# ABSTRACT

Title of dissertation: CAPILLARY ISOELECTRIC FOCUSING-BASED MULTIDIMENSIONAL PEPTIDE/PROTEIN SEPARATIONS FOR PROTEOMICS ANALYSIS

Yueju Wang, Doctor of Philosophy, 2005

Dissertation directed by: Professor Cheng S. Lee
Department of Chemistry and Biochemistry

With the completion of the human genome project, the proteomics has become the focus of research interest for better understanding the complex biological processes. The mass spectrometry (MS) detection of vast number and broad dynamic range of the proteins requires that sample fractionation and separation be performed prior to MS analysis. Realizing the limitations of gel-based proteomic techniques, capillary-based and gel free separation technologies are presented as attractive alternatives holding the promises of high separation efficiency and resolution, broad dynamic range, easy system automation as well as high throughput.

Coupled with laser free microdissection technology, the combination of CIEF with nano-RPLC in an automated and integrated platform was employed for comprehensive and sensitive proteome studies of limited protein quantities obtained from tissue samples. The peptides were first separated and concentrated by CIEF and were sequentially fractionated. All the CIEF fractions were further resolved by nano-RPLC,

followed by tandem MS analysis. A total of 6,866 fully tryptic peptides were detected, leading to the identification of 1,820 distinct proteins.

Due to limited peptide sequence coverage of identified proteins, the bottom-up approaches provide very limited molecular information about the intact proteins, particularly towards the detection of post-translational modifications. In contrast, top-down methods are advantageous for the detection of protein modifications. To improve separation efficiency and resolution of nano-RPLC separations for intact proteins, various chromatography conditions, including the chain length of the stationary phase, the column temperature, and the ion-pairing agent utilized in the mobile phase, were optimized using model proteins.

Building upon the experience in the development of automated and integrated multidimensional peptide separation platform and the optimization of protein chromatography separation, a top-down proteome characterization of yeast cell lysates was further evaluated. An overall system capacity of 4,320-7,200 was achieved and a total of 534 distinct yeast protein masses were measured, yet required a protein loading of only 9.6 μg. This protein loading is two to three orders of magnitude less than those used in current top-down proteome techniques, illustrating the potential usage of this proteome technology for the analysis of protein profiles within small cell populations or limited tissue samples.

# CAPILLARY ISOELECTRIC FOCUSING-BASED MULTIDIMENSIONAL PEPTIDE/PROTEIN SEPARATIONS FOR PROTEOMICS ANALYSIS

By

Yueju Wang

Dissertation submitted to the Faculty of the Graduate School of the
University of Maryland, College Park in partial fulfillment
of the requirements for the degree of
Doctor of Philosophy
2005

Advisory Committee:

Professor Cheng S. Lee, Chair
Professor Daniel E. Falvey
Professor Catherine C. Fenselau
Professor Sang Bok Lee
Professor William E. Bentley

TABLE OF CONTENTS

# LIST OF FIGURES

# LIST OF TABLES

# CHAPTER 1

# RECENT ADVANCES IN CAPILLARY SEPARATIONS FOR PROTEOMICS

Jonathan W. Cooper, Yueju Wang, and Cheng S. Lee

Electrophoresis 25, 3913-3926 (2004)

## 1.1 INTRODUCTION TO PROTEOMICS

As the sequence of the human genome continuously achieves further confidence, the door has already opened toward an effort at the fundamental understanding of complex biological processes, including development, differentiation, and signal transduction. These processes generally involve the coordinated expression and interaction of multiple genes and proteins in a synergistic effort. The identification and quantification of the multiple proteins that constitute and control a particular process is fundamental toward understanding the regulation of that biological system. Additionally, the ability to monitor the presence or absence of particular proteins, an increase or decrease in protein expression, a change in protein microheterogeneity, or a combination of these modifications may be useful toward the early detection and diagnosis of a wide spectrum of known diseases [1,2].

The information gained through proteomics, the large-scale analysis of gene products and their covalent modifications contained within a specific cell type at a particular cell state, will contribute greatly to our understanding not only of gene

function, but also of the role that individual proteins, and protein-protein complexes play in biological systems. For example, the transformation of a normal cell into a cancer cell requires multiple genetic modifications or changes, such as alterations in cell cycles specific for protein modifications or mechanisms of DNA repair. The identification of gene products either distinctive to cancers, or those playing a role related to their development, will help define the sequence of molecular events that eventually lead to cancer. It is clear that a profound impact will be made directly on disease related research ranging from the ability to enhance early detection and diagnosis of disease to the identification of biologically relevant targets for drug development and screening.

Mass spectrometry (MS) employing matrix-assisted laser desorption/ionization (MALDI) [3,4] and electrospray ionization (ESI) [5] has evolved to become an essential tool in the bioanalytical laboratory for the identification and sequencing of protein [6]. The vast number and broad dynamic range of the proteins present in the expressed proteome of a typical organism requires that several fractionation and/or separation steps be performed on the sample prior to MS analysis. Two-dimensional polyacrylamide gel electrophoresis (2-D PAGE) has seemingly remained the method of choice for separating thousands of proteins in a single run [7-10] while simultaneously offering a “differential display” analysis of protein expression. The two dimensions of a 2-D PAGE separation are isoelectric focusing in a pH gradient and sodium dodecyl sulfate (SDS)-PAGE. Each protein spot provides a rough measure of isoelectric point (pI) and molecular weight of the protein within 5-10%. However, 2-D PAGE is a relatively slow, labor intensive, and cumbersome technology. 2-D PAGE results from different laboratories can be difficult to compare, and sensitivity is limited

by the amount of a protein needed to visualize a spot, typically in the low-nanogram range for silver staining.

Gel protein identification and the study of protein modifications generally involve gel spot excision, proteolytic digestion, peptide extraction/concentration, MS analysis of each protein spot. Unfortunately, many of the most important regulatory proteins, expressed at extremely low levels, are excluded in the combined 2-D PAGE-MS technique unless extensive fractionation of large quantities of protein together with the processing of a large number of narrow-range gels [11]. The disadvantage of these strategies, however, is that they all require much larger amounts of proteins, and therefore may be impractical for studies of small cell populations or tissue samples. Furthermore, the 2-D PAGE-MS approach still struggles in the degree of demonstrated coverage for a given proteome (i.e. for proteins with isoelectric points (pIs), molecular masses, or hydrophobicity at the extremes), sensitivity, and throughput [11,12].

## 1.2 CAPILLARY SEPARATIONS IN PROTEOMICS

Recognizing the severe constrains of gel-based separation techniques, a considerable effort has been focused on the development of liquid phase-based or non-gel proteome technologies enabling the rapid, broad, and sensitive analysis of complex proteomic samples through the combination of various chromatography methods with MS or tandem MS analysis [13-18]. Not surprisingly, much of this work has centered on the evaluation of capillary chromatography separations for the analysis of peptide mixtures obtained from proteolytic digestion of cell lysates. While direct analysis of peptide mixtures obtained from the digestion of complex cell lysates offers a greater potential for the identification of lower abundance proteins than 2-D PAGE [13,16], this bottom-up (shotgun) approach [13-18] provides very limited molecular information about the intact proteins, particularly for the detection of post-translational modifications (PTMs) [19]. PTMs include co- or post-translation covalent modifications to the protein structure and proteolytic processing of the translated protein. Such modifications may be overlooked in analyses using peptide-based proteome technique, where only a fraction of the total theoretical peptide population of a given protein may be identified [13,14,18].

The top-down method [17,20-23], in which intact proteins rather than peptides are measured, may be advantageous for the detection of PTMs. Furthermore, the top-down approach to protein sequence analysis using tandem MS may allow complete protein characterization far more efficiently than shotgun proteome technology using tryptic peptides. Realization of the potentials of the top-down technique, however, requires the processing and the separation of intact proteins to be brought to the similar level as those routinely achieved in shotgun proteomics for peptides [13-18].

**Single Dimension Capillary Separations**

The utilization of high-efficiency capillary reversed-phase liquid chromatography (CRPLC) has become increasingly attractive for the analysis of complex peptide mixtures [24]. Smith and co-workers have developed a series of high-efficiency separations based on the combination of various capillary chromatography columns with inner diameters ranging from 15 to 150 μm [24,25]. Employing commercially available switching valves containing 150 μm channels, narrow bore separation columns operating at 10,000 psi were coupled with larger solid phase extraction columns. The integrated system offers an increase in sample processing capacity roughly 400 fold as to sample solution volume and roughly 10 fold for sample mass loading for both soluble and membrane protein tryptic digests. The ability to identify 1,100-1,500 unique peptides in a 5-hr period while covering a hydrophobicity range approaching 98% of all possible tryptic peptides in the sample was demonstrated using an 11.4 Tesla Fourier transform ion cyclotron (FTICR)-MS [25]. The high resolution and sensitivity, and, of particular utility, high mass accuracy of FTICR together with reproducible CRPLC separation made possible a new concept of “accurate mass-time tags” that could largely eliminate the need for time-consuming tandem MS measurements [26].

Horvath and co-workers [27,28] have employed displacement chromatography to achieve selective enrichment of trace analytes during reversed-phase separations. Based on the retention behavior of peptide components in the elution mode, selective analyte enrichment and high-resolution separation were achieved in a single step by the combination of an organic eluant such as acetonitrile with the displacer in elution-modified displacement chromatography. Accordingly, the sensitive ESI-MS

detection of a protein kinase A peptide substrate at low fmol levels, which was added as a trace marker component to a tryptic digest of bovine serum proteins or to a human growth hormone peptide digest, was achieved at a concentration ratio of $1:10^5$ or $1:10^6$.

In addition to the separation of complex peptide mixtures, single dimension separation techniques, including isoelectric focusing gel [29], capillary isoelectric focusing (CIEF) [30,31], capillary zone electrophoresis (CZE) [20], and RPLC [32,33], have been employed for processing protein mixtures prior to MS analysis. One characteristic inherent to capillary electrophoresis is the small sample volume that can be successfully applied to obtain a high-resolution analysis. As a good portion of the important proteins contained in a proteomic sample may be present at low levels, it becomes important to combine sample preparation/concentration in-line with the subsequent electrophoretic separations while avoiding analyte loss or dilution due to manual handling and transfer procedures.

For protein samples in high conductivity media, an on-capillary sample stacking method has been developed by Wei and Yeung [34] without the need for sample desalting. By employing an etched porous joint not only as a molecular sieve, but also as an electrical junction, proteins and peptides may be concentrated in the discreet plug determined by the size of the etched region. After stacking, the narrow sample zone was introduced into the separation portion of the capillary by either hydrodynamic or electrokinetic forces, and CZE was then completed for resolution of the concentrated analytes. Additionally, Janini and co-workers [35] have demonstrated an on column sample enrichment technique utilizing a $C_{18}$ impregnated solid phase extraction disk within the capillary flow path to collect and enrich the sample to be studied.

While CIEF involves the application of a mixture containing protein/peptide analytes and carrier ampholytes in the entire capillary, the column volume still limits sample loading. To increase sample loading and, in turn, the final concentrations of focused analytes, an approach based on the dynamic electrokinetic injection of proteins/peptides from a solution reservoir was demonstrated by Chen et al. [36]. The charged proteins and peptides continuously migrated into the column whereupon they encountered the pH gradient established by preexisting carrier ampholytes for focusing and separation. The dynamic introduction and focusing was directly controlled by various electrokinetic conditions, including applied electric field strength and the injection time. An increase in the loading capacity of yeast peptide was determined to range from 8 to 45-fold of that obtained in conventional CIEF, and an overall concentration factor of 1400-7700 was achieved in comparison with the concentrations of dilute yeast peptides originally present in the sample.

Still, the use of only a single separation dimension may not provide sufficient peak capacity for the resolution of complex protein and peptide mixtures, putting significant constraints on the detection sensitivity and dynamic range of the MS. It should be emphasized that the peak capacity of 2-D separation is the product of the peak capacities of the individual one-dimensional methods [37]. Thus, various non-gel-based 2-D separation schemes have been developed recently in an effort to alleviate the shortcomings in 2-D PAGE while reserving the ability to resolve complex peptide/protein mixtures prior to MS analysis.

## Multidimensional Capillary Separations

**Capillary liquid chromatography-capillary liquid chromatography.** Yates and co-workers have demonstrated a shotgun proteomics approach named multidimensional protein identification technology [14,15], which combines multidimensional liquid chromatography with ESI-tandem MS. The combination of strong cation exchange chromatography with high-efficiency nano-RPLC was employed by Shen and co-workers to obtain ultra-high-resolution of peptide mixtures in conjunction with tandem MS for characterization of the human plasma proteome [38]. The use of multidimensional chromatography separations has resulted in better utilization of the MS dynamic range and reduced discrimination among peptides during ionization, thus achieving a dynamic range of greater than 8 orders of magnitude in relative protein abundance. By using a total of 365 μg of human plasma, 800-1682 human proteins were identified, dependent on criteria used for the identification.

The selective detection of phosphopeptides from proteolytic digests is a challenging and highly relevant task in many proteomics applications. Phosphopeptides are generally present in small amounts with the need for selective isolation or enrichment before identification. Selective enrichment of phosphopeptides can be achieved using immobilized metal affinity chromatography (IMAC), followed by base elution [39]. Unfortunately, this method often results in the isolation of many nonphosphorylated peptides via nonspecific interactions. The selectivity of the IMAC toward phosphopeptides was significantly enhanced by converting all peptides to their corresponding methyl esters, drastically eliminating confounding binding via carboxylate groups [40]. Furthermore, Pinkse and co-workers [41] reported an automated method for

the enrichment of phosphopeptides from protein digests employing a 2-D column setup, with titanium oxide-based solid-phase as the first dimension and reversed-phase as the second dimension. Proteolytic digests of three different autophosphorylation forms of the 153 kDa homodimeric cGMP-dependent protein kinase were analyzed, and eight phosphorylation sites were identified, including two previously uncharacterized sites, namely, Ser-26 and Ser-44.

In addition to performing protein isoelectric focusing in a preparative-scale Rotofor [42-44], Yan et al. [45] have employed an anion exchange column to achieve protein fractionation in a chromatofocusing mode using a pH-gradient in the mobile phase. The collected fractions eluted from a pH gradient of 4-7 were injected into a nonporous reversed-phase column as the second separation dimension for further analysis. The proteins eluted from the reversed-phase column were identified using both on-line ESI-MS and off-line faction collection followed by proteolytic digestion prior to MALDI-MS. Recently, Meng et al. have demonstrated combination of preparative-scale acid-labile surfactant-PAGE with RPLC for protein fractionation [22,23]. Proteins eluted from RPLC were subjected to protein sequence analysis using tandem MS to facilitate the detection of incorrectly predicted translational start sites and proteolytic processing of proteins such as removal of signal peptides or activation of pro-proteins to create functional proteins. These approaches currently require the use of FTICR-MS/MS for obtaining protein-sequencing measurements [20-23] and are also limited by the relative scarcity of bioinformatic tools to efficiently analyze this type of data, although these are under development [21].

**Capillary liquid chromatography-capillary electrophoresis.** On-line coupling of size-exclusion chromatography with CZE was achieved by Stroink et al. via a reversed-phase trap column [46,47]. The size-resolved fraction retained in the trap column was then eluted into CZE for further analysis. A 2-D RPLC-CZE technique was developed by Issaq and co-workers [48,49] and employed towards the rapid and broad mapping of complex samples, including tryptic digests of cell extracts. Fractions from a micro-RPLC separation were collected every 30 s by an automated fraction collector into a 96-well microtiter plate. After concentration by drying under vacuum, the fractions were reconstituted with deionized water, and each was analyzed simultaneously in the second dimension by a 96-array CZE system based on charge-to-size ratio, and detected by UV absorption or laser-induced fluorescence.

Instead of using UV or fluorescence detection, Janini et al. [50] have combined RPLC-CZE separations with ESI-tandem MS towards the identification of peptides in complex mixtures. A serum sample was depleted of high-abundance proteins, digested with trypsin, and then separated by RPLC and collected into 96 fractions. These fractions, collected off-line from the RPLC separation, were subjected to sequential CZE separations through a sheathless ESI interface that was integrated on the separation capillary. A key feature of this work is the employment of RPLC in lieu of ion exchange fractionation, where there is a large degree of overlap. The CZE-MS results demonstrated less than 15% overlap between neighboring RPLC fractions, leading to a more sensitive proteome analysis.

**Capillary electrophoresis-liquid chromatography**. On-line combination of CIEF with CRPLC has been developed by Chen et al. [51,52]. In addition to analyte

focusing and concentration, CIEF as the first separation dimension resolves peptides on the basis of their differences in pI and offers greater resolving power than that achieved in strong cation exchange of a multidimensional liquid chromatography system [14,15]. The grouping of two highly resolving and completely orthogonal separation techniques of CIEF and CRPLC, together with analyte focusing and concentration, significantly enhances the dynamic range and sensitivity of MS toward the identification of lower abundance proteins.

**Capillary electrophoresis-capillary electrophoresis.** By using a dialysis interface, Yang et al. [53,54] have constructed a 2-D capillary electrophoresis system consisting of CIEF coupled with either CZE or capillary gel electrophoresis (CGE) for the analysis of model proteins. Mohan and co-workers [55,56] have developed an integrated multidimensional electrokinetic-based separation/concentration platform employing a microdialysis junction as the interface for on-line combination of CIEF with transient capillary isotachophoresis (CITP)/CZE coupled with ESI-FTICR-MS for achieving the high resolution and sensitive analysis of complex proteome mixtures. In addition to the high-resolving power afforded by both the CIEF and CZE separations, the electrokinetic focusing/stacking effects of CIEF and CITP greatly enhance the dynamic range and detection sensitivity of MS for protein identification. This multidimensional electrokinetic-based platform offers overall peak capacity comparable to those obtained using multidimensional liquid chromatography system, but with a much shorter run time and no need for column regeneration. Most importantly, a total of 1,174 unique proteins, corresponding to 26.5% proteome coverage, were identified from the cytosolic fraction of *S. oneidensis*, while requiring <500 ng of proteolytic digest loaded in the CIEF capillary.

The sensitive capabilities of the multidimensional electrokinetic-based approach are attributed to the concentration effect in CIEF, the electrokinetic stacking of CITP, the nanoscale peak volume in CZE, the “accurate mass tag” strategy for protein/peptide identification, and the high-sensitivity, high-resolution, and high-mass measurement accuracy of FTICR-MS.

Sheng and Pawliszyn [57] demonstrated a 2-D electrokinetic separation system by coupling micellar electrokinetic chromatography (MEKC) in the first dimension with CIEF in the second dimension. To afford the combination of these orthogonal separation mechanisms, a 10-port valve with two conditioning loops was employed to collect the fractions eluting from the first dimension, provide the dialysis desalting of each surfactant rich fraction, and also act as the direct interface between MEKC and CIEF. Within the dialysis loop, salt and other unwanted first dimension effluent components were eliminated and carrier ampholytes were added prior to the second dimension separation. Peak broadening during the dialysis did not have significant impact on the second dimension separation due to the inherent concentrating effect in CIEF.

Michaels and co-workers [58] detailed a 2-D electrokinetic separation system by combining submicellar capillary electrophoresis in the first dimension with CZE in the second dimension for high sensitivity protein analysis. Protein fractions from the first dimension separation were transferred to a second dimension capillary through an injection interface, where CZE was performed and followed by laser-induced fluorescence detection. Hu et al. [59] further combined capillary sieving electrophoresis on the basis of a SDS-pullulan buffer system with MEKC for the study of protein

expression in single mammalian cells. After a 6-min-long size-based separation, over 100 transfers of fractions from the first capillary were introduced into a second capillary for further separation by MEKC over an approximately 3.5-hr-long period. The ability to achieve sensitive protein profiling was demonstrated through the generation of protein fingerprints from single native MC3T3-E1 osteoprogenitor cells and MC3T3-E1 cells transfected with the human transcription regulator TWIST.

**Multidimensional proteome separations using microfluidics.** Thermal time constants in microfluidics tend to be extremely small due to the large surface area to volume ratio, reducing the onset of significant Joule heating during electrokinetic separations and thus allowing higher separation voltages for shorter analysis times and equivalent or better separation resolution than capillary-based techniques toward complex mixtures. In addition to reduced size and power requirements leading to improved portability, microfluidic systems also hold great promise for realizing multidimensional separations in a single integrated system. To this end, several research groups have explored the application of microfluidics to perform multidimensional peptide and protein separations.

Ramsey and co-workers have demonstrated 2-D separation of peptide mixtures in a microfluidic device using MEKC and CZE as the first and second dimensions, respectively [60,61]. Gottschlich et al. have also fabricated a spiral shaped glass channel coated with a $C_{18}$ stationary phase for performing RPLC separation of trypsin-digested peptides [62]. By employing a cross interface, the eluted peptides from MEKC [60,61] or RPLC [62] were sampled by a rapid CZE separation in a short glass microchannel. Additionally, Herr and co-workers have coupled CIEF with CZE for 2-D

separations of model proteins using plastic microfluidics [63]. Instead of using a cross interface [60-63], Wang et al. have combined CIEF with CZE or CGE using microfluidic valves [64].

In each of these examples, the multiple separation dimensions are performed serially, without the ability to simultaneously sample all proteins or peptides separated in the first dimension for parallel analysis in the second dimension. As an early step toward this goal, a microfabricated quartz device has been proposed by Becker and co-workers with a single channel for the first dimension and an array of 500 parallel channels with submicron dimensions as the second dimension positioned orthogonally to the first dimension channel [65]. In a further step, Chen et al. described a 2-D capillary electrophoresis system based on a 6-layer poly (dimethylsiloxane) (PDMS) microfluidic system [66]. The system consisted of a 25 mm-long microchannel for performing CIEF, with an intersecting array of parallel 60 mm-long microchannels for achieving CGE. This 6-layer PDMS microfluidic device, however, required the alignment, bonding, removal, re-alignment, and re-bonding of various combinations of the six layers to perform a full 2-D protein separation.

An integrated protein concentration/separation system, combining CIEF with CGE on a single-layer 2-D microfluidic network, has been reported by Li and co-workers [67]. The ability to introduce and isolate multiple separation media in plastic microfluidic network was one of two key requirements for achieving multidimensional protein separations. The second requirement resided in the quantitative transfer of focused proteins from the first to second separation dimensions without significant loss in the resolution acquired from the first dimension. Rather than sequentially sampling

protein analytes eluted from CIEF, focused proteins were electrokinetically transferred into an array of orthogonal microchannels and further resolved by CGE in a parallel and high throughput format. Resolved proteins were monitored using non-covalent, environment-sensitive, fluorescent probes such as SYPRO Red. A 2-D protein separation was completed in less than 10 min with an overall peak capacity of around 1,700 using a chip with planar dimensions of as small as 2 cm x 3 cm.

## 1.3 PROJECT DESCRIPTION

The sequencing of several organisms' genomes, including the human's one, has opened the way for the so-called postgenomic era, which is now routinely coined as "proteomics". The most basic task in proteomics remains the detection and identification of proteins from a biological sample, and the most traditional way to achieve this goal consists of protein separations performed by 2-D PAGE. Still, the 2-D PAGE-MS approach remains lacking in proteome coverage (for proteins having extreme pIs or molecular masses as well as for membrane proteins), dynamic range, sensitivity, and throughput. Consequently, considerable efforts have been devoted to the development of non-gel-based proteome separation technologies in an effort to alleviate the shortcomings in 2-D PAGE while reserving the ability to resolve complex protein and peptide mixtures prior to MS analysis.

It should be emphasized that the extremely high resolution of 2-D PAGE for protein separation is mostly contributed by isoelectric focusing in the first separation dimension. By transferring isoelectric focusing separation from gel to capillary format, it has been demonstrated that the focusing effect of CIEF not only contributes to high resolution protein/peptide separation [68,69], but also provides significant enhancement in analyte concentration. It should be noted that the entire CIEF capillary is initially filled with a solution containing proteins/peptides and carrier ampholytes for the creation of a pH gradient inside the capillary. Upon completion of analyte focusing, the self-sharpening effect greatly restricts analyte diffusion and contributes to analyte stacking in narrow focused bands.

This project therefore aims to further develop and optimize on-line combination of CIEF with nano-RPLC in an integrated platform for performing multidimensional separations of complex peptide and protein mixtures toward comprehensive and sensitive proteome studies. Chapter 2 demonstrates the ability to perform sensitive proteome analysis on the limited protein quantities available through tissue microdissection. CIEF combined with nano-RPLC in an automated and integrated platform not only provides systematic resolution of complex peptide mixtures based on their differences in pI and hydrophobicity, but also eliminates peptide loss and analyte dilution. In comparison with strong cation exchange chromatography [13-18], the significant advantages of electrokinetic focusing-based separations include high resolving power, high concentration and narrow analyte bands, and effective usage of ESI-tandem MS toward peptide identifications.

Through the use of CIEF-based multidimensional peptide separations, a total of 6,866 fully tryptic peptides were detected, leading to the identification of 1,820 distinct proteins. These high mass accuracy and high confidence identifications were generated from 3 proteome runs of a single glioblastoma multiforme tissue sample, each run consuming only 10 μg of total protein, an amount corresponding to 20,000 selectively isolated cells. Instead of performing multiple runs of multidimensional separations, the overall peak capacity can be greatly enhanced for mining deeper into tissue proteomics by increasing the number of CIEF fractions without an accompanying increase in sample consumption.

Building upon the experience in the development of CIEF-based multidimensional peptide separation platform, research efforts are later directed toward

the application of combined CIEF with nano-RPLC for concentrating and resolving intact proteins from complex cell lysates. To improve the peak capacity of nano-RPLC for the resolution of protein mixtures within individual CIEF fractions, effects of various chromatography conditions, including alkyl chain length in the stationary phase, capillary column temperature, and ion-pairing agent, on the resolution of intact proteins are studied and reported in Chapter 3. Optimal chromatography conditions include the use of $C_{18}$ column heated at 60 $^{0}$C and the addition of trifluoroacetic acid instead of heptafluorobutyric acid as the ion-paring agent in the mobile phase. Under optimized chromatography conditions, there are no significant differences in the separation performance of yeast cell lysates present in the native versus denatured states.

An integrated protein concentration/separation platform, combining CIEF with nano-RPLC, is developed and presented in Chapter 4 to provide significant protein concentration and high resolving power for the analysis of complex protein mixtures. Upon completion of protein focusing, the proteins are sequentially and hydrodynamically loaded into individual trap columns using a group of microinjection and microselection valves. Repeated protein loadings and injections into trap columns are carried out automatically until the entire CIEF capillary content is sampled and fractionated. Each CIEF fraction "parked" in separate trap columns is further resolved using nano-RPLC, and the eluants are analyzed using ESI MS.

By taking only 9 CIEF fractions, an overall system capacity of 4,320-7,200 is achieved in this study for the analysis of intact proteins obtained from the soluble fraction of yeast cell lysates. Further enhancement to the overall system capacity can be realized by increasing the number of CIEF fractions and slowing the solvent gradient in

nano-RPLC at the expense of analysis time. The CIEF-based multidimensional concentration/separation platform enables the measurement of 534 distinct yeast protein masses over a mass range of 5-70 kDa, yet requires a protein loading of only 9.6 μg. This protein loading is two to three orders of magnitude less than those used in current 2-D PAGE and top-down proteome techniques [22,23,42-45], illustrating the potential usage of this proteome technology for the analysis of protein profiles within small cell populations or limited tissue samples.

## 1.4 ACKNOWLEDGEMENT

We thank the National Cancer Institute (CA107988 and CA103086) for supporting portions of our research reviewed in this article.

# CHAPTER 2

# PROTEOME ANALYSIS OF MICRODISSECTED TUMOR TISSUE USING A CAPILLARY ISOELECTRIC FOCUSING-BASED MULTIDIMENSIONAL SEPARATION PLATFORM COUPLED WITH ESI-TANDEM MS

Yueju Wang, Paul A. Rudnick, Erin L. Evans, Jie Li, Zhengping Zhuang, Don L. DeVoe, Cheng S. Lee, and Brian M. Balgley

Submitted to Analytical Chemistry for Consideration of Publication

## 2.1 INTRODUCTION

Biological systems are typically multi-tiered and exhibit complex interdependent interactions. Thus, it is widely accepted that instead of the classic single gene or single marker approach, molecular profiling has supplanted the single gene approach enabling the simultaneous expression monitoring of many genes or proteins. Tissue specific genomics or proteomics data can only be generated if the samples investigated consist of homogenous cell populations, in which no unwanted cells of different types and/or developmental stages obscure the results. One of the main problems with the analysis of tissue samples, either at the level of genes or proteins, is the heterogeneous nature of the sample; many different cell types are typically present in tissue biopsies, and in the case of diseased tissue, small numbers of abnormal cells may lie within or adjacent to unaffected areas.

Infrared laser capture microdissection (LCM) technology [70,71] provides a straightforward method for procuring homogeneous subpopulations of cells or tumor structures for biochemical and molecular biological analyses [72]. LCM is the technique of choice for selectively isolating diseased cells from normal cells within a tissue specimen, followed by microgenomic analysis using oligonucleotide and cDNA arrays [73-75]. Through subsequent application of recently developed approaches of mRNA amplification in a pool of isolated total RNA, it is now possible to perform complex high-throughput mRNA expression profiling by microdissecting and processing even single-cell samples [76-78]. All of these molecular profiling tools may be applied to generate specific genetic fingerprints for defined and individual lesions and for certain stages of a disease, as well as for characterizing transitional and developmental changes.

Proteomics studies offer a powerful complementary approach to nucleic acid-based investigation. In the absence of protein amplification techniques, proteomic analysis of tissue specimens procured by LCM and other microdissection techniques [79-82] is severely constrained by limiting sample amounts ranging from $10^3$-$10^5$ cells, corresponding to a total protein content of 0.1-10 μg [71]. Cells isolated and captured by LCM have been directly analyzed using MALDI-MS [83-85]. The *m/z* signals or peaks obtained from MALDI-MS are correlated with protein distribution within a specific region of the tissue sample and can be used to construct ion density maps or specific molecular images for virtually every signal detected in the analysis. Additionally, Surface-enhanced laser desorption/ionization-mass spectrometry (SELDI-MS) has been reported as a relatively simple and rapid protein biomarker analysis tool with potential clinical utility [86-89]. Although SELDI-MS spectral peaks do not provide protein

identifications, the resulting fingerprint patterns have been explored for diagnostic applications including the early detection of several types of cancers. However, reproducibility of sample preparation and mass spectra among different laboratories has been problematic for both methodological and biological reasons, and little physical meaning can be attributed to the spectral peaks in the absence of identification [89].

Current proteome separation platforms, including 2-D PAGE and shotgun-based multidimensional liquid chromatography separations [13-18], however, require large cellular samples which are generally incompatible with the protein quantities obtained from LCM samples. While limited 2-D PAGE analyses of LCM-derived tissue samples have been attempted [90-93], these studies involve significant manual effort and time (from 3 hr to 4 days, depending on tissue type) to extract sufficient amounts of protein for obtaining good visual quality of gel patterns, while providing little proteome information beyond a relatively small number of high abundance protein identifications. In addition, the 2-D PAGE-MS approach suffers from low throughput and poor reproducibility, and remains lacking in proteome coverage, dynamic range, and sensitivity [11].

Peak capacity improvements in multidimensional liquid chromatography separations [13-18] have increased the number of detected peptides and proteins identified as a result of better use of the MS dynamic range and reduced discrimination during ionization. However, the minimal quantity of available sample from LCM captured cells has restricted analysis to the use of only a single chromatography separation prior to tandem MS analysis in recent studies [94,95] and limited the ability for mining deeper into the tissue proteome. Since the sizes of human tissue biopsies are

becoming significantly smaller due to early detection and diagnosis, a more effective discovery-based proteome technology is critically needed to enable sensitive studies of protein profiles within tissue specimens procured by LCM and other microdissection techniques [79-82].

As demonstrated in our previous studies [52,56], the key to establishing sensitive proteome analysis is attributed to high analyte concentrations in small peak volumes as the result of electrokinetic focusing/stacking and high resolving, multidimensional separation techniques in an integrated platform, thereby enhancing the dynamic range and detection sensitivity of MS. Our research efforts in this work further characterize and optimize the on-line combination of CIEF with nano-RPLC. Comparisons of peptide separations using CIEF versus strong cation exchange chromatography as the first separation dimension in multidimensional protein identification technology [13-18] are studied for their impacts on subsequent ESI-MS-based peptide identification. The capabilities of CIEF-based multidimensional separations for the analysis of protein profiles within small cell populations are demonstrated using a microdissected glioblastoma multiforme tissue sample.

## 2.2 EXPERIMENTAL SECTION

### Materials and Reagents

Fused-silica capillaries (100 μm i.d./365 μm o.d. and 50 μm i.d./365 μm o.d.) were acquired from Polymicro Technologies (Phoenix, AZ). Acetic acid, ammonium hydroxide, high resolution ampholyte 3-10, dithiothreitol (DTT), and iodoacetamide (IAM) were obtained from Sigma (St. Louis, MO). Acetonitrile, hydroxypropyl cellulose (average MW 100,000), tris(hydroxymethyl)aminomethane (Tris), and urea were purchased from Fisher Scientific (Pittsburgh, PA). Heptafluorobutyric acid (HFBA) was acquired from Pierce (Rockford, IL). All solutions were prepared using water purified by a Nanopure II system (Dubuque, IA) and further filtered with a 0.22 μm membrane (Costar, Cambridge, MA).

### Tissue Microdissection and Protein Digestion

Tumor tissues of glioblastoma multiforme were collected at the time of surgery. The tissue was completely covered with optimal cutting temperature medium, immediately frozen in liquid nitrogen, and stored at -80 $^{0}$C until analyzed. Selective tissue microdissection was performed as previously described [82]. Briefly, a single 10-μm-thick section was taken and stained with hematoxylin and eosin for histological evaluation. A semi-quantitative cell count was performed on tumor-rich (> 90% tumor cells) areas that were not compromised by inflammation, necrosis, or stromal or endothelial proliferation.

Subsequently, these areas were subjected to selective tumor dissection from serial sections. A fine needle rigidly attached to a 3-axis micromanipulator was used

to mechanically mill tissue around the periphery of the selected regions. The depth of cut was progressively increased by changing the z-axis on the manipulator while navigating along the desired path, until the region was fully separated from the bulk tissue. The needle could then be used to remove the small section from the cover slip for placement in a sample vial. This simple approach is analogous to traditional manual tissue dissection, but with a miniature cutting tool replacing the dissection scalpel, and a micropositioner suitable for automation used for cutting depth and path control. The primary goal was to selectively enrich 100,000 tumor cells from each tissue sample in less than 30 min, using 5-10 consecutive sections. These serial sections were not stained and tissue microdissection was performed under strict morphologic control. Procurement of normal brain or areas of inflammation, necrosis, hemorrhage, or stromal or vascular proliferation was strictly avoided.

The microdissected cells were placed directly into a microcentrifuge tube containing 20 mM Tris at pH 8.0. The cellular proteins were collected in the supernatant by centrifugation at 20,000g for 20 min. Proteins in the supernatant were denatured and reduced in solution containing 8 M urea and 10 mg/mL DTT. IAM was added to 20 mg/mL and the solution was incubated at 37 $^{0}$C for 1 hr in the dark. The solution was then diluted 4-fold with 100 mM ammonium acetate at pH 8.0. Trypsin was added at a 1:50 enzyme to substrate ratio and the solution was incubated at 37 $^{0}$C overnight. Tryptic digests were desalted using a Peptide MacroTrap column (Michrom Bioresources, Auburn, CA), lyophilized to dryness using a SpeedVac (Thermo, San Jose, CA), and then stored at -37 $^{0}$C.

**Integrated CIEF/Nano-RPLC Multidimensional Peptide Concentration/Separation**

An on-line combination of CIEF with nano-RPLC has been developed and described in detail in previous work [52] and was employed for systematically resolving peptide digests based on their differences in pI and hydrophobicity. To perform multidimensional peptide separations, a 80-cm CIEF capillary (100 μm i.d./365 μm o.d.) was coated with hydroxypropyl cellulose for the elimination of electroosmotic flow and protein adsorption onto the capillary wall [96]. The capillary was initially filled with a solution containing 2% ampholyte 3-10 and 1.67 mg/mL tryptic peptides.

Solutions of 0.5% ammonium hydroxide at pH 10.5 and 0.1 M acetic acid at pH 2.5 were employed as the catholyte and the anolyte, respectively. Focusing was performed at an electric field strength of 300 V/cm over the entire CIEF capillary. The current decreased continuously as the result of peptide focusing. Once the current reduced to ~10% of the original value, usually within 30 min, the focusing was considered to be complete. The focused peptides were sequentially and hydrodynamically fractionated into either 14 or 28 unique fractions. Nano-RPLC of each CIEF fraction was performed using an Ultimate pump (Dionex, Sunnyvale, CA) connected to a 15-cm pulled-tip fused silica capillary (50 μm i.d./365 μm o.d.) packed with 5-μm porous $C_{18}$ reversed-phase particles. Peptides were eluted using a 60-min linear gradient from 5 to 45% acetonitrile containing 0.02% HFBA and 0.02% formic acid at a flow rate of 200 nL/min. The eluants were monitored using a qTOF micro (Waters, Milford, MA) mass spectrometer and mass spectra were acquired from 500-1900 m/z for 1 sec, followed by 3 data dependent MS/MS scans from 50-1900 m/z for 3 sec each.

**Peptide Data Analysis**

The resulting MS data files were analyzed by ProteinLynx Global Server 2.0 (Waters) to de-isotope and lock-mass correct the raw data into peak list file suitable for database searching. Peptide and protein identifications were made using MASCOT 2.0 (Matrix Science, London, UK). Protein identifications are based on peptide identifications in the human International Protein Index (2.28) distributed and maintained by the European Bioinformatics Institute (http://www.ebi.ac.uk/IPI/IPIhuman.html). MASCOT searches were carried out at a precursor mass tolerance of 60 ppm, a 0.2 Da fragment mass tolerance; enzyme was trypsin (full); allowing 1 missed cleavage; carbamidomethyl as a fixed modification; and oxidized methionine, Y, S and T phosphorylations, and N-term and K acetylations as a variable modifications.

Because MASCOT does not consider mass accuracy when assigning significance scores, an empirical threshold in place of the MASCOT Identity Threshold was calculated using a reversed database search [97]. This threshold was calculated by searching the same data files with the same search parameters against a reversed human International Protein Index database. Hits to the reversed database, with the exception of those peptides occurring in the forward search or to peptides containing residues with mass differences beyond the resolution limits of the instrument (Q->K, I->L), were considered false positive. A threshold score corresponding to a user defined false positive rate can then be extrapolated from a simple linear regression of and exponential plot of MASCOT ions score versus the false positive rate. Runs containing >1,000 spectra typically produce a linear regression with an $R^2$ value of >0.98. In this study, the false positive rate was kept to less than 5%. Mass accuracy based thresholds (MATH) have

been shown to accurately reduce false negative identifications, while controllably limiting false positive identifications, and improve the predictive power of a typical MASCOT search using qTOF data sets [97]. MASCOT results were parsed using MP.pm (Calibrant Biosystems, Rockville, MD) and stored for reporting and data visualization in proteome BiNDR databases accessible by web-interface (Calibrant Biosystems).

## 2.3 RESULTS AND DISCUSSION

Gliomas are the most common primary tumors of the brain, with an incidence in the United States of nearly 20,000-25,000 new cases per year. Half of all gliomas, including the anaplastic astrocytomas and glioblastoma multiforme, exhibit aggressive behavior. In this study, a single 10-μm-thick tissue section was taken from a glioblastoma multiforme sample and stained with hematoxylin and eosin for histological evaluation (Fig. 2-1). A semiquantitative cell count was performed on tumor-rich areas (> 90% tumor cells) that were not compromised by inflammation, necrosis, or stromal or endothelial proliferation. Subsequently, these areas were subjected to careful tumor microdissection [82]. Selective enrichment of approximately 100,000 tumor cells was obtained from the microdisection of 5 -10 consecutive sections in each tissue sample.

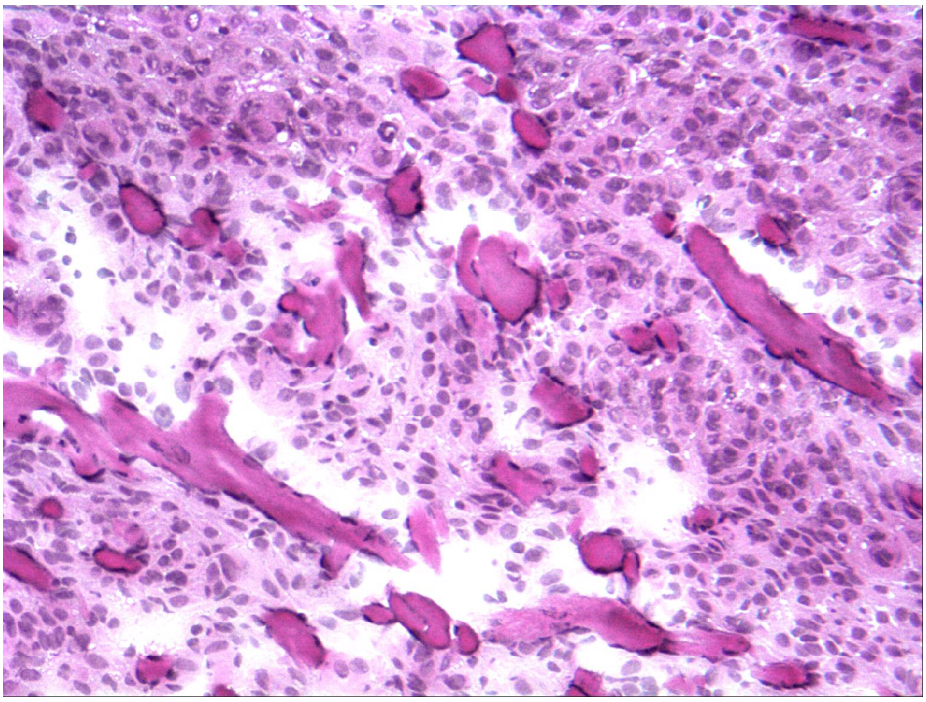

**Figure 2-1** Optical microscope photograph of stained glioblastoma multiforme tissue section

These microdissected cells contained roughly 50 μg protein for analysis. A 80-cm long capillary with a 100 μm i.d. employed in this study offered a peptide loading of 10 μg for each proteome analysis using a 1.67 mg/mL peptide digest solution prepared from the microdissection-procured tissue sample. As shown in Fig. 2-2, the CIEF separation performance of tryptic peptides obtained from the protein extract of glioblastoma multiforme was evaluated by hydrodynamically mobilizing focused proteins passing a UV detector placed near the cathodic end of the capillary. Initially, the entire content of the CIEF capillary was split into 14 individual fractions. All CIEF fractions were further resolved by nano-RPLC and the eluants were measured using ESI-tandem MS. Displayed in Fig. 2-3 are the base peak chromatograms of a representative CIEF/nano-RPLC analysis of tryptic peptides obtained from the microdissection of a glioblastoma multiforme sample.

The percentage of identified peptides present in more than one CIEF fraction was only around 10-15%, significantly less than 40-80% obtained from the multidimensional LC system using strong cation exchange coupled with reversed-phase separations [14]. A high degree of peptide overlapping in the first dimension unnecessarily burdens the subsequent separation and greatly reduces the overall peak capacity in a multidimensional separation system. The presence of high abundance peptides in multiple fractions negatively impacts the selection of low abundance peptides for tandem MS identification. Additionally, the poor resolution of low abundance peptides adversely affects their final concentrations in the eluting peaks prior to the ESI-MS analysis.

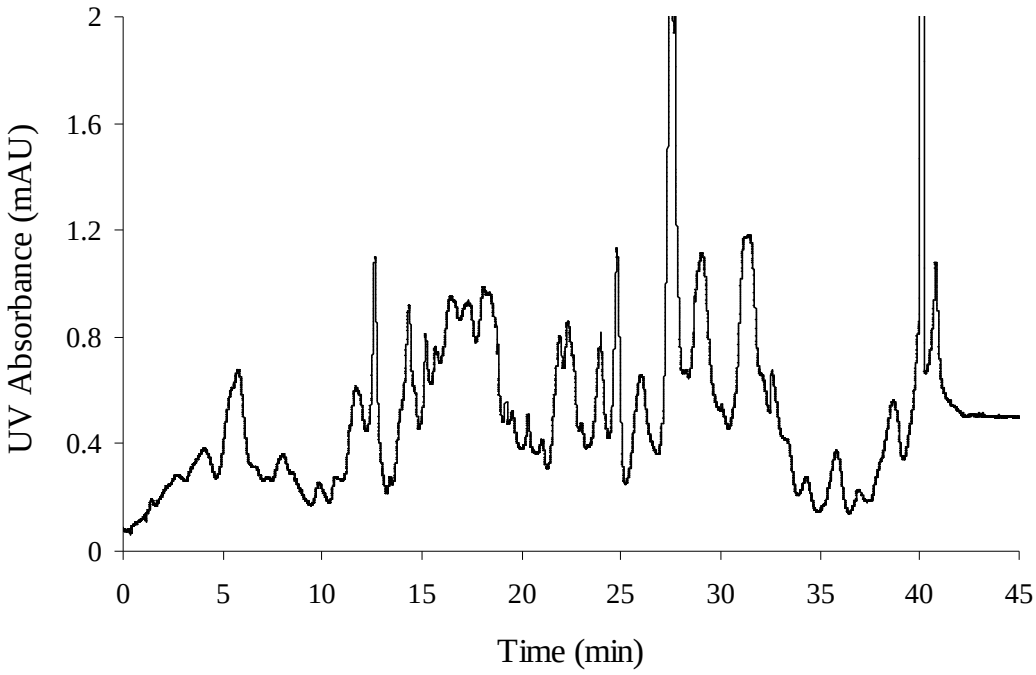


**Figure 2-2** CIEF-UV analysis of tryptic peptides obtained from microdissection-procured glioblastoma multiforme tissue sample. Capillary: hydroxypropyl cellulose coating, 80 cm x 100 μm i.d. x 365 μm o.d.; anolyte: 0.1 M acetic acid at pH 2.5; catholyte: 0.5% w/w ammonium hydroxide at pH 10.5; electric field strength: 300 V/cm; hydrodynamic mobilization; detection: UV absorbance at 280 nm, 7 cm from cathodic end.

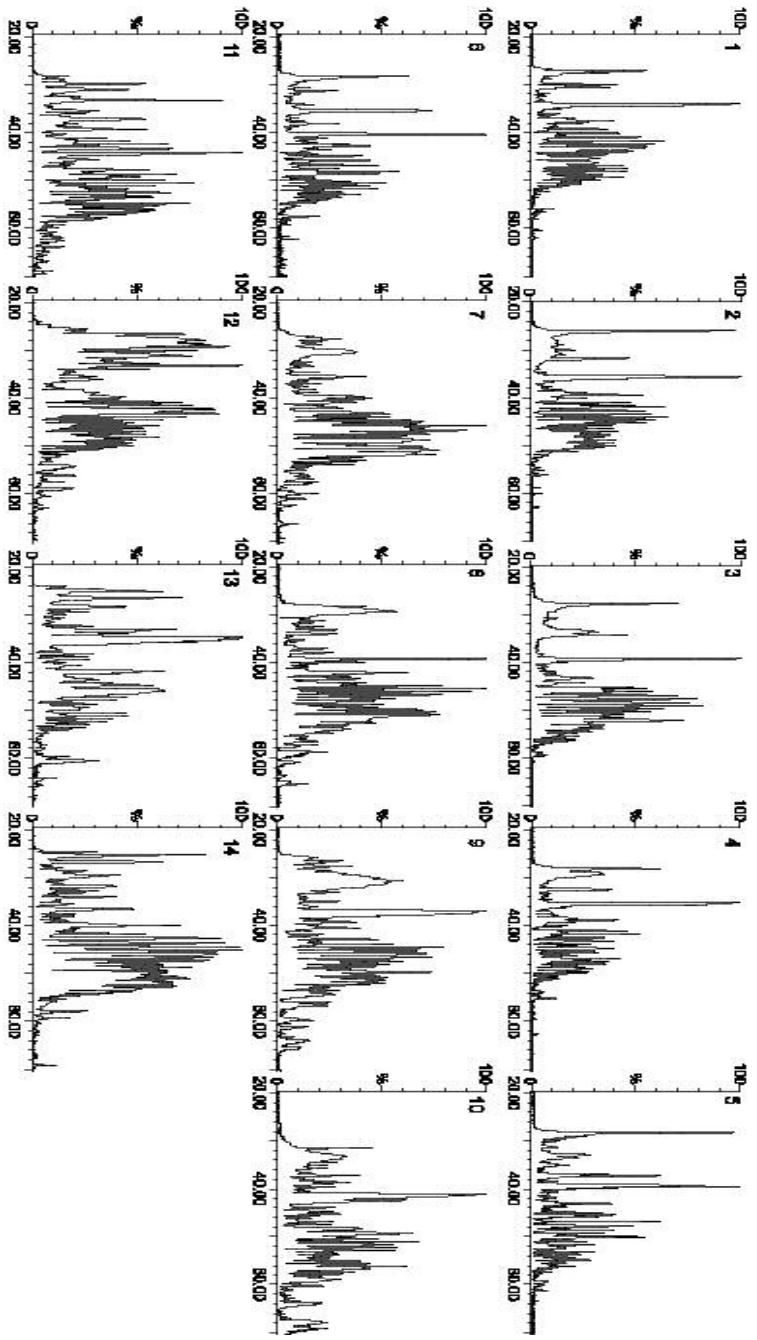

**Figure 2-3** Base peak chromatograms of a representative CIEF/nano-RPLC multidimensional separation of 10 μg peptide digest prepared from microdissection-procured glioblastoma multiforme tissue sample. Each number represents the sequence of CIEF fractions further analyzed by nano-RPLC from basic to acid pHs.

The high resolution nature of pI-based separations, including CIEF [52,69], was further supported by Stephenson and co-workers [98,99] who employed immobilized pH gradient gels in the first dimension, followed by RPLC and subsequent tandem MS analysis. The pI values of peptides identified in each CIEF fraction were calculated using the "iep" program developed by the European Molecular Biology Open Source Software Suite (EMBOSS) group. As shown in Fig. 2-4, the CIEF separation was able to cover a wide pH range of 3.1-10.8 using a 2% ampholyte 3-10 solution. In comparison with immobilized pH gradient gels [98,99], the significant advantages of CIEF include the ability to use higher electric fields resulting in rapid and ultrahigh resolution separations, improved reproducibility in pI fractions resulting from the use of gel free separation medium, and the amenability to automation and seamless coupling with nano-RPLC in an integrated platform while avoiding potential sample loss, analyte dilution, and any post-gel peptide extraction/concentration procedures.

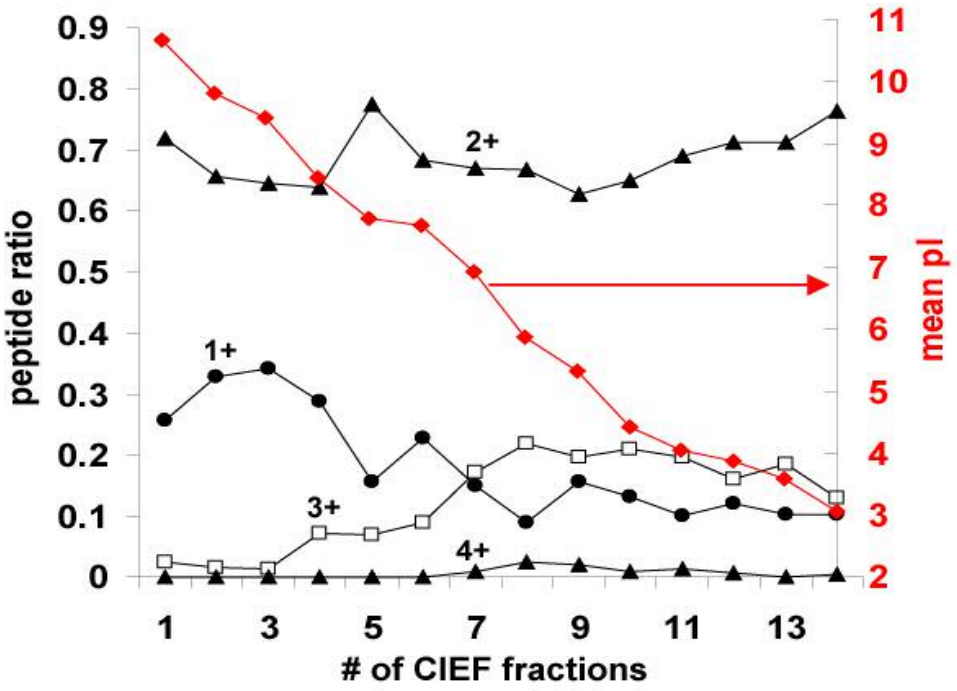


**Figure 2-4** Distribution of peptide's pI and solution charge state in each CIEF fraction.

In addition to the significant peptide fraction overlap resulting from strong cation exchange chromatography, peptides are separated in a mixed-mode based on their ionic charge and hydrophobicity [18]. The majority of doubly charged peptides are eluted over approximately 25% of the entire salt gradient [18]. Typically 70-90% of peptide identifications in shotgun proteomics are made through tandem MS fragmentation of doubly charged ions [14,18]. Therefore, fractions containing the majority of peptide identifications tend to be clustered at the early part of the salt elution gradient, corresponding to the presence of doubly charged peptides [18,99]. In contrast, CIEF provides an even distribution of doubly charged peptides over the entire pH gradient (Fig. 2-4), thereby maximizing the informative potential of MS measurements.

Due to the limited protein quantities extracted from microdissection-procured tissue specimens, a single RPLC separation was performed in recent studies [94,95] for the analysis of selected cell populations. However, the use of only a single separation dimension may not provide sufficient peak capacity for the resolution of complex peptide mixtures, putting significant burdens on the detection sensitivity and dynamic range of the MS. By employing CIEF-based multidimensional separations, a total of 6,866 fully tryptic peptides were detected, leading to the identification of 1,820 distinct proteins (see APPENDIX). These identifications were generated from 3 runs of a single glioblastoma multiforme tissue sample, with each run consuming only 10 μg of total protein and were based on high mass accuracy (60 ppm) and high confidence (5% false positive) hits to fully tryptic peptides.

This ultrasensitive capability of CIEF-based multidimensional separations may enable the use of proteome analysis for the assessment of specimen quality and reproducibility procured from the same tissue, and in turn, allow the evaluation and optimization of microdissection technologies [70,71,79-82] and tissue sample preparation. In addition to tracking the cumulative totals of protein identifications, the percentage of overlapping proteins was approximately 70% across any two runs (Fig. 2-5). A total of 700 proteins, corresponding to 38.5% of collective data set, were found in all three runs. For each additional run, the percentage increase in cumulative protein identifications was approximately 25-35% and decreased with increasing numbers of analysis runs. This percentage increase in cumulative protein identifications was higher than 10-15% obtained from the analysis of yeast cell lysates using multidimensional

liquid chromatography separations [100], likely as a result of the complexity of the human tissue proteome.

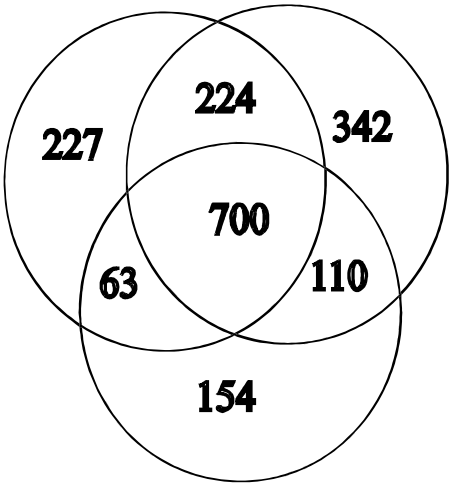


**Figure 2-5** The overlap in the proteins identified from three CIEF-nano-RPLC-ESI-MS/MS runs using a single glioblastoma multiforme tissue sample.

The intrinsic high resolution of CIEF allows the number of fractions sampled in the first separation dimension to be further increased. The excellent reproducibility together with straightforward fractionation enables user discretion as to which fractions are to be analyzed in the off-line approach, and interesting fractions may be revisited (reanalyzed) or repeatedly accumulated for identification of extremely low abundance peptides. By comparing the results obtained from runs containing 14 and 28 CIEF fractions, the number of distinct proteins identified from a single proteome experiment of 28 CIEF fractions was comparable or slightly higher than the cumulative data set achieved using two runs of 14 CIEF fractions. For the proteome analysis of limited tissue samples, further enhancement in the overall peak capacity for mining

deeper into the proteome can therefore be realized by simply increasing the number of CIEF fractions without an accompanying increase in sample consumption. In contrast, Peng and co-workers [18] have significantly increased the number of strong cation exchange chromatography fractions, but obtained comparable numbers of peptide and protein identifications as those reported by Washburn and colleagues [13].

A variety of protein classes, including structural proteins, metabolic enzymes, receptors, and proteins involved in transcription, translation, and post-translational modification of gene products, were identified from microdissection-procured glioblastoma multiforme tissue samples. A number of biologically relevant proteins, such as annexin I and nestin, were unambiguously identified. A total of 18 unique peptides (peptides matching on single database entry) (Table 2-1), corresponding to greater than 50% protein sequence coverage, led to the identification of annexin I which is related to tumor aggressiveness and angiogenesis, and found exclusively in tumor vessels [101,102]. On the other hand, nestin, which is linked to neural stem cell differentiation [103,104], was identified by 16 unique peptides (sequence in "italic" in Table 2-1) out of a total of 19 distinct peptide identifications. Examples of tandem MS spectra leading to peptide identifications are shown in Fig. 2-6.

For the identification of peptides eluted from multidimensional separations, tandem MS instruments such as a qTOF mass spectrometer employed in this study acquire peptide MS/MS spectra which encode the peptide sequences. Traditionally, this acquisition has been done in a data-dependent way, whereby the instrument relies on a preliminary scan, performed as the peptides enter the instrument, to select peptides for fragmentation and generation of tandem MS spectra. However, data-dependent scanning

cannot acquire spectra fast enough to identify all the peptides as they enter the MS instrument, so many peptide and subsequent protein identifications are missed. Newly introduced rapid-scanning linear ion-trap instruments can acquire MS/MS spectra up to five times faster than earlier generations of MS instruments. Furthermore, parallel, rather than serial, collision-induced dissociation (CID) of peptides has been demonstrated by several research groups [105-109] for increasing the mass spectrometric duty cycle. Thus, the use of rapid-scanning MS instruments or parallel (or data-independent) CID coupled with CIEF-based multidimensional separations should greatly increase the sequence coverage of identified proteins and total proteome coverage within limited tissue samples or small cell populations.

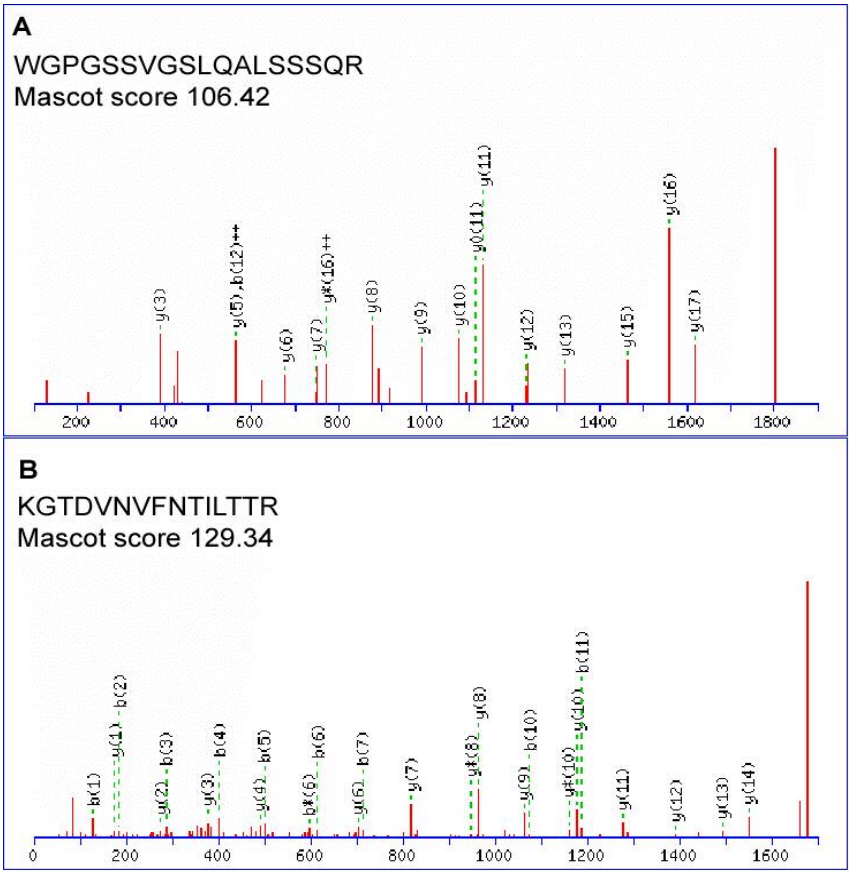


**Figure 2-6** MS/MS spectra of (A) WGPGSSVGSLQALSSSQR and (B) KGTDVNVFNTILTTR leading to the identification of nestin and annexin I , respectively.

