	# Genes in	p-value	FDR q-value
ANATOMICAL_STRUCTURE_DEVELOPMENT	1013	59	0.00E+00	0.00E+00
INTRACELLULAR_SIGNALING_CASCADE	667	47	0.00E+00	0.00E+00
NEGATIVE_REGULATION_OF_BIOLOGICAL_PROCESS	677	47	0.00E+00	0.00E+00
NEGATIVE_REGULATION_OF_CELLULAR_PROCESS	646	46	0.00E+00	0.00E+00
SIGNAL_TRANSDUCTION	1634	89	0.00E+00	0.00E+00
MULTICELLULAR_ORGANISMAL_DEVELOPMENT	1049	57	1.11E-16	4.03E-14
SYSTEM_DEVELOPMENT	861	50	1.11E-16	4.03E-14
CELL_DEVELOPMENT	577	40	4.44E-16	1.41E-13
BIOPOLYMER_METABOLIC_PROCESS	1684	68	3.23E-14	7.85E-12
PROTEIN_KINASE_CASCADE	293	27	3.40E-14	7.85E-12
ORGAN_DEVELOPMENT	571	36	2.29E-13	4.85E-11
REGULATION_OF_DEVELOPMENTAL_PROCESS	440	31	6.13E-13	1.20E-10
ENZYME_REGULATOR_ACTIVITY	323	26	2.30E-12	4.17E-10
TRANSCRIPTION	753	40	2.46E-12	4.17E-10
KINASE_ACTIVITY	369	27	8.04E-12	1.28E-09
REGULATION_OF_TRANSCRIPTION	566	33	1.87E-11	2.79E-09
PHOSPHOTRANSFERASE_ACTIVITY_ALCOHOL_GROUP_AS_ACCEPTOR	334	25	2.94E-11	4.15E-09
TRANSFERASE_ACTIVITY_TRANSFERRING_PHOSPHORUS_CONTAINING_GROUPS	424	28	3.70E-11	4.95E-09
REGULATION_OF_NUCLEOBASENUCLEOSIDENUCLEOTIDE_AND_NUCLEIC_ACID_METABOLIC_PROCESS	618	34	4.39E-11	5.57E-09
PROGRAMMED_CELL_DEATH	432	28	5.70E-11	6.90E-09
PROTEIN_METABOLIC_PROCESS	1231	50	7.88E-11	9.10E-09
POSITIVE_REGULATION_OF_CELLULAR_PROCESS	668	35	8.54E-11	9.44E-09
REGULATION_OF_MOLECULAR_FUNCTION	324	24	9.05E-11	9.54E-09
TRANSCRIPTION_DNA_DEPENDENT	636	34	9.39E-11	9.54E-09
RNA_BIOSYNTHETIC_PROCESS	638	34	1.02E-10	9.60E-09
POST_TRANSLATIONAL_PROTEIN_MODIFICATION	476	29	1.12E-10	1.02E-08
REGULATION_OF_CATALYTIC_ACTIVITY	276	22	1.36E-10	1.17E-08
REGULATION_OF_CELLULAR_METABOLIC_PROCESS	787	38	1.38E-10	1.17E-08
REGULATION_OF_METABOLIC_PROCESS	799	38	2.12E-10	1.74E-08
APOPTOSIS_GO	431	27	2.67E-10	2.10E-08
REGULATION_OF_PROGRAMMED_CELL_DEATH	342	24	2.73E-10	2.10E-08
NUCLEOBASENUCLEOSIDENUCLEOTIDE_AND_NUCLEIC_ACID_METABOLIC_PROCESS	1244	49	3.44E-10	2.57E-08
ANATOMICAL_STRUCTURE_MORPHOGENESIS	376	25	3.59E-10	2.61E-08
DNA_BINDING	602	32	3.87E-10	2.73E-08
POSITIVE_REGULATION_OF_BIOLOGICAL_PROCESS	709	35	4.18E-10	2.87E-08
ESTABLISHMENT_OF_LOCALIZATION	870	39	6.63E-10	4.34E-08
TRANSPORT	795	37	6.65E-10	4.34E-08
CELLULAR_PROTEIN_METABOLIC_PROCESS	1117	45	9.26E-10	5.88E-08
PROTEIN_AMINO_ACID_PHOSPHORYLATION	279	21	1.01E-09	6.12E-08
REGULATION_OF_TRANSCRIPTION_DNA_DEPENDENT	461	27	1.16E-09	6.87E-08
CELLULAR_MACROMOLECULE_METABOLIC_PROCESS	1131	45	1.36E-09	7.79E-08
