

Proteomics Analysis of the Endoplasmic Reticulum and Golgi Apparatus

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Abstract

Isolated rough and smooth microsomes of the endoplasmic reticulum and isolated Golgi apparatus from rat liver were analyzed by proteomics using mass spectrometry, identifying 1064 proteins among the three fractions. An additional 598 proteins were identified by biochemically subfractionating the rough and smooth microsomes by treatment with a high salt wash and the detergent Triton-X 114. Proteins were quantified by redundant peptide counts which enabled an assessment of the extent of cross-contamination between the endoplasmic reticulum and Golgi fractions and other organellar contamination. Results of this analysis revealed that the Golgi fraction was contaminated up to 30% by proteins of the endoplasmic reticulum and that the mitochondria constitute the largest source of organellar contamination for all three fractions. Hierarchical clustering of the distribution profiles of proteins among the three fractions assigned proteins to either the rough and/or smooth endoplasmic reticulum or the Golgi apparatus. In doing so, the protein disulphide isomerase, ERp44, was localized to the Golgi. This result was verified by immunolocalization with an ERp44 antibody. Furthermore, hierarchical clustering assigned a location for 176 previously uncharacterized proteins in the endoplasmic reticulum providing a subcellular context to their putative functions predicted by bioinformatics. Additionally, the biochemical subfractionation of the rough and smooth microsomes assigned proteins to the cytosolic, membrane or luminal subcompartments of the endoplasmic reticulum. These results guided the selection of uncharacterized membrane proteins for further characterization leading to the identification of 7 proteins upregulated by ER stress, which included 4 new molecular chaperones. Finally, a comparison of this work with previous proteomics analyses of these organelles showed that the proteomes of the endoplasmic reticulum and Golgi apparatus presented here may be the most comprehensive to date. The pipeline outlined in this thesis, which begins with well

characterized and homogenous preparations of subcellular fractions, is documented as a comprehensive and quantitative approach to organellar proteomics.

Résumé

L'analyse par protéomique des microsomes du Réticulum Endoplasmique rugueux, des microsomes du Réticulum Endoplasmique lisse et de l'appareil de Golgi a permis l'identification de 1064 protéines par spectrométrie de masse. Par ailleurs, le fractionnement biochimique des microsomes lisses et rugueux par lavage avec une solution saline concentrée suivi d'un traitement au détergent Triton X-114 a permis l'identification de 598 nouvelles protéines. Les protéines furent quantifiées en fonction du nombre de peptides identifiés par spectrométrie de masse. La quantification des protéines a permis d'évaluer le degré de contamination croisée présent dans les fractions du Réticulum Endoplasmique, de l'appareil de Golgi et celui provenant des autres organelles. Les résultats de cette analyse ont révélé que la fraction de Golgi était contaminée jusqu'à un maximum de 20% par les protéines provenant du Réticulum Endoplasmique et que les mitochondries constituaient la source essentielle de contamination dans ces trois fractions. La clustérisation hiérarchique des protéines quantifiées a permis de dresser le profile de distribution des différentes protéines et ainsi de les assigner au sein des différents compartiments, à savoir aux microsomes du Réticulum Endoplasmique rugueux et/ou lisses, ou alors à l'appareil de Golgi. De ce fait, la protéine disulphide isomerase, ERp44, a été localisée dans l'appareil de Golgi. Ce résultat a été confirmé par immunolocalisation avec l'anticorps ERp44. Par ailleurs, cette même clustérisation hiérarchique a permis de localiser pour la première fois 176 protéines dans le Réticulum Endoplasmique correspondant ainsi à leur fonction putative prédite par bioinformatique. De plus, le fractionnement biochimique des microsomes lisses et rugueux a permis d'assigner les protéines dans les compartiments subcellulaires du Réticulum Endoplasmique : cytosol, membrane ou lumière. Ces résultats ont également permis la sélection de protéines membranaires non encore

caractérisées parmi lesquelles 7 protéines sur-régulées par un stress dans le Réticulum Endoplasmique ont été identifiées. Parmi ces protéines, il y a 4 nouvelles molécules chaperonnes. Enfin, la comparaison des résultats présentés de cette étude avec ceux obtenus à partir d'autres analyses protéomiques équivalentes, sur les mêmes organelles, a montré que les protéomes du Réticulum Endoplasmique et de l'appareil de Golgi décrits dans cette thèse représentent les données les plus complètes à ce jour. Il est également montré que le développement d'un pipeline mettant en oeuvre des préparations bien caractérisées et homogènes représente à la fois une approche complète et quantitative de la protéomique des organelles.

Preface – Contribution of Authors

The work presented in this thesis is my own original contribution with the exception of:

1. The work presented in Chapters 1-5 is part of a paper published by Elsevier Limited (Gilchrist A, Au CE, Hiding J, Bell AW, Fernandez-Rodriguez J, Lesimple S, Nagaya H, Roy L, Gosline SJC, Hallett M, Paiement J, Kearney RE, Nilsson T and Bergeron JJM. 2006. Quantitative proteomics of the early secretory pathway. Cell. 127:1265-1281). The following are the contributions of my co-authors and colleagues:
 - a. The isolation of the RM and SM fractions, biochemical subfractionation, characterization of the RM and SM fractions by marker enzyme assay and by western blotting of marker proteins as well as the quantitative western blotting of albumin in the RM, SM and Golgi fractions was done by Line Roy.
 - b. Electron microscopy of the RM, SM and Golgi fractions was done by Dr. Jacques Paiement.
 - c. Isolation of the Golgi apparatus and plasma membrane fractions and the characterization of the Golgi and plasma membrane fractions by marker enzyme assay were performed by Ali Fazel.
 - d. Protein separation of the fractions by ID SDS-PAGE electrophoresis and band cutting as well as the destaining of gel pieces, reduction, alkylation and trypsinization of peptides (done robotically in a 96 well plate format using a MassPrep Workstation) was done by Nathalie Hamel and Line Roy.
 - e. Tandem mass spectrometry was done by Daniel Boismenu.

- f. Peaklist generation by distiller, matching of mass spectra to peptides using Mascot, grouping of peptides and operation of CellMapBase was performed by the bioinformatics group supervised by Dr. Robert E. Kearney.
 - g. The generation of a non-redundant protein list and the functional annotation of proteins identified by mass spectrometry in the RM, SM and Golgi fractions were done in collaboration with Catherine Au. I performed the analysis for the RM and SM fractions and Catherine Au performed the analysis for the Golgi fraction.
 - h. Principal coordinates analysis was done in collaboration with Sara J.C. Gosline.
 - i. Immunolocalization of ERp44 and sapreticulin and confocal microscopy was done by Dr. Hisao Nagaya.
 - j. Addition of an N-terminal cysteine and KLH conjugation of the peptide for the generation of the sapreticulin antibody was done by Line Roy.
2. The work presented in Chapter 6 is part of a paper submitted for publication (Jain MD, Nagaya H, Gilchrist A, Au CE, Ye Z, Rangarajan ES, Sacher M, Cygler M, and Bergeron JJM. 2007. The organization of the ER into domains by subcellular proteomics is predictive of protein function). Testing of selected proteins for upregulation under ER stress by RT-PCR and co-immunoprecipitation experiments were performed by Michael Jain. Construction of YFP chimeras and confocal microscopy was performed by Dr. Hisao Nagaya.

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Lastly, I would like to thank my husband, Michael Babics, for his love, encouragement and absolute confidence in me. Without his support, this work would not have been possible.

Original Contributions

This body of work characterizes the proteome of the ER and Golgi apparatus through the identification and quantitation of the proteins in these isolated compartments by mass spectrometry. Subcellular fractionation, protein separation and peptide generation by trypsinization, HPLC, tandem mass spectrometry, confocal microscopy, cell culture, immunoprecipitation, real-time PCR and bioinformatics were used for this characterization. My original contributions to the research and scientific knowledge are the following:

1. Developed quantitative proteomics combined with hierarchical clustering as a protein localization tool for organelles.
 - a. Performed the initial manual analysis of peptide counting which led to the automated computational procedure used for this thesis.
 - b. Identified, optimized and applied software for hierarchical clustering.
2. Used redundant peptide counting in combination with principal components analysis (PCO) to define the uniqueness of the protein makeup of isolated organelles and the homogeneity of organellar samples for proteomics.
 - a. Applied Matlab™ software to generate PCO plots.
3. Validated redundant peptide counting through biological observations.
 - a. Manually computed the redundant peptide counts for albumin and compared these results to quantitative western blotting.
 - b. Identified ERp44 as localized in the Golgi by redundant peptide counting and compared result to immunoblotting with anti-ERp44 antibody.

2. The first application of redundant peptide counting to estimate contamination in subcellular fractions from other organelles.
 - a. Developed and applied the idea of using % total peptides of marker proteins to estimate the amount of cross-contamination between the ER and Golgi fractions.
3. The first characterization of organellar contamination for the RM, SM and Golgi fractions.
 - a. Identified 23 functional categories as representative of the proteins identified in the RM, SM and Golgi fractions.
 - b. Assigned proteins to these categories.
 - c. Developed the idea of using the enrichment of protein categories by redundant peptide counting to characterize the fractions which led to the determination of organellar contamination of the RM, SM and Golgi fractions.
4. Characterized 1341 proteins in the ER and 527 proteins in the Golgi apparatus representing the most complete accounting of proteins in these structures to date.
5. Uncovered 324 proteins of unknown function of which 224 were localized to the RM, SM or Golgi by the quantitative protein localization tool developed in this thesis.
6. Established a pipeline for the analysis of proteomics data after mass spectrometry identification.
 - a. Contributed to the initial development of code for the redundancy reduction at the peptide to protein assignment (grouping)
 - b. Reduced redundancy at the protein level (due to SNPs or allelic isoforms) using BLASTp

7. Bioinformatic characterization of proteins of unknown function.
8. Contributed the sapreticulin antibody to community.

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Abbreviations

2D – Two dimensional

ADP – adenosine diphosphate

Assigned_Prot_Name – Assigned Protein Name

ATP – adenosine triphosphate

ATPase – adenosine triphosphatase

BLAST – Basic Local Alignment Search Tool

BSA - bovine serum albumin

CMBSEQID - CellMapBase sequence identifier

COG - conserved oligomeric Golgi complex

CREB - cAMP response-element-binding (CREB)

CYP – cytochrome p450

Da - Daltons

DAD-1 – Defender against death 1

DTT - Dithiothreitol

EM – electron microscopy

ER – endoplasmic reticulum

ERAD - ER associated degradation

ERES - ER exit sites

ERGIC - ER to Golgi intermediate compartment

ERM - ezrin-radixin-moesin

ESI – electrospray ionization

FAD - flavin adenine dinucleotide

GERL- Golgi ER and lysosomal associations

GFP – green fluorescent protein

Glc – Glucose

GlcNac – N-acetylglucosamine

GTP – guanine triphosphate

HERA - Human ER Aperçu database

Hsp70 – Heat shock protein of 70 kDa

Hsp90 - Heat shock protein of 90 kDa
ICAT - Isotope-Coded Affinity Tagging
ID Score - Identity Score
IP(3) – inositol triphosphate
IP3R1 - inositol 1,4,5-triphosphate receptor
iTRAQ - isotope tags for relative and absolute quantitation
m/z – mass to charge ration
MALDI – Matrix assisted laser desorption/ionization
Man – mannose
MDS- multidimensional scaling multidimensional scaling
MIR - myosin regulatory light chain-interacting protein
MS - mass spectrometry
MS/MS – tandem mass spectrometry
MuDPIT - Multidimensional Protein Identification Technology
MW - molecular weight
NAC - nascent-polypeptide-associated complex
NCBI – National Center for Biotechnology Information
nrdb – non-redundant protein database
NSF – N-ethylmaleimide-sensitive factor
PCA - principal coordinates analysis
PCR – polymerase chain reaction
PDI – protein disulphide isomerase
PHB - prohibitin-like domain
PIPES - piperazine-N,N'-bis(ethanesulfonic acid); 1,4-piperazinediethanesulfonic acid
PM – plasma membrane
PPI - peptidylprolyl isomerase
PRIDE - PRoteomics IDEntifications database
PTM - post-translational modification
RER - rough endoplasmic reticulum
RM – rough microsomes

RNC - ribosomal-nascent chain complex
SDS-PAGE – Sodium dodecyl sulphate polyacrylamide gel electrophoresis
SER – smooth endoplasmic reticulum
SM – smooth microsomes
SNAP - soluble N-ethylmaleimide-sensitive factor attachment proteins
SNARE –soluble NSF attachment protein receptor
SNP – single nucleotide polymorphism
SRP - signal recognition particle
TE - Transitional elements
Th - Thomsons
TMD - transmembrane domain
TRAM - Translocon-Associated Membrane protein
TRAP - Translocon Associated Protein
TX-114 - Triton X-114
UAS - ubiquitin associated domain
UBX - ubiquitin-like domain
UGGT - UDP:glucose glucosyltransferase
UNIRef90 – UniProt NRef database at 90% identity
UPR – unfolded protein response
VKORC1 - vitamin K epoxide reductase complex subunit 1
VTC – vesiculotubular cluster
YFP – yellow fluorescent protein

Introduction

This thesis focuses on the high-throughput identification and quantitation of proteins in isolated rough and smooth endoplasmic reticulum (ER) and Golgi apparatus of rat liver. The ER and Golgi apparatus are organelles that comprise the early secretory pathway and are responsible for folding and processing of newly synthesized proteins as well as lipid biosynthesis (Hebert & Molinari 2007, Spiro 2002). Proteins destined for secretion proceed sequentially through these organelles on their way to the plasma membrane (Harter & Reinhard 2000). The ER is the entry-point to the secretory pathway. Nascent proteins are translocated co-translationally into the lumen of the rough ER where they encounter resident molecular chaperones that facilitate their folding into the correct 3-dimensional configuration (Schrag et al 2003). After attaining the correct 3-dimensional structure, proteins advance to the Golgi apparatus for glycosylation (Schroder & Kaufman 2005). Recent advances in mass-spectrometry based proteomics have successfully mapped and quantified protein complements for several organelles (Yates et al 2005). Using this technology, we have generated a protein map of the organelles of the early secretory pathway (Gilchrist et al 2006).

For this study, a proteomics strategy was developed to assign proteins to their intracellular locations using isolated organelles. Rough and smooth microsomes of the ER were isolated by subcellular fractionation using highly rigorous protocols. Subcellular fractions were characterized by enzyme assays and electron microscopy to assess the degree of enrichment and homogeneity. For analysis by mass spectrometry, proteins in these samples were solubilized and separated by 1-dimensional SDS-PAGE gels. Each gel lane was cut into slices (1 mm) and subjected to trypsin digestion followed by tandem mass spectrometry. To quantify the identified proteins, the redundant peptide

counting approach (Blondeau et al 2004, Cox et al 2005, Gao et al 2005, Gao et al 2003, Girard et al 2005, Liu et al 2004, Pang et al 2002, Qian et al 2005, Rappsilber et al 2002, Zybaylov et al 2005) was used. Protein distribution profiles among the three organelles were established which enabled the assignment of proteins to a subcellular location based on their co-distribution with marker proteins.

Because of the complexity of organelles, enrichment strategies such as subcellular fractionation or immunodepletion are often employed in proteomic studies (Stasyk & Huber 2004). These approaches reduce sample complexity and serve to increase the number of less abundant proteins that can be detected (Stasyk & Huber 2004) since subcellular fractionation enriches for organelle specific proteins and diminishes all others. Proteins in highly enriched organellar fractions are more likely to be detected by the mass spectrometer due to the stochastic aspect of selecting peptides for fragmentation by the tandem mass spectrometer. As the abundance of a protein increases in a sample, so does the probability for its selection by the mass spectrometer.

For this study, subcellular fractionation was used to enrich for the organelles under study. This technique separates organelles based on their physical properties (size, density, charge, etc.) (De Duve & Beaufay 1981) and consists of two major steps: 1) homogenation to disrupt cellular organization and 2) fractionation of the homogenate to separate organelles. The resulting homogenate can then be further resolved by centrifugation into enriched fractions of organelles. These organelle rich fractions can serve as the starting point for organellar proteomics studies (Yates et al 2005).

Organellar proteomics aims to identify the compendium of proteins of the membrane-bound compartments of the cell (Au et al 2007). First

generation organellar proteomics studies isolated and analyzed one organelle at a time, often without quantifying the proteins they identified. These efforts include proteomics analyses of isolated Golgi apparatus (Bell et al 2001, Wu et al 2004) and ER (Knoblauch et al 2003). An analysis of the Golgi apparatus was performed by Bell et al. (Bell et al 2001) who examined the protein constituents of a Golgi membrane fraction by tandem mass spectrometry. They identified 81 proteins and characterized a novel Golgi protein called GPP34. An independent proteomics characterization of isolated hepatic Golgi apparatus also characterized exactly the same novel protein, which this group called GMX33 (Wu et al 2000a). Hence, based on these 2 examples, organelle proteomics characterizes proteins unattainable by other methods and immediately gives them context in terms of their subcellular location. A more recent proteomics analysis of the Golgi was performed by Wu et al. (Wu et al 2004). They used the MudPIT approach in their analysis of the Golgi apparatus and uncovered arginine dimethylation as a novel post-translational modification. As for a proteomics analysis of the ER, Knoblauch et al. (Knoblauch et al 2003) used 2D gels to characterize proteins of a soluble ER fraction representing the luminal contents of this organelle (Knoblauch et al 2003). They identified 141 known proteins and 6 proteins of unknown function, two of which were shown to be novel protein disulphide isomerases (Knoblauch et al 2003). These studies of the Golgi and ER fall into the “first generation” category of proteomics analyses since they were not quantitative. Within the last 5 years, the use of quantitative methods in organellar proteomics studies has become increasingly more common.

Blondeau et al. (Blondeau et al 2004) were the first to use a quantitative approach to protein characterization in organelles. They monitored the frequency of tandem mass spectra in 3 biological replicates of their sample - clathrin coated vesicles. Surprisingly, they found that

plotting the distribution of peptides assigned to proteins in the context of a lane of a 1- D SDS PAGE gel recapitulated the Coomassie Blue staining profile of the same proteins visualized in the gel. They went on to show that this method (redundant peptide counting) could accurately and statistically calculate the stoichiometry of the heavy and light chain of the clathrin coat as well as of the adaptin subunits. Furthermore, they were able to estimate how many vesicles were in plasma membrane derived clathrin coated vesicles compared to Golgi derived vesicles (based on the abundance of AP-1 and AP-2). This study tested the hypothesis that brain clathrin coated vesicles recycled synaptic vesicle constituents and their results confirmed the hypothesis, resolving a minor controversy in the field. More recent multi-organelle proteomics studies which encompass the ER and Golgi (Foster et al 2006a, Kislinger et al 2006) have also used quantitative methods in their analyses.

Two studies by Kislinger et al. (Kislinger et al 2006) and Foster et al. (Foster et al 2006a) analyzed multiple organelles of murine origin using quantitative approaches. Kislinger et al. (Kislinger et al 2006) identified proteins in four subcellular fractions (cytosol, microsomes (including ER and Golgi), mitochondria and nuclei) derived from six organs by tandem mass spectrometry. To determine tissue selectivity, they compared protein abundance with mRNA abundance derived from previous studies. As a way to gauge protein abundance, Kislinger et al. (Kislinger et al 2006) used the redundant peptide counting approach. A similar study was conducted by Foster et al. (Foster et al 2006a) who surveyed proteins in ten organelles of mouse liver including the ER and Golgi apparatus. To measure protein abundance, they used extracted peptide ion currents (Andersen et al 2003). Quantitative aspects of the Kislinger et al. (Kislinger et al 2006) and Foster et al. (Foster et al 2006a) studies enabled the assignment of proteins to specific organelles (Foster et al 2006a) and tissues (Kislinger et al 2006).

Both redundant peptide counting and extracted peptide ion currents are considered label-free methods of protein quantitation. Redundant peptide counting relies on the frequency of detection of tandem mass spectra derived from peptides for a given protein (Blondeau et al 2004, Cox et al 2005, Gao et al 2005, Gao et al 2003, Girard et al 2005, Liu et al 2004, Pang et al 2002, Qian et al 2005, Rappsilber et al 2002, Zybaylov et al 2005). The approach is described as “redundant” due to the observation that a peptide can generate multiple mass spectra. The method is based on the observation that the number of times a peptide is sampled is proportional to the abundance of its parent protein. In practice, redundant peptide counts are derived by taking the sum of all tandem mass spectra assigned to peptides for a given protein (Blondeau et al 2004, Cox et al 2005, Gao et al 2005, Gao et al 2003, Girard et al 2005, Liu et al 2004, Pang et al 2002, Qian et al 2005, Rappsilber et al 2002, Zybaylov et al 2005). Extracted total ion currents are determined by plotting the intensity of the signal as a peptide elutes from the chromatographic column over time. The area under this curve is the extracted ion current and, for the same peptide and experimental conditions, is linearly related to its amount (Andersen et al 2003). Using this quantitative approach, Andersen et al. (Andersen et al 2003) distinguished between proteins resident to the centrosome and contaminants which represented an important advance to the field.

Due to the difficulty in isolating organelles (DeDuve 1971), it is a challenge to distinguish bona fide organellar proteins from contaminating proteins. This is exactly the problem addressed by the development of protein correlation profiling by Andersen et al. (Andersen et al 2003). Protein correlation profiling involved tracking the abundance of peptides in all fractions of an analytical gradient (Andersen et al 2003). Distribution profiles of all identified proteins were compared to profiles of known

marker proteins. Protein distribution profiles that deviated from marker profiles were considered contaminants. Protein correlation profiling was used by Foster et al. (Foster et al 2006a) to assign 1400 proteins to 10 different organelles isolated from mouse liver homogenates. Similar to protein correlation profiling, LOPIT (localization of organelle proteins by isotope tagging), developed by Dunkley et al. (Dunkley et al 2006, Dunkley et al 2004), was used to map different subcompartments of the endomembrane system in the plant, *Arabidopsis thaliana*. In this approach, proteins were partially separated by centrifugation through density gradients. iTRAQ reagents were used to label proteins in different fractions of the gradient and protein distribution profiles were determined by measuring the relative iTRAQ reporter ion intensities across the gradients. As with protein correlation profiling, localization was established by comparing all profiles to marker protein profiles. Using this approach, Dunkley et al. (Dunkley et al 2006) assigned 527 proteins to the ER, Golgi, PM, vacuolar membrane and mitochondria. Both the Foster et al. (Foster et al 2006a) and Dunkley et al. (Dunkley et al 2006) studies relied on the behaviour of proteins in a single gradient to assign to them a subcellular localization. This approach is attractive, in theory; however, in practice, the approach is susceptible to incomplete separation of proteins in the gradient. Indeed, this has been a problem for cell biologists and since the latter half of the 20th century, the field has been challenged to develop methods to isolate organelles effectively (DeDuve 1971). The results of the Foster et al. (Foster et al 2006a) study support this point. When benchmarked against proteomics analyses of individual organelles, they identified, on average, only 30% of the proteins identified for each organelle (Foster et al 2006a). Therefore highly enriched isolated organelles may be required to gain insight into protein content and their distribution in cells and organs. In this scenario a “divide and conquer approach” is needed to map the proteome (Au et al 2007, Yates et al 2005).

The goal of this work was to create a protein map of the organelles of the secretory pathway – the rough and smooth ER and Golgi apparatus. This thesis describes the application of a subcellular localization method using a label free quantitative proteomics strategy to elucidate the proteome of the early secretory pathway from isolated subcellular fractions derived from the rough ER, smooth ER, and Golgi apparatus of rat liver parenchyma. In this thesis, I aim to:

1. Describe the methodology employed throughout the thesis and the pipeline established as a result of this work (Methods).
2. Quantify the extent of cross contamination between the ER and Golgi fractions as well as contamination from other organelles of the cell (Results: Assessment of contamination of RM, SM and Golgi fractions).
3. Define the proteome of the early secretory pathway with a subcellular localization for most proteins to the rough ER and/or smooth ER and Golgi apparatus (Results: Subcellular localization of proteins by proteomics).
4. Assign a membrane, cytosolic or luminal location to most proteins based on their distribution in various biochemical subfractions (Results: Biochemical subfractionation of ER fractions).
5. Estimate the completeness of the ER and Golgi protein identifications and show that proteomics, using well-isolated organelles, is a more comprehensive approach than other methods (Results: Completeness of ER and Golgi proteomics results).
6. Characterize the proteins of unknown function identified in the ER and the novel biology they represent (Results: Characterization of proteins of unknown function of the ER).

Literature Review

The secretory pathway in eukaryotic cells consists of separate organelles that work in succession to effect protein secretion to the extracellular environment. A protein destined for secretion transits through various specialized compartments that facilitate the different stages of protein synthesis and folding, modification, sorting and secretion. The ER is the entry point into the secretory pathway. Ribosomes docked on the membrane of the ER translate nascent proteins which enter the lumen of the ER for protein folding. The next step for an immature protein is the Golgi apparatus. Secretory protein cargo exits the ER in vesicles which ultimately end up in the Golgi apparatus. Glycosylation of proteins proceeds sequentially due to the distribution of resident Golgi enzymes in the cis, medial and trans Golgi cisternae. Communication and transport between the ER and Golgi occurs via vesicles, coated with either COPI or COPII coats, that fuse with these organelles.

1. The endoplasmic reticulum

The lace-like structure of the ER was first viewed by Keith Porter using the electron microscope (Porter et al 1945). The term “endoplasmic reticulum” was derived from observations that its structure is within the cytoplasm (endoplasmic) with a net-like appearance (reticulum). The general structure of the ER is an extensive membrane network of interconnected tubules and flattened sacs, enclosing a single cisternal space called the ER lumen. The ER membrane, a phospholipid bilayer, separates the cisternal space from the cytosol. The main functions of the ER include protein and lipid synthesis. It synthesizes the majority of lipids and integral membrane proteins for the organelles of the cell as well as the majority of proteins destined for secretion outside of the cell. Other

functions of the ER include calcium sequestration and detoxification. The ER is divided into different subcompartments: the rough ER and the smooth ER.

1.1 The rough endoplasmic reticulum

The rough endoplasmic reticulum (RER) is defined by the presence of numerous membrane bound ribosomes which dot the membrane surface, thus giving it its rough appearance. The RER is generally viewed as the entryway to the secretory pathway (Hebert & Molinari 2007). Proteins enter the secretory pathway via the membrane bound ribosomes that synthesize nascent polypeptides (Hebert & Molinari 2007). These immature proteins are transported into the lumen of the ER co-translationally, that is, before the end of protein synthesis (Blobel & Dobberstein 1975, Redman & Sabatini 1966). Ribosomes bound to the ER do not differ from ribosomes that synthesize proteins in the cytosol (Blobel & Dobberstein 1975, Lingappa et al 1984). The difference in their spatial distribution, whether they synthesize proteins on the ER or in the cytosol, lies in the protein they are making at the time (Lingappa et al 1984, Lingappa et al 1978). Translation is initiated in the cytoplasm by a series of initiation factors (Weissbach & Ochoa 1976). Elongation of the polypeptide continues through the action of these factors bound to aminoacyl-tRNA molecules (Mucha 2002). Targeting to the ER membrane is specified by a signal sequence at the N-terminus of the protein (Lingappa et al 1978). As the signal sequence emerges from the ribosome-mRNA complex, it is recognized and bound by the signal recognition particle (SRP) (Kurzchalia et al 1986, Walter & Blobel 1981). This step arrests protein synthesis (Meyer et al 1982, Walter & Blobel 1981) which does not resume until the ribosome docks onto the ER membrane. The ribosomal-nascent chain complex (RNC) bound to SRP is then targeted to the ER membrane where it binds by two interactions: 1) to the SRP receptor (Wiedmann et al 1987) and 2) to the Sec61 complex

also known as the translocon (Junnickel & Rapoport 1995). Binding of SRP-RNC to the SRP receptor causes the dissociation of the signal sequence from the SRP in a GTP dependant manner (Connolly et al 1991). After dissociation, the nascent polypeptide is transferred to the Sec61 α unit of the translocon (Gilmore & Blobel 1985, Krieg et al 1989, Wiedmann et al 1987).

As the synthesis of secretory proteins occurs, different factors interact with the newly synthesized polypeptide. Aside from the SRP, another complex which associates with ribosome bound polypeptides is the nascent-polypeptide-associated complex (NAC) (Rospert et al 2002, Wiedmann et al 1994). It has been proposed the NAC complex plays a role in mediating the proper translocation of proteins to the ER by controlling the accessibility of the translocon, and the signal recognition particle to ribosome bound nascent chains (Moller et al 1998) (Lauring et al 1995). These findings were all based on in vitro experiments. Moreover, the association of NAC with ribosomes and the cross-linking of NAC to short nascent polypeptides indicate that NAC might be involved in the folding of newly synthesized proteins (Wiedmann et al 1994). However, direct in vivo evidence for these hypotheses has yet to be produced.

NAC has also been implicated in the mitochondrial import of proteins (Funfschilling & Rospert 1999, George et al 1998, George et al 2002). A recent study localized ICD-1 β NAC to the mitochondria during embryogenesis and identified this protein as a suppressor of apoptosis in *C. elegans* (Bloss et al 2003). Based on this evidence, it has been proposed that ICD-1 β NAC may regulate the mitochondrial apoptotic program. In light of this conflicting evidence, the role of NAC remains unclear.

1.1.1 Translocation across the ER membrane

Once the SRP-RNC is docked onto the ER membrane, protein synthesis continues. The ribosome aligns and forms a tight seal with an aqueous pore that spans the ER membrane (Crowley et al 1993). This pore is called the translocon and is comprised of the trimeric Sec61 complex (Sec61 α , β and γ) (Johnson & van Waes 1999). Translocon constituents were first identified by photocross-linking experiments, using an approach that incorporated photoreactive probes into the newly synthesized polypeptide (Krieg et al 1989, Thrift et al 1991, Wiedmann et al 1989). As the nascent chain passed through the ER membrane, the probes were photolyzed resulting in the photo-crosslinking of proteins adjacent to them (Krieg et al 1989, Thrift et al 1991, Wiedmann et al 1989). The interacting proteins were then validated by reconstitution into proteoliposomes and were shown to be successful in protein translocation (Gorlich et al 1992a, Gorlich et al 1992b, Gorlich & Rapoport 1993, Nicchitta & Blobel 1990). This approach identified Sec61 α , β , γ and the Translocon-Associated Membrane protein (TRAM) as the core constituents of the translocon, since translocation of most proteins was successfully reconstituted by this core complex (Gorlich & Rapoport 1993). Another group of proteins found to be associated with the translocon and remain poorly characterized is the translocon-associated protein complex which has 4 subunits (TRAP α β δ γ). TRAP is postulated to play a role in the translocation of proteins whose signal sequences interact weakly with the translocon. This hypothesis is supported by the finding that the TRAP complex is necessary for the translocation of prion protein (Fons et al 2003). This protein is inefficiently transported by the core Sec61/TRAM complex, possibly due to properties of its signal sequence.

As translocation proceeds, proteins adjacent to the channel act on the nascent polypeptide as it enters the lumen of the RER. Before the

protein is completely synthesized, signal peptidase, a protease in the membrane of the ER, cleaves off the signal sequence (Evans et al 1986). Other proteins which have been located proximal to the translocon include p34 (Tazawa et al 1991) and p180 (Savitz & Meyer 1993). Both proteins were once considered candidates for the ribosome receptor, which was eventually shown to be Sec61 α (Osborne et al 2005, Prinz et al 2000, Raden et al 2000).

Another protein located transiently at the translocon is BiP. BiP is generally regarded as a molecular chaperone (Meunier et al 2002) (Kleizen & Braakman 2004). BiP forms a seal on the luminal side of both the inactive translocon and one that is in the early stages of translocation (Hamman et al 1998). Mechanistically, when BiP seals the translocon, it is in the ADP-bound conformation and it switches to the ATP bound state upon pore reopening (Alder et al 2005). A similar mechanism is used when BiP associates and dissociates from substrates in its role in protein folding.

Further modification of the nascent polypeptide also occurs by the action of the oligosaccharyl transferase. Glycoproteins make up the majority of proteins synthesized in the ER and the addition of sugars to proteins is one of the main functions of the organelle. The oligosaccharyl transferase is a complex of membrane proteins that transfers a preassembled oligosaccharide - Glc3-Man9-(GlcNac)₂ – en masse onto asparagine residues of newly synthesized proteins. The oligosaccharide is transferred to arginine residues of the form N-X-T/S by a process called N-linked glycosylation (reviewed in (Helenius & Aebi 2004)). The precursor oligosaccharide is first synthesized in the cytosol and held in the ER membrane by a dolichol lipid carrier. Nucleotide-sugar intermediates, formed in the cytosol, donate their sugars to dolichol in a specific order. Seven sugars are added on the cytoplasmic side and are all together

linked to the dolichol by a pyrophosphate bond. After the heptasaccharide is added to the dolichol carrier, the lipid linked oligosaccharide is flipped from the cytosolic side to the luminal side of the ER for further addition of four mannose and three glucose residues. This “flipping” is facilitated by a protein called RFT1 (Helenius et al 2002). In contrast to the addition of sugars on the cytosolic side of the ER membrane, sugars assembled on the luminal side are not nucleotide activated sugars but are instead dolichol phosphate bound monosaccharides. These sugars are also synthesized on the cytoplasmic side and are “flipped” into the lumen of the ER. However, the identity of the “flippase” that mediates this step remains unknown (Helenius & Aebi 2002).

1.2 Protein folding

The lumen of the ER provides an oxidating redox environment conducive for protein folding (Tu & Weissman 2004). Once translocated into the ER lumen, a newly synthesized protein encounters numerous molecular chaperones, ER resident proteins that function to fold nascent proteins. These proteins assist nascent proteins to attain the correct three dimensional conformations. Chaperones of the ER fall into two categories. They function either to keep proteins in a folding competent state (e.g. BiP and calnexin) or to catalyze protein folding reactions (e.g. protein disulphide isomerise or cis-trans prolyl isomerise) (Zapun et al 1999).

1.2.1 The calnexin cycle

Calnexin is an ER resident type I transmembrane protein that bears sequence similarity with calreticulin, another soluble luminal protein of the ER. Calnexin and calreticulin are both lectins in that they interact with monoglucosylated N-linked glycans (Ou et al 1993, Peterson et al 1995).

The calnexin/calreticulin cycle works in the following way (Schrage et al 2003). The newly synthesized protein bearing an N-linked glycan has the structure of Glc3-Man9-(GlcNac)2 (where Glc is glucose, Man is mannose, and GlcNac is N-acetylglucosamine). The cycle begins with the sequential trimming by glucosidase I and II of two terminal glucose residues leaving the N-linked oligosaccharide with the structure Glc1-Man9-(GlcNac)2. Calnexin or calreticulin bind to the monoglucosylated protein and this association permits enzymes such as protein disulphide isomerase to facilitate folding by catalyzing the exchange of disulfide bonds. When the protein is properly folded, it is released from calnexin or calreticulin by the action of glucosidase II. The enzyme re-enters and trims the final glucose on the glycan to generate a Man9-(GlcNac)2 oligosaccharide. If the protein remains misfolded, it is recognized by another member of the cycle known as UDP:glucose glucosyltransferase (UGGT). UGGT functions as a sensor of protein misfolding and acts on misfolded proteins by re-glucosylating the oligosaccharide, thus, re-forming the Glc1-Man9-(GlcNac)2 structure (Taylor et al 2004). Re-glucosylation by UGGT allows for another round of protein folding in which the cycle begins again with calnexin recognition followed by glucose trimming and so forth (Schrage et al 2003).

1.2.2 BiP

Another indicator of incompletely folded proteins is exposed hydrophobic residues (Hellman et al 1999). These residues are normally sequestered inside correctly folded proteins and away from the aqueous environment of the cell; therefore the exposure of hydrophobic domains is a hallmark of protein misfolding. The heat shock protein (HSP) family of proteins are responsible for recognition of exposed hydrophobic residues. Hsp70 and Hsp90 proteins have mainly been studied in the cytoplasm but they are also present in the lumen of the ER.

The protein BiP/GRP78 is a member of the Hsp70 family and an abundant resident protein of the ER. BiP and Hsp70 family members in general, are characterized by a nucleotide binding domain that binds ATP, and a substrate binding domain responsible for recognizing a series of hydrophobic residues. These domains work together to modulate the affinity and the duration of binding of incompletely folded proteins (Gething 1999). BiP also has other roles within the ER. It is involved in the translocation of newly synthesized precursors across the ER membrane (Matlack et al 1999), the retro-translocation of misfolded proteins as part of the ER-dependent degradation process (ERAD) (Chillaron & Haas 2000) and in the unfolded protein response (UPR) (Bertolotti et al 2000).

1.2.3 Protein disulphide isomerise and oxidative protein folding

The oxidizing environment of the ER is highly optimized for protein folding and disulphide bond formation. Protein disulphide isomerase, the first chaperone to be discovered (Goldberger et al 1963), catalyzes the formation as well as the rearrangement of disulphide bonds in incompletely folded proteins in a process called oxidative folding (Tu & Weissman 2004). Despite the fact that PDI has been known for over 40 years, the mechanisms behind oxidative folding have been understood only recently. Studies by Tu et al. (Tu et al 2000, Tu & Weissman 2002) have shown that oxidative protein folding is dependant on electron acceptors and consists of a relay system of electron transfers between the proteins Ero1, PDI and molecular oxygen. Ero1 was first discovered through a genetic screen in yeast, which identified mutants that were sensitive to the reducing agent DTT. These mutants accumulated normally disulphide bonded proteins in a reduced form in the ER (Frandsen & Kaiser 1998, Pollard et al 1998). The reduced form of these proteins suggested that Ero1 functioned upstream of PDI (Frandsen & Kaiser 1998, Pollard et al 1998). During oxidative folding, the relay of electron transfer

begins with the binding of Ero1 to FAD that is transported into the lumen of the ER. Ero1 then oxidizes PDI, becoming reduced in the process, and donates its electrons to molecular oxygen, the terminal electron acceptor. After oxidation by Ero1, PDI oxidizes cysteine pairs in incompletely folded proteins through disulphide bond formation.

Whether or not Ero1 interacts with the other PDIs of the ER remains to be seen. At present, there are four PDI homologs in yeast and seventeen in human (Ellgaard & Ruddock 2005). The only other PDI postulated to interact with Ero1 is the relatively unknown protein, ERp44. In a cross-linking experiment, human Ero1 formed a mixed disulphide cross-link with ERp44 (Anelli et al 2002). In another capacity, ERp44 has been shown to regulate the calcium concentration through its interaction with the IP3 receptor located in the ER membrane (Higo et al 2005). This regulation is dependant on the pH, calcium concentration and the presence of reduced cysteines in the third loop of the IP(3) type 1 receptor (Higo et al 2005). ERp44 represents a molecular chaperone which carries out a specialized role by coordinating protein folding with calcium levels in the ER.

1.3 Quality control in the endoplasmic reticulum

Protein folding in the ER is monitored by a quality control system which ensures that only properly assembled and functional proteins exit the ER. Proper function of the ER is disrupted when the load of unfolded nascent polypeptides surpasses the folding capacity of the ER. This perturbation of ER function known as “ER stress” occurs naturally during biological processes such as B cell differentiation into plasma cells (Reimold et al 2001) or during diseased states known as ER storage diseases (Rutishauser & Spiess 2002). Proteins that do not attain the proper conformation and stability are handled by the quality control machinery. Two mechanisms exist for coping with misfolded proteins: ER-

associated degradation (ERAD) and the unfolded protein response (UPR). ERAD identifies terminally misfolded proteins and retrotranslocates them to the cytosol for degradation by the ubiquitin-proteasome system (Meusser et al 2005). The UPR is an intracellular signalling pathway used by the ER to increase its folding capacity in order to handle an increased load of misfolded protein (Schroder & Kaufman 2005). The UPR is not separate from ERAD; rather, ERAD is one of the pathways activated by the UPR to accommodate for compromised protein folding.

1.3.1 ER associated degradation

Similar to unfolded protein recognition in the calnexin cycle, the glycosylation state of an incompletely folded protein determines its fate. Recent studies have identified two different lectins in the ER which function in ERAD. The first lectin is called EDEM in mammalian cells or Htm1 in yeast. Studies in mammalian cells suggest that EDEM helps misfolded glycoproteins exit the calnexin/calreticulin cycle and enter the degradation pathway (Molinari et al., 2003; Oda et al., 2003). Terminally misfolded proteins are recognized by EDEM/Htm1 after trimming of the N-linked glycan by α 1,2 mannosidase (Molinari et al 2003, Oda et al 2003). In fact, EDEM is a mannosidase homolog although catalytically inactive. It is thought that EDEM uses its mannosidase domain for glycoprotein recognition to sequester unstable glycoproteins after trimming by α 1,2 mannosidase (Molinari et al 2003, Oda et al 2003). A second lectin which was recently discovered is Yos9 (Cormier et al 2005). In 3 different studies, Yos9 was identified as necessary for degradation of a misfolded glycoprotein in yeast (Bhamidipati et al 2005, Kim et al 2005, Szathmary et al 2005). Yos9 contains a mannose binding domain similar to the mannose-6-phosphate receptor and an HDEL at its C- terminus localizing it to the lumen of the ER. Mutagenesis experiments revealed that the mannose binding domain of Yos9 is required for glycoprotein binding and mutations in this domain abolishes its capacity to sustain ERAD.

However, these same mutants show a stronger affinity for misfolded proteins. Therefore, how misfolded proteins are recognized by Yos9 and how they are delivered to the degradation machinery is not entirely clear at this time.

Once misfolded proteins are sorted out by the quality control machinery of the ER, they are generally retro-translocated through a pore complex to the cytosol for degradation. Although the identity of the pore is the subject of debate, the general evidence supports two candidates: the Sec61 complex (Pilon et al 1997) (Plempner et al 1997) (Zhou & Schekman 1999) and Derlin-1 (Lilley & Ploegh 2004, Ye et al 2004).

Proteins destined for degradation are extracted from the ER membrane and into the cytosol by a protein complex comprised of the AAA-ATPase Cdc48p/p97 coupled with the proteins Npl4p and Ufd1p (Jarosch et al 2002, Ye et al 2001, Ye et al 2004). Once in the cytosol, the proteins are ubiquitinated by E2 conjugating enzymes and E3 ligases associated with the ER membrane followed by degradation by the 26S proteasome.

1.3.2 The unfolded protein response

The UPR is a signal transduction pathway activated by an accumulation of unfolded proteins in the ER. The signaling events initiated by the UPR function to increase the size of the ER membrane. Resident proteins are also upregulated which include molecular chaperones and other protein modifying enzymes. The UPR also decreases the translation and import of proteins into the ER and increases the targeting of proteins for degradation via ERAD.

Sensors within the ER membrane initiate the signaling events of the UPR. These proteins are known as IRE1 α and β , PERK and ATF6. IRE1

is a highly conserved integral membrane protein kinase with a luminal domain which senses misfolded proteins, a cytosolic ribonuclease domain and a serine/threonine kinase domain. ER stress causes the intraluminal domain of IRE-1 to become activated by homodimerization and autophosphorylation. These changes cause the cytosolic ribonuclease domain to excise a 26 bp intron from mRNA encoding the X-box-binding protein (XBP1). Cleavage of XBP1 in metazoans or Hac1 in yeast produces an active transcription factor that moves to the nucleus and activates the transcription of genes encoding proteins involved in ER protein folding and modification, phospholipid biosynthesis and ERAD, and vesicular transport (Harding et al 2003) (Lee et al 2003) (Shaffer et al 2004) (Sriburi et al 2004). At present, the full complement of metazoan UPR target genes is still unknown.

PERK is a single spanning integral membrane kinase. The accumulation of misfolded proteins in the lumen of the ER activates PERK leading to the phosphorylation of the translation initiation factor eIF2 α . Since PERK directly phosphorylates eIF2 α and is not dependent on translocation to the nucleus or translation, this branch of the UPR elicits the fastest response. Phosphorylated eIF2 α inhibits the assembly of the 80S ribosome and causes a general attenuation of protein synthesis, thus decreasing the influx of proteins into the ER. Although most mRNAs are not translated under these conditions, a subset contain internal ribosome entry sites (Fernandez et al 2001) or upstream open reading frames (Harding et al 2000) which cause them to be preferentially translated. One of the mRNAs is ATF4, a member of the cAMP response-element-binding (CREB) family of transcription factors (Harding et al 2000). Since phosphorylation of eIF2 α also occurs in response to other cellular stresses which lead to the activation of other non-PERK eIF2 α kinases (Clemens 2001), genes downstream of ATF4 are generally important for the

recovery from different stresses, whether they originate from the ER or not.

ATF6 is translated initially as an ER-resident integral membrane protein. It is a bZIP transcription factor that migrates to the Golgi upon UPR induction where it is cleaved by the S1P and S2P proteases. Cleavage of ATF6 produces a cytosolic fragment that is an activated transcription factor (Ye et al 2000). The cytosolic fragment of ATF6 then moves to the nucleus where it induces the transcription of XBP1 (Yoshida et al 1998) among other factors.

Studies on gene expression analysis in yeast (Travers et al 2000) and mammals (Scheuner et al 2001) (Harding et al 2003) (Okada et al 2002) have identified UPR target genes and characterized their transcriptional profile depending on the branch of UPR activation. All these transcriptional studies have identified ER chaperones, protein folding enzymes and other proteins of the secretory pathway as target genes of the UPR. If homeostasis is not regained during the UPR, cells undergo apoptosis. In particular, PERK and ATF6 activation induce proapoptotic genes (Harding et al 2000) (Yoshida et al 2000).

Temporally, the UPR can be divided into an early and a late phase (Yoshida et al 2003). The early phase consists of the inhibition of protein synthesis through eIF2 α phosphorylation by PERK and the upregulation of ER chaperones to increase protein folding activities within the ER. The second phase involves the upregulation of genes involved in ERAD to enhance degradation to decrease the load of misfolded proteins in the ER. ATF6 has been implicated, in mammals, to induce the expression of the protein Herp which is thought to recruit the 26S proteasome to the ER membrane in times of ER stress (Ma & Hendershot 2004). In addition,

the IRE1/XBP1 pathway induces the expression of ERAD proteins such as EDEM, HRD1 and UGGT (Hosokawa et al 2003).

1.4 The smooth endoplasmic reticulum

Although the rough and the smooth endoplasmic reticulum (SER) comprise a continuous membrane, morphological and functional segregation exist within the organelle (Depierre & Dallner 1975). In contrast to the RER, the SER lacks bound ribosomes and is often abundant in cells with specialized functions, e.g. the rat liver hepatocyte. In these cells, the SER is expanded to accommodate for increased lipoprotein synthesis and detoxification of drugs (Baron et al 1982, Bolender & Weibel 1973, Jones & Fawcett 1966). The cytochrome 450s (CYP450) comprise a system for drug clearance in the liver (Guengerich 2006). These proteins are type I integral membrane proteins that make up a highly conserved superfamily of heme enzymes. Combined with the glucuronosyltransferases, also type I membrane proteins, endogenous steroids and xenobiotic chemicals are oxidized by CYP450 and made more hydrophilic by glucuronidation for elimination from the body. The CYP450 system also works with other systems in the liver to render lipophilic steroids and drugs more water soluble. These systems include the carboxylesterases (Sato & Hosokawa 2006) and glutathione-S-transferases (Sheehan et al 2001).

Along with detoxification, the SER is the site of lipid and sterol synthesis (Bishop & Bell 1988). In fact, the ER is the principal organelle for the synthesis of the major classes of lipids required for the generation of new membranes. The major products of lipid synthesis in the ER are phospholipids, cholesterol and ceramide. The assembly of phospholipids (e.g. phosphatidylcholine and phosphatidylethanolamine) can be regarded as a three step process. The first step involves the synthesis of lipids from hydrophilic precursors on the cytosolic leaflet of the ER membrane (Bell &

Coleman 1980). In the second step, the assembled phospholipid molecules are transported across the bilayer into the luminal side of the ER membrane. The exact mechanism for the energetically unfavorable translocation of phospholipids (Liu & Conboy 2005) is unknown at this time. However, current data strongly support the existence of a membrane protein or “flippase” that enables phospholipid flipping to occur (Pomorski & Menon 2006). The third step consists of the transport of lipids from the ER (Voelker 2003) to other organelles of the endomembrane system or to organelles which are unable to synthesize phospholipids for the assembly of new organellar membranes. For example, mitochondria can not synthesize the majority of the lipids required for its function; therefore, phosphatidylcholine, phosphatidylinositol and phosphatidylserine must be imported from the ER (Voelker 1989). Once imported into the mitochondria, phosphatidylserine, which is essential for mitochondrial function, is converted to phosphatidylethanolamine by phosphatidylserine decarboxylase 1 (Birner et al 2001).

1.5 Endoplasmic reticulum structure

One of the classical problems in cell biology is the question of how the structure and spatial arrangement of organelles influence their functions. Recent work on membrane curvature and the factors that contribute to the characteristic “sheets and tubules” morphology of the ER touches upon this problem. The RER has generally been characterized as membrane sheets studded with ribosomes that emanate from the nuclear membrane, whereas, the SER is described as a ribosome free network of tubules (Clermont et al 1980, Fawcett 1955, Hobman et al 1992, Staubli et al 1969). Recent work investigating the causes of membrane curvature showed that the reticulon and DPR protein families are responsible for generating and maintaining tubular structures in the ER (Voeltz et al 2006). Overexpression of these proteins in ER membranes of yeast resulted in the formation of long unbranched tubules (Voeltz et al 2006).

The proposed mechanism is that the reticulons and DP1 stabilize the curvature of ER tubules by wedging themselves into ER membranes, thus increasing the surface area of the membrane which is required for high curvature. Localization of these proteins revealed that they were almost exclusively distributed to the peripheral tubular ER and absent from the nuclear rim (Voeltz et al 2006). The same study also demonstrated that the loss of reticulon proteins resulted in a reduction in peripheral tubules and an increase in sheet-like structures (Voeltz et al 2006). However, merely the absence of reticulons does not fully explain the maintenance of ER sheets and additional factors are most likely required. Snapp et al. (Snapp et al 2003) demonstrated that highly ordered smooth ER membranes (OSER) can form through weak interactions between the cytosolic domains of overexpressed membrane proteins. Similarly, the overexpression of the poorly characterized protein, p180, led to the proliferation of stacked RER sheets in yeast cells (Becker et al 1999).

The functional significance of the segregation of ER membranes into sheets and tubules is still a mystery. However, it has been suggested that large polysomes arranged on the RER require an expanded surface area provided by a sheet-like structure (Shibata et al 2006). In contrast, smooth ER functions may be hindered by the presence of docked ribosomes since the enzymes that synthesize lipids and detoxifying proteins function on the cytosolic surface of the ER. Therefore, tubules are the ideal shape since they would restrict ribosome binding.

2. The Golgi apparatus

After their folding in the ER, newly synthesized proteins are transported to the Golgi apparatus for final maturation, before they move to their final destinations within the endomembrane system or in the extracellular space. The Golgi apparatus was first discovered in 1898 by Camillo Golgi (Bentivoglio 1998). The organelle consists of tightly stacked

membrane subunits which are commonly referred to as cisternae. These stacks divide the organelle into the cis Golgi network (CGN) (also called the intermediate compartment), the cis, medial and trans cisternae (Ehrenreich et al 1973) and the trans Golgi network (TGN) (Clermont et al 1995). Vesicles carrying secretory proteins from the ER fuse with the CGN and deposit their cargo for glycan side chain processing and proteolytic cleavage by resident Golgi enzymes. Cargo proteins subsequently progress through the stacks to the TGN where they are sorted and sent to either the cell surface or to other parts of the endomembrane system.

2.1 Oligosaccharide processing in the Golgi apparatus

Glycosylation reactions that take place in the Golgi apparatus are much more diverse than in the ER. Enzymes in the Golgi apparatus complete the final stages of N-linked oligosaccharide synthesis and the assembly of glycolipids, proteoglycans and O-linked oligosaccharides (Hirschberg & Snider 1987). The N-glycan transferred onto newly synthesized proteins in the ER is further modified in the Golgi by the addition of new sugars and proteolytic processing, through the sequential action of resident Golgi enzymes (Berger 1985). The outcome of N-linked oligosaccharide processing in the Golgi is the formation of complex oligosaccharides (Berger 1985).

Complex oligosaccharides are made by the combination of trimming of the N-linked glycan as well as through the addition of new sugars by glycosyltransferases (Berger 1985). These enzymes work sequentially (Kornfeld & Kornfeld 1985) and are organized within the Golgi stacks in the order in which they act (Rabouille et al 1995). Therefore, earlier steps in N-linked glycan processing are located toward the cis-face of the Golgi apparatus, whereas enzymes acting in later steps are distributed more towards the medial to trans-stacks (Rabouille et al 1995).

The sequence of complex oligosaccharide processing proceeds as follows: Mannose trimming that begins in the ER is continued in the Golgi by the action of α 1,2 mannosidase I, which trims 3 mannoses from N-linked glycan. This is followed by the addition of N-acetylglucosamine by N-acetylglucosamine transferase I enabling mannosidase II to remove two more mannoses thus yielding a 3 mannose core. An additional N-acetylglucosamine is then added by β 1,2 N-acetylglucosaminyltransferase II. Elongation of the oligosaccharide continues through the addition of galactose by β 1,4, galactosyltransferase, sialic acid by α 2,6 sialyltransferase or fucose by fucosyltransferase (Hirschberg & Snider 1987).

Post-translational modification in the Golgi apparatus also occurs by O-linked glycosylation. This reaction is carried out by glycosyl transferases and involves the addition of sugars to hydroxyl groups on specific serine and threonine residues (Young 2004). O-linked glycosylation is initiated by polypeptide:GalNAc transferase (ppGaNTase) and elongation continues through the action of glycosyl transferases, some of which are also involved in N-linked glycosylation (Ten Hagen et al 2003). Another modification to the O-linked glycan includes sulfation by sulfotransferase (Ouyang et al 1998). Sulfation also occurs on sugars that are incorporated into glycosaminoglycans which are the building blocks of proteoglycans, secreted proteins that form the extracellular matrix. Proteoglycan synthesis involves the polymerization of one or more glycosaminoglycan chains (long continuous repeating disaccharide units) (Toma et al 1996).

3. ER to Golgi transport

It is generally accepted that transport from the ER to the Golgi occurs sequentially through vesicles bearing two coat protein complexes (COPII and COPI coats). COPII vesicles bud from the ER and fuse

together forming a separate compartment called the ER-Golgi intermediate compartment (ERGIC). Transport through the early secretory pathway involves many budding and fusion events and require several components to facilitate these processes. Coat protein play a role in cargo selection and membrane deformation and membrane fusion is regulated by the Rab GTPases and SNARE proteins.

3.1 ER exit sites

Exit from the ER is mediated by COPII vesicles. The COPII coat consists of cytosolic protein subunits that come together to form the coat structure. Assembly of the COPII coat mediates the formation of transport vesicles from the ER. COPII subunits were first discovered as temperature sensitive sec mutants in yeast that accumulated ER tubules at restricted temperatures (Novick et al 1980). COPII vesicles form at ribosome free areas of the ER, which are continuous with the RER. These areas display convoluted invaginated morphology and are referred to as transitional elements (TEs) (Palade 1975). COPII coated buds form on the TEs and accumulate secretory cargo that have passed the quality control checkpoint of the ER (Aridor et al 1999) (Forster et al 2006). These buds, called ER exit sites (ERES) (Watson & Stephens 2005), transform into coated vesicles that rapidly shed their coats and fuse together or with nearby vesiculotubular cluster (VTCs) (Balch et al 1994, Bannykh & Balch 1997). VTCs are also known as the ER to Golgi intermediate compartment (ERGIC) (Hauri & Schweizer 1992, Schweizer et al 1991). The ERGIC is a distinct compartment from the ER and Golgi apparatus. The isolation of this compartment from Vero cells revealed that it was composed of smooth membrane bound vesicles and showed a distinct protein pattern from that of the ER or Golgi apparatus (Schweizer et al 1991).

3.2 Cargo selection by COPII vesicles

The core components required for COPII mediated budding consist of the COPII subunits, Sec23-Sec24 and Sec13-Sec31 (Barlowe et al 1994), the GTPase Sar1 (Nakano & Muramatsu 1989) and the GTP-GDP exchange factor, Sec12, which activates Sar1 (Matsuoka et al 1998). COPII assembly occurs by sequential binding of these components, beginning with the activation of Sar1 by Sec12p followed by the relocation of Sar1 to the ER membrane (Matsuoka et al 1998). Sec23-24 is then recruited to the ER membrane and binds to Sar1 through Sec23 (Matsuoka et al 1998). In addition to Sar1 binding, cargo binding to Sec24 stabilizes the membrane binding of Sec23-24 (Aridor et al 1999). The Sec13 and Sec31 proteins form the vesicle cage, which has a unique cuboctahedral structure (Stagg et al 2006). The Sar1-Sec23-Sec24-cargo complex then binds to Sec13-Sec31 (Matsuoka et al 1998).

Cargo selection and concentration by COPII occurs through the interaction of Sec24 with cytosolically exposed segments of transmembrane proteins or through the binding of transmembrane cargo receptors for luminal proteins (Aridor et al 1999, Forster et al 2006). Binding to transmembrane cargo is mediated by recognition motifs such as the di-acidic DXE motif (Nishimura et al 1999) or the tyrosine based sorting motif YXX ϕ , where ϕ is a bulky hydrophobic group (Aridor et al 2001). Several putative cargo receptors have been identified for soluble protein export from the ER. Erv29p has been shown to be involved in an active mechanism for packaging glycosylated pro-alpha-factor for ER export (Belden & Barlowe 2001). ERGIC-53, a mannose-binding lectin, has also been postulated to be a soluble cargo receptor (Appenzeller et al 1999). ERGIC-53 formed a complex with a cathepsin-Z related glycoprotein in the ER and dissociation took place in the intermediate compartment. The most recent evidence supporting soluble cargo receptors involves the homologous proteins Emp46 and Emp47.

Disruption of Emp46 and Emp47 function resulted in the failed secretion of specific glycoproteins from the ER (Sato & Nakano 2002). Furthermore, a number of cargo binding sites were identified on Sec24 which could account for the diversity in secretory proteins that have to be transported from the ER (Mootha et al 2003b).

COPII coated buds transform into coated vesicles that quickly shed their coats and fuse with one another or with nearby VTC membranes to form the intermediate compartment. Transport between the ER and the cis-Golgi is generally accepted as an ordered mechanism that is mediated by COPII and COPI coats. COPI is comprised of seven subunits (α , β , β' , γ , δ , ϵ , ζ) which assemble in the cytosol to form a complex called coatamer (Schekman & Orci 1996) (Rothman & Wieland 1996). COPI coats are generally observed on intermediate compartment membranes and at the lateral rims of Golgi cisternae (Appenzeller et al 1999, Lavoie et al 1999). COPI has been observed on vesicles emanating from the intermediate compartment which move towards the Golgi apparatus (Scales et al 1997)

3.3 Retrieval sequences

Despite the evidence that cargo selection occurs via interactions with the COPII coat, resident proteins of the ER do escape to the Golgi apparatus. To maintain ER proteins at steady state in the ER compartment, proteins that have escaped out of the ER are retrieved by binding to retrieval motifs, short stretches of amino acids at the C-termini of proteins. Two retrieval motifs for ER proteins are the KDEL (or HDEL) sequence for soluble luminal ER proteins and the di-lysine motif (K(X)KXX) for retrieval of transmembrane proteins (Pelham 1989). COPI coatamer interacts directly with the cytoplasmically oriented di-lysine motif for recycling back to the ER (Cosson & Letourneur 1994, Letourneur et al 1994). The KDEL sequence of soluble luminal proteins binds to the KDEL

receptor in the cis-Golgi network, thus returning proteins back to the ER (Pelham 1991). Several studies have shown that when the KDEL sequence is removed from a soluble ER protein, the protein is slowly secreted from the cell. Furthermore, if a KDEL sequence is added to a normally secreted protein, the protein is not secreted and is returned to the ER (Munro & Pelham 1987). Approximately 30% of all ER localized proteins have known ER retrieval motifs (Scott et al 2004). Therefore, how the majority of ER resident proteins are kept in the ER remains to be elucidated.

3.4 Membrane fusion

Transport throughout the secretory pathway involves many membrane fusion events. To ensure that a transport vesicle delivers its cargo to the correct organelle, specificity in targeting must be ensured. Recognition between a vesicle and its target membrane is mediated by SNAREs (soluble N-ethylmaleimide-sensitive factor) (Sollner et al 1993a, Sollner et al 1993b, Wilson et al 1989), SNAPs (soluble N-ethylmaleimide-sensitive factor attachment proteins) (Clary & Rothman 1990) and Rabs (Zerial & McBride 2001). SNARE proteins are localized in opposing vesicle and target membranes and catalyze membrane fusion by forming a fusion complex (Bonifacino & Glick 2004). The fusion complex bridges together the vesicle and target membrane which brings the lipid bilayers into close proximity and overcomes the energy barrier for membrane fusion to occur (Hanson et al 1997). NSF and SNAPs function to disassemble SNARE complexes after membrane fusion (Block et al 1988, Mayer et al 1996). Rabs are small monomeric GTPases, which are involved in docking and targeting a vesicle to the target membrane (Zerial & McBride 2001).

3.4.1 SNAREs

Most SNAREs are transmembrane proteins that possess an evolutionary conserved motif – a sequence of 60-70 amino acids arranged in heptad repeats which is called the SNARE motif (Paumet et al 2004). SNAREs are classified into Q- or R- SNAREs based on the presence of glutamine or arginine at the core of the four helix bundle. The different SNARE motifs divide the SNAREs further into Qa-, Qb-, Qc- and R-SNAREs (Fasshauer et al 1998, Sutton et al 1998). SNAREs were previously classified as either v- or t- SNAREs because it was assumed that they were separated into either vesicle (v-) for the donor compartment or at the target membrane (t-) for the acceptor compartment (Sollner et al 1993a). This terminology has since been changed to reflect SNARE structural motifs and is more useful in describing homotypic fusion events (Fasshauer et al 1998, Sutton et al 1998). Functional SNARE complexes contain two parallel four helix bundles requiring one of each of the Qa-, Qb-, Qc- and R- SNAREs (Sutton et al 1998). The zipper model describes how SNAREs effect membrane fusion. SNARE motifs come together starting from their cytosolic N-terminus and zip towards their C terminal membrane domains, compressing the membranes together to initiate membrane fusion (Hanson et al 1997, Lin & Scheller 1997). SNARE complexes are disassembled by the hexameric AAA ATPase, NSF (Block et al 1988, Malhotra et al 1988) and also require the presence of α -SNAP (Clary & Rothman 1990). The activity of NSF ensures that uncomplexed SNAREs are continually regenerated for further fusion events (Sollner et al 1993a). NSF uses the energy from ATP hydrolysis to dissociate the complexes (Whiteheart et al 1994). It was once thought that the disassembly of SNARE complexes by NSF and α SNAP was the principal force behind membrane fusion (Sollner et al 1993a). However, this model has since been replaced by the concept that the SNAREs, themselves, function as fusion catalysts (Mayer et al 1996).

SNAREs exist in specific subcellular compartments of the cell (Hay 2001). Examples are Sec22 and Bet1 that function in transport between the ER and Golgi apparatus (Hay et al 1996). Since membrane fusion is a dynamic process involving the recycling of membranes, SNAREs can reside on the organelle where fusion takes place as well as on intermediate compartments involved in membrane recycling. How SNAREs are properly sorted is not entirely clear; although, it has been shown that the cytoplasmic domains of SNAREs are essential for their proper sorting (West et al 1997, Zeng et al 2003). Furthermore, since SNAREs are distributed among many subcellular compartments (Hay 2001), SNAREs in these compartments must stay inactive until they return to their specific place of function. For these reasons, another level of regulation might be involved which could be at the level of tethering involving the Rab proteins (Zerial & McBride 2001).

3.4.2 Rabs

Rabs are small GTP-binding proteins that control the specificity of tethering and docking events between vesicles and target membranes (Zerial & McBride 2001). During membrane fusion events, Rabs are postulated to function before SNARE pairing occurs. Rabs have a distinct distribution among the organelles and regulate transport between these compartments (Zerial & McBride 2001). Although Rabs are generally associated with tethering and docking events, they have also been implicated in vesicle formation (Nuoffer et al 1994). Their role in vesicle budding was shown by using a mutant form of Rab1, which was able to initiate export from the ER and transport between Golgi compartments (Nuoffer et al 1994). Additionally, Rabs have been shown to interact with elements of the cytoskeleton. Rabs play a role in recruiting microtubule motors to membranes such as kinesin to endosomes (Hoepfner et al 2005) and dynein to the TGN (Matanis et al 2002) (Short et al 2002). These interactions with microtubule motors are consistent with their

function in the spatial regulation of membrane transport. A large number of Rabs are predicted from the human genome (>60) (Zerial & McBride 2001). Due to their abundance, they have been postulated to define organelles by creating unique protein scaffolds (Munro 2004, Pfeffer 2001).

3. Transport through the Golgi apparatus

Despite knowing much about the mechanisms governing the process of protein secretion (e.g. the calnexin cycle, glycosylation, SNARE mediated membrane fusion), the fundamental question of how proteins transit through the Golgi apparatus remains an unresolved matter. Two mechanisms have been debated over the years, the cisternal maturation, vesicular transport model, and a newer tubular continuity-based mechanism.

The cisternal maturation model proposes that the cisternae carrying secretory cargo move forward through the Golgi apparatus. New layers form at the cis face and old layers are dispersed at the trans face (Elsner et al 2003). As the cisternae mature, they progress through the stacks carrying secretory cargo, which is actively modified in the cisternae by resident Golgi enzymes. At the trans side of the Golgi apparatus, cargo is sorted for secretion to the extracellular space or dispersed to other parts of the cell.

Alternatively, the vesicular transport model proposes that the Golgi stacks are stable, long-lasting structures and that secretory cargo is transported from stack to stack by vesicles which bud off one cisternae and fuse with the next to deliver their secretory cargo (Elsner et al 2003). The vesicles proposed to shuttle cargo were identified and called COPI vesicles named for the coat that encapsulates them. This coat is made up of COPI subunits or coatomer (Orci et al 1986). In the cisternal

maturation model, COPI vesicles play a different role. Instead of shuttling cargo, they retrieve resident Golgi enzymes from more trans stacks for delivery to earlier stacks in a retrograde manner (Lin et al 1999). In this way, COPI vesicles are postulated to prevent resident Golgi enzymes from being secreted by replenishing the supply of resident Golgi enzymes to newly forming Golgi cisternae.

The debate surrounding Golgi transport has shifted from one model to the other over the years. The question of “what is in COPI vesicles” should have been able to resolve this controversy. However, experiments designed to test these models have resulted in inconclusive results. The most striking example came from two studies which used cryo-immuno electron microscopy to answer this question (Martinez-Menarguez et al 2001, Orci et al 2000). Using the same technique, they found conflicting results (Martinez-Menarguez et al 2001, Orci et al 2000). Orci et al. (Orci et al 2000) observed that the resident Golgi enzymes, mannosidase II and N-acetylglucosaminyl transferase I remained in the Golgi cisternae and were excluded in the COPI vesicles; whereas, the study by Martinez-Menarguez et al. (Martinez-Menarguez et al 2001) made the opposite conclusion and visualized mannosidase II in peri-Golgi vesicles.

Recently, two separate studies by Losev et al. (Losev et al 2006) and Matsuura-Tokita et al. (Matsuura-Tokita et al 2006) produced evidence in support of cisternal maturation. Using Golgi apparatus from *Saccharomyces cerevisiae* which are unstacked and therefore easier to visualize, they tagged resident membrane proteins of the cis and trans cisternae with green and red fluorescent proteins, respectively. They predicted that if Golgi cisternae are stable structures, consistent with the vesicular transport model, then the resident proteins should remain in place over time. However, if cisternal maturation is taking place and the cisternae are transitory, the cisternae should change color in time. Both

groups observed the shift from green to yellow to red representing a shift from an early green cis cisternae to medial yellow cisternae when both enzymes are present and ending with a red trans cisternae as the earlier green tagged enzyme is lost (Losev et al 2006, Matsuura-Tokita et al 2006). Furthermore, Losev et al. (Losev et al 2006) also showed that two cargo proteins (α factor and carboxypeptidase Y) in the cis cisternae traverse the Golgi at the same speed, which is another prediction of the cisternal maturation model. Matsuura et al. (Matsuura-Tokita et al 2006) addressed another aspect of cisternal maturation which is the role of the COPI vesicles. They found that in yeast with a mutation of the COPI coat, cisternal maturation still occurred but it slowed down approximately 3 fold. Therefore, the question still remains of how retrograde transport occurs without COPI vesicles. Other questions also remain to be addressed such as how the differential distribution of Golgi enzymes is maintained in the Golgi stacks and how relevant is the yeast Golgi system to the mammalian Golgi apparatus (Malhotra & Mayor 2006).

In contrast to the first two mechanisms, COPI vesicles play a minor role in the continuity-based model. This model has been of recent interest due to two studies that took advantage of technological developments in microscopy to address the debate about mechanisms of Golgi transport. However, membrane continuities between Golgi cisternae have been detected previously (Clermont et al 1994, Ladinsky et al 1999, Tanaka et al 1986). Two studies using EM tomography have shown that tubular connections form throughout the Golgi stack during active Golgi transport (Kweon et al 2004, Trucco et al 2004). The study by Kweon et al. (Kweon et al 2004) analyzed the distribution of Golgi enzymes (mannosidase II and galactosyltransferase) in the three-dimensional structure of the Golgi apparatus obtained by EM tomography. They found that, in contrast to the cisternal maturation model, 50- to 60- nm COPI coated buds and COPI-dependent vesicles were depleted of Golgi

enzymes (Kweon et al 2004) at steady state. They also found that Golgi enzymes were concentrated in pores or perforated zones near the cisternal rims of the Golgi. Furthermore, when Golgi-enzymes were enriched in round profiles, the authors showed by tomographic reconstruction that the round profiles were not vesicles but instead were cross-sections of cylinder-like structures near the perforated zone. In a separate but related study by the same group, Trucco et al. (Trucco et al 2004) showed that tubular continuities are formed across the Golgi subcompartments during active Golgi transport. A synchronized wave of secretory traffic was induced in cells by either blocking their exit from the ER using both a temperature and hydroxylation block or by arresting cargo in the intermediate compartment by a 15° C temperature shift. This wave of traffic was studied in model Golgi produced from Golgi ribbons by treatment with nocodazole. The authors found that during the duration of the traffic wave, tubular continuities are formed throughout the Golgi stacks. In addition, they observed that a secretory cargo-containing intermediate compartment fused with the cis-cisternae and the cargo was absorbed into the stack. This formed new cis cisternae and enlarged the already existing cis cisternae. This observation is at odds with predictions of the cisternal maturation model which states that the intermediate compartment does not combine with the pre-existing cis-cisternae but instead forms new cis- cisternae. In light of past and recent observations, a new model of Golgi transport has been proposed. This model states that ER-to-Golgi carriers fuse with the cis-Golgi and deliver their cargo and membranes to the cis-stack. This event triggers the formation of tubular connections between adjacent cisternae with incoming membranes redistribute throughout the Golgi stack. Cargo is initially excluded from the tubules and the membrane redistribution step and retained in the cis-Golgi cisternae. Transport proceeds as predicted by the cisternal maturation scheme; however, instead of COPI vesicles recycling Golgi enzymes back

to earlier cisternae, enzymes flow back through tubular connections (Trucco et al 2004).

4. Proteomics

Proteomics is defined as the large-scale elucidation of the functions of all proteins in a cell (Anderson & Anderson 1998). Proteomics technologies have made large scale organelle studies feasible, and provide powerful tools for studying organelles, their components and dynamics (Oda et al 1999, Yates 2004). The combination of large-scale proteomics studies with traditional cell-biology techniques provides a strategy for the functional characterization of organelles, the molecules they interact with in the cytoplasm and the discovery of novel proteins and functions for the organelles (Yates et al 2005).

An organellar proteomics study begins an enriched fraction containing the organelle of interest which is isolated by subcellular fractionation (Au et al 2007). Proteins isolated with the organelle are then identified using proteomics techniques such as mass spectrometry. There are some limitations to this approach which include contamination from other organelles, difficulty in identifying post-translational modifications and the variance seen in proteomes from different tissues (Yates et al 2005). A consideration when carrying out a proteomics analysis of isolated organelles involves discerning true resident proteins from contaminants. After subcellular fractionation, the enrichment of proteins in the isolated organelle will vary making it difficult to ascertain bona fide components of the organelle from contaminating proteins (Andersen et al 2003, Dunkley et al 2006, Dunkley et al 2004, Foster et al 2006a). Both types of proteins are present in the fraction and if proper controls for contamination are not used, contaminating proteins could be mistakenly considered part of the proteome. Recent organellar proteomics analyses have addressed this limitation by quantitatively analyzing more than one

organelle at a time and in doing so, attempt to distinguish true resident proteins from contaminants (Dunkley et al 2006, Foster et al 2006a, Kislinger et al 2006). Secondly, many proteins, especially membrane and important signaling proteins are post-translationally modified. These post-translational modifications (PTMs), which include phosphorylation and glycosylation, regulate the function of these proteins by changing their activity, interactions, and subcellular localizations. Until recently, determining PTMs has presented many challenges; however, advances in mass spectrometry have made the analysis of PTMs of proteins in signalling pathways more feasible (Mann & Jensen 2003, Olsen et al 2006, Rush et al 2005). Finally, the protein composition of an organelle in different tissues will vary, making it difficult to identify any “one” proteome for an organelle. A recent study by Kislinger et al. (Kislinger et al 2006) attempted to address this issue by comparing the proteomes of different organelles from different tissues with their mRNA abundance.

4.1 Subcellular fractionation

Subcellular fractionation is the most common strategy for the isolation of organelles. This approach to isolating organelles was pioneered by Claude (Claude 1975), Palade (Palade 1975) and de Duve (Duve 1975) and involves homogenizing tissue or cells followed by different centrifugation steps to separate cellular components. The separation is based on the size and density of the organelles using different time periods and centrifugation velocities (DeDuve 1971). To isolate the ER and Golgi apparatus, gradient centrifugation is used (Ehrenreich et al 1973, Paiement et al 2004). Sucrose is the most common gradient used but other alternatives exist such as Nycodenz, Percoll and Ficoll (Stasyk & Huber 2004).

Contamination by other organelles is always an issue with subcellular fractionation (Duve 1975). Indeed, DeDuve (Appelmans et al

1955), showed that for any organelle population, the sedimentation coefficients exhibit a Gaussian distribution; therefore, organelles are not completely separable (De Duve & Beaufay 1981, Duve 1975). Despite this, subcellular fractionation generates a sample that is highly enriched and reduced in complexity compared to the starting homogenate (Stasyk & Huber 2004). Protein concentrations in an enriched subcellular fraction exhibit a smaller range in protein concentration as compared to the starting homogenate. As an example, the Golgi apparatus comprises 1% of the total volume of the cell. After subcellular fractionation, it is enriched approximately 150 times by the measurement of galactosyltransferase activity (Dominguez et al 1999) in the homogenate vs. the subcellular fraction. Therefore, the dynamic range of protein concentration is reduced by subcellular fractionation.

Another factor in mass spectrometry based protein identification is the dynamic range of the mass spectrometer. Mann and colleagues showed that nano-electrospray mass spectrometry can detect proteins in the femtomolar range (Wilm et al 1996). However, in practice, the same group showed that the highly sensitive FT-ICR mass spectrometer exhibited a 10^4 dynamic range for a two protein mixture (de Godoy et al 2006). Therefore, efforts to decrease the range of protein concentration in a proteomic sample to within the effective dynamic range of the mass spectrometer when analyzing a complex protein mixture increases the likelihood of peptide and protein identification.

4.2 Protein separation

Although organellar preparations are reduced in complexity, subcellular fractions must be further resolved for optimal analysis by mass spectrometry. Three of the most common methods used are two dimensional gels (2D gels), 1D SDS-PAGE gels and two dimensional liquid chromatography (2D-LC). Two dimensional gels separate proteins

in the first dimension based on their isoelectric point and in the second dimension by their molecular weight. The resulting gels contain “spots” which are excised, digested with trypsin and the peptides extracted for analysis by the mass spectrometer. This method allows for thousands of proteins to be displayed at one time, serving as a protein map of a particular cell or tissue (Wirth & Vesterberg 1988). Two-dimensional gels are commonly stained with Coomassie blue or silver stain. Since 2D gel spots often contain only one protein, the intensity of the stain indicates that protein’s abundance. A further advantage to 2D gels is their detection of post-translationally modified proteins, which appear as an additional spot shifted on the gel (Wirth & Vesterberg 1988). However, 2D gels are limited in that they separate transmembrane proteins incompletely. This limitation is mainly due to the insolubility of membrane proteins in the non-detergent isoelectric focusing buffer for the first dimension separation and solubilised membrane proteins often precipitate at their isoelectric point (Santoni et al 2000). Consequently, for the detection of membrane proteins, either 1D SDS-PAGE gels or 2D-LC are used.

One-dimensional SDS-PAGE gels separate proteins based on their molecular weight. Sodium dodecyl sulphate (SDS), a detergent, denatures and binds to a protein proportional to its length. SDS also imparts a negative charge to a protein; therefore, proteins separate in an electric field based on their size (Righetti 2005). Similar to 2D gels, the bands of a 1D gel are excised, trypsinized and the peptides extracted. However, unlike 2D gels bands on a 1D gel contain multiple proteins. The major advantage to 1D gels is their ability to separate membrane as well as soluble proteins.

A recent advance in protein separation involves a gel-free approach using 2D-LC. The approach, called MudPIT (multi-dimensional protein identification technology) (Link et al 1999, Washburn et al 2001, Wolters et

al 2001), begins with proteolytically digesting proteins with trypsin followed by separation based on charge using strong cation exchange chromatography (SCX). This step is followed by reverse-phase chromatography which separates proteins based on hydrophobic interactions. A series of salt steps elute the peptides off the SCX column which are then trapped onto the reverse phase column. An organic solvent then elutes the reverse phase column that is connected in-line to a tandem mass spectrometer (Link et al 1999, Washburn et al 2001, Wolters et al 2001). This approach eliminates the use of gels by coupling protein separation with tandem mass spectrometry in one step.

4.3 Mass spectrometry

The mass spectrometer measures the ratio of a molecule's mass to charge (m/z). Because of this, it can be used in a variety of applications in the biological sciences. The use of mass spectrometry to analyze biological molecules greatly increased in the 1990's due to the improvements in ionization techniques (Aebersold & Mann 2003). Mass spectrometers measure molecules in the gas phase which limited the analysis of biological molecules because they are mainly large, non-volatile, polar molecules in the liquid phase. The development of two ionization techniques called matrix assisted laser desorption ionization (MALDI) (Karas & Hillenkamp 1988) and electrospray ionization (ESI) (Fenn et al 1989) overcame this limitation. These are two of the most popular ionization techniques credited with the success of mass spectrometry based proteomics (Aebersold & Goodlett 2001).

To generate ions in the gas phase using MALDI, proteins and a matrix material are mixed together, applied to a metal substrate and allowed to dry (Karas & Hillenkamp 1988). The resulting solid is then irradiated with a laser, which generates ions (Karas & Hillenkamp 1988). MALDI is usually coupled with a time of flight (TOF) analyzer, which

functions by detecting and recording the flight path of ions accelerated to a fixed amount of kinetic energy down a travel tube (Wiley & MacLaren 1955). The mass to charge ratio is determined by relating the time it takes an ion to reach the detector. MALDI ToF is most often used to measure the mass of intact peptides (Aebersold & Goodlett 2001) in the MS mode of the mass spectrometer. This approach is also known as peptide mass fingerprinting (James et al 1993, Mann et al 1993, Pappin et al 1993, Yates et al 1993).

In contrast to MALDI, ESI ionizes the proteins immediately out of a solution (Fenn et al 1989). Because of this property, it is often coupled to liquid based separation tools such as liquid chromatography. Proteins elute off a column and are sprayed directly into the mass spectrometer. ESI is most often coupled to a quadrupole, which guides peptide ions through the application of an electric field (Chernushevich et al 2001). Tandem MS is more commonly performed using ESI (Chernushevich et al 2001). Both peptide mass fingerprinting (James et al 1993, Mann et al 1993, Pappin et al 1993, Yates et al 1993) and tandem MS approaches measure the m/z values of intact peptides in the MS mode of the mass spectrometer. However, tandem MS involves a further step of peptide fragmentation to acquire the amino acid sequence of a particular peptide. In tandem MS, a peptide ion is selected and bombarded with an inert gas to fragment the peptide and several bonds within the peptide can be broken during fragmentation (Bowie et al 2002). Cleavage of the amide bond is most common for ESI, and depending on whether the charge is retained at the amino terminal fragment or carboxyl terminal fragment, an ion is designated as either a b or y ion, respectively (Bowie et al 2002). The amino acid series for a peptide after tandem MS can be determined by the m/z differences between the observed b or y ions (Bunkenborg & Matthiesen 2007). This process is very laborious to do manually and algorithms designed for de novo sequencing are still inaccurate

(Medzihradszky 2005). Complications arise in interpreting tandem mass spectra by de novo sequencing because often the y or b ion series are incomplete and difficult to interpret (Steen & Mann 2004). Presently, the most common method used to assign peptide sequences to tandem MS spectra is by searching against a protein sequence database (Steen & Mann 2004).

4.4 Peptide identification by searching protein sequence databases

Two major advances have contributed to the advancements in proteomics. The first is the development of algorithms designed to match mass spectra with peptide sequences by searching protein sequence databases and the second is the progress made in whole genome sequencing to populate these databases (Boguski & McIntosh 2003). Matching spectra to protein sequence databases is a less complicated problem than de novo sequencing because only a small fraction of possible peptide sequences actually occur (Steen & Mann 2004). Therefore, even though a mass spectrum does not have enough information to clearly identify its sequence through de novo sequencing, it may contain enough information to assign it to a peptide sequence in the database (Steen & Mann 2004). Several approaches exist to assign sequences to peptides via database searching. Two of the most commonly used methods are SEQUEST (Eng et al 1994) and Mascot (Perkins et al 1999) which are based on a cross-correlation and probability approaches, respectively. Both methods compare observed mass spectra to simulated mass spectra generated by theoretically digesting a protein database with trypsin and fragmenting the peptides. The difference between the two lies in the way they score and rank the assignments.

4.5 Quantitation

Several methods exist to measure the abundance of proteins in a proteomics experiment. These methods range from gel based approaches which rely on staining intensity, to isotopically labelling of peptides or labelling with chemical tags. Quantitation becomes especially important in proteomics experiments that rely on the degree of state changes of proteins. This section discusses commonly used methods for quantitation in proteomics experiments.

Quantification using 2D gels occurs by comparing the stain intensity between spots in 2 different samples to identify proteins that are increased or decreased in abundance (Fey & Larsen 2001). This approach pioneered the field of “quantitative proteomics.” Presently, other mass spectrometry based methods have superseded 2D gels for quantification purposes (Ong & Mann 2005). These methods were developed mainly to overcome the inherent limitations of 2D gels due to their bias against membrane proteins and their low resolution (Freiburghaus 1994).

Methods of measuring protein abundance come in two varieties – label and label-free. Label-free methods include counting the number of redundant peptides for a given protein (Blondeau et al 2004, Kislinger et al 2006, Liu et al 2004, Pang et al 2002) referred to as peptide counting (Blondeau et al 2004), redundant peptide counting (Kislinger et al 2006) or spectral counting (Liu et al 2004). This method, which was first applied by Pang et al. (Pang et al 2002) and in a high throughput study by Blondeau et al. (Blondeau et al 2004), is based on the observation that the number of peptides generated by a protein increases with increasing protein amount. It relies on the frequency of detection of tandem mass spectra and uses the total number of MS/MS signals for any peptide in a given protein as an index of protein abundance (Blondeau et al 2004, Cox et al 2005, Gao et al 2005, Gao et al 2003, Girard et al 2005, Liu et al 2004,

Pang et al 2002, Qian et al 2005, Rappsilber et al 2002, Zybaylov et al 2005). To determine the relative abundance between proteins in the sample, the number of redundant peptides for a protein is normalized to the total number of peptides in a sample or to the number of expected peptides or by the molecular weight.

A related approach to spectral counts involves using the extracted ion currents for peptides. This measurement is derived by plotting the intensity of the peptide signal as it elutes from the chromatographic column and measuring the area under this curve (Andersen et al 2003). In their application of this method in deciphering the proteome of the centrosome, Andersen et al. (Andersen et al 2003) used the average of the three most intense peptide extracted ion currents for the same protein as a measure of its abundance. Both peptide counting and extracted ion currents are simple and straightforward measures for estimating protein abundance which do not require manipulation of the samples and are applicable to any tandem mass spectrometry experiment.

Several limitations exist for the label free peptide based quantitative approach. First, tryptic peptides have different ionization efficiencies and propensities to “fly” in the mass spectrometer and some peptides may be either too small or large and are beyond the range of detection by the mass spectrometer (Ong et al 2003). Mallick et al. (Mallick et al 2007) used up to 500 biochemical attributes of peptides (e.g. charge and hydrophobicity of amino acids) to predict peptides that are more likely to be detected in a tandem mass spectrometry experiment. A peptide was designated “proteotypic” if it was observed over 50% of the time in experiments in which its parent protein was observed (Mallick et al 2007). Similarly, Lu et al. (Lu et al 2007) developed the Absolute Protein Expression Profiling (APEX) approach which predicts proteotypic peptides

and incorporates this prediction into redundant peptide counting to increase the accuracy of the abundance measurement.

As for quantitative labelling methods, a common strategy is to use stable isotope labeling (e.g., ^{12}C vs. ^{13}C , ^{14}N vs. ^{15}N , ^2H vs. ^1H). The method relies on the similar ionization efficiencies between both the light and heavy forms of the labelled peptide which produce the same signal in the mass spectrometer except for an offset in mass. Ways to introduce isotopes into the peptides include: 1) adding a “spike-in” isotopically labelled peptide (Kuhn et al 2004, Stemmann et al 2001) 2) introducing an isotopically labelled chemical tag into peptides (Gygi et al 1999, Ross et al 2004) 3) introducing the isotope into the cells metabolically (Ong, 2002 #521). Relative abundance is derived from determining the ratios of light to heavy peptides by measuring the extracted ion chromatogram or by signal intensities of the mass spectrometer.

The most straightforward approach to introducing stable isotope labelled peptides is by the “spike-in” method which involves introducing a known-quantity of a labelled peptide as an internal standard. This method served as the basis for the AQUA approach which was used to monitor the phosphorylation states of the protein, separase, during the *Xenopus* cell cycle (Stemmann et al 2001). Biomarker research also relies on this approach when using multiple reaction monitoring (MRM) to monitor selected peptides. However, the internal standard is added after tryptic digestion and therefore does not correct for losses during the previous processing steps. Since the internal standards must be selected and synthesized prior to the experiment, the stable isotope “spike-in” approach is generally applied to only a small number of proteins.

Peptides can also be coupled to a reagent such as ICAT which yields isotopically distinguishable fragment ions in the MS mode of the

mass spectrometer. In this approach, two related samples are chemically modified with a light and heavy version of isotopes present in the chemical tag. The first widespread application of this method was through the isotope-coded affinity tag (ICAT) method (Gygi et al 1999). The ICAT reagent is directed at cysteine residues in peptides. During an ICAT experiment, two samples (one control and experimental) are reduced and alkylated in the presence of the light and heavy ICAT reagent, respectively. Both samples are then combined, digested and the labelled peptides are isolated with an affinity column. The captured ICAT labelled peptides are then eluted off the column and analyzed by MS. An advantage of the ICAT approach is that it reduces the complexity of a sample since not all proteins contain cysteines (Gygi et al 1999). However, this same reason proves to be disadvantageous because some cysteine-poor proteins may only be identified and quantified by a single peptide (Ong et al 2003). These limitations were addressed in the development of the next generation stable-isotope chemical tags. The Isobaric Tag for Relative and Absolute Quantitation (iTRAQ) tag targets enables relative protein levels in four samples to be determined in a single mass spectrometry experiment (Ross et al 2004). The iTRAQ reagent has an N-hydroxysuccinimide ester group, which reacts with peptide N-termini and the primary amines of the C-terminal lysines of tryptic peptides (Ross et al 2004). It also contains a balance group and a reporter group whose masses increasingly differ by 1 Da. iTRAQ labelled peptides are isobaric rendering the mass spectra simple, with the difference in mass seen in the fragmentation spectra. When an iTRAQ-labelled peptide is subjected to collision-induced dissociation, the iTRAQ tag fragments between the reporter group, balance group and the peptide. The resulting reporter ions derived from the four versions of the iTRAQ reagent appear at 114.1 m/z, 115.1 m/z, 116.1 m/z, and 117.1 m/z in each MS/MS spectrum. The balance group is uncharged and, therefore, is not present in the MS/MS spectra. The ratios of peak areas of the iTRAQ reporter ions reflect the

relative abundances of the peptides and the proteins in the samples. The ITRAQ system is a common way to quantify proteins in proteomics studies (Ong et al 2003). Of relevance to organellar proteomics, the LOPIT strategy developed by Dunkley et al. (Dunkley et al 2006) used ITRAQ to map the proteomes of the organelles in *Arabidopsis thaliana*.

Metabolic labelling involves growing cells in media containing a light and heavy version of a stable isotope (Ong et al 2002). Proteins incorporate the labels through normal protein synthesis and turnover and all proteins within the cell are replaced by isotopically labelled versions. This method is the basis of the stable isotope labelling by amino acids in cell culture (SILAC) approach (Ong et al 2002). A stable-isotope labelled amino acid (e.g. leucine or arginine) is added to media of two cell populations for comparison. The cells incorporate the amino acid into their proteins after several rounds of cell growth. By mass spectrometry, the peptide pairs are distinguished by the difference in mass due to the labelled amino acid and quantitation of abundance occurs by comparing the intensities of these labelled peptides (Ong et al 2002).

In summary, the main difference between label and label-free methods is that quantitation by labeling measures the relative difference in protein abundance between control and treated samples; whereas, label-free methods do not rely on a protein by protein comparison and can determine the relative abundance among all proteins in a sample (Ong & Mann 2005).

4.6 Organellar proteomics

A large number of organelles have now been analyzed by proteomics. The first generation of organellar proteomics studies isolated and analyzed one organelle at a time to gain insight into their functions. Many of these studies produced a catalog of proteins that make up the

organelles, which include a number of previously uncharacterized proteins. The ability to translate from a list of proteins to new biology is the driving force behind a proteomics study (Yates et al 2005). At present, the major organelles have been analyzed by proteomics (Yates et al 2005). Furthermore, recent organellar proteomics studies have taken a systems approach and analyzed several organelles that constitute a pathway. This section focuses on the following topics: 1) studies which used proteomics findings to gain insight into the function of the organelle. 2) how these studies addressed the issue of contamination and 3) prior studies on organelles of the early secretory pathway (ER, Golgi and ERGIC).

4.6.1 Nucleus

Subcompartments of the nucleus which have been characterized by proteomics include the nuclear pore, nuclear envelope, the spliceosome and the nucleolus. The analysis of the yeast nuclear pore complex by Rout and colleagues led to the identification of 174 proteins (Rout et al 2000). To determine, nuclear pore proteins from contaminants, Rout and colleagues functionally characterized proteins identified in the enriched nuclear pore fraction by cross-referencing protein databases. Previously uncharacterized nuclear pore proteins were then screened to verify their localization to the nuclear pore. This screen involved a three step process which involved 1) localization of epitope-tagged proteins by immunofluorescence microscopy, 2) co-localization of proteins with the nuclear pore complex in a yeast strain in which the complexes cluster together and 3) co-fractionation of proteins with known nuclear pore components. After screening, twenty-nine proteins were localized to the nuclear pore by immunoelectron microscopy. This study led to biological insight into how molecules enter and exit the nuclear pore. Rout et al. (Rout et al 2000) proposed a new model for nuclear transport

based on “Brownian affinity gating” in which a stochastic mechanism selects for molecules to be transported into and out of the nucleus.

The nuclear envelope, which is one of least characterized structures of the nucleus, has also been characterized by proteomics. This is a double membrane structure comprised of an inner and outer membrane. Identification of proteins specific to the nuclear envelope is complicated since the outer envelope is continuous with the ER membrane. To determine nuclear envelope specific proteins, Schirmer et al. (Schirmer et al 2003) used a subtractive proteomics strategy. In this approach, they characterized a microsomal membrane fraction by mass spectrometry and subtracted the proteins in common with the nuclear envelope proteome. Prior studies on the nuclear envelope compiled a list of 13 resident proteins. All of these were identified including an additional 67 previously uncharacterized proteins. As a way to assign significance to these proteins, Schirmer et al. mapped the chromosomal locations of the human homologues of these proteins. Mutations in nuclear envelope proteins have been linked to a number of dystrophies and the idea was that the novel proteins could be associated with one or more of these dystrophies that have not been assigned a gene. Of the 67 previously uncharacterized proteins, 23 were mapped to regions of the genome that have been linked to various dystrophies.

4.6.2 Phagosome

Internalization of large macromolecular complexes and pathogens for degradation occurs by phagocytosis. During this process, the pathogen binds to receptors on the plasma membrane, which initiates the engulfment and subsequent internalization of the pathogen through the invagination of the plasma membrane. Newly formed phagosomes interact with the endocytic machinery and transform into a phagolysosome for degradation of the engulfed particles. To understand further the

function of phagosomes, subcellular fractionation of latex bead containing phagosomes was done. Isolation of phagosomes using latex beads confers the advantage that the latex bead containing phagosomes migrate to a part of the gradient away from all other organelles of the cell (Wetzel & Korn 1969). Therefore, a highly enriched phagosome preparation is obtained with minimal contamination.

Mass spectrometry identified 520 proteins in the phagosome preparation. Unexpectedly, a significant portion of the phagolysosome proteome identified was made up of ER proteins which were considered possible contaminants (Garin et al 2001). However, investigation into this observation led to the discovery that the ER contributes membrane to phagosome formation (Gagnon et al 2002) which then led to a mechanism explaining the process of antigen-cross presentation on MHC class I molecules (Guermónprez et al 2003, Houde et al 2003). Furthermore, independent confirmation of the involvement of ER in phagocytosis has recently been presented (Ackerman et al 2006, Becker et al 2005, Hatsuzawa et al 2006). The finding that the ER directly fuses with the plasma membrane also explains how ER proteins, such as calnexin and calreticulin reach the cell surface (Johnson et al 2001, Okazaki et al 2000).

4.6.3 Clathrin coated-vesicles

Clathrin coated vesicles (CCV) form at the plasma membrane as part of the endocytic process. Clathrin molecules and adaptor proteins are recruited to regions of the plasma membrane destined for endocytosis. At the plasma membrane, cytosolic domains of certain membrane proteins bind to the adaptor proteins which themselves bind to clathrin. Proteins that do not bind are excluded from the vesicles. A protein called dynamin functions in pinching off the neck of the coated pit, in a GTP dependent manner, thus forming a clathrin coated vesicle. Two hundred and nine proteins were identified in the CCV proteome included 8 previously

uncharacterized proteins. Further work showed two of these proteins, enthoprotin/epsinR and adaptin ear-binding coat-associated protein-2 (NECAP2), to be new components of CCVs that form at the trans-Golgi network and the plasma membrane, respectively (Ritter et al 2003, Wasiak et al 2002). A novel motif, WVQF, for interaction with AP1 and AP2 was also identified.

4.6.4 Mitochondria

Four separate attempts have been made to decipher the mitochondrial proteome from different tissues (Mootha et al 2003a, Prokisch et al 2004, Sickmann et al 2003, Taylor et al 2003) leading to the identification of 416-750 proteins. Mitochondria derived from the human heart was analyzed using two different approaches, 1D SDS-PAGE tandem MS approach (Taylor et al 2000) and multidimensional liquid chromatography/tandem MS (Gaucher et al 2004), identifying greater than 600 proteins. Sickmann et al. (Sickmann et al 2003) identified 750 proteins in the proteome of *S. cerevisiae* using a combination of 2D gels and 2-dimensional liquid chromatography. Mootha et al. (Mootha et al 2003a) and Prokisch et al. (Prokisch et al 2004) combined data from different data sources (expression profiling, subcellular localization, deletion phenotype screening, protein-protein interactions and computational analysis) to achieve a comprehensive “systems biology” view of the mitochondria. Mootha et al. (Mootha et al 2003a) investigated the diversity in mitochondrial proteomes derived from different mouse tissues (brain, kidney, heart and liver) and compared their proteomics data with RNA expression profiling studies of the same tissues. This study gave insight into the differences of mitochondria from other tissues as well as the correlation between RNA levels and protein (Mootha et al 2003a). Five-hundred and ninety-one proteins were identified in this study including 163 proteins not previously linked to the organelle. Based on the integration of this dataset with genotype data from patients with the

neurodegenerative disorder called Leigh syndrome, a single candidate gene, LRPPRC, was identified for this disease (Mootha et al 2003b).

4.6.5 ERGIC

A study by Breuza et al. (Breuza et al 2004) analyzed the protein composition of the ER-Golgi Intermediate Compartment (ERGIC) isolated from HepG2 hepatoma cell line. These cells were treated with Brefeldin A, an inhibitor of protein transport, causing the Golgi apparatus to fuse with the ER. Brefeldin A specifically inhibits the GTP exchange factor for the GTPase ARF (ADP ribosylation factor) which inhibits protein transport through the Golgi. After treatment with Brefeldin A, an ERGIC compartment resistant to the drug remains behind. This compartment was isolated by subcellular fractionation on Nycodenz gradients followed by immunoprecipitations using magnetic beads coupled to an antibody to the KDEL receptor. Twenty-four proteins were identified by MALDI time of flight and nanospray MS/MS (Breuza et al 2004). This study showed that the protein ERGIC-32, which shuttles between the ER and the Golgi, forms a complex with ERV46 and a previously uncharacterized protein SURF4 was identified as a cargo receptor (Breuza et al 2004).

4.6.6 Golgi

Four proteomics studies of the Golgi have been performed; two analyses used 2D gels, and the other two involved 1D SDS-PAGE and MUDPIT (Bell et al 2001, Taylor et al 2000, Wu et al 2004, Wu et al 2000b). These studies used a highly enriched Golgi fraction isolated by different methods of subcellular fractionation. The study by Bell et al. used the detergent Triton-X 114 to enrich for transmembrane containing proteins and separated the proteins using 1D SDS-PAGE gels. Using MALDI mass spectrometry and Edman sequencing, they uncovered 81 proteins. They also discovered and localized a protein they named GPP34 which was also uncovered by Taylor et al. (Taylor et al 2000) and

Wu et al. (Wu et al 2000a, Wu et al 2000b). This protein was named GMx33 (Taylor et al 2000, Wu et al 2004, Wu et al 2000a, Wu et al 2000b). In a more recent study of the Golgi using the MUDPIT approach, Wu et al. identified 421 proteins and 41 previously uncharacterized proteins. Furthermore, Wu et al. (Wu et al 2004) uncovered a novel post-translational modification, arginine dimethylation, in a subset of the Golgi and ER proteins identified in their study.

4.6.7 ER

The soluble luminal contents of the ER were analyzed in a study by Knoblach et al. (Knoblach et al 2003). They isolated ER from livers of Balb/C mice by subcellular fractionation and separated the proteins using 2D gels. Spots were excised and MALDI MS/MS was used to characterize the proteins in them. Of the 141 proteins, six previously uncharacterized proteins were identified including two new protein disulphide isomerases, ERp46 and Erp19. Both proteins contain thioredoxin motifs and were able to function as PDIs in yeast (Knoblach et al 2003).

4.6.8 Peroxisomes

Peroxisomes are ubiquitous organelles that produce hydrogen peroxide and are linked to several functions including fatty acid metabolism and plasmalogen synthesis. Marelli et al. (Marelli et al 2004) identified 70 out of 306 proteins with high probability of being peroxisomal proteins in *S. cerevisiae*. They delineated peroxisomal proteins from contaminants by using ICAT (Gygi et al 1999) to compare the relative abundance of identified proteins in an enriched vs. a crude contaminating fraction. The use of ICAT also served to reduce sample complexity (Gygi et al 1999). This study (Marelli et al 2004) led to insight into the regulation of peroxisome movement and location was made. Marelli et al. (Gygi et al 1999) identified the GTPase Rho1p on peroxisomal

membranes and showed that it is recruited to peroxisomes and interacts with the peroxisome membrane protein Pex25p. This was the first discovery of a link between peroxisomes and the cytoskeleton

4.6.9 Plasma membrane

One challenge for organellar proteomics is to characterize proteins on the cell surface within the context of disease. With this aim in mind, one of the most studied organelles by proteomics is the plasma membrane (Nielsen et al 2005, Nühse et al 2004 Sep, Tam et al 2004, Zhang et al 2003 Aug). An important breakthrough was made by Oh et al. (Oh et al 2004) in their proteomics analysis of the plasma membranes of lung endothelial cells isolated using the coated silica bead technology. Out of 2000 proteins identified, 2 were specific to lung endothelial cells. They also analyzed plasma membranes from lung endothelial cells of rats with breast adenocarcinoma. The comparison of the proteins between normal and diseased cells identified 12 proteins that were enriched in tumor epithelium. One of the proteins was annexin A1. Treatment of tumors in mice with antibodies targeted to annexin A1 resulted in tumor remission.

4.6.10 Proteomics of multiple organelles

Recently, there has been a shift towards comparative organelle studies in which multiple organelles are analyzed to gain insight into the relationship among the organelles under study. A study by Kislinger et al. (Kislinger et al 2006) identified proteins in four subcellular fractions (cytosol, microsomes, mitochondria and nuclei) from six organs by tandem mass spectrometry and compared protein expression in these organelles and tissues with mRNA expression. They assigned a subcellular location to 3274 of the 4768 proteins identified and determined tissue selectivity by comparing protein abundance with mRNA abundance derived from previous studies.

A study by Foster et al. (Foster et al 2006a) used protein correlation profiling to identify proteins in ten organelles of mouse liver including the ER and Golgi apparatus. This work extended a previous study that used the same method in its analysis of the mammalian centrosome (Andersen et al 2003). Protein correlation profiling involves tracking the abundance of peptides in all fractions of an analytical gradient. Distribution profiles of all identified proteins are compared to profiles of known marker proteins. Accordingly, protein distribution profiles that deviate from marker profiles were considered contaminants. In this study, Foster et al. (Foster et al 2006a) identified 1404 proteins with multiple locations assigned to 39% of the proteins.

Another study by Dunkley et al. (Dunkley et al 2006) used the localization of organelle proteins by isotope tagging technique (LOPIT) (Dunkley et al 2004) to map proteins to different subcompartments of the endomembrane system in the plant, *Arabidopsis thaliana*. In this approach, proteins were partially separated by centrifugation through density gradients and iTRAQ reagents were used to label proteins in different fractions of the gradient. A protein distribution profile was then determined by measuring the relative iTRAQ reporter ion intensities across the gradients. Localization was established by comparing all profiles to marker protein profiles using principal components analysis and partial least squares discriminant analysis. Using this approach, Dunkley et al. (Dunkley et al 2006) assigned 527 proteins to the ER, Golgi, PM, vacuolar membrane and mitochondria. They were also able to distinguish resident proteins from proteins trafficking through the secretory pathway.

Methods

Introduction

This section outlines the approach used for the proteomics analysis of the rough and smooth microsomes and Golgi apparatus. The multidisciplinary nature of proteomics bridges the fields of cell biology, protein chemistry, engineering and computer science. In general, a proteomics analysis involves multiple steps drawing from all of these disciplines. An organellar proteomics experiment begins with sample preparation which can involve subcellular fractionation and ends with a bioinformatics analysis of the data. Each step bears equal importance since the fidelity of a subsequent procedure relies on the previous one. For organellar proteomics, good quality subcellular fractions with minimal contamination are essential to achieve a comprehensive organellar proteome. Proper protein separation and mass spectrometry strategies ensure that the proteins present in the sample have a high probability of being identified. Furthermore, effective data collection and archiving enable current and future bioinformatics analyses. These steps as well as others are discussed in detail in the following sections.

Isolation of rough and smooth microsomes

Rough and smooth microsomes of the rat hepatic ER were isolated by subcellular fractionation. The isolation protocol was first used in a study by Paiement et al. (Paiement & Bergeron 1983) investigating the link between membrane fusion and N-linked glycosylation. The isolation of rough and smooth microsomes started with the homogenization of minced rat liver tissue using a Potter- Elvehjem homogenizer. Three biological replicates of the rough and smooth microsomes were made. For the preparation of the first biological replicate of the RM and SM fractions used in this study, 6 rats (200-225 g each) were used and produced 4 ml of RM at 19.8 mg/ml protein concentration and 6 ml of SM at 29.2 mg/ml.

For the second and third biological replicate, both were prepared in the same day. For the second replicate, 3 rats were used (200-225 g each) which generated 2 ml of RM at 26.5 mg/ml protein concentration and 3 ml of SM at 30 mg/ml protein concentration. For the third biological replicate, 3 rats were used (200-225 g each) generating 2 ml of RM at 30.5 mg/ml protein concentration and 3 ml of SM at 32.1 mg/ml protein concentration. Nuclei, mitochondria and total microsomal fractions were separated by successive centrifugation steps at increasing speeds. The first centrifugation step at 8,700 g for 13 minutes generated a nuclear fraction which was discarded. The remaining fraction was centrifuged at 43,000 g for 6 min and 40 seconds. This step generated a mitochondrial fraction which was also removed. Centrifugation of the remaining fraction at 111,000 g for 60 min yielded a pellet containing the total microsomes. The pellet was resuspended in 1.38 M sucrose, placed under a step-gradient of 1.0, 0.86, and 0.25 M sucrose and centrifuged at 300,000 X g, for 60 min. After centrifugation, a subfraction containing smooth microsomes and low density rough microsomes (1.17 g/cm^3) was distributed in the upper half of the 1.38 M sucrose step above the residual pellet. This fraction was washed once by centrifugation at 100,000 X g and resuspended in 0.25 M sucrose. The residual pellet containing the high density rough microsomes was recovered and resuspended in 0.25 M sucrose with 4 mM imidazole buffer, pH 7.4 and stored at -80°C .

Isolation of Golgi apparatus

The Golgi fraction was prepared exactly as per Dominguez et al. (Dominguez et al 1999) where it is referred to as the WNG fraction. Livers from three to 5 Sprague-Dawley rats weighing approximately 140 g each were used. Homogenates were prepared by gentle homogenization of finely minced rat liver, suspended in a 0.25M sucrose buffer with 5mM Tris-HCl (pH 7.4), 5 mM MgCl, 1 mM PMSF and 200 U/ml aprotinin, with the type B loose pestle of a Dounce homogenizer (12 strokes; Thomas

Scientific). The homogenates were filtered through two layers of cheese cloth and then incubated for two hours at 4°C. After incubation, a low-speed centrifugation at $400g_{max}$ for 5 minutes resulted in a supernatant (S1) and a pellet (P1) which was recovered and re-homogenized in half the original volume of buffer with five strokes of the type B pestle. The re-homogenized mixture underwent a second low speed centrifugation at $400g_{max}$ for 5 minutes, which produced a second supernatant (S2) and pellet (P2). S1 and S2 were combined and centrifuged for 10 minutes at $1,475g_{max}$. P2 was combined with P1 and resuspended in 1.22 M sucrose in STM buffer, containing the proteinase inhibitors PMSF (1 mM) and aprotinin (200 U/ml) at a concentration of 20% wt/vol original liver wet weight. A continuous gradient in STM buffer of 0.25–1.10 M sucrose was generated above the load zone. This was followed by centrifugation at $1,200 g_{av}$ for 30 min, followed by $83,000 g_{av}$ (SW27; Beckman Instruments, Inc.) for a period of 1 hour. After the centrifugation, the band approximately 1cm above the load zone was collected and the concentration adjusted to 0.4M sucrose in STM buffer. The recovered band was centrifuged at $1,475 g_{max}$ for 10 minutes to generate a pellet (P3). P3 was resuspended in 0.25 M sucrose in STM buffer followed by pelleting at $1,475 g_{max}$ for 10 minutes two times to increase enrichment of large membranes. The final pellet was resuspended in 0.25 M STM buffer and stored at -80° C until required for separation by SDS-PAGE. Three separate biological replicates of Golgi fraction were made.

Plasma Membrane Isolation

The homogenates used for isolation of the plasma membrane (PM) fraction were prepared by gentle homogenization of finely minced rat liver (from 1 Sprague-Dawley rat, ~200 g), suspended in a 0.25M sucrose buffer with 5mM Tris-HCl (pH 7.4), 5mM MgCl (STM), 1 mM PMSF and 200 U/ml aprotinin, with the type B loose pestle of a Dounce homogenizer (12 strokes; Thomas Scientific). The homogenates were filtered through

two layers of cheese cloth and then incubated on ice for 30 to 60 minutes. After incubation, a low-speed centrifugation at $400g_{max}$ for 5 minutes resulted in a supernatant (S1) and a pellet (P1) which was recovered and re-homogenized in half the original volume of buffer with five strokes of the type B pestle. The re-homogenized mixture underwent a second low speed centrifugation at $400g_{max}$ for 5 minutes, which produced a second supernatant (S2) and pellet (P2). S1 and S2 were combined and centrifuged for 10 minutes at $1,500g_{max}$, yielding S3 and P3. The supernatant (S3) was separated from the pellet (P3). Pellets P2 and P3 were combined and resuspended in 1.50 M buffered sucrose at a concentration of 10% wt/vol original liver wet weight. A continuous gradient in STM buffer of 0.25–1.42 M sucrose was generated above the load zone. This was followed by centrifugation at 25,000 rpm for 60 min for a period of 1 hour with no brake. After centrifugation, the band at the 1.42 M/1.0 M interface was collected and the sucrose concentration adjusted to 0.4 M. The recovered band was centrifuged at $1,575g_{max}$ for 10 min and then resuspended in homogenation buffer and stored at -80°C until required for SDS-PAGE,

Characterization of Isolated Organelles

After the isolation of the rough and smooth microsomes and Golgi apparatus, marker enzyme assays were carried out to estimate the enrichment of these organelles compared to the homogenate. The rationale behind the marker enzyme assay is that organelles have unique resident enzymes and the activity of a marker enzyme for a particular organelle indicates the degree of enrichment of that organelle. Moreover, the presence of enzyme activity associated with other organelles indicates the level of contamination. To measure the enrichment of the ER fractions, the activity of glucose-6-phosphatase was measured as previously done (Lavoie et al 1996). Similarly, for the Golgi fraction, galactosyl transferase activity was measured (Dominguez et al 1999).

The rough and smooth microsomes were ~ 4 times enriched compared to the homogenate and the Golgi fraction was ~110 times enriched. These results are discussed in more detail in *Results: Assessment of contamination of RM, SM and Golgi fractions*.

The isolated RM, SM and Golgi fractions were also characterized morphologically by electron microscopy (EM). This step was performed to verify the identity of the organelles and to identify contaminating organelles by their morphological characteristics. The isolated RM, SM and Golgi fractions were prepared for electron microscopy using the random sampling filtration apparatus of Baudhuin et al. (Baudhuin et al 1967) and has been described previously (Dominguez et al 1999). Membrane fractions were fixed at 4°C overnight with an equal volume of 5% glutaraldehyde in 100 mM sodium cacodylate buffer at pH 7.4 and then filtered on HA 0.45 µm filters (Millipore Corp, Billerica, MA). Post-fixation was done with reduced OsO₄ comprised of equal volumes of 4% OsO₄, 4% potassium ferrocyanide.

Electron micrographs of the RM, SM, and Golgi fractions that were analyzed by proteomics are shown in Figure 1. The RM fraction exhibited the characteristic rough appearance due to the ribosomes on the membranes; whereas the SM fraction is relatively free of ribosomes. However, ribosomes occasionally dot the SM membranes. The arrow in the SM micrograph points to the occasional ribosome studded profile. The Golgi fraction showed characteristic Golgi stacks.

Figure 1: EM characterization of random views of filtered preparations of isolated rough microsomes (RM), smooth microsomes (SM) and Golgi apparatus (G). The RM fraction shows ribosome-studded microsomal profiles. The SM fraction revealed a preponderance of smooth membranes with the occasional profile showing ribosome-studded microsomes (arrow). The arrows in the Golgi micrograph point to four separate Golgi stacks cut at different angles of section. Scale bar = 0.5 μ m.

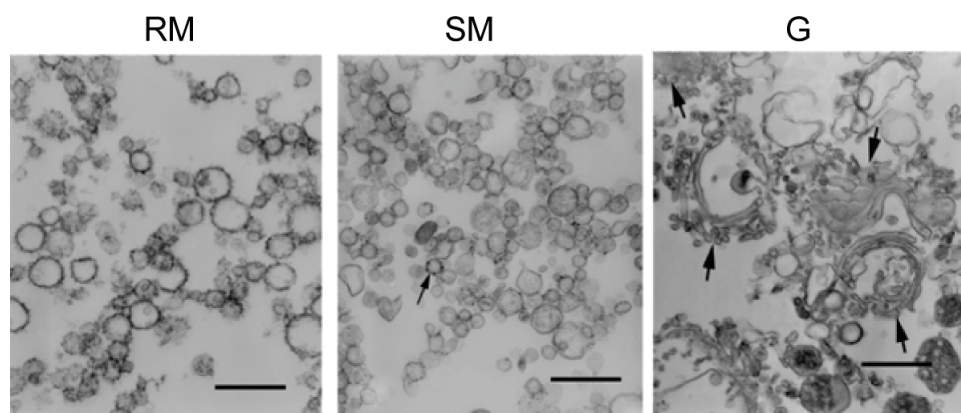


Figure 1

Biochemical subfractionation of the rough and smooth microsomes

One way to isolate proteins from subcellular fractions with similar physical characteristics (i.e. hydrophobic membrane proteins, soluble luminal proteins, soluble membrane associated cytosolic proteins) is by biochemically subfractionating the membranes using a detergent. This step also concentrates proteins of lower abundance in the total organellar preparations (i.e. RM and SM and Golgi fractions described previously).

Biochemical fractionation of RM and SM fractions was done with a high salt wash followed by Triton X-114 (TX-114) detergent phase extraction (Bordier 1981). The salt wash disrupts the interaction of cytosolic proteins associated with the membranes. TX-114 is a non-ionic detergent that forms mixed micelles with integral membrane proteins due to the replacement by the detergent of lipid molecules normally in contact with hydrophobic transmembrane segments. Hydrophilic proteins have minimal to no interaction with nonionic detergents (Bordier 1981) and are separated from the membrane proteins after an increase in temperature.

For salt wash treatment, RM and SM fractions were incubated at 1 $\mu\text{g}/\mu\text{L}$ in 3 mM imidazole buffer (pH 7.4) containing 0.25 M sucrose and 2 M KCl for 15 min on ice with agitation. Fractions were then centrifuged at 200,000 X g for 2 h. Next, the salt wash supernatant was mixed 9 to 1 with 100% trichloroacetic acid in acetone (100 g trichloroacetic acid in a final volume of 100 mL) containing 20 mM DTT and incubated at -20°C for 60 min. The precipitated proteins were collected by centrifugation, resuspended in acetone and incubated at -20°C overnight. For storage at -80°C , precipitated proteins were collected by centrifugation and the acetone was removed with a stream of nitrogen followed by sonication (two 2-3 sec bursts at 60%) assisted resuspension in distilled water.

For detergent treatment, the pelleted salt-washed microsomal fraction was treated with Triton X-114 according to a modified protocol of the Bordier procedure (Bordier 1981) to generate a soluble (aqueous phase), detergent soluble and detergent insoluble protein fractions. The TX-114 solution was prepared in the following manner. Triton X-114 was washed with butylated hydroxytoluene as follows: 40 g of Triton X-114 was mixed with 960 mL of 10 mM Tris-HCl, pH 7.4, containing 150 mM NaCl and 72.6 μ M butylated hydroxytoluene and stirred at 4°C for 6 h. The solution was then transferred to 1 L separatory funnels and incubated at 30°C overnight to effect phase separation. The lower detergent phase (approx. 400 mL) was collected while working at 30°C and repeatedly washed (3 times) with 600 mL of 72.6 μ M butylated hydroxytoluene in 10 mM Tris-HCl, pH 7.4, containing 150 mM NaCl by dissolution and stirring (6h) at 4°C until clear. The washed Triton X-114 was stored at 4°C.

For detergent phase extraction, the salt-washed pellets from RM and SM were resuspended in 3 volumes of 10 mM Tris-HCl pH 7.4, containing 150 mM NaCl. This preparation was then diluted with 1-volume of 40 mM Tris-HCl, pH 7.4, containing 600 mM NaCl plus 4% Triton X-114 to obtain a 10-fold excess of Triton to membrane protein to a final concentration of 1 μ g/ μ L. Mixtures were incubated on ice for 30 min. Centrifugation at 0°C (12,000 rpm, Beckman Ti60 rotor) of this suspension yielded a pellet (insoluble protein fraction) and a clear supernatant. To aid in the resolution of the aqueous and detergent phase proteins from the clear supernatant, a cushion of 1.5 % (w/v) sucrose, in 10 mM Tris-HCl, pH 7.4, 75 mM NaCl plus 0.06% Triton X-114 was used. The clear supernatant (at 4°C) was overlaid onto the sucrose cushion in a centrifuge tube. To effect phase separation (as evidenced by cloudiness), the tube was incubated at 30°C for 3 min. Centrifugation at room temperature yielded 3 phases (aqueous upper phase, detergent lower phase (oily droplet) and intermediate sucrose cushion).

Detergent phase proteins were extracted from the aqueous phase proteins 3 times. The protocol involved the following steps. In a second tube, fresh Triton X- 114 was added to the aqueous phase to yield 0.5% triton X-114. The cloudy suspension was clarified by incubation at 0°C and then layered onto the detergent phase/sucrose cushion previously isolated. The centrifuge tube was incubated at 30°C for phase separation (of the newly added solution) followed by centrifugation (as above) to remove the detergent phase from the aqueous phase and generated 3 layers (as above). The upper, aqueous and lower, detergent layers represent the aqueous and detergent phases. Aqueous phase proteins were recovered by trichloroacetic acid precipitation (as indicated above) and detergent phase proteins were recovered by precipitation with 9 volumes of ethanol/ether (4:1). Precipitated proteins were washed with acetone and any residual acetone was removed with a stream of nitrogen. The proteins were suspended by sonication (as above) in distilled water and stored at -80°C until required for separation by SDS-PAGE.

Protein Separation and in-gel trypsin digestion

Organelle fractions were solubilized in SDS or with additional 4 M urea and resolved on 7-15% gradient gels containing 4 M urea. This was followed by staining with Coomassie Brilliant blue G. For trypsinization and peptide extraction, whole gels for the RM and SM were divided into 90 - 93 bands. The Golgi gels were divided into ~70 bands. Treatments of the bands (destaining, reduction and alkylation, trypsinization) were performed robotically in a 96 well plate format using a MassPrep Workstation (MicroMass, Manchester, U.K.).

Bands were first dehydrated in 50 ul of acetonitrile followed by destaining with 50 µL each of 100 mM (NH₄)₂CO₃ and acetonitrile for 10 minutes. Bands were then dehydrated by the addition of 50 ul of

acetonitrile for 10 minutes. For reduction of cysteines and alkylation, the destained gel slices were then treated for 30 min with 50 μ l of 10 mM dithiothreitol (reduction of cysteines) and treated for 20 min with 50 μ l of 55 mM iodoacetamide (alkylation). An additional round of $(\text{NH}_4)_2\text{CO}_3$ and acetonitrile washes was performed followed by gel extraction with acetonitrile at 37°C. The gel slices were then incubated with trypsin (Promega Sequencing Grade Modified Trypsin, Promega V5111) (6 ng/ μ l in 50 mM $(\text{NH}_4)_2\text{CO}_3$) for 5 h at 37°C and the peptides were first extracted in 1% formic acid/ 2% acetonitrile followed by two further extractions with additions of acetonitrile.

Mass Spectrometry

The extracted peptides from robotic trypsin digestion were resolved using a CapLC (Waters, Milford, USA) system and analyzed by mass spectrometry (MS) in positive ion mode using an upgraded (with embedded personal computer control and acquisition system (EPCAS)) quadrupole time of flight (QToF-2) mass spectrometer (Micromass, Manchester, U.K.). The ion source was a Micromass nano electrospray ionization source (nanoESI) source. Extracted peptides were injected (pump C) onto a trapping guard column (u-Precolumn cartridge filled with PepMap C18, 5 μ m, 100 angstrom, 300 μ m i.d. x 5 mm (LC Packings, Sunnyvale, CA)). The trapping guard column was connected inline via a Cheminert 10 port valve (VICI, Brockville, ON, Canada) to an analytical preconditioned (see below) PicoFrit® (New Objective, Woburn, MA) column (filled with BioBasic packing C18, 5 μ m, 300 angstrom, 75 μ m i.d. x 10 cm). Prior to elution of the peptides, the sample bound to the guard column was washed with aqueous 0.1% formic acid, at a flow rate of 30 μ L/min for 5 min using pump C, and the analytical column was pre-equilibrated with 5% solvent B (acetonitrile 0.1% formic acid). For gradient elution, the 1 μ L/min combined flow from pumps A (solvent A: aqueous 0.1% formic acid) and B (solvent B: acetonitrile 0.1% formic acid)

was reduced to ~200 nL/min by column splitting with a Valco Tee and fused silica (5 m, 0.75 μ m inner diameter). Electrospray ionization (ESI) from the fritted-tip, located about 1 cm in front of and about 0.5 cm off centre to the sampling cone of the mass spectrometer, was performed with the capillary voltage set at 2000 V, the cone at 45 V, and the extractor at 3V. The collision cell was set at 10 V as default setting. Ar pressure was 4.4×10^{-5} mbar. The source block temperature was 80 °C and the multi-channel plate detector set at 2300 V.

For peptide extracts from gel slices corresponding to apparent MW >200kDa or <30kDa, a 30 min gradient was employed, and for proteins with apparent MW between 30 kDa and 200 kDa a 60 min gradient was employed. Gradients (started with sample injection) for the 30 min. and 60 min. gradient are shown in Table 1.

PicoFrit® columns were preconditioned before adjusting the spray as follows: 95% solvent B for 30 min; sequentially by steps of 10% for 10 min to 25% B; held at 25% B for 30 min. To set the voltage for the best plume, the voltage was increased from zero to the optimal voltage. Solvent was then adjusted to 5% B and chromatographic performance of the trapping column as well as the analytical column was assessed by analysis of 2 μ L PepMix (Sigma, H2016) employing the 15 min gradient (5% B from 0 to 5 min; to 40% B from 5 to 10.7 min; to 70% B from 10.7 to 12.9 min; to 95% B from 12.9 to 15 min; at 95% B from 15 to 20 min; and to 5% B from 20 to 29 min). Typically an optimal voltage of 2000 V is obtained and in order to maintain a good plume, the voltage must be increased as the column ages. The requirement for column replacement is monitored, diagnostically by the capillary voltage and the column is replaced when the required voltage reaches 3000 V. Nitrogen is not needed for nebulization because of low flow rates (200 nL/min) and column tip inner diameter (15 μ m). To accommodate the PicoFrit®

column, the QToF-2 was custom adapted as previously described (Blondeau et al., 2004). Briefly, the customization was as follows: the Micromass nanoflow probe was gutted and replaced with a Pasteur pipette that was fixed in place by hot melt glue. The pipette was cut such that 5 mm protruded from the housing near the Z-spray sampling cone. The PicoFrit® column was introduced from the forward end and was fixed in place with hot melt glue such that ~6 mm extended from the end of the pipette. The inlet end of the fused silica column was cut ~3 cm from the packing and connected to the solvent line via a stainless steel Valco zero dead volume connector. For operation, the dead volume connector was connected to the capillary power supply.

For MS analysis of biological samples, the mass spectrometer was operated in the Data Directed Analysis mode, with the threshold set to 6, and with up to 4 of the most intense doubly or triply charged precursor ions automatically selected for up to 5 fragmentation scans of 1 sec. Doubly or triply charged ions were targeted for fragmentation because this corresponds to the most likely charge state of tryptic peptides at low pH (0.1% formic acid). Survey scans of 1 sec were recorded from 350 to 1600 m/z with an interscan time of 0.1 sec and tandem MS scans of 1 sec. Tandem MS scans were collected sequentially for the selected precursor ions and were recorded from 50 to 2000 m/z. After selection and fragmentation, precursor ions were excluded from repeated selection for 60 sec after the end of the corresponding fragmentation duty cycle. Collisions energies were preprogrammed as follows: for doubly charged ions between 400-653 m/z, 653-740 m/z, 740-820 m/z, 820-1200 m/z, and 1200-1600 m/z, the energies were 25 V, 26 V, 28 V, 32 V and 55 V, respectively. For triply charge ions between 435-547 m/z, 547-605 m/z, 605-950 m/z and 950-1600 m/z, the energies were 14 V, 19 V, 24 V and 35 V, respectively. QToF calibration employed direct infusion of 500 of Glu-Fibrinopeptide (Sigma, F3261) from a gold-plated glass capillary, with

Table 1: Concentration of Solvent B for 30 min and 60 min gradient for peptide elution

30 min gradient	60 min gradient
5% B from 0 to 5 min	5% B from 0 to 5 min
40% B from 5 to 25 min	40% B from 5 to 45 min
70% B from 25 to 30 min	70% B from 45 to 53 min
95% B from 30 to 35 min	95% B from 53 to 58 min
95% B from 35 to 42 min	95% B from 58 to 60 min
5% B from 42 to 47 min	5% B from 60 to 65 min

collision energy set at 30 eV and the following y-ions: 175.1195, 246.1566, 333.1887, 480.2570, 627.3257, 684.3469, 813.3895, 942.4321, 1056.4750, 1171.5020, and 1285.5449 m/z. Calibration was updated when the temperature of the time of flight tube changed by greater than 0.5 °C. This temperature was monitored continuously via an insulated thermocouple taped to the flight tube.

Data processing

The raw data generated by the LC-QToF MS/tandem MS were transferred to a 40 terabyte server and automatically processed in a pipeline format (Kearney et al 2003). First, the raw data were processed to generate a peaklist of all tandem MS by employing Distiller (Matrix Science, <http://www.matrixscience.com/distiller.html>). Peaklists were searched using the Mascot Cluster (Matrix Science, <http://matrixscience.com/cluster.html>). The Mascot (Perkins et al 1999) search results were parsed into CellMapBase, our in-house relational database (Bencsath-Makkai et al 2003a, Bencsath-Makkai et al 2003b). Peptides were grouped to present a minimum set of protein identifications (Kearney et al 2005). Only peptides with less than 5% probability of being an incorrect assignment as determined by Mascot (Perkins et al 1999) were used for protein identifications. These peptides had Mascot scores greater than the Mascot calculated ID score for the peptides.

Peaklist Generation

For the generation of the peaklists, Distiller version 2.0.0 was used with the following peak detection parameters: minimum interaction 500; correlation threshold 0.7; minimum peak 50 m/z; maximum peak 100,000 m/z; minimum S/N 2; minimum peak width 0.01; maximum peak width 1; expected peak width 0.1; and maximum allowed precursor difference 3 Da. Baseline correction and reject width outliers were activated and re-gridding was done with a value of 20 data point per Da.

Mascot

The concatenated peaklist was searched against a copy of the National Center for Biotechnology Information non-redundant database (<ftp://ftp.ncbi.nih.gov/blast/db/FASTA/nr.gz>) (release: NCBI nrdb March 18, 2004) by employing Mascot Cluster version 1.9.03 with the following parameters specified: trypsin; 1 missed cleavage; fixed carbamidomethyl alkylation of cysteines; variable oxidation of methionines; 0.5 mass unit tolerances on parent and fragment ions; monoisotopic; limited to the *Rattus* taxonomy (30949 sequences). The false positive rate was found to be ~1.5% by repeating the search analysis, as above, against a randomized copy of the March 18, 2004 database.

Grouping

All protein identifications were made using peptides assigned by Mascot with less than 5% probability of being an incorrect assignment (false positive rate ~ 1.5% estimated by searching a randomized copy of the database). For generation of the minimum list of proteins, protein identifications were grouped based on common sets of peptides. This step was necessary to eliminate redundant identifications of the same gene sequence that arise due to homologous sequences, truncated or partial sequences, alternatively spliced proteins, strain-specific allelic variation or redundant assignments of tandem MS. Proteins within a group were called hits. Peptides assigned to hits may be unique or shared. Unique peptides were distinct peptide sequences that occurred only in one particular group. Shared peptides occurred in hits that fell into two or more groups. This scenario came up in proteins with high sequence similarity such as members of protein families, allelic isoforms, homologous sequences, truncated or partial sequences, alternatively spliced proteins, strain-specific allelic variation or redundant assignments of tandem MS. The top hit was a sequence that accounted for all

peptides assigned within a group. Often there was more than one top hit. The grouping algorithm randomly chose a representative protein sequence from the top hit(s). Only groups with at least one unique peptide were considered in this study. Therefore, in this study, the word protein means protein group and the accession number provided (usually an NCBI gi number) is for the representative top hit of a group.

Annotation

The non-redundant list of proteins identified in this study was manually annotated by literature search via the NCBI gi number and cross-referencing to GO annotations (Ashburner et al 2000) to categorize all identifications into 1 of 23 functional categories (Table 2). These categories reflected functions specific to the ER and Golgi apparatus and were necessary for us to organize the data in an understandable way. Proteins were also annotated for transmembrane segments and signal peptides (including insertion via lipid anchors) using TMHMM (Sonnhammer et al 1998) and SignalP (Bendtsen et al 2004), respectively. This was done to aid in distinguishing resident proteins (many would have a signal peptide) from non-residents or contaminants. Proteins were also assigned a protein name. This was done for two reasons. First, some of the NCBI descriptions were uninformative even for well-known proteins. An example is the protein with the NCBI description “BWK4,” which has since been removed from the database. A BLASTp analysis (Altschul et al 1990, Li et al 2002) revealed that this sequence was in fact, the protein disulphide isomerase, ERp44. Therefore, this protein was renamed “ERp44.” The second reason for assigning names to proteins was to have the ability to “collapse” proteins with greater than 90% similarity over the length of the protein. This step followed the rationale set forth by the UniREF90 database (Suzek et al 2007), in which proteins in the entire UniProt database are collapsed based on 90% sequence identity.

Several curation related difficulties were experienced, such as: i) non-descriptive names, ii) fused gene predictions, iii) incorrect gene predictions, iv) missing protein sequences and v) allelic isoforms. Examples for each case follow:

1. Vague or indecipherable names: The NCBI description “Similar to protein X” could mean either that it was a rat version of protein X, which was originally identified in mouse or that there was a 40% similarity to protein X, but it was not a rat homologue. We chose to use the “similar to” for proteins with similarity but that were not orthologs.
2. Fused genes: Peptides that were assigned to the protein represented by gi number 34879705 could be sorted into 2 groups based on BLASTp assignment to either ABO-family member 5 or to stomatin. Further analysis revealed that the two genes had been improperly fused in the rat database. Modifications were made to the in-house database.
3. Incorrect gene predictions: Proteins that should be nearly identical to each other displayed approximately only 65% identity, due to different lengths of intronic sequences due to incorrect gene prediction and/or editing of the rat genome. For example, the protein mannosidase II was split into two sequences. Exons that should have been assigned to one protein were assigned to two different sequences. Some exons were assigned to one sequence, whereas the other exons were assigned to another sequence. Each sequence showed homology with the NCBI non-redundant database sequence for mannosidase II, but they did not show any homology with each other.

4. Missing protein sequences: We knew from literature and experimental evidence that the protein SRP receptor β was in our sample but was not identified by limiting the search to the *Rattus* taxonomy. Its presence was confirmed by expanding the Mascot search to include mouse sequences which reflects the expected sequence conservation between these two species.
5. Allelic isoforms: Because the Sprague- Dawley rat strain is out-bred, the presence of allelic isoforms is possible and was detectable. Allelic isoforms are different sequences derived from the same gene that contain single nucleotide polymorphisms (SNPs). In the case of allelic isoforms, we added their peptides together. To do this, we chose to assign the same protein name to allelic protein pairs.

These curation steps were incorporated into our in-house database, CellMapBase and define a method currently in use for analyzing proteomics data (Au et al 2007).

Protein Quantitation

For quantification of proteins, redundant peptide counting or spectral counting (Blondeau et al 2004, Liu et al 2004) was employed. We prefer the term, redundant peptide counting, to spectral counting because redundant peptide counting emphasizes that the mass spectrometer repeatedly measured spectra assigned to peptides (many mass spectra remain unassigned). Therefore, the term, redundant peptide counting, will be used throughout this thesis. Redundant peptides are the number of mass spectra observed and assigned to peptide sequences for a given protein. In using the redundant peptide counting approach, the total number of redundant peptides assigned to a protein is added together and

this value is used as a measure of the protein's abundance, as represented by the following equation:

$$P_i = \sum_1^k 1$$

where P_i = redundant peptide counts for any given protein, i ; k is the number of times the peptide is observed (or the number of spectra).

Furthermore, for a proteomics sample, the total redundant peptide count for a sample is represented by the following equation:

$$R = \sum_{i=1}^n P_i$$

where R = total redundant peptide counts for a sample, P_i = the number of redundant peptides for protein i , and n is the number of proteins identified in a sample.

It has been demonstrated that the relative abundance of different proteins can be deduced by comparing their redundant peptide counts (Blondeau et al 2004, Kislinger et al 2006, Liu et al 2004, Pang et al 2002). Fifty-nine percent of all identified proteins in the three replicates of the RM, SM and Golgi fractions were identified with 5 or more redundant peptides (Figure 2). This is the number used as a cut-off for quantitation in this thesis. A protein must have greater than or equal to 5 redundant peptides for quantitation.

Proteins identified in this study were described by 3 numbers: unique peptides, shared peptides and total peptides. Determining the total peptides for proteins with only unique peptides was simple since these peptides are only assigned to one protein. However, the total peptide count for proteins with shared peptides was a number derived from apportioning shared peptides based on the number of unique peptides

each protein possesses. This is described for two proteins, A and B, by the following equation:

$$\text{Total}_A = \text{Unique}_A + \text{Shared}_{A+B} * \text{Unique}_A / (\text{Unique}_A + \text{Unique}_B)$$

For example, rab1A and rab1B are two proteins with 91% sequence identity by BLAST. Both proteins were uniquely identified in the Golgi fraction with 2 unique peptides for rab1A and 3 unique peptides for rab1B. Both proteins also shared 3 peptides. Following the formula outlined above, rab1A would have 3.2 total peptides ($\text{total peptides}_{\text{rab1A}} = 2 + 3 * 2 / 5$) and rab1B has 4.8 total peptides ($\text{total peptides}_{\text{rab1B}} = 3 + 3 * 3 / 5$). This algorithm has the advantage of preserving the total peptide count except for cases where peptides are shared among proteins with no unique peptides. As an additional step, total peptides for each protein were normalized to the total number of redundant peptides observed in a sample to account for the variance in each biological replicate. Therefore, the total peptide count for a protein is divided by the total number of assigned peptides in a sample and by 100 resulting in % total peptides. Both total peptides and % total peptides are used in this thesis.

Since shared peptides are apportioned between proteins based on the fraction of unique peptides, one might postulate that a potential bias may exist for larger proteins. Take, for example, two proteins of different size that share peptides and have unique peptides distinguishing them. The bias comes into play when apportioning the shared peptides since the longer protein may have more unique peptides which would result in higher redundant peptide counts. Practically, this situation does not have a major effect since many of proteins that share peptides belong to the same family and are generally within the same size range (e.g. cytochrome P450s, rabs, glucuronosyl transferase, carboxylesterases).

Several studies have been done to validate redundant peptide counting. For instance, using this approach, Blondeau et al. (Blondeau et al 2004) demonstrated the 1:1 stoichiometry of clathrin heavy and light chain in brain derived clathrin coated vesicles. Furthermore, it also showed the lack of such stoichiometry for clathrin coated vesicles derived from liver (Girard et al 2005). That redundant peptide counting was able to detect the stoichiometry of a well-known biological structure validates the utility of the approach in a biological experiment. In another study, redundant peptide counts were able to detect the relative concentrations of 6 different proteins spiked into yeast cell lysates (Liu et al 2004). A comparison of redundant peptide counting and derived ion chromatograms, another common quantitation method, revealed that redundant peptide counting was more reproducible and exhibited a greater dynamic range (Zybailov et al 2005). Despite the large and growing body of work validating redundant peptide counting, experiments were done by us to test this approach for this study. One experiment compared redundant peptide counting to quantitative western blotting (Figure 3). This involved comparing the relative abundance of albumin detected by redundant peptide counting in the RM, SM and Golgi fractions to albumin detected by quantitative western blotting with I^{125} secondary antibody (Figure 3). Both methods showed that there was an enrichment of albumin in the Golgi fraction as compared to the ER fractions. Furthermore, we took part in a study conducted by the Association of Biomolecular Resource Facilities (ABRF) in 2006 (Turck et al 2007) which aimed to compare different approaches in estimating protein abundance. The aim of the study was to determine the relative protein abundance of 8 proteins in two mixtures. In this study (Turck et al 2007), we were the only participants to use redundant peptide counting (indicated as spectral counts). To evaluate each method of quantitation, the % error of ratio between the expected and observed ratio was calculated using the following formula:

Figure 2: Histogram of redundant peptide count distribution for proteins in the RM, SM and Golgi total fractions. Redundant peptide counts for proteins observed in one or all of the three replicates of each subcellular fraction were added together. The number of redundant peptides identifying proteins is indicated on the x-axis and the number of proteins per peptide count range is indicated by the y-axis.

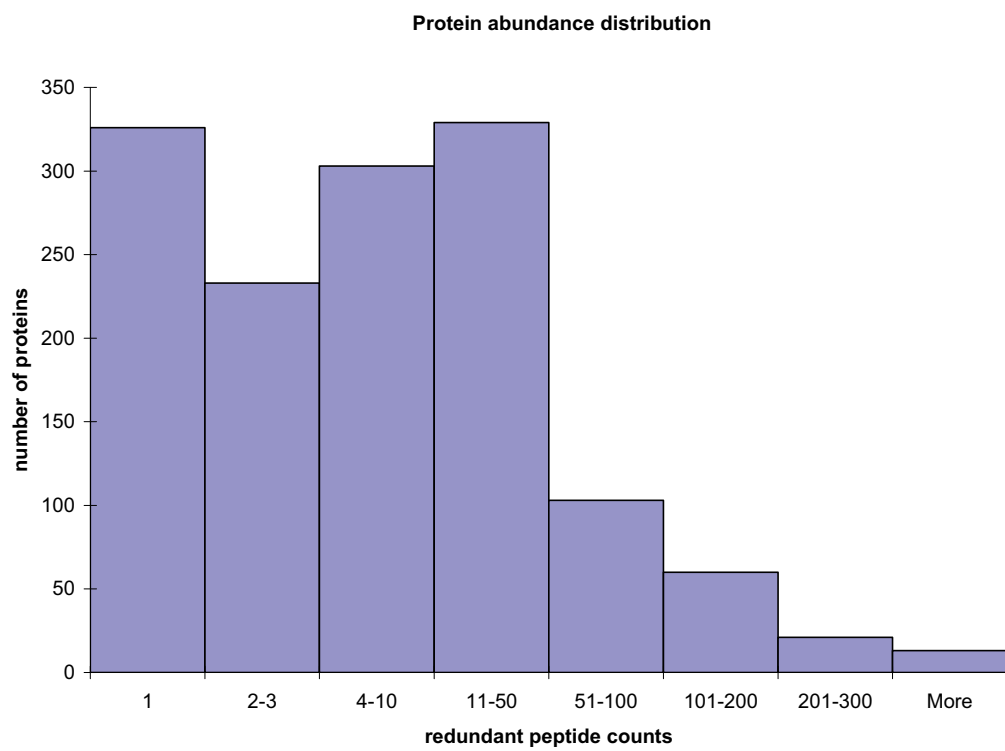


Figure 2

Figure 3: Comparison of redundant peptide counts with quantitative western blotting. The inset indicates the relative proportion of subcellular fractions within the linear response range for detecting albumin as visualized on X-ray films. The solid histograms represent the relative proportion of albumin antigenicity as deduced from γ counting (Bell et al., 2001) of the excised bands corresponding to albumin in RM, SM, and Golgi fractions. The white histograms represent peptide counts for albumin. In this and all other figures, error bars represent $\pm$ SD (n = 3) unless otherwise noted.

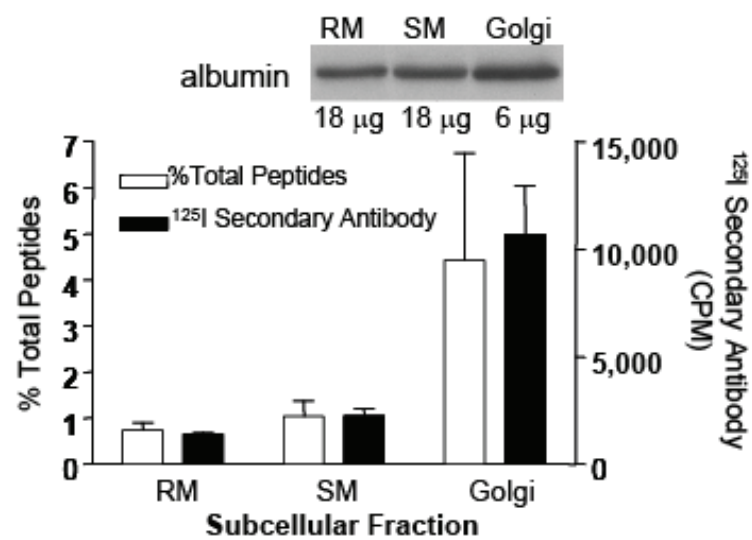


Figure 3

Table 2: Functional Categories Assigned to Proteins

Functional Category	Examples
Biosynthetic Cargo	Proteins that transit through the secretory pathway, e.g. albumin
Blood and other Cells Likely Contaminants (keratins)	Contaminants from sample preparation
Calcium Transport/Binding (Calcium Trans/Bind)	A key function of ER (Berridge 2002) (e.g. sarcoplasmic $\text{Ca}^{2+}/\text{Mg}^{2+}$ ATPase, Inositol 1,4,5 triphosphate receptor II)
Coat	COPII, COPI, clathrin coats
Cytoskeleton	Provide structure to ER and Golgi (Voeltz et al 2002) e.g. actin, microtubules
Detoxification (detox)	ER (e.g. cytochrome p450s)
GTPase	ER and Golgi (e.g. Rabs)
Lysosome Mitochondria Nucleus Peroxisome Plasma membrane	Organellar contaminants
Metabolism	e.g. glucose-6-phosphatase
Protein modification (Prot Mod)	Golgi glycosyltransferases
Protein Synthesis and Folding (Prot Syn/Fold)	Molecular chaperones (e.g. calnexin, BiP)
Proteasome/Ubiquitin	Proteasomal subunits
Signaling	Presenilin 1
Tethering Docking and Fusion (Teth/Dock/Fuse)	Rabs, Golgins
Traffic	p24s
Transcription	e.g. Sel1
Trypsin	Added to sample for peptide generation
Unknown	Proteins of unknown function

percent error of ratio = [(expected ratio – observed ratio)/expected ratio] x 100.

Of the 13 quantitative methods used in this study (Turck et al 2007), spectral counting produced one of the lowest % error or ratio at 50%. The results also revealed that this approach was as good as other methods of protein quantitation, including iTRAQ and derived ion chromatograms (Turck et al 2007).

Supplementary tables of proteins identified in the RM, SM and Golgi total and biochemical fractions

In proteomics, guidelines exist for the publication of protein and peptide identification results (Carr et al 2004), which address the issue of protein identifications that are based on a single peptide observation. Confidence in these identifications should be low since there is only one experimental observation to indicate that the protein is present in a sample. All protein identifications for the three replicates of the RM, SM and Golgi fraction and the biochemical subfractions of the RM and SM are indicated in table S1A. Single peptide identifications are indicated in table S1B. Table S1A and S1B reflect what was assigned by Mascot (Perkins et al 1999) (95% confidence) as observed by the mass spectrometer. Presented are: NCBI description; calculated molecular weight (MW); NCBI gi number; CMBSEQID (CellMapBase sequence identifier, an in-house reference number to identify a particular, exact sequence of amino acids and cross-references these tables); number of unique peptides (assigned only to the identified protein); number of distinct peptides (includes peptides shared between proteins); and percent (%) sequence coverage. Database entries representing partial N-terminal protein sequences, typically identified by calculated MW <5 kDa, reveal overestimated sequence coverage. The protein identifications were submitted to the PRoteomics IDentifications database PRIDE (<http://www.ebi.ac.uk/pride/>)

and Tranche (<http://www.proteomecommons.org/dev/dfs/>) for public access. For proteins identified by a single peptide in table S1B, Carr et al (Carr et al 2004) outlined several criteria for publication. These criteria are meant to assist other researchers to assess the quality of the peptide and protein identification. The following criteria are indicated in Carr et al. (Carr et al 2004) and are presented in table S1B:

1. To identify that a peptide was a tryptic peptide, the N-terminal flanking amino-acid corresponding to the amino acid (single letter amino acid abbreviation) in the cognate protein that is N-terminal to the assigned tryptic peptide is presented. START indicates that the peptide is the N-terminal tryptic peptide. M indicates that the initiator methionine has been removed and K or R indicate the presence of a lysine or arginine at the beginning of the tryptic peptide.
2. Peptide sequence
3. To identify that the peptide was a tryptic peptide, the C-terminal flanking amino acid is also presented. END indicates the C-terminal tryptic peptide. K or R indicates the presence of a lysine or arginine at the end of the tryptic peptide.
4. m/z value in Thomsons (Th) corresponds to the ion that was selected for tandem MS.
5. Charge corresponds to the charge state of the ion fragmented
6. Experimental peptide mass in Daltons (Da) corresponds to mass of the peptide as calculated from the m/z value and experimental charge of the ion fragmented
calculated peptide mass in Daltons corresponds to the mass of the assigned peptide as determined from the assigned peptide sequence
7. Delta value corresponds to the difference between the experimental and calculated peptide mass

8. The score from the database search engine used. MASCOT Score corresponds to the score assigned by the tandem MS database search program Mascot (<http://www.matrixscience.com>)
9. The cut-off for confidence in a peptide identification. Identity Score (ID Score) corresponds to the Mascot score that corresponds to assignment at 95% confidence (Perkins et al., 1999).

Table S1C reflects the curation of protein identifications into functional categories (Table 2), the assignment of protein names (Assigned_Prot_Name) (section 1.7.4 Annotation). A bioinformatics prediction for signal peptides was done since proteins moving through the secretory pathway have cleavable signal sequences. Transmembrane domain predictions were also performed to get an indication of the number of predicted membrane proteins and to compare the predictions with biochemical subfractionation. The table contains the following columns:

1. Assigned Prot_Name
2. Functional category
3. NCBI Description; calculated molecular weight (MW)
4. gi number
5. CMBSEQID
6. Membrane status as assigned based on TMHMM (Sonnhammer et al 1998) and/or literature search
7. Signal type as assigned by SignalP prediction (Bendtsen et al 2004)
8. Transmembrane domain (TMD) prediction (TMHMM, (Sonnhammer et al 1998) including starting amino acid
9. Length of the transmembrane segment (TMS)
10. Direction relative to the cytoplasm (IN = cytoplasmic)

11. UNIREF100 identifier (Apweiler et al 2004)
12. Refseq an NCBI identifier (Pruitt et al 2005).

Table S1D contains the peptide statistics for proteins by assigned protein name. Proteins with the same assigned protein name in table S1C have been grouped together and the redundant peptide counts (Total Peptides) and normalized redundant peptide counts (% Total Peptides) were added together. Table S2A contains the results of the hierarchical clustering of the mean % total peptide counts for the 3 biological replicates of the RM, SM and Golgi total fractions. Table S2B contains the results of the hierarchical clustering for the 3 replicates of the biochemical subfractionation for the RM and SM fractions. Contaminants were removed prior to clustering for both analyses. Results in tables S2A and S2B are discussed in *Results: Subcellular localization of proteins by Proteomics* and *Results: Biochemical Subfractionation of RM and SM fractions*, respectively. Table S3 contains the 43 new proteins identified in the Golgi biochemical subfractions which are discussed in *Results: Biochemical subfractionation of RM and SM fractions*. Table S4 contains the results of a comparison of Golgi proteins identified in the Foster et al. (Foster et al 2006a) study with Golgi proteins identified in the Golgi fraction. These results are discussed in *Discussion: Completeness of protein identifications in the RM, SM and Golgi fractions*. These tables are also available as a supplement to Gilchrist et al. (Gilchrist et al 2006).

Antibodies

Anti-calnexin antibodies were raised against amino acids 555-573 of canine calnexin (Ou et al 1993). Anti-ribophorin I was provided by Dr. G Kreibich (NYU Medical Center). Anti-mannosidase II was provided by Dr. M Farquhar (UDSD School of Medicine). Anti-tom20 was provided by Dr. G Shore (McGill University). Anti- α membrin was purchased from Stressgen (Ann Arbor, MI).

Principal Coordinates Analysis

In *Results: Assessment of Contamination of RM, SM and Golgi Fractions*, principal coordinates analysis (PCO) using Matlab was used to determine if the RM, SM and Golgi fractions are distinct from one another. The goal of the analysis was to reduce the 9 x 2000 matrix, X (3 biological replicates each for the RM, SM and Golgi with ca. 2000 points consisting of the % total peptide counts for the identified proteins), to a 9 x 2 dimensional space, Y. First, an n x n pairwise distance matrix, D, is calculated for X using the pdist function in Matlab with Euclidean distance specified as the distance measure. The Matlab function, cmdscale, takes D as its input to generate the 2 dimensional coordinates in Y. A graph of Y shows the scatter of points representing the 3 organelles in two dimensional space. Ideally, the three organelles would occupy 3 separate areas on the graph indicating that they are different entities.

Immunolabeling

For Western blotting, proteins in each fraction were separated on a 10% gel by SDS-PAGE, and transferred to nitrocellulose electrophoretically for 2 h at 400 mA at 15°C, employing a Trans-Blot® Electrophoretic Transfer Cell (BIO-RAD, Hercules, CA). The blots were blocked with 5% skim milk in 0.1% Tween 20® buffer and PBS (pH 7.4) and then incubated overnight at 4 °C with the following primary antibodies and dilutions: 1:5000 dilution for anti-calnexin; 1:5000 dilution for anti-ribophorin I; 1/1000 for anti-membrin; 1/1000 for anti-integrin β 1, 1/2000 for anti-mannosidase II and 1/5000 dilution for anti-tom20. Anti-integrin β 1 and anti- α -membrin were mouse polyclonal antibodies and the rest were rabbit polyclonal antibodies. After each antibody reaction, the blots were washed with 0.5% skim milk in 0.1% Tween 20® buffer and PBS (pH 7.4). Bands were visualized by chemiluminescence using the Western Lighting Chemiluminescence reagent (Perkin Elmer Life Sciences, Waltham, MA).

Marker Enzyme Assay

To test for glucose-6-phosphatase activity, the following protocol was used. In three separate tubes (one blank, 2 for testing) for each sample, 200 ml sodium cacodylate pH 6.5, 66.7 ml 0.15 M glucose-6-phosphatase, 183.3 ml H₂O was added and preincubated at 37 °C for 5 min. After incubation, 50 ml of membranes without phosphatases inhibitor was added to the tube. After 10 minutes incubation, the reaction was stopped by adding 0.33 ml of 10% trichloroacetic acid. Membranes were added to the blank after addition of trichloroacetic acid and incubated on ice for 10 minutes. After incubation, samples were centrifuged in a microfuge for 5 min. 400 ml of the samples were tested for phosphate content by the Ames and Dubin method (Ames & Dubin 1960). One ml of the Ames-Dubin mixture (1 part 10% ascorbic acid, 6 parts 0.42% ammonium molybdate in 1N H₂SO₄) was added to each sample in a glass tube and incubated at 45 °C for 20 minutes. The absorbance was read against the blank at 770 nm wavelength.

For the 5' nucleotidase enzyme assay, three separate tubes were used for each sample. In two of the tubes, 0.05 ml of 0.5 M Tris HCl (pH 8.5), 0.05 ml of 0.1 M MgCl₂, 0.05 ml of 1% Triton X-100 and 0.05 ml of the membrane prep without phosphatase inhibitors was added. Membranes were not added to the blank tube. At 30 sec intervals, 0.1 ml of 0.05M AMP (20.4 mg/ml) was added to each tube and incubated at 37 °C for 20 minutes in a dry bath. At the same interval, 300 ul of 25% trichloroacetic acid was added to stop the reaction. After the reaction was stopped, membrane was added to the blank tubes. Phosphate content was determined by the Ames and Dubin method (Ames & Dubin 1960). Galactosyl transferase activity was assayed according to Bergeron et al. (Bergeron et al 1982).

Hierarchical Clustering

Hierarchical clustering is discussed in *Results: Subcellular Localization of Proteins by Proteomics*. This method progressively calculates the pairwise distances between objects, which, in this case, are the protein localization profiles and creates a similarity matrix among proteins. For example, if there are 20 objects under consideration, the distances between each pair among the 20 objects are calculated and the closest or most similar pair of objects is merged together. The merged pair forms a new cluster and is considered a single object for the next round of pairwise distance calculations. This process continues until there is only 1 cluster left containing 20 objects. A correlation coefficient is calculated for each cluster (with 2 or more objects) which ranges from -1 to 1, with 1 meaning they are identical and -1 meaning that they are perfect opposites.

Cluster 3.0 (<http://bonsai.ims.u-tokyo.ac.jp/~mdehoon/software/cluster/>) and JAVA Treeview 1.6 (<http://jtreeview.sourceforge.net/>) programs were used for hierarchical clustering and graphical representation of protein expression data, respectively (de Hoon et al 2004, Eisen et al 1998). Hierarchical clustering of genes was performed using an uncentered Pearson correlation distance metric and average linkage aggregation. Selected clusters had correlation coefficients > 0.9 as determined by Cluster 3.0. The png images produced by TreeView were edited using the Adobe Illustrator software (San Jose, CA), by scaling the list of proteins, protein arrays, and the dendrogram for visualization. Original alignments between the elements in the original png files were maintained. All other data analysis and manipulation was done using Matlab and Excel.

Antibodies and Light Microscopy

Antibodies to ERp44 were a gift of Dr. R. Scherer, Albert Einstein College of Medicine and discussed in Wang et al. (Wang et al 2006). HepG2 cells cultured on coverslips were fixed with methanol for 5 min at -20°C. The fixed and permeabilized cells were blocked in 0.1% bovine serum albumin (BSA) in PIPES buffer, pH 7.5 with 150 mM NaCl for 30 min at room temperature and then incubated with the antibody solution (dilution 1:200) in the blocking buffer for 30 min at room temperature. Cells were washed three times with blocking buffer (for 5 min each) and then incubated with Alexa 594-conjugated anti-rabbit IgG antibody (Molecular Probes, Invitrogen, USA) for 30 min at room temperature. The cells were again washed three times with blocking buffer (5 min each), and the coverslips were mounted onto ProLong Gold (Invitrogen, USA). Images were taken with an inverted confocal laser scanning microscope (Zeiss LSM 510 META) with a 63× oil lens and processed by Adobe Photoshop version 7.0.

YFP visualization and immunofluorescence

For YFP visualization, HeLa cells were cultured on coverslips and transfected with YFP-tagged constructs. HeLa cells were selected for simplicity of morphology visualization. Cells were fixed with methanol for 5 min at 20°C, 36 hours after transfection. The fixed and permeabilized cells were blocked in 1% bovine serum albumin (BSA) in PIPES pH 7.5 w/ 150 mM NaCl buffer for 30 min and then incubated with anti-calnexin antibody in the blocking buffer for 1 hour at room temperature. Cells were washed 3 x 5 min. with blocking buffer and then incubated with Alexa 633-conjugated anti-Rabbit IgG antibody (Molecular Probes, Eugene, OR) for 30 min. at room temperature. The cells were again washed 3 x 5 min with blocking buffer, and the coverslips were mounted onto ProLong Gold (Invitrogen). Images were taken with an inverted confocal laser scanning

microscopy (Zeiss LSM 510 META) with a 63× oil objective lens and processed by LSM image Browser (Zeiss).

Bioinformatics Predictions of Transmembrane Segments and Signal Peptides

Transmembrane segment and signal peptide prediction was done using TMHMM 2.0 and SignalP, respectively, as a stand alone software package on a UNIX platform.

BLAST Analysis

FASTA formatted sequences for the proteins identified in the RM, SM and Golgi fractions were extracted from the NCBI non-redundant database. HERA (Scott et al 2004) sequences were provided by M. Scott. All other sequences were accessed as indicated in the publications (Huh et al 2003, Wiwatwattana & Kumar 2005) or directly from tables in the publications (Foster et al 2006a, Knoblach et al 2003, O'Brien et al 2005, Wu et al 2004). Sequence comparisons were done using the stand-alone BLAST application (http://www.ncbi.nlm.nih.gov/staff/tao/URLAPI/pc_setup.html#2). Proteins from each database (HERA, OrganelleDB) or study (Foster et al, Knoblach et al, O'Brien et al., Wu et al., Hugh et al. and Wiwatwattana et al.) were aligned pairwise with proteins identified in the RM and SM or Golgi fraction using BLASTp. The e-value was set at e^{-15} . For proteins that did not match, a random set of alignments were verified manually to minimize false negatives.

Characterization of Proteins of Unknown Function by Bioinformatics

Previously uncharacterized proteins were identified in the proteomics results for the RM, SM and Golgi fractions by their associated NCBI descriptions. These descriptions were generally uninformative and could include the words “hypothetical, similar to, RIKEN.” The NCBI gi

numbers for these proteins were compiled into a list which was used to retrieve protein sequences using the Batch Entrez (<http://www.ncbi.nlm.nih.gov/entrez/batchentrez.cgi?db=Protein>) feature of NCBI (www.ncbi.nlm.nih.gov). To confirm the unknown function status of these proteins, their sequences were compared using BLAST (Altschul et al 1990) to the NCBI non-redundant protein database. If a protein displayed significant similarity to another protein with a known function (% identity > 80% to mammalian proteins), it was considered a characterized protein and removed from the list. The remaining protein sequences for uncharacterized proteins were then submitted to the TMHMM (Sonnhammer et al 1998) and SignalP (Bendtsen et al 2004) web servers for transmembrane segment and signal peptide predictions. For protein domain predictions, sequences were submitted to InterProScan (Zdobnov & Apweiler 2001) in batch mode. Protein domain predictions were also obtained using CD-Search (Marchler-Bauer & Bryant 2004).

Selection of proteins of unknown function for YFP localization

TMHMM and SignalP as well as biochemical subfractionation results guided the selection of uncharacterized proteins for further validation by YFP localization and functional studies (M. Jain, personal communication). The majority of proteins selected were single spanning membrane proteins with large luminal domains. Bioinformatics predictions guided the initial selection and the predictions were validated by checking to see that the proteins were identified in the detergent fractions by proteomics. For the majority of the uncharacterized proteins selected for validation, the bioinformatics and biochemical subfractionation results agreed.

Sapreticulin Antibody

A synthetic peptide for the sapreticulin antibody was synthesized and purified (> 85%) as described previously (Ou et al., 1995) by the

Sheldon Biotechnology Center, McGill University. The sequence was KRTDLC DHALHRS which corresponds to amino acids 166-178 in the saposin B domain containing protein, which we named sapreticulin. The peptide sequence was searched by BLASTP (Altschul et al., 1990) against the NCBI nr protein database which confirmed that the sequence was not present in any other protein. An N-terminal cysteine was added to the protein which was then conjugated to KLH as described by the supplier (Pierce, Rockford, IL). Antibodies were raised to this KLH conjugated peptide as described by Ou et al. (Ou et al., 1995). HepG2 cells cultured on coverslips were fixed with methanol for 5 min at -20°C. The fixed and permeabilized cells were blocked in 0.1% bovine serum albumin (BSA) in PIPES pH 7.5 w/ 150 mM NaCl buffer for 30 min at room temperature and then incubated with the antibody solution (dilution 1:200) in blocking buffer for 30 min at room temperature. Cells were washed three times with blocking buffer (for 5 min each) and then incubated with Alexa 594-conjugated anti-rabbit IgG antibody (Molecular Probes, Invitrogen, USA) for 30 min at room temperature. The cells were again washed three times with blocking buffer (5 min each), and coverslips were mounted onto ProLong Gold (Invitrogen, USA). Images were taken with an inverted confocal laser scanning microscope (Zeiss LSM 510 META) with a 63× oil lens and processed by Adobe Photoshop version 7.0.

Results

Assessment of contamination of the RM, SM and Golgi fractions

Organelle isolation by subcellular fractionation is limited by contamination from other organelles of the cell. This section describes how the results of the proteomics analysis of the RM, SM and Golgi fractions are used to assess their levels of contamination. The results of the proteomic approach are compared to other ways to characterize the degree of contamination in these fractions, namely, marker enzyme assays, electron microscopy and western blotting for marker proteins.

Organellar contamination

Proteins identified in the RM, SM and Golgi fraction were assigned to 23 different functional categories (Table 2). These categories include functions of the ER (metabolism, detoxification, protein synthesis and folding, calcium transport and binding), functions of the Golgi (protein modification, traffic), components of the secretory pathway (coats), functions of proteins involved in membrane fusion (tethering docking and fusion, GTPase), likely contaminants from sample preparation (likely contaminants and trypsin), cell types other than hepatocytes (blood and other cells), other functions or category of proteins associated with ER and Golgi (signaling, transcription, proteasome), proteins of the cytoskeleton (cytoskeleton), soluble and membrane proteins that traffic through the secretory pathway (biosynthetic cargo), proteins of unknown function (unknown) and other organelles considered to be a source of contamination (mitochondria, nucleus, peroxisome, lysosome and plasma membrane). Redundant peptide counts were used to quantify the abundance of proteins identified in these fractions (Blondeau et al 2004, Cox et al 2005, Gao et al 2005, Gao et al 2003, Girard et al 2005, Liu et al 2004, Old et al 2005, Pang et al 2002, Qian et al 2005, Rappsilber et al

2002, Zybaïlov et al 2005). To account for the variation in size and complexity of the organelles, redundant peptide counts for any protein were normalized to the total number of assigned peptides in the proteomics experiment. This number is expressed as “% total peptides.” The sum of the % total peptides observed for proteins classified into mitochondria, nucleus, peroxisome, lysosome and plasma membrane represents the amount of contamination by these organelles (Table 3).

$$C = \sum_{i=1}^n P_i$$

where C is the amount of contamination

P is the % total peptides for a given protein

n is the number of proteins in a particular functional category

Mitochondria contributed the most peptides, making it the major contaminant in the three fractions.

Cross-contamination between the ER and Golgi fractions

Figure 4 shows plots of peptide counts for marker proteins detected in each biological replicate of the RM, SM and Golgi fractions. Indicated on the y- axis as “% of peptides” are the % total peptide counts for the marker proteins normalized to the highest % total peptide count observed for a particular protein in any one biological replicate. The maximum peptide count for these marker proteins is indicated as 100%. A maximum of 30% contamination is obtained by taking the maximum value of all marker proteins for a particular organelle from 3 biological replicates.

Ribophorin II is a member of the oligosaccharyl transferase which transfers a preassembled dolichol-linked oligosaccharide to asparagine residues of newly synthesized polypeptides. Sec61 α , the ribosome receptor (Prinz et al 2000) and a constituent of the translocon, is part of

the channel through which newly synthesized proteins enter the lumen of the ER for protein folding. Since ribosomes actively synthesize proteins through the translocon in the rough ER, ribophorin II and Sec61 α were used as marker proteins for the RM fraction. Based on redundant peptide counts, ribophorin II and Sec61 α levels are highest in the RM fractions and lowest in the Golgi (Figure 4, Table 4). Calnexin, protein disulphide isomerase A4 and calreticulin, abundant proteins of the ER, were selected as marker proteins equally distributed between the RM and the SM. These proteins show an equally high distribution between the RM and SM fractions and are low in the Golgi (Figure 4, Table 4).

The protein markers used for the Golgi apparatus were Golgin-84, GMX33, α 2, 6 sialyltransferase and α 1, 2 mannosidase. Of the 4, only α 1, 2 mannosidase was detected in the SM fractions, albeit at very low levels. Conversely, peptide counts for these Golgi marker proteins were high in the Golgi (Figure 4, Table 4). Additionally, peptides for glucose-6-phosphatase and galactosyl transferase, marker proteins of the ER and Golgi, respectively were identified only in their cognate isolated organelles (Figure 5, Table 4).

Cross-contamination among RM, SM and Golgi fractions was also determined by western blot of marker proteins using chemiluminescence (Figure 6), confirming the results obtained by peptide counts and enzyme assays. The results show that the Golgi is contaminated with ER by the detection of the ER markers, ribophorin I and calnexin, in the Golgi fraction. Detection of the Golgi markers, membrin and mannosidase II reveal some Golgi contamination in the SM fraction. Mannosidase II is more enriched in the SM as compared to membrin which could be due to the recycling of mannosidase II from the Golgi to the ER (Cole et al 1998). Plasma membrane contamination of the Golgi is minimal based on the detection of integrin β 1. The form of the protein detected in the Golgi is at

Table 3: Mean % Contamination of rough and smooth microsomal and Golgi fractions with other organelles

Fractions	% Contamination					
	Mitochondria	Peroxisomes	Lysosomes	Nucleus	PM	Total
RM	10.6	7.7	0.2	1.4	0.6	20.5
SM	11.7	3.2	0.08	0.36	2.9	18.24
Golgi	9.6	2.8	0.48	0.02	1.5	14.4

Values shown are the mean % total peptides for the three experiments.

Percent total peptides are redundant peptide counts for a protein normalized to all assigned peptides for a particular biological replicate times 100. Shown are the sum of % total peptides for all proteins in the indicated organelles and subcellular fractions. The last column indicates the total organellar contamination in the indicated fractions.

Figure 4: Cross contamination between ER (RM and SM) and Golgi (G) fractions. Values on the y-axis are % total peptide counts for the indicated protein in each biological replicate of the indicated subcellular fraction (RM1, RM2, RM3, etc.) normalized to the highest value for each protein observed in any one biological replicate. The maximal value (% total peptides) for a protein observed in any one biological replicate is set to 100%, and all other % total peptides are normalized to the maximum. Indicated on the x-axis is each biological replicate of a subcellular fraction (e.g. RM1 = RM fraction repeat number 1).

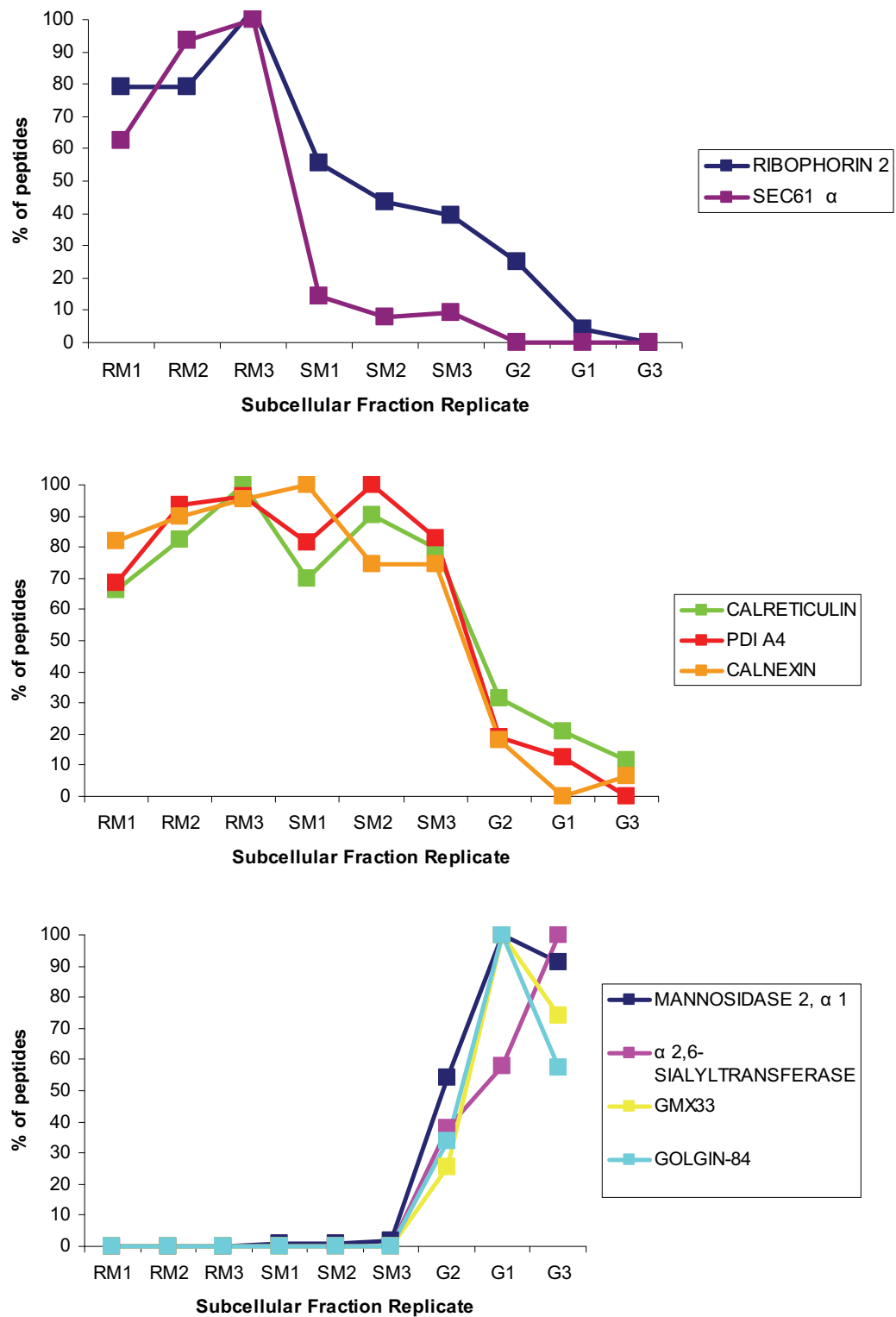


Figure 4

Table 4: Total Peptides for ER and Golgi Marker Proteins

Protein name	Biological Repeat for Subcellular Fraction									
	RM1	RM2	RM3	SM1	SM2	SM3	G1	G2	G3	Total
Ribophorin II	27	57	82	24	34	26	1	12	0	263
Sec61 α	7	22	26	2	2	2	0	0	0	61
Calreticulin	18	47	63	24	56	42	4	12	3	269
PDI A4	15.3	44	50	23	51	36	2	6	0	227.3
Calnexin	13	30	35	20	27	23	0	4	1	153
ERp44	0	1	2	1	2	1	3	6	15	31
Mannosidase II, α 1	0	0	0	1	2	4	74	79	91	251
α 2,6-Sialyltransferase	0	0	0	0	0	0	24.8	32	58	114.8
GMX33	0	0	0	0	0	0	6	3	6	15
Golgin-84	0	0	0	0	0	0	9	6	7	22

Values shown are the total peptides (redundant peptide counts with no normalization applied) for the marker proteins in Figure 4.

Figure 5: Detection of Glucose-6-phosphatase and Galactosyl transferase in the ER (RM and SM) and Golgi (G) fractions. Percent total peptides for glucose-6-phosphatase and glucose-6-phosphatase transport protein are added together to represent glucose-6-phosphatase. Similarly, % total peptides for β -1-3-galactosyltransferase-6, glycoprotein-4- β -galactosyltransferase 2, UDP-galactose:N-acetylgalactosamine α peptide- β 1,3-galactosyltransferase , β 1,3-galactosyltransferase polypeptide 1, β 1,4-galactosyltransferase polypeptide V are added together for galactosyltransferase. Glucose-6-phosphatase has a total of 40 peptides and galactosyltransferase has a total of 19 peptides in all fractions. Values on the y-axis are % total peptide counts for each biological replicate of the indicated subcellular fraction (RM1, RM2, RM3, etc.) normalized to the highest value for the markers observed in any biological replicate. The maximal value (% total peptides) was set as 100%, and all other % total peptides were normalized to this 100%.

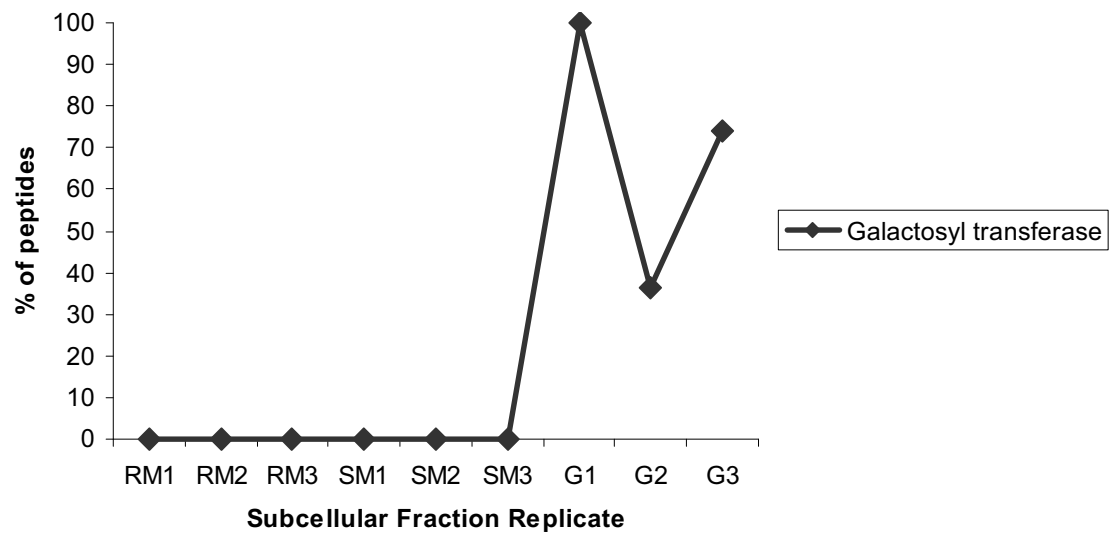
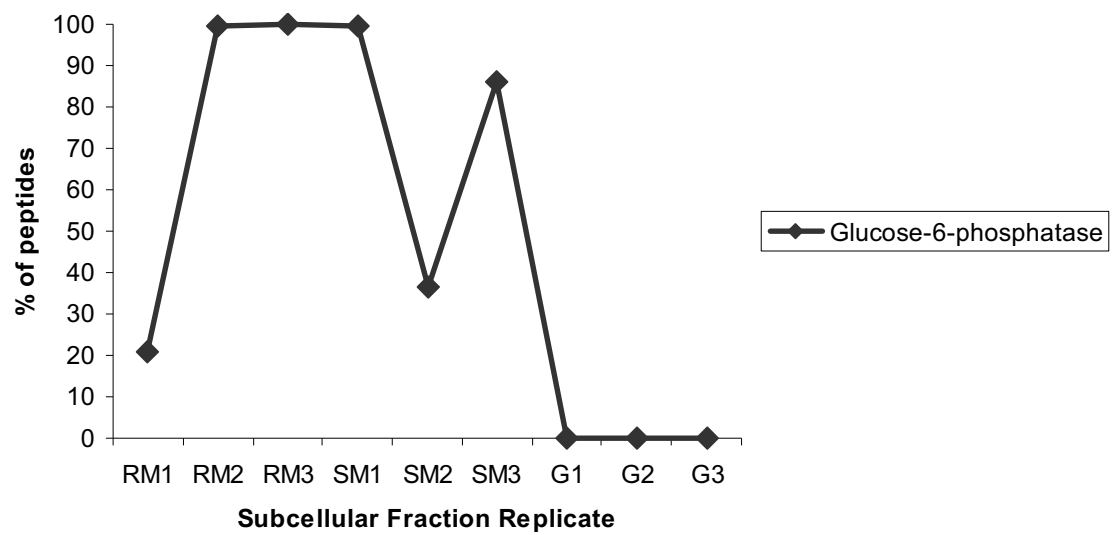


Figure 5

a precursor molecular weight which is different to that observed in the PM fraction. Mitochondrial contamination (anti-Tom20) of the RM and SM fractions is greater than that seen in the Golgi.

Reproducibility of the RM, SM and Golgi fraction preparation

One way the reproducibility of each biological replicate of the RM, SM and Golgi fractions was assessed was by using principal coordinates analysis (PCO) also known as multidimensional scaling multidimensional scaling (MDS) (Gower 1966). PCO allows for the visualization of the distance between variables by revealing the underlying dimensionality of large multidimensional datasets. This effectively reduces the dataset to a smaller number of dimensions which can be visualized in a 2 dimensional plot. A PCO analysis was carried out to determine the behaviour of the RM, SM and Golgi biological replicates and to give an indication of how similar the subcellular fractions were to one another (Figure 7). Nine variables represented each biological replicate of the RM, SM and Golgi fractions with ca. 2000 data points for each variable (redundant peptide counts for 2000 proteins). The goal was to reduce the 9 x 2000 matrix into a two dimensional, 9 x 2 plot. The analysis was done using the cmdscale function in Matlab which accepts a pairwise distance matrix as input. Euclidean distance was used as the distance measure. The arrangement of the first two sets of points returned by cmdscale gives a visual representation of the difference between the ER and Golgi fractions (Figure 7). The PCO plot shows that the space occupied by the RM and SM fractions differs to that of the Golgi (Figure 7). Furthermore, the biological replicates of the RM and SM fractions show less variability when compared to the Golgi repeats. Of the three Golgi replicates, the Golgi N2 sample is closest to the ER fractions indicating that it is more contaminated with ER proteins than the other two.

Table 5 shows the marker enzyme assays carried out on the RM, SM and Golgi fractions. The ratios of the enrichment of the Golgi marker enzyme galactosyl transferase in the RM and SM fractions to that observed in the Golgi fraction reveals low levels of Golgi contamination in the RM and SM fractions. Similarly, Golgi marker proteins were not detected in the RM and SM fractions by redundant peptide counting (Figure 4). As a measure of ER contamination of the Golgi fractions, the ratio of the enrichment of glucose-6-phosphatase in the Golgi fraction to that in the RM and SM fractions was measured and shows an average of 30% ER contamination (Table 5). The result obtained by looking at peptides for ER marker proteins in the Golgi biological replicates (Figure 4) reveals a maximum of 30% contamination.

Subcellular localization of proteins by proteomics

This section describes the assignment of proteins to the RM, SM or Golgi based on their distribution among these organelles by redundant peptide counting. The results show that this approach is able to assign known proteins to their cognate organelles. Furthermore, the method reveals that ERp44 is localized to the Golgi apparatus and not the ER as previously described (Anelli et al 2002).

Functions of Proteins Identified in the RM, SM and Golgi fractions

The assignment of proteins to 23 functional categories allowed us to identify functions which were enriched in a particular subcellular fraction. Figure 8 shows bar graphs depicting the enrichment of specific functional categories for the RM, SM and Golgi fractions. The height of the bars represents the sum of % total peptides for proteins in the

Figure 6: Immunoblots of marker proteins in rat liver homogenates, RM, SM, Golgi and PM fractions. Equal amounts of protein were applied to each lane in a 1D SDS gel with the immunoblot revealed by chemiluminescence. Only the precursor form of β -integrin is found in the Golgi fraction while the mature PM form is found in SM fractions indicating contamination of SM with PM. Abbreviations: H – homogenate; RM and SM - rough and smooth microsomes; SRM – stripped rough microsomes (microsomes treated with EDTA to remove ribosomes from membranes (Blobel & Dobberstein 1975); PM – plasma membrane; G – Golgi fraction.

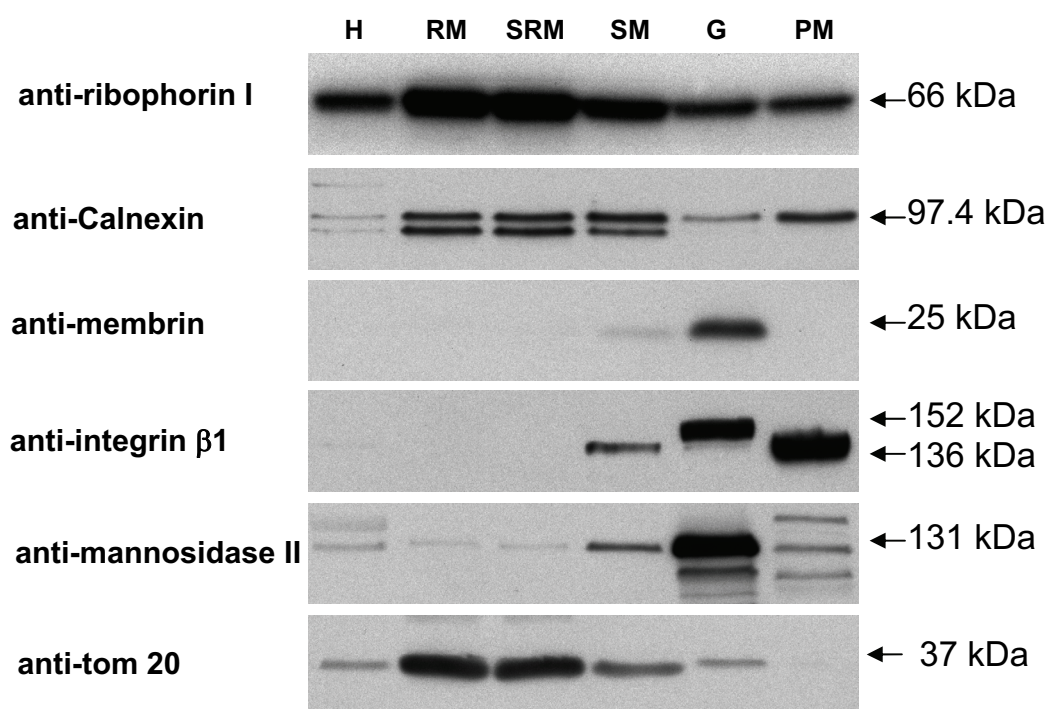


Figure 6

Figure 7: Principal coordinates analysis (PCO) of the biological replicates (n=1, 2, 3) of the RM and SM fractions shows that they are distinct from the Golgi fractions. A 9 x 2000 matrix comprising the 9 total biological replicates of the RM, SM and Golgi fractions and the abundance of 2000 proteins identified in these fractions was reduced by PCO to a 9 x 2 matrix which is represented in the figure.

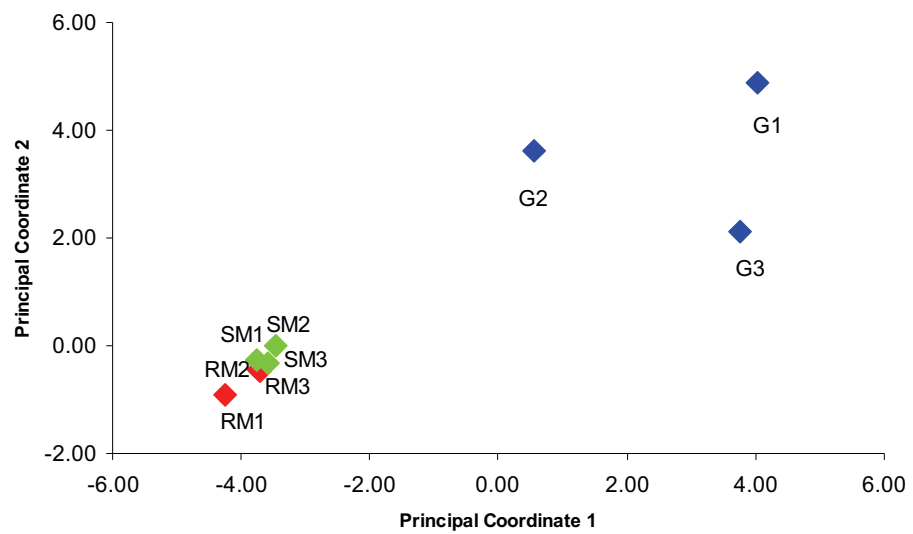


Figure 7

Table 5: Enrichment of marker enzymes in RM, SM, Golgi and PM fractions

Fractions	Glucose-6-phosphatase		Galactosyl transferase	
	Spec. Act.1	Enrichment over	Spec. Act.2	Enrichment over
Homogenate	4.5 ± 0.7	1.0	0.1 ± 0.01	1.0
RM	20.4 ± 4.9	4.5 ± 0.4	0.1 ± 0.01	0.7 ± 0.2
SM	17.3 ± 4.1	4.0 ± 0.3	0.3 ± 0.01	3.5 ± 0.2
PM	3.7 ± 0.1	1.06 ± 0.04	0.3 ± 0.1	3.8 ± 0.7
Golgi	7.3 ± 1.2	1.3 ± 0.2	10.4 ± 3.8	105.5 ± 26.4

Spec. Act.¹: μ mole of Pi liberated / h per mg of protein

Spec. Act.²: nmol of galactose transferred / min per mg of protein

specified functional category. Proteins were annotated mainly by literature search and categories were chosen to reflect the major functions of proteins in the early secretory pathway. For the RM fraction, the highest number of peptides is assigned to proteins involved in protein synthesis and folding (Figure 8). Proteins involved in both detoxification and protein synthesis and folding are the most abundant in SM and soluble biosynthetic cargo proteins account for the majority of the peptides for the Golgi fraction (Figure 8).

Co-distribution with Marker Proteins to Assign Subcellular Location

Since many proteins were identified in more than one subcellular fraction, it was difficult to assign proteins to a particular organelle. To address this problem, distribution profiles were determined for each protein using redundant peptide counts as an estimate of protein abundance. In addition, hierarchical clustering was used to group together proteins with similar distribution patterns (de Hoon et al 2004, Eisen et al 1998, Quackenbush 2001). Figure 9 shows the clustering results for 1,067 proteins identified in the RM, SM and Golgi fractions. Prior to this analysis, 320 proteins which belong to categories deemed contaminants were removed. These categories include organellar as well as likely contaminants (keratins, trypsin, and proteins from cells of non-hepatic origin). This step was done to simplify the analysis and to consider only those proteins that have a high probability of being resident to the organelles under study.

As seen in Figure 9, the branch lengths of the dendrogram indicate the degree of correlation between the distribution profiles of the proteins as assessed by the Pearson correlation pairwise similarity function. Also

Figure 8: Quantitative distribution of peptides assigned to proteins classified into 23 functional categories. A total of 35,645 tandem mass spectra were assigned to proteins in the indicated 23 categories. Shown are the mean sum % total peptides for proteins assigned to the indicated functional categories. The arrows indicate the categories with the highest abundance of peptides for each subcellular fraction.

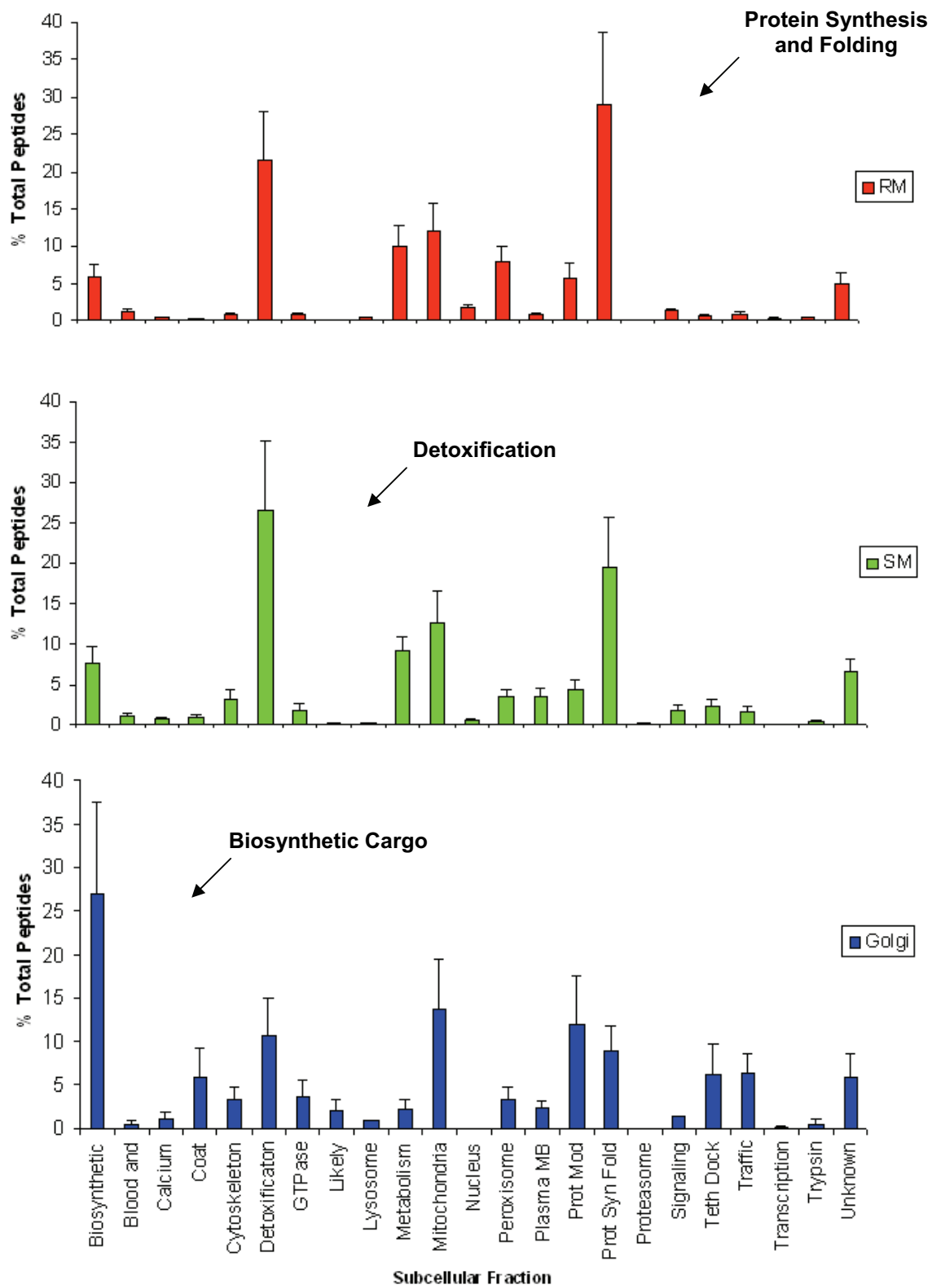


Figure 8

Figure 9: Hierarchical clustering of proteins that co-distribute with Sec61 α , p97, Calnexin, and MannII. The RM, SM, and Golgi data (n = 3) from Supplementary Table S1D (%total peptides) were averaged (Supplementary Table S2A) and used to generate the heat map. Clusters that contained Sec61 α , p97, calnexin, and MannII as markers were selected (Pearson correlation coefficient > 0.90). Pearson correlation coefficients for the selected clusters are indicated. Intensity scale indicates the % total peptides observed for each protein.

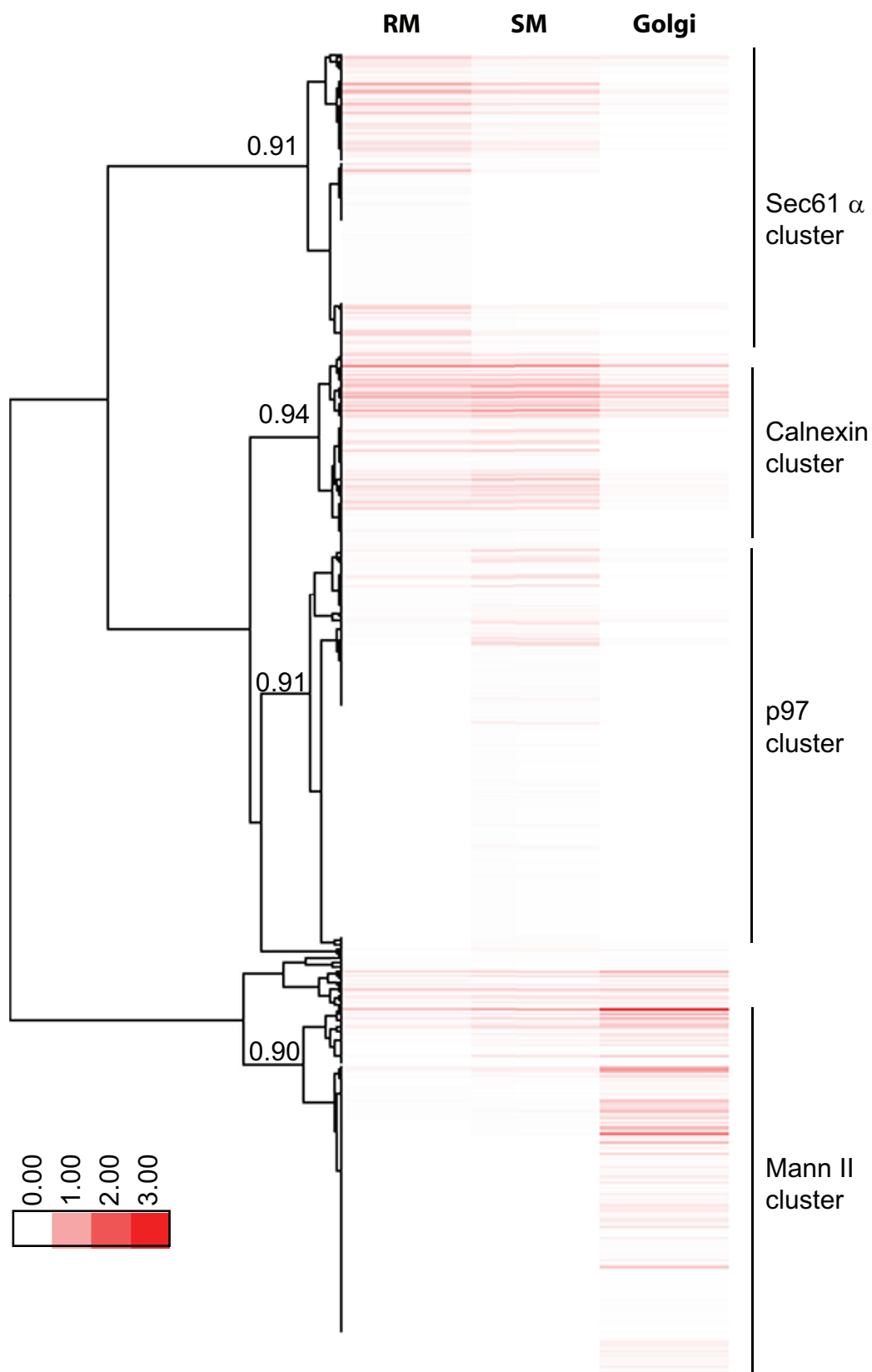


Figure 9

indicated is the Pearson correlation coefficient for the highest node in each cluster as calculated by Cluster 3.0 (de Hoon et al 2004). The Pearson correlation coefficient ranges between 1 and 0. A value of 1 indicates that they are perfectly correlated while a value of 0 means that there is no relationship. All clusters were selected to have correlation coefficients greater than 0.9. This indicates that proteins with similar patterns of expression are adjacent to one another and members of a particular cluster are most similar to one another.

Figure 10 shows the localization profile of proteins in the 4 clusters and their co-distribution with the specific marker proteins for the isolated organelle. The major functions of proteins in the 4 main clusters are seen in Figure 11. Proteins that clustered together had similar functions and these functions were consistent with the isolated organelles under study. The Sec61 α cluster consists of proteins which were highly abundant in the RM with few peptides observed in the SM or Golgi fractions. This cluster shows two distinct distribution profiles. One profile displays proteins whose peptides are mainly observed in the RM with little to no peptides in the SM or Golgi fraction. These proteins are mostly low abundance proteins with as little as 2 peptides observed in all 3 RM replicates. The other distribution profile contains proteins whose peptides are distributed approximately 80% in the RM with the rest in the SM or Golgi fractions. These proteins are more abundant with an average of 10 peptides among the three RM replicates. These proteins are, therefore, more likely to be detected in the SM and Golgi fractions. The majority of the peptides in this cluster are derived from proteins involved in protein synthesis and folding. Sec61 α , a member of the translocon complex, clustered with other translocon constituents namely TRAM, the integral membrane protein TRAP γ (translocon associated protein) and the putative ribosome receptor, p180 (Meyer et al 2000).

The calnexin cluster contains proteins that are equally abundant in the RM and SM fractions and are mainly in the detoxification and protein synthesis and folding categories. These proteins include glucosidase II, which removes the innermost glucose residues on N-linked glycoproteins for presentation of newly synthesized glycoproteins to the calnexin cycle for protein folding, as well as protein folding enzymes such as protein disulphide isomerase and Ero1, which provides the reducing equivalents for the oxidizing environment of the ER.

Also present were the protein folding enzyme peptidyl-cis-trans-isomerase, BiP and the hypoxia upregulated stress protein GRP170. Cytochrome p450s and other characteristic detoxification proteins of the liver ER were also found.

The AAA-ATPase protein p97 represents the cluster containing proteins predominantly expressed in the SM fraction. Included in this cluster is reticulon 3, a constituent of a family of proteins implicated in the tubular structure of the smooth ER (Voeltz et al 2006) and Derlin, a protein involved in ER associated degradation (ERAD) (Lilley & Ploegh 2004, Ye et al 2004).

The mannosidase II cluster contains classic Golgi marker proteins including the mannosidases, sialyltransferases and galactosyltransferases. Also included in the mannosidase II cluster is the RDEL terminating, protein disulphide isomerase protein, ERp44, which was thought until now to reside in ER. To validate this discovery, ERp44 was immunolocalized with a polyclonal antibody revealing a predominant juxtannuclear staining (Figure 12). ERp44 staining mainly overlaps with the Golgi marker, GM130. Reticular ER-like staining was also observed which is consistent with the minimal detection of ERp44 in the ER compared to the Golgi.

Figure 10: Distribution of proteins in individual clusters. Mean % total peptides for proteins in each of the clusters were normalized to 1 and plotted individually (Table S2A). ERp44, a RDEL-terminating member of the ER protein disulfide isomerase family, co-clusters with the Golgi marker MannII (correlation coefficient > 0.90).

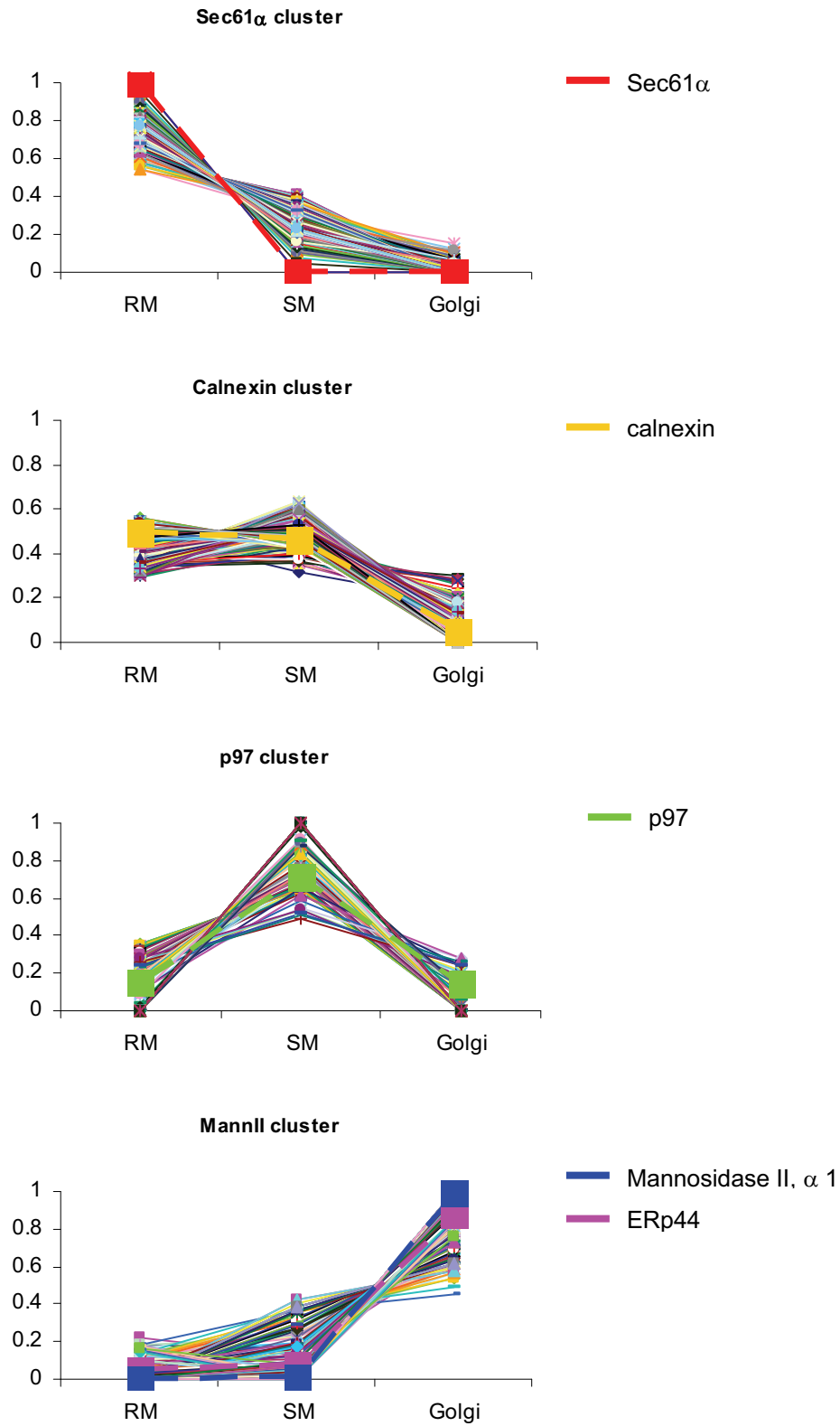


Figure 10

Figure 11: Functional categories of proteins in Sec61 α , calnexin, p97 and mannosidase II cluster. Functional categories of proteins observed for each cluster in Figure 9 are shown, with the particular subcellular fraction identified by color as seen in the boxes in the legend. Histograms represent the mean sum of % total peptides for proteins in the functional categories indicated. Proteins in functional categories designated as contaminants were removed.

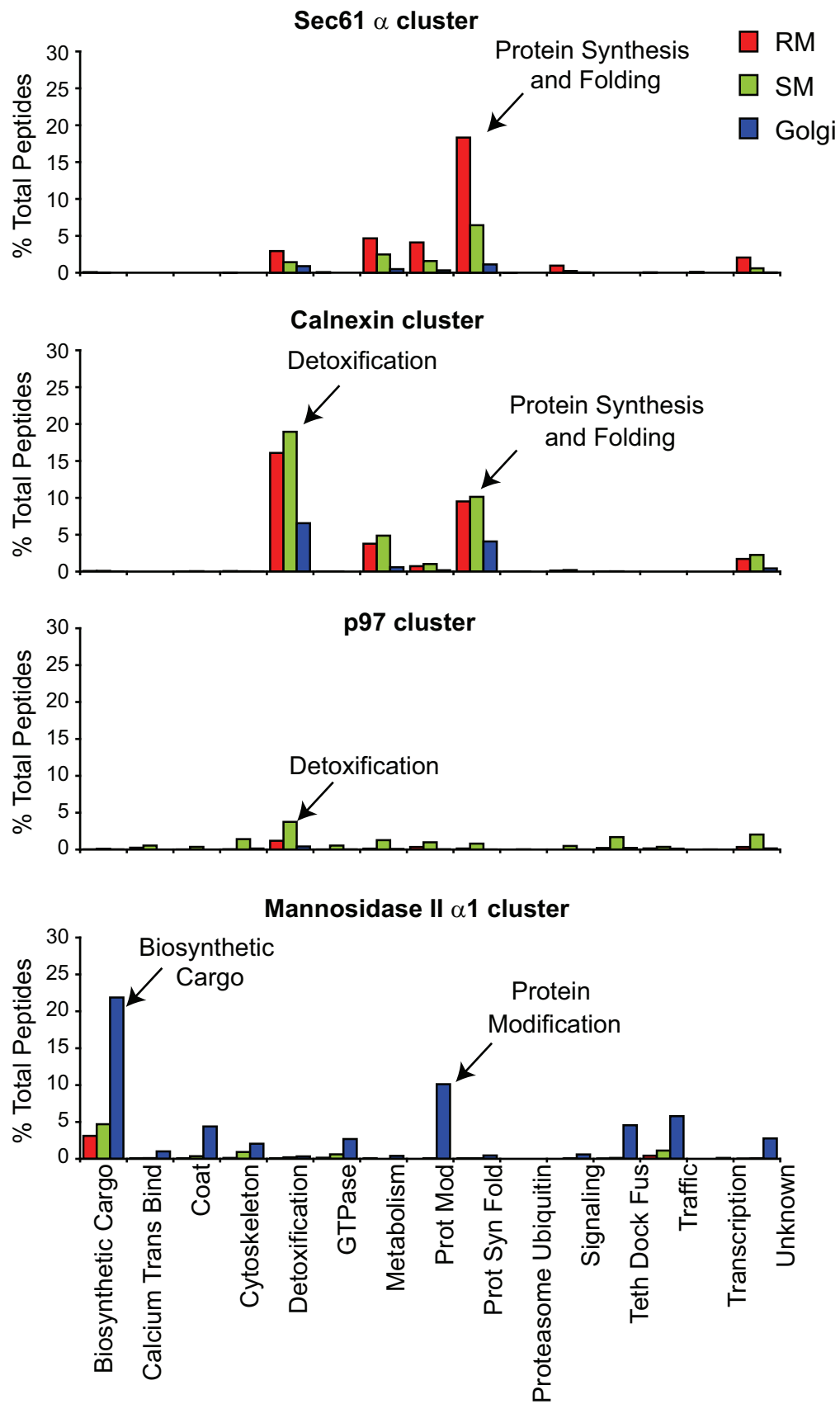


Figure 11

Figure 12: Immunolocalization of ERp44. Indirect immunofluorescence of ERp44 in HepG2 cells with an ERp44 antibody shows both a Golgi and ER localization as seen by colocalization with GM130, a cis-Golgi marker. Scale bar = 25 um.

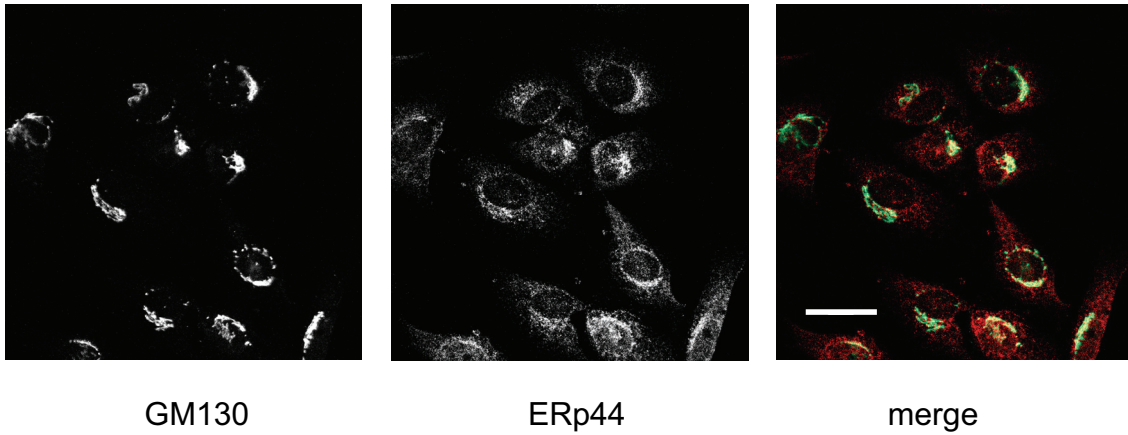


Figure 12

Biochemical subfractionation of the RM and SM fractions

Integral membrane proteins have proven difficult to study by proteomics (Wu & Yates 2003). This complication arises due to the intricacies in separating and recovering these proteins since they are insoluble in aqueous protein solvents. Integral membrane proteins represent approximately 30% of the human genome (Wallin & von Heijne 1998) and carry out many fundamental biological processes such as vesicle trafficking, membrane fusion, protein modification and translocation. This section describes the proteomics characterization of a membrane, soluble and membrane-associated cytosolic biochemical subfraction of the ER with the aim of increasing the coverage of proteins identified in the RM and SM and detecting lower abundance proteins.

Biochemical subfractionation increases the number of identified proteins

To increase the likelihood of detecting lower abundance proteins and to characterize different domains of the ER, RM and SM membranes were biochemically subfractionated. Membranes of the RM and SM total fraction were washed with a high molar salt solution to concentrate cytosolic membrane peripheral proteins resulting in a saltwash fraction (S). This step was followed by treatment with the detergent, Triton X-114, to extract and separate membrane proteins from soluble proteins. Triton X-114 treatment followed by a temperature shift partitions soluble and luminal proteins away from membrane proteins based on their separation into the aqueous (A) or the detergent (D) phase, respectively (Bordier 1981). After biochemical subfractionation, 589 proteins not previously identified in the total fractions were uncovered in the biochemical subfractions.

Hierarchical clustering of protein distribution in biochemical fractions

Hierarchical clustering of the mean redundant peptide count distributions of proteins identified in the biochemical subfractions (3 biological replicates) identified clusters of proteins with similar biochemical characteristics (Figure 13). Six clusters account for 77% of all assigned peptides. These clusters define proteins restricted to a limited number of functional categories (Figure 14). An analysis of the individual proteins in the most abundant categories is shown in Figure 15. Most of the proteins identified in the BiP cluster were molecular chaperones and protein-folding enzymes known to be soluble luminal ER proteins and were largely found in the aqueous phase after Triton X-114 phase separation. The actin cluster contains principally insoluble cytoskeletal proteins including molecular motors (kinesin family protein 13A, various myosins, and several components of the dynein/ dynactin complex) that mainly localize to smooth microsomes (Figure 15). The poly(A) binding protein cluster is made up of TX-114 insoluble proteins such as the ribosomes and other proteins involved in protein synthesis that localized to the rough microsomes. These proteins are mainly cytosolic proteins. Their discovery in the insoluble fraction indicates that they were not removed by the high salt wash, suggesting a strong interaction with the membrane of the rough ER. In contrast, the NAC α cluster consists of metabolic enzymes removed by the high salt treatment, which indicates that they are loosely associated with the cytosolic surface of the rough ER. This cluster also contains elongation factor 2 and consists largely of proteins involved in translation or folding. The cytochrome P450 cluster reflects a major function of the ER in lipid and steroid oxidation and drug detoxification. The ribophorin cluster defines integral membrane proteins (TX-114 soluble phase) of major functional significance in the ER for protein modification reactions that include N-linked glycosylation (Figure 15).

Bioinformatics prediction of transmembrane segments represents another way to identify integral membrane vs. soluble proteins. TMHMM is an algorithm based on a hidden Markov model which predicts transmembrane helices in proteins (Sonnhammer et al 1998). This program was used to predict membrane spanning regions for all proteins identified in this study (Table S1D). The performance of TMHMM vs. biochemical subfractionation with TX-114 was analyzed (Figure 16) by comparing TMHMM predictions for well-known integral membrane proteins with their behavior after TX-114 subfractionation. Proteins in the CYP2C11 cluster were verified as either membrane or soluble proteins by literature search when possible. Of the 101 proteins in this cluster, 11 were predicted genes or had no information about the presence or absence of transmembrane segments. Of the 15 proteins predicted to be soluble by TMHMM, 13 were documented membrane proteins in the literature. These proteins include members of the cytochrome p450 family, Rab7 and Rab2A as well as epoxide hydrolase. The majority of proteins in the BiP cluster were correctly predicted to be soluble proteins. Only one protein, Sel1 homolog (Schuberth & Buchberger 2005), in this cluster was correctly predicted as a membrane protein.

Figure 13: Protein Clusters in Biochemical Extracts from RM and SM Fractions. Mean % total peptide counts for the three biological replicates of each biochemical fraction of the RM and SM were clustered by hierarchical clustering using Pearson correlation (Table S2B). Shown are the BiP cluster, the actin cluster, the poly(A) binding protein cluster, the arginase and elongation factor 2 cluster, the cytochrome P450 cluster, and the ribophorin cluster.

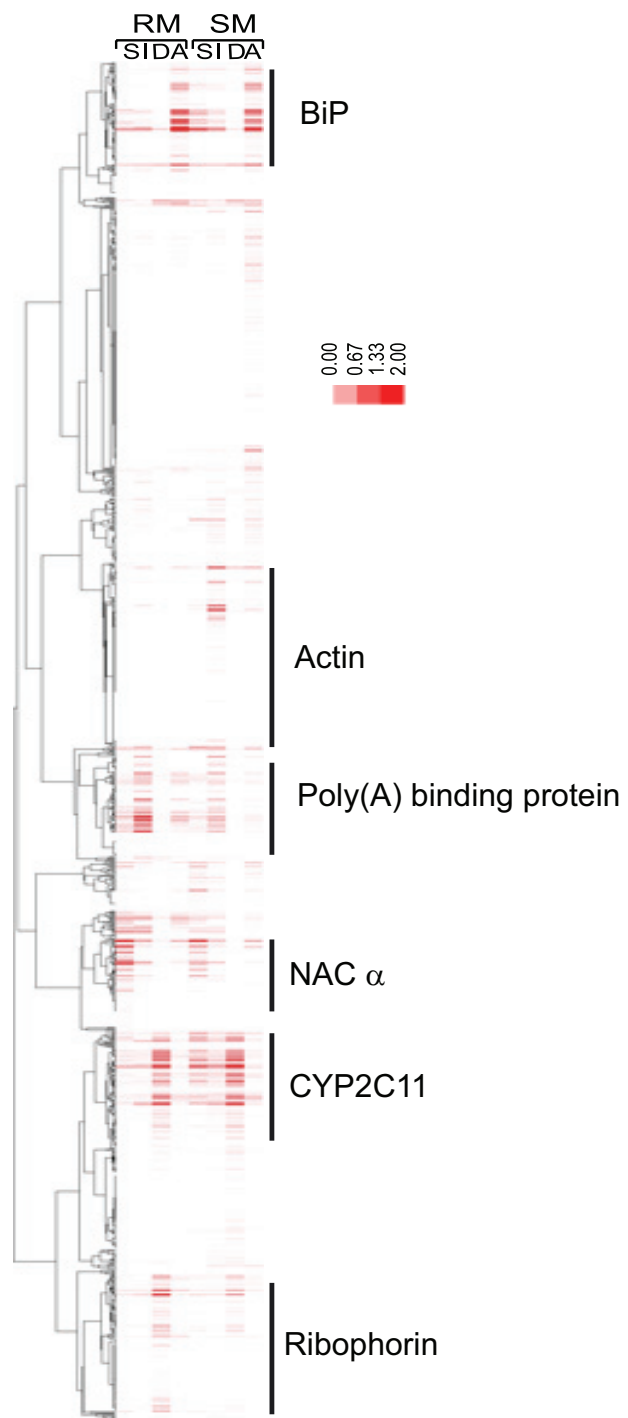


Figure 13

Figure 14: Functional categories of proteins in biochemical fractions clusters. Shown are the major categories of proteins observed for each cluster, with the particular biochemical extract identified by color as seen in the boxes in the legend. Histograms represent the mean sum % total peptide counts. The major categories are indicated by arrows. RS = RM salt wash, RI = RM insoluble, RD = RM detergent, RA = RM aqueous, SS = SM salt wash, SI = SM insoluble, SD = SM detergent, SA = SM aqueous.

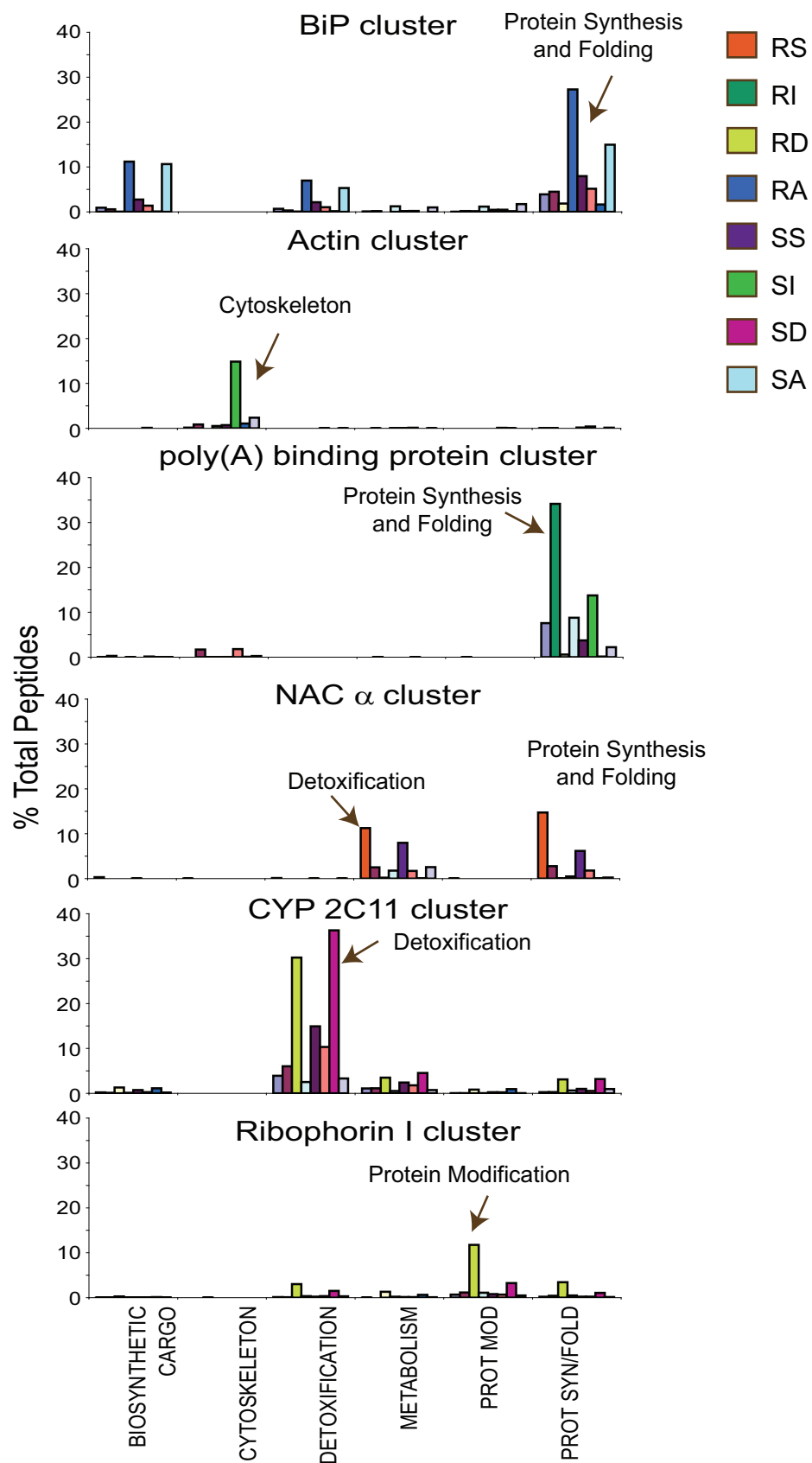
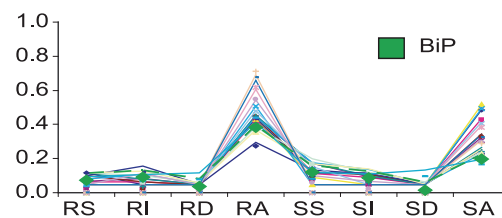


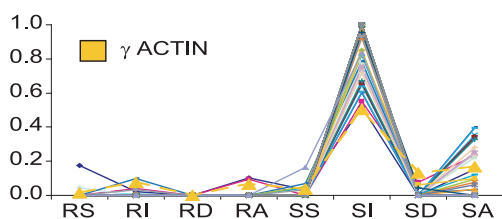
Figure 14

Figure 15: Distribution of proteins among the biochemical fractions in the selected clusters (Table S2B). Marker proteins in each cluster (excluding the ribosomal proteins) are indicated by a dashed line. Plotted values are mean % total peptide counts for each protein. RS = RM salt wash, RI = RM insoluble, RD = RM detergent, RA = RM aqueous, SS = SM salt wash, SI = SM insoluble, SD = SM detergent, SA = SM aqueous.

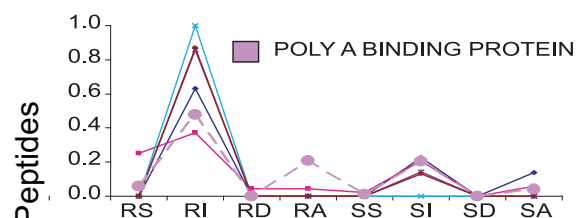
Protein Synthesis and Folding Proteins



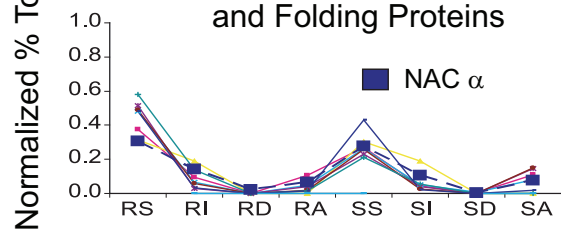
Cytoskeletal Proteins



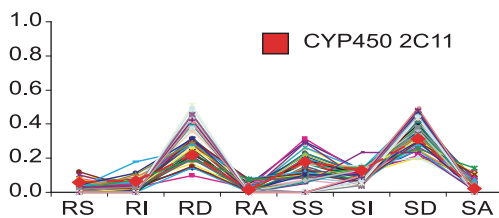
Protein Synthesis and Folding Proteins



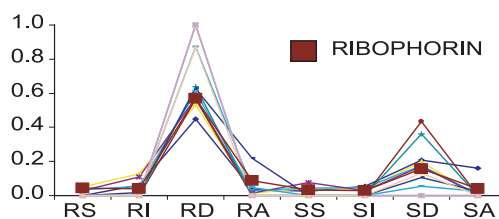
Metabolism and Protein Synthesis and Folding Proteins



Detoxification Proteins



Protein Modification Proteins



Biochemical Subfraction

Figure 15

Figure 16: Comparison of biochemical subfractionation with TX-114 to bioinformatic prediction of integral membrane proteins. Proteins in the CYP2C11 and BiP clusters were enriched in the detergent and aqueous biochemical subfraction after treatment with TX-114 (Bordier 1981) identifying them as membrane and soluble proteins, respectively. Proteins were also designated membrane or soluble based on bioinformatic predictions for transmembrane segments by TMHMM (Sonnhammer et al 1998). Both biochemical subfractionation and bioinformatic prediction were compared. The bar graph represents the number of proteins in the designated cluster predicted as either membrane or soluble by TMHMM (Sonnhammer et al 1998).

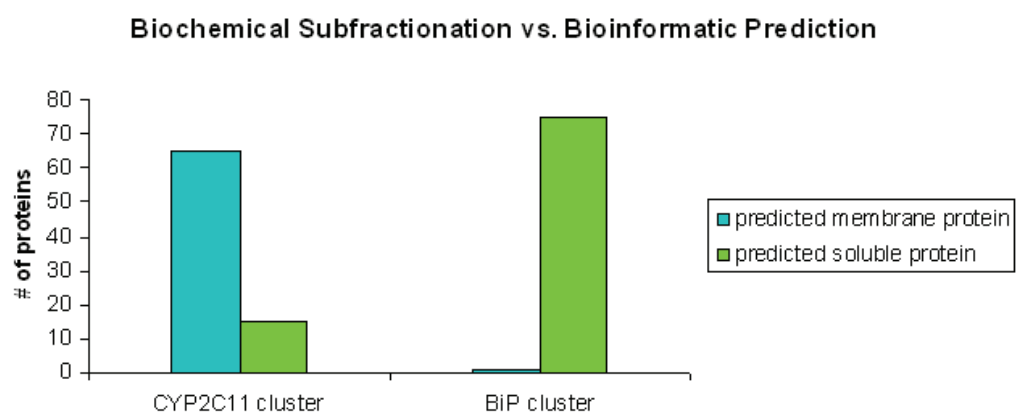


Figure 16

Completeness of protein identifications in the RM, SM and Golgi fractions

The objective of this section is to address the issue of the completeness of the list of proteins identified in the RM, SM and Golgi fractions. This was accomplished by comparing the proteins identified in these organelles to 1) the high-throughput localization study in *Saccharomyces cerevisiae* by Huh et al. study (Huh et al 2003). In addition, the comprehensiveness of this study was assessed by comparing the proteins identified in the RM, SM and Golgi fractions to 1) known ER and Golgi localized proteins contained in the protein localization databases, OrganelleDB (Wiwatwattana et al 2007) and HERA (Scott et al 2004) and 2) previous proteomics analyses of the ER and Golgi apparatus (Foster et al 2006a, Knoblach et al 2003, Wu et al 2004).

Comparison of proteins identified in the RM and SM fractions to ER localized proteins in *Saccharomyces cerevisiae*

A total of 1342 proteins were identified in the rough and smooth microsomal fractions (total and biochemical) excluding contaminants. A comparison of proteins identified in the ER with past proteomics analyses of these organelles (Foster et al 2006a, Knoblach et al 2003) reveals that the proteins identified in the ER fraction encompass the greatest number of proteins (Figure 17, Table 6) and have a greater coverage of ER localized proteins in yeast. Of the 293 yeast proteins localized to the ER by GFP (Huh et al 2003) 121 had rat orthologs based on the Inparanoid eukaryotic ortholog database (O'Brien et al 2005). Of these 121 proteins, 53 (44%) were identified in the RM and SM fractions (Figure 17, Table 6). This value decreased slightly to 42 % when contaminants were excluded from the dataset suggesting that either some of the proteins localized to the ER were retained in the ER due to misfolding of the GFP tag or that these proteins were indeed ER proteins but we misclassified as contaminants (mitochondria or plasma membrane). Prominent proteins

not identified in the ER fraction but localized to the ER in yeast include proteins involved in dolichol-linked oligosaccharide synthesis and phosphatidylinositol glycan anchor biosynthesis.

Comparison to Protein Localization Databases

A lower percentage of proteins present in the subcellular localization databases, HERA and OrganelleDB, were identified in the RM, SM and Golgi fractions (Figure 18 and 5.4). Fifty-two percent of HERA “kernel ER” proteins were present in the RM and SM fractions. Proteins in the HERA dataset which were not identified in the RM and SM fractions function in phosphatidylinositol glycan anchor biosynthesis, phospholipid synthesis and are members of the dolichol-linked oligosaccharide synthesis pathway. Closer inspection of HERA proteins not identified in the RM and SM fractions reveals proteins which are either 1) not present in rat 2) associated with the ER but function elsewhere (ex. Bcl-2 (Walter & Hajnoczky 2005), sterol regulatory element-binding transcription factor (Espenshade 2006) 3) low abundance proteins such as transcription factors and protein kinases 4) cell-type specific proteins (skeletal muscle, cardiac) or 5) plasma membrane contaminants (aquaporin 2, mucin) which were classified as ER in the HERA dataset. Taking these proteins out of the analysis increased the overlap to 65%.

The HERA dataset contains proteins involved mainly in detoxification and protein synthesis and folding, the two major functional categories for proteins identified in the RM and SM fraction. Approximately 33% of proteins in the RM and SM fraction that belong to these functions were identified in HERA. The remaining 66% of proteins identified in the RM and SM fractions absent from HERA and assigned to the detoxification category include many unidentified members of the cytochrome p450, glucuronosyl transferase and carboxylesterase families as well as cytosolic proteins potentially associated with the ER membrane.

As for the protein synthesis and folding category, many proteins absent from HERA consist of cytosolic protein folding proteins such as the chaperonins, heat shock proteins as well as proteins involved in translation e.g. the translation initiation and elongation factors. Aside from these two categories, the remaining proteins identified in the RM and SM fraction not included in HERA belong to the cytoskeleton, metabolism, protein modification, tethering docking and fusion and traffic categories. For many of these proteins, their association with the ER is apparent. As an example, cytoskeletal proteins that fractionate with the ER provide structure to the ER and cytosolic proteins in the tethering docking and fusion categories, which include the SNAREs and Rabs, are involved in membrane fusion events. These proteins are considered to define the “identity” of an organelle by providing specificity for membrane fusion events (Behnia & Munro 2005).

Similar analyses examining the completeness of the list of proteins identified in the Golgi fraction were also done. The Golgi list consists of 564 proteins with contaminants and biosynthetic cargo excluded. Contaminants and cargo were excluded because they were not considered resident proteins; in the case of cargo proteins, they only traffic through the Golgi apparatus and do not function in this organelle. Figure 19 shows the detection coverage of yeast proteins with rat orthologs localized to the Golgi by GFP (Huh et al 2003). These data are also presented in Table 8. As presented in the figure, the greatest coverage of Golgi yeast proteins is achieved by this study. Of the 43 yeast proteins localized to the Golgi in the Huh et al. study (Huh et al 2003), 18 have rat orthologs. Sixty seven percent of yeast orthologs were identified in the Golgi fraction when contaminants were included and 61% were identified when contaminants and biosynthetic cargo were removed (Figure 19, Table 8), again suggesting that the excluded contaminants were either *bona fide* Golgi proteins or were mislocalized by GFP. Furthermore, the

majority of Golgi proteins identified in the Foster et al. (Foster et al 2006b) and Wu et al. (Wu et al 2004) studies were also identified in the Golgi fraction (Figure 20, Table 9). The Wu et al. study (Wu et al 2004) classified 110 of the 421 proteins identified in their Golgi fraction as *bona fide* Golgi proteins by literature search. These 110 proteins were used as a benchmark for our Golgi study and the comparison revealed 80% of these proteins identified in the Golgi fraction (Figure 20, Table 9).

Less than half of the Golgi HERA proteins were identified in the Golgi fraction. Some of the missing proteins are expected to be of low abundance such as the protein kinases; however, many of the missing proteins are known sugar transferases of the Golgi. It is possible that these proteins have similar retention times as other more abundant proteins and are consequently missed. A comparison with the 110 *bona fide* Golgi proteins from the Wu et al. (Wu et al 2004) study yielded better results. Eighty percent of these proteins were identified in the Golgi fraction which is consistent with both studies using the same starting material (rat liver) (Figure 20).

Comparison to other Proteomics Studies of the ER and Golgi

Previous attempts at identifying the proteome of the ER and Golgi (Foster et al 2006a, Knoblach et al 2003, Wu et al 2004) have not achieved the level of coverage for these organelles as attained by this study (Figure 17 and 19). Compared to the 50% coverage of yeast ER localized proteins achieved by the proteomics analysis of the RM and SM fractions in this study, previous analyses have identified less than 6% of yeast ER proteins (Foster et al 2006a, Knoblach et al 2003) (Table 6). Furthermore, 90% of ER proteins uncovered in the Foster et al. (Foster et al 2006a) and Knoblach et al. (Knoblach et al 2003) studies were also identified in the RM and SM fractions. This leads to the conclusion that the

RM and SM protein list may be the most comprehensive of all ER proteomics analyses done to date.

Proteins identified in the Golgi fraction encompassed 67% of Golgi localized yeast proteins with rat orthologs; whereas, the Wu et al. (Wu et al 2004) study identified only 50% of these proteins (Figure 19, Table 8). An earlier study of Golgi membrane proteins by Bell et al. (Bell et al 2001) identified only 17% of Golgi localized yeast proteins (Figure 19, Table 8). However, this study specifically examined a detergent soluble membrane fraction of Golgi membranes and had therefore limited coverage of the Golgi proteome. The majority of proteins identified in the Foster et al. (Foster et al 2006a) and the Bell et al. (Bell et al 2001) studies were also detected in the Golgi fraction (Figure 20, Table 9). There is less overlap with the Wu et al. study (Wu et al 2004) (Figure 20, Table 9) when all proteins are considered which could be due to either transient and/or low-abundance proteins. Therefore, using yeast protein coverage as the standard for completeness, the list of proteins identified in the Golgi fraction is more comprehensive than any of the earlier studies of Bell et al. (Bell et al 2001) and Wu et al. (Wu et al 2004).

Conclusion

Based on the comparison with yeast proteins localized by GFP, it can be concluded that the compendium of proteins identified in the RM and SM fractions is at least 50% complete and the Golgi list is at least 60% complete. The ER and Golgi protein lists encompass the majority of proteins detected in prior proteomics studies of these organelles. Furthermore, the proteomic analysis of the RM, SM and Golgi fractions identified the highest number of proteins, suggesting that these protein lists may be the most comprehensive to date.

Figure 17: Completeness of compendium of proteins identified in the RM and SM fractions by comparison to yeast ER proteins. Proteins from different proteomics analyses of the ER and ER subcellular localization databases are compared to ER localized *Saccharomyces cerevisiae* proteins with rat orthologs from Huh et al. (Huh et al 2003) as measure of the extent of protein coverage and completeness. Comparison was done using BLASTp (Altschul et al 1990) with a cut-off e-value less than or equal to e^{-15} . The trend line is indicated by the dashed line.

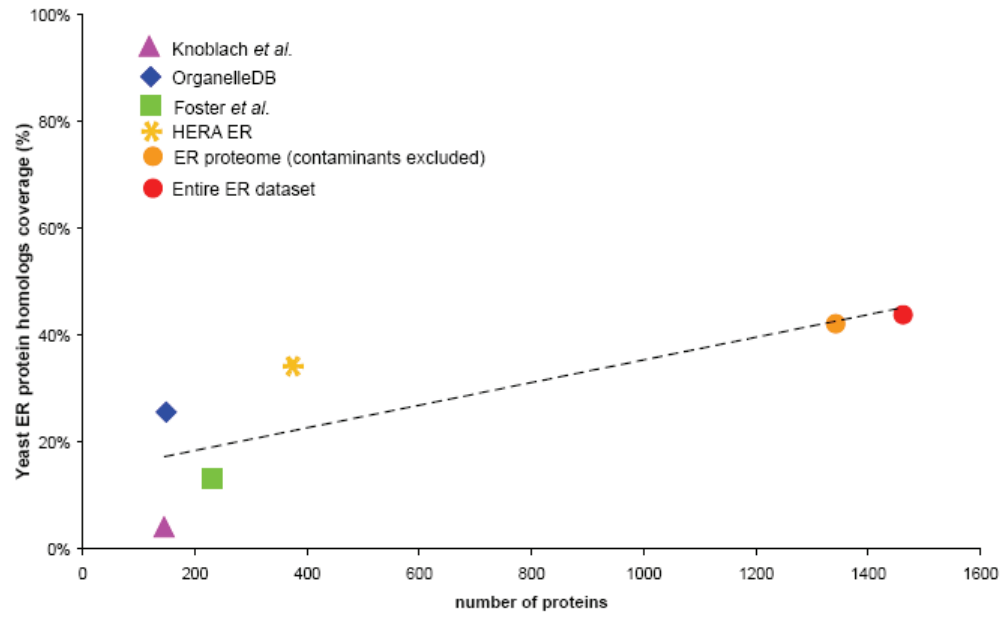


Figure 17

Table 6: Comparison of ER proteomics studies and databases with yeast ER GFP localized proteins (Huh et al 2003)

Dataset	# of proteins	% coverage
Knoblach et al.	145	4%
Organelle DB	149	26%
Foster et al. ER proteins	230	13%
HERA	372	35%
ER proteome (contaminants excluded)	1342	42%
ER proteome (contaminants included)	1764	44%

Protein sequences from the indicated datasets were compared to sequences of proteins localized to the ER in yeast (Huh et al 2003). Values in this table are shown in Figure 17. Comparison was done using BLASTp (Altschul et al 1990) with a cut-off e-value less than or equal to e^{-5} .

Figure 18: Comprehensiveness of compendium of proteins identified in the RM and SM fractions by comparison to other ER proteomics studies and ER subcellular localization databases. The overlap of proteins in the ER proteome with proteins identified in other ER proteomics studies and ER subcellular localization databases is used to measure the comprehensiveness of the ER proteome. Comparison was done using BLASTp (Altschul et al 1990) with a cut-off e-value less than or equal to e^{-15} .

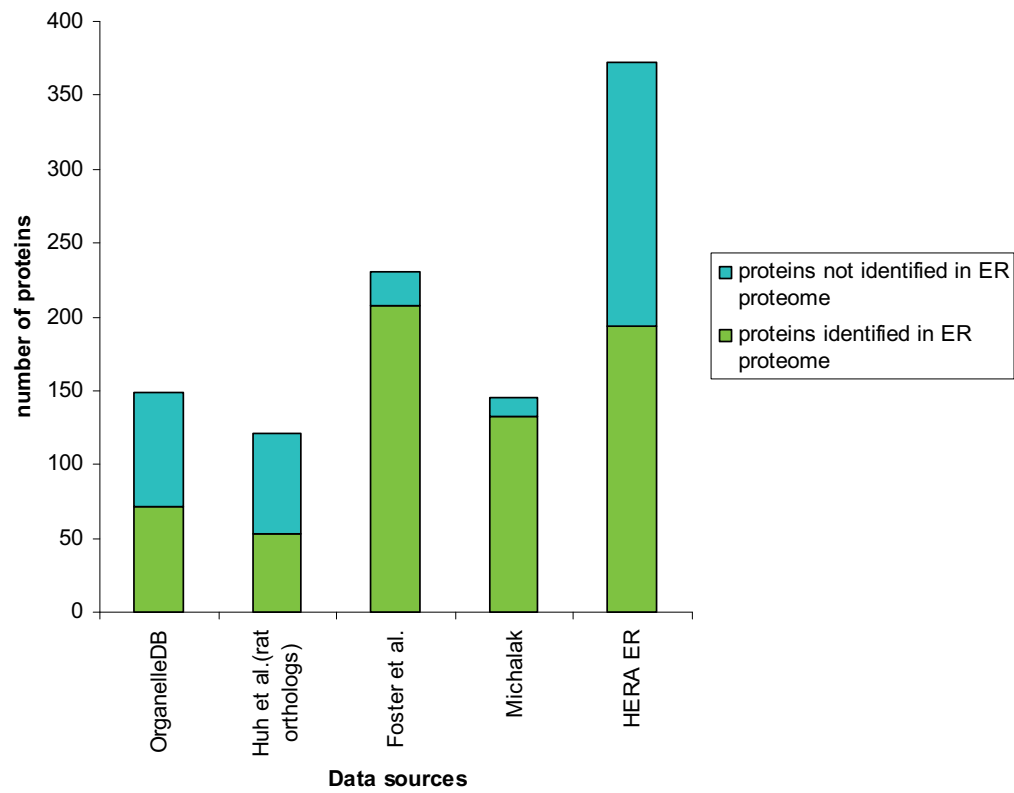


Figure 18

Table 7: Comparison of ER proteomics studies and databases with ER proteome

Database	# of proteins identified	# of proteins matched to ER proteome	% coverage
OrganelleDB	149	72	48%
Huh et al. (rat orthologs)	121	83	44%
Foster et al. ER	230	207	90%
Knoblach et al.	145	133	92%
HERA ER proteins	372	194	52%

Protein sequences identified in the RM and SM fractions were compared to protein sequences in the indicated databases. Values in this table are shown in Figure 18. Comparison was done using BLASTp (Altschul et al 1990) with a cut-off e-value less than or equal to e^{-15} .

Figure 19: Completeness of compendium of proteins identified in Golgi fractions by comparison to yeast Golgi proteins. Proteins from different proteomics analyses of the Golgi and Golgi subcellular localization databases are compared to Golgi localized *Saccharomyces cerevisiae* proteins with rat orthologs from Huh et al. (Huh et al 2003) as measure of the extent of protein coverage and completeness. Comparison was done using BLASTp (Altschul et al 1990) with a cut-off e-value less than or equal to e^{-15} . The trend line is indicated by the dashed line.

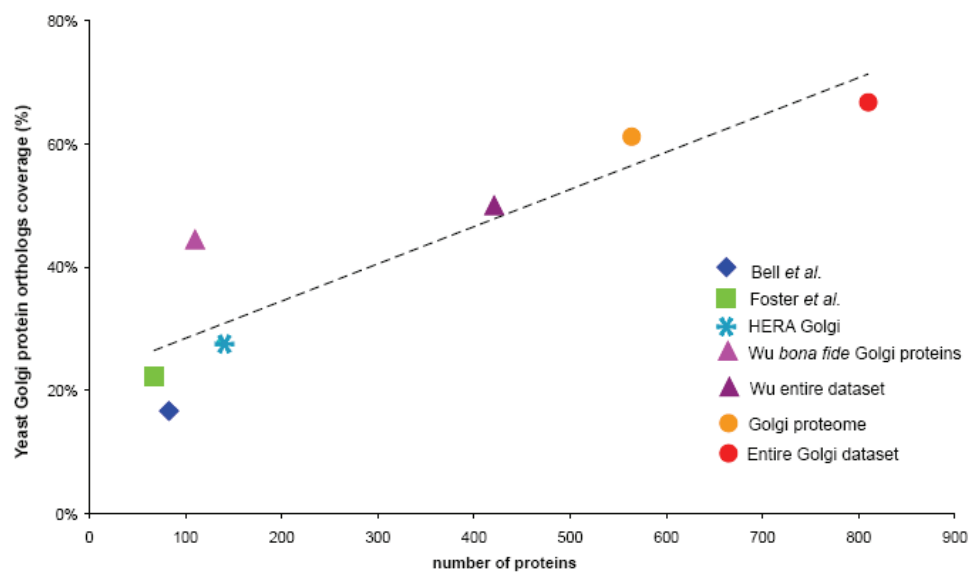


Figure 19

Table 8: Comparison of Golgi proteomics studies and databases with yeast Golgi GFP localized proteins (Huh et al 2003)

Dataset	# of proteins	% coverage
Organelle DB	23	11%
Foster et al. Golgi	67	22%
Bell et al.	83	17%
Wu et al. (literature confirmed)	110	44%
Wu et al.	421	50%
Golgi proteome (contaminants excluded)	564	61%

Protein sequences in the indicated datasets were compared to sequences of proteins localized to the Golgi apparatus in yeast (Huh et al 2003). Values in this table are shown in Figure 19. Comparison was done using BLASTp (Altschul et al 1990) with a cut-off e-value less than or equal to e^{-15} .

Figure 20: Comprehensiveness of compendium of proteins identified in the Golgi fractions by comparison to other Golgi proteomics studies and Golgi subcellular localization databases. The overlap of proteins in the Golgi proteome with proteins identified in other Golgi proteomics studies and Golgi subcellular localization databases is used to measure the comprehensiveness of the Golgi proteome. Comparison was done using BLASTp (Altschul et al 1990) with an e-value less than or equal to e^{-15} .

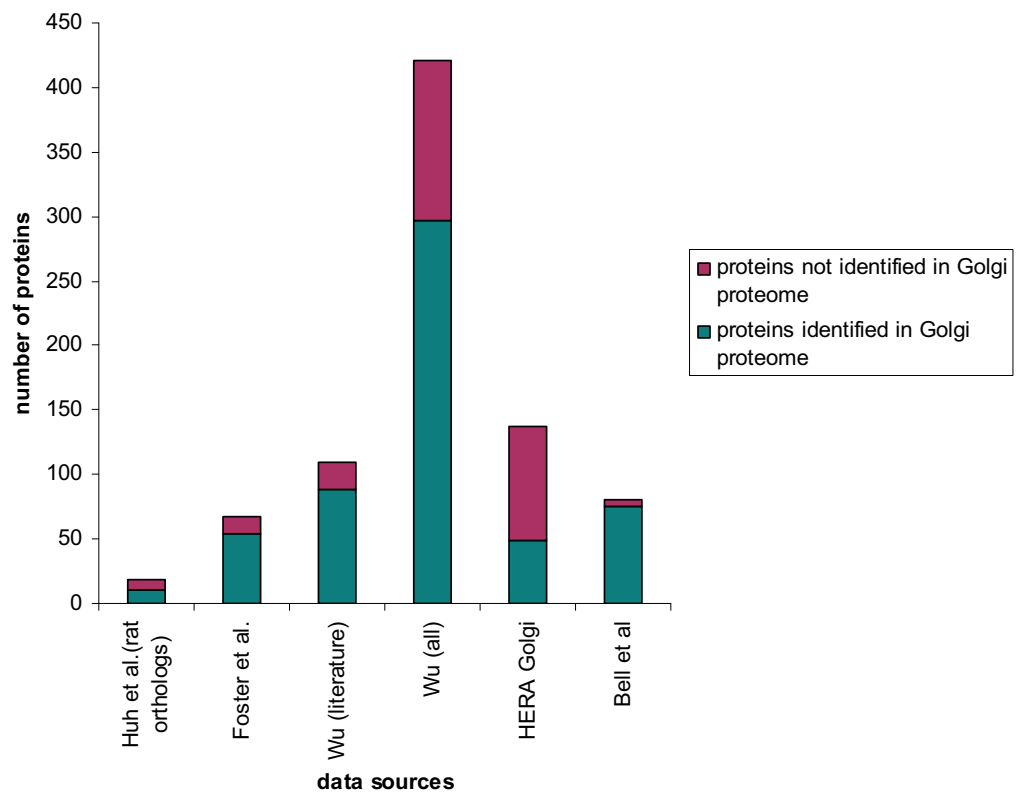


Figure 20

Table 9: Comparison of Golgi proteomics studies and databases with Golgi proteome

Database	# of proteins identified	# of proteins matched to Golgi proteome	% coverage
Huh et al. (rat orthologs)	18	16	89%
Foster et al. Golgi	67	54	81%
Wu et al. (literature)	110	88	80%
Wu et al. (all)	421	297	71%
HERA Golgi proteins	137	49	36%

Protein sequences in the Golgi proteome were compared to protein sequences in the indicated databases. Values in this table are shown in Figure 20. Comparison was done using BLASTp (Altschul et al 1990) with a cut-off e-value less than or equal to e^{-15} .

Characterization of proteins of unknown function

One hundred and seventy six previously uncharacterized proteins were identified in the RM and SM total fractions. These proteins are mainly predicted genes and translated open reading frames. For many of these sequences, this study provides the first evidence of their protein expression. This section describes the identification and bioinformatic characterization of proteins of unknown function and how this analysis led to the functional characterization of 5 novel molecular chaperones.

Distribution of uncharacterized proteins by peptide counts

The proteomics characterization of the RM and SM total fractions uncovered 176 previously uncharacterized proteins. Their predominant distribution by peptide counts in the RM and SM total fractions as well as their co-distribution with marker ER proteins support an ER localization for these proteins (Figure 23). One hundred seventy out of 176 uncharacterized proteins identified in the ER could be assigned to an RM, SM or ER (equally distributed between the RM and SM fractions) location by peptide counts and hierarchical clustering.

Bioinformatics predictions to guide selection for functional analysis

Bioinformatic predictions for the presence of signal peptides (Bendtsen et al 2004), transmembrane segments (Sonnhammer et al 1998), and protein domains (Marchler-Bauer & Bryant 2004) guided the selection of proteins for further functional analysis (Figure 22). The majority of uncharacterized proteins are predicted to be membrane proteins. Protein sequences were also probed for functional domains using InterPro (Zdobnov & Apweiler 2001). Furthermore, of the membrane proteins, single spanning membrane proteins represent the largest category (Figure 21).

Bioinformatic predictions and the partitioning of these proteins into the membrane, saltwash or soluble biochemical subfractions guided the selection of a number of uncharacterized ER proteins for further validation. Criteria for selection required that a protein possess a predicted single transmembrane segment and a large luminal domain. These features were chosen because they are characteristic of calnexin (Schrag et al 2001), a known membrane-bound molecular chaperone. Our rationale was that unknown proteins in the ER with these characteristics could represent other novel membrane bound molecular chaperones. Proteins were also selected if they possessed functional domains (Figure 22) indicative of a protein functioning in the secretory pathway. Of the 169 proteins, 18 proteins that fit these criteria (16 predicted to be integral membrane, two soluble) were chosen for independent validation of subcellular

Figure 21: Characterization of membrane topology of proteins of unknown function. Bioinformatics predictions of membrane spanning regions and cleavable signal peptides for unknown proteins localized to the ER by proteomics were done using TMHMM (Sonnhammer et al 1998) and SignalP (Bendtsen et al 2004) as well as biochemical subfractionation. Shown are proteins with bioinformatic and biochemical fractionation data. The pie charts show the proportion of proteins predicted as membrane, luminal or cytosolic categories. The number of single and multi-spanning membrane proteins is also indicated.

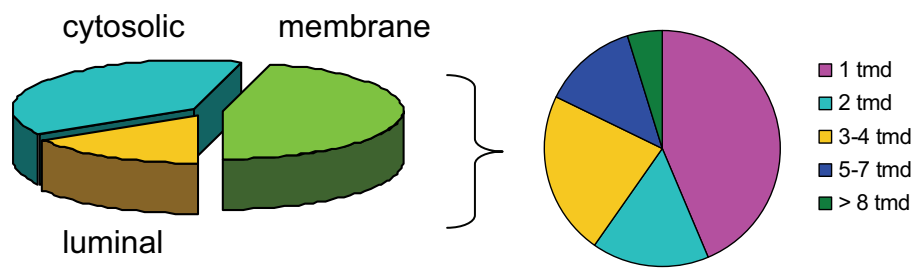


Figure 21

Figure 22: Protein domains in proteins of unknown function showing an ER localization by redundant peptide counts and YFP tagging. NCBI Conserved Domains (Marchler-Bauer & Bryant 2004) was used for protein domain prediction. TMHMM (Sonnhammer et al 1998) and SignalP (Bendtsen et al 2004) were used for transmembrane spanning region and signal peptide and signal anchor predictions.

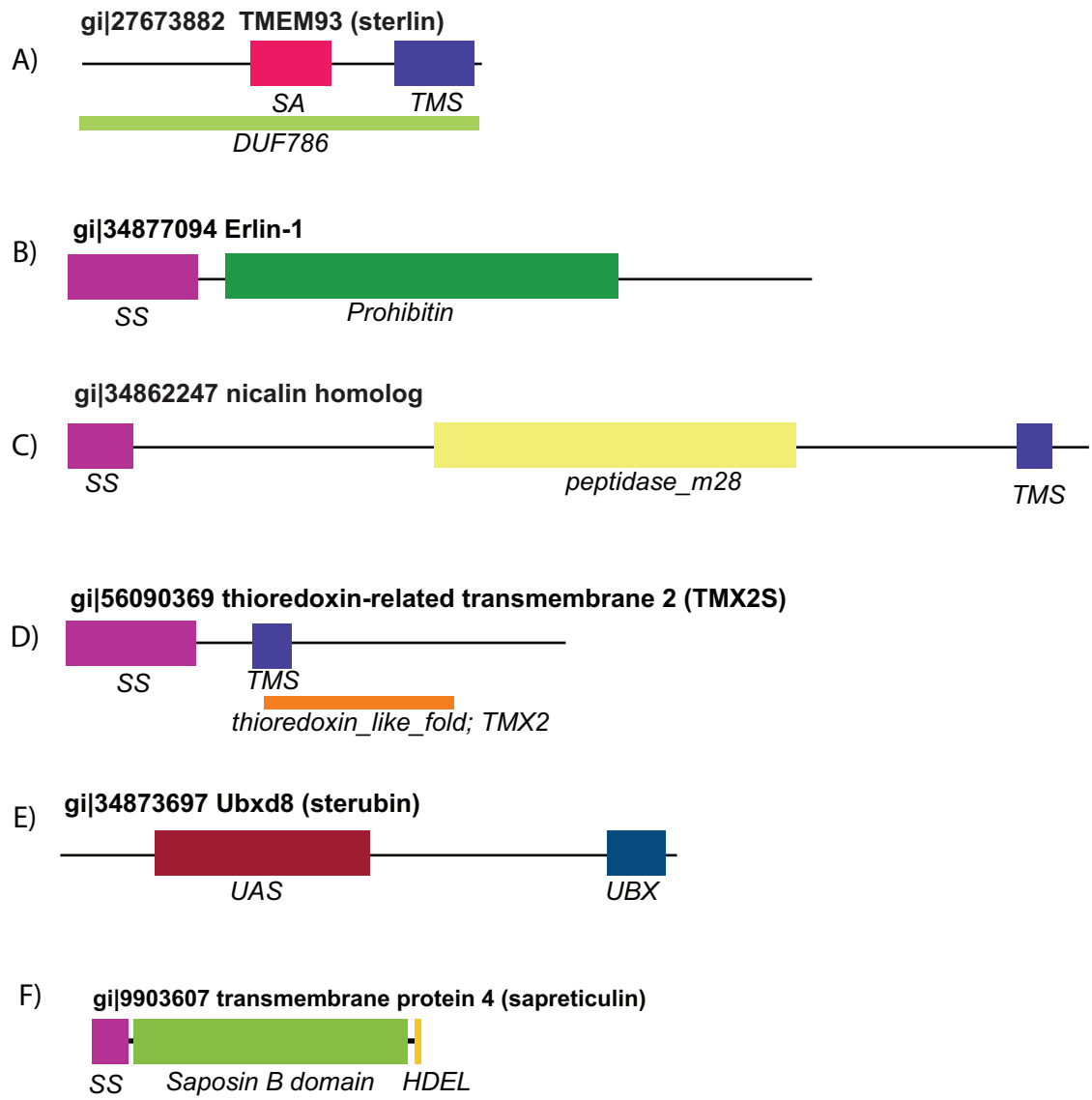


Figure 22

Figure 23: Selected proteins of unknown function and their localization by the distribution of redundant peptide counts. Shown are the mean % total peptides for each protein and a marker protein for the cluster. Values are normalized to 1 for visualization purposes.

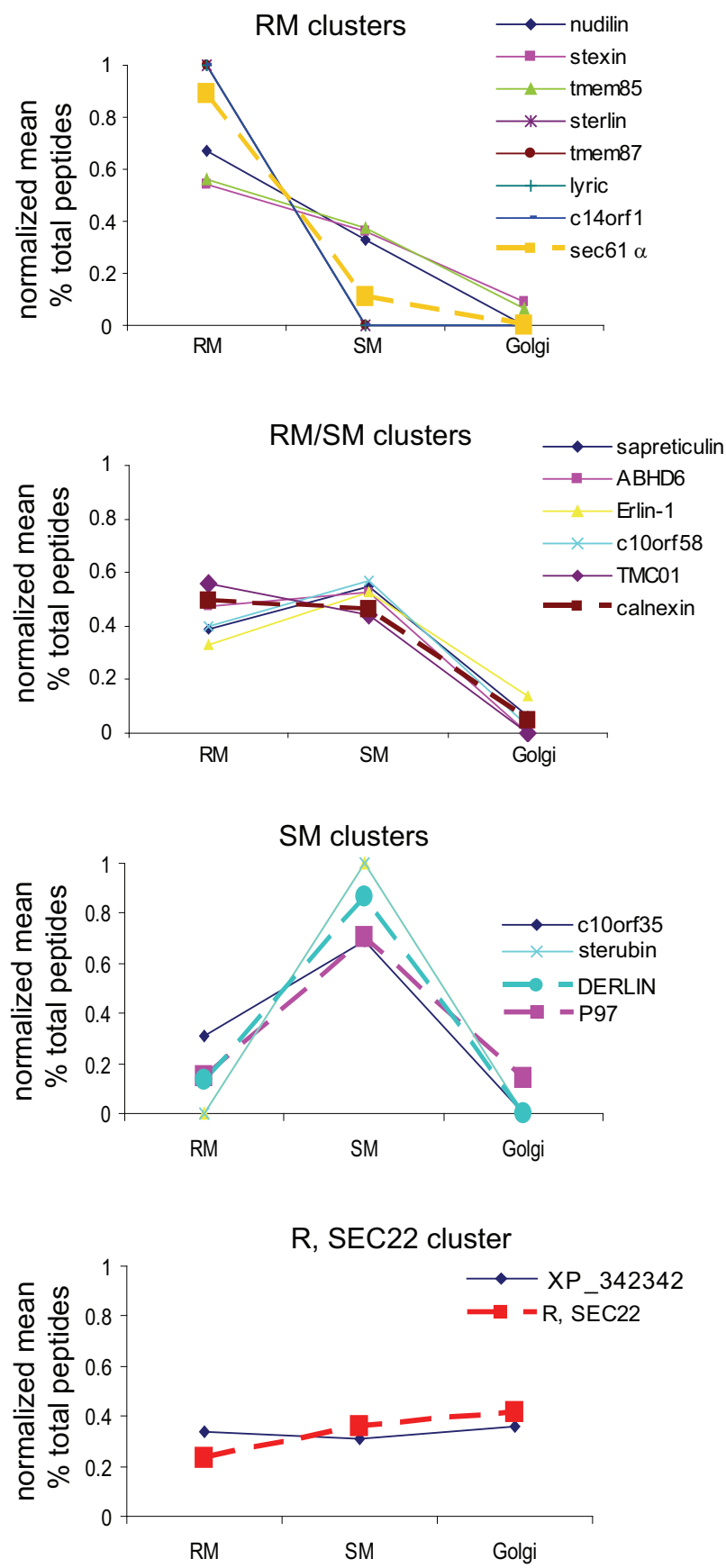


Figure 23

location by YFP tagging. Using monomeric YFP, they were expressed as fusion proteins and visualized by confocal microscopy (Dr. Hisao Nagaya personal communication). Fifteen of these proteins show an ER distribution by peptide counts (Figure 23) and YFP fluorescence validated the ER localization.