**Table 1**

List of Peptides Identified for Nestin and Annexin I

| Peptide Sequence | Exp. Mass | Error (Da) | Error (ppm) | Score |
|---|---|---|---|---|
| **Nestin** | | | | |
| EESEAEAPR | 1016.45 | 0.0060 | 5.9 | 43.00 |
| *SLEEDLETLK* | 1175.61 | 0.0151 | 12.9 | 47.54 |
| *AHADDELAALR* | 1180.59 | 0.0048 | 4.1 | 56.57 |
| *SAGQENLETLK* | 1188.62 | 0.0189 | 15.9 | 39.53 |
| *VGLNAQAACAPR* | 1226.64 | 0.0183 | 14.9 | 47.46 |
| *SLETEILESLK* | 1260.69 | 0.0114 | 9.0 | 62.59 |
| *EIQDSQVPLEK* | 1284.68 | 0.0208 | 16.2 | 51.25 |
| *DNLAEELEGVAGR* | 1371.67 | 0.0119 | 8.7 | 75.51 |
| *GEGEGQIWGLVEK* | 1400.70 | 0.0088 | 6.2 | 90.97 |
| *TLENQSHETLER* | 1455.70 | 0.0005 | 0.3 | 84.51 |
| *QGLQSQIAQVLEGR* | 1525.83 | 0.0087 | 5.7 | 58.40 |
| *VAIPASVLPGPEEPGGQR* | 1772.93 | 0.0166 | 9.3 | 66.26 |
| *VAIPASVLPGPEEPGGQR* | 1772.94 | 0.0016 | 0.9 | 52.76 |
| WGPGSSVGSLQALSSSQR | 1802.89 | 0.0018 | 1.0 | 106.42 |
| DLEEAGGLGTEFSELPGK | 1847.88 | 0.0003 | 0.2 | 64.77 |
| *SLEEEGQELPQSADVQR* | 1913.87 | 0.0219 | 11.5 | 59.02 |
| *SLDQEIARPLENENQEFLK* | 2272.14 | 0.0051 | 2.3 | 44.52 |
| *LGSLLPVLSPTSLPSPLPATLETPVPAFLK* | 3054.74 | 0.0233 | 7.6 | 27.71 |
| *SLEGNLETFLFPGTENQELVSSLQENLESLTALEK* | 3878.87 | 0.0655 | 16.9 | 57.72 |
| | | | | |
| **Annexin I** | | | | |
| *CLTAIVK* | 803.46 | 0.0006 | 0.7 | 31.89 |
| *VLDLELK* | 828.49 | 0.0092 | 11.1 | 34.98 |
| *NALLSLAK* | 828.50 | 0.0099 | 12.0 | 44.68 |
| *AMVSEFLK* | 965.48 | 0.0092 | 9.6 | 52.36 |
| *DITSDTSGDFR* | 1212.53 | 0.0078 | 6.4 | 57.74 |
| *TPAQFDADELR* | 1261.61 | 0.0190 | 15.1 | 76.96 |
| *CATSKPAFFAEK* | 1355.67 | 0.0157 | 11.6 | 46.84 |
| *GVDEATIIDILTK* | 1386.77 | 0.0123 | 8.9 | 72.57 |
| *GVDEATIIDILTKR* | 1542.86 | 0.0008 | 0.5 | 67.23 |
| *ALTGHLEEVVLALLK* | 1604.96 | 0.0112 | 7.0 | 90.92 |
| *KGTDVNVFNTILTTR* | 1677.88 | 0.0297 | 17.7 | 129.34 |
| *GLGTDEDTLIEILASR* | 1701.87 | 0.0088 | 5.2 | 129.79 |
| *KALTGHLEEVVLALLK* | 1733.09 | 0.0452 | 26.1 | 79.72 |
| *SEDFGVNEDLADSDAR* | 1738.73 | 0.0041 | 2.4 | 83.35 |
| *AAYLQETGKPLDETLK* | 1775.92 | 0.0060 | 3.4 | 62.79 |
| *AAYLQETGKPLDETLKK* | 1904.04 | 0.0117 | 6.1 | 76.35 |
| *MYGISLCQAILDETKGDYEK* | 2333.08 | 0.0122 | 5.2 | 31.02 |
| *GGPGSAVSPYPTFNPSSDVAALHK* | 2355.16 | 0.0090 | 3.8 | 103.65 |

## 2.4 CONCLUSION

To address the issue of cell heterogeneity in the tissue section, LCM [70,71] and other microdissection techniques [79-82] have been developed to provide a rapid and straightforward method for isolating selected subpopulations of cells for downstream molecular analysis, effectively enabling purification of the molecules of interest by eliminating DNA, RNA, or protein interference from the surrounding tissue. However, a more significant problem of microdissection-based tissue sample preparation is the lack of sample availability for mining deeper into the proteome using current 2-D PAGE [90-93] and shotgun technologies [13-18,94,95], greatly impacting the efforts toward the assessment of sample quality and the discovery of tumor biomarkers.

Coupled with the laser-free microdissection technology [82], CIEF-based multidimensional peptide separations were employed to enable the analysis of protein profiles within small cell populations procured from glioblastoma multiforme tissue samples. Compared with strong cation exchange chromatography utilized as the first dimension in multidimensional protein identification technology [13-18], CIEF not only contributed to high resolution peptide separation based on their differences in pI, but also allowed effective usage of MS-based peptide identifications by even distribution of doubly charged peptides over the entire pH gradient. Instead of performing multiple runs of multidimensional separations, comparable or even better proteome results can be achieved by simply increasing the number of CIEF fractions due to the intrinsic high resolution nature of electrokinetic focusing. This unique feature is particularly important for the proteome analysis of limited tissue samples.

The analysis of a single glioblastoma multiforme tissue sample led to the identification of a total of 6,866 fully tryptic peptides, corresponding to 1,820 distinct protein identifications. To greatly enhance the sequence coverage of identified proteins and total proteome coverage within limited tissue samples or small cell populations, our future work will focus on the application of rapid-scanning linear ion-trap instrumentation and/or data-independent CID [105-109] for increasing the mass spectrometric duty cycle. In addition to biomarker discovery, the ability to perform comprehensive and sensitive tissue proteome analysis will also allow the evaluation of sample quality and reproducibility for the validation and optimization of microdissection technologies.

## 2.5 ACKNOWLEDGEMENT

We thank the National Cancer Institute (CA103086 and CA107988) and the National Center for Research Resources (RR21239) for supporting portions of this research.

# CHAPTER 3

# EFFECTS OF CHROMATOGRAPHY CONDITIONS ON INTACT PROTEIN SEPARATIONS FOR TOP-DOWN PROTEOMICS

Yueju Wang, Brian M. Balgley, Paul A. Rudnick, and Cheng S. Lee

Journal of Chromatography A, 1073, 35-41 (2005)

## 3.1 INTRODUCTION

The vast number of proteins present in the proteome of a typical organism requires that separations be performed on the mixture prior to introduction into the mass spectrometer. 2-D PAGE is still the method of choice for separating thousands of proteins in a single run [7-10] while offering a "differential display" of protein expression. However, the identification of gel resolved proteins and the study of protein modifications typically involve the separate excision, proteolytic digestion, peptide extraction/concentration, and MS analysis of each protein spot [110,111]. All of these procedures, even when semi-automated using the commercially available robotic sample and liquid handling systems, are time-consuming tasks prone to significant sample loss and analyte dilution. Thus, the 2-D PAGE-MS approach remains lacking in proteome coverage, dynamic range, sensitivity, and throughput [11,12].

Consequently, considerable efforts have been devoted to the development of non-gel-based and bottom-up (or shotgun) proteome technologies through the combination of various chromatography methods with MS or tandem MS analysis [13-18]. These peptide separation techniques fully exploit the sensitivity achievable with conventional mass spectrometers (roughly $10^{-16}$ mol as opposed to $10^{-14}$ mol in

conjunction with 2-D PAGE), allowing many additional proteins to be identified. However, the bottom-up approaches provide very limited molecular information about the intact proteins where only a fraction of the total theoretical peptide population of a given protein may be identified.

By comparing with shotgun methodologies, the top-down proteome techniques [20-23], in which intact proteins rather than peptides are measured, are advantageous for the detection of PTMs [19]. PTMs include co- or post-translation covalent modifications to the protein structure and proteolytic processing of the translated protein. Furthermore, the top-down approaches to protein sequence analysis using tandem MS may allow complete protein characterization far more efficiently than shotgun proteome technologies using protein digests. In order to achieve the full potential of top-down approaches, the processing and separation of intact proteins still have to be brought to a similar level as those routinely achieved in shotgun proteomics.

A variety of separation technologies, including gel-based isoelectric focusing [29], CIEF [30,31], CZE [20], and RPLC [32,33], have been utilized for resolving intact proteins prior to MS analysis. The application of only a single separation dimension, however, provides insufficient peak capacity for the resolution of complex protein mixtures. Thus, several recent attempts have involved off-line combinations of preparative scale isoelectric focusing [42-44] or acid-labile surfactant-based polyacrylamide gel electrophoresis [22,23] with RPLC in the development of multidimensional protein separation platforms. The collected protein fractions from either isoelectric focusing or gel electrophoresis were further resolved using RPLC as the second separation dimension prior to MS analysis.

It is clear that RPLC plays a major role in both single and multidimensional protein separation platforms in an effort to increase the overall peak capacity for the resolution of complex intact protein mixtures such as cell lysates. Total peak capacity improvements in protein separations contribute to increased number of proteins identified in top-down proteomics due to better use of the MS dynamic range and reduced discrimination during ionization. Thus, the main objective of the present study is to carefully examine the effects of various chromatography conditions, including alkyl chain length in the stationary phase, capillary column temperature, and ion-pairing agent, on the resolution of intact proteins. By using nano-RPLC-ESI MS, we further investigate potential differences in chromatography separation and ESI measurement of yeast intact proteins as the result of the protein denaturation process. Denatured proteins collected in RPLC fractions can be directly subjected to proteolytic digestion for obtaining their corresponding peptides and peptide sequences, particularly toward the MS identification of high molecular mass proteins [42-45].

## 3.2 EXPERIMENTAL SECTION

### Materials and Chemicals

Fused-silica capillaries (50 μm i.d./365 μm o.d.) were acquired from Polymicro Technologies (Phoenix, AZ). Model proteins, including bovine serum albumin (bovine, pI 5.60, 66,433.0 Daltons), cytochrome c (equine, pI 9.59, 12,362.0 Daltons), myoglobin (equine, pI 7.36, 16,951.5 Daltons), and ribonuclease A (bovine, pI 8.64, 13,688.1 Daltons), DTT, and IAM were obtained from Sigma (St. Louis, MO). Acetonitrile, DNase, formic acid, glycerol, magnesium chloride, TFA, Tris, and urea were purchased from Fisher Scientific (Pittsburgh, PA). HFBA was acquired from Pierce (Rockford, IL). All solutions were prepared using water purified by a Nanopure II system (Dubuque, IA) and further filtered with a 0.22 μm membrane (Costar, Cambridge, MA).

### Soluble Fraction of Intact Proteins from *S. cerevisiae*

The yeast cells (Sigma) were suspended in a buffer which consisted of 10 mM Tris (pH 7.0), 5 mM magnesium chloride, 0.1 mM DTT, and 10% glycerol. The cells were disrupted by sonication for the release of cellular proteins. After sonication, DNase was added with a final concentration of 50 μg/mL for the cleavage and removal of nucleic acids. The cellular proteins were collected in the supernatant by centrifugation at 20,000g for 10 min. The protein solution was then desalted using a regenerated cellulose membrane (Millipore, Bedford, MA) with a 5,000 molecular weight cutoff.

Yeast cytosol proteins were denatured and reduced in a 20 mM Tris buffer containing 8 M urea and 0.1 M DTT for 2 hr at 37 $^{0}$C under a nitrogen atmosphere. Proteins were alkylated by adding excess IAM with a final concentration of 50 mM and

the reaction was allowed to proceed for 30 min at room temperature in the dark. A PD-10 size exclusion column (Amersham Pharmacia Biotech, Uppsala, Sweden) was employed for buffer exchange and proteins were eluted in a solution containing 2 M urea and 10 mM Tris at pH 8.0. The total protein concentration was determined using the Bradford method (Bio-Rad, Richmond, CA) and was around 2 mg/mL.

**Nano-RPLC-ESI-MS Analysis of Model Proteins and Soluble Fraction of Intact Proteins from *S. cerevisiae***

The tip at the end of a 16-cm-long fused silica capillary (50 μm i.d. x 365 μm o.d.) was flame-pulled and packed with 13 cm of 5-μm $C_4$- or $C_{18}$-bonded particles (Phenomenex, Torrance, CA). The $C_{18}$-bonded particles in methanol were introduced into the capillary by gradually increasing the pressure from 100 to 2,000 psi using an Agilent 1100 capillary LC pump (Avondale, PA). The packed capillary was left under pressure for 10 hr and then depressurized overnight. A microcross (Upchurch Scientific, Oak Harbor, WA) containing a platinum electrode was employed to apply an ESI voltage of 1.8 kV and reduce the flow of Agilent 1100 capillary LC pump from 2 μL/min to an effective flow rate of 200 nL/min. A 30-min linear gradient from 10% to 65% acetonitrile (containing 0.1% TFA or 0.02% HFBA) was utilized to perform intact model protein separations. The linear gradient was further extended from 30- to 60-min for the analysis of complex yeast cell lysates.

The eluants from nano-RPLC were monitored using a Micromass qTOF micro mass spectrometer (Manchester, United Kingdom). Mass spectra were collected from 600 to 1900 m/z using a scan time of 2.0 s. Automated analysis of the nano-RPLC-

ESI-MS data files were performed using Protein Trawler software (Bioanalyte, Portland, ME) [112,113]. The program summed all data within a specified time interval, utilized Micromass MaxEnt 1 to deconvolute multiply charged ions, centered the results, carried out a threshold selection, and reported the mass, intensity, and retention time of each protein in a text file. The program repeated this process across sequential portions of the chromatogram.

## 3.3 RESULTS AND DISCUSSION

The reduction of column i.d. from few hundred μm [13] to as small as 15 μm [24] in capillary liquid chromatography has resulted in higher peptide concentrations within smaller peak volumes, thus enabling more sensitive MS detection. Nano-RPLC equipped with a 50 μm i.d. capillary column was therefore employed in this study to evaluate the effects of various chromatography conditions on intact protein separations and allow ultrasensitive characterization of model proteins and yeast cell lysates using ESI-MS. Due to the use of ESI-MS detection, the differences in chromatography separation and protein intensity were further revealed among the samples containing the soluble fraction of yeast cell lysates in the native versus denatured/reduced/alkylated states.

### Effect of Alkyl Chain Length in the Stationary Phase on Intact Protein Separations

Four model proteins, including bovine serum albumin, cytochrome c, myoglobin, and ribonuclease A, were prepared in 10 mM Tris at pH 7.0 with a final concentration of 0.1 μM for each model protein. The effect of alkyl chain length in the stationary phase on chromatography separation of model proteins was studied and shown in Figs. 3-1A and 3-1B as the base peak chromatograms acquired from capillary columns packed with 5-μm $C_4$- and $C_{18}$-bonded particles, respectively. All protein peaks were directly identified on the basis of mass spectra of protein analytes taken from the average of scans under the peaks.

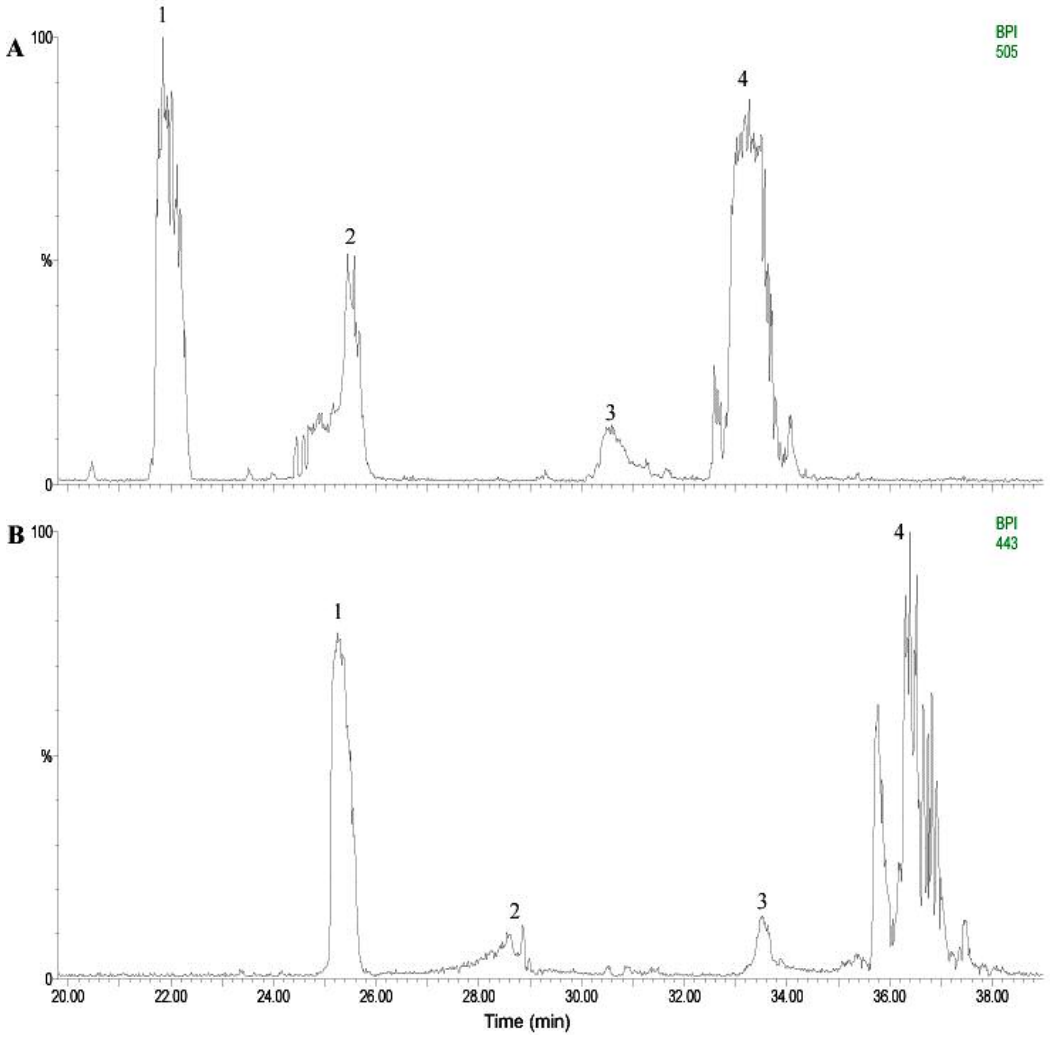


**Figure 3-1** Comparison of model protein separations using (A) $C_4$ and (B) $C_{18}$ columns. Column temperature: 25 $^0$C; elution order: 1-ribonuclease A, 2-cytochrome c, 3-bovine serum albumin, and 4-myoglobin; mobile phase: a 30-min linear gradient from 10% to 65% acetonitrile (containing 0.1% TFA) at a flow rate of 200 nL/min; sample loading: 100 femtomole for each model protein (1 μL injection of 0.1 μM protein solution).

As anticipated [114], the elution time of model proteins increased with increasing alkyl chain length. Furthermore, the reconstructed ion chromatograms were obtained using the most intense m/z ions from each protein envelope and displayed in Figs. 3-2A and 3-2B for the separations carried out by the $C_4$ and $C_{18}$ columns, respectively. Both the separation efficiency and resolution of model proteins achieved in the $C_{18}$ column were considerably better than those obtained from the $C_4$ column, particularly for early eluted proteins such as ribonuclease A and cytochrome c. Still, potential sample loss due to irreversible protein adsorption onto the $C_{18}$ stationary phase may outweigh the benefits of better separation performance and may adversely impact the ability to perform comprehensive proteome analysis, particularly toward the identification of low abundance proteins. Thus, both $C_4$ and $C_{18}$ reversed phase columns have been utilized by several research groups for the analysis complex protein mixtures such as cell lysates in top-down proteomics [22,23,42-45,112,113].

**Effect of Ion-Pairing Agent on Intact Protein Separations**

To improve chromatography separations, ion-pairing agents are commonly used to sharpen peak shapes [115]. In contrast to ion pairing agents of alkanesulfonic acids, perfluorinated carboxylic acids up to four carbon atoms are known to be volatile and therefore well suited for ESI-MS detection. The downside to the use of perfluorinated carboxylic acids is their ionization suppression effect. Some of the decrease in MS sensitivity, however, can be regained through increased analyte concentrations in sharpened peaks due to the “concentration sensitive” behavior of nano-ESI-MS [116].

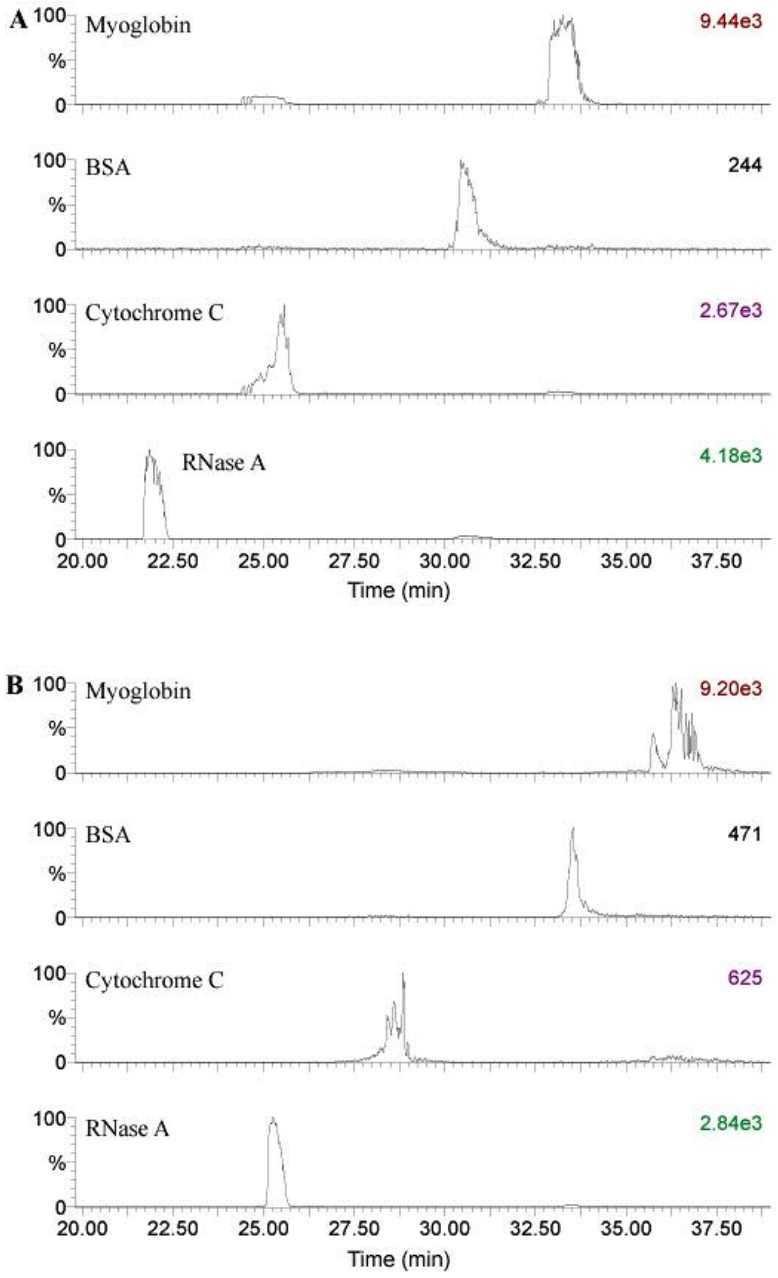


**Figure 3-2** Reconstructed ion chromatograms of model protein separations using (A) $C_4$ and (B) $C_{18}$ columns. Each model protein is represented using its most intense m/z ion from the ESI protein envelope: m/z 893.7 for myoglobin, m/z 1332.9 for bovine serum albumin, m/z 825.4 for cytochrome c, and m/z 1245.7 for ribonuclease A.

In shotgun proteomics, Yates and co-workers [13,14] have substituted acetic acid with 0.02% HFBA for the analysis of a trypsin-digested sample of soluble proteins from *S. cerevisiae* using strong cation exchange chromatography coupled with RPLC. By comparing with an acetic acid buffer system, more than three times as many peptides were identified using HFBA in their work. Adding HFBA improved the dynamic range of the analysis and allowed for the acquisition of more low-abundance peptides. By using a $C_{18}$ column, the effect of ion-paring agent on intact protein separations was investigated by adding either 0.1% TFA (Fig. 1B) or 0.02% HFBA (Fig. 3-3) into the mobile phase. In contrast to the conclusion obtained from shotgun proteome studies [13,14], the use of 0.02% HFBA as ion-pairing agent resulted in significant deterioration of separation resolution among model proteins, particularly between bovine serum albumin and myoglobin. Further increase in HFBA concentration contributed to dramatic reduction in protein ion intensities measured by ESI-MS (data not shown).

**Effect of Column Temperature on Intact Protein Separations**

At high column temperatures, the mobile phase viscosity is reduced, and concomitantly, the diffusivity of the analyte is enhanced. More importantly, the sorption kinetics of the analyte is also accelerated with increasing temperature. Consequently, the column efficiency is expected to be higher at elevated column temperatures [117,118]. Thus, the effect of column temperature on intact protein separation performance was evaluated by raising the column temperature from 25 to 60 $^0$C using a column heater. By comparing with the results shown in Fig. 3-1B, the base peak chromatogram displayed in Fig. 3-4 not only demonstrated improved separation resolution and efficiency among

various protein conformers at high column temperature, but also presented strong protein ion intensities as the result of enhanced ESI prior to MS detection. Due to the limitation on MS scan speed, no attempts were pursued in increasing the mobile phase flow rate for further enhancing the column efficiency and achieving high speed chromatography separations.

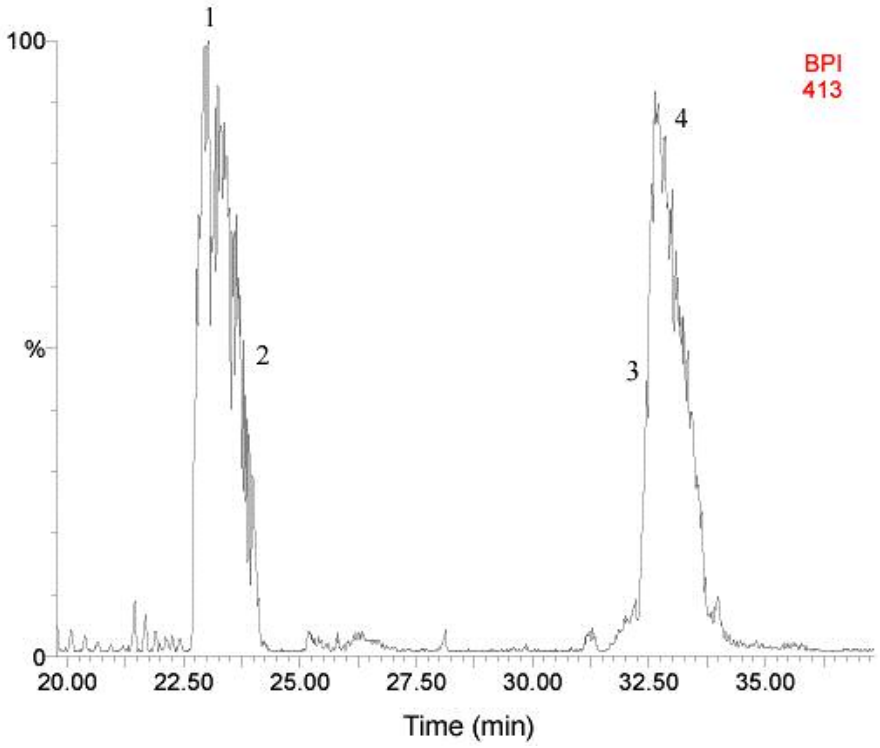


**Figure 3-3** Base peak chromatogram for illustrating the effect of ion-paring agent on nano-RPLC-ESI-MS separation of model proteins. $C_{18}$ column temperature: 25 $^{0}$C.; elution order: 1-ribonuclease A, 2-cytochrome c, 3-bovine serum albumin, and 4-myoglobin; mobile phase: a 30-min linear gradient from 10% to 65% acetonitrile (containing 0.02% HFBA) at a flow rate of 200 nL/min; sample loading: 100 femtomole for each model protein (1 μL injection of 0.1 μM protein solution).

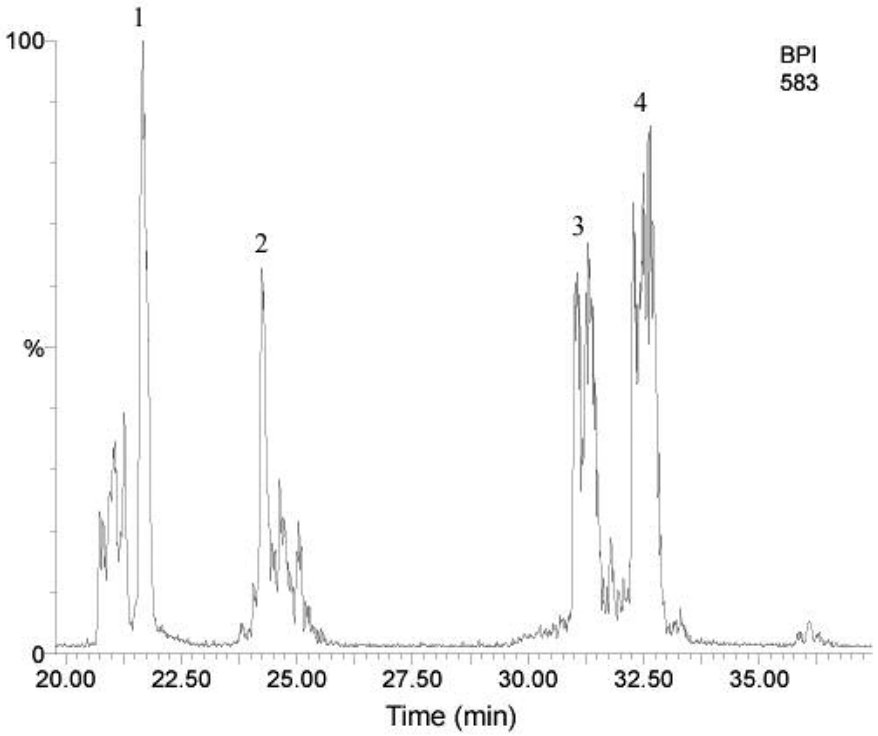


**Figure 3-4** Base peak chromatogram for illustrating the effect of column temperature on nano-RPLC-ESI-MS separation of model proteins. $C_{18}$ column temperature: 60 $^{0}$C.; elution order: 1-ribonuclease A, 2-cytochrome c, 3-bovine serum albumin, and 4-myoglobin; mobile phase: a 30-min linear gradient from 10% to 65% acetonitrile (containing 0.1% TFA) at a flow rate of 200 nL/min; sample loading: 100 femtomole for each model protein (1 μL injection of 0.1 μM protein solution).

**Nano-RPLC-ESI-MS Analysis of Native and Denatured/Reduced/Alkylated Yeast Cell Lysates**

In addition to the characterization of model proteins, the soluble fraction of intact proteins from *S. cerevisiae* in the native state was analyzed using nano-RPLC-ESI-MS in this study. As shown in Fig. 3-5A, the peak width ($4\sigma$) for a protein eluting from the column is as small as 10 s which corresponds to a peak capacity of 360 over a gradient run time of 60 min. Further enhancement in the peak capacity can be realized by slowing the solvent gradient in nano-RPLC and increasing the column length at the expense of analysis time [24]. Still, the peak capacity of any single dimension separations is insufficient for processing the number of proteins that expected from even a eukaryotic organism such as *S. cerevisiae* proteome (> 6,000 proteins).

It has been estimated that up to 10,000 proteins may be commonly present in human serum, most of which would be present at very low relative abundance [119]. The large variation of protein relative abundances having potential biological significance in mammalian systems (> 6-9 orders of magnitude) also presents a major analytical challenge for proteomics. Thus, the use of multidimensional protein separations, including combinations of isoelectric focusing [42-44,120] or polyacrylamide gel electrophoresis [22,23] with RPLC, not only contributes to reduction in protein complexity prior to MS analysis, but also increases the number of proteins identified due to better use of the MS dynamic range and reduced discrimination during ionization.

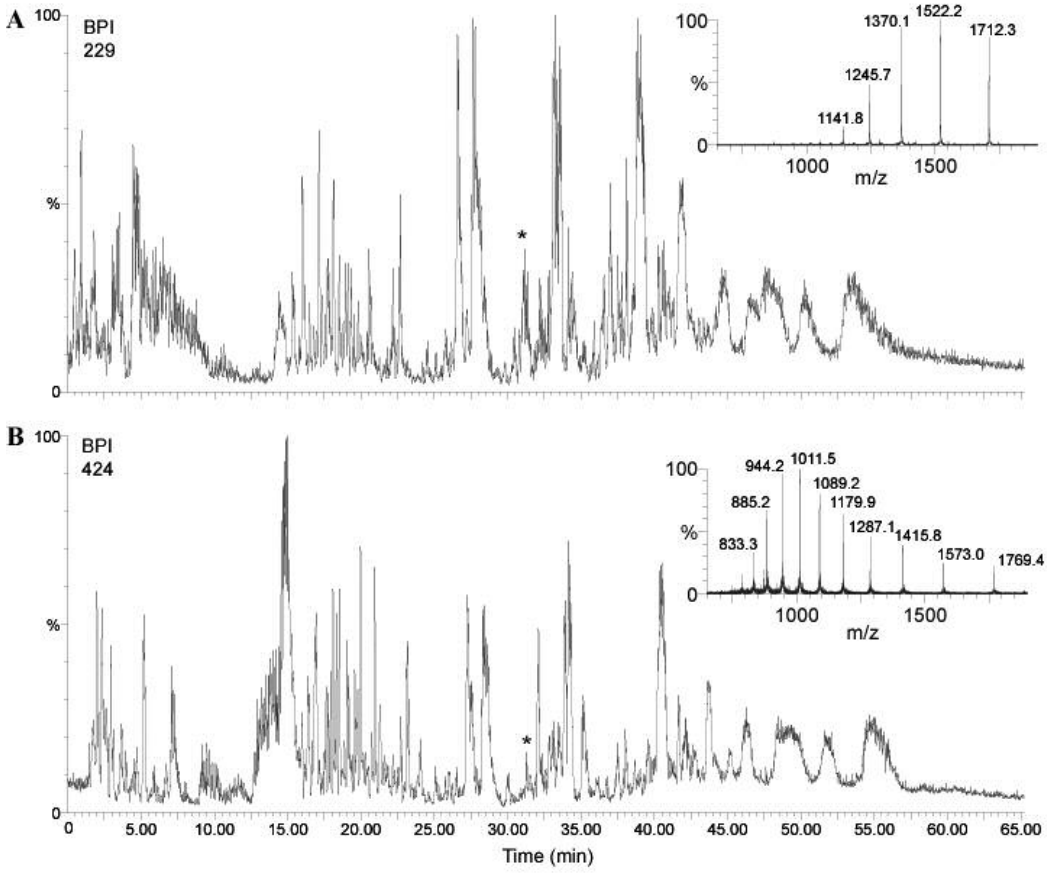


**Figure 3-5** Base peak chromatograms for the soluble fraction of yeast cell lysates in the (A) native and (B) denatured states using nano-RPLC-ESI MS. $C_{18}$ column temperature: 60 $^{0}$C.; mobile phase: a 60-min linear gradient from 10% to 65% acetonitrile (containing 0.1% TFA) at a flow rate of 200 nL/min; sample loading: 2 µg of total yeast protein (1 µL injection of 2 mg/mL yeast protein solution) spiked with ribonuclease A. Eluted ribonuclease A peaks are marked with * and the mass spectra taken from the average of scans under the peaks are shown as insets.

Top-down proteome approaches offer excellent molecular level information for the intact proteins, but currently require the use of FTICR-MS/MS for obtaining protein-sequencing measurements [20-23]. Furthermore, top-down technologies are also limited by the relative scarcity of bioinformatic tools to efficiently analyze this type of data, although these are under development [21]. Thus, on-line proteolytic digestion of eluted proteins or off-line fraction collection of resolved proteins followed by subsequent digestion [42-45] can greatly facilitate protein identification through peptide mass mapping or peptide sequences obtained from tandem MS using conventional mass spectrometers. Instead of spreading proteolytic peptides over the entire multidimensional separation in the bottom-up approach, the peptides and their sequences can be directly linked with the corresponding proteins in this combined top-down/bottom-up methodology, possibly resulting in increased peptide sequence coverage of identified proteins.

In order to implement the combined top-down/bottom-up proteome analysis in our future work, we therefore investigated potential differences in chromatography separation and ESI-MS measurement of yeast intact proteins present in the native versus denatured states. This is because these denatured, reduced, and alkylated proteins eluted from nano-RPLC can be directed toward to a miniaturized trypsin membrane reactor [121] for performing on-line and real time proteolytic digestion prior to MS analysis. The chromatography separation results obtained from the same yeast protein sample which was further denatured, reduced, and alkylated (Fig. 3-5B) were compared with the analysis using yeast proteins in the native state (Fig. 3-5A). In general, there were no significant differences in the separation efficiency and resolution

of native versus denatured proteins using nano-RPLC. The elution time of denatured, reduced, and alkylated proteins was slightly earlier than that of corresponding native proteins.

This is evidenced by comparing the elution times of ribonuclease A (labeled by * in Figs. 3-5A and 3-5B) which was spiked into the yeast protein samples. By comparing with the ESI protein envelope of native ribonuclease A (inset in Fig. 3-5A), the mass spectrum of denatured and alkylated ribonuclease A (inset in Fig. 3-5B) not only confirmed complete alkylation, but also displayed an increase in its average charge state as the result of denaturation process. The deconvoluted masses of native and alkylated ribonuclease A were measured as 13,690.7 and 14,147.5 daltons, respectively. The alkylation of each cysteine residue results in addition mass of 57.0 daltons. Thus, the difference in protein mass between native and alkylated ribonuclease A corresponds to the alkylation of all eight cysteines present in ribonuclease A. Furthermore, the protein denaturation process often results in improved MS intensity as the denatured state of a protein exhibits an open conformation and accepts more protons than the native state.

## 3.4 CONCLUSION

For top-down proteomics, total peak capacity improvements in protein separations will clearly contribute to increased number of proteins identified due to better use of the MS dynamic range and reduced discrimination during ionization. Thus, the effects of various chromatography conditions, including alkyl chain length in the stationary phase, capillary column temperature, and ion-pairing agent, on the resolution of intact proteins are examined in this study using nano-RPLC-ESI-MS. Optimal chromatography conditions include the use of $C_{18}$ column heated at 60 $^{0}$C and the addition of trifluoroacetic acid instead of heptafluorobutyric acid as the ion-paring agent in the mobile phase.

We further investigate potential differences in chromatography separation and ESI measurement of yeast intact proteins as the result of the protein denaturation process. Under optimized chromatography conditions, there are no significant differences in the separation performance of yeast cell lysates present in the native versus denatured states. Denatured yeast proteins resolved and eluted from nano-RPLC can be subjected to proteolytic digestion in an on- or off-line approach to provide improved protein sequence coverage toward protein identification in a combined top-down/bottom-up proteome platform. Due to the complexity of typical cell lysates, protein digests related to individual protein peaks resolved and eluted from nano-RPLC may require further separations prior to MS analysis. In this regard, the capillary format of the nanoscale trypsin membrane reactor recently developed in our laboratory [121] lends itself to further peptide concentration and separation using high speed capillary isotachophoresis/capillary zone electrophoresis prior to ESI-MS.

## 3.5 ACKNOWLEDGEMENT

Support for this work by the National Cancer Institute (CA107988) is gratefully acknowledged.

# CHAPTER 4

# INTEGRATED CAPILLARY ISOELECTRIC FOCUSING/NANO-REVERSED PHASE LIQUID CHROMATOGRAPHY COUPLED WITH ESI-MS FOR CHARACTERIZATION OF INTACT YEAST PROTEINS

Yueju Wang, Brian M. Balgley, Paul A. Rudnick, Don L. DeVoe, Cheng S. Lee

Journal of Proteome Research 4, 36-42 (2005)

## 4.1 INTRODUCTION

The vast number of proteins present in the proteome of a typical organism requires that separations be performed on the mixture prior to introduction into a mass spectrometer for protein identification and quantification. While direct analysis of peptide mixtures obtained from the digestion of complex cell lysates in current shotgun (bottom-up) proteome technologies [13-18,122,123] offers greater potential for the analysis of low abundance proteins than 2-D PAGE, bottom-up approaches provide very limited molecular information about the intact proteins, particularly towards the detection of PTMs [19]. Such modifications may be overlooked in analyses using peptide-based approaches, where only a fraction of the total theoretical peptide population of a given protein may be identified.

For example, the average number of unique peptides leading to each protein identification has been reported to be around 3.73-5.01 for the yeast proteome analysis together with 33.9%-42.1% of yeast proteins identified by only a single peptide

[13,14,18]. To enhance the ability of shotgun proteome approaches toward the identification of PTMs, Yates and co-workers have combined the proteolytic cleavage activities of different enzymes to generate overlapping peptides [124]. In such experiments, a protein mixture is digested using three different enzymes: trypsin that cleaves in a site-specific manner and two others (subtilisin and elastase) that cleave nonspecifically. The use of multiple enzymes for increased sequence coverage of proteins was further demonstrated by Choudhary et al. [125] for the analysis of human plasma.

In contrast, the top-down proteome techniques [20-23,126,127], in which intact proteins rather than peptides are measured, are advantageous for the detection of PTMs. Furthermore, top-down approaches to protein sequence analysis using tandem mass spectrometry ($MS^n$) may allow complete protein characterization far more efficiently than shotgun proteome technologies using protein digests. Realizing the potential of top-down approaches, however, requires that the processing and separation of intact proteins be brought to a similar level as those routinely achieved in shotgun proteomics.

Single dimension protein separations, including isoelectric focusing gel [29], CIEF [30,31], CZE [20], and RPLC [32,33], have been employed for processing protein mixtures prior to MS analysis. However, the use of only a single separation dimension may not provide sufficient peak capacity for the resolution of complex mixtures, putting significant constraints on the detection sensitivity and dynamic range of the MS.

Recent developments in multidimensional protein separations have been based on off-line combinations of preparative scale isoelectric focusing [42-44] or gel

electrophoresis [22,23,126] with RPLC for processing complex protein mixtures. Lubman and co-workers have performed isoelectric focusing in a Rotofor using approximately 10 mg of protein from whole cell lysates over a 5 hr period [42-44]. They have also employed an anion exchange column to achieve protein fractionation in a chromatofocusing mode [45] over a pH range of 4-7 due to the difficulty in obtaining reproducible, wide range pH-gradients. Additionally, acid-labile surfactant-based preparative polyacrylamide gel electrophoresis was utilized by Kelleher and co-workers for processing 1-300 [22,23,126] mg of total yeast proteins. The collected protein fractions from either isoelectric focusing or gel electrophoresis were further resolved using RPLC as the second separation dimension prior to MS analysis.

As demonstrated in our previous studies [52,56], the key to establishing ultrasensitive proteome analysis is attributed to high analyte concentrations in small peak volumes as the result of electrokinetic focusing/stacking and high-resolving multidimensional separation techniques, thereby effectively exploiting the dynamic range and detection sensitivity of MS. Building upon the experience in the development of CIEF-based shotgun proteome techniques [52-56], our research efforts in this work present the application of combined CIEF with nano-RPLC for concentrating and resolving intact proteins. The grouping of two highly resolving and completely orthogonal separation techniques greatly enhances the system peak capacity for analyzing complex protein mixtures while eliminating protein loss and dilution in an integrated and automated platform. Beyond the characterization of model proteins achieved by Zhou and Johnston [128], our results clearly illustrate the ability of CIEF/nano-RPLC coupled with ESI-MS to provide the detection of a large number of yeast protein envelopes and

deconvoluted molecular masses. Most significantly, all these measurements are carried out with a protein loading which is two to three orders of magnitude lower than those employed by the current top-down proteome separation techniques [22,23,42-45,126].

## 4.2 EXPERIMENTAL SECTION

### Materials and Reagents

Fused-silica capillaries (100 μm i.d./365 μm o.d. and 50 μm i.d./365 μm o.d.) were acquired from Polymicro Technologies (Phoenix, AZ). Acetic acid, ammonium hydroxide, DTT, and IAM were obtained from Sigma (St. Louis, MO). Acetonitrile, DNase, formic acid, glycerol, hydroxypropyl cellulose (average MW 100,000), magnesium chloride, thiourea, TFA, Tris, and urea were purchased from Fisher Scientific (Pittsburgh, PA). Pharmalyte 3-10 was acquired from Amersham Pharmacia Biotech (Uppsala, Sweden). All solutions were prepared using water purified by a Nanopure II system (Dubuque, IA) and further filtered with a 0.22 μm membrane (Costar, Cambridge, MA).

### Soluble Fraction of Intact Proteins from *S. cerevisiae*

The yeast cells (Sigma) were suspended in a buffer which consisted of 10 mM Tris (pH 8.0), 5 mM magnesium chloride, 0.1 mM DTT, and 10% glycerol. The cells were disrupted by sonication for the release of cellular proteins. After sonication, DNase was added to a final concentration of 50 μg/mL for the cleavage and removal of nucleic acids. The soluble proteins were collected in the supernatant by centrifugation at 20,000g for 10 min. The protein solution was then desalted using a regenerated cellulose membrane (Millipore, Bedford, MA) with a 5,000 Da molecular weight cutoff.

Yeast cytosolic proteins were denatured and reduced in a 10 mM Tris buffer containing 8 M urea and 100 mM DTT for 2 hr at 37 $^{0}$C under a nitrogen atmosphere. Proteins were alkylated by adding excess IAM to a final concentration of

250 mM and the reaction was allowed to proceed for 30 min at room temperature in the dark. A PD-10 size exclusion column (Amersham Pharmacia Biotech) was employed for buffer exchange and proteins were eluted in a solution containing 10 mM Tris. The total protein concentration was determined using the Bradford method (Bio-Rad, Richmond, CA) and was around 2 mg/mL.

**Integrated CIEF/Nano-RPLC Multidimensional Protein Concentration/Separation Platform**

An on-line combination of CIEF with nano-RPLC has been developed and described in detail in previous work [52] and was employed for systematically resolving complex peptide mixtures based on their differences in pI and hydrophobicity. To perform multidimensional protein separations, a 60-cm CIEF capillary (100 μm i.d./365 μm o.d.) was coated with hydroxypropyl cellulose for the elimination of electroosmotic flow and protein adsorption onto the capillary wall [96]. The capillary was initially filled with a solution containing 1% pharmalyte 3-10, 4 M urea, 2 M thiourea, and 2 mg/mL intact proteins obtained from the soluble fraction of yeast cell lysates. There were no column performance changes for more than 20 runs of CIEF separations using the coated capillary. The stability of hydroxypropyl coated capillaries has been further supported by the work of Shen and Smith [96].

Solutions of 0.5% ammonium hydroxide at pH 10.5 and 0.1 M acetic acid at pH 2.5 were employed as the catholyte and the anolyte, respectively. Focusing was performed at an electric field strength of 300 V/cm over the entire CIEF capillary. The current decreased continuously as the result of protein focusing. Once the current reduced

to ~10% of the original value, usually within 30 min, the focusing was considered to be complete. The focused proteins were sequentially and hydrodynamically loaded into an injection loop in a 6-port microinjection valve (Upchurch Scientific, Oak Harbor, WA). The loaded proteins were then injected into a $C_{18}$ reversed-phase trap column using a Harvard Apparatus 22 syringe pump (Holliston, MA) through a 6-port microselection valve (Upchurch Scientific).

Repeated protein loadings and injections into various trap columns were automated and controlled using LabView (National Instruments, Austin, TX) until the entire CIEF capillary content was sampled into 9 unique fractions. No significant band broadening in the CIEF capillary was anticipated over the entire protein loading and injection process for a period of approximately 10 min based on limited protein diffusion. Trap columns were prepared "in-house". The effluent end of a 8-cm-long fused-silica capillary (100 μm i.d./365 μm o.d.) was connected to an inline microfilter assembly (Upchurch Scientific). The $C_{18}$-bonded particles (5-μm diameter, 300-Å pores, Phenomenex, Torrance, CA) in methanol were introduced into the capillary by gradually increasing the pressure from 100 to 2,000 psi using an Agilent 1100 capillary LC pump (Avondale, PA). The capillary packed with 3 cm of $C_{18}$-bonded particles was left under pressure for 10 hr and then depressurized overnight.

Due to the highly charged and hydrophilic nature of carrier ampholytes (Pharmalyte 3-10) employed for the generation of a pH gradient during the CIEF step, ampholytes were eluted from the trap columns into a waste reservoir prior to the nano-RPLC separations using a 0.1% TFA solution. An Agilent 1100 capillary LC pump was then employed to generate a 40-min linear gradient from 10% to 65% acetonitrile

(containing 0.1% TFA and 0.3% formic acid) at a flow rate of 200 nL/min. Through the use of a second 6-port microselection valve (Upchurch Scientific), the mobile phase was delivered into the individual trap column, followed by a 13-cm-long capillary column (50 μm i.d. x 365 μm o.d.) packed with 5-μm porous $C_{18}$ reversed-phase particles.

All 9 isoelectric focusing fractions collected in the trap columns were analyzed in sequence from acidic to basic pI and the eluants from nano-RPLC were monitored using a Micromass qTOF mass spectrometer (Manchester, United Kingdom). A microcross (Upchurch Scientific) containing a platinum electrode was employed to apply an ESI voltage of 1.8 kV and was placed in-line with and upstream of the chromatography column. Mass spectra were collected from 600 to 1900 m/z using a scan time of 1.0 s. Automated analysis of the nano-RPLC-ESI MS data files were performed using Protein Trawler software (Bioanalyte, Portland, ME) [112,113].

Approximately 40-min of each nano-RPLC run was divided into 80 30-s slices. The mass spectra of these 30-s slices were summed and averaged, and Micromass MaxEnt1 was employed as the deconvolution algorithm over a mass range of 5-100 kDa. No baseline subtraction or smoothing was used, as these manipulations were empirically determined to interfere with protein mass deconvolution. Post-processing of the deconvoluted protein peaks was performed using routines provided with Protein Trawler. Briefly, peaks within 30 Da and occurring within 90-s were only included once and were considered to be the result of bleeding or band broadening of the same protein. Post-processing also included the elimination of 1/2 and 2X mass peaks which are common artifacts of the deconvolution algorithm

## 4.3 RESULTS AND DISCUSSION

### CIEF Separations of Intact Proteins from Soluble Fraction of Yeast Cell Lysates

Preparative scale isoelectric focusing separations have been performed using a Rotofor cell containing a solution pH gradient [42-44] , micro anion exchange chromatography combined with pH gradient elution [45], and gel membranes containing the desired pHs [98,99,129,130] for processing mgs of protein samples obtained from cell lysates. By taking advantage of the large surface area to volume ratio in fused-silica capillaries for effectively dissipating joule heating at high electric fields, CIEF not only establishes a rapid and high resolution protein/peptide separation, but also affords a typical concentration factor of at least 100 times as the result of the focusing effect. Furthermore, CIEF provides a direct capillary interface for on-line combination with nano-RPLC in an integrated and multidimensional separation platform for resolving complex peptide and protein mixtures as demonstrated in our previous studies [52] and this work, respectively.

As shown in Fig. 4-1, the CIEF separation performance of intact proteins from the soluble fraction of yeast cell lysates was initially evaluated by hydrodynamically mobilizing focused proteins passing a UV detector placed near the cathodic end of the capillary. Protein bandwidth after focusing was as small as 2.0 mm inside a 60-cm long CIEF capillary by applying electric field strength of 300 V/cm over a pH gradient from 3 to 10. This yielded to a sample concentration factor of ~300 and a baseline resolution (resolution, $R_s$, of 1.5) of ~ 200 peaks. Furthermore, a 60-cm long capillary with a 100 μm i.d. employed in this study offered a sample loading volume of ~4.8 μL and a total protein loading of ~9.6 μg using a 2 mg/mL yeast protein solution. Further enhancement

in sample loading can be achieved using the dynamic introduction and focusing approach demonstrated in our previous work [131].

**Integrated CIEF/Nano-RPLC Separations of Intact Proteins from Yeast Cell Lysates**

Instead of using the "stop and go" mode for on-line coupling of CIEF with capillary RPLC in the characterization of model proteins [128], a combination of computer controlled microinjection and microselection valves was utilized for automatically and reproducibly loading focused protein fractions into individual trap columns for the subsequent second dimension nano-RPLC analyses. As shown in Fig. 4-2, the yeast proteins were systematically resolved based on their differences in pI and hydrophobicity using the combined CIEF/nano-RPLC separations in an integrated platform.

The peak width for a protein eluting from the chromatography column (Fig. 4-2) was as small as 10 s which corresponds to a peak capacity of 160 over a gradient run time of 40 min. Further improvement in the peak capacity can be realized by slowing the solvent gradient in nano-RPLC and increasing the column length [24]. Because the separation mechanisms in CIEF and nano-RPLC are completely orthogonal, the overall peak capacity of multidimensional CIEF/nano-RPLC separations was estimated to be around 1,440 (9 fractions from CIEF x 160 from CRPLC) over a run time of approximately 6 hr. By acquiring and confidently deconvoluting 3-5 ESI protein envelopes (Fig. 4-3) over the elution of any single peak from nano-RPLC using qTOF-

MS, an overall system capacity of 4,320-7,200 was achieved in this study for the analysis of complex protein mixtures such as yeast cell lysates.

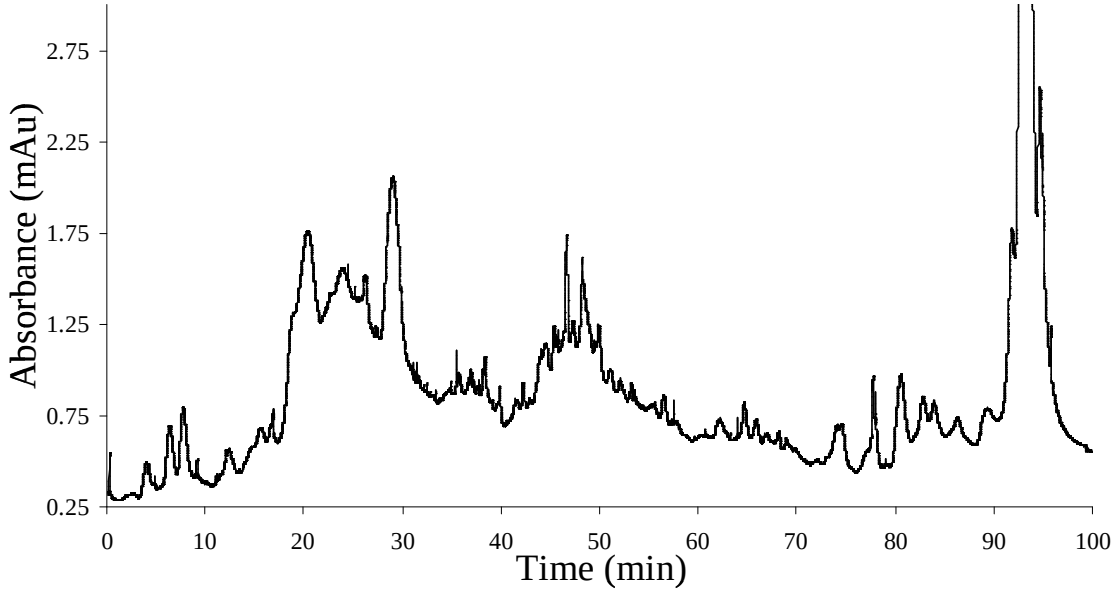


**Figure 4-1** CIEF-UV Analysis of intact proteins in the soluble fraction obtained from *S. cerevisiae* cell lysates. Capillary: hydroxypropyl cellulose coating, 60 cm x 100 µm i.d. x 365 µm o.d.; anolyte: 0.1 M acetic acid at pH 2.5; catholyte: 0.5% w/w ammonium hydroxide at pH 10.5; electric field strength: 300 V/cm; hydrodynamic mobilization; detection: UV absorbance at 280 nm, 7 cm from cathodic end.

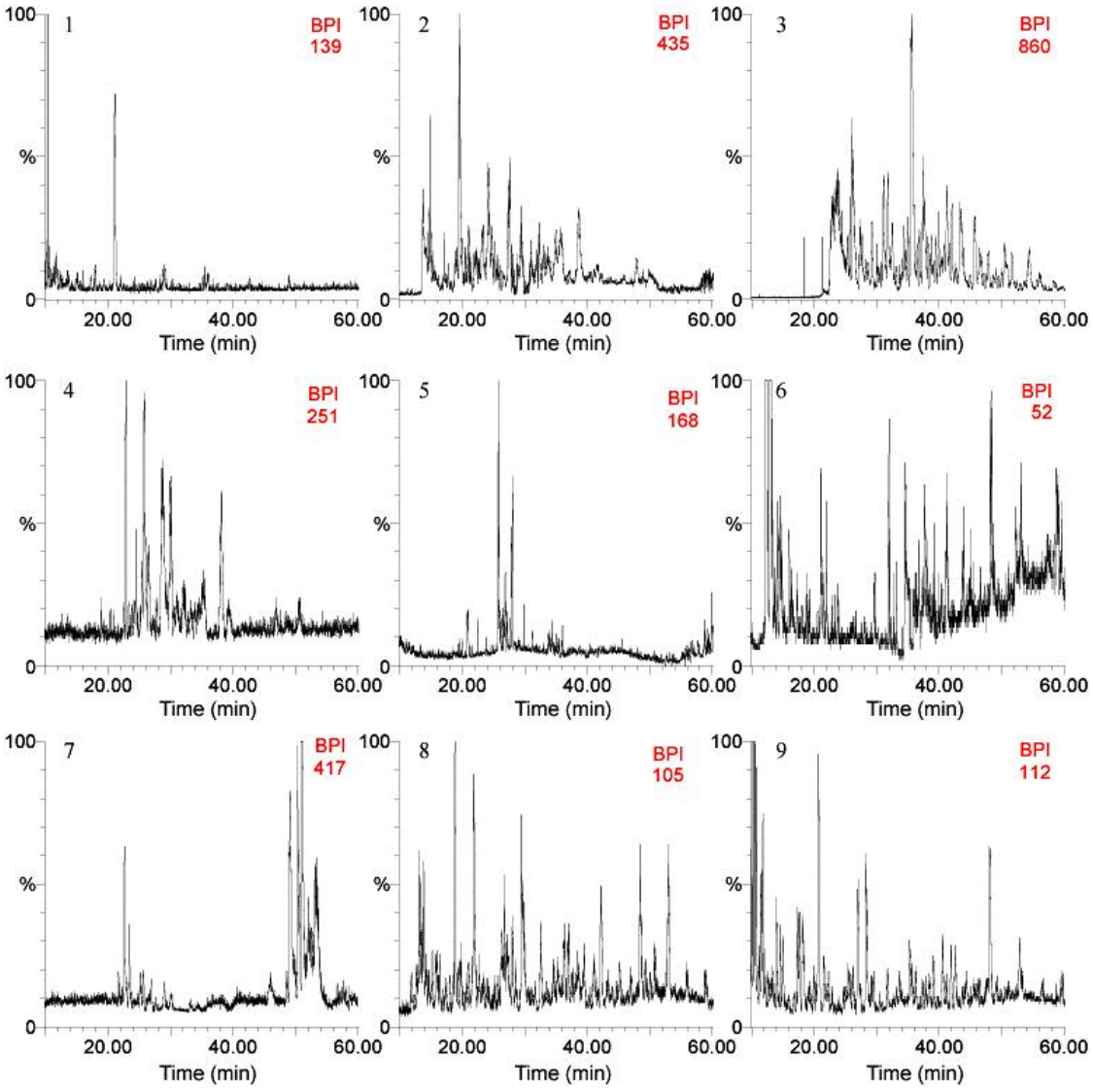


**Figure 4-2** Base peak chromatograms of a representative CIEF/nano-RPLC multidimensional separation of 9.6 µg of yeast intact proteins obtained from the soluble fraction of cell lysates. Each number represents the sequence of CIEF fractions further analyzed by nano-RPLC from acidic to basic pHs.

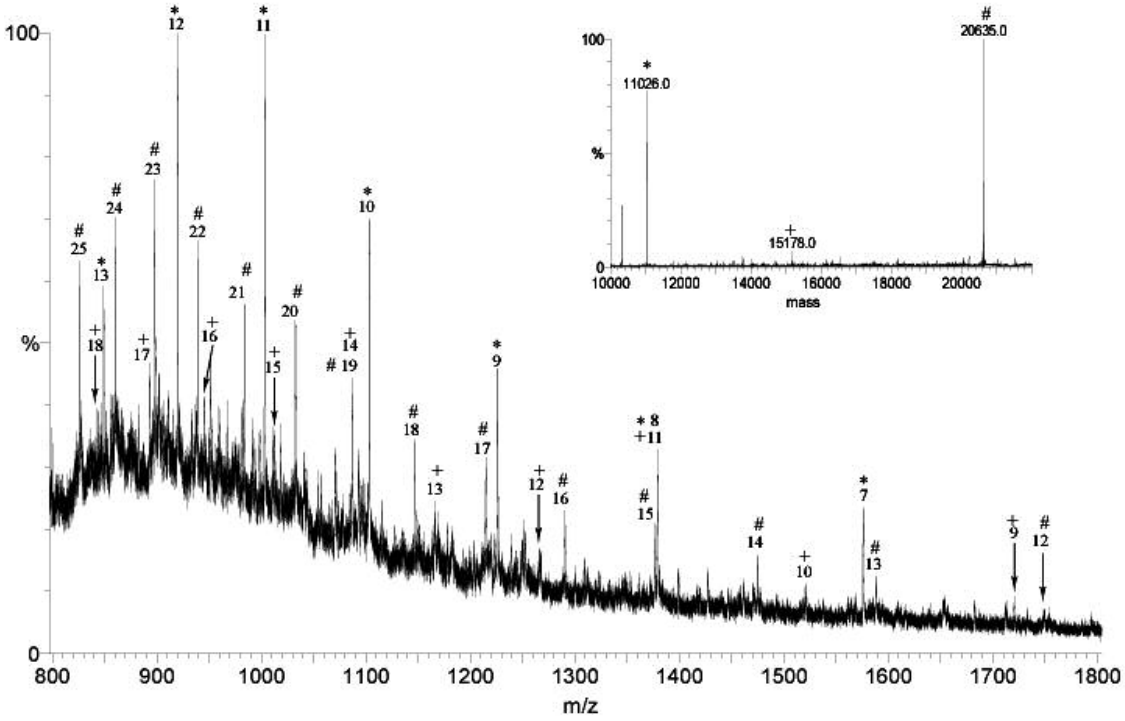


**Figure 4-3** The mass spectrum of a chromatography peak eluted at 35.7 min for the nano-RPLC separation of the second CIEF fraction. The inset presents deconvoluted protein masses which are labeled together with the corresponding protein envelopes using *, +, and #, respectively.