REGULATION_OF_APOPTOSIS	341	23	1.38E-09	7.79E-08
PHOSPHORYLATION	313	22	1.46E-09	8.03E-08
PROTEIN_KINASE_ACTIVITY	285	21	1.48E-09	8.03E-08
REGULATION_OF_GENE_EXPRESSION	673	33	1.57E-09	8.29E-08
REGULATION_OF_RNA_METABOLIC_PROCESS	471	27	1.84E-09	9.37E-08
PROTEIN_MODIFICATION_PROCESS	631	31	4.70E-09	2.34E-07
REGULATION_OF_SIGNAL_TRANSDUCTION	222	18	4.92E-09	2.40E-07
NEGATIVE_REGULATION_OF_DEVELOPMENTAL_PROCESS	197	17	5.14E-09	2.47E-07
TRANSCRIPTION_REPRESSOR_ACTIVITY	152	15	6.63E-09	3.06E-07
RESPONSE_TO_EXTERNAL_STIMULUS	312	21	7.40E-09	3.36E-07
REGULATION_OF_PROTEIN_KINASE_ACTIVITY	155	15	8.67E-09	3.86E-07
BIOPOLYMER_MODIFICATION	650	31	9.34E-09	4.09E-07
RNA_METABOLIC_PROCESS	841	36	9.97E-09	4.29E-07
REGULATION_OF_KINASE_ACTIVITY	157	15	1.03E-08	4.37E-07
CYTOSKELETAL_PROTEIN_BINDING	159	15	1.23E-08	4.95E-07
REGULATION_OF_TRANSFERASE_ACTIVITY	161	15	1.45E-08	5.77E-07
REGULATION_OF_BIOLOGICAL_QUALITY	419	24	1.48E-08	5.80E-07
NEGATIVE_REGULATION_OF_TRANSCRIPTION	188	16	1.76E-08	6.68E-07
POSITIVE_REGULATION_OF_CATALYTIC_ACTIVITY	165	15	2.03E-08	7.57E-07
GTPASE_REGULATOR_ACTIVITY	125	13	3.59E-08	1.30E-06
RESPONSE_TO_STRESS	508	26	3.66E-08	1.31E-06
MAPKKK_CASCADE_GO_0000165	104	12	3.74E-08	1.32E-06
RECEPTOR_ACTIVITY	583	28	4.20E-08	1.46E-06
REGULATION_OF_MAP_KINASE_ACTIVITY	67	10	4.26E-08	1.46E-06
CALMODULIN_BINDING	25	7	4.79E-08	1.62E-06
TRANSCRIPTION_FACTOR_ACTIVITY	354	21	6.51E-08	2.15E-06
CELL_SURFACE_RECEPTOR_LINKED_SIGNAL_TRANSDUCTION_GO_0007166	641	29	8.62E-08	2.81E-06
NEGATIVE_REGULATION_OF_NUCLEOBASENUCLEOSIDENUCLEOTIDE_AND_NUCLEIC_ACID_METABOLIC_PROCESS	211	16	8.87E-08	2.85E-06

SULFOTRANSFERASE_ACTIVITY	28	7	1.14E-07	3.61E-06
ACTIN_BINDING	76	10	1.46E-07	4.42E-06
CELL_PROLIFERATION_GO_0008283	513	25	1.69E-07	4.99E-06
TRANSMEMBRANE_TRANSPORTER_ACTIVITY	375	21	1.71E-07	4.99E-06
RESPONSE_TO_CHEMICAL_STIMULUS	314	19	2.02E-07	5.83E-06
NERVOUS_SYSTEM_DEVELOPMENT	385	21	2.64E-07	7.53E-06
TRANSFERASE_ACTIVITY_TRANSFERRING_SULFUR_CONTAINING_GROUPS	32	7	3.07E-07	8.57E-06
TRANSMEMBRANE_RECEPTOR_PROTEIN_TYROSINE_KINASE_SIGNALING_PATHWAY	83	10	3.40E-07	9.29E-06
PID_HIF1_TFPATHWAY	66	9	4.51E-07	1.21E-05
POSITIVE_REGULATION_OF_TRANSFERASE_ACTIVITY	86	10	4.76E-07	1.26E-05
POSITIVE_REGULATION_OF_DEVELOPMENTAL_PROCESS	218	15	7.73E-07	1.99E-05
PID_P53DOWNSTREAMPATHWAY	137	12	7.83E-07	1.99E-05

Extended Table 7