YFP localization vs. redundant peptide count localization

There is a discrepancy between the YFP localization and the protein distribution by redundant peptide counts for 3 of the 18 proteins. The subcellular localization of the YFP chimeras reveals a location inconsistent with an ER location, in contrast to the ER distribution observed by peptide counts (Figure 24 and Figure 25). During the course of this work 2 of these 3 were validated in the literature to reside in the ER (Figure 24 and Figure 25). The protein now known as the vitamin K epoxide reductase complex subunit 1 (VKORC1), localizes to the ER (Li et al 2004, Rost et al 2004), in agreement with our redundant peptide counting data (Figure 23). Furthermore, a new Q-SNARE named D-12, localizes to the ER and ERGIC (Okumura et al 2006). As for the protein UNQ501, an independent localization or function has yet to be published. Nevertheless, at least 15 of these proteins are genuine ER residents with the vitamin K epoxide reductase and the Q-SNARE D12 additionally confirmed by redundant peptide counting as ER residents.

Of the 15 proteins localized to the ER by peptide counts and YFP, only 1 protein, transmembrane protein 4 (renamed sapreticulin), has an ER retrieval HDEL sequence at the C-terminus (Figure 24). During the course of this study, this protein was identified and localized to the cytosol (Bornhauser & Lindholm 2005). To further characterize this protein, an anti-peptide antibody was raised in rabbits. The antibody was characterized for specificity by western blot (Figure 26a) revealing a single band at the expected molecular weight (21 kDa) in the post-injection

serum. Furthermore, the protein was immunolocalized in HegG2 cells with this antibody revealing an ER pattern (Figure 26b).

Upregulation of proteins by ER stress and characterization of novel molecular chaperones

Using the signal peptide and transmembrane segment prediction results as well as biochemical subfractionation results, 33 genes corresponding to single spanning membrane proteins were tested for upregulation by quantitative PCR following treatment with ER stress agents – tunicamycin, thapsigargin, DTT and glucose deprivation (Michael Jain personal communication). The rationale was that proteins upregulated during the unfolded protein response could potentially represent novel molecular chaperones. Of the 33 proteins, 7 proteins were upregulated by ER stress. Furthermore, 4 of the seven were shown to be novel molecular chaperones by their transient interaction with the cargo protein tyrosinase (Michael Jain personal communication).

Figure 24: Discrepancies between proteomics localization and YFP localization (I). (A) Redundant peptide counts show an ER localization for UNQ501 and the protein now known as the Vitamin K epoxide reductase (VKORC1) (Li et al 2004, Rost et al 2004). (B) However, YFP chimeras of these proteins and co-localization with calnexin in HepG2 cells show a perinuclear localization indicating a compartment other than ER. Colocalization with calnexin is shown.

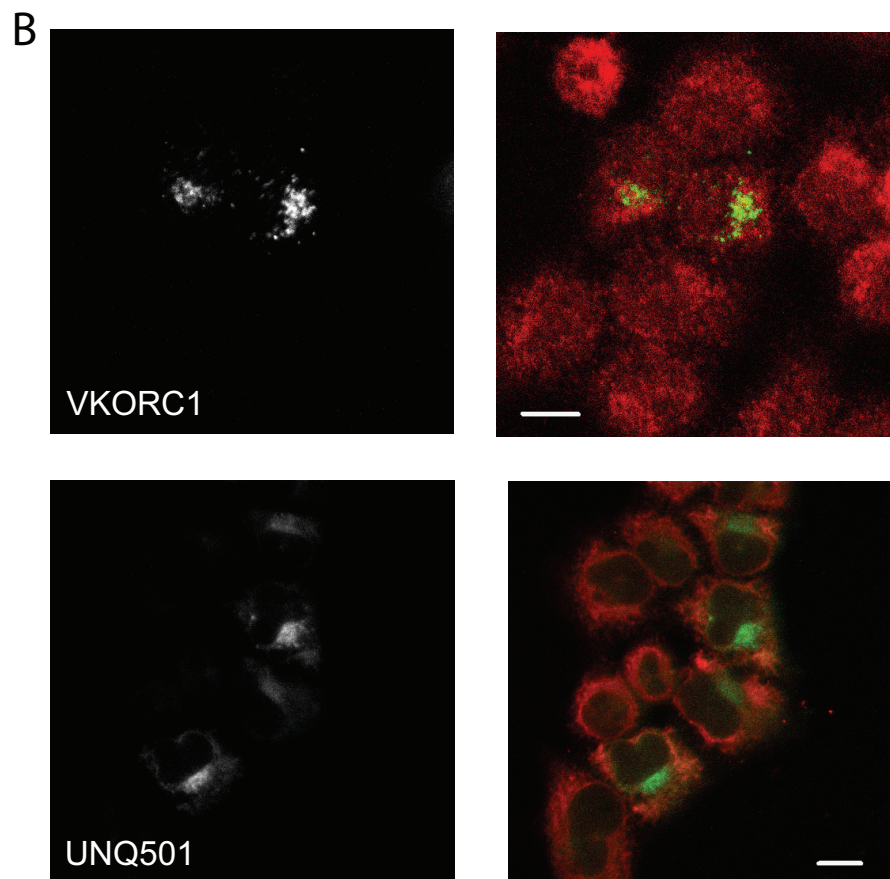
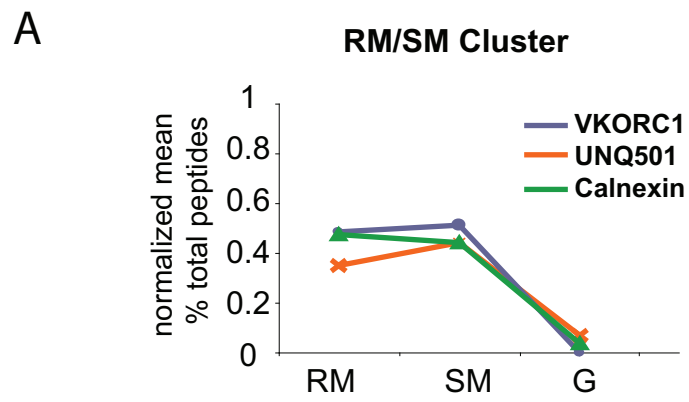
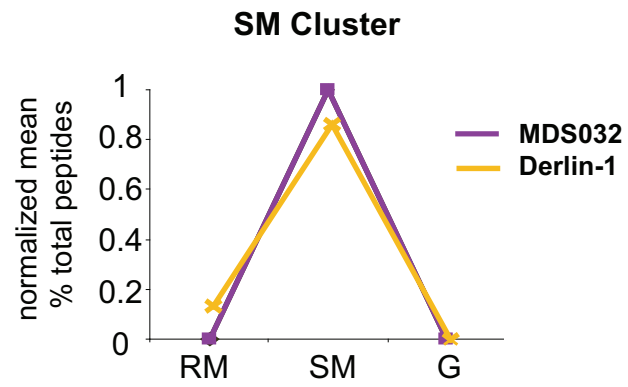


Figure 24

Figure 25: Discrepancies between proteomics localization and YFP localization (II). MDS032, now known to be the ER/ERGIC located Q-SNARE D12 (Okumura et al 2006) shows a smooth microsomal localization by redundant peptide counts. However, the YFP chimera primarily shows peri-nuclear staining indicating a location other than ER. Colocalization with calnexin is shown.

A



B

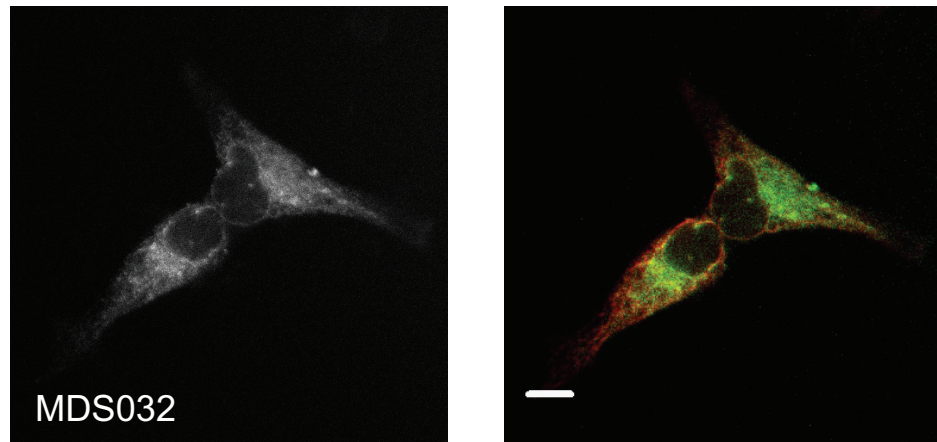


Figure 25

Figure 26: Sapreticulin antibody. Antibodies were raised against a peptide corresponding to amino acids 166-178 (KRTDLCDDHALHRS) of sapreticulin after coupling to KLH. (A) Shown are the results of western blot analysis of serum post-injection of the coupled peptide into a rabbit compared to pre-immune (PI) serum from the same rabbit. A single band of 21 kDa is observed which corresponds to the expected molecular weight (20.636 kDa) of the protein. (B) Immunolocalization of sapreticulin in HepG2 cells revealed an ER localization. Bar, 10 μ m.

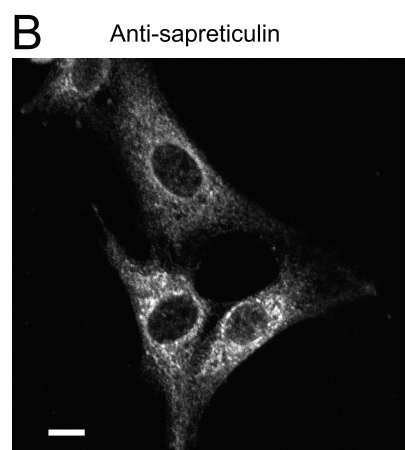
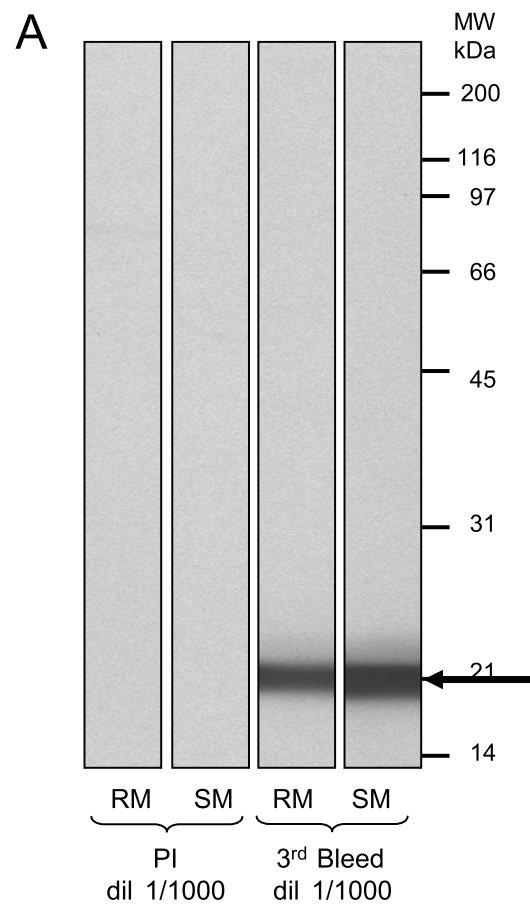


Figure 26

Discussion

The goal of this body of work was to create a protein map of the organelles of the early secretory pathway. During the course of this work, methods were developed which now comprise a functional proteomics pipeline that is currently in use. Research in this thesis contributed to the development of standard operating procedures for the preparation of samples, mass spectrometry, software for the identification of proteins from peptides and their scoring as well as a method to estimate the abundance of proteins (Results: The proteomics pipeline). Quantitative measurements of the abundance of proteins in highly enriched subcellular fractions enabled us to develop a subcellular localization tool based on protein distribution among the RM, SM and Golgi fractions. Using this tool, we were able to independently assess the levels of cross-contamination among these fractions as well as the amount of contamination from other organelles of the cell (Results: Assessment of contamination of RM, SM and Golgi fractions). As an extension of this approach, hierarchical clustering of protein distributions enabled the identification of clusters of proteins which could be assigned to one or more of the organelles (Results: Subcellular localization of proteins by proteomics). This approach revealed the localization of a previously known ER protein, a protein disulphide isomerase, ERp44, to the Golgi apparatus. Furthermore, the localization of proteins was extended by biochemical subfractionation which assigned proteins to either the cytosolic, membrane or luminal regions of the ER (Results: Biochemical subfractionation of RM and SM fractions). To assess the validity of the proteomic approach employed here, protein identifications of the RM, SM and Golgi fractions were compared to other existing datasets (Results: Completeness of protein identifications in the RM, SM and Golgi fractions). This analysis revealed that the use of highly enriched subcellular fractions is the optimal way to achieve a comprehensive

organelle proteome. Finally, the discovery of more than 150 proteins of unknown function in the ER and their subcellular localization by proteomics led to the identification of novel molecular chaperones and serves as a resource to the cell biology community (Results: Characterization of proteins of unknown function).

The proteomics pipeline

The experimental strategy of organellar proteomics described in Results: The proteomics pipeline is composed of three main steps: sample preparation, mass spectrometric analysis and data evaluation. Although subcellular fractionation does not completely separate organelles, the use of highly enriched subcellular fractions significantly increases the probability of identifying proteins that function in the organelle. After peptide identification by mass spectrometry and Mascot (Perkins et al 1999), proteins were grouped by a set of common peptides to identify the least number of proteins accounting for all identified peptides. This step along with a BLASTp analysis reduced redundancy in the protein lists returned by Mascot (Perkins et al 1999). The redundancy occurred because of the presence of allelic isoforms or SNPs in the NCBI non-redundant database. The grouping step also enabled quantitation of the proteins based on the number of redundant peptides. At the same time, assignment of proteins to functional categories by literature search lead to the identification of contaminating proteins which were excluded from many of the analyses presented in this thesis. This annotation step also provided a good way to view the landscape of proteins identified in the RM, SM and Golgi fractions. Using the proteomics pipeline, we were left at the end of the analysis with a non-redundant set of proteins with functional annotation and a measure of their relative abundance in each subcellular fraction. These steps, outlined in Results: The proteomics pipeline, are now automated and in use for every proteomics analysis performed at the Montreal Proteomics Center.

Contamination of the RM, SM and Golgi fractions

By redundant peptide counting and functional annotation, we were able to estimate the amount of cross-contamination between the ER and Golgi fractions. Quantitative subcellular localization by proteomics of marker proteins for the ER and Golgi apparatus identified a maximum of 30% contamination of ER in the Golgi fraction. Past proteomics studies of the Golgi apparatus also uncovered significant ER contamination of the Golgi (Taylor et al 2000, Wu et al 2004). An interpretation of this finding is that there was incomplete separation of the ER from the Golgi during the subcellular fractionation step and that the observed ER proteins were *bona fide* contaminants. However, Mogelsvang and Howell present an alternate explanation (Mogelsvang & Howell 2006). Electron microscope tomography and serial reconstructions of the Golgi apparatus revealed specialized regions of the ER associated with the trans-Golgi stack (Ladinsky et al 2002, Marsh et al 2001). Mogelsvang and Howell (Mogelsvang & Howell 2006) proposed that these ER – Golgi apparatus connections may be facilitating the modification of the lipid composition of the trans-Golgi membranes for sorting into “sphingolipid rich microdomains” or lipid rafts (Simons & Ikonen 1997). Alternatively, these connections could be facilitating cisternal maturation, one of the proposed transport mechanisms operating within the Golgi complex (Marsh et al 2001). These findings support earlier studies from the 1960s and 70s by Novikoff who identified ER, Golgi and lysosomal associations in various tissues, coining the term “GERL” for Golgi ER and lysosomal associations (Novikoff et al 1964, Novikoff & Novikoff 1977, Novikoff et al 1971). Therefore, the ER contamination observed in these studies may not be dismissed simply as incomplete Golgi complex isolation but instead may bear physiological relevance to the function of the Golgi apparatus.

Quantitation and subcellular localization by proteomics also enabled an estimate of contamination of the RM, SM and Golgi fractions by other organelles. The proteomics analysis of the Golgi fraction revealed that peptides derived from mitochondria account for an average of 10% of all peptides identified. This translates to a 10% mitochondrial contamination of the Golgi fraction. Prior morphometry work on the Golgi fraction showed that 84% of the profiles were Golgi and that the remaining profiles were either ER (14%), mitochondria (1%) or peroxisomal cores (1%) (Bell et al 2001). That mitochondria accounted for only 1% of the total volume of the Golgi fraction and 10% of all peptides observed can be explained by the high protein content of the mitochondria resulting in more peptides. Mitochondrial contamination of the RM and SM fractions was also highest among all the contaminating organelles for these fractions. Western blot analysis of the RM and SM fraction with an antibody to the mitochondrial protein, TOM20, supports this result (Figure 7). In contrast to Western blotting, the advantage of using redundant peptide counts to detect contamination is in the ability to compare the abundance of different proteins across a sample. Due to different affinities of antibodies, the amount of contamination can only be assessed one protein at a time on a western blot, i.e. the amount of contamination by TOM20 in Figure 7 can not be directly compared to integrin β 1.

None of the Golgi marker proteins were detected in the RM and SM fractions by redundant peptide counting (Results: Assessment of contamination of the RM, SM and Golgi fractions). This is not surprising and is most likely due to the small volume the Golgi occupies (1% total volume) in the rat liver hepatocyte as compared to the ER (14% total volume) (Blouin et al 1977). Thus, the concentration that a Golgi protein can attain in an ER fraction could not be high enough to out compete other more abundant ER proteins in the mass spectrometer. Prior to this study, the amount of organellar contamination of the RM and SM fraction was not

clear, mainly because other organelles such as the mitochondria and lysosomes were not detected in previous analyses by electron microscopy (Lavoie et al 1996). This limitation is due to the severe homogenation procedure used in ER microsomal preparation which results in fragmentation of mitochondrial and other organellar membranes (except peroxisomal cores) (Lavoie et al 1996). Electron microscopy analysis of the RM fraction has previously identified the presence of peroxisomal cores (Païement & Bergeron 1983). This is an expected finding since peroxisomal cores have the same density as the rough microsomes (1.20 g/cm^3) (Appelkvist et al 1981). By redundant peptide counting, peroxisomal peptides comprised 7.7% of all the peptides in the RM, making this organelle the second most prevalent contaminant (Table 3). In the RM and SM fractions, there were few morphological features to distinguish smooth microsomes from plasma membrane, mitochondria, Golgi or lysosomal membranes (Lavoie et al 1996). However, since the smooth ER makes up about 50% of the volume of the rat hepatocyte (Blouin et al 1977) the likelihood that the smooth membranes seen in the ER fractions are indeed smooth ER is high. Due to this limitation in detecting organellar contamination in the ER fractions, proteomics using peptide counts provides the first indication of the extent of organellar contamination of the ER fractions.

Proteomics coupled with the redundant peptide counting method has established a simple estimate of organellar contamination of the RM, SM and Golgi fractions. These estimates are in agreement with past morphological and biochemical studies of contamination in these fractions. In particular, the proteomics approach provided the first estimate of organellar contamination for the RM and SM fractions. The proteomics approach also enabled the analysis to estimate the reproducibility of the subcellular fractionation procedure and discovered that the 3 RM and SM biological replicates were more reproducible than the 3 Golgi preparations.

Proteome of the early secretory pathway

Proteins identified in the 3 subcellular fractions were often present in 2 or more of the fractions. Hierarchical clustering of protein distribution profiles by redundant peptide counting allowed us to assign proteins to one or more of the isolated organelles. In addition, the assignment of proteins to functional categories allowed us to determine the enrichment of functional categories for proteins identified in these fractions.

An inherent bias existed in our classification method in that proteins were assigned to only one functional category. An example of this was seen in the assignment of the NAC proteins to the protein synthesis and folding category. Recent studies have shown that β NAC (ICD-1) in *C. elegans* is localized to the mitochondria during embryogenesis and is a suppressor of apoptosis (Bloss et al 2003). Furthermore, β NAC is also known as a transcription factor called BTF3 (Zheng et al 1990). However, the largest body of evidence identified β NAC as a member of the NAC complex involved in protein synthesis, which was the reason why it was assigned to this category. Proteins with multiple functions were assigned to a functional category best supported by the literature. Furthermore, in choosing functional assignments, a protein was assigned to a single category which described its role in the secretory pathway or its status as a contaminant. This method deviates from the approach developed by the GO consortium (Ashburner et al 2000). GO terms are organized as connecting nodes of a network, with increasing specificity when moving from parent to child terms. In GO, a protein's function is described by three different ontologies – biological process, molecular function and cellular component (Ashburner et al 2000). For any given protein, its function may be described by a sub network of these three ontologies. Therefore, each protein has several GO terms describing its function, going from general to specific. We

aimed to simplify GO by selecting broad functional categories to describe the proteins identified in this study, which we considered to be more meaningful to other scientists. GO has also recognized the need for more streamlined categories and has addressed this need by introducing GO Slim (<http://www.geneontology.org/GO.slims.shtml>). However, this capability was not available at the time we were conducting this project. Another difference between our approach and the GO approach is the assignment of proteins to multiple functions using GO. Proteins annotated in GO may belong to multiple biological processes, molecular functions and cellular components which reflects the fact that a particular protein may function in several processes, carry out different molecular functions or interact with proteins from different cellular compartments (Ashburner et al 2000). In contrast, our approach assigned proteins to a single category which was best supported by the literature. Doing so made calculating the enrichment of functional categories in a subcellular fraction a more feasible task.

Since biological literature is constantly changing as more information is discovered about the functions of proteins, it was recognized that errors in our classification scheme may have been introduced by us or may evolve as more information is gathered about these proteins. It was for this reason that the proteomics data for this study was stored in CellMapBase, our in-house Oracle database. This database allows for retrieval and update of past proteomics results and the associated annotations. These data were also submitted to Tranche (<http://www.proteomecommons.org/dev/dfs/>) and Peptide Atlas (Desiere et al 2006) for access to the scientific community. The approach of using hierarchical clustering with peptide counts as an index of abundance is likely applicable to all current tandem mass spectrometry-based proteomics efforts. For organellar proteomics, the ability to assign proteins to different organelles becomes especially important in the

characterization of previously uncharacterized or “novel” proteins since knowledge of the location of a protein provides clues about its function.

Hierarchical clustering of redundant peptide counts of proteins identified in the RM, SM and Golgi fraction identified four major clusters. Clusters were selected by co-distribution with marker proteins for the three organelles under study. Sec61 α served as the marker protein for the RM, p97 for the SM, calnexin for the ER (equal distribution between the RM and SM) and mannosidase II for the Golgi. As a validation of the method, the majority of proteins identified in the clusters were known constituents of molecular machines that define functions for rough and/or smooth ER as well as the Golgi apparatus (Figure 10). Prominent proteins in these four clusters that define the rough and smooth ER and Golgi apparatus are discussed in the following sections.

Sec61 α cluster

The majority of proteins in the Sec61 α cluster that localized to the RM belong to the protein synthesis and folding category (Figure 10, Figure 11). Prominent proteins in this cluster include those involved in the translation and translocation of newly synthesized proteins. Four translation initiation factors (eIF2s1, eIF-4G, eIF-5A) as well as elongation factors (EF-2s1, EF1 α 1) make up the translational machinery localized to the RM.

Constituents of the translocon and translocon associated proteins also clustered with the Sec61 α . The nascent-polypeptide-associated complex (NAC) (Wiedmann et al 1994) (Rospert et al 2002) is made up of two subunits, α and β and associates with ribosome bound polypeptides. The proteomics results identified α NAC in the rough microsomes. β NAC, however, was much less abundant. The role of NAC in the cell is not entirely clear. Multiple studies exist supporting its association with

ribosome bound newly synthesized proteins as well as in translocation (Moller et al 1998) (Lauring et al 1995) (Wiedmann et al 1994). A recent study (Bloss et al 2003) localized ICD-1 (β NAC) to the mitochondria during embryogenesis and identified it as a suppressor of apoptosis in *C. elegans*. These results support the role of β NAC in the regulation of the mitochondrial apoptotic program. That β NAC was less abundant than α NAC in the RM functions supports its role elsewhere in the cell.

Not surprisingly, three proteins (p34, p180 and ribophorin I) once considered to be candidates for the ribosome receptor (Johnson & van Waes 1999), co-clustered with Sec61 α , now accepted as the ribosome receptor (Raden et al 2000) (Prinz et al 2000). Other proteins associated with the translocon and localized to the RM were TRAP α and γ (Translocon Associated Protein).

Proteins adjacent to the translocon that act on nascent polypeptides as they enter the lumen of the rough ER were also localized to RM cluster. Six of the seven members of the oligosaccharyltransferase complex were identified (ribophorin I and II, N33/IAP, STT3, OST-48, DAD-1) with all but DAD-1 co-clustering with Sec61 α . Another abundant protein identified in the Sec61 α cluster and localized to the RM is vigilin, a protein involved in RNA transport and metabolism (Kruse et al 2000). Vigilin contains a nuclear localization signal and multiple conserved RNA binding KH domains. Accordingly, vigilin has been localized in ribonuclear complexes containing eEF-1 α and tRNA in both the cytoplasmic and the nuclear fractions by immunoaffinity chromatography using anti-vigilin antibodies (Kruse et al 1998, Kruse et al 2000). A recent study showed that vigilin binds both free and membrane bound ribosomes indicating that binding does not depend on the translation of cytoplasmic or secretory proteins. This finding supports its general role in mRNA targeting to the

ribosome (Kruse et al 2003). This role is consistent with its abundance in the RM which is at a level similar to proteins of the oligosaccharyltransferase, essential proteins of the ER.

Calnexin Cluster

Proteins localized equally to the RM and SM clusters clustered with the ER marker calnexin and belong to two major functional categories – protein synthesis and folding and detoxification. Prominent proteins in these categories include proteins of the calnexin cycle and the cytochrome p450 detoxification system.

Constituents of the calnexin cycle which co-clustered with calnexin are glucosidase II, calreticulin and protein disulphide isomerases including ERp57. Interestingly, of the two glucosidases in the calnexin cycle, only glucosidase II was identified in the RM/SM cluster. Glucosidase I, an integral membrane protein, co-clustered with Sec61 α instead, which can be explained by its early action in the calnexin cycle which positions it closer to the oligosaccharyltransferase in the rough ER (Schrag et al 2003). Binding by calnexin and calreticulin permit enzymes such as the protein disulphide isomerases (PDIs) and peptidylprolyl isomerases (PPIs) to facilitate folding of proteins to the correct three dimensional structure. This happens through the catalysis of the exchange of disulfide bonds by PDIs or isomerisation of polypeptide conformations by PPIs (Bedard et al 2005, McCormick et al 2005, Pollock et al 2004). Of the 6 protein disulphide isomerases in the human genome, four were identified in the calnexin cluster. During formation of disulphide bonds in incompletely folded proteins, PDIs donate electrons to acceptor proteins. Ero1, a protein which directly oxidizes some members of the PDI family to facilitate electron transfer (Frandsen & Kaiser 1999, Tu et al 2000), also clustered with calnexin.

BiP, one of the most abundant identified ER chaperones, and the BiP associated proteins GRP94, ERp72, also co-clustered with calnexin. These results support past co-immunoprecipitation studies, which have shown BiP associated with these four accessory proteins during the folding of thyroglobulin (Kuznetsov et al 1997). Another BiP interacting protein, mammalian Grp170, also co-clustered with calnexin in agreement with the recent evidence showing the role of Grp170 as an alternate nucleotide exchange factor for BiP (Weitzmann et al 2006).

Another important function of the ER is the detoxification and clearance of drugs and other xenobiotics. The three most abundant protein families involved in this process and detected in the calnexin cluster are the cytochrome p450s, glucuronosyl transferases and the carboxylesterases. Of the 34 cytochrome p450s identified in the total ER fractions, 25 co-clustered with calnexin. Similarly, 5 out of 9 carboxylesterases showed the same equal distribution between the RM and SM fraction. Finally, of the 11 glucuronosyltransferases identified in the ER and Golgi fractions, 11 were identified in the RM and SM cluster.

p97 cluster

Proteins that clustered with p97 localize to the smooth microsomal clusters and belong to protein synthesis and folding and detoxification categories. Prominent proteins include p97, Derlin, reticulon 3 and short chain dehydrogenases/reductases. Derlin-1, which was identified as a component of the ERAD retro-translocation machinery and shown to interact with p97 (Lilley & Ploegh 2004, Ye et al 2004), displayed a similar pattern of distribution and co-clustered with p97. The abundance of p97 and Derlin in the SM fraction supports past observations of a “degradation compartment” of the ER. As support for this hypothesis, two studies have identified this compartment morphologically as a ribosome-free

compartment which accumulates misfolded proteins (Hobman et al 1994, Raposo et al 1995).

Reticulon 3, a member of the reticulon class of proteins (RTNs) is the only member of this class of proteins identified in the ER fractions of rat liver. Voeltz et al. (Voeltz et al 2006) showed that these proteins are predominantly localized to smooth ER tubules and excluded from the nuclear envelope. In addition, overexpression of reticulon 4a lead to the formation and maintenance of long tubules in yeast while deletion lead to loss of ER tubules (Voeltz et al 2006). Much of the work on the reticulons has been done on reticulon 4 and mostly in brain. For the first time, this study identifies reticulon 3 as an abundant member of this class of proteins expressed in the rat liver ER and localized it to the smooth microsomes.

Apart from the cytochrome p450s, other detoxification proteins clustered with p97 and localized to the smooth ER. The short chain dehydrogenase/reductase family of proteins were the most numerous and among the most abundant. Short-chain dehydrogenases/reductases (SDR) constitute a functionally heterogeneous superfamily of enzymes and are defined by a common folding pattern and sequence motif (Oppermann et al 2001). The 3 most abundant SDR proteins localized to the SM function in hormone and retinol metabolism.

Mannosidase II α 1 cluster

Proteins which clustered with mannosidase II were assigned to the Golgi fraction. The most abundant proteins in this cluster are those in the biosynthetic cargo category (Figure 11). This is consistent with the concentration of cargo in the Golgi observed by electron microscopy (Claude 1970, Dahan et al 1994). As biosynthetic cargo proteins traffic through the Golgi, they are post-translationally modified by sugar

transferases. Thirty-one Golgi sugar transferases co-clustered with mannosidase II α 1 and were assigned to the Golgi.

This proteomics localization approach led to the unexpected finding that ERp44, the RDEL-terminating PDI family member, co-distributed with mannosidase II (Figure 11). Previous localization studies on ERp44 using an HA-tagged ERp44 showed an ER localization (Anelli et al 2002). We confirmed the Golgi localization indicated by the peptide counts by indirect immunofluorescence using a polyclonal antibody to ERp44, revealing a predominant juxtanuclear staining typical of the Golgi and largely overlapping with the Golgi marker GM130 (Figure 13). Some reticular ER-like staining was also found which is consistent with the low peptide counts for ERp44 in the RM and SM fractions. This is the first time that a PDI ortholog with a C-terminal RDEL retrieval motif displayed a steady state Golgi distribution. A study by Anelli et al. (Anelli et al 2003) showed that ERp44 functions to retain the oxidoreductase ERO1 in the ER in a process called thiol-mediated protein retention. More recently, ERp44 has been shown to bind and inhibit the inositol 1,4,5-triphosphate receptor (IP3R1), a calcium release channel in the ER (Higo et al 2005). Inhibition of IP3R1 by ERp44 was dependent on free cysteine groups on IP3R1. Both these roles for ERp44 are consistent with its previously known ER localization. Therefore, the function of ERp44 in the Golgi apparatus remains to be determined.

The Rab and SNARE family of proteins also co-distributed with mannosidase II α 1. These protein families cooperate to ensure the fidelity of vesicle fusion to target membranes (Zerial & McBride 2001). The most prominent Rabs characterized here were Rab1A, 1B, 5, 6 14, 18. Sequence identity between Rab1A and 1B is high (>90%) but despite this, the proteomics method distinguished between the two. Both Rabs were equally abundant and showed an identical distribution among the ER

and Golgi fractions. Studies examining the regulation of Golgi structure and membrane traffic through the Golgi (Alvarez et al 2003, Wilson et al 1994) have identified Rab1A and Rab 1B as factors affecting these processes. Rab 6 was initially identified as a Golgi specific Rab (Goud et al 1990) and was localized to vesicles involved in retrograde transport from the Golgi to the ER (White et al 1999). Recent work has shown that Rab6 isoforms have varied, non-overlapping functions in membrane trafficking (Del Nery et al 2006). Although less understood mechanistically, Rab14 is a Golgi-localized Rab (Junutula et al 2004). Although 11 other Rabs were uncovered here, their abundance was much lower. Nine SNAREs were observed considerably extending our past proteomics effort to uncover Golgi SNAREs (Bell et al 2001). In this study, the Q-SNAREs Gos-28 and Syntaxin 5 were the most abundant.

A family of proteins which interact with Rabs is the conserved oligomeric Golgi (COG) complex (Ungar et al 2006). These proteins comprise a multisubunit peripheral membrane protein complex that controls several aspects of Golgi structure and function and is composed of 8 subunits, 5 of which were identified in this study. Recent work using COG3-siRNA to impair COG function in a mammalian cell line resulted in the accumulation of vesicles suggesting that the COG complex is involved in vesicle fusion (Zolov & Lupashin 2005). The accumulation of vesicles along with the interaction of COGs with Rab proteins suggested that this complex may be functioning as a tethering factor (Ungar et al 2006).

In summary, hierarchical clustering of protein distribution profiles determined by peptide counting assigns proteins to their cognate organelles. Four major clusters were identified by this approach. Examination of these clusters validates the approach of analyzing highly enriched subcellular fractions and quantifying proteins by redundant

peptide counting as a way to assign proteins to their respective organelles.

Completeness of the protein identifications for the RM, SM and Golgi fractions

Based on comparisons with yeast localized ER proteins in the Huh et al. study (Huh et al 2003), we determined that the list of proteins identified in the RM and SM fractions is at least 50% complete and the compendium of proteins identified in the Golgi is at least 60% complete. The proteins identified in RM, SM and Golgi fractions encompass the majority of proteins identified in prior proteomics analyses of these organelles (Bell et al 2001, Foster et al 2006a, Wu et al 2004). Furthermore, the proteomic analysis of the RM, SM and Golgi fractions detailed in this thesis identified the greatest number of proteins for these organelles. In sum, the comparison to Huh et al. supports the conclusion that the list of RM, SM and Golgi proteins from this study are the most comprehensive to date.

How valid was this analysis? A similar examination was performed by Andersen et al. (Andersen et al 2005) in their proteomics analysis of the human nucleolus. In their study, they determined by comparison to the yeast localization database of Huh et al. (Huh et al 2003) that their nucleolar proteome was 80% complete. Therefore, this is a common approach used to assess the completeness of a proteomics analysis. The validity of this approach depends on the quality of the Huh et al. (Huh et al 2003) localizations and whether proteins conserved between yeast and mammals are truly representative.

In their localization of yeast proteins, Huh et al. (Huh et al 2003) integrated a DNA sequence, encoding either a tandem affinity purification tag (TAP) or green fluorescent protein (GFP), by homologous

recombination. These tags were positioned in-frame with the 3'-end of the coding sequence of each gene and in its original chromosomal location. This approach does not affect the promoter and upstream regulatory sequences of the tagged genes with the aim that genes are expressed at endogenous levels and behave normally. In the first round of localization, GFP patterns were classified into 12 general subcellular localization patterns, such as the nucleus and mitochondria. In a second set of experiments, unknown proteins were co-localized with marker proteins tagged with red fluorescent protein. Using both approaches, Huh et al. (Huh et al 2003) identified a total of 22 compartments to which 75% of yeast proteins localized.

An analysis of the quality of the Huh et al. (Ross-Macdonald et al 1999) study suggests that the results are reliable and of high quality. First, a comparison of the localizations in Huh et al. (Huh et al 2003) with annotations for the localization of yeast proteins in SGD showed that there was 80% agreement with SGD. Second, results obtained by Huh et al. (Huh et al 2003) were comparable to the previous large-scale localization study of yeast proteins by immunofluorescence (Ross-Macdonald et al 1999). Third, a comparison with mass-spectrometry based organellar proteomics of the nucleolus and spindle pole, yielded good coverage (Ross-Macdonald et al 1999). Therefore, results of these comparisons suggest that the Huh et al. study (Ross-Macdonald et al 1999) is a reliable reference for subcellular localization in yeast.

The second question about the reliability of comparing to yeast localized proteins is whether proteins conserved between yeast and mammals are truly representative for a mammalian proteome. It is evident that studies in yeast have paved the way for analysis in mammals (Henry & Patton-Vogt 1998, Pelham 1999). In particular, the landmark study of Novick et al. (Novick et al 1980), identified temperature-sensitive

secretory mutants (sec) of *S. cerevisiae* which led to the elucidation of the molecular mechanisms involved in communication and transport between organelles. Importantly, these mechanisms are conserved in mammals (Novick et al 1980, Schekman & Novick 2004). An ideal comparison for the completeness of the proteome would be to benchmark against a localization study in mammals. Localization studies by GFP-tagging have been done previously in mammals (O'Rourke et al 2005); however, these studies mainly focused on uncharacterized proteins and would not yield a comprehensive comparison. Therefore, at this time, the study of Huh et al. (Huh et al 2003) remains the most comprehensive study for protein localization at the whole genome level.

Vision of the cell map

One of the goals of organellar proteomics is to create a complete, accurate and permanent protein map of the cell (Au et al 2007). MS analysis of isolated organelles is in a position to achieve this goal since the small volume of these structures ensures that protein concentrations in the sample are high. This overcomes the dynamic range problem of current MS-based proteomics efforts [34]. However, the benefit of subcellular fractionation is offset by the problem of contamination.

Two studies have tried to address the problem of contamination in similar ways (Dunkley et al 2006, Foster et al 2006a). Dunkley et al. (Dunkley et al 2006) have addressed this using an isotope tagging technique that enables the assignment of proteins to subcellular compartments. The method, called LOPIT (localization of organelle proteins by isotope tagging) determines the distribution of any given protein within an iodixanol density gradient. This distribution was measured using isotope tagging with ICAT (Dunkley et al 2004) and more recently iTRAQ (Dunkley et al 2006). The confidence in subcellular localization was determined by comparing protein distribution profiles to

the distribution of 12 known organellar proteins. Scores rating the confidence in subcellular localization were calculated using partial least squares discriminant analysis. Uncharacterized proteins were localized to an organelle when their scores match those of known organellar residents. This method attempts to overcome the contamination issue, as organelles will have different but overlapping distribution patterns that can be discriminated from one another using this statistical approach. LOPIT analysis on fractionated endomembranes from *Arabidopsis thaliana* callus cultures enabled the simultaneous localization of 527 proteins to the ER, plasma membrane, Golgi apparatus, vacuolar membrane and mitochondria/plastids.

A similar but label-free approach was used by Foster et al. (Foster et al 2006a) in their effort to map proteins of the endomembrane system of mouse liver. Using protein correlation profiling, they identified proteins in 10 organelles of mouse liver including the ER and Golgi apparatus. This work extended a previous study that used the same method in its analysis of the mammalian centrosome (Andersen et al 2003). Protein correlation profiling involves tracking the abundance of peptides in all fractions of an analytical gradient. Distribution profiles of all identified proteins are compared to profiles of known marker proteins. Accordingly, protein distribution profiles that deviate from marker profiles were considered contaminants. In this study, Foster et al. (Foster et al 2006a) identified 1404 proteins with multiple locations assigned to 39% of the proteins.

A comparison with the Foster et al study (Foster et al 2006a) emphasizes the strength in our approach of using highly enriched subcellular fractions for organellar proteomics. Their method of separating organelles in a single continuous sucrose gradient resulted in the identification of far fewer Golgi and ER proteins when compared to the work presented here. Furthermore, only 19 of the 67 proteins they

characterized as Golgi are accepted in the literature as true resident Golgi proteins (Table S4). The other 48 proteins are essentially known contaminants. By contrast, using highly enriched subcellular fractions, we identified and assigned to the Golgi a greater number of proteins (including the majority identified in the Foster et al study (Foster et al 2006a)) with a higher percentage of known resident Golgi proteins. This finding indicates that the “divide and conquer” approach of using highly enriched subcellular fractions is the optimal way to create the cell map.

Although the protein lists identified in the RM, SM and Golgi fractions are the most comprehensive to date, the number of proteins identified in this study falls short of the predicted number of proteins in the ER and Golgi complex based on the Huh et al study (Huh et al 2003). An extrapolation of the proteins localized to the ER and Golgi in yeast suggests that proteins associated with the ER and Golgi complex in humans is between 2850 and 4110 (Simpson & Pepperkok 2003), which is at maximum double the number of proteins identified in this study. This observation suggests that we may have reached the limit in detection for mass-spec based organellar proteomics. However, improvements in the data acquisition by the mass spectrometer used in this study could potentially identify more proteins. For example, the use of exclusion lists (Chen et al 2005) in which a peptide, once detected, is not sampled for a certain window of time could be implemented. This approach would aim to detect lower abundance proteins that are masked more abundant peptides. Another reason why proteins could have been missed by this study could be the transient association of proteins with the ER and Golgi. These proteins may be difficult to detect by mass-spectrometry may require the use of other approaches such as GFP localization to detect these transient protein-organelle interactions (Simpson & Pepperkok 2003). Finally, other high throughput means to functionally characterize proteins such as RNAi (Bard et al 2006) and protein-protein interactions

(Gavin et al 2006) could provide more information on the functions of many of the “novel” proteins identified in this study.

In summary, the approach of using highly enriched subcellular fractions for mass spectrometry based protein identification has yielded the most extensive and comprehensive protein map of the secretory pathway. Improved mass spectrometry data acquisition and analysis of different tissues could detect proteins beyond those identified in this study. Furthermore, other global approaches to studying protein function and localization would contribute to the goal of elucidating a comprehensive, accurate and permanent cell map.

Biochemical subfractionation and novel proteins

One of our goals for this study was to identify novel resident proteins of the target organelles. Although this aim was on the whole achieved, very few of these previously uncharacterized proteins have been investigated in detail. Over 300 “unknown proteins” were identified and localized to either the rough and/or smooth microsomes or Golgi apparatus in this study. Of these proteins, 176 were uncovered in the rough and smooth microsomal fractions and 170 proteins were assigned by hierarchical clustering of redundant peptide distributions to either a rough and/or smooth ER location. Furthermore, biochemical subfractionation and bioinformatics prediction (TMHMM and SignalP) assigned these proteins to either the cytosolic, membrane or luminal compartment of the ER membrane. These results guided the selection of 33 single spanning membrane proteins for further functional analysis by other members of the laboratory. They tested these genes for upregulation by quantitative PCR following treatment with ER stress agents and showed 7 to be upregulated by ER stress. Furthermore, four of the 7 were shown to be novel molecular chaperones (Michael Jain unpublished data).

The subcellular localization of these proteins by proteomics was compared to localization of YFP-chimeras. Both methods localized 15 of the 18 proteins tested to the ER. Two of the three proteins showing a discrepancy were validated separately by others as ER proteins during the course of this work (Li et al 2004, Okumura et al 2006, Rost et al 2004). Thus, the subcellular localization method by redundant peptide counts observed in highly enriched organelle preparations performed better than YFP localization.

Bioinformatic predictions for the presence of signal peptides (Bendtsen et al 2004), transmembrane segments (Sonnhammer et al 1998), and protein domains (Marchler-Bauer & Bryant 2004) guided the selection of proteins for further functional analysis (Figure 22). The large number of previously uncharacterized proteins in the RM and SM fractions required a method to screen for their functions. One facile way to narrow down the number of proteins to study was to test for their upregulation under ER stress. Furthermore, since molecular chaperones comprise a class of proteins that are upregulated during ER stress, novel molecular chaperones could be identified by their association with incompletely folded proteins. This strategy was chosen because the reagents and the assays were already established in our laboratory due to the Bergeron lab's research history with the protein folding protein, calnexin.

Using the signal peptide and transmembrane segment prediction results as well as biochemical subfractionation results, 33 genes corresponding to single spanning membrane proteins were tested for upregulation by quantitative PCR following treatment with ER stress agents – tunicamycin, thapsigargin, DTT and glucose deprivation (Michael Jain personal communication). The rationale was that proteins upregulated during the unfolded protein response could potentially

represent novel molecular chaperones. Of the 33 proteins, 7 proteins were upregulated by ER stress. Furthermore, 4 of the seven were shown to be novel molecular chaperones by their transient interaction with the cargo protein tyrosinase (Michael Jain personal communication).

Localization of uncharacterized proteins by redundant peptide counting and hierarchical clustering and the bioinformatics analysis of TMDs and protein domains allowed us to rename the 7 proteins upregulated by ER stress. The names associated with these proteins in the NCBI database were uninformative, revealing very little to no information about their function. Therefore, in order to describe their newly discovered functions, three of the 7 proteins were renamed to reflect their upregulation by ER stress (indicated by the prefix “ster”) and the functional domains they possess through the bioinformatics predictions. Sterubin and sterlin were two proteins which were upregulated by ER stress but did not function as molecular chaperones. Sterubin (Figure 22E) is a soluble protein assigned to the SM based on peptide counts and co-distribution with p97. The YFP-chimera of sterubin also localized to the ER. This protein contains an ubiquitin associated domain (UAS) and an ubiquitin-like domain (UBX) domain (Figure 22E). Sterubin is related to other UBA/UBX-containing proteins like Faf1 (Chu et al 1995) and p47 (Kondo et al 1997) and may serve as an adaptor molecule involved in shuttling proteins to the proteasome for degradation. Sterlin possesses a predicted signal anchor and a transmembrane segment as well as a domain of unknown function (DUF786) (Marchler-Bauer & Bryant 2004). This domain is conserved in several members of the eukaryotic kingdom from fungi to mammals. Although the domain provided no clues about the function of the protein, its conservation indicates that this protein may play an important role which was retained in the evolutionary process. The last protein stexin, which was upregulated during ER stress and identified as a molecular chaperone, has no

functional domains except for a cleaved signal sequence and a single transmembrane segment. The rest of the uncharacterized proteins upregulated during ER stress (TMX2, nicalin, erlin) have domains which may ascribe functions to these proteins. The clearest example is TMX2 which has an atypical single thioredoxin domain (Ellgaard & Frickel 2003). Thioredoxin domains are found in protein disulfide isomerases, classical members of the ER protein folding family. Nicalin has a predicted Zn peptidase domain (Figure 22C) which suggests that the protein may be involved in cleavage of polypeptides in the ER. A previous study found an effect of a nicalin homologue on nodal signaling and axial patterning in zebrafish (Haffner et al 2007) which suggests an important developmental role for an ER protein.

Erlin-1 is an abundant transmembrane ER protein with a prohibitin-like domain (PHB). Erlin-1 was upregulated in response to tunicamycin and associated transiently with the immature form of tyrosinase. Recently, Erlin-1 has been described as a protein of unknown function that localizes to a lipid raft-like microdomain of the ER in a cholesterol-dependent manner (Browman et al 2006). The functional significance of the prohibitin domain in an ER protein is unclear at present.

The luminal saposin domain containing protein with a cleaved signal sequence and a C-terminal HDEL ER retrieval signal did not upregulate under ER stress conditions (M. Jain personal communication). Another group described this protein as a cytosolic protein (MSAP) which interacts with the ezrin-radixin-moesin (ERM)-like myosin regulatory light chain-interacting protein (MIR) (Bornhauser & Lindholm 2005, Bornhauser et al 2003). Both proteins were co-localized in cell lines and in primary neurons. By contrast, we conclude an ER location for this protein by several lines of evidence: redundant peptide counting (Figure 23 see RM/SM clusters), the localization of an YFP chimera and its

immunolocalization (Figure 26B). The reticulated pattern of its localization, its saposin B domain and its soluble character lead to the proposal that the protein be named sapreticulin. The significance of its saposin B domain is unclear. Saposins are small lysosomal proteins that serve as activators of various lysosomal lipid-degrading enzymes (O'Brien & Kishimoto 1991). They most likely act by isolating the lipid substrate from the membrane surroundings, thus making it more accessible to the soluble degradative enzymes (Liepinsh et al 1997). Since the synthesis of mostly all of the major classes of lipids (phospholipids and cholesterol) necessary for the production of cell membranes occurs in the ER (Vance & Vance 2004), sapreticulin may represent a novel constituent of this process .

Conclusion

In summary, the subcellular localization method using redundant peptide counts for proteins detected in highly enriched subcellular fractions of isolated ER and Golgi apparatus has defined the most comprehensive ER and Golgi proteome to date. This approach should be platform independent since redundant peptide counts are normalized to the total number of peptides assigned in a proteomics experiment. Furthermore, this approach brings the realization of a Cell Map closer to reality. One can envision the introduction of proteins identified from other organelles (mitochondria, lysosomes) into the existing results. The distribution of proteins among a greater number of organelles would not only increase the coverage of the rat liver hepatocyte proteome but would also verify the state of the many proteins classified here as contaminants. This would be particularly useful for the many “unknown proteins” uncovered in these studies since many have no distinguishing features to assign them to a particular organelle.

An equally interesting investigation would be to survey the proteome of the secretory pathway in different tissues to see how

morphological differences translate into the types of proteins identified. This type of study was attempted by Kislinger et al. (Kislinger et al 2006) who compared different proteomes of different tissues with mRNA expression. However, the analysis of the organelles of the secretory pathway was incomplete since they used crude microsomal fractions.

Another avenue for future investigation lies in the elucidation of the functions of the many unknown proteins identified in the ER and Golgi proteomes. A strategy set forth by Bard et al. (Bard et al 2006) involving a genome wide RNAi screen in a *Drosophila* cell line has identified genes involved in protein secretion and Golgi organization. The same screen could be applied to the number of unknown Golgi proteins to observe the effect on Golgi organization and protein secretion. In general, the elucidation of function of these unknown proteins linked to their location will open up an entirely new area of investigation relevant to organelle identity and trafficking mechanisms.

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Appendix I

OCs	✓	DATE
DB	✓	10/10/07
APPROVED		

www.mcgill.ca/research/compliance/animal/forms/


McGill University Animal Care Committee

RENEWAL of Animal Use Protocol

For: Research ☒ Teaching ☐ project

For Office Use Only:

Protocol #: 4741

Approval end date: June 30, 2008

Facility Committee: Dow

Renewal#: 1st2nd

Principal Investigator: John J. M. Bergeron

Protocol # 4741

Protocol Title: Molecular Cytology of Membrane Dynamics

Category: C

Unit, Dept. & Address: Anatomy & Cell Biology, 3640 University St., room 148

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Funding source: Canadian Institutes of Health Research

17016 4546

Start of Funding: July 1, 2003

End of Funding: Sept. 30, 2008

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Emergency contact #2 + work AND home phone #s: Pamela Cameron, work 514-398-6352, home 514-845-1086

1. Personnel and Qualifications

List the names of the Principal Investigator and of all individuals who will be in contact with animals in this study and their employment classification (investigator, technician, research assistant, undergraduate/graduate student, fellow). Indicate if the Principal Investigator is not handling animals. If an undergraduate student is involved, the role of the student and the supervision received must be described. Training is mandatory for all personnel listed here. Refer to www.animalcare.mcgill.ca for details. Each person listed in this section must sign. (Space will expand as needed)

Name	Classification	Animal Related Training Information		Occupational Health Program *	Signature "Has read the original full protocol"
		UACC on-line Theory course	Workshops + others		
John Bergeron*	PI	2005		no	John Bergeron
Ali Fazel	Res. Assist.	2004	rat (2002) & mouse (2004)	yes (2004)	Ali Fazel
Pamela Cameron**	Technician	2004	mouse workshop 2004	yes (2004)	Pamela Cameron
Michael Jain**	Grad. Student	2004	mouse workshop 2003	yes (2004)	Michael Jain

*does not work with animals
**works with mice only

* Indicate for each person, if participating in the local Occupational Health Program, see <http://www.mcgill.ca/research/compliance/animal/occupational/> for details.

Approved by:

2. Approval Signatures

Principal Investigator/ Course Director		Date: 18-APR-2007
Chair, Facility Animal Care Committee		Date: 23 APRIL 2007
UACC Veterinarian		Date: 27/04/07
Chairperson, Ethics Subcommittee (D level or Teaching Protocols Only)		Date: _____
Approved Animal Use Period	Start: July 1, 2007	End: June 30, 2008

☐ Renewal requires submission of full Animal Use Protocol form

 26 APR 2007
TOTAL P.02



McGill University Internal Radioisotope Permit

30070194

Permit Holder & Position JOHN J.M. BERGERON, PROFESSOR & CHAIR Department ANATOMY AND CELL BIOLOGY	Building (Office) STRATHCONA & DENT. Room Number(s) SAD 1/53	Building (Lab) GENOME CTR. Room Number(s) 6400-6503	Laboratory Classification INTERMEDIATE Telephone 398-1259	Telephone 398-6352	PLEASE POST Date Issued 2006/09/01 Expiry Date 2007/08/31

PERSON(S) APPROVED TO WORK WITH RADIOISOTOPES

Name	Train.	Cond(s)	Class(es)	Radioisotope(s)
JOHN J.M. BERGERON, PROFESSOR	N	6	6	
ALI FAZEL, RESEARCH ASSISTANT	Y	1, 2, 4	2, 3, 4	C-14, H-3, I-125, P-32, S-35
FREDRIC LAPORTE, GRADUATE STUDENT	Y	6	6	
MARY DEBINA, LAB ASSISTANT	N	6	6	
PANELA CAMERON, TECHNICIAN	Y	1, 2, 4	2, 3, 4	C-14, H-3, I-125, P-32, S-35
MICHAEL JAIN, GRADUATE STUDENT	Y	1, 2, 4	2, 3, 4	H-3, I-125, P-32, S-35, C-14
HISAO NAGAYA, POST DOC	Y	1, 2, 4	2, 3, 4	C-14, H-3, I-125, P-32, S-35

GENERAL LICENCE CONDITIONS (OPEN AND/OR SEALED SOURCES)

- The permit must be posted with the CNSC safety poster in the permit holder's premises.
- Radioisotope handling shall be in accordance with the McGill Radiation Safety Policy Manual.
- The permit holder must ensure that all persons mandated to work with radioisotopes be properly trained in radiation safety prior to start of work.
- Radioactive work areas must be clearly identified with radiation warning signs.
- Smoking, eating, drinking, storage of foods or drink and the application of cosmetics and contact lenses are prohibited in areas where radioisotopes are used.
- All procedures involving radioactive materials should be carried out on spill trays or on benches lined with disposable absorbent material.
- Procedures that might produce airborne radioactive contamination should be carried out in a functioning fume hood.
- When hand or clothing contamination is possible, protective gloves and clothing must be worn.
- After handling radioactive material and especially before leaving the laboratory, personnel must ensure that all parts of their cloths are not contaminated.
- Purchase and disposal of radioisotopes must be kept electronically or documented in a log book.
- For disposal of radioactive waste, consult the McGill Radiation Safety Policy Manual and/or McGill WMP.
- Wipe tests must be performed and records be kept in a log book.
- The permit must reflect the exact conditions under which radioactive material is used. If changes must be made, contact the RSO at 398-1538.
- The device(s) containing the sealed source(s) must have a radiation symbol and an identification label bearing the name and telephone number of the permit holder.
- Leak tests must be performed on sealed sources equal to or greater than 50 MBq (1.35mCi).
- Extremity dosimeter (i.e. ring or wrist badges) must be worn if 50 MBq or more of P-32, Sr-89, Sr-90 & Y-90 are used.
- Workers using I-125 or I-131 on open bench (5 MBq), in a fume hood (50 MBq) or a vented glove

Approved Unsealed Radioisotope(s) and Location(s)

Isotope	Possession Limit	Stored	Handled
P-32	< 1 GBq (27 mCi)	6500 / 03	6400/03, 6500/02/03
I-125	< 400 MBq (11 mCi)	6500 / 03	6400/03, 6500/03
S-35	< 4 GBq (108 mCi)	6500 / 03	6400/03, 6500/02/03
C-14	< 40 MBq (1.1 mCi)	6500 / 03	6400/03, 6500/03
H-3	< 1 GBq (27 mCi)	6500 / 03	6400/03, 6500/02/03

Approved Sealed Radioisotope(s) and Location(s)

Isotope	Activity	Permanently Housed Source(s)	Handled	Accessibile Source(s)
		Stored	Handled	Stored
		****6 Accessibile Sealed Sources ****		

Please, refer to office file for complete list of sealed sources.

Personnel Conditions

- Must attend thyroid bioassays within 5 days of use if 50 MBq (1.35 mCi) of I-125 are manipulated in a fume hood.
- Must wear a whole-body film badge, if gamma, x-ray or high energy beta emitters are used.
- Must wear an extremity TLD dosimeter, if more than 50 MBq (1.35 mCi) of P-32, Sr-89, Sr-90 or Y-90 are used.
- Classified as Radiation User.
- Classified as Nuclear Energy Worker (NEW).
- Does not work with any radioisotopes but may be indirectly exposed.

Workload Classes

- Work load < 10MBq (270 uCi) of unsealed radioisotopes in open areas.
- Work load < 10MBq (270 uCi) of unsealed radioisotopes in a fume hood.
- Work load > 10MBq (270 uCi) of unsealed radioisotopes in open areas.
- Work load > 10 MBq (270 uCi) of unsealed radioisotopes in a fume hood.
- Work with sealed sources.
- Individual does not work with radioactive sources but normal working conditions involve presence in a room where radioactive material is used or stored.

Joseph Vinelli
 Joseph Vinelli
 EHS & Radiation Safety Officer
 McGill Environmental Health & Safety
 Date *Sept 5/06*

For:
 Dr. Janusz Kozinski, Chair
 McGill University Laboratory Safety Committee
 Associate Vice-Principal (Research)



McGill University

University Biohazards Committee



APPLICATION TO USE BIOHAZARDOUS MATERIALS*

No project should be commenced without prior approval of an application to use biohazardous materials. Submit this application to the Chair, Biohazards Committee, one month before starting new projects or expiry of a previously approved application.

1. PRINCIPAL INVESTIGATOR: John J. M. Bergeron

ADDRESS: 3640 University Street, Room 148, Montreal, P. Q.

TELEPHONE: 398-6352

FAX NUMBER: 398-5047

DEPARTMENT: Anatomy & Cell Biology

E-MAIL: john.bergeron@mcgill.ca

PROJECT TITLE: The Molecular Cytology of Membrane Dynamics

2. FUNDING SOURCE: CIHR ☒ NSERC ☐ NIH ☐ FQRNT ☐ FRSQ ☐
INTERNAL ☐ OTHER ☐ (specify)

Grant No.: MT 5065

Beginning date: July 1, 2003

End date: Sept 30, 2008

3. Indicate if this is

☐ Renewal use application: procedures have been previously approved and no alterations have been made to the protocol.

Approval End Date

☐ New funding source: project previously reviewed and approved under an application to another agency.

Agency

Approval End Date

☒ New project: project not previously reviewed or procedures and/or microorganism altered from previously approved application.

CERTIFICATION STATEMENT: The Biohazards Committee approves the experimental procedures proposed and certifies with the applicant that the experiment will be in accordance with the principles outlined in the "Laboratory Biosafety Guidelines" prepared by Health Canada and the CIHR, and in the "McGill Laboratory Biosafety Manual".

Containment Level (circle) ② 3

Principal Investigator/course director:

date: 12 MAY 2003
day month year

Chairperson Biohazards Committee:

date: 15-05-2003
day month year

Approved prior

beginning 07-07-2003 ending 30-09-2008
day month year day month year

date: 30-09-2008
day month year

* as defined in the "McGill Laboratory Biosafety manual"

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Table S1A. RM, SM, Golgi, COPI vesicle, and COPI GTPγS vesicle protein identifications

NCBI DESCRIPTION	MW	gnumber	CMBSEQID	UNIQUE PEPTIDES	DISTINCT PEPTIDES	% SEQUENCE COVERAGE
(P04692) Isoform 5 of P04692	28340	112443	11396	4	5	18.3673
(P08081) Isoform Non-brain of P08081	23570	56269651	126525	4	4	18.3486
(P08644) Isoform 2B of P08644	21490	495534	71624	1	3	20.7447
(P20290) Isoform 2 of P20290	17700	56605700	33279	3	3	25.9259
(P22626) Isoform A2 of P22626	36010	34855868	29411	7	7	28.1525
(Q00438) Isoform PYBP1 of Q00438	56940	57002	9454	12	12	41.1321
(Q5M828) Isoform 2 of Q5M828	19640	33086520	284155	2	2	8.8757
(Q810T5) Isoform 2 of Q810T5	66820	29650457	268104	1	1	1.5464
(Q9ESC1) Isoform 2 of Q9ESC1	73800	11225481	129647	1	1	1.5106
(Q9JHL4) Isoform 3 of Q9JHL4	48250	7248379	18910	5	5	16.4352
(Q9QUH6) Isoform 5 of Q9QUH6	127700	7514095	13883	1	1	0.60034
(Q9QZX8) Isoform 2 of Q9QZX8	76770	9624356	78114	3	3	7.4236
(Q9WVG6) Isoform 2 of Q9WVG6	63460	77539446	292598	1	1	2.5641
1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase beta 3	139400	32699414	166274	1	1	1.6207
10 days embryo whole body cDNA, RIKEN full-length enriched library, clone:261051121 product:proteasome (prosome, macropain) subunit, alpha type 2, full insert sequence TIB-55 BB8 cDNA, RIKEN full-length enriched library, clone:1730006B17 product:proteasome (prosome, macropain) subunit, alpha type 2, full insert sequence 2 days neonate thymus thymic cells cDNA, RIKEN full-length enriched library, clone:E430022A16 product:proteasome (prosome, macropain) subunit, alpha type 2, full insert sequence Bone marrow macrophage cDNA, RIKEN full-length enriched library, clone:I830087N08 product:proteasome (prosome, macropain) subunit, alpha type 2, full insert sequence Bone marrow macrophage cDNA, RIKEN full-length enriched library, clone:I830041K04 product:proteasome (prosome, macropain) subunit, alpha type 2, full insert sequence Proteasome (Prosome, macropain) subunit, alpha type 2 Adult male urinary bladder cDNA, RIKEN full-length enriched library, clone:9530069L07 product:proteasome (prosome)	25930	8394063	33375	1	1	5.9829
10 kDa heat shock protein, mitochondrial	10770	400542	121548	3	3	33.6634
10-Formyltetrahydrofolate Dehydrogenase	34040	42543697	723160	1	3	13.5484
10-formyltetrahydrofolate dehydrogenase 10-FTHFDH Aldehyde dehydrogenase 1 family member L1 FBP-Cl	99130	908915	62196	11	13	20.51
1110003H02Rik protein	35550	55741774	161453	7	7	30.7453
14-3-3 protein epsilon	29170	61216932	35616	9	11	48.2353
14-3-3 protein eta	28210	6981710	29710	1	3	15.0407
14-3-3 protein theta	27780	6981712	29711	4	7	29.7959
14-3-3 protein zeta/delta Protein kinase C inhibitor protein 1 KCIP-1 SEZ-2	27770	68085421	29712	7	10	49.7959
15 kDa selenoprotein precursor	17780	20139870	129368	3	3	23.4568

16 days embryo lung cDNA, RIKEN full-length enriched library, clone:8430440E03 product:ribosomal protein L21, full insert sequence Ribosomal protein L21, isoform 1 17 days pregnant adult female amnion cDNA, RIKEN full-length enriched library, clone:1920072G18 product:ribosomal protein L21, full insert sequence TIB-55 BB88 cDNA, RIKEN full-length enriched library, clone:1730098C20 product:ribosomal protein L21, full insert sequence Ribosomal protein L21 Rpl21 protein Adult male small intestine cDNA, RIKEN full-length enriched library, clone:2010205O04 product:ribosomal protein L21, full insert sequence Adult male brain cDNA, RIKEN full-length enriched library, clone:0710001D04 product:ribosomal protein L21, full insert sequence	18580	62645460	98375	3	8	46.25
17-beta hydroxysteroid dehydrogenase 13 precursor Short-chain dehydrogenase/reductase 9	33490	77416416	169811	16	18	64.6667
18-day embryo whole body cDNA, RIKEN full-length enriched library, clone:1110037P24 product:weakly similar to RE35789p Novel protein Hypothetical protein Tmem93 18-day embryo whole body cDNA, RIKEN full-length enriched library, clone:1110001A14 product:hypothetical protein, full insert sequence	12020	27673882	98449	1	1	10.9091
2'-5'-oligoadenylate synthetase 1 (2-5' joligo(A) synthetase 1 2-5A synthetase 1	41670	56790	134570	7	7	25.6983
2'-3'-cyclic-nucleotide 3'-phosphodiesterase CNP CNPase	47270	66912120	109735	1	1	3.0952
2,4-dienoyl-CoA reductase, mitochondrial precursor	36130	67476443	148907	17	17	57.9104
2-hydroxyphytanoyl-CoA lyase 2-hydroxyphytanoyl-Coenzyme A lyase	63620	50926767	187564	8	8	23.58
230 kDa phosphatidylinositol 4-kinase	231300	25742825	19300	8	8	5.3405
26S protease regulatory subunit 6B TAT-binding protein 7 TBP-7	47410	38970025	85752	2	2	7.177
26S protease regulatory subunit 8 Proteasome subunit p45 p45/SUG Proteasome 26S subunit ATPase 5 mSUG1	45630	49065782	62820	2	2	6.6502
27 kDa Golgi SNARE protein	24650	2316090	55435	6	6	33.9623
3,2-trans-enoyl-CoA isomerase, mitochondrial precursor Dodecenoyl-CoA isomerase Delta(3),delta(2)-enoyl-CoA isomerase D3,D2-enoyl-CoA isomerase	32250	8393243	51421	10	10	46.0208
3-alpha-hydroxysteroid dehydrogenase	37030	6708142	19230	10	13	59.3168
3-hydroxyacyl-CoA dehydrogenase type II	27250	7387724	83190	16	16	88.5057
3-hydroxyanthranilate 3,4-dioxygenase 3-HAO 3-hydroxyanthranilic acid dioxygenase 3-hydroxyanthranilate oxygenase	32580	9910256	42736	7	7	29.3706
3-hydroxyisobutyrate dehydrogenase, mitochondrial precursor	35300	83977457	55185	3	3	14.3284
3-keto-steroid reductase Estradiol 17-beta-dehydrogenase 7 17-beta-HSD 7 17-beta-hydroxysteroid dehydrogenase 7 PRL receptor-associated protein PRAP	37370	8393576	708	3	3	15.8683
3-ketacyl-CoA thiolase, mitochondrial Beta-ketothiolase Acetyl-CoA acyltransferase Mitochondrial 3-oxoacyl-CoA thiolase	41870	55544	96895	18	18	62.2166
3-oxo-5-alpha-steroid 4-dehydrogenase 1 Steroid 5-alpha-reductase 1 SR type 1	29780	25742565	43740	7	7	20.0772
3-oxo-5-beta-steroid 4-dehydrogenase Delta(4)-3-ketosteroid 5-beta-reductase Aldo-keto reductase family 1 member D1	37380	9438775	23758	16	16	49.3865
4-aminobutyrate aminotransferase, mitochondrial precursor (S)-3-amino-2-methylpropanate transaminase Gamma-amino-N-butyrate transaminase GABA transaminase GABA aminotransferase GABA-T L-AIBAT 4-aminobutyrate aminotransferase, brain isoform 4-aminobutyrate aminotransferase, liver isoform	56450	48429192	37174	1	1	2.4
4-trimethylaminobutyraldehyde dehydrogenase TMABADH Aldehyde dehydrogenase 9A1						
40S ribosomal protein S11	53650	78099320	104196	11	11	29.1498
40S ribosomal protein S12	18430	54039305	4834	14	14	60.7595
40S ribosomal protein S13	14510	78126139	132206	6	8	57.5758
40S ribosomal protein S13	17220	57730	4835	9	9	45.6954

40S ribosomal protein S14	16270	37231722	98434	9	9	41.7219
40S ribosomal protein S16	16450	57714	4837	10	10	55.4795
40S ribosomal protein S18	17720	50403620	60848	6	16	61.8421
40S ribosomal protein S19	16090	82654220	122667	13	13	57.931
40S ribosomal protein S20	13370	57720	4840	2	5	35.2941
40S ribosomal protein S21	9127	483517	37243	3	3	39.759
40S ribosomal protein S23	15810	730647	4842	4	4	23.7762
40S ribosomal protein S25	13740	74355904	4844	6	6	32.8
40S ribosomal protein S26	13020	6981488	75074	5	5	47.8261
40S ribosomal protein S27-like protein	9477	57741	120488	2	5	40.4762
40S ribosomal protein S28	7841	57726	1344	2	2	30.4348
40S ribosomal protein S3	26670	57728	60850	26	26	83.1276
40S ribosomal protein S30	6648	51338625	106720	2	2	18.6441
40S ribosomal protein S3a	29940	8394221	51618	27	27	73.1061
40S ribosomal protein S7	22130	66730357	4853	12	15	70.1031
40S ribosomal protein S9	22590	52788199	142294	19	24	65.9794
40S ribosomal protein SA	32820	8393693	51515	2	16	60
45 kDa calcium-binding protein precursor Cab45 Stromal cell-derived factor 4 SDF-4	42080	21263446	64664	10	10	37.9501
49 kDa protein	2429	262199	124397	1	1	47.619
5'-AMP-activated protein kinase catalytic subunit alpha-1 AMPK alpha-1 chain	62600	1703034	23444	1	1	3.1022
5'-nucleotidase precursor Ecto-5'-nucleotidase 5'-NT CD73 antigen	63970	202551	11455	17	17	38.7153
5'-AMP-activated protein kinase, catalytic alpha-2 chain	62260	728758	54292	2	2	3.9855
5'-AMP-activated protein kinase, gamma-1 subunit	36670	1335860	68651	5	5	20.1238
55 kDa type II phosphatidylinositol 4-kinase	54300	16758554	60536	2	2	5.0209
60 kDa heat shock protein, mitochondrial precursor Hsp60 60 kDa chaperonin CPN60 Heat shock protein 60 HSP-60 Mitochondrial matrix protein P1 HSP-65	60960	55778012	52609	12	18	42.5829
60S acidic ribosomal protein P0 L10E	34220	730581	23405	18	19	64.3533
60S acidic ribosomal protein P1	11500	57710	144430	2	2	51.7544
60S acidic ribosomal protein P2	11690	71795613	144431	2	8	78.2609
60S ribosomal protein L12	17850	57680	144419	11	11	68.4848
60S ribosomal protein L18a	20730	50403587	71631	12	12	46.0227
60S ribosomal protein L22	14760	52221202	4392	5	6	50.7812
60S ribosomal protein L23	14870	57688	4807	8	8	52.1429
60S ribosomal protein L23a	17700	62656804	144423	15	15	57.6923
60S ribosomal protein L24	17780	560493	4812	7	7	38.8535
60S ribosomal protein L26	17260	27672824	4813	13	13	51.0345
60S ribosomal protein L36	12250	34849736	65711	1	6	37.1429
60S ribosomal protein L37	11080	57121	3029	1	1	7.2165

60S ribosomal protein L39	6407	6981484	4822	1	1	19.6078
60S ribosomal protein L4	47310	1363989	85424	25	25	48.9311
60S ribosomal protein L40 CEP52	6181	973178	77849	1	1	13.4615
60S ribosomal protein L5	34460	57125	37237	18	18	51.5152
60S ribosomal protein L9	21890	57706	144428	11	13	63.5417
7-dehydrocholesterol reductase 7-DHC reductase Sterol delta-7-reductase	54160	81882109	9067	7	7	17.8344
78 kDa glucose-regulated protein precursor GRP 78 Immunoglobulin heavy chain-binding protein BiP Steroidogenesis-activator polypeptide	72350	38303969	28269	39	43	56.5749
9.5 days embryo parthenogenote cDNA, RIKEN full-length enriched library, clone:B130020K18 product:RAS-RELATED PROTEIN RAP-2B homolog 7 days neonate cerebellum cDNA, RIKEN full-length enriched library, clone:A730075J10 product:RAP2B, member of RAS oncogene family, full insert sequence Bone marrow macrophage cDNA, RIKEN full-length enriched library, clone:G530142K06 product:RAP2B, member of RAS oncogene family, full insert sequence Rap2b protein 7 days neonate cerebellum cDNA, RIKEN full-length enriched library, clone:A730042C18 product:RAS-RELATED PROTEIN RAP-2B homolog	20500	47117735	32753	1	1	6.5574
9.5 days embryo parthenogenote cDNA, RIKEN full-length enriched library, clone:B130042B20 product:myosin regulatory light chain A, smooth muscle homolog CRL-1722 L5178Y-R cDNA, RIKEN full-length enriched library, clone:I730047D20 product:Myosin regulatory light chain 2-A, smooth muscle isoform (Myosin RLC-A) homolog 14 days pregnant adult female placenta cDNA, RIKEN full-length enriched library, clone:I530020L12 product:Myosin regulatory light chain 2-A, smooth muscle isoform (Myosin RLC-A) homolog Osteoclast-like cell cDNA, RIKEN full-length enriched library, clone:I420005I07 product:Myosin regulatory light chain 2-A, smooth muscle isoform (Myosin RLC-A) homolog Bone marrow macrophage cDNA, RIKEN full-length enriched library, clone:I830027H03 product:Myosin regulatory light chain 2-A, smooth muscle isoform (Myosin RLC-A) homolog Myosin light chain, regulatory B-like RIKEN cDNA 2900073G15 18-day embryo whole body cDNA, RIKEN full-length enriched library, clone:1190017I13 product:myosin	19900	68533710	69379	3	10	79.6512
A-Raf proto-oncogene serine/threonine-protein kinase	67550	55757	90531	1	1	1.8212
ADP-ribosylation factor 4	20400	543844	10609	5	12	68.8889
ADP-ribosylation factor-like protein 1	20410	728889	23396	7	7	43.6464
ADP-ribosylation-like factor 6-interacting protein Arl6ip1 protein	23450	68534822	139514	1	1	3.9409
ADP-ribosyltransferase NAD+, poly (ADP-ribose polymerase)-like 3 (Predicted)	58870	56605734	298279	2	2	3.8023
AMBP protein precursor Alpha-1-microglobulin inter-alpha-trypsin inhibitor light chain ITI-LC Bikunin HI-30 Trypsalrin	38850	6978497	3629	8	8	28.9398
AP-1 complex subunit beta-1 Adapter-related protein complex 1 beta-1 subunit Beta-adaptin 1	104600	8392872	126513	15	28	39.0938
Adaptor protein complex AP-1 beta-1 subunit Golgi adaptor HA1/AP1 adaptin beta subunit Clathrin assembly protein complex 1 beta large chain						
AP-1 complex subunit sigma-1A Adapter-related protein complex 1 sigma-1A subunit Sigma-adaptin 1A Adaptor protein complex AP-1 sigma-1A subunit Golgi adaptor HA1/AP1 adaptin sigma-1A subunit Clathrin assembly protein complex 1 sigma-1A small chain Clathrin coat assembly protein AP19 HA1 19 kDa subunit Sigma 1a subunit of AP-1 clathrin	18730	34871704	74369	3	3	27.8481
AP-2 complex subunit sigma-1 Adapter-related protein complex 2 sigma-1 subunit Sigma-adaptin 3b Clathrin coat assembly protein AP17 Clathrin coat-associated protein AP17 Plasma membrane adaptor AP-2 17 kDa protein Clathrin assembly protein 2 small chain	17020	56961624	65700	3	3	24.6479
APOBEC1 complementation factor APOBEC1-stimulating protein	65620	81916405	61026	16	16	37.8788
ARF-related protein 1	22660	2492928	52078	7	7	45.7711

ARF6 protein ADP-ribosylation factor 6	20080	60552411	120856	6	7	45.1429
ARHG protein Ras homolog gene family, member G Rho G	21310	82524300	93024	1	1	9.9476
ARP2/3 complex 21 kDa subunit	19650	27665454	160418	4	4	24.7059
ARP3 actin-related protein 3 homolog	47360	70912366	71751	11	11	36.6029
ATP synthase B chain, mitochondrial precursor	28870	39645769	141484	16	16	56.6406
ATP synthase D chain, mitochondrial	18760	9506411	21505	13	13	78.2609
ATP synthase O subunit, mitochondrial precursor Oligomycin sensitivity conferral protein OSCP	23400	543880	142437	14	14	75.1174
ATP synthase alpha chain, mitochondrial precursor	55280	6729934	73367	38	38	70.7843
ATP synthase beta chain, mitochondrial precursor	56350	71681130	141479	14	34	83.3648
ATP synthase coupling factor 6, mitochondrial precursor ATPase subunit F6	12490	599963	60480	2	2	30.5556
ATP synthase delta chain, mitochondrial precursor	17600	457929	21504	2	2	13.6905
ATP synthase epsilon chain, mitochondrial	5636	258789	11887	1	1	16
ATP synthase gamma chain, mitochondrial	29930	6729936	69786	8	8	34.8148
ATP synthase protein 8 ATPase subunit 8 A6L	7642	5835182	98990	2	2	34.3284
ATP-binding cassette, sub-family B (MDR/TAP), member 10 Predicted	77390	58865904	264038	1	1	3.4965
ATP-binding cassette, sub-family C (CFTR/MRP), member 3	169300	3242460	52680	1	1	0.72226
ATP-binding cassette, sub-family F (GCN20), member 1	92870	34852051	231492	1	1	1.348
ATP-citrate synthase ATP-citrate (pro-S)-lyase Citrate cleavage enzyme	120600	8392839	126543	16	16	20.8182
ATPase 7B	156000	6006306	1565	2	2	3.0992
ATPase, H+ transporting, V1 subunit C, isoform 1 Predicted	43900	62652340	311925	1	1	4.1885
ATPase, H+ transporting, V1 subunit E isoform 1	26130	38454230	261145	5	5	30.0885
ATPase, H+ transporting, lysosomal 34kDa, V1 subunit D	28310	40786463	160475	1	1	4.8583
Aa1018	55960	32492572	302124	6	6	15.3061
Aa1064	42690	111387	148924	1	12	36.3636
Aa1064 Ac1-1060	536000	61098031	166227	72	83	23.0234
Ab1-219	52040	62646756	201751	9	9	26.0776
Ab2-076	103300	33086552	166325	2	2	3.6345
Ab2-132	39450	33086562	261456	9	9	29.8551
Ab2-225 Hypothetical protein RGD1306952	27900	56970828	244467	1	1	4.0816
Ab2-305	43570	33086580	166327	3	17	49.2308
Abhydrolase domain containing 14A	26760	57528269	203847	2	2	13.6364
Abhydrolase domain containing 14b	22620	56090461	151517	5	5	32.8571
Abhydrolase domain containing 6	38310	56090644	309746	5	5	16.3205
Ac1-581 Ab1-216 Ab1-181	56610	33086484	166238	21	21	48.3101
Ac1573	79140	32264637	263869	1	6	10.2857
Ac1873	86660	62643670	173317	19	19	28.3887
Ac2-067	27970	34862605	166240	1	1	5.9289

Ac2-120	237300	62659617	166242	3	3	1.5699
Ac2-155	102100	33086620	198808	1	1	1.0239
Ac2-190	60820	34866106	305592	11	11	26.7135
Ac2-233	161600	34870762	223700	10	10	15.6534
Ac2-256	71830	62177146	166247	1	1	1.374
Acetyl-CoA acetyltransferase, mitochondrial precursor	44690	66502	31496	7	7	24.5283
Acetyl-CoA carboxylase 1 ACC-alpha Biotin carboxylase	265200	202645	84141	1	1	0.59701
Acetyl-coenzyme A transporter 1 AT-1 Acetyl-CoA transporter Solute carrier family 33 member 1	61190	7768591	104182	5	5	13.4545
Acid phosphatase 6, lysophosphatidic	47280	72255521	193296	8	8	26.8765
Acidic leucine-rich nuclear phosphoprotein 32 family member B Proliferation-related acidic leucine-rich protein PAL31	31060	9971212	3001	4	4	18.3824
Aconitate hydratase, mitochondrial precursor Citrate hydro-lyase Aconitase	85430	60391194	338228	7	7	12.5641
Actin, cytoplasmic 2	41790	62645364	120792	13	30	91.2
Actin-like protein 2 Actin-related protein 2	44730	62899645	156591	7	8	26.1421
Actin-related protein 2/3 complex subunit 1A	41600	59797636	168831	5	5	21.3514
Acyl-coenzyme A dehydrogenase, short chain	44970	48734846	84143	8	8	24.1546
Acyl-coenzyme A oxidase 1, peroxisomal	74680	8394149	51604	27	27	60.0605
Acyl-coenzyme A oxidase 2, peroxisomal 3-alpha,7-alpha,12-alpha-trihydroxy-5-beta-cholestanoyl-CoA 24-hydroxylase 3-alpha,7-alpha,12-alpha-trihydroxy-5-beta-cholestanoyl-CoA oxidase	76800	21955130	3086	24	24	40.6755
Trihydroxycoprostanoil-CoA oxidase THCCox THCA-CoA oxidase						
Acyl-coenzyme A oxidase 3, peroxisomal Pristanoyl-CoA oxidase Branched-chain acyl-CoA oxidase BRACox	78450	2498208	42129	19	19	40.7143
Acyl-protein thioesterase 1 Lysophospholipase 1	24710	6981362	75037	1	1	4.7826
AcylCoA:Cholesterol Acyltransferase 2	60480	21392392	207716	6	6	11.2595
Adaptor protein complex AP-2, mu1 12 days embryo spinal ganglion cDNA, RIKEN full-length enriched library, clone:D130035H06 product:adaptor protein complex AP-2, mu1, full insert sequence 17 days embryo heart cDNA, RIKEN full-length enriched library, clone:i920019109 product:adaptor protein complex AP-2, mu1, full insert sequence Ap2m1 protein	49650	73536275	73521	13	13	40.9195
Adenine phosphoribosyltransferase APRT	19550	61556832	126504	1	1	7.2222
Adenosine kinase	40100	7448824	3608	1	3	8.5873
Adenosine kinase	37310	1373230	85486	1	3	10.1796
Adenosylhomocysteinase	47420	24158803	54409	10	10	29.2343
Adenylate kinase 2, isoform b	25530	77020256	340217	14	14	69.8276
Adenylate kinase isoenzyme 4, mitochondrial Adenylate kinase 3-like 1 ATP-AMP transphosphorylase	25200	8392885	181389	1	1	5.3812
Adipocyte-derived leucine aminopeptidase precursor	100700	8131852	605	17	17	23.7557
Adult male cerebellum cDNA, RIKEN full-length enriched library, clone:1500003H20 product:myosin regulatory light chain 2, brain (clone FY53) homolog CRL-1722 L5178Y-R cDNA, RIKEN full-length enriched library, clone:I730003N21 product:Myosin regulatory light chain (Nonmuscle myosin light chain 2) homolog Myosin regulatory light chain-like Mylc2b protein Adult male kidney cDNA, RIKEN full-length enriched library, clone:0610041E23 product:myosin regulatory light chain 2, brain (clone FY53) homolog	19780	62655515	88823	2	10	79.6512

Adult male lung cDNA, RIKEN full-length enriched library, clone:1200010H03 product:surfet gene 4, full insert sequence Bone marrow macrophage cDNA, RIKEN full-length enriched library, clone:1830028A12 product:surfet gene 4, full insert sequence Bone marrow macrophage cDNA, RIKEN full-length enriched library, clone:1830026D09 product:surfet gene 4, full insert sequence Bone marrow macrophage cDNA, RIKEN full-length enriched library, clone:1830012C22 product:surfet gene 4, full insert sequence Blastocyst blastocyst cDNA, RIKEN full-length enriched library, clone:11C0027M05 product:surfet gene 4, full insert sequence	30380	76443685	60957	6	6	27.5093
Adult male thymus cDNA, RIKEN full-length enriched library, clone:5830427H10 product:GL009 homolog Bone marrow macrophage cDNA, RIKEN full-length enriched library, clone:1830027D22 product:GL009 homolog 12 days embryo spinal cord cDNA, RIKEN full-length enriched library, clone:C530010F19 product:GL009 homolog Jegunal homolog 1 18-day embryo whole body cDNA, RIKEN full-length enriched library, clone:110014A23 product:CDNA FLJ14602 FIS, CLONE NT2RP1000191 homolog	21100	68534555	32612	1	1	6.5574
Advanced glycosylation end product-specific receptor precursor Receptor for advanced glycosylation end products	42660	498034	128256	1	1	3.4826
Atadin Protein Atf-6	207700	7513996	3616	1	1	0.49207
Afamin precursor Alpha-albumin Alpha-Alb	69340	543793	23759	2	2	5.4276
Aflatoxin B1 aldehyde reductase member 1	36740	433611	100616	6	6	23.8532
Ak3 protein	25490	40352787	270293	1	1	5.7269
Akr7a2 protein	37600	6815049	161251	3	3	12.7219
AIF-C1	36210	3377279	75909	2	4	16.9184
Alcohol sulfotransferase	33080	204671	148916	4	8	35.9155
Alcohol sulfotransferase Hydroxysteroid sulfotransferase ST ST-60	33530	68341957	157070	1	4	15.7895
Aldehyde dehydrogenase	48270	16073616	7845	17	18	61.6253
Aldehyde dehydrogenase 1A1	54460	38494348	72216	3	5	13.1737
Aldehyde oxidase	146900	4324710	95119	3	3	3.2258
Aldose 1-epimerase Galactose mutarolase	37890	84028322	290544	4	4	18.1287
All-trans-retinol 13,14-reductase precursor All-trans-13,14-dihydroretinol saturase RetSat RMT-7	67530	81871478	27636	20	20	38.7521
Alpha actinin 4	104900	77539778	319018	33	50	68.6059
Alpha globin	15520	62655914	114803	1	2	16.9014
Alpha isoform of regulatory subunit A, protein phosphatase 2	65320	55926139	36803	5	5	14.0917
Alpha-1 catenin	9484	92036	84182	1	1	14.6067
Alpha-1,3-mannosyl-glycoprotein 2-beta-N-acetylglucosaminyltransferase N-glycosyl-oligosaccharide-glycoprotein N-acetylglucosaminyltransferase I GNT-I GlcNAc-T I	51590	740930	2699	15	15	39.1499
Alpha-1,6-mannosyl-glycoprotein 2-beta-N-acetylglucosaminyltransferase Mannoside acetylglucosaminyltransferase 2 N-glycosyl-oligosaccharide-glycoprotein N-acetylglucosaminyltransferase II Beta-1,2-N-acetylglucosaminyltransferase II GNT-II GlcNAc-T II	51110	747976	60482	14	14	31.2217
Alpha-1-acid glycoprotein precursor Orosomucoid OMD	23580	72091	11470	1	1	4.3902
Alpha-1-antitrypsin precursor	46140	112889	11475	19	19	53.2847
Alpha-1-inhibitor III precursor	163800	83816939	11478	13	47	47.6642
Alpha-1-macroglobulin	167100	739596	126488	51	51	48.4

Alpha-1B-glycoprotein precursor Liver regeneration-related protein 1 C44	56480	57012547	155721	1	1	2.1442
Alpha-2 antiplasmin Serine (Or cysteine) proteinase inhibitor, clade F, member 1	46470	51261124	317738	10	10	35.8852
Alpha-2-HS-glycoprotein	37980	60552688	111646	11	11	45.1705
Alpha-2-globin chain Hba-a1 protein 2-alpha globin	15280	60688619	109334	1	11	75.3521
Alpha-2U globulin	20560	8307690	125352	1	8	34.8066
Alpha-ETF	34950	57527204	151400	11	11	55.2553
Alpha-actinin-1 Alpha-actinin cytoskeletal isoform Non-muscle alpha-actinin-1 F-actin cross linking protein	103000	4210985	37175	4	24	34.0807
Alpha-amylase	58830	58293772	106479	2	2	5.5662
Alpha-methylacyl-CoA racemase	41830	13637497	76476	4	4	15.1832
Alpha-parvin Actopaxin	42290	20138815	37085	1	1	3.7634
Alpha-soluble NSF attachment protein SNAP-alpha N-ethylmaleimide-sensitive factor attachment protein, alpha	33190	6094309	51376	18	18	74.9153
Alpha-tocopherol transfer protein Alpha-TTP	31850	731023	75128	3	3	21.223
Amine oxidase [flavin-containing] A	58870	8170739	101201	14	14	35.9615
Aminopeptidase N	109400	205109	11241	13	13	17.7202
Amphoterin	24890	9082303	17711	3	8	39.0698
Amyloid-like protein 2 precursor	86880	1703345	10860	1	1	1.9608
Amyotrophic lateral sclerosis 2 chromosomal region candidate gene protein 3 homolog	101600	75905813	256333	1	1	0.87623
Angiotensinogen precursor Angiotensin-1 Angiotensin I Ang I Angiotensin-2 Angiotensin II Ang II	51980	56585074	45123	8	8	26.4151
Angiotensin-3 Angiotensin III Ang III Des-Asp[1]-angiotensin II	25960	6981420	75054	1	1	8.1301
Anionic trypsin-1 precursor Anionic trypsin I Pretrypsinogen I	36360	71766	120574	11	11	50.6173
Annexin A3	35850	37999910	171244	8	8	31.0345
Annexin A4	35740	6978505	3633	15	15	50.4702
Annexin A5	79150	2506117	43654	2	2	3.5862
Antigen peptide transporter 1 APT1 Peptide transporter TAP1 ATP-binding cassette sub-family B member 2	105700	73695330	59082	4	33	46.0568
Ap2b1 protein	41430	6707431	114274	11	11	34.0599
Apoa5 protein	30060	6978515	3638	11	11	49.8069
Apolipoprotein A-I precursor	11440	91985	3639	1	1	10.7843
Apolipoprotein A-II precursor	44460	60552712	141420	16	16	50.3836
Apolipoprotein A-IV precursor	10250	2492915	136243	1	1	12.5
Apolipoprotein C-IV precursor Apo-C-IV Apolipoprotein E-linked ECL	35750	55824759	126501	20	20	51.6026
Apolipoprotein E precursor Apo-E	21510	9506391	95121	3	3	18.4211
Apolipoprotein M	66720	7619915	63059	19	19	45.7516
Apoptosis-inducing factor	34970	6573527	37797	28	28	82.0433
Arginase 1	51550	551296	45085	12	12	33.4056
Argininosuccinate lyase	46500	55767	45108	29	29	72.3301
Argininosuccinate synthase Citrulline--aspartate ligase						

Aromatic-L-amino-acid decarboxylase AADC DOPA decarboxylase DDC	54050	6978759	3735	2	2	7.2917
Aryl sulfotransferase	33910	55761	69784	9	9	46.0481
Asialoglycoprotein receptor 1	32850	7705290	120624	11	11	41.9014
Asialoglycoprotein receptor R2/3	34860	206649	44327	2	2	6.3123
Aspartate aminotransferase, cytoplasmic	46430	91997	84171	8	8	28.8136
Aspartate aminotransferase, mitochondrial precursor Transaminase A Glutamate oxaloacetate transaminase 2	47310	6980972	3905	21	21	51.3953
B-cell receptor-associated protein 31	27910	51948420	139656	11	11	37.1429
B-cell receptor-associated protein BAP29	28230	55742817	243481	1	1	6.639
BCS1-like	47390	56090628	232734	2	2	8.6124
BET1 homolog Golgi vesicular membrane-trafficking protein p18 rBET1	13230	9506425	35327	3	3	29.661
BET1-like protein Vesicle transport protein GOS15 Golgi SNARE with a size of 15 kDa GS15 GOS-15	12410	61889075	315291	3	3	44.1441
BWK4	46880	62648953	310568	23	23	62.5616
Ba1-647	42470	33086640	166334	14	14	38.5827
Band 3 anion transport protein	103200	20141169	66007	3	3	4.9622
Basigin precursor	29590	7709992	141056	5	5	29.4118
Bax inhibitor-1	26230	456209	23753	1	1	3.8298
Bcl-2 inhibitor of transcription	19530	62078455	215739	3	3	27.6243
Beta-1,4 N-acetylgalactosaminyltransferase 1 (N-acetylneuraminy)-galactosylglucosylceramide GM2/GD2 synthase GalNAc-T	59280	51858903	137529	2	2	5.8161
Beta-2-glycoprotein 1 precursor Beta-2-glycoprotein I Apolipoprotein H Apo-H B2GPI Beta(2)GPI	33200	57525	21485	5	5	14.4781
Beta-2-microglobulin precursor	11640	999862	27803	3	3	51.5152
Beta-catenin	85470	16758082	74416	18	20	33.9309
Beta-glucuronidase precursor	73270	758260	21055	3	3	6.7717
Beta-ureidopropionase Beta-alanine synthase N-carbamoyl-beta-alanine amidohydrolase	44040	51259277	44431	4	4	21.374
Betaine-homocysteine S-methyltransferase	44980	3913156	71708	31	31	79.8526
Bifunctional heparan sulfate N-deacetylase/N-sulfotransferase 1 Glucosaminyl N-deacetylase/N-sulfotransferase 1 NDST-1 [Heparan sulfate]-glucosamine N-sulfotransferase 1 HSNST 1 N-heparan sulfate sulfotransferase 1 N-HSST 1 Heparan sulfate N-deacetylase 1 Heparan sulfate N-sulfotransferase 1	100800	401136	44217	22	25	35.034
Bile acyl-CoA synthetase BACS Bile acid CoA ligase BA-CoA ligase BAL Cholate--CoA ligase Very long chain acyl-CoA synthetase-related protein VLACS-related VLACSR Fatty acid transport protein 5 FATP-5 Solute carrier family 27 member 5	76270	9963930	30001	39	39	73.6232
Bile salt export pump ATP-binding cassette sub-family B member 11 Sister of P-glycoprotein	146300	3075422	13065	4	4	4.6177
Biliverdin reductase A precursor Biliverdin-IX alpha-reductase BVR A	33570	285208	54374	2	2	7.7966
Block of proliferation 1 Predicted	82640	66730443	214565	1	1	0.82079
Brain Zn-finger protein Brain zinc finger protein	48300	58219528	307560	3	3	9.6244
Brain protein 44 0-44 protein	14260	730248	80419	3	3	30.7087
Brain protein 44-like protein	12450	66911415	92620	1	1	7.3394

C-4 methylsterol oxidase Methylsterol monooxygenase Neuropoep 1 RANP-1	34960	38649308	807	2	2	13.6519
C-reactive protein, petaxin related	25470	8393197	126549	5	5	32.6087
C-type lectin domain family 4 member F C-type lectin superfamily member 13 C-type lectin 13 Kupffer cell receptor	61100	68533633	60545	1	1	2.3636
C4b-binding protein alpha chain precursor C4bp	62270	899380	3668	1	1	2.1505
CAP , adenylate cyclase-associated protein 1	51590	59709467	130827	4	4	14.7679
CCA2 protein	37780	2563999	86059	2	2	7.3964
CCAAT displacement protein	175300	34871708	280644	3	22	13.7672
CD166 antigen precursor Activated leukocyte-cell adhesion molecule ALCAM MEIMD protein HB2 SB-10 antigen KG-CAM	65020	47605356	78164	5	5	14.9228
CD59 glycoprotein precursor Membrane attack complex inhibition factor MACIF MAC-inhibitory protein MAC-IP Protectin	13790	6978635	3690	1	1	7.1429
CDK5 regulatory subunit-associated protein 3 CDK5 activator-binding protein C53	57040	7330736	18021	10	10	27.7778
CDP-diacylglycerol--inositol 3-phosphatidylinositol synthase PtdIns synthase PI synthase	23610	7674155	70677	5	5	27.23
CLIP-associated protein 2 Cytoplasmic linker-associated protein 2	140600	77416394	60531	2	2	1.3219
CMP-N-acetylneuraminat-beta-galactosamide-alpha-2,3-sialyltransferase Beta-galactoside alpha-2,3-sialyltransferase Alpha 2,3-sialyltransferase IV Alpha 2,3-ST SIAT4-C	38040	57870642	722827	2	2	9.3093
CMP-N-acetylneuraminat-beta-galactosamide-alpha-2,6-sialyltransferase Beta-galactoside alpha-2,6-sialyltransferase Alpha 2,6-ST Sialyltransferase 1 ST6Gal I	46730	204255	141534	14	20	49.1315
COMM domain containing 10	22830	51948526	211553	1	1	6.9307
Cadherin-17 precursor Liver-intestine-cadherin LI-cadherin	91860	628001	127670	2	2	3.7485
Calcium-binding protein 4	1978	111445	148937	1	1	88.8889
Calcium-binding protein p22 Calcium-binding protein CHP Calcineurin homologous protein Sid 470	22430	46577577	25354	3	3	24.6154
Calcium-independent alpha-latrotoxin receptor 2 precursor	161100	3695131	70058	4	4	4.3206
Calcium-transporting ATPase type 2C member 1 ATPase 2C1 ATP-dependent Ca(2+) pump PMR1	100500	8134332	41219	13	13	20.5658
Calnexin precursor	67250	543922	69775	29	29	47.5465
Calpain small subunit 1	28080	19864480	76638	1	1	9.0226
Calreticulin precursor CRP55 Calregulin HACBP ERp60 CALBP Calcium-binding protein 3 CABP3	48000	55855	23403	33	33	81.25
Cam protein Calm2a-prov protein	16840	8394168	55585	5	5	54.3624
Canalicular multispecific organic anion transporter 1 ATP-binding cassette sub-family C member 2 Multidrug resistance-associated protein 2 Canalicular multidrug resistance protein	173400	6978669	3702	2	2	2.4659
Carbamoyl-phosphate synthase [ammonia], mitochondrial precursor Carbamoyl-phosphate synthetase I CPSase I	164600	8393186	45074	59	61	49.0667
Carbonic anhydrase III	29420	10120584	5972	16	16	68.0769
Carbonyl reductase 4	25290	55562775	166315	1	1	8.0508
Carboxylesterase RL1	62310	14331129	158916	3	14	33.6299
Carboxylesterase isoenzyme	61800	21426807	157137	10	18	51.2545
Carboxylesterase isozyme	2133	1478388	42034	1	1	60
Carboxylesterase precursor	62040	2641992	182047	11	15	42.9603

Carboxylesterase precursor	62240	3062827	13000	2	11	23.8859
Carboxylesterase precursor (Carboxylesterase 2) (Carboxylesterase)	62190	56541525	12999	3	12	26.2032
Carboxypeptidase D precursor Metallocarboxypeptidase D gp180	152600	6978699	3713	20	20	19.4485
Carcinoembryonic antigen-related cell adhesion molecule, secreted isoform CEACAM1a-4C2 precursor	51410	76496479	39119	5	5	11.5468
Cardiac alpha actin 1	42020	77993370	10199	1	17	40.8488
Carnitine O-palmitoyltransferase I, mitochondrial liver isoform	88130	48735405	63443	24	24	36.9987
Carnitine O-palmitoyltransferase II, mitochondrial precursor	74110	6978705	3716	6	6	12.1581
Catechol O-methyltransferase, membrane-bound form	29600	6978681	3708	13	13	53.4091
Cathepsin B precursor	35600	1942646	19199	3	3	13.9752
Cathepsin D precursor Cathepsin D 12 kDa light chain Cathepsin D 9 kDa light chain Cathepsin D 34 kDa heavy chain Cathepsin D 30 kDa heavy chain	44680	55882	141570	7	7	24.3243
Cathepsin H precursor	37100	6978721	3719	2	2	9.009
Cathepsin L precursor Major excreted protein MEP Cyclic protein 2 CP-2 Cathepsin L heavy chain Cathepsin L light chain	37660	38648869	141572	8	8	39.2216
Cathepsin Z precursor	34190	60688149	160297	1	1	3.9216
Cation-dependent mannose-6-phosphate receptor	31100	56090485	161476	11	11	38.8489
Cationic trypsin-3 precursor Cationic trypsin III Pretrypsinogen III	26270	27465583	31543	1	1	3.2389
Cc1-9	62860	62641625	194016	13	13	28.0142
Cc2-27	120500	33086672	166337	3	3	3.9486
Ccf5 protein	31980	37590247	252047	3	3	20.6897
Cd81 protein	25900	62641476	228910	3	3	25
Cell division cycle 42	21260	61889112	85184	7	7	36.6492
Cell growth regulator with EF hand domain 1 Cell growth regulatory gene 11 protein	30830	23396481	38628	1	1	3.9146
Cell surface protein CD36	52730	6707016	105482	1	1	3.6017
Centaurin-alpha 2	43520	9910340	42770	1	1	4.5213
Ceramidase	83490	16758458	60505	1	1	1.7083
Ceramide glucosyltransferase Glucosylceramide synthase GCS UDP-glucose:N-acylsphingosine D-glucosyltransferase UDP-glucose ceramide glucosyltransferase GLCT-1	44820	62648957	85745	1	1	2.7919
Chain L, 1.9a Structure Of The Therapeutic Antibody Campath-1h Fab In Complex With A Synthetic Peptide Antigen	23280	5542160	20841	5	5	32.2275
Chaperonin containing TCP1, subunit 2 Beta	57460	54400730	292700	14	14	38.3178
Chaperonin containing TCP1, subunit 3 Gamma	60650	40018616	169833	14	14	32.6606
Chloride intracellular channel protein 4 Intracellular chloride ion channel protein p64H1	28630	6685295	78195	11	11	55.336
Choline dehydrogenase	66390	55250736	160551	20	20	46.5776
Choline/ethanolamine phosphotransferase 1	46500	56090333	264754	1	1	2.6442
Chronic lymphocytic leukemia deletion region gene 6 protein homolog CLL deletion region gene 6 protein homolog	21680	81883037	141958	7	7	46.9388
Claithrin heavy chain	191600	9506497	95154	63	63	49.194
Claithrin light chain B	25120	203359	60578	1	1	3.9301

Claudin-3	23310	82617586	33971	2	2	11.8721
Clusterin	24930	11127974	36009	2	2	13.3028
Coagulation factor IX Christmas factor	31450	204146	149112	1	1	3.9007
Coatomer subunit beta Beta-COP	107000	55819	63721	51	51	67.9958
Coatomer subunit delta Delta-coat protein Delta-COP Archain	57200	81884175	221177	38	38	68.8845
Cofilin-2 Cofilin, muscle isoform	18710	62650690	74438	2	4	37.3494
Complement C1q subcomponent subunit A precursor	25920	62906846	355419	2	2	12.2449
Complement C4 precursor Complement C4 beta chain Complement C4 alpha chain C4a anaphylatoxin Complement C4 gamma chain	192200	29789265	162301	24	24	20.2648
Complement component 1 Q subcomponent-binding protein, mitochondrial precursor Glycoprotein	30740	9506435	80872	2	2	15.8273
gC1qBP C1qBP GC1q-R protein	105100	61211276	240055	1	1	1.2848
Complement component C6 precursor	62280	2499467	43431	8	8	20.2166
Complement component C9 precursor	140300	18426830	96883	10	10	10.5987
Complement inhibitory factor H	61680	9506513	35260	1	1	3.5778
Complement regulatory protein Crry precursor Antigen 512	117400	50400225	169306	1	1	0.5814
Connector enhancer of kinase suppressor of ras 2 Connector enhancer of KSR2 CNK2 Membrane-associated guanylate kinase-interacting protein MAGUIN	46520	57294	84230	2	20	52.8846
Contrapsin-like protease inhibitor 1 precursor	46480	220698	135016	1	19	50.4808
Contrapsin-like protease inhibitor 1 precursor	46650	50927309	88238	14	17	57.4163
Contrapsin-like protease inhibitor 6 precursor GPI-26 Serine protease inhibitor 3 SPI-3 SPI-2.2	21520	61557239	2681	1	1	4.3956
Core binding factor beta	42310	8927166	55277	9	9	35.2617
Core 1 UDP-galactose:N-acetylgalactosamine-alpha-R beta 1,3-galactosyltransferase	53850	9506507	95157	3	3	9.5041
Coronin-1B Coronin-2	52630	2996044	57161	1	1	2.5478
Cortactin isoform C	31880	78214365	95697	22	22	69.4444
Corticosteroid 11-beta-dehydrogenase isozyme 1 11-DH 11-beta-hydroxysteroid dehydrogenase 1 11-beta-HSD1	104600	3851160	7578	1	1	1.0022
Cp431	43020	6978661	3700	1	1	3.6745
Creatine kinase M-type Creatine kinase M chain M-CK	136400	67460104	92415	4	4	3.4959
Cullin-associated NEDD8-dissociated protein 1 Cullin-associated and neddylation-dissociated protein 1 p120 CAND1 TBP-interacting protein TIP120A TBP-interacting protein of 120 kDa A						
Cyclophilin B	20310	2143900	80354	19	19	78.1421
Cyp4a14 protein	57970	71051108	63760	10	35	72.619
Cystathionine beta-synthase	61450	543960	41205	2	2	7.1301
Cystathionine gamma-lyase CTL target antigen	43580	51261011	62524	24	24	75.6281
Cysteine-rich protein 2 GRP2 Protein ESP1	22700	737713	46143	2	2	23.0769
Cysteine-sulfinate decarboxylase	55250	6685331	35923	2	2	7.3022
Cyldylate kinase	25830	71043752	267331	1	1	8.8106
Cytochrome P450 17A1 CYPXVII P450-C17 P450c17 Steroid 17-alpha-hydroxylase/17,20 lyase	57250	940818	3722	9	9	25.8383
Cytochrome P450 1A2	58290	203832	3724	21	21	52.8265

Cytochrome P450 27, mitochondrial precursor	60730	62655087	63757	10	10	29.4559
Cytochrome P450 2B2 CYP11B2 P450E P450 PB4	55930	34855371	13404	4	13	37.4745
Cytochrome P450 2B3 CYP11B3	56380	28849945	63770	23	30	66.8024
Cytochrome P450 2C11	57180	56971259	63780	1	38	84.4
Cytochrome P450 2C13, male-specific	55860	205935	63782	4	34	84.898
Cytochrome P450 2C22	56210	203521	33163	1	23	61.7587
Cytochrome P450 2C23	56430	6166042	72763	5	32	67.8138
Cytochrome P450 2C7	56190	482947	45873	26	30	58.3673
Cytochrome P450 2C70 CYP11C70 P-450Md P450 P49	56160	56827	63786	1	23	61.7587
Cytochrome P450 2D2	56680	57812	63788	24	39	80.8
Cytochrome P450 2D5	57080	57818	63790	3	30	63.4921
Cytochrome P450 2E1	56630	51980637	21526	27	27	61.6633
Cytochrome P450 2c13	55840	71051773	84196	1	31	70.2041
Cytochrome P450 3A	57720	6978749	3731	1	9	24.3028
Cytochrome P450 3A18 CYP11A18 P450(6)beta-2	57310	5921916	104898	15	17	44.668
Cytochrome P450 3A2	57730	515799	87425	11	19	48.6111
Cytochrome P450 4A1	58210	56047	51420	6	8	19.2534
Cytochrome P450 4A12 CYP1A12 CYP1A8 P450-KP1 P450-PP1	58520	203757	78089	1	6	10.0394
Cytochrome P450 4A14 precursor CYP1A14 Lauric acid omega-hydroxylase P450-LA-omega 3	58230	28461155	21524	12	36	72.3866
Cytochrome P450 4F1 CYP1V1 P450-A3	59870	9665225	134595	11	17	45.0382
Cytochrome P450 4F4 CYP1V4	60050	27465575	80281	9	18	44.0613
Cytochrome P450 51A1	56710	870754	3732	11	11	33.002
Cytochrome P450 IIA1 (Hepatic steroid hydroxylase IIA1) gene	56000	51980506	126566	21	36	77.6423
Cytochrome P450 monooxygenase CYP2T1	55880	19705467	161231	10	10	26.0606
Cytochrome P450, family 2, subfamily d, polypeptide 13	56640	58477687	103927	13	27	54
Cytochrome P450, family 2, subfamily j, polypeptide 9	57970	59809108	125135	5	6	18.1275
Cytochrome P450, family 20, subfamily A, polypeptide 1	52000	40786491	337678	3	3	9.3074
Cytochrome P450, subfamily 2A, polypeptide 1	56350	6978741	3727	17	30	64.2276
Cytochrome b5	10800	6980893	3890	9	9	76.5957
Cytochrome b5 outer mitochondrial membrane isoform precursor	15220	7427560	39173	1	5	60
Cytochrome c oxidase polypeptide VIIa-liver/heart, mitochondrial precursor Cytochrome c oxidase subunit VIIa-L	9353	56025	90517	2	2	27.7108
Cytochrome c oxidase polypeptide VIIc, mitochondrial VIIIA	1117	1169069	71407	1	1	90
Cytochrome c oxidase polypeptide Va, mitochondrial precursor	16130	55971	63743	9	9	59.589
Cytochrome c oxidase polypeptide Vb, mitochondrial precursor VIA*	13910	53237117	21518	3	3	24.031
Cytochrome c oxidase subunit 2	25940	5835181	98989	1	7	30.837
Cytochrome c oxidase subunit 4 isoform 1, mitochondrial precursor Cytochrome c oxidase subunit IV isoform 1 COX IV-1 Cytochrome c oxidase polypeptide IV	19510	8393180	63740	11	11	50.8876

Cytochrome c oxidase subunit I	56980	1332384	68411	2	2	2	4.8638
Cytochrome c, somatic Adult male kidney cDNA, RIKEN full-length enriched library, clone:F520003L15 product:cytochrome c, somatic, full insert sequence ES cells cDNA, RIKEN full-length enriched library, clone:2410041L21 product:cytochrome c, somatic, full insert sequence. Adult male cerebellum cDNA, RIKEN full-length enriched library, clone:1500032A05 product:cytochrome c, somatic, full insert sequence 18-day embryo whole body cDNA, RIKEN full-length enriched library, clone:1100001H15 product:cytochrome c, somatic, full insert sequence Adult male kidney cDNA, RIKEN full-length enriched library, clone:0610031O08 product:cytochrome c, somatic, full insert sequence	11610	6978725	71180	8	8	8	52.381
Cytochrome oxidase subunit II	26010	829023	105670	1	7	7	26.4317
Cytochrome oxidase subunit II Cytochrome c oxidase subunit II	25930	58615680	142106	1	7	7	30.837
Cytokeratin type I	15550	55956	11221	1	1	1	5.3892
D-amino-acid oxidase DAMOX DAO DAO	38820	56972124	60497	2	2	2	7.2254
DAD1 protein	12500	48428847	13029	3	3	3	26.5487
DAMP-1 protein	19670	37693510	116798	2	2	2	11.0465
DOPA/tyrosine sulfotransferase	34840	688032	74919	9	9	9	36.7893
Da1-24	124000	33086684	287107	8	8	8	8.7814
Damage-specific DNA binding protein 1	126900	9843869	111030	5	5	5	7.1053
Ddx5	69240	56090441	161883	7	9	9	18.6992
Dehydrogenase/reductase (SDR family) member 1	34020	56090381	240184	10	10	10	48.5623
Dehydrogenase/reductase SDR family member 4 NADPH-dependent carbonyl reductase/NADP-retinol dehydrogenase CR PHCR Peroxisomal short-chain alcohol dehydrogenase NADPH-dependent retinol dehydrogenase/reductase NDRD	27580	48474726	131621	6	6	6	23.8462
Dehydrogenase/reductase SDR family member 8 precursor 17-beta-hydroxysteroid dehydrogenase 11 17-beta-HSD 11 17-beta-HSD XI 17betaHSDXI 17bHSD11 17bHSD11	32940	73620788	308340	14	16	16	60.0671
Delta-5 desaturase	52470	16758190	60408	2	2	2	6.9351
Delta-6 fatty acid desaturase Fatty acid desaturase 2	52380	7513959	36810	6	6	6	13.964
Delta-aminolevulinic acid dehydratase Porphobilinogen synthase ALADH	36030	6978483	3622	4	4	4	25.4545
Delta3,5-delta2,4-dienoyl-CoA isomerase, mitochondrial precursor	36200	478984	80356	10	10	10	34.8624
Dephospho-CoA kinase domain containing	27350	56090393	318309	2	2	2	10.4167
Derlin-1 Degradation in endoplasmic reticulum protein 1 Der1-like protein 1	28830	62652445	119910	4	4	4	18.7251
Destrin Actin-depolymerizing factor ADF	18390	7441446	123978	4	4	4	34.7561
Developmentally regulated GTP binding protein 1 NOD-derived CD11c +ve dendritic cells cDNA, RIKEN full-length enriched library, clone:F630119A02 product:developmentally regulated GTP binding protein 1, full insert sequence 0 day neonate cortex cDNA, RIKEN full-length enriched library, clone:G630068K21 product:developmentally regulated GTP binding protein 1, full insert sequence	40510	57528300	71226	9	9	9	37.6022
Diacylglycerol O-acyltransferase 1 Diglyceride acyltransferase	56870	9965432	145183	1	1	1	3.2129
Diamine oxidase-like protein 1	80090	40385889	216306	1	1	1	1.2857
Dihydrofolate reductase	21640	81871579	53424	2	2	2	13.9037
Dihydroliipoamide dehydrogenase E3 component of pyruvate dehydrogenase complex, 2-oxo-glutarate complex, branched chain keto acid dehydrogenase complex	54040	40786469	253447	4	4	4	11.1984

Dihydroorotate dehydrogenase, mitochondrial precursor Dihydroorotate oxidase DHodehase	42660	62665239	43490	5	5	21.519
Dihydropteridine reductase HDHPR Quinoid dihydropteridine reductase	25550	576089	23398	11	11	55.1867
Dihydroxyacetone kinase Glycerone kinase DHA kinase	59440	85718638	223736	14	14	38.0623
Dimerization Cofactor Of Hepatocyte Nuclei	11960	10835705	108686	2	2	23.0769
Dimethylalanine monooxygenase [N-oxide-forming] 1 Hepatic flavin-containing monooxygenase 1 FMO 1 Dimethylalanine oxidase 1	59830	78099773	339248	23	23	51.3158
Dimethylglycine dehydrogenase, mitochondrial precursor ME2GLYDH	96050	56689	82662	1	1	1.9837
Dipeptidyl peptidase IV	88000	6978773	3741	1	19	28.292
Disks large homolog 1 Synapse-associated protein 97 SAP-97	100600	6978763	3737	3	3	5.5982
DnaJ (Hsp40) homolog, subfamily A, member 1 Blastocyst blastocyst cDNA, RIKEN full-length enriched library, clone:1C0041A13 product:DnaJ (Hsp40) homolog, subfamily A, member 1, full insert sequence 14 days pregnant adult female placenta cDNA, RIKEN full-length enriched library, clone:I530018C07 product:DnaJ (Hsp40) homolog, subfamily A, member 1, full insert sequence	44870	51702257	8742	11	11	39.7985
DnaJ homolog subfamily A member 2 RDJ2	45770	2281451	1106	5	5	19.4175
DnaJ-like protein	25760	9910322	42765	1	1	3.139
Dnajc3 protein [Rattus norvegicus]	50240	38197558	318957	1	15	46.0137
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 63 kDa subunit precursor Ribophorin II RPN-II	69080	62512124	193923	32	32	68.1458
Dynactin 2	44150	51948450	260733	4	4	14.6766
Dynamitin 2	98230	729380	3740	5	6	9.4253
Dynein heavy chain, cytosolic	532000	294543	95169	3	3	0.86133
Dynein light chain 2, cytoplasmic Dynein light chain LC8-type 2 8 kDa dynein light chain DLC8 DLC8b	10350	56748619	129100	2	2	25.8427
EH-domain containing 1	60600	58865448	2280	3	14	29.588
EH-domain containing protein 2	60790	34536836	244145	7	18	46.5421
EIF2S1 protein	36110	9506571	103	11	11	46.9841
EIF3S6 protein	52220	62652368	55867	1	1	2.9213
ELAV (Embryonic lethal, abnormal vision, Drosophila)-like 1 Hu antigen R 3 days neonate thymus cDNA, RIKEN full-length enriched library, clone:A630073F18 product:ELAV-LIKE PROTEIN 1 (HU-ANTIGEN R) (HUR) (ELAV-LIKE GENERIC PROTEIN) (MELG), full insert sequence	36170	34870116	18691	2	2	9.5092
ENSEMBL:ENSRNOP00000002163 REFSEQ:XP_342451 PREDICTED: similar to lunapark	47640	34855225	271473	1	1	1.8824
ENSEMBL:ENSRNOP00000001183 REFSEQ:XP_216785 PREDICTED: similar to neuronal protein 15.6	17630	27669100	192375	2	2	17.8808
ENSEMBL:ENSRNOP00000023811 REFSEQ:XP_214570 PREDICTED: similar to NADH dehydrogenase (ubiquinone) 1 alpha subcomplex 2	10840	27682913	250139	3	3	34.0206
ER lumen protein retaining receptor 2 KDEL receptor 2 KDEL endoplasmic reticulum protein retention receptor 2	24450	61557025	4394	4	6	40.566
ERGIC-53 protein precursor ER-Golgi intermediate compartment 53 kDa protein Lectin, mannose-binding 1.p58	57960	29611707	77835	25	25	56.0928
ERO1-like	54120	19924061	33170	9	10	26.7241
ES cells cDNA, RIKEN full-length enriched library, clone:2410046L21 product:ribosomal protein L35a, full insert sequence Ribosomal protein L35a Rpl35a protein	12550	57119	14850	3	3	15.4545

ES1 protein homolog, mitochondrial precursor	28170	83302472	214426	3	3	17.2932
EZRIN [Rattus norvegicus]	54170	17902245	145232	2	11	21.3187
Ectonucleoside triphosphate diphosphohydrolase 5	47370	40786479	318787	18	18	59.0164
Ectonucleotide pyrophosphatase/phosphodiesterase 1 E-NPP 1 Phosphodiesterase I/nucleotide pyrophosphatase 1 Plasma-cell membrane glycoprotein PC-1 Alkaline phosphodiesterase I	102900	23396766	60453	15	15	26.6004
Nucleotide pyrophosphatase NPPase						
Ectonucleotide pyrophosphatase/phosphodiesterase 3	99090	806379	85379	4	4	6.0571
Electron transfer flavoprotein subunit beta Beta-ETF	27690	81884360	189992	9	9	36.4706
Electron transfer flavoprotein-ubiquinone oxidoreductase, mitochondrial precursor ETF-QO ETF-ubiquinone oxidoreductase ETF dehydrogenase Electron-transferring-flavoprotein dehydrogenase	68200	52000614	258013	23	23	46.4286
Elongation factor EF-1 alpha	50110	85057089	140182	10	22	56.71
Endo-alpha-D-mannosidase	51670	2642187	133253	6	6	23.0599
Endobrevin	7348	18655558	37566	4	4	63.0769
Endoplasmic reticulum protein 29	28570	60688521	157237	15	15	60
Endothelial differentiation-related factor 1 EDF-1 Multiprotein-bridging factor 1 MBF1 Calmodulin-associated peptide 19 CAP-19	16370	62510525	98538	2	2	17.5676
Engulfment and cell motility protein 1	28740	34876182	4981	1	1	7.2874
Eno1 protein [Rattus norvegicus]	51260	38649320	338764	9	16	46.822
Enoyl-CoA hydratase, mitochondrial precursor	31520	56072	15873	12	12	45.8621
Enoyl-Coenzyme A, hydratase/3-hydroxyacyl Coenzyme A dehydrogenase	78660	59809132	149061	45	45	59.2798
Epidermal growth factor receptor	134900	6478868	85744	11	11	11.7452
Epithelial-cadherin precursor E-cadherin Uvomorulin Cadherin-1 CD324 antigen E-Cad/CTF1 E-Cad/CTF2 E-Cad/CTF3	98720	6009482	1625	4	4	7.9007
Epoxide hydrolase 1 Microsomal epoxide hydrolase Epoxide hydratase	52580	77539448	17081	40	40	82.4176
Epsin 1	60160	41016934	105332	1	1	2.087
Erythroid spectrin alpha	276600	58865394	725563	11	12	6.9602
Erythroid spectrin beta	246300	47058982	726511	15	19	10.3416
Estradiol 17-beta-dehydrogenase 2 17-beta-HSD 2 17-beta-hydroxysteroid dehydrogenase 2	41970	3334165	68349	11	11	34.9081
Estrogen sulfotransferase, isoform 1 EST-1 Sulfotransferase, estrogen-preferring Estrone sulfotransferase	35510	1711599	109266	1	7	31.1864
Estrogen sulfotransferase, isoform 3 EST-3 Sulfotransferase, estrogen-preferring Estrone sulfotransferase	35420	6981594	75106	1	7	31.1864
Estrogen sulfotransferase, isoform 6 EST-6 Sulfotransferase, estrogen-preferring Estrone sulfotransferase	35300	913357	62242	1	6	29.1525
Estrogen-related receptor gamma Estrogen receptor-related protein 3	51310	50400205	17534	1	1	2.1834
Eukaryotic initiation factor 5A isoform I variant D Eukaryotic initiation factor 5A isoform I variant B Eukaryotic initiation factor 5A isoform I variant C Eukaryotic translation initiation factor 5A	16830	91207082	23682	6	6	50
Eukaryotic peptide chain release factor subunit 1 eRF1 Eukaryotic release factor 1	49030	68565348	41501	4	4	18.0778

Eukaryotic translation initiation factor 4A1 16 days embryo kidney cDNA, RIKEN full-length enriched library, clone:1920165Q08 product:eukaryotic translation initiation factor 4A1, full insert sequence 17 days embryo kidney cDNA, RIKEN full-length enriched library, clone:1920077H15 product:eukaryotic translation initiation factor 4A1, full insert sequence 16 days embryo heart cDNA, RIKEN full-length enriched library, clone:1920075M13 product:eukaryotic translation initiation factor 4A1, full insert sequence 17 days embryo heart cDNA, RIKEN full-length enriched library, clone:1920075G18 product:eukaryotic translation initiation factor 4A1, full insert sequence 17 days embryo kidney cDNA, RIKEN full-length enriched library, clone:1920054E16 product:eukaryotic translation initiation factor 4A1, full insert sequence CDNA, RIKEN full-length enriched library, clone:1730045F20 product:eukaryotic translation initiation factor 4A1, full insert sequence Blastocyst blastocyst cDNA, RIKEN full-leng	46150	40786436	55871	8	8	27.3399
Eukaryotic translation initiation factor 4H	27320	55741853	295040	1	1	9.2742
Evolutionarily conserved signaling intermediate in Toll pathway	49620	55741518	276570	1	1	3.2258
Exocyst complex component 2 Exocyst complex component Sec5 rSec5	104000	7513971	161256	1	1	1.6234
Exostosin-1 Glucuronosyl-N-acetylglucosaminyl-proteoglycan/N-acetylglucosaminyl-proteoglycan 4-alpha-N-acetylglucosaminyltransferase Multiple exostosins protein 1 homolog	86310	62652423	57456	1	1	2.1448
F-actin binding protein b-Nexilin	78390	40538878	173653	1	1	1.2195
F-actin capping protein alpha-2 subunit	32970	74355722	74410	10	13	66.0839
F-actin capping protein beta subunit	30630	54400732	83668	13	13	47.0588
FAM3C-like protein	24710	38454280	173223	10	10	53.7445
FK506-binding protein 2 precursor	15390	27661294	170945	9	9	65.7143
Faah protein	63360	6225312	29993	20	20	55.9585
Fatty acid binding protein FABP-1	3929	452977	23674	2	2	68.5714
Fatty acid synthase	272600	57890	43659	34	34	21.517
Fatty acid-binding protein, liver	14270	6978825	3760	10	10	80.315
Fatty aldehyde dehydrogenase Aldehyde dehydrogenase, microsomal Aldehyde dehydrogenase family A2 member A2 Aldehyde dehydrogenase 10	54080	399362	78151	18	18	46.4876
Ferritin light chain 1	20750	84000579	277663	10	10	69.3989
Fetuin-B precursor IRL685	41530	6562849	145181	10	10	39.9471
Fibrinogen gamma chain precursor	49650	1183937	3766	11	11	38.4439
Fibronectin precursor FN	272500	9506703	95208	27	27	16.7138
Fibronigen-like protein	30750	25282415	181007	4	4	13.1086
Ficolin-1 precursor Collagen/fibrinogen domain-containing protein 1 Ficolin-A Ficolin A M-Ficolin	36630	6714560	75919	1	1	5.0746
Flotillin-2 Reggie-1 REG-1	47040	4079709	101676	10	10	30.1402
Ftcd protein	58910	60688163	39875	16	16	46.5804
Fukutin related protein	54850	71043684	242747	1	1	3.0364
Fumarate hydratase, mitochondrial precursor Fumarase	54460	8393358	45080	1	7	25.8383
Fumarylacetoacetase Fumarylacetoacetate hydrolase Beta-diketonase FAA	45980	8393349	51443	18	18	55.3699
Furin precursor Paired basic amino acid residue cleaving enzyme PACE Dibasic-processing enzyme Prohormone convertase 3	86650	9506955	47234	1	1	1.6393

GD3 alpha 2,8-sialyltransferase	44010	6981540	75089	3	3	3	9.7368
GM2 activator protein	21520	27229316	157436	1	1	1	11.0553
GNB2 protein	37330	8927570	4326	3	7	7	27.3529
GPP34-related protein	32920	62644637	220058	2	3	3	12.9825
GTP cyclohydrolase 1 feedback regulatory protein GTP cyclohydrolase I feedback regulatory protein GFRP p35	9541	16975337	140831	2	2	2	31.3253
GTP-binding nuclear protein Ran GTPase Ran Ras-like protein TC4	24420	51338593	76611	2	2	2	11.1111
GTP-binding protein rab10 - rat	22610	420269	44648	9	12	12	59
GTPase HRas precursor Transforming protein p21 p21ras H-Ras-1 c-H-ras	21300	34861217	10323	1	3	3	19.0476
Galactokinase 1 Predicted	42380	56605662	206276	2	2	2	10.9694
Galactose-1-phosphate uridylyltransferase Gal-1-P uridylyltransferase UDP-glucose--hexose-1-phosphate uridylyltransferase	43310	68533665	71441	1	1	1	2.3747
Galectin-3	27200	57870645	71532	1	1	1	4.1985
Galectin-9	36320	1916610	18989	7	7	7	31.3665
Gamma-butyrobetaine dioxygenase Gamma-butyrobetaine,2-oxoglutarate dioxygenase Gamma-butyrobetaine hydroxylase Gamma-BBH	44550	5825482	139030	1	1	1	3.1008
Gamma-glutamyltransferase 5 precursor Gamma-glutamyltransferase-like activity 1 Gamma-glutamyl leukotrienase GGL Gamma glutamyl transpeptidase-related enzyme GGT-rel Gamma-glutamyltransferase 5 heavy chain Gamma-glutamyltransferase 5 light chain	61610	9506723	52613	1	1	1	2.6224
Gap junction beta-1 protein Connexin-32 Cx32	32000	8393444	51463	5	5	5	14.4876
Gene,	48610	22775474	113271	1	1	1	2.6432
General vesicular transport factor p115 Transcytosis-associated protein TAP Vesicle docking protein	107200	538153	71574	14	14	14	19.3952
Genethonin-1	35490	62078705	169873	5	5	5	18.6186
Glia maturation factor beta GMF-beta	16610	111660	149966	1	1	1	16.3121
Glial fibrillary acidic protein alpha Gfap protein	49960	62657131	26394	3	4	4	10.2326
Glucose phosphate isomerase	62830	46485440	295907	5	5	5	13.9785
Glutamate dehydrogenase, mitochondrial precursor	61420	92090591	3897	42	42	42	67.5627
Glutamine fructose-6-phosphate transaminase 1	76830	54400724	277551	1	1	1	2.3495
Glutamine synthetase	42270	61098201	28251	12	12	12	33.5121
Glutamyl aminopeptidase	108000	7159085	62885	2	2	2	2.328
Glutathione S-transferase Yb-1	25920	204503	126642	2	26	26	89.4495
Glutathione S-transferase Yb-2	25700	66613	28291	4	17	17	66.5138
Glutathione S-transferase alpha-3 Glutathione S-transferase Yc-1 GST Yc1 GST 2-2 GST AA GST A3-3	25320	576438	78049	9	18	18	81.448
Glutathione S-transferase alpha-4 Glutathione S-transferase Yk GST Yk GST 8-8 GST K GST A4-4	25510	54200030	28290	1	3	3	9.9099
Glutathione peroxidase	22260	121668	28283	11	11	11	55.7214
Glutathione transferase (EC 2.5.1.18) psi	3544	92300	84221	1	1	1	33.3333
Glutathione transferase omega 1	27670	12585231	55147	3	3	3	13.6929
Glyceraldehyde-3-phosphate dehydrogenase Gapd protein	35830	9798638	51456	2	17	17	63.6637

Glycerol kinase ATP-glycerol 3-phosphotransferase	Glycerokinase GK ATP-stimulated	57480	433211	18015	1	1	2.2901
glucocorticoid-receptor translocation promoter	ASTP	93710	8393466	51468	7	7	11.9565
Glycerol-3-phosphate acyltransferase, mitochondrial precursor	GPAT	80970	6980978	3907	1	1	2.0633
Glycerol-3-phosphate dehydrogenase, mitochondrial precursor	GPDH-M	32420	6137382	19169	9	9	45.8904
Glycine N-methyltransferase		56860	81914601	229000	2	2	6.0484
Glycylpeptide N-tetradecanoyltransferase 1	Peptide N-myristoyltransferase 1	28530	16758358	21695	15	15	61.2
N-myristoyltransferase 1 NMT 1	Type I N-myristoyltransferase	133600	8393450	51465	48	48	49.7011
Golgi SNAP receptor complex member 1	28 kDa Golgi SNARE protein	33780	50400215	54283	11	12	40.2685
GOS-28		47310	56090463	288023	7	7	22.467
Golgi apparatus protein 1 precursor	Golgi sialoglycoprotein MG-160 E-selectin ligand 1	111400	7513936	169300	33	33	45.3347
Golgi phosphoprotein 3	Coat-protein GPP34 Trans-Golgi protein	15780	81884637	199992	1	1	10.9489
Golgi reassembly stacking protein 2		53520	51260133	86608	17	17	41.3866
Golgin subfamily A member 2	Cis-Golgi matrix protein GM130	25210	77539774	29315	1	1	5.53
Golgin subfamily A member 7		25680	529588	33791	1	10	39.9083
Group specific component		22590	30750124	196203	2	2	14.0704
Growth factor receptor bound protein 2		51020	9910706	42862	4	4	12.5551
Gstm7 protein		40500	71089913	37194	7	13	48.4507
Guanidinoacetate N-Methyltransferase		35080	54037164	123232	19	19	77.918
Guanine deaminase	Guanine aminase						
Guanine nucleotide binding protein alpha inhibiting 2							
Guanine nucleotide binding protein, beta 2, related sequence 1	CRL-1722 L5178Y-R cDNA, RIKEN full-length enriched library, clone:1730096H10 product:guanine nucleotide binding protein, beta 2, related sequence 1, full insert sequence Blastocyst blastocyst cDNA, RIKEN full-length enriched library, clone:17C0024M22 product:guanine nucleotide binding protein, beta 2, related sequence 1, full insert sequence Blastocyst blastocyst cDNA, RIKEN full-length enriched library, clone:17C0014F18 product:guanine nucleotide binding protein, beta 2, related sequence 1, full insert sequence Blastocyst blastocyst cDNA, RIKEN full-length enriched library, clone:17C0013E14 product:guanine nucleotide binding protein, beta 2, related sequence 1, full insert sequence Mammary gland RCB-0527 Jyg-MC(B) cDNA, RIKEN full-length enriched library, clone:G930013E05 product:guanine nucleotide binding protein, beta 2, related sequence 1, full insert sequence 0 day neonate head cDNA, RIKEN full-length enriched library,						
Guanine nucleotide-binding protein G(q), alpha subunit		42140	7329187	37195	4	6	21.4485
Guanine nucleotide-binding protein alpha-11 subunit		42030	8925964	37192	5	7	27.0195
H2-K region expressed gene 4, rat orthologue RT1 class I, locus K64		49500	62665667	219015	1	1	5.5556
H3 histone, family 3A H3 histone, family 3B H3F3A protein		15330	56388767	16060	1	1	23.5294
HNRPK protein Heterogeneous nuclear ribonucleoprotein K		51030	38197650	72151	10	10	28.8793
Hdlbp protein		41290	38649090	338318	3	25	65.9517
Heat shock 27 kDa protein		22890	204665	71479	1	1	8.2524

Heat shock protein 8 13 days embryo liver cDNA, RIKEN full-length enriched library, clone:1920176M04 product:heat shock protein 8, full insert sequence 16 days embryo kidney cDNA, RIKEN full-length enriched library, clone:1920096J24 product:heat shock protein 8, full insert sequence 16 days embryo kidney cDNA, RIKEN full-length enriched library, clone:1920087N17 product:heat shock protein 8, full insert sequence 16 days embryo kidney cDNA, RIKEN full-length enriched library, clone:1920079M09 product:heat shock protein 8, full insert sequence 17 days pregnant adult female amnion cDNA, RIKEN full-length enriched library, clone:1920066C08 product:heat shock protein 8, full insert sequence 16 days embryo kidney cDNA, RIKEN full-length enriched library, clone:1920062J24 product:heat shock protein 8, full insert sequence 17 days embryo stomach cDNA, RIKEN full-length enriched library, clone:1920052L10 product:heat shock protein 8, full insert sequence 17 days embryo kidney cDNA, RIKEN full-l	70870	71051777	68722	9	36	57.2755
Heat shock protein 86 Heat shock protein 1, alpha	84810	54673763	82698	12	20	31.5143
Heme oxygenase 1	33010	6981032	3930	1	1	3.8062
Heme oxygenase 2 HO-2	35760	501035	68743	7	7	32.0635
Hemoglobin alpha-1 and alpha-2 chains	15330	6981010	3923	1	11	75.3521
Hemoglobin beta chain, major-form	15980	55823	28543	3	18	91.1565
Hemopexin precursor	51290	204621	16936	19	19	44.3478
Hepcidin precursor	9286	21542070	108861	2	2	28.5714
Heterogeneous nuclear ribonucleoprotein A1	34200	70819	29410	2	2	10.625
Heterogeneous nuclear ribonucleoprotein D0 hnRNP D0 AU-rich element RNA-binding protein 1	38190	9588096	47431	1	1	3.966
Heterogeneous nuclear ribonucleoprotein F	45730	82546819	17327	2	2	7.9518
Hexokinase, type I	102400	6981022	3926	1	1	0.87146
High affinity immunoglobulin epsilon receptor gamma-subunit precursor FcεRI gamma IgE Fc receptor gamma-subunit Fc-epsilon RI-gamma	9765	226241	84256	2	2	15.1163
Histidine ammonia lyase	72280	8393522	51482	5	5	13.3942
Histidine triad nucleotide binding protein	13780	34870743	82484	1	1	11.1111
Histidine triad protein 4	18890	21654864	153619	1	1	8.4337
Histidine-rich glycoprotein 1	59050	62657833	140379	1	4	7.619
Histidine-rich glycoprotein 2	58060	13358878	18186	2	5	9.1262
Histone H1.2	21990	444788	72598	3	3	15.0685
HnRNP protein	18280	3021529	57359	1	1	11.399
Hsd17b12 protein	34840	38494210	337296	12	12	52.5641
Hydrolase A	3058	807108	105537	2	2	46.6667
Hydroxyacid oxidase 3	39200	50925465	100475	8	8	25.4958
Hydroxyacylglutathione hydrolase Glyoxalase II Glx II Round spermatid protein RSP29	28900	3913728	15417	4	4	23.8462
Hydroxymethylglutaryl-CoA lyase, mitochondrial precursor HMG-CoA lyase HL 3-hydroxy-3-methylglutarate-CoA lyase	34190	38511566	68742	5	5	28.3077
Hydroxymethylglutaryl-CoA synthase, mitochondrial precursor HMG-CoA synthase 3-hydroxy-3-methylglutaryl coenzyme A synthase	56910	27485521	16963	23	25	49.0157
Hydroxysteroid (17-beta) dehydrogenase 8	26790	47087119	301041	2	2	9.6525
HYOU1 protein	111200	77404380	395638	46	46	56.2124

Hypothetical glutaredoxin/glutathione S-transferase C terminus containing protein	43450	27706734	166503	2	2	2	8.5938
Hypothetical protein	37380	51338711	8648	2	6	6	20.2941
Hypothetical protein	24090	83415090	163993	2	7	7	41.8605
Hypothetical protein	40560	58477247	71440	5	5	5	25.2101
Hypothetical protein	14900	25282411	132369	2	2	2	18.9781
Hypothetical protein Ccdc51	42310	62078929	366853	1	1	1	2.6385
Hypothetical protein D10Wsu52e	55250	50926851	54494	9	9	9	23.5644
Hypothetical protein DKFZp468N1517	6677	6981490	4847	3	3	3	33.9286
Hypothetical protein FLJ20445 Ring finger protein 153	31230	34862676	49021	1	1	1	4.6763
Hypothetical protein MG87 MOCO sulphurase C-terminal domain containing 2	38250	38511548	161253	9	9	9	23.6686
Hypothetical protein MGC72560	17720	40018580	139384	1	1	1	8.0745
Hypothetical protein MGC72996	20710	38454298	220427	1	1	1	5.2632
Hypothetical protein MGC94464	19290	56090373	282775	1	1	1	4.8485
Hypothetical protein Mettl7b	27900	66730429	244225	11	11	11	50
Hypothetical protein Ndufc2	14360	57164133	164223	2	2	2	18.3333
Hypothetical protein RGD1305677	21660	58585236	209082	1	1	1	8.1633
Hypothetical protein RGD1310224	33690	57164137	208921	6	6	6	34.3234
Hypothetical protein RPL37A	10280	57123	4820	3	3	3	42.3913
Hypothetical protein Tmem97	20950	56605746	300133	3	3	3	13.0682
Hypoxanthine-guanine phosphoribosyltransferase HGPRT HGPRTase	24480	68534712	16980	3	3	3	15.1376
INSIG2 membrane protein Insulin induced gene 2	24970	55250700	200861	1	1	1	4.8889
ITI heavy chain-related protein	1809	1041915	40462	1	2	2	93.75
Ig gamma-2A chain C region	25220	13399989	62937	1	1	1	4.4444
IgG receptor FcRN large subunit P51 precursor	40170	56437	15418	1	1	1	3.0055
Implantation-associated protein precursor IAP	37990	6016303	128379	6	6	6	14.0299
Importin beta-1 subunit Karyopherin beta-1 subunit Nuclear factor P97	97120	8393610	51498	3	3	3	4.8
Injury-inducible-protein I-55	58100	24475405	154010	2	2	2	3.9139
Inosine monophosphate dehydrogenase 2	55800	40018566	231448	1	1	1	2.7237
Inositol 1,4,5-trisphosphate receptor type 2 Type 2 inositol 1,4,5-trisphosphate receptor Type 2	307100	56508	37203	2	2	2	1.1107
InsP3 receptor IP3 receptor isoform 2 InsP3R2	156800	8393621	51500	8	8	8	6.5799
Insulin receptor precursor IR Insulin receptor subunit alpha Insulin receptor subunit beta	27740	68534170	11776	2	2	2	11.4173
Insulin-like growth factor binding 4 Insulin-like growth factor binding protein 4	66810	71896592	11211	2	2	2	5.141
Insulin-like growth factor-binding protein complex acid labile chain precursor ALS	30310	81883760	284296	5	5	5	23.6842
Integral membrane protein 2B	130800	56494	37168	4	4	4	3.4746
Integrin alpha-1 precursor Laminin and collagen receptor VLA-1 CD49a antigen	88490	8393636	51502	12	12	12	20.5257
Integrin beta-1 precursor Fibronectin receptor subunit beta Integrin VLA-4 subunit beta CD29 antigen	86930	24308466	153869	7	7	7	10.4193
Integrin beta3 subunit							

Inter-alpha-inhibitor H4 heavy chain	103600	9506819	47186	21	22	29.9356
Inter-alpha-trypsin inhibitor heavy chain H3 precursor ITI heavy chain H3 Inter-alpha-inhibitor heavy chain 3	99100	8393899	38418	13	13	23.4498
Intercellular adhesion molecule 1 precursor ICAM-1	60140	6981068	3942	3	3	6.9725
Interferon-induced protein 35 Predicted	31760	57526854	315195	4	4	20.6294
Interferon-inducible protein	14970	57605	17165	2	2	26.2774
Interleukin 1 receptor-like 1 ligand Predicted	25210	61740631	194234	3	3	15.4185
Iodothyrosine dehalogenase 1 precursor IYD-1	32850	81882575	258458	5	5	21.0526
Iron-responsive element-binding protein 1 (IRE-BP 1) (Iron regulatory protein 1) (IRP1) (Ferritin repressor protein) (Aconitate hydratase) Citrate hydro-lyase Aconitase	98130	8394162	51607	8	8	16.198
Ischemia responsive 94 kDa protein	94060	3360521	95874	1	1	1.0714
Isocitrate dehydrogenase [NADP] cytoplasmic Cytosolic NADP-isocitrate dehydrogenase	46730	627999	71492	12	12	44.9275
Oxalosuccinate decarboxylase IDH NADP(+)-specific ICDH IDP	39610	68565369	60501	1	1	3.2787
Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial precursor Isocitric dehydrogenase NAD(+)-specific ICDH	46440	6981112	3955	3	3	9.434
Isovaleryl-CoA dehydrogenase, mitochondrial precursor IVD	24550	62821823	272716	4	5	32.5472
KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 1 Predicted	48020	21490001	38912	2	2	6.6194
Kallistatin	3107	554464	66467	1	1	38.4615
Keratin K6	61830	81170669	318877	6	12	15.1042
Keratin, type II cytoskeletal 5 Cytokeratin-5 CK-5 Keratin-5 K5	54020	67678416	67836	33	38	70.8075
Keratin, type II cytoskeletal 8	32750	62650395	127122	4	4	18.1208
Ketohexokinase Hepatic fructokinase	43870	51948424	169834	2	2	5.4455
Kidney predominant protein NCU-G1	159600	31745148	166145	3	3	1.444
Kinesin-like protein KIF15	54350	81882198	70289	8	8	20.9205
Kynurenine 3-monoxygenase Kynurenine 3-hydroxylase	47780	8393641	51504	3	3	11.5294
Kynurenine/alpha-aminoadipate aminotransferase mitochondrial precursor (KAT/AadAT) (Kynurenine--oxoglutarate transaminase II) Kynurenine aminotransferase II Kynurenine--oxoglutarate aminotransferase II 2-aminoadipate transaminase 2-aminoadipate aminotransferase						
Alpha-aminoadipate aminotransferase AadAT	50610	204150	104163	14	14	41.3636
L-gulonolactone oxidase	36450	8393706	51518	7	29	87.9518
L-lactate dehydrogenase A chain LDH-A LDH muscle subunit LDH-M	38480	21617859	44348	3	3	15.427
L-serine dehydratase/L-threonine deaminase	25720	50400214	161241	3	3	18.0328
L-xylulose reductase XR Dicarboxyl/L-xylulose reductase	31470	56090371	205582	1	1	3.663
LEA_4 domain containing protein RGD1359600	29970	71122452	19687	1	1	4.943
LIM and SH3 domain protein 1 LASP-1	21830	59798059	29682	2	3	17.2589
LIN-7 homolog C LIN-7C mLin7C Mammalian LIN-seven protein 3 MALS-3 Vertebrate LIN 7 homolog 3 Veil-3 protein	47340	44890246	726783	4	4	15
LOC246208 protein	62200	45680888	339290	1	1	2.0333
LOC362065 protein Transmembrane protein	14550	57702	103229	2	2	18.6992
LOC495749 protein	83280	51243735	139643	14	24	37.5691

LOC495903 protein	28830	41350889	11293	6	6	40.1575
LOC495922 protein	28300	9507245	47332	4	7	27.9352
LOC496117 protein	17470	38649092	28295	11	11	85.8065
LOC496278 protein	19670	34858314	32844	6	6	47.619
LRRGT00021	27510	62639574	274007	2	2	7.2961
LRRGT00032	75370	62656183	216194	4	4	6.7548
LRRGT00050	166800	66793366	286877	1	1	0.94213
LRRGT00084 DnaJ (Hsp40) homolog, subfamily B, member 11 Predicted	40490	62543491	295796	13	13	44.6927
LRRGT00086	62990	37361858	209490	1	1	1.9784
LRRGT00111	44780	62650915	238730	6	6	18.9189
Lactate dehydrogenase A-like	42050	50927335	224451	3	4	10.733
Lactoylglutathione lyase Methylglyoxalase Aldoketomutase Glyoxalase I Glx I Ketone-aldehyde mutase S-D-lactoylglutathione methylglyoxal lyase	20820	81885359	251837	2	2	16.3043
LanC-like protein 1 40 kDa erythrocyte membrane protein p40	45240	6625487	126112	1	1	3.0075
Leucine zipper protein 1 Leucine zipper motif-containing protein	117200	9931329	42949	3	3	1.9029
Leucine zipper-EF-hand-containing transmembrane protein 1, mitochondrial precursor	83060	62510718	296680	10	10	20.1624
Leucine-rich repeat-containing protein 57	26720	81909634	240594	2	2	10.0418
Leucine-rich repeat-containing protein 59 Protein p34	34870	81910029	152512	14	14	52.7687
Leucyl-cystinyl aminopeptidase	117200	20138455	5106	1	1	1.4634
Leukemia inhibitory factor receptor precursor LIF receptor LIF-R CD118 antigen	122400	81870502	37205	3	3	3.2937
Leukocyte common antigen variant 4 precursor	132600	56560	111680	1	1	0.93857
Lipid phosphate phosphohydrolase 3 Phosphatidic acid phosphatase 2b Phosphatidate phosphohydrolase type 2b PAP2b PAP-2b PAP2-beta Differentially expressed in rat intestine 42 Drl42	35320	45477000	82681	2	2	7.3718
Lipid raft protein flotillin-1 Bone marrow macrophage cDNA, RIKEN full-length enriched library, clone:1830015L22 product:flotillin 1, full insert sequence Bone marrow macrophage cDNA, RIKEN full-length enriched library, clone:1830013M04 product:flotillin 1, full insert sequence	47510	40352785	8548	7	7	24.0654
Liver NTE-related protein	75650	21314221	198073	1	1	2.4927
Liver annexin-like protein	52010	7108713	62757	2	2	5.0847
Liver carboxylesterase 1 precursor	60170	2506388	43686	10	20	45.173
Liver carboxylesterase 10 precursor	62150	57554	146478	2	35	64.0708
Liver carboxylesterase 10 precursor	62140	56899	112141	1	35	65.8407
Liver carboxylesterase 3 precursor Carboxylesterase ES-3 pl 5.5 esterase ES-HTEL	61710	550147	78070	17	22	52.7629
Liver carboxylesterase 4 precursor	62270	550418	77793	20	35	72.1925
Liver carboxylesterase B-1 precursor Liver microsomal carboxylesterase	62490	562010	10945	1	29	56.328
Liver regeneration-related protein 1	17130	28194393	52861	1	1	6.2893
Liver regeneration-related protein LRRG03 Transferrin	76400	61566986	166406	3	45	56.7335
Liver regeneration-related protein LRRG04 Apolipoprotein C-I	9861	91989	3640	3	3	22.7273
Liver-specific transport protein	58710	529590	60454	1	1	2.243

Lon	105800	19173766	140367	1	1	1	1.3684
Long-chain fatty acid transport protein 1 Fatty acid transport protein 1 FATP-1 Solute carrier family 27 member 1	71280	2492888	60472	1	1	1	1.8576
Long-chain specific acyl-CoA dehydrogenase, mitochondrial precursor LCAD	47870	6978431	3599	13	13	13	30.6977
Long-chain-fatty-acyl-CoA ligase 1 Long-chain acyl-CoA synthetase 1 LACS 1 Long-chain-fatty-acyl-CoA ligase, liver isozyme	78180	25742739	85756	38	42	42	67.8112
Long-chain-fatty-acyl-CoA ligase 4 Long-chain acyl-CoA synthetase 4 LACS 4	74330	6016483	22152	4	4	4	8.9552
Long-chain-fatty-acyl-CoA ligase 5 Long-chain acyl-CoA synthetase 5 LACS 5	76400	6016484	60485	29	33	33	57.8331
Long-chain-fatty-acyl-CoA ligase 6	78180	417242	44475	3	3	3	3.7303
Low molecular mass ubiquinone-binding protein	9849	68341999	311481	1	1	1	15.8537
Low-density lipoprotein receptor precursor LDL receptor	96620	56570	106673	2	2	2	3.2992
Lupus La protein homolog La ribonucleoprotein La autoantigen homolog	47780	729919	37247	2	2	2	6.747
LysM, putative peptidoglycan-binding, domain containing 3	33700	57527470	204667	1	1	1	4.6667
Lysosomal acid lipase/cholesteryl ester hydrolase precursor LAL Acid cholesteryl ester hydrolase	45190	9653291	72321	1	1	1	3.2746
Sterol esterase Lipase A Cholesteryl esterase	48320	8392842	144356	1	1	1	2.8369
Lysosomal acid phosphatase precursor LAP	43970	6981144	3967	5	5	5	14.742
Lysosome-associated membrane glycoprotein 1 precursor	43130	205169	44157	4	4	4	11.9593
Lysosome-associated membrane glycoprotein 2 precursor	16730	7428180	39196	1	1	1	12.8378
Lysozyme	71620	55741637	269157	1	1	1	1.7572
Lysyl-tRNA synthetase	19200	77157795	166255	1	1	1	6.25
MAL2A Mal, T-cell differentiation protein 2	127300	9931450	42953	1	1	1	0.69384
MHC class II transactivator type I	1917	300525	182793	1	1	1	41.1765
MOBILFERRIN	144700	7514041	78121	3	3	3	3.3673
MYB binding protein 1a	12480	7514124	37207	3	3	3	23.4783
Macrophage migration inhibitory factor	20740	992637	69402	1	15	15	71.2707
Major urinary protein precursor	36480	81861572	118982	9	9	9	36.5269
Malate dehydrogenase, cytoplasmic Cytosolic malate dehydrogenase	35680	42476181	339913	17	17	17	63.3136
Malate dehydrogenase, mitochondrial	2943	11133293	36062	1	1	1	39.2857
Maleylacetate isomerase MAAI Glutathione S-transferase zeta 1 GSTZ1-1	273400	6981078	3946	24	24	24	12.6664
Mannose 6-phosphate/insulin-like growth factor II receptor	16550	1942287	19138	1	1	1	8.0537
Mannose-binding protein A precursor	114300	40786505	338661	3	3	3	3.7661
Mannosidase 2, alpha B1	91870	48427849	51409	29	29	29	46.8825
Mannosyl-oligosaccharide glucosidase Glycoprotein-processing glucosidase I	46560	8392833	11499	4	4	4	15.9145
Medium-chain specific acyl-CoA dehydrogenase, mitochondrial precursor MCAD	23400	62900631	274611	5	7	7	37.3272
Membrane-associated progesterone receptor component 2	76080	49258142	140638	3	3	3	7.8635
Membrane-bound aminopeptidase P X-prolyl aminopeptidase (Aminopeptidase P) 2, membrane-bound	68710	32363191	124359	1	1	1	2.7304
Merlin Moesin-ezrin-radixin-like protein Neurofibromin-2 Schwannomin	23750	56090359	259160	1	1	1	5.314
Mesenchymal stem cell protein DSCD75							

Mesoderm development candidate 2	25220	81883487	280160	7	7	42.4107
Metaxin 2 Predicted	29720	56605654	203309	5	5	22.8137
Methylmalonate-semialdehyde dehydrogenase [acylating], mitochondrial precursor MMSDH	57810	400269	37213	11	11	37.3832
Malonate-semialdehyde dehydrogenase [acylating]	45520	47938984	23872	7	7	31.2195
Microsomal dipeptidase precursor	20630	61889101	3224	7	7	44.6927
Microsomal signal peptidase 18 kDa subunit SPase 18 kDa subunit SPC18 Endopeptidase SP18 SEC11-like 1 Sid 2895	57430	17736804	16130	2	2	7.2978
Mid-1-related chloride channel 2	21450	54607147	111212	4	6	39.0625
Migration-inducing protein 5 Ras-related C3 botulinum toxin substrate 1, isoform Rac1	34150	1580888	77688	2	8	39.4904
Mitochondrial 2-oxoglutarate/malate carrier protein	53800	81170680	215394	2	2	6.1144
Mitochondrial antiviral signaling protein Interferon-beta promoter stimulator protein 1 IPS-1 Virus-induced signaling adapter	33150	2497984	63382	8	8	27.907
Mitochondrial carnitine/acylcarnitine carrier protein Carnitine/acylcarnitine translocase CAC Solute carrier family 25 member 20	31460	27702070	156740	11	11	51.4184
Mitochondrial carrier homolog 2	31450	51859428	140375	10	10	44.7552
Mitochondrial dicarboxylate carrier Solute carrier family 25 (Mitochondrial carrier, dicarboxylate transporter), member 10	10460	59800393	77128	4	4	36.8421
Mitochondrial import inner membrane translocase subunit TIM13	11040	5107153	12056	1	1	11.3402
Mitochondrial import inner membrane translocase subunit TIM8 A Deafness dystonia protein 1 homolog	18370	55741522	220289	1	1	7.8313
Mitochondrial protein, 18 kDa	42050	9506991	47245	1	1	3.2787
Mitogen-activated protein kinase 13 Stress-activated protein kinase 4 Mitogen-activated protein kinase p38 delta MAP kinase p38 delta	13580	81883452	237355	1	1	8.871
Mitogen-activated protein kinase kinase 1-interacting protein 1	13480	27692916	12815	3	3	36
Mitogen-activated protein-binding protein-interacting protein Late endosomal/lysosomal Mp1-interacting protein p14	53240	6981542	75090	4	4	9.7166
Monocarboxylate transporter 1 MCT 1	23340	6730147	73388	2	2	12.6761
Monoclonal Antibody Against The Main Immunog	40050	38197682	35920	1	1	2.957
Monocyte differentiation antigen CD14 precursor	33500	79158553	76956	5	5	23.4323
Monoglyceride lipase MGL	73330	5052048	176262	3	3	6.0423
Mpg-1 protein	165000	7514016	37180	4	4	3.1957
Multidrug resistance-associated protein 6 ATP-binding cassette sub-family C member 6 MRP-like protein 1 MLP-1	16150	49036094	216613	4	4	44.8276
Multiple coagulation factor deficiency protein 2 homolog precursor Neural stem cell-derived neuronal survival protein	21500	70166245	3277	1	1	7.1795
Myelin basic protein S	118100	480659	6153	29	29	37.5486
Myosin I heavy chain	131900	56733	63042	49	50	52.2007
Myosin Ib Myosin I alpha MMI-alpha MMla Myosin heavy chain myr 1	116100	6981242	75002	37	37	42.8429
Myosin Id Myosin heavy chain myr 4	126800	693995	105842	8	9	9.8464
Myosin Ie Myosin heavy chain myr 3	251100	23618899	217296	1	1	0.45935
Myosin VIIA	16960	34862212	69375	7	8	55.6291
Myosin, light polypeptide 6, alkali, smooth muscle and non-muscle, isoform 2						

Myosin-10 Myosin heavy chain, nonmuscle IIb Nonmuscle myosin heavy chain IIb NMMHC II-b NMMHC-IIb Cellular myosin heavy chain, type B Nonmuscle myosin heavy chain-B NMMHC-B	229000	7381235	78051	5	17	11.5385
Myristoylated alanine-rich C-kinase substrate (MARCKS) (Protein kinase C substrate 80 kDa protein).	29780	27705710	166436	2	2	10.356
N-acylsphingosine amidohydrolase 1	44440	40254747	338609	3	3	11.9289
N-deacetylase/N-sulfotransferase (heparan glucosaminy) 2 [Rattus norvegicus]	95740	34868948	210844	1	4	5.3635
N-ethylmaleimide sensitive factor	82650	6007811	9479	2	2	4.0323
NAD(P) dependent steroid dehydrogenase-like	40410	57164113	228858	22	22	75.1381
NADH dehydrogenase (Ubiquinone) Fe-S protein 1, 75kDa	79410	53850628	229389	20	20	37.9642
NADH dehydrogenase (Ubiquinone) Fe-S protein 7 Predicted	23950	56606108	213294	4	4	23.8532
NADH dehydrogenase (Ubiquinone) flavoprotein 1, 51kDa	50730	55741424	243054	8	8	22.6293
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 11 NADH-ubiquinone oxidoreductase subunit B14.7 Complex I-B14.7 Cl-B14.7	14850	52000746	204895	2	2	24.1135
NADH-cytochrome b5 reductase	34170	38303959	69488	6	20	82.392
NADH-ubiquinone oxidoreductase 24 kDa subunit, mitochondrial precursor	27380	83305118	291031	6	6	31.4516
NADH-ubiquinone oxidoreductase chain 4 NADH dehydrogenase subunit 4	51800	639984	98993	1	1	4.3573
NADP-dependent leukotriene B4 12-hydroxydehydrogenase 15-oxoprostaglandin 13-reductase	35720	6012071	1678	9	9	37.69
Dithiolethione-inducible gene 1 protein D3T-inducible gene 1 protein DIG-1	76930	205660	44210	1	37	62.5369
NADPH-cytochrome P450 reductase	20600	57033190	20922	6	13	68.5083
NOD-derived CD11c +ve dendritic cells cDNA, RIKEN full-length enriched library, clone: F630112117 product: ADP-ribosylation factor 3, full insert sequence	34910	13925523	78016	1	1	4.4444
Na(+)/H(+) exchange regulatory co-factor NHE-RF2	23380	27710456	74102	5	5	32.5581
Nascent polypeptide-associated complex subunit alpha Alpha-NAC/1.9.2	128900	1708980	67879	11	11	12.766
Nck-associated protein 1 NAP 1 p125Nap1 Membrane-associated protein HEM-2	40490	62531217	199168	11	11	45.3521
Ndufa10 protein	23410	62665359	215440	5	5	33.3333
Neighbor of Cox4 Predicted	325100	19705491	161237	2	2	0.66949
Nesprin-1	99690	3983131	63008	11	11	20.5298
Neural-cadherin precursor N-cadherin Cadherin-2	231500	111999	11249	10	49	27.8639
Neuronal myosin heavy chain	78400	37081094	116574	4	4	9.1808
Nicastrin precursor	58560	46485387	722226	1	1	3.5316
Nicotinate phosphoribosyltransferase-like protein	54930	67460593	219030	2	2	7.1429
Non-POU domain-containing octamer-binding protein NonO protein	60580	6978589	3674	1	1	2.2599
Non-muscle caldesmon CDM L-caldesmon	204200	92557	111676	2	2	1.4846
Nuclear pore membrane glycoprotein 210 precursor POM210 Nuclear pore protein gp210	50090	8515422	3157	17	18	51.1905
Nucleobindin 2 precursor	53510	871525	60416	36	37	77.7778
Nucleobindin-1 precursor CALNUC Bone 63 kDa calcium-binding protein	32560	7242160	44225	4	4	8.9041
Nucleophosmin NPM Nucleolar phosphoprotein B23 Numatrin Nucleolar protein NO38	17280	55926145	69495	6	6	53.2895
Nucleoside diphosphate kinase B	52350	81892269	318887	2	2	4.9462
Nucleotide exchange factor SIL1 precursor						

OTTMUSP00000005802 13 days embryo liver cDNA, RIKEN full-length enriched library, clone:2510015J15 product:S-phase kinase-associated protein 1A, full insert sequence Bone marrow macrophage cDNA, RIKEN full-length enriched library, clone:1830081B01 product:S-phase kinase-associated protein 1A, full insert sequence	18670	56090475	62616	2	2	11.6564
Oligoribonuclease, mitochondrial precursor Small fragment nuclease RNA exonuclease 2 homolog	26750	81910234	216886	1	1	3.3755
Ornithine aminotransferase	24280	206706	44333	1	1	8.9686
Ornithine carbamoyltransferase, mitochondrial precursor	39890	6981312	75019	17	17	57.6271
Oxidative 17 beta hydroxysteroid dehydrogenase type 6	37140	27545384	102628	7	9	36.3914
PEF protein with a long N-terminal hydrophobic domain	30010	56090329	201603	1	1	4.5936
PRA1 family protein 3 ARL-6-interacting protein 5 ADP-ribosylation-like factor 6-interacting protein 5	21550	57012987	54281	1	1	10.6383
Alp-5 Glutamate transporter EAAC1-interacting protein GTRAP3-18 Prenylated Rab acceptor protein 2 Protein JWa						
PREDICTED: Glycoprotein-4-beta-galactosyltransferase 2	44480	34867143	229568	5	5	16.0401
PREDICTED: Ras-GTPase-activating protein SH3-domain binding protein	51790	34870749	252580	4	4	10.5376
PREDICTED: T-cell, immune regulator 1, ATPase, H+ transporting, lysosomal V0 protein a isoform 3	93210	62641689	274163	1	1	1.6787
PREDICTED: branched chain keto acid dehydrogenase E1, beta polypeptide	42820	34865350	151463	1	1	3.0769
PREDICTED: cadherin 11	88040	34851208	199319	1	1	1.3819
PREDICTED: hypothetical protein XP_215541	120700	34855491	219134	25	25	28.0453
PREDICTED: hypothetical protein XP_217094	21180	27719651	278444	4	4	26.9841
PREDICTED: hypothetical protein XP_346694	37150	76559925	268188	5	11	39.6825
PREDICTED: hypothetical protein XP_579384	186300	62718645	221549	77	77	59.531
PREDICTED: hypothetical protein XP_579439	47620	62664450	225098	4	4	12.4169
PREDICTED: hypothetical protein XP_579502	83280	62665770	317748	1	12	20.191
PREDICTED: low density lipoprotein receptor-related protein associated protein 1	47360	34878475	237675	13	13	35.6098
PREDICTED: maternal embryonic message 3	91730	34851395	206594	11	11	19.9749
PREDICTED: mitogen-activated protein kinase kinase kinase 7 interacting protein 2 (predicted)	76330	90108450	226905	1	1	1.0101
PREDICTED: peanut-like 2 (Drosophila) (predicted)	53080	62656738	223925	1	1	3.0501
PREDICTED: peroxisome biogenesis factor 16 (predicted)	38600	62645408	235341	2	2	11.0119
PREDICTED: pyrroline-5-carboxylate reductase-like (predicted)	28860	62652621	268213	1	1	4.0146
PREDICTED: similar to 1700001K19Rik protein	24610	34867823	299198	1	1	3.653
PREDICTED: similar to 25 kDa FK506-binding protein	25180	27664664	289953	6	6	33.4821
PREDICTED: similar to 3,5-cyclic-GMP phosphodiesterase; rod phosphodiesterase beta subunit	98490	34875832	283891	1	1	1.1682
PREDICTED: similar to 5830458K16Rik protein	27750	34869300	246358	2	2	9.7959
PREDICTED: similar to 6-phosphogluconolactonase	30820	34877556	315711	2	2	10.9966
PREDICTED: similar to 60S acidic ribosomal protein P1	11560	27717711	214842	1	1	14.1593
PREDICTED: similar to 60S acidic ribosomal protein P2	11760	62660456	201232	1	7	75.6522
PREDICTED: similar to 60S ribosomal protein L27a	16590	62639430	273222	7	7	32.4324

PREDICTED: similar to 60S ribosomal protein L7	30310	27660180	154516	15	24	61.9231
PREDICTED: similar to ALG-2	21900	34853323	296012	4	4	23.5602
PREDICTED: similar to ATP-binding cassette, sub-family F (GCN20), member 2	71660	27707592	268287	3	3	6.0606
PREDICTED: similar to ATPase, H+ transporting, V1 subunit A, isoform 1	68270	34869154	264901	7	7	15.3971
PREDICTED: similar to Aa2-258	19970	27706932	292254	3	3	16.8605
PREDICTED: similar to Acyl-CoA dehydrogenase family member 8, mitochondrial precursor (ACAD-8) (Isobutyryl-CoA dehydrogenase)	14960	34860605	288262	2	2	14.6154
PREDICTED: similar to Aldose reductase (AR) (Aldehyde reductase)	35900	62648070	161456	1	2	6.962
PREDICTED: similar to Alg2 protein	47320	62648970	161569	2	2	6.988
PREDICTED: similar to Apolipoprotein C2	10700	27676424	215733	1	1	9.2784
PREDICTED: similar to Auh protein	33340	34873875	242939	3	3	13.3333
PREDICTED: similar to BCL2-like 13	46730	34858394	258284	2	2	7.1429
PREDICTED: similar to BTB (POZ) domain containing 14A	63110	34853069	292782	1	1	1.3675
PREDICTED: similar to Blvrb protein	22090	34855391	272510	4	4	30.5825
PREDICTED: similar to CCT (chaperonin containing TCP-1) zeta subunit	58020	76253725	288751	10	10	28.2486
PREDICTED: similar to Cab39 protein	39870	34877516	314871	1	1	3.2258
PREDICTED: similar to Cell death-inducing DNA fragmentation factor, alpha subunit-like effector B	24750	34875073	235633	2	2	14.6119
PREDICTED: similar to Chain A, Solution Structure Of Coactosin-Like Protein (Cofilin Family) From Mus Musculus	22140	34851815	211193	2	2	12.4378
PREDICTED: similar to Clptm1 protein	75280	27676422	265343	2	2	3.4639
PREDICTED: similar to Coiled-coil-helix-coiled-coil-helix domain containing 6	35250	34856405	277277	1	1	4.4586
PREDICTED: similar to Cysteine-rich with EGF-like domains 1	45700	81170413	208169	1	1	2.619
PREDICTED: similar to D15Mgi27 protein	49680	27665476	206392	2	2	6.4444
PREDICTED: similar to DEAD/H box polypeptide 36 protein	113800	34856989	204574	2	2	2.7
PREDICTED: similar to DKFZF586A0522 protein	21900	27664990	263674	4	4	27.9793
PREDICTED: similar to DNA segment, Chr 13, Wayne State University 177, expressed	21120	95102018	253829	1	1	10.1124
PREDICTED: similar to DXImx39e protein	15360	34933457	246770	1	1	7.8014
PREDICTED: similar to Dual specificity phosphatase 14	22270	62644625	209194	1	1	10.6061
PREDICTED: similar to ER-resident protein ERdj5	90750	34856469	269276	9	9	16.1412
PREDICTED: similar to Elastin microfibril interfacer 1	107600	34863280	233953	3	3	3.3432
PREDICTED: similar to Emopamil-binding protein-like (Emopamil-binding related protein)	23410	34874266	245607	1	1	4.3689
PREDICTED: similar to Epidermal growth factor receptor pathway substrate 8-like protein 2	82280	34861230	276611	2	2	3.8409
PREDICTED: similar to F-box protein 28	41070	27681007	262592	1	1	2.9891
PREDICTED: similar to FK506-binding protein 38	43560	81295379	221624	4	4	16.8734
PREDICTED: similar to Farsla protein	57720	66730413	312741	17	17	40.3543
PREDICTED: similar to GPI transamidase component PIG-T precursor (Phosphatidylinositol-glycan biosynthesis, class T protein) (Neuronal development-associated protein 7)	65550	34860689	195113	1	1	2.5862
PREDICTED: similar to LECT2	20890	34873621	209309	1	1	4.8128

PREDICTED: similar to MAP kinase kinase 3b	47090	34870816	238438	1	1	3.58
PREDICTED: similar to MGC108823 protein	48270	67846046	244814	8	11	38.8489
PREDICTED: similar to Mannose-P-dolichol utilization defect 1	26550	27673096	252753	2	2	10.1215
PREDICTED: similar to Metaxin 1, isoform 2	26260	34857966	262377	1	1	6.7227
PREDICTED: similar to Microsomal glutathione S-transferase 2 (Microsomal GST-2) (Microsomal GST-II)	16740	27690924	285736	3	3	25.1701
PREDICTED: similar to Microsomal triglyceride transfer protein	99190	34860789	198793	56	56	65.067
PREDICTED: similar to NADH dehydrogenase	15640	27660847	304373	3	3	27.3438
PREDICTED: similar to NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 6 (B14)	15220	27663138	280728	5	5	46.9231
PREDICTED: similar to NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 5	21660	34856800	235872	4	4	22.7513
PREDICTED: similar to NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 7	16570	34851467	298146	3	3	30.6569
PREDICTED: similar to NADH dehydrogenase (ubiquinone) Fe-S protein 5	12700	72086149	306807	2	2	22.6415
PREDICTED: similar to NADH dehydrogenase (ubiquinone) Fe-S protein 8	23970	27661165	313497	4	4	23.1132
PREDICTED: similar to NADH oxidoreductase	12500	27717677	167188	4	4	31.25
PREDICTED: similar to NADH-ubiquinone oxidoreductase 30 kDa subunit, mitochondrial precursor (Complex I-30KD) (CI-30KD)	30230	27702072	256004	9	9	40.5303
PREDICTED: similar to Nodal modulator 1	133400	34856103	215096	35	35	42.3394
PREDICTED: similar to PL6 protein	38050	34865897	314280	2	2	11.1429
PREDICTED: similar to PLS1 protein	70390	34865784	207221	4	7	17.9365
PREDICTED: similar to Poly(A) binding protein, cytoplasmic 4, isoform 1	72410	34870953	206311	2	8	17.2727
PREDICTED: similar to Proteasome 26S non-ATPase subunit 2	100200	72255509	255113	3	3	4.9559
PREDICTED: similar to Protein HSPC163	16090	27679416	225990	1	1	14.3885
PREDICTED: similar to Putative pre-mRNA splicing factor RNA helicase (DEAH box protein 15)	90980	34878065	276202	4	4	6.0377
PREDICTED: similar to RAB5B protein	34900	34862219	218278	5	8	31.8885
PREDICTED: similar to RCK	54310	34879288	208269	1	1	3.1056
PREDICTED: similar to RET-II	82410	34867583	302868	42	42	71.6049
PREDICTED: similar to RIKEN cDNA 0610010D20	34460	34865395	220359	6	6	32.0872
PREDICTED: similar to RIKEN cDNA 1110038M16	31550	34870283	246519	1	1	8.3333
PREDICTED: similar to RIKEN cDNA 1200009C21	25110	27730981	189964	1	1	6.422
PREDICTED: similar to RIKEN cDNA 1500009M05	15290	27696657	235838	4	4	36.2963
PREDICTED: similar to RIKEN cDNA 1700025G04	13890	27712468	318230	1	1	5.7851
PREDICTED: similar to RIKEN cDNA 1700027N10	31220	34874480	246387	1	1	3.9855
PREDICTED: similar to RIKEN cDNA 1810036I24	22620	34861791	303059	3	3	12.9353
PREDICTED: similar to RIKEN cDNA 1810074P20	89590	34867100	217843	11	11	18.6633
PREDICTED: similar to RIKEN cDNA 2210023G05	62910	27658990	227817	5	8	17.5
PREDICTED: similar to RIKEN cDNA 2510039O18	69480	34872456	235860	6	6	12.6183
PREDICTED: similar to RIKEN cDNA 2610019P18	28380	34871484	194048	1	1	4.8583
PREDICTED: similar to RIKEN cDNA 4732495G21 gene	41960	27687455	161693	2	13	31.9149

PREDICTED: similar to RIKEN cDNA 4921531G14	34870	34866113	263127	11	11	42.7609
PREDICTED: similar to RIKEN cDNA 9430083G14	29550	34881196	218419	2	2	10.566
PREDICTED: similar to RIKEN cDNA D930001I22	30110	62646328	359989	1	1	6.1069
PREDICTED: similar to RPP20 protein	15740	27663642	220097	1	1	10.7143
PREDICTED: similar to RS21-C6 protein	32140	34877104	218331	1	1	4.4983
PREDICTED: similar to Rab33B	25750	34857303	281147	6	6	34.9345
PREDICTED: similar to Ras-related protein R-Ras (P23)	23910	34856057	257746	1	2	12.844
PREDICTED: similar to Ras-related protein Rab	23230	81887426	161420	1	2	10.4762
PREDICTED: similar to Retinoic acid early inducible protein 1 beta precursor (RAE-1beta)	27450	62638284	367801	1	1	5.4852
PREDICTED: similar to SEC63-like	87720	34853169	209405	9	9	16.4474
PREDICTED: similar to SPFH domain family, member 2	37710	34879021	249650	15	18	61.0619
PREDICTED: similar to Sfrs7 protein	20570	34862692	226986	1	2	14.2077
PREDICTED: similar to Smhs2 homolog	49210	34874232	269978	1	1	3.9443
PREDICTED: similar to Stromal cell-derived factor 2 precursor (SDF-2)	24060	27673471	232984	1	1	3.653
PREDICTED: similar to TOLLIP protein	30310	34861256	225945	1	1	5.1095
PREDICTED: similar to Thioredoxin domain containing protein 5 precursor (Thioredoxin-like protein p46) (Endoplasmic reticulum protein ERp46)	46350	34875200	293536	7	7	19.9041
PREDICTED: similar to Transmembrane emp24 protein transport domain containing 4	26120	27697481	170045	11	12	50.6608
PREDICTED: similar to Tripartite motif protein 47	70030	27690552	251088	1	1	1.7134
PREDICTED: similar to Vesicle amine transport protein 1 homolog (T californica)	43120	76096306	312134	3	3	11.6337
PREDICTED: similar to alpha/beta hydrolase fold protein	48340	34857271	271294	1	1	5.8824
PREDICTED: similar to armadillo repeat-containing protein	31200	34855505	302905	1	1	7.4468
PREDICTED: similar to beta-1,3-N-acetylglucosaminyltransferase bGnT-6	47470	34861816	304110	3	3	11.8072
PREDICTED: similar to beta-1,3-galactosyltransferase-6	37150	27663478	210144	5	5	19.6923
PREDICTED: similar to cathepsin 1 precursor	40980	27681673	266171	1	1	2.2284
PREDICTED: similar to chromosome 5 open reading frame 15	28260	34870715	258441	3	3	14.3969
PREDICTED: similar to chromosome 9 open reading frame 7	18410	34853142	272157	1	1	5.2632
PREDICTED: similar to cytochrome P450 2C66; CYP2C66	56170	34862902	260440	2	5	9.7959
PREDICTED: similar to cytochrome c-1	35430	34866853	271135	8	8	40.184
PREDICTED: similar to cytoskeleton-associated protein 4	63550	34862422	306304	6	6	14.6087
PREDICTED: similar to dolichol-phosphate-mannose synthase	29250	34860748	191580	5	5	25.7692
PREDICTED: similar to early quiescence protein-1	24200	27677818	208059	2	2	11.8812
PREDICTED: similar to eukaryotic translation initiation factor 2, subunit 3, structural gene X-linked	51080	34880581	267441	3	3	8.0508
PREDICTED: similar to evolutionarily conserved G-patch domain containing	100900	34855741	271140	1	1	1.2128
PREDICTED: similar to follicular lymphoma variant translocation 1	36040	34878781	198248	3	3	12.9518
PREDICTED: similar to glucuronosyltransferase I	37070	34861582	228888	7	7	31.6418
PREDICTED: similar to glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) (EC 1.2.1.12) - mouse	34590	34869386	306407	1	3	11.1111

PREDICTED: similar to glycine-N-acyltransferase isoform a	33990	27681359	139592	4	4	18.9189
PREDICTED: similar to glycolate oxidase, short-chain alpha-hydroxy acid oxidase	40970	34859262	270415	13	13	48.6486
PREDICTED: similar to hypothetical protein	26440	34856654	302143	7	7	45.2282
PREDICTED: similar to hypothetical protein 6820428D13	64490	27688925	279415	1	1	1.9031
PREDICTED: similar to hypothetical protein BC013949	25320	27688745	274768	1	1	5.9908
PREDICTED: similar to hypothetical protein FLJ20254	76570	34863014	234260	1	1	1.7518
PREDICTED: similar to ilvB (bacterial acetolactate synthase)-like	68020	34862359	299827	20	20	52.057
PREDICTED: similar to immunoglobulin light chain	16750	62647397	161334	1	1	8.7248
PREDICTED: similar to mALDP	81940	34881747	306584	1	1	2.7137
PREDICTED: similar to mKIAA0002 protein	59590	34867525	249893	16	16	35.0365
PREDICTED: similar to mKIAA1311 protein	118700	34879262	281850	1	1	1.0377
PREDICTED: similar to magnesium-dependent phosphatase-1	18610	27700106	272326	1	1	10.9756
PREDICTED: similar to membrane progesterin receptor alpha	39280	27732829	204220	1	1	6.087
PREDICTED: similar to microsomal glutathione S-transferase 3	16730	27678076	164232	3	3	34.2105
PREDICTED: similar to mitochondrial inner membrane translocase component Tim17b	18380	34933423	256607	1	1	8.7209
PREDICTED: similar to novel cell death-regulatory protein GRIM19	16780	27668839	160674	5	5	41.6667
PREDICTED: similar to novel protein of unknown function (DUF423) family member	11780	27672946	240868	1	1	24.7788
PREDICTED: similar to phosphoinositide-3-kinase, regulatory subunit 4, p150	152400	83288384	268833	1	1	1.1782
PREDICTED: similar to polypeptide GalNAc transferase-T4	66710	77736615	167222	1	1	2.2491
PREDICTED: similar to protein phosphatase 1 (formerly 2C)-like	41040	34857062	230767	7	7	26.6667
PREDICTED: similar to protein tyrosine phosphatase-like (proline instead of catalytic arginine), member b	15720	34882969	201524	1	1	9.0909
PREDICTED: similar to purine-nucleoside phosphorylase	32300	34869683	209477	10	10	49.1349
PREDICTED: similar to pyrophosphatase	32770	34852506	276601	3	3	17.9931
PREDICTED: similar to ribosomal protein L10a	24720	27665840	215516	1	4	23.5023
PREDICTED: similar to ribosomal protein S12	14570	27717927	310080	2	4	28.0303
PREDICTED: similar to serine beta lactamase-like protein LACT-1	60420	34864295	314386	19	19	47.8182
PREDICTED: similar to serine protease inhibitor 2.4	46840	34867677	195578	5	6	21.4797
PREDICTED: similar to serologically defined colon cancer antigen 1 isoform a	118600	34855476	218537	2	2	1.8269
PREDICTED: similar to seven transmembrane domain protein	25290	84042519	227176	1	1	7.5893
PREDICTED: similar to signal peptidase 12kDa	11750	27667224	307512	1	1	11.7647
PREDICTED: similar to signal recognition particle 19kDa	16140	27683535	219536	1	1	9.7222
PREDICTED: similar to silingshot-2L	159400	34873212	264614	1	1	1.6073
PREDICTED: similar to solute carrier family 25 (mitochondrial carrier, Aralar), member 12	27180	34854800	195681	3	4	22.4409
PREDICTED: similar to stomatin-like protein 2	38410	72255527	299358	9	9	33.711
PREDICTED: similar to tetrapeptide repeat domain 11	16990	94711371	171146	6	6	40.1316
PREDICTED: similar to ubiquinol-cytochrome c reductase binding protein	13560	34866011	293181	5	5	43.2432
PREDICTED: similar to ubiquitin-conjugating enzyme E2, J1	30880	34867116	250662	3	3	14.7482

PREDICTED: similar to vesicle associated membrane protein 4	16370	62659601	164208	1	1	8.5106
PREDICTED: similar to zinc binding alcohol dehydrogenase, domain containing 2	40480	34932585	231239	1	1	3.9788
PREDICTED: similar to zinc metalloproteinase, STE24 homolog	54850	34870924	288219	2	2	5.6842
PREDICTED: thioredoxin domain containing 7	48760	62651585	278868	24	24	63.3708
PREDICTED: tumor rejection antigen gp96 (predicted)	92770	62651904	269402	58	60	68.5323
PRx III	28320	4336877	90537	3	3	14.3969
PRx IV Peroxiredoxin 4	31010	4336879	60442	16	17	64.4689
Paraoxonase 1	39360	60551577	198556	5	16	67.3239
Peptidyl-prolyl cis-trans isomerase, mitochondrial precursor PPIase Rotamase Cyclophilin F	21810	56268806	88229	1	1	4.3689
Peptidyl-prolyl isomerase A	17870	951425	45089	12	12	74.3902
Peripheral plasma membrane protein CASK Calcium/calmodulin-dependent serine protein kinase	103300	2497510	104145	11	11	17.0517
Peroxiredoxin 1	22110	56789700	43433	17	18	64.3216
Peroxiredoxin 2 (EC 1.11.1.-) (Thioredoxin peroxidase 1) (Thioredoxin- dependent peroxide reductase 1) (Thiol-specific antioxidant protein) (TSA).	21800	34849738	269931	3	3	17.6768
Peroxiredoxin-5, mitochondrial precursor Prx-V Peroxisomal antioxidant enzyme PLP Thioredoxin reductase Thioredoxin peroxidase PMP20 Antioxidant enzyme B166 AOEB166	22180	6103726	60487	2	2	14.0845
Peroxisomal 2,4-dienoyl-CoA reductase 2,4-dienoyl-CoA reductase 2 DCR-AKL pVI-AKL	31290	90109768	176638	8	8	32.1918
Peroxisomal biogenesis factor 3 Peroxin-3 Peroxisomal assembly protein PEX3	42210	8926847	12072	1	1	2.957
Peroxisomal membrane anchor protein	40970	4126962	155718	3	3	16.2234
Peroxisomal multifunctional enzyme type 2	79430	2492741	108354	34	34	55.6463
Peroxisomal trans-2-enoyl-CoA reductase RLF98 Peroxisomal 2,4-dienoyl CoA reductase px-2,4-DCR1	32430	6491860	34787	14	14	81.5182
Phenylalanine-tRNA synthetase-like, beta subunit	65650	51948478	254493	20	20	38.8795
Phosphate carrier protein, mitochondrial precursor PTP Solute carrier family 25 member 3	39450	20806141	69383	9	9	29.2135
Phosphatidylcholine transfer protein	24730	8393922	51565	1	1	5.6075
Phosphatidylethanolamine N-methyltransferase	22490	6981348	69787	1	1	6.5327
Phosphatidylinositol-binding clathrin assembly protein Clathrin assembly lymphoid myeloid leukemia protein rCALM	69290	44888251	60461	10	10	27.3438
Phosphoenolpyruvate carboxykinase, cytosolic [GTP] Phosphoenolpyruvate carboxylase PEPCK-C	69420	51859488	144363	10	10	24.2765
Phosphofructokinase, liver, B-type	85300	38197562	318741	4	4	8.0769
Phosphoglycerate kinase 1	44540	56585024	340218	9	9	32.6139
Phosphoinositide phosphatase SAC1	67040	62654523	60561	17	17	31.8569
Phospholemmann precursor	10470	1916012	78112	1	1	13.0435
Phospholipase B	161100	2696236	82680	1	1	1.3793
Phospholipid hydroperoxide glutathione peroxidase, nuclear	29400	14971097	1198	2	2	8.5603
Phosphoserine aminotransferase	40590	29692074	249141	1	1	2.973
Phytanoyl-CoA dioxygenase, peroxisomal precursor Phytanoyl-CoA alpha-hydroxylase PhyH	38590	6539658	55437	11	11	34.6154
Phytanic acid oxidase						
Pirin	32180	57164095	304888	1	1	4.1237

Plakoglobin	81780	1497985	37204	11	13	24.698
Plasma retinol-binding protein precursor PRBP RBP	23220	27685035	144413	12	12	54.2289
Plasminogen	90540	62638541	60419	26	27	42.8571
Plastin-3 T-plastin	70300	57381	136274	15	19	43.8596
Plectin 10	518400	40849904	699022	12	12	3.3831
Poly(rC)-binding protein 2 Alpha-CP2 hnRNP-E2	38580	61557337	2515	2	2	7.3973
Polyadenylate-binding protein 1 Poly(A)-binding protein 1 PABP 1	70700	52789215	161229	12	18	34.1195
PolymERIC-immunoglobulin receptor precursor Poly-Ig receptor PIgR Secretory component	84800	56465	128586	16	16	27.5683
Polypeptide N-acetylglucosaminyltransferase 1 Protein-UDP acetylglucosaminyltransferase 1	64230	1709559	68735	21	21	45.6172
UDP-GalNAc:polypeptide N-acetylglucosaminyltransferase 1 Polypeptide GalNAc transferase 1						
GalNAc-T1 pp-GaNTase 1 Polypeptide N-acetylglucosaminyltransferase 1 soluble form						
Polypeptide N-acetylglucosaminyltransferase 11 Protein-UDP acetylglucosaminyltransferase 11	69040	51315700	319029	7	7	16.9408
UDP-GalNAc:polypeptide N-acetylglucosaminyltransferase 11 Polypeptide GalNAc transferase 11						
GalNAc-T11 pp-GaNTase 11						
Potassium voltage-gated channel subfamily A member 6	58880	57667	63679	1	1	1.6981
Prenylated Rab acceptor protein 1 PRA1 family protein 1	20640	56404679	78175	4	4	22.1622
Prenylated SNARE protein Ykt6p	22310	2642348	78131	2	2	15.1515
Prenylcysteine oxidase precursor Chloride ion pump-associated 55 kDa protein	56290	62286984	68714	8	8	26.3889
Presenilin 1	52790	6174931	37272	1	1	4.0598
Probable ergosterol biosynthetic protein 28	15810	62651081	178365	1	1	9.2857
Probable isomerase MAWBP	31720	19743770	33171	6	6	36.8056
Probable mitochondrial import receptor subunit TOM40 homolog Translocase of outer membrane 40	37920	81864912	726780	3	3	16.8975
kDa subunit homolog 38 kDa mitochondrial outer membrane protein OM38						
Procollagen-lysine,2-oxoglutarate 5-dioxygenase 1 precursor Lysyl hydroxylase 1 LH1	83610	6093729	60574	3	3	6.044
Profilin 1 ES cells cDNA, RIKEN full-length enriched library, clone:2410026M17 product:profilin 1, full insert sequence Bone marrow macrophage cDNA, RIKEN full-length enriched library, clone:I830015F09 product:profilin 1, full insert sequence	14960	51702769	60726	8	8	67.8571
Programmed cell death 6-interacting protein ALG-2-interacting protein 1	44060	6319138	157870	2	2	6.9825
Prohibitin 17 days embryo heart cDNA, RIKEN full-length enriched library, clone:1920041N05 product:prohibitin, full insert sequence CRL-1722 L5178Y-R cDNA, RIKEN full-length enriched library, clone:I730071G06 product:prohibitin, full insert sequence	29820	66911717	4312	16	16	71.6912
Proliferation-associated 2G4, 38kDa	43660	51948384	304663	16	16	39.0863
Propionyl-CoA carboxylase alpha chain, mitochondrial precursor PCCase subunit alpha Propanoyl-CoA:carbon dioxide ligase subunit alpha	77710	129684	69597	3	3	6.5341
Prostaglandin E synthase 3 Cytosolic prostaglandin E2 synthase cPGES Telomerase-binding protein p23 Hsp90 co-chaperone Progesterone receptor complex p23 Sid 3177	18720	34862186	25274	1	1	8.125
Prostaglandin F2 receptor negative regulator precursor Prostaglandin F2-alpha receptor regulatory protein Prostaglandin F2-alpha receptor-associated protein CD315 antigen	98730	9507007	47252	2	2	3.5267
Prostaglandin G/H synthase 1 precursor	69030	603052	103863	1	1	2.99
Protease (Prosome, macropain) 28 subunit, alpha	28630	61098214	227267	4	4	24.0964
Proteasome (Prosome, macropain) 26S subunit, ATPase 3	49550	38304011	71853	1	1	3.6199

Proteasome (Prosome, macropain) subunit, beta type 1	26410	37231712	233720	1	1	7.5
Proteasome 26S non-ATPase subunit 12	52940	54400716	317815	2	2	4.1667
Proteasome activator subunit 2	26860	8394091	51596	3	3	22.2689
Proteasome subunit alpha type 6 Proteasome iota chain Macropain iota chain Multicatalytic endopeptidase complex iota chain 27 kDa prosomal protein PROS-27 p27K	27400	8394076	51591	2	2	9.3496
Proteasome subunit alpha type 7 Proteasome subunit RC6-1	28330	2118151	72897	1	1	5.9055
Proteasome subunit beta type 3 Proteasome theta chain Proteasome chain 13 Proteasome component C10-II	22960	8394082	51593	2	2	15.6098
Proteasome subunit beta type 6 precursor Proteasome delta chain Macropain delta chain Multicatalytic endopeptidase complex delta chain Proteasome subunit Y Proteasome chain 5	25160	464446	134694	1	1	4.6414
Protein C2orf18 homolog precursor	41090	81883393	167119	1	1	4.0323
Protein C6orf89 homolog	39570	40786457	205305	1	1	3.7356
Protein DJ-1 Contraception-associated protein 1 Protein CAP1 Fertility protein SP22	19970	56404680	20683	3	3	26.9841
Protein FAM62A Membrane-bound C2 domain-containing protein vp115	121200	8393755	51531	10	10	14.2463
Protein JTB precursor	16390	6016410	128391	1	1	8.9041
Protein LRP16	28640	32129697	214491	1	1	3.876
Protein LYRIC Lysine-rich CEACAM1 co-isolated protein Metastasis adhesion protein Metadherin	63970	56748899	118984	7	7	18.0723
Protein NDRG2 NDRG1-related protein Antidepressant-related protein ADRG123	40780	81867103	123716	7	7	37.7358
Protein O-linked-mannose beta-1,2-N-acetylglucosaminyltransferase 1 POMGnT1	75150	73621412	285106	6	6	13.0303
Protein YIPF3 YIP1 family member 3 Liver regeneration-related protein LRRGT00110	37970	81865839	234797	5	5	23.6311
Protein YIPF4 YIP1 family member 4	27280	81883039	227072	4	4	13.4146
Protein disulfide isomerase precursor	56950	38197382	69606	44	44	73.4774
Protein disulfide-isomerase A3 precursor Disulfide isomerase ER-60 ERp60 68 kDa microsomal protein p58 ERp57 Hlp-70 Q-2	56620	38382858	21556	40	40	68.3168
Protein disulfide-isomerase A4 precursor Protein ERp-72 ERp72 Calcium-binding protein 2 CaBP2	72720	78099786	227664	2	51	65.7854
Protein kinase C and casein kinase substrate in neurons 2 protein Synaptic dynamin-associated protein II Syndapin 2 Syndapin-II Sdpll	55980	6651163	74255	4	4	8.6066
Protein kinase C, alpha type	76790	56914	44893	1	1	1.7857
Protein transport protein SEC61 beta subunit	9988	27714473	161564	3	3	37.5
Protein transport protein Sec23A SEC23-related protein A	86160	34867969	141679	32	36	75.1634
Protein tyrosine phosphatase type IVA protein 1 Protein-tyrosine phosphatase 4a1 Protein-tyrosine phosphatase of regenerating liver 1 PRL-1 PTP(CAAXI)	19820	68566099	4701	1	1	8.6705
Protein-glutamine gamma-glutamyltransferase K Transglutaminase K TGase K TKG TG(K) Transglutaminase-1 Epidermal TGase	90770	67677918	31490	7	7	11.5291
Protein-tyrosine phosphatase-like N precursor	105200	1113923	11137	1	1	1.1329
Proteolipid protein 2	16560	62286961	166582	1	1	7.947
Prothrombin precursor Coagulation factor II Activation peptide fragment 1 Activation peptide fragment 2 Thrombin light chain Thrombin heavy chain	70410	56970	31503	10	10	22.5284
Proto-oncogene C-crk P38 Adapter molecule crk	33840	9506515	95160	1	1	5.5921

Proton-translocating ATPase d subunit isoform d1 B6-derived CD11 +ve dendritic cells cDNA, RIKEN full-length enriched library, clone:F730225D05 product:ATPase, H+ transporting, V0 subunit D isoform 1, full insert sequence	40300	58865424	55382	12	12	45.2991
Putative N-acetyltransferase Camello 4	24890	6651436	176270	5	5	27.9279
Putative O-acetyltransferase OACT5 O-acetyltransferase domain-containing protein 5	56020	81882826	305024	3	3	7.1869
Putative SKAP55 Src family associated phosphoprotein 2	40720	47482120	15613	1	1	4.1899
Putative glycogen storage disease type 1b protein	46310	3929215	78079	6	6	25.1748
Putative integral membrane transport protein	62420	19705489	161236	2	4	8.1522
Putative integral membrane transport protein	62210	19705487	161235	2	4	7.971
Putative secreted protein	61440	59676595	271057	2	3	9.2421
Putative secreted protein	65610	59676599	220519	2	3	7.5993
Putative secreted protein ZSIG11	33770	56090363	262914	1	1	4.5307
Pyruvate carboxylase, mitochondrial precursor	129800	7438124	40425	21	21	26.146
Pyruvate dehydrogenase (Lipoamide) beta	38980	56090293	203734	5	5	19.4986
Pyruvate kinase, isozymes R/L	62300	206213	44273	4	4	12.0209
RAB1A, member RAS oncogene family RAB1A protein	22680	51338716	21122	4	19	79.0244
RAB21, member RAS oncogene family	24160	51948448	311263	3	3	15.6951
RAB4A, member RAS oncogene family	23920	6981454	75065	2	4	22.5352
RAB6-interacting protein 2 ERC protein 1 ERC1 CAZ-associated structural protein 2 CAST2	108800	51701367	165980	1	1	1.1603
RAB7	23500	9837359	111003	14	14	65.7005
RAB9, member RAS oncogene family	22870	16758200	60413	6	6	38.3085
RAT liver glutathione S-transferase YA subunit mRNA	15290	2117744	72819	1	7	51.8797
RER1 protein	22990	84781666	32618	4	4	23.9796
RGPR-p117	116800	16758344	60469	1	1	1.0397
RIKEN cDNA 2810407C02 gene	15840	62643492	13862	2	2	24.8175
RNA terminal phosphate cyclase domain 1	39310	51948426	319337	1	1	3.8251
RNA-dependent initiation factor-2 kinase	58260	9506993	47246	1	1	2.1442
RPL34 protein Ribosomal protein L34	13290	34860562	136355	7	7	33.3333
RT1.A1(F) protein	39250	1483574	42127	1	4	13.2565
Rab GDP dissociation inhibitor alpha	50540	71534276	67742	1	3	11.1857
Rab GDP dissociation inhibitor beta Rab GDI beta Guanosine diphosphate dissociation inhibitor 2 GDI-2 GDI-3	50540	40254781	8623	6	8	21.3483
Rab-related GTP-binding protein Rab38, member of RAS oncogene family	23780	47125439	44313	1	1	5.2133
Rap guanine nucleotide exchange factor 4 cAMP-regulated guanine nucleotide exchange factor II cAMP-GEFII Exchange factor directly activated by cAMP 2 Epac 2	50120	4115911	173285	1	1	2.5229
Ras-related C3 botulinum toxin substrate 2 precursor p21-Rac2 EN-7 protein	21440	56605840	8458	1	3	16.6667
Ras-related protein Rab-11A Rab-11	24390	55249677	41486	1	10	54.1667
Ras-related protein Rab-11B	24490	9837357	19693	2	11	55.9633
Ras-related protein Rab-13	22900	46577668	169821	1	3	15.7635

Ras-related protein Rab-14	23930	46577632	34567	12	13	76.2791
Ras-related protein Rab-18	22980	81909560	161691	10	10	59.7087
Ras-related protein Rab-1B	22180	56605816	166705	1	17	85.5721
Ras-related protein Rab-2A	23540	92340	78145	6	11	60.8491
Ras-related protein Rab-30	23060	27678162	64372	3	4	22.1675
Ras-related protein Rab-35 Rab-1C GTP-binding protein RAY	23030	62900797	35585	1	2	12.9353
Ras-related protein Rab-4B	23630	929830	51602	2	4	24.4131
Ras-related protein Rab-5C	23430	27689505	161834	4	8	47.6852
Ras-related protein Rab-8B	23600	2500066	43492	3	6	30.4348
Ras-related protein Ral-A	23550	54038996	37231	2	2	14.0777
Ras-related protein Rap-1A	20990	54114993	4747	1	6	35.3261
Ras-related protein Rap-1b precursor GTP-binding protein smg p21B	20800	539995	130852	2	7	42.3913
Rat GCP360	364300	7441640	124005	63	63	25.2902
Rat MHC class I cell surface antigen mRNA, precursor	42090	420280	44652	2	5	15.9151
Rat alpha(1)-inhibitor 3, variant I precursor	165300	91949	6160	1	49	46.2677
Rat female-specific cytochrome P450 15-beta CYP2C12 Cytochrome P450 2C12	55890	59808903	3729	19	28	68.9796
Ratsg1	40610	18266700	111523	1	1	4.5699
Receptor-binding cancer antigen expressed on SiSo cells Estrogen receptor-binding fragment-associated gene 9 protein	24190	81883249	239738	4	4	34.2723
Reg receptor	104400	9910530	42827	2	2	2.5027
Regucalcin RC Senescence marker protein 30 SMP-30	33390	6970313	3576	14	14	60.2007
Related RAS viral (R-ras) oncogene homolog 2 Predicted	23400	61740635	86161	2	3	20.5882
Reticulon 3 protein isoform b RTN3-A1 Reticulon 3 protein isoform a	25370	57977317	64492	3	3	16.1017
Retinoic acid receptor responder (Tazarotene induced) 2 Predicted	18500	61740621	235290	2	2	14.1104
Retinoid-inducible serine carboxypeptidase precursor Serine carboxypeptidase 1	51170	48474727	140359	3	3	9.9558
Retinol dehydrogenase 10	38060	31324556	227390	2	2	9.6774
Retinol dehydrogenase 2 Retinol dehydrogenase type II RODH II 29 k-protein	35600	50926989	80376	9	19	66.877
Retinol dehydrogenase 7 Retinol dehydrogenase type III RODH III	35740	68534258	35165	5	21	60.5678
Retinol dehydrogenase type I	35660	841197	105752	7	22	70.0315
Retinol-binding protein I, cellular Cellular retinol-binding protein CRBP	15700	809309	105581	1	1	8.9552
Rh blood group protein RH30	46580	3445506	90519	1	1	4.2654

Rho GDP dissociation inhibitor (GDI) alpha Activated spleen cDNA, RIKEN full-length enriched library, clone:F830047D12 product:Rho GDP dissociation inhibitor (GDI) alpha, full insert sequence NOD-derived CD11c +ve dendritic cells cDNA, RIKEN full-length enriched library, clone:F630116C04 product:Rho GDP dissociation inhibitor (GDI) alpha, full insert sequence NOD-derived CD11c +ve dendritic cells cDNA, RIKEN full-length enriched library, clone:F630107K12 product:Rho GDP dissociation inhibitor (GDI) alpha, full insert sequence 6 days neonate spleen cDNA, RIKEN full-length enriched library, clone:F430003F06 product:Rho GDP dissociation inhibitor (GDI) alpha, full insert sequence Activated spleen cDNA, RIKEN full-length enriched library, clone:F830101O10 product:Rho GDP dissociation inhibitor (GDI) alpha, full insert sequence 12 days embryo whole body cDNA, RIKEN full-length enriched library, clone:E970002J06 product:Rho GDP dissociation inhibitor (GDI) alpha, full insert sequence	23410	55742827	17309	2	2	15.1961
Rho guanine nucleotide exchange factor 7 PAK-interacting exchange factor beta Beta-Pix	73140	2865596	2120	1	1	2.1672
Rho-related GTP-binding protein RhoB precursor H6	22120	51338594	113828	1	3	25.5102
Ribonuclease 4 precursor RNase 4 RL3	16900	9910536	42830	1	1	8.8435
Ribophorin I Ribophorin1	68400	71891579	337611	36	36	65.5116
Ribosomal protein L10 Lung RCB-0558 LLC cDNA, RIKEN full-length enriched library, clone:G730040A02 product:ribosomal protein L10, full insert sequence CRL-1722 L5178Y-R cDNA, RIKEN full-length enriched library, clone:I730035D10 product:ribosomal protein L10, full insert sequence Bone marrow macrophage cDNA, RIKEN full-length enriched library, clone:I830029J07 product:ribosomal protein L10, full insert sequence Bone marrow macrophage cDNA, RIKEN full-length enriched library, clone:I830032M03 product:ribosomal protein L10, full insert sequence Bone marrow macrophage cDNA, RIKEN full-length enriched library, clone:I830035M24 product:ribosomal protein L10, full insert sequence Bone marrow macrophage cDNA, RIKEN full-length enriched library, clone:I830048G21 product:ribosomal protein L10, full insert sequence Bone marrow macrophage cDNA, RIKEN full-length enriched library, clone:I830087L08 product:ribosomal protein L10, full insert sequence Bone marrow macrophage cDNA, RIKEN full-length enriched li	24600	50403574	37238	4	16	59.8131
Ribosomal protein L10a	24830	51702767	37218	3	15	61.2903
Ribosomal protein L15	24150	515865	1145	6	12	51.9608
Ribosomal protein L17	21400	71051098	139425	9	12	53.8043
Ribosomal protein L19 13 days embryo liver cDNA, RIKEN full-length enriched library, clone:I920026E09 product:ribosomal protein L19, full insert sequence	23470	51338626	4809	7	7	26.5306
Ribosomal protein L22-like 1	14470	34856770	32658	4	5	51.6393
Ribosomal protein L27	15800	60688496	4814	8	8	55.8824
Ribosomal protein L28 11 days embryo whole body cDNA, RIKEN full-length enriched library, clone:2700043M16 product:ribosomal protein L28, full insert sequence	15730	61889083	74518	8	8	40.146
Ribosomal protein L31 11 days embryo whole body cDNA, RIKEN full-length enriched library, clone:2700055G03 product:ribosomal protein L31, full insert sequence	14460	57115	4818	6	6	42.4
Ribosomal protein L32	15860	6981482	4819	5	5	30.3704
Ribosomal protein L7a	30000	62644799	4825	4	23	59.0226
Ribosomal protein L8	28020	78214309	4826	15	15	47.8599
Ribosomal protein S10 Activated spleen cDNA, RIKEN full-length enriched library, clone:F830201J18 product:ribosomal protein S10, full insert sequence Bone marrow macrophage cDNA, RIKEN full-length enriched library, clone:I830015I24 product:ribosomal protein S10, full insert sequence 5 days embryo whole body cDNA, RIKEN full-length enriched library, clone:I0C0045K06 product:ribosomal protein S10, full insert sequence	18920	68163545	32867	6	8	43.0303

Ribosomal protein S15	17040	8394212	4836	3	7	67.5862
Ribosomal protein S15a Bone marrow macrophage cDNA, RIKEN full-length enriched library, clone:1830091121 product:ribosomal protein S15a, full insert sequence Rps15a protein	14840	54039450	72161	7	8	60.7692
Ribosomal protein S2	28140	2920825	100993	3	19	65.3696
Ribosomal protein S24, isoform 2 Bone marrow macrophage cDNA, RIKEN full-length enriched library, clone:1830025E19 product:ribosomal protein S24, full insert sequence Rps24 protein	15420	57858	4843	4	4	29.3233
Ribosomal protein S27 Metalloprotein 1	9461	5924385	4845	1	4	39.2857
Ribosomal protein S27a	17950	37194821	127926	4	7	48.0769
Ribosomal protein S4, X-linked, X isoform RPS4X protein	29600	57135	4849	22	22	63.1179
Ribosomal protein S6 16 days embryo heart cDNA, RIKEN full-length enriched library, clone:1920028E16 product:ribosomal protein S6, full insert sequence Blastocyst blastocyst cDNA, RIKEN full-length enriched library, clone:1C0007K02 product:ribosomal protein S6, full insert sequence 12 days embryo male wolffian duct includes surrounding region cDNA, RIKEN full-length enriched library, clone:6720430M17 product:ribosomal protein S6, full insert sequence 17 days pregnant adult female amnion cDNA, RIKEN full-length enriched library, clone:1920079C04 product:ribosomal protein S6, full insert sequence	28680	8394224	74523	12	12	39.3574
Ribosomal protein S8	24210	62078585	4854	10	13	52.4038
Rpl11 protein	19020	71043900	2378	10	10	46.1078
Rpl36a protein NOD-derived CD11c +ve dendritic cells cDNA, RIKEN full-length enriched library, clone:F630020E11 product:ribosomal protein L36a, full insert sequence 16 days embryo heart cDNA, RIKEN full-length enriched library, clone:1920030G04 product:ribosomal protein L36a, full insert sequence Bone marrow macrophage cDNA, RIKEN full-length enriched library, clone:1830174F05 product:ribosomal protein L36a-like, full insert sequence	12440	62643486	111202	2	2	16.9811
S-adenosylmethionine synthetase alpha and beta forms	43700	92483	69363	3	3	10.5793
S-arrestin	44990	92737	84325	1	1	3.2258
S15 ribosomal protein	13360	40287237	337119	1	5	55.2632
SAR1A protein promoting vesicle budding from the endoplasmic reticulum	22410	57528164	160782	8	10	71.7172
SAR1a gene homolog CRL-1722 L5178Y-R cDNA, RIKEN full-length enriched library, clone:1730062K18 product:SAR1a gene homolog 1 (S. cerevisiae), full insert sequence Erythroblast cDNA, RIKEN full-length enriched library, clone:K0C0021G18 product:SAR1a gene homolog 1 (S. cerevisiae), full insert sequence	22400	56090263	119421	3	5	37.3737
SEC14-like protein 2 Alpha-tocopherol-associated protein TAP Supernatant protein factor SPF	46170	21542226	60562	6	8	28.2878
Squalene transfer protein	35310	7109256	75738	1	1	2.5641
SH3P13 SH3 domain protein 2 C1	44730	425789	100550	1	1	1.9512
SIIRX-1 precursor	87750	624918	140634	4	4	8.396
SP120	97480	585688	104192	8	8	13.0588
SWISS-PROT:P09811 REFSEQ_NP:NP_071604 ENSEMBL:ENSRNOP00000009183 Glycogen phosphorylase, liver form	41980	206150	168209	1	1	3.5135
SWISS-PROT:P12368 cAMP-dependent protein kinase type II-alpha regulatory subunit	33410	83305808	299568	14	14	43.771
SWISS-PROT:P24329 TREMBL:Q5I0D4 REFSEQ_NP:NP_036940	45110	8393557	51489	10	10	35.369
ENSEMBL:ENSRNOP0000000202 Thiosulfate sulfurtransferase	72810	729436	60584	3	52	64.3857
SWISS-PROT:P32755 TREMBL:O88655 REFSEQ_NP:NP_058929						
ENSEMBL:ENSRNOP00000001809 4-hydroxyphenylpyruvate dioxygenase						
SWISS-PROT:P38659 TREMBL:Q6P7S5 REFSEQ_NP:NP_446301						
ENSEMBL:ENSRNOP00000008728 Protein disulfide-isomerase A4 precursor						

SWISS-PROT:Q07936-1	TREMBL:Q8R513	ENSEMBL:ENSRNOP00000013988	38680	9845234	109734	12	12	40.118
REFSEQ:NP_063970	annexin A2		226300	967249	75000	43	84	45.589
SWISS-PROT:Q62812	TREMBL:Q62704	REFSEQ_NP:NP_037326						
ENSEMBL:ENSRNOP0000007398	Myosin-9		109700	57303	84180	32	32	37.5125
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2			101400	5200744	85749	1	1	2.7203
Sarcosine dehydrogenase, mitochondrial precursor SarDH			56960	49904285	38864	6	6	18.2711
Scavenger receptor class B member 1 SRB1 SR-BI			72260	9507019	47254	15	15	37.2057
Sec1 family domain-containing protein 1 Syntaxin-binding protein 1-like 2 Vesicle transport-related protein Ra410 Sly1p			28540	16924008	35326	6	6	27.9528
Sec22 homolog			52260	63101555	75284	12	12	33.1933
Sec61 alpha subunit homolog			20690	2498940	43395	5	5	29.4444
Secreted phosphoprotein 24 precursor Spp-24 Secreted phosphoprotein 2			34340	10764633	150292	2	2	10.356
Secretory carrier membrane protein 2			38370	34857962	169836	5	5	19.1977
Secretory carrier membrane protein 3			38000	487057	46139	5	5	21.5976
Secretory carrier-associated membrane protein 1 Secretory carrier membrane protein 1 SCAMP 37			68660	29336095	213126	10	10	26.9919
Sel1 (suppressor of lin-12) 1 homolog			52530	49256633	111519	4	4	11.0169
Selenium binding protein 2			41580	47939025	1271	1	1	5.7143
Selenoprotein P precursor			28130	34856334	31392	2	2	13.7405
Sepiapterin reductase			50510	9789715	167832	4	4	13.7615
Septin-7 CDC10 protein homolog			63790	6090881	70797	2	2	4.4326
Septin-9 Eseptin eighth septin Septin-like protein SLP			47680	77416574	19107	1	1	3.6446
Sequestosome-1 Ubiquitin-binding protein p62 Protein kinase C-zeta-interacting protein PKC-zeta-interacting protein			54550	60551378	68739	2	2	5.8455
Serine (Or cysteine) proteinase inhibitor, clade D, member 1			54890	58865362	341343	1	1	2.6477
Serine (Or cysteine) proteinase inhibitor, clade F, member 2 Predicted			55610	40018558	222317	4	4	13.8889
Serine (Or cysteine) proteinase inhibitor, clade G (C1 inhibitor), member 1, Angioedema, hereditary			44930	8393560	51490	1	1	2.6442
Serine protease hepsin Serine protease hepsin non-catalytic chain Serine protease hepsin catalytic chain			21310	40018550	319145	1	1	6.2176
Serine protease inhibitor, Kunitz type 2			45830	66655	31393	4	4	12.5604
Serine-pyruvate aminotransferase, mitochondrial precursor SPT Alanine-glyoxylate aminotransferase AGT			35580	8394021	41475	3	3	16.1812
Serine/threonine protein phosphatase			37190	999343	4597	6	6	23.2416
Serine/threonine protein phosphatase PP1-beta catalytic subunit			68310	497994	12071	1	1	2.4876
Serine/threonine-protein kinase PLK1 Polo-like kinase 1 PLK-1			92830	61214571	55278	1	1	0.80275
Serine/threonine-protein phosphatase 1 regulatory subunit 10 Phosphatase 1 nuclear targeting subunit Protein PNUITS MHC class I region proline-rich protein CAT53			51980	7993726	78346	1	1	3.0905
Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B delta isoform PP2A, subunit B, B-delta isoform PP2A, subunit B, B55-delta isoform PP2A, subunit B, PR55-delta isoform PP2A, subunit B, R2-delta isoform			76360	6175089	37301	1	43	54.8711
Serotransferrin precursor Transferrin Siderophilin Beta-1-metal-binding globulin			46560	55824765	280024	7	7	25.1799
Serpinh1 protein								

Serum albumin precursor	68720	72101	120645	49	49	80.2632
Serum amyloid A 4 Predicted	14970	57164089	301225	1	1	9.2308
Serum amyloid P-component precursor	26180	3183550	52390	12	12	57.0175
Serum paraoxonase/arylesterase 1	38460	1945471	19325	1	12	58.2609
Short chain 3-hydroxyacyl-CoA dehydrogenase, mitochondrial precursor HCDH Medium and short chain L-3-hydroxyacyl-coenzyme A dehydrogenase	34450	7387725	70622	13	13	71.6561
Short/branched chain specific acyl-CoA dehydrogenase, mitochondrial precursor SBCAD 2-methyl branched chain acyl-CoA dehydrogenase 2-MEBCAD 2-methylbutyryl-coenzyme A dehydrogenase 2-methylbutyryl-CoA dehydrogenase	47820	6978433	3600	1	1	5.0926
Shwachman-Bodian-Diamond syndrome Predicted	28750	56605652	227484	1	1	4
Sideroflexin 1	38560	545998	80422	1	9	37.2549
Sigma1 receptor Optoid receptor, sigma 1	25270	6434855	78339	6	6	41.704
Signal recognition particle 14 kDa protein SRP14	12510	27731985	38099	1	1	12.7273
Signal recognition particle receptor subunit beta SR-beta	29580	null	38101	10	10	44.2379
Similar to CG6105-PA	11460	47058994	288462	5	5	58.2524
Similar to SPI6	42300	56090431	224458	2	2	7.754
Similar to interferon-inducible GTPase	48190	62664492	237237	1	4	14.8681
Similar to phospholysine phosphohistidine inorganic pyrophosphate phosphata 5M590	29190	57528359	221017	1	1	7.7778
Single-stranded DNA-binding protein, mitochondrial precursor Mt-SSB M1SSB P16	17450	423723	44190	1	1	6.6225
Small GTP-binding protein rab5	23610	3309068	177419	5	8	47.907
Small nuclear ribonucleoprotein Sm D1 snRNP core protein D1 Sm-D1 Sm-D autoantigen	13280	34877889	3858	1	1	16.8067
Sodium channel protein type 3 subunit alpha Sodium channel protein type III subunit alpha Voltage-gated sodium channel subunit alpha Nav1.3 Sodium channel protein, brain III subunit alpha Voltage-gated sodium channel subtype III	221400	6981510	75080	1	1	0.35879
Sodium/calcium exchanger 1 precursor	108100	57209	44653	1	1	0.72091
Sodium/potassium-transporting ATPase alpha-1 chain precursor Sodium pump 1 Na+/K+ ATPase 1	113100	6978543	3651	20	20	25.0244
Sodium/potassium-transporting ATPase beta-1 chain	35230	6978549	3654	2	2	8.2237
Sodium/potassium-transporting ATPase subunit beta-3 Sodium/potassium-dependent ATPase beta-3 subunit ATPB-3 CD298 antigen	31830	6978553	3656	3	3	15.4122
Soluble calcium-activated nucleotidase 1 SCAN-1 Apyrase homolog	45660	71153846	231548	21	21	60.794
Solute carrier family 10, member 1	39300	8394279	11254	1	1	3.8674
Solute carrier family 2, facilitated glucose transporter member 2 Glucose transporter type 2, liver	57090	92281	75093	3	3	6.3218
Solute carrier family 21 member 4	62970	19071449	198521	1	3	6.338
Solute carrier organic anion transporter family member 1A1 Solute carrier family 21 member 1 Sodium-independent organic anion transporter 1 Organic anion-transporting polypeptide 1	74180	8394294	152150	4	5	10
Solute carrier organic anion transporter family member 1A4 Solute carrier family 21 member 5 Sodium-independent organic anion-transporting polypeptide 2 Brain digoxin carrier protein Brain-specific organic anion transporter OATP-B1	73250	3914190	43622	7	10	20.8775
Solute carrier organic anion transporter family member 2B1 Solute carrier family 21 member 9 Organic anion transporter moatp1	74210	9622206	47477	2	2	3.8123
Son protein	12550	34849639	313065	1	1	8.8496

Sorbitol dehydrogenase	42830	2506157	43660	13	13	39.8496
Sorting and assembly machinery component 50 homolog	51960	51948454	255631	2	2	4.4776
Sorting nexin 3	18760	79152346	75350	1	1	4.321
Spectrin alpha chain, brain	284600	62644670	3340	98	99	50.0809
Spectrin beta chain, brain 2	271100	3550975	3158	40	47	25.335
Sphingosine-1-phosphate lyase 1 SP-lyase SPL Sphingosine-1-phosphate aldolase	63760	37999349	269681	7	7	15.8451
Splicing factor, arginine/serine-rich 3	19330	62665747	4905	1	2	12.8049
Squalene monooxygenase Squalene epoxidase SE	64020	8394354	137571	1	1	2.0942
Squalene synthetase SQS SS Farnesyl-diphosphate farnesyltransferase FPP:FPP farnesyltransferase	48110	9506591	85115	10	10	31.9712
Stabilin-2 precursor Hyaluronan receptor for endocytosis 175 kDa stabilin-2 175 kDa hyaluronan receptor for endocytosis	155900	50401220	153825	9	12	11.3906
Staufen isoform Stau+16	54800	9754866	60405	2	2	5.2525
Sterol 12-alpha hydroxylase	57520	4587057	129969	1	4	10.02
Sterol 12alpha-hydroxylase P450	57590	5360891	75741	1	4	10.02
Sterol 8-isomerase	26740	8388884	140632	3	3	15.2174
Sterol carrier protein 2	58790	51980631	33159	3	3	6.7642
Steryl-sulfatase precursor Steroid sulfatase Steryl-sulfate sulfohydrolase Arylsulfatase C ASC	62680	6981598	75108	6	6	12.305
Stonin	81920	33636736	277960	1	1	0.95759
Stress-70 protein, mitochondrial precursor	73740	62664205	36413	8	11	21.6495
Stress-induced-phosphoprotein 1 ST11 Hsc70/Hsp90-organizing protein Hop	62570	54036435	82685	2	2	4.4199
Stromal cell-derived factor-1 gamma	13550	76563910	209385	1	1	11.7647
Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial precursor Fp Flavoprotein subunit of complex II	71620	52782765	96892	26	26	53.6585
Succinate dehydrogenase [ubiquinone] iron-sulfur protein (EC 1.3.5.1) (lp) (Iron-sulfur subunit of complex II)	31830	27716317	167087	8	8	26.9504
Succinyl-CoA ligase [GDP-forming] alpha-chain, mitochondrial precursor Succinyl-CoA synthetase, alpha chain SCS-alpha	35030	68574	45104	9	9	42.042
Sulfate anion transporter 1 SAT-1 Solute carrier family 26 member 1 Canalicular sulfate transporter	75450	431453	104202	3	3	6.9701
Sulfate/carbonate antiporter	61120	92782	75055	5	5	11.9134
Sulfated glycoprotein 1 precursor	54350	40254758	318917	6	6	18.4426
Sulfite oxidase	35760	543420	78152	8	8	34.8684
Sulfoltransferase 1C1 N-hydroxyarylamine sulfoltransferase HAST-I	16020	1213217	35188	4	4	32.2581
Superoxide dismutase [Cu-Zn]	24680	56691	111692	6	6	35.5856
Superoxide dismutase [Mn], mitochondrial precursor	36120	37589607	33179	12	12	30.8442
Synaptic glycoprotein SC2	25670	9507167	47308	1	1	5.1282
Synaptogyrin-1 p29	22560	5106930	36071	2	2	12.6214
Synaptojanin 2 binding protein	29070	6685966	34036	1	1	5.4475
Synaptosomal-associated protein 29 SNAP-29 Vesicle-membrane fusion protein SNAP-29 Soluble 29 kDa NSF attachment protein Golgi SNARE of 32 kDa Gs32	63340	14210270	19552	2	2	3.7415
Synaptotagmin III						

Syndecan 2	23220	6981520	41211	2	2	10.9005
Syndecan-1 precursor	33210	6981518	75082	1	1	6.0703
Syndecan-4 precursor SYND4 Ryudocan core protein	21960	6981522	75083	2	2	19.3069
Syntaxin 13	30470	3184552	52412	4	4	26.2172
Syntaxin 6	29060	51858907	78119	1	1	9.8039
Syntaxin binding protein Munc18-3 Syntaxin binding protein 3	68020	71051327	157267	3	3	6.0708
Syntaxin-4	34210	349321	37252	3	3	14.094
Syntaxin-5	34120	631892	78137	11	11	55.4817
Syntaxin-8	26910	3834382	78117	1	1	7.6271
T-cell surface glycoprotein CD1d precursor CD1d antigen	38540	8393070	12016	3	3	10.119
T-complex protein 1 subunit alpha TCP-1-alpha CCT-alpha	60360	6981642	75118	13	13	34.5324
T-kininogen I precursor	47700	6981138	3965	9	9	26.5116
TATA element modulatory factor	90260	6650548	60512	5	5	7.2215
TOM22	15490	71051674	171046	2	2	16.1972
TOM70 Translocase of outer mitochondrial membrane 70 homolog A	67440	68534716	726503	5	5	10.6557
TOR1D	28490	37590771	161242	2	2	9.5057
TREMBL:O35234 Diphor-1	52250	2331224	80899	1	13	35.654
TREMBL:O35813 Keratin 14	25680	2443314	22440	3	4	15.1515
TREMBL:Q32PW9 ENSEMBL:ENSRNOP00000009649 REFSEQ:XP_214147 PREDICTED: similar to Psmc6 protein	45800	34869622	309670	3	3	9.9256
TREMBL:Q5EBA4 ENSEMBL:ENSRNOP00000011158 REFSEQ:XP_001067526:XP_341250 PREDICTED: similar to Protein NipSnap1	33350	34879019	217815	4	4	16.5493
TREMBL:Q5PQV6 REFSEQ:XP_579556 ENSEMBL:ENSRNOP00000004864 Flavin containing monooxygenase 3	59980	62659523	246480	24	30	69.4915
TREMBL:Q6MG49,Q9WNT8 REFSEQ_NP:NP_446061 ENSEMBL:ENSRNOP00000001129 BAT3	114900	4587081	60486	1	1	1.184
TREMBL:Q9EPH2 REFSEQ_NP:NP_110489 ENSEMBL:ENSRNOP00000012663 Mac-MARCKS protein	19850	76363234	71714	1	1	7.5377
TREMBL:Q9ROT3,Q6P7A0 REFSEQ_NP:NP_071568 ENSEMBL:ENSRNOP00000014182 Protein kinase inhibitor p58	57580	8570528	104170	5	19	44.0476
TSH receptor suppressor element-binding protein-1	35530	9653686	93202	1	3	18.323
Tapasin Tap-binding protein	50040	46237539	140838	4	4	14.2241
Target of myb1 homolog	54090	56605806	200982	1	1	2.6423
Tax_id=10116 2-oxoglutarate carrier	34250	2497985	23402	1	7	28.3439
Tax_id=10116 3-mercaptopyruvate sulfurtransferase	32940	62652539	13392	3	3	11.7845
Tax_id=10116 33 kDa protein	33300	34872473	212891	1	1	4.0678
Tax_id=10116 35 kDa protein	34930	57463	31609	29	29	85.1485
Tax_id=10116 ADP-ribosylation factor 5	20530	56388751	10610	5	13	68.8889
Tax_id=10116 ATP synthase, H+ transporting, mitochondrial F0 complex, subunit e	8255	461587	11888	4	5	69.0141
Tax_id=10116 ATP-binding cassette, sub-family D (ALD), member 3	75320	6981450	75063	22	22	46.1305

Tax_id=10116 AdAptor protein complex AP-1, gAmma 1 subunit	77880	34851742	198626	3	3	3	7.8236
Tax_id=10116 Aldehyde dehydrogenase family 1, subfamily A4	54560	91935	83139	1	3	3	7.984
Tax_id=10116 Aldo-keto reductase family 1, member A1	36510	399660	37172	8	8	8	32.3077
Tax_id=10116 Aldolase A	39350	6978487	3624	4	5	5	12.6374
Tax_id=10116 Amine oxidase (flavin-containing)	58390	91974	74982	22	22	22	54.2308
Tax_id=10116 Annexin 1	38830	6978501	3631	6	7	7	28.6127
Tax_id=10116 Arylacetamide deacetylase	45690	8347733	5958	11	11	11	36.4322
Tax_id=10116 Brain lipid binding protein	14860	476082	71698	3	3	3	28.0303
Tax_id=10116 CD36 antigen (collagen type I receptor, thrombospondin receptor)-like 2	54090	38197654	157248	8	8	8	26.569
Tax_id=10116 Catalase	59760	6978607	3681	24	24	24	58.8235
Tax_id=10116 Coatomer protein complex, subunit beta 2 (beta prime)	102600	3023522	35931	40	40	40	60.442
Tax_id=10116 Cofilin 1	18530	8393101	87332	4	6	6	48.7952
Tax_id=10116 Complement component 5	134400	34853897	205903	1	1	1	1.1745
Tax_id=10116 Cysteine and glycine-rich protein 1	20610	8393206	51411	2	2	2	12.9534
Tax_id=10116 D-beta-hydroxybutyrate dehydrogenase, mitochondrial precursor	38350	482346	141497	17	17	17	58.1395
Tax_id=10116 D-dopachrome tautomerase	13130	895882	29986	7	7	7	76.2712
Tax_id=10116 DEAD (Asp-Glu-Ala-Asp) box polypeptide 1	97470	34863163	240056	24	24	24	35.3075
Tax_id=10116 Diazepam binding inhibitor	10030	54261671	4320	4	4	4	52.8736
Tax_id=10116 Dihydrodipicolinate decarboxylase E2	53460	34859889	232730	1	1	1	2.8926
Tax_id=10116 Dimethylarginine dimethylaminohydrolase 1	31430	6831527	104206	3	3	3	18.2456
Tax_id=10116 Ensembl locations (Chr-bp): 1-95678925 ribosomal protein L13A	23480	548747	106718	14	14	14	46.798
Tax_id=10116 Ensembl locations (Chr-bp): 10-40398095 annexin VI	75750	763181	127131	45	46	46	69.9851
Tax_id=10116 Ensembl locations (Chr-bp): 10-98947600 similar to GTP-binding regulatory protein alpha-13 chain - mouse	45080	34875240	194129	6	6	6	17.3469
Tax_id=10116 Ensembl locations (Chr-bp): 11-64934053 similar to homotensate 1, 2-dioxygenase	59620	34869194	303719	3	3	3	8.5981
Tax_id=10116 Ensembl locations (Chr-bp): 12-20846400 Procollagen-lysine, 2-oxoglutarate 5-dioxygenase 3	84910	30017429	286288	5	5	5	9.9865
Tax_id=10116 Ensembl locations (Chr-bp): 13-87313501 similar to NADH dehydrogenase (ubiquinone) Fe-S protein 2	38440	34880923	216920	5	5	5	19.3548
Tax_id=10116 Ensembl locations (Chr-bp): 14-37304188 similar to RIKEN cDNA 6030432N09	27020	34877284	194680	2	2	2	11.8852
Tax_id=10116 Ensembl locations (Chr-bp): 14-70683054 similar to leucine aminopeptidase	64550	34878080	204743	2	2	2	5.1581
Tax_id=10116 Ensembl locations (Chr-bp): 14-77957500 similar to Syntaxin 18	49850	34878414	291113	2	2	2	5.7604
Tax_id=10116 Ensembl locations (Chr-bp): 15-21359488 similar to mitogen inducible gene mig-2	95210	34869626	211833	5	5	5	9.7969
Tax_id=10116 Ensembl locations (Chr-bp): 15-56616580 similar to component of oligomeric golgi complex 2	72190	34874501	274159	7	7	7	15.109
Tax_id=10116 Ensembl locations (Chr-bp): 16-1479259 similar to annexin A11	72140	34876896	205775	2	2	2	3.4226
Tax_id=10116 Ensembl locations (Chr-bp): 16-73342360 similar to ankyrin	186300	34879099	195573	1	1	1	0.58685
Tax_id=10116 Ensembl locations (Chr-bp): 17-77022236 similar to aldo-keto reductase family 1, member C12	32180	34876320	221880	1	4	4	15.1408

Tax_id=10116	Ensembl_locations(Chr-bp):2-120296304 similar to fragile-X-related protein 1 isoform e	68720	34856814	266426	1	1	2.2913
Tax_id=10116	Ensembl_locations(Chr-bp):2-252454876 similar to crystallin, zeta	37130	34860973	210117	1	1	2.5714
Tax_id=10116	Ensembl_locations(Chr-bp):2-2908047 glutaredoxin 1 (thioltransferase)	11880	38181944	246362	1	1	10.2804
Tax_id=10116	Ensembl_locations(Chr-bp):2-30892343 similar to methylcrotonyl-Coenzyme A carboxylase 2 (beta)	66180	34853476	191730	2	2	5.6385
Tax_id=10116	Ensembl_locations(Chr-bp):3-105548427 similar to hypothetical protein FLJ10579	57210	34856697	285691	5	5	13.2296
Tax_id=10116	Ensembl_locations(Chr-bp):3-141766859 FK506 binding protein 2	11920	501064	43461	1	1	12.037
Tax_id=10116	Ensembl_locations(Chr-bp):3-155772538 similar to protective protein precursor - mouse	57110	34860773	247133	3	3	7.3267
Tax_id=10116	Ensembl_locations(Chr-bp):4-160981651 Serine protease	77790	7435632	13085	1	1	2.0173
Tax_id=10116	Ensembl_locations(Chr-bp):4-173856695;4-173883435 similar to RIKEN cDNA 1100001H23	68540	34858551	236607	2	2	3.9933
Tax_id=10116	Ensembl_locations(Chr-bp):4-30073201;4-30073201 similar to Pon2 protein	27380	34854947	217377	11	11	55.3279
Tax_id=10116	Ensembl_locations(Chr-bp):4-39132345 similar to RIKEN cDNA 8430437G11	61370	34854982	191057	10	10	21.4552
Tax_id=10116	Ensembl_locations(Chr-bp):4-56330652 similar to Impdh1 protein	60730	34855047	190455	1	1	1.4109
Tax_id=10116	Ensembl_locations(Chr-bp):4-97148803 Hypothetical RNA binding protein RDA288	43010	18041977	114376	1	1	2.8061
Tax_id=10116	Ensembl_locations(Chr-bp):5-157093377 similar to oligosaccharyltransferase	53840	34872203	206351	12	12	36.5702
Tax_id=10116	Ensembl_locations(Chr-bp):6-26565039 similar to dystrobrevin B (mDTN-B)	82140	34863056	279256	2	2	4.2234
Tax_id=10116	Ensembl_locations(Chr-bp):6-51287726 similar to synaptophysin-like protein	29400	34864274	311134	2	2	10.3448
Tax_id=10116	Ensembl_locations(Chr-bp):6-93096989;10-64690010 proteasome (prosome, macropain) subunit, alpha type 3	28420	8394066	45012	1	1	4.7059
Tax_id=10116	Ensembl_locations(Chr-bp):6-94917824 similar to CGI-86 protein	36250	34865689	214468	7	11	48.9164
Tax_id=10116	Ensembl_locations(Chr-bp):7-113905923 similar to eukaryotic translation elongation factor 1 delta (guanine nucleotide exchange protein)	31330	27662108	302099	1	1	4.2705
Tax_id=10116	Ensembl_locations(Chr-bp):7-120740849 similar to alpha-N-acetyl-galactosaminidase	54520	34867288	202900	1	1	3.5197
Tax_id=10116	Ensembl_locations(Chr-bp):8-12086308 similar to RIKEN cDNA 4931406C07	19160	34860352	266321	3	3	21.5909
Tax_id=10116	Ensembl_locations(Chr-bp):8-46234308 similar to RIKEN cDNA D130038B21	40890	34863198	270449	1	1	3.2698
Tax_id=10116	Ensembl_locations(Chr-bp):9-45566723 similar to RIKEN cDNA 2610509I15	47870	34875828	251780	4	4	13.3803
Tax_id=10116	Ensembl_locations(Chr-bp):9-85296295 nucleolin	77150	6981248	69638	10	10	18.2328
Tax_id=10116	Ensembl_locations(Chr-bp):None similar to CLCP	25370	34852289	287945	1	1	5.1724
Tax_id=10116	Ensembl_locations(Chr-bp):None similar to Dp111 protein	20580	34862308	288307	5	5	29.3478
Tax_id=10116	Ensembl_locations(Chr-bp):None similar to LRG-47	44620	27670133	160756	13	13	54.4304
Tax_id=10116	Ensembl_locations(Chr-bp):None similar to alpha glucosidase II, alpha subunit	20950	34861578	310313	13	13	63.6364
Tax_id=10116	Ensembl_locations(Chr-bp):None similar to betaine-homocysteine methyltransferase 2	46420	34861318	247159	1	1	4.0094
Tax_id=10116	Ensembl_locations(Chr-bp):X-139040465 similar to glypican 4	62280	34881641	253728	3	3	7.7899
Tax_id=10116	Eukaryotic translation Elongation factor 2	95280	8393296	51432	42	42	57.2261
Tax_id=10116	Ezrin-radixin-moesin binding phosphoprotein 50	38830	8132349	644	7	7	25.2809
Tax_id=10116	Flavin-containing monooxygenase 5	60060	62286643	187298	25	25	56.848

Tax_id=10116 Fructose-1,6- biphosphatase 1	39610	623562	149105	18	18	61.708
Tax_id=10116 Glucokinase reGulatory protein	68920	6978884	3782	3	3	8.7719
Tax_id=10116 Glutathione S-transferase theta 1	27470	56265	111659	1	1	5
Tax_id=10116 Glutathione S-transferase, mitochondrial	25490	42543496	110024	10	10	52.2124
Tax_id=10116 Glutathione S-transferase, pi	23440	56336	28297	4	4	30
Tax_id=10116 Glutathione S-transferase, theta 2	27440	769703	3914	6	6	31.5574
Tax_id=10116 Golgi resident protein GCP60	60480	51315724	295490	11	11	23.1939
Tax_id=10116 Guanine nucleotide binding protein, alpha inhibiting 3	40520	71899	3901	4	10	35.5932
Tax_id=10116 Hydroxy-delta-5-steroid deHydrogenase, 3 beta- and steroid delta-isomerase	42210	6981050	3937	19	19	64.3432
Tax_id=10116 HypotHetical protein XP_213403	19700	34872851	239897	1	1	8.1871
Tax_id=10116 HypotHetical protein XP_215523	21540	34854965	295192	1	1	4.6632
Tax_id=10116 HypotHetical protein XP_235050	101800	34864725	191344	1	1	1.31
Tax_id=10116 HypotHetical protein XP_341172	45130	34881421	311586	7	7	20.6186
Tax_id=10116 HypotHetical protein XP_342343	17520	34860574	313817	1	1	9.9379
Tax_id=10116 HypotHetical protein XP_346991	26610	34857419	273429	1	1	2.9046
Tax_id=10116 Integrin, alpha 6	141300	34855181	306780	1	1	1.1067
Tax_id=10116 Kan-1	46500	8392962	80318	21	21	76.1905
Tax_id=10116 Keratin 18	16960	587518	108078	3	13	80.2721
Tax_id=10116 Lactate dehydrogenase B	36610	6981146	3968	1	4	12.5749
Tax_id=10116 M4 protein	74540	16124253	136387	1	1	1.8651
Tax_id=10116 Major vault protein	95800	49256645	395977	1	24	45.7607
Tax_id=10116 Mannosidase 2, alpha 1	86580	34877940	205526	21	41	56.2667
Tax_id=10116 Methylenetetrahydrofolate dehydrogenase (NADP+ dependent), Methylenetetrahydrofolate cyclohydrolase, forMyltetrahydrofolate synthase	101000	901850	62122	35	35	45.9893
Tax_id=10116 Moesin	67740	32363196	71715	7	16	28.2496
Tax_id=10116 NADH dehydrogenase (ubiquinone) 1 alpha subcomplex 5	13410	6981260	75004	2	2	17.2414
Tax_id=10116 P450 (cytochrome) oxidoreductase	76960	66118	78074	1	37	62.5369
Tax_id=10116 PDZ and LIM domain protein 1	35530	8393153	40336	6	6	24.7706
Tax_id=10116 PDZ domain-containing protein	56890	8439549	78142	1	13	30.9751
Tax_id=10116 Peroxiredoxin 6	24820	5902791	60471	10	10	65.1786
Tax_id=10116 Peroxisomal membrane Protein 2	22580	585703	11779	6	6	34.0206
Tax_id=10116 Phenylalanine-4-hydroxylase	51820	6981330	75026	4	4	10.8168
Tax_id=10116 PhosPhoglucosutase 1	61400	8393951	51568	8	8	25.9786
Tax_id=10116 PhosPhoribosylaminoimidazole carboxylase, PhosPhoribosylaminoimidazole succinocarboxamide synthetase	47100	976252	111533	4	4	12.9412
Tax_id=10116 Ribosomal pRotein L14	23340	2500360	43519	8	8	31.7757
Tax_id=10116 Ribosomal pRotein L18	21660	54261673	37240	9	12	46.2766
Tax_id=10116 Ribosomal pRotein L3	46140	57698	144426	25	27	59.8015

Tax_id=10116	Secretory protein, 45kD	100300	34878986	235129	10	12	17.3121
Tax_id=10116	Serine/threonine kinaSe 16	34410	27465615	105853	4	4	22.623
Tax_id=10116	Signal recognition particle 54 kDa	79610	34865216	263863	3	3	8.2633
Tax_id=10116	Similar to 1-acylglycerol-3-phoSphate O-acyltransSferaSe 2	31100	34853099	274486	4	4	23.0216
Tax_id=10116	Similar to 1700013123Rik protein	22400	34853020	251303	1	1	7.4257
Tax_id=10116	Similar to 2210409H23Rik protein	47190	34866415	232409	2	2	5.2874
Tax_id=10116	Similar to 24-dehydrocholeSterol reductaSe	78850	34869959	290771	7	7	16.2356
Tax_id=10116	Similar to 25 kDa brain-Specific protein (p25-alpha)	30720	34853331	206115	1	1	5.6338
Tax_id=10116	Similar to 40S riboSomaL protein S2	28530	34876659	307172	2	9	35.7143
Tax_id=10116	Similar to 4930544L10Rik protein	37000	34858831	241539	2	2	8.1505
Tax_id=10116	Similar to 5730439E10Rik protein	88550	34865846	303924	31	31	49.2405
Tax_id=10116	Similar to 60S riboSomaL protein L10 (QM protein homolog)	11450	34853952	238486	1	8	62
Tax_id=10116	Similar to 60S riboSomaL protein L7a (Surfeit locuS protein 3) (PLA-X polypeptide)	26160	34869696	200139	1	10	33.0435
Tax_id=10116	Similar to 9130011E15Rik protein	79550	34863517	198410	5	5	8.8953
Tax_id=10116	Similar to 9630010P11Rik protein	161100	34855819	234438	1	1	0.54018
Tax_id=10116	Similar to A-kinaSe anchor protein 9 iSoform 2	441400	34854301	223472	1	1	0.23438
Tax_id=10116	Similar to ALY	21140	34875658	307156	1	1	5.5838
Tax_id=10116	Similar to AP47 protein - mouSe	61590	34877759	223265	6	6	16.7897
Tax_id=10116	Similar to ARL6IP2	79450	34861996	265779	13	13	26.7425
Tax_id=10116	Similar to ARP2/3 complex 16 kDa Subunit (P16-ARC) (Actin-related protein 2/3 complex Subunit 5)	34540	34880487	318590	5	5	21.0863
Tax_id=10116	Similar to ATP SulfurylaSe/APS kinaSe 2	80990	34862615	219419	6	6	12.5174
Tax_id=10116	Similar to ATP-binding caSSette tranSporter ABCG3	95680	34876022	243111	3	5	7.9478
Tax_id=10116	Similar to ATP-binding caSSette tranSporter ABCG3	67490	34879726	242256	2	4	10.084
Tax_id=10116	Similar to ATP-binding caSSette tranSporter Sub-family A member 6	191500	34875258	278570	5	5	4.6718
Tax_id=10116	Similar to ATP-binding caSSette tranSporter Sub-family A member 8a	187500	34875001	209410	17	17	14.8575
Tax_id=10116	Similar to Ac2-248	97230	34880787	207228	12	12	21.3548
Tax_id=10116	Similar to Actin monomer-binding protein	204100	34866518	244260	1	1	0.58824
Tax_id=10116	Similar to Alanyl-tRNA SynthetaSe (Alanine-tRNA ligaSe) (AlaRS)	108200	34851760	253193	1	1	1.9388
Tax_id=10116	Similar to Aldh8a1 protein	72630	34852829	197702	16	16	34.0944
Tax_id=10116	Similar to All-1 protein +GTE form - mouSe (fragment)	374300	34863265	267292	1	1	0.26178
Tax_id=10116	Similar to Alpha enolaSe (2-phoSpho-D-glycerate hydro-lySe) (Non-neural enolaSe) (NNE) (EnolaSe 1)	39350	34875256	313683	1	8	29.3296
Tax_id=10116	Similar to Alpha-2 catenin (Alpha-catenin related protein) (Alpha N-catenin)	51430	34856264	258471	2	2	6.5217
Tax_id=10116	Similar to Alpha-mannoSidaSe Ix (MannoSyl-oligoSaccharide 1,3-1,6-alpha-mannoSidaSe) (MAN Ix) (MannoSidaSe alpha claSS 2A member 2)	133000	34857364	209202	1	3	2.294
Tax_id=10116	Similar to Amyloid beta A4 precuSor protein-binding family B member 2 (Fe65-like protein)	53090	34877353	294691	1	1	2.7368
Tax_id=10116	Similar to Arginine-tRNA-protein tranSferaSe 1	51870	34859415	229620	1	1	1.5086

Tax_id=10116 Similar to Arvcf protein	122400	34869778	246886	2	2	2	2.4845
Tax_id=10116 Similar to B aggreSsive lymphoma	106500	34869208	269562	4	4	4	6.9286
Tax_id=10116 Similar to BC013491 protein	76140	34856101	235741	1	1	1	1.0294
Tax_id=10116 Similar to Band 4.1-like protein 5	114300	34879408	300797	2	3	3	3.0978
Tax_id=10116 Similar to CAD protein	245800	34862992	315461	5	7	7	3.6526
Tax_id=10116 Similar to CENTROMERIC PROTEIN E (CENP-E PROTEIN)	313000	34860597	241018	1	1	1	0.25679
Tax_id=10116 Similar to CG11388-PA	36250	34869404	241377	1	1	1	5.7402
Tax_id=10116 Similar to CG17660-PA	52310	34857630	293554	2	2	2	6.5076
Tax_id=10116 Similar to CG2144-PA	100600	34875840	237985	3	3	3	3.9301
Tax_id=10116 Similar to CG31613-PA	101500	34876364	249977	6	9	9	10.4009
Tax_id=10116 Similar to CG32774-PA	79590	34876775	221370	2	2	2	2.3192
Tax_id=10116 Similar to CG33130-PA	132700	34853057	208493	1	1	1	1.0842
Tax_id=10116 Similar to CG9346-PA	113900	34865480	232164	2	2	2	2.0263
Tax_id=10116 Similar to CMP-Sialic acid transPorter	36550	34867231	260011	1	1	1	3.5608
Tax_id=10116 Similar to CUB and SuShi multiple domainS 3	213400	34866475	195940	1	1	1	0.6208
Tax_id=10116 Similar to Calcium-binding mitochondrial carrier protein Aralar2 (Solute carrier family 25, member 13) (Citrin)	101200	34854954	309822	18	19	19	24.9725
Tax_id=10116 Similar to Cgn-pending protein	159200	34858031	242726	1	5	5	3.0561
Tax_id=10116 Similar to Coatomer gamma-2 Subunit (Gamma-2 coat protein) (Gamma-2 COP)	84430	34855105	309005	14	16	16	30.429
Tax_id=10116 Similar to Coatomer zeta-1 Subunit (Zeta-1 coat protein) (Zeta-1 COP) (CGI-120) (HSPC181)	23840	34868640	236737	7	7	7	46.4115
Tax_id=10116 Similar to Complement C5 precursor (Hemolytic complement)	42190	34853846	242533	1	1	1	4.244
Tax_id=10116 Similar to Component of oligomeric golgi complex 4	91040	34851754	245295	4	4	4	6.6667
Tax_id=10116 Similar to ConServed oligomeric Golgi complex Subunit 5 (13S Golgi transPort complex 90 kDa Subunit) (GTC-90) (Golgi transPort complex 1)	45860	34864220	242048	4	4	4	12.5891
Tax_id=10116 Similar to ConServed oligomeric Golgi complex Subunit 5 (13S Golgi transPort complex 90 kDa Subunit) (GTC-90) (Golgi transPort complex 1)	28170	34864228	311912	2	2	2	11.9522
Tax_id=10116 Similar to ConServed oligomeric Golgi complex component 8	70760	34851657	222168	5	5	5	12.776
Tax_id=10116 Similar to Cox7a2l protein	12650	27716471	268354	1	1	1	10.6195
Tax_id=10116 Similar to Cux/CDP (1B1)	157000	34873366	289275	2	21	21	14.2658
Tax_id=10116 Similar to D-glucuronyl C5-epimeraSe	93260	34863951	299013	8	8	8	14.3201
Tax_id=10116 Similar to DEAD/H (ASp-Glu-Ala-Asp/His) box polypeptide RIG-I	94370	34867138	315303	1	1	1	1.937
Tax_id=10116 Similar to DEAH (ASp-Glu-Ala-His) box polypeptide 29	145700	34854165	249374	2	2	2	1.926
Tax_id=10116 Similar to DNA Segment, Chr 12, ERATO Doi 551, expresSed	130300	34865806	300896	1	1	1	0.94017
Tax_id=10116 Similar to DNA-directed RNA polymeraSe II largeSt Subunit (RPB1)	197600	34871645	202233	1	1	1	0.61694
Tax_id=10116 Similar to DeSmoplaKin (DP) (250/210 kDa paraneoplaStic pemphiguS antigen)	327800	34875216	219502	3	3	3	1.8362
Tax_id=10116 Similar to Delta(14)-Sterol reductaSe (C-14 Sterol reductaSe) (Sterol C14-reductaSe) (Delta14-SR) (Transmembrane 7 Superfamily member 2) (Another new gene 1) (Putative Sterol reductaSe SR-1)	46050	34861496	283602	5	5	5	15.7518
Tax_id=10116 Similar to DnaJ (HSp40) homolog, Subfamily B, member 12	40330	34882652	201409	5	5	5	20

Tax_Id=10116 Similar to ENSANGP0000013261	15620	27689183	197176	1	1	1	7.2993
Tax_Id=10116 Similar to Epithelial protein IosSt in neoplasia (mEPLIN)	94450	34868179	277610	14	14	14	22.7433
Tax_Id=10116 Similar to FERM, RhoGEF and pleckstrin domain protein 2	179800	34877686	293497	6	6	6	5.5556
Tax_Id=10116 Similar to FERM, RhoGEF, and pleckstrin domain protein 1	23830	34876611	304176	1	1	1	6.422
Tax_Id=10116 Similar to FLJ00343 protein	279400	34881882	282403	5	6	6	3.0845
Tax_Id=10116 Similar to FLJ00354 protein	155900	34861517	210125	1	2	2	1.1561
Tax_Id=10116 Similar to FYVE and coiled-coil domain containing 1	174100	34866719	308794	2	2	2	1.0975
Tax_Id=10116 Similar to Farp1 protein	195200	34876071	216529	5	5	5	3.303
Tax_Id=10116 Similar to G protein-coupled receptor 108	59750	34853540	214715	2	2	2	5.2731
Tax_Id=10116 Similar to GE36	76150	34880541	272300	1	1	1	1.8895
Tax_Id=10116 Similar to GTP binding protein	36860	34859732	225450	2	2	2	6.7692
Tax_Id=10116 Similar to Gamma-Soluble NSF attachment protein (SNAP-gamma) (N-ethylmaleimide-Sensitive factor attachment protein, gamma)	45610	34932055	316372	4	4	4	12.5926
Tax_Id=10116 Similar to Golgi phosphoprotein 2	54350	34873592	231145	10	10	10	34.9896
Tax_Id=10116 Similar to Herc2	542900	34856238	254063	1	1	1	0.24125
Tax_Id=10116 Similar to Hypothetical protein 5031404N19	336600	34867996	239621	1	1	1	0.36089
Tax_Id=10116 Similar to Hypothetical protein 9030012M21	37150	34875719	205153	1	1	1	3.5608
Tax_Id=10116 Similar to Hypothetical protein FLJ35794	51380	27708530	166638	1	1	1	2.4775
Tax_Id=10116 Similar to Hypothetical protein KIAA0152	26440	34872654	268830	8	8	8	34.8548
Tax_Id=10116 Similar to Hypothetical protein KIAA0233	237700	34932058	265857	1	1	1	0.43394
Tax_Id=10116 Similar to IQ motif containing GTPase activating protein 1	193900	34857388	242453	2	4	4	3.4604
Tax_Id=10116 Similar to Integrin alpha 5 (fibronectin receptor alpha)	115500	34868649	259355	3	3	3	3.7843
Tax_Id=10116 Similar to Integrin beta-2 precursor (Cell Surface adhesion glycoproteinS LFA-1/CR3/P150.95 beta-Subunit) (CD18) (Complement receptor C3 beta-Subunit)	84530	34852369	241188	1	1	1	2.2164
Tax_Id=10116 Similar to KDEL containing protein 1	60890	34863399	261916	1	1	1	2.2814
Tax_Id=10116 Similar to KIAA0090 protein	91240	34872226	302513	26	26	26	39.2109
Tax_Id=10116 Similar to KIAA0315	211600	34867650	248510	16	16	16	12.11
Tax_Id=10116 Similar to KIAA0316 protein	140900	34879922	244528	1	1	1	1.0133
Tax_Id=10116 Similar to KIAA0342 protein	333800	34866451	266038	1	1	1	0.344
Tax_Id=10116 Similar to KIAA0372 gene product	169500	34852783	312697	8	8	8	7.7982
Tax_Id=10116 Similar to KIAA0635 gene product	147000	34877224	224112	2	2	2	1.1058
Tax_Id=10116 Similar to KIAA0695 protein	71450	34879447	314767	1	1	1	2.0934
Tax_Id=10116 Similar to KIAA0903-like protein	120900	34879170	275605	1	1	1	1.7658
Tax_Id=10116 Similar to KIAA0963 protein	162200	34862323	279597	1	1	1	0.68306
Tax_Id=10116 Similar to KIAA0970 protein	135200	34874472	295665	14	14	14	16.3934
Tax_Id=10116 Similar to KIAA0980 protein	221500	34858955	230119	3	3	3	2.2472
Tax_Id=10116 Similar to KIAA1055 protein	108500	34865572	211597	2	2	2	1.5856
Tax_Id=10116 Similar to KIAA1208 protein	154100	34864701	229899	5	5	5	4.3478

Tax_Id=10116 Similar to KIAA1407 protein	75980	34869160	295453	1	1	1	1.059
Tax_Id=10116 Similar to KIAA1414 protein	184500	34861977	207796	1	1	1	0.99707
Tax_Id=10116 Similar to KIAA1453 protein	119600	34875569	239514	1	1	1	0.73126
Tax_Id=10116 Similar to KIAA1509 protein	212500	34867549	239536	2	2	2	0.91104
Tax_Id=10116 Similar to KIAA1630 protein	148300	34876831	315956	1	1	1	1.1646
Tax_Id=10116 Similar to KIAA1724 protein	43370	34863046	197285	2	2	2	8.6842
Tax_Id=10116 Similar to KIAA1940 protein	82950	34856348	273209	1	1	1	1.4398
Tax_Id=10116 Similar to KIF13A	204000	34874048	266483	2	2	2	1.1501
Tax_Id=10116 Similar to Kinetochore-associated protein 1 (Rough deal homolog) (hRod) (HSROD)	222900	34872331	265212	1	1	1	0.61287
Tax_Id=10116 Similar to Leukotriene A-4 hydrolase (LTA-4 hydrolase) (Leukotriene A(4) hydrolase) (HMLC)	93570	34864937	286024	1	1	1	1.8116
Tax_Id=10116 Similar to Maltese-glucosylase, intestinal	494700	34855581	199085	1	1	1	0.90048
Tax_Id=10116 Similar to MannoSyl-oligoSaccharide 1,2-alpha-mannoSidaSe IC (ProceSSing alpha-1,2-mannoSidaSe IC) (Alpha-1,2-mannoSidaSe IC) (MannoSidaSe alpha clSS 1C member 1)	51490	34872059	315202	2	2	2	5.4945
Tax_Id=10116 Similar to Meningioma expressed antigen 6 (coiled-coil proline-rich)	57130	34865266	286300	3	3	3	8.9109
Tax_Id=10116 Similar to Myl9 protein	34570	34860268	240507	3	8	8	37.7419
Tax_Id=10116 Similar to Mylk protein	73330	34869218	268038	1	1	1	1.3867
Tax_Id=10116 Similar to MyoSin VI	167000	34865321	261550	10	10	10	9.022
Tax_Id=10116 Similar to N-acetylglucosaminyltransferase IVb	71740	34870693	194890	15	15	15	34.4
Tax_Id=10116 Similar to NOD3	118900	34868757	253799	2	2	2	2.2018
Tax_Id=10116 Similar to Nebulette (Actin-binding Z-disk protein)	121800	34877348	276942	1	1	1	1.4995
Tax_Id=10116 Similar to Nedd4 WW binding protein 4	32550	34860870	317802	1	1	1	3.413
Tax_Id=10116 Similar to Nit protein 2	34190	34868007	213226	8	8	8	26.2295
Tax_Id=10116 Similar to OligoSaccharyl transferase 3 CG7748-PA	141400	34866419	214259	2	7	7	7.2395
Tax_Id=10116 Similar to P3 protein	44450	27689253	262782	3	3	3	7.9602
Tax_Id=10116 Similar to PALS2-beta Splice variant	67230	34855859	233877	4	4	4	9.6506
Tax_Id=10116 Similar to POLYPOSIS LOCUS PROTEIN 1 HOMOLOG (TB2 PROTEIN HOMOLOG) (GP106)	21070	34878680	252129	4	4	4	16.2162
Tax_Id=10116 Similar to PTB-associated Splicing factor	65140	34871066	310879	1	1	1	2.6891
Tax_Id=10116 Similar to Peroxisomal proliferator-activated receptor A interacting complex 285 kDa protein (PPAR-alpha interacting complex protein 285)	329700	34861034	286770	9	9	9	4.4771
Tax_Id=10116 Similar to Potential phospholipid-transporting ATPase IG (ATPase class I type 11C) (ATPase IQ)	131400	34881712	292511	14	14	14	15.4246
Tax_Id=10116 Similar to Probable RNA-dependent helicase p72 (DEAD-box protein p72) (DEAD-box protein 17)	73940	34866944	195895	2	4	4	7.218
Tax_Id=10116 Similar to Prolactin regulatory element-binding protein	45370	34863006	293599	5	5	5	13.6691
Tax_Id=10116 Similar to Protein Njmu-R1	44430	34872893	315828	1	1	1	4.0712
Tax_Id=10116 Similar to Protein disulfide isomerase-related	89320	34869214	276048	25	25	25	41.5929
Tax_Id=10116 Similar to Protein transport protein Sec24A (SEC24-related protein A)	105700	34870707	295725	17	17	17	22.9885

