Quantitative Proteomic Analysis of 2-Methoxyestradiol Induced Apoptosis in MCF-7 Human Breast Cancer Cells

By

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- Ellisor, M.B., Gong, C., Hogan, M.J., Bazemore-Walker, C.R. A Statistically Validated Proteomic Platform for reliable label-free quantification using spectral counting. 59th ASMS Conference, 2011, Denver, CO *poster presentation*
- Poston, C.N., Ellisor, M.B., Gu, H., Bazemore-Walker, C.R. Identification of Authentic Lipid Raft Proteins in Rat Liver Using Quantitative Proteomics. ACS National Meeting and Exposition, 2009, Washington, DC, *poster presentation*
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Abstract

Reliable quantitation of protein abundance is fundamental in accurately determining differential protein expression associated with biological phenomena such as cell growth and differentiation, disease progression, and drug treatment. Furthermore, the ability to quantitatively monitor global and site-specific changes in phosphorylation and other post-translational modifications are required in order to discern the dynamic molecular events and signaling cascades involved in governing these systems in response to particular stimuli.

Mass spectrometry-based approaches have proven particularly effective for large-scale proteomic and phosphoproteomic analyses. However, many of the conventional quantitative strategies are typically not suitable for investigations pertaining to hormone sensitive cell lines such as estrogen-dependent MCF-7 human breast cancer cells. It is therefore critical to develop flexible and accurate quantitative proteomic and phosphoproteomic strategies that may be easily adapted to a wide range of scientific applications

We have successfully developed a practical and statistically validated two-dimensional LC-MS/MS platform (RP-RP-nanoESI-MS/MS) for proteomic analysis using label-free quantification. An additional advantage of this methodology is the use of an intermediate-pH during the first dimension of separation which prevents possible β-elimination of phosphopeptides in support of phosphoproteomic investigations. However, with the increase in experimental variation associated with TiO_2 phosphopeptide enrichment, we have established a robust and flexible phosphoproteomic strategy

utilizing a simple and cost-effective quantification method based on reductive isotopic diethylation.

2-Methoxyestradiol has shown considerable promise as an anticancer therapeutic agent with a broad spectrum of activity against multiple tumor cell lines. Evidence has shown that various cellular targets and pathways have been implicated in 2-ME induced apoptosis. However, conflicting reports suggest that the cytotoxic effects of 2-ME may operate through multiple mechanisms of action with varying degrees of contribution depending upon cell type. The MCF-7 human breast cancer cell line is commonly used as a cellular model for breast cancer investigations and has shown to be particularly sensitive to 2-ME treatment (IC_{50} – 0.45 μM).

Utilizing our global proteomic and phosphoproteomic strategies, we aimed to determine potential therapeutic targets and signaling pathways associated with 2-ME-induced apoptosis that may provide evidence for a unifying mechanism of action. Although our data supports many of the previously described mechanisms associated with 2-ME-induced apoptosis, we provided additional evidence that these individual mechanisms may be related to the effects generated by the disruption of the Mevalonate pathway which coincides with an increase in ER-related stress.

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Table of Contents

Table of Figures

List of Tables

Chapter 1

General Introduction

1.1 Mass Spectrometry Based Proteomics

Proteomics is the comprehensive study of the entire protein complement within a given cell, tissue, or organism under a defined set of environmental conditions at a particular point in time (1). Since proteins serve as vital components of the molecular machinery involved in cellular function, proteomic research focuses on elucidating protein expression, regulation, and biological function. Compared to the genome of an organism which remains constant, the proteome is in a continual state of flux, responding to changes in the internal or external cellular environment associated with cell growth and differentiation, disease progression, or drug treatment. It was once thought that mRNA expression levels accurately represented the amount of protein being expressed within a biological system. However, contrary to initial beliefs, mRNA expression levels were later shown not correlate with protein expression due to post-transcriptional mechanisms which regulate protein translation and post-translational modifications (2). Therefore, proteomic research attempts to elucidate and quantify the molecular components and protein networks involved in various cellular processes by determining differential protein expression, protein-protein interactions, and post-translational modifications directly at the protein level.

Initially, proteomic investigations of complex protein mixtures were typically conducted using traditional biochemical techniques involving two-dimensional (2-D) gel electrophoresis followed by Edman degradation sequencing. Utilizing this proteomic strategy, researchers were able to create unique 2-D protein maps, exploiting the orthogonality between protein charge and size (isoelectric focusing/SDS-PAGE) (3). Protein maps were then compared across samples using sophisticated computer

algorithms and spots of interest were excised and readily subjected to Edman degradation sequencing for protein identification in an automated fashion (4, 5). Despite the contributions of these techniques, their utility is limited due to the extreme laborious and time-consuming nature of these methods and the large amount of purified protein required for accurate identification which is often compromised by insufficient separation and co-migration of proteins within a single spot. The necessity for more sensitive and reliable methods for large-scale proteomics investigations led to rapid advancements in technology and the development of mass spectrometry-based proteomic methods for global high-throughput proteomic analyses.

In conjunction with advances in bioinformatic technology, mass spectrometry has become a powerful tool for analyzing biomolecules in an unbiased fashion based on the mass-to-charge ratio (*m/z*) of gas-phase analytes. Mass spectrometers consist of three basic components: the ion source, one or more mass analyzer(s), and an ion detector. With the development of soft ionization techniques that can preserve structural information such as electrospray ionization (ESI) and matrix assisted laser desorption ionization (MALDI), large biomolecules are readily volatilized and introduced into the mass analyzer where the ionized analytes can be separated and subsequently detected with high sensitivity, resolution, and mass accuracy (6, 7). Currently, there are two fundamental proteomic strategies, "top-down" proteomics which analyzes intact proteins and "bottom-up" proteomics which analyzes proteins at the peptide level (8).

Top-down proteomic approaches analyze samples at the protein level and provide explicit information about the protein sequence and structural modifications. An advantage of these strategies is their ability to directly locate and characterize post-

translational modifications (PTM) as well as their ability to differentiate between protein isoforms which may result from alternative splicing (9). However, these approaches suffer from several limitations. In general, top-down proteomic analyses require high resolution mass spectrometers and are typically limited to the analysis of purified proteins or simple protein mixtures due to the complexity of the spectra generated by multiply charged proteins and the difficulties associated with coupling these techniques online with high-performance liquid chromatography (HPLC). Generally, top-down proteomic applications utilize nonergodic disassociation methods, such as electron capture dissociation (ECD) or electron transfer disassociation (ETD), for protein fragmentation during tandem mass spectrometry (MS/MS) analysis, which permits fragmentation along the peptidic backbone, yielding primarily *c* and *z* ions (Figure 1.1), while preserving post-translational modifications (10, 11). Unfortunately, the low-efficiency of these fragmentation techniques require prolonged accumulation, activation, and detection times which prevent real-time analysis on an LC-timescale. In addition, proteins are generally difficult to work with under typical LC-MS conditions, mainly due to their poor solubility in MS-compatible buffers which hinders the analysis of hydrophobic proteins, *i.e.*, membrane proteins, or large proteins (MW > 50 kDa).

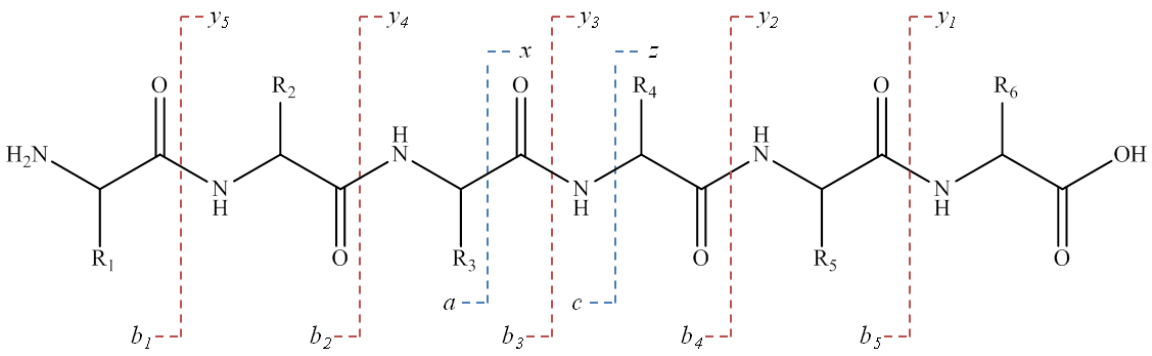

Figure 1. 1 - Nomenclature of Peptide Fragmentation.

In contrast, conventional bottom-up proteomic approaches focus on analyzing proteolytic peptides generated from site-specific proteases such as trypsin or Lys-C (12, 13). These approaches provide distinct advantages over top-down proteomic approaches and are routinely used for protein identification and quantification. Although the enzymatic digestion of proteins inherently increases the overall complexity of the sample, peptides are generally easier to work with and are readily soluble in MS-compatible buffers. As a result, highly complex peptide mixtures can be effectively resolved by a variety of LC-based chemistries using one or more dimensions of chromatography that can be directly coupled to mass spectrometry. In addition, peptides provide a much cleaner and easier to interpret MS/MS spectra compared to spectra generated from intact proteins. However, there are a few limitations to bottom-up proteomics, most notably its inadequacy in distinguishing between protein isoforms and determining PTMs. Peptide-based proteomic strategies do not identify proteins directly, and therefore must rely on reconstructing protein sequences from the obtained peptide data. In addition, current limitations in instrumentation generally result in only a small portion of the peptides being selected for MS/MS analysis, limiting this sequence coverage and creating a protein inference problem (14). The low sequence coverage may also result in totally excluding some peptides containing PTMs from ever being identified. Subsequently, various strategies and techniques have been investigated in order to maximize the overall sequence coverage and/or to enrich for particular PTMs.

Technical advances in instrumentation and the development of robust bioinformatic pipelines have allowed bottom-up proteomic approaches to emerge as a powerful and leading method for large-scale high-throughput proteomic analysis. In

general, bottom-up proteomic workflows involve three basic steps: sample preparation, data acquisition, and data analysis (Figure 1.2). Typically, proteins are extracted from samples in the presence of buffers containing protease inhibitors and in many cases detergents in order to assist in protein solubilization. Following protein extraction, samples may undergo a series of clean-up methods in order to remove contaminants such as salts, buffers, detergents, lipids, and particulates that could potentially interfere with downstream analyses (15). Prior to enzymatic digestion, intact proteins may undergo an enrichment or separation step. Depending upon the physiochemical characteristics of the sample, proteins are digested into peptides following routine in-solution or in-gel digestion protocols (16, 17). The complexity of the peptide mixture is inherently increased and therefore generally requires one or more dimensions of peptide fractionation or enrichment in order to reduce sample complexity prior to MS-analysis.

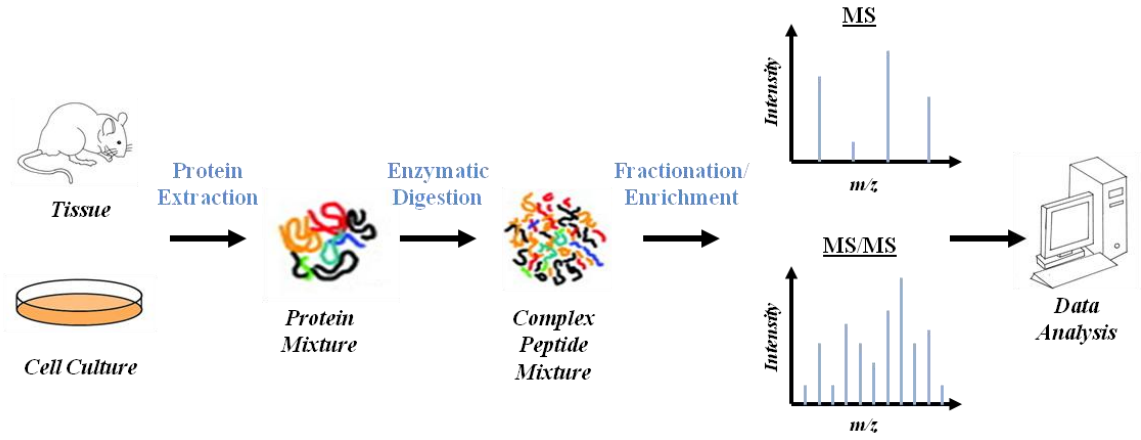

Figure 1. 2 - General Proteomic Workflow.

Peptides are then ionized into the gas-phase and subsequently analyzed based on their mass-to-charge ratio using one or more mass analyzers. During data acquisition, precursor ions identified in each full-scan mass spectrum (MS-scan) may be selected using data-dependent acquisition technology for further fragmentation in order to obtain

tandem mass spectra (MS/MS-scan) for peptide and PTM identification. Depending upon the parameters and capabilities of the instrument, 3-20 tandem mass spectra may be generated from a single MS-scan. Due to the complexity and overwhelming amount of data obtained during a typical analysis, MS-based proteomics rely heavily on computational methods for data analysis.

Although *de novo* sequencing methods are particularly useful when there is limited prior knowledge of a peptide's amino acid sequence, database searching methods are most commonly used for routine analysis of bottom-up proteomic data (18). Advanced searching algorithms such as Sequest, Mascot, X!Tandem, and OMSSA have been developed for database searching (19-22). Although each searching algorithm differs in the way that it processes data, they all attempt to achieve the same goal and accurately identify peptide sequences by comparing experimental MS/MS spectra to theoretical spectra generated *in silico* from peptide sequence databases. In order to reduce false positive identifications and increase confidence in peptide/protein assignments, data is commonly filtered using criteria such as quality scores generated by the searching algorithm which indicates the significance of the match between the experimental and theoretical spectra. Recently, substantial efforts have been made towards developing a universal scoring scheme in order to compare data across experimental platforms and search algorithms (23, 24). It should be noted that scores derived by database searching algorithms serve as a primary discriminating factor for peptide identification but are not reliable indicators of true positive identifications. Consequently, estimations of false discovery rates (FDR) and peptide/protein probability methods have been developed in order to statistically assess error associated with peptide/protein identification in a dataset,

which may be adjusted by filtering data with minimum threshold values correspond to an acceptable FDR (25-28).

The success of biological mass spectrometry is largely due to the development of "soft" ionization methods such as matrix assisted laser desorption ionization (MALDI) and electrospray ionization (ESI). Proteins and peptides are large, polar, nonvolatile, and thermally labile molecules that are difficult to transition into the gas-phase without extensive decomposition and fragmentation. These techniques allow biomolecules to be readily volatilized and introduced into the mass spectrometer while preserving their structural information.

In MALDI ionization, peptides/proteins are co-crystallized with excess matrix containing a chromophore that strongly absorbs radiation at a particular wavelength generated from a pulsating laser. As the matrix absorbs the energy and vaporizes into the gas-phase, it is accompanied by the intact molecular analytes with little transfer in the internal energy between the matrix and the analytes which allows ionization without extensive fragmentation. Although the ionization mechanism is not well understood, MALDI predominately generates singly charged analytes and is routinely applied to top-down proteomics approaches. In addition, MALDI is more tolerable of contaminants commonly found in proteomics workflows and can be useful for ionizing samples that are difficult to clean-up prior to MS-analysis. Unfortunately, the reproducibility associated with MALDI tends to be low due to homogeneity issues throughout the co-crystallized matrix and the strong influences in ionization associated with sample preparation.

Unlike MALDI, ESI produces ions from solution. The unique ability of ESI to transfer ions from solution into the gas phase at atmospheric pressure allows ESI to directly couple liquid chromatography separations to mass spectrometry analysis (LC-MS). Although the mechanism involved in producing gas phase ions by electrospray ionization is not fully understood, it is thought to occur through a series of droplet desolvation and Coulombic repulsion cycles until a single gaseous ion is formed. Another advantage of ESI is at its ability to impart multiple charges to an analyte, allowing the effective mass range of the mass spectrometer to be extended to thousands of daltons.

To a large extent, the information obtained during a proteomics experiment is determined by the performance of the mass analyzer. Although each type of mass analyzer has its advantages and disadvantages they all operate under the same concept measuring ions based on their mass-to-charge ratio. Mass analyzers may be separated into four basic classes: ion traps, time-of-flight, quadrupole, and Fourier transform. These mass analyzers may be used as stand-alone instruments or in combination to form hybrid instruments that allow one to take advantage of their individual strengths. Table 1.1 highlights the comparative features and applications of the most common instruments used in proteomics analyses.

1.2 Phosphoproteomics

Protein phosphorylation is a vital post-translational modification (PTM) that plays an integral role in regulating many molecular functions such as inter- and intracellular communication, differentiation, proliferation, cell cycle regulation, and apoptosis. Phosphorylation is a dynamic cellular event that is tightly regulated by protein kinases

Tabel 1. 1 - Performance Comparisons of the Mass Spectrometry Instruments (29).

Instrument	Applications	Resolution	Mass accuracy	Sensitivity	Dynamic range	Scan rate
LIT (LTQ)	Bottom-up protein identification in high-complexity, high-throughput analysis, LC-MS^n capabilities	2000	100 ppm	Femtomole	1e4	Fast
TQ (TSQ)	Bottom-up peptide and protein quantification; medium complexity samples, peptide and protein quantification (SRM, MRM, precursor, product, neutral fragment monitoring)	2000	100 ppm	Attomole	1e6	Moderate
LTQ-Orbitrap	Protein identification, quantification, PTM identification	100,000	2 ppm	Femtomole	1e4	Moderate
LTQ-FTICR, Q-FTICR	Protein identification, quantification, PTM identification, top-down protein identification	500,000	<2 ppm	Femtomole	1e4	Slow, slow
Q-TOF, IT-TOF	Bottom-up, top-down protein identification, PTM identification	10,000	2–5 ppm	Attomole	1e6	Moderate, fast
Q-LIT	Bottom-up peptide and protein quantification; medium complexity samples, peptide and protein quantification (SRM, MRM, precursor, product, neutral fragment monitoring)	2,000	100 ppm	Attomole	1e6	Moderate, fast

and phosphatases, which carefully control the phosphorylation status of particular proteins. Changes in protein phosphorylation may result in alterations of the activation status, subcellular location, and/or influence protein-protein interactions. Because of its ability to regulate various pathways involved in determining cell fate, many cancer therapeutics have been designed to target and inhibit phosphorylation events that activate signaling cascades which promote cell growth/proliferation.

The ability to quantitatively monitor global and site-specific changes in phosphorylation events allow us to gain a better understand of the key molecular components and signaling cascades involved in response to particular stimuli. However, phosphoproteomic analyses are inherently challenging due to the substoichiometric amount of phosphorylated proteins and the labile nature of the phosphate moiety. Even with recent advancements in instrumentation, phosphoproteomic analyses require the

selective enrichment of phosphopeptides prior to LC-MS analysis. Recently, several phosphopeptide enrichment methods have been developed (Fig 1.3).

Immobilized metal ion affinity chromatography (IMAC) is the most frequently used technique which is based on the high affinity of phosphates to certain trivalent metal ions (*e.g.* Fe^{3+}, Ga^{3+}, Al^{3+}, and Zr^{3+}) (30, 31). In IMAC, metal ions are immobilized onto a porous packing material. Phosphopeptides are retained by a strongly chelation effect between the metal ion and the phosphate group of phosphopeptide. Peptides are then eluted using a high pH elution buffer or by competing with a phosphate salt gradient. However, acidic peptides will also bind strongly to the IMAC material and competitively inhibit the enrichment of phosphorylated peptides. Therefore, samples may undergo additional chemical modifications, such as methyl esterfication, in order to improve the selectivity of IMAC for phosphorylated peptides (32).

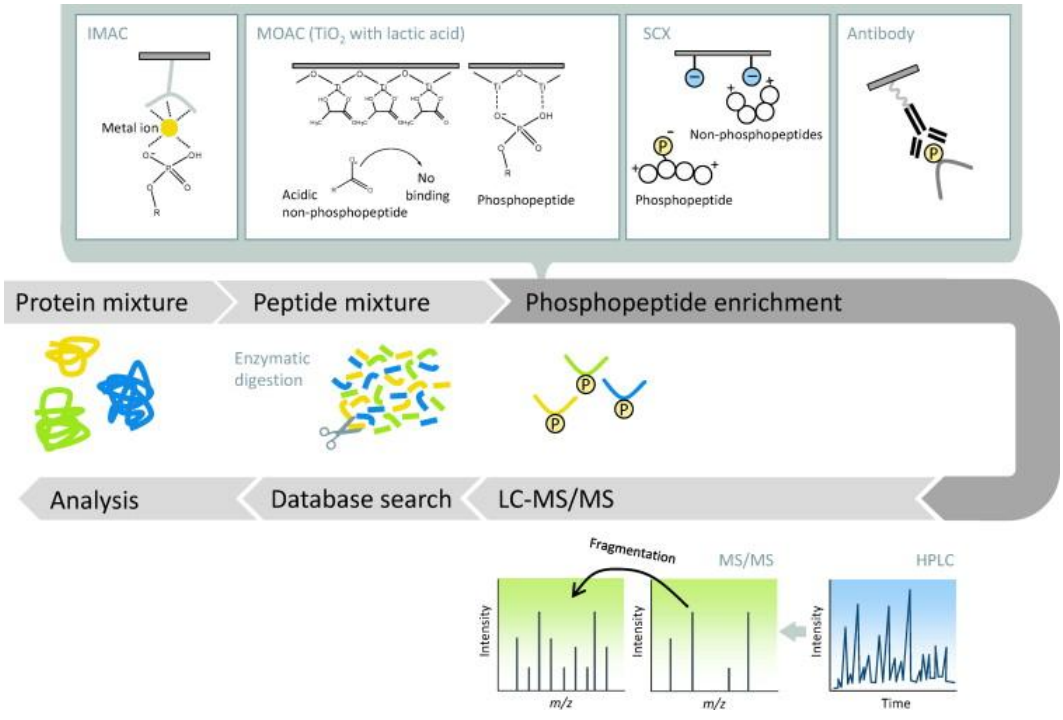

Figure 1. 3 - Phosphopeptide Enrichment Strategies and General Workflow (33).

Titanium dioxide (TiO_2) enrichment provides an alternative affinity-based method for the selective enrichment of phosphorylated peptides. As with IMAC, acidic peptides may interfere with TiO_2 enrichment, however, improvements in the selectivity for phosphorylated peptides do not require chemical modifications of the more abundant acidic residues. In order to improve the selectivity of phosphorylated peptides, samples are enriched in the presence of an acidic excluder such as lactic acid which effectively out competes acidic peptides (34).

It is estimated that at least 30% of all proteins are phosphorylated in mammalian cells, and that greater than 99% of all phosphorylation events occur on serine and threonine residues with less than 1% occurring on tyrosine (35). Although phosphorylation of tyrosine occurs much less often, it plays a vital role in many intracellular signaling pathways. Phosphoproteomic analyses focusing on phosphotyrosine signaling are generally enriched following well established immunoprecipitation (IP) protocols. Unlike phosphoserine/threonine antibodies which have only limited specificity, phosphotyrosine antibodies have proven to be highly selective and are commercially available. However, IP enrichment generally requires a substantial amount of starting material that may be difficult to obtain.

In addition to the challenges associated with the substochiometric levels of phosphorylated proteins, the ionization efficiency of phosphorylated peptides is relatively low compared to that of their non-phosphorylated counterparts. Furthermore, during collision-induced dissociation (CID), the conventional fragmentation technique in proteomic and phopshoproteomic analyses, protonated peptides are excelerated within the mass spectrometer and allowed to collide with a neutral gas (*e.g.*, argon, helium, or

nitrogen) causing peptide fragmentation generating a series of b- and y-ions (Fig. 1.1) (36). Although CID general causes cleavage at the peptide bond, peptides containing phosphorylated serine and thronine residues tend to fragment at the site of phosphorylation dominating fragmentation along the peptide backbone which yields a dominant neutral loss peak and minimizes valuable sequence information. Alternatively, electron capture dissociation (ECD) and electron transfer disassociation (ETD) techniques have been developed in order to provide a gentler fragmentation methods that permit fragmentation along the peptide backbone, generating a series of c- and z-ions while preserving the phosphorylated moiety and retaining site-specific information (Fig. 1.1) (10, 11). However, the compatibility of ECD and ETD fragmentation is not optimal for the analysis of trypsin digested samples which predominately generate 2+ peptides. During the electron transfer process the overall charge state is reduced increasing the *m/z* ratio which inhibits the analysis of peptides which exceed the mass range of the mass spectrometer (37).

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Chapter 2

Validation of 2D-RPLC-MS/MS Proteomic Platform

2.1 Introduction

Reliable quantitation of protein abundance is fundamental in accurately determining differential protein expression associated with biological perturbations such as cell growth and differentiation, disease progression, and drug treatment. Mass spectrometry-based approaches, usually featuring one or more dimensions of liquid chromatography, have proven particularly effective for large-scale proteomic analysis. Because large-scale proteomic analyses are often constricted by the analysis time and the number of replicates available, it is critical to develop flexible proteomic strategies that combine time-efficient separation schemes with simple and versatile methods of quantitation that can be statistically validated.

Two-dimensional liquid chromatography combined with tandem mass spectrometry (2D-LC-MS/MS) has become a commonly used technique for determining changes in protein expression within complex biological systems. The effectiveness of the two-dimensions of separation largely depends on the resolving power afforded by each separation mechanism and the overall orthogonality between each dimension (1-4). Typically, reversed-phase (RP) chromatography is used for LC-MS/MS in the second dimension because of the ease at which it can be directly coupled to mass spectrometry via electrospray ionization. Although various other modes of separation have shown good orthogonality to RPLC, strong cation exchange (SCX) chromatography has been conventionally used in the first dimension of fractionation due its high orthogonality to RPLC and its ability to be coupled off-line or on-line with RPLC-MS/MS (5-8). High-pH RPLC has been shown to be semi-orthogonal to low-pH RPLC and provides a promising alternative to SCX as it offers several advantages over its conventional counterpart, such as superior resolution, peak capacity, and the use of salt-free solvent systems that

eliminate the need to desalt the sample prior to RPLC-MS/MS analysis (1, 9-13). The orthogonality associated with common 2D-LC systems (*ie.* SCX-RP or HILIC-RP) is a result of the differences in retention mechanisms attributed to the stationary phases being utilized in each dimension of separation. In contrast, the orthogonality associated with low- and high-pH RP-RPLC is due to changes in the physiochemical properties of the analytes under varying pH conditions. Although the separation mechanism between each dimension is the same, dramatic differences in the pH of the mobile phases used during each dimension of separation may alter the overall charge, polarity, and relative hydrophobicity of most tryptic peptides, modifying their selectivity for the stationary phase (1, 11, 14). In addition, RP-RP has shown to provide greater peptide and protein identifications compared to SCX-RP, mainly resulting from its increased peak capacity and the uniform distribution of peptides across the elution gradient within the first dimension of separation (11, 13, 15).

Although 2D-LC has proven to effectively increase the dynamic range and proteomic coverage obtained during a proteomic analysis, the overall analysis time is inherently increased by the time required to sequentially sample each fraction collected during the first dimension by LC-MS/MS. One of the perennial challenges of 2D-LC-MS/MS experiments is the trade-off between proteome coverage and analysis time. In order to optimize proteomic coverage without excessively increasing the analysis time, several laboratories have demonstrated that pooling fractions collected during the first dimension of separation at equal time intervals reduces the overall analysis time while improving the efficiency of the available separation space in the second dimension (9, 16, 17).

While maximizing peptide and protein identifications provide valuable qualitative information about the composition of complex biological systems, accurate quantitative information is required to discern the dynamic molecular events that govern such systems. Over the past decade, several MS-based quantitation methods have been developed to determine changes in protein expression levels between two or more biological or treatment conditions. Labeling-based methods which utilize the incorporation and monitoring of various stable isotope labels have proven to provide accurate methods for quantifying relative protein abundances in complex samples (18-24). However, most labeling-based methods require costly reagents and are hindered by the number of possible comparisons, incomplete labeling, and increased sample complexity, which may demand sophisticated quantification software. Recently, label-free quantitation methods have gained increasing popularity because of their ability to provide simple, flexible, and cost-effective approaches that permit the analysis of an unrestricted number of samples (19, 25).

Currently, two label-free quantitation strategies are commonly used to assess relative protein abundance. Peak ion intensities from extracted ion chromatograms have been shown to correlate linearly with protein concentrations in complex protein mixtures, but due to slight shifts in retention times and variations in *m/z* values across individual LC-MS/MS runs, accurate quantitation requires precise computer algorithms to carefully align chromatographic peaks and calculate normalized peak area ratios for relative protein abundance (26-28). Alternatively, spectral counting provides a straightforward approach that does not have the computational requirements associated with peak intensity-based methods. With spectral counting, the total number of acquired MS/MS

spectra assigned to peptides corresponding to a particular protein is used as a measure of protein abundance. Spectral counting has been shown to be very accurate in measuring changes in protein abundance over a dynamic range of two orders of magnitude (29, 30). However, factors such as protein length and differences in instrument performance can artificially influence spectral counting results. Therefore, effective normalization methods are required to permit accurate quantitative comparisons across individual replicates. Various normalization strategies have been proposed in order to accurately assess spectral counting-based quantitative data (30-33). In particular, normalized spectral abundance factor (NASF) based methods provide simple, robust, and easily implemented methods for handling systematic/random variations from run to run as well as innate biases associated with the raw measurement (30, 33-35). In addition, the experimental variability inherent in the design of label-free proteomics requires the use of appropriate statistical methods in order to assess the significance in differentially expressed proteins (36).

Determining the appropriate statistical test may not always be straightforward due to the complex nature of quantitative proteomic experiments and inherent challenges associated with the statistical treatment of MS-based proteomic data. Generally, raw proteomic data is not suitable for statistical analysis and must be normalized and/or transformed prior to analysis (37). In addition, the random sampling effect associated within the mass spectrometer may result in missing values, particularly for low abundant peptides, which can drastically decrease the statistical power of the method. Various statistical approaches have been applied to bottom-up proteomic experiments in order to discern “normal” biological variability from significant experimental variations in protein

expression. As mentioned previously, proteomic experiments are often limited in the number of replicates available and may dictate which methods can be successfully applied to a particular data set. In general, statistical methods that require multiple replicates (*i.e.,* Student's t-test, LPE-test) often exhibit greater statistical power by factoring variability between biological replicates into significance calculations (36, 38). In contrast, other statistical methods (*i.e.,* G-test, Fisher's exact test, AC test) that weigh experimental results against fixed control or expected values absolve the requirement for multiple replicates at the expense of statistical power; replicates are simply pooled to "mimic" replicate analyses, and inter-replicate variability is unconsidered (36). An acute understanding of the experimental design and underlying assumptions and requirements of the statistical methods available will help ensure that the correct statistical approach is taken in order to accurately assess the biological implications of the acquired data.

Along with improvements in 2D-LC-MS/MS strategies, advances in computational and statistical methods have allowed label-free quantitation to emerge as a simple, reliable, and cost-effective method to determine significant changes in protein abundance. Still, the reproducibility of the proteomic method plays a major role in the accuracy of spectral counting-based label-free quantification. Here, we assessed the performance and reproducibility of our 2D-RP/RP-nanoESI-MS/MS proteomic platform (Fig. 2.1). Utilizing our methodology, we established a comprehensive and quantitative proteomic profile of the MCF-7 breast cancer cell line. In addition, we statistically validated the reliability of our proteomic platform for quantitative label-free proteomic comparisons, which may be easily adapted to a range of basic research and clinical applications.

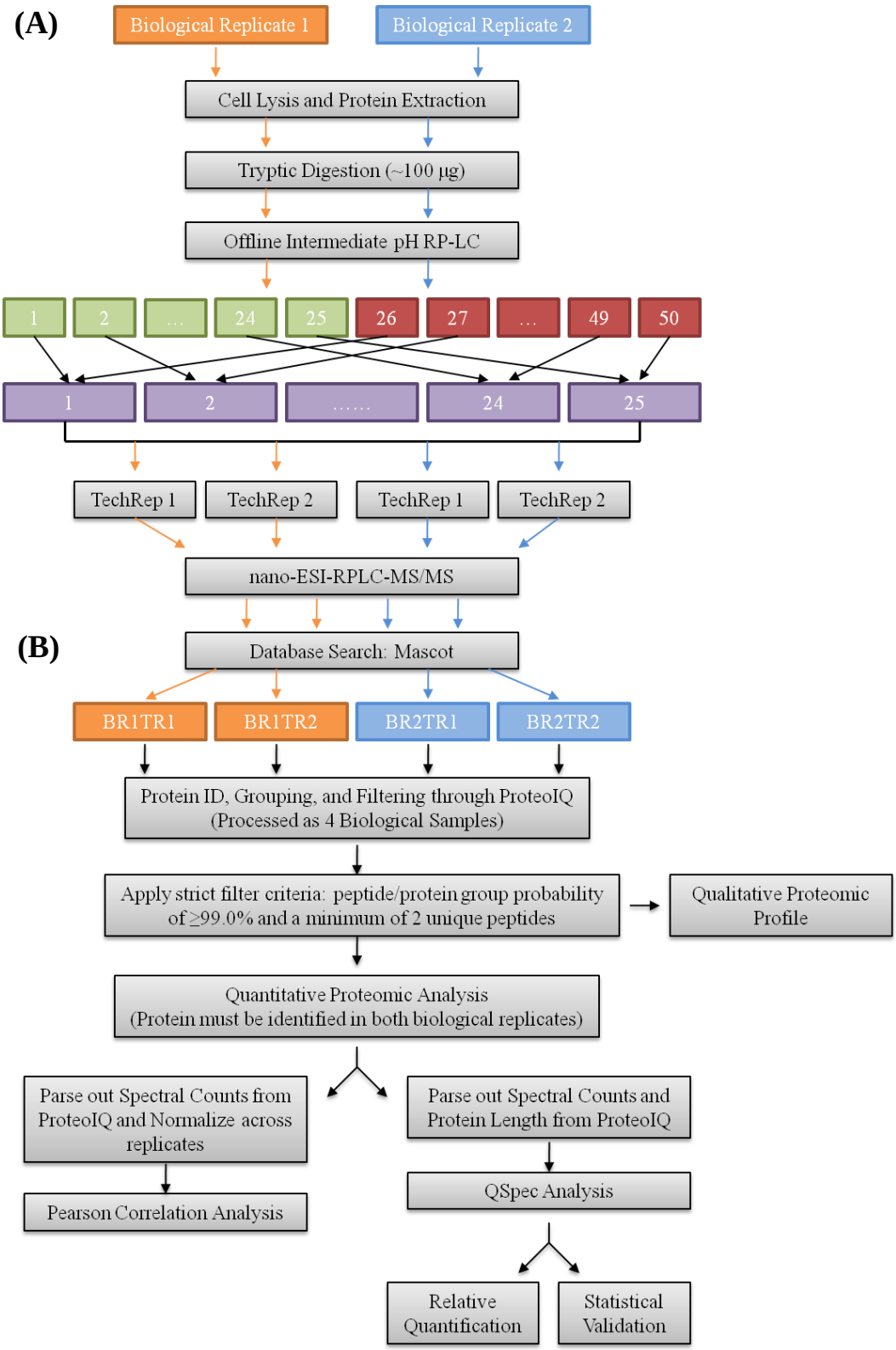

Figure 2. 1 – Proteomic Workflow. (A) Tryptic digests were created from two biological replicates (BR) of lysed MCF-7 cells and subsequently fractionated by offline RPLC at pH 7.5 (2 technical replicates (TR) per BR) prior to nano-RPLC-MS/MS at pH 2.0. **(B)** Acquired spectra were searched through Mascot Daemon and processed through ProteoIQ for data filtering and protein identification. Statistical software (QSpec) was used to determine relative abundance and assess significant experimental variation across biological replicates.

2.2 Experimental Methods

Cell Culture - MCF-7 human breast adenocarcinoma cells were purchased from the American Type Culture Collection (ATCC; Rockville, MD) and cultured to 60-70% confluency in GIBCO minimum essential medium (MEM) with Earle's salts and L-glutamine supplemented with 1.5 mg/ml sodium bicarbonate, 1 mM sodium pyruvate, MEM non-essential amino acids, 10% (v/v) fetal bovine serum (FBS), 100 units/ml penicillin, 100 μg/ml streptomycin and 10 mg/l insulin at 37 °C in a humidified atmosphere of 95% air and 5% CO_2. Cells were then washed with sterile PBS and incubated in serum-free medium at 37 °C for 24 hrs to synchronize them in G_0-phase (39). Following cell synchronization, cells were maintained in complete culture medium with 0.003% DMSO (vehicle control for a concurrent study) at 37 °C for 24 hrs under the same atmospheric conditions.

Cell Lysis and Protein Extraction - Cells were then incubated with cell dissociation solution (3 mM EDTA, 2.5 mM KCl, 150 mM NaCl, 1.5 mM KH_2PO_4, 8 mM Na_2HPO_4, pH 7.2) at 37 °C for 15 min. Cells were transferred to 50 ml conical vials (Corning, Inc.; Corning, NY) and centrifuged at 130 x *g* at 4 °C for 5 min. The supernatant was discarded and the resulting cellular pellet was washed with sterile PBS and then resuspended in lysis buffer (10 mM Tris-HCl (pH 7.5), 150 mM NaCl, 1% Triton X-100, 1 mM Na_3VO_4, 1 mM NaF, 1 mM sodium pyrophosphate, 1 mM β-glycerophosphate, and EDTA-free complete protease inhibitor cocktail). The suspension was incubated with end-over-end rotation for 60 min at 4 °C, followed by 15 manual strokes with a glass-teflon homogenizer. The lysate was centrifuged at 15,000 x *g* for 10 min at 4 °C in order to remove any cellular debris and the protein concentration of the

resulting extract (~4.0 mg/ml) was determined by BCA assay using a commercial protein assay kit (Thermo Scientific; Rockford, IL).

Protein Precipitation and Digestion - Protein (~3.0 mg) was precipitated with 5 times its volume of ice-cold acetone and incubated overnight at -20 °C. After pelleting by centrifugation at 16,000 x *g* for 10 min at 4 °C, the supernatant was carefully decanted and residual acetone was evaporated under nitrogen gas. The protein was resolubilized in 8 M urea, 50 mM ammonium bicarbonate (AMBIC), pH 8.5 and then reduced with 15 mM dithiothreitol (DTT) followed by carbamidomethylation with 30 mM iodoacetamide (IAM). An additional 15 mM DTT was added to the sample in order to quench any excess IAM. After dilution with 50 mM AMBIC to 1.6 M urea, proteins were digested with (1:50 w/w) trypsin and incubated at 37 °C overnight. The digestion was quenched with the addition of glacial acetic acid and samples were immediately stored at -80 °C until further analysis.

First Dimension Separation: Intermediate pH RPLC - Offline first dimension chromatographic separation was performed on an Agilent 1200 Series HPLC system using an Agilent Zorbax 300 Extended-C_{18} column (150 mm x 2.1 mm i.d., 3.5 µm packing particle size) at 35 °C. UV absorption was monitored at 214 nm. Approximately 100 µg of the tryptic digest was loaded onto the column and separated using the following gradient: 0-5 min, 0% solvent B (24 mM ammonium formate in 90% acetonitrile/10% water); 5-55 min, 0-50% B; 55-65 min, 50-70% B; 65-70 min, 70% B; 70-75 min, 70-0% B; 75-85 min, 0% B at 200 µL/min. Solvent A was composed of 24 mM ammonium formate, pH 7.5. Fractions were collected every minute for 50 min starting at the 10 min mark and subsequently evaporated to near dryness (~5 µl) using a

Savant SC110A SpeedVac Concentrator (Thermo Fisher Scientific; Waltham, MA). Samples were reconstituted in 20 µl of 0.1 M acetic acid and stored at -80 °C until further analysis.

Nano-RPLC-MS/MS Analysis - Peptides collected from the first dimension of separation were combined following a concatenated pooling strategy, where 3 µL of sample from fractions eluting during the first half of the gradient were combined with 3 µL of sample from fractions eluting during the second half of the gradient at equal 25 minute time intervals (*i.e.,* fraction *i* was pooled with fraction *i+25*) (9). Pooled samples were analyzed using an Agilent 1200 Series HPLC system coupled to an linear ion trap/Fourier transform (LTQ-FT) hybrid mass spectrometer (Thermo Finnigan) using an automated proteomic platform previously described (40). In brief, peptides were loaded via a microautosampler onto an analytical column (360 µm o.d. x 75 µm i.d. fused silica microcapillary, packed in-house with 10 cm of 5 µm Monitor-C_{18} particles (Column Engineering Inc; Ontario, CA) that was pulled to a fine tip using a P-2000 laser puller (Sutter Instrument; Novato, CA)). Peptides were eluted directly into the LTQ-FT using the following gradient: 0-50 min, 0-70% solvent B (acetonitrile with 0.1 M acetic acid); 50-53 min, 70-95% B; 53-55 min, 95-0% B; 55-90 min, 0% B. Solvent A was composed of aqueous 0.1 M acetic acid. The initial flow rate of ~200 nl/min was reduced to ~30 nl/min once peptides began to elute from the column, as determined from a bovine serum albumin peptide scouting run, as previously described (40). The mass spectrometer scan functions and HPLC solvent gradient were controlled by the Xcalibur data system. Spectra were acquired in the positive ion mode where each full MS survey scan (400-1800 *m/z*) was followed by nine data dependent MS/MS scans of the most intense ions

per survey spectrum, fragmenting selected ions via collision induced dissociation. Ions already selected for MS/MS analysis were dynamically excluded for 30 s with a repeat count of 2 and a repeat duration of 30 s. Two technical replicates were performed for each biological replicate.

Database Searching and Protein Identification - Acquired tandem mass spectra were converted to mascot generic files (.mgf) through the trans-proteomic pipeline (TPP; v4.4.0) and subsequently searched against a target/decoy International Protein Index (IPI) human database (v3.77) using Mascot Daemon (v2.2.0; Matrix Science). The Mascot search parameters were specified as a maximum of 1 missed tryptic cleavage; precursor ion mass tolerance of ±20 ppm; fragment ion tolerance mass tolerance of ±0.5 Da; a fixed modification of cysteine carbamidomethylation; and variable modifications of methionine oxidation and phosphorylation of serine, threonine, and tyrosine residues. Protein identification, grouping, and filtering were accomplished through ProteoIQ (v2.1.08; BioInquire, Athens, GA). Each replicate analysis was treated as an independent biological replicate within ProteoIQ for statistical validation purposes. An initial protein set was generated using the following criteria: minimum ion score of 28.0; peptide length of at least 4; peptide probability of 0.99; protein probability of 0.50; and a false discovery rate of 5.0%. A more stringent filter was then applied to the initial protein set specifying a peptide and protein group probability of ≥99.0% according to the PeptideProphet and ProteinProphet algorithms implemented within ProteoIQ and the identification of at least two peptides (41, 42). A non-redundant protein list was generated where uniquely identified protein groups were represented by the top scoring protein. Spectral counts

from proteins which were identified in replicates but did not meet the specified criteria were removed from those particular replicates and replaced with zero.

Optimization of Data-dependent Acquisition Parameters - Data-dependent acquisition parameters were optimized in order to increase the overall proteomic coverage while maintaining a high level of spectral counts. A test sample was generated from fractions 30-32 (Technical Replicate 2) in order to optimize the dynamic exclusion (DE) settings, primarily the DE duration. The DE duration was investigated at 10, 30, 50, 80, and 120 seconds with a fixed repeat count of 2, repeat duration of 30 s, and an exclusion list of 500. The sample was analyzed in duplicate at each DE duration value and subsequently processed as previously described above.

Quantification and Statistical Validation - Spectral counting was utilized for label-free relative quantification in order to evaluate experimental reproducibility and biological variance. For quantitative analysis, we required that each protein be identified in at least one technical replicate per biological replicate. Spectral count data parsed from ProteoIQ was globally normalized to reduce technical bias and permit comparisons across individual replicates. Normalized spectral abundance factors (NSAF) were calculated as previously described by Zybailov *et al*.: spectral abundance factors (SAF) were obtained for each protein by dividing the protein's spectral count by its length, and the NSAF values were determined by dividing the SAF values by the sum of the SAF values in each replicate (34, 36). Pearson's correlation coefficients were then established using $\log_2$-transformed NSAF values for comparing reproducibility across biological and technical replicates. For biological replicate comparisons, the $\log_2$-transformed NSAF values were represented as the average of the two technical replicates. In addition,

relative protein abundance and experimental variability were assessed through QSpec, a hierarchical Bayes statistical framework for the significance analysis of differential protein expression (43). A minimum Bayes factor of 30 and a maximum RBstat value of 10,000 were used to determine whether the observed variation in protein abundance was likely to be due to an experimental condition or normal biological variation.

2.3 Results

Label-free quantification by spectral counting provides a simple but reliable estimation of relative protein abundance, but the accuracy of measuring relative abundance relies on the reproducibility of the proteomic platform (25, 29, 30, 44, 45). We assessed the performance and reproducibility of our methodology in order to establish a comprehensive and quantitative proteomic profile of the MCF-7 breast cancer cell line.

Efficiency of 2D Separation – Tryptic peptides prepared from an MCF-7 whole cell lysate were subjected to a two-dimensional LC separation followed by MS/MS analysis. The first dimension of separation was conducted at an intermediate pH (pH 7.5) and was monitored by UV absorption at 214 nm. Comparison of chromatograms from replicate analyses indicated that the offline separation method was highly reproducible. Peptides began to elute from the column after approximately 10 minutes, at which time we began collecting fractions. Pooling fractions allowed us to exploit the entire separation capacity of the elution gradient in the second dimension while reducing the overall analysis time by half. Base peak chromatograms of pooled and individual fractions demonstrated that pooling fractions enhanced the overall orthogonality between the two dimensions of separation without compromising peptide identifications (Fig. 2.2).

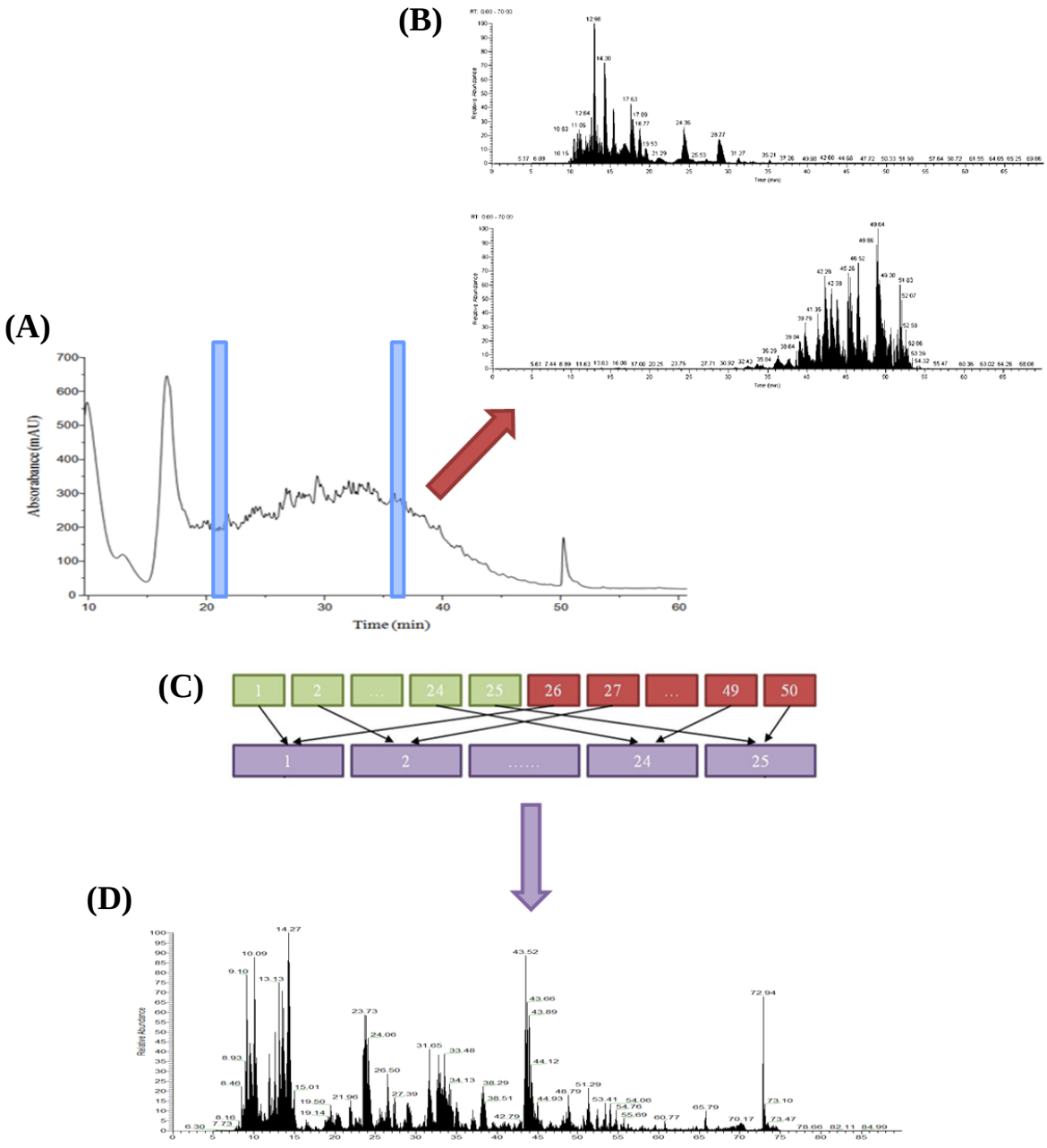

Figure 2. 2 - Concatenated Pooling Strategy. (A) Tryptic peptides from an MCF-7 whole cell lysate were fractionated off-line by intermediate pH RPLC (pH 7.5) and was monitored by UV absorption at 214 nm. Fractions were collected every minute for 50 min. starting at the 10 min. mark. **(B)** Fractions 11 and 36 were analyzed independently by RPLC-MS/MS. Respective chromatograms illustrate the insufficient use of separation space in the second dimension as well as the little in overlap between peptides detected during the second dimension of separation from fractions collected during the first and second half of the elution gradient during the first dimension of separation. **(C)** Fractions from the first half of the elution gradient were combined with fractions eluting during the second half of the gradient at equal 25 min. time intervals (*i.e.*, fraction *i* was combined with fraction *i*+25). **(D)** Base peak chromatogram of the concatenated sample for fractions 11 and 36.

The efficiency of the separation space afforded by the orthogonality of the RP-RPLC strategy is seen upon viewing the distribution of identified peptides across the two dimensions of separation (Fig. 2.3 A). Peptide retention times from the 2D online separation were parsed from Mascot result files using an in-house script and plotted against the 1D pooled fraction number. Approximately 65% of peptides were identified in only one fraction, and ~95% of peptides were identified in two or fewer fractions (Fig. 2.3 B), which may be attributed to the high resolution associated with reversed-phase chromatography.

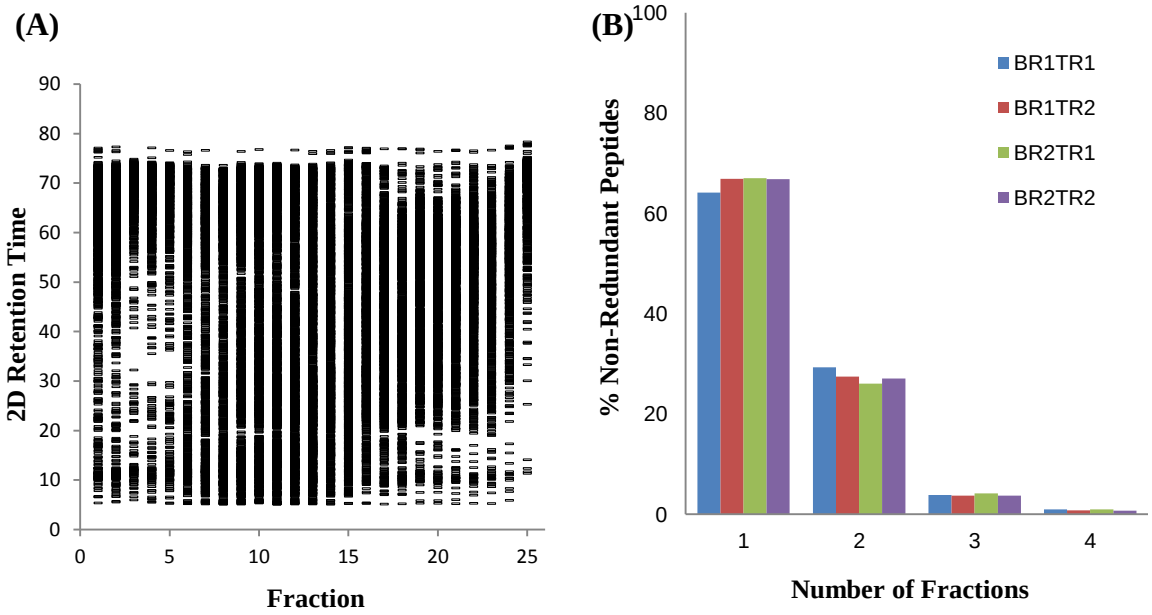

Figure 2. 3 - Efficiency of 2-D Separation Space. (A) Orthogonality map showing the distribution of peptides occupying the available 2-D separation space. **(B)** Percentage of non-redundant peptides identified across fractions.

Protein Identifications – The raw data were processed through our bioinformatic pipeline (Fig. 2.1 B), where acquired tandem mass spectra were searched against the IPI human database (v3.77) using Mascot Daemon (v2.2.0) and subsequently processed through ProteoIQ (v2.1.08) for protein identification, protein grouping, and filtering. A total of 30,599 non-redundant peptides were identified with a confidence threshold of

≥99.0% peptide probability and were used to identify 3,196 proteins (Appendix I) with a minimum of 2 unique peptides per protein at a confidence threshold of ≥99.0% protein probability. When proteins in a group with a group probability of ≥99.0% were indistinguishable, the probability of the group was attributed to the first listed protein, which was reported as a positive protein identification. When the data were searched against a decoy database using our stringent identification criteria, no false positives were identified. In order to establish a reliable baseline for quantitative proteomic comparisons of MCF-7 cells, we required that proteins be identified within each biological replicate. Increasing the stringency of the criteria produced a quantification list of 2,162 proteins (Subset of Appendix I), which were subsequently used to assess the reproducibility and experimental variability associated with the platform.

Evaluation of Reproducibility – Reproducibility across technical and biological replicates was evaluated using two independent calculations, the Pearson correlation and the Bland-Altman repeatability coefficient. Log_2-transformed NSAF values from proteins identified in both replicate runs were used to calculate the correlation coefficients (R). We observed a high correlation between both technical and biological replicates, $R = 0.92$ and 0.91, respectively (Fig. 2.4 A and B). Although Pearson correlation analyses are commonly used to assess the reproducibility of a method, strong correlation does not directly indicate strong agreement between two measurements. To address this concern, repeatability coefficients adopted by the British Standards Institution were calculated according to Bland and Altman, and the difference between the log_2-transformed NSAF values for two replicates was plotted against the mean of the two values (Fig. 2.4 C and D**)** (46). We calculated that the mean difference in values between biological replicates was

0.20 ± 0.04, and the mean difference in values between two technological replicates was -0.17 ± 0.03. We also noted that 95% of the differences in log_2-transformed normalized spectral counts fell within two standard deviations of the mean difference implying that the method provides an acceptable level of repeatability. Although somewhat arbitrary, the repeatability coefficient was determined to be 1.64 for the two biological replicates and 1.47 for the two technical replicates. In addition, the coefficient of variation (*CV*) was calculated across biological and technical replicates and was found to be 11.2% and 9.9%, respectively.

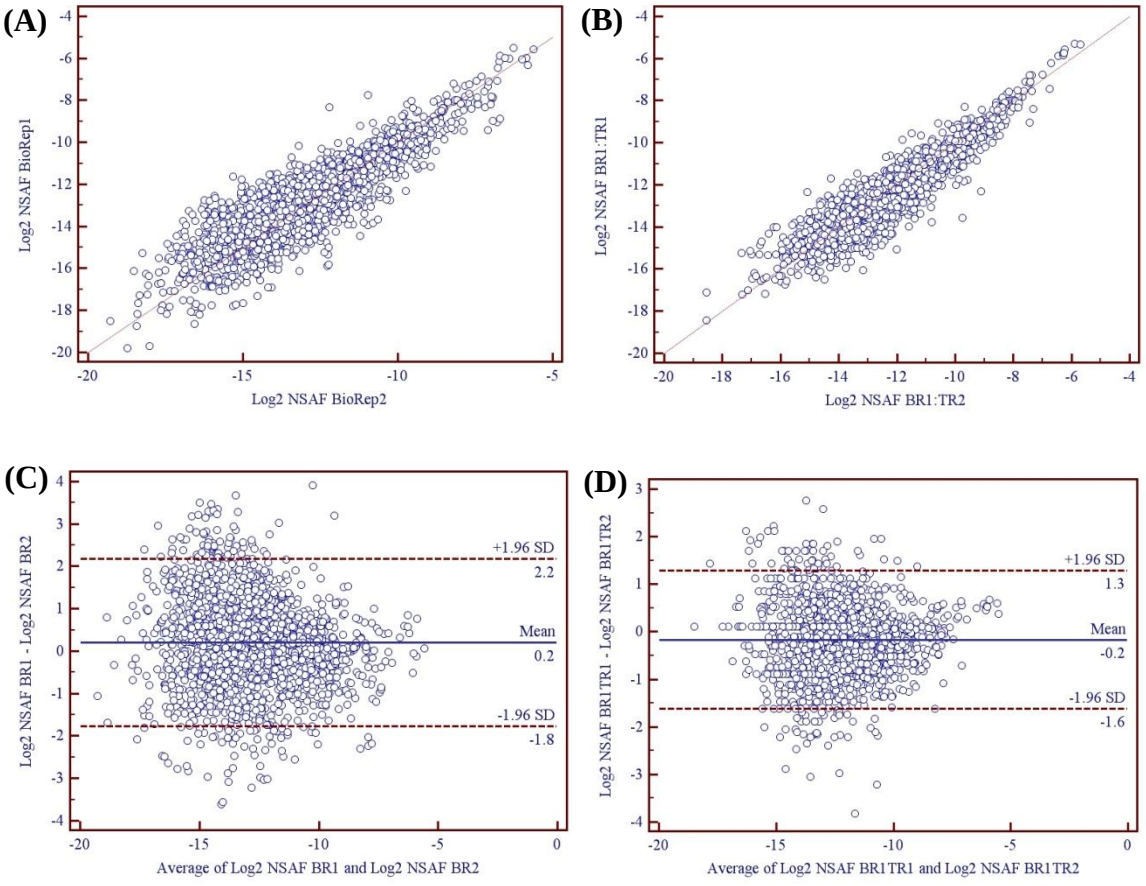

Figure 2. 4 - Reproducibility of Spectral Counting Quantification. (A) Pearson correlation plot between biological replicates. The log_2 transformed NSAF values from each technical replicate were averaged and plotted for each biological replicate. Correlation coefficient R = 0.91. **(B)** Pearson correlation plot between technical replicates from biological replicate 1. Correlation coefficient R = 0.92 **(C)** Bland-Altman plot of repeatability between biological replicates. Mean difference "bias" – 0.20 ± 0.04, repeatability coefficient – 1.64, percentage error – 10.7%, CV – 11.2%. **(D)** Bland-Altman plot of repeatability between technical replicates. Mean difference "bias" – -0.17 ± 0.03, repeatability coefficient – 1.47, percentage error – 7.7%, CV – 9.9%.

Identifying Significant Variation - Relative protein abundance is expressed in terms of NSAF values, described above. However, a recurrent problem in quantitative proteomics is the issue of identifying which proteins showing a change in abundance are significantly up- or down-regulated when the number of replicates is often limited. To address this problem, QSpec was specifically designed for large-scale spectral counting-based proteomic experiments, which implements a statistical framework that utilizes a hierarchical Bayes strategy to perform significance analysis on differential protein expression (43). The problem of having few replicates is partially offset by using this method, which pools information across all proteins to establish a regression model. Utilizing QSpec, we further evaluated the variability of our data. As shown in Figure 2.5, approximately 80% of the quantified proteins exhibited less than a two-fold change in

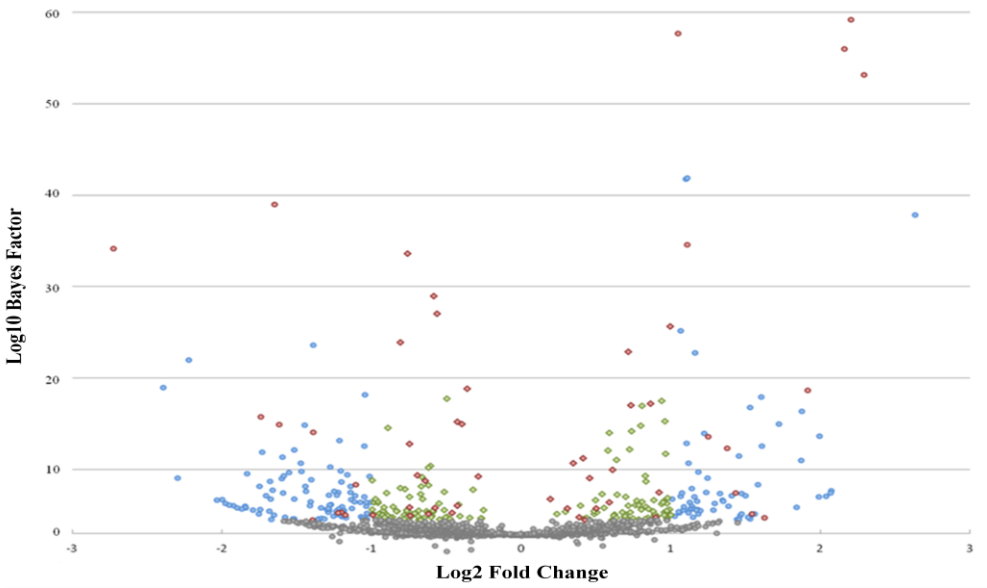

Figure 2. 5 - Volcano Plot for Significant Differential Protein Expression. (Blue) Proteins that a represent ≥ 2-fold change in protein expression across biological replicates and showed a statistical significance in differential expression (Bayes Factor ≥ 30). **(Green)** Proteins that showed statistical significance in differential expression, but showed little biological variation (< 2-fold). **(Red)** Proteins that, although showed significant biological and/or statistical variation, showed poor goodness-of-fit for either model in support of the null hypothesis or alternative hypothesis (RBStat >10,000).

protein expression with no significant statistical variation observed across biological replicates. In addition, only 163 proteins (7.5%) demonstrated significant variation (*i.e.*, 2-fold regulation, Bayes factor ≥30 and RBstat value <10,000) contributed to the experimental variability associated with spectral counting-based proteomic analyses.

Proteomic Profile - In comparison with previously published reports (5, 47, 48), we were able to establish the most comprehensive proteomic profile of the MCF-7 human breast cancer cell line to date (Table 2.1). We confidently identify 3,196 proteins with a minimum of 2 unique peptides per protein with a confidence threshold of ≥ 99.0% protein probability. In addition, we identified 588 proteins that have never before been described in any published accounts of the MCF-7 proteome. Each replicate required only ~40 hours of instrumental analysis time, due in part to the efficiency of our RP-RPLC separation scheme and concatenation strategy.

