

Organellar Proteomics of the Golgi Apparatus and Golgi Derived COPI Vesicles.

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List of Abbreviations

2D-PAGE	<u>2</u> - <u>D</u> imensional <u>P</u> oly <u>A</u> crylamide <u>G</u> el <u>E</u> lectrophoresis
ADP	<u>A</u> denosine <u>D</u> i <u>P</u> hosphate
ARF	<u>A</u> DP <u>R</u> ibosylation <u>F</u> actor
ATP	<u>A</u> denosine <u>T</u> ri <u>P</u> hosphate
BLAST	<u>B</u> asic <u>L</u> ocal <u>A</u> lignment <u>S</u> earch <u>T</u> ool
BLink	<u>B</u> last <u>L</u> ink
BSA	<u>B</u> ovine <u>S</u> erum <u>A</u> lbumin
CGN	<u>C</u> is <u>G</u> olgi <u>N</u> etwork
CMBSEQID	<u>C</u> ell <u>M</u> ap <u>B</u> ase <u>S</u> Equence <u>I</u> Dentifier
CMP	<u>C</u> ytidine <u>M</u> ono <u>P</u> hosphate
DNA	<u>D</u> eoxyribo <u>N</u> ucleic <u>A</u> cid
ECL	<u>E</u> nhanced <u>C</u> hemi <u>L</u> uminescence
EM	<u>E</u> lectron <u>M</u> icroscopy
EPCAS	<u>E</u> mbedded <u>P</u> ersonal <u>C</u> omputer-control and <u>A</u> cquisition <u>S</u> ystem
ER	<u>E</u> ndoplasmic <u>R</u> eticulum
ERGIC	<u>E</u> R <u>G</u> olgi <u>I</u> ntermediate <u>C</u> ompartment
ESI	<u>E</u> lectro <u>S</u> pray <u>I</u> onization
FTICR	<u>F</u> ourier <u>T</u> ransform <u>I</u> on <u>C</u> yclotron <u>R</u> esonance
GAP	<u>G</u> TPase <u>A</u> ctivating <u>P</u> rotein
GC MS	<u>G</u> as <u>C</u> hromatography <u>M</u> ass <u>S</u> pectrometry
GDP	<u>G</u> uanosine <u>D</u> i <u>P</u> hosphate
GEF	<u>G</u> uanine nucleotide <u>E</u> xchange <u>F</u> actors
GFP	<u>G</u> reen <u>F</u> luorescent <u>P</u> rotein
GO	<u>G</u> ene <u>O</u> ntology
GTP	<u>G</u> uanosine <u>T</u> ri <u>P</u> hosphate
GTPyS	Guanosine-5'-O-(3-thiotriphosphate)
HPLC	<u>H</u> igh <u>P</u> erformance <u>L</u> iquid <u>C</u> hromatography
HUPO	<u>H</u> uman <u>P</u> roteome <u>O</u> rganization
iCAT	<u>i</u> sotope- <u>C</u> oded <u>A</u> ffinity <u>T</u> ags

LC MS	<u>L</u> iquid <u>C</u> hromatography <u>M</u> ass <u>S</u> pectrometry
LOPIT	<u>L</u> ocalization of <u>O</u> rganelle <u>P</u> roteins by <u>I</u> sotope <u>T</u> agging
m/z	mass to charge ratio
MALDI	<u>M</u> atrix- <u>A</u> ssisted <u>L</u> aser <u>D</u> esorption/ <u>I</u> onization
MS	<u>M</u> ass <u>S</u> pectrometry
MudPIT	<u>M</u> ultidimensional <u>P</u> rotein- <u>I</u> dentification <u>T</u> echnology
NAD ⁺ /NADH	<u>N</u> icotinamide <u>A</u> denine <u>D</u> inucleotide
NCBI	<u>N</u> ational <u>C</u> enter for <u>B</u> iotecnology <u>I</u> nformation
PCP	<u>P</u> rotein <u>C</u> orrelation <u>P</u> rofiling
Pi	<u>i</u> norganic <u>P</u> hosphate
PM	<u>P</u> lasma <u>M</u> embrane
PMSF	<u>P</u> henyl <u>M</u> ethane <u>S</u> ulfonyl <u>F</u> luoride
rER	<u>r</u> ough <u>E</u> ndoplasmic <u>R</u> eticulum
RM	<u>R</u> ough <u>M</u> icrosomes
RNA	<u>R</u> ibo <u>N</u> ucleic <u>A</u> cid
SAGE	<u>S</u> erial <u>A</u> nalysis of <u>G</u> ene <u>E</u> xpression
SDS-PAGE	<u>S</u> odium <u>D</u> odecyl <u>S</u> ulfate <u>P</u> oly <u>A</u> crylamide <u>G</u> el <u>E</u> lectrophoresis
sER	<u>s</u> mooth <u>E</u> ndoplasmic <u>R</u> eticulum
SILAC	<u>S</u> table <u>I</u> sotope <u>L</u> abelling with <u>A</u> mino-acids in <u>C</u> ell -culture
SM	<u>S</u> mooth <u>M</u> icrosomes
SNARE	<u>S</u> oluble <u>N</u> SF <u>A</u> ttachment <u>P</u> rotein <u>R</u> Eceptor
SRM	<u>S</u> tripped <u>R</u> ough <u>M</u> icrosomes
SRP	<u>S</u> ignal <u>R</u> ecognition <u>P</u> article
tER	<u>t</u> ransitional <u>E</u> R
TGN	<u>T</u> rans <u>G</u> olgi <u>N</u> etwork
ToF	<u>T</u> ime of <u>F</u> light
UDP	<u>U</u> ridine <u>D</u> i <u>P</u> hosphate
UTR	<u>U</u> n <u>T</u> ranslated <u>R</u> egion
VSVG	<u>V</u> esicular <u>S</u> tomatitis <u>V</u> irus <u>G</u> lycoprotein

VTCs Vesicular Tubular Clusters

Abstract

Studying an organelle with traditional biochemistry, histology, or microscopy techniques allows the determination of the presence of up to three proteins simultaneously. Mass spectrometry based proteomics has changed the study of organelles; for the first time it is possible to investigate the whole protein complement of a subcellular compartment. In this work I demonstrate our ability to use redundant peptide counting as a quantitative technique to compare the relative abundance of different proteins in a complex sample, specifically, enriched organellar preparations. I present the pipeline that we use to isolate, characterize, and prepare samples for mass spectrometric analysis, followed by the automatic mass spectrometric data acquisition and data processing that result in the output of a list of protein identifications. A highly involved and time consuming manual annotation effort is applied to this preliminary list in order to generate a final set of tables where standardized functional categories and assigned names are applied to every protein identified in order facilitate the application of redundant peptide counting. The organelles of the early secretory pathway are processed by the pipeline, and after rigorous manual verification of the data, the proteomes of the rough microsomes, smooth microsomes, Golgi apparatus, and Golgi derived COPI GTP and COPI GTP γ S vesicles are determined. The focus of this thesis is on the proteomes of the Golgi and Golgi derived vesicles. The characteristics and most abundant proteins of the proteomes of the Golgi apparatus, COPI GTP, and COPI GTP γ S vesicles are described in detail. The hypothesis of cisternal maturation, a theory describing secretory cargo progress through the Golgi apparatus, is tested and eventually supported by our proteomics data. Finally, outlines of the abundant proteins of unknown function of the Golgi, COPI GTP and COPI GTP γ S vesicles are presented.

Resumé

Les techniques traditionnelles utilisées en biochimie, en histologie ainsi qu'en microscopie permettent la détermination d'un maximum de trois protéines à la fois dans l'étude d'une organelle. La mise en œuvre de la spectrométrie de masse en protéomique a complètement changé le panorama d'investigation des organelles. Pour la première fois, il est possible d'étudier le panel entier de protéines présent dans un compartiment sub-cellulaire. Dans cette étude, je démontre dans un premier temps que l'utilisation du dénombrement de peptides redondants permet la quantification des protéines et donc la capacité de comparer l'abondance relative de différentes protéines dans un échantillon complexe tel qu'une préparation d'organelle. Je présenterai par la suite le pipeline que nous utilisons pour isoler, caractériser et préparer les échantillons avant leur analyse par acquisition automatique par spectrométrie de masse laquelle est suivie par le traitement des données dont le résultat consiste à l'identification d'une liste de protéines. Un effort manuel important d'annotation est appliqué à cette liste préliminaire afin de générer un tableau final où sont assignées à la fois la fonction dans laquelle chaque protéine identifiée est impliquée, ainsi que l'attribution de la nomenclature la plus appropriée. Ce travail laborieux facilite par conséquent le dénombrement et l'attribution des peptides redondants aux protéines. Les organelles de la voie précoce de sécrétion sont analysées par le pipeline et après une vérification manuelle rigoureuse des données, les protéomes des microsomes rugueux, des microsomes lisses, de l'appareil de Golgi, et des vésicules dérivées du Golgi COPI GTP et COPI GTPyS sont déterminés. L'objectif de cette étude porte sur les protéomes du Golgi et des vésicules dérivées du Golgi dont les protéines les plus abondantes ainsi que leurs caractéristiques sont décrites en détail. L'hypothèse de la maturation des citernes de Golgi, théorie qui décrit la progression du cargo de sécrétion à travers l'appareil de Golgi a été

testée et a été par la suite confirmée par les données protéomiques obtenues. Enfin, les protéines abondantes identifiées dans l'appareil de Golgi et les vésicules COPI GTP et COPI GTP γ S dont les fonctions sont encore inconnues sont présentées.

Contributions of Authors

- 1) Part of the work presented in Chapters 3-8 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, 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 were performed by Line Roy.
 - b) Electron microscopy of the RM, SM and Golgi fractions was performed 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) Isolation of the COPI GTP vesicles and COPI GTP γ S vesicles was performed by Johan Hiding and the characterization performed by Dr. Julia Fernandez-Rodriguez, in the laboratory of Dr. Tommy Nilsson.
 - e) 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) were performed by Nathalie Hamel and Line Roy.

- f) Tandem mass spectrometry was performed by Daniel Boismenu.
 - g) Peaklist generation by distiller, matching of mass spectra to peptides using Mascot, grouping of peptides and operation of CellMapBase were performed by the bioinformatics group supervised by Dr. Robert E. Kearney.
 - h) 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 performed in collaboration with Annalyn Gilchrist.
 - i) Immunolocalization of ERp44 and sapreticulin and confocal microscopy were performed by Dr. Hisao Nagaya.
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 - 3) Cryoimmune electron micrographs of the Golgi apparatus presented in Chapters 3 and 4 were performed by Dr. Sophie Dahan.
 - 4) The Golgi retrograde transport assay presented in Chapter 7 was performed by Mr. Fred Laporte.

Original Contributions

1. Extension of the Golgi proteome to 246 proteins.
2. First proteomics analysis of Golgi derived COPI vesicles and COPI GTP γ S vesicles.
3. First use of proteomics to test a cell biological hypothesis.
4. Support for maturation model of Golgi transport.
5. Identification of over 100 novel proteins in the Golgi apparatus and COPI vesicles.

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Chapter 1 -- Introduction

Cell biologists have many questions regarding the function of the cell. One area of interest is secretion. For instance, how does the cell know to keep certain proteins in the cell while secreting others to the cell surface? This is one of the key discoveries emanating from cell biology, namely, the elucidation of the molecular mechanisms of the secretory pathway. The foundations of the field are the work of Nobel laureates Albert Claude, Christian DeDuve, George Palade and Gunter Blobel. These pioneers have been credited with the discovery of the basic organelles and associated structures of the secretory pathway, including, the ribosome, endoplasmic reticulum, Golgi apparatus and secretory vesicles. The signal hypothesis of Gunter Blobel elegantly accounted for the selection of messenger RNAs specific to secretory proteins being translated on the polyribosomes of the rough endoplasmic reticulum and translocated into the lumen of the ER (Blobel & Dobberstein 1975a, Blobel & Dobberstein 1975b). The work of Claude, Palade, LeBlond and several others worked out the trajectory of these secretory proteins from the endoplasmic reticulum to the stacked cisternae of the Golgi apparatus and onwards to their discharge from cells (Bennett et al 1974, Leblond 1963, Palade 1975, Palade 1971, Porter et al 1945, Weinstock & Leblond 1974).

In the late 1970s, Scheckman discovered genes in budding yeast required for proteins to be transported through the secretory pathway (Novick et al 1980). These genes, named sec genes, have orthologs in all metazoan species, and the determination of their function in yeast gave insight into their corresponding functions in mammalian cells (Schekman 2004). One of these genes, sec61, of the eponymous sec61 channel, is now accepted as the major avenue of transport for nascent signal sequence bearing secretory proteins across the membrane of the endoplasmic reticulum (Deshaies & Schekman 1987, Rapoport 1992, Rapoport et al 1992).

Another result of identifying the sec genes was the discovery of COPII coatamer complexes which are responsible for the selection of cargo for their packaging and transport from the endoplasmic reticulum to the Golgi apparatus (Barlowe et al 1994).

As is evident by the name, prior to the discovery of the COPII coatamer complex was the discovery of the COPI coatamer complex (Orci et al 1986). This discovery was a consequence of biochemical investigations attempting to decipher the machinery regulating transport through the Golgi apparatus. The Rothman group designed a cell free transport assay which mirrored the transport of a model secretory protein through the Golgi apparatus, but *in vitro* to facilitate observation. Using this cell free assay, dependent on cytosolic constituents as well as ATP and GTP, the Rothman lab was able to purify a complex of proteins which they named as COPI coatamer, that was required for transport of secretory cargo across the stacked cisternae of the Golgi apparatus (Fries & Rothman 1980, Melancon et al 1987). Great debate ensued. What was the *in vivo* correlate to these biochemically defined COPI coatamer complexes? Did the COPI coatamer complex structures contain secretory cargo or was it excluded? This debate raged for over a quarter of a century, culminating in the papers of Orci and Klumperman, who utilizing the same methodology on the same cell type, came up with opposite conclusions (Martinez-Menarguez et al 2001, Orci et al 2000).

It was in this context that I was given the opportunity to study the early secretory pathway using proteomics. When we commenced this work, the field of mass spectrometry based proteomics was in its infancy. Instead of looking at the spectra produced by just one sample, we decided to isolate organelles of the early secretory pathway; the rough and smooth endoplasmic reticulum (represented by the rough microsomal (RM) and smooth microsomal (SM) fractions), the Golgi apparatus, and the Golgi

derived COPI GTP vesicles and COPI GTP γ S vesicles. Over 5000 hours of mass spectrometer time went into this project, and the time required for manual analysis and assignment of the resulting spectra would have been prohibitive. To handle the amount of data generated by this project we developed an integrated high throughput pipeline which began at sample preparation and characterization, and continued with automated sample processing and mass spectrometric data analysis. This pipeline culminated in intensive manual verification of sequence identity and function.

We now had list of proteins identified in each organelle, but for cell biological applications we needed a method of quantitation for the proteins identified. An idea that was taking hold at the time was using spectral/peptide counts as an index of abundance. We decided to verify that we could reproduce the findings of other groups using this method before employing it ourselves. Peptide counting is now an accepted method of relative quantitation (Blondeau et al 2004, Cox et al 2005, Gao et al 2005, Gao et al 2003, Gilchrist et al 2006, Girard et al 2005, Kislinger et al 2006, Liu et al 2004, Mallick et al 2007, Olsen et al 2006, Pang et al 2002, Qian et al 2005, Rappsilber et al 2002, Zybaïlov et al 2005).

Armed with a list of over 2000 proteins, as well as data regarding their relative abundance, I tried to address the question of the role of COPI vesicles in biosynthetic cargo transport through the Golgi apparatus, as well as determining the identity of the Golgi apparatus, COPI GTP vesicles and COPI GTP γ S vesicles via their proteomes.

Chapter 2 -- Literature Review

2.1 The early secretory pathway.

The early secretory pathway consists of the endoplasmic reticulum, the ER Golgi intermediate compartment, the Golgi apparatus, and their associated structures. In the rat hepatocytes studied in this thesis, the membranes of the secretory pathway form the majority of the total cell membrane, due to the hepatocytes' role in serum protein production and secretion (Blouin et al 1977, Crane & Miller 1974, Noel & Rubinstein 1974, Palade 1975).

2.1.1 The endoplasmic reticulum.

The endoplasmic reticulum (ER) is a contiguous membrane comprised of different structural domains (Voeltz et al 2002). Two flattened sheets of endoplasmic reticulum membrane form the nuclear envelope (Voeltz et al 2002), the membrane and lumen of which are continuous with the more convoluted structures of the rough, smooth, and transitional endoplasmic reticulum (Levine & Rabouille 2005). The endoplasmic reticulum has many functions, including the translocation of secretory proteins into the lumen (Blobel & Dobberstein 1975a, Blobel & Dobberstein 1975b), the storage of calcium ions (Meldolesi & Pozzan 1998), the proper folding of proteins (Schroder & Kaufman 2005), and the synthesis of lipids, steroids, and the detoxification of xenobiotics (Miller 2005).

2.1.1.1 The rough endoplasmic reticulum.

The rough endoplasmic reticulum (rER) was named because of its rough appearance when viewed under the electron microscope. It is characterized by long, highly folded sections of membrane with many

ribosomes on the cytoplasmic surface. Secretory proteins being synthesized on ribosomes are targeted to regions on the rER called translocons, via signal sequences on the amino terminal end of newly synthesized proteins (Blobel & Dobberstein 1975a, Blobel & Dobberstein 1975b). When the signal sequence exits from the ribosome, it binds to the signal recognition particle (SRP), which in turn binds to the ER membrane in a GTP dependant manner (Millman & Andrews 1997, Simon & Blobel 1991). The amino terminal end of the protein being synthesized is then fed into the translocation channel, which feeds the peptide chain into the lumen of the ER (Crowley et al 1993). The channel itself is formed from a heterotrimeric complex of Sec61 proteins containing a large α subunit and two smaller β and γ subunits (Rapoport et al 1996). Protein folding and the formation of disulphide bonds occurs in the lumen of the endoplasmic reticulum, and is aided by chaperone proteins and protein disulphide isomerases (Kleizen & Braakman 2004).

2.1.1.2 The smooth endoplasmic reticulum.

The smooth endoplasmic reticulum (sER) is continuous with the rER but lacks the characteristic ribosomes of the latter structure and is more tubular (Depierre & Dallner 1975). The SNARE protein, syntaxin 17, has been demonstrated to localize uniquely to the sER (Steegmaier et al 2000). In hepatocytes, the sER is the site of lipid and sterol synthesis (Chesterton 1968), glycogen metabolism (Banhegyi & Mandl 2001), as well as detoxification of xenobiotics and drugs by members of the p450 enzyme family (Porter & Coon 1991). Proliferation of the sER in response to the administration of various drugs is a mechanism of providing space for the presence of upregulated detoxification enzymes (Bolender & Weibel 1973, Jones & Fawcett 1966). The pharmaceutical industry is very interested in detoxification enzymes because of their impact on drug toxicity, metabolism and excretion.

2.1.1.3 The transitional endoplasmic reticulum.

The transitional endoplasmic reticulum (tER) is similar to the rER, however, it contains fewer ribosomes. ER cargo exit sites characterized by the aggregation of COPII coats are found in this region (Hobman et al 1998). Cargo proteins travel from these exit sites to the ER Golgi intermediate compartment (ERGIC) and onwards to the Golgi apparatus.

2.1.2 The ER Golgi intermediate compartment.

The ER Golgi intermediate compartment (ERGIC), also called vesiculotubular clusters or pre-Golgi intermediates, was defined via the identification of the lectin ERGIC-53 that localizes to this region (Hauri et al 2000, Schweizer et al 1988). It is suggested by some that the ERGIC are transient cargo container structures that migrate to fuse and form the cis Golgi (Bannykh et al 1998, Stephens & Pepperkok 2001), and by others that the ERGIC is a stationary sorting compartment en route to the Golgi apparatus (Appenzeller-Herzog & Hauri 2006).

2.1.3 The Golgi apparatus.

The Golgi apparatus has fascinated cell biologists ever since its discovery in silver nitrate treated neural cells by the eponymous Camillo Golgi in 1898 (Golgi 1898). Its very existence was a matter of debate until it was seen using electron microscopy in 1954 (Sjostrand & Hanzon 1954). The site of post-translational protein modification, cargo concentration and sorting, its mechanisms of function are still poorly understood (Bergeron et al 1978, Kornfeld & Kornfeld 1985, Roth 1984, Tooze et al 1988).

2.1.3.1 Golgi ultrastructure.

The Golgi is characterized by tightly stacked membranous saccuoles also referred to as cisternae (Mollenhauer & Morre 1991). Cell types that are highly involved in secretion, such as the liver parenchymal cell, have highly developed Golgi, whereas cell types not involved in secretion have more modest Golgi. The Golgi apparatus is located adjacent to the centrosome in mammalian cells (Polishchuk & Mironov 2004).

The Golgi is divided into three regions: the cis Golgi network (CGN), the stacked cisternae, and the trans Golgi network (TGN). Proteins make their way through the Golgi apparatus beginning at the CGN, then proceed into the stacked cisternae, and finally into the TGN. The CGN is a system of anastomosing tubules on the side of the stacked cisternae facing the ERGIC (Rambourg & Clermont 1990). The stacked cisternae are closely opposed membranous sacks that resemble a stack of pancakes, and the stack itself is divided into cis, medial, and trans regions. The cisternae appear separate, but are interconnected via dilated tubules (Hermo et al 1991, Hermo & Smith 1998, Rambourg & Clermont 1990). Vesicle filled wells can be seen within the stacks (Hermo & Smith 1998, Ladinsky et al 1999). The TGN is on the opposite side of the cisternal stack to the CGN and was originally thought to be a part of the Golgi-ER-lysosome system (GERL) or the trans tubular network (Novikoff et al 1971, Rambourg et al 1979). Its structure varies greatly from one cell type to another (Clermont et al 1995), but it is generally organized as variations on a network of fenestrated cisternae and tubules.

2.1.3.2 Post-translational modification and the Golgi.

The Golgi apparatus is the site of many post-translational protein modifications such as the addition and/or removal of sugar groups performed by resident glycosidases and glycosyltransferases. Sulfation,

palmitoylation, acylation, methylation and the synthesis of glycolipids also occur here (Marsh & Howell 2002, Munro 1998). The most well known Golgi enzymes are mannosidase I and II. They are responsible for removing mannose from $\text{Glc}_{1-3}\text{Man}_{4-9}\text{GlcNac}_2$ -N-linked oligosaccharide chains (Tabas & Kornfeld 1979, Tulsiani et al 1982).

One of the interesting features of the Golgi apparatus is that different resident proteins are restricted to specific areas of the organelle. Examples of medial Golgi localized protein modification enzymes are GlcNAc transferase I (N-acetylglucosaminyltransferase I) and mannosidase II (Nilsson et al 1994). Beta-1,4-galactosyltransferase and alpha 2,6 sialyltransferase have been shown to be trans Golgi localized (Nilsson et al 1994). Some protein modification enzymes, such as N-acetylgalactosaminyltransferase I, are distributed over the cisternal stack (Rottger et al 1998).

2.1.3.3 Other Golgi components.

The Golgi matrix proteins GRASP65 and GM130 are integral to the cis Golgi (Barr et al 1997, Nakamura et al 1997, Nakamura et al 1995), GRASP55 and Golgin-45 to the medial Golgi (Pfeffer 2001, Shorter et al 1999), and golgin-245, golgin-97, and TGN38 to the trans Golgi (Gleeson et al 2004, Reaves et al 1992). Transporters for GDP-fructose, CMP-sialic acid, UDP-N-acetylglucosamine, UDP-N-acetylgalactosamine, and UDP-galactose, as well as nucleotide monophosphatases, nucleotide diphosphatases and nucleotide triphosphatases, NADH dehydrogenases, and furin are all found in the Golgi (Hirschberg et al 1998a).

2.1.4 COPI vesicles.

Identified via electron microscopy in isolated Golgi membranes treated with cytosol and ATP, the COPI protein complex was seen as a fuzzy coat

over the site of budding transport vesicles, as opposed to the regular lattice-like appearance of a clathrin coat (Orci et al 1986). Localized around the peri-Golgi region, these vesicles are of approximately 50nm to 60nm in diameter (Nickel et al 1997).

COPI vesicles were first isolated using the non-hydrolysable GTP analog, GTP γ S (Malhotra et al 1989, Melancon et al 1987). From these vesicles, the identity of its eight coat subunits was determined: seven COPI coatamer subunits (α , β , β' , γ , δ , ϵ , and ζ) (Duden et al 1991, Serafini et al 1991b, Stenbeck et al 1993, Waters et al 1991) and an ADP-ribosylation factor (ARF) which is a small GTPase (Serafini et al 1991a). The COPI coatamer subunits range in size from 21kDa (ζ) to 150kDa (α) (Gaynor et al 1998).

For the COPI coat to bind to a membrane, a myristoylated ARF-GTP must first associate with that membrane (Donaldson et al 1992, Helms & Rothman 1992). The seven COPI coatamer subunits assemble into a heptamer in the cytosol, and then bind to the ARF1 “primed” membrane as a unit (Hara-Kuge et al 1994). Release of the coat complex and ability to fuse with a target membrane occurs with the hydrolysis of ARF-GTP to ARF-GDP and Pi by the GTPase activating protein ARF-GAP1 (Tanigawa et al 1993). In order to start another cycle of coat binding and release, ARF1-GDP must be converted to ARF1-GTP by a guanine nucleotide exchange factor (GEF) (Jackson & Casanova 2000).

Studies on COPI vesicles resulted in the identification of the p24 family of integral membrane proteins. They are a major component of the vesicles, and are involved in vesicle budding (Stamnes et al 1995). Dimerization of p24 permits interactions between the p24 cytoplasmic tails and two binding sites on the COPI coatamer γ subunit (Bethune et al 2006).

Multiple roles for COPI vesicles have been proposed; anterograde ER to Golgi transport (Bednarek et al 1995, Pepperkok et al 1993, Peter et al 1993), intra Golgi transport (Orci et al 1986), and retrograde Golgi to ER transport (Cosson & Letourneur 1994, Letourneur et al 1994). The anterograde or retrograde direction of COPI vesicle intra Golgi transport is still under dispute.

2.2 Cisternal maturation and vesicular transport.

Transport of proteins and lipids through the secretory pathway involves a sequence of events that are only partly understood. Lipids and properly folded proteins leave the endoplasmic reticulum (ER) via vesicular structures. These either transfer their cargo to pre-existing structures (ER to Golgi, vesicular-tubular structures (VTCs)) that shuttle between the ER and the *cis*-face of the Golgi apparatus or fuse together to generate a new VTC. Transport/maturation of the VTCs then takes place along microtubules towards the Golgi apparatus, where they either release their biosynthetic cargo via vesicular carriers, or align themselves alongside the *cis*-most cisterna to become a new *cis* cisterna. Both scenarios have been considered as valid transport mechanisms for the past 40 years but differ fundamentally in their mode of action (see Figure 7.1 for schematics of both models). These models of transport are called cisternal maturation and vesicular transport. Vesicular transport involves pre-existing membrane structures to which vesicles fuse or bud, whereas cisternal maturation relies on the constant reformation of cisternal membrane structures. As cisternal maturation requires a constant input of new material, it was suggested that inhibiting protein synthesis should result in the collapse of the Golgi apparatus; however, the Golgi apparatus observed before and after inhibition of protein synthesis appears the same (Jamieson & Palade 1968).

This historical experiment contributed greatly to establish the vesicular transport model as the paradigm for the field. Since then, attention has focused on the particular roles of the vesicular transport intermediates observed in the pathway. In addition to the clathrin coated vesicles seen budding from the *trans*-most part of the Golgi apparatus (Bard & Malhotra

2006), two different types of vesicles have been identified. These are termed COPI (Orsi et al 1986) and COPII (Barlowe et al 1994) and are observed adjacent to Golgi stacked cisternae and transitional ER elements (e.g. ER export sites), respectively. Both types of vesicles have since been extensively characterized in terms of their corresponding molecular machinery including coat and the components for sorting, budding, tethering, and fusion (Lanoix et al 1999, Lanoix et al 2001, Lee et al 2004).

A combination of genetic and morphological evidence supports the role for COPI vesicles in transporting resident proteins of the secretory pathway. This was based on the key finding that the major coat complex of COPI coatamer binds directly to sorting signals of “pathway resident” proteins (Bethune et al 2006). The second key finding was that the *in vitro*-based transport assay classically used to study COPI vesicle function, that registers the correction of a glycosylation deficiency through the transfer of COPI vesicles, actually registers the transfer of the correcting glycosylation enzyme to the deficient cargo-containing membrane, not the other way around (Love et al 1998). In fact, as little as one COPI-derived vesicle is sufficient to correct the entire glycosylation deficiency of one Golgi cisterna (Ostermann 2001). Consistent with this, COPI vesicles generated *in vitro* were found to contain large amounts of Golgi resident proteins such as the protein modifying enzymes, mannosidase II and N-acetylglucosaminyltransferase I (Lanoix et al 1999, Lanoix et al 2001). Significant levels of the ER to Golgi recycling proteins, KDEL-receptor and rBet1, and the Golgi resident proteins, mannosidase II and giantin, were detected in coated cisternal rims as well as in peri-Golgi vesicles (Martinez-Menarguez et al 2001). When the distribution of vesicular stomatitis virus protein G (VSV-G) (a marker protein extensively used for

anterograde transport in the *in vitro*-based transport assay) was studied, very little was observed in peri-Golgi coated vesicles. Taken together, this would support a main role for COPI vesicles in recycling and maintenance of the resident proteins in the pathway. This conclusion is contradicted by similar studies, for example Orci et al. (Orci et al 2000), where investigation of the distribution of mannosidase II and N-acetylglucosaminyltransferase I was assessed by cryoimmune electron microscopy. They found that both enzymes were mainly absent from Golgi cisternal buds and vesicles. The same conclusion was recently reached by Kweon *et al.* (Kweon et al 2004), using electron microscope enhanced immunolabeling combined with serial or thick sections followed by 3D tilting analysis.

This confusion and controversy has been further exacerbated by the proposal that newly synthesized secretory cargo leave the stacked cisternae of the Golgi complex without a lag upon entry to the Golgi with first order kinetics and with different rates for each cargo (Hirschberg et al 1998b, Kweon et al 2004). Recently it has been concluded that neither resident Golgi enzymes nor anterograde directed secretory cargo are in COPI vesicles whether *in situ* or isolated, and that COPI vesicles preparations are inactive in the Golgi cell free transport assay (Kweon et al 2004). This has led to a model excluding any role for peri-Golgi vesicles in Golgi transport, but rather suggests that direct tubular continuities between heterogeneous Golgi cisternae account for the vehicle for content redistribution in the Golgi stack and resident protein retention (Kweon et al 2004).

2.3 Mass Spectrometry Based Proteomics.

The use of mass spectrometry (MS) for the identification of proteins created the field of proteomics. No longer was the researcher limited to identifying proteins with antibodies or enzyme assays. Multiple proteins in one sample could now be analyzed at one time.

Mass spectrometry is based on the fact that in gas phase ions behave in a manner dependent on their mass to charge ratio when subject to electric or magnetic fields. Mass spectrometers of all types have three common parts: an ion source, an analyzer, and a detector. The ion source ionizes the sample under study (for proteomics that is a peptide). The analyzer separates the ions by their mass to charge ratio (m/z). The detector measures relative intensities of different masses.

2.3.1 Mass spectrometric techniques used in proteomics.

2.3.1.1 Time of Flight (ToF).

As the name implies, time of flight mass spectrometers separate ions based on the amount of time it takes an ion to fly to the detector (Wollnik 1993). Time of flight is dependent on both the distance the ion must travel and the velocity of the ion. The velocity of the ion is dependent on its mass and charge. From the time of flight and charge state the mass of the ion can be calculated.

2.3.1.2 Fourier transform ion cyclotron resonance (FTICR).

An FTICR mass spectrometer determines the m/z value of ions based on their frequency in a fixed magnetic field (Marshall et al 1998). The output signal must be first subjected to Fourier transform to determine the m/z .

2.3.1.3 Tandem MS (MS/MS).

Tandem MS involves two rounds of mass spectrometric analysis. The first round involves the selection of an ion by the first analyzer. This ion is then subject to fragmentation while stabilized by the second analyzer. For proteomics analysis, the fragmentation is designed to only occur at peptide bonds. The third mass analyzer separates the resultant fragment. In this way we can determine the mass of the parent ion as well as the masses of the fragments. In proteomics, this allows the sequence of the parent ion to be determined (Boyd 1994).

2.3.1.4 Gas chromatography/MS (GC MS).

For GC MS, the sample is separated via gas chromatography before proceeding to the mass spectrometer.

2.3.1.5 Liquid chromatography/MS (LC MS).

LC MS involves sample separation by a liquid chromatography column prior to mass spectrometric analysis.

2.3.1.6 Electrospray ionization (ESI).

ESI is often used in proteomics due to its ability to cause ionization without fragmentation of macromolecules such as peptides (Fenn et al 1989). The peptide sample is injected through a very small, charged capillary which creates a fine mist of ionized particles in solution. When the solvent evaporates, lone charged ions proceed towards the mass analyzer. Proteins are digested into peptides by proteolytic enzymes prior to mass spectrometric analysis for this technique.

2.3.1.7 Matrix-assisted laser desorption/ionization (MALDI).

Also used in proteomics due to its ability to cause ionization without fragmentation of macromolecules, MALDI involves the mixing of the protein solution to be analyzed with a matrix in solvent followed by spotting on to a metal plate. When the solvent evaporates, a crystallized matrix containing sample is left on the plate. A laser directed at the sample spot causes ionization of the sample, and the matrix protects the sample from destruction during application of the laser (Karas & Hillenkamp 1988, Tanaka et al 1988). Undigested proteins are used for this technique.