Tax_Id=10116 Similar to Protein transPort protein Sec24D (SEC24-related protein D)	110300	34859959	219262	7	7	7	9.7126
Tax_Id=10116 Similar to RAB22, member RAS oncogene family	23730	34860889	296032	4	4	4	21.5962
Tax_Id=10116 Similar to RIKEN cDNA 0610008C08	18820	34880585	277830	2	2	2	15.8537
Tax_Id=10116 Similar to RIKEN cDNA 0610040B21	27040	34870174	239547	7	7	7	33.4694
Tax_Id=10116 Similar to RIKEN cDNA 0610041L09	37560	34855114	227312	2	2	2	7.8788
Tax_Id=10116 Similar to RIKEN cDNA 1110025H10	26400	34871118	269702	2	2	2	13.75
Tax_Id=10116 Similar to RIKEN cDNA 1110031I02	36810	34875673	300976	1	1	1	3.0581
Tax_Id=10116 Similar to RIKEN cDNA 1110055L24	27770	34854713	201498	1	1	1	7.6305
Tax_Id=10116 Similar to RIKEN cDNA 1200014J11	80090	34872727	249723	1	1	1	1.5603
Tax_Id=10116 Similar to RIKEN cDNA 1300006L01	34660	34865173	223033	5	5	5	16.4087
Tax_Id=10116 Similar to RIKEN cDNA 1300011P19	69740	34863012	258910	3	3	3	5.8085
Tax_Id=10116 Similar to RIKEN cDNA 1300013G12	59080	34879692	246703	2	2	2	6.5056
Tax_Id=10116 Similar to RIKEN cDNA 1300014E15	74920	34877442	203301	1	1	1	1.9288
Tax_Id=10116 Similar to RIKEN cDNA 1300017J02	74750	34865830	304054	17	18	18	32.5037
Tax_Id=10116 Similar to RIKEN cDNA 1700034M03 gene	122500	34854321	261953	1	1	1	0.94073
Tax_Id=10116 Similar to RIKEN cDNA 1810063B07 gene	31470	34868966	280249	2	2	2	11.5789
Tax_Id=10116 Similar to RIKEN cDNA 2010321J07	62770	27694215	169892	11	13	13	33.4545
Tax_Id=10116 Similar to RIKEN cDNA 2210404D11	57560	34873697	262247	4	4	4	16.2933
Tax_Id=10116 Similar to RIKEN cDNA 2310008M10	19420	34860558	316149	2	2	2	12.069
Tax_Id=10116 Similar to RIKEN cDNA 2310050P13	55910	34859909	271576	3	3	3	8.9286
Tax_Id=10116 Similar to RIKEN cDNA 2310079N02	20810	34851911	222133	3	3	3	26.0417
Tax_Id=10116 Similar to RIKEN cDNA 2410011G03	23970	34864767	297605	4	4	4	25.2427
Tax_Id=10116 Similar to RIKEN cDNA 2610020H15	71060	34872958	298062	1	1	1	1.9048
Tax_Id=10116 Similar to RIKEN cDNA 2610207I16	122600	34868438	250916	1	1	1	1.6901
Tax_Id=10116 Similar to RIKEN cDNA 2610318K02	17320	34856650	238667	2	2	2	18.125
Tax_Id=10116 Similar to RIKEN cDNA 2810025M15	71590	34880767	272641	1	1	1	4.0971
Tax_Id=10116 Similar to RIKEN cDNA 2810405J04	61290	34862460	198258	3	3	3	7.3214
Tax_Id=10116 Similar to RIKEN cDNA 3110038B19	46280	34879556	235525	9	9	9	38.149
Tax_Id=10116 Similar to RIKEN cDNA 4632417N05	35570	34851797	239422	1	1	1	6.4815
Tax_Id=10116 Similar to RIKEN cDNA 4732474A20 gene	70120	34862810	190227	1	3	3	5.7566
Tax_Id=10116 Similar to RIKEN cDNA 4921526O06	68350	34875183	247534	3	3	3	3.0744
Tax_Id=10116 Similar to RIKEN cDNA 4931400A14	231900	34878255	296181	2	2	2	0.9704
Tax_Id=10116 Similar to RIKEN cDNA 4932408F18	164100	34867309	293100	1	1	1	1.2943
Tax_Id=10116 Similar to RIKEN cDNA 4933412D19	51730	34858091	273635	1	1	1	2.6608
Tax_Id=10116 Similar to RIKEN cDNA 5630401D24	81090	34880803	213507	1	1	1	1.6667
Tax_Id=10116 Similar to RIKEN cDNA 5730406I15	24970	27678066	216144	8	8	8	46.9027
Tax_Id=10116 Similar to RIKEN cDNA 5730469M10	39980	34877094	208161	11	11	11	28.6119

Tax_id=10116 Similar to RIKEN cDNA 5730507E09	131000	34867616	273407	1	1	0.68435
Tax_id=10116 Similar to RIKEN cDNA 5730596K20	61690	34861548	267475	17	17	42.6763
Tax_id=10116 Similar to RIKEN cDNA 6430520C02	89840	34881696	266670	1	1	0.86634
Tax_id=10116 Similar to RIKEN cDNA 9530027K23	73500	34851643	224054	1	1	2.1962
Tax_id=10116 Similar to RIKEN cDNA 9630048K23	41350	34869346	228920	1	1	3.9886
Tax_id=10116 Similar to RIKEN cDNA C330023F11	105000	34881052	274975	14	14	22.9188
Tax_id=10116 Similar to RIKEN cDNA C920006C10	66760	34866542	287440	6	6	14.89
Tax_id=10116 Similar to RIKEN cDNA E330026B02	279300	34865864	264571	2	2	0.47207
Tax_id=10116 Similar to RIKEN cDNA G431004K08	303100	34872627	241842	3	3	1.6304
Tax_id=10116 Similar to RNA helicaSe	80570	34933204	287882	14	15	25.8904
Tax_id=10116 Similar to RNA helicaSe family	238800	34853214	288172	1	1	0.5717
Tax_id=10116 Similar to Rab24 protein	26250	34873657	250158	1	1	4.721
Tax_id=10116 Similar to Ribosome-binding protein 1 (RiboSome receptor protein) (mRRp)	143300	34858829	244957	44	44	35.574
Tax_id=10116 Similar to SH3 domain protein D19	125000	34857900	291964	1	1	0.69869
Tax_id=10116 Similar to START domain containing 10	53820	34858808	195138	4	4	11.7526
Tax_id=10116 Similar to Selective hybridizing clone	164100	34856144	203612	6	17	14.8876
Tax_id=10116 Similar to Semaphorin SubclaSS 4 member G	128000	34863455	222218	1	1	0.94991
Tax_id=10116 Similar to Serine/threonine kinaSe	179600	34874060	212247	1	1	0.4914
Tax_id=10116 Similar to Serologically defined breaSt cancer antigen 84	49120	34860248	275347	12	12	29.2237
Tax_id=10116 Similar to Short chain dehydrogenaSe reductaSe 9	40410	34866289	268103	2	2	5.9783
Tax_id=10116 Similar to Sialic-acid O-acetylSteraSe	56760	34863093	198275	1	1	2.3483
Tax_id=10116 Similar to Sidekick 2	185200	34875033	275767	1	1	0.59737
Tax_id=10116 Similar to Sideroflexin 2	38820	34863716	229993	2	2	7.2254
Tax_id=10116 Similar to Sif and Tiam1-like exchange factor	155900	34853702	204958	1	1	0.78684
Tax_id=10116 Similar to Signal recognition particle 68kDa	73120	34875372	300246	3	3	5.6923
Tax_id=10116 Similar to SlingShot 1	178100	34872826	271907	9	9	7.9751
Tax_id=10116 Similar to Solute carrier family 26, member 9	150000	34879705	268665	7	7	6.1901
Tax_id=10116 Similar to Solute carrier family 30 (zinc transPorter), member 6	51480	34862482	294808	1	1	3.4483
Tax_id=10116 Similar to Spectrin beta chain, brain 1 (Spectrin, non-erythroid beta chain 1) (Beta-II Spectrin) (Fodrin beta chain)	278400	34879632	300121	67	76	40.3407
Tax_id=10116 Similar to Stabilin-1	285900	34876981	262547	4	4	2.218
Tax_id=10116 Similar to Stabilin-2	93660	34864902	206065	7	7	12.5721
Tax_id=10116 Similar to Structural maintenance of chromoSomeS 1beta	147300	34867523	216707	1	1	1.1032
Tax_id=10116 Similar to SulfataSe modifying factor 2	25680	34872061	221314	2	2	11.7904
Tax_id=10116 Similar to Sulfide quinone reductaSe-like	78570	34856819	285775	1	1	2.3121
Tax_id=10116 Similar to Syntaxin 16 (Syn16)	41580	34860874	234670	2	2	7.3569
Tax_id=10116 Similar to T-box 1	54510	34861377	314602	1	1	2.0576
Tax_id=10116 Similar to TAFII140 protein	85530	34876351	313782	1	1	1.3072

Tax_id=10116 Similar to TOB3	70420	34873064	239142	8	8	17.8914
Tax_id=10116 Similar to TRS85 homolog	150900	34878190	194979	2	2	1.9245
Tax_id=10116 Similar to TTF-1 interacting protein 5	183400	34862191	316025	1	1	0.72115
Tax_id=10116 Similar to Tetratricopeptide repeat protein 7 (TPR repeat protein 7)	102100	34862046	196091	2	2	2.4096
Tax_id=10116 Similar to Tm9Sf1 protein	89670	34874167	211728	10	10	16.3728
Tax_id=10116 Similar to Transcriptional co-activator CRSP7 homolog	114600	34877464	272267	4	4	5.782
Tax_id=10116 Similar to Transferrin receptor protein 2 (TfR2)	89250	34871536	315288	19	19	30.1235
Tax_id=10116 Similar to Trim26 protein	47090	34852035	264688	1	1	4.6229
Tax_id=10116 Similar to TyroSine-protein kinaSe JAK1 (JanuS kinaSe 1) (JAK-1)	150400	34869913	290958	1	1	1.1459
Tax_id=10116 Similar to UDP-N-acetyl-alpha-D-galactoSamine:polypeptide N-acetyl-galactoSaminyltranSferaSe 2	82140	34851891	307730	27	27	41.1202
Tax_id=10116 Similar to UDP-glucuronate decarboxylaSe 1	20220	34881188	201012	1	1	4.4944
Tax_id=10116 Similar to UNR-interacting protein (Serine-threonine kinaSe receptor-aSSociated protein)	48180	34858563	269251	1	1	1.5909
Tax_id=10116 Similar to Uroplakin Ia (UPIa) (UPKa)	52100	34855791	301709	4	4	7.8556
Tax_id=10116 Similar to Vinculin (Metavinculin)	135500	34868946	268838	13	13	14.2972
Tax_id=10116 Similar to WAVE2	41650	34871786	222802	1	2	8.5561
Tax_id=10116 Similar to WD repeat domain 9 iSoform A	225200	34881323	312923	1	1	0.55276
Tax_id=10116 Similar to aSpantly beta-hydroxylaSe	60560	34866138	213158	8	8	17.3664
Tax_id=10116 Similar to actin - Hydra attenuata	13310	34871187	219221	1	1	5.7851
Tax_id=10116 Similar to actin related protein 2/3 complex Subunit 2	34350	34876797	205076	12	12	48.6667
Tax_id=10116 Similar to actin-binding protein homolog ABP-278	284700	34869526	231012	34	35	20.3523
Tax_id=10116 Similar to acyl-Coenzyme A dehydrogenaSe family, member 8	28470	34866733	288241	2	2	8.365
Tax_id=10116 Similar to acyltranSferaSe family member (5G933)	33640	34862502	237775	1	1	3.4843
Tax_id=10116 Similar to aldehyde dehydrogenaSe family 7, member A1	57290	34879551	245155	3	3	8.0153
Tax_id=10116 Similar to alpha 3 type VI collagen iSoform 1 precuSor	357700	34877775	307227	3	3	1.1522
Tax_id=10116 Similar to alpha glucocidaSe II, beta Subunit	59240	34860445	208522	16	16	30.2857
Tax_id=10116 Similar to alpha(1)-inhibitor 3, variant I	168100	34858402	296398	12	34	30.0727
Tax_id=10116 Similar to alpha-2u-globulin	61070	34868545	210822	1	7	9.8148
Tax_id=10116 Similar to alpha-catenin-like protein	21080	34852606	311543	1	1	5.8824
Tax_id=10116 Similar to alpha-mannoSidaSe	45930	34860045	248855	13	13	40.2948
Tax_id=10116 Similar to aminoadipate-Semialdehyde Synthase	92010	34855019	258586	1	1	2.0507
Tax_id=10116 Similar to amylo-1,6-glucosidaSe, 4-alpha-glucanotranSferaSe iSoform 1	180900	34859913	208010	1	1	1.192
Tax_id=10116 Similar to apoA-I binding protein	78970	34857927	303449	1	1	2.5035
Tax_id=10116 Similar to archvillin	236900	34876218	258828	1	1	0.61205
Tax_id=10116 Similar to arginine-rich, mutated in early Stage tumorS	26400	34865887	195759	12	12	37.8261
Tax_id=10116 Similar to autocrine motility factor receptor	68280	34851252	285136	1	1	3.1457
Tax_id=10116 Similar to bA261P9.2 (putative novel protein Similar to fly CG7340 and human putative aminopeptidaSe ZK353.6 in chromoSome 3 (EC 3.4.11.-))	99960	34860876	296511	1	1	1.6269

Tax_id=10116 Similar to band 7 protein (35.3 kD) (4N53)	39270	34863101	288335	12	15	47.7011
Tax_id=10116 Similar to beta1-Syntrophin	46920	34866568	190168	1	1	5.2506
Tax_id=10116 Similar to bile acid Coenzyme A: amino acid N-acyltranSferaSe	47980	34868484	273878	6	6	20.5479
Tax_id=10116 Similar to biotinidaSe	62250	34877005	196365	2	2	4.8301
Tax_id=10116 Similar to breakpoint cluSter region protein	177200	34852435	289382	1	1	0.50441
Tax_id=10116 Similar to bromodomain-containing protein BRD4 Short variant	159800	34862361	292562	1	1	0.62805
Tax_id=10116 Similar to bullouS pemphigoid antigen 1-b	1087000	34874618	233230	1	1	0.083005
Tax_id=10116 Similar to cDNA Sequence BC017158	51280	34859365	318242	2	2	8.0338
Tax_id=10116 Similar to cDNA Sequence BC030934	81010	34853075	266866	7	7	12.9655
Tax_id=10116 Similar to carbohydrate (chondroitin) Synthase 2	65060	27681143	278143	2	2	2.4955
Tax_id=10116 Similar to centromere/kinetochore protein zw10 homolog	88170	34863346	192125	5	5	9.7686
Tax_id=10116 Similar to chorein iSoform B	254800	34861677	218802	4	4	3.5952
Tax_id=10116 Similar to chromoSome 14 open reading frame 9	34520	34869712	209283	1	1	3.3846
Tax_id=10116 Similar to chromoSome 17 open reading frame 27	668500	34875599	199223	1	1	0.20315
Tax_id=10116 Similar to chromoSome 20 open reading frame 116	36120	34858705	275755	3	3	15.2381
Tax_id=10116 Similar to coat protein gamma-cop	138100	34856387	267886	42	44	48.0226
Tax_id=10116 Similar to coatomer protein complex Subunit alpha	139100	34860938	293534	72	72	67.3155
Tax_id=10116 Similar to cobl-related 1	135100	34854739	289448	3	3	3.0087
Tax_id=10116 Similar to coiled-coil protein	148900	34869656	304228	1	1	1.2298
Tax_id=10116 Similar to collagen alpha1 type VI-precursor	112800	34852376	201969	7	7	8.4826
Tax_id=10116 Similar to collagen type XIV	169900	34866496	308317	9	9	8.344
Tax_id=10116 Similar to complement component 8 alpha Subunit	62090	34869994	295319	1	1	5.1376
Tax_id=10116 Similar to complement component 8 beta Subunit	64810	34869943	204172	6	6	14.7368
Tax_id=10116 Similar to complement component factor h	43820	34880509	275354	2	2	5.0761
Tax_id=10116 Similar to copine III	59690	34867199	274130	2	2	4.6904
Tax_id=10116 Similar to copine IV	96010	34865971	245798	1	1	0.81301
Tax_id=10116 Similar to cyfokeratin	47590	34855041	245216	4	18	45.1537
Tax_id=10116 Similar to dJ14N1.2 (novel S-100/CaBP type calcium binding domain protein, Similar to trichohyalin)	133800	34858169	280707	1	1	0.96154
Tax_id=10116 Similar to dedicator of cyto-kineSIS 2	113200	34861140	200712	1	1	1.417
Tax_id=10116 Similar to development- and differentiation-enhancing factor 2	119200	34863212	230447	1	1	0.74697
Tax_id=10116 Similar to dolichyl-phoSphate beta-glucoSyltranSferaSe-like	47020	34856938	304061	2	2	5.9809
Tax_id=10116 Similar to eSteraSe 10	42940	34874491	305590	3	3	14.0992
Tax_id=10116 Similar to embryonic blasTocoelar extracellular matrix protein precursor	242800	34851569	303538	1	1	0.59199
Tax_id=10116 Similar to endophilin B1b	47410	34860931	263938	2	2	5.6471
Tax_id=10116 Similar to endoplasmic oxidoreductase 1 beta	57800	34876487	282876	4	5	11.4786
Tax_id=10116 Similar to erythrocyte band 7 integral membrane protein, protein 7.2B, Stomatatin	61240	34853860	265569	7	7	14.3646
Tax_id=10116 Similar to eukaryotic tranSlation initiation factor 3, Subunit 5 epSilon, 47kDa	35120	34858904	213255	1	1	5.7576

Tax_id=10116 Similar to eukaryotic translocation initiation factor 4G I	175000	34869741	239406	6	6	4.2112
Tax_id=10116 Similar to exoStoSeS (multiple) 2	93370	34856569	247469	2	2	3.4063
Tax_id=10116 Similar to expeSSed Sequence A1788959	65670	34876789	217594	13	17	34.4948
Tax_id=10116 Similar to family 4 cytochrome P450	66360	34878473	250367	6	6	16.6378
Tax_id=10116 Similar to ferrochelatase	71200	34932061	313806	1	1	1.9139
Tax_id=10116 Similar to glucan (1,4-alpha-), branching enzyme 1	43080	34867430	216271	3	3	9.2593
Tax_id=10116 Similar to glutaryl-CoA dehydrogenase precursor	49330	34851534	270372	2	2	6.5169
Tax_id=10116 Similar to glyoxylate reductase/hydroxypyruvate reductase	34140	34935094	265523	6	6	25.6329
Tax_id=10116 Similar to golgi phosphoprotein 4	73200	34857091	237211	26	26	43.68
Tax_id=10116 Similar to gp250 precursor	209000	34863171	283274	2	2	1.5516
Tax_id=10116 Similar to group XIII secreted phospholipase A2	25660	34882179	272967	4	4	25
Tax_id=10116 Similar to heterogeneous nuclear ribonucleoprotein D-like	58310	34876235	191966	1	2	4.1431
Tax_id=10116 Similar to histidyl-tRNA synthetase-like	82680	34878791	223302	1	1	0.96286
Tax_id=10116 Similar to hyaluronan receptor for endocytosis HARE precursor	58970	34868786	260956	1	4	9.6296
Tax_id=10116 Similar to hypothetical protein	97420	34861994	213193	7	7	11.5875
Tax_id=10116 Similar to hypothetical protein	103500	34864996	301836	2	2	3.388
Tax_id=10116 Similar to hypothetical protein	390800	34853159	241253	1	1	0.17361
Tax_id=10116 Similar to hypothetical protein	125800	34878417	272431	1	1	1.5233
Tax_id=10116 Similar to hypothetical protein	141900	34854842	233766	1	1	0.99923
Tax_id=10116 Similar to hypothetical protein 5832424M12	89010	34853466	213390	2	2	5.3086
Tax_id=10116 Similar to hypothetical protein 9930107J06	79800	34851601	290038	3	3	7.1023
Tax_id=10116 Similar to hypothetical protein BC002942	96350	34867679	290052	1	1	1.4134
Tax_id=10116 Similar to hypothetical protein CL25084	60710	34879636	242521	3	3	8.8889
Tax_id=10116 Similar to hypothetical protein D4Ertid765e	42320	34870159	200143	2	2	6.8354
Tax_id=10116 Similar to hypothetical protein E130308H01	113900	34865376	283779	2	2	2.7495
Tax_id=10116 Similar to hypothetical protein FLJ10375	107600	34866614	302504	1	1	1.7895
Tax_id=10116 Similar to hypothetical protein FLJ10737	91330	34872498	233304	1	1	1.7073
Tax_id=10116 Similar to hypothetical protein FLJ10849	58770	34876531	204932	2	2	5.5985
Tax_id=10116 Similar to hypothetical protein FLJ10890	138100	34856577	278036	2	2	1.9656
Tax_id=10116 Similar to hypothetical protein FLJ10900	93700	34872027	198580	1	1	1.8072
Tax_id=10116 Similar to hypothetical protein FLJ11274	34120	34866189	272995	1	1	5.5901
Tax_id=10116 Similar to hypothetical protein FLJ12681	90650	34870562	205672	1	1	2.4814
Tax_id=10116 Similar to hypothetical protein FLJ14681	65310	34858680	304442	1	1	1.2153
Tax_id=10116 Similar to hypothetical protein FLJ20531	57240	34871405	217607	1	1	1.938
Tax_id=10116 Similar to hypothetical protein FLJ20627	40260	34853516	295521	2	2	7.2626
Tax_id=10116 Similar to hypothetical protein FLJ21665	52020	34876595	213091	1	4	8.4233
Tax_id=10116 Similar to hypothetical protein FLJ21820	32850	34863103	317090	1	1	6.2284

Tax_Id=10116 Similar to hypothetical protein FLJ21963	91790	34865010	243174	1	1	1	2.1635
Tax_Id=10116 Similar to hypothetical protein FLJ30373	29880	34855399	229721	1	1	1	2.9197
Tax_Id=10116 Similar to hypothetical protein FLJ30596	61060	34854388	283019	1	1	1	2.5641
Tax_Id=10116 Similar to hypothetical protein FLJ31657	64050	34855501	263349	1	1	1	2.385
Tax_Id=10116 Similar to hypothetical protein MGC15523	132100	34875626	304037	12	12	12	14.4608
Tax_Id=10116 Similar to hypothetical protein MGC23920	24660	34889196	243905	4	4	4	22.87
Tax_Id=10116 Similar to hypothetical protein MGC26706	19680	34880064	228294	4	4	4	28.6585
Tax_Id=10116 Similar to hypothetical protein MGC37818	19860	34861397	316589	3	3	3	20.9302
Tax_Id=10116 Similar to hypothetical protein MGC38524	121800	34877564	273384	12	12	12	12.2109
Tax_Id=10116 Similar to hypothetical protein from EUROIMAGE 2021883	75830	34862247	195586	13	13	13	18.5294
Tax_Id=10116 Similar to immunoglobulin 4G6 light chain variable region	17890	34855968	195860	1	1	1	9.3168
Tax_Id=10116 Similar to inner membrane protein, mitochondrial (mitofilin)	82360	34855983	247605	22	22	22	39.4879
Tax_Id=10116 Similar to integrin alpha v Subunit	114700	34856480	299926	3	3	3	3.3816
Tax_Id=10116 Similar to intracellular membrane-associated calcium-independent phospholipase A2 gamma	107800	34865151	313999	1	1	1	0.62435
Tax_Id=10116 Similar to kidney ankyrin repeat-containing protein	127000	34860436	261449	1	1	1	1.1036
Tax_Id=10116 Similar to kinesin family protein KIF1a	218300	34877667	265199	2	2	2	1.0808
Tax_Id=10116 Similar to IdBP	110800	34875017	282341	2	2	2	2.4024
Tax_Id=10116 Similar to lectin, mannosyl-binding 2-like	44440	34875582	221907	3	3	3	8.9286
Tax_Id=10116 Similar to lipoprotein receptor-related protein	517200	34865759	268163	58	58	58	17.1815
Tax_Id=10116 Similar to lysosomal aspartylase-like 1	40920	34874392	217901	1	1	1	2.5496
Tax_Id=10116 Similar to lymphocyte cytosolic protein 1	80290	34875362	272629	1	3	3	4.8679
Tax_Id=10116 Similar to mKIAA0384 protein	101400	34856482	193681	2	2	2	3.0837
Tax_Id=10116 Similar to mKIAA0678 protein	96130	34865848	276172	2	2	2	3.7166
Tax_Id=10116 Similar to mKIAA1402 protein	86520	34853978	259133	1	1	1	2.0619
Tax_Id=10116 Similar to macrophage hemoglobin scavenger receptor CD163 precursor	119500	34858425	192759	2	2	2	2.3423
Tax_Id=10116 Similar to macrophage mannosylase receptor precursor	192400	34877265	296460	31	31	31	20.9166
Tax_Id=10116 Similar to malignant cell expression-enhanced gene/tumor progression-enhancer	33720	34854458	281230	1	1	1	7.1661
Tax_Id=10116 Similar to mannosyl-oligosaccharide alpha-1,2-mannosidase	31910	27705330	273814	12	12	12	42.953
Tax_Id=10116 Similar to medium-chain acyl-CoA synthetase	22360	34859067	258281	5	5	5	36
Tax_Id=10116 Similar to meiotic recombination protein REC14	28800	34863419	201803	1	1	1	6.2016
Tax_Id=10116 Similar to melanoma inhibitory activity protein 2	58930	34865264	225113	1	1	1	4
Tax_Id=10116 Similar to membrane receptor (5H375)	42380	34865609	318262	1	1	1	4.8649
Tax_Id=10116 Similar to methionyl aminopeptidase 1	53240	34860820	221417	1	1	1	2.3109
Tax_Id=10116 Similar to microtubule-associated protein 4	303100	34866431	264572	2	2	2	1.0892
Tax_Id=10116 Similar to mitochondria-associated granulocyte macrophage CSF signaling molecule	13800	27667166	288315	2	2	2	33.6
Tax_Id=10116 Similar to modifier of cell adhesion	227300	34865889	203448	2	2	2	0.90589

Tax_Id=10116 Similar to myoSin X	251600	34855017	249318	1	1	0.27347
Tax_Id=10116 Similar to myoSin heavy chain	229700	34869316	230006	2	2	0.7996
Tax_Id=10116 Similar to neuroblaStoma-amplified protein	163800	34863169	193119	3	3	2.9594
Tax_Id=10116 Similar to nicotinamide nucleotide tranSHydrogenaSe	120200	34854180	202296	22	22	24.1652
Tax_Id=10116 Similar to nondialthin coat protein zeta2-COP	18220	34873491	273036	1	1	6.0241
Tax_Id=10116 Similar to o-methyltranSferaSe family member (5C530)	24490	34868938	291365	3	3	20.1794
Tax_Id=10116 Similar to oSmotic StreSS protein	148000	34856875	290180	1	4	2.9456
Tax_Id=10116 Similar to oSteoclaSt inhibitory lectin	23540	34858508	255984	1	1	5.7971
Tax_Id=10116 Similar to oxySterol 7alpha-hydroxyylaSe	61430	34874781	201379	9	9	28.3054
Tax_Id=10116 Similar to p140mDia	140200	34878815	217100	1	1	1.0293
Tax_Id=10116 Similar to p53 inducible protein	164400	34870680	289228	3	14	12.3682
Tax_Id=10116 Similar to peptidyprolyl iSomerase D (cyclophilin D)	69130	34873471	283106	1	1	1.9324
Tax_Id=10116 Similar to phoSphatidylnoSitolglycan claSS N	89310	34878866	217052	1	1	2.0356
Tax_Id=10116 Similar to polioviruS receptor homolog	76950	34855325	279332	1	1	1.6925
Tax_Id=10116 Similar to probable nocturnin protein	16650	34861866	309047	2	2	6.8493
Tax_Id=10116 Similar to probable tranSMembrane protein FT27 - mouSe	39180	34877387	206786	5	5	20
Tax_Id=10116 Similar to procollagen, type VI, alpha 2	122100	34852378	258657	2	2	2.2867
Tax_Id=10116 Similar to programmed cell death 6 interacting protein	70550	34866400	306730	2	2	3.937
Tax_Id=10116 Similar to proline dehydrogenaSe (oxidaSe) 2	51070	34855688	288034	2	2	7.1895
Tax_Id=10116 Similar to protein 4.1, p4.1 - mouSe	105500	34871764	306783	2	2	3.148
Tax_Id=10116 Similar to protein RAKc	41260	34876322	249119	1	2	8.9136
Tax_Id=10116 Similar to protein tyroSine phoSphataSe, receptor type, D iSoform 3 precuSor	203600	34869007	215340	1	1	0.82827
Tax_Id=10116 Similar to putative mannoSyltranSferaSe	59900	34867585	231757	1	1	2.0638
Tax_Id=10116 Similar to putative protein, with at leaSt 6 tranSMembrane domains, of ancient origin (58.5 kD) (3N884)	65350	34865136	269355	3	3	5.7793
Tax_Id=10116 Similar to putative zinc finger tranScription factor OVO1	37260	27661858	294340	1	1	2.1407
Tax_Id=10116 Similar to regulator of nonSenSe tranScriptS 1	47750	34877805	234739	3	3	7.3227
Tax_Id=10116 Similar to repreSSor of eStrogen receptor activity	33420	34858436	262284	16	16	64.214
Tax_Id=10116 Similar to retinal Short-chain dehydrogenaSe/reductaSe	43630	34872444	294993	1	1	3.7783
Tax_Id=10116 Similar to riboSomal protein L27	22160	34875503	301863	1	1	10.8808
Tax_Id=10116 Similar to riboSomal protein S15	50300	34851670	224899	1	1	2.6316
Tax_Id=10116 Similar to riboSomal protein S5	29840	34854534	278725	14	14	48.8636
Tax_Id=10116 Similar to riboSomal protein S6 kinaSe, 52kDa, polypeptide 1	40530	34881360	216365	1	1	2.4064
Tax_Id=10116 Similar to riboSomal protein S6 kinaSe, polypeptide 4	86910	34935429	292778	1	1	1.5524
Tax_Id=10116 Similar to ring finger protein 20	122200	34868389	236982	1	1	0.66794
Tax_Id=10116 Similar to talin 2	284500	34864297	199727	2	5	2.0677
Tax_Id=10116 Similar to teStiS protein TEX15	282400	34866738	211558	1	1	0.67891

Tax_id=10116 Similar to the firSt amino acid waS determined to be iSoleucine rather than methionine by comparSon to mTEF1 (aSeSSion # L13853)	78480	34858488	267553	1	1	1.1065
Tax_id=10116 Similar to thyroid hormone receptor interactor 11	115700	34867565	247636	3	3	3.2129
Tax_id=10116 Similar to tolloid-like 2	23740	34883204	298591	1	1	5.5556
Tax_id=10116 Similar to tranSgelin 2	29970	34880944	266044	6	6	30.9701
Tax_id=10116 Similar to tranSthyretin (4L369)	16010	34861187	199559	1	1	11.3475
Tax_id=10116 Similar to tricarboxylate carrier	40660	34873877	278396	1	9	34.1463
Tax_id=10116 Similar to tropomodulin 3	46420	34864364	261414	5	5	18.8862
Tax_id=10116 Similar to tubulin, alpha 6	63060	34868254	298819	1	19	46.4664
Tax_id=10116 Similar to ubiquitin ligaSe E3 alpha-II	175300	34874398	274677	1	1	0.71244
Tax_id=10116 Similar to ubiquitous tetratricopeptide containing protein RoXaN	111900	34867257	230656	1	1	1.407
Tax_id=10116 Similar to uridindiphoSphoglucoSepyrophoSphorylaSe 2	89950	34879163	225159	12	12	19.7304
Tax_id=10116 Similar to vaScular endothelial zinc finger 1	82930	34872980	252804	1	1	3.0144
Tax_id=10116 Similar to veSicle tranSport through interaction with t-SNARES 1B homolog	35940	34866243	241548	2	2	6.9401
Tax_id=10116 Similar to villin-like protein	99190	34866628	253969	1	1	1.2458
Tax_id=10116 Similar to xylulokinaSe homolog	66490	34866669	229118	1	1	2.6016
Tax_id=10116 Similar to zinc finger protein 294	196200	34867507	309532	2	2	1.3196
Tax_id=10116 Similar to zinc finger protein, Subfamily 1A, 4	64460	34862217	313581	1	1	1.528
Tax_id=10116 Similar to zinc tranSporter 5	71030	34853639	259074	3	3	8.1538
Tax_id=10116 Similar to zinc tranSporter like 2	57350	34859877	257320	2	2	4.8638
Tax_id=10116 Solute carrier family 25, member 5	32900	728810	117684	1	16	50
Tax_id=10116 Syntaxin-7	29790	3152727	109585	3	3	14.9425
Tax_id=10116 T-complex protein 1, delta subunit	58100	52000745	166356	9	9	23.0056
Tax_id=10116 Thioredoxin	11670	57386	12218	3	3	22.8571
Tax_id=10116 Transitional endoplasmic reticulum ATPase	89350	641973	125172	46	46	63.7717
Tax_id=10116 Tropomyosin 4	28510	763182	44422	2	3	14.5161
Tax_id=10116 Tyrosine 3-monooxygenase/TrypTophan 5-monooxygenase acTiVaTion proTein, beTa polypepTide	28050	9507243	47331	4	8	40.2439
Tax_id=10116 Vanin 1	107100	34852937	310121	5	5	8.4995
Tax_id=10116 Vesicle-associated membrane protein-associated protein B	26920	4240464	57726	5	6	34.1564
Tax_id=10116 Vimentin	53730	57480	82925	2	2	5.794
Tax_id=10116 Von Willebrand factor	289700	34858467	251407	3	3	1.3611
Telomerase protein component 1 rTLP1 Telomerase-associated protein 1 Telomerase protein 1 p240 p230 p80 telomerase homolog	291700	47606056	169376	1	1	0.38037
Testis-specific farnesyl pyrophosphate synthetase	40800	37590777	78213	4	4	13.5977
Tetraspanin-31 Tspan-31 Sarcoma amplified sequence homolog	22660	62900748	260364	1	1	6.1905
Thioredoxin-related transmembrane protein 2	33870	56090369	227628	1	1	4.0678
Tissue-type transglutaminase	76930	9507185	47311	22	22	44.0233

Tmem32 protein 12 days embryo spinal cord cDNA, RIKEN full-length enriched library, clone:C530026I01 product: hypothetical protein, full insert sequence 10 days neonate cortex cDNA, RIKEN full-length enriched library, clone:A830005F13 product: weakly similar to CG15168 PROTEIN 16 days neonate cerebellum cDNA, RIKEN full-length enriched library, clone:9630048L06 product: weakly similar to CG15168 protein RE09053p	14680	27710182	244941	2	2	34.3511
Torsin-1A-interacting protein 2	61700	81885310	313574	2	2	5.3633
Torsin-2A precursor Torsin family 2 member A	35870	81884643	231792	2	2	9.3458
TorsinA	37980	22651450	188125	7	7	24.3243
Tpi1 protein	26720	38512111	340135	8	8	53.629
Tpst1 protein	42140	76779364	241393	9	9	33.5135
Trafficking protein particle complex subunit 3 BET3 homolog	20300	71153350	145735	1	1	7.2222
Trans-golgi network protein 1	38300	71051654	31491	10	10	38.9356
Transaldolase	37480	17433174	50402	1	1	2.9674
Transcobalamin-2 precursor Transcobalamin II TCII TC II	47420	5910985	90533	1	1	3.2787
Transcriptional activator protein PUR-alpha Purine-rich single-stranded DNA-binding protein alpha	34880	34878862	81816	4	4	21.8069
Transforming protein RhoA precursor	21780	47605935	76408	5	7	49.2228
Transketolase	67640	1729977	38668	32	32	59.39
Translocation-associated membrane protein 1	43030	81883693	275946	2	2	6.6845
Translocon-associated protein subunit alpha precursor TRAP-alpha Signal sequence receptor subunit alpha SSR-alpha Liver regeneration-related protein LRRG137	35630	71162390	166245	4	4	18.1818
Translocon-associated protein subunit delta precursor TRAP-delta Signal sequence receptor subunit delta SSR-delta	18980	8394364	152155	6	6	36.9942
Translocon-associated protein subunit gamma TRAP-gamma Signal sequence receptor subunit gamma SSR-gamma	21060	62906894	98326	2	2	12.973
Transmembrane 9 superfamily protein member 3 precursor	67540	34862730	140307	18	18	27.7683
Transmembrane and coiled-coil domain-containing protein 1	21170	81882981	91768	3	3	19.6809
Transmembrane emp24 domain-containing protein 10 precursor Transmembrane protein Tmp21 21 kDa transmembrane-trafficking protein	24860	62906896	60418	12	12	44.2922
Transmembrane emp24 domain-containing protein 2 precursor Membrane protein p24A RNP21.4	22730	3914232	78146	11	11	41.791
Transmembrane emp24 domain-containing protein 3 precursor	25510	62901119	305262	2	2	8.5973
Transmembrane emp24 domain-containing protein 5 precursor	26140	62287552	228279	7	7	25.3275
Transmembrane emp24 protein transport domain containing 9	27030	57528337	285748	13	14	46.383
Transmembrane protein 109 precursor Mitsugumin-23 Mg23	26240	81884639	282006	2	2	7.4074
Transmembrane protein 111	29980	71153386	63169	7	7	32.1839
Transmembrane protein 14C p11	11780	27734399	30411	1	1	25.2174
Transmembrane protein 33 DB83 protein	27980	4579688	137142	6	6	23.4818
Transmembrane protein induced by tumor necrosis factor alpha	40660	58219512	260939	1	1	4.9563
Transferrin precursor	15720	57425	31553	9	9	67.3469
Tricarboxylate transport protein, mitochondrial precursor Citrate transport protein C1P Tricarboxylate carrier protein Solute carrier family 25 member 1	33840	8394297	69776	6	6	21.2219

Trifunctional enzyme subunit alpha, mitochondrial precursor TP-alpha Long-chain enoyl-CoA hydratase Long chain 3-hydroxyacyl-CoA dehydrogenase	82510	510108	82392	32	32	52.6868
Trifunctional enzyme subunit beta, mitochondrial precursor TP-beta 3-ketoacyl-CoA thiolase Acetyl-CoA acyltransferase Beta-ketothiolase	51410	510110	43581	16	16	40.2105
Tripartite motif protein 25	71950	57164029	318709	2	2	4.1991
Tripeptidyl-peptidase 1 precursor Tripeptidyl-peptidase I TPP-I Tripeptidyl aminopeptidase	61330	20140356	75921	1	1	2.4867
Tropomyosin 5	28950	9653293	93198	4	5	17.7419
Tryptophan 2,3-dioxygenase	47860	59809151	11402	1	1	3.6946
Tubulin alpha-1 chain Alpha-tubulin 1 Testis-specific alpha-tubulin Tubulin H2-alpha	49920	55741524	31436	3	17	51.1161
Tubulin, beta polypeptide Beta 5-tubulin TUBB protein	49670	56754676	62620	3	21	64.8649
Tubulin, beta, 2	49800	40018568	270901	5	21	65.1685
Tumor protein, translationally-controlled 1 2 days neonate thymus thymic cells cDNA, RIKEN full-length enriched library, clone:E430014B07 product:tumor protein, translationally-controlled 1, full insert sequence CRL-1722 L5178Y-R cDNA, RIKEN full-length enriched library, clone:I730061H02 product:tumor protein, translationally-controlled 1, full insert sequence TIB-55 BB88 cDNA, RIKEN full-length enriched library, clone:I730042C17 product:tumor protein, translationally-controlled 1, full insert sequence 13 days pregnant adult female placenta cDNA, RIKEN full-length enriched library, clone:I530012I04 product:tumor protein, translationally-controlled 1, full insert sequence 5 days embryo whole body cDNA, RIKEN full-length enriched library, clone:I0C0031O13 product:tumor protein, translationally-controlled 1, full insert sequence Bone marrow macrophage cDNA, RIKEN full-length enriched library, clone:I830086J22 product:tumor protein, translationally-controlled 1, full insert sequence Bone m	19460	687712	38212	2	2	15.1163
Tumor-related protein Adult male medulla oblongata cDNA, RIKEN full-length enriched library, clone:6330565A20 product:Tumor-related protein (Hypothetical protein), full insert sequence Isochorismatase domain containing 1	32030	62664482	8904	1	1	4.7138
Type 2 lactosamine alpha-2,3-sialyltransferase CMP-NeuAc:beta-galactoside alpha-2,3-sialyltransferase VI ST3Gal VI Sialyltransferase 10	38140	48428498	722796	8	8	23.2628
Type I hair keratin KA27	45970	62656979	230035	2	9	21.2871
Type I keratin KA17	48120	71682170	301880	1	7	13.6259
Type I keratin KA22	50210	57012446	161849	1	4	10.6195
Type II keratin Kb15	57610	46485029	222258	1	8	11.2782
Tyrosine-protein kinase LYN	58660	294583	71712	1	2	4.6875
UDP glycosyltransferase 1 family polypeptide A1 UDP-glucuronosyltransferase 1A1	59660	695162	43597	10	19	42.0561
UDP glycosyltransferase 1 family polypeptide A7 UDP glycosyltransferase 1 family, polypeptide A6	60240	89276780	205347	1	22	51.6981
UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 1	37990	34854866	56042	10	10	33.7423
UDP-glucose 6-dehydrogenase UDP-Glc dehydrogenase UDP-GlcDH UDPGDH	54890	6136118	75904	4	4	15.213
UDP-glucose glycoprotein glucosyltransferase 1 precursor UDP-glucose ceramide glucosyltransferase-like 1 UDP-Glc:glycoprotein glucosyltransferase RUGT	174000	7677176	171823	55	55	49.0504
UDP-glucuronic acid decarboxylase 1 UDP-glucuronate decarboxylase 1 UGD UXS-1	47500	21326465	86062	3	3	14.0476
UDP-glucuronosyltransferase 1A5	60010	18308168	53066	8	17	38.0414
UDP-glucuronosyltransferase 1A6	60250	1890306	53068	1	22	51.6981
UDP-glucuronosyltransferase 1A7	59610	18308176	53069	4	13	33.145

UDP-glucuronosyltransferase 2B1 precursor, microsomal	60480	27545358	31600	17	20	51.2287
UDP-glucuronosyltransferase 2B12 precursor, microsomal	60920	458397	127236	1	15	40.9434
UDP-glucuronosyltransferase 2B2 precursor, microsomal	60990	207583	78055	2	21	50.9434
UDP-glucuronosyltransferase 2B3 precursor UDPGT Testosterone, dihydrotestosterone, and beta-estradiol specific 17-beta-hydroxysteroid specific UDPGTR-3 RLUG38	60520	31543923	31602	4	25	63.2075
UDP-glucuronosyltransferase 2B3 precursor, microsomal	60600	92287	84217	2	23	54.5283
UDP-glucuronosyltransferase 2B4 precursor UDPGT UDP-glucuronosyltransferase 2B12	61060	549157	80303	4	19	42.4528
UDP-glucuronosyltransferase 2B5 precursor UDPGT 17-beta-hydroxysteroid specific UDPGT-5	60590	55925581	31603	11	21	55.4717
UDP-glucuronosyltransferase R-21 UDPGT-21	18010	6981690	22316	1	1	7.5949
Ube2i-prov protein						
Ube2i3 protein Ubiquitin-conjugating enzyme E2L 3 Bladder RCB-0544 MBT-2 cDNA, RIKEN full-length enriched library, clone:G430072O21 product:ubiquitin-conjugating enzyme E2L 3, full insert sequence	17860	62658232	54899	2	2	24.026
Ubiquinol-cytochrome c reductase complex 11 kDa protein, mitochondrial precursor Mitochondrial hinge protein Cytochrome C1, nonheme 11 kDa protein Complex III subunit VIII	10420	62511137	277765	2	2	37.0787
Ubiquinol-cytochrome c reductase core protein I	52850	51948476	220138	15	15	37.7083
Ubiquinol-cytochrome c reductase core protein II	48400	55741544	139461	22	22	71.2389
Ubiquinol-cytochrome c reductase iron-sulfur subunit, mitochondrial precursor Rieske iron-sulfur protein RISP Liver regeneration-related protein LRRGT00195	29450	57114330	230682	8	8	27.3723
Ubiquinone biosynthesis protein COQ7 homolog Coenzyme Q biosynthesis protein 7 homolog	20140	7446711	30131	1	1	6.1453
Timing protein clk-1 homolog						
Ubiquitin specific protease 1 Predicted	87330	62543525	282121	1	1	1.0204
Ubiquitin-conjugating enzyme E2 G2 Ubiquitin-protein ligase G2 Ubiquitin carrier protein G2	18570	62665819	58922	1	1	14.5455
Ubiquitin-conjugating enzyme E2 N Ubiquitin-protein ligase N Ubiquitin carrier protein N Bendless-like ubiquitin-conjugating enzyme	17120	77417616	12328	2	2	20.3947
Ubiquitin-conjugating enzyme E2 variant 1 NOD-derived CD11c +ve dendritic cells cDNA, RIKEN full length enriched library, clone:F630102O04 product:ubiquitin-conjugating enzyme E2 variant 1, full insert sequence Adult inner ear cDNA, RIKEN full-length enriched library, clone:F930043P20 product:ubiquitin-conjugating enzyme E2 variant 1, full insert sequence	16350	62660106	82822	2	2	13.6054
Unc-13 homolog D Munc13-4						
Unc-13 homolog D Munc13-4	123500	5524667	20725	2	2	1.5625
Uncharacterized hematopoietic stem/progenitor cells protein MDS029 homolog	12100	27675590	164032	4	4	42.5926
Uncharacterized protein C20orf30 homolog	13200	81882492	190070	1	1	9.1667
Uncharacterized protein family UPF0227 member RGD1359682	33990	55741536	265453	1	1	4.5161
Up-regulated during skeletal muscle growth protein 5 Diabetes-associated protein in insulin-sensitive tissues	6408	81868653	171802	4	4	44.8276
Urinary protein 1 precursor RUP-1 Liver regeneration-related protein LRRG05	10960	6537316	37481	1	1	10.8911
Uroporphyrinogen decarboxylase	40450	5524747	44446	1	1	6.044
VAC14	88070	29293817	173122	2	2	3.0651
Vacuolar ATP synthase subunit B, brain isoform V-ATPase B2 subunit Vacuolar proton pump B isoform 2 Endomembrane proton pump 58 kDa subunit	56550	55716047	55432	4	4	10.1761
Vacuolar protein sorting 26 Vesicle protein sorting 26	38110	78099277	276682	1	1	3.9755
Vacuolar protein sorting 33A	67510	23396893	55286	1	1	3.5176
Vacuolar protein sorting-associated protein 45 ryps45	64890	51858559	19366	3	3	9.2982

Vacuolar proton translocating ATPase 116 kDa subunit a isoform 1 V-ATPase 116 kDa isoform a1	96330	206430	11413	1	1	1,432
Clahtin-coated vesicle/synaptic vesicle proton pump 116 kDa subunit Vacuolar proton pump subunit 1	45900	38197344	31214	3	3	15,7635
Vacuolar adenosine triphosphatase subunit Act16	41590	51858574	140635	5	5	22,1607
Vacuole membrane protein 1 Transmembrane protein 49	21600	6647578	19913	12	14	66,1538
Vascular endothelial cell specific protein 11 Septin 2	70690	3183199	78154	37	37	63,2258
Ventral midline antigen VEMA	70750	6978435	3601	14	14	31,2977
Very-long-chain acyl-CoA synthetase VLCS Very-long-chain-fatty-acid-CoA ligase VLACS THCA-CoA ligase Fatty-acid-coenzyme A ligase, very long-chain 1 Long-chain-fatty-acid-CoA ligase Fatty acid transport protein 2 FATP-2 Solute carrier family 27 member 2	135400	7514116	26418	11	11	12,5701
Very-long-chain specific acyl-CoA dehydrogenase, mitochondrial precursor VLCAD	26170	81867205	111524	5	5	25,8772
Vesicle associated protein	25160	9719420	6158	5	5	23,0415
Vesicle transport protein SEC20	12690	6981614	38248	1	4	34,4828
Vesicle transport through interaction with t-SNAREs homolog 1A	11480	56789137	23581	1	4	38,835
Vesicle-associated membrane protein 3 VAMP-3 Synaptobrevin-3 Cellubrevin CEB	24780	9502258	3011	3	3	18,1818
Vesicle-associated membrane protein 7	27270	90110085	318845	8	9	42,562
Vesicle-associated membrane protein-associated protein A VAMP-associated protein A VAMP-A VAP-A 33 kDa Vamp-associated protein VAP-33	24740	71043604	41516	18	18	65,1163
Vesicle-trafficking protein SEC22b SEC22 vesicle-trafficking protein-like 1	40390	27682691	139706	22	22	62,0112
Vesicular integral-membrane protein VIP36 precursor	141600	46397078	26167	32	54	48,1073
Vigilin High density lipoprotein-binding protein HDL-binding protein	17780	62511143	291525	1	1	11,1801
Vitamin K epoxide reductase complex subunit 1 Vitamin K1 2,3-epoxide reductase subunit 1	19780	62511142	165266	1	1	6,25
Vitamin K epoxide reductase complex subunit 1-like protein 1 VKORC1-like protein 1	87480	6136262	78166	7	7	11,4776
Vitamin K-dependent gamma-carboxylase Gamma-glutamyl carboxylase Vitamin K gamma glutamyl carboxylase	51910	6981412	75051	3	3	8,4599
Vitamin K-dependent protein C precursor Autoprothrombin IIA Anticoagulant protein C Blood coagulation factor XIV Vitamin K-dependent protein C light chain Vitamin K-dependent protein C heavy chain Activation peptide	30760	8810245	11037	17	17	77,7385
Voltage-dependent anion channel 1 2 days neonate thymus thymic cells cDNA, RIKEN full-length enriched library, clone:E430005O12 product:voltage-dependent anion channel 1, full insert sequence 17 days embryo stomach cDNA, RIKEN full-length enriched library, clone:1920191D06 product:voltage-dependent anion channel 1, full insert sequence 17 days embryo kidney cDNA, RIKEN full-length enriched library, clone:1920170K05 product:voltage-dependent anion channel 1, full insert sequence 17 days embryo stomach cDNA, RIKEN full-length enriched library, clone:1920087C06 product:voltage-dependent anion channel 1, full insert sequence 17 days pregnant adult female amnion cDNA, RIKEN full-length enriched library, clone:1920043H09 product:voltage-dependent anion channel 1 full insert sequence	31750	8810247	5942	4	5	21,3559
Voltage-dependent anion-selective channel protein 2 VDAC-2 Outer mitochondrial membrane protein porin 2 B36-VDAC	30800	15214186	5943	7	8	42,7562
Voltage-dependent anion-selective channel protein 3	78230	14161099	72067	4	6	13,7063
XLalphas protein	146300	2144323	80445	1	1	0,90158
Xanthine dehydrogenase/oxidase	96790	71164811	189334	5	5	7,9861
Xylosyltransferase 2 Xylosyltransferase II Peptide O-xylosyltransferase 2	25210	38454214	262403	2	2	10,917
Yif1b protein						

Zero beta-1 globin	16020	818015	105606	3	9	67.3469
Zgc:92860	8218	74354458	4821	5	5	51.4286
Zinc-alpha-2-glycoprotein precursor	34020	6978565	3662	2	2	8.1081
acetyl-CoA acyltransferase, 3-oxo acyl-CoA thiolase A, peroxisomal	44780	6978429	3598	7	7	25.8065
adaptor protein complex AP-2, alpha 2 subunit [Rattus norvegicus]	104000	55729	37177	27	34	49.467
aldolase B [Rattus norvegicus]	39600	1619606	116234	30	31	84.3407
alpha-1-inhibitor III precursor	19360	554401	66447	1	6	54.4379
apolipoprotein C-III precursor - rat	11030	91990	84170	1	1	19
bile canaliculus-specific membrane glycoprotein precursor	90930	204464	11237	1	19	24.8737
cAMP-dependent protein kinase, alpha-catalytic subunit (PKA C-alpha)	40620	125207	168211	1	4	11.396
cathepsin C	52240	8393218	51414	3	3	7.5758
cathepsin J peak 2 [rats, liver, Peptide Partial, 34 aa]	3838	245685	79044	1	1	58.8235
claudin 1	22870	61889099	318701	1	1	7.5829
cytochrome P450	57160	203695	126560	1	38	85.2
cytochrome P450	57190	203803	126576	7	33	77.5794
cytochrome P450, family 2, subfamily c, polypeptide 23	56490	56825	78212	1	28	60.9312
cytochrome c oxidase subunit VIc	8455	203519	63749	4	5	69.7368
cytochrome-c oxidase (EC 1.9.3.1) chain VIIa, hepatic - rat (fragment)	1246	7513957	80282	1	1	80
dihydropyrimidinase	56830	3122039	78138	7	7	17.341
divalent cation tolerant protein CUTA	16410	61212255	281056	1	1	5.8442
ezrin, p81 [Rattus norvegicus]	18790	56126	85113	1	1	5.625
ferritin, heavy polypeptide 1	21100	6978859	3774	7	7	36.8132
fibrinopeptide A	1740	229210	22617	1	1	100
fibrinopeptide B	1492	229196	22616	1	1	100
fumarase	54460	227665	168825	1	7	25.8383
glutathione S-transferase Ya subunit	25560	204493	28289	2	15	57.2072
glycerol-3-phosphate dehydrogenase 1 (soluble) [Rattus norvegicus]	37400	3023880	80790	10	10	41.8338
heat-responsive protein 12	14290	2425030	153343	8	8	62.7737
hemoglobin beta chain, minor - rat	15990	92362	84237	1	17	89.7959
histone H2B	13770	223096	135066	2	5	41.6
hypertension-induced protein S-2 - rat (fragment)	11250	539959	130834	2	5	69.3069
hypothetical protein XP_223792	115600	34868956	241419	16	16	23.8498
hypothetical protein XP_343009	87580	34862025	301974	1	1	1.0256
hypothetical protein XP_343478	31580	34865907	203844	1	1	4.7138
hypothetical protein XP_344851	46260	34854602	287423	1	1	3.2483
hypothetical protein XP_347087	13870	34866914	300655	1	1	7.1429
immunoglobulin heavy chain [Rattus sp.]	51460	243866	79012	5	5	15.5319

immunoglobulin kappa-chain	14860	204835	126680	1	1	1	9.6296
kynureninase (L-kynurenine hydrolase)	52450	3913969	157223	1	1	1	2.8017
lanosterol synthase	83330	13591981	37206	1	12	12	20.191
lin-7-Ba [Rattus norvegicus]	19930	3885830	158790	2	3	3	18.6813
lysozyme homolog AT-2, bone - rat (fragments)	3164	539969	130837	2	2	2	100
major vault protein - rat	99530	7514005	132766	1	24	24	41.8994
mannose-binding protein C (liver)	26100	205263	44167	4	4	4	20.082
null	12780	51702801	4817	7	10	10	72.1739
p105 coactivator	99330	1800307	177421	41	41	41	49.2045
peroxisome assembly factor-2 [Rattus norvegicus]	104300	2911135	169183	6	6	6	7.9755
phosphatidylethanolamine binding protein [Rattus norvegicus]	20800	8393910	51562	4	4	4	36.8984
proteasome (prosome, macropain) subunit, beta type 4	25790	310214	78104	2	2	2	8.1897
ribosomal protein L13	24240	510552	37239	6	10	10	37.9147
ribosomal protein L6	33570	2507315	42185	11	15	15	42.0875
roundabout (axon guidance receptor, Drosophila) homolog 2 [Rattus norvegicus]	176100	34867440	317126	1	1	1	0.43559
secreted frizzled-related protein 1	35350	34879084	271324	1	1	1	2.5559
senescence marker protein 2A	33200	32964821	69809	4	9	9	39.4366
sialyltransferase 1	25210	285193	41195	1	7	7	40.6542
similar to EST AA408438	42480	27713571	204725	10	10	10	36.3395
similar to 2310009N05Rik protein	30570	34932411	197729	2	2	2	7.3801
similar to 2310036102Rik protein	89350	34932104	265519	1	1	1	1.995
similar to 40S RIBOSOMAL PROTEIN S17	15680	34853950	250506	10	10	10	62.5
similar to 40S ribosomal protein S2 [Rattus norvegicus]	28120	34868798	193682	1	12	12	41.9847
similar to 60S RIBOSOMAL PROTEIN L13	20290	27714695	312086	2	3	3	11.236
similar to 60S RIBOSOMAL PROTEIN L18	21470	34932167	248463	3	6	6	32.9787
similar to 60S ribosomal protein L15	23920	34869871	293440	1	7	7	33.0049
similar to 60S ribosomal protein L36	12250	34856346	214593	1	6	6	37.7358
similar to 9530008L14Rik protein [Rattus norvegicus]	11600	34875157	310564	1	1	1	7.9208
similar to ARP1 actin-related protein 1 homolog A; actin-related protein 1 alpha; actin-related protein 1 homolog A (yeast); Arp1 contractin alpha; Arp1 centractin alpha	62980	34865224	222641	2	3	3	9.364
similar to ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9), isoform 2	14750	27685029	262837	1	1	1	5.7554
similar to ATP-binding cassette sub-family E member 1 (RNase L inhibitor) (Ribonuclease 4 inhibitor) (RNS4I) (HuhP68) [Rattus norvegicus]	65360	34851575	255150	9	9	9	20.3098
similar to Ab2-095 [Rattus norvegicus]	79240	34865464	276652	13	13	13	22.9555
similar to Adapter-related protein complex 2 alpha 1 subunit (Alpha-adaptin A) (Adaptor protein complex AP-2 alpha-1 subunit) (Clathrin assembly protein complex 2 alpha-A large chain) (100 kDa coated vesicle protein A) (Plasma membrane adaptor HA2/... [Rattus norvegicus]	104000	34856047	219335	16	23	23	33.8266
similar to Apoptosis inhibitor 5	36870	34878251	281550	1	1	1	5.4545

similar to Asparaginyl-tRNA synthetase, cytoplasmic (Asparagine--tRNA ligase) (AsnRS)	64130	34932063	238208	1	1	2.6882
similar to BLOCK 23	30630	34869320	240773	1	2	6.2963
similar to CCTeta, eta subunit of the chaperonin containing TCP-1 (CCT)	59660	27712178	161408	14	14	36.3971
similar to CG33130-PA	125000	34870072	215152	1	1	0.86207
similar to CG4241-PA	35190	34877651	194839	3	3	17.2956
similar to CG8014-PA	126100	34865967	261337	2	2	2.4757
similar to CG8014-PA	55190	34865850	245025	1	1	2.3158
similar to CGI-90 protein	52100	34867201	258588	1	1	2.1598
similar to Calcium-binding mitochondrial carrier protein Aralar2 (Solute carrier family 25, member 13) (Cltrn)	15470	27708576	166641	7	7	70.1389
similar to Cappa1 protein	32910	34859736	230796	8	11	59.4406
similar to Cc1-3 [Rattus norvegicus]	162200	34872293	256290	5	5	4.2479
similar to Conserved oligomeric Golgi complex subunit 5 (13S Golgi transport complex 90 kDa subunit) (GTC-90) (Golgi transport complex 1)	23020	34864266	295519	1	1	8.4906
similar to DNA (cytosine-5)-methyltransferase 3A (Dnmt3a) (DNA methyltransferase MmullIA) (DNA MTase MmullIA) (M.MmullIA)	59410	34871224	241066	1	1	1.3133
similar to Dysferlin (Dystrophy associated fer-1 like protein) (Fer-1 like protein 1) [Rattus norvegicus]	224600	34856330	229917	1	1	0.55923
similar to Elongation factor 1-alpha 1 (EF-1-alpha-1) (Elongation factor 1 A-1) (eEF1A-1) (Elongation factor Tu) (EF-Tu)	45440	34880757	223872	1	10	21.0402
similar to Endoplasmic reticulum mannosyl-oligosaccharide 1,2-alpha-mannosidase (ER alpha-1,2-mannosidase) (Mannosidase alpha class 1B member 1) (Man9GlcNAc2-specific processing alpha-mannosidase)	51600	34852997	290726	9	9	20.915
similar to Eukaryotic translation initiation factor 3 subunit 6 interacting protein (HSPC021/HSPC025)	66710	34866934	266163	5	5	12.234
similar to Exocyst complex component Sec6 (rSec6)	72270	34855314	276511	1	1	1.0819
similar to FK506 binding protein 11	22190	27664728	316692	5	5	26.3682
similar to Fc fragment of IgG binding protein; IgG Fc binding protein	583400	34855405	285938	1	1	0.16587
similar to G1 to phase transition 2	76550	27663980	171140	2	2	2.5568
similar to Gal beta 1,3GalNAc alpha 2,3-sialyltransferase [Rattus norvegicus]	26160	34866546	201171	6	6	36.4444
similar to Glutathione S-transferase, theta 3	44270	34852398	225794	5	5	15.736
similar to Glyceraldehyde 3-phosphate dehydrogenase (GAPDH) (38 kDa BFA-dependent ADP-ribosylation substrate) (BARS-38)	13770	34858500	247025	1	1	12.8788
similar to Glycine decarboxylase [Rattus norvegicus]	111900	34862790	260747	1	1	1.6882
similar to Golgi coiled coil protein GCC185	245100	34852562	311145	9	9	5.2162
similar to Growth-arrest-specific protein 2 (GAS-2)	61200	34856132	300461	14	14	32
similar to HTPAP protein	29160	34879054	255469	1	1	3.8462
similar to Heat shock cognate 71 kDa protein	64610	34855549	236971	1	18	30.5461
similar to Histone H2A.o (H2A.o) (H2A.2) (H2a-615)	21070	34858256	279473	1	2	24.7423
similar to Hypothetical protein CGI-109 precursor	20460	34879511	204384	5	5	24.7191
similar to Hypothetical protein KIAA0379	41000	27732065	190049	1	1	3.3333
similar to Igh-6 protein	79080	34935297	225182	2	2	3.0598

similar to KIAA0445 protein	198000	34877826	256921	2	2	0.9838
similar to KIAA0946 protein	84730	34864845	282355	1	1	4.3127
similar to LDL receptor adaptor protein	60620	34872138	266460	1	1	1.9713
similar to Liver carboxylesterase 1 precursor (Carboxylesterase ES-1) (E1) (ES-THET)	26910	34882067	308005	1	2	8.8353
similar to Man9-mannosidase	57920	34852693	212806	14	14	41.1417
similar to N-acetylneuraminic acid synthase (sialic acid synthase)	40050	27714479	225772	1	1	7.7994
similar to NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 9	42560	34858473	215768	11	11	39.7878
similar to NADH dehydrogenase (ubiquinone) 1 beta subcomplex 3	11280	34876452	287362	1	1	11
similar to NADH dehydrogenase (ubiquinone) 1 beta subcomplex 8	23240	34865197	292854	4	4	24.2424
similar to NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 10, 22kDa; NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 10 (22kD, PDSW)	20860	27667934	291828	8	8	50.5682
similar to NADH-ubiquinone oxidoreductase B9 subunit (Complex I-B9) (CI-B9)	11480	34854466	318196	2	2	33.9806
similar to NADH-ubiquinone oxidoreductase B15 subunit	15060	82617686	192715	1	1	19.3798
similar to NADP+-specific isocitrate dehydrogenase	14720	34857317	195949	1	1	9.5588
similar to Nag-pending protein	60300	34863173	240310	3	3	8.0074
similar to Nsap1-pending protein [Rattus norvegicus]	82690	34865422	221070	11	11	18.0723
similar to PKR-associating protein RAX	34390	34856450	191003	1	1	6.0703
similar to PalBH [Rattus norvegicus]	90550	34876995	233624	1	1	1.1292
similar to Phosphoacetylglucosamine mutase (PAGM) (Acetylglucosamine phosphomutase) (N-acetylglucosamine-phosphate mutase) (Phosphoglucumutase 3) [Rattus norvegicus]	50750	34865378	202185	1	1	2.1786
similar to Potentail helicase MOV-10 [Rattus norvegicus]	73800	27660592	154542	6	6	12.2511
similar to Proteasome activator complex subunit 2 (Proteasome activator 28-beta subunit) (PA28beta) (PA28b) (Activator of multicatalytic protease subunit 2) (11S regulator complex beta subunit) (REG-beta)	23620	34879501	244453	1	1	3.7915
similar to Protein transport protein Sec23B (SEC23-related protein B) [Rattus norvegicus]	86090	34858849	260808	5	9	14.4909
similar to Pyruvate kinase, M2 isozyme	57960	34875446	288218	1	1	1.8632
similar to RAB6, member RAS oncogene family	26610	34859460	290450	13	13	49.3617
similar to RIKEN cDNA 1600025D17	39820	34874446	296070	4	4	16.6205
similar to RIKEN cDNA 1810003N24	31780	34873957	230313	1	1	3.5088
similar to RIKEN cDNA 1810037C20	39480	34881760	200680	4	4	14.1689
similar to RIKEN cDNA 1810045K17	10150	34857339	270299	1	1	16.129
similar to RIKEN cDNA 2010005O13 [Rattus norvegicus]	15020	34880819	301426	1	1	7.4074
similar to RIKEN cDNA 2010012D11	22040	34875339	204593	2	2	10.7143
similar to RIKEN cDNA 2310001A20	57340	34859421	291250	5	19	46.3035
similar to RIKEN cDNA 2310041H06 [Rattus norvegicus]	21700	34865854	267421	3	3	21.5385
similar to RIKEN cDNA 2410002O22 gene [Rattus norvegicus]	22220	34853743	269534	1	1	5.9701
similar to RIKEN cDNA 2500002K03 gene	36950	34858565	307749	4	4	17.0149
similar to RIKEN cDNA 2810409H07 [Rattus norvegicus]	42320	34855205	260021	1	1	4.0214

similar to RIKEN cDNA 4732463H20 [Rattus norvegicus]	52510	34857987	192449	5	5	12.854
similar to RIKEN cDNA 9430097N02 [Rattus norvegicus]	81520	34869388	230365	1	1	1.5068
similar to RIKEN cDNA C920006C10	16670	27718855	264993	1	1	9.4595
similar to RIKEN cDNA D330038I09 [Rattus norvegicus]	96960	34862428	302704	3	3	4.1998
similar to RNA helicase A	150200	34880497	203449	2	2	2.0173
similar to RNA-binding protein isoform G3BP-2a	54070	34876568	211028	1	1	3.527
similar to Rap2c protein	13510	34881637	197399	1	1	10.2564
similar to Ras GTPase-activating-like protein IQGAP2	140700	34853552	197696	31	33	35.6109
similar to Ras suppressor protein 1 (Rsu-1) (RSP-1)	34760	34877253	195351	4	4	25.89
similar to SDF2 like protein 1 [Rattus norvegicus]	23400	34869825	263376	5	5	39.5455
similar to SLIT-ROBO Rho GTPase-activating protein 3; WAVE-associated Rac GTPase activating protein	35530	34879743	229135	1	1	3.7855
similar to SSC2	59620	34875179	315186	1	1	3.2075
similar to Sh3bgr1 protein	12800	27706424	198937	1	1	15.7895
similar to Succinyl-CoA ligase [ADP-forming] beta-chain, mitochondrial precursor (Succinyl-CoA synthetase, betaA chain) (SCS-betaA) (ATP-specific succinyl-CoA synthetase beta subunit) [Rattus norvegicus]	48250	34874487	313666	2	2	8.9888
similar to Succinyl-CoA ligase [GDP-forming] beta-chain, mitochondrial precursor (Succinyl-CoA synthetase, betaG chain) (SCS-betaG) (GTP-specific succinyl-CoA synthetase beta subunit)	39790	34857707	302398	5	5	19.1781
similar to Swiprosin 1	26760	72255531	250786	1	1	4.6025
similar to T-cell activation leucine repeat-rich protein	92210	34876057	221702	1	1	1.7435
similar to TRH3	44950	27693564	249505	5	5	17.6316
similar to Transmembrane 9 superfamily protein member 4	74800	34859018	260512	16	16	27.1739
similar to Txndc1 protein	31430	67078422	283888	1	1	4.3165
similar to UDP-galactose transporter	38530	34933455	208424	1	1	3.8251
similar to WD repeat domain 20 isoform 1	65240	34935498	289309	1	1	1.6807
similar to Wdr1 protein [Rattus norvegicus]	48550	34878397	292693	1	1	3.6117
similar to Wolf-Hirschhorn syndrome candidate 1 protein isoform 1; IL5 promoter RE11 region-binding protein; trithorax/ash1-related protein 5; multiple myeloma SET domain protein	152600	34878518	214625	1	1	1.0989
similar to actin-related protein 2	42030	34878017	194947	3	4	10.2981
similar to adaptor-related protein complex 2, beta 1 subunit	105700	34876358	254285	1	16	17.5975
similar to adenine nucleotide translocase	32800	34866578	257029	1	8	23.8255
similar to adipocyte-specific protein 4 [Rattus norvegicus]	55200	34873948	240031	16	16	39.1213
similar to alpha glucosidase II, alpha subunit [Rattus norvegicus]	89880	34861580	192728	27	27	45.3165
similar to ancient ubiquitous 46 kDa protein AUP46	46200	34856277	205068	4	4	18.5366
similar to apoptosis-inducing factor (AIF)-homologous mitochondrion-associated inducer of death; p53-responsive gene 3 [Rattus norvegicus]	14880	34852510	209377	1	1	10.2941
similar to aspartyl beta-hydroxylase	53800	34866148	285481	1	1	3.6961
similar to brain and kidney proline oxidase 2	30660	34869794	301508	2	2	8.1784

similar to butyrate-induced transcript 1	20610	34880723	260591	2	2	14.0449
similar to butyrate-induced transcript 1	28810	34864679	236762	1	1	4.0486
similar to cAMP-dependent protein kinase, beta-2-catalytic subunit (PKA C-beta-2)	73330	34861056	256498	1	4	6.135
similar to cDNA sequence BC003251	53180	34871409	253866	1	1	2.714
similar to carcinoma related gene	29600	34871082	257012	2	2	15.8915
similar to cation-transporting atpase	131900	34877696	273691	8	8	9.0226
similar to chromosome 20 open reading frame 169	20950	34860687	214268	1	1	11.5789
similar to component of oligomeric golgi complex 2	41480	34851897	272329	2	2	6.9519
similar to component of oligomeric golgi complex 2	41580	34851895	298383	2	2	9.4851
similar to contains transmembrane (TM) region and ATP binding region [Rattus norvegicus]	13790	27707476	281046	3	3	33.6
similar to coproporphyrinogen oxidase	49280	79749365	160701	7	7	17.1558
similar to endo B cytochrome	42970	34860580	202236	1	4	13.8381
similar to endonuclease G	32270	77917570	273385	1	1	4.4218
similar to enthoprotein; epsin 4; clathrin interacting protein localized in the trans-Golgi region	64680	34880606	203525	2	2	3.8721
similar to epiplakin	368200	34867002	318405	2	2	1.4649
similar to ethanol induced 6	15850	27686507	188139	1	1	16.2338
similar to glucan (1,4-alpha-), branching enzyme 1; DNA segment, Chr 16, ERATO Doi 536, expressed	32500	34867432	299017	2	2	9.8592
similar to glyceraldehyde-3-phosphate dehydrogenase	36450	34852715	210943	1	3	13.4731
similar to glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) (EC 1.2.1.12) - mouse	31550	34864978	296252	1	3	16.8919
similar to glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) (EC 1.2.1.12) - mouse	27870	27699577	156654	1	1	5.4475
similar to glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) (EC 1.2.1.12) - mouse	46820	34856839	252379	1	1	3.5545
similar to glycoprotein IIb - rat	274100	34873959	220383	6	6	3.5172
similar to golgi-associated microtubule-binding protein HOOK3; hook3 protein [Rattus norvegicus]	83230	34879033	220378	1	1	1.6506
similar to golgi-specific brefeldin A-resistance guanine nucleotide exchange factor 1	208100	34865240	218235	10	10	6.6383
similar to heat shock protein 105 kDa alpha	82350	34870188	195465	1	1	1.2295
similar to heparan sulfate 2-sulfotransferase	41850	34860929	259411	7	7	25.2809
similar to hepatocellular carcinoma autoantigen	13340	34869447	272734	1	1	4.918
similar to hexose-6-phosphate dehydrogenase GDH6PGL endoplasmic bifunctional protein	114800	34872615	251640	31	31	39.9417
similar to histocompatibility 13; presentilin-like protein 3	41780	34858994	305736	4	4	14.5503
similar to hypothetical protein A	36410	34869364	193827	1	1	3.4921
similar to hypothetical protein D4Erd89e	46520	34868399	231118	1	1	2.3641
similar to hypothetical protein FLJ14675	21510	34873570	196884	1	1	5.8824
similar to hypothetical protein FLJ20331 [Rattus norvegicus]	48370	34861003	248047	1	1	3.7471
similar to hypothetical protein FLJ22625	35090	34865046	243991	1	1	3.7267
similar to hypothetical protein FLJ22865	33930	34872934	263071	1	1	2.5559

similar to hypothetical protein MGC10084	42080	34851552	202821	1	1	1	3.5813
similar to hypothetical protein MGC23280	35980	34872804	277215	1	1	1	3.6585
similar to immunoglobulin alpha heavy chain	48960	34935283	224861	2	2	2	10.8647
similar to inhibitor of growth family, member 3	56500	34855011	234073	1	1	1	1.7751
similar to inter-alpha trypsin inhibitor, heavy chain 1 [Rattus norvegicus]	99190	34877130	227779	5	5	5	11.6592
similar to keratin associated protein 11-1	18900	27670141	269756	1	1	1	6.0109
similar to keratin type II, hair (b4) - mouse	105900	34868202	262043	14	15	15	31.9749
similar to keratinocytes associated protein 2	27650	34857976	235668	1	1	1	6.6667
similar to liver regeneration-related protein LRRG07 [Rattus norvegicus]	35400	34876593	287183	8	11	11	49.3548
similar to lysosomal apyrase-like 1	49290	34874388	305737	2	2	2	7.0938
similar to mCASP	35060	34873372	194891	10	10	10	38.535
similar to mKIAA0493 protein	110600	34866514	234949	6	6	6	8.3
similar to male enhanced antigen 2/golgi autoantigen, golgin subfamily a, 3 [Rattus norvegicus]	166100	34873054	267138	1	1	1	0.81191
similar to mannosyl-oligosaccharide 1,3-1,6-alpha-mannosidase	87810	34877942	294051	11	22	22	36.4205
similar to microchidia	55070	34869318	309715	1	1	1	1.8595
similar to mirror-image polydactyl gene 1	52780	34865613	265130	1	1	1	1.9397
similar to nonclathrin coat protein epsilon-COP	34650	34877816	259217	17	17	17	74.3506
similar to ornithine transporter	32800	27673563	205798	8	8	8	35.8804
similar to osteoclast stimulating factor 1	34620	34880977	297002	1	1	1	6.1093
similar to peroxisomal long chain acyl-CoA thioesterase la	46360	27667388	160562	1	1	1	3.0879
similar to placenta-specific 3 isoform 1; pregnancy-associated plasma protein-E; pregnancy-associated plasma preproprotein-A2	33400	34877698	287571	2	2	2	8.7542
similar to proline dehydrogenase; PRODH	12130	27665096	305160	1	1	1	14.9533
similar to rab20	32660	34879665	240940	1	1	1	2.349
similar to receptor-interacting protein 2	60780	34867073	242276	1	1	1	1.8553
similar to recombination activating 1 activation	24690	27692967	292043	1	1	1	9.0498
similar to retinal short-chain dehydrogenase/reductase 4	38310	34865424	315286	3	4	4	13.3136
similar to ribosomal protein S12; 40S ribosomal protein S12	12210	34869042	285721	1	2	2	28.5714
similar to ribosomal protein S2	21310	34879560	317435	2	3	3	18.1818
similar to serine protease OMI	49090	34856275	218478	5	5	5	15.0655
similar to sorting nexin 2	58530	34879535	319162	3	3	3	6.9364
similar to splicing coactivator subunit SFRm300; RNA binding protein; AT-rich element binding factor [Rattus norvegicus]	212600	34868816	290757	1	1	1	0.40589
similar to talin [Rattus norvegicus]	269500	34867875	230030	26	29	29	17.369
similar to thyroid hormone receptor interactor 11; thyroid receptor interacting protein 11	37170	34867559	280942	1	1	1	3.9039
similar to torsinB protein	17860	34853518	202385	1	1	1	8.642
similar to transducin (beta)-like 2	49610	34873382	294309	16	16	16	42.5339
similar to ubiquitin-protein ligase (EC 6.3.2.19) E1 - mouse	123600	34933178	317625	1	1	1	1.3489

stress 70 protein chaperone, microsome-associated, 60kD human homolog	51830	9507149	47300	4	4	12.5265
synaptogyrin 2	25710	6685963	60460	1	1	4.2735
taste receptor, type 1, member 2	202100	34872230	217700	6	9	7.123
transferrin receptor [Rattus norvegicus]	85020	34869255	269397	4	4	6.3745
tubulin beta chain 15 - rat	49940	92930	93455	3	20	57.5281
unknown	94390	34851379	292730	29	29	45.3052
unknown	46570	27677502	309339	13	13	44.9878
unknown	53820	34875854	222783	9	9	24.6285
unknown	28170	27722175	195164	9	9	47.541
unknown	35170	34870624	209664	10	10	42.492
unknown	13190	27705930	166454	3	3	38.3333
unknown	30510	34877499	258690	2	2	8.5185
unknown	84160	34880715	314842	1	1	1.4966
unknown	29280	34870857	233158	2	2	5.2632
unknown	17010	27707156	199239	2	2	16.3399
unknown	26610	84781644	345922	1	1	5.7613
unknown	167300	34869344	309548	1	1	0.65147
unknown	111800	34872548	263673	1	1	1.3374

Table S1B. Proteins identified by a single unique peptide

NCBI DESCRIPTION	MW	giumber	CMBSEQID	UNIQUE PEPTIDES	DISTINCT PEPTIDES	% SEQUENCE COVERAGE	N-TERM AA
(P08644) Isoform 2B of P08644	21490	495534	71624	1	3	21	R
(Q810T5) Isoform 2 of Q810T5	66820	29650457	268104	1	1	2	R
(Q9ESC1) Isoform 2 of Q9ESC1	73800	11225481	129647	1	1	2	R
(Q9QUH6) Isoform 5 of Q9QUH6	127700	7514095	13883	1	1	1	R
(Q9WVG6) Isoform 2 of Q9WVG6	63460	77539446	292598	1	1	3	K
1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase beta 3	139400	32699414	166274	1	1	2	R
10 days embryo whole body cDNA, RIKEN full-length enriched library, clone:261051121 product:proteasome (prosome, macropain) subunit, alpha type 2, full insert sequence TIB-55 BB88 cDNA, RIKEN full-length enriched library, clone:1730006B17 product:proteasome (prosome, macropain) subunit, alpha type 2, full insert sequence 2 days neonate thymus thymic cells cDNA, RIKEN full-length enriched library, clone:E430022A16 product:proteasome (prosome, macropain) subunit, alpha type 2, full insert sequence Bone marrow macrophage cDNA, RIKEN full-length enriched library, clone:1830087N08 product:proteasome (prosome, macropain) subunit, alpha type 2, full insert sequence Bone marrow macrophage cDNA, RIKEN full-length enriched library, clone:1830041K04 product:proteasome (prosome, macropain) subunit, alpha type 2, full insert sequence Proteasome (Prosome, macropain) subunit, alpha type 2 Adult male urinary bladder cDNA, RIKEN full-length enriched library, clone:9530069L07 product:proteasome (prosome,	25930	8394063	33375	1	1	6	R
10-Formyltetrahydrofolate Dehydrogenase	34040	42543697	723160	1	3	14	K
14-3-3 protein eta	28210	6981710	29710	1	3	15	K
18-day embryo whole body cDNA, RIKEN full-length enriched library, clone:1110037P24 product:weakly similar to RE35789p Novel protein Hypothetical protein Tmem93 18-day embryo whole body cDNA, RIKEN full-length enriched library, clone:1110001A14 product:hypothetical protein, full insert sequence	12020	27673882	98449	1	1	11	R
2',3'-cyclic-nucleotide 3'-phosphodiesterase CNPase	47270	66912120	109735	1	1	3	K
4-aminobutyrate aminotransferase, mitochondrial precursor (S)-3-amino-2-methylpropionate transaminase	56450	48429192	37174	1	1	2	K
Gamma-amino-N-butyrate transaminase GABA transaminase GABA aminotransferase GABA-AT GABA-T L AIBAT 4-aminobutyrate aminotransferase, brain isoform 4-aminobutyrate aminotransferase, liver isoform							
49 kDa protein	2429	262199	124397	1	1	48	R
5'-AMP-activated protein kinase catalytic subunit alpha-1 AMPK alpha-1 chain	62600	1703034	23444	1	1	3	R
60S ribosomal protein L36	12250	34849736	65711	1	6	37	R
60S ribosomal protein L37	11080	57121	3029	1	1	7	R
60S ribosomal protein L39	6407	6981484	4822	1	1	20	K
60S ribosomal protein L40 CEP52	6181	973178	77849	1	1	13	START
9.5 days embryo parthenogenote cDNA, RIKEN full-length enriched library, clone:B130020K18 product:RAS-RELATED PROTEIN RAP-2B homolog 7 days neonate cerebellum cDNA, RIKEN full-length enriched library, clone:A730075110 product:RAP2B, member of RAS oncogene family, full insert sequence Bone marrow macrophage cDNA, RIKEN full-length enriched library, clone:G530142K06 product:RAP2B, member of RAS oncogene family, full insert sequence Rap2b protein 7 days neonate cerebellum cDNA, RIKEN full-length enriched library, clone:A730042C18 product:RAS-RELATED PROTEIN RAP-2B homolog	20500	47117735	32753	1	1	7	K
A-Raf proto-oncogene serine/threonine-protein kinase	67550	55757	90531	1	1	2	R
ADP-ribosylation-like factor 6-interacting protein Arl6ip1 protein	23450	68534822	139514	1	1	4	K
ARHG protein Ras homolog gene family, member G Rho G	21310	82524300	93024	1	1	10	K
ATP synthase epsilon chain, mitochondrial	5636	258789	11887	1	1	16	R
ATP-binding cassette, sub-family B (MDR/TAP), member 10 Predicted	77390	58865904	264038	1	1	3	K
ATP-binding cassette, sub-family C (CFTR/MRP), member 3	169300	3242460	52680	1	1	1	R
ATP-binding cassette, sub-family F (GCN20), member 1	92870	34852051	231492	1	1	1	K

ATPase, H+ transporting, V1 subunit C, isoform 1 Predicted	43900	62652340	311925	1	1	4	K
ATPase, H+ transporting, lysosomal 34kDa, V1 subunit D	28310	40786463	160475	1	1	5	R
Aa1064	42690	111387	148924	1	12	36	R
Ab2-225 Hypothetical protein RGD1306952	27900	56970828	244467	1	1	4	R
Ac1573	79140	32264637	263869	1	6	10	R
Ac2-067	27970	34862605	168240	1	1	6	K
Ac2-155	102100	33086620	199808	1	1	1	K
Ac2-256	71830	62177146	168247	1	1	1	K
Acetyl-CoA carboxylase 1 ACC-alpha Biotin carboxylase	265200	202645	84141	1	1	1	R
Acyl-protein thioesterase 1 Lysophospholipase I	24710	6981362	75037	1	1	5	K
Adenine phosphoribosyltransferase APRT	19550	61556832	126504	1	1	7	R
Adenosine kinase	40100	7448824	3608	1	3	9	K
Adenosine kinase	37310	1373230	85486	1	3	10	R
Adenylate kinase isoenzyme 4, mitochondrial Adenylate kinase 3-like 1 ATP-AMP transphosphorylase	25200	8392885	181389	1	1	5	R
Adult male thymus cDNA, RIKEN full-length enriched library, clone:5830427H10 product:GL009 homolog Bone marrow macrophage cDNA, RIKEN full-length enriched library, clone:1830027D22 product:GL009 homolog 12 days embryo spinal cord cDNA, RIKEN full-length enriched library, clone:C530010F19 product:GL009 homolog Jagunal homolog 1 18-day embryo whole body cDNA, RIKEN full-length enriched library, clone:1110014A23 product:CDNA FLJ14602 FIS, CLONE NT2RP1000191 homolog	21100	68534555	32612	1	1	7	R
Advanced glycosylation end product-specific receptor precursor Receptor for advanced glycosylation end products	42660	498034	128256	1	1	3	K
Afadin Protein Af-6	207700	7513996	3616	1	1	0	R
Ak3 protein	25490	40352787	270293	1	1	6	K
Alcohol sulfotransferase Hydroxysteroid sulfotransferase ST ST-60	33530	68341957	157070	1	4	16	K
Alpha globin	15520	62655914	114803	1	2	17	K
Alpha-1 catenin	92036	94182	11470	1	1	15	R
Alpha-1-acid glycoprotein precursor Orosomucoid OMD	23580	72091	11470	1	1	4	K
Alpha-1B-glycoprotein precursor Liver regeneration-related protein 1 C44	56480	57012547	155721	1	1	2	R
Alpha-2-globin chain Hba-a1 protein 2-alpha globin	15280	60688619	109334	1	11	75	K
Alpha-2U globulin	20560	8307690	125352	1	8	35	R
Alpha-parvin Actopaxin	42290	20138815	37085	1	1	4	K
Amyloid-like protein 2 precursor	86880	1703345	10860	1	1	2	R
Amyotrophic lateral sclerosis 2 chromosomal region candidate gene protein 3 homolog	101600	75905813	256333	1	1	1	K
Anionic trypsin-1 precursor Anionic trypsin I Pretrypsinogen I	25960	6981420	75054	1	1	8	R
Apolipoprotein A-II precursor	11440	91985	3639	1	1	11	R
Apolipoprotein C-IV precursor Apo-C-IV Apolipoprotein E-linked ECL	10250	2492915	136243	1	1	13	R
B-cell receptor-associated protein BAP29	28230	55742817	243481	1	1	7	K
Bax inhibitor-1	26230	456209	23753	1	1	4	R
Block of proliferation 1 Predicted	82640	66730443	214565	1	1	1	R
Brain protein 44-like protein	12450	66911415	92620	1	1	7	R
C-type lectin domain family 4 member F C-type lectin superfamily member 13 C-type lectin 13 Kupffer cell receptor	61100	68533633	60545	1	1	2	R
C4b-binding protein alpha chain precursor C4bp	62270	899380	3688	1	1	2	R
CD59 glycoprotein precursor Membrane attack complex inhibition factor MAC1F MAC-inhibitory protein MAC	13790	6978635	3690	1	1	7	R
IP Protectin	22830	51948526	211553	1	1	7	K
COMM domain containing 10	1978	111445	148937	1	1	89	START
Calcium-binding protein 4	28030	19864480	76638	1	1	9	R
Calpain small subunit 1	25290	55562775	166315	1	1	8	R
Carbonyl reductase 4	2133	1478388	42034	1	1	60	START
Carboxylesterase isozyme	42020	77993370	10199	1	17	41	K

Cathepsin Z precursor	34190	60688149	160297	1	1	4	R
Cationic trypsin-3 precursor Cationic trypsin III Pretrypsinogen III	26270	27465583	31543	1	1	3	R
Cell growth regulator with EF hand domain 1 Cell growth regulatory gene 11 protein	30830	23396481	38628	1	1	4	K
Cell surface protein CD36	52730	6707016	105482	1	1	4	R
Ceratain-alpha 2	43520	9910340	42770	1	1	5	K
Ceramide	83490	16758458	60505	1	1	2	K
Ceramide glucosyltransferase Glucosylceramide synthase GCS UDP-glucose:N-acylsphingosine D-glucosyltransferase UDP-glucose ceramide glucosyltransferase GLCT-1	44820	62648957	85745	1	1	3	K
Choline/ethanolamine phosphotransferase 1	46500	56090333	264754	1	1	3	K
Clathrin light chain B	25120	203359	60578	1	1	4	R
Coagulation factor IX Christmas factor	31450	204146	149112	1	1	4	K
Complement component C6 precursor	105100	61211276	240055	1	1	1	K
Complement regulatory protein Cry precursor Antigen 512	61680	9506513	35260	1	1	4	K
Connector enhancer of kinase suppressor of ras 2 Connector enhancer of KSR2 CNK2 Membrane-associated guanylate kinase-interacting protein MAGUIN	117400	50400225	169306	1	1	1	K
Contrapsin-like protease inhibitor 1 precursor	46480	220698	135016	1	19	50	K
Core binding factor beta	21520	61557239	2681	1	1	4	K
Cortactin isoform C	52630	2996044	57161	1	1	3	R
Cp431	104600	3851160	7578	1	1	1	R
Creatine kinase M-type Creatine kinase M chain M-CK	43020	6978661	3700	1	1	4	K
Cytidylate kinase	25830	71043752	267331	1	1	9	R
Cytochrome P450 2C11	57180	56971259	63780	1	38	84	K
Cytochrome P450 2C22	56210	203521	33163	1	23	62	K
Cytochrome P450 2C70 CYP11C70 P-450Md P450 P49	56160	56827	63786	1	23	62	K
Cytochrome P450 2c13	55840	71051773	84196	1	31	70	K
Cytochrome P450 3A	57720	6978749	3731	1	9	24	R
Cytochrome P450 4A12 CYP11A12 CYP11A8 P450-KP1 P450-PP1	58520	203757	78089	1	6	10	R
Cytochrome b5 outer mitochondrial membrane isoform precursor	15220	7427560	39173	1	5	60	START
Cytochrome c oxidase polypeptide VIIc, mitochondrial VIIIA	1117	1169069	71407	1	1	90	START
Cytochrome c oxidase subunit 2	25940	5835181	98989	1	7	31	R
Cytochrome oxidase subunit II	26010	829023	105670	1	7	26	R
Cytochrome oxidase subunit II Cytochrome c oxidase subunit II	25930	58615680	142106	1	7	31	R
Cytokeratin type I	15550	55956	11221	1	1	5	R
Diacglycerol O-acyltransferase 1 Diglyceride acyltransferase	56870	9965432	145183	1	1	3	K
Diamine oxidase-like protein 1	80090	40385889	216306	1	1	1	R
Dimethylglycine dehydrogenase, mitochondrial precursor ME2GLYDH	96050	56689	82662	1	1	2	R
Dipeptidyl peptidase IV	88000	6978773	3741	1	19	28	K
Dnaj-like protein	25760	9910322	42765	1	1	3	R
Dnajc3 protein [Rattus norvegicus]	50240	38197558	318957	1	15	46	R
EIF3S6 protein	52220	62652368	55867	1	1	3	R
ENSEMBL:ENSRNOP0000002163 REFSEQ:XP_342451 PREDICTED: similar to lunapark	47640	34855225	271473	1	1	2	R
Enquifment and cell motility protein 1	28740	34876182	4981	1	1	7	R
Epsin 1	60160	41016934	105332	1	1	2	K
Estrogen sulfotransferase, isoform 1 EST-1 Sulfotransferase, estrogen-prefering Estrone sulfotransferase	35510	1711599	109266	1	7	31	K
Estrogen sulfotransferase, isoform 3 EST-3 Sulfotransferase, estrogen-prefering Estrone sulfotransferase	35420	6981594	75106	1	7	31	K
Estrogen sulfotransferase, isoform 6 EST-6 Sulfotransferase, estrogen-prefering Estrone sulfotransferase	35300	913357	62242	1	6	29	K
Estrogen-related receptor gamma Estrogen receptor-related protein 3	51310	50400205	17534	1	1	2	R
Eukaryotic translation initiation factor 4H	27320	55741853	295040	1	1	9	R
Evolutionarily conserved signaling intermediate in Toll pathway	49620	55741518	276570	1	1	3	R

Exocyst complex component 2 Exocyst complex component Sec5 rSec5	104000	7513971	161256	1	1	2	R
Exostosin-1 Glucuronosyl-N-acetylglucosaminyl-proteoglycan/N-acetylglucosaminyl-proteoglycan 4-alpha-N	86310	62652423	57456	1	1	2	K
acetylglucosaminyltransferase Multiple exostosins protein 1 homolog							
F-actin binding protein b-Nexilin	78390	40538878	173653	1	1	1	K
Ficolin-1 precursor Collagen/fibrinogen domain-containing protein 1 Ficolin-A Ficolin A M-Ficolin	36630	6714560	75919	1	1	5	K
Fukulin related protein	54850	71043684	242747	1	1	3	R
Fumarate hydratase, mitochondrial precursor Fumarase	54460	83933358	45080	1	7	26	R
Furin precursor Paired basic amino acid residue cleaving enzyme PACE Dibasic-processing enzyme	86650	9506955	47234	1	1	2	R
Prohormone convertase 3							
GM2 activator protein	21520	27229316	157436	1	1	11	K
GTPase HRas precursor Transforming protein p21 p21ras H-Ras-1 c-H-ras	21300	34861217	10323	1	3	19	R
Galactose-1-phosphate uridylyltransferase Gal-1-P uridylyltransferase UDP-glucose--hexose-1-phosphate	43310	68533665	71441	1	1	2	R
uridylyltransferase							
Galectin-3	27200	57870645	71532	1	1	4	K
Gamma-butyrobetaine dioxygenase Gamma-butyrobetaine,2-oxoglutarate dioxygenase Gamma-	44550	5825482	139030	1	1	3	K
butyrobetaine hydroxylase Gamma-BBH							
Gamma-glutamyltransferase 5 precursor Gamma-glutamyltransferase-like activity 1 Gamma-glutamyl	61610	9506723	52613	1	1	3	R
leukotrienase GGL Gamma glutamyl transpeptidase-related enzyme GGT-rel Gamma-glutamyltransferase 5							
heavy chain Gamma-glutamyltransferase 5 light chain							
Gene,	48610	22775474	113271	1	1	3	R
Gila maturation factor beta GMF-beta	16610	111660	148966	1	1	16	R
Glutamine fructose-6-phosphate transaminase 1	76830	54400724	277551	1	1	2	R
Glutathione S-transferase alpha-4 Glutathione S-transferase Yk GST Yk GST 8-8 GST K GST A4-4	25510	5420030	28290	1	3	10	R
Glutathione transferase (EC 2.5.1.18) psi	3544	92300	84221	1	1	33	START
Glycerol kinase ATP-glycerol 3-phosphotransferase Glycerokinase GK ATP-stimulated glucocorticoid-	57480	433211	18015	1	1	2	K
receptor translocation promoter ASTP							
Glycerol-3-phosphate dehydrogenase, mitochondrial precursor GPD-M GPDH-M	80970	6980978	3907	1	1	2	R
Golgin subfamily A member 7	15780	81884637	199992	1	1	11	K
Growth factor receptor bound protein 2	25210	77539774	29315	1	1	6	K
Gstm7 protein	25680	529588	33791	1	10	40	R
H2-K region expressed gene 4, rat orthologue RT1 class I, locus Ke4	49500	62665667	219015	1	1	6	R
H3 histone, family 3A H3 histone, family 3B H3F3A protein	15330	56388767	16060	1	1	24	R
Heat shock 27 kDa protein	22890	204665	71479	1	1	8	K
Heme oxygenase 1	33010	6981032	3930	1	1	4	R
Hemoglobin alpha-1 and alpha-2 chains	15330	6981010	3923	1	11	75	M
Heterogeneous nuclear ribonucleoprotein D0 hnRNP D0 AU-rich element RNA-binding protein 1	38190	9588096	47431	1	1	4	K
Hexokinase, type 1	102400	6981022	3926	1	1	1	K
Histidine triad nucleotide binding protein	13780	34870743	82484	1	1	11	K
Histidine triad protein 4	18890	21654864	153619	1	1	8	K
Histidine-rich glycoprotein 1	59050	62657833	140379	1	4	8	K
HnRNP protein	18280	3021529	57359	1	1	11	R
Hypothetical protein Ccdc51	42310	62078929	36853	1	1	3	K
Hypothetical protein FLJ20445 Ring finger protein 153	31230	34862676	49021	1	1	5	K
Hypothetical protein MGC72560	17720	40018580	139384	1	1	8	R
Hypothetical protein MGC72996	20710	38454298	220427	1	1	5	K
Hypothetical protein MGC9464	19290	56090373	282775	1	1	5	K
Hypothetical protein RGD1305677	21660	58585236	209082	1	1	8	R
INSIG2 membrane protein Insulin induced gene 2	24970	55250700	200861	1	1	5	M
IT1 heavy chain-related protein	1809	1041915	40462	1	2	94	START
Ig gamma-2A chain C region	25220	13399989	62937	1	1	4	K
IgG receptor FcRN large subunit P51 precursor	40170	56437	15418	1	1	3	K

Inosine monophosphate dehydrogenase 2	55800	40018566	231448		1	1	1	3	K
Ischemia responsive 94 kDa protein	94080	3360521	95874		1	1	1	1	R
Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial precursor Isocitric dehydrogenase NAD(+)-specific IDH	39610	68565369	60501		1	1	1	3	K
Keratin K6	3107	554464	66467		1	1	1	38	K
LEA 4 domain containing protein RGD1359600	31470	56090371	205582		1	1	1	4	K
LIM and SH3 domain protein 1 LASP-1	29970	71122452	19687		1	1	1	5	K
LOC362065 protein Transmembrane protein	62200	45680888	339290		1	1	1	2	K
LRRGT00050	166800	66793366	286877		1	1	1	1	K
LRRGT00086	62990	37361858	209490		1	1	1	2	K
LanC-like protein 1 40 kDa erythrocyte membrane protein p40	45240	6625487	126112		1	1	1	3	K
Leucyl-cystinyl aminopeptidase	117200	20138455	5106		1	1	1	1	R
Leukocyte common antigen variant 4 precursor	132600	56560	111680		1	1	1	1	R
Liver NTE-related protein	75650	21314221	198073		1	1	1	2	R
Liver carboxylesterase 10 precursor	62140	56899	112141		1	35	66	66	R
Liver carboxylesterase B-1 precursor Liver microsomal carboxylesterase	62490	562010	10945		1	29	56	56	K
Liver regeneration-related protein 1	17130	28194393	52861		1	1	1	6	K
Liver-specific transport protein	58710	529590	60454		1	1	2	2	K
Lon	105800	19173766	140367		1	1	1	1	K
Long-chain fatty acid transport protein 1 Fatty acid transport protein 1 FATP-1 Solute carrier family 27 member 1	71280	2492888	60472		1	1	1	2	K
Low molecular mass ubiquitinone-binding protein	9849	68341999	311481		1	1	1	16	R
LysM, putative peptidoglycan-binding, domain containing 3	33700	57527470	204667		1	1	1	5	R
Lysosomal acid lipase/cholesteryl ester hydrolase precursor LAL Acid cholesteryl ester hydrolase Sterol esterase Lipase A Cholesteryl esterase	45190	9653291	72321		1	1	1	3	R
Lysosomal acid phosphatase precursor LAP	48320	8392842	144356		1	1	1	3	R
Lysozyme	16730	7428180	39196		1	1	1	13	R
Lysyl-tRNA synthetase	71620	55741637	269157		1	1	1	2	R
MAL2A Mal, T-cell differentiation protein 2	19200	77157795	166255		1	1	1	6	R
MHC class II transactivator type I	127300	9931450	42953		1	1	1	1	K
MOBILFERRIN	1917	300525	182793		1	1	1	41	START
Major urinary protein precursor	20740	992637	69402		1	15	71	71	K
Maleylacetoacetate isomerase MAAI Glutathione S-transferase zeta 1 GSTZ1-1	2943	11133293	36062		1	1	39	39	K
Mannose-binding protein A precursor	16550	1942287	19138		1	1	1	8	K
Merlin Moesin-ezrin-radixin-like protein Neurofibromin-2 Schwannomin	68710	32363191	124359		1	1	3	3	K
Mesenchymal stem cell protein DSCD75	23750	56090359	259160		1	1	5	5	R
Mitochondrial import inner membrane translocase subunit TIM8 A Deafness dystonia protein 1 homolog	11040	5107153	12056		1	1	11	11	R
Mitochondrial protein, 18 kDa	18370	55741522	220289		1	1	1	8	R
Mitogen-activated protein kinase 13 Stress-activated protein kinase 4 Mitogen-activated protein kinase p38 delta MAP kinase p38 delta	42050	9506991	47245		1	1	3	3	K
Mitogen-activated protein kinase kinase 1-interacting protein 1	13580	81883452	237355		1	1	9	9	K
Monocyte differentiation antigen CD14 precursor	40050	38197682	35920		1	1	3	3	R
Myelin basic protein S	21500	70166245	3277		1	1	7	7	K
Myosin VIIA	251100	23618899	217296		1	1	0	0	R
N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 2 [Rattus norvegicus]	95740	34868948	210844		1	4	5	5	R
NADH-ubiquinone oxidoreductase chain 4 NADH dehydrogenase subunit 4	51800	639984	98993		1	1	4	4	R
NADPH-cytochrome P450 reductase	76930	205660	44210		1	37	63	63	R
Na(+)/H(+) exchange regulatory co-factor NHE-RF2	34910	13925523	78016		1	1	4	4	R
Nicotinate phosphoribosyltransferase-like protein	58560	46485387	722226		1	1	4	4	R
Non-muscle caldesmon CDM L-caldesmon	60580	6978589	3674		1	1	2	2	R
Oligoribonuclease, mitochondrial precursor Small fragment nuclease RNA exonuclease 2 homolog	26750	81910234	216886		1	1	3	3	M
Ornithine aminotransferase	24280	206706	44333		1	1	9	9	R

PEF protein with a long N-terminal hydrophobic domain	30010	56090329	201603	1	1	1	5	R
PRA1 family protein 3 AR1-6-interacting protein 5 ADP-ribosylation-like factor 6-interacting protein 5 Alp-5	21550	57012987	54281	1	1	1	11	K
Glutamate transporter EAAC1-interacting protein GTRAP3-18 Prenylated Rab acceptor protein 2 Protein Jwa								
PREDICTED: T-cell, immune regulator 1, ATPase, H ⁺ transporting, lysosomal V0 protein a isoform 3	93210	62641689	274163	1	1	1	2	K
PREDICTED: branched chain keto acid dehydrogenase E1, beta polypeptide								
PREDICTED: cadherin 11	42820	34865350	151463	1	1	1	3	R
PREDICTED: hypothetical protein XP_579502	88040	34851208	199319	1	1	1	1	K
PREDICTED: mitogen-activated protein kinase kinase kinase 7 interacting protein 2 (predicted)	83280	62665770	317748	1	1	12	20	K
PREDICTED: peanul-like 2 (Drosophila) (predicted)	76330	90108450	226905	1	1	1	1	K
PREDICTED: pyrroline-5-carboxylate reductase-like (predicted)	53080	62656738	223925	1	1	1	3	K
PREDICTED: similar to 1700001K19Rik protein	28860	62652621	268213	1	1	1	4	R
PREDICTED: similar to 3,5-cyclic-GMP phosphodiesterase, rod phosphodiesterase beta subunit	98490	34867823	299198	1	1	1	4	R
PREDICTED: similar to 60S acidic ribosomal protein P1	11560	27717711	214842	1	1	1	1	K
PREDICTED: similar to 60S acidic ribosomal protein P2	11760	62660456	201232	1	1	7	76	K
PREDICTED: similar to Aldose reductase (AR) (Aldehyde reductase)	35900	62648070	161456	1	1	2	7	K
PREDICTED: similar to Apolipoprotein C2	10700	27676424	215733	1	1	1	9	K
PREDICTED: similar to BTB (POZ) domain containing 14A	63110	34853069	292782	1	1	1	1	K
PREDICTED: similar to Cab39 protein	39870	34877516	314871	1	1	1	3	K
PREDICTED: similar to Coiled-coil-helix-coiled-coil-helix domain containing 6	35250	34856405	277277	1	1	1	4	K
PREDICTED: similar to Cysteine-rich with EGF-like domains 1	45700	81170413	208169	1	1	1	3	R
PREDICTED: similar to DNA segment, Chr 13, Wayne State University 177, expressed	21120	95102018	253829	1	1	1	10	R
PREDICTED: similar to DXImx39e protein	15360	34933457	246770	1	1	1	8	R
PREDICTED: similar to Dual specificity phosphatase 14	22270	62644625	209194	1	1	1	11	R
PREDICTED: similar to Emopamil-binding protein-like (Emopamil-binding related protein)	23410	34874266	245607	1	1	1	4	R
PREDICTED: similar to F-box protein 28	41070	27681007	262592	1	1	1	3	R
PREDICTED: similar to GPI transamidase component PIG-T precursor (Phosphatidylinositol-glycan biosynthesis, class T protein) (Neuronal development-associated protein 7)	65550	34860689	195113	1	1	1	3	R
PREDICTED: similar to LECT2	20890	34873621	209309	1	1	1	5	K
PREDICTED: similar to MAP kinase kinase 3b	47090	34870816	238438	1	1	1	4	K
PREDICTED: similar to Melaxin 1, isoform 2	26260	34857966	262377	1	1	1	7	K
PREDICTED: similar to Protein HSPC163	16090	27679416	225990	1	1	1	14	R
PREDICTED: similar to RCK	54310	34879288	208269	1	1	1	3	R
PREDICTED: similar to RIKEN cDNA 1110038M16	31550	34870283	246519	1	1	1	8	R
PREDICTED: similar to RIKEN cDNA 1200009C21	25110	27730981	189964	1	1	1	6	K
PREDICTED: similar to RIKEN cDNA 1700025G04	13890	27712468	318230	1	1	1	6	R
PREDICTED: similar to RIKEN cDNA 1700027N10	31220	34874480	246387	1	1	1	4	K
PREDICTED: similar to RIKEN cDNA 2610019P18	28380	34871484	194048	1	1	1	5	K
PREDICTED: similar to RIKEN cDNA D930001I22	30110	62646328	359989	1	1	1	6	K
PREDICTED: similar to RPP20 protein	15740	27663642	220097	1	1	1	11	R
PREDICTED: similar to RS21-C6 protein	32140	34877104	218331	1	1	1	4	K
PREDICTED: similar to Ras-related protein R-Ras (P23)	23910	34856057	257746	1	1	2	13	R
PREDICTED: similar to Retinoic acid early inducible protein 1 beta precursor (RAE-1beta)	23230	81887426	161420	1	1	2	10	K
PREDICTED: similar to Sfrs7 protein	27450	62638284	367801	1	1	1	5	K
PREDICTED: similar to Smhs2 homolog	20570	34862692	226986	1	1	2	14	K
PREDICTED: similar to Stromal cell-derived factor 2 precursor (SDF-2)	49210	34874232	269978	1	1	1	4	K
PREDICTED: similar to TOLLIP protein	24060	27673471	232984	1	1	1	4	R
PREDICTED: similar to Tripartite motif protein 47	30310	34861256	225945	1	1	1	5	R
PREDICTED: similar to alpha/beta hydrolase fold protein	70030	27690552	251068	1	1	1	2	R
PREDICTED: similar to armadillo repeat-containing protein	48340	34857271	271294	1	1	1	6	R
PREDICTED: similar to cathepsin 1 precursor	31200	34855505	302905	1	1	1	7	R
PREDICTED: similar to cathepsin 1 precursor	40980	27681673	266171	1	1	1	2	K

PREDICTED: similar to chromosome 9 open reading frame 7	18410	34853142	272157	1	1	5	K
PREDICTED: similar to evolutionarily conserved G-patch domain containing	100900	34855741	271140	1	1	1	K
PREDICTED: similar to glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) (EC 1.2.1.12) - mouse	34590	34869386	306407	1	3	11	K
PREDICTED: similar to hypothetical protein 6820428D13	64490	27688925	279415	1	1	2	R
PREDICTED: similar to hypothetical protein BC013949	25320	27668745	274768	1	1	6	R
PREDICTED: similar to hypothetical protein FLJ20254	76570	34863014	234260	1	1	2	K
PREDICTED: similar to immunoglobulin light chain	16750	62647397	161334	1	1	9	R
PREDICTED: similar to mALDP	81940	34881747	306584	1	1	3	R
PREDICTED: similar to mKIAA1311 protein	118700	34879262	281850	1	1	1	R
PREDICTED: similar to magnesium-dependent phosphatase-1	18610	27700106	272326	1	1	11	R
PREDICTED: similar to membrane progesterin receptor alpha	39280	27732829	204220	1	1	6	R
PREDICTED: similar to mitochondrial inner membrane translocase component Tim17b	18380	34933423	256607	1	1	9	R
PREDICTED: similar to novel protein of unknown function (DUF423) family member	11780	27672946	240868	1	1	25	R
PREDICTED: similar to phosphoinositide-3-kinase, regulatory subunit 4, p150	152400	83288384	268833	1	1	1	R
PREDICTED: similar to polypeptide GalNAc transferase-T4	66710	77736615	167222	1	1	2	R
PREDICTED: similar to protein tyrosine phosphatase-like (proline instead of catalytic arginine), member b	15720	34882969	201524	1	1	9	R
PREDICTED: similar to ribosomal protein L10a	24720	27665840	215516	1	4	24	K
PREDICTED: similar to seven transmembrane domain protein	25290	84042519	227176	1	1	8	K
PREDICTED: similar to signal peptidase 12kDa	11750	27667224	307512	1	1	12	K
PREDICTED: similar to signal recognition particle 19kDa	16140	27683535	219536	1	1	10	K
PREDICTED: similar to slingshot-2L	159400	34873212	264614	1	1	2	K
PREDICTED: similar to vesicle associated membrane protein 4	16370	62659601	164208	1	1	9	R
PREDICTED: similar to zinc binding alcohol dehydrogenase, domain containing 2	40480	34932585	231239	1	1	4	R
Peptidyl-prolyl cis-trans isomerase, mitochondrial precursor PPIase Rotamase Cyclophilin F	21810	56268806	88229	1	1	4	R
Peroxisomal biogenesis factor 3 Peroxin-3 Peroxisomal assembly protein PEX3	42210	8926847	12072	1	1	3	K
Phosphatidylcholine transfer protein	24730	8393922	51565	1	1	6	R
Phosphatidylethanolamine N-methyltransferase	22490	6981348	69787	1	1	7	R
Phospholemmann precursor	10470	1916012	78112	1	1	13	R
Phospholipase B	161100	2696236	82680	1	1	1	R
Phosphoserine aminotransferase	40590	29692074	249141	1	1	3	K
Pirin	32180	57164095	304888	1	1	4	K
Potassium voltage-gated channel subfamily A member 6	58880	57667	63679	1	1	2	R
Presenilin 1	52790	6174931	37272	1	1	4	R
Probable ergosterol biosynthetic protein 28	15810	62651081	178365	1	1	9	R
Prostaglandin E synthase 3 Cytosolic prostaglandin E2 synthase cPGES Telomerase-binding protein p23	18720	34862186	25274	1	1	8	K
Hsp90 co-chaperone Progesterone receptor complex p23 Sid 3177							
Prostaglandin G/H synthase 1 precursor	69030	603052	103863	1	1	3	K
Proteasome (Prosome, macropain) 26S subunit, ATPase 3	49560	38304011	71853	1	1	4	K
Proteasome (Prosome, macropain) subunit, beta type 1	26410	37231712	233720	1	1	8	R
Proteasome subunit alpha type 7 Proteasome subunit RC6-1	28330	2118151	72897	1	1	6	K
Proteasome subunit beta type 6 precursor Proteasome delta chain Macropain delta chain Multicatalytic endopeptidase complex delta chain Proteasome subunit Y Proteasome chain 5	25160	464446	134694	1	1	5	R
Protein C2orf18 homolog precursor	41090	81883393	167119	1	1	4	R
Protein C6orf89 homolog	39570	40786457	205305	1	1	4	R
Protein JTB precursor	16390	6016410	128391	1	1	9	K
Protein LRP16	28640	32129697	214491	1	1	4	K
Protein kinase C, alpha type	76790	56914	44893	1	1	2	K
Protein tyrosine phosphatase type IVA protein 1 Protein-tyrosine phosphatase 4a1 Protein-tyrosine phosphatase of regenerating liver 1 PRL-1 PTP(CAAXI)	19820	68566099	4701	1	1	9	R
Protein-tyrosine phosphatase-like N precursor	105200	1113923	11137	1	1	1	START
Proteolipid protein 2	16560	62286961	166582	1	1	8	R

Proto-oncogene C-crk P38 Adapter molecule crk	33840	9506515	95160	1	1	1	6	R
Putative SKAP55 Src family associated phosphoprotein 2	40720	47482120	15613	1	1	1	4	R
Putative secreted protein ZS/G11	33770	56090363	262914	1	1	1	5	R
RAB6-interacting protein 2 ERC protein 1 ERC1 OAZ-associated structural protein 2 CAST2	108800	51701367	165980	1	1	1	1	K
RAT liver glutathione S-transferase YA subunit mRNA	15290	2117744	72819	1	7	7	52	R
RGPR-p117	116800	16758344	60469	1	1	1	1	R
RNA terminal phosphate cyclase domain 1	39310	51948426	319337	1	1	1	4	K
RNA-dependent initiation factor-2 kinase	58260	9506993	47246	1	1	1	2	K
RT1A1(F) protein	39250	1483574	42127	1	4	4	13	R
Rab GDP dissociation inhibitor alpha	50540	71534276	67742	1	3	3	11	R
Rab-related GTP-binding protein Rab38, member of RAS oncogene family	23780	47125439	44313	1	1	1	5	R
Rap guanine nucleotide exchange factor 4 cAMP-regulated guanine nucleotide exchange factor II cAMP-GEFII Exchange factor directly activated by cAMP 2 Epac 2	50120	4115911	173285	1	1	1	3	K
Ras-related C3 botulinum toxin substrate 2 precursor p21-Rac2 EN-7 protein	21440	56605840	8458	1	1	3	17	K
Ras-related protein Rab-11A Rab-11	24390	55249677	41486	1	1	10	54	R
Ras-related protein Rab-13	22900	46577668	169821	1	1	3	16	K
Ras-related protein Rab-1B	22180	56605816	166705	1	1	17	86	K
Ras-related protein Rab-35 Rab-1C GTP-binding protein RAY	23030	62900797	35585	1	2	2	13	K
Ras-related protein Rap-1A	20990	54114993	4747	1	6	6	35	R
Rat alpha(1)-inhibitor 3, variant I precursor	165300	91949	6160	1	1	49	46	K
Ratsg1	40610	18266700	111523	1	1	1	5	R
Retinol-binding protein I, cellular Cellular retinol-binding protein CRBP	15700	809309	105581	1	1	1	9	K
Rh blood group protein RH30	46580	3445506	90519	1	1	1	4	R
Rho guanine nucleotide exchange factor 7 PAK-interacting exchange factor beta Beta-Pix	73140	2865596	2120	1	1	1	2	R
Rho-related GTP-binding protein RhoB precursor H6	22120	51338594	113828	1	3	3	26	K
Ribonuclease 4 precursor RNase 4 RL3	16900	9910536	42830	1	1	1	9	R
Ribosomal protein S27 Metallopanstimulin 1	9461	5924385	4845	1	4	4	39	K
S-arrestin	44990	92737	84325	1	1	1	3	K
S15 ribosomal protein	13360	40287237	337119	1	1	5	55	START
SH3P13 SH3 domain protein 2 C1	35310	7109256	75738	1	1	1	3	K
SIRR-1 precursor	44730	425789	100550	1	1	1	2	R
SWISS-PROT:P12368 cAMP-dependent protein kinase type II-alpha regulatory subunit	41980	206150	168209	1	1	1	4	K
Sarcosine dehydrogenase, mitochondrial precursor SarDH	101400	52000744	85749	1	1	1	3	R
Selenoprotein P precursor	41580	47939025	1271	1	1	1	6	R
Sequestosome-1 Ubiquitin-binding protein p62 Protein kinase C-zeta-interacting protein PKC-zeta-interacting protein	47680	77416574	19107	1	1	1	4	R
Serine (Or cysteine) proteinase inhibitor, clade F, member 2 Predicted	54890	58865362	341343	1	1	1	3	K
Serine protease hepsin Serine protease hepsin non-catalytic chain Serine protease hepsin catalytic chain	44930	8393560	51490	1	1	1	3	R
Serine protease inhibitor, Kunitz type 2	21310	40018550	319145	1	1	1	6	R
Serine/threonine-protein kinase PLK1 Polo-like kinase 1 PLK-1	68310	497994	12071	1	1	1	2	R
Serine/threonine-protein phosphatase 1 regulatory subunit 10 Phosphatase 1 nuclear targeting subunit	92830	61214571	55278	1	1	1	1	K
Protein PNUITS MHC class I region proline-rich protein CAT53	51980	7993726	78346	1	1	1	3	R
Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B delta isoform PP2A, subunit B, B-delta isoform PP2A, subunit B, B55-delta isoform PP2A, subunit B, PR55-delta isoform PP2A, subunit B, R2-delta isoform								
Serotransferrin precursor Transferrin Siderophilin Beta-1-metal-binding globulin	76380	6175089	37301	1	43	43	55	R
Serum amyloid A 4 Predicted	14970	57164089	301225	1	1	1	9	R
Serum paraoxonase/arylesterase 1	38460	1945471	19325	1	12	12	58	START
Short/branched chain specific acyl-CoA dehydrogenase, mitochondrial precursor SBCAD 2-methyl branched chain acyl-CoA dehydrogenase 2-MEBCAD 2-methylbutyryl-coenzyme A dehydrogenase 2-methylbutyryl-CoA dehydrogenase	47820	6978433	3600	1	1	1	5	R
Shwachman-Bodian-Diamond syndrome Predicted	28750	56605652	227484	1	1	1	4	K

Sideroflexin 1	38560	545998	80422	1	9	37	R
Signal recognition particle 14 kDa protein SRP14	12510	27731985	38099	1	1	13	M
Similar to interferon-inducible GTPase	48190	62664492	237237	1	4	15	R
Similar to phospholysine phosphohistidine inorganic pyrophosphate phosphata 5M590	29190	57528359	221017	1	1	8	R
Single-stranded DNA-binding protein, mitochondrial precursor Mt-SSB MSSB P16	17450	423723	44190	1	1	7	R
Small nuclear ribonucleoprotein Sm D1 snRNP core protein D1 Sm-D1 autoantigen	13280	34877889	3858	1	1	17	R
Sodium channel protein type 3 subunit alpha Sodium channel protein type III subunit alpha Voltage-gated sodium channel subunit alpha Nav1.3 Sodium channel protein, brain III subunit alpha Voltage-gated sodium channel subtype III	221400	6981510	75080	1	1	0	R
Sodium/calcium exchanger 1 precursor	108100	57209	44653	1	1	1	R
Solute carrier family 10, member 1	39300	8394279	11254	1	1	4	K
Solute carrier family 21 member 4	62970	19071449	198521	1	3	6	START
Son protein	12550	34849639	313065	1	1	9	R
Sorting nexin 3	18760	79152346	75350	1	1	4	K
Splicing factor, arginine/serine-rich 3	19330	62665747	4905	1	2	13	R
Squalene monooxygenase Squalene epoxidase SE	64020	8394354	137571	1	1	2	R
Sterol 12-alpha hydroxylase	57520	4587057	129969	1	4	10	K
Sterol 12alpha-hydroxylase P450	57590	5360891	75741	1	4	10	K
Stonin	81920	33636736	277960	1	1	1	K
Stromal cell-derived factor-1 gamma	13550	76563910	209385	1	1	12	K
Synaptogyrin-1 p29	25670	9507167	47308	1	1	5	K
Synaptosomal-associated protein 29 SNAP-29 Vesicle-membrane fusion protein SNAP-29 Soluble 29 kDa NSF attachment protein Golgi SNARE of 32 kDa Gs32	29070	6685966	34036	1	1	5	K
Syndecan-1 precursor	33210	6981518	75082	1	1	6	R
Syntaxin 6	29060	51858907	78119	1	1	10	R
Syntaxin-8	26910	3834382	78117	1	1	8	K
TREMBL:O35234 Diphor-1	52250	2331224	80899	1	13	36	K
TREMBL:Q6MG49:Q9WTN8 REFSEQ NP:NP_446061 ENSEMBL:ENSRNOP0000001129 BAT3	114900	4587081	60486	1	1	1	R
TREMBL:Q9EPH2 REFSEQ NP:NP_110489 ENSEMBL:ENSRNOP00000012663 Mac-MARCKS protein	19850	76363234	71714	1	1	8	R
TSH receptor suppressor element-binding protein-1	35530	9653686	93202	1	3	18	R
Target of myb1 homolog	54090	56605806	200982	1	1	3	K
Tax Id=10116 2-oxoglutarate carrier	34250	2497985	23402	1	7	28	K
Tax Id=10116 33 kDa protein	33300	34872473	212891	1	1	4	R
Tax Id=10116 Aldehyde dehydrogenase Family 1, subfamily A4	54560	91935	83139	1	3	8	R
Tax Id=10116 Complement Component 5	134400	34853897	205903	1	1	1	K
Tax Id=10116 Dihydroipomide branched chain transacylase E2	53460	34859889	232730	1	1	3	K
Tax Id=10116 Ensembl locations(Chr-bp):16-73342360 similar to ankyrin	186300	34879099	195573	1	1	1	K
Tax Id=10116 Ensembl locations(Chr-bp):17-77022236 similar to aldo-keto reductase family 1, member C-12	32180	34876320	221880	1	4	15	R
Tax Id=10116 Ensembl locations(Chr-bp):2-120296304 similar to fragile-X-related protein 1 isoform e	68720	34856814	266426	1	1	2	R
Tax Id=10116 Ensembl locations(Chr-bp):2-252454876 similar to crystallin, zeta	37130	34860973	210117	1	1	3	START
Tax Id=10116 Ensembl locations(Chr-bp):2-2908047 glutaredoxin 1 (thioltransferase)	11880	38181944	246362	1	1	10	K
Tax Id=10116 Ensembl locations(Chr-bp):3-141768859 FK506 binding protein 2	11920	501064	43461	1	1	12	M
Tax Id=10116 Ensembl locations(Chr-bp):4-160981651 Serine protease	77790	7435632	13085	1	1	2	K
Tax Id=10116 Ensembl locations(Chr-bp):4-56330652 similar to Impdh1 protein	60730	34855047	190455	1	1	1	K
Tax Id=10116 Ensembl locations(Chr-bp):4-97148803 Hypothetical RNA binding protein RDA288	43010	18041977	114376	1	1	3	R
Tax Id=10116 Ensembl locations(Chr-bp):6-93096989;10-64690010 proteasome (prosome, macropain) subunit, alpha type 3	28420	8394066	45012	1	1	5	K
Tax Id=10116 Ensembl locations(Chr-bp):7-113905923 similar to eukaryotic translation elongation factor 1 delta (guanine nucleotide exchange protein)	31330	27662108	302099	1	1	4	R
Tax Id=10116 Ensembl locations(Chr-bp):7-120740849 similar to alpha-N-acetyl-galactosaminidase	54520	34867288	202900	1	1	4	R

Tax Id=10116 Ensembl locations(Chr-bp):8-46234308 similar to RIKEN cDNA D130038B21	40890	34863198	270449	1	1	3	R
Tax Id=10116 Ensembl locations(Chr-bp):None similar to CLCP	28370	34852289	287945	1	1	5	K
Tax Id=10116 Ensembl locations(Chr-bp):None similar to betaine-homocysteine methyltransferase 2	46420	34861318	247159	1	1	4	R
Tax Id=10116 Glutathione S-transferase theta 1	27470	56265	111659	1	1	5	K
Tax Id=10116 Hypothetical protein XP_213403	19700	34872851	239897	1	1	8	K
Tax Id=10116 Hypothetical protein XP_215523	21540	34854965	295192	1	1	5	K
Tax Id=10116 Hypothetical protein XP_235050	101800	34864725	191344	1	1	1	K
Tax Id=10116 Hypothetical protein XP_342343	17520	34860574	313817	1	1	10	K
Tax Id=10116 Hypothetical protein XP_346991	26610	34857419	273429	1	1	3	R
Tax Id=10116 Integrin, alpha 6	141300	34855181	306780	1	1	1	K
Tax Id=10116 Lactate dehydrogenase B	36610	6981146	3968	1	4	13	K
Tax Id=10116 M4 protein	74540	16124253	136387	1	1	2	R
Tax Id=10116 Major vault protein	95800	49256645	395977	1	24	46	K
Tax Id=10116 P450 (cytochrome) oxidoreductase	76960	66118	78074	1	37	63	R
Tax Id=10116 PDZ domain-containing protein	56890	8439549	78142	1	13	31	R
Tax Id=10116 Similar to 17000131.23Rik protein	22400	34853020	251303	1	1	7	R
Tax Id=10116 Similar to 25 kDa brain-specific protein (p25-alpha)	30720	34853331	206115	1	1	6	R
Tax Id=10116 Similar to 60S ribosomal protein L10 (QM protein homolog)	11450	34853952	238486	1	8	62	R
Tax Id=10116 Similar to 60S ribosomal protein L7a (Surfeit locus protein 3) (PLA-X polypeptide)	26160	34869696	200139	1	10	33	K
Tax Id=10116 Similar to 96300107P1Rik protein	161100	34855819	234438	1	1	1	R
Tax Id=10116 Similar to A-kinase anchor protein 9 isoform 2	441400	34854301	223472	1	1	0	K
Tax Id=10116 Similar to ALY	21140	34875658	307156	1	1	6	R
Tax Id=10116 Similar to Actin monomer-binding protein	204100	34866518	244260	1	1	1	R
Tax Id=10116 Similar to Alanine-tRNA Synthetase (Alanine--tRNA ligase) (AlaRS)	108200	34851760	253193	1	1	2	K
Tax Id=10116 Similar to Ali-1 protein +GFE form - mouSe (fragment)	374300	34863265	267292	1	1	0	K
Tax Id=10116 Similar to Alpha enolase (2-phospho-D-glycerate hydro-lyase) (Non-neutral enolase) (NNE) (Enolase 1)	39350	34875256	313683	1	8	29	K
Tax Id=10116 Similar to Alpha-mannosidase IIx (Mannosyl-oligosaccharide 1,3-1,6-alpha-mannosidase) (MAN IIx) (Mannosidase alpha class 2A member 2)	133000	34857364	209202	1	3	2	R
Tax Id=10116 Similar to Anyloid beta A4 precursor protein-binding family B member 2 (Fe65-like protein)	53090	34877353	294691	1	1	3	K
Tax Id=10116 Similar to Arginine-tRNA-protein transferase 1	51870	34859415	229620	1	1	2	R
Tax Id=10116 Similar to BC013491 protein	76140	34856101	235741	1	1	1	K
Tax Id=10116 Similar to CENTROMERIC PROTEIN E (CENP-E PROTEIN)	313000	34860597	241018	1	1	0	K
Tax Id=10116 Similar to CG11388-PA	36250	34869404	241377	1	1	6	R
Tax Id=10116 Similar to CG33130-PA	132700	34853057	208493	1	1	1	K
Tax Id=10116 Similar to CMP-Sialic acid transporter	36550	34867231	260011	1	1	4	K
Tax Id=10116 Similar to CUB and SuShi multiple domains 3	213400	34866475	195940	1	1	1	R
Tax Id=10116 Similar to Cgn-pending protein	159200	34858031	242726	1	5	3	R
Tax Id=10116 Similar to Complement C5 precursor (Hemolytic complement)	42190	34853846	242533	1	1	4	R
Tax Id=10116 Similar to Cox7a21 protein	12650	27716471	268354	1	1	11	R
Tax Id=10116 Similar to DEAD/H (ASP-Glu-Ala-ASP/HIS) box polypeptide RIG-I	94370	34867138	315303	1	1	2	K
Tax Id=10116 Similar to DNA Segment, Chr 12, ERATO Doi 551, expressed	130300	34865806	300896	1	1	1	K
Tax Id=10116 Similar to DNA-directed RNA polymerase II large subunit (RPB1)	197600	34871645	202233	1	1	1	K
Tax Id=10116 Similar to ENSANGP00000013261	15620	27689183	197176	1	1	7	K
Tax Id=10116 Similar to FERM, RhoGEF, and pleckstrin domain protein 1	23830	34876611	304176	1	1	6	R
Tax Id=10116 Similar to FLJ00354 protein	155900	34861517	210125	1	2	1	R
Tax Id=10116 Similar to GE36	76150	34880541	272300	1	1	2	K
Tax Id=10116 Similar to Herc2	542900	34856238	254063	1	1	0	R
Tax Id=10116 Similar to Hypothetical protein 5031404N19	336600	34867996	239621	1	1	0	K
Tax Id=10116 Similar to Hypothetical protein 9030012M21	37150	34875719	205153	1	1	4	R

Tax	Id=10116	Similar to Hypothetical protein FLJ35794	51380	27708530	166638		1	1	2	K
Tax	Id=10116	Similar to Hypothetical protein KIAA0233	237700	34932058	265857		1	1	0	R
Tax	Id=10116	Similar to Integrin beta-2 precursor (Cell Surface adhesion glycoprotein S LFA-1/CR3/P150.95 beta-Subunit) (CD18) (Complement receptor C3 beta-Subunit)	84530	34852369	241188		1	1	2	K
Tax	Id=10116	Similar to KDEL containing protein 1	60890	34863399	261916		1	1	2	R
Tax	Id=10116	Similar to KIAA0316 protein	140900	34879922	244528		1	1	1	R
Tax	Id=10116	Similar to KIAA0342 protein	333800	34866451	266038		1	1	0	K
Tax	Id=10116	Similar to KIAA0895 protein	71450	34879447	314767		1	1	2	R
Tax	Id=10116	Similar to KIAA0903-like protein	120900	34879170	275605		1	1	2	R
Tax	Id=10116	Similar to KIAA0963 protein	162200	34862323	279597		1	1	1	R
Tax	Id=10116	Similar to KIAA1407 protein	75980	34869160	295453		1	1	1	K
Tax	Id=10116	Similar to KIAA1414 protein	184500	34861977	207796		1	1	1	R
Tax	Id=10116	Similar to KIAA1453 protein	119600	34875569	239514		1	1	1	K
Tax	Id=10116	Similar to KIAA1630 protein	148300	34876831	315956		1	1	1	K
Tax	Id=10116	Similar to KIAA1940 protein	82950	34856348	273209		1	1	1	R
Tax	Id=10116	Similar to Kinetochores-associated protein 1 (Rough deal homolog) (hRod) (HSROD) (Rod)	222900	34872331	265212		1	1	1	R
Tax	Id=10116	Similar to Leukotriene A-4 hydrolase (LTA-4 hydrolase) (Leukotriene A(4) hydrolase)	93570	34864937	286024		1	1	2	K
Tax	Id=10116	Similar to Maltese-glucosylase, intestinal	494700	34855581	199085		1	1	1	R
Tax	Id=10116	Similar to Myk protein	73330	34869218	268038		1	1	1	R
Tax	Id=10116	Similar to Nebulette (Actin-binding Z-disk protein)	121800	34877348	276942		1	1	1	K
Tax	Id=10116	Similar to Nedd4 WW binding protein 4	32550	34860870	317802		1	1	3	R
Tax	Id=10116	Similar to PTB-associated Splicing factor	65140	34871066	310879		1	1	3	R
Tax	Id=10116	Similar to Protein Njmu-R1	44430	34872893	315828		1	1	4	K
Tax	Id=10116	Similar to RIKEN cDNA 111003102	36810	34875673	300976		1	1	3	R
Tax	Id=10116	Similar to RIKEN cDNA 1110059L24	27770	34854713	201498		1	1	8	K
Tax	Id=10116	Similar to RIKEN cDNA 1200014J11	80090	34872727	249723		1	1	2	R
Tax	Id=10116	Similar to RIKEN cDNA 1300014E15	74920	34877442	203301		1	1	2	R
Tax	Id=10116	Similar to RIKEN cDNA 1700034M03 gene	122500	34854321	261953		1	1	1	R
Tax	Id=10116	Similar to RIKEN cDNA 2610020H15	71080	34872958	298062		1	1	2	R
Tax	Id=10116	Similar to RIKEN cDNA 2610207I16	122600	34868438	250916		1	1	2	K
Tax	Id=10116	Similar to RIKEN cDNA 2810025M15	71590	34880767	272641		1	1	4	R
Tax	Id=10116	Similar to RIKEN cDNA 4632417N05	35570	34851797	239422		1	1	6	R
Tax	Id=10116	Similar to RIKEN cDNA 4732474A20 gene	70120	34862810	190227		1	3	6	R
Tax	Id=10116	Similar to RIKEN cDNA 4932408F18	164100	34867309	293100		1	1	1	R
Tax	Id=10116	Similar to RIKEN cDNA 4933412D19	51730	34858091	273635		1	1	3	R
Tax	Id=10116	Similar to RIKEN cDNA 5630401D24	81090	34880803	213507		1	1	2	R
Tax	Id=10116	Similar to RIKEN cDNA 5730507E09	131000	34867616	273407		1	1	1	R
Tax	Id=10116	Similar to RIKEN cDNA 6430520C02	89840	34881696	266670		1	1	1	R
Tax	Id=10116	Similar to RIKEN cDNA 9530027K23	73500	34851643	224054		1	1	2	K
Tax	Id=10116	Similar to RIKEN cDNA 9630046K23	41350	34869346	228920		1	1	4	K
Tax	Id=10116	Similar to RNA helicase family	238800	34853214	288172		1	1	1	R
Tax	Id=10116	Similar to Rab24 protein	26250	34873657	250158		1	1	5	K
Tax	Id=10116	Similar to SH3 domain protein D19	125000	34857900	291964		1	1	1	R
Tax	Id=10116	Similar to Semaphorin Subclass 4 member G	128000	34863455	222218		1	1	1	R
Tax	Id=10116	Similar to Serine/threonine kinase	179600	34874060	212247		1	1	0	K
Tax	Id=10116	Similar to Sialic-acid O-acetyltransferase	56760	34863093	198275		1	1	2	K
Tax	Id=10116	Similar to Sidekick 2	185200	34875033	275767		1	1	1	K
Tax	Id=10116	Similar to Sif and Tiam1-like exchange factor	155900	34853702	204958		1	1	1	R
Tax	Id=10116	Similar to Solute carrier family 30 (zinc transporter), member 6	51480	34862482	294808		1	1	3	R
Tax	Id=10116	Similar to Structural maintenance of chromosome 1beta	147300	34867523	216707		1	1	1	K
Tax	Id=10116	Similar to Sulfide quinone reductase-like	78570	34856819	285775		1	1	2	K
Tax	Id=10116	Similar to T-box 1	54510	34861377	314602		1	1	2	R

Tax Id=10116 Similar to TAFII140 protein	85530	34876351	313782	1	1	1	1	R
Tax Id=10116 Similar to TTF-1 interacting protein 5	17300	34862191	316025	1	1	1	1	K
Tax Id=10116 Similar to Trim26 protein	47090	34852035	264688	1	1	1	5	R
Tax Id=10116 Similar to TyroSine-protein kinaSe JAK1 (JanuS kinaSe 1) (JAK-1)	150400	34869913	290958	1	1	1	1	R
Tax Id=10116 Similar to UDP-glucuronate decarboxylaSe 1	20220	34881188	201012	1	1	1	4	K
Tax Id=10116 Similar to UNR-interacting protein (Serine-threonine kinaSe receptor-aSociated protein)	48180	34858563	269251	1	1	1	2	R
Tax Id=10116 Similar to WAVE2	41650	34871786	222802	1	2	2	9	K
Tax Id=10116 Similar to WD repeat domain 9 iSoform A	225200	34881323	312923	1	1	1	1	K
Tax Id=10116 Similar to actin - Hydra attenuata	13310	34871187	219221	1	1	1	6	M
Tax Id=10116 Similar to acyltranSferaSe family member (5G933)	33640	34862502	237775	1	1	1	3	R
Tax Id=10116 Similar to alpha-2u-globulin	61070	34868545	210822	1	1	7	10	R
Tax Id=10116 Similar to alpha-catenin-like protein	21080	34852606	311543	1	1	1	6	K
Tax Id=10116 Similar to aminoadipate-Semialdehyde Synthase	92010	34855019	258586	1	1	1	2	K
Tax Id=10116 Similar to amylol-1,6-glucosidaSe, 4-alpha-glucanotranSferaSe iSoform 1	180900	34859913	208010	1	1	1	1	K
Tax Id=10116 Similar to apoA-I binding protein	78970	34857927	303449	1	1	1	3	K
Tax Id=10116 Similar to archivillin	236900	34876218	258828	1	1	1	1	K
Tax Id=10116 Similar to autocrine motility factor receptor	68290	34851252	285136	1	1	1	3	R
Tax Id=10116 Similar to ba261P9.2 (putative novel protein Similar to fly CG7340 and human putative aminopeptidaSe ZK353.6 in chromoSome 3 (EC 3.4.11.-))	99960	34860876	296511	1	1	1	2	R
Tax Id=10116 Similar to beta1-Syntrophin	46920	34866568	190168	1	1	1	5	K
Tax Id=10116 Similar to breakpoint cluSter region protein	177200	34852435	289382	1	1	1	1	R
Tax Id=10116 Similar to bromodomain-containing protein BRD4 Short variant	159800	34862361	292562	1	1	1	1	R
Tax Id=10116 Similar to bullous pemphigoid antigen 1-b	1087000	34874618	233230	1	1	1	0	K
Tax Id=10116 Similar to chromoSome 14 open reading frame 9	34520	34869712	209283	1	1	1	3	R
Tax Id=10116 Similar to chromoSome 17 open reading frame 27	668500	34875599	199223	1	1	1	0	R
Tax Id=10116 Similar to coiled-coil protein	148900	34869656	304228	1	1	1	1	R
Tax Id=10116 Similar to complement component 8 alpha Subunit	62090	34869994	295319	1	1	1	5	K
Tax Id=10116 Similar to copine IV	96010	34865971	245798	1	1	1	1	K
Tax Id=10116 Similar to dJ14N1.2 (novel S-100/CaBP type calcium binding domain protein, Similar to Trichohyalin)	133800	34858169	280707	1	1	1	1	R
Tax Id=10116 Similar to dedicator of cyto-kineSiS 2	113200	34861140	200712	1	1	1	1	K
Tax Id=10116 Similar to development- and differentiation-enhancing factor 2	119200	34863212	230447	1	1	1	1	K
Tax Id=10116 Similar to embryonic blasToocoeal extracellular matrix protein precuSor	242800	34851569	303538	1	1	1	1	K
Tax Id=10116 Similar to eukaryotic tranSlation initiation factor 3, Subunit 5 epSiIon, 47kDa	35120	34858904	213255	1	1	1	6	R
Tax Id=10116 Similar to ferrochelatase	71200	34932061	313806	1	1	1	2	R
Tax Id=10116 Similar to heterogeneous nuclear ribonucleoprotein D-like	58310	34876235	191966	1	1	2	4	K
Tax Id=10116 Similar to hiStidyl-tRNA Synthetase-like	82680	34878791	223302	1	1	1	1	R
Tax Id=10116 Similar to hyaluronan receptor for endocytosiS HARE precuSor	58970	34868786	260956	1	1	4	10	K
Tax Id=10116 Similar to hypothetical protein	390800	34853159	241253	1	1	1	0	R
Tax Id=10116 Similar to hypothetical protein	125800	34878417	272431	1	1	1	2	K
Tax Id=10116 Similar to hypothetical protein	141900	34854842	233766	1	1	1	1	R
Tax Id=10116 Similar to hypothetical protein	96350	34867679	290052	1	1	1	1	R
Tax Id=10116 Similar to hypothetical protein BC002942	107600	34866614	302504	1	1	1	2	K
Tax Id=10116 Similar to hypothetical protein FLJ10375	91330	34872498	233304	1	1	1	2	K
Tax Id=10116 Similar to hypothetical protein FLJ10737	93700	34872027	198580	1	1	1	2	K
Tax Id=10116 Similar to hypothetical protein FLJ11274	34120	34866189	272995	1	1	1	6	K
Tax Id=10116 Similar to hypothetical protein FLJ12681	90650	34870562	205672	1	1	1	2	K
Tax Id=10116 Similar to hypothetical protein FLJ14681	65310	34858680	304442	1	1	1	1	R
Tax Id=10116 Similar to hypothetical protein FLJ20531	57240	34871405	217607	1	1	1	2	K
Tax Id=10116 Similar to hypothetical protein FLJ21665	52020	34876595	213091	1	4	1	8	R
Tax Id=10116 Similar to hypothetical protein FLJ21820	32850	34863103	317090	1	1	1	6	R
Tax Id=10116 Similar to hypothetical protein FLJ21963	91790	34865010	243174	1	1	1	2	R

Tax	Id=10116	Similar to hypothetical protein FLJ30373	29880	34855399	229721	1	1	3	R
Tax	Id=10116	Similar to hypothetical protein FLJ30596	16050	34854388	283019	1	1	3	R
Tax	Id=10116	Similar to hypothetical protein FLJ31657	64050	34855501	253349	1	1	2	K
Tax	Id=10116	Similar to immunoglobulin 4G6 light chain variable region	17890	34855968	195860	1	1	9	R
Tax	Id=10116	Similar to intracellular membrane-associated calcium-independent phospholipase A2 gamma	107800	34865151	313999	1	1	1	K
Tax	Id=10116	Similar to kidney ankyrin repeat-containing protein	127000	34860436	261449	1	1	1	K
Tax	Id=10116	Similar to lysosomal aspartate-like 1	40920	34874392	217901	1	1	3	R
Tax	Id=10116	Similar to lymphocyte cytosolic protein 1	80290	34875362	272629	1	3	5	K
Tax	Id=10116	Similar to mKIAA1402 protein	86520	34853978	259133	1	1	2	R
Tax	Id=10116	Similar to malignant cell expression-enhanced gene/tumor progression-enhancer	33720	34854458	281230	1	1	7	R
Tax	Id=10116	Similar to meiotic recombination protein REC14	28800	34863419	201803	1	1	6	K
Tax	Id=10116	Similar to melanoma inhibitory activity protein 2	58930	34865264	225113	1	1	4	K
Tax	Id=10116	Similar to membrane receptor (5H375)	42380	34865609	318262	1	1	5	R
Tax	Id=10116	Similar to methionyl aminopeptidase 1	53240	34860820	221417	1	1	2	K
Tax	Id=10116	Similar to myosin X	251600	34855017	249318	1	1	0	K
Tax	Id=10116	Similar to nonclathrin coat protein zeta2-COP	18220	34873491	273036	1	1	6	R
Tax	Id=10116	Similar to osmotic stress protein	148000	34856875	290180	1	4	3	K
Tax	Id=10116	Similar to osteodistal inhibitory lectin	23540	34858508	255984	1	1	6	R
Tax	Id=10116	Similar to p140mDia	140200	34878815	217100	1	1	1	K
Tax	Id=10116	Similar to peptidylprolyl isomerase D (cyclophilin D)	69130	34873471	283106	1	1	2	R
Tax	Id=10116	Similar to phosphatidylinositol glycan class N	89310	34878866	217052	1	1	2	K
Tax	Id=10116	Similar to poliovirus receptor homolog	76950	34855325	279332	1	1	2	R
Tax	Id=10116	Similar to protein RAKC	41260	34876322	249119	1	2	9	K
Tax	Id=10116	Similar to protein tyrosine phosphatase, receptor type, D isoform 3 precursor	203600	34869007	215340	1	1	1	R
Tax	Id=10116	Similar to putative mannitol synthase	59900	34867585	231757	1	1	2	K
Tax	Id=10116	Similar to putative zinc finger transcription factor OVO1	37260	27661858	294340	1	1	2	R
Tax	Id=10116	Similar to retinal short-chain dehydrogenase/reductase	43630	34872444	294993	1	1	4	R
Tax	Id=10116	Similar to ribosomal protein L27	22160	34875503	301863	1	1	11	K
Tax	Id=10116	Similar to ribosomal protein S15	50300	34851670	224899	1	1	3	K
Tax	Id=10116	Similar to ribosomal protein S6 kinase, 52kDa, polypeptide 1	40530	34881360	216365	1	1	2	R
Tax	Id=10116	Similar to ribosomal protein S6 kinase, polypeptide 4	86910	34935429	292778	1	1	2	K
Tax	Id=10116	Similar to ring finger protein 20	122200	34868389	236982	1	1	1	K
Tax	Id=10116	Similar to teStS protein TEX15	282400	34866738	211558	1	1	1	R
Tax	Id=10116	Similar to the first amino acid was determined to be isoleucine rather than methionine by comparison to mTEF1 (aScSSion # L13853)	78480	34858488	267553	1	1	1	K
Tax	Id=10116	Similar to toll-like 2	23740	34883204	298591	1	1	6	K
Tax	Id=10116	Similar to transthyretin (4L369)	16010	34861187	199559	1	1	11	K
Tax	Id=10116	Similar to tricarboxylate carrier	40660	34873877	278396	1	9	34	R
Tax	Id=10116	Similar to tubulin, alpha 6	63060	34868254	298819	1	19	46	K
Tax	Id=10116	Similar to ubiquitin ligase E3 alpha-II	175300	34874398	274677	1	1	1	R
Tax	Id=10116	Similar to ubiquitous tetrapeptide containing protein RoXa	111900	34867257	230656	1	1	1	K
Tax	Id=10116	Similar to vascular endothelial zinc finger 1	82930	34872980	252804	1	1	3	R
Tax	Id=10116	Similar to villin-like protein	99190	34866628	253969	1	1	1	K
Tax	Id=10116	Similar to xylulokinase homolog	66490	34866669	229118	1	1	3	K
Tax	Id=10116	Similar to zinc finger protein, Subfamily 1A, 4	64460	34862217	313581	1	1	2	START
Tax	Id=10116	Solute carrier family 25, member 5	32900	728810	117684	1	16	50	K
Tax	Id=10116	Telomerase protein component 1 rTLP1 Telomerase-associated protein 1 Telomerase protein 1 p240 p230 p80 telomerase homolog	291700	47606056	169376	1	1	0	R
Tax	Id=10116	Tetraspanin-31 Sarcoma amplified sequence homolog	22660	62900748	260364	1	1	6	R
Tax	Id=10116	Thioredoxin-related transmembrane protein 2	33870	56090369	227628	1	1	4	K
Tax	Id=10116	Trafficking protein particle complex subunit 3 BE13 homolog	20300	71153350	145735	1	1	7	R
Tax	Id=10116	Transaldolase	37480	17433174	50402	1	1	3	K

Transcobalamin-2 precursor, Transcobalamin II TCII TC II	47420	5910985	90533	1	1	1	3	K
Transmembrane protein 14C p11	11780	27734399	30411	1	1		25	K
Transmembrane protein induced by tumor necrosis factor alpha	40660	58219512	260939	1	1	1	5	R
Tripeptidyl-peptidase 1 precursor Tripeptidyl-peptidase I TPP-I Tripeptidyl aminopeptidase	61330	20140356	75921	1	1	1	2	R
Tryptophan 2,3-dioxygenase	47860	59809151	11402	1	1	1	4	K
Tumor-related protein Adult male medulla oblongata cDNA, RIKEN full-length enriched library, clone:6330565A20 product:Tumor-related protein (Hypothetical protein), full insert sequence	32030	62664482	8904	1	1	1	5	R
Isochorismatase domain containing 1								
Type I keratin KA17	48120	71682170	301880	1	1	7	14	R
Type I keratin KA22	50210	57012446	161849	1	1	4	11	R
Type II keratin Kb15	57610	46485029	222258	1	1	8	11	R
Tyrosine-protein kinase LYN	58660	294583	71712	1	1	2	5	K
UDP-glycosyltransferase 1 family polypeptide A7 UDP-glycosyltransferase 1 family, polypeptide A6	60240	89276780	205347	1	1	22	52	R
UDP-glucuronosyltransferase 1A6	60250	1890306	53068	1	1	22	52	K
UDP-glucuronosyltransferase 2B12 precursor, microsomal	60920	458397	127236	1	1	15	41	R
Ube2-prov protein	18010	6981690	22316	1	1	1	8	K
Ubiquinone biosynthesis protein COQ7 homolog Coenzyme Q biosynthesis protein 7 homolog Timing protein clk-1 homolog	20140	7446711	30131	1	1	1	6	R
Ubiquitin specific protease 1 Predicted	87330	62543525	282121	1	1	1	1	K
Ubiquitin-conjugating enzyme E2 G2 Ubiquitin-protein ligase G2 Ubiquitin carrier protein G2	18570	62665819	58922	1	1	1	15	K
Uncharacterized protein C20orf30 homolog	13200	81882492	190070	1	1	1	9	R
Uncharacterized protein family UPF0227 member RGD1359682	33990	55741536	265453	1	1	1	5	K
Urinary protein 1 precursor RUP-1 Liver regeneration-related protein LRRG05	10960	6537316	37481	1	1	1	11	R
Uroporphyrinogen decarboxylase	40450	5524747	44446	1	1	1	6	R
Vacuolar protein sorting 26 Vesicle protein sorting 26	38110	78099277	276682	1	1	1	4	R
Vacuolar protein sorting 33A	67510	23396893	55286	1	1	1	4	R
Vacuolar proton translocating ATPase 116 kDa subunit a isoform 1 V-ATPase 116 kDa isoform a1 Clathrin-coated vesicle/synaptic vesicle protein pump 116 kDa subunit Vacuolar proton pump subunit 1 Vacuolar adenosine triphosphatase subunit Act116	96330	206430	11413	1	1	1	1	R
Vesicle-associated membrane 2	12690	6981614	38248	1	1	4	34	R
Vesicle-associated membrane protein 3 VAMP-3 Synaptobrevin-3 Cellubrevin CEB	11480	56789137	23581	1	1	4	39	R
Vitamin K epoxide reductase complex subunit 1 Vitamin K1 2,3-epoxide reductase subunit 1	17780	62511143	291525	1	1	1	11	R
Vitamin K epoxide reductase complex subunit 1-like protein 1 VKORC1-like protein 1	19780	62511142	165266	1	1	1	6	R
Xanthine dehydrogenase/oxidase	146300	2144323	80445	1	1	1	1	K
alpha-1-inhibitor III precursor	19360	554401	66447	1	1	6	54	K
apolipoprotein C-III precursor - rat	11030	91990	84170	1	1	1	19	K
ble canalicular-specific membrane glycoprotein precursor	90930	204464	11237	1	1	19	25	R
cAMP-dependent protein kinase, alpha-catalytic subunit (PKA C-alpha)	40620	125207	168211	1	1	4	11	R
cathepsin J peak 2 [rats, liver, Peptide Partial, 34 aa]	3838	245685	79044	1	1	1	59	START
claudin 1	22870	61889099	318701	1	1	1	8	K
cytochrome P450	57160	203695	126560	1	1	38	85	K
cytochrome P450, family 2, subfamily c, polypeptide 23	56490	58825	78212	1	1	28	61	R
cytochrome-c oxidase (EC 1.9.3.1) chain VIIa, hepatic - rat (fragment)	1246	7513957	80282	1	1	1	80	START
divalent cation tolerant protein CUTA	16410	61212255	281056	1	1	1	6	M
ezrin, p81 [Rattus norvegicus]	18790	56126	85113	1	1	1	6	K
fibrinopeptide A	1740	229210	22617	1	1	1	100	START
fibrinopeptide B	1492	229196	22616	1	1	1	100	START
fumarase	54460	227665	168825	1	1	7	26	K
hemoglobin beta chain, minor - rat	15990	92362	84237	1	1	17	90	K
hypothetical protein XP_343009	87580	34862025	301974	1	1	1	1	R
hypothetical protein XP_343478	31580	34865907	203844	1	1	1	5	K

hypothetical protein XP_344851	46260	34854602	287423	1	1	1	3	K
hypothetical protein XP_347087	13870	34866914	300655	1	1	1	7	K
immunoglobulin kappa-chain	14860	204835	126680	1	1	1	10	R
kynureninase (L-kynurenine hydrolase)	52450	3913969	157223	1	1	1	3	K
lanosterol synthase	83330	13591981	37206	1	12	12	20	R
major vault protein - rat	99530	7514005	132766	1	24	24	42	R
roundabout (axon guidance receptor, Drosophila) homolog 2 [Rattus norvegicus]	176100	34867440	317126	1	1	1	0	START
secreted frizzled-related protein 1	35350	34879084	271324	1	1	1	3	START
sialyltransferase 1	25210	285193	41195	1	7	7	41	K
similar to 2310036102Rik protein	89350	34932104	265519	1	1	1	2	R
similar to 40S ribosomal protein S2 [Rattus norvegicus]	28120	34868798	193682	1	12	12	42	K
similar to 60S ribosomal protein L15	23920	34869871	293440	1	7	7	33	R
similar to 60S ribosomal protein L36	12250	34856346	214593	1	6	6	38	R
similar to 9530008L14Rik protein [Rattus norvegicus]	11600	34875157	310564	1	1	1	8	K
similar to ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9), isoform 2	14750	27685029	262837	1	1	1	6	R
similar to Apoptosis inhibitor 5	36870	34878251	281550	1	1	1	5	K
similar to Asparaginyl-tRNA synthetase, cytoplasmic (Asparagine--tRNA ligase) (AsnRS)	64130	34932063	238208	1	1	1	3	K
similar to BLOCK 23	30630	34869320	240773	1	2	2	6	K
similar to CG33130-PA	125000	34870072	215152	1	1	1	1	K
similar to CG8014-PA	55190	34865850	245025	1	1	1	2	R
similar to CGI-90 protein	52100	34867201	258588	1	1	1	2	K
similar to Conserved oligomeric Golgi complex subunit 5 (13S Golgi transport complex 90 kDa subunit) (GTC-90) (Golgi transport complex 1)	23020	34864266	295519	1	1	1	8	K
similar to DNA (cytosine-5)-methyltransferase 3A (Dnmt3a) (DNA methyltransferase Mmullia) (Mmullia)	59410	34871224	241066	1	1	1	1	R
similar to Dysferlin (Dystrophy associated fer-1 like protein) (Fer-1 like protein 1) [Rattus norvegicus]	224600	34856330	229917	1	1	1	1	R
similar to Elongation factor 1-alpha 1 (EF-1-alpha-1) (Elongation factor 1 A-1) (eEF1A-1) (Elongation factor Tu) (EF-Tu)	45440	34880757	223872	1	10	10	21	K
similar to Exocyst complex component Sec6 (rSec6)	72270	34855314	276511	1	1	1	1	R
similar to Fc fragment of IgG binding protein: IgG Fc binding protein	583400	34855405	285938	1	1	1	0	R
similar to Glyceraldehyde 3-phosphate dehydrogenase (GAPDH) (38 kDa BFA-dependent ADP-ribosylation substrate) (BARS-38)	13770	34858500	247025	1	1	1	13	K
similar to Glycine decarboxylase [Rattus norvegicus]	111900	34862790	260747	1	1	1	2	R
similar to HTPAP protein	29160	34879054	255469	1	1	1	4	R
similar to Heat shock cognate 71 kDa protein	64610	34855549	236971	1	18	18	31	K
similar to Histone H2A.o (H2A.o) (H2A.2) (H2a-615)	21070	34858256	279473	1	2	2	25	R
similar to Hypothetical protein KIAA0379	41000	27732065	190049	1	1	1	3	K
similar to KIAA0946 protein	84730	34864845	282355	1	1	1	4	K
similar to LDL receptor adaptor protein	60620	34872138	266460	1	1	1	2	K
similar to Liver carboxylesterase 1 precursor (Carboxylesterase ES-1) (E1) (ES-THET)	26910	34882067	308005	1	2	2	9	R
similar to N-acetylneuraminic acid synthase (sialic acid synthase)	40050	27714479	225772	1	1	1	8	K
similar to NADH dehydrogenase (ubiquinone) 1 beta subcomplex 3	11280	34876452	287362	1	1	1	11	K
similar to NADH:ubiquinone oxidoreductase B15 subunit	15060	82617686	192715	1	1	1	19	K
similar to NADP+-specific isocitrate dehydrogenase	14720	34857317	195949	1	1	1	10	K
similar to PKR-associating protein RAX	34390	34856450	191003	1	1	1	6	R
similar to PalBH [Rattus norvegicus]	90550	34876995	233624	1	1	1	1	R
similar to Phosphoacetylglucosamine mutase (PAGM) (Acetylglucosamine phosphomutase) (N-acetylglucosamine-phosphate mutase) (Phosphoglucomutase 3) [Rattus norvegicus]	50750	34865378	202185	1	1	1	2	R

similar to Proteasome activator complex subunit 2 (Proteasome activator 28-beta subunit) (PA28beta) (PA28b) (Activator of multicatalytic protease subunit 2) (11S regulator complex beta subunit) (REG-beta)	23620	34879501	244453	1	1	4	K
similar to Pyruvate kinase, M2 isozyme	57960	34875446	288218	1	1	2	K
similar to RIKEN cDNA 181003N24	31780	34873957	230313	1	1	4	K
similar to RIKEN cDNA 1810045K17	10150	34857339	270299	1	1	16	K
similar to RIKEN cDNA 2010005O13 [Rattus norvegicus]	15020	34880819	301426	1	1	7	K
similar to RIKEN cDNA 241002O22 gene [Rattus norvegicus]	22220	34853743	269534	1	1	6	K
similar to RIKEN cDNA 2810409H07 [Rattus norvegicus]	42320	34855205	260021	1	1	4	K
similar to RIKEN cDNA 9430097N02 [Rattus norvegicus]	81520	34869388	230365	1	1	2	R
similar to RIKEN cDNA C920006C10	16670	27718855	264993	1	1	9	K
similar to RNA-binding protein isoform G3BP-2a	54070	34876568	211028	1	1	4	K
similar to Rap2c protein	13510	34881637	197399	1	1	10	K
similar to SLIT-ROBO Rho GTPase-activating protein 3; WAVE-associated Rac GTPase activating protein	35530	34879743	229135	1	1	4	R
similar to SSC2	59620	34875179	315186	1	1	3	K
similar to Sh3bgl protein	12800	27706424	198937	1	1	16	R
similar to Synprosin 1	26760	72255531	250786	1	1	5	K
similar to T-cell activation leucine repeat-rich protein	92210	34876057	221702	1	1	2	K
similar to Txnrd1 protein	31430	67078422	283888	1	1	4	K
similar to UDP-galactose transporter	38530	34933455	208424	1	1	4	K
similar to WD repeat domain 20 isoform 1	65240	34935498	289309	1	1	2	K
similar to Wdr1 protein [Rattus norvegicus]	48550	34878397	292693	1	1	4	K
similar to Wolf-Hirschhorn syndrome candidate 1 protein isoform 1; IL5 promoter RE11 region-binding protein; trithorax/ash1-related protein 5; multiple myeloma SET domain protein	152600	34878518	214625	1	1	1	K
similar to adaptor-related protein complex 2, beta 1 subunit	105700	34876358	254285	1	16	18	K
similar to adenine nucleotide translocase	32800	34866578	257029	1	8	24	R
similar to apoptosis-inducing factor (AIF)-homologous mitochondrion-associated inducer of death; p53-responsive gene 3 [Rattus norvegicus]	14880	34852510	209377	1	1	10	R
similar to aspartyl beta-hydroxylase	53800	34866148	285481	1	1	4	K
similar to butyrate-induced transcript 1	28810	34864679	236762	1	1	4	R
similar to cAMP-dependent protein kinase, beta-2-catalytic subunit (PKA C-beta-2)	73330	34861056	256498	1	4	6	R
similar to cDNA sequence BC003251	53180	34871409	253866	1	1	3	K
similar to chromosome 20 open reading frame 169	20950	34860687	214268	1	1	12	R
similar to endo B cytochrome	42970	34860580	202236	1	4	14	R
similar to endonuclease G	32270	77917570	273385	1	1	4	R
similar to ethanol induced 6	15850	27686507	168139	1	1	16	R
similar to glyceraldehyde-3-phosphate dehydrogenase	36450	34852715	210943	1	3	13	K
similar to glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) (EC 1.2.1.12) - mouse	31550	34864978	296252	1	3	17	K
similar to glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) (EC 1.2.1.12) - mouse	27870	27699577	156654	1	1	5	K
similar to glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) (EC 1.2.1.12) - mouse	46820	34856839	252379	1	1	4	R
similar to golgi-associated microtubule-binding protein HOOK3; hook3 protein [Rattus norvegicus]	83230	34879033	220378	1	1	2	K
similar to heat shock protein 105 kDa alpha	82350	34870188	195465	1	1	1	R
similar to hepatocellular carcinoma autoantigen	13340	34869447	272734	1	1	5	R
similar to hypothetical protein A	36410	34869364	193827	1	1	3	K
similar to hypothetical protein D4Etd89e	46520	34868399	231118	1	1	2	R
similar to hypothetical protein FLJ14675	21510	34873570	196884	1	1	6	R
similar to hypothetical protein FLJ20331 [Rattus norvegicus]	48370	34861003	248047	1	1	4	R
similar to hypothetical protein FLJ22625	35090	34865046	243991	1	1	4	R
similar to hypothetical protein FLJ22865	33930	34872934	263071	1	1	3	K
similar to hypothetical protein MGC10084	42080	34851552	202821	1	1	4	K
similar to hypothetical protein MGC23280	35980	34872804	277215	1	1	4	R
similar to inhibitor of growth family, member 3	56500	34855011	234073	1	1	2	R

similar to keratin associated protein 11-1	18900	27670141	269756	1	1	1	6	R
similar to keratinocytes associated protein 2	27650	34857976	235658	1	1	1	7	K
similar to male enhanced antigen 2/golgi autoantigen, golgin subfamily a, 3 [Rattus norvegicus]	166100	34873054	267138	1	1	1	1	K
similar to microchidia	55070	34869318	309715	1	1	1	2	K
similar to mirror-image polydactyly gene 1	52780	34865613	265130	1	1	1	2	R
similar to osteoclast stimulating factor 1	34620	34880977	297002	1	1	1	6	K
similar to peroxisomal long chain acyl-CoA thioesterase Ia	46360	27667388	160562	1	1	1	3	K
similar to proline dehydrogenase; PRODH	12130	27665096	305160	1	1	1	15	K
similar to rab20	32660	34879665	240940	1	1	1	2	K
similar to receptor-interacting protein 2	60780	34867073	242276	1	1	1	2	K
similar to recombination activating 1 activation	24690	27692967	292043	1	1	1	9	R
similar to ribosomal protein S12; 40S ribosomal protein S12	12210	34869042	285721	1	2	2	29	START
similar to splicing coactivator subunit SRm300; RNA binding protein; AT-rich element binding factor [Rattus norvegicus]	212600	34868816	290757	1	1	1	0	K
similar to thyroid hormone receptor interactor 11; thyroid receptor interacting protein 11	37170	34867559	280942	1	1	1	4	R
similar to torsinB protein	17860	34853518	202385	1	1	1	9	K
similar to ubiquitin-protein ligase (EC 6.3.2.19) E1 - mouse	123600	34933178	317625	1	1	1	1	R
synaptogyrin 2	25710	6685963	60460	1	1	1	4	R
unknown	84160	34880715	314842	1	1	1	1	R
unknown	26610	84781644	345922	1	1	1	6	R
unknown	167300	34869344	309548	1	1	1	1	K
unknown	111800	34872548	263673	1	1	1	1	R

CMBSEQID	PEPTIDE SEQUENCE	C-TERM AA	m/z	+ CHARGE	Experimental peptide mass	DELTA	Calculated peptide mass	MASCOT SCORE	ID SCORE
71624	SYGPIFIETSAK	T	656.84	2	1311.66	-0.01	1311.67	33.21	31
268104	ASEDEKLKLR	L	530.86	2	1059.71	0.15	1059.56	36.08	32
129647	RMVSASLHVR	L	578.32	2	1154.62	-0.01	1154.63	35.00	31
13883	SQPMVLR	G	423.73	2	845.44	0.00	845.44	41.38	33
292598	AGDTLSGTCLLIANK	R	767.27	2	1532.52	-0.27	1532.79	45.34	30
166274	DLIASILSEVTPTLEELR	S	1106.09	2	2210.17	0.00	2210.17	90.28	29
33375	GYSFSLTTFSPSGK	L	739.94	2	1477.86	0.15	1477.71	98.05	30
723160	AGLILFGNDDR	M	595.84	2	1189.66	0.06	1189.61	54.95	32
29710	NSVVEASEAAYKEAFEISK	E	691.23	3	2070.66	-0.35	2071.01	32.62	28
98449	EGPPFISEAAVR	G	636.90	2	1271.79	0.14	1271.65	88.97	30
109735	DLPLYFGWFLTK	K	823.96	2	1645.90	0.04	1645.85	48.65	30
37174	NLLAEVINIK	R	676.96	2	1351.90	0.05	1351.84	62.96	31
124397	FKDLGEEENFK	A	613.78	2	1225.55	-0.05	1225.60	63.68	31
23444	NHQDPLAVAYHLIIDNR	R	663.67	3	1987.99	-0.03	1988.02	40.04	29
65711	RAMELLK	V	430.81	2	859.61	0.12	859.49	33.11	33
3029	KYNWSAK	A	448.75	2	895.49	0.04	895.46	34.99	31
4822	QNRPIQWIR	M	436.60	3	1306.79	0.07	1306.73	37.17	31
77849	IIEPSLR	Q	414.28	2	826.55	0.06	826.49	40.48	31
32753	ASVDELFAEIVR	Q	674.86	2	1347.70	-0.01	1347.70	40.20	31
90531	IGTSGFTGVR	G	571.32	2	1140.63	0.03	1140.59	35.45	31
139514	WITEQQQR	F	538.75	2	1075.48	-0.03	1075.50	54.08	32
93024	EYPTVFDNYSQAQSAVDGR	T	1066.55	2	2131.09	0.11	2130.99	35.88	29
11887	DALKTEFK	A	476.26	2	950.51	0.00	950.51	49.26	32
264038	ILLDEATSALDAENEHLVQEALDR	L	926.81	3	2777.40	-0.01	2777.41	58.60	27
52680	SKILLALAEKG	I	571.84	2	1141.67	-0.03	1141.71	32.37	31
231492	GAVIVVSHDAR	L	562.31	2	1122.60	-0.01	1122.61	43.62	31

311925	VGTLIDLVLGSLDELAK	L	814.98	2	1627.94	0.04	1627.90	45.69	30
160475	TLAYITELDER	E	718.88	2	1435.74	-0.02	1435.76	30.99	30
148924	LELANIQAEILVAK	A	706.44	2	1410.86	0.05	1410.81	34.39	30
244467	NLEIWLNKYI	END	653.27	2	1304.52	-0.19	1304.71	36.27	31
263869	EGDYFTQQGEFR	V	738.90	2	1475.78	0.15	1475.63	84.28	31
166240	TPAGLOVLNDYLADK	S	809.27	2	1616.53	-0.31	1616.84	129.79	30
199808	DEQDPLLTR	T	543.85	2	1085.69	0.15	1085.54	31.16	31
166247	TLTLVHPLR	A	525.32	2	1048.63	-0.01	1048.64	40.97	31
84141	IGSFGPQEDLLFLR	A	796.44	2	1590.87	0.03	1590.84	82.92	30
75037	GLVNPANVTFK	V	580.38	2	1158.75	0.11	1158.64	47.69	32
126504	SFPDFPIPGVLFR	D	746.47	2	1490.92	0.13	1490.79	46.00	31
3608	DIKEIAR	K	422.80	2	843.58	0.10	843.48	35.66	32
85486	TFTLNLAPFISQFFK	E	931.10	2	1860.18	0.19	1859.98	109.74	30
181389	IWPYVYTLFSNK	I	765.96	2	1529.91	0.12	1529.79	39.61	31
32612	AAGTDGSDFOHR	E	631.31	2	1260.61	0.06	1260.55	101.95	31
128256	VLSPQGDWPDSVAR	I	763.73	2	1525.45	-0.30	1525.75	74.60	30
3616	VTRSQEELR	E	559.33	2	1116.65	0.07	1116.59	44.67	32
270293	GVLETFSGTETNK	I	691.90	2	1381.78	0.11	1381.67	38.25	30
157070	ELILTGFTFMR	K	664.35	2	1326.68	-0.02	1326.70	45.58	31
114803	IGNHAAEIGAETGR	L	755.06	2	1508.10	0.33	1507.77	68.74	30
84182	NAGNEODLGIQYR	A	739.40	2	1476.78	0.09	1476.70	99.64	31
11470	KPDLSPELR	K	527.85	2	1053.70	0.11	1053.58	65.44	31
155721	VLNIQGSFSTR	D	616.32	2	1230.63	-0.05	1230.67	69.44	31
109334	IGSHGGEYGEALQRMFAFPITK	T	856.34	3	2566.01	-0.22	2566.23	64.00	28
123352	IKENGVCTEFSLVADK	T	905.53	2	1809.04	0.14	1808.90	122.93	29
37085	VLIDWINDVLVGER	I	820.96	2	1639.91	0.02	1639.89	70.76	30
10860	VGGLEEEPDSVGPLR	E	777.41	2	1552.80	0.03	1552.77	30.68	30
256333	LKEHVIEK	E	498.26	2	994.50	-0.08	994.58	34.34	31
75054	LGEHNINVLGDEQFINAAK	I	737.59	3	2209.76	-0.34	2210.10	65.82	29
3639	TGTLNLMFLSR	L	635.77	2	1269.52	-0.08	1269.60	40.44	31
136243	VMEMVEPLVTR	T	668.31	2	1334.61	-0.05	1334.66	46.33	31
243481	NNDNTTEHVLETENKK	L	638.67	3	1913.00	0.13	1912.88	39.86	29
23753	KINFDAALK	F	531.33	2	1060.64	0.01	1060.63	53.59	32
214565	IYKPLR	T	395.21	2	788.41	-0.08	788.49	33.06	33
92620	LINYEMSK	R	507.31	2	1012.60	0.11	1012.49	31.06	31
60545	GLEEAQSEIQALR	G	722.47	2	1442.92	0.18	1442.74	78.42	31
3668	TQVTYECEGYR	L	767.93	2	1533.84	0.20	1533.64	31.21	30
3690	LEIANVQYR	C	553.25	2	1104.48	-0.12	1104.59	32.22	32
211553	LQSPQAVLQLGVSK	E	734.34	2	1466.66	-0.18	1466.85	51.63	30
148937	DDEVVDVGTVEEDLGK	S	867.87	2	1733.73	-0.02	1733.75	136.94	30
76638	ILGGVISAISEAAQYNPEPPPR	S	816.44	3	2446.31	0.03	2446.29	56.57	28
166315	TMIQQGGSIVNVGSIIGLK	G	966.11	2	1930.20	0.14	1930.06	36.67	30
42034	YPSPPPVNTVK	G	644.20	2	1286.38	-0.31	1286.69	93.49	31
10199	YPIEHGIITNWDMEK	I	980.94	2	1959.86	-0.04	1959.90	79.26	29

160297	NVNGVNYASVTR	N	647.43	2	1292.85	0.20	1292.65	61.34	30
31543	VSTVSLPR	S	429.80	2	857.59	0.09	857.50	43.50	32
38628	VDALSPEGAR	G	572.24	2	1142.47	-0.08	1142.56	31.65	31
105482	TYLDVEPTGFTLQFAK	R	971.97	2	1941.93	-0.08	1942.01	82.28	29
42770	LAFDPLPESELVPLITR	N	955.57	2	1909.13	0.07	1909.06	65.83	29
60505	SIDIAHTNLKPGK	V	697.39	2	1392.76	-0.01	1392.77	37.73	31
85745	LPGVSLKLPLK	G	582.87	2	1163.72	-0.04	1163.76	74.59	31
264754	LFQLPTPLSR	H	634.72	2	1267.42	-0.31	1267.73	56.90	31
60578	LQELDAASK	V	487.75	2	973.49	-0.02	973.51	42.55	32
149112	FGSGYVSGWGK	V	572.76	2	1143.51	-0.03	1143.53	58.67	31
240055	TIDLQLSDVFLK	A	690.34	2	1378.67	-0.06	1378.73	46.13	31
35260	LPQMSGFQK	G	575.83	2	1149.64	0.09	1149.55	44.62	31
169306	LSFIKR	C	382.25	2	762.49	0.01	762.48	49.19	33
135016	IAELFSDLDER	T	654.36	2	1306.71	0.07	1306.64	79.43	31
2681	LSRECEIK	Y	517.78	2	1033.55	0.03	1033.52	45.37	32
57161	YGLFPANVELR	Q	721.27	2	1440.53	-0.21	1440.74	52.42	30
7578	EELKCMLEK	Y	598.29	2	1194.57	0.01	1194.56	32.82	31
3700	LSVEALNSLTGEFK	G	754.34	2	1506.67	-0.13	1506.79	99.87	30
267331	IQTYLESTKPIDLYEEMGK	V	796.46	3	2386.36	0.16	2386.20	44.06	28
63780	VQEEIER	V	451.82	2	901.62	0.17	901.45	66.08	32
33163	TNGSPCDPSFLACVPCNLSSVIFQHR	F	1063.82	3	3188.43	-0.09	3188.52	33.44	26
63786	EYGPVFTMYLGMKPTVLYGYEVLK	E	977.14	3	2928.40	-0.07	2928.47	29.80	27
84196	IJSSPGIQVFNIFILLDYCPGNHNIYLK	N	1116.09	3	3345.24	0.47	3344.76	37.37	26
3731	LKEMFPVIEQYDILVK	Y	680.09	3	2037.25	0.16	2037.09	38.01	29
78089	KAQLQDEEELQK	V	729.95	2	1457.88	0.15	1457.74	61.20	30
39173	DGQGSDDPAVTYR	L	714.84	2	1427.67	0.04	1427.63	81.34	30
71407	SHYEEGPGK	N	502.22	2	1002.42	-0.02	1002.44	49.83	32
98989	LLEVDNRVLPMEPIR	M	669.43	3	2005.27	0.13	2005.14	43.56	29
105670	LNOATVTSNR	L	552.34	2	1102.67	0.09	1102.57	62.55	32
142106	MLISSEDLHSHWAPSLGLK	T	733.43	3	2197.27	0.13	2197.15	84.88	28
11221	DYQELMNTK	L	571.27	2	1140.52	0.01	1140.51	49.33	31
145183	YGILVDPIQVVSFLK	D	902.68	2	1803.34	0.29	1803.05	49.93	30
216306	HPVLGNLTK	K	489.78	2	977.54	-0.02	977.57	33.59	32
82662	NITDELGVLGAGPYAR	R	872.93	2	1743.85	-0.07	1743.92	109.37	30
3741	IVSDKDGYK	H	512.72	2	1023.42	-0.10	1023.52	40.27	31
42765	TKEELIR	G	444.70	2	887.39	-0.12	887.51	32.01	32
318957	AEAYLIEEMYDEAIDYEAQEQNENDQQIR	E	1240.39	3	3718.15	-0.47	3718.62	138.18	25
55867	HLVFPLLEFLSVK	E	771.45	2	1540.88	-0.02	1540.90	35.34	30
271473	TVAPALPR	R	412.79	2	823.57	0.07	823.49	31.83	31
4981	LLDENIQPDAPPPPIPK	E	991.99	2	1981.97	-0.14	1982.11	60.70	29
105332	NIVHNYSEAEIK	V	708.91	2	1415.80	0.09	1415.70	48.60	31
109266	YWEDIETFLARPDDLIVTPK	S	899.78	3	2696.32	-0.05	2696.37	71.84	27
75106	FMEGQVPYGSWYDHVK	S	653.60	3	1957.79	-0.07	1957.87	49.27	29
62242	LIEFLERDPLAELVDK	I	950.51	2	1899.00	-0.03	1899.04	33.02	29
17534	ELVVIIGWAK	H	564.26	2	1126.51	-0.16	1126.67	47.26	31
295040	TVATPLNQVANPNSAIFGGARPR	E	784.29	3	2349.86	-0.39	2350.25	50.75	28
276570	DLSVYNLLLDVFPK	E	818.49	2	1634.97	0.08	1634.89	72.94	30

161256	ASNTADTLFQEV LGR	K	811.46	2	1620.90	0.09	1620.81	112.63	30
57456	IAESYQNILAAIEGSR	F	867.85	2	1733.69	-0.21	1733.89	40.26	30
173653	QAEFEARR	R	494.77	2	987.53	0.06	987.47	35.31	32
75919	LTLGQFLEGTAGDSLTK	H	875.86	2	1749.71	-0.20	1749.91	84.52	30
242747	GWAVQLDLTLFASAR	Q	824.54	2	1647.07	0.19	1646.88	30.74	30
45080	THTQDAVPLTLGQEFSGYVQQVQYAMER	I	1066.32	3	3195.92	0.40	3195.53	110.17	27
47234	MLDGEVTDAREAR	S	711.38	2	1420.74	0.09	1420.65	31.36	30
157436	SLTLQDPPIVVPGDVIVSAEGK	T	1117.79	2	2233.57	0.35	2233.22	51.89	29
10323	TGEGFLCVFAINTK	S	835.92	2	1669.82	0.01	1669.81	65.88	30
71441	LPELTPAER	D	513.26	2	1024.51	-0.04	1024.56	32.18	31
71532	GNDIAHFHNP	F	644.36	2	1286.70	0.09	1286.62	35.10	31
139030	IDANNVAYTTGK	L	633.89	2	1265.76	0.14	1265.63	54.58	31
52613	LPWAQLFQPTIALLR	E	883.92	2	1765.82	-0.21	1766.02	53.51	30
113271	NVETMNYADIER	T	735.86	2	1469.72	0.07	1469.65	84.99	30
148966	LVLDEELEGVSPDELKDELPER	Q	875.08	3	2622.21	-0.12	2622.33	63.06	27
277551	VIFLEDDDDVAADVGR	L	867.02	2	1732.02	0.15	1731.87	87.84	30
28290	KPPPDGHYVDWR	T	739.96	2	1477.90	0.13	1477.77	36.84	30
84221	PMILGYWDIR	G	640.35	2	1278.69	0.05	1278.64	37.27	31
18015	LGQLNIDISNIK	A	664.33	2	1326.64	-0.11	1326.75	35.80	31
3907	LAFNLVQAAEEALPK	I	807.51	2	1613.00	0.12	1612.88	68.91	30
199992	IYAPQGLLLTDPIER	G	850.06	2	1698.11	0.18	1697.94	70.98	30
29315	FNSLNLVDYHR	S	753.94	2	1505.87	0.15	1505.73	34.01	30
33791	VDILENOLMDNR	M	738.38	2	1474.75	0.04	1474.71	40.03	30
219015	VSGYNLAAADLAHNFTDGLAIGASFR	G	898.43	3	2692.28	-0.08	2692.36	122.31	28
16060	FQSAAGALQEAASEAYLVGLFEDTNLCAIHAK	R	1146.54	3	3436.61	-0.09	3436.70	97.14	26
71479	AVTQSAEITPVTFEAR	A	917.07	2	1832.12	0.15	1831.97	44.86	29
3930	MNTLEMTPEVK	H	662.79	2	1323.57	0.03	1323.60	36.77	31
3923	VLSADDKTNIK	N	602.20	2	1202.39	-0.26	1202.65	87.36	31
47431	IFVGGLSPDTPPEEK	I	744.71	2	1487.40	-0.35	1487.75	82.89	30
3926	QTLMEVKK	R	488.86	2	975.70	0.15	975.54	32.74	32
82484	AQVAQPGGDTIFGK	I	694.90	2	1387.79	0.08	1387.71	61.31	31
153619	AGPEVSSPGTSESR	D	680.84	2	1359.67	0.04	1359.63	46.23	31
140379	AENGDFASFR	V	557.24	2	1112.46	-0.03	1112.49	48.00	31
73759	SSGSPYGGYSGGGGGYGSFR	R	955.96	2	1909.91	0.13	1909.78	30.49	29
366853	DLQNLMDLIR	G	616.72	2	1231.43	-0.19	1231.62	57.67	31
49021	LGPVYVLDLADR	L	715.36	2	1428.71	-0.09	1428.80	51.28	30
139384	TDEQALLSSILAK	T	694.79	2	1387.56	-0.20	1387.76	83.84	31
220427	FINDSEQVAR	A	589.80	2	1177.59	0.02	1177.57	63.61	31
282775	AVVESLPR	T	435.82	2	869.62	0.12	869.50	31.96	31
209082	GNIFNYWITISKPVFR	K	652.38	3	1954.11	0.07	1954.05	43.50	29
200861	AEGETESPRPK	K	400.92	3	1199.75	0.17	1199.58	37.30	31
40462	EKNGIDIYSLTVDSR	V	855.31	2	1708.61	-0.25	1708.86	104.48	30
62937	SISKPEGTPR	G	536.25	2	1070.48	-0.10	1070.57	37.72	32
15418	SKEQLFLEAIR	T	667.33	2	1332.65	-0.10	1332.74	87.42	31

231448	REDLWAPAGVTLK	E	489.93	3	1466.77	-0.08	1466.85	31.08	30
95874	FQSEERPK	L	575.29	2	1148.57	0.02	1148.55	53.49	31
60501	TPYTDVNIIVIR	E	696.41	2	1390.80	0.05	1390.75	64.59	30
66467	YEELQITAGR	H	590.26	2	1178.51	-0.08	1178.59	83.78	31
205582	KEEPPLODK	S	599.78	2	1197.55	-0.04	1197.59	34.75	31
19687	GFSVADTPELQR	I	709.93	2	1417.85	0.13	1417.72	49.36	31
339290	QSSLPAMSKVR	R	602.39	2	1202.76	0.12	1202.64	31.85	31
286877	DQVDSAVQELLQIK	A	793.45	2	1584.88	0.04	1584.84	52.69	30
209490	ERPGVYTNVAK	Y	617.42	2	1232.82	0.17	1232.65	32.45	31
126112	SLAENYFDSTGR	L	680.29	2	1358.56	-0.05	1358.61	36.55	31
5106	ANLINIFELAGLKG	V	793.87	2	1585.73	-0.15	1585.88	70.08	30
111680	LFLAEFQSIPR	V	660.90	2	1319.78	0.06	1319.72	69.00	31
198073	ILTGNAIALVLGGGAR	G	776.97	2	1551.93	0.02	1551.91	106.36	30
112141	AISEGVLTSALITTDSPKPIAKLIATLSGCK	T	1082.39	3	3244.13	0.33	3243.80	28.69	26
10945	MAIMLEK	F	490.82	2	979.62	0.11	979.51	39.23	31
52861	AASHWTSE	V	579.35	2	1156.68	0.12	1156.56	44.20	31
60454	AQLPETIQDVER	K	699.86	2	1397.70	-0.01	1397.71	37.70	31
140367	AQLSATVLTLLIK	Q	685.89	2	1369.77	-0.08	1369.85	50.95	30
60472	VLASYAQPIFLR	L	689.37	2	1376.72	-0.06	1376.78	67.46	31
311481	HVISYSLSPFEQR	A	781.96	2	1561.91	0.12	1561.79	93.19	31
204667	VNNLISDQDFFALR	S	826.32	2	1650.63	-0.20	1650.84	48.15	30
72321	LPDLLLEDLFGQK	Q	750.90	2	1499.78	-0.05	1499.82	98.60	30
144356	LQGGVLLAQILK	N	626.86	2	1251.71	-0.09	1251.79	93.51	31
39196	NYNPGDQSTDYGIQINSR	Y	1094.90	2	2187.78	-0.20	2187.98	107.78	28
269157	YLDLINDFVR	Q	690.85	2	1379.69	-0.06	1379.74	43.95	31
166255	ITLPAGPDILR	T	583.38	2	1164.75	0.06	1164.69	38.45	31
42953	ISLTLEK	G	458.71	2	915.41	-0.15	915.56	32.21	32
182793	DPAIFYK	E	427.28	2	852.54	0.11	852.44	59.59	31
69402	NGETFQMLVYGR	T	764.36	2	1526.70	-0.05	1526.76	117.48	30
36062	AITSGFNALEK	I	575.76	2	1149.51	-0.09	1149.60	63.58	31
19138	LANMEAEINTLK	S	681.84	2	1361.66	-0.02	1361.69	96.29	31
124359	IAQDLEMVGVNYFTIR	N	967.02	2	1932.02	0.08	1931.95	76.39	29
259160	DLAEQLYAGR	V	624.86	2	1247.71	0.06	1247.65	33.54	31
12056	FIDTSQFILNR	L	677.28	2	1352.55	-0.16	1352.71	87.13	31
220289	YLYANEVGEAFR	S	744.92	2	1487.83	0.13	1487.70	64.29	30
47245	QDINKTAWELPK	T	721.87	2	1441.72	-0.04	1441.76	36.06	30
237355	ELAPLFEELIK	V	651.39	2	1300.77	0.04	1300.73	51.30	30
35920	VPTQILFGTLR	V	622.85	2	1243.68	-0.05	1243.73	48.01	31
3277	GAYDAQGTLKIFK	L	749.83	2	1497.64	-0.14	1497.78	31.87	30
217296	GETVSTPLSR	E	523.84	2	1045.66	0.12	1045.54	36.94	32
210844	LGLYTFESLVR	F	649.38	2	1296.74	0.03	1296.71	56.33	30
98993	ELTMALHIPLMLLTINPK	L	769.45	3	2305.32	0.00	2305.32	47.68	28
44210	QYELVWHEDMDAAK	V	832.31	2	1662.60	-0.15	1662.76	43.58	30
78016	SVDPGSPASLSGLR	A	671.93	2	1341.84	0.15	1341.69	35.10	31
722226	SGLPNFLAVALGELGYR	A	980.95	2	1959.89	-0.19	1960.08	36.12	29
3674	LEQYTNAIEGTK	A	683.92	2	1365.82	0.14	1365.68	61.25	31
216886	LGVSLGAR	L	386.76	2	771.50	0.04	771.46	36.30	33
44333	IAIAALEVLEEHLAENADK	M	726.60	3	2176.77	-0.35	2177.12	28.46	28

201603	LSFEDEVMTASR	M	760.32	2	1518.62	-0.08	1518.70	55.60	30
54281	KTPWGIILDALEQQEDSINK	F	748.36	3	2242.05	-0.10	2242.15	38.53	28
274163	TTQNEIWQTFFGGR	Y	842.96	2	1683.91	0.11	1683.80	41.98	30
151463	AAVEQVPVEPYK	I	665.39	2	1328.76	0.06	1328.70	48.04	31
199319	VEAANVHDPK	F	596.76	2	1191.51	-0.11	1191.62	34.53	31
317748	AQTAHEGALNGVIFYAK	L	889.42	2	1776.83	-0.05	1776.88	60.14	29
226905	LRSSGPR	T	386.73	2	771.45	0.02	771.44	35.61	33
223925	STLVNSLFLDLYR	D	821.39	2	1640.77	-0.11	1640.88	32.23	30
268213	MAEAAQGLIR	A	594.80	2	1187.58	-0.05	1187.63	50.69	31
299198	NSPSYTLR	F	469.18	2	936.35	-0.12	936.47	36.94	31
283891	DEIQEILPTR	D	607.35	2	1212.68	0.04	1212.64	42.65	31
214842	AAGVNVFLFWPGLFAK	A	860.00	2	1717.98	0.06	1717.92	45.36	30
201232	ILDSVGIEADER	L	723.41	2	1444.81	0.11	1444.70	92.17	31
161456	AIGVSFNPLQIER	I	779.40	2	1556.78	-0.05	1556.83	102.03	30
215733	AAAGELYOK	T	475.71	2	949.41	-0.08	949.49	35.61	31
292782	RPLDTGPR	D	456.28	2	910.54	0.04	910.50	34.69	31
314871	DVAQIFNNILR	R	651.85	2	1301.69	-0.02	1301.71	35.67	31
277277	FQEQIAYODELVK	V	838.00	2	1673.98	0.12	1673.86	38.87	30
208169	LVEVLEGVCSK	S	616.90	2	1231.78	0.13	1231.65	37.36	31
253829	KPYVNDLEAEASLPEKK	G	677.22	3	2028.63	-0.45	2029.07	31.40	29
246770	ALDDFVLGSAR	L	582.32	2	1162.62	0.02	1162.60	44.13	31
209194	MISEGDIGGIAQTSSIFLGR	A	1091.05	2	2180.08	-0.04	2180.11	117.48	28
245607	GHQEASLAR	K	484.75	2	967.48	0.00	967.48	37.97	31
262592	QEVTKLOQOVK	T	684.95	2	1327.88	0.13	1327.75	39.12	31
195113	AFPVLLLDVAPWYLR	L	887.05	2	1772.08	0.08	1772.00	32.66	30
209309	LGTLPLQK	V	491.82	2	981.64	0.01	981.62	41.63	31
238438	IPEDILGEIAYSVIR	A	812.54	2	1623.06	0.14	1622.92	84.54	30
262377	ISNPWQSPSGTLPALR	T	862.45	2	1722.89	-0.01	1722.91	66.77	30
225990	FIMVPSGNMGVDFPTIEHNR	G	765.01	3	2292.02	-0.04	2292.07	82.60	28
208269	QILLYSATPLPSVQK	F	854.54	2	1707.07	0.10	1706.96	100.90	30
246519	HLHVGTIFDSGPGSDLIGALR	A	792.74	3	2375.20	-0.02	2375.22	33.73	28
189964	ENAYDLEANLAVLK	L	781.99	2	1561.97	0.17	1561.80	56.79	31
318230	NQENLEK	S	437.73	2	873.45	0.03	873.42	40.77	32
246387	VFDEEVVQIK	E	652.88	2	1303.75	0.04	1303.70	33.05	30
194048	LLSMELQELSR	T	732.39	2	1462.76	0.03	1462.73	52.37	31
359989	SFSPGLPPQSSSLTLK	Q	823.46	2	1644.91	0.04	1644.87	42.69	30
220097	GAIEALDPVEYTLR	K	838.50	2	1674.99	0.14	1674.85	44.02	30
218331	SECCPPSENPFEK	G	763.37	2	1524.72	0.06	1524.66	30.13	30
257746	LNVDFAEQLVK	T	716.93	2	1431.84	0.10	1431.74	94.73	31
161420	LVLVGDA5VGK	T	529.28	2	1056.54	-0.08	1056.62	35.79	31
367801	VHTTKTSGHPTLR	V	478.95	3	1433.82	0.04	1433.77	32.75	30
226986	VYVGNLGTGAGK	G	568.36	2	1134.70	0.10	1134.60	38.35	31
269978	VATGQELSNLLDTVFK	I	925.09	2	1848.16	0.20	1847.96	32.53	29
3232984	LTHINTGR	N	456.23	2	910.44	-0.05	910.50	32.41	31
225945	GPVYIGELPQDFLR	I	802.40	2	1602.79	-0.05	1602.84	53.91	30
251068	GLGSGEDELQK	L	566.75	2	1131.48	-0.06	1131.54	31.62	31
271294	IYVPLMLVNAADPLVHESLLTIPIK	S	921.18	3	2760.51	0.00	2760.51	62.25	28
302905	VGSHPEGGASWLSTAAFLSR	S	715.26	3	2142.76	-0.29	2143.04	29.58	29
266171	IPKTLDWR	D	514.85	2	1027.69	0.11	1027.58	38.06	31

272157	KGDAISYAR	I	490.75	2	979.49	-0.02	979.51	62.25	31
271140	AVITTDFAK	T	584.37	2	1166.72	0.14	1166.58	31.75	31
306407	LVIKGPVTFQER	D	807.41	2	1612.80	-0.13	1612.93	35.01	30
279415	DQGSFSELEK	D	652.87	2	1303.74	0.13	1303.61	35.61	30
274768	AAFTAFEEVQLPR	L	739.85	2	1477.70	-0.06	1477.76	55.04	30
234260	SLSPFAIAYLDR	L	676.83	2	1351.65	-0.06	1351.71	33.16	31
161334	FSGSGSGTDFTLK	I	652.26	2	1302.51	-0.10	1302.61	63.90	31
306584	GPQVPAGESTQEAAGATTAK	A	943.85	2	1885.69	-0.21	1885.90	70.76	29
281850	LSSGEDITELR	K	604.32	2	1206.62	0.05	1206.57	31.41	31
272326	TSEIEGANLLELFDLKG	Y	989.01	2	1976.01	0.00	1976.01	61.35	29
204220	SFQEVPSALAYALDISPVVHR	I	767.15	3	2298.42	0.22	2298.20	62.91	28
256607	NAPPFLEPNQLTPK	E	840.98	2	1679.95	0.09	1679.85	55.23	30
240868	LGALSGAGALSIIATYGAHGAQFPDAYGK	E	888.69	3	2663.05	-0.29	2663.33	78.88	27
268833	LAYAENIALLAETALR	F	866.48	2	1730.95	-0.01	1730.96	33.84	30
167222	SPTMAGGLFAVSK	K	641.28	2	1280.54	-0.10	1280.64	92.83	31
201524	QAGLYSISLPNK	Y	645.89	2	1289.76	0.06	1289.70	85.48	31
215516	KYDVFLEASELIK	Q	756.97	2	1511.93	0.11	1511.82	48.66	30
227176	ASVDVADLIGLNLVMSR	N	894.98	2	1787.95	0.00	1787.95	95.26	29
307512	WLPVQDSGTEDK	K	687.88	2	1373.74	0.09	1373.65	45.57	31
219536	QEDGSLCLVQFPSPR	K	818.51	2	1635.00	0.23	1634.77	35.64	30
264614	AVSELVSPDIIMQSHSENAISVK	E	818.62	3	2452.83	-0.41	2453.25	29.81	28
164208	HLNDDDDVTGSVK	S	650.27	2	1298.53	-0.08	1298.61	91.12	31
231239	FVGINASDINYSAGR	Y	792.41	2	1582.81	0.04	1582.77	33.23	30
88229	FPDENFTLK	H	555.80	2	1109.58	0.04	1109.54	47.15	30
12072	HSLSLDLEOK	L	641.83	2	1281.65	-0.04	1281.69	63.37	30
51565	LLDQSTGLYEYK	V	715.37	2	1428.72	0.01	1428.71	56.09	30
69787	SHCFQAMMSOPK	M	792.84	2	1583.67	0.02	1583.65	50.91	30
78112	TGEPDEEETGR	S	683.86	2	1365.71	0.14	1365.57	108.05	31
82680	GHAEMAIAIWNMLPEVGKK	T	747.71	3	2240.10	-0.01	2240.11	30.80	28
249141	LPYSVLLEIQK	Q	651.84	2	1301.67	-0.09	1301.76	51.84	31
304888	MLDPFLLDFEKF	G	765.95	2	1529.89	0.14	1529.75	65.70	31
63679	SSYLPTPHR	A	353.18	3	1056.53	-0.01	1056.54	39.70	31
37272	AAVQELSGSILTSDEPEER	G	1015.97	2	2029.92	-0.06	2029.98	29.46	29
178365	TFGIWTLLSSVIR	C	746.97	2	1491.93	0.09	1491.84	85.08	31
25274	LTFSCLGSDNFK	H	723.39	2	1444.77	0.11	1444.67	50.92	31
103863	IIIEYYVQHLSGYFLQLK	F	731.81	3	2192.39	0.21	2192.19	36.53	28
71853	LAGPQLVQMFIGDGAK	L	823.01	2	1644.01	0.14	1643.87	32.60	30
233720	FPYYVYNIIGGLDEEGK	G	1062.51	2	2123.00	-0.03	2123.02	44.71	29
72897	NYTDDAIETDOLTIK	L	863.91	2	1725.80	0.00	1725.79	47.67	30
134694	LAAIQSGGVER	Q	586.37	2	1170.72	0.08	1170.64	62.30	31
167119	GVLEDALDAFCQVGR	Q	825.39	2	1648.76	-0.03	1648.79	61.86	30
205305	ELFPVFTQLPEPK	D	782.00	2	1561.98	0.13	1561.85	44.15	31
128391	TPECGSGTGVEK	I	714.85	2	1427.69	0.07	1427.62	89.34	30
214491	VDLSTSTDWK	E	576.30	2	1150.59	0.04	1150.55	56.59	31
44893	LTDNFNLMVLGK	G	707.38	2	1412.75	0.01	1412.74	37.08	30
4701	APVLVALALIEGGMK	Y	749.47	2	1496.93	0.07	1496.86	54.70	30
111137	CGSGEGSGGLR	L	518.80	2	1035.59	0.15	1035.44	32.74	31
166582	HTAAPTDTDGP	END	590.26	2	1178.51	-0.01	1178.52	56.96	31

95160	IGDQEFDSLPALEPYK	I		992.98	2	1983.95	-0.03	1983.98	95.22	29
15613	NLLADVEITFVADTLK	G		825.04	2	1648.06	0.19	1647.87	60.16	30
262914	ETSATPEFSPGASNR	A		711.21	2	1420.41	-0.25	1420.66	50.55	30
165980	LSSTQQSIAEK	E		596.34	2	1190.67	0.06	1190.61	70.51	31
72819	KLPVDAK	Q		385.78	2	769.55	0.08	769.47	43.64	31
60469	VLEPDWLVLQR	R		684.40	2	1366.79	0.03	1366.76	40.95	30
319337	VGIEAAEMLLANLR	H		758.45	2	1514.89	0.08	1514.81	42.60	30
47246	LAVEILDNEKN	V		629.37	2	1256.73	0.07	1256.66	68.77	31
42127	YISVGYYDHTFVR	F		562.23	3	1683.67	-0.15	1683.83	45.05	30
67742	KFDLGQDVIDFTHALALYR	T		760.31	3	2277.91	-0.27	2278.17	96.55	29
44313	LQLWDIAQOER	F		664.87	2	1327.73	0.04	1327.69	52.31	31
173285	EQLAELEKTVK	Q		644.20	2	1286.39	-0.32	1286.71	31.46	31
8458	LAPITYQGLALAK	D		728.36	2	1454.71	-0.14	1454.85	36.98	30
41486	ENDMSPSNVVPIHVPTTENKPK	V		665.87	4	2659.44	0.14	2659.29	30.79	28
169821	SSNVNDEAFSSLAR	D		741.42	2	1480.83	0.11	1480.72	32.09	31
168705	IDSTPVK	S		380.18	2	758.34	-0.08	758.42	44.37	33
35585	FAGQMGIQLFETSAK	E		822.43	2	1642.84	0.04	1642.80	61.22	30
4747	VKDTEDVPMILVGNK	C		829.47	2	1656.93	0.06	1656.88	47.62	30
6160	SPLPKEPR	K		510.75	2	1019.48	-0.09	1019.58	42.80	32
111523	STGEAFVQFASQIEAK	A		921.52	2	1841.03	0.15	1840.88	50.32	30
105581	MLSNENFEYLR	A		780.85	2	1559.69	-0.01	1559.69	93.53	30
90519	ATISTLPLISAGAVLGK	V		863.02	2	1724.03	-0.02	1724.04	55.26	30
2120	KESAPQVLLPEEK	I		798.81	2	1595.60	-0.24	1595.84	37.41	30
113828	DEFPEVYPTVFENYVADIEVDGK	Q		925.50	3	2773.48	0.18	2773.30	54.66	27
42830	FNTFIHEDIWNIIR	S		852.85	2	1703.68	-0.16	1703.84	59.66	30
4845	DLLHPSPEEK	R		647.36	2	1292.71	0.08	1292.62	83.89	30
84325	AFATIDITDAEEDK	I		713.18	2	1424.35	-0.28	1424.63	34.24	31
337119	RGVDLDQLDMSYEQLMQLYSAR	Q		926.17	3	2775.48	0.16	2775.32	54.25	27
75738	AVAEILSK	A		415.79	2	829.57	0.08	829.49	45.40	33
100550	SEVTELR	L		495.26	2	988.52	-0.02	988.53	38.50	32
168209	MFESFIESVPLFK	S		795.41	2	1588.81	0.02	1588.78	42.13	30
85749	DILQVDLDADLSNEAFFSTHQLVR	A		948.43	3	2842.26	-0.16	2842.41	71.08	27
1271	LVYHLGLPYSFLTIPPVVEAIAK	I		867.16	3	2598.45	0.08	2598.38	49.07	27
19107	LTPTSAESSSTGTEDK	S		805.89	2	1609.77	0.04	1609.73	44.76	30
341343	LGLQDLFQSPDLR	G		751.46	2	1500.91	0.12	1500.79	91.90	31
51490	IVGGQDSSLGR	W		544.80	2	1087.58	0.02	1087.56	34.31	32
319145	SSDGASALSVP	K		573.79	2	1145.56	-0.01	1145.57	37.03	31
12071	LILYNDGDSLOQYER	D		906.59	2	1811.16	0.25	1810.91	30.37	30
55278	LVKQLSK	S		408.32	2	814.63	0.11	814.53	32.28	32
78346	SFFSEIISISDVK	F		779.91	2	1557.80	0.01	1557.79	58.70	30
37301	EGVCPASIDSAPVK	W		779.93	2	1557.84	0.11	1557.73	41.85	30
301225	DHGLSLOSTQK	A		671.80	2	1341.58	-0.08	1341.65	70.15	31
19325	GLVLALYKNHR	S		642.42	2	1282.82	0.06	1282.75	98.12	30
3600	IFDFQGLQHQAHVATQLEAAR	L		827.06	3	2478.17	-0.11	2478.28	55.94	28
227484	GEVQVSDKER	H		573.86	2	1145.71	0.14	1145.57	64.94	31

80422	SGDAPLTYNELGTAYVSATTGAVATALGLNAL	H		1083.21	3	3246.61	-0.09	3246.70	53.88	26
	TK									
38099	VLESEOFTELTR	L		839.38	2	1676.75	-0.15	1676.90	46.49	30
237237	DIDGTPLNVAVTGESAGK	S		900.89	2	1799.77	-0.12	1799.89	33.75	29
221017	ADGYVDNLAEAVDLLQHMDK	END		782.71	3	2345.12	-0.01	2345.12	61.88	28
44190	SLNRVQLLGR	V		578.36	2	1154.70	0.01	1154.69	31.59	31
3858	YFILPDSLPLDTLLVDVEPK	V		1144.19	2	2286.37	0.13	2286.24	33.70	28
75080	LKNISSK	Y		395.23	2	788.44	-0.04	788.48	35.63	33
44653	EMARILK	E		430.73	2	859.44	-0.06	859.49	34.76	33
11254	AAATEDATPAALEK	G		679.80	2	1357.59	-0.08	1357.67	85.80	31
198521	MGPDALPR	S		428.82	2	855.64	0.21	855.43	34.13	31
313065	SLPNEEIVQK	I		578.83	2	1155.64	0.03	1155.61	33.78	31
75350	TNLPIFK	L		416.76	2	831.51	0.03	831.49	42.47	33
4905	NPPGFAVFEDPRDAADAVR	E		774.12	3	2319.33	0.23	2319.09	42.92	28
137571	GVLLGDAYNLR	H		652.43	2	1302.84	0.11	1302.73	62.25	31
129969	DGISNWLGFMLR	F		704.78	2	1407.55	-0.15	1407.70	44.16	30
75741	VLDFTYAR	E		542.34	2	1082.66	0.08	1082.58	37.64	31
277960	IDRLPK	N		428.75	2	855.49	0.01	855.48	39.17	31
209385	ILNTPNCALQIVAR	L		791.91	2	1581.81	-0.05	1581.87	83.14	30
47308	AGGAFDPYTLVR	Q		633.84	2	1265.67	0.03	1265.64	78.11	31
34036	IDSNLDELSVGLGR	L		744.26	2	1486.51	-0.25	1486.76	107.13	30
75082	NQSPVDEGATGASQGLDR	K		958.03	2	1914.05	0.14	1913.91	107.13	29
78119	IGGELEEQAVMILDDFSHELESTQSR	L		946.08	3	2835.21	-0.07	2835.29	30.45	27
78117	IQEODAGLDALSSIIR	Q		965.10	2	1928.18	0.15	1928.02	103.96	30
80899	NNDLVAVNGESVEALDHDGVVEMIR	N		937.54	3	2809.60	0.24	2809.36	52.95	27
60486	LLGNTFVALSPLR	C		709.85	2	1417.68	-0.12	1417.79	33.82	31
71714	GDVTAEAAAGASPAK	A		687.32	2	1372.62	-0.03	1372.65	62.72	31
93202	SVGDGETVEFDVVEGEK	G		898.48	2	1794.95	0.13	1794.82	88.81	29
200982	VNLQSWADAFR	S		766.88	2	1531.74	-0.07	1531.81	37.31	30
23402	TSFHALTSILK	A		609.38	2	1216.75	0.07	1216.68	70.62	31
212891	KMDEADASSAVK	V		634.24	2	1266.47	-0.10	1266.58	42.38	31
83139	ANNTPYGLAAGVFTK	D		762.48	2	1522.95	0.17	1522.78	93.47	30
205903	GLLIGFLTVLSK	E		738.88	2	1475.75	-0.11	1475.86	100.93	31
232730	SYLENPAFMILLDK	END		835.51	2	1669.01	0.16	1668.84	51.53	30
195573	HGVTVDATTR	M		528.75	2	1055.48	-0.05	1055.54	37.82	31
221880	SSAQIALR	Y		423.23	2	844.44	-0.03	844.48	33.13	33
266426	GFLEFVEDFIQVPR	N		848.47	2	1694.93	0.06	1694.87	86.88	30
210117	MATGQKLMR	A		534.16	2	1086.31	-0.22	1086.53	31.62	31
246362	TQEILSQLPEK	R		652.41	2	1302.80	0.08	1302.72	61.39	31
43461	GVQVETISSGDGR	T		652.75	2	1303.48	-0.16	1303.64	41.37	30
13085	IQSFPWQYVFESPR	G		892.37	2	1782.73	-0.15	1782.87	77.60	30
190455	LVGIVTSR	D		422.83	2	843.64	0.12	843.52	34.77	32
114376	RPDQQLQGDGK	I		621.18	2	1240.35	-0.27	1240.62	60.42	31
45012	AVENSSTAIGR	C		609.38	2	1216.76	0.11	1216.64	37.96	31
302099	GVVDLQQAISK	L		643.34	2	1284.66	-0.05	1284.70	39.62	31
202900	TISPQNDILQNPLLIK	I		960.54	2	1919.07	-0.04	1919.11	43.56	29

270449	GVDSVFEPLLK	E	645.89	2	1289.76	0.08	1289.69	35.74	31
287945	NSNPALNDNLEK	G	664.88	2	1327.75	0.12	1327.64	60.22	31
247159	AGADVLQITFSAADR	M	899.94	2	1797.87	0.02	1797.85	80.56	30
111659	DLFLEAHEVILK	V	713.90	2	1425.78	-0.01	1425.79	82.67	30
239897	IVGGLELVDDLAK	E	734.36	2	1466.71	-0.17	1466.87	74.04	30
295192	TKIDSLGR	L	501.75	2	1001.49	-0.10	1001.59	59.46	32
191344	NACLOTSSLAVR	V	660.35	2	1318.69	0.02	1318.67	33.73	31
313817	SSAGNVLLGSADFYSR	F	822.39	2	1642.78	-0.02	1642.79	63.39	30
273429	VLESRR	E	436.76	2	871.50	-0.02	871.52	33.63	32
306780	SEDEVGSLIEYFR	V	836.83	2	1671.64	-0.12	1671.76	54.42	30
3968	SLADELALVDVLEDK	L	815.40	2	1628.79	-0.06	1628.85	71.03	30
136387	LGSTVFVANLDYK	V	713.89	2	1425.77	0.02	1425.75	66.53	30
395977	STLITDGSSPINLFSTAFGLLGSQGPPACK	END	1097.31	3	3288.91	0.23	3288.69	45.76	26
78074	AKEPAGENGGR	A	543.23	2	1084.45	-0.08	1084.53	37.18	31
78142	IMFLLDVKETAR	C	718.30	2	1434.59	-0.20	1434.79	30.61	30
251303	TLPVSDSALNAFEER	V	824.86	2	1647.71	-0.10	1647.81	100.15	30
206115	TITFEQFQEALEELAK	K	949.06	2	1896.11	0.16	1895.95	32.41	29
238486	IHIGQVMSIR	T	641.92	2	1281.83	0.10	1281.72	45.70	30
200139	KVNPLYEK	G	545.38	2	1088.74	0.12	1088.62	52.30	32
234438	EELDRHIR	I	534.21	2	1066.41	-0.14	1066.55	32.22	31
223472	QEKEQLLR	C	578.84	2	1155.67	0.01	1155.66	31.15	31
307156	SLGTADVHER	K	616.16	2	1230.31	-0.29	1230.60	45.90	31
244260	QGGENTFCLPK	T	625.89	2	1249.78	0.20	1249.58	34.79	31
253193	EIADLGEVLATAVIPQWQK	D	1041.14	2	2080.27	0.15	2080.12	30.70	29
267292	KIIPAPKPK	G	496.19	2	990.36	-0.29	990.66	36.12	32
313683	IDQLMIK	M	438.77	2	875.52	0.04	875.48	37.22	33
209202	LSVVSLLVNSPR	V	642.34	2	1282.67	-0.10	1282.76	43.15	30
294691	VRPPPPPADSVTR	R	694.92	2	1387.83	0.07	1387.76	47.63	31
229620	YQMIHK	D	466.91	2	931.81	0.31	931.49	33.94	32
235741	MGMLQER	A	440.78	2	879.55	0.16	879.39	62.24	32
241018	QEQLNIK	E	436.73	2	871.45	-0.03	871.48	35.04	32
241377	ELFEEFDNPLPGAVIGIAR	E	1069.03	2	2136.04	-0.05	2136.09	38.25	28
208493	TPTPSVELPHSR	S	711.47	2	1420.93	0.20	1420.73	33.65	30
260011	ASLSENVLGSPK	E	601.31	2	1200.60	-0.04	1200.63	75.43	31
195940	SGSSELSTVIGR	L	596.83	2	1191.64	0.03	1191.61	36.74	31
242726	LQELLEK	R	436.84	2	871.66	0.16	871.50	47.62	32
242533	ALVEGVDDLTDYQIK	D	903.02	2	1804.03	0.07	1803.96	33.75	30
268354	EAPPIIFATPTK	L	642.93	2	1283.84	0.12	1283.71	55.46	31
315303	IESFVVEDIESGVQNR	H	911.08	2	1820.14	0.25	1819.90	40.42	30
300896	ELGVLIDLK	Q	607.90	2	1213.78	0.06	1213.73	39.47	31
202233	LLVDSDNNPKIK	D	620.80	2	1239.58	-0.13	1239.72	32.08	31
197176	DPAKPVAAQK	T	526.83	2	1051.64	0.04	1051.60	40.92	31
304176	LGAPENSGISTLER	G	722.41	2	1442.80	0.07	1442.74	110.25	31
210125	TVEQENRTLR	G	623.35	2	1244.69	0.04	1244.65	32.16	31
272300	KYYEIVMLCGLLK	M	823.47	2	1644.92	0.06	1644.86	33.50	30
254063	VIGELGEDGWIR	V	672.47	2	1342.93	0.24	1342.69	43.80	31
239621	SSSISEMEELR	L	634.44	2	1266.86	0.28	1266.58	37.22	31
205153	EALGLWSALQK	I	664.92	2	1327.83	0.08	1327.75	44.73	31

166638	QLLAKELEEEK	M	665.28	2	1328.55	-0.17	1328.72	31.64	31
265857	DDELEESK	F	547.25	2	1092.49	0.05	1092.45	33.64	32
241188	LGDDLQALNEITESGR	I	893.59	2	1785.17	0.25	1784.93	36.37	30
261916	YFFLQSVSDGR	N	717.35	2	1432.68	0.01	1432.66	52.21	31
244528	SLLTLSPDITLKK	A	686.84	2	1371.67	-0.12	1371.80	35.09	31
266038	NHVLQCEVQR	N	641.81	2	1281.60	-0.03	1281.62	32.62	30
314767	SLLSMLSDLQVYK	D	748.91	2	1495.81	0.01	1495.80	48.05	30
275605	AHFGQELNVVQIEENSSK	S	1058.46	2	2114.90	-0.13	2115.02	36.73	29
279597	GMKWEFAFTR	S	627.76	2	1253.51	-0.07	1253.59	31.78	31
295453	KMDLLK	A	438.78	2	875.55	0.07	875.48	34.63	33
207796	SFATFLSHVLDLVSHPR	A	642.64	3	1924.91	-0.11	1925.02	40.53	29
239514	SPEGVSR	V	414.81	2	827.60	0.18	827.41	33.85	32
315956	LLLEQEFDFHLATK	F	895.94	2	1789.86	-0.07	1789.93	34.83	29
273209	SNEVISPEILK	M	614.92	2	1227.84	0.16	1227.67	41.51	31
265212	GYGREVNLLNK	E	688.36	2	1374.70	-0.06	1374.76	35.47	31
286024	DVDPDVAYSSIPYEK	G	849.51	2	1697.00	0.22	1696.78	33.70	30
199085	YTLPLYLTLMYK	A	849.47	2	1696.93	0.05	1696.88	33.85	30
268038	RLENAGSLK	V	494.34	2	986.67	0.12	986.55	33.02	32
276942	KDLENEIK	G	494.78	2	987.55	0.03	987.52	54.28	32
317802	DPEQQLNELNR	E	621.39	2	1240.76	0.16	1240.60	38.30	31
310879	LFVGNLPADITEDEFK	R	904.42	2	1806.83	-0.08	1806.90	35.03	29
315828	GAFFEGLGNAVSELR	I	833.30	2	1664.59	-0.26	1664.85	76.60	30
300976	VPEGNSAER	R	515.35	2	1028.69	0.20	1028.49	42.75	32
201498	GPDDLLIGMFYTDIDASFK	W	1060.48	2	2118.94	0.00	2118.95	62.96	29
249723	SSNRNSAVLYR	C	633.92	2	1265.83	0.18	1265.65	33.35	31
203301	GSLNEQIALVLIR	L	713.48	2	1424.94	0.10	1424.84	83.15	31
261953	IWQDVQLVKV	T	628.76	2	1255.51	-0.22	1255.73	35.61	31
298062	STGVNVNVSCLK	Y	616.76	2	1231.50	-0.15	1231.64	39.30	31
250916	LLGTITYAAEEIAAGGK	A	904.09	2	1806.16	0.22	1805.94	73.61	29
272641	IPENSLQDAAVLPVSYGTALAVDHR	A	950.11	3	2847.31	-0.21	2847.51	39.21	27
239422	VILFDIEPAQNLPFGITFVR	G	1192.46	2	2382.91	-0.40	2383.31	64.25	28
190227	TENGLWLNVEPLPSR	A	862.86	2	1723.70	-0.19	1723.89	55.77	30
293100	TVLIAADVLPGPLPQDEK	L	996.11	2	1990.20	0.14	1990.06	57.17	29
273635	NVTDDILALER	R	680.35	2	1358.68	-0.03	1358.70	80.34	31
213507	FSLPVFAFVMTK	F	701.97	2	1401.93	0.19	1401.74	51.95	31
273407	DLDMELR	E	518.65	2	1035.29	-0.17	1035.45	33.38	31
266670	RGVCGPR	A	401.22	2	800.43	0.03	800.41	39.86	32
224054	NLVPDTFFSFYDLR	R	924.03	2	1846.04	0.11	1845.93	35.53	29
228920	TDLSDVQELLQFVK	A	818.02	2	1634.02	0.16	1633.86	129.29	30
288172	IVGLSTALANAR	D	593.35	2	1184.68	-0.01	1184.69	33.75	31
250158	TGQSVDELFOK	V	626.36	2	1250.71	0.10	1250.61	45.38	31
291964	LSNSDRTR	N	474.69	2	947.37	-0.11	947.48	39.62	32
222218	EEGSSFTQSR	S	607.80	2	1213.58	0.06	1213.52	48.22	31
212247	TYSQMKEK	M	507.78	2	1013.54	0.05	1013.49	32.84	31
198275	ELSDTAAYQSVR	I	670.33	2	1338.65	0.00	1338.64	50.22	30
275767	TLFLAENSVK	L	561.37	2	1120.72	0.11	1120.61	33.93	32
204958	RFSWDWTGSLR	K	656.25	2	1310.48	-0.15	1310.64	34.89	31
294808	SLCGIPLGSSIFLPR	M	865.46	2	1728.91	-0.05	1728.96	70.06	30
216707	SNVMDALSFVMGEK	T	772.38	2	1542.74	0.04	1542.71	32.22	30
285775	ANIINFALTGIFGVK	K	839.97	2	1677.93	-0.02	1677.95	88.56	30
314602	GVPALLYTLR	S	551.82	2	1101.62	-0.04	1101.65	32.85	32

313782	EPSSINPOK	I	556.84	2	1111.67	0.09	1111.59	36.22	31
316025	SSPHTITEEDR	L	714.79	2	1427.57	-0.08	1427.66	36.35	30
264688	EOHLIDQATLEQLTEGR	E	736.41	3	2206.22	0.06	2206.16	89.46	28
290958	TTFQNLIEFEALK	END	862.53	2	1723.04	0.12	1722.92	50.30	30
201012	AAPILSPR	H	412.71	2	823.41	-0.08	823.49	42.08	31
269251	DPRSPLR	V	420.82	2	839.62	0.16	839.46	32.18	31
222802	FYTNPSYFFDLWK	E	864.47	2	1726.93	0.13	1726.80	53.10	30
312923	AAKIVTDVLLR	F	599.95	2	1197.88	0.14	1197.74	37.24	31
219221	PACAPSR	T	379.68	2	757.34	-0.02	757.35	48.10	33
237775	TTGTFVYDR	L	571.72	2	1141.42	-0.16	1141.58	78.91	31
210822	VFMQHINVLNSLGFK	F	631.48	3	1891.43	0.47	1890.97	68.94	29
311543	NLMNAVVTVK	M	608.84	2	1215.66	0.00	1215.66	61.91	32
258586	SIGPLTFVTGTGNVSK	G	862.91	2	1723.81	-0.11	1723.91	50.26	30
208010	GFIQVYVDQVEDIVAVTR	H	1083.56	2	2165.11	0.01	2165.10	39.41	28
303449	GNPSGIQPDILISLTAPK	K	911.00	2	1819.98	-0.02	1820.00	78.16	30
258828	VPAGDSSLDSPSK	T	630.32	2	1258.63	0.03	1258.60	85.69	31
285136	TYTGLSGALLGTVISAYR	A	978.57	2	1955.12	0.05	1955.07	53.60	29
296511	ATGFGVALLLAFGR	A	753.46	2	1504.91	0.04	1504.88	31.20	30
190168	DSATAQAWFSAHNSVGDLLVR	V	786.63	3	2356.86	-0.32	2357.18	84.77	28
289382	AEWRESIR	E	523.83	2	1045.64	0.11	1045.53	33.90	32
292562	LAELQEQLK	A	536.33	2	1070.65	0.06	1070.60	44.84	32
233230	SPASKLDK	S	423.13	2	844.26	-0.21	844.47	35.44	33
209283	VCQSPINVEGK	M	615.82	2	1229.63	0.03	1229.61	43.41	31
199223	VPFNINFDLSPR	H	709.86	2	1417.70	-0.03	1417.74	51.14	31
304228	TVEELLETGLIQVATR	E	886.65	2	1771.28	0.31	1770.97	30.50	30
295319	YNPVIDFEMQPIYQLLQHTNLGPLETK	R	1106.17	3	3315.49	-0.19	3315.68	55.79	26
245798	QNIPISTR	G	408.30	2	814.58	0.15	814.43	33.33	32
280707	LDFTFELMVFK	L	759.96	2	1517.90	0.12	1517.78	86.15	30
200712	GEADRVESLLQLFR	S	812.37	2	1622.73	-0.10	1622.83	129.40	30
230447	EISEVQR	M	487.32	2	972.62	0.09	972.52	46.98	32
303538	LAEAVGEFLVPVR	R	700.45	2	1398.89	0.10	1398.79	43.77	31
213255	IQDALSTVLQVAEDVLSGK	V	1025.44	2	2048.87	-0.20	2049.06	119.51	29
313806	VMEQLGYPNPYR	L	741.83	2	1481.64	-0.06	1481.70	78.61	30
191966	DAASVDKVLLEK	E	644.36	2	1286.70	-0.01	1286.71	35.44	31
223302	LFGIADK	I	382.22	2	762.42	0.00	762.43	37.02	33
260956	GLTGSLPSLLTR	L	607.87	2	1213.73	0.02	1213.70	49.19	31
241253	HSVQDR	S	371.24	2	740.47	0.12	740.36	35.91	30
272431	SLFVLPHTDHLVGYYIR	L	660.60	3	1978.78	-0.32	1979.10	33.25	29
233766	QDHLTGHMLTHQK	T	781.51	2	1561.01	0.27	1560.75	31.69	30
290052	LIONQVANYPYR	E	732.00	2	1461.99	0.22	1461.77	74.19	30
302504	ETLENQNLVYGASNIR	L	967.59	2	1933.17	0.18	1932.99	48.96	29
233304	AGFFGTIVEYGAER	K	758.91	2	1515.80	0.06	1515.74	48.65	31
198580	AVTSLDLPVAINLK	E	783.99	2	1565.96	0.02	1565.94	56.34	30
272995	APAAFGVLSFLMHAGLER	N	629.66	3	1885.97	-0.02	1885.99	43.88	29
205672	LLADDAEALSLLALNPFEGR	A	1064.46	2	2126.90	-0.22	2127.12	37.13	29
304442	LGTVMHR	V	415.28	2	828.54	0.11	828.43	61.09	33
217607	FLDRLGAER	D	595.39	2	1188.77	0.11	1188.66	45.34	31
213091	LAQVLSSTASLR	F	736.46	2	1470.91	0.03	1470.88	61.71	30
317090	APELPVVHTFLFPPIER	M	693.76	3	2078.25	0.09	2078.16	61.42	29
243174	VLAEHGVAALFTAPTAR	A	613.04	3	1836.10	0.07	1836.03	34.85	29

229721	YLQEARSR	E	511.81	2	1021.60	0.07	1021.53	37.23	31
283019	VAAQAVEDVNIAR	R	734.92	2	1467.82	0.02	1467.80	91.62	30
253349	HITSIFDDEFAHYK	R	570.97	3	1709.90	0.13	1709.77	36.98	29
198860	FSGSGGTDFLTIR	S	773.38	2	1544.74	-0.01	1544.75	47.44	30
313999	FPSLR	A	388.27	2	774.52	0.07	774.45	50.21	33
261449	TQDDITLQLFR	L	789.45	2	1576.90	0.09	1576.81	70.33	31
217901	GTGDFDLR	E	520.70	2	1039.38	-0.06	1039.44	45.04	31
272629	VNDIIVNWNITLK	E	872.35	2	1742.69	-0.23	1742.92	54.23	30
259133	ADVGDAVDTALEQINR	R	844.02	2	1686.03	0.20	1685.82	37.34	30
281230	TYLDWLEQPFPEAVPSLRPLL	R	880.92	3	2639.75	0.34	2639.41	38.09	27
201803	ENIETVVTGSLDDLK	V	866.52	2	1731.03	0.13	1730.89	66.54	30
225113	FFDNPWGFQNRPEDTELPSK	Q	857.80	3	2570.39	0.20	2570.19	50.94	28
318262	WDEVDPDFECFILSGYR	R	1124.14	2	2246.27	0.27	2246.00	57.14	29
221417	HAQANGFSVWR	S	593.35	2	1184.69	0.08	1184.61	54.09	31
249318	IIVDER	E	365.63	2	729.25	-0.15	729.40	33.79	33
273036	FQEPSLYTIK	A	613.32	2	1224.62	-0.02	1224.64	46.08	31
290180	QVYVDKLQELK	K	681.89	2	1361.77	0.02	1361.76	31.19	31
255984	FDTEELNFLSR	Y	750.45	2	1498.88	0.19	1498.69	48.40	30
217100	TAQNLSIFLGSFR	M	727.40	2	1452.79	0.02	1452.77	48.54	30
283106	IVLEFADIVPK	T	678.86	2	1355.71	-0.10	1355.81	31.87	31
217052	AESMFTNAVQILEQFK	E	928.38	2	1854.74	-0.18	1854.92	100.98	29
279332	ITWISLGGEAR	D	645.33	2	1288.65	-0.02	1288.68	38.98	31
249119	LNDGNLMPVLGFGTFASK	E	949.07	2	1896.12	0.17	1895.95	62.79	29
215340	SPOGLGASTAEISAR	T	722.92	2	1443.82	0.08	1443.73	41.71	31
231757	VPPEDVSLOTK	L	615.87	2	1229.73	0.07	1229.67	31.86	31
294340	LPELDLR	E	428.27	2	854.53	0.04	854.49	34.63	30
249993	FPNLFPPLKPTVAR	R	576.01	3	1725.01	0.05	1724.96	46.73	30
301863	IIDGTSRDPYSHALVAGIDR	Y	757.86	3	2270.57	0.44	2270.13	50.76	28
224899	VVPMKEKPEVK	T	676.42	2	1350.82	0.07	1350.76	45.39	30
216365	SSRESLDIK	E	517.76	2	1033.51	-0.03	1033.54	40.97	32
292778	TNOFAVAKISK	R	660.17	2	1318.33	-0.43	1318.76	35.97	31
236982	AELEDLR	Q	423.23	2	844.44	0.02	844.43	37.75	33
211558	YDLASGATEQLPLSGLR	A	895.99	2	1789.96	0.04	1789.92	36.07	29
267553	LKMALSVR	S	467.24	2	932.47	-0.08	932.55	32.71	32
298591	KTCEVETVPLEK	E	716.83	2	1431.64	-0.08	1431.73	45.04	31
199559	FHVPLLLSPWSYTTYR	G	660.60	3	1978.77	-0.26	1979.03	42.37	29
278396	ASHFTVTDPR	N	639.27	2	1276.53	-0.09	1276.62	39.81	31
298819	EDAANNYAR	G	512.22	2	1022.43	-0.01	1022.44	69.17	31
274677	LLAGLHVLLSK	S	582.33	2	1162.64	-0.10	1162.74	33.90	31
230656	LVQNLEAGNDLFR	E	818.47	2	1634.92	0.08	1634.84	42.17	30
252804	GGPPFAVFEDPRDAEDAVYGR	D	847.88	3	2540.63	0.47	2540.16	41.94	28
253969	LGESNVYVQR	L	639.86	2	1277.71	0.08	1277.64	34.46	31
229118	VVAFTGDNPASLAGMR	L	803.35	2	1604.69	-0.11	1604.80	81.46	30
313581	MTAVPLTSR	N	488.26	2	974.51	-0.02	974.52	35.81	32
171684	GTDIMYTGTLDCWR	K	852.90	2	1703.79	0.07	1703.73	54.08	30
169376	YPSLTLEFSR	S	606.90	2	1211.79	0.17	1211.62	53.96	31
260364	SSPCOMCGETFJK	H	772.81	2	1543.61	-0.04	1543.65	56.65	30
227628	QLPTLILFOGK	E	657.86	2	1313.70	-0.07	1313.77	31.64	31
145735	GALEMVQMAVEAK	F	696.78	2	1391.54	-0.14	1391.68	38.23	30
50402	LGFPQEEQIK	N	549.79	2	1097.57	0.00	1097.57	60.57	31

90533	ISGSLALYLALLR	A		723.92	2		1445.82	-0.04	1445.86	108.82	30
30411	AGSVPSLAAGLFFGGLAGLAYQLSQDPR	N		940.72	3		2819.14	-0.32	2819.46	53.98	27
260939	NWEDLQDDFGQIQETHR	L		715.41	3		2143.20	0.23	2142.97	34.74	29
75921	LFGSSFAHQASVAR	V		739.32	2		1476.63	-0.12	1476.75	70.08	31
11402	VFVDLFLNLSYLVR	H		884.99	2		1767.96	0.00	1767.96	48.88	30
8904	ILGIPVIITEQYPK	G		792.54	2		1583.07	0.14	1582.93	72.65	30
301880	LEGEIATYR	R		561.78	2		1121.55	-0.03	1121.57	61.26	31
161849	QVGGDVNVEMDAAPGVDLSR	I		1051.47	2		2100.93	-0.04	2100.97	109.40	29
222258	AEAESWYQTK	Y		606.75	2		1211.49	-0.06	1211.55	44.90	31
71712	VNTLETEWFFK	D		771.88	2		1541.74	0.00	1541.74	47.67	30
205347	SFGNNHFAASSPLMAPLR	E		645.03	3		1932.07	0.14	1931.93	70.55	29
53068	LPSNYLFR	G		504.82	2		1007.63	0.05	1007.58	49.98	31
127236	FVSWTYELPR	D		698.86	2		1395.72	0.00	1395.72	70.29	30
22316	DHPFGFVAVPTK	N		657.89	2		1313.76	0.08	1313.68	40.98	31
30131	IYAGQMAVLGR	T		589.81	2		1177.62	-0.01	1177.63	35.27	31
282121	HLFNIISR	K		500.25	2		998.49	-0.08	998.57	40.96	32
58922	ILLSVSMIAEPNDESGANVDASK	M		1238.07	2		2474.13	-0.09	2474.22	43.60	28
190070	TNLATGIPSSK	V		544.82	2		1087.62	0.03	1087.59	38.85	32
265453	NLYADIDAAWQALR	T		810.41	2		1618.81	0.00	1618.81	34.73	30
37481	CESLDSTGLCR	V		649.31	2		1296.61	0.07	1296.54	36.04	30
44446	LRDPAAVASELGVVFOATLTR	Q		797.85	3		2390.52	0.23	2390.30	62.83	29
276682	LFLAGYDPTPMR	D		741.23	2		1480.45	-0.29	1480.74	57.01	31
55286	EFTGSQNSVEPFDNLLLLDR	N		1206.16	2		2410.30	0.09	2410.22	63.65	28
11413	MQTNQPTTYNK	T		719.86	2		1437.70	0.05	1437.66	34.81	30
38248	LQQTQAAQVDEWDMR	V		936.87	2		1871.73	-0.21	1871.94	77.16	29
23581	LQQTQNVQVDEWDMR	V		958.33	2		1914.65	-0.29	1914.95	133.60	29
291525	LALCLAGLALSLYALHVK	A		642.77	3		1925.29	0.17	1925.12	104.32	29
165266	GFLLGSIFGK	D		548.30	2		1094.59	-0.02	1094.61	52.58	31
80445	IPAFGSIPIEFR	V		673.90	2		1345.79	0.05	1345.74	61.50	31
66447	NLHPLNELPLAYIED	END		949.43	2		1896.85	-0.11	1896.96	75.05	30
84170	TVQDALSMQESDIAVVAR	G		1018.50	2		2034.99	0.00	2034.99	144.87	29
11237	RTYTLADYLK	N		622.39	2		1242.77	0.11	1242.66	41.02	31
168211	FPSHFSSDLK	N		582.80	2		1163.59	0.03	1163.56	45.21	31
79044	DPENPFELTNHAVLLVGYGK	D		744.38	3		2230.13	-0.01	2230.14	63.20	29
318701	VFDSLNLNSTLQATR	A		896.57	2		1791.12	0.17	1790.95	84.32	30
126560	GTNVVSLSLHDDK	E		849.43	2		1696.85	-0.05	1696.90	49.88	30
78212	VQEEAWCLVEELQK	T		880.78	2		1759.55	-0.30	1759.85	99.96	30
80282	FENKVPEK	Q		495.77	2		989.53	0.01	989.52	47.76	32
281056	PALLPVASR	L		462.27	2		922.53	-0.03	922.56	36.65	31
85113	QRIDEFEAM	END		577.80	2		1153.59	0.08	1153.51	40.27	31
22617	ADIGTTSEFIDEGAGIR	END		870.51	2		1739.01	0.20	1738.80	99.76	29
22616	ATTDSDKVDISLAR	END		746.24	2		1490.47	-0.29	1490.76	145.82	31
168825	LNDHFPLVVWQTGSGTQTNMNVNEVISNR	A		1096.31	3		3285.90	0.31	3285.58	73.45	26
84237	EFTPSAQAAFKVVAGVASALAHK	Y		810.02	3		2427.05	-0.24	2427.29	65.51	29
301974	LLACLEGK	E		452.26	2		902.51	0.02	902.49	41.61	33
203844	VSSVCGVERMATLR	G		761.34	2		1520.67	-0.06	1520.73	33.70	30

287423	SQGGVQPIPSQGGK	L	670.38	2	1338.74	0.05	1338.69	46.24	30
300655	MSLHFQMLK	R	583.87	2	1165.72	0.16	1165.56	32.28	31
126680	FSGSGGTQYSLK	I	659.82	2	1317.62	0.00	1317.62	49.37	31
157223	SILLTGYLEYLLK	H	763.37	2	1524.73	-0.15	1524.88	78.64	30
37206	LYDAVAVLLSMR	N	683.81	2	1365.61	-0.12	1365.73	85.59	31
132766	IPPHYHYHVDQNSVSR	V	718.04	3	2151.11	0.03	2151.09	30.01	29
317126	MFGSRLR	Q	441.78	2	881.55	0.10	881.45	32.12	31
271324	MGVGRNAR	G	438.80	2	875.58	0.14	875.44	33.76	33
411195	FDSACTMGAYHPLIFEK	N	717.21	3	2148.61	-0.35	2148.96	83.73	29
165519	NLETLQQLGIEGENR	V	922.04	2	1842.06	0.14	1841.91	76.23	29
293682	AIGDYDGHVGLGVK	C	700.84	2	1399.67	-0.04	1399.71	58.28	31
293440	NPDTQWITK	F	551.72	2	1101.42	-0.13	1101.55	65.45	32
214593	QREELSNVLAAMR	K	506.33	3	1515.97	0.18	1515.78	65.53	31
310564	WGATVKPR	M	457.77	2	913.52	0.01	913.51	43.03	31
262837	SASQLPSR	L	423.27	2	844.53	0.09	844.44	37.62	33
281550	GTGLGFSQILQGEDIVR	E	951.99	2	1901.96	-0.06	1902.02	86.83	29
238208	SPVASIVYDLNPNFK	A	832.54	2	1663.06	0.20	1662.86	36.30	30
240773	TLGIATNISR	G	523.32	2	1044.62	0.03	1044.59	34.34	32
215152	LSAALSSLQR	D	523.31	2	1044.61	0.02	1044.59	32.12	32
245025	SYEFFNELYHR	F	752.94	2	1503.87	0.19	1503.68	39.75	30
258588	ESEDVELLWR	L	638.41	2	1274.81	0.19	1274.61	31.39	31
295519	TYTSQSHQAVIAEQLAK	L	663.21	3	1986.61	-0.43	1987.04	29.02	29
241066	DNGLLAR	Q	379.72	2	757.42	0.01	757.41	36.67	33
229917	TAEILAWGLR	N	621.95	2	1241.88	0.17	1241.71	44.09	31
223872	SGDAADVDMVPGK	A	638.27	2	1274.54	-0.08	1274.62	36.74	31
276511	RLPLADR	Y	420.76	2	839.50	0.01	839.50	34.99	31
285938	ISVINGGSK	A	437.75	2	873.49	-0.01	873.49	33.59	32
247025	IVSNASCTTKCLAPLAK	V	917.24	2	1832.47	-0.48	1832.95	58.22	29
260747	EMLQALGLASIDELIEK	T	936.99	2	1871.97	-0.02	1871.99	54.89	29
255469	IQPEELWLYR	N	673.75	2	1345.49	-0.21	1345.70	33.09	31
236971	SINPNEAVAYGAAVQAAILSGDK	S	753.87	3	2258.57	0.42	2258.15	50.54	28
279473	VGAGAPVYMAAVLEYLTAEILELAGNAAR	D	983.82	3	2948.45	-0.08	2948.53	117.75	27
190049	VHLARFVLDALDR	S	762.90	2	1523.79	-0.07	1523.86	36.35	31
282355	NTALHWAVLAGNTTVISLLLEAGGNVDAQNVK	G	1097.39	3	3289.16	0.41	3288.75	32.51	25
266460	APLSTVVSANTK	N	544.81	2	1087.60	0.02	1087.59	58.26	32
308005	HPSPPVVDITTK	G	632.85	2	1263.69	0.04	1263.65	95.41	31
225772	LPFDIPYVSGHETGIAISVAVALGAK	V	923.26	3	2766.76	0.26	2766.50	34.38	27
287362	IEGTPLEAMQK	K	616.87	2	1231.73	0.12	1231.61	56.32	31
192715	YKPAPLALPNLTDPAEYDVSPETR	K	910.17	3	2727.50	0.12	2727.38	78.50	27
195949	TIEAAAHGTVTR	H	678.30	2	1354.58	-0.11	1354.68	35.98	30
191003	SLLSLPNTDYIQLLSEIAK	E	1059.57	2	2117.12	-0.05	2117.16	45.92	29
233624	INSPHYLTK	I	536.84	2	1071.67	0.10	1071.57	37.90	32
202185	MGLLAVLRSK	Q	552.38	2	1102.75	0.09	1102.65	40.55	32

244453	DPHYMDYR	A		516.74	2		1031.46	0.01	1031.45	32.01		32
288218	KGDVVVLTR	X		550.28	2		1098.54	-0.13	1098.68	31.29		31
230313	DTKDVSTLTK	A		554.36	2		1106.70	0.12	1106.58	32.51		31
270299	VLSPVSTPFTAVLK	F		794.42	2		1586.84	-0.06	1586.89	54.09		30
301426	VLSGQDTEDR	S		560.26	2		1118.50	-0.02	1118.52	66.17		32
269534	LDVWKTNLGER	G		722.41	2		1442.80	0.01	1442.79	31.69		31
260021	IPAFNLVADIAGLVK	G		784.93	2		1567.84	-0.10	1567.93	82.50		30
230365	SVILHLSQLK	L		625.89	2		1249.77	-0.01	1249.78	85.79		31
264993	IAESLGGSGYSVER	L		712.87	2		1423.73	0.04	1423.69	45.57		30
211028	LPNFGVVDDSEPVQR	I		983.54	2		1965.06	0.10	1964.96	79.34		29
197399	SMVDLFAEIVR	Q		712.91	2		1423.80	0.10	1423.70	80.58		30
229135	VQLQDLQDFFR	K		761.42	2		1620.83	0.03	1620.80	47.06		30
315186	AFDNEVNAFLDNMFGPR	D		979.01	2		1956.01	0.13	1955.88	32.96		29
198937	ENNAVYAFGLTAPPGSK	E		924.98	2		1847.95	0.01	1847.94	72.80		29
250786	LGAPQTHLGLK	S		567.82	2		1133.63	-0.03	1133.66	36.44		31
221702	QINLNIEWTVEKLK	S		864.97	2		1727.92	0.00	1727.92	41.36		29
283888	VDVTEQTGLSGR	F		631.37	2		1260.73	0.09	1260.63	93.19		31
208424	ILTTALFSVLMNLR	S		804.46	2		1606.90	-0.01	1606.91	57.55		30
289309	LFNEERLIDK	S		638.81	2		1275.60	-0.08	1275.68	32.57		31
292693	YAPSGFYASGDISGK	L		816.81	2		1631.61	-0.17	1631.78	47.51		30
214625	AIEAASSLKSOAAIK	N		738.36	2		1474.71	-0.09	1474.80	31.08		30
254285	LQNDSVYTIAR	R		640.30	2		1278.59	-0.06	1278.66	33.14		31
257029	AAYYGIYDTAK	G		618.32	2		1234.62	0.03	1234.59	39.86		31
209377	NDGVGOISGFYVGR	L		734.85	2		1467.69	-0.02	1467.71	83.43		30
285481	LGYVDADGGDFDVDDAK	V		943.90	2		1885.78	-0.01	1885.79	68.95		29
236762	FSFTLPYPLR	M		620.91	2		1239.80	0.13	1239.67	42.93		31
256498	ILQAVEFPELVR	L		716.37	2		1430.73	-0.10	1430.83	46.76		31
253866	EGLSGQEWRLVK	G		750.98	2		1499.95	0.14	1499.81	33.99		30
214268	SSPSLDQMFDAEILGFSTPPGR	L		1184.53	2		2367.05	-0.06	2367.11	44.02		28
202236	STTFSTNYR	S		538.78	2		1075.54	0.04	1075.49	41.75		32
273385	ASGLLFVPNILAR	A		685.98	2		1369.94	0.13	1369.81	32.90		30
168139	RAPAAQPPATAAAPSAVGSPAAAPR	Q		751.96	3		2252.85	-0.35	2253.20	69.03		28
210943	VNHDNFGIVEGLMTTVHAITATQK	T		866.22	3		2595.65	0.34	2595.31	50.34		28
296252	VLISAPSANAPMFVMGVNHEK	Y		743.52	3		2227.54	0.43	2227.11	37.49		28
156654	GLMTTVHAITATQK	S		744.48	2		1486.95	0.17	1486.78	105.85		30
252379	GAAENIIPASTGAAK	A		685.93	2		1369.85	0.13	1369.72	31.78		30
220378	TTEELNEALSAK	E		653.20	2		1304.39	-0.25	1304.65	35.80		31
195465	FQEAERPR	V		581.29	2		1160.56	0.01	1160.56	31.18		31
272734	LPKPTR	S		356.24	2		710.46	0.01	710.44	36.01		30
193827	TLEEDEELFK	M		691.31	2		1380.61	-0.02	1380.63	53.60		31
231118	QQQFSLSEK	K		611.82	2		1221.63	0.04	1221.60	41.58		31
196884	EGLKSPWPSR	H		607.28	2		1212.54	-0.09	1212.63	40.91		31
248047	LATVPADFALLSNLLR	L		857.53	2		1713.04	0.06	1712.98	43.49		30
243991	VAEPSEASLGR	G		606.78	2		1211.55	-0.07	1211.61	82.54		31
263071	MAERIEER	I		517.31	2		1032.60	0.10	1032.50	32.90		32
202821	QWADIGFQGDPPK	T		738.90	2		1475.78	0.11	1475.67	34.65		31
277215	APSSLSAPSPEK	T		585.71	2		1169.41	-0.18	1169.59	37.94		31
234073	EEQMASIKK	D		532.35	2		1062.69	0.16	1062.54	31.33		31

269756	TYQSCVSSCR	R	688.28	2	1374.55	-0.02	1374.57	61.57	31
235658	ISSTLYQATAPALTPAK	V	867.04	2	1732.06	0.12	1731.94	89.24	30
267138	VLELEDELQESR	G	730.30	2	1458.59	-0.13	1458.72	44.99	31
309715	QEDSAQIIR	R	530.33	2	1058.65	0.12	1058.54	34.06	32
265130	MKHMESLK	M	583.82	2	1165.62	0.09	1165.53	32.75	31
297002	DIVEVLFTQPNVELNQONK	L	1114.68	2	2227.34	0.19	2227.15	36.80	29
160562	VAFSGILDIVDIR	N	709.45	2	1416.89	0.09	1416.80	31.97	31
305160	YVPYGPVMEVLPYLSR	R	941.97	2	1881.92	-0.05	1881.97	82.36	29
240940	YKMLDER	E	485.77	2	969.53	0.07	969.46	38.29	31
242276	CLIELEPVLR	T	621.32	2	1240.62	-0.06	1240.68	37.52	31
292043	LKDPYITVPNLPGLTGFIR	L	743.05	3	2226.14	-0.14	2226.28	59.21	29
285721	MAEGGVAAGVMDVNTALQEVLK	T	1145.60	2	2289.18	0.04	2289.13	28.79	28
290757	VKAVISPR	R	435.26	2	868.50	-0.05	868.55	31.64	31
280942	LDEANAALDSASR	L	666.78	2	1331.55	-0.08	1331.63	105.45	31
202385	NFVSQIVAEENLYPK	G	811.31	2	1620.60	-0.25	1620.85	63.36	30
317625	LAGTQPLEVLEAVQR	S	812.49	2	1622.97	0.07	1622.90	55.62	30
60460	YVSPQVWTR	L	588.80	2	1175.58	-0.05	1175.63	70.76	32
314842	DYSGDHVQQAK	Y	624.23	2	1246.45	-0.10	1246.56	67.30	31
345922	VPASASTQSQGSSR	V	681.89	2	1361.76	0.11	1361.65	55.11	31
309548	IAGLEEKALK	A	536.29	2	1070.56	-0.07	1070.63	38.18	32
263673	IENSLASILLELLK	G	722.00	2	1441.98	0.15	1441.84	31.39	30

Table S1C. Curation of protein identifications

ASSIGNED PROT NAME	FUNCTIONAL CATEGORY	NCBI DESCRIPTION	MW	ginumber	CMBSEQID
CHAPERONIN 10	PROT SYN/FOLD	10 kDa heat shock protein, mitochondrial	10770	400542	121548
14-3-3 PROTEIN EPSILON	SIGNALING	14-3-3 protein epsilon	29170	61216932	35616
14-3-3 PROTEIN ZETA/DELTA	SIGNALING	14-3-3 protein zeta/delta Protein kinase C inhibitor protein 1	27770	68085421	29712
15 KDA SELENOPROTEIN	PROT MOD	KCIP-1 SEZ-2 15 kDa selenoprotein precursor	17780	20139870	129368
ALCOHOL DEHYDROGENASE PAN1B-LIKE PROTEIN	METABOLISM	17-beta hydroxysteroid dehydrogenase 13 precursor Short-chain dehydrogenase/reductase 9	33490	77416416	169811
2,4-DIENOYL-COA REDUCTASE, MITOCHONDRIAL	MITOCHONDRIA	2,4-dienoyl-CoA reductase, mitochondrial precursor	36130	67476443	148907
2-HYDROXYPHYTYL-NOYL-COA LYASE	PEROXISOME	2-hydroxyphytyl-NOYL-COA lyase 2-hydroxyphytyl-NOYL-Coenzyme A lyase	63620	50926767	187564
3,2-TRANS-ENOYL-COA ISOMERASE, MITOCHONDRIAL	MITOCHONDRIA	3,2-trans-enoyl-CoA isomerase, mitochondrial precursor Dodecenoyl-CoA isomerase Delta(3), delta(2)-enoyl-CoA isomerase D3.D2-enoyl-CoA isomerase	32250	8393243	51421
3-ALPHA-HYDROXYSTEROID DEHYDROGENASE	DETOXIFICATION	3-alpha-hydroxysteroid dehydrogenase	37030	6708142	19230
3-HYDROXYACYL-COA DEHYDROGENASE TYPE II (TYPE II HADH)	DETOXIFICATION	3-hydroxyacyl-CoA dehydrogenase type II	27250	7387724	83190
3-KETOACYL-COA THIOLASE, MITOCHONDRIAL	MITOCHONDRIA	3-ketoacyl-CoA thiolase, mitochondrial Beta-ketothiolase Acetyl-CoA acyltransferase Mitochondrial 3-oxoacyl-CoA thiolase	41870	55544	96895
3-OXO-5-BETA-STEROID 4-DEHYDROGENASE	DETOXIFICATION	3-oxo-5-beta-steroid 4-dehydrogenase Delta(4)-3-ketosteroid 5 beta-reductase Aldo-keto reductase family 1 member D1	37380	9438775	23758
40S RIBOSOMAL PROTEIN S11	PROT SYN/FOLD	40S ribosomal protein S11	18430	54039305	4834
40S RIBOSOMAL PROTEIN S12	PROT SYN/FOLD	40S ribosomal protein S12	14510	78126139	132206
40S RIBOSOMAL PROTEIN S13	PROT SYN/FOLD	40S ribosomal protein S13	17220	57730	4835
40S RIBOSOMAL PROTEIN S14	PROT SYN/FOLD	40S ribosomal protein S14	16270	37231722	98434
40S RIBOSOMAL PROTEIN S16	PROT SYN/FOLD	40S ribosomal protein S16	16450	57714	4837
40S RIBOSOMAL PROTEIN S18	PROT SYN/FOLD	40S ribosomal protein S18	17720	50403620	60848
40S RIBOSOMAL PROTEIN S19	PROT SYN/FOLD	40S ribosomal protein S19	16090	82654220	122667
40S RIBOSOMAL PROTEIN S20	PROT SYN/FOLD	40S ribosomal protein S20	13370	57720	4840
40S RIBOSOMAL PROTEIN S21	PROT SYN/FOLD	40S ribosomal protein S21	9127	483517	37243
40S RIBOSOMAL PROTEIN S23	PROT SYN/FOLD	40S ribosomal protein S23	15810	730647	4842
40S RIBOSOMAL PROTEIN S25	PROT SYN/FOLD	40S ribosomal protein S25	13740	74355904	4844
40S RIBOSOMAL PROTEIN S26	PROT SYN/FOLD	40S ribosomal protein S26	13020	6981488	75074
40S RIBOSOMAL PROTEIN S27	PROT SYN/FOLD	40S ribosomal protein S27-like protein	9477	57741	120488
40S RIBOSOMAL PROTEIN S28	PROT SYN/FOLD	40S ribosomal protein S28	7841	57726	1344
40S RIBOSOMAL PROTEIN S3	PROT SYN/FOLD	40S ribosomal protein S3	26670	57728	60850
40S RIBOSOMAL PROTEIN S30	PROT SYN/FOLD	40S ribosomal protein S30	6648	51338625	106720
40S RIBOSOMAL PROTEIN S3A	PROT SYN/FOLD	40S ribosomal protein S3a	29940	8394221	51618
40S RIBOSOMAL PROTEIN S7	PROT SYN/FOLD	40S ribosomal protein S7	22130	66730357	4853
40S RIBOSOMAL PROTEIN S9	PROT SYN/FOLD	40S ribosomal protein S9	22590	52788199	142294
40S RIBOSOMAL PROTEIN SA	PROT SYN/FOLD	40S ribosomal protein SA	32820	8393693	51515
60 KDA HEAT SHOCK PROTEIN, MITOCHONDRIAL (HSP60) (60 KDa)	MITOCHONDRIA	60 kDa heat shock protein, mitochondrial precursor Hsp60 60 kDa chaperonin CPN60 Heat shock protein 60 HSP-60 Mitochondrial matrix protein P1 HSP-65	60960	55778012	52609

60S RIBOSOMAL PROTEIN P0	PROT SYN/FOLD	60S acidic ribosomal protein P0 L10E	34220	730581	23405
60S RIBOSOMAL PROTEIN P1	PROT SYN/FOLD	60S acidic ribosomal protein P1	11500	57710	144430
60S RIBOSOMAL PROTEIN P2	PROT SYN/FOLD	60S acidic ribosomal protein P2	11690	71795613	144431
60S RIBOSOMAL PROTEIN L12	PROT SYN/FOLD	60S ribosomal protein L12	17850	57680	144419
60S RIBOSOMAL PROTEIN L18A	PROT SYN/FOLD	60S ribosomal protein L18a	20730	50403587	71631
60S RIBOSOMAL PROTEIN L24	PROT SYN/FOLD	60S ribosomal protein L24	17780	560493	4812
60S RIBOSOMAL PROTEIN L36	PROT SYN/FOLD	60S ribosomal protein L36	12250	34849736	65711
60S RIBOSOMAL PROTEIN L4	PROT SYN/FOLD	60S ribosomal protein L4	47310	1363989	85424
60S RIBOSOMAL PROTEIN L5	PROT SYN/FOLD	60S ribosomal protein L5	34460	57125	37237
BIP	PROT SYN/FOLD	78 kDa glucose-regulated protein precursor GRP 78 Immunoglobulin heavy chain-binding protein BIP	72350	38303969	28269
NAD+ ADP-RIBOSYL TRANSFERASE 3 PARP-3	NUCLEUS	ADP-riboseyltransferase NAD+, poly (ADP-ribose polymerase)- Steroidogenesis-activator polypeptide	58870	56605734	298279
ALPHA-1-MICROGLOBULIN	BIOSYNTHETIC CARGO	AMBIP protein precursor Alpha-1-microglobulin Inter-alpha- trypsin inhibitor light chain ITI-LC Bikunin HI-30 Trypsatin like 3 (Predicted)	38850	6978497	3629
ARP3 ACTIN-RELATED PROTEIN 3 HOMOLOG	CYTOSKELETON	ARP3 actin-related protein 3 homolog	47360	70912366	71751
ATP SYNTHASE B CHAIN, MITOCHONDRIAL	MITOCHONDRIA	ATP synthase B chain, mitochondrial precursor	28870	39645769	141484
ATP SYNTHASE D CHAIN, MITOCHONDRIAL	MITOCHONDRIA	ATP synthase D chain, mitochondrial	18760	9506411	21505
ATP SYNTHASE OLIGOMYCIN SENSITIVITY CONFERRAL PROTEIN	MITOCHONDRIA	ATP synthase O subunit, mitochondrial precursor Oligomycin sensitivity conferral protein OSCP	23400	543880	142437
ATP SYNTHASE ALPHA CHAIN, MITOCHONDRIAL	MITOCHONDRIA	ATP synthase alpha chain, mitochondrial precursor	55280	6729934	73367
ATP SYNTHASE BETA CHAIN, MITOCHONDRIAL	MITOCHONDRIA	ATP synthase beta chain, mitochondrial precursor	56350	71681130	141479
ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR	MITOCHONDRIA	ATP synthase coupling factor 6, mitochondrial precursor	12490	599963	60480
ATP SYNTHASE DELTA CHAIN, MITOCHONDRIAL	MITOCHONDRIA	ATPase subunit F6 ATP synthase delta chain, mitochondrial precursor	17600	457929	21504
ATP SYNTHASE EPSILON CHAIN, MITOCHONDRIAL	MITOCHONDRIA	ATP synthase epsilon chain, mitochondrial	5636	258789	11887
ATP SYNTHASE GAMMA CHAIN, MITOCHONDRIAL	MITOCHONDRIA	ATP synthase gamma chain, mitochondrial	29930	6729936	69786
ATP CITRATE LYASE	METABOLISM	ATP-citrate synthase ATP-citrate (pro-S)-lyase Citrate cleavage enzyme	120600	8392839	126543
VITRONECTIN	BIOSYNTHETIC CARGO	Aa1018	55960	32492572	302124
APOLIPOPROTEIN B	BIOSYNTHETIC CARGO	Aa1064	42690	111387	148924
CCG1-INTERACTING FACTOR B	UNKNOWN	Abhydrolase domain containing 14b	22620	56090461	151517
FIBRINOGEN B BETA CHAIN	BIOSYNTHETIC CARGO	Ac1-581 Ab1-216 Ab1-181	56610	33086484	166238
SIMILAR TO OLIGOSACCHARYL TRANSFERASE 3	PROT MOD	Ac1573	79140	32264637	263869
FIBRINOGEN ALPHA/ALPHA-E CHAIN	BIOSYNTHETIC CARGO	Ac1873	86660	62643670	173317
MURINE COAGULATION FACTOR V	BIOSYNTHETIC CARGO	Ac2-120	237300	62659617	166242
AC2-155	UNKNOWN	Ac2-155	102100	33086620	199808
ACETYL-COA ACETYLTRANSFERASE, MITOCHONDRIAL	MITOCHONDRIA	Acetyl-CoA acetyltransferase, mitochondrial precursor	44690	66502	31496