Table 2. 1 Comparison of Proteomic Profile Studies of MCF-7 Cells

Protein IDs	Method	Instrument	Analysis Time	Confidence Threshold	Comments	Reference
3196	RP-RPLC-MS/MS	LTQ-FT	~ 40 hrs	99%	NSAF; 2 unique peptides	Current Work
2184	Gel-RPLC-MS/MS	LTQ-Orbitrap	~ 67 hrs	95%	NSAF; 2 unique peptides	(47)
2911	SCX-RPLC-MS/MS	Q-TOF	~ 110 hrs	95%	1123 - one unique peptide	(5)
1922	SCX-RPLC-MS/MS	LTQ	~ 40 hrs	Unknown	Only 1 unique peptide	(48)

In addition, our methodology allowed us to achieve a global representation of the entire MCF-7 proteome generated directly from a whole cell lysate without having to perform tedious and time-consuming subcellular fractionations experiments. We observed a good distribution of protein identifications across subcellular localizations for our entire data including the 588 novel proteins that were identified (Fig 2.6).

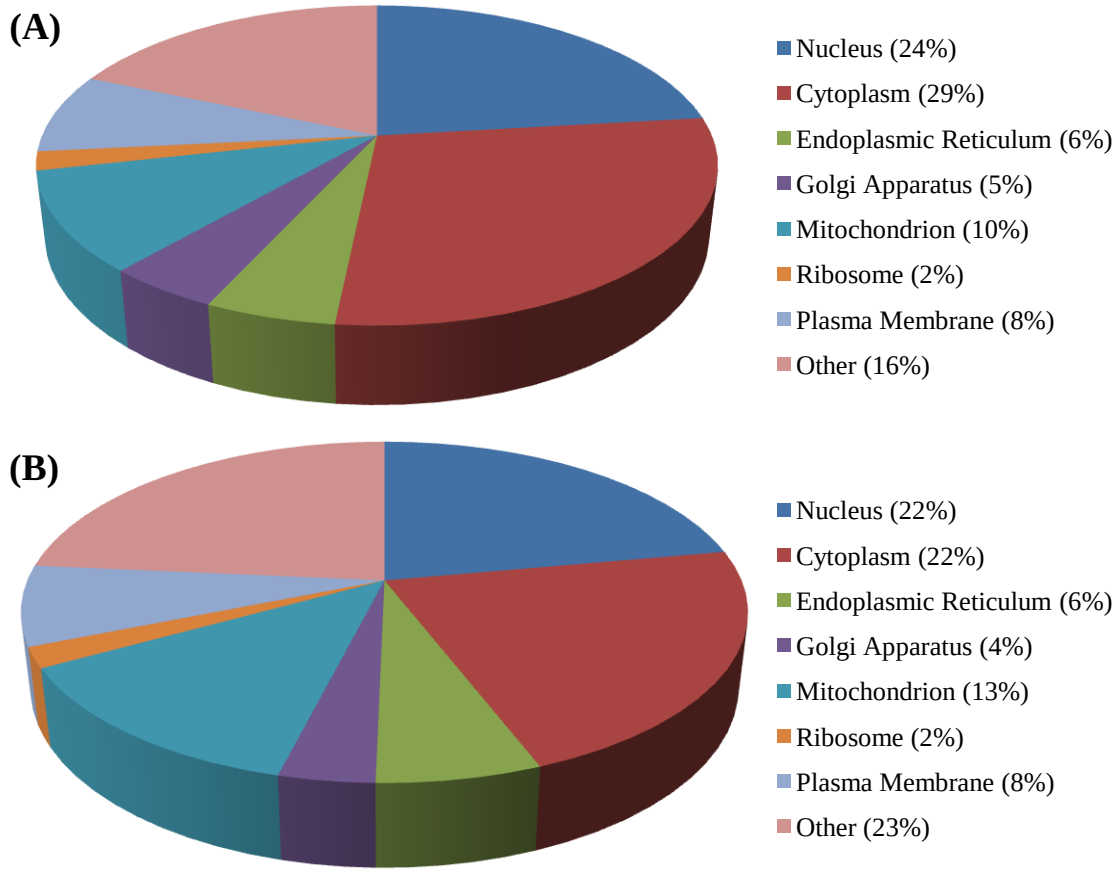

Figure 2. 6 - Distribution of Subcelluar Localizations. Subcellular localizations are according to Gene Ontology (GO). All subcellular locations were accounted for in proteins containing more than 1 localization. **(A)** Distribution of subcellular localizations for all 3,196 confidently identified proteins. **(B)** Distribution of subcellular localizations for the 588 proteins identified that have yet to be described in any previously published accounts of the MCF-7 proteome.

2.4 Discussion

The estrogen-dependent MCF-7 human breast cancer cell line is commonly used as a cellular model for breast cancer investigations. However, these investigations are typically limited in the number of suitable quantification strategies that may be applied as

a result of the hormone sensitive nature of MCF-7 cells. Presumably metabolic labeling strategies (*i.e.,* SILAC) provide the most accurate quantitative methods for determining relatively small changes in protein abundance or post-translational modifications as a result of its ability to reduce experimental error associated with sample processing by combining differentially labeled samples at the cellular level. Although metabolic labeling methods provide a reliable technique for determining relative protein abundance, these methods are not suitable for investigations using MCF-7 cells as they require the presence of hormones and other growth factors that are typically depleted from dialyzed serum used in metabolic labeling strategies (49, 50). It is therefore essential for us to develop a highly effective and efficient proteomic platform which incorporates a versatile and accurate method of quantification that is compatible with proteomic investigations involving the hormone sensitive MCF-7 breast cancer cell line.

Spectral counting-based label-free quantification methods provide a simple and versatile approach for accurately determining changes in relative protein abundance without the use of dialyzed serum. However, the accuracy of label-free quantification may be negatively impacted by the inherent experimental error associated within the design of the experiment. As mentioned previously, 2D-LC systems are commonly used to enhance the overall performance of proteomic analyses. However, each dimension of separation, as well as any additional steps required to process the samples as a result of the 2D-LC scheme (*i.e.,* desalting), could potentially compound the experimental variability associated with label-free quantification. Therefore, the reproducibility of the proteomic method plays a major role in the accuracy of spectral counting-based label-free

quantification and should be assessed in order to determine the overall performance and reliability of the 2D-LC proteomic platform.

Conventional 2D-LC-MS/MS systems have employed SCX in the first dimension of fractionation due to its orthogonality and its ability to be coupled with traditional RPLC-MS/MS. The orthogonality between SCX-RP is driven by the differences in separation mechanisms between the two dimensions of fractionation. During SCX chromatography peptides are primarily retained and separated according to their charge state using an elution gradient with an increasing salt concentration. Under typical SCX conditions, the majority of tryptic peptides are found in 2+ or 3+ charge states, making it difficult to adequately resolve these peptides during the first dimension of separation, reducing the overall peak capacity of the 2D-LC system. In addition, SCX chromatography requires that the samples be desalted prior to and possibly after fractionation which may lead to considerable sample losses and elevations in experimental error associated with spectral counting-based quantification.

As an alternative strategy to conventional SCX-RPLC, we have established an efficient and flexible intermediate-pH RP-RPLC separation scheme that is compatible with proteomic and phosphoproteomic investigations (9, 14). In addition to superior peak capacity and resolution, RPLC eliminates the need to desalt the sample prior to 2D-LC-MS/MS analysis, minimizing the experimental error associated with the 2D-LC system. Although high-pH RPLC (pH $\geq$10.0) is traditionally used during the first dimension of separation and has demonstrated to be orthogonal to conventional low-pH RPLC (pH 2.0), under high-pH conditions phosphorylated peptides may undergo β-elimination of the phosphate moiety (51). Therefore, we conducted the first dimension of separation at an

intermediate-pH (pH 7.5) in order to maintain an acceptable level of orthogonality while preventing phosphopeptides from undergoing possible β-elimination. In addition, we were able to improve the overall efficiency of the 2D-LC system by employing a concatenated pooling strategy (Fig 2.2). Base peak chromatograms of individual fractions collected during the first dimension of separation demonstrate the semi-orthogonal nature of intermediate-pH RP-RPLC and insufficient usage of the separation space available within the second dimension. However, fractions containing peptides collected during the first half of the elution gradient are chemically distinct from those collected during the second half and tend to occupy different regions of the second dimension elution gradient with little to no overlap between fractions. Pooling non-adjacent fractions at equal time intervals allowed us to take advantage of the entire separation space available within the second dimension of separation while reducing the analysis time by half without compromising peptide identifications. The enhanced efficiency and overall orthogonality of the concatenated RP-RPLC strategy is illustrated by the even distribution and dense coverage of identified peptides across the two dimensions of separation (Fig. 2.3 A). In addition, the efficiency is further demonstrated by our ability to resolve and confidently identify 30,599 non-redundant peptides. Approximately 95% of these peptides were identified in two or fewer fractions, which indicate little overlap between adjacent fractions and good overall separation efficiency (Fig. 2.3 B).

The efficiency of our RP-RPLC separation scheme and concatenation strategy has allowed us to confidently identify 3,196 proteins, including 588 proteins which have never before been described in any previously published account of the MCF-7 proteome. It is worth noting that because of the different instruments, data processing strategies, and

identification criteria and confidence thresholds used in each study, we are not able to make any direct comparisons between each 2D separation strategy and can only make general inferences about the overall performance of each proteomic platform. Utilizing a Gel-RPLC-MS/MS strategy, Qattan *et al.* confidently identified 2,184 proteins at a 95.0% protein probability. In addition to the laborious and time-consuming sample preparation techniques employed during this study (*i.e.,* subcellular fractionation, SDS-PAGE, in-gel digestion, etc.), ~67 hrs. of instrumental analysis time was required to analyze each replicate. In comparison, we identified ~81% of the proteins identified within this study requiring substantially less MS/MS analysis time (~30 hrs.). Although Sarvaiya *et al.* and Wang *et al.* both utilized conventional SCX-RPLC, they obtained drastically different numbers in confident protein identifications, 1,992 and 2,911 respectively. In order to reduce the overall MS/MS analysis time, Sarvaiya *et al.* collected relatively broad fractions (3 min.) within the first dimension of separation negating some of the benefits associated with SCX fractionation. In contrast, Wang *et al.* took full advantage of the separation capabilities of SCX in the first dimension of fractionation using a long shallow gradient while collecting nearly twice as many fractions, which resulted in a dramatic increase in the overall analysis time required per replicate (~110 hrs.). We were able to identify ~85% of the proteins identified by Sarvaiya *et al.* due to their less than ideal utilization of the separation capability of their 2D-LC system. In contrast, we only identified approximately 68% of the proteins identified by Wang *et al.* suggesting that SCX-RPLC and RP-RPLC provide complementary data. In addition, ~91% of the 4,340 unique proteins identified across all four studies were identified either by Wang *et al.* or within this study. Although our optimized RP-RPLC strategy provides complementary

data to an optimized SCX-RPLC strategy, our strategy allowed us to identify a greater number of proteins in approximately 1/3 of the time, ~40 hrs. and ~110 hrs., respectively. Utilizing our proteomic platform, we were therefore able to establish the most comprehensive proteomic profile of the MCF-7 human breast cancer cell line to date in a timely and cost effective manner.

Although comprehensive proteomics profiles provide valuable qualitative information about the composition of complex biological systems, accurate quantitative information is required to discern the dynamic molecular events that govern these systems. We therefore evaluated the reproducibility of our proteomic platform in order to assess the degree of experimental error associated with our 2D-LC strategy that may alter the performance and accuracy of spectral counting label-free quantification.

Various aspects of the experimental design including sample preparation and the random sampling associated with mass spectrometric analysis may contribute towards the variability associated with label-free quantitative proteomic investigations. In order to perform a robust analysis of our proteomic platform we first assessed the reproducibility of our 2D-LC-MS/MS system across technical and biological replicates. Two biological replicates of MCF-7 whole cell lysate tryptic digests were prepared independently and fractionated off-line by intermediate-pH RPLC in duplicate (technical replicates). Each technical replicate was subsequently analyzed by traditional nano-RPLC-MS/MS and processed through our bioinformatic pipeline. Pearson correlation coefficients are commonly used in proteomic studies to indicate reproducibility across individual analyses (52-54). We observed a high correlation between both technical and biological replicates, $R = 0.92$ and 0.91 respectively. In addition, our data is tightly clustered around

the line of best fit that nearly bisects the point of origin with the slope of ~0.95 indicating good reproducibility with approximately a 1:1 correlation between replicate analyses (Fig. 2.4 A and B). Although Pearson correlation analyses are commonly used to assess the reproducibility of a method, strong correlation does not directly indicate strong agreement between two measurements. Therefore, we also calculated the repeatability coefficients between technical and biological replicates according to Bland and Altman in order to assess the "precision" of the 2D-LC-MS/MS platform. Precision may be considered as how well a method produces the same result on a repeated measurement or how close measurements cluster around the mean of the measured values (55). The Bland Altman plots in Figure 2.4 C and D illustrate that the mean difference in spectral counts for each protein between replicates is approximately 0 and that ~98% of all the values are tightly clustered around the mean within ±1.96 SD. In addition, we observed surprisingly low coefficients of variation (*CV*) between biological and technical replicates (11.2% and 9.9%, respectively). In combination, these results indicate that we have developed a repeatable 2D-LC-MS/MS method suitable for label-free quantification.

Although biological variability is intrinsic to all organisms, increasing the number of biological replicates analyzed can effectively reduce the biological variation observed by producing a sample average that is truly representative of the population. Unfortunately, proteomic investigations are often limited in the number of biological replicates available for analysis making it difficult to discern true differences in protein expression from random fluctuations using traditional statistical approaches. Proteomic experiments often misuse traditional statistical tests; for example, the Student's *t*-test requires at least three independent experiments and falsely assumes that proteomic data

follows a normal distribution (56). To address these issues, we utilized QSpec, a statistical software package specifically designed to determine significant differential protein expression in large-scale spectral counting-based proteomic experiments with a limited number of biological replicates (≤ 2), in order to further evaluate the variability of our data. QSpec implements a statistical framework that utilizes a hierarchical Bayes method based on a Poisson distribution model that more accurately reflects the distribution associated with proteomic data and accounts for the paucity of information due to the limited number of available replicates. Only 7.5% (163 proteins) of the quantified proteins demonstrated significant variation across biological replicates using generally accepted significance thresholds for Bayesian statistics. In addition, proteins that showed the greatest amount of variation showed poor correlation with both the null and alternative hypothesis models (RBStat > 10,000) (Fig. 2.5 denoted in red). This is most likely due to a spectral count of "0" within one of the replicates, which artificially generates a large fold change, while also producing an abnormally high standard deviation for the spectral counts pertaining to that particular biological replicate.

In summary, we have successfully developed a practical and statistically validated two-dimensional LC-MS/MS platform (RP-RP-nanoESI-MS/MS) for proteomic analysis using label-free quantification, which may be easily adapted to a range of proteomic applications. An additional advantage of this methodology is the use of an intermediate-pH during the first dimension of separation which prevents possible β-elimination of phosphopeptides in support of phosphoproteomic investigations. Furthermore, utilizing our proteomic platform we were able to establish the most comprehensive proteomic

profile of the MCF-7 human breast cancer cell line to date, while requiring the most stringent identification criteria.

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Chapter 3

Quantitative Proteomic Analysis of 2-ME Induced Apoptosis

3.1 Introduction

In 2011, breast cancer was the most commonly diagnosed malignancy and second leading cause of cancer related deaths among women in the United States (1). As one of the most significant health concerns of modern times, considerable resources have been devoted towards breast cancer research and treatment. Conventional cancer therapies (radiotherapy and chemotherapy) have proven to effectively suppress cancer growth by inducing apoptosis, but their promiscuous properties cause undesirable side effects such as, nausea, emesis, and hair loss (2, 3). Therefore, the development of novel treatments is largely driven by the pursuit of effective new therapeutic agents possessing "selective toxicity" properties towards tumor cells. 2-Methoxyestradiol (2-ME) is a promising "new generation" anti-cancer agent with anti-proliferative, anti-angiogenic, and pro-apoptotic effects that has proven efficacious in targeting several tumor cell lines with little or no toxic side effects (4).

2-ME has been shown to be a potent inhibitor of tumor cell growth and has a seemingly profound specificity for malignant cells, showing particular sensitivity towards breast cancer cell lines (5). Evidence has shown that various cellular targets and pathways have been implicated in 2ME-induced apoptosis, including the disruption of microtubule dynamics, inhibition of hypoxia-inducible factor (HIF)-1α, and activation/regulation of the extrinsic and intrinsic apoptotic pathways (4-6) (Fig. 3.1). 2-ME inhibits the polymerization of tubulin and disrupts mitotic spindle formation, causing cells to undergo metaphase cell cycle arrest (G_2/M phases) which subsequently induces apoptosis (7-10). Furthermore, 2-ME has shown to directly activate the extrinsic apoptotic pathway through up-regulation of death receptor 5 (DR5), sensitizing cells towards its natural ligand (TRAIL) (11). In addition to activation of the extrinsic pathway, 2-ME has been

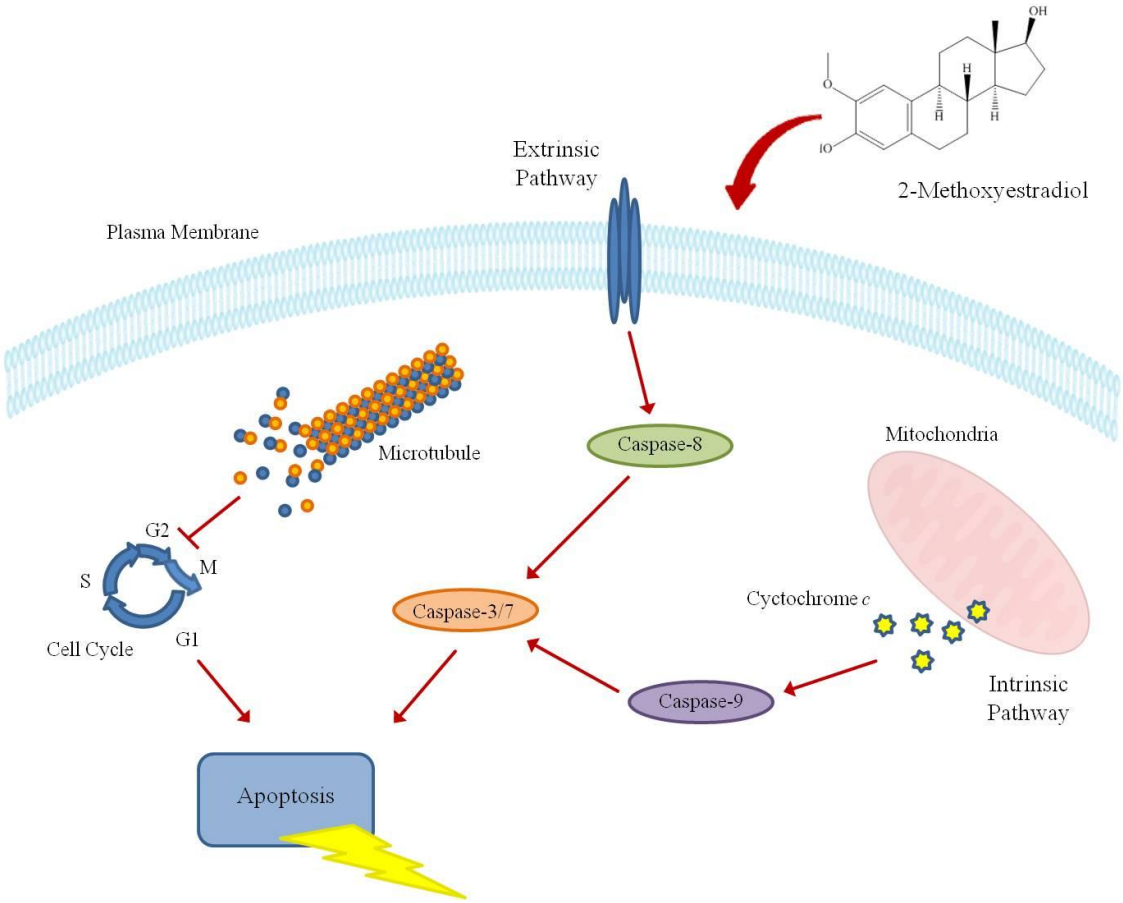

Figure 3. 1 – Mechanisms of Action Implicated in 2-ME Induced Apoptosis. 2-ME induces the intrinsic and extrinsic apoptotic pathways. In addition, 2-ME disrupts microtubule dynamics initiating cell cycle arrest and apoptosis.

shown to mediate apoptosis through the intrinsic apoptotic pathway via activation of the JNK/SAPK signaling pathway and regulation of apoptotic regulators such as Bcl-2 (anti-apoptotic) and Bax (pro-apoptotic) (12-15). However, despite ample observations about 2-ME, its exact mechanism of action is still not well understood.

The biological effects of 2-ME have been determined in large part by traditional biochemical assays, investigating the modes of action consistent with other microtubule disrupting agents (16-18). Unfortunately, traditional biochemical approaches are limited in scope, allowing only specific predetermined targets to be investigated. Recently, the development of high-throughput mass spectrometry-based proteomic strategies have

facilitated the global proteomic analysis of complex biological systems. The use of multidimensional liquid chromatography strategies combined with tandem mass spectrometry (2D-LC-MS/MS) has become a commonly used technique for resolving highly complex biological mixtures prior to MS/MS analysis. Various 2D-LC strategies have proven to effectively increase the proteomic coverage and dynamic range associated with proteomic investigations, permitting the ability to identify low abundant proteins and post-translational modifications responsible for regulating important biological functions. In addition to the development of new 2D-LC-MS/MS technologies, several MS-based quantification strategies have been established in order to accurately determine changes in protein expression in response to particular stimuli (*i.e.,* drug treatment). With advancements in bioinformatics and biostatistics, spectral counting-based label-free quantification has emerged as a cost effective, simple, and reliable method for determining significant changes in relative protein abundance.

In spectral counting-based quantification, the total number of acquired MS/MS spectra assigned to peptides corresponding to a particular protein is used as a measure of protein abundance and has been shown to be very accurate in measuring changes in protein expression over a dynamic range of two orders of magnitude (19, 20). However, factors such as protein length and differences in instrument performance can artificially influence spectral counting results. Therefore, effective normalization methods are required to permit accurate quantitative comparisons across different experimental conditions. Although various normalization strategies have been proposed, normalized spectral abundance factor (NASF) based methods provide simple, robust, and easily implemented methods for handling systematic/random variations from run to run as well

as innate biases associated with raw measurements (20-25). Even with precise quantitative measurements, the limited number of replicate samples typically available in a standard proteomic investigation presents unique challenges to the identification of significant differential protein expression. Consequently, QSpec, a statistical software package, was specifically designed to assess differential protein expression in large-scale spectral counting-based proteomic experiments that suffer from a limited number of biological replicates (26). Furthermore, the versatility of spectral counting-based quantification provides an alternative strategy for investigating hormone sensitive cell lines that are incompatible with metabolic labeling strategies (*i.e.,* SILAC) that deplete necessary hormones and growth factors from the culture media.

The estrogen-dependent MCF-7 human breast cancer cell line is commonly used as a cellular model for breast cancer investigations and has shown to be particularly sensitive to 2-ME treatment (IC_{50} – 0.45 μM) (4). Utilizing a RP-RPLC-MS/MS proteomic strategy with spectral counting-based quantification, we investigated differential protein expression following 2-ME exposure in order to determine potential therapeutic targets and signaling pathways associated with 2-ME-induced apoptosis in MCF-7 breast cancer cells. While a number of these proteins are consistent with previously reported findings, our data provides new insights into novel signaling pathways not previously implicated in 2-ME-induced apoptosis and could potentially clarify an ongoing dispute about 2-ME's role in microtubule disruption.

3.2 Experimental Methods

Cell Culture - MCF-7 human breast adenocarcinoma cells were purchased from the American Type Culture Collection (ATCC; Rockville, MD) and cultured to 60-70%

confluency in GIBCO minimum essential medium (MEM) with Earle's salts and L-glutamine supplemented with 1.5 mg/ml sodium bicarbonate, 1 mM sodium pyruvate, MEM non-essential amino acids, 10% (v/v) fetal bovine serum (FBS), 100 units/ml penicillin, 100 μg/ml streptomycin and 10 mg/l insulin at 37 °C in a humidified atmosphere of 95% air and 5% CO_2. Cells were then washed with sterile PBS and incubated in serum-free medium at 37 °C for 24 hrs to synchronize them in G_0-phase (27). Following cell synchronization, cells were treated with 2μM 2-ME or vehicle (0.003% DMSO) at 37 °C for 24 hrs under the same atmospheric conditions.

Cell Lysis and Protein Extraction - Cells were then incubated with cell dissociation solution (3 mM EDTA, 2.5 mM KCl, 150 mM NaCl, 1.5 mM KH_2PO_4, 8 mM Na_2HPO_4, pH 7.2) at 37 °C for 15 min. Cells were transferred to 50 ml conical vials (Corning, Inc.; Corning, NY) and centrifuged at 130 x *g* at 4 °C for 5 min. The supernatant was discarded and the resulting cellular pellet was washed with sterile PBS and then resuspended in lysis buffer (10 mM Tris-HCl (pH 7.5), 150 mM NaCl, 1% Triton X-100, 1 mM Na_3VO_4, 1 mM NaF, 1 mM sodium pyrophosphate, 1 mM β-glycerophosphate, and EDTA-free complete protease inhibitor cocktail). The suspension was incubated with end-over-end rotation for 60 min at 4 °C, followed by 15 manual strokes with a glass-teflon homogenizer. The lysate was centrifuged at 15,000 x *g* for 10 min at 4 °C in order to remove any cellular debris and the protein concentration of the resulting extract (~4.0 mg/ml) was determined by BCA assay using a commercial BCA protein assay kit (Thermo Scientific; Rockford, IL).

Protein Precipitation and Digestion - Protein (~3.0 mg) was precipitated with 5 times its volume of ice-cold acetone and incubated overnight at -20 °C. After pelleting by

centrifugation at 16,000 x *g* for 10 min at 4 °C, the supernatant was carefully decanted and residual acetone was evaporated under nitrogen gas. The protein was resolubilized in 8 M urea, 50 mM ammonium bicarbonate (AMBIC), pH 8.5 and then reduced with 15 mM dithiothreitol (DTT) followed by carbamidomethylation with 30 mM iodoacetamide (IAM). An additional 15 mM DTT was added to the sample in order to quench any excess IAM. After dilution with 50 mM AMBIC to 1.6 M urea, proteins were digested with (1:50 w/w) trypsin and incubated at 37 °C overnight. The digestion was quenched with the addition of glacial acetic acid and samples were immediately stored at -80 °C until further analysis.

First Dimension Separation: Intermediate pH RPLC - Offline first dimension chromatographic separation was performed on an Agilent 1200 Series HPLC system using an Agilent Zorbax 300 Extended-C_{18} column (150 mm x 2.1 mm i.d., 3.5 µm packing particle size) at 35 °C. UV absorption was monitored at 214 nm. Approximately 100 µg of the tryptic digest was loaded onto the column and separated using the following gradient: 0-5 min, 0% solvent B (24 mM ammonium formate in 90% acetonitrile/10% water); 5-55 min, 0-50% B; 55-65 min, 50-70% B; 65-70 min, 70% B; 70-75 min, 70-0% B; 75-85 min, 0% B at 200 µL/min. Solvent A was composed of 24 mM ammonium formate, pH 7.5. Fractions were collected every minute for 50 min starting at the 10 min mark and subsequently evaporated to near dryness (~5 µl) using a Savant SC110A SpeedVac Concentrator (Thermo Fisher Scientific; Waltham, MA). Samples were reconstituted in 20 µl of 0.1 M acetic acid and stored at -80 °C until further analysis.

Nano-RPLC-MS/MS Analysis - Peptides collected from the first dimension of separation were combined following the pooling strategy described by Song *et al*., where 3 μL of sample from fractions eluting during the first half of the gradient were combined with 3 μL of sample from fractions eluting during the second half of the gradient at equal 25 minute time intervals (*i.e.*, fraction *i* was pooled with fraction *i+25*) (28). Pooled samples were analyzed using an Agilent 1200 Series HPLC system coupled to a linear ion trap/Fourier transform (LTQ-FT) hybrid mass spectrometer (Thermo Finnigan) using an automated proteomic platform previously described (29). In brief, peptides were loaded via a microautosampler onto an analytical column (360 μm o.d. x 75 μm i.d. fused silica microcapillary, packed in-house with 10 cm of 5 μm Monitor-C_{18} particles (Column Engineering Inc; Ontario, CA) that was pulled to a fine tip using a P-2000 laser puller (Sutter Instrument; Novato, CA)). Peptides were eluted directly into the LTQ-FT using the following gradient: 0-50 min, 0-70% solvent B (acetonitrile with 0.1 M acetic acid); 50-53 min, 70-95% B; 53-55 min, 95-0% B; 55-90 min, 0% B. Solvent A was composed of aqueous 0.1 M acetic acid. The initial flow rate of ~200 nl/min was reduced to ~30 nl/min once peptides began to elute from the column, as determined from a bovine serum albumin peptide scouting run, as previously described (29). The mass spectrometer scan functions and HPLC solvent gradient were controlled by the Xcalibur data system. Spectra were acquired in the positive ion mode where each full MS survey scan (400-1800 *m/z*) was followed by nine data dependent MS/MS scans of the most intense ions per survey spectrum, fragmenting selected ions via collision induced dissociation. Ions already selected for MS/MS analysis were dynamically excluded for 30 s with a repeat

count of 1 and a repeat duration of 30 s. Two biological replicates from each biological treatment were analyzed in duplicate (technical replicates).

Database Searching and Protein Identification - Acquired tandem mass spectra were converted to Mascot Generic Files (.mgf) through the Trans-Proteomic Pipeline (TPP; v4.4.0) and subsequently searched against a concatenated target/decoy International Protein Index (IPI) human database (v3.77) using Mascot Daemon (v2.2.0; Matrix Science). The Mascot search parameters were specified as a maximum of 1 missed tryptic cleavage; precursor ion mass tolerance of ±20 ppm; fragment ion tolerance mass tolerance of ±0.5 Da; a fixed modification of cysteine carbamidomethylation; and variable modifications of methionine oxidation and phosphorylation of serine, threonine, and tyrosine residues. Protein identification, grouping, and filtering were accomplished through ProteoIQ (v2.1.08; BioInquire, Athens, GA). In ProteoIQ, technical replicates were merged and processed as a single biological sample in order to parse out total spectral counts for each biological replicate. An initial protein set was generated using the following criteria: minimum ion score of 28.0; peptide length of at least 4; peptide probability of 0.99; protein probability of 0.50; and a false discovery rate of 5.0%. A more stringent filter was then applied to the initial protein set specifying a peptide and protein group probability of ≥99.0% according to the PeptideProphet and ProteinProphet algorithms implemented within ProteoIQ and the identification of at least two peptides (30, 31). A non-redundant protein list was generated where uniquely identified protein groups were represented by the top scoring protein. Spectral counts from proteins which were identified in replicates but did not meet the specified criteria were removed from those particular replicates and replaced with zero.

Quantification and Functional Analysis - Significant differential protein expression was determined using QSpec, a statistical framework specifically designed for large-scale spectral counting-based quantification which utilizes a hierarchical Bayes method based on a Poisson distribution model (26). IPI accession numbers, raw spectral counts, and protein lengths for confidently identified proteins were parsed from ProteoIQ and submitted to QSpec for quantitative and statistical analysis. Differential protein expression was reported as fold change. In addition, corresponding Bayes factors and RBStat values were provided as a measurement of the statistical significance and "goodness-of-fit" - how well the supporting data fit the preferred model. A minimum Bayes factor of 30 and a maximum RBstat value of 10,000 were used to determine whether the observed variation in protein abundance was likely to be due to 2-ME exposure or normal biological variation. Differentially expressed proteins were further analyzed using the ingenuity pathway analysis (IPA) program in order to determine potential molecular targets and signaling pathways associated with 2-ME-induced apoptosis.

3.3 Results

In order to determine potential therapeutic targets and signaling pathways associated with 2-ME induced apoptosis, we utilized a RP-RPLC-MS/MS proteomic platform to determine differentially expressed proteins following 2-ME treatment in MCF-7 breast cancer cells. Following strict protein identification and quantification criteria, we identified 234 proteins that were significantly regulated following 2-ME exposure, of which 105 were found to be up-regulated while 129 were significantly down-regulated (Fig. 3.2). Using gene ontology and the IPA program, significantly regulated proteins were classified into seven groups based on molecular function:

apoptosis/cell death, proliferation, microtubule dynamics/structural organization, molecular/protein transport, cell cycle, translation/transcription, and other (Appendix II).

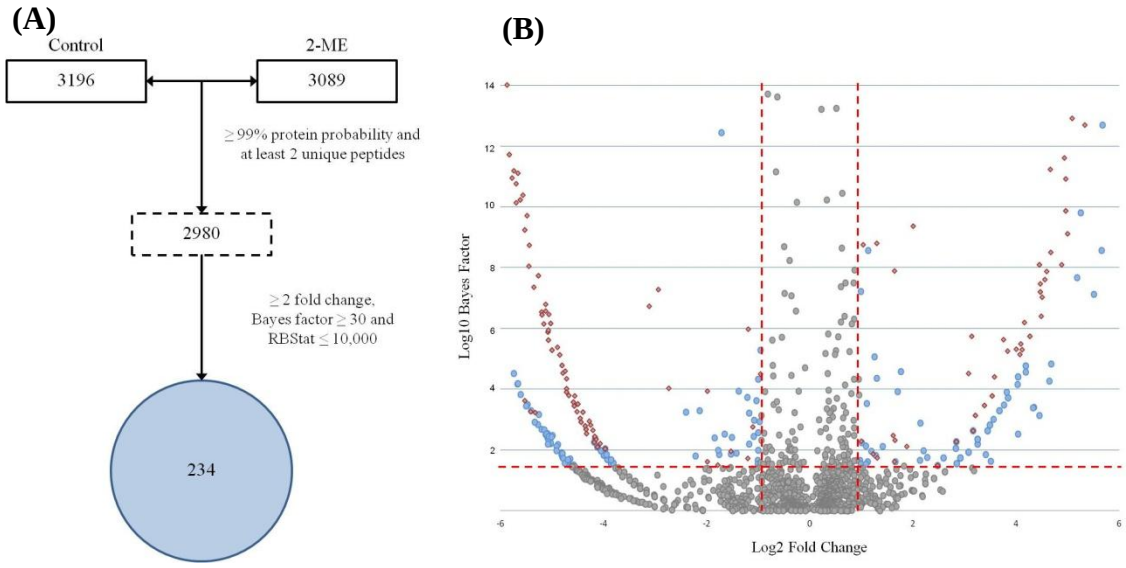

Figure 3. 2 Statistically Significant Differential Protein Expression. (A) Quantitative Flowchart. Solid rectangles indicate the number of proteins identified under each treatment condition. The dashed rectangle indicates the number of proteins identified across replicates with ≥99.0% protein probability and at least 2 unique peptides. The circle indicates significant differential protein expression which was determined utilizing QSpec, a bayesian based statistical software, with a significance threshold of ≥ 2 fold change, a Bayes factor of ≥30, and an RBStat ≤10,000 **(B)** Volcano plot for significant differential protein expression (blue) biologically and statistically significant (red) poor goodness-of-fit RBstat >10,000 (grey) not-significant

In support of increased apoptotic activity, we observed a general up-regulation in pro-apoptotic proteins (80 pro-apoptosis) and the down-regulation of proteins that promote cellular proliferation/growth (76 proliferation/anti-apoptosis). In addition, we observed evidence that supports activation of both the intrinsic and extrinsic apoptotic pathways. Proteins associated with DNA damage, mitochondrial cytochrome *c* release, ER stress, and molecules believed to serve as adapter proteins for death receptor signaling complexes were up-regulated, while proteins that initiate and promote proliferation and tumor progression were notably down-regulated (Table 3.1). Further examination of our data through IPA shows that the majority of the differentially expressed proteins are consistent with these findings and are implicated in cell death,

cellular transport, cell cycle regulation, proliferation, and small molecule biochemistry (Fig. 3.3)

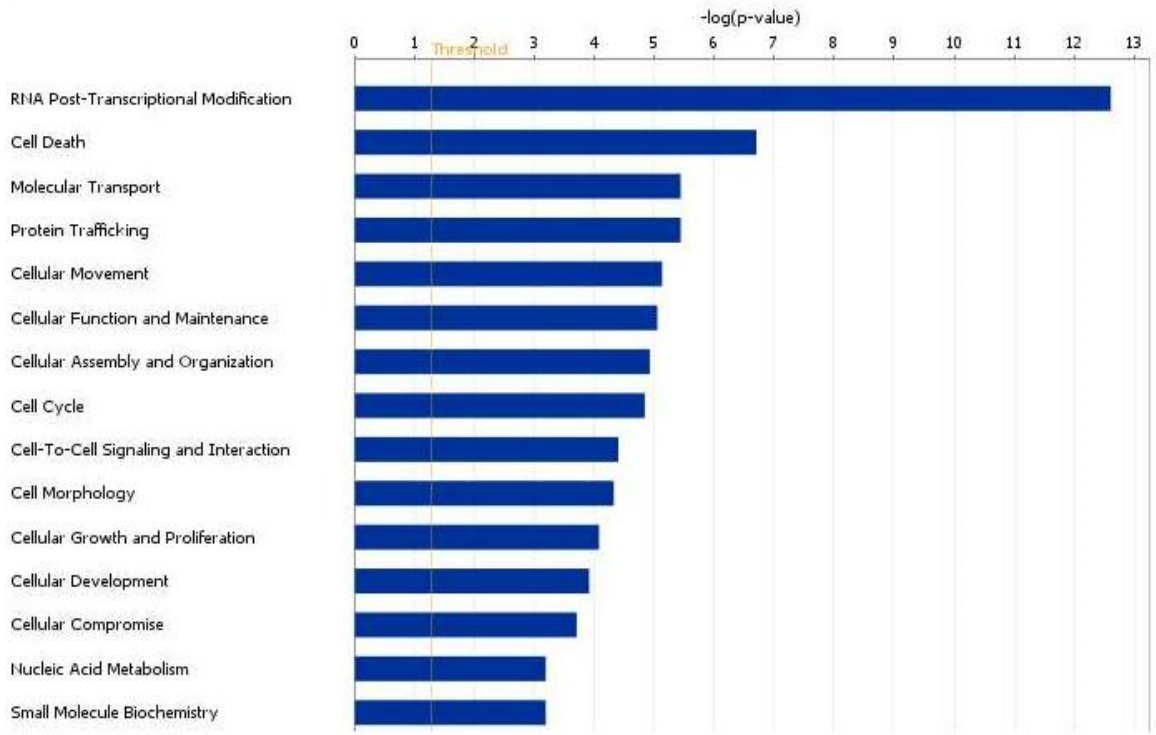

Figure 3. 3 - Molecular Functions of Differentially Expressed Proteins. Displayed are the top 15 molecular functions according to IPA analysis

Although there are conflicting reports of the exact mechanism, 2-ME has shown to be a potent inhibitor of microtubule polymerization. We identified significant perturbations in 34 structural proteins associated with microtubule dynamics and structural organization. Our results showed that 2-ME caused an up-regulation in proteins which actively depolymerize microtubules (*i.e.*, Stathmin-1) whilst down-regulating microtubule-associated proteins (MAPs) known to stabilize polymerized microtubules (*i.e.*, Microtubule-associated protein tau). In addition, 2-ME down-regulated microtubule binding proteins required for mitotic spindle formation. Not only did we observe changes

Table 3. 1 - Selected Proteins Differentially Expressed During 2-ME Induced Apoptosis.
↑ - Up-regulation ↓ - Down-regulation

Accession No.	Protein Name		Comments
Promotes Apoptosis/Cell Death			
IPI00007334	Apoptotic chromatin condensation inducer in the nucleus	↑	Induces chromatin condensation after caspase activation
IPI00022477	B-cell lymphoma/leukemia 10	↑	Involved in the NF-κB signaling cascade and serves as an adaptor protein for the NFR1-TRADD-RIP complex
IPI00018195	Mitogen-activated protein kinase 3	↑	Up-regulated in 2-ME induced apoptosis
IPI00008511	NADH dehydrogenase subunit 5	↑	Involved in mitochondrial cytochrome c release
IPI00020008	NEDD8	↑	Inhibits ER transcriptional activity inducing ER-stress
Promotes Proliferation/Cell Growth			
IPI00292134	Epidermal growth factor receptor substrate 15	↓	Initiates cell growth and proliferation
IPI00789008	Flotillin-2	↓	Lipid raft marker overexpressed in breast cancer
IPI00011593	Fos-related antigen 2	↓	Promotes breast cancer progression
IPI00021537	Opioid growth factor receptor	↓	Upregulates the cyclin-dependent kinase inhibitory pathway
Microtubule/Cytoskeleton Dynamics			
IPI00010133	Coronin-1A	↑	Tumor suppressor that regulates actin dynamics
IPI00550852	Dynactin subunit 4	↓	Required for microtubule anchoring at the centrosome
IPI00220173	Isoform Tau-B of Microtubule-associated protein tau	↓	Stablizes polymerized microtubules
IPI00220556	Pre-B-cell leukemia transcription factor-interacting protein 1	↓	Tethers ER-α to microtubules influencing ER-α signaling
IPI00479997	Stathmin 1	↑	Depolymerizes microtubules
Cell Cycle/Division			
IPI00217960	cAMP-dependent protein kinase catalytic subunit alpha	↓	Required for cells to enter into mitosis
IPI00215928	Centrin-2	↓	Required for centriole duplication
IPI00418336	Integrator complex subunit 3	↑	Involved in the G2/M checkpoint
IPI00293845	Telomere-associated protein RIF1	↑	Mediates cell cycle arrest in response to DNA damage
Other			
IPI00216085	Cytochrome c oxidase subunit 6B1	↓	Up-regulation enhances mitochondrial respiration and inhibits apoptosis
IPI00293817	Gamma-soluble NSF attachment protein	↓	Required for vesicular transport between the endoplasmic reticulum and the Golgi apparatus
IPI00220014	Isoform 2 of Isopentenyl-diphosphate Delta-isomerase 1	↓	Converts isopentenyl pyrophosphate (a toxic intermediate) to dimethylallyl pyrophosphate in the Mevalonate pathway
IPI00220648	Phosphomevalonate kinase	↑	Upstream kinase involved in the production of isopentenyl pyrophosphate in the Mevalonate pathway
IPI00748794	Sarcoplasmic/endoplasmic reticulum calcium ATPase 3	↓	Involved in Ca^{2+} transport, down-regulation affects Ca^{2+} homeostasis inducing ER-stress

in proteins that affect microtubule dynamics, we also observed the up-regulation of tumor suppressor proteins that are known to regulate actin dynamics (*i.e.,* Coronin-1A).

Proper mitotic spindle formation plays a vital role in cell division; aberrant spindle formation may cause cells to undergo cell cycle arrest. However, other key regulatory factors are required for cells to subsequently undergo apoptosis. We identified 23 proteins that mediate cell cycle arrest (Appendix II). Consistent with previous reports, our data suggests that 2-ME causes cells to undergo cellular arrest during G_2/M phase transition through the up-regulation of proteins involved in initiating G_2/M phase cell cycle arrest as well as those that serve as G_2/M phase checkpoint regulators. In addition, proteins that are required for cells to enter into mitosis or bypass specific cell cycle checkpoints were substantially down-regulated.

Apoptosis is known to considerably inhibit protein synthesis. In accordance with this observation, we observed the global down-regulation of transcription and translation factors and various ribosomal subunits responsible for protein synthesis. Most notably, we observed a significant down regulation in translation factors responsible for initiation and elongation, including translation initiation factor 4G (eIF4G) which is required for binding cellular mRNA to ribosomes and may play a central role in the shut-down mechanism of protein translation. In addition, the general decrease in protein synthesis is known to be a hallmark of ER related stress.

We observed a substantial increase in proteins related to ER-stress that may help facilitate 2-ME-induced apoptosis. Consistent with an overall decrease in protein synthesis, we detected an up-regulation of NEDD-8 which is known to inhibit ER transcriptional activity which induces ER-stress. Also of particular interest was the down-

regulation of Sarcoplasmic/endoplasmic reticulum calcium ATPase 3 (SERCA3), which affects Ca^{2+} homeostasis and may lead to irregularities in the Mevalonate pathway. This is further supported by the up-regulation of phosphomevalonate kinase and the down-regulation of isopentenyl-diphosphate delta-isomerase, two key components of the Mevalonate pathway.

3.4 Discussion

2-Methoxyestradiol has shown considerable promise as an anticancer therapeutic agent with a broad spectrum of activity against multiple tumor cell lines (4). Evidence has shown that various cellular targets and pathways have been implicated in 2-ME induced apoptosis. However, conflicting reports suggest that the cytotoxic effects of 2-ME may operate through multiple mechanisms of action with varying degrees of contribution depending upon cell type. Utilizing a global proteomic approach, we aimed to identify key factors and molecules involved in mediating 2-ME-induced apoptosis that may provide evidence for a unifying mechanism of action.

Consistent with known biological effects of 2-ME, we observed significant differential expression of proteins involved in mediating apoptosis through activation and regulation of the intrinsic and extrinsic apoptotic pathways. 2-ME has been shown to mediate apoptosis through activation of the c-Jun NH_2-terminal kinase (JNK) signaling pathway, leading to a decrease in the mitochondrial membrane potential and release of cytochrome *c* (32, 33). Although we did not observe differential expression of JNK, we did detect significant changes in other proteins involved in decreasing the mitochondrial membrane potential (*i.e.,* cytochrome b-c1 complex subunit Rieske, mitochondrial) as well as up-regulation of cytosolic cytochrome *c*. 2-ME is also known to mediate the

intrinsic pathway by regulating the expression levels between pro-apoptotic and anti-apoptotic Bcl-2 family members (12, 15, 34). Our data confirms that 2-ME causes an imbalance in the expression ratio of pro-/anti-apoptotic Bcl-2 related proteins favoring apoptosis. 2-ME substantially down-regulated Galectin-3, an anti-apoptotic Bcl-2 family member which is known to promote malignancy and the metastasis of human breast cancer cells (35, 36). Apoptosis was further promoted by the up-regulation of Bcl-10 and Bap-31, two pro-apoptotic Bcl-2 family members. In addition, Bap-31 is also thought to be involved in caspase-8 mediated apoptosis and may serve as a cross-linker between the intrinsic and extrinsic apoptosis pathways (37). 2-ME has also been shown to mediate the extrinsic apoptotic pathway through up-regulation of death receptor 5 (DR-5) (11). Although we did not detect an up-regulation of DR-5, we did detect significant increases in downstream proteins involved in death receptor signaling cascades. Following 24 hrs of 2-ME exposure, we are likely to only identify proteins involved late in the signaling cascade that are responsible for the execution of apoptosis to be differentially expressed. Although limited in scope, this work allowed us to determine signaling pathways that are fully committed to 2-ME-induced apoptosis.

2-ME has proven to be a potent inhibitor of microtubule dynamics, inhibiting tubulin polymerization and proper mitotic spindle formation. D'Amato *et. al* demonstrated that 2-ME interacts with tubulin at or near the colchicine binding site, thereby inhibiting polymerization (38). However, the mechanism in which 2-ME disrupts microtubule dynamics is debatable. Some reports have suggested that microtubule disruption is caused by 2-ME's ability to actively depolymerize microtubules, yet others have claimed that 2-ME disrupts microtubule function by merely preventing

polymerization (10, 39-41). In support of 2-ME's ability to actively depolymerize microtubules, our results indicated that 2-ME causes an up-regulation of Stathmin-1 which is responsible for depolymerizing microtubules while down-regulating the expression of CLIP-1 and PHF-tau which promote microtubule assembly and stability (42, 43). In addition, 2-ME has been shown to cause aberrant mitotic spindle formation which plays a vital role in cell division and causes cells to undergo cell cycle arrest. We observed the down-regulation of Dynactin and Nesprin-2 which are responsible for anchoring microtubules to the centrosome and maintaining subcellular spatial organization required for proper centrosome migration, respectively (44).

Although disruption of microtubule dynamics and mitotic spindle formation may play a vital role in initiating a prolonged interruption in the mitotic cycle, other key factors are required for cells to fully undergo cell cycle arrest and subsequent apoptosis. Atalla *et. al* suggested that as a result of 2-ME's ability to induce mitotic arrest at concentrations that do not effectively depolymerize tubulin filaments, 2-ME induces cellular arrest independently of microtubule disruption (10). We identified numerous proteins that serve as cell cycle checkpoint regulators or are responsible for initiating cell cycle arrest that may be working independently or in concert with the disruption of microtubule dynamics. Consistent with previous reports, the majority of these regulators cause cells to undergo mitotic arrest during the G_2/M transition phase.

In agreement with increased apoptosis, we observed the global down-regulation of transcription and translation factors responsible for protein synthesis, a hallmark of ER-stress. Although we are not able to determine whether apoptosis is a result of ER-stress or vice versa, we identified various proteins that induce ER-stress and/or are

involved in ER mediated apoptosis. Most notably, we identified the down-regulation of gamma-soluble NSF attachment protein which is required for the vesicular transport of misfolded proteins between the ER and golgi apparatus (45) and the up-regulation of Sec61-B which is required for protein translocation within the ER and is responsible for transducing apoptotic signals during ER-stress (46). Also of particular interest was the down-regulation of SERCA3, which affects Ca^{2+} homeostasis and may be required for maintaining the stability of HMG-CoA reductase, a key enzyme of the mevalonate pathway.

Interestingly, 2-ME treatment caused a significant up-regulation in phosphomevalonate kinase (PMK) and a down-regulation of isopenteynl pyrophosphate isomerase (IPI), two key components of the Mevalonate pathway (Fig. 3.4). The Mevalonate pathway plays a critical role in regulating the biosynthesis of various isoprenoids (*e.g.* cholesterol, ubiquinone, farnesyl isoprenoids, and dolichol) essential for multiple cellular processes involving cellular growth and proliferation, including the production of hormones, N-glycosylation of EGFR, and activation of Ras-related GTPases (47-49). As a result of its vital role in cell survival, new classes of therapeutic agents (*i.e.* statin and bisphophonates) have been developed that target the Mevalonate pathway (50). Our data indicates that 2-ME dysregulates the Mevalonate pathway through the up-regulation of PMK and down-regulation of IPI, possibly resulting in the bioaccumulation of isopentyl pyrophosphate (IPP) and preventing the production of downstream biomolecules essential for cell survival. Disruption of the mevalonate pathway is further supported by our data and may reveal a central mechanism for 2-ME induced apoptosis in MCF-7 cells.

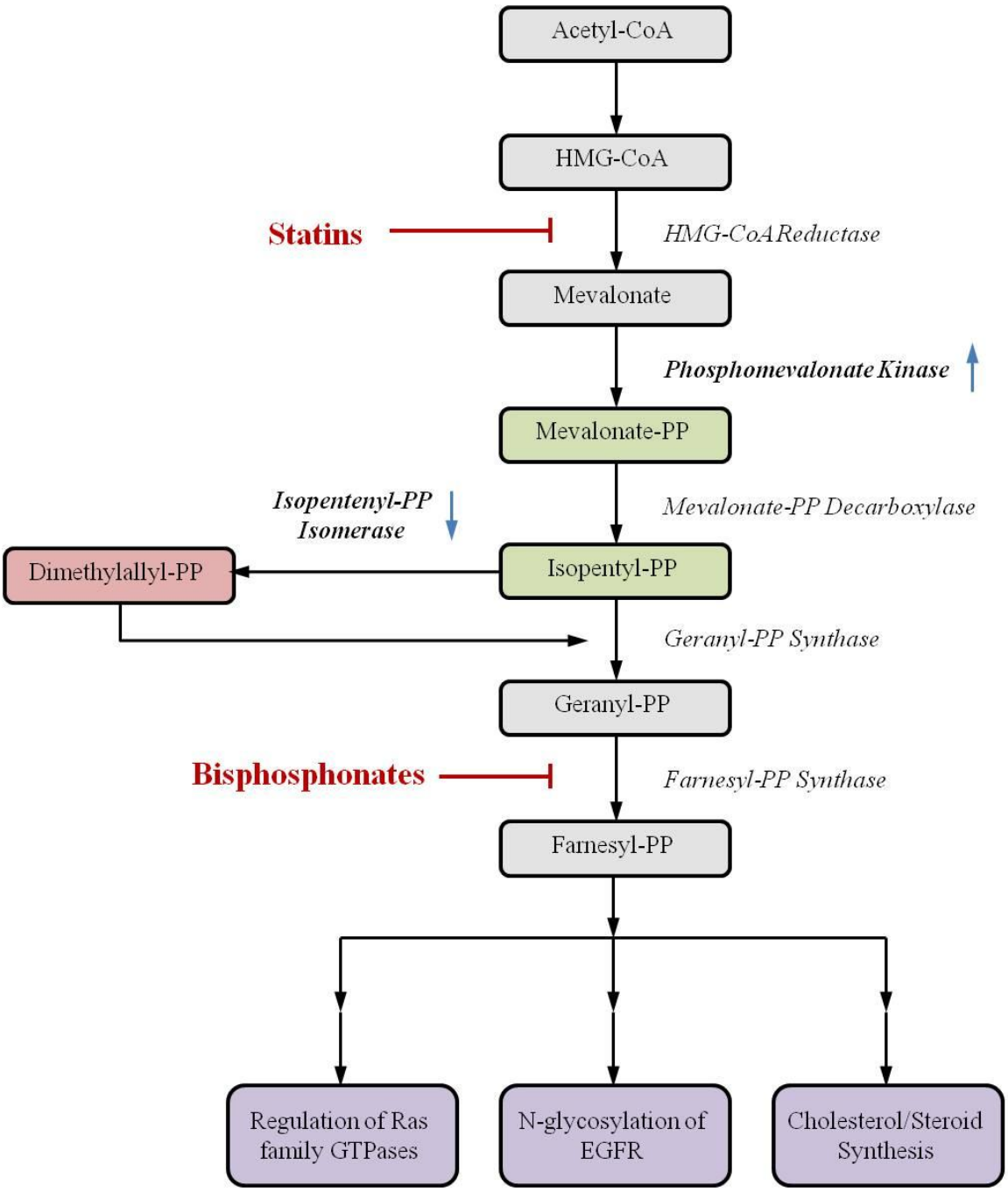

Figure 3. 4 – Overview of the Mevalonate Metabolic Pathway. The mevalonate pathway causes prenylation of Ras-related GTPases, the N-glycosylation of EGFR, and regulates the production of cholesterol and vital growth factors/hormones. Statins and Bisphosphonates are classes of anti-cancer drug developed to inhibit specific enzymes within the pathway in order to inhibit the production of downstream biomolecules. PP = pyrophosphate

Inhibiting the production of downstream metabolites within the mevalonate pathway prevents various cellular processes including N-glycosylation of EGFR, activation of Ras-related GTPases, and hormone synthesis. Consistent with aberrant EGFR function, we observed an overall down-regulation in the PI3K/Akt signaling pathway with the significant down-regulation of EGFR substrate 15, EGFR-bound protein 2, and Akt as well as the anti-apoptotic Bcl-2 family member Galectin-3. Furthermore, we observed the global down-regulation of Rho-GTPases which are responsible for actin cytoskeleton motility, transcriptional regulation, and vesicle trafficking (51). In addition, Rho-GTPases induce expression of p21-protein active kinase which inhibits stathmin-1 and microtubule depolymerization (52). As expected with the down-regulation of Rho-GTPases, we observed the down-regulation of p21-protein activated. Thus, perturbations to the mevalonate pathway may play a key role in the disruption of microtubule dynamics observed during 2-ME exposure. Disruption of the mevalonate pathway prevents the biosynthesis of various steroids, hormones, and growth factors required by hormone dependent MCF-7 cells and may explain the high sensitivity of MCF-7 cells towards 2-ME exposure. In addition to inhibiting the downstream activity of the mevalonate pathway, the bioaccumulation of IPP can lead to apoptosis. Räikkönen *et. al* recently showed that the accumulation of IPP leads to its conversion to triphosphoric acid 1-adenosin-5'-yl ester 3-(3-methylbut-3enyl) ester (ApppI), which interferes with mitochondrial function and consequently induces apoptosis (53).

These results suggest that 2-ME exposure regulates various factors that promote apoptosis and inhibits the expression of proteins that promote proliferation and aberrant cell growth. Our data supports many of the previously described mechanisms of action

associated with 2-ME, however we provided additional evidence that these individual mechanisms may be related to the effects generated by the disruption of the mevalonate pathway and the increase in ER-stress. Although limited in scope, this study is provides ample evidence and warrants further investigations into 2-ME's involvement in disrupting the mevalonate pathway.

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Chapter 4

Development of a Quantitative Phosphoproteomic Strategy Utilizing Isotopic Diethylation Labeling

4.1 Introduction

Protein phosphorylation is a vital post-translational modification (PTM) that plays an integral role in regulating many molecular functions such as inter- and intracellular communication, differentiation, proliferation, cell cycle regulation, and apoptosis (1). The dynamic nature of protein phosphorylation is tightly regulated by protein kinases and phosphatases, which carefully regulate the activation status, subcellular location, and protein-protein interactions of relevant signaling proteins. During the development or progression of diseases such as cancer, cells often lose their ability to regulate phosphorylation events. Thus, the ability to quantitatively monitor global and site-specific changes in phosphorylation allow us to gain a better understanding of the key molecular components and signaling cascades involved in such systems.

Phosphorylation often occurs on low abundance proteins at substoichiometric levels, which presents an inherent challenge uniquely associated with phosphoproteomic endeavors and requires the selective enrichment of phosphorylated peptides prior to LC-MS/MS analysis. Consequently, a number of techniques have been developed for the specific enrichment of phosphopeptides from their respective non-phosphorylated counterparts (2). Immobilized metal affinity chromatography (IMAC) has traditionally been the most commonly used enrichment strategy and separates phosphorylated peptides from non-phosphorylated peptides based largely on ionic interactions between the negatively charged phosphate group of the modified amino acid and the metal ions of the immobilized matrix (2). Unfortunately, acidic peptides are often co-purified using this strategy due to the negatively charged C-terminus and/or acidic amino acid (*i.e.*, glutamic

acid and/or aspartic acid) carboxyl groups. Carboxylic acids can be converted to methyl esters; however, the derivatization is often incomplete and may lead to deleterious side reactions. Titanium dioxide (TiO_2) provides a simpler and more effective alternative for the global enrichment of phosphorylated peptides based on the affinity of metal oxides for the phosphate moiety. Although acidic peptides can competitively inhibit the enrichment of phosphorylated peptides, the simple addition of an acidic excluder, such as lactic acid, can improve the selectivity of TiO_2 for phosphorylated peptides without the need to chemically modify the sample (3, 4).

Slight variations in the stoichiometry of phosphorylation activation can greatly impact cell signaling and homeostasis. Therefore, accurate quantitative information is required to discern the dynamic molecular events that govern such systems. Over the past decade, several MS-based quantitation methods have been utilized to determine changes in protein phosphorylation between two or more biological or treatment conditions. Labeling-based methods which utilize the incorporation and monitoring of various stable isotope labels have proven to provide accurate methods for quantifying relative protein abundances in complex samples (5-11). However, most labeling-based methods require costly reagents and are hindered by incomplete labeling, and increased sample complexity, which may demand sophisticated quantification software. Moreover, many of these labeling strategies are limited in their applications, as they may not be compatible with particular types of mass spectrometers and/or biological systems.

In order to address some of these issues, Hsu *et al.* recently developed a reductive amination labeling strategy that incorporates isotopically labeled dimethyl groups to the N-terminus and ε-amino group of lysine residues (12). Although this strategy provides an

inexpensive method for global quantification, the kinetic isotope effect associated with isotopically paired peptides ($^{2}H/^{1}H$) induces a differential chromatographic shift in retention time that increases the challenges associated with protein quantification of complex large-scale proteomic investigations. However, the use of isotopically labeled acetaldehyde (^{12}C and ^{13}C) provides an alternative diethylation method that eliminates the need to incorporate deuterium labels, abolishing shifts in LC retention time among isotopically paired peptides ($^{13}C/^{12}C$).

In addition, reductive diethylation labeling provides a quantification strategy that can be easily applied to proteomic investigations where conventional quantitative strategies are not suitable, such as those involving hormone sensitive cell lines that are not compatible with typical metabolic labeling procedures (*i.e.*, SILAC). Estrogen-dependant MCF-7 human breast cancer cells are commonly used as a cellular model for breast cancer investigations and has shown to be particularly sensitive to 2-methoxyestradiol (2-ME), a promising anticancer therapeutic agent that has shown a broad spectrum of activity against multiple cellular targets and signaling pathways.

We have established and validated a robust and flexible quantitative phosphoproteomic strategy (RP-TiO_2-RP-MS/MS) using reductive isotopic diethylation labeling (Fig. 4.1). To demonstrate the usefulness and applicability of this strategy, we preformed a quantitative phosphoproteomic analysis of 2-ME treated MCF-7 human breast cancer cells in order to determine potential therapeutic targets and signaling pathways associated with 2-ME induced apoptosis. Following stringent phosphopeptide identification criteria, we identify 11,382 unique phosphopeptides corresponding to 1,876 unique phosphoproteins with a 1% false discovery rate. Our data provides new insights

into novel signaling pathways not previously implicated in 2-ME-induced apoptosis while also being consistent with previously reported findings concerning 2-ME mediated phosphorylation.

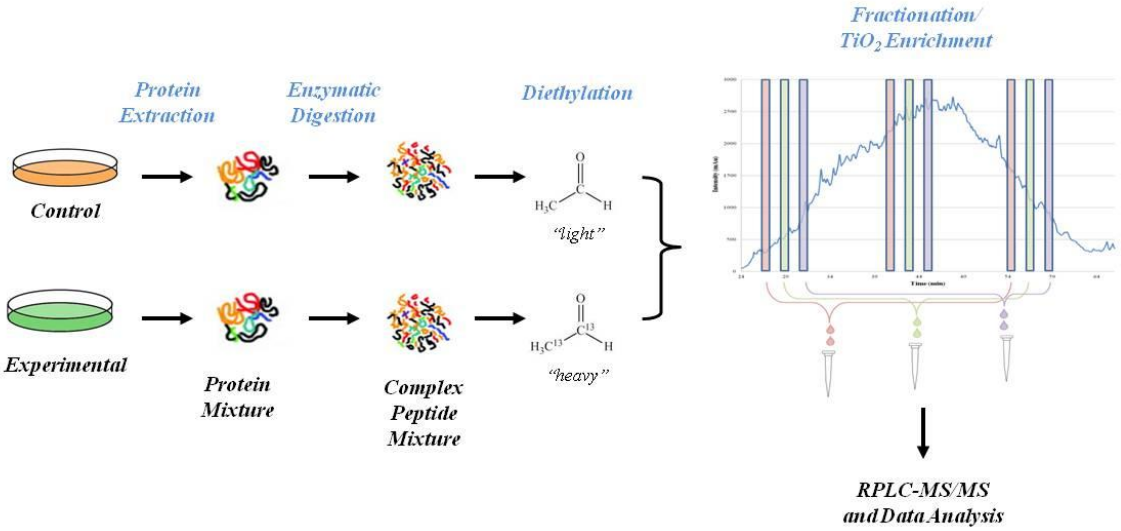

Figure 4. 1 – Phosphoproteomic Workflow. MCF-7 cells were treated with 2μm 2-ME or vehicle for 24 hrs. Whole cell lysates were generated in the presence of protease and phosphatase inhibitors. Following tryptic digestion, samples were diethylated with "heavy" or "light" labeled acetaldehyde and then combined at a 1:1 ratio. The combined sample was fractionated offline via intermediate pH RP-LC. Forty-five (45) fractions were collected and subsequently concatenated with 2 non-adjacent fractions at equal time intervals (14 total concatenated fractions). Phosphopeptides were enriched using TiO_2 spin columns and then analyzed by RPLC-MS/MS.