2.3.2 Interpretation of mass spectra.

The mass spectrometry (MS) analysis itself has inbuilt parameters which, to a certain extent, determine the degree of success of the entire exercise. There are two uncertainties in current MS characterization of peptides derived from proteins in biological samples. First, tryptic peptides have highly different efficiencies in their ionization and propensity to “fly”. Recently, attempts have been made to determine the biochemical attributes of such peptides (Mallick et al 2007). By simply tabulating which peptides are observed from past and ongoing proteomics efforts, the probability of flight can be determined empirically for each proteotypic peptide. High probability peptides can then be used as markers or signature peptides for each protein enabling identification with high confidence. Second, there is a stochastic aspect to further selection of the peptide that “flies” in the MS instrument for presentation to a collision cell for further fragmentation. The finite sampling time taken to select and fragment the parent tryptic peptides and assess the masses for these fragments represents the duty cycle. Sampling and fragmentation are incomplete and stochastic at present. It is, however, these MS fragmented peptides that are used to deduce the amino acid sequence of

the parent peptide. Hence, the quality and frequency of “tandem” mass spectra pointing to a specific peptide sequence varies between instrument platforms impacting identification and quantitation. Efforts to benchmark different MS platforms across the globe are underway through HUPO-based initiatives to circumvent this variable (Hermjakob 2006). Conceivably, commercially available peptide mixes will be needed to be included in future proteomics work to validate the performance and accuracy of the instrument(s) used. Once all the mass spectra have been collected from a sample, the data needs to be translated into peptide identifications. The identified peptides are linked to their parent protein sequence, and in this manner proteins are identified via proteomics. There are many commercial and open source software packages which are used to match spectra with peptide sequences. Mascot Cluster (Matrix Science, <http://matrixscience.com/cluster.html>) and Sequest (Sadygov et al 2004) are two that are popularly used.

2.3.3 Quantitation and proteomics.

The relative number of MS fragmented peptides is further used as a basis for a label-free quantitative method to score protein abundance. This running quantitation of their abundance termed “redundant peptide counting” is gathering popularity in the field (Blondeau et al 2004, Cox et al 2005, Gao et al 2005, Gao et al 2003, Gilchrist et al 2006, Girard et al 2005, Kislinger et al 2006, Liu et al 2004, Mallick et al 2007, Olsen et al 2006, Pang et al 2002, Qian et al 2005, Rappsilber et al 2002, Zybaylov et al 2005). It allows for quantitative comparison of proteins between fractions such that the relative abundance of a given protein can be determined. A protein that is synthesized in the ER and traverses the secretory pathway to be incorporated in the plasma membrane will be seen in multiple fractions. Knowing how much (in a relative sense) is seen in each fraction then gives rise to an intracellular distribution of each

protein as deduced by proteomics (Gilchrist et al 2006). Importantly, this simple way of determining relative protein abundance among subcellular fractions is an effective way of determining the degree of contamination. It also offers a means to identify biomarkers relevant for disease when comparing material from patient and control groups.

There are also methods for quantitation that use the incorporation of labels, such as SILAC (Stable isotope labeling with amino acids in cell culture) (Ong et al 2002), iCAT (isotope coded affinity tags) (Gygi et al 1999), and iTRAQ (a newer version of iCAT)(Ross et al 2004). These methods are much more involved than redundant peptide counting, all necessitating the use of isotopically labeled modifications. SILAC is for use in cell culture, so it can not be used for *in vivo* work, and the cost of iCAT and iTRAQ reagents can be prohibitive for large scale projects, as well as limiting the number of samples that can be compared to the number of labels available.

2.3.4 Sample preparation for proteomics.

In order to prepare a protein sample for tandem MS analysis, the protein components are size separated. Traditionally, this is done by 2 dimensional (2D) PAGE followed by silver staining. The density of each spot is then a convenient measure for relative abundance of each protein when comparing the same protein-spot between gels. The main drawback with 2D PAGE is that a large proportion of the proteome will never be seen due to the current inability of many proteins to enter the 1st dimension or to be resolved by their isoelectric point. Moreover, recent work shows that a significant number of spots seen on the gel each contain more than one protein species, sometimes up to five proteins. Though developments are being made, 2D PAGE has been overtaken by 1D SDS-PAGE. The entire sample is run in one lane, which after

separation, is cut into 1-2mm slices for further processing. The entire lane is processed allowing for a representation of the proteome. Following separation by PAGE, proteins are in-gel digested with proteolytic enzymes such as trypsin, and the peptides extracted from the gel.

Further separation methods prior to mass spectrometric analysis such as single or multiple dimensions of liquid chromatography or gas chromatography are used to provide better peak capacity (Aebersold & Mann 2003).

2.4 Proteomics and Cell Biology.

The characterization of organelles by tandem MS has led to new insights as to how these organelles are organized to effect their major functions.

2.4.1 Organellar proteomics.

2.4.1.1 Synaptic vesicles and clathrin coated vesicles from rat brain.

Using classical methods to isolate synaptic vesicles from rat brain homogenates, Takamori et al. (Takamori et al 2006) washed vesicles in sodium carbonate at pH 11, followed by either 1D or 2D PAGE to separate proteins. After in gel trypsinization and MS analysis they concluded that 410 different proteins had been characterized. Although no effort was made to provide a quantitative assessment of the MS data, they pursued quantitative Western blotting using standard curves of their cognate recombinant proteins to evaluate protein abundance. Co-purification of proteins with isolated synaptic vesicles enabled the authors to conclude that 7 of the 40 Rabs and related proteins identified by MS were constituents of the synaptic vesicles and that 12 of the 16 SNAREs characterized by MS were concluded to be genuine residents. For 14 proteins quantified by Western blotting, synaptophysin, synaptobrevin II, and the glutamate transporter VGlut2 were the most abundant. Taken together with their estimate of the lipid makeup of their preparations, they concluded that proteins overwhelm the surface of the synaptic vesicle with an excess of trafficking proteins to assure efficient membrane fusion reactions during synaptic transmission.

This proteomics-based characterization of synaptic vesicles now enables a comparison to the previously published proteomics-based characterization of clathrin coated vesicles that were also isolated from rat brain homogenates (Blondeau et al 2004). These investigators used redundant peptide counting (Blackstock & Weir 1999, Blondeau et al

2004) to test the hypothesis that brain clathrin coated vesicles have as their major cargo synaptic vesicle proteins for recycling. Indeed, of the 32 proteins that Blondeau et al. (Blondeau et al 2004) classified as synaptic vesicles proteins, 31 were observed by Takamori et al. (Takamori et al 2006). By contrast, of the 18 coat proteins, 1 endocytic accessory, and 7 novel proteins that were observed by Blondeau et al. (Blondeau et al 2004) and validated to be involved in endocytosis and/or clathrin trafficking, only 9 were detected by Takamori et al. (Takamori et al 2006). Hence, isolated synaptic vesicles lack to a large part the key endocytic components of clathrin coated vesicles from brain. Of further noteworthy significance, the 7 novel proteins characterized by Blondeau et al., have since been validated as new constituents of the clathrin and membrane trafficking machinery of clathrin coated vesicles (Blondeau et al 2004, Conner & Schmid 2005, McPherson 2007).

2.4.1.2 ER-phagosome controversy.

Further insight into organellar function emanated from the proteomics-based characterization of phagosomes isolated from macrophages (Garin et al 2001). Here, endoplasmic reticulum proteins, initially considered as contaminants (Garin et al 2001), were unexpectedly validated as genuine residents of early phagosomes (Gagnon et al 2002). These findings provided a fundamental insight into the mechanism of antigen cross presentation (Guermonprez et al 2003, Houde et al 2003). As the notion of ER being a contributor to phagocytosis has recently been challenged thereby questioning the validity of proteomics (Touret et al 2005). In this challenge, non-specific contamination was used as the main explanation for why Gagnon et al. (Gagnon et al 2002) observed ER specific proteins. Using antibodies to the luminal domain of calnexin, they showed that this ER-based marker could not be localized to any significant degree by immuno-based methods. This, in no way, excludes an ER contribution to phagocytosis. Indeed, by using antibodies to the cytoplasmic domain of

calnexin, it is clear that this part of calnexin persists in phagosomes longer than its luminal domain (Gagnon et al 2002). In addition, independent and substantial confirmation of the involvement of ER in phagocytosis has recently been presented (Ackerman et al 2006, Becker et al 2005, Hatsuzawa et al 2006). Nevertheless, more direct evidence may be necessary to address the arguments of Touret et al (Touret et al 2005).

2.4.1.3 Endosomes and p14.

Another noteworthy discovery based on an organellar proteomics effort is the determination of the function of endosomal p14. Originally characterized by a proteomics study of enriched endosomal fractions isolated from EpH4-mammary epithelial cell (Wunderlich et al 2001), p14 was subsequently found to be a scaffold for ERK1 signaling (Lunin et al 2004, Teis et al 2002), extending the concept of endosomes as signaling entities (Baass et al 1995). Most recently, mutations in the 3' UTR of p14 were identified in four offspring of a Mennonite family. The mutation resulted in reduced expression of p14 protein, a deficiency of endosomal biogenesis, and immunodeficiency likely linked to a defect in secretory lysosome formation (Bohn et al 2007).

2.4.1.4 The exosome.

When multivesicular endosomes fuse with the plasma membrane, exosomes (the vesicles from inside the endosomes) are released from the cell. It has been hypothesized that exosomes are somehow involved in intercellular signaling as part of the immune response (Peché et al 2003, Raposo et al 1996, Thery et al 2002, Zitvogel et al 1998). The proteome of exosomes produced by melanoma cell lines was determined via 2D-gel separation and tandem MS (Mears et al 2004). Forty-nine spots were subject to mass spectrometric analysis, and this resulted in the identification of proteins novel to exosomes, including p120 catenin, radixin, and immunoglobulin superfamily member 8 (PGRL). From

comparison to control samples, they confirmed the absence of proteins associated with lysosomes, mitochondria and the ER. Exosomes isolated from human urine were studied by Pisitkun et al. in the search for possible biomarkers of disease (Pisitkun et al 2004). Proteins were separated via 1D-SDS-PAGE followed by LC-MS/MS. Of the 295 proteins identified in this effort, the authors noted that 21 were proteins known to be involved in renal disease or blood pressure regulation.

2.4.1.5 The mitochondria.

The mitochondrion is an organelle involved in oxidative phosphorylation and ATP production. Isolation and proteomics characterization of the mitochondria from three different species has permitted the identification of 750 mitochondrial associated proteins (Gaucher et al 2004, Mootha et al 2003, Sickmann et al 2003, Taylor et al 2003). From mitochondria isolated from human heart, Taylor et al. identified 615 proteins using 1D-SDS-PAGE and LC-MS/MS (Taylor et al 2003). Eighty-one percent of the proteins, corresponding to 498 different identifications, belonged to classes of proteins of known functional significance. The other 19% belonged to classes of proteins that had not been characterized. The group expanded their coverage of the heart mitochondrial proteome in a second effort using multi-dimensional LC MS/MS (Gaucher et al 2004).

Mitochondria from *Saccharomyces cerevisiae* were analysed using 2D-PAGE LC MS/MS, 2D-PAGE LC-LC MS/MS and 1D-SDS-PAGE LC MS/MS in order to sidestep the problem of proteins being excluded by choice of separation technique (Sickmann et al 2003). From all three methods they identified a total of 750 proteins.

Prokisch et al. identified 546 proteins from mitochondria isolated from *S. cerevisiae* (Prokisch et al 2004). Yeast cells grown under four different conditions were subject to two different methods of mitochondrial

purification in order to generate both mitochondrial membrane and matrix fractions. The techniques LC MS/MS and LC FTICR were used for mass spectrometric analysis.

Mootha et al. isolated mitochondria from mouse brain, heart, kidney, and liver by gel-filtration chromatography followed by LC MS/MS, identifying 591 proteins, 163 of which were not previously identified as mitochondrial (Mootha et al 2003). Using human homologs of five of these newly identified proteins, they constructed GFP-fusion proteins in order to verify their sub-cellular location using confocal microscopy. They also compared the abundance of proteins they detected via proteomics with mRNA abundance, and the mitochondrial proteomes of the four tissue types. They confirmed that only a subset of mitochondrial proteins is shared between the tissue types, being indicative of functional specialization of the organelle.

2.4.1.6 The peroxisome.

Peroxisomes isolated from *S. cerevisiae* in both crude and purified fractions were subjected to iCAT based MS/MS in order to identify proteins enriched in the purified fractions (Marelli et al 2004). In this manner Marelli et al. were able to identify Rho1p as a peroxisomal protein.

2.4.1.7 The endoplasmic reticulum.

Proteomics analysis by 2D-PAGE and MALDI MS/MS of the contents of the endoplasmic reticulum lumen from the livers of Balb/C mice identified 141 proteins, of which 6 were novel (Knoblach et al 2003). Two of the novel proteins, ERp18 and ERp46, were protein disulphide isomerases.

Gilchrist et al. performed an analysis of the organelles of the early secretory pathway, including the rough and smooth endoplasmic reticulum, using 1D-SDS-PAGE and LC MS/MS (Gilchrist et al 2006). In

order to extend the proteome of the endoplasmic reticulum, they employed biochemical fractionation to their isolated rough and smooth endoplasmic reticulum fractions in order to enrich for low abundance proteins. Using this technique they extended the proteome by 35%.

2.4.1.8 The ERGIC.

ER-Golgi intermediate compartment membranes from HepG2 cells were isolated and then subjected to 1D-SDS-PAGE, MALDI MS/MS, and LC MS/MS (Breuza et al 2004). They identified four main categories of proteins: cargo receptors, proteins involved in membrane traffic, chaperones involved in protein maturation, and uncharacterized proteins. The novel protein, ERGIC-32, which is homologous to Erv46p and Erv41p, had its localization confirmed using confocal microscopy.

2.4.1.9 The Golgi apparatus.

Five separate proteomics analyses have been performed on the Golgi apparatus (Bell et al 2001, Gilchrist et al 2006, Taylor et al 2000, Wu et al 2004, Wu et al 2000). 2D-PAGE, 1D-SDS-PAGE, and multidimensional protein-identification technology (MudPIT) were the three separation strategies used in these studies. Bell et al. isolated a fraction enriched in Golgi membrane proteins and using MALDI MS and Edman sequencing they identified 81 proteins, 45 of which were considered Golgi resident, and 24 being ER or mitochondrial contaminants (Bell et al 2001). Using LC/LC MS/MS, Wu et al. identified 421 proteins in their Golgi sample, 110 of which were Golgi proteins (Wu et al 2004). A novel Golgi protein named GPP34 or GMx33 was identified by Bell et al., Taylor et al., and Wu et al., and was determined after further study to be a member of a novel family of trans Golgi proteins (Bell et al 2001, Taylor et al 2000, Wu et al 2004). Gilchrist et al. extended the Golgi proteome even further to

246 proteins by using Golgi derived COPI vesicles in their analysis (Gilchrist et al 2006).

2.4.1.10 The COPI vesicles.

COPI vesicles generated *in vitro*, with either hydrolysable GTP or non-hydrolysable GTP γ S, were isolated and analyzed by LC MS/MS after 1D-SDS-PAGE separation (Gilchrist et al 2006). There were 484 proteins identified in the COPI GTP vesicles and 909 in the COPI GTP γ S vesicles. Using their proteomics analysis of these vesicles and the Golgi apparatus, they were further able to test a controversial hypothesis in membrane trafficking through the Golgi and concluded that their data were consistent with the maturation hypothesis for Golgi transport.

2.4.1.11 The lysosome.

The lysosome, a degradative compartment of the cell containing many hydrolases, was studied by Bagshaw et al. (Bagshaw et al 2005). They isolated Triton-WR1339-filled lysosomes, which are known as 'tritosomes', and identified 215 proteins, 20 of which were novel, as well as many lipid raft proteins.

2.4.1.11 The nuclear envelope.

Schirmer et al. used a subtractive proteomics strategy to identify proteins of the nuclear envelope (Schirmer et al 2003). Because the nuclear envelope consists of endoplasmic reticulum membrane, they performed both a proteomics analysis of the endoplasmic reticulum and of the nuclear envelope. In this manner they subtracted the endoplasmic reticulum identified proteins from those identified in the nuclear envelope to generate a set of proteins that are unique to the nuclear envelope. They identified 13 previously identified components as well as 67 novel ones. Using immunolocalization, 8 of the 67 were tested and confirmed to be localized to the nuclear envelope.

2.4.2. Organelle contamination.

Isolated organelles are well suited to proteomics since the small volume of such structures ensure that protein concentrations in the sample are high. This overcomes the dynamic range problem of current MS-based proteomics efforts (Old et al 2005). This benefit, however, is counterbalanced by the problem of contamination.

Dunkley et al. (Dunkley et al 2004) have attempted to address this by an isotope tagging technique for quantitation and the assignment of proteins to subcellular compartments. The method has been named LOPIT (Localization of Organelle Proteins by Isotope Tagging). LOPIT scores the co-distribution of proteins within gradients with quantitation by iTRAQ. Fractionated endomembranes from *Arabidopsis thaliana* callus cultures enable the simultaneous localization of 527 proteins to the ER, plasma membrane, Golgi, vacuolar membrane, and mitochondria/plastids.

A label free quantitative method was applied by Foster et al. (Foster et al 2006) to map proteins of the endomembrane system of rat liver. They used protein correlation profiling (PCP) to localize 1400 proteins to 10 sub-cellular compartments resolved by rate zonal centrifugation of mouse liver homogenates. They concluded that 39% of all organellar proteins were found in multiple locations. By contrast, Gilchrist et al. characterized using proteomics highly enriched preparations of rough endoplasmic reticulum, smooth endoplasmic reticulum, Golgi apparatus, and a Golgi derived COPI vesicles, all derived from rat liver homogenates (Gilchrist et al 2006). They reported 2113 different proteins. They used a redundant peptide counting method as an index of protein abundance. They annotated 495 proteins as contaminants. Using hierarchical clustering (Kislinger et al 2006) to group protein distributions quantitatively, they concluded that Golgi contamination by ER was ~ 20% but that ER

contamination by Golgi was negligible. They also uncovered over 300 novel proteins, and could localize over 200 of these by proteomics.

Efforts are being made to improve the evaluation of mass spectra and identification of peptides. Presently, most of the time spent on a proteomics project goes into the manual work of sorting-out and annotating each protein identification. Current databases have a long way to go before being user friendly, as there is over representation of individual proteins and/or under representation of genes. More often than not, multiple entries are encountered for a given protein making redundant peptide counting a challenge which necessitates manual intervention. Moreover, factual annotation errors persist.

The goal of reaching the CAP (Complete, Accurate, Permanent) proteome for each organelle is still in the future but is achievable. By combining highly refined biochemical cell-fractions with 1D-gel based MS analysis, each proteome is near completion. It is likely that independent strategies are needed to achieve CAP status but already, proteomics goes a long way. What is evident is that cell fractionation and biochemistry, are now back in full swing. There is a central role for these types of methodologies which will persist for some time. Even if we reach CAP status for a given proteome of a given organelle, each proteome is likely to be cell-type specific and developmentally regulated as well as temporally specific. It is here that quantitative proteomics will prove its usefulness as we predict that the relative levels of proteins present in organelles will differ between cell-types, not just the makeup. This along with other cell-specific variations (i.e. post translational modifications and isoforms) will be the important determinants in organellar functions. Organellar proteomics in combination with genetic screens (e.g. RNA silencing) with image based localization (e.g. expression of open reading frames fused to fluorescent

proteins) and organellar protein interaction networks (Stuart et al 2007) may be an effective “systems biology” strategy to understand the cell.

Chapter 3 -- Validity of a quantitative proteomics method for organellar proteomics.

3.1 Abstract

Recent advances in mass spectrometry (MS) have enabled data-dependent acquisition of tandem mass spectra for a high throughput, reliable characterization of proteins in complex biological samples. Application of this method to purified organelles, i.e., rough microsomes, smooth microsomes, and Golgi fractions isolated from rat liver parenchyma reveals a correspondence between redundant peptide counts (as deduced from tandem MS) for proteins in these organelles, with relative protein content as determined by marker enzyme assays or immunoblots. For albumin (the major secretory protein of liver), we found a further correspondence by quantitative electron microscope immunolabeling of albumin in ultrathin cryosections of rat liver, when compared to peptide counts or quantitative immunoblotting of albumin in the isolated subcellular fractions. Tandem MS peptide counting as an estimate of relative protein abundance in isolated organelles now enables the characterization of several thousand proteins simultaneously in order to compare their global protein profiles.

At the commencement of this work, the methodology of peptide counting was just being introduced to the community, so we decided to perform a number of experiments to determine whether the technique was quantitative when in our hands. Peptide counting is now a widely used method of relative quantitation in proteomics (Blondeau et al 2004, Cox et al 2005, Gao et al 2005, Gao et al 2003, Gilchrist et al 2006, Girard et al 2005, Kislinger et al 2006, Liu et al 2004, Mallick et al 2007, Olsen et al

2006, Pang et al 2002, Qian et al 2005, Rappsilber et al 2002, Zybaïlov et al 2005).

3.2 Introduction

For organellar proteomics, it is relevant not only to determine what proteins are found in subcellular fractions, but also to estimate the relative abundance of each protein. We used tandem mass spectrometry to compare the protein content of the components of the early secretion apparatus of hepatocytes, i.e. the rough and smooth endoplasmic reticulum as well as the Golgi apparatus. In addition to enzymatic, immunoblot, and electron microscope based estimates of organelle enrichment, we have compared these data to the proteins characterized in these fractions by tandem mass spectrometry as quantified by an assessment of peptide abundance. This methodology was previously used to study isolated clathrin coated vesicles (Blondeau et al 2004). An accounting of the peptides characterized by tandem MS for this organelle illustrated the one-to-one stoichiometry of clathrin heavy and light chains. Furthermore, by the spiking of yeast cell lysates with 6 different proteins Liu et al. (Liu et al 2004) showed that spectral counts (peptide counts) were a valid indicator of relative protein abundance in 2D-LC tandem mass spectrometry, irrespective of the protein under analysis. As previously mentioned, peptide counts are now an accepted method of relative quantitation in proteomics (Blondeau et al 2004, Cox et al 2005, Gao et al 2005, Gao et al 2003, Gilchrist et al 2006, Girard et al 2005, Kislinger et al 2006, Liu et al 2004, Mallick et al 2007, Olsen et al 2006, Pang et al 2002, Qian et al 2005, Rappsilber et al 2002, Zybaylov et al 2005).

Proteins in rough and smooth microsomes, as well as in Golgi apparatus, isolated from rat liver parenchyma, were quantified using quantitative immunoblotting, marker enzyme assay, as well as redundant peptide counts. In addition, these data were compared to quantitative immunolabeling of one of these proteins, albumin, in ultra-thin

cryosections of rat liver parenchyma. A concordance of all of these methods supports the use of tandem mass spectrometry (tandem MS) to estimate relative amounts of specific proteins in organelles in a high throughput manner.

3.3 Methods

3.3.1 Organelle isolation.

This is detailed in the Sample preparation section of Chapter 4, specifically, 4.3.1.

3.3.2 Enzyme assays.

Glucose-6-phosphatase activity was assayed as per Farquhar et al. (Farquhar et al 1974). Galactosyl transferase activity was assayed as per Dominguez et al. (Dominguez et al 1999).

3.3.3 SDS-PAGE and immunoblots.

Organelle fractions were solubilized in SDS as described previously (Bell et al 2001, Dominguez et al 1999) 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 (Sigma, Oakville, Ontario, Canada). Quantitative immunoblotting with ¹²⁵I secondary antibody, and gamma counting was as described in Bell et al (Bell et al 2001). Albumin was purchased from Pierce Biotechnology (Rochford, IL, USA). Chemiluminescent immunoblotting was as described by NEN Life Science Products, 'Western Blot Chemiluminescent Reagents' (Albany, New York, USA).

3.3.4 Cryoimmune electron microscopy.

Liver samples were prepared as described by Dahan et al. (Dahan et al 1994). Cryosectioning of liver tissue samples was based on the procedures of Tokuyasu (Tokuyasu 1980), Griffiths et al. (Griffiths 1993, Griffiths et al 1984) and Geuze et al. (Geuze et al 1984). Specifically, tissue stubs were sectioned in a Reichert-Jung ultramicrotome equipped

with an FC4D cryochamber. 200 mesh Formvar-coated copper grids were carbon coated and then rendered hydrophilic using a glow-discharge apparatus. Sectioning was performed at -100°C and resultant sections were picked up with a copper loop filled with a 2.3 M sucrose solution. Section thickness was determined to be 50.4 ± 8.8 nm by the fold method of Small (Small 1968) as described in Weibel (Weibel 1979).

The Golgi fraction was prepared as described in Chapter 4, Section 4.3.1.2. The fraction was fixed with 4% paraformaldehyde/0.5% gluteraldehyde (final concentration) on ice for two hours. The membranes were centrifuged at 10000 *g* for 10 minutes. The supernatant was then discarded. The pellet was washed three times with 0.1 M cacodylate buffer and equilibrated for two to three hours in 2.3 M sucrose. After floating to the top of the sucrose, the pellet was then cut into small pieces, placed on nickel stubs, and quick-frozen in liquid nitrogen.

The immunolabeling procedure and staining was carried out as described in Dahan et al. ((Dahan et al 1994)). The sections were viewed using a Philips 400 T electron microscope, operating at 80 kV.

3.3.5 Peptide Counting.

3.3.5.1 The principle of peptide counting.

The principle of peptide counting is based on the fact that during mass spectrometric analysis, every peptide detected and sent for fragmentation was derived from a protein present in the original sample. The higher the concentration of protein X in the sample, the greater the number of peptides it will produce upon trypsin digestion. Each of the peptides that is detected and sent for fragmentation results in one tandem mass spectra. Simply by counting the number of tandem mass spectra

assigned to peptides, which are in turn matched back to protein X, gives an indication of the abundance of protein X.

3.3.5.2 Comparison between samples.

Because each sample subjected to mass spectrometric analysis generates a different total number of assigned mass spectra (hence identified peptides), we needed a method to compare protein abundance between samples. To normalize our data, we divided the number of peptides assigned to protein X by the number of all assigned peptides in the sample. This generated a result expressed as a percentage of total assigned peptides (% total peptides).

3.4 Results

3.4.1 Sensitivity of the approach.

The overall sensitivity of the in-gel tryptic digested 1D SDS-PAGE tandem MS approach was estimated by a dose response curve for purified albumin (Figure 3.1). Coomassie blue staining of 1D SDS-PAGE revealed a monotonic increase in density from 0.05 to 1.0 μ g of protein (inset and upper panel). Excision of the bands corresponding to albumin followed by in-gel tryptic digestion and tandem MS also revealed an increase in albumin peptides (lower panel) with protein amount. A sensitivity of circa 4pmols (250ng) is determined.

3.4.2 Complex protein mixtures.

The detection of albumin in rough and smooth microsomes and Golgi fractions isolated from rat liver parenchyma was estimated by quantitative immunoblotting (Figure 3.2, solid histograms). These data were compared to peptide counts for albumin by tandem MS in separate organelle preparations (Figure 3.2, open histograms). Whether by immunoblotting or peptide counts, a marked increase in albumin was observed in the isolated Golgi fractions. Therefore, at least for albumin, the peptide count method is a valid estimate of relative protein abundance in these subcellular fractions.

3.4.3 *In situ* distribution of albumin in rat liver parenchyma.

Albumin enrichment in Golgi apparatus was also verified by quantitative immunoelectron microscopy on ultra thin cryosections (Figure 3.3A). Albumin antigenicity was estimated by the analysis of 10 nm gold particles conjugated to secondary antibody (Figure 3.3A-C). As for the isolated RM, SM and Golgi fractions evaluated by quantitative immunoblotting or tandem MS (peptide counts), a marked increase in albumin antigenicity was detected in morphologically defined Golgi apparatus. Indeed the

resolution of the electron microscopy was greater and permitted detection of an increase in concentration from the cis-Golgi network to the stacked cisternae of the Golgi apparatus (Figure 3.3B, C).

The enrichment of albumin antigenicity from rough ER to the stacked cisternae of the Golgi apparatus was greater however by cryoimmune EM than that detected by quantitative immunoblotting or peptide counts of the corresponding subcellular fractions (cf. Figure 3.2 and 3.3C).

This was clarified by cryoimmune EM analysis of the isolated Golgi fraction. Using beta-COP as a marker for the cis Golgi network (Griffiths et al 1995, Oprins et al 1993) the isolated Golgi fraction was found to have a closely attached tubular compartment enriched in beta-COP which most likely corresponded to the cis Golgi network (Figure 3.4). This structure was diminished in albumin content as compared to the tightly opposed stacked cisternae of the Golgi apparatus (Figure 3.4B). Therefore, the isolated Golgi fraction contains both stacked cisternae with a high albumin content and cis Golgi elements with a low albumin content accounting for the apparent discrepancy between the data in Figure 3.2 and Figure 3.3C.

Therefore, whether by immunoblotting of isolated subcellular fractions, peptide counts of albumin in these fractions by tandem MS or cryoimmune electron microscopy, a coincident trend of albumin concentration from the endoplasmic reticulum to the Golgi apparatus was found.

3.4.4 Comparison of marker enzyme enrichment and marker protein peptides detected by tandem MS.

The enrichment for the marker enzyme of the hepatic endoplasmic reticulum, glucose-6-phosphatase was compared to that of the Golgi marker enzyme, galactosyl transferase in isolated subcellular fractions of rough and smooth microsomes and Golgi apparatus. The results (Figure

3.5) revealed the highest enrichment of the enzymatic activity for glucose-6-phosphatase in RM and SM fractions and of enzymatic activity for galactosyl transferase, in the Golgi fraction. Peptide counts for glucose-6-phosphatase as deduced from tandem MS (Figure 3.5, lower left panel) were high in RM and SM fractions but not Golgi fractions. Peptide counts for galactosyl transferase were only found in Golgi fractions (Figure 3.5, lower right panel). Hence, peptide counts detected marker proteins in their cognate organelles.

Using a chemiluminescent method of detection, immunoblotting of RM, SM and Golgi fractions revealed an enrichment of the ER marker calnexin in RM and SM fractions compared to homogenate, the Golgi marker mannosidase II in the isolated Golgi fraction as well as the Golgi SNARE membrin (Figure 3.6). Densitometric analysis indicated highest antigenicity for the markers in their cognate organelles (red histograms). Peptide counts for the same proteins as deduced from tandem MS showed highest levels of calnexin peptides in RM and SM fractions and of mannosidase II peptides detected in Golgi fractions (far right panel). The characterization of membrin in the same fractions was more variable but with the highest number of peptides detected in the isolated Golgi fraction. The variability is undoubtedly related to the low number of peptides detected for membrin (a total of 6 peptides spread amongst nine biological samples) as compared to either calnexin with (141 peptides detected) or mannosidase II (251 peptides detected).

Therefore, whether for soluble proteins (albumin) or integral membrane proteins (glucose-6-phosphatase, galactosyl transferase, calnexin, mannosidase II, but not membrin), peptide counts as deduced from tandem mass spectrometry represented a similar distribution of proteins as that found by immunoblotting or enzyme assay.

3.5 Discussion

The proteomics strategy we followed consisted of organelle isolation, protein separation by 1-D gels, cutting of the gel into bands followed by in-gel tryptic digestion, extraction of peptides, HPLC separation of tryptic peptides, and tandem MS. Based on the analysis of purified albumin, a sensitivity of detection of circa 4pmol was found for the overall methodology, and the efficiency of matching tandem mass spectra successfully to peptides was circa 50%. The sensitivity measurement is likely three times higher, since only one third of the of the extracted tryptic digest volume is submitted to the LC-QToF. The unassigned spectra are due to post translational modifications or sequences being absent from the database.

Albumin is the major secretory protein of rat liver parenchyma (Bergeron et al 1978). Analysis of well characterized, isolated subcellular fractions of rat liver parenchyma enriched in elements of the early secretory pathway revealed albumin as detected by quantitative immunoblotting in rough and smooth microsomes as well as Golgi fractions. The highest concentration of albumin was found in the isolated Golgi fraction confirming earlier studies (Bergeron et al 1978). The characterization of albumin content of these subcellular fractions by tandem MS also revealed the highest abundance of albumin peptides in the isolated Golgi fraction.

Analysis of the distribution of albumin in the same compartments *in situ*, by quantitative immuno-electron microscopy on ultra thin cryosections of liver parenchyma, also showed high concentrations in stacked, flattened cisternae of the Golgi complex. The high resolution of this method revealed in addition a distinction between the cis Golgi network with low albumin antigenicity, tightly applied to the Golgi stacked cisternae with high albumin content. When cryosections of the isolated Golgi fraction

were analyzed by this method, a distinct CGN with low albumin antigenicity tightly applied to the stacked Golgi cisternae (high albumin antigenicity) was also found. We have shown that quantitative EM immunolabeling as well as quantitative immunoblotting for albumin in isolated subcellular fractions demonstrate a comparable distribution in rough and smooth endoplasmic reticulum and Golgi apparatus as determined by peptide counts.

