Int J Clin Exp Pathol 2016;9(10):10483-10490
www.ijcep.com /ISSN:1936-2625/IJCEP0029512

Original Article

Application of iTRAQ to screen differentially expressed proteins in the hippocampus of a mouse model of Down syndrome

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Received March 31, 2016; Accepted July 14, 2016; Epub October 1, 2016; Published October 15, 2016

Abstract: Background: Down syndrome (DS) is characterized by mental retardation and the development of Alzheimer's disease (AD). However, the reason was not yet clear. Methods: Ts65Dn mice were used in this study. We collected their hippocampi and identified protein biomarkers using iTRAQ. We used bioinformatics to analyze differentially expressed proteins and western blots to preliminarily verify iTRAQ results. Results: A total of 2805 proteins were identified in the hippocampus of mouse. After calculating the index of significance (*p*-Value) and statistically analyzing differences between the DS and control groups, we found 374 significant differentially expressed proteins. These included protein binding, proteins with catalytic activity, and proteins with transferase activity. In addition, they were related to cellular processes, regulation of biological processes, and metabolic processes. The top 7 differentially regulated proteins were uncharacterized protein C2 orf 47 homolog (mitochondrial), isoform 2 of filamin A-interacting protein 1-like, zinc finger protein, isoform 1 of pericentriolar material 1 protein, SEC23-interacting protein, BAG family molecular chaperone regulator 3, and serpin H1. Conclusions: We observed differentially expressed proteins in the hippocampi of Ts65Dn mice that may be closely related to their neurological deficits. The new generation iTRAQ technology helps in the screening and identification of these proteins.

Keywords: Down syndrome, proteomics, iTRAQ, Ts65Dn, hippocampus

Introduction

Down syndrome (DS), also called trisomy 21, is one of the most common gross chromosomal abnormalities and affects approximately 1 in every 700 babies [1]. It is well-known that DS is a condition in which extra genetic material causes delays in child development, both mentally and physically. Intellectual disabilities are the foremost and most debilitating trait, which causes the loss of cognitive abilities and the development of early onset Alzheimer's disease (AD) [2]. The survival rate of people with DS has greatly improved in the past decades, with a current life expectancy of 60 years or longer [3]. Effective medical intervention and skills training can help many people with DS improve their growth, development, and IQ. However, large deficits in memory and learning abilities remain [4, 5]. Therefore, problems concerning cognitive mental retardation become more important to those with DS.

DS results from the presence of an extra chromosome 21. However, how trisomy 21 results in cognitive impairment remains unclear. Recently, different hypotheses have been advanced, including the "dosage imbalance hypothesis", "amplified developmental instability hypothesis", and "molecular misreading concept" [6-8]. Each of these theories focuses on the extra copy of chromosome 21 and its associated proteins, which change nerve development and metabolism in the DS brain, thereby destroying neural circuits. Research regarding protein function may be an important avenue to reveal the mechanism of mental retardation development in DS.

Proteomics, a high-throughput technology, has become a powerful platform for the discovery of biomarkers. As such, it can also be used for the identification of new biomarkers for DS. The application of proteomics in DS has made significant progress in the past 5 years. We also used two-dimensional gel electrophoresis (2-DE) and mass spectrometry (MS) to identify 29 differentially expressed proteins in maternal serum [9]. However, limited studies have focused on screening proteins related to neurological impairment in DS using proteomics. Shin et al. [10] first reported that they had discovered 9 proteins in the fetal human brain cortex, which were encoded on chromosome 21. Sun et al. [11] extracted proteins from the frontal cortex of fetal DS subjects and reported that 8 proteins participated in several pathways related to neurodevelopment. However, most research still use conventional 2-DE/MS approaches, which have less sensitivity, low resolution, poor reproducibility, and experimental bias. Most scholars indicate that the major limitation of current proteomic approaches is that the performance of putative candidate markers is not reproducible between studies or laboratories. Due to limitations of 2-DE/MS, most modern proteomic studies use shotgun proteomic analyses via ES-based MS systems, relying on isobaric tags for relative and absolute quantitation (iTRAQ) labeling for quantitative analyses. Such systems have been found to be very robust.

The studies by Shin et al. [10] and Sun et al. [11] investigated proteins from the cortex of DS subjects. However, it is well-known that the hippocampus is involved in memory formation, organization, and storing. It is particularly important in the consolidation of information from short-term memory to long-term memory and spatial navigation [12, 13]. Some research has shown that the hippocampus is one of the first regions of the brain to suffer damage, and memory loss and disorientation are among the earliest symptoms in Alzheimer's disease [14]. Recently, studies on the hippocampal tissue of DS subjects have attracted more and more attention [15, 16]. It is exciting and encouraging that researchers have begun to discover hippocampal proteins involved in DS using proteomics technology [17]. However, there were no studies regarding the application of iTRAQ.

The aim of this study is to discover differentially expressed proteins in the hippocampus of Ts65Dn mice [18, 19], which are a mouse model of DS. It is the first report identifying protein biomarkers involved in DS neurological impairment using iTRAQ.

Materials and methods

This study was conducted at the Changzhou Women and Children Hospital of Nanjing Medical University (Changzhou City, Jiangsu Province, China). The animals were bred at the Animal Center of Jiangsu University (Zhenjiang City, Jiangsu Province, China). All efforts were made to minimize the number of animals used and their suffering.

Animals

Six Ts65Dn mice (3 males, 3 females) carrying partial trisomy of chromosome 16 were purchased from The Jackson Laboratories (Bar Harbor, ME, USA). After culture reproduction, all first-generation mice were karyotyped using PCR according to The Jackson Laboratories protocol. We selected 5 Ts65Dn mice as the DS group (DS), and 5 normal mice as the control group (CG). The mice in both groups were age matched, and were older than 16~18 weeks. The animals' health and comfort were evaluated by the veterinary service. The animals had free access to water and food, per the methods of the Animal Center of Jiangsu University.

Methods

Sample collection

Anesthetized animals were euthanized using 10% chloral hydrate (Changzhou First People's Hospital, Changzhou, China). We removed the brain and isolated the hippocampus.

Protein preparation

Approximately 3 g frozen, treated hippocampal tissues were ground into a powder in liquid nitrogen and homogenized in extraction buffer (4% SDS, 1 mM DTT, 150 mM Tris-HCl, pH 8.0). After 3 min incubation in boiling water, homogenates were sonicated on ice. Crude extracts were again incubated in boiling water, and clarified by centrifugation for 10 min at 16,000 g at 25°C. Protein content was determined using the BCA protein assay reagent (Beyotime, Haimen, China).

Protein digestion and iTRAQ labeling

Protein digestion was performed according to the FASP procedure described by Wiśniewski

JR et al [20]. The resulting peptide mixture was labeled using the 4-plex/8-plex iTRAQ reagent according to the manufacturer's instructions (Applied Biosystems, Foster, CA, USA). Briefly, 200 μg of protein for each sample was incorporated into 30 μl STD buffer (4% SDS, 100 mM DTT, 150 mM Tris-HCl, pH 8.0). The detergent, DTT, and other low molecular weight components were removed using UA buffer (8 M urea, 150 mM Tris-HCl, pH 8.0) and repeated ultrafiltration (Microcon units, 30 kD). Iodoacetamide (0.5 M) in UA buffer (100 μl) was added to block reduced cysteine residues, and samples were incubated for 20 min in the dark. The filters were washed with 100 μl UA buffer three times, followed by two washes in 100 μl DS buffer (50 mM triethylammoniumbicarbonate, pH 8.5). Finally, the protein suspensions were digested overnight at 37°C with 2 μg trypsin (Promega, Beijing, China) in 40 μl DS buffer, and the resulting peptides were collected as the filtrate. The peptide content was estimated using UV light spectral density at 280 nm with an extinction coefficient of 1.1 of 0.1% (g/l) solution that was calculated based on the frequency of tryptophan and tyrosine in vertebrate proteins.

For labeling, each iTRAQ reagent was dissolved in 70 μl of ethanol and added to the respective peptide mixture. The samples were labeled as (CG)-114, (DS)-115, (CG)-116, and (DS)-117, were multiplexed, and vacuum dried.

Peptide fractionation with strong cation exchange (SCX) chromatography

iTRAQ labeled peptides were fractionated by SCX chromatography using the AKTA Purifier system (GE Healthcare, Uppsala, Sweden). The dried peptide mixture was reconstituted and acidified with 2 ml buffer A (10 mM KH_2PO_4 in 25% ACN, pH 2.7) and loaded onto a polysulfoethyl 4.6 × 100 mm column (5 μ, 200 Å, PolyLC Inc., Columbia, MD, USA). The peptides were eluted at a flow rate of 1 ml/min with a gradient of 0%-10% buffer B (500 mM KCl, 10 mM KH_2PO_4 in 25% ACN, pH 2.7) for 2 min, 10-20% buffer B for 25 min, 20%-45% buffer B for 5 min, and 50%-100% buffer B for 5 min. The elution was monitored by absorbance at 214 nm, and fractions were collected every 1 min. The collected fractions (approximately 30 fractions) were finally combined into 10 pools and desalted on C18 Cartridges [Empore™ SPE Cartridges C18 (standard density), bed I.D. 7 mm, volume 3 ml, Sigma, St. Louis, MO, USA]. Each fraction was concentrated by vacuum centrifugation and reconstituted in 40 μl 0.1% (v/v) trifluoroacetic acid. All samples were stored at -80°C until LC-MS analyses.

Liquid chromatography (LC) - electrospray Ionization (ESI) tandem MS (MS/MS) analyses by Q exactive

Experiments were performed on a Q Exactive mass spectrometer that was coupled to Easy nLC (Thermo Fisher Scientific, Waltham, MA, USA). Each fraction (10 μl) was injected for nanoLC-MS/MS analyses. The peptide mixture (5 μg) was loaded onto the C18-reversed phase column (15 cm long, 75 μm inner diameter) packed in-house with RP-C18 5 μm resin in buffer A (0.1% formic acid) and separated with a linear gradient of buffer B (80% acetonitrile and 0.1% formic acid) at a flow rate of 250 nl/min, controlled by IntelliFlow technology over 140 min. MS data were acquired using a data-dependent top 10 method dynamically choosing the most abundant precursor ions from the survey scan (300-1800 m/z) for HCD fragmentation. Determination of the target value is based on predictive Automatic Gain Control (pAGC). Dynamic exclusion duration was 60 s. Survey scans were acquired at a resolution of 70,000 at m/z 200 and resolution for HCD spectra was set to 17,500 at m/z 200. Normalized collision energy was 30 eV and the underfill ratio, which specifies the minimum percentage of the target value likely to be reached at maximum fill time, was defined as 0.1%. The instrument was run with the peptide recognition mode enabled.

Sequence database search and data analyses

MS/MS spectra were searched using the MASCOT engine (Matrix Science, London, UK; version 2.2) against a non-redundant International Protein Index (IPI) Arabidopsis sequence database v3.85 (released September 2011; 39,679 sequences) from the European Bioinformatics Institute (http://www.ebi.ac.uk/). For protein identification, the following options were used: peptide mass tolerance = 20 ppm, MS/MS tolerance = 0.1 Da, enzyme = trypsin, missed cleavage = 2, fixed modification = iTRAQ8plex (K), iTRAQ8plex (N-term), variable modification = oxidation (M), and decoy database pattern = reverse.

Table 1. The top 7 differentially expressed proteins in the hippocampus of Ts65Dn mice

Accession No.	Protein	Coverage (%)	DS/C	*p*-value
IPI00221850	Uncharacterized protein C2orf47 homolog, mitochondrial	5.84	5.865	1.23E-93
IPI00755058	Isoform 2 of filamin A-interacting protein 1-like	7.96	0.2	3.67E-92
IPI00756203	Zinc finger protein 575	6.69	4.798	5.42E-74
IPI00127764	Isoform 1 of pericentriolar material 1 protein	0.69	3.718	1.97E-52
IPI00116752	SEC23-interacting protein	1.5	3.163	1.01E-40
IPI00331334	BAG family molecular chaperone regulator 3	1.73	3.113	1.19E-39
IPI00114733	Serpin H1	6.24	3.063	1.41E-38

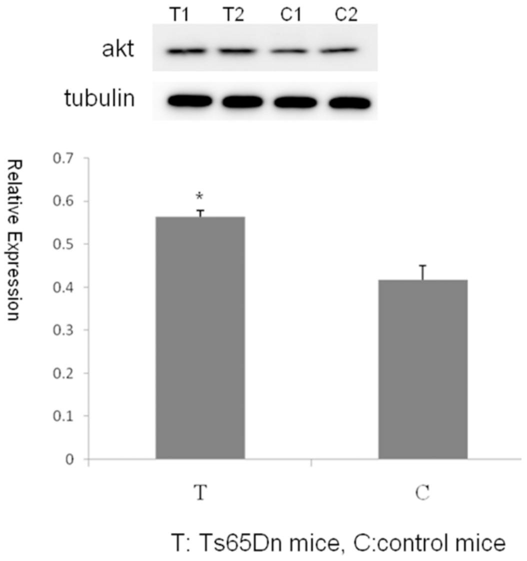

Figure 1. Western blot images using specific antibody against Akt.