Reproducibility of protein separation and identification using the combined CIEF/nano-RPLC-ESI MS approach was examined by performing multiple runs of identical yeast protein samples. For two analyses performed on consecutive days, the elution times of the same proteins in CRPLC differed by less than 0.3 min (data not shown). The elution times were slightly different, the shifts, however, were consistent across the analysis. The slight variation in elution times was mainly contributed by the difficulty in generating the same nanoflow rate using the current capillary LC pump equipped with an external flow splitter.

The intrinsic high resolution of CIEF allows the number of protein fractions sampled in the first separation dimension to be further increased. The excellent reproducibility of CIEF separation, together with the use of trap columns for "parking" the CIEF fractions in an automated platform, enables user discretion as to which fractions are to be analyzed in the off-line approach, and interesting fractions may be revisited (reanalyzed) or repeatedly accumulated for identification of extremely low abundance proteins. Further enhancement in the overall system capacity can be realized by increasing the number of CIEF fractions and slowing the solvent gradient in nano-RPLC at the expense of analysis time. To significantly reduce the overall run time, the ability to deposit eluted peptides/proteins onto MALDI target for subsequent MS analysis offers a promising platform for high-throughput proteome studies using a multiplexed LC system [132]. Recently, Ericson and co-workers have developed an automated non-contact deposition interface by employing a pulsed electric field for transferring the eluants from multiple parallel columns directly onto MALDI targets [133].

**ESI-MS Analysis of Intact Proteins Eluted from CIEF/Nano-RPLC Multidimensional Protein Separations**

The Protein Trawler program was utilized to automatically sum all data within a specified time interval, deconvolute multiply charged ions, carry out a threshold selection, eliminate deconvolution artifacts, and report protein mass, intensity, and retention time in a text file. The program repeated this process across sequential portions of the chromatogram of each nano-RPLC-ESI MS run. As a result, a total of 534 distinct protein masses between 5 and 70 kDa were identified from the CIEF/nano-RPLC-ESI MS analysis of intact proteins obtained from the soluble fraction of yeast cell lysates.

A 2-D map of identified protein masses is displayed in Fig. 4-4 with the estimated pI ranges for each CIEF fraction. By using 1% Pharmalyte 3-10, the CIEF separation was able to cover a wide pH range of 3.3-9.6. The pI range analyzed in this study was comparable to those reported using a Rotofor cell containing a solution pH gradient [42-44] and gel membranes containing immobilized pHs [98,99,129,130], but significantly wider than that obtained from micro anion exchange chromatography combined with pH gradient elution [45]. However, very basic proteins with pIs equal to or greater than 10 may not be resolved or could be lost to the catholyte using the currently available carrier ampholytes.

The competitive advantages of CIEF/nano-RPLC protein separations are mostly attributed to the high resolving power and analyte concentration effect in CIEF together with the elimination of analyte loss and dilution in an automated and integrated platform. The amount of intact proteins employed for performing yeast proteome analysis was around 9.6 μg (2 mg/mL x 4.8 μL of capillary volume in CIEF) which is two to three

orders of magnitude less than those utilized in current 2-D PAGE and top-down proteome techniques [22,23,42-45,126]. Instead of using significantly higher amounts of sample materials and additional sample fractionation procedures, the combination of analyte focusing/concentration with two highly resolving and orthogonal separation mechanisms in an integrated platform significantly enhances both the dynamic range and the sensitivity of MS toward the proteome analysis.

A database dump file “protein_properties.tab” containing computed molecular masses and pIs of translated yeast open reading frames (ORFs) was downloaded from the Saccharomyces Genome Database at Stanford University. By excluding ORFs with a “dubious” classification, a total of 5,792 “characterized” and “uncharacterized” gene products were used as the constituents of the predicted yeast proteome. The ratio of the number of deconvoluted protein masses to the number of predicted proteins in each molecular mass region was summarized in Fig. 4-5 from 5 to 70 kDa. Approximately 74% of predicted yeast proteins exhibit molecular masses within the range of 5-70 kDa. Due to the discrimination of the ESI process against MS detection of medium to high molecular weight proteins, the percentage of yeast proteome coverage was around 14%-58% in the molecular mass range of 5-30 kDa and decreased significantly with increasing molecular mass from 30 to 70 kDa. Such bias against high molecular mass proteins is in agreement with those reported using top-down protein identification and sequence measurements [22,23,42-45,126].

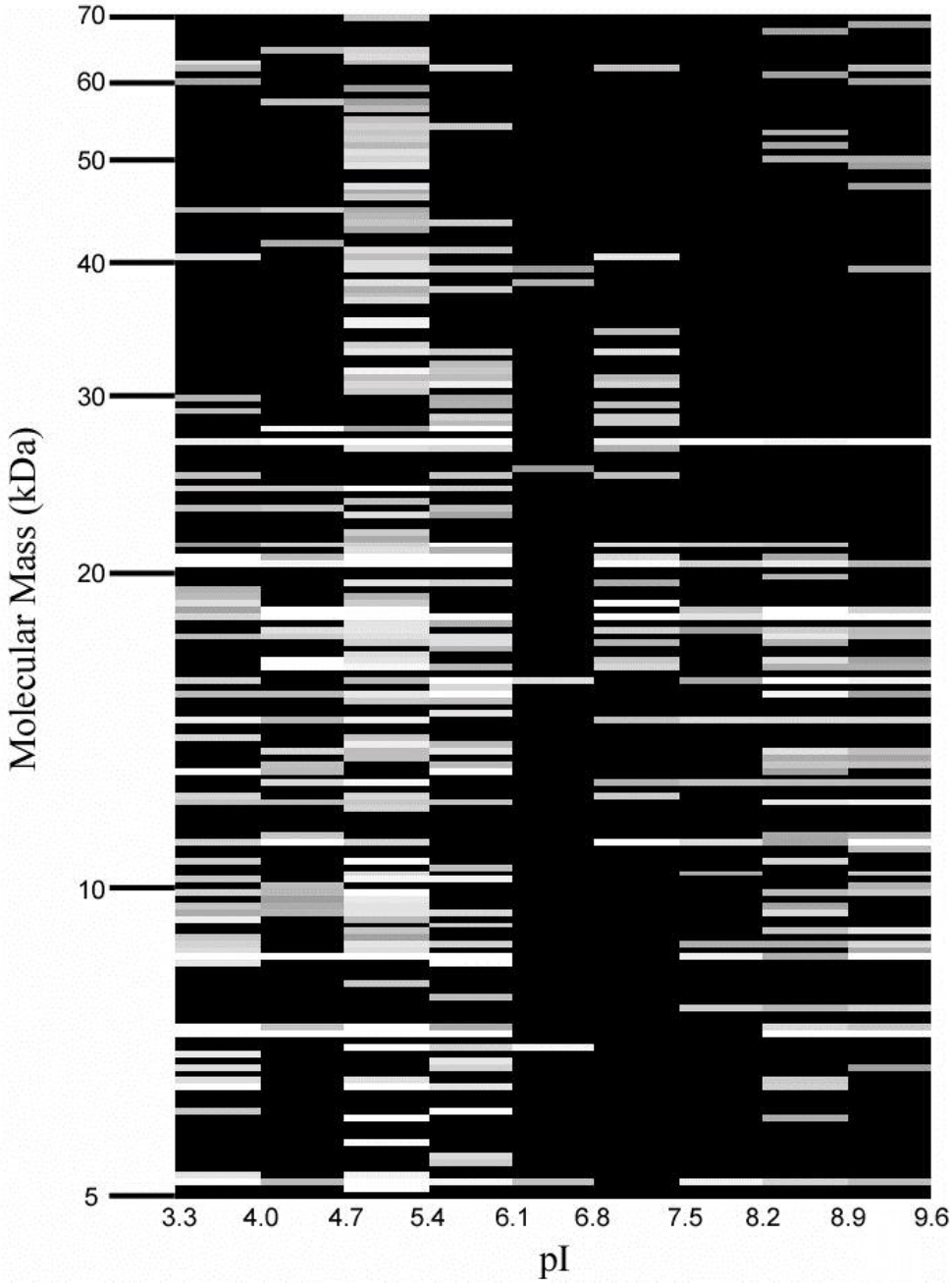


**Figure 4-4** 2-D map of deconvoluted protein masses versus pI within each CIEF fraction for the analysis of yeast cell lysates using CIEF/nano-RPLC-ESI MS. The logarithm of protein intensity is represented in gray scale on the map.

Improvements in protein detection can be achieved by enhancements in the deconvolution process for the ESI-multiply charged envelopes and employment of ultrahigh resolution and sensitivity of Fourier transform ion cyclotron resonance (FTICR)-MS. In comparison with shotgun proteomics [13-18,122,123], the lack of effective ESI of intact proteins may still adversely impact the ability to perform comprehensive proteome analysis using top-down techniques [20-23,126,127], particularly in the identification of low abundance proteins. As reported by Meng and co-workers [23], most of the 117 yeast gene products identified and characterized today are highly abundant proteins in the 5-39 kDa range.

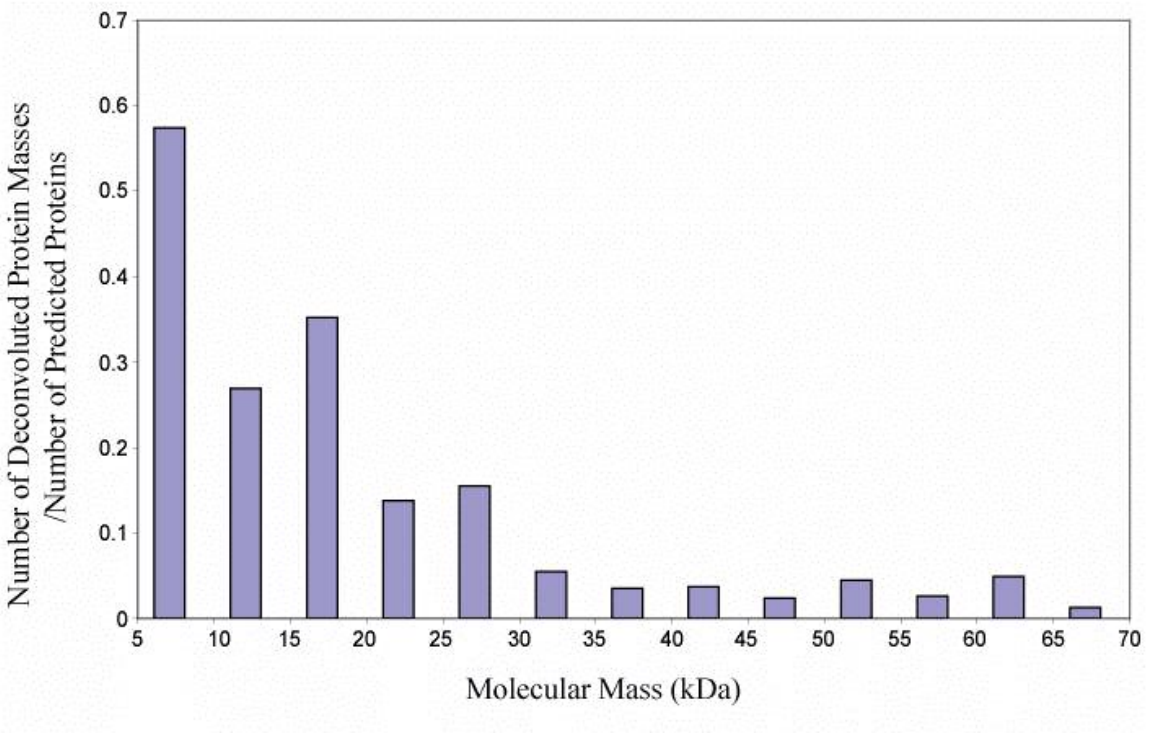


**Figure 4-5** The ratio of the number of deconvoluted protein masses to the number of predicted yeast proteins in individual molecular mass regions from 5 to 70 kDa.

## 4.4 CONCLUSION

As an automated and integrated approach, the on-line combination of CIEF with nano-RPLC offers analyte focusing for concentrating dilute protein samples of biological origin while providing excellent resolving power for the characterization of complex protein mixtures based on differences in pI and hydrophobicity. By obtaining a peak capacity of 1,440 from combined CIEF/nano-RPLC separations and acquiring 3-5 ESI protein envelopes over the elution of any chromatography peak using qTOF-MS, an overall system capacity of 4,320-7,200 is achieved in this study for the analysis of intact proteins obtained from the soluble fraction of *S. cerevisiae*. The intrinsic high resolution of CIEF allows the number of fractions sampled in the first separation dimension to be further increased. More CIEF fractions can be obtained by increasing the number of microselection valves and trap columns, or by employing microselection valves with a higher number of ports.

By using only the soluble fraction of yeast cell lysates, a total of 534 distinct protein masses were identified over a wide protein mass range of 5-70 kDa, requiring a protein loading of less than 10 μg. This protein loading is two to three orders of magnitude less than those utilized in current 2-D PAGE and top-down proteome techniques [22,23,42-45,126]. Future work includes directly coupling of CIEF/nano-RPLC separations with a newly developed nanoscale trypsin membrane reactor [121] for enabling real-time and effective digestion of resolved proteins in a combined top-down/bottom-up proteome analysis. Instead of spreading proteolytic peptides over the entire multidimensional separation as in shotgun proteomics, the proposed top-down/bottom-up proteome technology will allow direct correlation of the peptides and

their sequences with the corresponding proteins and measured protein masses, and will greatly facilitate the characterization of proteins containing PTMs.

## 4.5 ACKNOWLEDGEMENT

Support for this work by the National Cancer Institute (CA107988 and CA103086) is gratefully acknowledged.

# CHAPTER 5

# CONCLUSION

The sequencing of several organisms' genomes, including the human's one, has opened the way for the so-called postgenomic era, which is now routinely coined as "proteomics". The most basic task in proteomics remains the detection and identification of proteins from a biological sample, and the most traditional way to achieve this goal consists of protein separations performed by 2-D PAGE. Still, the 2-D PAGE-MS approach remains lacking in proteome coverage (for proteins having extreme isoelectric points or molecular masses as well as for membrane proteins), dynamic range, sensitivity, and throughput.

Consequently, considerable efforts have been devoted to the development of non-gel-based proteome separation technologies in an effort to alleviate the shortcomings in 2-D PAGE while reserving the ability to resolve complex protein and peptide mixtures prior to mass spectrometry analysis. Thus, this dissertation first reviewed recent advances in capillary-based separation techniques, including capillary liquid chromatography and capillary electrophoresis, and combinations of multiples of these separation mechanisms. In comparison with 2D-PAGE, the capillary-based separation technologies offer the capabilities of system automation, high throughput analysis, and increased detection dynamic range, and are becoming effective front-end tools for MS-based proteome analysis.

By transferring isoelectric focusing separation from gel to capillary format, it has been demonstrated that the focusing effect of CIEF not only contributes to high resolution protein/peptide separation, but also provides significant enhancement in

analyte concentration. Besides the analysis of tryptic peptides obtained from yeast cell lysates in our previous studies, CIEF-based multidimensional peptide separation platform was further developed and optimized in this work for enabling comprehensive and ultrasensitive characterization of protein profiles within limited tissue samples. In addition to establishing a micro-sample introduction technique, a combination of computer controlled microinjection and microselection valves was utilized for automatically and reproducibly fractionating pI-resolved peptides for the subsequent second dimension analyses. By using the combination of various carrier ampholytes, the separation range of CIEF has been extended to at least pI 12. The reduction of chromatography column inner diameter to as small as 50 μm together with the increase in the number of CIEF fractions significantly enhance both the overall separation peak capacity and the dynamic range and detection sensitivity of MS critically needed for performing comprehensive proteome studies.

In this study, protein profiles within small cell populations procured from glioblastoma multiforme tissues were analyzed using combined CIEF-nano-RPLC separations equipped with ESI-qTOF-MS. In comparison with strong cation exchange as the first separation dimension in current multidimensional chromatography system, CIEF not only exhibited higher separation resolution and less degree of peptide overlapping among fractions, but also allowed more effective usage of MS-based peptide identifications by providing an even distribution of doubly charged peptides over the entire pH gradient. Moreover, because of the high resolving power of CIEF, the number of peptide and protein identifications can be greatly increased by simply increasing the number of pI fractions instead of performing multiple proteome runs. The ability to mine

deep into the proteome of limited samples can therefore be realized without an accompanying increase in sample consumption.

Realizing the shortcomings of limited protein sequence coverage and thus limited intact molecular information obtained from bottom-up (shotgun) approaches, research efforts have also been made toward the development of top-down proteome techniques. Top-down methods, in which intact proteins rather than peptides are measured, are advantageous for the analysis of protein modifications. Building upon the experience in the development of CIEF-based shotgun proteome technologies, this project further aimed to expand the applications of combined CIEF-nano-RPLC separations for the analysis of complex protein mixtures such as yeast cell lysates.

As a first step toward the optimization of multidimensional protein separations, effects of various chromatography conditions, including alkyl chain length in the stationary phase, capillary column temperature, and ion-pairing agent, on the resolution of intact proteins have been studied using nano-RPLC-ESI MS. Optimal chromatography conditions included the use of $C_{18}$ column heated at 60 $^{0}$C and the addition of trifluoroacetic acid instead of heptafluorobutyric acid as the ion-paring agent in the mobile phase. Under optimized chromatography conditions, there were no significant differences in the separation performance of yeast cell lysates present in the native versus denatured states. As one of research directions in future proteome studies, denatured proteins resolved and eluted from nano-RPLC can be subjected to proteolytic digestion in an on- or off-line approach to provide improved protein sequence coverage toward protein identification in a combined top-down/bottom-up proteome platform.

As an automated and integrated approach, the on-line combination of CIEF with nano-RPLC offers analyte focusing for concentrating dilute protein samples of biological origin while providing excellent resolving power for the characterization of complex protein mixtures based on differences in pI and hydrophobicity. A key feature of combined CIEF-nano-RPLC separations in an integrated platform includes the elimination of analyte loss and dilution as the result of many manually operated sample handling, protein separation, and transfer steps in the current top-down processes. Sample loss and dilution may adversely impact the ability to perform comprehensive proteome analysis, particularly toward the identification of low abundance proteins.

By obtaining a peak capacity of 1,440 from combined CIEF/nano-RPLC separations and acquiring 3-5 ESI protein envelopes over the elution of any chromatography peak using qTOF-MS, an overall system capacity of 4,320-7,200 has been achieved in this study for the analysis of intact proteins obtained from the soluble fraction of yeast cell lysates. The CIEF-based multidimensional concentration/separation platform enabled the measurement of 534 distinct yeast protein masses over a mass range of 5-70 kDa, yet required a protein loading of only 9.6 μg. This protein loading is two to three orders of magnitude less than those used in current 2-D PAGE and top-down proteome techniques, illustrating the potential usage of this proteome technology for the analysis of protein profiles within small cell populations or limited tissue samples.

In conclusion, my research goal is to develop the novel bioanalytical technologies and tools that support comprehensive survey of proteins in cells and tissues, particular for the analysis of low abundance proteins. Instead of using significantly higher amounts of protein materials and additional sample fractionation procedures, the key to

establishing ultrasensitive proteome analysis is attributed to attain high analyte concentrations in small peak volumes as the result of electrokinetic focusing and high resolving multidimensional separation techniques in an integrated platform, thus enhancing the dynamic range and detection sensitivity of MS measurements. Future work includes the investigation of combined top-down and bottom-up approaches in order to leverage the unique capabilities provided by both approaches in an integrated platform. The integrated top-down/bottom-up proteome technology is expected to significantly increase the peptide sequence coverage of identified proteins and greatly facilitate the analysis of protein modifications. Realizing the potential of integrated top-down/bottom-up proteome technology, however, requires the development of novel bioinformatics tools to allow direct correlation of the peptides and their sequences with the corresponding proteins and measured protein masses in a single proteome analysis.