Characterization of the subcellular fractions by marker enzyme analysis confirmed their enrichment. Again, peptide counts of the marker proteins (glucose-6-phosphatase for ER, and galactosyl transferase for Golgi) confirmed the restriction of these proteins to their cognate organelles as well as the lack of cross contamination between ER and Golgi fractions. This was also confirmed by a chemiluminescent method of immunoblotting for further markers, as well as by enzyme assay. Peptide counts when abundant (i.e. for calnexin, mannosidase II, but not membrin) also showed a lack of cross contamination. The number of peptides detected for membrin was six which is the same as that for galactosyl transferase. Why membrin detection was more variable than that of galactosyl transferase remains unexplained.

The peptide count method as used here extends the application of this methodology as first utilized for the characterization of proteins in brain derived clathrin coated vesicles (Blondeau et al 2004). This peptide count methodology has also been analyzed by Liu et al., 2004 (Liu et al 2004), who showed an increase in peptides detected for six different proteins (including albumin) added to yeast lysates at four different concentrations. Therefore, as concluded by Liu et al., 2004 (Liu et al 2004), despite the many variable factors that may affect the acquisition of tandem mass spectra, these factors must average out such that redundant peptide (spectral) counts accurately reflect protein abundance even in complex

protein mixtures. Also as concluded by Liu et al. (Liu et al 2004), this methodology is particularly well suited to high throughput proteomics.

Figures

Figure 3.1. Sensitivity of the in-gel trypsin digested 1D SDS-PAGE tandem MS method.

(Inset) Dose dependent staining by Coomassie Brilliant blue of increasing amounts of purified albumin in 1D SDS PAGE. The amount of albumin applied to each lane of the gel is indicated. (Upper panel) Quantitation of Coomassie blue staining for two separate experiments revealing a dose-dependant increase in Coomassie blue staining with protein applied to the gel. (Lower panel) Peptide counts (two separate experiments) of albumin as characterized by tandem MS. Peptide counts increase with increased amounts of albumin subjected to 1D SDS-PAGE. Open symbols, experiment 1; closed symbols, experiment 2.

Figure 3.1

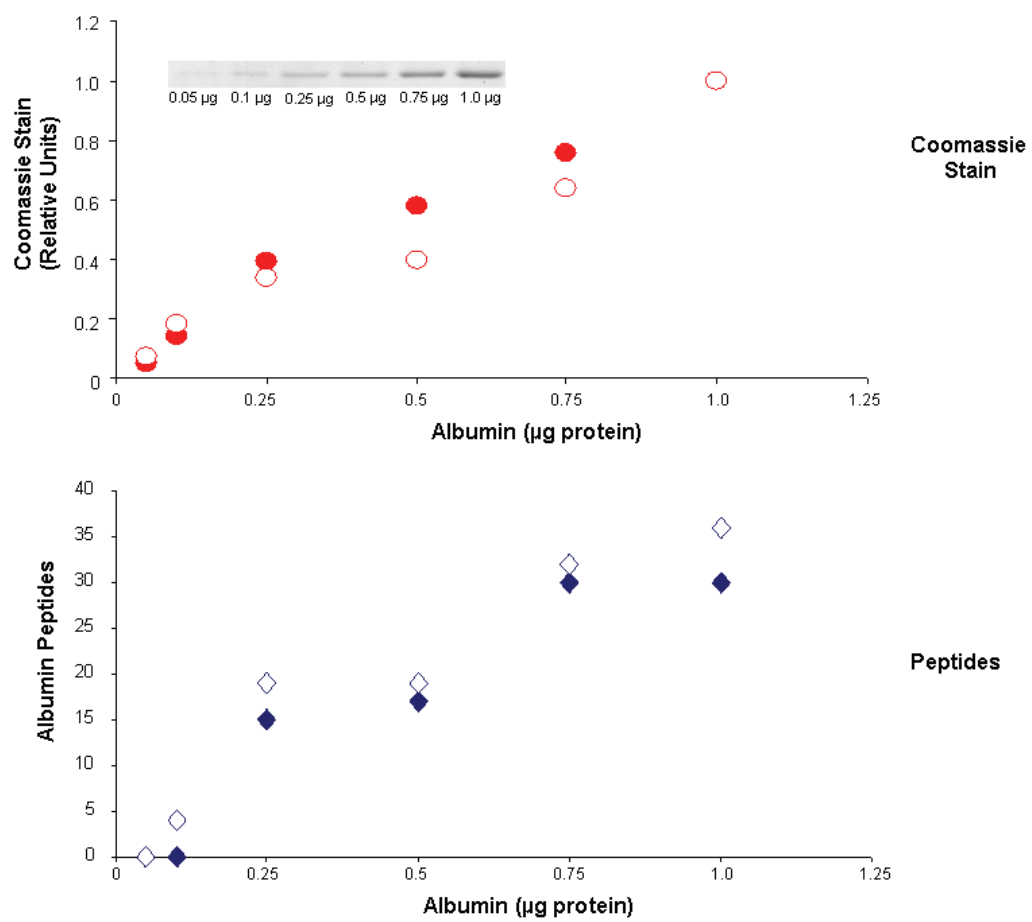


Figure 3.2. Characterization of albumin content in RM, SM and Golgi fractions.

Under linear conditions of detection, albumin content was estimated by quantitative immunoblotting with I^{125} labeled secondary antibody. 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 (lower) reveal the quantitative distribution of albumin antigenicity as deduced from gamma counting of the excised bands corresponding to albumin in RM, SM and Golgi fractions. Peptide counts corresponding to albumin in RM, SM and Golgi fractions are also shown for 3 separate preparations of the subcellular fractions. Peptide counts are represented on the ordinate as described. Different biological preparations were used for mass spectrometry and quantitative immunoblot analysis.

Figure 3.2

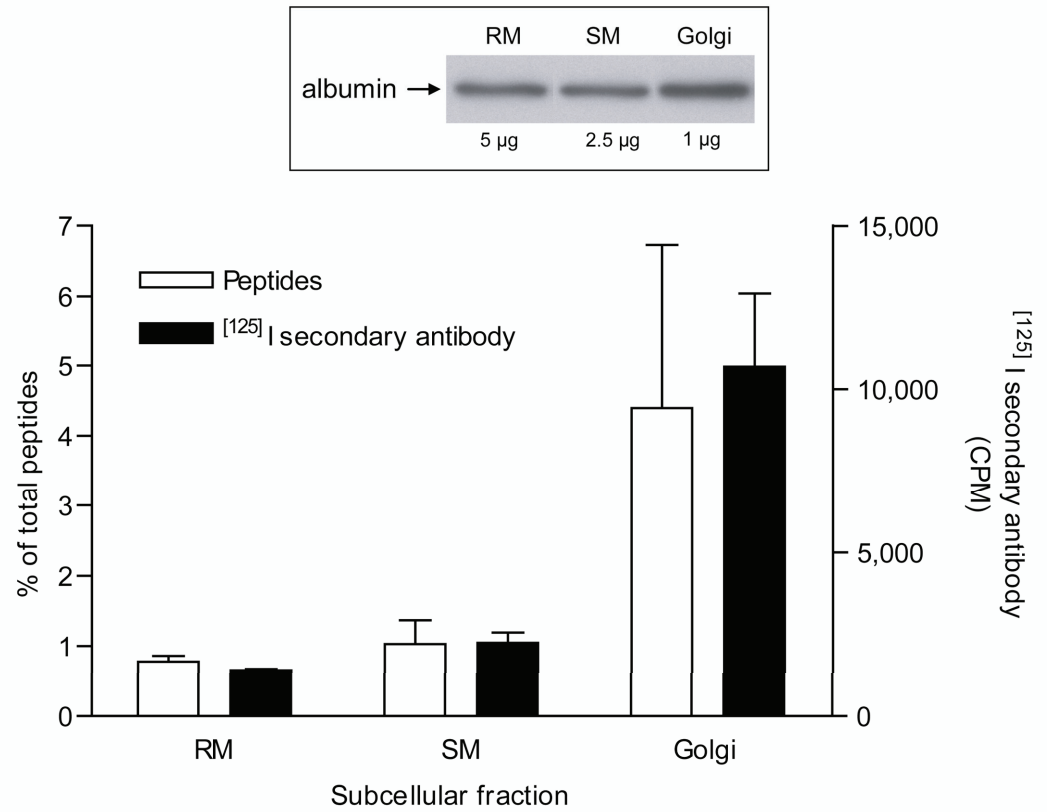


Figure 3.3. Albumin is concentrated in the Golgi apparatus from the CGN.

A Rat liver hepatocyte cryosections were immunolabeled for albumin with 10 nm gold particles. Immunoreactive albumin is detected within elements of the ER (****) in which it is homogenously distributed. Ends of rough ER cisternae (encircled by *dotted lines*) appear to taper and transform into tubular membranes which are distinct from the CGN (*arrows*). This compartment, characterized by tubular elements (*arrows*) around the Golgi apparatus, appears to have a higher gold particle density labeling for albumin than the flattened rough ER cisternae. The Golgi apparatus is highly labeled for albumin, within flattened cisternae (G) and peripheral distensions (d). **B** Enlarged view of the Golgi apparatus shown in A. The cis-Golgi network is delineated by dashed lines and indicated as cis. Golgi particles therein are encircled. The Golgi stacked cisternae and bulbous distensions at their rims are outlined by bold dashed lines. Trans-Golgi elements are indicated (trans) and defined as those on the opposite side of the cis-Golgi compartment. Albumin antigenicity, as deduced from the density of gold particles is markedly lower in the cis-Golgi network (gold particles encircled) as compared to the stacked cisternae and bulbous distensions of the Golgi and the associated tubulo-vesicular elements of the trans-Golgi network, all with a markedly higher density of gold particles. Bar, 400 nm. **C** Albumin concentrates in the Golgi apparatus. Ultrathin liver cryosections (n=36 micrographs from 4 animals) were immunolabeled with anti-albumin followed by goat anti-rabbit IgG 10 nm gold and the labeling density (particles/ μm^2) $\pm$ SEM was estimated in the individual compartments as described in Methods. Golgi stacks in which secretory vesicles were observed, were quantitatively analyzed to enable the identification of the cis vs. trans sides of the Golgi apparatus. Background labeling (as evaluated by labeling density measurements over mitochondria and peroxisomes) was subtracted from labeling densities over secretory compartments in albumin-labeled cryosections to yield the

values presented. Inset: The labeling density of albumin within individual cisternae of the rough ER (n=141 cisternae) and Golgi apparatus (n=128 cisternae) was determined to obtain a more precise quantitative estimate of the concentrative effect of the Golgi apparatus relative to the rough ER. The numbers (*n*) in brackets represent the absolute number of gold particles counted.

Figure 3.3

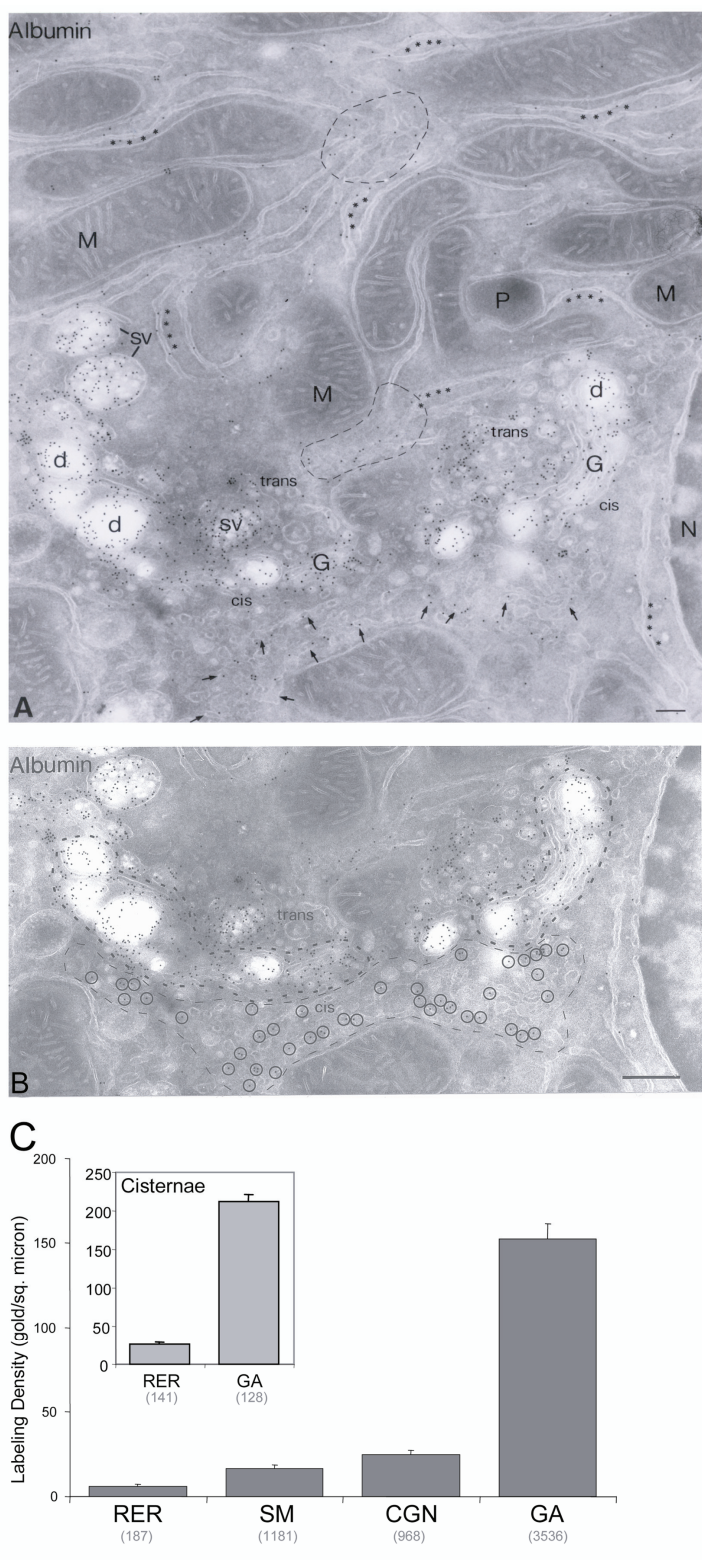


Figure 3.4. Distribution of albumin and β -COP in isolated rat liver Golgi fractions.

A Cryosections of the isolated Golgi fraction double-labeled for β -COP (10nm gold) and albumin (5nm gold). The broad dashed line indicates the outline of the cis-Golgi network overlaid with 10nm gold particles (arrowheads). The stacked flattened Golgi cisternae are overlaid by 5nm gold particles (arrows). The TGN with associated secretory vesicles (sv) is also indicated. Bar 400nm (n=10 Golgi profiles). **B** Gold particle labeling density of β -COP and albumin (n=10 Golgi apparatus profiles; 378 and 53 gold particles were scored for albumin and β -COP, respectively) in the two compartments.

Figure 3.4

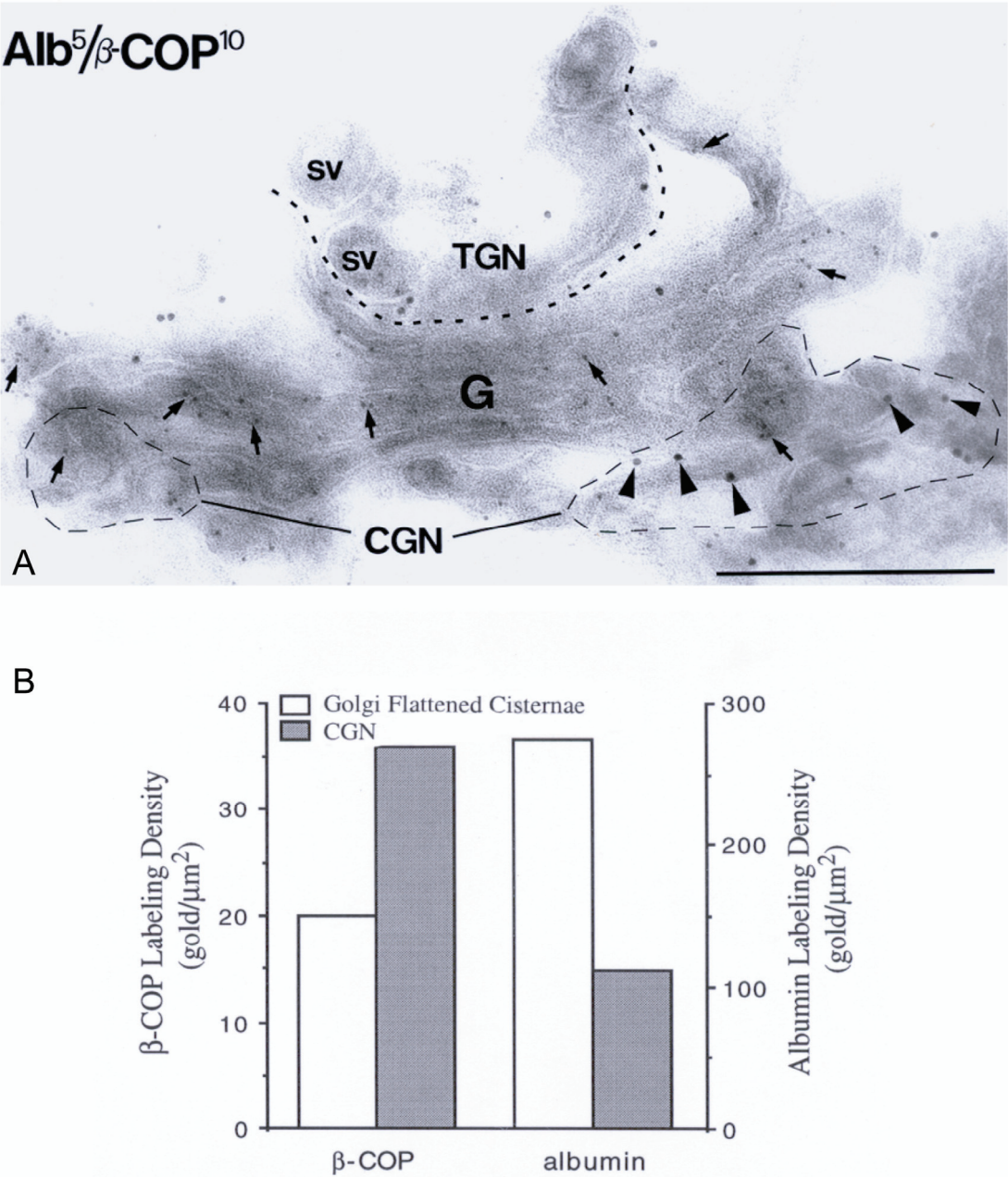


Figure 3.5. Comparison of marker enzyme activities and peptide counts for cognate marker proteins.

This figure was taken from (Gilchrist et al 2006). Upper panel. ER marker enzyme (glucose-6-phosphatase) and Golgi marker enzyme (galactosyl transferase) activities and enrichment in isolated subcellular fractions. Enzyme activities in the homogenate, RM, SM, and Golgi fractions are indicated for three separate biological preparations of each fraction (mean $\pm$ standard deviation). Lower Panels. Peptide counts corresponding to glucose-6-phosphatase and galactosyl transferase for 3 separate preparations for RM, SM and Golgi fractions. The total number of peptides characterized glucose-6-phosphatase was 40, and for galactosyl transferase there were 6. Variability is expected due to the 1,4,5 MS/Tandem MS duty cycle (duty cycle: for ever MS scan of 1 sec, up to 4 peptide ions are selected for up to 5 tandem MS scans of 1 sec (see also Tandem MS (MS/MS) analysis and Data Processing) employed for sampling peptides from the HPLC column.

Figure 3.5

FRACTIONS	GLUCOSE-6-PHOSPHATASE		GALACTOSYL TRANSFERASE	
	Spec. Act. 1	Enrichment over homogenate	Spec. Act. 2	Enrichment over homogenate
HOMOGENATE	4.5 ± 0.7	1.0	0.1 ± .01	1.0
RM	20.4 ± 4.9	4.5 ± 0.4	0.1 ± .01	0.7 ± 0.2
SM	17.3 ± 4.1	4.0 ± 0.3	0.3 ± .01	3.5 ± 0.2
Golgi	7.3 ± 1.2	1.3 ± 0.2	10.4 ± 3.8	105.5 ± 26.4

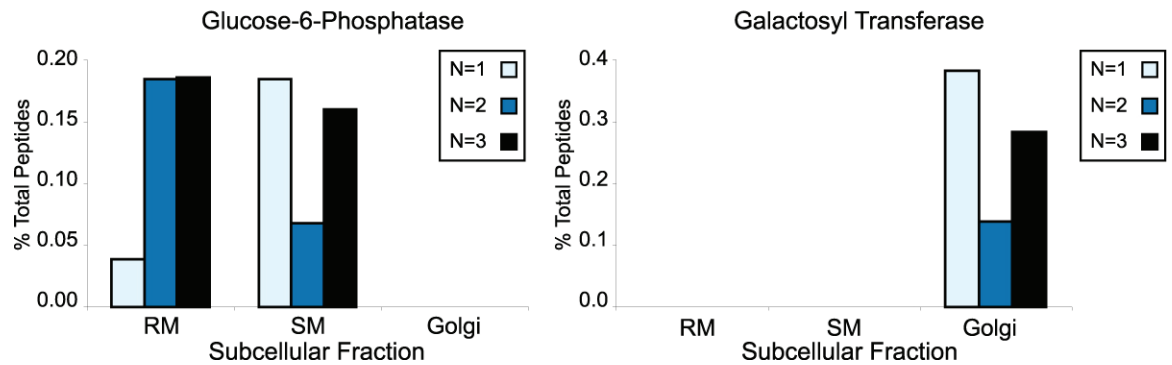
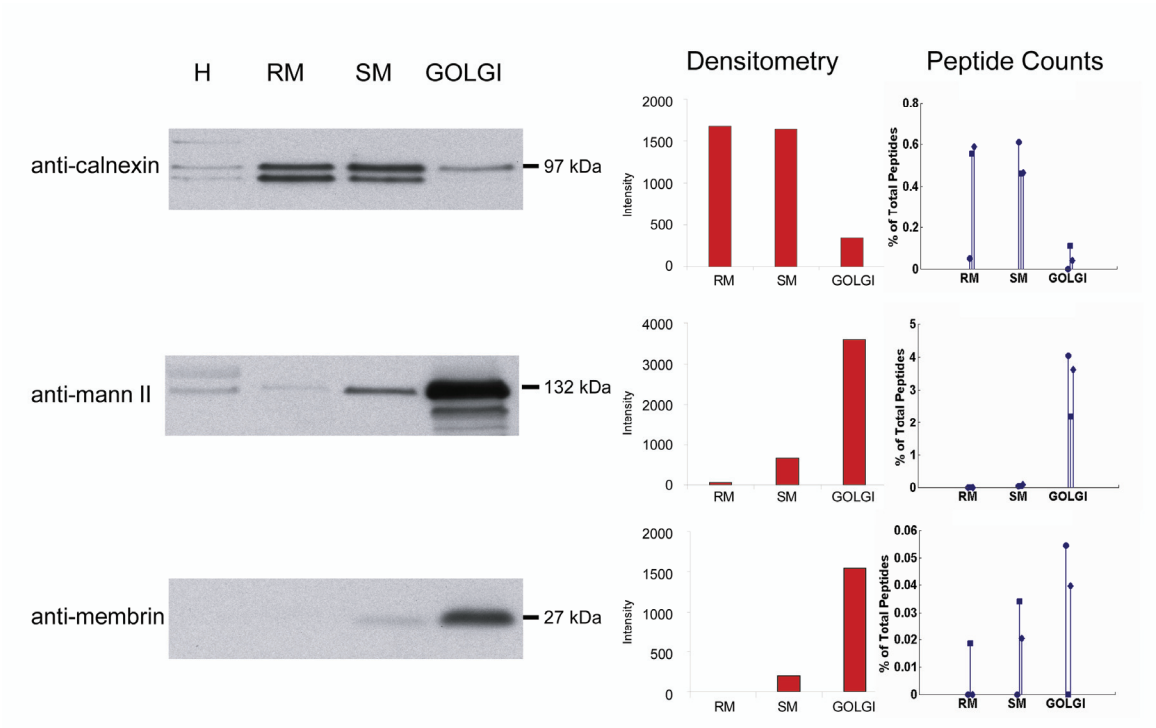


Figure 3.6. Marker proteins as detected by immunoblotting and peptide counting.

Left side: Immunoblots of markers in homogenate (H), rough microsomes (RM), smooth microsomes (SM) and Golgi fractions for calnexin (ER marker), mannosidase II and membrin (Golgi markers). 100 µgrams of protein was loaded onto each lane except for RM (140 µg) and immunoblots were visualized by ECL. Middle: Optical density of the measurements of immunoblot (histograms). Far right: Peptide counts detected for calnexin (141), mannosidase II (251), and membrin (6) for 3 separate experiments of RM, SM and Golgi fractions.

Figure 3.6



Chapter 4 -- The Pipeline

4.1 Abstract

For this project to come to fruition, a method of tracking every step of the experimental pathway and its resultant data had to be designed. The methods of organelle isolation, characterization, sample preparation for mass spectrometric analysis, the mass spectrometric analysis itself, collection of mass spectrometric data, database matching of spectra, and final tabulation of protein identifications is detailed here. This set of procedures and protocols comprise the first two parts of the pipeline that was developed to streamline this high throughput proteomics project.

4.2 Introduction

Due to the large amount of data being produced, an automated manner of sample processing and preliminary data analysis was needed in order not to be overwhelmed by the incoming flood of information. This methodology evolved into a standard operating procedure, the “pipeline”, which is comprised of manual sample preparation and characterization, automated size separation of proteins on 1D gels, automated in-gel trypsinization, automated mass spectrometry analysis (7 days a week, 24 hours a day), and automated preliminary data processing, followed by an exhaustive manual curation of the identified proteins.

The pipeline is comprised of three parts. The first part of the pipeline is manual sample preparation and characterization. For organellar proteomics we want our samples to be highly enriched, with minimal contamination, and of consistent quality. Our lab has many years of experience with organellar isolation using protocols that have been refined over decades. These organellar preparations are subjected to rigorous characterization by traditional methods such as electron microscopy, enzyme assay and western blot to verify their quality. Once the identity and homogeneity of the samples has been verified, the sample proceeds onwards to the second part of the pipeline. This part of the pipeline is automated and comprises the cutting of the 1D-SDS PAGE gel through to the construction of a list of proteins generated from the list of protein identifications from Mascot (see below). The last part of the pipeline involves the manual curation of all the protein identifications, and is described at length in Chapter 5.

4.3 Methods

4.3.1 Sample preparation.

4.3.1.1 Rough and smooth microsomes.

Rough and smooth microsomes from rat liver homogenates were isolated exactly as described by Paiement et al., (Paiement et al 2004). A brief outline of this procedure follows. A Potter-Elvehjem tissue grinder was used to homogenize finely minced rat liver. A series of centrifugations resulted in the separation of nuclei, then mitochondria, and finally total microsomes. The total microsomes fraction contained membrane from the rough and smooth endoplasmic reticulum as well as other cellular sources (e.g. plasma membrane, mitochondria). After suspension in 1.38M sucrose, the membrane mixture was placed under step gradients of 1M, 0.86M, and 0.25 M sucrose and then centrifuged at 300 000 X g for a period of 60 minutes. The pellet containing the rough microsomes were resuspended in 3 mM imidazole buffer (pH 7.4) containing 0.25 M sucrose and stored at -80° C. The smooth microsomes in the 1M sucrose step of the gradient were also resuspended in 3 mM imidazole buffer (pH 7.4) containing 0.25 M sucrose and stored at -80° C until required for separation by SDS-PAGE.

4.3.1.2 Golgi apparatus.

The Golgi fraction was prepared exactly as per Dominguez et al. (Dominguez et al 1999). The homogenates used for isolation of the Golgi fraction were prepared by gentle homogenization of finely minced liver with the type B loose pestle of a Dounce homogenizer (12 strokes; Thomas Scientific) in a 0.25M sucrose buffer with 5mM Tris-HCL (pH 7.4) and 5mM MgCl (STM), and containing the proteinase inhibitors PMSF (1 mM) and aprotinin (200 U/ml). Prior to a two hour incubation at 4°C, the homogenates were filtered through two layers of cheese cloth. The homogenate is subjected to a low-speed centrifugation at 400g_{max} for 5

minutes. The resultant fractions of this centrifugation step are a supernatant (S1) that was saved, and the pellet (P1) that was rehomogenized in half the original volume of buffer with five strokes of the type B pestle. A second low speed centrifugation at $400g_{max}$ for 5 minutes is performed on this rehomogenized mixture. This produced a supernatant (S2) and a pellet (P2). S1 and S2 were combined and then centrifuged for 10 minutes at $1475g_{max}$. 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 $1200g_{av}$ for 30 min, followed by $83000g_{av}$ in the rotor (SW27; Beckman Instruments, Inc.) for a period of 1 hour. After the centrifugation, the band approximately 1cm above the load zone was collected and adjusted to 0.4M sucrose in STM buffer. This was centrifuged at $1475g_{max}$ for 10 minutes to generate the pellet (P3). Resuspension in 0.25 M sucrose in STM buffer followed by pelleting at $1475g_{max}$ for 10 minutes was performed twice 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.

4.3.1.3 COPI vesicles.

The COPI vesicles were generated per Kartberg et al. (Kartberg et al 2005), using previously isolated and frozen rat liver Golgi fractions and rat liver cytosol (Stuart et al 1993). 400 μg of Golgi membranes and 12.5mg of rat liver cytosol are required for this reaction.

Prior to performing the vesicle generation assay, it is necessary to prepare isolated rat liver Golgi membranes (Dominguez et al 1999), rat liver cytosol (Stuart et al 1993), and purified His₆-tagged $\alpha\text{-SNAP}^{\text{dn}}$ mutant as per Barnard et al. (Barnard et al 1997). The use of an $\alpha\text{-SNAP}^{\text{dn}}$ mutant

prevents the newly formed vesicles from fusing back to the Golgi apparatus.

An aliquot of the Golgi fraction containing at least 400µg of protein is thawed, and the protein concentration determined by using the BioRad version of the Bradford protein assay reagent and BSA as a standard.

An aliquot of rat liver cytosol containing at least 12.5mg of protein is thawed then diluted with 5ml of KOAc assay buffer (25 mM HEPES, 115 mM KOAc, 2.5 mM MgCl₂, pH 7.0). To clear the cytosol, this mixture is centrifuged at 4°C for 1 hour at 157000*g*_{max}. To further clear the cytosol the supernatant from the previous centrifugation is transferred into new tubes and centrifuged again at 4°C for 15 minutes at 16000*g*. The protein concentration of the cytosol is determined using the BioRad version of the Bradford protein assay reagent and BSA as a standard.

The His₆-tagged α-SNAP^{dn} mutant was diluted to 1 mg/ml in KOAc assay buffer and then pre-warmed to 37°C.

Five reaction mixtures are made containing in each tube: 250µl of 10 X ATP regenerating system (26 mM of ATP, 100 mM creatine phosphate, 116 U/ml creatine kinase); 31µl of 40 mM GTP or 20µl of GTPγS 20µM (depending on whether you are generating vesicles with hydrolysable GTP or non-hydrolysable GTPγS); 25µl of 100 mM DTT; 25µl of 100X protease inhibitor cocktail (50 mM benzamidine HCl, 500 µg/ml leupeptine, 200 µg/ml soy bean trypsin inhibitor); 25µl of 1mg/ml α-SNAP^{dn} mutant; 12.5mg prepared rat liver cytosol; 400µg rat liver Golgi. The mixtures are made up to a final volume of 2.5ml per tube with KOAc assay buffer and vortexed less than one second each to mix. The tubes are then incubated for 30 minutes at 37°C, and the reaction terminated by transferring the tubes onto ice.

230µl of 3M KCl is added to each tube to detach the vesicles from the Golgi membranes. The reaction mixtures are divided into 0.3ml aliquots and delivered into microcentrifuge tubes prior to centrifugation at 16 000 g and 4°C for 15 minutes in order to separate the vesicles from the Golgi membranes. The supernatants are pooled. Care must be taken not to disturb the membrane pellets while removing the supernatants. Four tubes with a two-step sucrose cushion are prepared by adding 800µl of 20% wt/wt sucrose in KOAc assay buffer with 0.5M KCl into each of four ultra-clear SW-60 centrifuge tubes, followed by underlayering with 150 µl of 50% wt/wt sucrose in KOAc assay buffer with 0.5M KCl in each tube. Approximately 3 ml of the pooled supernatants is overlaid on the sucrose cushions of each tube. The tubes are centrifuged at 407000g_{max} at 4°C for three hours, and the vesicles are now collected from the 20%/50% sucrose interface. The vesicle fractions are pooled and the sucrose concentration adjusted by adding 1550µl of 65% sucrose (wt/wt) in KOAc assay buffer with 0.5M KCl, to a final approximate sucrose concentration of 55%. For the final purification step, vesicles were floated on a step gradient of sucrose containing a 20% (wt/wt) sucrose layer and a 50% (wt/wt) sucrose layer, in KOAc assay buffer with 0.5M KCl in an ultra-clear SW-60 centrifuge tubes. The pooled vesicles fractions were underlayered, and then spun at 337000 g_{max} at 4°C for 16 hours. Vesicles were collected from the 20%/50% interface and stored at -80° C until needed.

4.3.2 Sample characterization.

4.3.2.1 Preparation of samples for electron microscopy.

RM, SM. And Golgi fractions were prepared for electron microscopy using the random sampling filtration protocol as detailed by Bell et al. (Bell et al 2001).