The MASCOT search results for each SCX elution were further processed using ProteomicsTools (version 3.05), which includes the programs BuildSummary, Isobaric Labeling Multiple File Distiller, and Identified Protein iTraq Statistic Builder (Information can be accessed from the Research Center for Proteome Analysis http://www.proteomics.ac.cn/). The BuildSummary program was used for assembling protein identifications based on a target-decoy search in shotgun proteomics. All reported data were based on 99% confidence for protein identification as determined by false discovery rate (FDR) ≤ 1%. FDR = N (decoy)*2/[(N (decoy) + N (target)].

The Isobaric Labeling Multiple File Distiller and Identified Protein iTRAQ Statistic Builder programs were used to calculate the protein ratios, in which Sample REF was used as reference, base on the weighted average of the intensity of report ions in each identified peptide. The final ratios of protein were normalized to the median average protein ratio for an unequal mix of the different labeled samples.

We selected one proteins and verified the iTRAQ results using western blot. Proteins were extracted from the hippocampus and separated using 8% SDS-PAGE. After electrophoresis, proteins were electrotransferred to PVDF membranes. Blots were blocked for 2 h at room temperature with 5% nonfat milk in PBS. Membranes were incubated overnight at 4°C with polyclonal antibodies against Akt (Lot: ab-124341, Abcam, USA). Tubulin was used as an internal reference. Blots were developed using the ECL western blotting detection system (Shanghai Pik Wan Days Biotechnology Co. Ltd, Shanghai, China). The blots were scanned and the images were analyzed using Quantity One image processing software (BioRad Laboratories, USA). Protein levels are expressed relative to Tubulin expression.

Bioinformatics analyses

Functional classifications were performed using GOA (http://www.ebi.ac.uk/GOA/) according to the accession number of proteins in IPI. Some identified proteins were mapped to at least one annotation term within the GO biological process, molecular function, and cellular component catalogues.

Results

The hippocampi of Ts65Dn mice were labeled with iTRAQ 115 and 117, and the control samples were labeled with iTRAQ 114 and 116. Following tandem LC-ESI-MS, we identified 2,842 proteins with ≥95% confidence. However, after manually calculating the rate of iTRAQ

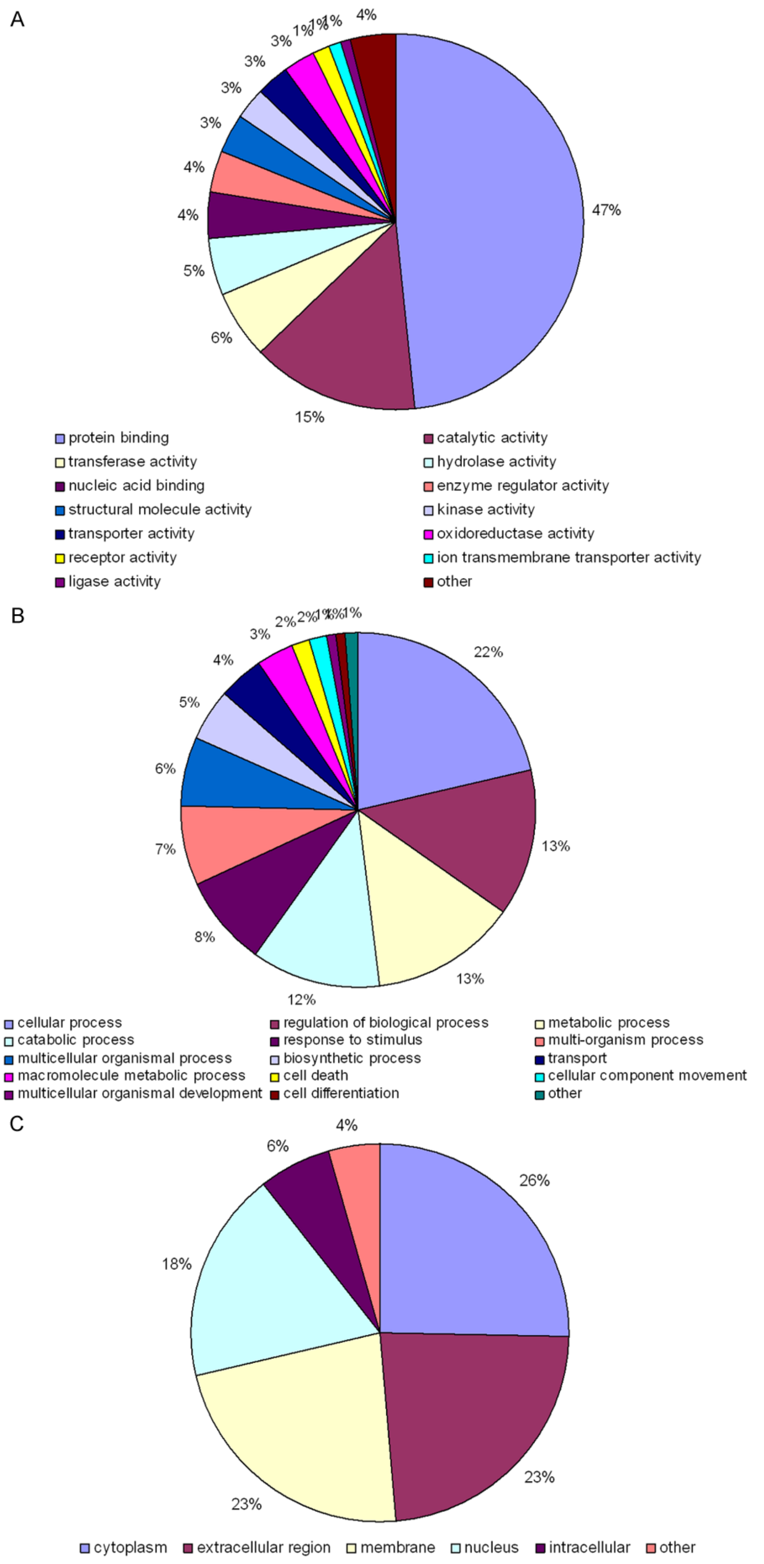

Figure 2. Classification of identified proteins based on GOA. (A) Molecular Function, (B) Biological Processes, and (C) Cellular Components.

(DS_115/Control and DS_117/Control), 2,805 proteins had a relative quantitation of two or more peptides derived from the analyses.

After calculating the index of significance (*p*-value) and statistically analyzing the differences between the DS and control groups, we termed proteins as differentially expressed if their *p*-values were lower than 0.05. Compared with the control group, there were 374 differentially expressed proteins in hippocampal tissues, including 195 proteins that were significantly increased and 179 that were decreased. The protein IPI, protein name, SwissProt AC, molecular weight (MW), coverage, molecular function, biological process, cellular component, and *p*-value of these proteins are shown in Supplementary Table 1. The top 7 proteins were uncharacterized protein C2 orf 47 homolog (mitochondrial), isoform 2 of filamin A-interacting protein 1-like, zinc finger protein, isoform 1 of pericentriolar material 1 protein, SEC-23-interacting protein, BAG family molecular chaperone regulator 3, and serpin H1. **Table 1** shows accession numbers, coverage, rate of DS/C, and *p*-values.

One proteins (Akt) were selected to preliminarily verify the iTRAQ results using western blot. Western blot images are shown in **Figure 1**, and the results confirmed that expression of these proteins are statistically different in the hippocampal region of DS mice.

By GOA, 374 proteins were mapped to at least one annotation term within the GO molecular function category including 334 (47%) protein binding proteins, 102 (15%) proteins with catalytic activity, 39 (6%) proteins with transferase activity, 35 (5%) proteins with hydrolase activity, and 27 (4%)

with nucleic acid binding activity (**Figure 2A**). In addition, they were mapped within the GO biological process category: cellular processes (238 proteins, 22%), regulation of biological processes (149 proteins, 13%), metabolic processes (148 proteins, 13%), catabolic processes (129, 12%), and response to stimulus (93, 8%) (**Figure 2B**). Within the GO cellular component catalogues, they were mapped as cytoplasmic (142, 26%), extracellular region (132, 23%), and membrane (128, 23%) (**Figure 2C**).

Discussion

It is well-known that Down syndrome (DS), the most common type of gross chromosomal abnormality, is characterized by intellectual disabilities and the development of Alzheimer's disease (AD). In recent years, with a prolonged life span, the problem of mental retardation in DS patients seems more prominent. For example, with effective medical intervention and skills training, the IQ of DS patients could be significantly improved. However, their memory, athletic ability, and learning ability still have great defects [4, 5]. In addition, DS patients are characterized by the early appearance of neurodegenerative diseases such as Alzheimer disease (AD): 11% of DS patients have AD pathology at 40 years of age and 100% have AD lesions at > 70 years of age [21].

However, how the extra chromosome 21 causes mental retardation was yet unclear. Current hypotheses suggested that research into the function of proteins might be an important avenue to reveal the cause of mental retardation in DS. Therefore, some prospective studies tried to discover proteins related to neurological impairments in DS using proteomic, one high-throughput technology. Limited reports have shown that proteomic approaches could contribute to the screening of candidate biomarkers of mental retardation. However, problems were also noted. First, most of the current, published studies involved only the fetal cerebral cortex although the hippocampus is predominantly responsible for learning and memory function. Therefore, protein research focused on the hippocampus are perhaps more meaningful. Second, most studies have used a conventional 2-DE/MS approach, which has less sensitivity, low resolution, poor reproducibility, and experimental bias. Third, mouse hippocampal tissue is very small and thus requires more sensitive proteomics technologies in order to discover differentially expressed proteins in DS mouse models. In this study, we applied a new proteomics platform termed iTRAQ (isobaric tags for relative and absolute quantitation) to screen differentially expressed proteins in the hippocampus of Ts65Dn mice. This technology was more quantitative, accurate, reliable, and reproducible, and was applicable to multiple parallel quantification analyses [22, 23].

Our research results indicate that iTRAQ could reliably screen differentially expressed proteins. In present study, we discovered 2,805 proteins that were closely related to biological metabolism, biological control, and stress responses. After further quantitative analyses, 374 significant differentially expressed proteins were found in Ts65Dn hippocampal tissues. They were predominantly protein binding and related to cellular processes, including cell communication, cell death, cell growth, cell differentiation, cell division, cell organization and biogenesis, cell proliferation, cellular homeostasis, development, regulation of biological processes, reproduction, response to stimuli, and transport. Increasing data show that enhanced apoptosis in DS may play a role in the mental deficiencies and neurodegeneration of AD [24]. Additionally, it was reported that disruption of neurogenesis and apoptosis, the two fundamental processes underlying brain building, could reduce neuron number in the DS hippocampal region [25]. Many differential proteins that we discovered were involved in cellular processes, particularly cell communication and cell death. We hypothesize that differentially expressed proteins play an important role in the neurological impairments observed in DS and future studies will examine this notion.

Acknowledgements

This study was supported by grants from the Project funding for the training of high level health professionals in Changzhou, Changzhou Research Program of Applied Basic (CJ20140055), the major projects of Jiangsu Maternal and Child Health (F201217), the project of the health department of Jiangsu Province (H201352) and the youth project of Health Bureau of Changzhou City (QN201405).

Disclosure of conflict of interest

None.