# APPENDIX

| Protein Number | ID | Description | Mass | pI | Peptide Hits | Distinct Peptides | % Coverage |
|---|---|---|---|---|---|---|---|
| 1 | IPI00025363.1 | GLIAL FIBRILLARY ACIDIC PROTEIN, ASTROCYTE. | 49880 | 5.2 | 217 | 41 | 77.55 |
| 2 | IPI00007752.1 | TUBULIN BETA-2 CHAIN. | 49831 | 4.52 | 179 | 22 | 72.13 |
| 3 | IPI00022434.1 | SERUM ALBUMIN PRECURSOR. | 69367 | 6.21 | 175 | 39 | 65.35 |
| 4 | IPI00031370.1 | TUBULIN, BETA POLYPEPTIDE. | 49953 | 4.52 | 174 | 21 | 68.31 |
| 5 | IPI00160897.1 | HYPOTHETICAL PROTEIN. | 49586 | 4.51 | 173 | 21 | 71.4 |
| 6 | IPI00220286.1 | POLYUBIQUITIN UBC. | 77039 | 7.94 | 172 | 6 | 65.11 |
| 7 | IPI00021439.1 | ACTIN, CYTOPLASMIC 1. | 41737 | 5.15 | 171 | 20 | 63.47 |
| 8 | IPI00021440.1 | ACTIN, CYTOPLASMIC 2. | 41793 | 5.16 | 170 | 20 | 63.47 |
| 9 | IPI00013475.1 | BETA TUBULIN (TUBULIN, BETA POLYPEPTIDE) (DJ40E16.7.1) (NOVEL PROTEIN SIMILAR TO TUBULIN BETA POLYPEPTIDE. | 49907 | 4.52 | 167 | 21 | 68.31 |
| 10 | IPI00142634.1 | TUBULIN BETA-5 CHAIN. | 49671 | 4.52 | 166 | 19 | 62.16 |
| 11 | IPI00011654.1 | TUBULIN BETA-1 CHAIN. | 49759 | 4.49 | 160 | 17 | 53.15 |
| 12 | IPI00180675.3 | TUBULIN, ALPHA 3. | 52312 | 4.82 | 155 | 25 | 59.02 |
| 13 | IPI00328696.7 | HEMOGLOBIN ALPHA CHAIN. | 15126 | 9.09 | 149 | 12 | 95.74 |
| 14 | IPI00387144.2 | TUBULIN ALPHA-1 CHAIN. | 50152 | 4.7 | 148 | 25 | 61.64 |
| 15 | IPI00396304.1 | TUBULIN, ALPHA, UBIQUITOUS. | 50152 | 4.7 | 148 | 25 | 61.64 |
| 16 | IPI00023598.1 | TUBULIN BETA-5 CHAIN. | 49631 | 4.54 | 146 | 19 | 64.86 |
| 17 | IPI00218816.1 | BETA GLOBIN. | 15998 | 7.32 | 146 | 12 | 93.88 |
| 18 | IPI00218343.3 | TUBULIN ALPHA-6 CHAIN. | 52631 | 5.13 | 145 | 23 | 50.74 |
| 19 | IPI00179709.4 | SPLICE ISOFORM 1 OF Q13748 TUBULIN ALPHA-2 CHAIN. | 49960 | 4.74 | 134 | 19 | 48 |
| 20 | IPI00375289.1 | SIMILAR TO TUBULIN ALPHA-3/ALPHA-7 CHAIN (ALPHA-TUBULIN 3/7). | 50839 | 4.74 | 134 | 19 | 47.06 |
| 21 | IPI00334432.1 | --none found in database-- | 15396 | 7.9 | 128 | 8 | 73.76 |
| 22 | IPI00257508.4 | DIHYDROPYRIMIDINASE RELATED PROTEIN-2. | 62294 | 6.33 | 126 | 24 | 66.96 |
| 23 | IPI00013683.2 | TUBULIN BETA-4 CHAIN. | 50433 | 4.57 | 122 | 15 | 47.11 |
| 24 | IPI00152453.1 | HYPOTHETICAL PROTEIN. | 88382 | 5.69 | 120 | 14 | 23.21 |
| 25 | IPI00384697.1 | SIMILAR TO ALPHA-FETOPROTEIN. | 47360 | 6.29 | 120 | 24 | 58.99 |
| 26 | IPI00216976.1 | ALDOLASE C, FRUCTOSE-BISPHOSPHATE. | 39456 | 6.86 | 119 | 23 | 75 |
| 27 | IPI00015786.2 | SPECTRIN ALPHA CHAIN, BRAIN. | 284897 | 5.05 | 116 | 61 | 34.32 |
| 28 | IPI00021428.1 | ACTIN, ALPHA SKELETAL MUSCLE. | 42051 | 5.05 | 116 | 12 | 31.3 |
| 29 | IPI00023006.1 | ACTIN, ALPHA CARDIAC. | 42019 | 5.05 | 116 | 12 | 31.3 |
| 30 | IPI00218345.1 | SPLICE ISOFORM 2 OF Q13748 TUBULIN ALPHA-2 CHAIN. | 46112 | 4.78 | 115 | 16 | 44.26 |
| 31 | IPI00007750.1 | TUBULIN ALPHA-4 CHAIN. | 49924 | 4.69 | 113 | 22 | 55.13 |
| 32 | IPI00003865.1 | SPLICE ISOFORM 1 OF P11142 HEAT SHOCK COGNATE 71 KDA PROTEIN. | 70898 | 5.16 | 112 | 26 | 43.96 |
| 33 | IPI00328163.1 | SIMILAR TO TUBULIN ALPHA 2. | 37218 | 4.62 | 110 | 19 | 71.64 |
| 34 | IPI00216773.3 | SIMILAR TO SERUM ALBUMIN PRECURSOR. | 45297 | 6.15 | 109 | 22 | 59.05 |
| 35 | IPI00177441.4 | SIMILAR TO TUBULIN ALPHA-3/ALPHA-7 CHAIN (ALPHA-TUBULIN 3/7). | 49859 | 4.77 | 106 | 13 | 38.89 |
| 36 | IPI00385560.1 | ACTIN ALPHA 1 SKELETAL MUSCLE PROTEIN. | 28151 | 5.96 | 104 | 10 | 37.01 |
| 37 | IPI00008603.1 | ACTIN, AORTIC SMOOTH MUSCLE. | 42009 | 5.05 | 103 | 10 | 28.38 |
| 38 | IPI00025416.1 | ACTIN, GAMMA-ENTERIC SMOOTH MUSCLE. | 41877 | 5.16 | 103 | 10 | 28.46 |
| 39 | IPI00000816.1 | 14-3-3 PROTEIN EPSILON. | 29174 | 4.36 | 100 | 18 | 70.2 |
| 40 | IPI00154491.1 | --none found in database-- | 44980 | 6.71 | 100 | 6 | 62.41 |
| 41 | IPI00215736.2 | ALPHA ENOLASE. | 47038 | 7.46 | 100 | 24 | 65.36 |
| 42 | IPI00328602.3 | HEAT SHOCK 90KDA PROTEIN 1, ALPHA. | 84674 | 4.66 | 99 | 29 | 41.8 |
| 43 | IPI00382950.1 | BETA-GLOBIN GENE FROM A THALASSEMIA PATIENT. | 18931 | 6.78 | 99 | 10 | 65.14 |
| 44 | IPI00383815.1 | HYPOTHETICAL PROTEIN. | 36299 | 5.52 | 96 | 21 | 56.78 |
| 45 | IPI00037070.1 | SPLICE ISOFORM 2 OF P11142 HEAT SHOCK COGNATE 71 KDA PROTEIN. | 53921 | 5.8 | 95 | 21 | 46.68 |
| 46 | IPI00328347.1 | PYRUVATE KINASE, M2 ISOZYME. | 57783 | 7.93 | 95 | 29 | 69.81 |
| 47 | IPI00022977.1 | CREATINE KINASE, B CHAIN. | 42644 | 5.3 | 94 | 22 | 71.65 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 48 | IPI00383237.1 | PYRUVATE KINASE, M1 ISOZYME. | 58168 | 7.93 | 93 | 28 | 66.23 |
| 49 | IPI00387164.1 | HYPOTHETICAL PROTEIN FLJ32377. | 43649 | 6.22 | 93 | 6 | 61.86 |
| 50 | IPI00180818.2 | FRUCTOSE-BISPHOSPHATE ALDOLASE A. | 39289 | 8.2 | 89 | 17 | 61.98 |
| 51 | IPI00395757.1 | ALDOLASE A. | 39420 | 8.2 | 89 | 17 | 61.81 |
| 52 | IPI00219018.1 | GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE. | 36053 | 8.73 | 88 | 16 | 58.21 |
| 53 | IPI00021263.1 | 14-3-3 PROTEIN ZETA/DELTA. | 27745 | 4.43 | 86 | 16 | 71.02 |
| 54 | IPI00220644.5 | PYRUVATE KINASE 3 ISOFORM 2. | 58293 | 7.78 | 86 | 27 | 62.66 |
| 55 | IPI00010728.3 | MICROTUBULE-ASSOCIATED PROTEIN 2 ISOFORM 3. | 202759 | 4.59 | 85 | 41 | 33.21 |
| 56 | IPI00003842.1 | SPLICE ISOFORM MAP2B OF P11137 MICROTUBULE-ASSOCIATED PROTEIN 2. | 199611 | 4.55 | 83 | 40 | 33.17 |
| 57 | IPI00334775.1 | HYPOTHETICAL PROTEIN. | 84843 | 5.01 | 82 | 24 | 35.41 |
| 58 | IPI00034283.1 | SIMILAR TO TUBULIN, BETA, 4. | 49857 | 4.51 | 81 | 11 | 33.18 |
| 59 | IPI00166768.1 | HYPOTHETICAL PROTEIN. | 36649 | 8.02 | 81 | 14 | 41.54 |
| 60 | IPI00029111.1 | DIHYDROPYRIMIDINASE RELATED PROTEIN-3. | 61963 | 6.45 | 77 | 20 | 51.05 |
| 61 | IPI00216005.3 | TUBULIN ALPHA-8 CHAIN. | 52591 | 4.91 | 75 | 13 | 32.63 |
| 62 | IPI00180776.1 | --none found in database-- | 27742 | 4.36 | 74 | 13 | 54.29 |
| 63 | IPI00216318.1 | TYROSINE 3-MONOOXYGENASE/TRYPTOPHAN 5-MONOOXYGENASE ACTIVATION PROTEIN, BETA POLYPEPTIDE. | 28082 | 4.47 | 74 | 14 | 66.26 |
| 64 | IPI00024067.1 | CLATHRIN HEAVY CHAIN 1. | 191615 | 5.42 | 73 | 28 | 22.93 |
| 65 | IPI00383331.1 | --none found in database-- | 15921 | 8.27 | 70 | 4 | 34.25 |
| 66 | IPI00216171.1 | ENOLASE 2. | 47269 | 4.65 | 67 | 16 | 58.99 |
| 67 | IPI00021369.1 | ALPHA CRYSTALLIN B CHAIN. | 20159 | 7.38 | 65 | 14 | 80.57 |
| 68 | IPI00169383.1 | PHOSPHOGLYCERETE KINASE 1. | 44615 | 8.27 | 65 | 18 | 54.68 |
| 69 | IPI00295540.1 | PHOSPHOGLYCERATE KINASE 1. | 44597 | 8.27 | 65 | 18 | 54.68 |
| 70 | IPI00220642.1 | TYROSINE 3-MONOOXYGENASE/TRYPTOPHAN 5-MONOOXYGENASE ACTIVATION PROTEIN, GAMMA POLYPEPTIDE. | 28303 | 4.52 | 64 | 15 | 63.97 |
| 71 | IPI00006664.4 | PEPTIDYL-PROLYL CIS-TRANS ISOMERASE A. | 17881 | 7.97 | 62 | 14 | 82.32 |
| 72 | IPI00010154.1 | RAB GDP DISSOCIATION INHIBITOR ALPHA. | 50583 | 4.75 | 62 | 20 | 57.49 |
| 73 | IPI00012011.1 | COFILIN, NON-MUSCLE ISOFORM. | 18502 | 8.29 | 60 | 12 | 72.89 |
| 74 | IPI00245171.3 | HEMOGLOBIN DELTA CHAIN. | 19496 | 8.24 | 60 | 9 | 57.06 |
| 75 | IPI00021716.1 | TRANSKETOLASE. | 67878 | 7.73 | 59 | 17 | 40.45 |
| 76 | IPI00328807.3 | TRIOSEPHOSPHATE ISOMERASE. | 26538 | 6.91 | 59 | 16 | 77.42 |
| 77 | IPI00306589.1 | UBIQUITIN B. | 25762 | 7.6 | 58 | 6 | 66.38 |
| 78 | IPI00333602.1 | --none found in database-- | 49640 | 4.45 | 58 | 8 | 21.27 |
| 79 | IPI00384875.1 | MUTANT BETA-GLOBIN. | 9689 | 8.52 | 58 | 5 | 66.29 |
| 80 | IPI00016801.1 | GLUTAMATE DEHYDROGENASE 1, MITOCHONDRIAL PRECURSOR. | 61398 | 7.91 | 56 | 20 | 44.62 |
| 81 | IPI00018146.1 | 14-3-3 PROTEIN TAU. | 27764 | 4.41 | 56 | 14 | 48.98 |
| 82 | IPI00335160.1 | --none found in database-- | 49595 | 4.63 | 56 | 7 | 15.16 |
| 83 | IPI00219217.1 | LACTATE DEHYDROGENASE B. | 36638 | 5.93 | 55 | 14 | 41.02 |
| 84 | IPI00292496.1 | BETA-TUBULIN 4Q. | 49776 | 4.52 | 55 | 7 | 15.09 |
| 85 | IPI00382845.1 | --none found in database-- | 18197 | 7.97 | 55 | 13 | 70.06 |
| 86 | IPI00382470.1 | HSP89-ALPHA-DELTA-N. | 63252 | 4.75 | 54 | 20 | 40.63 |
| 87 | IPI00182840.2 | SIMILAR TO BETA-TUBULIN 4Q. | 71234 | 5.13 | 53 | 6 | 9.09 |
| 88 | IPI00258879.2 | SIMILAR TO BETA ACTIN. | 41661 | 5.56 | 52 | 6 | 13.1 |
| 89 | IPI00027350.1 | PEROXIREDOXIN 2. | 21892 | 5.76 | 51 | 8 | 33.33 |
| 90 | IPI00174849.2 | --none found in database-- | 48278 | 4.73 | 51 | 6 | 12.01 |
| 91 | IPI00374080.1 | SIMILAR TO PEPTIDYLPROLYL ISOMERASE A (CYCLOPHILIN A). | 20754 | 6.36 | 51 | 11 | 55.56 |
| 92 | IPI00375400.1 | PEROXIREDOXIN 2 ISOFORM B. | 15989 | 6.53 | 51 | 8 | 44.9 |
| 93 | IPI00017855.1 | ACONITATE HYDRATASE, MITOCHONDRIAL PRECURSOR. | 85425 | 7.65 | 50 | 19 | 34.23 |
| 94 | IPI00385209.1 | --none found in database-- | 90518 | 8.19 | 50 | 19 | 32.25 |
| 95 | IPI00374165.1 | SIMILAR TO POTE PROTEIN. | 116971 | 6.69 | 46 | 9 | 8.96 |
| 96 | IPI00385600.1 | --none found in database-- | 69976 | 7.22 | 46 | 17 | 36.16 |
| 97 | IPI00219446.1 | PROSTATIC BINDING PROTEIN. | 21057 | 7.65 | 44 | 12 | 83.42 |
| 98 | IPI00384084.1 | --none found in database-- | 15980 | 8.72 | 44 | 4 | 31.51 |
| 99 | IPI00385497.1 | --none found in database-- | 18522 | 9.04 | 44 | 11 | 65.12 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 100 | IPI00005614.2 | SPLICE ISOFORM LONG OF Q01082 SPECTRIN BETA CHAIN, BRAIN 1. | 275518 | 5.28 | 43 | 30 | 17.5 |
| 101 | IPI00248359.2 | SIMILAR TO POTE PROTEIN. | 108369 | 6.84 | 42 | 7 | 7.08 |
| 102 | IPI00385244.1 | PHOSPHOGLYCERATE MUTASE 1 (BRAIN). | 28804 | 7.22 | 42 | 13 | 70.87 |
| 103 | IPI00291006.1 | MALATE DEHYDROGENASE, MITOCHONDRIAL PRECURSOR. | 35531 | 8.9 | 41 | 13 | 52.07 |
| 104 | IPI00010182.1 | SPLICE ISOFORM A 1 OF P07108 ACYL-COA-BINDING PROTEIN. | 9913 | 6.54 | 40 | 6 | 73.26 |
| 105 | IPI00216319.1 | TYROSINE 3/TRYPTOPHAN 5 -MONOOXYGENASE ACTIVATION PROTEIN, ETA POLYPEPTIDE. | 28219 | 4.47 | 40 | 8 | 32.52 |
| 106 | IPI00027146.1 | GLUTAMATE DEHYDROGENASE 2, MITOCHONDRIAL PRECURSOR. | 61434 | 8.67 | 38 | 14 | 25.27 |
| 107 | IPI00031461.1 | RAB GDP DISSOCIATION INHIBITOR BETA. | 50663 | 6.39 | 38 | 10 | 25.84 |
| 108 | IPI00218836.1 | SPLICE ISOFORM 2 OF P07108 ACYL-COA-BINDING PROTEIN. | 11793 | 5.24 | 38 | 5 | 53.85 |
| 109 | IPI00383071.1 | --none found in database-- | 26943 | 8.21 | 38 | 9 | 33.33 |
| 110 | IPI00384026.1 | HUMAN FULL-LENGTH CDNA 5-PRIME END OF CLONE CS0DN005YI08 OF ADULT BRAIN OF HOMO SAPIENS. | 29031 | 4.84 | 38 | 7 | 24.43 |
| 111 | IPI00182680.3 | SIMILAR TO ALPHA-TUBULIN. | 37407 | 4.53 | 37 | 9 | 22.94 |
| 112 | IPI00003269.1 | SIMILAR TO CYTOPLASMIC BETA-ACTIN. | 42003 | 5.29 | 36 | 4 | 11.17 |
| 113 | IPI00007702.1 | HEAT SHOCK-RELATED 70 KDA PROTEIN 2. | 70021 | 5.42 | 36 | 10 | 15.02 |
| 114 | IPI00018511.1 | TUBULIN BETA-4Q CHAIN. | 48435 | 4.91 | 36 | 5 | 10.14 |
| 115 | IPI00027388.3 | --none found in database-- | 17989 | 7.51 | 36 | 9 | 44.17 |
| 116 | IPI00160552.1 | TENASCIN-R. | 149548 | 4.44 | 36 | 15 | 15.39 |
| 117 | IPI00303476.1 | ATP SYNTHASE BETA CHAIN, MITOCHONDRIAL PRECURSOR. | 56560 | 5.07 | 36 | 14 | 44.23 |
| 118 | IPI00328230.1 | SPLICE ISOFORM SHORT OF Q01082 SPECTRIN BETA CHAIN, BRAIN 1. | 253113 | 5.16 | 36 | 27 | 17.02 |
| 119 | IPI00374162.1 | SIMILAR TO POTE PROTEIN. | 116972 | 6.99 | 36 | 6 | 5.01 |
| 120 | IPI00376456.1 | SIMILAR TO FKSG30. | 60497 | 5.62 | 36 | 6 | 9.74 |
| 121 | IPI00013890.1 | 14-3-3 PROTEIN SIGMA. | 27774 | 4.39 | 35 | 4 | 12.5 |
| 122 | IPI00025447.1 | ELONGATION FACTOR 1-ALPHA 1. | 50141 | 9.5 | 35 | 8 | 21.21 |
| 123 | IPI00219524.2 | SIMILAR TO PHOSPHOGLYCERATE MUTASE 1 (PHOSPHOGLYCERATE MUTASE ISOZYME B) (PGAM-B) (BPG-DEPENDENT PGAM 1). | 22850 | 6.04 | 35 | 11 | 75.25 |
| 124 | IPI00333015.1 | BETA-SPECTRIN 2 ISOFORM 2. | 251419 | 5.25 | 35 | 26 | 16.47 |
| 125 | IPI00386513.1 | SIMILAR TO STRATIFIN. | 24336 | 4.47 | 35 | 4 | 14.35 |
| 126 | IPI00216312.1 | VIMENTIN. | 53686 | 4.77 | 34 | 17 | 40.99 |
| 127 | IPI00307063.1 | TRUNCATED BETA-GLOBIN. | 6542 | 9.37 | 34 | 3 | 45.76 |
| 128 | IPI00184899.4 | DIHYDROPYRIMIDINASE RELATED PROTEIN-1. | 62184 | 7.03 | 33 | 9 | 23.95 |
| 129 | IPI00329351.3 | 60 KDA HEAT SHOCK PROTEIN, MITOCHONDRIAL PRECURSOR. | 61213 | 5.55 | 33 | 14 | 35.48 |
| 130 | IPI00006510.1 | TUBB1 HUMAN BETA TUBULIN 1, CLASS VI (DJ543J19.4) (BETA TUBULIN 1, CLASS VI. | 50327 | 4.82 | 32 | 4 | 6.43 |
| 131 | IPI00299399.3 | S100 CALCIUM-BINDING PROTEIN, BETA. | 10713 | 4.25 | 32 | 3 | 40.22 |
| 132 | IPI00018352.1 | UBIQUITIN CARBOXYL-TERMINAL HYDROLASE ISOZYME L1. | 24824 | 5.18 | 31 | 8 | 55.61 |
| 133 | IPI00387176.1 | HYPOTHETICAL PROTEIN FLJ32204. | 47488 | 4.72 | 31 | 15 | 39.02 |
| 134 | IPI00026119.2 | UBIQUITIN-ACTIVATING ENZYME E1. | 117849 | 5.5 | 30 | 17 | 25.61 |
| 135 | IPI00219301.3 | MYRISTOYLATED ALANINE-RICH PROTEIN KINASE C SUBSTRATE. | 31545 | 4.13 | 30 | 9 | 35.24 |
| 136 | IPI00298547.1 | RNA-BINDING PROTEIN REGULATORY SUBUNIT. | 19891 | 6.78 | 30 | 11 | 66.67 |
| 137 | IPI00335118.1 | --none found in database-- | 40424 | 5.23 | 30 | 8 | 21.53 |
| 138 | IPI00004358.2 | GLYCOGEN PHOSPHORYLASE, BRAIN FORM. | 96696 | 6.85 | 28 | 15 | 22.06 |
| 139 | IPI00008868.3 | MICROTUBULE-ASSOCIATED PROTEIN 1B (MAP 1B) [Contains: MAP1 LIGHT CHAIN LC1]. | 270620 | 4.44 | 28 | 20 | 12.56 |
| 140 | IPI00163249.3 | SIMILAR TO HEAT SHOCK COGNATE 71 KDA PROTEIN. | 63392 | 5.78 | 28 | 8 | 13.24 |
| 141 | IPI00220483.1 | SPLICE ISOFORM B1 OF P22626 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEINS A2/B1. | 43349 | 9.72 | 28 | 11 | 34.31 |
| 142 | IPI00291099.2 | SPLICE ISOFORM LONG OF P23471 RECEPTOR-TYPE PROTEIN-TYROSINE PHOSPHATASE ZETA PRECURSOR. | 260427 | 4.63 | 28 | 9 | 4.61 |
| 143 | IPI00374770.1 | MICROTUBULE-ASSOCIATED PROTEIN 1B ISOFORM 2. | 256710 | 4.43 | 28 | 20 | 13.24 |
| 144 | IPI00396378.1 | SPLICE ISOFORM A2 OF P22626 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEINS A2/B1. | 41925 | 9.58 | 28 | 11 | 35.34 |
| 145 | IPI00014850.2 | ASTROCYTIC PHOSPHOPROTEIN PEA-15. | 15040 | 4.66 | 27 | 8 | 70.77 |
| 146 | IPI00067590.1 | --none found in database-- | 9644 | 9.29 | 27 | 4 | 56.18 |
| 147 | IPI00220327.1 | KERATIN 1. | 66067 | 8.33 | 27 | 8 | 13.66 |
| 148 | IPI00384970.1 | HEAT SHOCK PROTEIN BETA. | 14066 | 4.4 | 27 | 5 | 32.31 |
| 149 | IPI00386715.1 | C-MYC PROMOTER-BINDING PROTEIN. | 37087 | 7.19 | 27 | 7 | 21.19 |
| 150 | IPI00014424.1 | ELONGATION FACTOR 1-ALPHA 2. | 50470 | 9.5 | 26 | 5 | 11.66 |
| 151 | IPI00022774.1 | TRANSITIONAL ENDOPLASMIC RETICULUM ATPASE (TER ATPASE) (15S MG(2+)-ATPASE P97 SUBUNIT) (VALOSIN CONTAINING PROTEIN) (VCP) [Contains: VALOSIN]. | 89322 | 4.89 | 26 | 16 | 25.43 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 152 | IPI00033946.1 | HEAT SHOCK 70KDA PROTEIN 1B. | 70025 | 5.31 | 26 | 13 | 29.64 |
| 153 | IPI00216283.1 | SPLICE ISOFORM SHORT OF P23471 RECEPTOR-TYPE PROTEIN-TYROSINE PHOSPHATASE ZETA PRECURSOR. | 163444 | 4.85 | 26 | 8 | 6.53 |
| 154 | IPI00216691.1 | PROFILIN 1. | 15054 | 8.46 | 26 | 9 | 87.86 |
| 155 | IPI00304925.1 | HEAT SHOCK 70 KDA PROTEIN 1. | 70052 | 5.31 | 26 | 13 | 29.64 |
| 156 | IPI00024323.3 | SIMILAR TO FKSG30. | 77208 | 7.25 | 25 | 4 | 5.99 |
| 157 | IPI00031523.1 | HEAT SHOCK PROTEIN 86. | 35674 | 4.27 | 25 | 5 | 15.71 |
| 158 | IPI00219757.6 | GLUTATHIONE S-TRANSFERASE P. | 24677 | 5.81 | 25 | 7 | 47.75 |
| 159 | IPI00234002.2 | SIMILAR TO HEAT SHOCK COGNATE 71 KDA PROTEIN. | 65588 | 5.44 | 25 | 8 | 12.03 |
| 160 | IPI00015671.1 | HYPOTHETICAL PROTEIN FLJ21665. | 49909 | 5.96 | 24 | 6 | 11.66 |
| 161 | IPI00233214.2 | CALMODULIN. | 16706 | 3.84 | 24 | 8 | 94.59 |
| 162 | IPI00293683.1 | MICROTUBULE-ASSOCIATED PROTEIN TAU ISOFORM 4. | 36760 | 10.06 | 24 | 9 | 40.34 |
| 163 | IPI00333562.1 | --none found in database-- | 36748 | 6.98 | 24 | 2 | 5.15 |
| 164 | IPI00007682.2 | VACUOLAR ATP SYNTHASE CATALYTIC SUBUNIT A, UBIQUITOUS ISOFORM. | 68304 | 5.16 | 23 | 9 | 17.18 |
| 165 | IPI00027175.1 | SORCIN. | 21676 | 5.2 | 23 | 7 | 61.11 |
| 166 | IPI00075248.1 | CALMODULIN 2. | 17557 | 3.89 | 23 | 7 | 66.45 |
| 167 | IPI00081025.1 | CALMODULIN. | 17163 | 3.82 | 23 | 7 | 67.76 |
| 168 | IPI00163984.2 | --none found in database-- | 33366 | 5.2 | 23 | 8 | 30.74 |
| 169 | IPI00181828.3 | COFILIN, MUSCLE ISOFORM. | 23759 | 8.2 | 23 | 5 | 27.98 |
| 170 | IPI00220171.1 | SPLICE ISOFORM FETAL-TAU OF P10636 MICROTUBULE-ASSOCIATED PROTEIN TAU. | 32813 | 10.77 | 23 | 8 | 37.46 |
| 171 | IPI00220173.1 | SPLICE ISOFORM TAU-B OF P10636 MICROTUBULE-ASSOCIATED PROTEIN TAU. | 39589 | 9.17 | 23 | 8 | 31.05 |
| 172 | IPI00220174.1 | SPLICE ISOFORM TAU-C OF P10636 MICROTUBULE-ASSOCIATED PROTEIN TAU. | 42472 | 7.43 | 23 | 8 | 28.85 |
| 173 | IPI00220362.2 | 10 KDA HEAT SHOCK PROTEIN, MITOCHONDRIAL. | 15224 | 10.05 | 23 | 5 | 39.01 |
| 174 | IPI00334215.1 | --none found in database-- | 45330 | 6.29 | 23 | 5 | 6.86 |
| 175 | IPI00386854.1 | HYPOTHETICAL PROTEIN. | 28412 | 4.51 | 23 | 8 | 36.55 |
| 176 | IPI00013769.1 | ALPHA ENOLASE, LUNG SPECIFIC. | 49477 | 5.97 | 22 | 5 | 13.54 |
| 177 | IPI00157721.4 | --none found in database-- | 42109 | 5.59 | 22 | 3 | 7.18 |
| 178 | IPI00258965.2 | SIMILAR TO ELONGATION FACTOR 1 ALPHA. | 45401 | 7.1 | 22 | 3 | 8.35 |
| 179 | IPI00291005.2 | CYTOSOLIC MALATE DEHYDROGENASE. | 36426 | 7.45 | 22 | 6 | 26.05 |
| 180 | IPI00293276.3 | MACROPHAGE MIGRATION INHIBITORY FACTOR (GLYCOSYLATION-INHIBITING FACTOR). | 12476 | 8.05 | 22 | 2 | 17.39 |
| 181 | IPI00383758.1 | GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, MUSCLE. | 35876 | 7.07 | 22 | 7 | 19.46 |
| 182 | IPI00386621.1 | SIMILAR TO CALMODULIN 2. | 16507 | 4.08 | 22 | 6 | 66.67 |
| 183 | IPI00396248.1 | SORCIN ISOFORM B. | 20345 | 4.92 | 22 | 6 | 36.07 |
| 184 | IPI00019683.3 | --none found in database-- | 48356 | 4.9 | 21 | 2 | 6.7 |
| 185 | IPI00022881.1 | SPLICE ISOFORM 1 OF P53675 CLATHRIN HEAVY CHAIN 2. | 187030 | 5.67 | 21 | 7 | 5.37 |
| 186 | IPI00024102.1 | TRANSALDOLASE. | 37540 | 6.8 | 21 | 8 | 25.52 |
| 187 | IPI00027497.2 | GLUCOSE-6-PHOSPHATE ISOMERASE. | 63147 | 8.55 | 21 | 7 | 21.51 |
| 188 | IPI00100470.1 | ALPHA-TUBULIN ISOTYPE H2-ALPHA. | 10899 | 3.91 | 21 | 4 | 48.98 |
| 189 | IPI00217506.1 | NUCLEOLIN. | 76344 | 4.31 | 21 | 8 | 16.12 |
| 190 | IPI00300446.1 | SPLICE ISOFORM 2 OF P53675 CLATHRIN HEAVY CHAIN 2. | 180296 | 5.58 | 21 | 7 | 5.56 |
| 191 | IPI00385804.1 | HYPOTHETICAL PROTEIN FLJ34423. | 74325 | 4.26 | 21 | 8 | 16.59 |
| 192 | IPI00017454.1 | HYPOTHETICAL PROTEIN FLJ13940. | 27546 | 8.59 | 20 | 2 | 11.62 |
| 193 | IPI00024915.2 | PEROXIREDOXIN 5, MITOCHONDRIAL PRECURSOR. | 22026 | 8.77 | 20 | 8 | 51.87 |
| 194 | IPI00026836.1 | MICROTUBULE-ASSOCIATED PROTEIN TAU ISOFORM 3. | 40007 | 10.13 | 20 | 8 | 33.94 |
| 195 | IPI00027429.1 | HYPOTHETICAL PROTEIN. | 18829 | 5.68 | 20 | 6 | 33.13 |
| 196 | IPI00179330.2 | UBIQUITIN AND RIBOSOMAL PROTEIN S27A PRECURSOR. | 17965 | 10.25 | 20 | 6 | 34.62 |
| 197 | IPI00215747.1 | FATTY ACID BINDING PROTEIN 7, BRAIN. | 14889 | 5.25 | 20 | 6 | 41.67 |
| 198 | IPI00219010.1 | FERRITIN, HEAVY POLYPEPTIDE 1. | 22178 | 6.34 | 20 | 5 | 31.05 |
| 199 | IPI00219568.2 | PHOSPHOGLYCERATE KINASE 2. | 44796 | 8.82 | 20 | 4 | 11.27 |
| 200 | IPI00220828.1 | THYMOSIN, BETA 4. | 5053 | 4.72 | 20 | 4 | 59.09 |
| 201 | IPI00296120.1 | SIMILAR TO SIMILARITY TO MONOUBIQUITIN/CARBOXY-EXTENSION PROTEIN FUSION. | 11722 | 11.17 | 20 | 6 | 52.94 |
| 202 | IPI00337838.1 | UBIQUITIN-52 AMINO ACID FUSION PROTEIN. | 14728 | 10.51 | 20 | 6 | 42.19 |
| 203 | IPI00376164.1 | THYMOSIN-LIKE 2. | 5040 | 6.82 | 20 | 4 | 59.09 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 204 | IPI00395917.1 | --none found in database-- | 22077 | 6.34 | 20 | 5 | 31.22 |
| 205 | IPI00006663.1 | ALDEHYDE DEHYDROGENASE, MITOCHONDRIAL PRECURSOR. | 56381 | 7.05 | 19 | 8 | 24.95 |
| 206 | IPI00015964.3 | NEUROMODULIN. | 28398 | 4.67 | 19 | 9 | 54.48 |
| 207 | IPI00021841.1 | APOLIPOPROTEIN A-I PRECURSOR. | 30778 | 5.5 | 19 | 9 | 34.83 |
| 208 | IPI00025499.1 | MICROTUBULE-ASSOCIATED PROTEIN TAU ISOFORM 2. | 45850 | 8.62 | 19 | 7 | 24.04 |
| 209 | IPI00215965.1 | HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1 ISOFORM B. | 38747 | 9.46 | 19 | 8 | 26.61 |
| 210 | IPI00216049.1 | SPLICE ISOFORM 1 OF Q07244 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN K. | 50976 | 5.18 | 19 | 9 | 26.13 |
| 211 | IPI00216746.1 | SPLICE ISOFORM 2 OF Q07244 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN K. | 51028 | 4.94 | 19 | 9 | 26.08 |
| 212 | IPI00217976.3 | MICROTUBULE-ASSOCIATED PROTEIN TAU ISOFORM 1. | 78878 | 6.69 | 19 | 7 | 13.98 |
| 213 | IPI00220175.1 | SPLICE ISOFORM TAU-E OF P10636 MICROTUBULE-ASSOCIATED PROTEIN TAU. | 42836 | 9.53 | 19 | 7 | 25.79 |
| 214 | IPI00220301.1 | PEROXIREDOXIN 6. | 25035 | 6.29 | 19 | 8 | 50.45 |
| 215 | IPI00220342.1 | DIMETHYLARGININE DIMETHYLAMINOHYDROLASE 1. | 31122 | 5.61 | 19 | 7 | 27.72 |
| 216 | IPI00258419.2 | SIMILAR TO HEAT SHOCK COGNATE 71 KDA PROTEIN. | 68249 | 4.91 | 19 | 7 | 11.27 |
| 217 | IPI00301277.1 | HEAT SHOCK 70 KDA PROTEIN 1-HOM. | 70375 | 5.82 | 19 | 7 | 15.6 |
| 218 | IPI00328348.2 | UBIQUITIN A-52 RESIDUE RIBOSOMAL PROTEIN FUSION PRODUCT 1. | 16175 | 10.6 | 19 | 5 | 34.75 |
| 219 | IPI00333785.1 | --none found in database-- | 20074 | 6.33 | 19 | 1 | 5.59 |
| 220 | IPI00375818.1 | SIMILAR TO GLUTAMATE DEHYDROGENASE 1, MITOCHONDRIAL PRECURSOR (GDH). | 18997 | 6.67 | 19 | 6 | 40.94 |
| 221 | IPI00376990.2 | HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1 ISOFORM A. | 34196 | 9.63 | 19 | 8 | 30.94 |
| 222 | IPI00396395.1 | NG,NG-DIMETHYLARGININE DIMETHYLAMINOHYDROLASE 1. | 30991 | 5.61 | 19 | 7 | 27.82 |
| 223 | IPI00396492.1 | --none found in database-- | 27478 | 4.8 | 19 | 4 | 13.58 |
| 224 | IPI00025252.1 | PROTEIN DISULFIDE ISOMERASE A3 PRECURSOR. | 56782 | 6.28 | 18 | 10 | 28.91 |
| 225 | IPI00105585.5 | --none found in database-- | 21666 | 4.14 | 18 | 6 | 46.63 |
| 226 | IPI00173781.3 | SIMILAR TO HEAT SHOCK PROTEIN HSP 90-ALPHA (HSP 86). | 64432 | 8.19 | 18 | 5 | 7.94 |
| 227 | IPI00247601.2 | SIMILAR TO GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER (GAPDH). | 72249 | 8 | 18 | 3 | 4.15 |
| 228 | IPI00333470.1 | --none found in database-- | 40503 | 6.04 | 18 | 2 | 4.63 |
| 229 | IPI00334610.1 | --none found in database-- | 41064 | 5.92 | 18 | 2 | 4.61 |
| 230 | IPI00375306.1 | PEROXIREDOXIN 5 PRECURSOR ISOFORM B. | 17394 | 9.01 | 18 | 7 | 57.06 |
| 231 | IPI00018939.1 | BA92K2.2. | 17967 | 10.03 | 17 | 5 | 24.36 |
| 232 | IPI00027230.1 | ENDOPLASMIN PRECURSOR. | 92469 | 4.48 | 17 | 9 | 16.19 |
| 233 | IPI00142798.2 | SIMILAR TO PEPTIDYLPROLYL ISOMERASE A (CYCLOPHILIN A). | 15631 | 9.78 | 17 | 6 | 43.97 |
| 234 | IPI00176590.2 | SIMILAR TO HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1 (HELIX-DESTABILIZING PROTEIN) (SINGLE-STRAND BINDING PROTEIN) (HNRNP CORE PROTEIN A1) (HDP). | 32353 | 7.32 | 17 | 7 | 26.73 |
| 235 | IPI00218570.1 | PHOSPHOGLYCERATE MUTASE 2 (MUSCLE). | 28850 | 9.33 | 17 | 4 | 14.23 |
| 236 | IPI00329801.5 | ANNEXIN A5. | 35806 | 4.66 | 17 | 8 | 31.66 |
| 237 | IPI00376165.1 | THYMOSIN-LIKE 4. | 5113 | 4.72 | 17 | 3 | 45.45 |
| 238 | IPI00000874.1 | PEROXIREDOXIN 1. | 22110 | 8.31 | 16 | 4 | 19.6 |
| 239 | IPI00010130.1 | GLUTAMINE SYNTHETASE. | 42064 | 6.88 | 16 | 7 | 21.72 |
| 240 | IPI00027499.1 | SPLICE ISOFORM 1 OF P06748 NUCLEOPHOSMIN. | 32575 | 4.39 | 16 | 7 | 30.95 |
| 241 | IPI00030809.1 | GAMMA-G GLOBIN. | 16969 | 6.34 | 16 | 1 | 6.45 |
| 242 | IPI00031012.2 | SIMILAR TO HEMOGLOBIN, GAMMA G. | 16126 | 7.23 | 16 | 1 | 6.8 |
| 243 | IPI00217471.1 | EPSILON GLOBIN. | 16203 | 9.1 | 16 | 1 | 6.8 |
| 244 | IPI00220706.1 | SIMILAR TO HEMOGLOBIN, GAMMA A. | 16128 | 7.23 | 16 | 1 | 6.8 |
| 245 | IPI00220740.1 | SPLICE ISOFORM 2 OF P06748 NUCLEOPHOSMIN. | 29465 | 4.22 | 16 | 7 | 34.34 |
| 246 | IPI00332720.1 | HEMOGLOBIN GAMMA-A AND GAMMA-G CHAINS. | 16009 | 7.23 | 16 | 1 | 6.85 |
| 247 | IPI00339269.1 | HEAT SHOCK 70 KDA PROTEIN 6. | 71028 | 6.01 | 16 | 6 | 11.04 |
| 248 | IPI00375307.1 | PEROXIREDOXIN 5 PRECURSOR ISOFORM C. | 12837 | 9.49 | 16 | 5 | 50.4 |
| 249 | IPI00382844.1 | ACONITASE. | 65347 | 7.92 | 16 | 5 | 12.33 |
| 250 | IPI00003362.1 | 78 KDA GLUCOSE-REGULATED PROTEIN PRECURSOR. | 72333 | 4.79 | 15 | 8 | 18.2 |
| 251 | IPI00009532.1 | 4-AMINOBUTYRATE AMINOTRANSFERASE, MITOCHONDRIAL PRECURSOR. | 56557 | 7.68 | 15 | 7 | 17 |
| 252 | IPI00016638.1 | ATP SYNTHASE ALPHA CHAIN, MITOCHONDRIAL PRECURSOR. | 59751 | 9.56 | 15 | 5 | 15.19 |
| 253 | IPI00021766.3 | SPLICE ISOFORM 1 OF Q9NQC3 RETICULON 4. | 129931 | 4.14 | 15 | 9 | 13.84 |
| 254 | IPI00086909.3 | SIMILAR TO EPSILON ISOFORM OF 14-3-3 PROTEIN. | 42284 | 4.58 | 15 | 4 | 12.83 |
| 255 | IPI00101135.1 | HYPOTHETICAL PROTEIN. | 65309 | 4.75 | 15 | 11 | 26.83 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 256 | IPI00177728.2 | CYTOSOLIC NONSPECIFIC DIPEPTIDASE. | 52954 | 5.81 | 15 | 9 | 26.47 |
| 257 | IPI00240029.5 | STATHMIN. | 17171 | 5.8 | 15 | 6 | 35.14 |
| 258 | IPI00299024.4 | BRAIN ACID SOLUBLE PROTEIN 1. | 22562 | 4.3 | 15 | 8 | 53.54 |
| 259 | IPI00333941.1 | --none found in database-- | 22028 | 8.48 | 15 | 6 | 33.33 |
| 260 | IPI00386492.1 | SIMILAR TO TRANSALDOLASE 1. | 35329 | 9.41 | 15 | 5 | 17.92 |
| 261 | IPI00395947.1 | 4-AMINOBUTYRATE AMINOTRANSFERASE PRECURSOR. | 62284 | 8.87 | 15 | 7 | 15.29 |
| 262 | IPI00012507.1 | GTP-BINDING NUCLEAR PROTEIN RAN. | 24423 | 7.59 | 14 | 6 | 34.72 |
| 263 | IPI00032826.1 | HSC70-INTERACTING PROTEIN. | 41332 | 4.92 | 14 | 6 | 21.14 |
| 264 | IPI00042578.2 | SIMILAR TO HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1 (HELIX-DESTABILIZING PROTEIN) (SINGLE-STRAND BINDING PROTEIN) (HNRNP CORE PROTEIN A1) (HDP). | 30383 | 8.2 | 14 | 5 | 19.08 |
| 265 | IPI00046057.1 | HUNC18B. | 68736 | 6.76 | 14 | 10 | 20.4 |
| 266 | IPI00063228.3 | SIMILAR TO EUKARYOTIC TRANSLATION ELONGATION FACTOR 1 ALPHA 2. | 41980 | 7.8 | 14 | 2 | 5.19 |
| 267 | IPI00077402.2 | SIMILAR TO UBIQUITIN AND RIBOSOMAL PROTEIN S27A PRECURSOR. | 22190 | 9.9 | 14 | 3 | 12.18 |
| 268 | IPI00084828.1 | SPLICE ISOFORM 1 OF Q64320 SYNTAXIN BINDING PROTEIN 1. | 67569 | 6.96 | 14 | 10 | 20.71 |
| 269 | IPI00156444.4 | SIMILAR TO HEAT SHOCK PROTEIN HSP 90-BETA (HSP 84) (HSP 90). | 53868 | 4.79 | 14 | 8 | 18.03 |
| 270 | IPI00164463.3 | --none found in database-- | 18122 | 6.66 | 14 | 6 | 43.11 |
| 271 | IPI00183526.1 | SIMILAR TO NUCLEOLIN. | 51357 | 4.43 | 14 | 5 | 14.26 |
| 272 | IPI00218733.1 | SUPEROXIDE DISMUTASE 1, SOLUBLE. | 15936 | 6.07 | 14 | 8 | 55.84 |
| 273 | IPI00289396.1 | HYPOTHETICAL PROTEIN FLJ30394. | 42500 | 6.39 | 14 | 8 | 26.06 |
| 274 | IPI00332208.2 | --none found in database-- | 23852 | 6.79 | 14 | 7 | 36.28 |
| 275 | IPI00382804.1 | EEF1A PROTEIN. | 24196 | 10.24 | 14 | 2 | 8.81 |
| 276 | IPI00383405.1 | --none found in database-- | 21680 | 8.32 | 14 | 7 | 41.27 |
| 277 | IPI00385358.1 | --none found in database-- | 23812 | 7.11 | 14 | 7 | 37.14 |
| 278 | IPI00395637.1 | --none found in database-- | 34937 | 8.92 | 14 | 7 | 23.56 |
| 279 | IPI00396452.1 | --none found in database-- | 24387 | 4.41 | 14 | 4 | 19.25 |
| 280 | IPI00003406.1 | DREBRIN. | 71425 | 4.1 | 13 | 7 | 14.48 |
| 281 | IPI00009802.1 | SPLICE ISOFORM V0 OF P13611 VERSICAN CORE PROTEIN PRECURSOR. | 372820 | 4.15 | 13 | 7 | 2.59 |
| 282 | IPI00012048.1 | NUCLEOSIDE DIPHOSPHATE KINASE A. | 17149 | 6.11 | 13 | 5 | 41.45 |
| 283 | IPI00014398.1 | SKELETAL MUSCLE LIM-PROTEIN 1. | 31895 | 8.37 | 13 | 5 | 22.86 |
| 284 | IPI00018206.1 | ASPARTATE AMINOTRANSFERASE, MITOCHONDRIAL PRECURSOR. | 47476 | 9.38 | 13 | 6 | 16.74 |
| 285 | IPI00047642.3 | --none found in database-- | 43066 | 9.43 | 13 | 3 | 6.3 |
| 286 | IPI00176692.2 | SIMILAR TO HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1 (HELIX-DESTABILIZING PROTEIN) (SINGLE-STRAND BINDING PROTEIN) (HNRNP CORE PROTEIN A1) (HDP-1) (TOPOISOMERASE-INHIBITOR SUPPRESSED). | 28788 | 9.73 | 13 | 4 | 17.31 |
| 287 | IPI00215629.1 | SPLICE ISOFORM V2 OF P13611 VERSICAN CORE PROTEIN PRECURSOR. | 182062 | 4.52 | 13 | 7 | 5.36 |
| 288 | IPI00215631.1 | SPLICE ISOFORM VINT OF P13611 VERSICAN CORE PROTEIN PRECURSOR. | 369688 | 4.13 | 13 | 7 | 2.61 |
| 289 | IPI00219029.1 | ASPARTATE AMINOTRANSFERASE 1. | 46247 | 7.01 | 13 | 8 | 26.63 |
| 290 | IPI00337778.2 | SIMILAR TO PHYTANOYL-COA HYDROXYLASE INTERACTING PROTEIN. | 39066 | 7.15 | 13 | 7 | 25 |
| 291 | IPI00374732.1 | SIMILAR TO PEPTIDYLPROLYL ISOMERASE A (CYCLOPHILIN A). | 19330 | 8.77 | 13 | 5 | 35.75 |
| 292 | IPI00374975.2 | PUTATIVE PHOSPHOGLYCERATE MUTASE 3. | 28777 | 6.63 | 13 | 4 | 24.8 |
| 293 | IPI00375531.1 | NM23-H1. | 19654 | 5.29 | 13 | 5 | 35.59 |
| 294 | IPI00375839.1 | SIMILAR TO PHOSPHOGLYCERATE MUTASE 1 (PHOSPHOGLYCERATE MUTASE ISOZYME B) (PGAM-B) (BPG-DEPENDENT PGAM 1). | 21007 | 6.16 | 13 | 3 | 11.58 |
| 295 | IPI00396476.1 | --none found in database-- | 58771 | 4.94 | 13 | 2 | 3.92 |
| 296 | IPI00001453.2 | ALPHA-INTERNEXIN. | 55391 | 5.09 | 12 | 7 | 14.83 |
| 297 | IPI00001734.2 | SPLICE ISOFORM 1 OF Q9Y617 PHOSPHOSERINE AMINOTRANSFERASE. | 40423 | 7.77 | 12 | 6 | 18.11 |
| 298 | IPI00007765.2 | STRESS-70 PROTEIN, MITOCHONDRIAL PRECURSOR. | 73680 | 6.01 | 12 | 11 | 20.47 |
| 299 | IPI00011107.2 | ISOCITRATE DEHYDROGENASE [NADP], MITOCHONDRIAL PRECURSOR. | 50909 | 8.95 | 12 | 7 | 18.58 |
| 300 | IPI00026260.1 | NUCLEOSIDE DIPHOSPHATE KINASE B. | 17298 | 8.69 | 12 | 5 | 42.11 |
| 301 | IPI00107634.2 | CHONDROITIN SULFATE PROTEOGLYCAN BEHAB/BREVICAN. | 99148 | 4.28 | 12 | 8 | 10.98 |
| 302 | IPI00163187.6 | HYPOTHETICAL PROTEIN. | 55136 | 7.26 | 12 | 7 | 15.6 |
| 303 | IPI00172579.1 | 4-TRIMETHYLAMINOBUTYRALDEHYDE DEHYDROGENASE. | 53802 | 5.61 | 12 | 6 | 15.18 |
| 304 | IPI00180730.1 | --none found in database-- | 50154 | 9.41 | 12 | 3 | 8.01 |
| 305 | IPI00186036.2 | --none found in database-- | 19050 | 8.35 | 12 | 5 | 17.42 |
| 306 | IPI00215628.1 | SPLICE ISOFORM V1 OF P13611 VERSICAN CORE PROTEIN PRECURSOR. | 265050 | 4.17 | 12 | 6 | 3.28 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 307 | IPI00215630.1 | SPLICE ISOFORM V3 OF P13611 VERSICAN CORE PROTEIN PRECURSOR. | 74293 | 7.38 | 12 | 6 | 12.06 |
| 308 | IPI00216900.1 | SIMILAR TO MICROTUBULE-ASSOCIATED PROTEIN 2. | 58954 | 10.4 | 12 | 5 | 16.99 |
| 309 | IPI00218319.1 | SPLICE ISOFORM 2 OF P06753 TROPOMYOSIN ALPHA 3 CHAIN. | 29033 | 4.44 | 12 | 6 | 27.02 |
| 310 | IPI00218320.1 | SPLICE ISOFORM 3 OF P06753 TROPOMYOSIN ALPHA 3 CHAIN. | 28955 | 4.46 | 12 | 6 | 27.13 |
| 311 | IPI00218474.2 | BETA ENOLASE. | 47003 | 7.84 | 12 | 4 | 11.95 |
| 312 | IPI00219478.1 | SPLICE ISOFORM 2 OF Q9Y617 PHOSPHOSERINE AMINOTRANSFERASE. | 35189 | 6.66 | 12 | 6 | 20.68 |
| 313 | IPI00261068.2 | --none found in database-- | 16467 | 8.76 | 12 | 4 | 18.67 |
| 314 | IPI00332474.1 | --none found in database-- | 18152 | 9.09 | 12 | 4 | 19.39 |
| 315 | IPI00374327.1 | MICROTUBULE-ASSOCIATED PROTEIN 2 ISOFORM 4. | 52874 | 10.3 | 12 | 5 | 18.92 |
| 316 | IPI00374399.1 | SIMILAR TO HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1 (HELIX-DESTABILIZING PROTEIN) (SINGLE-STRAND BINDING PROTEIN) (HNRNP CORE PROTEIN A1) (HDP). | 24239 | 9.6 | 12 | 5 | 26.84 |
| 317 | IPI00374686.1 | SIMILAR TO HYPOTHETICAL PROTEIN MGC37309. | 18838 | 8.9 | 12 | 5 | 28.66 |
| 318 | IPI00382894.1 | TPMSK3. | 28809 | 4.41 | 12 | 6 | 27.13 |
| 319 | IPI00386739.2 | CHONDROITIN SULFATE PROTEOGLYCAN BEHAB/BREVICAN. | 99118 | 4.28 | 12 | 8 | 10.98 |
| 320 | IPI00013808.1 | ALPHA-ACTININ 4. | 104854 | 5.12 | 11 | 7 | 11.75 |
| 321 | IPI00020599.1 | CALRETICULIN PRECURSOR. | 48142 | 4.04 | 11 | 6 | 23.02 |
| 322 | IPI00021383.1 | HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A3. | 39686 | 8.77 | 11 | 5 | 14.78 |
| 323 | IPI00021828.1 | CYSTATIN B. | 11140 | 7.73 | 11 | 3 | 45.92 |
| 324 | IPI00025366.1 | CITRATE SYNTHASE, MITOCHONDRIAL PRECURSOR. | 51706 | 8.21 | 11 | 5 | 12.23 |
| 325 | IPI00030144.1 | CYCLOPHILIN-LC. | 18182 | 9.76 | 11 | 4 | 20.73 |
| 326 | IPI00031045.1 | DESTRIN. | 18506 | 7.97 | 11 | 4 | 23.64 |
| 327 | IPI00062209.1 | HYPOTHETICAL PROTEIN. | 17098 | 6.38 | 11 | 2 | 5.1 |
| 328 | IPI00174760.2 | SIMILAR TO HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1 (HELIX-DESTABILIZING PROTEIN) (SINGLE-STRAND BINDING PROTEIN) (HNRNP CORE PROTEIN A1) (HDP). | 27551 | 5.21 | 11 | 5 | 20.88 |
| 329 | IPI00335314.1 | --none found in database-- | 34736 | 5.34 | 11 | 2 | 2.53 |
| 330 | IPI00374137.1 | SIMILAR TO PHOSPHATIDYLETHANOLAMINE-BINDING PROTEIN (PEBP) (PROSTATIC BINDING PROTEIN) (HCNPPP) (NEUROPOLYPEPTIDE H3) (RAF KINASE INHIBITOR PROTEIN) (RKIP). | 10844 | 5.7 | 11 | 2 | 22.92 |
| 331 | IPI00383539.1 | CITRATE SYNTHASE PRECURSOR ISOFORM B. | 44703 | 7.2 | 11 | 5 | 14.25 |
| 332 | IPI00386685.2 | CITRATE SYNTHASE PRECURSOR ISOFORM A. | 55633 | 8.96 | 11 | 5 | 11.24 |
| 333 | IPI00006482.1 | SPLICE ISOFORM LONG OF P05023 SODIUM/POTASSIUM-TRANSPORTING ATPASE ALPHA-1 CHAIN PRECURSOR. | 112896 | 5.15 | 10 | 6 | 7.82 |
| 334 | IPI00012007.2 | ADENOSYLHOMOCYSTEINASE. | 47716 | 6.29 | 10 | 5 | 16.2 |
| 335 | IPI00013944.2 | SPLICE ISOFORM C2 OF P07910 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEINS C1/C2. | 33688 | 4.69 | 10 | 5 | 19.28 |
| 336 | IPI00019359.2 | KERATIN, TYPE I CYTOSKELETAL 9. | 62064 | 4.89 | 10 | 7 | 13.96 |
| 337 | IPI00025318.1 | SH3 DOMAIN-BINDING GLUTAMIC ACID-RICH-LIKE PROTEIN. | 12774 | 4.91 | 10 | 3 | 28.95 |
| 338 | IPI00027107.3 | TU TRANSLATION ELONGATION FACTOR, MITOCHONDRIAL. | 49875 | 7.68 | 10 | 8 | 25.27 |
| 339 | IPI00029028.1 | FOUR AND A HALF LIM DOMAINS 1 PROTEIN ISOFORM C. | 22017 | 8.53 | 10 | 3 | 18.56 |
| 340 | IPI00055606.2 | LIM PROTEIN SLIMMER. | 36263 | 9.15 | 10 | 3 | 11.15 |
| 341 | IPI00072377.1 | TEMPLATE ACYIVATING FACTOR-I ALPHA. | 33489 | 3.95 | 10 | 4 | 17.93 |
| 342 | IPI00092176.2 | SIMILAR TO TYROSINE 3/TRYPTOPHAN 5 -MONOOXYGENASE ACTIVATION PROTEIN, EPSILON POLYPEPTIDE. | 27744 | 6.79 | 10 | 2 | 7.11 |
| 343 | IPI00107555.1 | PROFILIN 2 ISOFORM B. | 15088 | 5.88 | 10 | 3 | 29.29 |
| 344 | IPI00165579.3 | PP856. | 43908 | 6.44 | 10 | 6 | 22.19 |
| 345 | IPI00168184.1 | HYPOTHETICAL PROTEIN FLJ34068. | 56803 | 5.4 | 10 | 8 | 21.22 |
| 346 | IPI00168839.1 | FAM10A5. | 41378 | 4.68 | 10 | 4 | 12.74 |
| 347 | IPI00176715.2 | SIMILAR TO FERRITIN HEAVY CHAIN (FERRITIN H SUBUNIT). | 27186 | 6.5 | 10 | 3 | 16.1 |
| 348 | IPI00216592.1 | SPLICE ISOFORM C1 OF P07910 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEINS C1/C2. | 32356 | 4.68 | 10 | 5 | 20.14 |
| 349 | IPI00219468.1 | PROFILIN 2 ISOFORM A. | 15046 | 7.04 | 10 | 3 | 29.29 |
| 350 | IPI00236240.2 | SIMILAR TO FERRITIN HEAVY CHAIN (FERRITIN H SUBUNIT). | 47023 | 8.97 | 10 | 3 | 8.92 |
| 351 | IPI00289862.3 | PROTEIN KIAA0193. | 46382 | 4.39 | 10 | 4 | 11.84 |
| 352 | IPI00293579.1 | SPLICE ISOFORM MAP2C OF P11137 MICROTUBULE-ASSOCIATED PROTEIN 2. | 49768 | 10.19 | 10 | 4 | 17.83 |
| 353 | IPI00301311.1 | SET PROTEIN. | 32103 | 3.85 | 10 | 4 | 18.77 |
| 354 | IPI00302840.1 | SODIUM/POTASSIUM-TRANSPORTING ATPASE ALPHA-3 CHAIN. | 111735 | 5.02 | 10 | 6 | 8.79 |
| 355 | IPI00328587.4 | SIMILAR TO ENOLASE 1,. | 42342 | 5.71 | 10 | 5 | 8.51 |
| 356 | IPI00385025.1 | ISOCITRATE DEHYDROGENASE. | 46815 | 7.21 | 10 | 6 | 17.42 |
| 357 | IPI00385372.1 | --none found in database-- | 34547 | 4.97 | 10 | 5 | 21.29 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 358 | IPI00003021.1 | SODIUM/POTASSIUM-TRANSPORTING ATPASE ALPHA-2 CHAIN PRECURSOR. | 112265 | 5.33 | 9 | 5 | 6.47 |
| 359 | IPI00003479.1 | MITOGEN-ACTIVATED PROTEIN KINASE 1. | 41390 | 6.99 | 9 | 5 | 15.83 |
| 360 | IPI00013881.4 | HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN H. | 49229 | 6.25 | 9 | 4 | 13.36 |
| 361 | IPI00021304.1 | KERATIN, TYPE II CYTOSKELETAL 2 EPIDERMAL. | 65865 | 8.17 | 9 | 3 | 5.58 |
| 362 | IPI00022463.1 | SEROTRANSFERRIN PRECURSOR. | 77050 | 7.13 | 9 | 6 | 11.03 |
| 363 | IPI00024919.1 | THIOREDOXIN-DEPENDENT PEROXIDE REDUCTASE, MITOCHONDRIAL PRECURSOR. | 27693 | 7.88 | 9 | 6 | 26.95 |
| 364 | IPI00025054.1 | SPLICE ISOFORM LONG OF Q00839 HETEROGENOUS NUCLEAR RIBONUCLEOPROTEIN U. | 90479 | 5.8 | 9 | 6 | 10.44 |
| 365 | IPI00164792.1 | PROTHYMOSIN ALPHA. | 11828 | 3.38 | 9 | 5 | 36.11 |
| 366 | IPI00180240.1 | THYMOSIN-LIKE 3. | 5235 | 4.72 | 9 | 2 | 26.09 |
| 367 | IPI00218038.1 | ST13-LIKE TUMOR SUPPRESSOR. | 27407 | 4.72 | 9 | 4 | 22.5 |
| 368 | IPI00219209.1 | SPLICE ISOFORM 4 OF Q9NQC3 RETICULON 4. | 106360 | 4.13 | 9 | 7 | 11.98 |
| 369 | IPI00220503.4 | DYNACTIN 2. | 44820 | 4.81 | 9 | 7 | 23.89 |
| 370 | IPI00295624.1 | HYPOTHETICAL PROTEIN. | 71595 | 4.17 | 9 | 5 | 9.52 |
| 371 | IPI00299633.1 | DJ1071L10.1. | 5043 | 4.72 | 9 | 2 | 27.27 |
| 372 | IPI00302898.1 | PROTHYMOSIN ALPHA. | 12072 | 3.41 | 9 | 5 | 35.45 |
| 373 | IPI00332603.1 | --none found in database-- | 34063 | 8.19 | 9 | 4 | 19.11 |
| 374 | IPI00374151.1 | PEROXIREDOXIN 3 ISOFORM B. | 25839 | 7.54 | 9 | 6 | 28.99 |
| 375 | IPI00376163.1 | THYMOSIN-LIKE 1. | 5071 | 4.72 | 9 | 2 | 27.27 |
| 376 | IPI00376295.1 | MITOGEN-ACTIVATED PROTEIN KINASE 1. | 41404 | 7.16 | 9 | 5 | 15.83 |
| 377 | IPI00384369.1 | SIMILAR TO TROPOMYOSIN 1, ALPHA. | 32621 | 4.69 | 9 | 5 | 17.77 |
| 378 | IPI00386491.2 | SPLICE ISOFORM SHORT OF Q00839 HETEROGENOUS NUCLEAR RIBONUCLEOPROTEIN U. | 89724 | 5.6 | 9 | 6 | 10.58 |
| 379 | IPI00396479.1 | --none found in database-- | 24078 | 4.39 | 9 | 4 | 22.9 |
| 380 | IPI00003815.1 | RHO GDP-DISSOCIATION INHIBITOR 1. | 23207 | 4.74 | 8 | 3 | 30.88 |
| 381 | IPI00003881.1 | HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN F. | 45672 | 5.31 | 8 | 4 | 13.73 |
| 382 | IPI00004574.1 | IG KAPPA CHAIN C REGION. | 11609 | 5.68 | 8 | 3 | 51.89 |
| 383 | IPI00010779.1 | SPLICE ISOFORM 1 OF P07226 TROPOMYOSIN ALPHA 4 CHAIN. | 28522 | 4.36 | 8 | 4 | 15.73 |
| 384 | IPI00013508.2 | ALPHA-ACTININ 1. | 102974 | 5.04 | 8 | 4 | 5.49 |
| 385 | IPI00018140.2 | GRY-RBP. | 69633 | 8.88 | 8 | 5 | 9.79 |
| 386 | IPI00022314.1 | SUPEROXIDE DISMUTASE [MN], MITOCHONDRIAL PRECURSOR. | 24722 | 8.45 | 8 | 4 | 20.27 |
| 387 | IPI00027165.1 | SPLICE ISOFORM R-TYPE OF P30613 PYRUVATE KINASE, ISOZYMES R/L. | 61830 | 7.83 | 8 | 2 | 2.96 |
| 388 | IPI00027223.2 | ISOCITRATE DEHYDROGENASE [NADP] CYTOPLASMIC. | 46659 | 7 | 8 | 4 | 15.22 |
| 389 | IPI00027442.1 | ALANYL-TRNA SYNTHETASE. | 106801 | 5.13 | 8 | 6 | 10.23 |
| 390 | IPI00028888.1 | SPLICE ISOFORM 1 OF Q14103 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN D0. | 38434 | 8.01 | 8 | 5 | 18.31 |
| 391 | IPI00048940.3 | --none found in database-- | 29068 | 8.13 | 8 | 3 | 14.18 |
| 392 | IPI00074333.1 | HYPOTHETICAL PROTEIN. | 25826 | 5.61 | 8 | 5 | 24.35 |
| 393 | IPI00107117.1 | PEPTIDYLPROLYL ISOMERASE B. | 23743 | 10.07 | 8 | 4 | 16.2 |
| 394 | IPI00152471.1 | GUANINE NUCLEOTIDE-BINDING PROTEIN G(O), ALPHA SUBUNIT 2. | 40087 | 5.69 | 8 | 4 | 14.69 |
| 395 | IPI00164416.3 | --none found in database-- | 17889 | 7.88 | 8 | 3 | 16.46 |
| 396 | IPI00174920.2 | SIMILAR TO CITRATE SYNTHASE PRECURSOR. | 51440 | 7.23 | 8 | 4 | 9.87 |
| 397 | IPI00179589.1 | MYOTROPHIN. | 12895 | 5.18 | 8 | 5 | 63.56 |
| 398 | IPI00181260.1 | PHOSPHOFRUCTOKINASE, MUSCLE. | 85183 | 8.07 | 8 | 5 | 7.56 |
| 399 | IPI00217465.1 | H1 HISTONE FAMILY, MEMBER 2. | 21365 | 11.71 | 8 | 3 | 18.31 |
| 400 | IPI00218115.3 | SPLICE ISOFORM 1 OF P06753 TROPOMYOSIN ALPHA 3 CHAIN. | 32950 | 4.38 | 8 | 4 | 13.33 |
| 401 | IPI00218407.4 | ALDOLASE B. | 39473 | 7.96 | 8 | 1 | 1.92 |
| 402 | IPI00219585.1 | SPLICE ISOFORM 2 OF P08237 6-PHOSPHOFRUCTOKINASE, MUSCLE TYPE. | 81644 | 7.68 | 8 | 5 | 7.89 |
| 403 | IPI00220281.1 | GUANINE NUCLEOTIDE BINDING PROTEIN (G PROTEIN), ALPHA ACTIVATING ACTIVITY POLYPEPTIDE O. | 40051 | 5.19 | 8 | 4 | 14.69 |
| 404 | IPI00220684.1 | SPLICE ISOFORM 3 OF Q14103 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN D0. | 32835 | 8.43 | 8 | 5 | 21.24 |
| 405 | IPI00220827.1 | THYMOSIN, BETA 10. | 5026 | 5.02 | 8 | 3 | 63.64 |
| 406 | IPI00243603.2 | SIMILAR TO PYRUVATE KINASE, M1 ISOZYME (PYRUVATE KINASE MUSCLE ISOZYME) (CYTOSOLIC THYROID HORMONE-BINDING PROTEIN) (CTHBP) (THBP1). | 55507 | 6.45 | 8 | 5 | 10.16 |
| 407 | IPI00291928.1 | RAS-RELATED PROTEIN RAB-14. | 23927 | 6.13 | 8 | 4 | 22.79 |
| 408 | IPI00304824.3 | HYPOTHETICAL PROTEIN. | 24750 | 8.45 | 8 | 4 | 20.27 |
| 409 | IPI00332370.3 | PYRUVATE KINASE L. | 65043 | 7.75 | 8 | 2 | 2.81 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 410 | IPI00334441.1 | --none found in database-- | 10362 | 9.08 | 8 | 3 | 30.53 |
| 411 | IPI00334779.1 | SPLICE ISOFORM L-TYPE OF P30613 PYRUVATE KINASE, ISOZYMES R/L. | 58494 | 7.05 | 8 | 2 | 3.13 |
| 412 | IPI00374228.1 | SIMILAR TO MGC37309 PROTEIN. | 29623 | 8.26 | 8 | 3 | 12.46 |
| 413 | IPI00375401.1 | PEROXIREDOXIN 2 ISOFORM C. | 15819 | 9.49 | 8 | 2 | 13.38 |
| 414 | IPI00375676.1 | HYPOTHETICAL PROTEIN DKFZP686L19147. | 26825 | 5.61 | 8 | 5 | 23.24 |
| 415 | IPI00385058.1 | HYPOTHETICAL PROTEIN. | 25702 | 7.7 | 8 | 3 | 23.31 |
| 416 | IPI00385732.1 | --none found in database-- | 18987 | 8.78 | 8 | 5 | 26.49 |
| 417 | IPI00386745.1 | ACTININ, ALPHA 1. | 103058 | 5.07 | 8 | 4 | 5.49 |
| 418 | IPI00395553.1 | MYOTROPHIN. | 12764 | 5.18 | 8 | 5 | 64.1 |
| 419 | IPI00395915.1 | SIMILAR TO NS1-ASSOCIATED PROTEIN 1. | 58736 | 7.65 | 8 | 5 | 11.57 |
| 420 | IPI00396072.1 | HYPOTHETICAL PROTEIN. | 25674 | 8.45 | 8 | 3 | 23.5 |
| 421 | IPI00010810.1 | ELECTRON TRANSFER FLAVOPROTEIN ALPHA-SUBUNIT, MITOCHONDRIAL PRECURSOR. | 35080 | 8.57 | 7 | 5 | 24.62 |
| 422 | IPI00014177.1 | SEPTIN 2. | 41487 | 6.58 | 7 | 3 | 10.8 |
| 423 | IPI00015139.2 | SIMILAR TO HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1 (HELIX-DESTABILIZING PROTEIN) (SINGLE-STRAND BINDING PROTEIN) (HNRNP CORE PROTEIN A1) (HDP). | 25124 | 6.42 | 7 | 3 | 11.45 |
| 424 | IPI00015550.3 | PROTHYMOSIN ALPHA. | 11954 | 3.42 | 7 | 4 | 22.94 |
| 425 | IPI00015842.1 | RETICULOCALBIN 1 PRECURSOR. | 38890 | 4.61 | 7 | 5 | 20.24 |
| 426 | IPI00020956.1 | HEPATOMA-DERIVED GROWTH FACTOR. | 26788 | 4.39 | 7 | 6 | 37.92 |
| 427 | IPI00020984.1 | CALNEXIN PRECURSOR. | 67568 | 4.21 | 7 | 6 | 12.5 |
| 428 | IPI00023504.1 | RAS-RELATED PROTEIN RAB-3A. | 24984 | 4.62 | 7 | 3 | 17.73 |
| 429 | IPI00024990.6 | METHYLMALONATE-SEMIALDEHYDE DEHYDROGENASE [ACYLATING], MITOCHONDRIAL PRECURSOR. | 57840 | 8.69 | 7 | 5 | 11.59 |
| 430 | IPI00026230.1 | HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN H'. | 49264 | 6.25 | 7 | 3 | 9.58 |
| 431 | IPI00029997.1 | 6-PHOSPHOGLUCONOLACTONASE. | 27547 | 5.95 | 7 | 3 | 27.13 |
| 432 | IPI00046595.2 | SIMILAR TO PYRUVATE KINASE, M1 ISOZYME (PYRUVATE KINASE MUSCLE ISOZYME) (CYTOSOLIC THYROID HORMONE-BINDING PROTEIN) (CTHBP) (THBP1). | 38068 | 6.51 | 7 | 2 | 4.31 |
| 433 | IPI00056467.6 | SIMILAR TO TEMPLATE ACYIVATING FACTOR-I ALPHA. | 25908 | 4.73 | 7 | 3 | 18.3 |
| 434 | IPI00076042.2 | SHORT HEAT SHOCK PROTEIN 60 HSP60S2. | 27096 | 4.34 | 7 | 3 | 14.34 |
| 435 | IPI00100160.1 | HYPOTHETICAL PROTEIN. | 136376 | 5.54 | 7 | 5 | 4.55 |
| 436 | IPI00101645.1 | PUTATIVE ADENOSYLHOMOCYSTEINASE 3. | 66721 | 7.39 | 7 | 4 | 6.55 |
| 437 | IPI00159175.1 | HYPOTHETICAL PROTEIN. | 66668 | 7.44 | 7 | 4 | 6.7 |
| 438 | IPI00176697.3 | --none found in database-- | 29153 | 8.31 | 7 | 3 | 15.15 |
| 439 | IPI00179155.1 | --none found in database-- | 24613 | 4.99 | 7 | 4 | 24.35 |
| 440 | IPI00179377.2 | SIMILAR TO 60 KDA HEAT SHOCK PROTEIN, MITOCHONDRIAL PRECURSOR (HSP60) (60 KDA CHAPERONIN) (CPN60) (HEAT SHOCK PROTEIN 60) (HSP-60) (MITOCHONDRIAL MATRIX PROTEIN P1) (P60 LYMPHOCYTE PROTEIN) (HUCHA60). | 56672 | 5.38 | 7 | 4 | 11.93 |
| 441 | IPI00179721.3 | SIMILAR TO HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1 (HELIX-DESTABILIZING PROTEIN) (SINGLE-STRAND BINDING PROTEIN) (HNRNP CORE PROTEIN A1) (HDP-1) (TOPOISOMERASE-INHIBITOR SUPPRESSED). | 30103 | 6.4 | 7 | 3 | 10.39 |
| 442 | IPI00182938.3 | PUTATIVE ADENOSYLHOMOCYSTEINASE 2. | 71654 | 8.11 | 7 | 4 | 6.12 |
| 443 | IPI00186290.3 | ELONGATION FACTOR 2. | 97752 | 6.82 | 7 | 4 | 6.35 |
| 444 | IPI00215761.3 | ATP-DEPENDENT DNA HELICASE II, 70 KDA SUBUNIT. | 69712 | 6.61 | 7 | 6 | 12.99 |
| 445 | IPI00216134.1 | SPLICE ISOFORM 2 OF P09493 TROPOMYOSIN 1 ALPHA CHAIN. | 26549 | 4.47 | 7 | 3 | 13.66 |
| 446 | IPI00216757.1 | SPLICE ISOFORM SHORT OF P05023 SODIUM/POTASSIUM-TRANSPORTING ATPASE ALPHA-1 CHAIN PRECURSOR. | 74140 | 5.87 | 7 | 3 | 5.73 |
| 447 | IPI00216947.2 | SIMILAR TO HEAT SHOCK 70KD PROTEIN BINDING PROTEIN. | 34791 | 4.62 | 7 | 3 | 13.18 |
| 448 | IPI00217466.1 | H1 HISTONE FAMILY, MEMBER 3. | 22350 | 11.79 | 7 | 2 | 10.41 |
| 449 | IPI00217467.1 | H1 HISTONE FAMILY, MEMBER 4. | 21865 | 11.8 | 7 | 2 | 10.5 |
| 450 | IPI00217473.1 | ZETA GLOBIN. | 15637 | 8.51 | 7 | 1 | 4.93 |
| 451 | IPI00220683.1 | SPLICE ISOFORM 2 OF Q14103 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN D0. | 36272 | 8.34 | 7 | 4 | 15.48 |
| 452 | IPI00220685.1 | SPLICE ISOFORM 4 OF Q14103 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN D0. | 30672 | 8.73 | 7 | 4 | 18.12 |
| 453 | IPI00220766.1 | GLYOXALASE I. | 20720 | 5.08 | 7 | 3 | 25.54 |
| 454 | IPI00243289.4 | HYPOTHETICAL PROTEIN XP_292029. | 30355 | 5.04 | 7 | 1 | 2.6 |
| 455 | IPI00253411.2 | --none found in database-- | 38301 | 5.79 | 7 | 1 | 3.54 |
| 456 | IPI00290982.5 | DYNEIN HEAVY CHAIN, CYTOSOLIC. | 532367 | 6.36 | 7 | 5 | 1.74 |
| 457 | IPI00298289.1 | SPLICE ISOFORM 2 OF Q9NQC3 RETICULON 4. | 40318 | 4.41 | 7 | 3 | 13.67 |
| 458 | IPI00300020.3 | EXCITATORY AMINO ACID TRANSPORTER 2. | 62104 | 6.51 | 7 | 4 | 6.79 |
| 459 | IPI00328108.5 | DESMIN. | 53530 | 4.94 | 7 | 3 | 5.76 |
| 460 | IPI00328188.1 | FATTY ACID SYNTHASE. | 273427 | 6.41 | 7 | 5 | 3.03 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 461 | IPI00335276.3 | HYPOTHETICAL PROTEIN. | 43255 | 4.41 | 7 | 3 | 12.75 |
| 462 | IPI00337654.1 | PROTHYMOSIN ALPHA. | 8030 | 3.44 | 7 | 3 | 34.72 |
| 463 | IPI00374113.1 | SIMILAR TO PEPTIDYL-PRO CIS TRANS ISOMERASE. | 50546 | 8.56 | 7 | 2 | 2.79 |