The COPI vesicle preparations were pelleted onto a 20 μ l 50% (w/w) sucrose cushion at 45 000 rpm for 120 min at 4°C using a TLA45 rotor. The vesicle pellets were diluted into 100 mM (pH 7.4) phosphate buffer and then fixed for 2 h at 4°C with glutaraldehyde at a final concentration of 2.5% (wt/vol). Vesicles were collected after fixation by centrifugation at 14 000 rpm for 60 min at 4°C, using an Eppendorf centrifuge 5415 R. The sediments were processed for electron microscopy using a double fixation protocol with osmium tetroxide and tannic acid (Simionescu & Simionescu 1976). The samples were dehydrated in a graded ethanol series, and then embedded in Epon 812 (Serva) and polymerized for 48 h at 60°C. 60nm were cut at various depths through the entire pellet and mounted on Formvar coated grids. Samples were examined on a LEO 912 Omega Energy Filter Transmission Electron Microscope (Zeiss) at 120 kV accelerating voltage. Digital images were obtained by a side-mount MegaView III TEM CCD camera.

4.3.2.2 Quantification of vesicle profiles on electron micrographs.

For quantification, all vesicles were circled using Adobe® Photoshop® CS 8.0 (Adobe, San Jose, CA), filled with white, and the regions outside were darkened artificially to remove all other white spots. The number of white objects was automatically deduced by using the Volocity Classification 3.6.1 digital measurement system (Improvison, UK). The diameter of each vesicle was assessed as a function of its surface by Volocity Classification.

4.3.2.3 Enzyme assays.

Traditional biochemical characterization of our fractions was performed to assay the degree of enrichment of marker enzymes and was described in 3.3.2.

4.3.2.4 SDS-PAGE and immunoblots.

As described in Chapter 3, Section 3.3.3.

4.3.3 Tandem MS (MS/MS) analysis and data processing.

The following section has been adapted from Gilchrist et al. (Gilchrist et al 2006). For proteomics analysis of the 1D SDS gel resolved organelle fractions, extracted peptides from robotic (MassPREP Workstation, Micromass Manchester, U.K.) in-gel trypsin (Promega Sequencing Grade Modified Trypsin, Promega V5111) digestion were resolved by using a CapLC (Waters, Milford, USA) system and MS analysed in positive ion mode inline by using an upgraded (with embedded personal computer control and acquisition system (EPCAS)) quadrupole time of flight (QToF-2) MS (Micromass, Manchester, U.K.) equipped with a Micromass nanoESI source. Extracted peptides were injected (pump C) onto a trapping guard column (μ -Precolumn cartridge filled with PepMap C18, 5 μ m, 100 angstrom, 300 μ m i.d. x 5 mm (LC Packings, Sunnyvale, CA)) 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 at a flow rate of 200 nL/min with a 30 min or 60 min acetonitrile gradient (see below), the guard column-bound sample was washed with aqueous 0.1% formic acid, at a flow rate of 30 μ L/min for 5 min by using pump C and the analytical column was pre-equilibrated with 5% solvent B. 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 by employing 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 MS, was assisted 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 multichannel 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. For proteins with apparent MW between 30kDa and 200kDa a 60 min gradient was employed. Gradients (started with sample injection) were: 5% B from 0 to 5 min; to 40% B from 5 to 25 min; to 70% B from 25 to 30 min; to 95% B from 30 to 35 min; at 95% B from 35 to 42 min; and to 5% B from 42 to 47 min for the 30 min gradient; and 5% B from 0 to 5 min; to 40% B from 5 to 45 min; to 70% B from 45 to 53 min; to 95% B from 53 to 58 min; at 95% B from 58 to 60 min; and to 5% B from 60 to 65 min for the 60 min gradient. 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. In order 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 µL 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 µm).

In order 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; and for operation, the dead volume connector was connected to the capillary power supply.

For MS analysis of biological samples, the MS 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, collected sequentially for the selected precursor ions, 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; and 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 fmol/μL of Glu-Fibrinopeptide (Sigma, F3261) from a gold-plated glass capillary, with 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 >0.5 °C. The temperature was monitored continuously via an insulated thermocouple affixed to the flight tube.

4.3.4 Data processing.

After an LC-QToF MS/tandem MS proteomics analysis, the raw data was transferred to a 40 terabyte server and automatically processed in 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>). This was followed by database search analysis employing Mascot Cluster (Matrix Science, <http://matrixscience.com/cluster.html>); and then the Mascot search results were parsed into the in-house relational database termed CellMapBase (Bencsath-Makkai et al 2003a, Bencsath-Makkai et al 2003b). They were then scored for protein identifications and grouped in order to present a minimum set of protein identifications (Kearney et al 2005) to account for all the tandem MS assigned at 95% confidence (Matrix Science, <http://www.matrixscience.com/>). For generation of the peaklists, Distiller version 2.0.0 was employed, by using 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 points per Da. 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. Briefly, for generation of the minimum list of proteins (Kearney et al 2005), protein identifications were grouped based on redundant peptide assignments taking into account redundancies that arise due to homologous sequences, truncated or partial sequences, alternatively spliced proteins, strain-specific allelic variation or redundant assignments of tandem MS. In this process, peptides were assigned as unique to an identification or shared between 2 or more identifications. For quantification, redundant peptide counting (spectral counts), essentially as described by Blondeau et al. and Liu et al. (Blondeau et al 2004, Liu et al 2004) was employed. In the present case, peptides were grouped to their cognate proteins based on the gel resolved sample and shared peptides were apportioned to the cognate proteins based on the proportion of unique peptides. For comparison between samples, normalized (based on Total Peptides assigned in that biological repeat) % Total Peptides for n=3, Tables S1D) were employed.

4.3.5 Data analysis.

All protein identifications made by peptides assigned by Mascot at the 95% confidence level (false positive rate ~ 1.5% estimated by searching a randomized copy of the database) were tabulated into a relational database (CellMapBase) for further manipulations. The list of identified proteins is shown in Table S1A, and with peptide details provided according to the guidelines of Carr et al. (Carr et al 2004) for those proteins identified by a single unique peptide (assigned to only one identification, Table S1B). Curation and annotation of the data is covered in detail in the following chapter.

4.3.5.1 Principal coordinates analysis.

Related to hierarchical clustering, principal coordinates analysis was one more method we used to verify the homogeneity of our organellar preparations with our proteomics data instead of biochemical or microscopic techniques. It is a method with allows looking at all of our proteomics data for all 15 of our fractions (5 organelles with 3 biological replicates each) in a format that can be displayed on a flat medium. In its essence, a multidimensional dataset is projected onto two dimensions in order to visually compare how similar or how different are our 15 fractions from each other. This can be compared with drawing a cube in 2-dimensions; what we see is a 2-dimensional representation/projection of a 3-dimensional object onto a piece of paper.

4.4 Results

4.4.1 Evaluation of electron micrographs.

Figure 4.1 shows representative micrographs of the RM, SM, and Golgi fractions that were studied in this effort. Figure 4.2 shows a representative micrograph of a Golgi fraction revealing that it consists predominantly of intact, stacked Golgi cisternae covered with a perceptible coat with a few small vesicular profiles. In the inset of Figure 4.2, tannic acid staining demonstrates that some of these vesicular profiles are coated structures.

It is these Golgi fractions that were used to generate the COPI vesicles that are seen in Figure 4.3. They are negatively stained and decorated with gold-linked antibodies to cytoplasmic domain of p24 β_1 . Because the vesicles were filtered and subjected to negative stain and were not sectioned, this image counters the suggestion that what we identified as vesicular profiles were actually cross-sections of tubules.

Although the vesicles had been well characterized prior to this effort (Lanoix et al 1999, Lanoix et al 2001), a detailed morphological analysis of the vesicles had not been performed. In Figure 4.4, COPI GTP vesicles and COPI GTP γ S vesicles were subject to EM analysis in order to demonstrate that they were a morphologically homogeneous population. Examples of random fields containing many vesicles as well as higher magnification images of specific vesicles are shown for both COPI GTP vesicles and COPI GTP γ S vesicles. Morphometric analysis of vesicles showed that the COPI GTP vesicles were more uniform in size with over 70% of the vesicles scoring between 45 and 60nm in diameter. The COPI GTP γ S vesicles were more varied with regards to size with greater than 80% of the vesicles scoring between 45 and 75nm in diameter. This is likely because the COPI GTP γ S vesicles being unable to shed coat

proteins due to the presence of the non-hydrolysable GTP analog (GTP γ S).

To confirm that our vesicles were not the result of manual fragmentation of the Golgi cisternae as a consequence of the *in vitro* vesicle generation assay, Figure 4.5 shows micrographs of Golgi cisternae from control experiments performed at three different time points, showing intact Golgi cisternae still present after incubation. At experimental conditions, Golgi cisternae were collected after the *in vitro* vesicle generation assay at three time points to measure degradation of cisternae during the assay. A cisterna is defined as a profile where the length is over twice the width. As a percentage of the total profiles counted, the percentage of single and stacked cisternae drop slightly over the 30 minutes, however, the presence of fragmented cisternae referred to as “rest”, remain consistent below 5%. From this we believe that the vesicles generated in our assay are not a result of non specific fragmentation of the Golgi.

4.4.2 Enzyme assays.

Enzyme assay data was previously shown in Figure 3.5. To recap, Figure 3.5 shows enzyme enrichment in RM, SM, and Golgi fractions as compared to the starting homogenate for the endoplasmic reticulum marker enzyme glucose-6-phosphatase and the Golgi marker enzyme galactosyl transferase, as well a comparison to proteomics data for the same enzymes. Glucose-6-phosphatase activity was increased 4-fold in the RM and SM fractions with negligible change seen in the Golgi fraction. As the ER membrane of the liver parenchymal cell constitutes 45% of the total cell membrane (Blouin et al 1977) a 4-fold enrichment is expected. Golgi marker enzyme galactosyl transferase, activity is increased approximately 3-fold in the endoplasmic reticulum fractions and over 100-fold in the Golgi fractions. The Golgi, comprising only 2% of the total cell

membrane (Blouin et al 1977), makes this an expected result as well. When compared to the proteomics data we see that for glucose-6-phosphatase, peptides are detected in the RM and SM fractions and none in the Golgi apparatus. For galactosyl transferase we see the inverse; peptides are detected in the Golgi fractions but not in the RM or SM fractions. The enzyme assay data concurs with the proteomics data showing the marker enzymes enriched in their specific compartments but not enriched in others.

4.4.3 SDS-PAGE and Immunoblots.

In Figure 4.6, western blots displaying the concentration of five different marker proteins in various compartments are shown. The ER markers ribophorin I and calnexin are enriched in the RM and SM fractions. The Golgi markers membrin and mannosidase II are enriched in the Golgi compartment, and the plasma membrane protein integrin is enriched in the plasma membrane fractions. Although we see a prominent band for integrin in the Golgi apparatus, the higher molecular weight of this band indicates that this is a proprotein form of integrin that still has to be modified before export to the plasma membrane, and is not a contaminant.

4.4.4 Principal Coordinates Analysis.

In our case, the multidimensional dataset under analysis is our proteomics data. As seen in Figure 4.7, our 15 dimensions are RM n=1, RM n=2, RM n=3, SM n=1, SM n=2, SM n=3, Golgi n=1, Golgi n=2, Golgi n=3, COPI GTP n=1, COPI GTP n=2, COPI GTP n=3, COPI GTP γ S n=1, COPI GTP γ S n=2, and COPI GTP γ S n=3. Each point represents all the peptide counts for each fraction (dimension) projected onto our 2-dimensional graph. From this plot we see that each of the three fractions is distinct from the other two fractions; Golgi, COPI GTP vesicles, and COPI GTP γ S vesicles each occupy different areas of the plot. The three biological

replicates for each fraction, however, are located relatively close to each other on the plot. This confirms that our Golgi, COPI GTP vesicles and COPI GTP γ S vesicles are distinct entities, and that the biological replicates of a specific fraction are similar to the other biological replicates of that fraction. It also addresses the question of endoplasmic reticulum contamination of the Golgi. The RM and SM fractions are highly similar to each other, but very different from the Golgi, COPI GTP vesicles and COPI GTP γ S vesicles.

4.5 Discussion

Our highly detailed and exhaustive sample preparation and characterization give us a firm foundation on which to base our proteomics findings. Decades of experience in organelle isolation along with confirmation via electron microscopy, enzyme assay, and western blot give us confidence that the fractions we are loading onto the mass spectrometer are as highly enriched as possible. This reduces the presence of contaminants in our resulting proteomics data.

Regarding the *in vitro* generation of COPI GTP and COPI GTP γ S vesicles, it should be noted that our laboratory had previously isolated *in vivo* COPI vesicles (Lin et al 1999, Love et al 1998), however, the yield and homogeneity of these vesicles was not considered sufficient for mass spectrometric analysis, so we used their *in vitro* counterparts.

After the mass spectrometric analysis was performed, to further assure ourselves of the quality of our fractions, principal coordinates analysis of our proteomics data confirmed that for an organellar fraction, each biological replicate was more similar to other biological replicates of that fraction than to a replicate of a different organellar fraction (i.e. Golgi biological repeats n=1,2,3 are similar to each other but different and distinct from COPI GTP vesicles n=1,2,3 and COPI GTP γ S vesicles n=1,2,3). It also assured us that the RM and SM samples were very distinct from the Golgi, COPI GTP vesicles, and COPI GTP γ S vesicles samples.

The automated sample processing and mass spectrometric analysis allowed the collection of over 150 000 mass spectra. Using both in house and commercially available software, we processed the raw mass spectrometer output into a list of proteins we had identified in our sample.

A schematic representation of the whole pipeline is presented in Figure 4.8.

At this point in time we moved on to manual inspection and curation of these lists to render the data into a format easily manipulated and interpreted by cell biologists, and so began the annotation effort.

Figures

Figure 4.1. Electron micrographs of RM, SM, and Golgi fractions.

(This figure was taken from (Gilchrist et al 2006)). EM of random views of filtered preparations (Bell et al 2001) of isolated rough microsomes (RM) with ribosome studded microsomal profiles, smooth microsomes (SM) with a preponderance of smooth membranes and occasional profiles showing ribosome studded microsomes (arrow) and Golgi apparatus (G) with 4 different angles of section of Golgi profiles indicated by arrows. Bar, 0.5 μm .

Figure 4.1

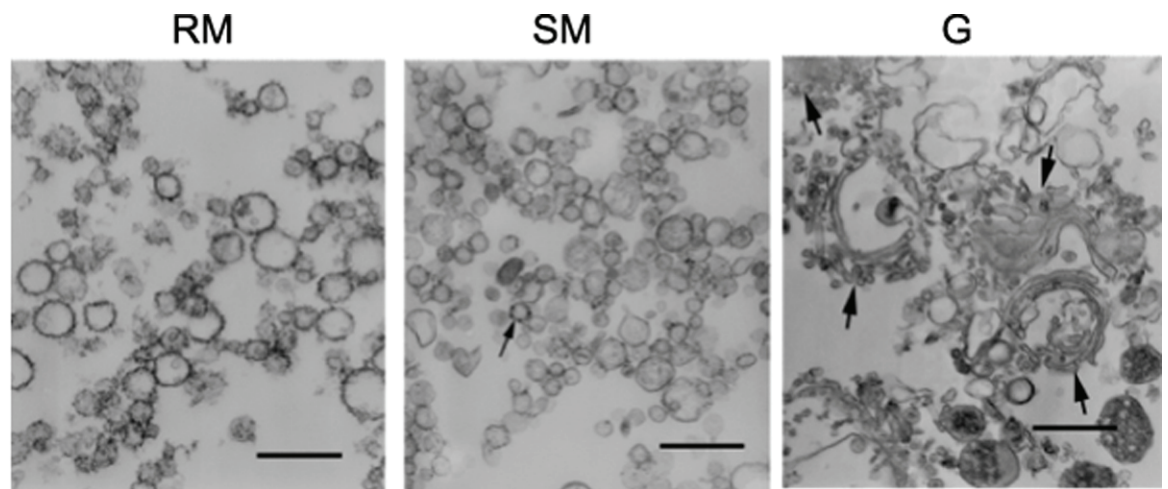


Figure 4.2. Electron micrographs of Golgi fractions.

Morphology of the Golgi fractions. An ultrathin cryosection of a Golgi fraction reveals that it consists predominantly of intact, stacked Golgi cisternae (Gs) covered with a perceptible coat with a few small vesicular profiles (arrowheads). Fuzzy coats can also be seen at the delimiting membrane of many of the Golgi-associated structures. Inset: Tannic acid treatment of a Golgi fractions fixed prior to Epon-embedding reveals some of the vesicular profiles to be coated (putative clathrin coats indicated with arrow, possible COPI coated buds are indicated by arrowheads). Bar 200 nm.

Figure 4.2

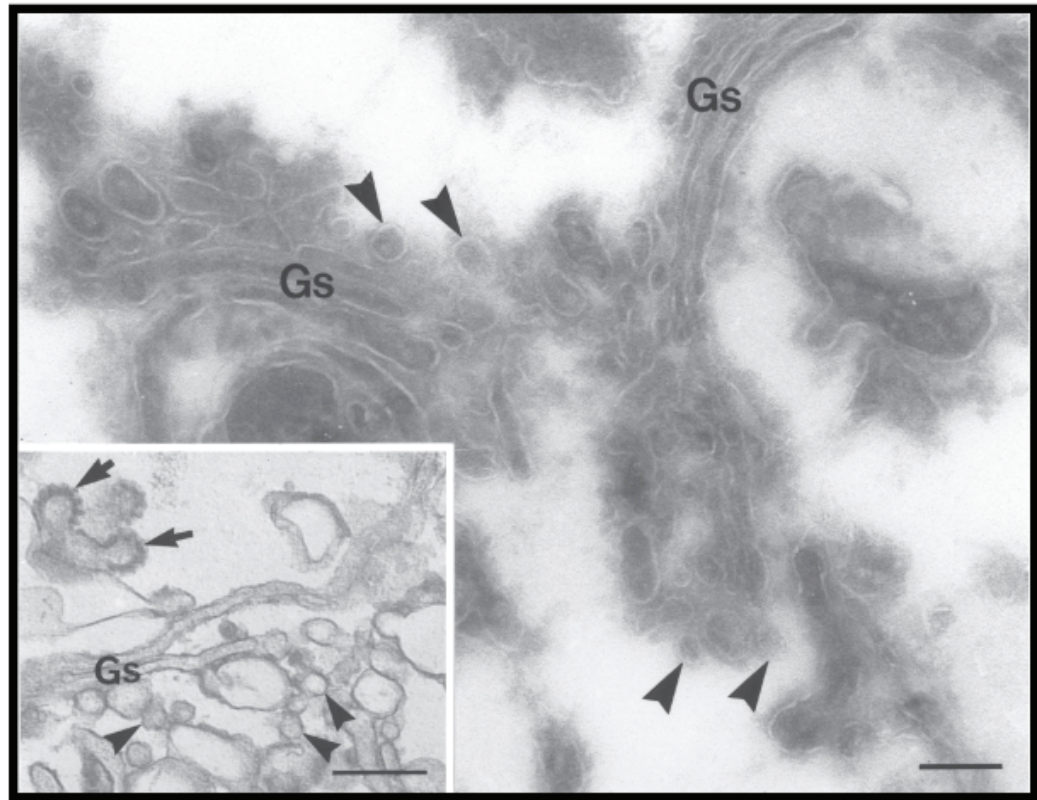


Figure 4.3. Negative stained COPI GTP vesicles.

Micrograph of purified vesicles transferred to grids and processed for negative stain. Immunolabeling using an antibody raised to the cytoplasmic domain of p24 β_1 often reveals a regular labeling around the vesicle. *Bar 100 and 50 nm.*

Figure 4.3

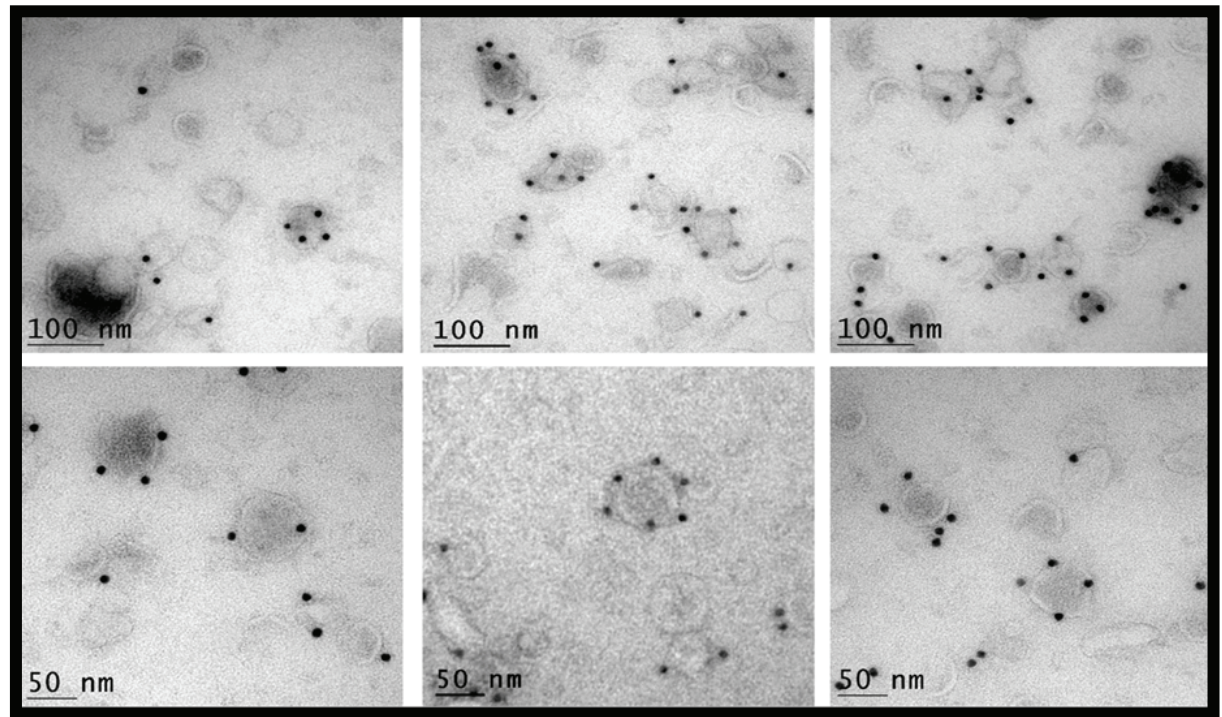


Figure 4.4. Quantitation of COPI GTP and COPI GTP γ S vesicles.

This figure was taken from (Gilchrist et al 2006). Ultrathin cryosections of floated vesicles reveal predominantly intact and homogenous vesicle populations. Vesicle fractions have been treated with tannic acid to reveal coat structures. Vesicles were generated by incubating purified rat liver Golgi with cytosol in the absence (A-F) or presence (G-L) of the non-hydrolysable GTP analogue, GTP γ S. **A. B. G. H.** Random fields of vesicles from processed fractions. Bars 250 nm. **C. D. I. J.** Larger magnifications of discrete vesicles. Bars 100nm (C, I), 50nm (D, J). **E. K.** Large vesicle (E) and clusters of vesicles (K) seen occasionally. Bars 100 nm. **F. L.** Size distributions of vesicles in the two fractions. In the absence of GTP γ S, vesicle profiles had an average diameter distribution of 45-60 nm (F) whereas in the presence of GTP γ S, vesicle profiles had an average diameter distribution of 45-75 nm (L). The larger diameter distribution seen in L is consistent with a coat. Roughly 800 vesicle profiles were measured in each fraction. Standard deviation is presented as error bars. The difference in darkness between A-E and G-K reflects variation in the degree of tannic acid staining.

Figure 4.4

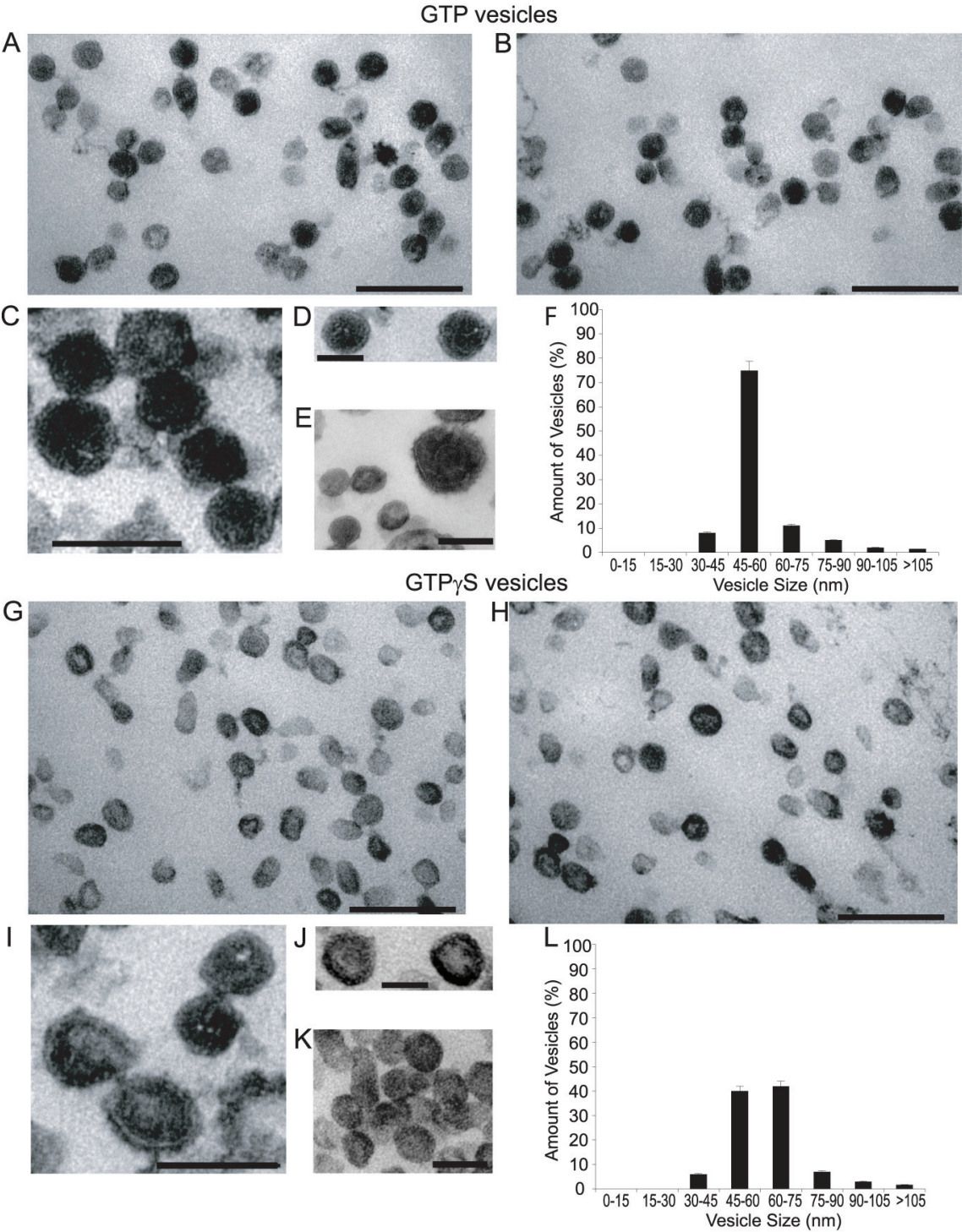


Figure 4.5. Golgi fractions before, during, and after COPI vesicle generation.

This figure was taken from (Gilchrist et al 2006). Golgi membranes under budding conditions. Purified rat liver Golgi membranes were incubated with cytosol under normal budding conditions (see 4.3.1) at 37°C for 0, 10 and 30 minutes. Membranes were then sedimented by low speed centrifugation leaving vesicles in the supernatant (see Figure 4.5 for micrographs of isolated vesicles). After removal of supernatant, membranes were fixed and processed for epon embedding and electron microscopy. Tannic acid and uranyl acetate were added to enhance contrast. Cisternal membranes were scored as the relative number of cisterna (All cist.), stacked cisterna and membrane remnants (Rest). Morphometry was according to Rabouille et al. (Rabouille et al., 1995). The number of stacks compared to free cisternae does not decrease significantly during incubation nor does the number of cisternae decrease. There does not appear to be any obvious fragmentation even after 30 minutes of incubation. The number of vesicular profiles were not scored as most, if not all, remained behind in the supernatant. Bars 100nm.

Figure 4.5

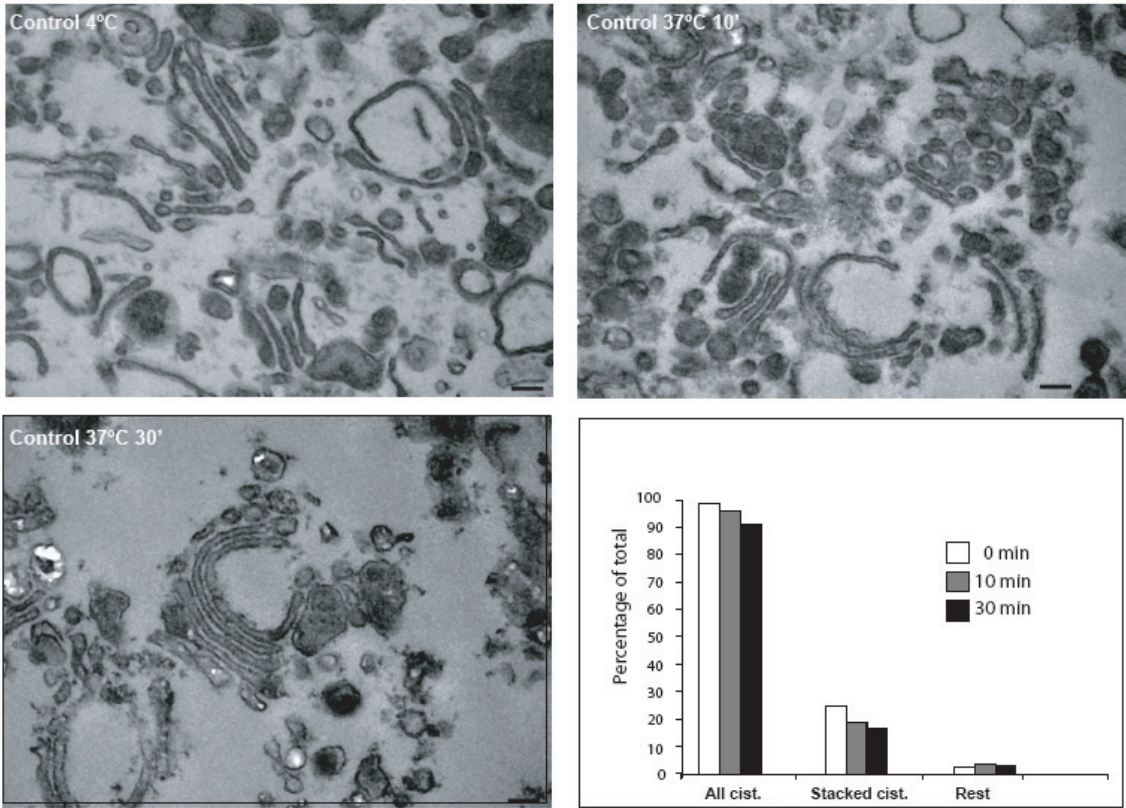


Figure 4.6. Western blots of marker proteins.

Western blots of five marker proteins are shown for H (homogenate), RM (rough microsomes), SRM (stripped rough microsomes, which are rough microsomes from which the ribosomes have been removed), SM (smooth microsomes), Golgi, and PM (plasma membrane). The first two blots are of the endoplasmic reticulum markers ribophorin I and calnexin. The third blot is of the Golgi marker, membrin. The fourth plot is for the plasma membrane marker, integrin $\beta 1$. It is detected in the Golgi apparatus, but in a precursor form of a higher molecular weight, and is therefore not contamination. The fifth and final blot is of the Golgi marker enzyme Mannosidase II.

Figure 4.6

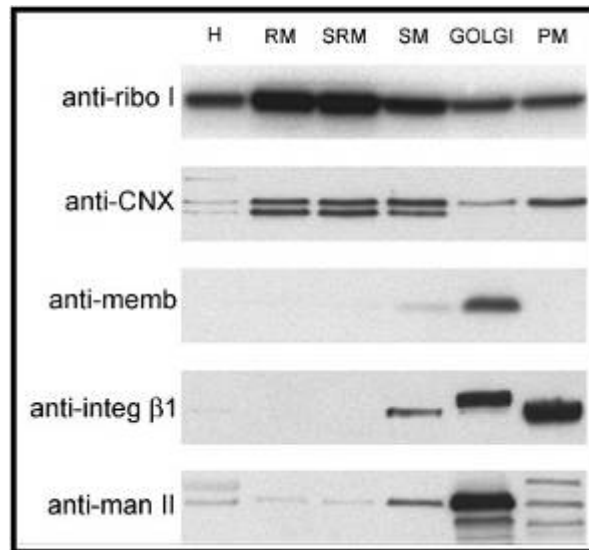


Figure 4.7. Principal components analysis of proteomics data.

The axes of the plot are in Euclidian units. RM (red), SM (green), Golgi (dark blue), COPI GTP vesicles (pink), and COPI GTP γ S vesicles (light blue). Note that RM and SM fractions occupy the same region of the plot, whereas Golgi, COPI GTP vesicles and COPI GTP γ S vesicles each occupy a distinct region of their own.