4.2 Experimental Methods

Cell Culture - MCF-7 human breast adenocarcinoma cells were purchased from the American Type Culture Collection (ATCC; Rockville, MD) and cultured to 60-70% confluency in GIBCO minimum essential medium (MEM) with Earle's salts and L-glutamine supplemented with 1.5 mg/ml sodium bicarbonate, 1 mM sodium pyruvate, MEM non-essential amino acids, 10% (v/v) fetal bovine serum (FBS), 100 units/ml penicillin, 100 μg/ml streptomycin and 10 mg/l insulin at 37 °C in a humidified atmosphere of 95% air and 5% CO_2. Cells were then washed with sterile PBS and incubated in serum-free medium at 37 °C for 24 hrs to synchronize them in G_0-phase

(13). Following cell synchronization, cells were treated with 2μM 2-ME or vehicle (0.003% DMSO) at 37 °C for 24 hrs under the same atmospheric conditions.

Cell Lysis and Protein Extraction - Cells were then incubated with cell dissociation solution (3 mM EDTA, 2.5 mM KCl, 150 mM NaCl, 1.5 mM KH_2PO_4, 8 mM Na_2HPO_4, pH 7.2) at 37 °C for 15 min. Cells were transferred to 50 ml conical vials (Corning, Inc.; Corning, NY) and centrifuged at 130 x *g* at 4 °C for 5 min. The supernatant was discarded and the resulting cellular pellet was washed with sterile PBS and then resuspended in lysis buffer (10 mM Tris-HCl (pH 7.5), 150 mM NaCl, 1% Triton X-100, 1 mM Na_3VO_4, 1 mM NaF, 1 mM sodium pyrophosphate, 1 mM β-glycerophosphate, and EDTA-free complete protease inhibitor cocktail). The suspension was incubated with end-over-end rotation for 60 min at 4 °C, followed by 15 manual strokes with a glass-teflon homogenizer. The lysate was centrifuged at 15,000 x *g* for 10 min at 4 °C in order to remove any cellular debris and the protein concentration of the resulting extract (~4.0 mg/ml) was determined by BCA assay using a commercial BCA protein assay kit (Thermo Scientific; Rockford, IL).

Protein Precipitation and Digestion - Protein (~3.0 mg) was precipitated with 5 times its volume of ice-cold acetone and incubated overnight at -20 °C. After pelleting by centrifugation at 16,000 x *g* for 10 min at 4 °C, the supernatant was carefully decanted and residual acetone was evaporated under nitrogen gas. The protein was resolubilized in 8 M urea, 50 mM ammonium bicarbonate (AMBIC), pH 8.5 and then reduced with 15 mM dithiothreitol (DTT) followed by carbamidomethylation with 30 mM iodoacetamide (IAM). An additional 15 mM DTT was added to the sample in order to quench any excess IAM. After dilution with 50 mM AMBIC to 1.6 M urea, proteins were digested

with (1:50 w/w) trypsin and incubated at 37 °C overnight. The digestion was quenched with the addition of glacial acetic acid and samples were immediately stored at -80 °C until further analysis.

Diethylation Labeling - Tryptic peptides (1.5 mg) were desalted using a C_{18} spin tip, dried under vacuum, and reconstituted in 500 μL of 100 mM sodium acetate buffer at pH 6.0. For biological replicate 1, samples were incubated with 30 μL of 40% (w/w) acetaldehyde-C^{12} (control) or acetaldehyde-C^{13} (2-ME treated) for 2 hrs at room temperature. Samples were then reduced with 20 μL of freshly prepared 0.6 M sodium cyanoborohydride ($NaBH_3CN$) and incubated for 1 hr at room temp. A second addition of 30 μL of 40% acetaldehyde-C^{12} or –C^{13} was added to each respective sample and incubated for 1 hr at room temp. Samples were then reduced with 20 μL of 0.6 M $NaBH_3CN$ and incubated for 1 hr at room temp. Samples were then reduced and incubated 3 additional times with the final incubation being left overnight (~14 hrs) at room temp. The reaction was then quenched with 25 μL of 25% (w/w) ammonium hydroxide (NH_4OH) and then immediately acidified with 20 μL of formic acid (CH_2O_2). Samples were then combined at a 1:1 ratio, dried under vacuum, reconstituted in 300 uL of 24 mM ammonium formate (pH 7.5) and stored at -80°C until further analysis. For biological replicate 2, samples were labeled following the same procedure, but with the inverse labels.

First Dimension Separation: Intermediate pH RPLC - Offline first dimension chromatographic separation was performed on an Agilent 1200 Series HPLC system using an Agilent Zorbax 300 Extended-C_{18} column (150 mm x 2.1 mm i.d., 3.5 μm packing particle size) at 35 °C. UV absorption was monitored at 214 nm. Approximately

500 µg of the diethylated tryptic digest was loaded onto the column and separated using the following gradient: 0-5 min, 0% solvent B (24 mM ammonium formate in 90% acetonitrile/10% water); 5-55 min, 0-50% B; 55-65 min, 50-70% B; 65-70 min, 70% B; 70-75 min, 70-0% B; 75-85 min, 0% B at 200 µL/min. Solvent A was composed of 24 mM ammonium formate, pH 7.5. Fractions were collected every minute for 45 min starting at the 24 min mark. Three non-adjacent fractions were pooled at equal time intervals (*i*, *i*+14, and *i*+28) and subsequently evaporated to near dryness (~5 µl) using a Savant SC110A SpeedVac Concentrator (Thermo Fisher Scientific; Waltham, MA). Samples were reconstituted in 100 µl of Buffer B and stored at -80 °C until further analysis.

TiO_2 Phosphopeptide Enrichment – Phosphopeptides were enriched using TiO_2 spin tips (GL Sciences Inc.; Tokyo, Japan). TiO_2 was activated with 200 µL of buffer A for 10 minutes and then centrifuged at 1,000 x g for 2 mins at room temp. An additional 200 µL of buffer A was added and immediately centrifuged following the same conditions. Tips were then conditioned with 200 µL of buffer B and centrifuged at 500 x g for 8 min at room temp. The eluent was collected, reloaded, and centrifuged again following the same conditions. This time the eluent was discarded as waste. Samples (100 µL) were then loaded and centrifuged at 500 x g for 8 min at room temp. The eluent was collected, reloaded, and centrifuged 2 additional times following the same procedure. Samples were then washed with 100 µL of buffer B followed by 3 consecutive washes with 100 µL of buffer A centrifuged at 800 x g for 2 min at room temp. The collection tube was replaced and samples were eluted with 100 µL of elution buffer I centrifuged at 500 x g for 5 min at room temp. Samples were then eluted with 100 µl of elution buffer II

centrifuged at 500 x g for 5 min at room temp and the acidified with 20 µL 50% acetic acid (AcOH). Samples were then dried under vacuum and reconstituted in 10 µL solvent A (0.1 M AcOH) and stored at -80°C until further analysis.

Nano-RPLC-MS/MS Analysis - Samples were analyzed using an Agilent 1200 Series HPLC system coupled to an LTQ-Orbitrap Velos hybrid mass spectrometer (Thermo Finnigan, San Jose, CA, USA) using an automated proteomic platform previously described (14). In brief, peptides were loaded via a microautosampler onto an analytical column (360 µm o.d. x 75 µm i.d PicoTip self pack column, New Objective, Woburn, MA) packed in-house with 12 cm of 3 µm Monitor-C_{18} particles (Column Engineering Inc; Ontario, CA). Peptides were eluted directly into the LTQ-Orbitrap using the following gradient at ~200 nL/min: 0-60 min, 0-35% solvent B (acetonitrile with 0.1 M acetic acid); 60-70 min, 35-70% B; 70-75 min, 70-0% B; 75-90 min, 0% B. Solvent A was composed of aqueous 0.1 M acetic acid. The mass spectrometer scan functions and HPLC solvent gradient were controlled by the Xcalibur data system. Spectra were acquired in the positive ion mode where each full MS survey scan performed in the Orbitrap analyzer (300-1700 *m/z*, R=60,000) was followed by 10 data-dependent MS/MS scans of the most intense ions per survey spectrum, fragmenting selected ions via collision induced dissociation. Ions already selected for MS/MS analysis were dynamically excluded for 30 s with a repeat count of 1 and a repeat duration of 30 s. Two biological replicates from each biological treatment were analyzed in duplicate (technical replicates).

Data Analysis - Acquired tandem mass spectra were converted to mascot generic files (.mgf) using MassMatrix jMass Spec Data File Conversion Tool (version 3.9) and

subsequently searched against a concatenated target/decoy International Protein Index (IPI) human database (v3.77) using Mascot Daemon (v2.2.0; Matrix Science). The Mascot search parameters were specified as a maximum of 1 missed tryptic cleavage; precursor ion mass tolerance of ±10 ppm; fragment ion tolerance mass tolerance of ±0.5 Da; a fixed modification of cysteine carbamidomethylation; and variable modifications of oxidation (M), phosphorylation (S,T,Y), diethylation +56 Da "light" (N-term., K, R, N, Q), and diethylation +60 Da "heavy" (N-term., K, R, N, Q). Protein identification and quantification was accomplished through the Isotopic Quantification module in ProteoIQ (v2.1.08; BioInquire, Athens, GA) using the following criteria: minimum ion score of 25.0; peptide length of at least 6; and a false discovery rate set at 1.0%.

Method Validation Using an α-Casein Standard Digest – An α-casein tryptic digest standard was prepared, desalted, and reconstituted in 100 mM sodium acetate at pH 6.0 (1 μg/μL) as described above. Equal volumes of sample (15 μL) were aliquoted and incubated with 4 μL of 40% (w/w) acetaldehyde-C^{12} (light label) or vehicle (unlabeled control) for 2 hrs at room temperature (vehicle – 100 mM sodium acetate, pH 6.0). Samples were then reduced with 4 μL of freshly prepared 0.6 M sodium cyanoborohydride ($NaBH_3CN$) or vehicle and incubated for 1 hr at room temp. A second addition of 4 μL of 40% acetaldehyde-C^{12} or vehicle was added to each respective sample and incubated for 1 hr at room temp. Samples were then reduced with 4 μL of 0.6 M $NaBH_3CN$ or vehicle and incubated for 1 hr at room temp. Samples were then reduced and incubated 3 additional times with the final incubation being left overnight (~14 hrs) at room temp. The reaction was then quenched with 8 μL of 25% (w/w) ammonium hydroxide (NH_4OH) and then immediately acidified with 16 μL of formic acid (CH_2O_2)

for both control and diethylated samples. Aliquots of each sample (33 μL) were then combined at a 1:1 ratio, dried under vacuum, reconstituted in 10 uL of 0.1 M AcOH. The remaining diethylated sample (33 μL) was dried under vacuum and reconstituted in 10 μL of 0.1 M AcOH. Samples were stored at -80°C until further analysis. Samples were generated in triplicate in order to test the labeling efficiency and assess any experimental effects on the stability of the phosphate moiety or influences in ionization.

Test samples were analyzed using an Agilent 1200 Series HPLC system coupled to an linear ion trap/Fourier transform (LTQ-FT) hybrid mass spectrometer (Thermo Finnigan). Peptides were diluted 10-fold in solvent A and loaded (4 μL) via a microautosampler onto an analytical column (360 μm o.d. x 75 μm i.d. fused silica microcapillary, packed in-house with 10 cm of 5 μm Monitor-C_{18} particles (Column Engineering Inc; Ontario, CA) that was pulled to a fine tip using a P-2000 laser puller (Sutter Instrument; Novato, CA)). Peptides were eluted directly into the LTQ-FT using the following gradient at 100 nL/min: 0-17 min, 0-70% solvent B (acetonitrile with 0.1 M acetic acid); 17-19 min, 70-95% B; 19-20 min, 95-0% B; 20-37 min, 0% B. Solvent A was composed of aqueous 0.1 M acetic acid. The mass spectrometer scan functions and HPLC solvent gradient were controlled by the Xcalibur data system. Spectra were acquired in the positive ion mode where each full MS survey scan (400-1800 *m/z*) was followed by a single data dependent MS/MS scans of the most intense ions per survey spectrum, fragmenting selected ions via collision induced dissociation. Ions already selected for MS/MS analysis were dynamically excluded for 30 s with a repeat count of 1 and a repeat duration of 30 s.

With a few key modifications to the original diethylation procedure (15), we reduced the reagent-to-peptide ratio and tested the labeling efficiency using a complex peptide mixture (MCF-7 whole cell lysate tryptic digest). The sample was desalted and diethylated as previously described within this section, except the reagent:peptide ratio was reduced from ~700 nmol reagent/pmol peptide to ~10 nmol reagent/pmol peptide. The sample was analyzed on the LTQ-FT instrument following the set-up and procedure described in chapter 3. The labeling efficiency was manually validated us the Xcalibur software.

4.3 Results

Protein phosphorylation is a vital post-translational modification that plays an integral role in tightly regulating many molecular functions including signal transduction, differentiation, proliferation, cell cycle control, metabolism, and apoptosis. The ability to quantitatively monitor global and site-specific changes in phosphorylation events allow us to gain a better understand of the key molecular components and signaling cascades involved in response to particular stimuli. We have established a robust and flexible phosphoproteomic strategy utilizing a simple and cost-effective quantification method based on reductive isotopic diethylation. The method was first validated using an α-casein standard tryptic digest to determine 1) the labeling efficiency, 2) the effect of the reaction conditions on the labile phosphate moiety, and 3) the effects of labeling on the ionization efficiency of phosphopeptides.

As shown in Figure 4.2, acetaldehyde will readily react with the N-terminus and lysine containing peptides at the ε-amino group to form a Schiff base which is easily reduced with $NaBH_3CN$. Using isotopically labeled acetaldehyde-C^{12} or -C^{13},

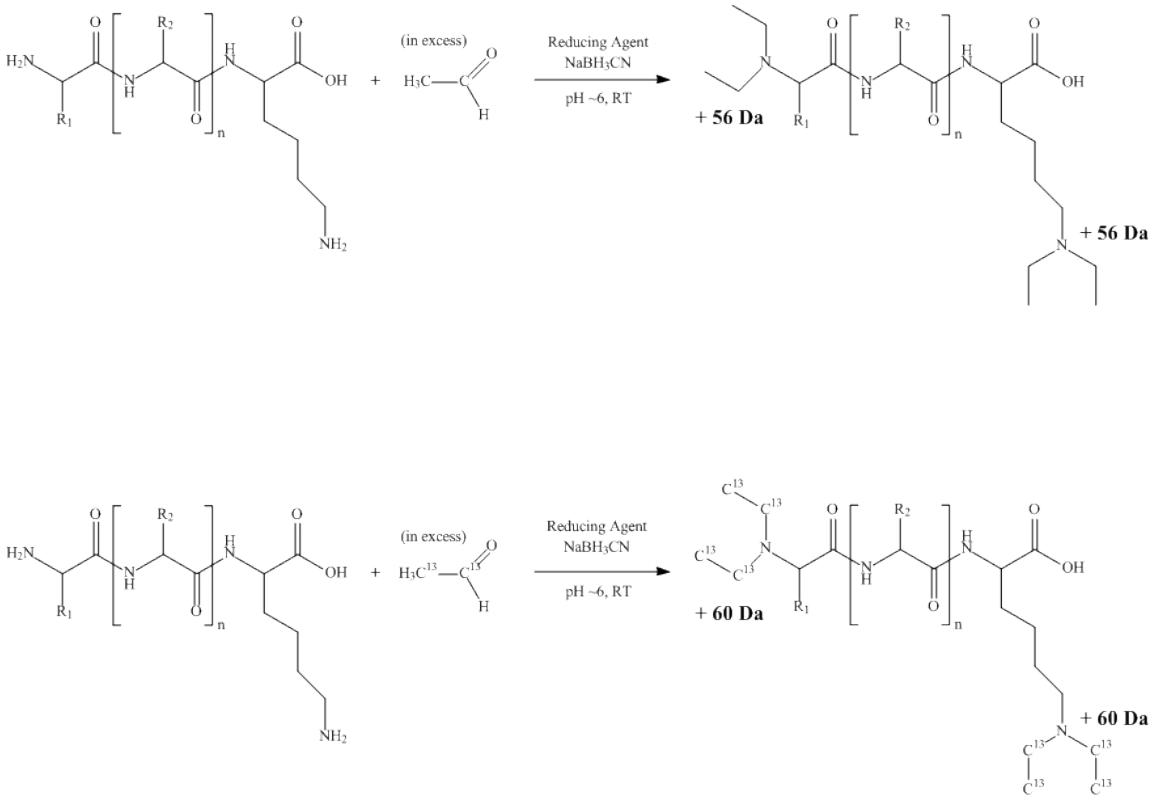

Figure 4. 2 - Diethylation Labeling Strategy. Peptides are reacted with "light" or "heavy" labeled acetaldehyde and then reduced with NaBH3CN. Following diethylation, the N-terminus and ε-amino group of lysine residues undergo a 56 Da or 60 Da mass shift

differentially labeled peptide pairs contain a 4 Da or 8 Da mass shift for conventional tryptic peptides containing a C-terminal arginine or lysine residue, respectively. However, the labeling efficiency directly influences the accuracy in quantification. Depending upon the completeness of the reaction, peptides may be completely labeled (diethylated), partially labeled (ethylated), or remain unlabeled.

Following diethylation of an α-casein standard digest, we manually validated (in triplicate) the labeling efficiency of three phosphorylated (2 mono- and 1 di-) and two non-phosphorylated peptides containing both C-terminal arginine or lysine residues

(Table 4.1). From the representative peptides, we were unable to successfully identify any partially or unlabeled peptides, suggesting near 100% labeling efficiency.

Table 4. 1 – Potential Labeling Conditions of Representative Phosphoyrlated Peptides. Following diethylation of an α-casein tryptic digest, samples were analyzed via RPLC-MS/MS in order to determine labeling efficiency. ND = not detected

TVDMEpSTEVFTK						
Charge State	Unlabeled (*m/z*)	RT	Peak Area	Diethylated (*m/z*)	RT	Peak Area
1+	1466.6	ND	ND	1578.6	24.22	6.34E+05
2+	733.8	ND	ND	789.8	24.22	1.59E+08
3+	489.5	ND	ND	526.8	24.22	8.78E+06
					Total	**1.69E+08**

β-Elimination of TVDMEpSTEVFTK						
Charge State	Unlabeled (*m/z*)	RT	Peak Area	Diethylated (*m/z*)	RT	Peak Area
1+	1368.6	ND	ND	1480.6	ND	ND
2+	684.8	ND	ND	740.8	ND	ND
3+	456.8	ND	ND	494.1	ND	ND

VPQLEIVPNpSAEER						
Charge State	Unlabeled (*m/z*)	RT	Peak Area	Diethylated (*m/z*)	RT	Peak Area
1+	1660.8	ND	ND	1716.8	ND	ND
2+	830.9	ND	ND	858.9	24.24	3.73E+08
3+	554.3	ND	ND	573	24.24	3.24E+08
					Total	**6.97E+08**

β-Elimination of VPQLEIVPNpSAEER						
Charge State	Unlabeled (*m/z*)	RT	Peak Area	Diethylated (*m/z*)	RT	Peak Area
1+	1562.8	ND	ND	1618.8	ND	ND
2+	781.9	ND	ND	809.9	ND	ND
3+	521.6	ND	ND	540.3	ND	ND

DIGpSEpSTEDQAMEDIK						
Charge State	Unlabeled (*m/z*)	RT	Peak Area	Diethylated (*m/z*)	RT	Peak Area
1+	1927.7	ND	ND	2039.7	ND	ND
2+	964.3	ND	ND	1020.3	25.06	1.39E+08
3+	643.2	ND	ND	680.5	25.06	2.08E+08
					Total	**3.47E+08**

β-Elimination of DIGpSEpSTEDQAMEDIK						
Charge State	Unlabeled (*m/z*)	RT	Peak Area	Diethylated (*m/z*)	RT	Peak Area
1+	1731.7	ND	ND	1843.7	ND	ND
2+	866.4	ND	ND	922.4	ND	ND
3+	577.9	ND	ND	615.2	ND	ND

Furthermore, we investigated the stability of the phosphate moiety under the labeling conditions and were unable to identify any peptides corresponding to the loss of the phosphate group while considering the possibility of all the potential degrees of labeling efficiency.

In addition to the challenges associated with the substochiometric levels of phosphorylated proteins, the ionization efficiency of phosphorylated peptides is relatively low compared to that of their non-phosphorylated counterparts. We investigated the potential influences in the ionization efficiency of phosphorylated peptides as a result of the increase in hydrophobicity resulting from diethylation. Tryptic peptides from a standard α-casein digest were diethylated with "light" labeled acetaldehyde and mixed at a 1:1 ratio with an unlabeled control and analyzed in tryplicate (Fig 4.3). Although the increase in hydrophobicity resulted in an increase in retention time (~ 0.5-1 min), we did not observe any significant changes in the ionization efficiency of the representative phosphorylated peptides.

In order assess the efficiency in phosphopeptide enrichment, we used an α-casein tryptic digest which provides a simple peptide mixture of non-phosphorylated and phosphorylated peptides with varying degrees of phosphorylation (9 total: 3 mono-, 2 di-, 1 tri-, and 3 quadruple-). Utilizing TiO_2 spin columns, we were able to effectively enrich phosphorylated peptides even though we observed an overall decrease in signal intensity following peptide enrichment (Fig 4.4). In addition, we were able to identify all singularly, doubly, and triply phosphorylated peptide and were only restricted in identifying the quadruple phosphorylated peptides following TiO_2 enrichment.

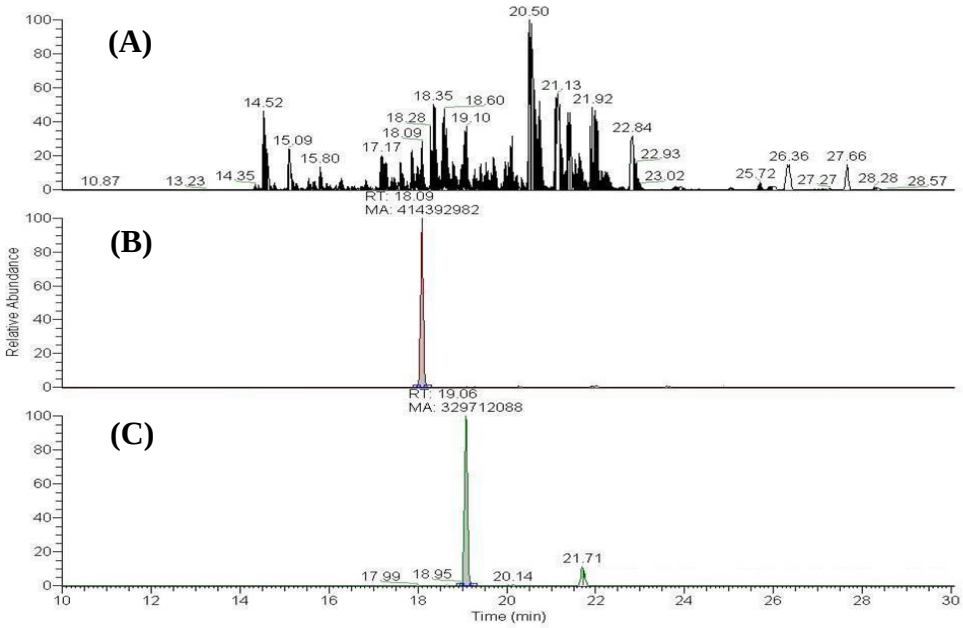

Figure 4. 3 - Ionization and Chromatographic Effects of Diethylation Labeling. (A) Base peak chromatogram from a 1:1 mixture of unlabeled:diethylated ("light") α-casein standard digest. **(B)** XIC of unlabled TVDMEpSTEVFTK. **(C)** XIC of diethylated "light" TVDMEpSTEVFTK.

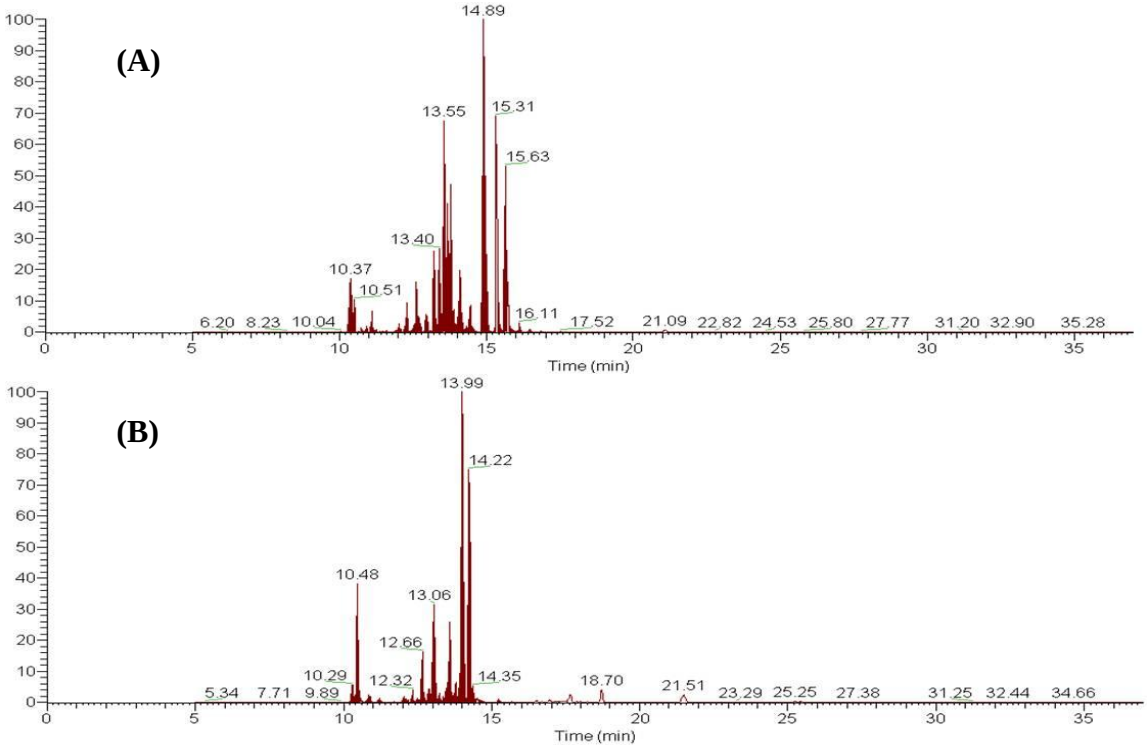

Figure 4. 4 – TiO_2 Enrichment of α-Casein. (A) Base peak chromatogram prior to TiO_2 enrichment. **(B)** Base peak chromatogram following TiO_2 enrichment

To demonstrate the usefulness and applicability of this strategy, we preformed a quantitative phosphoproteomic analysis of 2-ME-induced apoptosis in MCF-7 human breast cancer cells. We were able to identify 11,382 unique phosphopeptides corresponding to 1,876 unique phosphoproteins (data not shown). An initial survey of the phosphoproteomic data with IPA analysis software showed that the majority of the differential phosphorylation events are involved in cell cycle regulation, protein synthesis, cellular organization, and proliferation. Furthermore, this data supports our earlier findings pertaining to the mechanisms involved in 2-ME induced apoptosis particularly by mediating signaling cascades in response to ER-stress, the disruption in hormone synthesis, and those responsible for locking cells in G2/M cell cycle arrest.

4.4 Discussion

Protein phosphorylation plays an important role in regulating many molecular functions including inter- and intracellular signaling, proliferation, cell cycle regulation, and apoptosis. The ability to quantitatively monitor global and site-specific changes in phosphorylation is required in order to discern the dynamic molecular events and signaling cascades involved in governing these systems in response to biological perturbations such as cell growth and differentiation, disease progression, and drug response.

Mass spectrometry-based approaches have proven particularly effective for large-scale phosphoproteomic analyses. However, many of the conventional quantitative strategies are limited in their applications as a result of their incompatibility with particular types of biological systems, mass spectrometers, and/or experimental procedures specific to phosphoproteomics. Our research has predominately been

conducted using the MCF-7 cell line a cellular model for breast cancer investigations. In addition, this work has typically been conducted on either a LTQ-FT or LTQ-Orbitrap mass spectrometer utilizing collision-induced dissociation for MS/MS analysis.

Traditional metabolic labeling strategies (*i.e.,* SILAC) are presumably the most accurate quantification methods for determining relatively small changes in protein expression/modification as a result of its ability to reduce experimental error associated with sample processing by combining differentially labeled samples at the cellular level. However, these methods are typically not suitable for investigations pertaining to hormone sensitive cell lines, such as MCF-7 human breast cancer cells. Alternatively, chemical labeling strategies which incorporate isobaric mass tags (*e.g.,* iTRAQ and TMT) have been developed which allow samples to be differentially labeled at the peptide level. Unfortunately, these strategies are typically not compatible with linear ion trapping instruments which are unable to retain ions in the lower mass range during MS/MS analysis where the quantitiation based reporter ions are normally found (16). Recently, label-free quantitation methods (*i.e.,* spectral counting) have gained increasing popularity because of their ability to provide simple and cost-effective approaches for reliable protein quantification. However, the reproducibility of TiO_2 enrichment may negatively impact the accuracy of label-free quantification in phosphoproteomic analyses (17). It is therefore critical to develop flexible and accurate phosphoproteomic strategies that may be easily adapted to a wide range of scientific applications.

Recently, Barrios-Llerena *et al.* reported a relatively simple and inexpensive diethylation labeling strategy for global protein quantification that improves upon some of the drawbacks associated with similar dimethylation procedures. Most notably,

diethylation labeling eliminated differential shifts in the LC retention times between isotopically paired peptides observed in deuterium labeled dimethylation strategies. Therefore, we assessed the utility of diethylation labeling for quantitative phosphoproteomic analyses. Using an α-casein standard tryptic digest, we assessed the 1) labeling efficiency, 2) the effect of the reaction conditions on the phosphate moiety, and 3) the effects of labeling on the ionization efficiency of phosphopeptides.

We examined the labeling efficiency of 3 representative phosphorylated peptides and 2 non-phosphorylated peptides. Depending upon the degree of labeling following the diethylation procedure, peptides may be found as non-labled, partially labeled (ethylated), or completely labeled (diethylated). Utilizing peak intensities, we investigated the degree of labeling for each peptide under each potential labeling state corresponding to the +1, +2, and +3 charge states. Not only were we unable to identify any partially labeled or non-labeled peptides, we did not observe any losses of the phosphate moieties as a result of the labeling conditions for the 3 representative phosphorylated peptides. With an ~ 100% labeling efficiency and apparently little to no influence on the stability of the phosphate moiety, we confirmed that diethylation labeling provides- a promising global approach for phosphoproteomic analysis.

As mentioned previously, phosphorylation often occurs on low abundance proteins at substochiometric levels, which presents inherent challenges associated with phosphoproteomics and requires the selective enrichment of phosphorylated peptides prior to LC-MS/MS analysis. The use of 2D-LC-MS/MS strategies combined with selective phosphopeptide enrichment procedures has proven to effectively increase the identification of unique phosphorylated peptides and proteins responsible for regulating

important biological functions. Adapting our RP-RPLC-MS/MS scheme, we established RP-TiO_2-RP-MS/MS strategy for phosphoproteomic analysis (Fig. 4.1). During the first dimension of separation non-phosphorylated and phosphorylated peptides alike are evenly fractionated across the gradient. Conducting the first dimension of separation at an intermediate pH (pH 7.5), prevented the possible β-elimination of phosphorylated peptides while providing an acceptable level of orthogonality. Non-adjacent fractions at equal time intervals were concatenated. Concatenated samples were subsequently enriched for phosphopeptides using TiO_2 and analyzed by RPLC-MS/MS. Concatenating fractions allowed us to exploit the entire separation space in the second dimension while reducing the overall analysis time by half (Fig. 4.5).

Although we were able to identify 11,382 unique phosphopeptides corresponding to 1,876 unique phosphoproteins, our currently available software does not properly address the computational challenges associated with large scale phosphoproteomic analyses. Within ProteoIQ, regulation of protein phosphorylation is reported on the protein level rather than at the phosphorylation site and is therefore erroneously reported from phosphoproteins containing multiple phosphorylation sites. Although we were able to parse and export the peak intensities for each quantifiable phosphopeptide, additional efforts need to be taken in order to sum the intensities across all charge states for each phosphopeptide as well as those corresponding to the same phosphorylation site on unique peptides resulting from missed cleavages in order to obtain accurate site-specific quantification. In addition, proper statistical analysis needs to be conducted to further assess potential molecular targets and signaling pathways affected by 2-ME exposure.

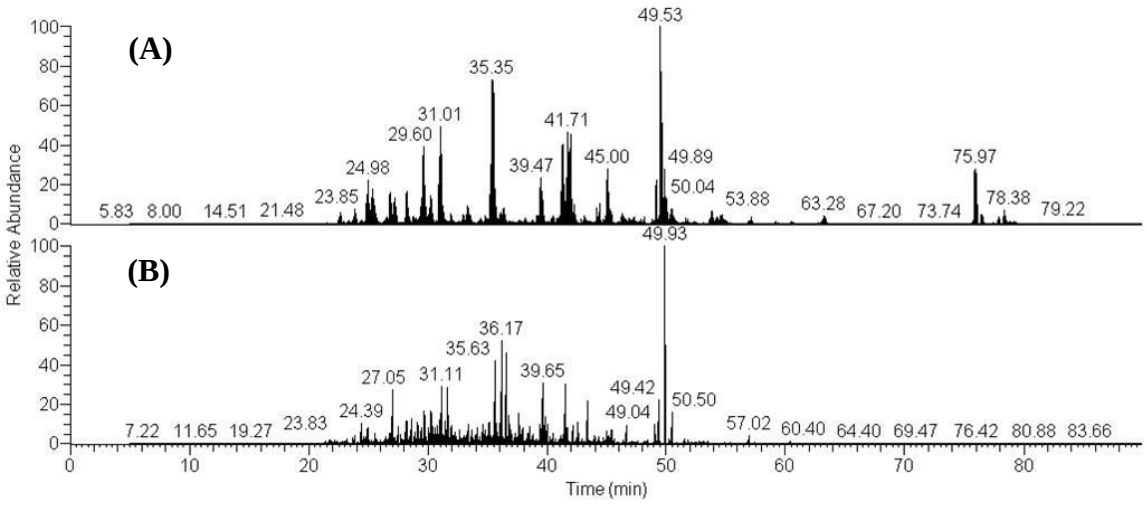

Figure 4. 5 - Distribution of Phosphorylated Peptides During the Second Dimension of Separation. Representative chromatograms from BioRep1 TechRep1 fraction 13 **(A)** Base peak chromatogram. **(B)** Neutral loss chromatogram corresponding to the loss of the phosphate moiety.

4.5 References

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Appendix I

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00398002	Isoform 3 of Plectin	b	B, D, L	4570	162	202	401	581
IPI00014898	Isoform 1 of Plectin	b	B, D, L	4684	164	202	402	583
IPI00026781	Fatty acid synthase		B, I, G, D, L	2511	426	496	554	613
IPI00302592	Isoform 2 of Filamin-A		K, B, D, L	2639	426	511	416	508
IPI00456969	cpic dynein 1 heavy chain 1	k	B, G, D, C	4646	170	205	136	209
IPI00019502	Isoform 1 of Myosin-9	x, o	K, B, D, L	1960	239	275	289	373
IPI00021812	Neuroblast differentiation-associated protein AHNAK		K	5890	94	159	259	253
IPI00296337	Isoform 1 of DNA-dependent protein kinase catalytic subunit		K	4128	186	206	160	254
IPI00553169	Uncharacterized protein			2315	384	470	399	488
IPI00607818	myosin-14 isoform 1			2003	130	250	270	280
IPI00289334	Isoform 1 of Filamin-B	p, e	K, B, L	2602	189	222	137	191
IPI00024067	Isoform 1 of Clathrin heavy chain 1	j	I, D, L	1675	225	288	317	354
IPI00554648	Keratin, type II cytoskeletal 8		K, B	483	2011	1429	1803	2440
IPI00009342	Ras GTPase-activating-like protein IQGAP1	p	K, J, B, L	1657	160	218	144	183
IPI00013933	Isoform DPI of Desmoplakin	b	B, I, L	2871	97	90	75	126
IPI00022774	Transitional er ATPase		K, J, B, E, H, D	806	181	272	241	218
IPI00554788	Keratin, type I cytoskeletal 18	d	B	430	1219	963	1657	1171
IPI00479186	Isoform M2 of Pyruvate kinase isozymes M1/M2		K, B, D, L	531	800	724	781	645
IPI00941899	66 kDa protein			605	721	625	663	568
IPI00186290	Elongation factor 2	r, g	B, D	858	285	274	405	395
IPI00382470	Isoform 2 of Heat shock protein HSP 90-alpha	k, p	B, D, L	854	551	601	567	730
IPI00784154	60 kDa heat shock protein, mitochondrial		B, I, D	573	131	224	421	308
IPI00013808	Alpha-actinin-4	o	K, J, B	911	149	223	176	201
IPI00021405	Isoform A of Prelamin-A/C	b	K, B	664	125	168	185	227

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00871535	Isoform 2 of Spectrin alpha chain, brain	b	B, D	2477	87	104	84	110
IPI00844215	Isoform 1 of Spectrin alpha chain, brain	b	B, D	2472	87	106	84	111
IPI00856098	p180/r receptor			1540	54	86	124	150
IPI00414676	Heat shock protein HSP 90-beta	l	B, I, D	724	457	518	544	605
IPI00013894	Stress-induced-phosphoprotein 1		K, B, G	543	90	138	196	211
IPI00003865	Isoform 1 of Heat shock cognate 71 kDa protein	l	B, D, L	646	401	408	542	619
IPI00216952	Isoform C of Prelamin-A/C	b	K, B	572	122	169	177	212
IPI00179298	482 kDa protein			4376	75	90	70	120
IPI00298994	Talin-1	c	B, D, L	2541	74	59	58	89
IPI00397526	Isoform 1 of Myosin-10		B	1976	91	159	80	112
IPI00027230	Endoplasmin	l, o	E, H, D	803	375	342	275	226
IPI00007752	Tubulin beta-2C chain	k, l	B, D, C	445	441	298	741	975
IPI00007765	Stress-70 protein, mitochondrial	l	B, I	679	117	200	226	288
IPI00027442	Alanyl-tRNA synthetase, cpic	g	B, D	968	109	127	122	167
IPI00645452	Tubulin, beta			426	474	317	764	991
IPI00021048	Isoform 1 of Myoferlin		K, L, A	2061	98	129	64	125
IPI00000877	Hypoxia up-regulated protein 1		E	999	168	164	95	122
IPI00003362	HSPA5 protein		K, E	655	240	227	331	376
IPI00783271	Leucine-rich PPR motif-containing protein, mitochondrial		K, B, I, C	1394	68	61	45	82
IPI00001159	tlal activator GCN1		B, I	2671	39	58	48	79
IPI00013508	Alpha-actinin-1		J, B, D	892	100	109	124	130
IPI00005614	Isoform Long of Spectrin beta chain, brain 1		K, J, B, D, L	2364	52	67	51	64
IPI00645078	Ubiquitin-like modifier-activating enzyme 1			1058	116	120	161	147

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00013475	Tubulin beta-2A chain	l, j	B, C	445	352	259	614	944
IPI00012837	Kinesin-1 heavy chain		B, C	963	69	83	76	100
IPI00304925	Heat shock 70 kDa protein 1A/1B		K, B, I, E, D	641	324	337	317	423
IPI00845339	cDNA FLJ54392, highly similar to Heat shock 70 kDa protein 1			641	324	337	316	420
IPI00013452	Bifunctional aminoacyl-tRNA synthetase	g	B, D	1512	99	111	60	101
IPI00297779	T-complex protein 1 subunit beta	l	K, J, B, D	535	83	98	116	133
IPI00465248	Isoform alpha-enolase of Alpha-enolase		K, B, D, L	434	377	383	653	592
IPI00002966	Heat shock 70 kDa protein 4		K, J, B	840	107	112	125	109
IPI00010951	Epiplakin		B, C	5090	10	14	88	152
IPI00009790	6-phosphofructokinase type C		B, D	784	72	94	108	127
IPI00787323	Similar to Keratin, type II cytoskeletal 8			443	1337	991	1071	1154
IPI00021439	Actin, cpic 1	l	B, D, C	375	1145	864	1192	1618
IPI00013683	Tubulin beta-3 chain	l	B, C	450	320	237	565	553
IPI00438229	Isoform 1 of tc intermediary factor 1-beta		K	835	117	111	122	150
IPI00169383	Phosphoglycerate kinase 1		B, D	417	238	280	269	263
IPI00295857	Isoform 1 of Coatomer subunit alpha		B, H, G, D	1224	58	85	65	100
IPI00009904	Protein disulfide-isomerase A4		E	645	101	140	145	160
IPI00218342	C-1-tetrahydrofolate synthase, cpic		B, I, D	935	98	86	125	133
IPI00010796	Protein disulfide-isomerase		E, H, L	508	214	227	425	398
IPI00021290	ATP-citrate synthase		K, J, B, D	1101	65	109	77	116
IPI00440493	ATP synthase subunit alpha, mitochondrial	h	I, L	553	77	91	174	120

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00930130	cDNA FLJ11352 fis, clone HEMBA1000020, highly similar to Tubulin beta-2C chain			397	439	290	559	779
IPI00420014	Isoform 1 of U5 small nuclear ribonucleoprotein 200 kDa helicase	g	K, J	2136	58	54	41	52
IPI00479145	Keratin, type I cytoskeletal 19			400	871	671	810	753
IPI00303476	ATP synthase subunit beta, mitochondrial	x, h	I, L	529	152	198	244	231
IPI00018246	Isoform 1 of Hexokinase-1	s	K, J, I, D	917	73	71	39	86
IPI00029601	Src substrate cortactin		B, C	550	56	61	127	108
IPI00911039	cDNA FLJ54408, highly similar to Heat shock 70 kDa protein 1			586	269	277	287	371
IPI00302925	59 kDa protein			547	74	90	105	149
IPI00217975	Lamin-B1	b	K	586	57	63	85	119
IPI00031522	Trifunctional enzyme subunit alpha, mitochondrial		J, B, I	763	72	83	62	97
IPI00789324	cDNA FLJ60424, highly similar to Junction plakoglobin			563	638	569	526	523
IPI00289499	Bifunctional purine biosynthesis protein PURH		I, D	592	80	123	70	103
IPI00023598	Tubulin beta-4 chain	k, l	B, D, C	444	310	230	604	788
IPI00216008	Isoform Long of Glucose-6-phosphate 1-dehydrogenase		B, D	561	129	192	216	238
IPI00795257	32 kDa protein			293	896	673	799	503
IPI00465439	Fructose-bisphosphate aldolase A		D	364	528	367	609	539
IPI00328753	Isoform 1 of Kinectin		E	1357	45	28	35	75
IPI00908770	cDNA FLJ53063, highly similar to Tubulin beta-7 chain			317	361	238	481	845
IPI00604620	Nucleolin	x	K, J, B	710	83	176	247	245

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00219018	Glyceraldehyde-3-phosphate dehydrogenase		K, B, D	335	929	670	804	508
IPI00792642	25 kDa protein			210	720	487	627	942
IPI00383581	cDNA FLJ61290, highly similar to Neutral alpha-glucosidase AB	l	E, G	995	80	207	95	121
IPI00022744	Isoform 1 of Exportin-2	b, f	K, B	971	83	182	146	150
IPI00025252	Protein disulfide-isomerase A3	l, p	E	505	106	151	166	195
IPI00011454	Isoform 2 of Neutral alpha-glucosidase AB	l	E, G	966	75	151	88	113
IPI00140420	Staphylococcal nuclease domain-containing protein 1		K, B, I	910	83	68	82	146
IPI00031461	cDNA FLJ60299, highly similar to Rab GDP dissociation inhibitor beta			449	102	121	116	135
IPI00006196	Isoform 2 of Nuclear mitotic apparatus protein 1	k	K, J, D	2101	52	70	13	13
IPI00100160	Isoform 1 of Cullin-associated NEDD8-dissociated protein 1	e	K	1230	78	77	78	88
IPI00302927	T-complex protein 1 subunit delta	l	K, J, B, D, C	539	52	76	59	93
IPI00218993	Isoform Beta of Heat shock protein 105 kDa		B	814	52	59	57	67
IPI00029012	Eukaryotic tl initiation factor 3 subunit A	r, g	K, B, D	1382	41	46	65	81
IPI00000816	14-3-3 protein epsilon	k, b	B, D	255	185	219	129	193
IPI00844578	ATP-dependent RNA helicase A	g	K, J, B	1270	68	81	93	88
IPI00024466	Isoform 1 of UDP-glucose:glycoprotein glucosyltransferase 1	l	E	1555	40	55	42	38
IPI00479262	eukaryotic tl initiation factor 4 gamma 1 isoform 1			1600	47	77	89	122
IPI00001639	Importin subunit beta-1	b	K, B, D	876	63	46	78	95

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00021263	14-3-3 protein zeta/delta	p	B, D	245	292	222	337	442
IPI00291175	Isoform 1 of Vinculin	c	B, D, C, L	1066	60	43	12	28
IPI00782992	Isoform 1 of Serine/arginine repetitive matrix protein 2		K	2752	31	33	45	82
IPI00219005	Peptidyl-prolyl cis-trans isomerase FKBP4	l	K, J, B, D, C	459	90	209	95	139
IPI00218343	Tubulin alpha-1C chain	l	B, C	449	285	301	427	289
IPI00008524	Isoform 1 of Polyadenylate-binding protein 1	r, g	K, B, D	636	97	132	127	152
IPI00026216	Puromycin-sensitive aminopeptidase		K, B, D	919	40	61	44	62
IPI00290566	T-complex protein 1 subunit alpha	l	K, J, B, G, D, C, L	556	35	39	65	79
IPI00025491	Eukaryotic initiation factor 4A-I	r, g	D	406	94	139	122	119
IPI00028031	cDNA FLJ56425, highly similar to Very-long-chain specific acyl-CoAdehydrogenase, mitochondrial			701	42	47	33	61
IPI00246058	Programmed cell death 6-interacting protein	b, d, o	B, D, C	868	73	76	70	68
IPI00792677	cDNA FLJ60097, highly similar to Tubulin alpha-ubiquitous chain			416	372	315	485	360
IPI00022462	Transferrin receptor protein 1	s	I, F, L	760	61	95	66	125
IPI00332371	Isoform 1 of 6-phosphofructokinase, liver type		B, D	780	58	155	141	96
IPI00010154	Rab GDP dissociation inhibitor alpha	p, o	B, D	447	86	105	116	106
IPI00910438	cDNA FLJ54574, highly similar to Staphylococcal nuclease domain-containing protein 1			889	76	60	76	123

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00180675	Tubulin alpha-1A chain	k, l	B, D, C	451	355	314	483	354
IPI00290770	cDNA FLJ44436 fis, clone UTERU2019706, highly similar to T-complex protein 1 subunit gamma			544	55	54	41	93
IPI00843975	Ezrin		J, B, D, L	586	53	82	120	108
IPI00006482	Isoform Long of Sodium/potassium-transporting ATPase subunit alpha-1	s	H, L	1023	41	66	82	65
IPI00643920	cDNA FLJ54957, highly similar to Transketolase			631	81	85	107	94
IPI00171903	Isoform 1 of Heterogeneous nuclear ribonucleoprotein M	g	K, J	730	38	47	53	78
IPI00010720	T-complex protein 1 subunit epsilon	l	J, B, D, C	541	41	42	53	78
IPI00291006	Malate dehydrogenase, mitochondrial		K, J, I, L	338	131	131	135	180
IPI00003527	Na(+)/H(+) exchange regulatory cofactor NHE-RF1		B, L	358	73	95	207	198
IPI00216049	Isoform 1 of Heterogeneous nuclear ribonucleoprotein K	p, g	K, J, B	463	143	123	122	177
IPI00844172	Myosin			1253	42	66	18	33
IPI00215948	Isoform 1 of Catenin alpha-1	c	B, D, L	906	54	55	39	71
IPI00011107	Isocitrate dehydrogenase [NADP], mitochondrial		I	452	52	85	82	137
IPI00794605	18 kDa protein			161	651	542	577	291
IPI00004860	Isoform Complexed of Arginyl-tRNA synthetase, cpic	g	K, J, B, I, D	660	28	35	35	63
IPI00011229	Cathepsin D		I	412	139	193	187	213
IPI00027497	Glucose-6-phosphate isomerase	x	K, J, B, D, L	558	144	161	130	178
IPI00004358	Glycogen phosphorylase, brain form		B	843	47	73	24	52

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00018146	14-3-3 protein theta		K, J, B	245	104	120	110	173
IPI00300371	Isoform 1 of Splicing factor 3B subunit 3	g	K	1217	71	62	47	85
IPI00299000	Proliferation-associated protein 2G4	f	K, J, B	394	151	213	187	254
IPI00072534	Isoform 1 of Protein unc-45 homolog A	e	K, B	944	20	52	29	37
IPI00026154	cDNA FLJ59211, highly similar to Glucosidase 2 subunit beta			535	67	120	114	130
IPI00783982	Coatomer subunit gamma		B, G, D	874	37	49	45	67
IPI00030781	Isoform Alpha of Signal transducer and activator of tc 1-alpha/beta	p	K, J, B, D	750	29	43	44	47
IPI00219078	Isoform 1 of Sarcoplasmic/er calcium ATPase 2	c, s	H	1042	50	62	38	68
IPI00742682	Nucleoprotein TPR	r, o, s	K, B	2363	19	22	30	49
IPI00022228	Vigilin		K, B, L	1268	54	38	40	79
IPI00894287	cDNA FLJ56889, moderately similar to Vigilin			1235	51	34	46	86
IPI00384489	AP-1 complex subunit beta-1 isoform c			919	37	51	34	60
IPI00465028	triosephosphate isomerase isoform 2			286	143	142	294	323
IPI00418313	interleukin enhancer-binding factor 3 isoform d		K, J, B, I	898	70	70	48	34
IPI00550069	Ribonuclease inhibitor		B	461	42	64	77	96
IPI00031420	UDP-glucose 6-dehydrogenase		D	494	49	59	71	84
IPI00646779	TUBB6 protein	l	B, C	447	150	122	253	352
IPI00012079	cDNA FLJ54492, highly similar to Eukaryotic tl initiation factor 4B	r, g	D	616	67	67	134	105
IPI00018398	26S protease regulatory subunit 6A	k, b	K, B	439	21	34	45	63

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00018465	T-complex protein 1 subunit eta	l	B, I, D	543	49	77	83	108
IPI00019912	Peroxisomal multifunctional enzyme type 2			736	50	47	54	55
IPI00018140	Isoform 1 of Heterogeneous nuclear ribonucleoprotein Q		K, B, E, H	623	51	61	37	46
IPI00418169	Isoform 2 of Annexin A2	x	B, L	357	85	145	156	158
IPI00644712	X-ray repair cross-complementing protein 6		K, B	609	142	244	68	79
IPI00003918	60S ribosomal protein L4	r, g	K, J, B, D, I	427	58	34	106	144
IPI00216318	Isoform Long of 14-3-3 protein beta/alpha	b	K, J, B, D	246	146	138	111	161
IPI00554469	Isoform 2 of Mitochondrial inner membrane protein		I	747	57	62	53	71
IPI00784156	Isoform 1 of AP-2 complex subunit beta		D, L	937	35	37	19	46
IPI00908469	cDNA FLJ52712, highly similar to Tubulin beta-6 chain			418	112	112	231	359
IPI00419880	40S ribosomal protein S3a	r, g, e	K, J, B, D, I	264	56	55	110	134
IPI00034049	Isoform 1 of Regulator of nonsense transcripts 1	d	B	1129	25	31	16	49
IPI00022143	Isoform 1 of Extended synaptotagmin-1			1104	32	44	28	78
IPI00020672	Isoform 1 of Dipeptidyl peptidase 3		B	737	58	69	56	63
IPI00604590	Nucleoside diphosphate kinase			292	129	152	215	326
IPI00016610	Poly(rC)-binding protein 1	g	K, B	356	78	100	131	106
IPI00940432	mitochondrial inner membrane protein isoform 2			659	55	62	51	67
IPI00021435	26S protease regulatory subunit 7	k, b	K, J, B, I	433	32	46	36	43
IPI00759723	Isoform Monomeric of Arginyl-tRNA synthetase, cpic	g	K, J, B, I, D	588	20	24	25	51

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00554737	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform	k	K, I, D	589	26	37	28	66
IPI00396485	Elongation factor 1-alpha 1	r, g	B, D	462	150	134	384	316
IPI00220834	X-ray repair cross-complementing protein 5	f	K, J, B	732	41	55	68	67
IPI00000846	Isoform 1 of Chromodomain-helicase-DNA-binding protein 4		K	1912	31	91	9	35
IPI00218319	Isoform 2 of Tropomyosin alpha-3 chain		B, D, C	248	77	124	161	154
IPI00883857	Isoform Long of Heterogeneous nuclear ribonucleoprotein U	g	K, B	825	79	75	61	71
IPI00016910	Eukaryotic tl initiation factor 3 subunit C	r, g	B, D	913	78	112	69	124
IPI00029485	Isoform p150 of Dynactin subunit 1	k, j	B, D, C	1278	28	21	20	32
IPI00007928	Pre-mRNA-processing-splicing factor 8	g	K	2335	17	41	20	39
IPI00220642	14-3-3 protein gamma	k	B, D	247	133	112	128	165
IPI00216951	Aspartyl-tRNA synthetase, cpic	r, g	K, B, D, L	501	89	99	64	81
IPI00030275	Heat shock protein 75 kDa, mitochondrial	l	I	704	75	60	65	74
IPI00396171	Isoform 1 of Microtubule-associated protein 4		B, C	1152	38	30	33	44
IPI00141318	Isoform 1 of cs-associated protein 4		E	602	36	45	62	55
IPI00744648	Isoform 1 of C-Jun-amino-terminal kinase-interacting protein 4		B	1321	27	41	29	18
IPI00299571	Isoform 2 of Protein disulfide-isomerase A6	l	E, L	492	57	72	81	75

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00304596	Non-POU domain-containing octamer-binding protein		K	471	40	38	32	81
IPI00025874	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1 precursor		E	646	89	96	110	126
IPI00020984	cDNA FLJ55574, highly similar to Calnexin			627	124	212	87	111
IPI00017617	Probable ATP-dependent RNA helicase DDX5		K, J	614	44	59	37	44
IPI00550363	Transgelin-2		L	199	28	21	65	136
IPI00550021	60S ribosomal protein L3	r, g	J, B, D, I	403	40	62	74	60
IPI00299402	Pyruvate carboxylase, mitochondrial		B, I	1178	23	24	27	44
IPI00010779	Isoform 1 of Tropomyosin alpha-4 chain		B, D, C	248	72	138	189	181
IPI00217952	Isoform 1 of Glucosamine--fructose-6-phosphate aminotransferase [isomerizing] 1	i	B, D	699	41	62	39	52
IPI00942539	39 kDa protein			342	64	109	110	117
IPI00027493	Isoform 2 of 4F2 cell-surface antigen heavy chain	h, s	L	529	56	82	46	64
IPI00012007	Adenosylhomocysteinase		B, D	432	51	55	43	69
IPI00419585	Peptidyl-prolyl cis-trans isomerase A	l	K, B, D	165	141	102	314	236
IPI00419237	Isoform 1 of c aminopeptidase		K, J, B, I	519	19	26	30	66
IPI00032038	Isoform 1 of Carnitine O-palmitoyltransferase 1, liver isoform		I, H	773	39	31	18	69
IPI00073772	Fructose-1,6-bisphosphatase 1		D	338	61	81	86	112
IPI00748794	Isoform SERCA3A of Sarcoplasmic/er calcium ATPase 3	s	K, E	999	32	60	24	40

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00218097	Uncharacterized protein			1312	25	38	29	16
IPI00027223	Isocitrate dehydrogenase [NADP] cpic		B, I, D	414	26	47	43	78
IPI00514053	Coatomer subunit delta		B, G, D	511	37	31	59	58
IPI00010740	Isoform Long of Splicing factor, proline- and glutamine-rich		K	707	72	51	50	80
IPI00014424	Elongation factor 1-alpha 2		K, B	463	141	161	442	367
IPI00418262	Fructose-bisphosphate aldolase	b	B, I, D, C	451	60	79	102	96
IPI00215637	ATP-dependent RNA helicase DDX3X		K, B	662	34	29	39	55
IPI00479217	Isoform Short of Heterogeneous nuclear ribonucleoprotein U	g	K, B	806	71	75	67	74
IPI00464999	HEAT repeat-containing protein 6			1181	17	23	18	45
IPI00006451	Vesicle-fusing ATPase	o	B, D	744	36	38	22	29
IPI00012268	26S proteasome non-ATPase regulatory subunit 2	k, b		908	46	50	34	60
IPI00007750	Tubulin alpha-4A chain	k, l	B, D, C	448	150	217	303	287
IPI00402183	Isoform 3 of Heterogeneous nuclear ribonucleoprotein Q		K, B, E, H	562	47	58	33	45
IPI00784044	Isoform 1 of Methylcrotonoyl-CoA carboxylase beta chain, mitochondrial		I	563	35	37	40	72
IPI00329536	Early e antigen 1		B, D	1411	21	21	17	32
IPI00017726	Isoform 1 of 3-hydroxyacyl-CoA dehydrogenase type-2		B, I, L	261	39	59	63	90
IPI00329791	Probable ATP-dependent RNA helicase DDX46		K	1031	26	35	25	24
IPI00026089	Splicing factor 3B subunit 1	g	K	1304	35	29	13	26
IPI00549248	Isoform 1 of Nucleophosmin	p, m	K, J, B	294	48	65	139	116
IPI00021428	Actin, alpha skeletal muscle		B, D	377	547	401	515	982

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00002459	Uncharacterized protein			667	31	53	33	29
IPI00003519	116 kDa U5 small nuclear ribonucleoprotein component	g	K, J, B	972	29	35	35	24
IPI00375441	Isoform 1 of Far upstream element-binding protein 1		K, J	644	44	56	24	70
IPI00295400	Isoform 1 of Tryptophanyl-tRNA synthetase, cpic	r, g	B, D	471	31	61	40	38
IPI00156374	Isoform 1 of Importin-4	o	K, B	1081	28	21	31	38
IPI00384689	Isoform 1 of Pyridoxal-dependent decarboxylase domain-containing protein 1			788	16	33	32	42
IPI00025512	Heat shock protein beta-1		K, B, D, C, L	205	116	121	249	266
IPI00643152	cDNA FLJ56386, highly similar to Heat shock 70 kDa protein 1L			705	200	158	163	239
IPI00219525	6-phosphogluconate dehydrogenase, decarboxylating		B, D	483	64	67	66	85
IPI00296039	Isoform 4 of Tropomyosin alpha-1 chain		B, D, C	284	41	54	116	115
IPI00641582	BAG family molecular chaperone regulator 3	l	D	575	25	27	48	47
IPI00848226	Guanine nucleotide-binding protein subunit beta-2-like 1		B, L	317	59	77	68	98
IPI00013214	cDNA FLJ55599, highly similar to DNA replication licensing factor MCM3			853	28	26	16	31
IPI00220219	Coatomer subunit beta'		B, G, D	906	42	46	25	42
IPI00002460	Isoform 1 of Annexin A7	f	K, D, L	488	38	43	27	47
IPI00396378	Isoform B1 of Heterogeneous nuclear ribonucleoproteins A2/B1	g	K, J, B	353	44	82	60	92

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00889541	Isoform 4 of Probable ATP-dependent RNA helicase DDX17		K	729	43	52	38	45
IPI00479786	KH-type splicing regulatory protein		K, B, D	711	34	31	37	61
IPI00221325	E3 SUMO-protein ligase RanBP2	k, l, o, s	K, D	3224	19	32	11	39
IPI00396370	Isoform 1 of Eukaryotic tl initiation factor 3 subunit B	r, g	B, D	814	42	48	22	53
IPI00011285	Calpain-1 catalytic subunit		B, L	714	65	82	25	37
IPI00645745	37 kDa protein			320	68	130	158	124
IPI00216135	Isoform 3 of Tropomyosin alpha-1 chain		B, D, C	284	60	72	123	137
IPI00329633	Threonyl-tRNA synthetase, cpic	r, g	B, D	723	30	32	31	41
IPI00008274	Isoform 1 of Adenylyl cyclase-associated protein 1	p	B, L	475	38	57	55	67
IPI00256684	Isoform B of AP-2 complex subunit alpha-1		D, L	955	17	31	14	38
IPI00604664	NADH-ubiquinone oxidoreductase 75 kDa subunit			741	39	32	32	38
IPI00301263	CAD protein		K, B, D	2225	28	29	16	34
IPI00940393	Elongation factor 1-alpha			395	132	124	285	254
IPI00221226	Annexin A6		B	673	27	34	30	27
IPI00413611	DNA topoisomerase 1		K, J, B	765	53	40	28	40
IPI00967467	33 kDa protein			285	60	92	125	120
IPI00011253	40S ribosomal protein S3	r, g	K, B, D	243	83	84	94	126
IPI00027107	Tu tl elongation factor, mitochondrial precursor		I	455	45	57	53	70
IPI00184330	DNA replication licensing factor MCM2	k, d	K	904	17	43	39	32
IPI00299608	Isoform 1 of 26S proteasome non-ATPase regulatory subunit 1	k, b		953	54	36	19	25