LYSOPHOSPHATIDIC ACID PHOSPHATASE	METABOLISM	Acid phosphatase 6, lysophosphatidic	47280	72255521	193296
PROLIFERATION RELATED ACIDIC LEUCINE RICH PROTEIN PAL3	NUCLEUS	Acidic leucine-rich nuclear phosphoprotein 32 family member B Proliferation-related acidic leucine-rich protein PAL 31	31060	9971212	3001
MITOCHONDRIAL ACONITASE	MITOCHONDRIA	Aconitate hydratase, mitochondrial precursor Citrate hydro-lyase Aconitase	85430	60391194	338228
ACTIN, GAMMA	CYTOSKELETON	Actin, cytoplasmic 2	41790	62645364	120792
ACTIN-LIKE PROTEIN 2 ACTIN-RELATED PROTEIN 2	CYTOSKELETON	Actin-like protein 2 Actin-related protein 2	44730	62899645	156591
ACYL-COENZYME A OXIDASE 1, PEROXISOMAL	PEROXISOME	Acyl-coenzyme A oxidase 1, peroxisomal	74680	8394149	51604
ACYL-COENZYME A OXIDASE 2, PEROXISOMAL	PEROXISOME	Acyl-coenzyme A oxidase 2, peroxisomal 3-alpha,7-alpha,12-alpha-trihydroxy-5-beta-cholestanoyl-CoA 24-hydroxylase 3-alpha,7-alpha,12-alpha-trihydroxy-5-beta-cholestanoyl-CoA oxidase Trihydroxycoprostanoyl-CoA oxidase THCCox THCA-CoA oxidase	76800	21955130	3086
ACYL-COENZYME A OXIDASE 3, PEROXISOMAL	PEROXISOME	Acyl-coenzyme A oxidase 3, peroxisomal Pristanoyl-CoA oxidase Branched-chain acyl-CoA oxidase BRCAox	78450	2498208	42129
ADENOSYLHOMOCYSTEINASE	METABOLISM	Adenosylhomocysteinase	47420	24158803	54409
ADENYLATE KINASE 2	MITOCHONDRIA	Adenylate kinase 2, isoform b	25530	77020256	340217
ADIPOCYTE-DERIVED LEUCINE AMINOPEPTIDASE	PROT MOD	Adipocyte-derived leucine aminopeptidase precursor	100700	8131852	605
AFAMIN	BIOSYNTHETIC CARGO	Afamin precursor Alpha-albumin Alpha-Alb	69340	543793	23759
AFLATOXIN B1 ALDEHYDE REDUCTASE MEMBER 1	DETOXIFICATION	Aflatoxin B1 aldehyde reductase member 1	36740	433611	100616
ALDEHYDE DEHYDROGENASE	METABOLISM	Aldehyde dehydrogenase	48270	16073616	7845
ESTRADIOL 17BETA-DEHYDROGENASE (EC 1.1.1.62), A-SPECIFIC	DETOXIFICATION	Aldo-keto reductase family 1, member C6	37000	76096330	217551
ALPHA-ACTININ 4	CYTOSKELETON	Alpha actinin 4	104900	77539778	319018
ALPHA GLOBIN	BLOOD + OTHER CELLS	Alpha globin	15520	62655914	114803
ALPHA-1-ANTIPROTEINASE	BIOSYNTHETIC CARGO	Alpha-1-antiproteinase precursor	46140	112889	11475
ALPHA-1 PROTEINASE INHIBITOR III	BIOSYNTHETIC CARGO	Alpha-1-inhibitor III precursor	163800	83816939	11478
ALPHA-1-MACROGLOBULIN	BIOSYNTHETIC CARGO	Alpha-1-macroglobulin	167100	739596	126488
ALPHA-2-HS-GLYCOPROTEIN	BIOSYNTHETIC CARGO	Alpha-2-HS-glycoprotein	37980	60552688	111646
HEMOGLOBIN ALPHA-1 AND ALPHA-2 CHAINS	BLOOD + OTHER CELLS	Alpha-2-globin chain Hba-a1 protein 2-alpha globin	15280	60688619	109334
ALPHA-2U GLOBULIN	BIOSYNTHETIC CARGO	Alpha-2U globulin	20560	8307690	125352
ALPHA-2U-GLOBULIN	BIOSYNTHETIC CARGO	Alpha-2u globulin PGCL2	20710	56269668	161585
ELECTRON TRANSFER FLAVOPROTEIN ALPHA-SUBUNIT, MITOC	MITOCHONDRIA	Alpha-ETF	34950	57527204	151400
ALPHA-ACTININ 1	CYTOSKELETON	Alpha-actinin-1 Alpha-actinin cytoskeletal isoform Non-muscle alpha-actinin-1 F-actin cross linking protein	103000	4210985	37175
ALPHA-METHYLACYL-COA RACEMASE	PEROXISOME	Alpha-methylacyl-CoA racemase	41830	13637497	76478
ALPHA-SOLUBLE NSF ATTACHMENT PROTEIN (ALPHA SNAP)	TETH/DOCK/FUS	Alpha-soluble NSF attachment protein SNAP-alpha N-ethylmaleimide-sensitive factor attachment protein, alpha	33190	6094309	51376

ANGIOTENSINOGEN	BIOSYNTHETIC CARGO	Angiotensinogen precursor Angiotensin-1 Angiotensin I Ang I	51980	56585074	45123
TRYPSIN I, ANIONIC	TRYPSIN	Angiotensin-2 Angiotensin II Ang II Angiotensin-3 Angiotensin III Ang III Des-Asp[1]-angiotensin II	25960	6981420	75054
ANNEXIN A3	TETH/DOCK/FUS	Antionic trypsin-1 precursor Antionic trypsin I Pretrypsinogen I	36360	71766	120574
ANNEXIN 5	TETH/DOCK/FUS	Annexin A3	35740	6978505	3633
APOLIPOPROTEIN A-I	BIOSYNTHETIC CARGO	Annexin A5	30060	6978515	3638
APOLIPOPROTEIN A-IV	BIOSYNTHETIC CARGO	Apolipoprotein A-I precursor	44460	60552712	141420
APOLIPOPROTEIN E	BIOSYNTHETIC CARGO	Apolipoprotein A-IV precursor	35750	55824759	126501
PROGRAMMED CELL DEATH PROTEIN 8, MITOCHONDRIAL	MITOCHONDRIA	Apolipoprotein E precursor Apo-E	66720	7619915	63059
ARGINASE 1	METABOLISM	Apoptosis-inducing factor	34970	6573527	37797
ARGININOSUCCINATE SYNTHASE	METABOLISM	Arginase 1	46500	55767	45108
ASPARTATE TRANSAMINASE	MITOCHONDRIA	Argininosuccinate synthase Citrulline--aspartate ligase	46430	91997	84171
ASPARTATE AMINOTRANSFERASE, MITOCHONDRIAL	MITOCHONDRIA	Aspartate aminotransferase, cytoplasmic	47310	6980972	3905
SIMILAR TO BCS1-LIKE	UNKNOWN	Aspartate aminotransferase, mitochondrial precursor	47390	56090628	232734
ERP44 (SIMILAR TO THIOREDOXIN DOMAIN CONTAINING 4; ENDO	PROT SYN/FOLD	Transaminase A Glutamate oxaloacetate transaminase 2	46880	62648953	310588
HAPTOGLOBIN	BIOSYNTHETIC CARGO	BCS1-like	42470	33086640	166334
SIMILAR TO BETA-2-GLYCOPROTEIN I	BIOSYNTHETIC CARGO	BW4	33200	57525	21485
BETA-2-MICROGLOBULIN	BIOSYNTHETIC CARGO	Beta-2-glycoprotein 1 precursor Beta-2-glycoprotein I	11640	999862	27803
BETA-GLUCURONIDASE	LYSOSOME	Apolipoprotein H Apo-H B2GPI Beta(2)GPI	73270	758260	21055
BETAINE--HOMOCYSTEINE S-METHYLTRANSFERASE	MITOCHONDRIA	Beta-2-microglobulin precursor	44980	3913156	71708
BILE ACID COA LIGASE	DETOXIFICATION	Beta-glucuronidase precursor	76270	9963930	30001
BILIVERDIN REDUCTASE A PRECURSOR	DETOXIFICATION	Betaine--homocysteine S-methyltransferase	33570	285208	54374
C-REACTIVE PROTEIN	BIOSYNTHETIC CARGO	Bile acyl-CoA synthetase BACS Bile acid CoA ligase BA-CoA ligase BAL Cholate--CoA ligase Very long chain acyl-CoA synthetase-related protein VLACS-related VLCSR Fatty acid transport protein 5 FATP-5 Solute carrier family 27 member 5	25470	8393197	126549
CDK5 REGULATORY SUBUNIT ASSOCIATED PROTEIN 3	SIGNALING	Biliverdin reductase A precursor Biliverdin-IX alpha-reductase BVR A	57040	7330736	18021
CDP-DIACYLGLYCEROL--INOSITOL 3-PHOSPHATIDYLTRANSFERASE	PROT MOD	C-reactive protein, pectatin related	23610	7674155	70677
ENDOPLASMIN PRECURSOR (ENDOPLASMIC RETICULUM PROTEIN)	PROT SYN/FOLD	CDK5 regulatory subunit-associated protein 3 CDK5 activator-binding protein C53	1978	111445	148937
CALNEXIN	PROT SYN/FOLD	GDP-diacylglycerol--inositol 3-phosphatidyltransferase Phosphatidylinositol synthase PtdIns synthase PI synthase	67250	543922	69775
CALRETICULIN	PROT SYN/FOLD	Calcium-binding protein 4	48000	55855	23403
CARBAMOYL-PHOSPHATE SYNTHASE [AMMONIA], MITOCHONDRIAL	MITOCHONDRIA	Calnexin precursor	164600	8393186	45074

CARBONIC ANHYDRASE III	METABOLISM	Carbonic anhydrase III	29420	10120584	5972
CARBOXYLESTERASE B-1	DETOXIFICATION	Carboxylesterase RL1	62310	14331129	158916
CARBOXYLESTERASE ESNA3	DETOXIFICATION	Carboxylesterase isoenzyme	61800	21426807	157137
CARBOXYLESTERASE 10	DETOXIFICATION	Carboxylesterase isoenzyme	2133	1478388	42034
CARBOXYLESTERASE ESNA2	DETOXIFICATION	Carboxylesterase precursor	62040	2641992	182047
CARBOXYLESTERASE 2	DETOXIFICATION	Carboxylesterase precursor	62240	3062827	13000
ACTIN, ALPHA CARDIAC	CYTOSKELETON	Cardiac alpha actin 1	42020	77993370	10199
CARNITINE O-PALMITOYLTRANSFERASE I, MITOCHONDRIAL	MITOCHONDRIA	Carnitine O-palmitoyltransferase I, mitochondrial liver isoform	88130	48735405	63443
CATHEPSIN B	LYSOSOME	Cathepsin B precursor	35600	1942646	19199
CATHEPSIN L	LYSOSOME	Cathepsin L precursor Major excreted protein MEP Cyclic protein 2 CP-2 Cathepsin L heavy chain Cathepsin L light chain	37660	38648869	141572
CC1-9	UNKNOWN	Cc1-9	62860	62641625	194016
CERAMIDASE	LYSOSOME	Ceramidase	83490	16758458	60505
CHOLINE DEHYDROGENASE, MITOCHONDRIAL	MITOCHONDRIA	Choline dehydrogenase	66390	55250736	160561
CLATHRIN HEAVY CHAIN	COAT	Clathrin heavy chain	191600	9506497	95154
COAGULATION FACTOR IX	BIOSYNTHETIC CARGO	Coagulation factor IX Christmas factor	31450	204146	149112
COFILIN, MUSCLE ISOFORM	CYTOSKELETON	Cofilin-2 Cofilin, muscle isoform	18710	62650690	74438
COMPLEMENT C4	BIOSYNTHETIC CARGO	Complement C4 precursor Complement C4 beta chain Complement C4 alpha chain C4a anaphylatoxin Complement C4 gamma chain	192200	29789265	162301
COMPLEMENT COMPONENT C9	BIOSYNTHETIC CARGO	Complement component C9 precursor	62280	2499467	43431
CONTRAPSIN-LIKE PROTEASE INHIBITOR 1	BIOSYNTHETIC CARGO	Contrapsin-like protease inhibitor 1 precursor	46520	57294	84230
CONTRAPSIN-LIKE PROTEASE INHIBITOR 3	BIOSYNTHETIC CARGO	Contrapsin-like protease inhibitor 3 precursor	45280	57231	84327
CONTRAPSIN-LIKE PROTEASE INHIBITOR 6	BIOSYNTHETIC CARGO	Contrapsin-like protease inhibitor 6 precursor CPI-26 Serine protease inhibitor 3 SPL-3 SPL-2.2	46650	50927309	88238
HYDROXYSTEROID 11-BETA DEHYDROGENASE 1	DETOXIFICATION	Corticosteroid 11-beta-dehydrogenase isozyme 1 11-DH 11-beta-hydroxysteroid dehydrogenase 1 11-beta-HSD1	31880	78214365	95697
TIP120	UNKNOWN	Cullin-associated NEDD8-dissociated protein 1 Cullin-associated and neddylation-dissociated protein 1 p120 CAND1 TBP-interacting protein TIP120A TBP-interacting protein of 120 kDa A	136400	67460104	92415
CYCLOPHILIN B	PROT SYN/FOLD	Cyclophilin B	20310	2143900	80354
CYTOCROME P450 4A2	DETOXIFICATION	Cyp4a14 protein	57970	71051108	63760
CYSTATHIONINE GAMMA-LYASE	METABOLISM	Cystathionine gamma-lyase CTL target antigen	43580	51261011	62524
CYTOCROME P450 1A2	DETOXIFICATION	Cytochrome P450 1A2	58290	203832	3724
CYTOCROME P450 27A1	DETOXIFICATION	Cytochrome P450 27, mitochondrial precursor	60730	62655087	63757

CYTOCHROME P450 2B2	DETOXIFICATION	Cytochrome P450 2B2 CYP1B2 P450E P450 PB4	55930	34855371	13404
CYTOCHROME P450 2B3	DETOXIFICATION	Cytochrome P450 2B3 CYP1B3	56380	28849945	63770
CYTOCHROME P450 2C11	DETOXIFICATION	Cytochrome P450 2C11	57180	56971259	63780
CYTOCHROME P450 2C13	DETOXIFICATION	Cytochrome P450 2C13, male-specific	55860	205935	63782
CYTOCHROME P450 2C22	DETOXIFICATION	Cytochrome P450 2C22	56210	203521	33163
CYTOCHROME P450 2C23	DETOXIFICATION	Cytochrome P450 2C23	56430	6166042	72763
CYTOCHROME P450 2C6	DETOXIFICATION	Cytochrome P450 2C6	56000	117223	63778
CYTOCHROME P450 2C7	DETOXIFICATION	Cytochrome P450 2C7	56190	482947	45873
CYTOCHROME P450 2D2	DETOXIFICATION	Cytochrome P450 2D2	56680	57812	63788
CYTOCHROME P450 2D5	DETOXIFICATION	Cytochrome P450 2D5	57080	57818	63790
CYTOCHROME P450 2E1	DETOXIFICATION	Cytochrome P450 2E1	56630	51980637	21526
CYTOCHROME P450 3A1	DETOXIFICATION	Cytochrome P450 3A	57720	6978749	3731
CYTOCHROME P450 3A18	DETOXIFICATION	Cytochrome P450 3A18 CYP11A18 P450(6)beta-2	57310	5921916	104898
CYTOCHROME P450 3A2	DETOXIFICATION	Cytochrome P450 3A2	57730	515799	87425
CYTOCHROME P450 4A3	DETOXIFICATION	Cytochrome P450 4A14 precursor CYP11A14 Lauric acid omega-hydroxylase P450-LA-omega 3	58230	28461155	21524
CYTOCHROME P450 2D3	DETOXIFICATION	Cytochrome P450, family 2, subfamily d, polypeptide 13	56640	58477687	103927
CYTOCHROME P450 2D4	DETOXIFICATION	Cytochrome P450, family 2, subfamily d, polypeptide 22	56680	62471444	33164
CYTOCHROME C OXIDASE POLYPEPTIDE VA, MITOCHONDRIAL	MITOCHONDRIA	Cytochrome c oxidase polypeptide Va, mitochondrial precursor	16130	55971	63743
CYTOCHROME C, SOMATIC	MITOCHONDRIA	Cytochrome c, somatic Adult male kidney cDNA, RIKEN full-length enriched library, clone:F520003L15 product:cytochrome c, somatic, full insert sequence ES cells cDNA, RIKEN full-length enriched library, clone:2410041L21 product:cytochrome c, somatic, full insert sequence. Adult male cerebellum cDNA, RIKEN full-length enriched library, clone:1500032A05 product:cytochrome c, somatic, full insert sequence 18-day embryo whole body cDNA, RIKEN full-length enriched library, clone:1100001H15 product:cytochrome c, somatic, full insert sequence Adult male kidney cDNA, RIKEN full-length enriched library, clone:0610031O08 product:cytochrome c, somatic, full insert sequence	11610	6978725	71180
D-AMINO ACID OXIDASE	PEROXISOME	D-amino-acid oxidase DAMOX DAO DAAO	38820	56972124	60497

DEHYDROGENASE/REDUCTASE SDR FAMILY MEMBER 4	PEROXISOME	Dehydrogenase/reductase SDR family member 4 NADPH-dependent carbonyl reductase/NADP-retinol dehydrogenase CR PHCR Peroxisomal short-chain alcohol dehydrogenase NADPH-dependent retinol dehydrogenase/reductase NDRD	27580	48474726	131621
ALCOHOL DEHYDROGENASE PAN1B	METABOLISM	Dehydrogenase/reductase SDR family member 8 precursor 17-beta-hydroxysteroid dehydrogenase 11 17-beta-HSD 11 17-beta-HSD XI 17betaHSDXI 17bHSD11 17betaHSD11	32940	73620788	308340
DELTA-AMINOLEVULINIC ACID DEHYDRATASE	DETOXIFICATION	Delta-aminolevulinic acid dehydratase Porphobilinogen synthase ALADH	36030	6978483	3622
DELTA3,5-DELTA2,4-DIENOYL-COA ISOMERASE, MITOCHONDRIAL	PEROXISOME	Delta3,5-delta2,4-dienoyl-CoA isomerase, mitochondrial precursor	36200	478984	80356
DIHYDROPTERIDINE REDUCTASE	METABOLISM	Dihydropteridine reductase HDHPR Quinoid dihydropteridine reductase	25550	576089	23398
DIMETHYLANILINE MONOOXYGENASE [N-OXIDE FORMING] 1	DETOXIFICATION	Dimethylaniline monooxygenase [N-oxide-forming] 1 Hepatic flavin-containing monooxygenase 1 FMO 1 Dimethylaniline oxidase 1	59830	78099773	339248
DNAJ HOMOLOGY SUBFAMILY A MEMBER 1	PROT SYN/FOLD	DnaJ (Hsp40) homolog, subfamily A, member 1 Blastocyst blastocyst cDNA, RIKEN full-length enriched library, clone:11C0041A13 product:DnaJ (Hsp40) homolog, subfamily A, member 1, full insert sequence 14 days pregnant adult female placenta cDNA, RIKEN full-length enriched library, clone:1530018C07 product:DnaJ (Hsp40) homolog, subfamily A, member 1, full insert sequence	44870	51702257	8742
PROTEIN KINASE INHIBITOR P58	SIGNALING	Dnajc3 protein [Rattus norvegicus]	50240	38197558	318957
RIBOPHORIN 2	PROT MOD	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 63 kDa subunit precursor Ribophorin II RPN-II	69080	62512124	193923
SIMILAR TO NADH DEHYDROGENASE (UBIQUINONE) 1 ALPHA SUBUNIT	MITOCHONDRIA	ENSEMBL:ENSRNOP0000023811 REFSEQ:XP_214570 PREDICTED: similar to NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 2	10840	27682913	250139
ERGIC-53 PROTEIN	TRAFFIC	ERGIC-53 protein precursor ER-Golgi intermediate compartment 53 kDa protein Lectin, mannose-binding 1 p58	57960	29611707	77835
OXIDOREDUCTASE ERO1-L	PROT SYN/FOLD	ERO1-like	54120	19924061	33170
ES1 PROTEIN	MITOCHONDRIA	ES1 protein homolog, mitochondrial precursor	28170	83302472	214426
EZRIN	CYTOSKELETON	EZRIN [Rattus norvegicus]	54170	17902245	145232
ECTONUCLEOSIDE TRIPHOSPHATE DIPHOSPHOHYDROLASE 5	PLASMA MB	Ectonucleoside triphosphate diphosphohydrolase 5	47370	40786479	318787
ELECTRON TRANSFER FLAVOPROTEIN BETA SUBUNIT	MITOCHONDRIA	Electron transfer flavoprotein subunit beta Beta-ETF	27690	81884360	189992
ELONGATION FACTOR 1-ALPHA 1 (EF-1-ALPHA-1)	PROT SYN/FOLD	Elongation factor EF-1 alpha	50110	85057089	140182
ENDOPLASMIC RETICULUM PROTEIN ERP29	PROT SYN/FOLD	Endoplasmic reticulum protein 29	28570	60688521	157237
ALPHA ENOLASE	METABOLISM	Eno1 protein [Rattus norvegicus]	51260	38649320	338764
ENOYL-COA HYDRATASE, MITOCHONDRIAL	MITOCHONDRIA	Enoyl-CoA hydratase, mitochondrial precursor	31520	56072	15873
PEROXISOMAL BIFUNCTIONAL ENZYME	PEROXISOME	Enoyl-Coenzyme A, hydratase/3-hydroxyacyl Coenzyme A dehydrogenase	78660	59809132	149061

ESTROGEN SULFOTRANSFERASE	DETOXIFICATION	Estrogen sulfotransferase, isoform 1 EST-1 Sulfotransferase, estrogen-preferring Estrone sulfotransferase	35510	1711599	109266
EUKARYOTIC TRANSLATION INITIATION FACTOR 5A	PROT SYN/FOLD	Eukaryotic initiation factor 5A isoform I variant D Eukaryotic initiation factor 5A isoform I variant B Eukaryotic initiation factor 5A isoform I variant C Eukaryotic translation initiation factor 5A	16830	91207082	23682
F-ACTIN CAPPING PROTEIN ALPHA-2 SUBUNIT PEPTIDYL-PROLYL CIS-TRANS ISOMERASE	CYTOSKELETON PROT SYN/FOLD	F-actin capping protein alpha-2 subunit FK506-binding protein 2 precursor	32970 15390	74355722 27661294	74410 170945
FATTY-ACID AMIDE HYDROLASE	PROT MOD	Faah protein	63360	6225312	29993
FATTY ACID SYNTHASE	PROT MOD	Fatty acid synthase	272600	57890	43659
FATTY ACID-BINDING PROTEIN, LIVER	PROT MOD	Fatty acid-binding protein, liver	14270	6978825	3760
ALDEHYDE DEHYDROGENASE FAMILY 3 MEMBER A2	DETOXIFICATION	Fatty aldehyde dehydrogenase Aldehyde dehydrogenase, microsomal Aldehyde dehydrogenase family 3 member A2	54080	399362	78151
FERRITIN LIGHT CHAIN	METABOLISM	Aldehyde dehydrogenase 10 Ferritin light chain 1	20750 41530	84000579 6562849	277663 145181
FETUIN-B	BIOSYNTHETIC CARGO	Fetuin-B precursor IRL685			
FIBRINOGEN GAMMA CHAIN	BIOSYNTHETIC CARGO	Fibrinogen gamma chain precursor	49650	1183937	3766
FIBRONECTIN 1	BIOSYNTHETIC CARGO	Fibronectin precursor FN	272500	9506703	95208
FIBRINOGEN	BIOSYNTHETIC CARGO	Fibrinogen-like protein	30750	25282415	181007
FORMIMIDOYLTRANSFERASE-CYCLODEAMINASE	METABOLISM	Ftcd protein	58910	60688163	39875
FUMARATE HYDRATASE, MITOCHONDRIAL	MITOCHONDRIA	Fumarate hydratase, mitochondrial precursor Fumarase	54460	8393358	45080
FUMARYLACETOACETASE	MITOCHONDRIA	Fumarylacetoacetase Fumarylacetoacetate hydrolase Beta-diketonase FAA	45980	8393349	51443
GTP CYCLOHYDROLASE FEEDBACK REGULATORY PROTEIN	SIGNALING	GTP cyclohydrolase 1 feedback regulatory protein GTP cyclohydrolase I feedback regulatory protein GFRP p35	9541	16975337	140831
RAB10	GTPASE	GTP-binding protein rab10 - rat	22610	420269	44648
DLST DIHYDROLIPOAMIDE SUCCINYLTRANSFERASE, EXON 15 A	MITOCHONDRIA	Gene,	48610	22775474	113271
GLIAL FIBRILLARY ACIDIC PROTEIN ALPHA	CYTOSKELETON	Glial fibrillary acidic protein alpha Gfap protein	49960	62657131	26394
GLUTAMATE DEHYDROGENASE, MITOCHONDRIAL	MITOCHONDRIA	Glutamate dehydrogenase, mitochondrial precursor	61420	92090591	3897
GLUTAMINE SYNTHETASE	METABOLISM	Glutamine synthetase	42270	61098201	28251
GLUTATHIONE S-TRANSFERASE YA-1	DETOXIFICATION	Glutathione S-transferase Ya-1	25640	66611	146667
GLUTATHIONE S-TRANSFERASE ALPHA	DETOXIFICATION	Glutathione S-transferase alpha-3 Glutathione S-transferase Yc-1 GST Yc1 GST 2-2 GST AA GST A3-3	25320	576438	78049
GLUTATHIONE S-TRANSFERASE 8	DETOXIFICATION	Glutathione S-transferase alpha-4 Glutathione S-transferase Yk GST Yk GST 8-8 GST K GST A4-4	25510	5420030	28290
GLUTATHIONE S-TRANSFERASE YC-2	DETOXIFICATION	Glutathione S-transferase alpha-5 Glutathione S-transferase Yc-2 GST Yc2 GST A5-5	25350	58331159	63272
GLUTATHIONE PEROXIDASE	DETOXIFICATION	Glutathione peroxidase	22260	121668	28283
GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE	METABOLISM	Glyceraldehyde-3-phosphate dehydrogenase Gapd protein	35830	9798638	51456

VITAMIN D-BINDING PROTEIN	BIOSYNTHETIC CARGO	Group specific component	53520	51260133	86608
GLUTATHIONE S-TRANSFERASE YB-3	DETOXIFICATION	Gstm7 protein	25680	529588	33791
GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE P	SIGNALING	Guanine nucleotide binding protein, beta 2, related sequence 1 CRL-1722 L5178Y-R cDNA, RIKEN full-length enriched library, clone:1730096H10 product:guanine nucleotide binding protein, beta 2, related sequence 1, full insert sequence Blastocyst blastocyst cDNA, RIKEN full-length enriched library, clone:11C0024M22 product:guanine nucleotide binding protein, beta 2, related sequence 1, full insert sequence Blastocyst blastocyst cDNA, RIKEN full-length enriched library, clone:11C0014F18 product:guanine nucleotide binding protein, beta 2, related sequence 1, full insert sequence Blastocyst blastocyst cDNA, RIKEN full-length enriched library, clone:11C0013E14 product:guanine nucleotide binding protein, beta 2, related sequence 1, full insert sequence Mammary gland RCB-0527 Jyg-MC(B) cDNA, RIKEN full-length enriched library, clone:G930013E05 product:guanine nucleotide binding protein, beta 2, related sequence 1, full insert sequence 0 day neonate head cDNA, RIKEN full-length enriched library,	35080	54037164	123232
VIGILIN (HIGH DENSITY LIPOPROTEIN-BINDING PROTEIN) (HDL-B	METABOLISM	Hdlbp protein	41290	38649090	338318
HEAT SHOCK 70 KDA PROTEIN 1/2	PROT SYN/FOLD	Heat shock 70 kDa protein 1/2	70090	396270	85008
HEAT-SHOCK COGNATE 70KD PROTEIN (44KD ATPASE N-TERMIN	PROT SYN/FOLD	Heat shock protein 8 13 days embryo liver cDNA, RIKEN full-length enriched library, clone:1920176M04 product:heat shock protein 8, full insert sequence 16 days embryo kidney cDNA, RIKEN full-length enriched library, clone:1920096J24 product:heat shock protein 8, full insert sequence 16 days embryo kidney cDNA, RIKEN full-length enriched library, clone:1920087N17 product:heat shock protein 8, full insert sequence 16 days embryo kidney cDNA, RIKEN full-length enriched library, clone:1920079M09 product:heat shock protein 8, full insert sequence 17 days pregnant adult female amnion cDNA, RIKEN full-length enriched library, clone:1920066C08 product:heat shock protein 8, full insert sequence 16 days embryo kidney cDNA, RIKEN full-length enriched library, clone:1920062I24 product:heat shock protein 8, full insert sequence 17 days embryo stomach cDNA, RIKEN full-length enriched library, clone:1920052L10 product:heat shock protein 8, full insert sequence 17 days embryo kidney cDNA, RIKEN full-l	70870	71051777	88722
HEAT SHOCK PROTEIN 86; HSP86	PROT SYN/FOLD	Heat shock protein 86 Heat shock protein 1, alpha	84810	54673763	82698
HEMOGLOBIN BETA CHAIN	BLOOD + OTHER CELLS	Hemoglobin beta chain, major-form	15980	55823	28543
HEMOPEXIN	BIOSYNTHETIC CARGO	Hemopeixin precursor	51290	204621	16936
HISTIDINE-RICH GLYCOPROTEIN HRG	UNKNOWN	Histidine-rich glycoprotein 1	59050	62657833	140379
CARBOXYLESTERASE 4	DETOXIFICATION	Hydrolase A	3058	807108	105537
HYDROXYACID OXIDASE 3	PEROXISOME	Hydroxyacid oxidase 3	39200	50925465	100475

HYDROXYACYLGLUTATHIONE HYDROLASE	MITOCHONDRIA		Hydroxyacylglutathione hydrolase	28900	3913728	15417
HYDROXYMETHYLGLUTARYL-COA SYNTHASE, MITOCHONDRIAL	MITOCHONDRIA		spermatid protein RSP29 Hydroxymethylglutaryl-CoA synthase, mitochondrial precursor	56910	27465521	16963
GRP170 (HYPOXIA UP-REGULATED 1)	PROT SYN/FOLD		HMG-CoA synthase 3-hydroxy-3-methylglutaryl coenzyme A synthase Hyou1 protein	111200	77404380	395638
PROSTAGLANDIN E SYNTHASE 2	METABOLISM		Hypothetical glutaredoxin/glutathione S-transferase C terminus containing protein	43450	27706734	166503
RAB2B	GTPASE		Hypothetical protein	24090	83415090	163993
40S RIBOSOMAL PROTEIN S29	PROT SYN/FOLD		Hypothetical protein DKFZp468N1517	6677	6981490	4847
SIMILAR TO RIKEN CDNA 0610006F02	UNKNOWN		Hypothetical protein Mett17b	27900	66730429	244225
SIMILAR TO PECO PROTEIN	PEROXISOME		Hypothetical protein RGD1310224	33690	57164137	208921
60S RIBOSOMAL PROTEIN L37A	PROT SYN/FOLD		Hypothetical protein RPL37A	10280	57123	4820
OPTINEURIN	UNKNOWN		Injury-inducible-protein I-55	58100	24475405	154010
INTER-ALPHA-INHIBITOR H4 HEAVY CHAIN	BIOSYNTHETIC CARGO		Inter-alpha-inhibitor H4 heavy chain	103600	9506819	47186
INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H3	BIOSYNTHETIC CARGO		Inter-alpha-trypsin inhibitor heavy chain H3 precursor ITI heavy chain H3 Inter-alpha-inhibitor heavy chain 3	99100	8393899	38418
ISOCITRATE DEHYDROGENASE [NADP] CYTOPLASMIC	METABOLISM		isocitrate dehydrogenase [NADP] cytoplasmic Cytosolic NADP-isocitrate dehydrogenase Oxalosuccinate decarboxylase IDH	46730	627999	71492
ISOVALERYL-COA DEHYDROGENASE, MITOCHONDRIAL	MITOCHONDRIA		NADP(+)-specific IDH IDP Isovaleryl-CoA dehydrogenase, mitochondrial precursor IVD	46440	6981112	3955
KERATIN K6	LIKELY CONTAMINANTS		Keratin K6	3107	554464	66467
CYTOKERATIN 15	LIKELY CONTAMINANTS		Keratin, type I cytoskeletal 15 Cytokeratin-15 CK-15 Keratin-15 K15 Type I keratin Ka15	48870	81891677	210892
KERATIN 5	LIKELY CONTAMINANTS		Keratin, type II cytoskeletal 5 Cytokeratin-5 CK-5 Keratin-5 K5	61830	81170669	318877
KERATIN, TYPE II CYTOSKELETAL 8	LIKELY CONTAMINANTS		Keratin, type II cytoskeletal 8	54020	67678416	67836
KETOHEXOKINASE	METABOLISM		Ketoheokinase Hepatic fructokinase	32750	62650395	127122
L-LACTATE DEHYDROGENASE	METABOLISM		L-lactate dehydrogenase A chain LDH-A LDH muscle subunit LDH-M	36450	8393706	51518
HEAT SHOCK PROTEIN 90: HSP90	PROT SYN/FOLD		LOC495860 protein	83280	51243735	139643
MICROSOMAL GLUTATHIONE S-TRANSFERASE 1	DETOXIFICATION		LOC496117 protein	17470	38649092	28295
ARP2/3 COMPLEX 20 KDA SUBUNIT	CYTOSKELETON		LOC496278 protein	19670	34858314	32844
LRRGT00057	UNKNOWN		LRRGT00057	268200	37654330	203325
DNAJ (HSP40) HOMOLOG, SUBFAMILY B, MEMBER 11	PROT SYN/FOLD		LRRGT00084 DnaJ (Hsp40) homolog, subfamily B, member 11 Predicted	40490	62543491	295796
LACTATE DEHYDROGENASE A-LIKE PROTEIN	METABOLISM		Lactate dehydrogenase A-like	42050	50927335	224451
LEUCINE ZIPPER-EF-HAND CONTAINING TRANSMEMBRANE PRO	MITOCHONDRIA		Leucine zipper-EF-hand-containing transmembrane protein 1, mitochondrial precursor	83060	62510718	296680
CARBOXYLESTERASE 1	DETOXIFICATION		Liver carboxylesterase 1 precursor	60170	2506388	43686
CARBOXYLESTERASE 3	DETOXIFICATION		Liver carboxylesterase 3 precursor Carboxylesterase ES-3 pl 5.5 esterase ES-HTEL	61710	550147	78070

SERINE PROTEASE INHIBITOR 2A; LIVER REGENERATION PROTEIN	BIOSYNTHETIC CARGO	Liver regeneration protein Iryan Ab1-021	68220	33086444	166149
TRANSFERRIN	BIOSYNTHETIC CARGO	Liver regeneration-related protein LRRG03 Transferrin	76400	61556986	166406
ACYL-COA DEHYDROGENASE, LONG-CHAIN SPECIFIC, MITOCHONDRIAL	MITOCHONDRIA	Long-chain specific acyl-CoA dehydrogenase, mitochondrial precursor LCAD	47870	6978431	3599
LONG-CHAIN-FATTY-ACID--COA LIGASE, LIVER ISOZYME	METABOLISM	Long-chain-fatty-acid--CoA ligase 1 Long-chain acyl-CoA synthetase 1 LACS 1 Long-chain-fatty-acid--CoA ligase, liver isozyme	78180	25742739	85766
LONG-CHAIN-FATTY-ACID--COA LIGASE 5	METABOLISM	Long-chain-fatty-acid--CoA ligase 5 Long-chain acyl-CoA synthetase 5 LACS 5	76400	6016484	60485
LONG-CHAIN-FATTY-ACID--COA LIGASE 6	PROT MOD	Long-chain-fatty-acid--CoA ligase 6	78180	417242	44475
LYSOSOMAL ACID LIPASE/CHOLESTERYL ESTER HYDROLASE	LYSOSOME	Lysosomal acid lipase/cholesteryl ester hydrolase precursor LAL Acid cholesteryl ester hydrolase Sterol esterase Lipase A Cholesteryl esterase	45190	9653291	72321
MACROPHAGE MIGRATION INHIBITORY FACTOR	BLOOD + OTHER CELLS	Macrophage migration inhibitory factor	12480	7514124	37207
MALATE DEHYDROGENASE, MITOCHONDRIAL	MITOCHONDRIA	Malate dehydrogenase, mitochondrial	35680	42476181	339913
MANNOSE-BINDING PROTEIN A	BIOSYNTHETIC CARGO	Mannose-binding protein A precursor	16550	1942287	19138
MANNOSIDASE 2, ALPHA B1	PROT MOD	Mannosidase 2, alpha B1	114300	40786505	338661
GLYCOPROTEIN PROCESSING GLUCOSIDASE I	PROT MOD	Mannosyl-oligosaccharide glucosidase Glycoprotein-processing glucosidase I	91870	48427849	51409
BOCA	PROT SYN/FOLD	Mesoderm development candidate 2	25220	81883487	280160
METHYLMALONATE-SEMIALDEHYDE DEHYDROGENASE [ACYLATING]	MITOCHONDRIA	Methylmalonate-semialdehyde dehydrogenase [acylating], mitochondrial precursor MMSDH Malonate-semialdehyde dehydrogenase [acylating]	57810	400269	37213
SIGNAL PEPTIDASE COMPLEX (18KD)	PROT SYN/FOLD	Microsomal signal peptidase 18 kDa subunit SPase 18 kDa subunit SPC18 Endopeptidase SP18 SEC11-like 1 Sid 2895	20630	61889101	3224
MITOCHONDRIAL 2-OXOGLUTARATE/MALATE CARRIER PROTEIN	MITOCHONDRIA	Mitochondrial 2-oxoglutarate/malate carrier protein	34150	1580888	77688
MITOCHONDRIAL IMPORT INNER MEMBRANE TRANSLOCASE SUBUNIT 1	MITOCHONDRIA	Mitochondrial import inner membrane translocase subunit TIM13	10460	59800393	77128
MITOCHONDRIAL IMPORT INNER MEMBRANE TRANSLOCASE SUBUNIT 2	MITOCHONDRIA	Mitochondrial import inner membrane translocase subunit TIM8 A Deafness dystonia protein 1 homolog	11040	5107153	12056
SIMILAR TO PUTATIVE NAD(P)H STEROID DEHYDROGENASE	UNKNOWN	NAD(P) dependent steroid dehydrogenase-like	40410	57164113	228858
NADH DEHYDROGENASE (UBIQUINONE) FE-S PROTEIN 1	MITOCHONDRIA	NADH dehydrogenase (Ubiquinone) Fe-S protein 1, 75kDa	79410	53850628	229389
SIMILAR TO NADH DEHYDROGENASE (UBIQUINONE) FE-S PROTEIN 2	MITOCHONDRIA	NADH dehydrogenase (Ubiquinone) Fe-S protein 2 Predicted	23950	56606108	213294
SIMILAR TO NADH DEHYDROGENASE (UBIQUINONE) FLAVOPROTEIN	MITOCHONDRIA	NADH dehydrogenase (Ubiquinone) flavoprotein 1, 51kDa	50730	55741424	243054
NADH-UBIQUINONE OXIDOREDUCTASE 24 KDA SUBUNIT, MITOCHONDRIAL	MITOCHONDRIA	NADH-ubiquinone oxidoreductase 24 kDa subunit, mitochondrial precursor	27380	83305118	291031
NADPH-CYTOCHROME P450 REDUCTASE	DETOXIFICATION	NADPH--cytochrome P450 reductase	76930	205660	44210
NADH DEHYDROGENASE 1 ALPHA SUBCOMPLEX 10-LIKE PROTEIN	MITOCHONDRIA	Ndufa10 protein	40490	62531217	199168
NESPRIN-1	NUCLEUS	Nesprin-1	325100	19705491	161237
NON-POU-DOMAIN-CONTAINING, OCTAMER BINDING PROTEIN	NUCLEUS	Non-POU domain-containing octamer-binding protein NonO protein	54930	67460593	219030
NUCLEAR PORE PROTEIN GP210 PRECURSOR	NUCLEUS	Nuclear pore membrane glycoprotein 210 precursor POM210 Nuclear pore protein gp210	204200	92557	111676

NUCLEOBINDIN 2 (CALNUC 2)	CALCIUM TRANS/BIND	Nucleobindin 2 precursor	50090	8515422	3157
NUCLEOSIDE DIPHOSPHATE KINASE B	MITOCHONDRIA	Nucleoside diphosphate kinase B	17280	55926145	69495
SIMILAR TO ENDOPLASMIC RETICULUM CHAPERONE SIL1 HOMOLOG	PROT SYN/FOLD	Nucleotide exchange factor SIL1 precursor	52350	81892269	318887
ORNITHINE TRANS-CARBAMOYLASE; ORNITHINE CARBAMOYLTRANSFERASE	MITOCHONDRIA	Ornithine carbamoyltransferase, mitochondrial precursor	39890	6981312	75019
OXIDATIVE 17 BETA HYDROXYSTEROID DEHYDROGENASE TYPE 6	DETOXIFICATION	Oxidative 17 beta hydroxysteroid dehydrogenase type 6	37140	27545384	102628
CERULOPLASMIN	BIOSYNTHETIC CARGO	PREDICTED: hypothetical protein XP_215541	120700	34855491	219134
COMPLEMENT COMPONENT 3	BIOSYNTHETIC CARGO	PREDICTED: hypothetical protein XP_579384	186300	62718645	221549
ALPHA-2-MACROGLOBULIN RECEPTOR-ASSOCIATED PROTEIN	BIOSYNTHETIC CARGO	PREDICTED: low density lipoprotein receptor-related protein associated protein 1	47360	34878475	237675
ACIDIC RIBOSOMAL PROTEIN P1	PROT SYN/FOLD	PREDICTED: similar to 60S acidic ribosomal protein P1	11560	27717711	214842
ACIDIC RIBOSOMAL PROTEIN P2, CYTOSOLIC	PROT SYN/FOLD	PREDICTED: similar to 60S acidic ribosomal protein P2	11760	62660456	201232
60S RIBOSOMAL PROTEIN L27A	PROT SYN/FOLD	PREDICTED: similar to 60S ribosomal protein L27a	16590	62639430	273222
NADH:UBIQUINONE OXIDOREDUCTASE PGIV SUBUNIT	MITOCHONDRIA	PREDICTED: similar to Aa2-258	19970	27706932	292254
SIMILAR TO ACYL-COA DEHYDROGENASE FAMILY MEMBER 8, MITOCHONDRIAL	MITOCHONDRIA	PREDICTED: similar to Acyl-CoA dehydrogenase family member 8, mitochondrial precursor (ACAD-8) (isobutyryl-CoA dehydrogenase)	14960	34860605	288262
CCT (CHAPERONIN CONTAINING TCP-1) ZETA SUBUNIT	PROT SYN/FOLD	PREDICTED: similar to CCT (chaperonin containing TCP-1) zeta subunit	58020	76253725	288751
SIMILAR TO MICROSOMAL TRIGLYCERIDE TRANSFER PROTEIN	PROT SYN/FOLD	PREDICTED: similar to Microsomal triglyceride transfer protein	99190	34860789	198793
SIMILAR TO NADH DEHYDROGENASE (UBIQUINONE) 1 ALPHA SUBUNIT	MITOCHONDRIA	PREDICTED: similar to NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 6 (B14)	15220	27663138	280728
NADH DEHYDROGENASE:UBIQUINONE FE-S PROTEIN 8	MITOCHONDRIA	PREDICTED: similar to NADH dehydrogenase (ubiquinone) Fe-S protein 8	23970	27661165	313497
SIMILAR TO NADH OXIDOREDUCTASE	MITOCHONDRIA	PREDICTED: similar to NADH oxidoreductase	12500	27717677	167188
SIMILAR TO NADH-UBIQUINONE OXIDOREDUCTASE 30 KDA SUBUNIT	MITOCHONDRIA	PREDICTED: similar to NADH-ubiquinone oxidoreductase 30 kDa subunit, mitochondrial precursor (Complex I-30KD) (CI-30KD)	30230	27702072	256004
SIMILAR TO PM5 PROTEIN; DNA SEGMENT, CHR 7, ERATO DOI 14	UNKNOWN	PREDICTED: similar to Nodal modulator 1	133400	34856103	215096
POLY(A) BINDING PROTEIN	PROT SYN/FOLD	PREDICTED: similar to Poly(A) binding protein, cytoplasmic 4, isoform 1	72410	34870953	206311
PRE-MRNA SPLICING FACTOR RNA HELICASE (DEAH BOX PROTEIN 15)	PROT SYN/FOLD	PREDICTED: similar to Putative pre-mRNA splicing factor RNA helicase (DEAH box protein 15)	90980	34878065	276202
SIMILAR TO RIKEN CDNA 0610010D20	UNKNOWN	PREDICTED: similar to RIKEN cDNA 0610010D20	34460	34865395	220359
CARBOXYLESTERASE ESN1	DETOXIFICATION	PREDICTED: similar to RIKEN cDNA 2210023G05	62910	27658990	227817
HYPOTHETICAL PROTEIN MGC40499	UNKNOWN	PREDICTED: similar to RIKEN cDNA 2610019P18	28380	34871484	194048
BETA-ACTIN	CYTOSKELETON	PREDICTED: similar to RIKEN cDNA 4732495G21 gene	41960	27687455	161693
SIMILAR TO SEC63	PROT SYN/FOLD	PREDICTED: similar to SEC63-like	87720	34853169	209405
SPFH DOMAIN FAMILY, MEMBER 2	UNKNOWN	PREDICTED: similar to SPFH domain family, member 2	37710	34879021	249650
ENDOPLASMIC RETICULUM PROTEIN ERP46	PROT SYN/FOLD	PREDICTED: similar to Thioredoxin domain containing protein 5 precursor (Thioredoxin-like protein p46) (Endoplasmic reticulum protein ERp46)	46350	34875200	293536

CARBOXYLESTERASE ESNA4	DETOXIFICATION	PREDICTED: similar to carboxylesterase isoenzyme gene	60750	34864823	286563
CYTOCHROME P450 2C18	DETOXIFICATION	PREDICTED: similar to cytochrome P450 2C66; CYP2C66	56170	34862902	260440
SIMILAR TO CYTOCHROME C-1	MITOCHONDRIA	PREDICTED: similar to cytochrome c-1	35430	34866853	271135
P63	TRAFFIC	PREDICTED: similar to cytoskeleton-associated protein 4	63550	34862422	306304
SIMILAR TO DOLICHOL-PHOSPHATE-MANNOSE SYNTHASE	PROT MOD	PREDICTED: similar to dolichol-phosphate-mannose synthase	29250	34860748	191580
DERMATOPONTIN	BIOSYNTHETIC CARGO	PREDICTED: similar to early quiescence protein-1	24200	27677818	208059
SIMILAR TO ARYLACETYL ACYL-COA N-ACYLTRANSFERASE	PROT MOD	PREDICTED: similar to glycine-N-acyltransferase isoform a	33990	27681359	139592
GLYCOLATE OXIDASE; SHORT-CHAIN ALPHA-HYDROXY ACID OX	PEROXISOME	PREDICTED: similar to glycolate oxidase; short-chain alpha-hydroxy acid oxidase	40970	34859262	270415
SIMILAR TO PURINE-NUCLEOSIDE PHOSPHORYLASE; PURINE-N	METABOLISM	PREDICTED: similar to purine-nucleoside phosphorylase	32300	34869683	209477
60S RIBOSOMAL PROTEIN L10A	PROT SYN/FOLD	PREDICTED: similar to ribosomal protein L10a	24720	27665840	215516
SIMILAR TO SERINE BETA LACTAMASE-LIKE PROTEIN LACT-1	MITOCHONDRIA	PREDICTED: similar to serine beta lactamase-like protein LACT-1	60420	34864295	314386
SERINE PROTEASE INHIBITOR 2.4 PRECURSOR	BIOSYNTHETIC CARGO	PREDICTED: similar to serine protease inhibitor 2.4	46840	34867677	195578
SOLUTE CARRIER FAMILY 25 (MITOCHONDRIAL CARRIER, ARAL	MITOCHONDRIA	PREDICTED: similar to solute carrier family 25 (mitochondrial carrier, Aralar), member 12	27180	34854800	195681
STOMATIN-LIKE PROTEIN 2	CYTOSKELETON	PREDICTED: similar to stomatin-like protein 2	38410	72255527	299358
SIMILAR TO ZINC BINDING ALCOHOL DEHYDROGENASE, DOMAIN	UNKNOWN	PREDICTED: similar to zinc binding alcohol dehydrogenase, domain containing 2	40480	34932585	231239
PROTEIN DISULFIDE ISOMERASE A6	PROT SYN/FOLD	PREDICTED: thioredoxin domain containing 7	48760	62651585	278868
PRX III	MITOCHONDRIA	PRx III	28320	4336877	90537
PRX IV	PEROXISOME	PRx IV Peroxiredoxin 4	31010	4336879	60442
PARAOXONASE 1	BIOSYNTHETIC CARGO	Paraoxonase 1	39360	60551577	198556
PEPTIDYL-PROLYL CIS-TRANS ISOMERASE A	PROT SYN/FOLD	Peptidylprolyl isomerase A	17870	951425	45089
PEROXIREDOXIN 1	PEROXISOME	Peroxiredoxin 1	22110	56789700	43433
PEROXIREDOXIN 5, MITOCHONDRIAL	MITOCHONDRIA	Peroxiredoxin-5, mitochondrial precursor Prx-V Peroxisomal antioxidant enzyme PLP Thioredoxin reductase Thioredoxin peroxidase PMP20 Antioxidant enzyme B166 AOEB166	22180	6103726	60487
PUTATIVE PEROXISOMAL 2,4-DIENOYL-COA REDUCTASE	PEROXISOME	Peroxisomal 2,4-dienoyl-CoA reductase 2,4-dienoyl-CoA reductase 2 DCR-AKL pVL-AKL	31290	90109768	176638
PEROXISOMAL MEMBRANE ANCHOR PROTEIN	PEROXISOME	Peroxisomal membrane anchor protein	40970	4128962	155718
PEROXISOMAL MULTIFUNCTIONAL ENZYME TYPE 2 (MFE-2) (D-B	PEROXISOME	Peroxisomal multifunctional enzyme type 2	79430	2492741	108364
PUTATIVE SHORT-CHAIN DEHYDROGENASE/REDUCTASE MRNA	PEROXISOME	Peroxisomal trans-2-enoyl-CoA reductase RLF98 Peroxisomal 2,4-dienoyl CoA reductase px-2,4-DCR1	32430	6491860	34787
SIMILAR TO PHENYLALANYL-TRNA SYNTHETASE BETA CHAIN (P	PROT SYN/FOLD	Phenylalanine-tRNA synthetase-like, beta subunit	65650	51948478	254493
PHOSPHATE CARRIER PROTEIN, MITOCHONDRIAL	MITOCHONDRIA	Phosphate carrier protein, mitochondrial precursor PTP Solute carrier family 25 member 3	39450	20806141	69383

PHYTANYL-COA DIOXYGENASE, PEROXISOMAL	PEROXISOME	Phytanoyl-CoA dioxygenase, peroxisomal precursor Phytanoyl-CoA alpha-hydroxylase PhyH Phytanic acid oxidase	38590	6539658	55437
PLASMA RETINOL-BINDING PROTEIN	BIOSYNTHETIC CARGO	Plasma retinol-binding protein precursor PRBP RBP	23220	27685035	144413
PLASMINOGEN	BIOSYNTHETIC CARGO	Plasminogen	90540	62638541	60419
PROCOLLAGEN-LYSINE:2-OXOGLUTARATE 5-DIOXYGENASE 1	PROT MOD	Procollagen-lysine:2-oxoglutarate 5-dioxygenase 1 precursor Lysyl hydroxylase 1 LH1	83610	6093729	60574
PROFILIN I	CYTOSKELETON	Profilin 1 ES cells cDNA, RIKEN full-length enriched library, clone:2410026M17 product:profilin 1, full insert sequence Bone marrow macrophage cDNA, RIKEN full-length enriched library, clone:I830015F09 product:profilin 1, full insert sequence	14960	51702769	60726
PROHIBITIN	MITOCHONDRIA	Prohibitin 17 days embryo heart cDNA, RIKEN full-length enriched library, clone:I920041N05 product:prohibitin, full insert sequence CRL-1722 L5178Y-R cDNA, RIKEN full-length enriched library, clone:I730071G06 product:prohibitin, full insert sequence	29820	66911717	4312
PROPIONYL-COA CARBOXYLASE ALPHA CHAIN, MITOCHONDRIA	MITOCHONDRIA	Propionyl-CoA carboxylase alpha chain, mitochondrial precursor PCCase subunit alpha Propanoyl-CoA: carbon dioxide ligase subunit alpha	77710	129684	69597
SIMILAR TO GI:13385412-LIKE PROTEIN SPLICE FORM I GLUT4 VESICLE PROTEIN	UNKNOWN	Protein C6orf89 homolog	39570	40786457	205305
	UNKNOWN	Protein FAM62A Membrane-bound C2 domain-containing protein vp115	121200	8393755	51531
PROTEIN DISULFIDE ISOMERASE	PROT SYN/FOLD	Protein disulfide isomerase precursor	56950	38197382	69606
PROTEIN DISULFIDE ISOMERASE A3	PROT SYN/FOLD	Protein disulfide-isomerase A3 precursor Disulfide isomerase ER-60 ERp60 58 kDa microsomal protein p58 ERp57 HIP-70 Q-2	56620	38382858	21566
PROTEIN DISULFIDE ISOMERASE A4	PROT SYN/FOLD	Protein disulfide-isomerase A4 precursor Protein ERp-72 ERp72 Calcium-binding protein 2 CaBP2	72720	78099786	227664
PROTHROMBIN	BIOSYNTHETIC CARGO	Prothrombin precursor Coagulation factor II Activation peptide fragment 1 Activation peptide fragment 2 Thrombin light chain Thrombin heavy chain	70410	56970	31503
PROTON-TRANSLOCATING ATPASE D SUBUNIT ISOFORM D1	LYSOSOME	Proton-translocating ATPase d subunit isoform d1 B6-derived CD11 +ve dendritic cells cDNA, RIKEN full-length enriched library, clone:F730225D05 product:ATPase, H+ transporting, V0 subunit D isoform 1, full insert sequence	40300	58865424	55382
PYRUVATE CARBOXYLASE, MITOCHONDRIAL	MITOCHONDRIA	Pyruvate carboxylase, mitochondrial precursor	129800	7438124	40425
RAB1A	GTPASE	RAB1A, member RAS oncogene family RAB1A protein	22680	51338716	21122
RAB7	GTPASE	RAB7	23500	9837359	111003
60S RIBOSOMAL PROTEIN L34	PROT SYN/FOLD	RPL34 protein Ribosomal protein L34	13290	34860562	136355
RAB GDI BETA	TRAFFIC	Rab GDP dissociation inhibitor beta Rab GDI beta Guanosine diphosphate dissociation inhibitor 2 GDI-2 GDI-3	50540	40254781	8623
CAMP-REGULATED GUANINE NUCLEOTIDE EXCHANGE FACTOR	TRAFFIC	Rap guanine nucleotide exchange factor 4 cAMP-regulated guanine nucleotide exchange factor II cAMP-GEFII Exchange factor directly activated by cAMP 2 Epac 2	50120	4115911	173285
RAB2A	GTPASE	Ras-related protein Rab-2A	23540	92340	78145
CYTOCHROME P450 2C12	DETOXIFICATION	Rat female-specific cytochrome P450 15-beta CYP2C12 Cytochrome P450 2C12	55890	59808903	3729

REGUCALCIN	METABOLISM	Regucalcin RC Senescence marker protein 30 SMP-30	33390	6970313	3576
RETICULON 3 PROTEIN ISOFORM B	UNKNOWN	Reticulon 3 protein isoform b RTN3-A1 Reticulon 3 protein isoform a	25370	57977317	64492
RETINOL DEHYDROGENASE TYPE II	DETOXIFICATION	Retinol dehydrogenase 2 Retinol dehydrogenase type II	35600	50926989	80376
RETINOL DEHYDROGENASE TYPE I	DETOXIFICATION	RODH II 29 k-protein Retinol dehydrogenase 7 Retinol dehydrogenase type III	35740	68534258	35165
RIBOPHORIN I	PROT MOD	RODH III Ribophorin I Ribophorin1	68400	71891579	337611
60S RIBOSOMAL PROTEIN L10	PROT SYN/FOLD	Ribosomal protein 10 Lung RCB-0558 LLC cDNA, RIKEN full-length enriched library, clone:G730040A02 product:ribosomal protein 10, full insert sequence CRL-1722 L5178Y-R cDNA, RIKEN full-length enriched library, clone:I730035D10 product:ribosomal protein 10, full insert sequence Bone marrow macrophage cDNA, RIKEN full-length enriched library, clone:I830029J07 product:ribosomal protein 10, full insert sequence Bone marrow macrophage cDNA, RIKEN full-length enriched library, clone:I830032M03 product:ribosomal protein 10, full insert sequence Bone marrow macrophage cDNA, RIKEN full-length enriched library, clone:I830035M24 product:ribosomal protein 10, full insert sequence Bone marrow macrophage cDNA, RIKEN full-length enriched library, clone:I830048G21 product:ribosomal protein 10, full insert sequence Bone marrow macrophage cDNA, RIKEN full-length enriched library, clone:I830087L08 product:ribosomal protein 10, full insert sequence Bone marrow macrophage cDNA, RIKEN full-length enriched li	24600	50403574	37238
60S RIBOSOMAL PROTEIN L15	PROT SYN/FOLD	Ribosomal protein L15	24150	515865	1145
60S RIBOSOMAL PROTEIN L27	PROT SYN/FOLD	Ribosomal protein L27	15800	60688496	4814
60S RIBOSOMAL PROTEIN L28	PROT SYN/FOLD	Ribosomal protein L28 11 days embryo whole body cDNA, RIKEN full-length enriched library, clone:2700043M16 product:ribosomal protein L28, full insert sequence	15730	61889083	74518
60S RIBOSOMAL PROTEIN L7A	PROT SYN/FOLD	Ribosomal protein L7a	30000	62644799	4825
60S RIBOSOMAL PROTEIN L8	PROT SYN/FOLD	Ribosomal protein L8	28020	78214309	4826
40S RIBOSOMAL PROTEIN S10	PROT SYN/FOLD	Ribosomal protein S10 Activated spleen cDNA, RIKEN full-length enriched library, clone:F83020J18 product:ribosomal protein S10, full insert sequence Bone marrow macrophage cDNA, RIKEN full-length enriched library, clone:I830015I24 product:ribosomal protein S10, full insert sequence 5 days embryo whole body cDNA, RIKEN full-length enriched library, clone:10C0045K06 product:ribosomal protein S10, full insert sequence	18920	68163545	32867
40S RIBOSOMAL PROTEIN S15	PROT SYN/FOLD	Ribosomal protein S15	17040	8394212	4836
40S RIBOSOMAL PROTEIN S15A	PROT SYN/FOLD	Ribosomal protein S15a Bone marrow macrophage cDNA, RIKEN full-length enriched library, clone:I830091I21 product:ribosomal protein S15a, full insert sequence Rps15a protein	14840	54039450	72161
40S RIBOSOMAL PROTEIN S2	PROT SYN/FOLD	Ribosomal protein S2	28140	2920825	100993

40S RIBOSOMAL PROTEIN S24	PROT SYN/FOLD	Ribosomal protein S24, isoform 2 Bone marrow macrophage cDNA, RIKEN full-length enriched library, clone:1830025E19 product:ribosomal protein S24, full insert sequence Rps24 protein	15420	57858	4843
40S RIBOSOMAL PROTEIN S27A	PROT SYN/FOLD	Ribosomal protein S27a	17950	37194821	127926
40S RIBOSOMAL PROTEIN S4	PROT SYN/FOLD	Ribosomal protein S4, X-linked, X isoform RPS4X protein	29600	57135	4849
40S RIBOSOMAL PROTEIN S6	PROT SYN/FOLD	Ribosomal protein S6 16 days embryo heart cDNA, RIKEN full-length enriched library, clone:1920028E16 product:ribosomal protein S6, full insert sequence Blastocyst blastocyst cDNA, RIKEN full-length enriched library, clone:11C0007K02 product:ribosomal protein S6, full insert sequence 12 days embryo male wolffian duct includes surrounding region cDNA, RIKEN full-length enriched library, clone:6720430M17 product:ribosomal protein S6, full insert sequence 17 days pregnant adult female amnion cDNA, RIKEN full-length enriched library, clone:1920079C04 product:ribosomal protein S6, full insert sequence	28680	8394224	74523
40S RIBOSOMAL PROTEIN S8	PROT SYN/FOLD	Ribosomal protein S8	24210	62078585	4854
60S RIBOSOMAL PROTEIN L11	PROT SYN/FOLD	Rpl11 protein	19020	71043900	2378
SEC14-LIKE PROTEIN 2	PROT MOD	SEC14-like protein 2 Alpha-tocopherol-associated protein TAP Supernatant protein factor SPF Squalene transfer protein	46170	21542226	60562
THIOSULFATE SULFURTRANSFERASE (RHODANASE)	MITOCHONDRIA	SWISS-PROT:P24329 TREMBL:Q510D4 REFSEQ NP:NP_036940 ENSEMBL:ENSRNOP00000000202 Thiosulfate sulfurtransferase	33410	83305808	299568
SARCOPLASMIC CA2+MG2+ ATPASE	CALCIUM TRANS/BIND	Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	109700	57303	84180
PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT ISOFORM 1	PROT SYN/FOLD	Sec61 alpha subunit homolog	52260	63101555	75284
SEL1L	TRANSCRIPTION	Sel1 (suppressor of lin-12) 1 homolog	68660	29338095	213126
SEPIAPTERIN REDUCTASE	METABOLISM	Sepiapterin reductase	28130	34856334	31392
HEPARIN COFACTOR II	BIOSYNTHETIC CARGO	Serine (Or cysteine) proteinase inhibitor, clade D, member 1	54550	60551378	68739
ALPHA-2-ANTIPLASMIN	BIOSYNTHETIC CARGO	Serine (Or cysteine) proteinase inhibitor, clade F, member 2 Predicted	54890	58865362	341343
SERINE-PYRUVATE AMINOTRANSFERASE, MITOCHONDRIAL	MITOCHONDRIA	Serine-pyruvate aminotransferase, mitochondrial precursor SPT Alanine--glyoxylate aminotransferase AGT	45830	66655	31393
HEAT SHOCK PROTEIN 47 PRECURSOR	PROT SYN/FOLD	Serpinh1 protein	46560	55824765	280024

SERUM ALBUMIN	BIOSYNTHETIC CARGO	Serum albumin precursor	68720	72101	120645
SERUM AMYLOID P-COMPONENT	BIOSYNTHETIC CARGO	Serum amyloid P-component precursor	26180	3183550	52390
SHORT CHAIN 3-HYDROXYACYL-COA DEHYDROGENASE, MITOCHONDRIA	MITOCHONDRIA	Short chain 3-hydroxyacyl-CoA dehydrogenase, mitochondrial precursor HCDH Medium and short chain L-3-hydroxyacyl-coenzyme A dehydrogenase	34450	7387725	70622
SIDEROFLEXIN 1 (TRICARBOXYLATE CARRIER PROTEIN)	MITOCHONDRIA	Sideroflexin 1	38560	545998	80422
SRP RECEPTOR BETA	PROT SYN/FOLD	Signal recognition particle receptor subunit beta SR-beta	29580	null	38101
FI1FO-ATP SYNTHASE G SUBUNIT	MITOCHONDRIA	Similar to CG6105-PA	11460	47058994	288462
SOLUTE CARRIER FAMILY 21 MEMBER 5	PLASMA MB	Solute carrier organic anion transporter family member 1A4 Solute carrier family 21 member 5 Sodium-independent organic anion-transporting polypeptide 2 Brain digoxin carrier protein Brain-specific organic anion transporter OATP-B1	73250	3914190	43622
SORBITOL DEHYDROGENASE	METABOLISM	Sorbitol dehydrogenase	42830	2506157	43660
SPHINGOSINE-1-PHOSPHATE LYASE 1	PROT MOD	Sphingosine-1-phosphate lyase 1 SP-lyase SPL Sphingosine-1-phosphate aldolase	63760	37999349	269681
FARNESYL-DIPHOSPHATE FARNESYLTRANSFERASE	PROT MOD	Squalene synthetase SQS SS Farnesyl-diphosphate farnesyltransferase FPP:FPP farnesyltransferase	48110	9506591	85115
GRP75	PROT SYN/FOLD	Stress-70 protein, mitochondrial precursor	73740	62664205	36413
FLAVOPROTEIN SUBUNIT OF SUCCINATE-UBIQUINONE REDUCTASE	MITOCHONDRIA	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial precursor Fp Flavoprotein subunit of complex II	71620	52782765	96892
SIMILAR TO SUCCINATE DEHYDROGENASE IP SUBUNIT	MITOCHONDRIA	Succinate dehydrogenase [ubiquinone] iron-sulfur protein (EC 1.3.5.1) (Ip) (Iron-sulfur subunit of complex II)	31830	27716317	167087
SUCCINYL-COA LIGASE [GDP-FORMING] ALPHA-CHAIN, MITOCHONDRIA	MITOCHONDRIA	Succinyl-CoA ligase [GDP-forming] alpha-chain, mitochondrial precursor Succinyl-CoA synthetase, alpha chain SCS-alpha	35030	68574	45104
SULFITE OXIDASE	MITOCHONDRIA	Sulfite oxidase	54350	40254758	318917
SUPEROXIDE DISMUTASE [CU-ZN]	MITOCHONDRIA	Superoxide dismutase [Cu-Zn]	16020	1213217	35188
SUPEROXIDE DISMUTASE [MN], MITOCHONDRIA	MITOCHONDRIA	Superoxide dismutase [Mn], mitochondrial precursor	24680	56691	111692
SYNAPTIC GLYCOPROTEIN SC2	PLASMA MB	Synaptic glycoprotein SC2	36120	37589607	33179
T-KININOGEN I	BIOSYNTHETIC CARGO	T-kininogen I precursor	47700	6981138	3965
MITOCHONDRIAL PRECURSOR PROTEINS IMPORT RECEPTOR	MITOCHONDRIA	TOM70 Translocase of outer mitochondrial membrane 70 homolog A	67440	68534716	726503
KERATIN 14	LIKELY CONTAMINANTS	TREMBL:O35813 Keratin 14	25680	2443314	22440
FLAVIN-CONTAINING MONOOXYGENASE 3	DETOXIFICATION	TREMBL:O6PQV6 REFSEQ_XP:XP_579556 ENSEMBL:ENSRNOP00000004864 Flavin containing monooxygenase 3	59980	62659523	246480
URATE OXIDASE	PEROXISOME	Tax_id=10116 35 kDa protein	34930	57463	31609
ATP SYNTHASE E CHAIN, MITOCHONDRIA	MITOCHONDRIA	Tax_id=10116 ATP synthase, H+ transporting, mitochondrial F0 complex, subunit e	8255	461587	11888

FRUCTOSE-BISPHOSPHATE ALDOLASE A	METABOLISM	Tax Id=10116 Aldolase A	39350	6978487	3624
CATALASE	PEROXISOME	Tax Id=10116 Catalase	59760	6978607	3681
COFILIN, NON-MUSCLE ISOFORM	CYTOSKELETON	Tax Id=10116 Cofilin 1	18530	8393101	87332
3-HYDROXYBUTYRATE DEHYDROGENASE (EC 1.1.1.30) - RAT	MITOCHONDRIA	Tax Id=10116 D-beta-hydroxybutyrate dehydrogenase, mitochondrial precursor	38350	482346	141497
D-DOPACHROME TAUTOMERASE	METABOLISM	Tax Id=10116 D-dopachrome tautomerase	13130	895882	29986
ACYL-COA-BINDING PROTEIN	METABOLISM	Tax Id=10116 Diazepam binding inhibitor	10030	54261671	4320
60S RIBOSOMAL PROTEIN L13A	PROT SYN/FOLD	Tax Id=10116 Ensembl_locations(Chr-bp):1-95678925	23480	548747	106718
ANNEXIN A6	TETH/DOCK/FUS	Tax Id=10116 Ensembl_locations(Chr-bp):10-40398095	75750	763181	127131
PROCOLLAGEN-LYSINE,2-OXOGLUTARATE 5-DIOXYGENASE 3	PROT MOD	Tax Id=10116 Ensembl_locations(Chr-bp):12-20846400	84910	30017429	286288
SIMILAR TO NADH DEHYDROGENASE (UBIQUINONE) FE-S PROT	MITOCHONDRIA	Procollagen-lysine, 2-oxoglutarate 5-dioxygenase 3 similar to NADH dehydrogenase (ubiquinone) Fe-S protein 2	38440	34880923	216920
PROTECTIVE PROTEIN	LYSOSOME	Tax Id=10116 Ensembl_locations(Chr-bp):3-155772538 similar to protective protein precursor - mouse	57110	34860773	247133
PARAOXONASE 2	BIOSYNTHETIC CARGO	Tax Id=10116 Ensembl_locations(Chr-bp):4-30073201;4-30073201 similar to Pon2 protein	27380	34854947	217377
SIMILAR TO OLIGOSACCHARYLTRANSFERASE	PROT MOD	Tax Id=10116 Ensembl_locations(Chr-bp):5-157093377 similar to oligosaccharyltransferase	53840	34872203	206351
DEHYDROGENASE/REDUCTASE (SDR FAMILY) MEMBER 7	DETOXIFICATION	Tax Id=10116 Ensembl_locations(Chr-bp):6-94917824 similar to CGI-86 protein	36250	34865689	214468
DP1L1 PROTEIN	UNKNOWN	Tax Id=10116 Ensembl_locations(Chr-bp):None similar to Dp1l1 protein	20580	34862308	288307
SIMILAR TO ALPHA GLUCOSIDASE II, ALPHA SUBUNIT	PROT MOD	Tax Id=10116 Ensembl_locations(Chr-bp):None similar to alpha glucosidase II, alpha subunit	20950	34861578	310313
FLAVIN-CONTAINING MONOOXYGENASE 5	DETOXIFICATION	Tax Id=10116 Flavin-containing monooxygenase 5	60060	62286643	187298
HYPOTHETICAL PROTEIN XP_234496	BIOSYNTHETIC CARGO	Tax Id=10116 Hypothetical protein XP_234496	43990	34935467	262615
KAN-1	PEROXISOME	Tax Id=10116 Kan-1	46500	8392962	80318
L-LACTATE DEHYDROGENASE B CHAIN	METABOLISM	Tax Id=10116 Lactate dehydrogenase B	36610	6981146	3968
MAJOR VAULT PROTEIN	PROT SYN/FOLD	Tax Id=10116 Major vault protein	95800	49256645	395977
C-1'-TETRAHYDROFOLATE SYNTHASE, CYTOPLASMIC	METABOLISM	Tax Id=10116 Methylene tetrahydrofolate dehydrogenase (NADP+ dependent), Methylene tetrahydrofolate cyclohydrolase, forMyltetrahydrofolate synthase	101000	901850	62122
MOESIN	CYTOSKELETON	Tax Id=10116 Moesin	67740	32363196	71715
PHOSPHOGLUCOMUTASE	METABOLISM	Tax Id=10116 Phosphoglucosmutase 1	61400	8393951	51568
MULTIFUNCTIONAL PROTEIN ADE2	METABOLISM	Tax Id=10116 Phosphoribosylaminimidazole carboxylase, Phosphoribosylaminoribosylaminimidazole succinocarboxamide synthetase	47100	976252	111533
60S RIBOSOMAL PROTEIN L14	PROT SYN/FOLD	Tax Id=10116 Ribosomal pRoteIn L14	23340	2500360	43519
60S RIBOSOMAL PROTEIN L18	PROT SYN/FOLD	Tax Id=10116 Ribosomal pRoteIn L18	21660	54261673	37240
60S RIBOSOMAL PROTEIN L3	PROT SYN/FOLD	Tax Id=10116 Ribosomal pRoteIn L3	46140	57698	144426
SIMILAR TO 5730439E10RIK PROTEIN	PROT MOD	Tax Id=10116 Similar to 5730439E10RIK protein	88550	34865846	303924
ANTITHROMBIN III	BIOSYNTHETIC CARGO	Tax Id=10116 Similar to Ac2-248	97230	34880787	207228
SIMILAR TO ALDH8A1 PROTEIN	DETOXIFICATION	Tax Id=10116 Similar to Aldh8a1 protein	72630	34852829	197702
CARBAMOYL-PHOSPHATE SYNTHETASE 2, ASPARTATE TRANS	MITOCHONDRIA	Tax Id=10116 Similar to CAD protein	245800	34862992	315461
U2-ASSOCIATED SR140 PROTEIN	UNKNOWN	Tax Id=10116 Similar to CG9346-PA	113900	34865480	232164

SIMILAR TO CALCIUM-BINDING MITOCHONDRIAL CARRIER PROTEIN	MITOCHONDRIA	Tax_id=10116 Similar to Calcium-binding mitochondrial carrier protein Aralar2 (Solute carrier family 25, member 13) (Citrin)	101200	34854954	309822
SIMILAR TO HEAT SHOCK COGNATE 71 KDA PROTEIN	PROT SYN/FOLD	Tax_id=10116 Similar to Heat Shock cognate 71 kDa protein	60040	34863953	258001
SIMILAR TO KDEL CONTAINING PROTEIN 1; ENDOPLASMIC RETICULUM	TRAFFIC	Tax_id=10116 Similar to KDEL containing protein 1	60890	34863399	261916
SIMILAR TO KIAA0090 PROTEIN	UNKNOWN	Tax_id=10116 Similar to KIAA0090 protein	91240	34872226	302513
SIMILAR TO KIAA0316 PROTEIN	UNKNOWN	Tax_id=10116 Similar to KIAA0316 protein	140900	34879922	244528
SIMILAR TO KIAA0372 GENE PRODUCT	UNKNOWN	Tax_id=10116 Similar to KIAA0372 gene product	169500	34852783	312697
SIMILAR TO KIAA0635 GENE PRODUCT	UNKNOWN	Tax_id=10116 Similar to KIAA0635 gene product	147000	34877224	224112
SIMILAR TO FIBRONECTIN TYPE III DOMAIN CONTAINING PROTEIN	UNKNOWN	Tax_id=10116 Similar to KIAA0970 protein	135200	34874472	295665
KINESIN FAMILY PROTEIN 13A	CYTOSKELETON	Tax_id=10116 Similar to KIF13A	204000	34874048	266483
SIMILAR TO KINETOCORE-ASSOCIATED PROTEIN 1 (ROUGH DENDRICLE ADHESION)	CYTOSKELETON	Tax_id=10116 Similar to Kinetochore-associated protein 1 (Rough deal homolog) (hRod) (HSROD) (Rod)	222900	34877231	265212
SIMILAR TO MENINGIOMA EXPRESSED ANTIGEN 6 (COILED-COIL)	UNKNOWN	Tax_id=10116 Similar to Meningioma expressed antigen 6 (coiled-coil,proline-rich)	57130	34865266	286300
SIMILAR TO NEBULETTE (ACTIN-BINDING Z-DISK PROTEIN)	CYTOSKELETON	Tax_id=10116 Similar to Nebulette (Actin-binding Z-disk protein)	121800	34877348	276942
SIMILAR TO NIT PROTEIN 2	UNKNOWN	Tax_id=10116 Similar to Nit protein 2	34190	34868007	213226
POLYPOSIS LOCUS PROTEIN 1 HOMOLOG (TB2 PROTEIN HOMOLOG)	UNKNOWN	Tax_id=10116 Similar to POLYPOSIS LOCUS PROTEIN 1 HOMOLOG (TB2 PROTEIN HOMOLOG) (GP106)	21070	34878680	252129
SIMILAR TO PROTEIN DISULFIDE ISOMERASE-RELATED	PROT SYN/FOLD	Tax_id=10116 Similar to Protein disulfide isomerase-related	89320	34869214	276048
SIMILAR TO ENDOPLASMIC RETICULUM THIOREDOXIN SUPERFAMILY	PROT SYN/FOLD	Tax_id=10116 Similar to RIKEN cDNA 0610040B21	27040	34870174	239547
SIMILAR TO RIKEN CDNA 1200014J11	UNKNOWN	Tax_id=10116 Similar to RIKEN cDNA 1200014J11	80090	34872727	249723
SIMILAR TO TRANSFERRIN	BIOSYNTHETIC CARGO	Tax_id=10116 Similar to RIKEN cDNA 1300017J02	74750	34865830	304054
UDP-GLUCURONOSYL TRANSFERASE GTNA2	DETOXIFICATION	Tax_id=10116 Similar to RIKEN cDNA 2010321J07	62770	27694215	169892
SIMILAR TO RIKEN CDNA 2310008M10	UNKNOWN	Tax_id=10116 Similar to RIKEN cDNA 2310008M10	19420	34860558	316149
SIMILAR TO NADH:UBIQUINONE OXIDOREDUCTASE B17.2 SUBUNIT	MITOCHONDRIA	Tax_id=10116 Similar to RIKEN cDNA 2410011G03	23970	34864767	297605
SIGNAL PEPTIDASE COMPLEX 25 KDA SUBUNIT	PROT SYN/FOLD	Tax_id=10116 Similar to RIKEN cDNA 5730406115	24970	27678066	216144
SIMILAR TO RIKEN CDNA 5730469M10	UNKNOWN	Tax_id=10116 Similar to RIKEN cDNA 5730469M10	39980	34877094	208161
SIMILAR TO RIKEN CDNA 9630046K23	UNKNOWN	Tax_id=10116 Similar to RIKEN cDNA 9630046K23	41350	34869346	228920
SIMILAR TO SIALIC-ACID O-ACETYLESTERASE	PROT MOD	Tax_id=10116 Similar to Sialic-acid O-acetyltransferase	56760	34863093	198275
TOB3	MITOCHONDRIA	Tax_id=10116 Similar to TOB3	70420	34873064	239142
UDP-GLUCURONATE DECARBOXYLASE 1	METABOLISM	Tax_id=10116 Similar to UDP-glucuronate decarboxylase 1	20220	34881188	201012
SIMILAR TO ASPARTYL BETA-HYDROXYLASE	METABOLISM	Tax_id=10116 Similar to aspartyl beta-hydroxylase	60560	34866138	213158
SIMILAR TO ALPHA GLUCOSIDASE II, BETA SUBUNIT	PROT MOD	Tax_id=10116 Similar to alpha glucosidase II, beta subunit	59240	34860445	208522
SIMILAR TO ALPHA-2U-GLOBULIN	BIOSYNTHETIC CARGO	Tax_id=10116 Similar to alpha-2u-globulin	61070	34868545	210822
ARMET PROTEIN	UNKNOWN	Tax_id=10116 Similar to arginine-rich, mutated in early Stage tumorS	26400	34865887	195759
BAND 7 PROTEIN (35.3 KD) (4N53)	UNKNOWN	Tax_id=10116 Similar to band 7 protein (35.3 kD) (4N53)	39270	34863101	288335
SIMILAR TO BILE ACID COENZYME A: AMINO ACID N-ACYL TRANSFERASE	PEROXISOME	Tax_id=10116 Similar to bile acid Coenzyme A: amino acid N-acyltransferase	47980	34868484	273878

BIOTINIDASE	PLASMA MB	Tax_Id=10116 Similar to biotinidase	62250	34877005	196365
SIMILAR TO COMPLEMENT COMPONENT 8 BETA SUBUNIT	BIOSYNTHETIC CARGO	Tax_Id=10116 Similar to complement component 8 beta	64810	34869943	204172
SIMILAR TO EMBRYONIC BLASTOCOELAR EXTRACELLULAR MATRIX	UNKNOWN	Subunit			
ENDOPLASMIC OXIDOREDUCTASE 1 BETA	PROT SYN/FOLD	Tax_Id=10116 Similar to embryonic blastocoelar extracellular matrix protein precursor	242800	34851569	303538
UDP-GLUCURONOSYLTRANSFERASE GTNA1	DETOXIFICATION	Tax_Id=10116 Similar to endoplasmic oxidoreductase 1 beta	57800	34876487	282876
SIMILAR TO GLYOXYLATE REDUCTASE/HYDROXYPYRUVATE REDUCTASE	PEROXISOME	Tax_Id=10116 Similar to expressed Sequence A1788959	65670	34876789	217594
TPA: SENATAXIN; DEAQ-BOX HELICASE; TRNA SPLICING ENDONUCLEASE	TRANSCRIPTION	Tax_Id=10116 Similar to glyoxylate reductase/hydroxypyruvate reductase	34140	34935094	265523
HYPOTHETICAL PROTEIN D4ERTD765E	UNKNOWN	Tax_Id=10116 Similar to hypothetical protein	390800	34853159	241253
SIMILAR TO HYPOTHETICAL PROTEIN FLJ30596	UNKNOWN	Tax_Id=10116 Similar to hypothetical protein	141900	34854842	233766
GLYCOSYLTRANSFERASE 25 DOMAIN CONTAINING 1	UNKNOWN	Tax_Id=10116 Similar to hypothetical protein D4ERTD765E	42320	34870159	200143
NICALIN HOMOLOG	SIGNALING	Tax_Id=10116 Similar to hypothetical protein FLJ30596	61060	34854388	283019
		Tax_Id=10116 Similar to hypothetical protein MGC38524	121800	34877564	273384
		Tax_Id=10116 Similar to hypothetical protein from EUROMAGE 2021883	75830	34862247	195586
SIMILAR TO INTRACELLULAR MEMBRANE-ASSOCIATED CALCIUM TRANSPORTER	METABOLISM	Tax_Id=10116 Similar to intracellular membrane-associated calcium-independent phospholipase A2 gamma	107800	34865151	313999
LIPOPROTEIN RECEPTOR-RELATED PROTEIN	PLASMA MB	Tax_Id=10116 Similar to lipoprotein receptor-related protein	517200	34865759	268163
SIMILAR TO MEDIUM-CHAIN ACYL-COA SYNTHETASE	MITOCHONDRIA	Tax_Id=10116 Similar to medium-chain acyl-CoA Synthetase	22360	34859067	258281
OSMOTIC STRESS PROTEIN	MITOCHONDRIA	Tax_Id=10116 Similar to osmotic stress protein	148000	34856875	290180
REPRESSOR OF ESTROGEN RECEPTOR ACTIVITY: B-CELL ASSOCIATED	MITOCHONDRIA	Tax_Id=10116 Similar to repressor of estrogen receptor activity	33420	34858436	262284
40S RIBOSOMAL PROTEIN S5	PROT SYN/FOLD	Tax_Id=10116 Similar to ribosomal protein S5	29840	34854534	278725
TUBULIN ALPHA 6	CYTOSKELETON	Tax_Id=10116 Similar to tubulin, alpha 6	63060	34868254	298819
ADENINE NUCLEOTIDE TRANSLOCATOR 2	MITOCHONDRIA	Tax_Id=10116 Solute carrier family 25, member 5	32900	728810	117684
THIOREDOXIN	PROT SYN/FOLD	Tax_Id=10116 Thioredoxin	11670	57386	12218
P97 (TRANSITIONAL ENDOPLASMIC RETICULUM ATPASE)	TETH/DOCK/FUS	Tax_Id=10116 Transitional endoplasmic reticulum ATPase	89350	641973	125172
SIMILAR TO BC032271 PROTEIN	UNKNOWN	Tmem32 protein 12 days embryo spinal cord cDNA, RIKEN full length enriched library, clone: C530026101 product: hypothetical protein, full insert sequence 10 days neonate cortex cDNA, RIKEN full-length enriched library, clone: A830005F13 product: weakly similar to CG15168 PROTEIN 16 days neonate cerebellum cDNA, RIKEN full-length enriched library, clone: 9630048L06 product: weakly similar to CG15168 protein	14680	27710182	244941
UNKNOWN (PROTEIN FOR MGC:72610)	UNKNOWN	BE09053n			
TRANSKETOLASE	METABOLISM	Torsin-1A-interacting protein 2	61700	81885310	313574
TRANSLOCON-ASSOCIATED PROTEIN ALPHA	PROT SYN/FOLD	Transketolase	67640	1729977	38668
		Translocon-associated protein subunit alpha precursor TRAP-alpha	35630	71162390	166245
		alpha Signal sequence receptor subunit alpha SSR-alpha			
		Liver regeneration-related protein LRRG137			

TRANSLOCON-ASSOCIATED PROTEIN, DELTA SUBUNIT	PROT SYN/FOLD	Translocon-associated protein subunit delta precursor TRAP-delta Signal sequence receptor subunit delta SSR-delta	18980	8394364	152155
COP-COATED VESICLE MEMBRANE PROTEIN P24 BETA 1	TRAFFIC	Transmembrane emp24 domain-containing protein 2 precursor Membrane protein p24A RNP214	22730	3914232	78146
30 KDA PROTEIN	UNKNOWN	Transmembrane protein 111	29980	71153386	63169
TRANSTHYRETIN	BIOSYNTHETIC CARGO	Transthyretin precursor	15720	57425	31553
TRICARBOXYLATE TRANSPORT PROTEIN, MITOCHONDRIAL	MITOCHONDRIA	Tricarboxylate transport protein, mitochondrial precursor Citrate transport protein CTP Tricarboxylate carrier protein	33840	8394297	69776
TRIFUNCTIONAL ENZYME ALPHA SUBUNIT, MITOCHONDRIAL	MITOCHONDRIA	Solute carrier family 25 member 1 Trifunctional enzyme subunit alpha, mitochondrial precursor TP-alpha Long-chain enoyl-CoA hydratase Long chain 3-hydroxyacyl-CoA dehydrogenase	82510	510108	82392
TRIFUNCTIONAL ENZYME BETA SUBUNIT, MITOCHONDRIAL	MITOCHONDRIA	Trifunctional enzyme subunit beta, mitochondrial precursor TP-beta 3-ketoacyl-CoA thiolase Acetyl-CoA acyltransferase Beta-ketothiolase	51410	510110	43581
TUBULIN ALPHA 1	CYTOSKELETON	Tubulin alpha-1 chain Alpha-tubulin 1	50150	55976173	31423
TUBULIN ALPHA 4	CYTOSKELETON	Tubulin alpha-1 chain Alpha-tubulin 1 Testis-specific alpha-tubulin Tubulin H2-alpha	49920	55741524	31436
TUBULIN BETA 5	CYTOSKELETON	Tubulin, beta polypeptide Beta 5-tubulin TUBB protein	49670	56754676	62620
SIMILAR TO KERATIN, TYPE II CYTOSKELETAL 5 (CYTOKERATIN	LIKELY CONTAMINANTS	Type II keratin Kb15	57610	46485029	222258
UDP-GLUCURONOSYLTRANSFERASE 1A1	DETOXIFICATION	UDP glycosyltransferase 1 family polypeptide A1 UDP-glucuronosyltransferase 1A1	59660	695162	43597
UDP-GLUCURONOSYLTRANSFERASE 1A6	DETOXIFICATION	UDP glycosyltransferase 1 family polypeptide A7 UDP glycosyltransferase 1 family, polypeptide A6	60240	89276780	205347
UDP-GLUCURONOSYLTRANSFERASE 2B12	DETOXIFICATION	UDP glycosyltransferase 2 family, polypeptide B4	61030	51948510	221298
UDP-GLUCOSE GLYCOPROTEIN:GLUCOSYLTRANSFERASE	PROT MOD	UDP-glucose:glycoprotein glucosyltransferase 1 precursor UDP-glucose ceramide glucosyltransferase-like 1 UDP--Glc:glycoprotein glucosyltransferase RUGT	174000	7677176	171823
UDP-GLUCURONOSYLTRANSFERASE 1A5	DETOXIFICATION	UDP-glucuronosyltransferase 1A5	60010	18308168	53066
UDP-GLUCURONOSYLTRANSFERASE 1A7	DETOXIFICATION	UDP-glucuronosyltransferase 1A7	59610	18308176	53069
UDP-GLUCURONOSYLTRANSFERASE 2A1	DETOXIFICATION	UDP-glucuronosyltransferase 2A1, microsomal (EC 2.4.1.17) (UDPGT) (UGT-QLF)	59860	112467	11410
UDP-GLUCURONOSYLTRANSFERASE 2B1	DETOXIFICATION	UDP-glucuronosyltransferase 2B1 precursor, microsomal	60480	27545358	31600
UDP-GLUCURONOSYLTRANSFERASE 2B2	DETOXIFICATION	UDP-glucuronosyltransferase 2B2 precursor, microsomal	60990	207583	78055
UDP-GLUCURONOSYLTRANSFERASE 2B3	DETOXIFICATION	UDP-glucuronosyltransferase 2B3 precursor UDPGT Testosterone, dihydrotestosterone, and beta-estradiol specific 17-beta-hydroxysteroid specific UDPGT-R3 RLUG38	60520	31543923	31602
UDP-GLUCURONOSYLTRANSFERASE 2B5	DETOXIFICATION	UDP-glucuronosyltransferase 2B5 precursor UDPGT 17-beta-hydroxysteroid specific UDPGT-r-5 UDP-glucuronosyltransferase R-21 UDPGT-r-21	60590	55925581	31603
UDP-GLUCURONOSYLTRANSFERASE 2B8	DETOXIFICATION	UDP-glucuronosyltransferase 2B8 precursor UDPGT UGT2B-RH4	60090	6136101	125219

UBIQUITIN-CONJUGATING ENZYME E2L 3	PROTEASOME/UBIQUITIN	Ube2/3 protein Ubiquitin-conjugating enzyme E2L 3 Bladder RCB-0544 MBT-2 cDNA, RIKEN full-length enriched library, clone: G430072O21 product:ubiquitin-conjugating enzyme E2L 3, full insert sequence	17860	62658232	54899
SIMILAR TO UBIQUINOL-CYTOCHROME C REDUCTASE CORE PROTEIN	MITOCHONDRIA	Ubiquinol-cytochrome c reductase core protein I	52850	51948476	220138
UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX CORE PROTEIN	MITOCHONDRIA	Ubiquinol-cytochrome c reductase core protein II	48400	55741544	139461
UBIQUINOL-CYTOCHROME C REDUCTASE IRON-SULFUR SUBUNIT	MITOCHONDRIA	Ubiquinol-cytochrome c reductase iron-sulfur subunit, mitochondrial precursor Rieske iron-sulfur protein RISP Liver regeneration-related protein LRRGT00195	29450	57114330	230682
MEMBRANE ASSOCIATED PROGESTERONE RECEPTOR COMPLEX	DETOXIFICATION	Ventral midline antigen VEMA	21600	6647578	19913
VERY-LONG-CHAIN ACYL-COA SYNTHETASE (VERY-LONG-CHAIN ACYL-COA SYNTHETASE)	PEROXISOME	Very-long-chain acyl-CoA synthetase VLCS Very-long-chain-fatty-acid-CoA ligase VLACS THCA-CoA ligase Fatty-acid-coenzyme A ligase, very long-chain 1 Long-chain-fatty-acid-CoA ligase Fatty acid transport protein 2 FATP-2 Solute carrier family 27 member 2	70690	3183199	78154
VIGILIN	PROT SYN/FOLD	Vigilin High density lipoprotein-binding protein HDL-binding protein	141600	46397078	26167
VITAMIN K-DEPENDENT GAMMA-CARBOXYLASE	PROT MOD	Vitamin K-dependent gamma-carboxylase Gamma-glutamyl carboxylase Vitamin K gamma glutamyl carboxylase	87480	6136262	78166
VITAMIN-K-DEPENDENT PROTEIN C	BIOSYNTHETIC CARGO	Vitamin K-dependent protein C precursor Autoprothrombin IIA Anticoagulant protein C Blood coagulation factor XIV Vitamin K-dependent protein C light chain Vitamin K-dependent protein C heavy chain Activation peptide	51910	6981412	75051
3-KETOACYL-COA THIOLEASE A, PEROXISOMAL	PEROXISOME	acetyl-CoA acyltransferase, 3-oxo acyl-CoA thiolase A, peroxisomal	44780	6978429	3598
FRUCTOSE-BISPHOSPHATE ALDOLASE B	METABOLISM	aldolase B [Rattus norvegicus]	39600	1619606	116234
BETA 2 GLOBIN	BLOOD + OTHER CELLS	beta 2 globin [rats, Sprague-Dawley, Peptide, 146 aa]	15860	8048915	371
CATHEPSIN C	LYSOSOME	cathepsin C	52240	8393218	51414
CYTOCHROME P450 2D1	DETOXIFICATION	cytochrome P450	57190	203803	126576
FERRITIN HEAVY CHAIN	METABOLISM	ferritin, heavy polypeptide 1	21100	6978859	3774
FIBRINOPEPTIDE A	BIOSYNTHETIC CARGO	fibrinopeptide A	1740	229210	22617
GLYCEROL-3-PHOSPHATE DEHYDROGENASE [NAD+], CYTOPLASMIC	METABOLISM	glycerol-3-phosphate dehydrogenase 1 (soluble) [Rattus norvegicus]	37400	3023880	80790
HEAT RESPONSIVE PROTEIN 12	PROT SYN/FOLD	heat-responsive protein 12	14290	2425030	153343
HYPERTENSION-INDUCED PROTEIN S-2	UNKNOWN	hypertension-induced protein S-2 - rat (fragment)	11250	539959	130834
MANNOSE-BINDING PROTEIN C PRECURSOR	BIOSYNTHETIC CARGO	mannose-binding protein C (liver)	26100	205263	44167
60S RIBOSOMAL PROTEIN L30	PROT SYN/FOLD	null	12780	51702801	4817
P105 COACTIVATOR	NUCLEUS	p105 coactivator	99330	1800307	177421
PHOSPHATIDYLETHANOLAMINE-BINDING PROTEIN	PROT MOD	phosphatidylethanolamine binding protein [Rattus norvegicus]	20800	8393910	51562
60S RIBOSOMAL PROTEIN L13	PROT SYN/FOLD	ribosomal protein L13	24240	510552	37239
60S RIBOSOMAL PROTEIN L6	PROT SYN/FOLD	ribosomal protein L6	33570	2507315	42185
40S RIBOSOMAL PROTEIN S17	PROT SYN/FOLD	similar to 40S RIBOSOMAL PROTEIN S17	15680	34853950	250506
60S RIBOSOMAL PROTEIN L7A (SURFEIT LOCUS PROTEIN 3) (PLA-X polypeptide)	PROT SYN/FOLD	similar to 60S ribosomal protein L7a (Surfeit locus protein 3) (PLA-X polypeptide)	26720	34855926	208919

60S RIBOSOMAL PROTEIN L7A (SURFEIT LOCUS PROTEIN 3) (PLA-X polypeptide)	PROT SYN/FOLD	similar to 60S ribosomal protein L7a (Surfeit locus protein 3) (PLA-X polypeptide)	35790	34857405	311989
CG33130-PA	UNKNOWN	similar to CG33130-PA	125000	34870072	215152
UNNAMED PROTEIN	UNKNOWN	similar to CG1-90 protein	52100	34867201	258588
CALCIUM-BINDING MITOCHONDRIAL CARRIER PROTEIN ARALAR2	MITOCHONDRIA	similar to Calcium-binding mitochondrial carrier protein Aralar2 (Solute carrier family 25, member 13) (Citrin)	15470	27708576	166641
F-ACTIN CAPPING PROTEIN ALPHA-1 SUBUNIT	CYTOSKELETON	similar to Cappa1 protein	32910	34859736	230796
CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 73 kDa	UNKNOWN	similar to Cleavage and polyadenylation specificity factor, 73 kDa subunit (CPSF 73 kDa subunit)	74350	34858109	240505
G1 TO PHASE TRANSITION 2	SIGNALING	similar to G1 to phase transition 2	76550	27663980	171140
AMPHOTERIN	NUCLEUS	similar to High mobility group protein 1 (HMG-1) (Amphoterin) (Heparin-binding protein p30)	48030	34861695	293750
SIMILAR TO NADH DEHYDROGENASE (UBIQUINONE) 1 ALPHA SUBUNIT	MITOCHONDRIA	similar to NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 9	42560	34858473	215768
TRINUCLEOTIDE REPEAT CONTAINING 5 (PREDICTED)	UNKNOWN	similar to RIKEN cDNA 1600025D17	39820	34874446	296070
YEAST-44.2 PROTEIN	UNKNOWN	similar to RIKEN cDNA 2810409H07 [Rattus norvegicus]	42320	34855205	260021
SDF2 LIKE PROTEIN 1	PROT MOD	similar to SDF2 like protein 1 [Rattus norvegicus]	23400	34869825	263376
SIMILAR TO ACTIN-RELATED PROTEIN 2	CYTOSKELETON	similar to actin-related protein 2	42030	34878017	194947
2610204L23RIK PROTEIN	UNKNOWN	similar to adipocyte-specific protein 4 [Rattus norvegicus]	55200	34873948	240031
ALPHA GLUCOSIDASE II, ALPHA SUBUNIT	PROT MOD	similar to alpha glucosidase II, alpha subunit [Rattus norvegicus]	89880	34861580	192728
COPROPORPHYRINOGEN OXIDASE	MITOCHONDRIA	similar to coproporphyrinogen oxidase	49280	79749365	160701
SIMILAR TO GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE	METABOLISM	similar to glyceraldehyde-3-phosphate dehydrogenase	41920	34854562	287450
SIMILAR TO GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE	METABOLISM	similar to glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) (EC 1.2.1.12) - mouse	31550	34864978	296252
SIMILAR TO HEXOSE-6-PHOSPHATE DEHYDROGENASE; GDH/6P	METABOLISM	similar to hexose-6-phosphate dehydrogenase GDH/6PGL endoplasmic bifunctional protein	114800	34872615	251640
INTER-ALPHA TRYPSIN INHIBITOR, HEAVY CHAIN 1	BIOSYNTHETIC CARGO	similar to inter-alpha trypsin inhibitor, heavy chain 1 [Rattus norvegicus]	99190	34877130	227779
MIRROR-IMAGE POLYDACTYLY GENE 1	UNKNOWN	similar to mirror-image polydactyly gene 1	52780	34865613	265130
ORNITHINE TRANSPORTER	MITOCHONDRIA	similar to ornithine transporter	32800	27673563	205798
SIMILAR TO RIBOSOMAL PROTEIN L10A	PROT SYN/FOLD	similar to ribosomal protein L10a	47220	34878384	298856
SIMILAR TO SERINE PROTEASE OMI	PROT MOD	similar to serine protease OMI	49090	34856275	218478
SIMILAR TO SPLICING COACTIVATOR SUBUNIT SRM300; RNA BINDING PROTEIN; AT-RICH ELEMENT BINDING FACTOR [Rattus norvegicus]	NUCLEUS	similar to splicing coactivator subunit SRm300; RNA binding protein; AT-rich element binding factor [Rattus norvegicus]	212600	34868816	290757
TALIN	CYTOSKELETON	similar to talin [Rattus norvegicus]	269500	34867875	230030
TASTE RECEPTOR, TYPE 1, MEMBER 2	PLASMA MB	taste receptor, type 1, member 2	202100	34872230	217700
SIMILAR TO PEROXISOMAL LONG-CHAIN ACYL-CoA OXIDASE	PEROXISOME	unknown	94390	34851379	292730
SIMILAR TO HYPOTHETICAL PROTEIN CGI-99	CYTOSKELETON	unknown	28170	27722175	195164
TROPOMYOSIN ALPHA	CYTOSKELETON	(P04692) Isoform 5 of P04692	28340	112443	11396

CLATHRIN LIGHT CHAIN A	COAT	(P08081) Isoform Non-brain of P08081	23570	56269651	126525
H-RAS-1/P21	GTPASE	(P08644) Isoform 2B of P08644	21490	495534	71624
SH3P7R2	UNKNOWN	(Q9JHL4) Isoform 3 of Q9JHL4	48250	7248379	18910
SOLUTE CARRIER FAMILY 21 MEMBER 10	PLASMA MB	(Q9QZX8) Isoform 2 of Q9QZX8	76770	9624356	78114
COACTIVATOR-ASSOCIATED ARGININE METHYLTRANSFERASE	NUCLEUS	(Q9WVG6) Isoform 2 of Q9WVG6	63460	77539446	292598
1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE	SIGNALING	1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase beta 3	139400	32699414	166274
PROTEASOME SUBUNIT ALPHA TYPE 2	PROTEASOME/UBIQUITINATION	10 days embryo whole body cDNA, RIKEN full-length enriched library, clone:261051121 product:proteasome (prosome, macropain) subunit, alpha type 2, full insert sequence T1B-55 BB88 cDNA, RIKEN full-length enriched library, clone:1730006B17 product:proteasome (prosome, macropain) subunit, alpha type 2, full insert sequence 2 days neonate thymus thymic cells cDNA, RIKEN full-length enriched library, clone:E430022A16 product:proteasome (prosome, macropain) subunit, alpha type 2, full insert sequence Bone marrow macrophage cDNA, RIKEN full-length enriched library, clone:1830087N08 product:proteasome (prosome, macropain) subunit, alpha type 2, full insert sequence Bone marrow macrophage cDNA, RIKEN full-length enriched library, clone:1830041K04 product:proteasome (prosome, macropain) subunit, alpha type 2, full insert sequence Proteasome (Prosome, macropain) subunit, alpha type 2 Adult male urinary bladder cDNA, RIKEN full-length enriched library, clone:9530069L07 product:proteasome (prosome)	25930	8394063	33375
10-FORMYLTETRAHYDROFOLATE DEHYDROGENASE	METABOLISM	10-Formyltetrahydrofolate Dehydrogenase	34040	42543697	723160
14-3-3 PROTEIN ETA	SIGNALING	14-3-3 protein eta	28210	6981710	29710
14-3-3 PROTEIN TAU	SIGNALING	14-3-3 protein theta	27780	6981712	29711
230 KDA PHOSPHATIDYLINOSITOL 4-KINASE	SIGNALING	230 kDa phosphatidylinositol 4-kinase	231300	25742825	19300
3-HYDROXYANTHRANILATE 3,4-DIOXYGENASE	METABOLISM	3-hydroxyanthranilate 3,4-dioxygenase 3-HAO 3-hydroxyanthranilic acid dioxygenase 3-hydroxyanthranilate oxygenase	32580	9910256	42736
ESTRADIOL 17 BETA-DEHYDROGENASE 7	DETOXIFICATION	3-keto-steroid reductase Estradiol 17-beta-dehydrogenase 7 17-beta-HSD 7 17-beta-hydroxysteroid dehydrogenase 7 PRL receptor-associated protein PRAP	37370	8393576	708
3-OXO-5-ALPHA-STEROID 4-DEHYDROGENASE 1	DETOXIFICATION	3-oxo-5-alpha-steroid 4-dehydrogenase 1 Steroid 5-alpha-reductase 1 SR type 1	29780	25742565	43740
4-TRIMETHYLAMINO BUTYRALDEHYDE DEHYDROGENASE	METABOLISM	4-trimethylaminobutyraldehyde dehydrogenase TMABADH	53650	78099320	104196
5'-NUCLEOTIDASE	PLASMA MB	Aldehyde dehydrogenase 9A1 5' -nucleotidase precursor Ecto-5' -nucleotidase 5' -NT CD73 antigen	63970	202551	11455

5'-AMP-ACTIVATED PROTEIN KINASE, GAMMA-1 SUBUNIT	SIGNALING	5'-AMP-activated protein kinase, gamma-1 subunit	36670	1335860	68651
60S RIBOSOMAL PROTEIN L22	PROT SYN/FOLD	60S ribosomal protein L22	14760	52221202	4392
60S RIBOSOMAL PROTEIN L26	PROT SYN/FOLD	60S ribosomal protein L26	17260	27672824	4813
MYOSIN REGULATORY LIGHT CHAIN	CYTOSKELETON	9.5 days embryo parthenogenote cDNA, RIKEN full-length enriched library, clone:B130042B20 product:myosin regulatory light chain A, smooth muscle homolog CRL-1722 L5178Y-R cDNA, RIKEN full-length enriched library, clone:I730047D20 product:Myosin regulatory light chain 2-A, smooth muscle isoform (Myosin RLC-A) homolog 14 days pregnant adult female placenta cDNA, RIKEN full-length enriched library, clone:I530020L12 product:Myosin regulatory light chain 2-A, smooth muscle isoform (Myosin RLC-A) homolog Osteoclast-like cell cDNA, RIKEN full-length enriched library, clone:I420005I07 product:Myosin regulatory light chain 2-A, smooth muscle isoform (Myosin RLC-A) homolog Bone marrow macrophage cDNA, RIKEN full-length enriched library, clone:I830027H03 product:Myosin regulatory light chain 2-A, smooth muscle isoform (Myosin RLC-A) homolog Myosin light chain, regulatory B-like RIKEN cDNA 2900073G15 18-day embryo whole body cDNA, RIKEN full-length enriched library, clone:1190017113 product:myosin	19900	68533710	69379
ADP-RIBOSYLATION FACTOR 4 CLATHRIN ADAPTIN-1, BETA 1	GTPASE COAT	ADP-ribosylation factor 4 AP-1 complex subunit beta-1 Adapter-related protein complex 1 beta-1 subunit Beta-adaptin 1 Adapter protein complex AP-1 beta-1 subunit Golgi adaptor HA1/AP1 adaptin beta subunit Clathrin assembly protein complex 1 beta large chain	20400 104600	543844 8392872	10609 126513
ADAPTER-RELATED PROTEIN COMPLEX 1 SIGMA 1A SUBUNIT	COAT	AP-1 complex subunit sigma-1A Adapter-related protein complex 1 sigma-1A subunit Sigma-adaptin 1A Adaptor protein complex AP-1 sigma-1A subunit Golgi adaptor HA1/AP1 adaptin sigma-1A subunit Clathrin assembly protein complex 1 sigma-1A small chain Clathrin coat assembly protein AP19 HA1 19 kDa subunit Sigma 1a subunit of AP-1 clathrin	18730	34871704	74369
CLATHRIN COAT ASSEMBLY PROTEIN AP17	COAT	AP-2 complex subunit sigma-1 Adapter-related protein complex 2 sigma-1 subunit Sigma-adaptin 3b Clathrin coat assembly protein AP17 Clathrin coat-associated protein AP17 Plasma membrane adaptor AP-2 17 kDa protein Clathrin assembly protein 2 small chain ARF6 protein ADP-ribosylation factor 6	17020	56961624	65700
ADP-RIBOSYLATION FACTOR 6	GTPASE	ARP2/3 complex 21 kDa subunit	20080	60552411	120856
ARP2/3 COMPLEX 21 KDA SUBUNIT	CYTOSKELETON	ARP2/3 complex 21 kDa subunit	19650	27665454	160418
ATPASE, H+ TRANSPORTING, V1 SUBUNIT E ISOFORM 1	LYSOSOME	ATPase, H+ transporting, V1 subunit E isoform 1	26130	38454230	261145
VACUOLAR ATP ASE	LYSOSOME	ATPase, H+ transporting, lysosomal 34kDa, V1 subunit D	28310	40786463	160475
ACETYL-COENZYME A ACETYLTTRANSFERASE 3-LIKE	UNKNOWN	Ab2-076	103300	33086552	166325
SIMILAR TO GLYCINE-N-ACYLTRANSFERASE	PROT MOD	Ab2-132	39450	33086562	261456
AB2-225	UNKNOWN	Ab2-225 Hypothetical protein RGD1306952	27900	56970828	244467
EUKARYOTIC TRANSLATION ELONGATION FACTOR 1 BETA 2	PROT SYN/FOLD	Ac2-067	27970	34862605	166240
ACETYL-COA CARBOXYLASE 1	MITOCHONDRIA	Acetyl-CoA carboxylase 1 ACC-alpha Biotin carboxylase	265200	202645	84141
SUPPRESSOR OF PROFILIN/P41 OF ACTIN-RELATED COMPLEX 3	CYTOSKELETON	Actin-related protein 2/3 complex subunit 1A	41600	59797636	168831

ADAPTOR-RELATED PROTEIN COMPLEX 2, MU 1 SUBUNIT	COAT	Adaptor protein complex AP-2, mu1 12 days embryo spinal ganglion cDNA, RIKEN full-length enriched library, clone:D130035H06 product:adaptor protein complex AP-2, mu1, full insert sequence 17 days embryo heart cDNA, RIKEN full-length enriched library, clone:I920019I09 product:adaptor protein complex AP-2, mu1, full insert sequence Ap2m1 protein	49650	73536275	73521
ADENINE PHOSPHORIBOSYLTRANSFERASE	METABOLISM	Adenine phosphoribosyltransferase APRT	19550	61556832	126504
ADENOSINE KINASE	METABOLISM	Adenosine kinase	40100	7448824	3608
AFLATOXIN B1 ALDEHYDE REDUCTASE MEMBER 2	DETOXIFICATION	Akr7a2 protein	37600	6815049	161251
HYDROXYSTEROID SULFOTRANSFERASE	DETOXIFICATION	Alcohol sulfotransferase	33080	204671	148916
ALDEHYDE DEHYDROGENASE FAMILY 1 MEMBER A1	DETOXIFICATION	Aldehyde dehydrogenase 1A1	54460	38494348	72216
ALDEHYDE OXIDASE	DETOXIFICATION	Aldehyde oxidase	146900	4324710	95119
ALDOSE1-EPIMERASE	METABOLISM	Aldose 1-epimerase Galactose mutarotase	37890	84028322	290544
ALPHA ISOFORM OF REGULATORY SUBUNIT A, PROTEIN PHOSPHATASE 2	SIGNALING	Alpha isoform of regulatory subunit A, protein phosphatase 2	65320	55926139	36803
ALPHA-1 CATENIN	CYTOSKELETON	Alpha-1 catenin	9484	92036	84182
ALPHA-1-ACID GLYCOPROTEIN PRECURSOR	BIOSYNTHETIC CARGO	Alpha-1-acid glycoprotein precursor Orosomucoid OMD	23580	72091	11470
ALPHA-2 ANTIPLASMIN	BIOSYNTHETIC CARGO	Alpha-2 antiplasmin Serine (Or cysteine) proteinase inhibitor, clade F, member 1	46470	51261124	317738
ALPHA-PARVIN	CYTOSKELETON	Alpha-parvin Actopaxin	42290	20138815	37085
ANNEXIN A4	TETH/DOKK/FUS	Annexin A4	35850	37999910	171244
CLATHRIN ADAPTIN-2, BETA 1	COAT	Ap2b1 protein	105700	73695330	59082
ARGININOSUCCINATE LYASE	METABOLISM	Argininosuccinate lyase	51550	551296	45085
AROMATIC-L-AMINO-ACID DECARBOXYLASE	METABOLISM	Aromatic-L-amino-acid decarboxylase AADC DOPA decarboxylase DDC	54050	6978759	3735
ARYL SULFOTRANSFERASE	DETOXIFICATION	Aryl sulfotransferase	33910	55761	69784
ASIALOGLYCOPROTEIN RECEPTOR 1	PLASMA MB	Asialoglycoprotein receptor 1	32850	7705290	120624
BETA-CATENIN	CYTOSKELETON	Beta-catenin	85470	16758082	74416
BETA-UREIDOPROPIONASE	MITOCHONDRIA	Beta-ureidopropionase Beta-alanine synthase N-carbamoyl-beta-alanine amidohydrolase	44040	51259277	44431
BILE SALT EXPORT PUMP (ATP-BINDING CASSETTE, SUB-FAMILY 11 SISTER OF P-GLYCOPROTEIN)	PLASMA MB	Bile salt export pump ATP-binding cassette sub-family B member 11 Sister of P-glycoprotein	146300	3075422	13065
ADENYLYL CYCLASE-ASSOCIATED PROTEIN 1	SIGNALING	CAP, adenylate cyclase-associated protein 1	51590	59709467	130827
CADHERIN-17 PRECURSOR	PLASMA MB	Cadherin-17 precursor Liver-intestine-cadherin LI-cadherin	91860	628001	127670
CALCIUM-BINDING PROTEIN P22	SIGNALING	Calcium-binding protein p22 Calcium-binding protein CHP	22430	46577577	25354
CALCIUM-INDEPENDENT ALPHA-LATROTOXIN RECEPTOR 2 PRECURSOR	PLASMA MB	Calcineurin homologous protein Sid 470 Calcium-independent alpha-latrotoxin receptor 2 precursor	161100	3695131	70058
CALMODULIN	PROT SYN/FOLD	Cam protein Calm2a-prov protein	16840	8394168	55585
CATECHOL O-METHYLTRANSFERASE, MEMBRANE-BOUND FORM	DETOXIFICATION	Catechol O-methyltransferase, membrane-bound form	29600	6978681	3708
6-PHOSPHOGLUCONATE DEHYDROGENASE; DECARBOXYLATIN	METABOLISM	Cc2-27	120500	33086672	166337

CCT5 PROTEIN	PROT SYN/FOLD	Cct5 protein	31980	37590247	252047
CDC42	GTPASE	Cell division cycle 42	21260	61889112	85184
CHAPERONIN CONTAINING TCP-1 BETA SUBUNIT	PROT SYN/FOLD	Chaperonin containing TCP1, subunit 2 Beta	57460	54400730	292700
CHAPERONIN CONTAINING TCP1, SUBUNIT 3 (GAMMA)	PROT SYN/FOLD	Chaperonin containing TCP1, subunit 3 Gamma	60650	40018616	169833
CHLORIDE INTRACELLULAR CHANNEL PROTEIN 4	PLASMA MB	Chloride intracellular channel protein 4 Intracellular chloride ion channel protein p64H1	28630	6685295	78195
COPI COATOMER BETA SUBUNIT	COAT	Coatomer subunit beta Beta-coat. protein Beta-COP	107000	55819	63721
COMPLEMENT COMPONENT 1, Q SUBCOMPONENT BINDING PROTEIN	MITOCHONDRIA	Complement component 1 Q subcomponent-binding protein, mitochondrial precursor Glycoprotein gC1qBP C1qBP GC1q-R protein	30740	9506435	80872
CORONIN 1B	SIGNALING	Coronin-1B Coronin-2	53850	9506507	95157
CORTACTIN ISOFORM C	CYTOSKELETON	Cortactin isoform C	52630	2996044	57161
CYSTATHIONINE BETA-SYNTHASE	METABOLISM	Cystathionine beta-synthase	61450	543960	41205
CYSTEINE-RICH PROTEIN 2	UNKNOWN	Cysteine-rich protein 2 CRP2 Protein ESP1	22700	737713	46143
CYSTEINE SULFINIC ACID DECARBOXYLASE	METABOLISM	Cysteine-sulfinate decarboxylase	55250	6685331	35923
SIMILAR TO UMP-CMP KINASE	SIGNALING	Cytidylate kinase	25830	71043752	267331
CYTOCHROME P450 17A1	DETOXIFICATION	Cytochrome P450 17A1 CYPXVII P450-C17 P450c17 Steroid 17-alpha-hydroxylase/17,20 lyase	57250	940818	3722
DOPA/TYROSINE SULFOTRANSFERASE	DETOXIFICATION	DOPA/tyrosine sulfotransferase	34840	688032	74919
B-FACTOR, PROPERDIN, ALTERNATIVE-COMPLEMENT PATHWAY	BIOSYNTHETIC CARGO	Daf1-24	124000	33086684	287107
DAMAGE-SPECIFIC DNA BINDING PROTEIN 1	NUCLEUS	Damage-specific DNA binding protein 1	126900	9843869	111030
DEHYDROGENASE/REDUCTASE SDR FAMILY MEMBER 1	UNKNOWN	Dehydrogenase/reductase (SDR family) member 1	34020	56090381	240184
DESTRIN	CYTOSKELETON	Destrin Actin-depolymerizing factor ADF	18390	7441446	123978
DIHYDROFOLATE REDUCTASE	METABOLISM	Dihydrofolate reductase	21640	81871579	53424
PTERIN-4-ALPHA-CARBINOLAMINE DEHYDRATASE	METABOLISM	Dimerization Cofactor Of Hepatocyte Nucleoside Diphosphate	11960	10835705	108686
DIPEPTIDYL PEPTIDASE 4	PLASMA MB	Dipeptidyl peptidase IV	88000	6978773	3741
PRESYNAPTIC PROTEIN SAP97	BIOSYNTHETIC CARGO	Disks large homolog 1 Synapse-associated protein 97 SAP-97	100600	6978763	3737
DYNEIN HEAVY CHAIN, CYTOSOLIC	CYTOSKELETON	Dynein heavy chain, cytosolic	532000	294543	95169
DYNEIN LIGHT CHAIN 2	CYTOSKELETON	Dynein light chain 2, cytoplasmic Dynein light chain LC8-type 2 8 kDa dynein light chain DLC8 DLC8b	10350	56748619	129100
EH-DOMAIN-CONTAINING PROTEIN 1 (MPAST1)	UNKNOWN	EH-domain containing protein 1	60600	58865448	2280
EH-DOMAIN CONTAINING PROTEIN 3	UNKNOWN	EH-domain containing protein 2	60790	34536836	244145
ECTO-NUCLEOTIDE PYROPHOSPHATASE/PHOSPHODIESTERASE	PLASMA MB	Ectonucleotide pyrophosphatase/phosphodiesterase 1 E-NPP 1 Phosphodiesterase I/nucleotide pyrophosphatase 1 Plasma-cell membrane glycoprotein PC-1 Alkaline phosphodiesterase I Nucleotide pyrophosphatase NPPase	102900	23396766	60453
EPIDERMAL GROWTH FACTOR RECEPTOR	PLASMA MB	Epidermal growth factor receptor	134900	6478868	85744
EPITHELIAL-CADHERIN	PLASMA MB	Epithelial-cadherin precursor E-cadherin Uvomorulin Cadherin-1 CD324 antigen E-Cad/CTF1 E-Cad/CTF2 E-Cad/CTF3	98720	6009482	1625
EPOXIDE HYDROLASE	DETOXIFICATION	Epoxide hydrolase 1 Microsomal epoxide hydrolase Epoxide hydratase	52580	77539448	17081
EPSIN 1	COAT	Epsin 1	60160	41016934	105332
ESTROGEN SULFOTRANSFERASE, ISOFORM 2	PROT MOD	Estrogen sulfotransferase, isoform 2 EST-2 Sulfotransferase, estrogen-preferring Estrone sulfotransferase	35360	1711600	109267

ESTROGEN SULFOTRANSFERASE, ISOFORM 6	METABOLISM	Estrogen sulfotransferase, isoform 6 EST-6	35300	913357	62242
ESTROGEN RECEPTOR-RELATED RECEPTOR GAMMA-1	TRANSCRIPTION	Estrogen-related receptor gamma Estrogen receptor-related protein 3	51310	50400205	17534
TRANSLATION INITIATION FACTOR EIF-4A	PROT SYN/FOLD	Eukaryotic translation initiation factor 4A1 16 days embryo kidney cDNA, RIKEN full-length enriched library, clone:1920165O08 product:eukaryotic translation initiation factor 4A1, full insert sequence 17 days embryo kidney cDNA, RIKEN full-length enriched library, clone:1920077H15 product:eukaryotic translation initiation factor 4A1, full insert sequence 16 days embryo heart cDNA, RIKEN full-length enriched library, clone:1920075M13 product:eukaryotic translation initiation factor 4A1, full insert sequence 17 days embryo heart cDNA, RIKEN full-length enriched library, clone:1920075G18 product:eukaryotic translation initiation factor 4A1, full insert sequence 17 days embryo kidney cDNA, RIKEN full-length enriched library, clone:1920054E16 product:eukaryotic translation initiation factor 4A1, full insert sequence CDNA, RIKEN full-length enriched library, clone:1730045F20 product:eukaryotic translation initiation factor 4A1, full insert sequence Blastocyst blastocyst cDNA, RIKEN full-length	46150	40786436	55871
SIMILAR TO WBSCR1	UNKNOWN	Eukaryotic translation initiation factor 4H	27320	55741853	295040
EXOCYST COMPLEX COMPONENT SEC5	TRAFFIC	Exocyst complex component 2 Exocyst complex component Sec5 rSec5	104000	7513971	161256
CAPPING PROTEIN (ACTIN FILAMENT) MUSCLE Z-LINE, BETA	CYTOSKELETON	F-actin capping protein beta subunit	30630	54400732	83668
SIMILAR TO GALACTOKINASE 1	METABOLISM	Galactokinase 1 Predicted	42380	56605662	206276
GALECTIN-9	PLASMA MB	Galectin-9	36320	1916610	18989
GAMMA-BUTYROBETAINE, 2-OXOGLUTARATE DIOXYGENASE	METABOLISM	Gamma-butyrobetaine dioxygenase Gamma-butyrobetaine, 2-oxoglutarate dioxygenase Gamma-butyrobetaine hydroxylase	44550	5825482	139030
GLUCOSE-6-PHOSPHATE ISOMERASE	METABOLISM	Gamma-BBH	62830	46485440	295907
GLUTATHIONE TRANSFERASE (EC 2.5.1.18) PSI	DETOXIFICATION	Glucose phosphate isomerase	3544	92300	84221
GLUTATHIONE TRANSFERASE OMEGA 1	DETOXIFICATION	Glutathione transferase (EC 2.5.1.18) psi	27670	12585231	55147
GLYCEROL-3-PHOSPHATE ACYL TRANSFERASE, MITOCHONDRIA	MITOCHONDRIA	Glutathione transferase omega 1	93710	8393466	51468
GLYCINE N-METHYL TRANSFERASE	PROT MOD	Glycerol-3-phosphate acyltransferase, mitochondrial precursor GPAT	32420	6137382	19169
GROWTH FACTOR RECEPTOR-BOUND PROTEIN 2	SIGNALING	Glycine N-methyltransferase	25210	77539774	29315
GUANIDINOACETATE N-METHYL TRANSFERASE	METABOLISM	Growth factor receptor bound protein 2	22590	30750124	196203
GUANINE DEAMINASE	METABOLISM	Guanidinoacetate N-methyltransferase	51020	9910706	42862
GUANINE NUCLEOTIDE-BINDING PROTEIN G(I), ALPHA-2 SUBUNIT	SIGNALING	Guanine deaminase Guanine Guanine aminase Guanine aminohydrolase GAH	40500	71089913	37194
GUANINE NUCLEOTIDE-BINDING PROTEIN, ALPHA-11 SUBUNIT	SIGNALING	Guanine nucleotide binding protein alpha inhibiting 2	42030	8925964	37192
HISTIDINE AMMONIA-LYASE	METABOLISM	Guanine nucleotide-binding protein alpha-11 subunit	72280	8393522	51482
HISTIDINE TRIAD NUCLEOTIDE-BINDING PROTEIN 1	NUCLEUS	Histidine ammonia lyase	13780	34870743	82484
SMOOTH MUSCLE-SPECIFIC 17BETA-HYDROXYSTEROID DEHYD	DETOXIFICATION	Histidine triad nucleotide binding protein	34840	38494210	337296
HYPOXANTHINE-GUANINE PHOSPHORIBOSYL TRANSFERASE	METABOLISM	Hsd17b12 protein	24480	68534712	16980

IMPORTIN BETA-1 SUBUNIT	NUCLEUS	Importin beta-1 subunit Karyopherin beta-1 subunit Nuclear factor P97	97120	8393610	51498
INOSITOL 1,4,5-TRISPHOSPHATE RECEPTOR TYPE 2	CALCIUM TRANS/BIND	Inositol 1,4,5-trisphosphate receptor type 2 Type 2 inositol 1,4,5-trisphosphate receptor Type 2 InsP3 receptor IP3 receptor isoform 2 InsP3R2	307100	56508	37203
INSULIN RECEPTOR	PLASMA MB	Insulin receptor precursor IR Insulin receptor subunit alpha	156800	8393621	51500
INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN COMPLEX A	BIOSYNTHETIC CARGO	Insulin receptor subunit beta	66810	71896592	11211
INTEGRIN BETA-1	PLASMA MB	Insulin-like growth factor-binding protein complex acid labile chain precursor ALS	88490	8393636	51502
IRON-RESPONSIVE ELEMENT BINDING PROTEIN 1 (IRE-BP 1) (IRP1)	PROT SYN/FOLD	Integrin beta-1 precursor Fibronectin receptor subunit beta	98130	8394162	51607
ISCHEMIA RESPONSIVE 94 KDA PROTEIN	PROT SYN/FOLD	Integrin VLA-4 subunit beta CD29 antigen	94060	3360521	95874
KALLISTATIN	BIOSYNTHETIC CARGO	Iron-responsive element-binding protein 1 (IRE-BP 1) (Iron regulatory protein 1) (IRP1) (Ferritin repressor protein) (Aconitate hydratase) Citrate hydro-lyase Aconitase	48020	21490001	38912
DIACETYL/L-XYLULOSE REDUCTASE	METABOLISM	Ischemia responsive 94 kDa protein	25720	50400214	161241
LIM AND SH3 DOMAIN PROTEIN 1	CYTOSKELETON	Kallistatin	29970	71122452	19687
LIN-7 HOMOLOG C	SIGNALING	L-xylulose reductase XR Dicarboxyl/L-xylulose reductase	21830	59798059	29682
PHOSPHOGLYCERATE MUTASE	METABOLISM	LIM and SH3 domain protein 1 LASP-1	28830	41350889	11293
14-3-3 PROTEIN GAMMA	SIGNALING	LIN-7 homolog C LIN-7C Mammalian LIN-seven protein 3 MALS-3 Vertebrate LIN 7 homolog 3 Veil-3 protein	28300	9507245	47332
SIMILAR TO SERINE HYDROXYMETHYL TRANSFERASE 1	MITOCHONDRIA	LOC495903 protein	75370	62656183	216194
LACTOYLGLUTATHIONE LYASE	PEROXISOME	LOC495922 protein	20820	81885359	251837
PUTATIVE TRANSCRIPTION FACTOR LUZP	UNKNOWN	LRRGT00032	117200	9931329	42949
LEUKOCYTE COMMON ANTIGEN VARIANT 4 PRECURSOR	SIGNALING	Lactoylglutathione lyase Methylglyoxalase Aldoketomutase Glyoxalase I Gix I Ketone-aldehyde mutase S-D-lactoylglutathione methylglyoxal lyase	132600	56560	111680
LIPID PHOSPHATE PHOSPHOHYDROLASE 3	PROT MOD	Leucine zipper protein 1 Leucine zipper motif-containing protein	35320	45477000	82681
PLASMA GLUTAMATE CARBOXYPEPTIDASE	BIOSYNTHETIC CARGO	Lipid phosphate phosphohydrolase 3 Phosphatidic acid phosphatase 2b Phosphatidate phosphohydrolase type 2b PAP2b PAP-2b PAP2-beta Differentially expressed in rat intestine 42 Dri42	52010	7108713	62757
LONG-CHAIN-FATTY-ACID--COA LIGASE 4	METABOLISM	Liver annexin-like protein	74330	6016483	22152
MHC CLASS II TRANSACTIVATOR TYPE I	TRANSCRIPTION	Long-chain-fatty-acid--CoA ligase 4 Long-chain acyl-CoA synthetase 4 LACS 4	127300	9931450	42953
CYTOSOLIC MALATE DEHYDROGENASE	METABOLISM	MHC class II transactivator type I	36480	81861572	118982
MALEYLACETOACETATE ISOMERASE	DETOXIFICATION	Malate dehydrogenase, cytoplasmic Cytosolic malate dehydrogenase	2943	11133293	36062
MANNOSE 6-PHOSPHATE/INSULIN-LIKE GROWTH FACTOR II RECEPTOR	PLASMA MB	Maleylacetoacetate isomerase MAAI Glutathione S-transferase zeta 1 GSTZ1-1	273400	6981078	3946
PROGESTERONE RECEPTOR MEMBRANE COMPONENT 2	DETOXIFICATION	Mannose 6-phosphate/insulin-like growth factor II receptor	23400	62900631	274611

MERLIN	UNKNOWN	Merlin Moesin-ezrin-radixin-like protein Neurofibromin-2 Schwannomin	68710	32363191	124359
MITOCHONDRIAL CARNITINE/ACYL CARNITINE CARRIER PROTEIN	MITOCHONDRIA	Mitochondrial carnitine/acylcarnitine carrier protein	33150	2497984	63382
MITOCHONDRIAL CARRIER HOMOLOG 2	MITOCHONDRIA	Carnitine/acylcarnitine translocase CAC Solute carrier family 25 member 20	31460	27702070	156740
MONOCARBOXYLATE TRANSPORTER 1	PLASMA MB	Mitochondrial carrier homolog 2	53240	6981542	75090
		Monocarboxylate transporter 1 MCT 1			
MULTIDRUG RESISTANCE-ASSOCIATED PROTEIN 6	PLASMA MB	Multidrug resistance-associated protein 6 ATP-binding cassette sub-family C member 6 MRP-like protein 1 MLP-1	165000	7514016	37180
MYOSIN IB	CYTOSKELETON	Myosin Ib Myosin I alpha MMI-alpha MMIIa Myosin heavy chain myr 1	131900	56733	63042
MYOSIN HEAVY CHAIN, NONMUSCLE TYPE B	CYTOSKELETON	Myosin-10 Myosin heavy chain, nonmuscle IIb Nonmuscle myosin heavy chain IIb NMMHC IIb NMMHC-IIb Cellular myosin heavy chain, type B Nonmuscle myosin heavy chain-B NMMHC-B	229000	7381235	78051
N-ETHYLMALIMIDE SENSITIVE FACTOR	TETH/DOCK/FUS	N-ethylmaleimide sensitive factor	82650	6007811	9479
NADP-DEPENDENT LEUKOTRIENE B4 12-HYDROXYDEHYDROGENASE	DETOXIFICATION	NADP-dependent leukotriene B4 12-hydroxydehydrogenase	35720	6012071	1678
		15-oxoprostaglandin 13-reductase Dithiolethione-inducible gene 1 protein D3T-inducible gene 1 protein DIG-1			
ADP-RIBOSYLATION FACTOR 3	GTPASE	NOD-derived CD11c +ve dendritic cells cDNA, RIKEN full-length enriched library, clone:F63011217 product:ADP-ribosylation factor 3, full insert sequence	20600	57033190	20922
NA(+)/H(+) EXCHANGE REGULATORY CO-FACTOR NHE-RF2	CYTOSKELETON	Na(+)/H(+) exchange regulatory co-factor NHE-RF2	34910	13925523	78016
NCK-ASSOCIATED PROTEIN 1	UNKNOWN	Nck-associated protein 1 NAP 1 p125Nap1 Membrane-associated protein HEM-2	128900	1708980	67879
NEURAL-CADHERIN	PLASMA MB	Neural-cadherin precursor N-cadherin Cadherin-2	99690	3983131	63008
NEURONAL MYOSIN HEAVY CHAIN	CYTOSKELETON	Neuronal myosin heavy chain	231500	111999	11249
NON-MUSCLE CALDESMON	CYTOSKELETON	Non-muscle caldesmon CDM L-caldesmon	60580	6978589	3674
NUCLEOBINDIN 1 (CALNOC 1)	CALCIUM TRANS/BIND	Nucleobindin-1 precursor CALNOC Bone 63 kDa calcium-binding protein	53510	871525	60416
SIMILAR TO PEF PROTEIN WITH A LONG N-TERMINAL HYDROPHOBIC DOMAIN	UNKNOWN	PEF protein with a long N-terminal hydrophobic domain	30010	56090329	201603
T-CELL, IMMUNE REGULATOR 1, ATPASE, H+ TRANSPORTING, L	LYSOSOME	PREDICTED: T-cell, immune regulator 1, ATPase, H+ transporting, lysosomal V0 protein a isoform 3	93210	62641689	274163
VACUOLAR SORTING PROTEIN 35	TRAFFIC	PREDICTED: maternal embryonic message 3	91730	34851395	206594
H5	GTPASE	PREDICTED: peanut-like 2 (Drosophila) (predicted)	53080	62656738	223925
SIMILAR TO 6-PHOSPHOGLUCONOLACTONASE	METABOLISM	PREDICTED: similar to 6-phosphoglucuronolactonase	30820	34877556	315711

ATPASE, H+ TRANSPORTING, V1 SUBUNIT A, ISOFORM 1	LYSOSOME	PREDICTED: similar to ATPase, H+ transporting, V1 subunit A, isoform 1	68270	34869154	264901
ALDOSE REDUCTASE	METABOLISM	PREDICTED: similar to Aldose reductase (AR) (Aldehyde reductase)	35900	62648070	161456
SIMILAR TO BILIVERDIN REDUCTASE B (FLAVIN REDUCTASE (NADH))	DETOXIFICATION	PREDICTED: similar to Bivrb protein	22090	34855391	272510
SIMILAR TO MO25 PROTEIN	UNKNOWN	PREDICTED: similar to Cab39 protein	39870	34877516	314871
COACTOSIN-LIKE 1	CYTOSKELETON	PREDICTED: similar to Chain A, Solution Structure Of Coactosin-Like Protein (Cofilin Family) From Mus Musculus	22140	34851815	211193
DKFZP586A0522 PROTEIN	UNKNOWN	PREDICTED: similar to DKFZP586A0522 protein	21900	27664990	263674
SIMILAR TO ER-RESIDENT PROTEIN ERDJ5	PROT SYN/FOLD	PREDICTED: similar to ER-resident protein ERdj5	90750	34856469	269276
SIMILAR TO EPIDERMAL GROWTH FACTOR RECEPTOR PATHWAY	SIGNALING	PREDICTED: similar to Epidermal growth factor receptor pathway substrate 8-like protein 2	82280	34861230	276611
SIMILAR TO FK506-BINDING PROTEIN 38	SIGNALING	PREDICTED: similar to FK506-binding protein 38	43560	81295379	221624
SIMILAR TO PHENYLALANINE-TRNA SYNTHETASE-LIKE	PROT SYN/FOLD	PREDICTED: similar to Farsla protein	57720	66730413	312741
SIMILAR TO NADH DEHYDROGENASE (UBIQUINONE) FE-S PROTEIN	MITOCHONDRIA	PREDICTED: similar to NADH dehydrogenase (ubiquinone) Fe-S protein 5	12700	72086149	306807
PLASTIN 1 (I ISOFORM)	CYTOSKELETON	PREDICTED: similar to PLS1 protein	70390	34865784	207221
SIMILAR TO RIKEN CDNA 1810074P20	UNKNOWN	PREDICTED: similar to RIKEN cDNA 1810074P20	89590	34867100	217843
PROTEIN KIAA0103 HOMOLOG	UNKNOWN	PREDICTED: similar to RIKEN cDNA 4921531G14	34870	34866113	263127
SIMILAR TO RIKEN CDNA 9430083G14	UNKNOWN	PREDICTED: similar to RIKEN cDNA 9430083G14	29550	34881196	218419
RAB33B	GTPASE	PREDICTED: similar to Rab33B	25750	34857303	281147
R-RAS (P23)	GTPASE	PREDICTED: similar to Ras-related protein R-Ras (P23)	23910	34856057	257746
RAB43	GTPASE	PREDICTED: similar to Ras-related protein Rab	23230	81887426	161420
SIMILAR TO SMHS2 HOMOLOG	UNKNOWN	PREDICTED: similar to Smhs2 homolog	49210	34874232	266978
SIMILAR TO GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE	METABOLISM	PREDICTED: similar to glyceraldehyde-3-phosphate dehydrogenase	35260	34875521	264061
SIMILAR TO GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE	METABOLISM	PREDICTED: similar to glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) (EC 1.2.1.12) - mouse	34590	34869386	306407
CCTTHETA, THETA SUBUNIT OF THE CHAPERONIN CONTAINING	PROT SYN/FOLD	PREDICTED: similar to mKIAA0002 protein	59590	34867525	249893
MAGNESIUM DEPENDENT PHOSPHATASE -1	SIGNALING	PREDICTED: similar to magnesium-dependent phosphatase-1	18610	27700106	272326
SIMILAR TO MICROSOMAL GLUTATHIONE S-TRANSFERASE 3	DETOXIFICATION	PREDICTED: similar to microsomal glutathione S-transferase 3	16730	27678076	164232
SIMILAR TO NOVEL CELL DEATH-REGULATORY PROTEIN GRIM1	NUCLEUS	PREDICTED: similar to novel cell death-regulatory protein GRIM19	16780	27668839	160674
SIMILAR TO PROTEIN PHOSPHATASE 2C EPSILON	SIGNALING	PREDICTED: similar to protein phosphatase 1 (formerly 2C)-like	41040	34857062	230767
INORGANIC DIPHOSPHATASE	SIGNALING	PREDICTED: similar to pyrophosphatase	32770	34852506	276601
PERIPHERAL PLASMA MEMBRANE PROTEIN CASK	SIGNALING	Peripheral plasma membrane protein CASK	103300	2497510	104145
PEROXIREDOXIN 2	PEROXISOME	Calcium/calmodulin-dependent serine protein kinase Peroxiredoxin 2 (EC 1.11.1.-) (Thioredoxin peroxidase 1) (Thioredoxin- dependent peroxide reductase 1) (Thiol-specific antioxidant protein) (TSA).	21800	34849738	269931

PEROXISOMAL ASSEMBLY PROTEIN PEX3	PEROXISOME	Peroxisomal biogenesis factor 3 Peroxin-3 Peroxisomal assembly protein PEX3	42210	8926847	12072
CALM	COAT	Phosphatidylinositol-binding clathrin assembly protein Clathrin assembly lymphoid myeloid leukemia protein rCALM	69290	44888251	60461
PHOSPHOENOLPYRUVATE CARBOXYKINASE, CYTOSOLIC [GTP]	METABOLISM	Phosphoenolpyruvate carboxykinase, cytosolic [GTP]	69420	51859488	144363
PHOSPHOGLYCERATE KINASE, TESTIS SPECIFIC	METABOLISM	Phosphoenolpyruvate carboxylase PEPCK-C	44540	56585024	340218
PHOSPHOSERINE AMINOTRANSFERASE	METABOLISM	Phosphoglycerate kinase 1	40590	29692074	249141
PIRIN	NUCLEUS	Phosphoserine aminotransferase	32180	57164095	304888
PLAKOGLOBIN	CYTOSKELETON	Pirin	81780	1497985	37204
T-PLASTIN	CYTOSKELETON	Plakoglobin	70300	57381	136274
POLYMERIC-IMMUNOGLOBULIN RECEPTOR	PLASMA MB	Plastin-3 T-plastin	84800	56465	128586
MAWDBP	UNKNOWN	Polymeric-immunoglobulin receptor precursor Poly-Ig receptor	31720	19743770	33171
HSP90 CO-CHAPERONE,P23	NUCLEUS	PIGR Secretory component	18720	34862186	25274
PROSTAGLANDIN F2 RECEPTOR NEGATIVE REGULATOR PRECURSOR	SIGNALING	Prostaglandin E synthase 3 Cytosolic prostaglandin E2 synthase cPGES Telomerase-binding protein p23 Hsp90 co-chaperone Progesterone receptor complex p23 Sid 3177	98730	9507007	47252
PROTEASOME ACTIVATOR 28-ALPHA SUBUNIT	PROTEASOME/UBIQUITIN	Prostaglandin F2 receptor negative regulator precursor	28630	61098214	227267
PROTEASOME (PROSOME, MACROPAIN) SUBUNIT, BETA TYPE 1	PROTEASOME/UBIQUITIN	Prostaglandin F2-alpha receptor regulatory protein	26410	37231712	233720
26S PROTEASOME NON-ATPASE REGULATORY SUBUNIT 12	PROTEASOME/UBIQUITIN	Protease (Prosome, macropain) 28 subunit, alpha	52940	54400716	317815
PROTEASOME ACTIVATOR COMPLEX SUBUNIT 2	PROTEASOME/UBIQUITIN	Proteasome (Prosome, macropain) subunit, beta type 1	26860	8394091	51596
PROTEASOME SUBUNIT ALPHA TYPE 6	PROTEASOME/UBIQUITIN	Proteasome 26S non-ATPase subunit 12	27400	8394076	51591
PROTEASOME SUBUNIT ALPHA TYPE 7	PROTEASOME/UBIQUITIN	Proteasome subunit alpha type 6 Proteasome iota chain Macropain iota chain Multicatalytic endopeptidase complex	28330	2118151	72897
PROTEASOME SUBUNIT BETA TYPE 3	PROTEASOME/UBIQUITIN	Proteasome subunit alpha type 7 Proteasome subunit RC6-1	22960	8394082	51593
PROTEASOME SUBUNIT BETA TYPE 6	PROTEASOME/UBIQUITIN	Proteasome subunit beta type 3 Proteasome theta chain Proteasome chain 13 Proteasome component C10-II	25160	4644446	134694
DJ-1 PROTEIN	UNKNOWN	Proteasome subunit beta type 6 precursor Proteasome delta chain Macropain delta chain Multicatalytic endopeptidase complex delta chain Proteasome subunit Y Proteasome chain 5	19970	56404680	20683
NDRG1 RELATED PROTEIN NDRG2B1	SIGNALING	Protein DJ-1 Contraception-associated protein 1 Protein CAP1 Fertility protein SP22	40780	81867103	123716
PROTEIN KINASE C AND CASEIN KINASE SUBSTRATE IN NEURO	SIGNALING	Protein NDRG2 NDRG1-related protein Antidepressant-related protein ADRG123	55980	6651163	74255
PROTEIN TRANSPORT PROTEIN SEC23A	COAT	Protein kinase C and casein kinase substrate in neurons 2 protein Synaptic dynamin-associated protein II Syndapin 2 Syndapin-II Sdpl	86160	34867969	141679

PROTO-ONCOGENE C-CRK	SIGNALING	Proto-oncogene C-crk P38 Adapter molecule crk	33840	9506515	95160
PUTATIVE N-ACETYLTRANSFERASE CAMELLO 4	PROT MOD	Putative N-acetyltransferase Camello 4	24890	6651436	176270
PUTATIVE SKAP55	SIGNALING	Putative SKAP55 Src family associated phosphoprotein 2	40720	47482120	15613
INTEGRAL MEMBRANE TRANSPORT PROTEIN UST5R	UNKNOWN	Putative integral membrane transport protein	62420	19705489	161236
INTEGRAL MEMBRANE TRANSPORT PROTEIN UST4R	UNKNOWN	Putative integral membrane transport protein	62210	19705487	161235
PYRUVATE DEHYDROGENASE E1 COMPONENT BETA SUBUNIT	MITOCHONDRIA	Pyruvate dehydrogenase (Lipoamide) beta	38980	56090293	203734
PYRUVATE KINASE, ISOZYMES R/L	METABOLISM	Pyruvate kinase, isozymes R/L	62300	206213	44273
RAB4A	GTPASE	RAB4A, member RAS oncogene family	23920	6981454	75065
RAB GDI ALPHA	TRAFFIC	Rab GDP dissociation inhibitor alpha	50540	71534276	67742
RAB-RELATED GTP-BINDING PROTEIN	GTPASE	Rab-related GTP-binding protein Rab38, member of RAS oncogene family	23780	47125439	44313
RAB14	GTPASE	Ras-related protein Rab-14	23930	46577632	34567
RAB18	GTPASE	Ras-related protein Rab-18	22980	81909560	161691
RAB1B	GTPASE	Ras-related protein Rab-1B	22180	56605816	166705
RAB30	GTPASE	Ras-related protein Rab-30	23060	27678162	64372
RAB35	GTPASE	Ras-related protein Rab-35 Rab-1C GTP-binding protein RAY	23030	62900797	35585
RAB4B	GTPASE	Ras-related protein Rab-4B	23630	929830	51602
RAB8A	GTPASE	Ras-related protein Rab-8A Oncogene c-mel	23670	82592520	33705
RAB8B	GTPASE	Ras-related protein Rab-8B	23600	2500066	43492
RAP1A	GTPASE	Ras-related protein Rap-1A	20990	54114993	4747
RAP1B	GTPASE	Ras-related protein Rap-1b precursor GTP-binding protein smg p21B	20800	539995	130852
GIANTIN	TETH/DOCK/FUS	Rat GCP360	364300	7441640	124005
R-RAS2	GTPASE	Related RAS viral (R-ras) oncogene homolog 2 Predicted	23400	61740635	86161
RETINOL-BINDING PROTEIN I, CELLULAR	METABOLISM	Retinol-binding protein I, cellular Cellular retinol-binding protein CRBP	15700	809309	105581

RHO GDP-DISSOCIATION INHIBITOR 1	SIGNALING	Rho GDP dissociation inhibitor (GDI) alpha Activated spleen cDNA, RIKEN full-length enriched library, clone:F830047D12 product:Rho GDP dissociation inhibitor (GDI) alpha, full insert sequence NOD-derived CD11c +ve dendritic cells cDNA, RIKEN full-length enriched library, clone:F630116C04 product:Rho GDP dissociation inhibitor (GDI) alpha, full insert sequence NOD-derived CD11c +ve dendritic cells cDNA, RIKEN full-length enriched library, clone:F630107K12 product:Rho GDP dissociation inhibitor (GDI) alpha, full insert sequence 6 days neonate spleen cDNA, RIKEN full-length enriched library, clone:F430003F06 product:Rho GDP dissociation inhibitor (GDI) alpha, full insert sequence Activated spleen cDNA, RIKEN full-length enriched library, clone:F830101O10 product:Rho GDP dissociation inhibitor (GDI) alpha, full insert sequence 12 days embryo whole body cDNA, RIKEN full-length enriched library, clone:E970002J06 product:Rho GDP dissociation inhibitor (GDI) alpha, full insert sequence	23410	55742827	17309
S-ADENOSYLMETHIONINE SYNTHETASE ALPHA AND BETA FORM GLYCOGEN PHOSPHORYLASE	PROT MOD METABOLISM	S-adenosylmethionine synthetase alpha and beta forms SWISS-PROT:P09811 REFSEQ_NP:NP_071604 ENSEMBL:ENSRNOP00000009183 Glycogen phosphorylase, liver form	43700 97480	92483 585688	69363 104192
4-HYDROXYPHENYLPYRUVATE DIOXYGENASE	METABOLISM	SWISS-PROT:P32755 TREMBL:Q88655 REFSEQ_NP:NP_058929 ENSEMBL:ENSRNOP00000001809 4-hydroxyphenylpyruvate dioxygenase	45110	8393557	51489
ANNEXIN A2	TETH/DOCK/FUS	SWISS-PROT:Q07936-1 TREMBL:Q8R513 ENSEMBL:ENSRNOP00000013988 REFSEQ:NP_063970 annexin A2	38680	9845234	109734
MYOSIN HEAVY CHAIN, NONMUSCLE TYPE A	CYTOSKELETON	SWISS-PROT:Q62812 TREMBL:Q62704 REFSEQ_NP:NP_037326 ENSEMBL:ENSRNOP00000007398 Myosin-9	226300	967249	75000
RSLY1P	TRAFFIC	Sect1 family domain-containing protein 1 Syntaxin-binding protein 1-like 2 Vesicle transport-related protein Ra410 Sly1p	72260	9507019	47254
SELENIUM-BINDING PROTEIN	UNKNOWN	Selenium binding protein 2	52530	49256633	111519
SEPTIN 7	GTPASE	Septin-7 CDC10 protein homolog	50510	9789715	167832
SERINE (OR CYSTEINE) PROTEINASE INHIBITOR, CLADE G (C1 IN BIOSYNTHETIC CARGO	BIOSYNTHETIC CARGO	Serine (Or cysteine) proteinase inhibitor, clade G (C1 inhibitor), member 1, Angioedema, hereditary	55610	40018558	222317
SERINE/THREONINE PROTEIN PHOSPHATASE 2A, CATALYTIC SUBUNIT	SIGNALING	Serine/threonine protein phosphatase	35580	8394021	41475
SERINE/THREONINE PROTEIN PHOSPHATASE PP1-BETA CATALYTIC SUBUNIT	SIGNALING	Serine/threonine protein phosphatase PP1-beta catalytic subunit	37190	999343	4597
SERINE PROTEASE INHIBITOR 6	BIOSYNTHETIC CARGO	Similar to SP16	42300	56090431	224458
SIMILAR TO PHOSPHOLYSINE PHOSPHOHISTIDINE INORGANIC PHOSPHATE	METABOLISM	Similar to phospholysine phosphohistidine inorganic pyrophosphate phosphata 5M590	29190	57528359	221017
SODIUM/POTASSIUM-TRANSPORTING ATPASE ALPHA-1 CHAIN	PLASMA MB	Sodium/potassium-transporting ATPase alpha-1 chain precursor Sodium pump 1 Na+/K+ ATPase 1	113100	6978543	3657

SODIUM/POTASSIUM-TRANSPORTING ATPASE BETA-1 CHAIN	PLASMA MB	Sodium/potassium-transporting ATPase beta-1 chain	35230	6978549	3654
SODIUM/POTASSIUM-TRANSPORTING ATPASE BETA-3 CHAIN	PLASMA MB	Sodium/potassium-transporting ATPase subunit beta-3 Sodium/potassium-dependent ATPase beta-3 subunit ATPB-3 CD298 antigen	31830	6978553	3656
SODIUM/BILE ACID COTRANSPORTER	PLASMA MB	Solute carrier family 10, member 1	39300	8394279	11254
ORGANIC ANION TRANSPORTER K8	PLASMA MB	Solute carrier family 21 member 4	62970	19071449	198521
SOLUTE CARRIER FAMILY 21 MEMBER 3	PLASMA MB	Solute carrier organic anion transporter family member 1A1 Solute carrier family 21 member 1 Sodium-independent organic anion transporter 1 Organic anion-transporting polypeptide 1	74180	8394294	152150
SOLUTE CARRIER FAMILY 21 MEMBER 9	PLASMA MB	Solute carrier organic anion transporter family member 2B1 Solute carrier family 21 member 9 Organic anion transporter moatp 1	74210	9622206	47477
SON PROTEIN	UNKNOWN	Son protein	12550	34849639	313065
SPECTRIN ALPHA CHAIN, BRAIN	CYTOSKELETON	Spectrin alpha chain, brain	284600	62644670	3340
SPECTRIN BETA CHAIN, BRAIN 2	CYTOSKELETON	Spectrin beta chain, brain 2	271100	3550975	3158
STABILIN-2	PLASMA MB	Stabilin-2 precursor Hyaluronan receptor for endocytosis 175 kDa stabilin-2 175 kDa hyaluronan receptor for endocytosis	155900	50401220	153825
NONSPECIFIC LIPID-TRANSFER PROTEIN, MITOCHONDRIAL PRE	MITOCHONDRIA	Sterol carrier protein 2	58790	51980631	33159
N-HYDROXYARYLAMINE SULFOTRANSFERASE	PROT MOD	Sulfotransferase 1C1 N-hydroxyarylamine sulfotransferase HAST-1	35760	543420	78152
T-COMPLEX PROTEIN 1, ALPHA SUBUNIT	PROT SYN/FOLD	T-complex protein 1 subunit alpha TCP-1-alpha CCT-alpha	60360	6981642	75118
PDZ DOMAIN-CONTAINING PROTEIN (DIPHOR 1)	BIOSYNTHETIC CARGO	TREMBL:Q35234 Diphor-1	52250	2331224	80899
PROTEASOME 26S ATPASE SUBUNIT 6	PROTEASOME/UBIQUITIN	TREMBL:Q32PW9 ENSEMBL:ENSRNOP0000009649 REFSEQ:XP_214147 PREDICTED: similar to Psmc6 protein	45800	34869622	309670
3-MERCAPTOPYRUVATE SULFURTRANSFERASE	MITOCHONDRIA	Tax_id=10116 3-mercaptopyruvate sulfurtransferase	32940	62652539	13392
ADP-RIBOSYLATION FACTOR 5	GTPASE	Tax_id=10116 ADP-ribosylation factor 5	20530	56388751	10610
ATP-BINDING CASSETTE, SUB-FAMILY D, MEMBER 3	PEROXISOME	Tax_id=10116 ATP-binding cassette, sub-family D (ALD), member 3	75320	6981450	75063

ALDEHYDE DEHYDROGENASE (NAD)	METABOLISM	Tax_id=101116 Aldehyde dehydrogenase ffamily 1, subfA4	54560	91935	83139
ALCOHOL DEHYDROGENASE [NADP+]	METABOLISM	Tax_id=101116 Aldo-keto reductase ffamily 1, member A1	36510	399660	37172
AMINE OXIDASE [FLAVIN-CONTAINING] B	MITOCHONDRIA	Tax_id=101116 Amine oxidase (flavin-containing)	58390	91974	74992
ANNEXIN A1 (ANNEXIN J) (LIPCORTIN J) (CALPACTIN II) (CHROM)	TETH/DOCK/FUS	Tax_id=101116 Annexin 1	38830	6978501	3631
FATTY ACID-BINDING PROTEIN, BRAIN	PROT MOD	Tax_id=101116 Brain lipid binding protein	14860	476098	71698
COP1 COATOMER BETA' SUBUNIT	COAT	Tax_id=101116 Coatomer protein complex, subunit beta 2 (beta prime)	102600	3023522	35931
COMPLEMENT COMPONENT 5	BIOSYNTHETIC CARGO	Tax_id=101116 Complement component 5	134400	34853897	205903
CYSTEINE-RICH PROTEIN 1	UNKNOWN	Tax_id=101116 Cysteine and glycine-rich protein 1	20610	8393206	51411
DEAD BOX PROTEIN 1	PROT SYN/FOLD	Tax_id=101116 DEAD (Asp-Glu-Ala-Asp) box polypeptide 1	97470	34863163	240056
DIHYDROLIPOAMIDE BRANCHED CHAIN TRANSACYLASE E2	MITOCHONDRIA	Tax_id=101116 Dihydrolipoamide branched chain transacylase E2	53460	34859889	232730
ING.NG-DIMETHYLARGININE DIMETHYLAMINOHYDROLASE 1	METABOLISM	Tax_id=101116 Dimethylarginine dimethylaminohydrolyase 1	31430	6831527	104206
SIMILAR TO HOMOGENITISATE 1, 2-DIOXYGENASE	METABOLISM	Tax_id=101116 Ensembl_locations(Chr-bp):1-64934053 similar to homogentisate 1, 2-dioxygenase	59620	34869194	303719
SIMILAR TO LEUCINE AMINOPEPTIDASE	METABOLISM	Tax_id=101116 Ensembl_locations(Chr-bp):14-70683054 similar to leucine aminopeptidase	64550	34878080	204743
SIMILAR TO MITOGEN INDUCIBLE GENE MIG-2	UNKNOWN	Tax_id=101116 Ensembl_locations(Chr-bp):15-21359488 similar to mitogen inducible gene mig-2	95210	34869626	211833
ANNEXIN A11	TETH/DOCK/FUS	Tax_id=101116 Ensembl_locations(Chr-bp):16-1479259 similar to annexin A11	72140	34876896	205775
SIMILAR TO ALDO-KETO REDUCTASE FAMILY 1, MEMBER C12	DETOXIFICATION	Tax_id=101116 Ensembl_locations(Chr-bp):17-77022236 similar to aldo-keto reductase family 1, member C12	32180	34876320	221880
FK506-BINDING PROTEIN 1A	PROT SYN/FOLD	Tax_id=101116 Ensembl_locations(Chr-bp):3-141766859 FK506 binding protein 2	11920	501064	43461
SIMILAR TO DYSTROBREVIN B	CYTOSKELETON	Tax_id=101116 Ensembl_locations(Chr-bp):6-26565039 similar to dystrobrevin B (mDITN-B)	82140	34863056	279256
PROTEASOME SUBUNIT ALPHA TYPE 3	PROTEASOME/UBIQUITIN	Tax_id=101116 Ensembl_locations(Chr-bp):6-93096989;10-64690010 proteasome (prosome, macropain) subunit, alpha type 3	28420	8394066	45012
SIMILAR TO RIKEN CDNA 4931406C07	UNKNOWN	Tax_id=101116 Ensembl_locations(Chr-bp):8-12086308 similar to RIKEN cDNA 4931406C07	19160	34860352	266321
NUCLEAR CHLORIDE ION CHANNEL PROTEIN	NUCLEUS	Tax_id=101116 Ensembl_locations(Chr-bp):None similar to CLCP	25370	34852289	287945
SIMILAR TO INTERFERON-G INDUCED GTPASE	GTPASE	Tax_id=101116 Ensembl_locations(Chr-bp):None similar to LRG-47	44620	27670133	160756
BETAINE-HOMOCYSTEINE METHYLTRANSFERASE 2	MITOCHONDRIA	Tax_id=101116 Ensembl_locations(Chr-bp):None similar to betaine-homocysteine methyltransferase 2	46420	34861318	247159
ELONGATION FACTOR 2	PROT SYN/FOLD	Tax_id=101116 Eukaryotic translation elongation factor 2	95280	8393296	51432
EZRIN-RADIXIN-MOESIN BINDING PHOSPHOPROTEIN 50	CYTOSKELETON	Tax_id=101116 Ezrin-radixin-moesin binding phosphoprotein 50	38830	8132349	644
FRUCTOSE-1,6-BISPHOSPHATASE	METABOLISM	Tax_id=101116 Fructose-1,6-bisphosphatase 1	39610	623562	149105
GLUTATHIONE S-TRANSFERASE 5	DETOXIFICATION	Tax_id=101116 Glutathione S-transferase theta 1	27470	56265	111659
GLUTATHIONE S-TRANSFERASE P	DETOXIFICATION	Tax_id=101116 Glutathione S-transferase, pi	23440	56336	28297
GLUTATHIONE S-TRANSFERASE YRS-YRS (GST 12-12) (GLUTATH)	DETOXIFICATION	Tax_id=101116 Glutathione S-transferase, theta 2	27440	769703	3914
GUANINE NUCLEOTIDE-BINDING PROTEIN G(K), ALPHA SUBUNIT	SIGNALING	Tax_id=101116 Guanine nucleotide binding protein, alpha inhibiting G3	40520	71899	3901
NADH-UBIQUINONE OXIDOREDUCTASE 13 KDA-B SUBUNIT	MITOCHONDRIA	Tax_id=101116 NADH dehydrogenase (ubiquinone) 1 alpha subcomplex 5	13410	6981260	75004
PDZ AND LIM DOMAIN PROTEIN 1	UNKNOWN	Tax_id=101116 PDZ and LIM domain protein 1	35530	8393153	40336
PEROXIREDOXIN 6	PEROXISOME	Tax_id=101116 Peroxiredoxin 6	24820	5902791	60471

PHENYLALANINE-4-HYDROXYLASE	METABOLISM	Tax_id=10116 Phenylalanine-4-hydroxylase	51820	6981330	75026
SEC14-LIKE PROTEIN 3	UNKNOWN	Tax_id=10116 Secretory protein, 45kD	100300	34878986	235129
COMPLEMENT COMPONENT C8 GAMMA SUBUNIT	BIOSYNTHETIC CARGO	Tax_id=10116 Similar to 1700013L23Rik protein	22400	34853020	251303
SIMILAR TO GLYCEROL-3-PHOSPHATE DEHYDROGENASE 1 (SO)	METABOLISM	Tax_id=10116 Similar to 2210409H23Rik protein	47190	34866415	232409
CLATHRIN AP47 PROTEIN	COAT	Tax_id=10116 Similar to ARP47 protein - mouSe	61590	34877759	232865
ARP2/3 COMPLEX 16 KDA SUBUNIT (P16-ARC) (ACTIN-RELATED)	CYTOSKELETON	Tax_id=10116 Similar to ARP2/3 complex 16 kDa Subunit (P16-ARC) (Actin-related protein 2/3 complex Subunit 5)	34540	34880487	318590
SIMILAR TO ATP SULFURYLASE/APS KINASE 2	METABOLISM	Tax_id=10116 Similar to ATP Sulfurylase/APS kinase 2	80990	34862615	219419
SIMILAR TO ATP-BINDING CASSETTE TRANSPORTER SUB-FAMILY	PLASMA MB	Tax_id=10116 Similar to ATP-binding cassette transporter Sub-family A member 6	191500	34875258	278570
SIMILAR TO ATP-BINDING CASSETTE TRANSPORTER SUB-FAMILY	PLASMA MB	Tax_id=10116 Similar to ATP-binding cassette transporter Sub-family A member 8a	187500	34875001	209410
SIMILAR TO ACTIN MONOMER-BINDING PROTEIN	CYTOSKELETON	Tax_id=10116 Similar to Actin monomer-binding protein	204100	34866518	244260
SIMILAR TO ALANYL--TRNA SYNTHETASE (ALANINE--TRNA LIGASE)	PROT SYN/FOLD	Tax_id=10116 Similar to Alanyl-tRNA Synthetase (Alanine--tRNA ligase) (AlaRS)	108200	34851760	253193
SIMILAR TO ALPHA-2 CATENIN	CYTOSKELETON	Tax_id=10116 Similar to Alpha-2 catenin (Alpha-catenin related protein) (Alpha N-catenin)	51430	34856264	258471
ARMADILLO REPEAT GENE DELETED IN VELO-CARDIO-FACIAL SYNDROME	CYTOSKELETON	Tax_id=10116 Similar to Arvcl protein	122400	34869778	246886
SIMILAR TO CG32774-PA	UNKNOWN	Tax_id=10116 Similar to CG32774-PA	79590	34876775	221370
HC PROTEIN	BIOSYNTHETIC CARGO	Tax_id=10116 Similar to Complement C5 precursor (Hemolytic complement)	42190	34853846	242533
EPLIN	CYTOSKELETON	Tax_id=10116 Similar to Epithelial protein lost in neoplasia (mEPLIN)	94450	34868179	277610
SIMILAR TO FERM, RHOGEF AND PLECKSTRIN DOMAIN PROTEIN	UNKNOWN	Tax_id=10116 Similar to FERM, RhoGEF and pleckstrin domain protein 2	179800	34877686	293497
SIMILAR TO FERM, RHOGEF, AND PLECKSTRIN DOMAIN PROTEIN	UNKNOWN	Tax_id=10116 Similar to FERM, RhoGEF, and pleckstrin domain protein 1	23830	34876611	304176
FILAMIN, ALPHA	CYTOSKELETON	Tax_id=10116 Similar to FLJ00343 protein	279400	34881882	282403
SIMILAR TO GE36	UNKNOWN	Tax_id=10116 Similar to GE36	76150	34880541	272300
GAMMA-SOLUBLE NSF ATTACHMENT PROTEIN (GAMMA SNAP)	TETHIDOCK/FUS	Tax_id=10116 Similar to Gamma-Soluble NSF attachment protein (SNAP-gamma) (N-ethylmaleimide-Sensitive factor attachment protein, gamma)	45610	34932055	316372
IQ MOTIF CONTAINING GTPASE ACTIVATING PROTEIN 1	SIGNALING	Tax_id=10116 Similar to IQ motif containing GTPase activating protein 1	193900	34857388	242453
SIMILAR TO PLEXIN	SIGNALING	Tax_id=10116 Similar to KIAA0315	211600	34867650	248510
LEUKOTRIENE A-4 HYDROLASE	METABOLISM	Tax_id=10116 Similar to Leukotriene A-4 hydrolase (LTA-4 hydrolase) (Leukotriene A(4) hydrolase)	93570	34864937	286024
SIMILAR TO MALTASE-GLUCOAMYLASE, INTESTINAL	PLASMA MB	Tax_id=10116 Similar to Maltase-glucoamylase, intestinal	494700	34855581	199085
MYOSIN LIGHT CHAIN KINASE	SIGNALING	Tax_id=10116 Similar to Mylk protein	73330	34869218	268038
SIMILAR TO NEDD4 WW BINDING PROTEIN 4	UNKNOWN	Tax_id=10116 Similar to Nedd4 WW binding protein 4	32550	34860870	317802

PALS2-BETA SPLICE VARIANT	BIOSYNTHETIC CARGO	Tax_id=10116 Similar to PALS2-beta Splice variant	67230	34855859	233877
SIMILAR TO POTENTIAL PHOSPHOLIPID-TRANSPORTING ATPAS	UNKNOWN	Tax_id=10116 Similar to Potential phoSpolipid-transPorting ATPase IG (ATPaSe class I type 11C) (ATPaSe IQ)	131400	34881712	292511
PROTEIN TRANSPORT PROTEIN SEC24A (SEC24-RELATED PRO	COAT	Tax_id=10116 Similar to Protein transPort protein Sec24A (SEC24-related protein A)	105700	34870707	295725
MITOCHONDRIAL GLUTAMATE CARRIER 1	MITOCHONDRIA	Tax_id=10116 Similar to RIKEN cDNA 1300006L01	34660	34865173	223033
ETA: EXPRESSED IN T-CELLS AND EOSINOPHILS IN ATOPIC DE	UNKNOWN	Tax_id=10116 Similar to RIKEN cDNA 2210404D11	57560	34873697	262247
SIMILAR TO RIKEN CDNA 3110038B19	UNKNOWN	Tax_id=10116 Similar to RIKEN cDNA 3110038B19	46280	34879556	235525
SIMILAR TO RIKEN CDNA C920006C10	UNKNOWN	Tax_id=10116 Similar to RIKEN cDNA C920006C10	66760	34866542	287440
SIMILAR TO ALPHA 3 TYPE VI COLLAGEN ISOFORM 4	BIOSYNTHETIC CARGO	Tax_id=10116 Similar to RIKEN cDNA E330026B02	279300	34865864	264571
SIMILAR TO START DOMAIN CONTAINING 10; SEROLOGICALLY D	UNKNOWN	Tax_id=10116 Similar to START domain containing 10	53820	34858808	195138
CYTOPLASMIC FMRT INTERACTING PROTEIN 1	UNKNOWN	Tax_id=10116 Similar to Selective hybridizing clone	164100	34856144	203612
SIDEROFLEXIN 2	MITOCHONDRIA	Tax_id=10116 Similar to Sideroflexin 2	38820	34863716	229983
SLINGSHOT 1L	SIGNALING	Tax_id=10116 Similar to SlingShot 1	178100	34872826	271907
SPECTRIN BETA-II CHAIN, BRAIN 1 (SPECTRIN, NON-ERYTHROID	CYTOSKELETON	Tax_id=10116 Similar to Spectrin beta chain, brain 1 (Spectrin, non-erythroid beta chain 1) (Beta-II Spectrin) (Fodrin beta chain)	278400	34879632	300121
STABILIN-1	PLASMA MB	Tax_id=10116 Similar to Stabilin-1	285900	34876981	262547
SIMILAR TO STABILIN-2	PLASMA MB	Tax_id=10116 Similar to Stabilin-2	93660	34864902	206065
TRANSFERRIN RECEPTOR PROTEIN 2 (TFR2)	PLASMA MB	Tax_id=10116 Similar to Transferrin receptor protein 2 (Tfr2)	89250	34871536	315288
SIMILAR TO UROPLAKIN IA	PLASMA MB	Tax_id=10116 Similar to Uroplakin Ia (UPIa) (UPKa)	52100	34855791	301709
SIMILAR TO VINCULIN (METAVINCULIN)	CYTOSKELETON	Tax_id=10116 Similar to Vinculin (Metavinculin)	135500	34868946	268838
WAVE2	CYTOSKELETON	Tax_id=10116 Similar to WAVE2	41650	34871786	222802
SIMILAR TO BETA ACTIN	CYTOSKELETON	Tax_id=10116 Similar to actin - Hydra attenuata	13310	34871187	219221
ARP2/3 COMPLEX 34 KDA SUBUNIT	CYTOSKELETON	Tax_id=10116 Similar to actin related protein 2/3 complex Subunit 2	34350	34876797	205076
FILAMIN B, BETA	CYTOSKELETON	Tax_id=10116 Similar to actin-binding protein homolog ABP-278	284700	34869526	231012
ALDEHYDE DEHYDROGENASE 7A1	DETOXIFICATION	Tax_id=10116 Similar to aldehyde dehydrogenase family 7, member A1	57290	34879551	245155
GLYCOGEN DEBRANCHING ENZYME	METABOLISM	Tax_id=10116 Similar to amylo-1,6-glucosidase, 4-alpha-glucanotransSferaSe isoform 1	180900	34859913	208010
SIMILAR TO APOA-I	BIOSYNTHETIC CARGO	Tax_id=10116 Similar to apoA-I binding protein	78970	34857927	303449
SIMILAR TO BETA1-SYNTROPHIN	CYTOSKELETON	Tax_id=10116 Similar to beta1-Syntrophin	46920	34866568	190168
CHOREIN, VPS13P	TRAFFIC	Tax_id=10116 Similar to chorein isoform B	254800	34861677	218802
SIMILAR TO CHROMOSOME 20 OPEN READING FRAME 116	UNKNOWN	Tax_id=10116 Similar to chromosome 20 open reading frame 116	36120	34858705	275755
COPI COATOMER ALPHA SUBUNIT	COAT	Tax_id=10116 Similar to coatomer protein complex Subunit alpha	139100	34880938	293534
CORDON-BLEU RELATED 1	UNKNOWN	Tax_id=10116 Similar to cbl-related 1	135100	34854739	289448
SIMILAR TO COMPLEMENT COMPONENT 8 ALPHA SUBUNIT	BIOSYNTHETIC CARGO	Tax_id=10116 Similar to complement component 8 alpha Subunit	62090	34869994	295319
SIMILAR TO ESTERASE 10; ESTERASE D	UNKNOWN	Tax_id=10116 Similar to eSteraSe 10	42940	34874491	305590

SIMILAR TO EUKARYOTIC TRANSLATION INITIATION FACTOR 3, 3, 3	PROT SYN/FOLD	Tax_id=10116 Similar to eukaryotic translation initiation factor 3, Subunit 5 epSilon, 47kDa	35120	34858904	213255
1,4-ALPHA-GLUCAN BRANCHING ENZYME	METABOLISM	Tax_id=10116 Similar to glucan (1,4-alpha)-, branching enzyme 1	43080	34867430	216271
SIMILAR TO GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE	METABOLISM	Tax_id=10116 Similar to glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) (EC 1.2.1.12) - mouse	36190	34873236	316038
GPP130	TETH/DOCK/FUS	Tax_id=10116 Similar to golgi.phosphoprotein 4	73200	34857091	237211
SORTLIN-RELATED RECEPTOR/LDL RECEPTOR MOSAIC 11	TRAFFIC	Tax_id=10116 Similar to gp230 precursor	209000	34863171	283274
SIMILAR TO HYPOTHETICAL PROTEIN CL25084	UNKNOWN	Tax_id=10116 Similar to hypothetical protein CL25084	60710	34879636	242521
SIMILAR TO DISHEVELLED-ASSOCIATED ACTIVATOR OF MORPHOGENESIS	UNKNOWN	Tax_id=10116 Similar to hypothetical protein E130308H01	113900	34865376	283779
TETRA TRICOPEPTIDE REPEAT DOMAIN 17	UNKNOWN	Tax_id=10116 Similar to hypothetical protein FLJ10890	138100	34856577	278036
UNKNOWN ZINC FINGER PROTEIN	UNKNOWN	Tax_id=10116 Similar to hypothetical protein FLJ20531	57240	34871405	217607
SIMILAR TO HYPOTHETICAL PROTEIN FLJ20627	UNKNOWN	Tax_id=10116 Similar to hypothetical protein FLJ20627	40260	34853516	295521
SIMILAR TO UROCANATE HYDRATASE	METABOLISM	Tax_id=10116 Similar to hypothetical protein MGC37818	19860	34861397	316589
IMMUNOGLOBULIN 4G6 LIGHT CHAIN	BLOOD + OTHER CELLS	Tax_id=10116 Similar to immunoglobulin 4G6 light chain variable region	17890	34855968	195860
LYMPHOCYTE CYTOSOLIC PROTEIN 1	CYTOSKELETON	Tax_id=10116 Similar to lymphocyte cytosolic protein 1	80290	34875362	272629
P120 CATENIN ISOFORM 2B	CYTOSKELETON	Tax_id=10116 Similar to mKIAA0384 protein	101400	34856482	193681
SIMILAR TO MACROPHAGE MANNANOSE RECEPTOR	BLOOD + OTHER CELLS	Tax_id=10116 Similar to macrophage mannoSe receptor precursor	192400	34877265	296460
MELANOMA INHIBITORY ACTIVITY PROTEIN 2(MIA2)	UNKNOWN	Tax_id=10116 Similar to melanoma inhibitory activity protein 2	58930	34865264	225113
SIMILAR TO MYOSIN HEAVY CHAIN	CYTOSKELETON	Tax_id=10116 Similar to myosin heavy chain	229700	34869316	230006
SIMILAR TO O-METHYLTRANSFERASE FAMILY MEMBER (5C530)	UNKNOWN	Tax_id=10116 Similar to o-methyltransferase family member (5C530)	24490	34868938	291365
P53 INDUCIBLE PROTEIN	SIGNALING	Tax_id=10116 Similar to p53 inducible protein	164400	34870680	289228
PEPTIDYLPROLYL ISOMERASE D (CYCLOPHILIN D)	PROT SYN/FOLD	Tax_id=10116 Similar to peptidylprolyl isomerase D (cyclophilin D)	69130	34873471	283106
SIMILAR TO PROBABLE NOCTURNIN PROTEIN	TRANSCRIPTION	Tax_id=10116 Similar to probable nocturnin protein	16650	34861866	309047
SIMILAR TO PROTEIN 4.1, P4.1 - MOUSE	UNKNOWN	Tax_id=10116 Similar to protein 4.1, P4.1 - mouse	105500	34871764	306783
PROTEIN RAKC	DETOXIFICATION	Tax_id=10116 Similar to protein RAKC	41260	34876322	249119
PROTEIN TYROSINE PHOSPHATASE, RECEPTOR TYPE, D ISOFORM	SIGNALING	Tax_id=10116 Similar to protein tyrosine phosphatase, receptor type, D isoform 3 precursor	203600	34869007	215340
TALIN 2	CYTOSKELETON	Tax_id=10116 Similar to talin 2	284500	34864297	199727
SIMILAR TO TESTIS PROTEIN TEX15	UNKNOWN	Tax_id=10116 Similar to testis protein TEX15	282400	34866738	211558
TRANSGELIN 2 (PREDICTED)	UNKNOWN	Tax_id=10116 Similar to transgelin 2	29970	34880944	266044
SIMILAR TO TRANSTHYRETIN (4L369)	BIOSYNTHETIC CARGO	Tax_id=10116 Similar to transthyretin (4L369)	16010	34861187	199559
SIMILAR TO UBIQUITIN LIGASE E3 ALPHA-II	PROTEASOME/UBIQUITIN	Tax_id=10116 Similar to ubiquitin ligase E3 alpha-II	175300	34874398	274677
SIMILAR TO URIDINDIPHOSPHOGLUCOSEPYROPHOSPHORYLASE	METABOLISM	Tax_id=10116 Similar to uridindiphosphoglucose pyrophosphorylase 2	89950	34879163	225159
SIMILAR TO VILIN-LIKE PROTEIN	CYTOSKELETON	Tax_id=10116 Similar to villin-like protein	99190	34866628	253969
SIMILAR TO ZINC FINGER PROTEIN, SUBFAMILY 1A, 4	TRANSCRIPTION	Tax_id=10116 Similar to zinc finger protein, subfamily 1A, 4	64460	34862217	313581
CHAPERONIN DELTA SUBUNIT	PROT SYN/FOLD	Tax_id=10116 T-complex protein 1, delta subunit	58100	52000745	166356
TROPOMYOSIN ALPHA 4 CHAIN	CYTOSKELETON	Tax_id=10116 Tropomyosin 4	28510	763182	44422
14-3-3 PROTEIN BETA/ALPHA	SIGNALING	Tax_id=10116 Tyrosine 3-monooxygenase/TrypTophan 5-monooxygenase acTivaTion proTein, betaT polypepTide	28050	9507243	47331
VESICLE-ASSOCIATED MEMBRANE PROTEIN-ASSOCIATED PROTEIN B	TRAFFIC	Tax_id=10116 Vesicle-associated membrane protein-associated protein B	26920	4240464	57726

TELOMERASE PROTEIN COMPONENT 1	NUCLEUS	Telomerase protein component 1 rTLP1 Telomerase-associated protein 1 Telomerase protein 1 p240 p230 p80 telomerase homolog	291700	47606056	169376
FARNESYL PYROPHOSPHATE SYNTHETASE	PROT MOD	Testis-specific farnesyl pyrophosphate synthetase	40800	37590777	78213
TISSUE-TYPE TRANSGLUTAMINASE	SIGNALING	Tissue-type transglutaminase	76930	9507185	47311
TORSINA	PROT SYN/FOLD	TorsinA	37980	22651450	188125
TRIOSEPHOSPHATE ISOMERASE	METABOLISM	Tpi1 protein	26720	38512111	340135
RHOA	GTPASE	Transforming protein RhoA precursor	21780	47605935	76408
P24 GAMMA 3	TRAFFIC	Transmembrane emp24 domain-containing protein 5 precursor	26140	62287552	228279
TROPOMYOSIN ISOFORM 6 SIMILAR TO TRANSLATIONALLY CONTROLLED TUMOR PROTEIN	CYTOSKELETON UNKNOWN	Tropomyosin 5 Tumor protein, translationally-controlled 1 2 days neonate thymus thymic cells cDNA, RIKEN full-length enriched library, clone:E430014B07 product:tumor protein, translationally-controlled 1, full insert sequence CRL-1722 L5178Y-R cDNA, RIKEN full-length enriched library, clone:I730061H02 product:tumor protein, translationally-controlled 1, full insert sequence TIB-55 BB88 cDNA, RIKEN full-length enriched library, clone:I730042C17 product:tumor protein, translationally-controlled 1, full insert sequence 13 days pregnant adult female placenta cDNA, RIKEN full-length enriched library, clone:I530012I04 product:tumor protein, translationally-controlled 1, full insert sequence 5 days embryo whole body cDNA, RIKEN full-length enriched library, clone:IDC0031O13 product:tumor protein, translationally-controlled 1, full insert sequence Bone marrow macrophage cDNA, RIKEN full-length enriched library, clone:I830086J22 product:tumor protein, translationally-controlled 1, full insert sequence Bone m	28950 19460	9653293 6877712	93198 38212
ISOCHORISMATASE DOMAIN CONTAINING 1	UNKNOWN	Tumor-related protein Adult male medulla oblongata cDNA, RIKEN full-length enriched library, clone:6330565A20 product:Tumor-related protein (Hypothetical protein), full insert sequence Isochorismatase domain containing 1	32030	62664482	8904
SIMILAR TO UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX	MITOCHONDRIA	Ubiquinol-cytochrome c reductase complex 11 kDa protein, mitochondrial precursor Mitochondrial hinge protein Cytochrome C1, nonheme 11 kDa protein Complex III subunit VIII	10420	62511137	277765
BENDLESS PROTEIN	PROTEASOME/UBIQUITIN	Ubiquitin-conjugating enzyme E2 N Ubiquitin-protein ligase N Ubiquitin carrier protein N Bendless-like ubiquitin-conjugating enzyme	17120	77417616	12328
UBIQUITIN-CONJUGATING ENZYME E2 VARIANT 1 UEV-1 CROC-1	PROTEASOME/UBIQUITIN	Ubiquitin-conjugating enzyme E2 variant 1 NOD-derived CD11c +ve dendritic cells cDNA, RIKEN full-length enriched library, clone:F630102O04 product:ubiquitin-conjugating enzyme E2 variant 1, full insert sequence Adult inner ear cDNA, RIKEN full-length enriched library, clone:F930043P20 product:ubiquitin-conjugating enzyme E2 variant 1, full insert sequence	16350	62660106	82822
URINARY PROTEIN 1	BIOSYNTHETIC CARGO	Urinary protein 1 precursor RUP-1 Liver regeneration-related protein LRRG05	10960	6537316	37481
UROPORPHYRINOGEN DECARBOXYLASE	DETOXIFICATION	Uroporphyrinogen decarboxylase	40450	5524747	44446

VACUOLAR ATP SYNTHASE SUBUNIT B, BRAIN ISOFORM	LYSOSOME	Vacuolar ATP synthase subunit B, brain isoform V-ATPase B2 subunit Vacuolar proton pump B isoform 2 Endomembrane proton pump 58 kDa subunit	56550	55716047	55432
SEPTIN 2	GTPASE	Vascular endothelial cell specific protein 11 Septin 2	41590	51858574	140635
R, VAMP A	TETH/DOCK/FUS	Vesicle-associated membrane protein-associated protein A VAMP-associated protein A VAMP-A VAP-A 33 kDa Vamp-associated protein VAP-33	27270	90110085	318845
R, SEC22	TETH/DOCK/FUS	Vesicle-trafficking protein SEC22b SEC22 vesicle-trafficking protein-like 1	24740	71043604	41516
GUANINE NUCLEOTIDE-BINDING PROTEIN G-S ALPHA	SIGNALING	XLalphas protein	78230	14161099	72067
XANTHINE DEHYDROGENASE/OXIDASE	PEROXISOME	Xanthine dehydrogenase/oxidase	146300	2144323	80445
ADAPTOR-RELATED PROTEIN COMPLEX 2 ALPHA 2 SUBUNIT	COAT	adaptor protein complex AP-2, alpha 2 subunit [Rattus norvegicus]	104000	55729	37177
CAMP-DEPENDENT PROTEIN KINASE C ALPHA	SIGNALING	CAMP-dependent protein kinase, alpha-catalytic subunit (PKA C-alpha)	40620	125207	168211
DIHYDROPYRIMIDINASE	METABOLISM	dihydropyrimidinase	56830	3122039	78138
SEC24C	COAT	hypothetical protein XP_223792	115600	34868956	241419
KYNURININASE	METABOLISM	kynureninase (L-kynurenine hydrolase)	52450	3913969	157223
LIN-7 PROTEIN	SIGNALING	lin-7-Ba [Rattus norvegicus]	19930	3885830	158790
LYSOZYME HOMOLOG AT-2, BINE - RAT (FRAGMENTS)	BIOSYNTHETIC CARGO	lysozyme homolog AT-2, bone - rat (fragments)	3164	539969	130837
PROTEASOME SUBUNIT BETA TYPE 4	PROTEASOME/UBIQUITIN	proteasome (prosome, macropain) subunit, beta type 4	25790	310214	78104
CLATHRIN ADAPTIN-2, ALPHA 1	COAT	similar to Adapter-related protein complex 2 alpha 1 subunit (Alpha-adaptin A) (Adaptor protein complex AP-2 alpha-1 subunit) (Clathrin assembly protein complex 2 alpha-A large chain) (100 kDa coated vesicle protein A) (Plasma membrane adaptor HA2/... [Rattus norvegicus])	104000	34856047	219335
SIMILAR TO ASPARAGINYL-TRNA SYNTHETASE, CYTOPLASMIC	PROT SYN/FOLD	similar to Asparaginyl-tRNA synthetase, cytoplasmic (Asparagine--tRNA ligase) (AsnRS)	64130	34932063	238208
CCTETA, ETA SUBUNIT OF THE CHAPERONIN CONTAINING TCP-	PROT SYN/FOLD	similar to CCTeta, eta subunit of the chaperonin containing TCP-1 (CCT1)	59660	27712178	161408
SIMILAR TO CG4241-PA	MITOCHONDRIA	similar to CG4241-PA	35190	34877651	194839
RSEC6	TRAFFIC	similar to Exocyst complex component Sec6 (rSec6)	72270	34855314	276511
SIMILAR TO GLUTATHIONE S-TRANSFERASE, THETA 3	DETOXIFICATION	similar to Glutathione S-transferase, theta 3	44270	34852398	225794
SIMILAR TO GROWTH-ARREST-SPECIFIC PROTEIN 2 (GAS-2)	SIGNALING	similar to Growth-arrest-specific protein 2 (GAS-2)	61200	34856132	300461
SIMILAR TO HYPOTHETICAL PROTEIN KIAA0379	UNKNOWN	similar to Hypothetical protein KIAA0379	41000	27732065	190049
N-ACETYLNEURAMINIC ACID SYNTHASE (SIALIC ACID SYNTHASE)	METABOLISM	similar to N-acetylneuraminic acid synthase (sialic acid synthase)	40050	27714479	225772
NEUROBLASTOMA AMPLIFIED GENE, NAG	UNKNOWN	similar to Nag-pending protein	60300	34863173	240310
PROTEIN TRANSPORT PROTEIN SEC23B (SEC23-RELATED PROTEIN B)	COAT	similar to Protein transport protein Sec23B (SEC23-related protein B) [Rattus norvegicus]	86090	34858849	260808
RAB6	GTPASE	similar to RAB6, member RAS oncogene family	26610	34859460	290450
SIMILAR TO RIKEN CDNA 4732463H20	UNKNOWN	similar to RIKEN cDNA 4732463H20 [Rattus norvegicus]	52510	34857987	192449
SIMILAR TO RAS GTPASE-ACTIVATING-LIKE PROTEIN IQGAP2	GTPASE	similar to Ras GTPase-activating-like protein IQGAP2	140700	34853552	197696
SIMILAR TO RAS SUPPRESSOR PROTEIN 1 (RSU-1) (RSP-1)	GTPASE	similar to Ras suppressor protein 1 (Rsu-1) (RSP-1)	34760	34877253	195351
SH3-BINDING DOMAIN GLUTAMIC ACID-RICH PROTEIN LIKE	UNKNOWN	similar to Sh3bgrl protein	12800	27706424	198937
UNNAMED PROTEIN PRODUCT2	UNKNOWN	similar to Swiprosin 1	26760	72255531	250786
SIMILAR TO WDR1 PROTEIN	UNKNOWN	similar to Wdr1 protein [Rattus norvegicus]	48550	34878397	292693
TUBULIN ALPHA CHAIN	CYTOSKELETON	similar to alpha-tubulin	45060	34872542	234717
SIMILAR TO ANCIENT UBIQUITOUS 46 KDA PROTEIN AUP46 PRE	UNKNOWN	similar to ancient ubiquitous 46 kDa protein AUP46	46200	34856277	205068
SIMILAR TO CDNA SEQUENCE BC003251	UNKNOWN	similar to cDNA sequence BC003251	53180	34871409	253866

SIMILAR TO ENDONUCLEASE G	NUCLEUS	similar to endonuclease G	32270	77917570	273385
SIMILAR TO SEPTIN 10	UNKNOWN	similar to ethanol induced 6	15850	27686507	168139
SIMILAR TO GLUCAN (1,4-ALPHA-), BRANCHING ENZYME 1; DNA	PROT MOD	similar to glucan (1,4-alpha-), branching enzyme 1; DNA segment, Chr.16, ERATO D01 536, expressed	32500	34867432	299017
SIMILAR TO GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE	METABOLISM	similar to glyceraldehyde-3-phosphate dehydrogenase	36450	34852715	210943
SIMILAR TO GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE	METABOLISM	similar to glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) (EC 1.2.1.12) - mouse	27870	27699577	156654
HEAT SHOCK PROTEIN 105 KDA ALPHA	PROT SYN/FOLD	similar to heat shock protein 105 kDa alpha	82350	34870188	195465
RAN BINDING PROTEIN 1	NUCLEUS	similar to hypothetical protein A	36410	34869364	193827
MYOSIN HEAD DOMAIN CONTAINING 1	CYTOSKELETON	similar to hypothetical protein FLJ22865	33930	34872934	263071
LIVER REGENERATION-RELATED PROTEIN	DETOXIFICATION	similar to liver regeneration-related protein LRRG07 [Rattus norvegicus]	35400	34876593	287183
LYSOSOMAL APYRASE-LIKE 1	LYSOSOME	similar to lysosomal apyrase-like 1	49290	34874388	305737
SIMILAR TO OSTEOCLAST STIMULATING FACTOR 1	UNKNOWN	similar to osteoclast stimulating factor 1	34620	34880977	297002
CREG	TRANSCRIPTION	similar to placenta-specific 3 isoform 1; pregnancy-associated plasma protein-E; pregnancy-associated plasma preproprotein-A2	33400	34877698	287571
SIMILAR TO PROLINE DEHYDROGENASE; PRODH	METABOLISM	similar to proline dehydrogenase; PRODH	12130	27665096	305160
RICK	SIGNALING	similar to receptor-interacting protein 2	60780	34867073	242276
UBIQUITIN-ACTIVATING ENZYME E1 1	PROTEASOME/UBIQUITIN	similar to ubiquitin-protein ligase (EC 6.3.2.19) E1 - mouse	123600	34933178	317625
ER-GOLGI INTERMEDIATE COMPARTMENT 32 KDA PROTEIN (ER)	TRAFFIC	unknown	35170	34870624	209664
SEC13 LIKE 1 PROTEIN	COAT	1110003H02Rik protein	35550	55741774	161453
45 KDA CALCIUM-BINDING PROTEIN	CALCIUM TRANS/BIND	45 kDa calcium-binding protein precursor Cab45 Stromal cell-derived factor 4 SDF-4	42080	21263446	64664
ARF-RELATED PROTEIN	GTPASE	ARF-related protein 1	22660	2492928	52078
ALPHA-1,6-MANNOSYL-GLYCOPROTEIN 2-BETA-N-ACETYLGLUC	PROT MOD	Alpha-1,6-mannosyl-glycoprotein 2-beta-N-acetylglucosaminyltransferase Mannoside acetylglucosaminyltransferase 2 N-glycosyl-oligosaccharide-glycoprotein N-acetylglucosaminyltransferase II Beta-1,2-N-acetylglucosaminyltransferase II GNT-II GlcNAc-T II	51110	747976	60482
ALPHA 2,6-SIALYL TRANSFERASE	PROT MOD	CMP-N-acetylneuraminate-beta-galactosamide-alpha-2,6-sialyltransferase Beta-galactoside alpha-2,6-sialyltransferase Alpha 2,6-ST Sialyltransferase 1 ST6Gal I	46730	204255	141534
SIMILAR TO DIHYDROLIPOAMIDE DEHYDROGENASE	METABOLISM	Dihydrolipoamide dehydrogenase E3 component of pyruvate dehydrogenase complex, 2-oxo-glutarate complex, branched chain keto acid dehydrogenase complex	54040	40786469	253447
MG160	PROT MOD	Golgi apparatus protein 1 precursor Golgi sialoglycoprotein MG-160 E-selectin ligand 1 ESL-1	133600	8393450	51465
TRANS-GOLGI PROTEIN GMX33	TETH/DOCK/FUS	Golgi phosphoprotein 3 Coat-protein GPP34 Trans-Golgi protein GMX33	33780	50400215	54283
GRASP55_65	TETH/DOCK/FUS	Golgi reassembly stacking protein 2	47310	56090463	288023
GOLGI AUTOANTIGEN, GOLGIN SUBFAMILY A MEMBER 2	TETH/DOCK/FUS	Golgin subfamily A member 2 Cis-Golgi matrix protein GM130	111400	7513936	169300
HYDROXYMETHYL GLUTARYL-COA LYASE, MITOCHONDRIAL	MITOCHONDRIA	Hydroxymethylglutaryl-CoA lyase, mitochondrial precursor HMG-CoA lyase HL 3-hydroxy-3-methylglutarate-CoA lyase	34190	38511566	68742

ACYL-COA DEHYDROGENASE, MEDIUM-CHAIN SPECIFIC, MITOCHONDRIAL PRECURSOR MCAD	MITOCHONDRIA	Medium-chain specific acyl-CoA dehydrogenase, mitochondrial precursor MCAD	46560	8392833	11499
ORNITHINE AMINOTRANSFERASE, MITOCHONDRIAL PRECURSOR	MITOCHONDRIA	Ornithine aminotransferase	24280	206706	44333
GOLGI PERIPHERAL MEMBRANE PROTEIN P65	TETHIDOCK/FUS	PREDICTED: hypothetical protein XP_579439	47620	62654450	225098
SIMILAR TO DNA SEGMENT, CHR 1, ERATO DOI 578, EXPRESSED	UNKNOWN	PREDICTED: similar to F-box protein 28	41070	27681007	262592
GOLGIN-84	TETHIDOCK/FUS	PREDICTED: similar to RET-1l	82410	34867583	302868
P24 ALPHA 2	TRAFFIC	PREDICTED: similar to Transmembrane emp24 protein transport domain containing 4	26120	27697481	170045
SIMILAR TO BETA-1,3-GALACTOSYLTRANSFERASE-6	PROT MOD	PREDICTED: similar to beta-1,3-galactosyltransferase-6	37150	27663478	210144
SIMILAR TO HTGN29 PROTEIN; KERATINOCYTES ASSOCIATED T	UNKNOWN	PREDICTED: similar to chromosome 5 open reading frame 15	28260	34870715	258441
GALACTOSYL GALACTOSYLXYLOSYLPROTEIN 3-BETA-GLUCURON	PROT MOD	PREDICTED: similar to glucuronosyltransferase I	37070	34861582	228888
POLYPEPTIDE N-ACETYL GALACTOSAMINYLTRANSFERASE	PROT MOD	Polypeptide N-acetylgalactosaminyltransferase 1 Protein-UDP acetylgalactosaminyltransferase 1 UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase 1 Polypeptide GalNAc transferase 1 GalNAc-T1 pp-GaNTase 1 Polypeptide N-acetylgalactosaminyltransferase 1 soluble form	64230	1709559	68735
R, YKT6	TETHIDOCK/FUS	Prenylated SNARE protein Ykt6p	22310	2642348	78131
RAB5C	GTPASE	Ras-related protein Rab-5C	23430	27689505	161834
SIMILAR TO GOLGI RESIDENT PROTEIN GCP60	TETHIDOCK/FUS	Tax_id=10116 Golgi resident protein GCP60	60480	51315724	295490
KERATIN 18	LIKELY CONTAMINANTS	Tax_id=10116 Keratin 18	16960	587518	108078
SIMILAR TO GOLGI MEMBRANE PROTEIN GP73	TRAFFIC	Tax_id=10116 Similar to Golgi phosphoprotein 2	54350	34873592	231145
SIMILAR TO EH DOMAIN BINDING PROTEIN 1	TRAFFIC	Tax_id=10116 Similar to KIAA0903-like protein	120900	34879170	275605
DVL-BINDING PROTEIN DAPLE	SIGNALING	Tax_id=10116 Similar to KIAA1509 protein	212500	34867549	239536
SIMILAR TO N-ACETYLGALACTOSAMINYLTRASNFRASE IVB	PROT MOD	Tax_id=10116 Similar to N-acetylglucosaminyltrasnfrase IVb	71740	34870693	194890
SIMILAR TO RIKEN CDNA 4931400A14	UNKNOWN	Tax_id=10116 Similar to RIKEN cDNA 4931400A14	231900	34878255	296181
MANNOSIDASE 1-BETA	PROT MOD	Tax_id=10116 Similar to alpha-mannoSidaSe	45930	34860045	248855
SIMILAR TO COMPLEMENT COMPONENT FACTOR H	BIOSYNTHETIC CARGO	Tax_id=10116 Similar to complement component factor h	43820	34880509	275354
TYROSYLPROTEIN SULFOTRANSFERASE-1	PROT MOD	Tpst1 protein	42140	76779364	241393
INTEGRAL MEMBRANE PROTEIN, TMP21-I (P23) DELTA 1	TRAFFIC	Transmembrane emp24 domain-containing protein 10 precursor Transmembrane protein Tmp21 21 kDa transmembrane-trafficking protein	24860	62906896	60418
CDA14 (PTX1)	TRAFFIC	similar to EST AA408438	42480	27713571	204725
ARP1 ACTIN-RELATED PROTEIN 1 ALPHA	CYTOSKELETON	similar to ARP1 actin-related protein 1 homolog A; actin-related protein 1 alpha; actin-related protein 1 homolog A (yeast); Arp1 contractin alpha; Arp1 contractin alpha	62980	34865224	222641
SIMILAR TO GAL BETA 1,3GALNAC ALPHA 2,3-SIALYLTRANSFERASE	PROT MOD	similar to Gal beta 1,3GalNAc alpha 2,3-sialyltransferase [Rattus norvegicus]	26160	34866546	201171
NOVEL MEMBER OF P24 FAMILY (TIRAP3B)	TRAFFIC	similar to Hypothetical protein CGI-109 precursor	20460	34879511	204384
MANNOSIDASE 2, ALPHA 1	PROT MOD	similar to Man9-mannosidase	57920	34852693	212806
SIMILAR TO CYTOKERATIN	LIKELY CONTAMINANTS	similar to cytokeratin	46840	34873210	190628

SIMILAR TO ENDO B CYTOKERATIN	LIKELY CONTAMINANTS	similar to endo B cytokeratin	42970	34860580	202236
GBF1	TRAFFIC	similar to golgi-specific brefeldin A-resistance guanine nucleotide exchange factor 1	208100	34865240	218235
SIMILAR TO HEPARAN SULFATE 2-SULFOTRANSFERASE	PROT MOD	similar to heparan sulfate 2-sulfotransferase	41850	34860929	259411
SIMILAR TO MKIAA0493 PROTEIN	UNKNOWN	similar to mkIAA0493 protein	110800	34866514	234949
0610009E20RIK PROTEIN	UNKNOWN	18-day embryo whole body cDNA, RIKEN full-length enriched library, clone:1110037P24 product:weakly similar to RE35789p Novel protein Hypothetical protein Tmem93 18-day embryo whole body cDNA, RIKEN full-length enriched library, clone:1110001A14 product:hypothetical protein, full insert sequence	12020	27673882	98449
2'-5'-OLIGOADENYLATE SYNTHETASE 1	SIGNALING	2'-5'-oligoadenylate synthetase 1 (2-5')oligo(A) synthetase 1 2-5A synthetase 1	41670	56790	134570
Qb. MEMBRIN	TETH/DOCK/FUS	27 kDa Golgi SNARE protein	24650	2316090	55435
7-DEHYDROCHOLESTEROL REDUCTASE	DETOXIFICATION	7-dehydrocholesterol reductase 7-DHC reductase Sterol delta-7-reductase	54160	81882109	9067
MHC CLASS I RT1.AB HEAVY CHAIN PRECURSOR	PLASMA.MB	A1b	39310	5912594	104733
AB2-305	UNKNOWN	Ab2-305	43570	33086580	166327
ABHYDROLASE DOMAIN CONTAINING 6	UNKNOWN	Abhydrolase domain containing 6	38310	56090644	309746
ACETYL-COA TRANSPORTER	PROT MOD	Acetyl-coenzyme A transporter 1 AT-1 Acetyl-CoA transporter Solute carrier family 33 member 1	61190	7768591	104182
ACYLCOA:CHOLESTEROL ACYLTRANSFERASE 2	PROT MOD	AcylCoA:Cholesterol Acyltransferase 2	60480	21392392	207716
SURFEIT LOCUS PROTEIN 4 (ERV29)	TRAFFIC	Adult male lung cDNA, RIKEN full-length enriched library, clone:1200010H03 product:surfet gene 4, full insert sequence Bone marrow macrophage cDNA, RIKEN full-length enriched library, clone:1830028A12 product:surfet gene 4, full insert sequence Bone marrow macrophage cDNA, RIKEN full-length enriched library, clone:1830026D09 product:surfet gene 4, full insert sequence Bone marrow macrophage cDNA, RIKEN full-length enriched library, clone:1830012C22 product:surfet gene 4, full insert sequence Blastocyst blastocyst cDNA, RIKEN full-length enriched library, clone:11C0027M05 product:surfet gene 4, full insert sequence	30380	76443685	60957
ALL-TRANS-13,14-DIHYDRORETINOL SATURASE	DETOXIFICATION	All-trans-retinol 13,14-reductase precursor All-trans-13,14-dihydroretinol saturase RetSat RMT-7	67530	81871478	27636
AMINE OXIDASE [FLAVIN-CONTAINING] A	MITOCHONDRIA	Amine oxidase [flavin-containing] A	58870	8170739	101201
BAP31 (B-CELL RECEPTOR-ASSOCIATED PROTEIN 31)	TRAFFIC	B-cell receptor-associated protein 31	27910	51948420	139656

IGD B-CELL RECEPTOR-ASSOCIATED PROTEIN (BAP) 29	TRAFFIC	B-cell receptor-associated protein BAP29	28230	55742817	243481
Qc, RBET1	TETH/DOCK/FUS	BET1 homolog Golgi vesicular membrane-trafficking protein p18 rBET1	13230	9506425	35327
BAX INHIBITOR-1	SIGNALING	Bax inhibitor-1	26230	456209	23763
BCL-2 INHIBITOR OF TRANSCRIPTION,	MITOCHONDRIA	Bcl-2 inhibitor of transcription	19530	62078455	215739
BRAIN PROTEIN 44	UNKNOWN	Brain protein 44 0-44 protein	14260	730248	80419
CHOLINE/ETHANOLAMINEPHOSPHOTRANSFERASE 1	PROT MOD	Choline/ethanolamine phosphotransferase 1	46500	56090333	264754
CORE BINDING FACTOR BETA SUBUNIT CYTOCHROME P450 4A1	TRANSCRIPTION DETOXIFICATION	Core binding factor beta Cytochrome P450 4A1	21520 58210	61557239 56047	2681 51420
CYTOCHROME P450 4A8	DETOXIFICATION	Cytochrome P450 4A12 CYP1A12 CYP1A8 P450-KP1 P450-PP1	58520	203757	78089
CYTOCHROME P450 4F1	DETOXIFICATION	Cytochrome P450 4F1 CYP1F1 P450-A3	59870	9665225	134595
CYTOCHROME P450 4F4	DETOXIFICATION	Cytochrome P450 4F4 CYP1F4	60050	27465575	80281
CYTOCHROME P450 4F6	DETOXIFICATION	Cytochrome P450 4F6 CYP1F6	61540	23463319	127733
CYTOCHROME P450 51A1	DETOXIFICATION	Cytochrome P450 51A1	56710	870754	3732
CYTOCHROME P450 2A1	DETOXIFICATION	Cytochrome P450 11A1 (Hepatic steroid hydroxylase 11A1) gene	56000	51980506	126566
CYTOCHROME P450 2T1	DETOXIFICATION	Cytochrome P450 monooxygenase CYP2T1	55880	19705467	161231
CYTOCHROME P450 2J3	DETOXIFICATION	Cytochrome P450, family 2, subfamily j, polypeptide 9	57970	59809108	125135
CYTOCHROME P450 20A1	DETOXIFICATION	Cytochrome P450, family 20, subfamily A, polypeptide 1	52000	40786491	337678
CYTOCHROME P450 2A2	DETOXIFICATION	Cytochrome P450, subfamily 2A, polypeptide 1	56350	6978741	3727
CYTOCHROME B5	DETOXIFICATION	Cytochrome b5	10800	6980893	3890
CYTOCHROME B5, MITOCHONDRIAL ISOFORM	MITOCHONDRIA	Cytochrome b5 outer mitochondrial membrane isoform precursor	16260	48735409	32875
CYTOCHROME C OXIDASE POLYPEPTIDE VB, MITOCHONDRIAL	MITOCHONDRIA	Cytochrome c oxidase polypeptide Vb, mitochondrial precursor VIA*	13910	53237117	21518
CYTOCHROME OXIDASE SUBUNIT II	MITOCHONDRIA	Cytochrome c oxidase subunit 2	25940	5835181	98989
CYTOCHROME C OXIDASE SUBUNIT IV ISOFORM 1, MITOCHONDRIAL	MITOCHONDRIA	Cytochrome c oxidase subunit 4 isoform 1, mitochondrial precursor Cytochrome c oxidase subunit IV isoform 1 COX IV-1	19510	8393180	63740
DAD1 (DEFENDER AGAINST CELL DEATH 1)	PROT MOD	Cytochrome c oxidase polypeptide IV DAD1 protein	12500	48428847	13029
DELTA-5 DESATURASE	PROT MOD	Delta-5 desaturase	52470	16758190	60408

DELTA-6 FATTY ACID DESATURASE	METABOLISM	Delta-6 fatty acid desaturase Fatty acid desaturase 2	52380	7513959	36810
DERLIN-1 (DEGRADATION IN ENDOPLASMIC RETICULUM PROTEIN 15.6)	PROT SYN/FOLD	Derlin-1 Degradation in endoplasmic reticulum protein 1 Derl1-like protein 1	28830	62652445	119910
SIMILAR TO NEURONAL PROTEIN 15.6	UNKNOWN	ENSEMBL:ENSRNOP00000011183 REFSEQ:XP_216785 PREDICTED: similar to neuronal protein 15.6	17630	27669100	192375
ELECTRON TRANSFERRING FLAVOPROTEIN, DEHYDROGENASE	MITOCHONDRIA	Electron transfer flavoprotein-ubiquinone oxidoreductase, mitochondrial precursor ETF-QO ETF-ubiquinone oxidoreductase ETF dehydrogenase Electron-transferring-flavoprotein dehydrogenase	68200	52000614	258013
ESTRADIOL 17 BETA-DEHYDROGENASE 2	DETOXIFICATION	Estradiol 17-beta-dehydrogenase 2 17-beta-HSD 2 17-beta-hydroxysteroid dehydrogenase 2	41970	3334165	68349
GLYCEROL-3-PHOSPHATE DEHYDROGENASE, MITOCHONDRIAL	MITOCHONDRIA	Glycerol-3-phosphate dehydrogenase, mitochondrial precursor GPD-M GPDH-M	80970	6980978	3907
HEME OXYGENASE 2	DETOXIFICATION	Heme oxygenase 2 HO-2	35760	501035	68743
GLUCOSE-6-PHOSPHATASE	METABOLISM	Hypothetical protein	40560	58477247	71440
MG87 PROTEIN	UNKNOWN	Hypothetical protein MG87 MOCO sulphurase C-terminal domain containing 2	38250	38511548	161253
SIMILAR TO NADH-UBIQUINONE OXIDOREDUCTASE B14.5B SUBUNIT	MITOCHONDRIA	Hypothetical protein Nduf2	14360	57164133	164223
SIMILAR TO RIKEN CDNA 1810020E01	UNKNOWN	Hypothetical protein RGD1305677	21660	58585236	209082
SIMILAR TO RIKEN CDNA 1810014L12	UNKNOWN	Hypothetical protein Tmem97	20950	56605746	300133
IMPLANTATION-ASSOCIATED PROTEIN	UNKNOWN	Implantation-associated protein precursor IAP	37990	6016303	128379
IODOTYROSINE DEHALOGENASE PROTEIN	UNKNOWN	Iodotyrosine dehalogenase 1 precursor IYD-1	32850	81882575	258458
KINESIN-LIKE PROTEIN KIF15	CYTOSKELETON	Kinesin-like protein KIF15	159600	31745148	166145
L-GULONOLACTONE OXIDASE	METABOLISM	L-gulonolactone oxidase	50610	204150	104163
RETINOL DEHYDROGENASE 11 (PREDICTED)	DETOXIFICATION	LRRGT00111	44780	62650915	238730
P34 PROTEIN	PROT SYN/FOLD	Leucine-rich repeat-containing protein 59 Protein p34	34870	81910029	152512
LOW MOLECULAR MASS UBIQUINONE-BINDING PROTEIN	PROTEASOME/UBIQUITIN	Low molecular mass ubiquinone-binding protein	9849	68341999	311481
LYSOSOMAL ACID PHOSPHATASE	LYSOSOME	Lysosomal acid phosphatase precursor LAP	48320	8392842	144356
LYSOSOMAL MEMBRANE GLYCOPROTEIN 1; LYSOSOMAL ASSOCIATED PROTEIN 1	LYSOSOME	Lysosome-associated membrane glycoprotein 1 precursor	43970	6981144	3967
LYSOSOMAL MEMBRANE GLYCOPROTEIN-TYPE B	LYSOSOME	Lysosome-associated membrane glycoprotein 2 precursor	43130	205169	44157
SIMILAR TO MESENCHYMAL STEM CELL PROTEIN DSCD75	UNKNOWN	Mesenchymal stem cell protein DSCD75	23750	56090359	259160
MID-1-RELATED CHLORIDE CHANNEL 2	PLASMA MB	Mid-1-related chloride channel 2	57430	17736804	16130

MITOCHONDRIAL DICARBOXYLATE CARRIER	MITOCHONDRIA	Mitochondrial dicarboxylate carrier Solute carrier family 25 (Mitochondrial carrier; dicarboxylate transporter), member 10	31450	51859428	140375
MONOGLYCERIDE LIPASE	METABOLISM	Monoglyceride lipase MGL	33500	79158553	76966
MYOSIN VIIA	CYTOSKELETON	Myosin VIIA	251100	23618899	217296
N-ACYLSPHINGOSINE AMIDOHYDROLASE (ACID CERAMIDASE)	PROT MOD	N-acylsphingosine amidohydrolase 1	44440	40254747	338609
RE70703P-LIKE PROTEIN	MITOCHONDRIA	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 11 NADH-ubiquinone oxidoreductase subunit B14.7	14850	52000746	204895
NADH-CYTOCHROME B5 REDUCTASE	DETOXIFICATION	Complex I-B14.7 C1-B14.7 NADH-cytochrome b5 reductase	34170	38303959	69488
SIMILAR TO HYPOTHETICAL PROTEIN COX4AL	UNKNOWN	Neighbor of Cox4 Predicted	23410	62665359	215440
NICASTRIN	PROT MOD	Nicastrin precursor	78400	37081094	116574
SIMILAR TO HYPOTHETICAL PROTEIN MGC18837	UNKNOWN	PREDICTED: hypothetical protein XP_217094	21180	27719651	278444
LANOSTEROL SYNTHASE	METABOLISM	PREDICTED: hypothetical protein XP_579502	83280	62665770	317748
SIMILAR TO PEROXISOME BIOGENESIS FACTOR 16	PEROXISOME	PREDICTED: peroxisome biogenesis factor 16 (predicted)	38600	62645408	235341
SIMILAR TO 3,5-CYCLIC-GMP PHOSPHODIESTERASE; ROD PHOSPHODIESTERASE BETA SUBUNIT	SIGNALING	PREDICTED: similar to 3,5-cyclic-GMP phosphodiesterase; rod phosphodiesterase beta subunit	98490	34875832	283891
RECEPTOR-TRANSPORTING PROTEIN 4 (28 KDA INTERFERON R	UNKNOWN	PREDICTED: similar to 5830458K16Rik protein	27750	34869300	246358
ALPHA-1,3-MANNOSYLTRANSFERASE ALG2	PROT MOD	PREDICTED: similar to Alg2 protein	47320	62648970	161589
SIMILAR TO CLEFT LIP AND PALATE ASSOCIATED TRANSMEMBR	PLASMA MB	PREDICTED: similar to C1ptm1 protein	75280	27676422	265343
SIMILAR TO CYSTEINE-RICH WITH EGF-LIKE DOMAINS 1	UNKNOWN	PREDICTED: similar to Cysteine-rich with EGF-like domains 1	45700	81170413	208169
SIMILAR TO INTERFERON-INDUCIBLE GTPASE	GTPASE	PREDICTED: similar to MGC108823 protein	48270	67846046	244814
SIMILAR TO MANNOSE-P-DOLICHOL UTILIZATION DEFECT 1	UNKNOWN	PREDICTED: similar to Mannose-P-dolichol utilization defect 1	26550	27673096	252753
SIMILAR TO NADH DEHYDROGENASE	MITOCHONDRIA	PREDICTED: similar to NADH dehydrogenase	15640	27660847	304373
SIMILAR TO NADH DEHYDROGENASE (UBIQUINONE) 1 BETA SUB	MITOCHONDRIA	PREDICTED: similar to NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 5	21660	34856800	235872
SIMILAR TO NADH DEHYDROGENASE (UBIQUINONE) 1 BETA SUB	MITOCHONDRIA	PREDICTED: similar to NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 7	16570	34851467	298146
26S PROTEASOME NON-ATPASE REGULATORY SUBUNIT 2	PROTEASOME/UBIQUITIN	PREDICTED: similar to Proteasome 26S non-ATPase subunit 2	100200	72255509	255113
RAB5A	GTPASE	PREDICTED: similar to RAB5B protein	34900	34862219	218278
RAB9-LIKE PROTEIN	GTPASE	PREDICTED: similar to RAB9B; member RAS oncogene family	22720	34881545	240722
SIMILAR TO RIKEN CDNA 1500009M05	UNKNOWN	PREDICTED: similar to RIKEN cDNA 1500009M05	15290	27696857	235838
PREDICTED E3 UBIQUITIN LIGASE	UNKNOWN	PREDICTED: similar to Zinc finger protein 364 (Rabring 7)	33870	34858089	298059
SIMILAR TO CATHEPSIN 1 PRECURSOR	LYSOSOME	PREDICTED: similar to cathepsin 1 precursor	40980	27681673	266171
SIMILAR TO FOLLICULAR LYMPHOMA VARIANT TRANSLOCATION	UNKNOWN	PREDICTED: similar to follicular lymphoma variant translocation 1	36040	34878781	198248

SIMILAR TO AAQ88810	UNKNOWN	PREDICTED: similar to hypothetical protein	26440	34856654	302143
SIMILAR TO HYPOTHETICAL PROTEIN FLJ20254	UNKNOWN	PREDICTED: similar to hypothetical protein FLJ20254	76570	34863014	234260
ILVB (BACTERIAL ACETOLACTATE SYNTHASE)-LIKE ISOFORM 1;	MITOCHONDRIA	PREDICTED: similar to ilvB (bacterial acetolactate synthase)-like	68020	34862359	299827
SIMILAR TO KERATIN COMPLEX 2, BASIC, GENE 7	LIKELY CONTAMINANTS	PREDICTED: similar to keratin complex 2, basic, gene 7	50810	34868200	246071
UNKNOWN3	UNKNOWN	PREDICTED: similar to leucine rich repeat containing 27	17070	34861166	264583
ATP-BINDING CASSETTE, SUB-FAMILY D (ALD), MEMBER 1	MITOCHONDRIA	PREDICTED: similar to mALDP	81940	34881747	306584
SIMILAR TO MITOCHONDRIAL INNER MEMBRANE TRANSLOCASE	MITOCHONDRIA	PREDICTED: similar to mitochondrial inner membrane translocase component Tim17b	18380	34933423	256607
SIMILAR TO HYPOTHETICAL PROTEIN MGC40107	UNKNOWN	PREDICTED: similar to novel protein of unknown function (DUF423) family member	11780	27672946	240868
SIMILAR TO PROTEIN TYROSINE PHOSPHATASE-LIKE PROTEIN 1	SIGNALING	PREDICTED: similar to protein tyrosine phosphatase-like (proline instead of catalytic arginine), member b	15720	34882969	201524
SIMILAR TO SEVEN TRANSMEMBRANE DOMAIN PROTEIN	UNKNOWN	PREDICTED: similar to seven transmembrane domain protein	25290	84042519	227176
TETRATRICOPEPTIDE REPEAT PROTEIN 11	UNKNOWN	PREDICTED: similar to tetratricopeptide repeat domain 11	16990	94711371	171146
UBIQUINOL-CYTOCHROME C REDUCTASE BINDING PROTEIN	MITOCHONDRIA	PREDICTED: similar to ubiquinol-cytochrome c reductase binding protein	13560	34866011	293181
SIMILAR TO NON-CANONICAL UBIQUITIN CONJUGATING ENZYME 1	PROTEASOME/UBIQUITIN	PREDICTED: similar to ubiquitin-conjugating enzyme E2, J1	30880	34867116	250662
ZMPSTE24 METALLOPROTEINASE	PROT MOD	PREDICTED: similar to zinc metalloproteinase, STE24 homolog	54850	34870924	288219
PHOSPHATIDYLETHANOLAMINE N-METHYLTRANSFERASE	PROT MOD	Phosphatidylethanolamine N-methyltransferase	22490	6981348	69787
PHOSPHOINOSITIDE PHOSPHATASE SAC1	PROT MOD	Phosphoinositide phosphatase SAC1	67040	62654523	60561
CHLORIDE ION PUMP-ASSOCIATED 55 KDA PROTEIN	PEROXISOME	Prelycysteine oxidase precursor Chloride ion pump-associated 55 kDa protein	56290	62286984	68714
PROSTAGLANDIN G/H SYNTHASE 1 PRECURSOR	BIOSYNTHETIC CARGO	Prostaglandin G/H synthase 1 precursor	69030	603052	103863
LYRIC	UNKNOWN	Protein LYRIC Lysine-rich CEACAM1 co-isolated protein	63970	56748899	118984
PROTEIN TRANSPORT PROTEIN SEC61 BETA SUBUNIT	PROT SYN/FOLD	Metastasis adhesion protein Metadherin	9988	27714473	161564
GLUCOSE-6-PHOSPHATASE, TRANSPORT PROTEIN 1	METABOLISM	Protein transport protein SEC61 beta subunit	46310	3929215	78079
RAB21	GTPASE	RAB21, member RAS oncogene family	24160	51948448	311263
RAB9A	GTPASE	RAB9, member RAS oncogene family	22870	16758200	60413

SELENOPROTEIN T	UNKNOWN	RIKEN cDNA 2810407C02 gene	15840	62643492	13862
MHC CLASS I RT1.AW3 PROTEIN	PLASMA MB	RT1A1(F)protein	39250	1483574	42127
RAB11A	GTPASE	Ras-related protein Rab-11A Rab-11	24390	55249677	41486
RAB11B	GTPASE	Ras-related protein Rab-11B	24490	9837357	19693
GTP-BINDING PROTEIN RAB13	GTPASE	Ras-related protein Rab-13	22900	46577668	169821
RAT MHC CLASS I CELL SURFACE ANTIGEN MRNA PRECURSOR	PLASMA MB	Rat MHC class I cell surface antigen mRNA, precursor	42090	420280	44652
UTROPHIN	CYTOSKELETON	Rattus norvegicus utrophin	391100	6981696	75129
SIDEROFLEXIN 3	MITOCHONDRIA	Sideroflexin-3	35430	8650526	55276
BRAIN SIGMA RECEPTOR	PLASMA MB	Sigma 1 receptor Opioid receptor, sigma 1	25270	6434855	78339
ZINC FINGER PROTEIN 183	UNKNOWN	Similar to RIKEN cDNA 2810428C21	38330	62339353	305856
RAB5	GTPASE	Small GTP-binding protein rab5	23610	3309068	177419
SOLUTE CARRIER FAMILY 12 MEMBER 5	PLASMA MB	Solute carrier family 12 member 5 Electroneutral potassium-chloride cotransporter 2 K-Cl cotransporter 2 Neuronal K-Cl cotransporter Furosemide-sensitive K-Cl cotransporter rKCC2	123600	27151682	161230
SQUALENE MONOOXYGENASE	DETOXIFICATION	Squalene monooxygenase Squalene epoxidase SE	64020	8394354	137571
CYTOCHROME P450 8B1	DETOXIFICATION	Sterol 12-alpha hydroxylase	57520	4587057	129969
3-BETA-HYDROXYSTEROID-DELTA(8),DELTA(7)-ISOMERASE	DETOXIFICATION	Sterol 8-isomerase	26740	8388884	140632
STERYL-SULFATASE	DETOXIFICATION	Steryl-sulfatase precursor Steroid sulfatase Steryl-sulfate sulfohydrolase Arylsulfatase C ASC	62680	6981598	75108
SULFATED GLYCOPROTEIN 1	BIOSYNTHETIC CARGO	Sulfated glycoprotein 1 precursor	61120	92782	75055
SYNAPTOTAGMIN III	TETHIDOCK/FUS	Synaptotagmin III	63340	14210270	19552
TAPASIN	PROT SYN/FOLD	Tapasin Tap-binding protein	50040	46237539	140838
ARYLACETAMIDE DEACETYLASE	DETOXIFICATION	Tax_id=10116 ArylAcetAmide deAcetylAse	45690	8347733	5958
LYSOSOME MEMBRANE PROTEIN II	LYSOSOME	Tax_id=10116 CD36 antigen (collagen type I receptor, thrombospondin receptor)-like 2	54090	38197654	157248
GTP-BINDING REGULATORY PROTEIN ALPHA-13 CHAIN - MOUSE	SIGNALING	Tax_id=10116 Ensembl_locations(Chr-bp):10-98947600 similar to GTP-binding regulatory protein alpha-13 chain - mouse	45080	34875240	194129
IFN-ALPHA RESPONSIVE TRANSCRIPTION FACTOR	TRANSCRIPTION	Tax_id=10116 Ensembl_locations(Chr-bp):15-33756303 similar to interferon stimulated gene factor 3 gamma	42060	27700390	263143
3 BETA-HYDROXYSTEROID DEHYDROGENASE TYPE III	DETOXIFICATION	Tax_id=10116 Hydroxy-delta-5-steroid deHydrogenase, 3 beta and steroid delta-isomerase	42210	6981050	3937
HYPOTHETICAL PROTEIN XP_224972	UNKNOWN	Tax_id=10116 HypoHetical protein XP_224972	34770	34879125	285270
PROTEIN FAM34A	UNKNOWN	Tax_id=10116 HypoHetical protein XP_341172	45130	34881421	311586

PEROXISOMAL MEMBRANE PROTEIN 2	PEROXISOME	Tax_Id=10116 Peroxisomal membrane Protein 2	22580	585703	11779
SIMILAR TO 1-ACYLGLYCEROL-3-PHOSPHATE O-ACYLTRANSFERASE	PROT MOD	Tax_Id=10116 Similar to 1-acylglycerol-3-phosphate O-acyltransferase 2	31100	34853099	274486
24-DEHYDROCHOLESTEROL REDUCTASE	DETOXIFICATION	Tax_Id=10116 Similar to 24-dehydrocholesterol reductase	78850	34869959	290771
ARL6IP2	UNKNOWN	Tax_Id=10116 Similar to ARL6IP2	79450	34861996	265779
ATP-BINDING CASSETTE TRANSPORTER ABCG3 (1)	UNKNOWN	Tax_Id=10116 Similar to ATP-binding cassette transporter ABCG3	95680	34876022	243111
SIMILAR TO ATP-BINDING CASSETTE TRANSPORTER ABCG3 (2)	UNKNOWN	Tax_Id=10116 Similar to ATP-binding cassette transporter ABCG3	67490	34879726	242256
SIMILAR TO ARGININE-TRNA-PROTEIN TRANSFERASE 1	PROT SYN/FOLD	Tax_Id=10116 Similar to Arginine-tRNA-protein transferase 1	51870	34859415	229620
SIMILAR TO BC013491 PROTEIN	UNKNOWN	Tax_Id=10116 Similar to BC013491 protein	76140	34856101	235741
SIMILAR TO CG7744-PA	UNKNOWN	Tax_Id=10116 Similar to CG7744-PA	73420	27662674	304800
SIMILAR TO DNA SEGMENT, CHR 16, BRIGHAM & WOMENS GENETICS 1547 EXPRESSED	UNKNOWN	Tax_Id=10116 Similar to DNA Segment, Chr 16, Brigham & Women's Genetics 1547 expressed	98700	34869279	294937
SIMILAR TO DNA-BINDING PROTEIN RFX1	TRANSCRIPTION	Tax_Id=10116 Similar to DNA-binding protein RFX1	109200	34851453	226741
SIMILAR TO DUB-1	PROTEASOME/UBIQUITINATION	Tax_Id=10116 Similar to DUB-1	82370	34859762	228869
DELTA(14)-STEROL REDUCTASE (C-14 STEROL REDUCTASE) (STEROL REDUCTASE)	DETOXIFICATION	Tax_Id=10116 Similar to Delta(14)-sterol reductase (C-14 sterol reductase) (sterol C14-reductase) (Delta14-SR) (Transmembrane 7 Superfamily member 2) (Another new gene 1) (Putative sterol reductase SR-1)	46050	34861496	283602
SIMILAR TO DNAJ (HSP40) HOMOLOG, SUBFAMILY B, MEMBER 1	PROT SYN/FOLD	Tax_Id=10116 Similar to DnaJ (Hsp40) homolog, Subfamily B, member 12	40330	34882652	201409
DOWN SYNDROME CELL ADHESION MOLECULE DSCAML1	CYTOSKELETON	Tax_Id=10116 Similar to Down Syndrome cell adhesion molecule DSCAML1	211000	34863302	224702
SIMILAR TO FLJ00354 PROTEIN	UNKNOWN	Tax_Id=10116 Similar to FLJ00354 protein	155900	34861517	210125
HERC2	TRAFFIC	Tax_Id=10116 Similar to Herc2	542900	34856238	254063
SIMILAR TO HYPOTHETICAL PROTEIN 5031404N19	UNKNOWN	Tax_Id=10116 Similar to Hypothetical protein 5031404N19	336600	34867996	239621
SIMILAR TO HOLOCENTRIC CHROMOSOME BINDING PROTEIN P	CYTOSKELETON	Tax_Id=10116 Similar to Hypothetical protein KIAA0056	130300	34860470	247233
SIMILAR TO HYPOTHETICAL PROTEIN KIAA0152	UNKNOWN	Tax_Id=10116 Similar to Hypothetical protein KIAA0152	26440	34872654	268830
INTEGRIN BETA-2 PRECURSOR (CELL SURFACE ADHESION GLYCOPROTEIN)	CYTOSKELETON	Tax_Id=10116 Similar to Integrin beta-2 precursor (Cell surface adhesion glycoprotein S LFA-1/CR3/CD11b, 95 beta-Subunit) (CD18) (Complement receptor C3 beta-Subunit)	84530	34852369	241188
SIMILAR TO KIAA0303	UNKNOWN	Tax_Id=10116 Similar to KIAA0303	247700	34853530	229044
SIMILAR TO KIAA0980 PROTEIN	UNKNOWN	Tax_Id=10116 Similar to KIAA0980 protein	221500	34858955	230119
SIMILAR TO YEAST NOT1 PROTEIN	UNKNOWN	Tax_Id=10116 Similar to KIAA1007 protein	262700	34851212	247833
SIMILAR TO UBIQUITIN SPECIFIC PROTEASE 36	PROTEASOME/UBIQUITINATION	Tax_Id=10116 Similar to KIAA1453 protein	119600	34875569	239514

SELENOPROTEIN I	PROT MOD	Tax_Id=10116 Similar to KIAA1724 protein	43370	34863046	197285
SIMILAR TO KIAA2019 PROTEIN	UNKNOWN	Tax_Id=10116 Similar to KIAA2019 protein	887700	34935525	217059
SIMILAR TO M-PHASE PHOSPHOPROTEIN 9; M PHASE PHOSPHO (MYC ANTAGONIST)	SIGNALING	Tax_Id=10116 Similar to M-phaSe phoSphoProtein 9	48800	34872316	229197
MNT (MYC ANTAGONIST)	TRANSCRIPTION	Tax_Id=10116 Similar to Myc antagoniSt Mnt	73510	34872745	286820
NOD3	UNKNOWN	Tax_Id=10116 Similar to NOD3	118900	34868757	253799
SIMILAR TO PLU1	UNKNOWN	Tax_Id=10116 Similar to PLU1	129000	34880236	194762
DNA-BINDING PROTEIN PROLACTIN REGULATORY ELEMENT BINDING	TRANSCRIPTION	Tax_Id=10116 Similar to Prolactin regulatory element-binding protein	45370	34863006	293599
SIMILAR TO RIKEN CDNA 0610008C08	UNKNOWN	Tax_Id=10116 Similar to RIKEN cDNA 0610008C08	18820	34880585	277830
COILED-COIL-HELIX-COILED-COIL-HELIX DOMAIN CONTAINING 3	UNKNOWN	Tax_Id=10116 Similar to RIKEN cDNA 0610041L09	37560	34855114	227312
SIMILAR TO RIKEN CDNA 1110007C09	UNKNOWN	Tax_Id=10116 Similar to RIKEN cDNA 1110007C09	22850	34874030	191708
SIMILAR TO ACYL-COA BINDING PROTEIN DOMAIN 5	UNKNOWN	Tax_Id=10116 Similar to RIKEN cDNA 1300014E15	74920	34877442	203301
SIMILAR TO RIKEN CDNA 1810063B07 GENE	UNKNOWN	Tax_Id=10116 Similar to RIKEN cDNA 1810063B07 gene	31470	34868966	280249
SIMILAR TO RIKEN CDNA 2610318K02	UNKNOWN	Tax_Id=10116 Similar to RIKEN cDNA 2610318K02	17320	34856650	238667
CYTochrome P450 NA2	DETOXIFICATION	Tax_Id=10116 Similar to RIKEN cDNA 4732474A20 gene	70120	34862810	190227
SIMILAR TO RIKEN CDNA 4930539I12	UNKNOWN	Tax_Id=10116 Similar to RIKEN cDNA 4930539I12	25260	34932978	295383
SIMILAR TO ARL6IP2	UNKNOWN	Tax_Id=10116 Similar to RIKEN cDNA 5730596K20	61690	34861548	267475
TCTA	UNKNOWN	Tax_Id=10116 Similar to RIKEN cDNA 9130410M22	23060	34932902	287769
SIMILAR TO RIKEN CDNA C330023F11	UNKNOWN	Tax_Id=10116 Similar to RIKEN cDNA C330023F11	105000	34881052	274975
SIMILAR TO RIKEN CDNA E330009P21 GENE	UNKNOWN	Tax_Id=10116 Similar to RIKEN cDNA E330009P21 gene	67850	34866429	300320
SLC26A9 ANION TRANSPORTER/EXCHANGE	PLASMA MB	Tax_Id=10116 Similar to Solute carrier family 26, member 9	150000	34879705	268665
SUPT6H	UNKNOWN	Tax_Id=10116 Similar to Supt6h	203400	34872813	219162
TATA BOX BINDING PROTEIN ASSOCIATED FACTOR 148	TRANSCRIPTION	Tax_Id=10116 Similar to TAFI48 protein	28070	34881098	248521
SIMILAR TO TAFI140 PROTEIN	PROT SYN/FOLD	Tax_Id=10116 Similar to TAFI140 protein	85530	34876351	313782
SIMILAR TO WD REPEAT MEMBRANE PROTEIN	UNKNOWN	Tax_Id=10116 Similar to WD repeat membrane protein	148000	34877378	284704
SIMILAR TO AXONEMAL HEAVY CHAIN DYNEIN TYPE 3	CYTOSKELETON	Tax_Id=10116 Similar to axonemal heavy chain dynein type 3	258100	34860087	203193
SIMILAR TO BREAKPOINT CLUSTER REGION PROTEIN	NUCLEUS	Tax_Id=10116 Similar to breakpoint cluSter region protein	177200	34852435	289382
CELL PROLIFERATION RELATED PROTEIN CAP	NUCLEUS	Tax_Id=10116 Similar to bromodomain-containing protein BRD4 Short variant	159800	34862361	292562
SIMILAR TO CDNA SEQUENCE BC017158	UNKNOWN	Tax_Id=10116 Similar to cDNA Sequence BC017158	51280	34859365	318242
SIMILAR TO DOLICHYL-PHOSPHATE BETA-GLUCOSYLTRANSFERASE	PROT MOD	Tax_Id=10116 Similar to dolichyl-phoSPhate beta-glucoSyltranSferaSe-like	47020	34856938	304061
SIMILAR TO EEA1	TRAFFIC	Tax_Id=10116 Similar to endoSomal protein	204800	34864971	310739
STOMATIN	PLASMA MB	Tax_Id=10116 Similar to erythrocyte band 7 integral membrane protein, protein 7.2B, Stomatin	61240	34853860	265569

LIPOMA HMGIC FUSION PARTNER-LIKE 2 (LHFPL2)	UNKNOWN	Tax_Id=10116 Similar to expreSSed Sequence A1447312	40980	34853130	301089
CYTOCHROME P450 4V3	DETOXIFICATION	Tax_Id=10116 Similar to family 4 cytochrome P450	66360	34878473	250367
SIMILAR TO GROUP XIII SECRETED PHOSPHOLIPASE A2	BIOSYNTHETIC CARGO A2	Tax_Id=10116 Similar to group XIII Secreted phoSpholipaSe A2	25660	34882179	272967
SIMILAR TO HISTIDYL-TRNA SYNTHETASE-LIKE UNKNOWN PROTEIN (1)	PROT SYN/FOLD UNKNOWN	Tax_Id=10116 Similar to hIstIdyl-TRNA Synthetase-like	82680	34878791	223302
SIMILAR TO SMILE PROTEIN	UNKNOWN	Tax_Id=10116 Similar to hypothetical protein	97420	34861994	213193
		Tax_Id=10116 Similar to hypothetical protein	103500	34864996	301836
SIMILAR TO HYPOTHETICAL PROTEIN BC002942	UNKNOWN	Tax_Id=10116 Similar to hypothetical protein BC002942	96350	34867679	290052
SIMILAR TO HYPOTHETICAL PROTEIN FLJ14681	UNKNOWN	Tax_Id=10116 Similar to hypothetical protein FLJ14681	65310	34858680	304442
SIMILAR TO HYPOTHETICAL PROTEIN FLJ21820	UNKNOWN	Tax_Id=10116 Similar to hypothetical protein FLJ21820	32850	34863103	317090
SIMILAR TO HYPOTHETICAL PROTEIN FLJ32934	UNKNOWN	Tax_Id=10116 Similar to hypothetical protein FLJ32934	110800	34858139	294206
RAB13	GTPASE	Tax_Id=10116 Similar to hypothetical protein MGC23920	24660	34869196	243905
SIMILAR TO HYPOTHETICAL PROTEIN MGC26706	UNKNOWN	Tax_Id=10116 Similar to hypothetical protein MGC26706	19680	34880064	228294
SIMILAR TO INNER MEMBRANE PROTEIN, MITOCHONDRIAL (MITOCHONDRIAL (mitofilin))	MITOCHONDRIA	Tax_Id=10116 Similar to inner membrane protein, mitochondrial (mitofilin)	82360	34855983	247605
SIMILAR TO NUCLEOLAR TRANSCRIPTION FACTOR 1	TRANSCRIPTION	Tax_Id=10116 Similar to methyl-CpG binding domain protein 3 like protein 2	82120	34860516	220741
SIMILAR TO NEUROBLASTOMA-AMPLIFIED PROTEIN	UNKNOWN	Tax_Id=10116 Similar to neuroblaStoma-amplified protein	163800	34863169	193119
SIMILAR TO NICOTINAMIDE NUCLEOTIDE TRANSHYDROGENASE	MITOCHONDRIA	Tax_Id=10116 Similar to nicotinamide nucleotide tranShydrogenaSe	120200	34854180	202296
CYTOCHROME P450 NA1	DETOXIFICATION	Tax_Id=10116 Similar to oxySterol 2alpha-hydroxylase	61430	34874781	201379
SIMILAR TO P66 ALPHA HOMOLOG	TRANSCRIPTION	Tax_Id=10116 Similar to p66 alpha homolog	66700	34877681	207944
SIMILAR TO POLYBROMO-1D	NUCLEUS	Tax_Id=10116 Similar to polybromo-1D	197500	34876969	310191
PUTATIVE MANNOSYLTRANSFERASE	PROT MOD	Tax_Id=10116 Similar to putative mannoSyLtranSferaSe	59900	34867585	231757

SIMILAR TO PUTATIVE PROTEIN, WITH AT LEAST 6 TRANSMEMBRANE DOMAINS, OF ANCIENT ORIGIN (58.5 kD) (3N884)	UNKNOWN	Tax_id=10116 Similar to putative protein, with at least 6 transmembrane domains, of ancient origin (58.5 kD) (3N884)	65350	34865136	269355
SIMILAR TO RETINAL SHORT-CHAIN DEHYDROGENASE/REDUCTASE	DETOXIFICATION	Tax_id=10116 Similar to retinal Short-chain dehydrogenase/reductase	43630	34872444	294993
SIMILAR TO VERY LONG-CHAIN ACYL-COA SYNTHETASE HOMOLOG 1	METABOLISM	Tax_id=10116 Similar to very long-chain acyl-CoA Synthetase homolog 1	77170	34932120	234511
VANIN 1	PLASMA MB	Tax_id=10116 Vanin 1	107100	34852937	310121
TRAM1	PROT SYN/FOLD	Translocation-associated membrane protein 1	43030	81883693	275946
TRANSLOCON-ASSOCIATED PROTEIN, GAMMA SUBUNIT	PROT SYN/FOLD	Translocon-associated protein subunit gamma TRAP-gamma Signal sequence receptor subunit gamma SSR-gamma	21060	62906894	98326
MEG-2-LIKE PROTEIN	UNKNOWN	Transmembrane and coiled-coil domain-containing protein 1	21170	81882981	91768
MITSUGUMIN 23	UNKNOWN	Transmembrane protein 109 precursor Mitsugumin-23 Mg23	26240	81884639	282006
DB83 PROTEIN	UNKNOWN	Transmembrane protein 33 DB83 protein	27980	4579688	137142
FIBROUS SHEATH PROTEIN	UNKNOWN	Tsga10 interacting protein	61460	51948361	252683
TUMOR NECROSIS FACTOR RECEPTOR TYPE II	PLASMA MB	Tumor necrosis factor receptor type II	45720	16225900	143647
TYPE I HAIR KERATIN	LIKELY CONTAMINANTS	Type I hair keratin KA27	45970	62656979	230035
TYPE I HAIR KERATIN KA28	LIKELY CONTAMINANTS	Type I hair keratin KA28	45840	57012440	161846
CYTOKERATIN 17	LIKELY CONTAMINANTS	Type I keratin KA17	48120	71682170	301880
UNCHARACTERIZED HEMATOPOIETIC STEM/PROGENITOR CELL	UNKNOWN	Uncharacterized hematopoietic stem/progenitor cells protein MDS029 homolog	12100	27675590	164032
DAPIT PROTEIN	UNKNOWN	Up-regulated during skeletal muscle growth protein 5 Diabetes-associated protein in insulin-sensitive tissues	6408	81868653	171802
UNCORTIN II	BIOSYNTHETIC CARGO	Urocortin-2 precursor Urocortin II Ucn II	11920	20532276	64824
VACUOLE MEMBRANE PROTEIN 1	UNKNOWN	Vacuole membrane protein 1 Transmembrane protein 49	45900	38197344	31214
ACYL-COA DEHYDROGENASE, VERY-LONG-CHAIN SPECIFIC, MITOCHONDRIAL PRECURSOR VLCAD	MITOCHONDRIA	Very-long-chain specific acyl-CoA dehydrogenase, mitochondrial precursor VLCAD	70750	6978435	3601
BNIP1 PROTEIN	SIGNALING	Vesicle transport protein SEC20	26170	81867205	111524
VESICULAR INTEGRAL-MEMBRANE PROTEIN VIP36	TRAFFIC	Vesicular integral-membrane protein VIP36 precursor	40390	27682691	139706
VITAMIN K EPOXIDE REDUCTASE COMPLEX SUBUNIT 1-LIKE PROTEIN	METABOLISM	Vitamin K epoxide reductase complex subunit 1 Vitamin K1 2,3-epoxide reductase subunit 1	17780	62511143	291525
VITAMIN K EPOXIDE REDUCTASE COMPLEX, SUBUNIT 1	METABOLISM	Vitamin K epoxide reductase complex subunit 1-like protein 1 VKORC1-like protein 1	19780	62511142	165266

VOLTAGE-DEPENDENT ANION CHANNEL 1	MITOCHONDRIA	Voltage-dependent anion channel 1 2 days neonate thymus thymic cells cDNA, RIKEN full-length enriched library, clone:E430005O12 product:voltage-dependent anion channel 1, full insert sequence 17 days embryo stomach cDNA, RIKEN full-length enriched library, clone:1920191D06 product:voltage-dependent anion channel 1, full insert sequence 17 days embryo kidney cDNA, RIKEN full-length enriched library, clone:1920170K05 product:voltage-dependent anion channel 1, full insert sequence 17 days embryo stomach cDNA, RIKEN full-length enriched library, clone:1920087C06 product:voltage-dependent anion channel 1, full insert sequence 17 days pregnant adult female amnion cDNA, RIKEN full-length enriched library, clone:1920043H09 product:voltage-dependent anion channel 1, full insert sequence	30760	8810245	11037
VOLTAGE-DEPENDENT ANION CHANNEL 2	MITOCHONDRIA	Voltage-dependent anion-selective channel protein 2 VDAC-2 Outer mitochondrial membrane protein porin 2 B36-VDAC	31750	8810247	5942
VOLTAGE-DEPENDENT ANION-SELECTIVE CHANNEL PROTEIN 3	MITOCHONDRIA	Voltage-dependent anion-selective channel protein 3	30800	15214186	5943
[PYRUVATE DEHYDROGENASE [LIPOAMIDE]] KINASE ISOZYME 4	MITOCHONDRIA	[Pyruvate dehydrogenase [lipoamide]] kinase isozyme 4, mitochondrial precursor Pyruvate dehydrogenase kinase isoform 4	46680	2772938	55168
CYTOCHROME C OXIDASE SUBUNIT VIC	MITOCHONDRIA	cytochrome c oxidase subunit Vlc	8455	203519	63749
2,3-OXIDOSQUALENE:LANOSTEROL CYCLASE	DETOXIFICATION	lanosterol synthase	83330	13591981	37206
OLFACTORY RECEPTOR MOR189-2	PLASMA MB	olfactory receptor Olr502	35720	47577533	310103
ROUNDABOUT (AXON GUIDANCE RECEPTOR, DROSOPHILA) HOMOLOG 2	BIOSYNTHETIC CARGO	roundabout (axon guidance receptor, Drosophila) homolog 2 [Rattus norvegicus]	176100	34867440	317126
DYSFERLIN (DYSTROPHY ASSOCIATED FER-1 LIKE PROTEIN)	CALCIUM TRANS/BIND	similar to Dysferlin (Dystrophy associated fer-1 like protein) (Fer-1 like protein 1) [Rattus norvegicus]	224600	34856330	229917
SIMILAR TO FK506 BINDING PROTEIN 11	UNKNOWN	similar to FK506 binding protein 11	22190	27664728	316692
SIMILAR TO FC FRAGMENT OF IGG BINDING PROTEIN; IGG FC BINDING PROTEIN	BIOSYNTHETIC CARGO	similar to Fc fragment of IgG binding protein; IgG Fc binding protein	583400	34855405	285938
SIMILAR TO NADH DEHYDROGENASE (UBIQUINONE) 1 BETA SUBUNIT	MITOCHONDRIA	similar to NADH dehydrogenase (ubiquinone) 1 beta subcomplex 3	11280	34876452	287362
SIMILAR TO NADH DEHYDROGENASE (UBIQUINONE) 1 BETA SUBUNIT	MITOCHONDRIA	similar to NADH dehydrogenase (ubiquinone) 1 beta subcomplex 8	23240	34865197	292854
SIMILAR TO NADH DEHYDROGENASE (UBIQUINONE) 1 BETA SUBUNIT	MITOCHONDRIA	similar to NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 10, 22kDa; NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 10 (22kD, PDSW)	20860	27667934	291828
SIMILAR TO NADH-UBIQUINONE OXIDOREDUCTASE B9 SUBUNIT	MITOCHONDRIA	similar to NADH-ubiquinone oxidoreductase B9 subunit (Complex I-B9) (CI-B9)	11480	34854466	318196
SIMILAR TO NADH-UBIQUINONE OXIDOREDUCTASE B15 SUBUNIT	MITOCHONDRIA	similar to NADH-ubiquinone oxidoreductase B15 subunit	15060	82617686	192715
SIMILAR TO PALBH	METABOLISM	similar to PalBH [Rattus norvegicus]	90550	34876995	233624
PROTO-ONCOGENE TYROSINE-PROTEIN KINASE ABL1 (P150) (C1 SIGNALING	(C1) SIGNALING	similar to Proto-oncogene tyrosine-protein kinase ABL1 (p150) (c-ABL)	129900	34861357	196976

SIMILAR TO RHBDF1 PROTEIN	PLASMA MB	similar to Rhbdf1 protein	96150	34875782	281804
SIMILAR TO SSC2	UNKNOWN	similar to SSC2	59620	34875179	315186
LAG1 LONGEVITY ASSURANCE HOMOLOG 2 (TRANSLOCATING C	UNKNOWN	similar to TRH3	44950	27693564	249505
THIOREDOXIN DOMAIN CONTAINING PROTEIN 1	UNKNOWN	similar to Txndc1 protein	31430	67078422	283888
SIMILAR TO B-IND1	SIGNALING	similar to butyrate-induced transcript 1	28810	34864679	236762
SIMILAR TO CARCINOMA RELATED GENE	UNKNOWN	similar to carcinoma related gene	29600	34871082	257012
ATPASE TYPE 13A1	MITOCHONDRIA	similar to cation-transporting atpase	131900	34877696	273691
SIMILAR TO HISTOCOMPATIBILITY 13; PRESENILIN-LIKE PROTEIN	PLASMA MB	similar to histocompatibility 13; presenilin-like protein 3	41780	34858994	305736
SIMILAR TO DISULFIDE ISOMERASE	UNKNOWN	similar to hypothetical protein FLJ22625	35090	34865046	243991
SIMILAR TO HYPOTHETICAL PROTEIN MGC10084	UNKNOWN	similar to hypothetical protein MGC10084	42080	34851552	202821
KERATIN TYPE II, HAIR (B4) - MOUSE	LIKELY CONTAMINANTS	similar to keratin type II, hair (b4) - mouse	105900	34868202	262043
SIMILAR TO KERATINOCYTES ASSOCIATED PROTEIN 2	UNKNOWN	similar to keratinocytes associated protein 2	27650	34857976	235658
SIMILAR TO PEPTIDYLPROLYL ISOMERASE A (CYCLOPHILIN A)	PROT SYN/FOLD	similar to peptidylprolyl isomerase A (cyclophilin A)	9589	34864413	268823
RAB20	GTPASE	similar to rab20	32660	34879665	240940
RETINAL SHORT-CHAIN DEHYDROGENASE/REDUCTASE 4	DETOXIFICATION	similar to retinal short-chain dehydrogenase/reductase 4	38310	34865424	315286
TRANSDUCIN (BETA)-LIKE 2	SIGNALING	similar to transducin (beta)-like 2	49610	34873382	294309
MICROSOMAL STRESS 70 PROTEIN ATPASE CORE	PROT SYN/FOLD	stress 70 protein chaperone, microsome-associated, 60kD human homolog	51830	9507149	47300
SIMILAR TO RIKEN CDNA C230094B15	UNKNOWN	unknown	100200	68051948	301870
SIMILAR TO RIKEN CDNA 2010107G23	UNKNOWN	unknown	13190	27705930	166454
PANCREATITIS-INDUCED PROTEIN 49	UNKNOWN	unknown	53820	34875854	222783
5-HYDROXYTRYPTAMINE 6 RECEPTOR	BLOOD + OTHER CELLS	5-hydroxytryptamine 6 receptor	46920	385709	68729

ATP-BINDING CASSETTE, SUB-FAMILY B, MEMBER 10	UNKNOWN	ATP-binding cassette, sub-family B (MDR/TAP), member 10 Predicted	77390	58865904	264038
SIMILAR TO MYO-INOSITOL MONOPHOSPHATASE A3	SIGNALING	Ac2-190	60820	34866106	305592
ALPHA-3 TYPE IV COLLAGEN	CYTOSKELETON	Alpha-3 type IV collagen	25400	4481745	120736
ALPHA-TOCOPHEROL TRANSFER PROTEIN	METABOLISM	Alpha-tocopherol transfer protein Alpha-TTP	31850	731023	75128
AMINOPEPTIDASE N	PLASMA MB	Aminopeptidase N	109400	205109	11241
ANTIGEN PEPTIDE TRANSPORTER 1	PROT SYN/FOLD	Antigen peptide transporter 1 APT1 Peptide transporter TAP1 ATP-binding cassette sub-family B member 2	79150	2506117	43654
BASIGIN	PLASMA MB	Basigin precursor	29590	7709992	141056
BRAIN PROTEIN 44-LIKE PROTEIN	UNKNOWN	Brain protein 44-like protein	12450	66911415	92620
BRAIN SPECIFIC NA+-DEPENDENT INORGANIC PHOSPHATE CO	PLASMA MB	Brain specific Na+-dependent inorganic phosphate cotransporter	61670	507415	60589
3 BETA-HYDROXY-DELTA 5-C27-STEROID OXIDOREDUCTASE	DETOXIFICATION	CCA2 protein	37780	2563999	86059
CD166 ANTIGEN	BLOOD + OTHER CELLS	CD166 antigen precursor Activated leukocyte-cell adhesion molecule ALCAM MEMD protein HB2 SB-10 antigen KG-CAM	65020	47605356	78164
CLASP2	CYTOSKELETON	CLIP-associating protein 2 Cytoplasmic linker-associated protein 2	140600	77416394	60531
CARCINOEMBRYONIC ANTIGEN-RELATED CELL ADHESION MOL	BIOSYNTHETIC CARGO	Carcinoembryonic antigen-related cell adhesion molecule, secreted isoform CEACAM1a-4C2 precursor	51410	76496479	39119
CARNITINE O-PALMITOYLTRANSFERASE II, MITOCHONDRIAL	MITOCHONDRIA	Carnitine O-palmitoyltransferase II, mitochondrial precursor	74110	6978705	3716
MANNOSE 6-PHOSPHATE RECEPTOR	PLASMA MB	Cation-dependent mannose-6-phosphate receptor	31100	56090485	161476
CD81 PROTEIN	PLASMA MB	Cd81 protein	25900	62641476	228910
PLATELET GLYCOPROTEIN IV	BLOOD + OTHER CELLS	Cell surface protein CD36	52730	6707016	105482
CYTOCHROME C OXIDASE SUBUNIT I	MITOCHONDRIA	Cytochrome c oxidase subunit I	56980	1332384	68411
DIHYDROOROTATE DEHYDROGENASE, MITOCHONDRIAL PRECU	MITOCHONDRIA	Dihydroorotate dehydrogenase, mitochondrial precursor Dihydroorotate oxidase DHODEHase	42660	62665239	43490

DIHYDROXYACETONE KINASE FAMILY PROTEIN	METABOLISM	Dihydroxyacetone kinase Glycerone kinase DHA kinase	59440	85718638	223736
ER LUMEN PROTEIN RETAINING RECEPTOR 2 (KDEL RECEPTOR)	TRAFFIC	ER lumen protein retaining receptor 2 KDEL receptor 2 KDEL endoplasmic reticulum protein retention receptor 2	24450	61557025	4394
ECTONUCLEOTIDE PYROPHOSPHATASE/PHOSPHODIESTERASE G PROTEIN BETA 2 SUBUNIT	PLASMA MB SIGNALING	Ectonucleotide pyrophosphatase/phosphodiesterase 3 GNB2 protein	99090	806379	85379
SIMILAR TO GENETHONIN 1	UNKNOWN	Genethonin-1	37330	8927570	4326
			35490	62078705	169873
GLUTAMYL AMINOPEPTIDASE	PLASMA MB	Glutamyl aminopeptidase	108000	7159085	62885
Qb, GOS28	TETH/DOCK/FUS	Golgi SNAP receptor complex member 1 28 kDa Golgi SNARE protein 28 kDa cis-Golgi SNARE p28 GOS-28	28530	16758358	21695
SIMILAR TO RIKEN CDNA C130038N16	UNKNOWN	Golgin subfamily A member 7	15780	81884637	19992
GUANINE NUCLEOTIDE BINDING PROTEIN (G PROTEIN) ALPHA 1	SIGNALING	Guanine nucleotide binding protein alpha 12	44070	71089929	37193
GUANINE NUCLEOTIDE-BINDING PROTEIN G(Q), ALPHA SUBUNIT	SIGNALING	Guanine nucleotide-binding protein G(q), alpha subunit	42140	7329187	37195
SIMILAR TO KE4	UNKNOWN	H2-K region expressed gene 4, rat orthologue RT1 class I, locus Ke4	49500	62665667	219015
HISTIDINE TRIAD PROTEIN 4	NUCLEUS	Histidine triad protein 4	18890	21654864	153619
G PROTEIN BETA 1 SUBUNIT	SIGNALING	Hypothetical protein	37380	51338711	8648
SIMILAR TO RIKEN CDNA 5730568A12	UNKNOWN	Hypothetical protein Cdc51	42310	62078929	366853
2400001E08RIK PROTEIN	UNKNOWN	Hypothetical protein MGC72560	17720	40018580	139384
INTEGRIN ALPHA-1 (LAMININ AND COLLAGEN RECEPTOR) (VLA-1)	PLASMA MB	Integrin alpha-1 precursor Laminin and collagen receptor VLA-1 CD49a antigen	130800	56494	37168
INTEGRIN BETA3 SUBUNIT	PLASMA MB	Integrin beta3 subunit	86930	24308466	153869
INTERCELLULAR ADHESION MOLECULE-1 PRECURSOR	CYTOSKELETON	Intercellular adhesion molecule 1 precursor ICAM-1	60140	6981068	3942
INTERFERON-INDUCIBLE PROTEIN	UNKNOWN	Interferon-inducible protein	14970	57605	17165
JUNCTIONAL ADHESION MOLECULE 1	PLASMA MB	Junctional adhesion molecule A precursor JAM-A Junctional adhesion molecule 1 JAM-1 CD321 antigen	32370	8650528	24909
KDEL RECEPTOR	TRAFFIC	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 1 Predicted	24550	62821823	272716
F-BOX ONLY PROTEIN 41	UNKNOWN	Kidney predominant protein NCU-G1	43870	51948424	169834
SIMILAR TO PROBABLE POLYPROTEIN-RELATED PROTEIN 4	UNKNOWN	LRRGT00021	27510	62639574	274007
SUCCINATE DEHYDROGENASE COMPLEX, SUBUNIT D, INTEGRAL MITOCHONDRIA	MITOCHONDRIA	Liver regeneration-related protein 1	17130	28194393	52861
LIVER-SPECIFIC TRANSPORT PROTEIN	PLASMA MB	Liver-specific transport protein	58710	529590	60454

LONG-CHAIN FATTY ACID TRANSPORT PROTEIN	BIOSYNTHETIC CARGO	Long-chain fatty acid transport protein 1 Fatty acid transport protein 1 FATP-1 Solute carrier family 27 member 1	71280	2492888	60472
SIMILAR TO KARS PROTEIN MAL2A	PROT SYN/FOLD UNKNOWN	Lysyl-tRNA synthetase MAL2A Mal, T-cell differentiation protein 2	71620 19200	55741637 77157795	269157 166255
SIMILAR TO METAXIN 2 RAC1	MITOCHONDRIA GTPASE	Metaxin 2 Predicted Migration-inducing protein 5 Ras-related C3 botulinum toxin substrate 1, isoform Rac1	29720 21450	56605654 54607147	203309 111212
HSPC242	UNKNOWN	Mitochondrial protein, 18 kDa	18370	55741522	220289
MITOGEN-ACTIVATED PROTEIN KINASE 1 INTERACTING	SIGNALING	Mitogen-activated protein kinase kinase 1-interacting protein 1	13580	81883452	237355
MYOSIN ID	CYTOSKELETON	Myosin Id Myosin heavy chain myr 4	116100	6981242	75002
NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4	MITOCHONDRIA	NADH-ubiquinone oxidoreductase chain 4 NADH dehydrogenase subunit 4	51800	639984	98993
SIMILAR TO ALG-2 BTB (POZ) DOMAIN CONTAINING 14A	PROT MOD UNKNOWN	PREDICTED: similar to ALG-2 PREDICTED: similar to BTB (POZ) domain containing 14A	21900 63110	34853323 34853069	296012 292782
SIMILAR TO METAXIN 1	MITOCHONDRIA	PREDICTED: similar to Metaxin 1, isoform 2	26260	34857966	262377
SIMILAR TO MICROSOMAL GLUTATHIONE S-TRANSFERASE 2 (MGST2)	DETOXIFICATION	PREDICTED: similar to Microsomal glutathione S-transferase 2 (Microsomal GST-2) (Microsomal GST-II)	16740	27690924	265736
SIMILAR TO EVOLUTIONARILY CONSERVED G-PATCH DOMAIN C	NUCLEUS	PREDICTED: similar to evolutionarily conserved G-patch domain containing	100900	34855741	271140
SIMILAR TO HYPOTHETICAL PROTEIN FLJ34922	UNKNOWN	PREDICTED: similar to schlafen 5	95800	34872914	315377
PHOSPHOLEMMAN	PLASMA MB	Phospholemmman precursor	10470	1916012	78112
PHOSPHOLIPASE B	PROT MOD	Phospholipase B	161100	2696236	82680
PHOSPHOLIPID HYDROPEROXIDE GLUTATHIONE PEROXIDASE, SIMILAR TO	NUCLEUS	Phospholipid hydroperoxide glutathione peroxidase, nuclear	29400	14971097	1198
SIMILAR TO PROBABLE MITOCHONDRIAL IMPORT RECEPTOR SUBUNIT TOM40	MITOCHONDRIA	Probable mitochondrial import receptor subunit TOM40 homolog Translocase of outer membrane 40 kDa subunit homolog 38 kDa mitochondrial outer membrane protein OM38	37920	81864912	726780
BARENTSZ- STAUFFEN LIKE	PROT SYN/FOLD	Protein CASC3 Cancer susceptibility candidate gene 3 protein homolog Barentsz protein Btz	75900	46395568	186570
GENE RICH CLUSTER, C3F GENE (PREDICTED)	UNKNOWN	Putative O-acyltransferase OACT5 O-acyltransferase domain-containing protein 5	56020	81882826	305024
TEX264 PROTEIN	UNKNOWN	Putative secreted protein ZSIG11	33770	56090363	262914
RER1	TRAFFIC	RER1 protein	22990	84781666	32618