Figure 4.7

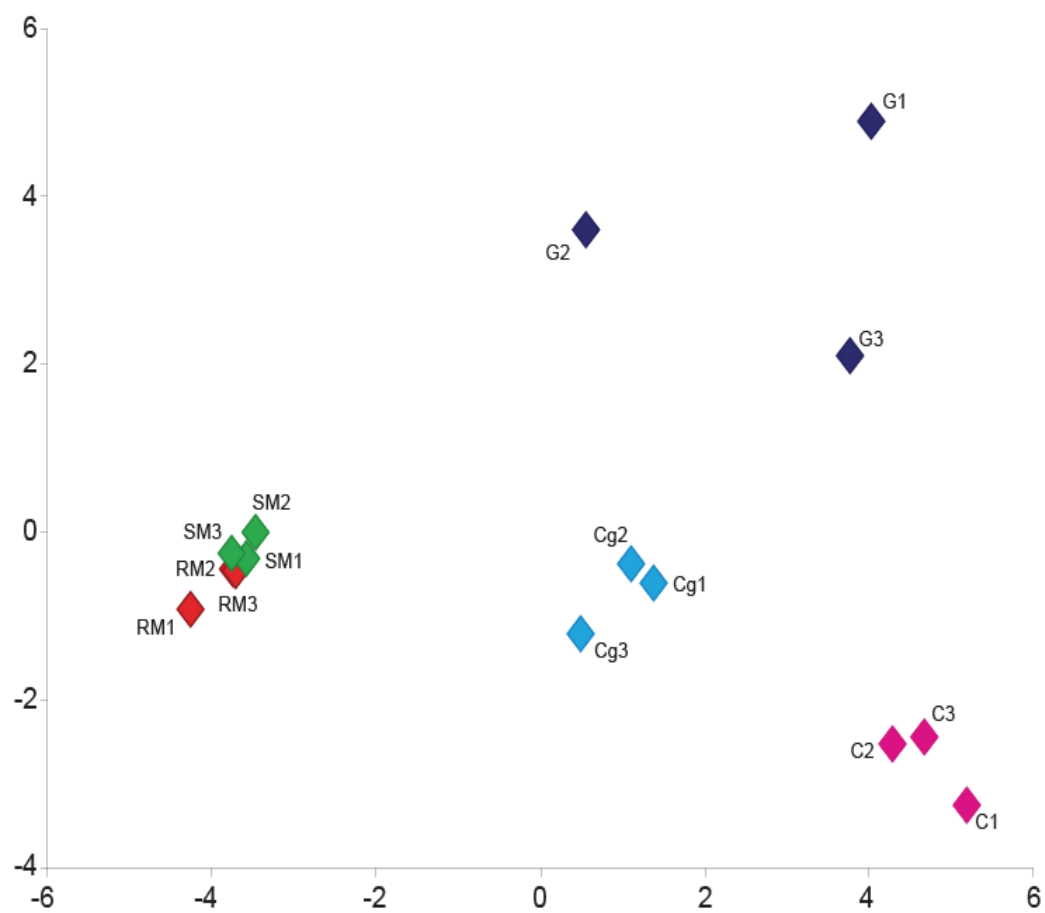
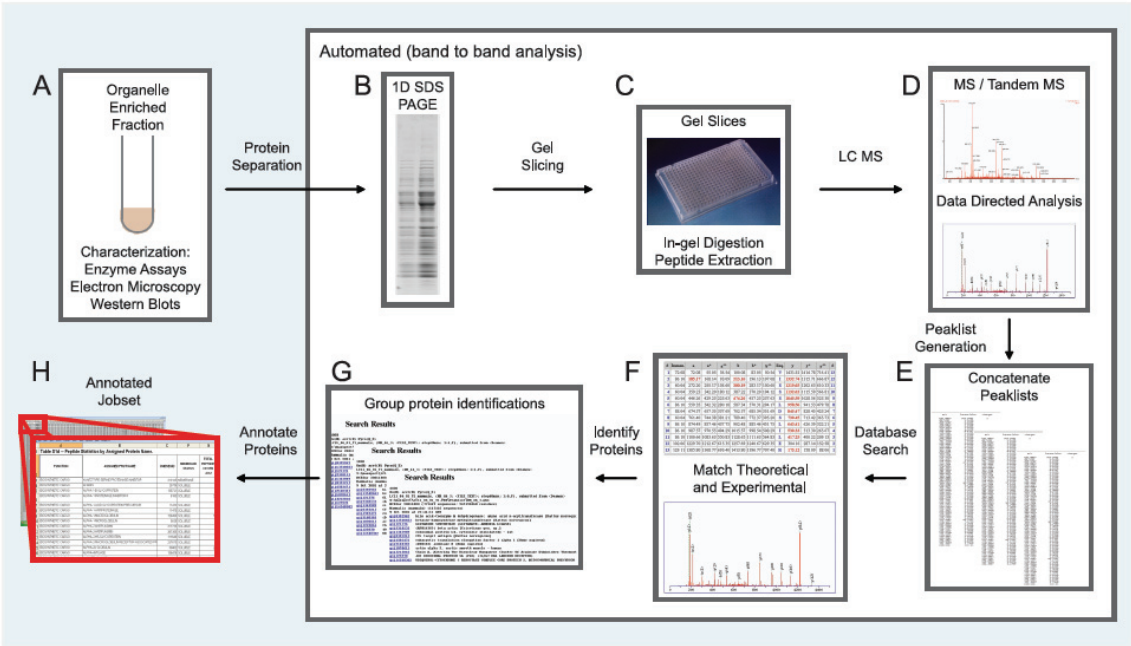


Figure 4.8. Schematic of the Pipeline.

This figure was taken from Au et al. (Au et al 2007). For organellar proteomics, highly enriched organelle fractions **A** are characterized by a combination of biochemical assays, Western blots, and electron microscopy. The proteins are then resolved by 1D-SDS PAGE **B**. Shown are two different amounts (25 and 75 μg protein) of rough microsomes isolated from rat liver homogenates (Gilchrist et al 2006), stained with Coomassie Brilliant Blue G. The stained gel is then robotically processed wherein gel-slices of 1.8 mm (83 slices per gel lane) of the complete gel lane are diced into cubes (~ 1 mm) and collected in a 96-well tray **C**. The tray is then transferred to a second robot for in-gel digestion with trypsin after reduction (with dithiothreitol) and alkylation (with iodoacetamide) and the peptides are extracted and transferred to a second 96-well tray. The extracted peptides are analysed by in-line LC-MS employing reversed phase chromatography with acetonitrile gradients in the presence of 0.1% formic acid to resolve the peptides in the mixture. MS analysis employs data directed analysis **D** whereby the MS cycles between MS and tandem MS modes, selecting the most intense doubly or triply charged ions (most likely charge state of tryptic peptides at low pH) for fragmentation, with a specified delay time before selecting the same m/z another time. For the CellMap project, a 1,4,5 duty cycle is employed. This corresponds to a 1 sec MS scan followed by up to 5 tandem MS scans of 1 sec each, for up to 4 selected ions fragmented. Shown **D** are typical MS (upper) and tandem MS (lower) scans. Each of the tandem MS are then converted into digital format by listing the m/z value and the charge state of the ion plus the m/z values and intensities of all fragmentation ions (4 peaklists are shown **E**). Typically for a 1-h LC separation 400 fragmentation spectra are recorded. For database search analysis, all individual peaklists for a gel-slice are concatenated into a single list. The matching of the tandem MS to tryptic peptides in a protein database involves the theoretical digestion of all proteins and fragmentation of all tryptic

peptides: experimental and calculated peptide masses are first matched, within a specified mass tolerance, followed by a scoring of the matching of the experimental and theoretical fragment ions, with the best fit indicated by the highest score. Confidence levels take into account the size of the database, reflecting on the probability of a random match. Shown **F** are the matching of experimental fragment ions (red) to the table of theoretical fragment ions (upper) and the matching of theoretical ions (black) in the tandem MS (lower). After matching tandem MS to peptides, the cognate proteins are tabulated. Shown **G** are search results for 3 gel slices, listing gel band identification, gi number and protein description. Subsequently the lists of proteins are grouped into one list for the sample (gel lane) and the minimum number of proteins required to account for all peptides (matched tandem MS) is generated. The final step of generation of the fully annotated protein list **H** is the most labour intensive step in the process and is presented in the next chapter.

Figure 4.8



Chapter 5 -- Generation of a comprehensive, meaningful, non-redundant protein list.

5.1 Abstract

After sample preparation, characterization, and automated mass spectrometric analysis, over 150 000 spectra had been collected. In order to have a comprehensive, meaningful, and non-redundant list of proteins produced by this proteomics effort, a detailed curation of each identified protein sequence was effected. The primary sequence of each protein identified through mass spectrometry was subjected to literature search, various bioinformatics prediction tools, and BLAST analysis in order to create a curated list of protein identifications. Examples of each type of problem in the database are shown, as well as the methods used to identify and correct the problem. Use of bioinformatics tools such as TMHMM and SignalP were also used to give added insight into the identified proteins.

5.2 Introduction

The list of proteins which was first compiled following Mascot analysis and clustering was data rich, but required further curation in order to yield biological insight. As the mass spectrometric data was being analyzed to generate peptide counts, we encountered a problem with assigning peptides to proteins. What we as biologists consider to be one protein (e.g. albumin), can have hundreds of entries in the database. Each sequence can be slightly different due to allelic isoforms, sequencing errors, or incorrect annotation in the database. When a program such as Mascot matches mass spectrometric data to the theoretically digested tryptic database, matches to multiple sequences can occur. But when we tabulate the peptides for albumin, we want all peptides that belong to the protein albumin to be counted as such, and not assigned to other sequences that are not readily identified by name as albumin.

An example of mass spectrometric data assigned by Mascot and then processed through the pipeline is shown in Table 1. Entries 1, 2, 3, 6, and 7 are examples of uninformative names. Nothing can be immediately determined regarding the nature of the identified protein from the database associated name. They could be proteins never identified before or well known proteins that were poorly annotated in the public database. Entries 17, 18, and 19 all have the same name which would lead one to believe they are the same protein, but when the sequences are compared, prove to be three different proteins. Entries 24 and 25 are examples of misleading names. Similar can mean virtually identical, with a 95% identity over the full sequence length, or it can mean a protein that has only 45% identity over the full sequence length, but is obviously functionally related. Entries 26 and 27 are examples of two proteins that might actually be allelic isoforms of the same protein, but have enough slight differences that they can be identified as two different sequences by

mass spectrometric. The difference in their calculated molecular weight is due to a splicing error which occurred during conceptual translation. This is just a small sampling of the problems that occurred when we first looked at the sequences identified by names from the public database. These types of problems affected approximately 25% of the sequences identified through proteomics.

We developed a common nomenclature for multiple sequences that we wished to be considered as the same protein in Cell Map Base (our local database). A BLAST analysis (Altschul et al 1990) was performed to find sequences with regions of high similarity (>90%) over the length. The whole database was compared against itself with search parameters being an e-value of 10^{-40} . This dealt with translated introns, fused genes (two or more separate transcripts that are listed in the NCBI database as one gene product), confusing names (for instance a gene was named RIK00009234, but the sequence matched that of albumin), and allelic isoforms due to variation between animals. Proteins that were deemed to be the same were given the same assigned protein name in order that their peptides would be counted towards one protein name for peptide counting.

5.3 Results

5.3.1 Translated introns.

The result of translated introns is most easily seen on a BLink diagram from NCBI (Figure 5.1). When looking at the horizontal bars that represent sequence similarity, on the left of the diagram, some bars look more like long beads on a string. The areas between these beads are caused by translated introns. This causes two sequences to register as non-identical to a BLAST program, but visual inspection of the alignments reveal that the sequences are the virtually the same when the intron regions are removed.

5.3.2 Fused genes.

Fused genes are the second problem we encountered. Many sequences in the rat database were created via conceptual translation of the genome. The result of this was one predicted protein sequence that contained more than one actual protein within it. Figure 5.2 illustrates an example of a fused gene sequence. The sequence has to be manually unraveled into its separate components, and the database then updated to contain the new individual sequences. This type of error was the most serious type of error we encountered, serendipitously, only comprising approximately 10 of over 2000 identified sequences.

5.3.4 Allelic isoforms.

Allelic isoforms are the simplest problem to solve. Because we use a pool of rats to obtain our liver fractions, and each rat is genetically unique, we expect to see different alleles of the same gene appear in our samples, an allele being “one of a set of alternative forms of a gene” (Alberts et al 2002). Often an allele is a result of a change of one or two amino acids in

the whole protein sequence; however, these slight changes register as different proteins in the database. For the purposes of peptide counting, we wish to consider all these allelic isoforms as the same protein, so we assign them the same protein name in order that their peptide counts are collapsed. Figure 5.3 illustrates an example of two different allelic isoforms of 10-formyltetrahydrofolate dehydrogenase.

5.3.5 Incomplete splicing of exons.

The last problem was incomplete splicing of exons. Two gene products could have no significant similarity when compared by BLAST, but when compared to the nrdb their match was the same. Further investigation revealed that one gene product contained two exons of the protein, and the other gene product contained two other exons for the protein, hence they both matched the parent sequence but not to each other, but are really identifications of the same protein.

5.3.6 Manual annotation of 23 functional categories.

As well as giving each protein an assigned protein name to allow for proper assignment of peptides, proteins were also assigned to one of 23 categories that were chosen for their relevance to membrane trafficking and biosynthetic cargo secretion. This allowed us to view how peptide abundance changed both for individual proteins and for whole categories of proteins. These are the categories:

5.3.6.1 Biosynthetic cargo:

Biosynthetic cargo proteins encompass all the secretory proteins of the liver. They include highly abundant blood serum proteins such as serum albumin. One of the main functions of the liver is the production and

secretion of serum proteins. This category encompasses over 20% of the peptide counts in the Golgi fractions.

5.3.6.2 Blood and other cells:

This category is for all proteins not from liver parenchymal cells, including blood cells and cells from all other contaminating tissues.

5.3.6.3 Calcium transport and binding:

Proteins assigned to this category are involved in the transport and sequestration of calcium in the cell.

5.3.6.4 Coat:

Many coat proteins were observed in our fractions. In the Golgi apparatus and COPI vesicles, the COPI coat proteins were most populous. We also identified subunits of the clathrin coat complex and the COPII coat complex in our samples.

5.3.6.5 Cytoskeleton:

Several cytoskeletal elements were characterized. Proteins in this category included all structural scaffolding elements of the cell, including many different isoforms of actin, dynein, dynamin, myosin, tubulin, and spectrin.

5.3.6.6 Detoxification:

These proteins were found in the highest concentrations in the smooth microsomes. The liver is the major site of detoxification of both endogenous and xenobiotic toxins, and the smooth endoplasmic reticulum is the cellular location where detoxification takes place. All enzymes

involved in reactions which lead to the oxidation and modification of lipophilic compounds as well as natural lipids and steroids into hydrophilic compounds.. This allows the eventual elimination of steroids and xenobiotics from the body.

5.3.6.7 GTPase:

Any protein that has the function of hydrolyzing GTP into GDP and Pi is included in this category as well as associated GEFs (guanosine nucleotide exchange factor) and GAPs (guanosine triphosphatase activating protein). This refers to G-proteins, Arfs, and Rabs among others.

5.3.6.8 Likely contaminants:

This category is reserved for keratins. Although there are endogenous keratins in the liver, we chose to label any keratin identified as a contaminant which may have come from stray hair or skin cells from rat or human sources.

5.3.6.9 Lysosome:

This is a contaminant category. Proteins that have been localized to the lysosomes such as LAMP are assigned here.

5.3.6.10 Metabolism:

Proteins involved in non-mitochondrial energy generation, such as those involved in glycolysis fit in this category. We also include proteins involved in the biosynthesis of lipids, amino acids etc.

5.3.6.11 Mitochondria:

This is a contaminant category. All proteins that have been localized to the mitochondria are in this category, and include the enzymes of the electron transport chain and cytochrome c.

5.3.6.12 Nucleus:

This is a contaminant category. Any nuclear proteins that are not directly involved in transcription fall into this category, for instance, histones.

5.3.6.13 Peroxisome:

This is a contaminant category. All proteins that have been localized to the peroxisome fall into this category.

5.3.6.14 Plasma membrane:

This is a contaminant category; however, as shown via Western blots, many plasma membrane proteins that are detected in the Golgi apparatus are in their precursor format. Plasma membrane proteins are post-transcriptionally modified in the Golgi apparatus before export to the plasma membrane.

5.3.6.15 Protein modification:

Proteins in this category perform all sorts of post-translational modifications to newly synthesized proteins. The Golgi-localized terminal sugar transferase enzymes are a major part of this category.

5.3.6.16 Protein synthesis and folding:

Proteins involved in the synthesis of new proteins and their subsequent folding into their three dimensional conformations belong in this category. This includes ribosomal proteins and chaperones such as calnexin.

5.3.6.17 Proteasome and ubiquitin:

Intimately associated with the endoplasmic reticulum, the proteasome is involved in the degradation of proteins. All subunits of the proteasome and all proteins involved in ubiquitination are included in this category.

5.3.6.18 Signaling:

Proteins that are involved in cellular signaling/signal transduction, such as kinases and phosphatases, are in this group.

5.3.6.19 Tethering, docking, and fusion:

This category contains proteins that are involved in the bringing together and fusion of two different membranes, such as SNAREs and tethering factors.

5.3.6.20 Traffic:

Proteins in this category are membrane proteins involved in membrane trafficking events.

5.3.6.21 Transcription:

Nuclear proteins that are directly involved in the transcription of DNA into mRNA are in this category. Examples are helicases, reverse transcriptases, and mRNA modifying enzymes.

5.3.6.22 Trypsin:

This is a contaminant category. Proteins are digested with trypsin after size separation on a 1D SDS-PAGE gel in order to prepare the sample for MS analysis. Any detected trypsin is assumed to be the result of this procedure.

5.3.6.23 Unknown:

Proteins were designated as unknown if they had been previously identified only as conceptual translations from a genomic database. This category also included proteins that had been identified in the cell, but their function was unknown (e.g. EMP70 family of proteins), and proteins which were somewhat similar to known sequences, but the similarity was not enough to confer knowledge of function.

5.3.7 SignalP and TMHMM predictions.

Once the proteins were assigned into their categories, we wished to know information regarding their membrane topology and location in the cell.

In order to determine whether or not a protein was a membrane protein we performed a TMHMM prediction (Sonnhammer et al 1998). The TMHMM program uses a hidden Markov model in order to predict the location and orientation of alpha helices in membrane-spanning proteins. An example of an output file is shown in Figure 5.4. The program gives us a list of predicted membrane domains showing the beginning and the end of each transmembrane segment, and whether the end is inside or outside the cell.

After this we performed a SignalP prediction (Bendtsen et al 2004) to determine if the sequence contained a signal sequence. SignalP

combines both neural networks and hidden Markov models to predict signal peptidase I cleavage sites. Figure 5.5 shows an example of an output file. If the protein contained a signal peptide within the first 70 amino acids, it was considered to be a secreted protein. We then compared this result with the TMHMM result. If a transmembrane domain was predicted within the first 70 amino acids, we considered it to be cleaved as a signal peptide, and the protein was a secreted soluble protein.

We came up against some problems using the TMHMM prediction program while performing this analysis. There were certain proteins that have been shown to be membrane proteins, but TMHMM consistently misidentified them as soluble proteins. The cytochrome p450 family of proteins was one of these groups. We are currently investigating what is different about these transmembrane sequence regions refractory to the TMHMM program.

As a consequence of this problem, we manually curated our list of proteins that were listed as membrane proteins or soluble proteins by computer prediction, and verified where possible that the prediction agreed with literature evidence. Another reason for problems with the predictions has to do with the errors in the rat database causing the sequences to contain transmembrane regions when they did not or vice versa.

5.3.8 Proteins missing from the rat database.

An example of a protein missing from the rat database is the protein CASP. Only CUT (alias splice isoform A of CCAAT displacement protein), a nuclear localized transcription factor, is found in the rat database (Neufeld et al 1992). All the peptides that matched to CUT in the rat database were manually mapped onto isoforms A, B, and C of CCAAT

displacement protein for both mouse and human sequences. This is shown in Figure 5.6. All peptides map to the splice isoforms known to be transmembrane domain containing and Golgi localized (Gillingham et al 2002). From this data we were able to construct the sequence for the rat protein CASP. It is difficult to estimate the prevalence of this type of problem. One has to be aware a sequence should be present before its absence is noted.

5.3.9 Tables of protein identifications.

Tables of all the proteins identified in this proteomics effort are presented in Appendix 2.

5.3.9.1 Descriptions of supplemental tables.

There are four supplemental tables found in Appendix 2. Brief descriptions of each of the tables are found below. Detailed legends are provided in Appendix 2 with the tables.

5.3.9.1.1 Table S1a description.

This table is a list of proteins that was identified by mass spectrometric analysis. No manual curation or inspection of the data was performed. This is the original output received after data processing.

5.3.9.1.2 Table S1b description.

As following the criteria of Carr et al. (Carr et al 2004), this table indicates all the proteins identified by one unique peptide. No manual curation or inspection of the data was performed.

5.3.9.1.3 Table S1c description.

This table contains all the manual annotations as well as TMHMM (Sonnhammer et al 1998) and SignalP (Bendtsen et al 2004) predictions performed on the data from Tables S1a and S1b.

5.3.9.1.4 Table S1d description.

For every assigned protein name, the total number of redundant peptide counts and the percentage of total redundant peptide counts is shown for each biological replicate of each organellar fraction.

5.3.10 Calculation of redundant peptide counts.

As previously discussed in Chapter 3, redundant peptide counts are now an accepted method of calculating relative abundance of protein in a complex sample. In Chapter 3 we were looking at specific proteins, and could perform the calculations manually, however, to look at all of our 2113 identified proteins in this manner would be prohibitive.

Because we have grouped together protein sequences we believe are allelic isoforms of the same protein under one assigned protein name, we can now automate the generation of peptide counts. For assigned protein names with only unique peptides, this is a simple matter of summing the number of peptides. For assigned protein names that share distinct peptides with another assigned protein name, we use a method of apportioning the shared peptides between the two.

The most effective way of demonstrating this method is an example. We have two proteins; A and B. Protein A has 10 unique peptides and protein B has 10 peptides, and protein A and protein B share 6 peptides in common. Since protein A and protein B have equal numbers of unique peptides, they split their shared peptides between them. In this way, the

total prorated redundant peptides for protein A is 13 and the total prorated redundant peptides for protein B is 13.

Once assigned protein names were entered into our Cell Map Base, the tables that are described in the previous section were generated.

5.4 Discussion

The lack of curation of the rat database was evident when we began the manual curation of our data. The authors of the study indicated that their mandate was to create a high quality draft genome, and that corrections of errors in the final sequence would not be made as they were for the human and mouse genome projects (Gibbs et al 2004). This caused many extra hours of work because of sequences containing unspliced introns and other artifacts of conceptual translation from the rat genome. As a result of our travails, a project to propagate our annotations to the public rat database has been discussed with other members of the scientific community.

A question which is often asked is why we spent so much time and effort on manual curation and annotation of our data when there are bioinformatic tools such as GO available for use (Ashburner et al 2000). When we began our proteomics analysis, the GO tool had just been created and existed in a form that was not conducive to a high throughput proteomics project. For one protein sequence there were three controlled vocabularies associated with it; one for biological process, one for cellular component and one for molecular function. Each vocabulary had a hierarchical tree of terms. For instance, consider the hierarchical tree for the molecular function ontology assigned to the protein 1,3-1,6-alpha-mannosidase shown in Figure 5.7. If we consider the terms associated with molecular function, we see that the first two levels, catalytic activity and hydrolase activity, are too vague, whereas further down the tree the terms are too specific. We determined that for our purposes, self assigned functional categories were superior to using the GO vocabulary.

For future proteomics work we are investigating whether GO slim, a reduced GO vocabulary, would be more adaptable to our needs.

Tables

Table 1. Examples of protein identifications before curation.

The following table gives examples of problems that needed to be addressed by manual curation of protein identifications. The column “#” indicates the number given to the protein by which it is referred to in the text. The column “NCBI description” is the description assigned to that specific sequence in the NCBI protein database. The column “MW” is the calculated molecular weight of the protein in Daltons. The column “Gi number” contains the gi number assigned to the protein sequence by the NCBI protein database. The “CMBSEQID” column indicates the CMBSEQID which is the identification number assigned to the sequence in our Cell Map Base.

Table 1 – Examples of protein identifications before curation.

#	NCBI DESCRIPTION	MW	Gi number	CMBSEQID
1	(P20290) Isoform 2 of P20290	17700	56605700	33279
2	(P22626) Isoform A2 of P22626	36010	34855868	29411
3	(Q00438) Isoform PYBP1 of Q00438	56940	57002	9454
4	1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase beta 3	139400	32699414	166274
5	3-oxo-5-alpha-steroid 4-dehydrogenase 1 Steroid 5-alpha-reductase 1 SR type 1	29780	25742565	43740
6	Aa1018	55960	32492572	302124
7	Aa1064	42690	111387	148924
8	Apoptosis-inducing factor	66720	7619915	63059
9	BET1 homolog Golgi vesicular membrane- trafficking protein p18 rBET1	13230	9506425	35327
10	BET1-like protein Vesicle transport protein GOS15 Golgi SNARE with a size of 15 kDa GS15 GOS-15	12410	61889075	315291
11	Cytochrome c oxidase polypeptide Va, mitochondrial precursor	16130	55971	63743
12	Cytochrome c oxidase polypeptide Vb, mitochondrial precursor VIA*	13910	53237117	21518
13	DnaJ homolog subfamily A member 2 RDJ2	45770	2281451	1106
14	Dnaj-like protein	25760	9910322	42765
15	Dnajc3 protein [Rattus norvegicus]	50240	38197558	318957
16	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
17	Hypothetical protein	37380	51338711	8648
18	Hypothetical protein	24090	83415090	163993
19	Hypothetical protein	40560	58477247	71440
20	Hypothetical protein RGD1305677	21660	58585236	209082
21	Liver regeneration-related protein LRRG03 Transferrin	76400	61556986	166406
22	Liver regeneration-related protein LRRG04 Apolipoprotein C-I	9861	91989	3640
23	Mitochondrial protein, 18 kDa	18370	55741522	220289
24	PREDICTED: similar to 25 kDa FK506-binding protein	25180	27664664	289953
25	PREDICTED: similar to 60S ribosomal protein L27a	16590	62639430	273222
26	S15 ribosomal protein	13360	40287237	337119
27	Tax_Id=10116 Similar to ribosomal protein S15	50300	34851670	224899
28	SWISS-PROT:P38659 TREMBL:Q6P7S5 REFSEQ_NP:NP_446301 ENSEMBL:ENSRNOP00000008728 Protein disulfide-isomerase A4 precursor	72810	729436	60584
29	Solute carrier family 10, member 1	39300	8394279	11254
30	Solute carrier family 21 member 4	62970	19071449	198521
31	similar to heparan sulfate 2-sulfotransferase	41850	34860929	259411

Figures

Figure 5.1. Translated introns.

This BLink plot from NCBI show an example of the easiest way to identify the presence of translated introns. When the identified sequence is displayed in this manner, you see that all the alignments look like a chain of sausages. The spaces between these sausages are representative of the translated introns.

Figure 5.1

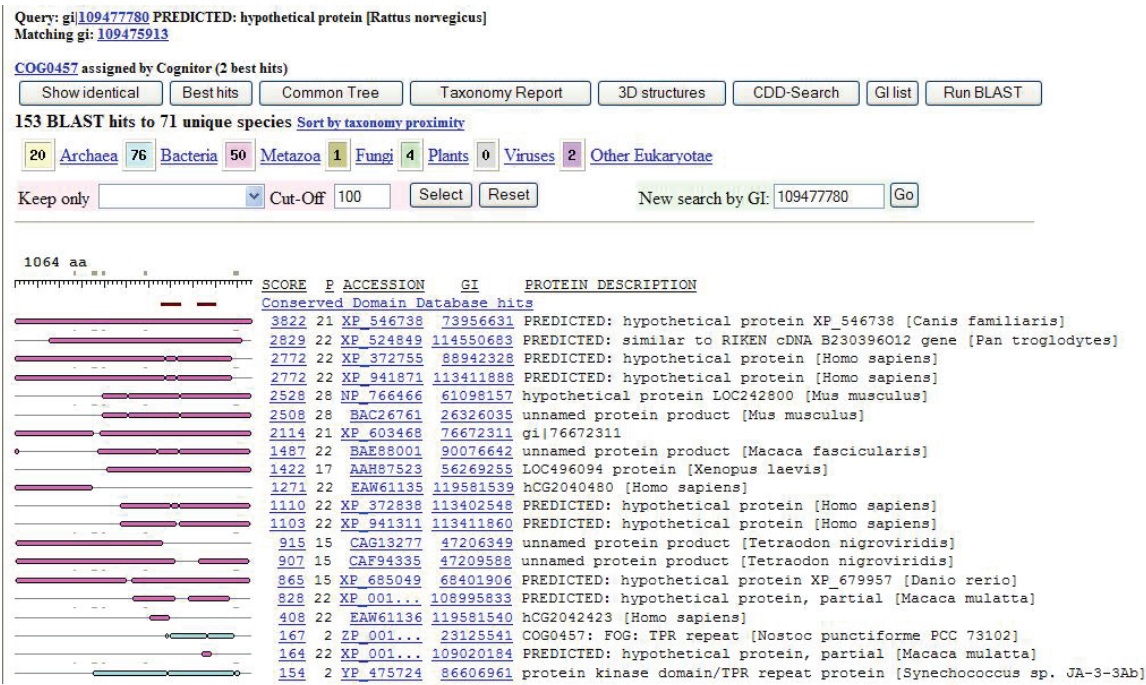


Figure 5.2. Fused gene products.

The protein gi|34879705 was identified by matching of tandem mass spectra. Closer inspection of the sequence revealed that this predicted gene product was actually three gene products that were fused together by the open reading frame prediction program. This fused gene product was manually split into three separate proteins and entered into our database as such.

Figure 5.2

ASSIGNED_PROTNAME	CMBSEQID	NRDB
SOLUTE CARRIER FAMILY 26, MEMBER 9; SLC26A9 ANION TRANSPORTER/EXCHANGER	268665	34879705
This is split into three proteins as shown in blue and red and green.		
1 mtsvspqalm nprkvdlik iivgalgvk tslhhgvhkf tfeeyqtdl gasilskii		
61 lddttklql wdtggqerf smvstfykgs dgcilafdv dpefealdi wrddvlakiv		
121 mveqsyprmvv lgnkidledr kvpgevahew ckekdmpye vsakndinvv qafevlasra		
181 lllrfvcmcs svdsylvpva smrkikvage edkeqkaree qpagsgrlegh kqglgqygeh		
241 shqtgescdq esarilglqc larfvkpwf lhrppggige elyrkaagpp hsfnsnshrel		
301 lwaprdlaps salnswnis evagrlvmvp dmsqtprryv vdraaysl dfekekddr		
361 aypvgelkm tfrccsakik aivglplvi swlpkykikd yilpdlggi sggcivpqvp		
421 mafallanip avnglyssff plityfflg iqhmvpqgta visilvgnic lqlapeskfq		
481 ifnathtety vdtvameaar lhvsatlaci taviqmalgf mgfgfvaiyi seefirgfmt		
541 aagqliliv lkyifgltp sytgpgsivf thidicknpl thniaslvfa lvsqvlvfv		
601 kelmarymsh inhpiptemi vvvvataisg scmkpkkyhgm qlveirghf pipavpmvsq		
661 wkdmvgtfats laivgyvini amgrtlanhk gydvdnsqem ialgcnsffg sffkihivcc		
721 alsvtlavdg aggksqvsi cvslvmitm lvgisylpl pkavilgalia vnlknsikql		
781 tdpuywlrks kldccvvvsv flssffislq ygvavgvafs lllvifqtqf mgstiaqvm		
841 dtdiynpntk ynrvgiegv kvtycpsly fanseifrk viaktgmdpq kvllakqyvl		
901 rkqekrmavp tqqrkslfmk tkbvislqel qdfesaastd pnnnqapvad ahisiytfsp		
961 dssataasel ptstqsprea sdalasvppf vtthtildm sgsvfvlmgd ikalakisls		
1021 yekigvqifi vnihaqyvnd isqgdfedg cvqmhvfps lvadavfaqa nareapahnf		
1081 qgagpgdtefs lydseedgss ywdleqawsl flfpppqafp tfvhsnliqh evvgkyshll		
1141 tvrgsdpslq pymlmahfvv vpaseegwv ppgfsgleqg flngrgaldn knsvmavlqa		
1201 lellirkyv pkrpfliag hdeevshlaq ylsrgpfrwi kplliskanr qcdvstpgni		
1261 stkerepgdf svsgstkgaa qisallqrg vqlafvldge sfledfipn lkcpfamivsv		
1321 tekgaldlmi qvnmtpghss appketsigi lsaavsr		
ASSIGNED_PROTNAME	CMBSEQID	NRDB
RAS-RELATED PROTEIN RAB-7B	none	50401091
1 mnprkvdlik liivgalgv ktsllhgvh kfteeyqtdl gasilskii liddttklq		
61 lwdtggqerf smvstfykgs dgcilafdv dpefealdi lwrddvlaki lpmegsyprmv		
121 vlgnkidled rkvsqevvhg wckekdmppf evsakndinv vqafevlasr allryqgtae		
181 nhldisiks pgqpskrcc		
ASSIGNED_PROTNAME	CMBSEQID	NRDB
SLC26A9 ANION TRANSPORTER/EXCHANGER	none	31321867
1 mnqprpryvv draayslsif ddefekddra ypvgeklmt frccsakfva fvgllpvlis		
61 wlpkykikdy iipdlggls ggcivpqgm afallanipa vnglyssff lityffligi		
121 hqmvpqgtfv isilvgnicl qlapeskfqi fmrvnetyv dtaamearil hvsatlacit		
181 aviaqmalgrm qgfgrvayis esfirgfmta agqlilivl kyifgltpis ytgpgsivft		
241 fidicknlph tniaslifa lvsqvlvfv elnarymsh hfpipptemiv vvvvataisgs		
301 ckmpkkyhmq lvgelrqgf tpavpmvsw kdmvgtfats laivgyvini mgttlaskhg		
361 ydvdsnqemi algcsnffgs ffrkihfvca lsvtldvda gkgsgvasic vsvlvmitml		
421 lvgisylplp kavilgalia nilknsikql dpyyhwksk lddccvvvsv lssffislpy		
481 gvavgvafs lllvifqtqf ngstiaqydm tdiynpnty nraeqiagkv lvtycsplyf		
541 anseifrqkv iaktgmdpqk vllakqkyrl kqektaipt qqrkslfmek ktvislqelq		
601 dfeasaptp nnnqapaaea hisiytfsp astaaceip astrespea dtlasvppfv		
661 tthtildms gvsfvlmgi kalakissy ekigvqifi nihaqyvndi shggvfedgc		
721 vqrshvfpsi hdavifaqan areapdrmf gapgdtefs ydseegpsy wdleqemfgt		
781 mfhettital		
ASSIGNED_PROTNAME	CMBSEQID	NRDB
UNNAMED PROTEIN PRODUCT BAC26171	none	6324834
1 maellaslpa waavilliffa tvsgstgprs renrgasip sqfseervia ikealkgalq		
61 iptvshsee snntalaefg eyirakevfa fssilvqhev vakysheifi qkdsqslapy		
121 mimahidvvp apegewevpp fslgerngi ygrgaldnkn svmailhale lllimyspk		
181 rffialghd eevsgkeagq kisallqarg vqlafvldge sflegfipn lekpvamisv		
241 tekgaldlmi qvnmtpghss appketsigi lsaavsrleq tpmnmpfggg pliktnklila		
301 nefspfinv lmlwifpi vsrimernpi thalvrtta ltmfmagikv nvipplakt		
361 incirhpsqt vhevielvkn tvaddrvqih vlrseplpi spsdqamgy qlletirsv		
421 fpevdvvpq iciantdth yanitngmyr fnplnlpqd fsgvhginek vsvqnyqnqv		
481 kfrifeiqna dtykepvppl hel		

Figure 5.3. Allelic isoforms.