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00305068	Pre-mRNA-processing factor 6	g	K	941	33	45	50	51
IPI00219678	Eukaryotic tl initiation factor 2 subunit 1	r, g	K, B, D	315	34	53	28	71
IPI00793199	annexin A4	p	B	321	54	60	42	48
IPI00453476	29 kDa protein			254	90	105	108	77
IPI00414717	Isoform 2 of ga protein 1		G	1203	37	27	32	40
IPI00032140	Serpin H1		B, E	418	35	42	38	44
IPI00024642	Isoform 1 of Coiled-coil domain-containing protein 47		E, H	483	34	34	15	52
IPI00017895	Isoform 1 of Glycerol-3-phosphate dehydrogenase, mitochondrial		I	727	19	31	16	37
IPI00000690	Isoform 1 of ap-inducing factor 1, mitochondrial		K, B, I, H, D	613	63	102	65	48
IPI00299024	Isoform 1 of Brain acid soluble protein 1		K, B, C, L	227	44	76	118	171
IPI00878314	110 kDa protein			1041	37	28	26	36
IPI00054042	Isoform 1 of General tc factor II-I	p	K, J, B	998	39	34	36	35
IPI00646304	Peptidyl-prolyl cis-trans isomerase B	l	E	216	127	168	85	140
IPI00004671	Golgin subfamily B member 1		G	3259	24	15	27	42
IPI00021808	Histidyl-tRNA synthetase, cpic	r, g	B, D	509	21	49	35	48
IPI00792375	Fructose-bisphosphate aldolase			336	50	66	88	84
IPI00909961	cDNA FLJ50720, highly similar to Homo sapiens tropomyosin 3 (TPM3), transcript variant 2, mRNA			203	66	98	67	72
IPI00216691	Profilin-1		K, B	140	97	108	230	259
IPI00218320	Isoform 3 of Tropomyosin alpha-3 chain		B, D, C	247	65	102	146	144

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00017367	Radixin, isoform CRA_a			604	34	33	25	55
IPI00017855	Aconitate hydratase, mitochondrial	i	K, I	780	24	28	8	32
IPI00220740	Isoform 2 of Nucleophosmin	p, m	K, J, B	265	40	47	110	99
IPI00002520	Serine hydroxymethyltransferase, mitochondrial		I	504	28	23	47	53
IPI00797038	Isoform 1 of Phosphoenolpyruvate carboxykinase [GTP], mitochondrial		I	640	34	32	26	52
IPI00014238	Isoform cpic of Lysyl-tRNA synthetase	g	K, B, I, D, L	597	28	37	30	41
IPI00221106	Splicing factor 3B subunit 2	g	K	895	27	32	30	79
IPI00170979	Isoform 2 of Ena/VASP-like protein		B, D, C	416	22	46	12	20
IPI00018206	Aspartate aminotransferase, mitochondrial		I, L	430	35	53	52	35
IPI00000875	cDNA FLJ56389, highly similar to Elongation factor 1-gamma			487	155	263	302	211
IPI00013788	HIV Tat-specific factor 1		K, J	755	61	108	34	52
IPI00006207	Isoform 2 of Leucine-rich repeat flightless-interacting protein 1		K, B, C	784	30	59	26	37
IPI00219077	Isoform 1 of Leukotriene A-4 hydrolase		K, J, B, D	611	46	39	11	40
IPI00449049	Poly [ADP-ribose] polymerase 1		K, J	1014	27	42	20	39
IPI00020599	Calreticulin	l	K, B, E, H, D	417	59	126	114	187
IPI00852685	Isoform 1 of Protein diaphanous homolog 1		B, C, L	1272	27	37	35	66
IPI00023048	Isoform 1 of Elongation factor 1-delta	r, g	D	281	58	85	78	132

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00217966	Isoform 1 of L-lactate dehydrogenase A chain		B, I, D	332	119	83	130	115
IPI00384369	Tropomyosin 1 alpha variant 6		B, D, C	248	46	66	122	117
IPI00022793	Trifunctional enzyme subunit beta, mitochondrial		I	474	49	47	40	57
IPI00033022	Isoform 1 of Dynamin-2	p	B, D, C, L	870	19	34	18	33
IPI00000874	Peroxiredoxin-1	f	K, B, I	199	100	151	134	115
IPI00217030	40S ribosomal protein S4, X isoform	r, g	B, D, I	263	30	44	53	58
IPI00470891	Isoform Long of Cold shock domain-containing protein E1		B	798	12	22	23	47
IPI00000873	Valyl-tRNA synthetase	g	B, I, D	1264	24	27	20	34
IPI00006079	Isoform 1 of Bcl-2-associated tc factor 1		K, J, B	920	26	50	30	46
IPI00295851	Coatomer subunit beta		B, G, D	953	35	57	39	58
IPI00298961	Exportin-1	k	K, J, B, D	1071	24	30	13	31
IPI00024403	Copine-3		B, D	537	37	34	31	39
IPI00031517	DNA replication licensing factor MCM6	k	K, J	821	31	48	36	40
IPI00293655	ATP-dependent RNA helicase DDX1		K, B	740	26	25	29	31
IPI00027626	T-complex protein 1 subunit zeta	l	B, D	531	36	48	80	57
IPI00641384	pt protein Sec16A	o	E, G	2357	19	27	17	34
IPI00465128	Isoform 1 of Large proline-rich protein BAT3	e	K, B, D	1132	40	38	9	15
IPI00293464	DNA damage-binding protein 1		K, B	1140	24	31	12	33
IPI00306369	tRNA (cytosine-5-)-methyltransferase NSUN2		K, J, B	767	30	18	23	35
IPI00018522	protein arginine N-methyltransferase 1 isoform 1		K, B, D	371	37	52	16	19
IPI00103994	Leucyl-tRNA synthetase, cpic	g	B, D	1176	25	27	11	22
IPI00329801	Annexin A5	p	B	320	38	64	56	64

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00007074	Tyrosyl-tRNA synthetase, cpic	b, g	K, B, D	528	31	25	23	47
IPI00031583	Isoform 2 of General vesicular transport factor p115		B, H, G, D	973	30	42	24	33
IPI00216134	tropomyosin alpha-1 chain isoform 7			248	65	84	129	139
IPI00219029	Aspartate aminotransferase, cpic		B, D	413	37	32	27	31
IPI00021700	Proliferating cell nuclear antigen	k, f	K, J, B	261	52	50	62	83
IPI00008530	60S acidic ribosomal protein P0	r, g	K, B, D, I	317	53	74	46	52
IPI00009104	RuvB-like 2	l	K, B	463	25	33	18	44
IPI00876962	Isoform 2 of Inverted formin-2		K, B, E	1240	29	40	27	44
IPI00012011	Cofilin-1	n	K, B, C	166	99	75	258	222
IPI00305383	Cytochrome b-c1 complex subunit 2, mitochondrial		I	453	25	43	29	36
IPI00306825	Isoform 1 of Tumor protein D54			206	42	101	86	85
IPI00215888	Signal recognition particle 72 kDa protein		J, B, D, L	671	23	27	21	33
IPI00787827	Isoform 2 of Presequence protease, mitochondrial		K, B, I	1038	21	33	22	38
IPI00024664	Isoform Long of Ubiquitin carboxyl-terminal hydrolase 5			858	30	27	22	41
IPI00797206	Protein			323	36	42	26	62
IPI00025273	Isoform Long of Trifunctional purine biosynthetic protein adenosine-3		B, D	1010	33	20	22	34
IPI00011416	Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial		I	328	25	59	35	36
IPI00000494	60S ribosomal protein L5	r, g	K, J, B, D, I	297	36	29	24	52
IPI00009822	Signal recognition particle 54 kDa protein		K, J, B, D	504	23	35	21	40

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00216230	Lamina-associated polypeptide 2, isoform alpha		K	694	32	35	41	40
IPI00291939	Structural maintenance of chromosomes protein 1A	k, g	K, J, B	1233	16	12	10	21
IPI00031812	Nuclease-sensitive element-binding protein 1	g	K, B	324	51	108	101	112
IPI00784614	septin-9 isoform a			586	31	32	48	50
IPI00026314	Isoform 1 of Gelsolin	b	B, D	782	50	106	70	56
IPI00009747	Lanosterol synthase		E, H	732	19	32	13	29
IPI00029079	GMP synthase [glutamine-hydrolyzing]		B, D	693	16	30	26	31
IPI00013847	Cytochrome b-c1 complex subunit 1, mitochondrial		I	480	17	32	17	49
IPI00012726	Isoform 1 of Polyadenylate-binding protein 4	r	B	644	22	22	37	33
IPI00936002	Isoform 2 of Alpha-aminoadipic semialdehyde dehydrogenase		K, B, I, D	511	35	37	20	40
IPI00640981	Isoform 4 of E3 ubiquitin-protein ligase UBR4		K, B, C	5176	28	17	4	23
IPI00298057	Periplakin		K, B, I, C, L	1756	2	9	19	32
IPI00412642	Isoform G of Kinesin light chain 1		B, D, C	564	34	50	49	59
IPI00216319	14-3-3 protein eta		B	246	67	72	64	99
IPI00015018	Inorganic pyrophosphatase	g	B, D	289	28	54	53	35
IPI00216047	Isoform 1 of SWI/SNF complex subunit SMARCC2		K, J	1214	11	21	9	24
IPI00853400	Isoform 1 of FK506-binding protein 15	l	B	1219	25	11	39	50
IPI00910719	cDNA FLJ55705, highly similar to Threonyl-tRNA synthetase, cpic			602	28	24	21	30
IPI00020501	Myosin-11		D	1972	29	46	36	44

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00064086	elongation factor 1-delta isoform 4			257	43	66	61	104
IPI00026665	cDNA FLJ75085, highly similar to Homo sapiens glutaminyl-tRNA synthetase (QARS), mRNA			793	27	37	15	19
IPI00106668	perilipin-3 isoform 3		B, F, G	422	24	27	36	51
IPI00854700	Isoform 1 of Shootin-1			631	34	30	38	46
IPI00246975	Glutathione S-transferase Mu 3	i	B	225	62	59	25	69
IPI00007188	ADP/ATP translocase 2	s	I	298	70	90	78	120
IPI00168388	Isoform 1 of Signal recognition particle 68 kDa protein		K, J, B, E, D, I	627	5	24	22	26
IPI00029629	E3 ubiquitin/ISG15 ligase TRIM25		K, J, B, D	630	24	24	32	27
IPI00011603	26S proteasome non-ATPase regulatory subunit 3	k, b		534	45	47	21	27
IPI00024993	Enoyl-CoA hydratase, mitochondrial		I	290	58	67	56	53
IPI00013890	Isoform 1 of 14-3-3 protein sigma	b, p, f	K, B	248	59	71	85	147
IPI00744692	Transaldolase		B, H, D	337	44	51	31	56
IPI00027252	Prohibitin-2		K, B, I	299	28	30	37	45
IPI00419979	Serine/threonine-protein kinase PAK 2	n, b, p	K, B, D, L	525	33	44	32	56
IPI00296053	Isoform Mitochondrial of Fumarate hydratase, mitochondrial		B, I	510	31	24	23	53
IPI00012303	Selenium binding protein 1			514	30	45	61	46
IPI00939159	Adenylyl cyclase-associated protein			433	23	49	39	40
IPI00384265	Isoform F of Constitutive coactivator of PPAR-gamma-like protein 1		B, L	1146	18	15	12	28

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00216308	Voltage-dependent anion-selective channel protein 1	b, s	I, L	283	68	68	92	156
IPI00020956	Hepatoma-derived growth factor	p, f	K, B	240	119	159	48	77
IPI00218200	B-cell receptor-associated protein 31	b	E, D, L	246	31	77	56	60
IPI00105598	Proteasome 26S non-ATPase subunit 11 variant (Fragment)	k, b		423	37	54	51	76
IPI00217223	Multifunctional protein ADE2		D	451	34	32	19	39
IPI00964764	cDNA FLJ55072, highly similar to Succinate dehydrogenase (ubiquinone) flavoprotein subunit, mitochondrial			616	25	32	28	35
IPI00016801	Glutamate dehydrogenase 1, mitochondrial		B, I	558	28	36	27	37
IPI00013495	Isoform 2 of ATP-binding cassette sub-family F member 1	r	B, I	807	24	31	44	36
IPI00218782	cDNA FLJ60094, highly similar to F-actin capping protein subunit beta			335	28	29	16	45
IPI00021537	Isoform 1 of Opioid growth factor receptor		K, B	677	26	36	45	56
IPI00008223	UV excision repair protein RAD23 homolog B		K, J, B	409	26	38	94	87
IPI00010810	Electron transfer flavoprotein subunit alpha, mitochondrial		I	333	39	54	65	98
IPI00107752	Isoform 2 of Dynamin-like 120 kDa protein, mitochondrial	b	I	997	24	20	29	18
IPI00220503	dynactin subunit 2	k, j, f	B, D, C	406	24	22	39	30
IPI00337465	Isoform P of Kinesin light chain 1		B, D, C	584	34	50	49	58

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00100716	Isoform 2 of Poly(U)-binding-splicing factor PUF60	b	K	542	22	38	43	35
IPI00009123	Isoform 1 of Nucleobindin-2		K, B, E, G, D, L	420	42	64	42	60
IPI00794807	15 kDa protein			134	297	182	240	215
IPI00945818	Isoform 2 of Lipopolysaccharide-responsive and beige-like anchor protein		E, G, L	2851	18	20	12	15
IPI00179953	Isoform 1 of Nuclear autoantigenic sperm protein	d, f, o	K, B	788	28	29	12	13
IPI00028091	Actin-related protein 3		B	418	27	28	21	50
IPI00746165	Isoform 1 of WD repeat-containing protein 1		B, D, C	606	22	31	29	31
IPI00016342	Ras-related protein Rab-7a	o	G	207	29	29	22	44
IPI00009032	Lupus La protein		K	408	28	26	23	41
IPI00221178	Isoform 2 of Tumor protein D54			186	31	97	80	68
IPI00104050	Thyroid hormone receptor-associated protein 3		K, J	955	24	22	32	41
IPI00642584	Isoform 1 of Uncharacterized protein KIAA0090			993	22	22	12	31
IPI00022648	Eukaryotic tl initiation factor 5	r, g	B, D	431	26	36	27	34
IPI00792422	Isoform 1 of WASH complex subunit FAM21A			1341	1	10	14	25
IPI00879437	Protein			279	79	109	120	154
IPI00304589	Isoform 1 of 182 kDa tankyrase-1-binding protein		K, B, D, C	1729	10	13	20	36
IPI00793443	Isoform 1 of Importin-5		K, J, B	1097	7	15	26	37
IPI00006865	Vesicle-trafficking protein SEC22b	o	E, G	215	20	29	47	55
IPI00006167	Protein phosphatase 1G		K, B	546	19	28	17	60
IPI00018931	Vacuolar protein sorting-associated protein 35	o	B, F, D	796	34	42	17	27

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00220527	Isoform 1A of Sorting nexin-1		B, G	457	33	35	13	27
IPI00024145	Isoform 2 of Voltage-dependent anion-selective channel protein 2	s	I	283	61	71	106	98
IPI00746182	Isoform 1 of pt protein Sec31A	o	B, E, D	1220	47	26	32	51
IPI00009368	Sideroflexin-1	s	I	322	36	40	46	40
IPI00021187	Isoform 1 of RuvB-like 1	d, j	K, J, B, G, C	456	26	33	15	19
IPI00291510	Inosine-5'-monophosphate dehydrogenase 2		D	514	21	25	31	32
IPI00910974	Phosphoglycerate kinase			161	82	123	137	95
IPI00011200	D-3-phosphoglycerate dehydrogenase			533	25	22	26	38
IPI00295386	Carbonyl reductase [NADPH] 1		B	277	26	25	25	40
IPI00021417	U4/U6.U5 tri-snRNP-associated protein 1		K, J, B, D	800	14	24	23	26
IPI00012066	poly(rC)-binding protein 2 isoform b			362	56	65	89	83
IPI00220301	Peroxiredoxin-6		B, D	224	59	82	58	62
IPI00033025	51 kDa protein			436	22	31	11	31
IPI00410214	Isoform 1 of 3'(2'),5'-bisphosphate nucleotidase 1		D	308	27	20	16	28
IPI00163849	cDNA FLJ60624, highly similar to Epidermal growth factor receptor substrate 15-like 1			910	17	31	27	29
IPI00007702	Heat shock-related 70 kDa protein 2		I	639	181	112	169	251
IPI00219420	Structural maintenance of chromosomes protein 3	k, j, p	K, B	1217	16	31	23	46
IPI00916111	Malate dehydrogenase		B, I, D	352	59	61	57	73
IPI00075248	Calmodulin		B, D, C, L	149	131	159	122	108

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00008982	Isoform Long of Delta-1-pyrroline-5-carboxylate synthase		B, I	795	8	21	9	32
IPI00337741	Acylamino-acid-releasing enzyme		B	732	14	16	20	26
IPI00022649	Isoform 1 of Solute carrier family 12 member 2	h, s	L	1212	20	33	25	32
IPI00640703	Exportin-5		K, J, B, D	1204	16	11	13	20
IPI00017297	Matrin-3		K	847	18	24	16	40
IPI00009532	cDNA FLJ56034, highly similar to 4-aminobutyrate aminotransferase, mitochondrial		I	515	15	17	18	31
IPI00411559	Isoform 1 of Structural maintenance of chromosomes protein 4	d	K, J, B	1288	23	26	26	23
IPI00037283	Isoform 5 of Dynamin-1-like protein	b	B, E, G, D	710	15	19	6	25
IPI00215914	ADP-ribosylation factor 1	o	B, G, D, L	181	82	89	51	68
IPI00219841	DNA ligase 1	k	K	919	38	48	13	18
IPI00028635	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2		K, E	631	32	30	23	38
IPI00644127	Isoleucyl-tRNA synthetase, cpic	g	K, J, B, D	1262	21	27	26	22
IPI00479722	Proteasome activator complex subunit 1	k, b	B	249	41	58	55	48
IPI00760715	Isoform 5 of Calpastatin			756	17	24	29	35
IPI00783097	Glycyl-tRNA synthetase	g	B, I, D	739	14	21	19	30
IPI00013122	Hsp90 co-chaperone Cdc37		B	378	30	39	82	65
IPI00297982	Eukaryotic tl initiation factor 2 subunit 3	r, g	D	472	30	36	25	31
IPI00029623	Proteasome subunit alpha type-6	k, b	K, B, I	246	54	31	62	32

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00334190	Stomatin-like protein 2		B, I, C	356	27	19	34	27
IPI00002214	Importin subunit alpha-2		K, B	529	26	28	54	61
IPI00479743	Isoform 1 of POTE ankyrin domain family member E			1075	501	348	448	481
IPI00290416	Isoform 1 of Obg-like ATPase 1		B	396	31	31	17	29
IPI00008164	Prolyl endopeptidase		K, B, D	710	13	11	12	23
IPI00396321	Leucine-rich repeat-containing protein 59		E, H	307	16	23	38	63
IPI00012442	Ras GTPase-activating protein-binding protein 1		K, B, D, L	466	15	23	39	58
IPI00375380	26S proteasome non-ATPase regulatory subunit 13 isoform 2			378	18	28	14	23
IPI00219913	Ubiquitin carboxyl-terminal hydrolase 14		B, L	494	20	17	12	47
IPI00015911	Dihydrolipoyl dehydrogenase, mitochondrial		B, I	509	16	35	32	61
IPI00183530	cDNA FLJ46302 fis, clone TESTI4036048, highly similar to Sorting nexin 1		B, G	557	31	35	13	23
IPI00456887	Heterogeneous nuclear ribonucleoprotein U-like protein 2		K	747	30	26	3	15
IPI00306960	Asparaginyl-tRNA synthetase, cpic	g	B, I, D	548	21	25	8	20
IPI00328328	Isoform 1 of Eukaryotic initiation factor 4A-II	r, g	D	407	58	62	43	54
IPI00465044	Protein RCC2	k	K, J, B, D, C	522	31	24	21	29
IPI00220373	Insulin-degrading enzyme	p	K, B, I, D	1019	17	26	9	16
IPI00297261	Tyrosine-protein phosphatase non-receptor type 1	p	E, D	435	18	16	18	13
IPI00008475	Hydroxymethylglutaryl-CoA synthase, cpic		B, D	520	24	11	13	20

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00017672	cDNA FLJ25678 fis, clone TST04067, highly similar to PURINE NUCLEOSIDE PHOSPHORYLASE		B, D, C	293	27	53	15	29
IPI00027834	Heterogeneous nuclear ribonucleoprotein L	g	K, B	589	29	17	26	41
IPI00640296	Heterogeneous nuclear ribonucleoprotein K			306	51	45	56	62
IPI00179964	Isoform 1 of Polypyrimidine tract-binding protein 1	g	K, J	531	33	37	39	53
IPI00101968	Isoform 3 of Drebrin-like protein	b	B, D, C	439	14	25	36	63
IPI00023919	26S protease regulatory subunit 8	k, b	K, J, B	406	23	17	15	23
IPI00021728	Eukaryotic tl initiation factor 2 subunit 2	r, g	D	333	32	88	51	43
IPI00551024	Bifunctional ATP-dependent dihydroxyacetone kinase/FAD-AMP lyase (cyclizing)		D	575	22	20	20	22
IPI00011126	26S protease regulatory subunit 4	k, b	K, J, B	440	17	35	44	37
IPI00024364	Isoform 1 of Transportin-1		K, B, D	898	16	35	22	26
IPI00456925	Isoform 1 of Drebrin-like protein	b	B, D, C	430	15	27	40	70
IPI00299573	60S ribosomal protein L7a	r, g	D	266	44	68	49	53
IPI00299254	Eukaryotic tl initiation factor 5B	r, g	B, D	1220	28	31	25	40
IPI00215965	Isoform A1-B of Heterogeneous nuclear ribonucleoprotein A1	g	K, J, B	372	30	66	29	57
IPI00297579	Chromobox protein homolog 3		K	183	16	52	140	70
IPI00028561	Isoform 1 of Kinesin heavy chain isoform 5C		B, C	957	19	19	22	35
IPI00419258	High mobility group protein	b	K, J	215	46	57	50	89

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
	B1							
IPI00026268	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1	p, f	L	340	26	29	21	26
IPI00014151	26S proteasome non-ATPase regulatory subunit 6	k, b		389	26	34	46	46
IPI00021924	Histone H1x		K	213	28	34	28	30
IPI00010896	Chloride intracellular channel protein 1	h, p	K, B, L	241	67	70	93	94
IPI00219301	Myristoylated alanine-rich C-kinase substrate		B, L	332	33	34	16	33
IPI00220739	Membrane-associated progesterone receptor component 1		K, J, E, H	195	100	100	59	55
IPI00396435	Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15		K	795	32	45	51	24
IPI00299095	Sorting nexin-2		B	519	24	50	15	33
IPI00329389	60S ribosomal protein L6	r, g	D, I	288	60	62	49	54
IPI00017334	Prohibitin	p	K, B, I	272	38	40	48	55
IPI00177728	Isoform 1 of cic non-specific dipeptidase	i	B	475	17	21	11	15
IPI00297211	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5		K, J	1052	28	39	30	38
IPI00008529	60S acidic ribosomal protein P2	r, g	D, I	115	65	83	94	71
IPI00017283	Isoleucyl-tRNA synthetase, mitochondrial	g	B, I	1012	21	21	15	37
IPI00410067	Isoform 1 of Zinc finger CCCH-type antiviral protein 1		K, B	902	10	14	13	24
IPI00291467	ADP/ATP translocase 3	b, s	I	298	62	54	56	95

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00030009	Isoform A of Bifunctional 3'-phosphoadenosine 5'-phosphosulfate synthase 2		D	614	14	22	7	33
IPI00448095	L-xylulose reductase			244	36	45	38	56
IPI00182757	Isoform 1 of Protein KIAA1967	b	K, B	923	38	29	29	32
IPI00257903	er metallopeptidase 1		E	904	14	24	13	13
IPI00299904	Isoform 1 of DNA replication licensing factor MCM7	k, f	K	719	12	10	30	29
IPI00033130	SUMO-activating enzyme subunit 1		K	346	28	49	9	30
IPI00645948	High-mobility group box 1			216	46	57	49	88
IPI00465179	6-phosphofructokinase, muscle type isoform 1			851	14	22	17	14
IPI00031131	Isoform 1 of Adipocyte pm-associated protein			416	26	14	32	30
IPI00295252	Isoform 1 of Phosphatidylinositol 3,4,5-trisphosphate-dependent Rac exchanger 1 protein	b	B, D, L	1659	29	21	7	23
IPI00016832	Isoform Short of Proteasome subunit alpha type-1	k, b	K, B	263	35	45	44	63
IPI00012048	Isoform 1 of Nucleoside diphosphate kinase A	e	K, B, I, H, D	152	111	114	116	208
IPI00008240	Methionyl-tRNA synthetase, cpic	g	B, I, D	900	20	35	16	21
IPI00008433	40S ribosomal protein S5	r, g	D	204	28	25	30	32
IPI00003818	Kynureninase		B, I, D	465	34	35	18	29
IPI00465233	Eukaryotic tl initiation factor 3, subunit E interacting protein			607	23	30	16	27
IPI00175169	Isoform 1 of ADP-ribosylation factor GTPase-activating protein 1	o	B, G	406	8	18	23	32

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00009253	Alpha-soluble NSF attachment protein		E, G, D	295	23	46	28	44
IPI00303207	ATP-binding cassette sub-family E member 1		B, I	599	18	24	23	30
IPI00005159	Actin-related protein 2		B	394	25	35	31	37
IPI00384051	Uncharacterized protein			249	41	37	32	42
IPI00171844	COP9 signalosome complex subunit 4		K, B	406	12	18	7	22
IPI00021840	40S ribosomal protein S6	r, g	K, J, D	249	46	42	77	43
IPI00018350	DNA replication licensing factor MCM5	k	K	734	8	12	17	16
IPI00012074	Isoform 1 of Heterogeneous nuclear ribonucleoprotein R	g	K, B	633	35	34	20	18
IPI00215911	DNA-(apurinic or apyrimidinic site) lyase		K, J, B, I, E, I	318	29	76	31	57
IPI00298547	Protein DJ-1		K, B, I, D	189	21	42	56	66
IPI00032959	Glycerol-3-phosphate dehydrogenase 1-like protein		B	351	22	37	14	35
IPI00033600	Isoform 1 of Protein phosphatase 1 regulatory subunit 7		K, B	360	19	12	6	11
IPI00335168	Isoform Non-muscle of Myosin light polypeptide 6		D	151	36	38	105	120
IPI00009771	Lamin-B2			620	13	27	21	47
IPI00010706	Glutathione synthetase		D	474	24	24	27	38
IPI00413895	Isoform 2 of Golgin subfamily A member 2		G	990	13	22	14	19
IPI00016702	Isoform 1 of Rab GTPase-activating protein 1	d	B, D, C	1069	24	35	19	28
IPI00106642	Dihydropyrimidinase-like 2		E	619	20	16	18	24
IPI00550689	UPF0027 protein C22orf28			505	14	27	12	17
IPI00185919	Isoform 1 of La-related protein 1			1096	7	17	15	31

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00008380	Serine/threonine-protein phosphatase 2A catalytic subunit alpha isoform		K, B, I, D, L	309	22	12	26	26
IPI00005158	Lon protease homolog, mitochondrial		B, I	959	21	31	19	24
IPI00009328	Eukaryotic initiation factor 4A-III		K, B	411	37	42	24	23
IPI00256861	Isoform 2 of Microtubule-actin cross-linking factor 1, isoforms 1/2/3/5		B, C	5430	6	10	9	28
IPI00788837	cDNA FLJ54752, highly similar to Poly(rC)-binding protein 2			282	48	62	89	82
IPI00030131	Isoform Beta of Lamina-associated polypeptide 2, isoforms beta/gamma		K	454	25	30	41	35
IPI00020632	Argininosuccinate synthase		B, E, D	450	19	25	29	43
IPI00006211	Isoform 1 of Vesicle-associated membrane protein-associated protein B/C		E, G, L	243	16	27	30	35
IPI00216088	Cellular retinoic acid-binding protein 2	p	K, J, B	138	128	226	215	109
IPI00005578	EH domain-containing protein 4		K, F, E	541	13	20	12	15
IPI00002519	Isoform 1 of Serine hydroxymethyltransferase, cic		K, B, I, D	483	21	24	16	34
IPI00008964	Ras-related protein Rab-1B	o	B, I, G	201	29	33	49	43
IPI00013881	Heterogeneous nuclear ribonucleoprotein H	g	K, J, B	449	26	24	33	57
IPI00293396	AP-1 complex subunit gamma-1 isoform a		B, G, D	825	22	29	13	18
IPI00017376	pt protein Sec23B		E, G	767	26	37	30	32
IPI00024175	Isoform 1 of Proteasome subunit alpha type-7	k, b	K, B	248	25	34	43	30

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00022334	Ornithine aminotransferase, mitochondrial		B, I	439	14	17	14	20
IPI00017375	pt protein Sec23A		E, G, D	765	25	30	13	30
IPI00795353	11 kDa protein			96	392	334	436	284
IPI00470467	NADPH--cytochrome P450 reductase		E	677	23	21	16	28
IPI00303063	147 kDa protein			1297	11	20	27	31
IPI00420108	Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial	i	K, B, I, H, L	453	13	18	13	18
IPI00015952	cDNA FLJ59571, highly similar to Eukaryotic tl initiation factor 4gamma 2			980	10	18	18	29
IPI00181409	Isoform Gamma of Lamina-associated polypeptide 2, isoforms beta/gamma		K	345	25	30	41	37
IPI00647400	Uncharacterized protein			611	26	26	18	35
IPI00021926	26S protease regulatory subunit 10B	k, b	K, B	389	16	24	16	32
IPI00642211	Aminopeptidase B		L	658	23	24	17	36
IPI00429689	Serine/threonine-protein phosphatase 2A catalytic subunit beta isoform		K, B, C	309	18	12	19	25
IPI00619958	Isoform 1 of Tumor protein D52		B, E	224	26	29	60	54
IPI00217465	Histone H1.2		K	213	66	69	105	130
IPI00297477	U2 small nuclear ribonucleoprotein A'	g	K	255	24	67	27	36
IPI00018349	DNA replication licensing factor MCM4	k	K, J	863	13	21	10	12
IPI00328715	Protein LYRIC		K, J, B, E	582	23	67	33	52
IPI00294879	Ran GTPase-activating protein	k, p	K, B, D, C	587	18	23	7	15

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
	1							
IPI00024804	Isoform SERCA1B of Sarcoplasmic/er calcium ATPase 1	s	H	1001	31	33	22	22
IPI00007682	V-type proton ATPase catalytic subunit A	h, s	I, D, L	617	33	33	8	22
IPI00015953	Isoform 1 of Nucleolar RNA helicase 2		K, J	783	13	46	12	20
IPI00829992	Isoform 3 of Myosin-Ic	o, s	K, J, B, L	1044	13	17	9	18
IPI00465132	Coatomer subunit epsilon	o	B, G, D	308	10	23	38	33
IPI00019383	cDNA FLJ56840, highly similar to Galactokinase			422	26	33	56	35
IPI00217468	Histone H1.5		K	226	32	47	69	71
IPI00217563	Isoform Beta-1A of Integrin beta-1	c	L	798	25	4	6	18
IPI00291928	Ras-related protein Rab-14	o	D, L	215	23	28	28	26
IPI00012998	Isoform 1 of Cleavage and polyadenylation specificity factor subunit 6		K	551	16	11	28	15
IPI00100151	Isoform 1 of 5'-3' exoribonuclease 2		K, J	950	18	12	11	20
IPI00028275	Isoform 1 of cs-associated protein 5	k	D	2032	12	15	16	15
IPI00005719	Isoform 1 of Ras-related protein Rab-1A	o	E, G	205	32	28	46	41
IPI00024661	pt protein Sec24C		B, E, G, D	1094	15	13	26	34
IPI00157790	proteasome-associated protein ECM29 homolog		K, B, E, C	2017	5	5	10	31
IPI00024915	Isoform Mitochondrial of Peroxiredoxin-5, mitochondrial		B, I	214	24	31	55	47
IPI00030706	Activator of 90 kDa heat shock protein ATPase homolog 1	l	B, E, D	338	16	17	20	36

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00017592	Isoform 1 of LETM1 and EF-hand domain-containing protein 1, mitochondrial		I	739	8	12	4	18
IPI00003925	Isoform 1 of Pyruvate dehydrogenase E1 component subunit beta, mitochondrial		I	359	26	15	12	30
IPI00643522	Ribosomal protein S6, isoform CRA_a			218	36	29	63	31
IPI00000634	Coiled-coil domain-containing protein 6		B, C	474	3	11	18	26
IPI00554742	Isoform 2 of ap inhibitor 5	b	K, J, B	504	13	18	17	13
IPI00098902	2-oxoglutarate dehydrogenase, mitochondrial		I	1023	15	19	14	18
IPI00215780	40S ribosomal protein S19	r, g	K, J, D, I	145	29	45	58	52
IPI00455473	Isoform 1 of Melanoma inhibitory activity protein 3	o	E	1907	13	28	9	21
IPI00395627	Isoform 1 of Calcyclin-binding protein		K, B	228	35	33	12	38
IPI00216587	40S ribosomal protein S8	r, g	B, D, I	208	68	119	97	122
IPI00220038	Isoform 2 of Serrate RNA effector molecule homolog	f	K, B	872	19	15	18	37
IPI00185374	26S proteasome non-ATPase regulatory subunit 12	k, b		456	5	7	7	20
IPI00028888	Isoform 1 of Heterogeneous nuclear ribonucleoprotein D0	g	K, J, B, D	355	11	29	39	41
IPI00024911	er resident protein 29	l	E	261	24	23	87	55
IPI00009923	Isoform 1 of Prolyl 4-hydroxylase subunit alpha-1		I, E	534	20	23	12	22
IPI00216171	Gamma-enolase		B, D, L	434	71	64	162	93
IPI00029019	Isoform 2 of Ubiquitin-associated protein 2-like			983	3	10	21	23
IPI00030363	Acetyl-CoA acetyltransferase, mitochondrial		I	427	18	32	15	14

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00220637	Seryl-tRNA synthetase, cpic	r, g	B, D	514	24	16	8	22
IPI00432363	Microtubule-actin cross-linking factor 1, isoform 4		B	5938	5	8	8	30
IPI00411453	Isoform 1 of AP-3 complex subunit delta-1		B, G	1153	16	19	0	7
IPI00641829	Isoform 2 of Spliceosome RNA helicase BAT1		K	443	34	36	13	15
IPI00017469	Sepiapterin reductase		B	261	12	12	27	32
IPI00550746	Nuclear migration protein nudC	k, f	K, B, G, D, C	331	21	33	33	37
IPI00003843	Isoform A1 of Tight junction protein ZO-2	b	K, B, L	1190	23	19	7	22
IPI00009542	Isoform 1 of Melanoma-associated antigen D2			606	16	51	29	44
IPI00004902	Isoform 1 of Electron transfer flavoprotein subunit beta		I	255	18	50	27	33
IPI00470498	Isoform 3 of Plasminogen activator inhibitor 1 RNA-binding protein		K, B, L	393	30	39	75	72
IPI00026848	Alpha-2-macroglobulin receptor-associated protein	l	B, E, L	357	16	22	41	66
IPI00909232	cDNA FLJ53542, highly similar to Heterogeneous nuclear ribonucleoproteins C			288	20	18	13	17
IPI00003783	Dual specificity mitogen-activated protein kinase kinase 2	n	D	400	15	15	15	21
IPI00465050	Isoform C of Lethal(2) giant larvae protein homolog 2	d	B	1020	5	19	7	18
IPI00329331	Isoform 1 of UTP--glucose-1-phosphate uridylyltransferase	i	B, D	508	19	12	12	31
IPI00550451	Serine/threonine-protein phosphatase PP1-alpha catalytic subunit	d	K, J, B, D	330	33	23	18	31

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00026230	Heterogeneous nuclear ribonucleoprotein H2	g	K, J, B	449	14	14	18	27
IPI00021695	Isoform D of pm calcium-transporting ATPase 1	s	L	1258	14	16	11	25
IPI00100292	Isoform 1 of Probable aminopeptidase NPEPL1			523	17	19	20	18
IPI00295813	Isoform 1 of UPF0577 protein KIAA1324			1013	31	28	8	11
IPI00007611	ATP synthase subunit O, mitochondrial	h	I, L	213	22	38	41	49
IPI00006025	Isoform 1 of Squamous cell carcinoma antigen recognized by T-cells 3		K, B	963	5	24	29	23
IPI00025084	Calpain small subunit 1		B, L	268	12	14	16	30
IPI00006725	Probable ATP-dependent RNA helicase DDX23	g	K	820	8	10	39	24
IPI00019918	ATP-dependent RNA helicase DDX19A	o, s	K, B	478	23	33	38	36
IPI00165261	Sec1 family domain-containing protein 1	o	B, E, G, L	642	7	13	11	33
IPI00101374	cDNA FLJ61658, highly similar to Transmembrane 9 superfamily protein member 1			815	15	12	10	10
IPI00156689	Synaptic vesicle membrane protein VAT-1 homolog		B	393	15	28	5	19
IPI00005969	F-actin-capping protein subunit alpha-1		B, D, C	286	19	52	32	57
IPI00294536	cDNA FLJ51909, highly similar to Serine-threonine kinase receptor-associatedprotein			363	23	20	30	33
IPI00220402	Protein phosphatase inhibitor 2			205	28	28	41	30
IPI00554711	Junction plakoglobin		K, B, D, C, L	745	11	16	8	25

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00646899	Uncharacterized protein			163	17	33	23	47
IPI00028055	Transmembrane emp24 domain-containing protein 10	o	H, G	219	26	33	31	25
IPI00012503	Isoform Sap-mu-0 of Proactivator polypeptide		G	524	28	35	45	43
IPI00644231	Isoform 1 of cpic FMR1-interacting protein 1	e	B	1253	8	21	2	9
IPI00020127	Replication protein A 70 kDa DNA-binding subunit	k	K, J, B	616	16	13	6	17
IPI00444371	Isoform 1 of WD repeat-containing protein 44		B, F, G, D	913	13	17	1	7
IPI00555956	Proteasome subunit beta type-4	k, b	K, B	264	15	33	18	29
IPI00059279	Exocyst complex component 4		B, F, G	974	13	15	9	24
IPI00030320	Probable ATP-dependent RNA helicase DDX6		B, D	483	19	13	6	35
IPI00062264	Isoform 4 of N-terminal kinase-like protein	n	K, B, G, C	781	15	43	12	10
IPI00641181	MARCKS-related protein		L	195	19	26	15	42
IPI00216592	Isoform C1 of Heterogeneous nuclear ribonucleoproteins C1/C2	g	K	293	20	13	13	17
IPI00030702	Isoform 1 of Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial		I	366	20	26	18	32
IPI00873935	Uncharacterized protein			514	10	19	28	27
IPI00386755	ERO1-like protein alpha	l	E, H	468	31	21	22	28
IPI00012535	DnaJ homolog subfamily A member 1	l		397	13	14	11	26
IPI00007084	Calcium-binding mitochondrial carrier protein Aralar2	s	I	675	15	12	2	8
IPI00215919	ADP-ribosylation factor 5	o	B, G, L	180	49	28	20	55
IPI00305692	Thioredoxin-like protein 1		B	289	13	61	13	39

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00337385	Isoform 1 of Pre-mRNA-processing factor 40 homolog A		K	957	13	20	15	17
IPI00005161	Actin-related protein 2/3 complex subunit 2		B, G	300	39	49	5	9
IPI00219910	22 kDa protein			207	14	24	25	47
IPI00163505	Isoform 1 of RNA-binding protein 39		K, J	530	9	17	25	23
IPI00034277	Isoform A of Probable cation-transporting ATPase 13A1			1204	15	13	12	17
IPI00221088	40S ribosomal protein S9	r, g	J, B, D, I	194	31	40	33	36
IPI00413108	33 kDa protein			300	57	101	57	57
IPI00003515	Thyroid receptor-interacting protein 11		K, B, G, C	1979	10	7	14	12
IPI00414320	cDNA FLJ55482, highly similar to Annexin A11	d	K, B, C	605	16	19	13	21
IPI00003348	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2		B, L	340	20	17	21	16
IPI00005024	Isoform 1 of Myb-binding protein 1A		K, J, B	1328	8	14	16	16
IPI00183002	Isoform 1 of Protein phosphatase 1 regulatory subunit 12A		B	1030	5	4	10	19
IPI00473014	Destrin		B	165	25	31	38	94
IPI00409671	Isoform 1 of ATP-dependent RNA helicase DDX42	m	K, J, B	938	14	13	13	22
IPI00221092	40S ribosomal protein S16	r, g	D	146	20	51	64	38
IPI00383670	Isoform 1 of Tumor protein D53		B	204	12	22	47	81
IPI00017451	Splicing factor 3A subunit 1	g	K, J	793	13	10	9	27
IPI00646240	Histone H2B			166	49	24	60	86
IPI00409635	Isoform 2 of Extended synaptotagmin-2		L	893	8	20	4	10

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00646377	Isoform 1 of Eukaryotic tl initiation factor 4 gamma 3			1585	6	14	12	25
IPI00217871	Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial		I	563	15	13	8	18
IPI00019884	Alpha-actinin-2	c	J, B, D, C	894	32	59	35	25
IPI00337541	NAD(P) transhydrogenase, mitochondrial		I	1086	26	18	14	10
IPI00178352	Isoform 1 of Filamin-C		B, D, C, L	2725	32	42	38	62
IPI00180730	Similar to Elongation factor 1-alpha 1			462	58	48	191	164
IPI00021634	Kinesin light chain 2		B, D, C	622	7	19	11	13
IPI00219446	Phosphatidylethanolamine-binding protein 1		B, I, G	187	33	31	74	70
IPI00025156	Isoform 1 of E3 ubiquitin-protein ligase CHIP		B	303	9	12	6	29
IPI00027350	Peroxiredoxin-2		B, I	198	42	39	56	77
IPI00000581	cDNA FLJ56307, highly similar to Ubiquitin thioesterase protein OTUB1			308	26	45	14	29
IPI00013485	40S ribosomal protein S2	r, g	K, J, D	293	33	34	22	45
IPI00013070	Isoform 1 of Heterogeneous nuclear ribonucleoprotein U-like protein 1	g	K	856	7	13	30	28
IPI00940237	ATP-dependent RNA helicase DDX39		K	427	26	31	7	10
IPI00290142	CTP synthase 1		D	591	20	24	21	16
IPI00003964	probable ubiquitin carboxyl-terminal hydrolase FAF-X isoform 4	d, j	B	2554	9	21	12	20
IPI00013068	Eukaryotic tl initiation factor 3 subunit E	r, g	K, B, D	445	14	27	7	17

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00337494	Isoform 1 of Calcium-binding mitochondrial carrier protein SCaMC-1	s	B, I	477	22	26	13	18
IPI00019540	Isoform 4 of Serine/threonine-protein phosphatase 6 regulatory subunit 3		K, B	793	27	41	7	17
IPI00022145	Isoform 1 of Nuclear ubiquitous casein and cyclin-dependent kinases substrate		K	243	21	15	13	18
IPI00030296	Eukaryotic tl initiation factor 4A, isoform 2, isoform CRA_b			312	28	39	17	20
IPI00384541	Isoform 1 of Regulation of nuclear pre-mRNA domain-containing protein 2			1461	21	15	4	12
IPI00334713	Isoform 3 of Heterogeneous nuclear ribonucleoprotein A/B		K, B	285	21	28	55	58
IPI00909083	eukaryotic peptide chain release factor GTP-binding subunit ERF3A isoform 2			636	14	26	22	23
IPI00186008	PCTP-like protein			291	35	49	70	59
IPI00059242	Synapse-associated protein 1		K	352	21	15	8	16
IPI00456359	Isoform 1 of Ataxin-2-like protein			1075	5	3	20	22
IPI00001539	3-ketoacyl-CoA thiolase, mitochondrial		I	397	21	25	13	15
IPI00014312	Isoform 1 of Cullin-3		K, G	768	9	19	17	23
IPI00219097	High mobility group protein B2	b	K, J, B	209	9	17	17	43
IPI00006252	Aminoacyl tRNA synthase complex-interacting multifunctional protein 1	x, b, c, p, g	K, B, E, G, D	312	12	11	20	36
IPI00619921	Isoform 4 of Death-inducer obliterator 1	q, b	K, B	2240	17	22	18	14

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00031397	Long-chain-fatty-acid--CoA ligase 3		I, E, H	720	13	32	22	17
IPI00030179	60S ribosomal protein L7	r, g	D	248	26	41	41	26
IPI00016339	Ras-related protein Rab-5C	o	F, L	216	26	12	21	21
IPI00022891	ADP/ATP translocase 1	s	I	298	47	47	51	82
IPI00328293	cDNA FLJ61739, highly similar to Serine/arginine repetitive matrix protein 1	q, g	K, D	916	23	22	36	40
IPI00005087	Tropomodulin-3		B, C	352	10	14	8	15
IPI00844508	cingulin			1203	14	10	15	28
IPI00000105	Major vault protein	o, s	K, B	893	17	16	13	14
IPI00003935	Histone H2B type 2-E		K	126	48	24	52	80
IPI00007927	Isoform 1 of Structural maintenance of chromosomes protein 2	d, j	K, B	1197	16	7	8	13
IPI00478410	Isoform Liver of ATP synthase subunit gamma, mitochondrial	h	I	298	17	20	22	24
IPI00004560	Isoform 2 of Serine/threonine-protein kinase DCLK1	n, e		740	11	19	26	24
IPI00009950	Vesicular integral-membrane protein VIP36	o	E, G	356	15	29	24	18
IPI00300074	Phenylalanyl-tRNA synthetase beta chain	r, g	B, D	589	7	12	4	23
IPI00217467	Histone H1.4		K	219	55	60	78	74
IPI00218236	Serine/threonine-protein phosphatase PP1-beta catalytic subunit	d	K, J, B	327	27	16	17	30
IPI00012102	N-acetylglucosamine-6-sulfatase			552	3	12	3	41
IPI00008454	DnaJ homolog subfamily B member 11	l	K, B, E	358	18	33	10	21
IPI00003269	Beta-actin-like protein 2		B, C	376	255	200	265	503

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00376005	Isoform 2 of Eukaryotic tl initiation factor 5A-1	r, o, s	K, B, E, D	184	14	13	42	78
IPI00908375	cDNA FLJ52821, highly similar to pt protein Sec23A			409	19	25	11	29
IPI00219930	Cellular retinoic acid-binding protein 1	p	B	137	22	25	41	42
IPI00215901	Isoform 1 of Adenylate kinase 2, mitochondrial		I	239	6	5	18	35
IPI00479306	Proteasome subunit beta type-5	k, b	K, B	263	34	30	36	37
IPI00178440	Elongation factor 1-beta	r, g	D	225	19	20	31	38
IPI00386189	Isoform 1 of N-alpha-acetyltransferase 15, NatA auxiliary subunit	x, e	K, B	866	21	8	7	19
IPI00018511	Putative tubulin beta-4q chain	l	B, C	434	74	84	116	92
IPI00465436	Catalase		I, E, G, D, L	527	2	12	9	15
IPI00936738	Isoform 1 of Torsin-1A-interacting protein 1		K	583	7	8	11	39
IPI00218922	Translocation protein SEC63 homolog	l, o	E	760	8	28	16	13
IPI00007320	tc factor 25		K	676	21	19	14	21
IPI00018873	Nicotinamide phosphoribosyltransferase	p	B, D	491	12	7	9	14
IPI00000001	Isoform Long of Double-stranded RNA-binding protein Staufen homolog 1		B	577	9	17	19	24
IPI00003419	Small acidic protein			183	26	26	47	33
IPI00022827	Isoform 1 of STE20-like serine/threonine-protein kinase	n, b	B, L	1235	6	11	11	8
IPI00218288	Isoform 2 of pt protein Sec24D		B, E, G, D	1033	7	13	18	18
IPI00478472	Isoform 1 of Protein GREB1			1949	15	14	7	10
IPI00554723	60S ribosomal protein L10	r, g	B, E, D, I	214	14	30	24	47

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00294065	Isoform 1 of Golgin subfamily A member 5	n	G	731	7	11	8	13
IPI00305267	Isoform 1 of Golgin subfamily A member 3		B, G	1498	6	2	16	21
IPI00006379	Nucleolar protein 58		K, J, B	529	16	31	6	7
IPI00009315	Golgi resident protein GCP60		I, G	528	26	32	13	23
IPI00029822	tc activator BRG1 isoform D			1678	12	16	14	19
IPI00007102	Uncharacterized protein C17orf25			504	23	30	13	38
IPI00012795	Eukaryotic tl initiation factor 3 subunit I	r, g	B, D	325	24	29	36	38
IPI00220362	10 kDa heat shock protein, mitochondrial	l	B, I	102	73	78	145	103
IPI00010153	60S ribosomal protein L23	r, g	J, B, D, I	140	25	20	23	41
IPI00012585	Beta-hexosaminidase subunit beta			556	22	19	9	21
IPI00026689	Putative uncharacterized protein DKFZp686L20222	k, j	K, B, D	303	18	25	15	17
IPI00412579	60S ribosomal protein L10a	r, g	D, I	217	29	45	23	32
IPI00015833	Coiled-coil-helix-coiled-coil-helix domain-containing protein 3, mitochondrial		I	227	4	5	16	31
IPI00100197	Isoform 1 of NSFL1 cofactor p47		K, G	370	25	49	56	77
IPI00747748	Isoform 2 of Serine/threonine-protein phosphatase 2B catalytic subunit alpha isoform		K, J, B, I, H, D	511	9	7	7	19
IPI00166010	Isoform 1 of CCR4-NOT tc complex subunit 1		D	2376	8	13	1	9
IPI00257508	Dihydropyrimidinase-related protein 2	p, e	B, I, D	572	19	17	6	12
IPI00218693	Adenine phosphoribosyltransferase		K, J, B, D	180	13	21	28	35
IPI00179473	Isoform 1 of Sequestosome-1	b, m, e	K, B, D	440	12	5	22	35

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00002335	huntingtin		K, J, B, E, G, D	3144	17	20	13	16
IPI00022694	Isoform Rpn10A of 26S proteasome non-ATPase regulatory subunit 4	k, b		377	19	15	34	41
IPI00902564	Isoform 1 of Eukaryotic tl initiation factor 2A	n	B	585	6	16	5	19
IPI00020436	Ras-related protein Rab-11B	d, o	I, L	218	15	23	12	27
IPI00375370	Protein SEC13 homolog			325	16	16	16	20
IPI00019848	Isoform 1 of Host cell factor 1		K, J, B, I	2035	8	4	5	13
IPI00219483	Isoform 2 of U1 small nuclear ribonucleoprotein 70 kDa	g	K	428	16	24	20	25
IPI00014197	Isoform 1 of Protein CDV3 homolog	f	B	258	35	40	27	22
IPI00939707	Protein KIAA0664			1309	9	21	10	20
IPI00376344	Isoform 1 of Myosin-Ib			1136	6	8	9	13
IPI00009906	Armadillo repeat-containing X-linked protein 3			379	13	18	8	13
IPI00031519	Isoform 1 of DNA (cytosine-5)-methyltransferase 1		K	1678	10	16	10	19
IPI00607714	Isoform 2 of UPF0663 transmembrane protein C17orf28		L	787	12	24	9	21
IPI00170935	Leucine-rich repeat-containing protein 47	r		583	8	9	15	20
IPI00005978	Serine/arginine-rich splicing factor 2	q, g	K	221	8	23	78	65
IPI00010860	Isoform p27-L of 26S proteasome non-ATPase regulatory subunit 9	k, b	K	223	8	3	22	27
IPI00029628	Reticulocalbin-2		E	317	4	5	27	30
IPI00007334	Isoform 1 of Apoptotic chromatin condensation inducer in the n	b	K, J, B, D	1341	16	28	12	14

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00006932	cDNA FLJ55988, highly similar to RNA-binding protein Luc7-like 2			458	12	15	17	43
IPI00026215	Flap endonuclease 1	k	K, J, I	380	23	37	35	33
IPI00004968	Pre-mRNA-processing factor 19		K, B, C	504	13	27	22	36
IPI00017184	EH domain-containing protein 1		L	534	15	9	6	5
IPI00022305	Basic leucine zipper and W2 domain-containing protein 2	e		419	18	27	15	19
IPI00216348	Isoform 2C of cpic dynein 1 intermediate chain 2	k	B, D, C	612	39	72	24	31
IPI00012201	Isoform 1 of Melanophilin		B	600	12	28	25	22
IPI00784320	Protein FAM83H			1179	3	15	1	13
IPI00011619	Bifunctional 3'-phosphoadenosine 5'-phosphosulfate synthase 1		D	624	9	13	8	14
IPI00339384	Isoform 1 of Retinol dehydrogenase 11		E	318	21	26	14	25
IPI00291783	Gem-associated protein 5		K, B, D	1508	8	12	27	22
IPI00293331	Ribonucleases P/MRP protein subunit POP1		K, J	1024	5	10	9	8
IPI00783378	Ubiquitin-conjugating enzyme E2 O			1292	8	4	14	13
IPI00217466	Histone H1.3		K	221	44	59	67	76
IPI00012490	Isoform XD of pm calcium-transporting ATPase 4	s	L	1241	9	15	13	26
IPI00234368	Isoform Short of Adenosine kinase		K, D	345	23	20	12	12
IPI00021831	cAMP-dependent protein kinase type I-alpha regulatory subunit	s	D	381	22	13	35	42
IPI00012828	3-ketoacyl-CoA thiolase, peroxisomal			424	13	10	10	10

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00550506	Isoform 1 of Rho guanine nucleotide exchange factor 16	b	D	709	24	20	2	12
IPI00022202	Isoform A of Phosphate carrier protein, mitochondrial	s	I	362	29	19	24	32
IPI00007058	Coronin-1B		B, C	489	18	38	23	30
IPI00291930	cDNA FLJ61629, highly similar to Clathrin interactor 1		B, G, D	643	8	18	11	22
IPI00008728	ATP-dependent Clp protease ATP-binding subunit clpX-like, mitochondrial	l	I	633	13	18	9	10
IPI00655641	Isoform 2 of tc elongation factor SPT5	q, d, g	K, J	1083	6	7	2	6
IPI00013272	Isoform 1 of Golgin subfamily A member 4		B, G	2230	15	21	1	8
IPI00007427	AGR2			195	20	16	39	55
IPI00292827	Serine/threonine-protein kinase MST4	n, b	B, G, D	416	12	30	7	27
IPI00012345	Isoform SRP55-1 of Serine/arginine-rich splicing factor 6	q, g	K, J	344	13	12	28	41
IPI00083708	Isoform 7 of Protein BAT2-like 2			2899	1	5	13	26
IPI00003482	2,4-dienoyl-CoA reductase, mitochondrial		K, J, B, I, L	335	12	22	23	33
IPI00217236	Tubulin-specific chaperone A	l	B, C	108	33	110	27	35
IPI00295485	Heat shock 70 kDa protein 4L	l	K, B	839	7	13	13	16
IPI00289862	Secernin-1		K, B	414	18	23	6	24
IPI00304417	Isocitrate dehydrogenase 3, beta subunit isoform a precursor		I	393	10	7	6	8
IPI00295098	Signal recognition particle receptor subunit beta		B, E	271	18	22	22	25
IPI00013468	Isoform 1 of Mitotic checkpoint protein BUB3	k	K, J, D	328	13	12	10	23

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00306332	60S ribosomal protein L24	r, g	D, I	157	17	20	66	43
IPI00005780	Isoform 3 of UDP-N-acetylglucosamine--peptide N-acetylglucosaminyltransferase 110 kDa subunit	p	K, B, D	1046	14	18	3	8
IPI00465361	60S ribosomal protein L13	r, g	D	211	16	30	99	59
IPI00376317	Isoform 1 of Enhancer of mRNA-decapping protein 4		K, B, D	1401	7	10	10	17
IPI00024157	Peptidyl-prolyl cis-trans isomerase FKBP3	l	K	224	3	46	28	39
IPI00019599	Isoform 1 of Ubiquitin-conjugating enzyme E2 variant 1	e	K, B, D	221	38	35	34	39
IPI00010080	Serine/threonine-protein kinase OSR1	n		527	17	13	4	19
IPI00429191	Eukaryotic peptide chain release factor subunit 1	r, g	B	437	17	22	2	16
IPI00021258	Isoform B of Arfaptin-1		D	373	9	17	16	11
IPI00240812	165 kDa protein			1448	21	26	30	17
IPI00021327	Isoform 1 of Growth factor receptor-bound protein 2	e	B, G, D	217	9	16	44	39
IPI00747764	cDNA FLJ53229, highly similar to Importin alpha-7 subunit		K, B	541	16	13	7	7
IPI00293088	Lysosomal alpha-glucosidase			952	17	13	14	26
IPI00291922	Proteasome subunit alpha type-5	k, b	K, B	241	23	32	20	37
IPI00001699	Isoform 1 of ap-associated speck-like protein containing a CARD	p	B	195	12	13	25	17
IPI00003704	Isoform 1 of RNA-binding protein 4		K, J, B	364	13	20	27	41
IPI00017763	Uncharacterized protein			386	29	24	21	30
IPI00171199	Isoform 2 of Proteasome subunit alpha type-3	k, b	K, B	248	20	19	10	29

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00025815	Isoform 2 of TAR DNA-binding protein 43		K, J	416	20	27	6	26
IPI00013296	40S ribosomal protein S18	r, g	B, D, I	152	103	79	78	109
IPI00479058	40S ribosomal protein S15	r, g	K, D	145	7	27	13	22
IPI00072377	Isoform 1 of Protein SET		K, B, E, D	290	14	34	85	54
IPI00006181	Eukaryotic tl initiation factor 3 subunit D	r, g	B, D	548	17	15	12	14
IPI00292753	Isoform 6 of GTPase-activating protein and VPS9 domain-containing protein 1	p	F, D	1487	5	10	5	9
IPI00005198	Interleukin enhancer-binding factor 2		K, J, B	390	11	25	26	21
IPI00216520	Isoform A of Arfaptin-1		D	341	9	19	14	11
IPI00221114	Isoform Beta of E3 ubiquitin-protein ligase TRIM33		K, J	1110	12	11	9	10
IPI00465431	Galectin-3	e	K, B, L	250	19	33	58	57
IPI00910128	cDNA FLJ59457, highly similar to NADPH:adrenodoxin oxidoreductase, mitochondrial			522	16	14	6	15
IPI00893541	14 kDa protein			123	62	84	104	105
IPI00021129	Isoform 1 of AP-3 complex subunit beta-1		G	1094	11	11	7	20
IPI00299155	Proteasome subunit alpha type-4	k, b	K, B	261	26	19	17	22
IPI00217477	High mobility group protein B3		K	200	17	9	4	16
IPI00023748	Nascent polypeptide-associated complex subunit alpha	q, r, o	K, B	215	10	49	44	30
IPI00658109	Isoform 1 of Creatine kinase U-type, mitochondrial		I	417	15	27	17	26
IPI00022256	Isoform 1 of AP-2 complex subunit mu		D, L	435	12	15	9	10

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00008148	Isoform 1 of GDNF family receptor alpha-1		L	465	13	19	13	19
IPI00002186	Brefeldin A-inhibited guanine nucleotide-exchange protein 2		B, D	1785	7	10	4	4
IPI00291419	cDNA FLJ53975, highly similar to Acetyl-CoA acetyltransferase, cic		K, J, B, I	426	2	18	15	19
IPI00185661	Ubiquitin carboxyl-terminal hydrolase 32		G	1604	3	10	0	10
IPI00017596	Microtubule-associated protein RP/EB family member 1	k, f	B, G, D, C	268	24	26	30	24
IPI00013860	3-hydroxyisobutyrate dehydrogenase, mitochondrial		I	336	6	11	8	37
IPI00025721	COP9 signalosome complex subunit 3	p	K, B	423	6	4	8	16
IPI00328319	Histone-binding protein RBBP4	d	K	425	20	42	9	22
IPI00012462	Eukaryotic tl initiation factor 2A			609	8	15	5	20
IPI00550900	tlally-controlled tumor protein		B	172	22	12	46	37
IPI00395865	Histone-binding protein RBBP7	f	K	425	17	32	53	43
IPI00411706	S-formylglutathione hydrolase		B	282	12	19	8	18
IPI00000861	Isoform 1 of LIM and SH3 domain protein 1	h	B, C	261	5	8	44	48
IPI00025366	Citrate synthase, mitochondrial		I	466	27	34	17	11
IPI00297084	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit		E, H	456	13	28	13	21
IPI00790937	60S ribosomal export protein NMD3	o	K, J, B	503	14	14	19	35

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00025057	Isoform 2 of Double-stranded RNA-specific adenosine deaminase		K, J, B	1200	9	12	6	15
IPI00027851	cDNA FLJ53927, highly similar to Beta-hexosaminidase alpha chain			540	11	15	8	14
IPI00290461	Eukaryotic tl initiation factor 3 subunit J	r, g	B, D	258	18	27	12	23
IPI00216184	Isoform 2 of Phosphatidylinositol-binding clathrin assembly protein		K, G	632	7	6	17	28
IPI00007423	Isoform 1 of Acidic leucine-rich nuclear phosphoprotein 32 family member B		K, B	251	21	24	11	28
IPI00005160	Actin-related protein 2/3 complex subunit 1B		B	372	19	23	9	23
IPI00019971	cDNA FLJ54775, highly similar to Syntaxin-binding protein 2			604	11	9	12	6
IPI00005705	Isoform Gamma-1 of Serine/threonine-protein phosphatase PP1-gamma catalytic subunit	k	K, J, B, D	323	23	17	15	24
IPI00020042	Isoform 1 of 26S protease regulatory subunit 6B	k, b	K, J, B, I	418	21	18	34	20
IPI00015856	cDNA FLJ56420, highly similar to Aspartyl aminopeptidase		B	493	12	21	10	17
IPI00023234	SUMO-activating enzyme subunit 2		K	640	17	14	15	25
IPI00329352	Nodal modulator 1			1222	6	14	19	25
IPI00290460	Eukaryotic tl initiation factor 3 subunit G	r, g	K, B, D	320	33	43	6	23
IPI00002134	26S proteasome non-ATPase regulatory subunit 5	k, b		504	10	11	21	18

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00442073	Cysteine and glycine-rich protein 1		K	193	29	35	38	65
IPI00411680	Isoform 1 of Protein-L-isoaspartate(D-aspartate) O-methyltransferase		B, E	227	9	11	18	18
IPI00003923	Isoform 1 of Uridine 5'-monophosphate synthase		K, B, D	480	5	8	7	13
IPI00019472	Neutral amino acid transporter B(0)	h, s	L	541	12	14	9	22
IPI00043863	Isoform 3 of Microtubule-associated protein 4		B, C	828	22	15	14	23
IPI00014177	Isoform 1 of Septin-2	d, j	K, J, B, L	361	13	19	9	20
IPI00550523	Atlastin-3		E	541	16	14	5	11
IPI00026105	Isoform SCPx of Non-specific lipid-transfer protein		K, J, B, I	547	13	13	12	18
IPI00239405	Isoform 1 of Nesprin-2		K, B, C, L	6885	0	8	16	18
IPI00219622	Proteasome subunit alpha type-2	k, b	K, B	234	3	6	4	26
IPI00642238	Isoform 1 of Heterochromatin protein 1-binding protein 3		K	553	13	5	7	15
IPI00010252	Isoform Alpha of E3 ubiquitin-protein ligase TRIM33		K, J	1127	12	10	7	7
IPI00012772	60S ribosomal protein L8	r, g	B, D, I	257	17	17	64	48
IPI00027341	Macrophage-capping protein		K, J, B	348	19	30	17	24
IPI00607628	Isoform 4 of GRIP1-associated protein 1			810	11	9	10	19
IPI00215884	Isoform ASF-1 of Serine/arginine-rich splicing factor 1	q, g	K, B	248	12	14	32	36
IPI00217943	Isoform 2 of Ras-related protein Rab-6A	o	G, D	208	16	21	7	17
IPI00010105	Eukaryotic tl initiation factor 6	r	K, J, B	245	14	8	10	24