| 464 | IPI00374247.1 | SIMILAR TO HEAT SHOCK PROTEIN HSP 90-BETA (HSP 84). | 11111 | 4.02 | 7 | 2 | 14.58 |
| 465 | IPI00376110.1 | SIMILAR TO RHO GDP-DISSOCIATION INHIBITOR 1 (RHO GDI 1) (RHO-GDI ALPHA). | 25377 | 6.3 | 7 | 2 | 13.9 |
| 466 | IPI00376262.1 | SIMILAR TO PEPTIDYL-PRO CIS TRANS ISOMERASE. | 27042 | 8.22 | 7 | 2 | 5.31 |
| 467 | IPI00376272.1 | SIMILAR TO CYCLOPHILIN-LC. | 23765 | 9.24 | 7 | 3 | 9.22 |
| 468 | IPI00376415.1 | SIMILAR TO PEPTIDYL-PRO CIS TRANS ISOMERASE. | 19047 | 10.51 | 7 | 2 | 7.56 |
| 469 | IPI00376771.1 | SIMILAR TO PEPTIDYL-PRO CIS TRANS ISOMERASE. | 19737 | 9.31 | 7 | 2 | 7.1 |
| 470 | IPI00382617.1 | P37 AUF1. | 31481 | 7.45 | 7 | 4 | 18.18 |
| 471 | IPI00382931.1 | PLACENTA IMMUNOREGULATORY FACTOR PLIF. | 19490 | 8.79 | 7 | 2 | 13.94 |
| 472 | IPI00386068.1 | HYPOTHETICAL PROTEIN. | 85409 | 5.16 | 7 | 5 | 7.27 |
| 473 | IPI00395343.1 | THYROID AUTOANTIGEN 70KDA (KU ANTIGEN). | 69843 | 6.61 | 7 | 6 | 12.97 |
| 474 | IPI00000230.1 | HYPOTHETICAL PROTEIN. | 34944 | 4.5 | 6 | 3 | 8.77 |
| 475 | IPI00003370.1 | SPLICE ISOFORM 1 OF Q16623 SYNTAXIN 1A. | 33023 | 4.88 | 6 | 5 | 28.13 |
| 476 | IPI00005719.1 | SPLICE ISOFORM 1 OF P11476 RAS-RELATED PROTEIN RAB-1A. | 22678 | 6 | 6 | 3 | 17.07 |
| 477 | IPI00006612.1 | CLATHRIN COAT ASSEMBLY PROTEIN AP180. | 92502 | 4.45 | 6 | 3 | 5.4 |
| 478 | IPI00008529.1 | 60S ACIDIC RIBOSOMAL PROTEIN P2. | 11665 | 4.14 | 6 | 4 | 69.57 |
| 479 | IPI00008964.1 | RAS-RELATED PROTEIN RAB-1B. | 22171 | 5.38 | 6 | 3 | 17.41 |
| 480 | IPI00009865.1 | KERATIN, TYPE I CYTOSKELETAL 10. | 59519 | 4.87 | 6 | 4 | 10.46 |
| 481 | IPI00010796.1 | PROTEIN DISULFIDE ISOMERASE PRECURSOR. | 57116 | 4.49 | 6 | 5 | 18.31 |
| 482 | IPI00011229.1 | CATHEPSIN D PRECURSOR. | 44552 | 6.5 | 6 | 4 | 11.65 |
| 483 | IPI00013991.1 | SPLICE ISOFORM 1 OF P07951 TROPOMYOSIN BETA CHAIN. | 32851 | 4.36 | 6 | 2 | 6.69 |
| 484 | IPI00014230.1 | COMPLEMENT COMPONENT 1, Q SUBCOMPONENT BINDING PROTEIN, MITOCHONDRIAL PRECURSOR. | 31362 | 4.47 | 6 | 3 | 9.57 |
| 485 | IPI00014581.1 | SPLICE ISOFORM 1 OF P09493 TROPOMYOSIN 1 ALPHA CHAIN. | 32709 | 4.39 | 6 | 3 | 9.51 |
| 486 | IPI00016513.1 | RAS-RELATED PROTEIN RAB-10. | 22541 | 8.61 | 6 | 2 | 11 |
| 487 | IPI00019888.1 | SUCCINATE SEMIALDEHYDE DEHYDROGENASE, MITOCHONDRIAL PRECURSOR. | 57215 | 8.37 | 6 | 4 | 10.09 |
| 488 | IPI00021751.2 | NEUROFILAMENT TRIPLET H PROTEIN. | 112479 | 6 | 6 | 2 | 1.36 |
| 489 | IPI00024107.1 | SPLICE ISOFORM 1 OF P37840 ALPHA-SYNUCLEIN. | 14460 | 4.37 | 6 | 2 | 13.57 |
| 490 | IPI00028196.2 | SIMILAR TO KIAA1765 PROTEIN. | 104424 | 9.71 | 6 | 2 | 3.01 |
| 491 | IPI00029091.1 | PUTATIVE NUCLEOSIDE DIPHOSPHATE KINASE. | 15529 | 8.83 | 6 | 3 | 27.01 |
| 492 | IPI00032904.1 | BETA-SYNUCLEIN. | 14288 | 4.09 | 6 | 2 | 14.18 |
| 493 | IPI00045410.2 | SIMILAR TO NUCLEOPHOSMIN 1. | 32995 | 4.34 | 6 | 2 | 6.73 |
| 494 | IPI00073958.1 | HYPOTHETICAL PROTEIN. | 18648 | 8.18 | 6 | 2 | 23.78 |
| 495 | IPI00140827.2 | SIMILAR TO SMT3 SUPPRESSOR OF MIF TWO 3 HOMOLOG 2. | 17755 | 6.25 | 6 | 2 | 13.75 |
| 496 | IPI00165028.1 | PROTHYMOSIN ALPHA. | 11349 | 3.41 | 6 | 3 | 24.76 |
| 497 | IPI00175108.2 | SIMILAR TO HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN K ISOFORM A. | 50289 | 4.89 | 6 | 3 | 6.54 |
| 498 | IPI00175156.2 | SIMILAR TO HEAT SHOCK 70KD PROTEIN BINDING PROTEIN. | 42873 | 5.05 | 6 | 3 | 10.68 |
| 499 | IPI00176998.2 | SIMILAR TO TROPOMYOSIN 3. | 28884 | 4.38 | 6 | 4 | 18.15 |
| 500 | IPI00178083.1 | HYPOTHETICAL PROTEIN FLJ35393. | 21697 | 4.51 | 6 | 4 | 24.46 |
| 501 | IPI00180954.2 | COLD-INDUCIBLE RNA-BINDING PROTEIN. | 18648 | 9.82 | 6 | 3 | 26.74 |
| 502 | IPI00185362.1 | SIMILAR TO NEURAL CELL ADHESION MOLECULE 1. | 66271 | 4.52 | 6 | 4 | 7.62 |
| 503 | IPI00215902.1 | ALDO-KETO REDUCTASE FAMILY 1, MEMBER B1. | 35853 | 6.99 | 6 | 4 | 11.71 |
| 504 | IPI00215916.1 | CYTOCHROME C. | 11749 | 10.16 | 6 | 2 | 27.62 |
| 505 | IPI00216975.1 | SPLICE ISOFORM 2 OF P07226 TROPOMYOSIN ALPHA 4 CHAIN. | 32723 | 4.38 | 6 | 2 | 6.69 |
| 506 | IPI00218467.1 | SPLICE ISOFORM 2-4 OF P37840 ALPHA-SYNUCLEIN. | 11372 | 8.88 | 6 | 2 | 16.96 |
| 507 | IPI00218667.1 | STATHMIN 2. | 24926 | 9.02 | 6 | 2 | 8.68 |
| 508 | IPI00218793.2 | PARATHYMOSIN. | 11530 | 3.83 | 6 | 3 | 22.55 |
| 509 | IPI00218820.1 | SPLICE ISOFORM 3 OF P07951 TROPOMYOSIN BETA CHAIN. | 28684 | 4.29 | 6 | 2 | 7.66 |
| 510 | IPI00220271.1 | ALDO-KETO REDUCTASE FAMILY 1, MEMBER A1. | 36573 | 6.79 | 6 | 4 | 18.46 |
| 511 | IPI00220709.3 | SPLICE ISOFORM 2 OF P07951 TROPOMYOSIN BETA CHAIN. | 32990 | 4.32 | 6 | 2 | 6.69 |
| 512 | IPI00220737.1 | SPLICE ISOFORM N-CAM 120 OF P13592 NEURAL CELL ADHESION MOLECULE 1, 120 KDA ISOFORM PRECURSOR. | 83770 | 4.5 | 6 | 4 | 6.04 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 513 | IPI00221222.1 | ACTIVATED RNA POLYMERASE II TRANSCRIPTION COFACTOR 4. | 14365 | 10.32 | 6 | 4 | 37.01 |
| 514 | IPI00258810.2 | --none found in database-- | 29189 | 9.77 | 6 | 3 | 12.02 |
| 515 | IPI00259825.2 | SIMILAR TO NUCLEOPHOSMIN 1. | 43866 | 4.97 | 6 | 2 | 4.95 |
| 516 | IPI00295684.1 | KERATIN 10. | 58827 | 4.82 | 6 | 4 | 10.62 |
| 517 | IPI00299149.1 | UBIQUITIN-LIKE PROTEIN SMT3B. | 10871 | 5.16 | 6 | 2 | 23.16 |
| 518 | IPI00302448.1 | NEURAL CELL ADHESION MOLECULE 1, 140 KDA ISOFORM PRECURSOR. | 93361 | 4.5 | 6 | 4 | 5.42 |
| 519 | IPI00332161.1 | IG GAMMA-1 CHAIN C REGION. | 36106 | 8.31 | 6 | 3 | 13.33 |
| 520 | IPI00333730.2 | --none found in database-- | 27500 | 5.01 | 6 | 3 | 19.84 |
| 521 | IPI00334144.1 | --none found in database-- | 22353 | 6.37 | 6 | 3 | 24.14 |
| 522 | IPI00334545.2 | --none found in database-- | 46431 | 4.7 | 6 | 1 | 1.68 |
| 523 | IPI00336008.1 | ALDEHYDE DEHYDROGENASE 5A1 PRECURSOR ISOFORM 1. | 58653 | 8.16 | 6 | 4 | 9.85 |
| 524 | IPI00374397.1 | SIMILAR TO TROPOMYOSIN 4. | 24982 | 4.87 | 6 | 2 | 8.84 |
| 525 | IPI00374519.1 | SIMILAR TO RAB1B, MEMBER RAS ONCOGENE FAMILY. | 22017 | 5.05 | 6 | 3 | 17.41 |
| 526 | IPI00374689.1 | SIMILAR TO ATP-DEPENDENT DNA HELICASE II, 70 KDA SUBUNIT (LUPUS KU AUTOANTIGEN PROTEIN P70) (KU70) (70 KDA SUBUNIT OF KU ANTIGEN) (THYROID-LUPUS AUTOANTIGEN) (TLAA) (CTC BOX BINDING FACTOR 75 KDA SUBUNIT) (CTCBF) (CTC75). | 54430 | 8.87 | 6 | 5 | 13.68 |
| 527 | IPI00375315.1 | SIMILAR TO HEAT SHOCK PROTEIN HSP 90-ALPHA (HSP 86). | 19507 | 4.44 | 6 | 2 | 12.2 |
| 528 | IPI00376005.1 | EUKARYOTIC INITIATION FACTOR 5A ISOFORM I VARIANT A. | 20170 | 7.02 | 6 | 3 | 25.54 |
| 529 | IPI00376012.1 | SIMILAR TO HYPOTHETICAL PROTEIN MGC37309. | 23413 | 9.19 | 6 | 3 | 11.66 |
| 530 | IPI00376379.1 | KERATIN 1B. | 61801 | 5.78 | 6 | 1 | 2.08 |
| 531 | IPI00376794.1 | SIMILAR TO THYMOSIN-LIKE 4. | 13915 | 4.7 | 6 | 1 | 4.8 |
| 532 | IPI00383445.1 | SIMILAR TO APOBEC-1 COMPLEMENTATION FACTOR. | 46268 | 9.19 | 6 | 3 | 8.29 |
| 533 | IPI00384938.1 | HYPOTHETICAL PROTEIN DKFZP686N02209. | 52852 | 8.61 | 6 | 3 | 9.13 |
| 534 | IPI00385332.1 | HYPOTHETICAL PROTEIN. | 51204 | 8.28 | 6 | 3 | 9.36 |
| 535 | IPI00385621.1 | PROTHYMOSIN ALPHA. | 11679 | 3.46 | 6 | 3 | 24.3 |
| 536 | IPI00386314.1 | FLJ00064 PROTEIN. | 30383 | 5.38 | 6 | 3 | 22.1 |
| 537 | IPI00395322.1 | EUKARYOTIC TRANSLATION INITIATION FACTOR 5A. | 16701 | 4.86 | 6 | 3 | 30.72 |
| 538 | IPI00395738.1 | --none found in database-- | 18721 | 9.95 | 6 | 3 | 26.59 |
| 539 | IPI00395871.1 | HUMAN FULL-LENGTH CDNA CLONE CS0DA009YK08 OF NEUROBLASTOMA OF HOMO SAPIENS. | 25230 | 4.35 | 6 | 4 | 21.24 |
| 540 | IPI00001593.1 | LYSOSOMAL PRO-X CARBOXYPEPTIDASE PRECURSOR. | 55800 | 7.23 | 5 | 3 | 9.88 |
| 541 | IPI00002966.1 | HEAT SHOCK 70 KDA PROTEIN 4. | 94300 | 4.9 | 5 | 3 | 5.6 |
| 542 | IPI00003925.3 | PYRUVATE DEHYDROGENASE E1 COMPONENT BETA SUBUNIT, MITOCHONDRIAL PRECURSOR. | 39219 | 6.63 | 5 | 4 | 14.21 |
| 543 | IPI00005089.1 | NEURONAL TROPOMODULIN. | 39595 | 4.93 | 5 | 2 | 7.41 |
| 544 | IPI00007102.1 | CGI-150 PROTEIN. | 55012 | 8.86 | 5 | 4 | 11.9 |
| 545 | IPI00008994.2 | SPLICE ISOFORM 1 OF Q9UN36 NDRG2 PROTEIN. | 40798 | 4.87 | 5 | 5 | 21.56 |
| 546 | IPI00009476.2 | SPLICE ISOFORM C OF P13592 NEURAL CELL ADHESION MOLECULE 1, 120 KDA ISOFORM PRECURSOR. | 83985 | 4.6 | 5 | 3 | 4.34 |
| 547 | IPI00011134.1 | HEAT SHOCK 70 KDA PROTEIN 7. | 26907 | 7.62 | 5 | 2 | 11.74 |
| 548 | IPI00011515.1 | PROTEIN KINASE C AND CASEIN KINASE SUBSTRATE IN NEURONS PROTEIN 1. | 50966 | 4.89 | 5 | 3 | 8.56 |
| 549 | IPI00012074.1 | HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN R. | 70943 | 8.32 | 5 | 4 | 7.9 |
| 550 | IPI00012503.1 | SPLICE ISOFORM SAP-MU-0 OF P07602 PROACTIVATOR POLYPEPTIDE PRECURSOR [Contains: SAPOSIN A (PROTEIN A); SAPOSIN B (SPHINGOLIPID ACTIVATOR PROTEIN 1) (SAP-1) (CEREBROSIDE SULFATE ACTIVATOR) (CSACT) (DISPERSIN) (SULFATIDE/GM1 ACTIVATOR); SAPOSIN C (CO-BETA-G | 58113 | 4.82 | 5 | 3 | 6.68 |
| 551 | IPI00013004.1 | SPLICE ISOFORM 1 OF O00764 PYRIDOXAL KINASE. | 35102 | 6.05 | 5 | 2 | 10.26 |
| 552 | IPI00013894.1 | STRESS-INDUCED-PHOSPHOPROTEIN 1. | 62639 | 6.78 | 5 | 3 | 7.73 |
| 553 | IPI00018853.1 | TROPOMYOSIN ISOFORM. | 28420 | 4.59 | 5 | 2 | 7.82 |
| 554 | IPI00022799.1 | SPLICE ISOFORM 2 OF P55087 AQUAPORIN 4. | 34830 | 7.75 | 5 | 3 | 11.15 |
| 555 | IPI00026781.1 | FATTY ACID SYNTHASE (EC 2.3.1.85) [Includes: EC 2.3.1.38; EC 2.3.1.39; EC 2.3.1.41; EC 1.1.1.100; EC 4.2.1.61; EC 1.3.1.10; EC 3.1.2.14]. | 273102 | 6.64 | 5 | 3 | 1.68 |
| 556 | IPI00027117.1 | SIMILAR TO RAN-SPECIFIC GTPASE-ACTIVATING PROTEIN (RAN BINDING PROTEIN 1) (RANBP1). | 23351 | 4.87 | 5 | 2 | 10.95 |
| 557 | IPI00027569.1 | HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN C-LIKE DJ845O24.4. | 32142 | 4.67 | 5 | 3 | 11.6 |
| 558 | IPI00027834.1 | HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN L. | 60187 | 7.13 | 5 | 4 | 8.24 |
| 559 | IPI00028946.1 | RETICULON PROTEIN 3. | 25609 | 8.76 | 5 | 1 | 4.66 |
| 560 | IPI00032458.4 | SIMILAR TO SODIUM/POTASSIUM-TRANSPORTING ATPASE ALPHA-4 CHAIN (SODIUM PUMP 4) (NA+/K+ ATPASE 4). | 110885 | 5.62 | 5 | 2 | 2.4 |
| 561 | IPI00032575.1 | HYPOTHETICAL PROTEIN. | 34793 | 5.28 | 5 | 4 | 19.17 |
| 562 | IPI00033600.1 | YEAST SDS22 HOMOLOG. | 41564 | 4.55 | 5 | 2 | 8.06 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 563 | IPI00064001.2 | --none found in database-- | 26127 | 8.44 | 5 | 1 | 5.53 |
| 564 | IPI00073603.2 | SIMILAR TO PEPTIDYL-PRO CIS TRANS ISOMERASE. | 23310 | 7.93 | 5 | 3 | 8.65 |
| 565 | IPI00076129.3 | --none found in database-- | 38230 | 5.25 | 5 | 2 | 6.48 |
| 566 | IPI00106604.3 | SIMILAR TO PEPTIDYL-PRO CIS TRANS ISOMERASE. | 19225 | 8.5 | 5 | 2 | 6.11 |
| 567 | IPI00161971.1 | HYPOTHETICAL PROTEIN. | 10870 | 5.73 | 5 | 1 | 12.63 |
| 568 | IPI00165677.1 | DJ681N20.2 (NOVEL PROTEIN SIMILAR TO FERRITIN, LIGHT POLYPEPTIDE. | 20075 | 5.56 | 5 | 3 | 22.86 |
| 569 | IPI00168728.1 | FLJ00385 PROTEIN. | 56111 | 7.64 | 5 | 2 | 5.89 |
| 570 | IPI00177423.2 | SIMILAR TO RETICULON PROTEIN 3 (NEUROENDOCRINE-SPECIFIC PROTEIN-LIKE 2) (NSP-LIKE PROTEIN II) (NSPLII). | 25523 | 8.76 | 5 | 1 | 4.66 |
| 571 | IPI00186711.2 | SIMILAR TO PLECTIN 1, INTERMEDIATE FILAMENT BINDING PROTEIN, 500KD. | 531990 | 5.76 | 5 | 5 | 1.3 |
| 572 | IPI00215884.1 | SPLICING FACTOR, ARGININE/SERINE-RICH 1 (SPLICING FACTOR 2, ALTERNATE SPLICING FACTOR). | 27745 | 10.77 | 5 | 4 | 16.53 |
| 573 | IPI00215914.1 | ADP-RIBOSYLATION FACTOR 1. | 20697 | 6.8 | 5 | 2 | 19.89 |
| 574 | IPI00215917.1 | ADP-RIBOSYLATION FACTOR 3. | 20601 | 7.6 | 5 | 2 | 19.89 |
| 575 | IPI00216135.1 | SPLICE ISOFORM 3 OF P09493 TROPOMYOSIN 1 ALPHA CHAIN. | 32876 | 4.42 | 5 | 2 | 6.69 |
| 576 | IPI00216320.1 | SPLICE ISOFORM 2 OF O00764 PYRIDOXAL KINASE. | 31808 | 5.82 | 5 | 2 | 11.27 |
| 577 | IPI00216393.1 | SPLICE ISOFORM NON-BRAIN OF P09496 CLATHRIN LIGHT CHAIN A. | 23662 | 4.17 | 5 | 4 | 20.64 |
| 578 | IPI00217903.2 | SIMILAR TO TUBULIN BETA. | 21641 | 4.54 | 5 | 2 | 12.77 |
| 579 | IPI00218108.1 | SPLICE ISOFORM 2 OF Q9UN36 NDRG2 PROTEIN. | 39289 | 5.05 | 5 | 5 | 22.41 |
| 580 | IPI00218109.1 | SPLICE ISOFORM 3 OF Q9UN36 NDRG2 PROTEIN. | 39679 | 5.06 | 5 | 5 | 22.22 |
| 581 | IPI00218591.1 | SPLICE ISOFORM ASF-2 OF Q07955 SPLICING FACTOR, ARGININE/SERINE-RICH 1. | 31868 | 5.7 | 5 | 4 | 14.09 |
| 582 | IPI00218592.1 | SPLICE ISOFORM ASF-3 OF Q07955 SPLICING FACTOR, ARGININE/SERINE-RICH 1. | 22329 | 8.16 | 5 | 4 | 20.5 |
| 583 | IPI00218919.1 | ATPASE, H+/K+ EXCHANGING, ALPHA POLYPEPTIDE. | 114091 | 5.54 | 5 | 2 | 2.71 |
| 584 | IPI00219824.1 | SPLICE ISOFORM SAP-MU-6 OF P07602 PROACTIVATOR POLYPEPTIDE PRECURSOR [Contains: SAPOSIN A (PROTEIN A); SAPOSIN B (SPHINGOLIPID ACTIVATOR PROTEIN 1) (SAP-1) (CEREBROSIDE SULFATE ACTIVATOR) (CSACT) (DISPERSIN) (SULFATIDE/GM1 ACTIVATOR); SAPOSIN C (CO-BETA-G | 58356 | 4.77 | 5 | 3 | 6.65 |
| 585 | IPI00219825.1 | SPLICE ISOFORM SAP-MU-9 OF P07602 PROACTIVATOR POLYPEPTIDE PRECURSOR [Contains: SAPOSIN A (PROTEIN A); SAPOSIN B (SPHINGOLIPID ACTIVATOR PROTEIN 1) (SAP-1) (CEREBROSIDE SULFATE ACTIVATOR) (CSACT) (DISPERSIN) (SULFATIDE/GM1 ACTIVATOR); SAPOSIN C (CO-BETA-G | 58484 | 4.77 | 5 | 3 | 6.64 |
| 586 | IPI00221098.1 | SPLICE ISOFORM 2 OF Q16623 SYNTAXIN 1A. | 29632 | 4.54 | 5 | 4 | 25.77 |
| 587 | IPI00221099.1 | SPLICE ISOFORM 3 OF Q16623 SYNTAXIN 1A. | 28995 | 5.2 | 5 | 4 | 26.69 |
| 588 | IPI00221189.1 | SPLICE ISOFORM 1 OF P55087 AQUAPORIN 4. | 32300 | 6.86 | 5 | 3 | 11.96 |
| 589 | IPI00239077.1 | HISTIDINE TRIAD NUCLEOTIDE BINDING PROTEIN 1. | 13802 | 6.96 | 5 | 2 | 34.92 |
| 590 | IPI00239540.2 | --none found in database-- | 36517 | 4.73 | 5 | 1 | 2.14 |
| 591 | IPI00243604.2 | SIMILAR TO HEAT SHOCK 70KD PROTEIN BINDING PROTEIN. | 34413 | 4.9 | 5 | 2 | 7.47 |
| 592 | IPI00247185.2 | --none found in database-- | 30007 | 9.92 | 5 | 3 | 12.69 |
| 593 | IPI00247776.2 | SIMILAR TO GLUTAMINE SYNTHETASE (GLUTAMATE--AMMONIA LIGASE). | 36070 | 6.44 | 5 | 2 | 6.01 |
| 594 | IPI00256777.2 | --none found in database-- | 12235 | 8.23 | 5 | 2 | 10.81 |
| 595 | IPI00259350.2 | SIMILAR TO ACONITASE 2. | 84975 | 6.98 | 5 | 2 | 3.9 |
| 596 | IPI00259901.2 | SIMILAR TO PEPTIDYLPROLYL ISOMERASE A (CYCLOPHILIN A). | 49928 | 9.15 | 5 | 2 | 7.62 |
| 597 | IPI00296039.5 | SPLICE ISOFORM 4 OF P09493 TROPOMYOSIN 1 ALPHA CHAIN. | 32848 | 4.4 | 5 | 2 | 6.69 |
| 598 | IPI00299147.4 | UBIQUITIN-LIKE PROTEIN SMT3A. | 14817 | 7.62 | 5 | 1 | 8.96 |
| 599 | IPI00301563.3 | RAN-SPECIFIC GTPASE-ACTIVATING PROTEIN. | 28792 | 8.49 | 5 | 2 | 8.73 |
| 600 | IPI00305457.3 | ALPHA-1-ANTITRYPSIN PRECURSOR. | 46737 | 5.31 | 5 | 4 | 15.31 |
| 601 | IPI00333204.1 | --none found in database-- | 45209 | 5 | 5 | 2 | 5.54 |
| 602 | IPI00333592.1 | --none found in database-- | 84896 | 6.47 | 5 | 3 | 5.61 |
| 603 | IPI00333982.2 | HUMAN FULL-LENGTH CDNA CLONE CS0DI019YF20 OF PLACENTA OF HOMO SAPIENS. | 57486 | 8.05 | 5 | 2 | 5.75 |
| 604 | IPI00375339.2 | SPLICE ISOFORM 1 OF Q13733 SODIUM/POTASSIUM-TRANSPORTING ATPASE ALPHA-4 CHAIN. | 114166 | 6.61 | 5 | 2 | 2.33 |
| 605 | IPI00375381.1 | --none found in database-- | 20961 | 4.8 | 5 | 1 | 6.01 |
| 606 | IPI00376170.1 | SIMILAR TO PEPTIDYL-PRO CIS TRANS ISOMERASE. | 19942 | 6.85 | 5 | 2 | 10.33 |
| 607 | IPI00376651.1 | SIMILAR TO SMT3 SUPPRESSOR OF MIF TWO 3 HOMOLOG 2. | 10814 | 7.52 | 5 | 1 | 12.63 |
| 608 | IPI00377005.1 | --none found in database-- | 28823 | 4.45 | 5 | 3 | 13.77 |
| 609 | IPI00382606.1 | FACTOR VII ACTIVE SITE MUTANT IMMUNOCONJUGATE. | 75553 | 7.01 | 5 | 2 | 4.42 |
| 610 | IPI00383556.1 | HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN UP2. | 24198 | 7.93 | 5 | 3 | 20.44 |
| 611 | IPI00383795.1 | MUTANT BETA-GLOBIN. | 1952 | 7.36 | 5 | 1 | 44.44 |
| 612 | IPI00383842.1 | HYPOTHETICAL PROTEIN. | 18605 | 9.11 | 5 | 1 | 9.09 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 613 | IPI00384653.1 | PROTHYMOSIN A14. | 11058 | 3.41 | 5 | 2 | 10.89 |
| 614 | IPI00395700.1 | --none found in database-- | 78434 | 9.06 | 5 | 3 | 6.13 |
| 615 | IPI00395771.1 | PROTEIN PHOSPHATASE-1 REGULATORY SUBUNIT 7 ALPHA2. | 36837 | 4.85 | 5 | 2 | 9.15 |
| 616 | IPI00395912.1 | HYPOTHETICAL PROTEIN. | 57156 | 7.76 | 5 | 2 | 5.76 |
| 617 | IPI00396462.1 | --none found in database-- | 20500 | 5.39 | 5 | 2 | 6.88 |
| 618 | IPI00003971.1 | SPLICE ISOFORM RTN1-A OF Q16799 RETICULON 1. | 83618 | 4.33 | 4 | 2 | 2.32 |
| 619 | IPI00004618.1 | IG GAMMA-4 CHAIN C REGION. | 35941 | 7.41 | 4 | 1 | 4.89 |
| 620 | IPI00005981.1 | NEURONAL PROTEIN. | 31454 | 8 | 4 | 3 | 14.89 |
| 621 | IPI00007346.1 | PEPTIDYL-PROLYL CIS-TRANS ISOMERASE H. | 19208 | 8.22 | 4 | 1 | 3.39 |
| 622 | IPI00007812.1 | VACUOLAR ATP SYNTHASE SUBUNIT B, BRAIN ISOFORM. | 56501 | 5.55 | 4 | 4 | 13.11 |
| 623 | IPI00009790.1 | 6-PHOSPHOFRUCTOKINASE, TYPE C. | 85596 | 7.6 | 4 | 3 | 4.46 |
| 624 | IPI00011454.1 | GLUCOSIDASE II ALPHA SUBUNIT. | 109438 | 6.18 | 4 | 4 | 7.04 |
| 625 | IPI00013164.1 | PERIPHERIN. | 53878 | 5.22 | 4 | 2 | 4.03 |
| 626 | IPI00014263.1 | SPLICE ISOFORM LONG OF Q15056 EUKARYOTIC TRANSLATION INITIATION FACTOR 4H. | 27385 | 7.36 | 4 | 2 | 16.94 |
| 627 | IPI00014587.1 | SPLICE ISOFORM BRAIN OF P09496 CLATHRIN LIGHT CHAIN A. | 27077 | 4.15 | 4 | 3 | 9.68 |
| 628 | IPI00014898.1 | SPLICE ISOFORM 1 OF Q15149 PLECTIN 1. | 531737 | 5.74 | 4 | 4 | 0.98 |
| 629 | IPI00016666.1 | METALLOTHIONEIN-III. | 6927 | 4.5 | 4 | 2 | 47.06 |
| 630 | IPI00016832.1 | SPLICE ISOFORM SHORT OF P25786 PROTEASOME SUBUNIT ALPHA TYPE 1. | 29556 | 6.6 | 4 | 3 | 15.21 |
| 631 | IPI00017763.3 | NUCLEOSOME ASSEMBLY PROTEIN 1-LIKE 4. | 42823 | 4.32 | 4 | 2 | 7.47 |
| 632 | IPI00018067.1 | SYNTAXIN 1B. | 33431 | 5.74 | 4 | 3 | 13.54 |
| 633 | IPI00019376.1 | HYPOTHETICAL PROTEIN FLJ10849. | 49398 | 6.8 | 4 | 4 | 9.32 |
| 634 | IPI00019755.1 | GLUTATHIONE TRANSFERASE OMEGA 1. | 27566 | 6.54 | 4 | 2 | 9.13 |
| 635 | IPI00019952.1 | NEURONAL MEMBRANE GLYCOPROTEIN M6-A. | 31210 | 4.95 | 4 | 1 | 5.04 |
| 636 | IPI00021840.1 | 40S RIBOSOMAL PROTEIN S6. | 28681 | 11.52 | 4 | 3 | 9.24 |
| 637 | IPI00022640.1 | NEUROGRANIN. | 7618 | 8.06 | 4 | 2 | 19.23 |
| 638 | IPI00023860.1 | NUCLEOSOME ASSEMBLY PROTEIN 1-LIKE 1. | 45374 | 4.09 | 4 | 2 | 6.91 |
| 639 | IPI00024129.1 | PEPTIDYL-PROLYL CIS-TRANS ISOMERASE C. | 22763 | 8.69 | 4 | 1 | 2.83 |
| 640 | IPI00024993.1 | ENOYL-COA HYDRATASE, MITOCHONDRIAL PRECURSOR. | 31371 | 8.19 | 4 | 3 | 18.28 |
| 641 | IPI00025491.1 | EUKARYOTIC INITIATION FACTOR 4A-I. | 46154 | 5.12 | 4 | 4 | 11.08 |
| 642 | IPI00026154.1 | PROTEIN KINASE C SUBSTRATE, 80 KDA PROTEIN, HEAVY CHAIN. | 59296 | 4.05 | 4 | 3 | 5.88 |
| 643 | IPI00026268.1 | GUANINE NUCLEOTIDE-BINDING PROTEIN G(I)/G(S)/G(T) BETA SUBUNIT 1. | 37377 | 5.85 | 4 | 3 | 11.47 |
| 644 | IPI00029623.1 | PROTEASOME SUBUNIT ALPHA TYPE 6. | 27399 | 6.74 | 4 | 3 | 14.23 |
| 645 | IPI00029631.1 | ENHANCER OF RUDIMENTARY HOMOLOG. | 12259 | 5.72 | 4 | 1 | 10.58 |
| 646 | IPI00031141.1 | 40S RIBOSOMAL PROTEIN SA. | 32854 | 4.51 | 4 | 3 | 16.95 |
| 647 | IPI00031169.1 | RAS-RELATED PROTEIN RAB-2A. | 23546 | 6.51 | 4 | 3 | 19.81 |
| 648 | IPI00031820.1 | PHENYLALANYL-TRNA SYNTHETASE ALPHA CHAIN. | 57564 | 7.96 | 4 | 2 | 4.92 |
| 649 | IPI00032230.2 | SPLICE ISOFORM A OF Q9Y2J2 BAND 4.1-LIKE PROTEIN 3. | 120678 | 4.84 | 4 | 3 | 3.5 |
| 650 | IPI00032256.1 | ALPHA-2-MACROGLOBULIN PRECURSOR. | 163278 | 6.39 | 4 | 4 | 3.19 |
| 651 | IPI00032808.1 | RAS-RELATED PROTEIN RAB-3D. | 24267 | 4.53 | 4 | 2 | 11.87 |
| 652 | IPI00061114.1 | RAS-RELATED PROTEIN RAB-3C. | 25952 | 4.85 | 4 | 2 | 11.45 |
| 653 | IPI00062037.1 | SIMILAR TO RIKEN CDNA 6720463E02 GENE. | 10350 | 7.5 | 4 | 3 | 42.7 |
| 654 | IPI00107552.1 | SIMILAR TO HEAT SHOCK 70KD PROTEIN BINDING PROTEIN. | 41305 | 4.98 | 4 | 2 | 7.05 |
| 655 | IPI00147581.1 | SIMILAR TO PEPTIDYLPROLYL ISOMERASE A (CYCLOPHILIN A). | 19853 | 9.05 | 4 | 2 | 6.67 |
| 656 | IPI00157890.1 | SIMILAR TO PEPTIDYLPROLYL ISOMERASE A. | 17712 | 6.14 | 4 | 2 | 7.55 |
| 657 | IPI00159927.1 | NEUROCAN CORE PROTEIN PRECURSOR. | 142973 | 5.03 | 4 | 1 | 1.59 |
| 658 | IPI00164538.1 | --none found in database-- | 15558 | 6.02 | 4 | 1 | 7.35 |
| 659 | IPI00167953.3 | BTB AND KELCH DOMAIN CONTAINING 3. | 69839 | 5 | 4 | 1 | 1.14 |
| 660 | IPI00173720.2 | --none found in database-- | 18469 | 7.97 | 4 | 1 | 3.59 |
| 661 | IPI00182986.3 | SIMILAR TO HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN C (C1/C2). | 32215 | 4.53 | 4 | 2 | 7.51 |
| 662 | IPI00183968.1 | HYPOTHETICAL PROTEIN FLJ35371. | 28223 | 4.41 | 4 | 3 | 11.52 |
| 663 | IPI00184471.2 | SIMILAR TO DESTRIN - PIG. | 11561 | 4.95 | 4 | 2 | 20.39 |
| 664 | IPI00215716.1 | SPLICE ISOFORM B OF Q9Y2J2 BAND 4.1-LIKE PROTEIN 3. | 96514 | 5.1 | 4 | 3 | 4.62 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 665 | IPI00215780.1 | 40S RIBOSOMAL PROTEIN S19. | 21585 | 11.6 | 4 | 3 | 16.24 |
| 666 | IPI00215942.1 | SPLICE ISOFORM 2 OF Q15149 PLECTIN 1. | 518447 | 5.46 | 4 | 4 | 1.01 |
| 667 | IPI00215943.1 | SPLICE ISOFORM 3 OF Q15149 PLECTIN 1. | 518006 | 5.45 | 4 | 4 | 1.01 |
| 668 | IPI00217296.1 | SPLICE ISOFORM 3 OF Q15257 PROTEIN PHOSPHATASE 2A, REGULATORY SUBUNIT B'. | 33481 | 6.24 | 4 | 2 | 7.14 |
| 669 | IPI00217872.1 | SPLICE ISOFORM 2 OF P36871 PHOSPHOGLUCOMUTASE. | 61928 | 5.72 | 4 | 3 | 7.79 |
| 670 | IPI00217966.1 | LACTATE DEHYDROGENASE A. | 36689 | 8.45 | 4 | 3 | 9.94 |
| 671 | IPI00218491.1 | SPLICE ISOFORM LONG OF P25786 PROTEASOME SUBUNIT ALPHA TYPE 1. | 30239 | 7 | 4 | 3 | 14.87 |
| 672 | IPI00218493.1 | HYPOXANTHINE PHOSPHORIBOSYLTRANSFERASE 1. | 24579 | 6.67 | 4 | 2 | 10.55 |
| 673 | IPI00218728.1 | PLATELET-ACTIVATING FACTOR ACETYLHYDROLASE, ISOFORM IB, ALPHA SUBUNIT (45KD). | 46638 | 7.4 | 4 | 3 | 8.54 |
| 674 | IPI00219328.1 | SPLICE ISOFORM 3 OF Q12906 INTERLEUKIN ENHANCER-BINDING FACTOR 3. | 82848 | 8.26 | 4 | 3 | 4.58 |
| 675 | IPI00219329.1 | SPLICE ISOFORM 4 OF Q12906 INTERLEUKIN ENHANCER-BINDING FACTOR 3. | 75554 | 8.58 | 4 | 3 | 5.01 |
| 676 | IPI00219330.1 | SPLICE ISOFORM 5 OF Q12906 INTERLEUKIN ENHANCER-BINDING FACTOR 3. | 74653 | 8.37 | 4 | 3 | 5.07 |
| 677 | IPI00219525.3 | PHOSPHOGLUCONATE DEHYDROGENASE. | 53140 | 7.25 | 4 | 3 | 8.49 |
| 678 | IPI00219526.2 | SPLICE ISOFORM 1 OF P36871 PHOSPHOGLUCOMUTASE. | 61318 | 6.73 | 4 | 3 | 7.84 |
| 679 | IPI00220894.1 | SPLICE ISOFORM SHORT OF Q15056 EUKARYOTIC TRANSLATION INITIATION FACTOR 4H. | 25200 | 8.41 | 4 | 2 | 18.42 |
| 680 | IPI00221136.3 | GLIA MATURATION FACTOR BETA. | 16992 | 6 | 4 | 2 | 18.62 |
| 681 | IPI00243423.1 | SIMILAR TO PEPTIDYL-PRO CIS TRANS ISOMERASE. | 17570 | 8.61 | 4 | 2 | 7.5 |
| 682 | IPI00248321.4 | SIMILAR TO PEPTIDYLPROLYL ISOMERASE A (CYCLOPHILIN A). | 23482 | 7.96 | 4 | 3 | 17.76 |
| 683 | IPI00258866.2 | SIMILAR TO GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER (GAPDH). | 76394 | 4.74 | 4 | 1 | 2.01 |
| 684 | IPI00293102.3 | SPLICE ISOFORM 2 OF Q15257 PROTEIN PHOSPHATASE 2A, REGULATORY SUBUNIT B'. | 40682 | 5.8 | 4 | 2 | 5.87 |
| 685 | IPI00298788.3 | SPLICE ISOFORM 1 OF Q12906 INTERLEUKIN ENHANCER-BINDING FACTOR 3. | 95384 | 9.02 | 4 | 3 | 3.91 |
| 686 | IPI00298789.1 | SPLICE ISOFORM 2 OF Q12906 INTERLEUKIN ENHANCER-BINDING FACTOR 3. | 76079 | 7.81 | 4 | 3 | 4.99 |
| 687 | IPI00300562.2 | RAS-RELATED PROTEIN RAB-3B. | 24758 | 4.61 | 4 | 2 | 11.87 |
| 688 | IPI00301364.2 | S-PHASE KINASE-ASSOCIATED PROTEIN 1A ISOFORM B. | 18658 | 4.15 | 4 | 2 | 15.95 |
| 689 | IPI00301975.1 | PLACENTAL RIBONUCLEASE INHIBITOR. | 49842 | 4.44 | 4 | 2 | 8.04 |
| 690 | IPI00328127.4 | VESICLE-ASSOCIATED MEMBRANE PROTEIN 2. | 12518 | 8.48 | 4 | 2 | 28.7 |
| 691 | IPI00328328.2 | EUKARYOTIC INITIATION FACTOR 4A-II. | 46394 | 5.13 | 4 | 4 | 11.06 |
| 692 | IPI00333105.1 | --none found in database-- | 33270 | 8.54 | 4 | 3 | 8.9 |
| 693 | IPI00333411.5 | SPLICE ISOFORM 1 OF Q15257 PROTEIN PHOSPHATASE 2A, REGULATORY SUBUNIT B'. | 36789 | 6.25 | 4 | 2 | 6.5 |
| 694 | IPI00334738.1 | --none found in database-- | 21933 | 6.1 | 4 | 2 | 13.33 |
| 695 | IPI00374056.1 | SIMILAR TO FERRITIN HEAVY CHAIN (FERRITIN H SUBUNIT). | 23034 | 7.28 | 4 | 1 | 4.93 |
| 696 | IPI00376109.1 | SIMILAR TO PROLYL 4-HYDROXYLASE, BETA SUBUNIT. | 69727 | 4.74 | 4 | 3 | 7.96 |
| 697 | IPI00376531.1 | SIMILAR TO PEPTIDYL-PRO CIS TRANS ISOMERASE. | 16359 | 9.41 | 4 | 2 | 8.05 |
| 698 | IPI00376539.1 | SIMILAR TO PEPTIDYL-PRO CIS TRANS ISOMERASE. | 12140 | 8.76 | 4 | 1 | 5.31 |
| 699 | IPI00376592.1 | SIMILAR TO TUC-4B. | 16598 | 9.15 | 4 | 1 | 7.74 |
| 700 | IPI00382995.1 | CYTOPLASMIC PROTEIN NDR1. | 39531 | 7.02 | 4 | 4 | 15.73 |
| 701 | IPI00383020.1 | SIMILAR TO 6-PHOSPHOGLUCONOLACTONASE. | 20237 | 10.32 | 4 | 2 | 22 |
| 702 | IPI00383111.1 | KERATIN 10. | 57247 | 4.72 | 4 | 2 | 5.53 |
| 703 | IPI00383182.1 | PP3895. | 14799 | 8.61 | 4 | 2 | 23.7 |
| 704 | IPI00383581.1 | ALPHA GLUCOSIDASE II ALPHA SUBUNIT. | 106874 | 6.06 | 4 | 4 | 7.2 |
| 705 | IPI00383751.1 | CALRETICULIN=CALCIUM BINDING PROTEIN. | 24455 | 4.17 | 4 | 2 | 19.16 |
| 706 | IPI00386819.1 | VACUOLAR ATP SYNTHASE CATALYTIC SUBUNIT A, OSTEOCLAST ISOFORM. | 68178 | 4.91 | 4 | 1 | 2.44 |
| 707 | IPI00395027.1 | CHONDROITIN SULFATE PROTEOGLYCAN BEHAB/BREVICAN. | 71671 | 4.11 | 4 | 2 | 3.13 |
| 708 | IPI00395742.1 | --none found in database-- | 40316 | 7.22 | 4 | 4 | 15.47 |
| 709 | IPI00395884.1 | --none found in database-- | 22145 | 9.15 | 4 | 2 | 10.61 |
| 710 | IPI00000861.1 | LIM AND SH3 DOMAIN PROTEIN 1. | 29717 | 7.07 | 3 | 3 | 13.79 |
| 711 | IPI00003348.1 | GUANINE NUCLEOTIDE-BINDING PROTEIN G(I)/G(S)/G(T) BETA SUBUNIT 2. | 37331 | 5.85 | 3 | 2 | 6.18 |
| 712 | IPI00003420.1 | T-CELL ACTIVATION PROTEIN. | 37031 | 5.28 | 3 | 1 | 3.06 |
| 713 | IPI00003856.1 | VACUOLAR ATP SYNTHASE SUBUNIT E. | 26145 | 8.37 | 3 | 1 | 6.19 |
| 714 | IPI00004902.1 | ELECTRON TRANSFER FLAVOPROTEIN BETA-SUBUNIT. | 27844 | 8.31 | 3 | 3 | 12.55 |
| 715 | IPI00005705.1 | SPLICE ISOFORM GAMMA-1 OF P36873 SERINE/THREONINE PROTEIN PHOSPHATASE PP1-GAMMA CATALYTIC SUBUNIT. | 36984 | 6.5 | 3 | 2 | 10.84 |
| 716 | IPI00005978.1 | SPLICING FACTOR, ARGININE/SERINE-RICH 2. | 25575 | 12.38 | 3 | 2 | 14.93 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 717 | IPI00006935.1 | EUKARYOTIC TRANSLATION INITIATION FACTOR 5AII. | 16793 | 5.28 | 3 | 1 | 7.84 |
| 718 | IPI00006980.1 | PROTEIN C14ORF166. | 28068 | 6.64 | 3 | 2 | 11.48 |
| 719 | IPI00008161.2 | POTASSIUM-TRANSPORTING ATPASE ALPHA CHAIN 2. | 115899 | 6.52 | 3 | 1 | 1.25 |
| 720 | IPI00008274.1 | ADENYLYL CYCLASE-ASSOCIATED PROTEIN. | 51673 | 8.2 | 3 | 3 | 6.95 |
| 721 | IPI00008453.1 | CORONIN 1C. | 53249 | 7.09 | 3 | 2 | 8.86 |
| 722 | IPI00008586.1 | NEUROGLYCAN C. | 57025 | 4.01 | 3 | 1 | 2.41 |
| 723 | IPI00009032.1 | LUPUS LA PROTEIN. | 46837 | 7.14 | 3 | 2 | 7.6 |
| 724 | IPI00010204.1 | SPLICE ISOFORM LONG OF P23152 SPLICING FACTOR, ARGININE/SERINE-RICH 3. | 19330 | 12.14 | 3 | 2 | 15.85 |
| 725 | IPI00010470.1 | SPLICE ISOFORM SNAP-25B OF P13795 SYNAPTOSOMAL-ASSOCIATED PROTEIN 25. | 23315 | 4.39 | 3 | 2 | 10.68 |
| 726 | IPI00010740.1 | SPLICE ISOFORM LONG OF P23246 SPLICING FACTOR, PROLINE-AND GLUTAMINE-RICH. | 76149 | 9.95 | 3 | 2 | 4.53 |
| 727 | IPI00011200.2 | D-3-PHOSPHOGLYCERATE DEHYDROGENASE. | 56650 | 6.7 | 3 | 3 | 7.88 |
| 728 | IPI00011253.1 | 40S RIBOSOMAL PROTEIN S3. | 26688 | 10.26 | 3 | 2 | 10.7 |
| 729 | IPI00012493.1 | 40S RIBOSOMAL PROTEIN S20. | 13373 | 10.71 | 3 | 2 | 19.33 |
| 730 | IPI00013043.1 | 25 KDA BRAIN-SPECIFIC PROTEIN. | 23694 | 10.12 | 3 | 1 | 7.31 |
| 731 | IPI00015473.3 | EXCITATORY AMINO ACID TRANSPORTER 1. | 59572 | 8.69 | 3 | 1 | 2.21 |
| 732 | IPI00016342.1 | RAS-RELATED PROTEIN RAB-7. | 23490 | 6.59 | 3 | 3 | 18.36 |
| 733 | IPI00016786.1 | SPLICE ISOFORM 2 OF P21181 CELL DIVISION CONTROL PROTEIN 42 HOMOLOG. | 21259 | 6.51 | 3 | 3 | 20.42 |
| 734 | IPI00017597.1 | MICROTUBULE-ASSOCIATED PROTEIN RP/EB FAMILY MEMBER 3. | 31982 | 5.23 | 3 | 1 | 3.56 |
| 735 | IPI00019329.1 | DYNEIN LIGHT CHAIN 1, CYTOPLASMIC. | 10366 | 7.5 | 3 | 2 | 17.98 |
| 736 | IPI00019599.1 | DNA-BINDING PROTEIN (EC 6.3.2.19) (DJ1185N5.1.4) (UBIQUITIN- CONJUGATING ENZYME E2 VARIANT 1. | 25797 | 8.47 | 3 | 3 | 13.12 |
| 737 | IPI00019901.1 | SPLICE ISOFORM 1 OF P35611 ALPHA ADDUCIN. | 80955 | 5.61 | 3 | 1 | 1.36 |
| 738 | IPI00019982.5 | VESICLE-ASSOCIATED MEMBRANE PROTEIN 3. | 11178 | 9.26 | 3 | 1 | 17.17 |
| 739 | IPI00020356.2 | MICROTUBULE-ASSOCIATED PROTEIN 1A (MAP 1A) (PROLIFERATION-RELATED PROTEIN P80) [Contains: MAP1 LIGHT CHAIN LC2]. | 306642 | 4.57 | 3 | 3 | 1.64 |
| 740 | IPI00021347.1 | UBIQUITIN-CONJUGATING ENZYME E2-18 KDA UBCH7. | 17862 | 8.79 | 3 | 1 | 14.29 |
| 741 | IPI00021842.1 | APOLIPOPROTEIN E PRECURSOR. | 36154 | 5.42 | 3 | 1 | 4.73 |
| 742 | IPI00022007.1 | WISKOTT-ALDRICH SYNDROME PROTEIN FAMILY MEMBER 1. | 61652 | 6.43 | 3 | 1 | 1.61 |
| 743 | IPI00022134.1 | PUTATIVE SMALL GTP-BINDING PROTEIN. | 18659 | 10.24 | 3 | 1 | 6.75 |
| 744 | IPI00022970.1 | NUCLEOPROTEIN TPR. | 265601 | 4.72 | 3 | 2 | 0.64 |
| 745 | IPI00024282.1 | RAS-RELATED PROTEIN RAB-8B. | 23584 | 9.54 | 3 | 1 | 5.31 |
| 746 | IPI00024638.1 | CREATINE KINASE, UBIQUITOUS MITOCHONDRIAL PRECURSOR. | 47037 | 8.47 | 3 | 2 | 4.32 |
| 747 | IPI00024911.1 | ENDOPLASMIC RETICULUM PROTEIN ERP29 PRECURSOR. | 28993 | 7.49 | 3 | 2 | 7.66 |
| 748 | IPI00024989.4 | SPLICE ISOFORM 1 OF P22061 PROTEIN-L-ISOASPARTATE(D-ASPARTATE) O-METHYLTRANSFERASE. | 27373 | 8.32 | 3 | 2 | 9.88 |
| 749 | IPI00025849.1 | ACIDIC LEUCINE-RICH NUCLEAR PHOSPHOPROTEIN 32 FAMILY MEMBER A. | 28585 | 3.72 | 3 | 3 | 16.06 |
| 750 | IPI00026133.1 | PARATHYROID HORMONE RECEPTOR PRECURSOR. | 62236 | 7.09 | 3 | 1 | 1.27 |
| 751 | IPI00026182.1 | CAPPING PROTEIN (ACTIN FILAMENT) MUSCLE Z-LINE, ALPHA 2. | 32949 | 5.65 | 3 | 3 | 16.43 |
| 752 | IPI00026271.1 | 40S RIBOSOMAL PROTEIN S14. | 16273 | 10.79 | 3 | 3 | 29.14 |
| 753 | IPI00026546.1 | PLATELET-ACTIVATING FACTOR ACETYLHYDROLASE IB BETA SUBUNIT. | 25569 | 5.8 | 3 | 3 | 28.38 |
| 754 | IPI00027423.1 | SERINE/THREONINE PROTEIN PHOSPHATASE PP1-ALPHA 1 CATALYTIC SUBUNIT. | 37512 | 6.25 | 3 | 2 | 10.61 |
| 755 | IPI00028481.1 | RAS-RELATED PROTEIN RAB-8. | 23668 | 9.54 | 3 | 1 | 5.31 |
| 756 | IPI00028627.3 | P PROTEIN. | 92894 | 7.18 | 3 | 1 | 0.72 |
| 757 | IPI00029744.1 | SINGLE-STRANDED DNA-BINDING PROTEIN, MITOCHONDRIAL PRECURSOR. | 17260 | 10.04 | 3 | 2 | 20.27 |
| 758 | IPI00029992.2 | SIMILAR TO 67 KDA LAMININ RECEPTOR. | 30715 | 4.2 | 3 | 2 | 14.44 |
| 759 | IPI00030296.1 | BM-010. | 36153 | 7.55 | 3 | 3 | 9.94 |
| 760 | IPI00030363.1 | ACETYL-COA ACETYLTRANSFERASE, MITOCHONDRIAL PRECURSOR. | 45200 | 9.21 | 3 | 2 | 7.03 |
| 761 | IPI00030962.6 | DNA-BINDING PROTEIN. | 19228 | 8.45 | 3 | 3 | 17.06 |
| 762 | IPI00031022.1 | SIMILAR TO HEAT SHOCK PROTEIN, 110 KDA. | 15689 | 4.38 | 3 | 2 | 21.62 |
| 763 | IPI00035033.8 | SIMILAR TO RAB12 PROTEIN. | 36315 | 8.57 | 3 | 1 | 3.24 |
| 764 | IPI00038378.2 | E-1 ENZYME. | 28933 | 4.4 | 3 | 2 | 13.03 |
| 765 | IPI00060801.1 | RAS-RELATED PROTEIN RAB-39B. | 24622 | 7.97 | 3 | 1 | 5.16 |
| 766 | IPI00061178.1 | SIMILAR TO RNA BINDING MOTIF PROTEIN, X CHROMOSOME. | 42142 | 10.21 | 3 | 3 | 8.21 |
| 767 | IPI00069363.1 | SIMILAR TO EUKARYOTIC INITIATION FACTOR 5A. | 16789 | 4.61 | 3 | 1 | 7.79 |
| 768 | IPI00070778.1 | --none found in database-- | 21273 | 7.21 | 3 | 3 | 20.42 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 769 | IPI00073180.5 | RAS-RELATED PROTEIN RAB-37. | 24684 | 6.28 | 3 | 1 | 4.95 |
| 770 | IPI00098624.1 | HYPOTHETICAL PROTEIN KIAA0968. | 59022 | 7.47 | 3 | 2 | 5.88 |
| 771 | IPI00107625.1 | SPLICE ISOFORM SNAP-25A OF P13795 SYNAPTOSOMAL-ASSOCIATED PROTEIN 25. | 23336 | 4.47 | 3 | 2 | 10.68 |
| 772 | IPI00140696.3 | --none found in database-- | 30066 | 8.06 | 3 | 3 | 8.99 |
| 773 | IPI00144127.2 | SIMILAR TO HEAT SHOCK 70KD PROTEIN BINDING PROTEIN. | 41649 | 5.11 | 3 | 2 | 8.13 |
| 774 | IPI00150205.1 | SIMILAR TO OCULOCUTANEOUS ALBINISM II (PINK-EYE DILUTION. | 90520 | 7.26 | 3 | 1 | 0.74 |
| 775 | IPI00150520.4 | --none found in database-- | 36881 | 4.32 | 3 | 1 | 3.15 |
| 776 | IPI00151594.4 | SIMILAR TO KERATIN 8. | 58664 | 7.24 | 3 | 2 | 3.88 |
| 777 | IPI00163974.2 | --none found in database-- | 18957 | 4.14 | 3 | 1 | 7.19 |
| 778 | IPI00165284.2 | HYPOTHETICAL PROTEIN. | 44123 | 4.17 | 3 | 1 | 2.31 |
| 779 | IPI00169392.2 | CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE II GAMMA. | 66963 | 8.52 | 3 | 2 | 5.13 |
| 780 | IPI00172450.1 | CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE II GAMMA ISOFORM 3. | 58365 | 7.19 | 3 | 2 | 5.98 |
| 781 | IPI00172452.1 | CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE II GAMMA ISOFORM 6. | 56944 | 7.31 | 3 | 2 | 6.15 |
| 782 | IPI00172636.1 | HYPOTHETICAL PROTEIN. | 54128 | 7.27 | 3 | 2 | 6.49 |
| 783 | IPI00176663.2 | SIMILAR TO ELONGATION FACTOR 1-ALPHA 1 (EF-1-ALPHA-1) (ELONGATION FACTOR 1 A-1) (EEF1A-1) (ELONGATION FACTOR TU) (EF-TU). | 19883 | 9.66 | 3 | 1 | 4.81 |
| 784 | IPI00176873.1 | --none found in database-- | 17875 | 8.04 | 3 | 1 | 14.29 |
| 785 | IPI00179415.3 | SERINE/THREONINE PROTEIN PHOSPHATASE 2B CATALYTIC SUBUNIT, ALPHA ISOFORM. | 63068 | 5.82 | 3 | 3 | 5.66 |
| 786 | IPI00182944.2 | SPLICE ISOFORM 3 OF Q13554 CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE II BETA CHAIN. | 54074 | 7.16 | 3 | 2 | 6.47 |
| 787 | IPI00183066.2 | SPLICE ISOFORM 7 OF Q13554 CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE II BETA CHAIN. | 50955 | 7.43 | 3 | 2 | 6.9 |
| 788 | IPI00183356.1 | RAS-RELATED PROTEIN RAB-4A. | 31568 | 9.61 | 3 | 1 | 3.81 |
| 789 | IPI00184363.1 | GLYCOLIPID TRANSFER PROTEIN. | 23850 | 7.49 | 3 | 1 | 7.18 |
| 790 | IPI00185565.6 | CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE II DELTA CHAIN. | 56297 | 7.42 | 3 | 2 | 6.21 |
| 791 | IPI00187143.1 | HYPOTHETICAL PROTEIN. | 27506 | 6.28 | 3 | 1 | 4.44 |
| 792 | IPI00215638.2 | ATP-DEPENDENT RNA HELICASE A. | 140877 | 6.76 | 3 | 2 | 2.28 |
| 793 | IPI00215715.1 | SPLICE ISOFORM B OF Q9UQM7 CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE II ALPHA CHAIN. | 55262 | 7.65 | 3 | 2 | 6.34 |
| 794 | IPI00215802.1 | SPLICE ISOFORM SHORT OF P23152 SPLICING FACTOR, ARGININE/SERINE-RICH 3. | 14203 | 10.5 | 3 | 2 | 20.97 |
| 795 | IPI00215983.1 | CARBONIC ANHYDRASE I. | 28870 | 7.14 | 3 | 2 | 15.71 |
| 796 | IPI00216131.1 | SPLICE ISOFORM 2 OF P22061 PROTEIN-L-ISOASPARTATE(D-ASPARTATE) O-METHYLTRANSFERASE. | 24562 | 6.51 | 3 | 2 | 11.01 |
| 797 | IPI00216184.1 | SPLICE ISOFORM II OF Q13492 PHOSPHATIDYLINOSITOL-BINDING CLATHRIN ASSEMBLY PROTEIN. | 68899 | 7.72 | 3 | 1 | 1.89 |
| 798 | IPI00216298.1 | THIOREDOXIN. | 11693 | 4.42 | 3 | 1 | 12.38 |
| 799 | IPI00216311.4 | VILLIN 2. | 69413 | 6.17 | 3 | 3 | 6.48 |
| 800 | IPI00216378.1 | CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE II GAMMA ISOFORM 1. | 62165 | 7.44 | 3 | 2 | 5.58 |
| 801 | IPI00216613.1 | SPLICE ISOFORM SHORT OF P23246 SPLICING FACTOR, PROLINE-AND GLUTAMINE- RICH. | 72263 | 9.74 | 3 | 2 | 4.78 |
| 802 | IPI00217236.2 | BETA-TUBULIN COFACTOR A. | 12855 | 4.94 | 3 | 2 | 18.52 |
| 803 | IPI00217297.1 | SPLICE ISOFORM 4 OF Q15257 PROTEIN PHOSPHATASE 2A, REGULATORY SUBUNIT B'. | 31859 | 6.42 | 3 | 1 | 2.85 |
| 804 | IPI00217507.3 | NEUROFILAMENT 3 (150KDA MEDIUM). | 102448 | 4.58 | 3 | 1 | 0.98 |
| 805 | IPI00218084.2 | SIMILAR TO EUKARYOTIC INITIATION FACTOR 5A. | 16773 | 4.61 | 3 | 1 | 7.79 |
| 806 | IPI00218130.1 | GLYCOGEN PHOSPHORYLASE. | 97092 | 7.03 | 3 | 2 | 3.33 |
| 807 | IPI00218187.1 | SPLICE ISOFORM GAMMA-2 OF P36873 SERINE/THREONINE PROTEIN PHOSPHATASE PP1-GAMMA CATALYTIC SUBUNIT. | 38518 | 5.99 | 3 | 2 | 10.39 |
| 808 | IPI00218236.3 | SERINE/THREONINE PROTEIN PHOSPHATASE PP1-BETA CATALYTIC SUBUNIT. | 40321 | 7.23 | 3 | 2 | 9.83 |
| 809 | IPI00218414.1 | CARBONIC ANHYDRASE II. | 29246 | 7.47 | 3 | 3 | 15 |
| 810 | IPI00219067.1 | GLUTATHIONE S-TRANSFERASE M2. | 25745 | 6.29 | 3 | 2 | 14.22 |
| 811 | IPI00219165.1 | SPLICE ISOFORM 2 OF Q13554 CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE II BETA CHAIN. | 56379 | 7.43 | 3 | 2 | 6.16 |
| 812 | IPI00219166.1 | SPLICE ISOFORM 5 OF Q13554 CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE II BETA CHAIN. | 58009 | 7.31 | 3 | 2 | 5.98 |
| 813 | IPI00219205.1 | KERATIN 8. | 53704 | 5.26 | 3 | 2 | 4.14 |
| 814 | IPI00219622.1 | PROTEASOME ALPHA 2 SUBUNIT. | 25899 | 7.55 | 3 | 1 | 8.12 |
| 815 | IPI00219684.1 | FATTY ACID BINDING PROTEIN 3. | 14858 | 6.8 | 3 | 2 | 17.29 |
| 816 | IPI00219812.1 | SPLICE ISOFORM RTN1-B OF Q16799 RETICULON 1. | 38950 | 4.9 | 3 | 1 | 3.65 |
| 817 | IPI00219813.1 | SPLICE ISOFORM RTN1-C OF Q16799 RETICULON 1. | 23576 | 9.25 | 3 | 1 | 6.25 |
| 818 | IPI00220158.1 | SPLICE ISOFORM 3 OF P35611 ALPHA ADDUCIN. | 84303 | 5.79 | 3 | 1 | 1.3 |
| 819 | IPI00220991.1 | SIMILAR TO ADAPTOR-RELATED PROTEIN COMPLEX 2, BETA 1 SUBUNIT. | 105692 | 4.98 | 3 | 3 | 4.94 |
| 820 | IPI00221234.1 | ANTIQUITIN. | 55366 | 6.85 | 3 | 3 | 7.44 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 821 | IPI00221305.2 | SPLICE ISOFORM 4 OF Q13554 CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE II BETA CHAIN. | 72727 | 7.93 | 3 | 2 | 4.67 |
| 822 | IPI00233929.2 | SIMILAR TO ALDOSE REDUCTASE (AR) (ALDEHYDE REDUCTASE). | 35858 | 8.02 | 3 | 2 | 6.01 |
| 823 | IPI00237671.1 | SIMILAR TO NEUROFILAMENT, LIGHT POLYPEPTIDE 68KDA. | 61517 | 4.32 | 3 | 1 | 1.66 |
| 824 | IPI00246022.2 | --none found in database-- | 49438 | 6.26 | 3 | 1 | 2.64 |
| 825 | IPI00251507.1 | SPLICE ISOFORM SYNAPSIN IB OF P17600 SYNAPSIN I. | 69876 | 10.44 | 3 | 3 | 7.17 |
| 826 | IPI00253279.1 | SPLICE ISOFORM 2 OF P35611 ALPHA ADDUCIN. | 69985 | 6.41 | 3 | 1 | 1.58 |
| 827 | IPI00259367.2 | SIMILAR TO ATPASE, H+ TRANSPORTING, LYSOSOMAL 31KD, V1 SUBUNIT E ISOFORM 1. | 26093 | 8.4 | 3 | 1 | 6.19 |
| 828 | IPI00259889.2 | SIMILAR TO AHCY PROTEIN. | 54363 | 7.48 | 3 | 1 | 2.62 |
| 829 | IPI00260188.2 | SIMILAR TO HEAT SHOCK 70KD PROTEIN BINDING PROTEIN. | 38191 | 5.73 | 3 | 1 | 4.08 |
| 830 | IPI00290738.1 | SPLICE ISOFORM I OF Q13492 PHOSPHATIDYLINOSITOL-BINDING CLATHRIN ASSEMBLY PROTEIN. | 70695 | 7.71 | 3 | 1 | 1.84 |
| 831 | IPI00290928.2 | GUANINE NUCLEOTIDE-BINDING PROTEIN, ALPHA-13 SUBUNIT. | 44050 | 8.13 | 3 | 1 | 2.92 |
| 832 | IPI00293126.1 | TUBULIN-SPECIFIC CHAPERONE B. | 27326 | 4.78 | 3 | 3 | 15.16 |
| 833 | IPI00294304.4 | HISTONE H1.0. | 20732 | 11.6 | 3 | 2 | 11.92 |
| 834 | IPI00296053.2 | FUMARATE HYDRATASE, MITOCHONDRIAL PRECURSOR. | 54694 | 9.17 | 3 | 2 | 6.85 |
| 835 | IPI00296678.1 | CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE (CAM KINASE) II GAMMA. | 59048 | 7.77 | 3 | 2 | 5.88 |
| 836 | IPI00298090.1 | SPLICE ISOFORM 6 OF Q13554 CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE II BETA CHAIN. | 55223 | 7.44 | 3 | 2 | 6.3 |
| 837 | IPI00299571.2 | PROTEIN DISULFIDE ISOMERASE A6 PRECURSOR. | 48212 | 4.7 | 3 | 3 | 9.52 |
| 838 | IPI00299977.1 | 14 KDA PHOSPHOHISTIDINE PHOSPHATASE. | 13833 | 5.98 | 3 | 2 | 24.8 |
| 839 | IPI00300096.2 | RAS-RELATED PROTEIN RAB-35. | 26927 | 9.24 | 3 | 1 | 4.64 |
| 840 | IPI00300568.3 | SPLICE ISOFORM SYNAPSIN IA OF P17600 SYNAPSIN I. | 73954 | 10.41 | 3 | 3 | 6.81 |
| 841 | IPI00302030.2 | RAS-RELATED PROTEIN RAB-30. | 23058 | 4.61 | 3 | 1 | 5.42 |
| 842 | IPI00304802.3 | DIHYDROLIPOAMIDE SUCCINYLTRANSFERASE COMPONENT OF 2-OXOGLUTARATE DEHYDROGENASE COMPLEX, MITOCHONDRIAL PRECURSOR. | 48640 | 9.19 | 3 | 1 | 3.09 |
| 843 | IPI00306351.2 | ESTERASE D. | 31463 | 7.02 | 3 | 1 | 7.8 |
| 844 | IPI00306959.5 | KERATIN 7. | 51419 | 5.14 | 3 | 2 | 4.26 |
| 845 | IPI00328744.2 | GUANINE NUCLEOTIDE BINDING PROTEIN (G PROTEIN) ALPHA 12. | 44251 | 10.42 | 3 | 1 | 2.89 |
| 846 | IPI00329441.1 | RAB11B. | 23339 | 5.35 | 3 | 1 | 5.19 |
| 847 | IPI00332724.1 | --none found in database-- | 38675 | 8 | 3 | 1 | 2.47 |
| 848 | IPI00332970.1 | SIMILAR TO RAB37, MEMBER OF RAS ONCOGENE FAMILY. | 24169 | 6.36 | 3 | 1 | 5.09 |
| 849 | IPI00333383.1 | ADAPTER-RELATED PROTEIN COMPLEX 2 BETA 1 SUBUNIT. | 104553 | 5.02 | 3 | 3 | 5.02 |
| 850 | IPI00333769.1 | --none found in database-- | 29617 | 8.75 | 3 | 3 | 9.06 |
| 851 | IPI00333776.1 | SPLICE ISOFORM 1 OF Q92823 NEURONAL CELL ADHESION MOLECULE PRECURSOR. | 143894 | 5.37 | 3 | 2 | 1.99 |
| 852 | IPI00333777.1 | SPLICE ISOFORM 2 OF Q92823 NEURONAL CELL ADHESION MOLECULE PRECURSOR. | 136618 | 5.82 | 3 | 2 | 2.1 |
| 853 | IPI00333778.1 | SPLICE ISOFORM 3 OF Q92823 NEURONAL CELL ADHESION MOLECULE PRECURSOR. | 130668 | 5.9 | 3 | 2 | 2.2 |
| 854 | IPI00333779.1 | SPLICE ISOFORM 4 OF Q92823 NEURONAL CELL ADHESION MOLECULE PRECURSOR. | 131046 | 5.6 | 3 | 2 | 2.2 |
| 855 | IPI00333781.1 | SPLICE ISOFORM 5 OF Q92823 NEURONAL CELL ADHESION MOLECULE PRECURSOR. | 144379 | 5.37 | 3 | 2 | 1.99 |
| 856 | IPI00334174.1 | SPLICE ISOFORM 2 OF P11476 RAS-RELATED PROTEIN RAB-1A. | 15331 | 8.3 | 3 | 2 | 17.02 |
| 857 | IPI00334271.1 | SPLICE ISOFORM 1 OF Q13554 CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE II BETA CHAIN. | 60387 | 7.31 | 3 | 2 | 5.72 |
| 858 | IPI00334344.1 | SPLICE ISOFORM 1 OF Q13555 CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE II GAMMA CHAIN. | 53011 | 7.38 | 3 | 2 | 6.57 |
| 859 | IPI00334587.1 | SPLICE ISOFORM 2 OF Q99729 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A/B. | 35968 | 6.95 | 3 | 1 | 4.22 |
| 860 | IPI00334713.1 | SPLICE ISOFORM 3 OF Q99729 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A/B. | 30588 | 8.18 | 3 | 1 | 4.91 |
| 861 | IPI00335789.1 | --none found in database-- | 73268 | 7.41 | 3 | 2 | 4.63 |
| 862 | IPI00336118.1 | CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE II GAMMA ISOFORM 4. | 55961 | 7.19 | 3 | 2 | 6.26 |
| 863 | IPI00374126.1 | SIMILAR TO 40S RIBOSOMAL PROTEIN SA (P40) (34/67 KDA LAMININ RECEPTOR) (COLON CARCINOMA LAMININ-BINDING PROTEIN) (NEM/1CHD4) (MULTIDRUG RESISTANCE-ASSOCIATED PROTEIN MGR1-AG). | 27902 | 4.62 | 3 | 2 | 9.24 |
| 864 | IPI00375127.1 | SIMILAR TO KIAA0038. | 32604 | 9.23 | 3 | 1 | 4.42 |
| 865 | IPI00375900.1 | SIMILAR TO PROTEIN 40KD. | 17887 | 4.4 | 3 | 2 | 14.02 |
| 866 | IPI00376220.1 | ADDUCIN 1 (ALPHA) ISOFORM D. | 73333 | 6.52 | 3 | 1 | 1.51 |
| 867 | IPI00376561.1 | SIMILAR TO TEMPLATE ACYIVATING FACTOR-I ALPHA. | 34608 | 4.24 | 3 | 1 | 3.28 |
| 868 | IPI00377060.1 | REGULATORY SUBUNIT PR 53 OF PROTEIN PHOSPHATASE 2A ISOFORM C. | 15387 | 7.14 | 3 | 1 | 6.06 |
| 869 | IPI00377174.1 | CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE IIB ISOFORM 4. | 57938 | 7.31 | 3 | 2 | 6 |
| 870 | IPI00377175.1 | SIMILAR TO ESTERASE D. | 32424 | 7.49 | 3 | 1 | 7.59 |
| 871 | IPI00377185.1 | CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE II DELTA ISOFORM 2. | 54114 | 7.13 | 3 | 2 | 6.49 |
| 872 | IPI00382475.1 | PNAS-20. | 9025 | 12.05 | 3 | 2 | 21.52 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 873 | IPI00382793.1 | --none found in database-- | 25223 | 9.28 | 3 | 1 | 6.48 |
| 874 | IPI00384016.1 | HUMAN FULL-LENGTH CDNA 5-PRIME END OF CLONE CS0DJ009YL13 OF T CELLS (JURKAT CELL LINE) OF HOMO SAPIENS. | 29625 | 8.5 | 3 | 1 | 5.02 |
| 875 | IPI00384121.1 | HUMAN FULL-LENGTH CDNA CLONE CS0DC015YM23 OF NEUROBLASTOMA OF HOMO SAPIENS. | 36455 | 5.02 | 3 | 3 | 14.16 |
| 876 | IPI00384514.1 | UEV1BS. | 17084 | 8.01 | 3 | 3 | 19.21 |
| 877 | IPI00385112.1 | SIMILAR TO RAB41. | 24162 | 9.2 | 3 | 1 | 5.12 |
| 878 | IPI00385140.1 | MASA. | 23759 | 4.65 | 3 | 2 | 16.19 |
| 879 | IPI00385786.1 | HYPOTHETICAL PROTEIN FLJ35170. | 23195 | 12.33 | 3 | 2 | 16.42 |
| 880 | IPI00385962.1 | --none found in database-- | 37493 | 6.68 | 3 | 3 | 9.51 |
| 881 | IPI00386604.1 | HYPOTHETICAL PROTEIN. | 51774 | 4.76 | 3 | 3 | 6.55 |
| 882 | IPI00386803.1 | LIM AND SH3 PROTEIN 1. | 36014 | 8.73 | 3 | 3 | 11.15 |
| 883 | IPI00394706.1 | PHAPI PROTEIN. | 15325 | 4.2 | 3 | 3 | 29.85 |
| 884 | IPI00394880.1 | ALPHA GLUCOSIDASE II ALPHA SUBUNIT. | 85834 | 6.22 | 3 | 3 | 6.23 |
| 885 | IPI00396440.1 | SIMILAR TO HYPOTHETICAL PROTEIN. | 58871 | 9.36 | 3 | 1 | 1.1 |
| 886 | IPI00396468.1 | --none found in database-- | 42695 | 6.38 | 3 | 2 | 3.27 |
| 887 | IPI00396539.1 | RAS-RELATED PROTEIN RAB-4B. | 23587 | 5.86 | 3 | 1 | 5.16 |
| 888 | IPI00000335.1 | HIT-17KDA. | 17162 | 9.61 | 2 | 1 | 12.27 |
| 889 | IPI00000581.1 | HSPC263. | 31686 | 4.64 | 2 | 2 | 9.09 |
| 890 | IPI00000875.1 | ELONGATION FACTOR 1-GAMMA. | 50119 | 6.64 | 2 | 2 | 5.26 |
| 891 | IPI00000949.1 | MU-CRYSTALLIN HOMOLOG. | 33776 | 4.79 | 2 | 1 | 6.69 |
| 892 | IPI00001683.1 | SPLICE ISOFORM LONG OF Q9Y5P2 TAXOL RESISTANT ASSOCIATED PROTEIN 3. | 14409 | 10.58 | 2 | 1 | 4.72 |
| 893 | IPI00001813.3 | HYPOTHETICAL PROTEIN KIAA1542. | 179055 | 9.23 | 2 | 1 | 0.42 |
| 894 | IPI00001816.1 | HYPOTHETICAL PROTEIN KIAA1541. | 55545 | 7.47 | 2 | 1 | 2.94 |
| 895 | IPI00002375.1 | TROPOMODULIN 1. | 40569 | 4.74 | 2 | 1 | 3.06 |
| 896 | IPI00003377.1 | SPLICE ISOFORM 1 OF Q16629 SPLICING FACTOR, ARGININE/SERINE-RICH 7. | 27367 | 12.33 | 2 | 1 | 5.88 |
| 897 | IPI00003391.2 | ODZ, ODD OZ/TEN-M HOMOLOG 1. | 305245 | 6.43 | 2 | 1 | 0.18 |
| 898 | IPI00003935.1 | HISTONE H2B.Q. | 13789 | 11 | 2 | 2 | 20.8 |
| 899 | IPI00004534.3 | PHOSPHORIBOSYLFORMYLGLYCINAMIDINE SYNTHASE. | 144664 | 5.55 | 2 | 1 | 1.64 |
| 900 | IPI00004839.1 | CRK-LIKE PROTEIN. | 33777 | 6.73 | 2 | 1 | 3.96 |
| 901 | IPI00005159.1 | ACTIN LIKE PROTEIN 2. | 44761 | 6.72 | 2 | 2 | 4.57 |
| 902 | IPI00005250.1 | REGULATOR OF G-PROTEIN SIGNALING 17. | 24359 | 5.43 | 2 | 1 | 2.38 |
| 903 | IPI00005859.1 | CYTOKERATIN TYPE II. | 59504 | 7.87 | 2 | 1 | 2.18 |
| 904 | IPI00006443.1 | LAMBDA-CRYSTALLIN HOMOLOG. | 34301 | 6.34 | 2 | 1 | 3.55 |
| 905 | IPI00007189.1 | SPLICE ISOFORM 1 OF P21181 CELL DIVISION CONTROL PROTEIN 42 HOMOLOG. | 21311 | 5.83 | 2 | 2 | 11.52 |
| 906 | IPI00007423.1 | ACIDIC LEUCINE-RICH NUCLEAR PHOSPHOPROTEIN 32 FAMILY MEMBER B. | 28788 | 3.67 | 2 | 2 | 11.55 |
| 907 | IPI00007906.1 | MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION. | 13695 | 7.24 | 2 | 1 | 4.13 |
| 908 | IPI00008040.1 | PROTEIN-ARGININE DEIMINASE TYPE I. | 74607 | 6.46 | 2 | 1 | 1.36 |
| 909 | IPI00008433.2 | 40S RIBOSOMAL PROTEIN S5. | 22876 | 10.31 | 2 | 2 | 15.69 |