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Supplementary Table 1. 374 proteins differentially expressed in hippocampal tissues of Ts65Dn

Accession	Name	SwissProt_AC	Coverage (%)	MW [kDa]	Molecular Function	Biological Process	Cellular Component	S/C *p* value
IPI00108150	RHO-ASSOCIATED PROTEIN KINASE 2.		8.65	160.5	catalytic activity; metal ion binding; motor activity; nucleotide binding; protein binding; transporter activity	cell communication; cell differentiation; cell division; cell organization and biogenesis; development; metabolic process; regulation of biological process; response to stimulus; transport	cytoplasm; cytoskeleton; membrane; mitochondrion	0.0304723
IPI00108378	LEUCINE-RICH REPEAT AND GUANYLATE KINASE DOMAIN-CONTAINING PROTEIN.	Q9D5S7	1.46	93.1	catalytic activity; nucleotide binding; protein binding	metabolic process	_	0.00524694
IPI00108391	POU DOMAIN, CLASS 3, TRANSCRIPTION FACTOR 4.	P62515	5.54	39.4	DNA binding	cell death; cell differentiation; development; metabolic process; regulation of biological process	nucleus	0.000227027
IPI00109033	ISOFORM 1 OF PROTEIN FAM54B.	Q9CWE0	4.15	31.7	_	_	_	5.96E-10
IPI00109089	BAG FAMILY MOLECULAR CHAPERONE REGULATOR 4.	Q8CI61	3.06	49.1	protein binding	cell communication; cell death; cell organization and biogenesis; cellular component movement; metabolic process; regulation of biological process; response to stimulus	cytoplasm; cytosol; membrane; nucleus	0.0221135
IPI00109611	PROTEIN FAM162A.	Q9D6U8	10.97	17.7	_	cell communication; cell death; cell organization and biogenesis; metabolic process; regulation of biological process; response to stimulus	cytoplasm; membrane; mitochondrion	0.0369242
IPI00111501	COMPLEXIN-2.	P84086	52.99	15.4	protein binding	cell communication; cell differentiation; development; regulation of biological process; response to stimulus; transport	cytoplasm; cytosol; membrane	0.0477629
IPI00112129	GLYCINE AMIDINOTRANSFERASE, MITOCHONDRIAL.	Q9D964	4.02	48.3	catalytic activity	development; metabolic process; response to stimulus	cytoplasm; membrane; mitochondrion	0.000168134
IPI00112139	OCIA DOMAIN-CONTAINING PROTEIN 2.	Q9D8W7	26.62	16.9	_	_	cytoplasm; endosome; membrane; mitochondrion	0.00804233
IPI00112709	UPF0565 PROTEIN C2ORF69 HOMOLOG.	Q9D9H8	3.56	41.7	_	_	extracellular	0.0022628
IPI00113143	6.8 KDA MITOCHONDRIAL PROTEOLIPID.	P56379	13.79	6.7	_	_	cytoplasm; membrane; mitochondrion	0.000701415
IPI00113240	METALLOTHIONEIN-2.	P02798	19.67	6.1	metal ion binding	cell communication; cellular homeostasis; regulation of biological process; response to stimulus	cytoplasm; nucleus	1.32E-08
IPI00113362	CRK-LIKE PROTEIN.	P47941	12.21	33.8	protein binding	development	_	0.00732873
IPI00114733	SERPIN H1.	P19324	6.24	46.5	enzyme regulator activity; protein binding	cell organization and biogenesis; metabolic process; regulation of biological process; response to stimulus	cytoplasm; endoplasmic reticulum; organelle lumen	1.41E-38
IPI00115056	TRAFFICKING PROTEIN PARTICLE COMPLEX SUBUNIT 3.	O55013	12.78	20.3	protein binding	transport	cytoplasm; cytosol; endoplasmic reticulum; Golgi; membrane	0.0199941
IPI00115097	COATOMER SUBUNIT BETA'.	O55029	0.77	102.4	protein binding; structural molecule activity	transport	cytoplasm; cytoskeleton; Golgi; membrane	0.0143213

IPI00115530	BETA-HEXOSAMINIDASE SUBUNIT BETA.	P20060	4.85	61.1	catalytic activity; protein binding	cell communication; cell differentiation; cell organization and biogenesis; cellular component movement; cellular homeostasis; development; metabolic process; regulation of biological process; reproduction; response to stimulus	cytoplasm; membrane; vacuole	0.0047568
IPI00115992	UNCHARACTERIZED PROTEIN.		7.2	13.7	_	_	_	3.49E-06
IPI00116372	MYELOID LEUKEMIA FACTOR 2.	Q99KX1	7.29	28	_	defense response; response to stimulus	cytoplasm; nucleus	0.0445597
IPI00116752	SEC23-INTERACTING PROTEIN.	Q6NZC7	1.5	110.7	metal ion binding; protein binding	_	cytoplasm; endoplasmic reticulum; membrane	1.01E-40
IPI00117811	AP-3 COMPLEX SUBUNIT DELTA-1.	O54774	14.1	135	transporter activity	cell communication; cell differentiation; cell organization and biogenesis; cellular component movement; cellular homeostasis; development; regulation of biological process; transport	cytoplasm; endosome; Golgi; membrane	0.02344
IPI00119094	PROSTAMIDE/PROSTAGLANDIN F SYNTHASE.	Q9DB60	13.43	21.7	catalytic activity; nucleotide binding	metabolic process	cytoplasm; cytosol	0.00732873
IPI00119124	FUN14 DOMAIN-CONTAINING PROTEIN 1.	Q9DB70	10.97	17.1	_	metabolic process; response to stimulus	cytoplasm; membrane; mitochondrion	1.49E-06
IPI00119346	CALRETININ.	Q08331	39.11	31.4	metal ion binding	_	_	0.0331125
IPI00119416	MUSCARINIC ACETYLCHOLINE RECEPTOR M1.	P12657	3.26	51.3	receptor activity; signal transducer activity	cell communication; regulation of biological process; response to stimulus; transport	membrane	0.00372267
IPI00120295	CLAUDIN-11.	Q60771	14.49	22.1	protein binding; structural molecule activity	cell communication; cellular homeostasis; development; reproduction	membrane	3.82E-11
IPI00120995	TRANSCRIPTION FACTOR CP2-LIKE PROTEIN 1.	Q3UNW5	2.51	54.7	DNA binding; protein binding	cell differentiation; cell organization and biogenesis; development; metabolic process; regulation of biological process	cytoplasm; membrane; mitochondrion; nucleus; organelle lumen	3.55E-16
IPI00121349	ISOFORM 1 OF PROTEIN PHOSPHATASE 1 REGULATORY SUBUNIT 1B.	Q60829	30.41	21.8	enzyme regulator activity; protein binding	cell communication; metabolic process; regulation of biological process; reproduction; response to stimulus	cytoplasm; nucleus	0.000377272
IPI00121558	TUBULIN ALPHA CHAIN-LIKE 3.	Q3UX10	12.56	50	catalytic activity; nucleotide binding; structural molecule activity	cell organization and biogenesis; cellular component movement; metabolic process	cytoplasm; cytoskeleton	3.24E-05
IPI00121627	CLEFT LIP AND PALATE TRANSMEMBRANE PROTEIN 1 HOMOLOG.	Q8VBZ3	2.26	75.2	_	cell differentiation; development; regulation of biological process	cell surface; membrane	6.75E-11
IPI00121736	PROGRAMMED CELL DEATH PROTEIN 6.	P12815	17.8	21.9	metal ion binding; protein binding	cell death; metabolic process; regulation of biological process; response to stimulus; transport	cytoplasm; endoplasmic reticulum; membrane; nucleus	0.0383616
IPI00122131	RAS AND RAB INTERACTOR 1.	Q921Q7	1.7	83	enzyme regulator activity; protein binding	cell communication; metabolic process; regulation of biological process; response to stimulus; transport	cytoplasm; cytoskeleton; membrane	0.00524694
IPI00122344	CYSTATHIONINE GAMMA-LYASE.	Q8VCN5	3.27	43.5	catalytic activity; protein binding	cell communication; cell death; cell growth; cell organization and biogenesis; cell proliferation; metabolic process; regulation of biological process; response to stimulus	cytoplasm; nucleus	0.00804233

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IPI00122421	60S RIBOSOMAL PROTEIN L27.	P61358	12.5	15.8	structural molecule activity	metabolic process	cytoplasm; ribosome	0.0284701
IPI00122522	GAMMA-GLUTAMYLTRANSPEPTIDASE 1.	Q60928	1.94	61.5	catalytic activity	defense response; development; metabolic process; regulation of biological process; reproduction; response to stimulus	membrane	0.000428266
IPI00123445	5'-AMP-ACTIVATED PROTEIN KINASE CATALYTIC SUBUNIT ALPHA-2.	Q8BRK8	3.08	62	catalytic activity; metal ion binding; nucleotide binding; protein binding	cell communication; cell death; cell organization and biogenesis; metabolic process; regulation of biological process; response to stimulus	cytoplasm; membrane; nucleus; organelle lumen	0.000137364
IPI00123542	GLUTAMATE RECEPTOR DELTA-1 SUBUNIT.	Q61627	2.08	112.1	receptor activity; signal transducer activity; transporter activity	cell communication; regulation of biological process; response to stimulus; transport	membrane	0.0335605
IPI00123623	HYALURONAN SYNTHASE 1.	Q61647	1.37	65.5	catalytic activity	cellular component movement; metabolic process; regulation of biological process; response to stimulus	membrane	0.0021948
IPI00123927	ALPHA-1-ANTITRYPSIN 1-5.	Q00898	11.62	45.9	enzyme regulator activity	metabolic process; regulation of biological process; response to stimulus	extracellular	0.0425307
IPI00124120	UNCHARACTERIZED PROTEIN.	Q9JLC8	0.24	520.4	nucleotide binding; protein binding	_	_	0.00620155
IPI00124181	SELENIDE, WATER DIKINASE 2.	P97364	4.65	47.8	catalytic activity	_	_	0.000173868
IPI00124284	DNA-DIRECTED RNA POLYMERASES I, II, AND III SUBUNIT RPABC3.	Q923G2	8.67	17.1	catalytic activity	metabolic process	cytoplasm; nucleus; organelle lumen	0.00116235
IPI00124499	KERATIN, TYPE II CYTOSKELETAL 79.	Q8VED5	2.26	57.5	catalytic activity; motor activity; structural molecule activity	_	cytoskeleton	0.00987844
IPI00124614	EPM2A-INTERACTING PROTEIN 1.	Q8VEH5	3.3	70.1	protein binding	_	cytoplasm; endoplasmic reticulum	0.0184077
IPI00124779	TRIMETHYLGUANOSINE SYNTHASE.	Q923W1	1.99	96.7	catalytic activity; metal ion binding	metabolic process; regulation of biological process	cytoplasm; nucleus; organelle lumen	1.60E-09
IPI00125397	ZINC TRANSPORTER 3.	P97441	18.04	41.8	transporter activity	cellular homeostasis; regulation of biological process; response to stimulus; transport	cytoplasm; membrane	0.0369895
IPI00125460	ATP SYNTHASE-COUPLING FACTOR 6, MITOCHONDRIAL.	P97450	35.19	12.5	catalytic activity; transporter activity	metabolic process; transport	cytoplasm; membrane; mitochondrion	0.0456058
IPI00126175	PROTEIN S100-A1.		15.96	10.5	metal ion binding; protein binding	metabolic process; regulation of biological process	cytoplasm; endoplasmic reticulum; nucleus	0.010706
IPI00126405	MYELIN-OLIGODENDROCYTE GLYCOPROTEIN.	Q61885	34.55	28.3	protein binding	_	membrane	0.000242579
IPI00126826	HISTAMINE N-METHYLTRANSFERASE.	Q91VF2	7.46	33.6	catalytic activity	cell communication; development; metabolic process; response to stimulus	cytoplasm; nucleus	0.0139462
IPI00126913	ISOFORM 1 OF ATPASE FAMILY AAA DOMAIN-CONTAINING PROTEIN 3.	Q925I1	2.88	66.7	catalytic activity; nucleotide binding; RNA binding	metabolic process	cytoplasm; membrane; mitochondrion	0.0307188
IPI00127358	SH3 DOMAIN-BINDING GLUTAMIC ACID-RICH-LIKE PROTEIN 3.	Q91VW3	27.96	10.5	catalytic activity	cellular homeostasis; regulation of biological process	cytoplasm; nucleus	0.0180603