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00217686	Putative rRNA methyltransferase 3		K, J	847	7	9	25	23
IPI00163496	Isoform 1 of Liprin-alpha-1	p	B	1202	5	10	5	16
IPI00028520	Isoform 1 of NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial		I	464	12	15	7	8
IPI00295209	Sorting nexin-5	o		404	16	23	19	24
IPI00031556	Isoform 1 of Splicing factor U2AF 65 kDa subunit	q, g	K	475	13	11	10	42
IPI00177938	Isoform 2 of Transducin-like enhancer protein 3	p	K	760	13	10	3	7
IPI00301109	Isoform 1 of Inorganic pyrophosphatase 2, mitochondrial	g	B, I	334	26	25	21	26
IPI00303318	Protein FAM49B			324	16	22	14	18
IPI00828098	protein ALO17 isoform 1			5256	10	10	12	15
IPI00015029	Prostaglandin E synthase 3	p	B, D	160	38	73	33	24
IPI00296215	Epithelial ca molecule		L	314	32	42	24	46
IPI00219604	Dual specificity mitogen-activated protein kinase kinase 1	j, p	B, G, D, L	393	8	9	12	10
IPI00219219	Galectin-1	b	K, B	135	5	4	29	39
IPI00024990	Methylmalonate-semialdehyde dehydrogenase [acylating], mitochondrial		K, J, I	535	9	20	10	12
IPI00002557	Coatomer subunit gamma-2		B, G	871	7	18	7	12
IPI00296526	N-acetyl-D-glucosamine kinase			390	9	14	9	25
IPI00219953	UMP-CMP kinase isoform a		K, B, D	228	3	2	12	20
IPI00024662	Chromobox protein homolog 5		K, J, B	191	9	2	11	24
IPI00790580	16 kDa protein			147	31	30	33	30
IPI00218474	Isoform 1 of Beta-enolase		B, D	434	126	78	190	123
IPI00295992	Isoform 2 of ATPase family AAA domain-containing			586	10	11	10	18

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
	protein 3A							
IPI00291755	Isoform 1 of Nuclear pore membrane glycoprotein 210	o, s	K, E	1887	6	13	7	9
IPI00293126	Tubulin-folding cofactor B	e	B	244	11	20	28	26
IPI00479997	Stathmin	p, e	B, C	149	18	28	41	42
IPI00032826	Hsc70-interacting protein	l	B	369	20	19	27	37
IPI00216293	Thiosulfate sulfurtransferase		I, L	297	18	26	11	17
IPI00746777	Alcohol dehydrogenase class-3		B, I	374	13	19	4	8
IPI00297322	ADP-ribosylation factor GTPase-activating protein 2	o	J, B, G, L	521	5	7	17	28
IPI00443909	Isoform 1 of Protein canopy homolog 2		E	182	8	12	26	19
IPI00027438	Flotillin-1		F, L, A	427	9	6	3	16
IPI00107357	Isoform 2 of Cleft lip and palate transmembrane protein 1	e		686	29	9	2	14
IPI00015947	DnaJ homolog subfamily B member 1	l	K, J, B	340	5	19	6	15
IPI00465059	Isoform 1 of Mitochondrial Rho GTPase 2	b	I, D, L	618	9	16	9	9
IPI00096066	Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial		I	432	11	23	9	20
IPI00290077	Keratin, type I cytoskeletal 15			456	142	83	82	155
IPI00005979	Isoform 1 of tl initiation factor eIF-2B subunit delta	r, g	B, D	523	4	5	11	10
IPI00013415	40S ribosomal protein S7	r, g	J, D, I	194	22	13	33	35
IPI00019600	Ubiquitin-conjugating enzyme E2 variant 2	f	K, B	145	21	27	24	30
IPI00090327	Vacuolar protein sorting-associated protein 45		F, G	570	13	9	9	15

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00025318	SH3 domain-binding glutamic acid-rich-like protein		K, B	114	22	22	31	57
IPI00025019	Proteasome subunit beta type-1	k, b	K, J, B, L	241	18	14	6	13
IPI00013862	Thymidylate kinase	d, f	D	212	14	15	19	7
IPI00007755	Ras-related protein Rab-21	o	F, E, G	225	16	18	6	14
IPI00419856	transportin-2 isoform 3			887	7	33	14	20
IPI00019223	Isoform 1 of A-kinase anchor protein 9	k, p	B, G, D, C	3911	7	7	4	12
IPI00221093	40S ribosomal protein S17	r, g	D, I	135	17	24	35	72
IPI00013004	Isoform 1 of Pyridoxal kinase	f	B, D	312	8	12	18	18
IPI00009982	Isoform 1 of Tudor and KH domain-containing protein		I	606	10	20	23	32
IPI00654777	cDNA FLJ36192 fis, clone TESTI2027450, highly similar to Eukaryotic tl initiation factor 3 subunit 5			372	3	12	28	34
IPI00000858	cDNA FLJ56180, highly similar to Negative elongation factor E			387	6	5	16	36
IPI00243221	nardilysin isoform a			1219	6	19	2	8
IPI00397904	Nuclear pore complex protein Nup93	o, s	K	819	8	2	26	19
IPI00401264	er resident protein 44	l	E	406	14	24	21	28
IPI00031564	Isoform 1 of Gamma-glutamylcyclotransferase		D	188	12	26	22	22
IPI00005688	Isoform 1 of Zinc finger protein 185		B, C	689	16	22	3	6
IPI00925804	Non-functional aryl hydrocarbon receptor interacting protein (Fragment)			368	7	16	9	11
IPI00019329	Dynein light chain 1, cpic	k, b	K, B, I, D, C, L	89	5	4	21	14

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00023542	Transmembrane emp24 domain-containing protein 9		E	235	16	22	19	25
IPI00916299	cDNA FLJ54595, highly similar to Golgi reassembly-stacking protein 2			405	14	18	15	19
IPI00026969	Isoform 1 of SEC23-interacting protein		B, E	1000	9	9	3	18
IPI00306436	Isoform Del-701 of Signal transducer and activator of tc 3	p	K, J, B, D, L	769	22	24	11	15
IPI00218414	Carbonic anhydrase 2		B, D	260	14	15	5	17
IPI00005537	cDNA FLJ60124, highly similar to Mitochondrial dicarboxylate carrier	r	I, I	442	29	18	13	29
IPI00000948	Transducin beta-like protein 2			447	12	14	10	10
IPI00306516	Mitochondrial import inner membrane translocase subunit TIM44	s	I	452	2	6	5	11
IPI00171798	Metastasis-associated protein MTA2		K, J	668	12	9	4	19
IPI00785096	Isoform 1 of Basic leucine zipper and W2 domain-containing protein 1		B	419	8	17	15	19
IPI00215719	60S ribosomal protein L18	r, g	B, D, I	188	29	21	45	20
IPI00002552	Isoform 1 of AP-1 complex subunit mu-2		G, D	423	20	25	17	25
IPI00293102	Isoform 2 of Serine/threonine-protein phosphatase 2A activator		K, J, B	358	13	21	19	24
IPI00868787	Isoform 1 of Protein TANC2			1990	3	2	7	16
IPI00373870	Isoform 1 of Chromodomain-helicase-DNA-binding protein 3		K	2000	11	12	2	10
IPI00465294	Cell division cycle 5-like protein	d	K, J, B	802	13	8	13	10

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00329338	Choline-phosphate cytidylyltransferase A		B, D	367	12	21	21	35
IPI00152535	Chromodomain-helicase-DNA-binding protein 5		K	1954	11	8	5	8
IPI00015148	Ras-related protein Rap-1b	p, f	B, D, L	184	16	15	9	25
IPI00023640	Programmed cell death protein 5	b	K, B	125	19	17	37	64
IPI00026305	Protein Hook homolog 1	o, e	B, C	728	8	12	10	11
IPI00220030	Isoform Alpha of Paxillin	c, p	B, C, L	557	3	2	19	30
IPI00300341	tc elongation factor B polypeptide 1	q, g	K, D	112	13	15	17	13
IPI00003881	Heterogeneous nuclear ribonucleoprotein F	g	K, J, B	415	16	19	36	33
IPI00329696	Regulator of microtubule dynamics protein 1		B, I, C	314	6	30	31	20
IPI00019812	Serine/threonine-protein phosphatase 5	q, j	K, B, G, D	499	4	9	13	21
IPI00019380	Nuclear cap-binding protein subunit 1	q, g	K, B, D	790	22	14	1	7
IPI00008438	40S ribosomal protein S10	r, g	K, J, B, D, I	165	11	12	17	22
IPI00011937	Peroxiredoxin-4		B, I	271	15	42	42	41
IPI00015285	Ethanolamine-phosphate cytidylyltransferase			389	14	15	10	15
IPI00103525	Isoform 1 of Paraspeckle component 1		K, J, B	523	2	9	7	16
IPI00743859	Isoform 2 of Catenin alpha-2		B, D, L	905	13	12	7	20
IPI00009866	Isoform 1 of Keratin, type I cytoskeletal 13			458	139	117	84	176
IPI00099550	Isoform 1 of Ubiquilin-1	b	K, B, E	589	4	8	3	10
IPI00644293	Doublecortin and CaM kinase-like 1			363	10	19	17	20
IPI00031023	Protein flightless-1 homolog		K, J, B, C	1269	3	8	4	18
IPI00031801	Isoform 1 of DNA-binding protein A		K, B	372	13	24	42	26

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00303292	Importin subunit alpha-1	b	K, B, D	538	6	9	11	5
IPI00784161	Isoform 1 of tc elongation factor SPT6		K, B	1726	35	16	15	4
IPI00013744	Integrin alpha-2	c, f	K, L	1181	6	14	6	12
IPI00441344	Isoform 1 of Beta-galactosidase		B	677	13	9	0	13
IPI00301311	Isoform 2 of Protein SET		K, B, E, D	277	22	39	81	54
IPI00179057	Isoform 2 of Cullin-4B	d	K	895	9	13	7	7
IPI00219156	60S ribosomal protein L30	r, g	B, D, I	115	25	7	42	23
IPI00024933	Isoform 1 of 60S ribosomal protein L12	r, g	D, I	165	38	33	25	37
IPI00026271	40S ribosomal protein S14	r, g	J, D, I	151	18	16	21	37
IPI00384456	Isoform GTBP-N of DNA mismatch repair protein Msh6		K	1360	8	6	2	5
IPI00006510	Tubulin beta-1 chain	l	B, C	451	67	70	102	82
IPI00025091	40S ribosomal protein S11	r, g	D, I	158	26	24	21	34
IPI00024095	Annexin A3		B, L	323	6	15	8	13
IPI00007764	Isoform 1 of Hematological and neurological expressed 1 protein		K	154	6	19	16	15
IPI00332106	Isoform 1 of Pre-B-cell leukemia tc factor-interacting protein 1	e	K, B, D, C	731	6	11	6	8
IPI00013895	Protein S100-A11	p	K, B	105	30	20	72	124
IPI00216298	Thioredoxin	p, f	K, B, I, D	105	12	15	41	42
IPI00002521	ATP synthase-coupling factor 6, mitochondrial	h	I	108	7	8	19	22
IPI00179026	Isoform 1 of Malignant T cell-amplified sequence 1	d	B	181	16	31	46	34
IPI00027434	Rho-related GTP-binding protein RhoC		D, L	193	11	20	19	35
IPI00014149	Tetratricopeptide repeat protein 35		K, I, E	297	12	16	13	12
IPI00220263	Isoform D of Syntaxin-16		B, H, G	308	5	6	6	14

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00470528	60S ribosomal protein L15	r, g	D, I	204	15	42	49	12
IPI00024705	PDZ domain-containing protein GIPC1		B, D	333	12	20	21	14
IPI00220766	Lactoylglutathione lyase		B	184	12	9	29	35
IPI00022215	Activity-dependent neuroprotector homeobox protein		K, J, B	1102	4	8	8	16
IPI00013184	N-alpha-acetyltransferase 10, NatA catalytic subunit	i	K, B	235	9	17	8	9
IPI00550364	Phosphoglucomutase-2		B, D	612	5	13	2	18
IPI00413140	Isoform 1 of Dynamin-1		B, C	864	6	20	7	7
IPI00033153	Nuclear RNA export factor 1	g	K, B, D	619	5	14	2	12
IPI00025849	Acidic leucine-rich nuclear phosphoprotein 32 family member A		K, B, E	249	14	21	38	36
IPI00172656	FAS-associated factor 2		B, E	445	21	23	12	24
IPI00152692	D-tyrosyl-tRNA(Tyr) deacylase 1		B	209	11	26	16	22
IPI00218728	Isoform 1 of Platelet-activating factor acetylhydrolase IB subunit alpha	k, e	K, J, B, D	410	16	14	3	8
IPI00001871	PRKC ap WT1 regulator protein	b	K, B, L	340	20	41	18	13
IPI00020567	Rho GTPase-activating protein 1	p	B, D	439	14	15	16	13
IPI00033030	Proteasomal ubiquitin receptor ADRM1		K, B	407	6	16	29	30
IPI00219358	Isoform 1 of Mannose-6-phosphate isomerase		B, D	423	9	13	7	7
IPI00479877	4-trimethylaminobutyraldehyde dehydrogenase		B, I, D, L	518	13	14	0	4
IPI00218493	Hypoxanthine-guanine phosphoribosyltransferase		B, D	218	5	11	9	21

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00293026	Isoform 1 of Elongation factor Tu GTP-binding domain-containing protein 1	r		1120	9	12	2	1
IPI00478231	Transforming protein RhoA	e	K, B, I, D, C, L	193	15	16	17	35
IPI00027397	Isoform 1 of Hematological and neurological expressed 1-like protein		K, B	190	11	12	18	21
IPI00030774	Isoform 4 of Tubulin-specific chaperone D	l		1248	3	6	3	18
IPI00152377	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3B		E	826	5	15	12	18
IPI00001960	Chloride intracellular channel protein 4	h, e	K, B, I, D, L	253	9	24	19	12
IPI00021016	Isoform 1 of Elongation factor Ts, mitochondrial		K, I	325	26	22	17	46
IPI00007694	Isoform 1 of Protein phosphatase methylesterase 1			386	12	5	11	25
IPI00003815	Rho GDP-dissociation inhibitor 1		B, D, C	204	36	43	85	84
IPI00008708	Ribosomal L1 domain-containing protein 1	r	K, J, I	490	12	12	5	4
IPI00021266	60S ribosomal protein L23a	r, g	D, I	156	20	19	42	24
IPI00006987	ATP-dependent RNA helicase DDX24		J, B	859	5	12	17	10
IPI00030243	Isoform 1 of Proteasome activator complex subunit 3	k, b	K, B	254	12	5	8	19
IPI00290928	Guanine nucleotide-binding protein subunit alpha-13	p, e	L	377	12	15	2	12
IPI00027444	Leukocyte elastase inhibitor		B	379	9	6	2	14

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00216346	cDNA FLJ58768, highly similar to Homo sapiens nucleolar protein 3 (ap repressor with CARD domain) (NOL3), mRNA			270	8	5	8	18
IPI00010320	Chromobox protein homolog 1		K	185	4	6	21	15
IPI00003217	Proteasome subunit beta type-7	k, b	K, B	277	12	11	16	19
IPI00384280	Prenylcysteine oxidase 1		L	505	12	18	14	16
IPI00247583	60S ribosomal protein L21	r, g	D, I	160	40	26	119	38
IPI00218465	Phospholipase A-2-activating protein	p		795	6	11	4	2
IPI00029468	Alpha-centractin	k	B, D, C	376	13	19	17	18
IPI00003479	Mitogen-activated protein kinase 1	d, p	K, B, D	360	17	18	11	5
IPI00008215	NADP-dependent malic enzyme		B, D	572	10	8	8	23
IPI00018342	Adenylate kinase isoenzyme 1		B, D	194	7	11	25	20
IPI00301618	Isoform 1 of Serologically defined colon cancer antigen 1		K, J, B	1076	3	6	2	8
IPI00107555	Profilin			188	10	15	11	18
IPI00019407	Sterol-4-alpha-carboxylate 3-dehydrogenase, decarboxylating		E	373	13	9	8	18
IPI00031820	Phenylalanyl-tRNA synthetase alpha chain	g	B, D	508	16	15	14	19
IPI00002412	Palmitoyl-protein thioesterase 1	o	K, G, D	306	6	5	17	11
IPI00013917	40S ribosomal protein S12	r, g	B, D, I	132	19	23	47	60
IPI00301936	cDNA FLJ60076, highly similar to ELAV-like protein 1			353	10	4	9	8
IPI00182533	60S ribosomal protein L28	r, g	D, I	137	7	11	20	22
IPI00171438	Thioredoxin domain-containing protein 5		E	432	1	3	10	35

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00328415	Isoform 1 of NADH-cytochrome b5 reductase 3		B, I, E	301	4	8	5	15
IPI00419473	Isoform 2 of tc factor BTF3		K	162	9	21	36	45
IPI00470674	NADH-cytochrome b5 reductase 1		I	305	20	15	13	8
IPI00010157	S-adenosylmethionine synthase isoform type-2		D	395	15	23	6	9
IPI00011609	Isoform II of Ubiquitin-protein ligase E3A		K, D	875	5	6	4	5
IPI00219468	Isoform IIa of Profilin-2		B	140	10	15	13	17
IPI00783872	Isoform 1 of Caprin-1	e	B, D	709	11	13	12	22
IPI00019888	Succinate-semialdehyde dehydrogenase, mitochondrial		I	535	9	17	8	15
IPI00017303	DNA mismatch repair protein Msh2		K	934	9	9	3	16
IPI00030915	Ubiquitin carboxyl-terminal hydrolase 8	d, f	K, B, D, L	1118	5	6	11	17
IPI00023673	Galectin-3-binding protein	c, p		585	3	4	5	14
IPI00333215	Isoform 1 of tc elongation factor A protein 1	q, g	K	301	3	17	10	12
IPI00294158	Biliverdin reductase A		B, D	296	11	7	7	15
IPI00456750	Niban-like protein 1			733	9	4	0	9
IPI00305282	Isoform 1 of DNA repair protein RAD50	d		1312	5	4	2	10
IPI00298949	Cyclin-G-associated kinase	n, d	B, G	1311	13	3	3	9
IPI00018195	Mitogen-activated protein kinase 3	q, n, d	K, B, D	379	15	26	13	4
IPI00294501	7-dehydrocholesterol reductase	e	E	475	26	18	17	35
IPI00024919	Thioredoxin-dependent peroxide reductase, mitochondrial		B, I	256	22	31	33	17
IPI00307155	Rho-associated protein kinase 2	n	B, D, L	1388	11	1	3	10

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00020950	Isoform Alpha-1 of Protein phosphatase 1A		D	382	10	11	4	15
IPI00021370	Isoform 1 of Ubiquitin-conjugating enzyme E2 K		B	200	14	10	15	5
IPI00012645	Isoform 1 of Spectrin beta chain, brain 2		B, D, C	2390	4	4	8	18
IPI00102069	Eukaryotic tl initiation factor 3 subunit M		B	374	3	5	6	23
IPI00221089	40S ribosomal protein S13	r, g	K, J, D, I	151	18	13	13	22
IPI00003406	Isoform 1 of Drebrin	e	B	649	10	10	14	24
IPI00295542	Nucleobindin-1		B, G	461	7	5	10	16
IPI00250153	Y-box-binding protein 2		K, B	364	14	23	36	15
IPI00019450	Isoform Long of 60 kDa SS-A/Ro ribonucleoprotein		K, J, B	538	6	7	10	2
IPI00293312	Isoform 2 of Zinc finger CCCH domain-containing protein 18		K	757	15	16	11	25
IPI00646105	pyrroline-5-carboxylate reductase 3			286	4	11	12	14
IPI00555744	Ribosomal protein L14 variant	r, g	B, D, I	220	19	16	23	26
IPI00220271	Alcohol dehydrogenase [NADP+]		D	325	10	13	4	8
IPI00016513	Ras-related protein Rab-10	o	G, L	200	32	83	12	25
IPI00013297	28 kDa heat- and acid-stable phosphoprotein	p, f		181	14	18	29	24
IPI00221035	Isoform 1 of tc factor BTF3		K	206	9	23	36	44
IPI00099463	Sphingosine-1-phosphate lyase 1	b	E	568	13	12	2	14
IPI00004273	Isoform 1 of RNA-binding protein 25	b	K, J, B	843	16	29	10	12
IPI00514234	Ladinin-1			517	2	6	11	12
IPI00014474	A-kinase anchor protein 8	j, p	K, J, I, G	692	18	18	2	11
IPI00026833	Adenylosuccinate synthetase isozyme 2		B, D, L	456	8	9	3	10

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00008552	Glutaredoxin-3		B	335	8	13	10	18
IPI00013466	ATPase ASNA1		K, J, B, E	348	23	16	3	14
IPI00014230	Complement component 1 Q subcomponent-binding protein, mitochondrial		K, I, L	282	16	21	19	11
IPI00328748	cDNA FLJ77177, highly similar to Homo sapiens arginine-rich, mutated in early stage tumors (ARMET), mRNA			234	6	2	14	20
IPI00294619	Protein TFG		B	400	6	10	17	12
IPI00640341	Isoform 1 of Peptidyl-prolyl cis-trans isomerase FKBP8	l, b	I	412	8	10	23	12
IPI00964541	Uncharacterized protein			144	51	51	50	57
IPI00218486	Isoform 1 of Protein phosphatase Slingshot homolog 3		K, B, C	659	6	7	3	10
IPI00744711	Polyribonucleotide nucleotidyltransferase 1, mitochondrial		B, I, L	783	11	26	20	13
IPI00549467	Omega-amidase NIT2		B, I	276	11	25	18	13
IPI00329629	DnaJ homolog subfamily C member 7	l	K, J, B, C	494	5	7	2	12
IPI00001661	regulator of chromosome condensation isoform a			452	13	16	2	4
IPI00291946	Ubiquitin carboxyl-terminal hydrolase 10		K, B	803	6	13	6	10
IPI00411937	Nucleolar protein 56		K, J	594	9	20	1	4
IPI00061525	Glucosamine 6-phosphate N-acetyltransferase	i	G, D	184	22	14	9	12
IPI00179330	Ubiquitin-40S ribosomal protein S27a	k, r, b, g	K, B, D, L	156	14	19	27	15
IPI00177965	5'-nucleotidase domain-containing protein 1			455	7	34	6	12

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00298348	Isoform 2 of Oxidation resistance protein 1		I	839	2	16	3	12
IPI00015894	Cdc42 effector protein 4		B	356	5	14	18	29
IPI00396279	Isoform 1 of CLIP-associating protein 1	k	B, G, D, C	1538	13	13	6	4
IPI00411614	WD repeat and HMG-box DNA-binding protein 1		K, J, B	1129	6	7	4	2
IPI00143753	Isoform 1 of U2-associated protein SR140			1029	6	20	11	16
IPI00413451	Serpin B6			409	4	12	5	9
IPI00030255	Procollagen-lysine,2-oxoglutarate 5-dioxygenase 3		E	738	5	7	9	12
IPI00001676	Isoform 2 of Nuclear pl protein 4 homolog		K, B, E, D	617	17	14	6	5
IPI00002212	Isoform B of Serine/threonine-protein kinase 24	n, b, p	B, D	443	1	21	4	13
IPI00027270	60S ribosomal protein L26	r, g	D	145	13	40	38	35
IPI00011916	Aminoacyl tRNA synthase complex-interacting multifunctional protein 2	b, g, e	K, B, D	320	14	14	27	7
IPI00219352	Isoform 1 of Cystathionine beta-synthase		K, J, B, D	551	8	11	14	16
IPI00183508	twinfilin-1	n	B	384	6	10	13	24
IPI00024971	Isoform 1 of Oxysterol-binding protein 1		B, G	807	9	7	2	15
IPI00305978	Aflatoxin B1 aldehyde reductase member 2		B, I, G	359	5	15	4	8
IPI00014053	Isoform 1 of Mitochondrial import receptor subunit TOM40 homolog	o, s	I	361	13	8	9	32
IPI00022745	Diphosphomevalonate decarboxylase		D	400	12	18	17	16

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00031836	Developmentally-regulated GTP-binding protein 1	q	K, B	367	5	8	13	15
IPI00032808	Ras-related protein Rab-3D	o	I, L	219	11	10	3	11
IPI00419373	Isoform 1 of Heterogeneous nuclear ribonucleoprotein A3	g	K, J	378	18	24	10	12
IPI00152981	Acyl-CoA dehydrogenase family member 9, mitochondrial		I	621	7	10	1	10
IPI00398812	Isoform 1 of Kinesin light chain 4		B, C	619	2	19	6	3
IPI00019376	Isoform 2 of Septin-11	d	B, C	439	8	1	6	12
IPI00037448	Glyoxylate reductase/hydroxypyruvate reductase	i	B	328	12	22	33	22
IPI00006980	UPF0568 protein C14orf166		K, B, C	244	9	12	5	20
IPI00023860	Nucleosome assembly protein 1-like 1		K	391	14	12	35	30
IPI00304071	Acyl-CoA synthetase family member 2, mitochondrial		I	615	6	10	3	7
IPI00554541	Isoform 1 of Acetolactate synthase-like protein			632	4	6	16	20
IPI00023149	Isoform B of Syntaxin-16		B, H, G	325	4	7	6	13
IPI00013871	Ribonucleoside-diphosphate reductase large subunit		B, D	792	7	23	9	13
IPI00171421	UPF0670 protein C8orf55			208	5	10	18	12
IPI00004534	Phosphoribosylformylglycinamidine synthase		B, D	1338	8	9	8	14
IPI00107104	UPF0368 protein Cxorf26			233	6	9	8	14
IPI00550882	Pyrroline-5-carboxylate reductase			346	6	10	15	10
IPI00465085	Isoform 1 of Nicotinate phosphoribosyltransferase		K, B, G, D	538	9	5	8	4
IPI00029133	ATP synthase subunit b, mitochondrial	h	I	256	12	24	22	26

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00375015	Isoform 2 of Deoxyuridine 5'-triphosphate nucleotidohydrolase, mitochondrial		K, I	164	2	4	14	18
IPI00015560	Isoform 1 of Elongator complex protein 2		K, J, B, G	826	14	19	7	13
IPI00339379	Isoform 2 of Rho guanine nucleotide exchange factor 1	f	B, D, L	879	14	9	9	8
IPI00002478	Isoform B of Endothelin-converting enzyme 1	b	F, L	770	13	11	1	14
IPI00101186	Isoform 1 of RRP12-like protein		K, J	1297	22	34	5	8
IPI00215918	ADP-ribosylation factor 4	o	B, G, L	180	32	18	19	37
IPI00292134	Isoform 1 of Epidermal growth factor receptor substrate 15	f, o	B, F, D, L	896	3	8	15	14
IPI00012545	Isoform TGN51 of Trans-Golgi network integral membrane protein 2		K, J, G, L	480	8	10	3	11
IPI00031169	Ras-related protein Rab-2A	o	E, G	212	10	12	20	18
IPI00465256	GTP:AMP phosphotransferase, mitochondrial		I	227	4	14	1	5
IPI00784233	Isoform 1 of PERQ amino acid-rich with GYF domain-containing protein 2			1299	0	1	13	17
IPI00011592	cpic dynein 1 light intermediate chain 2		B, C	492	3	8	10	11
IPI00302647	Isoform 1 of Coiled-coil and C2 domain-containing protein 1A		K, J, B, L	951	12	7	7	7
IPI00478758	Isoform 1 of UPF0557 protein C10orf119			642	1	10	3	11
IPI00023987	Phosphopantothenate--cysteine ligase		D	311	13	11	5	11

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00220835	pt protein Sec61 subunit beta	o, s	E	96	3	3	3	19
IPI00927892	Mitochondrial-processing peptidase subunit beta		I	489	8	3	7	8
IPI00550234	Isoform 1 of Actin-related protein 2/3 complex subunit 5		B	151	15	5	4	3
IPI00015361	Prefoldin subunit 5	l	K, B	154	8	1	28	14
IPI00021954	Golgi-specific brefeldin A-resistance guanine nucleotide exchange factor 1			1859	8	9	4	14
IPI00007675	cpic dynein 1 light intermediate chain 1	d, j	B, C, L	523	6	15	12	17
IPI00643041	GTP-binding nuclear protein Ran	d, j, p	K, B, D	216	39	33	27	42
IPI00334907	Isoform 1 of Phosphatidylinositol transfer protein beta isoform		B, G	271	7	6	3	7
IPI00005751	Serine palmitoyltransferase 2		I, E	562	5	10	5	13
IPI00001636	Ataxin-10		B	475	8	11	14	14
IPI00033494	Myosin regulatory light chain 12B		D	172	12	28	25	18
IPI00867509	Coronin-1C_i3 protein			527	20	20	13	13
IPI00009659	Regulation of nuclear pre-mRNA domain-containing protein 1B			326	10	13	5	10
IPI00298347	Isoform 2 of Tyrosine-protein phosphatase non-receptor type 11	p	B, I, D	593	5	4	2	14
IPI00554777	Asparagine synthetase [glutamine-hydrolyzing]	i	D	561	6	8	6	23
IPI00291607	Inositol 1,4,5-trisphosphate receptor type 3	h, s	K, J, B, E, H	2671	11	1	0	10
IPI00020719	Isoform 1 of Mitochondrial antiviral-signaling protein		I	540	6	8	8	10
IPI00374018	Isoform 1 of Protein			360	10	3	8	10

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
	FAM102B							
IPI00306398	Isoform 2 of NudC domain-containing protein 1			554	6	5	9	8
IPI00647650	cDNA FLJ35809 fis, clone TESTI2006016, highly similar to Eukaryotic tl initiation factor 3 subunit 3	r, g	B, D	366	16	12	15	18
IPI00219861	Isoform 1 of Low molecular weight phosphotyrosine protein phosphatase		K, B	158	10	13	10	11
IPI00477763	Serine/threonine-protein kinase MRCK beta	n, p	B, C	1711	3	13	6	11
IPI00216472	Isoform Non-brain of Clathrin light chain B			211	15	18	13	28
IPI00031107	Isoform 2 of Hydroxysteroid dehydrogenase-like protein 2		I	345	10	5	6	5
IPI00409659	Ubiquilin-2		K, B, L	624	4	10	8	7
IPI00031691	60S ribosomal protein L9	r, g	J, B, D, I	192	15	19	21	3
IPI00152441	Isoform 1 of Minor histocompatibility antigen H13		E, L	377	10	23	9	17
IPI00002349	Nuclear fragile X mental retardation-interacting protein 2		K, B	695	1	2	2	19
IPI00032003	Emerin		K, E	254	5	6	9	14
IPI00147874	Sialic acid synthase		B, D	359	18	15	14	18
IPI00396627	Isoform 1 of Zinc phosphodiesterase ELAC protein 2		K, I	826	11	10	9	10
IPI00607591	Isoform 1 of Rap1 GTPase-GDP dissociation stimulator 1			607	16	24	13	10
IPI00306290	Exportin-T		K, B	962	6	11	6	5
IPI00026673	Isoform 1 of Homeobox protein cut-like 1		K, J, B	1505	4	4	6	15

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00305092	Isoform 1 of Partner of Y14 and mago		K, J, B	204	5	8	5	13
IPI00022628	cDNA FLJ50558, highly similar to Homo sapiens microtubule-associated protein 7 (MAP7), mRNA			771	8	11	22	33
IPI00019927	26S proteasome non-ATPase regulatory subunit 7	k, b		324	17	24	13	14
IPI00183294	Isoform 1 of Nuclear pore complex protein Nup214	o, s	K, D	2090	3	1	5	18
IPI00953460	Uncharacterized protein			257	24	12	2	13
IPI00022664	Geranylgeranyl transferase type-2 subunit alpha			567	8	9	17	9
IPI00301364	Isoform 1 of S-phase kinase-associated protein 1	k	D	163	45	84	40	35
IPI00022020	Type II inositol-3,4-bisphosphate 4-phosphatase	p		924	5	6	3	9
IPI00005194	Ubiquitin domain-containing protein UBFD1			533	5	6	3	5
IPI00013174	Isoform 1 of RNA-binding protein 14		K, J	669	6	15	6	10
IPI00441473	Protein arginine N-methyltransferase 5	f	K, B, D	637	10	6	2	10
IPI00465045	Isoform 1 of Disco-interacting protein 2 homolog B		K	1576	5	9	8	7
IPI00017292	Isoform 1 of Catenin beta-1	b, c	K, B, D, C, L	781	6	8	7	17
IPI00456631	Isoform 1 of Lysine-specific histone demethylase 1A		K	852	19	14	5	8
IPI00013949	Small glutamine-rich tetratricopeptide repeat-containing protein alpha		B	313	1	7	27	41

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00217920	Isoform 1 of Aldehyde dehydrogenase family 16 member A1			802	10	9	5	9
IPI00645805	Isovaleryl-CoA dehydrogenase, mitochondrial		I	423	10	8	3	11
IPI00029557	GrpE protein homolog 1, mitochondrial	l	I	217	15	23	9	22
IPI00031804	Isoform 1 of Voltage-dependent anion-selective channel protein 3	s	I	283	21	15	16	19
IPI00220487	Isoform 1 of ATP synthase subunit d, mitochondrial	h	I	161	4	3	20	23
IPI00555565	Putative heat shock protein HSP 90-beta 4	l		505	85	153	94	73
IPI00005668	Aldo-keto reductase family 1 member C2		B	323	8	7	7	16
IPI00002270	UPF0364 protein C6orf211			441	21	15	16	26
IPI00306301	pyruvate dehydrogenase E1 alpha 1 isoform 2 precursor			428	8	8	5	10
IPI00007144	60S ribosomal protein L26-like 1	r, g	D	145	13	37	34	31
IPI00026202	60S ribosomal protein L18a	r, g	D, I	176	22	23	26	21
IPI00791573	Isoform 2 of Suppressor of G2 allele of SKP1 homolog	j		333	14	8	2	13
IPI00795701	7 kDa protein			65	14	13	20	21
IPI00844000	Isoform 1 of E3 UFM1-protein ligase 1		K, J, B, E	794	5	3	1	20
IPI00016786	Isoform 2 of Cell division control protein 42 homolog		B, D, L	191	25	16	28	53
IPI00218962	Uncharacterized protein			336	5	3	10	19
IPI00020021	Protein DEK	p	K	375	9	12	4	15
IPI00025861	Cadherin-1	b	B, L	882	14	8	9	7
IPI00289819	Cation-independent mannose-6-phosphate receptor	p	B, F	2491	9	7	2	12

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00016179	Protein S100-A13	o	K, B, D	98	12	22	33	38
IPI00793922	9 kDa protein			83	187	97	77	74
IPI00789155	cDNA FLJ31776 fis, clone NT2RI2008141, highly similar to CALUMENIN			323	7	19	9	17
IPI00001738	Nuclear pore complex protein Nup88	o, s	K, J, D	741	4	10	8	14
IPI00296190	UPF0765 protein C10orf58		I	229	9	11	10	13
IPI00026942	Isoform 1 of Erlin-2		B, E, L	339	6	4	2	8
IPI00023510	Ras-related protein Rab-5A	o	B, L	215	11	12	8	7
IPI00018813	Isoform 2 of COP9 signalosome complex subunit 2	p	K, J, B	450	6	10	4	12
IPI00101645	Putative adenosylhomocysteinase 3			611	10	14	1	6
IPI00002406	Basal ca molecule	c, p	L	628	6	12	6	12
IPI00219835	Isoform Gnas-2 of Guanine nucleotide-binding protein G(s) subunit alpha isoforms short	s	B, L	380	13	17	13	19
IPI00420025	Isoform 2 of Armadillo repeat-containing protein 10		I, E	308	2	12	18	4
IPI00021466	Isoform 1 of Polyadenylate-binding protein-interacting protein 1		B, D	479	9	7	3	2
IPI00470779	Alpha-taxilin	f	B	546	8	7	1	11
IPI00743802	Isoform Beta-2 of Protein phosphatase 1B			387	16	9	3	10
IPI00016703	24-dehydrocholesterol reductase	b, m	K, E, G	516	7	12	6	11
IPI00012069	NAD(P)H dehydrogenase [quinone] 1		B, D	274	11	23	12	12
IPI00071696	Protein CASP		G	678	8	6	11	24

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00182938	Isoform 1 of Putative adenosylhomocysteinase 2		E	530	9	11	1	10
IPI00789008	Flotillin-2	c	F, L, A	428	5	3	5	17
IPI00418194	198 kDa protein			1780	11	3	1	8
IPI00020416	Tripeptidyl-peptidase 2		B	1249	4	18	5	3
IPI00294398	Isoform 1 of Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial		B, I	314	5	4	7	10
IPI00217960	Isoform 2 of cAMP-dependent protein kinase catalytic subunit alpha	k, n, s	K, B, I, G, D, L	343	10	16	10	6
IPI00027378	Isoform 1 of UBX domain-containing protein 1		B	297	11	7	0	9
IPI00450768	Keratin, type I cytoskeletal 17		B	432	89	53	35	49
IPI00024580	Methylcrotonoyl-CoA carboxylase subunit alpha, mitochondrial		I	725	7	7	4	6
IPI00010415	Isoform 1 of cic acyl coenzyme A thioester hydrolase		K, J, B, I, D	380	12	7	5	7
IPI00016613	CSNK2A1 protein			397	4	8	6	12
IPI00294891	Uncharacterized protein			854	7	4	0	4
IPI00027445	Probable histidyl-tRNA synthetase, mitochondrial	r, g	B, I	506	6	3	7	21
IPI00554761	Non-histone chromosomal protein HMG-14		K, B	100	48	110	8	14
IPI00029750	Isoform 1 of 40S ribosomal protein S24	r, g	K, B, D	133	7	15	10	13
IPI00029778	Isoform 1 of Tumor suppressor p53-binding protein 1		K, B	1972	6	11	2	3
IPI00914566	Farnesyl pyrophosphate synthase		K, J, B, I, D	419	12	21	7	12

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00847689	Isoform 3 of Oxidoreductase HTATIP2	e	K, B	276	12	10	3	1
IPI00025310	Zinc finger protein 217		K	1048	0	3	16	7
IPI00017510	Cytochrome c oxidase subunit 2		I	227	9	4	6	22
IPI00219084	Isoform 2 of tc factor p65		K, B, D	537	6	9	8	6
IPI00217357	Isoform 1 of Cell division cycle and ap regulator protein 1	b, d, g	B	1150	13	8	7	12
IPI00184821	Isoform 1 of Bifunctional coenzyme A synthase		B	564	2	1	3	16
IPI00005162	Actin-related protein 2/3 complex subunit 3		B	178	8	17	9	17
IPI00296713	Isoform 1 of Granulins	p	I	593	0	6	6	21
IPI00008998	3-hydroxyacyl-CoA dehydratase 3		E	362	8	25	12	11
IPI00005745	Serine palmitoyltransferase 1		E	473	8	17	7	13
IPI00024670	Receptor expression-enhancing protein 5			189	13	17	20	27
IPI00015602	Mitochondrial import receptor subunit TOM70		I	608	13	11	8	19
IPI00071318	Isoform 1 of Putative RNA-binding protein Luc7-like 1		K	371	3	6	12	26
IPI00100656	Isoform 1 of Trans-2,3-enoyl-CoA reductase		B, E	308	9	27	0	8
IPI00289746	Isoform 2 of Serine/threonine-protein kinase PAK 1	n, b	B, G, D, L	553	6	14	14	15
IPI00386687	leucine-rich repeat flightless-interacting protein 1 isoform 1			640	12	17	10	14
IPI00644936	Isoform 3 of Guanine nucleotide-binding protein G(s) subunit alpha isoforms short	s	B, L	379	14	16	13	19

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00657706	Isoform 1 of Lysophospholipid acyltransferase 7			472	16	18	23	25
IPI00019345	Ras-related protein Rap-1A	p	D, L	184	9	11	9	21
IPI00095891	Isoform XLas-1 of Guanine nucleotide-binding protein G(s) subunit alpha isoforms XLas		L	1037	15	14	13	20
IPI00029764	Splicing factor 3A subunit 3	g	K, J	501	4	4	8	13
IPI00452747	Similar to Signal peptidase complex subunit 2			226	10	11	5	7
IPI00003965	Ubiquitin carboxyl-terminal hydrolase 7		K, B	1102	18	13	2	16
IPI00303258	LIM and cysteine-rich domains protein 1		K, B	365	4	3	2	23
IPI00063234	Protein kinase, cAMP-dependent, regulatory, type II, alpha, isoform CRA_b			382	15	27	16	14
IPI00100460	Aspartyl-tRNA synthetase, mitochondrial	g	K, B, I	645	6	9	6	6
IPI00006122	Isoform MEA6 of Cutaneous T-cell lymphoma-associated antigen 5			804	9	3	9	17
IPI00025974	Charged multivesicular body protein 4b	o	B, F, D	224	4	6	7	22
IPI00219512	Isoform 2 of Ubiquitin carboxyl-terminal hydrolase isozyme L5		K, B, D	316	2	10	6	11
IPI00003856	V-type proton ATPase subunit E 1	h, s	B, I, F, D	226	11	2	4	10
IPI00760846	Isoform 1 of Myosin-XVIIIa		B, C	2054	1	6	4	10
IPI00022082	Isoform 2 of Septin-8	d	B, C	429	13	4	6	9
IPI00016862	Isoform Mitochondrial of Glutathione reductase, mitochondrial		B, I, D	522	7	12	8	11

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00022597	NEDD8-conjugating enzyme Ubc12			183	16	14	13	14
IPI00926316	cDNA, FLJ79126, highly similar to Zyxin			415	5	1	2	24
IPI00007277	Isoform 1 of Leucine-rich repeat flightless-interacting protein 2			721	0	5	9	12
IPI00219299	Talin-2	c	B, L	2542	4	2	5	14
IPI00013774	Histone deacetylase 1		K, J, B, D	482	12	8	6	12
IPI00003949	Ubiquitin-conjugating enzyme E2 N		K, B, D	152	13	26	26	28
IPI00333619	Isoform 1 of Fatty aldehyde dehydrogenase		E	485	5	3	7	9
IPI00004838	Isoform Crk-II of Adapter molecule crk	p	K, B, F, D, L	304	2	8	10	14
IPI00022542	Rho-associated protein kinase 1	n, b, p	B, G, D, C	1354	5	1	4	5
IPI00016458	Isoform 1 of L-2-hydroxyglutarate dehydrogenase, mitochondrial		I	463	5	0	4	10
IPI00014361	GDP-L-fucose synthase		B	321	13	25	12	18
IPI00148063	Heme-binding protein 1		B, I, D	189	13	13	5	29
IPI00010204	Serine/arginine-rich splicing factor 3	q, g	K	164	17	6	13	25
IPI00010271	Isoform A of Ras-related C3 botulinum toxin substrate 1	b, c	D, L	192	19	25	21	26
IPI00217437	Tau-tubulin kinase			1649	227	168	270	458
IPI00014577	Ras-related protein Rab-18	o	L	206	14	18	13	16
IPI00016621	Isoform 2 of AP-2 complex subunit alpha-2		D, L	940	3	11	1	10
IPI00007402	Importin-7	p	K, B, G	1038	8	10	6	9
IPI00008485	cpic aconitate hydratase	i	B, I, E, G, D	889	7	18	5	2
IPI00551062	Isoform 1 of Protein canopy homolog 3		E	278	12	23	19	25

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00029046	Malectin	l	E	292	37	38	24	19
IPI00410666	Isoform 3 of Protein scribble homolog	f, e	B, L	1655	6	5	5	16
IPI00554786	Isoform 5 of Thioredoxin reductase 1, cpic	p, f	K, J, B, I, D	499	5	7	2	7
IPI00024719	Histone acetyltransferase type B catalytic subunit		K, B	419	11	17	9	7
IPI00000015	Serine/arginine-rich splicing factor 4	q, g	K	494	10	7	26	18
IPI00797574	Biorientation of chromosomes in cell division protein 1-like			3051	6	8	6	7
IPI00002372	Isoform 1 of ATP-binding cassette sub-family D member 3	s	D	659	6	7	5	6
IPI00007812	V-type proton ATPase subunit B, brain isoform	h, s	G, D, L	511	4	2	2	6
IPI00011604	Glycine cleavage system H protein, mitochondrial		I	173	0	1	21	2
IPI00006579	Cytochrome c oxidase subunit 4 isoform 1, mitochondrial		K, I	169	17	10	12	19
IPI00103467	Aldehyde dehydrogenase X, mitochondrial		K, J, I	517	5	0	9	9
IPI00032955	Isoform 1 of RING finger protein 114	e		228	10	10	11	8
IPI00219673	Isoform 1 of Glutathione S-transferase kappa 1			226	7	16	13	11
IPI00008531	REST corepressor 1		K	482	4	13	13	4
IPI00171152	Isoform 4 of Abhydrolase domain-containing protein 11		I	308	19	11	10	6
IPI00550239	Histone H1.0	b	K, G	194	10	7	20	17
IPI00010586	Isoform 2 of TATA element modulatory factor		K, B, G	1096	5	4	4	13
IPI00102864	Hexokinase-2	s	I, D	917	7	5	2	10
IPI00032304	Plastin-1		B	629	7	9	6	8

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00011569	Isoform 1 of Acetyl-CoA carboxylase 1		B, I, D	2346	9	12	1	8
IPI00007935	Isoform 1 of PDZ and LIM domain protein 5		B, D, L	596	4	7	5	11
IPI00006176	Isoform 1 of Hepatocyte growth factor-regulated tyrosine kinase substrate	p	B, F, D	777	7	5	7	14
IPI00156282	Isoform 1 of COP9 signalosome complex subunit 1	d	K, B	491	10	10	5	12
IPI00549389	Protein of unknown function DUF858, methyltransferase-like family protein		K	224	2	7	9	6
IPI00074870	DnaJ homolog subfamily C member 1	l	K, E, H	554	10	17	2	8
IPI00294742	Isoform 1 of La-related protein 7		K	582	11	7	7	9
IPI00025086	Cytochrome c oxidase subunit 5A, mitochondrial		I	150	4	2	18	16
IPI00220173	Isoform Tau-B of Microtubule-associated protein tau	b	B, D, C, L	381	13	8	4	9
IPI00012866	RAC-alpha serine/threonine-protein kinase	n, b, p	K, B, D, L	480	6	18	5	14
IPI00106495	Condensin complex subunit 3	d, j	K, B	1015	6	9	2	4
IPI00025796	NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial		I	264	7	7	4	11
IPI00107745	Isoform 1 of Luc7-like protein 3	b	K, J, L	432	9	7	7	15
IPI00168479	cDNA FLJ56357, highly similar to Homo sapiens apolipoprotein A-I binding protein (APOA1BP), mRNA			307	0	8	4	9

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00015920	Isoform 1 of Mitochondrial dicarboxylate carrier	s	K, J, I	287	24	11	2	25
IPI00395998	60S ribosomal protein L32	r, g	D, I	135	10	11	23	14
IPI00304612	60S ribosomal protein L13a	r, g	D	203	6	11	12	10
IPI00294627	Isoform 2 of Splicing factor 1		K, J, I	638	15	18	5	25
IPI00008575	Isoform 1 of KH domain-containing, RNA-binding, st-associated protein 1	d, p, f	K	443	10	6	4	19
IPI00888053	similar to hCG1643231			313	172	210	151	213
IPI00159899	Similar to Ankyrin repeat and FYVE domain-containing protein 1		B, F	1211	5	10	4	11
IPI00021338	Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial	i	I	647	9	4	4	1
IPI00827967	Isoform 2 of Putative GTP-binding protein Parf		K, B	730	4	7	2	10
IPI00102752	Isoform 1 of Putative RNA-binding protein 15		K, J	977	1	5	5	13
IPI00011284	Isoform Membrane-bound of Catechol O-methyltransferase		B, I, H, D, L	271	5	4	10	14
IPI00794397	charged multivesicular body protein 4A	o	F	265	2	4	10	10
IPI00033349	Prolactin regulatory element-binding protein	o	K, E	417	9	7	17	8
IPI00012197	dCTP pyrophosphatase 1		B, D	170	17	15	16	17
IPI00026991	Polypeptide N-acetylgalactosaminyltransferase 6		G	622	5	9	2	7
IPI00249080	Isoform 2 of N-acetylserotonin O-methyltransferase-like protein		B	605	3	10	6	14

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00012901	Isoform 1 of Trans-acting T-cell-specific tc factor GATA-3		K, J	443	7	6	3	8
IPI00456758	60S ribosomal protein L27a	r, g	D, I	148	14	15	25	23
IPI00017963	Small nuclear ribonucleoprotein Sm D2	g	K, D	118	24	9	11	30
IPI00012463	Isoform 1 of Putative deoxyribonuclease TATDN1		K	297	6	10	4	8
IPI00414482	Isoform 1 of General tc factor 3C polypeptide 1	q	K	2130	1	8	13	13
IPI00003327	ADP-ribosylation factor-like protein 3	d	K, B, G, C	182	12	17	1	15
IPI00377261	Isoform 1 of Far upstream element-binding protein 3	q	K	572	3	7	5	7
IPI00003833	Mitochondrial carrier homolog 2	s	I	303	16	23	13	17
IPI00028004	Proteasome subunit beta type-3	k, b	K, B	205	2	5	4	11
IPI00032635	Isoform 1 of Protein LSM14 homolog B			385	3	10	8	6
IPI00005861	Isoform 1 of U4/U6 small nuclear ribonucleoprotein Prp3		K, J, B	683	4	6	5	14
IPI00000760	N(G),N(G)-dimethylarginine dimethylaminohydrolase 2		B	285	1	1	8	12
IPI00024540	Isoform 1 of Endophilin-B2	p	K, B	395	5	6	2	10
IPI00550308	RNA-binding protein 12		K	932	8	2	3	9
IPI00640598	protein kinase C-binding protein 1 isoform a			1188	2	5	7	10
IPI00005202	progesterone receptor membrane component 2			247	9	11	7	10
IPI00478127	tc elongation factor A protein-like 3		K	200	1	14	26	42
IPI00298883	Isoform 1 of 5-azacytidine-induced protein 1	k, e	B, D	1083	4	5	8	6

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00000030	Isoform Delta-1 of Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit delta isoform	p	K, J, B	602	1	5	14	10
IPI00015973	Band 4.1-like protein 2		B, C, L	1005	8	32	7	5
IPI00291373	ATP-binding cassette sub-family D member 1	s	D	745	5	8	5	6
IPI00025277	Programmed cell death protein 6		K, B, E, H	191	9	13	5	14
IPI00217976	Isoform Tau-G of Microtubule-associated protein tau	b	B, D, C, L	776	12	8	8	6
IPI00908564	cDNA FLJ57619, highly similar to Delta 3,5-delta 2,4-dienoyl-CoA isomerase, mitochondrial			191	11	19	8	10
IPI00154451	cDNA FLJ55586, highly similar to MMS19-like protein			1051	8	7	3	18
IPI00000041	Rho-related GTP-binding protein RhoB	b, c, o, e	K, F, D, L	196	4	4	6	11
IPI00555957	Putative heat shock protein HSP 90-alpha A4	l	B	418	36	54	46	53
IPI00006754	DDB1- and CUL4-associated factor 7		K, J, B	342	3	8	3	6
IPI00555917	Paxillin variant (Fragment)			713	2	0	17	27
IPI00902909	cDNA FLJ16112 fis, clone 3NB692001853, highly similar to NUCLEOSOME ASSEMBLY PROTEIN 1-LIKE 1			323	14	14	28	16
IPI00872762	Succinyl-CoA ligase [GDP-forming] subunit alpha, mitochondrial		I	346	12	14	19	14
IPI00026530	Protein ERGIC-53	l, o	E, H, G	510	6	5	4	9

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00470649	Isoform 1 of Nicalin		K, J, E	563	4	5	4	5
IPI00293350	Translin-associated protein X	e	K, B	290	7	9	8	16
IPI00019755	Glutathione S-transferase omega-1	i	B, D	241	5	11	14	15
IPI00375843	Isoform 3 of Keratin, type II cytoskeletal 80			487	4	73	30	36
IPI00017344	Ras-related protein Rab-5B	o	F, L	215	8	6	6	11
IPI00006038	Isoform 1 of Nuclear pore complex protein Nup98-Nup96	k, o, s	K, D	1817	10	3	2	6
IPI00217232	Isoform 2 of Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial		I	441	11	8	2	13
IPI00453473	Histone H4		K	103	23	23	17	19
IPI00009057	Isoform A of Ras GTPase-activating protein-binding protein 2		B, D	482	9	13	3	17
IPI00917358	Uncharacterized protein			480	5	12	15	11
IPI00304435	Protein NipSnap homolog 1		I	284	5	6	1	15
IPI00027996	Isoform 1 of Coronin-7		B, G, D	925	8	5	2	8
IPI00376798	Isoform 1 of 60S ribosomal protein L11	r, g	J, D, I	178	29	37	36	30
IPI00719622	40S ribosomal protein S28	r, g	D	69	9	9	21	35
IPI00177008	Phosphoglycolate phosphatase			321	8	14	4	7
IPI00395887	Thioredoxin-related transmembrane protein 1	p, f	E	280	10	11	19	20
IPI00895852	cellular nucleic acid-binding protein isoform 5			171	3	11	8	16
IPI00019169	cDNA, FLJ96508, Homo sapiens SH3-domain GRB2-like 1 (SH3GL1), mRNA			368	5	8	1	11
IPI00304692	Heterogeneous nuclear ribonucleoprotein G	g	K	391	6	9	2	13
IPI00216057	Sorbitol dehydrogenase		I	357	2	5	11	12

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00032516	AP-1 complex subunit mu-1		G, D	423	10	12	5	9
IPI00298702	Isoform 1 of Zinc transporter ZIP6	h, s	E, L	755	8	12	10	7
IPI00258833	sorting nexin-6 isoform a			290	4	6	4	7
IPI00012313	Golgi phosphoprotein 3-like		B, G	285	10	8	8	5
IPI00027415	Isoform 1 of Probable ATP-dependent RNA helicase DHX36		K, B	1008	11	16	6	12
IPI00218733	Superoxide dismutase [Cu-Zn]		K, J, B, I, D, L	154	9	14	70	62
IPI00296913	ADP-sugar pyrophosphatase			219	10	16	6	8
IPI00219155	60S ribosomal protein L27	r, g	D, I	136	27	26	37	18
IPI00304082	Isochorismatase domain-containing protein 1			298	15	11	14	14
IPI00334282	Protein FAM3C			227	6	8	3	15
IPI00328156	Amine oxidase [flavin-containing] B		I	520	5	10	9	16
IPI00029744	Single-stranded DNA-binding protein, mitochondrial		I	148	2	4	8	11
IPI00644697	HEBP2 protein (Fragment)		B, I	214	3	0	5	13
IPI00001952	Endonuclease domain-containing 1 protein			500	6	3	5	4
IPI00294186	Isoform 1 of Serine beta-lactamase-like protein LACTB, mitochondrial		I	547	6	6	2	4
IPI00045396	Calumenin isoform 4		E, G	323	4	17	9	16
IPI00150269	Isoform 1 of U4/U6 small nuclear ribonucleoprotein Prp4	g	K	522	4	7	6	9
IPI00218850	Secretory carrier-associated membrane protein 2	o	K, J, F, G	329	5	8	10	9
IPI00427330	r maturation protein SBDS		K, J, B	250	9	9	6	6
IPI00218775	Peptidyl-prolyl cis-trans isomerase FKBP5	l	K, B	457	7	10	1	4

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00292059	Nuclear pore complex protein Nup153	o, s	K, J, B	1475	0	1	5	11
IPI00783313	Glycogen phosphorylase, liver form		B, D	847	7	11	6	11
IPI00329600	Probable saccharopine dehydrogenase		I	429	16	17	3	6
IPI00021985	Transmembrane 9 superfamily member 4			642	4	16	1	5
IPI00028618	methylated-DNA--protein-cysteine methyltransferase			238	12	1	11	9
IPI00103064	Isoform 3 of Exocyst complex component 7	o	B, D, L	735	9	11	0	1
IPI00060181	EF-hand domain-containing protein D2			240	13	9	15	19
IPI00163187	Fascin	f	B	493	4	4	6	12
IPI00430812	Isoform 1 of Cellular nucleic acid-binding protein		B, E	177	6	6	4	16
IPI00029048	Tubulin--tyrosine ligase-like protein 12			644	8	6	4	8
IPI00011913	Heterogeneous nuclear ribonucleoprotein A0	g	K	305	2	5	6	10
IPI00306689	Glutamine-dependent NAD(+) synthetase		D	706	9	3	1	6
IPI00000279	Similar to Zinc finger CCCH domain-containing protein 15		K, J, B, L	431	5	6	6	8
IPI00008179	Isoform 1 of Sulfotransferase family cic 2B member 1		B, D	365	10	3	2	12
IPI00008791	Probable cic iron-sulfur protein assembly protein CIAO1			339	3	10	2	9
IPI00008711	Wolframin		E	890	4	5	8	12
IPI00029561	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 10,		I	355	3	6	0	10

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
	mitochondrial							
IPI00217272	Isoform 1 of Acetoacetyl-CoA synthetase		B, D	672	4	8	6	6
IPI00026519	Peptidyl-prolyl cis-trans isomerase F, mitochondrial	l	I	207	3	16	16	9
IPI00026302	60S ribosomal protein L31	r, g	D, I	125	8	4	9	19
IPI00021347	Ubiquitin-conjugating enzyme E2 L3	f	K, B	154	5	1	4	17
IPI00021805	Microsomal glutathione S-transferase 1		K, I, E, H	155	7	13	1	24
IPI00149849	conserved oligomeric Golgi complex subunit 4	o	G	789	10	6	8	5
IPI00307572	Transmembrane protein 165			324	2	2	18	10
IPI00793702	7 kDa protein			57	80	16	84	85
IPI00306280	Density-regulated protein			198	10	25	12	15
IPI00065931	Isoform 2 of A-kinase anchor protein 13	b	K, B, D	2817	3	3	0	4
IPI00025329	60S ribosomal protein L19	r, g	D, I	196	20	38	30	28
IPI00414315	EPS8L2 protein		B	731	3	5	3	7
IPI00184262	Isoform 3 of Epithelial splicing regulatory protein 1		K, J, L	677	4	4	2	5
IPI00293867	D-dopachrome decarboxylase		B	118	11	15	43	34
IPI00005102	Isoform 1 of Spermine synthase		D	366	4	1	6	8
IPI00027443	cysteinyl-tRNA synthetase, cpic isoform c			831	8	5	0	5
IPI00298991	KIAA1033 protein			1174	12	15	4	7
IPI00019385	Translocon-associated protein subunit delta precursor		E	184	9	6	6	15
IPI00107831	Isoform 1 of Receptor-type tyrosine-protein phosphatase F	c	F, H, L	1907	8	2	12	7
IPI00009865	Keratin, type I cytoskeletal 10			584	25	9	31	26

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00640525	lysosomal protective protein isoform a precursor			498	7	13	3	8
IPI00004795	Methylosome subunit pICln		K, B, D, C, L	237	12	8	20	9
IPI00029731	60S ribosomal protein L35a	r, g	D, I	110	12	16	28	23
IPI00218235	dehydrogenase/reductase SDR family member 2 isoform 2		K, B, I	280	7	28	6	9
IPI00003394	Isoform SMN of Survival motor neuron protein		K, B, D	294	5	17	6	4
IPI00024913	Isoform Long of ES1 protein homolog, mitochondrial		I	268	6	1	10	20
IPI00060569	Isoform 2 of Monoacylglycerol lipase ABHD12			404	3	6	5	12
IPI00176593	Uncharacterized protein			395	11	13	17	13
IPI00411426	Vacuolar protein sorting-associated protein 26A		B, F, D	327	7	9	4	10
IPI00017448	40S ribosomal protein S21	r, g	B, D	83	5	8	25	38
IPI00219729	Mitochondrial 2-oxoglutarate/malate carrier protein	s	I	314	6	14	10	12
IPI00247871	Isoform 1 of tc elongation regulator 1		K	1098	7	6	1	6
IPI00254408	Isoform 2 of Nucleosome-remodeling factor subunit BPTF		K, J, B	2920	7	15	4	8
IPI00102997	Isoform 2 of ATPase WRNIP1		K, J, I	640	7	10	6	5
IPI00003377	Isoform 1 of Serine/arginine-rich splicing factor 7	q, g	K	238	5	12	6	13
IPI00013003	Isoform Long of Acetyl-CoA carboxylase 2		B, G, D	2458	9	8	5	7
IPI00002245	Isoform 1 of Acyl-CoA synthetase short-chain family member 3, mitochondrial		I	686	5	6	9	6

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00168165	CLASP2 protein			1515	6	8	9	6
IPI00289601	Histone deacetylase 2		K, B	582	12	4	3	11
IPI00550181	Charged multivesicular body protein 2b	o	K, B, I, F, D	213	18	20	15	23
IPI00015972	Cytochrome c oxidase subunit 6C		I	75	19	19	13	17
IPI00023711	Envoplakin		B	2033	1	3	3	8
IPI00296141	Dipeptidyl peptidase 2		D	492	8	8	5	11
IPI00412499	Isoform 1 of Rab GTPase-binding effector protein 2	o	B	569	4	7	6	15
IPI00187011	Zinc finger CCCH domain-containing protein 4			1303	0	2	10	33
IPI00300659	Parafibromin	q, d	K	531	5	5	4	6
IPI00012750	40S ribosomal protein S25	r, g	J, B, D, I	125	12	23	44	31
IPI00009896	Epoxide hydrolase 1		E, H	455	10	5	1	3
IPI00292499	Heat shock 70 kDa protein 14		D, I	509	5	9	1	4
IPI00294834	Isoform 1 of Aspartyl/asparaginyl beta-hydroxylase		E	758	4	5	1	1
IPI00021389	Copper chaperone for superoxide dismutase		K, B	274	3	11	6	8
IPI00220416	Cytochrome b-c1 complex subunit 7		I	111	16	30	12	20
IPI00016912	Tetratricopeptide repeat protein 1	l		292	7	2	11	17
IPI00301280	Transmembrane protein 43		K, E, G	400	5	8	2	7
IPI00747849	Isoform 1 of Sodium/potassium-transporting ATPase subunit beta-1	s	L, A	303	19	17	2	4
IPI00294159	Tricarboxylate transport protein, mitochondrial	s	I	311	8	12	16	19
IPI00063130	Transmembrane protein 205			189	25	29	23	31