RAS-RELATED PROTEIN RAL-A	GTPASE	Ras-related protein Ral-A	23550	54038996	37231
RHO B	GTPASE	Rho-related GTP-binding protein RhoB precursor H6	22120	51338594	113828
SCAVENGER RECEPTOR CLASS B MEMBER 1	PLASMA MB	Scavenger receptor class B member 1 SRB1 SR-BI	56960	49904285	38864
SECRETORY CARRIER MEMBRANE PROTEIN 3	TRAFFIC	Secretory carrier membrane protein 3	38370	34857962	169836
SECRETORY CARRIER-ASSOCIATED MEMBRANE PROTEIN 1	TRAFFIC	Secretory carrier-associated membrane protein 1 Secretory carrier membrane protein 1 SCAMP 37	38000	487057	46139
MEGF5	BIOSYNTHETIC CARGO	Slit homolog 3 protein precursor Slit-3 Multiple epidermal growth factor-like domains 5	167800	45477220	75902
SOLUTE CARRIER FAMILY 2, FACILITATED GLUCOSE TRANSPORTER	PLASMA MB	Solute carrier family 2, facilitated glucose transporter member 2 Glucose transporter type 2, liver	57090	92281	75093
SULFATE ANION TRANSPORTER 1	PLASMA MB	Sulfate anion transporter 1 SAT-1 Solute carrier family 26 member 1 Canalicular sulfate transporter Sulfate/carbonate antiporter	75450	431453	104202
SYNAPTOJANIN 2 BINDING PROTEIN	MITOCHONDRIA	Synaptotagmin 2 binding protein	22560	5106930	36071
Qa, SYNTAXIN 4	TETH/DOCK/FUS	Syntaxin-4	34210	349321	37262
NIP-SNAP1 PROTEIN (SNAP25-LIKE)	TETH/DOCK/FUS	TREMBL:Q5EBA4 ENSEMBL:ENSRNOP00000011158 REFSEQ:XP_001067526;XP_341250 PREDICTED: similar to Protein NlpSnap1	33350	34879019	217815
OCIA DOMAIN CONTAINING 1	UNKNOWN	Tax_id=10116 Ensembl_locations(Chr-bp):14-37304188 similar to RIKEN cDNA 6030432N09	27020	34877284	194680
SIMILAR TO SYNTAXIN 18	TETH/DOCK/FUS	Tax_id=10116 Ensembl_locations(Chr-bp):14-77957500 similar to Syntaxin 18	49850	34878414	291113
PANTOPHYSIN	TRAFFIC	Tax_id=10116 Ensembl_locations(Chr-bp):6-51287726 similar to synaptophysin-like protein	29400	34864274	311134
GLUCOKINASE REGULATORY PROTEIN	METABOLISM	Tax_id=10116 Glucokinase reGulatory protein	68920	6978884	3782
ZINC FINGER PROTEIN 536	UNKNOWN	Tax_id=10116 Similar to 9630010P11Rik protein	161100	34855819	234438
TRIBBLES HOMOLOG 2	SIGNALING	Tax_id=10116 Similar to AW319517 protein	61480	34863190	252701
CYTOCHROME C OXIDASE	MITOCHONDRIA	Tax_id=10116 Similar to Cox7a2l protein	12650	27716471	268354
SIMILAR TO FLJ00375 PROTEIN	UNKNOWN	Tax_id=10116 Similar to FLJ00375 protein	151500	34867944	192966
INTEGRIN ALPHA 5	PLASMA MB	Tax_id=10116 Similar to Integrin alpha 5 (fibronectin receptor alpha)	115500	34868649	259355
SIMILAR TO INTERFERON-INDUCED GUANYLATE-BINDING PROTEIN 1	SIGNALING	Tax_id=10116 Similar to Interferon-induced guanylate-binding protein 1 (Guanine nucleotide-binding protein 1)	80280	34860826	191887
MYOSIN, HEAVY POLYPEPTIDE 7B, CARDIAC MUSCLE, BETA	CYTOSKELETON	Tax_id=10116 Similar to KIAA1512 protein	248700	34859107	211488
UBX DOMAIN CONTAINING 2 (PREDICTED)	UNKNOWN	Tax_id=10116 Similar to RIKEN cDNA 1300013G12	59080	34879692	246703
SIMILAR TO RIKEN CDNA 2610020H15	UNKNOWN	Tax_id=10116 Similar to RIKEN cDNA 2610020H15	71060	34872958	298062
SIMILAR TO NAD(P) DEPENDENT STEROID DEHYDROGENASE-LIKE	UNKNOWN	Tax_id=10116 Similar to RIKEN cDNA 4632417N05	35570	34851797	239422
SIMILAR TO RIKEN CDNA 5330415H22	UNKNOWN	Tax_id=10116 Similar to RIKEN cDNA 5330415H22	44840	34874131	314793

RAB24	GTPASE	Tax_Id=10116 Similar to Rab24 protein	26250	34873657	250158
RIBOSOME-BINDING PROTEIN 1 (RIBOSOME RECEPTOR PROTEIN)	PROT SYN/FOLD	Tax_Id=10116 Similar to RiboSome-binding protein 1 (RiboSome receptor protein) (mRRp)	143300	34858829	244957
SIMILAR TO SPINSTER-LIKE PROTEIN	PLASMA MB	Tax_Id=10116 Similar to SpinSter-like protein	115400	34872719	285147
SIMILAR TO ACYLTRANSFERASE FAMILY MEMBER (5G933)	PROT MOD	Tax_Id=10116 Similar to acyltranSferaSe family member (5G933)	33640	34862502	237775
SIMILAR TO LECTIN, MANNOSE-BINDING 2-LIKE; VIP36-LIKE	TRAFFIC	Tax_Id=10116 Similar to lectin, mannoSe-binding 2-like	44440	34875582	221907
SIMILAR TO LEUCINE RICH REPEAT CONTAINING 16	UNKNOWN	Tax_Id=10116 Similar to leucine rich repeat containing 16	120700	34876156	290606
SIMILAR TO MANNOsyl-OLIGOSACCHARIDE ALPHA-1,2-MANNOSE	PROT MOD	Tax_Id=10116 Similar to mannoSyl-oligoSaccharide alpha-1,2-mannoSidaSe	31910	27705330	273814
SIMILAR TO MITOCHONDRIA-ASSOCIATED GRANULOCYTE MACROPHAGE CSF SIGNALING MOLECULE	MITOCHONDRIA	Tax_Id=10116 Similar to mitochondria-aSSociated granulocyte macrophage CSF Signaling molecule	13800	27667166	288315
MYOSIN HEAVY CHAIN 2B	CYTOSKELETON	Tax_Id=10116 Similar to myoSin heavy chain 2b	230900	34870888	198855
POMFIL1; NEURON NAVIGATOR 3	NUCLEUS	Tax_Id=10116 Similar to neuron navigator 3	186800	34864833	278518
NECT1; POLIOVIRUS RELATED RECEPTOR	PLASMA MB	Tax_Id=10116 Similar to poliovirus receptor homolog	76950	34855325	279332
SIMILAR TO PROLINE DEHYDROGENASE (OXIDASE) 2	METABOLISM	Tax_Id=10116 Similar to proline dehydrogenaSe (oxidaSe) 2	51070	34855688	268034
PUTATIVE PHEROMONE RECEPTOR	PLASMA MB	Tax_Id=10116 Similar to putative pheromone receptor	169800	34856154	285918
TORSIN FAMILY 2, MEMBER A	PROT SYN/FOLD	Torsin-2A precursor Torsin family 2 member A	35870	81884643	231792
SIMILAR TO UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 1 (UBN)	PROTEASOME/UBIQUITIN	Ubiquitin specific protease 1 Predicted	87330	62543525	282121
VASOPRESSIN V1b RECEPTOR	PLASMA MB	Vasopressin V1b receptor	47090	968900	111884
APOLIPOPROTEIN C-III	BIOSYNTHETIC CARGO	apolipoprotein C-III precursor - rat	11030	91990	84170

CLAUDIN-1	PLASMA MB	claudin 1	22870	61889099	318701
OLFACTORY RECEPTOR OLR406	PLASMA MB	olfactory receptor Olf406	34910	47577295	260312
RAP2C	GTPASE	similar to Rap2c protein	13510	34881637	197399
SPINDLIN-LIKE PROTEIN 2	UNKNOWN	similar to Spindlin-like protein 2 (SPIN-2)	32010	34882053	222106
SIMILAR TO T-CELL ACTIVATION LEUCINE REPEAT-RICH PROTEIN	UNKNOWN	similar to T-cell activation leucine repeat-rich protein	92210	34876057	221702
SIMILAR TO ACTIVATING TRANSCRIPTION FACTOR 7 INTERACTING PROTEIN 2	TRANSCRIPTION	similar to activating transcription factor 7 interacting protein 2	32900	34868272	243423
CONTAINS TRANSMEMBRANE (TM) REGION	UNKNOWN	similar to contains transmembrane (TM) region	30350	34855994	257142
ENVOPLAKIN	CYTOSKELETON	similar to envoplakin [Rattus norvegicus]	230800	34875366	316366
INTEGRIN ALPHA2B	PLASMA MB	similar to glycoprotein IIb - rat	274100	34873959	220383
SIMILAR TO HYPOTHETICAL PROTEIN MGC23280	UNKNOWN	similar to hypothetical protein MGC23280	35980	34872804	277215
TORSINB PROTEIN	PROT SYN/FOLD	similar to torsinB protein	17860	34853518	202385
UNKNOWN EXPRESSED AFTER PARTIAL HEPATECTOMY	UNKNOWN	Ab2-183	51860	33086568	194122
INTERFERON GAMMA INDUCED GTPASE	GTPASE	Ac2-233	161600	34870762	223700
ALPHA-1,3-MANNOSYL-GLYCOPROTEIN 2-BETA-N-ACETYLGLUCOSAMINYLTRANSFERASE	PROT MOD	Alpha-1,3-mannosyl-glycoprotein 2-beta-N-acetylglucosaminyltransferase N-glycosyl-oligosaccharide-glycoprotein N-acetylglucosaminyltransferase I GNT-1 GcNAc-T1	51590	740930	2699
AMYLOID-LIKE PROTEIN 2 PRECURSOR	PLASMA MB	Amyloid-like protein 2 precursor	86880	1703345	10860
APOLIPOPROTEIN C-IV PRECURSOR	BIOSYNTHETIC CARGO	Apolipoprotein C-IV precursor Apo-CIV ApoC-IV	10250	2492915	136243
BETA-1,4 N-ACETYL GALACTOSAMINYLTRANSFERASE	PROT MOD	Beta-1,4 N-acetyl galactosaminyltransferase 1 (N-acetylneuraminy)-galactosylglucosylceramide GM2/GD2 synthase GaINAc-T	59280	51858903	137529
HEPARAN SULFATE N-DEACETYLASE/N-SULFOTRANSFERASE	PROT MOD	Bifunctional heparan sulfate N-deacetylase/N-sulfotransferase 1 Glucosaminyl N-deacetylase/N-sulfotransferase 1 NDST-1 [Heparan sulfate]-glucosamine N-sulfotransferase 1 HSNST 1 N-heparan sulfate sulfotransferase 1 N-HSST 1 Heparan sulfate N-deacetylase 1 Heparan sulfate N-sulfotransferase 1	100800	401136	44217
CCAAT DISPLACEMENT PROTEIN (CASP)	TETH/DOCK/FUS	CCAAT displacement protein	175300	34871708	280644
CARBOXYPEPTIDASE D	PROT MOD	Carboxypeptidase D precursor Metallocarboxypeptidase D gp180	152600	6978699	3713
SIMILAR TO CHROMOSOME 13 OPEN READING FRAME 1	UNKNOWN	Chronic lymphocytic leukemia deletion region gene 6 protein homolog CLL deletion region gene 6 protein homolog	21680	81883037	141958
CORE1 UDP-GALACTOSE:N-ACETYL GALACTOSAMINE-ALPHA-R	PROT MOD	Core1 UDP-galactose:N-acetyl galactosamine-alpha-R beta 1,3 galactosyltransferase	42310	8927166	55277
DAMP-1 PROTEIN	PLASMA MB	DAMP-1 protein	19670	37693510	116798
ENDO-ALPHA-D-MANNOSIDASE	PROT MOD	Endo-alpha-D-mannosidase	51670	2642187	133253

EXOCYST COMPLEX COMPONENT SEC8	TRAFFIC	Exocyst complex component 4 Exocyst complex component Sec8 rSec8	110600	24418659	80377
FURIN PRECURSOR	PROT MOD	Furin precursor Paired basic amino acid residue cleaving enzyme PACE Dbasic-processing enzyme Prohormone convertase 3	86650	9506955	47234
GD3 ALPHA 2,8-SIALYLTRANSFERASE	PROT MOD	GD3 alpha 2,8-sialyltransferase	44010	6981540	75089
GPP34 RELATED PROTEIN	TETH/DOCK/FUS	GPP34-related protein	32920	62644637	220068
TRANSCYTOSIS ASSOCIATED PROTEIN/P115	TETH/DOCK/FUS	General vesicular transport factor p115 Transcytosis-associated protein TAP Vesicle docking protein	107200	538153	71574
HEME OXYGENASE 1	DETOXIFICATION	Heme oxygenase 1	33010	6981032	3930
MP51 PROTEIN	BLOOD + OTHER CELLS	Mpg-1 protein	73330	5052048	176262
N-DEACETYLASE/N-SULFOTRANSFERASE (HEPARAN GLUCOSAMINYL)	PROT MOD	N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 2 [Rattus norvegicus]	95740	34868948	210844
GLYCOPROTEIN-4-BETA-GALACTOSYL TRANSFERASE 2	PROT MOD	PREDICTED: Glycoprotein-4-beta-galactosyltransferase 2	44480	34867143	229568
SIMILAR TO PL6 PROTEIN	SIGNALING	PREDICTED: similar to PL6 protein	38050	34865897	314280
SIMILAR TO RIKEN CDNA 2510039O18	UNKNOWN	PREDICTED: similar to RIKEN cDNA 2510039O18	69480	34872456	235860
SIMILAR TO N-ACETYLLACTOSAMINIDE BETA-1,3-N-ACETYLGLUCOSAMINYLTRANSFERASE	PROT MOD	PREDICTED: similar to beta-1,3-N-acetylglucosaminyltransferase bGnT-6	47470	34861816	304110
PRENYLATED RAB ACCEPTOR 1	GTPASE	Prenylated Rab acceptor protein 1 PRA1 family protein 1	20640	56404679	78175
NATURAL KILLER CELL-SPECIFIC ANTIGEN KLIP1	BLOOD + OTHER CELLS	Protein YIPF3 YIP1 family member 3 Liver regeneration-related protein LRRGT00110	37970	81885839	234797
RGPR-P117	UNKNOWN	RGPR-p117	116800	16758344	60469
RHO-GEF 7	GTPASE	Rho guanine nucleotide exchange factor 7 PAK-interacting exchange factor beta Beta-Pix	73140	2865596	2120
SAR1 HOMOLOG	GTPASE	SAR1A protein promoting vesicle budding from the endoplasmic reticulum	22410	57528164	160782
SEC22 HOMOLOG	TETH/DOCK/FUS	Sec22 homolog	28540	16924008	35326
SERINE PROTEASE HEPSIN	PLASMA MB	Serine protease hepsin Serine protease hepsin non-catalytic chain Serine protease hepsin catalytic chain	44930	8393560	51490
KUNITZ TYPE SERINE PROTEINASE INHIBITOR	BIOSYNTHETIC CARGO	Serine protease inhibitor, Kunitz type 2	21310	40018550	319145
SIMILAR TO HPS5 PROTEIN	TRAFFIC	Serum amyloid A 4 Predicted	14970	57164089	301225
SOLUBLE CALCIUM-ACTIVATED NUCLEOTIDASE SCAN-1 (UDPAS)	PROT MOD	Soluble calcium-activated nucleotidase 1 SCAN-1 Apyrase homolog	45660	71153846	231548
Qa. SYNTAXIN 5	TETH/DOCK/FUS	Syntaxin-5	34120	631892	78137
TORID	UNKNOWN	TORID	28490	37590771	161242
DENSIN 180	CYTOSKELETON	Tax_id=101116 Ensembl_locations(Chr-bp):2-256243636 Densin-180 variant D	32790	8570180	24769

SIMILAR TO AMYLOID BETA A4 PRECURSOR PROTEIN-BINDING	UNKNOWN	Tax_Id=10116 Similar to Amyloid beta A4 precursor protein-binding family B member 2 (Fe65-like protein)	53090	34877353	294691
COG5	TETH/DOCK/FUS	Tax_Id=10116 Similar to ConServed oligomeric Golgi complex Subunit 5 (13S Golgi transPort complex 90 kDa Subunit) (GTC90) (Golgi.transPort complex 1)	45860	34864220	242048
D-GLUCURONYL C5-EPIMERASE	PROT MOD	Tax_Id=10116 Similar to D-glucuronyl C5-epimerase	93260	34863951	299013
SIMILAR TO DNA SEGMENT, CHR 12, ERATO DOI 551, EXPRESSED	UNKNOWN	Tax_Id=10116 Similar to DNA Segment, Chr 12, ERATO DOI 551, expreSSed	130300	34865806	300896
GROWTH ARREST SPECIFIC 2	SIGNALING	Tax_Id=10116 Similar to GAS2-related protein	94280	27674275	209378
SIMILAR TO KIELIN	SIGNALING	Tax_Id=10116 Similar to Kielin	222300	34855063	263135
FAM13C1	UNKNOWN	Tax_Id=10116 Similar to RIKEN cDNA 1200015N20	81340	34852453	252381
SEROLOGICALLY DEFINED BREAST CANCER ANTIGEN NY-BR-84	UNKNOWN	Tax_Id=10116 Similar to Serologically defined breast cancer antigen 84	49120	34860248	275347
TRANSCRIPTIONAL CO-ACTIVATOR CRSP7 HOMOLOG	TRANSCRIPTION	Tax_Id=10116 Similar to Transcriptional co-activator CRSP7 homolog	114600	34877464	272267
UDP-N-ACETYL-ALPHA-D-GALACTOSAMINE:POLYPEPTIDE N-ACETYLTRANSFERASE	PROT MOD	Tax_Id=10116 Similar to UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetyltransferase 2	82140	34851891	307730
QUIESCIN Q6-LIKE 1	MITOCHONDRIA	Tax_Id=10116 Similar to cDNA Sequence BC030934	81010	34853075	266866
EXOSTOSES (MULTIPLE) 2	PROT SYN/FOLD	Tax_Id=10116 Similar to exoStoSeS (multiple) 2	93370	34856569	247469
SIMILAR TO HYPOTHETICAL PROTEIN DJ667H12.2	UNKNOWN	Tax_Id=10116 Similar to hypothetical protein DJ667H12.2	57230	34865452	195844
PRESENILIN-BINDING PROTEIN	SIGNALING	Tax_Id=10116 Similar to modifier of cell adhesion	227300	34865889	203448
Qb, VT1 1B	TETH/DOCK/FUS	Tax_Id=10116 Similar to vesicle transport through interaction with t-SNARES 1B homolog	35940	34866243	241548
TRANS-GOLGI NETWORK INTEGRAL MEMBRANE PROTEIN (TGN38)	TRAFFIC	Trans-golgi network protein 1	38300	71051654	31491
TRANSMEMBRANE 9 SUPERFAMILY MEMBER 3	UNKNOWN	Transmembrane 9 superfamily protein member 3 precursor	67540	34862730	140307
INTEGRAL TYPE I PROTEIN P24 GAMMA4	TRAFFIC	Transmembrane emp24 domain-containing protein 3 precursor	25510	62901119	305262
Qb, VT1 1A	TETH/DOCK/FUS	Vesicle transport through interaction with t-SNARES homolog 1A	25160	9719420	6158
R, VAMP 3	TETH/DOCK/FUS	Vesicle-associated membrane protein 3 VAMP-3 Synaptobrevin-3 Cellubrevin CEB	11480	56789137	23581
XYLOSYL TRANSFERASE II	PROT MOD	Xylosyltransferase 2 Xylosyltransferase II Peptide O-xylosyltransferase 2	96790	71164811	189334
AB2-095	UNKNOWN	similar to Ab2-095 [Rattus norvegicus]	79240	34865464	276652
ALPHA-1,2-MANNOSIDASE	PROT MOD	similar to Endoplasmic reticulum mannosyl-oligosaccharide 1,2-alpha-mannosidase (ER alpha-1,2-mannosidase) (Mannosidase alpha class 1B member 1) (Man9GlcNAc2-specific processing alpha-mannosidase)	51600	34852997	290726
GOLGI COILED COIL PROTEIN GCC185 (GOLGIN FAMILY MEMBER 1)	TETH/DOCK/FUS	similar to Golgi coiled coil protein GCC185	245100	34852562	311145
SIMILAR TO KIAA0802 PROTEIN	UNKNOWN	similar to KIAA0802 protein	105700	34878269	270395

ENHANCER FACTOR-1-ALPHA	TRANSCRIPTION	similar to Nuclease sensitive element binding protein 1 (Y box binding protein-1) (Y-box transcription factor) (YB-1) (CCAAT-binding transcription factor I subunit A) (CBF-A) (Enhancer factor I subunit A) (EF1-A) (DNA-binding protein B) (DBPB),...	48860	34871368	260805
SIMILAR TO RIKEN CDNA 1810037C20	UNKNOWN	similar to RIKEN cDNA 1810037C20	39480	34881760	200680
TRANSMEMBRANE 9 SUPERFAMILY MEMBER 4	UNKNOWN	similar to Transmembrane 9 superfamily protein member 4	74800	34859018	260512
SIMILAR TO WD REPEAT DOMAIN 20 ISOFORM 2	UNKNOWN	similar to WD repeat domain 20 isoform 1	65240	34935498	289309
COG2	TETHIDOCK/FUS	similar to component of oligomeric golgi complex 2	41580	34851895	298383
UDP-GALACTOSE:N-ACETYLGALACTOSAMINEALPHA- PEPTIDE B	PROT MOD	similar to contains transmembrane (TM) region and ATP binding region [Rattus norvegicus]	13790	27707476	281046
AXONEMAL DYNEIN HEAVY CHAIN 9	CYTOSKELETON	similar to mkIAA0357 protein	119700	34870863	302855
SYNAPTOGYRIN 2	TETHIDOCK/FUS	synaptogyrin 2	25710	6685963	60460
TRANSFERRIN RECEPTOR	PLASMA MB	transferrin receptor [Rattus norvegicus]	85020	34869255	269397
PROTEIN FAM20B PRECURSOR	UNKNOWN	unknown	46570	27677502	309339
HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A2/B1	NUCLEUS	(P22626) Isoform A2 of P22626	36010	34855868	294111
POLYPYRIMIDINE TRACT-BINDING PROTEIN 1	NUCLEUS	(Q00438) Isoform PYBP1 of Q00438	56940	57002	9454
60S RIBOSOMAL PROTEIN L21	PROT SYN/FOLD	16 days embryo lung cDNA, RIKEN full-length enriched library, clone:8430440E03 product:ribosomal protein L21, full insert sequence Ribosomal protein L21, isoform 1 17 days pregnant adult female amnion cDNA, RIKEN full-length enriched library, clone:1920072G18 product:ribosomal protein L21, full insert sequence TIB-55 BB88 cDNA, RIKEN full-length enriched library, clone:1730098C20 product:ribosomal protein L21, full insert sequence Ribosomal protein L21 Rpl21 protein Adult male small intestine cDNA, RIKEN full-length enriched library, clone:2010205O04 product:ribosomal protein L21, full insert sequence Adult male brain cDNA, RIKEN full-length enriched library, clone:0710001D04 product:ribosomal protein L21, full insert sequence	18580	62645460	98375
26S PROTEASE REGULATORY SUBUNIT 6B	PROTEASOME/UBIQUITI	26S protease regulatory subunit 6B TAT-binding protein 7 TBP	47410	38970025	85752
60S RIBOSOMAL PROTEIN L23	PROT SYN/FOLD	60S ribosomal protein L23	14870	57688	4807
60S RIBOSOMAL PROTEIN L23A	PROT SYN/FOLD	60S ribosomal protein L23a	17700	62656804	144423
APOBEC-1 COMPLEMENTATION FACTOR LONG ISOFORM	PROT SYN/FOLD	APOBEC1 complementation factor APOBEC1-stimulating protein	65620	81916405	61026
ATP SYNTHASE PROTEIN 8	MITOCHONDRIA	ATP synthase protein 8 ATPase subunit 8 A6L	7642	5835182	98990
RIBOSOMAL PROTEIN L22P/L17E	PROT SYN/FOLD	Ac2-210	25080	32527737	251790
ADVANCED GLYCOSYLATION END PRODUCT-SPECIFIC RECEPTOR	BLOOD + OTHER CELLS	Advanced glycosylation end product-specific receptor precursor Receptor for advanced glycosylation end products	42660	498034	128256
S-AFADIN	CYTOSKELETON	Afadin Protein Af-6	207700	7513996	3616

ASPARTYL-TRNA SYNTHETASE	PROT SYN/FOLD	Aspartyl-tRNA synthetase Aspartate-tRNA ligase AspRS	57130	47938978	45103
CANALICULAR MULTISPECIFIC ORGANIC ANION TRANSPORTER	PLASMA MB	Canalicular multispecific organic anion transporter 1 ATP-binding cassette sub-family C member 2 Multidrug resistance-associated protein 2 Canalicular multidrug resistance protein	173400	6978669	3702
PROBABLE RNA-DEPENDENT HELICASE P68 (DEAD-BOX PROTEIN DEVELOPMENTALLY REGULATED GTP-BINDING PROTEIN 1	PROT SYN/FOLD GTPASE	Ddx5 Developmentally regulated GTP binding protein 1 NOD-derived CD11c +ve dendritic cells cDNA, RIKEN full-length enriched library, clone:F630119A02 product:developmentally regulated GTP binding protein 1, full insert sequence 0 day neonate cortex cDNA, RIKEN full-length enriched library, clone:G630068K21 product:developmentally regulated GTP binding protein 1, full insert sequence	69240 40510	56090441 57528300	161883 71226
DIMETHYLGLYCINE DEHYDROGENASE, MITOCHONDRIAL	MITOCHONDRIA	Dimethylglycine dehydrogenase, mitochondrial precursor ME2GLYDH	96050	56689	82662
DNAJ HOMOLOG SUBFAMILY A MEMBER 2	PROT SYN/FOLD	DnaJ homolog subfamily A member 2 RDJ2	45770	2281451	1108
EUKARYOTIC TRANSLATION INITIATION FACTOR 2 SUBUNIT 1	PROT SYN/FOLD	EIF2S1 protein	36110	9506571	103
60S RIBOSOMAL PROTEIN L35A	PROT SYN/FOLD	ES cells cDNA, RIKEN full-length enriched library, clone:2410046L21 product:ribosomal protein L35a, full insert sequence Ribosomal protein L35a Rpl35a protein	12550	57119	14850
EUKARYOTIC PEPTIDE CHAIN RELEASE FACTOR SUBUNIT 1 (ER	PROT SYN/FOLD	Eukaryotic peptide chain release factor subunit 1 eRF1	49030	68565348	41501
FICOLIN 1 PRECURSOR	BIOSYNTHETIC CARGO	Ficolin-1 precursor Collagen/fibrinogen domain-containing protein 1 Ficolin-A Ficolin A M-Ficolin	36630	6714560	75919
GLYCEROL KINASE	SIGNALING	Glycerol kinase ATP:glycerol 3-phosphotransferase Glycerokinase GK ATP-stimulated glucocorticoid-receptor translocation promoter ASTP	57480	433211	18015
HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN K	NUCLEUS	HNRPK protein Heterogeneous nuclear ribonucleoprotein K	51030	38197650	72151
RIBONUCLEOPROTEIN F	NUCLEUS	Heterogeneous nuclear ribonucleoprotein F	45730	82546819	17327
HISTONE H1.2	NUCLEUS	Histone H1.2	21990	444788	72598
HYALURONAN SYNTHASE 1	PROT MOD	Hyaluronan synthase 1	65730	27229296	159543
P55	UNKNOWN	Hypothetical protein D10Wsu52e	55250	50926851	54494
KERATIN, TYPE I CYTOSKELETAL 19	LIKELY CONTAMINANTS	Keratin, type I cytoskeletal 19 Cytokeratin-19 CK-19 Keratin-19 K19 Type I keratin Ka19	44640	73920214	222832
KYNURENINE/ALPHA-AMINOADIPATE AMINOTRANSFERASE	METABOLISM	Kynurenine/alpha-aminoadipate aminotransferase mitochondrial precursor (KAT/AadAT) (Kynurenine--oxoglutarate transaminase II) Kynurenine aminotransferase II Kynurenine--oxoglutarate aminotransferase II 2-aminoadipate transaminase 2-aminoadipate aminotransferase Alpha-aminoadipate aminotransferase AadAT	47780	8393641	51504

60S RIBOSOMAL PROTEIN L35	PROT SYN/FOLD	LOC495749, protein	14550	57702	103229
PUTATIVE RNA BINDING PROTEIN 1	NUCLEUS	LRRG100079	70520	37361844	231196
MITOCHONDRIAL LON PROTEASE HOMOLOG	MITOCHONDRIA	Lon	105800	19173766	140367
MYELIN BASIC PROTEIN S	BIOSYNTHETIC CARGO	Myelin basic protein S	21500	70166245	3277
MYOSIN LIGHT CHAIN ALKALI, SMOOTH-MUSCLE ISOFORM	CYTOSKELETON	Myosin, light polypeptide 6, alkali, smooth muscle and non-muscle, isoform 2	16960	34862212	69375
SIMILAR TO MITOGEN-ACTIVATED PROTEIN KINASE KIN	SIGNALING	PREDICTED: mitogen-activated protein kinase kinase kinase 7 interacting protein 2 (predicted)	76330	90108450	226905
60S RIBOSOMAL PROTEIN L7	PROT SYN/FOLD	PREDICTED: similar to 60S ribosomal protein L7	30310	27660180	154516
ATP-BINDING CASSETTE, SUB-FAMILY F (GCN20), MEMBER 2	BIOSYNTHETIC CARGO	PREDICTED: similar to ATP-binding cassette, sub-family F (GCN20), member 2	71660	27707592	268287
DEAD/H BOX POLYPEPTIDE 36 PROTEIN	UNKNOWN	PREDICTED: similar to DEAD/H box polypeptide 36 protein	113800	34856989	204574
SIMILAR TO MAP KINASE KINASE 3B	SIGNALING	PREDICTED: similar to MAP kinase kinase 3b	47090	34870816	238438
SIMILAR TO RIKEN CDNA 1700027N10	UNKNOWN	PREDICTED: similar to RIKEN cDNA 1700027N10	31220	34874480	246387
HYPOTHETICAL PROTEIN FLJ14494	UNKNOWN	PREDICTED: similar to RNA pseudouridylylate synthase domain containing 4	52220	34863026	266306
SPLICING FACTOR, ARGININE/SERINE-RICH 7, 35 kDa	PROT SYN/FOLD	PREDICTED: similar to Sfrs7 protein	20570	34862692	226986
SIMILAR TO KIAA1074 PROTEIN	UNKNOWN	PREDICTED: similar to ankyrin repeat domain 26	80070	34877470	202835
PHOSPHOFRUCTOKINASE, LIVER, B-TYPE	METABOLISM	Phosphofructokinase, liver, B-type	85300	38197562	318741
POLY(UC)-BINDING PROTEIN 2 ALPHA-CP2 HNRNP-E2	NUCLEUS	Poly(UC)-binding protein 2 Alpha-CP2 hnRNP-E2	38580	61557337	2515
ALG-2 INTERACTING PROTEIN 1	SIGNALING	Programmed cell death 6-interacting protein ALG-2-interacting protein 1	44060	6319138	157870
RECEPTOR-TYPE TYROSINE PHOSPHATASE V PRECU	SIGNALING	Receptor-type tyrosine-protein phosphatase V precursor	187300	725329	59236
60S RIBOSOMAL PROTEIN L17	PROT SYN/FOLD	Embryonic stem cell protein-tyrosine phosphatase ES cell phosphatase Osteostesticular protein-tyrosine phosphatase OST-PTP	21400	71051098	139425
60S RIBOSOMAL PROTEIN L19	PROT SYN/FOLD	Ribosomal protein L19 13 days embryo liver cDNA, RIKEN full-length enriched library, clone:1920026E09 product:ribosomal protein L19, full insert sequence	23470	51338626	4809
60S RIBOSOMAL PROTEIN L31	PROT SYN/FOLD	Ribosomal protein L31 11 days embryo whole body cDNA, RIKEN full-length enriched library, clone:2700055G03 product:ribosomal protein L31, full insert sequence	14460	57115	4818
60S RIBOSOMAL PROTEIN L32	PROT SYN/FOLD	Ribosomal protein L32	15860	6981482	4819
RYANODINE RECEPTOR TYPE II	CALCIUM TRANS/BIND	Ryanodine receptor type II	62520	1930136	19063
SMALL NUCLEAR RIBONUCLEOPROTEIN SM D1	NUCLEUS	Small nuclear ribonucleoprotein Sm D1 snRNP core protein D1 Sm-D1 Sm-D autoantigen	13280	34877889	3858
SODIUM/CALCIUM EXCHANGER 1 PRECURSOR	CALCIUM TRANS/BIND	Sodium/calcium exchanger 1 precursor	108100	57209	44653
SYNAPTOTAGMIN X	TETH/DOCK/FUS	Synaptotagmin X	56410	7441534	2110

GLUTAREDOXIN	PROT SYN/FOLD	Tax_id=10116 Ensembl_locations(Chr-bp):2-2908047 glutaredoxin 1 (thioltransferase)	11880	38181944	246362
SIMILAR TO METHYLCROTONOYL-COENZYME A CARBOXYLASE	METABOLISM	Tax_id=10116 Ensembl_locations(Chr-bp):2-30892343 similar to methylcrotonoyl-Coenzyme A carboxylase 2 (beta)	66180	34853476	191730
GLUTATHIONE S-TRANSFERASE, MITOCHONDRIAL HYPOTHETICAL PROTEIN XP_231157	MITOCHONDRIA UNKNOWN	Tax_id=10116 Glutathione S-transferase, mitochondrial Tax_id=10116 Hypothetical protein XP_231157	25490 115700	42543496 34853657	110024 209125
SIMILAR TO 60S RIBOSOMAL PROTEIN L19	PROT SYN/FOLD	Tax_id=10116 Similar to 60S ribosomal protein L19	24360	34881946	232570
SIMILAR TO ALL-1 PROTEIN +GTE FORM - MOUSE (FRAGMENT)	UNKNOWN	Tax_id=10116 Similar to All-1 protein +GTE form - mouse (fragment)	374300	34863265	267292
SIMILAR TO B AGGRESSIVE LYMPHOMA	UNKNOWN	Tax_id=10116 Similar to B aggressive lymphoma	106500	34869208	269562
HISTONE H3	NUCLEUS	Tax_id=10116 Similar to CG31613-PA	101500	34876364	249977
SIMILAR TO DNA SEGMENT ON CHROMOSOME X AND Y (UNIQUE)	UNKNOWN	Tax_id=10116 Similar to DNA Segment on chromosome X and Y (unique) 155 expressed Sequence	112100	34932999	262653
SIMILAR TO ERA G-PROTEIN-LIKE 1; GTPASE, HUMAN HOMOLOG	GTPASE	Tax_id=10116 Similar to Era G-protein-like 1	52770	34873187	218788
SIMILAR TO ADIPONUTRIN	UNKNOWN	Tax_id=10116 Similar to GS2 like	50130	34867787	278047
SIMILAR TO GTP BINDING PROTEIN	UNKNOWN	Tax_id=10116 Similar to GTP binding protein	36860	34859732	225450
SIMILAR TO IDN3 PROTEIN ISOFORM A	UNKNOWN	Tax_id=10116 Similar to IDN3 protein isoform A	297800	34854352	234794
RIKEN CDNA 2410066K11	UNKNOWN	Tax_id=10116 Similar to KIAA1992 protein	132600	34854749	269290
MYOSIN BINDING PROTEIN C, FAST-TYPE	CYTOSKELETON	Tax_id=10116 Similar to Myosin binding protein C, fast-type	81100	34856029	217827
NUCLEAR FACTOR OF ACTIVATED T-CELLS, CYTOPLASMIC, CAL	TRANSCRIPTION	Tax_id=10116 Similar to NFAT1-A	124800	34860796	295712
SIMILAR TO PEROXISOMAL PROLIFERATOR-ACTIVATED RECEPTOR	PEROXISOME	Tax_id=10116 Similar to Peroxisomal proliferator-activated receptor A interacting complex 285 kDa protein (PPAR-alpha interacting complex protein 285)	329700	34861034	286770
PROBABLE RNA-DEPENDENT HELICASE P72 (DEAD-BOX PROTEIN)	PROT SYN/FOLD	Tax_id=10116 Similar to Probable RNA-dependent helicase p72 (DEAD-box protein p72) (DEAD-box protein 17)	73940	34866944	195895
SIMILAR TO HOMOPROTOPORTECHUATE CATABOLISM BIFUNCTIONAL PHF1 PROTEIN	METABOLISM UNKNOWN	Tax_id=10116 Similar to RIKEN cDNA 1110025H10 Tax_id=10116 Similar to RIKEN cDNA 1110054G21	26400 101700	34871118 34854019	269702 233179
PROBABLE UPF0334 KINASE-LIKE PROTEIN	UNKNOWN	Tax_id=10116 Similar to RIKEN cDNA 2310079N02	20810	34851911	222133
SIMILAR TO RIKEN CDNA 2610207116	UNKNOWN	Tax_id=10116 Similar to RIKEN cDNA 2610207116	122600	34868438	250916
SIMILAR TO RIKEN CDNA 2810405J04	UNKNOWN	Tax_id=10116 Similar to RIKEN cDNA 2810405J04	61290	34862460	198258
SIMILAR TO EXOCYST COMPLEX COMPONENT SEC6	TRAFFIC	Tax_id=10116 Similar to RIKEN cDNA E430013E20 gene	81050	34851597	259373
GCN1 GENERAL CONTROL OF AMINO-ACID SYNTHESIS 1-LIKE 1	PROT SYN/FOLD	Tax_id=10116 Similar to RIKEN cDNA G431004K08	303100	34872627	241842
RNA HELICASE	NUCLEUS	Tax_id=10116 Similar to RNA helicase	80570	34933204	287882
SIMILAR TO RNA HELICASE FAMILY	NUCLEUS	Tax_id=10116 Similar to RNA helicase family	238800	34853214	288172
SIMILAR TO SPECTRIN BETA CHAIN, BRAIN 4 (SPECTRIN, NON-E	CYTOSKELETON	Tax_id=10116 Similar to Spectrin beta chain, brain 4 (Spectrin, non-erythroid beta chain 4) (Beta-V Spectrin) (BSPECV)	402100	34856723	275665
PALLADIN	TRAFFIC	Tax_id=10116 Similar to Sulfide quinone reductase-like precursor	78570	34856819	285775
SIMILAR TO ALPHA 3 TYPE VI COLLAGEN ISOFORM 1	BIOSYNTHETIC CARGO	Tax_id=10116 Similar to alpha 3 type VI collagen isoform 1	357700	34877775	307227
SIMILAR TO ALPHA-TUBULIN	CYTOSKELETON	Tax_id=10116 Similar to alpha-tubulin	45240	34852918	268840
SIMILAR TO BULLOUS PEMPFIGOID ANTIGEN 1-B	CYTOSKELETON	Tax_id=10116 Similar to bullous pemphigoid antigen 1-b	1087000	34874618	233230

CARBOHYDRATE (CHONDROITIN) SYNTHASE 2	PROT MOD	Tax_id=10116 Similar to carbohydrate (chondroitin) Synthase 2	65060	27681143	278143
SIMILAR TO CHROMOSOME 17 OPEN READING FRAME 27	UNKNOWN	Tax_id=10116 Similar to chromosome 17 open reading frame 27	668500	34875599	199223
COLLAGEN ALPHA1 TYPE VI-PRECURSOR	BIOSYNTHETIC CARGO	Tax_id=10116 Similar to collagen alpha1 type VI-precursor	112800	34852376	201969
SIMILAR TO DEVELOPMENT- AND DIFFERENTIATION-ENHANCING	SIGNALING	Tax_id=10116 Similar to development- and differentiation-enhancing factor 2	119200	34863212	230447
SIMILAR TO FORMIN-LIKE PROTEIN	CYTOSKELETON	Tax_id=10116 Similar to formin-like protein	123000	34873916	239048
GLUTARYL-COA DEHYDROGENASE	MITOCHONDRIA	Tax_id=10116 Similar to glutaryl-CoA dehydrogenase precursor	49330	34851534	270372
SIMILAR TO ALPHA TUBULIN	CYTOSKELETON	Tax_id=10116 Similar to hypothetical protein FLJ21665	52020	34876595	213091
SIMILAR TO HYPOTHETICAL PROTEIN FLJ32784	UNKNOWN	Tax_id=10116 Similar to hypothetical protein FLJ32784	138000	34872260	228083
SIMILAR TO INTERLEUKIN-1 RECEPTOR ASSOCIATED KINASE 4	SIGNALING	Tax_id=10116 Similar to interleukin-1 receptor associated kinase 4	57750	34867776	244001
SIMILAR TO MYOCARDIN-RELATED TRANSCRIPTION FACTOR A	TRANSCRIPTION	Tax_id=10116 Similar to myocardin-related transcription factor A	123400	34867047	275363
SIMILAR TO NUCLEAR DOMAIN 10 PROTEIN	NUCLEUS	Tax_id=10116 Similar to nuclear domain 10 protein	85380	34873520	275895
PROCOLLAGEN, TYPE VI, ALPHA 2	BIOSYNTHETIC CARGO	Tax_id=10116 Similar to procollagen, type VI, alpha 2	122100	34852378	258657
SIMILAR TO XYLULOKINASE HOMOLOG; XYLULOKINASE (H. INFEL)	METABOLISM	Tax_id=10116 Similar to xylulokinase homolog	66490	34866669	229118
TITIN	UNKNOWN	Tax_id=10116 Titin	1375000	34856454	293312
VON WILLEBRAND FACTOR	BIOSYNTHETIC CARGO	Tax_id=10116 Von Willebrand factor	289700	34858467	251407
TRANSLATION INITIATION FACTOR EIF-2B BETA SUBUNIT	PROT SYN/FOLD	Translation initiation factor eIF-2B beta subunit	38880	2494306	112447
TRYPTOPHAN 2,3-DIOXYGENASE	METABOLISM	Tryptophan 2,3-dioxygenase	47860	59809151	11402
TYPE I KERATIN KA22	LIKELY CONTAMINANTS	Type I keratin KA22	50210	57012446	161849
UDP-GLUCOSE 6-DEHYDROGENASE	METABOLISM	UDP-glucose 6-dehydrogenase UDP-Glc dehydrogenase UDP-GlcDH UDPGDH	54890	6136118	75904
60S RIBOSOMAL PROTEIN L38	PROT SYN/FOLD	Zgc92860	8218	74354458	4821
HYPOTHETICAL PROTEIN XP_343009	UNKNOWN	hypothetical protein XP_343009	87580	34862025	301974
HYPOTHETICAL PROTEIN XP_347082	UNKNOWN	hypothetical protein XP_347082	10270	34862408	222136
PEROXISOME ASSEMBLY FACTOR-2	PEROXISOME	peroxisome assembly factor-2 [Rattus norvegicus]	104300	2911135	169183
PROSTAGLANDIN E RECEPTOR 3; RAT KIDNEY PROSTAGLANDIN	BIOSYNTHETIC CARGO	prostaglandin E receptor 3 (subtype EP3)	39630	6981434	75057
SIMILAR TO 3000004C01RIK PROTEIN	UNKNOWN	similar to 3000004C01RIK protein	31860	34881333	281752
SIMILAR TO 60S RIBOSOMAL PROTEIN L7	PROT SYN/FOLD	similar to 60S RIBOSOMAL PROTEIN L7	50520	34877407	254343
ATP-BINDING CASSETTE SUB-FAMILY E MEMBER 1	LYSOSOME	similar to ATP-binding cassette sub-family E member 1 (RNase L inhibitor) (Ribonuclease 4 inhibitor) (RNS4I) (HuHP68) [Rattus norvegicus]	65360	34851575	255150
SIMILAR TO APOPTOSIS INHIBITOR 5	SIGNALING	similar to Apoptosis inhibitor 5	36870	34878251	281550
EUKARYOTIC TRANSLATION INITIATION FACTOR 3 SUBUNIT 6 IN	PROT SYN/FOLD	similar to Eukaryotic translation initiation factor 3 subunit 6 interacting protein (HSPC021/HSPC025)	66710	34866934	266163
RABCONNECTIN	TRAFFIC	similar to KIAA0856 protein	278000	34863411	215246
SIMILAR TO POTENTIAL HELICASE MOV-10	NUCLEUS	similar to Potential helicase MOV-10 [Rattus norvegicus]	73800	27660592	154542

SIMILAR TO RAS PROTEIN ACTIVATOR LIKE 2 ISOFORM 2; RAS GTPASE			similar to RAS protein activator like 2 isoform 2; Ras GTPase activating protein-like; Ras protein activator like 1	34760	34880852	276474
PUTATIVE RNA BINDING PROTEIN, PARTNER TO NOB1	UNKNOWN		similar to RIKEN cDNA 1810003N24	31780	34873957	230313
SIMILAR TO RIKEN CDNA 2410002022 GENE	UNKNOWN		similar to RIKEN cDNA 2410002022 gene [Rattus norvegicus]	22220	34853743	269534
DEOXYRIBOSE-PHOSPHATE ALDOLASE-LIKE	METABOLISM		similar to RIKEN cDNA 2500002K03 gene	36950	34858565	307749
SIMILAR TO RIKEN CDNA A930015D22	UNKNOWN		similar to RIKEN cDNA A930015D22	48920	34861327	218587
METHIONINE ADENOSYLTRANSFERASE II ALPHA SUBUNIT	METABOLISM		similar to RIKEN cDNA D630045P18	37180	34853482	239818
SUCCINYL-COA LIGASE [ADP-FORMING] BETA-CHAIN, MITOCHONDRIAL	MITOCHONDRIA		similar to Succinyl-CoA ligase [ADP-forming] beta-chain, mitochondrial precursor (Succinyl-CoA synthetase, betaA chain) (SCS-betaA) (ATP-specific succinyl-CoA synthetase beta subunit) [Rattus norvegicus]	48250	34874487	313666
SUCCINYL-COA LIGASE [GDP-FORMING] BETA-CHAIN, MITOCHONDRIAL	MITOCHONDRIA		similar to Succinyl-CoA ligase [GDP-forming] beta-chain, mitochondrial precursor (Succinyl-CoA synthetase, betaG chain) (SCS-betaG) (GTP-specific succinyl-CoA synthetase beta subunit)	39790	34857707	302398
SIMILAR TO APOPTOSIS-INDUCING FACTOR (AIF)-HOMOLOGOUS	MITOCHONDRIA		similar to apoptosis-inducing factor (AIF)-homologous mitochondrial-associated inducer of death; p53-responsive gene 3 [Rattus norvegicus]	14880	34852510	209377
PROLINE DEHYDROGENASE	METABOLISM		similar to brain and kidney proline oxidase 2	30660	34869794	301508
SIMILAR TO CYTOKERATIN ENDOA - MOUSE	LIKELY CONTAMINANTS		similar to cyokeratin EndoA - mouse	53620	34881863	292930
SIMILAR TO EXPRESSED SEQUENCE AU041483	UNKNOWN		similar to expressed sequence AU041483	63520	34869200	245616
SIMILAR TO RNA BINDING PROTEINS	UNKNOWN		similar to hepatocellular carcinoma autoantigen	13340	34869447	272734
SIMILAR TO HYPOTHETICAL PROTEIN MGC7793	UNKNOWN		similar to hypothetical protein MGC7793	139600	34855606	249584
SIMILAR TO MICRORCHIDIA (ZINC FINGER CW-TYPE COILED-COIL) NUCLEUS	NUCLEUS		similar to microrchidia	55070	34869318	309715
SIMILAR TO PUTATIVE ODORANT RECEPTOR	PLASMA MB		similar to putative odorant receptor	137500	34854788	252389
SIMILAR TO RIBOSOMAL PROTEIN L7, CYTOSOLIC [VALIDATED]	PROT SYN/FOLD		similar to ribosomal protein L7, cytosolic [validated] - rat	28840	34866562	206770
SIMILAR TO SORTING NEXIN 17	TRAFFIC		similar to sorting nexin 17 [Rattus norvegicus]	16590	27716735	167115
SIMILAR TO RIKEN CDNA 1110020C03	UNKNOWN		unknown	29280	34870857	233158
2' 3' CYCLIC NUCLEOTIDE 3' PHOSPHODIESTERASE	SIGNALING		2' 3' -cyclic-nucleotide 3' -phosphodiesterase CNP CNPase	47270	66912120	109735
5'-AMP-ACTIVATED PROTEIN KINASE, CATALYTIC ALPHA-1 CHAIN	SIGNALING		5' -AMP-activated protein kinase catalytic subunit alpha-1 AMPK alpha-1 chain	62600	1703034	23444
5'-AMP-ACTIVATED PROTEIN KINASE, CATALYTIC ALPHA-2 CHAIN	SIGNALING		5'-AMP-activated protein kinase, catalytic alpha-2 chain	62260	728758	54292
60S RIBOSOMAL PROTEIN L37	PROT SYN/FOLD		60S ribosomal protein L37	11080	57121	3029
ADP-RIBOSYLATION FACTOR-LIKE 1	GTPASE		ADP-ribosylation factor-like protein 1	20410	728889	23396
RHO-RELATED GTP-BINDING PROTEIN RHOG	GTPASE		ARHG protein Ras homolog gene family, member G Rho G	21310	82524300	93024
ADRENOLEUKODYSTROPHY RELATED PROTEIN	PEROXISOME		ATP-binding cassette sub-family D member 2 Adrenoleukodystrophy-related protein	83370	81917721	15419
ATP-BINDING CASSETTE, SUB-FAMILY F (GCN20), MEMBER 1	PROT SYN/FOLD		ATP-binding cassette, sub-family F (GCN20), member 1	92870	34852051	231492

SIMILAR TO VACUOLAR ATP SYNTHASE SUBUNIT C (V-ATPASE C)	MITOCHONDRIA	ATPase, H+ transporting, V1 subunit C, isoform 1 Predicted	43900	62652340	311925
TUMOR NECROSIS FACTOR ALPHA-INDUCED ADIPOSE-RELATED	PLASMA MB	Ab1-219	52040	62646756	201751
ADENYLATE CYCLASE, TYPE VIII	SIGNALING	Adenylate cyclase type 8 Adenylate cyclase type VIII ATP pyrophosphate-lyase 8 Ca(2+)/calmodulin-activated adenylyl cyclase	139800	8392852	119254
ADENYLATE KINASE ISOENZYME 4, MITOCHONDRIAL	MITOCHONDRIA	Adenylate kinase isoenzyme 4, mitochondrial Adenylate kinase 3-like 1 ATP-AMP transphosphorylase	25200	8392885	181389
O-GLCNAC TRANSFERASE-INTERACTING PROTEIN OF 98 KDA	PROT MOD	Anyotrophic lateral sclerosis 2 chromosomal region candidate gene protein 3 homolog	101600	75905813	256333
CALCIUM CHANNEL ISOFORM ALPHA1E7	CALCIUM TRANS/BIND	Calcium channel isoform alpha 1E7	259200	14578563	9007
CALPAIN SMALL SUBUNIT 1	BIOSYNTHETIC CARGO	Calpain small subunit 1	28080	19864480	76638
CARBOXYPEPTIDASE A1 PRECURSOR	PROT MOD	Carboxypeptidase A1 precursor	47150	8393183	111631
CLATHRIN LIGHT CHAIN B	COAT	Clathrin light chain B	25120	203359	60578
CLAUDIN-3	PLASMA MB	Claudin-3	23310	82617586	33971
COPI COATOMER DELTA SUBUNIT	COAT	Coatomer subunit delta Delta-coat protein Delta-COP Archain	57200	81884175	221177
COLORRECTAL TUMOR SUPPRESSOR	CYTOSKELETON	Colorectal tumor suppressor	157900	6978755	3733
KERATIN, TYPE II CYTOSKELETAL 1 (CYTOKERATIN 1) (67 KDA C	LIKELY CONTAMINANTS	Cytokeratin type I	15550	55956	11221
DNA POLYMERASE BETA	NUCLEUS	DNA polymerase beta	36540	206276	44281
DEATH EFFECTOR DOMAIN-CONTAINING PROTEIN	SIGNALING	Death effector domain-containing protein Death effector domain-containing testicular molecule	36850	3930224	54966
DYNAMIN 2	CYTOSKELETON	Dynammin 2	98230	729380	3740
DYNAMIN-1	CYTOSKELETON	Dynammin-1 D100 Dynammin, brain B-dynammin	95930	56054	67605
EUKARYOTIC TRANSLATION INITIATION FACTOR 3 SUBUNIT 6	PROT SYN/FOLD	EIF3S6 protein	52220	62652368	55867

RNA-BINDING PROTEIN HUR	PROT SYN/FOLD	ELAV (Embryonic lethal, abnormal vision, Drosophila)-like 1 Hu antigen R 3 days neonate thymus cDNA, RIKEN full-length enriched library, clone:A630073F18 product:ELAV-LIKE PROTEIN 1 (HU-ANTIGEN R) (HUR) (ELAV-LIKE GENERIC PROTEIN) (MELG), full insert sequence	36170	34870116	18691
ERYTHROID SPECTRIN ALPHA	CYTOSKELETON	Erythroid spectrin alpha	276600	58865394	725563
ERYTHROID SPECTRIN BETA	CYTOSKELETON	Erythroid spectrin beta	246300	47058982	726511
FATTY ACID BINDING PROTEIN FABP-1	METABOLISM	Fatty acid binding protein FABP-1	3929	452977	23674
FLOTILIN-2	PLASMA MB	Flotillin-2 Reggie-1 REG-1	47040	4079709	101676
GRIP-ASSOCIATED PROTEIN 1 LONG FORM	SIGNALING	GRIP1-associated protein 1 GRASP-1	96070	8980841	60564
GTPASE	GTPASE	GTP-binding nuclear protein Ran GTPase Ran Ras-like protein TC4	24420	51338593	76611
GAP JUNCTION BETA-1 PROTEIN (CONNEXIN 32) (CX32) (GAP JU	PLASMA MB	Gap junction beta-1 protein Connexin-32 Cx32	32000	8393444	51463
HEPATOMA-DERIVED GROWTH FACTOR 3	SIGNALING	Hepatoma-derived growth factor 3	74000	19424218	171803
L-SERINE DEHYDRATASE/L-THREONINE DEAMINASE	METABOLISM	L-serine dehydratase/L-threonine deaminase	38480	21617859	44348
LAMININ-5 ALPHA 3 CHAIN	BIOSYNTHETIC CARGO	Laminin-5 alpha 3 chain	190400	27545378	116280
2810002D13RIK PROTEIN	UNKNOWN	Leucine-rich repeat-containing protein 57	26720	81909634	240594
FLOTILLIN-1	BIOSYNTHETIC CARGO	Lipid raft protein flotillin-1 Bone marrow macrophage cDNA, RIKEN full-length enriched library, clone:I830015L22 product:flotillin 1, full insert sequence Bone marrow macrophage cDNA, RIKEN full-length enriched library, clone:I830013M04 product:flotillin 1, full insert sequence	47510	40352785	8548
LIVER NTE-RELATED PROTEIN	UNKNOWN	Liver NTE-related protein	75650	21314221	198073
MEMBRANE-BOUND AMINOPEPTIDASE P	PLASMA MB	Membrane-bound aminopeptidase P X-prolyl aminopeptidase (Aminopeptidase P) 2, membrane-bound	76080	49258142	140638
MICROSOMAL DIPEPTIDASE	PROT MOD	Microsomal dipeptidase precursor	45520	47938984	23872
SYNTROPHIN-ASSOCIATED SERINE/THREONINE KINASE SAS T11	SIGNALING	Microtubule-associated serine/threonine-protein kinase 1 Syntrophin-associated serine/threonine-protein kinase	171000	60389868	200842
MONOCYTE DIFFERENTIATION ANTIGEN CD14 PRECURSOR	BIOSYNTHETIC CARGO	Monocyte differentiation antigen CD14 precursor	40050	38197682	35920
MYOSIN I HEAVY CHAIN	CYTOSKELETON	Myosin I heavy chain	118100	480659	6153
MYOSIN IE	CYTOSKELETON	Myosin le Myosin heavy chain myr 3	126800	693995	105842
S-PHASE KINASE-ASSOCIATED PROTEIN 1A	SIGNALING	OTTMUSP00000005802 T3 days embryo liver cDNA, RIKEN full-length enriched library, clone:Z510015J15 product:S-phase kinase-associated protein 1A, full insert sequence Bone marrow macrophage cDNA, RIKEN full-length enriched library, clone:I830081B01 product:S-phase kinase-associated protein 1A, full insert sequence	18670	56090475	62616
P20-CGGBP	NUCLEUS	P20-CGGBP CGGBP1 protein CGG triplet repeat binding protein 1 Trinucleotide repeat DNA binding protein p20- CGGBP	18820	27672382	55652
MKIAA0523 PROTEIN	UNKNOWN	PREDICTED: similar to CDNA sequence BC030477	64790	66730417	255746
SIMILAR TO CELL DEATH-INDUCING DNA FRAGMENTATION FAC	NUCLEUS	PREDICTED: similar to Cell death-inducing DNA fragmentation factor, alpha subunit-like effector B	24750	34875073	236633

EH-DOMAIN CONTAINING 2; EH DOMAIN CONTAINING 2	UNKNOWN		PREDICTED: similar to EH-domain containing 2	61240	67846074	287406
EMILIN	CYTOSKELETON		PREDICTED: similar to Elastin microfibril interfacer 1	107600	34863280	233953
SIMILAR TO M PHASE PHOSPHOPROTEIN 6	PROT SYN/FOLD		PREDICTED: similar to M phase phosphoprotein 6	18880	34866285	221944
SIMILAR TO RIKEN CDNA 1110038M16	UNKNOWN		PREDICTED: similar to RIKEN cDNA 1110038M16	31550	34870283	246519
SIMILAR TO RIKEN CDNA 2010002A20	UNKNOWN		PREDICTED: similar to RIKEN cDNA 2010002A20	29160	34873218	256476
SIMILAR TO DJ881L22.2 (NOVEL PROTEIN)	UNKNOWN		PREDICTED: similar to RIKEN cDNA D930001122	30110	62646328	359989
SIMILAR TO TOLLIP PROTEIN	SIGNALING		PREDICTED: similar to TOLLIP protein	30310	34861256	225945
ABHYDROLASE DOMAIN CONTAINING PROTEIN 2	UNKNOWN		PREDICTED: similar to alpha/beta hydrolase fold protein	48340	34857271	271294
SIMILAR TO KIAA1311 PROTEIN	UNKNOWN		PREDICTED: similar to KIAA1311 protein	118700	34879262	281850
PHOSPHOINOSITIDE-3-KINASE; REGULATORY SUBUNIT 4, P150	TRAFFIC		PREDICTED: similar to phosphoinositide-3-kinase, regulatory subunit 4, p150	152400	83288384	268833
SIMILAR TO MKIAA3002 PROTEIN	UNKNOWN		PREDICTED: similar to round spermatid basic protein 1-like	92310	34854016	266462
SIMILAR TO SEROLOGICALLY DEFINED COLON CANCER ANTIGEN 1	TRANSCRIPTION		PREDICTED: similar to serologically defined colon cancer antigen 1 isoform a	118600	34855476	218537
TESTIS-SPECIFIC SERINE KINASE 4	SIGNALING		PREDICTED: similar to testis-specific serine kinase 4	37430	27700101	197055
PHOSPHATIDYLCHOLINE TRANSFER PROTEIN	PROT MOD		Phosphatidylcholine transfer protein	24730	8393922	51565
PLECTIN 10	CYTOSKELETON		Plectin 10	518400	40849904	699022
POTASSIUM VOLTAGE-GATED CHANNEL SUBFAMILY A MEMBER 6	PLASMA MB		Potassium voltage-gated channel subfamily A member 6	58880	57667	63679
PROTEIN LRP16	UNKNOWN		Protein LRP16	28640	32129697	214491
PROTEIN KINASE C ALPHA	SIGNALING		Protein kinase C, alpha type	76790	56914	44893
PROTEIN TYROSINE PHOSPHATASE 4A1	SIGNALING		Protein tyrosine phosphatase type IVA protein 1 Protein-tyrosine phosphatase 4a1 Protein-tyrosine phosphatase of regenerating liver 1 PRL-1 PTP(CAAXI)	19820	68566099	4701
PROTEIN-GLUTAMINE GAMMA-GLUTAMYLTRANSFERASE K	PROT MOD		Protein-glutamine gamma-glutamyltransferase K Transglutaminase K TGase K TGK TG(K) Transglutaminase-1 Epidermal TGase	90770	67677918	31490
CAST2	TRAFFIC		RAB6-interacting protein 2 ERC protein 1 ERC1 CAZ-associated structural protein 2 CAST2	108800	51701367	165980
MOMO	TRANSCRIPTION		RING finger protein 34 RING finger protein MOMO	42680	76363370	273497
RSB-11-77	UNKNOWN		RSB-11-77	42090	32996717	166313
RAB PROTEINS GERANYLGERANYLTRANSFERASE COMPONENT 1	PROT MOD		Rab proteins geranylgeranyltransferase component A 1 Rab escort protein 1 REP-1 Choroideraemia protein homolog	72480	8393110	86616
RAC2	GTPASE		Ras-related C3 botulinum toxin substrate 2 precursor p21-Rac2 EN-7 protein	21440	56605840	8458
RETINOL DEHYDROGENASE 10	DETOXIFICATION		Retinol dehydrogenase 10	38060	31324556	227390
RIBOSOMAL PROTEIN S6 KINASE ALPHA 1	PROT SYN/FOLD		Ribosomal protein S6 kinase alpha-1 S6K-alpha 1 90 kDa ribosomal protein S6 kinase 1 p90-RSK 1 Ribosomal S6 kinase 1 RSK-1 pp90RSK1 MAP kinase-activated protein kinase 1a MAPKAPK1A	82880	206772	37242

RAT INSULIN RECEPTOR RELATED RECEPTOR 1 (SIRR-1)	PLASMA MB	SIRR-1 precursor	44730	425789	100550
SMPTB	NUCLEUS	SMPTB	63720	33414511	185761
SP120	NUCLEUS	SP120	87750	624918	140634
CAMP-DEPENDENT PROTEIN KINASE TYPE II-ALPHA REGULATORY SUBUNIT	SIGNALING	SWISS-PROT:P12368 cAMP-dependent protein kinase type II-alpha regulatory subunit	41980	206150	168209
SCAFFOLDING PROTEIN SLIPR	CYTOSKELETON	Scaffolding protein SLIPR	129400	7650497	138308
SEMINAL VESICLE SECRETORY PROTEIN II PRECURSOR	BIOSYNTHETIC CARGO	Seminal vesicle secretory protein 2 precursor	45540	207115	11343
PKC-ZETA-INTERACTING PROTEIN	SIGNALING	Sequestosome-1 Ubiquitin-binding protein p62 Protein kinase C-zeta-interacting protein II SVS II	47680	77416574	19107
SER/THR PROTEIN PHOSPHATASE 2A SUBUNIT B	SIGNALING	Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B delta isoform PP2A, subunit B, B-delta isoform PP2A, subunit B, B55-delta isoform PP2A, subunit B, PR55-delta isoform PP2A, subunit B, R2-delta isoform	51980	7993726	78346
2',5'-OLIGOADENYLATE SYNTHETASE-LIKE 9	PROT SYN/FOLD	Solute carrier family 30 (Zinc transporter), member 4	47660	56268809	203002
Sorting nexin 3	BIOSYNTHETIC CARGO	Sorting nexin 3	18760	79152346	75350
SPlicing factor, ARGinine/SERine-RICH 3	NUCLEUS	Splicing factor, arginine/serine-rich 3	19330	62665747	4905
NEURAL ZINC FINGER FACTOR 3	TRANSCRIPTION	Suppression of tumorigenicity protein 18 Neural zinc finger factor 3 NFZ-3 C2-HC type zinc finger protein r-MyT3	113500	7514025	169317
SYNDECAN-2 PRECURSOR	PLASMA MB	Syndecan 2	23220	6981520	41211
SYNDECAN-1 PRECURSOR	PLASMA MB	Syndecan-1 precursor	33210	6981518	75082
SYNDECAN-4 PRECURSOR	PLASMA MB	Syndecan-4 precursor SYND4 Ryudocan core protein	21960	6981522	75083
ADAPTOR PROTEIN COMPLEX AP-1, GAMMA 1 SUBUNIT	COAT	Tax_id=10116 AdAptor protein complex AP-1, gamma 1 subunit	77880	34851742	198626
CADHERIN 7	PLASMA MB	Tax_id=10116 Cadherin 7	91340	34878884	214165
CYTOCHROME P450 NA4	DETOXIFICATION	Tax_id=10116 Ensembl_locations(Chr-bp):1-81087649 similar to cytochrome P450, family 2, subfamily s, polypeptide 1	83140	34855468	199155
SIMILAR TO FRAGILE-X-RELATED PROTEIN 1 ISOFORM E	UNKNOWN	Tax_id=10116 Ensembl_locations(Chr-bp):2-120296304 similar to fragile-X-related protein 1 isoform e	68720	34856814	266426
SIMILAR TO CALGIZZARIN	CALCIUM TRANS/BIND	Tax_id=10116 Ensembl_locations(Chr-bp):2-186570454 similar to endothelial monocyte-activating polypeptide	16840	34858021	215128
SIMILAR TO HYPOTHETICAL PROTEIN FLJ10579	UNKNOWN	Tax_id=10116 Ensembl_locations(Chr-bp):3-105548427 similar to hypothetical protein FLJ10579	57210	34856697	285691
3-HYDROXYISOBUTYRYL-COENZYME A HYDROLASE	METABOLISM	Tax_id=10116 Ensembl_locations(Chr-bp):9-45566723 similar to RIKEN cDNA 2610509J15	47870	34875828	251780
GLYPICAN 4	BIOSYNTHETIC CARGO	Tax_id=10116 Ensembl_locations(Chr-bp):X-139040485 similar to glypican 4	62280	34881641	253728
UNKNOWN1	UNKNOWN	Tax_id=10116 HypoHetical protein XP_235050	101800	34864725	191344
HYPOTHETICAL PROTEIN XP_342343	UNKNOWN	Tax_id=10116 HypoHetical protein XP_342343	17520	34860574	313817
M4 PROTEIN	UNKNOWN	Tax_id=10116 M4 protein	74540	16124253	136387

MYOSIN LIGHT CHAIN 1, SLOW-TWITCH MUSCLE BVENTRICULAR	CYTOSKELETON	Tax Id=10116 Myosin, light polypeptide 3	22160	763179	21125
DHM1 PROTEIN	TRANSCRIPTION	Tax Id=10116 Similar to 5-3 exoribonucleaSe 2	128500	34858884	242779
SIMILAR TO AFADIN	CYTOSKELETON	Tax Id=10116 Similar to AF-6 protein	16820	34853794	305979
SIMILAR TO ATP BINDING CASSETTE GENE, SUB-FAMILY A (ABC family A (ABC1), member 13	UNKNOWN	Tax Id=10116 Similar to ATP binding caSSette gene, Sub-family A (ABC1), member 13	646000	34879278	202444
SIMILAR TO BAND 4.1-LIKE PROTEIN 5	BLOOD + OTHER CELLS	Tax Id=10116 Similar to Band 4.1-like protein 5	114300	34879408	300797
SIMILAR TO CDT1 PROTEIN	UNKNOWN	Tax Id=10116 Similar to CDT1 protein	66840	34851851	203175
SIMILAR TO CENTROMERIC PROTEIN E (CENP-E PROTEIN)	CYTOSKELETON	Tax Id=10116 Similar to CENTROMERIC PROTEIN E (CENP-E PROTEIN)	313000	34860597	241018
DEAD-BOX PROTEIN ABSTRAKT HOMOLOG	PROT SYN/FOLD	Tax Id=10116 Similar to DEAD-box protein abStrakt homolog	165600	34873643	261560
DEAH (ASP-GLU-ALA-HIS) BOX POLYPEPTIDE 29; NUCLEIC ACID	PROT SYN/FOLD	Tax Id=10116 Similar to DEAH (ASP-Glu-Ala-HIS) box polypeptide 29	145700	34854165	249374
DESMOPLAKIN (DP) (250/210 KDA PARANEOPLASTIC PEMPHIGUS)	CYTOSKELETON	Tax Id=10116 Similar to DeSmoplakin (DP) (250/210 kDa paraneoplastic pemphigus antigen)	327800	34875216	219502
SIMILAR TO ENSANGP00000013261	UNKNOWN	Tax Id=10116 Similar to ENSANGP00000013261	15620	27689183	197176
FARP1 PROTEIN	UNKNOWN	Tax Id=10116 Similar to Farp1 protein	195200	34876071	216529
SIMILAR TO HYPOTHETICAL PROTEIN KIAA0233	UNKNOWN	Tax Id=10116 Similar to Hypothetical protein KIAA0233	237700	34932058	265857
CULLIN 4A	PROTEASOME/UBIQUITIN	Tax Id=10116 Similar to KIAA0695 protein	71450	34879447	314767
SIMILAR TO KIAA1407 PROTEIN	UNKNOWN	Tax Id=10116 Similar to KIAA1407 protein	75980	34869160	295453
SIMILAR TO LEK1	CYTOSKELETON	Tax Id=10116 Similar to LEK1	337700	34881142	192027
GUANINE NUCLEOTIDE EXCHANGE FACTOR GEF-H1	SIGNALING	Tax Id=10116 Similar to Lbc1 protein	113100	34857950	264247
SIMILAR TO LEUCINE-RICH REPEAT-CONTAINING PROTEIN 2	UNKNOWN	Tax Id=10116 Similar to Leucine-rich repeat-containing protein 2	45980	34866388	316728
SIMILAR TO MYOSIN VI	CYTOSKELETON	Tax Id=10116 Similar to MyoSin VI	167000	34865321	261550
SIMILAR TO NBL4	SIGNALING	Tax Id=10116 Similar to NBL4	95230	34878636	198264
PHF3	UNKNOWN	Tax Id=10116 Similar to PHD finger protein 3	226400	34874598	295897
SIMILAR TO PROLYL 4-HYDROXYLASE ALPHA IIA SUBUNIT	PROT MOD	Tax Id=10116 Similar to Prolyl 4-hydroxylaSe alpha Ila	66900	34870735	212585
	Subunit				

SRP RECEPTOR ALPHA SUBUNIT	PROT SYN/FOLD	Tax_id=10116 Similar to RIKEN cDNA 1300011P19	69740	34863012	256910
UNNAMED PROTEIN PRODUCT3	UNKNOWN	Tax_id=10116 Similar to RIKEN cDNA 1600013K19	91910	34867853	282761
DEAD (ASP-GLU-ALA-ASP) BOX POLYPEPTIDE 42	PROT SYN/FOLD	Tax_id=10116 Similar to RIKEN cDNA 1810047H21 gene	103600	27690029	238446
SIMILAR TO CAP-BINDING PROTEIN COMPLEX INTERACTING PR	NUCLEUS	Tax_id=10116 Similar to RIKEN cDNA 4931407K02	161300	34867357	282579
SIMILAR TO RIKEN CDNA 5730519E19 GENE	UNKNOWN	Tax_id=10116 Similar to RIKEN cDNA 5730519E19 gene	118100	34862241	227985
SB/CB404 PROTEIN	UNKNOWN	Tax_id=10116 Similar to RIKEN cDNA 9530027K23	73500	34851643	224054
SIMILAR TO RIKEN CDNA C730036B14 GENE	UNKNOWN	Tax_id=10116 Similar to RIKEN cDNA C730036B14 gene	216400	34865292	282808
SIMILAR TO RHO GTPASE ACTIVATING PROTEIN 2	SIGNALING	Tax_id=10116 Similar to Rho GTPase activating protein 2	89740	34877029	276572
SIMILAR TO SEMAPHORIN SUBCLASS 4 MEMBER G	PLASMA MB	Tax_id=10116 Similar to Semaphorin Subclass 4 member G	128000	34863455	222218
SHORT CHAIN DEHYDROGENASE REDUCTASE 9	DETOXIFICATION	Tax_id=10116 Similar to Short chain dehydrogenase reductase 9	40410	34866289	268103
SIMILAR TO SIGNAL RECOGNITION PARTICLE 68KDA	PROT SYN/FOLD	Tax_id=10116 Similar to Signal recognition particle 68kDa	73120	34875372	300246
SIMILAR TO STRUCTURAL MAINTENANCE OF CHROMOSOMES 1	NUCLEUS	Tax_id=10116 Similar to Structural maintenance of chromosome S 1beta	147300	34867523	216707
SIMILAR TO TETRATRICOPEPTIDE REPEAT PROTEIN 7 (TPR REP	UNKNOWN	Tax_id=10116 Similar to Tetratricopeptide repeat protein 7 (TPR repeat protein 7)	102100	34862046	196091
SIMILAR TO TRIM26 PROTEIN	UNKNOWN	Tax_id=10116 Similar to Trim26 protein	47090	34852035	264688
ARCHVILLIN	CYTOSKELETON	Tax_id=10116 Similar to archvillin	236900	34876218	258828
AUTOCRINE MOTILITY FACTOR RECEPTOR	PROTEASOME/UBIQUITIN	Tax_id=10116 Similar to autocrine motility factor receptor	68280	34851252	285136
SIMILAR TO BN280G18.3 (NOVEL PROTEIN)	UNKNOWN	Tax_id=10116 Similar to bn280G18.3 (novel protein)	38950	34868997	199323
SIMILAR TO CENTROMERE/KINETOCHORE PROTEIN ZW10 HOM	CYTOSKELETON	Tax_id=10116 Similar to centromere/kinetochore protein zw10 homolog	88170	34863346	192125
SIMILAR TO CHROMOSOME 2 OPEN READING FRAME 3; TRANSC	NUCLEUS	Tax_id=10116 Similar to chromosome 2 open reading frame 3	83470	34856267	196107
COPI COATOMER GAMMA-1 SUBUNIT	COAT	Tax_id=10116 Similar to coat protein gamma-cop	138100	34856387	267886
DJ1070B1.1 (KIAA0316 AND KIAA0967 PROTEINS)	UNKNOWN	Tax_id=10116 Similar to dj1070B1.1 (Similar to KIAA0316 and KIAA0967 proteins)	233200	34881575	253851
SIMILAR TO EXPRESSED SEQUENCE C87860	UNKNOWN	Tax_id=10116 Similar to expressed Sequence C87860	54690	34857072	242229
SIMILAR TO HYPOTHETICAL PROTEIN 4932411E22	UNKNOWN	Tax_id=10116 Similar to hypothetical protein 4932411E22	69500	34873297	232623
SIMILAR TO HYPOTHETICAL PROTEIN 5832424M12	UNKNOWN	Tax_id=10116 Similar to hypothetical protein 5832424M12	89010	34853466	213390
SIMILAR TO SEPTIN 6	GTPASE	Tax_id=10116 Similar to hypothetical protein FLJ10849	58770	34876531	204932
SIMILAR TO HYPOTHETICAL PROTEIN FLJ10900	UNKNOWN	Tax_id=10116 Similar to hypothetical protein FLJ10900	93700	34872027	198580
SIMILAR TO HYPOTHETICAL PROTEIN FLJ30373	UNKNOWN	Tax_id=10116 Similar to hypothetical protein FLJ30373	29880	34855399	229721
SIMILAR TO KIDNEY ANKYRIN REPEAT-CONTAINING PROTEIN	UNKNOWN	Tax_id=10116 Similar to kidney ankyrin repeat-containing protein	127000	34860436	261449
SIMILAR TO KINESIN FAMILY Y PROTEIN KIF1A	CYTOSKELETON	Tax_id=10116 Similar to kinesin family protein KIF1a	218300	34877667	265199
KINESIN FAMILY MEMBER 5C	CYTOSKELETON	Tax_id=10116 Similar to mKIAA0531 protein	114400	34854278	296600
SIMILAR TO MYELOID/LYMPHOID OR MIXED-LINEAGE LEUKEMIA	UNKNOWN	Tax_id=10116 Similar to myeloid/lymphoid or mixed-lineage leukemia 2	561200	34868150	316308
HEMATOPOIETIC GROWTH FACTOR RECEPTOR	BIOSYNTHETIC CARGO	Tax_id=10116 Similar to myeloproliferative leukemia virus oncogene	60890	34871078	277020
P140MDIA	SIGNALING	Tax_id=10116 Similar to p140mDia	140200	34878815	217100
SIMILAR TO CELL-CYCLE AND APOPTOSIS REGULATORY PROTE	SIGNALING	Tax_id=10116 Similar to p30 DBC protein	76270	34852526	276810
RENT1 PROTEIN	NUCLEUS	Tax_id=10116 Similar to regulator of nonSenSe transScriptS 1	47750	34877605	234739

RETINOBLASTOMA-ASSOCIATED FACTOR 600	TRANSCRIPTION	Tax_Id=10116 Similar to retinoblastoma-associated factor 600	577500	34872228	271261
ROOTLETIN	UNKNOWN	Tax_Id=10116 Similar to rootletin	234800	34872243	290689
TROPOMODULIN 3	CYTOSKELETON	Tax_Id=10116 Similar to tropomodulin 3	46420	34864364	261414
SIMILAR TO UBIQUITIN SPECIFIC PROTEASE 28	PROTEASOME/UBIQUITIN	Tax_Id=10116 Similar to ubiquitin specific protease 28	135800	34863342	319220
SIMILAR TO UBIQUITOUS TETRATRICOPEPTIDE CONTAINING PROTEIN	UNKNOWN	Tax_Id=10116 Similar to ubiquitous tetratricopeptide containing protein RoXan	111900	34867257	230656
VIMENTIN	CYTOSKELETON	Tax_Id=10116 Vimentin	53730	57480	82925
TRANSALDOLASE	METABOLISM	Transaldolase	37480	17433174	50402
SIMILAR TO ESTROGEN-RESPONSIVE FINGER PROTEIN	TRANSCRIPTION	Tripartite motif protein 25	71950	57164029	318709
TYROSINE-PROTEIN KINASE LYN	SIGNALING	Tyrosine-protein kinase LYN	58660	294583	71712
RING FINGER TRANSCRIPTION FACTOR	TRANSCRIPTION	Ubiquitin ligase protein RING2 RING finger protein 2 RING finger protein 1B RING1b	37620	27712522	33698
MUNC13-4 PROTEIN	TETHODOCK/FUS	Unc-13 homolog D Munc13-4	123500	5524667	20725
VACUOLAR PROTEIN SORTING 33A	TRAFFIC	Vacuolar protein sorting 33A	67510	23396893	55286
VACUOLAR PROTON TRANSLOCATING ATPASE 116 KDA SUBUNIT	MITOCHONDRIA	Vacuolar proton translocating ATPase 116 kDa subunit a isoform 1 V-ATPase 116 kDa isoform a1 Clathrin-coated vesicle/synaptic vesicle proton pump 116 kDa subunit	96330	206430	11413
ZINC FINGER	TRANSCRIPTION	Vacuolar proton pump subunit 1 Vacuolar adenosine triphosphatase subunit Ac116 Zinc finger protein	130500	7514121	134827
HYPOTHETICAL PROTEIN XP_344851	UNKNOWN	hypothetical protein XP_344851	46260	34854602	287423
OLFACTORY RECEPTOR MOR164-2	PLASMA MB	olfactory receptor Olr1265	35790	47577731	233320
SIMILAR TO ATP SYNTHASE, H+ TRANSPORTING, MITOCHONDRIAL F0 COMPLEX, SUBUNIT C (SUBUNIT 9), ISOFORM 2	MITOCHONDRIA	similar to ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9), isoform 2	14750	27685029	262837
DNAJC13	UNKNOWN	similar to CG8014-PA	126100	34865967	261337
SIMILAR TO HYPOTHETICAL PROTEIN KIAA0586	UNKNOWN	similar to Hypothetical protein KIAA0586	39910	34865368	294179
IMMUNOGLOBULIN HEAVY CHAIN CONSTANT REGION MU	BLOOD + OTHER CELLS	similar to IgH-6 protein	79080	34935297	225182
SIMILAR TO KIAA0789 PROTEIN	UNKNOWN	similar to KIAA0789 protein	40750	34872839	235178
SIMILAR TO DEDICATOR OF CYTOKINESIS PROTEIN 6	SIGNALING	similar to KIAA1771 protein	233300	34869877	199377
SIMILAR TO LDL RECEPTOR ADAPTOR PROTEIN	SIGNALING	similar to LDL receptor adaptor protein	60620	34872138	266460
PRKRA PROTEIN KINASE, INTERFERON-INDUCIBLE DOUBLE STRAND	SIGNALING	similar to PKR-associating protein RAX	34390	34856450	191003
SIMILAR TO RIKEN CDNA 1810045K17	UNKNOWN	similar to RIKEN cDNA 1810045K17	10150	34857339	270299
UNKNOWN4	UNKNOWN	similar to RIKEN cDNA C920006C10	16670	27718855	264993
RNA HELICASE A	NUCLEUS	similar to RNA helicase A	150200	34880497	203449
SIMILAR TO SLIT-ROBO RHO GTPASE-ACTIVATING PROTEIN 3; WAVE-ASSOCIATED RAC GTPASE ACTIVATING PROTEIN	SIGNALING	similar to SLIT-ROBO Rho GTPase-activating protein 3; WAVE-associated Rac GTPase activating protein	35530	34879743	229135
SIMILAR TO TRAV8-1	UNKNOWN	similar to TRAV8-1	14930	27699808	236003
B-IND1	SIGNALING	similar to butyrate-induced transcript 1	20610	34880723	260591
SIMILAR TO PKA C-BETA-2	SIGNALING	similar to cAMP-dependent protein kinase, beta-2-catalytic subunit (PKA C-beta-2)	73330	34861056	256498
SIMILAR TO CYCLIN G-ASSOCIATED KINASE	SIGNALING	similar to cyclin G-associated kinase	29950	34879280	254251
SIMILAR TO CYTOSOLIC BETA-ACTIN	CYTOSKELETON	similar to cytoplasmic beta-actin	27270	34881817	287459
ENTHOPROTEIN	COAT	similar to enthoprotein; epsin 4; clathrin interacting protein localized in the trans-Golgi region	64680	34880606	203525
EPIPLAKIN	CYTOSKELETON	similar to epiplakin	368200	34867002	318405

SIMILAR TO HYPOTHETICAL PROTEIN C230069C04 (1)	UNKNOWN		similar to hypothetical protein C230069C04	54880	34862585	263392
SIMILAR TO HYPOTHETICAL PROTEIN FLJ20331	UNKNOWN		similar to hypothetical protein FLJ20331 [Rattus norvegicus]	48370	34861003	248047
SIMILAR TO HYPOTHETICAL PROTEIN MGC22776	UNKNOWN		similar to hypothetical protein MGC22776	19210	34875293	302017
SERINE (OR CYSTEINE) PROTEINASE INHIBITOR, CLADE A (ALPHA-1 ANTITRYPSIN), MEMBER 9	PROT SYN/FOLD		similar to serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antitrypsin, antitrypsin), member 9	46840	34935459	300510
SIMILAR TO SOLUTE CARRIER FAMILY 22 MEMBER 6 ISOFORM b; renal organic anion transporter 1; para-aminohippurate transporter	PLASMA MB		similar to solute carrier family 22 member 6 isoform b; renal organic anion transporter 1; para-aminohippurate transporter	60990	34861829	307740
SORTING NEXIN 2	TRAFFIC		similar to sorting nexin 2	58530	34879535	319162
ACTIN RELATED PROTEIN 2/3 COMPLEX, SUBUNIT 5-LIKE	CYTOSKELETON		unknown	17010	27707156	199239
SIMILAR TO RIKEN CDNA 2010315L10	UNKNOWN		unknown	30510	34877499	258690
TRANSCRIPTION FACTOR BTF3	TRANSCRIPTION		(P20290) Isoform 2 of P20290	17700	56605700	33279
EGF, LATROPHILIN AND SEVEN TRANSMEMBRANE DOMAIN CONTAINING	PLASMA MB		(Q9ESC1) Isoform 2 of Q9ESC1	73800	11225481	129647
3' EXONUCLEASE	NUCLEUS		3' histone mRNA exonuclease 1 3' -5' exonuclease ER11	39580	78098993	241027
ALF-C1	NUCLEUS		ALF-C1	36210	3377279	75909
SIMILAR TO BLOCK OF PROLIFERATION 1	UNKNOWN		Block of proliferation 1 Predicted	82640	66730443	214565
BRAIN ZN-FINGER PROTEIN	TRANSCRIPTION		Brain Zn-finger protein Brain zinc finger protein	48300	58219528	307560
C-TYPE LECTIN 13	PLASMA MB		C-type lectin domain family 4 member F C-type lectin superfamily member 13 C-type lectin 13 Kupffer cell receptor	61100	68533633	60545
CATHEPSIN D	LYSOSOME		Cathepsin D precursor Cathepsin D 12 kDa light chain	44680	55882	141570
CATHEPSIN Z	LYSOSOME		Cathepsin D 9 kDa light chain Cathepsin D 34 kDa heavy chain Cathepsin D 30 kDa heavy chain	34190	60688149	160297
CENTAURIN-ALPHA2 PROTEIN	GTPASE		Centaurin-alpha 2	43520	9910340	42770
SIMILAR TO COMPLEMENT COMPONENT 1, Q SUBCOMPONENT, C1Q	BIOSYNTHETIC CARGO		Complement C1q subcomponent subunit A precursor	25920	62906846	355419
COMPLEMENT INHIBITORY FACTOR H	BIOSYNTHETIC CARGO		Complement inhibitory factor H	140300	18426830	96883
MEMBRANE-ASSOCIATED GUANYLATE KINASE-INTERACTING PROTEIN	SIGNALING		Connector enhancer of kinase suppressor of ras 2 Connector enhancer of KSR2 CNK2 Membrane-associated guanylate kinase-interacting protein MAGUIN	117400	50400225	169306
EDF-1 PROTEIN	SIGNALING		Endothelial differentiation-related factor 1 EDF-1 Multiprotein-bridging factor 1 MBF1 Calmodulin-associated peptide 19 CAP19	16370	62510525	98538
GM2 ACTIVATOR PROTEIN	LYSOSOME		GM2 activator protein	21520	27229316	157436
GLUTAMATE--CYSTEINE LIGASE REGULATORY SUBUNIT	METABOLISM		Glutamate--cysteine ligase regulatory subunit Gamma-glutamylcysteine synthetase Gamma-ECS GCS light chain	30550	8393446	51464
			Glutamate--cysteine ligase modifier subunit			

PEPTIDE N-MYRISTOYLTRANSFERASE 1	PROT MOD	Glycylpeptide N-tetradecanoyltransferase 1 Peptide N-myristoyltransferase 1 Myristoyl-CoA; protein N-myristoyltransferase 1 NMT 1 Type I N-myristoyltransferase	56860	81914601	229000
HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN D0	NUCLEUS	Heterogeneous nuclear ribonucleoprotein D0 hnRNP D0 AU-rich element RNA-binding protein 1	38190	9588096	47431
HYPOTHETICAL PROTEIN YGEH	UNKNOWN	Hypothetical protein ygeH	95100	2143952	80375
INTERFERON-INDUCED 35 KDA PROTEIN	SIGNALING	Interferon-induced protein 35 Predicted	31760	57526854	315195
LANTHIONINE SYNTHETASE C-LIKE PROTEIN 1	SIGNALING	LanC-like protein 1 40 kDa erythrocyte membrane protein p40	45240	6625487	126112
LUPUS LA PROTEIN HOMOLOG	TRANSCRIPTION	Lupus La protein homolog La ribonucleoprotein La autoantigen homolog	47780	729919	37247
LYSOZYME C, TYPE 1 PRECURSOR	LYSOSOME	Lysozyme	16730	7428180	39196
PAR INTERACTING PROTEIN	NUCLEUS	MYB binding protein 1a	144700	7514041	78121
MITOGEN-ACTIVATED PROTEIN KINASE 13	SIGNALING	Mitogen-activated protein kinase 13 Stress-activated protein kinase 4 Mitogen-activated protein kinase p38 delta MAP kinase p38 delta	42050	9506991	47245
NASCENT POLYPEPTIDE-ASSOCIATED COMPLEX ALPHA POLYPEPTIDE	PROT SYN/FOLD	Nascent polypeptide-associated complex subunit alpha Alpha-NAC Alpha-NAC/1.9.2	23380	27710456	74102
NUCLEOPHOSMIN	NUCLEUS	Nucleophosmin NPM Nucleolar phosphoprotein B23 Numatrin Nucleolar protein NO38	32560	7242160	44225
CADHERIN-11	PLASMA MB	PREDICTED: cadherin 11	88040	34851208	199319
FK506-BINDING PROTEIN 3	PROT SYN/FOLD	PREDICTED: similar to 25 kDa FK506-binding protein	25180	27664664	289953
CLATHRIN AP-3, BETA 3B	COAT	PREDICTED: similar to AP-3 complex beta3B subunit	119100	34857415	191978
AU-BINDING ENOYL-COA HYDRATASE	PEROXISOME	PREDICTED: similar to Auh protein	33340	34873875	242939
SIMILAR TO CDNA SEQUENCE BC003236	UNKNOWN	PREDICTED: similar to BC003236 protein	70080	34859748	277682
SIMILAR TO PROBABLE RNA HELICASE	NUCLEUS	PREDICTED: similar to RCK	54310	34879288	208269
SIMILAR TO APOLIPOPROTEIN L3 (APOLIPOPROTEIN L-III) (APOL)	BIOSYNTHETIC CARGO	PREDICTED: similar to RIKEN cDNA 2210421G13	39900	27662274	245688
RIBONUCLEASE P PROTEIN SUBUNIT P20	NUCLEUS	PREDICTED: similar to RPP20 protein	15740	27663642	220097
SIMILAR TO EUKARYOTIC TRANSLATION INITIATION FACTOR 2, 3	PROT SYN/FOLD	PREDICTED: similar to eukaryotic translation initiation factor 2, subunit 3, structural gene X-linked	51080	34880581	267441
SIMILAR TO H3 HISTONE FAMILY, MEMBER I	NUCLEUS	PREDICTED: similar to histone 1, H3g	33280	34876396	213604
SIMILAR TO KIAA0363	UNKNOWN	PREDICTED: similar to KIAA0363 protein	138500	34879082	246047
SLINGSHOT-2L	SIGNALING	PREDICTED: similar to slingshot-2L	159400	34873212	264614
PEPTIDYL-PROLYL CIS-TRANS ISOMERASE, MITOCHONDRIAL	MITOCHONDRIA	Peptidyl-prolyl cis-trans isomerase, mitochondrial precursor PPIase Rotamase Cyclophilin F	21810	56268806	88229
SIMILAR TO PROLIFERATION-ASSOCIATED PROTEIN 1	NUCLEUS	Proliferation-associated 2G4, 38kDa	43660	51948384	304663
RNA-DEPENDENT INITIATION FACTOR-2 KINASE	PROT SYN/FOLD	RNA-dependent initiation factor-2 kinase	58260	9506993	47246
RATSG1	NUCLEUS	Ratsg1	40610	18266700	111523
60S RIBOSOMAL PROTEIN L44	PROT SYN/FOLD	RpL36a protein NOD-derived CD11c +ve dendritic cells cDNA, RIKEN full-length enriched library, clone:F630020E11 product:ribosomal protein L36a, full insert sequence 16 days embryo heart cDNA, RIKEN full-length enriched library, clone:1920030G04 product:ribosomal protein L36a, full insert sequence Bone marrow macrophage cDNA, RIKEN full-length enriched library, clone:1830174F05 product:ribosomal protein L36a-like, full insert sequence	12440	62643486	111202

SH3 AND MULTIPLE ANKYRIN REPEAT DOMAINS PROTEIN 2	CYTOSKELETON	SH3 and multiple ankyrin repeat domains protein 2	134300	7513954	13148
PNUTS-PUTATIVE PROTEIN PHOSPHATASE 1 NUCLEAR TARGET	NUCLEUS	Serine/threonine-protein phosphatase 1 regulatory subunit 10 Phosphatase 1 nuclear targeting subunit Protein PNUTS MHC class I region proline-rich protein CAT53	92830	61214571	55278
SERUM DEPRIVATION RESPONSE GENE	UNKNOWN	Serum deprivation-response protein Phosphatidylserine-binding protein	46390	81884184	272310
SHWACHMAN-BODIAN-DIAMOND SYNDROME PROTEIN HOMOLOG	UNKNOWN	Shwachman-Bodian-Diamond syndrome Predicted	28750	56605652	227484
RNA-BINDING PROTEIN STAUFEN	PROT SYN/FOLD	Staufen isoform Stau+16	54800	9754866	60405
STRESS-INDUCED-PHOSPHOPROTEIN 1 (ST11)	SIGNALING	Stress-induced-phosphoprotein 1 ST11 Hsc70/Hsp90-organizing protein Hop	62570	54036435	82685
TSH RECEPTOR SUPPRESSOR ELEMENT-BINDING PROTEIN-1	TRANSCRIPTION	TSH receptor suppressor element-binding protein-1	35530	9653686	93202
SIMILAR TO TARDBP PROTEIN	UNKNOWN	Tax_id=10116 33 kDa protein	33300	34872473	212891
NUCLEOLIN	NUCLEUS	Tax_id=10116 Ensembl_locations(Chr-bp):9-85296295 nucleolin	77150	6981248	69538
SIMILAR TO 60S RIBOSOMAL PROTEIN L29	PROT SYN/FOLD	Tax_id=10116 Similar to 60S RIBOSOMAL PROTEIN L29 (P23)	16820	34880973	233078
CLATHRIN AP-3, BETA 1	COAT	Tax_id=10116 Similar to Adapter-related protein complex 3 beta 1 Subunit (Beta-adaptin 3A) (AP-3 complex beta-3A)	129800	34853134	203467
CD83 ANTIGEN	PLASMA MB	Subunit (Beta-3A-adaptin)	29030	34875124	281345
SIMILAR TO (RETINAL SHORT-CHAIN DEHYDROGENASE/REDUCTASE) BOX POLYPEPTIDE 28; DE	DETOXIFICATION	Tax_id=10116 Similar to Cgn-pending protein	159200	34858031	242726
SIMILAR TO DEAD (ASP-GLU-ALA-ASP) BOX POLYPEPTIDE 28; DE	PROT SYN/FOLD	Tax_id=10116 Similar to DEAD (ASP-Glu-Ala-ASP) box polypeptide 28	64620	34851714	284837
SIMILAR TO DEAD/H (ASP-GLU-ALA-ASP/HIS) BOX POLYPEPTIDE	PROT SYN/FOLD	Tax_id=10116 Similar to DEAD/H (ASP-Glu-Ala-ASP/HIS) box polypeptide RG-I	94370	34867138	315303
SIMILAR TO DNA SEGMENT CHR 10 ERATO DOI 739 EXPRESSED	UNKNOWN	Tax_id=10116 Similar to DNA Segment Chr 10 ERATO Doi 739 expressed like (21705)	118000	34864839	315844
SIMILAR TO HYPOTHETICAL PROTEIN KIAA0555	UNKNOWN	Tax_id=10116 Similar to Hypothetical protein KIAA0555	108700	34879361	286232
SIMILAR TO KIAA0342 PROTEIN	UNKNOWN	Tax_id=10116 Similar to KIAA0342 protein	333800	34866451	266038
NEBULIN	CYTOSKELETON	Tax_id=10116 Similar to Nebulin	913200	34854661	287849
SIMILAR TO QUINONE-REDUCTASE PROTEIN	UNKNOWN	Tax_id=10116 Similar to RIKEN cDNA 2810025M15	71590	34880767	272641
SIMILAR TO RIKEN CDNA 5630401D24	UNKNOWN	Tax_id=10116 Similar to RIKEN cDNA 5630401D24	81090	34880803	213507
SIMILAR TO RIKEN CDNA 5730409F24	UNKNOWN	Tax_id=10116 Similar to RIKEN cDNA 5730409F24	38500	34861617	317744
ZDHC9 PROTEIN	UNKNOWN	Tax_id=10116 Similar to RIKEN cDNA 9530098M12	30200	34881592	267183
SIMILAR TO RHO-RELATED BTB DOMAIN-CONTAINING PROTEIN	SIGNALING	Tax_id=10116 Similar to Rho-related BTB domain-containing protein 3	77710	34852777	300892
SIDEKICK 2; DROSOPHILA SIDEKICK-LIKE; CHICKEN SIDEKICK 2	PLASMA MB	Tax_id=10116 Similar to Sidekick 2	185200	34875033	275767
SIMILAR TO ZINC FINGER PROTEIN 35 (ZFP-35)	UNKNOWN	Tax_id=10116 Similar to Zinc finger protein 35 (Zfp-35)	87610	34878337	217979
ASH1 (ABSENT, SMALL, OR HOMEOTIC)-LIKE	UNKNOWN	Tax_id=10116 Similar to aSh1 (abSent, Small, or homeotic)-like	336900	34857960	247038
SIMILAR TO ACYL-COENZYME A DEHYDROGENASE FAMILY, MEMBER 8	MITOCHONDRIA	Tax_id=10116 Similar to acyl-Coenzyme A dehydrogenase family, member 8	28470	34866733	288241
COILED-COIL PROTEIN	TRAFFIC	Tax_id=10116 Similar to coiled-coil protein	148900	34869656	304228
COLLAGEN TYPE XIV	BIOSYNTHETIC CARGO	Tax_id=10116 Similar to collagen type XIV	169900	34866496	308317
COPINE III	TRAFFIC	Tax_id=10116 Similar to copine III	59690	34867199	274130
EUKARYOTIC TRANSLATION INITIATION FACTOR 4 GAMMA, 3	PROT SYN/FOLD	Tax_id=10116 Similar to eukaryotic translation initiation factor 4, gamma, 3	181400	34872195	316191

EUKARYOTIC TRANSLATION INITIATION FACTOR 4G I	PROT SYN/FOLD	Tax_id=101116 Similar to eukaryotic translation initiation factor 4G I	175000	34869741	239406
HYDROCEPHALUS-INDUCING PROTEIN	UNKNOWN	Tax_id=101116 Similar to hydrocephalus-inducing protein	144600	34851748	250307
SIMILAR TO HIGH GLUCOSE-REGULATED PROTEIN 8	UNKNOWN	Tax_id=101116 Similar to hypothetical protein FLJ31657	64050	34855501	253349
MEIOTIC RECOMBINATION PROTEIN REC14	NUCLEUS	Tax_id=101116 Similar to meiotic recombination protein REC14	28800	34863419	201803
SIMILAR TO METHIONYL AMINOPEPTIDASE 1	PROT MOD	Tax_id=101116 Similar to methionyl aminopeptidase 1	53240	34860820	221417
MICROTUBULE-ASSOCIATED PROTEIN 4	CYTOSKELETON	Tax_id=101116 Similar to microtubule-associated protein 4	303100	34866431	264572
GOLGI-ASSOCIATED MICROTUBULE-BINDING PROTEIN	CYTOSKELETON	Tax_id=101116 Similar to thyroid hormone receptor interactor 11	115700	34867565	247636
SIMILAR TO VASCULAR ENDOTHELIAL ZINC FINGER 1	TRANSCRIPTION	Tax_id=101116 Similar to vascular endothelial zinc finger 1	82930	34872980	252804
TRANSCRIPTIONAL ACTIVATOR PROTEIN PUR-ALPHA	NUCLEUS	Transcriptional activator protein PUR-alpha Purine-rich single-stranded DNA-binding protein alpha	34880	34878862	81816
TROPONIN T, FAST SKELETAL MUSCLE ISOFORMS BETA/ALPHA	CYTOSKELETON	Troponin T, fast skeletal muscle isoforms beta/alpha	30750	78883516	31540
UBIQUITIN-LIKE PROTEIN SUMO-1 CONJUGATING ENZYME	PROTEASOME/UBIQUITIN	Ube2i-prov protein	18010	6981690	22316
HISTONE H2B	NUCLEUS	histone H2B	13770	223096	135066
HISTONE H2A	NUCLEUS	similar to Histone H2A.o (H2A/o) (H2A.2) (H2a-615)	21070	34858256	279473
NADP+-SPECIFIC ISOCITRATE DEHYDROGENASE	MITOCHONDRIA	similar to NADP+-specific isocitrate dehydrogenase	14720	34857317	195949
(HNRNP-Q) (SYNAPTOTAGMIN BINDING, CYTOPLASMIC RNA INTERACTING)	NUCLEUS	similar to Nsap1-pending protein [Rattus norvegicus]	82690	34865422	221070
BIPHENYL HYDROLASE-LIKE (SERINE HYDROLASE, BREAST EPITHELIAL)	DETOXIFICATION	similar to RIKEN cDNA 2010012D11	22040	34875339	204593
NUDT16 PROTEIN	UNKNOWN	similar to RIKEN cDNA 2310041H06 [Rattus norvegicus]	21700	34865854	267421
XPA BINDING PROTEIN 1	NUCLEUS	similar to RIKEN cDNA 2410004J02	40230	34862639	270236
TUBBY RELATED PROTEIN 2	TRANSCRIPTION	similar to Tubby related protein 2 (Tubby-like protein 2) (P4-6 protein) [Rattus norvegicus]	48750	34856083	256460
PEROXISOMAL ACYL-COA THIOESTERASE 2B; LIKELY ORTHOLOG	PEROXISOME	similar to peroxisomal long chain acyl-CoA thioesterase la	46360	27667388	160562
RB BINDING PROTEIN	NUCLEUS	similar to retinoblastoma-binding protein 1 isoform I; retinoblastoma-binding protein 1	158900	34865364	211734
TELOMERIC AND TETRAPLEX DNA BINDING PROTEIN QTP42 V	NUCLEUS	telomeric and tetraplex DNA binding protein qTP42 V - rat (fragment)	4079	7446334	72931
MITOCHONDRIAL TRANSCRIPTION FACTOR A	MITOCHONDRIA	transcription factor A, mitochondrial	28140	4877353	75905
SIMILAR TO HYPOTHETICAL PROTEIN FLJ13089	UNKNOWN	unknown	111800	34872548	263673
BICAUDAL D PROTEIN	UNKNOWN	Bicaudal D protein	93420	38454268	223054
GALECTIN-3	TRANSCRIPTION	Galectin-3	27200	57870645	71532
HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1	NUCLEUS	Heterogeneous nuclear ribonucleoprotein A1	34200	70819	29410
HOMEODOMAIN PROTEIN OTX2	NUCLEUS	Homeobox protein OTX2	31640	27699029	44484
HYDROXYSTEROID (17-BETA) DEHYDROGENASE 8	DETOXIFICATION	Hydroxysteroid (17-beta) dehydrogenase 8	26790	47087119	301041
N-MYC PROTO-ONCOGENE PROTEIN	TRANSCRIPTION	N-myc proto-oncogene protein	49690	61556942	103852
RAS-GTPASE-ACTIVATING PROTEIN SH3-DOMAIN BINDING PROTEIN	TRAFFIC	PREDICTED: Ras-GTPase-activating protein SH3-domain binding protein	51790	34870749	252580
SIMILAR TO PROTEIN CGI-117 (PROTEIN HSPC111)	UNKNOWN	PREDICTED: similar to DNA segment, Chr 13, Wayne State University 177 expressed	21120	95102018	253829
SYNAPTIC VESICLE MEMBRANE PROTEIN VAT-1 HOMOLOG	UNKNOWN	PREDICTED: similar to Vesicle amine transport protein 1 homolog (T. californica)	43120	76096306	312134
SIMILAR TO HYPOTHETICAL PROTEIN BC013949	UNKNOWN	PREDICTED: similar to hypothetical protein BC013949	25320	27668745	274788
PEROXISOME PROLIFERATOR-ACTIVATED RECEPTOR GAMMA (1-BETA)	PEROXISOME	Peroxisome proliferator-activated receptor gamma coactivator 1-beta PPAR gamma coactivator-1beta PPARGC-1beta PGC-1-beta	109400	28570176	279034
SIGNAL RECOGNITION PARTICLE 14 KDA PROTEIN	PROT SYN/FOLD	Signal recognition particle 14 kDa protein SRP14	12510	27731985	38009

SPHINGOSINE 1-PHOSPHATE RECEPTOR EDG-1	PLASMA MB	Sphingosine 1-phosphate receptor Edg-1 Sphingosine 1-phosphate receptor 1 S1P1	42750	8393290	51431
ZETA-CRYSTALLIN	CYTOSKELETON	Tax_Id=10116 Ensembl_locations(Chr-bp):2-252454876 similar to crystallin, zeta	37130	34860973	210117
PLASMINOGEN ACTIVATOR INHIBITOR 1 RNA-BINDING PROTEIN	SIGNALING	Tax_Id=10116 Ensembl_locations(Chr-bp):4-97148803 Hypothetical RNA binding protein RDA288	43010	18041977	114376
SIMILAR TO ALY	TRANSCRIPTION	Tax_Id=10116 Similar to ALY	21140	34875658	307156
SIMILAR TO ATP-BINDING CASSETTE TRANSPORTER SUB-FAMILY	UNKNOWN	Tax_Id=10116 Similar to Abca3 protein	108000	34860091	282004
SIMILAR TO B CELL PHOSPHOINOSITIDE 3-KINASE ADAPTOR	UNKNOWN	Tax_Id=10116 Similar to B cell phosphoinositide 3-kinase adaptor	103600	34862928	233246
SIMILAR TO CALMODULIN 4 (CALCIUM-BINDING PROTEIN DD112)	PROT SYN/FOLD	Tax_Id=10116 Similar to Calmodulin 4 (Calcium-binding protein Dd112)	16820	34876599	290493
FLASH	SIGNALING	Tax_Id=10116 Similar to FLASH	219700	34867106	267985
PTB-ASSOCIATED SPLICING FACTOR	TRANSCRIPTION	Tax_Id=10116 Similar to PTB-associated Splicing factor	65140	34871066	310879
PROTEIN TRANSPORT PROTEIN SEC24D (SEC24-RELATED PROTEIN)	COAT	Tax_Id=10116 Similar to Protein transport protein Sec24D (SEC24-related protein D)	110300	34859959	219262
SIMILAR TO RIKEN CDNA 1700034M03 GENE	UNKNOWN	Tax_Id=10116 Similar to RIKEN cDNA 1700034M03 gene	122500	34854321	261953
SIMILAR TO ACTIVE BREAKPOINT CLUSTER REGION-RELATED PROTEIN	SIGNALING	Tax_Id=10116 Similar to active breakpoint cluster region-related protein isoform a	138700	34872879	248137
CYTOCHROME P450 NA5	DETOXIFICATION	Tax_Id=10116 Similar to cytochrome P450RA1-2	95320	34862888	279884
FERROCHELATASE	MITOCHONDRIA	Tax_Id=10116 Similar to ferrochelatase	71200	34932061	313806
SPLICING FACTOR 3B, SUBUNIT 1, 155KD	NUCLEUS	Tax_Id=10116 Splicing factor 3b, Subunit 1, 155kD	146000	34875872	194817
UBIQUINONE BIOSYNTHESIS PROTEIN COQ7 HOMOLOG	MITOCHONDRIA	Ubiquinone biosynthesis protein COQ7 homolog Coenzyme Q biosynthesis protein 7 homolog Timing protein clk-1 homolog	20140	7446711	30131
SIMILAR TO NEURONAL APOPTOSIS INHIBITORY PROTEIN	SIGNALING	similar to neuronal apoptosis inhibitory protein	158900	34853608	241983
SIMILAR TO PUTATIVE ZN-FINGER PROTEIN C47S	UNKNOWN	similar to putative Zn-finger protein C47S	31790	34874602	251444
NUCLEOLAR TRANSCRIPTION FACTOR 1 (UPSTREAM BINDING FACTOR 1)	TRANSCRIPTION	(P25977) Isoform UB2 of P25977	84970	112465	11409
AMILORIDE-SENSITIVE CATION CHANNEL 1, NEURONAL	PLASMA MB	(Q62962) Isoform 2 of Q62962	63120	35902696	106925
60S RIBOSOMAL PROTEIN L39	PROT SYN/FOLD	60S ribosomal protein L39	6407	6981484	4822
60S RIBOSOMAL PROTEIN L40	PROT SYN/FOLD	60S ribosomal protein L40 CEP62	6181	973178	77849
CANALICULAR MULTISPECIFIC ORGANIC ANION TRANSPORTER	PLASMA MB	ATP-binding cassette, sub-family C (CFTR/MRP), member 3	169300	3242460	52680
SHORT CHAIN ACYL-COA DEHYDROGENASE	MITOCHONDRIA	Acyl-coenzyme A dehydrogenase, short chain	44970	48734846	84143

JAGUNAL HOMOLOG 1	UNKNOWN	Adult male thymus cDNA, RIKEN full-length enriched library, clone:5830427H10 product:GL009 homolog Bone marrow macrophage cDNA, RIKEN full-length enriched library, clone:1830027D22 product:GL009 homolog 12 days embryo spinal cord cDNA, RIKEN full-length enriched library, clone:C530010F19 product:GL009 homolog Jagunal homolog 1 18-day embryo whole body cDNA, RIKEN full-length enriched library, clone:1110014A23 product:CDNA FLJ14602 FIS, CLONE NT2RP1000191 homolog	21100	68534555	32612
ADENYLATE KINASE 3 ALPHA-LIKE 1	MITOCHONDRIA	Ak3 protein	25490	40352787	270293
AMYLOID BETA A4 PRECURSOR PROTEIN-BINDING FAMILY B MEMBER 3	BIOSYNTHETIC CARGO	Amyloid beta A4 precursor protein-binding family B member 3 Fe65-like protein 2 Fe65L2	54910	2293387	157236
C-4 METHYL STEROL OXIDASE	DETOXIFICATION	C-4 methylsterol oxidase Methylsterol monooxygenase Neuropilin 1 RANP-1	34960	38649308	807
C4B-BINDING PROTEIN ALPHA CHAIN	BIOSYNTHETIC CARGO	C4b-binding protein alpha chain precursor C4bp	62270	899380	3668
CARBONYL REDUCTASE 4	DETOXIFICATION	Carbonyl reductase 4	25290	55562775	166315
CATHEPSIN H	LYSOSOME	Cathepsin H precursor	37100	6978721	3719
CYTOCHROME C OXIDASE POLYPEPTIDE VIIC, MITOCHONDRIAL	MITOCHONDRIA	Cytochrome c oxidase polypeptide VIic, mitochondrial VIIIA	1117	1169069	71407
DIACYLGLYCEROL O-ACYLTRANSFERASE 1	PROT MOD	Diacylglycerol O-acyltransferase 1 Diglyceride acyltransferase	56870	9965432	145183
HEXOKINASE, TYPE I	METABOLISM	Hexokinase, type I	102400	6981022	3926
HNRNP PROTEIN	NUCLEUS	HnRNP protein	18280	3021529	57359
SIMILAR TO RIKEN CDNA 5730470L24	UNKNOWN	Hypothetical protein RGD1311316	23580	62644110	229302
INSIG2 MEMBRANE PROTEIN (INSULIN INDUCED GENE 2)	PROT SYN/FOLD	INSIG2 membrane protein Insulin induced gene 2	24970	55250700	200861
INOSITOL 1,4,5-TRISPHOSPHATE RECEPTOR TYPE 1	CALCIUM TRANS/BIND	Inositol 1,4,5-trisphosphate receptor type 1	19180	204967	126700
CARNITINE DEFICIENCY-ASSOCIATED GENE EXPRESSED IN VENTRICLE 1	UNKNOWN	Intraflagellar transport 81 Carnitine deficiency-associated protein expressed in ventricle 1 CDV-1 protein	79030	48474223	282022
CG6210-LIKE	UNKNOWN	LOC362065 protein Transmembrane protein	62200	45680888	339290
LRRGT00033	UNKNOWN	LRRGT00033	230300	37654282	223419
SIMILAR TO COAGULATION FACTOR XI; PLASMA THROMBOPLASTIN	BIOSYNTHETIC CARGO	LRRGT00086	62990	37361858	209490
MYOSIN HEAVY CHAIN, CARDIAC MUSCLE ALPHA ISOFORM	CYTOSKELETON	Myosin heavy chain, cardiac muscle alpha isoform MyHC-alpha	223500	8393804	51542
SIMILAR TO SMFN PROTEIN	NUCLEUS	Oligoribonuclease, mitochondrial precursor Small fragment nuclease RNA exonuclease 2 homolog	26750	81910234	216886
SIMILAR TO CD7 PROTEIN	PLASMA MB	PREDICTED: similar to Cd7 protein	22880	27690996	222889
NEDD8 ULTIMATE BUSTER-1	PROTEASOME/UBIQUITIN	PREDICTED: similar to NEDD8 ultimate buster-1 (BS4 protein)	73130	34853974	279528

EUKARYOTIC TRANSLATION INITIATION FACTOR 3, SUBUNIT 12	PROT SYN/FOLD	PREDICTED: similar to RIKEN cDNA 120009C21	25110	27730981	189964
SIMILAR TO RS21-C6 PROTEIN	UNKNOWN	PREDICTED: similar to RS21-C6 protein	32140	34877104	218331
STROMAL CELL-DERIVED FACTOR 2 (SDF-2)	BLOOD + OTHER CELLS	PREDICTED: similar to Stromal cell-derived factor 2 precursor (SDF-2)	24060	27673471	232984
SIMILAR TO HYPOTHETICAL PROTEIN FLJ31364	NUCLEUS	PREDICTED: similar to hypothetical protein 6820428D13	64490	27688925	279415
MEMBRANE PROGESTIN RECEPTOR ALPHA	DETOXIFICATION	PREDICTED: similar to membrane progesterin receptor alpha	39280	27732829	204220
SIMILAR TO REGULATOR OF G-PROTEIN SIGNALING RGS18	SIGNALING	PREDICTED: similar to regulator of G-protein signaling RGS18	27660	34880519	259576
SIMILAR TO SEX-DETERMINATION PROTEIN HOMOLOG FEM1B	UNKNOWN	PREDICTED: similar to sex-determination protein homolog Fem1b	70240	27720561	314220
SP12	PROT SYN/FOLD	PREDICTED: similar to signal peptidase 12kDa	11750	27667224	307512
SIMILAR TO ZINEDIN	SIGNALING	PREDICTED: similar to zinedin	81440	34855229	315735
SIMILAR TO HSPC288	UNKNOWN	Probable ergosterol biosynthetic protein 28	15810	62651081	178365
RNA 3'-TERMINAL PHOSPHATE CYCLASE	NUCLEUS	RNA terminal phosphate cyclase domain 1	39310	51948426	319337
SH3P13	UNKNOWN	SH3P13 SH3 domain protein 2 C1	35310	7109256	75738
POLYCOMB-GROUP PROTEIN	UNKNOWN	Scm-like with four mbt domains 1	97510	8100077	78111
SIMILAR TO RIKEN CDNA 1100001H23	UNKNOWN	Tax_id=10116 Ensembl_locations(Chr-bp):4-173856695;4-173883435 similar to RIKEN cDNA 1100001H23	68540	34858551	236607
INOSINE MONOPHOSPHATE DEHYDROGENASE 1	METABOLISM	Tax_id=10116 Ensembl_locations(Chr-bp):4-56330652 similar to Impdh1 protein	60730	34855047	190455
SIMILAR TO 2810022L02RIK PROTEIN	UNKNOWN	Tax_id=10116 Ensembl_locations(Chr-bp):9-56745024 similar to 2810022L02Rik protein	31270	348777015	195304
GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE (GAPDH)	METABOLISM	Tax_id=10116 Hypothetical protein XP_340782	19430	34870634	206459
SIMILAR TO 25 KDA BRAIN-SPECIFIC PROTEIN (P25-ALPHA)	UNKNOWN	Tax_id=10116 Similar to 25 kDa brain-Specific protein (p25-alpha)	30720	34853331	206115
SIMILAR TO OTTHUMP0000028696	UNKNOWN	Tax_id=10116 Similar to A1428795 protein	225500	34872984	229208
SIMILAR TO CALMODULIN REGULATED SPECTRIN-ASSOCIATED	UNKNOWN	Tax_id=10116 Similar to CG33130-PA	132700	34853057	208493
FRUCTOSAMINE-3-KINASE-RELATED PROTEIN	SIGNALING	Tax_id=10116 Similar to Hypothetical protein 9030012M21	37150	34875719	205153
SIMILAR TO KIAA1208 PROTEIN	UNKNOWN	Tax_id=10116 Similar to KIAA1208 protein	154100	34864701	229899
HYPOTHETICAL PROTEIN LOC303749	UNKNOWN	Tax_id=10116 Similar to RIKEN cDNA 1110031I02	36810	34875673	300976
UDP-N-ACETYLGLUCOSAMINE (UDP-GLCNAC) TRANSPORTER	PROT MOD	Tax_id=10116 Similar to RIKEN cDNA 2310050P13	55910	34859909	271576
SIMILAR TO RIKEN CDNA 4932408F18	UNKNOWN	Tax_id=10116 Similar to RIKEN cDNA 4932408F18	164100	34867309	293100
SIMILAR TO RIBONUCLEASE III (RNASE III) (P241)	NUCLEUS	Tax_id=10116 Similar to Ribonuclease III (RNase III) (p241)	170500	34854376	206108
SIMILAR TO SHORT TRANSIENT RECEPTOR POTENTIAL CHANNEL	PLASMA MB	Tax_id=10116 Similar to Short transient receptor potential channel 3 (TrpC3) (Htrp3)	118800	34873770	228349
SIMILAR TO SULFATASE MODIFYING FACTOR 2	PROT MOD	Tax_id=10116 Similar to Sulfatase modifying factor 2	25680	34872061	221314
COPINE IV	TRAFFIC	Tax_id=10116 Similar to copine IV	96010	34865971	245798

SIMILAR TO DJ545L17.1 (NOVEL PROTEIN SIMILAR TO RAD21 (S. pombe))	UNKNOWN	Tax_id=10116 Similar to dJ545L17.1 (novel protein Similar to RAD21 (S. pombe)) homolog (KIAA0078))	23480	34858963	293085
SIMILAR TO ENDOPHILIN B1b	PROT MOD	Tax_id=10116 Similar to endophilin B1b	47410	34860931	263938
FIDGETIN	UNKNOWN	Tax_id=10116 Similar to fidgetin	84370	34854854	247355
HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN D-LIKE; A+	NUCLEUS	Tax_id=10116 Similar to heterogeneous nuclear ribonucleoprotein D-like	58310	34876235	191966
SIMILAR TO HYPOTHETICAL PROTEIN FLJ32785	UNKNOWN	Tax_id=10116 Similar to hypothetical protein FLJ32785	89490	34858137	311347
LENG8_PREDICTED PROTEIN	UNKNOWN	Tax_id=10116 Similar to leukocyte receptor cluster member 8	103400	34854521	313918
LUNG ALPHA/BETA HYDROLASE FOLD PROTEIN 3	UNKNOWN	Tax_id=10116 Similar to lung alpha/beta hydrolase fold protein 3	50090	34877891	224186
RHOBTB2	GTPASE	Tax_id=10116 Similar to mKIAA0717 protein	79880	34874404	284812
SIMILAR TO MKIAA1707 PROTEIN	UNKNOWN	Tax_id=10116 Similar to mKIAA1707 protein	124200	34868019	273598
MEMBRANE BOUND O-ACYL TRANSFERASE	PROT MOD	Tax_id=10116 Similar to malignant cell expression-enhanced gene/tumor progression-enhancer	33720	34854458	281230
SIMILAR TO MEMBRANE RECEPTOR (5H375)	UNKNOWN	Tax_id=10116 Similar to membrane receptor (5H375)	42380	34865609	318262
SIMILAR TO TOLLOID-LIKE 2	SIGNALING	Tax_id=10116 Similar to tollid-like 2	23740	34883204	298591
TRANSMEMBRANE PROTEIN INDUCED BY TUMOR NECROSIS FACTOR	UNKNOWN	Transmembrane protein induced by tumor necrosis factor alpha	40660	58219512	260939
CYTOCHROME-C OXIDASE (EC 1.9.3.1) CHAIN VIIa, HEPATIC	MITOCHONDRIA	cytochrome-c oxidase (EC 1.9.3.1) chain VIIa, hepatic - rat (fragment)	1246	7513957	80282
HYPOTHETICAL PROTEIN XP_347087	UNKNOWN	hypothetical protein XP_347087	13870	34866914	300655
SIMILAR TO GLYCINE DECARBOXYLASE	MITOCHONDRIA	similar to Glycine decarboxylase [Rattus norvegicus]	111900	34862790	260747
SIMILAR TO KIAA0445 PROTEIN	UNKNOWN	similar to KIAA0445 protein	198000	34877826	256921
SIMILAR TO PHOSPHOACETYLGLUCOSAMINE MUTASE (PAGM)	METABOLISM	similar to Phosphoacetylglucosamine mutase (PAGM) (Acetylglucosamine phosphomutase) (N-acetylglucosamine-phosphate mutase) (Phosphoglucosamine mutase) [Rattus norvegicus]	50750	34865378	202185
RNA-BINDING PROTEIN ISOFORM G3BP-2A	SIGNALING	similar to RNA-binding protein isoform G3BP-2a	54070	34876568	211028
HEAT SHOCK PROTEIN 60 (LIVER); HEAT SHOCK 60KD PROTEIN	PROT SYN/FOLD	similar to heat shock protein 60 (liver); heat shock 60kD protein 1 (chaperonin)	30730	34860223	220421
SIMILAR TO HYPOTHETICAL PROTEIN MGC27616	UNKNOWN	similar to hypothetical protein MGC27616	108100	34871738	239371
SIMILAR TO INHIBITOR OF GROWTH FAMILY, MEMBER 3	TRANSCRIPTION	similar to inhibitor of growth family, member 3	56500	34855011	234073
SIMILAR TO OOCYTE-TESTIS GENE 1	UNKNOWN	similar to oocyte-testis gene 1 [Rattus norvegicus]	99590	34864546	279578
AA2-020	UNKNOWN	(Q5M828) Isoform 2 of Q5M828	19640	33086520	284155
HISTONE ACETYLTRANSFERASE	NUCLEUS	(Q810T5) Isoform 2 of Q810T5	66820	29650457	268104
TESTIS-SPECIFIC A-KINASE-ANCHORING-PROTEIN	SIGNALING	A-kinase anchor protein 14 Testis-specific A-kinase-anchoring protein TAKAP-80 TAKAP-1.2	55760	46395561	137155
ADP-RIBOSYLATION FACTOR-LIKE 6 INTERACTING PROTEIN 1	UNKNOWN	ADP-ribosylation-like factor 6-interacting protein Arf6p1 protein	23450	68534822	139514

ATP-BINDING CASSETTE PROTEIN C12 VARIANT A	UNKNOWN	ATP-binding cassette protein C12 variant A	144200	37778161	337364
BAND 3 ANION TRANSPORT PROTEIN	PLASMA MB	Band 3 anion transport protein	103200	20141169	66007
CLUSTERIN	BIOSYNTHETIC CARGO	Clusterin	24930	11127974	36009
COMPLEMENT REGULATORY PROTEIN	PLASMA MB	Complement regulatory protein Cry precursor Antigen 5I2	61680	9506513	35260
CYTOCHROME C OXIDASE POLYPEPTIDE VIIA-LIVER/HEART, MITOCHONDRIA	MITOCHONDRIA	Cytochrome c oxidase polypeptide VIIa-liver/heart, mitochondrial precursor Cytochrome c oxidase subunit VIIa-L	9353	56025	90517
SIMILAR TO RIKEN CDNA 6720485C15	UNKNOWN	Dephospho-CoA kinase domain containing	27350	56090393	318309
R. VAMP8	TETH/DOCK/FUS	Endobrevin	7348	18655558	37566
EVOLUTIONARILY CONSERVED SIGNALING INTERMEDIATE IN TOLL PATHWAY	SIGNALING	Evolutionarily conserved signaling intermediate in Toll pathway	49620	55741518	276570
F-ACTIN BINDING PROTEIN B-NEXILIN	CYTOSKELETON	F-actin binding protein b-Nexilin	78390	40538878	173663
N-RAS	GTPASE	GTPase NRas precursor Transforming protein N-Ras	21240	68534734	41183
GLIA MATURATION FACTOR BETA	CYTOSKELETON	Glia maturation factor beta GMF-beta	16610	111660	148966
UNKNOWN (PROTEIN FOR MGC:72996)	UNKNOWN	Hypothetical protein MGC72996	20710	38454298	220427
SIMILAR TO RIKEN CDNA 4933403F05	UNKNOWN	LEA 4 domain containing protein RGD1359600	31470	56090371	205582
NEURAL STEM CELL DERIVED NEURONAL SURVIVAL PROTEIN	TRAFFIC	Multiple coagulation factor deficiency protein 2 homolog precursor Neural stem cell-derived neuronal survival protein	16150	49036094	216613
NEURONAL NICOTINIC ACETYLCHOLINE RECEPTOR SUBUNIT	PLASMA MB	Neuronal acetylcholine receptor protein subunit alpha-10 precursor Nicotinic acetylcholine receptor subunit alpha 10	49820	68051992	176273
OBSCURIN	GTPASE	NACHR alpha 10	88460	28273604	261258
SIMILAR TO GLUCOKINASE	UNKNOWN	PREDICTED: similar to ATP-dependent glucokinase	53920	34863772	279185
SIMILAR TO BCL2-LIKE 13	MITOCHONDRIA	PREDICTED: similar to BCL2-like 13	46730	34858394	258284
CDNA SEQUENCE BC023105	UNKNOWN	PREDICTED: similar to CDNA sequence BC023105	47510	34932132	297879
COILED-COIL-HELIX-COILED-COIL-HELIX DOMAIN CONTAINING 6	UNKNOWN	PREDICTED: similar to Coiled-coil-helix-coiled-coil-helix domain containing 6	35250	34856405	277277
GPI TRANSAMIDASE COMPONENT PIG-T PRECURSOR (PHOSPHATIDYLINOSITOL-GLYCAN BIOSYNTHESIS, CLASS T PROTEIN) (NEURONAL DEVELOPMENT-ASSOCIATED PROTEIN 7)	METABOLISM	PREDICTED: similar to GPI transamidase component PIG-T precursor (Phosphatidylinositol-glycan biosynthesis, class T protein) (Neuronal development-associated protein 7)	65550	34860689	195113
GOA	SIGNALING	PREDICTED: similar to Tripartite motif protein 47	70030	27690552	251068
POTASSIUM VOLTAGE-GATED CHANNEL SUBFAMILY KQT MEMBER 2	PLASMA MB	Potassium voltage-gated channel subfamily KQT member 2	93950	3641300	51393
		Voltage-gated potassium channel subunit Kv7.2 Potassium channel subunit alpha KvLQT2 KQT-like 2			

PRESENILIN 1	SIGNALING	Presenilin 1	52790	6174931	37272
SERINE/THREONINE-PROTEIN KINASE PLK	SIGNALING	Serine/threonine-protein kinase PLK1 Polo-like kinase 1 PLK-1	68310	497994	12071
SIMILAR TO CDNA SEQUENCE BC003324	UNKNOWN	Similar to cDNA sequence BC003324	22440	51948382	314265
SIMILAR TO PROTEIN CGI-51	UNKNOWN	Sorting and assembly machinery component 50 homolog	51960	51948454	255631
SYNTAXIN BINDING PROTEIN MUNC18-3	TETH/DOCK/FUS	Syntaxin binding protein Munc18-3 Syntaxin binding protein 3	68020	71051327	157267
HYPOTHETICAL PROTEIN XP_346991	UNKNOWN	Tax_id=10116 HypoHelical protein XP_346991	26610	34857419	273429
SIMILAR TO 60S RIBOSOMAL PROTEIN L29 (P23)	PROT SYN/FOLD	Tax_id=10116 Similar to 60S RIBOSOMAL PROTEIN L29 (P23)	16860	34860240	261531
SIMILAR TO A-KINASE ANCHOR PROTEIN 9 ISOFORM 2; YOTIAO;	SIGNALING	Tax_id=10116 Similar to A-kinase anchor protein 9 isoform 2	441400	34854301	223472
SIMILAR TO BRCA1 INTERACTING PROTEIN C-TERMINAL HELICA	UNKNOWN	Tax_id=10116 Similar to BRCA1 interacting protein C-terminal helicaSe 1	114500	34872948	221550
CUB AND SUSHI MULTIPLE DOMAINS 3	UNKNOWN	Tax_id=10116 Similar to CUB and SuShi multiple domains 3	213400	34866475	195940
SIMILAR TO FYVE AND COILED-COIL DOMAIN CONTAINING 1	SIGNALING	Tax_id=10116 Similar to FYVE and coiled-coil domain containing 1	174100	34866719	308794
SIMILAR TO KIAA0528 PROTEIN	UNKNOWN	Tax_id=10116 Similar to KIAA0528 protein	131100	34858585	263505
SIMILAR TO MYOSIN HEAVY CHAIN A (MHCA)	CYTOSKELETON	Tax_id=10116 Similar to MyoSin heavy chain A (MHCA)	92190	34878271	241434
SIMILAR TO PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE 3-KIN	SIGNALING	Tax_id=10116 Similar to Phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic subunit, delta isoform (PI3-kinase p110 subunit delta) (PtdIns-3-kinase p110) (PI3K) (p110delta)	111000	34872607	194716
TYPE I TRANSMEMBRANE C-TYPE LECTIN RECEPTOR DCL-1	UNKNOWN	Tax_id=10116 Similar to RIKEN cDNA 1110055L24	27770	34854713	201498
SIMILAR TO RIKEN CDNA 3000003F02	UNKNOWN	Tax_id=10116 Similar to RIKEN cDNA 3000003F02	80990	34867913	317963
SIMILAR TO RIKEN CDNA 4930548H24	UNKNOWN	Tax_id=10116 Similar to RIKEN cDNA 4930548H24	50800	34881177	287094
INTRAMEMBRANE PROTEASE	PROT MOD	Tax_id=10116 Similar to SPPL2b	87570	34873981	306369
SIMILAR TO SERINE/THREONINE KINASE	SIGNALING	Tax_id=10116 Similar to Serine/threonine kinase	179600	34874060	212247
T-BOX TRANSCRIPTION FACTOR TBX10 (T-BOX PROTEIN 10)	TRANSCRIPTION	Tax_id=10116 Similar to T-box 1	54510	34861377	314602
SIMILAR TO TYROSINE-PROTEIN KINASE JAK1 (JANUS KINASE 1)	SIGNALING	Tax_id=10116 Similar to TyroSine-protein kinase JAK1 (Janus kinase 1) (JAK-1)	150400	34869913	290958
ANGIOMOTIN LIKE 1; JUNCTION-ENRICHED AND ASSOCIATED PH	UNKNOWN	Tax_id=10116 Similar to angiominin like 1	88040	34860492	250115
SIMILAR TO BA261P9.2 (PUTATIVE NOVEL PROTEIN SIMILAR TO	UNKNOWN	Tax_id=10116 Similar to ba261P9.2 (putative novel protein similar to fly CG7340 and human putative aminopeptidase ZK353.6 in chromoSome 3 (EC 3.4.11.-))	99960	34860876	296511
SIMILAR TO BUTYROPHILIN-LIKE PROTEIN	BIOSYNTHETIC CARGO	Tax_id=10116 Similar to butyrophilin-like protein	56340	34862769	204977
SIMILAR TO HOOK HOMOLOG 2	UNKNOWN	Tax_id=10116 Similar to hook homolog 2	70280	34851423	289211

SIMILAR TO HYPOTHETICAL PROTEIN FLJ10375	UNKNOWN	Tax_id=10116 Similar to hypothetical protein FLJ10375	107600	34866614	302504
SIMILAR TO HYPOTHETICAL PROTEIN FLJ10737	UNKNOWN	Tax_id=10116 Similar to hypothetical protein FLJ10737	91330	34872498	233304
SIMILAR TO INTEGRIN ALPHA V SUBUNIT	PLASMA MB	Tax_id=10116 Similar to integrin alpha v Subunit	114700	34856480	299926
NAKED CUTICLE-2	UNKNOWN	Tax_id=10116 Similar to naked cuticle homolog 2	50280	34853337	310990
SIMILAR TO PUTATIVE ZINC FINGER TRANSCRIPTION FACTOR OVO1	TRANSCRIPTION	Tax_id=10116 Similar to putative zinc finger transcription factor OVO1	37260	27661858	294340
RIG-1 PROTEIN	BIOSYNTHETIC CARGO	Tax_id=10116 Similar to rig-1 protein	152300	34863083	191924
THIOREDOXIN-RELATED TRANSMEMBRANE PROTEIN 2	UNKNOWN	Thioredoxin-related transmembrane protein 2	33870	56090369	227628
SIMILAR TO UBIQUITIN-CONJUGATING ENZYME E2G 2; UBIQUITIN	PROTEASOME/UBIQUITIN	Ubiquitin-conjugating enzyme E2 G2 Ubiquitin-protein ligase G2 Ubiquitin carrier protein G2	18570	62665819	58922
WD-REPEAT PROTEIN 13	UNKNOWN	WD repeat protein 13	53660	34933412	65960
UNKNOWN (PROTEIN FOR MGC:72987)	UNKNOWN	Yif1b protein	25210	38454214	262403
AXIN 1 PROTEIN	SIGNALING	axin 1	92860	7513916	68755
HYPOTHETICAL PROTEIN XP_343478	UNKNOWN	hypothetical protein XP_343478	31580	34865907	203844
SECRETED FRIZZLED-RELATED PROTEIN 1	SIGNALING	secreted frizzled-related protein 1	35350	34879084	271324
AFG3 ATPASE FAMILY GENE 3-LIKE 2	PROT MOD	similar to 2310036102Rik protein	89350	34932104	265519
SIMILAR TO 2610042L04RIK PROTEIN	UNKNOWN	similar to 2610042L04Rik protein	35150	34882725	237032
SIMILAR TO 9530008L14RIK PROTEIN	UNKNOWN	similar to 9530008L14Rik protein [Rattus norvegicus]	11600	34875157	310564
SIMILAR TO RHO GUANINE NUCLEOTIDE EXCHANGE FACTOR 4	SIGNALING	similar to Rho guanine nucleotide exchange factor 4 isoform a; APC-stimulated guanine nucleotide exchange factor	77300	34874641	288425
ALPHA-CATENIN RELATED PROTEIN	CYTOSKELETON	similar to alpha-catenin related protein	81630	34868416	257171
SIMILAR TO HYPOTHETICAL PROTEIN D4ERTD89E	UNKNOWN	similar to hypothetical protein D4ERTD89e	46520	34868399	231118
SIMILAR TO HYPOTHETICAL PROTEIN MGC45873	UNKNOWN	unknown	57950	34873128	290208
3-HYDROXYISOBUTYRATE DEHYDROGENASE, MITOCHONDRIAL	MITOCHONDRIA	3-hydroxyisobutyrate dehydrogenase, mitochondrial precursor	35300	83977457	55185
BETA-ALANINE OXOGLUTARATE AMINOTRANSFERASE	MITOCHONDRIA	4-aminobutyrate aminotransferase, mitochondrial precursor (S)-3-amino-2-methylpropanoate transaminase Gamma-amino-N-butyrate transaminase GABA transaminase GABA aminotransferase GABA-AT GABA-T L-AIBAT 4-aminobutyrate aminotransferase, brain isoform 4-aminobutyrate aminotransferase, liver isoform	56450	48429192	37174
ATP-BINDING CASSETTE, SUB-FAMILY B, MEMBER 9 PRECURSOR	PROT SYN/FOLD	ATP-binding cassette sub-family B member 9 precursor ATP-binding cassette transporter 9 ABC transporter 9 protein TAP-like protein TAPL	84030	6045150	104172
DORZ1	UNKNOWN	Abhydrolase domain containing 14A	26760	57528269	203847
ALPHA-AMYLASE	BIOSYNTHETIC CARGO	Alpha-amylase	58830	58293772	106479

ANKYRIN G107	SIGNALING	ANKYRIN G107	106900	18376635	53239
APOLIPOPROTEIN A-V	BIOSYNTHETIC CARGO	ApoA5 protein	41430	6707431	114274
APOLIPOPROTEIN A-II	BIOSYNTHETIC CARGO	Apolipoprotein A-II precursor	11440	91985	3639
APOLIPOPROTEIN M	BIOSYNTHETIC CARGO	Apolipoprotein M	21510	9506391	95121
ASIALOGLYCOPROTEIN RECEPTOR (RHL2) Qc, GS15	PLASMA MB TETH/DOCK/FUS	Asialoglycoprotein receptor R2/3 BET1-like protein Vesicle transport protein GOS15 Golgi SNARE with a size of 15 kDa GS15 GOS-15	34860 12410	206649 61889075	44327 315291
COMM DOMAIN CONTAINING 10	UNKNOWN	COMM domain containing 10	22830	51948526	211553
DYNACTIN COMPLEX 50 KDA SUBUNIT Qa, SYNTAXIN 2	CYTOSKELETON TETH/DOCK/FUS	Dynactin 2 Epimorphin	44150 33360	51948450 349313	260733 11925
FAM3C-LIKE PROTEIN	UNKNOWN	FAM3C-like protein	24710	38454280	173223
GRAB PROTEIN	TRAFFIC	GRAB	41910	19705545	161254
SIMILAR TO GENERAL TRANSCRIPTION FACTOR IIF POLYPEPTIDE	TRANSCRIPTION	General transcription factor IIF, polypeptide 1, 74kDa	57180	56090552	219560
INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 4	BIOSYNTHETIC CARGO	Insulin-like growth factor binding 4 Insulin-like growth factor binding protein 4	27740	68534170	11776
INTEGRAL MEMBRANE PROTEIN 2B P24 GAMMA 1	UNKNOWN TRAFFIC	Integral membrane protein 2B Interleukin 1 receptor-like 1 ligand Predicted	30310 25210	81883760 61740631	284296 194234
NAD+-SPECIFIC ISOCITRATE DEHYDROGENASE A-SUBUNIT	MITOCHONDRIA	Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial precursor Isocitric dehydrogenase NAD(+)-specific ICDH	39610	68565369	60501
APOLIPOPROTEIN C-I	BIOSYNTHETIC CARGO	Liver regeneration-related protein LRRG04 Apolipoprotein C-I	9861	91989	3640
METABOTROPIC GLUTAMATE RECEPTOR 7 PRECURSOR	PLASMA MB	Metabotropic glutamate receptor 7 precursor mGluR7	102200	547904	37198
LATE ENDOSOMAL/LYSOSOMAL MP1 INTERACTING PROTEIN	LYSOSOME	Mitogen-activated protein-binding protein-interacting protein Late endosomal/lysosomal Mp1-interacting protein p14	13480	27692916	12815
BRANCHED CHAIN KETO ACID DEHYDROGENASE E1, BETA POL	MITOCHONDRIA	PREDICTED: branched chain keto acid dehydrogenase E1, beta polypeptide	42820	34865350	151463
CALCIUM CHANNEL BETA 4 SUBUNIT	CALCIUM TRANS/BIND	PREDICTED: calcium channel beta 4 subunit	57960	423788	100500
SIMILAR TO RING FINGER PROTEIN 10	UNKNOWN	PREDICTED: ring finger protein 10 (predicted)	88540	62659003	265735
PHOSPHOPANTOTHENOYLCOYSTEINE SYNTHETASE	METABOLISM	PREDICTED: similar to 6330579817Rik protein	33910	34870890	191085
SIMILAR TO EXPRESSED SEQUENCE AW556797	UNKNOWN	PREDICTED: similar to D15Mgi27 protein	49680	27665476	206392
SIMILAR TO LECT2	SIGNALING	PREDICTED: similar to LECT2	20890	34873621	209309
PROTEIN FAM18B (NPD008) (CGI-148).	UNKNOWN	PREDICTED: similar to RIKEN cDNA 1810036124	22620	34861791	303059

SIMILAR TO ECOTROPIC VIRAL INTEGRATION SITE 5	UNKNOWN	PREDICTED: similar to ecotropic viral integration site 5-like	83090	34870058	316795
R, VAMP 4	TETH/DOCK/FUS	PREDICTED: similar to vesicle associated membrane protein 4	16370	62659601	164208
PERIPHERIN	CYTOSKELETON	Peripherin	53550	92597	75052
PXF PROTEIN	PEROXISOME	Peroxisomal biogenesis factor 19 Peroxin-19 Peroxisomal farnesylated protein	32500	62903182	1659
UDP-N-ACETYL-ALPHA-D-GALACTOSAMINE:POLYPEPTIDE N-ACETYL-GLUCOSAMINE 11 TRANSFERASE	PROT MOD	Polypeptide N-acetylgalactosaminyltransferase 11 Protein-UDP acetylgalactosaminyltransferase 11 UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase 11 Polypeptide GalNAc transferase 11 GalNAc-T11 pp-GalNTase 11	69040	51315700	319029
YIP1	GTPASE	Protein YIPF4 YIP1 family member 4	27280	81883039	227072
PROTEIN-TYROSINE PHOSPHATASE-LIKE N	SIGNALING	Protein-tyrosine phosphatase-like N precursor	105200	1113923	11137
BC004044 (DENTIN MATRIX PROTEIN 4)	UNKNOWN	Putative secreted protein	65610	59676599	220519
(RCAS1) TYPE II RECEPTOR LIKE CANCER ASSOCIATED SURFACE GLYCOPROTEIN	UNKNOWN	Receptor-binding cancer antigen expressed on SiSo cells Estrogen receptor-binding fragment-associated gene 9 protein	24190	81883249	239738
SIMILAR TO CHO FUNCTIONALLY UNKNOWN TYPE II TRANSMEMBRANE PROTEIN	UNKNOWN	Retinoic acid receptor responder (Tazarotene induced) 2 Predicted	18500	61740621	235290
RETINOID-INDUCIBLE SERINE CARBOXYPEPTIDASE	PROT MOD	Retinoid-inducible serine carboxypeptidase precursor Serine carboxypeptidase 1	51170	48474727	140359
S-ARRESTIN	SIGNALING	S-arrestin	44990	92737	84325
SARCOSINE DEHYDROGENASE	MITOCHONDRIA	Sarcosine dehydrogenase, mitochondrial precursor SarDH	101400	52000744	85749
SECRETED PHOSPHOPROTEIN 24	BIOSYNTHETIC CARGO	Secreted phosphoprotein 24 precursor Spp-24 Secreted phosphoprotein 2	20690	2498940	43395
SELENOPROTEIN P	BIOSYNTHETIC CARGO	Selenoprotein P precursor	41580	47939025	1271
ACYL-COA DEHYDROGENASE, SHORT/BRANCHED CHAIN SPECIFIC	MITOCHONDRIA	Short/branched chain specific acyl-CoA dehydrogenase, mitochondrial precursor SBCAD 2-methyl branched chain acyl-CoA dehydrogenase 2-MEBCAD 2-methylbutyryl-coenzyme A dehydrogenase 2-methylbutyryl-CoA dehydrogenase	47820	6978433	3600
Qbc, SNAP29	TETH/DOCK/FUS	Synaptosomal-associated protein 29 SNAP-29 Vesicle-membrane fusion protein SNAP-29 Soluble 29 kDa NSF attachment protein Golgi SNARE of 32 kDa Gs32	29070	6685966	34036
TATA ELEMENT MODULATORY FACTOR	TRANSCRIPTION	TATA element modulatory factor	90260	6650548	60512
COG3	TETH/DOCK/FUS	Tax_Id=10116 Ensembl_locations(Chr-bp):15-56616580 similar to component of oligomeric golgi complex 2	72190	34874501	274159
SERINE PROTEASE	BIOSYNTHETIC CARGO	Tax_Id=10116 Ensembl_locations(Chr-bp):4-160981651 Serine protease	77790	7435632	13085
SIMILAR TO RIKEN CDNA 8430437G11	UNKNOWN	Tax_Id=10116 Ensembl_locations(Chr-bp):4-39132345 similar to RIKEN cDNA 8430437G11	61370	34854982	191057
D130038B21	UNKNOWN	Tax_Id=10116 Ensembl_locations(Chr-bp):8-46234308 similar to RIKEN cDNA D130038B21	40890	34863198	270449
SERINE/THREONINE PROTEIN KINASE 16	SIGNALING	Tax_Id=10116 Serine/threonine kinase 16	34410	27465615	105853

RING FINGER PROTEIN 121	UNKNOWN	Tax_Id=10116 Similar to 4930544L 10Rik protein	37000	34858831	241539
SIMILAR TO 9130011E15RIK PROTEIN	UNKNOWN	Tax_Id=10116 Similar to 9130011E15Rik protein	79550	34863517	198410
SIMILAR TO APOPTOTIC CHROMATIN CONDENSATION INDUCER	NUCLEUS	Tax_Id=10116 Similar to Apoptotic chromatin condensation inducer in the nucleus (Acinus)	156800	34874127	238120
COPI COATOMER GAMMA-2 SUBUNIT	COAT	Tax_Id=10116 Similar to Coatomer gamma-2 Subunit (Gamma 2 coat protein) (Gamma-2 COP)	84430	34855105	309005
COPI COATOMER ZETA-1 SUBUNIT	COAT	Tax_Id=10116 Similar to Coatomer zeta-1 Subunit (Zeta-1 coat protein) (Zeta-1 COP) (CGI-120) (HSPC181)	23840	34868640	236737
COG4	TETH/DOCK/FUS	Tax_Id=10116 Similar to Component of oligomeric golgi complex 4	91040	34851754	245295
SIMILAR TO CONSERVED OLIGOMERIC GOLGI COMPLEX SUBUNIT	COAT	Tax_Id=10116 Similar to Conserved oligomeric Golgi complex Subunit 5 (13S Golgi transport complex 90 kDa Subunit) (GTC90) (Golgi transport complex 1)	28170	34864228	311912
COG8	TETH/DOCK/FUS	Tax_Id=10116 Similar to Conserved oligomeric Golgi complex component 8	70760	34851657	222168
SIMILAR TO DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT	TRANSCRIPTION	Tax_Id=10116 Similar to DNA-directed RNA polymerase II large subunit (RPB1)	197600	34871645	202233
SIMILAR TO G PROTEIN-COUPLED RECEPTOR 108	SIGNALING	Tax_Id=10116 Similar to G protein-coupled receptor 108	59750	34853540	214715
SIMILAR TO G-PROTEIN COUPLED RECEPTOR 113	SIGNALING	Tax_Id=10116 Similar to G-protein coupled receptor 113	105200	34863284	309118
SIMILAR TO HYPOTHETICAL PROTEIN KIAA0645	UNKNOWN	Tax_Id=10116 Similar to Hypothetical protein KIAA0645	153700	34878957	300384
DEHYDROGENASE E1 AND TRANSKETOLASE DOMAIN CONTAINING	METABOLISM	Tax_Id=10116 Similar to KIAA1630 protein	148300	34876831	315956
SIMILAR TO P3 PROTEIN	UNKNOWN	Tax_Id=10116 Similar to P3 protein	44450	27689253	262782
SIMILAR TO PROTEIN KINASE NJMU-R1	UNKNOWN	Tax_Id=10116 Similar to Protein Njmu-R1	44430	34872893	315828
UNNAMED PROTEIN PRODUCT1	UNKNOWN	Tax_Id=10116 Similar to RIKEN cDNA 1200002K10 gene	98650	34853708	249884
SIMILAR TO RIKEN CDNA 4921513020; CDNA SEQUENCE, CLONED	UNKNOWN	Tax_Id=10116 Similar to RIKEN cDNA 4921513020	282700	34867735	191004
SOLUTE CARRIER FAMILY 35, MEMBER B3 (PREDICTED)	UNKNOWN	Tax_Id=10116 Similar to RIKEN cDNA 4921526006	68350	34875183	247534
SIMILAR TO RIKEN CDNA 4921529018	UNKNOWN	Tax_Id=10116 Similar to RIKEN cDNA 4921529018	153300	34865399	221195
BTB (POZ) DOMAIN CONTAINING 7 (PREDICTED)	UNKNOWN	Tax_Id=10116 Similar to RIKEN cDNA 5730507E09	131000	34867616	273407
SIMILAR TO SIF AND TIAM1-LIKE EXCHANGE FACTOR	UNKNOWN	Tax_Id=10116 Similar to Sif and Tiam1-like exchange factor	155900	34853702	204958

TRANSMEMBRANE 9 SUPERFAMILY MEMBER 1	UNKNOWN	Tax_Id=10116 Similar to Tm9SF1 protein	89670	34874167	211728
SIMILAR TO TRIPLE FUNCTIONAL DOMAIN PROTEIN (PTPRF INTERACTING PROTEIN)	SIGNALING	Tax_Id=10116 Similar to Triple functional domain protein (PTPRF interacting protein)	352100	34854901	310374
SIMILAR TO WD REPEAT DOMAIN 9 ISOFORM A: CAMP RESPONSE ELEMENT-BINDING PROTEIN	SIGNALING	Tax_Id=10116 Similar to WD repeat domain 9 isoform A	225200	34881323	312923
SIMILAR TO AMINOADIPATE-SEMIALDEHYDE SYNTHASE	METABOLISM	Tax_Id=10116 Similar to aminoadipate-Semialdehyde Synthase	92010	34855019	258586
SIMILAR TO BETA-1,4-GALACTOSYLTRANSFERASE V	PROT MOD	Tax_Id=10116 Similar to beta-1,4-galactosyltransferase V	33110	34860732	275497
FBXL4 PROTEIN	UNKNOWN	Tax_Id=10116 Similar to FBXL4 protein	71160	34867089	218543
SIMILAR TO FERTILIZATION ANTIGEN-1; FA-1	UNKNOWN	Tax_Id=10116 Similar to fertilization antigen-1	11520	34872581	319241
SIMILAR TO FLJ12716 PROTEIN	UNKNOWN	Tax_Id=10116 Similar to hypothetical protein	125800	34878417	272431
UNKNOWN5	UNKNOWN	Tax_Id=10116 Similar to hypothetical protein A930013K19	71010	34878581	285571
SIMILAR TO HYPOTHETICAL PROTEIN DKFZP547C176	UNKNOWN	Tax_Id=10116 Similar to hypothetical protein DKFZP547C176	41180	34863409	227549
SIMILAR TO FLJ21963	UNKNOWN	Tax_Id=10116 Similar to hypothetical protein FLJ21963	91790	34865010	243174
KINESIN-RELATED MITOTIC MOTOR PROTEIN	CYTOSKELETON	Tax_Id=10116 Similar to kinesin-related mitotic motor protein	129800	34862680	209577
COG1	TETH/DOCK/FUS	Tax_Id=10116 Similar to ldlbp	110800	34875017	282341
OSTEOCLAST INHIBITORY LECTIN	PROT SYN/FOLD	Tax_Id=10116 Similar to osteoclast inhibitory lectin	23540	34858508	255984
SIMILAR TO PROBABLE TRANSMEMBRANE PROTEIN FT27 - MOUSE	UNKNOWN	Tax_Id=10116 Similar to probable transmembrane protein FT27 - mouse	39180	34877387	206786
RING FINGER PROTEIN 20; HOMOLOG OF S. CEREVISIAE BRE1	PROTEASOME/UBIQUITINATION	Tax_Id=10116 Similar to ring finger protein 20	122200	34868389	236982
SIMILAR TO ZINC TRANSPORTER 5	UNKNOWN	Tax_Id=10116 Similar to zinc transporter 5	71030	34853639	259074
SIMILAR TO ZINC TRANSPORTER LIKE 2	CALCIUM TRANS/BIND	Tax_Id=10116 Similar to zinc transporter like 2	57350	34859877	257320
BET3	TETH/DOCK/FUS	Trafficking protein particle complex subunit 3 BET3 homolog	20300	71153350	145735
TYPE 2 LACTOSAMINE ALPHA-2,3-SIALYLTRANSFERASE	PROT MOD	Type 2 lactosamine alpha-2,3-sialyltransferase CMP-NeuAc:beta-galactoside alpha-2,3-sialyltransferase VI ST3Gal VI Sialyltransferase 10	38140	48428498	722796
BETA 1,3-GALACTOSYLTRANSFERASE POLYPEPTIDE 1	PROT MOD	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 1	37990	34854866	56042
UDP-GLUCURONATE DECARBOXYLASE	METABOLISM	UDP-glucuronic acid decarboxylase 1 UDP-glucuronate decarboxylase 1 UGD UXS-1	47500	21326465	86062
SIMILAR TO VACUOLAR PROTEIN SORTING 26; VACUOLE PROTEIN SORTING 26	TRAFFIC	Vacuolar protein sorting 26 Vesicle protein sorting 26	38110	78099277	276682

VESICLE ASSOCIATED PROTEIN	COAT	Vesicle associated protein	135400	7514116	26418
DIHYDROPYRIDINE-SENSITIVE L-TYPE, CALCIUM CHANNEL BETA 3	CALCIUM TRANS/BIND	Voltage-dependent L-type calcium channel subunit beta-3	54560	6978583	3671
ZINC-ALPHA-2-GLYCOPROTEIN	BIOSYNTHETIC CARGO	CAB3 Calcium channel voltage-dependent subunit beta 3	34020	6978565	3662
PQ LOOP REPEAT CONTAINING 1	UNKNOWN	Zinc-alpha-2-glycoprotein precursor	30570	34932411	197729
SIMILAR TO APG16L BETA ISOFORM	UNKNOWN	similar to 2310009N05Rik protein			
VACUOLAR PROTON-TRANSLOCATING ATPASE 100 KDA SUBUNIT	LYSOSOME	similar to APG16L beta isoform [Rattus norvegicus]	36440	34858802	281500
		similar to Cc1-3 [Rattus norvegicus]	162200	34872293	256290
GAG	LIKELY CONTAMINANTS		67670	34869861	216646
PUTATIVE PHOSPHATIDIC ACID PHOSPHATASE	METABOLISM	similar to Gag	29160	34879054	255469
ALDEHYDE DEHYDROGENASE 1 FAMILY, MEMBER L2	DETOXIFICATION	similar to HTPAP protein			
GOLGI-ASSOCIATED MICROTUBULE-BINDING PROTEIN HOOK3;	CYTOSKELETON	similar to RIKEN cDNA D330038109 [Rattus norvegicus]	96960	34862428	302704
MALE ENHANCED ANTIGEN 2/GOLGI AUTOANTIGEN, GOLGIN SUBFAMILY A, 3	TETH/DOCK/FUS	similar to golgi-associated microtubule-binding protein HOOK3; hook3 protein [Rattus norvegicus]	83230	34879033	220378
SIMILAR TO NESPRIN-2	CYTOSKELETON	similar to male enhanced antigen 2/golgi autoantigen, golgin subfamily a, 3 [Rattus norvegicus]	166100	34873054	267138
COPI COATOMER EPSILON SUBUNIT	COAT	similar to nesprin-2	152400	34865470	310579
SIMILAR TO THYROID HORMONE RECEPTOR INTERACTOR 11; THYROID RECEPTOR INTERACTING PROTEIN 11	UNKNOWN	similar to nonclathrin coat protein epsilon-COP	34650	34877816	259217
SIMILAR TO HYPOTHETICAL PROTEIN FLJ22419	UNKNOWN	similar to thyroid hormone receptor interactor 11; thyroid receptor interacting protein 11	37170	34867559	280942
FOR PROTEASOMAL ATPASE (SUG1)	PROTEASOME/UBIQUITIN	unknown	99380	34873842	308914
AC2-256	UNKNOWN	26S protease regulatory subunit 8 Proteasome subunit p45	45630	49065782	62820
ACTIVATING SIGNAL COINTEGRATOR 1 COMPLEX SUBUNIT 1	NUCLEUS	p45/SUG Proteasome 26S subunit ATPase 5 mSUG1	71830	62177146	166247
ALPHA 1-B GLYCOPROTEIN	BIOSYNTHETIC CARGO	Ac2-256	41180	56090367	229337
CALCIUM-TRANSPORTING ATPASE TYPE 2C, MEMBER 1	CALCIUM TRANS/BIND	Activating signal cointegrator 1 complex subunit 1	56480	57012547	155721
		Alpha-1B-glycoprotein precursor Liver regeneration-related protein 1 C44	100500	8134332	41219
COMPLEMENT FACTOR 6	BIOSYNTHETIC CARGO	Calcium-transporting ATPase type 2C member 1 ATPase 2C1 ATP-dependent Ca(2+) pump PMR1			
COPPER-TRANSPORTING ATPASE 1	PROT MOD	Complement component C6 precursor	105100	61211276	240055
		Copper-transporting ATPase 1 Copper pump 1 Menkes disease-associated protein homolog	162100	16258817	12003
CYTOCHROME P450 11B3	DETOXIFICATION		57180	595823	108087
DNAJ-LIKE PROTEIN	PROT SYN/FOLD	Cytochrome P-450 11-beta hydroxylase	25760	9910322	42765

EXOSTOSIN-1	PROT MOD	Exostosin-1 Glucuronosyl-N-acetylglucosaminyl-proteoglycan/N-acetylglucosaminyl-proteoglycan 4-alpha-N-acetylglucosaminyltransferase Multiple exostosins protein 1 homolog	86310	62652423	57456
SIMILAR TO FUKUTIN-RELATED PROTEIN	PROT MOD	Fukutin related protein	54850	71043684	242747
GLUCOSAMINE--FRUCTOSE-6-PHOSPHATE AMINOTRANSFERASE	METABOLISM	Glutamine fructose-6-phosphate transaminase 1	76830	54400724	277551
HEPCIDIN	BIOSYNTHETIC CARGO	Hepcidin precursor	9286	21542070	108861
RING FINGER PROTEIN 153	PROTEASOME/UBIQUITIN	Hypothetical protein FLJ20445 Ring finger protein 153	31230	34862676	49021
IGG RECEPTOR FcRN LARGE SUBUNIT P51	BLOOD + OTHER CELLS	IgG receptor FcRN large subunit P51 precursor	40170	56437	15418
KYNURENINE 3-HYDROXYLASE	METABOLISM	Kynurenine 3-monooxygenase Kynurenine 3-hydroxylase	54350	81882198	70289
GLUTAMYL-PROLYL-TRNA SYNTHETASE	PROT SYN/FOLD	LRRGT00050	168800	66793366	286877
LEUKEMIA INHIBITOR FACTOR RECEPTOR ALPHA-CHAIN	PLASMA MB	Leukemia inhibitory factor receptor precursor LIF receptor LIF-R CD118 antigen	122400	81870502	37205
LOW-DENSITY LIPOPROTEIN RECEPTOR	PLASMA MB	Low-density lipoprotein receptor precursor LDL receptor	96620	56570	106673
SIMILAR TO CDNA SEQUENCE BC003322	UNKNOWN	LysM, putative peptidoglycan-binding, domain containing 3	33700	57527470	204667
HYPOTHETICAL PROTEIN XP_238476	UNKNOWN	PREDICTED: similar to 1700001K19Rik protein	24610	34867823	299198
PRA1 FAMILY PROTEIN 2 (JM4 PROTEIN)	GTPASE	PREDICTED: similar to DXImx39e protein	15360	34933457	246770
VPS26	TRAFFIC	PREDICTED: similar to Dcra	29720	34867703	287732
SIMILAR TO MAGEB3	UNKNOWN	PREDICTED: similar to MAGEB3	38250	67846038	291571
SIMILAR TO MITOCHONDRIAL CARRIER TRIPLE REPEAT 1	MITOCHONDRIA	PREDICTED: similar to Mitochondrial carrier triple repeat 1	34420	34877540	303709
SIMILAR TO PROTEIN HSPC163	UNKNOWN	PREDICTED: similar to Protein HSPC163	16090	27679416	225990
SIMILAR TO RIKEN CDNA 281042815	UNKNOWN	PREDICTED: similar to RIKEN cDNA 281042815	18770	27668986	291986
SIMILAR TO SPECKLE-TYPE POZ PROTEIN-LIKE 1; POZ 56 PROTEIN	UNKNOWN	PREDICTED: similar to TPOZ2	40870	27692515	169806
UDP-N-ACETYL-ALPHA-D-GALACTOSAMINE:POLYPEPTIDE N-ACETYLTRANSFERASE	PROT MOD	PREDICTED: similar to polypeptide GalNAc transferase-T4	66710	77736615	167222
SIMILAR TO SIGNAL RECOGNITION PARTICLE 19KDA; SIGNAL RECOGNITION PARTICLE 19KDA	PROT SYN/FOLD	PREDICTED: similar to signal recognition particle 19kDa	16140	27683535	219536
UDP-GALNAC:POLYPEPTIDE N-ACETYLGLACTOSAMINYLTRANSFERASE	PROT MOD	Polypeptide N-acetylglucosaminyltransferase 10 Protein-UDP acetylglucosaminyltransferase 10 UDP-GalNAc;polypeptide N-acetylglucosaminyltransferase 10 Polypeptide GalNAc transferase 10 GalNAc-T10 pp-GalNTase 10	69120	51315730	72049
26S PROTEASE REGULATORY SUBUNIT 6A	PROTEASOME/UBIQUITIN	Proteasome (Prosome, macropain) 26S subunit, ATPase 3	49550	38304011	71853
SIMILAR TO O-MANNOSYL N-ACETYLGLUCOSAMINYLTRANSFERASE	PROT MOD	Protein O-linked-mannose beta-1,2-N-acetylglucosaminyltransferase 1 POM/GnT1	75150	73621412	285106
FAMILY WITH SEQUENCE SIMILARITY 20, MEMBER A (PREDICTED)	BIOSYNTHETIC CARGO	Putative secreted protein	61440	59676595	271057
REG RECEPTOR	PROT MOD	Reg receptor	104400	9910530	42827
SECRETORY CARRIER MEMBRANE PROTEIN 2	TRAFFIC	Secretory carrier membrane protein 2	34340	10764633	150292

SEPTIN-LIKE PROTEIN	GTPASE	Septin-9 Eseptin eighth septin Septin-like protein SLP	63790	6090881	70797
PROTEIN KINASE (EC 2.7.1.37), MYOTONIC DYSTROPHY-ASSOCIATED PROTEIN KINASE	SIGNALING	Serine/threonine-protein kinase MRCK alpha CDC42-binding protein kinase alpha Myotonic dystrophy kinase-related CDC42-binding kinase alpha Myotonic dystrophy protein kinase-like alpha MRCK alpha	197100	81174934	60508
SHORT TRANSIENT RECEPTOR POTENTIAL CHANNEL 2	PLASMA MB	Short transient receptor potential channel 2 TrpC2 rTRP2	99610	4877836	138976
STONIN	COAT	Stonin	81920	33636736	277960
BAT3 (HLA-B ASSOCIATED TRANSCRIPT 3)	UNKNOWN	TREMBL:Q6MG49;Q9WTN8 REFSEQ_NP:NP_446061 ENSEMBL:ENSRNOP0000001129 BAT3	114900	4587081	60486
SIMILAR TO MITOGEN ACTIVATED PROTEIN KINASE KINASE	SIGNALING	Tax_id=10116 Ensembl_locations(Chr-bp):11-81385238 similar to mitogen-activated protein kinase kinase 13	62180	27665594	259662
SIMILAR TO RIKEN CDNA 2810002104	UNKNOWN	Tax_id=10116 Ensembl_locations(Chr-bp):6-109338222 similar to RIKEN cDNA 2810002104	45290	34935370	313692
HYPOTHETICAL PROTEIN XP_215523	UNKNOWN	Tax_id=10116 HypoHetical protein XP_215523	21540	34854965	295192
HYPOTHETICAL PROTEIN XP_343384	UNKNOWN	Tax_id=10116 HypoHetical protein XP_343384	69230	34863314	308477
SIGNAL RECOGNITION PARTICLE 54 KDA	PROT SYN/FOLD	Tax_id=10116 Signal recognition particle 54 kDa	79610	34865216	263863
ATP-DEPENDENT ZINC METALLOPROTEASE	PROT MOD	Tax_id=10116 Similar to ATP-dependent zinc metalloprotease	85690	34851878	314287
SIMILAR TO ALPHA-MANNOSIDASE IIX (MANNOSYL-OLIGOSACCHARIDE 1,3-1,6-ALPHA-MANNOSIDASE) (MAN IIX)	PROT MOD	Tax_id=10116 Similar to Alpha-mannosidase Iix (MannoSyl-oligoSaccharide 1,3-1,6-alpha-mannoSidaSe) (MAN Iix) (MannoSidaSe alpha class 2A member 2)	133000	34857364	209202
SIMILAR TO CG2144-PA	UNKNOWN	Tax_id=10116 Similar to CG2144-PA	100600	34875840	237985
SIMILAR TO CMP-SIALIC ACID TRANSPORTER	PROT MOD	Tax_id=10116 Similar to CMP-Sialic acid transPorter	36550	34867231	260011
ALPHA N-CATENIN	SIGNALING	Tax_id=10116 Similar to ENSANGP00000019826	159200	27732405	221731
SIMILAR TO ETHANOLAMINE KINASE (EKI)	SIGNALING	Tax_id=10116 Similar to Ethanolamine kinaSe (EKI)	43710	34858587	250733
FORMIN HOMOLOG 2 DOMAIN CONTAINING 1	UNKNOWN	Tax_id=10116 Similar to F H1/FH2 domainS-containing protein (Formin homolog overexpresSed in Spleen) (FHOS) (Formin homology 2 domain containing 1)	68180	34851604	317496
SIMILAR TO KDEL (LYS-ASP-GLU-LEU) ENDOPLASMIC RETICULUM RESIDENT PROTEIN	TRAFFIC	Tax_id=10116 Similar to KDEL (Lys-ASp-Glu-Leu) endoplasmic reticulum protein retention receptor 3	27420	34867041	283557
SIMILAR TO KIAA1055 PROTEIN	UNKNOWN	Tax_id=10116 Similar to KIAA1055 protein	108500	34865572	211597
SIMILAR TO RAB6IP1	UNKNOWN	Tax_id=10116 Similar to KIAA1091 protein	38000	34861343	274376

ALPHA-1,2-MANNOSIDASE IC	PROT MOD	Tax_Id=10116 Similar to MannoSyl-oligoSaccharide 1,2-alpha-mannoSidase IC (ProceSSing alpha-1,2-mannoSidase IC) (Alpha-1,2-mannoSidase IC) (MannoSidase alpha clasS 1C member 1) (HMIQ)	51490	34872059	315202
SIMILAR TO RIKEN CDNA C330027C09	UNKNOWN	Tax_Id=10116 Similar to RIKEN cDNA C330027C09	101300	34869119	273781
SIMILAR TO SH3 DOMAIN PROTEIN D19	UNKNOWN	Tax_Id=10116 Similar to SH3 domain protein D19	125000	34857900	291964
SPIR-1	TRAFFIC	Tax_Id=10116 Similar to Spir-1 protein	66730	34932106	284460
TRS85 HOMOLOG	TRAFFIC	Tax_Id=10116 Similar to TRS85 homolog	150900	34878190	194979
BROMODOMAIN ADJACENT TO ZINC FINGER DOMAIN_2A (PRED)	UNKNOWN	Tax_Id=10116 Similar to TTF-J interacting protein 5	183400	34862191	316025
UDP-N-ACETYL-ALPHA-D-GALACTOSAMINE:POLYPEPTIDE N-AC	PROT MOD	Tax_Id=10116 Similar to UDP-N-acetyl-alpha-D-galactoSamine:polypeptide N-acetylGalactoSaminytranSferaSe 3	74480	34854862	247675
SORTING NEXIN 23	TRAFFIC	Tax_Id=10116 Similar to chromoSome 20 open reading frame 23	177300	34859296	313987
HYPOTHETICAL PROTEIN (3)	UNKNOWN	Tax_Id=10116 Similar to hypothetical protein	166900	34872142	230780
SIMILAR TO HYPOTHETICAL PROTEIN C230030N03	UNKNOWN	Tax_Id=10116 Similar to hypothetical protein C230030N03	133800	34874915	193616
SIMILAR TO HYPOTHETICAL PROTEIN MGC15523	UNKNOWN	Tax_Id=10116 Similar to hypothetical protein MGC15523	132100	34875626	304037
SIMILAR TO HYPOTHETICAL PROTEIN MGC19022	UNKNOWN	Tax_Id=10116 Similar to hypothetical protein MGC19022	626600	34862645	250792
SIMILAR TO RME-8	TRAFFIC	Tax_Id=10116 Similar to mKIAA0678 protein	96130	34865848	276172
CHONDROITIN SULFATE GLUCURONYLTRANSFERASE	PROT MOD	Tax_Id=10116 Similar to mKIAA1402 protein	86520	34853978	259133
SIMILAR TO MACROPHAGE HEMOGLOBIN SCAVENGER RECEPT	BLOOD + OTHER CELLS	Tax_Id=10116 Similar to macrophage hemoglobin Scavenger receptor CD163 precursor	119500	34858425	192759
SIMILAR TO MATRILIN-4 PRECURSOR	BIOSYNTHETIC CARGO	Tax_Id=10116 Similar to matrilin-4 precursor	68970	34860683	276968
SIMILAR TO PANCREATITIS INDUCED PROTEIN 49	UNKNOWN	Tax_Id=10116 Similar to pancreatitiS-induced protein 49	54860	34853103	232078
POLYCYSTIC KIDNEY DISEASE 1-LIKE 3	PLASMA MB	Tax_Id=10116 Similar to polycyStic kidney diSeaSe 1-like 3	150800	34851921	221805
SIMILAR TO POLYCYSTIC KIDNEY DISEASE-LIKE 2 PROTEIN	PLASMA MB	Tax_Id=10116 Similar to polycyStic kidney diSeaSe-like 2 protein	68780	34878682	217412
SIMILAR TO TEKTN 3; TESTICULAR MICROTUBULES-RELATED P	CYTOSKELETON	Tax_Id=10116 Similar to tektin 3	57610	34870851	284187
SIMILAR TO TRIPARTITE MOTIF PROTEIN 8; RING FINGER PROTE	UNKNOWN	Tax_Id=10116 Similar to tripartite motif protein 8	102500	34863676	250614
VACUOLE 14 PROTEIN; VAC14 PROTEIN; HYDIN	CYTOSKELETON	VAC14	88070	29293817	173122
VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN 45	TRAFFIC	Vacuolar protein sorting-associated protein 45 nyps45	64890	51858559	19366
R, VAMP 2	TETH/DOCK/FUS	Vesicle-associated membrane 2	12690	6981614	36248
R, VAMP 7	TETH/DOCK/FUS	Vesicle-associated membrane protein 7	24780	9502258	3011
SIMILAR TO DIVALENT CATION TOLERANT PROTEIN CUTA	UNKNOWN	divalent cation tolerant protein CUTA	16410	61212255	281056
HYPOTHETICAL PROTEIN XP_219683	UNKNOWN	hypothetical protein XP_219683	102000	34861395	198827
SIMILAR TO 40S RIBOSOMAL PROTEIN S2	PROT SYN/FOLD	similar to 40S ribosomal protein S2	25730	34879332	271484
DNAJ (HSP40) HOMOLOG, SUBFAMILY C, MEMBER 13	PROT SYN/FOLD	similar to CG8014-PA	55190	34865850	245025

SIMILAR TO DEAD/DEAH BOX HELICASE DDX37	NUCLEUS	similar to DEAH (Asp-Glu-Ala-His) box polypeptide 37; DEAD/DEAH box helicase DDX37; DEAD/H (Asp-Glu-Ala-His) box polypeptide 37 [Rattus norvegicus]	125500	34872286	239799
SIMILAR TO DKFZP586G1517 PROTEIN	UNKNOWN	similar to DKFZP586G1517 protein	50150	34853508	234819
SIMILAR TO DNA (CYTOSINE-5)-METHYLTRANSFERASE 3A (DNMT3A)	NUCLEUS	similar to DNA (cytosine-5)-methyltransferase 3A (Dnmt3a) (DNA methyltransferase Mmull1A) (DNA MTase Mmull1A) (M.Mmull1A)	59410	34871224	241066
SIMILAR TO HYPOTHETICAL PROTEIN KIAA1383	UNKNOWN	similar to Hypothetical protein KIAA1383	96280	34851995	212350
HUNTINGTIN INTERACTING PROTEIN 14 (HIP 14)	TETH/DOCK/FUS	similar to KIAA0946 protein	84730	34864845	282355
SIMILAR TO RIKEN CDNA 1200014P05	UNKNOWN	similar to RIKEN cDNA 1200014P05	97320	34859177	239276
OXYSTEROL BINDING PROTEIN-LIKE 11	UNKNOWN	similar to RIKEN cDNA 9430097N02 [Rattus norvegicus]	81520	34869388	230365
WOLF-HIRSCHHORN SYNDROME CANDIDATE 1 PROTEIN ISOFORM 1; IL5 PROMOTER REII REGION-BINDING PROTEIN; TRITHORAX/ASH1-RELATED PROTEIN 5; MULTIPLE MYELOMA SET DOMAIN PROTEIN	UNKNOWN	similar to Wolf-Hirschhorn syndrome candidate 1 protein isoform 1; IL5 promoter REII region-binding protein; trithorax/ash1-related protein 5; multiple myeloma SET domain protein	152600	34878518	214625
SIMILAR TO COMPONENT OF OLIGOMERIC GOLGI COMPLEX 2	COAT	similar to component of oligomeric golgi complex 2	41480	34851897	272329
SYNAPTIC RAS-GAP 1	GTPASE	(Q9QUH6) Isoform 5 of Q9QUH6	127700	7514095	13883
55 KDA TYPE II PHOSPHATIDYLINOSITOL 4-KINASE	SIGNALING	55 kDa type II phosphatidylinositol 4-kinase	54300	16758554	60536
RAP2B	GTPASE	9.5 days embryo parthenogenote cDNA, RIKEN full-length enriched library, clone:B130020K18 product:RAS-RELATED PROTEIN RAP-2B homolog 7 days neonate cerebellum cDNA, RIKEN full-length enriched library, clone:A730075I10 product:RAP2B, member of RAS oncogene family, full insert sequence Bone marrow macrophage cDNA, RIKEN full-length enriched library, clone:G530142K06 product:RAP2B, member of RAS oncogene family, full insert sequence Rap2b protein 7 days neonate cerebellum cDNA, RIKEN full-length enriched library, clone:A730042C18 product:RAS-RELATED PROTEIN RAP-2B homolog	20500	47117735	32763
A-RAF PROTO-ONCOGENE SERINE/THREONINE-PROTEIN KINASE ATPASE 7B	SIGNALING PROT MOD	A-Raf proto-oncogene serine/threonine-protein kinase ATPase 7B	67550 156000	55757 6006306	90531 1565
ALDO-KETO REDUCTASE FAMILY 1 MEMBER E1	DETOXIFICATION	Aldo-keto reductase family 1, member E1	34500	56605762	218884
MEMBRANE ATTACK COMPLEX INHIBITION FACTOR	BLOOD + OTHER CELLS	CD59 glycoprotein precursor Membrane attack complex inhibition factor MACIF MAC-inhibitory protein MAC-IP Protectin	13790	6978635	3690
ALPHA-2,3-SIALYLTRANSFERASE ST3GAL IV	PROT MOD	CMP-N-acetylneuraminate-beta-galactosamide-alpha-2,3-sialyltransferase Beta-galactoside alpha-2,3-sialyltransferase Alpha 2,3-sialyltransferase IV Alpha 2,3-ST SIAT4-C	38040	57870642	722827
CHONDROITIN 6-SULFOTRANSFERASE	PROT MOD	Carbohydrate sulfotransferase 3 Chondroitin 6-O-sulfotransferase 1 C6ST-1 Galactose/N-acetylglucosamine/N-acetylglucosamine 6-O-sulfotransferase 0 GST-0	54020	61211366	55190

CELL GROWTH REGULATORY GENE 11 PROTEIN	UNKNOWN	Cell growth regulator with EF hand domain 1 Cell growth regulatory gene 11 protein	30830	23396481	38628
CERAMIDE GLUCOSYLTRANSFERASE	PROT MOD	Ceramide glucosyltransferase Glucosylceramide synthase GCS UDP-glucose:N-acylsphingosine D-glucosyltransferase UDP-glucose ceramide glucosyltransferase GLCT-1	44820	62648957	85745
CHAIN L, 1.9A STRUCTURE OF THE THERAPEUTIC ANTIBODY CALBLOOD + OTHER CELLS		Chain L, 1.9a Structure Of The Therapeutic Antibody Campath-1h Fab In Complex With A Synthetic Peptide Antigen	23280	5542160	20841
TSGA10	UNKNOWN	Cp431	104600	3851160	7578
CREATINE KINASE, M CHAIN	METABOLISM	Creatine kinase M-type Creatine kinase M chain M-CK	43020	6978661	3700
DIAMINE OXIDASE-LIKE PROTEIN 1	UNKNOWN	Diamine oxidase-like protein 1	80090	40385889	216306
EYES ABSENT 2 HOMOLOG SIMILAR TO RIKEN CDNA 2810433K01	UNKNOWN UNKNOWN	Drosophila-type eyes absent 2-like protein ENSEMBL:ENSRNOP0000020637 REFSEQ:XP_214527 PREDICTED: similar to RIKEN cDNA 2810433K01	58060 29420	61097896 27679138	242823 190728
ENGULFMENT AND CELL MOTILITY PROTEIN 1	CYTOSKELETON	Engulfment and cell motility protein 1	28740	34876182	4981
GALACTOSE-1-PHOSPHATE URIDYLTRANSFERASE	METABOLISM	Galactose-1-phosphate uridylyltransferase Gal-1-P uridylyltransferase UDP-glucose--hexose-1-phosphate uridylyltransferase	43310	68533665	71441
GAMMA-GLUTAMYLTRANSFERASE 5	METABOLISM	Gamma-glutamyltransferase 5 precursor Gamma-glutamyltransferase-like activity 1 Gamma-glutamyl leukotrienase GGL Gamma glutamyl transpeptidase-related enzyme GGT-rel Gamma-glutamyltransferase 5 heavy chain Gamma-glutamyltransferase 5 light chain	61610	9506723	52613
HEAT SHOCK 27 KDA PROTEIN	PROT SYN/FOLD	Heat shock 27 kDa protein	22890	204665	71479
HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR GAMMA	BLOOD + OTHER CELLS	High affinity immunoglobulin epsilon receptor gamma-subunit precursor FcεRI gamma IgE Fc receptor gamma-subunit Fc-epsilon RI-gamma	9765	226241	84256
HISTONE DEACETYLASE 4	NUCLEUS	Histone deacetylase 4	18710	12963266	122642
YIP1P-INTERACTING FACTOR: LIVER PROTEIN	TETH/DOCK/FUS	Hypothetical protein	14900	25282411	132369
IG GAMMA-2A CHAIN C REGION	BLOOD + OTHER CELLS	Ig gamma-2A chain C region	25220	13399989	62937
IMP (INOSINE MONOPHOSPHATE) DEHYDROGENASE 2	METABOLISM	Inosine monophosphate dehydrogenase 2	55800	40018566	231448
INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 5 PRECURSOR	(BIOSYNTHETIC CARGO	Insulin-like growth factor-binding protein 5 precursor IGFBP-5	30300	6981088	3949
LOC246208 PROTEIN	UNKNOWN	LOC246208 protein	47340	44890246	726783
LAMIN B RECEPTOR	NUCLEUS	Lamin-B receptor Integral nuclear envelope inner membrane protein NBP60	70720	81861075	40763
LEUCYL-CYSTINYL AMINOPEPTIDASE SIMILAR TO MHC CLASS I PROTEIN	PROT MOD BIOSYNTHETIC CARGO	Leucyl-cystinyl aminopeptidase MHC class I protein RT1 class I, CE7	117200 39930	20138455 62665606	5106 290515
MHC CLASS II ANTIGEN RT1.B BETA CHAIN	PLASMA MB	MHC class II antigen RT1.B beta chain	22020	1762640	38923
MICROTUBULE ASSOCIATED PROTEIN 1A	CYTOSKELETON	Microtubule associated protein 1A	15800	56619	111687
SIMILAR TO RIKEN CDNA D430028G21	UNKNOWN	Mitochondrial antiviral signaling protein Interferon-beta promoter stimulator protein 1 IPS-1 Virus-induced signaling adapter	53800	81170680	215394

CHAIN A, THE CRYSTAL STRUCTURE OF THE FAB FRAGMENT OF MYOSIN VA	PLASMA MB CYTOSKELETON	Monoclonal Antibody Against The Main Immung Myosin-5A Myosin Va Dilute myosin heavy chain, non-muscle	23340 211800	6730147 6577099	73388 63044
MARCKS	CYTOSKELETON	Myristoylated alanine-rich C-kinase substrate (MARCKS) (Protein kinase C substrate 80 kDa protein).	29780	27705710	166436
NICOTINATE PHOSPHORIBOSYLTRANSFERASE-LIKE PROTEIN	METABOLISM	Nicotinate phosphoribosyltransferase-like protein	58560	46485387	722226
OLFACTORY RECEPTOR MOR263-6	PLASMA MB	Olfactory receptor 7, rat orthologue of mouse MOR263-3	34210	47834335	277221
PRA1 FAMILY PROTEIN 3 (ADP-RIBOSYLATION-LIKE FACTOR 6 IN	GTPASE	PRA1 family protein 3 ARL-6-interacting protein 5 ADP-ribosylation-like factor 6-interacting protein 5 Alp-5 Glutamate transporter EAAC1-interacting protein GTRAP3-18 Prenylated Rab acceptor protein 2 Protein JWa	21550	57012987	54281
DELTA 1-PYRROLINE-5-CARBOXYLATE REDUCTASE	METABOLISM	PREDICTED: pyrroline-5-carboxylate reductase-like (predicted)	28860	62652621	268213
APOLIPOPROTEIN C2	BIOSYNTHETIC CARGO	PREDICTED: similar to Apolipoprotein C2	10700	27676424	215733
SIMILAR TO DUAL SPECIFICITY PHOSPHATASE 14	SIGNALING	PREDICTED: similar to Dual specificity phosphatase 14	22270	62644625	209194
EMOPAMIL BINDING RELATED PROTEIN	UNKNOWN	PREDICTED: similar to Emopamil-binding protein-like (Emopamil-binding related protein)	23410	34874266	245607
SIMILAR TO CGI-35 PROTEIN	UNKNOWN	PREDICTED: similar to Protein C14orf111 homolog	23360	95102022	234912
SIMILAR TO RIKEN CDNA 1700025G04 GENE	UNKNOWN	PREDICTED: similar to RIKEN cDNA 1700025G04	13890	27712468	318230
SIMILAR TO RIKEN CDNA 1700045I19	UNKNOWN	PREDICTED: similar to RIKEN cDNA 1700045I19	28360	27708820	208800
SIMILAR TO RETINOIC ACID EARLY INDUCIBLE PROTEIN 1 BETA	UNKNOWN	PREDICTED: similar to Retinoic acid early inducible protein 1 beta precursor (RAE-1beta)	27450	62638284	367801
SIMILAR TO RIKEN CDNA A730063F07 GENE	UNKNOWN	PREDICTED: similar to SUMO/sentrin specific protease 5	85750	34869267	243468
SIMILAR TO ABNORMAL SPINDLE	CYTOSKELETON	PREDICTED: similar to abnormal spindle	364500	34880454	243295
SIMILAR TO ARMADILLO REPEAT-CONTAINING PROTEIN	UNKNOWN	PREDICTED: similar to armadillo repeat-containing protein	31200	34855505	302905
SIMILAR TO CHROMOSOME 9 OPEN READING FRAME 7	UNKNOWN	PREDICTED: similar to chromosome 9 open reading frame 7	18410	34853142	272157
HIST3H3	NUCLEUS	PREDICTED: similar to histone 1, H3g	15430	27671651	163757
IMMUNOGLOBULIN LIGHT CHAIN	BLOOD + OTHER CELLS	PREDICTED: similar to immunoglobulin light chain	16750	62647397	161334
SIMILAR TO RIKEN CDNA 1810015P03	TRAFFIC	PREDICTED: similar to transmembrane emp24 protein transport domain containing 6	27610	34851659	275967
PLASMA MEMBRANE CALCIUM-TRANSPORTING ATPASE 4	PLASMA MB	Plasma membrane calcium-transporting ATPase 4	133100	14285346	39788
HYPOTHETICAL PROTEIN LOC298851	UNKNOWN	Protein C2orf18 homolog precursor	41090	81883393	167119

JTB PROTEIN	UNKNOWN	Protein JTB precursor	16390	6016410	128391
PROTEOLIPID PROTEIN 2	UNKNOWN	Proteolipid protein 2	16560	62286961	166582
RAT MHC CLASS II A-BETA RT1.B-B-BETA	BIOSYNTHETIC CARGO	Rat MHC class II A-beta RT1.B-b-beta	22030	554474	66476
RH BLOOD GROUP PROTEIN RH30	BLOOD + OTHER CELLS	Rh blood group protein RH30	46580	3445506	90519
RIBONUCLEASE 4	BLOOD + OTHER CELLS	Ribonuclease 4 precursor RNase 4 RL3	16900	9910536	42830
SODIUM CHANNEL PROTEIN TYPE III ALPHA SUBUNIT	PLASMA MB	Sodium channel protein type 3 subunit alpha Sodium channel protein type III subunit alpha Voltage-gated sodium channel subunit alpha Nav1.3 Sodium channel protein, brain III subunit alpha Voltage-gated sodium channel subtype III	221400	6981510	75080
STROMAL CELL DERIVED FACTOR 1 GAMMA	BLOOD + OTHER CELLS	Stromal cell-derived factor-1 gamma	13550	76563910	209385
SYNAPTOGYRIN 1	TETH/DOCK/FUS	Synaptogyrin-1 p29	25670	9507167	47308
Qa. SYNTAXIN 13	TETH/DOCK/FUS	Syntaxin 13	30470	3184552	52412
Qc. SYNTAXIN 6	TETH/DOCK/FUS	Syntaxin 6	29060	51858907	78119
Qc. SYNTAXIN 8	TETH/DOCK/FUS	Syntaxin-8	26910	3834382	78117
B-TOMOSYN ISOFORM	TETH/DOCK/FUS	Syntaxin-binding protein 5 Tomosyn-1 Lethal(2) giant larvae protein homolog 3	127700	81917877	21456
T-CELL SURFACE GLYCOPROTEIN CD1D	BLOOD + OTHER CELLS	T-cell surface glycoprotein CD1d precursor CD1d antigen	38540	8393070	12016
TOM22 PROTEIN	MITOCHONDRIA	TOM22	15490	71051674	171046
MAC-MARCKS PROTEIN	CYTOSKELETON	TREMBL:Q9EPH2 REFSEQ NP:NP_110489 ENSEMBL:ENSRNOP00000012663 Mac-MARCKS protein	19850	76363234	71714
MEMBRANE ASSOCIATED GUANYLATE KINASE INTERACTING PR	UNKNOWN	Tax_id=10116 Ensembl_locations(Chr-bp):1-37869999 similar to hypothetical protein 6820402C05	60130	34853572	231037
SIMILAR TO MENA PROTEIN	CYTOSKELETON	Tax_id=10116 Ensembl_locations(Chr-bp):13-98108982 similar to mena protein	88490	34881078	196358
ANKYRIN	CYTOSKELETON	Tax_id=10116 Ensembl_locations(Chr-bp):16-73342360 similar to ankyrin	186300	34879099	195573

SIMILAR TO TRANSLATION ELONGATION FACTOR 1 DELTA (GUA)	PROT SYNIFOLD	Tax_id=10116 Ensembl_locations(Chr-bp):7-113905923 similar to eukaryotic translation elongation factor 1 delta (guanine nucleotide exchange protein)	31330	27662108	302099
SIMILAR TO ALPHA-N-ACETYL-GALACTOSAMINIDASE	PROT MOD	Tax_id=10116 Ensembl_locations(Chr-bp):7-120740849 similar to alpha-N-acetyl-galactosaminidase	54520	34867288	202900
SIMILAR TO SP140 PROTEIN	UNKNOWN	Tax_id=10116 Ensembl_locations(Chr-bp):9-84465266 similar to Sp140 protein	104400	34877740	306790
INTRAFLAGELLAR TRANSPORT PROTEIN 20-LIKE PROTEIN	UNKNOWN	Tax_id=10116 HypoHetical protein XP_213403	19700	34872851	239897
HYPOTHETICAL PROTEIN XP_235398	UNKNOWN	Tax_id=10116 HypoHetical protein XP_235398	98020	34866792	248288
SIMILAR TO 4631428G15 PROTEIN	UNKNOWN	Tax_id=10116 Similar to 4631428G15 protein	148800	34878459	250964
SIMILAR TO A530083I02RIK PROTEIN	UNKNOWN	Tax_id=10116 Similar to A530083I02RIK protein	184100	34876687	308809
SIMILAR TO CG11388-PA	UNKNOWN	Tax_id=10116 Similar to CG11388-PA	36250	34869404	241377
SIMILAR TO CG17660-PA	UNKNOWN	Tax_id=10116 Similar to CG17660-PA	52310	34857630	293564
SIMILAR TO COLORECTAL MUTANT CANCER PROTEIN (MCC PR)	UNKNOWN	Tax_id=10116 Similar to Colorectal mutant cancer protein (MCC protein)	126800	34879375	199763
SIMILAR TO DNA MISMATCH REPAIR PROTEIN MLH3 (MUTL PRO)	NUCLEUS	Tax_id=10116 Similar to DNA mismatch repair protein Mlh3 (MutL protein homolog 3)	157700	34867420	219867
DNA-DEPENDENT PROTEIN KINASE CATALYTIC SUBUNIT	NUCLEUS	Tax_id=10116 Similar to DNA-dependent protein kinase catalytic Subunit	470400	34870011	251203
SIMILAR TO HYPOTHETICAL PROTEIN FLJ35794	UNKNOWN	Tax_id=10116 Similar to HypoHetical protein FLJ35794	51380	27708530	166638
SIMILAR TO HYPOTHETICAL PROTEIN KIAA0934	UNKNOWN	Tax_id=10116 Similar to HypoHetical protein KIAA0934	194300	34876285	253215
INHIBITOR OF GROWTH PROTEIN 1	SIGNALING	Tax_id=10116 Similar to ING1 protein	31190	34879659	227451
SIMILAR TO KIAA0963 PROTEIN	UNKNOWN	Tax_id=10116 Similar to KIAA0963 protein	162200	34862323	279597
SIMILAR TO B-TOMOSYN ISOFORM	TETH/DOCK/FUS	Tax_id=10116 Similar to KIAA1006 protein	106300	34869352	253264
SIMILAR TO KIAA1414 PROTEIN	UNKNOWN	Tax_id=10116 Similar to KIAA1414 protein	184500	34861977	207796
SIMILAR TO LIV-1 PROTEIN, ESTROGEN REGULATED	PLASMA MB	Tax_id=10116 Similar to LIV-1 protein, estrogen regulated	85430	34878347	277425
SIMILAR TO NMI PROTEIN	UNKNOWN	Tax_id=10116 Similar to Nmi protein	31120	34854824	192515
RAB22A	GTPASE	Tax_id=10116 Similar to RAB22, member RAS oncogene family	23730	34860889	296032
SIMILAR TO RBP1-LIKE PROTEIN ISOFORM 1	UNKNOWN	Tax_id=10116 Similar to RBP1-like protein isoform 1	67150	27682805	167845
G PROTEIN-COUPLED RECEPTOR 89	SIGNALING	Tax_id=10116 Similar to RIKEN cDNA 4933412D19	51730	34858091	273635
SIMILAR TO SOLUTE CARRIER FAMILY 9 (SODIUM/HYDROGEN E)	MITOCHONDRIA	Tax_id=10116 Similar to RIKEN cDNA 6430520C02	89840	34881696	266670
SIMILAR TO RIKEN CDNA C820004H04	UNKNOWN	Tax_id=10116 Similar to RIKEN cDNA C820004H04	111800	34869133	272177
SIMILAR TO RIKEN CDNA D930036F22 GENE	UNKNOWN	Tax_id=10116 Similar to RIKEN cDNA D930036F22 gene	12830	27662972	294302

RAP1 GUANINE NUCLEOTIDE-EXCHANGE FACTOR PDZ-GEF2B	GTPASE	Tax_id=10116 Similar to Rap1 guanine nucleotide-exchange factor PDZ-GEF2B	252400	34870741	252747
SMC4 STRUCTURAL MAINTENANCE OF CHROMOSOMES 4-LIKE	NUCLEUS	Tax_id=10116 Similar to SMC4 protein	163900	34857050	301164
SIMILAR TO SEC23-INTERACTING PROTEIN p125	UNKNOWN	Tax_id=10116 Similar to Sec23-interacting protein p125	107800	34859392	284142
SIMILAR TO SECRETED GEL FORMING MUCIN	BIOSYNTHETIC CARGO	Tax_id=10116 Similar to Secreted gel-forming mucin	293900	34861766	270223
SMYD1	TRANSCRIPTION	Tax_id=10116 Similar to Skm-BOP2	57130	34855974	276020
SIMILAR TO SOLUTE CARRIER FAMILY 30 (ZINC TRANSPORTER)	PLASMA MB	Tax_id=10116 Similar to Solute carrier family 30 (zinc transporter), member 6	51480	34862482	294808
SIMILAR TO STOMATIN RELATED OLFACTORY PROTEIN SRO	UNKNOWN	Tax_id=10116 Similar to Stomatin related olfactory protein SRO	36800	34857327	207620
Qa, SYNTAXIN 16	TETHIDOCK/FUS	Tax_id=10116 Similar to Syntaxin 16 (Syn16)	41580	34860874	234670
SIMILAR TO TRANSCRIPTION FACTOR E3	TRANSCRIPTION	Tax_id=10116 Similar to Transcription factor E3	61600	34933434	287807
RLBP1 PROTEIN	UNKNOWN	Tax_id=10116 Similar to cellular retinaldehyde-binding protein	43870	34857275	269045
SIMILAR TO CHROMOSOME 10 OPEN READING FRAME 3	UNKNOWN	Tax_id=10116 Similar to chromoSome 10 open reading frame 3	90190	34862686	216923
SIMILAR TO CHROMOSOME 14 OPEN READING FRAME 9	UNKNOWN	Tax_id=10116 Similar to chromoSome 14 open reading frame 9	34520	34869712	209283
MEMBRALIN SPLICE VARIANT 2	UNKNOWN	Tax_id=10116 Similar to chromoSome 19 open reading frame 6	60460	34862329	219400
SIMILAR TO CHROMOBX HOMOLOG 2 (DROSOPHILA PC CLASS)	NUCLEUS	Tax_id=10116 Similar to chromobox homolog 2 (Drosophila Pc class)	55490	34882763	317761
CORONIN 2A	CYTOSKELETON	Tax_id=10116 Similar to coronin, actin binding protein, 2A	60470	34868360	191842
SIMILAR TO CALCIUM BINDING DOMAIN PROTEIN, SIMILAR TO THE LIKELY CONTAMINANTS	UNKNOWN	Tax_id=10116 Similar to dJ14N1.2 (novel S-100/CaBP type calcium binding domain protein, Similar to trichohyalin)	133800	34858169	280707
SIMILAR TO DEDICATOR OF CYTO-KINESIS 2	SIGNALING	Tax_id=10116 Similar to dedicator of cyto-kinesis 2	113200	34861140	200712
MITOGEN-ACTIVATED PROTEIN KINASE KINASE 3 ISOFORM 1	SIGNALING	Tax_id=10116 Similar to hypothetical protein	74350	34873993	286816
SIMILAR TO VACUOLAR PROTEIN SORTING 13D	TRAFFIC	Tax_id=10116 Similar to hypothetical protein	465500	34872448	294934
ENGULFMENT AND CELL MOTILITY PROTEIN 3	CYTOSKELETON	Tax_id=10116 Similar to hypothetical protein 9930107J06	79800	34851601	290038
SIMILAR TO HYPOTHETICAL PROTEIN C230069C04 (2)	UNKNOWN	Tax_id=10116 Similar to hypothetical protein C230069C04	88310	34858101	286208
SOLUTE CARRIER FAMILY 39 (ZINC TRANSPORTER), MEMBER 9	UNKNOWN	Tax_id=10116 Similar to hypothetical protein FLJ11274	34120	34866189	272995
SIMILAR TO HYPOTHETICAL PROTEIN FLJ12681	UNKNOWN	Tax_id=10116 Similar to hypothetical protein FLJ12681	90650	34870562	205672
SIMILAR TO HYPOTHETICAL PROTEIN FLJ13511	UNKNOWN	Tax_id=10116 Similar to hypothetical protein FLJ13511	152600	34861042	205697
SIMILAR TO HYPOTHETICAL PROTEIN FLJ32000	UNKNOWN	Tax_id=10116 Similar to hypothetical protein FLJ32000	118000	34870861	275469

SIMILAR TO LOW AFFINITY SODIUM-GLUCOSE COTRANSPORTER	METABOLISM	Tax_Id=10116 Similar to low affinity Sodium-glucose cotranSporter	67850	34852422	211877
SIMILAR TO LYSOSOMAL APYRASE-LIKE 1	LYSOSOME	Tax_Id=10116 Similar to lySoSomal apyraSe-like 1	40920	34874392	217901
TRANSCRIPTION FACTOR 20 (STROMELYSIN 1 PDGF-RESPONSIVE)	TRANSCRIPTION	Tax_Id=10116 Similar to mKlAA0292 protein	199400	34867313	311710
SIMILAR TO MKIAA0515 PROTEIN	UNKNOWN	Tax_Id=10116 Similar to mKlAA0515 protein	172900	34853592	286188
SIMILAR TO MITOTIC KINESIN RELATED PROTEIN	CYTOSKELETON	Tax_Id=10116 Similar to mitotic kinesin-related protein	229600	34862643	291449
SIMILAR TO MYOSIN X	CYTOSKELETON	Tax_Id=10116 Similar to myoSin X	251600	34855017	249318
COPI COATOMER ZETA-2 SUBUNIT	COAT	Tax_Id=10116 Similar to nonclathrin coat protein zeta2-COP	18220	34873491	273036
SIMILAR TO PARANEOPLASTIC ANTIGEN LIKE 5	UNKNOWN	Tax_Id=10116 Similar to paranepoPlastic antigen like 5	49680	27682149	207724
SIMILAR TO PHOSPHATIDYLINOSITOL GLYCAN CLASS N	PLASMA MB	Tax_Id=10116 Similar to phoSphatidyInoSitoGlycan claSS N	89310	34878866	217052
SIMILAR TO PLEXIN 1	SIGNALING	Tax_Id=10116 Similar to plexin 1	204500	34856403	308345
TEA DOMAIN-CONTAINING TRANSCRIPTION FACTOR	UNKNOWN	Tax_Id=10116 Similar to the firSt amino acid waS determined to be iSoleucine rather than methionine by compariSon to mTEF1 (aSceSSion # L13853)	78480	34858488	267553
QaA SYNTAXIN 7	TETHIDOCK/FUS	Tax_Id=10116 Syntaxin-7	29790	3152727	109585
SARCOMA AMPLIFIED SEQUENCE (PREDICTED)	UNKNOWN	Tetraspanin-31 Tspan-31 Sarcoma amplified sequence homolog	22660	62900748	260364
TRANSCOBALAMIN II	BIOSYNTHETIC CARGO	Transcobalamin-2 precursor Transcobalamin II TCII TC II	47420	5910985	90533
TRANSMEMBRANE PROTEIN 14C (P11)	UNKNOWN	Transmembrane protein 14C p11	11780	27734399	30411
TRIPEPTIDYL-PEPTIDASE I	LYSOSOME	Tripeptidyl-peptidase 1 precursor Tripeptidyl-peptidase I TPP-I	61330	20140356	75921
SIMILAR TO CHROMOSOME 20 OPEN READING FRAME 30	UNKNOWN	Tripeptidyl aminopeptidase Uncharacterized protein C20orf30 homolog	13200	81882492	190070
SIMILAR TO CDNA SEQUENCE BC005632	UNKNOWN	Uncharacterized protein family UPF0227 member RGD1359682	33990	55741536	265453
X-LINKED INTERLEUKIN-1 RECEPTOR ACCESSORY PROTEIN-LIKE	BIOSYNTHETIC CARGO	X-linked interleukin-1 receptor accessory protein-like 1 precursor IL1RAPL-1	79770	34222486	241488
GLUTAMATE RECEPTOR KA1 SUBUNIT	PLASMA MB	glutamate receptor, ionotropic, kainate 4 precursor	107300	475546	119817
CHAIN H, 1.9A STRUCTURE OF THE THERAPEUTIC ANTIBODY CAb	BLOOD + OTHER CELLS	immunoglobulin heavy chain [Rattus sp.]	51460	243866	79012
IMMUNOGLOBULIN KAPPA-CHAIN	BLOOD + OTHER CELLS	immunoglobulin kappa-chain	14860	204835	126680

OLFACTORY RECEPTOR OLR1063	PLASMA MB	olfactory receptor OLR1063	35540	47578031	302444
BCL-2-ASSOCIATED TRANSCRIPTION FACTOR	TRANSCRIPTION	similar to Bcl-2-associated transcription factor [Rattus norvegicus]	92060	34852810	216315
PYRUVATE KINASE, M2 ISOZYME	METABOLISM	similar to Pyruvate kinase, M2 isozyme	57960	34875446	288218
SIMILAR TO RIKEN CDNA 1500016H10	PROT SYN/FOLD	similar to RIKEN cDNA 1500016H10	14000	34882737	231235
SIMILAR TO RIKEN CDNA 2010005013	UNKNOWN	similar to RIKEN cDNA 2010005013 [Rattus norvegicus]	15020	34880819	301426
UDP-GALACTOSE TRANSPORTER	METABOLISM	similar to UDP-galactose transporter	38530	34933455	208424
PROTEIN SYS1 HOMOLOG	TRAFFIC	similar to chromosome 20 open reading frame 169	20950	34860687	214268
KRUPPEL-LIKE ZINC FINGER PROTEIN GLIS3	UNKNOWN	similar to hypothetical protein E230012L24	47320	34862740	246776
AMINOPEPTIDASE O (AP-O)	METABOLISM	similar to hypothetical protein FLJ14675	21510	34873570	196884
SIMILAR TO IMMUNOGLOBULIN ALPHA HEAVY CHAIN	BLOOD + OTHER CELLS	similar to immunoglobulin alpha heavy chain	48960	34935283	224861
SIMILAR TO KERATIN ASSOCIATED PROTEIN 11-1	LIKELY CONTAMINANTS	similar to keratin associated protein 11-1	18900	27670141	269756
SERINE/THREONINE PROTEIN PHOSPHATASE WITH EF-HAND MOTIF	SIGNALING	similar to protein phosphatase with EF-hands-2 [Rattus norvegicus]	84100	34876562	308740
SIMILAR TO PUTATIVE PROTEIN AT THE X CHROMOSOMAL L1CAM	UNKNOWN	similar to putative protein at the X chromosomal L1cam locus	64310	34864432	293919
SIMILAR TO RECOMBINATION ACTIVATING GENE 1	UNKNOWN	similar to recombination activating 1 activation	24690	27692967	292043
SIMILAR TO TRANSMEMBRANE GAMMA-CARBOXYGLUTAMIC ACID	PROT MOD	similar to transmembrane gamma-carboxyglutamic acid protein 4	45410	34856617	203605
HYPOTHETICAL PROTEIN XP_216137	UNKNOWN	unknown	26610	84781644	345922
SIMILAR TO KIAA1204 PROTEIN	UNKNOWN	unknown	167300	34869344	309548
SIMILAR TO HYPOTHETICAL PROTEIN MDS025	UNKNOWN	unknown	37550	34875130	276318
SIMILAR TO HYPOTHETICAL PROTEIN B230358A15	UNKNOWN	unknown	84160	34880715	314842

CMBSEQID	MEMBRANE STATUS	SIGNAL TYPE	TMD	UNIREF100	REFSEQ
121548	SOLUBLE			P26772	
35616	SOLUBLE			P42655 P62260	
29712	SOLUBLE			P63102 Q52KK1 Q6IRF4	
129368	SOLUBLE	cleavable signal peptide		Q923V8	
169811	SOLUBLE	cleavable signal peptide		Q5M875	
148907	SOLUBLE	cleavable signal peptide		Q64591 Q6PCV4	
187564	SOLUBLE			Q8CHM7	
51421	SOLUBLE			P23965	
19230	SOLUBLE			P23457 Q5BKC8 Q6LDE6 Q6LDE7	
83190	SOLUBLE	cleavable signal peptide		O70351	
96895	SOLUBLE			P13437	
23758	SOLUBLE			P31210	
4834	SOLUBLE				
132206	SOLUBLE			Q6PDW1	
4835	SOLUBLE				
98434	SOLUBLE			Q6PDV6	
4837	SOLUBLE				
60848	SOLUBLE			P25232 P62271	XP_215328.1
122667	SOLUBLE				
4840	SOLUBLE			P60868	XP_233622.1
37243	SOLUBLE			P05765	
4842	SOLUBLE				
4844	SOLUBLE			P62853 Q3SYP7	XP_217121.1
75074	SOLUBLE				
120488	SOLUBLE				
1344	SOLUBLE			P62859	
60850	SOLUBLE			P17073 P62909	XP_341889.1
106720	SOLUBLE			P62864	
51618	SOLUBLE			P49242	
4853	SOLUBLE			P23821 P62083	
142294	SOLUBLE				
51515	SOLUBLE			P38983	
52609	SOLUBLE			P63039	

23405	SOLUBLE			P19945		
144430	SOLUBLE			P19944		XP_343404.1
144431	SOLUBLE	cleavable signal peptide		P02401	Q499W9	
144419	SOLUBLE			P23358		
71631	SOLUBLE			P62718		XP_214302.1
4812	SOLUBLE			P83732		
65711	SOLUBLE			Q6PDV5		
85424	SOLUBLE			P50878		
37237	SOLUBLE			P09895		
28269	SOLUBLE	cleavable signal peptide		P06761		
298279	SOLUBLE			Q5U2U3		XP_217264.2
3629	SOLUBLE	cleavable signal peptide		P19603	Q63336	
				Q64240		
71751	SOLUBLE			Q4V7C7		
141484	SOLUBLE	cleavable signal peptide		P19511		
21505	SOLUBLE			P31399		
142437	SOLUBLE			Q06647		
73367	MEMBRANE			P15999		
141479	SOLUBLE	cleavable signal peptide		P10719	Q499W0	
60480	SOLUBLE			P21571		
21504	SOLUBLE	cleavable signal peptide		P35434		
11887	SOLUBLE			P29418		
69786	SOLUBLE			P35435		
				UPI000011257C		
126543	SOLUBLE			P16638		
302124	SOLUBLE	cleavable signal peptide		Q7TQ11		
148924	SOLUBLE			Q7TMA5		
151517	SOLUBLE			Q6DGG1		XP_217255.1
166238	SOLUBLE			Q7TME5		
263869	MEMBRANE		23 20 IN-OUT 52 20 OUT- IN 78 23 IN-OUT 115 20 OUT-IN 141 21 IN-OUT 171 18 OUT-IN 200 23 IN-	Q7TQ74		
173317	SOLUBLE	cleavable signal peptide		Q7TQ70		XP_342268.1
166242	SOLUBLE			Q7TPK2		
199808	SOLUBLE			Q7TP30		
31496	SOLUBLE			P17764		

193296	SOLUBLE	cleavable signal peptide		Q4FZU0	
3001	SOLUBLE			Q9EST6	
338228	SOLUBLE			Q6P6V3 Q9ER34	
120792	SOLUBLE			P63259	
156591	SOLUBLE			Q5M7U6	
51604	SOLUBLE			P07872 P11354	
3086	SOLUBLE			P97562	
42129	SOLUBLE			Q63448	
54409	SOLUBLE			P10760	
340217	SOLUBLE			UPI0000110EC7	
605	SOLUBLE	cleavable signal peptide		Q6P7C6	
23759	SOLUBLE	cleavable signal peptide		Q9JJ22 Q9JJ22-2	
100616	SOLUBLE			P36953	
7845	SOLUBLE			P38918	
217551	SOLUBLE			Q91ZD7	
319018	SOLUBLE			Q3MHS3	
114803	SOLUBLE			Q6P786	
11475	SOLUBLE	cleavable signal peptide		Q63910	
11478	SOLUBLE	cleavable signal peptide	7 18 IN-OUT	P17475 Q6AYZ5	
126488	SOLUBLE	cleavable signal peptide		P14046 Q6LDP2	
111646	SOLUBLE	cleavable signal peptide		Q63041	
109334	SOLUBLE			P24090 Q5BKD2	
125352	SOLUBLE	cleavable signal peptide		Q91V15	
161586	SOLUBLE	cleavable signal peptide		Q63022 Q63213	
151400	SOLUBLE	cleavable signal peptide		Q8K1Q6	XP_216422.1
37175	SOLUBLE			Q5M7W0	
76478	SOLUBLE			Q9Z1P2	
51376	SOLUBLE			P70473	
				P54921	

45123	SOLUBLE	cleavable signal peptide			P01015	
75054	SOLUBLE	cleavable signal peptide			P00762	
120574	SOLUBLE				P14669 Q642C2	
3633	SOLUBLE				P14668	
3638	SOLUBLE	cleavable signal peptide			P04639 Q5EBB2	
141420	SOLUBLE	cleavable signal peptide			P02651 Q5BK92	
126501	SOLUBLE	cleavable signal peptide			P02650	
63059	SOLUBLE				Q548E3 Q9JM53	
37797	SOLUBLE				P07824 Q5BK93	
45108	SOLUBLE				P09034	
84171	SOLUBLE				P13221	
3905	SOLUBLE	cleavable signal peptide			P00507 Q64551	
232734	SOLUBLE				Q5XIM0	XP_217434.2
310568	SOLUBLE	cleavable signal peptide			Q5VLR5	XP_216396.2
166334	SOLUBLE	cleavable signal peptide			Q7TP23	
21485	SOLUBLE	cleavable signal peptide			P26644	
27803	SOLUBLE				P07151	
21055	SOLUBLE	cleavable signal peptide			P06760	
71708	SOLUBLE				O09171	
30001	SOLUBLE	cleavable signal peptide	7 23 IN-OUT		Q9ES38	
54374	SOLUBLE				P46844	
126549	SOLUBLE	cleavable signal peptide			P48199 Q5BK94	
18021	SOLUBLE				Q9JLH7	
70677	MEMBRANE		20 23 OUT-IN 141 20 IN-OUT 175 23 OUT-IN		P70500	
148937	SOLUBLE				Q7M079	
69775	MEMBRANE	cleavable signal peptide	484 23 OUT-IN		P35565	
23403	SOLUBLE	cleavable signal peptide			P10452 P18418	
45074	SOLUBLE				P07756	

13404	MEMBRANE	cleavable signal peptide	5 18 IN-OUT	P04167 Q64579 Q64582	
63770	MEMBRANE	cleavable signal peptide	5 20 IN-OUT	P13107 Q64585	
63780	MEMBRANE	cleavable signal peptide		P08683 Q63141 Q64554	
63782	MEMBRANE	cleavable signal peptide	5 18 IN-OUT	P20814 P22693 Q64587	
33163	MEMBRANE	cleavable signal peptide	2 19 IN-OUT	P19225 UPI000016796B	
72763	MEMBRANE	cleavable signal peptide	3 23 IN-OUT	P24470 Q63914 Q64534	
63778	MEMBRANE	cleavable signal peptide		P05178	
45873	MEMBRANE	cleavable signal peptide		P05179	
63788	MEMBRANE	signal anchor	9 18 IN-OUT	P10634	
63790	MEMBRANE	signal anchor	4 23 OUT-IN 301 23 IN-OUT	P12939	
21526	MEMBRANE	cleavable signal peptide	2 22 IN-OUT	P05182	
3731	MEMBRANE	cleavable signal peptide	4 23 OUT-IN 217 23 IN-OUT	Q6LEQ2	
104898	MEMBRANE	signal anchor	7 23 IN-OUT 219 23 OUT-IN	Q64581	
87425	MEMBRANE	cleavable signal peptide	4 23 OUT-IN 219 23 IN-OUT 301 23 OUT-IN	P05183	
21524	MEMBRANE	cleavable signal peptide	15 18 OUT-IN 113 20 IN-OUT	P20817	
103927	MEMBRANE	signal anchor	4 23 OUT-IN 305 23 IN-OUT	O35106 P12938 Q5FVU3	
33164	MEMBRANE	signal anchor	7 20 IN-OUT	Q566D3 Q64680 P11240	
63743	SOLUBLE	cleavable signal peptide			
71180	SOLUBLE				
60497	SOLUBLE	cleavable signal peptide		O35078	

131621	SOLUBLE				Q8VID1	
308340	SOLUBLE	cleavable signal peptide	4 20 OUT-IN		Q6AYS8	XP_213994.2
3622	SOLUBLE				P06214	
80356	SOLUBLE				Q62651 UPI0000167964	
23398	SOLUBLE				P11348	
339248	MEMBRANE	cleavable signal peptide	509 23 OUT-IN		P36365 Q6P7Q5	
8742	SOLUBLE				P63036	
318957	SOLUBLE	cleavable signal peptide				
193923	MEMBRANE	cleavable signal peptide	539 23 OUT-IN 573 23 IN-OUT 605 18 OUT-IN		P25235 Q6P9X0	
250139	SOLUBLE					
77835	MEMBRANE	cleavable signal peptide	483 23 OUT-IN		Q62902	
33170	SOLUBLE	cleavable signal peptide			UPI00000E73E1	
214426	SOLUBLE	cleavable signal peptide			P56571 Q68FS5	XP_215368.1
145232	SOLUBLE					
318787	MEMBRANE	cleavable signal peptide	5 18 OUT-IN 29 23 IN-OUT		Q6P6S9	
18992	SOLUBLE					XP_214922.1
140182	SOLUBLE				P62630 Q5BJW8 Q64718 Q78ED4	XP_215242.2
157237	SOLUBLE	cleavable signal peptide	7 23 IN-OUT		P52555 P80749 Q5BKC2	
338764	SOLUBLE					
15873	SOLUBLE				P14604	
149061	SOLUBLE				Q5EBD2	

109266	SOLUBLE				P52844		
23682	SOLUBLE						
74410	SOLUBLE				Q3T1K5		
170945	SOLUBLE	cleavable signal peptide			UPI00001820BB		
29993	MEMBRANE	cleavable signal peptide	7 23 IN-OUT		P97612 Q5BKA3		
43659	MEMBRANE				O09187 O09190 P12785 Q63577 Q64717		
3760	SOLUBLE				P02692		
78151	MEMBRANE		463 18 OUT-IN		P30839		
277663	SOLUBLE				Q6P7T1		
145181	SOLUBLE	cleavable signal peptide			Q9QX79		
3766	SOLUBLE	cleavable signal peptide			P02680 P02680-2		
95208	SOLUBLE	cleavable signal peptide			P04937 Q6LDX9		
181007	SOLUBLE	cleavable signal peptide			Q8K583		
39875	SOLUBLE				O88618 Q5BKB7		
45080	SOLUBLE	cleavable signal peptide			P14408		
51443	SOLUBLE				P25093		
140831	SOLUBLE				P70552		
44648	MEMBRANE						
113271	SOLUBLE				Q8CJG5		
26394	SOLUBLE				Q9R1Q3	XP 346411.1	
3897	SOLUBLE	cleavable signal peptide			P10860 Q66HI8		
28251	SOLUBLE				Q6LC16		
146667	SOLUBLE				P09606		
78049	SOLUBLE				P00502		
28290	SOLUBLE				P14942		
63272	SOLUBLE						
28283	SOLUBLE	cleavable signal peptide			O08946 P04041 Q4PIY2		
51456	SOLUBLE				Q9QWU4	XP_216453.1	

86608	SOLUBLE	cleavable signal peptide		Q68FY4	
33791	SOLUBLE				
123232	SOLUBLE				
338318	SOLUBLE			Q6P513	
85008	SOLUBLE			Q07439	
68722	SOLUBLE			P63018 Q4FZY7	
82698	SOLUBLE			Q91XW0	
28543	SOLUBLE			P02091	
16936	SOLUBLE	cleavable signal peptide	5 18 IN-OUT	P20059	
140379	SOLUBLE	cleavable signal peptide		Q99PS8	
105537	SOLUBLE			Q9QV19	
100475	SOLUBLE			Q07523	

15417	SOLUBLE				O35952		
16963	SOLUBLE				P22791		
395638	SOLUBLE	cleavable signal peptide		13 23 IN-OUT	Q6P136		
166503	SOLUBLE	cleavable signal peptide			UPI000017FFAE		
163993	MEMBRANE				Q3B7V5		
4847	SOLUBLE						
244225	SOLUBLE	cleavable signal peptide		10 23 OUT-IN	Q562C4		
208921	SOLUBLE				Q5M884	XP_214465.2	
4820	SOLUBLE						
154010	SOLUBLE				Q8CJH5		
47186	SOLUBLE	cleavable signal peptide		7 20 IN-OUT	O35802		
38418	SOLUBLE	cleavable signal peptide			Q63416		
71492	SOLUBLE				P41562 P80300		
3955	SOLUBLE	cleavable signal peptide			P12007		
66467	SOLUBLE				Q63282		
210892	SOLUBLE				Q6IFV3	XP_213482.2	
318877	SOLUBLE				Q6P6Q2 Q7TN97		
67836	SOLUBLE	signal anchor			Q10758		
127122	SOLUBLE				P97550 Q02974		
51518	SOLUBLE				P04642		
139643	SOLUBLE				Q68GV5	XP_217339.1	
28295	MEMBRANE			12 23 IN-OUT 131 19 OUT-IN			
32844	SOLUBLE	cleavable signal peptide					
203325	SOLUBLE	cleavable signal peptide			Q6TXE2		
295796	SOLUBLE	cleavable signal peptide		5 23 IN-OUT	Q6TUG0		
224451	SOLUBLE				Q7TNA8		
296680	MEMBRANE			205 23 IN-OUT	Q5XIN6	XP_223541.2	
43686	SOLUBLE	cleavable signal peptide			P10959 Q63106 Q64626		
78070	SOLUBLE	cleavable signal peptide			Q63108		

166149	SOLUBLE				Q7TMB9	
166406	SOLUBLE	cleavable signal peptide			Q7TNX0	
3599	SOLUBLE	cleavable signal peptide			P15650	
85756	MEMBRANE		21 23 IN-OUT		P18163	
60485	MEMBRANE	signal anchor	7 23 IN-OUT		O88813	
44475	MEMBRANE	signal anchor	21 23 IN-OUT		P33124 Q63835	
72321	SOLUBLE	cleavable signal peptide			Q64194	
37207	SOLUBLE				P30904	
33913	SOLUBLE				Q6GSM4	
19138	SOLUBLE				P19999	
					UPI00001121CE	
338661	MEMBRANE	cleavable signal peptide	20 23 IN-OUT		Q6P762	
51409	MEMBRANE	signal anchor	40 23 IN-OUT		O88941	
280160	SOLUBLE	cleavable signal peptide			Q5U2R7	XP_218854.1
37213	MEMBRANE	cleavable signal peptide	174 23 IN-OUT		Q02253	
3224	MEMBRANE		21 23 IN-OUT		Q6P9X2	
77688	SOLUBLE					
77128	SOLUBLE				P62076	
12056	MEMBRANE				Q9WVA1	
228858	MEMBRANE		288 23 IN-OUT		Q5PPL3	XP_219730.2
229389	SOLUBLE				Q66HF1	XP_217417.2
213294	SOLUBLE	cleavable signal peptide			Q5RJN0	XP_343166.1
243054	SOLUBLE				Q5XIH3	XP_215176.2
291031	SOLUBLE				P19234 Q6PDU9	XP_343639.1
44210	MEMBRANE		20 23 IN-OUT		P00388	
199168	SOLUBLE	cleavable signal peptide			Q561S0	XP_234089.2
161237	SOLUBLE				Q8VHJ9	NP_599208.1
219030	SOLUBLE				Q5FVM4	
111676	MEMBRANE	cleavable signal peptide	1809 23 OUT-IN		P11654	

3157	SOLUBLE	cleavable signal peptide		Q9J185	
69495	SOLUBLE			P19804	
318887	SOLUBLE	cleavable signal peptide		Q6P6S4	
75019	SOLUBLE			P00481	Q63407
102628	MEMBRANE	signal anchor	10 18 OUT-IN	O54753	
219134	SOLUBLE	cleavable signal peptide		UPI00001	CEDAC
221549	SOLUBLE	cleavable signal peptide	9 23 IN-OUT	UPI00001	D1A63
237675	SOLUBLE			UPI00001	D0C4B
214842	SOLUBLE			UPI00001	C9D52
201232	SOLUBLE	cleavable signal peptide		UPI00001	9B6E0
273222	SOLUBLE			UPI00001	C705B
292254	SOLUBLE			UPI00001	7E147
288262	SOLUBLE			UPI00001	CFEE5
288751	SOLUBLE			Q3MHS9	
198793	SOLUBLE	cleavable signal peptide		UPI00001	7E18D
280728	SOLUBLE			UPI00001	82984
313497	SOLUBLE			UPI00001	80449
167188	SOLUBLE			UPI00001	7E24F
256004	SOLUBLE	cleavable signal peptide		UPI00001	7EC12
215096	SOLUBLE	cleavable signal peptide		UPI00001	80F4C
206311	SOLUBLE			UPI00001	CE8C3
276202	SOLUBLE			UPI00001	CF7C4
220359	SOLUBLE			UPI00001	D0BF1
227817	SOLUBLE	cleavable signal peptide	7 20 IN-OUT	UPI00001	80E7B
194048	SOLUBLE	cleavable signal peptide		UPI00001	CD14E
161693	SOLUBLE			UPI00001	D08D1
209405	MEMBRANE	signal anchor	13 23 IN-OUT 69 23 OUT-IN 191 23 IN-OUT	UPI00001	C79D9
249650	SOLUBLE	cleavable signal peptide		UPI00001	D1639
293536	SOLUBLE	cleavable signal peptide		UPI00001	D1016
				UPI00001	D1120

286563	SOLUBLE	cleavable signal peptide		UPI00001CEC61	
260440	MEMBRANE	cleavable signal peptide	2 19 IN-OUT	UPI00001CEBD2	
271135	SOLUBLE	cleavable signal peptide		UPI00001CFD4B	
306304	MEMBRANE		86 23 IN-OUT	UPI00001CFC2F	
191580	SOLUBLE			UPI00001CF3A2	
208059	SOLUBLE	cleavable signal peptide		UPI00001CBC39	
139592	SOLUBLE			UPI00001C7619	
270415	SOLUBLE			UPI0000181D12	
209477	SOLUBLE			UPI00001D0D54	
215516	SOLUBLE			UPI00001CA225	
314386	SOLUBLE	cleavable signal peptide		UPI00001CFF0B	
195578	SOLUBLE	cleavable signal peptide		UPI00001CFA7C	
195681	SOLUBLE	cleavable signal peptide		UPI00001CF14D	
299358	SOLUBLE	cleavable signal peptide		Q4FZT0 UPI00001811E2	
231239	SOLUBLE			UPI00001D137B	
278868	SOLUBLE	cleavable signal peptide	7 20 IN-OUT	UPI00001CFB6B	XP_343129.1
90537	SOLUBLE	cleavable signal peptide		Q9Z0V6	
60442	SOLUBLE	cleavable signal peptide		Q9Z0V5	
198556	SOLUBLE	cleavable signal peptide		Q5BJN6	XP_342640.1
45089	SOLUBLE			Q5BK98	
43433	SOLUBLE			Q63716	
60487	SOLUBLE	cleavable signal peptide		Q9R063	
176638	SOLUBLE			Q9Z2M4	
155718	SOLUBLE			Q9Z2Z4	
108354	SOLUBLE	cleavable signal peptide		P97852	
34787	SOLUBLE	cleavable signal peptide		Q9WVK3	
254493	SOLUBLE			Q68FT7	XP_217455.2
69363	MEMBRANE		256 23 OUT-IN 308 20 IN-OUT	P16036	

55437	SOLUBLE				P57093 Q9QY64		
144413	SOLUBLE	cleavable signal peptide			P04916		
60419	SOLUBLE	cleavable signal peptide			Q01177 Q5BKB6 Q9ROW3	NP_445943.1	
60574	SOLUBLE	cleavable signal peptide			Q63321		
60726	SOLUBLE						
4312	SOLUBLE	cleavable signal peptide			P67779 Q4V8M6		
69597	SOLUBLE				P14882		
205305	MEMBRANE			57 23 IN-OUT	Q6P6G2		
51531	MEMBRANE			54 23 IN-OUT	Q3T1L3 Q9Z1X1		
69606	SOLUBLE	cleavable signal peptide			P04785 P13700		
21556	SOLUBLE	cleavable signal peptide			P11598		
227664	SOLUBLE	cleavable signal peptide			P38659 Q6P7S5		
31503	SOLUBLE	cleavable signal peptide			P18292		
55382	SOLUBLE				Q5M7T6		
40425	SOLUBLE				P52873 Q5RKM0	XP_346578.1	
21122	MEMBRANE						
111003	MEMBRANE				P09527 Q4AEF6		
136355	SOLUBLE						
8623	SOLUBLE				Q6P797		
173285	SOLUBLE				Q9Z1C7		
78145	MEMBRANE				P05712		
3729	MEMBRANE	cleavable signal peptide	5 18 IN-OUT		Q64648		

3576	SOLUBLE			68 23 IN-OUT 170 23 OUT- IN	Q03336 Q63496 Q925W3 Q8VBU0	NP_543185.1
64492	MEMBRANE					
80376	SOLUBLE	cleavable signal peptide			P50170	
35165	MEMBRANE	cleavable signal peptide			P55006 Q4KMB6	
337611	MEMBRANE	cleavable signal peptide		439 20 OUT-IN	Q6P7A7	
37238	SOLUBLE					
1145	SOLUBLE					
4814	SOLUBLE				Q5BJ97	
74518	SOLUBLE				Q642E2	
4825	SOLUBLE					
4826	SOLUBLE					
32867	SOLUBLE				P63326	
4836	SOLUBLE					
72161	SOLUBLE					
100993	SOLUBLE				O55211	

4843	SOLUBLE				P62850 Q6PEC9	
127926	SOLUBLE				Q6PED0	
4849	SOLUBLE					
74523	SOLUBLE				P62755	
4854	SOLUBLE					
2378	SOLUBLE				Q4V8I6	
60562	SOLUBLE				Q99MS0	
299568	SOLUBLE					
84180	MEMBRANE			60 20 IN-OUT 84 23 OUT- IN 260 20 IN-OUT 299 23 OUT-IN 759 23 IN-OUT 836 23 OUT-IN 930 20 IN- OUT	P11507 P11507-2	
75284	MEMBRANE	signal anchor		33 23 IN-OUT 75 23 OUT- IN 118 21 IN-OUT 143 23 OUT-IN 172 22 IN-OUT 203 18 OUT-IN 241 23 IN- OUT 283 23 OUT-IN 413 23 IN-OUT 440 23 OUT-IN	Q505I3	
213126	MEMBRANE				UPI000005CD43	
31392	SOLUBLE	cleavable signal peptide			P18297	
68739	SOLUBLE	cleavable signal peptide			Q5BKA6 Q64268	
341343	SOLUBLE	cleavable signal peptide			Q68FT8	
31393	SOLUBLE				P09139 Q9R2C7	
280024	SOLUBLE	cleavable signal peptide			Q5RJR9	

120645	SOLUBLE	cleavable signal peptide		P02770 P11382		
52390	SOLUBLE	cleavable signal peptide		P23680 Q63539		
70622	SOLUBLE	cleavable signal peptide		Q9WVK7		
80422	MEMBRANE		264 23 IN-OUT 301 23 OUT-IN	Q63965		
38101	SOLUBLE	signal anchor	34 23 IN-OUT			
288462	SOLUBLE			Q6PDU7		
43622	MEMBRANE	cleavable signal peptide	21 23 IN-OUT 58 23 OUT-IN 87 23 IN-OUT 157 23 OUT-IN 191 23 IN-OUT 243 23 OUT-IN 316 23 IN-OUT 353 23 OUT-IN 511 23 IN-OUT 548 23 OUT-IN 589 23 IN-OUT	O35913 O55224		
43660	SOLUBLE	cleavable signal peptide		P27867		
269681	SOLUBLE			Q8CHN6		
85115	MEMBRANE			Q02769		
36413	SOLUBLE	cleavable signal peptide		P48721 UPI0000170CC4		
96892	SOLUBLE			Q920L2		
167087	SOLUBLE			UPI00001C9571		
45104	SOLUBLE			P13086		
318917	SOLUBLE	cleavable signal peptide		Q6F6W0		
35188	SOLUBLE			P07632		
111692	SOLUBLE			P07895		
33179	MEMBRANE		85 23 IN-OUT 165 20 OUT-IN 196 20 IN-OUT 253 23 OUT-IN	Q64232		
3965	SOLUBLE	cleavable signal peptide		P01048 UPI0000163B79		
726503	SOLUBLE	cleavable signal peptide		Q75Q39		
22440	SOLUBLE					
246480	SOLUBLE	cleavable signal peptide				
31609	SOLUBLE					
11888	MEMBRANE					

3624	SOLUBLE								
3681	SOLUBLE								
87332	SOLUBLE								
141497	SOLUBLE								NP_446447.1
29986	SOLUBLE								
4320	SOLUBLE						Q2V4X5		
106718	SOLUBLE								
127131	SOLUBLE								
286288	SOLUBLE		cleavable signal peptide						
216920	SOLUBLE		cleavable signal peptide						
247133	SOLUBLE		cleavable signal peptide						
217377	SOLUBLE		cleavable signal peptide						
206351	MEMBRANE		cleavable signal peptide		40 23 IN-OUT 453 23 OUT-IN				
214468	SOLUBLE		cleavable signal peptide		5 23 IN-OUT				
288307	MEMBRANE		signal anchor		43 23 IN-OUT 89 23 OUT-IN 118 23 IN-OUT				
310313	SOLUBLE		cleavable signal peptide		13 20 IN-OUT				
187298	MEMBRANE		cleavable signal peptide		510 23 OUT-IN				
262615	SOLUBLE		cleavable signal peptide						
80318	SOLUBLE								
3968	SOLUBLE								
395977	SOLUBLE								
62122	SOLUBLE								
71715	SOLUBLE								
51568	SOLUBLE								
111533	SOLUBLE								
43519	SOLUBLE								
37240	SOLUBLE								
144428	SOLUBLE								
303924	SOLUBLE								
207228	SOLUBLE								
197702	SOLUBLE								
315461	SOLUBLE								
232164	SOLUBLE								

309822	MEMBRANE	cleavable signal peptide				
258001	SOLUBLE					
261916	SOLUBLE	cleavable signal peptide				
302513	SOLUBLE	cleavable signal peptide				
244528	SOLUBLE					
312697	SOLUBLE					
224112	SOLUBLE					
295665	MEMBRANE		1197 23 OUT-IN			
266483	SOLUBLE					
265212	SOLUBLE					
286300	SOLUBLE					
276942	SOLUBLE					
213226	SOLUBLE					
252129	MEMBRANE	signal anchor	31 23 IN-OUT 84 23 OUT-IN			
276048	SOLUBLE					
239547	SOLUBLE					
249723	SOLUBLE					
304054	SOLUBLE	cleavable signal peptide				
169892	MEMBRANE	cleavable signal peptide	7 23 IN-OUT 509 23 OUT-IN			
316149	MEMBRANE	signal anchor	57 23 IN-OUT 107 23 OUT-IN 142 23 IN-OUT			
297605	SOLUBLE					
216144	MEMBRANE		80 23 IN-OUT 112 23 OUT-IN			
208161	MEMBRANE		135 23 OUT-IN			
228920	SOLUBLE					
198275	SOLUBLE	cleavable signal peptide				
239142	SOLUBLE					
201012	SOLUBLE					
213158	MEMBRANE					
208522	SOLUBLE	cleavable signal peptide				
210822	SOLUBLE	cleavable signal peptide				
195759	MEMBRANE	signal anchor				
288335	SOLUBLE	cleavable signal peptide	7 20 IN-OUT			
273878	SOLUBLE					

196365	MEMBRANE	signal anchor				
204172	SOLUBLE					
303538	SOLUBLE	cleavable signal peptide				
282876	SOLUBLE					
217594	MEMBRANE	cleavable signal peptide	538 23 OUT-IN			
265523	SOLUBLE	cleavable signal peptide				
241253	SOLUBLE					
233766	SOLUBLE					
200143	SOLUBLE					
283019	SOLUBLE					
273384	SOLUBLE					
195586	MEMBRANE	signal anchor	12 23 IN-OUT 638 23 OUT-IN			
313999	SOLUBLE					
268163	MEMBRANE	cleavable signal peptide	4540 23 OUT-IN			
258281	SOLUBLE					
290180	MEMBRANE		183 20 IN-OUT 222 23 OUT-IN 280 23 IN-OUT 312 23 OUT-IN 482 23 IN-OUT			
262284	SOLUBLE	cleavable signal peptide				
278725	SOLUBLE	cleavable signal peptide				
298819	SOLUBLE					
117684	MEMBRANE		112 23 IN-OUT 209 23 OUT-IN			
12218	SOLUBLE					
125172	SOLUBLE					
244941	MEMBRANE	cleavable signal peptide	5 23 IN-OUT 42 23 OUT-IN			
313574	SOLUBLE				Q6P752	
38668	SOLUBLE				P50137	
166245	MEMBRANE	cleavable signal peptide	208 23 OUT-IN		Q7TPJ0	XP_341516.1

152155	MEMBRANE	cleavable signal peptide	146 20 OUT-IN	Q07984		
78146	MEMBRANE	cleavable signal peptide	4 20 OUT-IN 169 23 IN-OUT	Q63524		
63169	MEMBRANE	signal anchor	15 23 OUT-IN 115 23 IN-OUT		XP_232272.2	
31553	SOLUBLE	cleavable signal peptide		P02767 Q547K9		
69776	SOLUBLE	cleavable signal peptide		P32089 Q498T8		
82392	SOLUBLE	cleavable signal peptide		Q64428		
43581	SOLUBLE			Q60587		
31423	SOLUBLE			Q6P9V9		
31436	SOLUBLE			Q5XIF6	XP_237302.1	
62620	SOLUBLE			P69897		
222258	SOLUBLE			Q6IFZ4		
43597	MEMBRANE	cleavable signal peptide	7 23 IN-OUT 493 23 OUT-IN	Q5DT04 Q64550 Q64635		
205347	MEMBRANE	cleavable signal peptide	488 23 OUT-IN	Q6T5E9		
221298	MEMBRANE	cleavable signal peptide	494 23 OUT-IN	Q68G19	XP_346460.1	
171823	SOLUBLE	cleavable signal peptide		Q9JLA3		
53066	MEMBRANE	cleavable signal peptide	489 23 OUT-IN	Q8VD45		
53069	MEMBRANE	cleavable signal peptide	489 23 OUT-IN	Q8VD43		
11410	SOLUBLE	cleavable signal peptide	492 23 OUT-IN	UPI0000178B8E		
31600	MEMBRANE	cleavable signal peptide	494 23 OUT-IN	P09875		
78055	MEMBRANE	cleavable signal peptide	495 23 OUT-IN	P08541		
31602	MEMBRANE	cleavable signal peptide	495 23 OUT-IN	P08542 P16915		
31603	MEMBRANE	cleavable signal peptide	495 23 OUT-IN	P19488 P19489		
125219	MEMBRANE	cleavable signal peptide	496 23 OUT-IN	Q62789		

54899	SOLUBLE						
220138	SOLUBLE	cleavable signal peptide			Q68FY0	XP_217267.2	
139461	SOLUBLE				Q5XIR3	XP_215042.1	
230682	SOLUBLE	cleavable signal peptide			P20788 Q6Q113	XP_214457.2	
19913	MEMBRANE			20 23 OUT-IN	Q549C4		
78154	MEMBRANE	cleavable signal peptide		5 23 OUT-IN 266 23 IN-OUT	P97524		
26167	SOLUBLE				Q9Z1A6		
78166	MEMBRANE			116 23 IN-OUT 160 23 OUT-IN 195 20 IN-OUT 249 23 OUT-IN 278 23 IN-OUT	O88496		
75051	SOLUBLE	cleavable signal peptide			P31394		
3598	SOLUBLE	cleavable signal peptide			UPI000016852C		
116234	SOLUBLE						
371	SOLUBLE						
51414	SOLUBLE	cleavable signal peptide			UPI0000049A8F		
126576	MEMBRANE	signal anchor		4 23 OUT-IN 301 23 IN-OUT			
3774	SOLUBLE				UPI0000163C2E		
22617	SOLUBLE						
80790	SOLUBLE						
153343	SOLUBLE				UPI000001679A7		
130834	SOLUBLE						
44167	SOLUBLE	cleavable signal peptide			UPI00000168267		
4817	SOLUBLE						
177421	SOLUBLE				UPI000000E741D		
51562	SOLUBLE						
37239	SOLUBLE				UPI000001679E1		
42185	SOLUBLE				UPI000001679A0		
250506	SOLUBLE				UPI000001CF113		
208919	SOLUBLE				UPI000001CF4E6		

311989	SOLUBLE				UPI00001CEE0A	
215152	SOLUBLE	cleavable signal peptide			UPI00001D081E	
258588	SOLUBLE	cleavable signal peptide			UPI00001CF684	
166641	SOLUBLE				UPI00001C8924	
230796	SOLUBLE				UPI00001CEF4D	
240505	SOLUBLE				UPI00001CEE92	
171140	SOLUBLE	cleavable signal peptide			UPI00001C98FC	
293750	SOLUBLE				UPI00001CEA7A	
215768	SOLUBLE	cleavable signal peptide			UPI00001CF5B3	
296070	SOLUBLE				UPI00001D0171	
260021	SOLUBLE	cleavable signal peptide				
263376	SOLUBLE	cleavable signal peptide				
194947	SOLUBLE				UPI00001D0BF6	
240031	SOLUBLE	cleavable signal peptide				
192728	SOLUBLE					
160701	SOLUBLE				Q387D0	
287450	SOLUBLE				UPI000017ED67	
296252	SOLUBLE	cleavable signal peptide			UPI00001CE72B	
					UPI00001CFC83	
251640	SOLUBLE				UPI00001CF8A5	
227779	SOLUBLE	cleavable signal peptide				
265130	SOLUBLE				UPI00001CF9EA	
205798	SOLUBLE	cleavable signal peptide			UPI00001CC87E	
298856	SOLUBLE				UPI00001D014B	
218478	MEMBRANE	cleavable signal peptide	106 20 IN-OUT		UPI00001CF4FA	
290757	SOLUBLE					
230030	SOLUBLE					
217700	MEMBRANE		1612 23 OUT-IN 1647 23 IN-OUT 1684 23 OUT-IN 1719 23 IN-OUT 1745 23 OUT-IN		UPI00001CF880	
292730	SOLUBLE				UPI0000181D18	
195164	SOLUBLE				UPI00001CDC62	
11396	SOLUBLE				P04692-5	

126525	SOLUBLE			P08081+2 Q5PPP1	
71624	SOLUBLE			P08644+2	
18910	SOLUBLE			Q9JHL4-3	
78114	MEMBRANE		26 23 IN-OUT 68 22 OUT- IN 96 23 IN-OUT 171 23 OUT-IN 206 23 IN-OUT 255 23 OUT-IN 335 23 IN- OUT 372 23 OUT-IN 401 23 IN-OUT 532 23 OUT-IN 567 23 IN-OUT 619 23 OUT-IN	Q9QZX8-2	
292598	SOLUBLE	cleavable signal peptide		Q4AE68	
166274	SOLUBLE			Q62887 Q99JE6 Q9QW29	
33375	SOLUBLE				
723160	SOLUBLE			UPI0000237CD3	
29710	SOLUBLE			P11576	
29711	SOLUBLE			P68255	
19300	SOLUBLE			O08662	
42736	SOLUBLE			P46953 P70474 Q5RKK0 Q64556	
708	MEMBRANE	cleavable signal peptide		Q62904	
43740	MEMBRANE		15 20 OUT-IN 113 18 IN- OUT 145 23 OUT-IN	P24008	
104196	SOLUBLE			Q6GMM4 Q9JLJ3	
11455	MEMBRANE	cleavable signal peptide	563 23 OUT-IN	P21588	

68651	SOLUBLE			P80385	
4392	SOLUBLE			Q6PDV8	
4813	SOLUBLE				
69379	SOLUBLE				
10609	MEMBRANE				
126513	SOLUBLE			P52303	
74369	SOLUBLE				
65700	SOLUBLE			P62744	XP_346535.1
120856	MEMBRANE			Q5BKA5	
160418	SOLUBLE				
261145	SOLUBLE			Q6PCU2	
160475	SOLUBLE			Q6P503	
166329	SOLUBLE			Q7TP61	
261456	SOLUBLE			Q7TP56	
244467	SOLUBLE			Q7TP52	XP_226908.2
166240	SOLUBLE		59 23 IN-OUT	Q7TPK5	
84141	SOLUBLE			P11497 P97902	
168831	SOLUBLE			Q99PD4	

73521	SOLUBLE				P84092	
126504	SOLUBLE				P36972	
3608	SOLUBLE				Q64640	NP_037027.1
161251	SOLUBLE				Q6P765	
148916	SOLUBLE				P15709	
72216	SOLUBLE				P51647	
95119	SOLUBLE				Q9R240	Q9Z0U5
290544	SOLUBLE				Q66HG4	XP_233806.2
36803	SOLUBLE				Q5XI34	XP_341765.1
84182	SOLUBLE					
11470	SOLUBLE	cleavable signal peptide			P02764	
317738	SOLUBLE	cleavable signal peptide			Q80ZA3	
37085	SOLUBLE				Q9HB97	
171244	SOLUBLE				P55260	NP_077069.2
59082	SOLUBLE				P62944-2	Q3ZB97
45085	SOLUBLE				P20673	Q6AZ85
3735	SOLUBLE				P14173	Q6LEG4
69784	SOLUBLE				P17988	Q548D2
120624	MEMBRANE	signal anchor	40	23 IN-OUT	P02706	
74416	SOLUBLE					
44431	SOLUBLE				Q03248	
13065	MEMBRANE		61	23 IN-OUT 143	O70127	
			23 IN-OUT 320	23 OUT-IN 354		
			23 IN-OUT 754	23 OUT-IN 797		
			23 IN-OUT 886	32 OUT-IN 978		
			23 IN-OUT			
130827	SOLUBLE				Q5FVS8	
127670	MEMBRANE	cleavable signal peptide	784	23 OUT-IN	P55281	
25354	SOLUBLE					
70058	MEMBRANE	cleavable signal peptide	854	23 OUT-IN 889	O88923	
			18 IN-OUT 921	23 OUT-IN 956		
			20 IN-OUT 995	23 OUT-IN 1055		
			23 IN-OUT 1082	23 OUT-IN		
55585	SOLUBLE					
3708	SOLUBLE	cleavable signal peptide	2	23 IN-OUT	P22734	
166337	SOLUBLE				Q71P11	

252047	SOLUBLE				Q6PCT4		
85184	MEMBRANE				Q6P9Y3		
292700	SOLUBLE				Q5XIM9		XP_216891.2
169833	SOLUBLE				Q6P502		
78196	MEMBRANE						
63721	SOLUBLE				P23514		
80872	SOLUBLE	cleavable signal peptide			O35796		
95157	SOLUBLE				O89046		
57161	SOLUBLE				O70419		
41206	SOLUBLE				P32232		
46143	SOLUBLE				P36201		
35923	SOLUBLE				Q546T1 Q64577		
267331	SOLUBLE	cleavable signal peptide			Q64611 Q9R1F6		
3722	MEMBRANE	cleavable signal peptide			Q4KM73		
74919	SOLUBLE				UPI00001CF786		
287107	SOLUBLE	cleavable signal peptide			P11715 Q68FY2		
111030	SOLUBLE				Q6LAE5		
240184	SOLUBLE				P52847		
123978	SOLUBLE				Q71P05		
53424	SOLUBLE				Q9ESW0		
108686	SOLUBLE				Q6AXY8		XP_214194.2
3741	MEMBRANE	signal anchor		7 23 IN-OUT	Q7M0E3		
3737	SOLUBLE				UPI000011156C		
95169	SOLUBLE				P14740		
129100	SOLUBLE				UPI0000129841		
2280	SOLUBLE				Q62696		
244145	SOLUBLE				P38650		
60453	MEMBRANE				Q78P75		
					Q641Z6		
					Q8R491		
				57 23 IN-OUT	Q91XQ3 Q920C8		
					Q924C3		
85744	MEMBRANE	cleavable signal peptide		647 23 OUT-IN 774 23 IN-OUT	Q9QX70		
1625	MEMBRANE	cleavable signal peptide		713 23 OUT-IN	O35794 Q9JIV9		
17081	MEMBRANE	cleavable signal peptide			Q9R0T4		
105332	SOLUBLE				P07687		
109267	SOLUBLE				O88339		
					P52845		

62242	SOLUBLE				P49890		
17534	SOLUBLE				P62510 Q5QJE4 Q75151 Q75152 Q6P3V8		
55871	SOLUBLE						
295040	SOLUBLE				Q5XI72	XP_213755.2 XP_347155.1	
161256	SOLUBLE				O54921		
83668	SOLUBLE				Q5XI32	XP_216562.2	
206276	SOLUBLE				Q5RKH2	XP_213528.2	
18989	MEMBRANE				P97840 P97840-2		
139030	SOLUBLE				Q9QZU7		
295907	SOLUBLE				Q6P6V0	XP_214908.2	
84221	SOLUBLE				Q7M0B7		
55147	SOLUBLE				Q9Z339		
51468	SOLUBLE				O35349 P97564 P97565 P97566		
19169	SOLUBLE				P13255		
29315	SOLUBLE				P62994 Q5BKA7		
196203	SOLUBLE				UPI0000190F9E		
42862	SOLUBLE	cleavable signal peptide			Q9WT16		
37194	SOLUBLE				Q45QN0		
37192	SOLUBLE				Q9JID2		
51482	SOLUBLE				P21213 Q5EBB8		
82484	SOLUBLE						
337296	MEMBRANE	cleavable signal peptide	7 18 IN-OUT		Q6P7R8		
16980	SOLUBLE				P27605 P70469 Q4KMC5 Q62926		

51498	SOLUBLE				P52296	
37203	MEMBRANE			2226 23 OUT-IN 2260 23 IN-OUT 2302 23 OUT-IN 2345 23 IN-OUT 2395 23 OUT-IN 2522 23 IN-OUT 958 23 OUT-IN	P29995 Q99P56	
51500	MEMBRANE	cleavable signal peptide			P15127 P97681	
11211	SOLUBLE	cleavable signal peptide			P35859	
51502	MEMBRANE	cleavable signal peptide		730 23 OUT-IN	P49134	
51607	SOLUBLE				Q63270	
95874	SOLUBLE				O88600	
38912	SOLUBLE	cleavable signal peptide			P97569	NP_659565.1
161241	SOLUBLE	cleavable signal peptide			Q920P0	
19687	SOLUBLE				Q499R9 Q99MZ8	
29682	SOLUBLE				Q79210	
11293	SOLUBLE				Q6P0K6	
47332	SOLUBLE					
216194	SOLUBLE				Q6TXG7	
251837	SOLUBLE					XP_215365.1
42949	SOLUBLE				Q9ESV1	
111680	MEMBRANE			446 22 OUT-IN 709 23 IN- OUT	P04157 P04157-4	
82681	MEMBRANE	signal anchor		34 23 IN-OUT 83 20 OUT- IN 123 23 IN-OUT 196 20 OUT-IN 227 18 IN-OUT 259 18 OUT-IN	P97544	
62757	SOLUBLE	cleavable signal peptide			Q9JLV0	
22152	SOLUBLE				O35547	
42953	SOLUBLE	cleavable signal peptide			Q9GJEO	
118982	SOLUBLE					
36062	SOLUBLE				P57113	
3946	MEMBRANE	cleavable signal peptide		2291 23 OUT-IN	Q63002 Q63757	
274611	MEMBRANE			40 23 OUT-IN	Q5XIU9	XP_342240.1

124359	SOLUBLE				Q63648		
63382	MEMBRANE	signal anchor	13 19 IN-OUT 74 23 OUT- IN 108 23 IN-OUT	P97521		NP_446417.1	
156740	MEMBRANE						
75090	MEMBRANE	cleavable signal peptide	15 23 OUT-IN 58 23 IN- OUT 84 23 OUT-IN 113 23 IN-OUT 150 23 OUT-IN 177 23 IN-OUT 255 23 OUT-IN 324 18 IN-OUT 345 23 OUT-IN 380 20 IN- OUT 414 23 OUT-IN	P53987			
37180	MEMBRANE		40 22 OUT-IN 81 20 IN- OUT 110 20 OUT-IN 136 20 IN-OUT 170 23 OUT-IN 308 20 IN-OUT 342 23 OUT-IN 423 23 IN-OUT 450 18 OUT-IN 529 23 IN- OUT 989 23 OUT-IN 1068 23 IN-OUT	O88269			
63042	SOLUBLE			Q05096			
78051	SOLUBLE			Q9JLT0			
9479	SOLUBLE			Q9QUL6			
1678	SOLUBLE			P97584 Q5EBD3			
20922	MEMBRANE						
78016	SOLUBLE			Q920G2			
67879	SOLUBLE			P55161			
63008	MEMBRANE	cleavable signal peptide	724 23 OUT-IN	Q9R0T5 Q9Z1Y3			
11249	SOLUBLE			Q63731			
3674	SOLUBLE			Q62736			
60416	SOLUBLE	cleavable signal peptide		P97623 Q497A4			
				Q63083			
201603	SOLUBLE			Q641Z8		XP_238392.2	
274163	SOLUBLE	cleavable signal peptide	398 23 OUT-IN 441 23 IN- OUT 540 23 OUT-IN 575 23 IN-OUT 635 23 OUT-IN 770 23 IN-OUT	UPI000018330D			
206594	SOLUBLE			UPI00001D13DB			
223925	SOLUBLE			UPI00001D04F2			
315711	SOLUBLE			UPI00001D0F55			

264901	SOLUBLE				UPI00001D0792	
161456	SOLUBLE				UPI000017F39F	
272510	SOLUBLE	cleavable signal peptide			UPI00001CE7A7	
314871	SOLUBLE				UPI0000183016	
211193	SOLUBLE	signal anchor			UPI00001D14D3	
263674	SOLUBLE	cleavable signal peptide	10 23 OUT-IN		UPI00001CA1B5	
269276	MEMBRANE	signal anchor	21 23 IN-OUT		UPI00001CF190	
276611	SOLUBLE				UPI00001CEB27	
221624	MEMBRANE		381 20 OUT-IN		Q3B7U9	
312741	SOLUBLE				Q505J8	
306807	SOLUBLE				UPI000018073F	
207221	SOLUBLE				UPI000018157F	
217843	SOLUBLE				UPI00001D0083	
263127	SOLUBLE				UPI00001CF65A	
218419	MEMBRANE	cleavable signal peptide	138 23 IN-OUT		UPI00001CFD06	
281147	MEMBRANE				UPI00001D17A5	
257746	MEMBRANE				UPI000017EEFD	
161420	SOLUBLE				UPI0000181911	
269978	SOLUBLE	cleavable signal peptide			Q53B90	
264061	SOLUBLE				UPI00001C8CE8	
306407	SOLUBLE				UPI000019BC70	
249893	SOLUBLE				UPI00001D0E0B	
272326	SOLUBLE				UPI00001D076A	
164232	MEMBRANE	cleavable signal peptide	10 18 OUT-IN 64 18 IN-OUT 85 20 OUT-IN 117 23 IN-OUT		UPI00001D06BF	
160674	MEMBRANE	signal anchor	29 23 IN-OUT		UPI00001810E3	
230767	MEMBRANE	signal anchor			UPI0000181D94	
276601	SOLUBLE				UPI00001CC6CB	
104145	SOLUBLE				UPI000017E6E6	
269931	SOLUBLE				UPI00001D15CC	
					Q62915	
					UPI000019B77D	

12072	SOLUBLE	signal anchor			Q9JJK4	
60461	SOLUBLE				O55011 O55012	
144363	SOLUBLE				P07379	
340218	SOLUBLE				Q5M945	
249141	SOLUBLE				Q80YG1	
304888	SOLUBLE				Q5M827	XP_343785.1
37204	SOLUBLE				P70565	
136274	SOLUBLE				Q63598	
128586	MEMBRANE	cleavable signal peptide	644 23 OUT-IN		P15083	
33171	SOLUBLE					NP_612539.1
25274	SOLUBLE					
47252	MEMBRANE	cleavable signal peptide	831 23 OUT-IN		Q62786	
227267	SOLUBLE				Q6P9V7	
233720	SOLUBLE				Q6PDW4	
317815	SOLUBLE				Q5XIC6	XP_213502.2
51596	SOLUBLE				Q4QR96	
51591	SOLUBLE				P60901	
72897	SOLUBLE				P48004	
51593	SOLUBLE				P40112	
134694	SOLUBLE					
20683	SOLUBLE				O88767	
123716	SOLUBLE				Q8VBU2 Q8VBW2 Q8V100 Q8V101	
74255	SOLUBLE				Q9QY17 Q9QY18 Q9QY19 Q9QY20	
141679	SOLUBLE					

17309	SOLUBLE				Q5XI73	XP_340951.1
69363	SOLUBLE				P13444 Q5FVU2	
104192	SOLUBLE					
51489	SOLUBLE					
109734	SOLUBLE					
75000	SOLUBLE					
47254	SOLUBLE				Q62843 Q62991	
111519	SOLUBLE				Q8VIF7	
167832	MEMBRANE				Q9WVC0	
222317	SOLUBLE	cleavable signal peptide			Q6P734	
41475	SOLUBLE				P62716 Q6LDK0	
4597	SOLUBLE				P37140	
224458	SOLUBLE				Q6AYF8	XP_341523.1
221017	SOLUBLE				Q5I0D5	
3651	MEMBRANE			95 23 IN-OUT 130 20 OUT- IN 290 23 IN-OUT 322 23 OUT-IN 776 23 IN-OUT 802 23 OUT-IN 850 23 IN- OUT 913 20 OUT-IN 953 23 IN-OUT 985 18 OUT-IN	P06685 Q64609	

3654	MEMBRANE	signal anchor	35 23 IN-OUT	P07340 UPI0000167A69	
3656	MEMBRANE	signal anchor	38 23 IN-OUT	Q63377	
11254	MEMBRANE	signal anchor	26 23 OUT-IN 61 23 IN-OUT 119 23 OUT-IN 154 23 IN-OUT 191 20 OUT-IN 222 23 IN-OUT 282 23 OUT-IN	P26435 Q5BK99	
198521	MEMBRANE		103 23 IN-OUT 140 23 OUT-IN 215 23 IN-OUT 252 23 OUT-IN 410 23 IN-OUT 447 23 OUT-IN 498 23 IN-OUT	P70502 P70502-7	
152150	MEMBRANE		21 23 IN-OUT 58 23 OUT-IN 87 23 IN-OUT 244 23 OUT-IN 312 23 IN-OUT 354 23 OUT-IN 388 23 IN-OUT 514 23 OUT-IN 549 23 IN-OUT 600 23 OUT-IN	P46720	
47477	MEMBRANE		43 23 IN-OUT 80 23 OUT-IN 109 23 IN-OUT 183 23 OUT-IN 218 23 IN-OUT 266 23 OUT-IN 360 23 IN-OUT 397 23 OUT-IN 432 20 IN-OUT 549 23 OUT-IN 591 20 IN-OUT 639 23 OUT-IN	Q9JHI3	
313065	SOLUBLE			Q6PDU3	
3340	SOLUBLE			O88663 P16086 P70477	
3158	SOLUBLE			O88197 Q9ES68 Q9QWN8	
153825	MEMBRANE		1325 23 OUT-IN	Q8CFM6	
33159	SOLUBLE			Q642G0	NP_612517.1
78152	SOLUBLE			P50237 Q5M8B5	
75118	SOLUBLE			P28480	
80899	SOLUBLE				
309670	SOLUBLE				
13392	SOLUBLE	cleavable signal peptide			
10610	MEMBRANE				
75063	MEMBRANE	cleavable signal peptide	125 23 IN-OUT 225 23 OUT-IN 306 23 IN-OUT		