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IPI00127691	GLUTATHIONE SYNTHETASE.	P51855	5.06	52.2	catalytic activity; metal ion binding; nucleotide binding; protein binding	metabolic process; response to stimulus	_	0.0383616
IPI00127764	ISOFORM 1 OF PERICENTRIOLAR MATERIAL 1 PROTEIN.	Q9R0L6	0.69	228.7	protein binding	cell differentiation; cell organization and biogenesis; cell proliferation; development; regulation of biological process	cytoplasm; cytoskeleton; membrane; nucleus	1.97E-52
IPI00128040	SERINE PROTEASE HTRA1.	Q9R118	2.92	51.2	catalytic activity; protein binding	cell communication; cell growth; cell organization and biogenesis; metabolic process; regulation of biological process; response to stimulus	cytoplasm; cytosol; extracellular	0.0139462
IPI00128249	ALPHA-2-HS-GLYCOPROTEIN.	P29699	6.96	37.3	enzyme regulator activity	cell communication; cell growth; cell organization and biogenesis; defense response; development; regulation of biological process; reproduction; response to stimulus; transport	extracellular	0.00194904
IPI00128945	PROTEASOME SUBUNIT BETA TYPE-2.	Q9R1P3	12.94	22.9	catalytic activity	metabolic process; response to stimulus	cytoplasm; cytosol; nucleus; proteasome	5.08E-11
IPI00128989	V-TYPE PROTON ATPASE SUBUNIT S1.	Q9R1Q9	2.16	51	catalytic activity; nucleotide binding; transporter activity	cell death; transport	cytoplasm; membrane; vacuole	0.012587
IPI00129417	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN D-LIKE.	Q9Z130	16.28	33.5	DNA binding; nucleotide binding; RNA binding	metabolic process; regulation of biological process	cytoplasm; nucleus	0.0256739
IPI00130376	CYTOCHROME C OXIDASE SUBUNIT 1.	P00397	7.78	56.8	catalytic activity; metal ion binding; transporter activity	metabolic process; transport	cytoplasm; membrane; mitochondrion	0.0383616
IPI00130589	SUPEROXIDE DISMUTASE [CU-ZN].	P08228	47.4	15.9	antioxidant activity; catalytic activity; metal ion binding; protein binding	cell communication; cell death; cell differentiation; cell organization and biogenesis; cellular component movement; cellular homeostasis; coagulation; development; metabolic process; regulation of biological process; reproduction; response to stimulus; transport	cytoplasm; cytosol; extracellular; membrane; mitochondrion; nucleus; organelle lumen	0.00183542
IPI00131058	MYOTUBULARIN-RELATED PROTEIN 9.	Q9Z2D0	2.02	62.9	catalytic activity; enzyme regulator activity; protein binding	metabolic process; regulation of biological process	cytoplasm	0.00278269
IPI00131211	CGMP-GATED CATION CHANNEL ALPHA-1.	P29974	2.34	79.4	nucleotide binding; transporter activity	response to stimulus; transport	membrane	0.00383149
IPI00131540	VESICLE TRANSPORT THROUGH INTERACTION WITH T-SNARES HOMOLOG 1A.	O89116	3.69	25	protein binding	cell organization and biogenesis; transport	cytoplasm; Golgi; membrane	0.00106116
IPI00131674	TRYPSINOGEN 7.		3.24	26.4	catalytic activity	metabolic process	_	0.0253546
IPI00131896	BRAIN PROTEIN 44.	Q9D023	19.69	14.3	transporter activity	metabolic process; transport	cytoplasm; membrane; mitochondrion	3.49E-06
IPI00132248	SOMATOSTATIN.	P60041	28.45	12.7	protein binding	cellular component movement; regulation of biological process; response to stimulus	extracellular	3.81E-07
IPI00132276	VESICLE-ASSOCIATED MEMBRANE PROTEIN 3.	P63024	38.83	11.5	protein binding	cell differentiation; cell organization and biogenesis; metabolic process; regulation of biological process; transport	cytoplasm; endosome; membrane	0.0122281

IPI00132278	COMPLEXIN-1.	P63040	56.72	15.1	protein binding; transporter activity	cell communication; transport	cytoplasm; cytosol; membrane	0.00219647
IPI00132388	BASIC LEUCINE ZIPPER AND W2 DOMAIN-CONTAINING PROTEIN 1.	Q9CQC6	10.5	48	protein binding	metabolic process; regulation of biological process	cytoplasm	0.0135859
IPI00132938	MYELOID-ASSOCIATED DIFFERENTIATION MARKER.	O35682	8.44	35.3	_	_	membrane	0.00334361
IPI00132940	NADH DEHYDROGENASE [UBIQUINONE] 1 ALPHA SUBCOMPLEX SUBUNIT 1.	O35683	14.29	8.1	_	metabolic process; transport	cytoplasm; membrane; mitochondrion	0.00207942
IPI00133167	MITOCHONDRIAL IMPORT INNER MEMBRANE TRANSLOCASE SUBUNIT TIM16.	Q9CQV1	10.4	13.8	_	metabolic process; regulation of biological process; response to stimulus; transport	cytoplasm; membrane; mitochondrion	0.0383616
IPI00133289	MITOCHONDRIAL IMPORT RECEPTOR SUBUNIT TOM7 HOMOLOG.	Q9D173	30.91	6.2	transporter activity	transport	cytoplasm; membrane; mitochondrion	0.00334361
IPI00133342	PUTATIVE UNCHARACTERIZED PROTEIN.	Q9CPQ8	21.71	14.2	transporter activity	metabolic process; transport	cytoplasm; membrane; mitochondrion	1.67E-09
IPI00133744	NADH DEHYDROGENASE [UBIQUINONE] 1 ALPHA SUBCOMPLEX ASSEMBLY FACTOR 4.	Q9D1H6	8.09	20.1	protein binding	cell organization and biogenesis	cytoplasm; membrane; mitochondrion	0.00301512
IPI00134017	CYSTEINE AND HISTIDINE-RICH DOMAIN-CONTAINING PROTEIN 1.	Q9D1P4	4.53	37.3	metal ion binding; protein binding	cell organization and biogenesis; metabolic process; regulation of biological process; response to stimulus	_	0.0154766
IPI00136683	ACYL-COENZYME A THIOESTERASE 2, MITOCHONDRIAL.	Q9QYR9	14.13	49.6	catalytic activity	metabolic process	cytoplasm; mitochondrion; organelle lumen	7.42E-07
IPI00136691	PUTATIVE UNCHARACTERIZED PROTEIN (FRAGMENT).		5.26	23.8	DNA binding; metal ion binding	metabolic process; regulation of biological process	nucleus	0.000224024
IPI00137229	ISOFORM 2 OF CELLULAR NUCLEIC ACID-BINDING PROTEIN.	P53996	8.82	18.7	metal ion binding	cell proliferation; metabolic process; regulation of biological process	cytoplasm; cytosol; endoplasmic reticulum; nucleus	0.0199725
IPI00139364	SERINE/ARGININE-RICH SPLICING FACTOR 4.	Q8VE97	2.66	55.9	nucleotide binding; RNA binding	metabolic process; regulation of biological process	nucleus; organelle lumen	7.28E-07
IPI00153266	PROBABLE SACCHAROPINE DEHYDROGENASE.	Q8R127	8.62	47.1	catalytic activity; nucleotide binding	metabolic process	cytoplasm; mitochondrion	2.03E-11
IPI00153381	CYTOCHROME B-C1 COMPLEX SUBUNIT 9.	Q8R1I1	26.56	7.4	catalytic activity; transporter activity	metabolic process; transport	cytoplasm; membrane; mitochondrion	0.000250734
IPI00153813	UNCHARACTERIZED PROTEIN.		4.22	102.6	_	_	_	4.61E-23
IPI00153827	DIPHTHAMIDE BIOSYNTHESIS PROTEIN 1.	Q5NCQ5	3.88	48	protein binding	cell proliferation; metabolic process	cytoplasm; nucleus	8.35E-16
IPI00165902	MITOCHONDRIAL IMPORT INNER MEMBRANE TRANSLOCASE SUBUNIT TIM10.	P62073	22.22	10.3	metal ion binding; protein binding; transporter activity	cell organization and biogenesis; transport	cytoplasm; membrane; mitochondrion	0.0312196
IPI00170249	ISOFORM 1 OF REGULATORY-ASSOCIATED PROTEIN OF MTOR.	Q8K4Q0	2.02	149.4	protein binding	cell communication; cell growth; regulation of biological process; response to stimulus	cytoplasm; vacuole	0.00961595

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IPI00177205	GTP-BINDING PROTEIN RHEB.	Q921J2	20.11	20.4	catalytic activity; metal ion binding; nucleotide binding; protein binding	cell communication; metabolic process; regulation of biological process; response to stimulus	membrane; nucleus; spliceosomal complex	0.0273981
IPI00187452	SUCCINATE DEHYDROGENASE [UBIQUINONE] CYTOCHROME B SMALL SUBUNIT, MITOCHONDRIAL.	Q9CXV1	10.69	17	metal ion binding	metabolic process; transport	cytoplasm; membrane; mitochondrion	0.00286189
IPI00221411	SERINE/THREONINE-PROTEIN PHOSPHATASE 2A 55 KDA REGULATORY SUBUNIT BGAMMA ISOFORM.	Q8BG02	7.83	51.4	enzyme regulator activity; protein binding	cell communication; regulation of biological process; response to stimulus	_	9.10E-34
IPI00221782	UNCHARACTERIZED PROTEIN C18ORF19 HOMOLOG.	Q8BGY7	11.72	31.6	_	_	cytoplasm; membrane; mitochondrion	0.000409551
IPI00221826	ISOFORM SHORT OF SERINE/ARGININE-RICH SPLICING FACTOR 3.	P84104	7.26	14.2	nucleotide binding	_	_	3.07E-10
IPI00221850	UNCHARACTERIZED PROTEIN C2ORF47 HOMOLOG, MITOCHONDRIAL.	Q8BHE8	5.84	33	_	_	cytoplasm; mitochondrion	1.23E-93
IPI00222105	ISOFORM 2 OF LIPID PHOSPHATE PHOSPHATASE-RELATED PROTEIN TYPE 2.	Q8VCY8	1.99	48.4	catalytic activity	_	membrane	3.20E-06
IPI00222208	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN U-LIKE PROTEIN 2.	Q00PI9	9.53	84.9	protein binding	_	nucleus	0.00886652
IPI00222263	ISOFORM 1 OF DISKS LARGE-ASSOCIATED PROTEIN 2.	Q8BJ42	4.72	119	_	cell communication	cytoskeleton; membrane	0.000336971
IPI00222393	ISOFORM 1 OF PROTEIN FAM164A.	Q8BJH1	12.04	35.1	metal ion binding	_	_	0.00370343
IPI00222419	CYTOCHROME C, SOMATIC.	P62897	55.24	11.6	metal ion binding	cell death; metabolic process; transport	cytoplasm; membrane; mitochondrion	9.81E-05
IPI00222514	28S RIBOSOMAL PROTEIN S27, MITOCHONDRIAL.	Q8BK72	5.54	47.7	_	_	cytoplasm; mitochondrion; ribosome	0.00881552
IPI00222548	60S RIBOSOMAL PROTEIN L29.	P47915	11.88	17.6	structural molecule activity	metabolic process	cytoplasm; ribosome	6.79E-10
IPI00222578	SELENOPROTEIN W.	P63300	11.36	9.6	_	cellular homeostasis; regulation of biological process	_	0.0139462
IPI00222759	SYNAPTIC VESICLE MEMBRANE PROTEIN VAT-1 HOMOLOG-LIKE.	Q80TB8	31.89	45.8	catalytic activity; metal ion binding; nucleotide binding	metabolic process	_	0.00409707
IPI00222935	INTEGRIN BETA.		2.22	84.5	protein binding; receptor activity	cell communication; development; metabolic process; regulation of biological process; response to stimulus	membrane	0.0043074
IPI00223437	COATOMER SUBUNIT GAMMA.	Q9QZE5	3.43	97.5	structural molecule activity	transport	cytoplasm; Golgi; membrane; nucleus	2.45E-07
IPI00223713	HISTONE H1.2.	P15864	19.34	21.3	DNA binding; protein binding	cell organization and biogenesis; metabolic process	chromosome; nucleus	1.05E-17
IPI00223714	HISTONE H1.4.	P43274	18.72	22	DNA binding; protein binding	cell organization and biogenesis; metabolic process	chromosome; nucleus	6.41E-15

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IPI00223907	ANKYRIN AND ARMADILLO REPEAT-CONTAINING PROTEIN.	A2RT91	0.82	165.2	protein binding	_	membrane	0.000128371
IPI00223987	LEUCYL-CYSTINYL AMINOPEPTIDASE.	Q8C129	2.05	117.2	catalytic activity; metal ion binding; protein binding	metabolic process	cytoplasm; membrane	0.00881552
IPI00224075	COPINE-1.	Q8C166	7.09	58.8	protein binding	_	_	0.00196948
IPI00226515	TRANSGELIN.	P37804	19.4	22.6	protein binding	cell organization and biogenesis; development	cytoplasm	0.0276405
IPI00226551	ISOFORM 2 OF MYOSIN-ID.	Q5SYD0	1.27	109.2	catalytic activity; motor activity; nucleotide binding	_	cytoskeleton	6.05E-12
IPI00226771	BRI3-BINDING PROTEIN.	Q8BXV2	7.51	28.2	_	_	cytoplasm; membrane; mitochondrion	0.00842123
IPI00226932	ISOFORM 1 OF UNCHARACTERIZED PROTEIN KIAA0090.	Q8C7X2	2.31	111.5	_	_	cytoplasm; endoplasmic reticulum; membrane	5.39E-11
IPI00227900	ISOFORM 2 OF CAMP-DEPENDENT PROTEIN KINASE CATALYTIC SUBUNIT ALPHA.	P05132	16.03	39.8	catalytic activity; nucleotide binding	metabolic process	_	1.14E-09
IPI00227970	ISOFORM 2 OF EXOCYST COMPLEX COMPONENT 7.	O35250	1.84	75.1	protein binding	transport	cytoplasm; membrane	5.88E-06
IPI00228306	ISOFORM 2 OF RAC-GAMMA SERINE/ THREONINE-PROTEIN KINASE.	Q9WUA6	7.87	54.6	catalytic activity; nucleotide binding; protein binding	metabolic process	_	0.0488747
IPI00228580	ISOFORM 1 OF PROTEIN FAM123A.	Q8CCJ4	3.27	69.9	protein binding	cell communication; regulation of biological process; response to stimulus	membrane	0.0343749
IPI00228935	UNCHARACTERIZED PROTEIN.		3.34	38	_	_	_	1.49E-18
IPI00229392	RAS-RELATED GTP-BINDING PROTEIN A.	Q80X95	2.24	36.5	nucleotide binding; protein binding	cell communication; cell death; regulation of biological process; reproduction; response to stimulus	cytoplasm; Golgi; nucleus; vacuole	0.000209556
IPI00229525	GUANINE NUCLEOTIDE-BINDING PROTEIN G(OLF) SUBUNIT ALPHA.	Q8CGK7	13.12	44.3	catalytic activity; metal ion binding; nucleotide binding; protein binding; signal transducer activity	cell communication; metabolic process; regulation of biological process; response to stimulus	membrane	0.000179791
IPI00230006	CAMP-DEPENDENT PROTEIN KINASE INHIBITOR ALPHA.	P63248	19.74	8	catalytic activity; enzyme regulator activity	metabolic process; regulation of biological process; transport	cytoplasm; nucleus	1.39E-25
IPI00230264	HISTONE H2A.X.	P27661	36.36	15.1	DNA binding; protein binding	cell organization and biogenesis; metabolic process; regulation of biological process; reproduction; response to stimulus	chromosome; nucleus; organelle lumen	0.000209556
IPI00230320	CARBONIC ANHYDRASE 1.	P13634	8.05	28.3	catalytic activity; metal ion binding	metabolic process	cytoplasm	9.13E-05
IPI00230449	HIPPOCALCIN-LIKE PROTEIN 1.	P62748	54.92	22.3	metal ion binding; protein binding	cell communication; regulation of biological process; response to stimulus	extracellular	0.0184077
IPI00230470	ISOFORM 2 OF ALPHA-ENDOSULFINE.	P60840	41.88	12.9	protein binding; signal transducer activity; transporter activity	cell communication; regulation of biological process; transport	_	0.000513155
IPI00230730	HISTONE H3.2.	P84228	40.44	15.4	DNA binding	cell organization and biogenesis; metabolic process; regulation of biological process	chromosome; nucleus; organelle lumen	7.72E-07
IPI00230766	PARVALBUMIN ALPHA.	P32848	56.36	11.9	metal ion binding	_	cytoplasm	0.000800162