| 910 | IPI00008527.1 | 60S ACIDIC RIBOSOMAL PROTEIN P1. | 11514 | 3.95 | 2 | 1 | 14.04 |
| 911 | IPI00009439.1 | SYNAPTOTAGMIN I. | 47573 | 8.33 | 2 | 2 | 4.98 |
| 912 | IPI00009867.1 | KERATIN, TYPE II CYTOSKELETAL 5. | 62461 | 8.25 | 2 | 1 | 2.03 |
| 913 | IPI00010271.1 | SPLICE ISOFORM A OF P15154 RAS-RELATED C3 BOTULINUM TOXIN SUBSTRATE 1. | 21450 | 8.65 | 2 | 2 | 12.5 |
| 914 | IPI00010320.1 | CHROMOBOX PROTEIN HOMOLOG 1. | 21418 | 4.57 | 2 | 1 | 5.95 |
| 915 | IPI00010405.3 | SPLICE ISOFORM LONG OF Q01973 TYROSINE-PROTEIN KINASE TRANSMEMBRANE RECEPTOR ROR1 PRECURSOR. | 104313 | 7.17 | 2 | 1 | 0.75 |
| 916 | IPI00010720.1 | T-COMPLEX PROTEIN 1, EPSILON SUBUNIT. | 59671 | 5.34 | 2 | 2 | 6.1 |
| 917 | IPI00011604.1 | GLYCINE CLEAVAGE SYSTEM H PROTEIN, MITOCHONDRIAL PRECURSOR. | 18911 | 4.56 | 2 | 1 | 11.56 |
| 918 | IPI00011666.2 | SIMILAR TO HYPOTHETICAL PROTEIN KIAA0415. | 164677 | 8.46 | 2 | 1 | 0.66 |
| 919 | IPI00011932.3 | SIMILAR TO HEAT SHOCK 70 KDA PROTEIN 12A. | 79538 | 7.41 | 2 | 2 | 3.61 |
| 920 | IPI00011937.1 | PEROXIREDOXIN 4. | 30540 | 6.24 | 2 | 1 | 2.95 |
| 921 | IPI00012136.1 | SPLICE ISOFORM BI-1-GGCAG OF O00555 VOLTAGE-DEPENDENT P/Q-TYPE CALCIUM CHANNEL ALPHA-1A SUBUNIT. | 282365 | 9.1 | 2 | 2 | 0.68 |
| 922 | IPI00012388.1 | TRANSCRIPTION INTERMEDIARY FACTOR 1-BETA. | 88550 | 5.55 | 2 | 1 | 3.59 |
| 923 | IPI00013075.1 | P60 KATANIN. | 55965 | 6.88 | 2 | 1 | 1.02 |
| 924 | IPI00013157.1 | C367G8.3 (NOVEL PROTEIN SIMILAR TO RPL23A. | 17508 | 10.92 | 2 | 1 | 8.33 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 925 | IPI00013179.1 | PROSTAGLANDIN-H2 D-ISOMERASE PRECURSOR. | 21029 | 7.94 | 2 | 2 | 17.37 |
| 926 | IPI00013193.1 | SPLICE ISOFORM 1 OF Q13402 MYOSIN VIIA. | 254406 | 8.74 | 2 | 1 | 0.23 |
| 927 | IPI00013698.1 | ACID CERAMIDASE PRECURSOR. | 44650 | 7.71 | 2 | 2 | 8.61 |
| 928 | IPI00013838.1 | 51C PROTEIN. | 126809 | 9.16 | 2 | 1 | 0.44 |
| 929 | IPI00013877.2 | SPLICE ISOFORM 1 OF P31942 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN H3. | 36926 | 6.87 | 2 | 2 | 7.8 |
| 930 | IPI00013896.1 | GUANINE NUCLEOTIDE -BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN 12.3. | 35077 | 7.77 | 2 | 2 | 7.26 |
| 931 | IPI00013917.1 | 40S RIBOSOMAL PROTEIN S12. | 14395 | 6.75 | 2 | 1 | 7.63 |
| 932 | IPI00014312.1 | SPLICE ISOFORM 1 OF Q13618 CULLIN HOMOLOG 3. | 88930 | 8.7 | 2 | 1 | 0.65 |
| 933 | IPI00014589.1 | SPLICE ISOFORM BRAIN OF P09497 CLATHRIN LIGHT CHAIN B. | 25190 | 4.28 | 2 | 2 | 13.97 |
| 934 | IPI00015029.1 | TELOMERASE-BINDING PROTEIN P23. | 18697 | 4.11 | 2 | 1 | 7.5 |
| 935 | IPI00015141.1 | CREATINE KINASE, SARCOMERIC MITOCHONDRIAL PRECURSOR. | 47520 | 8.31 | 2 | 1 | 1.43 |
| 936 | IPI00015911.1 | DIHYDROLIPOAMIDE DEHYDROGENASE, MITOCHONDRIAL PRECURSOR. | 54150 | 7.76 | 2 | 1 | 2.75 |
| 937 | IPI00016621.2 | ADAPTER-RELATED PROTEIN COMPLEX 2 ALPHA 2 SUBUNIT. | 105162 | 6.82 | 2 | 2 | 4.84 |
| 938 | IPI00016932.1 | INOSITOL POLYPHOSPHATE 5-PHOSPHATASE. | 138585 | 6.49 | 2 | 1 | 0.4 |
| 939 | IPI00017340.5 | PLACENTAL THROMBIN INHIBITOR. | 42590 | 4.93 | 2 | 2 | 7.98 |
| 940 | IPI00017448.1 | 40S RIBOSOMAL PROTEIN S21. | 9111 | 8.75 | 2 | 1 | 12.05 |
| 941 | IPI00017596.1 | MICROTUBULE-ASSOCIATED PROTEIN RP/EB FAMILY MEMBER 1. | 29999 | 4.76 | 2 | 2 | 10.45 |
| 942 | IPI00017726.1 | SPLICE ISOFORM 1 OF Q99714 3-HYDROXYACYL-COA DEHYDROGENASE TYPE II. | 26923 | 7.94 | 2 | 2 | 14.18 |
| 943 | IPI00018259.3 | GROUP IID SECRETORY PHOSPHOLIPASE A2 PRECURSOR. | 16546 | 8.27 | 2 | 1 | 3.45 |
| 944 | IPI00018524.1 | HISTONE H2A.E. | 13805 | 11.53 | 2 | 1 | 14.96 |
| 945 | IPI00018534.1 | HISTONE H2B.C. | 13821 | 11 | 2 | 2 | 20.8 |
| 946 | IPI00018952.1 | U2 SMALL NUCLEAR RIBONUCLEOPROTEIN AUXILIARY FACTOR 35 KDA SUBUNIT RELATED-PROTEIN 1. | 57643 | 9.9 | 2 | 1 | 1.04 |
| 947 | IPI00019512.2 | SIMILAR TO MYOSIN HEAVY CHAIN, NONMUSCLE TYPE B (CELLULAR MYOSIN HEAVY CHAIN, TYPE B) (NONMUSCLE MYOSIN HEAVY CHAIN-B) (NMMHC-B). | 229928 | 5.25 | 2 | 2 | 0.66 |
| 948 | IPI00019600.1 | MMS2. | 16363 | 8.43 | 2 | 2 | 13.79 |
| 949 | IPI00019642.1 | HYPOTHETICAL PROTEIN KIAA0291. | 115837 | 6.7 | 2 | 2 | 3.06 |
| 950 | IPI00019927.2 | 26S PROTEASOME NON-ATPASE REGULATORY SUBUNIT 7. | 37025 | 6.75 | 2 | 1 | 5.25 |
| 951 | IPI00020101.1 | HISTONE H2B.A/G/K. | 13775 | 11 | 2 | 2 | 20.8 |
| 952 | IPI00020436.2 | RAS-RELATED PROTEIN RAB-11B. | 24488 | 5.73 | 2 | 2 | 9.17 |
| 953 | IPI00020850.1 | SERINE/THREONINE PROTEIN PHOSPHATASE 2A, 55 KDA REGULATORY SUBUNIT B, BETA ISOFORM. | 51710 | 6.4 | 2 | 1 | 3.16 |
| 954 | IPI00020906.1 | INOSITOL-1(OR 4)-MONOPHOSPHATASE. | 30189 | 4.91 | 2 | 2 | 13 |
| 955 | IPI00020955.1 | 3-OXO-5-BETA-STEROID 4-DEHYDROGENASE. | 37377 | 7.58 | 2 | 1 | 1.84 |
| 956 | IPI00021266.1 | 60S RIBOSOMAL PROTEIN L23A. | 17695 | 11.16 | 2 | 1 | 8.33 |
| 957 | IPI00021794.2 | LYSOSOMAL PROTECTIVE PROTEIN PRECURSOR. | 54466 | 6.59 | 2 | 1 | 1.25 |
| 958 | IPI00022004.1 | SPLICE ISOFORM 2 OF Q92556 ENGULFMENT AND CELL MOTILITY PROTEIN 1. | 28742 | 6.37 | 2 | 1 | 2.43 |
| 959 | IPI00022082.2 | SIMILAR TO SEPTIN KIAA0202B. | 84898 | 9.51 | 2 | 1 | 1.44 |
| 960 | IPI00022334.1 | ORNITHINE AMINOTRANSFERASE, MITOCHONDRIAL PRECURSOR. | 48535 | 7.05 | 2 | 1 | 2.51 |
| 961 | IPI00022892.2 | THY 1 MEMBRANE GLYCOPROTEIN PRECURSOR. | 17935 | 8.93 | 2 | 1 | 9.32 |
| 962 | IPI00023591.1 | TRANSCRIPTIONAL ACTIVATOR PROTEIN PUR-ALPHA. | 34911 | 6.39 | 2 | 1 | 9.01 |
| 963 | IPI00023785.2 | DEAD BOX POLYPEPTIDE 17 ISOFORM P82. | 80272 | 8.37 | 2 | 2 | 2.74 |
| 964 | IPI00024157.1 | FK506-BINDING PROTEIN 3. | 25177 | 9.96 | 2 | 1 | 4.91 |
| 965 | IPI00024913.1 | SPLICE ISOFORM LONG OF P30042 ES1 PROTEIN HOMOLOG, MITOCHONDRIAL PRECURSOR. | 28142 | 8.4 | 2 | 2 | 13.06 |
| 966 | IPI00026216.3 | PUROMYCIN-SENSITIVE AMINOPEPTIDASE. | 103302 | 5.44 | 2 | 2 | 2.5 |
| 967 | IPI00026272.1 | HISTONE H2A.M. | 14041 | 11.66 | 2 | 1 | 14.73 |
| 968 | IPI00026516.1 | SUCCINYL-COA:3-KETOACID-COENZYME A TRANSFERASE, MITOCHONDRIAL PRECURSOR. | 56158 | 7.52 | 2 | 2 | 4.42 |
| 969 | IPI00026958.1 | SPLICE ISOFORM SHORT OF P22570 NADPH:ADRENODOXIN OXIDOREDUCTASE, MITOCHONDRIAL PRECURSOR. | 53809 | 8.4 | 2 | 1 | 1.02 |
| 970 | IPI00027139.1 | INOSITOL POLYPHOSPHATE 1-PHOSPHATASE. | 43998 | 4.91 | 2 | 1 | 3.01 |
| 971 | IPI00027464.1 | SPLICE ISOFORM 1 OF P06705 CALCINEURIN B SUBUNIT ISOFORM 1. | 19169 | 4.4 | 2 | 1 | 5.92 |
| 972 | IPI00027487.1 | CREATINE KINASE, M CHAIN. | 43101 | 7.28 | 2 | 1 | 1.57 |
| 973 | IPI00027770.1 | SYNAPTOPHYSIN. | 33845 | 4.41 | 2 | 2 | 7.03 |
| 974 | IPI00027809.1 | SPLICE ISOFORM 1 OF P16299 SERINE/THREONINE PROTEIN PHOSPHATASE 2B CATALYTIC SUBUNIT, BETA ISOFORM. | 59024 | 5.75 | 2 | 2 | 3.44 |
| 975 | IPI00028006.1 | PROTEASOME SUBUNIT BETA TYPE 2. | 22836 | 7.04 | 2 | 1 | 5.47 |
| 976 | IPI00028508.1 | RAS-RELATED PROTEIN RAB-11A. | 24394 | 6.53 | 2 | 2 | 9.26 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 977 | IPI00029751.1 | SPLICE ISOFORM 1 OF Q12860 CONTACTIN PRECURSOR. | 113320 | 5.69 | 2 | 1 | 0.88 |
| 978 | IPI00031128.1 | SIMILAR TO RIKEN CDNA 2610024G14 GENE. | 78458 | 8.86 | 2 | 1 | 0.72 |
| 979 | IPI00031562.1 | H2A HISTONE FAMILY, MEMBER L. | 14121 | 11.66 | 2 | 1 | 14.62 |
| 980 | IPI00032234.1 | HISTONE H2B. | 13890 | 11 | 2 | 2 | 20.63 |
| 981 | IPI00033025.1 | SEPTIN 7. | 48787 | 9.14 | 2 | 2 | 8.37 |
| 982 | IPI00033153.1 | NUCLEAR RNA EXPORT FACTOR 1. | 70182 | 8.7 | 2 | 1 | 0.81 |
| 983 | IPI00043499.1 | PROBABLE UROCANATE HYDRATASE. | 74831 | 6.78 | 2 | 1 | 0.74 |
| 984 | IPI00044779.1 | TC4 PROTEIN. | 12233 | 9.8 | 2 | 2 | 26.61 |
| 985 | IPI00045512.1 | HEMICENTIN. | 613704 | 6.44 | 2 | 1 | 0.09 |
| 986 | IPI00048961.2 | SIMILAR TO 60S RIBOSOMAL PROTEIN L7A (SURFEIT LOCUS PROTEIN 3) (PLA-X POLYPEPTIDE). | 23850 | 10.75 | 2 | 1 | 5.16 |
| 987 | IPI00056357.1 | HYPOTHETICAL PROTEIN. | 18795 | 6.68 | 2 | 1 | 6.36 |
| 988 | IPI00059685.1 | HYPOTHETICAL PROTEIN. | 44004 | 7.7 | 2 | 2 | 8.74 |
| 989 | IPI00062003.1 | SIMILAR TO ACETYL-COENZYME A ACETYLTRANSFERASE 1. | 17201 | 10.57 | 2 | 1 | 10.49 |
| 990 | IPI00063234.1 | SIMILAR TO PROTEIN KINASE, CAMP-DEPENDENT, REGULATORY, TYPE II, ALPHA. | 43067 | 4.71 | 2 | 2 | 8.9 |
| 991 | IPI00063472.2 | SIMILAR TO PROTEASOME SUBUNIT ALPHA TYPE 6 (PROTEASOME IOTA CHAIN) (MACROPAIN IOTA CHAIN) (MULTICATALYTIC ENDOPEPTIDASE COMPLEX IOTA CHAIN) (27 KDA PROSOMAL PROTEIN) (PROS-27) (P27K). | 35186 | 10.07 | 2 | 1 | 4.19 |
| 992 | IPI00065073.1 | HYPOTHETICAL PROTEIN FLJ25413. | 16636 | 9.01 | 2 | 1 | 4.11 |
| 993 | IPI00073442.4 | SIMILAR TO RIKEN CDNA 1600013K19. | 24867 | 10.82 | 2 | 1 | 2.25 |
| 994 | IPI00075558.4 | SIMILAR TO 60S RIBOSOMAL PROTEIN L7A (SURFEIT LOCUS PROTEIN 3) (PLA-X POLYPEPTIDE). | 21549 | 10.99 | 2 | 1 | 5.85 |
| 995 | IPI00081836.1 | DJ86C11.1. | 13906 | 11.53 | 2 | 1 | 14.84 |
| 996 | IPI00082404.2 | SIMILAR TO 60S RIBOSOMAL PROTEIN L7A (SURFEIT LOCUS PROTEIN 3) (PLA-X POLYPEPTIDE). | 21953 | 11.22 | 2 | 1 | 5.7 |
| 997 | IPI00088730.3 | --none found in database-- | 30919 | 9.18 | 2 | 1 | 2.42 |
| 998 | IPI00101405.1 | FARNESYL DIPHOSPHATE SYNTHASE. | 48275 | 6.02 | 2 | 2 | 7.16 |
| 999 | IPI00102165.1 | H2A HISTONE FAMILY, MEMBER J ISOFORM 1. | 16610 | 10.88 | 2 | 1 | 12.26 |
| 1000 | IPI00104450.2 | SIMILAR TO PHOSPHOSERINE AMINOTRANSFERASE ISOFORM 1. | 40331 | 5.98 | 2 | 2 | 6.78 |
| 1001 | IPI00145399.2 | SIMILAR TO 67 KDA LAMININ RECEPTOR. | 27169 | 4.54 | 2 | 1 | 5.33 |
| 1002 | IPI00145540.3 | SIMILAR TO TROPOMYOSIN 3. | 24801 | 4.17 | 2 | 1 | 6.67 |
| 1003 | IPI00148061.2 | SIMILAR TO LACTATE DEHYDROGENASE 1, A CHAIN. | 25626 | 8.01 | 2 | 1 | 5.13 |
| 1004 | IPI00151138.1 | SIMILAR TO 60S ACIDIC RIBOSOMAL PROTEIN P1. | 10091 | 4.26 | 2 | 1 | 16.67 |
| 1005 | IPI00152635.1 | ADAMTS-17 PRECURSOR. | 121100 | 8.09 | 2 | 1 | 0.46 |
| 1006 | IPI00152785.1 | DJ193B12.2. | 13906 | 11 | 2 | 2 | 20.63 |
| 1007 | IPI00152906.1 | HISTONE H2B.B. | 13805 | 11 | 2 | 2 | 20.8 |
| 1008 | IPI00154852.1 | FLJ00246 PROTEIN. | 157811 | 4.72 | 2 | 1 | 0.4 |
| 1009 | IPI00156689.1 | HYPOTHETICAL PROTEIN. | 41920 | 6.25 | 2 | 2 | 7.89 |
| 1010 | IPI00163147.4 | --none found in database-- | 44915 | 5.01 | 2 | 2 | 4.6 |
| 1011 | IPI00163328.3 | GLYCOGEN PHOSPHORYLASE, LIVER FORM. | 97208 | 7.17 | 2 | 1 | 1.42 |
| 1012 | IPI00163743.2 | HYPOTHETICAL PROTEIN KIAA0169. | 195699 | 6.71 | 2 | 2 | 0.86 |
| 1013 | IPI00164623.2 | COMPLEMENT C3 PRECURSOR [Contains: C3A ANAPHYLATOXIN]. | 187235 | 6.34 | 2 | 2 | 1.56 |
| 1014 | IPI00165049.1 | SIMILAR TO HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1 (HELIX-DESTABILIZING PROTEIN) (SINGLE-STRAND BINDING PROTEIN) (HNRNP CORE PROTEIN A1) (HDP-1) (TOPOISOMERASE-INHIBITOR SUPPRESSED). | 34495 | 9.51 | 2 | 1 | 2.18 |
| 1015 | IPI00166293.1 | HYPOTHETICAL PROTEIN FLJ33901. | 13908 | 11 | 2 | 2 | 20.63 |
| 1016 | IPI00166342.1 | HYPOTHETICAL PROTEIN FLJ33648. | 27035 | 5.06 | 2 | 1 | 2.07 |
| 1017 | IPI00167313.1 | HYPOTHETICAL PROTEIN FLJ40089. | 65287 | 9.17 | 2 | 1 | 0.89 |
| 1018 | IPI00168895.1 | FORKHEAD TRANSCRIPTION FACTOR. | 18064 | 7.7 | 2 | 1 | 3.36 |
| 1019 | IPI00170645.1 | HISTONE H2A. | 13988 | 11.55 | 2 | 1 | 14.73 |
| 1020 | IPI00171874.1 | RAS GUANYL RELEASING PROTEIN 3. | 78332 | 6.79 | 2 | 1 | 0.87 |
| 1021 | IPI00175039.2 | SIMILAR TO NEUROFIBROMIN. | 78168 | 7.39 | 2 | 1 | 0.71 |
| 1022 | IPI00175190.2 | SIMILAR TO DJ702J19.1 (GLYCINE CLEAVAGE SYSTEM PROTEIN H (AMINOMETHYL CARRIER)). | 18883 | 4.4 | 2 | 1 | 11.56 |
| 1023 | IPI00176593.1 | SIMILAR TO ACTIN-RELATED PROTEIN 2. | 44705 | 6.33 | 2 | 2 | 4.57 |
| 1024 | IPI00176610.1 | SIMILAR TO UNACTIVE PROGESTERONE RECEPTOR, 23 KD. | 18694 | 4.16 | 2 | 1 | 7.5 |
| 1025 | IPI00176755.2 | SIMILAR TO 60S RIBOSOMAL PROTEIN L23A. | 17707 | 11.16 | 2 | 1 | 8.33 |
| 1026 | IPI00176799.1 | SIMILAR TO HYPOTHETICAL PROTEIN. | 85105 | 4.55 | 2 | 2 | 4.15 |
| 1027 | IPI00178188.3 | DYNEIN LIGHT CHAIN 2B, CYTOPLASMIC. | 10855 | 7.68 | 2 | 2 | 21.88 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 1028 | IPI00178416.1 | RAS GUANYL RELEASING PROTEIN 3 (CALCIUM AND DAG-REGULATED). | 78203 | 6.79 | 2 | 1 | 0.87 |
| 1029 | IPI00179437.3 | RHO-SPECIFIC GUANINE NUCLEOTIDE EXCHANGE FACTOR P114. | 118022 | 6.74 | 2 | 1 | 0.48 |
| 1030 | IPI00180277.3 | SIMILAR TO KERATIN 8, TYPE II CYTOSKELETAL - HUMAN. | 42608 | 4.46 | 2 | 1 | 2.9 |
| 1031 | IPI00180671.2 | DKFZP564O123 PROTEIN. | 30196 | 10.17 | 2 | 1 | 1.82 |
| 1032 | IPI00181738.1 | PROTEIN PHOSPHATASE 3 CATALYTIC SUBUNIT BETA3. | 58081 | 6.01 | 2 | 2 | 3.5 |
| 1033 | IPI00182180.1 | CGI-77 PROTEIN. | 33813 | 5.93 | 2 | 1 | 1.71 |
| 1034 | IPI00184845.1 | UNCHARACTERIZED HEMATOPOIETIC STEM/PROGENITOR CELLS PROTEIN MDS026. | 14995 | 7.99 | 2 | 1 | 10.22 |
| 1035 | IPI00185361.3 | SIMILAR TO RIKEN CDNA 2810021H22 GENE. | 68501 | 9.89 | 2 | 2 | 1.33 |
| 1036 | IPI00215717.1 | SPLICE ISOFORM C OF Q9Y2J2 BAND 4.1-LIKE PROTEIN 3. | 69521 | 6.16 | 2 | 2 | 4.41 |
| 1037 | IPI00215753.1 | SPLICE ISOFORM 2 OF Q13402 MYOSIN VIIA. | 250489 | 8.87 | 2 | 1 | 0.23 |
| 1038 | IPI00215756.1 | SPLICE ISOFORM 5 OF Q13402 MYOSIN VIIA. | 240657 | 9 | 2 | 1 | 0.24 |
| 1039 | IPI00215758.1 | SPLICE ISOFORM 6 OF Q13402 MYOSIN VIIA. | 250982 | 8.58 | 2 | 1 | 0.23 |
| 1040 | IPI00215759.1 | SPLICE ISOFORM 7 OF Q13402 MYOSIN VIIA. | 249977 | 8.58 | 2 | 1 | 0.23 |
| 1041 | IPI00215907.1 | SPLICE ISOFORM 2 OF Q16629 SPLICING FACTOR, ARGININE/SERINE-RICH 7. | 15573 | 10.08 | 2 | 1 | 10.37 |
| 1042 | IPI00216106.1 | SPLICE ISOFORM 3 OF Q9NTK5 PUTATIVE GTP-BINDING PROTEIN PTD004. | 31440 | 8.01 | 2 | 1 | 5.4 |
| 1043 | IPI00216313.1 | VISININ-LIKE 1. | 22142 | 4.76 | 2 | 2 | 12.04 |
| 1044 | IPI00216347.1 | SPLICE ISOFORM 2B OF Q13409 DYNEIN INTERMEDIATE CHAIN 2, CYTOSOLIC. | 70645 | 4.88 | 2 | 2 | 4.91 |
| 1045 | IPI00216348.1 | SPLICE ISOFORM 2C OF Q13409 DYNEIN INTERMEDIATE CHAIN 2, CYTOSOLIC. | 68426 | 4.95 | 2 | 2 | 5.07 |
| 1046 | IPI00216349.1 | SPLICE ISOFORM 2D OF Q13409 DYNEIN INTERMEDIATE CHAIN 2, CYTOSOLIC. | 67552 | 4.77 | 2 | 2 | 5.12 |
| 1047 | IPI00216403.1 | H4 HISTONE FAMILY, MEMBER C. | 11367 | 11.91 | 2 | 1 | 11.65 |
| 1048 | IPI00216456.2 | HISTONE H2A.L. | 13974 | 11.66 | 2 | 1 | 14.73 |
| 1049 | IPI00216457.3 | H2A HISTONE FAMILY, MEMBER O. | 14095 | 11.55 | 2 | 1 | 14.62 |
| 1050 | IPI00216459.1 | H2B HISTONE FAMILY, MEMBER E. | 13989 | 11 | 2 | 2 | 20.63 |
| 1051 | IPI00216492.1 | SPLICE ISOFORM 2 OF P31942 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN H3. | 35239 | 6.87 | 2 | 2 | 8.16 |
| 1052 | IPI00216493.1 | SPLICE ISOFORM 3 OF P31942 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN H3. | 31525 | 7.36 | 2 | 2 | 9.09 |
| 1053 | IPI00216494.1 | SPLICE ISOFORM 4 OF P31942 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN H3. | 22322 | 5.51 | 2 | 2 | 12.56 |
| 1054 | IPI00216495.1 | SPLICE ISOFORM 5 OF P31942 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN H3. | 16084 | 6.39 | 2 | 2 | 18.62 |
| 1055 | IPI00216496.1 | SPLICE ISOFORM 6 OF P31942 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN H3. | 15413 | 6.39 | 2 | 2 | 19.42 |
| 1056 | IPI00216641.1 | SPLICE ISOFORM 2 OF Q12860 CONTACTIN PRECURSOR. | 111867 | 5.52 | 2 | 1 | 0.89 |
| 1057 | IPI00216731.1 | H1 HISTONE FAMILY, MEMBER T, TESTIS-SPECIFIC. | 22019 | 12.28 | 2 | 1 | 5.31 |
| 1058 | IPI00217423.3 | HYALURONAN BINDING PROTEIN. | 56575 | 4.13 | 2 | 1 | 1.72 |
| 1059 | IPI00217442.1 | MULTIPLE ANKYRIN REPEATS SINGLE KH DOMAIN PROTEIN ISOFORM 2. | 277175 | 5.69 | 2 | 1 | 0.23 |
| 1060 | IPI00217469.1 | H1 HISTONE FAMILY, MEMBER 1. | 21842 | 11.76 | 2 | 1 | 5.12 |
| 1061 | IPI00217497.1 | SPLICE ISOFORM BI-1(V1) OF O00555 VOLTAGE-DEPENDENT P/Q-TYPE CALCIUM CHANNEL ALPHA-1A SUBUNIT. | 256777 | 8.56 | 2 | 2 | 0.75 |
| 1062 | IPI00217498.1 | SPLICE ISOFORM BI-1(V1)-GGCAG OF O00555 VOLTAGE-DEPENDENT P/Q-TYPE CALCIUM CHANNEL ALPHA-1A SUBUNIT. | 282209 | 9.08 | 2 | 2 | 0.68 |
| 1063 | IPI00217499.1 | SPLICE ISOFORM BI-1(V2) OF O00555 VOLTAGE-DEPENDENT P/Q-TYPE CALCIUM CHANNEL ALPHA-1A SUBUNIT. | 280944 | 8.92 | 2 | 2 | 0.68 |
| 1064 | IPI00217906.1 | SIMILAR TO GUANINE NUCLEOTIDE BINDING PROTEIN (G PROTEIN), ALPHA INHIBITING ACTIVITY POLYPEPTIDE 2. | 38473 | 5.14 | 2 | 1 | 3.54 |
| 1065 | IPI00218445.1 | SPLICE ISOFORM SHORT OF Q9Y5P2 TAXOL RESISTANT ASSOCIATED PROTEIN 3. | 12654 | 10.3 | 2 | 1 | 5.45 |
| 1066 | IPI00218468.1 | SPLICE ISOFORM 2-5 OF P37840 ALPHA-SYNUCLEIN. | 13109 | 4.18 | 2 | 1 | 4.76 |
| 1067 | IPI00218482.1 | SPLICE ISOFORM SHORT OF P30042 ES1 PROTEIN HOMOLOG, MITOCHONDRIAL PRECURSOR. | 24729 | 8.25 | 2 | 2 | 14.77 |
| 1068 | IPI00218767.1 | SPLICE ISOFORM 2 OF P35557 HEXOKINASE D. | 52136 | 4.78 | 2 | 1 | 1.07 |
| 1069 | IPI00218768.1 | SPLICE ISOFORM 3 OF P35557 HEXOKINASE D. | 52035 | 4.88 | 2 | 1 | 1.08 |
| 1070 | IPI00218862.1 | SPLICE ISOFORM 2 OF P16299 SERINE/THREONINE PROTEIN PHOSPHATASE 2B CATALYTIC SUBUNIT, BETA ISOFORM. | 58013 | 5.34 | 2 | 2 | 3.5 |
| 1071 | IPI00219005.1 | FK506-BINDING PROTEIN 4. | 51805 | 5.11 | 2 | 2 | 7.63 |
| 1072 | IPI00219153.1 | RIBOSOMAL PROTEIN L22 PROPROTEIN. | 14787 | 9.75 | 2 | 1 | 8.59 |
| 1073 | IPI00219218.2 | LACTATE DEHYDROGENASE C. | 36253 | 7.86 | 2 | 1 | 3.61 |
| 1074 | IPI00219219.1 | BETA-GALACTOSIDASE BINDING LECTIN PRECURSOR. | 14716 | 5.15 | 2 | 2 | 22.96 |
| 1075 | IPI00219304.1 | SPLICE ISOFORM 2 OF P06705 CALCINEURIN B SUBUNIT ISOFORM 1. | 24979 | 4.81 | 2 | 1 | 4.63 |
| 1076 | IPI00219448.1 | SPLICE ISOFORM 2 OF O00154 CYTOSOLIC ACYL COENZYME A THIOESTER HYDROLASE. | 27041 | 7 | 2 | 2 | 10.98 |
| 1077 | IPI00219532.1 | SPLICE ISOFORM 1 OF Q92556 ENGULFMENT AND CELL MOTILITY PROTEIN 1. | 83829 | 6.22 | 2 | 1 | 0.83 |
| 1078 | IPI00219563.1 | SPLICE ISOFORM A OF Q9NQ66 1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE BETA 1. | 138567 | 6.12 | 2 | 1 | 0.41 |
| 1079 | IPI00219593.1 | PROTEIN KINASE, CAMP-DEPENDENT, REGULATORY, TYPE II, BETA. | 46346 | 4.55 | 2 | 1 | 3.83 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 1080 | IPI00219675.1 | SPLICE ISOFORM B OF P15154 RAS-RELATED C3 BOTULINUM TOXIN SUBSTRATE 1. | 23467 | 8.82 | 2 | 2 | 11.37 |
| 1081 | IPI00219774.1 | PROTEIN KINASE, CAMP-DEPENDENT, REGULATORY, TYPE II, ALPHA. | 45518 | 4.7 | 2 | 2 | 8.42 |
| 1082 | IPI00219953.1 | UMP-CMP KINASE. | 25855 | 8.1 | 2 | 1 | 6.58 |
| 1083 | IPI00220067.6 | LEUCINE AMINOPEPTIDASE. | 56049 | 7.8 | 2 | 2 | 6.36 |
| 1084 | IPI00220403.1 | H2B HISTONE FAMILY, MEMBER F. | 13950 | 11 | 2 | 2 | 20.63 |
| 1085 | IPI00220578.1 | GUANINE NUCLEOTIDE BINDING PROTEIN (G PROTEIN), ALPHA INHIBITING ACTIVITY POLYPEPTIDE 3. | 40532 | 5.37 | 2 | 1 | 3.39 |
| 1086 | IPI00220803.1 | MARCKS-LIKE PROTEIN. | 19529 | 4.34 | 2 | 2 | 14.36 |
| 1087 | IPI00220834.4 | ATP-DEPENDANT DNA HELICASE II. | 82705 | 5.58 | 2 | 2 | 4.1 |
| 1088 | IPI00220855.1 | SIMILAR TO H2A HISTONE FAMILY, MEMBER O. | 14019 | 11.55 | 2 | 1 | 14.73 |
| 1089 | IPI00221118.1 | SPLICE ISOFORM LONG OF P22570 NADPH:ADRENODOXIN OXIDOREDUCTASE, MITOCHONDRIAL PRECURSOR. | 54451 | 8.33 | 2 | 1 | 1.01 |
| 1090 | IPI00232721.2 | SIMILAR TO NUCLEAR RNA EXPORT FACTOR 2. | 102429 | 8.02 | 2 | 1 | 0.65 |
| 1091 | IPI00232796.2 | SIMILAR TO STRESS-INDUCED-PHOSPHOPROTEIN 1 (STI1) (HSP70/HSP90-ORGANIZING PROTEIN) (TRANSFORMATION-SENSITIVE PROTEIN IEF SSP 3521). | 60808 | 6.66 | 2 | 1 | 2.43 |
| 1092 | IPI00235690.2 | SIMILAR TO TEMPLATE ACYIVATING FACTOR-I ALPHA. | 34369 | 4 | 2 | 1 | 4.38 |
| 1093 | IPI00239692.1 | SIMILAR TO 40S RIBOSOMAL PROTEIN SA (P40) (34/67 KD LAMININ RECEPTOR). | 9847 | 10.06 | 2 | 1 | 14.29 |
| 1094 | IPI00240020.5 | KERATIN, TYPE II CYTOSKELETAL 6A. | 59914 | 8.16 | 2 | 1 | 2.13 |
| 1095 | IPI00241841.4 | KERATIN 6L. | 57836 | 7.22 | 2 | 1 | 2.24 |
| 1096 | IPI00244083.3 | SPLICE ISOFORM 1 OF P35557 HEXOKINASE D. | 55643 | 5.16 | 2 | 1 | 1.01 |
| 1097 | IPI00246053.1 | SIMILAR TO PEPTIDYLPROLYL ISOMERASE A (CYCLOPHILIN A). | 24298 | 8.68 | 2 | 2 | 4.91 |
| 1098 | IPI00246188.1 | SIMILAR TO PEPTIDYL-PRO CIS TRANS ISOMERASE. | 18294 | 8.75 | 2 | 2 | 6.55 |
| 1099 | IPI00246616.1 | HYPOTHETICAL PROTEIN KIAA0291. | 112981 | 6.76 | 2 | 2 | 3.13 |
| 1100 | IPI00246673.2 | SIMILAR TO CYTOKERATIN 8. | 59070 | 5.63 | 2 | 1 | 2.1 |
| 1101 | IPI00247629.2 | SIMILAR TO RPL7A PROTEIN. | 51100 | 10.78 | 2 | 1 | 2.38 |
| 1102 | IPI00251211.2 | SIMILAR TO HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1 (HELIX-DESTABILIZING PROTEIN) (SINGLE-STRAND BINDING PROTEIN) (HNRNP CORE PROTEIN A1). | 62657 | 8.01 | 2 | 1 | 1.23 |
| 1103 | IPI00251464.2 | HYPOTHETICAL PROTEIN XP_294997. | 33925 | 6.93 | 2 | 1 | 1.63 |
| 1104 | IPI00255316.1 | HISTONE 1, H2AD. | 14107 | 11.55 | 2 | 1 | 14.62 |
| 1105 | IPI00257462.2 | HISTONE H2B.H. | 13805 | 11 | 2 | 2 | 20.8 |
| 1106 | IPI00258043.1 | --none found in database-- | 11621 | 10.09 | 2 | 2 | 23.81 |
| 1107 | IPI00259806.2 | --none found in database-- | 29109 | 7.13 | 2 | 2 | 8.55 |
| 1108 | IPI00260178.2 | SIMILAR TO KERATIN 8, TYPE II CYTOSKELETAL - HUMAN. | 53411 | 4.87 | 2 | 1 | 2.28 |
| 1109 | IPI00260388.3 | PHD FINGER PROTEIN 2. | 121232 | 9.72 | 2 | 1 | 0.54 |
| 1110 | IPI00290078.1 | KERATIN, TYPE II CYTOSKELETAL 4. | 57295 | 6.55 | 2 | 1 | 2.06 |
| 1111 | IPI00290416.1 | SPLICE ISOFORM 1 OF Q9NTK5 PUTATIVE GTP-BINDING PROTEIN PTD004. | 44744 | 7.99 | 2 | 1 | 3.79 |
| 1112 | IPI00290566.1 | T-COMPLEX PROTEIN 1, ALPHA SUBUNIT. | 60344 | 5.96 | 2 | 2 | 4.5 |
| 1113 | IPI00291262.2 | CLUSTERIN PRECURSOR. | 55192 | 6.57 | 2 | 2 | 4.83 |
| 1114 | IPI00291347.1 | SPLICE ISOFORM BI-1(V2,V3) OF O00555 VOLTAGE-DEPENDENT P/Q-TYPE CALCIUM CHANNEL ALPHA-1A SUBUNIT. | 282651 | 9.1 | 2 | 2 | 0.68 |
| 1115 | IPI00291373.1 | ADRENOLEUKODYSTROPHY PROTEIN. | 82909 | 9.2 | 2 | 1 | 0.67 |
| 1116 | IPI00291383.1 | HEMICENTIN. | 613518 | 6.48 | 2 | 1 | 0.09 |
| 1117 | IPI00291419.2 | CYTOSOLIC ACETOACETYL-COENZYME A THIOLASE. | 41296 | 6.7 | 2 | 1 | 2.77 |
| 1118 | IPI00291764.1 | H2A HISTONE FAMILY, MEMBER C. | 14091 | 11.55 | 2 | 1 | 14.62 |
| 1119 | IPI00293655.2 | ATP-DEPENDENT HELICASE DDX1. | 86436 | 7.04 | 2 | 2 | 3.85 |
| 1120 | IPI00293665.4 | KERATIN, TYPE II CYTOSKELETAL 6B. | 59868 | 8.16 | 2 | 1 | 2.13 |
| 1121 | IPI00293867.3 | D-DOPACHROME TAUTOMERASE. | 12712 | 7.42 | 2 | 1 | 11.02 |
| 1122 | IPI00294178.1 | SERINE/THREONINE PROTEIN PHOSPHATASE 2A, 65 KDA REGULATORY SUBUNIT A, BETA ISOFORM. | 66201 | 4.57 | 2 | 1 | 3 |
| 1123 | IPI00295542.1 | NUCLEOBINDIN 1 PRECURSOR. | 53821 | 4.92 | 2 | 2 | 7.81 |
| 1124 | IPI00296350.3 | KERATIN, TYPE II CYTOSKELETAL 6F. | 59936 | 8.16 | 2 | 1 | 2.13 |
| 1125 | IPI00297714.1 | GAMMA-SYNUCLEIN. | 13301 | 4.62 | 2 | 2 | 22.83 |
| 1126 | IPI00298306.3 | SERINE-PROTEIN KINASE ATM. | 350644 | 6.75 | 2 | 1 | 0.16 |
| 1127 | IPI00298363.2 | FAR UPSTREAM ELEMENT BINDING PROTEIN 2. | 72709 | 8.05 | 2 | 2 | 3.25 |
| 1128 | IPI00299076.1 | RECEPTOR-BINDING CANCER ANTIGEN EXPRESSED ON SISO CELLS. | 24377 | 6.08 | 2 | 1 | 2.35 |
| 1129 | IPI00299145.4 | TYPE II KERATIN K6H. | 60025 | 8.16 | 2 | 1 | 2.13 |
| 1130 | IPI00299573.4 | RIBOSOMAL PROTEIN L7A. | 29996 | 11.32 | 2 | 1 | 4.14 |
| 1131 | IPI00300725.2 | KERATIN, TYPE II CYTOSKELETAL 6C. | 60069 | 8.16 | 2 | 1 | 2.13 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 1132 | IPI00301909.3 | HYPOTHETICAL PROTEIN. | 36629 | 9.67 | 2 | 1 | 1.57 |
| 1133 | IPI00302712.1 | SPLICE ISOFORM 2A OF Q13409 DYNEIN INTERMEDIATE CHAIN 2, CYTOSOLIC. | 71755 | 4.92 | 2 | 2 | 4.84 |
| 1134 | IPI00302925.1 | T-COMPLEX PROTEIN 1, THETA SUBUNIT. | 59621 | 5.3 | 2 | 2 | 4.01 |
| 1135 | IPI00303133.3 | HISTONE H2B.J. | 13761 | 11 | 2 | 2 | 20.8 |
| 1136 | IPI00303315.1 | H2A HISTONE FAMILY, MEMBER A. | 14135 | 11.66 | 2 | 1 | 14.62 |
| 1137 | IPI00304490.3 | HYPOTHETICAL PROTEIN KIAA1764. | 119885 | 6.17 | 2 | 1 | 0.78 |
| 1138 | IPI00304692.1 | HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN G. | 42332 | 10.39 | 2 | 2 | 6.14 |
| 1139 | IPI00305692.2 | THIOREDOXIN-LIKE PROTEIN. | 35546 | 4.88 | 2 | 2 | 11.95 |
| 1140 | IPI00306301.1 | PYRUVATE DEHYDROGENASE E1 COMPONENT ALPHA SUBUNIT, SOMATIC FORM, MITOCHONDRIAL PRECURSOR. | 43296 | 8.14 | 2 | 1 | 3.33 |
| 1141 | IPI00328202.2 | GUANINE NUCLEOTIDE-BINDING PROTEIN G(I), ALPHA-2 SUBUNIT. | 40320 | 5.2 | 2 | 1 | 3.39 |
| 1142 | IPI00328343.6 | PROBABLE ATP-DEPENDENT RNA HELICASE P47. | 53243 | 5.51 | 2 | 2 | 6.44 |
| 1143 | IPI00329665.2 | HISTONE H2B.S. | 13813 | 11.05 | 2 | 2 | 20.8 |
| 1144 | IPI00329717.3 | HISTONE H2B.R. | 13773 | 11 | 2 | 2 | 20.8 |
| 1145 | IPI00332418.2 | RIBOSOMAL PROTEIN L7A. | 27358 | 11.16 | 2 | 1 | 4.56 |
| 1146 | IPI00332452.3 | HYPOTHETICAL PROTEIN FLJ20288. | 73616 | 8.19 | 2 | 1 | 0.87 |
| 1147 | IPI00332511.4 | SERINE/THREONINE PROTEIN PHOSPHATASE 2A, 55 KDA REGULATORY SUBUNIT B, ALPHA ISOFORM. | 58255 | 7.23 | 2 | 1 | 2.76 |
| 1148 | IPI00333841.3 | SEPTIN KIAA0202D. | 52498 | 6.66 | 2 | 1 | 2.43 |
| 1149 | IPI00334168.1 | --none found in database-- | 49350 | 4.85 | 2 | 1 | 2.49 |
| 1150 | IPI00335053.1 | --none found in database-- | 37874 | 9.99 | 2 | 1 | 1.98 |
| 1151 | IPI00335449.1 | PROTEIN PHOSPHATASE 2 (FORMERLY 2A), REGULATORY SUBUNIT A (PR 65), BETA ISOFORM. | 73585 | 4.69 | 2 | 1 | 2.7 |
| 1152 | IPI00336094.1 | SPLICE ISOFORM 2 OF Q99714 3-HYDROXYACYL-COA DEHYDROGENASE TYPE II. | 25984 | 7.29 | 2 | 2 | 14.68 |
| 1153 | IPI00337415.1 | GUANINE NUCLEOTIDE-BINDING PROTEIN G(I), ALPHA-1 SUBUNIT. | 41147 | 6.27 | 2 | 1 | 3.32 |
| 1154 | IPI00339230.1 | SPLICE ISOFORM 3 OF Q16629 SPLICING FACTOR, ARGININE/SERINE-RICH 7. | 15257 | 9.88 | 2 | 1 | 10.61 |
| 1155 | IPI00339285.1 | HISTONE H2B.N. | 13776 | 10.89 | 2 | 2 | 20.8 |
| 1156 | IPI00373922.1 | SIMILAR TO 60S RIBOSOMAL PROTEIN L7A (SURFEIT LOCUS PROTEIN 3) (PLA-X POLYPEPTIDE). | 27765 | 11.35 | 2 | 1 | 4.49 |
| 1157 | IPI00373935.1 | SIMILAR TO 40S RIBOSOMAL PROTEIN SA (P40) (34/67 KDA LAMININ RECEPTOR) (COLON CARCINOMA LAMININ-BINDING PROTEIN) (NEM/1CHD4) (MULTIDRUG RESISTANCE-ASSOCIATED PROTEIN MGR1-AG). | 30638 | 4.43 | 2 | 2 | 13.5 |
| 1158 | IPI00374199.1 | SIMILAR TO TROPOMYOSIN 3. | 19174 | 4.45 | 2 | 1 | 8.24 |
| 1159 | IPI00374249.1 | SIMILAR TO ENSANGP00000025329. | 26487 | 10.87 | 2 | 1 | 4.7 |
| 1160 | IPI00374259.1 | ATAXIA TELANGIECTASIA MUTATED PROTEIN ISOFORM 2. | 195978 | 6.75 | 2 | 1 | 0.29 |
| 1161 | IPI00374876.1 | HYPOTHETICAL PROTEIN XP_353305. | 21818 | 10.24 | 2 | 1 | 2.65 |
| 1162 | IPI00375843.1 | HYPOTHETICAL PROTEIN DKFZP686J1375. | 54176 | 5.05 | 2 | 1 | 2.26 |
| 1163 | IPI00376041.1 | HYPOTHETICAL PROTEIN. | 63446 | 4.69 | 2 | 1 | 0.89 |
| 1164 | IPI00376493.1 | PHD FINGER PROTEIN 2 ISOFORM B. | 120992 | 10.07 | 2 | 1 | 0.54 |
| 1165 | IPI00376647.1 | SIMILAR TO PEPTIDYLPROLYL ISOMERASE A. | 17978 | 6.27 | 2 | 2 | 6.96 |
| 1166 | IPI00376664.1 | SIMILAR TO PEPTIDYLPROLYL ISOMERASE A. | 14624 | 6.08 | 2 | 2 | 8.15 |
| 1167 | IPI00376688.1 | N-ACYLSPHINGOSINE AMIDOHYDROLASE (ACID CERAMIDASE) 1 ISOFORM B. | 46494 | 7.97 | 2 | 2 | 8.27 |
| 1168 | IPI00376972.1 | BETA ISOFORM OF REGULATORY SUBUNIT B55, PROTEIN PHOSPHATASE 2 ISOFORM B. | 52017 | 7.02 | 2 | 1 | 3.14 |
| 1169 | IPI00376973.1 | BETA ISOFORM OF REGULATORY SUBUNIT B55, PROTEIN PHOSPHATASE 2 ISOFORM C. | 49333 | 6.7 | 2 | 1 | 3.31 |
| 1170 | IPI00376974.1 | BETA ISOFORM OF REGULATORY SUBUNIT B55, PROTEIN PHOSPHATASE 2 ISOFORM D. | 50371 | 6.58 | 2 | 1 | 3.24 |
| 1171 | IPI00376997.1 | HISTONE H2B.L. | 13805 | 11 | 2 | 2 | 20.8 |
| 1172 | IPI00377199.1 | HISTONE H2B.D. | 17842 | 11.46 | 2 | 2 | 16.46 |
| 1173 | IPI00382458.1 | SPLICE ISOFORM 2 OF Q13618 CULLIN HOMOLOG 3. | 86234 | 8.1 | 2 | 1 | 0.67 |
| 1174 | IPI00382459.1 | SPLICE ISOFORM 3 OF Q13618 CULLIN HOMOLOG 3. | 81093 | 8.72 | 2 | 1 | 0.71 |
| 1175 | IPI00382480.1 | IG HEAVY CHAIN V-III REGION BRO. | 13227 | 6.49 | 2 | 1 | 4.17 |
| 1176 | IPI00382536.1 | IG HEAVY CHAIN V-II REGION MCE. | 13792 | 8.76 | 2 | 1 | 4 |
| 1177 | IPI00382725.1 | CEI-A PROTEIN PRECURSOR. | 19292 | 11.9 | 2 | 1 | 2.81 |
| 1178 | IPI00383317.1 | PRO2275. | 13097 | 9.66 | 2 | 1 | 15 |
| 1179 | IPI00383853.1 | HYPOTHETICAL PROTEIN. | 40660 | 7.4 | 2 | 2 | 5.48 |
| 1180 | IPI00384339.2 | KATNA1 PROTEIN. | 41120 | 10.09 | 2 | 1 | 1.38 |
| 1181 | IPI00384365.1 | SIMILAR TO CHROMOSOME 8 OPEN READING FRAME 2. | 25355 | 8.57 | 2 | 1 | 3.93 |
| 1182 | IPI00384536.1 | HYPOTHETICAL PROTEIN KIAA1764. | 108166 | 5.6 | 2 | 1 | 0.86 |
| 1183 | IPI00385149.1 | HYPOTHETICAL PROTEIN. | 14577 | 3.63 | 2 | 2 | 10.29 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 1184 | IPI00385216.1 | LAMBDA-CRYSTALLIN. | 35419 | 6.1 | 2 | 1 | 3.45 |
| 1185 | IPI00385314.1 | TRIM28 PROTEIN. | 79474 | 5.85 | 2 | 1 | 3.98 |
| 1186 | IPI00385447.1 | DJ224A6.1.2 (CELL DIVISION CYCLE 42. | 26643 | 6.51 | 2 | 2 | 9.44 |
| 1187 | IPI00385928.1 | HYPOTHETICAL PROTEIN FLJ90472. | 78431 | 8.86 | 2 | 1 | 0.72 |
| 1188 | IPI00386438.2 | KERATIN, TYPE II CYTOSKELETAL 6D. | 42468 | 5.05 | 2 | 1 | 3.13 |
| 1189 | IPI00394837.1 | RAS-RELATED C3 BOTULINUM TOXIN SUBSTRATE 1 ISOFORM RAC1C. | 16797 | 9.23 | 2 | 2 | 16.22 |
| 1190 | IPI00395319.1 | HYPOTHETICAL PROTEIN KIAA1595. | 54113 | 10 | 2 | 2 | 1.7 |
| 1191 | IPI00395561.1 | SPLICE ISOFORM B OF Q9NQ66 1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE BETA 1. | 133703 | 6.35 | 2 | 1 | 0.43 |
| 1192 | IPI00000051.2 | PREFOLDIN SUBUNIT 1. | 14210 | 6.81 | 1 | 1 | 9.02 |
| 1193 | IPI00000494.1 | MSTP030. | 34363 | 10.21 | 1 | 1 | 4.71 |
| 1194 | IPI00000534.2 | SIMILAR TO KIAA1671 PROTEIN. | 193711 | 8.64 | 1 | 1 | 0.28 |
| 1195 | IPI00000760.1 | NG,NG-DIMETHYLARGININE DIMETHYLAMINOHYDROLASE 2. | 29644 | 5.9 | 1 | 1 | 5.61 |
| 1196 | IPI00001348.4 | HYPOTHETICAL PROTEIN KIAA0542. | 144083 | 11.42 | 1 | 1 | 0.41 |
| 1197 | IPI00002135.1 | TRANSFORMING ACIDIC COILED-COIL-CONTAINING PROTEIN 3. | 90360 | 4.69 | 1 | 1 | 0.6 |
| 1198 | IPI00002647.2 | WISKOTT-ALDRICH SYNDROME PROTEIN FAMILY MEMBER 4. | 68189 | 6.68 | 1 | 1 | 1.12 |
| 1199 | IPI00002949.5 | --none found in database-- | 52314 | 4.93 | 1 | 1 | 2.77 |
| 1200 | IPI00003327.1 | ADP-RIBOSYLATION FACTOR-LIKE PROTEIN 3. | 20456 | 7.35 | 1 | 1 | 12.09 |
| 1201 | IPI00003399.1 | TYPE II MEMBRANE PROTEIN. | 20652 | 4.55 | 1 | 1 | 8.79 |
| 1202 | IPI00004203.5 | HYPOTHETICAL PROTEIN FLJ22059. | 98900 | 8.11 | 1 | 1 | 0.78 |
| 1203 | IPI00004290.1 | HYPOTHETICAL PROTEIN DJ434O14.5. | 87055 | 5.72 | 1 | 1 | 0.66 |
| 1204 | IPI00004408.1 | SPLICE ISOFORM 2 OF Q9UEY8 GAMMA ADDUCIN. | 79155 | 6.26 | 1 | 1 | 1.7 |
| 1205 | IPI00004450.1 | TESTES SPECIFIC HETEROGENOUS NUCLEAR RIBONUCLEOPROTEIN G-T. | 42784 | 10.72 | 1 | 1 | 3.57 |
| 1206 | IPI00004488.1 | VACUOLAR ATP SYNTHASE SUBUNIT F. | 13358 | 5.19 | 1 | 1 | 10.08 |
| 1207 | IPI00004501.1 | SPLICE ISOFORM 1 OF P11277 SPECTRIN BETA CHAIN, ERYTHROCYTE. | 246322 | 4.9 | 1 | 1 | 0.47 |
| 1208 | IPI00004557.3 | SIMILAR TO KIAA0367. | 315796 | 4.05 | 1 | 1 | 0.17 |
| 1209 | IPI00004656.1 | BETA-2-MICROGLOBULIN PRECURSOR. | 13715 | 6.51 | 1 | 1 | 8.4 |
| 1210 | IPI00004838.1 | SPLICE ISOFORM CRK-II OF P46108 PROTO-ONCOGENE C-CRK. | 33872 | 5.44 | 1 | 1 | 5.59 |
| 1211 | IPI00004924.1 | DEF-6 PROTEIN. | 73910 | 5.89 | 1 | 1 | 1.58 |
| 1212 | IPI00005198.1 | NF45 PROTEIN. | 44697 | 8.32 | 1 | 1 | 2.71 |
| 1213 | IPI00005474.3 | PHOSPHOLYSINE PHOSPHOHISTIDINE INORGANIC PYROPHOSPHATE PHOSPHATASE. | 29193 | 6.36 | 1 | 1 | 7.78 |
| 1214 | IPI00005589.1 | WUGSC:H_DJ0844F09.1 PROTEIN. | 15751 | 11.6 | 1 | 1 | 9.63 |
| 1215 | IPI00005646.1 | HYPOTHETICAL PROTEIN KIAA0635. | 99213 | 5.64 | 1 | 1 | 1.06 |
| 1216 | IPI00005824.1 | VELI 1. | 25997 | 9.1 | 1 | 1 | 6.87 |
| 1217 | IPI00005969.1 | F-ACTIN CAPPING PROTEIN ALPHA-1 SUBUNIT. | 32923 | 5.42 | 1 | 1 | 5.94 |
| 1218 | IPI00006079.1 | HYPOTHETICAL PROTEIN KIAA0164. | 106122 | 10.61 | 1 | 1 | 1.96 |
| 1219 | IPI00006158.1 | LYMPHOID-RESTRICTED MEMBRANE PROTEIN. | 62093 | 5.74 | 1 | 1 | 1.44 |
| 1220 | IPI00006254.1 | PERIPHERAL BENZODIAZEPINE RECEPTOR INTERACTING PROTEIN. | 200150 | 4.78 | 1 | 1 | 0.27 |
| 1221 | IPI00006328.1 | ATPASE INHIBITOR, MITOCHONDRIAL PRECURSOR. | 12249 | 10.05 | 1 | 1 | 9.43 |
| 1222 | IPI00006504.1 | SPLICE ISOFORM 1 OF Q9NR50 TRANSLATION INITIATION FACTOR EIF-2B GAMMA SUBUNIT. | 50240 | 6.41 | 1 | 1 | 1.11 |
| 1223 | IPI00007087.1 | F-BOX ONLY PROTEIN 2. | 33257 | 4.01 | 1 | 1 | 4.07 |
| 1224 | IPI00007834.1 | SPLICE ISOFORM 1 OF Q01484 ANKYRIN 2. | 430344 | 4.77 | 1 | 1 | 0.2 |
| 1225 | IPI00007847.1 | UEV1AS. | 11842 | 9.46 | 1 | 1 | 8.74 |
| 1226 | IPI00007926.1 | RCL. | 19108 | 4.69 | 1 | 1 | 9.77 |
| 1227 | IPI00008055.1 | HYPOTHETICAL PROTEIN KIAA1285. | 87733 | 6 | 1 | 1 | 0.51 |
| 1228 | IPI00008200.1 | HYPOTHETICAL PROTEIN KIAA1197. | 157165 | 9.54 | 1 | 1 | 0.54 |
| 1229 | IPI00008332.1 | MYELIN TRANSCRIPTION FACTOR 1. | 122329 | 4.53 | 1 | 1 | 0.89 |
| 1230 | IPI00008418.1 | SPLICE ISOFORM 1 OF Q9NR28 SMAC PROTEIN, MITOCHONDRIAL PRECURSOR. | 27131 | 5.72 | 1 | 1 | 5.02 |
| 1231 | IPI00008511.1 | NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5. | 67027 | 9.32 | 1 | 1 | 1.16 |
| 1232 | IPI00008524.1 | POLYADENYLATE-BINDING PROTEIN 1. | 70671 | 10 | 1 | 1 | 1.73 |
| 1233 | IPI00008998.1 | HSPC121. | 44423 | 9.47 | 1 | 1 | 5.63 |
| 1234 | IPI00009159.2 | SIMILAR TO 40S RIBOSOMAL PROTEIN S6 (PHOSPHOPROTEIN NP33). | 28425 | 10.82 | 1 | 1 | 2.38 |
| 1235 | IPI00009227.2 | BCL-2-ASSOCIATED TRANSCRIPTION FACTOR SHORT FORM. | 100216 | 10.57 | 1 | 1 | 2.07 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 1236 | IPI00009328.2 | PROBABLE ATP-DEPENDENT HELICASE DDX48. | 46871 | 6.69 | 1 | 1 | 1.95 |
| 1237 | IPI00009468.3 | SIMILAR TO VACUOLAR PROTEIN SORTING 35. | 140263 | 7.25 | 1 | 1 | 0.8 |
| 1238 | IPI00009887.1 | SPLICE ISOFORM 2 OF Q9HBY8 SERINE/THREONINE-PROTEIN KINASE SGK2. | 47604 | 7.5 | 1 | 1 | 1.17 |
| 1239 | IPI00009922.1 | DC50. | 12349 | 11 | 1 | 1 | 5.5 |
| 1240 | IPI00009995.2 | ETS TRANSCRIPTION FACTOR. | 62711 | 6.68 | 1 | 1 | 0.86 |
| 1241 | IPI00010270.1 | RAS-RELATED C3 BOTULINUM TOXIN SUBSTRATE 2. | 21429 | 7.7 | 1 | 1 | 5.21 |
| 1242 | IPI00010402.1 | SH3 DOMAIN-BINDING GLUTAMIC ACID-RICH-LIKE PROTEIN 3. | 10438 | 4.56 | 1 | 1 | 10.75 |
| 1243 | IPI00010415.2 | SPLICE ISOFORM 1 OF O00154 CYTOSOLIC ACYL COENZYME A THIOESTER HYDROLASE. | 41796 | 8.66 | 1 | 1 | 3.16 |
| 1244 | IPI00010420.1 | HYPOTHETICAL PROTEIN. | 35022 | 10.46 | 1 | 1 | 3.49 |
| 1245 | IPI00010496.1 | HYPOTHETICAL PROTEIN KIAA1045. | 48030 | 5.88 | 1 | 1 | 3.98 |
| 1246 | IPI00010970.2 | HYPOTHETICAL PROTEIN KIAA1617. | 101667 | 6.68 | 1 | 1 | 0.55 |
| 1247 | IPI00011274.1 | JKTBP2. | 46438 | 9.98 | 1 | 1 | 3.81 |
| 1248 | IPI00011603.2 | 26S PROTEASOME NON-ATPASE REGULATORY SUBUNIT 3. | 60978 | 8.75 | 1 | 1 | 0.94 |
| 1249 | IPI00011702.2 | PROTEIN KIAA0406. | 122069 | 5.85 | 1 | 1 | 0.92 |
| 1250 | IPI00011730.2 | SIMILAR TO ELASTIN MICROFIBRIL INTERFACE LOCATED PROTEIN 5. | 82647 | 7.76 | 1 | 1 | 0.78 |
| 1251 | IPI00011964.1 | ADDUCIN 2 ISOFORM F. | 56350 | 5.3 | 1 | 1 | 2.38 |
| 1252 | IPI00011982.1 | ADDUCIN 2 ISOFORM G. | 46168 | 5.26 | 1 | 1 | 2.91 |
| 1253 | IPI00012341.1 | SPLICE ISOFORM SRP40-1 OF Q13243 SPLICING FACTOR, ARGININE/SERINE-RICH 5. | 31264 | 12.1 | 1 | 1 | 1.84 |
| 1254 | IPI00012345.2 | SPLICE ISOFORM SRP55-1 OF Q13247 SPLICING FACTOR, ARGININE/SERINE-RICH 6. | 39587 | 11.94 | 1 | 1 | 2.62 |
| 1255 | IPI00012441.1 | SPLICE ISOFORM 1 OF O43426 SYNAPTOJANIN 1. | 173346 | 7.44 | 1 | 1 | 0.83 |
| 1256 | IPI00012451.1 | GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT 4. | 37567 | 5.85 | 1 | 1 | 2.94 |
| 1257 | IPI00012682.1 | SIMILAR TO DEATH-ASSOCIATED PROTEIN. | 11880 | 10.72 | 1 | 1 | 7.48 |
| 1258 | IPI00012751.1 | 40S RIBOSOMAL PROTEIN S28. | 7841 | 11.33 | 1 | 1 | 13.04 |
| 1259 | IPI00012893.2 | SPLICE ISOFORM 1 OF O43566 REGULATOR OF G-PROTEIN SIGNALING 14. | 64601 | 9.25 | 1 | 1 | 0.67 |
| 1260 | IPI00013290.1 | SIMILAR TO HEPATOMA-DERIVED GROWTH FACTOR, RELATED PROTEIN 2. | 74230 | 7.62 | 1 | 1 | 2.24 |
| 1261 | IPI00013296.1 | 40S RIBOSOMAL PROTEIN S18. | 17719 | 11.6 | 1 | 1 | 7.24 |
| 1262 | IPI00013396.1 | U1 SMALL NUCLEAR RIBONUCLEOPROTEIN C. | 17394 | 10.14 | 1 | 1 | 7.55 |
| 1263 | IPI00013415.1 | 40S RIBOSOMAL PROTEIN S7. | 22127 | 10.86 | 1 | 1 | 11.34 |
| 1264 | IPI00013485.1 | 40S RIBOSOMAL PROTEIN S2. | 31324 | 10.9 | 1 | 1 | 4.44 |
| 1265 | IPI00013860.1 | 3-HYDROXYISOBUTYRATE DEHYDROGENASE, MITOCHONDRIAL PRECURSOR. | 35329 | 8.26 | 1 | 1 | 5.65 |
| 1266 | IPI00013888.1 | INTEGRAL MEMBRANE PROTEIN 2A. | 29741 | 5.49 | 1 | 1 | 1.52 |
| 1267 | IPI00013949.1 | SMALL GLUTAMINE-RICH TETRATRICOPEPTIDE REPEAT-CONTAINING PROTEIN. | 34063 | 4.51 | 1 | 1 | 2.88 |
| 1268 | IPI00014151.1 | 26S PROTEASOME NON-ATPASE REGULATORY SUBUNIT 6. | 45531 | 5.29 | 1 | 1 | 3.86 |
| 1269 | IPI00014439.1 | DIHYDROPTERIDINE REDUCTASE. | 25804 | 7.45 | 1 | 1 | 7.38 |
| 1270 | IPI00014455.3 | R31167_1, PARTIAL PROTEIN. | 53887 | 5.07 | 1 | 1 | 1 |
| 1271 | IPI00014537.1 | SPLICE ISOFORM 1 OF O43852 CALUMENIN PRECURSOR. | 37107 | 4.23 | 1 | 1 | 3.49 |
| 1272 | IPI00014754.3 | SIMILAR TO 40S RIBOSOMAL PROTEIN SA (P40) (34/67 KDA LAMININ RECEPTOR) (COLON CARCINOMA LAMININ-BINDING PROTEIN) (NEM/1CHD4) (MULTIDRUG RESISTANCE-ASSOCIATED PROTEIN MGR1-AG). | 23486 | 4.21 | 1 | 1 | 2.83 |
| 1273 | IPI00014925.1 | ATP-DEPENDENT DNA HELICASE Q4. | 133077 | 8.12 | 1 | 1 | 0.83 |
| 1274 | IPI00015018.1 | INORGANIC PYROPHOSPHATASE. | 32660 | 5.64 | 1 | 1 | 3.46 |
| 1275 | IPI00015115.1 | SIMILAR TO AC45. | 25310 | 9.99 | 1 | 1 | 4.46 |
| 1276 | IPI00015148.3 | RAS-RELATED PROTEIN RAP-1B. | 20825 | 5.39 | 1 | 1 | 6.52 |
| 1277 | IPI00015157.1 | HYPOTHETICAL PROTEIN. | 16313 | 10.38 | 1 | 1 | 9.03 |
| 1278 | IPI00015180.1 | APICAL-LIKE PROTEIN. | 176410 | 7.09 | 1 | 1 | 0.37 |
| 1279 | IPI00015351.1 | AD039. | 24178 | 5.56 | 1 | 1 | 4.27 |
| 1280 | IPI00015526.2 | SPLICE ISOFORM 1 OF Q9H9B1 HISTONE-LYSINE N-METHYLTRANSFERASE, H3 LYSINE-9 SPECIFIC 5. | 138182 | 5.83 | 1 | 1 | 0.39 |
| 1281 | IPI00015730.1 | PROSTAGLANDIN F2-ALPHA RECEPTOR. | 40055 | 9.11 | 1 | 1 | 1.67 |
| 1282 | IPI00015826.1 | ATP-BINDING CASSETTE, SUB-FAMILY B, MEMBER 10, MITOCHONDRIAL PRECURSOR. | 79099 | 10.41 | 1 | 1 | 0.81 |
| 1283 | IPI00015891.1 | PREFOLDIN SUBUNIT 4. | 15314 | 4.15 | 1 | 1 | 8.96 |
| 1284 | IPI00015973.1 | BAND 4.1-LIKE PROTEIN 2. | 112588 | 5.13 | 1 | 1 | 1 |
| 1285 | IPI00016456.1 | ADENOVIRUS 5 E1A-BINDING PROTEIN. | 66203 | 8.3 | 1 | 1 | 1.6 |
| 1286 | IPI00016664.1 | FORKHEAD BOX PROTEIN E2. | 52389 | 11.25 | 1 | 1 | 1 |
| 1287 | IPI00016734.1 | HOMEOBOX PROTEIN ENGRAILED-1. | 40101 | 10.09 | 1 | 1 | 1.28 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 1288 | IPI00016768.1 | L-LACTATE DEHYDROGENASE A-LIKE. | 41943 | 8.89 | 1 | 1 | 1.57 |
| 1289 | IPI00016783.1 | NUCLEAR TRANSITION PROTEIN 2. | 15641 | 12.14 | 1 | 1 | 4.35 |
| 1290 | IPI00017025.2 | SIMILAR TO PEPTIDYL-PRO CIS TRANS ISOMERASE. | 21072 | 7.74 | 1 | 1 | 2.55 |
| 1291 | IPI00017297.1 | MATRIN 3. | 94623 | 6.19 | 1 | 1 | 2.48 |
| 1292 | IPI00017367.1 | RADIXIN. | 68564 | 6.3 | 1 | 1 | 1.54 |
| 1293 | IPI00017704.1 | COACTOSIN-LIKE PROTEIN. | 15945 | 5.31 | 1 | 1 | 11.27 |
| 1294 | IPI00017870.1 | BA13B9.3. | 55152 | 4.55 | 1 | 1 | 1.8 |
| 1295 | IPI00018195.1 | MITOGEN-ACTIVATED PROTEIN KINASE 3. | 43136 | 6.74 | 1 | 1 | 3.96 |
| 1296 | IPI00018214.1 | SPLICE ISOFORM 1 OF P25912 MAX PROTEIN. | 18275 | 6.25 | 1 | 1 | 6.25 |
| 1297 | IPI00018262.1 | ACIDIC LEUCINE-RICH NUCLEAR PHOSPHOPROTEIN 32 FAMILY MEMBER C. | 26762 | 3.86 | 1 | 1 | 4.7 |
| 1298 | IPI00018272.1 | PYRIDOXINE-5'-PHOSPHATE OXIDASE. | 29988 | 7.09 | 1 | 1 | 3.45 |
| 1299 | IPI00018342.2 | ADENYLATE KINASE ISOENZYME 1. | 21635 | 8.99 | 1 | 1 | 7.22 |
| 1300 | IPI00018398.2 | 26S PROTEASE REGULATORY SUBUNIT 6A. | 49204 | 4.87 | 1 | 1 | 3.19 |
| 1301 | IPI00018465.1 | T-COMPLEX PROTEIN 1, ETA SUBUNIT. | 59367 | 7.73 | 1 | 1 | 2.58 |
| 1302 | IPI00018590.1 | SIMILARITY BY BLASTN TO AF063018. | 40925 | 9.71 | 1 | 1 | 1.63 |
| 1303 | IPI00018693.1 | OLFACTORY RECEPTOR 1Q1. | 35616 | 8.96 | 1 | 1 | 1.59 |
| 1304 | IPI00018768.1 | TRANSLIN. | 26183 | 6.41 | 1 | 1 | 5.26 |
| 1305 | IPI00018871.1 | HYPOTHETICAL PROTEIN FLJ10702. | 21539 | 8.62 | 1 | 1 | 12.37 |
| 1306 | IPI00018931.2 | VACUOLAR PROTEIN SORTING 35. | 91707 | 5.17 | 1 | 1 | 1.26 |
| 1307 | IPI00018963.1 | SPLICE ISOFORM 1 OF Q9NVD7 ALPHA-PARVIN. | 42244 | 5.74 | 1 | 1 | 1.34 |
| 1308 | IPI00019171.1 | SH3-CONTAINING GRB2-LIKE PROTEIN 2. | 39962 | 5.14 | 1 | 1 | 4.55 |
| 1309 | IPI00019345.1 | RAS-RELATED PROTEIN RAP-1A. | 20987 | 6.55 | 1 | 1 | 6.52 |
| 1310 | IPI00019355.1 | REGULATORY PROTEIN TSC-22. | 15680 | 4.87 | 1 | 1 | 8.33 |
| 1311 | IPI00019884.1 | ALPHA-ACTININ 2. | 103854 | 5.13 | 1 | 1 | 1.68 |
| 1312 | IPI00019904.1 | SPLICE ISOFORM 1 OF P35612 BETA ADDUCIN. | 80854 | 5.73 | 1 | 1 | 1.65 |
| 1313 | IPI00019997.1 | HYPOTHETICAL PROTEIN FLJ11215. | 21834 | 8.7 | 1 | 1 | 8.12 |
| 1314 | IPI00020008.1 | UBIQUITIN-LIKE PROTEIN NEDD8. | 9072 | 9 | 1 | 1 | 17.28 |
| 1315 | IPI00020075.1 | HYPOTHETICAL PROTEIN FLJ11342. | 33933 | 8.77 | 1 | 1 | 6.21 |
| 1316 | IPI00020273.1 | ATP-SENSITIVE INWARD RECTIFIER POTASSIUM CHANNEL 10. | 42508 | 8.2 | 1 | 1 | 1.32 |
| 1317 | IPI00020546.1 | ASH1. | 332768 | 9.95 | 1 | 1 | 0.2 |
| 1318 | IPI00021034.1 | COLLAGEN ALPHA 1(IV) CHAIN PRECURSOR. | 160611 | 8.42 | 1 | 1 | 0.3 |
| 1319 | IPI00021122.1 | OLFACTORY RECEPTOR 17-1. | 32021 | 10.42 | 1 | 1 | 2.02 |
| 1320 | IPI00021338.1 | DIHYDROLIPOAMIDE ACETYLTRANSFERASE COMPONENT OF PYRUVATE DEHYDROGENASE COMPLEX, MITOCHONDRIAL PRECURSOR. | 65781 | 5.95 | 1 | 1 | 2.44 |
| 1321 | IPI00021396.1 | VASCULAR ENDOTHELIAL GROWTH FACTOR RECEPTOR 2 PRECURSOR. | 151527 | 5.64 | 1 | 1 | 0.37 |
| 1322 | IPI00021435.1 | PROTEASOME 26S ATPASE SUBUNIT 2. | 48634 | 5.65 | 1 | 1 | 2.54 |
| 1323 | IPI00021808.1 | HISTIDYL-TRNA SYNTHETASE. | 57410 | 5.56 | 1 | 1 | 0.98 |
| 1324 | IPI00021819.1 | CYTOCHROME P450 2D6. | 55802 | 7.26 | 1 | 1 | 1.21 |
| 1325 | IPI00021885.1 | SPLICE ISOFORM ALPHA-E OF P02671 FIBRINOGEN ALPHA/ALPHA-E CHAIN PRECURSOR [Contains: FIBRINOPEPTIDE A]. | 94973 | 5.87 | 1 | 1 | 1.73 |
| 1326 | IPI00021954.1 | GOLGI-SPECIFIC BREFELDIN A-RESISTANCE GUANINE NUCLEOTIDE EXCHANGE FACTOR 1. | 206446 | 5.5 | 1 | 1 | 0.32 |
| 1327 | IPI00022326.1 | OLFACTORY RECEPTOR 10A5. | 35519 | 8.94 | 1 | 1 | 1.58 |
| 1328 | IPI00022432.1 | TRANSTHYRETIN PRECURSOR. | 15887 | 5.58 | 1 | 1 | 8.84 |
| 1329 | IPI00023004.2 | EUKARYOTIC TRANSLATION INITIATION FACTOR 1A, Y-CHROMOSOMAL. | 16311 | 4.84 | 1 | 1 | 7.69 |
| 1330 | IPI00023048.2 | ELONGATION FACTOR 1-DELTA. | 31122 | 4.63 | 1 | 1 | 3.2 |
| 1331 | IPI00023138.1 | RAS-RELATED C3 BOTULINUM TOXIN SUBSTRATE 3. | 21379 | 8.27 | 1 | 1 | 5.21 |
| 1332 | IPI00023258.2 | SIMILAR TO TRANSCRIPTION INITIATION FACTOR TFIID 105 KDA SUBUNIT (TAFII-105) (TAFII105). | 101928 | 9.88 | 1 | 1 | 0.73 |
| 1333 | IPI00023601.1 | PROTEOGLYCAN LINK PROTEIN PRECURSOR. | 40166 | 7.45 | 1 | 1 | 3.39 |
| 1334 | IPI00024664.1 | SPLICE ISOFORM LONG OF P45974 UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 5. | 95786 | 4.65 | 1 | 1 | 1.86 |
| 1335 | IPI00024670.2 | POLYPOSIS LOCUS PROTEIN 1. | 21133 | 8.29 | 1 | 1 | 5.95 |
| 1336 | IPI00024920.1 | ATP SYNTHASE DELTA CHAIN, MITOCHONDRIAL PRECURSOR. | 17490 | 5.19 | 1 | 1 | 8.33 |
| 1337 | IPI00025084.1 | CALCIUM-DEPENDENT PROTEASE, SMALL SUBUNIT. | 28316 | 4.82 | 1 | 1 | 8.58 |
| 1338 | IPI00025329.1 | 60S RIBOSOMAL PROTEIN L19. | 23466 | 12.03 | 1 | 1 | 8.67 |
| 1339 | IPI00025340.1 | HYPOTHETICAL PROTEIN. | 31698 | 6.51 | 1 | 1 | 4.73 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 1340 | IPI00025477.2 | SPLICE ISOFORM ALPHA-1B-1 OF Q00975 VOLTAGE-DEPENDENT N-TYPE CALCIUM CHANNEL ALPHA-1B SUBUNIT. | 264305 | 8.75 | 1 | 1 | 0.47 |
| 1341 | IPI00025710.1 | PROTEIN C21ORF59. | 33224 | 7.55 | 1 | 1 | 1.72 |
| 1342 | IPI00025961.1 | HYPOTHETICAL PROTEIN KIAA1411. | 170604 | 5.1 | 1 | 1 | 0.39 |
| 1343 | IPI00026138.2 | SIMILAR TO RIBOSOMAL PROTEIN S3A. | 29847 | 10.3 | 1 | 1 | 3.79 |
| 1344 | IPI00026167.1 | NHP2-LIKE PROTEIN 1. | 14174 | 8.64 | 1 | 1 | 8.59 |
| 1345 | IPI00026314.1 | GELSOLIN PRECURSOR, PLASMA. | 85698 | 6.19 | 1 | 1 | 1.66 |
| 1346 | IPI00026519.1 | PEPTIDYL-PROLYL CIS-TRANS ISOMERASE, MITOCHONDRIAL PRECURSOR. | 22040 | 9.95 | 1 | 1 | 2.42 |
| 1347 | IPI00026533.4 | HYPOTHETICAL PROTEIN FLJ20032. | 130277 | 7.85 | 1 | 1 | 0.43 |
| 1348 | IPI00027500.1 | TRANSFORMING PROTEIN RHOA. | 21768 | 5.89 | 1 | 1 | 5.18 |
| 1349 | IPI00027626.1 | T-COMPLEX PROTEIN 1, ZETA SUBUNIT. | 58024 | 6.65 | 1 | 1 | 3.95 |
| 1350 | IPI00027717.1 | COMPONENT OF GEMS 4. | 119990 | 6 | 1 | 1 | 0.66 |
| 1351 | IPI00027860.1 | PROBABLE SERINE PROTEASE HTRA4 PRECURSOR. | 50979 | 8.07 | 1 | 1 | 1.05 |
| 1352 | IPI00027862.2 | PROBABLE SERINE PROTEASE HTRA3 PRECURSOR. | 48608 | 7.1 | 1 | 1 | 3.97 |
| 1353 | IPI00027996.1 | 70 KDA WD-REPEAT TUMOR REJECTION ANTIGEN HOMOLOG. | 100575 | 5.55 | 1 | 1 | 1.19 |
| 1354 | IPI00028004.2 | PROTEASOME SUBUNIT BETA TYPE 3. | 22949 | 6.51 | 1 | 1 | 7.8 |
| 1355 | IPI00028277.2 | SIMILAR TO KIAA1752 PROTEIN. | 61383 | 4.83 | 1 | 1 | 2.6 |
| 1356 | IPI00028448.1 | BRAIN-SPECIFIC ANGIOGENESIS INHIBITOR 3 PRECURSOR. | 171491 | 7.06 | 1 | 1 | 0.33 |
| 1357 | IPI00028454.1 | HYPOTHETICAL PROTEIN KIAA1692. | 97050 | 6.65 | 1 | 1 | 0.7 |
| 1358 | IPI00028951.2 | POTENTIAL PHOSPHOLIPID-TRANSPORTING ATPASE VA. | 167688 | 8.43 | 1 | 1 | 0.33 |
| 1359 | IPI00028975.2 | SPLICE ISOFORM II OF Q14141 SEPTIN 6. | 49717 | 6.65 | 1 | 1 | 2.3 |
| 1360 | IPI00029208.1 | MYOSIN LIGHT CHAIN ALKALI, SMOOTH-MUSCLE ISOFORM. | 16830 | 4.19 | 1 | 1 | 8.67 |
| 1361 | IPI00029413.1 | OLFACTORY RECEPTOR 10A1. | 25309 | 8.94 | 1 | 1 | 2.2 |
| 1362 | IPI00029485.2 | SPLICE ISOFORM P150 OF Q14203 DYNACTIN 1. | 141695 | 5.58 | 1 | 1 | 1.72 |
| 1363 | IPI00029534.1 | AMIDOPHOSPHORIBOSYLTRANSFERASE PRECURSOR. | 57399 | 6.74 | 1 | 1 | 1.16 |
| 1364 | IPI00029626.1 | ELF-1 RELATED PROTEIN. | 70984 | 6.08 | 1 | 1 | 0.75 |