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00289113	Isoform 2 of E3 ubiquitin-protein ligase LRSAM1	o	B	696	3	5	2	10
IPI00219451	Isoform 5 of cic acyl coenzyme A thioester hydrolase		K, J, B, I, D	350	5	7	5	7
IPI00296259	Isoform 1 of Transmembrane emp24 domain-containing protein 4		E	227	9	14	6	7
IPI00002149	GTP-binding protein SAR1b		E, G, D	198	9	5	2	12
IPI00015806	Isoform 1 of General tc factor 3C polypeptide 3	q	K	886	8	7	4	10
IPI00016405	Isoform 1 of OCIA domain-containing protein 1		I, F	245	4	0	4	13
IPI00171412	sulfatase modifying factor 2 isoform b precursor			320	11	3	8	18
IPI00103090	Isoform 1 of RNA polymerase-associated protein LEO1		K	666	9	7	12	8
IPI00004668	Isoform 1 of Alpha-(1,6)-fucosyltransferase		G	575	5	12	3	7
IPI00010414	PDZ and LIM domain protein 1		B, C	329	2	1	4	16
IPI00375358	Isoform 1 of Replication factor C subunit 1	k	K	1148	0	4	1	11
IPI00294840	Absent in melanoma 1 protein			1723	6	3	3	2
IPI00218130	Glycogen phosphorylase, muscle form		B, D	842	7	14	6	9
IPI00181135	Branched-chain-amino-acid aminotransferase		K, B, I	352	3	10	0	2
IPI00549343	Vesicle-associated membrane protein 3	o	H, L	100	12	10	8	17
IPI00021320	7SK snRNA methylphosphate capping enzyme			689	1	5	3	6

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00010700	Isoform 1 of Large proline-rich protein BAT2		K, B	2157	3	2	3	7
IPI00017160	Vacuolar protein sorting-associated protein VTA1 homolog	o	B, F	307	10	11	9	12
IPI00171626	Lysophosphatidylcholine acyltransferase 1	i	E, G	534	4	2	4	7
IPI00333776	Isoform 1 of Neuronal ca molecule		L	1304	7	3	0	7
IPI00291093	DNA-directed RNA polymerases I, II, and III subunit RPABC1	q, g	K	210	9	0	2	8
IPI00008527	60S acidic ribosomal protein P1	r, g	B, D, I	114	39	59	41	11
IPI00413324	60S ribosomal protein L17	r, g	D	184	14	23	23	28
IPI00022431	cDNA FLJ55606, highly similar to Alpha-2-HS-glycoprotein			433	34	42	14	26
IPI00646917	Cleavage and polyadenylation specificity factor subunit 5	q, g	K	227	5	18	6	17
IPI00025869	Alpha-galactosidase A		B, G	429	2	6	2	11
IPI00032903	Peptidyl-tRNA hydrolase 2, mitochondrial	r, b	I	179	0	7	4	12
IPI00293009	Isoform 1 of Rab GTPase-binding effector protein 1	b, o	B	862	1	5	4	8
IPI00220327	Keratin, type II cytoskeletal 1		C, L	644	11	5	3	2
IPI00103654	Isoform 1 of Serine/threonine-protein phosphatase 4 regulatory subunit 2		K, J, B, C	417	24	7	4	9
IPI00028006	Proteasome subunit beta type-2	k, b	K, B	201	15	11	4	19
IPI00409640	Isoform 1 of Lipolysis-stimulated lipoprotein receptor		L	649	3	3	2	9
IPI00642816	Signal recognition particle 9 kDa protein		B, D	86	6	11	6	13

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00419575	Protein of unknown function DUF410 family protein		B, D	328	3	12	5	8
IPI00297910	Tumor-associated calcium signal transducer 2	f	D, L	323	13	7	4	9
IPI00220267	Argininosuccinate lyase		B, D	464	7	6	3	2
IPI00744036	tight junction protein ZO-3		L	952	3	2	0	12
IPI00165026	Isoform 1 of SET domain-containing protein 3			594	4	6	7	22
IPI00015954	GTP-binding protein SAR1a		B, E, G	198	8	9	6	12
IPI00221222	Activated RNA polymerase II tcal coactivator p15		K, J	127	10	8	30	16
IPI00014843	Isoform 1 of Leucine-rich repeat-containing protein 16A		K, B, D	1371	0	4	6	2
IPI00003933	Isoform 1 of Hydroxyacylglutathione hydrolase, mitochondrial		B, I	308	2	3	0	10
IPI00071059	Isoform Epsilon of ap regulator BAX	b	B, I, E, D	164	3	2	4	8
IPI00015944	cDNA FLJ56452, highly similar to Echinoderm microtubule-associated protein-like 2		B, C	815	3	8	5	11
IPI00029469	Beta-centractin		B, C	376	9	19	11	10
IPI00639842	cDNA FLJ56362			582	1	4	15	10
IPI00216393	Isoform Non-brain of Clathrin light chain A		D, L	218	8	12	28	24
IPI00013256	Isoform 1 of Cleavage stimulation factor subunit 2	q, g	K, J	577	2	5	5	9
IPI00009791	Isoform WB of pm calcium-transporting ATPase 2	s	B, E, H, L	1243	6	6	10	13
IPI00221345	Isoform 1 of YTH domain family protein 1			559	9	6	4	7
IPI00029534	Amidophosphoribosyltransfera se		D	517	10	11	5	7

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00016249	Isoform 1 of Fragile X mental retardation syndrome-related protein 1	b, e	K, J, B	621	1	9	2	8
IPI00216132	Isoform Alpha I of Ribosomal protein S6 kinase beta-1	n, d, p	K, B, I, D	525	7	23	3	4
IPI00218918	Annexin A1	d, p	K, B	346	6	4	6	10
IPI00002188	Brefeldin A-inhibited guanine nucleotide-exchange protein 1			1849	3	5	2	3
IPI00219344	Hippocalcin-like protein 1			193	6	2	1	1
IPI00873472	Isoform 1 of pt protein Sec24A		B, E, G, D	1093	5	9	7	7
IPI00178150	Isoform 1 of Chromosome-associated kinesin KIF4A		K, B, D, C	1232	1	0	5	11
IPI00034015	Isoform 1 of CUGBP Elav-like family member 1		K, B	486	7	4	5	9
IPI00005038	Ribonuclease UK114		K, J, B	137	5	5	6	7
IPI00221091	40S ribosomal protein S15a	r, g	B, I, D, I	130	18	24	20	21
IPI00001757	Isoform 1 of RNA-binding protein 8A	q, g	K, J, B, D	174	11	19	10	41
IPI00006034	Cysteine-rich protein 2			208	12	11	14	18
IPI00412607	60S ribosomal protein L35	r, g	J, B, D, I	123	17	20	24	26
IPI00028264	Exocyst complex component 8	o	K, B	725	1	5	5	7
IPI00296022	Cytochrome b-c1 complex subunit 6, mitochondrial		I	91	12	11	31	28
IPI00002408	Isoform 1 of RNA polymerase II-associated protein 3			665	0	6	2	4
IPI00434965	Isoform 2 of ADP-ribosylation factor-like protein 6-interacting protein 4		K	352	36	34	21	28
IPI00070809	Isoform SV1 of Cell division protein kinase 11A	n, b, j	K, B	777	14	10	0	6
IPI00291328	NADH dehydrogenase [ubiquinone] flavoprotein 2, mitochondrial		I	249	2	12	2	6

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00297252	Isoform 1 of Extracellular sulfatase Sulf-2		E, G	870	2	6	3	13
IPI00412147	Long-chain fatty acid transport protein 4	s	E, L	643	4	8	2	6
IPI00306195	Isoform 2 of Proline-rich AKT1 substrate 1		B, D	276	1	5	6	8
IPI00010882	Isoform DFF45 of DNA fragmentation factor subunit alpha (Fragment)	b	K, B, I, D, L	331	1	5	10	8
IPI00016925	Protein C10			126	1	0	8	16
IPI00010182	Isoform 1 of Acyl-CoA-binding protein			87	26	10	21	19
IPI00642705	Isoform 2 of AT-rich interactive domain-containing protein 1A		K, J	2068	4	5	2	4
IPI00154473	Isoform 1 of Elongation factor G, mitochondrial		I	751	7	9	1	3
IPI00307257	Isoform 1 of TBC1 domain family member 9B			1250	3	1	1	12
IPI00000811	Proteasome subunit beta type-6	k, b	K, B	239	10	13	9	25
IPI00183046	Isoform 3 of Tyrosine-protein phosphatase non-receptor type 6	b, p	K, B, D	556	0	2	3	8
IPI00921566	Ankyrin-3	p	B, C	4377	5	2	2	6
IPI00183400	Isoform 1 of Casein kinase I isoform alpha	n, d, j, p	K, B, D, C	337	12	4	3	11
IPI00607814	xaa-Pro aminopeptidase 1 isoform 2		B	642	4	6	1	7
IPI00019148	Immunoglobulin-binding protein 1	p	B	339	0	6	18	9
IPI00556594	Isoform 1 of Zinc finger CCHC domain-containing protein 8			707	2	8	11	8

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00930678	small nuclear ribonucleoprotein Sm D2 isoform 2			108	12	7	11	24
IPI00019353	Isoform 1 of Acylglycerol kinase, mitochondrial	i	I	422	2	5	4	5
IPI00299524	Condensin complex subunit 1	d, j	K, B	1401	7	0	3	4
IPI00455199	Isoform 2 of DnaJ homolog subfamily C member 2		K, B, D	568	6	8	1	2
IPI00376199	Isoform 1 of Interferon regulatory factor 2-binding protein 2		K	587	0	8	4	6
IPI00290462	Carbonyl reductase [NADPH] 3		K, J, B, D	277	10	7	7	15
IPI00297178	119 kDa protein			1041	10	8	10	17
IPI00300567	Isoform 1 of 3,2-trans-enoyl-CoA isomerase, mitochondrial		I	302	6	10	6	4
IPI00022002	cDNA FLJ54536, highly similar to Mitochondrial 28S ribosomal protein S27			428	12	14	8	12
IPI00383046	Carboxymethylenebutenolidase homolog		B, D	245	7	12	5	4
IPI00177890	54 kDa protein			473	4	6	1	3
IPI00007019	Peptidyl-prolyl cis-trans isomerase-like 1	l		166	6	8	8	14
IPI00385631	Isoform 1 of Zinc finger ZZ-type and EF-hand domain-containing protein 1			2961	6	1	4	9
IPI00026625	Isoform 1 of Nuclear pore complex protein Nup155	o, s	K	1391	6	6	1	5
IPI00003819	Isoform 1 of Low affinity cationic amino acid transporter 2	h, s	B, L	658	16	31	3	8
IPI00465054	Putative uncharacterized protein DKFZp686C1054			439	3	8	5	3

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00009010	tRNA methyltransferase 112 homolog			125	3	10	23	12
IPI00141561	Conserved oligomeric Golgi complex subunit 1	o	G	980	4	3	4	5
IPI00023409	Isoform 1 of Regulator of nonsense transcripts 3B	q, g	K, B, D	483	4	0	2	5
IPI00217882	Sortilin	e	K, F, E, H, G, L	831	11	12	26	14
IPI00007347	Isoform 1 of Conserved oligomeric Golgi complex subunit 5	o	K, J, B, G, D	839	6	2	1	7
IPI00024821	26S proteasome non-ATPase regulatory subunit 14	k, b		310	15	13	6	7
IPI00328840	THO complex subunit 4	q, g	K, J, B, D	264	5	11	19	8
IPI00010400	1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase beta-3		D	1234	5	2	4	3
IPI00003168	Phosphoribosyl pyrophosphate synthase-associated protein 2			369	5	13	0	11
IPI00297626	Syntaxin-binding protein 3	o	K, J, B, D, L	592	9	5	4	5
IPI00645702	CTP synthase 2		I, D	586	5	10	8	6
IPI00386271	Calcium-binding mitochondrial carrier protein Aralar1	s	I	678	11	4	3	2
IPI00024934	Methylmalonyl-CoA mutase, mitochondrial		I	750	3	6	3	4
IPI00293735	Elongator complex protein 1	n	K, J, B	1332	2	4	2	5
IPI00337495	Isoform 2 of Procollagen-lysine,2-oxoglutarate 5-dioxygenase 2		E	758	3	6	2	2
IPI00014340	Isoform 1 of Protein phosphatase 1 regulatory subunit 12C		B	782	9	8	5	10
IPI00023530	Cell division protein kinase 5	f	K, B, D, C	292	7	14	5	4

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00022184	Isoform 3 of Pumilio homolog 2		B	1064	0	7	0	7
IPI00399089	LDLR chaperone MESD		E	234	13	25	4	6
IPI00465308	Isoform 1 of GPI transamidase component PIG-S		E	555	0	1	3	3
IPI00026337	Isoform 1 of Ran-binding protein 3	o	K, B	567	6	2	4	4
IPI00215928	Centrin-2	k, j	K, B, D, C	172	7	5	6	9
IPI00030116	cDNA FLJ55543, highly similar to Phosphoacetylglucosamine mutase			570	9	12	5	13
IPI00003128	Isoform IIb of Prolyl 4-hydroxylase subunit alpha-2		E	535	5	8	9	6
IPI00004416	Charged multivesicular body protein 2a	o	F, D	222	4	15	6	15
IPI00012341	Isoform SRP40-1 of Serine/arginine-rich splicing factor 5	q, g	K	272	2	3	17	13
IPI00300127	N-acetyltransferase 10	i	K, J	1025	1	7	0	3
IPI00292020	Spermidine synthase		D	302	5	8	22	14
IPI00045946	Isoform 1 of ATP-dependent zinc metalloprotease YME1L1		I	773	6	2	6	11
IPI00306382	Isoform 1 of Secretory carrier-associated membrane protein 3	o		347	12	12	6	5
IPI00009607	Ras-related protein Rap-2c	p	B, D	183	9	21	8	6
IPI00063408	Probable 2-oxoglutarate dehydrogenase E1 component DHKTD1, mitochondrial		I	919	6	7	4	12
IPI00384745	HSR1 protein			561	2	7	7	9
IPI00021828	Cystatin-B		K, J, B	98	24	25	39	17
IPI00301058	Vasodilator-stimulated phosphoprotein		B, D, L	380	4	8	7	20
IPI00021766	Isoform 1 of Reticulon-4	x, b	B, E, L	1192	15	15	11	6

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00026964	Cytochrome b-c1 complex subunit Rieske, mitochondrial		I	274	6	6	6	7
IPI00167572	Protein FAM98B			330	2	4	3	6
IPI00012382	U1 small nuclear ribonucleoprotein A	g	K	282	5	11	5	10
IPI00062120	Protein S100-A16		K, J, B, D	103	12	14	10	11
IPI00386718	Isoform Short of Probable global tc activator SNF2L2		K, J	1572	6	7	1	7
IPI00100796	Charged multivesicular body protein 5	o	K, B, F, D	219	3	5	17	16
IPI00005179	Isoform 1 of DNA-directed RNA polymerases I and III subunit RPAC1	q	K	346	2	4	3	5
IPI00217841	Isoform 2 of Band 4.1-like protein 5		B, C, L	505	2	2	1	8
IPI00003031	Isoform 2 of Isochorismatase domain-containing protein 2, mitochondrial		K, B, I	221	4	2	8	10
IPI00218606	40S ribosomal protein S23	r, g	D, I	143	8	14	14	12
IPI00032905	Vacuolar protein sorting-associated protein 33B	o	B	617	3	4	4	5
IPI00477355	KIF1-binding protein	e	I	621	9	21	14	15
IPI00470610	Pyrroline-5-carboxylate reductase 2			320	7	5	3	2
IPI00018671	Dual specificity protein phosphatase 3		K, D	185	4	3	4	2
IPI00006713	DnaJ homolog subfamily C member 3	l	B, E	504	20	14	5	5
IPI00033036	Methionine aminopeptidase 2		B	478	7	5	2	8
IPI00748962	Similar to 40S ribosomal protein S11			161	11	6	7	12
IPI00026824	Heme oxygenase 2	s	E, H, L	370	10	6	0	1

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00027285	Isoform SM-B' of Small nuclear ribonucleoprotein-associated proteins B and B'	q, g	K, D	240	4	2	8	18
IPI00026952	Plakophilin-3	c	K	797	3	4	1	12
IPI00328170	Mannosyl-oligosaccharide glucosidase	l	E	837	5	7	1	5
IPI00299977	14 kDa phosphohistidine phosphatase		B, D	125	6	2	25	14
IPI00027448	ATP synthase subunit g, mitochondrial	h	I	103	18	5	24	20
IPI00939720	Baculoviral IAP repeat-containing protein 6	b		4829	8	15	0	6
IPI00012912	Carnitine O-palmitoyltransferase 2, mitochondrial		I	658	7	11	5	1
IPI00005490	Golgi phosphoprotein 3	f	B, I, F, G, D, L	298	5	7	8	9
IPI00003627	Isoform 1 of Actin-like protein 6A	p	K, L	429	10	5	2	4
IPI00022434	Uncharacterized protein			627	45	44	11	42
IPI00297492	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3A		E	705	11	9	10	12
IPI00007722	Adenosine monophosphate deaminase 2			890	7	2	3	2
IPI00002496	Isoform 2 of Mannose-1-phosphate guanyltransferase beta			387	5	10	10	4
IPI00953461	La-related protein 4B			738	4	3	4	10
IPI00027009	Isoform 1 of Protein kinase C and casein kinase substrate in neurons protein 2		B, D	486	10	4	2	9

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00410330	Isoform 1 of tcal repressor p66-alpha		K, J	633	6	8	7	11
IPI00291544	Squalene monooxygenase		E, H	574	2	5	1	5
IPI00162563	Isoform 1 of E3 ubiquitin-protein ligase BRE1B		K	1001	9	15	10	4
IPI00027180	CAAX prenyl protease 1 homolog		E, G	475	12	12	9	12
IPI00251559	E3 ubiquitin-protein ligase BRE1A		K, J	977	4	2	9	8
IPI00016287	Threonine synthase-like 1			743	3	8	3	6
IPI00030098	Protein FAM50A		K	339	4	5	2	0
IPI00019269	WD repeat-containing protein 61			305	2	5	9	8
IPI00179589	14 kDa protein			130	10	13	26	13
IPI00006615	Isoform 1 of Caseinolytic peptidase B protein homolog		I	707	7	3	1	9
IPI00788907	Isoform 1 of Serine/threonine-protein phosphatase PGAM5, mitochondrial		I	289	14	24	10	14
IPI00296099	Thrombospondin-1	b, c		1170	9	5	1	7
IPI00017341	SF3A2 protein (Fragment)	g	K	481	10	6	8	10
IPI00395694	Isoform 2 of Transportin-3	o	K, B	923	0	2	6	11
IPI00292376	GEM-interacting protein		D	970	1	5	3	6
IPI00219160	60S ribosomal protein L34	r, g	D, I	117	7	13	15	19
IPI00012970	Isoform 1 of Serine/threonine-protein phosphatase 6 catalytic subunit	d	B, D	305	0	9	6	5
IPI00101782	Isoform 1 of Mannose-1-phosphate guanyltransferase alpha			420	3	7	2	6
IPI00014263	Isoform Long of Eukaryotic tl initiation factor 4H	r, g	B, D	248	3	6	37	21
IPI00425404	Isoform 1 of Kinesin-like protein KIF21A		B, C	1674	8	0	7	5

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00019966	Isoform 1 of UPF0489 protein C5orf22			442	2	4	2	2
IPI00789454	9 kDa protein			84	10	12	6	9
IPI00647217	Superkiller viralicidic activity 2-like 2		K, J	1042	3	3	5	9
IPI00744637	Isoform 1 of RUN and FYVE domain-containing protein 1	o	B, F	708	2	0	2	9
IPI00154975	DnaJ homolog subfamily C member 9	l		260	4	11	11	7
IPI00218546	Isoform 2 of BAG family molecular chaperone regulator 1		K, B, I, D	311	2	6	2	4
IPI00299193	Synaptojanin-2-binding protein		I	145	4	11	2	5
IPI00180954	Cold-inducible RNA-binding protein		K, B	172	2	2	7	21
IPI00031651	Uncharacterized protein C7orf50			194	11	19	7	22
IPI00300333	Isoform 1 of RNA polymerase II-associated factor 1 homolog		K	531	2	5	4	6
IPI00006702	cDNA FLJ56414, highly similar to Homo sapiens proline-, glutamic acid-, leucine-rich protein 1 (PELP1), mRNA	q	K, B	1180	0	10	2	1
IPI00006103	CD2 antigen cpic tail-binding protein 2	g	K, B	341	3	6	14	10
IPI00005914	Sedoheptulokinase		B	478	4	3	1	11
IPI00922172	cDNA FLJ57598, highly similar to Homo sapiens golgi phosphoprotein 3-like (GOLPH3L), mRNA			241	8	2	3	0
IPI00011996	Isoform 1 of Ubiquitin-conjugating enzyme E2 Z	b	K, J, B	354	7	6	7	26

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00045660	Isoform 1 of Uncharacterized protein C1orf31		I	125	0	0	1	14
IPI00168885	Isoform 1 of Putative ATP-dependent RNA helicase DHX57			1386	1	4	7	5
IPI00165041	TCOF1 protein		K, J	1450	6	1	0	9
IPI00465160	Isoform 1 of ATP-binding cassette sub-family F member 3			709	1	3	8	8
IPI00008483	Amine oxidase [flavin-containing] A		I	527	11	8	4	2
IPI00024660	Isoform 1 of IST1 homolog	d		364	3	6	7	13
IPI00902997	cDNA FLJ33692 fis, clone BRAWH2003000			301	14	15	12	12
IPI00005613	Splicing factor U2AF 35 kDa subunit	q, g	K	240	4	3	6	14
IPI00514301	Isoform 1 of Peripheral pm protein CASK	n, c	K, B, D, L	926	5	9	2	3
IPI00293817	Gamma-soluble NSF attachment protein		I, E, G	312	1	0	7	6
IPI00106913	Isoform 1 of Dehydrogenase/reductase SDR family member 4		I	278	9	9	4	6
IPI00000192	Isoform F of Protein SON		K, J	2426	3	3	8	11
IPI00023086	39S ribosomal protein L15, mitochondrial	r	I	296	3	0	3	5
IPI00018780	Isoform 2 of CDK5 regulatory subunit-associated protein 3			419	2	5	5	11
IPI00013678	Isoform 1 of Metaxin-1	o	I	466	11	9	9	8
IPI00455510	Isoform 2 of Prothymosin alpha	q	K	110	48	70	9	14
IPI00008986	Large neutral amino acids transporter small subunit 1	h, e, s	B, D, L	507	13	20	11	31

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00293434	Signal recognition particle 14 kDa protein		B, D	136	9	5	9	12
IPI00299116	Podocalyxin-like protein 1 precursor			528	4	7	12	22
IPI00646689	Thioredoxin domain-containing protein 17		B, D	123	7	11	23	13
IPI00008418	Diablo homolog, mitochondrial precursor	b	B, I, D	315	7	21	7	16
IPI00456429	Ubiquitin-60S ribosomal protein L40	k, r, b, g	K, B, D, I, L	128	6	16	19	13
IPI00152303	Phosphatidylinositol-5-phosphate 4-kinase type-2 gamma		B	421	1	2	18	12
IPI00419844	U4/U6.U5 tri-snRNP-associated protein 2		K	565	0	3	7	7
IPI00220014	Isoform 2 of Isopentenyl-diphosphate Delta-isomerase 1		I, D	284	9	15	11	11
IPI00964989	Protein			137	19	32	27	45
IPI00465428	Isoform 1 of Vacuolar protein sorting-associated protein 13C	m		3753	0	3	0	5
IPI00329742	Fumarylacetoacetate hydrolase domain-containing protein 2A			314	3	2	1	3
IPI00020944	Squalene synthase		E, H	417	10	11	4	10
IPI00328361	Seryl-tRNA synthetase, mitochondrial	g	B, I	518	2	9	3	13
IPI00166865	CDGSH iron-sulfur domain-containing protein 2		I, E	135	3	9	3	3
IPI00018272	Pyridoxine-5'-phosphate oxidase		D	261	10	9	18	6
IPI00384282	Cytovillin 2 (Fragment)			141	7	12	10	7
IPI00332097	Isoform 4 of Breast carcinoma-amplified sequence 3		K	965	1	1	2	6

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00029400	Isoform 1 of Zinc finger Ran-binding domain-containing protein 2		K	330	14	23	0	2
IPI00554590	Isoform 1 of Rab3 GTPase-activating protein non-catalytic subunit		B	1393	3	2	2	7
IPI00152510	ATP-dependent RNA helicase DDX54 isoform 1		K, J	882	2	5	7	8
IPI00007321	cDNA FLJ60607, highly similar to Acyl-protein thioesterase 1			263	2	6	4	17
IPI00023780	Isoform 2 of DnaJ homolog subfamily C member 5	l	L	167	7	9	2	2
IPI00028083	tl initiation factor eIF-2B subunit beta	r, g	B, D	351	7	5	8	6
IPI00305374	Isoform 1 of THO complex subunit 1	b, p	K, J, B	657	16	16	0	4
IPI00163230	COP9 signalosome complex subunit 6		K, B	327	8	7	0	8
IPI00413587	Isoform 1 of BH3-interacting domain death agonist	b	B, I, D	195	5	8	16	23
IPI00178953	Isoform 4 of Zinc finger protein 638		K, B	1139	3	10	6	9
IPI00418497	Isoform 2 of Mitochondrial import inner membrane translocase subunit TIM50	o, s	K, I	456	5	4	7	10
IPI00002432	Isoform 1 of Protein Hook homolog 2	o	B, C	719	1	1	7	6
IPI00916739	Elongation factor Ts			169	6	8	1	3
IPI00219153	60S ribosomal protein L22	r, g	B, D, I	128	13	13	12	17
IPI00217661	ribonucleoprotein PTB-binding 1		K, B	756	4	4	2	6

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00018627	Isoform 1 of N-alpha-acetyltransferase 50, NatE catalytic subunit	i	B	169	9	6	2	8
IPI00010865	Casein kinase II subunit beta	p	B, D, L	215	2	8	3	16
IPI00220797	Isoform 2 of Alpha-endosulfine		B	117	5	9	9	17
IPI00006052	Prefoldin subunit 2	l		154	6	8	23	12
IPI00013306	Isoform 1 of Glycerophosphodiester phosphodiesterase domain-containing protein 3			318	8	8	3	7
IPI00550968	cDNA FLJ38504 fis, clone HCHON2000156, highly similar to Mortality factor 4-like protein 1			348	4	5	1	10
IPI00005737	Isoform 1 of Surfeit locus protein 4		E, G	269	7	3	4	4
IPI00011274	Isoform 1 of Heterogeneous nuclear ribonucleoprotein D-like		K, B	420	5	11	6	12
IPI00015897	Isoform 1 of Cysteine and histidine-rich domain-containing protein 1			332	3	4	2	5
IPI00025049	Cation-dependent mannose-6-phosphate receptor		F	277	2	4	6	6
IPI00026829	Isoform Long of Deoxyhypusine synthase	r	D	369	3	3	0	5
IPI00217519	Ras-related protein Ral-A	d, p	D, L	206	8	5	2	16
IPI00031982	Isoform 1 of Nck-associated protein 1	b	L	1128	4	4	3	4
IPI00783781	Nuclear pore complex protein Nup205	o, s	K	2012	4	3	3	10
IPI00005511	PHD finger-like domain-containing protein 5A	g	K	110	2	5	4	17

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00002894	DNA polymerase delta catalytic subunit	k	K	1107	7	11	5	4
IPI00414860	60S ribosomal protein L37a	r, g	D, I	92	23	24	30	41
IPI00023647	Isoform 1 of Ubiquitin-like modifier-activating enzyme 6		B	1052	2	8	0	2
IPI00296353	Isoform 1 of Rho GTPase-activating protein 18	p	D	663	2	9	2	4
IPI00014311	cDNA FLJ56037, highly similar to Cullin-2			764	3	10	7	5
IPI00170692	Isoform 1 of Vesicle-associated membrane protein-associated protein A		E, L	249	2	9	4	8
IPI00100329	Isoform 1 of Inositol-tetrakisphosphate 1-kinase	p	D	414	9	3	7	5
IPI00166749	Mitochondrial-processing peptidase subunit alpha		I	525	6	3	3	20
IPI00002853	Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit epsilon isoform	p	B	467	1	0	1	6
IPI00005605	Isoform 1 of Protein NDRG3	e	B	375	5	6	6	4
IPI00374054	Isoform 2 of Protein enabled homolog		B, D, C	570	8	4	2	7
IPI00030351	Isoform 1 of Disks large homolog 1		E, D, L	904	3	9	1	7
IPI00181391	bifunctional protein NCOAT isoform b			863	6	3	4	12
IPI00005658	Ubiquitin-like protein 4A		B, D	157	4	2	3	16
IPI00305304	LAG1 longevity assurance homolog 2		K, E	380	4	12	9	1
IPI00026182	F-actin-capping protein subunit alpha-2		B, D	286	10	10	10	9
IPI00010402	Putative uncharacterized protein			226	17	43	21	27

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00419791	Isoform 1 of Arginine/serine-rich coiled-coil protein 2			434	3	5	4	12
IPI00014137	Isoform 1 of Oxysterol-binding protein-related protein 2			480	3	4	3	0
IPI00019903	tlal activator of cytochrome c oxidase 1		I	297	11	16	6	12
IPI00007926	Deoxyribonucleoside 5'-monophosphate N-glycosidase	i, f	K, J, B	174	5	10	12	12
IPI00062336	Isoform 2 of Regulation of nuclear pre-mRNA domain-containing protein 1A			289	3	2	10	14
IPI00301561	Thyroid receptor-interacting protein 6	c	K, B, C	476	1	3	1	11
IPI00024976	Mitochondrial import receptor subunit TOM22 homolog	s	I	142	7	5	8	6
IPI00009634	Sulfide:quinone oxidoreductase, mitochondrial		B, I	450	1	5	1	8
IPI00019205	Enhanced at puberty protein 1		K	796	0	1	0	7
IPI00001754	Junctional adhesion molecule A	c	L	299	0	2	1	7
IPI00007818	Cleavage and polyadenylation specificity factor subunit 3	q, g	K	684	8	3	7	9
IPI00009070	Isoform 1 of HBS1-like protein	r, p		684	1	3	1	3
IPI00029695	Isoform A of SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily B member 1	d	K, J	385	3	9	2	0
IPI00029175	WASH complex subunit strumpellin			1159	5	7	2	0
IPI00006438	Isoform 1 of er-Golgi intermediate compartment protein 3		E, G	383	5	6	2	6

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00295741	Cathepsin B		B, I, A	339	9	7	4	7
IPI00029264	Cytochrome c1, heme protein, mitochondrial		B, I	325	9	16	25	14
IPI00871620	Isoform RMO1-RAPH1 of Ras-associated and pleckstrin homology domains-containing protein 1	p	K, B, C, L	1250	0	2	4	4
IPI00017450	General tc factor IIF subunit 1	q, g	K	517	3	4	7	8
IPI00029444	UPF0160 protein MYG1, mitochondrial		K, I	376	6	2	2	6
IPI00014264	Arf-GAP with coiled-coil, ANK repeat and PH domain-containing protein 2			778	11	14	0	3
IPI00030207	GDP-mannose 4,6 dehydratase		B	372	9	5	0	4
IPI00329625	cDNA FLJ56153, highly similar to Homo sapiens transforming growth factor beta regulator 4 (TBRG4), transcript variant 1, mRNA			642	4	4	7	12
IPI00006952	Beta-lactamase-like protein 2			288	4	9	6	5
IPI00419531	Cleavage and polyadenylation specificity factor subunit 2	q, g	K	782	6	2	3	1
IPI00302458	Exportin-7	s	K, B	1087	6	3	2	4
IPI00016007	Myosin-Vc			1742	5	1	0	3
IPI00784324	Isoform 1 of Synaptotagmin-like protein 2		B, L	934	8	1	2	11
IPI00010214	Protein S100-A14		B, L	104	8	10	13	21
IPI00877817	P40			338	5	4	2	8
IPI00006957	Isoform 1 of Dehydrogenase/reductase SDR family member 7			339	3	4	0	1
IPI00013455	Isoform 1 of CAP-Gly domain-containing linker protein 1	k, j	B, F, D	1438	0	2	7	10

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00103925	Immunity-related GTPase family Q protein			623	24	17	13	37
IPI00216048	Phosphatidylinositol transfer protein alpha isoform		B	270	5	0	6	8
IPI00554811	Actin-related protein 2/3 complex subunit 4		B, C	168	7	12	3	7
IPI00038378	Isoform 1 of Enolase-phosphatase E1		K, B	261	2	5	3	6
IPI00644708	nucleolysin TIAR isoform 2			392	6	5	3	12
IPI00871617	Isoform 1 of Lys-63-specific deubiquitinase BRCC36		K	291	7	3	6	1
IPI00032831	Synaptosomal-associated protein 29	o	K, J, B, L	258	2	2	9	14
IPI00218847	Isoform 2 of Low molecular weight phosphotyrosine protein phosphatase		K, B	158	6	7	6	3
IPI00167515	Isoform 1 of Prostaglandin reductase 2		B, I	351	4	1	4	5
IPI00217872	Isoform 2 of Phosphoglucomutase-1		B, D	580	3	6	1	7
IPI00157144	glycogen [starch] synthase, muscle isoform 2			673	5	24	3	4
IPI00917650	family with sequence similarity 38, member A	h	E, L	2521	2	2	6	5
IPI00016932	Isoform 1 of Phosphatidylinositol-3,4,5-trisphosphate 5-phosphatase 2	c	B, D, C, L	1258	5	3	2	7
IPI00942338	Uncharacterized protein			418	81	15	45	66
IPI00029266	Small nuclear ribonucleoprotein E	q, g	K, D	92	0	16	8	8
IPI00045511	Isoform 1 of Chloride channel CLIC-like protein 1		K, B, E, H, G	551	1	2	0	12
IPI00298935	Isoform 1 of Lysine-specific demethylase 3B		K, J	1761	1	4	3	10

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00180154	Isoform 1 of Ataxin-2		K, J, B, G	1313	2	1	3	3
IPI00009322	115 kDa protein			1000	8	2	7	5
IPI00303832	RNA polymerase-associated protein RTF1 homolog		K, J	710	1	8	3	3
IPI00021785	Cytochrome c oxidase subunit 5B, mitochondrial		I	129	4	10	1	6
IPI00643720	2-oxoglutarate dehydrogenase-like, mitochondrial		I	1010	7	4	2	5
IPI00294739	Isoform 1 of SAM domain and HD domain-containing protein 1		K	626	2	1	3	5
IPI00293078	Probable ATP-dependent RNA helicase DDX27		K	796	1	5	1	4
IPI00217950	Non-histone chromosomal protein HMG-17		K, B	90	0	0	30	16
IPI00044761	Pseudouridylate synthase 7 homolog			661	5	3	3	6
IPI00022283	Trefoil factor 1			84	43	18	35	46
IPI00010346	Neurolysin, mitochondrial		B, I	704	8	8	8	8
IPI00004397	cDNA FLJ55177, highly similar to Ras-related protein Ral-B	b, d, p	D, L	228	7	5	0	12
IPI00012440	Plasma alpha-L-fucosidase			467	2	2	1	7
IPI00217766	Lysosome membrane protein 2	c		478	2	5	1	5
IPI00024623	Short/branched chain specific acyl-CoA dehydrogenase, mitochondrial		I	432	8	7	1	5
IPI00234252	SWI/SNF complex subunit SMARCC1		K, J	1105	5	6	0	2
IPI00022018	Dolichol-phosphate mannosyltransferase		E	260	10	13	2	2
IPI00028412	Sjoegren syndrome/scleroderma autoantigen 1	d, j		199	0	0	2	7

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00003588	Eukaryotic tl elongation factor 1 epsilon-1	g	K, J, B, D	174	2	17	2	2
IPI00300096	Ras-related protein Rab-35	m, o	L	201	14	20	14	15
IPI00018452	Copine-1			537	0	2	1	5
IPI00549189	Thimet oligopeptidase		B	689	4	5	2	3
IPI00034159	V-type proton ATPase subunit d 1	h, s		351	10	10	4	14
IPI00220993	Isoform CNPI of 2',3'-cyclic-nucleotide 3'-phosphodiesterase		B	401	3	1	3	5
IPI00293946	UBX domain-containing protein 4		K, E	508	4	3	5	9
IPI00026970	FACT complex subunit SPT16	q, g	K	1047	4	9	2	2
IPI00300052	Keratin, type II cuticular Hb4			600	201	128	171	166
IPI00844214	Isoform 1 of Beta-catenin-like protein 1		K, J	563	12	14	0	6
IPI00221354	Isoform Short of RNA-binding protein FUS	g	K, J, B	525	8	8	2	1
IPI00102128	Isoform 1 of Protein arginine N-methyltransferase 6		K, B	375	2	4	4	6
IPI00014481	Angio-associated migratory cell protein	x, e	B, L	434	0	2	5	8
IPI00016373	Ras-related protein Rab-13	c, o	B, G, L	203	20	9	2	9
IPI00011662	Kunitz-type protease inhibitor 2		B	252	6	11	6	6
IPI00300086	Nicotinate-nucleotide pyrophosphorylase [carboxylating]		B, D	297	21	16	7	6
IPI00032851	Coatomer subunit zeta-1		B, G, D	177	4	6	3	8
IPI00002535	Peptidyl-prolyl cis-trans isomerase FKBP2	l	E	142	3	9	4	7
IPI00003635	cDNA FLJ56280, highly similar to er-Golgi intermediate compartment		E, G	235	6	4	4	3

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
	protein 1							
IPI00170786	WW domain-binding protein 11		K, B	641	4	1	2	10
IPI00647163	Isoform 2 of tc elongation factor A protein-like 4		K	358	0	5	3	9
IPI00291608	Isoform 1 of PEST proteolytic signal-containing nuclear protein	d	K	178	2	5	6	17
IPI00170972	UPF0553 protein C9orf64			341	1	4	1	3
IPI00180386	Isoform GN-1L of Glycogenin-1		D	350	6	5	3	5
IPI00641924	28S ribosomal protein S9, mitochondrial	r	I, I	396	3	3	4	7
IPI00216237	60S ribosomal protein L36	r, g	J, D, I	105	14	9	4	20
IPI00296191	Isoform 1 of V-type proton ATPase subunit H	h, s	D, L	483	1	4	5	3
IPI00746004	40S ribosomal protein S27-like	r	K, I	84	10	23	14	9
IPI00103247	Isoform 1 of Heterogeneous nuclear ribonucleoprotein L-like		K	542	6	6	2	0
IPI00004310	Ly6/PLAUR domain-containing protein 3		L	346	3	6	2	2
IPI00328987	Bystin	c	K, J, B	437	6	3	9	7
IPI00332511	Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B alpha isoform	p		447	6	9	5	12
IPI00019906	Isoform 2 of Basigin		I, L	269	7	10	9	14
IPI00455518	MORC family CW-type zinc finger protein 2			1032	13	11	8	0
IPI00009111	Trophoblast glycoprotein	c	B, E	420	0	0	2	12

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00301051	Isoform 1 of NHL repeat-containing protein 2			726	6	7	5	2
IPI00102896	Ras-related protein Rab-2B	o	E, G, L	216	8	7	6	7
IPI00028122	Isoform 1 of PC4 and SFRS1-interacting protein		K, J, D	530	7	6	0	2
IPI00018768	Translin		K, B	228	6	2	5	2
IPI00873518	MAD1 mitotic arrest deficient-like 1			804	1	0	3	5
IPI00027809	serine/threonine-protein phosphatase 2B catalytic subunit beta isoform isoform a			525	5	3	6	10
IPI00165528	Isoform 2 of Ubiquitin carboxyl-terminal hydrolase 47			1287	3	6	3	3
IPI00303722	Protein FAM136A		B, I	138	5	2	2	4
IPI00011250	Ubiquitin carboxyl-terminal hydrolase isozyme L3		B	230	1	2	6	1
IPI00025729	Calcium signal-modulating cyclophilin ligand	p	E	296	3	2	0	1
IPI00004958	cDNA FLJ55986			519	10	14	11	8
IPI00745105	Isoform 1 of UPF0585 protein C16orf13			204	3	4	3	4
IPI00063784	Isoform Long of Vesicle transport through interaction with t-SNAREs homolog 1B	f	G	232	3	1	2	7
IPI00001589	Mitochondrial import inner membrane translocase subunit Tim13	o, s	I	95	0	0	5	7
IPI00216654	Isoform Beta of Nucleolar and coiled-body phosphoprotein 1	d, j	K, J, B	709	7	18	2	3
IPI00644297	helicase SKI2W			1246	4	4	2	4
IPI00006442	Coilin		K, J	576	4	2	6	6
IPI00003802	Alpha-mannosidase 2		G	1144	7	4	0	0
IPI00815770	Isoform 1 of Sorting nexin-3	o	B	162	6	14	8	8

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00016670	RhoA activator C11orf59		F, G, L	161	0	2	3	9
IPI00376229	Isoform 1 of Phosphofurin acidic cluster sorting protein 1		G, D	963	1	2	3	9
IPI00019733	mRNA export factor	s	K, B, C	368	4	5	0	4
IPI00329332	Syntaxin-12		G	276	7	8	3	5
IPI00179757	Kinesin-like protein KIF1C		B, E, G, C	1103	1	4	1	7
IPI00412415	Isoform 1 of Bromodomain adjacent to zinc finger domain protein 1A		K	1556	7	2	5	2
IPI00027505	Isoform 1 of Integrin alpha-V	c	L	1048	7	4	0	4
IPI00241841	Keratin, type II cytoskeletal 79			535	140	98	117	102
IPI00291016	Isoform 2 of NADH dehydrogenase [ubiquinone] flavoprotein 3, mitochondrial		K, J, B, I	473	0	1	2	6
IPI00375631	Ubiquitin-like protein ISG15		B, D	165	10	27	18	15
IPI00024701	Isoform 1 of Collagen type IV alpha-3-binding protein	n, p, f	B, I, E, G, D	624	6	15	9	12
IPI00008219	UV excision repair protein RAD23 homolog A		K	363	4	19	2	10
IPI00329236	Protein kinase C delta type	n, b, p	K, B, E, D, L	676	3	6	5	2
IPI00007731	Isoform 1 of BAG family molecular chaperone regulator 5	l, b		447	0	4	4	7
IPI00647099	ATPase, Na+/K+ transporting, alpha 4 polypeptide			477	6	7	5	7
IPI00014808	Platelet-activating factor acetylhydrolase IB subunit gamma		B	231	12	6	4	8
IPI00023001	Protein FAM162A			154	6	7	3	4
IPI00301021	Isoform 1 of Translocon-associated protein subunit alpha		E	286	5	6	3	6

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00783302	Isoform 1 of Pentatricopeptide repeat-containing protein 3, mitochondrial		I	689	3	14	5	8
IPI00554649	Isoform 1 of Cysteine protease ATG4B	o	B	393	6	6	2	3
IPI00026670	tc elongation factor B polypeptide 2	q, g	K, D	118	17	25	13	20
IPI00106687	Latexin		B	222	30	19	12	30
IPI00016634	Protein C20orf11		K	228	3	5	4	2
IPI00013623	Isoform 1 of Long-chain fatty acid transport protein 3		I	811	5	3	3	3
IPI00328798	Isoform 1 of B-cell CLL/lymphoma 9-like protein		K	1499	2	1	6	9
IPI00014376	ras-related protein Rab-31	o	L	195	9	3	1	6
IPI00022239	Methionine aminopeptidase 1		B	386	7	1	11	13
IPI00031526	Uncharacterized protein C19orf43			176	3	9	2	5
IPI00884105	Lysosome-associated membrane glycoprotein 1			417	2	5	12	13
IPI00026219	Cleavage and polyadenylation specificity factor subunit 1	q, g	K	1443	4	4	5	4
IPI00021978	Peroxisomal membrane protein 11B	p	I	259	2	4	1	5
IPI00007673	Coiled-coil-helix-coiled-coil-helix domain-containing protein 2, mitochondrial		I	151	7	8	15	6
IPI00169430	Isoform 1 of Spermatid perinuclear RNA-binding protein	e	K, B	672	3	4	0	0
IPI00006907	Probable fructose-2,6-bisphosphatase TIGAR			270	6	14	5	2
IPI00010368	Isoform 1 of Kinesin-like protein KIF2A	k, e	B, D, C	686	6	5	2	8

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00025341	D-beta-hydroxybutyrate dehydrogenase, mitochondrial	i	I	343	2	7	1	4
IPI00796237	DUSP3 protein			144	2	4	1	2
IPI00334715	Isoform 1 of Glucocorticoid receptor DNA-binding factor 1	q, p	K, B, D	1513	0	8	7	7
IPI00013976	Laminin subunit beta-1	c		1786	0	6	2	6
IPI00012834	Isoform Gamma-3 of Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit gamma isoform	p	K	524	2	3	2	7
IPI00169400	Isoform 1 of 28S ribosomal protein S5, mitochondrial	r	I, I	430	7	4	4	5
IPI00011875	Protein Red		K	557	4	5	12	14
IPI00103599	BRI3-binding protein		I	251	7	10	4	6
IPI00872048	Ataxin 3 variant ref			370	2	2	4	6
IPI00760554	HLA class I histocompatibility antigen, A-69 alpha chain			365	9	16	10	13
IPI00024871	Isoform 2 of Core-binding factor subunit beta		K	187	3	5	3	4
IPI00748145	Isoform 1 of Guanine nucleotide-binding protein G(i) subunit alpha-2	p	K, D, L	355	7	11	1	6
IPI00103497	Isoform 1 of Splicing factor, arginine/serine-rich 12		K	508	0	0	2	4
IPI00005634	Tetratricopeptide repeat protein 37			1564	2	2	3	4
IPI00382979	Isoform 2 of DDB1- and CUL4-associated factor 5		I	860	4	2	0	2
IPI00013698	N-acylsphingosine amidohydrolase (Acid ceramidase) 1, isoform CRA_c			546	1	10	4	8

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00219682	Erythrocyte band 7 integral membrane protein		C, L	288	3	5	1	3
IPI00305289	Kinesin-like protein KIF11	d, j	B, D, C	1056	4	4	4	4
IPI00742996	RING finger protein 214			703	0	3	0	9
IPI00295889	Signal recognition particle 19 kDa protein		K, J, B, I, D	144	4	9	4	3
IPI00031521	Replication factor C subunit 3	k	K	356	5	4	1	7
IPI00215687	Isoform 3 of Glutaminase kidney isoform, mitochondrial		I	598	5	1	3	9
IPI00220710	Isoform 1 of Acyl-coenzyme A thioesterase 9, mitochondrial		I	439	6	0	1	4
IPI00030911	Vesicle-associated membrane protein 8		I, L	100	4	5	5	14
IPI00029056	Selenide, water dikinase 1			392	2	10	13	7
IPI00410287	Isoform 2 of 5'-AMP-activated protein kinase catalytic subunit alpha-1	n, p	D	574	11	7	4	13
IPI00002424	Pleckstrin homology domain-containing family F member 2			249	5	2	5	4
IPI00029819	Neurogenic locus notch homolog protein 3	g	K, D, L	2321	2	3	2	8
IPI00000728	Isoform 1 of Ubiquitin carboxyl-terminal hydrolase 15			981	0	4	2	6
IPI00012493	40S ribosomal protein S20	r, g	B, D	119	12	16	24	17
IPI00013830	SNW domain-containing protein 1	g	K, J	536	0	1	7	8
IPI00292894	Pre-rRNA-processing protein TSR1 homolog		K, J	804	3	0	4	5
IPI00396218	SCY1-like protein 2	n	B, F, G	929	1	3	0	2
IPI00008787	Alpha-N-acetylglucosaminidase	i		743	2	3	7	6

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00921849	cDNA FLJ57046, highly similar to Lysosomal alpha-glucosidase			644	7	4	2	11
IPI00005631	Isoform 1 of GRIP and coiled-coil domain-containing protein 2	o	B, G	1583	0	3	0	7
IPI00026111	Isoform 1 of Transmembrane and coiled-coil domain-containing protein 1		E, G	188	12	8	4	13
IPI00030847	Transmembrane 9 superfamily member 3			589	6	7	0	7
IPI00295772	lanosterol 14-alpha demethylase isoform 1		E, H	509	2	8	0	6
IPI00012895	Isoform 1 of Carbonic anhydrase 12			354	0	7	1	7
IPI00867672	Uncharacterized protein			266	2	3	8	9
IPI00004977	Isoform 3 of Guanine nucleotide exchange factor VAV2	x, b, p	B, D, L	839	3	5	4	9
IPI00056357	UPF0556 protein C19orf10			173	6	9	9	12
IPI00430472	Activating signal cointegrator 1 complex subunit 3		B	2202	4	3	5	5
IPI00305438	Isoform 1 of Vacuolar protein sorting-associated protein 16 homolog		B	839	1	3	6	7
IPI00165434	YLP motif-containing protein 1			2146	0	0	3	8
IPI00081836	Histone H2A type 1-H		K	128	20	33	28	14
IPI00333763	Glutaredoxin-related protein 5, mitochondrial		I	157	2	5	16	3
IPI00032406	DnaJ homolog subfamily A member 2	l		412	2	9	2	5
IPI00301419	COP9 signalosome complex subunit 7a		K, J, B	275	5	10	0	7
IPI00182469	Isoform 1AB of Catenin delta-	c	K, B, D, L	962	8	4	1	7

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
	1							
IPI00296078	Isoform 1 of Zinc finger tc factor Trps1		K	1281	0	1	0	5
IPI00032374	Isoform 2 of Ribosomal RNA processing protein 1 homolog B		K, J, D	740	0	5	3	3
IPI00006362	Isoform 2 of Endothelial differentiation-related factor 1	e	K, J, B	139	5	4	7	12
IPI00026320	E3 ubiquitin-protein ligase UBR5	f	K	2799	0	0	2	6
IPI00014310	Cullin-1	k, b	D	776	5	6	6	7
IPI00396131	cDNA FLJ56221, highly similar to YTH domain protein 3			588	7	6	5	9
IPI00024502	Ubiquilin-4		K, B, E, D	601	1	0	0	10
IPI00018278	Histone H2A.V		K	128	12	25	20	15
IPI00005045	ATP-binding cassette sub-family F member 2		I	623	5	2	3	6
IPI00180240	Thymosin beta-4-like protein 3		B, C	44	14	16	39	122
IPI00216516	Isoform OA3-312 of Leukocyte surface antigen CD47	c	L	312	6	6	3	7
IPI00010717	Mevalonate kinase	i	B, D	396	2	6	2	0
IPI00009146	TRAF-type zinc finger domain-containing protein 1			582	4	1	4	9
IPI00001985	Isoform 1 of Vacuolar protein sorting-associated protein 18 homolog	o		973	6	6	2	4
IPI00029267	U2 small nuclear ribonucleoprotein B"	g	K	225	0	5	4	5
IPI00219617	Isoform 1 of Ribose-phosphate pyrophosphokinase 2			318	5	6	10	8
IPI00302850	Small nuclear ribonucleoprotein Sm D1	g	K, B, D	119	12	1	7	12

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00009480	COP9 signalosome complex subunit 8		K, B	209	2	9	4	4
IPI00016763	Putative GTP-binding protein 6			516	6	5	6	3
IPI00549970	Growth hormone inducible transmembrane protein			325	9	1	1	22
IPI00027485	Eukaryotic tl initiation factor 4E	r, g	B, D	217	10	15	2	6
IPI00797279	E3 ubiquitin-protein ligase UHRF1 isoform 2			806	5	4	0	0
IPI00016568	Adenylate kinase isoenzyme 4, mitochondrial		I	223	9	2	2	1
IPI00012497	Beta-adrenergic receptor kinase 1		B, D, L, A	689	1	4	0	3
IPI00007756	Ras-related protein Rab-22A	o	L	194	7	5	3	3
IPI00028366	Histone-lysine N-methyltransferase SETD7		K	366	2	0	1	10
IPI00019025	Partitioning defective 6 homolog beta	d	K, B, D, L	372	2	3	3	1
IPI00655650	40S ribosomal protein S26	r, g	D	115	12	6	16	8
IPI00170596	Paired amphipathic helix protein Sin3a		K, J	1273	5	9	3	0
IPI00186721	Isoform 1 of Golgi-associated PDZ and coiled-coil motif-containing protein	o	B, G, L	462	0	4	4	4
IPI00402008	103 kDa protein			943	3	2	0	6
IPI00217413	ATP-dependent RNA helicase DHX29	r	B, I	1369	3	6	20	3
IPI00021536	Calmodulin-like protein 5	p		146	2	5	3	10
IPI00414554	Actin-related protein 2/3 complex subunit 5-like protein		B, C	153	8	6	6	2
IPI00178431	ATP-dependent DNA helicase Q1		K	649	0	2	5	17

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00218292	Isoform Short of Ubiquitin fusion degradation protein 1 homolog		K, B, D	307	4	12	6	5
IPI00028376	Mitochondrial import inner membrane translocase subunit Tim8 A	o, s	I	97	4	1	6	12
IPI00000190	CD81 antigen	m, f	L	236	1	2	13	7
IPI00011635	Isoform 2 of Bcl-2-like protein 13		K, I	485	6	9	1	2
IPI00014319	Influenza virus NS1A-binding protein		K, B, C	642	2	2	0	10
IPI00013877	Isoform 1 of Heterogeneous nuclear ribonucleoprotein H3		K	346	3	0	2	8
IPI00029665	Cob(I)yrinic acid a,c-diamide adenosyltransferase, mitochondrial		I	250	5	9	3	4
IPI00011998	breast cancer anti-estrogen resistance protein 1 isoform 4			888	2	3	6	6
IPI00549381	39S ribosomal protein L1, mitochondrial	r	I	325	6	6	2	3
IPI00104128	Signal peptidase complex catalytic subunit SEC11A		E, H	179	4	5	0	1
IPI00106698	Protein pelota homolog	r, d, f	K, B	385	1	1	9	6
IPI00220150	Isocitrate dehydrogenase [NAD] subunit gamma, mitochondrial		K, J, I	393	2	5	1	3
IPI00103142	NudC domain-containing protein 2			157	0	6	2	5
IPI00022265	Coiled-coil domain-containing protein 22			627	6	0	0	0
IPI00005740	Neighbor of COX4		K, B, I	210	5	4	5	4
IPI00181504	UBR7 protein			361	10	11	9	11
IPI00015838	Cell growth-regulating nucleolar protein		K, J	379	3	8	0	0

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00334159	von Hippel-Lindau binding protein 1, isoform CRA_b	l	K, B	233	12	8	15	10
IPI00553131	UDP-glucose 4-epimerase		D	348	4	6	4	2
IPI00855873	Isoform 1 of Transmembrane protein 192		K, B, G	271	0	3	2	2
IPI00101987	Isoform 1 of BRCA1-A complex subunit MERIT40		K, B	329	2	11	5	8
IPI00023728	Gamma-glutamyl hydrolase		D	318	8	3	4	5
IPI00479905	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 10		I	172	7	10	6	11
IPI00182293	Guanylate kinase		D	197	2	3	3	5
IPI00253281	Isoform 2 of Epidermal growth factor receptor kinase substrate 8-like protein 1		B	596	4	7	5	8
IPI00013396	U1 small nuclear ribonucleoprotein C		K	159	0	0	8	15
IPI00290337	Epidermal growth factor receptor kinase substrate 8	p, f		822	0	1	1	4
IPI00024523	Isoform A of DnaJ homolog subfamily B member 6	l	K, J, B	326	0	3	4	6
IPI00033143	Eukaryotic tl initiation factor 3 subunit K	r, g	K, B, D	218	6	8	0	3
IPI00002804	Serine/threonine-protein kinase N2	n, p	K, B	984	4	3	3	3
IPI00181702	Isoform 1 of Splicing factor, arginine/serine-rich 15		K, J	1147	6	5	4	0
IPI00009305	Glucosamine-6-phosphate isomerase 1		B	289	2	5	2	3
IPI00017669	Isoform 1 of SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily E member 1		K, J	411	2	6	2	11

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00414612	Isoform 1 of Putative hexokinase HKDC1		K, J, I	917	8	7	1	6
IPI00152182	Isoform 1 of Kelch domain-containing protein 4			520	4	5	4	5
IPI00294911	Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial		I	280	1	3	11	14
IPI00017381	Replication factor C subunit 4	k	K	363	3	0	4	2
IPI00152898	Isoform 1 of AP-1 complex subunit sigma-1A		G, D	158	15	18	18	11
IPI00604527	Threonyl-tRNA synthetase, mitochondrial	g	B, I	718	7	0	0	6
IPI00024320	Putative RNA-binding protein 3		K, B	157	0	0	1	12
IPI00654731	Isoform 1 of Probable ATP-dependent RNA helicase DDX58		B, D	925	2	4	0	0
IPI00746412	Isoform 1 of SRSF2-interacting protein		K	1463	5	5	0	1
IPI00646963	Uncharacterized protein			211	7	4	0	7
IPI00328932	Isoform 1 of Vacuolar protein-sorting-associated protein 36	o	K, B	386	5	10	4	7
IPI00019226	Isoform 1 of Bromodomain-containing protein 8	p	K, J, I	1235	6	6	5	3
IPI00438170	Isoform 1 of Sorting nexin-12	o		172	6	8	7	5
IPI00433576	Hepatocellular carcinoma-associated antigen 59			196	0	0	8	7
IPI00375527	inosine-5'-monophosphate dehydrogenase 1 isoform a			599	3	1	3	7
IPI00335541	Isoform 1 of Protein timeless homolog	d, j	K	1208	10	8	2	3

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00023532	cDNA FLJ59751, weakly similar to Mus musculus spermatogenesis associated, serine-rich 2 (Spats2), mRNA			588	1	0	1	9
IPI00012870	RAC-beta serine/threonine-protein kinase		K, I, H, D, L	481	6	10	5	12
IPI00024417	Huntingtin-interacting protein 1-related protein		B, C	1068	0	2	2	4
IPI00027993	Ras-related protein Rab-25	o	B, L	213	5	6	2	3
IPI00023122	Isoform 1 of PDZ and LIM domain protein 7	e	B	457	2	2	4	8
IPI00028957	Isoform 2 of Ubiquitin conjugation factor E4 A			1073	2	0	2	9
IPI00005728	RER1 protein		G	214	2	9	0	2
IPI00304742	Serine/threonine-protein kinase 10	n		968	0	0	2	8
IPI00553175	Isoform 1 of Zinc finger CCCH-type with G patch domain-containing protein		K	531	6	14	8	21
IPI00012315	Nucleoside diphosphate kinase 3	b	I	169	4	6	1	5
IPI00217013	Isoform 1 of Serine/threonine-protein phosphatase 4 regulatory subunit 3A		K, B, C	833	1	3	3	3
IPI00549789	Isoform 2 of TBC1 domain family member 23			684	0	4	2	2
IPI00017412	Isoform 1 of Replication factor C subunit 2	k	K	354	4	6	1	0
IPI00013721	Serine/threonine-protein kinase PRP4 homolog	n	K, J	1007	0	3	0	6
IPI00169285	Putative phospholipase B-like 2			589	2	2	5	6
IPI00032825	Transmembrane emp24 domain-containing protein 7		E	224	5	16	4	13

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00031554	ATP-dependent RNA helicase DDX50		K, J	737	6	5	1	1
IPI00296907	Isoform 1 of Peroxisomal acyl-coenzyme A oxidase 1		B, I	660	3	6	0	0
IPI00022348	Isoform PML-1 of Probable tc factor PML		K, J, B	882	2	3	0	5
IPI00385042	Nucleolar GTP-binding protein 1		K, J, B	634	0	8	1	4
IPI00001891	Isoform Long of Ancient ubiquitous protein 1		K, J, E	476	1	6	7	5
IPI00008449	Isoform 3 of Pre-mRNA 3'-end-processing factor FIP1		K	520	7	11	9	20
IPI00937278	26S proteasome non-ATPase regulatory subunit 8	k, b	K, J, B	350	3	13	5	7
IPI00002405	2'-5'-oligoadenylate synthase 3		H	1087	3	4	1	0
IPI00291893	DCN1-like protein 1			259	4	6	0	3
IPI00009688	Phosphatidylinositol-5-phosphate 4-kinase type-2 alpha			406	5	5	0	2
IPI00651738	Isoform 1 of 1,2-dihydroxy-3-keto-5-methylthiopentene dioxygenase		K, B, L	179	7	24	13	18
IPI00743121	sphingomyelin phosphodiesterase 4 isoform 1			837	7	4	0	6
IPI00022078	Protein NDRG1		K, B, L	394	4	2	0	2
IPI00168501	Isoform 4 of Zinc finger CCCH domain-containing protein 14		K, B	571	7	3	10	5
IPI00027831	Glutamate-rich WD repeat-containing protein 1		K, J	446	2	2	1	4
IPI00478834	Isoform 1 of Arginine and glutamate-rich protein 1			273	0	1	0	8
IPI00028481	Ras-related protein Rab-8A	o	G, L	207	3	0	6	6
IPI00170770	Isoform 1 of PHD finger protein 3	q	K	2039	6	9	2	2

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00411710	Eukaryotic tl initiation factor 4 gamma, 3			630	2	3	2	7
IPI00221128	Isoform 4 of InaD-like protein		B, L	1524	2	3	1	1
IPI00418471	Vimentin	b	B, D, C, L	466	121	112	97	151
IPI00014938	SAP domain-containing ribonucleoprotein		K	210	3	1	7	10
IPI00007940	erlin-1			348	3	3	0	6
IPI00075081	Isoform 1 of Fanconi anemia group D2 protein	d	K	1471	3	6	2	6
IPI00167985	Zinc finger protein 579		K	562	0	5	5	5
IPI00293845	Isoform 1 of Telomere-associated protein RIF1	d	K, B, C	2472	2	1	2	6
IPI00219616	Ribose-phosphate pyrophosphokinase 1		D	318	6	2	10	10
IPI00554681	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5		I	116	3	3	4	8
IPI00604624	Isoform 1 of NIF3-like protein 1		B, I	377	1	3	0	3
IPI00009946	Mitochondrial import receptor subunit TOM34		B, I	309	0	3	9	7
IPI00293276	Macrophage migration inhibitory factor	f	B	115	30	33	29	23
IPI00032957	SUMO-conjugating enzyme UBC9	d, j	K, B	158	5	17	0	2
IPI00019195	Ribonuclease P protein subunit p38		K, J	283	6	10	1	3
IPI00219685	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 13			227	3	3	4	8
IPI00018871	cDNA FLJ56285, highly similar to ADP-ribosylation factor-like protein 8B			238	3	7	4	12