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IPI00263028	CDKN2A-INTERACTING PROTEIN.	Q8BI72	3.37	59.7	protein binding; RNA binding	cell communication; cell growth; cell organization and biogenesis; metabolic process; regulation of biological process; response to stimulus	nucleus; organelle lumen	0.00409707
IPI00263879	60S RIBOSOMAL PROTEIN L35.	Q6ZWV7	8.13	14.5	structural molecule activity	metabolic process	cytoplasm; ribosome	0.0243816
IPI00263903	ISOFORM 5 OF ALPHA-TUBULIN N-ACETYLTRANSFERASE.	Q8K341	5.16	35.1	catalytic activity	_	_	6.48E-09
IPI00270098	ISOFORM GP95-TRKB OF BDNF/NT-3 GROWTH FACTORS RECEPTOR.	P15209	1.47	53.2	catalytic activity; nucleotide binding; protein binding; receptor activity; signal transducer activity	cell communication; cell differentiation; development; metabolic process; regulation of biological process; response to stimulus; transport	cytoplasm; cytosol; membrane	0.00636178
IPI00270362	RAP GUANINE NUCLEOTIDE EXCHANGE FACTOR 4 ISOFORM 3.	Q9EQZ6	1.38	99.4	enzyme regulator activity	cell communication; metabolic process; regulation of biological process; response to stimulus; transport	cytoplasm; cytosol	0.00965231
IPI00271430	UNCHARACTERIZED PROTEIN (FRAGMENT).		9.76	14.1	structural molecule activity	metabolic process	cytoplasm; mitochondrion; ribosome	0.000209556
IPI00271726	39S RIBOSOMAL PROTEIN L28, MITOCHONDRIAL.	Q9D1B9	8.56	30.2	structural molecule activity	metabolic process	cytoplasm; mitochondrion; organelle lumen; ribosome	1.01E-05
IPI00272622	METHIONINE AMINOPEPTIDASE 1.	Q8BP48	2.85	43.2	catalytic activity; metal ion binding	metabolic process	_	0.0307188
IPI00274656	MITOCHONDRIAL-PROCESSING PEPTIDASE SUBUNIT BETA.	Q9CXT8	4.29	54.6	catalytic activity; metal ion binding	metabolic process	cytoplasm; membrane; mitochondrion; organelle lumen	0.0171585
IPI00275198	ISOFORM STEP20 OF TYROSINE-PROTEIN PHOSPHATASE NON-RECEPTOR TYPE 5.	P54830	12.64	19.8	catalytic activity	metabolic process	_	0.000728067
IPI00281212	UNCHARACTERIZED PROTEIN.		0.86	127.8	protein binding	cell communication; regulation of biological process; response to stimulus	membrane	2.23E-06
IPI00283755	UNCHARACTERIZED PROTEIN.		0.22	466.4	catalytic activity; motor activity; nucleotide binding	cellular component movement	cytoskeleton	3.28E-15
IPI00308276	KELCH REPEAT AND BTB DOMAIN-CONTAINING PROTEIN 3.	Q8BHI4	1.15	69.5	protein binding	_	_	0.0176651
IPI00308332	ARMADILLO REPEAT-CONTAINING X-LINKED PROTEIN 3.	Q8BHS6	5.01	42.6	protein binding	metabolic process; regulation of biological process	cytoplasm; membrane; mitochondrion	8.71E-06
IPI00312172	VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN 4A.	Q8VEJ9	3.66	48.9	catalytic activity; nucleotide binding; protein binding; RNA binding	cell division; metabolic process; transport	cytoplasm; endosome; membrane	0.0105569
IPI00314456	KELCH DOMAIN-CONTAINING PROTEIN 8A.	Q91XA8	4.29	38.8	protein binding	_	_	0.0442722
IPI00314865	YTH DOMAIN FAMILY PROTEIN 2.		2.59	62.2	_	_	_	1.37E-28
IPI00316469	DOLICHYL-DIPHOSPHOOLIGOSACCHARIDE--PROTEIN GLYCOSYLTRANSFERASE SUBUNITSTT3B.	Q3TDQ1	1.82	93.2	catalytic activity	metabolic process	cytoplasm; endoplasmic reticulum; membrane	8.02E-07

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IPI00316491	HEMOGLOBIN SUBUNIT BETA-2.	P02089	78.91	15.9	metal ion binding; transporter activity	response to stimulus; transport	cytoplasm; cytosol; membrane	7.26E-19
IPI00318982	26S PROTEASOME NON-ATPASE REGULATORY SUBUNIT 12.	Q9D8W5	18.42	52.9	protein binding	_	proteasome	0.00752679
IPI00319525	GLYCOGEN PHOSPHORYLASE, LIVER FORM.	Q9ET01	4.94	97.4	catalytic activity; nucleotide binding	metabolic process	cytoplasm; membrane	0.0356578
IPI00319652	GLUTATHIONE PEROXIDASE 1.	P11352	5.47	22.3	antioxidant activity; catalytic activity	metabolic process; response to stimulus	_	7.92E-05
IPI00321497	VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN 33B.	P59016	2.11	70.5	protein binding	cell organization and biogenesis; transport	cytoplasm; endosome; membrane; vacuole	0.00233101
IPI00321646	ISOFORM 1 OF PROTEASOME-ASSOCIATED PROTEIN ECM29 HOMOLOG.	Q6PDI5	3.91	203.6	_	metabolic process	cytoplasm; cytoskeleton; endoplasmic reticulum; endosome; nucleus; proteasome	1.47E-07
IPI00322209	KERATIN, TYPE II CYTOSKELETAL 8.	P11679	3.67	54.5	catalytic activity; motor activity; protein binding; structural molecule activity	cell communication; cell death; cell differentiation; cell organization and biogenesis; development; metabolic process; regulation of biological process; response to stimulus	cytoplasm; cytoskeleton; membrane; nucleus; organelle lumen	0.0031756
IPI00323182	SERINE/THREONINE-PROTEIN KINASE 32C.	Q8QZV4	3.07	55.2	catalytic activity; metal ion binding; nucleotide binding	metabolic process	_	4.97E-13
IPI00323510	ISOFORM 1 OF LYSINE-SPECIFIC DEMETHYLASE 6A.	O70546	1.36	154.3	catalytic activity; metal ion binding; protein binding	cell organization and biogenesis; metabolic process; reproduction	nucleus; organelle lumen	0.0243816
IPI00330146	ISOFORM 1 OF NUCLEAR FRAGILE X MENTAL RETARDATION-INTERACTING PROTEIN2.	Q5F2E7	2.46	75.6	catalytic activity; RNA binding	metabolic process	cytoplasm; nucleus; ribosome	0.0435348
IPI00330619	PROTEIN VAC14 HOMOLOG.	Q80WQ2	3.58	88	enzyme regulator activity	cell death; metabolic process; regulation of biological process; response to stimulus	cytoplasm; endoplasmic reticulum; endosome; membrane; vacuole	0.00301512
IPI00331014	UPF0670 PROTEIN C8ORF55 HOMOLOG.	Q80ZW2	7.73	23.8	_	_	extracellular	0.0149431
IPI00331064	VOLTAGE-DEPENDENT R-TYPE CALCIUM CHANNEL SUBUNIT ALPHA-1E.	Q61290	0.75	257	transporter activity	cell communication; cellular component movement; cellular homeostasis; defense response; regulation of biological process; response to stimulus; transport	membrane	8.75E-11
IPI00331163	S-PHASE KINASE-ASSOCIATED PROTEIN 1.	Q9WTX5	58.9	18.7	catalytic activity; protein binding	cell organization and biogenesis; metabolic process	cytoplasm; cytosol; nucleus	0.0335605
IPI00331334	BAG FAMILY MOLECULAR CHAPERONE REGULATOR 3.	Q9JLV1	1.73	61.8	protein binding	cell death; development; regulation of biological process	cytoplasm; cytosol; membrane	1.19E-39
IPI00337844	E3 SUMO-PROTEIN LIGASE RANBP2.	Q9ERU9	0.36	340.9	catalytic activity; metal ion binding; protein binding	metabolic process; transport	membrane; nucleus	9.12E-19
IPI00338412	ISOFORM 2 OF FIBROBLAST GROWTH FACTOR 12.	P61329	13.81	20.4	protein binding	_	_	3.50E-05
IPI00344703	ADAM METALLOPEPTIDASE WITH THROMBOSPONDIN TYPE 1 MOTIF, 17.		0.62	124.1	catalytic activity; metal ion binding	metabolic process	extracellular	5.49E-05

IPI00344786	PROTEIN NJMU-R1.	Q9CYI0	3.56	44.4	_	_	_	0.00405811
IPI00345779	ISOFORM RPN10E OF 26S PROTEASOME NON-ATPASE REGULATORY SUBUNIT 4.	O35226	5.77	27.9	metal ion binding	metabolic process; regulation of biological process; response to stimulus	_	0.00578086
IPI00346834	KERATIN, TYPE II CYTOSKELETAL 2 ORAL.	Q3UV17	1.52	62.8	catalytic activity; motor activity; structural molecule activity	_	cytoskeleton	0.00732873
IPI00348094	UNCHARACTERIZED PROTEIN.		11.09	50.4	catalytic activity; nucleotide binding; structural molecule activity	cell organization and biogenesis; cellular component movement; metabolic process	cytoplasm; cytoskeleton	0.0427295
IPI00349069	PUTATIVE GTP-BINDING PROTEIN PARF.	Q5U3K5	1.66	79.8	nucleotide binding	cell communication; regulation of biological process; response to stimulus	cytoplasm; cytoskeleton; nucleus	0.00636178
IPI00349306	PEPTIDYL-PROLYL CIS-TRANS ISOMERASE G.	A2AR02	1.86	88.3	catalytic activity	metabolic process	cytoplasm; nucleus; organelle lumen	2.92E-06
IPI00352475	28 KDA HEAT- AND ACID-STABLE PHOSPHOPROTEIN.	Q3UHX2	16.02	20.6	protein binding	cell communication; cell proliferation; regulation of biological process; response to stimulus	extracellular	3.13E-07
IPI00355099	ISOFORM 2 OF LEUCINE-RICH REPEAT-CONTAINING PROTEIN 16C.	Q3V3V9	5.42	79.7	_	_	_	0.0312196
IPI00357660	PUTATIVE UNCHARACTERIZED PROTEIN.		5.98	20.8	enzyme regulator activity	cell communication; metabolic process; regulation of biological process; response to stimulus	_	6.02E-20
IPI00357789	SHC SH2 DOMAIN-BINDING PROTEIN 1-LIKE PROTEIN.	Q3TTP0	1.72	70.9	_	_	_	0.00389586
IPI00378120	GLUTAREDOXIN-RELATED PROTEIN 5, MITOCHONDRIAL.	Q80Y14	21.05	16.3	catalytic activity; metal ion binding	cellular homeostasis; development; regulation of biological process	cytoplasm; mitochondrion; nucleus	0.02344
IPI00378156	ISOFORM 1 OF RAB GTPASE-ACTIVATING PROTEIN 1.	A2AWA9	2.26	120.7	catalytic activity; enzyme regulator activity; motor activity; protein binding; transporter activity	cell organization and biogenesis; metabolic process; regulation of biological process; transport	cytoplasm; cytoskeleton; cytosol; membrane	0.0425307
IPI00378224	THIOREDOXIN DOMAIN-CONTAINING PROTEIN 15.	Q6P6J9	6.1	38.1	_	cellular homeostasis; regulation of biological process	membrane	2.99E-15
IPI00378764	VGF NERVE GROWTH FACTOR INDUCIBLE.		2.11	68.2	protein binding	cell communication; development; metabolic process; regulation of biological process; reproduction; response to stimulus; transport	cytoplasm; extracellular; membrane	0.0137219
IPI00380780	ELONGATOR COMPLEX PROTEIN 1.	Q7TT37	2.63	149.5	catalytic activity; DNA binding; enzyme regulator activity; nucleotide binding	cell communication; cellular component movement; metabolic process; regulation of biological process; response to stimulus	cytoplasm; nucleus; organelle lumen	1.73E-13
IPI00380816	ISOFORM 4 OF NUCLEAR EXPORT MEDIATOR FACTOR NEMF.	Q8CCP0	2.89	47.6	_	metabolic process	_	0.0135859
IPI00381151	ISOFORM 2 OF PROTEIN FAM186A.	Q9D9R9	24.04	11.6	_	_	_	0.0167231
IPI00381599	RETROTRANSPOSON-LIKE PROTEIN 1.	Q7M732	0.4	198.9	catalytic activity; RNA binding	development; metabolic process	membrane	0.0216479
IPI00399483	40S RIBOSOMAL PROTEIN S30.	P62862	16.95	6.6	structural molecule activity	metabolic process	cytoplasm; ribosome	2.75E-09
IPI00403381	NADH DEHYDROGENASE [UBIQUINONE] FLAVOPROTEIN 3, MITOCHONDRIAL.	Q8BK30	10.58	11.8	_	metabolic process; transport	cytoplasm; membrane; mitochondrion	2.10E-07