| 1365 | IPI00029717.1 | SPLICE ISOFORM ALPHA OF P02671 FIBRINOGEN ALPHA/ALPHA-E CHAIN PRECURSOR [Contains: FIBRINOPEPTIDE A]. | 69757 | 8.17 | 1 | 1 | 2.33 |
| 1366 | IPI00030023.1 | HISTAMINE N-METHYLTRANSFERASE. | 33295 | 4.98 | 1 | 1 | 3.42 |
| 1367 | IPI00030126.1 | PROBABLE G PROTEIN-COUPLED RECEPTOR GPR18. | 38062 | 9.65 | 1 | 1 | 1.21 |
| 1368 | IPI00030154.1 | PROTEASOME ACTIVATOR COMPLEX SUBUNIT 1. | 28723 | 5.83 | 1 | 1 | 4.82 |
| 1369 | IPI00030267.1 | HYPOTHETICAL PROTEIN. | 180827 | 6.72 | 1 | 1 | 0.3 |
| 1370 | IPI00030536.2 | SPLICE ISOFORM 1 OF Q9HCH5 SYNAPTOTAGMIN-LIKE PROTEIN 2. | 102666 | 8.15 | 1 | 1 | 0.66 |
| 1371 | IPI00030907.1 | ALPHA-2 CATENIN. | 105282 | 5.53 | 1 | 1 | 0.52 |
| 1372 | IPI00031422.3 | CARDIAC SODIUM CHANNEL ALPHA SUBUNIT NAV1.5. | 226812 | 5.15 | 1 | 1 | 0.45 |
| 1373 | IPI00031519.1 | SPLICE ISOFORM 1 OF P26358 DNA (CYTOSINE-5)-METHYLTRANSFERASE 1. | 183165 | 7.81 | 1 | 1 | 0.37 |
| 1374 | IPI00031522.2 | TRIFUNCTIONAL ENZYME ALPHA SUBUNIT, MITOCHONDRIAL PRECURSOR (TP-ALPHA) (78 KDA GASTRIN-BINDING PROTEIN) [Includes: LONG-CHAIN ENOYL-COA HYDRATASE (EC 4.2.1.17); LONG CHAIN 3-HYDROXYACYL-COA DEHYDROGENASE (EC 1.1.1.35)]. | 83000 | 9.52 | 1 | 1 | 1.83 |
| 1375 | IPI00031812.1 | NUCLEASE SENSITIVE ELEMENT BINDING PROTEIN 1. | 35924 | 10.31 | 1 | 1 | 5.86 |
| 1376 | IPI00032050.2 | WW DOMAIN BINDING PROTEIN 2. | 28087 | 5.72 | 1 | 1 | 3.83 |
| 1377 | IPI00032461.1 | GUANINE DEAMINASE. | 51003 | 5.45 | 1 | 1 | 2.64 |
| 1378 | IPI00033904.2 | SIMILAR TO RIBOSOMAL PROTEIN S3A. | 29971 | 10.47 | 1 | 1 | 3.79 |
| 1379 | IPI00034319.1 | DIVALENT CATION TOLERANT PROTEIN CUTA. | 16833 | 4.87 | 1 | 1 | 17.31 |
| 1380 | IPI00035766.2 | SIMILAR TO PEPTIDYL-PRO CIS TRANS ISOMERASE. | 17525 | 7.89 | 1 | 1 | 3.14 |
| 1381 | IPI00037283.1 | DYNAMIN-LIKE PROTEIN DYMPLE ISOFORM. | 78061 | 6.68 | 1 | 1 | 1 |
| 1382 | IPI00037448.1 | GLYOXYLATE REDUCTASE. | 35668 | 7.44 | 1 | 1 | 5.49 |
| 1383 | IPI00043606.1 | HYPOTHETICAL PROTEIN FLJ31030. | 66043 | 9 | 1 | 1 | 0.7 |
| 1384 | IPI00045051.1 | PUR-BETA. | 33241 | 5.06 | 1 | 1 | 4.17 |
| 1385 | IPI00045396.1 | SPLICE ISOFORM 2 OF O43852 CALUMENIN PRECURSOR. | 37135 | 4.18 | 1 | 1 | 3.49 |
| 1386 | IPI00045438.1 | SOLUTE CARRIER FAMILY 26, MEMBER 9 ISOFORM A. | 86988 | 8.33 | 1 | 1 | 0.63 |
| 1387 | IPI00045498.1 | JKTBP1DELTA6. | 27191 | 8.99 | 1 | 1 | 6.56 |
| 1388 | IPI00045527.1 | PROTEOGLYCAN LINK PROTEIN. | 40894 | 6.5 | 1 | 1 | 3.33 |
| 1389 | IPI00045729.1 | HYPOTHETICAL PROTEIN FLJ14981. | 48585 | 5.33 | 1 | 1 | 1.11 |
| 1390 | IPI00045864.1 | HYPOTHETICAL PROTEIN FLJ14710. | 65622 | 9.1 | 1 | 1 | 1.04 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 1391 | IPI00047526.3 | SIMILAR TO 40S RIBOSOMAL PROTEIN S3A (V-FOS TRANSFORMATION EFFECTOR PROTEIN). | 22075 | 10.46 | 1 | 1 | 5.18 |
| 1392 | IPI00050096.4 | SIMILAR TO MITOCHONDRIAL ACONITASE. | 41937 | 10.03 | 1 | 1 | 2.71 |
| 1393 | IPI00050933.5 | SIMILAR TO PHOSPHOSERINE AMINOTRANSFERASE ISOFORM 1. | 41929 | 8.04 | 1 | 1 | 2.88 |
| 1394 | IPI00052316.2 | SIMILAR TO PEPTIDYLPROLYL ISOMERASE A. | 16975 | 6.59 | 1 | 1 | 3.31 |
| 1395 | IPI00056312.1 | HYPOTHETICAL PROTEIN FLJ25628. | 22502 | 4.56 | 1 | 1 | 4.5 |
| 1396 | IPI00056521.1 | SPLICE ISOFORM 1 OF Q969W9 TRANSMEMBRANE PROSTATE ANDROGEN-INDUCED PROTEIN. | 31609 | 6.89 | 1 | 1 | 1.74 |
| 1397 | IPI00058448.3 | SIMILAR TO PROTEIN TYROSINE PHOSPHATASE. | 70608 | 8.12 | 1 | 1 | 1.3 |
| 1398 | IPI00059975.1 | SPLICE ISOFORM 2 OF Q9HCH5 SYNAPTOTAGMIN-LIKE PROTEIN 2. | 42736 | 9.42 | 1 | 1 | 1.6 |
| 1399 | IPI00060031.1 | SIMILAR TO HYPOTHETICAL PROTEIN FLJ10702. | 21416 | 7.93 | 1 | 1 | 12.37 |
| 1400 | IPI00060762.2 | SIMILAR TO RIBOSOMAL PROTEIN L7. | 33826 | 10.99 | 1 | 1 | 3.09 |
| 1401 | IPI00063849.1 | SPLICE ISOFORM 2 OF Q9NP97 DYNEIN LIGHT CHAIN 2A, CYTOPLASMIC. | 5060 | 5.71 | 1 | 1 | 19.15 |
| 1402 | IPI00064239.1 | HYPOTHETICAL PROTEIN KIAA1784. | 127547 | 5.18 | 1 | 1 | 0.43 |
| 1403 | IPI00064351.1 | HYPOTHETICAL PROTEIN FLJ14825. | 43273 | 5.12 | 1 | 1 | 1.32 |
| 1404 | IPI00064352.1 | HYPOTHETICAL PROTEIN FLJ14824. | 17023 | 7.68 | 1 | 1 | 8.11 |
| 1405 | IPI00064579.3 | BTB/POZ DOMAIN CONTAINING PROTEIN 6. | 45925 | 5.33 | 1 | 1 | 1.46 |
| 1406 | IPI00066374.1 | SMOOTH MUSCLE AND NON-MUSCLE MYOSIN ALKALI LIGHT CHAIN ISOFORM 4. | 12939 | 4.53 | 1 | 1 | 11.21 |
| 1407 | IPI00068174.2 | SIMILAR TO PEPTIDYLPROLYL ISOMERASE A (CYCLOPHILIN A). | 38117 | 9.04 | 1 | 1 | 1.44 |
| 1408 | IPI00070907.4 | HYPOTHETICAL PROTEIN XP_351183. | 32585 | 5.97 | 1 | 1 | 2.01 |
| 1409 | IPI00074224.8 | --none found in database-- | 17143 | 4.84 | 1 | 1 | 7.33 |
| 1410 | IPI00074962.1 | ANKYRIN 2 ISOFORM 1. | 433745 | 4.79 | 1 | 1 | 0.2 |
| 1411 | IPI00075272.1 | HYPOTHETICAL PROTEIN FLJ32194. | 44434 | 6.79 | 1 | 1 | 3.72 |
| 1412 | IPI00076579.3 | SIMILAR TO T-COMPLEX PROTEIN 1, ALPHA SUBUNIT (TCP-1-ALPHA) (CCT- ALPHA). | 54758 | 6.73 | 1 | 1 | 1.98 |
| 1413 | IPI00083938.1 | SIMILAR TO 40S RIBOSOMAL PROTEIN S16. | 16412 | 10.6 | 1 | 1 | 7.53 |
| 1414 | IPI00084423.4 | SIMILAR TO 60S RIBOSOMAL PROTEIN L17 (L23) (AMINO ACID STARVATION-INDUCED PROTEIN) (ASI). | 13053 | 10.85 | 1 | 1 | 12.28 |
| 1415 | IPI00091258.4 | SIMILAR TO 3-5 RNA EXONUCLEASE. | 81440 | 5.07 | 1 | 1 | 0.94 |
| 1416 | IPI00097447.4 | SIMILAR TO ADENYLYL CYCLASE-ASSOCIATED PROTEIN 1 (CAP 1). | 49300 | 8.01 | 1 | 1 | 2.44 |
| 1417 | IPI00097790.1 | WAS PROTEIN FAMILY, MEMBER 2. | 54284 | 5.16 | 1 | 1 | 1.41 |
| 1418 | IPI00098756.2 | SIMILAR TO ADAPTOR-RELATED PROTEIN COMPLEX 2, BETA 1 SUBUNIT. | 100424 | 5.95 | 1 | 1 | 1.22 |
| 1419 | IPI00101968.1 | HYPOTHETICAL PROTEIN FLJ14461. | 49042 | 4.72 | 1 | 1 | 2.51 |
| 1420 | IPI00102498.2 | SOLUTE CARRIER FAMILY 26, MEMBER 9 ISOFORM B. | 101680 | 8.63 | 1 | 1 | 0.54 |
| 1421 | IPI00102896.1 | RAS-RELATED PROTEIN RAB-2B. | 24214 | 7.97 | 1 | 1 | 5.56 |
| 1422 | IPI00103616.1 | DYSLEXIA SUSCEPTIBILITY 1 CANDIDATE GENE 1 PROTEIN. | 48455 | 9.27 | 1 | 1 | 1.43 |
| 1423 | IPI00103647.1 | CILIARY DYNEIN HEAVY CHAIN 7. | 461143 | 5.82 | 1 | 1 | 0.17 |
| 1424 | IPI00104136.2 | SIMILAR TO NUCLEAR RNA HELICASE, DECD VARIANT OF DEAD BOX FAMILY. | 49130 | 5.39 | 1 | 1 | 2.34 |
| 1425 | IPI00104899.2 | SIMILAR TO 60S RIBOSOMAL PROTEIN L17 (L23). | 12755 | 10.8 | 1 | 1 | 9.01 |
| 1426 | IPI00105119.1 | HYPOTHETICAL PROTEIN FLJ25373. | 46520 | 6.62 | 1 | 1 | 1.21 |
| 1427 | IPI00106663.1 | HYPOTHETICAL PROTEIN KIAA0849. | 107911 | 5.22 | 1 | 1 | 0.52 |
| 1428 | IPI00140345.3 | SIMILAR TO 40S RIBOSOMAL PROTEIN SA (P40) (34/67 KDA LAMININ RECEPTOR). | 36157 | 4.69 | 1 | 1 | 2.99 |
| 1429 | IPI00141564.1 | HYPOTHETICAL PROTEIN. | 78194 | 6.6 | 1 | 1 | 0.84 |
| 1430 | IPI00141809.2 | SIMILAR TO HIGH MOBILITY GROUP PROTEIN HOMOLOG HMG4. | 23922 | 10.34 | 1 | 1 | 2.84 |
| 1431 | IPI00141925.1 | ZINC FINGER PROTEIN 342. | 50810 | 8.98 | 1 | 1 | 1.05 |
| 1432 | IPI00144153.1 | SIMILAR TO PROTEIN 40KD. | 14077 | 7.68 | 1 | 1 | 7.75 |
| 1433 | IPI00145331.2 | BA317E16.3. | 14167 | 11 | 1 | 1 | 8.66 |
| 1434 | IPI00146260.1 | SIMILAR TO ACTIVATED RNA POLYMERASE II TRANSCRIPTIONAL COACTIVATOR P15 (PC4) (P14). | 14229 | 10.39 | 1 | 1 | 11.02 |
| 1435 | IPI00146935.1 | DYNAMIN-LIKE PROTEIN. | 81891 | 6.8 | 1 | 1 | 0.95 |
| 1436 | IPI00148255.1 | SECOND MITOCHONDRIA-DERIVED ACTIVATOR OF CASPASE ISOFORM SMAC-DELTA, PRECURSOR. | 22284 | 5.73 | 1 | 1 | 6.15 |
| 1437 | IPI00152108.1 | F-BOX ONLY PROTEIN 2. | 33328 | 4.01 | 1 | 1 | 4.05 |
| 1438 | IPI00152242.1 | HYPOTHETICAL PROTEIN. | 19735 | 10.27 | 1 | 1 | 7.56 |
| 1439 | IPI00154890.1 | PROTEIN SERINE/THREONINE PHOSPHATASE 4 SUBUNIT PP4RMEG. | 107004 | 4.38 | 1 | 1 | 0.53 |
| 1440 | IPI00156774.2 | SIMILAR TO RAS-RELATED C3 BOTULINUM TOXIN SUBSTRATE 1 ISOFORM RAC1. | 21543 | 9.14 | 1 | 1 | 7.29 |
| 1441 | IPI00157556.5 | --none found in database-- | 64711 | 8.57 | 1 | 1 | 0.85 |
| 1442 | IPI00157813.1 | MAX PROTEIN. | 15395 | 7.24 | 1 | 1 | 7.46 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 1443 | IPI00158128.1 | SPLICE ISOFORM 3 OF P25912 MAX PROTEIN. | 12099 | 5.93 | 1 | 1 | 9.71 |
| 1444 | IPI00160587.2 | SIMILAR TO 40S RIBOSOMAL PROTEIN S6 (PHOSPHOPROTEIN NP33). | 26351 | 11.05 | 1 | 1 | 2.59 |
| 1445 | IPI00160836.3 | --none found in database-- | 42157 | 4.58 | 1 | 1 | 2.67 |
| 1446 | IPI00161313.2 | SIMILAR TO FOLATE HYDROLASE. | 88682 | 6.06 | 1 | 1 | 0.5 |
| 1447 | IPI00161846.2 | SIMILAR TO PROTEIN 40KD. | 19072 | 7.51 | 1 | 1 | 5.71 |
| 1448 | IPI00164007.1 | SMALL GTP-BINDING PROTEIN. | 6306 | 5.56 | 1 | 1 | 15.09 |
| 1449 | IPI00165222.2 | --none found in database-- | 11625 | 6.51 | 1 | 1 | 6.67 |
| 1450 | IPI00165486.5 | SIMILAR TO RIBOSOMAL PROTEIN S2. | 45408 | 10.48 | 1 | 1 | 3.06 |
| 1451 | IPI00166058.1 | SIMILAR TO HYPOTHETICAL GENE LOC136555. | 12255 | 9.65 | 1 | 1 | 3.6 |
| 1452 | IPI00166250.1 | HYPOTHETICAL PROTEIN FLJ37882. | 44031 | 9.96 | 1 | 1 | 1.6 |
| 1453 | IPI00166271.1 | HYPOTHETICAL PROTEIN FLJ34952. | 13616 | 11.47 | 1 | 1 | 4.72 |
| 1454 | IPI00166825.1 | SIMILAR TO HYPOTHETICAL PROTEIN FLJ14981. | 50662 | 5.48 | 1 | 1 | 1.06 |
| 1455 | IPI00167002.2 | ETS-RELATED TRANSCRIPTION FACTOR ELF-1. | 67456 | 4.84 | 1 | 1 | 0.81 |
| 1456 | IPI00167400.4 | HYPOTHETICAL PROTEIN FLJ40200. | 58798 | 6.55 | 1 | 1 | 1.93 |
| 1457 | IPI00167491.2 | SIMILAR TO ZINC FINGER PROTEIN 432. | 71162 | 10.05 | 1 | 1 | 0.8 |
| 1458 | IPI00167784.1 | HYPOTHETICAL PROTEIN FLJ36749. | 27957 | 8.61 | 1 | 1 | 2.4 |
| 1459 | IPI00167879.1 | HYPOTHETICAL PROTEIN FLJ36000. | 15015 | 8.14 | 1 | 1 | 3.52 |
| 1460 | IPI00167967.1 | HYPOTHETICAL PROTEIN FLJ35542. | 24855 | 8.1 | 1 | 1 | 2.64 |
| 1461 | IPI00168368.1 | HYPOTHETICAL PROTEIN FLJ90378. | 34237 | 7.84 | 1 | 1 | 2.17 |
| 1462 | IPI00168438.1 | HYPOTHETICAL PROTEIN. | 16885 | 9.68 | 1 | 1 | 3.9 |
| 1463 | IPI00168509.2 | HYPOTHETICAL PROTEIN FLJ13725. | 131873 | 6.24 | 1 | 1 | 0.49 |
| 1464 | IPI00170744.1 | MYELOID ELF-1 LIKE FACTOR. | 70730 | 5.3 | 1 | 1 | 0.75 |
| 1465 | IPI00170796.1 | SPLICE ISOFORM 1 OF Q9UBQ0 VACUOLAR PROTEIN SORTING 29. | 20506 | 6.79 | 1 | 1 | 7.14 |
| 1466 | IPI00171160.1 | SIMILAR TO 37 KDA LEUCINE-RICH REPEAT (LRR) PROTEIN. | 51800 | 8.34 | 1 | 1 | 1.36 |
| 1467 | IPI00171230.1 | HYPOTHETICAL PROTEIN KIAA1081. | 115109 | 6.24 | 1 | 1 | 0.9 |
| 1468 | IPI00171480.1 | HYPOTHETICAL PROTEIN FLJ90246. | 69856 | 7.12 | 1 | 1 | 0.77 |
| 1469 | IPI00171741.2 | PIGGYBAC TRANSPOSABLE ELEMENT DERIVED 4. | 67004 | 9.62 | 1 | 1 | 1.2 |
| 1470 | IPI00171903.1 | HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN M. | 77516 | 9.1 | 1 | 1 | 2.19 |
| 1471 | IPI00172421.3 | S-PHASE KINASE-ASSOCIATED PROTEIN 1A ISOFORM A. | 18063 | 4.08 | 1 | 1 | 8.75 |
| 1472 | IPI00172585.1 | SERINE/THREONINE-PROTEIN KINASE SGK3. | 57108 | 6.92 | 1 | 1 | 1.01 |
| 1473 | IPI00173565.3 | --none found in database-- | 28163 | 5.27 | 1 | 1 | 2.77 |
| 1474 | IPI00175146.2 | HYPOTHETICAL PROTEIN KIAA0546. | 218331 | 8.12 | 1 | 1 | 0.26 |
| 1475 | IPI00175151.2 | SIMILAR TO HYPOTHETICAL PROTEIN. | 223811 | 8.03 | 1 | 1 | 0.25 |
| 1476 | IPI00176219.1 | SIMILAR TO NEPHRONECTIN SHORT ISOFORM. | 61907 | 8.38 | 1 | 1 | 0.88 |
| 1477 | IPI00176375.1 | HYPOTHETICAL PROTEIN. | 185782 | 6.9 | 1 | 1 | 0.36 |
| 1478 | IPI00176686.2 | SIMILAR TO RIBOSOMAL PROTEIN L6. | 32336 | 10.93 | 1 | 1 | 2.79 |
| 1479 | IPI00176721.1 | SIMILAR TO RIBOSOMAL PROTEIN S2. | 31392 | 11.08 | 1 | 1 | 4.47 |
| 1480 | IPI00176823.1 | SIMILAR TO 60 KDA HEAT SHOCK PROTEIN, MITOCHONDRIAL PRECURSOR (HSP60) (60 KDA CHAPERONIN) (CPN60) (HEAT SHOCK PROTEIN 60) (HSP-60) (MITOCHONDRIAL MATRIX PROTEIN P1) (P60 LYMPHOCYTE PROTEIN) (HUCHA60). | 12103 | 8.44 | 1 | 1 | 11.82 |
| 1481 | IPI00176841.1 | SIMILAR TO S-PHASE KINASE-ASSOCIATED PROTEIN 1A ISOFORM A. | 16920 | 4.53 | 1 | 1 | 9.4 |
| 1482 | IPI00176996.2 | --none found in database-- | 26168 | 7.97 | 1 | 1 | 2.94 |
| 1483 | IPI00177010.2 | SIMILAR TO TRANSLATION INITIATION FACTOR EIF-4A II - MOUSE. | 46056 | 4.64 | 1 | 1 | 3.42 |
| 1484 | IPI00178607.5 | BH3 INTERACTING DOMAIN DEATH AGONIST ISOFORM 1. | 31798 | 6.91 | 1 | 1 | 5.28 |
| 1485 | IPI00179076.1 | DJ1172N10.1 (UBIQUITIN SPECIFIC PROTEASE 9, X CHROMOSOME. | 172064 | 5.47 | 1 | 1 | 0.4 |
| 1486 | IPI00179357.1 | TITIN. | 3.82E+06 | 6.25 | 1 | 1 | 0.01 |
| 1487 | IPI00180139.3 | --none found in database-- | 55267 | 8.39 | 1 | 1 | 1.22 |
| 1488 | IPI00180384.1 | HYPOTHETICAL PROTEIN KIAA0944. | 461773 | 5.82 | 1 | 1 | 0.17 |
| 1489 | IPI00181391.4 | SIMILAR TO MENINGIOMA EXPRESSED ANTIGEN 5. | 110453 | 6.21 | 1 | 1 | 0.61 |
| 1490 | IPI00181684.1 | ELKS. | 108793 | 6.57 | 1 | 1 | 0.95 |
| 1491 | IPI00181771.1 | --none found in database-- | 10322 | 8.32 | 1 | 1 | 5.62 |
| 1492 | IPI00181921.1 | ADDUCIN 2 ISOFORM C. | 46551 | 4.98 | 1 | 1 | 2.85 |
| 1493 | IPI00183349.6 | R31155_1. | 84252 | 10.02 | 1 | 1 | 1.22 |
| 1494 | IPI00183643.1 | GOLIATH PROTEIN. | 46405 | 9.05 | 1 | 1 | 2.63 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 1495 | IPI00183664.2 | --none found in database-- | 42485 | 9.5 | 1 | 1 | 2.48 |
| 1496 | IPI00183679.2 | SPLICE ISOFORM 2 OF Q969W9 TRANSMEMBRANE PROSTATE ANDROGEN-INDUCED PROTEIN. | 27900 | 6.51 | 1 | 1 | 1.98 |
| 1497 | IPI00184119.2 | --none found in database-- | 106202 | 8.98 | 1 | 1 | 0.62 |
| 1498 | IPI00184284.2 | SPLICE ISOFORM 2 OF Q9UBQ0 VACUOLAR PROTEIN SORTING 29. | 20927 | 7.07 | 1 | 1 | 6.99 |
| 1499 | IPI00184799.2 | --none found in database-- | 24156 | 8.94 | 1 | 1 | 3.88 |
| 1500 | IPI00185197.3 | SIMILAR TO CGI-55 PROTEIN. | 40188 | 6.87 | 1 | 1 | 1.36 |
| 1501 | IPI00185238.3 | --none found in database-- | 62594 | 8.38 | 1 | 1 | 0.88 |
| 1502 | IPI00185256.2 | SEX COMB ON MIDLEG HOMOLOG 1 ISOFORM 2. | 72072 | 9.68 | 1 | 1 | 0.77 |
| 1503 | IPI00185798.2 | --none found in database-- | 34164 | 6.97 | 1 | 1 | 5.97 |
| 1504 | IPI00186101.2 | --none found in database-- | 32528 | 8.22 | 1 | 1 | 2.99 |
| 1505 | IPI00186586.4 | SIMILAR TO HYPOTHETICAL PROTEIN FLJ10101. | 54698 | 8.17 | 1 | 1 | 1.21 |
| 1506 | IPI00186815.2 | SPLICE ISOFORM 2 OF O43566 REGULATOR OF G-PROTEIN SIGNALING 14. | 38536 | 8.46 | 1 | 1 | 1.13 |
| 1507 | IPI00187110.2 | SIMILAR TO SEX COMB ON MIDLEG-LIKE 1. | 73354 | 9.71 | 1 | 1 | 0.76 |
| 1508 | IPI00215719.1 | 60S RIBOSOMAL PROTEIN L18. | 22659 | 12.28 | 1 | 1 | 5.5 |
| 1509 | IPI00215879.1 | SPLICE ISOFORM SRP55-3 OF Q13247 SPLICING FACTOR, ARGININE/SERINE-RICH 6. | 38419 | 11.56 | 1 | 1 | 2.69 |
| 1510 | IPI00215911.1 | APEX NUCLEASE. | 35554 | 8.26 | 1 | 1 | 5.35 |
| 1511 | IPI00215918.1 | ADP-RIBOSYLATION FACTOR 4. | 20511 | 7.26 | 1 | 1 | 11.67 |
| 1512 | IPI00215919.1 | ADP-RIBOSYLATION FACTOR 5. | 20530 | 6.79 | 1 | 1 | 11.67 |
| 1513 | IPI00215948.1 | ALPHA2(E)-CATENIN. | 102776 | 6.25 | 1 | 1 | 0.54 |
| 1514 | IPI00216139.1 | SPLICE ISOFORM I OF Q14141 SEPTIN 6. | 48873 | 6.8 | 1 | 1 | 2.34 |
| 1515 | IPI00216141.1 | SPLICE ISOFORM V OF Q14141 SEPTIN 6. | 49167 | 6.8 | 1 | 1 | 2.33 |
| 1516 | IPI00216163.3 | SPLICE ISOFORM 1 OF Q9NP97 DYNEIN LIGHT CHAIN 2A, CYTOPLASMIC. | 13364 | 9.89 | 1 | 1 | 10.26 |
| 1517 | IPI00216256.1 | SPLICE ISOFORM SHORT OF O75083 WD-REPEAT PROTEIN 1. | 58002 | 6.89 | 1 | 1 | 3 |
| 1518 | IPI00216443.1 | SPLICE ISOFORM 3 OF Q9H9B1 HISTONE-LYSINE N-METHYLTRANSFERASE, H3 LYSINE-9 SPECIFIC 5. | 125404 | 5.74 | 1 | 1 | 0.43 |
| 1519 | IPI00216470.1 | PHOSPHATIDYLINOSITOL-4-PHOSPHATE 5-KINASE TYPE II BETA. | 47378 | 7.37 | 1 | 1 | 3.37 |
| 1520 | IPI00216472.1 | SPLICE ISOFORM NON-BRAIN OF P09497 CLATHRIN LIGHT CHAIN B. | 23181 | 4.34 | 1 | 1 | 4.74 |
| 1521 | IPI00216704.1 | SPLICE ISOFORM 2 OF P11277 SPECTRIN BETA CHAIN, ERYTHROCYTE. | 267680 | 5.03 | 1 | 1 | 0.43 |
| 1522 | IPI00216719.1 | ELKS EPSILON. | 128086 | 5.8 | 1 | 1 | 0.81 |
| 1523 | IPI00216720.1 | ELKS GAMMA. | 81967 | 6.6 | 1 | 1 | 1.25 |
| 1524 | IPI00217009.1 | FK506-BINDING PROTEIN 1A. | 15727 | 10.14 | 1 | 1 | 9.72 |
| 1525 | IPI00217154.1 | SPLICE ISOFORM 1 OF Q9HBY8 SERINE/THREONINE-PROTEIN KINASE SGK2. | 41175 | 6.73 | 1 | 1 | 1.36 |
| 1526 | IPI00217683.1 | SPLICE ISOFORM 2 OF Q02952 A-KINASE ANCHOR PROTEIN 12. | 181647 | 4.1 | 1 | 1 | 1.19 |
| 1527 | IPI00217691.1 | SIMILAR TO NUCLEAR FACTOR. | 110097 | 6.52 | 1 | 1 | 0.51 |
| 1528 | IPI00218013.3 | TRIPIN. | 144718 | 8.2 | 1 | 1 | 0.4 |
| 1529 | IPI00218075.1 | PROTEIN FAM9B. | 22438 | 5.08 | 1 | 1 | 2.69 |
| 1530 | IPI00218242.1 | SPLICE ISOFORM ALPHA-2 OF O15165 PROTEIN C18ORF1. | 32072 | 6.59 | 1 | 1 | 1.74 |
| 1531 | IPI00218243.1 | SPLICE ISOFORM BETA-1 OF O15165 PROTEIN C18ORF1. | 27600 | 7.57 | 1 | 1 | 2.02 |
| 1532 | IPI00218244.1 | SPLICE ISOFORM BETA-2 OF O15165 PROTEIN C18ORF1. | 25772 | 8.34 | 1 | 1 | 2.17 |
| 1533 | IPI00218310.1 | EXOSOME COMPLEX EXONUCLEASE RRP41. | 27637 | 6.6 | 1 | 1 | 1.95 |
| 1534 | IPI00218371.1 | PHOSPHORIBOSYL PYROPHOSPHATE SYNTHETASE 1-LIKE 1. | 34839 | 6.31 | 1 | 1 | 4.09 |
| 1535 | IPI00218782.1 | F-ACTIN CAPPING PROTEIN BETA SUBUNIT. | 30629 | 5.78 | 1 | 1 | 4.78 |
| 1536 | IPI00218847.1 | ACID PHOSPHATASE 1 ISOFORM B. | 17977 | 6.88 | 1 | 1 | 6.96 |
| 1537 | IPI00219077.1 | LEUKOTRIENE A4 HYDROLASE. | 69285 | 6.1 | 1 | 1 | 2.13 |
| 1538 | IPI00219114.1 | SPLICE ISOFORM P135 OF Q14203 DYNACTIN 1. | 127404 | 5.09 | 1 | 1 | 1.92 |
| 1539 | IPI00219126.2 | SPLICE ISOFORM 3 OF O43566 REGULATOR OF G-PROTEIN SIGNALING 14. | 64745 | 8.82 | 1 | 1 | 0.67 |
| 1540 | IPI00219127.1 | SPLICE ISOFORM 4 OF O43566 REGULATOR OF G-PROTEIN SIGNALING 14. | 21781 | 10.15 | 1 | 1 | 1.99 |
| 1541 | IPI00219157.1 | RIBOSOMAL PROTEIN L27A. | 16561 | 11.64 | 1 | 1 | 7.43 |
| 1542 | IPI00219207.1 | SPLICE ISOFORM 3 OF Q9NQC3 RETICULON 4. | 22395 | 9.78 | 1 | 1 | 7.04 |
| 1543 | IPI00219274.1 | SYNAPTOTAGMIN II. | 46830 | 8.12 | 1 | 1 | 2.39 |
| 1544 | IPI00219365.1 | MOESIN. | 67820 | 6.32 | 1 | 1 | 1.56 |
| 1545 | IPI00219451.1 | SPLICE ISOFORM 5 OF O00154 CYTOSOLIC ACYL COENZYME A THIOESTER HYDROLASE. | 38991 | 8.47 | 1 | 1 | 3.43 |
| 1546 | IPI00219452.1 | SPLICE ISOFORM 6 OF O00154 CYTOSOLIC ACYL COENZYME A THIOESTER HYDROLASE. | 36568 | 7.88 | 1 | 1 | 3.65 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 1547 | IPI00219616.1 | PHOSPHORIBOSYL PYROPHOSPHATE SYNTHETASE 1. | 34834 | 6.98 | 1 | 1 | 4.09 |
| 1548 | IPI00219861.1 | ACID PHOSPHATASE 1 ISOFORM C. | 18042 | 6.73 | 1 | 1 | 6.96 |
| 1549 | IPI00219865.1 | SPLICE ISOFORM 2 OF Q9NR28 SMAC PROTEIN, MITOCHONDRIAL PRECURSOR. | 21233 | 4.48 | 1 | 1 | 6.45 |
| 1550 | IPI00219929.1 | SPLICE ISOFORM 2 OF P25912 MAX PROTEIN. | 17202 | 6.52 | 1 | 1 | 6.62 |
| 1551 | IPI00220002.1 | SPLICE ISOFORM 2 OF O75781 PARALEMMIN. | 37157 | 4.62 | 1 | 1 | 4.08 |
| 1552 | IPI00220026.1 | SPLICE ISOFORM 2 OF P22303 ACETYLCHOLINESTERASE PRECURSOR. | 69909 | 6.91 | 1 | 1 | 0.93 |
| 1553 | IPI00220323.5 | SPLICE ISOFORM ALPHA-1 OF O15165 PROTEIN C18ORF1. | 36484 | 6.82 | 1 | 1 | 1.52 |
| 1554 | IPI00220365.2 | EUKARYOTIC TRANSLATION INITIATION FACTOR 4 GAMMA, 1 ISOFORM 4. | 154805 | 4.82 | 1 | 1 | 0.71 |
| 1555 | IPI00220373.1 | INSULYSIN. | 118022 | 6.74 | 1 | 1 | 0.59 |
| 1556 | IPI00220412.1 | S100 CALCIUM BINDING PROTEIN A1. | 10546 | 4.13 | 1 | 1 | 22.34 |
| 1557 | IPI00220431.1 | SPLICE ISOFORM ALPHA-1B-2 OF Q00975 VOLTAGE-DEPENDENT N-TYPE CALCIUM CHANNEL ALPHA-1B SUBUNIT. | 251759 | 8.59 | 1 | 1 | 0.49 |
| 1558 | IPI00220573.1 | MYOSIN REGULATORY LIGHT CHAIN MRCL3. | 19794 | 4.4 | 1 | 1 | 6.43 |
| 1559 | IPI00220617.1 | HYPOTHETICAL PROTEIN. | 90203 | 7.88 | 1 | 1 | 1.81 |
| 1560 | IPI00220738.1 | SPLICE ISOFORM CRK-I OF P46108 PROTO-ONCOGENE C-CRK. | 22936 | 4.96 | 1 | 1 | 8.33 |
| 1561 | IPI00220754.1 | SPLICE ISOFORM 1 OF Q9UEY8 GAMMA ADDUCIN. | 75671 | 6.8 | 1 | 1 | 1.78 |
| 1562 | IPI00220791.1 | SPLICE ISOFORM 2 OF P49418 AMPHIPHYSIN. | 71929 | 4.37 | 1 | 1 | 1.53 |
| 1563 | IPI00220918.1 | SPLICE ISOFORM 2 OF P26358 DNA (CYTOSINE-5)-METHYLTRANSFERASE 1. | 184819 | 7.92 | 1 | 1 | 0.37 |
| 1564 | IPI00220919.1 | SPLICE ISOFORM 3 OF P26358 DNA (CYTOSINE-5)-METHYLTRANSFERASE 1. | 144465 | 7.48 | 1 | 1 | 0.47 |
| 1565 | IPI00220993.1 | SPLICE ISOFORM CNPI OF P09543 2',3'-CYCLIC NUCLEOTIDE 3'-PHOSPHODIESTERASE. | 45099 | 8.76 | 1 | 1 | 2.74 |
| 1566 | IPI00221088.1 | RIBOSOMAL PROTEIN S9. | 22591 | 11.32 | 1 | 1 | 5.67 |
| 1567 | IPI00221089.1 | RIBOSOMAL PROTEIN S13. | 17222 | 11.19 | 1 | 1 | 9.93 |
| 1568 | IPI00221092.1 | RIBOSOMAL PROTEIN S16. | 16445 | 10.81 | 1 | 1 | 7.53 |
| 1569 | IPI00221225.1 | ANNEXIN IV. | 36085 | 5.9 | 1 | 1 | 2.18 |
| 1570 | IPI00221286.1 | SPLICE ISOFORM SRP40-2 OF Q13243 SPLICING FACTOR, ARGININE/SERINE-RICH 5. | 12528 | 10.56 | 1 | 1 | 4.67 |
| 1571 | IPI00221287.1 | SPLICE ISOFORM SRP40-4 OF Q13243 SPLICING FACTOR, ARGININE/SERINE-RICH 5. | 30663 | 12.18 | 1 | 1 | 1.86 |
| 1572 | IPI00221354.1 | SPLICE ISOFORM SHORT OF P35637 RNA-BINDING PROTEIN FUS. | 53355 | 9.59 | 1 | 1 | 2.29 |
| 1573 | IPI00221391.1 | NADH DEHYDROGENASE SUBUNIT 5. | 67012 | 9.32 | 1 | 1 | 1.16 |
| 1574 | IPI00232416.2 | SIMILAR TO TAU TUBULIN KINASE 2. | 51904 | 8.27 | 1 | 1 | 1.95 |
| 1575 | IPI00232533.2 | EUKARYOTIC TRANSLATION INITIATION FACTOR 1A, X-CHROMOSOMAL. | 22218 | 9.37 | 1 | 1 | 5.61 |
| 1576 | IPI00232922.1 | SPLICE ISOFORM 6 OF P07202 THYROID PEROXIDASE PRECURSOR. | 67293 | 7.96 | 1 | 1 | 0.98 |
| 1577 | IPI00232923.1 | SPLICE ISOFORM 2-3 OF P07202 THYROID PEROXIDASE PRECURSOR. | 96475 | 7.33 | 1 | 1 | 0.69 |
| 1578 | IPI00232924.1 | SPLICE ISOFORM 2-4 OF P07202 THYROID PEROXIDASE PRECURSOR. | 92031 | 7.01 | 1 | 1 | 0.72 |
| 1579 | IPI00233255.2 | SIMILAR TO PROTEIN-TYROSINE PHOSPHATASE, NON-RECEPTOR TYPE 11 (PROTEIN-TYROSINE PHOSPHATASE 2C) (PTP-2C) (PTP-1D) (SH-PTP3) (SH- PTP2) (SHP-2). | 64013 | 6.74 | 1 | 1 | 1.43 |
| 1580 | IPI00233820.2 | CATALASE. | 59625 | 7.41 | 1 | 1 | 1.71 |
| 1581 | IPI00234131.2 | SIMILAR TO 60 KDA HEAT SHOCK PROTEIN, MITOCHONDRIAL PRECURSOR (HSP60) (60 KDA CHAPERONIN) (CPN60) (HEAT SHOCK PROTEIN 60) (HSP-60) (MITOCHONDRIAL MATRIX PROTEIN P1) (P60 LYMPHOCYTE PROTEIN) (HUCHA60). | 61092 | 4.91 | 1 | 1 | 1.57 |
| 1582 | IPI00235352.1 | SIMILAR TO PHOSPHATIDYLINOSITOL-4-PHOSPHATE 5-KINASE, TYPE II, BETA. | 32317 | 9.91 | 1 | 1 | 4.98 |
| 1583 | IPI00235412.1 | DYNAMIN 1-LIKE. | 79442 | 6.92 | 1 | 1 | 0.99 |
| 1584 | IPI00236274.2 | SIMILAR TO KH-TYPE SPLICING REGULATORY PROTEIN (FUSE BINDING PROTEIN 2). | 85529 | 10.18 | 1 | 1 | 1.25 |
| 1585 | IPI00237806.1 | SPLICE ISOFORM 3 OF P11277 SPECTRIN BETA CHAIN, ERYTHROCYTE. | 242656 | 4.99 | 1 | 1 | 0.47 |
| 1586 | IPI00237884.1 | A-KINASE ANCHOR PROTEIN 12 ISOFORM 1. | 191482 | 4.07 | 1 | 1 | 1.12 |
| 1587 | IPI00239789.1 | HYPOTHETICAL PROTEIN. | 47921 | 6.91 | 1 | 1 | 2.82 |
| 1588 | IPI00242253.4 | SIMILAR TO RETICULOCALBIN 1 PRECURSOR. | 36289 | 4.46 | 1 | 1 | 5.18 |
| 1589 | IPI00243499.2 | SIMILAR TO AMINOPEPTIDASE PUROMYCIN SENSITIVE. | 30397 | 4.47 | 1 | 1 | 3.68 |
| 1590 | IPI00243595.2 | FLJ00153 PROTEIN. | 54312 | 8.78 | 1 | 1 | 1.41 |
| 1591 | IPI00243913.3 | SIMILAR TO NEUROFILAMENT-LIKE PROTEIN. | 115538 | 4.56 | 1 | 1 | 0.56 |
| 1592 | IPI00244116.1 | SIMILAR TO HYPOTHETICAL PROTEIN MGC27277. | 50892 | 8.49 | 1 | 1 | 1.4 |
| 1593 | IPI00244567.2 | GUANINE NUCLEOTIDE-BINDING PROTEIN G(I)/G(S)/G(O) GAMMA-2 SUBUNIT. | 7719 | 8.22 | 1 | 1 | 22.86 |
| 1594 | IPI00246067.2 | SIMILAR TO KERATIN 8, TYPE II CYTOSKELETAL - HUMAN. | 45740 | 5.03 | 1 | 1 | 2.13 |
| 1595 | IPI00246556.2 | --none found in database-- | 17536 | 6.53 | 1 | 1 | 3.92 |
| 1596 | IPI00246975.2 | GLUTATHIONE S-TRANSFERASE MU 3. | 26428 | 5.19 | 1 | 1 | 7.59 |
| 1597 | IPI00247493.1 | HYPOTHETICAL PROTEIN KIAA0679. | 103071 | 4.56 | 1 | 1 | 0.65 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 1598 | IPI00248099.2 | SIMILAR TO CHROMATIN ASSEMBLY FACTOR 1 SUBUNIT C (CAF-1 SUBUNIT C) (CHROMATIN ASSEMBLY FACTOR I P48 SUBUNIT) (CAF-I 48 KDA SUBUNIT) (CAF-IP48) (RETINOBLASTOMA BINDING PROTEIN P48) (RETINOBLASTOMA-BINDING PROTEIN 4) (RBBP-4) (MSI1 PROTEIN HOMOLOG).... | 48212 | 4.9 | 1 | 1 | 3.04 |
| 1599 | IPI00248597.2 | --none found in database-- | 8151 | 4.52 | 1 | 1 | 6.85 |
| 1600 | IPI00248708.3 | --none found in database-- | 148561 | 9.04 | 1 | 1 | 0.37 |
| 1601 | IPI00248956.1 | SPLICE ISOFORM A OF Q9UH03 NEURONAL-SPECIFIC SEPTIN 3. | 39345 | 7.22 | 1 | 1 | 3.48 |
| 1602 | IPI00249627.2 | --none found in database-- | 29061 | 8.71 | 1 | 1 | 3.37 |
| 1603 | IPI00249656.1 | SIMILAR TO RIKEN CDNA 2310039E09. | 41899 | 8.64 | 1 | 1 | 2.75 |
| 1604 | IPI00252153.1 | HYPOTHETICAL PROTEIN FLJ33253. | 63244 | 8.17 | 1 | 1 | 1.26 |
| 1605 | IPI00254157.3 | --none found in database-- | 44064 | 5 | 1 | 1 | 3.33 |
| 1606 | IPI00256143.2 | --none found in database-- | 27979 | 5.78 | 1 | 1 | 2.77 |
| 1607 | IPI00256684.1 | SPLICE ISOFORM B OF O95782 ADAPTER-RELATED PROTEIN COMPLEX 2 ALPHA 1 SUBUNIT. | 105370 | 7.72 | 1 | 1 | 1.88 |
| 1608 | IPI00257898.2 | SIMILAR TO HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN G (HNRNP G) (RNA BINDING MOTIF PROTEIN, X CHROMOSOME) (GLYCOPROTEIN P43). | 41987 | 9.61 | 1 | 1 | 2.56 |
| 1609 | IPI00257932.1 | SIMILAR TO HYPOTHETICAL PROTEIN MGC15737. | 23307 | 4.45 | 1 | 1 | 4.37 |
| 1610 | IPI00258370.2 | SIMILAR TO CALCIUM-BINDING TRANSPORTER. | 28389 | 6.99 | 1 | 1 | 1.95 |
| 1611 | IPI00258514.2 | SIMILAR TO 78 KDA GLUCOSE-REGULATED PROTEIN PRECURSOR (GRP 78) (IMMUNOGLOBULIN HEAVY CHAIN BINDING PROTEIN) (BIP) (ENDOPLASMIC RETICULUM LUMENAL CA(2+) BINDING PROTEIN GRP78). | 67459 | 4.94 | 1 | 1 | 3.45 |
| 1612 | IPI00258904.2 | SIMILAR TO PEPTIDYL-PRO CIS TRANS ISOMERASE. | 18513 | 8.01 | 1 | 1 | 2.91 |
| 1613 | IPI00260715.2 | SPLICE ISOFORM LONG OF P35637 RNA-BINDING PROTEIN FUS. | 56239 | 9.49 | 1 | 1 | 2.17 |
| 1614 | IPI00260755.2 | SIMILAR TO DJ1100H13.4 (PUTATIVE RHOGAP DOMAIN CONTAINING PROTEIN). | 66290 | 8.46 | 1 | 1 | 0.84 |
| 1615 | IPI00289348.1 | HYPOTHETICAL PROTEIN FLJ30766. | 27508 | 7.29 | 1 | 1 | 2.04 |
| 1616 | IPI00289551.1 | STEROL/RETINOL DEHYDROGENASE. | 35645 | 8.77 | 1 | 1 | 1.89 |
| 1617 | IPI00289572.1 | SPLICE ISOFORM 1 OF P07202 THYROID PEROXIDASE PRECURSOR. | 102931 | 6.75 | 1 | 1 | 0.64 |
| 1618 | IPI00289573.3 | SPLICE ISOFORM 2 OF P07202 THYROID PEROXIDASE PRECURSOR. | 96667 | 6.79 | 1 | 1 | 0.68 |
| 1619 | IPI00289575.1 | SPLICE ISOFORM 4 OF P07202 THYROID PEROXIDASE PRECURSOR. | 98295 | 6.94 | 1 | 1 | 0.67 |
| 1620 | IPI00289576.3 | SPLICE ISOFORM 5 OF P07202 THYROID PEROXIDASE PRECURSOR. | 84549 | 6.33 | 1 | 1 | 0.79 |
| 1621 | IPI00289819.2 | CATION-INDEPENDENT MANNOSE-6-PHOSPHATE RECEPTOR PRECURSOR. | 274966 | 5.82 | 1 | 1 | 0.24 |
| 1622 | IPI00290461.1 | EUKARYOTIC TRANSLATION INITIATION FACTOR 3 SUBUNIT 1. | 29062 | 4.45 | 1 | 1 | 4.26 |
| 1623 | IPI00290462.3 | CARBONYL REDUCTASE 3. | 30850 | 6.06 | 1 | 1 | 5.78 |
| 1624 | IPI00290557.1 | SIMILAR TO UBIQUITIN UBF-FL. | 65644 | 9.19 | 1 | 1 | 1.04 |
| 1625 | IPI00290842.2 | MICROTUBULE-ASSOCIATED PROTEIN 4 ISOFORM 4. | 109619 | 4.82 | 1 | 1 | 1.06 |
| 1626 | IPI00290857.1 | KERATIN, TYPE II CYTOSKELETAL 3. | 64511 | 6.41 | 1 | 1 | 1.59 |
| 1627 | IPI00291165.2 | POLYRIBONUCLEOTIDE NUCLEOTIDYLTRANSFERASE 1. | 86456 | 7.86 | 1 | 1 | 0.89 |
| 1628 | IPI00291579.4 | KINESIN FAMILY MEMBER 23 ISOFORM 1. | 112994 | 8.84 | 1 | 1 | 0.71 |
| 1629 | IPI00291922.2 | PROTEASOME SUBUNIT ALPHA TYPE 5. | 26411 | 4.45 | 1 | 1 | 5.39 |
| 1630 | IPI00291993.1 | SPLICE ISOFORM M4 OF P52272 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN M. | 77469 | 9.29 | 1 | 1 | 2.19 |
| 1631 | IPI00292434.3 | SPLICE ISOFORM M1-M2 OF P52272 HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN M. | 73575 | 9.45 | 1 | 1 | 2.32 |
| 1632 | IPI00292776.1 | HYPOTHETICAL PROTEIN KIAA1508. | 65597 | 8.95 | 1 | 1 | 0.7 |
| 1633 | IPI00293080.1 | HYPOTHETICAL PROTEIN. | 140183 | 8.58 | 1 | 1 | 0.39 |
| 1634 | IPI00293338.5 | SMC5 PROTEIN. | 131136 | 8.53 | 1 | 1 | 0.62 |
| 1635 | IPI00293380.2 | SUPERFAST MYOSIN REGULATORY LIGHT CHAIN 2. | 21332 | 4.43 | 1 | 1 | 3.14 |
| 1636 | IPI00293884.4 | KINESIN-LIKE PROTEIN KIF23. | 101041 | 8.83 | 1 | 1 | 0.79 |
| 1637 | IPI00293975.1 | GLUTATHIONE PEROXIDASE 1. | 21899 | 6.5 | 1 | 1 | 8.96 |
| 1638 | IPI00294158.1 | BILIVERDIN REDUCTASE A PRECURSOR. | 33428 | 6.41 | 1 | 1 | 4.73 |
| 1639 | IPI00294566.1 | HYPOTHETICAL PROTEIN. | 55210 | 7.23 | 1 | 1 | 1.98 |
| 1640 | IPI00294632.1 | PUTATIVE DYNEIN LIGHT CHAIN PROTEIN DJ8B22.1. | 10535 | 6.93 | 1 | 1 | 5.62 |
| 1641 | IPI00294980.1 | PEPSINOGEN. | 8716 | 10.47 | 1 | 1 | 5.48 |
| 1642 | IPI00295386.3 | CARBONYL REDUCTASE 1. | 30375 | 8.49 | 1 | 1 | 5.78 |
| 1643 | IPI00295392.3 | 60S RIBOSOMAL PROTEIN L3. | 45978 | 10.89 | 1 | 1 | 2.99 |
| 1644 | IPI00295461.1 | SPLICE ISOFORM 1 OF Q12884 SEPRASE. | 87821 | 6.87 | 1 | 1 | 0.66 |
| 1645 | IPI00295589.1 | EUKARYOTIC TRANSLATION INITIATION FACTOR 4GI. | 175535 | 5.01 | 1 | 1 | 0.63 |
| 1646 | IPI00296191.1 | VACUOLAR ATP SYNTHASE SUBUNIT H. | 55883 | 6.44 | 1 | 1 | 4.76 |
| 1647 | IPI00296241.3 | HISTO-BLOOD GROUP ABO SYSTEM TRANSFERASE (NAGAT) [Includes: GLYCOPROTEIN-FUCOSYLGALACTOSIDE ALPHA-N-ACETYLGALACTOSAMINYLTRANSFERASE (EC 2.4.1.40) (FUCOSYLGLYCOPROTEIN ALPHA-N-ACETYLGALACTOSAMINYLTRANSFERASE) (HISTO-BLOOD GROUP A | 40934 | 9.24 | 1 | 1 | 1.41 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| | | TRANSFERASE) (A TRANSFERA | | | | | |
| 1648 | IPI00296291.1 | HP1-BP74 PROTEIN. | 61436 | 10.26 | 1 | 1 | 0.72 |
| 1649 | IPI00297587.1 | HYPOTHETICAL PROTEIN FLJ25874. | 32161 | 8.14 | 1 | 1 | 1.71 |
| 1650 | IPI00297597.1 | NUCLEAR RNA HELICASE. | 49078 | 5.67 | 1 | 1 | 2.34 |
| 1651 | IPI00298237.1 | TRIPEPTIDYL-PEPTIDASE I PRECURSOR. | 61229 | 6.42 | 1 | 1 | 2.49 |
| 1652 | IPI00298347.1 | PROTEIN-TYROSINE PHOSPHATASE, NON-RECEPTOR TYPE 11. | 68011 | 7.31 | 1 | 1 | 1.35 |
| 1653 | IPI00298394.2 | SIMILAR TO HYPOTHETICAL PROTEIN. | 123425 | 6.65 | 1 | 1 | 0.54 |
| 1654 | IPI00298497.3 | FIBRINOGEN BETA CHAIN PRECURSOR [Contains: FIBRINOPEPTIDE B]. | 55928 | 8.38 | 1 | 1 | 3.05 |
| 1655 | IPI00299000.1 | PROLIFERATION-ASSOCIATED PROTEIN 2G4. | 43787 | 6.52 | 1 | 1 | 4.31 |
| 1656 | IPI00299155.3 | PROTEASOME SUBUNIT ALPHA TYPE 4. | 29484 | 7.86 | 1 | 1 | 8.43 |
| 1657 | IPI00299608.2 | 26S PROTEASOME NON-ATPASE REGULATORY SUBUNIT 1. | 108488 | 5.06 | 1 | 1 | 1.94 |
| 1658 | IPI00299755.1 | PHOSPHATIDYLINOSITOL 3-KINASE. | 100988 | 6.7 | 1 | 1 | 0.68 |
| 1659 | IPI00300285.2 | HYPOTHETICAL PROTEIN DKFZP564D1378. | 29776 | 6.17 | 1 | 1 | 7.78 |
| 1660 | IPI00300587.2 | SIMILAR TO HP4 OLFACTORY RECEPTOR. | 38231 | 8.89 | 1 | 1 | 1.46 |
| 1661 | IPI00301023.3 | SPLICE ISOFORM 1 OF O75781 PARALEMMIN. | 42076 | 4.64 | 1 | 1 | 3.62 |
| 1662 | IPI00301154.1 | POLYADENYLATE-BINDING PROTEIN 3. | 70031 | 10.2 | 1 | 1 | 1.74 |
| 1663 | IPI00301288.2 | HYPOTHETICAL PROTEIN FLJ90754. | 178834 | 5.11 | 1 | 1 | 0.31 |
| 1664 | IPI00301610.3 | HYPOTHETICAL PROTEIN KIAA1994. | 113760 | 5.47 | 1 | 1 | 1.07 |
| 1665 | IPI00302227.3 | HYPOTHETICAL PROTEIN FLJ23447. | 56555 | 10.15 | 1 | 1 | 1.17 |
| 1666 | IPI00302309.2 | HYPOTHETICAL PROTEIN FLJ10890. | 108741 | 5.79 | 1 | 1 | 0.52 |
| 1667 | IPI00302966.2 | HYPOTHETICAL PROTEIN FLJ10890. | 129687 | 6.56 | 1 | 1 | 0.44 |
| 1668 | IPI00303335.1 | NEBULIN. | 773214 | 9.49 | 1 | 1 | 0.1 |
| 1669 | IPI00304111.1 | EXTRACELLULAR SIGNAL-RELATED KINASE 1C. | 38249 | 6.14 | 1 | 1 | 4.48 |
| 1670 | IPI00304577.3 | SPLICE ISOFORM A OF O95782 ADAPTER-RELATED PROTEIN COMPLEX 2 ALPHA 1 SUBUNIT. | 107555 | 7.06 | 1 | 1 | 1.84 |
| 1671 | IPI00304911.3 | VACUOLAR ATP SYNTHASE SUBUNIT B, KIDNEY ISOFORM. | 56980 | 5.52 | 1 | 1 | 3.9 |
| 1672 | IPI00305092.2 | PYM PROTEIN. | 28286 | 10.71 | 1 | 1 | 3.13 |
| 1673 | IPI00305461.1 | INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H2 PRECURSOR. | 106596 | 6.94 | 1 | 1 | 0.63 |
| 1674 | IPI00305469.1 | SIMILAR TO V-CRK AVIAN SARCOMA VIRUS CT10 ONCOGENE HOMOLOG. | 22906 | 5.13 | 1 | 1 | 8.33 |
| 1675 | IPI00305486.1 | SPLICE ISOFORM 1 OF P49418 AMPHIPHYSIN. | 76257 | 4.28 | 1 | 1 | 1.44 |
| 1676 | IPI00305491.3 | HYPOTHETICAL SERINE/THREONINE PROTEIN PHOSPHATASE. | 58129 | 6.97 | 1 | 1 | 1.76 |
| 1677 | IPI00306667.2 | SPLICE ISOFORM CNPII OF P09543 2',3'-CYCLIC NUCLEOTIDE 3'-PHOSPHODIESTERASE. | 51085 | 9.59 | 1 | 1 | 2.4 |
| 1678 | IPI00306840.1 | SPHINGOSINE-1-PHOSPHATE PHOSPHATASE 1. | 48889 | 9.18 | 1 | 1 | 1.36 |
| 1679 | IPI00306870.1 | DJ148E22.2 (NOVEL PABPC1. | 33332 | 9.29 | 1 | 1 | 3.77 |
| 1680 | IPI00306929.4 | SPLICE ISOFORM 1 OF Q8IUG5 MYOSIN XVIIIB. | 285185 | 6.88 | 1 | 1 | 0.19 |
| 1681 | IPI00307219.2 | --none found in database-- | 52180 | 9.67 | 1 | 1 | 1.27 |
| 1682 | IPI00307516.4 | HYPOTHETICAL PROTEIN FLJ32752. | 122765 | 7.23 | 1 | 1 | 0.54 |
| 1683 | IPI00307702.1 | H53_GS1. | 58017 | 8.33 | 1 | 1 | 1.12 |
| 1684 | IPI00328268.5 | EIF4GII. | 176652 | 5.02 | 1 | 1 | 0.63 |
| 1685 | IPI00328319.4 | CHROMATIN ASSEMBLY FACTOR 1 SUBUNIT C. | 50614 | 4.65 | 1 | 1 | 2.86 |
| 1686 | IPI00329276.1 | B-CELL NOVEL PROTEIN ISOFORM 3. | 77401 | 8.71 | 1 | 1 | 0.86 |
| 1687 | IPI00329389.2 | 60S RIBOSOMAL PROTEIN L6. | 32597 | 11.29 | 1 | 1 | 2.79 |
| 1688 | IPI00329391.1 | SIMILAR TO DIHYDROLIPOAMIDE S-ACETYLTRANSFERASE PRECURSOR. | 68997 | 7.94 | 1 | 1 | 2.32 |
| 1689 | IPI00329442.1 | FIBROBLAST ACTIVATION PROTEIN, ALPHA. | 87713 | 6.63 | 1 | 1 | 0.66 |
| 1690 | IPI00329607.5 | ZINC FINGER PROTEIN 93 (ZINC FINGER PROTEIN HTF34). | 53858 | 10.26 | 1 | 1 | 1.06 |
| 1691 | IPI00329633.3 | THREONYL-TRNA SYNTHETASE. | 83435 | 6.64 | 1 | 1 | 1.24 |
| 1692 | IPI00332047.1 | --none found in database-- | 10605 | 4.79 | 1 | 1 | 8.51 |
| 1693 | IPI00332128.1 | --none found in database-- | 48426 | 4.7 | 1 | 1 | 2.3 |
| 1694 | IPI00332371.1 | 6-PHOSPHOFRUCTOKINASE, LIVER TYPE. | 85048 | 7.38 | 1 | 1 | 1.92 |
| 1695 | IPI00332570.3 | POLYADENYLATE-BINDING PROTEIN 2. | 58518 | 9.77 | 1 | 1 | 2.11 |
| 1696 | IPI00332604.1 | FLJ00140 PROTEIN. | 64716 | 10.19 | 1 | 1 | 1.04 |
| 1697 | IPI00333134.2 | SPLICE ISOFORM 2 OF O43426 SYNAPTOJANIN 1. | 144887 | 7.34 | 1 | 1 | 0.99 |
| 1698 | IPI00333196.1 | --none found in database-- | 56744 | 8.49 | 1 | 1 | 1.19 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 1699 | IPI00333323.1 | --none found in database-- | 45158 | 10.72 | 1 | 1 | 3.4 |
| 1700 | IPI00333763.5 | SIMILAR TO RIKEN CDNA 2900070E19 GENE. | 16628 | 6.78 | 1 | 1 | 8.92 |
| 1701 | IPI00334255.1 | HYPOTHETICAL PROTEIN FLJ39802. | 69109 | 8 | 1 | 1 | 0.97 |
| 1702 | IPI00334272.2 | SIMILAR TO MYOSIN:SUBUNIT=REGULATORY LIGHT CHAIN. | 31859 | 6.24 | 1 | 1 | 3.91 |
| 1703 | IPI00334324.1 | --none found in database-- | 26794 | 10.04 | 1 | 1 | 3.69 |
| 1704 | IPI00334763.1 | --none found in database-- | 42146 | 8.37 | 1 | 1 | 2.9 |
| 1705 | IPI00334877.1 | --none found in database-- | 15754 | 10.25 | 1 | 1 | 7.97 |
| 1706 | IPI00335168.4 | SMOOTH MUSCLE AND NON-MUSCLE MYOSIN ALKALI LIGHT CHAIN ISOFORM 1. | 16930 | 4.29 | 1 | 1 | 8.61 |
| 1707 | IPI00335186.3 | SPLICE ISOFORM 3 OF P07202 THYROID PEROXIDASE PRECURSOR. | 102739 | 7.25 | 1 | 1 | 0.65 |
| 1708 | IPI00335929.1 | SERUM/GLUCOCORTICOID REGULATED KINASE-LIKE ISOFORM 2. | 53306 | 7.24 | 1 | 1 | 1.08 |
| 1709 | IPI00337584.1 | SCAVENGER RECEPTOR CLASS A, MEMBER 3 ISOFORM 1. | 70062 | 6.66 | 1 | 1 | 0.92 |
| 1710 | IPI00337806.1 | --none found in database-- | 153097 | 4.94 | 1 | 1 | 0.72 |
| 1711 | IPI00337814.1 | HYPOTHETICAL PROTEIN. | 55244 | 7.23 | 1 | 1 | 1.98 |
| 1712 | IPI00373980.1 | SIMILAR TO CG11206-PA. | 71306 | 7.2 | 1 | 1 | 0.77 |
| 1713 | IPI00373982.1 | SIMILAR TO 40S RIBOSOMAL PROTEIN S16. | 14346 | 10.41 | 1 | 1 | 8.53 |
| 1714 | IPI00374005.1 | SIMILAR TO TRIOSEPHOSPHATE ISOMERASE 1. | 10312 | 10.22 | 1 | 1 | 8.51 |
| 1715 | IPI00374119.1 | SMOOTH MUSCLE AND NON-MUSCLE MYOSIN ALKALI LIGHT CHAIN ISOFORM 3. | 17557 | 4.24 | 1 | 1 | 8.28 |
| 1716 | IPI00374239.1 | SIMILAR TO 40S RIBOSOMAL PROTEIN S3. | 13211 | 5.17 | 1 | 1 | 10.74 |
| 1717 | IPI00374318.1 | SIMILAR TO 60S RIBOSOMAL PROTEIN L27A. | 12538 | 12.1 | 1 | 1 | 9.73 |
| 1718 | IPI00374566.1 | SIMILAR TO PROTEIN 40KD. | 17755 | 4.47 | 1 | 1 | 6.1 |
| 1719 | IPI00374734.1 | SIMILAR TO MITOCHONDRIAL IMPORT RECEPTOR SUBUNIT TOM22 HOMOLOG (TRANSLOCASE OF OUTER MEMBRANE 22 KDA SUBUNIT HOMOLOG) (HTOM22) (1C9-2). | 32926 | 4.63 | 1 | 1 | 1.68 |
| 1720 | IPI00374918.1 | HYPOTHETICAL PROTEIN XP_353349. | 10953 | 9.56 | 1 | 1 | 4.95 |
| 1721 | IPI00374976.1 | ELKS DELTA. | 124904 | 5.91 | 1 | 1 | 0.83 |
| 1722 | IPI00375145.1 | SPLICE ISOFORM SHORT OF P45974 UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 5. | 93308 | 4.71 | 1 | 1 | 1.92 |
| 1723 | IPI00375210.1 | SIMILAR TO RIBOSE-PHOSPHATE PYROPHOSPHOKINASE III (PHOSPHORIBOSYL PYROPHOSPHATE SYNTHETASE III) (PRS-III). | 38356 | 6.7 | 1 | 1 | 3.72 |
| 1724 | IPI00375223.1 | HYPOTHETICAL PROTEIN LOC255743. | 55697 | 8.61 | 1 | 1 | 0.98 |
| 1725 | IPI00375731.1 | HYPOTHETICAL PROTEIN DKFZP686E2459. | 110338 | 6.12 | 1 | 1 | 1.31 |
| 1726 | IPI00375802.1 | HYPOTHETICAL PROTEIN DKFZP781B1340. | 65111 | 5.4 | 1 | 1 | 0.86 |
| 1727 | IPI00375907.2 | HYPOTHETICAL PROTEIN LOC200186. | 74180 | 7.01 | 1 | 1 | 0.71 |
| 1728 | IPI00375927.1 | HYPOTHETICAL PROTEIN DKFZP686F07114. | 123331 | 6.7 | 1 | 1 | 0.54 |
| 1729 | IPI00376018.1 | CYTOPLASMIC DYNEIN LIGHT CHAIN 2A ISOFORM B. | 7342 | 7.53 | 1 | 1 | 19.05 |
| 1730 | IPI00376108.1 | SIMILAR TO AMINOPEPTIDASE PUROMYCIN SENSITIVE. | 46093 | 4.66 | 1 | 1 | 2.44 |
| 1731 | IPI00376139.1 | PHOSPHOINOSITIDE-3-KINASE, CLASS 3. | 101549 | 6.79 | 1 | 1 | 0.68 |
| 1732 | IPI00376426.1 | SIMILAR TO HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1 (HELIX-DESTABILIZING PROTEIN) (SINGLE-STRAND BINDING PROTEIN) (HNRNP CORE PROTEIN A1) (HDP-1) (TOPOISOMERASE-INHIBITOR SUPPRESSED). | 21265 | 6.25 | 1 | 1 | 5.82 |
| 1733 | IPI00376452.1 | SIMILAR TO 40S RIBOSOMAL PROTEIN S20. | 14339 | 10.53 | 1 | 1 | 9.45 |
| 1734 | IPI00376740.1 | SIMILAR TO GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE. | 26342 | 8.9 | 1 | 1 | 2.48 |
| 1735 | IPI00376747.1 | SIMILAR TO HYPOTHETICAL PROTEIN. | 232554 | 6.84 | 1 | 1 | 0.28 |
| 1736 | IPI00376825.1 | SIMILAR TO DJ834A16.1 (SIMILAR TO PGAM). | 14527 | 4.64 | 1 | 1 | 7.75 |
| 1737 | IPI00376841.1 | SIMILAR TO GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, LIVER (GAPDH). | 21168 | 7.66 | 1 | 1 | 3.63 |
| 1738 | IPI00376910.1 | HYPOTHETICAL PROTEIN XP_352987. | 15467 | 10.35 | 1 | 1 | 3.6 |
| 1739 | IPI00376992.1 | MLL/SEPTIN6 FUSION PROTEIN. | 63143 | 8.15 | 1 | 1 | 1.79 |
| 1740 | IPI00377006.1 | SODIUM CHANNEL PROTEIN TYPE V ALPHA SUBUNIT. | 227485 | 5.18 | 1 | 1 | 0.45 |
| 1741 | IPI00377087.1 | GELSOLIN ISOFORM B. | 80641 | 5.6 | 1 | 1 | 1.78 |
| 1742 | IPI00377132.1 | BH3 INTERACTING DOMAIN DEATH AGONIST ISOFORM 3. | 11263 | 10.22 | 1 | 1 | 15.15 |
| 1743 | IPI00377238.1 | TITIN ISOFORM N2-A. | 3.82E+06 | 6.25 | 1 | 1 | 0.01 |
| 1744 | IPI00382569.1 | --none found in database-- | 25911 | 8.95 | 1 | 1 | 2.2 |
| 1745 | IPI00382574.1 | --none found in database-- | 13463 | 5.56 | 1 | 1 | 10.17 |
| 1746 | IPI00382629.2 | --none found in database-- | 158768 | 7.09 | 1 | 1 | 0.44 |
| 1747 | IPI00382632.1 | --none found in database-- | 18183 | 5.68 | 1 | 1 | 6.13 |
| 1748 | IPI00382644.1 | PUTATIVE EUKARYOTIC TRANSLATION INITIATION FACTOR 1A. | 16329 | 4.73 | 1 | 1 | 7.69 |
| 1749 | IPI00382716.1 | --none found in database-- | 11418 | 9.85 | 1 | 1 | 6.86 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 1750 | IPI00382803.2 | SPLICE ISOFORM 1 OF P27816 MICROTUBULE-ASSOCIATED PROTEIN 4. | 126443 | 5.39 | 1 | 1 | 0.91 |
| 1751 | IPI00382869.1 | FARNESYL PYROPHOSPHATE SYNTHETASE LIKE-4 PROTEIN. | 39750 | 4.61 | 1 | 1 | 3.45 |
| 1752 | IPI00383134.1 | SIMILAR TO BA92K2.2 (SIMILAR TO UBIQUITIN). | 16874 | 9.67 | 1 | 1 | 3.36 |
| 1753 | IPI00383234.1 | AMPHIPHYSIN I VARIANT CT2. | 60634 | 3.81 | 1 | 1 | 1.76 |
| 1754 | IPI00383296.1 | RIBONUCLEOPROTEIN. | 73621 | 9.29 | 1 | 1 | 2.32 |
| 1755 | IPI00383323.1 | --none found in database-- | 35570 | 10.05 | 1 | 1 | 5.97 |
| 1756 | IPI00383607.1 | HYPOTHETICAL PROTEIN. | 200087 | 6.54 | 1 | 1 | 0.28 |
| 1757 | IPI00383660.2 | KIAA1508 PROTEIN. | 68838 | 8.74 | 1 | 1 | 0.67 |
| 1758 | IPI00383752.1 | DELTA 3, DELTA 2-ENOYL-COA ISOMERASE. | 12656 | 8.51 | 1 | 1 | 3.45 |
| 1759 | IPI00383786.1 | NEBULIN. | 111660 | 9.61 | 1 | 1 | 0.72 |
| 1760 | IPI00383911.1 | HYPOTHETICAL PROTEIN FLJ36307. | 20450 | 10.4 | 1 | 1 | 8.6 |
| 1761 | IPI00384065.1 | HYPOTHETICAL PROTEIN FLJ90034. | 58059 | 6.94 | 1 | 1 | 0.79 |
| 1762 | IPI00384187.1 | HYPOTHETICAL PROTEIN. | 40100 | 6.8 | 1 | 1 | 3.43 |
| 1763 | IPI00384282.1 | CYTOVILLIN 2. | 16302 | 9.83 | 1 | 1 | 6.38 |
| 1764 | IPI00384366.1 | SIMILAR TO RIKEN CDNA 5133400G04 GENE. | 20847 | 10.09 | 1 | 1 | 2.66 |
| 1765 | IPI00384463.1 | EUKARYOTIC TRANSLATION INITIATION FACTOR 4 GAMMA. | 153361 | 4.9 | 1 | 1 | 0.72 |
| 1766 | IPI00384476.1 | E74-LIKE FACTOR 1. | 67498 | 4.84 | 1 | 1 | 0.81 |
| 1767 | IPI00384504.1 | SIMILAR TO BCL-2-ASSOCIATED TRANSCRIPTION FACTOR. | 57763 | 11.73 | 1 | 1 | 3.55 |
| 1768 | IPI00384544.1 | MYOSIN REGULATORY LIGHT CHAIN. | 19779 | 4.44 | 1 | 1 | 6.4 |
| 1769 | IPI00384582.2 | SIMILAR TO MICROTUBULE-ASSOCIATED PROTEIN 4. | 89580 | 10.27 | 1 | 1 | 1.28 |
| 1770 | IPI00384584.1 | B-CELL NOVEL PROTEIN ISOFORM 2. | 72185 | 8.11 | 1 | 1 | 0.92 |
| 1771 | IPI00384585.1 | B-CELL NOVEL PROTEIN ISOFORM 1. | 73779 | 8.4 | 1 | 1 | 0.9 |
| 1772 | IPI00384758.1 | HYPOTHETICAL PROTEIN FLJ39514. | 69992 | 6.76 | 1 | 1 | 0.94 |
| 1773 | IPI00385001.1 | HYPOTHETICAL PROTEIN DKFZP686L1653. | 182480 | 6.89 | 1 | 1 | 0.37 |
| 1774 | IPI00385055.1 | HYPOTHETICAL PROTEIN. | 100447 | 5.72 | 1 | 1 | 0.55 |
| 1775 | IPI00385120.1 | HYPOTHETICAL PROTEIN. | 6196 | 10.36 | 1 | 1 | 16.67 |
| 1776 | IPI00385347.1 | HYPOTHETICAL PROTEIN DKFZP779O048. | 12455 | 8.75 | 1 | 1 | 10 |
| 1777 | IPI00385371.1 | B-IND1 PROTEIN. | 43543 | 8.19 | 1 | 1 | 5.68 |
| 1778 | IPI00385399.1 | MITOGEN-ACTIVATED PROTEIN KINASE 3. | 43109 | 6.74 | 1 | 1 | 3.96 |
| 1779 | IPI00385414.1 | HYPOTHETICAL PROTEIN. | 66055 | 7.28 | 1 | 1 | 1.01 |
| 1780 | IPI00385659.1 | HYPOTHETICAL PROTEIN. | 16156 | 8.48 | 1 | 1 | 5.84 |
| 1781 | IPI00385699.1 | NUCLEASE SENSITIVE ELEMENT BINDING PROTEIN 1. | 35369 | 9.5 | 1 | 1 | 5.94 |
| 1782 | IPI00385860.1 | GPR18-ISO. | 38034 | 9.75 | 1 | 1 | 1.2 |
| 1783 | IPI00386245.1 | AMPHIPHYSIN I VARIANT NC1. | 62173 | 3.83 | 1 | 1 | 1.72 |
| 1784 | IPI00386350.1 | HYPOTHETICAL PROTEIN FLJ13874. | 19784 | 9.33 | 1 | 1 | 5.52 |
| 1785 | IPI00386445.1 | RIBOSOMAL PROTEIN S2. | 21721 | 11.51 | 1 | 1 | 6.4 |
| 1786 | IPI00386533.1 | EUKARYOTIC TRANSLATION INITIATION FACTOR 4 GAMMA, 1 ISOFORM 3. | 158517 | 4.86 | 1 | 1 | 0.7 |
| 1787 | IPI00386534.1 | EUKARYOTIC TRANSLATION INITIATION FACTOR 4 GAMMA, 1 ISOFORM 2. | 166589 | 4.86 | 1 | 1 | 0.66 |
| 1788 | IPI00386623.1 | HYPOTHETICAL PROTEIN. | 34580 | 7.23 | 1 | 1 | 6.71 |
| 1789 | IPI00386631.1 | HYPOTHETICAL PROTEIN KIAA0910. | 145331 | 7.69 | 1 | 1 | 0.99 |
| 1790 | IPI00386639.1 | ELASTIC TITIN. | 883025 | 5.19 | 1 | 1 | 0.06 |
| 1791 | IPI00386795.1 | SIMILAR TO DIFFERENTIALLY EXPRESSED IN FDCP (MOUSE HOMOLOG) 6. | 69043 | 5.65 | 1 | 1 | 1.69 |
| 1792 | IPI00387125.1 | BA196N14.4.2 (PRO1085 PROTEIN, ISOFORM 2, SIMILAR TO PROTEIN SERINE/THREONINE PHOSPHATASE 4 REGULATORY SUBUNIT 1. | 38508 | 6.05 | 1 | 1 | 1.5 |
| 1793 | IPI00395423.1 | HYPOTHETICAL PROTEIN FLJ14719. | 94705 | 6.77 | 1 | 1 | 0.72 |
| 1794 | IPI00395469.1 | SPLICE ISOFORM 3 OF O00154 CYTOSOLIC ACYL COENZYME A THIOESTER HYDROLASE. | 42728 | 10.1 | 1 | 1 | 3.02 |
| 1795 | IPI00395532.1 | PRO3063. | 26233 | 4.53 | 1 | 1 | 4.7 |
| 1796 | IPI00395643.1 | REGULATOR OF G-PROTEIN SIGNALLING 14. | 61575 | 8.47 | 1 | 1 | 0.71 |
| 1797 | IPI00395748.1 | SPLICE ISOFORM 4 OF O00154 CYTOSOLIC ACYL COENZYME A THIOESTER HYDROLASE. | 49170 | 10.05 | 1 | 1 | 2.65 |
| 1798 | IPI00395750.1 | SPLICE ISOFORM LONG OF O75083 WD-REPEAT PROTEIN 1. | 67541 | 6.67 | 1 | 1 | 2.58 |
| 1799 | IPI00395788.1 | BH3 INTERACTING DOMAIN DEATH AGONIST. | 26556 | 6.78 | 1 | 1 | 6.28 |
| 1800 | IPI00395835.1 | PUTATIVE C-MYC-RESPONSIVE ISOFORM 2. | 16187 | 6.79 | 1 | 1 | 11.49 |
| 1801 | IPI00395865.1 | HISTONE ACETYLTRANSFERASE TYPE B SUBUNIT 2. | 51576 | 5.07 | 1 | 1 | 2.84 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 1802 | IPI00395972.1 | --none found in database-- | 152969 | 4.94 | 1 | 1 | 0.72 |
| 1803 | IPI00395982.1 | --none found in database-- | 55277 | 8.31 | 1 | 1 | 1.22 |
| 1804 | IPI00395998.1 | RIBOSOMAL PROTEIN L32. | 15860 | 11.9 | 1 | 1 | 9.63 |
| 1805 | IPI00396023.1 | COMPLEXIN 1. | 15030 | 4.63 | 1 | 1 | 10.45 |
| 1806 | IPI00396111.1 | CYLD PROTEIN. | 107316 | 5.27 | 1 | 1 | 0.52 |
| 1807 | IPI00396152.1 | MICROTUBULE-ASSOCIATED PROTEIN 4 ISOFORM 3. | 119232 | 4.94 | 1 | 1 | 0.97 |
| 1808 | IPI00396171.1 | MICROTUBULE-ASSOCIATED PROTEIN 4 ISOFORM 2. | 122596 | 5.14 | 1 | 1 | 0.94 |
| 1809 | IPI00396265.1 | NERF-1B. | 57389 | 9.43 | 1 | 1 | 0.94 |
| 1810 | IPI00396293.1 | PMEPA1 VARIANT A PROTEIN. | 26201 | 6.85 | 1 | 1 | 2.11 |
| 1811 | IPI00396344.1 | --none found in database-- | 41771 | 7.8 | 1 | 1 | 1.25 |
| 1812 | IPI00396426.1 | HYPOTHETICAL PROTEIN. | 33285 | 7.08 | 1 | 1 | 1.71 |
| 1813 | IPI00396437.1 | SIMILAR TO SRC HOMOLOGY 3 DOMAIN-CONTAINING PROTEIN HIP-55. | 48294 | 4.72 | 1 | 1 | 2.55 |
| 1814 | IPI00396482.1 | --none found in database-- | 24793 | 9.8 | 1 | 1 | 5.43 |
| 1815 | IPI00396485.1 | --none found in database-- | 50183 | 7.42 | 1 | 1 | 2.41 |
| 1816 | IPI00396508.1 | DNAJ (HSP40) HOMOLOG, SUBFAMILY C, MEMBER 6. | 102814 | 8.08 | 1 | 1 | 0.64 |
| 1817 | IPI00396540.1 | SCAVENGER RECEPTOR CLASS A, MEMBER 3 ISOFORM 2. | 57359 | 6.11 | 1 | 1 | 1.17 |
| 1818 | IPI00396558.1 | SIMILAR TO MEMBRANE PROTEIN OF CHOLINERGIC SYNAPTIC VESICLES. | 32559 | 6.72 | 1 | 1 | 4.67 |
| 1819 | IPI00396589.1 | INTERLEUKIN ENHANCER BINDING FACTOR 2, 45KD. | 43062 | 4.93 | 1 | 1 | 2.82 |
| 1820 | IPI00396653.1 | SEX COMB ON MIDLEG HOMOLOG 1. | 68325 | 9.91 | 1 | 1 | 0.81 |