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00023004	Eukaryotic tl initiation factor 1A, Y-chromosomal		B	144	4	6	20	20
IPI00514897	Brefeldin A-inhibited guanine nucleotide-exchange protein 3			2177	1	2	0	5
IPI00025178	Pre-mRNA-splicing factor SPF27		K, J	225	0	0	3	7
IPI00290684	Bifunctional polynucleotide phosphatase/kinase		K, J	521	1	1	1	6
IPI00015891	Prefoldin subunit 4	l	D	134	5	3	18	18
IPI00299214	Thymidine kinase, cic		B, D	234	5	5	10	5
IPI00176574	12 kDa protein			106	1	10	4	11
IPI00008167	Sodium/potassium-transporting ATPase subunit beta-3	s	B, L, A	279	6	0	1	2
IPI00020472	Isoform 1 of Transmembrane protein 111		G	261	8	2	0	1
IPI00219037	Histone H2A.x	d	K	143	11	22	23	21
IPI00550852	Dynactin subunit 4		K, B, C	460	6	7	9	7
IPI00789041	Isoform 1 of Pinin	c	K, J, B, L	717	2	0	3	5
IPI00167909	Isoform 1 of Echinoderm microtubule-associated protein-like 3		B, C	896	6	1	2	6
IPI00004324	Trafficking protein particle complex subunit 3		B, E, G, D	180	6	2	3	4
IPI00073713	Isoform 1 of RNA-binding protein Musashi homolog 2		B	328	0	0	3	5
IPI00018798	DnaJ homolog subfamily C member 17	l		304	0	0	7	8
IPI00008961	Telomeric repeat-binding factor 2-interacting protein 1		K, B	399	2	4	2	12
IPI00014400	dnaJ homolog subfamily B member 12	l	E	409	4	1	0	2
IPI00006440	28S ribosomal protein S7, mitochondrial	r	I, I	242	3	2	0	4

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00030730	Phenol sulfotransferase 1A5*1A possible alternative splicing form			301	3	2	0	8
IPI00411356	Vacuolar protein sorting-associated protein 4A	d, o	B	437	0	3	2	6
IPI00411984	cDNA FLJ16404 fis, clone UTERU2008019, highly similar to Serine/threonine-protein kinase 3			519	4	6	1	1
IPI00011302	CD59 glycoprotein		L	128	14	12	2	3
IPI00101600	Isoform 1 of CWF19-like protein 1			538	2	5	8	5
IPI00337694	Isoform 1 of Rap guanine nucleotide exchange factor 6	p	B, L	1601	6	4	0	0
IPI00185146	Importin-9		K, B	1041	4	3	3	1
IPI00011118	ribonucleoside-diphosphate reductase subunit M2 isoform 1			449	10	4	6	3
IPI00100247	Thioredoxin-related transmembrane protein 4			349	2	9	0	2
IPI00158615	THO complex subunit 2		K	1478	1	1	3	3
IPI00166013	Uncharacterized protein C20orf4			384	0	5	0	1
IPI00032506	Uncharacterized protein C14orf142			100	12	11	16	17
IPI00012733	C-X-C chemokine receptor type 7		L	362	2	0	2	6
IPI00807463	nuclear factor NF-kappa-B p100 subunit isoform b	p	K, B, D	899	6	6	0	2
IPI00220578	Guanine nucleotide-binding protein G(k) subunit alpha		B, G, L	354	11	9	6	8
IPI00011693	UPF0293 protein C16orf42			312	0	8	2	5
IPI00000792	Quinone oxidoreductase		B, G, D	329	0	6	2	4
IPI00215720	Isoform 1 of Fragile X mental retardation 1 protein		K, J, B	594	2	1	2	8

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00003813	Isoform 1 of ca molecule 1	b, c, e	L	442	12	8	0	0
IPI00056494	60S ribosomal protein L36a-like	r	B, I	106	1	6	4	10
IPI00027808	DNA-directed RNA polymerase II subunit RPB2	q, g	K	1174	1	2	4	2
IPI00014513	tcal repressor protein YY1		K, L	414	9	13	1	2
IPI00384861	Isoform 1 of ARF GTPase-activating protein GIT1		B	761	11	5	4	0
IPI00413659	Isoform 2 of Probable alpha-ketoglutarate-dependent dioxygenase ABH5			394	5	2	0	3
IPI00412497	Dynein, light chain, roadblock-type 1			148	3	4	5	8
IPI00329692	Isoform Long of Glycylpeptide N-tetradecanoyltransferase 1	b	B, D, L	496	2	3	3	7
IPI00008868	Microtubule-associated protein 1B		B, D, C, L	2468	6	5	1	2
IPI00290544	Isoform 2 of Ganglioside-induced differentiation-associated protein 1		B	290	7	6	6	8
IPI00220317	DNA polymerase alpha catalytic subunit	k, f	K, J, B	1462	11	13	4	7
IPI00477971	Transducin beta-like protein 3		K, J	808	1	6	9	11
IPI00165393	Acidic leucine-rich nuclear phosphoprotein 32 family member E		K, B	268	1	4	2	5
IPI00299456	Fructose-1,6-bisphosphatase isozyme 2		D	339	18	16	10	11
IPI00026087	Barrier-to-autointegration factor		K, B, D	89	5	8	11	4
IPI00019400	Thiopurine S-methyltransferase	i	B, D	245	4	6	2	0

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00018288	DNA-directed RNA polymerase II subunit RPB3	q, g	K, B	275	0	0	1	9
IPI00010404	Splicing factor 3B subunit 5	g	K	86	1	5	4	17
IPI00009844	GMP reductase 2		D	348	2	0	0	6
IPI00443534	cDNA FLJ46889 fis, clone UTERU3017995, highly similar to Homo sapiens likely ortholog of rat p47			143	0	8	5	3
IPI00304540	Isoform 3 of Protein FAM40A		K	440	7	5	0	1
IPI00026516	Succinyl-CoA:3-ketoacid-coenzyme A transferase 1, mitochondrial	i	I	520	3	2	0	7
IPI00304409	Calcium-regulated heat stable protein 1		B	147	2	2	10	12
IPI00008569	Synaptobrevin homolog YKT6	o	B, I, F, E, G, D	198	2	6	8	8
IPI00220871	60S ribosomal protein L37	r, g	D, I	97	0	4	11	11
IPI00412224	WD repeat-containing protein 11			1224	5	8	3	4
IPI00107113	Isoform 1 of U3 small nucleolar RNA-associated protein 14 homolog A		K, J	771	0	6	2	4
IPI00155601	MACRO domain-containing protein 1		I	325	0	9	1	10
IPI00023504	Ras-related protein Rab-3A	o	B, L	220	8	4	3	2
IPI00550766	Ribosomal RNA processing protein 1 homolog A		K, J	461	4	8	7	7
IPI00002495	Isoform 1 of Epsin-1		K, B, L	551	0	1	7	0
IPI00743576	Isoform 2 of V-type proton ATPase 116 kDa subunit a isoform 1	h, s	K, J, B, G, L	831	6	5	1	5
IPI00014235	Isoform 1 of Rab3 GTPase-activating protein catalytic subunit		K, J, B	981	6	5	4	2

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00301204	Retinol dehydrogenase 13		I	331	2	4	5	3
IPI00294943	Protein ariadne-1 homolog		B	557	5	3	6	7
IPI00027192	cDNA, FLJ79184, highly similar to Procollagen-lysine, 2-oxoglutarate 5-dioxygenase 1			774	4	1	2	6
IPI00018434	Isoform 1 of Tumor susceptibility gene 101 protein	d, o, e	K, J, B, L	390	9	5	0	4
IPI00299033	Importin subunit alpha-3		K, B	521	12	17	17	6
IPI00028387	Isoform 1 of DDRGK domain-containing protein 1		E	314	1	0	4	11
IPI00016746	Isoform 1 of Core-binding factor subunit beta		K	182	1	5	5	4
IPI00784119	V-type proton ATPase subunit S1	h		470	1	4	5	2
IPI00013723	Peptidyl-prolyl cis-trans isomerase NIMA-interacting 1	l, d	K	163	0	2	4	6
IPI00006164	Integrin-linked kinase-associated serine/threonine phosphatase 2C		B	392	4	6	7	4
IPI00376259	Isoform 1 of SLIT-ROBO Rho GTPase-activating protein 1	p	D	1085	1	0	0	14
IPI00397721	Biogenesis of lysosome-related organelles complex 1 subunit 3		B, D	202	3	2	4	5
IPI00384571	MRPL43 protein (Fragment)			145	6	4	3	2
IPI00169413	28S ribosomal protein S34, mitochondrial		I, I	218	1	2	0	2
IPI00465141	DNA topoisomerase I, mitochondrial		I	601	3	5	2	5
IPI00100673	Charged multivesicular body protein 3	d, o	B, F, D	222	3	3	2	2
IPI00640980	Isoform 2 of Sorting nexin-27	p, o	B, D	528	2	3	3	6
IPI00023322	Zinc finger protein ubi-d4	b	K, J, B	391	0	2	7	6
IPI00043638	Isoform 2 of La-related protein			605	0	0	1	8

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
	4							
IPI00045536	Isoform 3 of Chitinase domain-containing protein 1			362	4	9	7	3
IPI00413778	FKBP1A protein	l	B, D	145	2	1	3	3
IPI00908488	cDNA FLJ60932, highly similar to T-complex protein 1 subunit zeta-2			493	8	9	2	6
IPI00306043	Isoform 1 of YTH domain family protein 2			579	3	4	3	6
IPI00396185	N-alpha-acetyltransferase 35, NatC auxiliary subunit		K, J, B, L	725	4	2	8	2
IPI00748037	Beta-soluble NSF attachment protein		E, G	298	0	3	2	5
IPI00100193	Alpha- and gamma-adaptin-binding protein p34	o	B	315	2	2	1	7
IPI00007814	V-type proton ATPase subunit C 1	h, s	B, D, L	382	2	4	2	4
IPI00000845	84 kDa protein			744	0	2	3	1
IPI00005129	Isoform 1 of Secretory carrier-associated membrane protein 1	o	F, G	338	2	2	0	3
IPI00220827	Thymosin beta-10		B, C	44	15	10	12	17
IPI00399212	similar to RAN binding protein 1			201	8	35	22	19
IPI00025239	NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial		I	463	6	3	3	2
IPI00013146	28S ribosomal protein S22, mitochondrial		I, I	360	2	0	2	4
IPI00290158	Isoform 7 of Serine/threonine-protein kinase MARK2	n, e	L	692	3	4	2	6
IPI00018946	cDNA FLJ56439, highly similar to Pantothenate kinase 4			781	0	5	3	6

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00032355	Pumilio homolog 1 (Drosophila), isoform CRA_c			1224	3	5	0	5
IPI00031708	Fumarylacetoacetase		D	419	5	2	2	6
IPI00168255	membrane protein FAM174B			159	0	13	2	0
IPI00922910	Ubiquitin carboxyl-terminal hydrolase			509	11	4	2	10
IPI00171411	Golgi membrane protein 1			410	7	8	0	4
IPI00414858	Isoform 1 of Conserved oligomeric Golgi complex subunit 3		G	828	5	2	0	0
IPI00010845	NADH dehydrogenase [ubiquinone] iron-sulfur protein 8, mitochondrial		I	210	1	0	5	5
IPI00176702	Calmodulin-regulated spectrin-associated protein 3		B, C	1249	0	0	1	6
IPI00384028	cDNA FLJ56176, highly similar to Poly(A) polymerase alpha	q, g	K, J, B	761	2	4	2	1
IPI00102875	Isoform 3 of Zinc finger FYVE domain-containing protein 19			403	14	5	12	3
IPI00012989	Lysosomal alpha-mannosidase			1011	2	2	0	1
IPI00219381	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 2		I	99	0	3	6	4
IPI00218466	cDNA FLJ59739, highly similar to pt protein Sec61 subunit alpha isoform 1			482	8	4	2	4
IPI00335385	Scavenger mRNA-decapping enzyme DcpS		K, B, D	337	8	7	19	5
IPI00299507	Condensin complex subunit 2	k, j	K, B	741	3	8	5	7
IPI00003968	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9,		I	377	1	4	2	1

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
	mitochondrial							
IPI00300299	Signal peptidase complex subunit 3		E, H	180	5	3	0	4
IPI00290542	Isoform 1 of Signal transducing adapter molecule 2		B, F, D	525	1	2	1	6
IPI00184772	Uncharacterized protein			2049	0	0	2	5
IPI00168336	LEM domain-containing protein 2		K	503	3	2	0	4
IPI00013195	39S ribosomal protein L49, mitochondrial	r	I, I	166	2	2	3	4
IPI00060627	Coiled-coil domain-containing protein 124		K	223	2	2	2	6
IPI00012835	C-terminal-binding protein 1	n, e	K, J, B	440	3	4	3	2
IPI00297160	Isoform 12 of CD44 antigen		K, B, G, L	361	4	6	0	0
IPI00020196	Armadillo repeat-containing protein 6			501	0	3	2	5
IPI00010120	Isoform 1 of C-terminal-binding protein 2	e	K	445	2	4	2	8
IPI00003768	Isoform 1 of Pescadillo homolog	f	K, J	588	4	6	0	5
IPI00418240	nebulette isoform 2			270	0	1	22	3
IPI00220906	Isoform 1 of Acyl-coenzyme A thioesterase 2, mitochondrial		I	483	5	5	0	1
IPI00002525	Neudesin			172	2	0	5	10
IPI00012202	Methylosome protein 50		K, B, D	342	0	4	1	2
IPI00026904	cDNA FLJ59367, highly similar to Adenylosuccinate lyase			498	6	5	2	8
IPI00472855	HLA class I histocompatibility antigen, A-30 alpha chain			365	5	15	10	11
IPI00022479	Uncharacterized protein			4862	0	2	3	5

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00168262	Procollagen galactosyltransferase 1		E	622	2	0	5	3
IPI00291578	Isoform 1 of Phosphoribosyl pyrophosphate synthase-associated protein 1			356	3	4	2	4
IPI00303568	Prostaglandin E synthase 2		K, B, I, G, D	377	4	0	1	2
IPI00478453	cDNA FLJ61662, highly similar to CCR4-NOT tc complex subunit 3		K, B, D	718	2	0	6	8
IPI00016250	Fragile X mental retardation syndrome-related protein 2		B	698	1	3	0	0
IPI00218924	Calcium-binding protein p22		B, D	195	0	10	2	0
IPI00034099	Isoform 2 of Epithelial splicing regulatory protein 2		K	717	3	0	2	8
IPI00333913	Isoform 1 of Neuroblastoma-amplified sequence			2371	5	0	1	4
IPI00878015	12 kDa protein			106	18	9	0	0
IPI00007426	PRA1 family protein 3		B, E	188	2	5	6	3
IPI00063903	Up-regulated during skeletal muscle growth protein 5		I	58	6	13	1	7
IPI00297284	insulin-like growth factor-binding protein 2 precursor	p		328	0	0	6	5
IPI00016608	Transmembrane emp24 domain-containing protein 2	o	H, G	201	6	4	0	3
IPI00239077	Histidine triad nucleotide-binding protein 1	p	K, B, C	126	6	3	13	15
IPI00419731	Isoform 1 of Cysteine-rich with EGF-like domain protein 2		E	353	0	25	1	10
IPI00026167	NHP2-like protein 1	g	K, J	128	4	6	13	6
IPI00006970	Mitochondrial 28S ribosomal protein S2	r	I	319	7	4	4	2
IPI00221240	Isoform 2 of Leucyl-cystinyl aminopeptidase		H, L	1011	3	7	2	13

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00004669	Polypeptide N-acetylgalactosaminyltransferase 2		G	571	5	4	6	5
IPI00328571	Actin nucleation promoting factor			465	0	0	2	4
IPI00027178	AP-1 complex subunit gamma-like 2		F, G	785	2	5	1	1
IPI00215768	Glutamate--cysteine ligase catalytic subunit		D	637	2	3	2	3
IPI00009320	Isoform 1 of Transmembrane protein 85	b		183	3	8	2	4
IPI00293564	Hydroxymethylglutaryl-CoA lyase, mitochondrial		I	325	4	3	0	6
IPI00221233	B-cell receptor-associated protein 29	b	E	241	7	0	1	1
IPI00019359	Keratin, type I cytoskeletal 9			623	19	2	13	11
IPI00025039	rRNA 2'-O-methyltransferase fibrillarin		K, J	321	5	4	4	5
IPI00019924	Tubulin-specific chaperone C	l	B, C	346	2	1	3	2
IPI00219291	Uncharacterized protein	h	I	98	6	3	2	5
IPI00007343	RING finger protein 113A			343	1	0	1	3
IPI00165949	Isoform 2 of er aminopeptidase 1	x	E, D	948	3	4	0	0
IPI00183500	Isoform 1 of Nuclear cap-binding protein subunit 2	q, g	K, B, D	156	1	3	0	11
IPI00334914	Isoform 1 of TRM1-like protein			733	7	8	2	5
IPI00479962	Myosin-Vb	o		1849	0	0	1	4
IPI00464952	Serine/arginine-rich splicing factor 11	q, g	K, J	484	15	8	3	0
IPI00412792	tc factor BTF3 homolog 4			158	2	1	11	8
IPI00020075	Abhydrolase domain-containing protein 10, mitochondrial		I	306	4	3	2	4

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00384497	3-hydroxyacyl-CoA dehydratase 2		E	254	9	13	5	3
IPI00099996	Mitochondrial ribonuclease P protein 1		I	403	2	4	2	8
IPI00164724	Isoform 2 of BRCA1-A complex subunit BRE	b, p	K, B	383	2	1	0	4
IPI00177437	Isoform 1 of Crooked neck-like protein 1		K, B	848	4	10	4	3
IPI00022697	Developmentally-regulated GTP-binding protein 2	p	B, I	364	2	0	0	4
IPI00011643	Isoform 2 of Kunitz-type protease inhibitor 1			513	5	2	3	4
IPI00025285	V-type proton ATPase subunit G 1	h, s	D, L	118	1	2	2	6
IPI00411886	Nucleolar complex protein 2 homolog		K, J	749	2	1	0	2
IPI00550821	Isoform 1 of Cleavage and polyadenylation specificity factor subunit 7	q, g	K	471	2	0	4	4
IPI00291901	Interferon regulatory factor 3		K, B, D, L	427	3	3	0	2
IPI00333420	Isoform 1 of Serine/threonine-protein kinase SRPK2	n, e	K, J, B	688	1	2	4	4
IPI00177509	Trafficking protein particle complex subunit 5		E, G	188	3	6	0	6
IPI00013212	Tyrosine-protein kinase CSK	n	B, G, D, L	450	4	1	0	4
IPI00022790	Microfibrillar-associated protein 1			439	10	3	11	9
IPI00334532	Isoform 2 of Neural ca molecule L1	c, e	L	1253	1	0	4	6
IPI00057097	Deoxynucleotidyltransferase terminal-interacting protein 1		K	329	0	6	9	4
IPI00216085	Cytochrome c oxidase subunit 6B1		I	86	5	7	1	17
IPI00303105	Small ubiquitin-related		K, B	101	2	9	2	5

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
	modifier 1							
IPI00004839	Crk-like protein		D	303	1	0	4	2
IPI00216675	Isoform Alpha' of Caspase-7	b	B, H, D	336	9	8	13	6
IPI00174442	Isoform 1 of Protein FAM98A			519	2	5	6	3
IPI00002203	Isoform 1 of BRCA2 and CDKN1A-interacting protein	d	K	314	0	2	5	4
IPI00029155	Isoform 1 of Single Ig IL-1-related receptor	p		410	5	12	5	7
IPI00220302	Isoform 1 of Pre-mRNA-splicing regulator WTAP	d	K, J	396	2	4	0	8
IPI00478657	G-rich sequence factor 1		B, I	480	2	0	0	9
IPI00019004	Translocation protein SEC62	s	E	399	1	2	1	5
IPI00029997	6-phosphogluconolactonase		B, D	258	3	4	2	1
IPI00018009	Enhancer of mRNA-decapping protein 3		B, D	508	0	3	0	6
IPI00045051	tcal activator protein Pur-beta		K	312	4	5	1	9
IPI00030968	Isoform 1 of Uncharacterized protein C9orf142			204	3	1	2	3
IPI00829652	RNA-binding protein 16		K	1271	6	1	0	5
IPI00010255	Rhomboid domain-containing protein 2			364	0	0	0	7
IPI00304187	RNA-binding protein 28		K, J, G	759	3	0	1	5
IPI00027464	Calcineurin subunit B type 1	b	D	170	1	6	0	4
IPI00028570	Isoform 1 of Glycogen synthase kinase-3 beta	n	K, J, B, D	420	3	1	2	1
IPI00640551	Exportin 5			158	0	2	5	6
IPI00001466	Echinoderm microtubule-associated protein-like 4	j	B, C	981	3	4	3	6
IPI00384154	Isoform 2 of Poly(A) polymerase alpha	q, g	K, J, B	285	4	2	0	1
IPI00010207	Ubiquitin-fold modifier 1		K, B	85	2	0	12	17
IPI00003438	DnaJ homolog subfamily C member 8	l, g		253	3	8	22	18

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00220648	Phosphomevalonate kinase	n	B, D	192	2	5	1	3
IPI00026994	PRA1 family protein 2	o	F	178	2	1	5	2
IPI00337315	Isoform 1 of E3 ubiquitin-protein ligase RBBP6		K, J	1792	2	2	2	1
IPI00023161	39S ribosomal protein L46, mitochondrial		I, I	279	1	1	10	6
IPI00292537	Isoform 2 of Nuclear factor NF-kappa-B p105 subunit	b, p	K, J, B, I, D	969	4	3	2	2
IPI00024781	Small EDRK-rich factor 2			59	3	4	4	13
IPI00004472	Isoform 1 of Serine/threonine-protein kinase WNK1	n, h	B	2382	4	5	12	9
IPI00297487	Cathepsin H			335	0	0	4	7
IPI00005715	Isoform 1 of Ubiquitin conjugation factor E4 B	b	K, B	1302	4	1	0	3
IPI00025344	NADH dehydrogenase [ubiquinone] iron-sulfur protein 6, mitochondrial		I	124	3	3	3	4
IPI00302990	Isoform 1 of WD repeat-containing protein 55		K, J, B	383	6	0	6	4
IPI00935516	Heat shock factor-binding protein 1		K, C	76	0	3	5	10
IPI00748303	Uncharacterized protein			1056	4	1	1	5
IPI00009817	Isoform 2 of Coiled-coil-helix-coiled-coil-helix domain-containing protein 8			96	3	5	1	3
IPI00220079	Isoform 2 of Nuclear receptor coactivator 3		K, B, G	1409	0	2	4	6
IPI00073763	Semaphorin-4C		L	833	1	0	1	4
IPI00004363	STE20/SPS1-related proline-alanine-rich protein kinase	n	K, B, C	547	9	7	2	3
IPI00412404	ATP-dependent RNA helicase SUPV3L1, mitochondrial		K, I	786	0	2	1	1

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00157734	Isoform 1 of Exocyst complex component 3	o		756	2	4	0	3
IPI00022254	Isoform 1 of Ubiquitin-like-conjugating enzyme ATG3	o	B, D	314	3	3	0	2
IPI00293746	Isoform 1 of Multiple myeloma tumor-associated protein 2			263	1	0	3	3
IPI00295081	Tubulin gamma-1 chain	k	B, D, C	451	4	2	4	5
IPI00553067	Isoform 1 of Coiled-coil domain-containing protein 132			964	4	3	0	3
IPI00153051	Isoform 1 of Poly(A) RNA polymerase, mitochondrial	q	B, I	582	4	2	0	5
IPI00187143	Isoform 2 of Ras-related protein Rab-4B	o	L	248	6	1	5	3
IPI00219919	DNA methyltransferase 1-associated protein 1		K	467	0	3	0	2
IPI00010133	Coronin-1A		K, B, L	461	6	2	4	4
IPI00017305	Ribosomal protein S6 kinase alpha-1	n, p	D	735	12	0	0	0
IPI00154668	Coiled-coil domain-containing protein 93			631	1	2	3	4
IPI00329650	Nucleoporin NUP53	o, s	K, J, L	326	0	0	3	5
IPI00329593	Isoform 2 of ADP-dependent glucokinase			496	2	1	5	1
IPI00797186	Isoform 4 of Protein MON2 homolog	o		1717	3	4	0	3
IPI00015808	Nucleolar GTP-binding protein 2		K, J	731	3	6	2	1
IPI00452731	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 7		I	113	0	1	4	6
IPI00328526	Isoform ARPP-19 of cAMP-regulated phosphoprotein 19		B	112	6	4	5	16
IPI00215920	ADP-ribosylation factor 6	b, c, o	B, F, G, L	175	3	8	1	1

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00219034	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 8		I	172	0	0	9	7
IPI00024387	Hepatocyte nuclear factor 3-alpha		K	473	0	2	3	4
IPI00658145	Isoform 1 of BRCA1-associated protein required for ATM activation protein 1		K	821	0	1	0	6
IPI00010438	Isoform SNAP-23a of Synaptosomal-associated protein 23	o	K, J, H, G, L	211	4	3	2	2
IPI00024920	ATP synthase subunit delta, mitochondrial	h	I	168	7	18	8	25
IPI00328737	Isoform 1 of Zinc finger protein 598			904	2	4	2	3
IPI00019994	Isoform 1 of Gamma-taxilin	d	K, B, D	528	0	1	3	9
IPI00552897	Isoform 1 of Mediator of DNA damage checkpoint protein 1	d	K, J	2089	5	6	0	0
IPI00220567	5-formyltetrahydrofolate cyclo-ligase		B, G, D, L	203	2	3	3	3
IPI00472164	Wiskott-Aldrich syndrome protein family member 2	x	B	498	0	0	1	6
IPI00216219	Isoform Long of Tight junction protein ZO-1	b	K, B, G, L	1748	0	2	0	9
IPI00006608	Isoform APP770 of Amyloid beta A4 protein (Fragment)	n, c	B, G, L	770	2	8	4	4
IPI00022275	Phosphatidylinositide phosphatase SAC1		E, G	587	10	11	3	15
IPI00011770	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 4		I	81	3	3	3	6
IPI00301202	magnesium transporter protein 1			367	2	11	0	5
IPI00604756	Nuclear receptor-binding	n, g	B	535	2	4	1	7

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
	protein							
IPI00305833	WD40 repeat-containing protein SMU1		K, B	513	0	3	2	8
IPI00152671	Protein FAM91A1			838	0	4	9	10
IPI00419433	Isoform 1 of Rab11 family-interacting protein 1	o	B	1283	3	0	0	4
IPI00006197	Isoform 1 of Nuclear valosin-containing protein-like		K, J, B	856	7	1	0	2
IPI00020008	NEDD8	m	K	81	3	0	4	9
IPI00554752	cAMP-dependent protein kinase type II-beta regulatory subunit	k, s	B, D	418	2	3	4	4
IPI00009922	SRA stem-loop-interacting RNA-binding protein, mitochondrial		K, I	109	2	3	8	5
IPI00418412	Uncharacterized protein			586	1	2	3	6
IPI00293260	Isoform 1 of DnaJ homolog subfamily C member 10	l	E	793	1	3	0	5
IPI00016736	Isoform 1 of 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase gamma-1	p	B, D, L	1290	3	6	1	1
IPI00419194	Isoamyl acetate-hydrolyzing esterase 1 homolog			248	2	3	4	3
IPI00142716	Isoform 1 of DnaJ homolog subfamily C member 21	l	I	531	1	0	0	5
IPI00007057	Rabenosyn-5	o	F, L	784	0	0	0	9
IPI00025311	Isoform 1 of Breast carcinoma-amplified sequence 1		B	584	0	2	0	4
IPI00034006	Tyrosine-protein phosphatase non-receptor type 23			1636	0	7	5	5
IPI00414197	Isoform 1 of WD repeat-containing protein 26		K, J, B	661	4	1	3	5

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00333696	Isoform 3 of HEAT repeat-containing protein 5B			1982	2	2	3	3
IPI00023461	Isoform 4 of Afadin	c, p	K, J, D, L	1824	0	0	3	6
IPI00027342	Adenylyl cyclase-associated protein 2	p	L	477	3	3	0	4
IPI00026570	cytochrome c oxidase subunit VIIa polypeptide 2 (liver) precursor		I	115	8	6	2	6
IPI00032971	Oxysterol-binding protein-related protein 10			764	2	2	0	4
IPI00412987	Glia maturation factor, beta	n, p		154	2	10	5	5
IPI00013930	Syntaxin-6		G, L	255	1	5	2	4
IPI00296432	Isoform 1 of Protein IWS1 homolog		K	819	5	3	0	3
IPI00025616	DNA polymerase delta subunit 2	k	K	469	4	0	3	12
IPI00398922	Protein phosphatase 1 regulatory subunit 14B		B	199	5	6	2	4
IPI00024129	Peptidyl-prolyl cis-trans isomerase C	l, p	B	212	0	6	2	3
IPI00220099	Isoform B of Syntaxin-3		L	252	4	6	4	7
IPI00217851	Isoform 1 of Phosphatase and actin regulator 4			702	5	2	3	2
IPI00290511	Isoform 1 of Leucine-rich repeat-containing protein 68			691	0	5	1	0
IPI00030877	15 kDa selenoprotein isoform 1 precursor			165	0	0	0	2
IPI00306723	CCAAT/enhancer-binding protein zeta		K	1054	3	5	4	0
IPI00032827	Pre-mRNA branch site protein p14	g	K	125	4	3	2	2
IPI00301503	Isoform 1 of Transformer-2 protein homolog beta		K	288	2	4	4	1
IPI00394926	DNA polymerase delta subunit	k	K	466	2	2	0	2

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
	3							
IPI00010590	Isoform 1 of Lymphoid-specific helicase	d, j	K	838	2	3	1	2
IPI00022421	Cytochrome c oxidase subunit 7A-related protein, mitochondrial		I	114	1	2	3	6
IPI00745433	Isoform 1 of Protein argonaute-2	r	K, B, D	859	6	0	0	3
IPI00181617	Isoform 1 of RNA-binding protein 34		K, J	430	3	0	0	1
IPI00220342	N(G),N(G)-dimethylarginine dimethylaminohydrolase 1		B, I	285	1	0	3	3
IPI00024062	Isoform 1 of Band 4.1-like protein 1		B, D, C, L	881	6	5	1	4
IPI00219068	Isoform 1 of N-alpha-acetyltransferase 30, NatC catalytic subunit	i	B	362	18	13	0	2
IPI00001022	Isoform 2 of Probable hydrolase PNKD		K, B, I	142	5	6	0	5
IPI00257882	Xaa-Pro dipeptidase			493	2	2	0	5
IPI00013946	Synaptogyrin-2			224	12	8	4	7
IPI00017373	Replication protein A 14 kDa subunit	k	K, B	121	1	0	3	4
IPI00023591	tcal activator protein Pur-alpha		K, B	322	3	6	6	5
IPI00419273	Isoform 1 of Cullin-4A			759	0	0	4	6
IPI00061780	Isoform 1 of E3 ubiquitin-protein ligase Itchy homolog		K, B, D, L	903	0	0	9	6
IPI00479697	Isoform 2 of Mitochondrial carrier homolog 1	s	I	372	7	4	2	8
IPI00020906	Inositol monophosphatase 1	p	B	277	3	1	0	2
IPI00008756	cDNA FLJ59296, highly similar to Bullous pemphigoid antigen 1 isoforms1/2/3/4/5/8			5537	1	1	4	2

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00003505	Isoform 1 of Thyroid receptor-interacting protein 13		K	432	3	3	2	2
IPI00028005	Nuclear pore complex protein Nup107	k, o, s	K, D	925	0	1	0	4
IPI00045839	Isoform 3 of Prolyl 3-hydroxylase 1		E	804	2	1	1	5
IPI00017704	Coactosin-like protein		B, C	142	0	3	2	11
IPI00065276	Isoform 2 of Tether containing UBX domain for GLUT4			647	3	0	2	2
IPI00180403	TBC1 domain family member 30			924	4	2	3	4
IPI00298558	Programmed cell death protein 10	x	B, G, D, L	212	4	4	1	5
IPI00473047	cDNA FLJ40287 fis, clone TESTI2027909, highly similar to 5'-AMP-ACTIVATED PROTEIN KINASE, GAMMA-1 SUBUNIT	n, p	K, D	340	5	1	1	1
IPI00032597	RNA-binding motif protein, X-linked 2			322	6	4	2	6
IPI00102897	Rab-like protein 3			236	1	2	2	3
IPI00006715	Double-strand-break repair protein rad21 homolog	k, b	K, J	631	2	3	4	6
IPI00030360	RUN domain-containing protein 2A			375	1	3	2	0
IPI00015756	Isoform 1 of Receptor-type tyrosine-protein phosphatase kappa	c, p	L	1439	5	7	5	5
IPI00029697	Isoform 2 of Exosome complex exonuclease RRP45		K, J, B, D	456	5	5	0	0
IPI00386043	Isoform 1 of Protein odr-4 homolog			454	4	6	3	2
IPI00307259	DnaJ homolog subfamily C member 13			2243	3	3	2	2

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00946481	Protein			329	1	0	1	5
IPI00215790	60S ribosomal protein L38	r, g	D, I	70	9	1	7	6
IPI00017342	Rho-related GTP-binding protein RhoG		D, L	191	0	1	0	6
IPI00410079	Isoform 1 of Regulator of microtubule dynamics protein 3	b, e	K, B, I, C	470	2	9	4	2
IPI00328243	Phospholipase D3		E	490	4	5	1	1
IPI00015077	Eukaryotic tl initiation factor 1		B	113	0	2	1	4
IPI00022450	TBC1 domain family member 5			795	2	0	1	5
IPI00000897	HELZ protein		K	1943	0	2	5	2
IPI00300631	Scaffold attachment factor B1		K, J	915	3	2	0	2
IPI00219036	Endoribonuclease Dicer	x	B, D	1922	0	2	8	13
IPI00656021	vacuolar protein sorting-associated protein 53 homolog isoform 1	o	F, G	832	1	2	0	2
IPI00215995	Isoform Alpha-3A of Integrin alpha-3	c	L	1051	2	0	1	10
IPI00294603	Similar to Zinc finger MYM-type protein 5		K	1379	7	2	3	9
IPI00170796	Isoform 1 of Vacuolar protein sorting-associated protein 29	o	B, F	182	10	10	11	8
IPI00016669	GTP-binding protein Rheb	p	D, L	184	0	4	0	4
IPI00006658	Isoform 2 of Peptidyl-prolyl cis-trans isomerase NIMA-interacting 4	l	K, J, B, I, C	156	0	0	1	10
IPI00218495	Isoform 2 of DNA-3-methyladenine glycosylase		K	293	3	3	2	6
IPI00166785	Isoform 2 of Membrane magnesium transporter 1		B, E, G, L	196	13	10	5	6
IPI00020178	Isoform 1 of Signal transducing adapter molecule 1	p	B, F, D	540	5	4	0	0

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00016639	Protein kinase C iota type	n	K, B, F, D, L	596	2	4	9	4
IPI00428288	Isoform 4 of 39S ribosomal protein L43, mitochondrial	r	I, I	159	2	1	3	6
IPI00007364	Claudin-3		L	220	1	1	2	6
IPI00032995	LanC-like protein 2		K, B, D, L	450	6	7	5	2
IPI00005118	Hexokinase-3	s	I, D	923	4	2	0	3
IPI00027035	GPN-loop GTPase 1 isoform a			388	4	0	1	3
IPI00003373	Occludin	b	D, L	522	0	1	0	3
IPI00007853	Gamma-interferon-inducible lysosomal thiol reductase		L	261	6	1	6	7
IPI00024787	Very long-chain acyl-CoA synthetase		I, E, H	620	0	7	0	0
IPI00024282	Ras-related protein Rab-8B	o	I, L	207	3	0	0	5
IPI00103554	tcal repressor p66-beta		K, J	593	3	6	7	6
IPI00019447	Isoform 1 of Fanconi anemia group I protein	d	K	1268	1	8	7	5
IPI00031618	Isoform 3 of Protein DDI1 homolog 2			419	0	0	3	5
IPI00027422	Isoform Beta-4C of Integrin beta-4	c	L	1822	0	0	0	7
IPI00022282	Isoform Alpha of Glucocorticoid receptor	p, g	K, J, B	777	1	0	0	4
IPI00218848	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit E	h	I	72	12	7	12	6
IPI00007166	Immediate early response 3-interacting protein 1		E, G	82	0	5	0	0
IPI00157820	Isoform 2 of Thioredoxin reductase 2, mitochondrial		B, I	522	2	4	1	0
IPI00006092	Phosphomannomutase 2		B, D	246	7	8	3	6
IPI00031115	Golgin subfamily A member 1		G	767	2	1	0	2
IPI00005657	Prefoldin subunit 6	l		129	2	3	7	3

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00006991	Cyclin-dependent kinase inhibitor 1B	k	K, B, D	198	0	0	4	0
IPI00477505	Isoform 1 of Serine/threonine-protein phosphatase 6 regulatory ankyrin repeat subunit A		K	1086	2	0	1	2
IPI00007061	Vesicle transport protein GOT1B	o	E, G	138	0	0	0	4
IPI00294618	Proline-rich protein PRCC		K	491	0	3	1	1
IPI00301434	BolA-like protein 2			152	1	2	16	10
IPI00001091	AFG3-like protein 2		I	797	1	1	2	8
IPI00004045	Isoform A of RNA-binding protein with multiple splicing		K, B	196	2	5	7	8
IPI00168878	Torsin-1A-interacting protein 2		E	470	1	0	2	5
IPI00387077	Isoform 1 of Solute carrier family 12 member 9	s	L	914	0	0	2	4
IPI00031570	Nucleoside-triphosphatase C1orf57			190	4	3	4	6
IPI00062860	Putative ataxin-7-like protein 3B			97	5	10	2	4
IPI00000171	TSC22 domain family protein 4		K	395	3	3	1	2
IPI00168884	Renin receptor			350	2	0	0	5
IPI00221300	tl initiation factor eIF-2B subunit alpha	r, g	B, D, L	305	4	1	0	5
IPI00018963	Isoform 1 of Alpha-parvin	c	K, B, D, L	372	1	4	0	2
IPI00025333	Isoform 3 of Anamorsin	b	K, J, B	299	3	2	2	3
IPI00009901	Nuclear transport factor 2	o	B, D	127	3	5	6	5
IPI00301163	KTEL motif-containing protein 1		E	392	6	7	8	7
IPI00009841	RNA-binding protein EWS isoform 1			661	16	2	3	5
IPI00032472	cAMP-dependent protein kinase inhibitor beta			78	2	6	0	3

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00070643	Isoform Long of FAS-associated factor 1		K, B, D	650	3	1	5	2
IPI00553153	Putative uncharacterized protein DKFZp564G0422	x	I	107	0	4	4	9
IPI00186681	Isoform 1 of Acyl-CoA-binding domain-containing protein 5			534	4	0	0	3
IPI00164935	Isoform 2 of TSC22 domain family protein 2			756	2	5	3	9
IPI00296374	Zinc finger protein-like 1		K, G	310	1	2	3	1
IPI00009976	Transmembrane emp24 domain-containing protein 1	p	L	227	2	2	3	3
IPI00183695	Protein S100-A10	p		97	1	1	5	4
IPI00167941	Midasin		K	5596	2	1	5	1
IPI00783186	Isoform 2 of Ankyrin repeat domain-containing protein 17		K, B	2602	2	0	1	1
IPI00004312	Isoform 1 of Signal transducer and activator of tc 2		K, B, D, L	851	2	3	2	7
IPI00304331	Galactosylgalactosylxylosylprotein 3-beta-glucuronosyltransferase 3		G	335	0	2	2	4
IPI00018415	Transmembrane 9 superfamily member 2		F	663	3	2	2	4
IPI00013164	Isoform 1 of Peripherin			470	65	50	57	78
IPI00014266	Isoform 1 of Bromodomain-containing protein 3		K	726	1	1	2	1
IPI00060521	FLYWCH family member 2			140	7	6	5	4
IPI00025490	Mdm2 (Fragment)			256	3	1	4	2
IPI00782974	Isoform 1 of Uncharacterized protein C17orf85			620	1	5	6	8
IPI00480056	RAB4A, member RAS oncogene family variant		B, F, H, D, L	218	5	4	8	6
IPI00477526	Conserved hypothetical protein			483	1	2	0	2

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00010331	Isoform 2 of NAD-dependent deacetylase sirtuin-5		I	299	0	0	1	6
IPI00333010	Calcium homeostasis er protein		B, E	916	1	3	1	1
IPI00064162	Deubiquitinating protein VCIP135	j	B, E, G	1222	3	3	0	0
IPI00293074	Isoform 2 of Choline transporter-like protein 2	s	L	709	6	8	5	2
IPI00023972	Probable ATP-dependent RNA helicase DDX47		K, J	455	2	4	3	0
IPI00297641	Keratin, type I cuticular Ha8			456	5	11	16	9
IPI00843802	Isoform 1 of Protein KIAA0284		B, C	1590	2	0	3	2
IPI00031091	EF-hand domain-containing protein D1		I	239	9	5	2	1
IPI00456722	Isoform 2 of Ral GTPase-activating protein subunit alpha-1		K, B, I	2083	0	0	0	4
IPI00003807	Lysosomal acid phosphatase			423	0	3	4	8
IPI00301421	Isoform 1 of Nuclear-interacting partner of ALK	d, j	K	502	0	4	5	2
IPI00644482	Proteasome assembly chaperone 2		K	264	1	2	2	6
IPI00335641	cDNA FLJ61243, highly similar to MKL/myocardin-like protein 2	e	K, B	1099	2	0	0	4
IPI00173589	17 kDa protein			155	14	8	8	17
IPI00217059	Isoform 2 of Coiled-coil domain-containing protein 50		B	482	0	1	2	6
IPI00017964	Small nuclear ribonucleoprotein Sm D3	q, g	K, B, D	126	3	20	10	21
IPI00005107	Niemann-Pick C1 protein		F, E	1278	0	1	0	4
IPI00465113	cDNA FLJ58573, highly similar to Exonuclease 3'-5' domain-like-containing protein			621	0	0	1	4

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
	2							
IPI00298409	Phosducin-like protein	p		301	1	1	2	2
IPI00013654	Isoform 2 of Dynactin subunit 3	k, j	B, D, C	176	1	1	2	3
IPI00247295	Isoform 4 of Nesprin-1		K, J, B, G, C	8749	4	4	2	4
IPI00025717	Metaxin-2	o	I	263	0	1	1	4
IPI00333068	Actin-related protein 2/3 complex subunit 1A		B	370	2	1	0	5
IPI00794229	9 kDa protein			73	4	4	0	0
IPI00002324	Isoform 1 of Methionine adenosyltransferase 2 subunit beta		K, I, D	334	2	0	2	2
IPI00216694	Plastin-3		B	630	1	2	1	6
IPI00748807	Isoform 1 of Nuclear pore complex protein Nup160	k, o, s	K, D	1436	2	0	0	4
IPI00028160	Isoform 1 of Porphobilinogen deaminase		K, B, D	361	3	2	0	5
IPI00001477	Isoform 1 of Epithelial discoidin domain-containing receptor 1	n, c		913	1	4	0	0
IPI00744194	ATPase, P-type, K/Mg/Cd/Cu/Zn/Na/Ca/Na/H-transporter family protein			149	4	1	5	2
IPI00020510	CDGSH iron-sulfur domain-containing protein 1		I	108	4	3	1	0
IPI00024255	G patch domain and KOW motifs-containing protein		K, J	476	2	2	1	11
IPI00021167	Isoform 1 of Interferon-inducible double stranded RNA-dependent protein kinase activator A	n	B	313	2	4	0	5

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00024283	WD repeat and FYVE domain-containing protein 1		K, D	410	6	2	0	2
IPI00100192	Isoform 3 of cic 5'-nucleotidase 3		B, I, E, D	286	0	5	2	1
IPI00019997	Protein lin-7 homolog C	o	L	197	4	5	1	4
IPI00185533	Isoform A of Nucleoporin SEH1	k, o, s	K, D	360	3	2	0	1
IPI00005904	Probable ATP-dependent RNA helicase DDX20		K, B, D, C	824	0	0	2	4
IPI00180292	Isoform 5 of Brain-specific ag inhibitor 1-associated protein 2	p	K, J, B, L	520	4	0	0	1
IPI00444452	Isoform 1 of Putative helicase MOV-10		B	1003	1	3	0	3
IPI00413293	cDNA FLJ56343, highly similar to Torsin A			364	1	4	2	2
IPI00216932	Isoform 1 of Acetyl-coenzyme A synthetase 2-like, mitochondrial		I	689	4	4	3	2
IPI00301579	cDNA FLJ59142, highly similar to Epididymal secretory protein E1			201	10	6	2	3
IPI00306056	Ribonuclease P protein subunit p25		K	199	0	5	6	7
IPI00413170	Isoform 2 of Protein FAM98C			267	0	5	4	3
IPI00440727	Isoform 1 of Bromodomain-containing protein 4	n	K, J, B	1362	0	0	3	1
IPI00384867	Isoform 2 of Adenosine 3'-phospho 5'-phosphosulfate transporter 1	s	G	392	0	1	2	8
IPI00029741	Integrin beta-5	c	L	799	6	2	1	2
IPI00385267	Signal recognition particle receptor subunit alpha		E	638	6	4	0	4
IPI00015580	Isoform 3 of Formin-binding protein 1-like		B, C, L	547	5	4	3	3

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00041325	H/ACA ribonucleoprotein complex subunit 2		K, J	153	9	1	0	6
IPI00555902	Isoform 1 of OCIA domain-containing protein 2		F	154	2	4	1	4
IPI00432337	Isoform 2 of er lectin 1		E	429	1	0	1	7
IPI00001735	Isoform 1 of Nuclear receptor corepressor 2		K, J	2525	3	1	0	5
IPI00442146	101 kDa protein			917	1	2	1	3
IPI00027165	Isoform R-type of Pyruvate kinase isozymes R/L		D	574	41	18	24	21
IPI00937995	Actin-like protein (Fragment)			103	73	15	20	39
IPI00294211	Pre-mRNA-splicing factor ATP-dependent RNA helicase PRP16	q, g	K	1227	2	1	2	5
IPI00329025	Protein jagunal homolog 1		E	183	3	0	0	0
IPI00745955	Probable rRNA-processing protein EBP2		K, J	306	4	3	4	10
IPI00014232	ADP-ribosylation factor-like protein 6-interacting protein 1		B, E, D	203	3	9	4	12
IPI00218144	Cytochrome c oxidase copper chaperone		B, I	63	2	20	2	10
IPI00604483	Isoform 4 of Dipeptidyl peptidase 9		B, D	836	2	0	0	2
IPI00182180	OTU domain-containing protein 6B			323	6	3	2	5
IPI00017454	Putative tubulin-like protein alpha-4B		B, C	241	10	11	4	8
IPI00301923	Isoform 1 of Cell division protein kinase 9	q, n, f, g	K, J	372	1	0	2	5
IPI00941732	tc elongation factor B polypeptide 3	q, g	K	798	1	1	1	6
IPI00217442	ANKHD1-EIF4EBP3 protein			2617	2	0	3	0
IPI00013454	Isoform 1 of Regulator of G-protein signaling 10		B, L	173	2	5	4	6

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00294242	28S ribosomal protein S31, mitochondrial		I, I	395	0	0	4	3
IPI00004497	Isoform 1 of Breakpoint cluster region protein	n, p	D	1271	0	2	2	3
IPI00022302	Isoform 1 of Sorting nexin-24	o		169	0	1	0	4
IPI00552569	DNA excision repair protein ERCC-6-like	k	D	1250	5	2	3	4
IPI00009407	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit DAD1	b		113	6	4	5	6
IPI00303158	Isoform 1 of N-acylneuraminate cytidylyltransferase		K	434	0	3	0	4
IPI00023832	SH3 and PX domain-containing protein 2B	e	B	911	1	0	2	4
IPI00329572	Protein kinase C and casein kinase substrate in neurons 3, isoform CRA_b		B, L	425	0	0	4	5
IPI00011593	Isoform 1 of Fos-related antigen 2		K, J	326	7	5	1	2
IPI00165506	Polymerase delta-interacting protein 2		K, I	368	3	2	1	2
IPI00030362	Proteolipid protein 2	h	E, L	152	2	3	6	11
IPI00894533	Protein			103	0	2	0	3
IPI00008207	er mannosyl-oligosaccharide 1,2-alpha-mannosidase	l, i	E	699	2	2	7	0
IPI00032050	WW domain-binding protein 2			261	3	2	2	1
IPI00220007	cDNA FLJ55764, highly similar to Apolipoprotein-L2			451	2	2	0	5
IPI00790298	20 kDa protein			171	17	3	13	14
IPI00024802	TATA-binding protein-associated factor 172		K	1849	0	2	0	3
IPI00169168	Isoform 3 of F-box only			276	2	0	2	5

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
	protein 22							
IPI00165981	Isoform 1 of NFX1-type zinc finger-containing protein 1			1918	5	0	0	3
IPI00178972	Isoform 1 of DDB1- and CUL4-associated factor 11			546	4	10	1	3
IPI00176706	Splicing factor 45		K	401	0	0	27	10
IPI00021267	Ephrin type-A receptor 2	n, b, p	L	976	4	1	3	2
IPI00012340	Serine/arginine-rich splicing factor 9	q, g	K	221	3	2	2	2
IPI00293613	Serine/threonine-protein kinase TBK1	n	B, D, L	729	3	2	2	2
IPI00382452	Isoform 1 of Charged multivesicular body protein 1a	d, o	K, B	196	2	0	1	9
IPI00001543	Mitochondrial import inner membrane translocase subunit Tim10	o, s	I	90	0	0	5	6
IPI00005948	Isoform 1 of Methylthioribose-1-phosphate isomerase		K, B	369	2	0	0	7
IPI00030418	Tetraspanin-31			210	1	0	0	9
IPI00027175	Sorcin	p	B, L	198	3	2	0	4
IPI00797771	Isoform 2 of Uncharacterized protein C20orf117			1661	0	0	2	4
IPI00181997	Isoform 2 of Methyltransferase-like protein 2B			313	1	0	4	9
IPI00030383	Isoform Alpha of Nuclear inhibitor of protein phosphatase 1	f	K, J, B	351	5	6	10	4
IPI00107869	Isoform 2 of WW domain-containing oxidoreductase	b	K, B, I, G	363	5	1	0	0
IPI00798360	18 kDa protein			162	11	7	10	14
IPI00220546	Isoform 2 of Galactocerebrosidase		I	407	2	2	0	0

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00029011	Isoform 1 of Kinesin-like protein KIF1B	b	B, I, C	1816	0	1	0	4
IPI00018402	Tubulin-specific chaperone E	l	K, B, C, L	527	3	1	0	3
IPI00477468	RNA polymerase-associated protein CTR9 homolog		K	1173	4	4	2	2
IPI00394788	Probable alanyl-tRNA synthetase, mitochondrial	g	B, I	985	3	1	0	4
IPI00030530	Isoform 1 of Transmembrane protein 55B		F	277	2	4	0	3
IPI00004489	Adenylyltransferase and sulfurtransferase MOCS3		B, D	460	4	1	2	4
IPI00030408	Isoform 1 of M-phase phosphoprotein 8	d	K, B	860	0	3	0	1
IPI00060031	ADP-ribosylation factor-like protein 8A	d, j	B, F	186	3	5	1	5
IPI00020418	Ras-related protein R-Ras	p	L	218	2	0	0	2
IPI00183118	Isoform 1 of MAP/microtubule affinity-regulating kinase 3	n		776	0	0	0	3
IPI00640947	Isoform 2 of tRNA-dihydrouridine synthase 3-like			482	3	4	4	0
IPI00009235	Translocon-associated protein subunit gamma		E, H	185	6	8	9	6
IPI00009030	Isoform LAMP-2A of Lysosome-associated membrane glycoprotein 2		L	410	6	2	1	5
IPI00291643	SPRY domain-containing protein 4		K, I	207	2	3	0	2
IPI00014068	Isoform 1 of Serine/threonine-protein kinase PAK 4	n, p	G	591	0	2	4	0
IPI00003016	Striatin-4		B	753	0	0	0	7
IPI00306471	Coiled-coil domain-containing protein 94			323	0	4	11	1
IPI00002564	DNA repair protein XRCC1		K	633	0	1	3	3

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00014849	[Pyruvate dehydrogenase [lipoamide]] kinase isozyme 3, mitochondrial	p	I	406	1	2	1	12
IPI00019178	Phosphoserine phosphatase		B	225	2	5	0	2
IPI00293857	Isoform 1A of Beta-arrestin-1	o	K, B, D, L	418	2	0	3	9
IPI00173549	synaptopodin-2 isoform a			1261	0	0	5	10
IPI00036742	Isoform 1 of Protein virilizer homolog		K	1812	0	2	0	1
IPI00005648	Scaffold attachment factor B2		K, B	953	0	6	4	4
IPI00106506	Isoform 1 of Evolutionarily conserved signaling intermediate in Toll pathway, mitochondrial		K, B, I	431	1	0	5	3
IPI00328354	Isoform 1 of Melanoma-associated antigen D1	b	B, L	778	0	2	1	5
IPI00166395	Isoform 1 of Acyl-CoA synthetase family member 3, mitochondrial		I	576	1	2	0	6
IPI00165547	Isoform 2 of Phosphatidylinositol 4-kinase beta	p	B, I, F, E, G	801	0	2	7	6
IPI00026940	Nuclear pore complex protein Nup50	o, s	K	468	0	0	2	4
IPI00556619	Isoform 2 of Thioredoxin-related transmembrane protein 2			258	3	1	2	4
IPI00443799	Isoform 1 of Putative sodium-coupled neutral amino acid transporter 10	h		1119	1	2	0	0
IPI00550165	Dehydrogenase/reductase SDR family member 7B			325	2	0	2	0
IPI00031616	22 kDa protein			206	0	2	3	6
IPI00947393	Uncharacterized protein			42	2	3	0	9

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00013939	Isoform 1 of Replication protein A 32 kDa subunit	k	K, J	270	3	6	2	1
IPI00022316	28S ribosomal protein S18b, mitochondrial	r	I, I	258	9	0	2	7
IPI00412880	Isoform 1 of Histone-arginine methyltransferase CARM1		K, B, D	585	3	6	4	1
IPI00099311	Isoform 1 of tRNA (adenine-N(1)-)-methyltransferase non-catalytic subunit TRM6		K	497	4	5	2	2
IPI00100213	Isoform 1 of Ribonucleoside-diphosphate reductase subunit M2 B		K, J, B	351	6	0	3	5
IPI00375731	Putative uncharacterized protein DKFZp686E2459		K, J	995	0	0	1	3
IPI00178187	Isoform 1 of EH domain-binding protein 1		B	1231	1	2	4	4
IPI00019451	MRG-binding protein		K	204	0	0	3	4
IPI00014174	Mortality factor 4-like protein 2		K, J	288	0	1	2	2
IPI00375330	Isoform 1 of Wings apart-like protein homolog	d, j	K, B	1190	10	6	0	3
IPI00022585	cDNA FLJ56047, highly similar to A kinase anchor protein 1, mitochondrial			945	6	1	1	5
IPI00103242	Isoform 1 of Protein POF1B			595	0	0	2	3
IPI00003648	Isoform Delta of Poliovirus receptor-related protein 1	c	H, L	517	6	2	0	0
IPI00465275	Isoform 1 of Ran-binding protein 9		K, B, D	729	2	0	1	3
IPI00028369	Isoform 1 of Protein lunapark			428	6	5	1	2
IPI00019018	Isoform 1 of Delta(14)-sterol reductase		E	418	4	3	2	2
IPI00005184	Isoform Long of tc intermediary factor 1-alpha		K, B	1050	2	4	0	0

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00332376	Ubiquitin-conjugating enzyme E2 D2			147	2	4	3	4
IPI00010187	Elongation of very long chain fatty acids protein 1		E	279	3	1	2	8
IPI00790949	Uncharacterized protein			69	3	5	5	2
IPI00018783	Inosine triphosphate pyrophosphatase		B	194	8	8	7	7
IPI00030389	Isoform Long of Active breakpoint cluster region-related protein	b, p	D	859	2	2	2	2
IPI00007052	Mitochondrial fission 1 protein	b	I	152	9	4	21	18
IPI00640416	19 kDa protein			171	2	6	0	0
IPI00297655	Neurogenic locus notch homolog protein 2	g, e	K, D, L	2471	6	7	3	0
IPI00140827	Uncharacterized protein			95	8	5	9	19
IPI00020530	Acyl-coenzyme A thioesterase 13		B, I	140	1	2	1	3
IPI00011564	Syndecan-4			198	2	2	1	3
IPI00000335	Histidine triad nucleotide-binding protein 2, mitochondrial	b	I	163	4	6	6	10
IPI00009505	Isoform 1 of Beta-2-syntrophin		B, C	540	3	1	2	2
IPI00023087	Ubiquitin-conjugating enzyme E2 T			197	0	5	0	0
IPI00152853	Isoform 1 of Phostensin		B, C	613	1	4	0	2
IPI00376165	Thymosin-like 4			44	9	8	11	10
IPI00032409	Isoform 1 of Mitogen-activated protein-binding protein-interacting protein			125	7	1	0	1
IPI00002803	Isoform 1 of Serine/threonine-protein kinase N1	n, p	K, B, F, L	942	0	4	0	0
IPI00025346	Isoform 1 of Peroxisomal membrane protein PEX14	o, s	K	377	3	6	2	2

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00384047	Isoform 1 of Trafficking protein particle complex subunit 6B		E, G	158	0	0	4	7
IPI00885081	Isoform 2 of Hepatoma-derived growth factor-related protein 2		K	670	3	3	2	2
IPI00031655	Vacuolar protein-sorting-associated protein 25	o	K, B, I, F	176	0	4	0	3
IPI00022386	Thioredoxin domain-containing protein 9			226	2	6	0	0
IPI00555938	T-box 2 variant (Fragment)			317	4	2	2	4
IPI00328911	E3 ubiquitin-protein ligase HECTD1			2612	0	0	4	3
IPI00163391	Isoform 1 of Putative methyltransferase METT10D			562	0	0	2	4
IPI00217053	Isoform 3 of Protein PRRC1		G	462	2	3	4	2
IPI00186581	osteosarcoma amplified 9, er lectin isoform 2 precursor			612	2	2	2	4
IPI00297455	A-kinase anchor protein 8-like		K, B	646	0	5	2	6
IPI00164215	TSPYL protein		K, J	438	0	1	0	7
IPI00043598	Isoform 4 of Inhibitor of nuclear factor kappa-B kinase-interacting protein		E	377	3	1	0	2
IPI00299084	Transmembrane protein 33			247	2	2	0	4
IPI00023191	cDNA FLJ54710, highly similar to Target of Myb protein 1			501	1	2	0	2
IPI00744182	SH3 domain-binding protein 5	p	B, I	455	0	0	0	5
IPI00607605	Isoform 1 of Macrophage erythroblast attacher	d, c	K, B, C, L	396	0	0	0	3
IPI00645608	Interferon regulatory factor 2-binding protein 1		K	584	0	0	3	2
IPI00299517	BRISC complex subunit Abro1			415	1	0	0	6

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00289876	Isoform 1 of Syntaxin-7		F	261	5	0	5	4
IPI00163644	Oxysterol-binding protein			890	4	12	1	2
IPI00014624	AP-3 complex subunit sigma-1		G	293	5	6	0	5
IPI00073779	Isoform 1 of 28S ribosomal protein S35, mitochondrial		I, I	323	1	7	0	0
IPI00401285	DNL-type zinc finger protein		I	178	0	0	2	4
IPI00386418	Isoform 2 of Myelin expression factor 2	q	K, J, G	576	0	2	3	1
IPI00003004	Mitochondrial glutamate carrier 1	s	K, J, I	323	1	1	3	4
IPI00306708	cDNA FLJ58333, highly similar to T-lymphokine-activated killer cell-originated protein kinase	n, j		333	0	0	2	4
IPI00027728	High affinity cationic amino acid transporter 1	h, s	L	629	2	0	2	2
IPI00031109	Mimitin, mitochondrial		I	169	0	0	3	6
IPI00032879	Isoform 1 of Adenylate kinase isoenzyme 6		K, J	172	0	0	1	3
IPI00005040	Isoform 1 of Medium-chain specific acyl-CoA dehydrogenase, mitochondrial		I	421	2	4	1	0
IPI00028946	Isoform 3 of Reticulon-3	b	E, G	236	4	7	5	1
IPI00018968	NEDD8-activating enzyme E1 regulatory subunit	d, p	B, L	534	10	11	0	2
IPI00030278	Isoform 1 of TNF receptor-associated factor 2	b, p	B, D	501	0	2	0	2
IPI00012833	Serine/threonine-protein phosphatase 4 catalytic subunit		K, B, C	307	2	1	3	7
IPI00217862	U3 small nucleolar RNA-interacting protein 2		K, J	475	4	0	3	5
IPI00032892	Geranylgeranyl pyrophosphate synthase		B, D	300	2	3	0	2
IPI00005667	NEDD4-binding protein 1		K, J	896	3	0	1	1

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00021408	Isoform 2 of Diphosphoinositol polyphosphate phosphohydrolase 2		B	181	2	0	4	4
IPI00031629	Phosducin-like protein 3	b	B	239	4	0	4	6
IPI00477962	Isoform 1 of UDP-N-acetylhexosamine pyrophosphorylase-like protein 1	i		507	0	0	2	2
IPI00719051	82 kDa protein			710	2	2	3	4
IPI00010544	Isoform 1 of Tight junction-associated protein 1		G	557	0	0	4	4
IPI00395663	Ankyrin repeat and SAM domain-containing protein 1A		B	1134	0	0	4	3
IPI00100030	Isoform 1 of GPI transamidase component PIG-T		B, E	578	3	3	1	5
IPI00023334	Isoform 1 of 39S ribosomal protein L4, mitochondrial	r	I, I	311	1	8	12	4
IPI00294701	CDK-activating kinase assembly factor MAT1	k, q, f, g	K, B	309	1	2	3	0
IPI00293327	P2X purinoceptor 4	h, p	L	388	0	0	0	5
IPI00413817	Serine incorporator 1		E, L	453	4	7	5	10
IPI00289501	Neurosecretory protein VGF			615	1	0	2	5
IPI00165230	Isoform 1 of DAZ-associated protein 1	e	K, J, B	407	2	2	0	6
IPI00329591	Isoform 1 of Required for meiotic nuclear division protein 1 homolog		I	449	0	2	2	3
IPI00290305	TP53-regulating kinase	n	K	253	10	8	6	4
IPI00019996	SAFB-like tc modulator isoform b			1016	0	5	0	1
IPI00006408	Nitric oxide synthase-interacting protein		K, B, D	301	0	0	2	7