IPI00404182	RHO-RELATED GTP-BINDING PROTEIN RHOB.	P62746	33.67	22.1	nucleotide binding; protein binding	cell communication; cell death; cell differentiation; cell division; development; regulation of biological process; response to stimulus; transport	cytoplasm; endosome; membrane; nucleus	0.0319832
IPI00404590	PUTATIVE UNCHARACTERIZED PROTEIN.		11.73	19.2	DNA binding	cell organization and biogenesis; metabolic process	chromosome; nucleus	7.24E-09
IPI00405328	ISOFORM 2 OF B-CELL LYMPHOMA/ LEUKEMIA 11A.	Q9QYE3	3.19	47.4	metal ion binding	_	_	0.0343749
IPI00405596	PHOSPHOACETYLGLUCOSAMINE MUTASE ISOFORM 2.		2.59	55	catalytic activity; metal ion binding	development; metabolic process; reproduction	cytoplasm; cytosol	0.00817131
IPI00406204	UNCHARACTERIZED PROTEIN.		0.93	142.2	protein binding; receptor activity; signal transducer activity	cell communication; regulation of biological process; response to stimulus	membrane	0.000149265
IPI00406841	PUTATIVE UNCHARACTERIZED PROTEIN.		14.85	11.1	_	_	nucleus	0.000267841
IPI00407499	ISOFORM 1 OF 4-AMINOBUTYRATE AMINOTRANSFERASE, MITOCHONDRIAL.	P61922	49.2	56.4	catalytic activity; protein binding	cell communication; metabolic process; reproduction; response to stimulus	cytoplasm; mitochondrion; organelle lumen	0.0110359
IPI00407660	MAWMS1 PROTEIN.		16.13	6.9	_	_	_	2.25E-09
IPI00408500	ISOFORM 2 OF PURINE-RICH ELEMENT-BINDING PROTEIN GAMMA.	Q8R4E6	5.54	36.9	_	_	_	0.00922571
IPI00408895	TRANS-GOLGI NETWORK INTEGRAL MEMBRANE PROTEIN 1.	Q62313	4.53	37.8	_	_	cytoplasm; Golgi; membrane; nucleus	0.0171585
IPI00420812	ISOFORM 1 OF UREA TRANSPORTER 1.	Q8VHL0	1.82	42.1	transporter activity	transport	membrane	0.000660251
IPI00421000	ISOFORM 2 OF DIACYLGLYCEROL KINASE BETA.	Q6NS52	6.04	89.4	catalytic activity	cell communication; regulation of biological process; response to stimulus	_	0.0149431
IPI00421085	CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR SUBUNIT 6.	Q6NVF9	7.44	59.1	nucleotide binding; RNA binding	cell organization and biogenesis; metabolic process	nucleus; organelle lumen	0.00795102
IPI00421240	SPERM-ASSOCIATED ANTIGEN 17.	Q5S003	0.74	246.2	protein binding	_	cytoplasm; cytoskeleton	1.19E-13
IPI00453531	PROTEIN PRUNE HOMOLOG.	Q8BIW1	3.74	50.2	catalytic activity; metal ion binding	_	cytoplasm; membrane; nucleus	0.000212435
IPI00453613	ISOFORM 2 OF E3 UBIQUITIN-PROTEIN LIGASE HUWE1.	Q7TMY8	0.62	369.5	_	_	membrane	5.65E-07
IPI00453835	PUTATIVE UNCHARACTERIZED PROTEIN.		5.82	48.6	protein binding	cell communication; regulation of biological process; response to stimulus	_	0.0184077
IPI00457668	ISOFORM 3 OF SEC1 FAMILY DOMAIN-CONTAINING PROTEIN 1.	Q8BRF7	4.52	67.4	_	transport	_	0.0191766
IPI00458368	UNCHARACTERIZED PROTEIN.		1.16	134	_	_	_	0.000311118
IPI00459442	RETICULON-1 ISOFORM RTN1-C.		47.6	23.5	_	_	cytoplasm; endoplasmic reticulum	0.0331125
IPI00461624	KLHDC4 PROTEIN.		4.05	48.6	protein binding	_	_	0.00935989
IPI00461653	VPS26A PROTEIN.		13.04	19	protein binding	transport	cytoplasm; endosome; membrane	0.0458598
IPI00463297	60S RIBOSOMAL PROTEIN L36.		28.85	12.1	structural molecule activity	metabolic process	cytoplasm; ribosome	0.0105569

IPI00464114	ISOFORM 1 OF TRANSPORTIN-3.	Q6P2B1	3.68	104.1	_	transport	cytoplasm; nucleus	0.0112927
IPI00465812	BAND 4.1-LIKE PROTEIN 1 ISOFORM A.	Q9Z2H5	29.12	98.3	protein binding; structural molecule activity	cell organization and biogenesis	cytoplasm; cytoskeleton; membrane	0.0327634
IPI00466588	RAS-RELATED PROTEIN RAP-2C.	Q8BU31	31.15	20.7	catalytic activity; nucleotide binding; transporter activity	cell communication; cellular component movement; metabolic process; regulation of biological process; response to stimulus; transport	cytoplasm; cytosol; endosome; membrane	0.0284701
IPI00466991	UNCHARACTERIZED PROTEIN.		2.17	78.9	catalytic activity; nucleotide binding	_	_	3.17E-27
IPI00468850	FUMARYLACETOACETATE HYDROLASE DOMAIN-CONTAINING PROTEIN 1.	Q8R0F8	2.64	25.1	catalytic activity; metal ion binding	metabolic process	cytoplasm; cytosol; membrane; mitochondrion	0.00112433
IPI00468999	PHOSPHATIDATE CYTIDYLYLTRANSFERASE 2.	Q99L43	16.44	51.3	catalytic activity	cell communication; metabolic process; regulation of biological process; response to stimulus	cytoplasm; endoplasmic reticulum; membrane; mitochondrion	0.000383838
IPI00471176	HEPATOCYTE CELL ADHESION MOLECULE.	Q640R3	25.36	46.3	protein binding	regulation of biological process	cytoplasm; membrane	0.0135859
IPI00471416	ISOFORM 2 OF COILED-COIL DOMAIN-CONTAINING PROTEIN 90B, MITOCHONDRIAL.	Q8C3X2	10.36	25.6	_	_	_	0.0250468
IPI00471447	UBA3 PROTEIN (FRAGMENT).		8.9	49.3	catalytic activity; nucleotide binding	metabolic process	_	0.0488747
IPI00473748	MICROTUBULE-ASSOCIATED PROTEIN.	P27546	12.05	113.7	protein binding	_	cytoskeleton	0.0425307
IPI00474158	ISOFORM 3 OF SERINE/ARGININE-RICH SPLICING FACTOR 7.	Q8BL97	7.64	17.9	_	_	_	0.000456055
IPI00474465	PUTATIVE UNCHARACTERIZED PROTEIN.		16.5	11.7	enzyme regulator activity	cell communication; metabolic process; regulation of biological process; response to stimulus	_	9.39E-21
IPI00474904	UNCHARACTERIZED PROTEIN.		2.13	75.1	catalytic activity; protein binding	cell proliferation; development; metabolic process; regulation of biological process	cytoplasm; endoplasmic reticulum; membrane	0.0327634
IPI00480233	NADH DEHYDROGENASE SUBUNIT 5.		1.15	68.4	catalytic activity	metabolic process; transport	cytoplasm; membrane; mitochondrion	0.0397751
IPI00515199	UNCHARACTERIZED PROTEIN.		1.46	64.9	metal ion binding; nucleotide binding	_	nucleus	0.0474931
IPI00515505	ISOFORM 3 OF SERINE/ARGININE-RICH SPLICING FACTOR 1.	Q6PDM2	20.92	21.8	_	_	_	0.00452719
IPI00515675	ISOFORM 2 OF STERILE ALPHA AND TIR MOTIF-CONTAINING PROTEIN 1.	Q6PDS3	1.67	79	protein binding	_	_	0.0491731
IPI00553538	HISTONE H3.1.	P68433	40.44	15.4	DNA binding; protein binding	cell organization and biogenesis; metabolic process; regulation of biological process	chromosome; nucleus; organelle lumen	0.00383149
IPI00553774	HISTONE H2B TYPE 3-A.	Q9D2U9	48.41	14	DNA binding	cell organization and biogenesis; metabolic process	chromosome; nucleus	0.00499659

IPI00555113	60S RIBOSOMAL PROTEIN L18.	P35980	22.87	21.6	structural molecule activity	metabolic process	cytoplasm; cytosol; ribosome	0.012587
IPI00607961	TRANSMEMBRANE PROTEIN 33 ISOFORM 2.		8.94	27.9	_	_	membrane	0.00301512
IPI00608064	FERROCHELATASE (FRAGMENT).		2.51	44.7	catalytic activity; metal ion binding; RNA binding	cell differentiation; cell organization and biogenesis; development; metabolic process; regulation of biological process; response to stimulus	cytoplasm; membrane; mitochondrion	0.0307188
IPI00608074	ISOFORM 2 OF UNCHARACTERIZED PROTEIN CXORF38 HOMOLOG.	Q8C5K5	12.94	23.1	_	_	_	6.62E-12
IPI00622766	WD REPEAT-CONTAINING PROTEIN 61 ISOFORM B.		9.66	22.5	protein binding	cell differentiation; cell organization and biogenesis; development; metabolic process; regulation of biological process	chromosome; cytoplasm; nucleus; organelle lumen	2.68E-05
IPI00623191	ISOFORM 2 OF COLLAGEN ALPHA-1(I) CHAIN.	P11087	1.47	117.7	protein binding; structural molecule activity	_	extracellular	4.81E-06
IPI00624773	UNCHARACTERIZED PROTEIN.		3.17	104.5	protein binding; receptor activity; signal transducer activity	cell communication; cell organization and biogenesis; regulation of biological process; transport	_	0.000377272
IPI00625118	ISOFORM 2 OF PHOSPHATASE AND ACTIN REGULATOR 4.	Q501J7	2.85	73.4	receptor activity; signal transducer activity; transcription regulator activity	cell organization and biogenesis; metabolic process; regulation of biological process; response to stimulus	_	5.82E-05
IPI00625175	UNCHARACTERIZED PROTEIN.		2.13	58.1	_	_	_	1.16E-15
IPI00625369	ISOFORM 2 OF UBINUCLEIN-1.	Q4G0F8	1.99	119.3	_	cell differentiation; development	_	0.000516625
IPI00626451	ISOFORM 3 OF DENN DOMAIN-CONTAINING PROTEIN 4B.	Q3U1Y4	2.02	151.5	_	_	membrane	2.13E-21
IPI00647981	Y BOX PROTEIN 1.		10.75	24.7	DNA binding; protein binding	cell differentiation; development; metabolic process; regulation of biological process	cytoplasm; nucleus	2.31E-16
IPI00648041	21 KDA PROTEIN.		6.29	20.8	_	metabolic process; regulation of biological process	_	1.56E-08
IPI00648201	ISOFORM 2 OF ESTRADIOL 17-BETA-DEHYDROGENASE 11.	Q9EQ06	11.21	25.3	catalytic activity; nucleotide binding	metabolic process	_	0.00767832
IPI00648806	ISOFORM 2 OF PROTEIN FAM114A2.	Q8VE88	3.06	53.3	_	_	_	0.0263599
IPI00648829	UNCHARACTERIZED PROTEIN.		5.58	22.9	_	_	cytoplasm; mitochondrion	1.90E-09
IPI00649131	ISOFORM 3 OF HETEROCHROMATIN PROTEIN 1-BINDING PROTEIN 3.	Q3TEA8	6.4	56.8	DNA binding	cell organization and biogenesis; metabolic process	chromosome; nucleus	0.0263599
IPI00649136	UNCHARACTERIZED PROTEIN.		17.48	17	structural molecule activity	metabolic process	cytoplasm; ribosome	0.0318971
IPI00649422	ISOFORM 1 OF LUC7-LIKE PROTEIN 3.	Q5SUF2	5.09	51.4	DNA binding; RNA binding	cell death; metabolic process; response to stimulus	membrane; nucleus; organelle lumen	0.0273981
IPI00649531	UNCHARACTERIZED PROTEIN.		2.78	104.9	catalytic activity; nucleotide binding	metabolic process	_	4.56E-26
IPI00649603	ARGINYL-TRNA--PROTEIN TRANSFERASE 1.		2.36	58.3	catalytic activity	metabolic process	cytoplasm; nucleus	0.0415471
IPI00649678	UNCHARACTERIZED PROTEIN.		7.32	54.3	nucleotide binding; protein binding	metabolic process	cytoplasm	0.000119947