# REFERENCES


1. Persidis, A. (1998). “An ambitious drug development platform attempts to link gene sequence to expressed phenotype under various physiological states,” *Nat. Biotech*. 16, 393-394.
2. Hood, L. (2002). “A personal view of molecular technology and how it has changed biology,” *J. Prot. Res*. 1, 399-409.
3. Hillenkamp, F., Karas, M., Beavis, R. C., and Chait, B. T. (1991). “Matrix-assisted laser desorption/ionization mass spectrometry of biopolymers,” *Anal. Chem*. 63, 1193A-1202A.
4. Fenselau, C. (1997). “MALDI-MS and strategies for protein analysis,” *Anal. Chem*. 69, 661A-665A.
5. Kebarle, P., Tang, L. (1993). “From ions in solution to ions in the gas phase,” *Anal. Chem.* 65, 972A-986A.
6. Yates, J. R. III (1998). “Mass spectrometry and the age of the proteome,” *J. Mass Spectrom*. 33, 1-19.
7. Klose, J., Kobalz, U. (1995). “Two-dimensional electrophoresis of proteins: an updated protocol and implications for a functional analysis of the genome,” *Electrophoresis* 16, 1034-1059.
8. Jungblut, P., Thiede, B., Zimny-Arndt, U., Muller, E.-C., Scheler, C., Wittmann-Liebold, B., and Otto, A. (1996). “Resolution power of two-dimensional electrophoresis and identification of proteins from gels,” *Electrophoresis* 17, 839-847.

9. Rabilloud, T. (2000). “Detecting proteins separated by 2-D gel electrophoresis,” *Anal. Chem*. 72, 48A-55A.

10. Righetti, P. G., Castagna, A., and Herbert, B. (2001). “Prefractionation techniques in proteome analysis,” *Anal. Chem*. 73, 320A-326A.

11. Gygi, S. P., Corthals, G. L., Zhang, Y., Rochon, Y., and Aebersold, R. (2000). “Evaluation of two-dimensional gel electrophoresis based proteome analysis technology,” *Proc. Natl. Acad. Sci. USA* 97, 9390-9395.

12. Smith, R. D. (2000). “Probing proteomes-seeing the whole picture,” *Nat. Biotech*. 18, 1041-1042.

13. Washburn, M. P., Wolters, D., and Yates, J. R. III (2001). “Large-scale analysis of the yeast proteome by multidimensional protein identification technology,” *Nat. Biotech*. 19, 242-247.

14. Wolters, D. A., Washburn, M. P., and Yates, J. R. III (2001). “An automated multidimensional protein identification technology for shotgun proteomics,” *Anal. Chem*. 73, 5683-5690.

15. Washburn, M. P., Ulaszek, R., Deciu, C., Schieltz, D. M., and Yates, J. R. III (2002). “Analysis of quantitative proteomic data generated via multidimensional protein identification technology,” *Anal. Chem*. 74, 1650-1657.

16. Gygi, S. P., Rist, B., Griffin, T. J., Eng, J., and Aebersold, R. (2002). “Proteome analysis of low-abundance proteins using multidimensional chromatography and isotope-coded affinity tags,” *J. Prot. Res*. 1, 47-54.

17. VerBerkmoes, N. C., Bundy, J. L., Hauser, L., Asano, K. G., Razumovskaya, J., Larimer, F., Hettich, R. L., and Stephenson, J. J. Jr. (2002). “Integrating top-

down and bottom-up mass spectrometric approaches for proteomic analysis of *Shewanella Oneidensis*," *J. Prot. Res*. 1, 239-252.

18. Peng, J., Elias, J. E., Thoreen, C. C., Licklider, L. J., and Gygi, S. P. (2003). "Evaluation of multidimensional chromatography coupled with tandem mass spectrometry (LC/LC-MS/MS) for large-scale protein analysis: the yeast proteome," *J. Prot. Res*. 2, 43-50.
19. Mann, M., Jensen, O. N. (2003). "Proteomics analysis of post-translational modifications," *Nat. Biotech*. 21, 255-261.
20. Valaskovic, G. A., Kelleher, N. L., and Mclafferty, F. W. (1996). "Attomole protein characterization by capillary electrophoresis mass spectrometry," *Science* 273, 1199-1202.
21. Meng, F., Cargile, B. J., Miller, L. M., Forbes, A. J., Johnson, J. R., and Kelleher, N. L. (2001). "Informatics and multiplexing of intact protein identification in bacteria and the archaea," *Nat. Biotech*. 19, 952-957.
22. Meng, F., Cargile, B. J., Patrie, S. M., Johnson, J. R., McLoughlin, S. M., and Kelleher, N. L. (2002). "Processing complex mixtures of intact proteins for direct analysis by mass spectrometry," *Anal. Chem*. 74, 2923-2929.
23. Meng, F., Du, Y., Miller, L. M., Patrie, S. M., Robinson, D. E., and Kelleher, N. L. (2004). "Molecular-level description of proteins from *Saccharomyces cerevisiae* using quadrupole FT hybrid mass spectrometry for top down proteomics," *Anal. Chem.* 76, 2852-2858.
24. Shen, Y., Moore, R. J., Zhao, R., Blonder, J., Auberry, D. L., Masselon, C., Paša-Tolić, L., Hixson, K. K., Auberry, K. J., and Smith, R. D. (2003). "High-

efficiency on-line solid-phase extraction coupling to 15-150-μm-i.d. liquid chromatography for proteome analysis," *Anal. Chem*. 75, 3596-3605.

25. Shen, Y., Tolic, N., Masselon, C., Paša-Tolić, L., Camp, D. G., Hixson, K. K., Zhao, R., Anderson, G. A., and Smith, R. D. (2004). "Ultrasensitive proteomics using high-efficiency on-line micro-SPE-nanoLC-nanoESI MS and MS/MS," *Anal. Chem.* 76, 144-154.

26. Petritis, K., Kangas, L. J., Ferguson, P. L., Anderson, G. A., Paša-Tolić, L., Lipton, M. S., Auberry, K. J., Strittmatter, E. F., Shen, Y., Zhao, R., and Smith, R. D. (2003). "Use of artificial neural networks for the accurate prediction of peptide liquid chromatography elution times in proteome analysis," *Anal. Chem.* 75, 1039-1048.

27. Wilkins, J. A., Xiang, R., and Horvath, C. (2002). "Selective enrichment of low-abundance peptides in complex mixtures by elution-modified displacement chromatography and their identification by electrospray ionization mass spectrometry," *Anal. Chem.* 74, 3933-3941.

28. Xiang, R., Horvath, C., and Wilkins, J. A. (2003). "Elution-modified displacement chromatography coupled with electrospray ionization-MS: on-line detection of trace peptides at low-femtomole level in peptide digests," *Anal. Chem.* 75, 1819-1827.

29. Ogorzalek Loo, R. R., Cavalcoti, J. D., VanBogelen, R. A., Mitchell, C., Loo, J. A., Moldover, B., and Andrews, P. C. (2001). "Virtual 2-D gel electrophoresis: visualization and analysis of the *E. Coli* proteome by mass spectrometry," *Anal. Chem*. 73, 4063-4070.

30. Tang, Q., Harrata, A. K., and Lee, C. S. (1997). “Two-dimensional analysis of recombinant *E. Coli* proteins using capillary isoelectric focusing-electrospray ionization mass spectrometry,” *Anal. Chem.* 69, 3177-3182.

31. Jensen, P. K., Pasa-Tolic, L., Anderson, G. A., Horner, J. A., Lipton, M. S., Bruce, J. E., and Smith, R. D. (1999). “Probing proteomes using capillary isoelectric focusing-electrospray ionization fourier transform ion cyclotron resonance mass spectrometry,” *Anal. Chem.* 71, 2076-2084.

32. Li, W., Hendrickson, C. L., Emmett, M. R., and Marshall, A. G. (1999). “Identification of intact proteins in mixtures by alternated capillary liquid chromatography electrospray ionization and LC-ESI infrared multiphoton dissociation fourier transform ion cyclotron resonance mass spectrometry,” *Anal. Chem.* 71, 4397-4402.

33. Lee, S.-W., Berger, S. J., Martinovic, S., Pasa-Tolic, L., Anderson, G. A., Shen, Y., Zhao, R., and Smith, R. D. (2002). “Direct mass spectrometric analysis of intact proteins of the yeast large ribosomal subunit using capillary LC/FTICR,” *Proc. Natl. Acad. Sci. USA* 99, 5942-5947.

34. Wei, W., Yeung, E. S. (2002). “On-line concentration of proteins and peptides in capillary zone electrophoresis with an etched porous joint,” *Anal. Chem*. 74, 3899-3905.

35. Janini, G. M., Zhou, M., Yu, L., Blonder, J., Gignac, M., Conrads, T. P., Issaq, H. J., and Veenstra, T. D. (2003). “On-column sample enrichment for capillary electrophoresis sheathless electrospray ionization mass spectrometry: evaluation for peptide analysis and protein identification,” *Anal. Chem*. 75, 5984-5993.

36. Chen, J., Gao, J., and Lee, C. S. (2003). “Dynamic enhancements of sample loading and analyte concentration in capillary isoelectric focusing for proteome studies,” *J. Prot. Res*. 2, 249-254.

37. Giddings, J. C. (1991). *United Separation Science*, John Wiley & Sons, New York.

38. Shen, Y., Jacobs, J. M., Camp, D. G. II, Fang, R., Moore, R. J., Smith, R. D., Xiao, W., Davis, R. W., and Tompkins, R. G. (2004). “Ultra-high-efficiency strong cation exchange LC/RPLC/MS/MS for high dynamic range characterization of the human plasma proteome,” *Anal. Chem.* 76, 1134-1144.

39. Porath, J., Olin, B. (1983). “Immobilized metal ion affinity adsorption and affinity chromatography of biomaterials,” *Biochem.* 22, 1621-1630.

40. Ficarro, S. B., McCleland, M. L., Stukenberg, P. T., Burke, D. J., Ross, M. M., Shabanowitz, J., Hunt, D. F., and White, F. M. (2002). “Phosphoproteome analysis by mass spectrometry and its application to *Saccharomyces cerevisiae*,” *Nat. Biotech.* 20, 301-305.

41. Pinkse, M. W., Uitto, P. M., Hilhorst, M. J., Ooms, B., and Heck, A. J. (2004). “Selective isolation at the femtomole level of phosphopeptides from proteolytic digests using 2D-nanoLC-ESI-MS/MS and titanium oxide precolumns,” *Anal Chem*. 76, 3935-3943.

42. Wall, D. B., Kachman, M. T., Gong, S., Hinderer, R., Parus, S., Misek, D. E., Hanash, S. M., and Lubman, D. M. (2000). “Isoelectric focusing nonporous RP HPLC: a two-dimensional liquid-phase separation method for mapping of

cellular proteins with identification using MALDI-TOF mass spectrometry," *Anal. Chem.* 72, 1099-1111.

43. Kachman, M. T., Wang, H., Schwartz, D. R., Cho, K. R., and Lubman, D. M. (2002). "A 2-D liquid separations/mass mapping methods for interlysate comparison of ovarian cancers," *Anal. Chem.* 74, 1779-1791.

44. Zhu, K., Kim, J., Yoo, C., Miller, F. R., and Lubman, D. M. (2003). "High sequence coverage of proteins isolated from liquid separations of breast cancer cells using capillary electrophoresis-time-of-flight MS and MALDI-TOF MS mapping," *Anal. Chem.* 75, 6209-6217.

45. Yan, F., Subramanian, B., Nakeff, A., Barder, T. J., Parus, S. J., and Lubman, D. M. (2003). "A comparison of drug-treated and untreated HCT-116 human colon adenocarcinoma cells using a 2-D liquid separation mapping method based upon chromatofocusing PI fractionation," *Anal. Chem.* 75, 2299-2308.

46. Stroink, T., Wiese, G., Teeuwsen, J., Lingeman, H., Waterval, J. C. M., Bult, A., de Jong, G. J., and Underberg, W. J. M. (2003). "On-line coupling of size-exclusion chromatography and capillary zone electrophoresis via a reversed-phase C18 trapping column for the analysis of structurally related enkephalins in cerebrospinal fluid," *Electrophoresis* 24, 897-903.

47. Stroink, T., Schravendijk, P., Wiese, G., Teeuwsen, J., Lingeman, H., Waterval, J. C. M., Bult, A., de Jong, G. J., and Underberg, W. J. M. (2003). "On-line coupling of size-exclusion chromatography and capillary zone electrophoresis via a reversed-phase C18 trapping column for the determination of peptides in biological samples," *Electrophoresis* 24, 1126-1134.

48. Issaq, H. J., Chan, K. C., Liu, C. S., and Li, Q. (2001). “Multidimensional high performance liquid chromatography – capillary electrophoresis separation of a protein digest: an update,” *Electrophoresis* 22, 1133 -1135.

49. He, Y., Yeung, E. S., Chan, K. C., Issaq, H. J. (2002). “Two dimensional mapping of cancer cell extracts by liquid chromatography-capillary electrophoresis with ultraviolet absorbance detection,” *J. Chromatogr. A* 979, 81-89.

50. Janini, G. M., Chan, K. C., Conrads, T. P., Issaq, H. J., and Veenstra, T. D. (2004). “Two-dimensional liquid chromatography-capillary zone electrophoresis-sheathless electrospray ionization-mass spectrometry: evaluation for peptide analysis and protein identification,” *Electrophoresis* 25, 1973-1980.

51. Chen, J., Baehrecke, E. H., Shen, Y., Smith, R. D., and Lee, C. S. (2002). “Integration of capillary isoelectric focusing with capillary reversed-phase liquid chromatography for two-dimensional proteomics separation,” *Electrophoresis* 23, 3143 -3148.

52. Chen, J., Balgley, B. M., DeVoe, D. L., and Lee, C. S. (2003). “Capillary isoelectric focusing-based multidimensional concentration/separation platform for ultrasensitive proteome analysis,” *Anal Chem*. 75, 3145-3152.

53. Yang, C., Liu, H., Yang, Q., Zhang, L., Zhang, W., and Zhang, Y. (2003). ”On-line hyphenation of capillary isoelectric focusing and capillary gel electrophoresis by a dialysis interface,” *Anal Chem*. 75, 215-218.

54. Yang, C., Zhang, L., Liu, H., Zhang, W., and Zhang, Y. (2003). ”Two-dimensional capillary electrophoresis involving capillary isoelectric focusing and capillary zone electrophoresis,” *J. Chromatogr A.* 1018, 97-103.

55. Mohan, D., Shen, Y., Smith, R. D., and Lee, C. S. (2002). “On-line coupling of capillary isoelectric focusing with transient isotachophoresis/zone electrophoresis: a two-dimensional separation system for proteomics,” *Electrophoresis* 23, 3160-3167.

56. Mohan, D., Paša-Tolić, L., Masselon, C. D., Tolic, N., Bogdanov, B., Hixson, K. K., Smith, R. D., and Lee, C. S. (2003). “Integration of electrokinetic-based multidimensional separation/concentration platform with ESI-FTICR-MS for proteome analysis of *Shewanella oneidensis*,” *Anal Chem*. 75, 4432-4440.

57. Sheng, L., Pawliszyn, J. (2002). “Comprehensive two dimensional separation based on coupling micellar electrokinetic chromatography with capillary isoelectric focusing,” *Analyst* 127, 1159-1163.

58. Michels, D. A., Hu, S., Schoenherr, R. M., Eggertson, M. J., and Dovichi, N. J. (2002). **“**Fully automated two-dimensional capillary electrophoresis for high sensitivity protein analysis,” *Mol. Cell Proteomics* 1, 69-74.

59. Hu, S., Michels, D. A., Fazal, M. A., Ratisoontorn, C., Cunningham, M. L., and Dovichi, N. J. (2004). “Capillary sieving electrophoresis/micellar electrokinetic capillary chromatography for two-dimensional protein fingerprinting of single mammalian cells,” *Anal Chem*. 76, 4044-4049.

60. Rocklin, R. D., Ramsey, R. S., and Ramsey, J. M. (2000). "A microfabricated fluidic device for performing two-dimensional liquid phase separations," *Anal. Chem.* 72, 5244-5249.

61. Ramsey, J. D., Jacobson, S. C., Culbertson, C. T., and Ramsey, J. M. (2003). "High efficiency, two-dimensional separations of protein digests on microfluidic devices," *Anal. Chem.* 75, 3758-3764.

62. Gottschlich, N., Jacobson, S. C., Culbertson, C. T., and Ramsey, J. M. (2001). "Two-dimensional electrochromatography/capillary electrophoresis on a microchip," *Anal. Chem.* 73, 2669-2674.

63. Herr, A. E., Molho, J. I., Drouvalakis, K. A., Mikkelsen, J. C., Utz, P. J., Santiago, J. G., and Kenny, T. W. (2003). "On-chip coupling of isoelectric focusing and free solution electrophoresis for multidimensional separations," *Anal. Chem.* 75, 1180-1187.

64. Wang, Y.-C., Choi, M. H., and Han, J. (2004). "Two-dimensional protein separation with advanced sample and buffer isolation using microfluidic valves," *Anal. Chem.* 76, 4426-4431.

65. Becker, H., Lowack, K., and Manz, A. (1998). "Planar quartz chips with submicron channels for two-dimensional capillary electrophoresis applications," *J. Micromech. Microeng.* 8, 24-28.

66. Chen, X., Wu, H., Mao, C., and Whitesides, G. M. (2002). "A prototype two-dimensional capillary electrophoresis system fabricated in poly(dimethylsiloxane)," *Anal. Chem.* 74, 1772-1778.

67. Li, Y., Buch, J. S., Rosenberger, F., DeVoe, D. L., and Lee, C. S. (2004). "Integration of isoelectric focusing with parallel SDS gel electrophoresis for multidimensional protein separations in a plastic microfluidic network," *Anal. Chem.* 76, 742-748.

68. Conti, M., Gelfi, C., and Righetti, P. G. (1995). "Screening of umbilical cord blood hemoglobins by isoelectric focusing in capillaries," *Electrophoresis* 16, 1485-1491.

69. Shen, Y., Berger, S. J., Anderson, G. A., and Smith, R. D. (2000). "High-efficiency capillary isoelectric focusing of peptides," *Anal. Chem.* 72, 2154-2159.

70. Emmert-Buck, M. R., Bonner, R. F., Smith, P. D., Chuaqui, R. F., Zhuang, Z., Goldstein, S. R., Weiss, R. A., and Liotta, L. A. (1996). "Laser capture microdissection," *Science* 274, 998-1001.

71. Bonner, R. F., Emmert-Buck, M. R., Cole, K., Pohida, T., Chuaqui, R. F., Goldstein, S. R., and Liotta, L. A. (1997). "Laser capture microdissection: molecular analysis of tissue," *Science* 278, 1481-1483.

72. Wittliff, J. L., Erlander, M. G. (2002). "Laser capture microdissection and its applications in genomics and proteomics," *Methods Enzym.* 356, 12-25.

73. Goldsworthy, S. M., Stockton, P. S., Trempus, C. S., Foley, J. F., and Maronpot, R. R. (1999). "Effects of fixation on RNA extraction and amplification from laser capture microdissected tissue," *Mol. Carcinog.* 25, 86-91.

74. Kitahara, O., Furukawa, Y., Tanaka, T., Kihara, C., Ono, K., Yanagawa, R., Nita, M. E., Takagi, T., Nakamura, Y., and Tsunoda, T. (2001). "Alterations of

gene expression during colorectal carcinogenesis revealed by cDNA microarrays after laser capture microdissection of tumor tissues and normal epithelia," *Cancer Res.* 61, 3544-3549.

75. Taylor, T. B., Nambiar, P. R., Raja, R., Cheung, E., Rosenberg, D. W., and Anderegg, B. (2004). "Microgenomics: identification of new expression profiles via small and single-cell sample analyses," *Cytometry* 59, 254-261.

76. Van Gelder, R. N., von Zastrow, M. E., Yool, A., Dement, W. C., Barchas, J. D., and Eberwine, J. H. (1990). "Amplified RNA synthesized from limited quantities of heterogeneous cDNA," *Proc. Natl. Acad. Sci. USA* 87, 1663-1667.

77. Luo, L., Salunga, R. C., Guo, H., Bittner, A., Joy, K. C., Galindo, J. E., Xiao, H., Rogers, K. E., Wan, J. S., Jackson, M. R., and Erlander, M. G. (1999). "Gene expression profiles of laser-captured adjacent neuronal subtypes," *Nat. Med.* 1, 117-122.

78. Kabbarah, O., Pinto, K., Mutch, D. G., and Goodfellow, P. J. (2003). "Expression profiling of mouse endometrial cancers microdissected from ethanol-fixed paraffin-embedded tissues," *Am. J. Pathol.* 162, 755-762.

79. Wong, M. H., Saam, J. R., Stappenbeck, T. S., Rexer, C. H., and Gordon, J. I. (2000). "Genetic mosaic analysis based on cre recombinase and navigated laser capture microdissection," *Proc. Natl. Acad. Sci. USA* 97, 12601-12606.

80. Mouledous, L., Hunt, S., Harcourt, R., Harry, J., Williams, K. L., and Gutstein, H. B. (2003). "Navigated laser capture microdissection as an alternative to direct histological staining for proteomic analysis of brain samples," *Proteomics* 3, 610-615.

81. DeSouza, A. I., McGregor, E., Dunn, M. J., and Rose, M. L. (2004). "Preparation of human heart for laser microdissection and proteomics," *Proteomics* 4, 578-586.

82. Furuta, M., Weil, R. J., Vortmeyer, A. O., Huang, S., Lei, J., Huang, T.-N., Lee, Y.-S., Bhowmick, D. A., Lubensky, I. A., Oldfield, E. H., and Zhuang, Z. (2004). "Protein patterns and proteins that identify subtype of glioblastoma multiforme," *Oncogene* 23, 6806-6814.

83. Xu, B. J., Caprioli, R. M., Sanders, M. E., and Jensen, R. A. (2002). "Direct analysis of laser capture microdissected cells by MALDI mass spectrometry," *J. Am. Soc. Mass Spectrom.* 13, 1292-1297.

84. Bhattacharya, S. H., Gal, A. A., and Murray, K. K. (2003). "Laser capture microdissection MALDI for direct analysis of archival tissue," *J. Prot. Res.* 2, 95-98.

85. Chaurand, P., Sanders, M. E., Jensen, R. A., and Caprioli, R. M. (2004). "Proteomics in diagnostic pathology: profiling and imaging proteins directly in tissue section," *Am. J. Pathol.* 165, 1057-1068.

86. Paweletz, C. P., Trock, B., Pennanen, M., Tsangaris, T., Magnant, C., Liotta, L. A., and Petricoin, E. F. (2001). "Proteomic patterns of nipple aspirate fluids obtained by SELDI-TOF: potential for new biomarkers to aid in the diagnosis of breast cancer," *Dis. Markers* 17, 301-307.

87. Petricoin, E. F., Zoon, K. C., Kohn, E. C., Barrett, J. C., and Liotta, L. A. (2002). "Clinical proteomics: translating benchside promise into bedside reality," *Nat. Rev. Drug Discovery* 1, 683-695.

88. Wulfkuhle, J. D., Liotta, L. A., and Petricoin, E. F. (2003). "Proteomic applications for the early detection of cancer," *Nat. Rev. Cancer* 3, 267-275.

89. Cottingham, K. (2003). "Clinical proteomics: are we there yet," *Anal. Chem.* 75, 472A-476A.

90. Ornstein, D. K., Gillespie, J. W., Paweletz, C. P., Duray, P. H., Herring, J., Vocke, C. D., Topalian, S. L., Bostwick, D. G., Linehan, W. M., Petricoin, E. F., and Emmert-Buck, M. R. (2000). "Proteomic analysis of laser capture microdissected human prostate cancer and in vitro prostate cell lines," *Electrophoresis* 21, 2235-2242.

91. Craven, R. A., Banks, R. E. (2001). "Laser capture microdissection and proteomics: possibilities and limitation," *Proteomics* 1, 1200-1204.

92. Craven, R. A., Totty, N., Harnden, P., Selby, P. J., and Banks, R. E. (2002). "Laser capture microdissection and two-dimensional polyacrylamide gel electrophoresis: evaluation of tissue preparation and sample limitations," *Am. J. Pathol.* 160, 815-822.

93. Ahram, M., Flaig, M. J., Gillespie, J. W., Duray, P. H., Linehan, W. M., Ornstein, D. K., Niu, S., Zhao, Y., Petricoin, E. F., and Emmert-Buck, M. R. (2003). "Evaluation of ethanol-fixed, paraffin-embedded tissues for proteomic applications," *Proteomics* 3, 413-421.

94. Wu, S.-L., Hancock, W. S., Goodrich, G. G., and Kunitake, S. T. (2003). "An approach to the proteomic analysis of a breast cancer cell line (SKBR-3)," *Proteomics* 3, 1037-1046.

95. Zang, L., Toy, D. P., Hancock, W. S., Sgroi, D. C., and Karger, B. L. (2004). "Proteomic analysis of ductal carcinoma of the breast using laser capture microdissection, LC-MS, and $^{16}O/^{18}O$ isotopic labeling," *J. Prot. Res.* 3, 604-612.

96. Shen, Y. F., Smith, R. D. (2002). "High-resolution capillary isoelectric focusing of proteins using highly hydrophilic-substituted cellulose-coated capillaries," *J. Microcol. Sep.* 12, 135-141.

97. Rudnick, P. A., Wang, Y., Evans, E. L., Lee, C. S., and Balgley, B. M. (2005). "Large scale interpretation of MASCOT results using a mass accuracy based threshold effectively reduces false negative identifications," submitted to *J. Prot. Res.*

98. Cargile, B. J., Talley, D. L., and Stephenson, J. L. Jr. (2004). "Immobilized pH gradients as a first separation dimension in shotgun proteomics and analysis of the accuracy of pI predictability of peptides," *Electrophoresis* 25, 936-945.

99. Essader, A. S., Cargile, B. J., Bundy, J. L., and Stephenson, J. L. Jr. (2005). "A comparison of immobilized pH gradient isoelectric focusing and strong-cation-exchange chromatography as a first dimension in shotgun proteomics," *Proteomics* 5, 24-34.

100. Liu, H., Sadygov, R. G., Yates, J. R. III (2004). "A model for random sampling and estimation of relative protein abundance in shotgun proteomics," *Anal. Chem*. 76, 4193-4201.

101. Wang, Y., Serfass, L., Roy, M. O., Wong, J., Bonneau, A. M., and Georges, E. (2004). "Annexin-I expression modulates drug resistance in tumor cells," *Biochem. Biophys. Res. Commun.* 314, 565-570.

102. Cicek, M., Samant, R. S., Kinter, M., Welch, D. R., and Casery, G. (2004). "Identification of metastasis-associated proteins through protein analysis of metastatic MDA-MB-435 and metastasis-suppressed BRMS1 transfected-MDA-MB-435 cells," *Clin. Exp. Metastasis* 21, 149-157.

103. Wiese, C., Rolletschek, A., Kania, G., Blyszczuk, P., Tarasov, K. V., Tarasova, Y., Wersto, R. P., Boheler, K. R., and Wobus, A. M. (2004). "Nestin expression – a property of multi-lineage progenitor cells?," *Cell. Mol. Life Sci.* 61, 2510-2522.

104. Thomas, S. K., Messam, C. A., Spengler, B. A., Biedler, J. L., and Ross, R. A. (2004). "Nestin is a potential mediator of malignancy in human neuroblastoma cells," *J. Biol. Chem.* 279, 27994-27999.

105. Masselon, C., Anderson, G. A., Harkewicz, R., Bruce, J. E., Pasa-Tolic, L., and Smith, R. D. (2000). "Accurate mass multiplexed tandem mass spectrometry for high-throughput polypeptide identification from mixtures," *Anal. Chem.* 72, 1918-1924.

106. Williams, J. D., Flanagan, M., Lopez, L., Fischer, S., and Miller, L. A. D. (2003). "Using accurate mass electrospray ionization-time-of-flight mass spectrometer with in-source collision-induced dissociation to sequence peptide mixtures," *J. Chromatogr. A* 1020, 11-26.

107. Purvine, S., Eppel, J.-T., Yi, E. C., and Goodlett, D. R. (2003). “Shotgun collision-induced dissociation of peptides using a time of flight mass analyzer,” *Proteomics* 3, 847-850.

108. Venable, J. D., Dong, M.-Q., Wohlschlegel, J., Dillin, A., and Yates, J. R. III (2004). “Automated approach for quantitative analysis of complex peptide mixtures from tandem mass spectra,” *Nat. Methods* 1, 39-45.

109. Wilson, J., Vachet, R. W. (2004). “Multiplexed MS/MS in a quadrupole ion trap mass spectrometer,” *Anal. Chem.* 76, 7346-7353.

110. Shevchenko, A., Wilm, M., Vorm, O., and Mann, M. (1996). “Mass spectrometric sequencing of proteins from silver-stained polyacrylamide gels,” *Anal. Chem.* 68, 850-858.

111. Shevchenko, A., Jensen, O. N., Podtelejnikov, A. V., Sagliocco, F., Wilm, M., Vorm, O., Mortensen, P., Shevchenko, A., Boucherie, H., and Mann, M. (1996). “Linking genome and proteome by mass spectrometry: large-scale identification of yeast proteins from two dimensional gels,” *Proc. Natl. Acad. Sci. USA* 93, 14440-14445.

112. Williams, T. L., Leopold, P., and Musser, S. (2002). “Automated postprocessing of electrospray LC/MS data for profiling protein expression in bacteria,” *Anal. Chem.* 74, 5807-5813.

113. Williams, T. L., Callahan, J. H., Monday, S. R., Feng, P. C. H., and Musser, S. M. (2004). “Relative quantitation of intact proteins of bacterial cell extracts using coextracted proteins as internal standards,” *Anal. Chem.* 76, 1002-1007.

114. Wilce, M. C. J., Aguilar, M.-I., and Hearn, M. T. W. (1995). "Physicochemical basis of amino acid hydrophobicity scales" evaluation of four new scales of amino acid hydrophobicity coefficients derived from RP-HPLC of peptides," *Anal. Chem.* 67, 1210-1219.

115. Apffel, A., Fischer, S., Goldberg, G., Goodley, P. C., and Kuhlmann, F. E. (1995). "Enhanced sensitivity for peptide mapping with electrospray liquid chromatography-mass spectrometry in the presence of signal suppression due to trifluoroacetic acid-containing mobile phases,"*J. Chromatogr. A* 712, 177-190.

116. Juraschek, R., Dulcks, T., and Karas, M. (1999). "Nanoelectrospray – more than just a minimized-flow electrospray ionization source," *J. Am. Soc. Mass Spectrom.* 10, 300-308.

117. Chloupek, R. C., Hancock, W. S., Marchylo, B. A., Kirkland, J. J., Boyes, B. E., and Snyder, L. R. (1994). "Temperature as a variable in reversed-phase high-performance liquid chromatographic separations of peptide and protein samples : II. selectivity effects observed in the separation of several peptide and protein mixtures," *J. Chromatogr. A* 686, 45-59.

118. Chen, H., Horvath, Cs. (1995). "High speed high-performance liquid chromatography of peptides and proteins," *J. Chromatogr. A* 705, 3-20.

119. Adkins, J. N., Varnum, S. M., Auberry, K. J., Moore, R. J., Angell, N. H., Smith, R. D., Springer, D. L., and Pounds, J. G. (2002). "Toward a human blood serum proteome: analysis by multidimensional separation coupled with mass spectrometry," *Mol. Cell. Proteomics* 1, 947-955.

120. Wang, Y., Balgley, B. M., Rudnick, P. A., Evans, E. L., DeVoe, D. L., and Lee, C. S. (2005). "Integrated capillary isoelectric focusing/nano-reversed phase liquid chromatography coupled with ESI-MS for characterization of intact yeast proteins," *J. Prot. Res.* 4, 36-42.

121. Cooper, J. W., Chen, J., Li, Y., and Lee, C. S. (2003). "Membrane-based nanoscale proteolytic reactor enabling protein digestion, peptide separation, and protein identification using mass spectrometry," *Anal. Chem.* 75, 1067-1074.

122. Wu, S.-L., Choudhary, G., Ramstrom, M., Bergquist, J., and Hancock, W. S. (2003). "Evaluation of shotgun sequencing for proteomic analysis of human plasma using HPLC coupled with either ion trap or fourier transform mass spectrometry," *J. Prot. Res.* 2, 383-393.

123. Corbin, R. W., Paliy, O., Yang, F., Shabanowitz, J., Platt, M., Lyons, C. E., Root, K., McAuliffe, J., Jordan, M. I., Kustu, S., Soupene, E., and Hunt, D. F. (2003). "Toward a protein profile of *Escherichia coli*: comparison to its transcription profile," *Proc. Natl. Acad. Sci. USA* 100, 9232-9237.

124. MacCoss, M. J., McDonald, W. H., Saraf, A., Sadygov, R., Clark, J. M., Tasto, J. J., Gould, K. L., Wolters, D., Washburn, M., Weiss, A., Clark, J. I., and Yates, J. R. III (2002). "Shotgun identification of protein modifications from protein complexes and lens tissue," *Proc. Nat. Acad. Sci. USA* 99, 7900-7905.

125. Choudhary, G., Wu, S.-L., Shieh, P., and Hancock, W. S. (2003). "Multiple enzymatic digestion for enhanced sequence coverage of proteins in complex proteomic mixtures using capillary LC with ion trap MS/MS," *J. Prot. Res.* 2, 59-67.

126. Du, Y., Meng, F., Patrie, S. M., Miller, L. M., and Kelleher, N. L. (2004). ”Improved molecular weight-based processing of intact proteins for interrogation by quadrupole-enhanced FT MS/MS,” *J. Prot. Res.* 3, 801-806.

127. Amunugama, R., Hogan, J. M., Newton, K. A., and McLuckey, S. A. (2004). “Whole protein dissociation in a quadrupole ion trap: identification of a priori unknown modified protein,” *Anal. Chem.* 76, 720-727.

128. Zhou, F., Johnston, M. V. (2004). “Protein characterization by on-line capillary isoelectric focusing, reversed-phase liquid chromatography, and mass spectrometry,” *Anal. Chem.* 76, 2734-2740.

129. Zuo, X., Echan, L., Hembach, P., Tang, H. Y., Speicher, K. D., Santoli, D., and Speicher, D. W. (2001). “Towards global analysis of mammalian proteomes using sample prefractionation prior to narrow pH range two-dimensional gels and using one-dimensional gels for insoluble and large proteins,” *Electrophoresis* 22, 1603-1615.

130. Zuo, X., Speicher, D. W. (2002). “Comprehensive analysis of complex proteomes using microscale solution isoelectrofocusing prior to narrow pH range two-dimensional electrophoresis,” *Proteomics* 2, 58-68.

131. Chen, J., Gao, J., and Lee, C. S. (2003). “Dynamic enhancements in sample loading and analyte concentration for capillary isoelectric focusing,” *J. Prot. Res.* 2, 249-254.

132. Lee, H., Criffin, T. J., Gygi, S. P., Rist, B., and Aebersold, R. (2002). “Development of a multiplexed microcapillary liquid chromatography system for high-throughput proteome analysis,” Anal. Chem. 74, 4353-4360.

133. Ericson, C., Phung, Q. T., Horn, D. M., Peters, E. C., Fitchett, J. R., Ficarro, S. B., Salomon, A. R., Brill, L. M., and Brock, A. (2003). “An automated noncontact deposition interface for liquid chromatography matrix-assisted laser desorption/ionization mass spectrometry,” *Anal. Chem.* 75, 2309-2315.