83139	SOLUBLE					
37172	SOLUBLE					
74982	MEMBRANE			489 23 OUT-IN		
3631	SOLUBLE					
71698	SOLUBLE					
35931	SOLUBLE					
205903	SOLUBLE	cleavable signal peptide				
51411	SOLUBLE					
240056	SOLUBLE					
232730	SOLUBLE					
104206	SOLUBLE					
303719	SOLUBLE					
204743	SOLUBLE					
211833	SOLUBLE					
205775	SOLUBLE					
221880	SOLUBLE					
43461	SOLUBLE					
279256	SOLUBLE					
45012	SOLUBLE					
266321	SOLUBLE					
287945	SOLUBLE					
160756	MEMBRANE					
247159	SOLUBLE					
51432	SOLUBLE					
644	SOLUBLE					
149105	SOLUBLE					
111659	SOLUBLE					
28297	SOLUBLE					
3914	SOLUBLE					
3901	SOLUBLE					
75004	SOLUBLE					
40336	SOLUBLE					
60471	SOLUBLE					

75026	SOLUBLE						
235129	SOLUBLE						
251303	SOLUBLE	cleavable signal peptide					
232409	SOLUBLE						
223265	SOLUBLE						
318590	SOLUBLE						
219419	SOLUBLE						
278570	MEMBRANE	signal anchor		32 20 IN-OUT 218 23 OUT- IN 264 23 IN-OUT 301 23 OUT-IN 330 23 IN-OUT 367 23 OUT-IN 840 18 IN- OUT 1083 23 OUT-IN 1117 20 IN-OUT 1141 23 OUT- IN 1180 23 IN-OUT			
209410	MEMBRANE	signal anchor		31 18 IN-OUT 222 23 OUT- IN 265 23 IN-OUT 297 23 OUT-IN 332 23 IN-OUT 359 23 OUT-IN 394 23 IN- OUT 915 20 OUT-IN 1042 23 IN-OUT 1079 23 OUT- IN 1157 23 IN-OUT 1194 23 OUT-IN 1223 23 IN-			
244260	SOLUBLE						
253193	SOLUBLE						
258471	SOLUBLE						
246886	SOLUBLE						
221370	SOLUBLE						
242533	SOLUBLE						
277610	SOLUBLE						
293497	SOLUBLE						
304176	SOLUBLE						
282403	SOLUBLE						
272300	SOLUBLE						
316372	SOLUBLE						
242453	SOLUBLE						
248510	MEMBRANE	signal anchor		40 23 IN-OUT			
286024	SOLUBLE						
199085	MEMBRANE			208 23 IN-OUT			
268038	SOLUBLE						
317802	MEMBRANE	signal anchor		54 23 IN-OUT			

233877	SOLUBLE				
292511	MEMBRANE			369 23 OUT-IN 422 20 IN-OUT 1034 23 OUT-IN	
295725	SOLUBLE				
223033	MEMBRANE			12 20 IN-OUT	
262247	SOLUBLE				
235525	SOLUBLE				
287440	SOLUBLE				
264571	SOLUBLE				
195138	SOLUBLE				
203612	SOLUBLE				
229993	MEMBRANE			170 23 OUT-IN 252 23 IN-OUT 289 23 OUT-IN	
271907	SOLUBLE				
300121	SOLUBLE				
262547	MEMBRANE			58 23 IN-OUT 2565 23 OUT-IN	
206065	MEMBRANE	cleavable signal peptide			
315288	MEMBRANE			102 23 IN-OUT	
301709	MEMBRANE			87 23 IN-OUT 197 23 OUT-IN 231 23 IN-OUT	
268838	SOLUBLE				
222802	SOLUBLE				
219221	SOLUBLE				
205076	SOLUBLE				
231012	SOLUBLE				
245155	SOLUBLE	cleavable signal peptide			
208010	SOLUBLE				
303449	SOLUBLE				
190168	SOLUBLE				
218802	SOLUBLE				
275755	SOLUBLE	cleavable signal peptide		4 18 OUT-IN	
293534	SOLUBLE				
289448	SOLUBLE				
295319	SOLUBLE	cleavable signal peptide			
305590	SOLUBLE				

213255	SOLUBLE	cleavable signal peptide				
216271	SOLUBLE					
316038	SOLUBLE					
237211	MEMBRANE					
283274	MEMBRANE		1791 23 OUT-IN			
242521	MEMBRANE		65 23 IN-OUT			
283779	SOLUBLE					
278036	SOLUBLE	cleavable signal peptide				
217607	SOLUBLE					
295521	MEMBRANE		332 23 OUT-IN			
316589	SOLUBLE					
195860	SOLUBLE					
272629	SOLUBLE					
193681	SOLUBLE					
296460	MEMBRANE	signal anchor	7 23 IN-OUT 1634 23 OUT-IN			
225113	SOLUBLE	cleavable signal peptide				
230006	SOLUBLE					
291365	SOLUBLE	cleavable signal peptide	10 23 OUT-IN			
289228	SOLUBLE					
283106	MEMBRANE	cleavable signal peptide	525 20 OUT-IN			
309047	SOLUBLE					
306783	SOLUBLE					
249119	SOLUBLE					
215340	MEMBRANE		1167 23 OUT-IN			
199727	SOLUBLE					
211558	SOLUBLE					
266044	SOLUBLE					
199559	SOLUBLE					
274677	MEMBRANE		1620 23 OUT-IN			
225159	SOLUBLE					
253969	SOLUBLE					
313581	SOLUBLE					
166356	SOLUBLE					
44422	SOLUBLE					
47331	SOLUBLE					
57726	MEMBRANE		220 23 OUT-IN			

169376	SOLUBLE				O08653		
78213	MEMBRANE				Q6GT82		
47311	SOLUBLE				Q9WVJ6		
188125	SOLUBLE	cleavable signal peptide			Q8K3L8		NP_695215.1
340135	SOLUBLE				Q6P793		
76408	MEMBRANE				P61589		
228279	MEMBRANE	cleavable signal peptide		5 23 OUT-IN 195 23 IN-OUT	Q6AXN3		XP_214123.2
93198	SOLUBLE				P97726		
38212	SOLUBLE				P63029		
8904	SOLUBLE	cleavable signal peptide		7 23 IN-OUT			
277765	SOLUBLE				Q5M9I5		XP_345569.1
12328	SOLUBLE				Q9EQX9		
82822	SOLUBLE						
37481	SOLUBLE	cleavable signal peptide			P81827 Q53ZD7		
44446	SOLUBLE				P32362		

55432	SOLUBLE			P62815		
140635	MEMBRANE			Q91Y81		
318845	MEMBRANE		219 23 OUT-IN	Q6P723 Q9Z270		
41516	MEMBRANE		191 23 IN-OUT	Q4KM74		
72067	SOLUBLE			Q63803		
80445	SOLUBLE			P22985		
37177	SOLUBLE					
168211	SOLUBLE					
78138	SOLUBLE			UPI0000129870		
241419	SOLUBLE			UPI00001D0CDF		
157223	SOLUBLE			UPI000012E177		
158790	SOLUBLE					
130837	SOLUBLE					
78104	SOLUBLE			UPI0000167973		
219335	SOLUBLE					
238208	SOLUBLE			UPI00001D1315		
161408	SOLUBLE			UPI00001C8C99		
194839	MEMBRANE		186 23 IN-OUT	UPI00001D0F77		
276511	SOLUBLE			UPI00001CE7DD		
225794	SOLUBLE			UPI00001D15AC		
300461	SOLUBLE			UPI00001CE8AA		
190049	SOLUBLE			UPI00001C83AC		
225772	SOLUBLE			UPI000018096E		
240310	SOLUBLE			UPI00001CF9A0		
260808	SOLUBLE					
290450	MEMBRANE			UPI00001CEA56		
192449	SOLUBLE					
197696	MEMBRANE			UPI00001CECE0		
195351	SOLUBLE			UPI00001D1212		
198937	SOLUBLE			UPI00001CD5DD		
250786	SOLUBLE			Q4FZY0		
				UPI00001808E0		
292693	SOLUBLE					
234717	SOLUBLE			UPI00001CF88C		
205068	MEMBRANE	signal anchor	23 23 OUT-IN	UPI000017FDCE		
253866	SOLUBLE			UPI00001D04B6		

273385	SOLUBLE	cleavable signal peptide		Q3V5X8	
168139	SOLUBLE	cleavable signal peptide		UPI0000182170	
299017	SOLUBLE			UPI000017FFEA	
				UPI00001D06E4	
210943	SOLUBLE			UPI00001D15EC	
156654	SOLUBLE			UPI00001C810A	
195466	SOLUBLE			UPI00001D084A	
193827	SOLUBLE			UPI00001D0766	
263071	SOLUBLE	signal anchor		UPI00001D056C	
287183	SOLUBLE				
305737	MEMBRANE		162 23 OUT-IN	UPI00001D0E3A	
297002	SOLUBLE	cleavable signal peptide		UPI00001D0A8A	
287571	SOLUBLE			UPI00001D1232	
305160	SOLUBLE			UPI00001CB397	
242276	SOLUBLE			UPI0000181DE1	
317625	SOLUBLE	cleavable signal peptide		UPI00001D16AF	
209664	MEMBRANE	signal anchor	42 23 OUT-IN 271 23 IN-OUT	UPI00001D03B5	
161453	SOLUBLE			Q5XFW8	XP_216257.1
64664	SOLUBLE	cleavable signal peptide	13 23 IN-OUT	Q91ZS3	
52078	MEMBRANE			Q63055	
60482	MEMBRANE	signal anchor	12 18 IN-OUT	Q09326	
141534	MEMBRANE	signal anchor	9 18 IN-OUT	P13721	
253447	SOLUBLE			Q6P6R2	
51465	MEMBRANE	cleavable signal peptide	1138 23 OUT-IN	Q62638	
54283	SOLUBLE			Q9ERE4	
288023	SOLUBLE			Q68G33	XP_346654.1
169300	MEMBRANE			Q62839	
68742	SOLUBLE	cleavable signal peptide		P97519	

11499	SOLUBLE				P08503		
44333	SOLUBLE				Q6LDF6		
225098	SOLUBLE				UPI00001D0130		
262592	SOLUBLE				UPI00001CBDDb		
302868	MEMBRANE			693 23 OUT-IN	UPI000017F5A9		
170045	MEMBRANE	cleavable signal peptide		10 23 OUT-IN 195 20 IN-OUT	UPI0000182A1D		
210144	MEMBRANE	cleavable signal peptide		12 19 IN-OUT	UPI0000180178		
258441	MEMBRANE	cleavable signal peptide		190 20 OUT-IN	UPI00001D040D		
228888	MEMBRANE	cleavable signal peptide		7 23 IN-OUT	UPI0000180E75		
68735	MEMBRANE	cleavable signal peptide		7 23 IN-OUT	Q10473		
78131	SOLUBLE				Q35487		
161834	MEMBRANE				UPI000017ED6D		
295490	SOLUBLE						
108078	SOLUBLE						
231145	SOLUBLE	cleavable signal peptide		13 23 IN-OUT			
275605	SOLUBLE						
239536	SOLUBLE	cleavable signal peptide					
194890	MEMBRANE	cleavable signal peptide		7 23 IN-OUT			
296181	SOLUBLE						
248855	MEMBRANE						
275354	SOLUBLE	cleavable signal peptide					
241393	MEMBRANE	cleavable signal peptide			Q3KR92		
60418	MEMBRANE	cleavable signal peptide		15 23 OUT-IN 186 23 IN-OUT	Q63584 Q9R0W6		
204725	MEMBRANE	signal anchor			UPI00001C8F2F		
222641	SOLUBLE				UPI00001CE61F		
201171	MEMBRANE	cleavable signal peptide		12 23 IN-OUT			
204384	MEMBRANE	cleavable signal peptide		148 23 IN-OUT	UPI00001D12FE		
212806	MEMBRANE				UPI00001D15F6		
190628	SOLUBLE				UPI00001D0520		

202236	SOLUBLE				UPI00001CFEB9		
218235	SOLUBLE				UPI00001CE622		
259411	MEMBRANE	signal anchor			UPI000017F21B		
234949	SOLUBLE				UPI00001CFD3D		
98449	MEMBRANE	signal anchor		46 23 OUT-IN 85 23 IN-OUT			
134570	SOLUBLE				Q05961		
55435	MEMBRANE			192 20 IN-OUT	O08566 O35165		
9067	MEMBRANE	signal anchor		33 23 OUT-IN 147 23 IN-OUT 174 23 OUT-IN 298 23 IN-OUT 325 23 OUT-IN 410 23 IN-OUT	Q9ZZZ8		
104733	MEMBRANE			286 23 OUT-IN	Q9QYP8		
166327	MEMBRANE	cleavable signal peptide			Q7TP48		
309746	MEMBRANE	signal anchor		7 23 IN-OUT	Q5XI64	XP_223871.2	
104182	MEMBRANE			73 23 IN-OUT 110 20 OUT-IN 142 18 IN-OUT 260 19 OUT-IN 299 23 IN-OUT 345 23 OUT-IN 380 20 IN-OUT 409 23 OUT-IN 507 23 IN-OUT		NP_071588.1	
207716	MEMBRANE			120 23 IN-OUT 157 23 OUT-IN 191 23 IN-OUT 303 23 OUT-IN 338 23 IN-OUT 413 23 OUT-IN 440 23 IN-OUT 472 23 OUT-IN	Q8K1M9		
60957	SOLUBLE			63 23 OUT-IN 92 23 IN-OUT 177 23 OUT-IN 206 20 IN-OUT 240 23 OUT-IN			
27636	SOLUBLE	cleavable signal peptide		2 23 IN-OUT	Q8VHE9		
101201	SOLUBLE				P21396		
139656	MEMBRANE	signal anchor		7 23 IN-OUT 44 20 OUT-IN 102 20 IN-OUT	Q6AY58	XP_215226.1	

243481	MEMBRANE	signal anchor	7 23 IN-OUT 44 20 OUT-IN 103 20 IN-OUT	Q5XIU4	XP_216681.1
35327	MEMBRANE		96 20 IN-OUT	Q62896	
23753	MEMBRANE	signal anchor	29 20 IN-OUT 52 20 OUT- IN 84 23 IN-OUT 111 23 OUT-IN 140 23 IN-OUT	P55062	
215739	SOLUBLE	cleavable signal peptide	166 20 OUT-IN	Q5X186	
80419	SOLUBLE			P38718	
264754	MEMBRANE		83 23 IN-OUT 115 18 OUT- IN 181 23 IN-OUT 213 23 OUT-IN 248 23 IN-OUT 285 20 OUT-IN 317 23 IN- OUT 370 20 OUT-IN	Q6AXM5	XP_227571.2
2681	SOLUBLE			Q66HA7	
51420	MEMBRANE	cleavable signal peptide	10 23 OUT-IN 117 23 IN- OUT	P08516	
78089	MEMBRANE	signal anchor	10 23 OUT-IN 116 23 IN- OUT		NP_113793.1
134595	MEMBRANE	cleavable signal peptide		P33274	NP_062569.1
80281	MEMBRANE	cleavable signal peptide	15 21 OUT-IN 80 23 IN- OUT	P51869	
127733	MEMBRANE	cleavable signal peptide		P51871	
3732	MEMBRANE	cleavable signal peptide	21 23 IN-OUT	Q64549 Q64654	
126566	MEMBRANE	cleavable signal peptide	5 20 IN-OUT	Q642C5	
161231	MEMBRANE	cleavable signal peptide	7 18 IN-OUT	Q91Y29	
125135	MEMBRANE	cleavable signal peptide	10 23 OUT-IN 75 23 IN- OUT	P51590 Q5EBD7	
337678	MEMBRANE	cleavable signal peptide	5 20 IN-OUT	Q6P7D4	
3727	MEMBRANE	cleavable signal peptide	5 20 IN-OUT	P15149 Q5EBB3	
3890	MEMBRANE			P00173	
32875	MEMBRANE		119 23 IN-OUT	P04166 Q9QWG1	
21518	SOLUBLE	cleavable signal peptide		P12075	
98989	MEMBRANE	signal anchor	26 23 IN-OUT 63 23 OUT- IN	P00406 Q37738 Q5UAJ6 Q80W17	
63740	MEMBRANE		103 18 IN-OUT	P10888	
13029	MEMBRANE	signal anchor	29 23 OUT-IN 56 23 IN- OUT 93 20 OUT-IN		
60408	MEMBRANE		134 23 OUT-IN 268 23 IN- OUT 310 23 OUT-IN	Q9EPV4	

36810	MEMBRANE		132 23 OUT-IN 265 20 IN-OUT 304 23 OUT-IN	Q9Z122		
119910	MEMBRANE		20 23 IN-OUT 57 23 OUT-IN 99 18 IN-OUT 120 18 OUT-IN 157 23 IN-OUT	Q5RKH9		
192375	MEMBRANE	cleavable signal peptide	85 23 OUT-IN			
258013	SOLUBLE			Q6UPE1		NP_942037.1
68349	MEMBRANE	signal anchor	10 20 OUT-IN 41 23 IN-OUT	Q62730		
3907	MEMBRANE	cleavable signal peptide	7 23 IN-OUT	P35571		
68743	MEMBRANE		295 20 OUT-IN	P23711		
71440	MEMBRANE		29 23 OUT-IN 58 23 IN-OUT 118 23 OUT-IN 152 23 IN-OUT 179 23 OUT-IN 214 23 IN-OUT 256 23 OUT-IN 291 18 IN-OUT 323 23 OUT-IN	P43428 Q5FVC9		
161253	SOLUBLE	cleavable signal peptide	20 20 OUT-IN	O88994		
164223	MEMBRANE	signal anchor	57 20 OUT-IN	Q5PQZ9		XP_214989.1
209082	MEMBRANE		32 23 OUT-IN 66 23 IN-OUT 108 23 OUT-IN	Q5HZA9		
300133	MEMBRANE	cleavable signal peptide	12 23 IN-OUT 64 23 OUT-IN 98 23 IN-OUT 140 23 OUT-IN	Q5U3Y7		XP_220741.1
128379	MEMBRANE	cleavable signal peptide	186 20 OUT-IN 212 23 IN-OUT 269 23 OUT-IN 304 18 IN-OUT	O35777		
258458	MEMBRANE	signal anchor	2 19 IN-OUT	Q5BK17		
166145	SOLUBLE			Q7TN17		
104163	MEMBRANE		251 23 IN-OUT	P10867		
238730	MEMBRANE	signal anchor	41 23 IN-OUT	Q6TUD3		
152512	MEMBRANE		244 23 OUT-IN	Q5RJR8 Q63742		XP_213436.1
311481	MEMBRANE	signal anchor	46 18 IN-OUT	Q7TQ16		
144356	MEMBRANE	cleavable signal peptide	7 23 IN-OUT 382 23 OUT-IN	P20611		
3967	MEMBRANE	cleavable signal peptide	374 23 OUT-IN	P14562 P97620		
44157	MEMBRANE		361 23 OUT-IN	P17046		
259160	SOLUBLE	cleavable signal peptide	5 23 IN-OUT	Q5XIE1		XP_235418.1
16130	MEMBRANE	cleavable signal peptide	2 18 IN-OUT 151 23 OUT-IN 182 23 IN-OUT 298 23 OUT-IN	Q8VIF1		

140375	SOLUBLE	cleavable signal peptide		O89035	
76956	SOLUBLE			Q32PZ2 Q8R431	
217296	SOLUBLE			Q8CJE3	
338609	MEMBRANE	cleavable signal peptide		Q6P7S1	
204895	MEMBRANE		21 23 IN-OUT 58 23 OUT-IN	Q80W89	
69488	MEMBRANE	cleavable signal peptide		P20070	
215440	SOLUBLE			Q5FVL2	
116574	MEMBRANE	cleavable signal peptide	669 23 OUT-IN	Q8CGU6 Q8CH12	
278444	MEMBRANE	signal anchor	15 23 OUT-IN 57 23 IN-OUT 84 23 OUT-IN 164 23 IN-OUT	UPI000017E10A	
317748	SOLUBLE			UPI000019B5F2	
235341	SOLUBLE			UPI000017F003	
283891	SOLUBLE			UPI00001D0B24	
246358	MEMBRANE		222 23 OUT-IN	UPI00001D07A4	
161569	SOLUBLE			UPI000017EC6D	
265343	MEMBRANE	cleavable signal peptide	355 23 OUT-IN 390 23 IN-OUT 417 18 OUT-IN 478 20 IN-OUT 507 23 OUT-IN	UPI000017F451	
208169	MEMBRANE	cleavable signal peptide	363 20 OUT-IN 387 20 IN-OUT	Q4V7F2	
244814	MEMBRANE			UPI00000180F07	
252753	MEMBRANE		45 23 OUT-IN 74 23 IN-OUT 106 18 OUT-IN 130 23 IN-OUT 213 23 OUT-IN 64 23 OUT-IN	Q4V797	
304373	MEMBRANE			UPI000001801ED	
235872	MEMBRANE	cleavable signal peptide	73 23 IN-OUT	UPI0000017EAB8	
298146	SOLUBLE			UPI000001C9183	
255113	SOLUBLE			UPI000001CEDC8	
218278	MEMBRANE			UPI000001D141A	
240722	MEMBRANE	cleavable signal peptide		Q4FZT9	
235838	MEMBRANE	signal anchor	38 23 OUT-IN	UPI000001D07C8	
298059	SOLUBLE			UPI000001CFB7E	
266171	SOLUBLE	cleavable signal peptide		UPI0000017FB23	
198248	SOLUBLE	cleavable signal peptide	12 23 IN-OUT	UPI000001805B1	
				UPI000001827EE	
				UPI000001CC96D	
				UPI000001D09A7	

302143	MEMBRANE	cleavable signal peptide	159 23 OUT-IN	UPI00001831B1	
234260	MEMBRANE		563 23 OUT-IN	UPI00001CF988	
299827	SOLUBLE	cleavable signal peptide	12 23 IN-OUT	UPI00001CFC25	
246071	SOLUBLE			UPI000017FE76	
264583	SOLUBLE			UPI00001CEB24	
306584	SOLUBLE	cleavable signal peptide		UPI0000180310	
256607	MEMBRANE		111 23 OUT-IN	UPI00001D16C6	
240868	MEMBRANE	cleavable signal peptide	65 23 IN-OUT 92 20 OUT-IN	UPI0000181FBE	
201524	MEMBRANE		15 23 OUT-IN 50 23 IN-OUT 92 23 OUT-IN	UPI00001D1A6E	
227178	MEMBRANE		4 23 OUT-IN 38 23 IN-OUT 99 23 OUT-IN 141 18 IN-OUT 168 23 OUT-IN 197 23 IN-OUT	Q2TA63 UPI0000181B67	
171148	MEMBRANE		122 23 IN-OUT	P84817 UPI00001CB823	
293181	SOLUBLE			UPI0000180B5B	
250662	MEMBRANE		246 23 OUT-IN	UPI00001CF637	
288219	MEMBRANE	cleavable signal peptide	20 18 OUT-IN 79 23 IN-OUT 121 23 OUT-IN 171 23 IN-OUT 197 23 OUT-IN 349 20 IN-OUT 383 23 OUT-IN	UPI000017E57E	
69787	MEMBRANE	signal anchor	15 18 OUT-IN 45 23 IN-OUT 87 20 OUT-IN 108 18 IN-OUT 157 23 OUT-IN	Q5BK89	
60561	MEMBRANE		521 23 OUT-IN 550 20 IN-OUT	Q9ES21	
68714	SOLUBLE	cleavable signal peptide	OUT	Q99ML5	
103863	SOLUBLE	cleavable signal peptide		Q62731 Q63684 Q63921	
118984	MEMBRANE	signal anchor	50 23 IN-OUT	Q9Z1W6	
161564	MEMBRANE		68 23 OUT-IN	UPI00001C91F7	
78079	MEMBRANE		7 20 IN-OUT 49 23 OUT-IN 78 23 IN-OUT 134 23 OUT-IN 169 20 IN-OUT 220 20 IN-OUT 260 23 IN-OUT 302 21 OUT-IN 329 23 IN-OUT 366 23 OUT-IN 395 23 IN-OUT	Q9Z296	
311263	MEMBRANE	cleavable signal peptide		Q6AXT5	XP_216895.2
60413	MEMBRANE			UPI0000133184	

13862	SOLUBLE		22 23 IN-OUT	Q5POZ8	
42127	MEMBRANE		288 23 OUT-IN	Q31257	
41486	MEMBRANE				
19693	MEMBRANE				
169821	MEMBRANE			P35286 Q8K3X5	
44652	MEMBRANE	cleavable signal peptide	309 23 OUT-IN	Q31265	
75129	SOLUBLE			O55147	
55276	MEMBRANE		228 23 IN-OUT 265 23 OUT-IN	Q9JHY2	
78339	MEMBRANE	cleavable signal peptide	9 23 IN-OUT	Q9ROC9	
305856	SOLUBLE			Q5PPN1	
177419	MEMBRANE			O88565	
161230	MEMBRANE		98 23 OUT-IN 133 23 IN-OUT 165 23 OUT-IN 192 23 IN-OUT 229 20 OUT-IN 255 21 IN-OUT 396 23 OUT-IN 439 23 IN-OUT 481 23 OUT-IN 535 20 IN-OUT 558 20 OUT-IN 598 23 IN-OUT	Q63633	
137571	MEMBRANE	cleavable signal peptide	21 23 IN-OUT 517 18 OUT-IN 546 20 IN-OUT	P52020 Q4V8L3	
129969	MEMBRANE	cleavable signal peptide		Q9WTN7	
140632	MEMBRANE	signal anchor	29 23 OUT-IN 64 23 IN-OUT 117 23 OUT-IN 146 23 IN-OUT 183 23 OUT-IN	Q548M8	
75108	MEMBRANE	cleavable signal peptide	183 23 OUT-IN 212 23 IN-OUT	P15589	
75055	SOLUBLE	cleavable signal peptide		P10960 Q62841 Q64190	
19552	MEMBRANE	signal anchor	52 23 IN-OUT	P40748	
140838	MEMBRANE	cleavable signal peptide	416 23 OUT-IN	UPI00000E760E Q99JC6	
5958	MEMBRANE	cleavable signal peptide	5 18 IN-OUT 32 23 OUT-IN 105 20 IN-OUT		
157248	MEMBRANE	cleavable signal peptide	7 23 IN-OUT 434 23 OUT-IN		
194129	SOLUBLE				
263143	SOLUBLE				
3937	SOLUBLE	cleavable signal peptide			
285270	SOLUBLE				
311586	MEMBRANE		20 23 OUT-IN 54 23 IN-OUT 144 23 OUT-IN 357 23 IN-OUT		

11779	MEMBRANE		31 23 OUT-IN 74 23 IN-OUT 111 23 OUT-IN 163 23 IN-OUT			
274486	MEMBRANE	cleavable signal peptide	4 18 OUT-IN 28 23 IN-OUT 123 20 OUT-IN			
290771	MEMBRANE	cleavable signal peptide	4 23 OUT-IN 183 18 IN-OUT 210 23 OUT-IN 390 23 IN-OUT			
265779	MEMBRANE		595 23 OUT-IN 619 23 IN-OUT			
243111	MEMBRANE		113 23 IN-OUT 538 23 OUT-IN 572 23 IN-OUT 623 20 OUT-IN 649 23 IN-OUT 816 20 OUT-IN			
242256	MEMBRANE		403 23 OUT-IN 437 23 IN-OUT 495 23 OUT-IN			
229620	SOLUBLE					
235741	SOLUBLE					
304800	MEMBRANE	cleavable signal peptide	15 19 OUT-IN 266 23 IN-OUT 347 23 OUT-IN 376 23 IN-OUT 408 18 OUT-IN			
294937	MEMBRANE		647 23 IN-OUT 741 23 OUT-IN 776 20 IN-OUT 799 23 OUT-IN			
226741	SOLUBLE					
228869	SOLUBLE					
283602	MEMBRANE		103 23 IN-OUT 129 23 OUT-IN 256 23 IN-OUT 288 18 OUT-IN 356 23 IN-OUT			
201409	MEMBRANE		243 23 IN-OUT			
224702	SOLUBLE					
210125	SOLUBLE					
254063	SOLUBLE					
239621	SOLUBLE					
247233	SOLUBLE					
268830	SOLUBLE	cleavable signal peptide				
241188	MEMBRANE		699 23 OUT-IN			
229044	SOLUBLE	cleavable signal peptide	20 23 IN-OUT			
230119	SOLUBLE					
247833	SOLUBLE					
239514	SOLUBLE					

197285	MEMBRANE	cleavable signal peptide	103 23 IN-OUT 140 20 OUT-IN 172 23 IN-OUT 214 23 OUT-IN 249 23 IN- OUT 284 20 OUT-IN 312 23 IN-OUT 338 23 OUT-IN		
217059	SOLUBLE	cleavable signal peptide			
229197	SOLUBLE				
286820	SOLUBLE				
253799	SOLUBLE				
194762	SOLUBLE				
293599	MEMBRANE		313 20 OUT-IN 391 23 IN- OUT		
277830	MEMBRANE		75 20 OUT-IN		
227312	MEMBRANE	cleavable signal peptide	12 23 IN-OUT		
191708	SOLUBLE				
203301	MEMBRANE		647 23 OUT-IN		
280249	MEMBRANE		208 23 OUT-IN		
238667	MEMBRANE		70 23 IN-OUT 107 20 OUT- IN		
190227	SOLUBLE	signal anchor	21 20 IN-OUT		
295383	SOLUBLE				
267475	MEMBRANE		456 23 OUT-IN 480 23 IN- OUT		
287769	MEMBRANE		147 20 IN-OUT		
274979	MEMBRANE		821 23 OUT-IN		
300320	SOLUBLE				
268665	MEMBRANE		429 23 OUT-IN 458 18 IN- OUT 508 23 OUT-IN 537 23 IN-OUT 579 20 OUT-IN 611 20 IN-OUT 664 20 OUT-IN 704 23 IN-OUT 736 23 OUT-IN 795 32 IN- OUT		
219162	SOLUBLE				
248521	SOLUBLE				
313782	SOLUBLE				
284704	SOLUBLE				
203193	SOLUBLE	signal anchor			
289382	SOLUBLE				
292562	SOLUBLE				
318242	SOLUBLE				
304061	MEMBRANE	cleavable signal peptide	7 23 IN-OUT		
310739	SOLUBLE				
265569	MEMBRANE		291 23 OUT-IN		

301089	MEMBRANE		169 23 IN-OUT 246 23 OUT-IN 281 23 IN-OUT 329 23 OUT-IN 13 23 IN-OUT			
250367	MEMBRANE	cleavable signal peptide				
272967	SOLUBLE	cleavable signal peptide				
223302	SOLUBLE					
213193	MEMBRANE		64 20 IN-OUT			
301836	MEMBRANE		9 23 IN-OUT 93 23 OUT-IN 136 23 IN-OUT 168 20 OUT-IN 200 23 IN-OUT 232 23 OUT-IN 321 18 IN- OUT 348 23 OUT-IN 377 18 IN-OUT			
290052	MEMBRANE		117 23 IN-OUT 183 23 OUT-IN 368 23 IN-OUT 405 23 OUT-IN 457 23 IN- OUT 509 23 OUT-IN 543 23 IN-OUT			
304442	MEMBRANE	cleavable signal peptide	248 23 OUT-IN 277 23 IN- OUT 321 23 OUT-IN 355 23 IN-OUT 382 23 OUT-IN 417 20 IN-OUT 456 18 OUT-IN			
317090	SOLUBLE					
294206	MEMBRANE	signal anchor	21 23 IN-OUT 48 23 OUT- IN 320 23 IN-OUT			
243905	MEMBRANE					
228294	SOLUBLE					
247605	SOLUBLE	signal anchor				
220741	SOLUBLE					
193119	SOLUBLE					
202296	MEMBRANE	cleavable signal peptide	476 23 OUT-IN 505 23 IN- OUT 554 23 OUT-IN 596 23 IN-OUT 622 18 OUT-IN 646 18 IN-OUT 673 18 OUT-IN 702 23 IN-OUT 739 23 OUT-IN 774 23 IN- OUT 816 23 OUT-IN 851 23 IN-OUT			
201379	MEMBRANE	signal anchor				
207944	SOLUBLE					
310191	SOLUBLE					
231757	MEMBRANE		34 23 IN-OUT 123 23 OUT- IN 152 18 IN-OUT 179 20 OUT-IN 203 18 IN-OUT 230 23 OUT-IN 334 18 IN- OUT 356 23 OUT-IN 390 23 IN-OUT			

269355	MEMBRANE		44 18 IN-OUT 114 18 OUT- IN 168 23 IN-OUT			
294993	SOLUBLE	cleavable signal peptide	7 23 IN-OUT			
234511	SOLUBLE					
310121	MEMBRANE					
275946	MEMBRANE	signal anchor	30 23 IN-OUT 80 23 OUT- IN 125 23 IN-OUT 167 19 OUT-IN 197 18 IN-OUT 218 23 OUT-IN 252 23 IN- OUT 294 23 OUT-IN		XP_232596.2	
98326	MEMBRANE		29 23 IN-OUT 55 23 OUT- IN 138 20 IN-OUT 162 23 OUT-IN	Q08013 Q6P6U5		
91768	MEMBRANE	cleavable signal peptide	10 22 OUT-IN 90 20 IN- OUT	Q5I0H4 Q71D10		
282006	MEMBRANE	cleavable signal peptide	10 23 OUT-IN 84 23 IN- OUT 130 23 OUT-IN 154 23 IN-OUT 186 20 OUT-IN 27 23 OUT-IN 96 23 IN- OUT 170 23 OUT-IN	Q6AYQ4	XP_342026.1	
137142	MEMBRANE			Q9Z142		
252683	SOLUBLE			Q66MI6	XP_341992.1	
143647	MEMBRANE		243 23 OUT-IN	Q91ZM6		
230035	SOLUBLE	cleavable signal peptide		Q6IFW1	XP_220966.2	
161846	SOLUBLE	cleavable signal peptide		Q6IFW0		
301880	SOLUBLE			Q6IFU8	XP_213478.2	
164032	SOLUBLE	cleavable signal peptide	13 19 OUT-IN	UPI000017E541		
171802	MEMBRANE		23 23 OUT-IN	Q9JJW3		
64824	SOLUBLE	cleavable signal peptide		Q91WW1		
31214	MEMBRANE		79 20 IN-OUT 113 23 OUT- IN 255 23 IN-OUT 282 18 OUT-IN 306 23 IN-OUT 371 18 OUT-IN	Q91ZQ0		
3601	SOLUBLE			P45953		
111524	MEMBRANE		203 18 IN-OUT	Q8VHI8		
139706	MEMBRANE	cleavable signal peptide	325 23 OUT-IN	UPI0000182448		
291525	MEMBRANE	cleavable signal peptide	10 20 OUT-IN 101 23 IN- OUT 127 23 OUT-IN	Q6TEK4		
165266	MEMBRANE	cleavable signal peptide	17 20 IN-OUT 89 23 OUT- IN 118 18 IN-OUT 140 23 OUT-IN	Q6TEK3		

11037	MEMBRANE					
5942	MEMBRANE				P81155 Q9JI32	
5943	MEMBRANE				Q9ESR2 Q9JI31 Q9R1Z0 Q9WTU2	
55158	SOLUBLE				O54937	
63749	SOLUBLE	cleavable signal peptide		20 23 OUT-IN		
37206	SOLUBLE				UPI00000E8107	
310103	MEMBRANE	signal anchor		25 23 OUT-IN 60 18 IN- OUT 92 23 OUT-IN 142 23 IN-OUT 198 23 OUT-IN 241 20 IN-OUT 275 18 OUT-IN	UPI000001C81C9 XP_230110.1	
317126	SOLUBLE					
229917	MEMBRANE			1905 23 OUT-IN		
316692	MEMBRANE	cleavable signal peptide		155 23 OUT-IN	UPI00000180296	
285938	SOLUBLE				UPI000001D1AB2	
287362	MEMBRANE			63 23 OUT-IN	UPI000001D11D7	
292854	SOLUBLE	cleavable signal peptide			UPI000001CE61B	
291828	SOLUBLE				UPI00000180E3B	
318196	MEMBRANE	signal anchor		36 23 OUT-IN	UPI000001CE77F	
192715	MEMBRANE					
233624	SOLUBLE			88 18 OUT-IN	UPI0000018052B	
196976	SOLUBLE				UPI000001CF058	

281804	MEMBRANE		406 23 OUT-IN 678 23 IN-OUT 710 23 OUT-IN 739 20 IN-OUT 762 23 OUT-IN 796 23 IN-OUT	UPI00001D0335	
315186	MEMBRANE		243 23 OUT-IN 277 23 IN-OUT 331 20 OUT-IN 400 23 IN-OUT 466 23 OUT-IN	UPI00001D1137	
249505	MEMBRANE	signal anchor	46 23 OUT-IN 136 20 IN-OUT 175 23 OUT-IN 210 23 IN-OUT 264 23 OUT-IN 299 23 IN-OUT	UPI0000181E78	
283888	MEMBRANE	cleavable signal peptide	4 23 OUT-IN 139 23 IN-OUT 181 23 OUT-IN	Q52KJ9 UPI00001CFA1C	
236762	MEMBRANE		85 23 IN-OUT 127 20 OUT-IN 167 23 IN-OUT 209 20 OUT-IN	UPI00001CFF0A	
257012	MEMBRANE		74 23 IN-OUT 133 20 OUT-IN 173 23 IN-OUT	UPI00001D043F	
273691	MEMBRANE		61 23 IN-OUT 93 23 OUT-IN 439 20 IN-OUT 1042 23 OUT-IN 1090 23 IN-OUT	UPI00001828EA	
305736	MEMBRANE	signal anchor	1127 18 OUT-IN 32 23 OUT-IN 75 19 IN-OUT 103 23 OUT-IN 210 23 IN-OUT 258 20 OUT-IN 290 23 IN-OUT 317 20 OUT-IN	UPI00001CF30C	
243991	MEMBRANE		283 23 OUT-IN	UPI00001CFC94	
202821	SOLUBLE			UPI00001D1434	
262043	SOLUBLE			UPI00001CFE3A	
235658	MEMBRANE		120 23 OUT-IN 154 23 IN-OUT 191 23 OUT-IN	UPI00001CEE83	
268823	SOLUBLE			UPI00001CFFEF	
240940	MEMBRANE			UPI00001D1073	
315286	SOLUBLE	cleavable signal peptide	5 18 IN-OUT	UPI00001CF9D7	
294309	SOLUBLE	cleavable signal peptide	9 23 IN-OUT	UPI00001D0815	
47300	SOLUBLE	cleavable signal peptide	7 20 IN-OUT	UPI00000E791F	
301870	SOLUBLE	cleavable signal peptide		P84551 UPI00001CFF92	
166454	MEMBRANE		92 23 IN-OUT	UPI000017E25A	
222783	MEMBRANE		71 23 IN-OUT	UPI00001D0B3C	
68729	MEMBRANE	cleavable signal peptide	28 23 OUT-IN 63 23 IN-OUT 100 23 OUT-IN 143 23 IN-OUT 185 23 OUT-IN 267 23 IN-OUT 304 20 OUT-IN	P31388	

264038	MEMBRANE	cleavable signal peptide	136 23 OUT-IN 179 23 IN-OUT 279 23 OUT-IN 358 23 IN-OUT 395 23 OUT-IN	Q5FVL8		
305592	SOLUBLE	cleavable signal peptide	7 23 IN-OUT	Q7TPJ5	XP_232655.2	
120736	SOLUBLE			Q63122		
75128	SOLUBLE			P41034		
11241	MEMBRANE	signal anchor	12 23 IN-OUT	P15684		
43654	MEMBRANE	cleavable signal peptide	7 23 IN-OUT 39 23 OUT-IN 68 23 IN-OUT 117 23 OUT-IN 164 23 IN-OUT 206 23 OUT-IN 290 23 IN-OUT	P36370		
141056	MEMBRANE	cleavable signal peptide	210 23 OUT-IN	P26453 P26453-2 Q6GT74		
92620	SOLUBLE			P63031 Q4V8N5		
60589	MEMBRANE		69 23 IN-OUT 116 23 OUT-IN 145 23 IN-OUT 206 23 OUT-IN 233 23 IN-OUT 301 23 OUT-IN 340 23 IN-OUT 402 23 OUT-IN 436 23 IN-OUT 468 23 OUT-IN	Q62634		
86059	MEMBRANE		252 23 OUT-IN 281 23 IN-OUT	O35048		
78164	MEMBRANE	cleavable signal peptide	528 23 OUT-IN	O35112 O55172		
60531	SOLUBLE			Q99JD4		
39119	SOLUBLE	cleavable signal peptide		Q9JHL6		
3716	SOLUBLE	cleavable signal peptide		P18886 P97781		
161476	MEMBRANE	cleavable signal peptide	189 23 OUT-IN	Q6AY20	XP_232335.1	
228910	MEMBRANE	signal anchor	13 23 IN-OUT 62 23 OUT-IN 91 23 IN-OUT 204 23 OUT-IN	Q6P9V1		
105482	MEMBRANE	signal anchor	7 23 IN-OUT 441 23 OUT-IN	Q925W0		
68411	MEMBRANE	signal anchor	15 23 OUT-IN 62 23 IN-OUT 104 23 OUT-IN 147 23 IN-OUT 184 23 OUT-IN 236 23 IN-OUT 268 23 OUT-IN 303 23 IN-OUT 340 23 OUT-IN 375 23 IN-OUT 412 23 OUT-IN 455 23 IN-OUT	Q95938		
43490	SOLUBLE	signal anchor	13 20 IN-OUT	Q63707		

223736	SOLUBLE					Q4KLZ6	
4394	MEMBRANE	cleavable signal peptide	56 23 IN-OUT 116 23 OUT- IN 151 18 IN-OUT 178 23 OUT-IN		UPI00001CEB5D Q5U305		
85379	MEMBRANE	signal anchor	23 23 IN-OUT		P97675		
4326	MEMBRANE						
169873	SOLUBLE	cleavable signal peptide	2 23 IN-OUT		Q5FVN1		
62865	MEMBRANE	signal anchor	20 20 IN-OUT		P50123 Q64200 Q9JLQ7 Q9JLQ9		
21695	MEMBRANE		230 20 IN-OUT		Q62931		
19992	SOLUBLE				Q6AYQ1	XP_341458.1	
37193	SOLUBLE				Q45QM2		
37195	SOLUBLE				P82471		
219015	MEMBRANE	cleavable signal peptide	9 20 IN-OUT 128 23 OUT- IN 163 23 IN-OUT 205 23 OUT-IN 384 23 IN-OUT 416 23 OUT-IN 445 23 IN- OUT		UPI0000167970 Q6MGB4	XP_215320.2	
153619	SOLUBLE				Q8K3P7		
8648	SOLUBLE						
366853	MEMBRANE		354 23 OUT-IN		Q5PPN7		
139384	SOLUBLE				Q6P791		
37168	MEMBRANE	cleavable signal peptide	7 23 IN-OUT 1143 23 OUT- IN		P18614		
153869	MEMBRANE	cleavable signal peptide	718 23 OUT-IN		Q8R2H2		
3942	MEMBRANE	cleavable signal peptide	12 20 IN-OUT 493 23 OUT- IN		Q00238		
17165	MEMBRANE		58 23 OUT-IN 108 23 IN- OUT		P26376		
24909	MEMBRANE	cleavable signal peptide	239 23 OUT-IN		Q9JHY1		
272716	MEMBRANE	cleavable signal peptide	56 23 IN-OUT 116 23 OUT- IN 151 18 IN-OUT 178 23 OUT-IN		Q569A6		
169834	MEMBRANE	cleavable signal peptide	370 23 OUT-IN		Q68FV6	XP_215623.1	
274007	MEMBRANE				Q6TXH8		
52861	SOLUBLE	cleavable signal peptide	208 23 IN-OUT		Q812B0		
60454	MEMBRANE		144 20 OUT-IN 172 23 IN- OUT 198 20 OUT-IN 230 23 IN-OUT 257 20 OUT-IN 341 23 IN-OUT 373 23 OUT-IN 402 23 IN-OUT 428 23 OUT-IN 462 23 IN- OUT 488 23 OUT-IN		Q63314		

60472	SOLUBLE	cleavable signal peptide	13 23 IN-OUT	P97849	NP_446032.1
269157	SOLUBLE			Q5XIM7	XP_214694.2
166255	MEMBRANE		32 23 IN-OUT 69 23 OUT- IN 103 23 IN-OUT 148 23 OUT-IN	Q7TPB7	
203309	SOLUBLE			Q5UIZ9	XP_213632.2
111212	MEMBRANE			Q6RUV5	
220289	SOLUBLE			Q5XIG9	XP_214075.1
237355	SOLUBLE			Q5U204	XP_342348.1
75002	SOLUBLE				NP_037115.1
98993	MEMBRANE	cleavable signal peptide	23 23 IN-OUT 60 23 OUT- IN 94 19 IN-OUT 116 23 OUT-IN 145 23 IN-OUT 194 23 OUT-IN 221 23 IN- OUT 258 20 OUT-IN 284 20 IN-OUT 308 23 OUT-IN 351 23 IN-OUT 393 23 OUT-IN 436 23 IN-OUT	P05508 Q7HKW3 Q9T528	
296012	SOLUBLE			UPI0000181133	
292782	SOLUBLE			UPI000017F463	
262377	SOLUBLE			UPI00001CEEAF	
265736	MEMBRANE	cleavable signal peptide	64 23 OUT-IN 106 23 IN- OUT	UPI000017FA90	
271140	SOLUBLE			UPI00001CE817	
315377	SOLUBLE			UPI00001D052F	
78112	MEMBRANE	cleavable signal peptide	2 19 IN-OUT 35 23 OUT-IN	O08589	
82680	MEMBRANE	cleavable signal peptide	1421 23 OUT-IN	UPI0000167BB7 O54728	
1198	SOLUBLE			Q91XR8	
726780	SOLUBLE			Q75Q40	
186570	SOLUBLE			Q8K3X0	
305024	MEMBRANE		40 23 OUT-IN 69 23 IN- OUT 111 23 OUT-IN 176 23 IN-OUT 236 23 OUT-IN 279 23 IN-OUT 371 23 OUT-IN 427 18 IN-OUT 454 20 OUT-IN 5 23 IN-OUT	Q5FVN0	
262914	SOLUBLE	cleavable signal peptide		Q5XIF0	XP_217261.2
32618	MEMBRANE		39 23 OUT-IN 63 23 IN- OUT 140 23 OUT-IN	Q498C8	

37231	SOLUBLE				P63322		
113828	SOLUBLE				P62747		
38864	MEMBRANE	signal anchor		9 23 IN-OUT 440 23 OUT- IN	P97943		
169836	MEMBRANE			171 23 IN-OUT 198 23 OUT-IN 233 23 IN-OUT 275 23 OUT-IN	UPI00001C7DDF		
46139	MEMBRANE			154 23 IN-OUT 181 23 OUT-IN 216 23 IN-OUT 258 23 OUT-IN	P56603		
75902	SOLUBLE	cleavable signal peptide			O88280		
75093	MEMBRANE	cleavable signal peptide		7 20 IN-OUT 94 23 OUT-IN 152 23 IN-OUT 189 23 OUT-IN 218 20 IN-OUT 302 23 OUT-IN 337 20 IN- OUT 366 23 OUT-IN 400 23 IN-OUT 432 20 OUT-IN 458 23 IN-OUT	P12336 Q6LE98		
104202	MEMBRANE			68 23 IN-OUT 94 23 OUT- IN 184 23 IN-OUT 280 20 OUT-IN 291 23 IN-OUT 346 23 OUT-IN 381 23 IN- OUT 416 23 OUT-IN 476 23 IN-OUT	P45380		
36071	MEMBRANE			178 23 OUT-IN	Q9WVJ4		
37252	MEMBRANE			274 23 IN-OUT	Q08850		
217815	SOLUBLE						
194680	SOLUBLE						
291113	MEMBRANE			410 23 IN-OUT			
311134	MEMBRANE			103 23 OUT-IN 213 23 IN- OUT			
3782	SOLUBLE						
234438	SOLUBLE	cleavable signal peptide					
252701	SOLUBLE						
268354	MEMBRANE			85 23 IN-OUT			
192966	SOLUBLE						
259355	MEMBRANE	cleavable signal peptide		1007 23 OUT-IN			
191887	SOLUBLE						
211488	SOLUBLE						
246703	SOLUBLE	cleavable signal peptide					
298062	MEMBRANE	signal anchor		4 23 OUT-IN 516 23 IN- OUT			
239422	MEMBRANE			297 23 OUT-IN			
314793	SOLUBLE						

250158	MEMBRANE						
244957	SOLUBLE						
285147	MEMBRANE			33 23 OUT-IN 62 23 IN-OUT 94 23 OUT-IN 123 23 IN-OUT 155 20 OUT-IN 208 23 IN-OUT 259 18 OUT-IN 297 23 IN-OUT 401 23 OUT-IN 573 23 IN-OUT 610 23 OUT-IN 639 20 IN-OUT 732 23 OUT-IN 767 20 IN-OUT 796 23 OUT-IN 850 23 IN-OUT 899 23 OUT-IN 934 20 IN-OUT 958 23 OUT-IN 1000 23 IN-OUT 1042 23 OUT-IN			
237775	MEMBRANE	signal anchor		7 23 IN-OUT			
221907	MEMBRANE	cleavable signal peptide		358 23 OUT-IN			
290606	SOLUBLE						
273814	MEMBRANE	signal anchor					
288315	SOLUBLE	cleavable signal peptide					
198855	SOLUBLE			172 20 IN-OUT			
278518	SOLUBLE						
279332	MEMBRANE	cleavable signal peptide		351 23 OUT-IN 529 23 IN-OUT			
268034	SOLUBLE	cleavable signal peptide					
285918	MEMBRANE			431 23 OUT-IN 465 23 IN-OUT 502 23 OUT-IN 544 20 IN-OUT 578 23 OUT-IN 657 23 IN-OUT 976 23 OUT-IN 1010 23 IN-OUT 1047 23 OUT-IN 1089 20 IN-OUT 1123 23 OUT-IN 1321 23 IN-OUT 1358 23 OUT-IN 1393 23 IN-OUT 1430 23 OUT-IN			
231792	SOLUBLE	cleavable signal peptide		7 23 IN-OUT	Q6AYR4	XP_342416.1	
282121	SOLUBLE				Q569C3		
111884	MEMBRANE	signal anchor		38 23 OUT-IN 72 23 IN-OUT 114 23 OUT-IN 149 23 IN-OUT 200 23 OUT-IN 285 23 IN-OUT 317 23 OUT-IN	P48974		
84170	SOLUBLE	cleavable signal peptide					

318701	MEMBRANE	cleavable signal peptide	5 23 IN-OUT 77 23 OUT-IN 119 23 IN-OUT 161 23 OUT-IN	UPI000021C5DA	
260312	SOLUBLE	signal anchor	27 23 OUT-IN 61 23 IN- OUT 98 23 OUT-IN 141 23 IN-OUT 197 23 OUT-IN 240 23 IN-OUT 272 23 OUT-IN	UPI00001C87D6	XP_231200.1
197399	MEMBRANE			UPI00001D184B	
222106	SOLUBLE			UPI00001D18FD	
221702	MEMBRANE	signal anchor	26 20 OUT-IN 120 23 IN- OUT 262 23 OUT-IN 305 23 IN-OUT	UPI000017FFDA	
243423	SOLUBLE			UPI00001D035C	
257142	SOLUBLE	cleavable signal peptide	7 20 IN-OUT	UPI00001CE8B6	
316366	SOLUBLE				
220383	MEMBRANE		2459 23 OUT-IN	UPI00001D060E	
277215	SOLUBLE	signal anchor	5 23 IN-OUT	UPI00001D0500	
202385	SOLUBLE	cleavable signal peptide	13 23 IN-OUT	UPI00001CF0D7	
194122	MEMBRANE		196 23 OUT-IN	Q7TP53	
223700	MEMBRANE	cleavable signal peptide		Q7TPJ1	
2699	MEMBRANE	cleavable signal peptide	7 23 IN-OUT	Q09325	
10860	MEMBRANE	cleavable signal peptide	12 23 IN-OUT 696 23 OUT- IN	P15943	
136243	SOLUBLE	cleavable signal peptide		P55797	
137529	MEMBRANE	cleavable signal peptide	7 20 IN-OUT	Q10468	
44217	MEMBRANE	signal anchor	19 23 IN-OUT	Q02353	
280644	MEMBRANE			UPI00001D08E2	
3713	MEMBRANE	cleavable signal peptide	1298 23 OUT-IN	O35850 Q9JHW1	
141958	SOLUBLE			Q5M7T2	
55277	MEMBRANE	cleavable signal peptide	7 23 IN-OUT	Q9JJ05	
116798	MEMBRANE	signal anchor	27 23 OUT-IN 148 23 IN- OUT	Q811A2	
133253	MEMBRANE			O35390	

80377	SOLUBLE				Q62824		
47234	MEMBRANE	cleavable signal peptide	5 18 IN-OUT 713 23 OUT-IN		P23377		
75089	MEMBRANE	signal anchor	9 23 IN-OUT		P97877		
220058	SOLUBLE				Q66H74		XP_227445.1
71574	SOLUBLE				P41542		
3930	MEMBRANE		266 23 OUT-IN		P06762 Q5BK87		
176262	SOLUBLE	cleavable signal peptide			Q9WV57		
210844	MEMBRANE	signal anchor	19 23 IN-OUT				
229568	MEMBRANE	signal anchor			UPI00001CF67C		
314280	MEMBRANE	cleavable signal peptide	12 23 IN-OUT 38 23 OUT-IN 72 23 IN-OUT 98 23 OUT-IN 127 23 IN-OUT 164 20 OUT-IN 190 19 IN-OUT 223 23 OUT-IN		UPI00001D00B7		
235860	MEMBRANE	cleavable signal peptide	21 20 IN-OUT 592 23 OUT-IN		UPI000001CF8AF		
304110	MEMBRANE	cleavable signal peptide	7 23 IN-OUT		UPI000001CEB09		
78175	MEMBRANE		78 35 IN-OUT 142 23 OUT-IN		Q35394		
234797	MEMBRANE		146 23 IN-OUT 183 23 OUT-IN 212 23 IN-OUT 238 23 OUT-IN 272 23 IN-OUT		Q6TUD4		XP_217351.2
60469	SOLUBLE				Q925T1		
2120	SOLUBLE				O55043		
160782	MEMBRANE				Q5HZY2		
35326	MEMBRANE		188 23 IN-OUT 225 23 OUT-IN		Q62891		
51490	MEMBRANE	signal anchor	20 23 IN-OUT		Q05511		
319145	MEMBRANE	cleavable signal peptide	12 18 IN-OUT 139 23 OUT-IN		Q6P796		
301225	SOLUBLE	cleavable signal peptide			Q5M878		XP_344894.1
231548	MEMBRANE	signal anchor			Q4V8N9 Q8K4Y7		
78137	MEMBRANE		280 20 IN-OUT		Q08851		
161242	MEMBRANE		58 23 OUT-IN 87 23 IN-OUT 124 23 OUT-IN 196 23 IN-OUT		Q925D4		
24769	SOLUBLE						

294691	SOLUBLE					
242048	SOLUBLE					
299013	MEMBRANE					
300896	MEMBRANE	signal anchor	54 23 IN-OUT			
209378	SOLUBLE					
263135	SOLUBLE					
252381	SOLUBLE					
275347	MEMBRANE		395 23 OUT-IN			
272267	MEMBRANE		776 23 OUT-IN 811 20 IN-OUT 834 20 OUT-IN 866 23 IN-OUT 898 23 OUT-IN 927 23 IN-OUT 959 20 OUT-IN			
307730	MEMBRANE					
266866	MEMBRANE	cleavable signal peptide	663 23 OUT-IN			
247469	MEMBRANE	signal anchor	24 23 IN-OUT			
195844	SOLUBLE					
203448	SOLUBLE					
241548	MEMBRANE					
31491	MEMBRANE	cleavable signal peptide	304 20 OUT-IN	P19814 Q4G0B6		
140307	MEMBRANE	cleavable signal peptide	221 23 OUT-IN 287 23 IN-OUT 324 23 OUT-IN 358 23 IN-OUT 390 23 OUT-IN 446 23 IN-OUT 483 23 OUT-IN 512 23 IN-OUT 549 23 OUT-IN 5 19 OUT-IN 183 23 IN-OUT			
305262	MEMBRANE	cleavable signal peptide		Q6AY25	XP_217216.2	
6158	MEMBRANE		193 23 IN-OUT	Q9JI51 Q9JI51-2		
23581	MEMBRANE		83 20 IN-OUT	P63025		
189334	MEMBRANE	cleavable signal peptide	13 23 IN-OUT	Q9EPI0		
276652	SOLUBLE	cleavable signal peptide				
290726	MEMBRANE		122 20 IN-OUT	UPI00001CF09A		
311145	SOLUBLE			UPI00001D15EE		
270395	SOLUBLE			UPI00001D0324		

260805	SOLUBLE				UPI00001D04B3	
200680	MEMBRANE	signal anchor		7 23 IN-OUT	UPI00001D186F	
260512	MEMBRANE	cleavable signal peptide		282 23 OUT-IN 348 23 IN-OUT 380 23 OUT-IN 415 23 IN-OUT 452 23 OUT-IN 502 23 IN-OUT 534 23 OUT-IN 569 23 IN-OUT 606 23 OUT-IN	UPI000001CF2C4	
289309	SOLUBLE				UPI000001CFAC8	
298383	SOLUBLE				UPI000001D14E3	
281046	MEMBRANE					
302855	SOLUBLE				UPI00001D0488	
60460	MEMBRANE			37 23 IN-OUT 79 23 OUT-IN 113 23 IN-OUT 155 23 OUT-IN	UPI00000135B31	
269397	MEMBRANE			58 23 IN-OUT		
309339	MEMBRANE			7 19 IN-OUT	UPI00000181A67	
294111	SOLUBLE	signal anchor				
9454	SOLUBLE				Q00438-2	
98375	SOLUBLE				Q6PDW2	
85752	SOLUBLE				Q63570	
4807	SOLUBLE	cleavable signal peptide			P62832	XP_213448.1
144423	SOLUBLE				P62752	
61026	SOLUBLE				Q8CH55 Q8CH56 Q8CH57 Q8CH58 Q923K9 Q924K3	
98990	MEMBRANE	signal anchor		7 20 IN-OUT	P11608 Q35736 Q5UAJ5 Q7TPJ7 Q63495	
251790	SOLUBLE					
128256	MEMBRANE	cleavable signal peptide		339 23 OUT-IN		
3616	SOLUBLE				O35889 O35890	

45103	SOLUBLE				P15178		
3702	MEMBRANE	signal anchor	29 23 OUT-IN 63 23 IN-OUT 100 18 OUT-IN 129 23 IN-OUT 161 23 OUT-IN 310 23 IN-OUT 352 23 OUT-IN 436 18 IN-OUT 458 23 OUT-IN 542 23 IN-OUT 584 23 OUT-IN 969 23 IN-OUT 1020 23 OUT-IN 1102 23 IN-OUT		Q63120 Q63145		
161883	SOLUBLE				Q6AY11	XP_213508.1	
71226	SOLUBLE				Q510F0		
82662	SOLUBLE	signal anchor			Q63342	NP_620802.1	
1106	SOLUBLE				Q35824	NP_114468.1	
103	SOLUBLE						
14850	SOLUBLE				P04646		
41501	SOLUBLE						
75919	SOLUBLE	cleavable signal peptide			Q9WTS8	NP_112638.1	
18015	SOLUBLE	cleavable signal peptide			Q63060		
72151	SOLUBLE				Q5D059		
17327	SOLUBLE				Q794E4		
72598	SOLUBLE				P15865		
159543	MEMBRANE	cleavable signal peptide	21 23 IN-OUT 53 23 OUT-IN 408 23 IN-OUT 435 23 OUT-IN 464 23 IN-OUT 501 23 OUT-IN 544 23 IN-OUT		Q8CH93		
54494	SOLUBLE				Q6AYT3	XP_343186.1	
222832	SOLUBLE				Q5M7V2 Q63279 Q6S6J4 Q64602		
51504	SOLUBLE						

103229	SOLUBLE					XP 216052.1
231196	SOLUBLE				Q6TUG5	
140367	SOLUBLE	cleavable signal peptide			Q924S5	
3277	SOLUBLE				P02688	
69375	SOLUBLE					
226905	SOLUBLE				Q5U303	
154516	SOLUBLE				UPI0000182B91	
268287	SOLUBLE				UPI00001C8FA0	
					UPI0000182BFD	
204574	SOLUBLE				UPI00001CEE14	
238438	SOLUBLE	cleavable signal peptide			UPI00001D045A	
246387	SOLUBLE	cleavable signal peptide			UPI000017FF69	
266306	SOLUBLE				UPI00001CFF23	
226986	SOLUBLE				UPI00001CFC47	
202835	MEMBRANE		674 20 OUT-IN		UPI00001D1223	
318741	SOLUBLE				Q6P783	
2515	SOLUBLE				Q6AYU5	
157870	SOLUBLE				Q9QZA2	
59236	SOLUBLE	cleavable signal peptide			Q64612	
139425	SOLUBLE				Q4G093	
4809	SOLUBLE				P84100	
4818	SOLUBLE				P62902	
4819	SOLUBLE				Q63ZV8	
19063	MEMBRANE		174 20 IN-OUT 247 23 OUT-IN 386 23 IN-OUT 443 23 OUT-IN 524 20 IN- OUT		O08661	
3858	SOLUBLE					
44653	MEMBRANE	cleavable signal peptide	75 19 OUT-IN 131 23 IN- OUT 168 20 OUT-IN 200 19 IN-OUT 233 23 OUT-IN 795 23 IN-OUT 832 23 OUT-IN 874 20 IN-OUT 903 23 OUT-IN 946 23 IN- OUT		Q01728 UPI0000167A49	
2110	MEMBRANE		55 23 IN-OUT		O08625	

246362	SOLUBLE					
191730	SOLUBLE					
110024	SOLUBLE					
209125	SOLUBLE	cleavable signal peptide				
232570	SOLUBLE					
267292	SOLUBLE					
269562	SOLUBLE					
249977	SOLUBLE					
262653	SOLUBLE					
218788	SOLUBLE					
278047	SOLUBLE					
225450	SOLUBLE					
234794	SOLUBLE					
269290	SOLUBLE					
217827	SOLUBLE					
295712	SOLUBLE					
286770	SOLUBLE					
195895	SOLUBLE					
269702	SOLUBLE					
233179	MEMBRANE		226 20 IN-OUT 260 18 OUT-IN 531 23 IN-OUT 585 23 OUT-IN 670 23 IN- OUT 738 23 OUT-IN 826 23 IN-OUT			
222133	SOLUBLE					
250916	SOLUBLE	cleavable signal peptide				
198258	SOLUBLE					
259373	SOLUBLE					
241842	SOLUBLE	cleavable signal peptide				
287882	SOLUBLE					
288172	SOLUBLE					
275665	SOLUBLE					
285775	SOLUBLE					
307227	SOLUBLE	cleavable signal peptide				
268840	SOLUBLE					
233230	SOLUBLE					

278143	MEMBRANE					
199223	SOLUBLE					
201969	SOLUBLE	cleavable signal peptide				
230447	SOLUBLE					
239048	SOLUBLE					
270372	SOLUBLE					
213091	SOLUBLE					
228083	SOLUBLE					
244001	SOLUBLE					
275363	SOLUBLE					
275895	SOLUBLE					
258657	SOLUBLE	cleavable signal peptide				
229118	SOLUBLE					
293312	SOLUBLE					
251407	SOLUBLE					
112447	SOLUBLE				O08956 Q62818	
11402	SOLUBLE				P21643 Q5EBC2 Q6LBW3	
161849	SOLUBLE				Q6IFU7	
75904	SOLUBLE				O70199	
4821	SOLUBLE				Q3TIG5	
301974	SOLUBLE				UPI00001CF92A	
222136	SOLUBLE				UPI00001CFC5E	
169183	SOLUBLE	cleavable signal peptide				
75057	MEMBRANE		28 23 OUT-IN 71 23 IN- OUT 108 23 OUT-IN 151 23 IN-OUT 206 23 OUT-IN 258 23 IN-OUT		UPI0000163A80	
281752	SOLUBLE	cleavable signal peptide			UPI00001D17BB	
254343	SOLUBLE	cleavable signal peptide			UPI00001D0BC3	
255150	SOLUBLE					
281550	SOLUBLE				UPI00001D125A	
266163	SOLUBLE				UPI00001CFDSA	
215246	SOLUBLE				UPI00001CFF74	
154542	SOLUBLE					

276474	SOLUBLE				UPI00001D0A7E	
230313	SOLUBLE				UPI00001D0622	
269534	SOLUBLE					
307749	SOLUBLE				UPI00001CF5C0	
218587	MEMBRANE			54 23 IN-OUT 110 23 OUT- IN 145 18 IN-OUT 172 23 OUT-IN 214 23 IN-OUT 251 23 OUT-IN 280 20 IN- OUT	UPI00001CF053	
239818	SOLUBLE				UPI00001CF419	
313666	SOLUBLE					
302398	SOLUBLE				UPI00001CF541	
209377	SOLUBLE					
301508	SOLUBLE				UPI00001D07EC	
292930	SOLUBLE				UPI00001D186E	
245616	MEMBRANE			172 23 IN-OUT	UPI00001D0769	
272734	SOLUBLE				UPI00001D07B9	
249584	SOLUBLE				UPI00001CF4A5	
309715	SOLUBLE				UPI00001D0784	
252389	MEMBRANE	cleavable signal peptide		279 23 OUT-IN 313 23 IN- OUT 350 23 OUT-IN 396 23 IN-OUT 433 20 OUT-IN 459 23 IN-OUT 1050 23 OUT-IN 1093 20 IN-OUT 1137 23 OUT-IN 1172 23 IN-OUT 1204 23 OUT-IN	UPI00001CE768	
206770	SOLUBLE				UPI00001CFD27	
167115	SOLUBLE					
233158	SOLUBLE				UPI00001CF7D6	
109735	SOLUBLE				P13233 Q4V796	
23444	SOLUBLE				Q64575	
54292	SOLUBLE				P54645	
3029	SOLUBLE				Q09137	
23396	MEMBRANE				P61212	
93024	SOLUBLE				Q32PX6	
15419	SOLUBLE	cleavable signal peptide			Q9QY44	
231492	SOLUBLE				UPI00001D152D	

311925	SOLUBLE			Q5FVI6		
201751	MEMBRANE		202 23 IN-OUT 246 23 OUT-IN 293 23 IN-OUT 348 23 OUT-IN	Q7TP88		
119254	MEMBRANE		181 23 OUT-IN 210 20 IN- OUT 244 20 OUT-IN 270 23 IN-OUT 317 23 OUT-IN 708 23 IN-OUT 740 19 OUT-IN 779 23 IN-OUT 832 20 OUT-IN 856 23 IN- OUT	P40146		
181389	SOLUBLE	cleavable signal peptide		Q9WUS0		
256333	SOLUBLE			Q8R2H6 Q8R2H7 Q8R4G3 Q923K6		
9007	MEMBRANE		90 20 IN-OUT 129 23 OUT- IN 158 23 IN-OUT 221 23 OUT-IN 296 23 IN-OUT 328 23 OUT-IN 476 23 IN- OUT 503 23 OUT-IN 603 23 IN-OUT 681 23 OUT-IN 1131 23 IN-OUT 1204 23 OUT-IN 1271 23 IN-OUT 1384 23 OUT-IN 1453 23 IN-OUT 1495 23 OUT-IN 1624 18 IN-OUT 1588 20 OUT-IN 1682 23 IN-OUT			
76638	SOLUBLE			Q64537		
111631	SOLUBLE	cleavable signal peptide		P00731 UPI00001432A8		
60578	SOLUBLE			P08082		
33971	MEMBRANE	cleavable signal peptide	7 23 IN-OUT 78 23 OUT-IN 121 23 IN-OUT 163 23 OUT-IN	Q63400		
221177	SOLUBLE	cleavable signal peptide		Q66H80	XP_217133.2	
3733	MEMBRANE	cleavable signal peptide	5 23 IN-OUT 1099 23 OUT- IN	Q63155		
11221	SOLUBLE			Q63115		
44281	SOLUBLE			P06766		
54966	SOLUBLE			Q9Z2K0		
3740	SOLUBLE			P39052		
67605	SOLUBLE			P21575		
55867	SOLUBLE			Q641X8		

18691	SOLUBLE					
725563	SOLUBLE				Q6XDA1	
726511	SOLUBLE				Q6XDA0	
23674	SOLUBLE				Q9QV50	
101676	MEMBRANE				Q9QX33 Q9Z2S8	
					Q9Z2S9	
60564	SOLUBLE				Q9JHZ3 Q9JHZ4	
76611	SOLUBLE					
51463	MEMBRANE	cleavable signal peptide	23 23 IN-OUT 76 20 OUT- IN 131 23 IN-OUT 192 23 OUT-IN		P08033	
171803	SOLUBLE				Q925G1	
44348	SOLUBLE				P09367	
					UPI00001684FB	
116280	SOLUBLE	cleavable signal peptide			P70570	
240594	SOLUBLE				Q5FVI3	
8548	SOLUBLE				Q6P2A7	
198073	SOLUBLE				Q8K3H9	
140638	MEMBRANE	cleavable signal peptide			Q95MA2	
23872	SOLUBLE	cleavable signal peptide			P31430 Q6IN35	
200842	SOLUBLE				Q810W7 Q810W8	
35920	SOLUBLE	cleavable signal peptide			Q63691 Q6GT04	
6153	SOLUBLE				Q63355	
105842	SOLUBLE				Q63356	
62616	SOLUBLE				XP_213290.1	
55652	SOLUBLE					
255746	SOLUBLE	cleavable signal peptide	17 20 IN-OUT		Q505J3	
235633	SOLUBLE				UPI00001CB000	
					UPI000018133C	

287406	SOLUBLE				Q4V8H8	
233953	SOLUBLE	cleavable signal peptide			UPI00001CE791	
					UPI0000180741	
221944	SOLUBLE				UPI00001CFA4A	
246519	MEMBRANE			166 23 IN-OUT	UPI00001CF7A0	
255476	MEMBRANE	cleavable signal peptide		217 23 OUT-IN	UPI00001D0587	
359989	MEMBRANE	cleavable signal peptide		55 23 IN-OUT 92 23 OUT-IN 145 23 IN-OUT 182 23 OUT-IN 216 23 IN-OUT	UPI00001C859B	
225945	SOLUBLE				UPI00001CEB28	
					UPI000017E212	
281850	SOLUBLE				UPI00001D12DF	
268833	SOLUBLE				UPI00001D00B2	
266462	SOLUBLE				UPI00001CF433	
218537	SOLUBLE				UPI00001CE7BA	
197055	SOLUBLE				UPI0000180DEE	
51565	SOLUBLE				P53809 Q9Z2N9	
699022	SOLUBLE				Q6S396	
63679	MEMBRANE			171 23 OUT-IN 255 23 IN-OUT 290 23 OUT-IN 377 23 IN-OUT 438 23 OUT-IN	P17659 P19025	
214491	SOLUBLE	cleavable signal peptide			Q8K4G6	
44893	SOLUBLE				P05696	
4701	SOLUBLE				Q4QRA5 Q78EG7 Q8VH48	
31490	MEMBRANE				P23606 Q4QRA6	
165980	SOLUBLE				Q811U3 Q8CIY9	
273497	SOLUBLE	cleavable signal peptide			Q6AYH3 Q8CIP0	XP_341083.1
166313	SOLUBLE				Q80WN5	
86616	SOLUBLE				P37727	
8458	MEMBRANE				Q5U1Y2	XP_345855.1
227390	MEMBRANE	cleavable signal peptide		5 23 OUT-IN 34 20 IN-OUT	Q80ZF7	
37242	SOLUBLE				Q63531	

100550	MEMBRANE	cleavable signal peptide		Q63720		
185761	SOLUBLE			Q80XZ1		
140634	SOLUBLE			Q63555		
168209	SOLUBLE					
138308	SOLUBLE			Q9JK71		
11343	SOLUBLE	cleavable signal peptide		P22006		
19107	SOLUBLE			O08623 Q8CH59		
78346	SOLUBLE			P56932 Q66HR7		
203002	SOLUBLE		115 23 OUT-IN 144 20 IN-OUT 178 23 OUT-IN 213 23 IN-OUT 274 23 OUT-IN 308 23 IN-OUT	Q5POX4		
75350	SOLUBLE			Q5U211		
4905	SOLUBLE					
169317	SOLUBLE					
41211	MEMBRANE	cleavable signal peptide	157 23 OUT-IN	Q6IRK3		
75082	MEMBRANE	cleavable signal peptide	257 23 OUT-IN	P26260		
75083	MEMBRANE	cleavable signal peptide	152 23 OUT-IN	P34901		
198626	SOLUBLE					
214165	MEMBRANE	cleavable signal peptide	642 23 OUT-IN			
199155	SOLUBLE		542 23 OUT-IN			
266426	SOLUBLE	cleavable signal peptide				
215128	SOLUBLE					
285691	SOLUBLE					
251780	SOLUBLE					
253728	SOLUBLE					
191344	SOLUBLE					
313817	SOLUBLE					
136387	SOLUBLE					

258910	SOLUBLE	cleavable signal peptide			
282761	SOLUBLE				
238446	SOLUBLE				
282579	SOLUBLE				
222795	SOLUBLE				
224054	SOLUBLE				
282808	MEMBRANE	cleavable signal peptide	90 23 IN-OUT		
276572	SOLUBLE				
222218	MEMBRANE		998 23 OUT-IN		
268103	SOLUBLE				
300246	SOLUBLE				
216707	SOLUBLE				
196091	SOLUBLE				
264688	SOLUBLE				
258828	SOLUBLE				
285136	MEMBRANE	cleavable signal peptide	83 20 OUT-IN 122 20 IN-OUT 145 18 OUT-IN 187 23 IN-OUT		
199323	MEMBRANE		312 23 OUT-IN		
192129	SOLUBLE				
196107	SOLUBLE				
267886	SOLUBLE				
253851	SOLUBLE				
242229	SOLUBLE				
232623	SOLUBLE				
213390	SOLUBLE				
204932	MEMBRANE				
198580	MEMBRANE	signal anchor	20 23 OUT-IN 96 20 IN-OUT		
229721	SOLUBLE	cleavable signal peptide			
261449	SOLUBLE				
265199	SOLUBLE				
296600	SOLUBLE				
316308	SOLUBLE				
277020	SOLUBLE	cleavable signal peptide			
217100	SOLUBLE				
276810	SOLUBLE				
234739	SOLUBLE				

271261	SOLUBLE					
290689	SOLUBLE					
261414	SOLUBLE					
319220	SOLUBLE					
230656	SOLUBLE					
82925	SOLUBLE					
50402	SOLUBLE					
318709	SOLUBLE				Q6P7B3	
71712	SOLUBLE				Q07014	
33698	SOLUBLE					
20729	SOLUBLE				Q9R189	
55286	SOLUBLE				Q63615	
11413	MEMBRANE			400 23 OUT-IN 443 23 IN-OUT 541 23 OUT-IN 570 23 IN-OUT 636 23 OUT-IN 772 23 IN-OUT	P25286	
134827	SOLUBLE				Q63681	
287423	SOLUBLE				UPI000001CE797	
233320	MEMBRANE	signal anchor		33 23 IN-OUT 65 19 OUT-IN 104 23 IN-OUT 141 23 OUT-IN 206 23 IN-OUT 243 23 OUT-IN	UPI00000182E24	XP_236114.1
262837	MEMBRANE			78 23 IN-OUT 115 23 OUT-IN	UPI000001CAB0E	
261337	SOLUBLE				UPI000001D008C	
294179	SOLUBLE				UPI000001CFA1E	
225182	SOLUBLE				UPI000001CFA84	
235178	SOLUBLE				UPI000001D0976	
199377	SOLUBLE				UPI000001CF764	
266460	SOLUBLE				UPI000001CF868	
191003	SOLUBLE				UPI0000017E04D	
270299	SOLUBLE				UPI000001CEE65	
264993	SOLUBLE	cleavable signal peptide			UPI000001C9F63	
203449	SOLUBLE				UPI000001D0A2F	
229135	SOLUBLE				UPI000001D09D8	
236003	SOLUBLE	cleavable signal peptide			UPI000001CC370	
260591	MEMBRANE			149 23 IN-OUT	UPI000001D1798	
256498	SOLUBLE				UPI000001CF013	
254251	SOLUBLE				UPI000001D09AF	
287459	SOLUBLE				UPI000001D1884	
203525	SOLUBLE				UPI000001D1757	
318405	SOLUBLE				UPI000001CFDB4	

263392	MEMBRANE	cleavable signal peptide	475 23 OUT-IN	UPI00001CFC44	
248047	SOLUBLE				
302017	SOLUBLE	cleavable signal peptide		UPI00001D0EAE	
300510	SOLUBLE	cleavable signal peptide		UPI00001CFAC6	
307740	MEMBRANE	cleavable signal peptide	15 23 OUT-IN 141 18 IN-OUT 168 20 OUT-IN 192 23 IN-OUT 224 23 OUT-IN 251 20 IN-OUT 365 23 OUT-IN 400 18 IN-OUT 427 20 OUT-IN 459 23 IN-OUT 486 23 OUT-IN	UPI00001CEAD0	
319162	SOLUBLE			UPI00001D12EA	
199239	SOLUBLE			UPI0000182CC0	
258690	MEMBRANE		243 23 OUT-IN	UPI00001D0F57	
33279	SOLUBLE			Q5U3Y8	XP 215460.1
129647	MEMBRANE	cleavable signal peptide	479 23 OUT-IN 514 18 IN-OUT 546 23 OUT-IN 581 23 IN-OUT 618 23 OUT-IN	Q9ESC1-2	
241027	SOLUBLE			Q5FVR4	
75909	SOLUBLE			O88311	
214565	SOLUBLE			Q562C2	
307560	SOLUBLE			Q6U6G5	
60545	MEMBRANE	signal anchor	45 23 IN-OUT	P10716 Q4KMB0	
141570	SOLUBLE	cleavable signal peptide		P24268	
160297	SOLUBLE	cleavable signal peptide		Q5BKD9 Q9R1T3	
42770	SOLUBLE			Q9JK15	
355419	SOLUBLE	cleavable signal peptide		P31720 Q5RJK1	
96883	SOLUBLE	cleavable signal peptide		Q91YB6	
169306	SOLUBLE			Q9R093 Q9Z1T4	
98538	SOLUBLE			P69736	
157436	SOLUBLE	cleavable signal peptide	5 23 IN-OUT	Q8CJH4	NP_758838.1
51464	SOLUBLE			P48508	

229000	SOLUBLE				Q8K1Q0	
47431	SOLUBLE	cleavable signal peptide			Q9JJ51 Q9JJ52 Q9JJ53 Q9JJ54	
80375	SOLUBLE					
315195	SOLUBLE				Q5M849	
126112	SOLUBLE				Q9ER29 Q9QX69	
37247	SOLUBLE				P38656	NP_112381.1
39196	SOLUBLE	cleavable signal peptide			Q6PDV1	
78121	SOLUBLE				UPI00000E85AB	
47245	SOLUBLE				Q9WTY9	
74102	SOLUBLE					
44225	SOLUBLE				P13084 Q63698 Q64269	
199319	MEMBRANE	cleavable signal peptide	618 23 OUT-IN		UPI000019BDF0	
289953	SOLUBLE				UPI000018229C	
191978	SOLUBLE				UPI00001CE91A	
242939	SOLUBLE	cleavable signal peptide			UPI00001D10E4	
277682	SOLUBLE				UPI00001CEF50	
208269	SOLUBLE				UPI00001D09B7	
245688	SOLUBLE				UPI00001CA071	
220097	SOLUBLE				UPI000017F661	
267441	SOLUBLE				UPI000017E138	
213604	SOLUBLE				UPI00001D117C	
246047	SOLUBLE				UPI00001D0C60	
264614	SOLUBLE				UPI00001D0521	
88229	SOLUBLE	cleavable signal peptide			P29117	
304663	SOLUBLE				Q6AYD3	XP_213828.2
47246	SOLUBLE				Q63184	
111523	SOLUBLE				Q8VHV7	
111202	SOLUBLE					

13148	SOLUBLE				Q9QX74		
55278	SOLUBLE				UPI000017068F		
					O55000 Q6MG09		
272310	SOLUBLE						XP_237121.2
227484	SOLUBLE				Q5RK30		XP_213759.1
60405	SOLUBLE				Q9ET50		
82685	SOLUBLE				O35814		
93202	SOLUBLE				P97752		
212891	SOLUBLE						
69538	SOLUBLE						
233078	SOLUBLE						
203467	SOLUBLE						
281345	MEMBRANE			204 23 IN-OUT			
242726	SOLUBLE						
284837	SOLUBLE						
315303	SOLUBLE						
315844	SOLUBLE						
286232	SOLUBLE						
266038	SOLUBLE						
287849	SOLUBLE						
272641	SOLUBLE						
213507	SOLUBLE						
317744	SOLUBLE						
267163	MEMBRANE	signal anchor		36 20 IN-OUT 59 23 OUT- IN 184 23 IN-OUT			
300892	SOLUBLE						
275767	MEMBRANE			524 23 IN-OUT 1363 23 OUT-IN			
217979	SOLUBLE						
247038	SOLUBLE						
288241	SOLUBLE	cleavable signal peptide					
304228	MEMBRANE	signal anchor		7 23 IN-OUT			
308317	SOLUBLE	cleavable signal peptide		12 20 IN-OUT			
274130	SOLUBLE						
316191	SOLUBLE						

239406	SOLUBLE					
250307	SOLUBLE					
253349	SOLUBLE					
201803	SOLUBLE					
221417	SOLUBLE					
264572	SOLUBLE					
247636	SOLUBLE					
252804	SOLUBLE					
81816	SOLUBLE					
31540	SOLUBLE				P09739 Q304F4	
22316	SOLUBLE				P63281	
135066	SOLUBLE					
279473	SOLUBLE				UPI00001CEF1B	
195949	SOLUBLE				UPI00001CE8EE	
221070	SOLUBLE					
204593	SOLUBLE	cleavable signal peptide			UPI00001D113E	
267421	SOLUBLE					
270236	SOLUBLE	cleavable signal peptide			UPI00001CF964	
256460	SOLUBLE					
160562	SOLUBLE				UPI00001822A8	
211734	SOLUBLE				UPI00001CF9FE	
72931	SOLUBLE					
75905	SOLUBLE				UPI0000167962	
263673	SOLUBLE				UPI00001D095C	
223054	SOLUBLE				Q712J3	
71532	SOLUBLE				P08699	
29410	SOLUBLE				Q510M7	
44484	SOLUBLE					
301041	SOLUBLE	cleavable signal peptide			Q6MGB5	XP_342097.1
103852	SOLUBLE				Q63379	
252580	SOLUBLE				UPI000017F395	
253829	SOLUBLE				Q1RP77	
312134	SOLUBLE				UPI0000183039	
					Q3MIE4	
274768	SOLUBLE				UPI0000180D5D	
279034	SOLUBLE				UPI000017FC64	
					Q811R2-2	
38099	SOLUBLE					

51431	MEMBRANE		48 23 OUT-IN 82 23 IN-OUT 119 23 OUT-IN 161 23 IN-OUT 203 23 OUT-IN 259 23 IN-OUT 296 20 OUT-IN	P48303 Q4V7F6	
210117	SOLUBLE				
114376	SOLUBLE				
307156	SOLUBLE				
282004	MEMBRANE		342 23 OUT-IN 385 23 IN-OUT 422 23 OUT-IN 457 23 IN-OUT 489 23 OUT-IN 523 23 IN-OUT		
233246	SOLUBLE				
290493	SOLUBLE				
267985	SOLUBLE				
310879	SOLUBLE				
219262	SOLUBLE				
261953	SOLUBLE	cleavable signal peptide			
248137	SOLUBLE				
279884	SOLUBLE				
313806	SOLUBLE				
194817	SOLUBLE				
30131	SOLUBLE			O08887 Q63619	
241983	SOLUBLE			UPI00001CECF0	
251444	SOLUBLE			UPI00001D01B3	
11409	SOLUBLE			P25977-2	
106925	SOLUBLE			Q62962-2	
4822	SOLUBLE			P02404	
77849	SOLUBLE			P62986	
52680	MEMBRANE		37 20 OUT-IN 69 23 IN-OUT 101 23 OUT-IN 130 23 IN-OUT 172 19 OUT-IN 302 23 IN-OUT 344 23 OUT-IN 425 23 IN-OUT 451 18 OUT-IN 532 23 IN-OUT 569 23 OUT-IN 968 23 IN-OUT 1010 23 OUT-IN 1072 23 IN-OUT 1099 23 OUT-IN 1190 23 IN-OUT	UPI0000016797E	
84143	SOLUBLE	cleavable signal peptide		Q6IMX3	

32612	SOLUBLE	signal anchor	40 23 IN-OUT 97 23 OUT- IN 139 23 IN-OUT	Q4KM64	
270293	SOLUBLE	cleavable signal peptide		Q6P2A5	
157236	SOLUBLE			O35827	
807	MEMBRANE	cleavable signal peptide	55 23 OUT-IN 101 23 IN- OUT 194 23 OUT-IN	O35532	
3668	SOLUBLE	cleavable signal peptide		Q63514	
166315	SOLUBLE			Q7TS56	
3719	SOLUBLE	cleavable signal peptide		P00786	
71407	SOLUBLE			P80432	
145183	MEMBRANE		137 23 OUT-IN 172 23 IN- OUT 198 23 OUT-IN 343 23 IN-OUT 436 20 OUT-IN 462 23 IN-OUT	Q9ERM3	
3926	SOLUBLE			P05708	
57359	SOLUBLE			O70592	
229302	SOLUBLE			Q5FWT9	
200861	SOLUBLE	signal anchor	27 23 OUT-IN 69 23 IN- OUT 131 18 OUT-IN 153 23 IN-OUT 185 23 OUT-IN	Q80UA9	
126700	SOLUBLE			P29994	
282022	SOLUBLE			P83829	
339290	MEMBRANE	signal anchor	13 23 IN-OUT 233 20 OUT- IN 265 23 IN-OUT 302 18 OUT-IN 332 23 IN-OUT 379 23 OUT-IN 434 23 IN- OUT 471 23 OUT-IN	Q6P689	
223419	SOLUBLE			Q6TXG6	
209490	SOLUBLE			Q6TUF8	
51542	SOLUBLE			P02563 Q63351	
216886	SOLUBLE			Q5U1X1	XP_217137.1
222889	MEMBRANE	cleavable signal peptide	146 23 OUT-IN	UPI00001CB348	
279528	SOLUBLE			UPI00001CF42E	

189964	SOLUBLE				UPI00001816CA	
218331	SOLUBLE	cleavable signal peptide			UPI00001D0F20	
232984	SOLUBLE		12 23 IN-OUT		UPI00001CB008	
279415	SOLUBLE	cleavable signal peptide			UPI000001CB15C	
204220	MEMBRANE	cleavable signal peptide	71 23 IN-OUT 103 23 OUT- IN 132 23 IN-OUT 169 23 OUT-IN 244 20 IN-OUT 314 23 OUT-IN		UPI000001830B3	
259576	SOLUBLE				UPI0000018124E	
314220	SOLUBLE	cleavable signal peptide			UPI0000017E95E	
307512	MEMBRANE	signal anchor	20 23 OUT-IN 47 23 IN- OUT		UPI000001CC60E	
315735	SOLUBLE	cleavable signal peptide			UPI00000182C93	
178365	MEMBRANE	cleavable signal peptide	5 23 IN-OUT 47 23 OUT-IN 76 23 IN-OUT 108 23 OUT- IN			
319337	SOLUBLE				Q68FS8	XP 215694.2
75738	SOLUBLE				Q9JKT0	
78111	SOLUBLE				UPI000000E7DFC	
236607	SOLUBLE	cleavable signal peptide				
190455	SOLUBLE	cleavable signal peptide				
195304	SOLUBLE					
206459	SOLUBLE	signal anchor	43 23 OUT-IN			
206115	SOLUBLE	cleavable signal peptide				
229208	SOLUBLE					
208493	SOLUBLE					
205153	SOLUBLE					
229899	MEMBRANE	signal anchor	20 23 IN-OUT 1314 23 OUT-IN			
300976	SOLUBLE	signal anchor	39 23 IN-OUT			
271576	MEMBRANE		181 20 IN-OUT 215 23 OUT-IN 315 20 IN-OUT 349 23 OUT-IN 383 23 IN- OUT 420 22 OUT-IN 448 20 IN-OUT 471 23 OUT-IN			
293100	SOLUBLE					
206108	SOLUBLE					
228349	MEMBRANE	cleavable signal peptide	530 23 OUT-IN 565 23 IN- OUT 652 23 OUT-IN 763 23 IN-OUT 800 20 OUT-IN 831 23 IN-OUT			
221314	SOLUBLE	cleavable signal peptide				
245798	SOLUBLE					

293085	SOLUBLE						
263938	SOLUBLE						
247355	SOLUBLE						
191966	SOLUBLE						
311347	SOLUBLE						
313918	SOLUBLE						
224186	MEMBRANE	signal anchor	26 23 IN-OUT				
284812	SOLUBLE						
273598	SOLUBLE						
281230	MEMBRANE	signal anchor	5 18 OUT-IN 35 23 IN-OUT 72 23 OUT-IN 245 23 IN-OUT				
318262	MEMBRANE		78 23 IN-OUT 115 23 OUT-IN 144 23 IN-OUT 199 23 OUT-IN 233 23 IN-OUT 335 23 OUT-IN				
298591	SOLUBLE						
260939	MEMBRANE		138 19 OUT-IN 163 20 IN-OUT 192 23 OUT-IN 266 20 IN-OUT 305 20 OUT-IN	Q5HZE2			
80282	SOLUBLE						
300656	SOLUBLE	cleavable signal peptide			UPI00001CFDC3		
260747	SOLUBLE						
256921	SOLUBLE				UPI00001D02CB		
202185	SOLUBLE						
211028	SOLUBLE						
220421	SOLUBLE	cleavable signal peptide			UPI00001FB84 UPI00001CEF75		
239371	SOLUBLE				UPI00001D08E6		
234073	SOLUBLE				UPI00001CF470		
279578	SOLUBLE						
284155	MEMBRANE		7 18 IN-OUT 114 23 OUT-IN	Q5M828-2			
268104	SOLUBLE				Q810T5-2		
137155	SOLUBLE				O35817		
139514	MEMBRANE	signal anchor	42 20 IN-OUT 66 23 OUT-IN 136 18 IN-OUT 158 23 OUT-IN	Q7TMZ5		NP_942032.1	

337364	MEMBRANE		127 20 IN-OUT 156 23 OUT-IN 180 23 IN-OUT 269 23 OUT-IN 298 23 IN- OUT 712 23 OUT-IN 769 23 IN-OUT 853 32 OUT-IN 959 23 IN-OUT	Q6Y305	
66007	MEMBRANE		423 23 OUT-IN 466 23 IN- OUT 508 23 OUT-IN 543 20 IN-OUT 582 23 OUT-IN 617 23 IN-OUT 678 19 OUT-IN 717 23 IN-OUT 799 23 OUT-IN 858 23 IN- OUT	P23562	
36009	SOLUBLE			Q9ERD1	
35260	MEMBRANE	cleavable signal peptide	483 23 OUT-IN	Q63135 Q63612	
90517	MEMBRANE		53 23 IN-OUT	P35171	
318309	MEMBRANE		202 23 OUT-IN	Q6AY55	XP 340918.1
37566	MEMBRANE			UPI0000111953	
276570	SOLUBLE			Q5XIC2	XP_217092.2
173653	SOLUBLE			Q9Z2J4	
41183	SOLUBLE			Q04970 Q4KMB1	
148966	SOLUBLE			Q63228	
220427	MEMBRANE		135 23 OUT-IN 164 23 IN- OUT	Q6PCT6	
205582	MEMBRANE		134 23 IN-OUT	Q5XIJ4	XP 225853.1
216613	SOLUBLE	cleavable signal peptide		Q8K5B3	
176273	MEMBRANE	cleavable signal peptide	238 23 OUT-IN 267 20 IN- OUT 301 23 OUT-IN 426 20 IN-OUT	Q9JLB5	
261258	SOLUBLE			Q80ZF5	
279185	SOLUBLE	cleavable signal peptide		UPI0000180ED9	
258284	MEMBRANE		409 23 OUT-IN	UPI00001CF567	
297879	SOLUBLE			UPI00001D1329	
277277	SOLUBLE			UPI00001CF504	
195113	MEMBRANE	cleavable signal peptide	524 23 OUT-IN	UPI00001CF398	
251068	SOLUBLE			UPI00001CB2BF	
51393	MEMBRANE		93 23 IN-OUT 125 23 OUT- IN 168 20 IN-OUT 232 23 OUT-IN 290 23 IN-OUT	O88943	

37272	MEMBRANE		82 19 IN-OUT 132 23 OUT- IN 161 23 IN-OUT 193 23 OUT-IN 224 18 IN-OUT 246 23 OUT-IN 281 18 IN- OUT 405 23 OUT-IN 432 23 IN-OUT	P97529 P97887		
12071	SOLUBLE			Q62673		
314265	SOLUBLE			Q6AYA0	XP 213771.2	
255631	SOLUBLE			Q6AXV4	XP 217005.2	
157267	SOLUBLE			Q99PV2		
273429	SOLUBLE					
261531	SOLUBLE					
223472	SOLUBLE					
221550	SOLUBLE					
195940	MEMBRANE		1856 23 OUT-IN			
308794	SOLUBLE					
263505	SOLUBLE					
241434	SOLUBLE					
194716	SOLUBLE					
201498	MEMBRANE	cleavable signal peptide	187 23 IN-OUT			
317953	SOLUBLE					
287094	SOLUBLE					
306369	MEMBRANE		171 23 IN-OUT 240 23 OUT-IN 269 23 IN-OUT 311 20 OUT-IN 364 23 IN- OUT 430 18 OUT-IN 460 23 IN-OUT			
212247	SOLUBLE					
314602	SOLUBLE					
290958	SOLUBLE					
250115	SOLUBLE					
296511	SOLUBLE					
204977	SOLUBLE	cleavable signal peptide				
289211	SOLUBLE					

302504	MEMBRANE		419 23 OUT-IN 520 23 IN-OUT 557 19 OUT-IN 617 17 IN-OUT 643 23 OUT-IN 711 23 IN-OUT 762 23 OUT-IN			
233304	SOLUBLE					
299926	MEMBRANE		981 23 OUT-IN			
310990	SOLUBLE					
294340	SOLUBLE					
191924	SOLUBLE					
227628	MEMBRANE	cleavable signal peptide	20 20 OUT-IN 103 23 IN-OUT	Q5XIK2		XP_230274.1
58922	SOLUBLE					
65960	SOLUBLE					
262403	MEMBRANE		124 20 OUT-IN 156 23 IN-OUT 206 23 OUT-IN	Q6PEC3		
68755	SOLUBLE			UPI00001679D2		
203844	SOLUBLE			UPI00001D00BC		
271324	SOLUBLE	cleavable signal peptide	12 20 IN-OUT	UPI00001D1029		
265519	MEMBRANE		145 18 OUT-IN 251 20 IN-OUT	UPI000017F121		
237032	SOLUBLE			UPI00001D1A11		
310564	MEMBRANE		25 20 IN-OUT 59 23 OUT-IN			
288425	SOLUBLE			UPI00001D015C		
257171	SOLUBLE			UPI00001CF6BA		
231118	SOLUBLE	cleavable signal peptide		UPI00001CF6EF		
290208	SOLUBLE			UPI00001CF8F1		
55185	SOLUBLE	cleavable signal peptide		P29266		
37174	SOLUBLE			O70539 P50554		
104172	MEMBRANE	cleavable signal peptide	7 23 IN-OUT 82 23 OUT-IN 116 23 IN-OUT 182 23 OUT-IN 224 23 IN-OUT 320 23 OUT-IN 404 23 IN-OUT	Q9QYJ4		
203847	SOLUBLE	cleavable signal peptide	7 18 IN-OUT	Q5I0C4		
106479	SOLUBLE	cleavable signal peptide	13 20 IN-OUT	Q99N59		

53239	SOLUBLE					Q8VDA0		
114274	SOLUBLE	cleavable signal peptide				Q5FVT8 Q9QUH3		
3639	SOLUBLE	cleavable signal peptide				P04638		
95121	SOLUBLE	cleavable signal peptide				P14630 Q5EBB9 Q9QXI9		
44327	MEMBRANE				59 23 IN-OUT	P08290		
315291	MEMBRANE				87 20 IN-OUT			
211553	SOLUBLE					Q68FS9	XP 341612.1	
260733	SOLUBLE					Q6AYH5	XP 216906.2	
11929	MEMBRANE				267 23 IN-OUT	P50279 Q08846 Q08847 Q08848		
173223	SOLUBLE	cleavable signal peptide			7 23 IN-OUT	Q810F4		
161254	SOLUBLE					Q99NH3		
219560	SOLUBLE					Q6AY96	XP 236789.2	
11776	SOLUBLE	cleavable signal peptide				P21744 Q68J74	XP 340898.1	
284296	MEMBRANE				52 23 IN-OUT	Q5XIE8	XP 214228.1	
194234	MEMBRANE	cleavable signal peptide			193 23 IN-OUT	Q5BK85		
60501	SOLUBLE					Q99NA5		
3640	SOLUBLE	cleavable signal peptide				P19939 Q53ZD8		
37198	MEMBRANE	cleavable signal peptide			593 23 OUT-IN 628 20 IN-OUT 657 18 OUT-IN 756 20 IN-OUT 790 23 OUT-IN 819 23 IN-OUT	P35400		
12815	SOLUBLE							
151463	SOLUBLE	cleavable signal peptide				UPI00001CA61E		
100500	SOLUBLE					UPI000017956B		
265735	SOLUBLE					UPI00001D0942		
191085	SOLUBLE					UPI00001CF7CB		
206392	MEMBRANE	cleavable signal peptide			45 20 OUT-IN 77 23 IN-OUT 131 23 OUT-IN 174 23 IN-OUT 201 23 OUT-IN 249 23 IN-OUT 281 18 OUT-IN 311 23 IN-OUT 343 23 OUT-IN 378 20 IN-OUT 407 23 OUT-IN	UPI000017E7B7		
209309	SOLUBLE	cleavable signal peptide				UPI00001D10CC		
303059	MEMBRANE				53 23 OUT-IN 122 23 IN-OUT 149 20 OUT-IN	UPI00001823C0		

316795	SOLUBLE			UPI00001D0830		
164208	SOLUBLE		118 20 OUT-IN	UPI00001803AD		
75052	SOLUBLE			P21807		
1659	SOLUBLE			Q9QYU1		
319029	MEMBRANE	signal anchor	7 23 IN-OUT	Q6P6V1		
227072	MEMBRANE		117 20 IN-OUT 140 23 OUT-IN 169 23 IN-OUT 195 23 OUT-IN 226 20 IN-OUT	Q5M7T4		
11137	MEMBRANE	cleavable signal peptide	569 23 OUT-IN	Q63259		
220519	SOLUBLE	cleavable signal peptide	9 23 IN-OUT	Q5FV72		
239738	MEMBRANE	cleavable signal peptide		UPI00001D08A6 Q5PQP2		
235290	SOLUBLE	cleavable signal peptide		Q5BK77		
140359	MEMBRANE	cleavable signal peptide	7 23 IN-OUT	Q920A6		
84325	SOLUBLE			P15887		
85749	SOLUBLE			O88499 Q64380		
43395	SOLUBLE					
1271	SOLUBLE	cleavable signal peptide		P25236 UPI000016794E		
3600	SOLUBLE			P70584		
34036	SOLUBLE			Q9Z2P6		
60512	SOLUBLE			Q9QYA5		
274159	SOLUBLE					
13085	SOLUBLE	cleavable signal peptide				
191057	MEMBRANE	signal anchor	10 19 OUT-IN 35 23 IN-OUT 62 20 OUT-IN 149 18 IN-OUT 171 19 OUT-IN 196 23 IN-OUT			
270449	SOLUBLE					
105853	SOLUBLE					

241539	MEMBRANE		50 23 OUT-IN 79 18 IN-OUT 101 20 OUT-IN 140 23 IN-OUT 175 18 OUT-IN 294 23 IN-OUT		
198410	SOLUBLE				
238120	SOLUBLE				
309005	SOLUBLE				
236737	SOLUBLE				
245295	SOLUBLE				
311912	SOLUBLE				
222168	SOLUBLE	cleavable signal peptide			
202233	SOLUBLE				
214715	MEMBRANE	cleavable signal peptide	245 20 OUT-IN 277 23 IN-OUT 314 23 OUT-IN 349 21 IN-OUT 384 20 OUT-IN 424 23 IN-OUT 456 20 OUT-IN		
309118	MEMBRANE	cleavable signal peptide	655 23 OUT-IN 690 23 IN-OUT 732 23 OUT-IN 761 23 IN-OUT 812 23 OUT-IN 847 23 IN-OUT 879 23 OUT-IN		
300384	SOLUBLE				
315956	SOLUBLE				
262782	MEMBRANE		102 18 OUT-IN 140 23 IN-OUT 172 23 OUT-IN 201 23 IN-OUT 233 23 OUT-IN 275 20 IN-OUT 304 23 OUT-IN 333 20 IN-OUT 362 23 OUT-IN		
315828	SOLUBLE				
249884	SOLUBLE				
191004	SOLUBLE				
247534	MEMBRANE		250 20 OUT-IN 282 23 IN-OUT 319 23 OUT-IN 478 23 IN-OUT 515 20 OUT-IN 541 23 IN-OUT 568 20 OUT-IN		
221195	SOLUBLE				
273407	SOLUBLE	cleavable signal peptide			
204958	SOLUBLE				

211728	MEMBRANE		424 23 OUT-IN 494 23 IN-OUT 526 23 OUT-IN 560 23 IN-OUT 597 23 OUT-IN 656 23 IN-OUT 688 23 OUT-IN 723 20 IN-OUT 757 23 OUT-IN		
310374	SOLUBLE				
312923	SOLUBLE				
258586	SOLUBLE				
275497	MEMBRANE	cleavable signal peptide	13 23 IN-OUT		
218543	SOLUBLE				
319241	SOLUBLE	cleavable signal peptide			
272431	SOLUBLE				
285571	SOLUBLE				
227549	SOLUBLE				
243174	SOLUBLE				
209577	SOLUBLE				
282341	SOLUBLE				
255984	MEMBRANE	signal anchor	42 23 IN-OUT		
206786	MEMBRANE	cleavable signal peptide	16 18 IN-OUT 85 23 OUT-IN 127 23 IN-OUT 153 20 OUT-IN 228 19 IN-OUT 307 23 OUT-IN 336 23 IN-OUT		
236982	SOLUBLE				
259074	MEMBRANE		143 23 OUT-IN 172 23 IN-OUT 209 20 OUT-IN 307 21 IN-OUT 337 23 OUT-IN 372 23 IN-OUT 409 23 OUT-IN 476 23 IN-OUT 503 23 OUT-IN		
257320	MEMBRANE		37 23 IN-OUT 69 20 OUT-IN 101 23 IN-OUT 141 23 OUT-IN 266 23 IN-OUT 293 23 OUT-IN 476 23 IN-OUT		
145735	MEMBRANE			Q5U1Z2	XP_342918.1
722796	MEMBRANE	signal anchor	5 23 IN-OUT	P61943	
56042	MEMBRANE	cleavable signal peptide	7 20 IN-OUT		
86062	SOLUBLE	cleavable signal peptide	20 19 IN-OUT		
276682	SOLUBLE			Q6AY86	XP_342141.1

26418	SOLUBLE				Q9Z2Q1		
3671	SOLUBLE				P54287		
3662	SOLUBLE	cleavable signal peptide			Q63523 Q63678		
197729	MEMBRANE	cleavable signal peptide		15 23 OUT-IN 49 20 IN-OUT 78 23 OUT-IN 146 20 IN-OUT 169 23 OUT-IN	UPI0000183329		
281500	SOLUBLE						
256290	SOLUBLE			988 23 OUT-IN 1031 18 IN-OUT 1135 23 OUT-IN 1164 23 IN-OUT 1231 23 OUT-IN 1365 23 IN-OUT			
216646	SOLUBLE				UPI00001D07E2		
255469	MEMBRANE	cleavable signal peptide		10 20 OUT-IN 49 23 IN-OUT 86 23 OUT-IN 147 18 IN-OUT 179 18 OUT-IN 209 20 IN-OUT	UPI00001D1035		
302704	SOLUBLE						
220378	SOLUBLE						
267138	SOLUBLE						
310579	SOLUBLE				UPI00001CF9D8		
259217	SOLUBLE				UPI0000180AD2		
280942	SOLUBLE				UPI00001CFB06		
308914	SOLUBLE				UPI00001D05E1		
62820	SOLUBLE				P62198		
166247	MEMBRANE			557 23 OUT-IN	Q7TP18		
229337	SOLUBLE				Q5X11	XP_215419.2	
155721	SOLUBLE	cleavable signal peptide					
41219	MEMBRANE			83 18 IN-OUT 104 16 OUT-IN 269 18 IN-OUT 301 23 OUT-IN 701 23 IN-OUT 776 20 OUT-IN 844 20 IN-OUT 873 23 OUT-IN	Q64566 Q64567	NP_571982.1	
240055	SOLUBLE	cleavable signal peptide			Q811M5		
12003	SOLUBLE			644 23 IN-OUT 697 23 OUT-IN 740 23 IN-OUT 767 23 OUT-IN 929 23 IN-OUT 976 23 OUT-IN 1351 23 IN-OUT 1377 23 OUT-IN	P70705		
108087	MEMBRANE				Q64539		
42765	SOLUBLE				Q9QZW8		

57456	SOLUBLE	cleavable signal peptide	7 20 IN-OUT			
242747	MEMBRANE	cleavable signal peptide	7 23 IN-OUT	Q4KLJ4 UPI00001C6FCF		
277551	SOLUBLE			Q5XI08	XP_216205.2	
108861	SOLUBLE	cleavable signal peptide	4 23 OUT-IN	Q99MH3		
49021	MEMBRANE		97 23 IN-OUT 139 23 OUT-IN 209 20 IN-OUT 238 19 OUT-IN			
15418	MEMBRANE	cleavable signal peptide	299 23 OUT-IN	P13599		
70289	MEMBRANE		386 23 OUT-IN 421 23 IN-OUT	O8867		
286877	SOLUBLE			Q6TXE9		
37205	MEMBRANE	cleavable signal peptide	831 23 OUT-IN	O70535		
106673	MEMBRANE	cleavable signal peptide	806 23 OUT-IN	P35952		
204667	MEMBRANE		217 23 OUT-IN	Q5M836		
299198	SOLUBLE			UPI00001CF9		
246770	MEMBRANE		49 23 IN-OUT 76 23 OUT-IN	UPI00001D16D8		
287732	SOLUBLE			UPI00001D06F0		
291571	SOLUBLE			Q4V8D8 UPI00001CD667		
303709	SOLUBLE		173 23 IN-OUT 215 23 OUT-IN	UPI00001802E6		
225990	MEMBRANE	cleavable signal peptide	5 23 IN-OUT 56 23 OUT-IN 118 20 IN-OUT	UPI00001CBD1A		
291988	SOLUBLE			UPI000018042A		
169806	SOLUBLE			UPI00001C7D93		
167222	MEMBRANE	cleavable signal peptide	13 23 IN-OUT	Q3KR95 UPI0000182D08		
219536	SOLUBLE			UPI00001CCF1F		
72049	MEMBRANE	cleavable signal peptide	12 20 IN-OUT	Q925R7		
71853	SOLUBLE			Q6P6U2		
285106	MEMBRANE	signal anchor		Q5XIN7	XP_342886.1	
271057	SOLUBLE	cleavable signal peptide	9 20 IN-OUT	Q5FV73 UPI00001812BB		
42827	MEMBRANE		29 23 IN-OUT	Q9JMA8		
150292	SOLUBLE	signal anchor	134 23 IN-OUT 161 23 OUT-IN 196 23 IN-OUT 241 23 OUT-IN	Q9ERM7		

70797	MEMBRANE				Q9QZJ7 Q9QZJ8 Q9QZP9 Q9QZR6	
60508	SOLUBLE				O54874	
138976	MEMBRANE			343 23 OUT-IN 378 23 IN- OUT 450 23 OUT-IN 550 23 IN-OUT 611 23 OUT-IN	Q9R283	
277960	SOLUBLE				Q7TNJ9	NP_891999.1
60486	SOLUBLE					
259662	SOLUBLE					
313692	SOLUBLE					
295192	SOLUBLE					
308477	SOLUBLE					
263863	SOLUBLE					
314287	SOLUBLE					
209202	SOLUBLE	signal anchor		7 20 IN-OUT		
237985	MEMBRANE	cleavable signal peptide		7 23 IN-OUT 366 23 OUT- IN 401 20 IN-OUT 435 23 OUT-IN 478 23 IN-OUT 628 18 OUT-IN 657 23 IN- OUT 689 23 OUT-IN 724 19 IN-OUT 817 23 OUT-IN 862 23 IN-OUT 889 20 OUT-IN		
260011	SOLUBLE	signal anchor		10 23 OUT-IN 41 23 IN- OUT 115 23 OUT-IN 144 18 IN-OUT 176 20 OUT-IN 207 23 IN-OUT 239 23 OUT-IN 274 23 IN-OUT 300 18 OUT-IN		
221731	SOLUBLE					
250733	SOLUBLE					
317496	SOLUBLE					
283557	SOLUBLE			43 23 IN-OUT 80 19 OUT- IN 105 20 IN-OUT 134 20 OUT-IN 166 20 IN-OUT		
211597	SOLUBLE					
274376	SOLUBLE					

315202	SOLUBLE					
273781	SOLUBLE					
291964	SOLUBLE					
284460	SOLUBLE					
194979	SOLUBLE					
316025	SOLUBLE					
247675	MEMBRANE					
313987	SOLUBLE					
230780	SOLUBLE					
193616	SOLUBLE					
304037	MEMBRANE	cleavable signal peptide	9 23 IN-OUT 36 23 OUT-IN 83 23 IN-OUT 120 23 OUT- IN 149 23 IN-OUT 228 23 OUT-IN 323 18 IN-OUT 344 23 OUT-IN 491 23 IN- OUT			
250792	SOLUBLE					
276172	SOLUBLE					
259133	MEMBRANE	cleavable signal peptide	13 23 IN-OUT			
192759	MEMBRANE	cleavable signal peptide	20 23 IN-OUT 1047 23 OUT-IN			
276968	SOLUBLE	cleavable signal peptide				
232078	SOLUBLE	cleavable signal peptide	87 23 IN-OUT			
221805	MEMBRANE		814 23 OUT-IN 1031 23 IN- OUT 1079 23 OUT-IN 1122 23 IN-OUT 1164 23 OUT- IN 1207 23 IN-OUT 1272 23 OUT-IN			
217412	MEMBRANE	signal anchor	33 23 IN-OUT 275 23 OUT- IN 314 23 IN-OUT 364 23 OUT-IN 407 23 IN-OUT 464 23 OUT-IN			
284187	SOLUBLE					
250614	SOLUBLE				Q80W92	
173122	SOLUBLE				O08700	
193668	SOLUBLE					
38248	SOLUBLE		93 23 IN-OUT			
3011	MEMBRANE	cleavable signal peptide	192 23 IN-OUT	Q9JHW5		
281056	SOLUBLE	cleavable signal peptide		UPI0000183321	XP_215338.2	
198827	SOLUBLE			UPI00001CEB04		
271484	SOLUBLE		43 23 OUT-IN	UPI00001D0C7E		
245025	SOLUBLE			UPI00001D00AF		

239799	SOLUBLE						
234819	SOLUBLE					UPI00001CE6BE	
241066	SOLUBLE					UPI00001D03F9	
212350	SOLUBLE	cleavable signal peptide				UPI00001D14B9	
282355	MEMBRANE			416 20 OUT-IN 467 23 IN-OUT 494 20 OUT-IN 594 23 IN-OUT 650 23 OUT-IN		UPI00001CFCA8	
239276	SOLUBLE					UPI00001CF34F	
230366	SOLUBLE						
214625	SOLUBLE					UPI0000182C44	
272329	SOLUBLE					UPI00001D148F	
13883	SOLUBLE					Q9QUH6-5	
60536	SOLUBLE					Q99M64	
32753	MEMBRANE					P61227	
90531	SOLUBLE					P14056	
1565	MEMBRANE			646 20 IN-OUT 680 23 OUT-IN 723 23 IN-OUT 755 18 OUT-IN 915 23 IN-OUT 959 23 OUT-IN 1312 23 IN-OUT		Q9QUG4	
218884	SOLUBLE					Q5U1Y4	XP 225536.2
3690	MEMBRANE	cleavable signal peptide		7 20 IN-OUT 103 20 OUT-IN		P27274	
722827	MEMBRANE	cleavable signal peptide		7 20 IN-OUT		P61131	
55190	SOLUBLE	signal anchor		20 19 IN-OUT		Q9QZL2	

38628	SOLUBLE	cleavable signal peptide			P97586	
85745	MEMBRANE	signal anchor	10 23 OUT-IN 283 23 IN-OUT 310 20 OUT-IN		O55149 Q9R0E0	
20841	SOLUBLE					
7578	SOLUBLE				Q9Z220	
3700	SOLUBLE				P00564	
216306	SOLUBLE	cleavable signal peptide			Q6IMK6	
242823	SOLUBLE				Q6UN47	
190728	SOLUBLE					
4981	SOLUBLE					
71441	SOLUBLE				P43424 Q4KM61	
52613	SOLUBLE	signal anchor	7 23 IN-OUT		Q9QWE9	NP_062108.1
71479	SOLUBLE				P42930 Q63922	
84256	SOLUBLE	cleavable signal peptide	24 23 OUT-IN		Q9QWA8	
122642	SOLUBLE				Q99F99	
132369	SOLUBLE				O35946	
62937	SOLUBLE				P20760	
231448	SOLUBLE				UPI0000111CCD	
3949	SOLUBLE	cleavable signal peptide			Q6F9U9	
726783	SOLUBLE				P24594	
40753	SOLUBLE		214 23 IN-OUT 258 23 OUT-IN 301 20 IN-OUT 330 20 OUT-IN 457 23 IN-OUT 489 18 OUT-IN 525 23 IN-OUT 557 23 OUT-IN		Q6NYB8	
5106 ?					O08984	
290515	SOLUBLE	cleavable signal peptide	110 23 IN-OUT 311 23 OUT-IN		P97629 Q11009	
38923	MEMBRANE		150 23 IN-OUT		Q861P9	
111687	SOLUBLE				P79590	
215394	SOLUBLE				Q63330	
					Q66HG9	XP_230537.2

73388	SOLUBLE				UPI0000110B4C		
63044	SOLUBLE				Q9QYF3		
166436	SOLUBLE				UPI00001CD470		
722228	SOLUBLE				Q6XQN1		
277221	MEMBRANE	signal anchor		25 23 OUT-IN 60 23 IN-OUT 97 23 OUT-IN 140 23 IN-OUT 196 23 OUT-IN 237 23 IN-OUT 274 18 OUT-IN	Q6MFX2	XP_227976.1	
54281	MEMBRANE			36 23 IN-OUT 62 23 OUT-IN 97 18 IN-OUT 119 23 OUT-IN	Q9ES40 Q9JKD1		
268213	SOLUBLE				UPI00001CFD51		
215733	SOLUBLE	cleavable signal peptide			UPI000017F6A9		
209194	SOLUBLE				UPI00001804E3		
245607	MEMBRANE	cleavable signal peptide		10 23 OUT-IN 45 23 IN-OUT 98 23 OUT-IN 125 23 IN-OUT 162 23 OUT-IN	UPI00001808C0		
234912	SOLUBLE				Q1RP75		
318230	SOLUBLE				UPI00001CFA6C		
208800	SOLUBLE				UPI00001CBB9B		
367801	SOLUBLE	cleavable signal peptide			UPI00001815D9		
243468	SOLUBLE				UPI00001C6D86		
243296	SOLUBLE				UPI00001D0754		
302905	SOLUBLE				UPI00001D0A15		
272157	MEMBRANE	cleavable signal peptide			UPI000017FFE4		
163757	SOLUBLE				UPI00001CF064		
161334	SOLUBLE	cleavable signal peptide		32 23 IN-OUT 59 23 OUT-IN 101 23 IN-OUT			
275967	MEMBRANE	cleavable signal peptide			UPI00001C8BAD		
39788	MEMBRANE			201 23 OUT-IN	UPI00001813CD		
167119	MEMBRANE	cleavable signal peptide		366 23 OUT-IN 409 23 IN-OUT 843 23 OUT-IN 919 20 IN-OUT 968 20 OUT-IN 990 23 IN-OUT 1027 23 OUT-IN	Q63127 Q63445 Q64542 Q64543 Q64544 Q64545		
				88 20 IN-OUT 117 20 OUT-IN 143 19 IN-OUT 176 23 OUT-IN 211 23 IN-OUT 259 23 OUT-IN 301 23 IN-OUT	Q5RKH7		

128391	MEMBRANE	cleavable signal peptide	104 23 OUT-IN	O88823		
166582	MEMBRANE	signal anchor	25 18 OUT-IN 49 20 IN-OUT 83 23 OUT-IN 112 23 IN-OUT	Q6P742		XP_217597.1
66476	SOLUBLE			Q31286		
90519	SOLUBLE	signal anchor	12 23 IN-OUT 44 23 OUT-IN 71 23 IN-OUT 113 23 OUT-IN 137 23 IN-OUT 169 23 OUT-IN 212 18 IN-OUT 244 23 OUT-IN 279 23 IN-OUT 333 23 OUT-IN 376 23 IN-OUT 9 20 IN-OUT	O88298		
42830	SOLUBLE	cleavable signal peptide		O55004		
75080	MEMBRANE		125 23 IN-OUT 192 23 OUT-IN 221 23 IN-OUT 247 23 OUT-IN 402 23 IN-OUT 707 23 OUT-IN 742 23 IN-OUT 829 23 OUT-IN 912 23 IN-OUT 1157 20 OUT-IN 1197 23 IN-OUT 1229 23 OUT-IN 1278 23 IN-OUT 1397 23 OUT-IN 1478 20 IN-OUT 1507 23 OUT-IN 1536 23 IN-OUT 1609 23 OUT-IN 1699 23 IN-OUT	P08104		
209385	SOLUBLE	cleavable signal peptide		Q80YV8		
47308	SOLUBLE		27 18 IN-OUT 70 23 OUT-IN 105 23 IN-OUT 147 23 OUT-IN	Q62876		
52412	SOLUBLE		244 23 IN-OUT	Q70319		
78119	SOLUBLE		235 20 IN-OUT	Q63635		
78117	SOLUBLE		211 23 IN-OUT	Q9Z2Q7		
21456	SOLUBLE			Q9WU70 Q9WU71 Q9Z152		
12016	MEMBRANE	cleavable signal peptide	303 23 OUT-IN	Q63493		
171046	SOLUBLE			Q75Q41		
71714	SOLUBLE		84 18 IN-OUT			
231037	SOLUBLE					
196358	SOLUBLE					
195573	SOLUBLE					

302099	SOLUBLE					
202900	SOLUBLE	cleavable signal peptide				
306790	SOLUBLE					
239897	SOLUBLE					
248288	SOLUBLE					
250964	SOLUBLE					
308809	SOLUBLE					
241377	MEMBRANE	cleavable signal peptide	69 23 IN-OUT			
293554	MEMBRANE	cleavable signal peptide	188 23 IN-OUT 220 20 OUT-IN 295 23 IN-OUT 321 20 OUT-IN 361 20 IN-OUT 400 18 OUT-IN			
199763	SOLUBLE	cleavable signal peptide				
219867	SOLUBLE					
251203	SOLUBLE					
166638	SOLUBLE					
253215	SOLUBLE					
227451	SOLUBLE					
279597	SOLUBLE					
253264	SOLUBLE					
207798	SOLUBLE					
277429	MEMBRANE		333 23 OUT-IN 362 23 IN-OUT 434 20 OUT-IN 666 23 IN-OUT 693 20 OUT-IN 732 23 IN-OUT			
192515	SOLUBLE					
296032	MEMBRANE					
167845	SOLUBLE					
273635	SOLUBLE	signal anchor	28 23 OUT-IN 62 15 IN-OUT 96 23 OUT-IN 284 23 IN-OUT 334 23 OUT-IN 376 23 IN-OUT 418 23 OUT-IN			
266670	MEMBRANE	cleavable signal peptide	24 21 IN-OUT 75 18 OUT-IN 99 23 IN-OUT 183 18 OUT-IN 213 23 IN-OUT 303 23 OUT-IN 346 20 IN-OUT 385 23 OUT-IN 428 23 IN-OUT 460 20 OUT-IN 486 20 IN-OUT 515 20 OUT-IN 547 23 IN-OUT 574 23 OUT-IN			
272177	SOLUBLE					
294302	SOLUBLE					

252747	SOLUBLE					
301164	SOLUBLE					
284142	SOLUBLE					
270223	SOLUBLE	cleavable signal peptide				
276020	SOLUBLE					
294808	MEMBRANE	signal anchor		38 18 IN-OUT 65 23 OUT- IN 100 23 IN-OUT 137 23 OUT-IN 204 20 IN-OUT 233 23 OUT-IN		
207620	SOLUBLE			67 23 IN-OUT		
234670	SOLUBLE			345 20 IN-OUT		
287807	SOLUBLE					
269045	SOLUBLE					
216923	SOLUBLE					
209283	MEMBRANE			260 23 IN-OUT 292 23 OUT-IN		
219400	SOLUBLE	cleavable signal peptide		15 23 OUT-IN 243 23 IN- OUT 309 20 OUT-IN 335 18 IN-OUT 367 19 OUT-IN 392 23 IN-OUT		
317761	SOLUBLE					
191842	SOLUBLE					
280707	SOLUBLE					
200712	SOLUBLE					
286816	SOLUBLE					
294934	SOLUBLE					
290038	SOLUBLE					
286208	SOLUBLE					
272995	MEMBRANE	cleavable signal peptide		5 23 IN-OUT 37 23 OUT-IN 119 23 IN-OUT 191 23 OUT-IN 226 20 IN-OUT 255 23 OUT-IN 297 23 IN- OUT		
205672	MEMBRANE	signal anchor		24 23 IN-OUT 102 23 OUT- IN 520 23 IN-OUT 594 23 OUT-IN		
205697	SOLUBLE					
275469	SOLUBLE					

211877	SOLUBLE	signal anchor	29 20 OUT-IN 55 20 IN-OUT 84 23 OUT-IN 127 23 IN-OUT 159 23 OUT-IN 188 20 IN-OUT 254 20 OUT-IN 286 23 IN-OUT 338 23 OUT-IN 380 23 IN-OUT 417 19 OUT-IN 442 23 IN-OUT 484 23 OUT-IN 598 20 IN-OUT		
217901	SOLUBLE		301 23 OUT-IN		
311710	SOLUBLE				
286188	SOLUBLE				
291449	SOLUBLE	cleavable signal peptide			
249318	SOLUBLE				
273036	SOLUBLE				
207724	SOLUBLE				
217052	MEMBRANE	cleavable signal peptide	2 23 IN-OUT 432 23 OUT-IN 474 20 IN-OUT 497 18 OUT-IN 527 23 IN-OUT 553 20 OUT-IN 609 23 IN-OUT 646 23 OUT-IN		
308345	SOLUBLE	cleavable signal peptide			
267553	SOLUBLE				
109585	SOLUBLE		237 23 IN-OUT	NP_068641.1	
260364	MEMBRANE	signal anchor	12 23 IN-OUT 44 23 OUT-IN 73 20 IN-OUT 174 20 OUT-IN	Q5U1V9	XP_343218.1
90533	SOLUBLE	cleavable signal peptide		Q9R0D6	
30411	MEMBRANE		7 23 IN-OUT 34 23 OUT-IN 63 20 IN-OUT 87 20 OUT-IN	Q924P2	
75921	SOLUBLE	cleavable signal peptide	IN	Q9EQV6	
190070	MEMBRANE	signal anchor	45 23 OUT-IN 80 23 IN-OUT	Q5BJP5	
265453	SOLUBLE	cleavable signal peptide		Q5XIJ5	XP_216853.2
241488	SOLUBLE	cleavable signal peptide		P59824	
119817	MEMBRANE	cleavable signal peptide	544 23 OUT-IN 587 23 IN-OUT 624 23 OUT-IN 805 23 IN-OUT	UPI0000167F6F	
79012	SOLUBLE	cleavable signal peptide			
126680	SOLUBLE				

302444	SOLUBLE	signal anchor	24 23 OUT-IN 59 23 IN-OUT 96 23 OUT-IN 138 23 IN-OUT 193 23 OUT-IN 236 23 IN-OUT 273 18 OUT-IN	UPI000017FDA1	XP_222380.2
216315	SOLUBLE				
288218	SOLUBLE			UPI00001D0DFC	
231235	SOLUBLE			UPI00001D1A15	
301426	MEMBRANE	signal anchor	36 23 OUT-IN 63 23 IN-OUT 95 23 OUT-IN		
208424	MEMBRANE	cleavable signal peptide	37 20 IN-OUT 66 23 OUT-IN 138 23 IN-OUT 170 23 OUT-IN 205 23 IN-OUT 242 22 OUT-IN 270 23 IN-OUT 297 18 OUT-IN	UPI00001D16C7	
214268	SOLUBLE		48 23 IN-OUT 100 20 OUT-IN 126 20 IN-OUT 150 23 OUT-IN	UPI00001CF39A	
246776	SOLUBLE	cleavable signal peptide		UPI00001CEBC1	
196884	SOLUBLE	cleavable signal peptide		UPI00001D10C8	
224861	SOLUBLE			UPI00001CFAD8	
269756	SOLUBLE			UPI00001CB5EB	
308740	SOLUBLE				
293919	SOLUBLE			UPI00001CFF2C	
292043	MEMBRANE	cleavable signal peptide	10 18 OUT-IN 69 23 IN-OUT 96 23 OUT-IN 160 23 IN-OUT 186 20 OUT-IN 23 23 IN-OUT 318 23 OUT-IN	UPI0000181987	
203605	SOLUBLE	signal anchor		UPI00001CF251	
345922	MEMBRANE		62 23 IN-OUT 94 19 OUT-IN 121 23 IN-OUT 202 23 OUT-IN	Q4G068 UPI00001C8AC0	
309548	SOLUBLE			UPI00001D0773	
276318	SOLUBLE		313 23 OUT-IN	UPI00001D1108	
314842	MEMBRANE		584 23 OUT-IN	UPI00001D1772	

Table S1D. Peptide statistics by assigned protein name

FUNCTION	CMBSEQID	CMBSEQID LIST	gnumber	ASSIGNED PROT NAME	MEMBRANE STATUS	TOTAL PEPTIDES N=1 RM AQU	TOTAL PEPTIDES N=2 RM AQU
BIOSYNTHETIC CARGO	319145	319145	40018550	KUNITZ TYPE SERINE PROTEINASE INHIBITOR	MEMBRANE	0	0
BIOSYNTHETIC CARGO	23759	23759	543793	AFAMIN	SOLUBLE	0	2
BIOSYNTHETIC CARGO	6160	6160 11478 66447 84131 256838 296398	91949	ALPHA-1 PROTEINASE INHIBITOR III	SOLUBLE	27	51
BIOSYNTHETIC CARGO	11470	11470	72091	ALPHA-1-ACID GLYCOPROTEIN PRECURSOR	SOLUBLE	0	0
BIOSYNTHETIC CARGO	11475	11475	112889	ALPHA-1-ANTIPTROTEINASE	SOLUBLE	5	14
BIOSYNTHETIC CARGO	126488	126488	739596	ALPHA-1-MACROGLOBULIN	SOLUBLE	13	31
BIOSYNTHETIC CARGO	3629	3629	6978497	ALPHA-1-MICROGLOBULIN	SOLUBLE	0	2
BIOSYNTHETIC CARGO	317738	317738	51261124	ALPHA-2 ANTIPLASMIN	SOLUBLE	0	0
BIOSYNTHETIC CARGO	341343	341343	58865362	ALPHA-2-ANTIPLASMIN	SOLUBLE	0	0
BIOSYNTHETIC CARGO	111646	111646	60552688	ALPHA-2-HS-GLYCOPROTEIN	SOLUBLE	0	2
BIOSYNTHETIC CARGO	237675	237675	34878475	ALPHA-2-MACROGLOBULIN RECEPTOR-ASSOCIATED PROTEIN	SOLUBLE	0	4
BIOSYNTHETIC CARGO	69402	36387 69402 125352	992637	ALPHA-2U GLOBULIN	SOLUBLE	23	51
BIOSYNTHETIC CARGO	106479	106479	58293772	ALPHA-AMYLASE	SOLUBLE	0	0
BIOSYNTHETIC CARGO	45123	45123	56585074	ANGIOTENSINOGEN	SOLUBLE	0	2
BIOSYNTHETIC CARGO	207228	207228	34880787	ANTITHROMBIN III	SOLUBLE	0	4
BIOSYNTHETIC CARGO	3638	3638	6978515	APOLIPOPROTEIN A-I	SOLUBLE	0	2
BIOSYNTHETIC CARGO	3639	3639	91985	APOLIPOPROTEIN A-II	SOLUBLE	0	0
BIOSYNTHETIC CARGO	141420	141420	60552712	APOLIPOPROTEIN A-IV	SOLUBLE	0	7
BIOSYNTHETIC CARGO	114274	114274	6707431	APOLIPOPROTEIN A-V	SOLUBLE	0	0
BIOSYNTHETIC CARGO	166227	148924 166227	61098031	APOLIPOPROTEIN B	SOLUBLE	0	29
BIOSYNTHETIC CARGO	3640	3640	91989	APOLIPOPROTEIN C-I	SOLUBLE	0	0
BIOSYNTHETIC CARGO	84170	84170	91990	APOLIPOPROTEIN C-III	SOLUBLE	0	0
BIOSYNTHETIC CARGO	136243	136243	2492315	APOLIPOPROTEIN C-IV PRECURSOR	SOLUBLE	0	0
BIOSYNTHETIC CARGO	126501	126501	55824759	APOLIPOPROTEIN E	SOLUBLE	1	9
BIOSYNTHETIC CARGO	95121	95121	9506391	APOLIPOPROTEIN M	SOLUBLE	0	0
BIOSYNTHETIC CARGO	268287	268287	27707592	ATP-BINDING CASSETTE, SUB-FAMILY F (GCN20), MEMBER 2	SOLUBLE	0	0
BIOSYNTHETIC CARGO	287107	287107	33086684	B-FACTOR, PROPERDIN, ALTERNATIVE-COMPLEMENT PATHWAY C3/C5 CONVERTASE	SOLUBLE	0	0
BIOSYNTHETIC CARGO	27803	27803	999862	BETA-2-MICROGLOBULIN	SOLUBLE	0	1
BIOSYNTHETIC CARGO	126549	126549	8393197	C-REACTIVE PROTEIN	SOLUBLE	2	7
BIOSYNTHETIC CARGO	3668	3668	899380	C4B-BINDING PROTEIN ALPHA CHAIN	SOLUBLE	0	0
BIOSYNTHETIC CARGO	76638	76638	19864480	CALPAIN SMALL SUBUNIT 1	SOLUBLE	0	0
BIOSYNTHETIC CARGO	39119	39119	76496479	CARCINOEMBRYONIC ANTIGEN-RELATED CELL ADHESION MOLECULE, SECRETED ISOFORM CEACAM1A-4C2	SOLUBLE	0	0
BIOSYNTHETIC CARGO	219134	219134	34855491	CERULOPLASMIN	SOLUBLE	1.1	6
BIOSYNTHETIC CARGO	36009	36009	11127974	CLUSTERIN	SOLUBLE	0	0
BIOSYNTHETIC CARGO	149112	149112	204146	COAGULATION FACTOR IX	SOLUBLE	0	1
BIOSYNTHETIC CARGO	201969	201969	34852376	COLLAGEN ALPHA1 TYPE VI-PRECURSOR	SOLUBLE	0	0
BIOSYNTHETIC CARGO	308317	308317	34866496	COLLAGEN TYPE XIV	SOLUBLE	0	0
BIOSYNTHETIC CARGO	162301	162301	29789265	COMPLEMENT C4	SOLUBLE	0	7
BIOSYNTHETIC CARGO	221549	221549	62718645	COMPLEMENT COMPONENT 3	SOLUBLE	9.9	31
BIOSYNTHETIC CARGO	205903	205903	34853897	COMPLEMENT COMPONENT 5	SOLUBLE	0	0

BIOSYNTHETIC CARGO	251303	251303	34853020	COMPLEMENT COMPONENT C8 GAMMA SUBUNIT	SOLUBLE	0	0
BIOSYNTHETIC CARGO	43431	43431	2499467	COMPLEMENT COMPONENT C9	SOLUBLE	0	5
BIOSYNTHETIC CARGO	96883	96883	18426830	COMPLEMENT INHIBITORY FACTOR H	SOLUBLE	0	0
BIOSYNTHETIC CARGO	84230	84230 135016	57294	CONTRAPSIN-LIKE PROTEASE INHIBITOR 1	SOLUBLE	4	23
BIOSYNTHETIC CARGO	88238	88238	50927309	CONTRAPSIN-LIKE PROTEASE INHIBITOR 6	SOLUBLE	1	14
BIOSYNTHETIC CARGO	208059	208059	27677818	DERMATOPONTIN	SOLUBLE	0	1
BIOSYNTHETIC CARGO	145181	145181	6562849	FETUIN-B	SOLUBLE	0	1
BIOSYNTHETIC CARGO	181007	181007	25282415	FIBRINOGEN	SOLUBLE	0	1
BIOSYNTHETIC CARGO	173317	173317	62643670	FIBRINOGEN ALPHA/ALPHA-E CHAIN	SOLUBLE	2	9
BIOSYNTHETIC CARGO	166238	166238	33086484	FIBRINOGEN B BETA CHAIN	SOLUBLE	0	1
BIOSYNTHETIC CARGO	3766	3766	1183937	FIBRINOGEN GAMMA CHAIN	SOLUBLE	0	7
BIOSYNTHETIC CARGO	22617	22617	229210	FIBRINOPEPTIDE A	SOLUBLE	0	1
BIOSYNTHETIC CARGO	95208	95208	9506703	FIBRONECTIN 1	SOLUBLE	0	7
BIOSYNTHETIC CARGO	75919	75919	6714560	FICOLIN 1 PRECURSOR	SOLUBLE	0	0
BIOSYNTHETIC CARGO	8548	8548	40352785	FLOTILLIN-1	SOLUBLE	0	0
BIOSYNTHETIC CARGO	253728	253728	34881641	GLYPICAN 4	SOLUBLE	0	0
BIOSYNTHETIC CARGO	166334	166334	33086640	HAPTOGLOBIN	SOLUBLE	3	10
BIOSYNTHETIC CARGO	242533	242533	34853846	HC PROTEIN	SOLUBLE	0	0
BIOSYNTHETIC CARGO	16936	16936	204621	HEMOPEXIN	SOLUBLE	0	6
BIOSYNTHETIC CARGO	68739	68739	60551378	HEPARIN COFACTOR II	SOLUBLE	0	3
BIOSYNTHETIC CARGO	18186	18186 140379	13358878	HISTIDINE-RICH GLYCOPROTEIN HRG	SOLUBLE	0	4
BIOSYNTHETIC CARGO	11776	11776	68534170	INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 4	SOLUBLE	0	0
BIOSYNTHETIC CARGO	11211	11211	71896592	INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN	SOLUBLE	0	0
BIOSYNTHETIC CARGO	227779	227779	34877130	INTER-ALPHA TRYPSIN INHIBITOR, HEAVY CHAIN 1	SOLUBLE	0	1
BIOSYNTHETIC CARGO	47186	47186	9506819	INTER-ALPHA-INHIBITOR H4 HEAVY CHAIN	SOLUBLE	0	4
BIOSYNTHETIC CARGO	38418	38418	8393899	INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H3	SOLUBLE	0	1
BIOSYNTHETIC CARGO	38912	38912	21490001	KALLISTATIN	SOLUBLE	0	0
BIOSYNTHETIC CARGO	60472	60472	2492888	LONG-CHAIN FATTY ACID TRANSPORT PROTEIN	SOLUBLE	0	0
BIOSYNTHETIC CARGO	130837	130837	539969	LYSOZYME HOMOLOG AT-2, BINE - RAT (FRAGMENTS)	SOLUBLE	0	0
BIOSYNTHETIC CARGO	19138	19138	1942287	MANNOSE-BINDING PROTEIN A	SOLUBLE	0	3
BIOSYNTHETIC CARGO	44167	44167	205263	MANNOSE-BINDING PROTEIN C PRECURSOR	SOLUBLE	1	4
BIOSYNTHETIC CARGO	35920	35920	38197682	MONOCYTE DIFFERENTIATION ANTIGEN CD14	SOLUBLE	0	0
BIOSYNTHETIC CARGO	166242	166242	62659617	MURINE COAGULATION FACTOR V	SOLUBLE	0	0
BIOSYNTHETIC CARGO	3277	3277	70166245	MYELIN BASIC PROTEIN S	SOLUBLE	0	0
BIOSYNTHETIC CARGO	233877	233877	34855859	PALS2-BETA SPLICE VARIANT	SOLUBLE	0	0
BIOSYNTHETIC CARGO	198556	19325 198556	60551577	PARAOXONASE 1	SOLUBLE	0	4
BIOSYNTHETIC CARGO	217377	217377	34854947	PARAOXONASE 2	SOLUBLE	0	5
BIOSYNTHETIC CARGO	62757	62757	7108713	PLASMA GLUTAMATE CARBOXYPEPTIDASE	SOLUBLE	0	0
BIOSYNTHETIC CARGO	144413	144413	27685035	PLASMA RETINOL-BINDING PROTEIN	SOLUBLE	3	4
BIOSYNTHETIC CARGO	60419	60419 124523	62638541	PLASMINOGEN	SOLUBLE	7	12
BIOSYNTHETIC CARGO	3737	3737	6978763	PRESYNAPTIC PROTEIN SAP97	SOLUBLE	0	0
BIOSYNTHETIC CARGO	258657	258657	34852378	PROCOLLAGEN, TYPE VI, ALPHA 2	SOLUBLE	0	0
BIOSYNTHETIC CARGO	103863	103863	603052	PROSTAGLANDIN G/H SYNTHASE 1 PRECURSOR	SOLUBLE	0	0
BIOSYNTHETIC CARGO	31503	31503	56970	PROTHROMBIN	SOLUBLE	0	6
BIOSYNTHETIC CARGO	317126	317126	34867440	ROUNDABOUT (AXON GUIDANCE RECEPTOR, DROSOPHILA) HOMOLOG 2	SOLUBLE	0	0
BIOSYNTHETIC CARGO	43395	43395	2498940	SECRETED PHOSPHOPROTEIN 24	SOLUBLE	0	0
BIOSYNTHETIC CARGO	1271	1271	47939025	SELENOPROTEIN P	SOLUBLE	0	0

BIOSYNTHETIC CARGO	222317	222317	81892278	SERINE (OR CYSTEINE) PROTEINASE INHIBITOR, CLADE G (C1 INHIBITOR), MEMBER 1, (ANGIOEDEMA, HEREDITARY)	SOLUBLE	0	0
BIOSYNTHETIC CARGO	13085	13085	7435832	SERINE PROTEASE	SOLUBLE	0	0
BIOSYNTHETIC CARGO	195578	195578	34867677	SERINE PROTEASE INHIBITOR 2.4 PRECURSOR	SOLUBLE	0	2
BIOSYNTHETIC CARGO	224458	224458	55090431	SERINE PROTEASE INHIBITOR 6	SOLUBLE	0	0
BIOSYNTHETIC CARGO	120645	120645	72101	SERUM ALBUMIN	SOLUBLE	41	74
BIOSYNTHETIC CARGO	52390	52390	3183550	SERUM AMYLOID P-COMPONENT	SOLUBLE	1	6
BIOSYNTHETIC CARGO	307227	307227	34877775	SIMILAR TO ALPHA 3 TYPE VI COLLAGEN ISOFORM 1 PRECURSOR; COLLAGEN VI, ALPHA-3 POLYPEPTIDE	SOLUBLE	0	0
BIOSYNTHETIC CARGO	264571	264571	34865864	SIMILAR TO ALPHA 3 TYPE VI COLLAGEN ISOFORM 4	SOLUBLE	0	0
BIOSYNTHETIC CARGO	210822	210822	34868545	SIMILAR TO ALPHA-2U-GLOBULIN	SOLUBLE	0	0
BIOSYNTHETIC CARGO	303449	303449	34857927	SIMILAR TO APOA1	SOLUBLE	0	0
BIOSYNTHETIC CARGO	21485	21485	319920	SIMILAR TO BETA-2-GLYCOPROTEIN I	SOLUBLE	0	2
BIOSYNTHETIC CARGO	209490	209490	37361858	SIMILAR TO COAGULATION FACTOR XI; PLASMA THROMBOPLASTIN ANTECEDENT	SOLUBLE	0	0
BIOSYNTHETIC CARGO	355419	355419	62908846	SIMILAR TO COMPLEMENT COMPONENT 1, Q SUBCOMPONENT, ALPHA POLYPEPTIDE	SOLUBLE	0	0
BIOSYNTHETIC CARGO	295319	295319	34869994	SIMILAR TO COMPLEMENT COMPONENT 8 ALPHA SUBUNIT	SOLUBLE	0	0
BIOSYNTHETIC CARGO	204172	204172	34869943	SIMILAR TO COMPLEMENT COMPONENT 8 BETA SUBUNIT	SOLUBLE	0	2
BIOSYNTHETIC CARGO	275354	275354	34880509	SIMILAR TO COMPLEMENT COMPONENT FACTOR H	SOLUBLE	0	0
BIOSYNTHETIC CARGO	285938	285938	34855405	SIMILAR TO FC FRAGMENT OF IGG BINDING PROTEIN; IGG FC-BINDING PROTEIN	SOLUBLE	0	0
BIOSYNTHETIC CARGO	272967	272967	34882179	SIMILAR TO GROUP XIII SECRETED PHOSPHOLIPASE A2	SOLUBLE	0	0
BIOSYNTHETIC CARGO	304054	304054	34865830	SIMILAR TO TRANSFERRIN	SOLUBLE	0	9
BIOSYNTHETIC CARGO	199559	199559	34861187	SIMILAR TO TRANSTHYRETIN (4L369)	SOLUBLE	0	0
BIOSYNTHETIC CARGO	75055	75055	92782	SULFATED GLYCOPROTEIN 1	SOLUBLE	0	0
BIOSYNTHETIC CARGO	75350	75350	79152346	Sorting nexin 3	SOLUBLE	0	0
BIOSYNTHETIC CARGO	3965	3965	6981138	T-KININOGEN I	SOLUBLE	0	3
BIOSYNTHETIC CARGO	166406	37301 166406	61556986	TRANSFERRIN	SOLUBLE	27	62
BIOSYNTHETIC CARGO	31553	31553	57425	TRANSTHYRETIN	SOLUBLE	1	5
BIOSYNTHETIC CARGO	37481	37481	6537316	URINARY PROTEIN 1	SOLUBLE	0	0
BIOSYNTHETIC CARGO	86608	86608	51260133	VITAMIN D-BINDING PROTEIN	SOLUBLE	0	4
BIOSYNTHETIC CARGO	75051	75051	6981412	VITAMIN-K-DEPENDENT PROTEIN C	SOLUBLE	0	3
BIOSYNTHETIC CARGO	302124	302124	32492572	VITRONECTIN	SOLUBLE	0	1
BIOSYNTHETIC CARGO	251407	251407	34858467	VON WILLEBRAND FACTOR	SOLUBLE	0	0
BIOSYNTHETIC CARGO	3662	3662	6978565	ZINC-ALPHA-2-GLYCOPROTEIN	SOLUBLE	0	0
BLOOD + OTHER CELLS	128256	128256	498034	ADVANCED GLYCOSYLATION END PRODUCT-SPECIFIC RECEPTOR	MEMBRANE	0	0
BLOOD + OTHER CELLS	78164	78164	47605356	CD166 ANTIGEN	MEMBRANE	0	0
BLOOD + OTHER CELLS	234797	234797	81885839	NATURAL KILLER CELL-SPECIFIC ANTIGEN KLIP1	MEMBRANE	0	0
BLOOD + OTHER CELLS	105482	105482	6707016	PLATELET GLYCOPROTEIN IV	MEMBRANE	0	0
BLOOD + OTHER CELLS	296460	296460	34877265	SIMILAR TO MACROPHAGE MANNOSE RECEPTOR	MEMBRANE	0	0
BLOOD + OTHER CELLS	109334	3923 109334	60688619	HEMOGLOBIN ALPHA-1 AND ALPHA-2 CHAINS	SOLUBLE	5	10
BLOOD + OTHER CELLS	28543	28543 28546 84237	55823	HEMOGLOBIN BETA CHAIN	SOLUBLE	6	10
BLOOD + OTHER CELLS	195860	195860	34855968	IMMUNOGLOBULIN 4G6 LIGHT CHAIN	SOLUBLE	0	0
BLOOD + OTHER CELLS	225182	225182	34935297	IMMUNOGLOBULIN HEAVY CHAIN CONSTANT REGION MU	SOLUBLE	0	0
BLOOD + OTHER CELLS	37207	37207	38181546	MACROPHAGE MIGRATION INHIBITORY FACTOR	SOLUBLE	0	0
BLOOD + OTHER CELLS	176262	176262	5052048	MPS1 PROTEIN	SOLUBLE	0	0

BLOOD + OTHER CELLS	300797	300797	34879408	SIMILAR TO BAND 4.1-LIKE PROTEIN 5	SOLUBLE	0	0
BLOOD + OTHER CELLS	232984	232984	27673471	STROMAL CELL-DERIVED FACTOR 2 (SDF-2)	SOLUBLE	0	0
CALCIUM TRANS/BIND	229917	229917	34856330	DYSFERLIN (DYSTROPHY ASSOCIATED FER-1 LIKE PROTEIN)	MEMBRANE	0	0
CALCIUM TRANS/BIND	37203	37203	56508	INOSITOL 1,4,5-TRISPHOSPHATE RECEPTOR TYPE 2	MEMBRANE	0	0
CALCIUM TRANS/BIND	84180	84180	57303	SARCOPLASMIC CA2+MG2+ ATPASE	MEMBRANE	0	1
CALCIUM TRANS/BIND	257320	257320	34859877	SIMILAR TO ZINC TRANSPORTER LIKE 2	MEMBRANE	0	0
CALCIUM TRANS/BIND	44653	44653	57209	SODIUM/CALCIUM EXCHANGER 1 PRECURSOR	MEMBRANE	0	0
CALCIUM TRANS/BIND	64664	64664	21263446	45 KDA CALCIUM-BINDING PROTEIN	SOLUBLE	0	0
CALCIUM TRANS/BIND	268188	85740 268188	76559925	CALUMENIN	SOLUBLE	0	0
CALCIUM TRANS/BIND	60416	60416	871525	NUCLEOBINDIN 1 (CALNUC1)	SOLUBLE	0	0
CALCIUM TRANS/BIND	3157	3157	8515422	NUCLEOBINDIN 2 (CALNUC2)	SOLUBLE	0	4
COAT	74369	74369	34871704	ADAPTER-RELATED PROTEIN COMPLEX 1 SIGMA 1A SUBUNIT	SOLUBLE	0	0
COAT	198626	198626	34851742	ADAPTOR PROTEIN COMPLEX AP-1, GAMMA 1 SUBUNIT	SOLUBLE	0	0
COAT	37177	37177	55729	ADAPTOR-RELATED PROTEIN COMPLEX 2 ALPHA 2 SUBUNIT	SOLUBLE	0	0
COAT	73521	73521	73536275	ADAPTOR-RELATED PROTEIN COMPLEX 2, MU 1 SUBUNIT	SOLUBLE	0	0
COAT	60461	60461	44888251	CALM	SOLUBLE	0	0
COAT	126513	126513	8392872	CLATHRIN ADAPTIN-1, BETA 1	SOLUBLE	0	0
COAT	219335	219335	34856047	CLATHRIN ADAPTIN-2, ALPHA 1	SOLUBLE	0	0
COAT	59082	59082	73695330	CLATHRIN ADAPTIN-2, BETA 1	SOLUBLE	0	0
COAT	223265	223265	34877759	CLATHRIN AP47 PROTEIN	SOLUBLE	0	0
COAT	65700	65700	56961624	CLATHRIN COAT ASSEMBLY PROTEIN AP17	SOLUBLE	0	0
COAT	95154	95154	9506497	CLATHRIN HEAVY CHAIN	SOLUBLE	0	2
COAT	126525	126525	56269651	CLATHRIN LIGHT CHAIN A	SOLUBLE	0	0
COAT	60578	60578	203359	CLATHRIN LIGHT CHAIN B	SOLUBLE	0	0
COAT	293534	293534	34880938	COPI COATOMER ALPHA SUBUNIT	SOLUBLE	0	0
COAT	63721	63721	55819	COPI COATOMER BETA SUBUNIT	SOLUBLE	0	0
COAT	35931	35931	3023522	COPI COATOMER BETA' SUBUNIT	SOLUBLE	0	0
COAT	221177	221177	81884175	COPI COATOMER DELTA SUBUNIT	SOLUBLE	0	0
COAT	259217	259217	34877816	COPI COATOMER EPSILON SUBUNIT	SOLUBLE	0	0
COAT	267886	267886	34856387	COPI COATOMER GAMMA-1 SUBUNIT	SOLUBLE	0	0
COAT	236737	236737	34868640	COPI COATOMER ZETA-1 SUBUNIT	SOLUBLE	0	0
COAT	203525	203525	34880606	ENTHOPROTEIN	SOLUBLE	0	0
COAT	105332	105332	41016934	EPSIN 1	SOLUBLE	0	0
COAT	141679	141679	34867969	PROTEIN TRANSPORT PROTEIN SEC23A	SOLUBLE	0	0
COAT	260808	260808	34858849	PROTEIN TRANSPORT PROTEIN SEC23B (SEC23-RELATED PROTEIN B)	SOLUBLE	0	0
COAT	295725	295725	34870707	PROTEIN TRANSPORT PROTEIN SEC24A (SEC24-RELATED PROTEIN A)	SOLUBLE	0	0
COAT	219262	219262	34859959	PROTEIN TRANSPORT PROTEIN SEC24D (SEC24-RELATED PROTEIN D)	SOLUBLE	0	0
COAT	161453	161453	55741774	SEC13 LIKE 1 PROTEIN	SOLUBLE	0	0
COAT	241419	241419	34868956	SEC24C	SOLUBLE	0	0
COAT	311912	295519 311912	34864228	SIMILAR TO CONSERVED OLIGOMERIC GOLGI COMPLEX SUBUNIT 5 (13S GOLGI TRANSPORT COMPLEX 90 KDA SUBUNIT) (GTC-90) (GOLGI TRANSPORT COMPLEX 1)	SOLUBLE	0	0
COAT	26418	26418	7514116	VESICLE ASSOCIATED PROTEIN	SOLUBLE	0	0

CYTOSKELETON	241188	241188	34852369	INTEGRIN BETA-2 PRECURSOR (CELL SURFACE ADHESION GLYCOPROTEINS LFA-1/CR3/P150.95 BETA-SUBUNIT) (CD18) (COMPLEMENT RECEPTOR C3 BETA-SUBUNIT)	MEMBRANE	0	0
CYTOSKELETON	3942	3942	6981068	INTERCELLULAR ADHESION MOLECULE-1 PRECURSOR	MEMBRANE	0	0
CYTOSKELETON	95123	95123 287770	9506405	ACTIN RELATED PROTEIN 2/3 COMPLEX	SOLUBLE	0	0
CYTOSKELETON	199239	199239	27707156	ACTIN RELATED PROTEIN 2/3 COMPLEX, SUBUNIT 5-LIKE	SOLUBLE	0	0
CYTOSKELETON	10199	10199	77993370	ACTIN, ALPHA CARDIAC	SOLUBLE	3.5	0
CYTOSKELETON	120792	120792	62645364	ACTIN, GAMMA	SOLUBLE	4.5	18
CYTOSKELETON	156591	156591	62899645	ACTIN-LIKE PROTEIN 2 ACTIN-RELATED PROTEIN 2	SOLUBLE	0	4
CYTOSKELETON	84182	84182	92036	ALPHA-1 CATENIN	SOLUBLE	0	0
CYTOSKELETON	37175	37175	4210385	ALPHA-ACTININ 1	SOLUBLE	0	0
CYTOSKELETON	319018	319018	77539778	ALPHA-ACTININ 4	SOLUBLE	0	7
CYTOSKELETON	37085	37085	20138815	ALPHA-PARVIN	SOLUBLE	0	0
CYTOSKELETON	258828	258828	34876218	ARCHVILLIN	SOLUBLE	0	0
CYTOSKELETON	246886	246886	34869778	ARMADILLO REPEAT GENE DELETED IN VELO-CARDIO-FACIAL SYNDROME (ARVCF) PROTEIN	SOLUBLE	0	0
CYTOSKELETON	222641	222641	34865224	ARP1 ACTIN-RELATED PROTEIN 1 ALPHA	SOLUBLE	0	0
CYTOSKELETON	318590	318590	34880487	ARP2/3 COMPLEX 16 KDA SUBUNIT (P16-ARC) (ACTIN-RELATED PROTEIN 2/3 COMPLEX SUBUNIT 5)	SOLUBLE	0	0
CYTOSKELETON	32844	32844	34858314	ARP2/3 COMPLEX 20 KDA SUBUNIT	SOLUBLE	0	0
CYTOSKELETON	160418	160418	27665454	ARP2/3 COMPLEX 21 KDA SUBUNIT	SOLUBLE	0	0
CYTOSKELETON	205076	205076	34876797	ARP2/3 COMPLEX 34 KDA SUBUNIT	SOLUBLE	0	0
CYTOSKELETON	71751	71751	70912366	ARP3 ACTIN-RELATED PROTEIN 3 HOMOLOG	SOLUBLE	0	2
CYTOSKELETON	161693	161693	27687455	BETA-ACTIN	SOLUBLE	0	0
CYTOSKELETON	74416	74416	16758082	BETA-CATENIN	SOLUBLE	0	0
CYTOSKELETON	83668	83668	54400732	CAPPING PROTEIN (ACTIN FILAMENT) MUSCLE Z-LINE, BETA	SOLUBLE	0	0
CYTOSKELETON	211193	211193	34851815	COACTOSIN-LIKE 1	SOLUBLE	0	0
CYTOSKELETON	74438	74438	62650690	COFILIN, MUSCLE ISOFORM	SOLUBLE	0	0
CYTOSKELETON	87332	87332	8393101	COFILIN, NON-MUSCLE ISOFORM	SOLUBLE	0	3
CYTOSKELETON	57161	57161	2996044	CORTACTIN ISOFORM C	SOLUBLE	0	0
CYTOSKELETON	219502	219502	34875216	DESMOPLAKIN (DP) (250/210 KDA PARANEOPLASTIC PEMPHIGUS ANTIGEN)	SOLUBLE	0	0
CYTOSKELETON	123978	123978	7441446	DESTRIN	SOLUBLE	0	0
CYTOSKELETON	260733	260733	51948450	DYNACTIN COMPLEX 50 KDA SUBUNIT	SOLUBLE	0	0
CYTOSKELETON	3740	3740	729380	DYNAMIN 2	SOLUBLE	0	0
CYTOSKELETON	95169	95169	294543	DYNEIN HEAVY CHAIN, CYTOSOLIC	SOLUBLE	0	0
CYTOSKELETON	129100	129100	56748619	DYNEIN LIGHT CHAIN 2	SOLUBLE	0	0
CYTOSKELETON	233953	233953	34863280	EMILIN	SOLUBLE	0	0
CYTOSKELETON	318405	318405	34867002	EPIPLAKIN	SOLUBLE	0	0
CYTOSKELETON	277610	277610	34868179	EPLIN	SOLUBLE	0	0
CYTOSKELETON	725563	725563	58865394	ERYTHROID SPECTRIN ALPHA	SOLUBLE	0	0
CYTOSKELETON	726511	726511	47058982	ERYTHROID SPECTRIN BETA	SOLUBLE	0	0
CYTOSKELETON	145232	145232	17902245	EZRIN	SOLUBLE	0	0
CYTOSKELETON	644	644	8132349	EZRIN-RADIXIN-MOESIN BINDING PHOSPHOPROTEIN 50	SOLUBLE	0	0
CYTOSKELETON	173653	173653	40538878	F-ACTIN BINDING PROTEIN B-NEXILIN	SOLUBLE	0	0
CYTOSKELETON	230796	230796	34859736	F-ACTIN CAPPING PROTEIN ALPHA-1 SUBUNIT	SOLUBLE	0	0
CYTOSKELETON	74410	74410	74355722	F-ACTIN CAPPING PROTEIN ALPHA-2 SUBUNIT	SOLUBLE	0	0
CYTOSKELETON	231012	231012	34869526	FILAMIN B, BETA	SOLUBLE	0	0

CYTOSKELETON	282403	282403	34881882	FILAMIN, ALPHA	SOLUBLE	0	0
CYTOSKELETON	148966	111660	111660	GLIA MATURATION FACTOR BETA	SOLUBLE	0	0
CYTOSKELETON	26394	26394	62657131	GLIAL FIBRILLARY ACIDIC PROTEIN ALPHA	SOLUBLE	0	0
CYTOSKELETON	220378	220378	34879033	GOLGI-ASSOCIATED MICROTUBULE-BINDING PROTEIN	SOLUBLE	0	0
CYTOSKELETON	266483	266483	34874048	HOOK3: HOOK3 PROTEIN	SOLUBLE	0	0
CYTOSKELETON	166145	166145	31745148	KINESIN FAMILY PROTEIN 13A	SOLUBLE	0	0
CYTOSKELETON	19687	19687	71122452	KINESIN-LIKE PROTEIN KIF15	SOLUBLE	0	0
CYTOSKELETON	272629	272629	34875362	LIM AND SH3 DOMAIN PROTEIN 1	SOLUBLE	0	0
CYTOSKELETON	264572	264572	34866431	LYMPHOCYTE CYTOSOLIC PROTEIN 1	SOLUBLE	0	0
CYTOSKELETON	71715	71715	32363196	MICROTUBULE-ASSOCIATED PROTEIN 4	SOLUBLE	0	0
CYTOSKELETON	263071	263071	34872934	MOESIN	SOLUBLE	0	3
CYTOSKELETON	75000	75000	967249	MYOSIN HEAD DOMAIN CONTAINING 1	SOLUBLE	0	0
CYTOSKELETON	78051	78051	7381235	MYOSIN HEAVY CHAIN, NONMUSCLE TYPE A	SOLUBLE	0	0
CYTOSKELETON	6153	6153	480659	MYOSIN HEAVY CHAIN, NONMUSCLE TYPE B	SOLUBLE	0	0
CYTOSKELETON	63042	63042	56733	MYOSIN I HEAVY CHAIN	SOLUBLE	0	0
CYTOSKELETON	75002	75002	6981242	MYOSIN IB	SOLUBLE	0	0
CYTOSKELETON	105842	105842	693995	MYOSIN ID	SOLUBLE	0	0
CYTOSKELETON	69375	69375	34862212	MYOSIN IE	SOLUBLE	0	0
CYTOSKELETON	69379	69379	68533710	MYOSIN LIGHT CHAIN ALKALI, SMOOTH-MUSCLE ISOFORM	SOLUBLE	0	0
CYTOSKELETON	217296	217296	23618899	MYOSIN REGULATORY LIGHT CHAIN	SOLUBLE	0	0
CYTOSKELETON	78016	78016	13925523	MYOSIN VIIA	SOLUBLE	0	0
CYTOSKELETON	11249	11249	111999	NA(+)/H(+) EXCHANGE REGULATORY CO-FACTOR NHE-RF2	SOLUBLE	0	0
CYTOSKELETON	3674	3674	6978589	NEURONAL MYOSIN HEAVY CHAIN	SOLUBLE	0	0
CYTOSKELETON	193681	193681	34856482	NON-MUSCLE CALDESMON	SOLUBLE	0	0
CYTOSKELETON	37204	37204	1497985	P120 CATENIN ISOFORM 2B	SOLUBLE	0	0
CYTOSKELETON	207221	207221	34865784	PLAKOGLOBIN	SOLUBLE	0	0
CYTOSKELETON	699022	699022	40849904	PLASTIN 1 (I ISOFORM)	SOLUBLE	0	0
CYTOSKELETON	60726	60726	51702769	PLECTIN 10	SOLUBLE	0	0
CYTOSKELETON	3616	3616	7513996	PROFILIN I	SOLUBLE	0	0
CYTOSKELETON	244260	244260	34866518	S-AFADIN	SOLUBLE	0	0
CYTOSKELETON	213091	213091	34876595	SIMILAR TO ACTIN MONOMER-BINDING PROTEIN	SOLUBLE	0	0
CYTOSKELETON	258471	258471	34856264	SIMILAR TO ALPHA TUBULIN	SOLUBLE	0	0
CYTOSKELETON	219221	219221	34871187	SIMILAR TO ALPHA-2 CATENIN	SOLUBLE	0	0
CYTOSKELETON	190168	190168	34866568	SIMILAR TO BETA ACTIN	SOLUBLE	0	0
CYTOSKELETON	233230	233230	34874618	SIMILAR TO BETA1-SYNTROPHIN	SOLUBLE	0	0
CYTOSKELETON	192125	192125	34863346	SIMILAR TO BULLOUS PEMPFIGOID ANTIGEN 1-B	SOLUBLE	0	0
CYTOSKELETON	241018	241018	34860597	SIMILAR TO CENTROMERE/KINETOCHORE PROTEIN ZW10	SOLUBLE	0	0
CYTOSKELETON	279256	279256	34863056	HOMOLOG	SOLUBLE	0	0
CYTOSKELETON	195164	195164	27722175	SIMILAR TO CENTROMERIC PROTEIN E (CENP-E PROTEIN)	SOLUBLE	0	0
CYTOSKELETON	265199	265199	34877667	SIMILAR TO DYSTROBREVIN B	SOLUBLE	0	0
CYTOSKELETON	265212	265212	34872331	SIMILAR TO HYPOTHETICAL PROTEIN CGI-99	SOLUBLE	0	4
CYTOSKELETON	261550	261550	34865321	SIMILAR TO KINESIN FAMILY PROTEIN KIF1A	SOLUBLE	0	0
CYTOSKELETON	276942	276942	34877348	SIMILAR TO KINETOCHORE-ASSOCIATED PROTEIN 1	SOLUBLE	0	1
CYTOSKELETON	253969	253969	34866628	(ROUGH DEAL HOMOLOG) (HROD) (HSROD) (ROD)	SOLUBLE	0	0
CYTOSKELETON	268838	268838	34868946	SIMILAR TO MYOSIN VI	SOLUBLE	0	0
CYTOSKELETON	194947	194947	34878017	SIMILAR TO NEBULETTE (ACTIN-BINDING Z-DISK PROTEIN)	SOLUBLE	0	0
CYTOSKELETON	253969	253969	34866628	SIMILAR TO VILLIN-LIKE PROTEIN	SOLUBLE	0	0
CYTOSKELETON	268838	268838	34868946	SIMILAR TO VINCULIN (METAVINCULIN)	SOLUBLE	0	0
CYTOSKELETON	194947	194947	34878017	SIMILAR TO ACTIN-RELATED PROTEIN 2	SOLUBLE	0	0

CYTOSKELETON	3340	3340	62644670	SPECTRIN ALPHA CHAIN, BRAIN	SOLUBLE	0	0
CYTOSKELETON	3158	3158	3550975	SPECTRIN BETA-II CHAIN, BRAIN 2	SOLUBLE	0	0
CYTOSKELETON	300121	300121	34879632	SPECTRIN BETA-II CHAIN, BRAIN 1 (SPECTRIN, NON-ERYTHROID BETA CHAIN 1) (BETA-II SPECTRIN) (FODRIN BETA CHAIN)	SOLUBLE	0	0
CYTOSKELETON	299358	299358	72255527	STOMATIN-LIKE PROTEIN 2	SOLUBLE	0	5
CYTOSKELETON	168831	168831	59797636	SUPPRESSOR OF PROFILIN/P41 OF ACTIN-RELATED COMPLEX 2/3	SOLUBLE	0	0
CYTOSKELETON	136274	136274	57381	T-PLASTIN	SOLUBLE	0	0
CYTOSKELETON	230030	230030	34867875	TALIN	SOLUBLE	0	1
CYTOSKELETON	199727	199727	34864297	TALIN 2	SOLUBLE	0	0
CYTOSKELETON	261414	261414	34864364	TROPOMODULIN 3	SOLUBLE	0	0
CYTOSKELETON	11396	11396	112443	TROPOMYOSIN ALPHA	SOLUBLE	0	0
CYTOSKELETON	44422	44422	763182	TROPOMYOSIN ALPHA 4 CHAIN	SOLUBLE	0	0
CYTOSKELETON	93198	93198	null	TROPOMYOSIN ISOFORM 6	SOLUBLE	0	0
CYTOSKELETON	31436	31436	55741524	TUBULIN ALPHA 4	SOLUBLE	0	0
CYTOSKELETON	298819	298819	34868254	TUBULIN ALPHA 6	SOLUBLE	0	0
CYTOSKELETON	270901	270901	40018568	TUBULIN BETA 5	SOLUBLE	0	0
CYTOSKELETON	82925	82925	57480	VIMENTIN	SOLUBLE	0	0
CYTOSKELETON	222802	222802	34871786	WAVE2	SOLUBLE	0	0
CYTOSKELETON	210117	210117	34860973	ZETA-CRYSTALLIN	SOLUBLE	0	0
DETOXIFICATION	290771	290771	34869959	24-DEHYDROCHOLESTEROL REDUCTASE	MEMBRANE	0	0
DETOXIFICATION	86059	86059	81861101	3 BETA-HYDROXY-DELTA 5-C27-STEROID OXIDOREDUCTASE	MEMBRANE	0	0
DETOXIFICATION	140632	140632	8388884	3-BETA-HYDROXYSTEROID-DELTA(8), DELTA(7)-ISOMERASE	MEMBRANE	0	0
DETOXIFICATION	43740	43740	25742565	3-OXO-5-ALPHA-STEROID 4-DEHYDROGENASE 1	MEMBRANE	0	0
DETOXIFICATION	9067	9067	81882109	7-DEHYDROCHOLESTEROL REDUCTASE	MEMBRANE	0	0
DETOXIFICATION	78151	78151	399362	ALDEHYDE DEHYDROGENASE FAMILY 3 MEMBER A2	MEMBRANE	0	5
DETOXIFICATION	5958	5958	8347733	ARYLACETAMIDE DEACETYLASE	MEMBRANE	0	0
DETOXIFICATION	807	807	38649308	C-4 METHYL STEROL OXIDASE	MEMBRANE	0	0
DETOXIFICATION	3890	3890	6980893	CYTOCHROME B5	MEMBRANE	0	0
DETOXIFICATION	3722	3722	940818	CYTOCHROME P450 17A1	MEMBRANE	0	0
DETOXIFICATION	3724	3724	203832	CYTOCHROME P450 1A2	MEMBRANE	0	5
DETOXIFICATION	337678	337678	40786491	CYTOCHROME P450 20A1	MEMBRANE	0	0
DETOXIFICATION	63757	63757	62655087	CYTOCHROME P450 27A1	MEMBRANE	0	2
DETOXIFICATION	126566	126566	51980506	CYTOCHROME P450 2A1	MEMBRANE	0	0
DETOXIFICATION	3727	3727	6978741	CYTOCHROME P450 2A2	MEMBRANE	0	0
DETOXIFICATION	13404	13404	34855371	CYTOCHROME P450 2B2	MEMBRANE	0	0
DETOXIFICATION	63770	63770	28849945	CYTOCHROME P450 2B3	MEMBRANE	15	28
DETOXIFICATION	126560	126560	203695	CYTOCHROME P450 2C11	MEMBRANE	0	11
DETOXIFICATION	3729	3729	59808903	CYTOCHROME P450 2C12	MEMBRANE	0	0
DETOXIFICATION	63782	63782	205935	CYTOCHROME P450 2C13	MEMBRANE	0	5.5
DETOXIFICATION	260440	260440	34862902	CYTOCHROME P450 2C18	MEMBRANE	0	0
DETOXIFICATION	63786	63786	58827	CYTOCHROME P450 2C22	MEMBRANE	0	1
DETOXIFICATION	72763	72763	6166042	CYTOCHROME P450 2C23	MEMBRANE	2	16
DETOXIFICATION	63778	63778	231660 253344	CYTOCHROME P450 2C6	MEMBRANE	0	1.7
DETOXIFICATION	45873	45873	482947	CYTOCHROME P450 2C7	MEMBRANE	1	4.8
DETOXIFICATION	126576	126576	203803	CYTOCHROME P450 2D1	MEMBRANE	0	0
DETOXIFICATION	63788	63788	57812	CYTOCHROME P450 2D2	MEMBRANE	0	6.4
DETOXIFICATION	103927	103927	58477687	CYTOCHROME P450 2D3	MEMBRANE	0	1.6
DETOXIFICATION	63790	63790	57818	CYTOCHROME P450 2D5	MEMBRANE	0	0
DETOXIFICATION	21526	21526	51980637	CYTOCHROME P450 2E1	MEMBRANE	0	1

DETOXIFICATION	125135	125135	59803108	CYTOCHROME P450 2J3	MEMBRANE	0	0
DETOXIFICATION	161231	161231	19705467	CYTOCHROME P450 2T1	MEMBRANE	0	0
DETOXIFICATION	63758	3731 63758	27465619	CYTOCHROME P450 3A1	MEMBRANE	0	0
DETOXIFICATION	104898	104898	5921916	CYTOCHROME P450 3A18	MEMBRANE	0	5.8333
DETOXIFICATION	87425	87425	515799	CYTOCHROME P450 3A2	MEMBRANE	0	1.1667
DETOXIFICATION	51420	51420	46048525	CYTOCHROME P450 4A1	MEMBRANE	0	0
DETOXIFICATION	63760	63760	71051108	CYTOCHROME P450 4A2	MEMBRANE	0	6
DETOXIFICATION	21524	21524	28461155	CYTOCHROME P450 4A3	MEMBRANE	0	0
DETOXIFICATION	78089	78089	203757	CYTOCHROME P450 4A8	MEMBRANE	0	0
DETOXIFICATION	134595	134595	9665225	CYTOCHROME P450 4F1	MEMBRANE	0	0
DETOXIFICATION	80281	80281	27465575	CYTOCHROME P450 4F4	MEMBRANE	0	0
DETOXIFICATION	250367	250367	34878473	CYTOCHROME P450 4V3	MEMBRANE	0	0
DETOXIFICATION	3732	3732	6978751	CYTOCHROME P450 51A1	MEMBRANE	0	0
DETOXIFICATION	129969	75741 129969	4587057	CYTOCHROME P450 8B1	MEMBRANE	0	0
DETOXIFICATION	201379	201379	34874781	CYTOCHROME P450 NA1	MEMBRANE	0	0
DETOXIFICATION	283602	283602	34861496	DELTA(14)-STEROL REDUCTASE (C-14 STEROL REDUCTASE) (STEROL C14-REDUCTASE) (DELTA14-SR) (TRANSMEMBRANE 7 SUPERFAMILY MEMBER 2) (ANOTHER NEW GENE 1) (PUTATIVE STEROL REDUCTASE SR-1)	MEMBRANE	0	0
DETOXIFICATION	17081	17081	77539448	EPOXIDE HYDROLASE	MEMBRANE	0	0
DETOXIFICATION	68349	68349	3334165	ESTRADIOL 17 BETA-DEHYDROGENASE 2	MEMBRANE	0	0
DETOXIFICATION	708	708	8393576	ESTRADIOL 17 BETA-DEHYDROGENASE 7	MEMBRANE	0	0
DETOXIFICATION	187298	187298	62286643	FLAVIN-CONTAINING MONOOXYGENASE 5	MEMBRANE	0	4
DETOXIFICATION	3930	3930	6981032	HEME OXYGENASE 1	MEMBRANE	0	0
DETOXIFICATION	68743	68743	501035	HEME OXYGENASE 2	MEMBRANE	0	0
DETOXIFICATION	19913	19913	6647578	MEMBRANE ASSOCIATED PROGESTERONE RECEPTOR COMPONENT 1	MEMBRANE	0	2
DETOXIFICATION	204220	204220	27732829	MEMBRANE PROGESTIN RECEPTOR ALPHA	MEMBRANE	0	0
DETOXIFICATION	28295	28295	38649092	MICROSOMAL GLUTATHIONE S-TRANSFERASE 1	MEMBRANE	3	4
DETOXIFICATION	69488	69488 123616	38303959	NADH-CYTOCHROME B5 REDUCTASE	MEMBRANE	0	0
DETOXIFICATION	78074	44210 78074	66118	NADPH-CYTOCHROME P450 REDUCTASE	MEMBRANE	0	3
DETOXIFICATION	102628	102628	27545384	OXIDATIVE 17 BETA HYDROXYSTEROID DEHYDROGENASE TYPE 6	MEMBRANE	0	1
DETOXIFICATION	274611	274611	62900631	PROGESTERONE RECEPTOR MEMBRANE COMPONENT 2	MEMBRANE	0	0
DETOXIFICATION	227390	227390	31324556	RETINOL DEHYDROGENASE 10	MEMBRANE	0	0
DETOXIFICATION	238730	238730	62650915	RETINOL DEHYDROGENASE 11 (PREDICTED)	MEMBRANE	0	0
DETOXIFICATION	105752	35165 105752	841197	RETINOL DEHYDROGENASE TYPE I	MEMBRANE	3	10.6667
DETOXIFICATION	285736	285736	27690924	SIMILAR TO MICROSOMAL GLUTATHIONE S-TRANSFERASE 2 (MICROSOMAL GST-2) (MICROSOMAL GST-II)	MEMBRANE	0	0
DETOXIFICATION	164232	164232	27678076	SIMILAR TO MICROSOMAL GLUTATHIONE S-TRANSFERASE 3	MEMBRANE	0	0
DETOXIFICATION	337296	337296	81892292	SMOOTH MUSCLE-SPECIFIC 17BETA-HYDROXYSTEROID DEHYDROGENASE TYPE 3	MEMBRANE	0	0
DETOXIFICATION	137571	137571	83943354	SQUALENE MONOOXYGENASE	MEMBRANE	0	0
DETOXIFICATION	75108	75108	6981598	STERYL-SULFATASE	MEMBRANE	0	0
DETOXIFICATION	43597	43597	695162	UDP-GLUCURONOSYLTRANSFERASE 1A1	MEMBRANE	1.25	8.4
DETOXIFICATION	53066	53066	18308168	UDP-GLUCURONOSYLTRANSFERASE 1A5	MEMBRANE	0	2.8
DETOXIFICATION	205347	53068 205347	89276780	UDP-GLUCURONOSYLTRANSFERASE 1A6	MEMBRANE	0	8.4
DETOXIFICATION	53069	53069	18308176	UDP-GLUCURONOSYLTRANSFERASE 1A7	MEMBRANE	0	2.8
DETOXIFICATION	31600	31600	27545358	UDP-GLUCURONOSYLTRANSFERASE 2B1	MEMBRANE	0	1.05

DETOXIFICATION	80303	80303 127236 221298	549157	UDP-GLUCURONOSYL TRANSFERASE 2B12	MEMBRANE	1.25	13.65
DETOXIFICATION	78055	78055 146466	207583	UDP-GLUCURONOSYL TRANSFERASE 2B2	MEMBRANE	2.25	6.8125
DETOXIFICATION	31602	31602 84217	31543923	UDP-GLUCURONOSYL TRANSFERASE 2B3	MEMBRANE	0	5.4511
DETOXIFICATION	31603	31603	55925581	UDP-GLUCURONOSYL TRANSFERASE 2B5	MEMBRANE	2.25	12.5364
DETOXIFICATION	217594	217594	34876789	UDP-GLUCURONOSYL TRANSFERASE GTNA1	MEMBRANE	0	2.1
DETOXIFICATION	169892	169892	27694215	UDP-GLUCURONOSYL TRANSFERASE GTNA2	MEMBRANE	0	3
DETOXIFICATION	37206	37206	13591981	2,3-OXIDOSQUALENE/LANOSTEROL CYCLASE	SOLUBLE	0	0
DETOXIFICATION	3937	3937	6981050	3 BETA-HYDROXY STEROID DEHYDROGENASE TYPE III	SOLUBLE	0	0
DETOXIFICATION	19230	19230	6708142	3-ALPHA-HYDROXY STEROID DEHYDROGENASE	SOLUBLE	0	3
DETOXIFICATION	83190	83190	7387724	3-HYDROXYACYL-COA DEHYDROGENASE TYPE II (TYPE II HADH) (ENDOPLASMIC RETICULUM-ASSOCIATED AMYLOID BETA-PEPTIDE BINDING PROTEIN)	SOLUBLE	0	6
DETOXIFICATION	23758	23758	456303	3-OXO-5-BETA-STEROID 4-DEHYDROGENASE	SOLUBLE	0	3
DETOXIFICATION	100616	100616	433611	AFLATOXIN B1 ALDEHYDE REDUCTASE MEMBER 1	SOLUBLE	0	1
DETOXIFICATION	161251	161251	6815049	AFLATOXIN B1 ALDEHYDE REDUCTASE MEMBER 2	SOLUBLE	0	0
DETOXIFICATION	302704	302704	34862428	ALDEHYDE DEHYDROGENASE 1 FAMILY, MEMBER L2	SOLUBLE	0	0
DETOXIFICATION	245155	245155	34879551	ALDEHYDE DEHYDROGENASE 7A1	SOLUBLE	0	0
DETOXIFICATION	72216	72216	38494348	ALDEHYDE DEHYDROGENASE FAMILY 1 MEMBER A1	SOLUBLE	0	0
DETOXIFICATION	95119	95119	4324710	ALDEHYDE OXIDASE	SOLUBLE	0	0
DETOXIFICATION	27636	27636	81871478	ALL-TRANS-13,14-DIHYDRORETINOL SATURASE	SOLUBLE	0	0
DETOXIFICATION	69784	69784	55761	ARYL SULFOTRANSFERASE	SOLUBLE	0	0
DETOXIFICATION	30001	30001	9963930	BILE ACID COA LIGASE	SOLUBLE	0	8
DETOXIFICATION	54374	54374	285208	BILIVERDIN REDUCTASE A PRECURSOR	SOLUBLE	0	1
DETOXIFICATION	204593	204593	34875339	BIPHENYL HYDROLASE-LIKE (SERINE HYDROLASE; BREAST EPITHELIAL MUCIN-ASSOCIATED ANTIGEN)	SOLUBLE	0	0
DETOXIFICATION	166315	166315	55562775	CARBONYL REDUCTASE 4	SOLUBLE	0	0
DETOXIFICATION	43686	43686	2506388	CARBOXYL ESTERASE 1	SOLUBLE	5.6667	13.0606
DETOXIFICATION	84186	42034 84186 112141 146478 196665	92053	CARBOXYL ESTERASE 10	SOLUBLE	56.8926	67.8496
DETOXIFICATION	12999	12999 13000	56541525	CARBOXYL ESTERASE 2	SOLUBLE	1.1419	3
DETOXIFICATION	78070	78070	550147	CARBOXYL ESTERASE 3	SOLUBLE	4.0305	32.6337
DETOXIFICATION	77793	77793 105537	550418	CARBOXYL ESTERASE 4	SOLUBLE	35.2136	47.8318
DETOXIFICATION	10945	10945 123735 158916	562010	CARBOXYL ESTERASE B-1	SOLUBLE	10.061	25.6242
DETOXIFICATION	227817	227817	27658990	CARBOXYL ESTERASE ESNA1	SOLUBLE	0	0
DETOXIFICATION	182047	182047	2641992	CARBOXYL ESTERASE ESNA2	SOLUBLE	0	0
DETOXIFICATION	157137	157137	21426807	CARBOXYL ESTERASE ESNA3	SOLUBLE	11.9936	20
DETOXIFICATION	3708	3708	6978681	CATECHOL O-METHYL TRANSFERASE; MEMBRANE-BOUND FORM	SOLUBLE	0	0
DETOXIFICATION	190227	190227	34862810	CYTOCHROME P450 NA2	SOLUBLE	0	0
DETOXIFICATION	214468	214468	34865689	DEHYDROGENASE/REDUCTASE (SDR FAMILY) MEMBER 7	SOLUBLE	0	0
DETOXIFICATION	3622	3622	6978483	DELTA-AMINOLEVULINIC ACID DEHYDRATASE	SOLUBLE	0	1
DETOXIFICATION	339248	339248	78099773	DIMETHYLANILINE MONOOXYGENASE [N-OXIDE FORMING]	MEMBRANE	0	3
DETOXIFICATION	74919	74919	3915863	DOPA/TYROSINE SULFOTRANSFERASE	SOLUBLE	0	0
DETOXIFICATION	75106	75106 109266	6981594	ESTROGEN SULFOTRANSFERASE	SOLUBLE	0	1
DETOXIFICATION	246480	246480	62659523	FLAVIN-CONTAINING MONOOXYGENASE 3	SOLUBLE	0	8
DETOXIFICATION	28283	28283	121668	GLUTATHIONE PEROXIDASE	SOLUBLE	0	1
DETOXIFICATION	111659	111659	56265	GLUTATHIONE S-TRANSFERASE 5	SOLUBLE	0	0
DETOXIFICATION	28290	28290	27720723	GLUTATHIONE S-TRANSFERASE 8	SOLUBLE	0	0
DETOXIFICATION	78049	78049	576438	GLUTATHIONE S-TRANSFERASE ALPHA	SOLUBLE	0	0

DETOXIFICATION	28297	28297	56336	GLUTATHIONE S-TRANSFERASE P	SOLUBLE	0	0
DETOXIFICATION	146667	28289 51474 146667	66611	GLUTATHIONE S-TRANSFERASE YA-1	SOLUBLE	3	11
DETOXIFICATION	126642	126642 164858	204503	GLUTATHIONE S-TRANSFERASE YB-1 SUBUNIT	SOLUBLE	3	12 3333
DETOXIFICATION	185727	28291 40315 185727	33356830	GLUTATHIONE S-TRANSFERASE YB-2 SUBUNIT	SOLUBLE	0	8.6667
DETOXIFICATION	33791	33791	529588	GLUTATHIONE S-TRANSFERASE YB-3	SOLUBLE	0	0
DETOXIFICATION	3914	3914	769703	GLUTATHIONE S-TRANSFERASE YRS-YRS (GST 12-12)	SOLUBLE	0	0
				(GLUTATHIONE S-TRANSFERASE SUBUNIT 12) (GST CLASS THETA)			
DETOXIFICATION	84221	84221	92300	GLUTATHIONE TRANSFERASE (EC 2.5.1.18) PSI	SOLUBLE	0	0
DETOXIFICATION	55147	55147	12585231	GLUTATHIONE TRANSFERASE OMEGA 1	SOLUBLE	0	0
DETOXIFICATION	301041	301041	47087119	HYDROXYSTEROID (17-BETA) DEHYDROGENASE 8	SOLUBLE	0	0
DETOXIFICATION	95697	95697	78214365	HYDROXYSTEROID 11-BETA DEHYDROGENASE 1	SOLUBLE	14	35
DETOXIFICATION	69809	69809 148916 157070	32964821	HYDROXYSTEROID SULFOTRANSFERASE	SOLUBLE	0	0
DETOXIFICATION	287183	287183	34876593	LIVER REGENERATION-RELATED PROTEIN	SOLUBLE	0	0
DETOXIFICATION	36062	36062	11133293	MALEYLACETOACETATE ISOMERASE	SOLUBLE	0	0
DETOXIFICATION	1678	1678	6012071	NADP-DEPENDENT LEUKOTRIENE B4 12-HYDROXYDEHYDROGENASE	SOLUBLE	0	0
DETOXIFICATION	249119	249119	34876322	PROTEIN RAKC	SOLUBLE	0	0
DETOXIFICATION	315286	315286	34865424	RETINAL SHORT-CHAIN DEHYDROGENASE/REDUCTASE 4	SOLUBLE	0	0
DETOXIFICATION	80376	80376	50926989	RETINOL DEHYDROGENASE TYPE II	SOLUBLE	0	5.3333
DETOXIFICATION	268103	268103	34866289	SHORT CHAIN DEHYDROGENASE REDUCTASE 9	SOLUBLE	0	0
DETOXIFICATION	197702	197702	34852829	SIMILAR TO ALDH8A1 PROTEIN	SOLUBLE	0	1
DETOXIFICATION	272510	272510	34855391	SIMILAR TO BILIVERDIN REDUCTASE B (FLAVIN REDUCTASE (NADPH))	SOLUBLE	0	0
DETOXIFICATION	225794	225794	34852398	SIMILAR TO GLUTATHIONE S-TRANSFERASE, THETA 3	SOLUBLE	0	0
DETOXIFICATION	294993	294993	34872444	SIMILAR TO RETINAL SHORT-CHAIN DEHYDROGENASE/REDUCTASE	SOLUBLE	0	0
DETOXIFICATION	44446	44446	5524747	UROPORHYRINOGEN DECARBOXYLASE	SOLUBLE	0	0
GTPASE	20922	20922	57033190	ADP-RIBOSYLATION FACTOR 3	MEMBRANE	0	0
GTPASE	10609	10609	543844	ADP-RIBOSYLATION FACTOR 4	MEMBRANE	0	0
GTPASE	10610	10610	56388751	ADP-RIBOSYLATION FACTOR 5	MEMBRANE	0	0
GTPASE	120856	120856	60552411	ADP-RIBOSYLATION FACTOR 6	MEMBRANE	0	0
GTPASE	23396	23396	728889	ADP-RIBOSYLATION FACTOR-LIKE 1	MEMBRANE	0	0
GTPASE	52078	52078	2492928	ARF-RELATED PROTEIN	MEMBRANE	0	0
GTPASE	85184	85184	61889112	CDC42	MEMBRANE	0	0
GTPASE	169821	169821	46577668	GTP-BINDING PROTEIN RAB13	MEMBRANE	0	0
GTPASE	223700	223700	34870762	INTERFERON GAMMA INDUCED GTPASE	MEMBRANE	0	0
GTPASE	78175	78175	56404679	PRENYLATED RAB ACCEPTOR 1	MEMBRANE	0	0
GTPASE	257746	257746	34856057	R-RAS (P23)	MEMBRANE	0	0
GTPASE	86161	86161	61740635	R-RAS2	MEMBRANE	0	0
GTPASE	44313	44313	47125439	RAB-RELATED GTP-BINDING PROTEIN	MEMBRANE	0	0
GTPASE	44648	44648	420269	RAB10	MEMBRANE	0	1
GTPASE	243905	243905	34869196	RAB13	MEMBRANE	0	0
GTPASE	34567	34567	46577632	RAB14	MEMBRANE	0	0
GTPASE	161691	161691	81909560	RAB18	MEMBRANE	0	0
GTPASE	21122	21122	51338716	RAB1A	MEMBRANE	0	0
GTPASE	166705	84231 166705	56605816	RAB1B	MEMBRANE	0	0
GTPASE	240940	240940	34879665	RAB20	MEMBRANE	0	0
GTPASE	311263	311263	51948448	RAB21	MEMBRANE	0	0
GTPASE	250158	250158	34873657	RAB24	MEMBRANE	0	0
GTPASE	78145	78145	92340	RAB2A	MEMBRANE	0	0

GTPASE	163993	163993	83415090	RAB2B	MEMBRANE	0	0
GTPASE	64372	64372	27678162	RAB30	MEMBRANE	0	0
GTPASE	281147	281147	34857303	RAB33B	MEMBRANE	0	0
GTPASE	177419	177419	3309068	RAB5	MEMBRANE	0	0
GTPASE	218278	218278	34862219	RAB5A	MEMBRANE	0	0
GTPASE	161834	161834	27689505	RAB5C	MEMBRANE	0	0
GTPASE	290450	290450	34859460	RAB6	MEMBRANE	0	0
GTPASE	111003	111003	9837359	RAB7	MEMBRANE	0	0
GTPASE	43492	43492	2500066	RAB8B	MEMBRANE	0	0
GTPASE	60413	60413	16758200	RAB9A	MEMBRANE	0	0
GTPASE	111212	111212	54607147	RAC1	MEMBRANE	0	0
GTPASE	8458	8458	56605840	RAC2	MEMBRANE	0	0
GTPASE	4747	4747	54114993	RAP1A	MEMBRANE	0	0
GTPASE	130852	130852	539995	RAP1B	MEMBRANE	0	0
GTPASE	197399	197399	34881637	RAP2C	MEMBRANE	0	0
GTPASE	76408	76408	47605935	RHOA	MEMBRANE	0	0
GTPASE	160782	119421	160782	SAR1 HOMOLOG	MEMBRANE	0	0
GTPASE	140635	140635	51858574	SEPTIN 2	MEMBRANE	0	0
GTPASE	167832	167832	9789715	SEPTIN 7	MEMBRANE	0	0
GTPASE	160756	160756	27670133	SIMILAR TO INTERFERON-G INDUCED GTPASE	MEMBRANE	0	0
GTPASE	244814	237237	244814	SIMILAR TO INTERFERON-INDUCIBLE GTPASE	MEMBRANE	0	0
GTPASE	197696	197696	34853552	SIMILAR TO RAS GTPASE-ACTIVATING-LIKE PROTEIN	MEMBRANE	0	0
				IQGAP2			
GTPASE	204932	204932	34876531	SIMILAR TO SEPTIN 6	MEMBRANE	0	0
GTPASE	227072	227072	81883039	YIP1	MEMBRANE	0	0
GTPASE	42770	42770	9910340	CENTAURIN-ALPHA2 PROTEIN	SOLUBLE	0	0
GTPASE	71226	71226	57528300	DEVELOPMENTALLY REGULATED GTP-BINDING PROTEIN 1	SOLUBLE	0	0
GTPASE	76611	76611	51338593	GTPASE	SOLUBLE	0	0
GTPASE	71624	71624	495534	H-RAS-1/P21	SOLUBLE	0	0
GTPASE	223925	223925	62656738	H5	SOLUBLE	0	0
GTPASE	35585	35585	62900797	RAB35	SOLUBLE	0	0
GTPASE	37231	37231	54038996	RAS-RELATED PROTEIN RAL-A	SOLUBLE	0	0
GTPASE	113828	113828	51338594	RHO B	SOLUBLE	0	0
GTPASE	2120	2120	2865596	RHO-GEF 7	SOLUBLE	0	0
GTPASE	93024	93024	82524300	RHO-RELATED GTP-BINDING PROTEIN RHOG	SOLUBLE	0	0
GTPASE	195351	195351	34877253	SIMILAR TO RAS SUPPRESSOR PROTEIN 1 (RSU-1) (RSP-1)	SOLUBLE	0	0
LIKELY CONTAMINANTS	301880	301880	71682170	CYTOKERATIN 17	SOLUBLE	0	0
LIKELY CONTAMINANTS	22440	22440	2443314	KERATIN 14	SOLUBLE	0	0
LIKELY CONTAMINANTS	108078	108078	587518	KERATIN 18	SOLUBLE	0	0
LIKELY CONTAMINANTS	318877	318877	81170669	KERATIN 5	SOLUBLE	0	0
LIKELY CONTAMINANTS	66467	66467	554464	KERATIN K6	SOLUBLE	0	3
LIKELY CONTAMINANTS	262043	262043	34868202	KERATIN TYPE II, HAIR (B4) - MOUSE	SOLUBLE	0	0
LIKELY CONTAMINANTS	11221	11221	55956	KERATIN, TYPE II CYTOSKELETAL 1 (CYTOKERATIN 1) (67	SOLUBLE	0	0
				KDA CYTOKERATIN)			
LIKELY CONTAMINANTS	67836	67836	67678416	KERATIN, TYPE II CYTOSKELETAL 8	SOLUBLE	0	0
LIKELY CONTAMINANTS	202236	202236	34860580	SIMILAR TO ENDO B CYTOKERATIN	SOLUBLE	0	0
LIKELY CONTAMINANTS	222258	222258	46485029	SIMILAR TO KERATIN, TYPE II CYTOSKELETAL 5	SOLUBLE	0	0
				(CYTOKERATIN 5) (K5) (CK 5) (58 KDA CYTOKERATIN)			
LIKELY CONTAMINANTS	230035	191456	230035	TYPE I HAIR KERATIN	SOLUBLE	0	0
LIKELY CONTAMINANTS	161849	161849	57012446	TYPE I KERATIN KA22	SOLUBLE	0	0
LYSOSOME	144356	144356	8392842	LYSOSOMAL ACID PHOSPHATASE	MEMBRANE	0	0

LYSOSOME	305737	305737	34874388	LYSOSOMAL APYRASE-LIKE 1	LYSOSOMAL	0	0
LYSOSOME	3967	3967	6981144	LYSOSOMAL MEMBRANE GLYCOPROTEIN 1; LYSOSOMAL ASSOCIATED MEMBRANE PROTEIN 1 (120 KDA)	MEMBRANE	0	0
LYSOSOME	44157	44157	205169	LYSOSOMAL MEMBRANE GLYCOPROTEIN-TYPE B	MEMBRANE	0	0
LYSOSOME	157248	157248	38197654	LYSOSOME MEMBRANE PROTEIN II	MEMBRANE	0	0
LYSOSOME	255150	255150	34851575	ATP-BINDING CASSETTE SUB-FAMILY E MEMBER 1	SOLUBLE	0	0
LYSOSOME	264901	264901	34869154	ATPASE, H ⁺ -TRANSPORTING, V1 SUBUNIT A, ISOFORM 1	SOLUBLE	0	0
LYSOSOME	261145	261145	38454230	ATPASE, H ⁺ -TRANSPORTING, V1 SUBUNIT E ISOFORM 1	SOLUBLE	0	0
LYSOSOME	21055	21055	758260	BETA-GLUCURONIDASE	SOLUBLE	0	2
LYSOSOME	19199	19199	1942646	CATHEPSIN B	SOLUBLE	0	1
LYSOSOME	51414	51414 79044	8393218	CATHEPSIN C	SOLUBLE	0	3
LYSOSOME	141570	141570	55882	CATHEPSIN D	SOLUBLE	0	0
LYSOSOME	3719	3719	6978721	CATHEPSIN H	SOLUBLE	0	0
LYSOSOME	141572	141572	38648869	CATHEPSIN L	SOLUBLE	0	1
LYSOSOME	160297	160297	60688149	CATHEPSIN Z	SOLUBLE	0	0
LYSOSOME	60505	60505	81867389	CERAMIDASE	SOLUBLE	0	1
LYSOSOME	157436	157436	27229316	GM2 ACTIVATOR PROTEIN	SOLUBLE	0	0
LYSOSOME	12815	12815	27692916	LATE ENDOSOMAL/LYSOSOMAL MP1 INTERACTING PROTEIN	SOLUBLE	0	0
LYSOSOME	72321	72321	20138456	LYSOSOMAL ACID LIPASE/CHOLESTERYL ESTER HYDROLASE	SOLUBLE	0	3
LYSOSOME	39196	39196	7428180	LYSOZYME C, TYPE 1 PRECURSOR	SOLUBLE	0	0
LYSOSOME	247133	247133	34860773	PROTECTIVE PROTEIN	SOLUBLE	0	1
LYSOSOME	55382	55382	58865424	PROTON-TRANSLOCATING ATPASE D SUBUNIT ISOFORM D1	SOLUBLE	0	1
LYSOSOME	266171	266171	27681673	SIMILAR TO CATHEPSIN 1 PRECURSOR	SOLUBLE	0	0
LYSOSOME	274163	274163	62641689	T-CELL, IMMUNE REGULATOR 1, ATPASE, H ⁺ -TRANSPORTING, LYSOSOMAL V0 PROTEIN A ISOFORM 3	SOLUBLE	0	0
LYSOSOME	160475	160475	40786463	VACUOLAR ATPASE	SOLUBLE	0	0
LYSOSOME	55432	55432	55716047	VACUOLAR ATP SYNTHASE SUBUNIT B, BRAIN ISOFORM	SOLUBLE	0	0
LYSOSOME	256290	256290	34872293	VACUOLAR PROTON-TRANSLOCATING ATPASE 100 KDA SUBUNIT ISOFORM A2	SOLUBLE	0	0
METABOLISM	36810	36810	7513959	DELTA-6 FATTY ACID DESATURASE	MEMBRANE	0	0
METABOLISM	71440	71440	58477247	GLUCOSE-6-PHOSPHATASE	MEMBRANE	0	0
METABOLISM	78079	78079	3929215	GLUCOSE-6-PHOSPHATASE, TRANSPORT PROTEIN 1	MEMBRANE	0	0
METABOLISM	195113	195113	34860689	GPI TRANSAMIDASE COMPONENT PIG-T PRECURSOR (PHOSPHATIDYLINOSITOL-GLYCAN BIOSYNTHESIS, CLASS T PROTEIN).	MEMBRANE	0	0
METABOLISM	104163	104163	204150	L-GULONOLACTONE OXIDASE	MEMBRANE	0	0
METABOLISM	60485	60485	6016484	LONG-CHAIN-FATTY-ACID--COA LIGASE 5	MEMBRANE	2	14.8571
METABOLISM	85756	85756	25742739	LONG-CHAIN-FATTY-ACID--COA LIGASE, LIVER ISOZYME	MEMBRANE	1	11.1429
METABOLISM	255469	255469	34879054	PUTATIVE PHOSPHATIDIC ACID PHOSPHATASE	MEMBRANE	0	0
METABOLISM	213158	213158	34866138	SIMILAR TO ASPARTYL BETA-HYDROXYLASE	MEMBRANE	0	0
METABOLISM	291525	291525	62511143	VITAMIN K EPOXIDE REDUCTASE COMPLEX SUBUNIT 1-LIKE PROTEIN	MEMBRANE	0	0
METABOLISM	165266	165266	62511142	VITAMIN K EPOXIDE REDUCTASE COMPLEX, SUBUNIT 1	MEMBRANE	0	0

METABOLISM	216271	216271	34867430	1,4-ALPHA-GLUCAN BRANCHING ENZYME	SOLUBLE	0	0
METABOLISM	62196	216271	908915	10-FORMYL TETRAHYDROFOLATE DEHYDROGENASE	SOLUBLE	0	0
METABOLISM	42736	42736	9910256	3-HYDROXYANTHRANILATE 3,4-DIOXYGENASE	SOLUBLE	0	0
METABOLISM	251780	251780	34875828	3-HYDROXYISOBUTYRYL-COENZYME A HYDROLASE	SOLUBLE	0	0
METABOLISM	51489	51489	8393557	4-HYDROXYPHENYLPYRUVATE DIOXYGENASE	SOLUBLE	0	0
METABOLISM	104196	104196	78099320	4-TRIMETHYLAMINO BUTYRALDEHYDE DEHYDROGENASE	SOLUBLE	0	0
METABOLISM	166337	166337	33086672	6-PHOSPHOGLUCONATE DEHYDROGENASE, DECARBOXYLATING	SOLUBLE	0	0
METABOLISM	4320	4320	54261671	ACYL-COA-BINDING PROTEIN	SOLUBLE	0	0
METABOLISM	126504	126504	61556832	ADENINE PHOSPHORIBOSYL TRANSFERASE	SOLUBLE	0	0
METABOLISM	85486	85486	1373230	ADENOSINE KINASE	SOLUBLE	0	0
METABOLISM	54409	54409	24158803	ADENOSYLHOMOCYSTEINASE	SOLUBLE	0	4
METABOLISM	11560	11560 84144	38382840	ALCOHOL DEHYDROGENASE 1	SOLUBLE	0	7
METABOLISM	308340	308340	73620788	ALCOHOL DEHYDROGENASE PAN1B	SOLUBLE	0	4.3077
METABOLISM	169811	169811	77416416	ALCOHOL DEHYDROGENASE PAN1B-LIKE PROTEIN	SOLUBLE	3	9.6923
METABOLISM	37172	37172	399660	ALCOHOL DEHYDROGENASE [NADP+]	SOLUBLE	0	0
METABOLISM	7845	7845	16073616	ALDEHYDE DEHYDROGENASE	SOLUBLE	0	7
METABOLISM	83139	83139	91935	ALDEHYDE DEHYDROGENASE (NAD)	SOLUBLE	0	0
METABOLISM	161456	161456	62648070	ALDOSE REDUCTASE	SOLUBLE	0	0
METABOLISM	290544	290544	84028322	ALDOSE 1-EPIMERASE	SOLUBLE	0	0
METABOLISM	338764	313683 338764	38649320	ALPHA ENOLASE	SOLUBLE	0	3
METABOLISM	75128	75128	731023	ALPHA-TOCOPHEROL TRANSFER PROTEIN	SOLUBLE	0	0
METABOLISM	37797	37797	6573527	ARGININASE 1	SOLUBLE	9	31
METABOLISM	45085	45085	551296	ARGININOSUCCINATE LYASE	SOLUBLE	0	0
METABOLISM	45108	45108	55767	ARGININOSUCCINATE SYNTHASE	SOLUBLE	0	14
METABOLISM	3735	3735	6978759	AROMATIC-L-AMINO-ACID DECARBOXYLASE	SOLUBLE	0	0
METABOLISM	126543	126543	8392839	ATP CITRATE LYASE	SOLUBLE	0	1
METABOLISM	62122	62122	901850	C-1-TETRAHYDROFOLATE SYNTHASE, CYTOPLASMIC	SOLUBLE	0	1
METABOLISM	5972	5972	10120584	CARBONIC ANHYDRASE III	SOLUBLE	0	12
METABOLISM	41205	41205	543960	CYSTATHIONINE BETA-SYNTHASE	SOLUBLE	0	0
METABOLISM	62524	62524	51261011	CYSTATHIONINE GAMMA-LYASE	SOLUBLE	2	9
METABOLISM	35923	35923	6685331	CYSTEINE SULFINIC ACID DECARBOXYLASE	SOLUBLE	0	0
METABOLISM	118982	118982	81861572	CYTOSOLIC MALATE DEHYDROGENASE	SOLUBLE	0	0
METABOLISM	29986	29986	895882	D-DOPACHROME TAUTOMERASE	SOLUBLE	0	2
METABOLISM	315956	315956	34876831	DEHYDROGENASE E1 AND TRANSKETOLASE DOMAIN CONTAINING PROTEIN 1	SOLUBLE	0	0
METABOLISM	307749	307749	34858565	DEOXYRIBOSE-PHOSPHATE ALDOLASE-LIKE	SOLUBLE	0	0
METABOLISM	161241	161241	50400214	DIACETYL-L-XYLULOSE REDUCTASE	SOLUBLE	0	0
METABOLISM	53424	53424	81871579	DIHYDROFOLATE REDUCTASE	SOLUBLE	0	0
METABOLISM	23398	23398	576089	DIHYDROPTERIDINE REDUCTASE	SOLUBLE	0	1
METABOLISM	78138	78138	3122039	DIHYDROPYRIMIDINASE	SOLUBLE	0	0
METABOLISM	223736	223736	85718638	DIHYDROXYACETONE KINASE FAMILY PROTEIN	SOLUBLE	0	0
METABOLISM	62242	62242	1711602	ESTROGEN SULFOTRANSFERASE, ISOFORM 6	SOLUBLE	0	0
METABOLISM	23674	23674	null	FATTY ACID BINDING PROTEIN FABP-1	SOLUBLE	0	0
METABOLISM	3774	3774	6978859	FERRITIN HEAVY CHAIN	SOLUBLE	0	5
METABOLISM	277663	277663	84000579	FERRITIN LIGHT CHAIN	SOLUBLE	6	21
METABOLISM	39875	39875	60688163	FORMIMIDOYLTRANSFERASE-CYCLODEAMINASE	SOLUBLE	0	0
METABOLISM	149105	149105	623562	FRUCTOSE-1,6-BISPHOSPHATASE	SOLUBLE	0	0
METABOLISM	3624	3624	6978487	FRUCTOSE-BISPHOSPHATE ALDOLASE A	SOLUBLE	0	0
METABOLISM	116234	116234	1619606	FRUCTOSE-BISPHOSPHATE ALDOLASE B	SOLUBLE	9	39

METABOLISM	139030	139030	5825482	GAMMA-BUTYROBETAINE,2-OXOGLUTARATE DIOXYGENASE	SOLUBLE	0	0
METABOLISM	3782	3782	6978884	GLUCOKINASE	SOLUBLE	0	0
METABOLISM	295907	295907	46485440	GLUCOSE-6-PHOSPHATE ISOMERASE	SOLUBLE	0	0
METABOLISM	28251	28251	61098201	GLUTAMINE SYNTHETASE	SOLUBLE	1	7
METABOLISM	51456	51456 170936	9798638	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE	SOLUBLE	0	2
METABOLISM	80790	80790	3023880	GLYCEROL-3-PHOSPHATE DEHYDROGENASE [NAD ⁺], CYTOPLASMIC	SOLUBLE	0	1
METABOLISM	208010	208010	34859913	GLYCAGEN DEBRANCHING ENZYME	SOLUBLE	0	0
METABOLISM	104192	104192	585688	GLYCAGEN PHOSPHORYLASE	SOLUBLE	0	0
METABOLISM	196203	196203	30750124	GUANIDINOACETATE N-METHYLTRANSFERASE	SOLUBLE	0	0
METABOLISM	42862	42862	9910706	GUANINE DEAMINASE	SOLUBLE	0	0
METABOLISM	3926	3926	6981022	HEXOKINASE, TYPE I	SOLUBLE	0	0
METABOLISM	51482	51482	8393522	HISTIDINE AMMONIA-LYASE	SOLUBLE	0	0
METABOLISM	16980	16980	68534712	HYPOXANTHINE-GUANINE PHOSPHORIBOSYLTRANSFERASE	SOLUBLE	0	0
METABOLISM	190455	190455	34855047	INOSINE MONOPHOSPHATE DEHYDROGENASE 1	SOLUBLE	0	0
METABOLISM	71492	71492	627999	ISOCITRATE DEHYDROGENASE [NADP] CYTOPLASMIC	SOLUBLE	0	4
METABOLISM	127122	127122	62650395	KETOHEXOKINASE	SOLUBLE	0	1
METABOLISM	157223	157223	3913969	KYNURENINASE	SOLUBLE	0	0
METABOLISM	51504	51504	8393641	KYNURENINE/ALPHA-AMINOADIPATE AMINOTRANSFERASE	SOLUBLE	0	0
METABOLISM	51518	51518 237201 286597	8393706	L-LACTATE DEHYDROGENASE	SOLUBLE	0	13
METABOLISM	3968	3968	6981146	L-LACTATE DEHYDROGENASE B CHAIN	SOLUBLE	0	0
METABOLISM	44348	44348	21617859	L-SERINE DEHYDRATASE/L-THREONINE DEAMINASE	SOLUBLE	0	0
METABOLISM	224451	224451	50927335	LACTATE DEHYDROGENASE A-LIKE PROTEIN	SOLUBLE	0	0
METABOLISM	317748	317748	62665770	LANOSTEROL SYNTHASE	SOLUBLE	0	0
METABOLISM	286024	286024	34864937	LEUKOTRIENE A-4 HYDROLASE	SOLUBLE	0	0
METABOLISM	22152	22152	6016483	LONG-CHAIN-FATTY-ACID-COA LIGASE 4	SOLUBLE	0	0
METABOLISM	193296	193296	72255521	LYSOPHOSPHATIDIC ACID PHOSPHATASE	SOLUBLE	0	0
METABOLISM	76956	76956	79158553	MONOGLYCERIDE LIPASE	SOLUBLE	0	0
METABOLISM	111533	111533	976252	MULTIFUNCTIONAL PROTEIN ADE2	SOLUBLE	0	0
METABOLISM	225772	225772	27714479	N-ACETYLNEURAMINIC ACID SYNTHASE (SIALIC ACID SYNTHASE)	SOLUBLE	0	0
METABOLISM	104206	104206	6831527	NG,NG-DIMETHYLARGININE DIMETHYLAMINOHYDROLASE 1	SOLUBLE	0	0
METABOLISM	75026	75026	6981330	PHENYLALANINE-4-HYDROXYLASE	SOLUBLE	0	0
METABOLISM	144363	144363	51859488	PHOSPHOENOLPYRUVATE CARBOXYKINASE, CYTOSOLIC [GTP]	SOLUBLE	0	0
METABOLISM	318741	318741	38197562	PHOSPHOFRUCTOKINASE, LIVER, B-TYPE	SOLUBLE	0	0
METABOLISM	51568	51568	8393951	PHOSPHOGLUCOMUTASE	SOLUBLE	0	1
METABOLISM	340218	340218	56585024	PHOSPHOGLYCERATE KINASE, TESTIS SPECIFIC	SOLUBLE	0	0
METABOLISM	207767	207767	34858123	PHOSPHOGLYCERATE MUTASE	SOLUBLE	0	0
METABOLISM	249141	249141	29692074	PHOSPHOSERINE AMINOTRANSFERASE	SOLUBLE	0	0
METABOLISM	301508	301508	34869794	PROLINE DEHYDROGENASE	SOLUBLE	0	0
METABOLISM	166503	166503	27706734	PROSTAGLANDIN E SYNTHASE 2	SOLUBLE	0	0
METABOLISM	108686	108686	10835705	PTERIN-4-ALPHA-CARBINOLAMINE DEHYDRATASE	SOLUBLE	0	0
METABOLISM	44273	44273	206213	PYRUVATE KINASE, ISOZYMES R/L	SOLUBLE	0	0
METABOLISM	3576	3576	6970313	REGUCALCIN	SOLUBLE	1	3
METABOLISM	105581	105581	null	RETINOL-BINDING PROTEIN I, CELLULAR	SOLUBLE	0	0
METABOLISM	31392	31392	34856334	SEPIAPTERIN REDUCTASE	SOLUBLE	0	1

METABOLISM	315711	315711	34877556	SIMILAR TO 6-PHOSPHOGLUCONOLACTONASE	SOLUBLE	0	0
METABOLISM	258586	258586	34855019	SIMILAR TO AMINOADIPATE-SEMIALDEHYDE SYNTHASE	SOLUBLE	0	0
METABOLISM	219419	219419	34862615	SIMILAR TO ATP SULFURYLASE/APS KINASE 2	SOLUBLE	0	0
METABOLISM	253447	253447	40786469	SIMILAR TO DIHYDROLIPOAMIDE DEHYDROGENASE	SOLUBLE	0	0
METABOLISM	206276	206276	56605662	SIMILAR TO GALACTOKINASE 1	SOLUBLE	0	0
METABOLISM	248817	210943 248817	34852868	SIMILAR TO GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE (2)	SOLUBLE	0	0
METABOLISM	262638	262638	34853387	SIMILAR TO GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE (3)	SOLUBLE	0	0
METABOLISM	156654	156654	27699577	SIMILAR TO GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE (4)	SOLUBLE	0	0
METABOLISM	290393	290393	34862792	SIMILAR TO GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE (5)	SOLUBLE	0	0
METABOLISM	296252	296252	34864978	SIMILAR TO GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE (6)	SOLUBLE	0	0
METABOLISM	232409	232409	34866415	SIMILAR TO GLYCEROL-3-PHOSPHATE DEHYDROGENASE 1 (SOLUBLE)	SOLUBLE	0	0
METABOLISM	251640	251640	34872615	SIMILAR TO HEXOSE-6-PHOSPHATE DEHYDROGENASE; GDH6PGL ENDOPLASMIC BIFUNCTIONAL PROTEIN	SOLUBLE	15	34
METABOLISM	303719	303719	34869194	SIMILAR TO HOMOGENITISATE 1,2-DIOXYGENASE	SOLUBLE	0	0
METABOLISM	269702	269702	34871118	SIMILAR TO HOMOPROTECATECHUATE CATABOLISM BIFUNCTIONAL ISOMERASE/DECARBOXYLASE	SOLUBLE	0	0
METABOLISM	313999	313999	34865151	SIMILAR TO INTRACELLULAR MEMBRANE-ASSOCIATED CALCIUM-INDEPENDENT PHOSPHOLIPASE A2 GAMMA	SOLUBLE	0	1
METABOLISM	204743	204743	34878080	SIMILAR TO LEUCINE AMINOPEPTIDASE	SOLUBLE	0	0
METABOLISM	191730	191730	34853476	SIMILAR TO METHYLCROTONOYL-COENZYME A CARBOXYLASE 2 (BETA); NON-BIOTIN CONTAINING SUBUNIT OF 3-METHYLCROTONYL-COA CARBOXYLASE; BIOTIN CARBOXYLASE	SOLUBLE	0	0
METABOLISM	233624	233624	34876995	SIMILAR TO PALBH	SOLUBLE	0	0
METABOLISM	202185	202185	34865378	SIMILAR TO PHOSPHOACETYLGLUCOSAMINE MUTASE (PAGM) (ACETYLGLUCOSAMINE PHOSPHOMUTASE) (N-ACETYLGLUCOSAMINE-PHOSPHATE MUTASE) (PHOSPHOGLUCOMUTASE 3)	SOLUBLE	0	0
METABOLISM	221017	221017	57528359	SIMILAR TO PHOSPHOLYSINE PHOSPHOHISTIDINE INORGANIC PYROPHOSPHATE PHOSPHATA (5M590)	SOLUBLE	0	0
METABOLISM	268034	268034	34855688	SIMILAR TO PROLINE DEHYDROGENASE (OXIDASE) 2	SOLUBLE	0	0
METABOLISM	305160	305160	27665096	SIMILAR TO PROLINE DEHYDROGENASE; PRODH	SOLUBLE	0	0
METABOLISM	209477	209477	34869683	SIMILAR TO PURINE-NUCLEOSIDE PHOSPHORYLASE; PURINE-NUCLEOSIDE PHOPSHORYLASE	SOLUBLE	0	4
METABOLISM	225159	225159	34879163	SIMILAR TO URIDINDIPHOSPHOGLUCOSEPYROPHOSPHORYLASE 2	SOLUBLE	0	0
METABOLISM	316589	316589	34861397	SIMILAR TO UROCANATE HYDRATASE	SOLUBLE	0	0
METABOLISM	229118	229118	34866669	SIMILAR TO XYLOKINASE HOMOLOG; XYLULOKINASE (H. INFLUENZAE) HOMOLOG	SOLUBLE	0	0
METABOLISM	43660	43660	2506157	SORBITOL DEHYDROGENASE	SOLUBLE	0	1
METABOLISM	50402	50402	17433174	TRANSALDOLASE	SOLUBLE	0	0
METABOLISM	38668	38668	1729977	TRANSKETOLASE	SOLUBLE	0	3

METABOLISM	340135	340135	38512111	TRIOSEPHOSPHATE ISOMERASE	SOLUBLE	0	0
METABOLISM	11402	11402	59809151	TRYPTOPHAN 2,3-DIOXYGENASE	SOLUBLE	0	0
METABOLISM	75904	75904	6136118	UDP-GLUCOSE 6-DEHYDROGENASE	SOLUBLE	0	0
METABOLISM	86062	86062	21326465	UDP-GLUCURONATE DECARBOXYLASE	SOLUBLE	0	0
METABOLISM	201012	201012	34881188	UDP-GLUCURONATE DECARBOXYLASE 1	SOLUBLE	0	1
METABOLISM	338318	338318	38649090	VIGILIN (HIGH DENSITY LIPOPROTEIN-BINDING PROTEIN) (HDL-BINDING PROTEIN)	SOLUBLE	0	0
MITOCHONDRIA	117684	117684	728810	ADENINE NUCLEOTIDE TRANSLOCATOR 2	MEMBRANE	2	10
MITOCHONDRIA	74982	74982	91974	AMINE OXIDASE [FLAVIN-CONTAINING] B	MEMBRANE	0	0
MITOCHONDRIA	73367	73367	6729934	ATP SYNTHASE ALPHA CHAIN, MITOCHONDRIAL	MEMBRANE	5	43.5119
MITOCHONDRIA	11888	11888	461587	ATP SYNTHASE E CHAIN, MITOCHONDRIAL	MEMBRANE	0	1
MITOCHONDRIA	98990	98990	5835182	ATP SYNTHASE PROTEIN 8	MEMBRANE	0	0
MITOCHONDRIA	273691	273691	34877696	ATPASE TYPE 13A1	MEMBRANE	0	0
MITOCHONDRIA	63443	63443	48735405	CARNITINE O-PALMITOYL TRANSFERASE 1, MITOCHONDRIAL LIVER ISOFORM	MEMBRANE	0	1
MITOCHONDRIA	32875	32875	48735409	CYTOCHROME B5, MITOCHONDRIAL ISOFORM	MEMBRANE	0	0
MITOCHONDRIA	288354	288354	27716471	CYTOCHROME C OXIDASE	MEMBRANE	0	0
MITOCHONDRIA	90517	90517	56025	CYTOCHROME C OXIDASE POLYPEPTIDE VIIA-LIVER/HEART, MITOCHONDRIAL	MEMBRANE	0	0
MITOCHONDRIA	68411	68411	1332384	CYTOCHROME C OXIDASE SUBUNIT I	MEMBRANE	0	0
MITOCHONDRIA	63740	63740	8393180	CYTOCHROME C OXIDASE SUBUNIT IV ISOFORM 1, MITOCHONDRIAL	MEMBRANE	0	0
MITOCHONDRIA	105670	105670	829023	CYTOCHROME OXIDASE SUBUNIT II	MEMBRANE	0	0
MITOCHONDRIA	3907	3907	6980978	GLYCEROL-3-PHOSPHATE DEHYDROGENASE, MITOCHONDRIAL	MEMBRANE	0	0
MITOCHONDRIA	296680	296680	62510718	LEUCINE ZIPPER-EF-HAND CONTAINING TRANSMEMBRANE PROTEIN 1	MEMBRANE	0	2
MITOCHONDRIA	37213	37213	400269	METHYLMALONATE-SEMIALDEHYDE DEHYDROGENASE [ACYLATING], MITOCHONDRIAL	MEMBRANE	0	1
MITOCHONDRIA	63382	63382	2497984	MITOCHONDRIAL CARNITINE/ACYL-CARNITINE CARRIER PROTEIN	MEMBRANE	0	0
MITOCHONDRIA	156740	156740	27702070	MITOCHONDRIAL CARRIER HOMOLOG 2	MEMBRANE	0	0
MITOCHONDRIA	223033	223033	34865173	MITOCHONDRIAL GLUTAMATE CARRIER 1	MEMBRANE	0	0
MITOCHONDRIA	12056	12056	5107153	MITOCHONDRIAL IMPORT INNER MEMBRANE TRANSLOCASE SUBUNIT TIM8 A	MEMBRANE	0	0
MITOCHONDRIA	98993	98993	639984	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4	MEMBRANE	0	0
MITOCHONDRIA	290180	290180	34856875	OSMOTIC STRESS PROTEIN	MEMBRANE	0	0
MITOCHONDRIA	69383	69383	20806141	PHOSPHATE CARRIER PROTEIN, MITOCHONDRIAL	MEMBRANE	0	1
MITOCHONDRIA	266866	266866	34853075	QUIESCIN Q6-LIKE 1	MEMBRANE	0	0
MITOCHONDRIA	204895	204895	52000746	RE70703P-LIKE PROTEIN	MEMBRANE	0	0
MITOCHONDRIA	80422	80422	null	SIDEROFLEXIN 1 (TRICARBOXYLATE CARRIER PROTEIN)	MEMBRANE	0	1
MITOCHONDRIA	229993	229993	34863716	SIDEROFLEXIN 2	MEMBRANE	0	0
MITOCHONDRIA	262837	262837	27685029	SIMILAR TO ATP SYNTHASE, H+ TRANSPORTING, MITOCHONDRIAL F0 COMPLEX, SUBUNIT C (SUBUNIT 9), ISOFORM 2	MEMBRANE	0	0
MITOCHONDRIA	258284	258284	34858394	SIMILAR TO BCL2-LIKE 13	MEMBRANE	0	0
MITOCHONDRIA	309822	309822	34854954	SIMILAR TO CALCIUM-BINDING MITOCHONDRIAL CARRIER PROTEIN ARALAR2 (SOLUTE CARRIER FAMILY 25, MEMBER 13) (CITRIN)	MEMBRANE	1	21.9545
MITOCHONDRIA	194839	194839	34877651	SIMILAR TO CG4241-PA	MEMBRANE	0	0
MITOCHONDRIA	256607	256607	34933423	SIMILAR TO MITOCHONDRIAL INNER MEMBRANE TRANSLOCASE COMPONENT TIM17B	MEMBRANE	0	0

MITOCHONDRIA	304373	304373	27660847	SIMILAR TO NADH DEHYDROGENASE	MEMBRANE	0	0
MITOCHONDRIA	287362	287362	34876452	SIMILAR TO NADH DEHYDROGENASE (UBIQUINONE) 1 BETA SUBCOMPLEX 3	MEMBRANE	0	0
MITOCHONDRIA	235872	235872	34856800	SIMILAR TO NADH DEHYDROGENASE (UBIQUINONE) 1 BETA SUBCOMPLEX 5; NADH DEHYDROGENASE (UBIQUINONE) 1 BETA SUBCOMPLEX 5	MEMBRANE	0	0
MITOCHONDRIA	164223	164223	57164133	SIMILAR TO NADH-UBIQUINONE OXIDOREDUCTASE B14.5B SUBUNIT	MEMBRANE	0	0
MITOCHONDRIA	318196	318196	34854466	SIMILAR TO NADH-UBIQUINONE OXIDOREDUCTASE B9 SUBUNIT (COMPLEX I-B9) (CI-B9)	MEMBRANE	0	0
MITOCHONDRIA	192715	192715	82617686	SIMILAR TO NADH:UBIQUINONE OXIDOREDUCTASE B15 SUBUNIT	MEMBRANE	0	0
MITOCHONDRIA	202296	202296	34854180	SIMILAR TO NICOTINAMIDE NUCLEOTIDE TRANSHYDROGENASE	MEMBRANE	0	0
MITOCHONDRIA	36071	36071	5106930	SYNAPTJANIN 2 BINDING PROTEIN	MEMBRANE	0	0
MITOCHONDRIA	11413	11413	206430	VACUOLAR PROTON TRANSLOCATING ATPASE 116 KDA SUBUNIT A ISOFORM 1	MEMBRANE	0	0
MITOCHONDRIA	11037	11037	8810245	VOLTAGE-DEPENDENT ANION CHANNEL 1	MEMBRANE	0	0
MITOCHONDRIA	5942	5942	8810247	VOLTAGE-DEPENDENT ANION CHANNEL 2	MEMBRANE	0	0
MITOCHONDRIA	5943	5943	15214186	VOLTAGE-DEPENDENT ANION-SELECTIVE CHANNEL PROTEIN 3 (VDAC-3) (RVDAC3) (OUTER MITOCHONDRIAL MEMBRANE PROTEIN PORIN.3)	MEMBRANE	0	0
MITOCHONDRIA	148907	148907	67476443	2,4-DIENOLYL-COA REDUCTASE, MITOCHONDRIAL	SOLUBLE	0	3
MITOCHONDRIA	51421	51421	8393243	3,2-TRANS-ENOYL-COA ISOMERASE, MITOCHONDRIAL	SOLUBLE	0	3
MITOCHONDRIA	141497	141497	482346	3-HYDROXYBUTYRATE DEHYDROGENASE (EC 1.1.1.30) - RAT	SOLUBLE	3	22
MITOCHONDRIA	55185	55185	83977457	3-HYDROXYISOBUTYRATE DEHYDROGENASE; MITOCHONDRIAL	SOLUBLE	0	0
MITOCHONDRIA	96895	96895	55544	3-KETOACYL-COA THIOLEASE, MITOCHONDRIAL	SOLUBLE	0	5
MITOCHONDRIA	13392	13392	62652539	3-MERCAPTOPYRUVATE SULFURTRANSFERASE	SOLUBLE	0	0
MITOCHONDRIA	52609	52609	55778012	60 KDA HEAT SHOCK PROTEIN, MITOCHONDRIAL (HSP60) (60 KDA CHAPERONIN)	SOLUBLE	0	3
MITOCHONDRIA	31496	31496	66502	ACETYL-COA ACETYLTRANSFERASE, MITOCHONDRIAL	SOLUBLE	0	2
MITOCHONDRIA	84141	84141	202645	ACETYL-COA CARBOXYLASE 1	SOLUBLE	0	0
MITOCHONDRIA	3599	3599	6978431	ACYL-COA DEHYDROGENASE, LONG-CHAIN SPECIFIC, MITOCHONDRIAL	SOLUBLE	0	6
MITOCHONDRIA	11499	11499	8392833	ACYL-COA DEHYDROGENASE, MEDIUM-CHAIN SPECIFIC, MITOCHONDRIAL	SOLUBLE	0	0
MITOCHONDRIA	3600	3600	6978433	ACYL-COA DEHYDROGENASE, SHORT/BRANCHED CHAIN SPECIFIC, MITOCHONDRIAL	SOLUBLE	0	0
MITOCHONDRIA	3601	3601	6978435	ACYL-COA DEHYDROGENASE, VERY-LONG-CHAIN SPECIFIC, MITOCHONDRIAL	SOLUBLE	0	0
MITOCHONDRIA	340217	340217	77020256	ADENYLATE KINASE 2	SOLUBLE	1	18
MITOCHONDRIA	270293	270293	40352787	ADENYLATE KINASE 3 ALPHA-LIKE 1	SOLUBLE	0	0
MITOCHONDRIA	181389	181389	8392885	ADENYLATE KINASE ISOENZYME 4, MITOCHONDRIAL	SOLUBLE	0	0
MITOCHONDRIA	101201	101201	null	AMINE OXIDASE [FLAVIN-CONTAINING] A	SOLUBLE	0	0
MITOCHONDRIA	3905	3905	6980972	ASPARTATE AMINOTRANSFERASE, MITOCHONDRIAL	SOLUBLE	1	4
MITOCHONDRIA	84171	84171	91997	ASPARTATE TRANSAMINASE	SOLUBLE	0	2
MITOCHONDRIA	141484	141484	39645769	ATP SYNTHASE B CHAIN, MITOCHONDRIAL	SOLUBLE	0	5
MITOCHONDRIA	141479	126508 141479	71681130	ATP SYNTHASE BETA CHAIN, MITOCHONDRIAL	SOLUBLE	23	67

MITOCHONDRIA	60480	60480	599963	ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL PRECURSOR	SOLUBLE	0	0
MITOCHONDRIA		21505	9506411	ATP SYNTHASE D CHAIN, MITOCHONDRIAL	SOLUBLE	0	4
MITOCHONDRIA	21504	21504	457929	ATP SYNTHASE DELTA CHAIN, MITOCHONDRIAL	SOLUBLE	1	4
MITOCHONDRIA	11887	11887	null	ATP SYNTHASE EPSILON CHAIN, MITOCHONDRIAL	SOLUBLE	0	1
MITOCHONDRIA	69786	69786	6729936	ATP SYNTHASE GAMMA CHAIN, MITOCHONDRIAL	SOLUBLE	0	7
MITOCHONDRIA	142437	142437	543880	ATP SYNTHASE OLIGOMYCIN SENSITIVITY CONFERRAL PROTEIN, MITOCHONDRIAL	SOLUBLE	2	17
MITOCHONDRIA	306584	306584	34881747	ATP-BINDING CASSETTE, SUB-FAMILY D (ALD), MEMBER 1	SOLUBLE	0	0
MITOCHONDRIA	215739	215739	62078455	BCL-2 INHIBITOR OF TRANSCRIPTION,	SOLUBLE	0	0
MITOCHONDRIA	37174	37174	48429192	BETA-ALANINE OXOGLUTARATE AMINOTRANSFERASE	SOLUBLE	0	0
MITOCHONDRIA	44431	44431	51259277	BETA-UREIDOPROPIONASE	SOLUBLE	0	0
MITOCHONDRIA	71708	71708	3913156	BETAINE--HOMOCYSTEINE S-METHYLTRANSFERASE	SOLUBLE	4	24
MITOCHONDRIA	247159	247159	34861318	BETAINE-HOMOCYSTEINE METHYLTRANSFERASE 2	SOLUBLE	0	0
MITOCHONDRIA	151463	151463	34865350	BRANCHED CHAIN KETO ACID DEHYDROGENASE E1, BETA POLYPEPTIDE	SOLUBLE	0	0
MITOCHONDRIA	166641	166641	27708576	CALCIUM-BINDING MITOCHONDRIAL CARRIER PROTEIN ARALAR2 (SOLUTE CARRIER FAMILY 25, MEMBER 13) (CITRIN)	SOLUBLE	1	4
MITOCHONDRIA	45074	45074	8393186	CARBAMOYL-PHOSPHATE SYNTHASE [AMMONIA], MITOCHONDRIAL	SOLUBLE	15	32
MITOCHONDRIA	315461	315461	34862992	CARBAMOYL-PHOSPHATE SYNTHETASE 2, ASPARTATE TRANS-CARBAMYLASE, AND DIHYDROOROTASE	SOLUBLE	0	0
MITOCHONDRIA	3716	3716	6978705	CARNITINE O-PALMITOYL TRANSFERASE II, MITOCHONDRIAL	SOLUBLE	0	0
MITOCHONDRIA	160551	160551	55250736	CHOLINE DEHYDROGENASE, MITOCHONDRIAL	SOLUBLE	0	1
MITOCHONDRIA	80872	80872	9506435	COMPLEMENT COMPONENT 1, Q SUBCOMPONENT BINDING PROTEIN, MITOCHONDRIAL	SOLUBLE	0	0
MITOCHONDRIA	160701	160701	79749365	COPROPORPHYRINOGEN OXIDASE	SOLUBLE	0	2
MITOCHONDRIA	63743	63743	55971	CYTOCHROME C OXIDASE POLYPEPTIDE VA, MITOCHONDRIAL	SOLUBLE	0	0
MITOCHONDRIA	21518	21518	53237117	CYTOCHROME C OXIDASE POLYPEPTIDE VB, MITOCHONDRIAL	SOLUBLE	0	0
MITOCHONDRIA	71407	71407	1169069	CYTOCHROME C OXIDASE POLYPEPTIDE VIIC, MITOCHONDRIAL	SOLUBLE	0	0
MITOCHONDRIA	63749	63749	34849861	CYTOCHROME C OXIDASE SUBUNIT VIC	SOLUBLE	0	0
MITOCHONDRIA	71180	71180	6978725	CYTOCHROME C, SOMATIC	SOLUBLE	1	5
MITOCHONDRIA	80282	80282	7513957	CYTOCHROME-C OXIDASE (EC 1.9.3.1) CHAIN VIIA, HEPATIC	SOLUBLE	0	0
MITOCHONDRIA	232730	232730	34859889	DIHYDROLIPOAMIDE BRANCHED CHAIN TRANSACYLASE E2	SOLUBLE	0	0
MITOCHONDRIA	43490	43490	62665239	DIHYDROOROTATE DEHYDROGENASE, MITOCHONDRIAL PRECURSOR	SOLUBLE	0	0
MITOCHONDRIA	82662	82662	56689	DIMETHYLGLYCINE DEHYDROGENASE, MITOCHONDRIAL	SOLUBLE	0	0
MITOCHONDRIA	113271	113271	22775474	DLST DIHYDROLIPOAMIDE SUCCINYLTRANSFERASE, EXON 15 AND COMPLETE CDS	SOLUBLE	0	1
MITOCHONDRIA	151400	151400	57527204	ELECTRON TRANSFER FLAVOPROTEIN ALPHA-SUBUNIT, MITOCHONDRIAL	SOLUBLE	0	1

MITOCHONDRIA	189992	189992	81884360	ELECTRON TRANSFER FLAVOPROTEIN BETA SUBUNIT	SOLUBLE	0	2
MITOCHONDRIA	258013	258013	52000614	ELECTRON TRANSFERRING FLAVOPROTEIN, DEHYDROGENASE	SOLUBLE	0	0
MITOCHONDRIA	15873	15873	56072	ENOYL-COA HYDRATASE, MITOCHONDRIAL	SOLUBLE	0	3
MITOCHONDRIA	214426	214426	83302472	ES1 PROTEIN	SOLUBLE	0	1
MITOCHONDRIA	288462	288462	47058994	F1FO-ATP SYNTHASE G SUBUNIT	SOLUBLE	0	2
MITOCHONDRIA	313806	313806	34932061	FERROCHELATASE	SOLUBLE	0	0
MITOCHONDRIA	96892	96892	52782765	FLAVOPROTEIN SUBUNIT OF SUCCINATE-UBIQUINONE REDUCTASE	SOLUBLE	0	10
MITOCHONDRIA	45080	45080	83933358	FUMARATE HYDRATASE, MITOCHONDRIAL	SOLUBLE	0	1
MITOCHONDRIA	51443	51443	83933349	FUMARYLACETOACETASE	SOLUBLE	0	1
MITOCHONDRIA	3897	3897	92090591	GLUTAMATE DEHYDROGENASE, MITOCHONDRIAL	SOLUBLE	0	32
MITOCHONDRIA	270372	270372	34851534	GLUTARYL-COA DEHYDROGENASE	SOLUBLE	0	0
MITOCHONDRIA	110024	110024	42543496	GLUTATHIONE S-TRANSFERASE, MITOCHONDRIAL	SOLUBLE	0	0
MITOCHONDRIA	51468	51468	8393466	GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE, MITOCHONDRIAL (GPAT)	SOLUBLE	0	0
MITOCHONDRIA	15417	15417	3913728	HYDROXYACYLGLUTATHIONE HYDROLASE	SOLUBLE	0	1
MITOCHONDRIA	68742	68742	38511566	HYDROXYMETHYLGLUTARYL-COA LYASE, MITOCHONDRIAL	SOLUBLE	0	0
MITOCHONDRIA	16963	16963	27465521	HYDROXYMETHYLGLUTARYL-COA SYNTHASE, MITOCHONDRIAL	SOLUBLE	4	17
MITOCHONDRIA	299827	299827	34862359	ILVB (BACTERIAL ACETOLACTATE SYNTHASE)-LIKE ISOFORM 1: ACETOLACTATE SYNTHASE HOMOLOG	SOLUBLE	0	0
MITOCHONDRIA	3955	3955	6981112	ISOVALERYL-COA DEHYDROGENASE, MITOCHONDRIAL	SOLUBLE	0	1
MITOCHONDRIA	339913	339913	42476181	MALATE DEHYDROGENASE, MITOCHONDRIAL	SOLUBLE	5	19
MITOCHONDRIA	77688	23402 77688	1580888	MITOCHONDRIAL 2-OXOGLUTARATE/MALATE CARRIER PROTEIN	SOLUBLE	0	3
MITOCHONDRIA	338228	338228	60391194	MITOCHONDRIAL ACONITASE	SOLUBLE	0	3
MITOCHONDRIA	140375	140375	51859428	MITOCHONDRIAL DICARBOXYLATE CARRIER	SOLUBLE	0	0
MITOCHONDRIA	77128	77128	59800393	MITOCHONDRIAL IMPORT INNER MEMBRANE TRANSLOCASE SUBUNIT TIM13 A	SOLUBLE	0	0
MITOCHONDRIA	140367	140367	19173766	MITOCHONDRIAL LON PROTEASE HOMOLOG	SOLUBLE	0	0
MITOCHONDRIA	726503	726503	68534716	MITOCHONDRIAL PRECURSOR PROTEINS IMPORT RECEPTOR	SOLUBLE	0	1
MITOCHONDRIA	60501	60501	68565369	NAD+-SPECIFIC ISOCITRATE DEHYDROGENASE A-SUBUNIT	SOLUBLE	0	0
MITOCHONDRIA	229389	229389	53850628	NADH DEHYDROGENASE (UBIQUINONE) FE-S PROTEIN 1	SOLUBLE	0	11
MITOCHONDRIA	199168	199168	62531217	NADH DEHYDROGENASE 1 ALPHA SUBCOMPLEX 10-LIKE PROTEIN	SOLUBLE	0	8
MITOCHONDRIA	313497	313497	27661165	NADH DEHYDROGENASE: UBIQUINONE FE-S PROTEIN 8	SOLUBLE	0	5
MITOCHONDRIA	75004	75004	6981260	NADH-UBIQUINONE OXIDOREDUCTASE 13 KDA-B SUBUNIT	SOLUBLE	0	0
MITOCHONDRIA	291031	291031	83305118	NADH-UBIQUINONE OXIDOREDUCTASE 24 KDA SUBUNIT, MITOCHONDRIAL	SOLUBLE	0	6
MITOCHONDRIA	292254	292254	27706932	NADH-UBIQUINONE OXIDOREDUCTASE PGIV SUBUNIT	SOLUBLE	0	3
MITOCHONDRIA	195949	195949	34857317	NADP+-SPECIFIC ISOCITRATE DEHYDROGENASE	SOLUBLE	0	0
MITOCHONDRIA	33159	33159	51980631	NONSPECIFIC LIPID-TRANSFER PROTEIN, MITOCHONDRIAL PRECURSOR	SOLUBLE	0	0
MITOCHONDRIA	69495	69495	55926145	NUCLEOSIDE DIPHOSPHATE KINASE B	SOLUBLE	0	1

MITOCHONDRIA	44333	44333	206706	ORNITHINE AMINOTRANSFERASE, MITOCHONDRIAL PRECURSOR	SOLUBLE	0	0
MITOCHONDRIA	75019	75019	6981312	ORNITHINE TRANSCARBAMYLASE; ORNITHINE CARBAMOYLTRANSFERASE	SOLUBLE	0	7
MITOCHONDRIA	205798	205798	27673563	ORNITHINE TRANSPORTER	SOLUBLE	0	4
MITOCHONDRIA	88229	88229	56268806	PEPTIDYL-PROLYL CIS-TRANS ISOMERASE, MITOCHONDRIAL	SOLUBLE	0	0
MITOCHONDRIA	60487	60487	6103726	PEROXIREDOXIN 5, MITOCHONDRIAL	SOLUBLE	0	1
MITOCHONDRIA	63059	63059	7619915	PROGRAMMED CELL DEATH PROTEIN 8, MITOCHONDRIAL	SOLUBLE	0	7
MITOCHONDRIA	4312	4312	66911717	PROHIBITIN	SOLUBLE	0	3
MITOCHONDRIA	69597	69597	129684	PROPIONYL-COA CARBOXYLASE ALPHA CHAIN, MITOCHONDRIAL	SOLUBLE	0	1
MITOCHONDRIA	90537	90537	4336877	PRX III	SOLUBLE	0	2
MITOCHONDRIA	40425	40425	7438124	PYRUVATE CARBOXYLASE, MITOCHONDRIAL	SOLUBLE	0	9
MITOCHONDRIA	203734	203734	56090293	PYRUVATE DEHYDROGENASE E1 COMPONENT BETA SUBUNIT, MITOCHONDRIAL	SOLUBLE	0	0
MITOCHONDRIA	262284	262284	34858436	REPRESSOR OF ESTROGEN RECEPTOR ACTIVITY; B-CELL ASSOCIATED PROTEIN	SOLUBLE	0	3
MITOCHONDRIA	85749	85749	52000744	SARCOSINE DEHYDROGENASE	SOLUBLE	0	0
MITOCHONDRIA	31393	31393	66655	SERINE--PYRUVATE AMINOTRANSFERASE, MITOCHONDRIAL	SOLUBLE	0	1
MITOCHONDRIA	70622	70622	7387725	SHORT CHAIN 3-HYDROXYACYL-COA DEHYDROGENASE, MITOCHONDRIAL	SOLUBLE	1	1
MITOCHONDRIA	84143	84143	48734846	SHORT CHAIN ACYL-COA DEHYDROGENASE	SOLUBLE	0	0
MITOCHONDRIA	288262	288262	34860605	SIMILAR TO ACYL-COA DEHYDROGENASE FAMILY MEMBER 8, MITOCHONDRIAL PRECURSOR (ACAD-8) (ISOBUTYRYL-COA DEHYDROGENASE)	SOLUBLE	0	1
MITOCHONDRIA	288241	288241	34866733	SIMILAR TO ACYL-COENZYME A DEHYDROGENASE FAMILY Y, MEMBER 8	SOLUBLE	0	0
MITOCHONDRIA	209377	209377	34852510	SIMILAR TO APOPTOSIS-INDUCING FACTOR (AIF)-HOMOLOGOUS MITOCHONDRION-ASSOCIATED INDUCER OF DEATH: P53-RESPONSIVE GENE 3	SOLUBLE	0	0
MITOCHONDRIA	271135	271135	34866853	SIMILAR TO CYTOCHROME C-1	SOLUBLE	0	3
MITOCHONDRIA	260747	260747	34862790	SIMILAR TO GLYCINE DECARBOXYLASE	SOLUBLE	0	0
MITOCHONDRIA	247605	247605	34855983	SIMILAR TO INNER MEMBRANE PROTEIN, MITOCHONDRIAL (MITOFILIN); MOTOR PROTEIN	SOLUBLE	0	0
MITOCHONDRIA	258281	258281	34859067	SIMILAR TO MEDIUM-CHAIN ACYL-COA SYNTHETASE	SOLUBLE	0	1
MITOCHONDRIA	262377	262377	34857966	SIMILAR TO METAXIN 1	SOLUBLE	0	0
MITOCHONDRIA	203309	203309	56605654	SIMILAR TO METAXIN 2	SOLUBLE	0	0
MITOCHONDRIA	288315	288315	27667166	SIMILAR TO MITOCHONDRIA-ASSOCIATED GRANULOCYTE MACROPHAGE CSF SIGNALING MOLECULE; MITOCHONDRIA ASSOCIATED GRANULOCYTE MACROPHAGE CSF SIGNALING MOLECULE	SOLUBLE	0	0
MITOCHONDRIA	250139	250139	27682913	SIMILAR TO NADH DEHYDROGENASE (UBIQUINONE) 1 ALPHA SUBCOMPLEX, 2, 8KDA; NADH DEHYDROGENASE (UBIQUINONE) 1 ALPHA SUBCOMPLEX, 2 (8KD, B8)	SOLUBLE	0	1
MITOCHONDRIA	280728	280728	27663138	SIMILAR TO NADH DEHYDROGENASE (UBIQUINONE) 1 ALPHA SUBCOMPLEX, 6 (B14); NADH DEHYDROGENASE (UBIQUINONE) 1 ALPHA SUBCOMPLEX, 6 (14KD, B14)	SOLUBLE	0	0

MITOCHONDRIA	215768	215768	34858473	SIMILAR TO NADH DEHYDROGENASE (UBIQUINONE) 1	SOLUBLE	0	5
MITOCHONDRIA	292854	292854	34865197	ALPHA SUBCOMPLEX, 9	SOLUBLE	0	0
MITOCHONDRIA	291828	291828	27667934	BETA SUBCOMPLEX 8	SOLUBLE	0	0
				SIMILAR TO NADH DEHYDROGENASE (UBIQUINONE) 1			
				BETA SUBCOMPLEX, 10, 22KDA; NADH DEHYDROGENASE (UBIQUINONE) 1 BETA SUBCOMPLEX, 10 (22KD, PDSW)			
MITOCHONDRIA	298146	298146	34851467	SIMILAR TO NADH DEHYDROGENASE (UBIQUINONE) 1	SOLUBLE	0	0
MITOCHONDRIA	216920	216920	34880923	BETA SUBCOMPLEX, 7	SOLUBLE	0	3
MITOCHONDRIA	306807	306807	72086149	SIMILAR TO NADH DEHYDROGENASE (UBIQUINONE) FE-S	SOLUBLE	0	0
MITOCHONDRIA	213294	213294	56606108	PROTEIN 5	SOLUBLE	0	2
MITOCHONDRIA	243054	243054	55741424	SIMILAR TO NADH DEHYDROGENASE (UBIQUINONE) FE-S	SOLUBLE	0	5
MITOCHONDRIA	167188	167188	27717877	FLAVOPROTEIN 1	SOLUBLE	0	1
MITOCHONDRIA	256004	256004	27702072	SIMILAR TO NADH OXIDOREDUCTASE	SOLUBLE	1	7
				SIMILAR TO NADH-UBIQUINONE OXIDOREDUCTASE 30 KDA SUBUNIT, MITOCHONDRIAL PRECURSOR (COMPLEX I-30KD) (CI-30KD)			
MITOCHONDRIA	297605	297605	34864767	SIMILAR TO NADH-UBIQUINONE OXIDOREDUCTASE B17.2	SOLUBLE	0	1
MITOCHONDRIA	726780	726780	81864912	SUBUNIT	SOLUBLE	0	0
				SIMILAR TO PROBABLE MITOCHONDRIAL IMPORT RECEPTOR SUBUNIT TOM40 HOMOLOG (TRANSLOCASE OF OUTER MEMBRANE 40 KDA SUBUNIT HOMOLOG)			
MITOCHONDRIA	314386	314386	34864295	SIMILAR TO SERINE BETA LACTAMASE-LIKE PROTEIN	SOLUBLE	0	3
MITOCHONDRIA	216194	216194	62656183	LACT-1	SOLUBLE	0	0
MITOCHONDRIA	167087	167087	27716317	SIMILAR TO SERINE HYDROXYMETHYL TRANSFERASE 1	SOLUBLE	0	1
MITOCHONDRIA	277765	277765	62511137	SIMILAR TO SUCCINATE DEHYDROGENASE IP SUBUNIT	SOLUBLE	0	0
				SIMILAR TO UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX 11 KDA PROTEIN, MITOCHONDRIAL PRECURSOR (MITOCHONDRIAL HINGE PROTEIN)			
				(CYTOCHROME C1, NONHEME 11 KDA PROTEIN) (COMPLEX III SUBUNIT VIII)			
MITOCHONDRIA	220138	220138	51948476	SIMILAR TO UBIQUINOL-CYTOCHROME C REDUCTASE	SOLUBLE	0	12
MITOCHONDRIA	311925	311925	62652340	CORE PROTEIN 1	SOLUBLE	0	0
				SIMILAR TO VACUOLAR ATP SYNTHASE SUBUNIT C (V-ATPASE C SUBUNIT) (VACUOLAR PROTON PUMP C SUBUNIT)			
MITOCHONDRIA	195681	195681	34854800	SOLUTE CARRIER FAMILY 25 (MITOCHONDRIAL CARRIER, ARALAR), MEMBER 12	SOLUBLE	0	1.0455
MITOCHONDRIA	52861	52861	28194393	SUCCINATE DEHYDROGENASE COMPLEX, SUBUNIT D, INTEGRAL MEMBRANE PROTEIN	SOLUBLE	0	0
MITOCHONDRIA	313666	313666	34874487	SUCCINYL-COA LIGASE [ADP-FORMING] BETA-CHAIN, MITOCHONDRIAL PRECURSOR (SUCCINYL-COA SYNTHETASE, BETA CHAIN) (SCS-BETAA) (ATP-SPECIFIC SUCCINYL-COA SYNTHETASE BETA SUBUNIT)	SOLUBLE	0	0

MITOCHONDRIA	45104	45104	68574	SUCCINYL-COA LIGASE [GDP-FORMING] ALPHA-CHAIN, MITOCHONDRIAL	SOLUBLE	0	1
MITOCHONDRIA	302398	302398	34857707	SUCCINYL-COA LIGASE [GDP-FORMING] BETA-CHAIN, MITOCHONDRIAL (SUCCINYL-COA SYNTHETASE, BETA-CHAIN) (SCS-BETAG) (GTP-SPECIFIC SUCCINYL-COA SYNTHETASE BETA SUBUNIT)	SOLUBLE	0	0
MITOCHONDRIA	318917	318917	40254758	SULFITE OXIDASE	SOLUBLE	0	1
MITOCHONDRIA	35188	35188	1213217	SUPEROXIDE DISMUTASE [CU-ZN]	SOLUBLE	0	6
MITOCHONDRIA	111692	111692	56691	SUPEROXIDE DISMUTASE [MNI], MITOCHONDRIAL	SOLUBLE	0	3
MITOCHONDRIA	299568	299568	83305808	THIOSULFATE SULFURTRANSFERASE (RHODANASE)	SOLUBLE	1	6
MITOCHONDRIA	239142	239142	34873064	TOB3	SOLUBLE	0	1
MITOCHONDRIA	69776	69776	8394297	TRICARBOXYLATE TRANSPORT PROTEIN, MITOCHONDRIAL	SOLUBLE	0	2
MITOCHONDRIA	82392	82392	510108	TRIFUNCTIONAL ENZYME ALPHA SUBUNIT,	SOLUBLE	2	25
MITOCHONDRIA	43581	43581	510110	TRIFUNCTIONAL ENZYME BETA SUBUNIT, MITOCHONDRIAL	SOLUBLE	0	11
MITOCHONDRIA	293181	293181	34866011	UBIQUINOL-CYTOCHROME C REDUCTASE BINDING PROTEIN	SOLUBLE	0	0
MITOCHONDRIA	139461	139461	55741544	UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX CORE PROTEIN 2, MITOCHONDRIAL	SOLUBLE	4	20
MITOCHONDRIA	230682	230682	57114330	UBIQUINOL-CYTOCHROME C REDUCTASE IRON-SULFUR SUBUNIT, MITOCHONDRIAL	SOLUBLE	0	3
MITOCHONDRIA	30131	30131	7446711	UBIQUINONE BIOSYNTHESIS PROTEIN COQ7 HOMOLOG	SOLUBLE	0	0
NUCLEUS	111676	111676	92557	NUCLEAR PORE PROTEIN GP210 PRECURSOR	MEMBRANE	0	1
NUCLEUS	160674	160674	27668839	SIMILAR TO NOVEL CELL DEATH-REGULATORY PROTEIN GRIM19	MEMBRANE	0	0
NUCLEUS	221070	221070	34865422	(HNRNP-Q) (SYNAPTOTAGMIN BINDING, CYTOPLASMIC RNA INTERACTING PROTEIN)	SOLUBLE	0	0
NUCLEUS	75909	75909	3377279	ALF-C1	SOLUBLE	0	0
NUCLEUS	293750	293750	34861695	AMPHOTERIN	SOLUBLE	0	0
NUCLEUS	292562	292562	34862361	CELL PROLIFERATION RELATED PROTEIN CAP	SOLUBLE	0	0
NUCLEUS	292598	292598	77539446	COACTIVATOR-ASSOCIATED ARGININE METHYLTRANSFERASE 1 ISOFORM D	SOLUBLE	0	0
NUCLEUS	111030	111030	9843869	DAMAGE-SPECIFIC DNA BINDING PROTEIN 1	SOLUBLE	0	0
NUCLEUS	29410	29410	70819	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1	SOLUBLE	0	0
NUCLEUS	29411	29411	34855868	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A2/B1	SOLUBLE	0	0
NUCLEUS	191966	191966	34876235	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN D-LIKE, A-U-RICH ELEMENT RNA BINDING FACTOR	SOLUBLE	0	0
NUCLEUS	47431	47431	9588096	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN D0	SOLUBLE	0	0
NUCLEUS	72151	72151	38197650	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN K	SOLUBLE	0	0
NUCLEUS	82484	82484	34870743	HISTIDINE TRIAD NUCLEOTIDE-BINDING PROTEIN 1	SOLUBLE	0	0
NUCLEUS	153619	153619	21654864	HISTIDINE TRIAD PROTEIN 4	SOLUBLE	0	0
NUCLEUS	288104	288104	29650457	HISTONE ACETYLTRANSFERASE	SOLUBLE	0	0
NUCLEUS	72598	72598	444788	HISTONE H1.2	SOLUBLE	0	0
NUCLEUS	279473	279473	34858256	HISTONE H2A	SOLUBLE	0	0
NUCLEUS	249977	249977	34876364	HISTONE H3	SOLUBLE	0	0

NUCLEUS	57359	57359	3021529	HNRNP PROTEIN	SOLUBLE	0	0
NUCLEUS	25274	25274	34862186	HSP90 CO-CHAPERONE P23	SOLUBLE	0	0
NUCLEUS	51498	51498	8393610	IMPORTIN BETA-1 SUBUNIT	SOLUBLE	0	0
NUCLEUS	201803	201803	34863419	MEIOTIC RECOMBINATION PROTEIN REC14	SOLUBLE	0	0
NUCLEUS	298279	298279	56605734	NAD+ ADP-RIBOSYLTRANSFERASE 3 PARP-3	SOLUBLE	1	0
NUCLEUS	161237	161237	19705491	NESPRIN-1	SOLUBLE	0	1
NUCLEUS	219030	219030	67460593	NON-POU-DOMAIN-CONTAINING, OCTAMER BINDING PROTEIN	SOLUBLE	0	0
NUCLEUS	287945	287945	34852289	NUCLEAR CHLORIDE ION CHANNEL PROTEIN	SOLUBLE	0	0
NUCLEUS	69538	69538	6981248	NUCLEOLIN	SOLUBLE	0	0
NUCLEUS	44225	44225	7242160	NUCLEOPHOSMIN	SOLUBLE	0	0
NUCLEUS	177421	177421	1800307	P105 COACTIVATOR	SOLUBLE	0	5
NUCLEUS	78121	78121	7514041	PAR INTERACTING PROTEIN	SOLUBLE	0	0
NUCLEUS	1198	1198	14971097	PHOSPHOLIPID HYDROPEROXIDE GLUTATHIONE PEROXIDASE, NUCLEAR	SOLUBLE	0	0
NUCLEUS	304888	304888	57164095	PIRIN	SOLUBLE	0	0
NUCLEUS	55278	55278	61214571	PNUTS-PUTATIVE PROTEIN PHOSPHATASE 1 NUCLEAR TARGETING SUBUNIT	SOLUBLE	0	0
NUCLEUS	2515	2515	61557337	POLY(RC)-BINDING PROTEIN 2 ALPHA-CP2 HNRNP-E2	SOLUBLE	0	0
NUCLEUS	9454	9454	57002	POLYPYRIMIDINE TRACT-BINDING PROTEIN 1	SOLUBLE	0	0
NUCLEUS	3001	3001	9971212	PROLIFERATION RELATED ACIDIC LEUCINE RICH PROTEIN PAL31	SOLUBLE	0	2
NUCLEUS	193827	193827	34869364	RAN BINDING PROTEIN 1	SOLUBLE	0	0
NUCLEUS	111523	111523	18266700	RATSG1	SOLUBLE	0	0
NUCLEUS	234739	234739	34877805	RENT1 PROTEIN	SOLUBLE	0	0
NUCLEUS	220097	220097	27663642	RIBONUCLEASE P PROTEIN SUBUNIT P20	SOLUBLE	0	0
NUCLEUS	17327	17327	82546819	RIBONUCLEOPROTEIN F	SOLUBLE	0	0
NUCLEUS	319337	319337	51948426	RNA 3'-TERMINAL PHOSPHATE CYCLASE	SOLUBLE	0	0
NUCLEUS	287882	287882	34933204	RNA HELICASE	SOLUBLE	0	0
NUCLEUS	203449	203449	34880497	RNA HELICASE A	SOLUBLE	0	0
NUCLEUS	289382	289382	34852435	SIMILAR TO BREAKPOINT CLUSTER REGION PROTEIN	SOLUBLE	0	0
NUCLEUS	235633	235633	34875073	SIMILAR TO CELL DEATH-INDUCING DNA FRAGMENTATION FACTOR, ALPHA SUBUNIT-LIKE EFFECTOR B	SOLUBLE	0	0
NUCLEUS	273385	273385	77917570	SIMILAR TO ENDONUCLEASE G	SOLUBLE	0	0
NUCLEUS	271140	271140	34855741	SIMILAR TO EVOLUTIONARILY CONSERVED G-PATCH DOMAIN CONTAINING	SOLUBLE	0	0
NUCLEUS	279415	279415	27688925	SIMILAR TO HYPOTHETICAL PROTEIN FLJ1364	SOLUBLE	0	0
NUCLEUS	309715	309715	34869318	SIMILAR TO MICRORCHIDIA (ZINC FINGER CW-TYPE COILED-COIL DOMAIN PROTEIN 1)	SOLUBLE	0	0
NUCLEUS	154542	154542	27660592	SIMILAR TO POTENTIAL HELICASE MOV-10	SOLUBLE	0	0
NUCLEUS	208269	208269	34879288	SIMILAR TO PROBABLE RNA HELICASE	SOLUBLE	0	0
NUCLEUS	304663	304663	51948384	SIMILAR TO PROLIFERATION-ASSOCIATED PROTEIN 1	SOLUBLE	0	0
NUCLEUS	288172	288172	34853214	SIMILAR TO RNA HELICASE FAMILY	SOLUBLE	0	0
NUCLEUS	216886	216886	81910234	SIMILAR TO SMFN PROTEIN	SOLUBLE	0	0
NUCLEUS	290757	290757	34868816	SIMILAR TO SPLICING COACTIVATOR SUBUNIT SRM300; RNA BINDING PROTEIN; AT-RICH ELEMENT BINDING FACTOR	SOLUBLE	0	0
NUCLEUS	216707	216707	34867523	SIMILAR TO STRUCTURAL MAINTENANCE OF CHROMOSOMES 1BETA	SOLUBLE	0	0