Allelic isoforms cause confusion for peptide counting. When they are listed as two separate proteins, as they appear in public databases, this results in a splitting of the peptide counts between the sequences. So that the sequences were considered as one protein identification for the purposes of peptide counting, they were given the same “assigned protein name”. This was performed by BLASTing the database of sequences against itself, and then scanning the hits for almost identical proteins. Here we see the results for two isoforms of 10-formyltetrahydrofolate dehydrogenase. The red arrows indicate the amino acid differences between the two sequences.

Figure 5.3

```

Query= gi|42543697|pdb|1S3I|A Chain A, Crystal Structure Of The N
Terminal Hydrolase Domain Of 10- Formyltetrahydrofolate Dehydrogenase
      (310 letters)

Database: allGolgi_COPI_GTPgS_RM_SM_seq.txt
        2142 sequences; 1,198,328 total letters

Searching.....done

Sequences producing significant alignments:

                                Score      E
                                (bits) Value
gi|908915|gb|AAA70429.1| 10-formyltetrahydrofolate dehydrogenase      624    e-180
gi|34862428|ref|XP_235005.2| similar to RIKEN cDNA D330038I09 [R...    471    e-134

>gi|908915|gb|AAA70429.1| 10-formyltetrahydrofolate dehydrogenase
    Length = 902

    Score = 624 bits (1609), Expect = e-180
    Identities = 304/309 (98%), Positives = 305/309 (98%)

Query: 1   MKIAVIGQSLFGQEVYCYQLRKEGHEVVGVFPTIPDKDGKADPDGLEAEKDGVPVFKFPRWR 60
          MKIAVIGQSLFGQEVYCYQLRKEGHEVVGVFPTIPDKDGKADP GLEAEKDG VFKFPRWR
Sbjct: 1   MKIAVIGQSLFGQEVYCYQLRKEGHEVVGVFPTIPDKDGKADPLGLEAEKDGRAVFKFPRWR 60

Query: 61   ARGQALPEVVAKYQALGAELNVLPFCSQFIPMEVINAPRHGSIYHPSLLPRHRGASAIN 120
          ARGQALPEVVAKYQALGAELNVLPFCSQFIPMEVINAPRHGSIYHPSLLPRHRGASAIN
Sbjct: 61   ARGQALPEVVAKYQALGAELNVLPFCSQFIPMEVINAPRHGSIYHPSLLPRHRGASAIN 120

Query: 121  WTLIHGDKKGGFTIFWADDGLDTGDLQLQKECEVLPDDTVSTLYNRFLFPEGIKGMVQAV 180
          WTLIHGDKKGGFTIFWADDGLDTGDLQLQKECEVLPDDTVSTLYNRFLFPEGIKGMVQAV
Sbjct: 121  WTLIHGDKKGGFTIFWADDGLDTGDLQLQKECEVLPDDTVSTLYNRFLFPEGIKGMVQAV 180

Query: 181  RLIAEGTAPRCQPQSEEGATYEGIQKKTAKINWDQPAEAIHNWIRGNDKVPGAWTEACGQ 240
          RLIAEGTAPRCQPQSEEGATYEGIQKKTAKINWDQPAEAIHNWIRGNDKVPGAWTEACGQ
Sbjct: 181  RLIAEGTAPRCQPQSEEGATYEGIQKKTAKINWDQPAEAIHNWIRGNDKVPGAWTEACGQ 240

Query: 241  KLTFNNTLNTSGLSTQGEALPIPGAHRPGVVTKAGLILFGNDRMLLVKNIQLEDGKMM 300
          KLTFNNTLNTSGLSTQGEALPIPGAHRPGVVTKAGLILFGN+ RMLLVKNIQLEDGKMM
Sbjct: 241  KLTFNNTLNTSGLSTQGEALPIPGAHRPGVVTKAGLILFGNEHRMLLVKNIQLEDGKMM 300

Query: 301  PASQFFKGS 309
          PASQFFKGS
Sbjct: 301  PASQFFKGS 309

```

Figure 5.4. TMHMM prediction.

TMHMM (Sonnhammer et al 1998) was used to predict the existence and location of transmembrane regions for the proteins in our database. The sequence is inputted into the program, and the output file contains the predicted location and orientation of transmembrane segment(s). This figure shows the output for the sequence

Figure 5.4

TMHMM result

HELP with output formats

```
# gi_109460116_ref_XP_220013.3 Length: 721
# gi_109460116_ref_XP_220013.3 Number of predicted TMHs: 9
# gi_109460116_ref_XP_220013.3 Exp number of AAs in TMHs: 204.50213
# gi_109460116_ref_XP_220013.3 Exp number, first 60 AAs: 0
# gi_109460116_ref_XP_220013.3 Total prob of N-in: 0.00382
gi_109460116_ref_XP_220013.3 TMHMM2.0 outside 1 354
gi_109460116_ref_XP_220013.3 TMHMM2.0 TMhelix 355 377
gi_109460116_ref_XP_220013.3 TMHMM2.0 inside 378 420
gi_109460116_ref_XP_220013.3 TMHMM2.0 TMhelix 421 443
gi_109460116_ref_XP_220013.3 TMHMM2.0 outside 444 457
gi_109460116_ref_XP_220013.3 TMHMM2.0 TMhelix 458 480
gi_109460116_ref_XP_220013.3 TMHMM2.0 inside 481 491
gi_109460116_ref_XP_220013.3 TMHMM2.0 TMhelix 492 514
gi_109460116_ref_XP_220013.3 TMHMM2.0 outside 515 523
gi_109460116_ref_XP_220013.3 TMHMM2.0 TMhelix 524 546
gi_109460116_ref_XP_220013.3 TMHMM2.0 inside 547 579
gi_109460116_ref_XP_220013.3 TMHMM2.0 TMhelix 580 602
gi_109460116_ref_XP_220013.3 TMHMM2.0 outside 603 616
gi_109460116_ref_XP_220013.3 TMHMM2.0 TMhelix 617 639
gi_109460116_ref_XP_220013.3 TMHMM2.0 inside 640 645
gi_109460116_ref_XP_220013.3 TMHMM2.0 TMhelix 646 668
gi_109460116_ref_XP_220013.3 TMHMM2.0 outside 669 682
gi_109460116_ref_XP_220013.3 TMHMM2.0 TMhelix 683 705
gi_109460116_ref_XP_220013.3 TMHMM2.0 inside 706 721
```

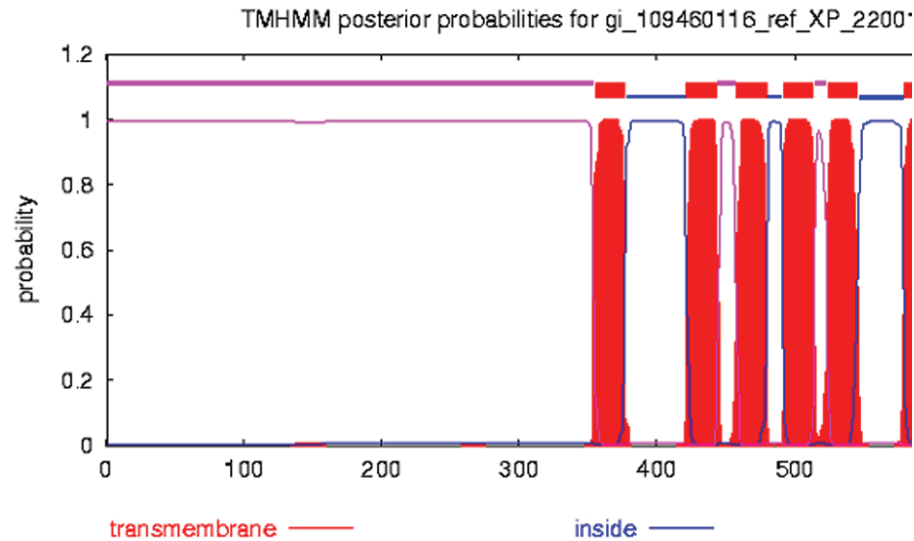


Figure 5.5. SignalP prediction.

The SignalP (Bendtsen et al 2004) program was used to identify possible signal peptides present in the protein sequences in our database. The program scanned the first 70 amino acids of each sequence in order to make its prediction. An example of the output file is shown in this figure.

Figure 5.5



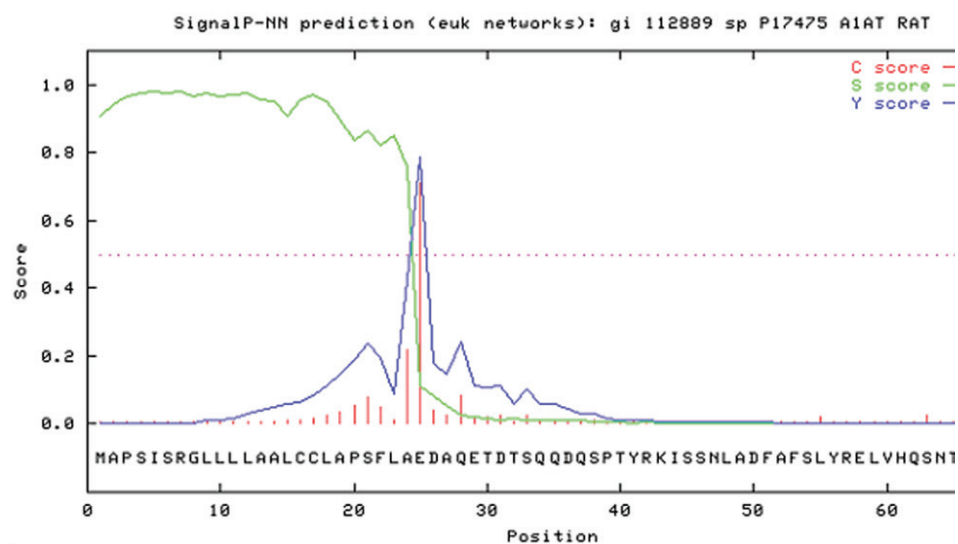
SignalP 3.0 Server - prediction results

Technical University of Denmark

Using neural networks (NN) and hidden Markov models (HMM) trained on eukaryotes

>gi_112889_sp_P17475_A1AT_RAT Alpha-1-antiproteinase precursor _Alpha-1-antitrypsin_ _Alpha-1-proteinase inhibitor_

SignalP-NN result:



```
# data
>gi_112889_sp_P17475_ length = 70
# Measure Position Value Cutoff signal peptide?
max. C 25 0.709 0.32 YES
max. Y 25 0.788 0.33 YES
max. S 5 0.982 0.87 YES
mean S 1-24 0.929 0.48 YES
D 1-24 0.859 0.43 YES
# Most likely cleavage site between pos. 24 and 25: FLA-ED
```

SignalP-HMM result:

Figure 5.6. Identifying CASP.

CASP, a splice isoform of the transcription factor CCAAT displacement protein (also known as CUT), localizes to the Golgi apparatus. Only CUT was found in the rat database. All the peptides that were originally matched to CUT in the rat database were manually matched with sequences for all the isoforms of CCAAT displacement protein for mouse and human sequences. The peptides for the three different CUT sequences in the rat database are shown in three tables at the top of the figure, and are coloured in green, red, and blue. These peptides are matched to their locations on the mouse and human sequences, shown below the peptide tables. CCAAT displacement protein isoform A is CUT. Isoforms B and C are equivalent to CASP. Note that all the peptides match to isoforms B and C, and to the beginning portion of isoform A. The end portion of isoform A is what is removed in the splice variants, and none of our peptides match to this region of the protein.

Figure 5.6

```
CMBSEQID      GI
289275        34873366
  SLQSENATLR   TKYDEETAK   LQNDFAEK
  SQAETIALEK   EIAQLVEDVQR   APDVAIEVLTR

CMBSEQID      GI
280644        34871708
  EQLSSANHSLQLASQIQK  SFQGEIDALSK  ADEIEMIMTDLER  ELDATATVLANR
  LQTLQTALEK          APDVEQAIEVLTR  EAEAAFLTVYK
  KLQETQMSTTSK        SSLEVELAAK   SQAETIALEK     ADEIEMIMTDLER
  ELDATATVLANR        EIAQLVEDVQR  SLQSENATLR     LQTLQTALEK
  APDVEQAIEVLTR       LRENSASQISQLEQQQNAK  EAEAAFLTVYK    ETLEEYNKEFAEVK
  ENSASQISQLEQQQNAK   LHDietenqk   SKEAEAAFLTVYK  LQNDFAEKER
  EAETLREQLSSANHSLQLASQIQK
  TRTEFLDLK          SFQGEIDALSK  APDVEQAIEVLTR  ETLEEYNKEFAEVK
  IREYEQTLK
  SQAETIALEK          EIAQLVEDVQR  APDVEQAIEVLTR
  ELDATATVLANR        LQTLQTALEK  APDVEQAIEVLTR
  APDVEQAIEVLTR
```

```
CMBSEQID      GI
194891        34873372
  YLGLSPWDK      FHESDNGAAAGDLWQ      CAELQIHLTEATAK
  MAQHTIQALQSELDCLR
  MAQHTIQALQSELDCLR      LEQDLSTIQSIQRPDAEGASEQGL  NQELEAESR
                                EK
                                FLQSYPGR
  MAQHTIQALQSELDCLRADNIK  MAQHTIQALQSELDCLR      LEQDLSTIQSIQRPDAEGAS
                                EQGLEK
  GIGSDDELTR      LEQDLSTIQSIQRPDAEGASEQGL
                                EK
  GIGSDDELTR      MAQHTIQALQSELDCLR      LEQDLSTIQSIQRPDAEGAS
                                EQGLEK
  NQELEAESR      FLQSYPGR
  GIGSDDELTR      NQELEAESR      YSSQYEER
  FLQSYPGR
```

```
>gi|41282038|ref|NP_941004.1| CCAAT displacement protein isoform b [Mus musculus]
MAANVGSMFQYWKRFDLQQLRELDATATVLANRQDESEQSRKRLIEQSREFKKNTPEDLRKQVAPLLKS
FQGEIDALSKRSKEAEAAFLTVYKRRLIDVDPVPALDVGQQLKIKVQRLLHDIETENQKLRETL EEYNKEF
AEVKNQEVTIKALKEKIREYEQTLKSQAETIALEKEQKLQNDFAEKERKLQETQMSTTSKLEEAHKLQT
LQTALEKTRTEFLDLKTKYDEETAKADEIEMIMTDLERANQRAEVAQREAE TLREQLSSANHSLQLASQ
IQAPDVEQAIEVLTRSSLEVELAAKEREIAQLVEDVQRLQASLTKLRENSASQISQLEQQQNAKNSTLK
QLEEKLKGQADYEEVKELNTLKSMEFAPSEGAGTQDSTKPLEVLLLEKNRSLQSENATLRISNSDLGR
CAELQIHLTEATAKAVEQKELIARLEQDLSTIQSIQRPDAEGASEQGLEKIPAPIKEATALFYGPSMSSS
GTLPEGQVDSLSSIISSQRERFRTRNQELEAESRMAQHTIQALQSELDCLRADNIKLFEEKFLQSYPGR
GIGSDDELTRYSSQYEERLDPFSSFSKRERQRKYLGSLPDKATLGMGRILLSNKTARTIGFFYTFLHC
LVFLVLVKLAWSESVERDCAATCAKKFADHLHKFHESDNGAAAGDLWQ
```

```
>gi|31652240|ref|NP_853530.1| CCAAT displacement protein isoform a [Homo sapiens]
MLCVRGARLKRELDATATVLANRQDESEQSRKRLIEQSREFKKNTPEDLRKQVAPLLKSFQGEIDALSKR
SKEAEAAFLNVYKRLIDVDPVPALDLGQQLKLVQRLHDIETENQKRLETLEEYNKEFAEVKNQEVTIK
ALKEKIREYEQTLKNQAETIALEKEQKLQNDFAEKERKLQETQMSTTSKLEEAHKVQSLQTALEKTRTE
LFDLTKYDEETAKADEIEMIMTDLERANQRAEVAQREAE TLREQLSSANHSLQLASQIQAPDVEQAIE
VLTRSSLEVELAAKEREIAQLVEDVQRLQASLTKLRENSASQISQLEQQQNAKNSTLKQLEKLKGQAD
YEEVKELNLSMEFAPSEGAGTQDAKPLEVLLLEKNRSLQSENATLRISNSDLGSGARRKGKDQPES
RRPGSLPAPPPSQLPRNPGEQASNTNGTHQFSPAGLSQDFFSSSLASPSLPLASTGKFALNSLLQRQLMQ
SFYSKAMQEAGSTSMIFSTGPYSTNSISSQSPDQSPDVGMPSPSQSESAGSVSEGEEMDTAEIARQV
KEQLIKHNIGQRIFGHYVLGLSQGSVSEILARPKPWNKLTVRGKEPFHKMKQFLSDEQNILALRSIQGRQ
RENPGQSLNRLFQEVPKRRNGSEGNITRIRASETGSDEAIAKSILEQAKRELQVQKTAEPAPQSSASGSG
NSDEPIRSILQQARREMAQQAALDPALKQAPLSQSDITILTPKLLSTSPMPTVSSYPPLAISLKKPSAA
PEAGASALPNPPALKKEAQDAPGLDPQGAADCAQGVLRQVKNVEVGRSGAWKDHWSAVQPERRNAASSEE
AKAETGGGKEKGGSGSGSGSPRAERSQLQGPSSSEYWKWPSAESPSQSSELSTGASRSETPQNSP
LPSSPIVPMKPTKPSVPPLTPQYEVYMYQEVDTIELTRQVKEKLAKNGICQRIFGEKVLGLSQGSVSD
```

MLSRPKPWSKLTQKGREPFIRMQLWNLGELGQGVLPVQGGQQGPVLHVSVTSIQDPLQQGCVSSESTPKTS
 ASCSPAPESPMSSSESVKSLTELVLQQPCPPIEASKDKSKPPEPSDPPASDSQPTTPLPLSGHSALSISQELV
 AMSPELDITYGITKRKVEVLTNNLGQRLFGETILGLTQGSVSDLLARPKPWHKLSLKGREPFVIRMQLWNL
 DPNNEKLMMDMKRMEKKAYMKRRHSSVSDSQCEPPSVGTEYSQGASQPQHQKPRVVLAPEEKEALK
 RAYQQKPYPSPKTIEDLATQLNLKTSTVINWFHNYRSRIRRELFIEEIQAGSQGAGASDPSARSRAA
 PSSEGDSCDGVATEGPGSADTEEPKSGQEAEREVEPRPAEQTEPPPSGTPGPDADDDHEGGPVGPG
 PLPSPASATATAAPAPEDAATSAAPGEGPAAPSSAPPPSNSSSSSAPRRPSSLQSLFGLPEAAGARD
 SRDNPLRKKKAANLNSIIHRLEKAASREEPIEWEF

>gi|31652236|ref|NP_001904.2| CCAAT displacement protein isoform b [Homo sapiens]
 MAANVGSMFYWKRFDLQQLR**ELDATATVLANR**QDESEQSRKRLIEQSREFKKNTPEDLRKQVAPLLKS
 FQGEIDALSKRSKEAAEAFNLVYKRLIDVPDPVPALDLGQQQLQKLVQRLHDIETENQKLRETL EEYNKEF
 AEVKNQEVTIKALKEK**IREYEQTLKNQAETIALEKEQKLQNDFAEKERKLQETQMSTTSKLEEA**EHKVQS
 LQTAL**ETRT**ELFDL**TKYDEET**TA**KADEIEMIMTDLER**ANQRAEVAQREAE**TLREQLSSANHSLQLASQ**
 IQ**KAPDVEQAI**EV**LTRSSLEVELA**AKERE**IAQLVEDVQRLQASLTKLRENSASQISQLEQQLSAKN**STLK
 QLEEK**LGQADYEEVKELN**ILKSMEFAPSEGAGTQDAAKPLEVLLLEKNRSLQSENAALRISNSDLSGR
 CAELQVR**ITEAVATATEQRELIARLEQDLSIIQSIQRPDAEGAAEHRLEKIPEPIKEAT**ALFYGPAAPAS
 GALPEGQVDSLLSISSQRERFRARNQ**ELEAENRLAQHTLQALQSE**LSLRADNIKLF**EKIKFLQSY**PGR
 GSGSD**DELTRYSSQYEER**LDPFSSFSKRERQRKYL**SLSPWDKATLSMGR**LVL**SNKMARTIGFFYT**TLFLHC
 LVFLVLYKLAWSES**MERDCATFCAKKFADHLHKFHENDNGAAAGDLWQ**

>gi|31652238|ref|NP_852477.1| CCAAT displacement protein isoform c [Homo sapiens]
 MAANVGSMFYWKRFDLQQLR**ELDATATVLANR**QDESEQSRKRLIEQSREFKKNTPEDLRKQVAPLLKS
 FQGEIDALSKRSKEAAEAFNLVYKRLIDVPDPVPALDLGQQQLQKLVQRLHDIETENQKLRETL EEYNKEF
 AEVKNQEVTIKALKEK**IREYEQTLKNQAETIALEKEQKLQNDFAEKERKLQETQMSTTSKLEEA**EHKVQS
 LQTAL**ETRT**ELFDL**TKYDEET**TA**KADEIEMIMTDLER**ANQRAEVAQREAE**TLREQLSSANHSLQLASQ**
 IQ**KAPDVAIEVLTRSSLEVELA**AKERE**IAQLVEDVQRLQASLTKLRENSASQISQLEQQLSAKN**STLKQ
 LEELKGQADYEEVKELN**ILKSMEFAPSEGAGTQDAAKPLEVLLLEKNRSLQSENAALRISNSDLSGR**CA
 ELQVR**ITEAVATATEQRELIARLEQDLSIIQSIQRPDAEGAAEHRLEKIPEPIKEAT**ALFYGPAAPASGA
 LPEGQVDSLLSISSQRERFRARNQ**ELEAENRLAQHTLQALQSE**LSLRADNIKLF**EKIKFLQSY**PGRGS
 GSDD**DELTRYSSQYEER**LDPFSSFSKRERQRKYL**SLSPWDKATLSMGR**LVL**SNKMARTIGFFYT**TLFLHCLV
 FLVLYKLAWSES**MERDCATFCAKKFADHLHKFHENDNGAAAGDLWQ**

>gi|41282038|ref|NP_941004.1| CCAAT displacement protein isoform b [Mus musculus]
 MAANVGSMFYWKRFDLQQLR**ELDATATVLANR**QDESEQSRKRLIEQSREFKKNTPEDLRKQVAPLLKS
 FQGEIDALSKRSK**EAEAAFLTVYKRLIDVPDPVPALDVGQQL**EIKVQRLHDIETENQKLRETL EEYNKEF
 AEVKNQEVTIKALKEK**IREYEQTLKSQAETIALEKEQKLQNDFAEKERKLQETQMSTTSKLEEA**EHKLQT
 LQTAL**ETRT**ELFDL**TKYDEET**TA**KADEIEMIMTDLER**ANQRAEVAQREAE**TLREQLSSANHSLQLASQ**
 IQ**KAPDVEQAI**EV**LTRSSLEVELA**AKERE**IAQLVEDVQRLQASLTKLRENSASQISQLEQQLN**AKNSTLK
 QLEEK**LGQADYEEVKELN**TLKSMEFAPSEGAGTQDSTKPLEVLLLEKNRSLQSENA**TLRISNSDLSGR**CA
 ELQ**VIHLTEATAKAVEQKELIARLEQDLSIIQSIQRPDAEGASEQGLEKIPEPIKEAT**ALFYG**PSMSSS**
 GTLPEGQVDSLLSISSQRERFR**TRNQELEAESRMAQHTIQALQSE**LSLRADNIKLF**EKIKFLQSY**PGR
 GIGSD**DELTRYSSQYEER**LDPFSSFSKRERQRKYL**LGSLPWDKATLSMGR**LIL**SNKTARTIGFFYT**TLFLHC
 LVFLVLYKLAWSES**VERDCAATCAKKFADHLHKFHESDNGAAAGDLWQ**

>gi|38348586|ref|NP_034116.2| CCAAT displacement protein isoform a [Mus musculus]
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 SK**EAEAAFLTVYKRLIDVPDPVPALDVGQQL**EIKVQRLHDIETENQKLRETL EEYNKEF**AEVKNQEVTIK**
 ALKEK**IREYEQTLKSQAETIALEKEQKLQNDFAEKERKLQETQMSTTSKLEEA**EHKL**QTLQTALEKTRTE**
 LFDL**TKYDEET**TA**KADEIEMIMTDLER**ANQRAEVAQREAE**TLREQLSSANHSLQLASQIQKAPDVEQAI**
 EV**LTRSSLEVELA**AKERE**IAQLVEDVQRLQASLTKLRENSASQISQLEQQLN**AKNSTLKQLEEK**LGQAD**
 YEEVKELN**TLKSMEFAPSEGAGTQDSTKPLEVLLLEKNRSLQSENA**TLRISNSDLSGSARRKGRDQ**PE**
 RRPGLPASPPQLPRNTGEQVSN**TNGTHHFS**PAGLSQDFFSSNLASPSLPLASTGKFALNSLQRQ**LMQ**
 SFYSKAMQEAGSTSTIFSTG**PYSTNSISSPSPLQQSPDVNGMAPSPSQSESAGSISEGEEIDTA**EIARQV
 KEQLIKHNIGQRI**FGHYVLGLSQGSVSEILARPKPW**NKLTVRGKEPF**HKMKQFLSDEQNILALRSIQGRQ**
 RENPGQSLNRL**FQEVPKRRNRSEGNITTRIRASE**TGSDEAIKSILEQAKRELQVQK**TAE**FPVQTSSTSSG
 NSDDAIRSILQARREMEAAQ**AALDPALKPAPLSQPD**LTLTPKHLSAP**PMSTVSTYPP**LAISLKKTPAA
 PETSTAALPSAPAL**KKEAQDVPTLDPPGSADAAQGVLRPMKSELV**RGSTWKDPWWSP**IQPERRNLTS**SEE
 TKADETTASGKERAGSSQ**PRAERSQLQG**PSASAEYWK**EWPSAES**PYSQSS**ELSLTGASRSET**PQNSPLPS
 SPIVMAKPAKPSVPPL**TEQYEV**MYQEVD**TI**ELTRQVKEKLAKNGICQ**RIFGEKVLGLSQGSV**SDMLS
 RPKPWSKLTQKGREPFIRMQLWNLGELGQGVLPVQGGQQGPVLHVSASLQDPLQQGCVSSESTPKTS
 SPAPESPMSSSESVKSLTELVLQQPCPAI**ETSK**EGKPP**EPSDPPASDSQPTT**PLPLSGHSALSISQELVAMS
 PELDITYGITKRKVEVLTNNLGQRLFGETILGLTQGSVSDLLARPKPWHKLSLKGREPFVIRMQLWNLDPN
 NVEKLMMDMKRMEKKAYMKRRHSSVSDSQCEPPSVGIDYSQGASQPQHQKPRVVLAPEEKEALKRAY
 QQKPYPSKTIEELATQLNLKTSTVINWFHNYRSRIRRELFIEEIQAGSQGAGASDPSARSRAAPSS
 EGDSCDGV**EATDAE**EPG**GNIVATKSQGLAE**VAAAPAD**REEATQPAEKAKAQPLCSGTPGQDDGEDASRP**
 RPLPEGLADAPAPVPVSLA**APAGEDAATSATAPATATEAPGAARAGPAERS**SALPSTAPANAPARRPSS
 LQSLFGLPEAAGARDNPVRKKKAANLNSIIHRLEKAASREEPIEWEF

Figure 5.7. Gene Ontology (GO).

The GO controlled vocabulary for the protein 1,3-1,6-alpha-mannosidase.

The tree of terms for the molecular function category is displayed.

Figure 5.7



the Gene Ontology

Advanced SearchBLAST searchBrowseHelp

Search GO ☒ Terms ☐ Genes or proteins ☐ Exact Match

Filter tree view ?

Filter by ontology

Ontology

AllBiological ProcessCellular ComponentMolecular Function

Filter Gene Product Counts

Data source

AllCGDdictyBaseFlyBase

Set filters

Remove all filters

☐ all : all [218887]

☐ ☐ GO:0008150 : biological_process [140488]

☐ ☐ GO:0005575 : cellular_component [152782]

☐ ☐ GO:0003674 : molecular_function [143288]

☐ ☐ GO:0003824 : catalytic activity [45863]

☐ ☐ GO:0016787 : hydrolase activity [15187]

☐ ☐ GO:0016798 : hydrolase activity, acting on glycosyl bonds [1283]

☐ ☐ GO:0004553 : hydrolase activity, hydrolyzing O-glycosyl compounds [1021]

☐ ☐ GO:0015923 : mannosidase activity [84]

☐ ☐ GO:0015924 : mannosyl-oligosaccharide mannosidase activity [34]

☐ ☐ **GO:0004572 : mannosyl-oligosaccharide 1,3-1,6-alpha-mannosidase activity [6]**

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Chapter 6 --Proteomes of the Golgi apparatus and COPI vesicles.

6.1 Abstract

After generating a highly curated list of proteins with their associated peptide counts, we were able to start looking closely at the proteomes of our samples and the relative abundances of identified proteins. This provided us with our first opportunity to examine the total protein complement of our organelle. The largest proportion of redundant peptide counts from the Golgi apparatus were assigned to proteins in the biosynthetic cargo functional category. For the COPI vesicles generated with hydrolysable GTP the representation was highest for the functional category of protein modification enzymes, and for the COPI vesicles generated with GTP γ S the peptide counts were spread over a number of categories.

6.2 Introduction

The Golgi apparatus has fascinated cell biologists ever since its discovery by Camillo Golgi in 1898 (Golgi 1898). In the past, the organelle has been investigated by isolation followed by enzyme assays, western blots, electron microscopic analysis, *in vitro* assays etc. as well as *in vivo* studies using immunofluorescence. All of these techniques are limited in that it is only possible to study a few proteins at the same time. Proteomics analysis allows us to look at the whole protein complement of the organelle at the same time. Instead of comparing the abundance of two proteins we now have access to data on hundreds of proteins.

6.3 Results

Looking at the distribution of redundant peptide counts across our 23 categories (Figure 6.1), we are able to discern a picture of the protein make up of our organelles. The Golgi apparatus is enriched in biosynthetic cargo proteins, the COPI GTP vesicles are enriched in protein modification enzymes, and the COPI GTP γ S vesicles are enriched in coat proteins.

6.3.1 Proteome of the Golgi apparatus.

As seen in Figure 6.1, the largest proportion of redundant peptide counts for the isolated Golgi apparatus preparations are in the functional category of biosynthetic cargo. Seeing as though hepatocytes produce the majority of the proteins present in serum (Crane & Miller 1974, Noel & Rubinstein 1974, Palade 1975), and these proteins are concentrated in the Golgi before secretion (Glaumann & Ericsson 1970, Peters et al 1971), this is an expected result. Other non-contaminant functional categories of interest are: coat, detoxification, GTPase, protein modification, protein synthesis and folding, tethering/docking/fusion, traffic, and unknown.

6.3.1.1 Biosynthetic cargo.

The Golgi is the site of concentration of biosynthetic cargo before it is packaged for secretion to the cell surface and the blood plasma. Over 20% of the total peptides were assigned to proteins in this category. Figure 6.2 shows the nine most abundant biosynthetic cargo proteins, with the most abundant by far being serum albumin.