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00006378	Coiled-coil domain-containing protein 72			64	0	7	9	9
IPI00022477	B-cell lymphoma/leukemia 10	b	K, B, D	233	6	4	9	9
IPI00031516	Isoform 1 of GA-binding protein subunit beta-1		K	395	2	3	4	1
IPI00002580	Phosphatidylinositol-4-phosphate 3-kinase C2 domain-containing subunit alpha		K, B, G, L	1686	5	4	1	4
IPI00218463	Mitochondrial import inner membrane translocase subunit Tim16	o, s	I	125	0	0	5	2
IPI00059764	Isoform 1 of Zinc finger protein 428			188	3	11	5	3
IPI00011997	Isoform 1 of UPF0488 protein C8orf33			229	0	0	5	4
IPI00032533	WD repeat-containing protein 18			432	6	5	2	3
IPI00004454	Isoform 1 of Dolichol-phosphate mannosyltransferase subunit 3		E	92	1	1	2	10
IPI00414168	E3 ubiquitin-protein ligase MARCH5		I, E	278	2	5	0	2
IPI00011307	Bifunctional methylenetetrahydrofolate dehydrogenase/cyclohydrolase, mitochondrial		I	350	2	2	2	0
IPI00479125	SLIT-ROBO Rho GTPase-activating protein 2	p	D	1071	0	0	0	3
IPI00375879	Uncharacterized protein KIAA1467			622	0	0	0	5
IPI00427739	Isoform 1 of Leucine-rich repeat-containing protein 1		B	524	1	0	10	13

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00019355	Isoform 2 of TSC22 domain family protein 1		K, B	144	3	4	1	6
IPI00007346	Peptidyl-prolyl cis-trans isomerase H	l	K, B	177	0	0	1	3
IPI00022442	Acyl carrier protein, mitochondrial		I	156	4	4	3	0
IPI00059139	V-type proton ATPase subunit E 2	h, s	D	226	3	1	2	2
IPI00171459	Inactive hydroxysteroid dehydrogenase-like protein 1		I	330	2	3	1	0
IPI00410110	Isoform 1 of Probable ATP-dependent RNA helicase DHX40			779	3	0	0	0
IPI00027799	Isoform 2 of Protein FAM107B			306	0	3	2	5
IPI00015195	Cleavage stimulation factor subunit 3	q, g	K	717	2	4	0	0
IPI00007306	Isoform 1 of Craniofacial development protein 1	c		299	8	6	3	4
IPI00337659	Isoform 2 of Serine/threonine-protein kinase tousled-like 2	n, d	K	750	2	1	0	2
IPI00412492	Isoform 1 of Plexin-D1	p	L	1925	2	5	1	2
IPI00300504	Isoform 1 of Regulator of nonsense transcripts 2		K, B	1272	0	0	0	5
IPI00022276	28S ribosomal protein S28, mitochondrial		I, I	187	0	0	2	3
IPI00013180	Protein BUD31 homolog		K	144	2	1	3	3
IPI00965548	Protein			249	3	3	2	0
IPI00001716	Isoform 2 of tRNA pseudouridine synthase A, mitochondrial		K, J, I	399	2	2	2	2
IPI00470924	Isoform 2 of Transmembrane and TPR repeat-containing protein 3			914	4	2	0	2

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00303214	Isoform 1 of Peroxisomal leader peptide-processing protease			566	0	0	4	8
IPI00186826	Ephrin receptor			935	1	3	3	0
IPI00009335	Brain protein 16			390	0	2	4	2
IPI00006602	nuclear distribution protein nudE-like 1 isoform A			328	5	2	3	5
IPI00011167	TBC1 domain family member 10A			508	2	0	0	3
IPI00011898	tl initiation factor eIF-2B subunit epsilon	r, g	K, B, D	721	2	3	1	0
IPI00032881	28S ribosomal protein S23, mitochondrial		I, I	190	2	2	0	1
IPI00101524	Isoform 1 of Vacuolar-sorting protein SNF8	o	K, B, F	258	2	5	0	3
IPI00550037	28S ribosomal protein S15, mitochondrial	r	I, I	257	0	0	1	4
IPI00002790	Isoform 1 of Protein sel-1 homolog 1		E	794	2	2	1	2
IPI00030738	Isoform 2 of Cytospin-B		K	790	4	4	7	13
IPI00017940	LMBR1 domain-containing protein 2			695	0	3	0	0
IPI00480049	Isoform B of Inositol polyphosphate 5-phosphatase OCRL-1	p	D	893	0	2	10	4
IPI00059264	Vacuolar protein sorting-associated protein 26B	o	B, D	336	0	0	1	5
IPI00064666	Protein FAM84B		B, L	310	4	1	0	0
IPI00166638	Isoform 1 of UPF0598 protein C8orf82		I	216	5	9	2	0
IPI00013651	49 kDa protein			439	7	9	2	5
IPI00007941	Protein HEXIM1		K, J, B	359	0	0	0	5
IPI00384176	Isoform 1 of Protein polybromo-1	j	K	1689	2	2	0	0

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00177428	Isoform 2 of Mitochondrial intermembrane space import and assembly protein 40	o, s	I	155	3	10	3	3
IPI00016802	NAD-dependent deacetylase sirtuin-1	e	K, J, B	747	0	2	6	5
IPI00746351	Isoform 1 of Exosome complex exonuclease RRP44		K, J, B, D	958	0	0	2	6
IPI00005966	13kDa differentiation-associated protein variant (Fragment)		I	146	0	6	2	2
IPI00106646	Isoform 1 of 45 kDa calcium-binding protein		B, G, L	362	6	6	10	4
IPI00012773	Isoform Long of Metastasis-associated protein MTA1	p	K, J, B	715	0	3	0	2
IPI00307591	Zinc finger protein 609		K	1411	4	2	0	0
IPI00418234	Isoform A of Methyl-CpG-binding protein 2		K	486	0	0	0	4
IPI00030357	Dihydrofolate reductase	k	D	187	0	0	2	4
IPI00025890	Isoform 1 of N-alpha-acetyltransferase 25, NatB auxiliary subunit		B	972	0	0	1	3
IPI00013773	Isoform 1 of Receptor-interacting serine/threonine-protein kinase 1	b, p	B, I, D, L	671	0	2	1	0
IPI00156793	DNA repair protein complementing XP-C cells		K, B	940	5	6	1	0
IPI00465315	Cytochrome c	b	K, I, D	105	15	1	0	0
IPI00009958	COP9 signalosome complex subunit 5	r	K, J, B	334	0	3	0	3
IPI00102096	Isoform 1 of Stromal membrane-associated protein 1		L	467	0	1	1	4
IPI00000057	Conserved oligomeric Golgi complex subunit 2		G	738	2	3	0	5

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00554538	Uncharacterized protein			555	0	4	0	3
IPI00844323	Isoform 5 of Protein BAT2-like 1			2229	0	0	2	1
IPI00018276	Isoform 3 of Seizure 6-like protein 2		E, L	853	1	0	4	5
IPI00329005	Isoform 2 of Aftiphilin	o	K, J, B, G, D	909	0	0	0	3
IPI00018120	28S ribosomal protein S29, mitochondrial		K, J, I	398	0	5	0	1
IPI00023186	TOM1-like protein 1		F, G, D	476	0	0	1	2
IPI00003606	E3 ubiquitin-protein ligase RNF14	p	K, B	474	0	0	2	3
IPI00023704	Lipoma-preferred partner	c	K, B, L	612	1	0	0	4
IPI00013457	Isoform 1 of Zinc finger protein 207		K, J	478	5	5	2	1
IPI00385987	Isoform 1 of Sn1-specific diacylglycerol lipase beta		L	672	1	0	0	2
IPI00749454	cDNA FLJ56561		L	792	3	6	4	2
IPI00077853	Isoform 1 of Oxysterol-binding protein-related protein 9			736	0	1	0	4
IPI00219217	L-lactate dehydrogenase B chain		B, I, D	334	19	2	12	17
IPI00167492	Uncharacterized protein C4orf32			132	1	3	36	37
IPI00790530	Nuclear pore complex protein Nup85	k, o, s	K, B, D, C	656	1	1	2	4
IPI00004392	Isoform p26 of 7,8-dihydro-8-oxoguanine triphosphatase		B	197	0	8	2	6
IPI00029631	Enhancer of rudimentary homolog	d		104	1	2	1	6
IPI00008752	Isoform 1 of Metallothionein-1G			62	0	3	4	8
IPI00025478	Interferon regulatory factor 9		K, B, D	393	5	2	0	0
IPI00013236	Isoform 2 of Vesicle-associated membrane protein 7	o	F, E, G, L	260	1	0	2	2

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00015102	Isoform 1 of CD166 antigen	c, p		583	3	2	0	2
IPI00163185	arf-GAP with GTPase, ANK repeat and PH domain-containing protein 3 isoform a	p	B	911	5	10	0	0
IPI00470631	Isoform 1 of Ubiquinone biosynthesis protein COQ9, mitochondrial		I	318	5	17	6	10
IPI00024214	Isoform 1 of Telomeric repeat-binding factor 2	d	K, J, B, G	500	0	1	0	3
IPI00289807	Isoform 1 of tRNA-nucleotidyltransferase 1, mitochondrial		I	434	0	0	0	4
IPI00015864	2-5A-dependent ribonuclease	n	B, I	741	4	0	0	0
IPI00016006	Isoform 1 of Gephyrin		B, C, L	736	8	14	6	2
IPI00305461	Inter-alpha (Globulin) inhibitor H2, isoform CRA_a			947	3	4	0	0
IPI00306049	Isoform 1 of Protein misato homolog 1		B, I	570	2	2	2	6
IPI00160021	NFU1 iron-sulfur cluster scaffold homolog, mitochondrial isoform 1			230	2	4	4	3
IPI00154645	Isoform 1 of TBC1 domain family member 15		B, I	691	0	1	2	2
IPI00411531	Isoform 2 of General tc factor 3C polypeptide 5	q	K	509	1	0	7	4
IPI00549664	Testis-expressed sequence 10 protein		K, J	929	7	6	6	3
IPI00296635	1,4-alpha-glucan-branching enzyme		D	702	5	2	0	2
IPI00022543	GPI-anchor transamidase		E	395	0	1	4	0
IPI00023556	Isoform 1 of RNA polymerase II subunit A C-terminal domain phosphatase SSU72		K, B	194	0	0	0	7

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00554701	Cytochrome b-c1 complex subunit 9		I	63	8	7	0	5
IPI00016077	Protein NipSnap homolog 2		I	286	0	0	0	4
IPI00786897	26 kDa protein			232	4	8	8	15
IPI00042580	Isoform 1 of Apolipoprotein O			198	2	0	0	1
IPI00174771	Isoform 1 of Rab11 family-interacting protein 4	o	F	637	0	0	0	3
IPI00302030	Ras-related protein Rab-30	o	L	203	5	5	0	0
IPI00100947	Leukocyte receptor cluster member 1			264	1	10	2	6
IPI00550733	Isoform 1 of TBC1 domain family member 2B			963	10	7	6	4
IPI00171769	FUN14 domain-containing protein 2		I	189	2	2	0	4
IPI00013271	Derlin-1	o	E	251	4	0	0	3
IPI00100930	cDNA FLJ58610			263	0	0	0	3
IPI00009917	Isoform 3 of Protein LAS1 homolog		K, J	675	1	0	1	3
IPI00031563	DET1- and DDB1-associated protein 1			102	0	1	4	6
IPI00395463	Charged multivesicular body protein 7		B	453	0	4	2	2
IPI00296922	Laminin subunit beta-2	c		1798	2	0	0	0
IPI00915872	Trinucleotide repeat containing 6B			745	0	0	0	3
IPI00419802	Isoform 1 of 3-hydroxyisobutyryl-CoA hydrolase, mitochondrial		I	386	0	0	1	7
IPI00007943	STAM-binding protein		K, B	424	0	0	3	2
IPI00017597	Isoform 1 of Microtubule-associated protein RP/EB family member 3	d, j	B, C	281	6	2	0	0
IPI00410485	Serine/threonine-protein kinase TAO3	n	B, I, L	898	2	2	4	5

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00006558	Isoform 1 of Endophilin-B1	b, p	B, I, G	365	0	0	5	6
IPI00045939	2-aminoethanethiol dioxygenase		I	270	0	0	1	3
IPI00006504	Isoform 1 of tl initiation factor eIF-2B subunit gamma	r, g	B, D	452	2	3	2	2
IPI00003565	26S proteasome non-ATPase regulatory subunit 10	k, b	K, B	226	5	5	2	4
IPI00294008	ZW10 interactor	k, d	K, B, D	277	0	0	0	3
IPI00012479	Putative nascent polypeptide-associated complex subunit alpha-like protein			213	0	28	19	11
IPI00299468	Acyl-CoA desaturase		E	359	5	8	7	1
IPI00855946	Sorting nexin-30	o	B	437	1	2	2	4
IPI00027745	Isoform Long of Beta-glucuronidase			651	1	6	3	6
IPI00297931	Isoform 1 of Synergin gamma		B, G	1314	2	2	2	4
IPI00100775	Isoform 1 of UPF0366 protein C11orf67			122	2	1	0	3
IPI00410324	Isoform 1 of Protein LSM12 homolog			195	0	0	0	3
IPI00242630	Isoform 1 of HEAT repeat-containing protein 2			855	2	0	2	3
IPI00307592	ATP-binding cassette sub-family A member 2 isoform a			2436	3	0	0	0
IPI00418336	Isoform 2 of Integrator complex subunit 3		K	1042	0	0	0	18
IPI00001885	Sorting nexin-8			465	6	7	0	0
IPI00456965	Isoform 1 of Ubiquinone biosynthesis methyltransferase COQ5, mitochondrial		I	327	10	8	2	2
IPI00014398	four and a half LIM domains protein 1 isoform 5			296	8	0	1	2
IPI00024619	Uncharacterized protein C16orf61			79	0	0	0	5

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00061108	Isoform 1 of r-recycling factor, mitochondrial	r	I	262	0	0	0	4
IPI00011511	Isoform 2 of Cat eye syndrome critical region protein 5	i	I	423	0	0	2	3
IPI00018370	Isoform 2 of Supervillin		K, B, L	1788	0	0	3	1
IPI00020508	Isoform 1 of N(2),N(2)-dimethylguanosine tRNA methyltransferase			659	0	0	0	4
IPI00254162	cDNA FLJ55936, highly similar to Polypyrimidine tract-binding protein 2		K	548	0	2	8	8
IPI00220421	Isoform 2 of Arf-GAP with Rho-GAP domain, ANK repeat and PH domain-containing protein 1	p	B, G, D, L	1199	0	0	0	3
IPI00855846	UPF0727 protein C6orf115			81	0	0	1	4
IPI00018451	Calcium and integrin-binding protein 1	b, c	K, B, E, L	191	0	0	0	3
IPI00307200	Switch-associated protein 70		K, B, L	585	2	2	2	6
IPI00410249	Isoform 2 of Zinc transporter ZIP11	h, s		335	3	3	0	2
IPI00020495	28S ribosomal protein S36, mitochondrial	r	I, I	103	0	0	10	5
IPI00021518	Isoform 1 of DNA damage-binding protein 2		K	427	1	0	1	3
IPI00002330	Ubiquitin carboxyl-terminal hydrolase 3	k	K	520	1	0	2	4
IPI00008714	Annexin A9		D	345	0	2	1	6
IPI00024368	Isoform Long of Probable phospholipid-transporting ATPase IIA			1047	2	7	2	8
IPI00395568	Isoform 1 of PHD finger protein 6		K, J	365	0	0	0	4
IPI00166784	E3 SUMO-protein ligase		K	247	0	1	4	9

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
	NSE2							
IPI00220102	Isoform 3 of DnaJ homolog subfamily B member 2	l		324	0	0	2	5
IPI00745568	Isoform 1 of TIP41-like protein		B	272	2	0	0	4
IPI00184363	Glycolipid transfer protein		B	209	6	6	2	5
IPI00151358	Isoform 1 of Cleft lip and palate transmembrane protein 1-like protein	b		538	5	1	4	9
IPI00005050	28S ribosomal protein S14, mitochondrial	r	I, I	128	0	0	2	3
IPI00010873	Tryptophan-rich protein		K, J	174	0	0	3	9
IPI00012429	Protein of unknown function UPF0118 family protein			886	2	0	2	0
IPI00006516	Isoform 1 of Uracil-DNA glycosylase	i	K, I	304	0	0	0	4
IPI00328985	Isoform 1 of THO complex subunit 6 homolog			341	2	0	0	8
IPI00303954	cytochrome b5 type B precursor			150	4	2	0	1
IPI00374574	Isoform 1 of Inositol polyphosphate 5-phosphatase K		E, D	448	4	0	0	0
IPI00170924	Histidine triad nucleotide-binding protein 3		K, J, B, I	182	2	0	0	0
IPI00294610	Isoform 1 of DnaJ homolog subfamily A member 3, mitochondrial	l, b	K, B, I, D	480	2	3	5	5
IPI00006113	DNA-directed RNA polymerase II subunit RPB9	q, g	K	125	0	0	2	0
IPI00028912	vascular endothelial zinc finger 1	x	K, J	521	4	0	0	4
IPI00163659	Isoform 3 of Protein CASC5	k	K, D	1746	0	0	3	2
IPI00007909	Prenylated Rab acceptor protein 1		B, G, L	185	0	2	0	4

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00023101	cd protein RCD1 homolog		K, D	299	0	0	0	4
IPI00009466	similar to coiled-coil-helix-coiled-coil-helix domain containing 2			184	1	2	1	2
IPI00296157	Isoform 1 of All-trans-retinol 13,14-reductase		E	610	0	0	2	2
IPI00291316	Isoform 1 of Rho guanine nucleotide exchange factor 2	b, d, j	B, G, D, C, L	986	1	0	3	3
IPI00166996	Isoform 1 of E3 ubiquitin-protein ligase synoviolin		K, J, E	617	1	4	0	3
IPI00749237	6.8 kDa mitochondrial proteolipid		I	58	4	3	1	2
IPI00401321	Protein arginine N-methyltransferase 3		B	531	5	0	1	2
IPI00465100	Isoform 2 of Zinc finger protein 574		K	986	0	0	2	2
IPI00478003	Alpha-2-macroglobulin		D	1474	2	2	0	0
IPI00383598	Cytochrome c oxidase polypeptide VIa			86	4	4	4	2
IPI00020191	Isoform 1 of Protein tyrosine phosphatase type IVA 2		B, L	167	12	6	0	5
IPI00168554	Sulfiredoxin-1		B, D	137	0	0	0	4
IPI00009544	RalA-binding protein 1	p	D	655	6	9	0	4
IPI00215997	CD9 antigen	c	L	228	2	4	0	9
IPI00925571	Lemur tyrosine kinase 2			1454	0	0	2	3
IPI00019463	Interferon-induced, double-stranded RNA-activated protein kinase	r, n	D	551	0	4	1	0
IPI00009885	Peptidyl-prolyl cis-trans isomerase FKBP11	l		201	5	3	0	0
IPI00024348	Peroxisomal membrane protein PEX13	o		403	1	0	0	3
IPI00015736	Isoform 1 of Ubiquitin-like modifier-activating enzyme 5		K, B	404	0	0	0	3

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00374563	Agrin	p		2045	0	0	0	3
IPI00022091	Isoform 1 of Cell division cycle protein 16 homolog	k, j, f	K, B, D, C	620	0	0	2	3
IPI00292009	Isoform 2 of Palladin		K, B, C	1106	3	2	0	1
IPI00031063	Repressor of RNA polymerase III tc MAF1 homolog		K, B	256	0	1	0	3
IPI00006682	Protein phosphatase 1 regulatory subunit 3D			299	2	2	0	3
IPI00220528	Small nuclear ribonucleoprotein F	q, g	K, D	86	3	0	1	8
IPI00009009	Protein CWC15 homolog		K	229	0	0	1	6
IPI00006863	Sperm-associated antigen 7		K	293	0	0	8	2
IPI00024658	OTU domain-containing protein 7B		K, B	843	0	2	2	4
IPI00022465	Isoform 1 of Citron Rho-interacting kinase	n, d, j, e	B	2027	9	0	1	3
IPI00386220	Protein FAM18B			205	0	4	0	0
IPI00027463	Protein S100-A6	p	K, B, D, L	90	0	0	9	10
IPI00152143	Zinc finger protein 519		K	540	0	0	0	4
IPI00014301	Oxidase (Cytochrome c) assembly 1-like		I	496	0	1	2	2
IPI00056504	Ubiquitin-conjugating enzyme E2 E3		K, J, B	207	0	4	0	0
IPI00556641	Isoform 2 of Phosphatidate phosphatase LPIN3		K	852	5	1	0	0
IPI00008867	Glycogen [starch] synthase, liver		B, D, C	703	0	4	0	2
IPI00073602	Exosome complex exonuclease MTR3		K, J, B, D	272	2	0	0	3
IPI00300384	Isoform 1 of Receptor tyrosine-protein kinase erbB-2	n, p, f	K, B, L	1255	0	1	6	6
IPI00001580	Isoform 1 of FYVE and coiled-coil domain-containing protein 1			1478	0	0	0	3

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00182933	Isoform 2 of Cytochrome b5		B, I, E, H	98	3	7	4	3
IPI00216999	Pumilio domain-containing protein C14orf21			636	0	0	0	2
IPI00017801	Isoform 1 of Mitogen-activated protein kinase kinase kinase 3		D	626	3	2	2	2
IPI00418603	Ubiquitin-conjugating enzyme E2 R2			238	1	4	0	3
IPI00181047	Isoform 2 of Calcium-independent phospholipase A2-gamma	i	B, E, G	720	3	0	0	1
IPI00010348	Deoxyribonuclease-2-alpha	b		360	3	2	2	4
IPI00152627	C11orf30 protein			1337	0	0	0	3
IPI00333016	Isoform 3 of DnaJ homolog subfamily C member 11	l		507	0	0	4	4
IPI00016472	Isoform 2 of Zinc finger CCCH domain-containing protein 13			1564	0	0	2	8
IPI00007001	39S ribosomal protein L11, mitochondrial	r	I, I	192	1	2	2	3
IPI00007327	Isoform 1 of Tapasin		E, H	448	4	3	0	2
IPI00739464	similar to actin, gamma 1			152	0	6	0	0
IPI00018037	Surfeit locus protein 2			256	7	0	1	0
IPI00411901	Isoform 1 of Disks large homolog 5	p	B, L	1919	0	0	1	3
IPI00024714	Isoform 1 of Regulator of G-protein signaling 12		K, B, L	1447	0	0	0	3
IPI00015351	Isoform 1 of UPF0424 protein C1orf128			211	2	2	2	1
IPI00005502	Atrophin 1		K, B	1191	0	0	1	3
IPI00180781	Isoform 1 of Mixed lineage kinase domain-like protein	n		471	0	3	1	2
IPI00479523	Isoform 2 of Triple functional domain protein	n, b	B, D	2921	0	0	2	7

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00883655	Dihydropyrimidinase-like 2 long form (Fragment)			165	2	1	0	2
IPI00411705	Isoform 1 of Chronic lymphocytic leukemia deletion region gene 6 protein			196	3	3	0	0
IPI00009333	Transmembrane protein 9			183	0	0	0	3
IPI00012575	Pirin		K, B	290	0	0	7	7
IPI00470594	Isoform 1 of UPF0485 protein C1orf144			152	1	3	7	13
IPI00015804	tRNA-dihydrouridine synthase 2-like		B, I, E	493	1	0	4	4
IPI00432751	Isoform 3 of Autophagy-related protein 16-1	o	B	470	0	0	1	4
IPI00152900	cDNA FLJ55829, highly similar to Homo sapiens leucine zipper and CTNNBIP1 domain containing (LZIC), mRNA			211	3	1	2	0
IPI00297113	E3 ubiquitin-protein ligase TRIM32		K, B	653	1	0	3	0
IPI00006099	r biogenesis protein BMS1 homolog		K, J	1282	3	4	0	0
IPI00009949	Proteasome inhibitor PI31 subunit	k, b		271	7	2	0	0
IPI00100106	Isoform 3 of Synembryn-A		B	537	0	2	0	0
IPI00307409	39S ribosomal protein L9, mitochondrial	r	I, I	267	0	3	2	3
IPI00013981	Proto-oncogene tyrosine-protein kinase Yes		B, D, L	543	4	4	4	2
IPI00015865	Poly(ADP-ribose) glycohydrolase ARH3		K, J, B	363	0	3	0	0
IPI00024698	Isoform 1 of Polyglutamine-binding protein 1		K, J, B	265	0	1	3	4
IPI00550440	Transmembrane protein			371	0	6	0	0

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
	C2orf18							
IPI00935692	hypothetical protein XP_002348229			105	3	7	13	19
IPI00871174	C-Myc-binding protein		K, B, I	103	4	4	11	2
IPI00106549	Diphthamide biosynthesis protein 2			489	2	0	3	4
IPI00329088	Isoform 1 of Chromodomain-helicase-DNA-binding protein 1-like		K, J, B, L	897	2	0	0	4
IPI00382816	Fetal beta-MHC binding factor			398	0	0	0	3
IPI00305552	cDNA FLJ39671 fis, clone SMINT2008917			158	0	0	0	5
IPI00022463	Serotransferrin	h, s		698	0	3	0	1
IPI00152990	253 kDa protein			2246	0	0	1	2
IPI00010427	Transmembrane protein 93			110	3	0	1	1
IPI00016559	Probable tRNA(His) guanylyltransferase		B, I	298	2	5	2	5
IPI00414896	Isoform 1 of Ribonuclease T2			256	0	0	0	3
IPI00014147	PCNA-associated factor		K, I	111	0	0	2	12
IPI00374362	Importin subunit alpha-8		K, B	516	0	1	1	4
IPI00003389	Mitochondrial ornithine transporter 1	s	I	301	1	2	0	0
IPI00395569	Isoform 1 of Neurobeachin-like protein 1			2604	0	0	3	2
IPI00185769	cDNA FLJ61700, highly similar to ATP-dependent DNA helicase Q5		K, J, B	1018	0	0	0	3
IPI00059687	hypothetical protein LOC147339 isoform a			404	0	0	0	4
IPI00179172	Isoform 2 of Liprin-beta-1	c	L	1005	0	0	4	0
IPI00305668	28S ribosomal protein S6, mitochondrial	r	I	125	4	1	7	9
IPI00013789	SET and MYND domain-containing protein 5			418	4	7	0	0

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00001541	Mitochondrial import inner membrane translocase subunit Tim9	o, s	I	89	0	4	0	3
IPI00302176	Isoform 1 of H/ACA ribonucleoprotein complex subunit 1		K, J	217	4	3	3	2
IPI00007401	Importin-8	p	K, B	1037	0	0	0	3
IPI00016605	UPF0587 protein C1orf123			160	0	0	0	4
IPI00329057	Isoform 1 of F-box/LRR-repeat protein 18			805	2	2	0	0
IPI00011578	Isoform 1 of Neuroplastin	c	L	282	4	0	0	2
IPI00215998	CD63 antigen		B, L	238	3	0	0	0
IPI00740961	DKFZP586J0619 protein			2408	0	0	0	3
IPI00185361	ATP-dependent RNA helicase DDX55			600	0	0	3	2
IPI00005792	Isoform 1 of Polyadenylate-binding protein 2	q, g	K, J, B	306	4	2	3	2
IPI00032087	Disco-interacting protein 2 homolog C		K	1556	0	0	0	3
IPI00305545	Isoform 1 of Lariat debranching enzyme		K	544	6	0	2	2
IPI00164481	Isoform 2 of Double-stranded RNA-binding protein Staufen homolog 2		K, J, B, E	538	2	1	0	6
IPI00296370	Uncharacterized protein			338	5	8	6	10
IPI00012885	Isoform 1 of Focal adhesion kinase 1	n, b	B, D, C, L	1052	0	1	0	2
IPI00004500	NEDD4-binding protein 3		B	544	0	1	1	3
IPI00375452	Solute carrier family 19 (Folate transporter), member 1, isoform CRA_f		L	613	0	0	0	4

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00003870	Putative ATP-dependent Clp protease proteolytic subunit, mitochondrial		I	277	0	2	3	0
IPI00009148	Diphosphoinositol polyphosphate phosphohydrolase 1		B	172	0	0	2	3
IPI00012107	Fatty-acid amide hydrolase 1		B, C	579	3	0	0	0
IPI00290094	Splicing factor, arginine/serine-rich 8		K	951	1	3	0	2
IPI00159072	regulator of differentiation 1 isoform 2			524	11	11	1	2
IPI00004337	Zinc finger and BTB domain-containing protein 11		K	1053	4	0	1	0
IPI00167198	Isoform 2 of U4/U6 small nuclear ribonucleoprotein Prp31		K	364	2	4	5	1
IPI00018240	Isoform 1 of Protein SDA1 homolog	o	K, J	687	4	5	0	0
IPI00916281	Protein			38	2	0	2	5
IPI00290032	Transient receptor potential cation channel subfamily M member 7	h, s	L	1865	3	0	0	0
IPI00783656	39S ribosomal protein L38, mitochondrial		B, I, I	380	0	0	1	3
IPI00008692	Isoform 1 of Keratin, type I cuticular Ha6			467	4	6	7	6
IPI00411730	Isoform 1 of Serine/threonine-protein phosphatase 4 regulatory subunit 1	n, p		950	0	0	0	3
IPI00061777	Coiled-coil domain-containing protein 97			343	0	0	0	4
IPI00028415	Isoform PBX1a of Pre-B-cell leukemia tc factor 1	e	K, J, B	430	0	0	0	3

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00399254	Isoform 1 of OTU domain-containing protein 4			1114	2	0	0	0
IPI00000733	U3 small nucleolar RNA-associated protein 18 homolog		K, J	573	3	1	0	0
IPI00375677	Mitochondrial ribosomal protein L21 isoform d	r	I, I	209	0	0	1	4
IPI00004974	cDNA FLJ55772, highly similar to Rab5 GDP/GTP exchange factor			505	0	0	0	2
IPI00016871	Tyrosine-protein kinase Fgr	n	D, L	529	4	4	4	2
IPI00748953	Isoform 1 of Histone deacetylase complex subunit SAP130		K	1048	4	1	0	0
IPI00176527	ATP synthase subunit epsilon-like protein, mitochondrial	h	I	51	1	2	3	5
IPI00030023	Histamine N-methyltransferase		B	292	1	0	0	3
IPI00304693	Isoform 2 of Arf-GAP domain and FG repeats-containing protein 1	e	K, G	522	0	0	0	3
IPI00000643	BAG family molecular chaperone regulator 2	l, b		211	0	3	1	1
IPI00030820	Isoform 1 of 39S ribosomal protein L47, mitochondrial	r	I, I	250	3	0	0	3
IPI00908692	cDNA FLJ60521, highly similar to Protein kinase-like protein C9orf96			161	2	1	3	7
IPI00022536	Isoform 1 of Ribosomal protein S6 kinase alpha-4	n	K, J, B	772	0	0	3	1
IPI00298925	Isoform Long of tc initiation factor TFIID subunit 5	q, g	K, J	800	5	0	0	0
IPI00017337	Isoform A of Annexin A13	e	L	316	4	0	0	2
IPI00298301	Myosin-3		B, D	1940	1	0	1	2
IPI00063962	Protein DPCD			203	0	0	0	3
IPI00293167	Stromal cell-derived factor 2			211	0	0	0	3

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00549761	Chitobiosyldiphosphodolichol beta-mannosyltransferase		E	464	1	1	5	5
IPI00302453	Isoform 1 of Dynein heavy chain 9, axonemal		B, C	4486	5	2	3	8
IPI00004656	Beta-2-microglobulin		L	119	0	1	2	5
IPI00289758	Calpain-2 catalytic subunit		B, L	700	0	3	0	2
IPI00028883	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 8, mitochondrial		I, E	186	2	0	0	4
IPI00018117	Death-associated protein 1			102	1	0	0	5
IPI00470526	Protein TRIQK		E	86	3	0	0	1
IPI00024305	Mothers against decapentaplegic homolog 3		K, B, D, L	425	0	0	0	6
IPI00410657	Isoform 2 of mRNA cap guanine-N7 methyltransferase	q, g	K	504	2	2	0	0
IPI00019459	TGF-beta-activated kinase 1 and MAP3K7-binding protein 1		D	504	0	0	0	3
IPI00171611	Histone H3.2		K	136	2	0	12	4
IPI00004247	Isoform 1 of Phosphorylase b kinase regulatory subunit alpha, skeletal muscle isoform		D, L	1223	0	0	0	3
IPI00938023	similar to TRIMCyp			221	3	9	12	19
IPI00021058	Solute carrier family 4 sodium bicarbonate cotransporter member 7			1135	0	0	1	4
IPI00793874	Sideroflexin-3	s	I	325	2	1	0	0
IPI00011217	NADH dehydrogenase [ubiquinone] iron-sulfur protein 4, mitochondrial		I	175	0	0	0	3
IPI00026496	Nucleoplasmin-3		K, J	178	3	0	0	4
IPI00329583	Isoform 1 of Spermatogenesis-associated protein 5	e	B, I	893	0	0	1	2

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00888430	Isoform 1 of Dynein heavy chain 17, axonemal		B, C	4485	2	0	1	4
IPI00031802	Tumor necrosis factor ligand superfamily member 13B	p, f	L	285	0	0	3	3
IPI00218081	dermatan-sulfate epimerase-like protein			1222	0	2	0	0
IPI00029730	Syntaxin-4		B, D, L	297	0	0	0	3
IPI00028277	Isoform 1 of Alpha-ketoglutarate-dependent dioxygenase FTO		K	505	5	3	0	0
IPI00248126	Septin-14	d	B, C	432	4	1	1	1
IPI00645814	Isoform 2 of MAP7 domain-containing protein 1		B, C	803	0	0	2	2
IPI00158296	204 kDa protein			1809	0	0	0	3
IPI00010463	GTP-binding protein 1	p		669	0	0	0	2
IPI00024620	Enhancer of yellow 2 tc factor homolog		K	101	0	0	0	3
IPI00470537	Isoform 1 of AT-rich interactive domain-containing protein 2		K	1835	2	0	0	3
IPI00063760	Zinc finger protein 234		K	700	0	1	2	0
IPI00071824	Isoform 1 of cs-associated protein 2	b, d	B	683	0	0	0	2
IPI00550192	Isoform 1 of Probable Xaa-Pro aminopeptidase 3		I	507	8	10	6	9
IPI00386786	Isoform 2 of Syntaxin-5		K, J, E, G	301	5	6	1	0
IPI00216990	Isoform 1 of Uncharacterized protein KIAA2026			2103	3	0	0	0
IPI00015522	Growth/differentiation factor 5			501	0	0	5	2
IPI00056314	Pre-rRNA-processing protein TSR2 homolog			191	0	0	0	2
IPI00013002	Ubiquitin-conjugating enzyme E2 C	k, d, j	D	179	2	0	0	4

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00410590	Isoform 2 of Protein LSM14 homolog A		B	463	0	0	1	4
IPI00017603	Coagulation factor VIII	c	L	2351	0	0	0	4
IPI00382985	Isoform 1 of Ribonuclease H2 subunit C		K	164	0	0	1	3
IPI00003386	E3 ubiquitin-protein ligase RBX1		K, B, D	108	3	0	0	0
IPI00002501	Cyclic AMP-dependent tc factor ATF-1		K	271	0	0	4	2
IPI00011757	RNA polymerase II elongation factor ELL2		K	640	2	2	2	2
IPI00004237	Phosphorylase b kinase regulatory subunit alpha, liver isoform		D, L	1235	0	0	0	2
IPI00002968	Molybdopterin synthase sulfur carrier subunit		B, D	88	0	1	0	3
IPI00303944	Isoform 1 of Putative methyltransferase NSUN4			384	0	0	0	4
IPI00015578	Isoform 1 of Palmdelphin		B	551	4	2	0	0
IPI00014516	Isoform 1 of Caldesmon		B, D, C, L	793	0	0	0	3
IPI00022164	Isoform 1 of Rho guanine nucleotide exchange factor 12	b	B, D	1544	4	1	0	0
IPI00964394	Protein			142	1	3	2	4
IPI00157757	cDNA FLJ56489, highly similar to NEDD9-interacting protein with calponin homology and LIM domains	p	B, C	1086	0	0	1	2
IPI00021156	Isoform 4 of Kalirin	n, b, p	B, D	1288	0	0	0	2
IPI00794307	hypothetical protein			140	0	0	1	4
IPI00937782	Isoform 1 of Intersectin-2		B	1697	2	0	3	2
IPI00007404	Isoform 1 of Ubiquitin-like modifier-activating enzyme ATG7	o	B	703	0	0	2	0
IPI00306929	Myosin XVIIIB			2569	0	0	1	3

Accession No.	Protein Name	Biological Function	Cellular Location	Length	BR1TR1 SpC	BR1TR2 SpC	BR2TR1 SpC	BR2TR2 SpC
IPI00892641	Protein			58	1	2	0	0
IPI00298281	Laminin subunit gamma-1	c		1609	0	0	3	0
IPI00027096	39S ribosomal protein L19, mitochondrial	r	K, I, I	292	0	0	0	3
IPI00009464	Isoform 1 of Exosome component 10		K, J, B	885	0	0	0	3
IPI00879874	52 kDa protein			447	2	2	1	1
IPI00043526	cDNA FLJ55603			710	2	0	0	0
IPI00100154	Toll-interacting protein	p	B, D	274	0	0	3	0
IPI00328885	immunoglobulin-like and fibronectin type III domain-containing protein 1		K, B	3708	0	0	0	2
IPI00299010	Isoform 1 of Paraplegin		I	795	2	4	0	0
IPI00297572	Intron-binding protein aquarius		K	1486	0	0	2	0
IPI00218694	Isoform 2 of Caldesmon		B, D, C, L	564	0	0	0	2
IPI00303335	Nebulin		B, D	6669	0	0	1	5
IPI00743820	Isoform 2 of Leiomodin-3		B, C	348	0	0	3	0

*** a) angiogenesis b) apoptosis c) cell adhesion d) cell cycle e) cell differentiation f) cell proliferation g) gene expression**

h) ion transport i) metabolic process j) mitosis k) mitotic cell cycle l) protein folding m) protein localization n) protein phosphorylation

o) protein transport p) signal transduction q) transcription r) translation s) transmembrane transport

Appendix II

Accession No.	Protein Name	Molecular Function*	Fold Change	BayesFactor	RBstat
IPI00000041	Rho-related GTP-binding protein RhoB	a,b,c,d,e	-18.3	182.4	7705.6
IPI00000735	Tetraspanin-13	a	7.5	54.5	33.6
IPI00001539	3-ketoacyl-CoA thiolase, mitochondrial	b	-2.3	1612.3	252.6
IPI00001699	Isoform 1 of Apoptosis-associated speck-like protein containing a CARD	a,b,d	-2.0	96.9	31.5
IPI00002335	Huntingtin	a,b,c,d	1.9	34.5	19.7
IPI00002525	Neudesin	b	-16.0	67.0	2477.3
IPI00002790	Isoform 1 of Protein sel-1 homolog 1	g	7.2	35.8	31.5
IPI00002926	Vacuolar protein sorting-associated protein 37B	d	3.3	8440.9	5799.8
IPI00003168	Phosphoribosyl pyrophosphate synthase-associated protein 2		-16.7	93.0	4093.9
IPI00003377	Isoform 1 of Serine/arginine-rich splicing factor 7	d	-18.0	244.2	9463.5
IPI00004416	Charged multivesicular body protein 2a	d	-2.7	78.7	5.0
IPI00005129	Isoform 1 of Secretory carrier-associated membrane protein 1	d	3.5	29.9	238.2
IPI00005194	Ubiquitin domain-containing protein UBFD1	a,b	-15.3	48.4	1475.4
IPI00005668	Aldo-keto reductase family 1 member C2	b	-30.3	128.7	5.5
IPI00005688	Isoform 1 of Zinc finger protein 185	a,b,d	12.8	1991.0	389.5
IPI00006025	Isoform 1 of Squamous cell carcinoma antigen recognized by T-cells 3	b	-3.6	250.5	845.1
IPI00006181	Eukaryotic translation initiation factor 3 subunit D	b,f	-2.3	156.8	12.2
IPI00006442	Coilin	e	3.4	38283.1	6.7
IPI00006957	Isoform 1 of Dehydrogenase/reductase SDR family member 7	e	2.4	65.6	300.6
IPI00007334	Isoform 1 of Apoptotic chromatin condensation inducer in the nucleus	a,b	1.9	6453.9	96.4
IPI00007764	Isoform 1 of Hematological and neurological expressed 1 protein	b	-38.4	1472.8	3.1
IPI00007927	Isoform 1 of Structural maintenance of chromosomes protein 2	e	-2.9	257.3	10.2
IPI00008511	NADH dehydrogenase subunit 5	a	9.5	154.2	64.4
IPI00008961	Telomeric repeat-binding factor 2-interacting protein 1	e	-15.3	48.4	1217.1
IPI00009943	Tumor protein, translationally-controlled 1	a	18.2	59330.4	5471.1
IPI00010133	Coronin-1A	a,b,c,d,e	9.5	222.0	111.7

Accession No.	Protein Name	Molecular Function*	Fold Change	BayesFactor	RBstat
IPI00010418	Isoform 2 of Myosin-Ic	d	36.2	4.7E+07	9.3
IPI00011274	Isoform 1 of Heterogeneous nuclear ribonucleoprotein D-like	f	-35.1	320.7	3.3
IPI00011593	Isoform 1 of Fos-related antigen 2	a,b	-14.1	36.6	1647.8
IPI00011916	Aminoacyl tRNA synthase complex-interacting multifunctional protein 2	b	1.9	38.5	5.1
IPI00011996	Isoform 1 of Ubiquitin-conjugating enzyme E2 Z	b	-15.7	106.9	8700.7
IPI00012462	Eukaryotic translation initiation factor 2A	f	-35.6	464.9	4.0
IPI00012726	Isoform 1 of Polyadenylate-binding protein 4	b,f	-71.1	3.7E+06	13.5
IPI00012998	Isoform 1 of Cleavage and polyadenylation specificity factor subunit 6	f	-3.4	99.4	1002.4
IPI00013184	N-alpha-acetyltransferase 10, NatA catalytic subunit	a,b	2.4	1.2E+05	42.3
IPI00013256	Isoform 1 of Cleavage stimulation factor subunit 2	b,f	-15.3	48.4	990.5
IPI00013455	Isoform 1 of CAP-Gly domain-containing linker protein 1	c	-17.4	124.1	8190.9
IPI00013698	N-acylsphingosine amidohydrolase (Acid ceramidase) 1, isoform CRA_c	a	10.9	426.9	311.2
IPI00013723	Peptidyl-prolyl cis-trans isomerase NIMA-interacting 1	a,b,c,e,f	-14.6	35.4	508.9
IPI00014147	PCNA-associated factor	a,b	-16.0	67.0	3586.2
IPI00015809	Probable O-sialoglycoprotein endopeptidase		9.5	222.0	126.7
IPI00015894	Cdc42 effector protein 4	c	-2.6	8656.8	216.3
IPI00016006	Isoform 1 of Gephyrin	a,c	6.0	54.4	712.9
IPI00016621	Isoform 2 of AP-2 complex subunit alpha-2	a,d	11.2	672.3	392.1
IPI00016912	Tetratricopeptide repeat protein 1	c	-4.7	64.0	34.6
IPI00017292	Isoform 1 of Catenin beta-1	a,b	-15.5	71.0	6128.6
IPI00017669	Isoform 1 of SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily E member 1	a,c,e	2.3	90.4	307.1
IPI00017964	Small nuclear ribonucleoprotein Sm D3	f	16.3	25337.7	1793.7
IPI00018195	Mitogen-activated protein kinase 3	a,b,c	16.2	14274.1	1207.8
IPI00018627	Isoform 1 of N-alpha-acetyltransferase 50, NatE catalytic subunit	b	-15.7	106.9	9181.2
IPI00019178	Phosphoserine phosphatase	a	9.5	154.2	80.3
IPI00019376	Isoform 2 of Septin-11	c,e	16.3	25337.7	2368.3
IPI00020008	NEDD8	a,e,f	12.8	1991.0	371.0
IPI00020495	28S ribosomal protein S36, mitochondrial	.	-17.4	124.1	9804.9

Accession No.	Protein Name	Molecular Function*	Fold Change	BayesFactor	RBstat
IPI00021327	Isoform 1 of Growth factor receptor-bound protein 2	a,b,c	-2.1	4159.9	5951.8
IPI00021537	Isoform 1 of Opioid growth factor receptor	b	-93.2	1.6E+09	16.9
IPI00021805	Microsomal glutathione S-transferase 1	a,b	-37.1	470.8	3.6
IPI00022002	cDNA FLJ54536, highly similar to Mitochondrial 28S ribosomal protein S27		-39.0	676.6	6.9
IPI00022256	Isoform 1 of AP-2 complex subunit mu	d	-40.5	830.0	19.4
IPI00022477	B-cell lymphoma/leukemia 10	a	2.0	34.2	82.7
IPI00022628	cDNA FLJ50558, highly similar to Homo sapiens microtubule-associated protein 7 (MAP7), mRNA	b,c	-50.9	15434.6	492.0
IPI00023001	Protein FAM162A	a	-14.5	48.2	3213.8
IPI00023149	Isoform B of Syntaxin-16	d	-27.9	76.1	7.2
IPI00023322	Zinc finger protein ubi-d4	a,f	-14.6	35.4	591.4
IPI00023526	Isoform 1 of Ras-related protein Rab-6A	d	45.4	1.3E+07	4.3
IPI00023748	Nascent polypeptide-associated complex subunit alpha	b,f	-2.0	21288.0	19.0
IPI00024281	Isoform 1 of Survival of motor neuron protein-interacting protein 1	g	10.9	426.9	124.5
IPI00024781	Small EDRK-rich factor 2	a	21.8	1354.6	6.9
IPI00026111	Isoform 1 of Transmembrane and coiled-coil domain-containing protein 1	b,g	-32.8	175.1	5.5
IPI00026964	Cytochrome b-c1 complex subunit Rieske, mitochondrial	a	-14.1	36.6	2924.5
IPI00027438	Flotillin-1	b,c	-28.2	81.7	4.1
IPI00027443	cysteinyl-tRNA synthetase, cytoplasmic isoform c	a,f	-15.5	71.0	9132.3
IPI00029175	WASH complex subunit strumpellin	d	-14.1	36.6	1586.9
IPI00030383	Isoform Alpha of Nuclear inhibitor of protein phosphatase 1	a,b	8.4	84.9	88.7
IPI00030774	Isoform 4 of Tubulin-specific chaperone D	c	-27.7	53.4	9.1
IPI00031107	Isoform 2 of Hydroxysteroid dehydrogenase-like protein 2	g	-28.0	56.1	7.3
IPI00031627	DNA-directed RNA polymerase II subunit RPB1	a,f	7.5	54.5	59.5
IPI00031655	Vacuolar protein-sorting-associated protein 25	d	4.8	57.2	44.9
IPI00033075	Protein BAT5		7.5	54.5	79.6
IPI00045511	Isoform 1 of Chloride channel CLIC-like protein 1	a,d	10.9	426.9	230.5
IPI00045660	Isoform 1 of Uncharacterized protein C1orf31	g	-16.7	93.0	3165.8
IPI00060031	ADP-ribosylation factor-like protein 8A	e	10.9	426.9	109.7

Accession No.	Protein Name	Molecular Function*	Fold Change	BayesFactor	RBstat
IPI00063234	Protein kinase, cAMP-dependent, regulatory, type II, alpha, isoform CRA_b	b,d	-2.1	274.2	16.4
IPI00075081	Isoform 1 of Fanconi anemia group D2 protein	a,b,e	4.6	95.8	71.0
IPI00103654	Isoform 1 of Serine/threonine-protein phosphatase 4 regulatory subunit 2	e	2.1	3353.3	495.6
IPI00106668	perilipin-3 isoform 3	a,b,d	-90.0	3.3E+08	113.9
IPI00151358	Isoform 1 of Cleft lip and palate transmembrane protein 1-like protein	b	-14.6	35.4	662.6
IPI00152510	ATP-dependent RNA helicase DDX54 isoform 1	f	-16.0	67.0	1878.4
IPI00152900	cDNA FLJ55829, highly similar to Homo sapiens leucine zipper and CTNNBIP1 domain containing (LZIC), mRNA		7.5	54.5	54.3
IPI00158615	THO complex subunit 2	b,d	-14.6	35.4	686.1
IPI00158627	Isoform 2 of A-kinase anchor protein 1, mitochondrial	a,c	7.5	54.5	123.0
IPI00163084	Pre-mRNA-splicing factor SYF1	f	7.2	35.8	26.5
IPI00165026	Isoform 1 of SET domain-containing protein 3	a,e	2.5	23037.7	106.3
IPI00165393	Acidic leucine-rich nuclear phosphoprotein 32 family member E	a	11.2	672.3	163.2
IPI00165547	Isoform 2 of Phosphatidylinositol 4-kinase beta	a,b,c	-14.6	35.4	679.0
IPI00167941	Midasin	a	4.4	45.1	135.4
IPI00170786	WW domain-binding protein 11	g	-15.3	48.4	1190.6
IPI00175169	Isoform 1 of ADP-ribosylation factor GTPase-activating protein 1	d	-2.0	374.9	29.8
IPI00178150	Isoform 1 of Chromosome-associated kinesin KIF4A	e	-16.7	93.0	2314.9
IPI00178953	Isoform 4 of Zinc finger protein 638	f	-16.0	67.0	1875.7
IPI00178972	Isoform 1 of DDB1- and CUL4-associated factor 11		-15.5	71.0	6769.9
IPI00180386	Isoform GN-1L of Glycogenin-1		9.5	222.0	121.7
IPI00181135	Branched-chain-amino-acid aminotransferase		-14.5	48.2	6140.0
IPI00185919	Isoform 1 of La-related protein 1	d,g	-4.4	1967.8	71.4
IPI00215928	Centrin-2	e	-3.4	70.4	7.0
IPI00216085	Cytochrome c oxidase subunit 6B1	b	-25.2	51.7	4.2
IPI00216088	Cellular retinoic acid-binding protein 2	d	-2.0	1.9E+26	2030.8
IPI00216508	Isoform 2 of Sorting nexin-3	b,d	-16.7	93.0	2986.8
IPI00217121	Uncharacterized protein C19orf21		-16.0	67.0	1648.7
IPI00217766	Lysosome membrane protein 2	a	2.7	130.2	7.1

Accession No.	Protein Name	Molecular Function*	Fold Change	BayesFactor	RBstat
IPI00217960	Isoform 2 of cAMP-dependent protein kinase catalytic subunit alpha	a,b,c,d,e	-34.7	332.7	20.7
IPI00218200	B-cell receptor-associated protein 31	a,b	1.6	2.5E+06	22.9
IPI00218848	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit E	d,g	-32.0	303.2	4.9
IPI00219451	Isoform 5 of Cytosolic acyl coenzyme A thioester hydrolase	g	11.7	1040.0	303.8
IPI00219616	Ribose-phosphate pyrophosphokinase 1	a	13.5	3019.3	725.8
IPI00220014	Isoform 2 of Isopentenyl-diphosphate Delta-isomerase 1	g	-34.2	346.6	6.1
IPI00220173	Isoform Tau-B of Microtubule-associated protein tau	a,b,c,d	-30.3	95.4	17.7
IPI00220261	Isoform A of Syntaxin-16	d	7.5	54.5	39.2
IPI00220263	Isoform D of Syntaxin-16	d	-27.9	76.1	7.6
IPI00220556	Isoform 3 of Pre-B-cell leukemia transcription factor-interacting protein 1	c	-15.3	48.4	1535.3
IPI00220567	5-formyltetrahydrofolate cyclo-ligase	a	5.6	30.6	300.8
IPI00220648	Phosphomevalonate kinase	a	12.8	1991.0	403.9
IPI00220766	Lactoylglutathione lyase	a,b	-2.1	939.7	3150.7
IPI00220835	Protein transport protein Sec61 subunit beta	d	2.1	137.2	131.4
IPI00221300	Translation initiation factor eIF-2B subunit alpha	a,b,f	2.1	34.7	367.7
IPI00239077	Histidine triad nucleotide-binding protein 1	b	-33.6	283.1	143.0
IPI00239405	Isoform 1 of Nesprin-2	c,e	-34.0	156.6	3395.1
IPI00241841	Keratin, type II cytoskeletal 79	c	-238.9	5.1E+29	2103.2
IPI00250153	Y-box-binding protein 2	a,b,f	-2.3	5299.3	6.7
IPI00251559	E3 ubiquitin-protein ligase BRE1A	f	-17.4	124.1	7396.8
IPI00292059	Nuclear pore complex protein Nup153	d	-16.7	93.0	5120.5
IPI00292134	Isoform 1 of Epidermal growth factor receptor substrate 15	b,d	-3.2	339.4	62.6
IPI00292537	Isoform 2 of Nuclear factor NF-kappa-B p105 subunit	a,b,c	8.4	84.9	125.0
IPI00293817	Gamma-soluble NSF attachment protein	d	-15.3	48.4	1250.3
IPI00293845	Isoform 1 of Telomere-associated protein RIF1		9.5	222.0	105.9
IPI00294742	Isoform 1 of La-related protein 7	f	-18.3	182.4	7640.7
IPI00295741	Cathepsin B	a,b	-25.7	34.3	6.4
IPI00295889	Signal recognition particle 19 kDa protein	a	2.2	40.9	12.9
IPI00298058	Isoform 1 of Transcription elongation factor SPT5	a,d	9.5	222.0	205.9
IPI00298949	Cyclin-G-associated kinase	b	-26.1	38.3	11.1

Accession No.	Protein Name	Molecular Function*	Fold Change	BayesFactor	RBstat
IPI00299116	Podocalyxin-like protein 1 precursor	c	4.0	5.1E+16	433.8
IPI00299468	Acyl-CoA desaturase	a	16.3	337.5	4.2
IPI00299517	BRISC complex subunit Abro1		10.6	71.0	27.6
IPI00301202	Magnesium transporter protein 1	a,d	9.5	222.0	109.0
IPI00301579	Niemann-Pick disease, type C2	d	7.2	35.8	85.1
IPI00302850	Small nuclear ribonucleoprotein Sm D1		-34.3	253.9	4.4
IPI00303105	Small ubiquitin-related modifier 1	a,b,c,d	7.2	35.8	57.2
IPI00303882	Isoform B of Perilipin-3	a,b,d	50.8	4.8E+12	7.1
IPI00304540	Isoform 3 of Protein FAM40A	c	-14.1	36.6	1538.9
IPI00306195	Isoform 2 of Proline-rich AKT1 substrate 1	a,b	-15.3	48.4	1237.4
IPI00306518	Isoform 3 of Fanconi anemia group I protein	e	9.5	222.0	98.9
IPI00328298	Isoform 2 of Structural maintenance of chromosomes protein 4	e	7.1	185.8	8544.1
IPI00328748	mesencephalic astrocyte-derived neurotrophic factor	a,b	-32.3	268.4	497.0
IPI00332936	Isoform 2 of Zinc finger CCCH-type antiviral protein 1	g	25.5	67736.5	95.3
IPI00334410	Isoform 2 of Myosin-XVIIIa	b	-15.3	48.4	1513.5
IPI00335001	Isoform 1 of Huntingtin-interacting protein K	a	7.2	35.8	58.6
IPI00335280	Isoform 1 of Ribulose-phosphate 3-epimerase	g	5.6	30.6	401.4
IPI00383597	Isoform A of Anion exchange protein 2	a,d	9.5	222.0	134.7
IPI00384857	Isoform 2 of Hematological and neurological expressed 1 protein		50.5	3.7E+08	1724.2
IPI00385631	Isoform 1 of Zinc finger ZZ-type and EF-hand domain-containing protein 1		-14.6	35.4	1117.7
IPI00386258	Isoform 1 of Mitochondrial carrier homolog 1	a,b	8.9	429.5	7298.9
IPI00386271	Calcium-binding mitochondrial carrier protein Aralar1	d	4.4	774.2	1748.4
IPI00386687	leucine-rich repeat flightless-interacting protein 1 isoform 1	f	-2.0	34.0	21.8
IPI00395694	Isoform 2 of Transportin-3	d	-18.3	182.4	8692.6
IPI00397860	Isoform 1 of Cytochrome b5	d	10.9	426.9	145.0
IPI00409659	Ubiquilin-2	b	-16.0	67.0	1632.4
IPI00410067	Isoform 1 of Zinc finger CCCH-type antiviral protein 1	g	-44.8	3123.6	4.9
IPI00410618	Uncharacterized protein KIAA1143		-14.6	35.4	725.0
IPI00412497	Dynein, light chain, roadblock-type 1	d	-14.6	35.4	575.6
IPI00412499	Isoform 1 of Rab GTPase-binding effector protein 2	d	-28.2	67.5	6.0

Accession No.	Protein Name	Molecular Function*	Fold Change	BayesFactor	RBstat
IPI00414442	cDNA FLJ56403, highly similar to CDK5 regulatory subunit-associated protein 3	a,c	14.3	5132.5	693.3
IPI00418194	Synaptotagmin-like 2	d	-15.5	71.0	6264.8
IPI00418336	Isoform 2 of Integrator complex subunit 3	a,e	7.2	35.8	98.1
IPI00418412	Uncharacterized protein		14.1	7993.5	1627.3
IPI00419575	Protein of unknown function DUF410 family protein	b	-24.2	30.1	4.5
IPI00419791	Isoform 1 of Arginine/serine-rich coiled-coil protein 2	g	-16.7	93.0	2919.0
IPI00429689	Serine/threonine-protein phosphatase 2A catalytic subunit beta isoform	a,b	-53.7	33220.4	6.5
IPI00433576	Hepatocellular carcinoma-associated antigen 59	b	-17.4	124.1	5032.9
IPI00465431	Galectin-3	b	-3.3	2.8E+12	6408.2
IPI00472058	Neuronal protein		11.2	672.3	170.5
IPI00477355	KIF1-binding protein	c	-2.0	45.0	16.5
IPI00477802	Isoform 2 of Transcription elongation factor A protein-like 1	f	-18.3	182.4	6733.4
IPI00478277	15 kDa protein		-42.6	1948.5	3181.1
IPI00478453	cDNA FLJ61662, highly similar to CCR4-NOT transcription complex subunit 3	f	-15.3	48.4	1010.6
IPI00479997	Stathmin 1	b,c	1.692	172972.438	677.759
IPI00480056	RAB4A, member RAS oncogene family variant	d	-15.3	48.4	955.7
IPI00514399	Uncharacterized protein		-29.7	152.7	4.2
IPI00549664	Testis-expressed sequence 10 protein	g	-14.5	48.2	3079.2
IPI00549970	Growth hormone inducible transmembrane protein	a	7.1	113.6	1674.4
IPI00550165	Dehydrogenase/reductase SDR family member 7B	e,g	7.2	35.8	97.3
IPI00550852	Dynactin subunit 4	c	-17.4	124.1	3297.1
IPI00553131	UDP-glucose 4-epimerase	g	6.0	54.4	703.1
IPI00553153	ATPase inhibitory factor 1	a,b	-16.0	67.0	2113.7
IPI00554541	Isoform 1 of Acetolactate synthase-like protein		-5.3	1733.8	229.6
IPI00554777	Asparagine synthetase [glutamine-hydrolyzing]	a	-33.7	216.7	11.0
IPI00554811	Actin-related protein 2/3 complex subunit 4	c	18.1	37055.7	2725.8
IPI00640416	19 kDa protein		9.5	222.0	172.4
IPI00641181	MARCKS-related protein	a,b,d	2.2	3.7E+08	26.6
IPI00642238	Isoform 1 of Heterochromatin protein 1-binding protein 3	f	-32.8	161.3	4.2
IPI00642693	OGFR protein	b	85.2	7.7E+17	90.7

Accession No.	Protein Name	Molecular Function*	Fold Change	BayesFactor	RBstat
IPI00642904	Polyadenylate-binding protein 4 isoform 1	f	37.9	6.4E+09	30.0
IPI00644482	Proteasome assembly chaperone 2	a,b	-14.6	35.4	713.0
IPI00645307	Isoform 1 of Isopentenyl-diphosphate Delta-isomerase 1		25.0	18163.8	4.8
IPI00645702	CTP synthase 2	b	-2.9	73.7	4.6
IPI00646377	Isoform 1 of Eukaryotic translation initiation factor 4 gamma 3	f	-45.6	2812.2	7.6
IPI00748794	Isoform SERCA3A of Sarcoplasmic/endoplasmic reticulum calcium ATPase 3	d	-91.0	7.5E+08	904.2
IPI00759646	low molecular weight phosphotyrosine protein phosphatase isoform d	a,b,c	8.9	429.5	6077.3
IPI00783302	Isoform 1 of Pentatricopeptide repeat-containing protein 3, mitochondrial	f	-14.6	35.4	691.8
IPI00784029	Isoform 1 of Oxidoreductase HTATIP2	a,b	20.2	2556.2	5.7
IPI00789008	Flotillin-2	b	-25.8	45.0	32.6
IPI00789454	9 kDa protein		14.3	5132.5	639.1
IPI00793081	11 kDa protein		7.2	35.8	181.6
IPI00794397	Charged multivesicular body protein 4A	d	-24.0	32.2	94.2
IPI00797206	Protein		-100.9	2.1E+10	4.8
IPI00797537	Isoform 1 of NudC domain-containing protein 1	a	7.1	185.8	4046.6
IPI00827972	Isoform 1 of Putative GTP-binding protein Parf	b	10.9	426.9	189.4
IPI00830108	Isoform 1 of DnaJ homolog subfamily C member 2	a,e,f	8.4	84.9	56.1
IPI00844014	chromosome 9 open reading frame 114	a	9.5	222.0	134.7
IPI00847689	Isoform 3 of Oxidoreductase HTATIP2	a,b	-26.0	46.8	1331.7
IPI00848328	Similar to Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial precursor	b	-51.1	14600.9	4.3
IPI00868787	Isoform 1 of Protein TANC2	g	-27.1	37.4	91.6
IPI00876962	Isoform 2 of Inverted formin-2	c	-83.2	5.4E+07	5.5
IPI00878985	Isoform 1 of Inverted formin-2	c	68.7	7.5E+16	73.1
IPI00887557	Similar to hCG1644442		20.0	2436.7	180.6
IPI00916739	Elongation factor Ts	f	-15.7	106.9	9371.4
IPI00921849	cDNA FLJ57046, highly similar to Lysosomal alpha-glucosidase	g	-16.0	67.0	1716.5
IPI00925387	Uncharacterized protein		11.3	43.2	3.1
IPI00937278	26S proteasome non-ATPase regulatory subunit 8	a	18.2	59330.4	3924.8

Accession No.	Protein Name	Molecular Function*	Fold Change	BayesFactor	RBstat
IPI00941155	Growth hormone-inducible transmembrane protein	a	14.3	5132.5	1009.0
IPI00945153	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 6	a,d	8.4	84.9	58.2
IPI00945818	Isoform 2 of Lipopolysaccharide-responsive and beige-like anchor protein	b,d	-49.0	6617.8	31.0
IPI00966227	12 kDa protein		64.0	1.5E+11	18.0
IPI00967562	Heterogeneous nuclear ribonucleoprotein D (AU-rich element RNA binding protein 1, 37kDa)	b,d	16.3	25337.7	2299.0
IPI00971041	Hypothetical protein LOC55793 isoform 4		7.1	113.6	1927.7
*** a) Apoptosis/Cell Death b) Proliferation/Cell Growth c) Microtubule Dynamics/Cytoskeleton**					
d) Molecular/Protein Transport e) Cell Cycle/Division f) Translation/Transcription g) Other					