IPI00650034	COILED-COIL DOMAIN-CONTAINING PROTEIN 45 ISOFORM 2.		1.4	90.7	_	_	_	0.00839725
IPI00652299	PUTATIVE UNCHARACTERIZED PROTEIN.		5.22	12.3	_	_	_	0.000890399
IPI00652708	ISOFORM 2 OF PROTEIN TWEETY HOMOLOG 2.	Q3TH73	7.66	52.1	_	_	membrane	1.22E-15
IPI00652802	ARF-GAP WITH GTPASE, ANK REPEAT AND PH DOMAIN-CONTAINING PROTEIN 1ISOFORM 2.		1.62	89	catalytic activity; enzyme regulator activity; metal ion binding; nucleotide binding; protein binding	cell communication; metabolic process; regulation of biological process; response to stimulus	cytoplasm; cytosol	0.00247329
IPI00653306	UNCHARACTERIZED PROTEIN.		3.44	45.9	_	cell differentiation; development; metabolic process	membrane	5.91E-05
IPI00653963	UNCHARACTERIZED PROTEIN.		16.11	20.4	catalytic activity; nucleotide binding; signal transducer activity	cell communication; cell death; metabolic process; regulation of biological process; response to stimulus	cytoplasm; cytosol; membrane; mitochondrion	0.00157991
IPI00654251	UNCHARACTERIZED PROTEIN (FRAGMENT).		0.71	142.8	catalytic activity; DNA binding; nucleotide binding; protein binding	cell differentiation; cell organization and biogenesis; development; metabolic process; regulation of biological process	chromosome; nucleus; organelle lumen	0.0139462
IPI00654255	PUTATIVE UNCHARACTERIZED PROTEIN.		23.38	21.9	catalytic activity; nucleotide binding	cell communication; regulation of biological process; response to stimulus; transport	cytoplasm; nucleus	3.86E-25
IPI00654263	PUTATIVE UNCHARACTERIZED PROTEIN (FRAGMENT).		4.1	24.8	nucleotide binding	_	_	0.00732873
IPI00654285	CUTANEOUS T-CELL LYMPHOMA-ASSOCIATED ANTIGEN 5 HOMOLOG ISOFORM 3.		1.71	85.6	protein binding	cell organization and biogenesis; transport	cytoplasm; membrane; nucleus	0.000168134
IPI00655041	EXOCYST COMPLEX COMPONENT 2.	Q9D4H1	1.19	103.9	protein binding	regulation of biological process; transport	cytoplasm	1.73E-05
IPI00661245	REGULATORY FACTOR X DOMAIN CONTAINING 2.		1.1	157.5	DNA binding	metabolic process; regulation of biological process	_	2.81E-31
IPI00666485	40S RIBOSOMAL PROTEIN S21-LIKE.		30.38	8.8	structural molecule activity	metabolic process	cytoplasm; ribosome	0.000227027
IPI00675855	UNCHARACTERIZED PROTEIN (FRAGMENT).		8.32	112.5	_	cell organization and biogenesis; metabolic process; regulation of biological process; reproduction	cytoplasm; cytoskeleton; mitochondrion; nucleus	0.00141236
IPI00675985	BTB/POZ DOMAIN-CONTAINING PROTEIN KCTD16.	Q5DTY9	4.45	48.9	protein binding	cell communication; cell organization and biogenesis; regulation of biological process; response to stimulus	membrane	0.0343658
IPI00719927	UNCHARACTERIZED PROTEIN.		10.21	116.4	metal ion binding; protein binding	_	membrane	0.0352067
IPI00742400	ISOFORM 2 OF CAMP-DEPENDENT PROTEIN KINASE CATALYTIC SUBUNIT BETA.	P68181	17.16	39.4	catalytic activity; nucleotide binding	metabolic process	_	9.14E-05
IPI00750932	MKIAA0422 PROTEIN (FRAGMENT).		2.3	43.5	catalytic activity; nucleotide binding	cell communication; metabolic process; regulation of biological process; response to stimulus	_	9.41E-14
IPI00752684	UNCHARACTERIZED PROTEIN.		4.7	52.5	protein binding	_	cytoplasm	0.0491731
IPI00753038	SORBITOL DEHYDROGENASE.	Q64442	4.48	38.2	catalytic activity; metal ion binding; nucleotide binding	cellular component movement; metabolic process	cytoplasm; membrane; mitochondrion	0.0319832

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IPI00753152	UNCHARACTERIZED PROTEIN.		18.5	22.5	nucleotide binding	cell organization and biogenesis; metabolic process	cytoplasm; nucleus	0.0343658
IPI00753794	UNCHARACTERIZED PROTEIN (FRAGMENT).		2.65	77.5	metal ion binding	metabolic process; regulation of biological process; transport	cytoplasm; membrane; nucleus	0.0474931
IPI00755058	ISOFORM 2 OF FILAMIN A-INTERACTING PROTEIN 1-LIKE.	Q6P6L0	7.96	23.5	_	_	_	3.67E-92
IPI00755966	UNCHARACTERIZED PROTEIN.		26.92	8.6	protein binding	cell communication; cell death; cell differentiation; cell division; cell organization and biogenesis; cell proliferation; cellular homeostasis; development; regulation of biological process; reproduction; response to stimulus; transport	cytoplasm; cytoskeleton; cytosol; membrane; mitochondrion	0.0343749
IPI00756203	ZINC FINGER PROTEIN 575.	Q3TXZ1	6.69	26.3	DNA binding; metal ion binding	metabolic process; regulation of biological process	nucleus	5.42E-74
IPI00756448	UNCHARACTERIZED PROTEIN.		29.69	6.8	_	_	_	0.0427295
IPI00756953	ISOFORM 4 OF PROTEIN XRP2.	Q9EPK2	3.23	34.9	catalytic activity; enzyme regulator activity; nucleotide binding	metabolic process; regulation of biological process	cytoplasm; membrane	1.09E-13
IPI00757912	UNCHARACTERIZED PROTEIN.		9.09	14.6	catalytic activity	_	cytoplasm; mitochondrion	0.0297411
IPI00761677	GTP-BINDING PROTEIN 1.	O08582	3.14	72.3	catalytic activity; nucleotide binding	metabolic process; regulation of biological process	cytoplasm; cytosol	0.0101475
IPI00762814	UNCHARACTERIZED PROTEIN.		0.99	452.3	catalytic activity; protein binding	metabolic process	_	0.0210297
IPI00762862	METABOTROPIC GLUTAMATE RECEPTOR 2.	Q14BI2	4.13	95.8	receptor activity; signal transducer activity	cell communication; regulation of biological process; response to stimulus; transport	membrane	0.0383616
IPI00775828	ISOFORM 2 OF VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN 26B.	Q8C0E2	4.61	32.4	_	transport	membrane	0.00257602
IPI00798595	ISOFORM ZETA OF LAMINA-ASSOCIATED POLYPEPTIDE 2, ISOFORMS ALPHA/ZETA.	Q61033	10.22	25	_	_	nucleus	0.00383149
IPI00828599	UNCHARACTERIZED PROTEIN.		11.27	22.7	_	_	_	7.35E-09
IPI00828758	UNCHARACTERIZED PROTEIN.		8.33	21	_	_	cytoplasm; membrane; mitochondrion	0.0284701
IPI00830613	ISOFORM 1 OF BAND 4.1-LIKE PROTEIN 1.	Q9Z2H5	29.12	98.3	protein binding; structural molecule activity	cell organization and biogenesis	cytoplasm; cytoskeleton; membrane	9.45E-05
IPI00830707	UNCHARACTERIZED PROTEIN.		10.01	93.8	metal ion binding; protein binding	cell communication; cell differentiation; cellular component movement; development; regulation of biological process; response to stimulus	membrane	0.00732263
IPI00831124	UNCHARACTERIZED PROTEIN.		3.62	25.7	catalytic activity	metabolic process	cytoplasm	0.00922571
IPI00831330	TROPOMYOSIN ALPHA-1 CHAIN ISOFORM 6.		37.5	28.5	structural molecule activity	development	cytoplasm; cytoskeleton	0.0101475
IPI00831694	UNCHARACTERIZED PROTEIN.		2.72	80.5	catalytic activity; protein binding	cell death; cell proliferation; development; metabolic process	_	0.00886652

IPI00845802	HEMOGLOBIN ALPHA, ADULT CHAIN 2.		87.32	15.1	metal ion binding; transporter activity	transport	cytoplasm; cytosol	0.0273981
IPI00850288	PUTATIVE PROTEIN PHOSPHATASE 1 REGULATORY INHIBITOR SUBUNIT 3G.	Q9CW07	5.76	37.8	protein binding	metabolic process; regulation of biological process	cytoplasm	5.02E-07
IPI00854922	POM121-LIKE PROTEIN 2 ISOFORM 2.		4.26	51.3	_	_	_	5.25E-09
IPI00855125	UNCHARACTERIZED PROTEIN.		0.68	178.6	_	_	membrane	0.00372267
IPI00856133	ISOFORM 1 OF PROTEIN UNC-80 HOMOLOG.	Q8BLN6	0.25	363.3	_	_	membrane	0.0243816
IPI00856136	ISOFORM 2 OF ZINC FINGER PROTEIN 532.	Q6NXK2	1.67	95.4	_	_	_	0.010706
IPI00856140	UNCHARACTERIZED PROTEIN.		8.72	21.9	enzyme regulator activity	cell communication; metabolic process; regulation of biological process; response to stimulus	_	2.18E-06
IPI00856307	COSTARS FAMILY PROTEIN C6ORF115 HOMOLOG.	Q4KML4	16.05	9	_	_	_	2.24E-12
IPI00856717	UNCHARACTERIZED PROTEIN.		3.15	62.7	_	_	_	2.18E-25
IPI00856749	UNCHARACTERIZED PROTEIN.		4.88	22.9	catalytic activity; RNA binding	metabolic process	nucleus; organelle lumen	1.64E-36
IPI00857233	UNCHARACTERIZED PROTEIN.		37.5	9.4	protein binding	_	_	0.000839264
IPI00857687	ISOFORM 2 OF BRO1 DOMAIN-CONTAINING PROTEIN BROX.	Q8K2Q7	39.81	11.8	_	_	_	0.0331125
IPI00857698	PROTEIN KINASE JNK1.		12.24	26.9	catalytic activity; nucleotide binding; signal transducer activity	cell communication; metabolic process; regulation of biological process; response to stimulus	_	0.000183164
IPI00857865	54 KDA PROTEIN.		34.73	54.1	catalytic activity; nucleotide binding; protein binding	metabolic process	_	0.0105569
IPI00858016	UNCHARACTERIZED PROTEIN.		4.02	37.6	_	_	_	0.0491731
IPI00874728	ISOFORM 2 OF TROPOMYOSIN BETA CHAIN.	P58774	20.42	32.9	protein binding; structural molecule activity	_	cytoplasm; cytoskeleton	0.0119087
IPI00875863	UNCHARACTERIZED PROTEIN.		3.11	53.9	metal ion binding; nucleotide binding	cell communication; regulation of biological process; response to stimulus	cytoplasm; membrane; mitochondrion	0.00351945
IPI00875916	UNCHARACTERIZED PROTEIN.		2.83	34.7	RNA binding	metabolic process	nucleus; organelle lumen; spliceosomal complex	0.0149431
IPI00876427	UNCHARACTERIZED PROTEIN.		10.64	54.9	metal ion binding; nucleotide binding	_	_	3.96E-15
IPI00876489	TYROSINE-PROTEIN PHOSPHATASE NON-RECEPTOR TYPE SUBSTRATE 1 ISOFORM 1.		26.52	56	protein binding	cell organization and biogenesis; cellular component movement; regulation of biological process; transport	membrane	9.69E-07
IPI00876558	UNCHARACTERIZED PROTEIN.		0.81	166.5	protein binding; receptor activity; signal transducer activity	cell communication; development; regulation of biological process; response to stimulus	membrane	0.0176041
IPI00877206	UNCHARACTERIZED PROTEIN.		1.91	166.2	protein binding	cell organization and biogenesis	cytoskeleton	0.00372267
IPI00877337	ISOFORM 2 OF DEHYDROGENASE/REDUCTASE SDR FAMILY MEMBER 7B.	Q99J47	4.78	34	catalytic activity	metabolic process	_	4.73E-05