6.3.1.2 Coat.

Surprisingly, we see an enrichment of proteins of the COPII coat in the Golgi apparatus. Referring to Figure 6.3, we see that six different subunits

of the COPII coats are identified in the Golgi apparatus and the GTP γ S vesicles, but are virtually absent from the RM, SM, and COPI vesicles.

6.3.1.3 Detoxification.

Detoxification enzymes are known to localize to the smooth endoplasmic reticulum, however, we identified seven detoxification proteins that were at comparable levels in ER and Golgi apparatus. Figure 6.4 displays these seven proteins.

6.3.1.4 GTPase.

There is one Rab that we see highly enriched in the Golgi apparatus as compared to the COPI GTP and COPI GTP γ S vesicles. This Rab is Rab6. Figure 6.5 shows the distribution of percentage total peptides for Rab6 over the three organelles.

6.3.1.5 Protein modification.

The Golgi is the site of protein modification via terminal glycosylation. Many different protein modification enzymes were identified. The 7 most abundant protein modification enzymes are shown in Figure 6.6. It should be noted that for the majority of protein modification enzymes they were more highly enriched in the COPI GTP vesicles as compared to the Golgi apparatus.

6.3.1.6 Tethering, docking, and fusion.

Membrane budding and fusion events are integral to the functioning of the Golgi. Vesicles arriving from the vesicular tubular clusters fuse with the cis Golgi of the Golgi, secretory vesicles are budded off the trans Golgi, and COPI vesicles are postulated to bud off from and fuse back to different cisternae of the Golgi stack. These varied membrane trafficking events are evidenced by a wide variety of tethering, docking, and fusion

proteins identified in the Golgi apparatus. The most abundant of these proteins in the Golgi apparatus are shown in Figure 6.7.

6.3.1.7 Unknown.

One abundant protein of unknown function was identified primarily in the Golgi apparatus. This protein is shown in Figure 6.8. A more extensive discussion of proteins of unknown function is found in Chapter 7.

6.3.2 Proteomes of the COPI GTP vesicles and COPI GTP γ S vesicles.

Referring back to Figure 6.1, we see that the largest proportion of redundant peptide counts for the isolated COPI GTP vesicle preparations are in the functional category of protein modification. For the GTP γ S vesicles, the category with the most peptides is that of coat proteins. As GTP γ S is a non-hydrolysable analog of GTP, and release of coat proteins requires the hydrolysis of GTP, it is expected that we have more coat proteins attached to the GTP γ S vesicles than our GTP vesicles. Other non-contaminant functional categories of interest for our vesicles are: calcium transport and binding, GTPase, tethering/docking/fusion, traffic, and unknown. It should be noted that most of the proteins identified in the COPI GTP vesicles are well known Golgi localized proteins, and though they are detected in higher abundance in the COPI GTP vesicles, that does not obviate their Golgi localization. The GTP γ S vesicles are heterogeneous in nature, and are not enriched in any specific category of proteins other than the aforementioned coat proteins.

6.3.2.1 Coat.

As expected, the most abundant coat proteins of the COPI GTP and COPI GTP γ S vesicles are the subunits of the COPI coat. The distribution of percentage total peptides is shown in Figure 6.9. All seven members of the coat complex are represented. These are: alpha, beta, beta prime,

gamma, delta, epsilon, and zeta. Two forms of gamma and delta were identified.

Having identified all COPI coatamer proteins, we decided to apply the methodology of Blondeau et al. (Blondeau et al 2004) to the subunits of the COPI coat complex to determine whether we could detect a 1:1 stoichiometry. Figure 6.10A shows the distribution of percentage total peptides for the seven subunits in the COPI GTPyS fraction. Figure 6.10B shows the percentage total peptides normalized to percentage total peptides per kDa in order to compare molar abundance between the subunits. Six of the seven subunits show approximate 1:1 molar stoichiometry. The zeta subunit is underrepresented which may be due to its small size or to the manner it binds to the complex.

6.3.2.2 Calcium transport and binding.

Three abundant calcium transport and binding proteins were enriched in the COPI GTP vesicles. The distribution of their percentage total peptides is shown in Figure 6.11. Two of these proteins, Calnuc 1 and Calnuc 2, were previously localized to the Golgi apparatus (Lin et al 1998), however, we see greater than a two-fold increase of these proteins in our COPI vesicles. The third protein, Cab45, has also been Golgi localized (Scherer et al 1996). The involvement of calcium in membrane fusion events has been demonstrated previously (Beckers & Balch 1989), and these proteins could act as a calcium reservoir for membrane fusion events that the vesicles will be involved in subsequently.

6.3.2.3 GTPase.

Our COPI GTP vesicles are enriched in the Rab proteins Rab1A, Rab1B, and Rab14, as seen in Figure 6.12, all of which have been Golgi localized (Nuoffer et al 1994, Proikas-Cezanne et al 2006). There are many other Rab proteins detected, but at much lower abundance. Low levels of ARF

proteins are detected in all the fractions, with the highest amounts in COPI GTPyS vesicles. We detected ARF1, ARF3, ARF4, ARF5, and ARF6.

6.3.2.4 Protein modification.

There is a whole cohort of Golgi localized protein modification enzymes that are enriched in the COPI GTP vesicles. The most abundant are shown in Figure 6.13. The Golgi marker protein, mannosidase II, is the most highly abundant protein modification protein, followed by various glycosyl transferase enzymes.

6.3.2.5 Tethering, docking, and fusion.

There are four abundant tethering/docking/fusion proteins enriched in the COPI GTP vesicles. These proteins are: Golgin-84, GM130, GPP130, and CASP and can be seen in Figure 6.14.

6.3.2.6 Traffic.

Traffic proteins enriched in the COPI GTP vesicles are ERGIC-53, VIP36, and a few members of the p24 family of proteins as seen in Figure 6.15.

6.3.2.7 Unknown.

There are 11 proteins of unknown function that are enriched in the COPI GTP vesicles. They are shown in Figure 6.16 and discussed along with all identified proteins of unknown function in Chapter 7.

6.4 Discussion

A summary cartoon, Figure 6.17, shows the proteomes of the Golgi apparatus, COPI vesicles, and COPI GTP γ S vesicles.

Seven hundred proteins were identified in the Golgi apparatus. Twenty-five percent of the peptides identified in this sample belonged to proteins in the category of biosynthetic cargo and ten percent belonged to proteins in the category of protein modification. Compared to the proteomics analysis of the Golgi performed by Wu et al. (Wu et al 2004) which identified 106 Golgi resident proteins, we expanded the Golgi proteome to 246 Golgi resident proteins, all of which were literature verified. Our comparison of proteomes did not include the 85 biosynthetic cargo proteins we identified, since Wu et al. treated their Golgi to exclude cargo proteins and we wanted to make an unbiased comparison.

There were two unexpected results in the proteome of the Golgi apparatus: the enrichment of COPII subunits and the presence of a few detoxification proteins at levels higher than would be expected for contaminants.

Previously it has been suggested that COPII coat proteins localize to exit sites on the endoplasmic reticulum (Forster et al 2006, Liu & Lippincott-Schwartz 2005, Palmer & Stephens 2004, Watson et al 2005), however, we clearly detect the presence of multiple COPII subunits in our Golgi fraction in much higher abundances than in the RM and SM fractions in all three of our Golgi biological replicates. The cis Golgi is known to be isolated with our Golgi fraction, and as Mardones et al. show that tubules containing Golgi cis-medial matrix proteins associate with ER exit sites (Mardones et al 2006), it is likely that COPII coatamer is isolated along with the cis Golgi in our fractions.

The presence of detoxification proteins in the Golgi fraction in levels higher than would be expected for contaminants opens the question of whether detoxification enzymes traffic between the endoplasmic reticulum and Golgi apparatus. Our proteomics data seems to suggest that certain proteins do traffic, but further study regarding the amino acid sequences of these proteins needs to be performed.

Although it would have been interesting to look at which tethering docking and fusion proteins were enriched in each compartment, the relatively low abundance of these proteins as detected by peptide counts does not allow an accurate statement to be made about their distribution other than they are seen to be present. The same problem was encountered when looking at any GTPases other than the most abundant. Looking at proteomics data regarding the distribution of ARFs in the Golgi and vesicle fractions, all we could say is that they were detected but at levels too low to speculate as to their distribution.

The difference between COPI vesicles generated with hydrolysable GTP and those generated with non-hydrolysable GTP γ S becomes evident with proteomics analysis. Vesicles generated with hydrolysable GTP contain a subset of proteins identified in the Golgi apparatus, as opposed to vesicles generated with GTP γ S which have a large variety of protein content. Repeated cycles of GTP hydrolysis are likely involved in the selection of vesicular contents, and generating vesicles without GTP hydrolysis negates this active selection. Thus we see GTP γ S vesicles contain almost double the number of proteins (by name) than COPI GTP vesicles due to lack of specificity in protein selection. From this data, we determine that vesicles generated with GTP are more representative of what would be seen *in vivo*.

Figures

Figure 6.1. Distribution of peptides over 23 functional categories.

This figure was taken from (Gilchrist et al 2006). The three histograms show the proteomes of the Golgi apparatus (dark blue), COPI GTP vesicles (pink) and COPI GTP γ S vesicles (light blue), respectively. The abscissa contains the previously described 23 functional categories assigned during the manual annotation effort. The ordinate is expressed as percentage of total assigned peptides. Each coloured bar is the mean of n=3 biological replicates, with the standard deviation indicated by error bars. The number of different proteins identified for each organelle is shown in the upper right hand corner of each histogram. An arrow indicates the functional category assigned the largest proportion of the percentage total peptides.

Figure 6.1

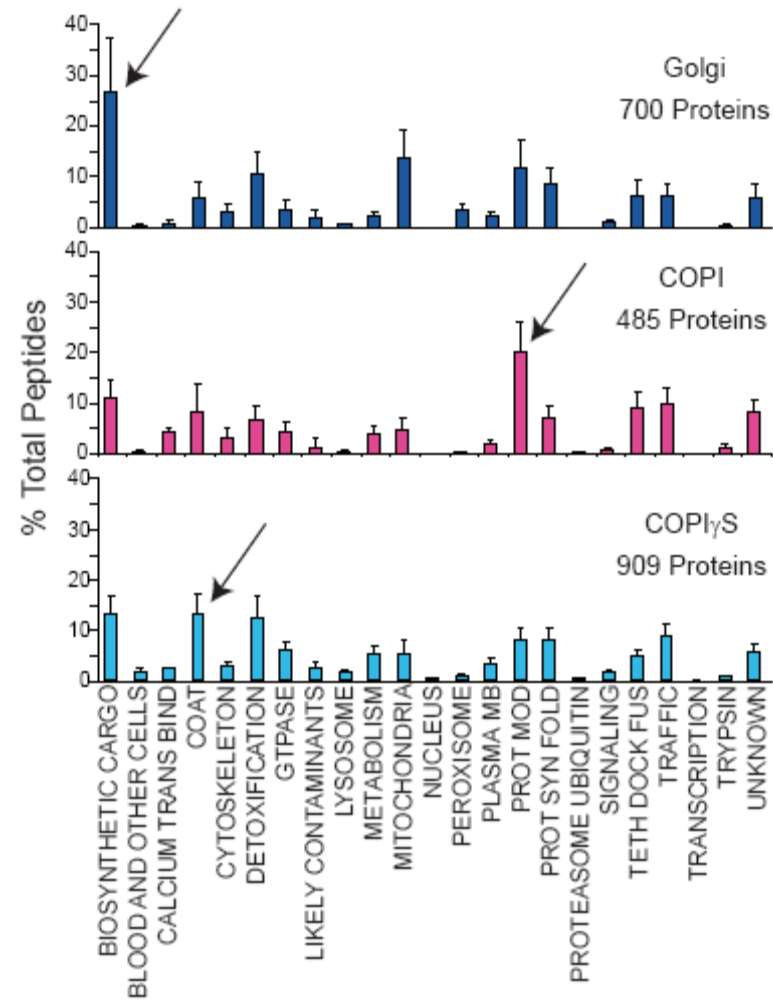


Figure 6.2. Abundant biosynthetic cargo proteins of the Golgi apparatus.

The abscissa contains the nine most abundant biosynthetic cargo proteins in the Golgi apparatus. The ordinate is expressed as percentage of total assigned peptides. The n=3 biological replicates are plotted individually for each protein. Golgi apparatus (dark blue), COPI GTP vesicles (pink) and COPI GTP γ S vesicles (light blue).

Figure 6.2

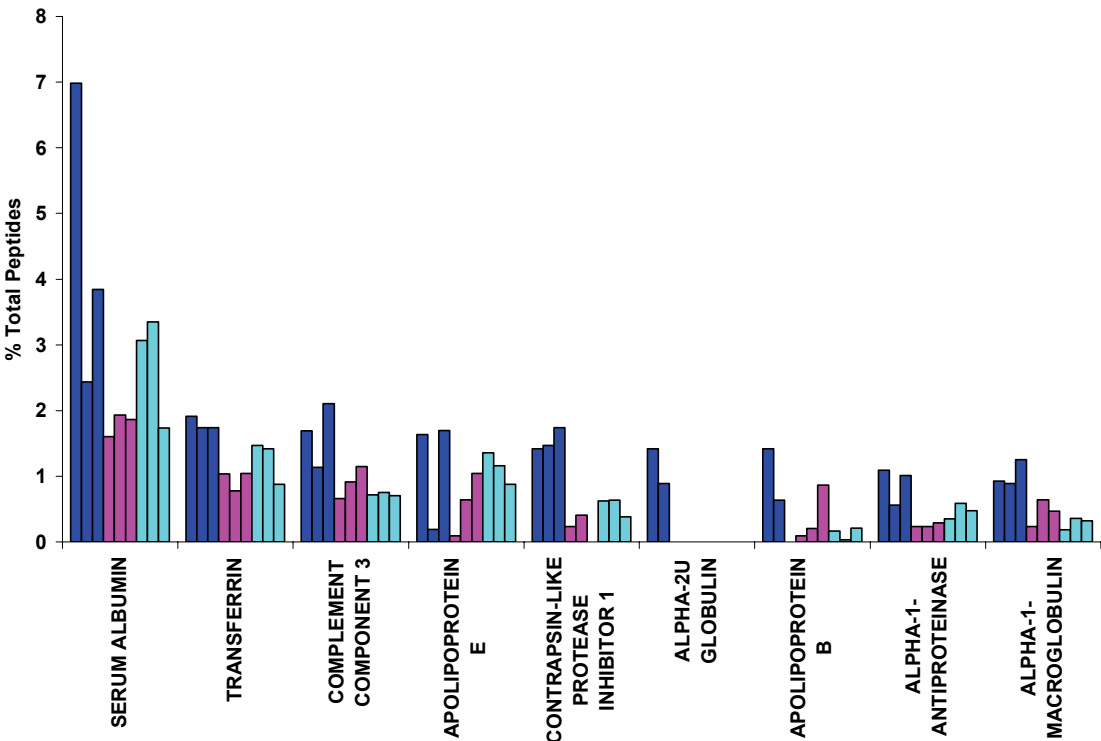


Figure 6.3. Abundant coat proteins of the Golgi apparatus.

The abscissa contains the six most abundant coat proteins enriched in the Golgi apparatus. The ordinate is expressed as percentage of total assigned peptides. The n=3 biological replicates are plotted individually for each protein. RM (green), SM (red), Golgi apparatus (dark blue), COPI GTP vesicles (pink) and COPI GTP γ S vesicles (light blue).

Figure 6.3

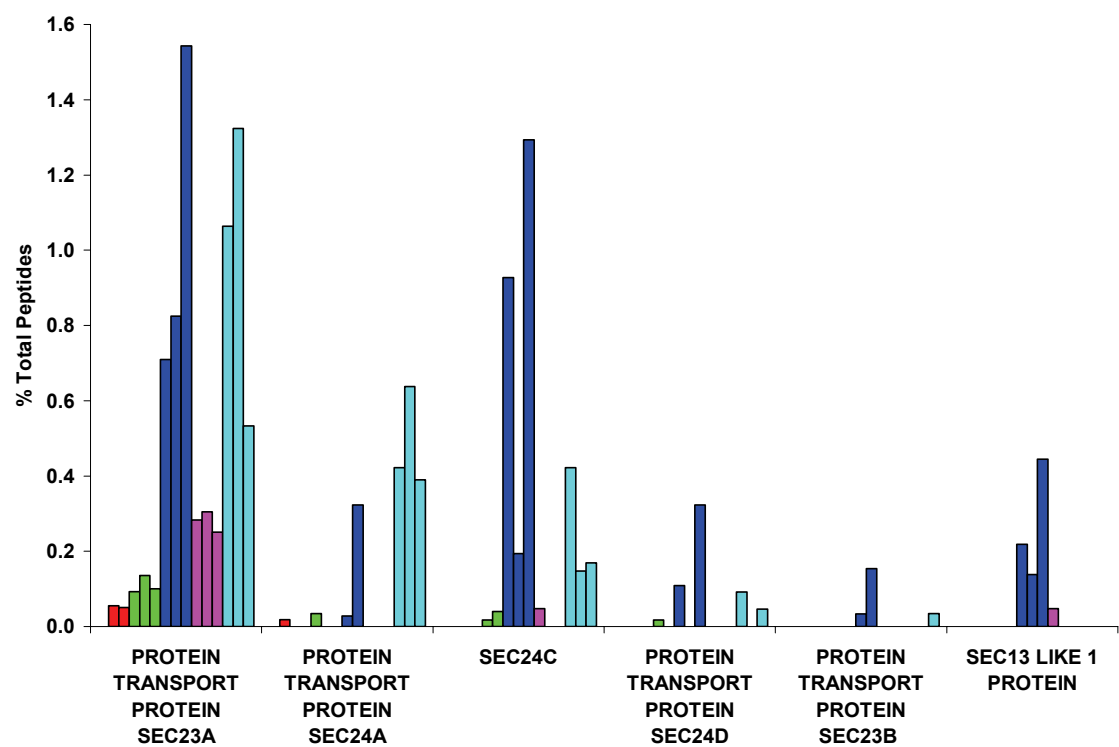


Figure 6.4. Abundant detoxification proteins of the Golgi apparatus.

This plot contains data from isolated rough microsomes (RM) that are representative of the rough endoplasmic reticulum, and smooth microsomes (SM) that are representative of the smooth endoplasmic reticulum in order to demonstrate that the proteins are truly present in the Golgi apparatus and are not the result of endoplasmic reticulum contamination. The abscissa contains the seven most abundant detoxification proteins enriched in the Golgi apparatus. The ordinate is expressed as percentage of total assigned peptides. The n=3 biological replicates are plotted individually for each protein. RM (red), SM (green), Golgi apparatus (dark blue), COPI GTP vesicles (pink) and COPI GTP γ S vesicles (light blue).

Figure 6.4

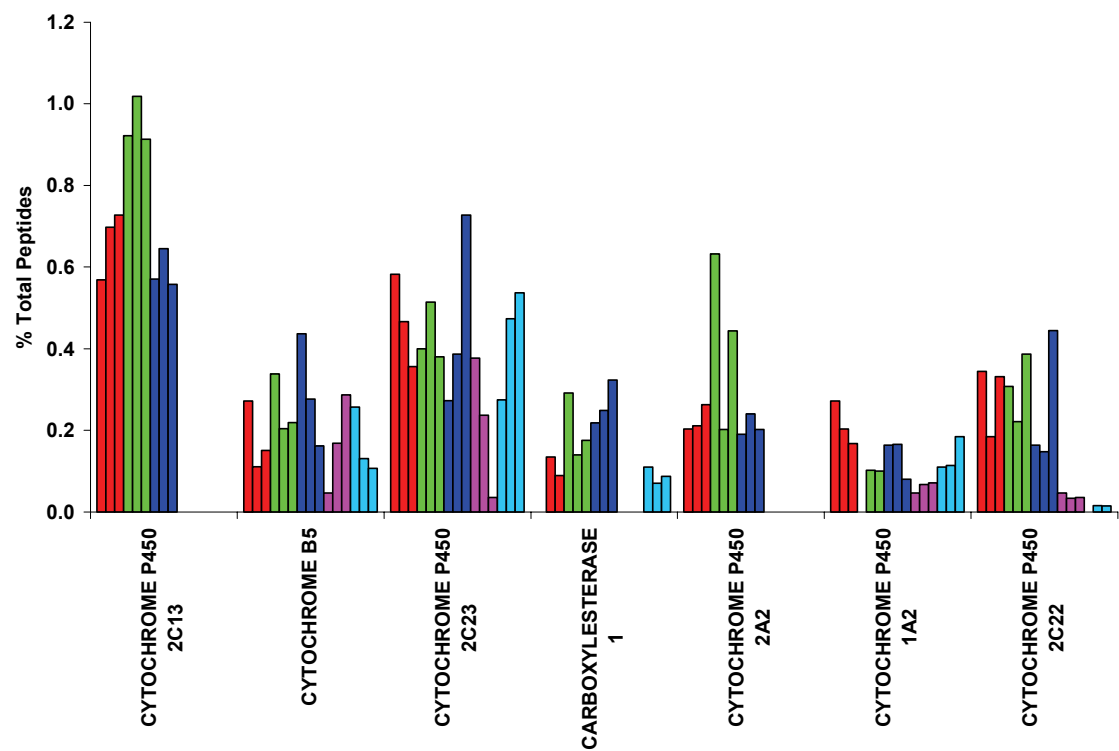


Figure 6.5. Abundant GTPase protein of the Golgi apparatus.

The abscissa shows Rab6, the most abundant GTPase protein enriched in the Golgi apparatus. The ordinate is expressed as percentage of total assigned peptides. The n=3 biological replicates are plotted individually for each protein. Golgi apparatus (dark blue), COPI GTP vesicles (pink) and COPI GTP γ S vesicles (light blue).

Figure 6.5

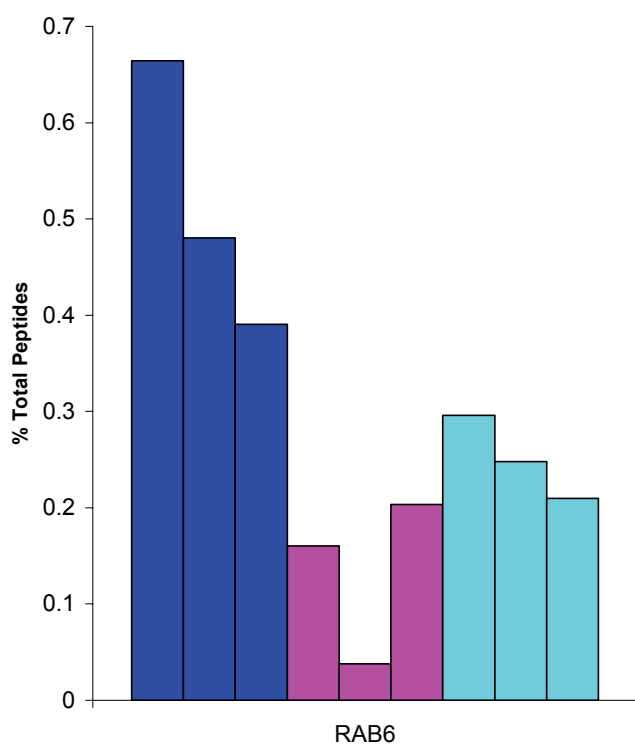


Figure 6.6. Abundant protein modification proteins of the Golgi apparatus.

The abscissa shows the seven most abundant protein modification proteins enriched in the Golgi apparatus. The ordinate is expressed as percentage of total assigned peptides. The n=3 biological replicates are plotted individually for each protein. Golgi apparatus (dark blue), COPI GTP vesicles (pink) and COPI GTP γ S vesicles (light blue).

Figure 6.6

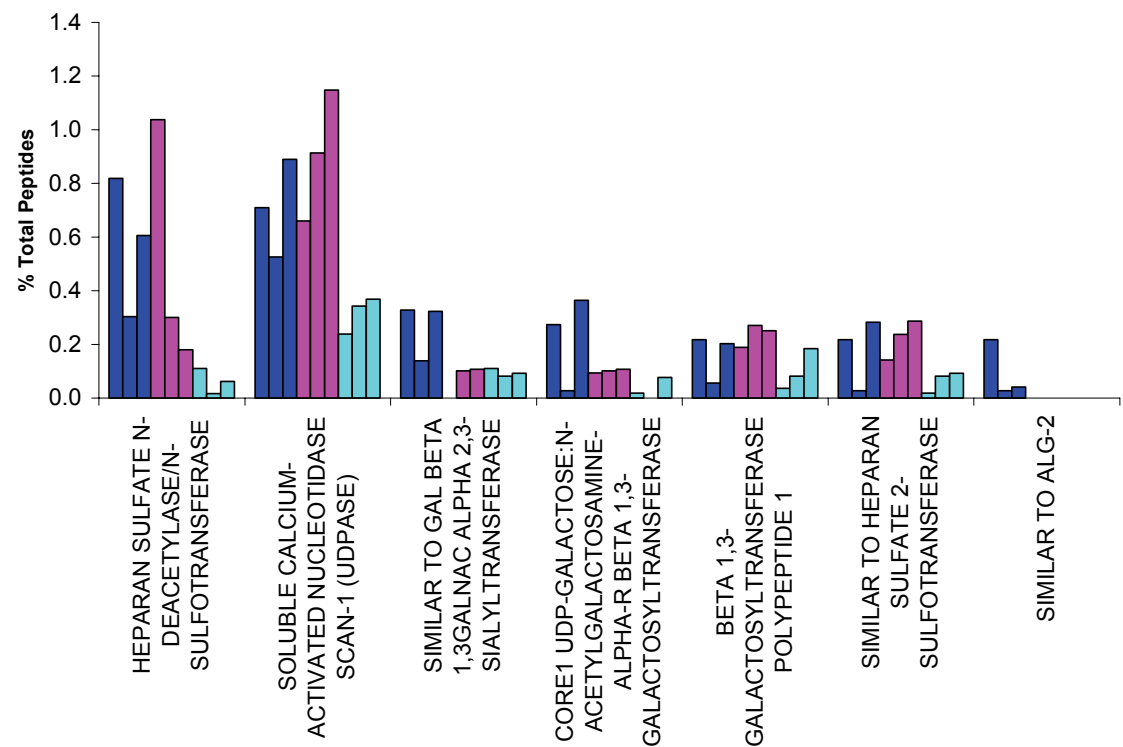


Figure 6.7. Abundant tethering/docking/fusion proteins of the Golgi apparatus.

The abscissa shows the four most abundant tethering/docking/fusion proteins enriched in the Golgi apparatus. The ordinate is expressed as percentage of total assigned peptides. The n=3 biological replicates are plotted individually for each protein. Golgi apparatus (dark blue), COPI GTP vesicles (pink) and COPI GTP γ S vesicles (light blue).

Figure 6.7

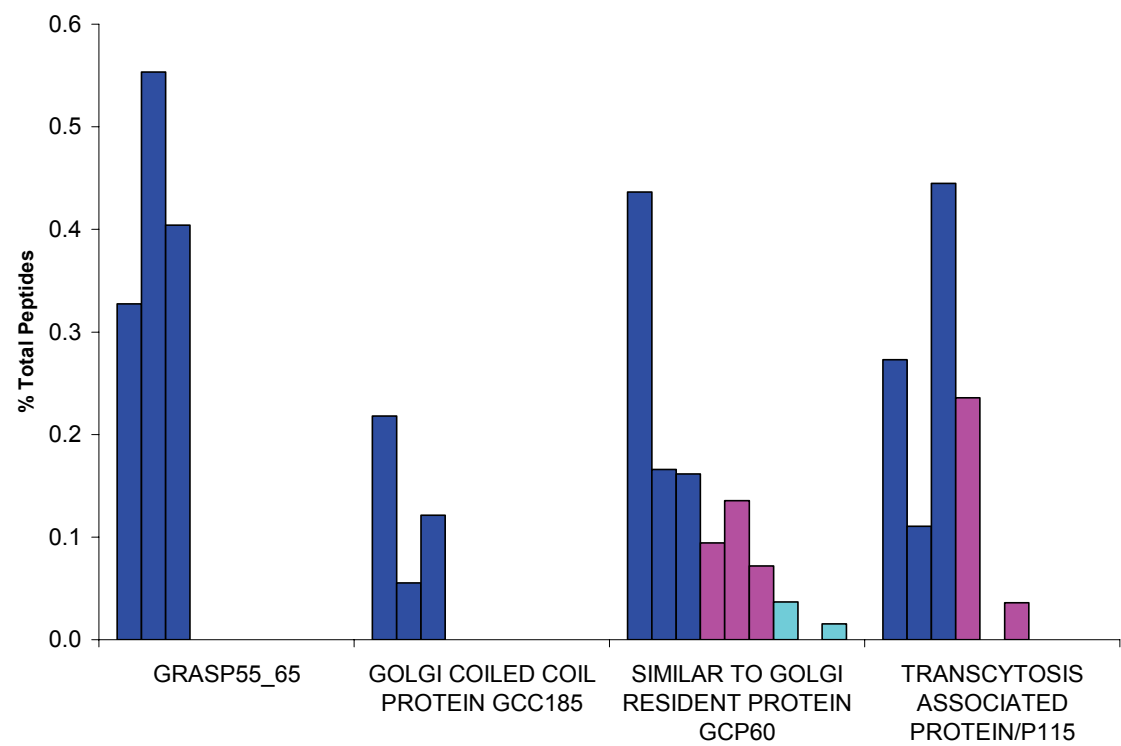


Figure 6.8. Abundant novel protein of the Golgi apparatus.

The abscissa shows the protein Similar to Riken cDNA 3110038B19, the abundant protein of unknown function that is enriched in the Golgi apparatus. The ordinate is expressed as percentage of total assigned peptides. The n=3 biological replicates are plotted individually for each protein. Golgi apparatus (dark blue), COPI GTP vesicles (pink) and COPI GTP γ S vesicles (light blue).

Figure 6.8

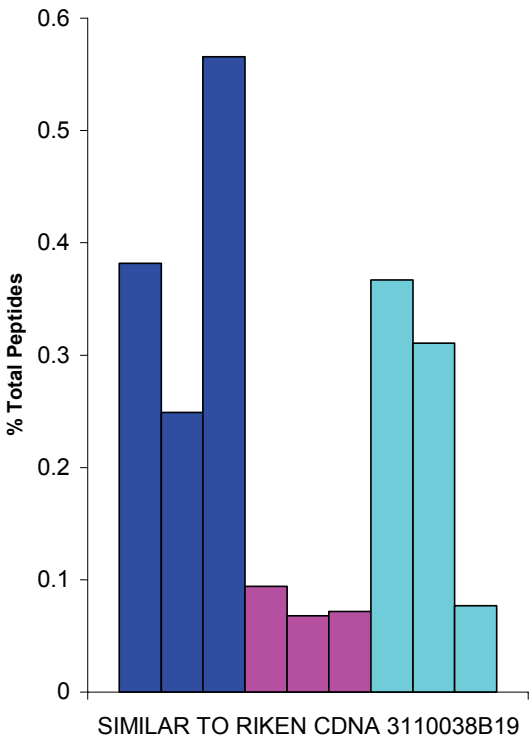


Figure 6.9. Abundant coat proteins of the COPI GTP vesicles and COPI GTPyS vesicles.

The abscissa shows the nine most abundant coat proteins enriched in the COPI GTP vesicles and COPI GTPyS vesicles. They are all subunits of the COPI coatamer complex. The ordinate is expressed as percentage of total assigned peptides. The n=3 biological replicates are plotted individually for each protein. Golgi apparatus (dark blue), COPI GTP vesicles (pink) and COPI GTPyS vesicles (light blue).

Figure 6.9

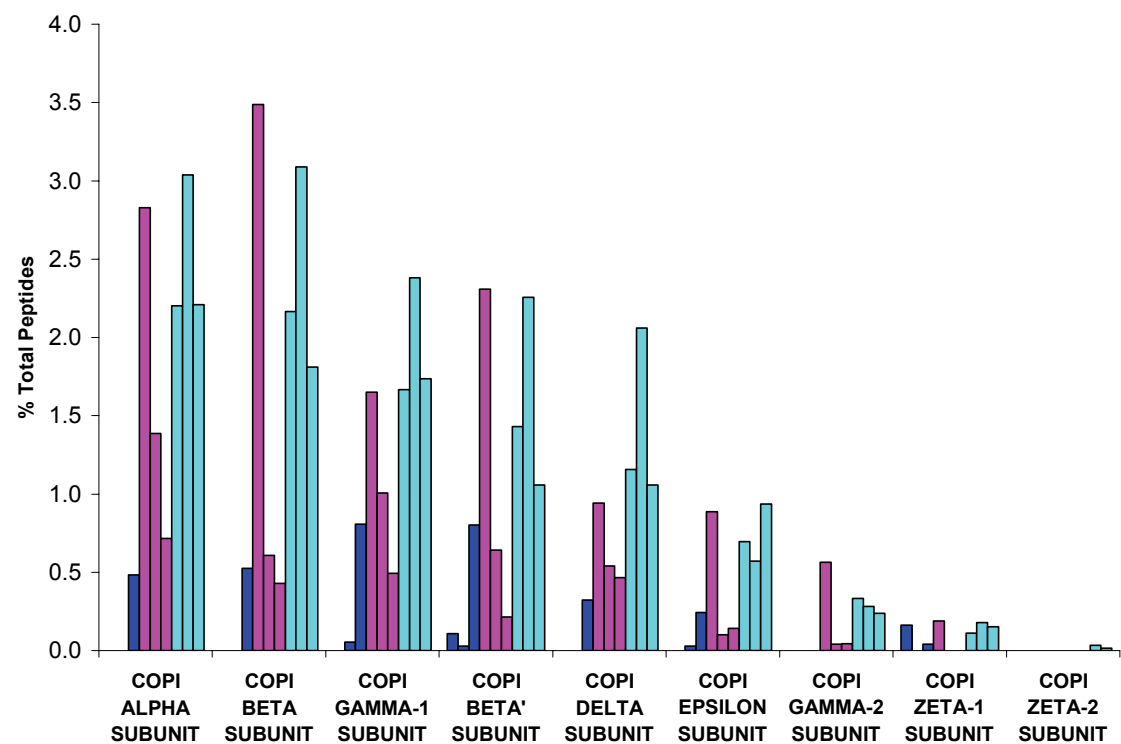


Figure 6.10. Stoichiometry of COPI coatamer subunits in the COPI GTP γ S vesicles.