Database_Pathway Annotation	# Genes in Gene Set	# Genes in O	p-value	FDR q-value
<i>Nudix Dependent Genes</i>				
REACTOME_IMMUNE_SYSTEM	933	92	0.00E+00	0.00E+00
REACTOME_CYTOKINE_SIGNALING_IN_IMMUNE_SYSTEM	270	49	0.00E+00	0.00E+00
REACTOME_INTERFERON_SIGNALING	159	38	0.00E+00	0.00E+00
REACTOME_INTERFERON_ALPHA_BETA_SIGNALING	64	24	0.00E+00	0.00E+00
KEGG_PATHWAYS_IN_CANCER	328	34	3.57E-14	3.63E-12
REACTOME_INTERFERON_GAMMA_SIGNALING	63	15	3.24E-12	2.28E-10
KEGG_CYTOKINE_CYTOKINE_RECEPTOR_INTERACTION	267	27	2.69E-11	1.75E-09
REACTOME_ADAPTIVE_IMMUNE_SYSTEM	539	39	4.15E-11	2.51E-09
REACTOME_DEVELOPMENTAL_BIOLOGY	396	29	9.85E-09	4.63E-07
REACTOME_ANTIVIRAL_MECHANISM_BY_IFN_STIMULATED_GENES	66	12	1.29E-08	5.81E-07
KEGG_MAPK_SIGNALING_PATHWAY	267	23	1.70E-08	7.20E-07
REACTOME_AXON_GUIDANCE	251	22	2.53E-08	1.04E-06
KEGG_TOLL_LIKE_RECEPTOR_SIGNALING_PATHWAY	102	14	3.47E-08	1.37E-06
REACTOME_TRANSMEMBRANE_TRANSPORT_OF_SMALL_MOLECULES	413	28	8.95E-08	3.16E-06
REACTOME_HEMOSTASIS	466	30	9.75E-08	3.30E-06
REACTOME_INNATE_IMMUNE_SYSTEM	279	22	1.64E-07	5.28E-06
REACTOME_SIGNALING_BY_FGFR_MUTANTS	44	9	2.98E-07	9.35E-06
KEGG_CHEMOKINE_SIGNALING_PATHWAY	190	17	7.16E-07	2.00E-05
KEGG_FC_EPSILON_RI_SIGNALING_PATHWAY	79	11	8.73E-07	2.36E-05
KEGG_REGULATION_OF_ACTIN_CYTOSKELETON	216	18	9.65E-07	2.58E-05
<i>Nudix Independent Genes</i>				
KEGG_PATHWAYS_IN_CANCER	328	30	1.55E-15	4.39E-13
REACTOME_SIGNALING_BY_RHO_GTPASES	113	15	1.01E-10	9.60E-09
REACTOME_SIGNALING_BY_GPCR	920	40	9.59E-10	5.94E-08
REACTOME_PLATELET_ACTIVATION_SIGNALING_AND_AGGREGATION	208	18	1.75E-09	9.06E-08
KEGG_PROSTATE_CANCER	89	12	6.25E-09	2.94E-07
REACTOME_TRANSMEMBRANE_TRANSPORT_OF_SMALL_MOLECULES	413	24	1.13E-08	4.69E-07
KEGG_ENDOCYTOSIS	183	16	1.20E-08	4.92E-07
KEGG_MAPK_SIGNALING_PATHWAY	267	19	1.57E-08	6.03E-07
REACTOME_HEMOSTASIS	466	25	2.70E-08	9.94E-07
KEGG_AXON_GUIDANCE	129	13	5.23E-08	1.75E-06
KEGG_REGULATION_OF_ACTIN_CYTOSKELETON	216	16	1.22E-07	3.84E-06
REACTOME_SIGNALLING_BY_NGF	217	16	1.30E-07	4.04E-06
KEGG_ALDOSTERONE_REGULATED_SODIUM_REABSORPTION	42	8	1.36E-07	4.17E-06
REACTOME_NRAGE_SIGNALS_DEATH_THROUGH_JNK	43	8	1.65E-07	4.94E-06
KEGG_FOCAL_ADHESION	201	15	2.74E-07	7.75E-06
KEGG_WNT_SIGNALING_PATHWAY	151	13	3.34E-07	9.21E-06
KEGG_CYTOKINE_CYTOKINE_RECEPTOR_INTERACTION	267	17	4.32E-07	1.17E-05
KEGG_ADIPOCYTOKINE_SIGNALING_PATHWAY	67	9	5.14E-07	1.35E-05
KEGG_PANCREATIC_CANCER	70	9	7.53E-07	1.95E-05