IPI00880460	ISOFORM 4 OF CCR4-NOT TRANSCRIPTION COMPLEX SUBUNIT 10.	Q8BH15	3.95	58.6	_	_	_	0.0101475
IPI00880733	UNCHARACTERIZED PROTEIN.		5.53	23.4	_	_	membrane	0.00554508
IPI00881670	ISOFORM 2 OF TUDOR DOMAIN-CONTAINING PROTEIN 5.	Q5VCS6	2.01	105.3	_	_	_	4.96E-21
IPI00881939	UNCHARACTERIZED PROTEIN.		1.71	162.9	protein binding; receptor activity; signal transducer activity	cell communication; regulation of biological process; response to stimulus	membrane	0.000662188
IPI00885363	UNCHARACTERIZED PROTEIN.		9.49	17.5	_	_	_	3.25E-10
IPI00885364	ISOFORM 7 OF SH3 DOMAIN-CONTAINING KINASE-BINDING PROTEIN 1.	Q8R550	12.73	12	protein binding	cell organization and biogenesis; cellular component movement; regulation of biological process	cytoplasm; nucleus	1.67E-09
IPI00885399	LEUCINE-RICH REPEAT AND WD REPEAT-CONTAINING PROTEIN KIAA1239.	Q6P5U7	0.8	197.3	protein binding	_	_	0.000113032
IPI00885454	UNCHARACTERIZED PROTEIN.		21.88	7.3	_	_	membrane	1.33E-06
IPI00885539	UNCHARACTERIZED PROTEIN.		2.62	41.7	_	cell organization and biogenesis	nucleus	0.0221135
IPI00885547	PUTATIVE UNCHARACTERIZED PROTEIN.		15.38	12.2	_	cell organization and biogenesis; metabolic process; regulation of biological process; transport	cytoplasm; endoplasmic reticulum; Golgi; membrane	2.35E-06
IPI00886083	UNCHARACTERIZED PROTEIN.		2.73	53.7	catalytic activity	metabolic process	cytoplasm; mitochondrion	1.63E-07
IPI00886310	ISOFORM 2 OF WASH COMPLEX SUBUNIT FAM21.	Q6PGL7	1.76	136	catalytic activity; metal ion binding	metabolic process	cytoplasm	0.0135859
IPI00895063	UNCHARACTERIZED PROTEIN.		20.19	11.2	catalytic activity	metabolic process	nucleus; organelle lumen	0.000466007
IPI00895403	UNCHARACTERIZED PROTEIN.		1.34	262	DNA binding; protein binding; transporter activity	cell communication; cell death; cell differentiation; cell growth; cell organization and biogenesis; cellular homeostasis; development; metabolic process; regulation of biological process; response to stimulus; transport	membrane	0.02344
IPI00896032	ISOFORM 2 OF UPF0600 PROTEIN C5ORF51 HOMOLOG.	Q8BR90	6.19	26.1	_	_	_	0.0065562
IPI00896072	UNCHARACTERIZED PROTEIN (FRAGMENT).		1.58	87.8	_	cell communication; regulation of biological process; response to stimulus	_	3.58E-14
IPI00915477	OBSCURIN ISOFORM 2.	A2AAJ9	0.44	830.7	enzyme regulator activity; protein binding	cell communication; regulation of biological process; response to stimulus	membrane	1.25E-05
IPI00918136	UNCHARACTERIZED PROTEIN.		17.02	10.3	_	_	_	0.0171585
IPI00918333	MYELIN EXPRESSION FACTOR 2 ISOFORM 3.		11.09	59.5	nucleotide binding	_	_	4.40E-05
IPI00918940	UNCHARACTERIZED PROTEIN.		12.4	29.4	protein binding	transport	membrane	1.19E-07
IPI00919121	UNCHARACTERIZED PROTEIN.		5.02	62.3	catalytic activity	metabolic process	cytoplasm; membrane	0.0185271
IPI00923037	UNCHARACTERIZED PROTEIN.		79.1	22.6	protein binding	_	_	0.000336971
IPI00927961	UNCHARACTERIZED PROTEIN.		11.83	54.4	catalytic activity; nucleotide binding; protein binding	cell communication; cell differentiation; cell organization and biogenesis; cell proliferation; cellular component movement; cellular homeostasis; development; metabolic process; regulation of biological process; response to stimulus	_	0.0120504

IPI00928096	UNCHARACTERIZED PROTEIN.		2	84.9	protein binding	_	_	1.08E-16
IPI00929786	ISOFORM 1 OF LA-RELATED PROTEIN 1.	Q6ZQ58	1.49	121.1	RNA binding	_	cytoplasm	0.0269704
IPI00929874	ISOFORM 2 OF UNCHARACTERIZED PROTEIN KIAA0564 HOMOLOG.	Q8CC88	1.35	116.1	catalytic activity; nucleotide binding	_	_	0.0307188
IPI00930820	ISOFORM 3 OF SYNAPTOJANIN-2-BINDING PROTEIN.	Q9D6K5	11.88	11.1	protein binding	_	_	0.0273981
IPI00943994	SMALL NUCLEAR RIBONUCLEOPROTEIN F.	P62307	15.12	9.7	RNA binding	metabolic process	nucleus; spliceosomal complex	0.0312196
IPI00954626	ISOFORM 3 OF RECEPTOR-TYPE TYROSINE-PROTEIN PHOSPHATASE EPSILON.	P49446	1.95	71.4	catalytic activity	metabolic process	membrane	1.41E-14
IPI00956990	INNER NUCLEAR MEMBRANE PROTEIN MAN1.		1.96	100.1	nucleotide binding	cell communication; cell differentiation; development; regulation of biological process; response to stimulus	membrane; nucleus	7.68E-05
IPI00957025	UNCHARACTERIZED PROTEIN.		23.33	13.4	_	_	_	0.020506
IPI00969956	PROTEASOME ACTIVATOR COMPLEX SUBUNIT 2 ISOFORM 2.		16.88	26.1	_	_	proteasome	0.0243816
IPI00970487	UNCHARACTERIZED PROTEIN.		7.02	72.7	protein binding; transporter activity	metabolic process; regulation of biological process; transport	_	0.000683489
IPI00970530	UNCHARACTERIZED PROTEIN.		10.32	14.1	_	_	_	1.09E-06
IPI00975221	UNCHARACTERIZED PROTEIN.		4.86	91.1	_	_	_	0.00667092
IPI00985596	HEMOGLOBIN SUBUNIT BETA-1-LIKE ISOFORM 5.		62.42	16.7	metal ion binding	_	_	4.81E-37
IPI00985807	UNCHARACTERIZED PROTEIN.		10.93	26.6	catalytic activity; nucleotide binding	metabolic process	cytoplasm; mitochondrion	2.26E-08
IPI00986015	PROTEIN DISULFIDE-ISOMERASE A6-LIKE.		25	47.2	_	cellular homeostasis; regulation of biological process	_	5.04E-08
IPI00986912	UNCHARACTERIZED PROTEIN.		12.07	13	protein binding; structural molecule activity	transport	cytoplasm; Golgi; membrane	0.0405836
IPI00987092	UNCHARACTERIZED PROTEIN.		0.59	129.5	catalytic activity	metabolic process	membrane	2.50E-05
IPI00987373	UNCHARACTERIZED PROTEIN.		21.15	6.2	_	_	_	0.000428266
IPI00987376	SRP54C PROTEIN.		2.6	55.5	catalytic activity; nucleotide binding; RNA binding	transport	cytoplasm	0.0383616
IPI00987645	PROTEIN PRRC2A ISOFORM 2.		0.7	228.9	protein binding; receptor activity; signal transducer activity	cell communication; cell death; cell differentiation; cell organization and biogenesis; cell proliferation; metabolic process; regulation of biological process; response to stimulus; transport	membrane	0.00087902
IPI00987813	UNCHARACTERIZED PROTEIN.		2.31	147.7	protein binding	_	membrane	1.73E-13
IPI00987890	UNCHARACTERIZED PROTEIN.		20.96	52.5	catalytic activity; metal ion binding	cell communication; metabolic process; regulation of biological process; response to stimulus	_	5.10E-05
IPI00988018	UNCHARACTERIZED PROTEIN.		17.18	58.2	protein binding; transporter activity	cell organization and biogenesis; response to stimulus; transport	cytoplasm; membrane; vacuole	1.68E-05
IPI00988328	TUBULIN BETA-3 CHAIN-LIKE.		27.09	50	catalytic activity; nucleotide binding	cell organization and biogenesis; metabolic process	_	0.00271561
IPI00988468	UNCHARACTERIZED PROTEIN.		12.66	9.1	protein binding	development; response to stimulus	extracellular	4.54E-06

IPI00988539	UNCHARACTERIZED PROTEIN.		30.46	52.2	protein binding; structural molecule activity	cell differentiation; cell organization and biogenesis; development; metabolic process; regulation of biological process	cytoplasm; cytoskeleton; cytosol; membrane	0.0435348
IPI00988573	UNCHARACTERIZED PROTEIN.		2.37	70.9	catalytic activity; motor activity	metabolic process; regulation of biological process	chromosome; cytoskeleton; nucleus; organelle lumen	0.0199941
IPI00988950	HEMOGLOBIN SUBUNIT BETA-1-LIKE.		84.35	15.7	metal ion binding; transporter activity	transport	cytoplasm; cytosol	4.40E-10
IPI00989397	SRC SUBSTRATE CORTACTIN.		20.27	32.2	DNA binding	_	membrane	0.00452719
IPI00989707	UNCHARACTERIZED PROTEIN.		1.72	58.9	protein binding	_	membrane	0.00141236
IPI00989807	77 KDA PROTEIN.		1.8	76.6	_	_	membrane	2.78E-05
IPI00990071	UNCHARACTERIZED PROTEIN.		6.77	29.6	protein binding	cell organization and biogenesis; response to stimulus	extracellular; membrane	5.71E-16
IPI00990418	VOLTAGE-GATED CHLORIDE CHANNEL CLC-4A.		1.02	76.4	protein binding; transporter activity	transport	membrane	0.00112433
IPI00990426	UBIQUITIN-LIKE MODIFIER-ACTIVATING ENZYME ATG7-LIKE ISOFORM 1.		1.51	66	catalytic activity	_	membrane	0.0216479
IPI01007845	ISOFORM 2 OF HISTONE-LYSINE N-METHYLTRANSFERASE MLL.	P55200	0.56	429.1	DNA binding; metal ion binding; protein binding	_	nucleus	1.77E-11
IPI01008219	NEUREXIN II ISOFORM 3.		1.26	163	protein binding	cell communication; cell organization and biogenesis; development; transport	membrane	0.00881552
IPI01026773	UNCHARACTERIZED PROTEIN.		10.48	83	protein binding	cell communication; regulation of biological process; response to stimulus	cytoplasm; membrane	0.0387157
IPI01026887	PROTEIN.		3.16	27.8	protein binding	cell differentiation; cell organization and biogenesis; cell proliferation; cellular component movement; development; metabolic process; regulation of biological process; response to stimulus	extracellular	0.00732873
IPI01027424	ISOFORM 4 OF SERINE/THREONINE-PROTEIN KINASE BRSK1.	Q5RJI5	7.49	35.1	catalytic activity; nucleotide binding	metabolic process	membrane	0.00804233
IPI01027599	LAMININ SUBUNIT ALPHA-1 PRECURSOR.		0.55	337.9	catalytic activity; motor activity; protein binding; structural molecule activity	cell communication; cell differentiation; cell organization and biogenesis; cellular component movement; development; regulation of biological process; response to stimulus	cytoplasm; cytoskeleton; extracellular; membrane	0.0184077
IPI01027799	11 KDA PROTEIN.		21.78	11.4	protein binding	cell organization and biogenesis; metabolic process	cytoplasm; cytosol	0.02344