NUCLEUS	3858	3858	34877889	SMALL NUCLEAR RIBONUCLEOPROTEIN SMD1	SOLUBLE	0	0
NUCLEUS	140634	140634	624918	SP120	SOLUBLE	0	0
NUCLEUS	4905	4905	62665747	SPlicing FACTOR, ARGININE/SERINE-RICH 3	SOLUBLE	0	0
NUCLEUS	169376	169376	47606056	TELOMERASE PROTEIN COMPONENT 1	SOLUBLE	0	0
NUCLEUS	81816	81816	34878862	TRANSCRIPTIONAL ACTIVATOR PROTEIN PUR-ALPHA	SOLUBLE	0	0
PEROXISOME	75063	75063	6981450	ATP-BINDING CASSETTE, SUB-FAMILY D, MEMBER 3	MEMBRANE	0	0
PEROXISOME	11779	11779	585703	PEROXISOMAL MEMBRANE PROTEIN 2	MEMBRANE	0	0
PEROXISOME	78154	78154	3183199	VERY-LONG-CHAIN ACYL-COA SYNTHETASE (VERY-LONG-CHAIN-FATTY-ACYL-COA LIGASE)	MEMBRANE	0	24
PEROXISOME	187564	187564	50926767	2-HYDROXYPHYTYL-ACYL COA LYASE	SOLUBLE	0	3
PEROXISOME	3598	3598	6978429	3-KETOACYL-COA THIOLEASE A, PEROXISOMAL	SOLUBLE	0	2
PEROXISOME	51604	51604	8394149	ACYL-COENZYME A OXIDASE 1, PEROXISOMAL	SOLUBLE	2	15
PEROXISOME	3086	3086	21955130	ACYL-COENZYME A OXIDASE 2, PEROXISOMAL	SOLUBLE	3	7
PEROXISOME	42129	42129	2498208	ACYL-COENZYME A OXIDASE 3, PEROXISOMAL	SOLUBLE	1	10
PEROXISOME	76476	76476	13637497	ALPHA-METHYLACYL-COA RACEMASE	SOLUBLE	0	1
PEROXISOME	242939	242939	34873875	AU-BINDING ENOYL-COA HYDRATASE	SOLUBLE	0	0
PEROXISOME	3681	3681	6978607	CATALASE	SOLUBLE	34	31
PEROXISOME	68714	68714	62286984	CHLORIDE ION PUMP-ASSOCIATED 55 KDA PROTEIN	SOLUBLE	0	0
PEROXISOME	60497	60497	56972124	D-AMINO ACID OXIDASE	SOLUBLE	0	1
PEROXISOME	131621	131621	48474726	DEHYDROGENASE/REDUCTASE SDR FAMILY MEMBER 4	SOLUBLE	0	2
PEROXISOME	80356	80356	478984	DELTA3,5-DELTA2,4-DIENOYL-COA ISOMERASE,	SOLUBLE	0	2
PEROXISOME	270415	270415	34859262	MITOCHONDRIAL GLYCOLATE OXIDASE; SHORT-CHAIN ALPHA-HYDROXY ACID OXIDASE	SOLUBLE	4	12
PEROXISOME	100475	100475	50925465	HYDROXYACID OXIDASE 3	SOLUBLE	1	7
PEROXISOME	80318	80318	8392962	KAN-1	SOLUBLE	5	13
PEROXISOME	251837	251837	81885359	LACTOYL-GLUTATHIONE LYASE	SOLUBLE	0	0
PEROXISOME	43433	43433	56789700	PEROXIREDOXIN 1	SOLUBLE	1.4	4.9524
PEROXISOME	269931	269931	34849738	PEROXIREDOXIN 2	SOLUBLE	0	0
PEROXISOME	60471	60471	5902791	PEROXIREDOXIN 6	SOLUBLE	0	0
PEROXISOME	160562	160562	27667388	PEROXISOMAL ACYL-COA THIOESTERASE 2B; LIKELY ORTHOLOG OF MOUSE PEROXISOMAL ACYL-COA THIOESTERASE 2B	SOLUBLE	0	0
PEROXISOME	12072	12072	8926847	PEROXISOMAL ASSEMBLY PROTEIN PEX3	SOLUBLE	0	0
PEROXISOME	149061	149061	59809132	PEROXISOMAL BIFUNCTIONAL ENZYME	SOLUBLE	12	25
PEROXISOME	155718	155718	4126962	PEROXISOMAL MEMBRANE ANCHOR PROTEIN	SOLUBLE	0	0
PEROXISOME	108354	108354	2492741	PEROXISOMAL MULTIFUNCTIONAL ENZYME TYPE 2 (MFE-2) (D-BIFUNCTIONAL PROTEIN) (DBP) (17-BETA-HYDROXYSTEROID DEHYDROGENASE 4)	SOLUBLE	8	33
PEROXISOME	169183	169183	2911135	PEROXISOME ASSEMBLY FACTOR-2	SOLUBLE	0	0
PEROXISOME	55437	55437	6539658	PHYTYL-ACYL-COA DIOXYGENASE; PEROXISOMAL PRX IV	SOLUBLE	0	0
PEROXISOME	60442	60442	4336879		SOLUBLE	12.6	21.0476
PEROXISOME	176638	176638	90109768	PUTATIVE PEROXISOMAL 2,4-DIENOYL-COA REDUCTASE	SOLUBLE	0	3
PEROXISOME	34787	34787	6491860	PUTATIVE SHORT-CHAIN DEHYDROGENASE/REDUCTASE MRNA, COMPLETE CDS	SOLUBLE	1	8
PEROXISOME	273878	273878	34868484	SIMILAR TO BILE ACID COENZYME A: AMINO ACID N-ACYL TRANSFERASE; GLYCINE N-CHOLYL TRANSFERASE	SOLUBLE	0	2

PEROXISOME	265523	265523	34935094	SIMILAR TO GLYOXYLATE REDUCTASE/HYDROXYPYRUVATE REDUCTASE	SOLUBLE	0	0
PEROXISOME				SIMILAR TO PEGI PROTEIN	SOLUBLE	0	1
PEROXISOME	208921	208921	57164137		SOLUBLE	1	0
PEROXISOME	292730	292730	34851379	SIMILAR TO PEROXISOMAL LON PROTEASE	SOLUBLE	0	0
PEROXISOME	286770	286770	34861034	SIMILAR TO PEROXISOMAL PROLIFERATOR-ACTIVATED RECEPTOR A INTERACTING COMPLEX 285 KDA PROTEIN (PPAR-ALPHA INTERACTING COMPLEX PROTEIN 285)	SOLUBLE	0	0
PEROXISOME							
PEROXISOME	235341	235341	62645408	SIMILAR TO PEROXISOME BIOGENESIS FACTOR 16	SOLUBLE	0	0
PEROXISOME	31609	31609	56971244	URATE OXIDASE	SOLUBLE	0	6
PEROXISOME	80445	80445	2144323	XANTHINE DEHYDROGENASE/OXIDASE	SOLUBLE	0	0
PLASMA MB	11455	11455	202551	5-NUCLEOTIDASE	MEMBRANE	0	0
PLASMA MB	11241	11241	205109	AMINOPEPTIDASE N	MEMBRANE	0	0
PLASMA MB	10860	10860	1703345	AMYLOID-LIKE PROTEIN 2 PRECURSOR	MEMBRANE	0	0
PLASMA MB	44327	44327	206649	ASIALOGLYCOPROTEIN RECEPTOR (RHL2)	MEMBRANE	0	0
PLASMA MB	120624	120624	7705290	ASIALOGLYCOPROTEIN RECEPTOR 1	MEMBRANE	0	0
PLASMA MB	66007	66007	20141169	BAND 3 ANION TRANSPORT PROTEIN	MEMBRANE	0	0
PLASMA MB	141056	141056	7709992	BASIGIN	MEMBRANE	0	0
PLASMA MB	13065	13065	3075422	BILE SALT EXPORT PUMP (ATP-BINDING CASSETTE, SUB- FAMILY B, MEMBER 11) (SISTER OF P-GLYCOPROTEIN)	MEMBRANE	0	0
PLASMA MB							
PLASMA MB	196365	196365	34877005	BIOTINIDASE	MEMBRANE	0	1
PLASMA MB	78339	78339	6434855	BRAIN SIGMA RECEPTOR	MEMBRANE	0	0
PLASMA MB	60545	60545	68533633	C-TYPE LECTIN 13	MEMBRANE	0	0
PLASMA MB	199319	199319	34851208	CADHERIN-11	MEMBRANE	0	0
PLASMA MB	127670	127670	628001	CADHERIN-17 PRECURSOR	MEMBRANE	0	0
PLASMA MB	70058	70058	3695131	CALCIUM-INDEPENDENT ALPHA-LATROTOXIN RECEPTOR 2 PRECURSOR	MEMBRANE	0	0
PLASMA MB	3702	3702	6978669	CANALICULAR MULTISPECIFIC ORGANIC ANION TRANSPORTER 1	MEMBRANE	0	0
PLASMA MB	52680	52680	3242460	CANALICULAR MULTISPECIFIC ORGANIC ANION TRANSPORTER 2	MEMBRANE	0	0
PLASMA MB	228910	228910	62641476	CD81 PROTEIN	MEMBRANE	0	0
PLASMA MB	78195	78195	6885295	CHLORIDE INTRACELLULAR CHANNEL PROTEIN 4	MEMBRANE	0	0
PLASMA MB	33971	33971	82617586	CLAUDIN-3	MEMBRANE	0	0
PLASMA MB	35260	35260	9506513	COMPLEMENT REGULATORY PROTEIN	MEMBRANE	0	0
PLASMA MB	116798	116798	37693510	DAMP-1 PROTEIN	MEMBRANE	0	0
PLASMA MB	3741	3741 11237	6978773	DIPEPTIDYLPEPTIDASE 4	MEMBRANE	0	0
PLASMA MB	60453	60453	23396766	ECTO-NUCLEOTIDE	MEMBRANE	0	0
PLASMA MB				PYROPHOSPHATASE/PHOSPHODIESTERASE-1			
PLASMA MB	318787	318787	40786479	ECTONUCLEOSIDE TRIPHOSPHATE DIPHOSPHOHYDROLASE 5	MEMBRANE	3	23
PLASMA MB	85379	85379	806379	ECTONUCLEOTIDE	MEMBRANE	0	0
PLASMA MB	129647	129647	11225481	PYROPHOSPHATASE/PHOSPHODIESTERASE 3 EGF, LATROPHILIN AND SEVEN TRANSMEMBRANE DOMAIN CONTAINING PROTEIN 1	MEMBRANE	0	0
PLASMA MB							
PLASMA MB	85744	85744	6478868	EPIDERMAL GROWTH FACTOR RECEPTOR	MEMBRANE	0	0
PLASMA MB	1625	1625	6009482	EPITHELIAL-CADHERIN	MEMBRANE	0	0
PLASMA MB	101676	101676	4079709	FLOTILIN-2	MEMBRANE	0	0
PLASMA MB	18989	18989	1916610	GALECTIN-9	MEMBRANE	0	0
PLASMA MB	51463	51463	8393444	GAP JUNCTION BETA-1 PROTEIN (CONNEXIN 32) (CX32) (GAP JUNCTION 28 KDA LIVER PROTEIN)	MEMBRANE	0	0
PLASMA MB	62885	62885	7159085	GLUTAMYL AMINOPEPTIDASE	MEMBRANE	0	0

PLASMA MB	51500	51500	8393621	INSULIN RECEPTOR	MEMBRANE	0	0
PLASMA MB	259355	259355	34868649	INTEGRIN ALPHA 5	MEMBRANE	0	0
PLASMA MB	37168	37168	56494	INTEGRIN ALPHA-1 (LAMININ AND COLLAGEN RECEPTOR) (LA-1) (CD49A)	MEMBRANE	0	0
PLASMA MB	220383	220383	34873959	INTEGRIN ALPHA2B	MEMBRANE	0	0
PLASMA MB	51502	51502	8393636	INTEGRIN BETA-1	MEMBRANE	0	0
PLASMA MB	153869	153869	24308466	INTEGRIN BETA3 SUBUNIT	MEMBRANE	0	0
PLASMA MB	288163	288163	34865759	LIPOPROTEIN RECEPTOR-RELATED PROTEIN	MEMBRANE	0	4
PLASMA MB	60454	60454	529590	LIVER-SPECIFIC TRANSPORT PROTEIN	MEMBRANE	0	0
PLASMA MB	161476	161476	56090485	MANNOSE 6-PHOSPHATE RECEPTOR	MEMBRANE	0	0
PLASMA MB	3946	3946	6981078	MANNOSE 6-PHOSPHATE/INSULIN-LIKE GROWTH FACTOR II RECEPTOR	MEMBRANE	0	0
PLASMA MB	140638	140638	49258142	MEMBRANE-BOUND AMINOPEPTIDASE P	MEMBRANE	0	0
PLASMA MB	16130	16130	17736804	MID-1-RELATED CHLORIDE CHANNEL 2	MEMBRANE	0	0
PLASMA MB	75090	75090	6981542	MONOCARBOXYLATE TRANSPORTER 1	MEMBRANE	0	0
PLASMA MB	37180	37180	7514016	MULTIDRUG RESISTANCE-ASSOCIATED PROTEIN 6	MEMBRANE	0	0
PLASMA MB	279332	279332	34855325	NECT1: POLIOVIRUS RELATED RECEPTOR	MEMBRANE	0	0
PLASMA MB	63008	63008	3983131	NEURAL-CADHERIN	MEMBRANE	0	0
PLASMA MB	198521	198521	19071449	ORGANIC ANION TRANSPORTER K8	MEMBRANE	0	0
PLASMA MB	78112	78112	1916012	PHOSPHOLEMMAN	MEMBRANE	0	0
PLASMA MB	128586	128586	56465	POLYMERIC-IMMUNOGLOBULIN RECEPTOR	MEMBRANE	0	0
PLASMA MB	63679	63679	116435	POTASSIUM VOLTAGE-GATED CHANNEL SUBFAMILY A MEMBER 6	MEMBRANE	0	0
PLASMA MB	100550	100550	425789	RAT INSULIN RECEPTOR RELATED RECEPTOR 1 (SIRR-1)	MEMBRANE	0	0
PLASMA MB	44652	44652	420280	RAT MHC CLASS I CELL SURFACE ANTIGEN MRNA PRECURSOR	MEMBRANE	0	0
PLASMA MB	38864	38864	49904285	SCAVENGER RECEPTOR CLASS B MEMBER 1	MEMBRANE	0	0
PLASMA MB	51490	51490	8393560	SERINE PROTEASE HEPsin	MEMBRANE	0	0
PLASMA MB	275767	275767	34875033	SIDEKICK 2; DROSOPHILA SIDEKICK-LIKE; CHICKEN SIDEKICK 2-LIKE	MEMBRANE	0	0
PLASMA MB	278570	278570	34875258	SIMILAR TO ATP-BINDING CASSETTE TRANSPORTER SUB-FAMILY A MEMBER 6	MEMBRANE	0	0
PLASMA MB	209410	209410	34875001	SIMILAR TO ATP-BINDING CASSETTE TRANSPORTER SUB-FAMILY A MEMBER 8A	MEMBRANE	0	0
PLASMA MB	265343	265343	27676422	SIMILAR TO CLEFT LIP AND PALATE ASSOCIATED TRANSMEMBRANE PROTEIN 1	MEMBRANE	0	0
PLASMA MB	305736	305736	34858994	SIMILAR TO HISTOCOMPATIBILITY 13; PRESENILIN-LIKE PROTEIN 3	MEMBRANE	0	0
PLASMA MB	299926	299926	34856480	SIMILAR TO INTEGRIN ALPHA V SUBUNIT	MEMBRANE	0	0
PLASMA MB	199085	199085	34855581	SIMILAR TO MALTASE-GLUCOAMYLASE; INTESTINAL	MEMBRANE	0	0
PLASMA MB	222218	222218	34863455	SIMILAR TO SEMAPHORIN SUBCLASS 4 MEMBER G	MEMBRANE	0	0
PLASMA MB	206065	206065	34864902	SIMILAR TO STABILIN-2	MEMBRANE	0	0
PLASMA MB	301709	301709	34855791	SIMILAR TO UROPLAKIN IA	MEMBRANE	0	0
PLASMA MB	286665	286665	34879705	SLC26A9 ANION TRANSPORTER/EXCHANGE	MEMBRANE	0	0
PLASMA MB	11254	11254	8394279	SODIUM/BILE ACID COTransporter	MEMBRANE	0	0
PLASMA MB	3651	3651	6978543	SODIUM/POTASSIUM-TRANSPORTING ATPASE ALPHA-1 CHAIN	MEMBRANE	0	0
PLASMA MB	3654	3654	6978549	SODIUM/POTASSIUM-TRANSPORTING ATPASE BETA-1 CHAIN	MEMBRANE	0	0
PLASMA MB	3656	3656	6978553	SODIUM/POTASSIUM-TRANSPORTING ATPASE BETA-3 CHAIN	MEMBRANE	0	0

PLASMA MB	75093	75093	92281	SOLUTE CARRIER FAMILY 2, FACILITATED GLUCOSE TRANSPORTER, MEMBER 2	MEMBRANE	0	0
PLASMA MB		78114	9624356	SOLUTE CARRIER FAMILY 21 MEMBER 10	MEMBRANE	0	0
PLASMA MB		152150	8394294	SOLUTE CARRIER FAMILY 21 MEMBER 3	MEMBRANE	0	0
PLASMA MB		43622	3914190	SOLUTE CARRIER FAMILY 21 MEMBER 5	MEMBRANE	0	0
PLASMA MB		47477	9622206	SOLUTE CARRIER FAMILY 21 MEMBER 9	MEMBRANE	0	0
PLASMA MB		262547	34876981	STABLIN-1	MEMBRANE	0	0
PLASMA MB		153825	50401220	STABLIN-2	MEMBRANE	0	0
PLASMA MB		265569	34853860	STOMATIN	MEMBRANE	0	0
PLASMA MB		104202	431453	SULFATE ANION TRANSPORTER 1	MEMBRANE	0	0
PLASMA MB		33179	37589607	SYNAPTIC GLYCOPROTEIN SC2	MEMBRANE	0	1
PLASMA MB		75082	6981518	SYNDECAN-1 PRECURSOR	MEMBRANE	0	0
PLASMA MB		41211	6981520	SYNDECAN-2 PRECURSOR	MEMBRANE	0	0
PLASMA MB		75083	6981522	SYNDECAN-4 PRECURSOR	MEMBRANE	0	0
PLASMA MB		217700	34872230	TASTE RECEPTOR, TYPE 1, MEMBER 2	MEMBRANE	0	3
PLASMA MB		269397	34869255	TRANSFERRIN RECEPTOR	MEMBRANE	0	0
PLASMA MB		315288	34871536	TRANSFERRIN RECEPTOR PROTEIN 2 (TFR2)	MEMBRANE	0	0
PLASMA MB		201751	62646756	TUMOR NECROSIS FACTOR ALPHA-INDUCED ADIPOSE- RELATED PROTEIN	MEMBRANE	0	0
PLASMA MB		310121	34852937	VANIN 1	MEMBRANE	0	0
PLASMA MB		318701	61889099	CLAUDIN-1	MEMBRANE	0	0
PROT MOD		104182	7768591	ACETYL-COA TRANSPORTER	MEMBRANE	0	0
PROT MOD		207716	21392392	ACYLCOA-CHOLESTEROL ACYLTRANSFERASE 2	MEMBRANE	0	0
PROT MOD		265519	34932104	AFG3 ATPASE FAMILY GENE 3-LIKE 2	MEMBRANE	0	0
PROT MOD		141534	204255	ALPHA 2,6-SIALYLTRANSFERASE	MEMBRANE	0	0
PROT MOD		290726	34852997	ALPHA-1,2-MANNOSIDASE	MEMBRANE	0	0
PROT MOD		2699	740930	ALPHA-1,3-MANNOSYL-GLYCOPROTEIN 2-BETA-N- ACETYLGLUCOSAMINYLTRANSFERASE	MEMBRANE	0	0
PROT MOD		60482	747976	ALPHA-1,6-MANNOSYL-GLYCOPROTEIN 2-BETA-N- ACETYLGLUCOSAMINYLTRANSFERASE	MEMBRANE	0	0
PROT MOD		56042	34854866	BETA 1,3-GALACTOSYL TRANSFERASE POLYPEPTIDE 1	MEMBRANE	0	0
PROT MOD		137529	51858903	BETA-1,4 N-ACETYL GALACTOSAMINYLTRANSFERASE	MEMBRANE	0	0
PROT MOD		278143	27681143	CARBOHYDRATE (CHONDROITIN) SYNTHASE 2	MEMBRANE	0	0
PROT MOD		3713	6978699	CARBOXYPEPTIDASE D	MEMBRANE	0	0
PROT MOD		70677	7674155	CDP-DIACYLGLYCEROL-INOSITOL 3- PHOSPHATIDYLTRANSFERASE	MEMBRANE	0	1
PROT MOD		264754	56090333	CHOLINE/ETHANOLAMINEPHOSPHOTRANSFERASE 1	MEMBRANE	0	0
PROT MOD		55277	8927166	CORE1 UDP-GALACTOSE:N-ACETYL GALACTOSAMINE- ALPHA-R BETA 1,3-GALACTOSYL TRANSFERASE	MEMBRANE	0	0
PROT MOD		299013	34863951	D-GLUCURONYL C5-EPIMERASE	MEMBRANE	0	0
PROT MOD		13029	48428847	DADI1 (DEFENDER AGAINST CELL DEATH 1)	MEMBRANE	0	0
PROT MOD		60408	16758190	DELTA-5 DESATURASE	MEMBRANE	0	0
PROT MOD		145183	9965432	DIACYLGLYCEROL O-ACYLTRANSFERASE 1	MEMBRANE	0	0
PROT MOD		133253	2642187	ENDO-ALPHA-D-MANNOSIDASE	MEMBRANE	0	0
PROT MOD		29993	6225312	FATTY-ACID AMIDE HYDROLASE	MEMBRANE	0	1
PROT MOD		47234	9506955	FURIN PRECURSOR	MEMBRANE	0	0
PROT MOD		228888	34861582	GALACTOSYL GALACTOSYLXYLOSYLPROTEIN 3-BETA- GLUCURONOSYL TRANSFERASE 3	MEMBRANE	0	0
PROT MOD		75089	6981540	GD3 ALPHA 2,8-SIALYLTRANSFERASE	MEMBRANE	0	0

PROT MOD	51409	51409	48427849	GLYCOPROTEIN PROCESSING GLUCOSIDASE I	MEMBRANE	0	4
PROT MOD	229568	229568	34867143	GLYCOPROTEIN-4-BETA-GALACTOSYLTRANSFERASE 2	MEMBRANE	0	0
PROT MOD	44217	44217	401136	HEPARAN SULFATE N-DEACETYLASE/N-SULFOTRANSFERASE	MEMBRANE	0	0
PROT MOD	82681	82681	45477000	LIPID PHOSPHATE PHOSPHOHYDROLASE 3	MEMBRANE	0	0
PROT MOD	44475	44475	417242	LONG-CHAIN-FATTY-ACID--COA LIGASE 6	MEMBRANE	0	0
PROT MOD	248855	248855	34860045	MANNOSIDASE 1-BETA	MEMBRANE	0	0
PROT MOD	205526	196264 205526	34877940	MANNOSIDASE 2, ALPHA 1	MEMBRANE	0	0
PROT MOD	338661	338661	40786505	MANNOSIDASE 2, ALPHA B1	MEMBRANE	0	1
PROT MOD	281230	281230	34854458	MEMBRANE BOUND O-ACYL TRANSFERASE	MEMBRANE	0	0
PROT MOD	51465	51465	8393450	MG160	MEMBRANE	0	0
PROT MOD	116574	116574	37081094	NICASTRIN	MEMBRANE	0	0
PROT MOD	69787	69787	6981348	PHOSPHATIDYLETHANOLAMINE N-METHYL TRANSFERASE	MEMBRANE	0	0
PROT MOD	60561	60561	62654523	PHOSPHOINOSITIDE PHOSPHATASE SAC1	MEMBRANE	0	0
PROT MOD	82680	82680	2696236	PHOSPHOLIPASE B	MEMBRANE	0	0
PROT MOD	68735	68735	1709559	POLYPEPTIDE N-ACETYLGALACTOSAMINYLTRANSFERASE	MEMBRANE	0	0
PROT MOD	231757	231757	34867585	PUTATIVE MANNOSYLTRANSFERASE	MEMBRANE	0	0
PROT MOD	176270	176270	6651436	PUTATIVE N-ACETYLTRANSFERASE CAMELLO 4	MEMBRANE	0	0
PROT MOD	140359	140359	48474727	RETINOID-INDUCIBLE SERINE CARBOXYPEPTIDASE	MEMBRANE	0	0
PROT MOD	193923	193923	62512124	RIBOPHORIN 2	MEMBRANE	0	15
PROT MOD	337611	337611	71891579	RIBOPHORIN I	MEMBRANE	13	25
PROT MOD	197285	197285	34863046	SELENOPROTEIN I	MEMBRANE	0	0
PROT MOD	274486	274486	34853099	SIMILAR TO 1-ACYLGLYCEROL-3-PHOSPHATE O-ACYLTRANSFERASE 2	MEMBRANE	0	0
PROT MOD	237775	237775	34862502	SIMILAR TO ACYLTRANSFERASE FAMILY MEMBER (5G933)	MEMBRANE	0	0
PROT MOD	210144	210144	27663478	SIMILAR TO BETA-1,3-GALACTOSYLTRANSFERASE-6	MEMBRANE	0	0
PROT MOD	201171	201171	34866546	SIMILAR TO GAL BETA 1,3GALNAC ALPHA 2,3-SIALYLTRANSFERASE	MEMBRANE	0	0
PROT MOD	259411	259411	34860929	SIMILAR TO HEPARAN SULFATE 2-SULFOTRANSFERASE	MEMBRANE	0	0
PROT MOD	273814	273814	27705330	SIMILAR TO MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE	MEMBRANE	0	0
PROT MOD	194890	194890	34870693	SIMILAR TO N-ACETYLGALACTOSAMINYLTRASNFERASE IVB	MEMBRANE	0	0
PROT MOD	304110	304110	34861816	SIMILAR TO N-ACETYLLACTOSAMINIDE BETA-1,3-N-ACETYLGALACTOSAMINYLTRANSFERASE (POLY-N-ACETYLLACTOSAMINE EXTENSION ENZYME)	MEMBRANE	0	0
PROT MOD	214259	214259 263869	34866419	SIMILAR TO OLIGOSACCHARYL TRANSFERASE 3	MEMBRANE	0	2
PROT MOD	206351	206351	34872203	SIMILAR TO OLIGOSACCHARYL TRANSFERASE	MEMBRANE	0	1
PROT MOD	218478	218478	34856275	SIMILAR TO SERINE PROTEASE OMI	MEMBRANE	0	1
PROT MOD	231548	231548	71153846	SOLUBLE CALCIUM-ACTIVATED NUCLEOTIDASE SCAN-1 (UDPASE)	MEMBRANE	0	0
PROT MOD	722796	722796	48428498	TYPE 2 LACTOSAMINE ALPHA-2,3-SIALYLTRANSFERASE	MEMBRANE	0	0
PROT MOD	241393	241393	76779364	TYROSYLPROTEIN SULFOTRANSFERASE-1	MEMBRANE	0	0
PROT MOD	319029	319029	51315700	UDP-N-ACETYL-ALPHA-D-GALACTOSAMINE:POLYPEPTIDE N-ACETYLGALACTOSAMINYLTRANSFERASE 11 (GALNAC-T11)	MEMBRANE	0	0

PROT MOD	307730	307730	34851891	UDP-N-ACETYL-ALPHA-D-GALACTOSAMINE:POLYPEPTIDE N-ACETYL GALACTOSAMINYL TRANSFERASE 2; PPGANTASE-T2	MEMBRANE	0	0
PROT MOD	271576	271576	34859909	UDP-N-ACETYLGLUCOSAMINE (UDP-GLCNAC) TRANSPORTER	MEMBRANE	0	0
PROT MOD	78166	78166	6136262	VITAMIN K-DEPENDENT GAMMA-CARBOXYLASE	MEMBRANE	1	3
PROT MOD	189334	189334	71164811	XYLOSYLTRANSFERASE II	MEMBRANE	0	0
PROT MOD	288219	288219	34870924	ZMPSTE24 METALLOPROTEINASE	MEMBRANE	0	0
PROT MOD	129388	129388	20139870	15 KDA SELENOPROTEIN	SOLUBLE	0	5
PROT MOD	605	605	8131852	ADIPOCYTE-DERIVED LEUCINE AMINOPEPTIDASE	SOLUBLE	3	10
PROT MOD	192728	192728	34861580	ALPHA GLUCOSIDASE II, ALPHA SUBUNIT	SOLUBLE	13	13
PROT MOD	161569	161569	62648970	ALPHA-1,3-MANNOSYLTRANSFERASE ALG2	SOLUBLE	0	0
PROT MOD	78213	78213	37590777	FARNESYL PYROPHOSPHATE SYNTHETASE	MEMBRANE	0	0
PROT MOD	85115	85115	9506591	FARNESYL-DIPHOSPHATE FARNESYLTRANSFERASE	MEMBRANE	0	2
PROT MOD	43659	43659	57890	FATTY ACID SYNTHASE	MEMBRANE	0	2
PROT MOD	71698	71698	476082	FATTY ACID-BINDING PROTEIN, BRAIN	SOLUBLE	0	0
PROT MOD	3760	3760	6978825	FATTY ACID-BINDING PROTEIN, LIVER	SOLUBLE	2	8.8889
PROT MOD	19169	19169	6137382	GLYCINE N-METHYLTRANSFERASE	SOLUBLE	0	0
PROT MOD	23872	23872	47938984	MICROSOMAL DIPEPTIDASE	SOLUBLE	0	0
PROT MOD	338609	338609	40254747	N-ACYLSPHINGOSINE AMIDOHYDROLASE (ACID CERAMIDASE)	MEMBRANE	0	0
PROT MOD	78152	78152	543420	N-HYDROXYARYLAMINE SULFOTRANSFERASE	SOLUBLE	0	0
PROT MOD	256333	256333	75905813	O-GLCNAC TRANSFERASE-INTERACTING PROTEIN OF 98 KDA	SOLUBLE	0	0
PROT MOD	229000	229000	81914601	PEPTIDE N-MYRISTOYLTRANSFERASE 1	SOLUBLE	0	0
PROT MOD	51565	51565	8393922	PHOSPHATIDYLCHOLINE TRANSFER PROTEIN	SOLUBLE	0	0
PROT MOD	51562	51562	8393910	PHOSPHATIDYLETHANOLAMINE-BINDING PROTEIN	SOLUBLE	0	1
PROT MOD	60574	60574	6093729	PROCOLLAGEN-LYSINE:2-OXOGLUTARATE 5- DIOXYGENASE 1	SOLUBLE	0	0
PROT MOD	286288	286288	30017429	PROCOLLAGEN-LYSINE:2-OXOGLUTARATE 5- DIOXYGENASE 3	SOLUBLE	0	2
PROT MOD	31490	31490	67677918	PROTEIN-GLUTAMINE GAMMA-GLUTAMYLTRANSFERASE K	MEMBRANE	0	0
PROT MOD	69363	69363	92483	S-ADENOSYLMETHIONINE SYNTHETASE ALPHA AND BETA FORMS	SOLUBLE	0	0
PROT MOD	263376	263376	34869825	SDF2 LIKE PROTEIN 1	SOLUBLE	2	5
PROT MOD	60562	60562	21542226	SEC14-LIKE PROTEIN 2	SOLUBLE	0	0
PROT MOD	303924	303924	34865846	SIMILAR TO 5730439E10RIK PROTEIN	SOLUBLE	1	9
PROT MOD	296012	296012	34853323	SIMILAR TO ALG-2	SOLUBLE	0	0
PROT MOD	310313	310313	34861578	SIMILAR TO ALPHA GLUCOSIDASE II, ALPHA SUBUNIT	SOLUBLE	6	9
PROT MOD	208522	208522	34860445	SIMILAR TO ALPHA GLUCOSIDASE II, BETA SUBUNIT	SOLUBLE	3	6
PROT MOD	139592	139592	27681359	SIMILAR TO ARYLACETYL ACYL-COA N- ACYLTRANSFERASE	SOLUBLE	0	1
PROT MOD	191580	191580	34860748	SIMILAR TO DOLICHOL-PHOSPHATE-MANNOSE SYNTHASE	SOLUBLE	0	2
PROT MOD	304061	304061	34856938	SIMILAR TO DOLICHYL-PHOSPHATE BETA- GLUCOSYLTRANSFERASE-LIKE	MEMBRANE	0	0
PROT MOD	299017	299017	34867432	SIMILAR TO GLUCAN (1,4-ALPHA-), BRANCHING ENZYME 1; DNA SEGMENT, CHR 16, ERATO DOI 536, EXPRESSED	SOLUBLE	0	0
PROT MOD	261456	261456	33086562	SIMILAR TO GLYCINE-N-ACYLTRANSFERASE	SOLUBLE	0	0

PROT MOD	221417	221417	34860820	SIMILAR TO METHIONYLAMINOPEPTIDASE 1	SOLUBLE	0	0
PROT MOD	198275	198275	34863093	SIMILAR TO SULFIC-ACID O-ACETYLESTERASE	SOLUBLE	0	1
PROT MOD	221314	221314	34872061	SIMILAR TO SULFATASE MODIFYING FACTOR 2	SOLUBLE	0	0
PROT MOD	269681	269681	37999349	SPHINGOSINE-1-PHOSPHATE LYASE 1	SOLUBLE	0	2
PROT MOD	281046	281046	27707476	UDP-GALACTOSE:N-ACETYL GALACTOSAMINEALPHA-PEPTIDE BETA1,3-GALACTOSYLTRANSFERASE	MEMBRANE	0	0
PROT MOD	171823	171823	7677176	UDP-GLUCOSE GLYCOPROTEIN:GLUCOSYLTRANSFERASE	SOLUBLE	7	36
PROT SYNIFOLD	43654	43654	2506117	ANTIGEN PEPTIDE TRANSPORTER 1	MEMBRANE	0	0
PROT SYNIFOLD	69775	69775	543922	CALNEXIN	MEMBRANE	0	9
PROT SYNIFOLD	247469	247469	34856569	EXOSTOSES (MULTIPLE) 2	MEMBRANE	0	0
PROT SYNIFOLD	255984	255984	76574685	OSTEOCLAST INHIBITORY LECTIN	MEMBRANE	0	0
PROT SYNIFOLD	152512	152512	81910029	P34 PROTEIN	MEMBRANE	0	0
PROT SYNIFOLD	283106	283106	34873471	PEPTIDYLPROLYL ISOMERASE D (CYCLOPHILIN D)	MEMBRANE	0	0
PROT SYNIFOLD	75284	75284	63107555	PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT	MEMBRANE	0	1
PROT SYNIFOLD	161564	161564	27714473	ISOFORM 1	MEMBRANE	0	0
PROT SYNIFOLD	3224	3224	61889101	SIGNAL PEPTIDASE COMPLEX (18KD)	MEMBRANE	0	1
PROT SYNIFOLD	216144	216144	27678066	SIGNAL PEPTIDASE COMPLEX 25 KDA SUBUNIT	MEMBRANE	0	1
PROT SYNIFOLD	201409	201409	34882652	SIMILAR TO DNAJ (HSP40) HOMOLOG, SUBFAMILY B, MEMBER 12	MEMBRANE	0	0
PROT SYNIFOLD	269276	269276	34856469	SIMILAR TO ER-RESIDENT PROTEIN ERDJ5	MEMBRANE	0	0
PROT SYNIFOLD	209405	209405	34853169	SIMILAR TO SEC63	MEMBRANE	0	1
PROT SYNIFOLD	307512	307512	27667224	SP12	MEMBRANE	0	0
PROT SYNIFOLD	140838	140838	46237539	TAPASIN	MEMBRANE	0	0
PROT SYNIFOLD	275946	275946	81883693	TRAM1	MEMBRANE	0	0
PROT SYNIFOLD	166245	166245	71162390	TRANSLOCON-ASSOCIATED PROTEIN ALPHA	MEMBRANE	3	5
PROT SYNIFOLD	152155	152155	8394364	TRANSLOCON-ASSOCIATED PROTEIN, DELTA SUBUNIT	MEMBRANE	4	14
PROT SYNIFOLD	32867	32867	68163545	40S RIBOSOMAL PROTEIN S10	SOLUBLE	0	7
PROT SYNIFOLD	4834	4834	54039305	40S RIBOSOMAL PROTEIN S11	SOLUBLE	6	10
PROT SYNIFOLD	132206	132206 310080	78126139	40S RIBOSOMAL PROTEIN S12	SOLUBLE	2	1
PROT SYNIFOLD	4835	4835	54261703	40S RIBOSOMAL PROTEIN S13	SOLUBLE	6	8
PROT SYNIFOLD	98434	98434	37231722	40S RIBOSOMAL PROTEIN S14	SOLUBLE	4	1.1111
PROT SYNIFOLD	4836	4836	8394212	40S RIBOSOMAL PROTEIN S15	SOLUBLE	1	2
PROT SYNIFOLD	72161	72161	54039450	40S RIBOSOMAL PROTEIN S15A	SOLUBLE	7	5
PROT SYNIFOLD	4837	4837	54039370	40S RIBOSOMAL PROTEIN S16	SOLUBLE	12	10
PROT SYNIFOLD	250506	250506	34853950	40S RIBOSOMAL PROTEIN S17	SOLUBLE	2	3
PROT SYNIFOLD	60848	60848	50403620	40S RIBOSOMAL PROTEIN S18	SOLUBLE	10	16
PROT SYNIFOLD	122667	122667	82654220	40S RIBOSOMAL PROTEIN S19	SOLUBLE	10	7
PROT SYNIFOLD	100993	100993 193682 307172	2920825	40S RIBOSOMAL PROTEIN S2	SOLUBLE	12	18
PROT SYNIFOLD	4840	4840	56090271	40S RIBOSOMAL PROTEIN S20	SOLUBLE	4	0
PROT SYNIFOLD	37243	37243	483517	40S RIBOSOMAL PROTEIN S21	SOLUBLE	2	5
PROT SYNIFOLD	4842	4842	730647	40S RIBOSOMAL PROTEIN S23	SOLUBLE	2	1
PROT SYNIFOLD	4843	4843	57858	40S RIBOSOMAL PROTEIN S24	SOLUBLE	6	6
PROT SYNIFOLD	4844	4844	74355904	40S RIBOSOMAL PROTEIN S25	SOLUBLE	7	2
PROT SYNIFOLD	75074	75074	6981488	40S RIBOSOMAL PROTEIN S26	SOLUBLE	1	4
PROT SYNIFOLD	120488	4845 120488	133902	40S RIBOSOMAL PROTEIN S27	SOLUBLE	3	4
PROT SYNIFOLD	127926	127926	37194821	40S RIBOSOMAL PROTEIN S27A	SOLUBLE	0	5
PROT SYNIFOLD	1344	1344	51338623	40S RIBOSOMAL PROTEIN S28	SOLUBLE	2	5
PROT SYNIFOLD	4847	4847	6981490	40S RIBOSOMAL PROTEIN S29	SOLUBLE	0	1

PROT SYNIFOLD	60850	60850	57164151	40S RIBOSOMAL PROTEIN S3	SOLUBLE	23	28
PROT SYNIFOLD	106720	106720	51338625	40S RIBOSOMAL PROTEIN S30	SOLUBLE	1	0
PROT SYNIFOLD	51618	51618	8394221	40S RIBOSOMAL PROTEIN S3A	SOLUBLE	5	10
PROT SYNIFOLD	4849	4849	56090273	40S RIBOSOMAL PROTEIN S4	SOLUBLE	16	18
PROT SYNIFOLD	278725	278725	34854534	40S RIBOSOMAL PROTEIN S5	SOLUBLE	1	3
PROT SYNIFOLD	74523	74523	8394224	40S RIBOSOMAL PROTEIN S6	SOLUBLE	2	7
PROT SYNIFOLD	4853	4853	66730357	40S RIBOSOMAL PROTEIN S7	SOLUBLE	5	12
PROT SYNIFOLD	4854	4854	62078585	40S RIBOSOMAL PROTEIN S8	SOLUBLE	10	9
PROT SYNIFOLD	142294	142294	52788199	40S RIBOSOMAL PROTEIN S9	SOLUBLE	6	8
PROT SYNIFOLD	51515	51515 74609	8393693	40S RIBOSOMAL PROTEIN SA	SOLUBLE	16	37
PROT SYNIFOLD	37238	37238 238486	50403574	60S RIBOSOMAL PROTEIN L10	SOLUBLE	0	0
PROT SYNIFOLD	37218	37218 215516	51702767	60S RIBOSOMAL PROTEIN L10A	SOLUBLE	9	16
PROT SYNIFOLD	2378	2378	71043900	60S RIBOSOMAL PROTEIN L11	SOLUBLE	0	2
PROT SYNIFOLD	144419	144419	27706782	60S RIBOSOMAL PROTEIN L12	SOLUBLE	7	7
PROT SYNIFOLD	37239	37239	510552	60S RIBOSOMAL PROTEIN L13	SOLUBLE	2	4
PROT SYNIFOLD	106718	106718	548747	60S RIBOSOMAL PROTEIN L13A	SOLUBLE	1	1
PROT SYNIFOLD	43519	43519	2500360	60S RIBOSOMAL PROTEIN L14	SOLUBLE	1	0
PROT SYNIFOLD	1145	1145 293440	515865	60S RIBOSOMAL PROTEIN L15	SOLUBLE	7	20
PROT SYNIFOLD	139425	139425	71051098	60S RIBOSOMAL PROTEIN L17	SOLUBLE	0	0
PROT SYNIFOLD	37240	37240 248463	54261673	60S RIBOSOMAL PROTEIN L18	SOLUBLE	12	16.64
PROT SYNIFOLD	71631	71631	50403587	60S RIBOSOMAL PROTEIN L18A	SOLUBLE	0	1
PROT SYNIFOLD	4809	4809	51338626	60S RIBOSOMAL PROTEIN L19	SOLUBLE	0	0
PROT SYNIFOLD	98375	98375 226038 241516	62645460	60S RIBOSOMAL PROTEIN L21	SOLUBLE	0	0
PROT SYNIFOLD	4392	4392	52221202	60S RIBOSOMAL PROTEIN L22	SOLUBLE	0	0
PROT SYNIFOLD	4807	4807	56090279	60S RIBOSOMAL PROTEIN L23	SOLUBLE	0	0
PROT SYNIFOLD	144423	144423	62656804	60S RIBOSOMAL PROTEIN L23A	SOLUBLE	0	0
PROT SYNIFOLD	4812	4812	560493	60S RIBOSOMAL PROTEIN L24	SOLUBLE	3	2
PROT SYNIFOLD	4813	4813	27672824	60S RIBOSOMAL PROTEIN L26	SOLUBLE	0	0
PROT SYNIFOLD	4814	4814 301863	60688496	60S RIBOSOMAL PROTEIN L27	SOLUBLE	4	4
PROT SYNIFOLD	273222	273222	62639430	60S RIBOSOMAL PROTEIN L27A	SOLUBLE	2	0
PROT SYNIFOLD	74518	74518	61889083	60S RIBOSOMAL PROTEIN L28	SOLUBLE	1	2
PROT SYNIFOLD	144426	144426	38454246	60S RIBOSOMAL PROTEIN L3	SOLUBLE	5	17
PROT SYNIFOLD	4817	4817	51702801	60S RIBOSOMAL PROTEIN L30	SOLUBLE	4	5
PROT SYNIFOLD	4818	4818	57115	60S RIBOSOMAL PROTEIN L31	SOLUBLE	0	0
PROT SYNIFOLD	4819	4819	6981482	60S RIBOSOMAL PROTEIN L32	SOLUBLE	0	0
PROT SYNIFOLD	136355	136355	34860562	60S RIBOSOMAL PROTEIN L34	SOLUBLE	0	1
PROT SYNIFOLD	103229	103229	57702	60S RIBOSOMAL PROTEIN L35	SOLUBLE	0	0
PROT SYNIFOLD	14850	14850	57119	60S RIBOSOMAL PROTEIN L35A	SOLUBLE	0	0
PROT SYNIFOLD	65711	65711 214593	34849736	60S RIBOSOMAL PROTEIN L36	SOLUBLE	2	5
PROT SYNIFOLD	3029	3029	57121	60S RIBOSOMAL PROTEIN L37	SOLUBLE	0	0
PROT SYNIFOLD	4820	4820	56972097	60S RIBOSOMAL PROTEIN L37A	SOLUBLE	1	0
PROT SYNIFOLD	4821	4821	74354458	60S RIBOSOMAL PROTEIN L38	SOLUBLE	0	0
PROT SYNIFOLD	4822	4822	6981484	60S RIBOSOMAL PROTEIN L39	SOLUBLE	0	0
PROT SYNIFOLD	85424	85424	1363989	60S RIBOSOMAL PROTEIN L4	SOLUBLE	2	7
PROT SYNIFOLD	77849	77849	9737178	60S RIBOSOMAL PROTEIN L40	SOLUBLE	0	0
PROT SYNIFOLD	111202	111202	62643486	60S RIBOSOMAL PROTEIN L44	SOLUBLE	0	0
PROT SYNIFOLD	37237	37237	57125	60S RIBOSOMAL PROTEIN L5	SOLUBLE	0	8
PROT SYNIFOLD	42185	42185	2507315	60S RIBOSOMAL PROTEIN L6	SOLUBLE	0	7
PROT SYNIFOLD	154516	154516	27660180	60S RIBOSOMAL PROTEIN L7	SOLUBLE	0	0
PROT SYNIFOLD	4825	4825 200139	62644799	60S RIBOSOMAL PROTEIN L7A	SOLUBLE	21	30.36
PROT SYNIFOLD	4826	4826	78214309	60S RIBOSOMAL PROTEIN L8	SOLUBLE	3	16
PROT SYNIFOLD	160533	160533	27666954	60S RIBOSOMAL PROTEIN L9	SOLUBLE	0	0
PROT SYNIFOLD	23405	23405	730581	60S RIBOSOMAL PROTEIN P0	SOLUBLE	26	30

PROT SYNIFOLD	144430	144430	56090277	60S RIBOSOMAL PROTEIN P1	SOLUBLE	2	2
PROT SYNIFOLD	144431	144431	71795613	60S RIBOSOMAL PROTEIN P2	SOLUBLE	0	3
PROT SYNIFOLD	214842	214842	27717711	ACIDIC RIBOSOMAL PROTEIN P1	SOLUBLE	0	1
PROT SYNIFOLD	201232	201232	62660456	ACIDIC RIBOSOMAL PROTEIN P2, CYTOSOLIC	SOLUBLE	0	0
PROT SYNIFOLD	61026	61026	81916405	APOBEC-1 COMPLEMENTATION FACTOR LONG ISOFORM	SOLUBLE	0	0
PROT SYNIFOLD	231492	231492	34852051	ATP-BINDING CASSETTE, SUB-FAMILY F (GCN20), MEMBER 1	SOLUBLE	0	0
PROT SYNIFOLD	28269	28269	38303969	BIP	SOLUBLE	157,927	113.04
PROT SYNIFOLD	280160	280160	81883487	BOCA	SOLUBLE	0	3
PROT SYNIFOLD	55585	55585	8394168	CALMODULIN	SOLUBLE	0	0
PROT SYNIFOLD	23403	23403	55855	CALRETICULIN	SOLUBLE	38	90
PROT SYNIFOLD	288751	288751	76253725	CCT (CHAPERONIN CONTAINING TCP-1) ZETA SUBUNIT	SOLUBLE	0	1
PROT SYNIFOLD	252047	252047	37590247	CCT5 PROTEIN	SOLUBLE	0	0
PROT SYNIFOLD	161408	161408	27712178	CCTETA, ETA SUBUNIT OF THE CHAPERONIN CONTAINING TCP-1 (CCT)	SOLUBLE	0	0
PROT SYNIFOLD	249893	249893	34867525	CCTTHETA, THETA SUBUNIT OF THE CHAPERONIN CONTAINING TCP-1 (CCT)	SOLUBLE	0	0
PROT SYNIFOLD	121548	121548	400542	CHAPERONIN 10	SOLUBLE	0	0
PROT SYNIFOLD	292700	292700	54400730	CHAPERONIN CONTAINING TCP-1 BETA SUBUNIT	SOLUBLE	0	0
PROT SYNIFOLD	169833	169833	40018616	CHAPERONIN CONTAINING TCP1, SUBUNIT 3 (GAMMA)	SOLUBLE	0	0
PROT SYNIFOLD	166356	166356	52000745	CHAPERONIN DELTA SUBUNIT	SOLUBLE	0	0
PROT SYNIFOLD	80354	80354	2143900	CYCLOPHILIN B	SOLUBLE	24	33
PROT SYNIFOLD	240056	240056	34863163	DEAD BOX PROTEIN 1	SOLUBLE	0	0
PROT SYNIFOLD	249374	249374	34854165	DEAH (ASP-GLU-ALA-HIS) BOX POLYPEPTIDE 29; NUCLEIC ACID HELICASE DDX	SOLUBLE	0	0
PROT SYNIFOLD	119910	119910	62652445	DERLIN-1 (DEGRADATION IN ENDOPLASMIC RETICULUM PROTEIN 1) (DER1-LIKE PROTEIN 1)	MEMBRANE	0	0
PROT SYNIFOLD	295796	295796	62543491	DNAJ (HSP40) HOMOLOG, SUBFAMILY B, MEMBER 11	SOLUBLE	4	13
PROT SYNIFOLD	8742	8742	51702257	DNAJ HOMOLOG SUBFAMILY A MEMBER 1	SOLUBLE	0	3
PROT SYNIFOLD	1106	1106	2281451	DNAJ HOMOLOG SUBFAMILY A MEMBER 2	SOLUBLE	0	0
PROT SYNIFOLD	140182	140182 223872	85057089	ELONGATION FACTOR 1-ALPHA 1 (EF-1-ALPHA-1)	SOLUBLE	3	12
PROT SYNIFOLD	51432	51432	8393296	ELONGATION FACTOR 2	SOLUBLE	0	0
PROT SYNIFOLD	282876	282876	34876487	ENDOPLASMIC OXIDOREDUCTASE 1 BETA	SOLUBLE	0	0
PROT SYNIFOLD	157237	157237	60688521	ENDOPLASMIC RETICULUM PROTEIN ERP29	SOLUBLE	6	20
PROT SYNIFOLD	293536	293536	34875200	ENDOPLASMIC RETICULUM PROTEIN ERP46	SOLUBLE	1	6
PROT SYNIFOLD	269402	269402	62651904	ENDOPLASMIC RETICULUM PRECURSOR (ENDOPLASMIC RETICULUM PROTEIN 99) (94 KDA GLUCOSE-REGULATED PROTEIN) (GRP94) (ERP99) (POLYMORPHIC TUMOR REJECTION ANTIGEN 1) (TUMOR REJECTION ANTIGEN GP96)	SOLUBLE	77	79,9474
PROT SYNIFOLD	310568	310568	62648953	ERP44 (SIMILAR TO THIOREDOXIN DOMAIN CONTAINING 4; ENDOPLASMIC RETICULUM RESIDENT PROTEIN 44KDA)	SOLUBLE	8	19
PROT SYNIFOLD	41501	41501	68565348	EUKARYOTIC PEPTIDE CHAIN RELEASE FACTOR SUBUNIT 1 (ERF1) (EUKARYOTIC RELEASE FACTOR 1) (TB3-1) (C11 PROTEIN)	SOLUBLE	0	0
PROT SYNIFOLD	166240	166240	34862605	EUKARYOTIC TRANSLATION ELONGATION FACTOR 1 BETA 2	SOLUBLE	0	0
PROT SYNIFOLD	103	103	9506571	EUKARYOTIC TRANSLATION INITIATION FACTOR 2 SUBUNIT 1	SOLUBLE	0	0

PROT SYNIFOLD	55867	55867	62652368	EUKARYOTIC TRANSLATION INITIATION FACTOR 3	SOLUBLE	0	0
PROT SYNIFOLD	266163	266163	34866934	SUBUNIT 6	SOLUBLE	0	0
PROT SYNIFOLD	189964	189964	27730981	SUBUNIT 6 INTERACTING PROTEIN	SOLUBLE	0	0
PROT SYNIFOLD	239406	239406	34869741	EUKARYOTIC TRANSLATION INITIATION FACTOR 3,	SOLUBLE	0	0
PROT SYNIFOLD	23682	23682	91207082	SUBUNIT 12 [MUS MUSCULUS]	SOLUBLE	0	0
PROT SYNIFOLD	43461	43461	501064	EUKARYOTIC TRANSLATION INITIATION FACTOR 4G I	SOLUBLE	0	1
PROT SYNIFOLD	289953	289953	27664664	EUKARYOTIC TRANSLATION INITIATION FACTOR 5A	SOLUBLE	0	0
PROT SYNIFOLD	241842	241842	34872627	FK506-BINDING PROTEIN 1A	SOLUBLE	0	0
PROT SYNIFOLD	246362	246362	38181944	FK506-BINDING PROTEIN 3	SOLUBLE	0	0
PROT SYNIFOLD	395638	395638	77404380	GCN1 GENERAL CONTROL OF AMINO-ACID SYNTHESIS 1-	SOLUBLE	0	0
PROT SYNIFOLD	36413	36413 246743	62664205	LIKE 1	SOLUBLE	0	0
PROT SYNIFOLD	153343	153343	2425030	GLUTAREDOXIN	SOLUBLE	19	39
PROT SYNIFOLD	195465	195465	34870188	GRP170 (HYPOXIA UP-REGULATED 1)	SOLUBLE	0	2
PROT SYNIFOLD	280024	280024	55824765	GRP75	SOLUBLE	0	0
PROT SYNIFOLD	82698	82698	54673763	HEAT RESPONSIVE PROTEIN 12	SOLUBLE	0	0
PROT SYNIFOLD	139643	139643	51243735	HEAT SHOCK PROTEIN 105 KDA ALPHA	SOLUBLE	0	0
PROT SYNIFOLD	68722	68722 236971 311124	71051777	HEAT SHOCK PROTEIN 47 PRECURSOR	SOLUBLE	0	5
PROT SYNIFOLD	200861	200861	55250700	HEAT SHOCK PROTEIN 86: HSP86	SOLUBLE	0	0
PROT SYNIFOLD	51607	51607	8394162	HEAT SHOCK PROTEIN 90: HSP90	SOLUBLE	0	2.0526
PROT SYNIFOLD	95874	95874	3360521	HEAT SHOCK COGNATE 70KD PROTEIN (44KD ATPASE N-TERMINAL FRAGMENT)	SOLUBLE	9.073	23.96
PROT SYNIFOLD	132766	132766 395977	7514005	INSIG2 MEMBRANE PROTEIN (INSULIN INDUCED GENE 2)	SOLUBLE	0	0
PROT SYNIFOLD	47300	47300	9507149	IRON-RESPONSIVE ELEMENT BINDING PROTEIN 1 (IRE-BP 1) (IRON REGULATORY PROTEIN 1) (IRP1) (FERRITIN REPRESSOR PROTEIN) (ACONITATE HYDRATASE)	SOLUBLE	0	0
PROT SYNIFOLD	74102	74102	27710456	ISCHEMIA RESPONSIVE 94 KDA PROTEIN	SOLUBLE	0	0
PROT SYNIFOLD	33170	33170	19924061	MAJOR VAULT PROTEIN	SOLUBLE	0	6
PROT SYNIFOLD	170945	170945	27661294	MICROSOMAL STRESS 70 PROTEIN ATPASE CORE	SOLUBLE	0	0
PROT SYNIFOLD	45089	45089	951425	NASCENT POLYPEPTIDE-ASSOCIATED COMPLEX ALPHA POLYPEPTIDE	SOLUBLE	0	0
PROT SYNIFOLD	161229	161229 206311	52789215	OXIDOREDUCTASE ERO1-L	SOLUBLE	0	5
PROT SYNIFOLD	276202	276202	34878065	PEPTIDYL-PROLYL CIS-TRANS ISOMERASE	SOLUBLE	1	4
PROT SYNIFOLD	161883	161883	56090441	PEPTIDYL-PROLYL CIS-TRANS ISOMERASE A	SOLUBLE	1	4
PROT SYNIFOLD	195895	195895	34866944	POLY(A) BINDING PROTEIN	SOLUBLE	4	11
PROT SYNIFOLD	69606	69606	38197382	PRE-MRNA SPLICING FACTOR RNA HELICASE (DEAH BOX PROTEIN 15)	SOLUBLE	0	0
PROT SYNIFOLD	21556	21556	38382858	PROBABLE RNA-DEPENDENT HELICASE P68 (DEAD-BOX PROTEIN P68) (DEAD-BOX PROTEIN 5)	SOLUBLE	0	0
PROT SYNIFOLD	60584	60584 227664	729436	PROBABLE RNA-DEPENDENT HELICASE P72 (DEAD-BOX PROTEIN P72) (DEAD-BOX PROTEIN 17)	SOLUBLE	122	90
PROT SYNIFOLD	278868	278868	62651585	PROTEIN DISULFIDE ISOMERASE	SOLUBLE	83	70
PROT SYNIFOLD	244957	244957	34858829	PROTEIN DISULFIDE ISOMERASE A3	SOLUBLE	34	52
PROT SYNIFOLD	18691	18691	34870116	PROTEIN DISULFIDE ISOMERASE A4	SOLUBLE	30	41.4881
PROT SYNIFOLD	60405	60405	9754866	PROTEIN DISULFIDE ISOMERASE A6	SOLUBLE	0	0
PROT SYNIFOLD	47246	47246	9506993	RIBOSOME-BINDING PROTEIN 1 (RIBOSOME RECEPTOR PROTEIN) (MRP) P180	SOLUBLE	0	0
PROT SYNIFOLD	38099	38099	27731985	RNA-BINDING PROTEIN HUR	SOLUBLE	0	0
PROT SYNIFOLD	237486	237486 237486	34875539	RNA-BINDING PROTEIN STAUFEIN	SOLUBLE	0	0
PROT SYNIFOLD				RNA-DEPENDENT INITIATION FACTOR-2 KINASE	SOLUBLE	0	0
PROT SYNIFOLD				SIGNAL RECOGNITION PARTICLE 14 KDA PROTEIN	SOLUBLE	0	0
PROT SYNIFOLD				SIMILAR TO 60S RIBOSOMAL PROTEIN L29	SOLUBLE	0	0

PROT SYN/FOLD	253193	253193	34851760	SIMILAR TO ALANYL-TRNA SYNTHETASE (ALANINE--TRNA LIGASE) (ALARS)	SOLUBLE	0	0
PROT SYN/FOLD	229620	229620	34859415	SIMILAR TO ARGININE-TRNA-PROTEIN TRANSFERASE 1	SOLUBLE	0	0
PROT SYN/FOLD	238208	238208	34932063	SIMILAR TO ASPARAGINYL-TRNA SYNTHETASE, CYTOPLASMIC (ASPARAGINE--TRNA LIGASE) (ASNRS)	SOLUBLE	0	0
PROT SYN/FOLD	315303	315303	34867138	SIMILAR TO DEAD/H (ASP-GLU-ALA-ASP/HIS) BOX POLYPEPTIDE RIG-I: RNA HELICASE	SOLUBLE	0	0
PROT SYN/FOLD	318887	318887	81892269	SIMILAR TO ENDOPLASMIC RETICULUM CHAPERONE SIL1 HOMOLOG	SOLUBLE	0	1
PROT SYN/FOLD	239547	239547	34870174	SIMILAR TO ENDOPLASMIC RETICULUM THIOREDOXIN SUPERFAMILY MEMBER, 18 K	SOLUBLE	0	1
PROT SYN/FOLD	267441	267441	34880581	SIMILAR TO EUKARYOTIC TRANSLATION INITIATION FACTOR 2, SUBUNIT 3, STRUCTURAL GENE X-LINKED	SOLUBLE	0	0
PROT SYN/FOLD	213255	213255	34858904	SIMILAR TO EUKARYOTIC TRANSLATION INITIATION FACTOR 3, SUBUNIT 5 EPSILON, 47KDA; EUKARYOTIC TRANSLATION INITIATION FACTOR 3, SUBUNIT 5 (EPSILON, 47KD)	SOLUBLE	0	0
PROT SYN/FOLD	223302	223302	34878791	SIMILAR TO HISTIDYL-TRNA SYNTHETASE-LIKE	SOLUBLE	0	0
PROT SYN/FOLD	269157	269157	55741637	SIMILAR TO KARS PROTEIN	SOLUBLE	0	0
PROT SYN/FOLD	198793	198793	34860789	SIMILAR TO MICROSOMAL TRIGLYCERIDE TRANSFER PROTEIN	SOLUBLE	7	34
PROT SYN/FOLD	312741	312741	66730413	SIMILAR TO PHENYLALANINE-TRNA SYNTHETASE-LIKE	SOLUBLE	0	0
PROT SYN/FOLD	254493	254493	51948478	SIMILAR TO PHENYLALANYL-TRNA SYNTHETASE BETA CHAIN (PHENYLALANINE--TRNA LIGASE BETA CHAIN) (PHERS)	SOLUBLE	0	1
PROT SYN/FOLD	276048	276048	34869214	SIMILAR TO PROTEIN DISULFIDE ISOMERASE-RELATED	SOLUBLE	12	19
PROT SYN/FOLD	300246	300246	34875372	SIMILAR TO SIGNAL RECOGNITION PARTICLE 68KDA	SOLUBLE	0	0
PROT SYN/FOLD	313782	313782	34876351	SIMILAR TO TAF1140 PROTEIN	SOLUBLE	0	0
PROT SYN/FOLD	226986	226986	34862692	SPLICING FACTOR, ARGinine/SERine-RICH 7, 35 kDa	SOLUBLE	0	0
PROT SYN/FOLD	258910	258910	34863012	SRP RECEPTOR ALPHA SUBUNIT	SOLUBLE	0	0
PROT SYN/FOLD	38101	38101	null	SRP RECEPTOR BETA	SOLUBLE	0	3
PROT SYN/FOLD	75118	75118	6981642	T-COMPLEX PROTEIN 1, ALPHA SUBUNIT	SOLUBLE	0	0
PROT SYN/FOLD	12218	12218	34849734	THIOREDOXIN	SOLUBLE	0	2
PROT SYN/FOLD	231792	231792	81884643	TORSIN FAMILY 2, MEMBER A	SOLUBLE	0	0
PROT SYN/FOLD	188125	188125	22651450	TORSINA	SOLUBLE	0	0
PROT SYN/FOLD	202385	202385	34853518	TORSINB PROTEIN	SOLUBLE	0	0
PROT SYN/FOLD	55871	55871	40786436	TRANSLATION INITIATION FACTOR EIF-4A	SOLUBLE	0	0
PROT SYN/FOLD	98326	98326	62906894	TRANSLOCIN-ASSOCIATED PROTEIN, GAMMA SUBUNIT	MEMBRANE	0	0
PROT SYN/FOLD	26167	26167	46397078	VIGILIN	SOLUBLE	1	4
PROTEASOME/UBIQUITIN	285136	285136	34851252	AUTOCRINE MOTILITY FACTOR RECEPTOR	MEMBRANE	0	0
PROTEASOME/UBIQUITIN	311481	311481	68341999	LOW MOLECULAR MASS UBIQUINONE-BINDING PROTEIN	MEMBRANE	0	0
PROTEASOME/UBIQUITIN	250662	250662	34867116	SIMILAR TO NON-CANONICAL UBIQUITIN CONJUGATING ENZYME 1	MEMBRANE	0	0
PROTEASOME/UBIQUITIN	274677	274677	34874398	SIMILAR TO UBIQUITIN LIGASE E3 ALPHA-I1	MEMBRANE	0	0
PROTEASOME/UBIQUITIN	85752	85752	38970025	26S PROTEASE REGULATORY SUBUNIT 6B	SOLUBLE	0	0
PROTEASOME/UBIQUITIN	317815	317815	54400716	26S PROTEASOME NON-ATPASE REGULATORY SUBUNIT 12	SOLUBLE	0	0

PROTEASOME/UBIQUITIN	255113	255113	72255509	26S PROTEASOME NON-ATPASE REGULATORY SUBUNIT 2	SOLUBLE	0	0	0
PROTEASOME/UBIQUITIN	12328	12328	77417616	BENDLESS PROTEIN	SOLUBLE	0		0
PROTEASOME/UBIQUITIN	314767	314767	34879447	CULLIN 4A	SOLUBLE	0		0
PROTEASOME/UBIQUITIN	233720	233720	37231712	PROTEASOME (PROSOME, MACROPAIN) SUBUNIT, BETA TYPE 1	SOLUBLE	0		0
PROTEASOME/UBIQUITIN	309670	309670	34869622	PROTEASOME 26S ATPASE SUBUNIT 6	SOLUBLE	0		0
PROTEASOME/UBIQUITIN	227267	227267	61098214	PROTEASOME ACTIVATOR 28-ALPHA SUBUNIT	SOLUBLE	0		0
PROTEASOME/UBIQUITIN	51596	51596	8394091	PROTEASOME ACTIVATOR COMPLEX SUBUNIT 2	SOLUBLE	0		0
PROTEASOME/UBIQUITIN	33375	33375	8394063	PROTEASOME SUBUNIT ALPHA TYPE 2	SOLUBLE	0		0
PROTEASOME/UBIQUITIN	45012	45012	8394066	PROTEASOME SUBUNIT ALPHA TYPE 3	SOLUBLE	0		0
PROTEASOME/UBIQUITIN	51591	51591	8394076	PROTEASOME SUBUNIT ALPHA TYPE 6	SOLUBLE	0		0
PROTEASOME/UBIQUITIN	72897	72897	2118151	PROTEASOME SUBUNIT ALPHA TYPE 7	SOLUBLE	0		0
PROTEASOME/UBIQUITIN	51593	51593	8394082	PROTEASOME SUBUNIT BETA TYPE 3	SOLUBLE	0		0
PROTEASOME/UBIQUITIN	78104	78104	310214	PROTEASOME SUBUNIT BETA TYPE 4	SOLUBLE	0		0
PROTEASOME/UBIQUITIN	134694	134694	464446	PROTEASOME SUBUNIT BETA TYPE 6	SOLUBLE	0		0
PROTEASOME/UBIQUITIN	239514	239514	34875569	SIMILAR TO UBIQUITIN SPECIFIC PROTEASE 36	SOLUBLE	0		0
PROTEASOME/UBIQUITIN	58922	58922	62665819	SIMILAR TO UBIQUITIN-CONJUGATING ENZYME E2G 2;	SOLUBLE	0		0
PROTEASOME/UBIQUITIN	317625	317625	34933178	UBIQUITIN-CONJUGATING ENZYME 7 HOMOLOG	SOLUBLE	0		0
PROTEASOME/UBIQUITIN	82822	82822	62660106	UBIQUITIN-ACTIVATING ENZYME E1 1	SOLUBLE	0		0
PROTEASOME/UBIQUITIN	54899	54899	62658232	UBIQUITIN-CONJUGATING ENZYME E2L 3	SOLUBLE	0		0
PROTEASOME/UBIQUITIN	22316	22316	6981690	UBIQUITIN-LIKE PROTEIN SUMO-1 CONJUGATING ENZYME CROC-1	SOLUBLE	0		0
SIGNALING	260591	260591	34880723	B-IND1	MEMBRANE	0		0
SIGNALING	23753	23753	456209	BAX INHIBITOR-1	MEMBRANE	0		0
SIGNALING	111524	111524	81867205	BNIP1 PROTEIN	MEMBRANE	0		0
SIGNALING	4326	4326	8927570	G PROTEIN BETA 2 SUBUNIT	MEMBRANE	0		0
SIGNALING	111680	111680	56560	LEUKOCYTE COMMON ANTIGEN VARIANT 4 PRECURSOR	MEMBRANE	0		0
SIGNALING	195586	195586	34862247	NICALIN HOMOLOG	MEMBRANE	0		8
SIGNALING	37272	37272	6174931	PRESENILIN 1	MEMBRANE	0		0
SIGNALING	47252	47252	9507007	PROSTAGLANDIN F2 RECEPTOR NEGATIVE REGULATOR PRECURSOR	MEMBRANE	0		0
SIGNALING	215340	215340	34869007	PROTEIN TYROSINE PHOSPHATASE, RECEPTOR TYPE, D ISOFORM 3 PRECURSOR; PROTEIN TYROSINE PHOSPHATASE, RECEPTOR TYPE, DELTA POLYPEPTIDE; PROTEIN TYROSINE PHOSPHATASE DELTA	MEMBRANE	0		0
SIGNALING	11137	11137	1113923	PROTEIN-TYROSINE PHOSPHATASE-LIKE N	MEMBRANE	0		0
SIGNALING	236762	236762	34864679	SIMILAR TO B-IND1	MEMBRANE	0		0
SIGNALING	221624	221624	81295379	SIMILAR TO FK506-BINDING PROTEIN 38	MEMBRANE	0		0
SIGNALING	214715	214715	34853540	SIMILAR TO G PROTEIN-COUPLED RECEPTOR 108	MEMBRANE	0		0
SIGNALING	314280	314280	34865897	SIMILAR TO PL6 PROTEIN	MEMBRANE	0		0
SIGNALING	248510	248510	34867650	SIMILAR TO PLEXIN	MEMBRANE	0		0
SIGNALING	230767	230767	34857062	SIMILAR TO PROTEIN PHOSPHATASE 2C EPSILON	MEMBRANE	0		0
SIGNALING	201524	201524	34882969	SIMILAR TO PROTEIN TYROSINE PHOSPHATASE-LIKE PROTEIN PTPLB	MEMBRANE	0		0
SIGNALING	166274	166274	32699414	1-PHOSPHATIDYL INOSITOL-4,5-BISPHOSPHATE	SOLUBLE	0		0
SIGNALING	47331	47331	9507243	PHOSPHODIESTERASE BETA 3	SOLUBLE	0		0
SIGNALING	35616	35616	61216932	14-3-3 PROTEIN BETA/ALPHA	SOLUBLE	0		1

SIGNALING	29710	29710	6981710	14-3-3 PROTEIN ETA	SOLUBLE	0	0
SIGNALING	47332	47332	9507245	14-3-3 PROTEIN GAMMA	SOLUBLE	0	0
SIGNALING	29711	29711	6981712	14-3-3 PROTEIN TAU	SOLUBLE	0	0
SIGNALING	29712	29712	68085421	14-3-3 PROTEIN ZETA/Delta	SOLUBLE	0	1
SIGNALING	109735	109735	66912120	2' 3' CYCLIC NUCLEOTIDE 3' PHOSPHODIESTERASE	SOLUBLE	0	0
SIGNALING	134570	134570	56790	2' 5'-OLIGOADENYLATE SYNTHETASE 1	SOLUBLE	0	0
SIGNALING	19300	19300	25742825	230 KDA PHOSPHATIDYLINOSITOL 4-KINASE	SOLUBLE	0	0
SIGNALING	23444	23444	1703034	5'-AMP-ACTIVATED PROTEIN KINASE, CATALYTIC ALPHA-1 CHAIN	SOLUBLE	0	0
SIGNALING	54292	54292	728758	5'-AMP-ACTIVATED PROTEIN KINASE, CATALYTIC ALPHA-2 CHAIN	SOLUBLE	0	0
SIGNALING	68651	68651	1335860	5'-AMP-ACTIVATED PROTEIN KINASE, GAMMA-1 SUBUNIT	SOLUBLE	0	0
SIGNALING	130827	130827	59709467	ADENYLYL CYCLASE-ASSOCIATED PROTEIN 1	SOLUBLE	0	0
SIGNALING	157870	157870 306730	6319138	ALG-2 INTERACTING PROTEIN 1	SOLUBLE	0	0
SIGNALING	36803	36803	55926139	ALPHA ISOFORM OF REGULATORY SUBUNIT A, PROTEIN PHOSPHATASE 2	SOLUBLE	0	0
SIGNALING	25354	25354	46577577	CALCIUM-BINDING PROTEIN P22	SOLUBLE	0	0
SIGNALING	168211	168211	125207	CAMP-DEPENDENT PROTEIN KINASE C ALPHA	SOLUBLE	0	0
SIGNALING	168209	168209	206150	CAMP-DEPENDENT PROTEIN KINASE TYPE II-ALPHA REGULATORY CHAIN	SOLUBLE	0	0
SIGNALING	18021	18021	7330736	CDK5 REGULATORY SUBUNIT ASSOCIATED PROTEIN 3	SOLUBLE	0	1
SIGNALING	95157	95157	9506507	CORONIN 1B	SOLUBLE	0	0
SIGNALING	239536	239536	34867549	DVL-BINDING PROTEIN DAPLE	SOLUBLE	0	0
SIGNALING	98538	98538	62510525	EDF-1 PROTEIN	SOLUBLE	0	0
SIGNALING	276570	276570	55741518	EVOLUTIONARILY CONSERVED SIGNALING INTERMEDIATE IN TOLL PATHWAY	SOLUBLE	0	0
SIGNALING	205153	205153	34875719	FRUCTOSAMINE-3-KINASE-RELATED PROTEIN	SOLUBLE	0	0
SIGNALING	8648	8648	51338711	G PROTEIN BETA 1 SUBUNIT	SOLUBLE	0	0
SIGNALING	171140	171140	27663980	G1 TO PHASE TRANSITION 2	SOLUBLE	0	0
SIGNALING	18015	18015	433211	GLYCEROL KINASE	SOLUBLE	0	0
SIGNALING	251068	251068	27690552	GOA	SOLUBLE	0	0
SIGNALING	29315	29315	77539774	GROWTH FACTOR RECEPTOR-BOUND PROTEIN 2	SOLUBLE	0	0
SIGNALING	140831	140831	16975337	GTP CYCLOHYDROLASE I FEEDBACK REGULATORY PROTEIN	SOLUBLE	0	1
SIGNALING	194129	194129	34875240	GTP-BINDING REGULATORY PROTEIN ALPHA-13 CHAIN - MOUSE	SOLUBLE	0	0
SIGNALING	123232	123232	54037164	GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN 12.3	SOLUBLE	21	27
SIGNALING	37194	37194	71089913	GUANINE NUCLEOTIDE-BINDING PROTEIN G(I), ALPHA-2 SUBUNIT (ADENYLYLATE CYCLASE-INHIBITING G ALPHA PROTEIN)	SOLUBLE	0	0
SIGNALING	3901	3901	71899	GUANINE NUCLEOTIDE-BINDING PROTEIN G(K), ALPHA SUBUNIT	SOLUBLE	0	0
SIGNALING	37195	37195	7329187	GUANINE NUCLEOTIDE-BINDING PROTEIN G(Q), ALPHA SUBUNIT	SOLUBLE	0	0
SIGNALING	72067	72067	14161099	GUANINE NUCLEOTIDE-BINDING PROTEIN G-S ALPHA	SOLUBLE	0	0
SIGNALING	37192	37192	8925964	GUANINE NUCLEOTIDE-BINDING PROTEIN, ALPHA-11 SUBUNIT	SOLUBLE	0	0
SIGNALING	276601	276601	34852506	INORGANIC DIPHOSPHATASE	SOLUBLE	0	0
SIGNALING	315195	315195	57526854	INTERFERON-INDUCED 35 KDA PROTEIN	SOLUBLE	0	0

SIGNALING	242453	242453	34857388	IQ MOTIF CONTAINING GTPASE ACTIVATING PROTEIN 1	SOLUBLE	0	0
SIGNALING				LANTHIONINE SYNTHETASE C-LIKE PROTEIN 1	SOLUBLE	0	0
SIGNALING	126112	126112	6625487	LIN-7 HOMOLOG C	SOLUBLE	0	0
SIGNALING	29682	29682	59798059	LIN-7 PROTEIN	SOLUBLE	0	0
SIGNALING	158790	158790	3885830	MAGNESIUM DEPENDENT PHOSPHATASE -1	SOLUBLE	0	0
SIGNALING	272326	272326	27700106	MEMBRANE-ASSOCIATED GUANYLATE KINASE-	SOLUBLE	0	0
SIGNALING	169306	169306	50400225	INTERACTING PROTEIN 1 MAGUIN-1	SOLUBLE	0	0
SIGNALING	47245	47245	9506991	MITOGEN-ACTIVATED PROTEIN KINASE 13	SOLUBLE	0	0
SIGNALING	237355	237355	81883452	MITOGEN-ACTIVATED PROTEIN KINASE 1	SOLUBLE	0	0
SIGNALING				INTERACTING PROTEIN 1	SOLUBLE	0	0
SIGNALING	268038	268038	34869218	MYOSIN LIGHT CHAIN KINASE	SOLUBLE	0	0
SIGNALING	123716	123716	81867103	NDRG1 RELATED PROTEIN NDRG2B1	SOLUBLE	0	0
SIGNALING	217100	217100	34878815	P140MDIA	SOLUBLE	0	0
SIGNALING	289228	289228	34870680	P53 INDUCIBLE PROTEIN	SOLUBLE	0	0
SIGNALING	104145	104145	2497510	PERIPHERAL PLASMA MEMBRANE PROTEIN CASK	SOLUBLE	0	0
SIGNALING	19107	19107	77416574	PKC-ZETA-INTERACTING PROTEIN	SOLUBLE	0	0
SIGNALING	114376	114376	18041977	PLASMINOGEN ACTIVATOR INHIBITOR 1 RNA-BINDING PROTEIN (PAI-RBP1)	SOLUBLE	0	0
SIGNALING	191003	191003	34856450	PRKRA PROTEIN KINASE, INTERFERON-INDUCIBLE	SOLUBLE	0	0
SIGNALING	44893	44893	125552	DOUBLE STRANDED RNA DEPENDENT ACTIVATOR	SOLUBLE	0	0
SIGNALING	74255	74255	6651163	PROTEIN KINASE C ALPHA	SOLUBLE	0	0
SIGNALING				PROTEIN KINASE C AND CASEIN KINASE SUBSTRATE IN NEURONS 2 PROTEIN	SOLUBLE	0	0
SIGNALING	318957	104170 318957	38197558	PROTEIN KINASE INHIBITOR P58	SOLUBLE	0	12
SIGNALING	4701	4701	68566099	PROTEIN TYROSINE PHOSPHATASE 4A1	SOLUBLE	0	0
SIGNALING	95160	95160	9506515	PROTO-ONCOGENE C-CRK	SOLUBLE	0	0
SIGNALING	15613	15613	47482120	PUTATIVE SKAP55	SOLUBLE	0	0
SIGNALING	17309	17309	55742827	RHO GDP-DISSOCIATION INHIBITOR 1	SOLUBLE	0	0
SIGNALING	242276	242276	34867073	RICK	SOLUBLE	0	0
SIGNALING	211028	211028	34876568	RNA-BINDING PROTEIN ISOFORM G3BP-2A	SOLUBLE	0	0
SIGNALING	84325	84325	92737	S-ARRESTIN	SOLUBLE	0	0
SIGNALING	62616	62616	56090475	S-PHASE KINASE-ASSOCIATED PROTEIN 1A	SOLUBLE	0	0
SIGNALING	271324	271324	34879084	SECRETED FRIZZLED-RELATED PROTEIN 1	SOLUBLE	0	0
SIGNALING	78346	78346	7993726	SER/THR PROTEIN PHOSPHATASE 2A SUBUNIT B	SOLUBLE	0	0
SIGNALING	105853	105853	27465615	SERINE/THREONINE PROTEIN KINASE 16	SOLUBLE	0	0
SIGNALING	41475	41475	8394021	SERINE/THREONINE PROTEIN PHOSPHATASE 2A, CATALYTIC SUBUNIT, BETA ISOFORM	SOLUBLE	0	0
SIGNALING	4597	4597	6981388	SERINE/THREONINE PROTEIN PHOSPHATASE PP1-BETA CATALYTIC SUBUNIT	SOLUBLE	0	0
SIGNALING	12071	12071	497994	SERINE/THREONINE-PROTEIN KINASE PLK	SOLUBLE	0	0
SIGNALING	283891	283891	34875832	SIMILAR TO 3,5-CYCLOC-GMP PHOSPHODIESTERASE; ROD PHOSPHODIESTERASE BETA SUBUNIT	SOLUBLE	0	0
SIGNALING	223472	223472	34854301	SIMILAR TO A-KINASE ANCHOR PROTEIN 9 ISOFORM 2; YOTIAO; A-KINASE ANCHORING PROTEIN 450; AKAP120-LIKE PROTEIN; CENTROSOME- AND GOLGI-LOCALIZED PROTEIN; KINASE N-ASSOCIATED PROTEIN; PROTEIN KINASE A ANCHORING PROTEIN 9; A-KINASE ANCHOR PROTEIN_350kD...	SOLUBLE	0	0
SIGNALING	281550	281550	34878251	SIMILAR TO APOPTOSIS INHIBITOR 5	SOLUBLE	0	0
SIGNALING	230447	230447	34863212	SIMILAR TO DEVELOPMENT- AND DIFFERENTIATION-ENHANCING FACTOR 2; PYK2 C TERMINUS-ASSOCIATED PROTEIN	SOLUBLE	0	0

SIGNALING	276611	276611	34861230	SIMILAR TO EPIDERMAL GROWTH FACTOR RECEPTOR PATHWAY SUBSTRATE 8-LIKE PROTEIN 2	SOLUBLE	0	0
SIGNALING	308794	308794	34866719	SIMILAR TO FYVE AND COILED-COIL DOMAIN CONTAINING 1	SOLUBLE	0	0
SIGNALING	300461	300461	34856132	SIMILAR TO GROWTH-ARREST-SPECIFIC PROTEIN 2 (GAS-1)	SOLUBLE	0	0
SIGNALING	266460	266460	34872138	SIMILAR TO LDL RECEPTOR ADAPTOR PROTEIN	SOLUBLE	0	0
SIGNALING	209309	209309	34873621	SIMILAR TO LECT2	SOLUBLE	0	0
SIGNALING	238438	238438	34870816	SIMILAR TO MAP KINASE KINASE 3B	SOLUBLE	0	0
SIGNALING	226905	226905	90108450	SIMILAR TO MITOGEN-ACTIVATED PROTEIN KINASE KINASE KINASE 7 INTERACTING PROTEIN 2	SOLUBLE	0	0
SIGNALING	305592	305592	34866106	SIMILAR TO MYO-INOSITOL MONOPHOSPHATASE A3	SOLUBLE	0	0
SIGNALING	256498	256498	34861056	SIMILAR TO PKA C-BETA-2	SOLUBLE	0	0
SIGNALING	212247	212247	34874060	SIMILAR TO SERINE/THREONINE KINASE	SOLUBLE	0	0
SIGNALING	229135	229135	34879743	SIMILAR TO SLIT-ROBO RHO GTPASE-ACTIVATING PROTEIN 3; WAVE-ASSOCIATED RAC GTPASE ACTIVATING PROTEIN	SOLUBLE	0	0
SIGNALING	225945	225945	34861256	SIMILAR TO TOLLIP PROTEIN	SOLUBLE	0	0
SIGNALING	298591	298591	34883204	SIMILAR TO TOLL-1-LIKE 2	SOLUBLE	0	0
SIGNALING	290958	290958	34869913	SIMILAR TO TYROSINE-PROTEIN KINASE JAK1 (JANUS KINASE 1) (JAK-1)	SOLUBLE	0	0
SIGNALING	267331	267331	71043752	SIMILAR TO UMP-CMP KINASE	SOLUBLE	0	0
SIGNALING	312923	312923	34881323	SIMILAR TO WD REPEAT DOMAIN 9 ISOFORM A; CAMP RESPONSE ELEMENT BINDING AND BETA-TRANSDUCIN FAMILY-LIKE	SOLUBLE	0	0
SIGNALING	271907	271907	34872826	SLINGSHOT 1L	SOLUBLE	0	0
SIGNALING	264614	264614	34873212	SLINGSHOT-2L	SOLUBLE	0	0
SIGNALING	82685	82685	54036435	STRESS-INDUCED-PHOSPHOPROTEIN 1 (STI1)	SOLUBLE	0	0
SIGNALING	47311	47311	9507185	TISSUE-TYPE TRANSGLUTAMINASE	SOLUBLE	0	0
SIGNALING	294309	294309	34873382	TRANSDUCIN (BETA)-LIKE 2	SOLUBLE	0	0
SIGNALING	71712	71712	294583	TYROSINE-PROTEIN KINASE LYN	SOLUBLE	0	0
TETH/DOCK/FUS	145735	145735	71153350	BET3	MEMBRANE	0	0
TETH/DOCK/FUS	280644	280644	34871708	CCAAT DISPLACEMENT PROTEIN (CASP)	MEMBRANE	0	0
TETH/DOCK/FUS	124005	124005	7441640	GIANTIN	MEMBRANE	0	0
TETH/DOCK/FUS	169300	169300	7513936	GOLGI AUTOANTIGEN, GOLGIN SUBFAMILY A MEMBER 2 (GM130)	MEMBRANE	0	0
TETH/DOCK/FUS	302868	302868	34867583	GOLGIN-84	MEMBRANE	0	0
TETH/DOCK/FUS	237211	237211	34857091	GPP130	MEMBRANE	0	0
TETH/DOCK/FUS	37252	37252	349321	Qa, SYNTAXIN 4	MEMBRANE	0	0
TETH/DOCK/FUS	78137	78137	631892	Qa, SYNTAXIN 5	MEMBRANE	0	0
TETH/DOCK/FUS	21695	21695	16758358	Qb, GOS28	MEMBRANE	0	0
TETH/DOCK/FUS	55435	55435	2316090	Qb, MEMBRIN	MEMBRANE	0	0
TETH/DOCK/FUS	6158	6158	9719420	Qb, VTI 1A	MEMBRANE	0	0
TETH/DOCK/FUS	241548	241548	34866243	Qb, VTI 1B	MEMBRANE	0	0
TETH/DOCK/FUS	315291	315291	61889075	Qc, GS15	MEMBRANE	0	0
TETH/DOCK/FUS	35327	35327	9506425	Qc, RBET1	MEMBRANE	0	0
TETH/DOCK/FUS	41516	41516	71043604	R, SEC22	MEMBRANE	0	0
TETH/DOCK/FUS	23581	23581	56789137	R, VAMP 3	MEMBRANE	0	0
TETH/DOCK/FUS	318845	318845	90110085	R, VAMP A	MEMBRANE	0	0
TETH/DOCK/FUS	37566	37566	18655558	R, VAMP8	MEMBRANE	0	0
TETH/DOCK/FUS	35326	35326	16924008	SEC22 HOMOLOG	MEMBRANE	0	0
TETH/DOCK/FUS	291113	291113	34878414	SIMILAR TO SYNTAXIN 18	MEMBRANE	0	0
TETH/DOCK/FUS	60460	60460	6685963	SYNAPTODYRIN 2	MEMBRANE	0	0

TETH/DOCK/FUS	19552	19552	14210270	SYNAPTOTAGMIN III	MEMBRANE	0	0
TETH/DOCK/FUS	51376	51376	6094309	ALPHA-SOLUBLE NSF ATTACHMENT PROTEIN (ALPHA SNAP)	SOLUBLE	0	1
TETH/DOCK/FUS	3633	3633	6978505	ANNEXIN 5	SOLUBLE	0	1
TETH/DOCK/FUS	3631	3631	6978501	ANNEXIN A1 (ANNEXIN I) (LIPOCORTIN I) (CALPACTIN II) (CHROMOBINDIN 9) (P35) (PHOSPHOLIPASE A2 INHIBITORY PROTEIN)	SOLUBLE	0	0
TETH/DOCK/FUS	205775	205775	34876896	ANNEXIN A11	SOLUBLE	0	0
TETH/DOCK/FUS	109734	109734	9845234	ANNEXIN A2	SOLUBLE	0	0
TETH/DOCK/FUS	120574	120574	71766	ANNEXIN A3	SOLUBLE	1	7
TETH/DOCK/FUS	171244	171244	37999910	ANNEXIN A4	SOLUBLE	0	0
TETH/DOCK/FUS	127131	127131	763181	ANNEXIN A6	SOLUBLE	0	5
TETH/DOCK/FUS	282341	282341	34875017	COG1	SOLUBLE	0	0
TETH/DOCK/FUS	298383	298383	34851895	COG2	SOLUBLE	0	0
TETH/DOCK/FUS	274159	274159	34874501	COG3	SOLUBLE	0	0
TETH/DOCK/FUS	245295	245295	34851754	COG4	SOLUBLE	0	0
TETH/DOCK/FUS	242048	242048	34864220	COG5	SOLUBLE	0	0
TETH/DOCK/FUS	222168	222168	34851657	COG8	SOLUBLE	0	0
TETH/DOCK/FUS	316372	316372	34932055	GAMMA-SOLUBLE NSF ATTACHMENT PROTEIN (GAMMA SNAP)	SOLUBLE	0	0
TETH/DOCK/FUS	311145	311145	34852562	GOLGI COILED COIL PROTEIN GCC185 (GOLGIN FAMILY MEMBER)	SOLUBLE	0	0
TETH/DOCK/FUS	225098	225098	62654450	GOLGI PERIPHERAL MEMBRANE PROTEIN P65	SOLUBLE	0	0
TETH/DOCK/FUS	220058	220058	62644637	GPP34 RELATED PROTEIN	SOLUBLE	0	0
TETH/DOCK/FUS	288023	288023	56090463	GRASP55_65	SOLUBLE	0	0
TETH/DOCK/FUS	267138	267138	34873054	MALE ENHANCED ANTIGEN 2/GOLGI AUTOANTIGEN, GOLGIN SUBFAMILY A, 3	SOLUBLE	0	0
TETH/DOCK/FUS	20725	20725	5524667	MUNC13-4 PROTEIN	SOLUBLE	0	0
TETH/DOCK/FUS	9479	9479	6007811	N-ETHYLMALIMIDE SENSITIVE FACTOR	SOLUBLE	0	0
TETH/DOCK/FUS	217815	217815	34879019	NIPSNAPT PROTEIN (SNAP25-LIKE)	SOLUBLE	0	0
TETH/DOCK/FUS	125172	125172	641973	P97 (TRANSITIONAL ENDOPLASMIC RETICULUM ATPASE)	SOLUBLE	1	7
TETH/DOCK/FUS	34036	34036	6685966	Qbc, SNAP29	SOLUBLE	0	0
TETH/DOCK/FUS	164208	164208	62659601	R, VAMP 4	SOLUBLE	0	0
TETH/DOCK/FUS	78131	78131	2642348	R, YKT6	SOLUBLE	0	0
TETH/DOCK/FUS	295490	295490	51315724	SIMILAR TO GOLGI RESIDENT PROTEIN GCP60	SOLUBLE	0	0
TETH/DOCK/FUS	157267	157267	71051327	SYNTAXIN BINDING PROTEIN MUNC18-3	SOLUBLE	0	0
TETH/DOCK/FUS	54283	54283	50400215	TRANS-GOLGI PROTEIN GMX33	SOLUBLE	0	0
TETH/DOCK/FUS	71574	71574	538153	TRANSCYTOSIS ASSOCIATED PROTEIN/P115	SOLUBLE	0	0
TRAFFIC	139656	139656	51948420	BAP31 (B-CELL RECEPTOR-ASSOCIATED PROTEIN 31)	MEMBRANE	0	0
TRAFFIC	204725	204725	27713571	CD414 (PTX1)	MEMBRANE	0	0
TRAFFIC	304228	304228	34869656	COILED-COIL PROTEIN	MEMBRANE	0	0
TRAFFIC	78146	78146	3914232	COP-COATED VESICLE MEMBRANE PROTEIN P24 BETA 1	MEMBRANE	0	0
TRAFFIC	209664	209664	34870624	ER-GOLGI INTERMEDIATE COMPARTMENT 32 KDA PROTEIN (ERGIC-32) (HT034)	MEMBRANE	0	0
TRAFFIC	77835	77835	29611707	ERGIC-53 PROTEIN	MEMBRANE	0	3
TRAFFIC	243481	243481	55742817	IGD B-CELL RECEPTOR-ASSOCIATED PROTEIN (BAP) 29	MEMBRANE	0	0
TRAFFIC	60418	60418	62906896	INTEGRAL MEMBRANE PROTEIN, TMP21-i (P23) DELTA 1	MEMBRANE	0	0
TRAFFIC	305262	305262	62901119	INTEGRAL TYPE I PROTEIN P24 GAMMA4	MEMBRANE	0	0
TRAFFIC	272716	272716	62821823	KDEL RECEPTOR	MEMBRANE	0	0

TRAFFIC	204384	204384	34879511	NOVEL MEMBER OF P24 FAMILY (TIRAP3B)	MEMBRANE	0	0
TRAFFIC	285748	170045 285748	57528337	P24 ALPHA 2	MEMBRANE	0	0
TRAFFIC	194234	194234	81888420	P24 GAMMA 1	MEMBRANE	0	0
TRAFFIC	228279	228279	62287552	P24 GAMMA 3	MEMBRANE	0	0
TRAFFIC	306304	306304	34862422	P63	MEMBRANE	0	4
TRAFFIC	311134	311134	34864274	PANTOPHYSIN	MEMBRANE	0	0
TRAFFIC	32618	32618	84781666	RER1	MEMBRANE	0	0
TRAFFIC	169836	169836	34857962	SECRETORY CARRIER MEMBRANE PROTEIN 3	MEMBRANE	0	0
TRAFFIC	46139	46139	487057	SECRETORY CARRIER-ASSOCIATED MEMBRANE PROTEIN 1	MEMBRANE	0	0
TRAFFIC	221907	221907	34875582	SIMILAR TO LECTIN, MANNOSE-BINDING 2-LIKE; VIP36-LIKE	MEMBRANE	0	0
TRAFFIC	283274	283274	34863171	SORTILIN-RELATED RECEPTOR/LDL RECEPTOR MOSAIC 11	MEMBRANE	0	0
TRAFFIC	31491	31491	71051654	TRANS-GOLGI NETWORK INTEGRAL MEMBRANE PROTEIN (TGN38)	MEMBRANE	0	0
TRAFFIC	57726	57726	4240464	VESICLE-ASSOCIATED MEMBRANE PROTEIN-ASSOCIATED PROTEIN B	MEMBRANE	0	0
TRAFFIC	139706	139706	27682691	VESICULAR INTEGRAL-MEMBRANE PROTEIN VIP36	MEMBRANE	0	0
TRAFFIC	173285	173285	4115911	CAMP-REGULATED GUANINE NUCLEOTIDE EXCHANGE FACTOR II	SOLUBLE	1	0
TRAFFIC	165980	165980	51701367	CAST2	SOLUBLE	0	0
TRAFFIC	218802	218802	34861677	CHOREIN; VPS13P	SOLUBLE	0	0
TRAFFIC	274130	274130	34867199	COPINE III	SOLUBLE	0	0
TRAFFIC	245798	245798	34865971	COPINE IV	SOLUBLE	0	0
TRAFFIC	4394	4394	61557025	ER LUMEN PROTEIN RETAINING RECEPTOR 2 (KDEL RECEPTOR 2)	MEMBRANE	0	0
TRAFFIC	161256	161256	7513971	EXOCYST COMPLEX COMPONENT SEC5	SOLUBLE	0	0
TRAFFIC	218235	218235	34865240	GBF1	SOLUBLE	0	0
TRAFFIC	254063	254063	34856238	HERC2	SOLUBLE	0	0
TRAFFIC	216613	216613	49036094	NEURAL STEM CELL DERIVED NEURONAL SURVIVAL PROTEIN	SOLUBLE	0	0
TRAFFIC	285775	285775	34856819	PALLIDIN	SOLUBLE	0	0
TRAFFIC	268833	268833	83288384	PHOSPHOINOSITIDE-3-KINASE, REGULATORY SUBUNIT 4, P150	SOLUBLE	0	0
TRAFFIC	67742	67742	71534276	RAB GDI ALPHA	SOLUBLE	0	0
TRAFFIC	8623	8623	40254781	RAB GDI BETA	SOLUBLE	0	1
TRAFFIC	252580	252580	34870749	RAS-GTPASE-ACTIVATING PROTEIN SH3-DOMAIN BINDING PROTEIN	SOLUBLE	0	0
TRAFFIC	276511	276511	34855314	RSEC6	SOLUBLE	0	0
TRAFFIC	47254	47254	9507019	RSLY1P	SOLUBLE	0	0
TRAFFIC	275605	275605	34879170	SIMILAR TO EH DOMAIN BINDING PROTEIN 1	SOLUBLE	0	0
TRAFFIC	231145	231145	34873592	SIMILAR TO GOLGI-MEMBRANE PROTEIN GP73	SOLUBLE	0	0
TRAFFIC	301225	301225	57164089	SIMILAR TO HPS5 PROTEIN	SOLUBLE	0	0
TRAFFIC	261916	261916	34863399	SIMILAR TO KDEL CONTAINING PROTEIN 1; ENDOPLASMIC RETICULUM-RESIDENT KDEL PROTEIN	SOLUBLE	0	1
TRAFFIC	276682	276682	78099277	SIMILAR TO VACUOLAR PROTEIN SORTING 26; VACUOLE PROTEIN SORTING 26; H BETA 58	SOLUBLE	0	0
TRAFFIC	319162	319162	34879535	SORTING NEXIN 2	SOLUBLE	0	0
TRAFFIC	60957	60957	76443685	SURFET LOCUS PROTEIN 4 (ERV29)	SOLUBLE	0	0
TRAFFIC	55286	55286	23396893	VACUOLAR PROTEIN SORTING 33A	SOLUBLE	0	0
TRAFFIC	206594	206594	34851395	VACUOLAR SORTING PROTEIN 35	SOLUBLE	0	0

TRANSCRIPTION	293599	293599	34863006	DNA-BINDING PROTEIN PROLACTIN REGULATORY ELEMENT BINDING (PREB)	MEMBRANE	0	0
TRANSCRIPTION	213126	213126	29336095	SEL1L	MEMBRANE	0	5
TRANSCRIPTION	272267	272267	34877464	TRANSCRIPTIONAL CO-ACTIVATOR CRSP7 HOMOLOG	MEMBRANE	0	0
TRANSCRIPTION	307560	307560	58219528	BRAIN ZN-FINGER PROTEIN	SOLUBLE	0	0
TRANSCRIPTION	2681	2681	61557239	CORE BINDING FACTOR BETA SUBUNIT	SOLUBLE	0	0
TRANSCRIPTION	287571	287571	34877698	CREG	SOLUBLE	0	0
TRANSCRIPTION	17534	17534	50400205	ESTROGEN RECEPTOR-RELATED RECEPTOR GAMMA-1	SOLUBLE	0	0
TRANSCRIPTION	71532	71532	57870645	GALECTIN-3	SOLUBLE	0	0
TRANSCRIPTION	37247	37247	729919	LUPUS LA PROTEIN HOMOLOG	SOLUBLE	0	0
TRANSCRIPTION	42953	42953	9931450	MHC CLASS II TRANSACTIVATOR TYPE I	SOLUBLE	0	0
TRANSCRIPTION	310879	310879	34871066	PTB-ASSOCIATED SPLICING FACTOR	SOLUBLE	0	0
TRANSCRIPTION	307156	307156	34875658	SIMILAR TO ALY	SOLUBLE	0	0
TRANSCRIPTION	202233	202233	34871645	SIMILAR TO DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (RPB1)	SOLUBLE	0	0
TRANSCRIPTION	318709	318709	57164029	SIMILAR TO ESTROGEN-RESPONSIVE FINGER PROTEIN	SOLUBLE	0	0
TRANSCRIPTION	234073	234073	34855011	SIMILAR TO INHIBITOR OF GROWTH FAMILY, MEMBER 3	SOLUBLE	0	0
TRANSCRIPTION	309047	309047	34861866	SIMILAR TO PROBABLE NOCTURNIN PROTEIN	SOLUBLE	0	0
TRANSCRIPTION	294340	294340	27661858	SIMILAR TO PUTATIVE ZINC FINGER TRANSCRIPTION FACTOR OVO1	SOLUBLE	0	0
TRANSCRIPTION	218537	218537	34855476	SIMILAR TO SEROLOGICALLY DEFINED COLON CANCER ANTIGEN 1 ISOFORM A	SOLUBLE	0	0
TRANSCRIPTION	252804	252804	34872980	SIMILAR TO VASCULAR ENDOTHELIAL ZINC FINGER 1	SOLUBLE	0	0
TRANSCRIPTION	313581	313581	34862217	SIMILAR TO ZINC FINGER PROTEIN, SUBFAMILY 1A, 4	SOLUBLE	0	0
TRANSCRIPTION	314602	314602	34861377	T-BOX TRANSCRIPTION FACTOR TBX10 (T-BOX PROTEIN 10)	SOLUBLE	0	0
TRANSCRIPTION	60512	60512	6650548	TATA ELEMENT MODULATORY FACTOR	SOLUBLE	0	0
TRANSCRIPTION	241253	241253	34853159	TPA: SENATAXIN; DEAXQ-BOX HELICASE; TRNA SPLICING ENDONUCLEASE REGULATOR 1	SOLUBLE	0	0
TRANSCRIPTION	33279	33279	56605700	TRANSCRIPTION FACTOR BTF3	SOLUBLE	0	0
TRANSCRIPTION	93202	93202	null	TSH RECEPTOR SUPPRESSOR ELEMENT-BINDING PROTEIN-1	SOLUBLE	0	0
TRYPSIN	75054	75054	6981420	TRYPSIN I, ANIONIC	SOLUBLE	26	25
UNKNOWN	239738	239738	81883249	(RCAS1) TYPE II RECEPTOR LIKE CANCER ASSOCIATED SURFACE ANTIGEN (RCAS1) TYPE II RECEPTOR LIKE CANCER ASSOCIATED SURFACE ANTIGEN	MEMBRANE	0	0
UNKNOWN	98449	98449	27673882	0610009E20RIK PROTEIN	MEMBRANE	0	0
UNKNOWN	63169	63169	71153386	30 KDA PROTEIN	MEMBRANE	0	1
UNKNOWN	284155	284155	33086520	AA2-020	MEMBRANE	0	0
UNKNOWN	291250	166327 291250	34859421	AB2-305	MEMBRANE	0	0
UNKNOWN	309746	309746	56090644	ABHYDROLASE DOMAIN CONTAINING 6	MEMBRANE	0	0
UNKNOWN	139514	139514	68534822	ADP-RIBOSYLATION FACTOR-LIKE 6 INTERACTING PROTEIN 1	MEMBRANE	0	0
UNKNOWN	195759	195759	34865887	ARMET PROTEIN	MEMBRANE	8	13
UNKNOWN	243111	243111	34876022	ATP-BINDING CASSETTE TRANSPORTER ABCG3 (1)	MEMBRANE	0	0
UNKNOWN	264038	264038	58865904	ATP-BINDING CASSETTE, SUB-FAMILY B, MEMBER 10	MEMBRANE	0	0
UNKNOWN	339290	339290	45680888	CG6210-LIKE	MEMBRANE	0	0

UNKNOWN	227312	227312	34855114	COILED-COIL-HELIX-COILED-COIL-HELIX DOMAIN CONTAINING 3	MEMBRANE	0	0
UNKNOWN	195940	195940	34866475	GUB AND SUSHI MULTIPLE DOMAINS 3	MEMBRANE	0	0
UNKNOWN	171802	171802	81868653	DAPIT PROTEIN	MEMBRANE	0	0
UNKNOWN	137142	137142	4579688	DB83 PROTEIN	MEMBRANE	0	0
UNKNOWN	288307	288307	34862308	DP1L1 PROTEIN	MEMBRANE	1	3.5
UNKNOWN	273209	273209	34856348	F-BOX ONLY PROTEIN 41	MEMBRANE	0	0
UNKNOWN	305024	305024	81882826	GENE RICH CLUSTER, C3F GENE (PREDICTED)	MEMBRANE	0	0
UNKNOWN	51531	51531	8393755	GLUT4 VESICLE PROTEIN	MEMBRANE	0	2
UNKNOWN	128379	128379	6016303	IMPLANTATION-ASSOCIATED PROTEIN	MEMBRANE	0	0
UNKNOWN	284296	284296	81883760	INTEGRAL MEMBRANE PROTEIN 2B	MEMBRANE	0	0
UNKNOWN	161235	161235	19705487	INTEGRAL MEMBRANE TRANSPORT PROTEIN UST4R	MEMBRANE	0	0
UNKNOWN	161236	161236	19705489	INTEGRAL MEMBRANE TRANSPORT PROTEIN UST5R	MEMBRANE	0	0
UNKNOWN	17165	17165	34861203	INTERFERON-INDUCIBLE PROTEIN	MEMBRANE	0	0
UNKNOWN	258458	258458	81882575	IODOTYROSINE DEHALOGENASE PROTEIN	MEMBRANE	0	0
UNKNOWN	249505	249505	27693564	LAG1 LONGEVITY ASSURANCE HOMOLOG 2 (TRANSLCATING CHAIN-ASSOCIATING MEMBRANE PROTEIN HOMOLOG 3) (TRAM HOMOLOG 3)	MEMBRANE	0	0
UNKNOWN	118984	118984	56748899	LYRIC	MEMBRANE	0	0
UNKNOWN	166255	166255	77157795	MAL2A	MEMBRANE	0	0
UNKNOWN	91768	91768	81882981	MEG-2-LIKE PROTEIN	MEMBRANE	0	0
UNKNOWN	282006	282006	81884639	MIT SUGUMIN 23	MEMBRANE	0	0
UNKNOWN	222783	222783	34875854	PANCREATITIS-INDUCED PROTEIN 49	MEMBRANE	0	0
UNKNOWN	252129	252129	34878680	POLYPOSIS LOCUS PROTEIN 1 HOMOLOG (TB2 PROTEIN HOMOLOG) (GP106)	MEMBRANE	0	3.5
UNKNOWN	197729	197729	34932411	PQ LOOP REPEAT CONTAINING 1	MEMBRANE	0	0
UNKNOWN	309339	309339	27677502	PROTEIN FAM20B PRECURSOR	MEMBRANE	0	0
UNKNOWN	311586	311586	34881421	PROTEIN FAM34A	MEMBRANE	0	0
UNKNOWN	246358	246358	34869300	RECEPTOR-TRANSPORTING PROTEIN 4 (28 KDA INTERFERON RESPONSIVE PROTEIN)	MEMBRANE	0	0
UNKNOWN	64492	64492	57977317	RETICULON 3 PROTEIN ISOFORM B	MEMBRANE	0	1
UNKNOWN	241539	241539	34858831	RING FINGER PROTEIN 121	MEMBRANE	0	0
UNKNOWN	275347	275347	34860248	SEROLOGICALLY DEFINED BREAST CANCER ANTIGEN NY-BR-84 HOMOLOG	MEMBRANE	0	0
UNKNOWN	310564	310564	34875157	SIMILAR TO 9530008L14RIK PROTEIN	MEMBRANE	0	0
UNKNOWN	302143	302143	34856654	SIMILAR TO AAQ88810	MEMBRANE	0	0
UNKNOWN	203301	203301	34877442	SIMILAR TO ACYL-COA BINDING PROTEIN DOMAIN 5	MEMBRANE	0	0
UNKNOWN	205068	205068	34856277	SIMILAR TO ANCIENT UBIQUITOUS 46 KDA PROTEIN AUP46 PRECURSOR	MEMBRANE	0	0
UNKNOWN	267475	267475	34861548	SIMILAR TO ARL6IP2	MEMBRANE	0	0
UNKNOWN	242256	242256	34879726	SIMILAR TO ATP-BINDING CASSETTE TRANSPORTER ABCG3 (2)	MEMBRANE	0	0
UNKNOWN	244941	244941	27710182	SIMILAR TO BC032271 PROTEIN	MEMBRANE	0	1
UNKNOWN	257012	257012	34871082	SIMILAR TO CARCINOMA RELATED GENE	MEMBRANE	0	0
UNKNOWN	208169	208169	81170413	SIMILAR TO CYSTEINE-RICH WITH EGF-LIKE DOMAINS 1	MEMBRANE	0	0
UNKNOWN	243991	243991	34865046	SIMILAR TO DISULFIDE ISOMERASE	MEMBRANE	0	0
UNKNOWN	300896	300896	34865806	SIMILAR TO DNA SEGMENT, CHR 12, ERATO DOI 551, EXPRESSED	MEMBRANE	0	0
UNKNOWN	206392	206392	27665476	SIMILAR TO EXPRESSED SEQUENCE AW556797	MEMBRANE	0	0

UNKNOWN	295665	295665	34874472	SIMILAR TO FIBRONECTIN TYPE III DOMAIN CONTAINING PROTEIN 3A	MEMBRANE	0	1
UNKNOWN		316692	27664728	SIMILAR TO FK506 BINDING PROTEIN 11	MEMBRANE	0	0
UNKNOWN	205305	205305	81885239	SIMILAR TO GI:13385412-LIKE PROTEIN SPLICE FORM I	MEMBRANE	0	0
UNKNOWN	258441	258441	34870715	SIMILAR TO HTGN29 PROTEIN; KERATINOCYTES ASSOCIATED TRANSMEMBRANE PROTEIN 2	MEMBRANE	0	0
UNKNOWN	290052	290052	34867679	SIMILAR TO HYPOTHETICAL PROTEIN BC002942	MEMBRANE	0	0
UNKNOWN	242521	242521	34879636	SIMILAR TO HYPOTHETICAL PROTEIN CL25084	MEMBRANE	0	0
UNKNOWN	302504	302504	34866614	SIMILAR TO HYPOTHETICAL PROTEIN FLJ10375	MEMBRANE	0	0
UNKNOWN	198580	198580	34872027	SIMILAR TO HYPOTHETICAL PROTEIN FLJ10900	MEMBRANE	0	0
UNKNOWN	304442	304442	34858680	SIMILAR TO HYPOTHETICAL PROTEIN FLJ14681	MEMBRANE	0	0
UNKNOWN	234260	234260	34863014	SIMILAR TO HYPOTHETICAL PROTEIN FLJ20254	MEMBRANE	0	0
UNKNOWN	295521	295521	34853516	SIMILAR TO HYPOTHETICAL PROTEIN FLJ20627	MEMBRANE	0	0
UNKNOWN	265857	265857	34932058	SIMILAR TO HYPOTHETICAL PROTEIN KIAA0233	MEMBRANE	0	0
UNKNOWN	278444	278444	27719651	SIMILAR TO HYPOTHETICAL PROTEIN MGC18837	MEMBRANE	0	0
UNKNOWN	240868	240868	27672946	SIMILAR TO HYPOTHETICAL PROTEIN MGC40107	MEMBRANE	0	0
UNKNOWN	219015	219015	62665667	SIMILAR TO KE4	MEMBRANE	0	0
UNKNOWN	235658	235658	34857976	SIMILAR TO KERATINOCYTES ASSOCIATED PROTEIN 2	MEMBRANE	0	0
UNKNOWN	229899	229899	34864701	SIMILAR TO KIAA1208 PROTEIN	MEMBRANE	0	0
UNKNOWN	252753	252753	27673096	SIMILAR TO MANNOSE-P-DOLICHOYL UTILIZATION DEFECT 1	MEMBRANE	0	0
UNKNOWN	318262	318262	34865609	SIMILAR TO MEMBRANE RECEPTOR (5H375)	MEMBRANE	0	0
UNKNOWN	239422	239422	34851797	SIMILAR TO NAD(P) DEPENDENT STEROID DEHYDROGENASE-LIKE	MEMBRANE	0	0
UNKNOWN	317802	317802	34860870	SIMILAR TO NEDD4 WW BINDING PROTEIN 4	MEMBRANE	0	0
UNKNOWN	192375	192375	27663100	SIMILAR TO NEURONAL PROTEIN 15.6	MEMBRANE	0	0
UNKNOWN	262782	262782	27689253	SIMILAR TO P3 PROTEIN	MEMBRANE	0	0
UNKNOWN	292511	292511	34881712	SIMILAR TO POTENTIAL PHOSPHOLIPID-TRANSPORTING ATPASE IG (ATPASE CLASS I TYPE 11C) (ATPASE IQ)	MEMBRANE	0	0
UNKNOWN	206786	206786	34877387	SIMILAR TO PROBABLE TRANSMEMBRANE PROTEIN FT27 - MOUSE	MEMBRANE	0	0
UNKNOWN	228858	228858	57164113	SIMILAR TO PUTATIVE NAD(P)H STEROID DEHYDROGENASE	MEMBRANE	2	12
UNKNOWN	269355	269355	34865136	SIMILAR TO PUTATIVE PROTEIN, WITH AT LEAST 6 TRANSMEMBRANE DOMAINS, OF ANCIENT ORIGIN (58.5 KD) (3N884)	MEMBRANE	0	0
UNKNOWN	277830	277830	34880585	SIMILAR TO RIKEN CDNA 0610008C08	MEMBRANE	0	0
UNKNOWN	246519	246519	34870283	SIMILAR TO RIKEN CDNA 1110038M16	MEMBRANE	0	0
UNKNOWN	235838	235838	27696657	SIMILAR TO RIKEN CDNA 1500009M05	MEMBRANE	0	0
UNKNOWN	300133	300133	56605746	SIMILAR TO RIKEN CDNA 1810014L12	MEMBRANE	0	0
UNKNOWN	209082	209082	58585236	SIMILAR TO RIKEN CDNA 1810020E01	MEMBRANE	0	0
UNKNOWN	200680	200680	34881760	SIMILAR TO RIKEN CDNA 1810037C20	MEMBRANE	0	0
UNKNOWN	280249	280249	34868966	SIMILAR TO RIKEN CDNA 1810063B07 GENE	MEMBRANE	0	0
UNKNOWN	166454	166454	27705930	SIMILAR TO RIKEN CDNA 2010107G23	MEMBRANE	0	0
UNKNOWN	258690	258690	34877499	SIMILAR TO RIKEN CDNA 2010315L10	MEMBRANE	0	0
UNKNOWN	316149	316149	34860558	SIMILAR TO RIKEN CDNA 2310008M10	MEMBRANE	0	0
UNKNOWN	235860	235860	34872456	SIMILAR TO RIKEN CDNA 2510039O18	MEMBRANE	0	0
UNKNOWN	298062	298062	34872958	SIMILAR TO RIKEN CDNA 2610020H15	MEMBRANE	0	0
UNKNOWN	238667	238667	34856650	SIMILAR TO RIKEN CDNA 2610318K02	MEMBRANE	0	0
UNKNOWN	205582	205582	56090371	SIMILAR TO RIKEN CDNA 4933403F05	MEMBRANE	0	0
UNKNOWN	208161	208161	34877094	SIMILAR TO RIKEN CDNA 5730469M10	MEMBRANE	0	0

UNKNOWN	318309	318309	56090393	SIMILAR TO RIKEN CDNA 6720485C15	MEMBRANE	0	0
UNKNOWN	191057	191057	34854982	SIMILAR TO RIKEN CDNA 8430437G11	MEMBRANE	0	0
UNKNOWN	218419	218419	34881196	SIMILAR TO RIKEN CDNA 9430083G14	MEMBRANE	0	0
UNKNOWN	274975	274975	34881052	SIMILAR TO RIKEN CDNA C330023F11	MEMBRANE	0	0
UNKNOWN	227176	227176	84042519	SIMILAR TO SEVEN TRANSMEMBRANE DOMAIN PROTEIN	MEMBRANE	0	0
UNKNOWN	301836	301836	34864996	SIMILAR TO SMILE PROTEIN	MEMBRANE	0	0
UNKNOWN	315186	315186	34875179	SIMILAR TO SSC2	MEMBRANE	0	0
UNKNOWN	221702	221702	34876057	SIMILAR TO T-CELL ACTIVATION LEUCINE REPEAT-RICH PROTEIN	MEMBRANE	0	0
UNKNOWN	259074	259074	34853639	SIMILAR TO ZINC TRANSPORTER 5	MEMBRANE	0	0
UNKNOWN	274007	274007	62639574	SIMILAR TO PROBABLE POL POLYPROTEIN-RELATED PROTEIN 4	MEMBRANE	0	0
UNKNOWN	247534	247534	34875183	SOLUTE CARRIER FAMILY 35, MEMBER B3 (PREDICTED)	MEMBRANE	0	0
UNKNOWN	171146	171146	94711371	TETRAPEPTIDE REPEAT PROTEIN 11	MEMBRANE	0	0
UNKNOWN	283888	283888	67078422	THIOREDOXIN DOMAIN CONTAINING PROTEIN 1	MEMBRANE	0	0
UNKNOWN	227628	227628	56090369	THIOREDOXIN-RELATED TRANSMEMBRANE PROTEIN 2	MEMBRANE	0	0
UNKNOWN	161242	161242	37590771	TORID	MEMBRANE	0	0
UNKNOWN	211728	211728	34874167	TRANSMEMBRANE 9 SUPERFAMILY MEMBER 1	MEMBRANE	0	0
UNKNOWN	140307	140307	34862730	TRANSMEMBRANE 9 SUPERFAMILY MEMBER 3	MEMBRANE	0	0
UNKNOWN	260512	260512	34859018	TRANSMEMBRANE 9 SUPERFAMILY MEMBER 4	MEMBRANE	0	0
UNKNOWN	260939	260939	58219512	TRANSMEMBRANE PROTEIN INDUCED BY TUMOR NECROSIS FACTOR ALPHA	MEMBRANE	0	0
UNKNOWN	201498	201498	34854713	TYPE 1 TRANSMEMBRANE C-TYPE LECTIN RECEPTOR DCL-1	MEMBRANE	0	0
UNKNOWN	262403	262403	38454214	UNKNOWN (PROTEIN FOR MGC:72987)	MEMBRANE	0	0
UNKNOWN	220427	220427	38454298	UNKNOWN (PROTEIN FOR MGC:72986)	MEMBRANE	0	0
UNKNOWN	213193	213193	34861994	UNKNOWN PROTEIN (1)	MEMBRANE	0	0
UNKNOWN	31214	31214	38197344	VACUOLE MEMBRANE PROTEIN 1	MEMBRANE	0	0
UNKNOWN	139384	139384	40018580	2400001E08RIK PROTEIN	SOLUBLE	0	0
UNKNOWN	240031	240031	34873948	2610204L23RIK PROTEIN	SOLUBLE	0	3
UNKNOWN	240594	240594	81909634	2810002D13RIK PROTEIN	SOLUBLE	0	0
UNKNOWN	276652	276652	34865464	AB2-095	SOLUBLE	0	0
UNKNOWN	244467	244467	56970828	AB2-225	SOLUBLE	0	0
UNKNOWN	271294	271294	34857271	ABHYDROLASE DOMAIN CONTAINING PROTEIN 2	SOLUBLE	0	0
UNKNOWN	199808	199808	33086620	AC2-155	SOLUBLE	0	0
UNKNOWN	166325	166325	33086552	ACETYL-COENZYME A ACETYL TRANSFERASE 3-LIKE	SOLUBLE	0	0
UNKNOWN	265779	265779	34861996	ARL6IP2	MEMBRANE	0	0
UNKNOWN	288335	288335	34863101	BAND 7 PROTEIN (35.3 KD) (4N53)	SOLUBLE	0	1
UNKNOWN	220519	220519	59676599	BC004044 (DENTIN MATRIX PROTEIN 4)	SOLUBLE	0	0
UNKNOWN	80419	80419	730248	BRAIN PROTEIN 44	SOLUBLE	0	0
UNKNOWN	92620	92620	66911415	BRAIN PROTEIN 44-LIKE PROTEIN	SOLUBLE	0	0
UNKNOWN	292782	292782	34853069	BTB (POZ) DOMAIN CONTAINING 14A	SOLUBLE	0	0
UNKNOWN	273407	273407	34867616	BTB (POZ) DOMAIN CONTAINING 7 (PREDICTED)	SOLUBLE	0	0
UNKNOWN	194016	194016	62641625	CC1-9	SOLUBLE	2	11
UNKNOWN	151517	151517	56090461	CCG1-INTERACTING FACTOR B	SOLUBLE	0	1
UNKNOWN	215152	215152	34870072	CG33130-PA	SOLUBLE	0	0
UNKNOWN	277277	277277	34856405	COILED-COIL-HELIX-COILED-COIL-HELIX DOMAIN CONTAINING 6 (PREDICTED)	SOLUBLE	0	0
UNKNOWN	211553	211553	51948526	COMM DOMAIN CONTAINING 10	SOLUBLE	0	0
UNKNOWN	289448	289448	34854739	CORDON-BLEU RELATED 1	SOLUBLE	0	0

UNKNOWN	51411	51411	8393206	CYSTEINE-RICH PROTEIN 1	SOLUBLE	0	0
UNKNOWN	46143	46143	737713	CYSTEINE-RICH PROTEIN 2	SOLUBLE	0	0
UNKNOWN	203612	203612	34856144	CYTOPLASMIC FMR1 INTERACTING PROTEIN 1	SOLUBLE	0	0
UNKNOWN	270449	270449	34863198	D130038B21	SOLUBLE	0	0
UNKNOWN	204574	204574	34856989	DEAD/H BOX POLYPEPTIDE 36 PROTEIN	SOLUBLE	0	0
UNKNOWN	240184	240184	56090381	DEHYDROGENASE/REDUCTASE SDR FAMILY MEMBER 1	SOLUBLE	0	0
UNKNOWN	20683	20683	56404680	DJ-1 PROTEIN	SOLUBLE	0	0
UNKNOWN	263674	263674	27664990	DKFZF586A0522 PROTEIN	SOLUBLE	0	0
UNKNOWN	261337	261337	34865967	DNAJC13	SOLUBLE	0	0
UNKNOWN	203847	203847	57528269	DORZ1	SOLUBLE	0	0
UNKNOWN	244145	244145	34536836	EH-DOMAIN CONTAINING PROTEIN 3	SOLUBLE	0	0
UNKNOWN	2280	2280	58865448	EH-DOMAIN-CONTAINING PROTEIN 1 (MPAST1)	SOLUBLE	0	0
UNKNOWN	262247	262247	34873697	E7EA: EXPRESSED IN T-CELLS AND EOSINOPHILS IN ATOPIC DERMATITIS	SOLUBLE	0	0
UNKNOWN	173223	173223	38454280	FAM3C-LIKE PROTEIN	SOLUBLE	0	0
UNKNOWN	216529	216529	34876071	FARP1 PROTEIN	SOLUBLE	0	0
UNKNOWN	273384	273384	34877564	GLYCOSYLTRANSFERASE 25 DOMAIN CONTAINING 1	SOLUBLE	0	10
UNKNOWN	220289	220289	55741522	HSPC242	SOLUBLE	0	0
UNKNOWN	130834	130834	539959	HYPERTENSION-INDUCED PROTEIN S-2	SOLUBLE	0	0
UNKNOWN	233766	233766	34854842	HYPOTHETICAL PROTEIN (1)	SOLUBLE	0	0
UNKNOWN	200143	200143	34870159	HYPOTHETICAL PROTEIN D4ERTD765E	SOLUBLE	0	1
UNKNOWN	300976	300976	34875673	HYPOTHETICAL PROTEIN LOC303749	SOLUBLE	0	0
UNKNOWN	194048	194048	34871484	HYPOTHETICAL PROTEIN MGC40499	SOLUBLE	0	1
UNKNOWN	313817	313817	34860574	HYPOTHETICAL PROTEIN XP_342343	SOLUBLE	0	0
UNKNOWN	301974	301974	34862025	HYPOTHETICAL PROTEIN XP_343009	SOLUBLE	0	0
UNKNOWN	203844	203844	34865907	HYPOTHETICAL PROTEIN XP_343478	SOLUBLE	0	0
UNKNOWN	287423	287423	34854602	HYPOTHETICAL PROTEIN XP_344851	SOLUBLE	0	0
UNKNOWN	273429	273429	34857419	HYPOTHETICAL PROTEIN XP_346991	SOLUBLE	0	0
UNKNOWN	300655	300655	34866914	HYPOTHETICAL PROTEIN XP_347087	SOLUBLE	0	0
UNKNOWN	8904	8904	62664482	ISOCHORISMATASE DOMAIN CONTAINING 1	SOLUBLE	0	0
UNKNOWN	32612	32612	68534555	JAGUNAL HOMOLOG 1	SOLUBLE	0	0
UNKNOWN	198073	198073	21314221	LIVER NTE-RELATED PROTEIN	SOLUBLE	0	0
UNKNOWN	136387	136387	16124253	M4 PROTEIN	SOLUBLE	0	0
UNKNOWN	33171	33171	19743770	MAWDBP	SOLUBLE	0	0
UNKNOWN	225113	225113	34865264	MELANOMA INHIBITORY ACTIVITY PROTEIN 2(MIA2)	SOLUBLE	0	0
UNKNOWN	124359	124359	32363191	MERLIN	SOLUBLE	0	0
UNKNOWN	161253	161253	38511548	MG87 PROTEIN	SOLUBLE	0	0
UNKNOWN	265130	265130	34865613	MIRROR-IMAGE POLYDACTYLY GENE 1	SOLUBLE	0	0
UNKNOWN	67879	67879	1708980	NCK-ASSOCIATED PROTEIN 1	SOLUBLE	0	0
UNKNOWN	240310	240310	34863173	NEUROBLASTOMA AMPLIFIED GENE, NAG	SOLUBLE	0	0
UNKNOWN	253799	253799	34868757	NOD3	SOLUBLE	0	0
UNKNOWN	267421	267421	34865854	NUDT16 PROTEIN	SOLUBLE	0	0
UNKNOWN	194680	194680	34877284	OCIA DOMAIN CONTAINING 1	SOLUBLE	0	0
UNKNOWN	154010	154010	24475405	OPTINEURIN	SOLUBLE	0	1
UNKNOWN	54494	54494	50926851	P55	SOLUBLE	0	0
UNKNOWN	40336	40336	8393153	PDZ AND LIM DOMAIN PROTEIN 1	SOLUBLE	0	0
UNKNOWN	78142	78142	8439549	PDZ DOMAIN-CONTAINING PROTEIN (DIPHOR 1)	SOLUBLE	0	0
UNKNOWN	298059	298059	34858089	PREDICTED E3 UBIQUITIN LIGASE	SOLUBLE	0	0
UNKNOWN	222133	222133	34851911	PROBABLE UPF0334 KINASE-LIKE PROTEIN	SOLUBLE	0	0
UNKNOWN	263127	263127	34866113	PROTEIN KIAA0103 HOMOLOG	SOLUBLE	0	0
UNKNOWN	214491	214491	32129697	PROTEIN LRP16	SOLUBLE	0	0

UNKNOWN	230313	230313	34873957	PUTATIVE RNA BINDING PROTEIN, PARTNER TO NOB1	SOLUBLE	0	0
UNKNOWN							
UNKNOWN	42949	42949	9931329	PUTATIVE TRANSCRIPTION FACTOR LUZP	SOLUBLE	0	0
UNKNOWN	60469	60469	16758344	RGPR-P117	SOLUBLE	0	0
UNKNOWN	224054	224054	34851643	SB-CB404 PROTEIN	SOLUBLE	0	0
UNKNOWN	235129	235129	34878986	SEC14-LIKE PROTEIN 3	SOLUBLE	0	0
UNKNOWN	111519	111519	49256633	SELENIUM-BINDING PROTEIN	SOLUBLE	0	0
UNKNOWN	13862	13862	62643492	SELENOPROTEIN T	SOLUBLE	0	0
UNKNOWN	198937	198937	27706424	SH3-BINDING DOMAIN GLUTAMIC ACID-RICH PROTEIN LIKE	SOLUBLE	0	0
UNKNOWN							
UNKNOWN	75738	75738	7109256	SH3P13	SOLUBLE	0	0
UNKNOWN	18910	18910	7248379	SH3P7R2	SOLUBLE	0	0
UNKNOWN	227484	227484	56605652	SHWACHMAN-BODIAN-DIAMOND SYNDROME PROTEIN HOMOLOG	SOLUBLE	0	0
UNKNOWN	206115	206115	34853331	SIMILAR TO 25 KDA BRAIN-SPECIFIC PROTEIN (P25-ALPHA)	SOLUBLE	0	0
UNKNOWN							
UNKNOWN	198410	198410	34863517	SIMILAR TO 9130011E15RIK PROTEIN	SOLUBLE	0	0
UNKNOWN	267292	267292	34863265	SIMILAR TO ALL-1 PROTEIN +GTE FORM - MOUSE (FRAGMENT)	SOLUBLE	0	0
UNKNOWN	294691	294691	34877353	SIMILAR TO AMYLOID BETA A4 PRECURSOR PROTEIN- BINDING FAMILY B MEMBER 2 (FE65-LIKE PROTEIN)	SOLUBLE	0	0
UNKNOWN							
UNKNOWN	269562	269562	34869208	SIMILAR TO B AGGRESSIVE LYMPHOMA	SOLUBLE	0	0
UNKNOWN	296511	296511	34860876	SIMILAR TO BA261P9.2 (PUTATIVE NOVEL PROTEIN SIMILAR TO FLY CG7340 AND HUMAN PUTATIVE AMINOPEPTIDASE ZK353.6 IN CHROMOSOME 3 (EC 3.4.11.-))	SOLUBLE	0	0
UNKNOWN							
UNKNOWN	235741	235741	34856101	SIMILAR TO BC013491 PROTEIN	SOLUBLE	0	0
UNKNOWN	232734	232734	56090628	SIMILAR TO BCS1-LIKE	SOLUBLE	0	3
UNKNOWN	214565	214565	66730443	SIMILAR TO BLOCK OF PROLIFERATION 1	SOLUBLE	0	0
UNKNOWN	208493	208493	34853057	SIMILAR TO CALMODULIN REGULATED SPECTRIN- ASSOCIATED PROTEIN 1	SOLUBLE	0	0
UNKNOWN	253866	253866	34871409	SIMILAR TO CDNA SEQUENCE BC003251	SOLUBLE	0	0
UNKNOWN	318242	318242	34859365	SIMILAR TO CDNA SEQUENCE BC017158	SOLUBLE	0	0
UNKNOWN	221370	221370	34876775	SIMILAR TO CG32774-PA	SOLUBLE	0	0
UNKNOWN	235290	235290	61740621	SIMILAR TO CHO FUNCTIONALLY UNKNOWN TYPE II TRANSMEMBRANE PROTEIN	SOLUBLE	0	0
UNKNOWN	141958	141958	81883037	SIMILAR TO CHROMOSOME 13 OPEN READING FRAME 1	SOLUBLE	0	0
UNKNOWN							
UNKNOWN	199223	199223	34875599	SIMILAR TO CHROMOSOME 17 OPEN READING FRAME 27	SOLUBLE	0	0
UNKNOWN	275755	275755	34858705	SIMILAR TO CHROMOSOME 20 OPEN READING FRAME 116	SOLUBLE	0	0
UNKNOWN							
UNKNOWN	283779	283779	34865376	SIMILAR TO DISHEVELLED-ASSOCIATED ACTIVATOR OF MORPHOGENESIS 1	SOLUBLE	0	0
UNKNOWN	359989	359989	62646328	SIMILAR TO DJ881L22.2 (NOVEL PROTEIN)	MEMBRANE	0	0
UNKNOWN	262592	262592	27681007	SIMILAR TO DNA SEGMENT, CHR 1, ERATO DOI 578, EXPRESSED	SOLUBLE	0	0
UNKNOWN							
UNKNOWN	303538	303538	34851569	SIMILAR TO EMBRYONIC BLASTOCOELAR EXTRACELLULAR MATRIX PROTEIN PRECURSOR	SOLUBLE	0	1
UNKNOWN	197176	197176	27689183	SIMILAR TO ENSANGP0000013261	SOLUBLE	0	0
UNKNOWN	305590	305590	34874491	SIMILAR TO ESTERASE 10; ESTERASE D	SOLUBLE	0	0

UNKNOWN	293497	293497	34877686	SIMILAR TO FERM, RHOGEF AND PLECKSTRIN DOMAIN PROTEIN 2	SOLUBLE	0	0
UNKNOWN	304176	304176	34876611	SIMILAR TO FERM, RHOGEF, AND PLECKSTRIN DOMAIN PROTEIN 1; CHONDROCYTE-DERIVED EZRIN-LIKE PROTEIN	SOLUBLE	0	0
UNKNOWN	210125	210125	34861517	SIMILAR TO FLJ0354 PROTEIN	SOLUBLE	0	0
UNKNOWN	272431	272431	34878417	SIMILAR TO FLJ12716 PROTEIN	SOLUBLE	0	0
UNKNOWN	243174	243174	34865010	SIMILAR TO FLJ21963	SOLUBLE	0	0
UNKNOWN	198248	198248	34878781	SIMILAR TO FOLLICULAR LYMPHOMA VARIANT	SOLUBLE	0	0
UNKNOWN	266426	266426	34856814	TRANSLOCATION 1	SOLUBLE	0	0
UNKNOWN	272300	272300	34880541	SIMILAR TO FRAGILE-X-RELATED PROTEIN 1 ISOFORM E	SOLUBLE	0	0
UNKNOWN	169873	169873	81882827	SIMILAR TO GE36	SOLUBLE	0	0
UNKNOWN	225450	225450	34859732	SIMILAR TO GENETHONIN 1	SOLUBLE	0	0
UNKNOWN	253349	253349	34855501	SIMILAR TO GTP BINDING PROTEIN	SOLUBLE	0	0
UNKNOWN	178365	178365	62651081	SIMILAR TO HIGH GLUCOSE-REGULATED PROTEIN 8	SOLUBLE	0	0
UNKNOWN	239621	239621	34867996	SIMILAR TO HSPC288	MEMBRANE	0	0
UNKNOWN	213390	213390	34853466	SIMILAR TO HYPOTHETICAL PROTEIN 5031404N19	SOLUBLE	0	0
UNKNOWN	274768	274768	27668745	SIMILAR TO HYPOTHETICAL PROTEIN 5832424M12	SOLUBLE	0	0
UNKNOWN	215440	215440	62665359	SIMILAR TO HYPOTHETICAL PROTEIN BC013949	SOLUBLE	0	0
UNKNOWN	231118	231118	34868399	SIMILAR TO HYPOTHETICAL PROTEIN COX4L	SOLUBLE	0	0
UNKNOWN	285691	285691	34856697	SIMILAR TO HYPOTHETICAL PROTEIN D4ERTD89E	SOLUBLE	0	0
UNKNOWN	233304	233304	34872498	SIMILAR TO HYPOTHETICAL PROTEIN FLJ10579	SOLUBLE	0	0
UNKNOWN	263673	263673	34872548	SIMILAR TO HYPOTHETICAL PROTEIN FLJ10737	SOLUBLE	0	0
UNKNOWN	248047	248047	34861003	SIMILAR TO HYPOTHETICAL PROTEIN FLJ13089	SOLUBLE	0	0
UNKNOWN	317090	317090	34863103	SIMILAR TO HYPOTHETICAL PROTEIN FLJ20331	SOLUBLE	0	0
UNKNOWN	229721	229721	34855399	SIMILAR TO HYPOTHETICAL PROTEIN FLJ21820	SOLUBLE	0	0
UNKNOWN	283019	283019	34854388	SIMILAR TO HYPOTHETICAL PROTEIN FLJ30373	SOLUBLE	0	0
UNKNOWN	268830	268830	34872654	SIMILAR TO HYPOTHETICAL PROTEIN FLJ30596	SOLUBLE	0	1
UNKNOWN	190049	190049	27732065	SIMILAR TO HYPOTHETICAL PROTEIN KIAA0152	SOLUBLE	0	0
UNKNOWN	202821	202821	34851552	SIMILAR TO HYPOTHETICAL PROTEIN KIAA0379	SOLUBLE	0	0
UNKNOWN	277215	277215	34872804	SIMILAR TO HYPOTHETICAL PROTEIN MGC10084	SOLUBLE	0	0
UNKNOWN	228294	228294	34880064	SIMILAR TO HYPOTHETICAL PROTEIN MGC23280	SOLUBLE	0	0
UNKNOWN	302513	302513	34872226	SIMILAR TO HYPOTHETICAL PROTEIN MGC26706	SOLUBLE	0	0
UNKNOWN	244528	244528	34879922	SIMILAR TO KIAA0090 PROTEIN	SOLUBLE	0	3
UNKNOWN	266038	266038	34866451	SIMILAR TO KIAA0316 PROTEIN	SOLUBLE	0	1
UNKNOWN	312697	312697	34852783	SIMILAR TO KIAA0342 PROTEIN	SOLUBLE	0	0
UNKNOWN	224112	224112	34877224	SIMILAR TO KIAA0372 GENE PRODUCT	SOLUBLE	0	0
UNKNOWN	230119	230119	34858955	SIMILAR TO KIAA0635 GENE PRODUCT	SOLUBLE	0	1
UNKNOWN	281850	281850	34879262	SIMILAR TO KIAA0980 PROTEIN	SOLUBLE	0	0
UNKNOWN	295453	295453	34869160	SIMILAR TO KIAA1311 PROTEIN	SOLUBLE	0	0
UNKNOWN	261449	261449	34860436	SIMILAR TO KIAA1407 PROTEIN	SOLUBLE	0	0
UNKNOWN				SIMILAR TO KIDNEY ANKYRIN REPEAT-CONTAINING PROTEIN	SOLUBLE	0	0
UNKNOWN	286300	286300	34865266	SIMILAR TO MENINGIOMA EXPRESSED ANTIGEN 6 (COILED-COIL PROLINE-RICH)	SOLUBLE	0	3
UNKNOWN	259160	259160	56090359	SIMILAR TO MESENCHYMAL STEM CELL PROTEIN DSCD75	SOLUBLE	0	0
UNKNOWN	211833	211833	34869626	SIMILAR TO MITOGEN INDUCIBLE GENE MIG-2	SOLUBLE	0	0
UNKNOWN	234949	234949	34866514	SIMILAR TO MKIAA0493 PROTEIN	SOLUBLE	0	0
UNKNOWN	314871	314871	34877516	SIMILAR TO MO25 PROTEIN	SOLUBLE	0	0
UNKNOWN	193119	193119	34863169	SIMILAR TO NEUROBLASTOMA-AMPLIFIED PROTEIN	SOLUBLE	0	0
UNKNOWN	213226	213226	34868007	SIMILAR TO NIT PROTEIN 2	SOLUBLE	0	1

UNKNOWN	291365	291365	34868938	SIMILAR TO O-METHYLTRANSFERASE FAMILY MEMBER (GC530)	SOLUBLE	0	0
UNKNOWN	297002	297002	34880977	SIMILAR TO OSTEOCLAST STIMULATING FACTOR 1	SOLUBLE	0	0
UNKNOWN	201603	201603	81910619	SIMILAR TO PEF PROTEIN WITH A LONG N-TERMINAL HYDROPHOBIC DOMAIN (PEFLIN)	SOLUBLE	0	0
UNKNOWN	215096	215096	34856103	SIMILAR TO PM5 PROTEIN; DNA SEGMENT, CHR 7, ERATO DOI 156, EXPRESSED	SOLUBLE	13	17
UNKNOWN	306783	306783	34871764	SIMILAR TO PROTEIN 4.1, P4.1 - MOUSE	SOLUBLE	0	0
UNKNOWN	253829	253829	95102018	SIMILAR TO PROTEIN CGI-117 (PROTEIN HSPC111)	SOLUBLE	0	0
UNKNOWN	255631	255631	51948454	SIMILAR TO PROTEIN CGI-51	SOLUBLE	0	0
UNKNOWN	315828	315828	34872893	SIMILAR TO PROTEIN KINASE NJMU-R1	SOLUBLE	0	0
UNKNOWN	272641	272641	34880767	SIMILAR TO QUINONE-REDUCTASE PROTEIN	SOLUBLE	0	0
UNKNOWN	244225	244225	66730429	SIMILAR TO RIKEN CDNA 0610006F02	SOLUBLE	0	0
UNKNOWN	220359	220359	34865395	SIMILAR TO RIKEN CDNA 0610010D20	SOLUBLE	0	1
UNKNOWN	236607	236607	34858551	SIMILAR TO RIKEN CDNA 1100001H23	SOLUBLE	0	0
UNKNOWN	249723	249723	34872727	SIMILAR TO RIKEN CDNA 1200014J11	SOLUBLE	1	0
UNKNOWN	246387	246387	34874480	SIMILAR TO RIKEN CDNA 1700027N10	SOLUBLE	0	0
UNKNOWN	261953	261953	34854321	SIMILAR TO RIKEN CDNA 1700034M03 GENE	SOLUBLE	0	0
UNKNOWN	270299	270299	34857339	SIMILAR TO RIKEN CDNA 1810045K17	SOLUBLE	0	0
UNKNOWN	217843	217843	34867100	SIMILAR TO RIKEN CDNA 1810074P20	SOLUBLE	0	0
UNKNOWN	269534	269534	34853743	SIMILAR TO RIKEN CDNA 2410002O22 GENE	SOLUBLE	0	0
UNKNOWN	250916	250916	34868438	SIMILAR TO RIKEN CDNA 2610207H16	SOLUBLE	0	0
UNKNOWN	198258	198258	34862460	SIMILAR TO RIKEN CDNA 2810405J04	SOLUBLE	0	0
UNKNOWN	235525	235525	34879556	SIMILAR TO RIKEN CDNA 3110038B19	SOLUBLE	0	0
UNKNOWN	192449	192449	34857987	SIMILAR TO RIKEN CDNA 4732463H20	SOLUBLE	0	0
UNKNOWN	296181	296181	34878255	SIMILAR TO RIKEN CDNA 4931400A14	SOLUBLE	0	0
UNKNOWN	266321	266321	34860352	SIMILAR TO RIKEN CDNA 4931406C07	SOLUBLE	0	0
UNKNOWN	293100	293100	34867309	SIMILAR TO RIKEN CDNA 4932408F18	SOLUBLE	0	0
UNKNOWN	213507	213507	34880803	SIMILAR TO RIKEN CDNA 5630401D24	SOLUBLE	0	0
UNKNOWN	366853	366853	62078929	SIMILAR TO RIKEN CDNA 5730568A12	MEMBRANE	0	0
UNKNOWN	228920	228920	34869346	SIMILAR TO RIKEN CDNA 96300046K23	SOLUBLE	0	3
UNKNOWN	199992	199992	81884637	SIMILAR TO RIKEN CDNA C130038N16	SOLUBLE	0	0
UNKNOWN	287440	287440	34866542	SIMILAR TO RIKEN CDNA C920006C10	SOLUBLE	0	0
UNKNOWN	272734	272734	34869447	SIMILAR TO RNA BINDING PROTEINS	SOLUBLE	0	0
UNKNOWN	218331	218331	34877104	SIMILAR TO RS21-C6 PROTEIN	SOLUBLE	0	0
UNKNOWN	168139	168139	27686507	SIMILAR TO SEPTIN 10	SOLUBLE	0	0
UNKNOWN	204958	204958	34853702	SIMILAR TO SIF AND TIAM1-LIKE EXCHANGE FACTOR	SOLUBLE	0	0
UNKNOWN	269978	269978	34874232	SIMILAR TO SMHS2 HOMOLOG	MEMBRANE	0	0
UNKNOWN	195138	195138	34858808	SIMILAR TO START DOMAIN CONTAINING 10; SEROLOGICALLY DEFINED COLON CANCER ANTIGEN 28	SOLUBLE	0	0
UNKNOWN	212891	212891	34872473	SIMILAR TO TARDBP PROTEIN	SOLUBLE	0	0
UNKNOWN	211558	211558	34866738	SIMILAR TO TESTIS PROTEIN TEX15	SOLUBLE	0	0
UNKNOWN	196091	196091	34862046	SIMILAR TO TETRATRIPEPTIDE REPEAT PROTEIN 7 (TPR REPEAT PROTEIN 7)	SOLUBLE	0	0
UNKNOWN	280942	280942	34867559	SIMILAR TO THYROID HORMONE RECEPTOR INTERACTOR 11; THYROID RECEPTOR INTERACTING PROTEIN 11	SOLUBLE	0	0
UNKNOWN	38212	38212	687712	SIMILAR TO TRANSLATIONALLY CONTROLLED TUMOR PROTEIN (TCTP) (P23) (HISTAMINE-RELEASING FACTOR) (HRF)	SOLUBLE	0	0
UNKNOWN	264688	264688	34852035	SIMILAR TO TRIM26 PROTEIN	SOLUBLE	0	0

UNKNOWN	230656	230656	34867257	SIMILAR TO UBIQUITOUS TETRATRICOPEPTIDE CONTAINING PROTEIN ROXAN; ROTAVIRUS X ASSOCIATED NON-STRUCTURAL PROTEIN	SOLUBLE	0	0
UNKNOWN							
UNKNOWN	295040	295040	55741853	SIMILAR TO WBSCR1	SOLUBLE	0	0
UNKNOWN	289309	289309	34935498	SIMILAR TO WD REPEAT DOMAIN 20 ISOFORM 2	SOLUBLE	0	0
UNKNOWN	292693	292693	34878397	SIMILAR TO WDR1 PROTEIN	SOLUBLE	0	0
UNKNOWN	231239	231239	34932585	SIMILAR TO ZINC BINDING ALCOHOL DEHYDROGENASE, DOMAIN CONTAINING 2	SOLUBLE	0	1
UNKNOWN							
UNKNOWN	313065	313065	34849639	SON PROTEIN	SOLUBLE	0	0
UNKNOWN	249650	249650	34879021	SPFH DOMAIN FAMILY, MEMBER 2	SOLUBLE	0	4
UNKNOWN	312134	312134	76096306	SYNAPTIC VESICLE MEMBRANE PROTEIN VAT-1	SOLUBLE	0	0
UNKNOWN				HOMOLOG			
UNKNOWN	278036	278036	34856577	TETRATRICOPEPTIDE REPEAT DOMAIN 17	SOLUBLE	0	0
UNKNOWN	262914	262914	56090363	TEX264 PROTEIN	SOLUBLE	0	0
UNKNOWN	92415	92415	67460104	TIP120	SOLUBLE	0	0
UNKNOWN	266044	266044	34880944	TRANSGELIN 2 (PREDICTED)	SOLUBLE	0	0
UNKNOWN	296070	296070	34874446	TRINUCLEOTIDE REPEAT CONTAINING 5 (PREDICTED)	SOLUBLE	0	3
UNKNOWN							
UNKNOWN	232164	232164	34865480	U2-ASSOCIATED SR140 PROTEIN	SOLUBLE	0	1
UNKNOWN	246703	246703	34879692	UBX DOMAIN CONTAINING 2 (PREDICTED)	SOLUBLE	0	0
UNKNOWN	164032	164032	27675590	UNCHARACTERIZED HEMATOPOIETIC STEM/PROGENITOR CELLS PROTEIN MDS029 HOMOLOG	SOLUBLE	0	0
UNKNOWN							
UNKNOWN	313574	313574	81885310	UNKNOWN (PROTEIN FOR MGC:72610)	SOLUBLE	0	1
UNKNOWN	217607	217607	34871405	UNKNOWN ZINC FINGER PROTEIN	SOLUBLE	0	0
UNKNOWN	191344	191344	34864725	UNKNOWN1	SOLUBLE	0	0
UNKNOWN	264993	264993	27718855	UNKNOWN4	SOLUBLE	0	0
UNKNOWN	258588	258588	34867201	UNNAMED PROTEIN	SOLUBLE	0	0
UNKNOWN	250786	250786	72255531	UNNAMED PROTEIN PRODUCT2	SOLUBLE	0	0
UNKNOWN	260021	260021	34855205	YEAST-44.2 PROTEIN	SOLUBLE	0	1
UNKNOWN	234438	234438	34855819	ZINC FINGER PROTEIN 536	SOLUBLE	0	0

10.5556	28.5968	29.4163	17.541	5.1667	6.5	2	0	2.087	5.3939	13.8095	28.9628	14.8828	8
1	30.426	54.1961	9.2954	4.4167	8.3788	0	2.4762	7.3705	0	18.3472	36.0205	10.6021	2
2.0556	15.3764	25.5047	21.8018	3.875	5.3894	2.5	4.4762	8.9353	0	17.8187	31.7205	34.5044	2.6667
2	40.9837	46.4246	22.9991	3.5417	3.1485	2.5	3.4762	6.2594	3.697	13.9293	24.0494	30.7464	1.3333
0	4.6123	15.2401	12.8655	1.125	0	0	1.1429	0	0	3.4524	4.6114	12.9826	0
6.3333	4.2658	9.4585	10.7841	0	0	0	0	0	0	5.2857	6.2513	14.1784	0
0	8	0	0	0	0	0	0	0	0	0	0	1	0
0	12	27	24	3	3	1	2	0	0	13	15	13	0
0	0	0	0	0	2	3	0	0	0	0	2	0	6
2	0	0	0	1	19	5	2	4	0	0	7	8	6
0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	3	0	0	0	0	0	0	0	2
0	0	0	0	0	3	2	0	0	0	0	1	0	2
0	0	0	0	0	0	0	0	0	0	0	0	0	1
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0	0	0	0	0	0	0	0	0	0	0	0	0	2
0	15	11	9	0	3	4	0	1	0	3	5	6	0
0	0	0	0	0	3	0	0	0	0	0	0	0	0
3	23.5	60	49.2	3	29	21	3	0	0	8.35	25.5814	38.5606	2
0	0	0	0	0	0	0	0	0	0	0	0	0	2
0	0	0	0	0	0	0	1	0	0	0	0	1	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0
10.5952	0	0	0	0	0	0	0	0	0	0	1	0	0
98.2727	0	0	2	0	7	4	5	6	14.4444	25.0909	34.3906	31.6216	48.0882
4.8545	0	0	0	0	0	0	0	0	0	0	1.4111	4	3.8627
27.6038	0	0	0	0	1.2	0	0	0	0	9.8312	10.7538	22.4912	24.0407
96.761	0	0	2	4	6.6	4	4.8	6.75	6.5556	24.8623	36.1169	26.2075	45.3847
22.7673	0	0	0	0	2.2	0	1.2	2.25	0	6.2156	11.4053	16.3797	26.4744
5.2727	0	0	0	0	0	0	0	0	0	0	1.3	0	1.1111
6.4545	0	0	0	0	0	0	0	0	0	0	0	0	0
29.4182	0	0	0	0	2	0	2	1	0	7	15.2889	17	21.0261
0	7	16	4	0	3	1	0	0	0	1	12	4	4
0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	5	0	0	0	0	0	0	0	0	4	2	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0
2	13	15	16	0	1	4	4	1	2	6	12	11	4
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0	0	0	0	0	0	0	0	0	0	0	0	0	4
8	12	19	15	0	4	8	2	1	3	11	12	21	4
2	0	0	0	0	2	1	0	1	0	0	2	1	3
0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	8	0	10.3077	8.3077	14.375	2.5	9.3529	14.75	9.6923

[illegible]

[illegible]

22	10	8	9	27	57	32	23	49	24	32	31	34	7
0	0	0	0	3	1	3	1	1	3	1	0	3	0
2	0	0	0	9	57	26	18	14	26	14	23	26	2
6	1	0	0	20	45	48	14	8	13	16	20	23	0
1	8	9	1	6	20	16	4	1	1	8	12	12	0
0	0	0	0	24	41	19	7	5	8	7	7	15	1
4	0	0	0	11	20.5185	22	7	14	5	8	15	13	0
4	3	0	0	20	39.8077	22	11	10.6667	3	7	10.1111	10.8889	7
0	1	0	0	10	41	41	3	13	4	9	9	13.5385	1
30	4	3	2	19	29	20	18	34.6667	34	12	18	16	7
0	0	0	0	9	23.0714	11.0202	12	7.0556	0	8.1579	0	10	0
13	0	0	0	16	94	40	3	0	0	11	13	19	6
1	0	0	0	1	1	3	11	20	5	5	4	9	1
6	0	0	0	13	18	23	8	8	5	11	11	3	6
4	0	0	0	32	40	15	24	15	4	17	13	15	0
0	0	0	0	16	27	12	6	1	2	6	11	11	0
0	0	0	0	9	13	2	4	2	2	2	5	7	0
4	0	0	0	13	63	31	0	0	0	2	11	10	0
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3	0	0	0	32	47.6104	28	11.9167	7	0	3	10	11	3
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0	0	0	0	3	10	6	10	4	1	5	6	8	0
0	0	0	0	2	13.4815	6	3	2	2	4	8	7	0
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4	0	0	0	17	86	69	18	14	7	6	11	11	0
8	0	0	0	8	9	12	3	2	5	3	4	4	0
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0	0	0	0	0	2	0	4	2.4	3	0	4.16	2	0
2	0	0	0	2	12	3	0	0	0	3	2	2	0
0	0	0	0	0	2	0	3	5	1	1	0	0	0
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2	0	0	0	4	15	17	1	0	0	1	1	6	1
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0	0	0	0	1	10	3	0	0	0	0	0	1	0
0	0	0	0	0	2	1	6	3	2	0	2	11	0
0	0	0	0	0	0	0	0	0	0	0	1	0	0
3	0	0	0	47	180	112	17	10	10	16	12	18	2
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6	0	0	0	0	0	0	32	63	20	10	21	18	0
0	0	0	0	21	54	20	35	29	20	7	21	24	0
0	0	0	0	16	35	19	26	24	17	14	19	32	0
22	4	0	0	33	118.3896	71	10.0833	0	6	13	21	20	0
7	0	0	0	20	74	31	0	0	2	5	8	12	3
1	0	0	0	1	7	2	15	9	7	1	16	16	0
13	1	1	0	44	109.9286	102.9798	22	18.9444	17	17.8421	37	35	6

2	0	2	1	3	16	7	0	3	12	4	2	5	4	2
5	0	0	0	3	10	17.889	4.5		12		0	4.667	6	2
	0	0	0	0	5	1	0		0		1	1	1	1
0	0	0	0	0	0	5.111	4.5		0		0	2.333	0	0
0	0	0	0	3	8	1	1		4	1	1	3	4.8	0
0	0	0	0	0	0	0	0		0	0	0	0	0	0
211.5123	17.4286	20.125	14.9333	24.3846	57.3012	43.8182	26.2973	33.8667	26.6842	54.1639	51.3731	70.3448	106.6116	
7	0	0	0	0	0	0	0	0	0	0	0	2	1	
86	0	0	0	3	10	4	4	18	8	18	47	63	34	
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0	0	0	0	8	20	3	24	30	30	13	20	28.6222	0	
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18	0	0	0	0	1	1	2	0	2	5	12	10	7	
4	0	0	0	0	0	0	0	0	0	0	0	0	7	
131	1	2	3	14.8571	15.1809	8	1	9	11	18	65.9062	52	49.6	
14	0	0	0	3	0	0	0	0	0	0	1	2	6	
0	0	0	0	1	0	0	4	1	2	0	0	0	0	
0	0	0	0	0	0	0	0	0	0	0	0	0	0	
0	0	0	0	1	0	0	4	6	3	1	6	4	0	

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10	22	0	2	0	93.9167	74	55.871	0	8	0	5	12	11
1.25	4.2105	0	0	0	38.1604	9.6921	15.098	0	0	0	0	1	1
3.75	15.7895	0	0	0	78.8287	33.4639	39.902	0	6	0	0	1	5
4	4	0	5	0	2	2	1	0	0	0	0	2	4
1	0	0	0	0	3	0	0	0	0	0	0	0	0
24	15.9091	0	3	0	3	0	0	0	0	0	1	10	5
7	27	0	0	0	4	4	0	0	0	0	2	4	2
0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	7	1	0	0	0	0	0	0	0
1	0	0	0	0	5	0	0	0	0	0	0	0	0
0	0	0	0	0	1.5	0	0	0	0	0	0	0	0
1	0	0	0	0	2.5	0	0	0	0	0	0	0	0
0	0	0	2	3	22.25	36	10	0	2	0	3	0	0
0	0	0	0	0	22.125	0	0	0	0	0	0	0	0
11	16	0	3	0	73	41	49	2	0	0	2	14	9
0	0	0	0	0	0	1	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	1	0	0	0	0	0
0	0	0	2	1	0	0	0	0	0	0	0	4	5
0	0	0	2	0	0	1	0	0	0	0	1	0	0
0	0	0	1	2	0	1	0	0	0	0	1	0	3
0	0	0	2	0	0	0	0	0	0	0	0	1	0
0	0	0	0	0	6	3	0	0	0	0	0	3	5
9	15	14	26	19	9	19	13	20	21	8	9	11	27
0	0	4	8	4	6	1	0	1	2	2	7	5	4
0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	11	14	14	11	4	5	12	17	7	11	12	11
0	1	0	3	1	6	3	0	0	1	0	1	6	4
9	17	1	12	9	10	4	7	3	6	0	0	6	5
0	0	0	0	0	0	0	0	0	0	0	1	0	0
4	0	0	5	0	0	0	0	0	0	0	0	3	3
0	0	8.125	21.5385	13.7148	16.5517	7.0769	3	12.4545	7.5	3.75	17.4167	22.12	14.8
0	0	17.875	18.4615	32.4	25.4483	15.9231	9	9.5455	7.5	11.25	20.5833	11.88	22.2
0	4.0345	3.0833	6.0494	0	2.0455	0	0	2.1765	0	0	0	0	4.0702
32	38.9655	3	7	9	19	24	5	14	17	4	3	29	23
11	13.8667	28.0685	90.7916	61.479	49.7828	65.7684	32.7059	19.4902	33.1198	21.8333	14	81.1495	66.6252
0	0	4.0092	5.1017	1.3074	8.1306	2.6187	0	2.75	1.3986	1.1417	3.9	1.2637	2.6632
58	2.6667	31.6076	80.7264	27.9124	62.6474	43.3062	11.6364	17.2976	24.5141	13.8423	29.9889	59.836	45.6903
0	0	0	0	0	0	0	0	0	0	0	0	0	0
5	6	4.1481	9.1011	9.2857	24.0154	13.1739	2	9	8.1944	1	10	13	19.3865
13	16.7368	9	31.5321	15.4348	26.3676	23.2785	7	13	9	0	13	30.1963	19
3.2	3.8667	4.9	17.1008	22.8509	24.0428	21.515	5.2941	7.25	6.3214	3.875	0	21.0569	27.8362
1	3.6	10.1832	36.5968	18.6151	34.9679	28.3394	6.3636	20.0357	17.4516	4.3077	1.1111	34.9863	12.6284
4.4271	4.7513	17.5714	33.5766	17.4197	20.9627	19.2556	7.5	18.2433	12.422	8.1071	2	22.0824	22.7703
15.0485	21.118	2.7857	19.0704	21.4945	20.601	17.0558	14.3167	18.0101	11.9863	13.681	0	29.4952	27.7518
7.3452	4.5663	0	9.8598	9.5927	11.7409	9.6863	2.7833	6.8066	16.3995	3.2774	0	16.6243	7.5472
6.1792	8.5645	2.6429	13.4932	7.4931	7.6954	9.0024	5.4	11.94	7.1923	4.9345	0	11.798	10.9306
6	5.2632	12	29	28.9286	19	7	4	15	5	2	7	17.1721	27

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6.8063	13.8935	11.6632	26.8949	14.8864	16.2139	14.5	1.0909	11.8376	8.3333	2.5	1.1282	19.6666	19.0756
7.2609	2.4232	20.2556	41.122	5.233	11.5737	18.5254	3.0818	14.1298	12.6	1.45	3.1026	27.5778	9.6667
0	7.2464	6.4648	18.7742	19.8158	15.4679	4.3092	3.0818	11.3613	9.4214	3.4	0	22.2339	28.8291
7.087	1.8116	19.9269	27.5918	14.1828	16.6417	13.3321	1.2909	15.0389	5.681	3.4	11.359	22.5189	21.2478
2.2688	4.2749	6.2018	7.3314	3.684	7.3069	0	0	0	0	0	4.5128	3.4567	9.3601
1.0909	1	1.1	2.1676	4.5944	0	0	0	0	0	0	5.3077	3.2143	8.7161
0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	14	27	23	13	5	0	14	12	4	10	13	15
12.5	12	0	0	0	4	5	0	0	0	0	2	8.875	3
10	13	0	1	0	26	24	4	3	3	0	2	16	4
14	13	0	0	0	3	3	0	0	0	0	2	3	1
5	5	0	0	0	5	2	2	0	0	0	0	3	2
0	3	0	0	0	2	0	0	0	0	0	0	1	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0
1	1	0	0	0	0	0	0	0	0	0	0	0	0
2.5	2	0	0	0	0	0	0	0	0	0	0	0	0
1	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	13	14	8	8	11.8403	2	10	4	0	12	10.7692	10.625
2	3	0	0	0	7	3	0	0	0	0	0	2	0
17	11	16.4706	59.6374	33.9394	54.1494	49.7258	11	10.2857	12.4	1	29.58	31.4762	48.5412
0	1	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	1	0	0	0	1
0	0	0	0	0	0	0	0	0	0	0	0	0	0
14.3333	17.2845	0	5	0	1.5	0	0	3	0	0	9.5	8.2308	8.7692
63.8372	96.6632	0	4	2	33.6842	19.5429	9	9.7143	11.1111	5.7143	33.7353	56.0784	39.9241
1.1	6.7851	0	0	0	1.25	0	0	0	0	0	0	0	1.2222
33.0894	24.9685	0	0	0	11.7084	7.284	0	0	1.8611	0	7.4817	19.512	16.5926
59.1601	102.2817	0	0	0	28.2442	18.8122	6	12.8571	16.3095	14.2222	40.4534	37.849	38.1142
29.58	31.0498	0	0	0	11.4882	8.361	0	6.4286	2.7183	4.0635	15.8296	26.3298	11.6
3.3	1.2023	0	0	0	0	0	0	0	0	0	0	0	0
0	11.9991	0	0	0	0	0	0	0	0	0	0	0	1.2222
10.6	39.2948	0	0	0	11.75	3	2	7	3	6	12	14	11.5556
8	5	1	9	0	4	3	0	1	0	0	2	14	7
0	0	1	0	0	0	0	0	0	0	0	0	0	0
0	0	3	9	0	9.375	8	0	0	0	0	8	9	3
2	4	0	0	0	0	1	0	0	0	0	0	1	1
12	12	23	16	16	23	8	4	13	8	2	25	29	24
0	3	0	0	0	2	3	1	0	0	0	1	2	0
5	5	0	0	0	5	0	0	0	0	0	0	3	1
20	11	23	18	13	26	11	8	13	10	0	19	28	22
4	4	0	0	0	9	5	1	1	0	0	0	4	0
1	1	0	0	0	1	0	1	0	0	0	0	0	0
1.2	0	0	0	0	0	0	0	0	0	0	0	0	0
9.0632	23.2353	0	0	0	12.3333	3.3846	0	12.25	16.594	5	3.875	14.1058	11.8571

9	10	0	0	2	0	28	29	7	15	22	1	10	8	8
0	0	0	0	0	0	0	0	0	0	0	0	0	1	2
1	1	0	0	0	0	10	19	4	8	15	1	2	6	4
4	2	0	0	0	0	31.9677	36.619	14	8	11	0	3	6	7
1	0	2	0	3	0	7	13	0	5	1	0	3	7	10
4	1	0	0	0	0	13.26	21	4	2	8.28	0	4.16	6	4
4	4	0	0	0	0	6	11	1	2	6	0	3	9	12
4.8	3.5	0	0	0	0	14.5455	16.625	8	7	0	0	3	7	4
4	0	0	0	0	0	17	29	6	2	4	0	5	7	9
5	7	0	0	0	0	4	6	4	9	14	7	8	6	6
2	6	0	0	0	0	21.1935	20.1899	6	0	0	0	0	6	2
8	21	0	0	0	0	19	56	34	3	0	0	4	10	5
0	0	0	0	0	0	5	4	3	4	10	1	3	5	4
8	8	0	0	0	0	7	29	13	4	5	0	5	2	5
3	7	0	0	0	0	48	39	9	12	8	0	6	9	6
0	0	0	0	0	0	25	40	4	5	0	0	4	5	2
0	0	0	0	0	0	11	12	0	2	2	0	1	5	1
5	4	0	0	0	0	18.8889	38	12	0	0	0	1	4	2
0	0	0	0	0	0	14	9	1	7	0	0	4	6	7
6	2	0	0	0	0	17	41.5	14	3	4	0	3	5	7
0	0	0	0	0	0	17	24	2	0	0	0	0	3	0
0	0	0	0	0	0	14	10	2	3	0	0	0	0	1
0	0	0	0	0	0	12	17	0	2	2	0	2	4	7
1	0	0	0	0	0	0	1	0	3	7	0	2	2	1
0	0	0	0	0	0	9	9	1	3	3	3	2	1	2
0	0	0	0	0	0	2	7	0	7	10	0	5	11	10
0	1	0	0	0	0	14	16	4	3	5	0	2	6	7
1	0	0	0	0	0	0	1	0	8	14	0	2	9	9
2	2	0	0	0	0	6	7	3	0	0	0	0	2	1
0	3	0	0	0	0	10	8	4	0	0	0	1	0	1
0	0	0	0	0	0	11	7	3	0	0	0	0	0	2
3	2	0	0	0	0	11	52	23	3	2	1	0	3	2
2.5	2	0	0	0	0	8.5	6	11	1	0	0	1	0	3
0	0	0	0	0	0	1	1	0	2	2	1	0	3	4
0	0	0	0	0	0	2	0	0	2	0	1	0	0	0
0	0	0	0	0	0	7	9	7	0	0	0	0	1	2
0	0	0	0	0	0	0	0	0	3	1	0	2	1	2
0	0	0	0	0	0	2	1	0	0	0	0	0	0	0
3	3	0	0	0	0	7.875	17	10.9091	1	0	0	3	1	5
0	0	0	0	0	0	0	1	0	0	0	0	0	0	0
0	0	0	0	0	0	1	3	1	0	0	0	0	0	0
0	0	0	0	0	0	0	1	0	5	1	1	1	2	1
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6	3	0	0	0	0	34	52	22	2	5	1	1	5	4
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2	1	0	0	0	0	0	1	0	19	8	3	7	11	6
1	1	0	0	0	0	22	41	0	15	7.75	3	5	13	9
0	0	0	0	0	0	24	27	1	9	11	0	7	8	8
14	14	0	0	0	0	32	70.5	21	7	5	0	7	16	12
4	4	0	0	1	0	17	49	11	2	2	0	1	6	5
0	0	0	0	0	0	6	14	0	7	0	0	2	6	5
6	18	0	0	3	0	26.8065	77.8101	23	12	11	5	12	12	17

2	3	0	1	0	4	5	2	0	4	2	2	0	2	2
2	3	0	0	0	4	6	7.3333	3.5	6.667	2	2	2	0	2
0	0	0	0	0	1	3	0	1	0	0	0	0	2	0
0	0	0	0	0	0	3	3.6667	3.5	3.333	0	0	0	0	0
0	0	0	0	0	7	19	0	0	7	0	0	0	1	1
0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
132.9866	182.6891	3.75	9.8824	2	66.0783	63.7826	43.4762	65.5652	41.4154	14	52.642	63.2308	70	70
3	2	0	0	0	0	0	0	0	0	0	0	1	1	1
0	1	0	0	0	7	0	0	0	1	0	0	1	0	0
69	68	0	0	0	22	28	2	15	28	5	24	56	42	42
7	3	0	0	0	7	7	1	3	1	0	1	3	2	2
1	0	0	0	0	2	1	0	0	0	0	0	1	0	0
6	4	0	0	0	12	6.8571	2	6	2	0	0	1	2	2
1	4	0	0	0	8	13	0	9	4	0	1	2	2	2
1	2	0	0	0	0	0	0	0	0	0	0	0	0	0
5	7	0	0	0	6	2	1	2	0	0	2	3	1	1
1	9	0	0	0	8	13	0	0	5	0	3	5	2	2
5	3	0	0	0	7	7	1	0	2	0	2	2	1	1
29	50	0	1	0	15	17	4	12	7	0	20	21	29	29
1	2	0	0	0	4	13	1	1	11	0	0	3	5	5
0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
0	0	1	1	1	2	2	0	0	0	0	0	1	5	5
5	4	0	1	1	0	0	0	1	0	0	2	1	2	2
3	0	0	0	0	8	6	3	0	1	0	0	2	1	1
0	0	0	0	0	1	1	0	0	0	0	0	0	0	0
4	10	0	0	0	34.8387	53	17	15.6923	33.8621	12	3	11	10	10
0	3	0	0	0	17	15	2	17	17	17	3	8	8	8
0	2.5	0	0	0	0	0	0	0	0	0	0	0	1	1
22	19	0	0	0	9	5	0	3	4	0	7	14	11	11
4	4	0	0	0	0	0	0	1	0	0	0	1	0	0
17.5238	167.6914	0	0	3	79.5333	36.7073	13	41.9048	13.9286	10	50.8696	35.7895	47.8776	47.8776
10	19	0	0	0	3	1	0	4	0	0	1	2	1	1
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	1	0	0	0	1	1	0	0	0	0	0	0	0	0
0	0	0	0	0	2	2	0	0	2	0	0	3	0	0

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0	0	1	1	7	0	0	0	0.04896	0.082372	0	0.025107	0	0	0.021566	0.035829
0	3	0	0	1	0	0	0	0	0	0.5959	0.50213	0.34549	0	0.043131	0
1	0	3	0	10	0	0	0	0.073439	0.13729	0	0	0	0	0	0
0	0	0	0	2	0	0	0	0.02448	0	0	0	0	0	0	0
0	0	1	0	0	0	0	0	0.04896	0	0.074488	0.050213	0	0	0.064697	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1	0	0	0	8	0	0	0	0.2448	0.082372	0.5959	0.55235	0.076775	0	0.021566	0
0	0	0	0	2	0	0	0	0.02448	0.027457	0	0	0	0	0	0
0	0	0	5	0	0	0	0	0.02448	0.10983	0	0	0	0.11834	0.15096	0.071659
2	0	0	21	0	5	0	0	0.78335	1.4552	0	0	0	0.11834	0.36662	0.25081
0	0	0	2	0	0	0	0	0	0	0	0	0	0	0.021566	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.021566	0.035829
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0.02448	0	0	0	0	0	0.021566	0
1	0	0	0	2	0	0	0	0	0	0	0	0	0	0.021566	0
6	0	0	0	28	2	0.23952	0.24712	0.41616	0.037244	0.037244	0	0	0.17751	0.34505	0.28664
0	0	0	0	0	0	0	0	0	0	0.26071	0.20085	0.15355	0.059172	0.064697	0.14332
0	0	0	0	2	0	0	0	0.02448	0	0	0	0	0	0	0
8	0	5	18	1	3	0.2394	0.082372	0.46512	0	0	0	0	0	0.021566	0.035829
0	0	0	0	0	0	0	0	0.073439	0	0.11173	0.27617	0.15355	0	0	0
1	0	0	0	0	0	0	0	0.073439	0	0	0	0	0	0	0
0	2	0	2	0	0	0	0	0	0	0.18622	0.15064	0.11516	0	0.021566	0
0	0	0	0	0	0	0	0	0	0.10983	0	0.025107	0	0	0	0
0	0	0	0	1	0	0	0	0	0	0	0	0	0	0.021566	0
0	0	0	0	0	0	0	0	0.02448	0	0	0	0	0	0	0
0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	1	0	0	0	0.26928	0.054915	0.14898	0.40171	0.23033	0	0.043131	0
0	0	1	3	0	0	0	0	0.19584	0.10983	0	0.025107	0	0	0.043131	0
0	0	0	0	0	0	0	0	0.1224	0.027457	0.037244	0.10043	0.038388	0	0.021566	0
0	0	0	0	0	0	0	0	0	0	0	0	0.038388	0	0	0
0	0	0	0	0	0	0	0	0.14688	0.10983	0.037244	0.12553	0.038388	0	0	0
0	0	1	0	0	0	0	0	0.073439	0	0.074488	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0.02448	0	0	0	0	0	0	0

1	0	0	0	0	0	0	0.02448	0	0	0	0	0	0.059172	0.10783	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0.021566	0.035829	
0	0	0	0	0	0	0	0.02448	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0.14688	0.10983	0	0	0	0	0	0	0
0	0	0	1	0	0	0	0.073439	0.027457	0	0	0	0	0	0	0
5	0	0	6	3	18	0.05988	0.14688	0.082372	0	0	0	0.059172	0.21566	0.10749	
0	0	0	0	0	0	0	0.02448	0.027457	0	0.050213	0	0	0	0	0.035829
0	0	0	0	0	0	0	0.04896	0	0.074488	0.12553	0.038388	0	0	0	0
0	0	0	0	15	1	0.11976	0.612	0.63152	0.18622	0.25107	0.42226	0.23669	0.51768	0.28664	
0	0	0	0	3	0	0	0.26928	0.13729	0	0	0	0	0	0	0
0	0	0	1	0	0	0	0	0	0.14898	0.025107	0	0	0	0	0
2	0	0	1	12	1	0.23952	0.4896	0.3844	0.22346	0.30128	0.26871	0.059172	0.10783	0.17915	
0	0	0	0	0	0	0	0.073439	0.16474	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0.02448	0	0.14898	0.17575	0.076775	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0.038388	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0.059172	0.086263	0.10749	
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0.17751	0.30192	0.17915	
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	1	1	0	0	0	0	0	0	0	0.021566	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0.043131	0	0

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% TOTAL PEPTIDES N=1 RM SLT	% TOTAL PEPTIDES N=2 RM SLT	% TOTAL PEPTIDES N=3 RM SLT	% TOTAL PEPTIDES N=1 RM TOT	% TOTAL PEPTIDES N=2 RM TOT	% TOTAL PEPTIDES N=3 RM TOT	% TOTAL PEPTIDES N=1 SM AQU	% TOTAL PEPTIDES N=2 SM AQU	% TOTAL PEPTIDES N=3 SM AQU	% TOTAL PEPTIDES N=1 SM DET	% TOTAL PEPTIDES N=2 SM DET	% TOTAL PEPTIDES N=3 SM DET	% TOTAL PEPTIDES N=1 SM INS	% TOTAL PEPTIDES N=2 SM INS	% TOTAL PEPTIDES N=3 SM INS
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0.033473	0	0.063412	0.015926	0	0	0	0	0	0
0	0.12415	0.049826	0.1165	0.62742	0.68619	1.9861	1.2682	1.6404	0	0	0	0.40067	0	0.10484
0	0	0	0	0	0	0	0.021137	0	0	0	0	0	0	0
0	0	0	0.038835	0.073814	0.10042	0.29791	0.21137	0.24128	0	0	0	0	0	0
0	0.12415	0	0.27184	0.16608	0.28452	0.82754	0.14796	1.1148	0	0	0	0.21972	0.087367	0
0	0	0	0	0	0	0	0	0.015926	0	0	0	0	0	0
0	0	0	0	0	0	0	0.042274	0.015926	0	0	0	0	0	0
0	0	0	0	0	0	0	0.021137	0.015926	0	0	0	0	0	0
0	0	0	0	0	0.050209	0.033102	0.063412	0.047778	0	0	0	0.012925	0	0
0	0	0	0	0.036907	0.050209	0.033102	0.10569	0.12741	0	0	0	0.012925	0	0
0	0	0	0.31068	0.38753	0.23431	1.0924	0.84549	0.74853	0	0	0	0.29727	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0.066203	0.10569	0.031852	0	0	0	0	0	0
0	0	0	0	0.018454	0	0.033102	0.10569	0.095557	0	0	0	0.012925	0	0
0	0	0	0	0.036907	0	0.042274	0.042274	0.079631	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0.038835	0.092268	0.050209	0.099305	0.084549	0.12741	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0.11173	0	0	0.41477	0.51883	0.69513	0.76094	0.92371	0	0.28506	0.057471	0.19387	0.087367	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0.016736	0	0	0	0	0.028506	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0.15634	0.036907	0.16736	0.099305	0.29592	0.22297	0	0	0	0.012925	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0.012925	0	0
0	0	0	0	0	0	0	0	0	0	0.085519	0.17241	0	0	0
0	0	0	0	0.018454	0	0	0.021137	0.063704	0	0	0	0	0	0
0	0	0	0	0	0	0	0.042274	0.079631	0.21994	0.085519	0.057471	0.0517	0.034947	0
0	0	0	0	0.073814	0.050209	0.16551	0.21137	0.14333	0	0	0	0.0517	0	0
0	0	0	0	0	0.016736	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0.012925	0	0
0	0	0	0	0	0	0	0	0	0	0.085519	0.17241	0	0	0
0	0	0	0	0.092268	0.066946	0.33102	0.34539	0.14333	0	0	0	0.19387	0.05242	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0.02585	0.017473	0
0.079777	0.12415	0	0	0.073814	0	0	0	0	0	0	0	0	0	0
0	0.031037	0	0	0.018454	0.050209	0.23171	0.12682	0.27074	0	0.028506	0	0.064625	0.017473	0
0.15955	0.24829	0.24913	0.15634	0.29626	0.45188	0.86064	0.66919	1.3378	0	0.057013	0	0.21972	0.13979	0
0	0	0	0	0	0.016736	0.033102	0.021137	0.015926	0	0	0	0	0	0

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0	0	0	0	0	0	0.018454	0.033473	0	0	0	0	0	0	0.085519	0.057471	0.02585	0
0	0	0	0	0	0.038835	0.018454	0.016736	0	0	0	0	0	0.21994	0.057013	0.11905	0.064625	0.017473
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0.25755	0.14017	0.033102	0.07398	0.047778	0.17595	0.32579	0.12378	0.14217	0.02621	0.02621	0.02621
0.15955	0.12415	0	0	0.19417	0.038835	0.34011	0.26151	0.033102	0.2008	0.12741	0.6305	0.44388	1.0256	0.2068	0.14852	0.14852	0.14852
0	0	0	0	0	0	0.083041	0.036262	0	0	0	0	0.06372	0.2069	0.014966	0.020366	0.020366	0.020366
0.27922	0	0	0.64773	0.72233	0.43673	0.34804	0	0	0.042274	0.084939	2.1156	0.92194	2.0254	0.80263	0.24754	0.24754	0.24754
0	0	0	0	0.48155	0.21837	0.50273	0.13241	0.13241	0.084549	0.04247	0.81693	0.6392	1.101	0.22932	0.18638	0.18638	0.18638
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0.073814	0.10042	0	0	0	0.073314	0.24434	0.19157	0.084012	0.081542	0.081542	0.081542
0	0	0	0	0	0	0.092268	0.10042	0	0	0	0.073314	0.21176	0.095785	0.096937	0.040771	0.040771	0.040771
0	0	0	0	0	0	0.018454	0	0	0	0	0	0.057013	0	0	0	0	0
0	0	0.099651	0.038835	0.038835	0.055361	0.083682	0	0	0	0	0.073314	0.11403	0.28736	0.1034	0.034947	0.034947	0.034947
0	0	0	0	0	0.036907	0	0	0	0	0	0	0.085519	0.057471	0.012925	0.017473	0.017473	0.017473
0	0	0	0	0	0.036907	0.050209	0	0	0	0	0	0.085519	0.11494	0.012925	0	0	0
0	0	0	0	0	0.055361	0	0	0	0	0	0.073314	0.085519	0.057471	0.02585	0.017473	0.017473	0.017473
0.31911	0.3414	0.14948	0.56893	0.56893	0.35834	0.52618	0	0	0	0	1.3585	0.97955	2.1874	0.5117	0.31931	0.31931	0.31931
0	0	0	0	0	0.018454	0.13389	0	0	0	0	0	0.11403	0	0	0	0	0
0	0	0	0.038835	0.038835	0.018454	0.016736	0	0	0	0.031852	0	0.085519	0.11494	0	0.017473	0.017473	0.017473
0	0.062073	0	0.27184	0.27184	0.22144	0.15063	0.099305	0.099305	0.084549	0.015926	0.65982	0.65564	0.8046	0.21972	0.50673	0.50673	0.50673
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0.14253	0.17241	0.012925	0	0	0
0.079777	0.09311	0.24913	0.3452	0.3452	0.40598	0.31297	0.033102	0.033102	0.042274	0.031852	1.2348	0.65037	1.4235	0.25288	0.22715	0.22715	0.22715
0	0	0	0	0	0	0.016736	0	0	0	0	0	0	0	0	0	0	0
0.15955	0.21726	0.1993	0.31068	0.31068	0.33216	0.52859	0.099305	0.099305	0.042274	0.19111	2.346	1.1403	1.4368	0.21972	0.29705	0.29705	0.29705
0.11966	0.031037	0	0.31068	0.31068	0.20299	0.30126	0	0	0	0	0.80645	0.65564	0.74713	0.12925	0.15726	0.15726	0.15726
0.079777	0.12415	0	0.69903	0.69903	0.62742	0.82008	0.033102	0.033102	0.14796	0.079631	2.1994	1.5678	2.3563	0.37482	0.33199	0.33199	0.33199
0	0	0	0	0	0.10684	0.035235	0	0	0.084549	0	0.17107	0.29932	0	0.059085	0.12814	0.12814	0.12814
0	0	0	0.04315	0.04315	0.055361	0.05523	0	0	0.021137	0	0.23152	0.14781	0.18568	0.070244	0.034947	0.034947	0.034947
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.012925	0.017473	0.017473	0.017473
0	0	0	0.038835	0.038835	0.018454	0.033473	0	0	0	0	0.073314	0.028506	0.057471	0.02585	0.017473	0.017473	0.017473
0.35899	0	0	0.34951	0.34951	0.46203	0.42582	0.21847	0.21847	0.26421	0.2212	2.1841	0.94478	0.9387	0.50246	0.34947	0.34947	0.34947
0	0	0	0	0	0	0.018454	0.016736	0	0	0	0	0.028506	0	0	0.017473	0.017473	0.017473
0	0	0	0	0	0	0	0	0	0	0.015926	0	0.057013	0	0.02585	0.05242	0.05242	0.05242
0.039888	0	0	0.038835	0.038835	0.20299	0.13389	0	0	0	0.015926	0.073314	0.14253	0.11494	0.1551	0.17473	0.17473	0.17473
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0.055361	0.066946	0	0	0	0	0.028506	0	0.012925	0	0	0
0	0	0	0	0	0	0.055361	0.066946	0	0	0	0	0.028506	0	0.012925	0	0	0
0.17095	0.21366	0.35603	0.89575	0.89575	0.41758	0.59302	0.099305	0.099305	0.17277	0.2786	1.8328	0.67531	1.405	0.47967	0.30393	0.30393	0.30393
0	0	0	0.059716	0.059716	0.20879	0.098837	0	0	0	0.18574	0.36657	0.18418	0.28101	0.056432	0.075983	0.075983	0.075983
0.085475	0.042732	0.23735	0.41802	0.41802	0.47083	0.49419	0	0	0.043193	0.030956	0.12219	0.49113	0.65569	0.11286	0.037991	0.037991	0.037991
0	0	0	0.059716	0.059716	0.13919	0.032946	0	0	0	0	0	0.061392	0	0	0	0	0
0	0.064772	0	0.17291	0.17291	0.37616	0.27228	0	0	0.047955	0.051062	0.2728	0.27323	0.46307	0.059267	0.042227	0.042227	0.042227

0	0.064772	0.26876	0.53629	0.53447	0.24908	0.26481	0.14387	0.22127	0.85507	0.76667	0.84405	0.20956	0.25336
0.098771	0.22876	0	0.71251	0.66471	0.17744	0.066203	0.15347	0.038592	1.485	1.1722	0.30074	0.20956	0.25336
0.17855	0.27732	0	0.69199	0.58536	0.57748	0.088271	0	0.11541	0.47396	0.53518	1.1388	0.19992	0.075296
0.13866	0.19427	0.1842	0.54094	0.4438	0.51458	0.044135	0.1498	0.028852	1.4609	0.78654	0.8151	0.21509	0.23296
0.045587	0	0	0.13407	0.085097	0.21728	0	0.047955	0.068083	0.45467	0.20899	0.21172	0.09444	0
0	0	0	0.20527	0.11536	0.2373	0	0.023059	0.015926	0.080645	0.061791	0.26405	0	0
0	0	0	0	0	0.016736	0	0	0	0	0	0	0	0
0.079777	0	0	0.50485	0.2768	0.21757	0	0	0	1.0264	0.76967	1.3218	0.16802	0.087367
0	0	0	0	0.036907	0	0.19861	0.26421	0.19111	0	0	0	0.0517	0.087367
0.079777	0.12415	0	0	0.12918	0.13389	0.19861	0.21137	0.20704	0	0.028506	0	0.33605	0.41936
0	0	0	0	0	0	0.066203	0.29592	0.20704	0	0	0	0.038775	0.05242
0	0	0	0	0.018454	0	0.066203	0.10569	0.079631	0	0	0	0.064625	0.034947
0	0	0	0	0	0	0.033102	0	0.047778	0	0	0	0.02585	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0.021137	0.015926	0	0	0	0	0
0	0	0	0	0	0	0.066203	0.052843	0.031852	0	0	0	0	0
0	0	0	0	0	0	0.066203	0.021137	0	0	0	0	0	0
0	0.031037	0	0.1165	0.092268	0.10042	0	0	0	0.95308	0.39909	0.45977	0.1034	0.20689
0	0	0	0	0	0	0	0.042274	0.047778	0	0	0	0.090474	0.05242
0.11966	0	0	0.32427	0.47207	0.64537	0.066203	0.35933	0.17519	1.2075	1.7	1.9505	0.69988	0.86888
0	0	0	0	0	0	0.066203	0	0.015926	0	0	0	0	0
0.039888	0	0	0	0	0.016736	0	0	0	0	0	0	0	0
0	0	0	0	0.018454	0	0	0	0	0	0	0	0	0
0	0	0	0	0.13533	0.089415	0.46382	0.30297	0.27527	0	0.14253	0	0.019387	0
0.19944	0.18622	0.7197	0.9744	0.63463	0.52923	1.5918	1.3493	1.5395	0	0.11403	0.11494	0.43537	0.34148
0	0	0	0	0.02604	0.066946	0.12786	0.023251	0.10806	0	0	0	0.016156	0
0	0	0	0.38179	0.19845	0.37642	0.79579	0.69942	0.39765	0	0	0	0.15133	0.12728
0.19146	0.2095	0.32663	0.96553	0.66649	0.43862	1.5023	1.2505	1.6289	0	0	0	0.36505	0.32871
0.047866	0.069832	0	0.24138	0.21047	0.27414	0.87635	0.62524	0.4945	0	0	0	0.14848	0.14609
0	0	0	0	0.02399	0	0.03678	0.069753	0.019147	0	0	0	0	0
0	0	0	0	0	0	0	0	0.1911	0	0	0	0	0
0.079777	0.031037	0	0.27184	0.28213	0.28452	0.696	0.22405	0.62581	0	0	0	0.15187	0.05242
0	0	0	0.038835	0.22144	0.066946	0.13241	0.1691	0.079631	0.073314	0.25656	0	0.0517	0.05242
0	0	0	0	0	0	0	0	0	0.073314	0	0	0	0
0	0	0	0	0.073814	0.033473	0	0	0	0.21994	0.25656	0	0.12117	0.13979
0	0	0	0	0	0	0.033102	0.042274	0.063704	0	0	0	0	0.017473
0.15955	0.031037	0.099651	0.23301	0.22144	0.1841	0.13241	0.25365	0.19111	1.6862	0.4561	0.91954	0.29727	0.13979
0	0	0	0	0	0	0.033102	0	0.047778	0	0	0	0.02585	0.05242
0	0	0	0	0	0	0.13241	0.10569	0.079631	0	0	0	0.064625	0
0.079777	0.031037	0.14948	0.42718	0.22144	0.35146	0.13241	0.42274	0.17519	1.6862	0.51311	0.74713	0.33605	0.19221
0	0.031037	0	0	0.036907	0.016736	0.099305	0.084549	0.063704	0	0	0	0.11632	0.087367
0	0	0	0	0	0	0	0.021137	0.015926	0	0	0	0.012925	0
0	0	0	0	0	0	0	0.025365	0	0	0	0	0	0
0.41116	0.25784	0.71624	0.097087	0.1726	0.24886	0.32083	0.19157	0.37005	0	0	0	0.15941	0.059141

0	0	0	0	0	0	0	0	0.033102	0.021137	0	0	0	0	0	0	0	0	0.012925	0
0	0	0	0	0	0	0	0	0.099305	0.063412	0.15926	0	0	0	0	0	0	0	0.1034	0.017473
0	0	0	0	0	0	0	0	0	0.12682	0.063704	0	0	0	0	0	0	0	0.012925	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0.099305	0.021137	0.079631	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0.19861	0.084549	0.047778	0	0	0	0	0	0	0	0	0
0.039888	0	0	0	0	0	0	0	0	0.042274	0.031852	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0.021137	0.079631	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0.021137	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0.042274	0.015926	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0.16551	0.14796	0.063704	0	0	0	0	0	0	0	0	0.017473
0.23933	0.3414	0.34878	0	0.29526	0.16736	0.33102	0.50729	0.33102	0.50729	0.22297	0	0.028506	0	0	0.11632	0	0.11632	0.24463	0
0.039888	0.062073	0	0.0863	0.19137	0.12971	0.099305	0.063412	0.099305	0.063412	0.079631	0.14663	0.43379	0.17241	0.13848	0.12911	0	0.13848	0.12911	0
0.039888	0	0	0.30205	0.32533	0.38912	0.099305	0.10569	0.099305	0.10569	0.079631	0.65982	0.27887	0.4023	0.055392	0.20289	0	0.055392	0.20289	0
0	0	0	0	0	0	0	0	0.13241	0.1691	0.063704	0	0	0	0	0	0	0	0	0
0	0	0.049826	0	0.12918	0.033473	0.16551	0.10569	0.16551	0.10569	0.047778	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0.031706	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0.033102	0	0.031852	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0.063412	0.015926	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0.23171	0.14796	0.15926	0	0	0	0	0.02585	0	0.02585	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0.057013	0	0.02585	0.017473	0	0.02585	0.017473	0
2.7124	2.1105	3.2387	2.3689	1.0334	1.272	0.52963	0.76094	0.52963	0.76094	0.71667	0	0	0.057471	1.4217	1.1882	0	1.4217	1.1882	0
0	0	0	0	0	0	0	0	0.099305	0.042274	0	0	0	0	0	0	0	0.012925	0	0
1.1169	0.15518	0.049826	0.49931	0.5167	0.23431	0.72824	0.29592	0.72824	0.29592	0.23889	0	0	0	0	0	0	0.012925	0	0
0	0	0	0	0	0	0	0	0	0.042274	0.095557	0	0	0	0	0	0	0	0	0
0	0	0.049826	0.038835	0	0.033473	0.16551	0.084549	0.16551	0.084549	0.095557	0	0	0	0	0.090474	0.05242	0.090474	0.05242	0
1.4759	1.3035	0.44843	0.46602	0.2399	0.32682	0.033102	0.021137	0.033102	0.021137	0.063704	0	0	0	0	0.077549	0.069893	0.077549	0.069893	0
0	0	0	0	0.073814	0.083682	0.52963	0.67639	0.52963	0.67639	0.3663	0	0.028506	0	0.16802	0.10484	0	0.16802	0.10484	0
0	0	0	0	0	0	0	0.021137	0	0.021137	0	0	0	0	0.012925	0	0	0.012925	0	0
1.5556	1.9243	1.7937	0.73786	0.59051	0.35146	0.39722	0.27478	0.39722	0.27478	0.20704	0	0.028506	0.057471	0.19387	0.19221	0	0.19387	0.19221	0
0	0	0	0	0	0	0.066203	0.042274	0.066203	0.042274	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0.099305	0.10569	0.099305	0.10569	0.095557	0	0	0	0.012925	0	0	0.012925	0	0
0	0	0	0	0	0	0.16551	0.14796	0.16551	0.14796	0.14333	0	0	0	0.012925	0.034947	0	0.012925	0.034947	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0.039888	0.031037	0	0	0	0	0	0	0	0	0	0	0	0	0.02585	0.017473	0	0.02585	0.017473	0
0	0	0	0	0	0	0	0	0	0.021137	0	0	0	0	0.012925	0	0	0.012925	0	0
0	0	0	0	0	0	0	0.042274	0	0.042274	0	0	0	0	0	0	0	0	0	0
0.39888	0.031037	0.29895	0.19417	0.14763	0.11715	0	0.021137	0	0.021137	0.031852	0	0	0	0	0	0	0	0	0
0.039888	0	0	0	0	0.016736	0.033102	0.10569	0.033102	0.10569	0	0	0	0	0.038775	0	0	0.038775	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0.057013	0.11494	0.077549	0.034947	0	0.077549	0.034947	0
0	0	0	0	0.018454	0.016736	0	0	0	0	0.015926	0	0	0	0	0	0	0	0	0
0	0	0.049826	0	0.018454	0.016736	0	0	0	0	0	0	0	0	0	0.017473	0	0	0.017473	0
0	0	0	0	0.092268	0	0.033102	0.12682	0.033102	0.12682	0.047778	0	0	0	0	0	0	0	0	0
0.15955	0	0	0	0.22144	0.16736	0.19861	0.29592	0.19861	0.29592	0.25482	0	0	0	0.038775	0.017473	0	0.038775	0.017473	0
0	0	0	0	0	0.016736	0	0.10569	0	0.10569	0.031852	0	0	0	0.038775	0.10484	0	0.038775	0.10484	0
0	0	0	0.038835	0.036907	0.050209	0.29791	0.19023	0.29791	0.19023	0.31852	0	0	0	0.20105	0.087367	0	0.20105	0.087367	0
0.039888	0.031435	0	0	0	0	0	0	0	0	0.031852	0	0	0	0	0	0	0	0	0
2.7922	2.4205	3.7369	1.8641	1.1626	1.1213	0.86064	1.0357	0.86064	1.0357	0.71667	0	0.057013	0	0.2585	0.31452	0	0.2585	0.31452	0

0	0	0	0	0	0	0	0	0	0.033102	0.021137	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0.039888	0.031037	0	0	0	0	0	0	0	0	0	0.031852	0	0	0	0	0	0	0	0	0	0.077549	0.034947	0	0
0.039888	0	0.049826	0	0.018454	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0.042274	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0.033473	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0.036907	0	0.027894	0	0	0	0.031852	0	0	0	0	0	0	0	0	0.019387	0	0	0	0
0.039888	0	0	0	0	0	0	0.016736	0	0	0.021137	0.015926	0	0	0	0	0	0	0	0	0.02585	0.034947	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0.031852	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0.033102	0.042274	0.031852	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0.062073	0	0.31068	0.33216	0.33473	0.76134	0.7398	0.52556	0	0	0	0	0	0	0	0	0	0	0	0.2585	0.19221	0	0	0
0	0	0	0	0	0	0.066203	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.017473	0	0
0	0	0	0	0	0	0	0	0	0	0	0.015926	0	0	0	0	0	0	0	0	0.067086	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0.042274	0.015926	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0.018454	0.016736	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0.015926	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0.016736	0	0	0	0	0	0	0	0	0	0	0	0	0.057471	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0.015926	0	0	0	0	0	0	0	0	0.012925	0.034947	0	0	0
0	0	0	0	0	0	0	0	0	0	0.19023	0.095557	0	0	0	0	0	0	0	0	0	0	0.034947	0	0
0	0	0	0	0	0	0	0	0	0	0.063412	0.047778	0	0	0	0	0	0	0	0	0.1034	0.017473	0	0	0
0	0	0	0	0	0	0	0	0	0	0.021137	0.015926	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0.11966	0.09311	0.1993	0.07767	0.12918	0.033473	0.13241	0.1691	0.11148	0	0.1691	0.11148	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0.87754	0.96214	0.99651	0.58252	0.35062	0.41841	0.29791	0.48616	0.079631	0	0	0	0	0	0	0	0	0	0	0	0.038775	0.069893	0	0	0

0.11966	0.15518	0.049826	0.038835	0.036907	0.033473	0	0.084549	0.047778	0	0	0	0	0.012925	0.034947
0.079777	0	0.049826	0.07767	0.036907	0.083682	0	0	0	0	0	0	0	0.012925	0.034947
0.079777	0.031037	0	0.07767	0.036907	0.066946	0	0	0.015926	0	0	0	0	0.24557	0.13251
0.079777	0.062073	0	0	0.018454	0	0	0	0	0	0	0	0	0.012925	0.017473
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0.83765	1.4587	0.89686	0.85437	0.62742	0.87029	0	0.042274	0.015926	0	0	0	0	0.59455	0.66399
0	0	0	0	0	0	0	0	0.015926	0	0	0	0	0	0
0	0	0	0	0	0	0	0.063412	0	0.073314	0.085519	0.057471	0.32312	0.15726	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0.03256	0	0.085519	0.22989	0.02585	0.034947	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0.14663	0.11403	0.28736	0.038775	0	0
0	0	0	0	0	0	0	0	0.031852	0	0.028506	0	0	0	0
0	0	0	0	0	0	0.033102	0.021137	0	0	0	0	0	0	0
0	0	0	0	0.073814	0.066946	0	0	0	0.073314	0.028506	0.057471	0	0	0
0	0	0.049826	0	0	0	0	0	0	0	0	0	0	0	0
0	0.031037	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0.015926	0	0	0	0.012925	0	0
0	0	0	0	0	0	0	0	0.015926	0	0	0	0.038775	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0.038775	0	0
0	0	0	0	0	0	0	0	0.015926	0.36657	0.19954	0.11494	0	0	0
0	0	0	0	0	0	0.066203	0.063412	0.047778	0.5132	0.17104	0.34483	0.02585	0	0
0	0	0.099651	0	0.14763	0.13389	0.43032	0.33819	0.23889	0	0	0.11494	0.038775	0.017473	0
0	0	0	0	0	0	0	0	0	0	0.028506	0.057471	0	0	0
0.039888	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0.063412	0.095557	0	0.028506	0	0.090474	0.05242	0
0	0	0	0	0	0	0	0.021137	0	0	0	0	0.077549	0.017473	0
0	0	0	0	0	0	0	0	0	0	0	0	0.1034	0	0
0	0	0	0	0	0	0.033102	0.021137	0.031852	0	0.028506	0	0.12925	0.15726	0
0	0	0	0	0	0	0	0	0	0	0	0	0.16802	0.40189	0
0	0	0	0	0	0	0	0	0	0	0.028506	0.057471	0.012925	0	0

0.91743	1.5208	1.1958	1.2427	0.57206	0.56904	0.23171	0.19023	0.15926	0	0.057013	0	0.3619	0.50673
0.039888	0.031037	0.14948	0.038835	0	0.050209	0	0	0	0	0	0	0	0
0.71799	0.43451	1.2955	0.54369	0.42443	0.43515	0.066203	0.021137	0.015926	0	0	0	0.12925	0.33199
0.55844	0.24829	0.64773	0.62136	0.36907	0.38494	0	0.084549	0.031852	0	0	0	0.41318	0.63986
0.15955	0.031037	0.049826	0.31068	0.22144	0.20084	0	0.021137	0	0.14663	0.085519	0	0.090474	0.22715
0.27922	0.15518	0.3986	0.27184	0.12918	0.25105	0.033102	0.084549	0.015926	0	0	0	0.17138	0.36694
0.27922	0.43451	0.24913	0.31068	0.27184	0.21757	0	0.084549	0.063704	0	0	0	0.077549	0.19221
0.43877	0.33106	0.14948	0.27184	0.18659	0.18224	0.23171	0.10146	0.056741	0	0	0	0.188	0.29049
0.11966	0.40348	0.1993	0.34951	0.16608	0.22659	0.033102	0.084549	0	0	0	0	0.21972	0.50673
0.71799	1.0759	1.6941	0.46602	0.33216	0.26778	0.23171	0.10569	0.11148	0	0	0	0.0517	0.10484
0.47866	0.21898	0	0.31681	0	0.16736	0	0.042274	0.095557	0	0	0	0.27392	0.35278
0.11966	0	0	0.42718	0.2399	0.31799	0.19861	0.1691	0.33445	0	0	0	0.24557	0.97851
0.43877	0.62073	0.24913	0.19417	0.073814	0.15063	0.033102	0	0	0	0	0	0.064625	0.069893
0.31911	0.24829	0.24913	0.42718	0.20299	0.050209	0.19861	0.1691	0.12741	0	0	0	0.090474	0.50673
0.95732	0.46555	0.1993	0.66019	0.2399	0.25105	0	0.063412	0.11148	0	0	0	0.6204	0.68146
0.23933	0.031037	0.099651	0.23301	0.20299	0.1841	0	0	0	0	0	0	0.32312	0.69893
0.15955	0.062073	0.099651	0.07767	0.092288	0.11715	0	0	0	0	0	0	0.14217	0.20968
0	0	0	0.07767	0.20299	0.16736	0	0.10569	0.063704	0	0	0	0.24414	0.66399
0.43877	0.15518	0.29895	0.27184	0.38753	0.25105	0	0	0	0	0	0	0.18095	0.15726
0.47534	0.21726	0	0.1165	0.18454	0.1841	0.099305	0.12682	0.031852	0	0	0	0.21972	0.72514
0.079777	0	0	0.038835	0.073814	0.066946	0	0	0	0	0	0	0.21972	0.41936
0.39888	0.12415	0.049826	0.19417	0.11072	0.13389	0	0	0	0	0	0	0.18095	0.17473
0.11966	0.062073	0.099651	0.15534	0.14763	0.11715	0	0	0	0	0	0	0.1551	0.29705
0.35899	0.40348	0.1993	0.19417	0.073814	0.13389	0	0.021137	0	0	0	0	0	0.017473
0.11966	0.3414	0.34878	0.038835	0.036907	0.050209	0	0	0	0	0	0	0.11632	0.15726
0.35899	0.49659	0.3986	0.34951	0.2399	0.40167	0	0	0	0	0	0	0.02585	0.12231
0.31911	0.15518	0.24913	0.23301	0.2399	0.1841	0.033102	0	0.015926	0	0	0	0.18095	0.27957
0.19944	0.40348	0.29895	0.31068	0.38753	0.16736	0	0.021137	0	0	0	0	0	0.017473
0.079777	0.12415	0	0.07767	0.036907	0.033473	0	0.042274	0.031852	0	0	0	0.077549	0.12231
0.039888	0.031037	0.14948	0.07767	0.055361	0.066946	0	0	0.047778	0	0	0	0.12925	0.13979
0	0.031037	0.049826	0.038835	0.018454	0.033473	0	0	0	0	0	0	0.14217	0.12231
0.71799	0.43451	0.34878	0.23301	0.20299	0.1841	0	0.063412	0.031852	0	0	0	0.14217	0.90861
0.11966	0.062073	0.24913	0.1165	0.073814	0.066946	0	0.052843	0.031852	0	0	0	0.10986	0.10484
0.15955	0.21726	0.1993	0.23301	0.055361	0.10042	0	0	0	0	0	0	0.012925	0.017473
0.19944	0.074488	0.14948	0	0.076767	0.033473	0	0	0	0	0	0	0.02585	0
0	0	0	0.1165	0.036907	0.033473	0	0	0	0	0	0	0.090474	0.15726
0.11966	0.15518	0.049826	0.038835	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0.02585	0.017473
0.039888	0	0	0.038835	0.018454	0.10042	0.033102	0.063412	0.047778	0	0	0	0.10178	0.29705
0	0	0	0	0	0	0	0	0	0	0	0	0	0.017473
0	0	0	0	0	0.016736	0	0	0	0	0	0	0.012925	0.05242
0.23933	0.09311	0.099651	0	0.036907	0.1841	0	0	0	0	0	0	0	0.017473
0	0	0	0	0.018454	0	0	0	0	0	0	0	0	0
0.6781	0.31037	0.49826	0.62136	0.22144	0.30126	0.066203	0.12682	0.047778	0	0	0	0.43945	0.90861
0	0	0	0	0.018454	0	0	0	0	0	0	0	0	0
0	0	0.049826	0	0	0.016736	0	0	0	0	0	0	0	0
1.2764	1.9553	0.99651	0.38835	0.38753	0.30126	0	0.042274	0.015926	0	0	0	0	0.017473
1.3961	0.90006	0.99651	0.27184	0.38753	0.40167	0	0.021137	0.015926	0	0	0	0.28435	0.71641
1.0371	0.74488	0.84704	0.54369	0.35062	0.53556	0	0	0	0	0	0	0.3102	0.47178
0.40221	0	0.29895	0.50485	0.38753	0.33473	0	0.29592	0.22297	0	0	0	0.4136	1.2319
0	0	0.099651	0.19417	0.14763	0.20084	0.099305	0.084549	0.063704	0	0.028506	0	0.21972	0.85619
0.59832	0.27933	0.34878	0.038835	0.29526	0.26778	0	0	0	0	0	0	0.077549	0.24463
0.87754	0.58797	0.84704	0.6929	0.68278	0.58577	0.19861	0.12682	0.28667	0	0.085519	0	0.34647	1.3596

0	0.09311	0.1993	0.07767	0.092268	0.068946	0.086203	0.042274	0.047778	0	0.028506	0	0	0.0517	0.087367
0.1795	0.37244	0.59791	0	0.086117	0.10042	0.033102	0.042274	0.047778	0	0	0	0	0.0517	0.10484
0	0	0.038835	0.018454	0.016736	0	0	0	0	0	0	0	0	0.012925	0.05242
0.1795	0	0	0.043058	0	0	0	0	0	0	0	0	0	0	0.05242
0.039888	0.12415	0.049826	0.038835	0.055361	0.080335	0	0	0	0	0	0	0	0.090474	0.33199
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.017473
1.049	1.0511	1.3296	2.1035	0.94802	1.1773	3.529	2.811	2.9095	0.27493	0.28171	0.11494	0.85406	1.1145	0
0	0	0	0	0	0.033473	0.033102	0.063412	0.031852	0	0	0	0	0.090474	0
0	0	0	0	0	0	0	0	0.015926	0	0	0	0	0	0
0.15955	0.55866	0.3986	0.69903	0.86732	1.0544	1.1255	1.4585	1.083	0	0	0	0	0.28435	0.48925
0	0	0	0	0	0	0	0.14796	0.047778	0	0	0	0	0.090474	0.12231
0	0	0	0	0	0	0	0.021137	0	0	0	0	0	0.02585	0.017473
0	0.031037	0	0	0.018454	0	0	0.12682	0.063704	0	0	0	0	0.1551	0.11982
0	0	0	0	0	0	0	0.021137	0.063704	0	0	0	0	0.1034	0.22715
0	0	0	0	0	0	0	0.021137	0.031852	0	0	0	0	0	0
0.31911	0.15518	0.049826	0.38835	0.40598	0.25105	0.59583	0.61298	0.79631	0	0.028506	0	0	0.090474	0.12231
0.11966	0.24829	0.049826	0.07767	0.11072	0.11715	0	0.021137	0.031852	0	0	0	0	0.19387	0.29705
0	0	0	0	0	0.016736	0	0	0	0	0	0	0	0.0517	0.22715
0	0	0	0	0	0	0	0	0	0.073314	0.028506	0.057471	0.02585	0.034947	0
0	0	0	0.07767	0.092268	0.033473	0.099305	0.10569	0.063704	0	0.028506	0.057471	0	0	0
0.11966	0.15518	0.14948	0	0.073814	0.050209	0.033102	0.063412	0	0	0	0	0.1034	0.10484	0
0	0	0	0	0	0	0	0	0	0	0	0	0.012925	0.017473	0
3.5102	3.1657	2.292	0.62136	0.77415	0.88604	0.19861	0.084549	0.15926	0	0	0	0.45029	0.92609	0
0.95732	0.9311	1.4948	0.50485	0.36907	0.47903	0	0	0.047778	0	0	0	0.21972	0.2621	0
0	0	0	0	0	0	0	0	0.039815	0	0	0	0	0	0
0.079777	0	0.099651	0.19417	0.22144	0.16736	0.23171	0.46502	0.3026	0	0	0	0.11632	0.087367	0
0	0	0	0	0	0	0.23171	0.084549	0.063704	0	0	0	0	0	0
0.039888	0.27933	0.54808	0.69903	1.2162	0.87029	1.6418	0.3704	2.6707	0	0	0.17241	1.028	0.6414	0
0	0	0	0	0.018454	0.033473	0.19861	0.21137	0.3026	0	0	0	0.038775	0.017473	0
0.15955	0.031037	0.099651	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0.015926	0	0	0	0.012925	0.017473	0
0.15955	0.18622	0.14948	0.038835	0.11072	0.066946	0	0	0	0	0	0	0.02585	0.034947	0

[illegible]

% TOTAL PEPTIDES N=3 SM INS	% TOTAL PEPTIDES N=1 SM SLT	% TOTAL PEPTIDES N=2 SM SLT	% TOTAL PEPTIDES N=3 SM SLT	% TOTAL PEPTIDES N=1 SM TOT	% TOTAL PEPTIDES N=2 SM TOT	% TOTAL PEPTIDES N=3 SM TOT	% TOTAL PEPTIDES N=1 GOLGI AQU	%TOTAL PEPTIDES N=1 GOLGI DET	% TOTAL PEPTIDES N=1 GOLGI TOT	% TOTAL PEPTIDES N=2 GOLGI TOT	% TOTAL PEPTIDES N=3 GOLGI TOT
0	0	0	0	0	0	0	0	0.069396	0	0	0
0	0	0	0	0	0	0.019984	0	0	0.054555	0.027663	0
0	0.46779	0.41308	0.12739	1.1989	0.76583	0.43965	1.1506	0	2.0731	1.6321	1.4147
0	0	0	0	0	0	0	0	0	0	0	0
0	0.035984	0.068847	0	0	0.034037	0.039968	3.6611	0	1.0911	0.56247	1.0105
0.047824	0.14394	0.068847	0	0.39963	0.44248	0.3797	0.31381	0	0.92744	0.8852	1.253
0	0	0	0	0	0	0.019984	0.1046	0	0.10911	0.11065	0.04042
0	0	0	0	0	0	0	0.52301	0	0.16367	0.082988	0.12126
0	0	0	0	0	0.017018	0	0	0	0	0.027663	0
0	0	0	0	0	0.068074	0.039968	0.73222	0	0.27278	0.35961	0.76799
0	0	0	0	0	0.017018	0.039968	0	0	0	0	0
0.047824	0.57575	0.20654	0.38217	0.95297	0.42546	0.4996	0.73222	0.069396	1.4184	0.8852	0
0	0	0	0	0	0	0	0	0	0	0	0.080841
0	0	0	0	0	0	0	0.41841	0	0.16367	0.055325	0.16168
0	0	0	0	0.030741	0.017018	0.019984	0.62762	0	0.16367	0.27663	0.52546
0	0	0	0	0	0.051055	0	0.1046	0	0.38189	0.027663	0.2021
0	0	0	0	0	0	0	0	0	0.054555	0	0
0	0	0	0	0	0.085092	0.079936	0	0	0.32733	0	0.32336
0	0	0	0	0	0	0	0	0	0.16367	0.055325	0.24252
0.047824	0.21591	0.10327	0	0.44692	0.42546	0.55955	0.1046	0.13879	1.4184	0.63624	0
0	0	0	0	0	0	0	0	0	0.054555	0	0
0	0	0.034423	0	0	0	0	0	0.13879	0	0.082988	0
0	0	0	0	0	0	0	0	0.069396	0	0	0
0	0.32386	0.13769	0	0.27667	0.11913	0.17986	0.52301	0.97155	1.6367	0.19364	1.6977
0	0	0	0	0	0	0	0	0	0	0.055325	0
0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0.13879	0	0.16598	0
0	0	0	0	0	0	0	0	0	0.054555	0.16598	0.04042
0.047824	0.035984	0	0	0.061482	0.017018	0.039968	0.1046	0.13879	0.16367	0.082988	0
0.047824	0.035984	0	0	0.092223	0.10211	0.079936	0.62762	0.069396	0.38189	0.27663	0.12126
0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0.017018	0	0	0	0	0	0
0	0	0	0	0	0.017018	0	0	0.13879	0	0.16598	0
0.047824	0	0.068847	0	0.1637	0.068074	0.21982	0	0	0.38189	0.24896	0.080841
0	0	0	0	0.030741	0	0	0	0	0	0.027663	0.12126
0	0	0	0	0	0	0	0	0	0	0	0
0.14347	0	0	0	0	0	0	0	0	0	0	0
0	0	0.10327	0	0	0.017018	0	0	0	0	0	0
0	0.071968	0.034423	0	0.12296	0.034037	0.079936	0.1046	0	0	0.055325	0.04042
0.14347	0.32386	0.27539	0	0.55334	0.34037	0.3797	1.046	0	1.6912	1.1342	2.1019
0	0	0	0	0	0.034037	0	0	0	0	0	0

[illegible]

2.672	0	0.27539	0	0.1537	0.20422	0.21982	0	0	0	0	0.082988	0
0.72205	0	0	0	0	0.017018	0.019984	0	0	0	0	0	0
1.9083	0	0.20654	0	0	0.017018	0.09992	0	0	0	0.054555	0	0
0.047824	0	0	0	0	0.034037	0.079936	0	0	0	0	0.055325	0
0	0	0	0	0	0	0	0	0	0	0	0.027663	0
0	0	0	0	0.030741	0.17018	0.09992	0	0	0	0	0	0
0	0	0	0	0.061482	0.068074	0.039968	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0.47824	0	0.068847	0	0.092223	0	0	0	0	0.13879	0	0	0.36378
0	0	0	0	0	0	0	0	0	0	0	0	0
2.3434	0.071968	0	0	0.061482	0.23826	0.17986	0	0	0.21822	0	0.16598	0.76799
0	0	0	0	0	0	0	0	0	0	0	0.027663	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0.035984	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0.068074	0.09992	0	0	0	0	0	0
0	0	0	0	0.030741	0	0	0	0	0	0	0	0
0	0	0	0	0.030741	0.017018	0.059952	0	0	0	0	0	0
0	0	0	0.12739	0.092223	0.051055	0.09992	0	0	0	0	0.027663	0
0	0	0	0	0.030741	0.068074	0.15987	0	0	0	0	0.027663	0.080841
0.62171	0.71968	0.72289	1.0191	0.27667	0.1872	0.53567	0.20921	0.48577	0	0	0.27663	0.24252
0	0.035984	0.068847	0.25478	0.21519	0.085092	0.079936	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0.23912	0.43181	0.5852	0.89172	0.33815	0.20422	0.21982	0	0.62457	0.43644	0.27663	0.16168	0
0	0	0.034423	0	0.030741	0.10211	0.079936	0	0	0	0	0	0
0.33477	0.10795	0.20654	0	0	0.10211	0.09992	0	0.069396	0.16367	0.16598	0.080841	0
0	0	0	0	0.030741	0	0	0	0	0	0	0	0
0	0	0	0	0	0.051055	0.059952	0	0	0	0.055325	0	0
0.14347	0.44817	0.25818	0.47771	0.5354	0.37645	0.29576	0	0.24674	0.19094	0.11987	0	0
0.43042	0.34349	0.25818	1.4331	0.63275	0.20218	0.44365	0	0.8636	0.19094	0.23974	0.2021	0
0	0.078318	0	0	0	0	0.081338	0	0	0	0	0	0
0.23912	0.50378	0.5852	0.50955	0.092223	0.49353	0.45963	0.41841	0.20819	0.054555	0.055325	0.16168	0
1.5641	0.70134	1.1401	2.7813	0.43037	1.381	1.3314	0	1.5578	0.54555	0.74911	0.56589	0
0	0.098956	0.048143	0.14544	0.11989	0.021506	0.053222	0	0.10675	0	0	0	0
0.5565	0.62244	0.84386	1.7634	0.92188	1.0183	0.91308	0	1.4821	0.57035	0.64556	0.5578	0
0	0	0	0	0	0	0	0	0.086745	0	0	0	0
0.095648	0.32386	0.28208	0.12739	0.30741	0.22124	0.38742	0	0.62457	0.16367	0.14819	0.44462	0
0.33477	0.46779	0.30981	0	0.39963	0.1389	0.3797	0.1046	0.90215	0.27278	0.38728	0.72757	0
0.25319	0.26089	0.21761	0.49363	0	0.35835	0.5628	0	0.60024	0.19342	0.43445	0.080841	0
0.30433	0.72097	0.60074	0.54875	0.034157	0.59541	0.25237	0	0.53833	0.054555	0.374	0.088925	0
0.35868	0.65647	0.42761	1.0328	0.061482	0.37581	0.45504	0	0.25098	0	0.33402	0.32336	0
0.69468	0.64808	0.41261	1.7428	0	0.50196	0.55459	0.1046	0.20125	0	0.2621	0.36378	0
0.13311	0.24493	0.56453	0.4175	0	0.28292	0.15082	0	0.12954	0	0.15076	0	0
0.25825	0.42965	0.24758	0.6286	0	0.20078	0.21844	0	0.25098	0	0	0	0
0.1913	0.53976	0.17212	0.25478	0.21519	0.29224	0.53957	0	0.27759	0.10911	0.11065	0.12126	0

0	0	0	0	0	0.030741	0.017018	0.019984	0	0	0	0	0.054555	0	0	0
0	0	0	0	0	0.030741	0.071477	0.1199	0	0	0	0	0.054555	0	0	0
0	0.099385	0	0	0	0	0	0.024639	0	0	0.10409	0	0	0	0	0
0.079707	0.20562	0.068847	0	0	0	0.27229	0.14534	0	0	0	0	0.062241	0	0	0
0.35071	0.19877	0.17212	1.0191	0.061482	0	0.32335	0.36959	0	0	0.10409	0.054555	0.15906	0	0	0
0	0	0	0	0	0	0.01872	0.097545	0	0	0	0	0	0	0	0
0.8335	0.6717	0.27539	0.61146	0.81079	0	0.41355	0.60377	0	0	0.24289	0.16367	0.30429	0.33347	0	0
0.31427	0.33585	0.27539	0.40764	0.44958	0	0.26549	0.43777	0	0	0.24289	0	0	0.11116	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0.071968	0	0	0	0.11528	0.034037	0.077081	0	0	0	0	0	0	0	0
0	0.071968	0	0	0	0.069167	0.051055	0.12276	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0.017018	0.039968	0	0	0	0	0	0	0	0
0	0.071968	0	0	0.12739	0	0.085092	0.079936	0	0	0.13879	0	0.027663	0.04042	0	0
0	0	0	0	0	0	0.017018	0.039968	0	0	0	0	0	0	0	0
0.047824	0.035984	0	0	0.061482	0	0	0.039968	0	0	0	0	0	0	0	0
0	0	0	0	0.061482	0	0.10211	0.019984	0	0	0	0	0	0	0	0
0.43042	0.96129	0.66506	1.2739	0.68429	0	0.57052	0.80853	0	0	0.83276	0.28218	0.23974	0.28294	0	0
0	0.035984	0	0	0.092223	0	0	0.27978	0	0	0	0	0	0	0	0
0	0.071968	0	0	0.061482	0.017018	0.039968	0.039968	0	0	0	0	0	0	0	0
0.095648	0.21591	0.27539	0.38217	0.52259	0.30633	0	0.51958	0	0	0.13879	0	0.055325	0	0	0
0	0	0	0	0	0	0	0	0	0	0.069396	0	0	0	0	0
0	0	0	0	0	0	0.034037	0	0	0	0	0	0	0	0	0
0.1913	0.50378	0.41308	0.12739	0.39963	0.36873	0.36873	0.33497	0.20921	0.83276	0.21822	0.13278	0.16168	0	0	0
0	0	0	0	0	0	0	0.019984	0	0	0	0	0	0	0	0
0.33477	0.50378	0.34423	0.50955	0.49185	0.57862	0.57862	0.45963	0.31381	0.34698	0.43644	0.41494	0.2021	0	0	0
0	0.25189	0.34423	0	0.36889	0.28931	0.28931	0.29976	0	0.55517	0.27278	0.11065	0.080841	0	0	0
0.23912	1.0795	1.1704	0	0.86074	0.85092	0.85092	0.93255	0	0.83276	0.16367	0.33195	0	0	0	0
0	0.07524	0.074143	0	0.073778	0.19997	0.19997	0.096393	0	0	0	0	0	0	0	0
0.047824	0.10795	0.034423	0.12739	0.030741	0.073746	0.073746	0.10468	0	0.069396	0.054555	0.033195	0	0	0	0
0	0	0	0	0.030741	0	0	0	0	0	0	0	0	0	0	0
0	0.035984	0	0	0.092223	0.051055	0.051055	0.09992	0	0	0	0	0.055325	0	0	0
0.26303	1.0334	0.6721	0	0.96794	0.67377	0.67377	0.74388	0	0	0	0	0.39834	0	0	0
0	0	0	0	0.030741	0.017018	0.017018	0.059952	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0.43824	0.3058	0.38358	0.66879	0.96209	0.42246	0.42246	0.59029	0	0.26525	0	0	0.44842	0.2021	0	0
0	0	0.063929	0	0.06013	0.094454	0.094454	0.26047	0	0	0	0	0.11211	0	0	0
0.10956	0.12232	0.063929	0	0.24052	0.27158	0.27158	0.12849	0	0.17683	0.054555	0.28026	0.067367	0	0	0
0	0	0	0	0	0	0	0.042163	0	0	0	0	0	0	0	0
0	0.17039	0.038112	0	0.13873	0.17648	0.17648	0.12926	0	0.37268	0.054555	0.12147	0	0	0	0

0.052172	0.42597	0.28686	0.31847	0.034682	0.33469	0.38121	0.20921	0.59629	0.27278	0.091099	0
0.14738	0.50845	0.43373	0.18471	0.096375	0.46933	0.19318	0	0.36901	0.21822	0.20986	0.28294
0.14738	0.40883	0.32432	0.43312	0	0.37839	0.57612	0	0.58454	0.18185	0.24816	0.18189
0.061736	0.54116	0.19556	0.43312	0.34918	0.38323	0.42462	0	0.27244	0.090926	0.14297	0.15494
0	0	0	0	0.13873	0.058828	0.18705	0	0	0	0.060733	0
0	0	0	0	0.16316	0.054702	0.17418	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0
0	0.50378	0.41308	0.50955	0.30741	0.22124	0.29976	0	0	0	0	0.080841
0	0	0	0	0.061482	0.15104	0.059952	0	0	0	0	0
0.1913	0.10795	0.10327	0	0.061482	0.27229	0.079936	0.41841	0.13879	0.10911	0.38728	0
0	0	0	0	0.061482	0.051055	0.019984	0	0	0	0	0
0.095648	0	0	0	0	0.051055	0.039968	0	0	0	0	0
0	0	0	0	0	0.017018	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0.082988	0
0	0	0	0	0	0	0	0.1046	0	0.054555	0	0
0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0
0.095648	0.35984	0.13769	0	0.36889	0.18327	0.21233	0	0.20819	0	0	0.12126
0	0	0	0	0	0.034037	0	0	0	0	0	0
0.52606	0.37012	0.42685	0.12739	0.90931	0.53567	0.97005	0.1046	0.27759	0	0.11987	0.04042
0	0	0	0	0	0	0	0	0	0	0	0
0	0	0.034423	0	0	0	0.019984	0	0	0	0.055325	0
0	0	0	0	0	0	0	0	0	0	0	0
0	0.10795	0	0	0.29204	0.14007	0.17524	1.0012	0	0.21822	0.24896	0.32336
0.43042	0.34956	0.38248	0.72793	1.0371	0.95436	0.79784	0.67589	0	0.23806	0.55828	0.47458
0	0	0	0	0	0	0.024425	0	0	0	0	0
0	0	0.064066	0	0.22999	0.33206	0.33159	0.18736	0	0	0.060522	0
0.28694	0.46265	0.56143	1.8117	1.2436	0.64413	0.76167	0.70961	0	0.33654	0.56029	0.4273
0	0.23133	0.093572	0.51764	0.48662	0.44809	0.23181	0.35481	0	0.13462	0.093382	0
0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0.024425	0	0	0	0	0
0.095648	0.25189	0.10327	0.76433	0.36889	0.23826	0.23093	0	0	0	0.11065	0.16168
0	0.035984	0	0	0.061482	0.23826	0.13989	0	0.069396	0.054555	0	0
0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0.24593	0.15317	0.059952	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0.017018	0.019984	0	0	0	0	0
0.1913	0.46779	0.27539	0.25478	0.76852	0.49353	0.47962	0	0.41638	0.16367	0.027663	0
0.047824	0	0	0	0.030741	0.034037	0	0	0	0	0	0.04042
0	0	0	0	0	0.051055	0.019984	0	0	0	0	0
0.38259	0.46779	0.34423	0	0.58408	0.47651	0.43965	0	0.069396	0.16367	0.11065	0
0.047824	0.035984	0	0	0	0.068074	0	0	0	0	0.027663	0
0.047824	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0
0	0.44081	0.57122	0.63694	0.11912	0.24006	0.23695	0	0	0	0	0

0	0.10795	0.24096	0	0.030741	0.085092	0.039968	0.1046	0	0	0.055325	0.04042
0.047824	0	0	0.12739	0	0	0	0	0	0	0.027663	0
0	0	0.034423	0	0	0	0	0	0	0	0	0
0	0	0.034423	0	0.12296	0.085092	0.079936	0	0	0	0.082988	0.080841
0	0.071968	0	0	0.030741	0	0.019984	0	0	0.054555	0.082988	0
0.095648	0.17992	0.24096	0	0.061482	0.11913	0.09992	0.52301	0	0.32733	0.49793	0.12126
0	0	0	0	0	0.051055	0.019984	0	0	0	0	0
0	0	0	0	0.092223	0.017018	0.039968	0	0	0	0	0
0.43042	0.35984	0.41308	0.63694	0.24593	0.39142	0.43965	0	0	0	0.41494	0.04042
0.047824	0	0.10327	0	0	0.017018	0	0	0	0	0.082988	0
0	0	0	0	0	0.034037	0.019984	0	0	0.054555	0	0
0.095648	0	0	0	0.21519	0.15317	0.17986	0.20921	0	0.054555	0.33195	0.04042
0	0	0	0	0.061482	0.10211	0.059952	0	0	0	0	0
0	0.035984	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0.034037	0	0	0	0	0	0
0	0.10795	0.10327	0	0	0.051055	0.019984	0	0	0	0	0
0	0.035984	0	0	0	0.017018	0	0	0	0	0	0
0	0.071968	0	0	0	0	0	0	0	0	0	0
0	0.035984	0	0	0	0	0	0	0	0	0	0
0	0.035984	0.10327	0.12739	0	0.051055	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0
0	0.071968	0	0	0	0	0	0	0	0	0	0
0	0	0.13769	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0.019984	0	0	0	0	0
0	0	0	0	0	0.017018	0	0	0	0	0	0
0	0	0	0	0	0	0.019984	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0.027663	0.04042
0	0	0	0	0	0	0	0	0	0	0	0
0	0.035984	0.068847	0.25478	0	0	0.09992	0	0	0	0	0

0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.48504
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0.061482	0.034037	0.019984	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0.069396	0.10911	0.055325	0.12126	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0.071968	0	0	0	0.030741	0.034037	0.09992	0.09992	0	0	0	0	0.027663	0	0	0
0	0	0	0	0.12739	0.061482	0.017018	0	0	0	0	0	0	0	0	0	0
0	0.21591	0	0	0.38217	0.55334	0.25528	0.19984	0	0	0	0	0.16367	0.027663	0.04042	0	0
0	0	0	0	0	0.030741	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0.030741	0.017018	0	0	0	0	0	0	0	0	0	0
0	0.035984	0	0	0	0.061482	0.085092	0.09992	0	0	0	0	0	0	0.04042	0	0
0	0	0	0	0	0.030741	0.10589	0.09992	0.09992	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0.095648	0.10795	0.17212	0	0	0.21519	0.15317	0.079936	0.20921	0	0.16367	0	0.13831	0	0	0	0
0	0	0	0	0	0.061482	0.051055	0.019984	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0.034037	0	0	0	0	0	0.027663	0	0	0	0
0	0	0	0	0	0	0.017018	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0.047824	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0.019984	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0.14394	0.17212	0	0.092223	0.017018	0	0	0	0	0	0	0	0	0	0	0
0.047824	0	0	0	0	0	0	0	0	0	0	0	0.21822	0.027663	0.04042	0	0
0	0	0	0	0	0.1537	0.068074	0.09992	0	0	0.054555	0	0	0	0	0	0
0	0.53976	0.17212	0	0.18445	0.13615	0.27835	0.1046	0	0.054555	0.055325	0	0	0	0	0	0
0	0	0.34423	0	0	0	0	0	0	0	0.027663	0	0	0	0	0	0
0	0	0	0	0	0	0.051055	0.019984	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0.017018	0.019984	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0.034423	0	0	0	0	0.019984	0	0	0	0	0	0.13831	0	0	0

0.33477	0.53976	0.75731	0.12739	0.30741	0.13615	0.15987	0	0	0	0	0.16598	0.2021
0	0	0	0	0	0.017018	0.039968	0	0	0	0	0	0
0.1913	0.28787	0.51635	0.12739	0.061482	0.10211	0.079936	0	0	0	0	0.082988	0.080841
0.60954	0.28787	0.37866	0	0.092223	0.10211	0.13989	0	0	0	0.054555	0.11065	0.04042
0	0.17992	0.034423	0	0.092223	0.11913	0.19984	0	0.069396	0	0	0	0
0.1913	0.071968	0.28503	0	0.12788	0.10211	0.079936	0	0	0	0	0	0
0.047824	0.071968	0.20654	0	0.092223	0.15317	0.23981	0	0	0	0.055325	0	0
0.38259	0.25189	0	0	0.092223	0.11913	0.079936	0	0	0	0.062241	0	0
0.28694	0.071968	0.13769	0	0.1537	0.11913	0.17986	0	0	0	0	0	0
0.1913	0.32386	0.48193	0.89172	0.24593	0.10211	0.1199	0.1046	0	0.054555	0.082988	0.12126	0
0.28694	0	0	0	0	0.10211	0.039968	0	0	0	0.027663	0	0
1.626	0.10795	0	0	0.12296	0.17018	0.09992	0	0	0	0	0	0.080841
0.14347	0.14394	0.34423	0.12739	0.092223	0.085092	0.079936	0	0	0	0.027663	0.04042	0
0.62171	0.14394	0.17212	0	0.1537	0.34037	0.09992	0	0	0	0	0	0
0.43042	0.43181	0.27539	0	0.18445	0.15317	0.1199	0	0	0.054555	0	0	0
0.1913	0.17992	0	0	0.12296	0.085092	0.039968	0	0	0.054555	0	0	0
0	0.071968	0.08847	0	0.030741	0.085092	0.019984	0	0	0	0.027663	0	0
0.57389	0	0	0	0.030741	0.068074	0.039968	0	0	0	0	0	0
0.047824	0.25189	0	0	0.12296	0.10211	0.13989	0	0	0	0.055325	0	0
0.66954	0.10795	0.13769	0	0.092223	0.085092	0.13989	0	0	0	0.027663	0	0
0.095648	0	0	0	0	0.051055	0	0	0	0	0	0	0
0.095648	0.10795	0	0	0	0	0.019984	0	0	0	0	0	0
0	0.071968	0.06847	0	0.061482	0.068074	0.13989	0	0	0	0	0	0
0	0.10795	0.24096	0	0.061482	0.034037	0.019984	0	0	0	0	0	0
0.047824	0.10795	0.10327	0.38217	0.061482	0.017018	0.039968	0	0	0	0	0	0
0	0.25189	0.34423	0	0.1537	0.1872	0.19984	0	0	0	0	0	0
0.1913	0.10795	0.17212	0	0.061482	0.10211	0.13989	0	0	0	0	0	0
0	0.28787	0.48193	0	0.061482	0.15317	0.17986	0	0	0	0	0	0
0.14347	0	0	0	0	0.034037	0.019984	0	0	0	0	0	0
0.1913	0	0	0	0.030741	0	0.019984	0	0	0	0	0	0
0.14347	0	0	0	0	0	0.039968	0	0	0	0	0	0
1.1	0.10795	0.06847	0.12739	0	0.051055	0.039968	0	0	0	0	0	0
0.52606	0.035984	0	0	0.030741	0	0.059952	0	0	0	0.055325	0	0
0	0.071968	0.06847	0.12739	0	0.051055	0.079936	0	0	0.054555	0.027663	0	0
0	0.071968	0	0.12739	0	0	0	0	0	0	0	0	0
0.33477	0	0	0	0	0.017018	0.039968	0	0	0	0	0	0
0	0.10795	0.034423	0	0.061482	0.017018	0.039968	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0.52172	0.035984	0	0	0.092223	0.017018	0.09992	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0.047824	0	0	0	0	0	0	0	0	0	0	0	0
0	0.17992	0.034423	0.12739	0.030741	0.034037	0.019984	0	0	0.054555	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
1.0521	0.071968	0.17212	0.12739	0.030741	0.085092	0.079936	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0.6837	0.27539	0.38217	0.21519	0.1872	0.1199	0	0	0	0.055325	0	0
0	0.53976	0.26678	0.38217	0.1537	0.22124	0.17986	0	0	0	0	0	0
0.047824	0.32386	0.37866	0	0.21519	0.13615	0.15987	0	0	0	0.027663	0	0
1.0043	0.25189	0.17212	0	0.21519	0.27229	0.23981	0	0	0	0	0	0
0.52606	0.071968	0.06847	0	0.030741	0.10211	0.09992	0	0	0	0.055325	0	0
0	0.25189	0	0	0.061482	0.10211	0.09992	0	0	0	0.082988	0	0
1.1	0.43181	0.37866	0.63694	0.36889	0.20422	0.33973	0.20921	0	0	0.11065	0.080841	0

0.095648	0	0.13769	0.25478	0	0.034037	0.039968	0	0	0	0.054555	0.055325	0
0.35071	0.12594	0.22949	0.25478	0.061482	0	0.13989	0	0	0	0	0	0.04042
0	0.035984	0	0	0	0.034037	0	0	0	0	0	0	0
0.17535	0.12594	0.11474	0	0	0	0	0	0	0	0	0	0
0	0	0.24096	0	0	0.017018	0.019984	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
2.0792	2.3593	1.4257	1.7834	1.6183	1.0761	1.3989	2.9616	0.13879	0.64375	1.2664	0.28294	0
0	0	0	0	0	0.017018	0.019984	0	0	0	0	0	0
0	0	0.034423	0	0	0.017018	0	0	0	0	0	0	0
0.095648	0.53976	0.96386	0.63694	0.73778	0.95303	0.83933	0.83682	0	0.21822	0.33195	0.12126	0
0.047824	0.10795	0.034423	0	0.030741	0.051055	0.039968	0	0	0	0	0	0
0	0	0	0	0	0.017018	0	0	0	0	0	0	0
0.095648	0.21591	0.068847	0	0	0.017018	0.039968	0	0	0	0	0	0
0	0.32386	0.13769	0	0.030741	0.034037	0.039968	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0.054555	0.055325	0	0
0.047824	0.071968	0	0	0.061482	0.051055	0.019984	0	0	0	0	0	0
0	0	0.17212	0	0.092223	0.085092	0.039968	0	0	0	0	0	0
0.047824	0	0.068847	0	0.061482	0.034037	0.019984	0	0	0	0	0.04042	0
0.1913	0.43181	0.24096	0	0.61482	0.35739	0.57954	0.73222	0.27759	0.43644	0.27663	0.56589	0
0.047824	0.035984	0.37866	0	0	0.051055	0.09992	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0.017018	0.09992	0	0	0	0	0	0
0	0.035984	0	0	0.061482	0.017018	0.039968	0.31381	0	0	0.027663	0	0
0.14347	0	0.034423	0	0	0.034037	0.019984	0	0	0	0	0.04042	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0.81301	0.56467	1.1656	1.5287	0.092223	0.1872	0.19984	0	0	0.054555	0	0.080841	0
0.095648	0.61173	0.5852	2.1656	0.092223	0.13615	0.15987	0.1046	0	0	0.027663	0	0
0	0	0	0	0	0	0.019984	0	0	0	0	0	0
0	0.10795	0.13769	0	0.21519	0.23826	0.21982	0.41841	0	0.16367	0.082988	0.04042	0
0	0.035984	0	0	0	0.017018	0	0	0	0	0	0	0
0.62171	1.5079	0.47947	1.2739	1.5638	0.60908	0.95679	1.7782	0	0.65466	0.94053	0.28294	0
0	0.14394	0	0	0.030741	0.034037	0.019984	0.20921	0	0.16367	0.16598	0.60631	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0	0	0	0	0.04042	0
0	0	0.068847	0	0	0.051055	0	0	0	0	0	0	0

Table S2A. Hierarchical clustering of proteins identified in RM, SM, and Golgi total fractions

CMBSEQID List	Assigned Prot Name	Function	Cluster	Mean % Total Peptides		
				RM	SM	Golgi
3724	CYTOCHROME P450 1A2	DETOXIFICATION	1	0.214063	0.067343	0.13683
144430	60S RIBOSOMAL PROTEIN P1	PROT SYN/FOLD	1	0.078961	0.024668	0.036627
78055 146466	UDP-GLUCURONOSYLTRANSFERASE 2B2	DETOXIFICATION	1	0.51822	0.252628	0.237007
31602 84217	UDP-GLUCURONOSYLTRANSFERASE 2B3	DETOXIFICATION	1	0.618277	0.31817	0.203967
28251	GLUTAMINE SYNTHETASE	METABOLISM	1	0.098128	0.043185	0.036168
53068 205347	UDP-GLUCURONOSYLTRANSFERASE 1A6	DETOXIFICATION	1	0.461013	0.212863	0.134061
169811	ALCOHOL DEHYDROGENASE PAN1B-LIKE PROTEIN	METABOLISM	1	0.338833	0.148623	0.10742
8742	DNAJ HOMOLOG SUBFAMILY A MEMBER 1	PROT SYN/FOLD	1	0.041341	0.018007	0.013473
152155	TRANSLOCON-ASSOCIATED PROTEIN, DELTA SUBUNIT	PROT SYN/FOLD	1	0.259803	0.106722	0.082219
51515 74609	40S RIBOSOMAL PROTEIN SA	PROT SYN/FOLD	1	0.35532	0.15598	0.086268
1344	40S RIBOSOMAL PROTEIN S28	PROT SYN/FOLD	1	0.07281	0.021593	0.018185
98434	40S RIBOSOMAL PROTEIN S14	PROT SYN/FOLD	1	0.105492	0.037991	0.027663
4821	60S RIBOSOMAL PROTEIN L38	PROT SYN/FOLD	1	0.073669	0.028254	0.018185
4834	40S RIBOSOMAL PROTEIN S11	PROT SYN/FOLD	1	0.159133	0.055998	0.027406
4817	60S RIBOSOMAL PROTEIN L30	PROT SYN/FOLD	1	0.085753	0.030231	0.018442
4818	60S RIBOSOMAL PROTEIN L31	PROT SYN/FOLD	1	0.129597	0.043664	0.027406
169892	UDP-GLUCURONOSYLTRANSFERASE GTNA2	DETOXIFICATION	2	0.185977	0.130681	0
13404	CYTOCHROME P450 2B2	DETOXIFICATION	2	0.03947	0.027113	0
60848	40S RIBOSOMAL PROTEIN S18	PROT SYN/FOLD	2	0.190677	0.128428	0
237675	ALPHA-2-MACROGLOBULIN RECEPTOR-ASSOCIATED PROTEIN	BIOSYNTHETIC CARGO	2	0.029039	0.018995	0
106720	40S RIBOSOMAL PROTEIN S30	PROT SYN/FOLD	2	0.029681	0.018995	0
98375 226038 241516	60S RIBOSOMAL PROTEIN L21	PROT SYN/FOLD	2	0.14004	0.089815	0
23398	DIHYDROPTERIDINE REDUCTASE	METABOLISM	2	0.152983	0.094497	0
142294	40S RIBOSOMAL PROTEIN S9	PROT SYN/FOLD	2	0.247393	0.150897	0
4825 200139	60S RIBOSOMAL PROTEIN L7A	PROT SYN/FOLD	2	0.409037	0.24243	0
37797	ARGINASE 1	METABOLISM	2	1.5581	0.883637	0.082473
4853	40S RIBOSOMAL PROTEIN S7	PROT SYN/FOLD	2	0.26835	0.161734	0.018442
37240 248463	60S RIBOSOMAL PROTEIN L18	PROT SYN/FOLD	2	0.161713	0.105735	0.009221
31600	UDP-GLUCURONOSYLTRANSFERASE 2B1	DETOXIFICATION	2	0.273783	0.148157	0.058675
80303 127236 221298	UDP-GLUCURONOSYLTRANSFERASE 2B12	DETOXIFICATION	2	0.439947	0.250194	0.121293
193923	RIBOPHORIN 2	PROT MOD	2	1.1576	0.611993	0.128835
250506	40S RIBOSOMAL PROTEIN S17	PROT SYN/FOLD	2	0.066588	0.036892	0.009221
116234	FRUCTOSE-BISPHOSPHATE ALDOLASE B	METABOLISM	2	1.382667	0.832913	0.182674
295796	DNAJ (HSP40) HOMOLOG, SUBFAMILY B, MEMBER 11	PROT SYN/FOLD	2	0.067804	0.039489	0.009221
2378	60S RIBOSOMAL PROTEIN L11	PROT SYN/FOLD	2	0.139538	0.08575	0.022694
238667	SIMILAR TO RIKEN CDNA 2610318K02	UNKNOWN	2	0.078389	0.051934	0.009221
268830	SIMILAR TO HYPOTHEITICAL PROTEIN KIAA0152	UNKNOWN	2	0.164787	0.109831	0.027663
62122	C-1-TETRAHYDROFOLATE SYNTHASE, CYTOPLASMIC	METABOLISM	2	0.344247	0.160446	0.056237
160533	60S RIBOSOMAL PROTEIN L9	PROT SYN/FOLD	2	0.200625	0.087837	0.027663
4835	40S RIBOSOMAL PROTEIN S13	PROT SYN/FOLD	2	0.154268	0.062658	0.027406
166245	TRANSLOCON-ASSOCIATED PROTEIN ALPHA	PROT SYN/FOLD	2	0.17523	0.072905	0.018442
337611	RIBOPHORIN 1	PROT MOD	2	1.28372	0.546343	0.128377
4826	60S RIBOSOMAL PROTEIN L8	PROT SYN/FOLD	2	0.18088	0.07759	0.018442
37218 215516	60S RIBOSOMAL PROTEIN L10A	PROT SYN/FOLD	2	0.328357	0.13102	0.026947
106718	60S RIBOSOMAL PROTEIN L13A	PROT SYN/FOLD	2	0.2067	0.082673	0.018185
4854	40S RIBOSOMAL PROTEIN S8	PROT SYN/FOLD	2	0.213557	0.097096	0.020747
43519	60S RIBOSOMAL PROTEIN L14	PROT SYN/FOLD	2	0.095696	0.045272	0.009221
23405	60S RIBOSOMAL PROTEIN P0	PROT SYN/FOLD	2	0.653817	0.30428	0.06383
51409	GLYCOPROTEIN PROCESSING GLUCOSIDASE I	PROT MOD	2	0.55279	0.233793	0.009221
71440	GLUCOSE-6-PHOSPHATASE	METABOLISM	2	0.064229	0.027155	0

144419	60S RIBOSOMAL PROTEIN L12	PROT SYN/FOLD	2	0.226793	0.095886	0
4843	40S RIBOSOMAL PROTEIN S24	PROT SYN/FOLD	2	0.066659	0.028254	0
37243	40S RIBOSOMAL PROTEIN S21	PROT SYN/FOLD	2	0.121015	0.051824	0
74518	60S RIBOSOMAL PROTEIN L28	PROT SYN/FOLD	2	0.030254	0.013323	0
78166	VITAMIN K-DEPENDENT GAMMA-CARBOXYLASE	PROT MOD	2	0.096774	0.038501	0
302143	SIMILAR TO AAQ88810	UNKNOWN	2	0.030826	0.012334	0
122667	40S RIBOSOMAL PROTEIN S19	PROT SYN/FOLD	2	0.241883	0.105254	0.009221
37239	60S RIBOSOMAL PROTEIN L13	PROT SYN/FOLD	2	0.383713	0.152507	0.018185
139425	60S RIBOSOMAL PROTEIN L17	PROT SYN/FOLD	2	0.303473	0.121653	0.018442
195164	SIMILAR TO HYPOTHETICAL PROTEIN CGI-99	CYTOSKELETON	2	0.15492	0.053911	0
32867	40S RIBOSOMAL PROTEIN S10	PROT SYN/FOLD	2	0.238097	0.084762	0
176270	PUTATIVE N-ACETYLTRANSFERASE CAMELLO 4	PROT MOD	2	0.055501	0.020494	0
4814 301863	60S RIBOSOMAL PROTEIN L27	PROT SYN/FOLD	2	0.04935	0.018007	0
23682	EUKARYOTIC TRANSLATION INITIATION FACTOR 5A	PROT SYN/FOLD	2	0.065515	0.02368	0
154516	60S RIBOSOMAL PROTEIN L7	PROT SYN/FOLD	2	0.476623	0.170403	0.009221
276048	SIMILAR TO PROTEIN DISULFIDE ISOMERASE-RELATED	PROT SYN/FOLD	2	0.275577	0.101782	0.009221
233078 237486	SIMILAR TO 60S RIBOSOMAL PROTEIN L29	PROT SYN/FOLD	2	0.017309	0.005673	0
222133	PROBABLE UPE0334 KINASE-LIKE PROTEIN	UNKNOWN	2	0.017309	0.005673	0
4845 120488	40S RIBOSOMAL PROTEIN S27	PROT SYN/FOLD	2	0.098345	0.056398	0
4844	40S RIBOSOMAL PROTEIN S25	PROT SYN/FOLD	2	0.118366	0.066755	0
278725	40S RIBOSOMAL PROTEIN S5	PROT SYN/FOLD	2	0.24432	0.137064	0
144423	60S RIBOSOMAL PROTEIN L23A	PROT SYN/FOLD	2	0.33036	0.180247	0
62524	CYSTATHIONINE GAMMA-LYASE	METABOLISM	2	0.559943	0.293297	0.018185
269681	SPHINGOSINE-1-PHOSPHATE LYASE 1	PROT MOD	2	0.092549	0.048748	0
42185	60S RIBOSOMAL PROTEIN L6	PROT SYN/FOLD	2	0.35368	0.184933	0
215440	SIMILAR TO HYPOTHETICAL PROTEIN COX4AL	UNKNOWN	2	0.03519	0.018007	0
152512	P34 PROTEIN	PROT SYN/FOLD	2	0.347887	0.169303	0.013473
37237	60S RIBOSOMAL PROTEIN L5	PROT SYN/FOLD	2	0.359047	0.174097	0.018442
4813	60S RIBOSOMAL PROTEIN L26	PROT SYN/FOLD	2	0.288523	0.131504	0
4812	60S RIBOSOMAL PROTEIN L24	PROT SYN/FOLD	2	0.219003	0.101161	0
214842	ACIDIC RIBOSOMAL PROTEIN P1	PROT SYN/FOLD	2	0.024675	0.011346	0
240056	DEAD BOX PROTEIN 1	PROT SYN/FOLD	2	0.101847	0.050325	0
263127	PROTEIN KIAA0103 HOMOLOG	UNKNOWN	2	0.11973	0.058595	0
74523	40S RIBOSOMAL PROTEIN S6	PROT SYN/FOLD	2	0.217357	0.103309	0
111524	BNIP1 PROTEIN	SIGNALING	2	0.01173	0.005673	0
234438	ZINC FINGER PROTEIN 536	UNKNOWN	2	0.01173	0.005673	0
171802	DAPIT PROTEIN	UNKNOWN	2	0.02346	0.011346	0
267421	NUDT16 PROTEIN	UNKNOWN	2	0.02346	0.011346	0
303924	SIMILAR TO 5730439E10RIK PROTEIN	PROT MOD	3	0.43593	0.036414	0
4840	40S RIBOSOMAL PROTEIN S20	PROT SYN/FOLD	3	0.099341	0.010247	0
74102	NASCENT POLYPEPTIDE-ASSOCIATED COMPLEX ALPHA POLYPEP	PROT SYN/FOLD	3	0.109213	0.012334	0
1678	NADP-DEPENDENT LEUKOTRIENE B4 12-HYDROXYDEHYDROGENA	DETOXIFICATION	3	0.041984	0.005673	0
98326	TRANSLOCON-ASSOCIATED PROTEIN GAMMA SUBUNIT	PROT SYN/FOLD	3	0.04935	0.006661	0
75284	PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT ISOFORM	PROT SYN/FOLD	3	0.37099	0.045162	0
194016	CC1-9	UNKNOWN	3	0.088902	0.011346	0
144426	60S RIBOSOMAL PROTEIN L3	PROT SYN/FOLD	3	0.2067	0.030341	0
26167	VIGILIN	PROT SYN/FOLD	3	1.252433	0.187065	0
240031	2610204L23RIK PROTEIN	UNKNOWN	3	0.082751	0.012334	0
4809	60S RIBOSOMAL PROTEIN L19	PROT SYN/FOLD	3	0.14626	0.006661	0
210943 248817	SIMILAR TO GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE	METABOLISM	3	0.011158	0	0
807	C-4 METHYL STEROL OXIDASE	DETOXIFICATION	3	0.011158	0	0
318262	SIMILAR TO MEMBRANE RECEPTOR (5H375)	UNKNOWN	3	0.011158	0	0
295453	SIMILAR TO KIAA1407 PROTEIN	UNKNOWN	3	0.011158	0	0

269276	SIMILAR TO ER-RESIDENT PROTEIN ERD15	PROT SYN/FOLD	3	0.011158	0	0
134570	2'-5'-OLIGOADENYLATE SYNTHETASE 1	SIGNALING	3	0.011158	0	0
33279	TRANSCRIPTION FACTOR BTF3	TRANSCRIPTION	3	0.011158	0	0
3616	S-AFADIN	CYTOSKELETON	3	0.017309	0	0
71226	DEVELOPMENTALLY REGULATED GTP-BINDING PROTEIN 1	GTPASE	3	0.074596	0	0
111533	MULTIFUNCTIONAL PROTEIN ADE2	METABOLISM	3	0.016736	0	0
213158	SIMILAR TO ASPARTLY BETA-HYDROXYLASE	METABOLISM	3	0.053141	0	0
209405	SIMILAR TO SEC63	PROT SYN/FOLD	3	0.0766	0	0
218478	SIMILAR TO SERINE PROTEASE OMI	PROT MOD	3	0.006151	0	0
85740 268188	CALUMENIN	CALCIUM TRANS/BIND	3	0.006151	0	0
202185	SIMILAR TO PHOSPHOACETYLGLUCOSAMINE MUTASE (PAGM) (AC	METABOLISM	3	0.01173	0	0
68739	HEPARIN COFACTOR II	BIO SYNTHETIC CARGO	3	0.01173	0	0
130837	LYSOZYME HOMOLOG AT-2, BINE - RAT (FRAGMENTS)	BIO SYNTHETIC CARGO	3	0.006151	0	0
4819	60S RIBOSOMAL PROTEIN L32	PROT SYN/FOLD	3	0.036747	0	0
75051	VITAMIN-K-DEPENDENT PROTEIN C	BIO SYNTHETIC CARGO	3	0.006151	0	0
23674	FATTY ACID BINDING PROTEIN FABP-1	METABOLISM	3	0.01173	0	0
118984	LYRIC	UNKNOWN	3	0.064801	0	0
166315	CARBONYL REDUCTASE 4	DETOXIFICATION	3	0.006151	0	0
239547	SIMILAR TO ENDOPLASMIC RETICULUM THIOREDOXIN SUPERFAM	PROT SYN/FOLD	3	0.01173	0	0
285775	PALLIDIN	TRAFFIC	3	0.006151	0	0
140831	GTP CYCLOHYDROLASE I FEEDBACK REGULATORY PROTEIN	SIGNALING	3	0.01173	0	0
42770	CENTAUIN-ALPHA2 PROTEIN	GTPASE	3	0.006151	0	0
252580	RAS-GTPASE-ACTIVATING PROTEIN SH3-DOMAIN BINDING PROTEIN	TRAFFIC	3	0.01173	0	0
318741	PHOSPHOFRUCTOKINASE, LIVER, B-TYPE	METABOLISM	3	0.006151	0	0
227484	SHWACHMAN-BODIAN-DIAMOND SYNDROME PROTEIN HOMOLOG	UNKNOWN	3	0.01173	0	0
197285	SELENOPROTEIN I	PROT MOD	3	0.006151	0	0
246387	SIMILAR TO RIKEN CDNA 1700027N10	UNKNOWN	3	0.01173	0	0
307512	SPI2	PROT SYN/FOLD	3	0.006151	0	0
246362	GLUTAREDOXIN	PROT SYN/FOLD	3	0.006151	0	0
171140	G1 TO PHASE TRANSITION 2	SIGNALING	3	0.012358	0	0
4822	60S RIBOSOMAL PROTEIN L39	PROT SYN/FOLD	3	0.006151	0	0
77849	60S RIBOSOMAL PROTEIN L40	PROT SYN/FOLD	3	0.006151	0	0
47246	RNA-DEPENDENT INITIATION FACTOR-2 KINASE	PROT SYN/FOLD	3	0.006151	0	0
205153	FRUCTOSAMINE-3-KINASE-RELATED PROTEIN	SIGNALING	3	0.006151	0	0
211028	RNA-BINDING PROTEIN ISOFORM G3BP-2A	SIGNALING	3	0.006151	0	0
307560	BRAIN ZN-FINGER PROTEIN	TRANSCRIPTION	3	0.006151	0	0
37247	LUPUS LA PROTEIN HOMOLOG	TRANSCRIPTION	3	0.006151	0	0
301836	SIMILAR TO SMILE PROTEIN	UNKNOWN	3	0.006151	0	0
178365	SIMILAR TO HSPC288	UNKNOWN	3	0.006151	0	0
270299	SIMILAR TO RIKEN CDNA 1810045K17	UNKNOWN	3	0.006151	0	0
293100	SIMILAR TO RIKEN CDNA 4932408F18	UNKNOWN	3	0.006151	0	0
218331	SIMILAR TO RS21-C6 PROTEIN	UNKNOWN	3	0.006151	0	0
312697	SIMILAR TO KIA0372 GENE PRODUCT	UNKNOWN	3	0.024716	0	0
201232	ACIDIC RIBOSOMAL PROTEIN P2, CYTOSOLIC	PROT SYN/FOLD	3	0.014353	0	0
98449	0610009E20RIK PROTEIN	UNKNOWN	3	0.017881	0	0
300133	SIMILAR TO RIKEN CDNA 1810014L12	UNKNOWN	3	0.017881	0	0
338318	VIGILIN (HIGH DENSITY LIPOPROTEIN-BINDING PROTEIN) (HDL-BIN	METABOLISM	3	0.017625	0	0
295665	SIMILAR TO FIBRONECTIN TYPE III DOMAIN CONTAINING PROTEIN	UNKNOWN	3	0.077817	0	0
217296	MYOSIN VIIA	CYTOSKELETON	3	0.005579	0	0
264572	MICROTUBULE-ASSOCIATED PROTEIN 4	CYTOSKELETON	3	0.005579	0	0
209490	SIMILAR TO COAGULATION FACTOR XI; PLASMA THROMBOPLASTIN	BIO SYNTHETIC CARGO	3	0.005579	0	0
3688	C4B-BINDING PROTEIN ALPHA CHAIN	BIO SYNTHETIC CARGO	3	0.005579	0	0
227817	CARBOXYL-ESTERASE ESN1	DETOXIFICATION	3	0.007997	0	0

271576	UDP-N-ACETYLGLUCOSAMINE (UDP-GLCNAC) TRANSPORTER	PROT MOD	3	0.030254	0	0
37206	2,3-OXIDOSQUALENE:LANOSTEROL CYCLASE	DETOXIFICATION	3	0.005579	0	0
3926	HEXOKINASE, TYPE I	METABOLISM	3	0.005579	0	0
193296	LYSOPHOSPHATIDIC ACID PHOSPHATASE	METABOLISM	3	0.005579	0	0
268034	SIMILAR TO PROLINE DEHYDROGENASE (OXIDASE) 2	METABOLISM	3	0.005579	0	0
145183	DIACYLGLYCEROL O-ACYLTRANSFERASE 1	PROT MOD	3	0.005579	0	0
60574	PROCOLLAGEN-LYSINE 2-OXOGLUTARATE 5-DIOXYGENASE 1	PROT MOD	3	0.005579	0	0
286288	PROCOLLAGEN-LYSINE 2-OXOGLUTARATE 5-DIOXYGENASE 3	PROT MOD	3	0.005579	0	0
4820	60S RIBOSOMAL PROTEIN L37A	PROT SYN/FOLD	3	0.005579	0	0
111202	60S RIBOSOMAL PROTEIN L44	PROT SYN/FOLD	3	0.005579	0	0
249374	DEAH (ASP-GLU-ALA-HIS) BOX POLYPEPTIDE 29; NUCLEIC ACID HELICASE	PROT SYN/FOLD	3	0.005579	0	0
189964	EUKARYOTIC TRANSLATION INITIATION FACTOR 3, SUBUNIT 12 [MUS MUSCULA]	PROT SYN/FOLD	3	0.005579	0	0
47300	MICROSOMAL STRESS 70 PROTEIN ATPASE CORE	PROT SYN/FOLD	3	0.005579	0	0
223302	SIMILAR TO HISTIDYL-TRNA SYNTHETASE-LIKE	PROT SYN/FOLD	3	0.005579	0	0
315195	INTERFERON-INDUCED 35 KDA PROTEIN	SIGNALING	3	0.005579	0	0
234073	SIMILAR TO INHIBITOR OF GROWTH FAMILY, MEMBER 3	TRANSCRIPTION	3	0.005579	0	0
39290	CG6210-LIKE	UNKNOWN	3	0.005579	0	0
290052	SIMILAR TO HYPOTHETICAL PROTEIN BC002942	UNKNOWN	3	0.005579	0	0
242521	SIMILAR TO HYPOTHETICAL PROTEIN CL25084	UNKNOWN	3	0.005579	0	0
315186	SIMILAR TO SSC2	UNKNOWN	3	0.005579	0	0
260939	TRANSMEMBRANE PROTEIN INDUCED BY TUMOR NECROSIS FACTOR	UNKNOWN	3	0.005579	0	0
300655	HYPOTHETICAL PROTEIN XP_347087	UNKNOWN	3	0.005579	0	0
75738	SH3P13	UNKNOWN	3	0.005579	0	0
206115	SIMILAR TO 25 KDA BRAIN-SPECIFIC PROTEIN (P25-ALPHA)	UNKNOWN	3	0.005579	0	0
269562	SIMILAR TO B AGGRESSIVE LYMPHOMA	UNKNOWN	3	0.005579	0	0
208493	SIMILAR TO CALMODULIN REGULATED SPECTRIN-ASSOCIATED PROTEIN	UNKNOWN	3	0.005579	0	0
359989	SIMILAR TO DJ881L22.2 (NOVEL PROTEIN)	UNKNOWN	3	0.005579	0	0
229721	SIMILAR TO HYPOTHETICAL PROTEIN FLJ30373	UNKNOWN	3	0.005579	0	0
236607	SIMILAR TO RIKEN CDNA 1100001H23	UNKNOWN	3	0.005579	0	0
250916	SIMILAR TO RIKEN CDNA 261020716	UNKNOWN	3	0.005579	0	0
4842	40S RIBOSOMAL PROTEIN S23	PROT SYN/FOLD	3	0.012945	0	0
190455	INOSINE MONOPHOSPHATE DEHYDROGENASE 1	METABOLISM	3	0.012945	0	0
98538	EDF-1 PROTEIN	SIGNALING	3	0.018524	0	0
200861	INSIG2 MEMBRANE PROTEIN (INSULIN INDUCED GENE 2)	PROT SYN/FOLD	3	0.012945	0	0
245798	COPINE IV	TRAFFIC	3	0.012945	0	0
241253	TPA: SENATAXIN; DEAXQ-BOX HELICASE; TRNA SPLICING ENDONUCLEASE	TRANSCRIPTION	3	0.012945	0	0
300976	HYPOTHETICAL PROTEIN LOC303749	UNKNOWN	3	0.012945	0	0
249723	SIMILAR TO RIKEN CDNA 1200014J11	UNKNOWN	3	0.012945	0	0
217607	UNKNOWN ZINC FINGER PROTEIN	UNKNOWN	3	0.012945	0	0
239406	EUKARYOTIC TRANSLATION INITIATION FACTOR 4G1	PROT SYN/FOLD	3	0.041914	0	0
161883	PROBABLE RNA-DEPENDENT HELICASE P68 (DEAD-BOX PROTEIN P68)	PROT SYN/FOLD	3	0.029611	0	0
60405	RNA-BINDING PROTEIN STAUFEN	PROT SYN/FOLD	3	0.012302	0	0
250662	SIMILAR TO NON-CANONICAL UBQUITIN CONJUGATING ENZYME 1	PROTEASOME/UBQUITIN	3	0.012302	0	0
219015	SIMILAR TO KE4	UNKNOWN	3	0.012302	0	0
93202	TSH RECEPTOR SUPPRESSOR ELEMENT-BINDING PROTEIN-1	TRANSCRIPTION	3	0.04921	0	0
206351	SIMILAR TO OLIGOSACCHARYLTRANSFERASE	PROT MOD	4	0.243103	0.018995	0.055327
4836	40S RIBOSOMAL PROTEIN S15	PROT SYN/FOLD	4	0.095696	0.013323	0.018185
60850	40S RIBOSOMAL PROTEIN S3	PROT SYN/FOLD	4	0.7946	0.201143	0.122693
4849	40S RIBOSOMAL PROTEIN S4	PROT SYN/FOLD	4	0.458457	0.111408	0.068542
51618	40S RIBOSOMAL PROTEIN S3A	PROT SYN/FOLD	4	0.467757	0.081176	0.05461
53069	UDP-GLUCURONOSYLTTRANSFERASE 1A7	DETOXIFICATION	4	0.077284	0.014054	0
214259 263869	SIMILAR TO OLIGOSACCHARYL TRANSFERASE 3	PROT MOD	4	0.065375	0.011346	0
85424	60S RIBOSOMAL PROTEIN L4	PROT SYN/FOLD	4	0.381353	0.065256	0

207716	ACYLCOA:CHOLESTEROL ACYLTRANSFERASE 2	PROT MOD	4	0.034045	0.006661	0
308304	P63	TRAFFIC	4	0.029039	0.006673	0
244957	RIBOSOME-BINDING PROTEIN 1 (RIBOSOME RECEPTOR PROTEIN)	PROT SYN/FOLD	4	0.313823	0.061748	0
312741	SIMILAR TO PHENYLALANINE-TRNA SYNTHETASE-LIKE	PROT SYN/FOLD	4	0.085181	0.016908	0
61026	APOEC-1 COMPLEMENTATION FACTOR LONG ISOFORM	PROT SYN/FOLD	4	0.058177	0.012334	0
254493	SIMILAR TO PHENYLALANYL-TRNA SYNTHETASE BETA CHAIN (PHE)	PROT SYN/FOLD	4	0.180733	0.037512	0
308317	COLLAGEN TYPE XIV	BIOSYNTHETIC CARGO	4	0.024605	0.005673	0
263376	SDF2 LIKE PROTEIN 1	PROT MOD	4	0.029039	0.006661	0
273384	GLYCOSYLTRANSFERASE 25 DOMAIN CONTAINING 1	UNKNOWN	4	0.024675	0.005673	0
103	EUKARYOTIC TRANSLATION INITIATION FACTOR 2 SUBUNIT 1	PROT SYN/FOLD	4	0.072167	0.017018	0
213126	SEL1L	TRANSCRIPTION	4	0.028467	0.006661	0
203612	CYTOPLASMIC FMRI INTERACTING PROTEIN 1	UNKNOWN	4	0.025247	0.005673	0
273222	60S RIBOSOMAL PROTEIN L27A	PROT SYN/FOLD	4	0.066659	0.016908	0
289953	EK506-BINDING PROTEIN 3	PROT SYN/FOLD	4	0.041914	0.010247	0
140182 223872	ELONGATION FACTOR 1-ALPHA 1 (EF-1-ALPHA-1)	PROT SYN/FOLD	4	0.760517	0.159754	0.045132
100993 193682 307172	40S RIBOSOMAL PROTEIN S2	PROT SYN/FOLD	4	0.433213	0.138673	0.041136
37238 238486	60S RIBOSOMAL PROTEIN L10	PROT SYN/FOLD	4	0.16139	0.047359	0.009221
123232	GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PRO	SIGNALING	4	0.676883	0.17161	0.041136
12999 13000	CARBOXYLESTERASE 2	DETOXIFICATION	4	0.030995	0.008142	0
316692	SIMILAR TO FK506 BINDING PROTEIN 11	UNKNOWN	4	0.071595	0.018995	0
195586	NICALIN HOMOLOG	SIGNALING	4	0.082751	0.022581	0
282006	MITUGUMIN 23	UNKNOWN	4	0.024103	0.006661	0
51432	ELONGATION FACTOR 2	PROT SYN/FOLD	4	0.450983	0.129414	0.009221
136355	60S RIBOSOMAL PROTEIN L34	PROT SYN/FOLD	4	0.062293	0.018995	0
1145 293440	60S RIBOSOMAL PROTEIN L15	PROT SYN/FOLD	4	0.14934	0.046261	0
47311	TISSUE-TYPE TRANSGLUTAMINASE	SIGNALING	4	0.018454	0.005673	0
128379	IMPLANTATION-ASSOCIATED PROTEIN	UNKNOWN	4	0.022315	0.006661	0
4392	60S RIBOSOMAL PROTEIN L22	PROT SYN/FOLD	4	0.133958	0.038501	0
71631	60S RIBOSOMAL PROTEIN L18A	PROT SYN/FOLD	4	0.059865	0.017018	0
302513	SIMILAR TO KIAA090 PROTEIN	UNKNOWN	4	0.170442	0.048238	0
75074	40S RIBOSOMAL PROTEIN S26	PROT SYN/FOLD	4	0.042556	0.012334	0
294309	TRANSDUCIN (BETA)-LIKE 2	SIGNALING	4	0.105492	0.030741	0
215096	SIMILAR TO PM5 PROTEIN; DNA SEGMENT, CHR 7, ERATO DOI 156.	UNKNOWN	4	0.483633	0.141525	0
45873	CYTOCHROME P450 2C7	DETOXIFICATION	5	0.450223	0.293979	0.172493
299358	STOMATIN-LIKE PROTEIN 2	CYTOSKELETON	5	0.053071	0.037991	0.018442
13029	DAD1 (DEFENDER AGAINST CELL DEATH 1)	PROT MOD	5	0.081034	0.061082	0.027406
63770 72759	CYTOCHROME P450 2B3	DETOXIFICATION	5	0.425287	0.348461	0.09052
103927	CYTOCHROME P450 2D3	DETOXIFICATION	5	0.198013	0.14458	0.050253
31803	UDP-GLUCURONOSYLTRANSFERASE 2B5	DETOXIFICATION	5	0.499773	0.385677	0.129612
72161	40S RIBOSOMAL PROTEIN S15A	PROT SYN/FOLD	5	0.107427	0.082053	0.027406
19913	MEMBRANE ASSOCIATED PROGESTERONE RECEPTOR COMPONENT	DETOXIFICATION	5	0.354717	0.367777	0.170893
78151	ALDEHYDE DEHYDROGENASE FAMILY 3 MEMBER A2	DETOXIFICATION	5	0.36662	0.33448	0.17305
28269	BIP	PROT SYN/FOLD	5	1.409607	1.364433	0.73103
9067	7-DEHYDROCHOLESTEROL REDUCTASE	DETOXIFICATION	5	0.09627	0.086228	0.036168
3732	CYTOCHROME P450 51A1	DETOXIFICATION	5	0.059293	0.055009	0.022694
273868	PROTEIN DISULFIDE ISOMERASE A6	PROT SYN/FOLD	5	0.54299	0.46853	0.221107
4837	40S RIBOSOMAL PROTEIN S16	PROT SYN/FOLD	5	0.084255	0.067743	0.036627
157137	CARBOXYLESTERASE ESNA3	DETOXIFICATION	5	0.279497	0.27936	0.090777
95697	HYDROXYSTEROID 11-BETA DEHYDROGENASE 1	DETOXIFICATION	5	0.88173	0.861563	0.282417
43597	UDP-GLUCURONOSYLTRANSFERASE 1A1	DETOXIFICATION	5	0.63545	0.65828	0.21684
195759	ARMT PROTEIN	UNKNOWN	5	0.098055	0.101669	0.03637
87425	CYTOCHROME P450 3A2	DETOXIFICATION	5	0.265263	0.251474	0.071205
23403	CALRETICULIN	PROT SYN/FOLD	5	0.873583	0.84338	0.22381

217377	PARAOXONASE 2		BIOSYNTHETIC CARGO	5	0.085112	0.095996	0.027663
53066	UDP-GLUCURONOSYLTRANSFERASE 1A5		DETOXIFICATION	5	0.122448	0.138351	0.03737
144431	60S RIBOSOMAL PROTEIN P2		PROT SYN/FOLD	5	0.062179	0.067124	0.013473
263674	DKFZP586A0522 PROTEIN		UNKNOWN	5	0.077242	0.081176	0.018185
63782 84196	CYTOCHROME P450 2C13		DETOXIFICATION	5	0.664673	0.951087	0.591237
63788	CYTOCHROME P450 2D2		DETOXIFICATION	5	0.23039	0.352183	0.208627
33163 63786	CYTOCHROME P450 2C22		DETOXIFICATION	5	0.2869	0.305357	0.25216
63778 231660 253344	CYTOCHROME P450 2C6		DETOXIFICATION	5	0.295843	0.304877	0.236237
126576	CYTOCHROME P450 2D1		DETOXIFICATION	5	0.283553	0.297444	0.219127
28295	MICROSOMAL GLUTATHIONE S-TRANSFERASE 1		DETOXIFICATION	5	0.390477	0.510033	0.35116
69606	PROTEIN DISULFIDE ISOMERASE		PROT SYN/FOLD	5	1.07633	1.262663	0.883253
63780 126560	CYTOCHROME P450 2C11		DETOXIFICATION	5	1.03888	1.04759	0.620183
161564	PROTEIN TRANSPORT PROTEIN SEC61 BETA SUBUNIT		PROT SYN/FOLD	5	0.088331	0.086739	0.054812
269402	ENDOPLASMIN PRECURSOR (ENDOPLASMIC RETICULUM PROTEIN		PROT SYN/FOLD	5	0.928507	1.043223	0.626043
69488 123616	NADH-CYTOCHROME B5 REDUCTASE		DETOXIFICATION	5	0.271643	0.31932	0.154757
63757	CYTOCHROME P450 27A1		DETOXIFICATION	5	0.029039	0.037002	0.018442
77793 105337	CARBOXYLESTERASE 4		DETOXIFICATION	5	0.690213	0.883133	0.441377
42034 84186 112141 14647	CARBOXYLESTERASE 10		DETOXIFICATION	5	0.712753	0.929767	0.42364
85756	LONG-CHAIN-FATTY-ACID--COA LIGASE, LIVER ISOZYME		METABOLISM	5	1.055	1.262133	0.432435
3224	SIGNAL PEPTIDASE COMPLEX (18KD)		PROT SYN/FOLD	5	0.041984	0.046261	0.018185
63760	CYTOCHROME P450 4A2		DETOXIFICATION	5	0.502367	0.60937	0.267143
28283	GLUTATHIONE PEROXIDASE		DETOXIFICATION	5	0.017881	0.022691	0.009221
157237	ENDOPLASMIC RETICULUM PROTEIN ERP29		PROT SYN/FOLD	5	0.194323	0.224423	0.095693
21556	PROTEIN DISULFIDE ISOMERASE A3		PROT SYN/FOLD	5	1.309013	1.554533	0.620413
274611	PROGESTERONE RECEPTOR MEMBRANE COMPONENT 2		DETOXIFICATION	5	0.051247	0.069722	0.02925
17081	EPOXIDE HYDROLASE		DETOXIFICATION	5	0.484483	0.68778	0.268287
68722 236971 311124	HEAT-SHOCK COGNATE 70KD PROTEIN (44KD ATPASE N-TERMINAL		PROT SYN/FOLD	5	0.54159	0.75031	0.287659
28858	SIMILAR TO PUTATIVE NAD(P)H STEROID DEHYDROGENASE		UNKNOWN	5	0.31982	0.515133	0.19261
288307	DP1L1 PROTEIN		UNKNOWN	5	0.031399	0.054239	0.018185
21526	CYTOCHROME P450 2E1		DETOXIFICATION	5	0.224587	0.349	0.113673
161253	MG87 PROTEIN		UNKNOWN	5	0.017309	0.025657	0.009221
290771	24-DEHYDROCHOLESTEROL REDUCTASE		DETOXIFICATION	6	0.03519	0.055998	0
708	ESTRADIOL 17 BETA-DEHYDROGENASE 7		DETOXIFICATION	6	0.024675	0.039489	0
60561	PHOSPHOINOSITIDE PHOSPHATASE SAC1		PROT MOD	6	0.049922	0.080078	0
75741 129969	CYTOCHROME P450 8B1		DETOXIFICATION	6	0.012302	0.018995	0
78079	GLUCOSE-6-PHOSPHATASE, TRANSPORT PROTEIN 1		METABOLISM	6	0.072076	0.110308	0
274486	SIMILAR TO 1-ACYLGLYCEROL-3-PHOSPHATE O-ACYLTRANSFERASE		PROT MOD	6	0.017881	0.027265	0
76956	MONOGLYCERIDE LIPASE		METABOLISM	6	0.019096	0.028254	0
60461	CALM		COAT	6	0.034045	0.049847	0
54899	UBIQUITIN-CONJUGATING ENZYME E2L 3		PROTEASOME/UBIQUITIN	6	0.01173	0.017018	0
28289 51474 146667	GLUTATHIONE S-TRANSFERASE YA-1		DETOXIFICATION	6	0.251663	0.42023	0.013473
126642 164858	GLUTATHIONE S-TRANSFERASE YB-1 SUBUNIT		DETOXIFICATION	6	0.251337	0.41561	0
51456 170936	GLYERALDEHYDE 3-PHOSPHATE DEHYDROGENASE		METABOLISM	6	0.13089	0.215927	0
161569	ALPHA-1,3-MANNOSYLTRANSFERASE ALG2		PROT MOD	6	0.006151	0.010247	0
4847	40S RIBOSOMAL PROTEIN S29		PROT SYN/FOLD	6	0.006151	0.010247	0
104170 318957	PROTEIN KINASE INHIBITOR P58		SIGNALING	6	0.106143	0.182147	0
311586	PROTEIN FAM34A		UNKNOWN	6	0.029039	0.049847	0
201379	CYTOCHROME P450 NA1		DETOXIFICATION	6	0.029039	0.033817	0
126543	ATP CITRATE LYASE		METABOLISM	6	0.024103	0.028254	0
78049	GLUTATHIONE S-TRANSFERASE ALPHA		DETOXIFICATION	6	0.172182	0.19871	0
251640	SIMILAR TO HEXOSE-6-PHOSPHATE DEHYDROGENASE; GDH/6PGL		METABOLISM	6	0.325857	0.376927	0
3774	FERRITIN HEAVY CHAIN		METABOLISM	6	0.030756	0.034915	0
45108	ARGININOSUCCINATE SYNTHASE		METABOLISM	6	0.416773	0.498763	0

204220	MEMBRANE PROGESTIN RECEPTOR ALPHA	DETOXIFICATION	6	0.005579	0.006661	0
281230	MEMBRANE BOUND O-ACYL TRANSFERASE	PROT MOD	6	0.005579	0.006661	0
227176	SIMILAR TO SEVEN TRANSMEMBRANE DOMAIN PROTEIN	UNKNOWN	6	0.005579	0.006661	0
201524	SIMILAR TO PROTEIN TYROSINE PHOSPHATASE-LIKE PROTEIN PTF	SIGNALING	6	0.005579	0.006661	0
38668	TRANSKETOLASE	METABOLISM	6	0.450517	0.535107	0
269355	SIMILAR TO PUTATIVE PROTEIN, WITH AT LEAST 6 TRANSMEMBRANE	UNKNOWN	6	0.066659	0.078978	0
80281	CYTCHROME P450 4F4	DETOXIFICATION	6	0.064229	0.080994	0
5968	ARYLACETAMIDE DEACETYLASE	DETOXIFICATION	6	0.0987	0.126739	0
134595	CYTCHROME P450 4F1	DETOXIFICATION	6	0.058078	0.075466	0
125135	CYTCHROME P450 2J3	DETOXIFICATION	6	0.017309	0.022581	0
70677	CDP-DIACYLGLYCEROL--INOSITOL 3-PHOSPHATIDYL TRANSFERASE	PROT MOD	6	0.017309	0.022581	0
305024	GENE RICH CLUSTER, C3F GENE (PREDICTED)	UNKNOWN	6	0.017309	0.022581	0
188125	TORSINA	PROT SYN/FOLD	6	0.012302	0.01592	0
3729	CYTCHROME P450 2C12	DETOXIFICATION	6	0.047871	0.064873	0
235741	SIMILAR TO BC013491 PROTEIN	UNKNOWN	6	0.01173	0.01592	0
252753	SIMILAR TO MANNOSE-P-DOLICHOL UTILIZATION DEFECT 1	UNKNOWN	6	0.017309	0.02357	0
65711 214593	60S RIBOSOMAL PROTEIN L36	PROT SYN/FOLD	6	0.05257	0.06972	0
120574	ANNEXIN A3	TETHIDOCKFUS	6	0.034045	0.045272	0
275755	SIMILAR TO CHROMOSOME 20 OPEN READING FRAME 116	UNKNOWN	6	0.02346	0.03133	0
43660	SORBITOL DEHYDROGENASE	METABOLISM	6	0.080108	0.109317	0.009221
51518 237201 286597	L-LACTATE DEHYDROGENASE	METABOLISM	6	0.261563	0.36273	0.018442
208161	SIMILAR TO RIKEN CDNA 5730469M10	UNKNOWN	6	0.12588	0.18014	0.009221
35165 105752	RETINOL DEHYDROGENASE TYPE I	DETOXIFICATION	6	0.412453	0.795197	0.13278
129368	15 KDA SELENOPROTEIN	PROT MOD	6	0.029611	0.054899	0.009221
149305	FRUCTOSE-1,6-BISPHOSPHATASE	METABOLISM	6	0.041984	0.08575	0.013473
208522	SIMILAR TO ALPHA GLUCOSIDASE II, BETA SUBUNIT	PROT MOD	6	0.098345	0.19965	0.036627
30001	BILE ACID COA LIGASE	DETOXIFICATION	6	0.48057	0.80501	0.05343
60485	LONG-CHAIN-FATTY-ACID--COA LIGASE 5	METABOLISM	6	0.319963	0.551417	0.064947
308340	ALCOHOL DEHYDROGENASE PAN1B	METABOLISM	6	0.135793	0.250153	0.030177
249650	SPFH DOMAIN FAMILY, MEMBER 2	UNKNOWN	6	0.08064	0.156553	0.013473
3708	CATECHOL O-METHYLTRANSFERASE, MEMBRANE-BOUND FORM	DETOXIFICATION	6	0.109074	0.146544	0.018185
85115	FARNESYL-DIPHOSPHATE FARNESYLTRANSFERASE	PROT MOD	6	0.061652	0.082165	0.013473
44210 78074	NADPH-CYTCHROME P450 REDUCTASE	DETOXIFICATION	6	0.71551	0.883637	0.165207
278444	SIMILAR TO HYPOTHETICAL PROTEIN MGC18837	UNKNOWN	6	0.184383	0.233063	0.03637
395638	GRP170 (HYPOXIA UP-REGULATED 1)	PROT SYN/FOLD	6	0.351497	0.416453	0.063574
337296	SMOOTH MUSCLE-SPECIFIC 17BETA-HYDROXYSTEROID DEHYDRO	DETOXIFICATION	6	0.125238	0.185443	0.036627
246480	FLAVIN-CONTAINING MONOOXYGENASE 3	DETOXIFICATION	6	0.33336	0.50008	0.09144
38101	SRP RECEPTOR BETA	PROT SYN/FOLD	6	0.064872	0.090435	0.018185
10945 123735 158916	CARBOXYLESTERASE B-1	DETOXIFICATION	6	0.241997	0.38884	0.076001
192728	ALPHA GLUCOSIDASE II, ALPHA SUBUNIT	PROT MOD	6	0.215413	0.336153	0.077251
128566	CYTCHROME P450 2A1	DETOXIFICATION	6	0.249967	0.402537	0.103603
288335	BAND 7 PROTEIN (35.3 KD) (4N53)	UNKNOWN	6	0.043955	0.069844	0.018442
244225	SIMILAR TO RIKEN CDNA 0610006F02	UNKNOWN	6	0.178953	0.260837	0.064033
104898	CYTCHROME P450 3A18	DETOXIFICATION	6	0.132573	0.13921	0.020747
11560 84144	ALCOHOL DEHYDROGENASE 1	METABOLISM	6	0.27071	0.286973	0.027406
60584 227664	PROTEIN DISULFIDE ISOMERASE A4	PROT SYN/FOLD	6	0.748083	0.7648	0.091697
3937	3 BETA-HYDROXYSTEROID DEHYDROGENASE TYPE III	DETOXIFICATION	6	0.333073	0.276137	0.026947
217594	UDP-GLUCURONOSYLTRANSFERASE GTNA1	DETOXIFICATION	6	0.145482	0.128203	0.020244
45089	PEPTIDYL-PROLYL CIS-TRANS ISOMERASE A	PROT SYN/FOLD	6	0.148624	0.123741	0.018442
310313	SIMILAR TO ALPHA GLUCOSIDASE II, ALPHA SUBUNIT	PROT MOD	6	0.113503	0.107231	0.018185
78070	CARBOXYLESTERASE 3	DETOXIFICATION	6	0.318887	0.29788	0.020174
69775	CALNEXIN	PROT SYN/FOLD	6	0.548077	0.511317	0.050357
166327 291250	AB2-305	UNKNOWN	6	0.20055	0.182369	0.018442

21524	CYTOCHROME P450 4A3	DETOXIFICATION	6	0.400883	0.38428	0.037053
51420	CYTOCHROME P450 4A1	DETOXIFICATION	6	0.039768	0.038755	0
277663	FERRITIN LIGHT CHAIN	METABOLISM	6	0.1296	0.128935	0
240940	RAB20	GTPASE	6	0.005579	0.005673	0
275946	TRAM1	PROT SYN/FOLD	6	0.005579	0.005673	0
274677	SIMILAR TO UBIQUITIN LIGASE E3 ALPHA-II	PROTEASOME/UBIQUITIN	6	0.005579	0.005673	0
273209	F-BOX ONLY PROTEIN 41	UNKNOWN	6	0.005579	0.005673	0
191580	SIMILAR TO DOLICHOL-PHOSPHATE-MANNOSE SYNTHASE	PROT MOD	6	0.02346	0.02368	0
18021	CDK5 REGULATORY SUBUNIT ASSOCIATED PROTEIN 3	SIGNALING	6	0.017881	0.018007	0
291525	VITAMIN K EPOXIDE REDUCTASE COMPLEX SUBUNIT 1-LIKE PROTEIN	METABOLISM	6	0.01173	0.012334	0
69787	PHOSPHATIDYLETHANOLAMINE N-METHYL TRANSFERASE	PROT MOD	6	0.01173	0.012334	0
132766 395977	MAJOR VAULT PROTEIN	PROT SYN/FOLD	6	0.029039	0.030341	0
221314	SIMILAR TO SULFATASE MODIFYING FACTOR 2	PROT MOD	6	0.006151	0.006661	0
235658	SIMILAR TO KERATINOCYTES ASSOCIATED PROTEIN 2	UNKNOWN	6	0.006151	0.006661	0
280160	BOCA	PROT SYN/FOLD	6	0.011158	0.012334	0
309746	ABHDROLASE DOMAIN CONTAINING 6	UNKNOWN	6	0.011158	0.012334	0
132206 310080	40S RIBOSOMAL PROTEIN S12	PROT SYN/FOLD	6	0.067231	0.049337	0
216144	SIGNAL PEPTIDASE COMPLEX 25 KDA SUBUNIT	PROT SYN/FOLD	6	0.096337	0.075393	0
91768	MEG-2-LIKE PROTEIN	UNKNOWN	6	0.077817	0.061082	0
71715	MOESIN	CYTOSKELETON	6	0.011158	0.009455	0
63790	CYTOCHROME P450 2D5	DETOXIFICATION	6	0.164977	0.13974	0
33170	OXIDOREDUCTASE ERO1-L	PROT SYN/FOLD	6	0.047492	0.0396	0
92415	TIP120	UNKNOWN	6	0.007689	0.006382	0
217843	SIMILAR TO RIKEN CDNA 1810074P20	UNKNOWN	6	0.028467	0.024668	0
4807	60S RIBOSOMAL PROTEIN L23	PROT SYN/FOLD	6	0.041984	0.039489	0
195351	SIMILAR TO RAS SUPPRESSOR PROTEIN 1 (RSU-1) (RSP-1)	GTPASE	6	0.006151	0.005673	0
286300	SIMILAR TO MENINGIOMA EXPRESSED ANTIGEN 6 (COILED-COIL PROTEIN)	UNKNOWN	6	0.006151	0.005673	0
213255	SIMILAR TO EUKARYOTIC TRANSLATION INITIATION FACTOR 3, SUBUNIT 1	PROT SYN/FOLD	6	0.006151	0.005673	0
298591	SIMILAR TO TOLLOID-LIKE 2	SIGNALING	6	0.006151	0.005673	0
161229 206311	POLY(A) BINDING PROTEIN	PROT SYN/FOLD	6	0.018454	0.017018	0
63169	30 KDA PROTEIN	UNKNOWN	6	0.047563	0.044174	0
43740	3-OXO-5-ALPHA-STEROID 4-DEHYDROGENASE 1	DETOXIFICATION	7	0.029611	0.081066	0.009221
339248	DIMETHYLANILINE MONOOXYGENASE [N-OXIDE FORMING] 1	DETOXIFICATION	7	0.21285	0.580557	0.063778
27636	ALL-TRANS-13,14-DIHYDRORETINOL SATURASE	DETOXIFICATION	7	0.103063	0.25483	0.04042
156591	ACTIN-LIKE PROTEIN 2 ACTIN-RELATED PROTEIN 2	CYTOSKELETON	7	0.012302	0.0396	0.009221
161231	CYTOCHROME P450 2T1	DETOXIFICATION	7	0.024675	0.074039	0.018185
238730	RETINOL DEHYDROGENASE 11 (PREDICTED)	DETOXIFICATION	7	0.030254	0.081066	0.018442
274975	SIMILAR TO RIKEN CDNA C330023F11	UNKNOWN	7	0.03526	0.091535	0.018185
80376	RETINOL DEHYDROGENASE TYPE II	DETOXIFICATION	7	0.056084	0.280607	0.033195
3576	REGUCALIN	METABOLISM	7	0.017881	0.095996	0.009221
5972	CARBONIC ANHYDRASE III	METABOLISM	7	0.052499	0.25209	0.063778
60726	PROFILIN I	CYTOSKELETON	7	0.011158	0.053911	0.009221
125172	P97 (TRANSITIONAL ENDOPLASMIC RETICULUM ATPASE)	TE/TH/DOCK/FUS	7	0.107427	0.502687	0.1002
153343	HEAT RESPONSIVE PROTEIN 12	PROT SYN/FOLD	7	0.01173	0.086849	0.018442
75108	STERYL-SULFATASE	DETOXIFICATION	7	0.040769	0.077001	0
140632	3-BETA-HYDROXYSTEROID-DELTA(8),DELTA(7)-ISOMERASE	DETOXIFICATION	7	0.018524	0.035904	0
252129	POLYPOSIS LOCUS PROTEIN 1 HOMOLOG (TB2 PROTEIN HOMOLOG)	UNKNOWN	7	0.017309	0.033599	0
224451	LACTATE DEHYDROGENASE A-LIKE PROTEIN	METABOLISM	7	0.006866	0.012332	0
78138	DIHYDROPYRIMIDINASE	METABOLISM	7	0.005579	0.010247	0
60408	DELTA-5 DESATURASE	PROT MOD	7	0.005579	0.010247	0
262638	SIMILAR TO GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE	METABOLISM	7	0.0216	0.03967	0
187298	FLAVIN-CONTAINING MONOOXYGENASE 5	DETOXIFICATION	7	0.214637	0.4495	0.018442
29993	FATTY-ACID AMIDE HYDROLASE	PROT MOD	7	0.067804	0.15558	0.009221

171823	UDP-GLUCOSE GLYCOPROTEIN:GLUCOSYL TRANSFERASE	PROT MOD	7	0.26606	0.591363	0.027663
209903	COMPLEMENT COMPONENT 5	BIOSYNTHETIC CARGO	7	0.005579	0.011346	0
3722	CYTOCROME P450 17A1	DETOXIFICATION	7	0.034618	0.070929	0
254063	HERC2	TRAFFIC	7	0.006151	0.012334	0
84180	SARCOPLASMIC CA2+MG2+ ATPASE	CALCIUM TRANS/BIND	7	0.252403	0.53813	0
258458	IODOTYROSINE DEHALOGENASE PROTEIN	UNKNOWN	7	0.034618	0.075503	0
296070	TRINUCLEOTIDE REPEAT CONTAINING 5 (PREDICTED)	UNKNOWN	7	0.01173	0.025657	0
32612	JAGUNAL HOMOLOG 1	UNKNOWN	7	0.006151	0.013323	0
258910	SRP RECEPTOR ALPHA SUBUNIT	PROT SYN/FOLD	7	0.005579	0.012334	0
51531	GLUT4 VESICLE PROTEIN	UNKNOWN	7	0.005579	0.012334	0
166454	SIMILAR TO RIKEN CDNA 2010107G23	UNKNOWN	7	0.017309	0.038501	0
68349	ESTRADIOL 17 BETA-DEHYDROGENASE 2	DETOXIFICATION	7	0.050781	0.124001	0
127926	40S RIBOSOMAL PROTEIN S27A	PROT SYN/FOLD	7	0.047492	0.116493	0
605	ADIPOCYTE-DERIVED LEUCINE AMINOPEPTIDASE	PROT MOD	7	0.011158	0.026167	0
249505	LAG1 LONGEVITY ASSURANCE HOMOLOG 2 (TRANSLOCATING CHA	UNKNOWN	7	0.017881	0.042565	0
257012	SIMILAR TO CARCINOMA RELATED GENE	UNKNOWN	7	0.005579	0.013323	0
283602	DELTA(14)-STEROL REDUCTASE (C-14 STEROL REDUCTASE) (STER	DETOXIFICATION	7	0.018454	0.061192	0
82698	HEAT SHOCK PROTEIN 86: HSP86	PROT SYN/FOLD	7	0.010252	0.036066	0
32844	ARP2/3 COMPLEX 20 KDA SUBUNIT	CYTOSKELETON	7	0.006151	0.018007	0
225794	SIMILAR TO GLUTATHIONE S-TRANSFERASE, THETA 3	DETOXIFICATION	7	0.006151	0.018007	0
285736	SIMILAR TO MICROSMAL GLUTATHIONE S-TRANSFERASE 2 (MICR	DETOXIFICATION	7	0.01173	0.035904	0
156654	SIMILAR TO GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE	METABOLISM	7	0.005579	0.017018	0
103229	60S RIBOSOMAL PROTEIN L35	PROT SYN/FOLD	7	0.012945	0.039489	0
250367	CYTOCROME P450 4V3	DETOXIFICATION	7	0.006151	0.018995	0
161408	CCTETA, ETA SUBUNIT OF THE CHAPERONIN CONTAINING TCP-1 (C	PROT SYN/FOLD	7	0.006151	0.018995	0
154010	OPTINEURIN	UNKNOWN	7	0.006151	0.018562	0
102628	OXIDATIVE 17 BETA HYDROXYSTEROID DEHYDROGENASE TYPE 6	DETOXIFICATION	7	0.047358	0.12338	0
64492	RETICULON 3 PROTEIN ISOFORM B	UNKNOWN	7	0.01173	0.032828	0
213193	UNKNOWN PROTEIN (1)	UNKNOWN	7	0.006151	0.016908	0
193119	SIMILAR TO NEUROBLASTOMA-AMPLIFIED PROTEIN	UNKNOWN	7	0.006151	0.016908	0
267475	SIMILAR TO ARL6IP2	UNKNOWN	7	0.04935	0.173763	0.013473
162301	COMPLEMENT C4	BIOSYNTHETIC CARGO	8	0.022888	0.078978	0.031915
85486	ADENOSINE KINASE	METABOLISM	8	0.005579	0.018007	0.009221
161834 247408	RAB5C	GTPASE	8	0.01359	0.084454	0.030309
265779	ARL6IP2	UNKNOWN	8	0.030826	0.17908	0.081299
205076	ARP2/3 COMPLEX 34 KDA SUBUNIT	CYTOSKELETON	8	0.011158	0.02368	0.009221
139656	BAP31 (B-CELL RECEPTOR-ASSOCIATED PROTEIN 31)	TRAFFIC	8	0.046348	0.097574	0.03637
137142	DB83 PROTEIN	UNKNOWN	8	0.05543	0.106243	0.036627
3727	CYTOCROME P450 2A2	DETOXIFICATION	8	0.226087	0.426193	0.210927
318845	R. VAMP A	TEETH/DOCK/FUS	8	0.058078	0.125825	0.063574
60957	SURFEIT LOCUS PROTEIN 4 (ERV29)	TRAFFIC	8	0.094482	0.201181	0.091235
59082	CLATHRIN ADAPTIN-2, BETA 1	COAT	9	0.017309	0.12842	0
19230	3-ALPHA-HYDROXYSTEROID DEHYDROGENASE	DETOXIFICATION	9	0.012302	0.090825	0
39875	FORMIMIDOYLTRANSFERASE-CYCLODEAMINASE	METABOLISM	9	0.005579	0.0396	0
119910	DERLIN-1 (DEGRADATION IN ENDOPLASMIC RETICULUM PROTEIN 1	PROT SYN/FOLD	9	0.006151	0.038979	0
201012	UDP-GLUCURONATE DECARBOXYLASE 1	METABOLISM	9	0.006151	0.061483	0
171146	TETRATRICOPEPTIDE REPEAT PROTEIN 11	UNKNOWN	9	0.005579	0.062181	0
214468	DEHYDROGENASE/REDUCTASE (SDR FAMILY) MEMBER 7	DETOXIFICATION	9	0.035762	0.153017	0
244941	SIMILAR TO BC032271 PROTEIN	UNKNOWN	9	0.005579	0.02368	0
100616	AFLATOXIN B1 ALDEHYDE REDUCTASE MEMBER 1	DETOXIFICATION	9	0.006151	0.030341	0
139643	HEAT SHOCK PROTEIN 90: HSP90	PROT SYN/FOLD	9	0.032238	0.155797	0
171244	ANNEXIN A4	TEETH/DOCK/FUS	9	0.01173	0.063059	0
240184	DEHYDROGENASE/REDUCTASE SDR FAMILY MEMBER 1	UNKNOWN	9	0.017309	0.088937	0

319018	ALPHA-ACTININ 4		CYTOSKELETON	9	0	0.505557	0.064547
37194	GUANINE NUCLEOTIDE-BINDING PROTEIN G(I), ALPHA-2 SUBUNIT (7)		SIGNALING	9	0	0.103331	0.013473
63042	MYOSIN IB		CYTOSKELETON	9	0	0.150931	0.018442
3340	SPECTRIN ALPHA CHAIN, BRAIN		CYTOSKELETON	9	0	0.19258	0.027663
3633	ANNEXIN 5		TETHIDOCK/FUS	9	0	0.063169	0.009221
127131	ANNEXIN A6		TETHIDOCK/FUS	9	0.035762	0.766183	0.049641
197696	SIMILAR TO RAS GTPASE-ACTIVATING-LIKE PROTEIN IQGAP2		GTPASE	9	0.006151	0.291907	0
104192	GLYCOGEN PHOSPHORYLASE		METABOLISM	9	0	0.036414	0
111212	RAC1		GTPASE	9	0	0.015127	0
249893	CCTHETA, THETA SUBUNIT OF THE CHAPERONIN CONTAINING TCP-1		PROT SYN/FOLD	9	0	0.034915	0
37175	ALPHA-ACTININ 1		CYTOSKELETON	9	0	0.01199	0
71492	ISOCITRATE DEHYDROGENASE [NADP] CYTOPLASMIC		METABOLISM	9	0	0.029242	0
51489	4-HYDROXYPHENYLPIRUVATE DIOXYGENASE		METABOLISM	9	0	0.030741	0
288751	CCT (CHAPERONIN CONTAINING TCP-1) ZETA SUBUNIT		PROT SYN/FOLD	9	0	0.040588	0
43659	FATTY ACID SYNTHASE		PROT MOD	9	0	0.07885	0
244145	EH-DOMAIN CONTAINING PROTEIN 3		UNKNOWN	9	0	0.029353	0
268103	SHORT CHAIN DEHYDROGENASE REDUCTASE 9		DETOXIFICATION	9	0	0.016908	0
71624	H-RAS-1/P21		GTPASE	9	0	0.050835	0
120856	ADP-RIBOSYLATION FACTOR 6		GTPASE	9	0	0.041577	0
243111	ATP-BINDING CASSETTE TRANSPORTER ABCG3 (1)		UNKNOWN	9	0	0.037402	0
197702	SIMILAR TO ALDH8A1 PROTEIN		DETOXIFICATION	9	0	0.072428	0
169833	CHAPERONIN CONTAINING TCP1, SUBUNIT 3 (GAMMA)		PROT SYN/FOLD	9	0	0.072428	0
219335	CLATHRIN ADAPTIN-2, ALPHA 1		COAT	9	0	0.007772	0
3158	SPECTRIN BETA CHAIN, BRAIN 2		CYTOSKELETON	9	0	0.012334	0
42949	PUTATIVE TRANSCRIPTION FACTOR LUZP		UNKNOWN	9	0	0.012334	0
145232	EZRIN		CYTOSKELETON	9	0	0.018909	0
28291 40315 185727	GLUTATHIONE S-TRANSFERASE YB-2 SUBUNIT		DETOXIFICATION	9	0	0.353643	0
37177	ADAPTOR-RELATED PROTEIN COMPLEX 2 ALPHA 2 SUBUNIT		COAT	9	0	0.067221	0
126513	CLATHRIN ADAPTIN-1, BETA 1		COAT	9	0	0.120103	0
3731 63758	CYTOCHROME P450 3A1		DETOXIFICATION	9	0	0.008213	0
73521	ADAPTOR-RELATED PROTEIN COMPLEX 2, MU 1 SUBUNIT		COAT	9	0	0.012334	0
23758	3-OXO-5-BETA-STEROID 4-DEHYDROGENASE		DETOXIFICATION	9	0	0.044174	0
148966	GLIA MATURATION FACTOR BETA		CYTOSKELETON	9	0	0.012334	0
19169	GLYCINE N-METHYLTRANSFERASE		PROT MOD	9	0	0.044174	0
268838	SIMILAR TO VINCULIN (METAVINCULIN)		CYTOSKELETON	9	0	0.012334	0
292700	CHAPERONIN CONTAINING TCP-1 BETA SUBUNIT		PROT SYN/FOLD	9	0	0.044174	0
304061	SIMILAR TO DOLICHYL-PHOSPHATE BETA-GLUCOSYLTRANSFERASE		PROT MOD	9	0	0.012334	0
231118	SIMILAR TO HYPOTHETICAL PROTEIN D4ERTD89E		UNKNOWN	9	0	0.012334	0
65700	CLATHRIN COAT ASSEMBLY PROTEIN AP17		COAT	9	0	0.012334	0
209477	SIMILAR TO PURINE-NUCLEOSIDE PHOSPHORYLASE; PURINE-NUC		METABOLISM	9	0	0.021593	0
3622	DELTA-AMINOLEVULINIC ACID DEHYDRATASE		DETOXIFICATION	9	0	0.012334	0
75118	T-COMPLEX PROTEIN 1, ALPHA SUBUNIT		PROT SYN/FOLD	9	0	0.021593	0
139514	ADP-RIBOSYLATION FACTOR-LIKE 6 INTERACTING PROTEIN 1		UNKNOWN	9	0	0.012334	0
205068	SIMILAR TO ANCIENT UBIQUITOUS 46 KDA PROTEIN AUP46 PRECUR		UNKNOWN	9	0	0.012334	0
243991	SIMILAR TO DISULFIDE ISOMERASE		UNKNOWN	9	0	0.012334	0
262247	ETEA: EXPRESSED IN T-CELLS AND EOSINOPHILS IN ATOPIC DERM		UNKNOWN	9	0	0.012334	0
271294	ABHYDROLASE DOMAIN CONTAINING PROTEIN 2		UNKNOWN	9	0	0.012334	0
130827	ADENLYL CYCLASE-ASSOCIATED PROTEIN 1		SIGNALING	9	0	0.012334	0
182047	CARBOXYLESTERASE ESNA2		DETOXIFICATION	9	0	0.008142	0
3624	FRUCTOSE-BISPHOSPHATE ALDOLASE A		METABOLISM	9	0	0.034322	0
109734	ANNEXIN A2		TETHIDOCK/FUS	9	0	0.093355	0
161236	INTEGRAL MEMBRANE TRANSPORT PROTEIN UST5R		UNKNOWN	9	0	0.056985	0
236762	SIMILAR TO B-IND1		SIGNALING	9	0	0.013323	0

3631	ANNEXIN A1 (ANNEXIN I) (LIPOCORTIN I) (CALPACTIN II) (CHROMOB)	TETH/DOCK/FUS	9	0	0.031954	0
246703	UBX DOMAIN CONTAINING 2 (PREDICTED)	UNKNOWN	9	0	0.013323	0
317748	LANOSTEROL SYNTHASE	METABOLISM	9	0	0.02368	0
173653	F-ACTIN BINDING PROTEIN B-NEXLIN	CYTOSKELETON	9	0	0.013323	0
136274	T-PLASTIN	CYTOSKELETON	9	0	0.10028	0
144363	PHOSPHOENOLPYRUVATE CARBOXYKINASE, CYTOSOLIC (GTP)	METABOLISM	9	0	0.037512	0
75106 109266	ESTROGEN SULFOTRANSFERASE	DETOXIFICATION	9	0	0.02368	0
51607	IRON-RESPONSIVE ELEMENT BINDING PROTEIN 1 (IRE-BP 1) (IRON)	PROT SYN/FOLD	9	0	0.013323	0
277830	SIMILAR TO RIKEN CDNA 061008C08	UNKNOWN	9	0	0.013323	0
284155	AA2-020	UNKNOWN	9	0	0.013323	0
285691	SIMILAR TO HYPOTHETICAL PROTEIN FLJ10579	UNKNOWN	9	0	0.02368	0
74438	COFILIN, MUSCLE ISOFORM	CYTOSKELETON	9	0	0.017083	0
230030	TALIN	CYTOSKELETON	9	0	0.056508	0
260591	B-IND1	SIGNALING	9	0	0.02357	0
227628	THIOREDOXIN-RELATED TRANSMEMBRANE PROTEIN 2	UNKNOWN	9	0	0.010247	0
51411	CYSTEINE-RICH PROTEIN 1	UNKNOWN	9	0	0.024668	0
37231	RAS-RELATED PROTEIN RAL-A	GTPASE	9	0	0.006661	0
26394	GLIAL FIBRILLARY ACIDIC PROTEIN ALPHA	CYTOSKELETON	9	0	0.020494	0
33791	GLUTATHIONE S-TRANSFERASE YB-3	DETOXIFICATION	9	0	0.011946	0
313574	UNKNOWN (PROTEIN FOR MGC:72610)	UNKNOWN	9	0	0.010247	0
43492	RAB8B	GTPASE	9	0	0.021925	0
60472	LONG-CHAIN FATTY ACID TRANSPORT PROTEIN	BIOSYNTHETIC CARGO	9	0	0.010247	0
308794	SIMILAR TO FYVE AND COILED-COIL DOMAIN CONTAINING 1	SIGNALING	9	0	0.007137	0
165266	VITAMIN K EPOXIDE REDUCTASE COMPLEX, SUBUNIT 1	METABOLISM	9	0	0.010247	0
223736	DIHYDROXYACETONE KINASE FAMILY PROTEIN	METABOLISM	9	0	0.010247	0
213091	SIMILAR TO ALPHA TUBULIN	CYTOSKELETON	9	0	0.010247	0
20922	ADP-RIBOSYLATION FACTOR 3	GTPASE	9	0	0.011346	0
230796	F-ACTIN CAPPING PROTEIN ALPHA-1 SUBUNIT	CYTOSKELETON	9	0	0.010247	0
68743	HEME OXYGENASE 2	DETOXIFICATION	9	0	0.011346	0
318242	SIMILAR TO CDNA SEQUENCE BC017158	UNKNOWN	9	0	0.026167	0
86059	3 BETA-HYDROXY-DELTA 5-C27-STEROID OXIDOREDUCTASE	DETOXIFICATION	9	0	0.010247	0
221624	SIMILAR TO FK506-BINDING PROTEIN 38	SIGNALING	9	0	0.011346	0
337678	CYTOCHROME P450 20A1	DETOXIFICATION	9	0	0.010247	0
158790	LIN-7 PROTEIN	SIGNALING	9	0	0.011346	0
227390	RETINOL DEHYDROGENASE 10	DETOXIFICATION	9	0	0.010247	0
104145	PERIPHERAL PLASMA MEMBRANE PROTEIN CASK	SIGNALING	9	0	0.011346	0
161241	DIACETYL-L-XYLULOSE REDUCTASE	METABOLISM	9	0	0.010247	0
37252	Oa, SYNTAXIN 4	TETH/DOCK/FUS	9	0	0.011346	0
294993	SIMILAR TO RETINAL SHORT-CHAIN DEHYDROGENASE/REDUCTAS	DETOXIFICATION	9	0	0.010247	0
255631	SIMILAR TO PROTEIN CGI-51	UNKNOWN	9	0	0.011346	0
3782	GLUCOKINASE REGULATORY PROTEIN	METABOLISM	9	0	0.010247	0
227312	COILED-COIL-HELIX-COILED-COIL-HELIX DOMAIN CONTAINING 3	UNKNOWN	9	0	0.010247	0
161235	INTEGRAL MEMBRANE TRANSPORT PROTEIN UST4R	UNKNOWN	9	0	0.010247	0
87332	COFILIN, NON-MUSCLE ISOFORM	CYTOSKELETON	9	0	0.031265	0
6153	MYOSIN I HEAVY CHAIN	CYTOSKELETON	9	0	0.011346	0
190049	SIMILAR TO HYPOTHETICAL PROTEIN KIAA0379	UNKNOWN	9	0	0.010247	0
205775	ANNEXIN A11	TETH/DOCK/FUS	9	0	0.010247	0
283891	SIMILAR TO 3,5-CYCLIC-GMP PHOSPHODIESTERASE; ROD PHOSPH	SIGNALING	9	0	0.010247	0
203844	HYPOTHETICAL PROTEIN XP_343478	UNKNOWN	9	0	0.010247	0
46143	CYSTEINE-RICH PROTEIN 2	UNKNOWN	9	0	0.010247	0
139384	2400001E08RIK PROTEIN	UNKNOWN	9	0	0.010247	0
168211	CAMP-DEPENDENT PROTEIN KINASE C ALPHA	SIGNALING	9	0	0.010247	0
251068	GOA	SIGNALING	9	0	0.010247	0

75904	UDP-GLUCOSE 6-DEHYDROGENASE	METABOLISM	9	0	0.010247	0
12328	BENDLESS PROTEIN	PROTEASOMES/UBIQUITIN	9	0	0.010247	0
113828	RHO B	GTPASE	9	0	0.006661	0
140635	SEPTIN 2	GTPASE	9	0	0.006661	0
45085	ARGININOSUCCINATE LYASE	METABOLISM	9	0	0.006661	0
16980	HYPOXANTHINE-GUANINE PHOSPHORIBOSYLTRANSFERASE	METABOLISM	9	0	0.006661	0
11249	NEURONAL MYOSIN HEAVY CHAIN	CYTOSKELETON	9	0	0.012583	0
57726	VESICLE-ASSOCIATED MEMBRANE PROTEIN-ASSOCIATED PROTEIN	TRAFFIC	9	0	0.029278	0
287183	LIVER REGENERATION-RELATED PROTEIN	DETOXIFICATION	9	0	0.006382	0
212247	SIMILAR TO SERINE/THREONINE KINASE	SIGNALING	9	0	0.006661	0
231012	FILAMIN B, BETA	CYTOSKELETON	9	0	0.036414	0
225159	SIMILAR TO URIDINE DIPHOSPHOGLUCOSE PYROPHOSPHORYLASE 2	METABOLISM	9	0	0.058595	0
266321	SIMILAR TO RIKEN CDNA 4931406C07	UNKNOWN	9	0	0.006661	0
282876	ENDOPLASMIC OXIDOREDUCTASE 1 BETA	PROT SYN/FOLD	9	0	0.006661	0
118982	CYTOSOLIC MALATE DEHYDROGENASE	METABOLISM	9	0	0.081066	0
19687	LIM AND SH3 DOMAIN PROTEIN 1	CYTOSKELETON	9	0	0.006661	0
69784	ARYL SULFOTRANSFERASE	DETOXIFICATION	9	0	0.011346	0
253829	SIMILAR TO PROTEIN CGI-117 (PROTEIN HSPC111)	UNKNOWN	9	0	0.006661	0
84221	GLUTATHIONE TRANSFERASE (EC 2.5.1.18) PSI	DETOXIFICATION	9	0	0.006661	0
274007	SIMILAR TO PROBABLE POLYPROTEIN-RELATED PROTEIN 4	UNKNOWN	9	0	0.022581	0
55147	GLUTATHIONE TRANSFERASE OMEGA 1	DETOXIFICATION	9	0	0.006661	0
151517	CCG1-INTERACTING FACTOR B	UNKNOWN	9	0	0.011346	0
198073	LIVER NTE-RELATED PROTEIN	UNKNOWN	9	0	0.006661	0
40336	PDZ AND LIM DOMAIN PROTEIN 1	UNKNOWN	9	0	0.022581	0
211833	SIMILAR TO MITOGEN INDUCIBLE GENE MIG-2	UNKNOWN	9	0	0.006661	0
37566	R, VAMP8	TE/TH/DOCK/FUS	9	0	0.006661	0
271324	SECRETED FRIZZLED-RELATED PROTEIN 1	SIGNALING	9	0	0.006661	0
223472	SIMILAR TO A-KINASE ANCHOR PROTEIN 9 ISOFORM 2; YOTIAO; A-1	SIGNALING	9	0	0.006661	0
283888	THIOREDOXIN DOMAIN CONTAINING PROTEIN 1	UNKNOWN	9	0	0.006661	0
310564	SIMILAR TO 9530008L14RIK PROTEIN	UNKNOWN	9	0	0.006661	0
12071	SERINE/THREONINE-PROTEIN KINASE PLK	SIGNALING	9	0	0.006661	0
36803	ALPHA ISOFORM OF REGULATORY SUBUNIT A, PROTEIN PHOSPHATASE 1	SIGNALING	9	0	0.006661	0
235129	SEC14-LIKE PROTEIN 3	UNKNOWN	9	0	0.006661	0
67879	NCK-ASSOCIATED PROTEIN 1	UNKNOWN	9	0	0.006661	0
262403	UNKNOWN (PROTEIN FOR MGC:72987)	UNKNOWN	9	0	0.006661	0
302504	SIMILAR TO HYPOTHETICAL PROTEIN FLJ10375	UNKNOWN	9	0	0.006661	0
2280	EH-DOMAIN-CONTAINING PROTEIN 1 (MPAST1)	UNKNOWN	9	0	0.006661	0
277277	COILED-COIL-HELIX-COILED-COIL-HELIX DOMAIN CONTAINING 6 (P)	UNKNOWN	9	0	0.006661	0
62196	10-FORMYL TETRAHYDROFOLATE DEHYDROGENASE	METABOLISM	9	0	0.068252	0
313683 338764	ALPHA ENOLASE	METABOLISM	9	0	0.051824	0
51568	PHOSPHOGLUCOMUTASE	METABOLISM	9	0	0.028364	0
55585	CALMODULIN	PROT SYN/FOLD	9	0	0.005673	0
293536	ENDOPLASMIC RETICULUM PROTEIN ERP46	PROT SYN/FOLD	9	0	0.005673	0
265519	AFG3 ATPASE FAMILY GENE 3-LIKE 2	PROT MOD	9	0	0.005673	0
104206	NG-NG-DIMETHYLARGININE DIMETHYLAMINOHYDROLASE 1	METABOLISM	9	0	0.005673	0
116574	NICASTRIN	PROT MOD	9	0	0.005673	0
31392	SEPIAPTERIN REDUCTASE	METABOLISM	9	0	0.005673	0
272510	SIMILAR TO BILVERDIN REDUCTASE B (FLAVIN REDUCTASE (NADPH))	DETOXIFICATION	9	0	0.005673	0
4320	ACYL-COA-BINDING PROTEIN	METABOLISM	9	0	0.005673	0
54409	ADENOSYLHOMOCYSTEINASE	METABOLISM	9	0	0.005673	0
78152	N-HYDROXYARYLAMINE SULFOTRANSFERASE	PROT MOD	9	0	0.005673	0
53424	DIHYDROFOLATE REDUCTASE	METABOLISM	9	0	0.005673	0
221017	SIMILAR TO PHOSPHOLYSINE PHOSPHOHISTIDINE INORGANIC PYR	METABOLISM	9	0	0.005673	0

280249	SIMILAR TO RIKEN CDNA 1810063B07 GENE	UNKNOWN	9	0	0.005673	0
29682	LIN-7 HOMOLOG C	SIGNALING	9	0	0.005673	0
283779	SIMILAR TO DISHEVELLED-ASSOCIATED ACTIVATOR OF MORPHOGENESIS	UNKNOWN	9	0	0.005673	0
276601	INORGANIC DIPHOSPHATASE	SIGNALING	9	0	0.005673	0
274130	COPINE III	TRAFFIC	9	0	0.005673	0
273429	HYPOTHETICAL PROTEIN XP_346991	UNKNOWN	9	0	0.005673	0
290958	SIMILAR TO TYROSINE-PROTEIN KINASE JAK1 (JANUS KINASE 1) (JAK1)	SIGNALING	9	0	0.005673	0
4597	SERINE/THREONINE PROTEIN PHOSPHATASE PP1-BETA CATALYTIC SUBUNIT	SIGNALING	9	0	0.005673	0
29711	14-3-3 PROTEIN TAU	SIGNALING	9	0	0.005673	0
221370	SIMILAR TO CG32774-PA	UNKNOWN	9	0	0.005673	0
8623	RAB GDI BETA	TRAFFIC	9	0	0.005673	0
276570	EVOLUTIONARILY CONSERVED SIGNALING INTERMEDIATE IN TOLL-LIKE RECEPTOR SIGNALING	SIGNALING	9	0	0.005673	0
232734	SIMILAR TO BCST1-LIKE	UNKNOWN	9	0	0.005673	0
111519	SELENIUM-BINDING PROTEIN	UNKNOWN	9	0	0.005673	0
293599	DNA-BINDING PROTEIN PROLACTIN REGULATORY ELEMENT BINDING PROTEIN	TRANSCRIPTION	9	0	0.005673	0
198937	SH3-BINDING DOMAIN GLUTAMIC ACID-RICH PROTEIN LIKE	UNKNOWN	9	0	0.005673	0
296511	SIMILAR TO BA261P9.2 (PUTATIVE NOVEL PROTEIN SIMILAR TO FLY GUANINE NUCLEOTIDE-BINDING PROTEIN G-S ALPHA)	UNKNOWN	9	0	0.005673	0
72067	GUANINE NUCLEOTIDE-BINDING PROTEIN G-S ALPHA	SIGNALING	9	0	0.04135	0
104196	4-TRIMETHYLAMINO BUTYRALDEHYDE DEHYDROGENASE	METABOLISM	9	0	0.01592	0
12218	THIOREDOXIN	PROT SYN/FOLD	9	0	0.01592	0
644	EZRIN-RADIXIN-MOESIN BINDING PHOSPHOPROTEIN 50	CYTOSKELETON	9	0	0.01592	0
22152	LONG-CHAIN-FATTY-ACID--COA LIGASE 4	METABOLISM	9	0	0.01592	0
80790	GLYCEROL-3-PHOSPHATE DEHYDROGENASE [NAD+], CYTOPLASMIC	METABOLISM	9	0	0.01592	0
3914	GLUTATHIONE S-TRANSFERASE YRS-YRS (GST 12-12) (GLUTATHIONE S-TRANSFERASE YRS-YRS)	DETOXICATION	9	0	0.033927	0
271907	SLINGSHOT 1L	SIGNALING	9	0	0.017018	0
300461	SIMILAR TO GROWTH-ARREST-SPECIFIC PROTEIN 2 (GAS-2)	SIGNALING	9	0	0.047359	0
266044	TRANSGLUTININ 2 (PREDICTED)	UNKNOWN	9	0	0.017018	0
157267	SYNTAXIN BINDING PROTEIN MUNC18-3	TETH/DCK/FUS	9	0	0.017018	0
228294	SIMILAR TO HYPOTHETICAL PROTEIN MGC26706	UNKNOWN	9	0	0.017018	0
18910	SH3P7R2	UNKNOWN	9	0	0.017018	0
78142 80899	PDZ DOMAIN-CONTAINING PROTEIN (DIPHOR 1)	UNKNOWN	9	0	0.057496	0
78213	FARNESYL PYROPHOSPHATE SYNTHETASE	PROT MOD	9	0	0.01592	0
124359	MERLIN	UNKNOWN	9	0	0.01592	0
300121	SPECTRIN BETA-II CHAIN, BRAIN 1 (SPECTRIN, NON-ERYTHROID BETA-2)	CYTOSKELETON	10	0	0.038979	0.018185
86161	R-RAS2	GTPASE	10	0	0.018007	0.009221
69379 88823 240507	MYOSIN REGULATORY LIGHT CHAIN	CYTOSKELETON	10	0	0.030341	0.009221
29986	D-DOPACHROME TAUTOMERASE	METABOLISM	10	0	0.055409	0.018442
166356	CHAPERONIN DELTA SUBUNIT	PROT SYN/FOLD	10	0	0.038501	0.013473
35616	14-3-3 PROTEIN EPSILON	SIGNALING	10	0	0.058396	0.013473
248510	SIMILAR TO PLEXIN	SIGNALING	10	0	0.0396	0.009221
29712	14-3-3 PROTEIN ZETA/DELTA	SIGNALING	10	0	0.078	0.018185
75000	MYOSIN HEAVY CHAIN, NONMUSCLE TYPE A	CYTOSKELETON	11	0.033473	0.181067	0.146767
74919	DOPA/TYROSINE SULFOTRANSFERASE	DETOXICATION	11	0	0.021593	0.013473
83668	CAPPING PROTEIN (ACTIN FILAMENT) MUSCLE Z-LINE, BETA	CYTOSKELETON	11	0	0.026473	0.018185
123716	NDRG1 RELATED PROTEIN NDRG2B1	SIGNALING	11	0	0.033927	0.022694
47332	14-3-3 PROTEIN GAMMA	SIGNALING	11	0	0.018673	0.013473
257746	R-RAS (P23)	GTPASE	11	0	0.010247	0.009221
213226	SIMILAR TO NIT PROTEIN 2	UNKNOWN	11	0	0.011346	0.009221
206594	VACUOLAR SORTING PROTEIN 35	TRAFFIC	11	0	0.044174	0.036168
96883	COMPLEMENT INHIBITORY FACTOR H	BIOSYNTHETIC CARGO	12	0.028467	0	0.022694
23759	AFAMIN	BIOSYNTHETIC CARGO	12	0.011158	0.006661	0.027406
22817	FIBRINOPEPTIDE A	BIOSYNTHETIC CARGO	12	0.01173	0.005673	0.022694
261456	SIMILAR TO GLYCINE-N-ACYL TRANSFERASE	PROT MOD	12	0.022315	0.006661	0.046103

71751	ARP3 ACTIN-RELATED PROTEIN 3 HOMOLOG	CYTOSKELETON	12	0.012945	0	0.018442
194947	SIMILAR TO ACTIN-RELATED PROTEIN 2	CYTOSKELETON	12	0.005579	0	0.009221
164232	SIMILAR TO MICROSOMAL GLUTATHIONE S-TRANSFERASE 3	DETOXIFICATION	12	0.005579	0	0.009221
229899	SIMILAR TO KIAA1208 PROTEIN	UNKNOWN	12	0.018524	0	0.03637
44167	MANNOSE-BINDING PROTEIN C PRECURSOR	BIOSYNTHETIC CARGO	13	0.01173	0.012334	0.018185
355419	SIMILAR TO COMPLEMENT COMPONENT 1, Q SUBCOMPONENT, AL	BIOSYNTHETIC CARGO	13	0.006151	0.005673	0.009221
237237 244814	SIMILAR TO INTERFERON-INDUCIBLE GTPASE	GTPASE	13	0.012945	0.010247	0.018185
37301 166406	TRANSFERRIN	BIOSYNTHETIC CARGO	13	0.766853	0.980393	1.796033
104163	L-GULONOLACTONE OXIDASE	METABOLISM	13	0.054929	0.055998	0.122893
78145	RAB2A	GTPASE	13	0.09627	0.123741	0.263212
148924 166227	APOLIPOPROTEIN B	BIOSYNTHETIC CARGO	13	0.3112	0.47731	0.68488
111003	RAB7	GTPASE	13	0.127027	0.186907	0.300547
235838	SIMILAR TO RIKEN CDNA 1500009M05	UNKNOWN	13	0.018524	0.02357	0.03637
60419 124523	PLASMINOGEN	BIOSYNTHETIC CARGO	13	0.162426	0.074497	0.25783
304054	SIMILAR TO TRANSFERRIN	BIOSYNTHETIC CARGO	13	0.06345	0.028364	0.091935
104182	ACETYL-COA TRANSPORTER	PROT MOD	13	0.016736	0.011346	0.026947
302124	VITROTECTIN	BIOSYNTHETIC CARGO	13	0.072167	0.028254	0.077762
280024	HEAT SHOCK PROTEIN 47 PRECURSOR	PROT SYN/FOLD	13	0.011158	0.006661	0.013473
272967	SIMILAR TO GROUP XIII SECRETED PHOSPHOLIPASE A2	BIOSYNTHETIC CARGO	14	0.01173	0.018007	0.018185
160418	ARP2/3 COMPLEX 21 KDA SUBUNIT	CYTOSKELETON	14	0.024675	0.040588	0.03637
80354	CYCLOPHILIN B	PROT SYN/FOLD	14	0.34846	0.51725	0.42632
3890	CYTOCHROME B5	DETOXIFICATION	14	0.17773	0.254063	0.291583
217815	NIPSNAP1 PROTEIN (SNAP25-LIKE)	TEITHIDOCK/FUS	14	0.01173	0.01592	0.018442
83190	3-HYDROXYACYL-COA DEHYDROGENASE TYPE II (TYPE II HADH) (B	DETOXIFICATION	14	0.08769	0.137903	0.165463
41516	R, R-SC22	TEITHIDOCK/FUS	14	0.164143	0.253157	0.294403
3760	FATTY ACID-BINDING PROTEIN, LIVER	PROT MOD	14	0.059293	0.149432	0.10066
338609	N-ACYLSPHINGOSINE AMIDOHYDROLASE (ACID CERAMIDASE)	PROT MOD	14	0.005579	0.011346	0.009221
13862	SELENOPROTEIN T	UNKNOWN	14	0.005579	0.011346	0.009221
44648	RAB10	GTPASE	14	0.077671	0.067535	0.06797
19325 198556	PARAOXONASE 1	BIOSYNTHETIC CARGO	14	0.38429	0.415987	0.415047
198793	SIMILAR TO MICROSOMAL TRIGLYCERIDE TRANSFER PROTEIN	PROT SYN/FOLD	14	0.920833	0.99128	1.125563
72763 78212	CYTOCHROME P450 2C23	DETOXIFICATION	14	0.46827	0.431073	0.462543
316149	SIMILAR TO RIKEN CDNA 2310008M10	UNKNOWN	14	0.017309	0.01592	0.018442
170945	PEPTIDYL-PROLYL CIS-TRANS ISOMERASE	PROT SYN/FOLD	14	0.029039	0.024668	0.031658
141420	APOLIPOPROTEIN A-IV	BIOSYNTHETIC CARGO	15	0.060437	0.055009	0.216897
173317	FIBRINOGEN ALPHA/ALPHA-E CHAIN	BIOSYNTHETIC CARGO	15	0.16593	0.092412	0.502597
120645	SERUM ALBUMIN	BIOSYNTHETIC CARGO	15	0.730823	1.027787	4.4191
52390	SERUM AMYLOID P-COMPONENT	BIOSYNTHETIC CARGO	15	0.016736	0.024668	0.118644
31553	TRANSTHYRETIN	BIOSYNTHETIC CARGO	15	0.046348	0.077989	0.345477
3157	NUCLEOBINDIN 2 (CALNUC 2)	CALCIUM TRANS/BIND	15	0.070954	0.074626	0.325602
221549	COMPLEMENT COMPONENT 3	BIOSYNTHETIC CARGO	15	0.300827	0.42447	1.642433
144413	PLASMA RETINOL-BINDING PROTEIN	BIOSYNTHETIC CARGO	15	0.053714	0.080078	0.295173
85184	CDC42	GTPASE	15	0.017881	0.02368	0.082473
6160 11478 66447 84131 24	ALPHA-1 PROTEINASE INHIBITOR III	BIOSYNTHETIC CARGO	15	0.476703	0.80146	1.706633
204593	BIPHENYL HYDROLASE-LIKE (SERINE HYDROLASE, BREAST EPITHE	DETOXIFICATION	15	0.005579	0.006661	0.018442
126549	C-REACTIVE PROTEIN	BIOSYNTHETIC CARGO	15	0.041341	0.091423	0.259927
21122	RAB1A	GTPASE	15	0.090763	0.172389	0.46824
228279	P23 GAMMA 3	TRAFFIC	15	0.041984	0.074515	0.217815
126488	ALPHA-1-MACROGLOBULIN	BIOSYNTHETIC CARGO	15	0.240813	0.40727	1.02188
209664	ER-GOLGI INTERMEDIATE COMPARTMENT 32 KDA PROTEIN (ERGIC	TRAFFIC	15	0.029039	0.057496	0.141797
36387 69402 125352	ALPHA-2U GLOBULIN	BIOSYNTHETIC CARGO	16	0.31084	0.62601	0.767867
43886	CARBOXYLESTERASE 1	DETOXIFICATION	16	0.074915	0.20245	0.263513
219134	CERULOPLASMIN	BIOSYNTHETIC CARGO	16	0.053071	0.147198	0.23723

218278	RAB5A		GTPASE	16	0.021028	0.07058	0.10698
55435	Qb. MEMBRIN		TETHIDOCK/FUS	16	0.006151	0.018007	0.031658
139706	VESICULAR INTEGRAL-MEMBRANE PROTEIN VIP36		TRAFFIC	16	0.082683	0.264903	0.49035
130852	RAP1B		GTPASE	16	0	0.039967	0.141337
84231 166705	RAB1B		GTPASE	16	0	0.140457	0.397397
76408	RHOA		GTPASE	16	0	0.022691	0.06383
3901	GUANINE NUCLEOTIDE-BINDING PROTEIN G(K), ALPHA SUBUNIT		SIGNALING	16	0	0.017163	0.046103
10199	ACTIN: ALPHA CARDIAC		CYTOSKELETON	16	0.008926	0.056917	0.146567
62620 93455 270901	TUBULIN BETA 5		CYTOSKELETON	16	0.047492	0.159867	0.384063
161691	RAB18		GTPASE	16	0.006151	0.058485	0.126892
32618	RER1		TRAFFIC	16	0.005579	0.035904	0.07679
27803	BETA-2-MICROGLOBULIN		BIOSYNTHETIC CARGO	16	0	0.039489	0.082219
95154	CLATHRIN HEAVY CHAIN		COAT	16	0	0.20385	0.44287
69375	MYOSINLIGHT CHAIN ALKALI, SMOOTH-MUSCLE ISOFORM		CYTOSKELETON	16	0	0.012334	0.027406
23285	CLATHRIN AP47 PROTEIN		COAT	16	0	0.005673	0.013473
216613	NEURAL STEM CELL DERIVED NEURONAL SURVIVAL PROTEIN		TRAFFIC	16	0	0.005673	0.013473
3713	CARBOXYPEPTIDASE D		PROT MOD	16	0	0.011346	0.027406
74416	BETA-CATENIN		CYTOSKELETON	16	0	0.018995	0.027663
19138	MANNOSE-BINDING PROTEIN A		BIOSYNTHETIC CARGO	16	0	0.016908	0.022694
4326	G PROTEIN BETA 2 SUBUNIT		SIGNALING	16	0	0.020494	0.027663
120792	ACTIN: GAMMA		CYTOSKELETON	16	0.065888	0.623043	1.08143
8458	RAC2		GTPASE	16	0	0.007564	0.013473
316372	GAMMA-SOLUBLE NSF ATTACHMENT PROTEIN (GAMMA SNAP)		TETHIDOCK/FUS	16	0	0.028254	0.049641
68651	5'-AMP-ACTIVATED PROTEIN KINASE, GAMMA-1 SUBUNIT		SIGNALING	16	0	0.005673	0.009221
341343	ALPHA-2-ANTIPLASMIN		BIOSYNTHETIC CARGO	16	0	0.005673	0.009221
164032	UNCHARACTERIZED HEMATOPOIETIC STEM/PROGENITOR CELLS F		UNKNOWN	16	0	0.005673	0.009221
194129	GTP-BINDING REGULATORY PROTEIN ALPHA-13 CHAIN - MOUSE		SIGNALING	16	0	0.005673	0.009221
201498	TYPE I TRANSMEMBRANE C-TYPE LECTIN RECEPTOR DCL-1		UNKNOWN	16	0	0.005673	0.009221
294340	SIMILAR TO PUTATIVE ZINC FINGER TRANSCRIPTION FACTOR OVO		TRANSCRIPTION	16	0	0.005673	0.009221
3965	T-KINOGEN I		BIOSYNTHETIC CARGO	17	0.01173	0.012334	0.095747
84230 135016	CONTRAPSIN-LIKE PROTEASE INHIBITOR 1		BIOSYNTHETIC CARGO	17	0.205483	0.240343	1.540867
126501	APOLIPOPROTEIN E		BIOSYNTHETIC CARGO	17	0.119869	0.191887	1.176013
60418	INTEGRAL MEMBRANE PROTEIN, TMP21-I (P23) DELTA 1		TRAFFIC	17	0.129672	0.18878	1.147363
78146	COP-COATED VESICLE MEMBRANE PROTEIN P24 BETA 1		TRAFFIC	17	0.035762	0.121144	0.835883
170045 285748	P24 ALPHA 2		TRAFFIC	17	0.066588	0.167913	1.105137
31436	TUBULIN ALPHA 4		CYTOSKELETON	17	0.006151	0.030741	0.12126
77835	ERGIC-53 PROTEIN		TRAFFIC	17	0.042485	0.151407	0.640963
51376	ALPHA-SOLUBLE NSF ATTACHMENT PROTEIN (ALPHA SNAP)		TETHIDOCK/FUS	17	0.024675	0.069831	0.26203
34567	RAB14		GTPASE	17	0.005579	0.035858	0.193833
6158	Qb. VTI 1A		TETHIDOCK/FUS	17	0	0.006661	0.03637
47254	RSLY1P		TRAFFIC	17	0	0.038501	0.244304
74410	F-ACTIN CAPPING PROTEIN ALPHA-2 SUBUNIT		CYTOSKELETON	17	0	0.013323	0.05461
37204	PLAKOGLOBIN		CYTOSKELETON	17	0	0.012334	0.054812
36009	CLUSTERIN		BIOSYNTHETIC CARGO	17	0	0.010247	0.049641
169836	SECRETORY CARRIER MEMBRANE PROTEIN 3		TRAFFIC	17	0	0.011346	0.053893
18186 140379	HISTIDINE-RICH GLYCOPROTEIN HRG		BIOSYNTHETIC CARGO	17	0.006151	0	0.0501
43431	COMPLEMENT COMPONENT C9		BIOSYNTHETIC CARGO	17	0.012302	0.005673	0.108246
95208	FIBRONECTIN 1		BIOSYNTHETIC CARGO	17	0.011158	0.005673	0.07274
36413 246743	GRP75		PROT SYN/FOLD	17	0.012302	0.006661	0.082987
84170	APOLIPOPROTEIN C-III		BIOSYNTHETIC CARGO	17	0.005579	0	0.027663
253447	SIMILAR TO DIHYDROLIPOAMIDE DEHYDROGENASE		METABOLISM	17	0.006151	0	0.027663
7845	ALDEHYDE DEHYDROGENASE		METABOLISM	17	0.054218	0.005673	0.260953
31503	PROTHROMBIN		BIOSYNTHETIC CARGO	17	0.01173	0	0.063574

121548	CHAPERONIN 10	PROT SYN/FOLD	17	0.006151	0	0.036627
220359	SIMILAR TO RIKEN CDNA 0610010D20	UNKNOWN	17	0.01173	0.005673	0.055327
287107	B-FACTOR, PROPERDIN, ALTERNATIVE-COMPLEMENT PATHWAY C	BIOSYNTHETIC CARGO	17	0.006151	0	0.086985
11475	ALPHA-1-ANTI-PROTEINASE	BIOSYNTHETIC CARGO	17	0.071023	0.024668	0.888023
3766	FIBRINOGEN GAMMA CHAIN	BIOSYNTHETIC CARGO	17	0.029611	0.019984	0.403167
166238	FIBRINOGEN B BETA CHAIN	BIOSYNTHETIC CARGO	17	0.018454	0.013323	0.608023
47186	INTER-ALPHA-INHIBITOR H4 HEAVY CHAIN	BIOSYNTHETIC CARGO	17	0.017881	0.012334	0.336513
88238	CONTRAPSIN-LIKE PROTEASE INHIBITOR 6	BIOSYNTHETIC CARGO	17	0.023675	0.030341	0.552603
160756	SIMILAR TO INTERFERON-G INDUCED GTPASE	GTPASE	17	0.005579	0.005673	0.131602
207228	ANTITHROMBIN III	BIOSYNTHETIC CARGO	17	0.006151	0.022581	0.32192
111646	ALPHA-2-HS-GLYCOPROTEIN	BIOSYNTHETIC CARGO	17	0.016736	0.036014	0.466793
16936	HEMOPEXIN	BIOSYNTHETIC CARGO	17	0.018454	0.03971	0.519497
86608	VITAMIN D-BINDING PROTEIN	BIOSYNTHETIC CARGO	17	0.01173	0.036014	0.4296
141679	PROTEIN TRANSPORT PROTEIN SEC23A	COAT	17	0.03519	0.109431	1.025693
3638	APOLIPOPROTEIN A-I	BIOSYNTHETIC CARGO	17	0.012302	0.017018	0.203884
295725	PROTEIN TRANSPORT PROTEIN SEC24A (SEC24-RELATED PROTEIN)	COAT	17	0.006151	0.011346	0.117008
310568	ERP44 (SIMILAR TO THIOREDOXIN DOMAIN CONTAINING 4; ENDOPLASMIC RETICULUM CHAPERONE)	PROT SYN/FOLD	17	0.017309	0.028254	0.311987
166334	HAPTOGLOBIN	BIOSYNTHETIC CARGO	17	0.006151	0.043664	0.678913
293534	COPI COATOMER ALPHA SUBUNIT	COAT	17	0	0.010247	0.16168
177419	RAB5	GTPASE	17	0	0.006618	0.090927
3629	ALPHA-1-MICROGLOBULIN	BIOSYNTHETIC CARGO	17	0	0.006661	0.086727
290450	RAB6	GTPASE	17	0	0.025679	0.5117
219262	PROTEIN TRANSPORT PROTEIN SEC24D (SEC24-RELATED PROTEIN)	COAT	17	0	0.005673	0.144157
39119	CARCINOEMBRYONIC ANTIGEN-RELATED CELL ADHESION MOLECULE	BIOSYNTHETIC CARGO	17	0	0.005673	0.055327
145181	FETUIN-B	BIOSYNTHETIC CARGO	17	0	0.005673	0.245737
241419	SEC24C	COAT	17	0	0.018995	0.80486
51465	MG160	PROT MOD	17	0	0.012334	0.57361
60416	NUCLEOBINDIN 1 (CALNUC 1)	CALCIUM TRANS/BIND	17	0	0.017018	0.614784
248855	MANNOSEDASE 1-BETA	PROT MOD	17	0	0.005673	0.19569
235525	SIMILAR TO RIKEN CDNA 3110038B19	UNKNOWN	17	0	0.011346	0.398913
196264 205526	MANNOSEDASE 2, ALPHA 1	PROT MOD	17	0	0.048238	3.300233
273814	SIMILAR TO MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE	PROT MOD	17	0	0.005673	0.330627
260512	TRANSMEMBRANE 9 SUPERFAMILY MEMBER 4	UNKNOWN	17	0	0.006661	0.399954
45123	ANGIOTENSINOGEN	BIOSYNTHETIC CARGO	17	0	0	0.126892
114274	APOLIPOPROTEIN A-V	BIOSYNTHETIC CARGO	17	0	0	0.153838
38418	INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H3	BIOSYNTHETIC CARGO	17	0	0	0.209367
68735	POLYPEPTIDE N-ACETYL GALACTOSAMINYL TRANSFERASE	PROT MOD	17	0	0	0.19569
35327	Qc, RBET1	TEITH/DOCK/FUS	17	0	0	0.023353
231145	SIMILAR TO GOLGI MEMBRANE PROTEIN GP73	TRAFFIC	17	0	0	0.1044
228888	GALACTOSYL GALACTOSYLXYLOSYL PROTEIN 3-BETA-GLUCURONIDASE	PROT MOD	17	0	0	0.10517
44475	LONG-CHAIN-FATTY-ACID--COA LIGASE 6	PROT MOD	17	0	0	0.027193
276652	AB2-095	UNKNOWN	17	0	0	0.131144
259411	SIMILAR TO HEPARAN SULFATE 2-SULFOTRANSFERASE	PROT MOD	17	0	0	0.176274
78137	Qa, SYNTAXIN 5	TEITH/DOCK/FUS	17	0	0	0.14482
295490	SIMILAR TO GOLGI RESIDENT PROTEIN GCP60	TEITH/DOCK/FUS	17	0	0	0.2547
210144	SIMILAR TO BETA-1,3-GALACTOSYL TRANSFERASE-6	PROT MOD	17	0	0	0.054812
78175	PRENYLATED RAB ACCEPTOR 1	GTPASE	17	0	0	0.049843
229568	GLYCOPROTEIN-4-BETA-GALACTOSYL TRANSFERASE 2	PROT MOD	17	0	0	0.045132
141958	SIMILAR TO CHROMOSOME 13 OPEN READING FRAME 1	UNKNOWN	17	0	0	0.113673
272716	KDEL RECEPTOR	TRAFFIC	17	0	0	0.021515
235290	SIMILAR TO CHO FUNCTIONALLY UNKNOWN TYPE II TRANSMEMBRANE PROTEIN	UNKNOWN	17	0	0	0.045591
260808	PROTEIN TRANSPORT PROTEIN SEC23B (SEC23-RELATED PROTEIN)	COAT	17	0	0	0.062437
21485	SIMILAR TO BETA-2-GLYCOPROTEIN I	BIOSYNTHETIC CARGO	17	0	0	0.090061

221177	COPI COATOMER DELTA SUBUNIT	COAT	17	0	0	0.107787
63721	COPI COATOMER BETA SUBUNIT	COAT	17	0	0	0.175153
231548	SOLUBLE CALCIUM-ACTIVATED NUCLEOTIDASE SCAN-1 (UDPASE)	PROT MOD	17	0	0	0.70802
173223	FAM3C-LIKE PROTEIN	UNKNOWN	17	0	0	0.104453
267886	COPI COATOMER GAMMA-1 SUBUNIT	COAT	17	0	0	0.287912
64664	45 KDA CALCIUM-BINDING PROTEIN	CALCIUM TRANS/BIND	0	0	0	0.058605
311145	GOLGI COILED COIL PROTEIN GGC185 (GOLGIN FAMILY MEMBER)	TETHIDOCK/FUS	17	0	0	0.131602
211728	TRANSMEMBRANE 9 SUPERFAMILY MEMBER 1	UNKNOWN	17	0	0	0.107787
281147	RAB33B	GTPASE	17	0	0	0.088553
44217	HEPARAN SULFATE N-DEACETYLASE/N-SULFOTRANSFERASE	PROT MOD	17	0	0	0.57631
227072	YIP1	GTPASE	17	0	0	0.026947
106479	ALPHA-AMYLASE	BIOSYNTHETIC CARGO	17	0	0	0.026947
282341	COG1	TETHIDOCK/FUS	17	0	0	0.026947
62757	PLASMA GLUTAMATE CARBOXYPEPTIDASE	BIOSYNTHETIC CARGO	17	0	0	0.031658
220058	GPP34 RELATED PROTEIN	TETHIDOCK/FUS	17	0	0	0.026947
317738	ALPHA-2 ANTIPLASMIN	BIOSYNTHETIC CARGO	17	0	0	0.122639
54283	TRANS-GOLGI PROTEIN GMX33	TETHIDOCK/FUS	17	0	0	0.217613
241539	RING FINGER PROTEIN 121	UNKNOWN	17	0	0	0.026947
222641	ARP1 ACTIN-RELATED PROTEIN 1 ALPHA	CYTOSKELETON	17	0	0	0.026947
259217	COPI COATOMER EPSILON SUBUNIT	COAT	17	0	0	0.090061
275347	SEROLOGICALLY DEFINED BREAST CANCER ANTIGEN NY-BR-84 H	UNKNOWN	17	0	0	0.085808
206392	SIMILAR TO EXPRESSED SEQUENCE AW556797	UNKNOWN	17	0	0	0.026947
10610	ADP-RIBOSYLATION FACTOR 5	GTPASE	17	0	0	0.026947
305592	SIMILAR TO MYO-INOSITOL MONOPHOSPHATASE A3	SIGNALING	17	0	0	0.351523
242048	COG5	TETHIDOCK/FUS	17	0	0	0.059064
276682	SIMILAR TO VACUOLAR PROTEIN SORTING 26; VACUOLE PROTEIN	TRAFFIC	17	0	0	0.026947
55277	CORE1 UDP-GALACTOSE:N-ACETYL GALACTOSAMINE-ALPHA-R BE	PROT MOD	17	0	0	0.221408
124005	GIANTIN	TETHIDOCK/FUS	17	0	0	0.445654
51504	KYURENINE/ALPHA-AMINOADIPATE AMINOTRANSFERASE	METABOLISM	17	0	0	0.027663
296012	SIMILAR TO ALG-2	PROT MOD	17	0	0	0.095434
251780	3-HYDROXYISOBUTYRYL-COENZYME A HYDROLASE	METABOLISM	17	0	0	0.027663
302704	ALDEHYDE DEHYDROGENASE 1 FAMILY, MEMBER L2	DETOXIFICATION	17	0	0	0.027663
311134	PANTOPHYSIN	TRAFFIC	17	0	0	0.036627
258441	SIMILAR TO HTGN29 PROTEIN; KERATINOCYTES ASSOCIATED TRA	UNKNOWN	17	0	0	0.031658
235860	SIMILAR TO RIKEN CDNA 2510039018	UNKNOWN	17	0	0	0.027663
95121	APOLIPOPROTEIN M	BIOSYNTHETIC CARGO	17	0	0	0.018442
194890	SIMILAR TO N-ACETYL GLUCOSAMINYL TRANSFERASE IVB	PROT MOD	17	0	0	0.018442
35931	COPI COATOMER BETA' SUBUNIT	COAT	17	0	0	0.312718
222317	SERINE (OR CYSTEINE) PROTEINASE INHIBITOR, CLADE G (C1 INHI	BIOSYNTHETIC CARGO	17	0	0	0.040879
21695	Qb. GOS28	TETHIDOCK/FUS	17	0	0	0.335486
71574	TRANSCYTOSIS ASSOCIATED PROTEIN/P115	TETHIDOCK/FUS	17	0	0	0.276017
309339	PROTEIN FAM20B PRECURSOR	UNKNOWN	17	0	0	0.067826
200680	SIMILAR TO RIKEN CDNA 1810037C20	UNKNOWN	17	0	0	0.040879
163993	RAB2B	GTPASE	17	0	0	0.032273
237211	GPP130	TETHIDOCK/FUS	17	0	0	0.37596
197729	PQ LOOP REPEAT CONTAINING 1	UNKNOWN	17	0	0	0.022694
169300	GOLGI AUTOANTIGEN: GOLGIN SUBFAMILY A MEMBER 2 (GM130)	TETHIDOCK/FUS	17	0	0	0.658207
722796	TYPE 2 LACTOSAMINE ALPHA-2,3-SIALYL TRANSFERASE	PROT MOD	17	0	0	0.158143
105853	SERINE/THREONINE PROTEIN KINASE 16	SIGNALING	17	0	0	0.022694
230767	SIMILAR TO PROTEIN PHOSPHATASE 2C EPSILON	SIGNALING	17	0	0	0.022694
256498	SIMILAR TO PKA C-BETA-2	SIGNALING	17	0	0	0.018442
241393	TYROSYL PROTEIN SULFOTRANSFERASE-1	PROT MOD	17	0	0	0.244153
204384	NOVEL MEMBER OF P24 FAMILY (TIRAP3B)	TRAFFIC	17	0	0	0.236367

275605	SIMILAR TO EH DOMAIN BINDING PROTEIN 1	TRAFFIC	17	0	0	0.022694
75089	GD3 ALPHA 2,8-SIALYLTRANSFERASE	PROT MOD	17	0	0	0.103993
274159	COG3	TETHIDOCK/FUS	17	0	0	0.103993
31491	TRANS-GOLGI NETWORK INTEGRAL MEMBRANE PROTEIN (TGN38)	TRAFFIC	17	0	0	0.109166
60482	ALPHA-1,6-MANNOSYL-GLYCOPROTEIN 2-BETA-N-ACETYLGLUCOSYL	PROT MOD	17	0	0	0.346976
2689	ALPHA-1,3-MANNOSYL-GLYCOPROTEIN 2-BETA-N-ACETYLGLUCOSYL	PROT MOD	17	0	0	0.069104
140307	TRANSMEMBRANE 9 SUPERFAMILY MEMBER 3	UNKNOWN	17	0	0	0.494727
234949	SIMILAR TO MKIAA0493 PROTEIN	UNKNOWN	17	0	0	0.063114
4394	ER LUMEN PROTEIN RETAINING RECEPTOR 2 (KDEL RECEPTOR 2)	TRAFFIC	17	0	0	0.04303
284296	INTEGRAL MEMBRANE PROTEIN 2B	UNKNOWN	17	0	0	0.036883
236737	COPI COATOMER ZETA-1 SUBUNIT	COAT	17	0	0	0.06803
288023	GRASP55_65	TETHIDOCK/FUS	17	0	0	0.42826
23396	ADP-RIBOSYLATION FACTOR-LIKE 1	GTPASE	17	0	0	0.041136
201171	SIMILAR TO GAL BETA 1,3GALNAC ALPHA 2,3-SIALYLTRANSFERASE	PROT MOD	17	0	0	0.263
168831	SUPPRESSOR OF PROFILIN/P41 OF ACTIN-RELATED COMPLEX 2/3	CYTOSKELETON	17	0	0	0.009221
302868	GOLGIN-84	TETHIDOCK/FUS	17	0	0	0.313307
60460	SYNAPTOGYRIN 2	TETHIDOCK/FUS	17	0	0	0.027406
269702	SIMILAR TO HOMOPROTECATECHUATE CATABOLISM BIFUNCTIONAL	METABOLISM	17	0	0	0.009221
199239	ACTIN RELATED PROTEIN 2/3 COMPLEX, SUBUNIT 5-LIKE	CYTOSKELETON	17	0	0	0.009221
38912	KALLISTATIN	BIOSYNTHETIC CARGO	17	0	0	0.009221
315956	DEHYDROGENASE E1 AND TRANSKETOLASE DOMAIN CONTAINING	METABOLISM	17	0	0	0.009221
60413	RAB9A	GTPASE	17	0	0	0.009221
258586	SIMILAR TO AMINOADIPATE-SEMIALDEHYDE SYNTHASE	METABOLISM	17	0	0	0.009221
257320	SIMILAR TO ZINC TRANSPORTER LIKE 2	CALCIUM TRANS/BIND	17	0	0	0.009221
75002	MYOSIN ID	CYTOSKELETON	17	0	0	0.009221
1271	SELENOPROTEIN P	BIOSYNTHETIC CARGO	17	0	0	0.009221
311263	RAB21	GTPASE	17	0	0	0.009221
255469	PUTATIVE PHOSPHATIDIC ACID PHOSPHATASE	METABOLISM	17	0	0	0.013473
139592	SIMILAR TO ARYLACETYL ACYL-CoA N-ACYLTRANSFERASE	PROT MOD	17	0	0	0.009221
11776	INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 4	BIOSYNTHETIC CARGO	17	0	0	0.013473
281046	UDP-GALACTOSE:N-ACETYL GALACTOSAMINEALPHA-PEPTIDE BETA	PROT MOD	17	0	0	0.009221
137529	BETA-1,4-N-ACETYL GALACTOSAMINYLTRANSFERASE	PROT MOD	17	0	0	0.013473
255984	OSTEOCLAST INHIBITORY LECTIN	PROT SYN/FOLD	17	0	0	0.009221
304110	SIMILAR TO N-ACETYLLACTOSAMINIDE BETA-1,3-N-ACETYLLGLUCO	PROT MOD	17	0	0	0.013473
11137	PROTEIN-TYROSINE PHOSPHATASE-LIKE N	SIGNALING	17	0	0	0.009221
319029	UDP-N-ACETYL-ALPHA-D-GALACTOSAMINE:POLYPEPTIDE N-ACETY	PROT MOD	17	0	0	0.013473
214715	SIMILAR TO G PROTEIN-COUPLED RECEPTOR 108	SIGNALING	17	0	0	0.009221
166240	EUKARYOTIC TRANSLATION ELONGATION FACTOR 1 BETA 2	PROT SYN/FOLD	17	0	0	0.013473
230447	SIMILAR TO DEVELOPMENT- AND DIFFERENTIATION-ENHANCING F	SIGNALING	17	0	0	0.009221
314280	SIMILAR TO PL6 PROTEIN	SIGNALING	17	0	0	0.013473
209309	SIMILAR TO LECT2	SIGNALING	17	0	0	0.009221
84325	S-ARRESTIN	SIGNALING	17	0	0	0.013473
226905	SIMILAR TO MITOGEN-ACTIVATED PROTEIN KINASE KINASE	SIGNALING	17	0	0	0.009221
312923	SIMILAR TO WD REPEAT DOMAIN 9 ISOFORM A; CAMP RESPONSE	SIGNALING	17	0	0	0.009221
145735	BET3	TETHIDOCK/FUS	17	0	0	0.013473
315291	Qc, GS15	TETHIDOCK/FUS	17	0	0	0.013473
20725	MUNC13-4 PROTEIN	TETHIDOCK/FUS	17	0	0	0.009221
313999	SIMILAR TO INTRACELLULAR MEMBRANE-ASSOCIATED CALCIUM-B	METABOLISM	17	0	0	0.009221
225098	GOLGI PERIPHERAL MEMBRANE PROTEIN P65	TETHIDOCK/FUS	17	0	0	0.013473
34036	Qbc, SNAP29	TETHIDOCK/FUS	17	0	0	0.013473
78131	R, YKT6	TETHIDOCK/FUS	17	0	0	0.009221
220378	GOLGI-ASSOCIATED MICROTUBULE-BINDING PROTEIN HOOK3; HO	CYTOSKELETON	17	0	0	0.013473
140359	RETINOID-INDUCIBLE SERINE CARBOXYPEPTIDASE	PROT MOD	17	0	0	0.009221

208059	DERMATOPONTIN		BIOSYNTHETIC CARGO	17	0	0	0.009221
86062	UDP-GLUCURONATE DECARBOXYLASE		METABOLISM	17	0	0	0.013473
221907	SIMILAR TO LECTIN, MANNOSE-BINDING 2-LIKE; VIP36-LIKE		TRAFFIC	17	0	0	0.009221
301225	SIMILAR TO HPS5 PROTEIN		TRAFFIC	17	0	0	0.013473
239738	(RCAS1) TYPE II RECEPTOR LIKE CANCER ASSOCIATED SURFACE		UNKNOWN	17	0	0	0.013473
222783	PANCREATITIS-INDUCED PROTEIN 49		UNKNOWN	17	0	0	0.049641
300896	SIMILAR TO DNA SEGMENT, CHR 12, ERATO DOI 551, EXPRESSED		UNKNOWN	17	0	0	0.009221
206786	SIMILAR TO PROBABLE TRANSMEMBRANE PROTEIN FT27 - MOUSE		UNKNOWN	17	0	0	0.013473
82925	VIMENTIN		CYTOSKELETON	17	0	0	0.009221
243174	SIMILAR TO FLJ21963		UNKNOWN	17	0	0	0.009221
315828	SIMILAR TO PROTEIN KINASE NJMU-R1		UNKNOWN	17	0	0	0.013473
200143	HYPOTHETICAL PROTEIN DAERTD765E		UNKNOWN	17	0	0	0.009221
272431	SIMILAR TO FLJ12716 PROTEIN		UNKNOWN	17	0	0	0.013473
211553	COMM DOMAIN CONTAINING 10		UNKNOWN	17	0	0	0.013473
203847	DORZ1		UNKNOWN	17	0	0	0.009221
273407	BTB (POZ) DOMAIN CONTAINING 7 (PREDICTED)		UNKNOWN	17	0	0	0.013473
270449	D130038B21		UNKNOWN	17	0	0	0.009221
247534	SOLUTE CARRIER FAMILY 35, MEMBER B3 (PREDICTED)		UNKNOWN	17	0	0	0.013473
80419	BRAIN PROTEIN 44		UNKNOWN	17	0	0	0.009221
218419	SIMILAR TO RIKEN CDNA 9430083G14		UNKNOWN	17	0	0	0.009221
259074	SIMILAR TO ZINC TRANSPORTER 5		UNKNOWN	17	0	0	0.013473
290726	ALPHA-1,2-MANNOSIDASE		PROT MOD	17	0	0	0.076588
56042	BETA 1,3-GALACTOSYLTRANSFERASE POLYPEPTIDE 1		PROT MOD	17	0	0	0.158548
189334	XYLOSYLTRANSFERASE II		PROT MOD	17	0	0	0.095232
198410	SIMILAR TO 9130011E15RIK PROTEIN		UNKNOWN	17	0	0	0.085808
230119	SIMILAR TO KIA0980 PROTEIN		UNKNOWN	17	0	0	0.013473
161453	SEC13 LIKE 1 PROTEIN		COAT	17	0	0	0.26705
251303	COMPLEMENT COMPONENT C8 GAMMA SUBUNIT		BIOSYNTHETIC CARGO	17	0	0	0.018185
84182	ALPHA-1 CATENIN		CYTOSKELETON	17	0	0	0.018185
13085	SERINE PROTEASE		BIOSYNTHETIC CARGO	17	0	0	0.018185
260733	DYNACTIN COMPLEX 50 KDA SUBUNIT		CYTOSKELETON	17	0	0	0.053893
3640	APOLIPOPROTEIN C-I		BIOSYNTHETIC CARGO	17	0	0	0.018185
275354	SIMILAR TO COMPLEMENT COMPONENT FACTOR H		BIOSYNTHETIC CARGO	17	0	0	0.018185
3639	APOLIPOPROTEIN A-II		BIOSYNTHETIC CARGO	17	0	0	0.018185
299013	D-GLUCURONYL C5-EPIMERASE		PROT MOD	17	0	0	0.036168
220519	BC004044 (DENTIN MATRIX PROTEIN 4)		UNKNOWN	17	0	0	0.018185
3662	ZINC-ALPHA-2-GLYCOPROTEIN		BIOSYNTHETIC CARGO	17	0	0	0.036168
204958	SIMILAR TO SIF AND TIAM1-LIKE EXCHANGE FACTOR		UNKNOWN	17	0	0	0.018185
181007	FIBRINOGEN		BIOSYNTHETIC CARGO	17	0	0	0.036168
280942	SIMILAR TO THYROID HORMONE RECEPTOR INTERACTOR 11; THY1		UNKNOWN	17	0	0	0.018185
245155	ALDEHYDE DEHYDROGENASE 7A1		DETOXIFICATION	17	0	0	0.018185
35326	SEC22 HOMOLOG		TETH/DOCK/FUS	17	0	0	0.036168
289309	SIMILAR TO WD REPEAT DOMAIN 20 ISOFORM 2		UNKNOWN	17	0	0	0.018185
245295	COG4		TETH/DOCK/FUS	17	0	0	0.053893
202233	SIMILAR TO DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT		TRANSCRIPTION	17	0	0	0.018185
267138	MALE ENHANCED ANTIGEN 2/GOLGI AUTOANTIGEN, GOLGIN SUBF		TETH/DOCK/FUS	17	0	0	0.018185
164208	R, VAMP 4		TETH/DOCK/FUS	17	0	0	0.018185
194234	P24 GAMMA 1		TRAFFIC	17	0	0	0.018185
26418	VESICLE ASSOCIATED PROTEIN		COAT	17	0	0	0.26608
222168	COG8		TETH/DOCK/FUS	17	0	0	0.067367
60512	TATA ELEMENT MODULATORY FACTOR		TRANSCRIPTION	17	0	0	0.094977
41195 141634	ALPHA 2,6-SIALYLTRANSFERASE		PROT MOD	17	0	0	1.528033
52078	ARF-RELATED PROTEIN		GTPASE	17	0	0	0.068542

133253	ENDO-ALPHA-D-MANNOSIDASE		PROT MOD	17	0	0	0.063317
307730	UDP-N-ACETYL-ALPHA-D-GALACTOSAMINE:POLYPEPTIDE N-ACETYL		PROT MOD	17			0.262852
227779	INTER-ALPHA TRYPSIN INHIBITOR, HEAVY CHAIN 1		BIOSYNTHETIC CARGO	17	0	0	0.063778
43395	SECRETED PHOSPHOPROTEIN 24		BIOSYNTHETIC CARGO	17	0	0	0.088285
295519 311912	SIMILAR TO CONSERVED OLIGOMERIC GOLGI COMPLEX SUBUNIT 4		COAT	17	0	0	0.04042
280644 289275	CCAAT DISPLACEMENT PROTEIN (CASP)		TEETH/DOCK/FUS	17	0	0	0.063778
218235	GBF1		TRAFFIC	17	0	0	0.13094
204725	CDA14 (PTX1)		TRAFFIC	17	0	0	0.04042
191057	SIMILAR TO RIKEN CDNA 8430437G11		UNKNOWN	17	0	0	0.04042
262782	SIMILAR TO P3 PROTEIN		UNKNOWN	17	0	0	0.04042

Table S2B. Hierarchical clustering of proteins identified in biochemical fractions of RM and SM

				Mean % Total Peptides									
CMBSEQID List	Assigned Prot Name	Function	Cluster	RM					SM				
				SLT	INS	DET	AQU	SLT	INS	DET	AQU	SLT	AQU
16936	HEMOPEXIN	BIOSYNTHETIC CARGO	1	0	0	0	0.06727	0	0	0.03801	0.09098		
144413	PLASMA RETINOL-BINDING PROTEIN	BIOSYNTHETIC CARGO	1	0	0	0.02483	0.10167	0.012	0.01293	0.07738	0.13103		
	POLYPOSIS LOCUS PROTEIN 1												
	HOMOLOG (Tb2 PROTEIN HOMOLOG)												
252129	(GP106)	UNKNOWN	1	0.01035	0	0.01674	0.04687	0.01147	0.01013	0.01916	0.05148		
219134	CERULOPLASMIN	BIOSYNTHETIC CARGO	2	0	0	0	0.18294	0.02295	0.09804	0	0.27325		
145181	FETUIN-B	BIOSYNTHETIC CARGO	2	0	0	0	0.01731	0	0.01097	0	0.0287		
129368	15 KDA SELENOPROTEIN	PROT MOD	2	0	0	0	0.10487	0.02399	0.03471	0.019	0.11038		
	UDP-GLUCOSE												
	GLYCOPROTEIN:GLUCOSYLTRANSFERASE												
171823	SE	PROT MOD	2	0.02069	0.09928	0.12256	0.72636	0.28759	0.35459	0.10061	1.06393		
	INTER-ALPHA-INHIBITOR H4 HEAVY CHAIN		2	0	0	0	0.03264	0.012	0	0	0.06975		
162301	COMPLEMENT C4	BIOSYNTHETIC CARGO	2	0.01035	0.00719	0	0.13034	0.03546	0.02737	0.0095	0.20976		
	PEPTIDYL-PROLYL CIS-TRANS ISOMERASE		2	0.02695	0	0	0.09836	0.03442	0.02457	0	0.17409		
3760	FATTY ACID-BINDING PROTEIN, LIVER	PROT MOD	2	0	0.07653	0	0.19483	0.09336	0.06356	0.0095	0.36858		
3965	T-KININOGEN I	BIOSYNTHETIC CARGO	2	0	0	0	0.04279	0	0.00431	0	0.05688		
204172	8 BETA SUBUNIT	BIOSYNTHETIC CARGO	2	0	0	0	0.01632	0	0	0	0.02339		
23759	AFAMIN	BIOSYNTHETIC CARGO	2	0	0	0	0.01632	0	0	0	0.02645		
	SERINE PROTEASE INHIBITOR 2.4												
195578	PRECURSOR	BIOSYNTHETIC CARGO	2	0	0	0	0.01632	0	0	0	0.02471		
181007	FIBRINOGEN	BIOSYNTHETIC CARGO	2	0	0	0	0.00816	0	0	0	0.01284		
	TRINUCLEOTIDE REPEAT CONTAINING 5												
296070	(PREDICTED)	UNKNOWN	2	0	0	0	0.03363	0	0	0	0.05209		
43431	COMPLEMENT COMPONENT C9	BIOSYNTHETIC CARGO	2	0	0	0	0.0408	0	0	0.0095	0.05872		
43686	CARBOXYLESTERASE 1	DETOXIFICATION	2	0	0	0	0.31665	0.03598	0.00646	0.04751	0.34735		
213126	SEL 1L	TRANSCRIPTION	2	0	0	0	0.07741	0	0.00431	0.01916	0.09057		
84131 256838 296398	ALPHA-1 PROTEINASE INHIBITOR III	BIOSYNTHETIC CARGO	2	0.05799	0.02157	0	1.41273	0.33609	0.1685	0	1.63157		
	CONTRAPSIN-LIKE PROTEASE												
84230 135016	INHIBITOR 1	BIOSYNTHETIC CARGO	2	0	0.02157	0	0.39565	0.11339	0.05321	0	0.44611		
	ADIPOCYTE-DERIVED LEUCINE												
605	AMINOPEPTIDASE	PROT MOD	2	0	0	0	0.14148	0.04246	0.01693	0	0.17576		
395638	GRP170 (HYPOXIA UP-REGULATED 1)	PROT SYN/FOLD	2	0.04765	0.04545	0	1.14594	0.19631	0.13121	0	1.1656		
126488	ALPHA-1-MACROGLOBULIN	BIOSYNTHETIC CARGO	2	0.04138	0.01438	0	0.80532	0.07093	0.1183	0	0.69677		
126549	C-REACTIVE PROTEIN	BIOSYNTHETIC CARGO	2	0	0.00719	0	0.16111	0.012	0.03318	0	0.1734		
78070	CARBOXYLESTERASE 3	DETOXIFICATION	2	0	0.00863	0	0.59338	0.02136	0.09287	0	0.63095		
207228	ANTITHROMBIN III	BIOSYNTHETIC CARGO	2	0	0	0	0.06925	0	0.00431	0	0.07812		
166334	HAPTOGLOBIN	BIOSYNTHETIC CARGO	2	0	0	0	0.22385	0.01147	0	0	0.24968		
182047	CARBOXYLESTERASE ESNA2	DETOXIFICATION	2	0	0	0	0.05908	0	0	0	0.0637		
232734	SIMILAR TO BCS1-LIKE	UNKNOWN	2	0	0	0	0.02448	0	0	0	0.03037		
44167	MANNOSE-BINDING PROTEIN C												
	PRECURSOR	BIOSYNTHETIC CARGO	2	0	0	0	0.09836	0.012	0	0	0.10469		
293536	ENDOPLASMIC RETICULUM PROTEIN												
	ERP46	PROT SYN/FOLD	2	0	0	0	0.10553	0.012	0	0	0.12665		

237675	ALPHA-2-MACROGLOBULIN RECEPTOR-ASSOCIATED PROTEIN	BIOSYNTHETIC CARGO	2	0	0	0	0.08755	0	0.00431	0	0.08873
12989	CARBOXYLESTERASE 2	DETOXIFICATION	2	0	0	0	0.0917	0	0.00539	0	0.08639
121548	CHAPERONIN 10	PROT SYN/FOLD	2	0	0	0	0.01831	0	0	0	0.01766
232164	U2-ASSOCIATED SR140 PROTEIN	UNKNOWN	2	0	0	0	0.0196	0	0	0	0.0194
126501	APOLIPOPROTEIN E	BIOSYNTHETIC CARGO	2	0	0	0	0.18492	0.15385	0.00431	0	0.20607
3157	NUCLEOBINDIN 2 (CALNUC 2)	CALCIUM TRANS/BIND	2	0	0	0	0.10586	0.05789	0	0	0.15256
154010	OPTINEURIN	UNKNOWN	2	0	0	0	0.01731	0.012	0	0	0.0287
288307	DP1L1 PROTEIN	UNKNOWN	2	0.01661	0	0.02078	0.07598	0.06645	0.03772	0.0095	0.12898
22617	FIBRINOPEPTIDE A	BIOSYNTHETIC CARGO	2	0	0	0	0.01731	0.01147	0.00582	0	0.01235
221549	COMPLEMENT COMPONENT 3	BIOSYNTHETIC CARGO	2	0.21899	0.07177	0.0128	0.81446	0.19975	0.16766	0.019	0.95588
37301	166406 TRANSFERRIN	BIOSYNTHETIC CARGO	2	0.43553	0.10112	0.00837	1.54823	0.55223	0.18212	0	1.38853
120645	SERUM ALBUMIN	BIOSYNTHETIC CARGO	2	0.16803	0.30561	0.01242	2.12693	0.72246	0.33302	0.019	1.82597
	SIMILAR TO HEXOSE-6-PHOSPHATE DEHYDROGENASE; GDH/6PGL										
251640	ENDOPLASMIC BIFUNCTIONAL PROTEIN	METABOLISM	2	0.02069	0.11365	0	0.69582	0.15281	0.16618	0	0.67557
77793	105537 CARBOXYLESTERASE 4	DETOXIFICATION	2	0.24253	0.17411	0.02559	1.97877	0.94526	0.3269	0	1.46057
157137	CARBOXYLESTERASE ESNA3	DETOXIFICATION	2	0.03694	0.01438	0	0.67184	0.37316	0.09988	0	0.51529
10945	123735 158916 CARBOXYLESTERASE B-1	DETOXIFICATION	2	0.03923	0.01582	0	0.61829	0.28085	0.09819	0	0.66536
120574	ANNEXIN A3	TETH/DOCK/FUS	2	0	0	0	0.07708	0.03442	0.00582	0	0.06923
173317	FIBRINOGEN ALPHA/ALPHA-E CHAIN	BIOSYNTHETIC CARGO	2	0	0.01194	0	0.17743	0.03546	0.03774	0	0.09488
36387	69402 125352 ALPHA-2U GLOBULIN	BIOSYNTHETIC CARGO	2	0	0.00719	0	1.28083	0.38815	0.11503	0	0.89547
60584	227664 PROTEIN DISULFIDE ISOMERASE A4	PROT SYN/FOLD	2	0.08304	0.16273	0	1.72773	0.54536	0.20369	0.0095	1.20173
112141	146478 196665 CARBOXYLESTERASE 10	DETOXIFICATION	2	0.36845	0.09809	0.02559	2.58863	0.48666	0.40242	0.07632	1.49353
	ENDOPLASMIC RETICULUM PROTEIN										
157237	ERP29	PROT SYN/FOLD	2	0.05981	0.01913	0	0.4477	0.08188	0.0679	0	0.33311
23403	CALRETICULIN	PROT SYN/FOLD	2	0.37227	0.17883	0.02511	2.27997	0.71352	0.28975	0	1.22233
195759	ARMET PROTEIN	UNKNOWN	2	0.05763	0.00719	0	0.4122	0.10192	0.01444	0	0.20435
80354	CYCLOPHILIN B	PROT SYN/FOLD	2	0.17471	0.35625	0.00837	1.27001	0.22426	0.22741	0.0095	0.66837
	ENDOPLASMIN PRECURSOR (ENDOPLASMIC RETICULUM PROTEIN 99) (94 KDA GLUCOSE-REGULATED PROTEIN) (GRP94) (ERP99) (POLYMORPHIC TUMOR REJECTION ANTIGEN 1) (TUMOR REJECTION ANTIGEN GP96)										
269402	ANTIGEN GP96	PROT SYN/FOLD	2	0.2891	0.49772	0.06754	3.38827	1.08709	0.7637	0.05747	1.56097
28269	BIP	PROT SYN/FOLD	2	1.14323	1.4162	0.57588	6.0105	1.85613	1.34925	0.22386	3.08317
21556	PROTEIN DISULFIDE ISOMERASE A3	PROT SYN/FOLD	2	0.70616	0.54042	0.14826	3.45433	1.53627	0.74397	0.15808	1.9481
27868	PROTEIN DISULFIDE ISOMERASE A6	PROT SYN/FOLD	2	0.33974	0.39343	0.05474	1.58967	0.60838	0.46265	0.0095	1.02351
31553	TRANS-THYRETIN	BIOSYNTHETIC CARGO	2	0	0	0	0.17059	0.02295	0.00431	0	0.12242
11475	ALPHA-1-ANTITRYPSIN	BIOSYNTHETIC CARGO	2	0	0	0	0.27811	0.03494	0	0	0.25019
280024	HEAT SHOCK PROTEIN 47 PRECURSOR	PROT SYN/FOLD	2	0	0	0	0.04995	0.012	0	0	0.04237
31503	PROTHROMBIN	BIOSYNTHETIC CARGO	2	0	0	0	0.05811	0	0.00431	0	0.04594
86238	CONTRAPSIN-LIKE PROTEASE INHIBITOR 6	BIOSYNTHETIC CARGO	2	0	0	0	0.16166	0	0	0	0.1302
86608	VITAMIN D-BINDING PROTEIN	BIOSYNTHETIC CARGO	2	0	0	0	0.10586	0	0	0	0.08516
304054	SIMILAR TO TRANSFERRIN	BIOSYNTHETIC CARGO	2	0	0	0	0.11005	0	0	0	0.08731
3638	APOLIPOPROTEIN A-1	BIOSYNTHETIC CARGO	2	0	0	0	0.05293	0	0	0	0.04064
	SIMILAR TO GI:13385412-LIKE PROTEIN										
205305	SPLICE FORM I	UNKNOWN	2	0	0	0	0.00915	0	0	0	0.00705

227817	CARBOXYLESTERASE ESNA1	DETOXIFICATION	2	0	0	0	0.04826	0	0	0	0.04189
220359	SIMILAR TO RIKEN CDNA 0610010D20	UNKNOWN	2	0	0	0	0.02647	0	0	0	0.02339
52390	SERUM AMYLOID P-COMPONENT	BIOSYNTHETIC CARGO	2	0	0	0	0.09638	0	0.00582	0	0.06708
341343	ALPHA-2-ANTIPLASMIN	BIOSYNTHETIC CARGO	2	0	0	0	0.01831	0	0	0	0.01235
141420	APOLIPOPROTEIN A-IV	BIOSYNTHETIC CARGO	2	0	0	0	0.14864	0	0	0	0.10376
68739	HEPARIN COFACTOR II	BIOSYNTHETIC CARGO	2	0	0	0	0.03363	0	0	0	0.02339
228920	SIMILAR TO RIKEN CDNA 9630046K23	UNKNOWN	2	0	0	0	0.03363	0	0	0	0.02339
3774	FERRITIN HEAVY CHAIN	METABOLISM	2	0	0	0	0.11402	0	0	0	0.06923
	SIMILAR TO ENDOPLASMIC RETICULUM THIOREDOXIN SUPERFAMILY MEMBER, 18 K	PROT SYN/FOLD	2	0	0	0	0.06307	0	0	0	0.0389
208059	DERMATOPONTIN	BIOSYNTHETIC CARGO	2	0	0	0	0.01731	0	0	0	0.01103
	SIMILAR TO EMBRYONIC BLASTOCYLEAR EXTRACELLULAR										
303538	MATRIX PROTEIN PRECURSOR	UNKNOWN	2	0	0	0	0.01731	0	0	0	0.01103
194048	HYPOTHETICAL PROTEIN MGC40499	UNKNOWN	2	0	0	0	0.00816	0	0	0	0.00531
277663	FERRITIN LIGHT CHAIN	METABOLISM	2	0.05318	0.02875	0	0.41636	0.012	0.03469	0	0.24978
	ERP44 (SIMILAR TO THIOREDOXIN DOMAIN CONTAINING 4; ENDOPLASMIC RETICULUM RESIDENT PROTEIN 44KDA)	PROT SYN/FOLD	2	0	0.05917	0	0.44285	0.04798	0.01875	0	0.23753
18186 140379	HISTIDINE-RICH GLYCOPROTEIN HRG	BIOSYNTHETIC CARGO	2	0	0	0	0.03264	0	0	0	0.01766
273384	GLYCOSYLTRANSFERASE 25 DOMAIN CONTAINING 1	UNKNOWN	2	0	0	0	0.09991	0	0.00431	0	0.05473
	SIMILAR TO ENDOPLASMIC RETICULUM CHAPERONE SIL1 HOMOLOG	PROT SYN/FOLD	2	0	0	0	0.01731	0	0	0	0.00705
318887	BOCA	PROT SYN/FOLD	2	0	0	0	0.08855	0	0	0	0.04279
280160	ENDOPLASMIC OXIDOREDUCTASE 1 BETA	PROT SYN/FOLD	2	0	0	0	0.02746	0	0	0	0.01327
282876	SIMILAR TO MENINGIOMA EXPRESSED ANTIGEN 6 (COILED-COIL PROLINE-RICH)	UNKNOWN	2	0	0	0	0.02448	0	0	0	0.01103
286300	CC1-9	UNKNOWN	2	0	0.00719	0	0.17544	0	0.00431	0	0.08171
69606	PROTEIN DISULFIDE ISOMERASE	PROT SYN/FOLD	2	0.64808	0.80717	0.97666	5.03663	1.01029	0.85871	1.17536	2.0546
104170 318957	PROTEIN KINASE INHIBITOR P58	SIGNALING	2	0	0.01438	0.06754	0.24436	0.05893	0.03471	0.05717	0.14266
60419 124523	PLASMINOGEN	BIOSYNTHETIC CARGO	3	0.11708	0.1291	0	0.23764	0.07445	0.04869	0	0.09712
3766	FIBRINOGEN GAMMA CHAIN	BIOSYNTHETIC CARGO	3	0	0.06518	0	0.10288	0	0.00431	0	0.05372
263376	SDF2 LIKE PROTEIN 1	PROT MOD	3	0	0.02691	0	0.09903	0	0.01875	0	0.03442
	SIMILAR TO PROTEIN DISULFIDE ISOMERASE-RELATED	PROT SYN/FOLD	3	0.10451	0.21525	0	0.68744	0.04642	0.10781	0	0.15758
276048	DNAJ (HSP40) HOMOLOG, SUBFAMILY B, MEMBER 11	PROT SYN/FOLD	3	0	0.06274	0.02117	0.22253	0.012	0	0.02866	0.08957
295796	ALPHA-1-MICROGLOBULIN	BIOSYNTHETIC CARGO	3	0	0	0	0.01632	0	0	0	0.00531
3629	INTER-ALPHA TRYPSIN INHIBITOR, HEAVY CHAIN 1	BIOSYNTHETIC CARGO	3	0	0	0	0.01731	0	0	0	0.00531
227779	HEAVY CHAIN 1	BIOSYNTHETIC CARGO	3	0	0	0	0.04576	0	0	0	0.00705
85740 268188	CALUMENIN	CALCIUM TRANS/BIND	3	0	0	0	0.03264	0	0	0	0.00705
306304	P63	TRAFFIC	3	0	0	0	0.03264	0	0	0	0.00705
	SIMILAR TO SIALIC-ACID O-ACETYLESTERASE	PROT MOD	3	0	0	0	0.00816	0	0	0	0
198275			3	0	0	0	0.00816	0	0	0	0

123978	DESTRAIN	CYTOSKELETON	6	0	0	0	0	0	0.01444	0	0.03533
71698	FATTY ACID-BINDING PROTEIN, BRAIN	PROT MOD	6	0	0	0	0	0	0.00431	0	0.01062
	SERINE/THREONINE PROTEIN PHOSPHATASE 2A, CATALYTIC										
41475	SUBUNIT, BETA ISOFORM	SIGNALING	6	0	0	0	0	0	0.00862	0	0.02297
37085	ALPHA-PARVIN	CYTOSKELETON	6	0	0	0	0	0	0.00431	0	0.01634
193681	P120 CATENIN ISOFORM 2B	CYTOSKELETON	6	0	0	0	0	0	0.00431	0	0.01634
271907	SLINGSHOT 1L	SIGNALING	6	0	0	0	0	0	0.01444	0	0.05466
233877	PALS2-BETA SPLICE VARIANT	BIOSYNTHETIC CARGO	6	0	0	0	0	0	0.00862	0	0.03616
158790	LIN-7 PROTEIN	SIGNALING	6	0	0	0	0	0	0.00862	0	0.03616
46143	CYSTEINE-RICH PROTEIN 2	UNKNOWN	6	0	0	0	0	0	0.00431	0	0.01766
	SIMILAR TO GLUCAN (1,4-ALPHA-); BRANCHING ENZYME 1; DNA SEGMENT, CHR 16, ERATO DOI.536, EXPRESSED										
299017	AFATOXIN B1 ALDEHYDE REDUCTASE	PROT MOD	6	0	0	0	0	0	0.00431	0	0.02114
161251	MEMBER 2	DETOXIFICATION	6	0	0	0	0	0	0.00862	0	0.02696
42862	GUANINE DEAMINASE	METABOLISM	6	0	0	0	0	0	0.01594	0	0.04851
340135	TRIOSEPHOSPHATE ISOMERASE	METABOLISM	6	0	0	0	0	0	0.00862	0	0.03002
	HYPOXANTHINE-GUANINE										
16980	PHOSPHORIBOSYLTRANSFERASE	METABOLISM	6	0	0	0	0	0	0.00431	0	0.01409
18910	SH3P7R2	UNKNOWN	6	0	0	0	0	0	0.00431	0	0.01409
248510	SIMILAR TO PLEXIN	SIGNALING	6	0	0	0	0	0	0.03877	0.0095	0.12625
126543	ATP CITRATE LYASE	METABOLISM	6	0.01661	0.02632	0	0.00816	0.02399	0.04763	0	0.11521
	CHAPERONIN CONTAINING TCP-1 BETA										
292700	SUBUNIT	PROT SYN/FOLD	6	0	0.02632	0	0	0.02399	0.05344	0	0.09446
	N-HYDROXYARYLAMINE										
78152	SULFOTRANSFERASE	PROT MOD	6	0	0.00719	0	0	0	0.01747	0	0.03706
269276	SIMILAR TO ER-RESIDENT PROTEIN ERDJ5	PROT SYN/FOLD	6	0	0.00719	0	0	0	0.01875	0	0.03533
	10-FORMYLTETRAHYDROFOLATE										
62196	DEHYDROGENASE	METABOLISM	6	0	0.02389	0	0	0	0.04029	0	0.10733
217843	SIMILAR TO RIKEN CDNA 1810074P20	UNKNOWN	6	0	0.02157	0	0	0.01147	0.04787	0	0.1108
	3-ALPHA-HYDROXYSTEROID										
19230	DEHYDROGENASE	DETOXIFICATION	6	0	0.05021	0	0.02448	0	0.04636	0	0.21798
5972	CARBONIC ANHYDRASE III	METABOLISM	6	0	0.12268	0	0.09792	0.03598	0.09095	0.0095	0.52411
	DELTA-AMINOLEVULINIC ACID										
3622	DEHYDRATASE	DETOXIFICATION	6	0	0	0	0.00816	0	0.00582	0	0.04636
75106	ESTROGEN SULFOTRANSFERASE	DETOXIFICATION	6	0	0	0	0.00816	0	0.02154	0	0.10591
127122	KETOHEXOKINASE	METABOLISM	6	0	0	0	0.00816	0	0.01165	0	0.07679
	3-OXO-5-BETA-STEROID 4-										
23758	DEHYDROGENASE	DETOXIFICATION	6	0	0.02157	0	0.02448	0	0.0304	0	0.18972
3576	REGUCALIN	METABOLISM	6	0	0.02157	0	0.05359	0.01147	0.03622	0	0.26441
54409	ADENOSYLMOMOCYSTEINASE	METABOLISM	6	0	0.01438	0	0.04179	0	0.02177	0	0.12573
29886	D-DOPACHROME TAUTOMERASE	METABOLISM	6	0	0.01913	0	0.04378	0	0.0319	0	0.15227
45123	ANGIOTENSINOGEN	BIOSYNTHETIC CARGO	6	0	0	0	0.02547	0	0	0	0.06792
19138	MANNOSE-BINDING PROTEIN A	BIOSYNTHETIC CARGO	6	0	0	0	0.02448	0	0	0	0.06138
31392	SEPIAPTERIN REDUCTASE	METABOLISM	6	0	0	0	0.00816	0	0	0	0.01766
338661	MANNOSIDASE 2, ALPHA B1	PROT MOD	6	0	0	0	0.00816	0	0	0	0.01766
111646	ALPHA-2-HS-GLYCOPROTEIN	BIOSYNTHETIC CARGO	6	0	0	0	0.01632	0	0.00431	0	0.0481

209477	SIMILAR TO PURINE-NUCLEOSIDE PHOSPHORYLASE; PURINE-NUCLEOSIDE PHOSPHORYLASE	METABOLISM	6	0	0	0	0.04179	0	0.01165	0	0.09526
286288	PROCOLLAGEN-LYSINE,2-	PROT MOD	6	0	0	0	0.01632	0	0.00862	0	0.04237
87332	OXOGLUTARATE 5-DIOXYGENASE 3	CYTOSKELETON	6	0	0	0	0.02448	0	0.00431	0	0.09914
4320	COFILIN, NON-MUSCLE ISOFORM	METABOLISM	6	0	0	0	0.00915	0	0	0	0.03359
54374	ACYL-COA-BINDING PROTEIN	DETOXIFICATION	6	0	0	0	0.00816	0	0	0	0.02738
33170	BILVERDIN REDUCTASE A PRECURSOR	PROT SYN/FOLD	6	0	0	0	0.0408	0	0	0	0.1389
193296	OXIDOREDUCTASE ERO1L	METABOLISM	6	0	0	0	0.00915	0	0	0	0.04411
71492	LYSOPHOSPHATIDIC ACID PHOSPHATASE	METABOLISM	6	0	0	0	0.03264	0	0	0	0.19151
218478	ISOCITRATE DEHYDROGENASE [NADP]	PROT MOD	6	0	0	0	0.00816	0	0	0	0.04411
151517	SIMILAR TO SERINE PROTEASE OMI	UNKNOWN	6	0	0.00719	0	0.01731	0	0	0	0.05913
72216	CCG1-INTERACTING FACTOR B	DETOXIFICATION	6	0	0.00719	0	0	0	0	0	0.0503
104196	ALDEHYDE DEHYDROGENASE FAMILY 1 MEMBER A1	METABOLISM	6	0	0.00719	0	0	0	0	0	0.11031
295907	4-TRIMETHYLAMINO BUTYRALDEHYDE DEHYDROGENASE	METABOLISM	6	0	0.00719	0	0	0	0	0	0.07988
42736	GLUCOSE-6-PHOSPHATE ISOMERASE	METABOLISM	6	0	0.00719	0	0	0	0.00431	0	0.06351
118982	3-HYDROXYANTHRANILATE 3,4-DIOXYGENASE	METABOLISM	6	0	0.01438	0	0	0	0.00431	0	0.10018
211833	CYTOSOLIC MALATE DEHYDROGENASE	UNKNOWN	6	0	0.00719	0	0	0	0.00431	0	0.0433
60726	SIMILAR TO MITOGEN INDUCIBLE GENE MIG-2	CYTOSKELETON	6	0	0.03886	0	0.00915	0	0.01875	0	0.18576
153343	PROFILIN 1	PROT SYN/FOLD	6	0	0.02632	0	0.00915	0	0.02888	0	0.19515
47332	HEAT RESPONSIVE PROTEIN 12	SIGNALING	6	0	0.00719	0	0	0	0.01067	0	0.07451
313683	14-3-3 PROTEIN GAMMA	METABOLISM	6	0	0.01438	0	0.02448	0.01147	0.00862	0	0.17964
51562	ALPHA ENOLASE	PROT MOD	6	0	0.00719	0	0.00816	0	0	0	0.05872
28291	PHOSPHATIDYLETHANOLAMINE-BINDING PROTEIN	DETOXIFICATION	6	0	0.06757	0	0.07072	0	0.03686	0	0.65139
8623	GLUTATHIONE S-TRANSFERASE YB-2 SUBUNIT	TRAFFIC	6	0	0.01438	0	0.00816	0	0.00862	0	0.11894
38418	RAB GDI BETA	BIO SYNTHETIC CARGO	6	0	0	0	0.00816	0	0	0	0.06901
80790	INTER-ALPHA-TRYPSIN INHIBITOR	METABOLISM	6	0	0	0	0.00816	0	0.00431	0	0.08037
51568	GLYCEROL-3-PHOSPHATE DEHYDROGENASE [NAD+],	METABOLISM	6	0	0	0	0.00816	0	0.00431	0	0.08957
213226	PHOSPHOGLUCOMUTASE	UNKNOWN	6	0	0	0	0.00816	0	0.00431	0	0.13236
43659	SIMILAR TO NIT PROTEIN 2	PROT MOD	6	0	0.01438	0	0.01632	0	0.01293	0	0.38451
19169	FATTY ACID SYNTHASE	PROT MOD	6	0	0	0	0	0	0.00582	0	0.11122
75026	GLYCINE N-METHYLTRANSFERASE	METABOLISM	6	0	0	0	0	0	0	0	0.06087
249119	PHENYLALANINE-4-HYDROXYLASE	DETOXIFICATION	6	0	0	0	0	0	0	0	0.01409
95119	PROTEIN RAKC	DETOXIFICATION	6	0	0	0	0	0	0	0	0.02911
37175	ALDEHYDE OXIDASE	CYTOSKELETON	6	0	0	0	0	0	0	0	0.07658
317625	ALPHA-ACTININ 1	PROTEASOME/UBIQUITIN	6	0	0	0	0	0	0	0	0.01634
161456	UBIQUITIN-ACTIVATING ENZYME E1 1	METABOLISM	6	0	0	0	0	0	0	0	0.02165
	ALDOSE REDUCTASE		6	0	0	0	0	0	0	0	

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266321	SIMILAR TO RIKEN CDNA 4931406C07	UNKNOWN	6	0	0	0	0	0	0.00431	0	0.03799
29712	14-3-3 PROTEIN ZETADELTA	SIGNALING	6	0	0	0	0.00816	0	0.02134	0	0.19321
171244	ANNEXIN A4	TETH/DOCK/FUS	6	0	0	0	0	0.03598	0.01444	0	0.12582
51411	CYSTEINE-RICH PROTEIN 1	UNKNOWN	6	0	0	0	0	0.01147	0	0	0.03574
148924	166227 APOLIPOPROTEIN B	BIOSYNTHETIC CARGO	6	0.03724	0.04744	0.17423	0.27517	0.10639	0.10969	0.11418	0.79326
260021	YEAST 44.2 PROTEIN	UNKNOWN	6	0	0.00719	0	0.00816	0	0	0	0.0194
126642	164858 GLUTATHIONE S-TRANSFERASE YB-1 SUBUNIT	DETOXIFICATION	7	0.18646	0.12652	0	0.2795	0.10795	0.15215	0	0.44707
18021	CDK5 REGULATORY SUBUNIT	SIGNALING	7	0.04651	0.04848	0.00837	0.00816	0.012	0.03902	0.019	0.09529
7845	ALDEHYDE DEHYDROGENASE	METABOLISM	7	0.01661	0.0909	0	0.08458	0	0.01594	0	0.10633
36413	246743 GRP75	PROT SYN/FOLD	7	0	0.0407	0	0.02547	0.01147	0.01444	0	0.02907
51489	4-HYDROXYPHENILPYRUVATE DIOXYGENASE	METABOLISM	7	0	0.02691	0	0	0	0	0	0.06669
82698	HEAT SHOCK PROTEIN 86: HSP86	PROT SYN/FOLD	7	0	0.06575	0	0	0.02869	0.04452	0	0.14646
	IRON-RESPONSIVE ELEMENT BINDING PROTEIN 1 (IRE-BP 1) (IRON REGULATORY PROTEIN 1) (IRP1) (FERRITIN REPRESSOR PROTEIN) (ACONITATE HYDRATASE)	PROT SYN/FOLD	7	0	0.01438	0	0	0.01147	0.01165	0	0.03716
216271	1,4-ALPHA-GLUCAN BRANCHING ENZYME	METABOLISM	7	0	0.00719	0	0	0	0.00431	0	0.01808
	SIMILAR TO START DOMAIN CONTAINING 10; SEROLOGICALLY DEFINED COLON CANCER ANTIGEN 28	UNKNOWN	7	0	0.01438	0	0	0	0.00862	0	0.02471
195138	104192 GLYCOCEN PHOSPHORYLASE	METABOLISM	7	0.01035	0.0292	0	0	0	0.00431	0	0.0287
82822	UBIQUITIN-CONJUGATING ENZYME E2 VARIANT 1 UEV-1 CROC-1	PROTEASOME/UBIQUITIN	7	0	0.01194	0	0	0	0	0	0.01062
149105	FRUCTOSE-1,6-BISPHOSPHATASE	METABOLISM	7	0	0.24662	0	0	0	0.17585	0	0.26889
	S-ADENOSYLMETHIONINE SYNTHETASE ALPHA AND BETA FORMS	PROT MOD	7	0	0.05858	0	0	0	0.03038	0	0.04678
69363	60562 SEC14-LIKE PROTEIN 2	PROT MOD	7	0	0.02632	0	0	0	0.01293	0	0.03127
92415	TIP120	UNKNOWN	7	0	0.02389	0	0	0	0.00862	0	0.02738
205775	ANNEXIN A11	TETH/DOCK/FUS	7	0	0.02389	0	0	0.01147	0.00431	0	0.02339
316589	SIMILAR TO UROCANATE HYDRATASE FARNESYL PYROPHOSPHATE	METABOLISM	8	0	0	0	0	0	0	0.019	0.05649
78213	SYNTHETASE	PROT MOD	8	0	0	0	0	0	0.00431	0.01916	0.03574
123716	NDRG1 RELATED PROTEIN NDRG2B1	SIGNALING	8	0	0.00719	0	0	0	0.01013	0.01916	0.03176
51531	GLUT4 VESICLE PROTEIN	UNKNOWN	8	0	0	0.02521	0.01632	0.01147	0.03471	0.06697	0.08394
188125	TORSINA	PROT SYN/FOLD	8	0	0	0.02078	0	0	0	0.05543	0.03616
144363	PHOSPHOENOLPYRUVATE CARBOXYKINASE, CYTOSOLIC [GTP]	METABOLISM	8	0	0.00719	0	0	0	0.00582	0.06651	0.06006
218419	SIMILAR TO RIKEN CDNA 9430083G14	UNKNOWN	8	0	0	0	0	0	0	0.0095	0.01062
111680	LEUKOCYTE COMMON ANTIGEN VARIANT 4 PRECURSOR	SIGNALING	8	0	0	0	0	0	0	0.0095	0.00531
274677	SIMILAR TO UBIQUITIN LIGASE E3 ALPHA-II	PROTEASOME/UBIQUITIN	8	0	0	0	0	0	0	0.0095	0.00705
295521	SIMILAR TO HYPOTHETICAL PROTEIN FLJ20627	UNKNOWN	8	0	0	0	0	0	0	0.0095	0.00705
166238	FIBRINOGEN B BETA CHAIN	BIOSYNTHETIC CARGO	9	0	0.11782	0	0.00816	0.02399	0.16075	0	0.05607

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73521	ADAPTOR-RELATED PROTEIN COMPLEX	COAT	11	0	0	0	0	0	0.1375	0	0.01766
3340	2. MU 1 SUBUNIT SPECTRIN ALPHA CHAIN, BRAIN	CYTOSKELETON	11	0	0.01438	0	0	0.0918	1.7263	0.019	0.25345
	SPECTRIN BETA-II CHAIN, BRAIN 1 (SPECTRIN, NON-ERYTHROID BETA CHAIN 1) (BETA-II SPECTRIN) (FODRIN CHAIN 1) (BETA CHAIN)										
300121	BETA CHAIN	CYTOSKELETON	11	0	0.00719	0	0	0.06885	1.17064	0	0.13231
63042	MYOSIN IB	CYTOSKELETON	11	0	0.00719	0	0	0	1.37388	0.10182	0.16494
293534	COPI COATOMER ALPHA SUBUNIT	COAT	11	0	0	0	0	0	0.04029	0	0.00705
	230 KDA PHOSPHATIDYLINOSITOL 4- KINASE	SIGNALING	11	0	0	0	0	0	0.03483	0	0.00705
289228	P53 INDUCIBLE PROTEIN	SIGNALING	11	0	0	0	0	0	0.02973	0	0.00708
69379 88823	MYOSIN REGULATORY LIGHT CHAIN	CYTOSKELETON	11	0	0	0	0	0	0.46103	0	0.01808
277610	EPLIN	CYTOSKELETON	11	0	0	0	0	0	0.15274	0	0.01235
3158	SPECTRIN BETA CHAIN, BRAIN 2	CYTOSKELETON	11	0	0	0	0	0	0.46154	0	0.03116
69375	MYOSIN LIGHT CHAIN ALKALI, SMOOTH-										
	MUSCLE ISOFORM	CYTOSKELETON	11	0	0.01194	0	0	0.01147	0.33875	0	0
75002	MYOSIN ID	CYTOSKELETON	11	0	0	0	0	0	0.6195	0.02866	0
	INTERFERON GAMMA INDUCED GTPASE	GTPASE	11	0	0	0	0	0	0.02027	0	0
261550	SIMILAR TO MYOSIN VI	CYTOSKELETON	11	0	0	0	0	0	0.06335	0	0
216529	FARP1 PROTEIN	UNKNOWN	11	0	0	0	0	0	0.03748	0	0
	SMILAR TO ACTIN-RELATED PROTEIN 2	CYTOSKELETON	11	0	0	0	0	0	0.01951	0	0
44422	TROPOMYOSIN ALPHA 4 CHAIN	CYTOSKELETON	11	0	0	0	0	0	0.00646	0	0
725563	ERYTHROID SPECTRIN ALPHA	CYTOSKELETON	11	0	0	0	0	0	0.16852	0	0
233953	EMILIN	CYTOSKELETON	11	0	0	0	0	0	0.02887	0	0
298819	TUBULIN ALPHA 6	CYTOSKELETON	11	0	0	0	0	0	0.09532	0	0
10609	ADP-RIBOSYLATION FACTOR 4	GTPASE	11	0	0	0	0	0	0.00716	0	0
	L-SERINE DEHYDRATASE/L-THREONINE DEAMINASE	METABOLISM	11	0	0	0	0	0	0.00862	0	0
76611	GTPASE	GTPASE	11	0	0	0	0	0	0.00862	0	0
	ACTIN RELATED PROTEIN 2/3 COMPLEX,										
199239	SUBUNIT 5-LIKE	CYTOSKELETON	11	0	0	0	0	0	0.00862	0	0
20725	MUNC13-4 PROTEIN	TETH/DOCK/FUS	11	0	0	0	0	0	0.00615	0	0
	SIMILAR TO HYPOTHEITICAL PROTEIN										
213390	5832424M12	UNKNOWN	11	0	0	0	0	0	0.00862	0	0
	SIMILAR TO TETRATRICOPEPTIDE REPEAT PROTEIN 7 (TPR REPEAT PROTEIN 7)										
196091	RNA-BINDING PROTEIN HUR	UNKNOWN	11	0	0	0	0	0	0.00862	0	0
18691	5'-AMP-ACTIVATED PROTEIN KINASE, CATALYTIC ALPHA-2 CHAIN	PROT SYN/FOLD	11	0	0	0	0	0	0.00862	0	0
54292	SIMILAR TO PKA C-BETA-2	SIGNALING	11	0	0	0	0	0	0.00862	0	0
256498	MYOSIN IE	SIGNALING	11	0	0	0	0	0	0.00862	0	0
105842	ERYTHROID SPECTRIN BETA	CYTOSKELETON	11	0	0	0	0	0	0.05544	0	0
726511	TROPOMODULIN 3	CYTOSKELETON	11	0	0	0	0	0	0.09869	0	0
261414	FLOTILIN-1	CYTOSKELETON	11	0	0	0	0	0	0.03598	0	0
8548	GLYPICAN 4	BIOSYNTHETIC CARGO	11	0	0	0	0	0	0.07369	0	0
253728	PROTEIN-GLUTAMINE GAMMA- GLUTAMYLTRANSFERASE K	BIOSYNTHETIC CARGO	11	0	0	0	0	0	0.01875	0	0
31490	DYNAMIN 2	PROT MOD	11	0	0	0	0	0	0.04915	0	0
3740	CYTOSKELETON	CYTOSKELETON	11	0	0	0	0	0	0.03598	0	0

78346	SER/THR PROTEIN PHOSPHATASE 2A SUBUNIT B	SIGNALING	11	0	0	0	0	0	0	0.01596	0	0
85752	26S PROTEASE REGULATORY SUBUNIT 6B	PROTEASOME/UBIQUITIN	11	0	0	0	0	0	0	0.00619	0	0
29682	LN-7 HOMOLOG C	SIGNALING	11	0	0	0	0	0	0	0.01165	0	0
43654	ANTIGEN PEPTIDE TRANSPORTER 1	PROT SYN/FOLD	11	0	0	0	0	0	0	0.00582	0	0
93024	RHO-RELATED GTP-BINDING PROTEIN RHOG	GTPASE	11	0	0	0	0	0	0	0.00582	0	0
82925	VIMENTIN	CYTOSKELETON	11	0	0	0	0	0	0	0.00582	0	0
219502	DESMOPLAKIN (DP) (250/210 KDA PARANEOPlastic PEMPHIGUS ANTIGEN)	CYTOSKELETON	11	0	0	0	0	0	0	0.00582	0	0
23396	ADP-RIBOSYLATION FACTOR-LIKE 1	GTPASE	11	0	0	0	0	0	0	0.01013	0	0
227390	RETINOL DEHYDROGENASE 10	DETOXIFICATION	11	0	0	0	0	0	0	0.01013	0	0
221177	COPI COATOMER DELTA SUBUNIT	COAT	11	0	0	0	0	0	0	0.01013	0	0
318405	EPIPLAKIN	CYTOSKELETON	11	0	0	0	0	0	0	0.01594	0	0
268483	KINESIN FAMILY PROTEIN 13A	CYTOSKELETON	11	0	0	0	0	0	0	0.00479	0	0
203525	ENTHOPROTIN	COAT	11	0	0	0	0	0	0	0.01013	0	0
295453	SIMILAR TO KIAA1407 PROTEIN	UNKNOWN	11	0	0	0	0	0	0	0.01594	0	0
268103	SHORT CHAIN DEHYDROGENASE REDUCTASE 9	DETOXIFICATION	11	0	0	0	0	0	0	0.01013	0	0
35920	MONOCYTE DIFFERENTIATION ANTIGEN CD14 PRECURSOR	BIO SYNTHETIC CARGO	11	0	0	0	0	0	0	0.01594	0	0
75350	Sorting nexin 3	BIO SYNTHETIC CARGO	11	0	0	0	0	0	0	0.00582	0	0
229721	SIMILAR TO HYPOTHETICAL PROTEIN FLJ30373	UNKNOWN	11	0	0	0	0	0	0	0.00582	0	0
265857	SIMILAR TO HYPOTHETICAL PROTEIN KIAA0233	UNKNOWN	11	0	0	0	0	0	0	0.01594	0	0
264993	UNKNOWN4	UNKNOWN	11	0	0	0	0	0	0	0.00582	0	0
313817	HYPOTHETICAL PROTEIN XP_342343	UNKNOWN	11	0	0	0	0	0	0	0.01013	0	0
258690	SIMILAR TO RIKEN CDNA 2010315L10	UNKNOWN	11	0	0	0	0	0	0	0.01013	0	0
224054	SB:CB404 PROTEIN	UNKNOWN	11	0	0	0	0	0	0	0.00582	0	0
197176	SIMILAR TO ENSANGP00000013261	UNKNOWN	11	0	0	0	0	0	0	0.00582	0	0
191344	UNKNOWN1	UNKNOWN	11	0	0	0	0	0	0	0.00582	0	0
359989	SIMILAR TO DJ881L22.2 (NOVEL PROTEIN)	UNKNOWN	11	0	0	0	0	0	0	0.00582	0	0
136387	M4 PROTEIN	UNKNOWN	11	0	0	0	0	0	0	0.00582	0	0
3029	60S RIBOSOMAL PROTEIN L37	PROT SYN/FOLD	11	0	0	0	0	0	0	0.00582	0	0
231492	ATP-BINDING CASSETTE, SUB-FAMILY F (GCN20), MEMBER 1	PROT SYN/FOLD	11	0	0	0	0	0	0	0.00582	0	0
249374	DEAH (ASP-GLU-ALA-HIS) BOX POLYPEPTIDE 29; NUCLEIC ACID HELICASE DDXX	PROT SYN/FOLD	11	0	0	0	0	0	0	0.00582	0	0
268833	PHOSPHOINOSITIDE-3-KINASE, REGULATORY SUBUNIT 4, P150	TRAFFIC	11	0	0	0	0	0	0	0.00582	0	0
55867	EUKARYOTIC TRANSLATION INITIATION FACTOR 3 SUBUNIT 6	PROT SYN/FOLD	11	0	0	0	0	0	0	0.00582	0	0
285136	AUTOCRINE MOTILITY FACTOR RECEPTOR	PROTEASOME/UBIQUITIN	11	0	0	0	0	0	0	0.00582	0	0
260591	B-IND1	SIGNALING	11	0	0	0	0	0	0	0.00582	0	0
4701	PROTEIN TYROSINE PHOSPHATASE 4A1	SIGNALING	11	0	0	0	0	0	0	0.00582	0	0

51565	PHOSPHATIDYLCHOLINE TRANSFER PROTEIN	PROT MOD	11	0	0	0	0	0	0	0.00431	0	0
256333	O-GLCNAC TRANSFERASE-INTERACTING PROTEIN OF 98 KDA	PROT MOD	11	0	0	0	0	0	0	0.00431	0	0
50402	TRANSALDOLASE	METABOLISM	11	0	0	0	0	0	0	0.00431	0	0
204932	SIMILAR TO SEPTIN 6	GTPASE	11	0	0	0	0	0	0	0.00431	0	0
76638	CALPAIN SMALL SUBUNIT 1	BIO SYNTHETIC CARGO	11	0	0	0	0	0	0	0.00431	0	0
78051	MYOSIN HEAVY CHAIN, NONMUSCLE TYPE B	CYTOSKELETON	11	0	0	0	0	0	0	0.12099	0	0
699022	PLECTIN 10	CYTOSKELETON	11	0	0	0	0	0	0	0.10607	0	0
241018	SIMILAR TO CENTROMERIC PROTEIN E (CENP-E PROTEIN)	CYTOSKELETON	11	0	0	0	0	0	0	0.00431	0	0
265199	SIMILAR TO KINESIN FAMILY PROTEIN KIF1A	CYTOSKELETON	11	0	0	0	0	0	0	0.00431	0	0
60578	CLATHRIN LIGHT CHAIN B	COAT	11	0	0	0	0	0	0	0.00431	0	0
11249	NEURONAL MYOSIN HEAVY CHAIN	CYTOSKELETON	11	0	0	0	0	0	0	0.10047	0	0
130834	HYPERTENSION-INDUCED PROTEIN S-2	UNKNOWN	11	0	0	0	0	0	0	0.02423	0	0
214491	PROTEIN LRP16	UNKNOWN	11	0	0	0	0	0	0	0.00431	0	0
266426	SIMILAR TO FRAGILE-X-RELATED PROTEIN 1 ISOFORM E	UNKNOWN	11	0	0	0	0	0	0	0.00431	0	0
192125	SIMILAR TO CENTROMERE/KINETOCHORE PROTEIN ZW10 HOMOLOG	CYTOSKELETON	11	0	0	0	0	0	0	0.02737	0	0
267886	COPI COATOMER GAMMA-1 SUBUNIT	COAT	11	0	0	0	0	0	0	0.00431	0	0
23872	MICROSOMAL DIPEPTIDASE	PROT MOD	11	0	0	0	0	0	0	0.0375	0	0
272716	KDEL RECEPTOR	TRAFFIC	11	0	0	0	0	0	0	0.01293	0	0
258828	ARCHVILIN	CYTOSKELETON	11	0	0	0	0	0	0	0.00431	0	0
240594	281002D13RIK PROTEIN	UNKNOWN	11	0	0	0	0	0	0	0.01293	0	0
298059	PREDICTED E3 UBIQUITIN LIGASE	UNKNOWN	11	0	0	0	0	0	0	0.00431	0	0
	SIMILAR TO UBIQUITOUS TETRATRICOPEPTIDE CONTAINING PROTEIN ROXAN; ROTAVIRUS X ASSOCIATED NON-STRUCTURAL PROTEIN	UNKNOWN	11	0	0	0	0	0	0	0.00431	0	0
230656	PROTEIN	UNKNOWN	11	0	0	0	0	0	0	0.00431	0	0
264688	SIMILAR TO TRIM26 PROTEIN	UNKNOWN	11	0	0	0	0	0	0	0.00431	0	0
198073	LIVER NTE-RELATED PROTEIN	UNKNOWN	11	0	0	0	0	0	0	0.00431	0	0
287423	HYPOTHETICAL PROTEIN XP_344851	UNKNOWN	11	0	0	0	0	0	0	0.00431	0	0
246519	SIMILAR TO RIKEN CDNA 1110038M16	UNKNOWN	11	0	0	0	0	0	0	0.00431	0	0
248047	SIMILAR TO HYPOTHETICAL PROTEIN FLJ20331	UNKNOWN	11	0	0	0	0	0	0	0.00431	0	0
281850	SIMILAR TO KIAA1311 PROTEIN	UNKNOWN	11	0	0	0	0	0	0	0.00431	0	0
271294	ABHYDROLASE DOMAIN CONTAINING PROTEIN 2	UNKNOWN	11	0	0	0	0	0	0	0.00431	0	0
223302	SIMILAR TO HISTIDYL-TRNA SYNTHETASE-LIKE	PROT SYN/FOLD	11	0	0	0	0	0	0	0.00431	0	0
300246	SIMILAR TO SIGNAL RECOGNITION PARTICLE 68KDA	PROT SYN/FOLD	11	0	0	0	0	0	0	0.00431	0	0
255113	26S PROTEASOME NON-ATPASE REGULATORY SUBUNIT 2	PROTEASOME/UBIQUITIN	11	0	0	0	0	0	0	0.00431	0	0
314767	CULLIN 4A	PROTEASOME/UBIQUITIN	11	0	0	0	0	0	0	0.00431	0	0

109735	2' 3' CYCLIC NUCLEOTIDE 3'-PHOSPHODIESTERASE	SIGNALING	11	0	0	0	0	0	0	0.00431	0	0
23444	5'-AMP-ACTIVATED PROTEIN KINASE, CATALYTIC ALPHA-1 CHAIN	SIGNALING	11	0	0	0	0	0	0	0.00431	0	0
168209	CAMP-DEPENDENT PROTEIN KINASE TYPE II-ALPHA REGULATORY CHAIN	SIGNALING	11	0	0	0	0	0	0	0.00431	0	0
217100	P140MDIA	SIGNALING	11	0	0	0	0	0	0	0.00431	0	0
19107	PKC-ZETA-INTERACTING PROTEIN	SIGNALING	11	0	0	0	0	0	0	0.00431	0	0
191003	PRKRA PROTEIN KINASE, INTERFERON-INDUCIBLE DOUBLE STRANDED RNA DEPENDENT ACTIVATOR	SIGNALING	11	0	0	0	0	0	0	0.00431	0	0
44893	PROTEIN KINASE C ALPHA	SIGNALING	11	0	0	0	0	0	0	0.00431	0	0
261449	SIMILAR TO KIDNEY ANKYRIN REPEAT-CONTAINING PROTEIN	UNKNOWN	11	0	0	0	0	0	0	0.00431	0	0
261337	DNAJC13	UNKNOWN	11	0	0	0	0	0	0	0.00431	0	0
62616	1A	SIGNALING	11	0	0	0	0	0	0	0.00431	0	0
55286	VACUOLAR PROTEIN SORTING 33A	TRAFFIC	11	0	0	0	0	0	0	0.00431	0	0
266460	SIMILAR TO LDL RECEPTOR ADAPTOR PROTEIN	SIGNALING	11	0	0	0	0	0	0	0.00431	0	0
229135	SIMILAR TO SLIT-ROBO RHO GTPASE-ACTIVATING PROTEIN 3; WAVE-ASSOCIATED RAC GTPASE ACTIVATING PROTEIN	SIGNALING	11	0	0	0	0	0	0	0.00431	0	0
225945	SIMILAR TO TOLLIP PROTEIN	SIGNALING	11	0	0	0	0	0	0	0.00431	0	0
71712	TYROSINE-PROTEIN KINASE LYN	SIGNALING	11	0	0	0	0	0	0	0.00431	0	0
198580	FLJ10900	UNKNOWN	11	0	0	0	0	0	0	0.00431	0	0
165980	CAS2	TRAFFIC	11	0	0	0	0	0	0	0.00431	0	0
6153	MYOSIN I HEAVY CHAIN	CYTOSKELETON	11	0	0	0	0	0	0.08493	0.42699	0	0
285691	SIMILAR TO HYPOTHETICAL PROTEIN	UNKNOWN	11	0	0	0	0	0	0.01147	0.05194	0	0
296012	FLJ10579	PROT MOD	11	0	0.00719	0	0	0	0	0.02607	0.0095	0
75904	SIMILAR TO ALG-2	METABOLISM	11	0	0.01194	0	0	0	0.01147	0.03469	0	0
266163	UDP-GLUCOSE 6-DEHYDROGENASE EUKARYOTIC TRANSLATION INITIATION FACTOR 3 SUBUNIT 6 INTERACTING PROTEIN	PROT SYN/FOLD	11	0	0.00719	0	0	0	0	0.01875	0	0
230447	SIMILAR TO DEVELOPMENT- AND DIFFERENTIATION-ENHANCING FACTOR 2; PYK2 C TERMINUS-ASSOCIATED PROTEIN	SIGNALING	11	0	0.01194	0	0	0	0	0.02737	0	0
60472	LONG-CHAIN FATTY ACID TRANSPORT PROTEIN	BIOSYNTHETIC CARGO	13	0	0.00719	0	0	0	0	0.00582	0.0095	0
75128	ALPHA-TOCOPHEROL TRANSFER PROTEIN	METABOLISM	13	0	0.03108	0	0	0	0	0.01444	0.019	0
223736	DIHYDROXYACETONE KINASE FAMILY PROTEIN	METABOLISM	13	0	0.09345	0	0	0	0	0.06938	0.05732	0
219015	SIMILAR TO KE4	UNKNOWN	13	0	0.00719	0	0	0	0	0	0.0095	0
62620	93455 270901	CYTOSKELETON	14	0	1.13519	0	0	0	0.02399	1.33444	0.02851	0.26175
10610	ADP-RIBOSYLATION FACTOR 5	GTPASE	14	0	0.02157	0	0	0	0	0.02838	0	0
258657	PROCOLLAGEN, TYPE VI, ALPHA 2	BIOSYNTHETIC CARGO	14	0	0.00719	0	0	0	0	0.00862	0	0

251407	VON WILLEBRAND FACTOR	BIOSYNTHETIC CARGO	14	0	0.00719	0	0	0	0.00862	0	0
119421	160782 SARI HOMOLOG	GTPASE	14	0	0.04604	0	0	0	0.05647	0	0
47311	TISSUE-TYPE TRANSGLUTAMINASE	SIGNALING	14	0	0.2339	0	0	0	0.26183	0	0.00705
309047	SIMILAR TO PROBABLE NOCTURNIN PROTEIN	TRANSCRIPTION	14	0	0.01972	0	0	0	0.02224	0	0
136355	60S RIBOSOMAL PROTEIN L34	PROT SYN/FOLD	14	0	0.16154	0	0.02647	0	0.19417	0	0
31436	TUBULIN ALPHA 4	CYTOSKELETON	14	0	0.54422	0.00837	0.00915	0.02295	0.46495	0.07647	0
268287	ATP-BINDING CASSETTE, SUB-FAMILY F (GCN20), MEMBER 2	BIOSYNTHETIC CARGO	14	0	0.01438	0	0	0	0.01013	0	0
246362	GLUTAREDOXIN	PROT SYN/FOLD	14	0	0.00719	0	0	0	0.00582	0	0
281550	SIMILAR TO APOPTOSIS INHIBITOR 5	SIGNALING	14	0	0.00719	0	0	0	0.00582	0	0
285775	PALLIDIN	TRAFFIC	14	0	0.00719	0	0	0	0.00582	0	0
204574	DEAD/H BOX POLYPEPTIDE 36 PROTEIN	UNKNOWN	14	0	0.01194	0	0	0	0.01013	0	0
4842	40S RIBOSOMAL PROTEIN S23	PROT SYN/FOLD	14	0.0133	0.10462	0	0.04808	0	0.0709	0	0
37218	215516 60S RIBOSOMAL PROTEIN L10A	PROT SYN/FOLD	14	0.03989	1.46905	0	0.42918	0.03598	0.95003	0	0.23405
65711	214593 60S RIBOSOMAL PROTEIN L36	PROT SYN/FOLD	14	0.0133	0.38976	0	0.09903	0.012	0.30685	0	0.0481
4837	40S RIBOSOMAL PROTEIN S16	PROT SYN/FOLD	14	0.13441	0.59489	0.17184	0.36688	0.26425	0.17671	0.02866	0.07322
72161	40S RIBOSOMAL PROTEIN S15A	PROT SYN/FOLD	14	0.06425	0.33966	0	0.18967	0.05789	0.08103	0	0.01634
1344	40S RIBOSOMAL PROTEIN S28	PROT SYN/FOLD	14	0.04728	0.2039	0.01242	0.09903	0.04798	0.02306	0	0.0481
4835	40S RIBOSOMAL PROTEIN S13	PROT SYN/FOLD	14	0.15882	0.6344	0.0128	0.22165	0.25121	0.21418	0	0.01766
144430	60S RIBOSOMAL PROTEIN P1	PROT SYN/FOLD	14	0.09747	0.25779	0.02953	0.07455	0.13082	0.07824	0.0095	0.05209
60848	40S RIBOSOMAL PROTEIN S18	PROT SYN/FOLD	14	0.20125	0.52112	0.09565	0.46745	0.12882	0.30382	0.06788	0.08027
4844	40S RIBOSOMAL PROTEIN S25	PROT SYN/FOLD	14	0.14031	0.26837	0	0.21095	0.07741	0.17087	0	0.05035
144419	60S RIBOSOMAL PROTEIN L2	PROT SYN/FOLD	14	0.27218	0.6605	0	0.25175	0.10535	0.40631	0	0.16504
4814	307863 60S RIBOSOMAL PROTEIN L27	PROT SYN/FOLD	14	0.06798	0.18288	0	0.13079	0	0.11444	0	0.02471
4817	60S RIBOSOMAL PROTEIN L30	PROT SYN/FOLD	14	0.14362	0.3658	0	0.19386	0.012	0.24692	0	0.02823
161453	SEC13 LIKE 1 PROTEIN	COAT	14	0	0.03167	0	0	0	0.00862	0	0
3616	S-AFADIN	CYTOSKELETON	14	0	0.01913	0	0	0	0.00582	0	0
225450	SIMILAR TO GTP BINDING PROTEIN	UNKNOWN	14	0	0.01913	0	0	0	0.00582	0	0
201969	COLLAGEN ALPHA1 TYPE VI- PRECURSOR	BIOSYNTHETIC CARGO	14	0	0.13035	0	0	0	0.06226	0	0
278143	CARBOHYDRATE (CHONDROITIN) SYNTHASE 2	PROT MOD	14	0	0.01194	0	0	0	0.00582	0	0
71631	60S RIBOSOMAL PROTEIN L18A	PROT SYN/FOLD	14	0.02659	0.60333	0	0.00816	0	0.24491	0	0
269702	SIMILAR TO HOMOPROTECATEHUATE CATABOLISM BIFUNCTIONAL ISOMERASE/DECARBOXYLASE	METABOLISM	14	0	0.01438	0	0	0	0.00582	0	0
14850	60S RIBOSOMAL PROTEIN L35A	PROT SYN/FOLD	14	0	0.03826	0	0	0	0.01444	0	0
307974	HYPOTHETICAL PROTEIN XP_343009	UNKNOWN	14	0	0.01194	0	0	0	0.00431	0	0
44273	PYRUVATE KINASE, ISOZYMES R/L	METABOLISM	14	0	0.03351	0	0	0	0.01444	0	0.00705
240310	NEUROBLASTOMA AMPLIFIED GENE, NAG	UNKNOWN	14	0	0.02389	0	0	0	0.00862	0	0.00531
74518	60S RIBOSOMAL PROTEIN L28	PROT SYN/FOLD	14	0.02695	0.29842	0	0.03628	0	0.13598	0	0
11445	293440 60S RIBOSOMAL PROTEIN L15	PROT SYN/FOLD	14	0	1.07951	0	0.33953	0	0.49401	0	0.05647
4826	60S RIBOSOMAL PROTEIN L8	PROT SYN/FOLD	14	0.03322	1.29667	0	0.25451	0.04694	0.53399	0.0095	0.08252
4820	60S RIBOSOMAL PROTEIN L37A	PROT SYN/FOLD	14	0	0.12744	0	0.01996	0	0.03772	0	0
4836	40S RIBOSOMAL PROTEIN S15	PROT SYN/FOLD	14	0.04356	0.44137	0	0.03628	0.13886	0.15217	0	0.01409
4847	40S RIBOSOMAL PROTEIN S29	PROT SYN/FOLD	14	0	0.08014	0	0.00816	0.012	0.0304	0	0
214842	ACIDIC RIBOSOMAL PROTEIN P1	PROT SYN/FOLD	14	0	0.04789	0	0.00816	0.012	0.02178	0	0
302124	VITRONECTIN	BIOSYNTHETIC CARGO	14	0.04728	0.12744	0	0.00816	0	0.058	0.0095	0.01235
37238	238486 60S RIBOSOMAL PROTEIN L10	PROT SYN/FOLD	14	0.23255	0.47498	0	0	0	0.30455	0	0.04594

8742	DNAJ HOMOLOG SUBFAMILY A MEMBER	PROT SYN/FOLD	14	0.14144	0.2099	0.02559	0.02448	0.01147	0.11724	0	0.03217
106718	60S RIBOSOMAL PROTEIN L13A	PROT SYN/FOLD	14	0.12334	0.65299	0	0.02812	0.05997	0.40445	0	0
98375	226038 60S RIBOSOMAL PROTEIN L21	PROT SYN/FOLD	14	0.0938	0.20802	0	0	0.04694	0.15072	0	0
4834	40S RIBOSOMAL PROTEIN S11	PROT SYN/FOLD	14	0.15179	0.46929	0	0.21051	0.11735	0.22311	0	0.01808
4849	40S RIBOSOMAL PROTEIN S4	PROT SYN/FOLD	14	0.48482	1.29122	0.01242	0.52115	0.22218	0.57419	0	0.0388
4843	40S RIBOSOMAL PROTEIN S24	PROT SYN/FOLD	14	0.0864	0.54534	0	0.17787	0.05446	0.11877	0	0.0287
250506	40S RIBOSOMAL PROTEIN S17	PROT SYN/FOLD	14	0.11	0.28411	0.00837	0.10101	0.05789	0.08686	0	0.01593
4854	LACTATE DEHYDROGENASE A-LIKE PROTEIN	PROT SYN/FOLD	14	0.30644	0.94338	0.03724	0.30965	0.08396	0.28703	0	0.12964
100993	193682 40S RIBOSOMAL PROTEIN S2	PROT SYN/FOLD	14	0.45492	1.71607	0.02483	0.41386	0.16272	0.47659	0	0.06177
23405	60S RIBOSOMAL PROTEIN P0	PROT SYN/FOLD	14	0.77085	2.888	0.02078	0.88275	0.48247	0.93536	0.02851	0.20403
4845	120488 40S RIBOSOMAL PROTEIN S27	PROT SYN/FOLD	14	0.01661	0.33437	0.05803	0.11998	0.04746	0.15925	0.0095	0.04279
37240	248463 60S RIBOSOMAL PROTEIN L18	PROT SYN/FOLD	14	0.23087	1.3078	0	0.40276	0.08188	0.53813	0	0.08599
4825	200139 60S RIBOSOMAL PROTEIN L7A	PROT SYN/FOLD	14	0.23372	2.34993	0.04966	0.86826	0.14134	0.88327	0	0.17296
161229	206311 POLY(A) BINDING PROTEIN	PROT SYN/FOLD	14	0.0565	0.46515	0	0.20392	0.012	0.19718	0	0.03748
75074	40S RIBOSOMAL PROTEIN S26	PROT SYN/FOLD	14	0.08381	0.2686	0.00837	0.06175	0.03546	0.13191	0	0.03043
142294	40S RIBOSOMAL PROTEIN S9	PROT SYN/FOLD	14	0.24081	0.98164	0.01242	0.18504	0.06989	0.3378	0	0.03922
144426	60S RIBOSOMAL PROTEIN L3	PROT SYN/FOLD	14	0.50043	1.77757	0	0.27513	0.1014	0.71693	0	0.03176
273222	60S RIBOSOMAL PROTEIN L27A	PROT SYN/FOLD	14	0.07347	0.31155	0	0.03992	0	0.15345	0	0.01593
37239	60S RIBOSOMAL PROTEIN L13	PROT SYN/FOLD	14	0.54072	1.09786	0	0.10917	0.23573	0.57743	0	0.0583
43519	60S RIBOSOMAL PROTEIN L14	PROT SYN/FOLD	14	0.10709	0.29485	0	0.01996	0.04694	0.11728	0	0
4812	60S RIBOSOMAL PROTEIN L24	PROT SYN/FOLD	14	0.24114	0.55009	0	0.09451	0.09336	0.21727	0	0.01634
74523	40S RIBOSOMAL PROTEIN S6	PROT SYN/FOLD	14	0.27767	0.99502	0	0.09704	0.119	0.24321	0	0.04453
85424	60S RIBOSOMAL PROTEIN L4	PROT SYN/FOLD	14	0.49558	3.5586	0	0.1245	0.12383	0.80005	0	0.08027
11402	TRYPTOPHAN 2,3-DIOXYGENASE SIMILAR TO XYLULOXINASE HOMOLOG;	METABOLISM	15	0	0.00719	0	0	0	0	0	0
	XYLULOXINASE (H. INFLUENZAE)										
229118	HOMOLOG	METABOLISM	15	0	0.01438	0	0	0	0	0	0
	SIMILAR TO METHYLCROTONOYL-COENZYME A CARBOXYLASE 2 (BETA); NON-BIOTIN CONTAINING SUBUNIT OF 3-METHYLCROTONYL-COA										
191730	CARBOXYLASE; BIOTIN CARBOXYLASE	METABOLISM	15	0	0.01913	0	0	0	0	0	0
51504	KYNURENINE/ALPHA-AMINOADIPATE AMINOTRANSFERASE	METABOLISM	15	0	0.00719	0	0	0	0	0	0
233230	SIMILAR TO BULLOUS PEMPHIGOID ANTIGEN 1-B	CYTOSKELETON	15	0	0.01194	0	0	0	0	0	0
44653	SODIUM/CALCIUM EXCHANGER 1 PRECURSOR	CALCIUM TRANS/BIND	15	0	0.01194	0	0	0	0	0	0
	SIMILAR TO ALPHA 3 TYPE VI COLLAGEN ISOFORM 1 PRECURSOR; COLLAGEN VI, ALPHA-3 POLYPEPTIDE										
307227	FICOLIN 1 PRECURSOR	BIO SYNTHETIC CARGO	15	0	0.02632	0	0	0	0	0	0
75919	3277 MYELIN BASIC PROTEIN S	BIO SYNTHETIC CARGO	15	0	0.01194	0	0	0	0	0	0
238438	SIMILAR TO MAP KINASE KINASE 3B	SIGNALING	15	0	0.00719	0	0	0	0	0	0
199223	READING FRAME 27	UNKNOWN	15	0	0.01194	0	0	0	0	0	0
230313	PUTATIVE RNA BINDING PROTEIN, PARTNER TO NOB1	UNKNOWN	15	0	0.00719	0	0	0	0	0	0

267292	SIMILAR TO ALL-1 PROTEIN +GTE FORM 1	UNKNOWN	15	0	0.01194	0	0	0	0	0	0	0	0	0
18015	MOUSE (FRAGMENT) GLYCEROL KINASE	SIGNALING	15	0	0.00719	0	0	0	0	0	0	0	0	0
246387	SIMILAR TO RIKEN CDNA 1700027N10	UNKNOWN	15	0	0.00719	0	0	0	0	0	0	0	0	0
272734	SIMILAR TO RNA BINDING PROTEINS	UNKNOWN	15	0	0.00719	0	0	0	0	0	0	0	0	0
269534	SIMILAR TO RIKEN CDNA 2410002O22 GENE	UNKNOWN	15	0	0.01438	0	0	0	0	0	0	0	0	0
226986	SPLICING FACTOR, ARGININE/SERINE-RICH 7, 35 kDa	PROT SYN/FOLD	15	0	0.00719	0	0	0	0	0	0	0	0	0
250916	SIMILAR TO RIKEN CDNA 2610207116	UNKNOWN	15	0	0.00719	0	0	0	0	0	0	0	0	0
11062	DNAJ HOMOLOG SUBFAMILY A MEMBER 2	PROT SYN/FOLD	15	0	0.06042	0	0	0	0	0.01013	0	0	0	0
276202	PRE-MRNA SPLICING FACTOR RNA HELICASE (DEAH BOX PROTEIN 15)	PROT SYN/FOLD	15	0	0.02875	0	0	0	0	0.00431	0	0	0	0
157870 306730	ALG-2 INTERACTING PROTEIN 1	SIGNALING	15	0	0.03826	0	0	0	0	0.00582	0	0	0	0
269681	SPHINGOSINE-1-PHOSPHATE LYASE 1	PROT MOD	16	0	0.12662	0.08438	0.03463	0.02399	0.02027	0.03394	0.01409			
278725	40S RIBOSOMAL PROTEIN S5	PROT SYN/FOLD	16	0.08014	0.4532	0.18743	0.05359	0.07145	0.10588	0.07738	0.00705			
254063	HERC2	TRAFFIC	16	0	0.03945	0.02559	0	0	0.00431	0	0	0	0	0
130291	DAD1 (DEFENDER AGAINST CELL DEATH)	PROT MOD	16	0	0.09327	0.11277	0	0.02399	0.02457	0.03394	0	0	0	0
	RECEPTOR-TRANSPORTING PROTEIN 4 (28 KDA INTERFERON RESPONSIVE PROTEIN)	UNKNOWN	16	0	0.01194	0.02915	0	0	0.00862	0	0	0	0	0
246358														
28289 51474 146667	GLUTATHIONE S-TRANSFERASE YA-1	DETOXIFICATION	17	0.43192	0.22173	0	0.26862	0.43186	0.24528	0	0.42216			
11560 84144	ALCOHOL DEHYDROGENASE 1	METABOLISM	17	0.30984	0.21116	0	0.08458	0.45291	0.20002	0.0095	0.35376			
224451	LACTATE DEHYDROGENASE A-LIKE PROTEIN	METABOLISM	17	0.01053	0	0	0	0.02395	0.00631	0	0.01345			
43660	SORBITOL DEHYDROGENASE	METABOLISM	17	0.13736	0.0407	0	0.01731	0.15385	0	0	0.13766			
78049	GLUTATHIONE S-TRANSFERASE ALPHA PEPTIDYL-PROLYL CIS-TRANS	DETOXIFICATION	17	0.46175	0.05751	0	0	0.54966	0.07285	0	0.29415			
45089	ISOMERASE A	PROT SYN/FOLD	17	0.37223	0.03594	0	0.07091	0.39255	0.03748	0	0.15104			
45108	ARGINOSUCCINATE SYNTHASE	METABOLISM	18	0.44064	1.02129	0.05436	0.16	1.36254	1.04532	0.01916	0.42102			
156654	SIMILAR TO GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE (4)	METABOLISM	18	0.0133	0.01438	0	0	0.02295	0.02027	0	0.01235			
68722 236971 311124	HEAT-SHOCK COGNATE 70KD PROTEIN (44KD ATPASE N-TERMINAL FRAGMENT)	PROT SYN/FOLD	18	0.63859	0.77696	0.19433	0.55001	0.85783	1.02535	0.19894	0.73231			
201232	ACIDIC RIBOSOMAL PROTEIN P2, CYTOSOLIC	PROT SYN/FOLD	18	0.05983	0.06104	0	0	0.08023	0.07592	0	0	0	0	0
61026	APOBEC-1 COMPLEMENTATION FACTOR LONG ISOFORM	PROT SYN/FOLD	18	0.07129	0.12862	0	0	0.08032	0.14082	0	0	0	0	0
63770 72759	CYTCHROME P450 2B3	DETOXIFICATION	19	0.10936	0.22904	0.29423	0.72923	0.53284	0.30135	0.31224	0.77439			
208522	SIMILAR TO ALPHA GLUCOSIDASE II, BETA SUBUNIT	PROT MOD	19	0	0	0.15504	0.1363	0.23729	0.04612	0.1347	0.21822			
140831	GTP CYCLOHYDROLASE I FEEDBACK REGULATORY PROTEIN	SIGNALING	19	0	0	0	0.00816	0.012	0.00582	0	0.00531			
37177	ADAPTOR-RELATED PROTEIN COMPLEX 2 ALPHA 2 SUBUNIT	COAT	20	0.01035	0.01913	0	0	0.35503	0.29402	0	0.23456			
126513	CLATHRIN ADAPTIN-1, BETA 1	COAT	20	0	0	0	0	0.20336	0.14466	0	0.12358			

[illegible]

106720	40S RIBOSOMAL PROTEIN S30	PROT SYN/FOLD	26	0.07347	0.10219	0	0.01996	0	0	0	0
4853	40S RIBOSOMAL PROTEIN S7	PROT SYN/FOLD	26	0.32095	0.62721	0	0.23433	0.09284	0.10586	0	0.04942
4809	60S RIBOSOMAL PROTEIN L19	PROT SYN/FOLD	26	0.19095	0.20272	0	0	0.03598	0.15044	0	0
51618	40S RIBOSOMAL PROTEIN S3A	PROT SYN/FOLD	26	0.816	0.89777	0	0.19971	0.31054	0.21751	0	0.03442
144431	60S RIBOSOMAL PROTEIN P2	PROT SYN/FOLD	26	0.38328	0.34471	0	0.07024	0.2034	0.16908	0	0.04105
139425	60S RIBOSOMAL PROTEIN L17	PROT SYN/FOLD	26	0.29763	0.2105	0	0	0.08396	0.12868	0	0
42185	60S RIBOSOMAL PROTEIN L6	PROT SYN/FOLD	26	1.09756	1.04123	0	0.05712	0.39624	0.33359	0	0.01235
154516	60S RIBOSOMAL PROTEIN L7	PROT SYN/FOLD	26	0.87634	0.7941	0	0	0.23417	0.2766	0	0
	GCNT GENERAL CONTROL OF AMINO-ACID SYNTHESIS 1-LIKE 1	PROT SYN/FOLD	26	0.01035	0.00719	0	0	0	0	0	0
261456	ACYLTRANSFERASE	PROT MOD	26	0.11154	0.05983	0	0	0.01147	0	0	0.00531
111533	MULTIFUNCTIONAL PROTEIN ADE2	METABOLISM	26	0.0133	0.00719	0	0	0	0	0	0
222133	PROBABLE UPF0334 KINASE-LIKE PROTEIN	UNKNOWN	26	0.03399	0.01438	0	0	0	0	0	0
312697	SIMILAR TO KIAA0372 GENE PRODUCT	UNKNOWN	26	0.04433	0.03826	0	0.00915	0	0.00582	0	0.00531
318709	SIMILAR TO ESTROGEN-RESPONSIVE FINGER PROTEIN	TRANSCRIPTION	27	0.01035	0	0	0	0	0.01013	0	0
269562	SIMILAR TO B AGGRESSIVE LYMPHOMA	UNKNOWN	27	0.0133	0.00719	0	0	0	0.01165	0	0
198258	SIMILAR TO RIKEN CDNA 2810405J04	UNKNOWN	27	0.05686	0.02389	0	0	0.01147	0.04355	0	0
37797	ARGINASE 1	METABOLISM	28	2.6872	1.24553	0.19957	0.58819	2.4345	0.93768	0.03801	0.66908
116234	FRUCTOSE-BISPHOSPHATE ALDOLASE B	METABOLISM	28	2.9832	0.73903	0	0.82737	2.1237	0.35042	0.019	0.871
201012	UDP-GLUCURONATE DECARBOXYLASE 1	METABOLISM	28	0.02364	0.01194	0.00837	0.00816	0.02347	0	0	0
307749	DEOXYRIBOSE-PHOSPHATE ALDOLASE-LIKE	METABOLISM	28	0.02364	0.01438	0	0	0.02295	0.01444	0	0
240056	DEAD BOX PROTEIN 1	PROT SYN/FOLD	28	0.13926	0.09868	0	0	0.13822	0.10889	0	0.01766
4807	60S RIBOSOMAL PROTEIN L23	PROT SYN/FOLD	28	0.26995	0.10831	0	0	0.1978	0.10714	0	0
62524	CYSTATHIONINE GAMMA-LYASE	METABOLISM	28	1.75787	0.23622	0	0.17743	0.95973	0.19246	0.02866	0.29301
51518 237201	286597 L-LACTATE DEHYDROGENASE	METABOLISM	28	1.39851	0.07955	0	0.10608	0.62812	0.10539	0	0.39477
38668	TRANSKETOLASE	METABOLISM	28	0.9454	0.11306	0	0.03363	0.50518	0.05216	0	0.2879
308317	COLLAGEN TYPE XIV	BIO SYNTHETIC CARGO	28	0.06798	0	0	0	0.03442	0	0	0
	NASCENT POLYPEPTIDE-ASSOCIATED COMPLEX ALPHA POLYPEPTIDE	PROT SYN/FOLD	28	0.25303	0	0	0	0.13582	0	0	0
289953	FK506-BINDING PROTEIN 3	PROT SYN/FOLD	28	0.12152	0	0	0	0.07093	0	0	0
	RIBOSOME-BINDING PROTEIN 1 (RIBOSOME RECEPTOR PROTEIN)	PROT SYN/FOLD	28	1.64103	0.01194	0	0	0.75478	0.01165	0.04766	0
244957	(MRRP) P180	PROT SYN/FOLD	28	0.41806	0.02157	0	0	0.19871	0.04939	0	0
144423	60S RIBOSOMAL PROTEIN L23A	PROT SYN/FOLD	28	0.19204	0.01438	0	0	0.0894	0.01013	0	0
4818	60S RIBOSOMAL PROTEIN L31	PROT SYN/FOLD	28	0.10822	0.01438	0	0	0.04746	0	0	0
103229	60S RIBOSOMAL PROTEIN L35	PROT SYN/FOLD	28	0.10822	0.01438	0	0	0.04746	0	0	0
	DEVELOPMENTALLY REGULATED GTP-BINDING PROTEIN 1	GTPASE	28	0.29541	0.01438	0	0	0.10192	0.02457	0	0
71226	BINDING PROTEIN 1	PROT SYN/FOLD	28	0.32059	0.00719	0	0	0.1163	0.00582	0	0.00705
4392	60S RIBOSOMAL PROTEIN L22	PROT SYN/FOLD	28	0.32059	0.00719	0	0	0.1163	0.00582	0	0.00705
	SIMILAR TO 60S RIBOSOMAL PROTEIN L29	PROT SYN/FOLD	28	0.03322	0	0	0	0.01147	0	0	0
233078 237486	L29	PROT SYN/FOLD	28	1.4094	0	0	0.12019	0.44709	0.00582	0	0.0194
37237	60S RIBOSOMAL PROTEIN L5	PROT SYN/FOLD	28	1.4094	0	0	0.12019	0.44709	0.00582	0	0.0194
307560	BRAIN ZN-FINGER PROTEIN	TRANSCRIPTION	28	0.05355	0	0	0	0.01147	0	0	0

140182	223872	ELONGATION FACTOR 1-ALPHA 1 (EF-1-ALPHA-1)	PROT SYN/FOLD	28	2.9893	1.2522	0.0128	0.24017	1.08632	0.7298	0	0.14747
	2378	60S RIBOSOMAL PROTEIN L11	PROT SYN/FOLD	28	0.43621	0.06274	0	0.02547	0.20519	0.09266	0	0.01103
	26167	VIGILIN	PROT SYN/FOLD	28	2.39943	0.59699	0	0.06175	0.82396	0.23082	0	0
	4819	60S RIBOSOMAL PROTEIN L32	PROT SYN/FOLD	28	0.14114	0.03108	0	0	0.06645	0.00862	0	0
	54494	P55	UNKNOWN	28	0.12742	0.0407	0	0	0.06541	0.01165	0	0
	42770	GENTAURIN-ALPHA2 PROTEIN	GTPASE	28	0.01035	0	0	0	0.01147	0	0	0
	23398	DIHYDROPTERIDINE REDUCTASE	METABOLISM	28	0.24296	0	0	0.00816	0.24461	0	0	0.01766
		VIGILIN (HIGH DENSITY LIPOPROTEIN-BINDING PROTEIN) (HDL-BINDING PROTEIN)	METABOLISM	28	0.07175	0	0	0	0.0722	0.00862	0	0
	62122	C-1-TETRAHYDROFOLATE SYNTHASE, BIPHENYL HYDROLASE-LIKE (SERINE HYDROLASE, BREAST EPITHELIAL MUCIN-ASSOCIATED ANTIGEN)	METABOLISM	28	1.07594	0.07111	0	0.03562	0.96758	0.04915	0	0.03931
	204593	60S RIBOSOMAL PROTEIN L26	DETOXIFICATION	28	0.0133	0	0	0	0.01147	0	0	0
	37247	LUPUS LA PROTEIN HOMOLOG	PROT SYN/FOLD	28	0.30062	0.00719	0	0	0.2566	0.00582	0	0.00705
		STRESS-INDUCED-PHOSPHOPROTEIN 1 (STI1)	TRANSCRIPTION	28	0.05355	0	0	0	0.04246	0	0	0
	82685		SIGNALING	28	0.01661	0	0	0	0.01147	0	0	0
	4821	60S RIBOSOMAL PROTEIN L38	PROT SYN/FOLD	28	0.14403	0.02632	0	0	0.11391	0.00582	0	0
	51432	ELONGATION FACTOR 2	PROT SYN/FOLD	28	1.12774	0.33739	0	0	1.12084	0.19249	0	0.01593
	270299	SIMILAR TO RIKEN CDNA 1810045K17	UNKNOWN	28	0.01035	0	0	0	0.012	0.00431	0	0
	23674	FATTY ACID BINDING PROTEIN FABP-1	METABOLISM	28	0.01661	0	0	0	0	0.00582	0	0
	160533	60S RIBOSOMAL PROTEIN L9	PROT SYN/FOLD	28	0.40881	0.09393	0	0.00915	0.08396	0.10739	0	0
		PROBABLE RNA-DEPENDENT HELICASE P68 (DEAD-BOX PROTEIN P68) (DEAD-BOX PROTEIN 5)										
	161883		PROT SYN/FOLD	28	0.28023	0.04129	0	0	0.04877	0.09698	0	0
	103	EUKARYOTIC TRANSLATION INITIATION FACTOR 2 SUBUNIT 1	PROT SYN/FOLD	28	0.16508	0.01972	0	0	0.02295	0.02027	0	0
	62757	PLASMA GLUTAMATE CARBOXYPEPTIDASE	BIOSYNTHETIC CARGO	28	0.0432	0	0	0	0	0	0	0.00531
	1678	NADP-DEPENDENT LEUKOTRIENE B4 12-HYDROXYDEHYDROGENASE	DETOXIFICATION	28	0.11118	0	0	0	0	0	0	0.03043
		PROTEIN KINASE C AND CASEIN KINASE SUBSTRATE IN NEURONS 2 PROTEIN										
	74255		SIGNALING	28	0.05763	0	0	0	0	0	0	0.01235
	217607	UNKNOWN ZINC FINGER PROTEIN	UNKNOWN	28	0.01661	0	0	0	0	0	0	0.00705
	23682	EUKARYOTIC TRANSLATION INITIATION FACTOR 5A	PROT SYN/FOLD	28	0.13482	0	0	0.01731	0.02295	0.00431	0	0.01766
		EUKARYOTIC PEPTIDE CHAIN RELEASE FACTOR SUBUNIT 1 (ERF1)										
	41501	EUKARYOTIC RELEASE FACTOR 1) (TB3-1) (C11 PROTEIN)	PROT SYN/FOLD	28	0.09675	0.01972	0	0	0	0	0	0
		COMPLEMENT INHIBITORY FACTOR H SIMILAR TO PHENYLALANINE-TRNA	BIOSYNTHETIC CARGO	28	0.19386	0	0	0	0.012	0	0	0
	312741	SYNTHETASE-LIKE SIMILAR TO PHENYLALANYL-TRNA	PROT SYN/FOLD	28	0.47787	0.00719	0	0	0.04694	0.00431	0	0.00531
		SYNTHETASE BETA CHAIN (PHENYLALANINE--TRNA LIGASE BETA CHAIN) (PHERS)										
	254493		PROT SYN/FOLD	28	0.42777	0.01194	0	0.00816	0.05997	0	0	0

267441	SIMILAR TO EUKARYOTIC TRANSLATION INITIATION FACTOR 2, SUBUNIT 3, STRUCTURAL GENE X-LINKED	PROT SYN/FOLD	28	0.0432	0	0	0	0	0	0	0	0	0	0
227484	SHWACHMAN-BODIAN DIAMOND SYNDROME PROTEIN HOMOLOG	UNKNOWN	28	0.02069	0	0	0	0	0	0	0	0	0	0
84170	APOLIPOPROTEIN C-III	BIO SYNTHETIC CARGO	29	0	0	0	0	0	0	0.01147	0	0.0095	0	0
3729	CYTOCHROME P450 2C12	DETOXIFICATION	29	0	0	0.05429	0	0.09751	0.05028	0.1715	0	0	0	0
3890	CYTOCHROME B5	DETOXIFICATION	29	0.22602	0.03886	0.46485	0	0.63624	0.15039	0.67005	0	0	0	0
126576	CYTOCHROME P450 2D1	DETOXIFICATION	29	0.36842	0.06211	0.47598	0.01996	0.70563	0.32203	1.08215	0.05642	0	0	0
87425	CYTOCHROME P450 3A2	DETOXIFICATION	29	0.09457	0.04129	0.40253	0.01867	0.46333	0.23534	0.69999	0.12044	0	0	0
63788	CYTOCHROME P450 2D2	DETOXIFICATION	29	0.16335	0.11357	0.44453	0.14092	0.9345	0.41632	0.66105	0.28414	0	0	0
103927	CYTOCHROME P450 2D3	DETOXIFICATION	29	0.10534	0.03803	0.1294	0.03089	0.40899	0.15137	0.27746	0.15591	0	0	0
63790	CYTOCHROME P450 2D5	DETOXIFICATION	29	0.15896	0.10748	0.27512	0.01996	0.43528	0.17167	0.33635	0.14169	0	0	0
140838	TAPASIN	PROT SYN/FOLD	29	0	0.01972	0.06754	0	0.07741	0.00862	0.05732	0	0	0	0
240940	RAB20	GTPASE	29	0	0	0.02559	0	0.04246	0.02607	0.01916	0	0	0	0
44475	LONG-CHAIN-FATTY-ACID--COA LIGASE 6	PROT MOD	29	0	0	0.0186	0.00915	0.01273	0.01301	0.01011	0	0	0	0
78151	ALDEHYDE DEHYDROGENASE FAMILY 3 MEMBER A2	DETOXIFICATION	30	0.24671	0.28923	0.8524	0.14148	0.82056	0.35667	0.95319	0.19821	0	0	0
33163	CYTOCHROME P450 2C22	DETOXIFICATION	30	0.07016	0.10879	0.37731	0.01731	0.24444	0.21208	0.36574	0.06708	0	0	0
45873	CYTOCHROME P450 2C7	DETOXIFICATION	30	0.10709	0.68503	0.97296	0.07286	0.62349	0.41716	0.95319	0.03719	0	0	0
5958	ARYLACETAMIDE DEACETYLASE	DETOXIFICATION	30	0	0	0.26131	0	0.11987	0.03167	0.2504	0	0	0	0
126566	CYTOCHROME P450 2A1	DETOXIFICATION	30	0.04138	0.06215	0.87428	0	0.39469	0.16035	0.66595	0	0	0	0
31602	UDP-GLUCURONOSYLTRANSFERASE 2B3	DETOXIFICATION	30	0.15196	0.14503	0.68331	0.06329	0.38876	0.14087	0.71598	0.06789	0	0	0
19325	PARAOXONASE 1	BIO SYNTHETIC CARGO	30	0.20828	0.11955	1.29253	0.10586	0.73524	0.2575	1.12798	0.17483	0	0	0
29993	FATTY-ACID AMIDE HYDROLASE MICROSO MAL GLUTATHIONE S-	PROT MOD	30	0.03322	0.02389	0.38179	0.01731	0.21971	0.11727	0.33094	0.03002	0	0	0
28295	TRANSFERASE 1	DETOXIFICATION	30	0.19204	0.25102	2.05617	0.16574	0.45252	0.28385	1.64103	0.1109	0	0	0
31600	UDP-GLUCURONOSYLTRANSFERASE 2B1	DETOXIFICATION	30	0.02159	0.02752	0.39525	0.01823	0.0695	0.03383	0.33637	0.03301	0	0	0
21524	CYTOCHROME P450 4A3	DETOXIFICATION	30	0	0.22084	0.92237	0.03661	0.33963	0.24332	0.85238	0.08648	0	0	0
43597	UDP-GLUCURONOSYLTRANSFERASE 1A1	DETOXIFICATION	30	0.24688	0.21277	1.40817	0.21362	0.45272	0.40728	1.30437	0.18356	0	0	0
31603	UDP-GLUCURONOSYLTRANSFERASE 2B5	DETOXIFICATION	30	0.17238	0.12235	1.19163	0.16551	0.38995	0.16993	1.02085	0.07426	0	0	0
78055	UDP-GLUCURONOSYLTRANSFERASE 2B2	DETOXIFICATION	30	0.10918	0.14734	0.95024	0.10965	0.37563	0.20689	0.98598	0.08609	0	0	0
69775	CALNEXIN	PROT SYN/FOLD	30	0.08163	0.10462	1.01801	0.1009	0.43405	0.1821	0.97866	0.11344	0	0	0
3732	CYTOCHROME P450 51A1	DETOXIFICATION	30	0.03322	0.01194	0.11171	0	0.06645	0.04612	0.15824	0	0	0	0
17081	EPOXIDE HYDROLASE	DETOXIFICATION	30	0.27	0.10706	1.15213	0	0.96675	0.42048	1.50848	0	0	0	0
63778	231660	CYTOCHROME P450 2C6	30	0.06189	0.20746	0.53069	0.0276	0.32404	0.31329	0.72001	0.06514	0	0	0
63780	126560	CYTOCHROME P450 2C11	30	0.49283	0.57735	1.90807	0.13552	1.54091	1.11891	2.7264	0.20629	0	0	0
63782	84196	CYTOCHROME P450 2C13	30	0.39071	0.3941	1.43563	0.04488	1.07657	0.70764	2.07423	0.05502	0	0	0
85756	LONG-CHAIN-FATTY-ACID--COA LIGASE, LIVER ISOZYME	METABOLISM	30	0.97214	0.87841	2.6116	0.20037	1.96047	1.2432	3.4502	0.38101	0	0	0
3727	CYTOCHROME P450 2A2	DETOXIFICATION	30	0.04138	0.05799	0.72708	0	0.67826	0.34586	1.23296	0	0	0	0
274611	PROGESTERONE RECEPTOR	DETOXIFICATION	30	0	0.01254	0.12545	0	0.08992	0.05101	0.18834	0.00705	0	0	0
267475	MEMBRANE COMPONENT 2	DETOXIFICATION	30	0	0.05496	0.25153	0	0.20427	0.1829	0.38461	0	0	0	0
	SIMILAR TO ARL6IP2	UNKNOWN	30	0	0.05496	0.25153	0	0.20427	0.1829	0.38461	0	0	0	0

102628	OXIDATIVE 17 BETA HYDROXYSTEROID DEHYDROGENASE TYPE 6	DETOXIFICATION	30	0	0.01078	0.12589	0.00816	0.04979	0.06241	0.1568	0.02818
187298	FLAVIN-CONTAINING MONOOXYGENASE 5	DETOXIFICATION	30	0.02069	0.03826	0.4828	0.03264	0.29116	0.27403	0.70669	0.06659
318845	R. VAMP A	TETH/DOCK/FUS	30	0	0.1775	0	0	0.0944	0.09313	0.23915	0
41516	R. SEC22	TETH/DOCK/FUS	30	0.01035	0.02157	0.19514	0	0.09388	0.13172	0.29338	0.00705
35165 105752	RETINOL DEHYDROGENASE TYPE I	DETOXIFICATION	30	0.11966	0	0.81743	0.22014	0.5685	0.37165	1.35586	0.23463
21526	CYTOCHROME P450 2E1	DETOXIFICATION	30	0.07347	0.02632	0.56411	0.01731	0.32222	0.18639	1.12302	0.09228
339248	DIMETHYLANILINE MONOOXYGENASE [N OXIDE FORMING] 1	DETOXIFICATION	30	0.09675	0.05496	0.49166	0.04279	0.33265	0.20945	1.02061	0.19239
246480	FLAVIN-CONTAINING MONOOXYGENASE 3	DETOXIFICATION	30	0.08677	0.1243	0.49993	0.1385	0.27067	0.30362	0.98215	0.24345
708	ESTRADIOL 17 BETA-DEHYDROGENASE 7	DETOXIFICATION	30	0	0	0.04599	0	0.02399	0.00582	0.06682	0.01062
44210 78074	NADPH-CYTOCHROME P450 REDUCTASE	DETOXIFICATION	30	0.06798	0.11959	1.22903	0.02448	0.74997	0.31531	2.04117	0.0869
3937	3 BETA-HYDROXYSTEROID DEHYDROGENASE TYPE III	DETOXIFICATION	30	0.02659	0.09268	0.68204	0	0.47547	0.08513	1.03929	0
19913	MEMBRANE ASSOCIATED PROGESTERONE RECEPTOR COMPONENT 1	DETOXIFICATION	30	0.14067	0.11181	0.85254	0.04378	0.34808	0.22378	1.10289	0.03574
111003	RAB7	GTPASE	30	0.02659	0.0341	0.24564	0.01831	0.11787	0.06359	0.32189	0.05872
69488 123616	NADH-CYTOCHROME B5 REDUCTASE ALL-TRANS-13,14-DIHYDRORETINOL SATURASE	DETOXIFICATION	30	0.05023	0.01438	0.47664	0	0.19871	0.0955	0.73641	0
27636	INTEGRAL MEMBRANE PROTEIN, TMP21-1	DETOXIFICATION	30	0.01035	0.06934	0.39344	0	0.16584	0.13531	0.60398	0
60418	I (P23) DELTA 1	TRAFFIC	30	0.01035	0.00719	0.20888	0	0.08888	0.09419	0.31707	0
137142	DBR3 PROTEIN	UNKNOWN	30	0	0.00719	0.09593	0	0.02399	0.03016	0.12535	0
236838	SIMILAR TO RIKEN CDNA 1500009M05	UNKNOWN	30	0	0	0.02915	0	0.012	0	0.03816	0
166454	SIMILAR TO RIKEN CDNA 2010107G23	UNKNOWN	30	0	0	0.04966	0	0.012	0	0.0626	0
78145	RAB2A	GTPASE	30	0.01035	0	0.11633	0.01831	0.012	0.05649	0.17784	0.06525
80376	RETINOL DEHYDROGENASE TYPE II	DETOXIFICATION	30	0	0.02516	0.3003	0.08013	0.12229	0.15043	0.35582	0.12515
308340	ALCOHOL DEHYDROGENASE PAN1B	METABOLISM	30	0.03399	0.02632	0.18384	0.0443	0.05789	0.0892	0.25084	0.08078
72763 78212	CYTOCHROME P450 2C23	DETOXIFICATION	30	0.06094	0.16505	0.92047	0.21624	0.2592	0.36077	0.81525	0.25768
80303 127236 221298	UDP-GLUCURONOSYLTRANSFERASE 2B12	DETOXIFICATION	30	0.11118	0.17252	0.82567	0.23294	0.34377	0.1717	0.82193	0.20998
198793	SIMILAR TO MICROSMAL TRIGLYCERIDE TRANSFER PROTEIN	PROT SYN/FOLD	30	0.1703	0.16873	2.02033	0.53614	0.55179	0.32977	2.1528	0.83879
228858	SIMILAR TO PUTATIVE NAD(P)H STEROID DEHYDROGENASE	UNKNOWN	30	0.05468	0.05323	0.77858	0.19275	0.27172	0.15625	0.74666	0.26869
77835	ERGIC-53 PROTEIN	TRAFFIC	30	0.0133	0.01972	0.25535	0.05194	0.10036	0.05066	0.23968	0.18206
3724	CYTOCHROME P450 1A2	DETOXIFICATION	30	0.02991	0.08965	0.23554	0.09571	0.10483	0.17797	0.31088	0.17572
60485	LONG-CHAIN-FATTY-ACID-COA LIGASE 5	METABOLISM	30	0.07805	0.22276	0.68197	0.27302	0.37947	0.45479	0.80412	0.27532
249650	SPFH DOMAIN FAMILY, MEMBER 2	UNKNOWN	30	0	0.01797	0.14564	0.03264	0.09492	0.11684	0.16743	0.05382
63760	CYTOCHROME P450 4A2	DETOXIFICATION	30	0.30898	0.73196	1.74417	0.04896	0.51952	0.62789	1.68765	0.0424
30001	BILE ACID COA LIGASE	DETOXIFICATION	30	0.03989	0.51844	1.42344	0.09274	0.30812	0.69827	1.61933	0.20024
84180	SARCOPLASMIC CA2+/MG2+ ATPASE	CALCIUM TRANS/BIND	30	0	0.34485	0.76216	0.00816	0.04746	0.25431	0.93987	0.06361

161253	MG87 PROTEIN	UNKNOWN	30	0	0.00719	0.02078	0	0	0.00582	0.019	0
171802	DAPIT PROTEIN	UNKNOWN	30	0	0.00719	0.0332	0	0	0.02027	0.0436	0
134595	CYTOCHROME P450 4F1	DETOXIFICATION	30	0	0	0.16525	0	0.02399	0.05519	0.16974	0
80281	CYTOCHROME P450 4F4	DETOXIFICATION	30	0	0	0.15235	0	0.02399	0.0459	0.12695	0
44648	RAB10	GTPASE	30	0	0	0.11037	0.00816	0.01439	0.04454	0.10492	0.00939
244225	SIMILAR TO RIKEN CDNA 0610006F02 DERLIN-1 (DEGRADATION IN ENDOPLASMIC RETICULUM PROTEIN 1) (DER1-LIKE PROTEIN 1)	UNKNOWN	30	0.0133	0.06101	0.47001	0.00915	0.09492	0.14893	0.38042	0.04064
119910	SIMILAR TO PUTATIVE PROTEIN, WITH AT LEAST 6 TRANSMEMBRANE DOMAINS, OF ANCIENT ORIGIN (58.5 KD) (3N884)	PROT SYN/FOLD	30	0	0	0.06235	0	0	0.02027	0.0531	0
269355		UNKNOWN	30	0	0	0.08341	0	0	0.02457	0.05701	0
217594	UDP-GLUCURONOSYLTRANSFERASE GTNA1	DETOXIFICATION	30	0.0152	0.02219	0.34943	0.01714	0	0.03148	0.29179	0.03868
34567	RAB14	GTPASE	30	0	0.00719	0.06522	0	0	0.00517	0.06147	0
161231	CYTOCHROME P450 2T1	DETOXIFICATION	30	0	0	0.1347	0	0	0.02737	0.132	0
51420	CYTOCHROME P450 4A1	DETOXIFICATION	30	0	0	0.08315	0	0	0.01178	0.09021	0
9067	7-DEHYDROCHOLESTEROL REDUCTASE IODOTYROSINE DEHALOGENASE	DETOXIFICATION	30	0	0	0.14691	0	0	0.01596	0.12489	0
258458	PROTEIN P24 GAMMA 3	UNKNOWN	30	0	0	0.15078	0	0	0.02027	0.13576	0
228279	P24	TRAFFIC	30	0	0	0.19667	0	0.01147	0.03319	0.16427	0.00531
263674	DKFZP586A0522 PROTEIN P24 ALPHA 2	UNKNOWN	30	0.0133	0.00719	0.14991	0	0.012	0.02609	0.14537	0.00531
170045	285748	TRAFFIC	30	0	0	0.34472	0	0.05841	0.00431	0.31178	0
278444	MGC18837	UNKNOWN	30	0	0.01913	0.54948	0	0.11339	0.08231	0.5637	0
208161	SIMILAR TO RIKEN CDNA 5730469M10 24-DEHYDROCHOLESTEROL REDUCTASE	UNKNOWN	30	0	0	0.35166	0.00915	0.04798	0.03167	0.38073	0.00531
290771	ALPHA-1,3-MANNOSYLTRANSFERASE ALG2	DETOXIFICATION	30	0	0	0.05464	0	0	0	0.03816	0
161569	ATP-BINDING CASSETTE TRANSPORTER ABCG3 (1)	PROT MOD	30	0	0	0.01242	0	0	0	0.0095	0
243111		UNKNOWN	30	0	0	0.02511	0	0	0	0.019	0
198248	SIMILAR TO FOLLICULAR LYMPHOMA VARIANT TRANSLOCATION 1	UNKNOWN	30	0	0	0.02511	0	0	0	0.019	0
164032	UNCHARACTERIZED HEMATOPOIETIC STEM/PROGENITOR CELL'S PROTEIN MDS029 HOMOLOG	UNKNOWN	30	0	0	0.02953	0	0	0	0.02444	0
139656	BAP31 (B-CELL RECEPTOR-ASSOCIATED PROTEIN 31)	TRAFFIC	30	0	0	0.17568	0	0.012	0.01596	0.12505	0
176270	PUTATIVE N-ACETYLTRANSFERASE CAMELLO 4	PROT MOD	30	0	0	0.08784	0	0.01147	0.02306	0.12535	0.00531
125135	CYTOCHROME P450 2J3	DETOXIFICATION	30	0	0	0.04157	0	0	0.00862	0.04766	0

298062	SIMILAR TO RIKEN CDNA 2610020H15	UNKNOWN	32	0	0	0	0	0.00431	0.0095	
	UBX DOMAIN CONTAINING 2									
246703	(PREDICTED)	UNKNOWN	32	0	0	0	0	0.00431	0.0095	0
19992	SIMILAR TO RIKEN CDNA C130038N16	UNKNOWN	32	0	0	0	0	0.00431	0.0095	0
86161	R-RAS2	GTPASE	32	0	0	0	0	0	0.02851	0.00705
	PROSTAGLANDIN F2 RECEPTOR NEGATIVE REGULATOR PRECURSOR	SIGNALING	32	0	0	0	0	0		
47252	GUANINE NUCLEOTIDE-BINDING PROTEIN G-S ALPHA	SIGNALING	32	0	0	0	0	0	0.02444	0.00531
72067	GUANINE NUCLEOTIDE-BINDING PROTEIN, ALPHA-11 SUBUNIT	SIGNALING	32	0	0	0	0	0	0.03056	0.00705
37192	INTEGRAL MEMBRANE TRANSPORT PROTEIN UST5R	UNKNOWN	32	0	0	0	0	0	0.0392	0.00705
161236	MANNOSEDASE 2, ALPHA 1	PROT MOD	32	0	0	0.0128	0	0.00431	0.21072	0.04054
196264	GTP-BINDING REGULATORY PROTEIN ALPHA-13 CHAIN - MOUSE	SIGNALING	32	0	0	0.00837	0	0	0.11464	0
35327	Qc. RBET1	TETH/DOCK/FUS	32	0	0	0.00837	0	0.00431	0.05732	0
64372	RAB30	GTPASE	32	0	0	0	0	0	0.0115	0
51465	MG160	PROT MOD	32	0	0	0	0	0	0.04782	0
	SIMILAR TO PROLINE DEHYDROGENASE (OXIDASE) 2	METABOLISM	32	0	0	0	0	0	0.01916	0
268034	TORSIN FAMILY 2, MEMBER A	PROT SYN/FOLD	32	0	0	0	0	0	0.01109	0
190227	CYTOCHROME P450 NA2	DETOXIFICATION	32	0	0	0	0	0	0.02444	0
	SIMILAR TO ACYLTRANSFERASE FAMILY MEMBER (5G933)	PROT MOD	32	0	0	0	0	0	0.0095	0
169821	GTP-BINDING PROTEIN RAB13	GTPASE	32	0	0	0	0	0	0.01029	0
32618	RER1	TRAFFIC	32	0	0	0	0	0	0.019	0
250158	RAB24	GTPASE	32	0	0	0	0	0	0.0095	0
	SECRETORY CARRIER MEMBRANE PROTEIN 3	TRAFFIC	32	0	0	0	0	0	0.019	0
169836	INTERCELLULAR ADHESION MOLECULE- 1 PRECURSOR	CYTOSKELETON	32	0	0	0	0	0	0.07647	0
	CARCINOEMBRYONIC ANTIGEN- RELATED CELL ADHESION MOLECULE, SECRETED ISOFORM CEACAM1A-4C2	BIOSYNTHETIC CARGO	32	0	0	0	0	0	0.08598	0
234438	ZINC FINGER PROTEIN 536	UNKNOWN	32	0	0	0	0	0	0.0095	0
82680	PHOSPHOLIPASE B	PROT MOD	32	0	0	0	0	0	0.0095	0
194680	OGIA DOMAIN CONTAINING 1 SIMILAR TO MANNOSYL- OLIGOSACCHARIDE ALPHA-1,2- MANNOSEDASE	UNKNOWN	32	0	0	0	0	0	0.0095	0
273814	MANNOSEDASE	PROT MOD	32	0	0	0	0	0	0.019	0
262914	TEX264 PROTEIN	UNKNOWN	32	0	0	0	0	0	0.0095	0
197399	RAP2C	GTPASE	32	0	0	0	0	0	0.0095	0
	INTEGRAL MEMBRANE TRANSPORT PROTEIN UST4R	UNKNOWN	32	0	0	0	0	0	0.019	0
37231	RAS-RELATED PROTEIN RAL-A	GTPASE	32	0	0	0	0	0	0.0095	0
166255	MAL2A	UNKNOWN	32	0	0	0	0	0	0.019	0
366853	SIMILAR TO RIKEN CDNA 5730568A12	UNKNOWN	32	0	0	0	0	0	0.0095	0
199157	SIMILAR TO KARS PROTEIN	PROT SYN/FOLD	32	0	0	0	0	0	0.0095	0
92620	BRAIN PROTEIN 44-LIKE PROTEIN	UNKNOWN	32	0	0	0	0	0	0.0095	0

277215	SIMILAR TO HYPOTHETICAL PROTEIN	UNKNOWN	32	0	0	0	0	0	0	0	0	0	0.0095	0
MGC23280		PROT SYN/FOLD											0	0
202385	TORSINB PROTEIN	UNKNOWN	32	0	0	0	0	0	0	0	0	0	0.0095	0
220289	HSPC242	UNKNOWN	32	0	0	0	0	0	0	0	0	0	0.0095	0
305592	SIMILAR TO MYO-INOSITOL	SIGNALING	32	0	0	0	0	0	0	0	0	0	0.0095	0
37252	MONOPHOSPHATASE A3	TETH/DOCK/FUS	32	0	0	0	0	0	0	0	0	0	0.0095	0
	Qa. SYNTAXIN 4	UNKNOWN	32	0	0	0	0	0	0	0	0	0	0.0095	0
239422	SIMILAR TO NAD(P) DEPENDENT	UNKNOWN	32	0	0	0	0	0	0	0	0	0	0.0095	0
21695	STEROID DEHYDROGENASE-LIKE	TETH/DOCK/FUS	32	0	0	0	0	0	0	0	0	0	0.0095	0
Qb. GOS28		TRAFFIC	32	0	0	0	0	0	0	0	0	0	0.0095	0
204384	NOVEL MEMBER OF P24 FAMILY	TRAFFIC	32	0	0	0	0	0	0	0	0	0	0.0095	0
(TIRAP3B)		TRAFFIC	32	0	0	0	0	0	0	0	0	0	0.0095	0
311134	PANTOPHYSIN	TRAFFIC	32	0	0	0	0	0	0	0	0	0	0.0095	0
46139	SECRETORY CARRIER-ASSOCIATED	TRAFFIC	32	0	0	0	0	0	0	0	0	0	0.0095	0
MEMBRANE PROTEIN 1		UNKNOWN	32	0	0	0	0	0	0	0	0	0	0.0095	0
264038	ATP-BINDING CASSETTE, SUB-FAMILY B,	UNKNOWN	32	0	0	0	0	0	0	0	0	0	0.0095	0
MEMBER 10		UNKNOWN	32	0	0	0	0	0	0	0	0	0	0.0095	0
17165	INTERFERON-INDUCIBLE PROTEIN	UNKNOWN	32	0	0	0	0	0	0	0	0	0	0.0095	0
273209	F-BOX ONLY PROTEIN 41	UNKNOWN	32	0	0	0	0	0	0	0	0	0	0.01916	0
292782	BTB (POZ) DOMAIN CONTAINING 14A	UNKNOWN	32	0	0	0	0	0	0	0	0	0	0.01916	0
8648	G PROTEIN BETA 1 SUBUNIT	SIGNALING	32	0	0	0	0	0	0	0	0	0	0.0133	0
	SIMILAR TO PROBABLE POL	UNKNOWN	32	0	0	0	0	0	0	0	0	0	0.01916	0
274007	POLYPROTEIN-RELATED PROTEIN 4	UNKNOWN	32	0	0	0	0	0	0	0	0	0	0.01916	0
	GUANINE NUCLEOTIDE-BINDING	SIGNALING	32	0	0	0	0	0	0	0	0	0.00582	0.07483	0
37195	PROTEIN G(Q), ALPHA SUBUNIT	SIGNALING	32	0	0	0	0	0	0	0	0.012	0.01013	0.06245	0.00705
26354	CALCIUM-BINDING PROTEIN P22	SIGNALING	32	0	0	0	0	0	0	0	0	0.02295	0.0265	0.09671
	GUANINE NUCLEOTIDE-BINDING	UNKNOWN	32	0	0	0	0.03478	0	0.04694	0.02963	0.17229	0	0	0
37194	PROTEIN G(I), ALPHA-2 SUBUNIT	SIGNALING	32	0	0	0	0	0	0	0.02295	0.0265	0.09671	0.02645	0
	(ADENYLATE CYCLASE-INHIBITING G	UNKNOWN	32	0	0	0	0	0	0.04694	0.02963	0.17229	0	0	0
ALPHA PROTEIN)		UNKNOWN	32	0	0	0	0.00837	0	0.01147	0.01444	0.07754	0	0	0
265779	ARL6IP2	UNKNOWN	33	0	0	0	0	0	0.02347	0.00862	0.06651	0	0	0
228294	SIMILAR TO HYPOTHETICAL PROTEIN	GTPASE	33	0	0	0	0	0	0.02879	0.04439	0.0408	0	0	0
MGC26706		DETOXIFICATION	33	0	0.00719	0.00837	0	0	0	0.02609	0.019	0.00531	0	0
169873	SIMILAR TO GENETHONIN 1	GTPASE	33	0	0	0	0	0	0	0.03203	0.03326	0	0	0
21122	RAB1A	GTPASE	33	0	0	0	0	0	0	0.03203	0.03326	0	0	0
	SIMILAR TO MICROSOMAL	DETOXIFICATION	33	0	0	0.04184	0	0	0	0.08699	0.15883	0	0	0
164232	GLUTATHIONE S-TRANSFERASE 3	GTPASE	33	0	0	0	0	0	0	0.01293	0.0095	0	0	0
4747	RAP1A	GTPASE	33	0	0	0	0	0	0	0.01165	0.0095	0	0	0
130852	RAP1B	GTPASE	33	0	0	0	0	0	0	0.04915	0.03816	0	0	0
3782	GLUCOKINASE REGULATORY PROTEIN	DETOXIFICATION	33	0	0	0	0	0	0	0.08699	0.15883	0	0	0
139384	2400001E08RIK PROTEIN	UNKNOWN	33	0	0	0	0	0	0	0.01242	0	0.02457	0.05294	0.00531
213193	UNKNOWN PROTEIN (1)	UNKNOWN	33	0	0	0.00837	0	0	0	0.02511	0	0.04636	0.05717	0.01062
	DEHYDROGENASE/REDUCTASE (SDR	UNKNOWN	33	0	0	0	0.03358	0	0	0.03471	0.06788	0.00705	0	0
214468	FAMILY) MEMBER 7	DETOXIFICATION	33	0	0	0	0	0	0	0.01242	0	0.01596	0.02851	0.00705
221624	SIMILAR TO FK506-BINDING PROTEIN 38	SIGNALING	33	0	0	0	0	0	0	0.01242	0	0.01596	0.02851	0.00705
85184	GDC42	GTPASE	33	0	0	0	0.02511	0	0	0.04636	0.05717	0.01062	0	0
161691	RAB18	GTPASE	33	0	0	0	0.03358	0	0	0.03471	0.06788	0.00705	0	0
205068	SIMILAR TO ANCIENT UBIQUITOUS 46	UNKNOWN	33	0	0	0	0	0	0	0.01242	0	0.01596	0.02851	0.00705
	KDA PROTEIN AUP46 PRECURSOR	UNKNOWN	33	0	0.05476	0.13454	0.00816	0	0	0.11047	0.23637	0.06527	0	0
288335	BAND 7 PROTEIN (35.3 KD) (4N53)	UNKNOWN	33	0	0	0	0	0	0	0.01147	0.01013	0.0095	0.00705	0
71624	H-RAS-1/P21	GTPASE	33	0	0	0	0	0	0	0.01147	0.01013	0.0095	0.00705	0

130837	LYSOZYME HOMOLOG AT-2, BINE - RAT (FRAGMENTS)	BIOSYNTHETIC CARGO	36	0	0.00719	0.04157	0	0	0.00582	0.019	0.00705
236658	SIMILAR TO KERATINOCYTES ASSOCIATED PROTEIN 2	UNKNOWN	36	0	0.00719	0.05398	0	0	0.01013	0.02444	0
337611	RIBOPHORIN I	PROT MOD	36	0.33461	0.32219	4.3848	0.66483	0.25033	0.21379	1.20735	0.31344
38101	SRP RECEPTOR BETA	PROT SYN/FOLD	36	0.0133	0.01194	0.21379	0.03363	0.03546	0.03622	0.0721	0.01235
201409	SIMILAR TO DNAJ (HSP40) HOMOLOG, SUBFAMILY B, MEMBER 12	PROT SYN/FOLD	36	0	0.00719	0.04157	0	0	0.00582	0.0095	0
206351	SIMILAR TO OLIGOSACCHARYLTRANSFERASE	PROT MOD	36	0.06058	0.15845	0.65282	0.01731	0.05446	0.04481	0.23999	0
193923	RIBOPHORIN 2	PROT MOD	36	0.22862	0.3917	4.2547	0.20477	0.31818	0.3429	1.23826	0.06097
51409	GLYCOPROTEIN PROCESSING GLUCOSIDASE I	PROT MOD	36	0.06058	0.23855	1.25355	0.03264	0.16629	0.06078	0.37438	0.00531
263127	PROTEIN KIAA0103 HOMOLOG	UNKNOWN	36	0.01035	0.03945	0.27527	0	0.04746	0.01875	0.07738	0.00705
98326	TRANSLOCIN-ASSOCIATED PROTEIN, GAMMA SUBUNIT	PROT SYN/FOLD	36	0.01661	0.03167	0.19591	0	0.012	0	0.04766	0
152512	P34 PROTEIN	PROT SYN/FOLD	36	0.10746	0.07944	0.85064	0	0.08188	0.02609	0.32793	0
268830	SIMILAR TO HYPOTHETICAL PROTEIN KIAA0152	UNKNOWN	36	0.0133	0.0341	0.39382	0	0.02399	0.01444	0.15929	0
238730	RETINOL DEHYDROGENASE 11 (PREDICTED)	DETOXIFICATION	36	0	0	0.10883	0	0.012	0.01444	0.0531	0
71440	GLUCOSE-6-PHOSPHATASE	METABOLISM	36	0	0	0.05464	0	0	0.01165	0.02851	0
201379	CYTOCHROME P450 NA1	DETOXIFICATION	36	0	0	0.1143	0	0.012	0.02025	0.06682	0
60957	SURFTEIT LOCUS PROTEIN 4 (ERV29)	TRAFFIC	36	0	0	0.25601	0	0.02295	0.06814	0.16305	0
68349	ESTRADIOL 17 BETA-DEHYDROGENASE 2	DETOXIFICATION	36	0	0	0.09265	0	0.012	0	0.03801	0
238667	SIMILAR TO RIKEN CDNA 2610318K02	UNKNOWN	36	0	0	0.10873	0	0.012	0	0.0436	0
78079	GLUCOSE-6-PHOSPHATASE, TRANSPORT PROTEIN 1	METABOLISM	36	0	0	0.15904	0	0	0.01013	0.05717	0
3224	SIGNAL PEPTIDASE COMPLEX (18KD)	PROT SYN/FOLD	36	0	0	0.1597	0.00816	0	0	0.05717	0
300133	SIMILAR TO RIKEN CDNA 1810014L12	UNKNOWN	36	0	0	0.02915	0	0	0	0.0095	0
317748	LANOSTEROL SYNTHASE	METABOLISM	36	0	0	0.1014	0	0	0	0.05701	0
252753	SIMILAR TO MANNOSE-P-DOLICHOL UTILIZATION DEFECT 1	UNKNOWN	36	0	0	0.03358	0	0	0	0.019	0
140632	3-BETA-HYDROXYSTEROID-DELTA(8),DELTA(7)-ISOMERASE	DETOXIFICATION	36	0	0	0.10392	0	0	0.00582	0.04782	0
13862	SELENOPROTEIN T	UNKNOWN	36	0	0	0.08314	0	0	0.00582	0.03816	0
250367	CYTOCHROME P450 4V3	DETOXIFICATION	36	0	0	0.04157	0	0	0	0.019	0
192375	SIMILAR TO NEURONAL PROTEIN 15.6	UNKNOWN	36	0	0	0.02078	0	0	0	0.0095	0
318242	SIMILAR TO CDNA SEQUENCE BC017158	UNKNOWN	36	0	0	0.02078	0	0	0	0.0095	0
316692	SIMILAR TO FK506 BINDING PROTEIN 11	UNKNOWN	36	0	0	0.22178	0	0	0	0.08704	0
63169	30 KDA PROTEIN	UNKNOWN	36	0	0.00719	0.16029	0.00816	0	0.01013	0.08145	0
161834	247408 RAB5C	GTPASE	36	0	0	0.10974	0	0.03598	0.01005	0.04196	0
91768	MEG-2-LIKE PROTEIN	UNKNOWN	36	0	0.01438	0.15904	0	0.03598	0.01165	0.05294	0
166327	291250 AB2-305	UNKNOWN	36	0.0133	0.00719	0.67805	0	0.11891	0.03598	0.44211	0
274975	SIMILAR TO RIKEN CDNA C330023F11	UNKNOWN	36	0	0	0.19809	0	0.0688	0.01596	0.11585	0
166145	KINESIN-LIKE PROTEIN KIF15	CYTOSKELETON	36	0	0	0.0128	0	0	0.00431	0	0
291525	VITAMIN K EPOXIDE REDUCTASE COMPLEX SUBUNIT 1-LIKE PROTEIN	METABOLISM	36	0	0	0.01242	0	0	0.00431	0	0

227312	COILED-COIL-HELIX-COILED-COIL-HELIX DOMAIN CONTAINING 3	UNKNOWN	36	0	0	0	0.01674	0	0	0.00582	0	0
315286	RETINAL SHORT-CHAIN DEHYDROGENASE/REDUCTASE 4	DETOXIFICATION	36	0	0	0	0.01674	0	0	0.00431	0	0
235741	SIMILAR TO BC013491 PROTEIN	UNKNOWN	36	0	0	0	0.02117	0	0	0.00582	0	0
209405	SIMILAR TO SEC63	PROT SYN/FOLD	36	0	0	0	0.04561	0.00816	0	0	0	0
214259	SIMILAR TO OLIGOSACCHARYL TRANSFERASE 3	PROT MOD	36	0	0	0	0.46064	0.02547	0	0	0.02851	0.01409
213158	SIMILAR TO ASPARTLY BETA- HYDROXYLASE	METABOLISM	36	0	0	0	0.06301	0	0	0	0	0.00531
311263	RAB21	GTPASE	36	0	0	0	0.02483	0	0	0	0	0
37206	2,3-OXIDOSQUALENE:LANOSTEROL CYCLASE	DETOXIFICATION	36	0	0	0	0.09932	0	0	0	0	0
78089	CYTOCHROME P450 4A8	DETOXIFICATION	36	0	0	0	0.01064	0	0	0	0	0
243991	SIMILAR TO DISULFIDE ISOMERASE	UNKNOWN	36	0	0	0	0.02483	0	0	0	0	0
98449	0610009E20RIK PROTEIN	UNKNOWN	36	0	0	0	0.02483	0	0	0	0	0
275946	TRAM1	PROT SYN/FOLD	36	0	0	0	0.02511	0	0	0	0	0
242256	SIMILAR TO ATP-BINDING CASSETTE TRANSPORTER ABCG3 (2)	UNKNOWN	36	0	0	0	0.02511	0	0	0	0	0
75055	SULFATED GLYCOPROTEIN 1	BIOSYNTHETIC CARGO	36	0	0	0	0.0332	0	0	0	0	0
233624	SIMILAR TO PALBH	METABOLISM	36	0	0	0	0.01674	0	0	0	0	0
239514	SIMILAR TO UBIQUITIN SPECIFIC PROTEASE 36	PROTEASOME/UBIQUITIN	36	0	0	0	0.02117	0	0	0	0	0
317126	ROUNDABOUT (AXON GUIDANCE RECEPTOR, DROSOPHILA) HOMOLOG 2	BIOSYNTHETIC CARGO	36	0	0	0	0.00837	0	0	0	0	0
137571	SQUALENE MONOOXYGENASE	DETOXIFICATION	36	0	0	0	0.02078	0	0	0	0	0
47300	MICROSOMAL STRESS 70 PROTEIN ATPASE CORE	PROT SYN/FOLD	36	0	0	0	0.05436	0	0	0	0	0
236762	SIMILAR TO B-IND1	SIGNALING	36	0	0	0	0.02078	0	0	0	0	0
209082	SIMILAR TO RIKEN CDNA 1810020E01	UNKNOWN	36	0	0	0	0.00837	0	0	0	0	0
283888	THIOREDOXIN DOMAIN CONTAINING PROTEIN 1	UNKNOWN	36	0	0	0	0.02078	0	0	0	0	0
103863	PROSTAGLANDIN G/H SYNTHASE 1 PRECURSOR	BIOSYNTHETIC CARGO	36	0	0	0	0.00837	0	0	0	0	0
241188	INTEGRIN BETA-2 PRECURSOR (CELL SURFACE ADHESION GLYCOPROTEINS LFA-1/CR3/P150.95 BETA-SUBUNIT) (CD18) (COMPLEMENT RECEPTOR C3 BETA-SUBUNIT)	CYTOSKELETON	36	0	0	0	0.0128	0	0	0	0	0
337678	CYTOCHROME P450 20A1 DYSFERLIN (DYSTROPHY ASSOCIATED)	DETOXIFICATION	36	0	0	0	0.06716	0	0	0	0	0
229917	FER-1 LIKE PROTEIN	CALCIUM TRANS/BIND	36	0	0	0	0.00837	0	0	0	0	0
197285	SELENOPROTEIN I	PROT MOD	36	0	0	0	0.01242	0	0	0	0	0
285938	SIMILAR TO FC FRAGMENT OF IGG BINDING PROTEIN; IGG FC BINDING PROTEIN	BIOSYNTHETIC CARGO	36	0	0	0	0.00837	0	0	0	0	0
264754	CHOLINE/ETHANOLAMINEPHOSPHOTRA NSFERASE 1	PROT MOD	36	0	0	0	0.04195	0	0	0	0	0

201524	SIMILAR TO PROTEIN TYROSINE PHOSPHATASE-LIKE PROTEIN PTPLB	SIGNALING	36	0	0	0.05032	0	0	0	0	0	0
280249	SIMILAR TO RIKEN CDNA 1810063B07 GENE	UNKNOWN	36	0	0	0.00837	0	0	0	0	0	0
231757	PUTATIVE MANNOSYLTRANSFERASE	PROT MOD	36	0	0	0.00837	0	0	0	0	0	0
	N-ACYLSPHINGOSINE											
338609	AMIDOHYDROLASE (ACID CERAMIDASE)	PROT MOD	36	0	0	0.0128	0	0	0	0	0	0
288219	ZMPSTE24 METALLOPROTEINASE	PROT MOD	36	0	0	0.00837	0	0	0	0	0	0
229620	SIMILAR TO ARGININE-TRNA-PROTEIN TRANSFERASE 1	PROT SYN/FOLD	36	0	0	0.0128	0	0	0	0	0	0
	SIMILAR TO DOLICHYL-PHOSPHATE											
304061	BETA-GLUCOSYLTRANSFERASE-LIKE	PROT MOD	36	0	0	0.01674	0	0	0	0	0	0
19552	SYNAPTOTAGMIN III	TETH/DOCK/FUS	36	0	0	0.0128	0	0	0	0	0	0
313782	SIMILAR TO TAFI140 PROTEIN	PROT SYN/FOLD	36	0	0	0.00837	0	0	0	0	0	0
208169	SIMILAR TO CYSTEINE-RICH WITH EGF-LIKE DOMAINS 1	UNKNOWN	36	0	0	0.0128	0	0	0	0	0	0
290052	SIMILAR TO HYPOTHETICAL PROTEIN BC002942	UNKNOWN	36	0	0	0.00837	0	0	0	0	0	0
	SIMILAR TO SEVEN TRANSMEMBRANE											
227176	DOMAIN PROTEIN	UNKNOWN	36	0	0	0.0128	0	0	0	0	0	0
240868	SIMILAR TO HYPOTHETICAL PROTEIN MGC40107	UNKNOWN	36	0	0	0.00837	0	0	0	0	0	0
307836	SIMILAR TO SMILE PROTEIN	UNKNOWN	36	0	0	0.0128	0	0	0	0	0	0
315186	SIMILAR TO SSC2	UNKNOWN	36	0	0	0.00837	0	0	0	0	0	0
134570	2'-5'-OLIGOADENYLATE SYNTHETASE 1	SIGNALING	36	0	0	0.03752	0	0	0	0	0	0
234260	SIMILAR TO HYPOTHETICAL PROTEIN FLJ20254	UNKNOWN	36	0	0	0.01242	0	0	0	0	0	0
202821	SIMILAR TO HYPOTHETICAL PROTEIN MGC10084	UNKNOWN	36	0	0	0.00837	0	0	0	0	0	0
128379	IMPLANTATION-ASSOCIATED PROTEIN	UNKNOWN	36	0	0	0.07591	0	0	0	0	0	0
210125	SIMILAR TO FLJ00354 PROTEIN	UNKNOWN	36	0	0	0.01242	0	0	0	0	0	0
304442	SIMILAR TO HYPOTHETICAL PROTEIN FLJ14681	UNKNOWN	36	0	0	0.03396	0	0	0	0	0	0
239621	SIMILAR TO HYPOTHETICAL PROTEIN 5031404N19	UNKNOWN	36	0	0	0.01242	0	0	0	0	0	0
295665	SIMILAR TO FIBRONECTIN TYPE III DOMAIN CONTAINING PROTEIN 3A	UNKNOWN	36	0	0	0.18944	0.00816	0	0	0	0	0
118984	LYRIC	UNKNOWN	36	0	0	0.23371	0	0	0	0.0095	0	0
302143	SIMILAR TO AAQ8810	UNKNOWN	36	0	0	0.12508	0	0	0	0.0095	0	0
294309	TRANSUDCIN (BETA)-LIKE 2	SIGNALING	36	0	0.02632	0.39766	0	0.02399	0	0	0	0
75108	STERYL-SULFATASE	DETOXIFICATION	36	0	0	0.06311	0	0	0.00431	0.0095	0	0
	ACYLCOA:CHOLESTEROL											
207716	ACYLTRANSFERASE 2	PROT MOD	36	0	0	0.06311	0	0	0	0.0095	0	0
	DNA-BINDING PROTEIN PROLACTIN REGULATORY ELEMENT BINDING											
293599	(PREB)	TRANSCRIPTION	36	0	0	0.05869	0	0	0	0.0095	0	0

216144	SIGNAL PEPTIDASE COMPLEX 25 KDA SUBUNIT	PROT SYN/FOLD	36	0	0	0.13363	0.00816	0	0.00431	0.019	0
75284	PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT ISOFORM 1	PROT SYN/FOLD	36	0	0.0341	0.66328	0.00816	0	0.01596	0.08552	0
316149	SIMILAR TO RIKEN CDNA 2310008M10	UNKNOWN	36	0	0.01913	0.28848	0.00915	0.012	0.01013	0.0436	0.00531
36810	DELTA-6 FATTY ACID DESATURASE SIMILAR TO HYPOTHETICAL PROTEIN	METABOLISM	36	0	0	0.15258	0	0	0	0.03831	0
215440	COX4AL	UNKNOWN	36	0	0	0.07504	0	0	0	0.01916	0
302513	SIMILAR TO KIAA0090 PROTEIN	UNKNOWN	37	0	0	0.71988	0.02448	0	0.00582	0.15401	0.01062
76956	MONOGLYCERIDE LIPASE	METABOLISM	37	0	0.01438	0.02078	0	0.012	0.02394	0	0
60413	RAB9A	GTPASE	37	0	0	0.01242	0	0	0.02178	0	0
237237	SIMILAR TO INTERFERON-INDUCIBLE GTPASE	GTPASE	37	0	0.00719	0.05803	0	0.012	0.05601	0	0
317090	SIMILAR TO HYPOTHETICAL PROTEIN FLJ21820	UNKNOWN	37	0	0	0.01242	0	0	0.01013	0	0
193119	SIMILAR TO NEUROBLASTOMA- AMPLIFIED PROTEIN	UNKNOWN	37	0	0	0.0128	0	0	0.00862	0	0
259160	SIMILAR TO MESENCHYMAL STEM CELL PROTEIN DSCD75	UNKNOWN	37	0	0	0.00837	0	0	0.00431	0	0

Table S3. Proteins identified only in Golgi biochemical fractions

Assigned Prot Name	FUNCTION	Membrane Status
KUNITZ TYPE SERINE PROTEINASE INHIBITOR	BIOSYNTHETIC CARGO	MEMBRANE
APOLIPOPROTEIN C-IV PRECURSOR	BIOSYNTHETIC CARGO	SOLUBLE
HEPARIN COFACTOR II	BIOSYNTHETIC CARGO	SOLUBLE
SIMILAR TO ALPHA-2U-GLOBULIN	BIOSYNTHETIC CARGO	SOLUBLE
SIMILAR TO COMPLEMENT COMPONENT 8 BETA SUBUNIT	BIOSYNTHETIC CARGO	SOLUBLE
MPS1 PROTEIN	BLOOD + OTHER CELLS	SOLUBLE
CYTOCHROME P450 2C12	DETOXIFICATION	MEMBRANE
CYTOCHROME P450 2C18	DETOXIFICATION	MEMBRANE
CYTOCHROME P450 2D5	DETOXIFICATION	MEMBRANE
HEME OXYGENASE 1	DETOXIFICATION	MEMBRANE
GLUTATHIONE S-TRANSFERASE YB-1 SUBUNIT	DETOXIFICATION	SOLUBLE
INTERFERON GAMMA INDUCED GTPASE	GTPASE	MEMBRANE
SAR1 HOMOLOG	GTPASE	MEMBRANE
RHO-GEF 7	GTPASE	SOLUBLE
LYSOSOMAL APYRASE-LIKE 1	LYSOSOME	MEMBRANE
MONOGLYCERIDE LIPASE	METABOLISM	SOLUBLE
SIMILAR TO HEXOSE-6-PHOSPHATE DEHYDROGENASE; GDH/6PGL ENDOPLASMIC BIFURCATED	METABOLISM	SOLUBLE
SIDEROFLEXIN 1 (TRICARBOXYLATE CARRIER PROTEIN)	MITOCHONDRIA	MEMBRANE
MITOCHONDRIAL ACONITASE	MITOCHONDRIA	SOLUBLE
ORNITHINE AMINOTRANSFERASE, MITOCHONDRIAL PRECURSOR	MITOCHONDRIA	SOLUBLE
ACYL-COENZYME A OXIDASE 2, PEROXISOMAL	PEROXISOME	SOLUBLE
AMYLOID-LIKE PROTEIN 2 PRECURSOR	PLASMA MB	MEMBRANE
SERINE PROTEASE HEPsin	PLASMA MB	MEMBRANE
SLC26A9 ANION TRANSPORTER/EXCHANGE	PLASMA MB	MEMBRANE
CDP-DIACYLGLYCEROL--INOSITOL 3-PHOSPHATIDYLTRANSFERASE	PROT MOD	MEMBRANE
FURIN PRECURSOR	PROT MOD	MEMBRANE
EXOSTOSES (MULTIPLE) 2	PROT SYN/FOLD	MEMBRANE
40S RIBOSOMAL PROTEIN S5	PROT SYN/FOLD	SOLUBLE
DVL-BINDING PROTEIN DAPLE	SIGNALING	SOLUBLE
Qb, VTI 1B	TETH/DOCK/FUS	MEMBRANE
R, VAMP 3	TETH/DOCK/FUS	MEMBRANE
COG2	TETH/DOCK/FUS	SOLUBLE
INTEGRAL TYPE I PROTEIN P24 GAMMA4	TRAFFIC	MEMBRANE
SECRETORY CARRIER-ASSOCIATED MEMBRANE PROTEIN 1	TRAFFIC	MEMBRANE
TRANSCRIPTIONAL CO-ACTIVATOR CRSP7 HOMOLOG	TRANSCRIPTION	MEMBRANE
30 KDA PROTEIN	UNKNOWN	MEMBRANE
IODOTYROSINE DEHALOGENASE PROTEIN	UNKNOWN	MEMBRANE
THIOREDOXIN DOMAIN CONTAINING PROTEIN 1	UNKNOWN	MEMBRANE
TORID	UNKNOWN	MEMBRANE
RGPR-P117	UNKNOWN	SOLUBLE
SIMILAR TO AMYLOID BETA A4 PRECURSOR PROTEIN-BINDING FAMILY B MEMBER 2 (F)	UNKNOWN	SOLUBLE
SIMILAR TO DNA SEGMENT, CHR 1, ERATO DOI 578, EXPRESSED	UNKNOWN	SOLUBLE
SIMILAR TO RIKEN CDNA 4931400A14	UNKNOWN	SOLUBLE

CMBSEQID LIST	ginumber	TOTAL PEPTIDES N=1 GOLGI AQU	TOTAL PEPTIDES N=1 GOLGI DET	% TOTAL PEPTIDES N=1 GOLGI AQU	% TOTAL PEPTIDES N=1 GOLGI DET
319145	40018550	0	1	0	0.069396
136243	2492915	0	1	0	0.069396
68739	60551378	1	0	0.1046	0
210822	34868545	3	0	0.31381	0
204172	34869943	1	0	0.1046	0
176262	5052048	0	1	0	0.069396
3729	59808903	0	1.5383	0	0.10675
260440	34862902	0	1.25	0	0.086745
63790	57818	0	3.6167	0	0.25098
3930	6981032	0	1	0	0.069396
126642 164858	204503	1	0	0.1046	0
223700	34870762	0	2	0	0.13879
119421 160782	57528164	0	1	0	0.069396
2120	2865596	0	1	0	0.069396
305737	34874388	0	1	0	0.069396
76956	79158553	0	2	0	0.13879
251640	34872615	2	0	0.20921	0
80422 278396	545998	0	1	0	0.069396
338228	60391194	1	0	0.1046	0
44333	206706	1	0	0.1046	0
3086	21955130	1	0	0.1046	0
10860	1703345	0	1	0	0.069396
51490	8393560	0	1	0	0.069396
268665	34879705	0	1	0	0.069396
70677	7674155	0	1	0	0.069396
47234	9506955	0	1	0	0.069396
247469	34856569	0	2	0	0.13879
278725	34854534	0	1	0	0.069396
239536	34867549	1	0	0.1046	0
241548	34866243	0	2	0	0.13879
23581	56789137	0	1	0	0.069396
298383	34851895	0	1	0	0.069396
305262	62901119	0	2	0	0.13879
46139	487057	0	2	0	0.13879
272267	34877464	0	2	0	0.13879
63169	71153386	0	1	0	0.069396
258458	68163439	0	1	0	0.069396
283888	67078422	0	2	0	0.13879
161242	37590771	0	2	0	0.13879
60469	16758344	0	1	0	0.069396
294691	34877353	0	1	0	0.069396
262592	27681007	1	0	0.1046	0
296181	34878255	1	0	0.1046	0

Table S4. Comparison with Golgi Proteins Identified in Foster et al. study

	Foster et al protein accession	Description
Golgi	gi 126722 sp P27046 MA2A1_MOUSE	MA2A1_MOUSE Alpha-mannosidase 2 (Alpha-mannosidase II) (Mannosyl-oligosaccharide 1,3-1,6-alpha-mannosidase) (MAN II) (Golgi alpha-mannosidase II) (Mannosidase alpha class 2A member 1) (AMAN II)
Non-Golgi	gi 1710017 sp P35293 RAB18_MOUSE	RAB18_MOUSE Ras-related protein Rab-18
Non-Golgi	gi 1172773 sp P42669 PURA_MOUSE	PURA_MOUSE Transcriptional activator protein Pur-alpha (Purine-rich single-stranded DNA-binding protein alpha)
Non-Golgi	gi 29611958 sp P57716 NICA_MOUSE	NICA_MOUSE Nicastatin precursor
Cargo	gi 81881746 sp Q9DBK8 Q9DBK8_MOUSE	Q9DBK8_MOUSE Mus musculus adult male liver cDNA, RIKEN full-length enriched library, clone:1300004A21 product:inter alpha-trypsin inhibitor, heavy chain 4, full insert sequence
Golgi	gi 13124070 sp Q9JIF7 COPB_MOUSE	COPB_MOUSE Coatomer subunit beta (Beta-coat protein) (Beta-COP)
Golgi	gi 121143 sp P27808 MGAT1_MOUSE	MGAT1_MOUSE Alpha-1,3-mannosyl-glycoprotein 2-beta-N-acetylglucosaminyltransferase (N-glycosyl-oligosaccharide-glycoprotein N-acetylglucosaminyltransferase I) (GNT-I) (GlcNAc-T I)
Cargo	gi 231557 sp Q00623 APOA1_MOUSE	APOA1_MOUSE Apolipoprotein A-I precursor (Apo-AI) (ApoA-I)
Golgi	gi 68052854 sp Q921V5 MGAT2_MOUSE	MGAT2_MOUSE Alpha-1,6-mannosyl-glycoprotein 2-beta-N-acetylglucosaminyltransferase (Mannoside acetylglucosaminyltransferase 2) (N-glycosyl-oligosaccharide-glycoprotein N-acetylglucosaminyltransferase II) (Beta-1,2-N-acetylglucosaminyltransferase II) (GNT-II) (GlcNAc-T II)
Golgi	gi 17376706 sp Q61543 GSLG1_MOUSE	GSLG1_MOUSE Golgi apparatus protein 1 precursor (Golgi sialoglycoprotein MG-160) (E-selectin ligand 1) (ESL-1) (Selel)
Non-Golgi	gi 132739 sp P14118 RL19_HUMAN	RL19_HUMAN 60S ribosomal protein L19
Non-Golgi	gi 51316255 sp Q62WY3 RS27L_MOUSE	RS27L_MOUSE 40S ribosomal protein S27-like protein
Cargo	gi 136465 sp P07309 TTHY_MOUSE	TTHY_MOUSE Transhyretin precursor (Prealbumin)
Golgi	gi 85681904 sp Q9Z1Z0 VDP_MOUSE	VDP_MOUSE General vesicular transport factor p115 (Transcytosis-associated protein) (TAP) (Vesicle docking protein)
Cargo	gi 1722806 sp P29788 VTNC_MOUSE	VTNC_MOUSE Vitronectin precursor (Serum spreading factor) (S-protein)
Golgi	gi 51315982 sp Q8BMP6 GCP60_MOUSE	GCP60_MOUSE Golgi resident protein GCP60 (Acyl-CoA-binding domain-containing protein 3) (Golgi phosphoprotein 1) (GOLPH1) (Golgi complex-associated protein 1) (GOCAP1) (PBR- and PKA-associated protein 7) (Peripherial benzodiazepine receptor-associated protein PAP7)
Non-Golgi	gi 6174886 sp Q35386 PAHX_MOUSE	PAHX_MOUSE Phytanoyl-CoA dioxygenase, peroxisomal precursor (Phytanoyl-CoA alpha-hydroxylase) (PhyH) (Phytanic acid oxidase) (Lupus nephritis-associated peptide 1)
Golgi	gi 127822 sp P15535 B4GT1_MOUSE	B4GT1_MOUSE Beta-1,4-galactosyltransferase 1 (Beta-1,4-GalTase 1) (Beta4Gal-T1) (b4Gal-T1) (UDP-galactose:beta-N-acetylglucosamine beta-1,4-galactosyltransferase 1) (UDP-Gal:beta-GlcNAc beta-1,4-galactosyltransferase 1) [Includes: Lactose synthase A protein ; N-acetylglucosamine synthase (Nal synthetase); Beta-N-acetylglucosaminylglycopeptide beta-1,4-galactosyltransferase ; Beta-N-acetylglucosaminyl-glycolipid beta-1,4-galactosyltransferase]
Non-Golgi	gi 81918016 sp Q9Z2X1 Q9Z2X1_MOUSE	Q9Z2X1_MOUSE Heterogeneous nuclear ribonucleoprotein F
Cargo	gi 5915682 sp P07724 ALBU_MOUSE	ALBU_MOUSE Serum albumin precursor
Golgi	gi 1170851 sp P45700 MA1A1_MOUSE	MA1A1_MOUSE Mannosyl-oligosaccharide 1,2-alpha-mannosidase 1A (Processing alpha-1,2-mannosidase 1A) (Alpha-1,2-mannosidase 1A) (Mannosidase alpha class 1A member 1) (Man(9)-alpha-mannosidase) (Man9-mannosidase)
Golgi	gi 50400632 sp Q9CRA5 GOLP3_MOUSE	GOLP3_MOUSE Golgi phosphoprotein 3 (Coat-protein GPP34)
Non-Golgi	gi 1730067 sp P53657 KPYR_MOUSE	KPYR_MOUSE Pyruvate kinase isozymes R/L (L-PK)
Non-Golgi	gi 46396669 sp Q35737 HNRH1_MOUSE	HNRH1_MOUSE Heterogeneous nuclear ribonucleoprotein H (hnRNP H)

Non-Golgi	gi133890 sp P25111 RS25_HUMAN	RS25_HUMAN 40S ribosomal protein S25
Golgi	gi48428831 sp P61924 COPZ1_MOUSE	COPZ1_MOUSE Coatomer subunit zeta-1 [Zeta-1 coat protein] [Zeta-1 COP]
Non-Golgi	gi151316667 sp Q6ZVU9 RS27_MOUSE	RS27_MOUSE 40S ribosomal protein S27
Non-Golgi	gi13195690 ref NP_077239.1	ribosomal protein S27a [Mus musculus]
Non-Golgi	gi154039459 sp P62274 RS29_MOUSE	RS29_MOUSE 40S ribosomal protein S29
Non-Golgi	gi13878823 sp Q9ER39 TOR1A_MOUSE	TOR1A_MOUSE Torsin A precursor (Torsin family 1 member A) (Dystonia 1 protein)
Golgi	gi181898070 sp Q8BYH5 Q8BYH5_MOUSE	Q8BYH5_MOUSE Mus musculus adult male spinal cord cDNA, RIKEN full-length enriched library, clone:A330065C10 product:GOLGI-SPECIFIC BREFELDIN A-RESISTANCE GUANINE NUCLEOTIDE EXCHANGE FACTOR 1 (BFA-RESISTANT GEF 1) homolog
Golgi	gi181917443 sp Q9ET41 Q9ET41_MOUSE	Q9ET41_MOUSE Coatomer protein alpha subunit
Non-Golgi	gi121993 sp P27661 H2AFX_MOUSE	H2AFX_MOUSE Histone H2A.x (H2afx)
Non-Golgi	gi125090336 sp Q61584 FXR1_MOUSE	FXR1_MOUSE Fragile X mental retardation syndrome-related protein 1
Non-Golgi	gi1416914 sp P32233 DRG1_MOUSE	DRG1_MOUSE Developmentally-regulated GTP-binding protein 1 (DRG 1) (Protein NEDD3) (Neural precursor cell expressed developmentally down-regulated protein 3)
Golgi	gi181875543 sp Q8BWP9 Q8BWP9_MOUSE	Q8BWP9_MOUSE Mus musculus adult liver tumor cDNA, RIKEN full-length enriched library, clone:C730040C13 product:similar to 130 kDa GOLGI-LOCALIZED PHOSPHOPROTEIN (GPP130/GIMPC)
Golgi	gi147117662 sp P61211 ARL1_MOUSE	ARL1_MOUSE ADP-ribosylation factor-like protein 1
Non-Golgi	gi181915143 sp Q8VCX0 Q8VCX0_MOUSE	Q8VCX0_MOUSE Cytochrome P450, family 2, subfamily d, polypeptide 13
Non-Golgi	gi13633865 sp Q9QUJ0 RHOA_MOUSE	RHOA_MOUSE Transforming protein RhoA precursor
Golgi	gi32469790 sp Q9QYE6 GOGA5_MOUSE	GOGA5_MOUSE Golgin subfamily A member 5 (Golgin-84) (Sumiko protein) (Ret-ii protein)
Golgi	gi181885500 sp Q6PAK0 Q6PAK0_MOUSE	Q6PAK0_MOUSE Golgi1 protein
Non-Golgi	gi167460966 sp Q99K48 NONO_MOUSE	NONO_MOUSE Non-POU domain-containing octamer-binding protein (NonO protein)
Non-Golgi	gi12497642 sp P70194 CLC4F_MOUSE	CLC4F_MOUSE C-type lectin domain family 4 member F (C-type lectin superfamily member 13) (C-type lectin 13) (Kupffer cell receptor)
Non-Golgi	gi121994 sp P17317 H2AZ_HUMAN	H2AZ_HUMAN Histone H2A.z (H2A/z)
Non-Golgi	gi134922200 sp Q9R049 AMFR_MOUSE	AMFR_MOUSE Autocrine motility factor receptor (AMF receptor)
Non-Golgi	gi163735444 ref XP_129159.5	PREDICTED: apobec-1 complementation factor isoform 1 [Mus musculus]
Non-Golgi	gi121970 sp P20670 H2AO_HUMAN	H2AO_HUMAN Histone H2A.o (H2A.o) (H2A.2) (H2a-615)
Non-Golgi	gi121264500 sp P35980 RL18_MOUSE	RL18_MOUSE 60S ribosomal protein L18
Non-Golgi	gi167461015 sp Q6NZJ6 IF4G1_MOUSE	IF4G1_MOUSE Eukaryotic translation initiation factor 4 gamma 1 (eIF-4 gamma 1) (eIF-4G1) (eIF-4G 1)
Unknown	gi181884928 sp Q6NSU0 Q6NSU0_MOUSE	Q6NSU0_MOUSE D6Wsu176e protein
Non-Golgi	gi138074304 ref XP_193995.2	similar to 60S ribosomal protein [Mus musculus]
Non-Golgi	UniProt/Swiss-Prot Q8BRF7 SCFD1_MOUSE	SCFD1_MOUSE Sec1 family domain-containing protein 1
Unknown	UniProt/TrEMBL Q91XE8 Q91XE8_MOUSE	Q91XE8_MOUSE Hypothetical LOC235043
Cargo	UniProt/TrEMBL Q99K47 Q99K47_MOUSE	Q99K47_MOUSE Fibrinogen, alpha polypeptide
Unknown	gi181881522 sp Q9D758 Q9D758_MOUSE	Q9D758_MOUSE Mus musculus adult male tongue cDNA, RIKEN full-length enriched library, clone:2310032E02 product:zinc finger protein 289, full insert sequence
Non-Golgi	gi120978553 sp Q9CR00 PSD9_MOUSE	PSD9_MOUSE 26S proteasome non-ATPase regulatory subunit 9 (26S proteasome regulatory subunit p27)
Golgi	gi13878803 sp P58021 TM9S2_MOUSE	TM9S2_MOUSE Transmembrane 9 superfamily protein member 2 precursor
Unknown	gi181879422 sp Q8VEK0 Q8VEK0_MOUSE	Q8VEK0_MOUSE DNA segment, Chr. 9, Wayne State University 20, expressed (Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4932704103 product:DJ234P15.3 (NOVEL PROTEIN SIMILAR TO (PREDICTED) YEAST AND WORM PROTEINS) homolog)

Non-Golgi	gi 42560197 sp Q91VC3 DDX48_MOUSE	DDX48_MOUSE Probable ATP-dependent RNA helicase DDX48 (DEAD box protein 48)
Unknown	gi 81903613 sp Q9CR27 CCD53_MOUSE	CCD53_MOUSE Coiled-coil domain-containing protein 53
Non-Golgi	gi 20455216 sp Q9Z204 HNRPC_MOUSE	HNRPC_MOUSE Heterogeneous nuclear ribonucleoproteins C1/C2 (hnRNP C1 / hnRNP C2)
Unknown	gi 81877390 sp Q8CAP0 Q8CAP0_MOUSE	Q8CAP0_MOUSE Mus musculus 16 days neonate thymus cDNA, RIKEN full-length enriched library, clone:A130095H06 product:hypothetical protein, full insert sequence
Golgi	gi 62287508 sp Q91Y74 SIA4C_MOUSE	SIA4C_MOUSE CMP-N-acetylneuraminate-beta-galactosamide-alpha-2,3-sialyltransferase (Beta-galactoside alpha-2,3-sialyltransferase) (Alpha 2,3-sialyltransferase IV) (Alpha 2,3-ST) (SIA4-C)
Non-Golgi	gi 3915627 sp P11609 CD1D1_MOUSE	CD1D1_MOUSE T-cell surface glycoprotein CD1d1 precursor (CD1.1 antigen)
Non-Golgi	gi 549148 sp P35545 UBIM_MOUSE	UBIM_MOUSE Ubiquitin-like protein FUBI (Monoclonal nonspecific suppressor factor beta) (MNSF-beta)
Unknown	gi 81894640 sp Q7TQK5 Q7TQK5_MOUSE	CCD93_MOUSE Coiled-coil domain-containing protein 93
Non-Golgi	fp IP 00625088 IP 00625088.1	PREDICTED: SIMILAR TO 40S RIBOSOMAL PROTEIN S29