A Number of peptides identified for the seven subunits of COPI coatamer expressed as a percentage of total peptides. **B** Normalization of the total peptides taking into account their calculated mass is consistent with a similar molar abundance for six of the seven subunits of the COPI coat as observed by the LC-QToF by peptide counting. The number of total peptides characterized is indicated above the histogram. Only the zeta subunit appears under represented.

Figure 6.10

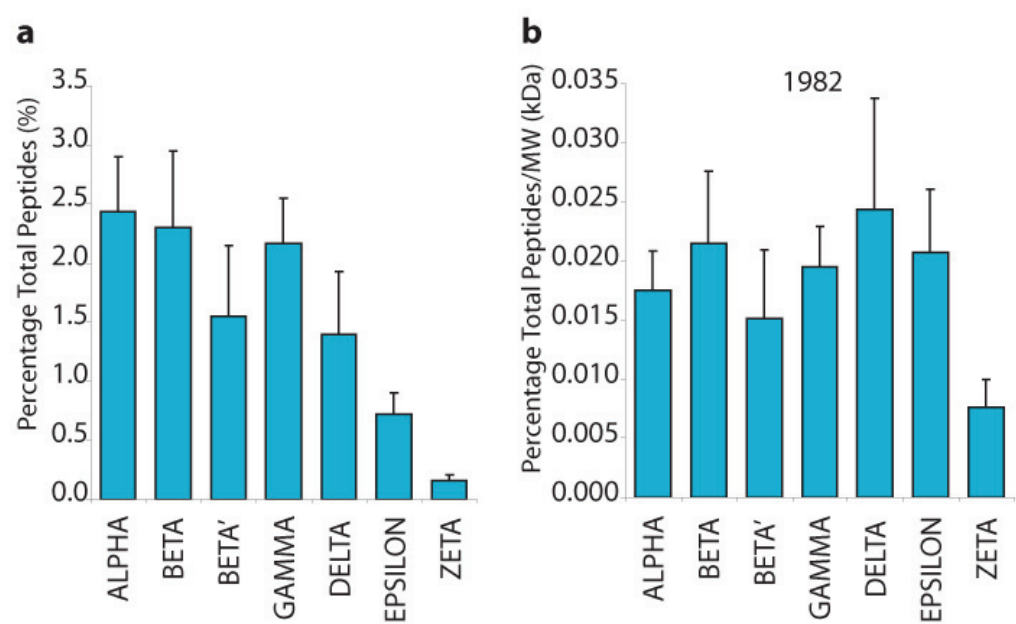


Figure 6.11. Abundant calcium transport and binding proteins of the COPI GTP vesicles.

The abscissa shows the three most abundant calcium transport and binding proteins enriched in the COPI GTP vesicles. The ordinate is expressed as percentage of total assigned peptides. The n=3 biological replicates are plotted individually for each protein. Golgi apparatus (dark blue), COPI GTP vesicles (pink) and COPI GTP γ S vesicles (light blue).

Figure 6.11

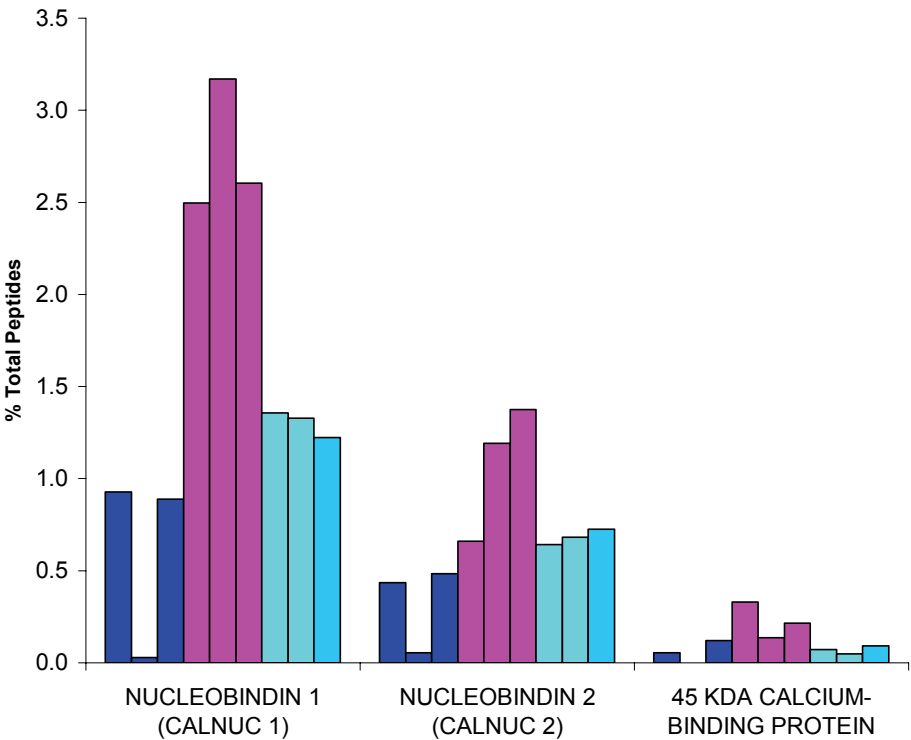


Figure 6.12. Abundant GTPase proteins of the COPI GTP vesicles.

The abscissa shows the three most abundant GTPase proteins enriched in the COPI GTP vesicles. The ordinate is expressed as percentage of total assigned peptides. The n=3 biological replicates are plotted individually for each protein. Golgi apparatus (dark blue), COPI GTP vesicles (pink) and COPI GTP γ S vesicles (light blue).

Figure 6.12

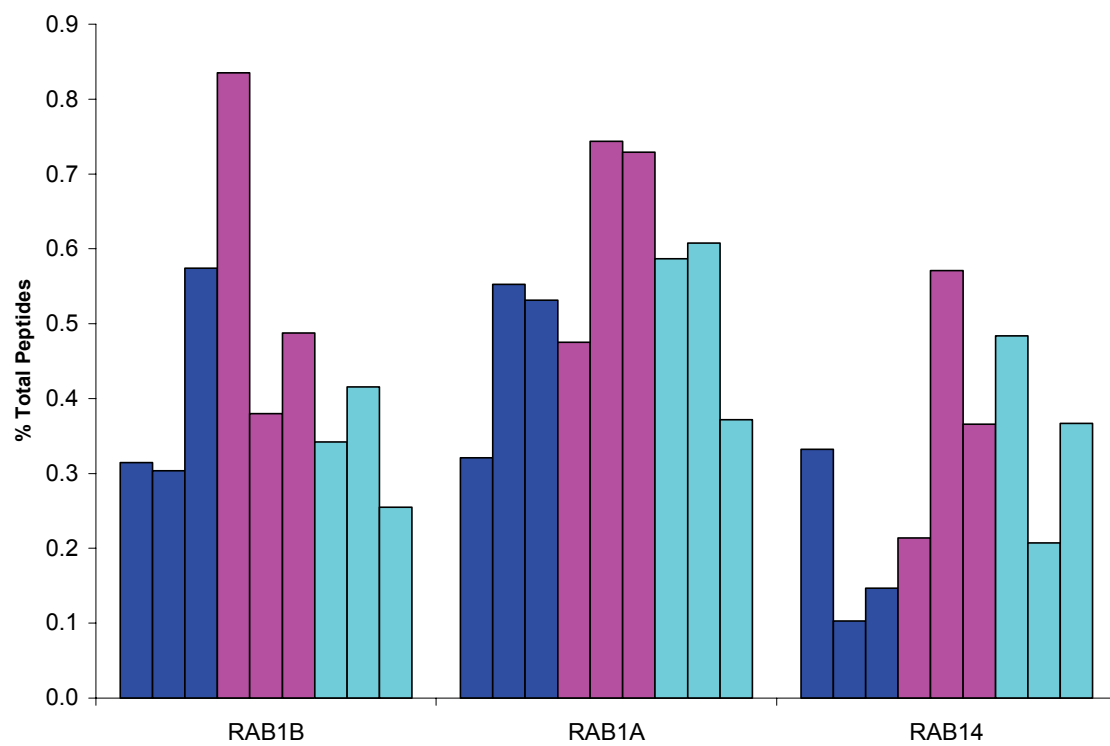


Figure 6.13. Abundant protein modification proteins of the COPI GTP vesicles.

The abscissa shows the three most abundant protein modification proteins enriched in the COPI GTP vesicles. The ordinate is expressed as percentage of total assigned peptides. The n=3 biological replicates are plotted individually for each protein. Golgi apparatus (dark blue), COPI GTP vesicles (pink) and COPI GTP γ S vesicles (light blue).

Figure 6.13

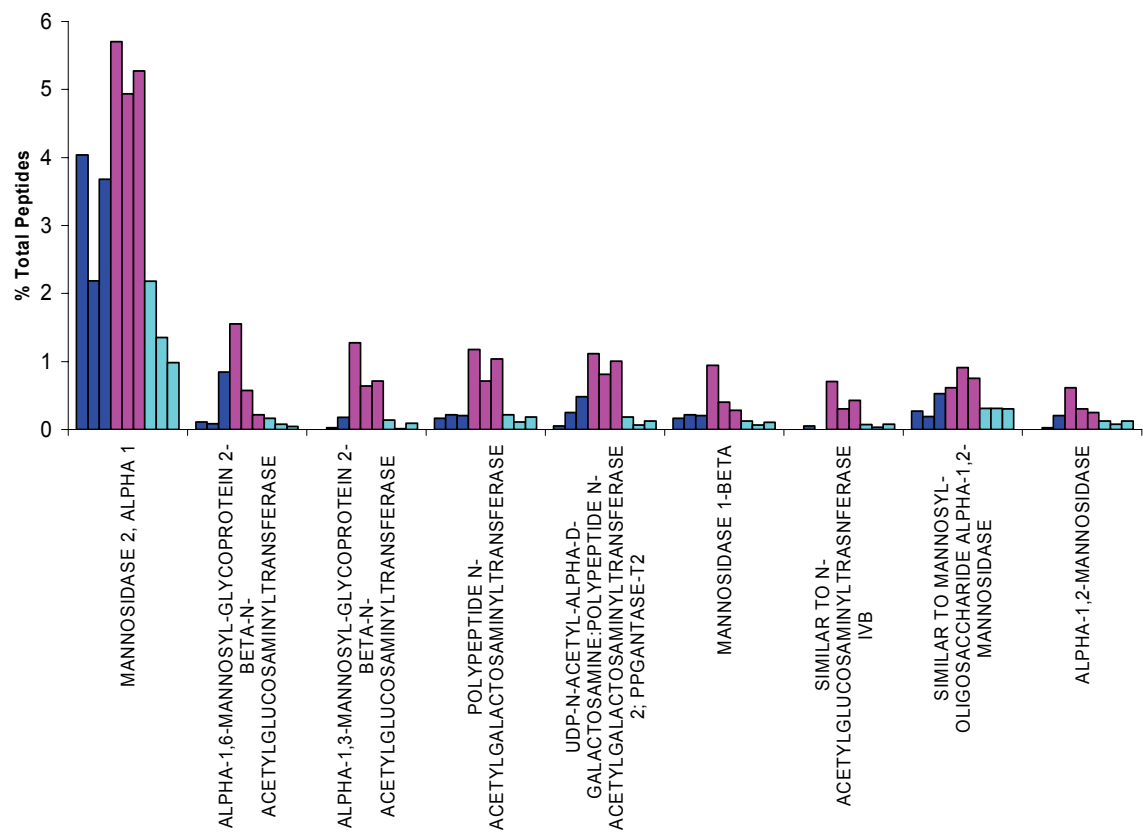


Figure 6.14. Abundant tethering/docking/fusion proteins of the COPI GTP vesicles.

The abscissa shows the three most abundant tethering/docking/fusion proteins enriched in the COPI GTP vesicles. The ordinate is expressed as percentage of total assigned peptides. The n=3 biological replicates are plotted individually for each protein. Golgi apparatus (dark blue), COPI GTP vesicles (pink) and COPI GTP γ S vesicles (light blue).

Figure 6.14

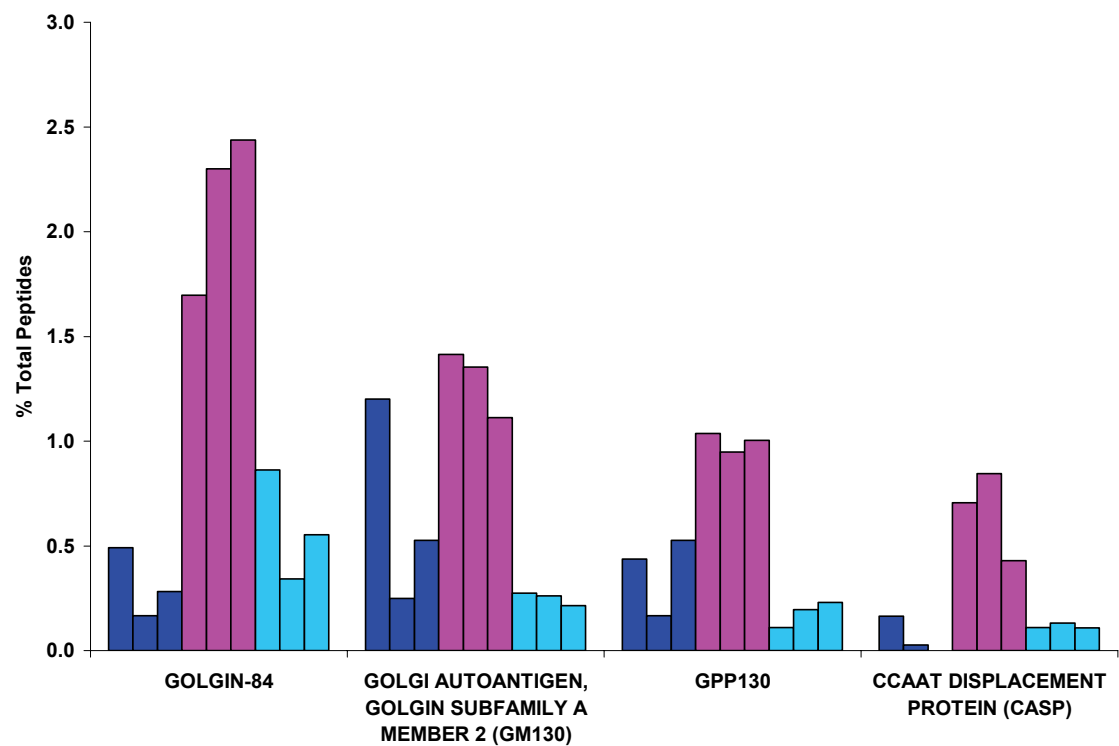


Figure 6.15. Abundant traffic proteins of the COPI GTP vesicles.

The abscissa shows the three most abundant traffic proteins enriched in the COPI GTP vesicles. The ordinate is expressed as percentage of total assigned peptides. The n=3 biological replicates are plotted individually for each protein. Golgi apparatus (dark blue), COPI GTP vesicles (pink) and COPI GTP γ S vesicles (light blue).

Figure 6.15

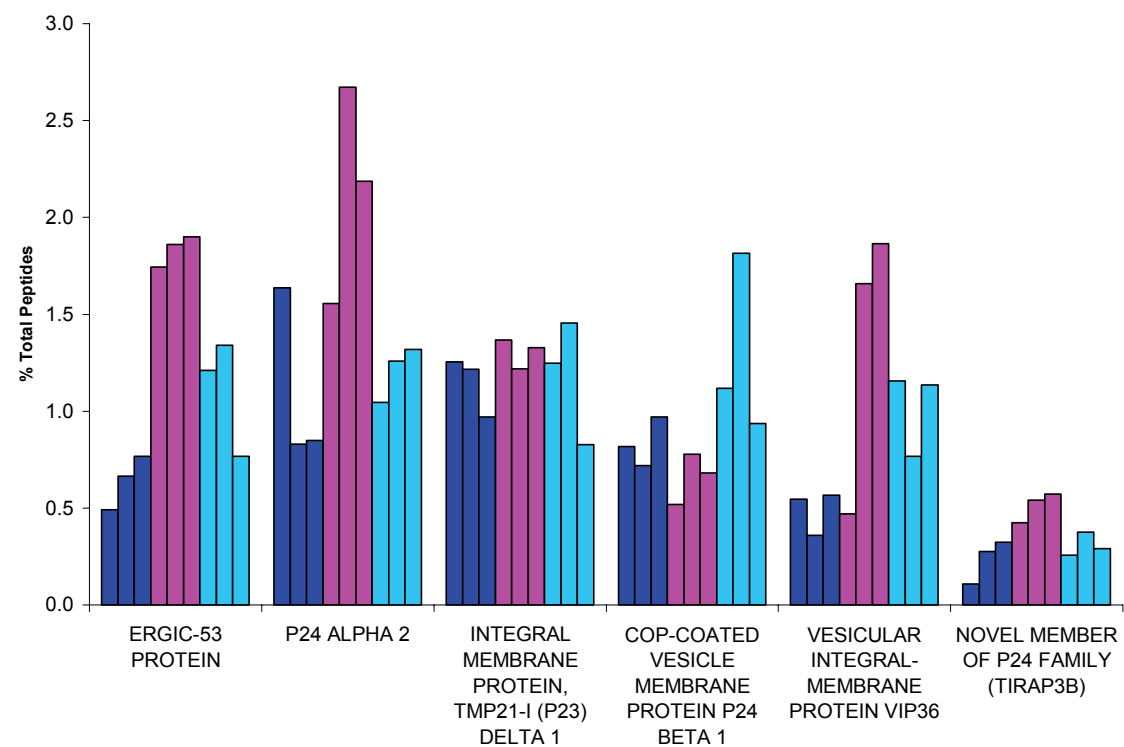


Figure 6.16. Abundant unknown proteins of the COPI GTP vesicles.

The abscissa shows the three most abundant proteins of unknown function enriched in the COPI GTP vesicles. The ordinate is expressed as percentage of total assigned peptides. The n=3 biological replicates are plotted individually for each protein. Golgi apparatus (dark blue), COPI GTP vesicles (pink) and COPI GTP γ S vesicles (light blue).

Figure 6.16

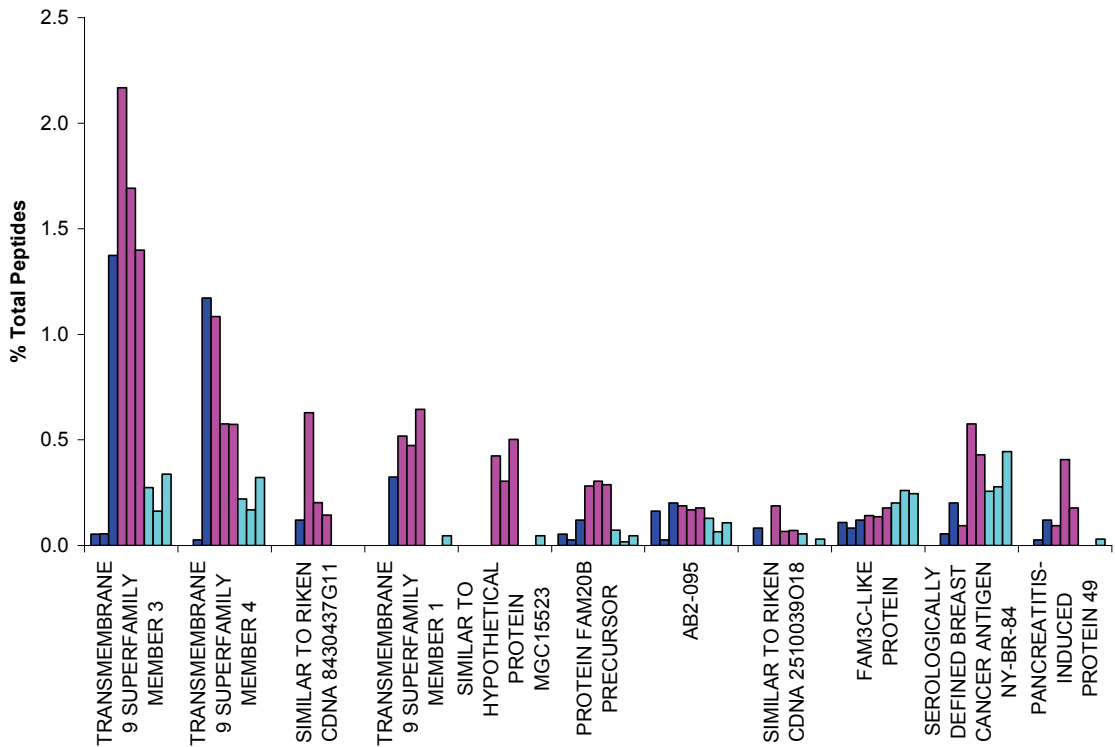
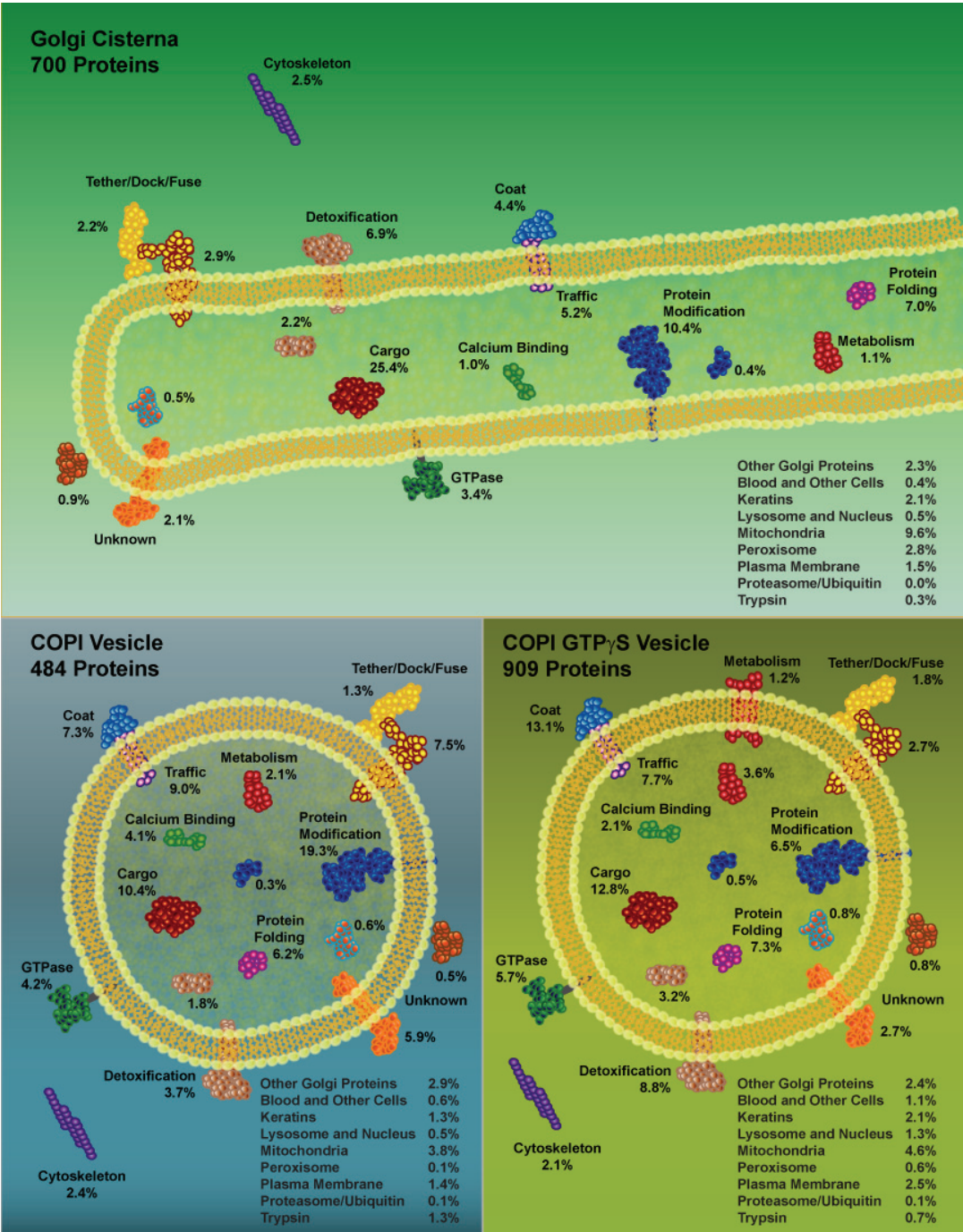


Figure 6.17. Proteomes of the Golgi, COPI vesicles, and COPI GTPγS vesicles.

The following are schematic cartoons of the major groups of proteins represented in each of the organelles. The numbers next to each group express the percentage total peptides assigned to that functional group and localization (i.e. luminal, transmembrane, or cytosolic membrane associated). The text in the bottom right hand corner of each panel shows the percentage total peptides assigned to contaminant categories.

Figure 6.17



Chapter 7 – The maturation hypothesis

7.1 Abstract

The vehicle and mechanisms for protein transport through the Golgi complex remain as controversial and elusive since the rival vesicular transport and cisternal maturation models were first proposed. Complexity has increased further as a consequence of a more recent model abandoning a role for peri-Golgi vesicles in transport and proposing instead intercisternal continuity and a single continuous Golgi compartment with different rates of egress for different secretory cargo. Here we show by the analysis of 109,654 tandem mass spectra, the characterization of 34338 peptides and the assignment of 1268 different proteins in isolated hepatic Golgi cisternae and COPI vesicles, a main role for COPI in the recycling of Golgi resident proteins during secretion. Recycling requires the hydrolysis of GTP for active sorting of Golgi resident proteins and diminishment of entry of anterograde directed soluble secretory cargo.

7.2 Introduction

We have investigated the entire protein content of COPI-derived vesicles of rat liver Golgi fractions by tandem mass spectrometry (MS) and compared this with the protein content of cisternal membranes, as well as with vesicles formed in the presence of the non-hydrolysable analogue, GTP γ S, to monitor the effect of impaired sorting. Vesicles were formed under conditions where their fusion to Golgi membranes was blocked through addition of a dominant-negative mutant of α -SNAP (α -SNAP^{dn}), an accessory protein for SNARE-dependent fusion. Comparing the total protein content of COPI GTP vesicles with that of Golgi cisternae, we find on average a 2.5-fold lower density of anterograde soluble biosynthetic cargo and on average, a 1.9-fold higher density of resident proteins of the pathway. Under conditions where GTP hydrolysis is blocked, the bias for resident proteins and against soluble anterograde cargo is decreased. Both of these findings support a main role for peri-Golgi COPI GTP vesicles in the transport of resident proteins consistent with a cisternal maturation scenario, which is dependent on GTP hydrolysis. I

7.3 Results

7.3.1 Quantitation via peptide counting reveals enrichment of Golgi resident proteins in COPI GTP vesicles

Each protein identified in our study was assigned to a functional group such as tethering, docking and fusion (e.g. tethering factors, SNARE proteins and accessory proteins) or biosynthetic cargo (i.e. anterograde directed soluble cargo). By summing the number of peptides identified at the 95% confidence level and assigned to proteins (Blondeau et al 2004), it is possible to get a representation of each functional group in the total subcellular fraction as well as providing a direct means for comparing between subcellular fractions (Blondeau et al 2004, Gibbs et al 2004). In the first instance, comparing within the subcellular fraction, the numbers expressed as percentages were used as an indication of the total representation of a functional group of proteins.

Comparison of n=3 separate subcellular isolations for each organelle revealed a consistent increase in the abundance of tandem mass spectra assigned to Golgi resident proteins in COPI GTP vesicles as compared to the Golgi fractions. By contrast, soluble biosynthetic cargo showed a significant decrease in COPI GTP vesicles as compared to the Golgi fraction as seen in Figure 7.2. Analysis of individual proteins in Figure 7.3 (Table 2) revealed an increase for each Golgi resident protein in COPI GTP vesicles, and a decrease for individual anterograde directed soluble cargo as well as ER resident proteins in COPI GTP vesicles as compared to Golgi fractions (Table 3). To further illustrate the point, the distribution profiles over the five fractions (RM, SM, Golgi, COPI GTP vesicles, and COPI GTP γ S vesicles) for 9 highly abundant (greater than an average of 0.15% total peptides over the 15 samples which is equivalent to greater

than 91 peptides) biosynthetic cargo proteins and 9 highly abundant protein modification enzymes were plotted in Figure 7.6. For each of the biosynthetic cargo proteins we see little in the RM and SM fractions, a high concentration in the Golgi, and a drop to levels slightly higher than those found in the RM and SM fractions for the COPI GTP vesicles. For the protein modification enzymes we see little to none present in the RM and SM fractions, more in the Golgi apparatus, and a high concentration in the COPI GTP vesicles.

Soluble biosynthetic cargo was not enriched in the COPI GTP vesicles however we did not know if Golgi resident soluble proteins behaved in this manner. Figure 7.5 compares the behaviour of serum albumin, the most abundant secretory protein, with that of calnexin (Lin et al 1998), a highly abundant Golgi resident protein, and shows that the resident protein is highly enriched in the COPI GTP vesicles but not the COPI GTP γ S vesicles.

Those Golgi proteins found to decrease in COPI GTP vesicles (e.g. TGN38, and α -2,3 sialyl transferase) are known to be resistant to Brefeldin A collapse into the ER (Chege & Pfeffer 1990, Ladinsky & Howell 1992) and may not be subject to inter organelle transport in COPI vesicles. Rab6 content was diminished 3.8 fold in COPI GTP vesicles compared to Golgi fractions (Table 3) and this is consistent with its known exclusion from COPI structures in retrograde transport (Girod et al 1999). At least 12 different Rabs were characterized with Rab1 the most prominent. Seven increased significantly in abundance of tandem mass spectra for COPI GTP vesicles compared to Golgi cisternae.

7.3.2 Retrograde transport.

Although our proteomics analysis comprises 34338 peptide identifications (Table S1d) and more than 1200 proteins we have emphasized those

relevant to the prevailing controversy in membrane trafficking through the Golgi apparatus i.e. the role of COPI vesicles. The compartments analyzed here, COPI GTP vesicles and COPI GTP γ S vesicles, were generated from Golgi fractions in a cell free system. In contrast to recent findings (Kweon et al 2004), COPI vesicles generated here function well in a retrograde cell-free assay delivering N-acetylglucosaminyltransferase I to a lec1 Golgi fraction devoid of this enzyme as shown in Figure 7.4 (see also Lanoix et al. (Lanoix et al 1999), and Ostermann (Ostermann 2001)). COPI GTP γ S vesicles are about 3.5 times less active than COPI GTP vesicles in this assay. Furthermore, as documented previously, generation of COPI vesicles is strictly dependent on the coatamer protomer of COPI (Lanoix et al 1999). Taken together the data support a role for peri-Golgi COPI vesicles in the acquisition of Golgi resident enzymes during budding and their delivery back to the Golgi by membrane fusion. The *in vitro* generation and efficient sorting of Golgi resident proteins into these vesicles is COPI dependant and from the proteomic data, take place from all parts of the Golgi stacked cisternae. The functional trajectory of the COPI vesicles in the cell-free fusion assay is deduced to be directed mainly towards the cis-Golgi subcompartment of VSV-G containing lec1 Golgi cisternae (Chen et al 1999).

7.4 Discussion

By generating COPI vesicles with hydrolysable and non-hydrolysable GTP in a cell free system and analyzing these organelles by mass spectrometry, a clear picture emerges of concentrated resident proteins in COPI vesicles requiring GTP hydrolysis for the concentrative effect. This resolves conclusively a major requirement of the maturation hypothesis that resident proteins be concentrated in COPI vesicles. Morphological methods have clearly given different results in the test of the maturation hypothesis (Martinez-Menarguez et al 2001, Orci et al 2000). As opposed to a requirement of the maturation hypothesis for concentration of resident proteins in COPI vesicles, no such requirement of concentration of secretory cargo in COPI vesicles is necessary to support the rival vesicular transport hypothesis. Our proteomics data clearly support the maturation hypothesis.

That the vehicle driving maturation is the complement of peri-Golgi COPI vesicles and not the intra-cisternal continuities is supported by the work shown here as well as prior studies. Hence, inhibition of vesicle consumption through fusion increases the amount of *medial* enzymes in the vesicle fraction whereas *cis* markers remain unchanged, *in vitro* (Lanoix et al 2001). Inhibition of vesicle fusion also occurs naturally during mitosis when the entire Golgi apparatus is converted into vesicles and convoluted tubular structures. The process requires COPI for vesicle formation; depletion of COPI coatamer results in the absence of vesicles and the formation of long tubules (Misteli & Warren 1994), thus highlighting a cellular machinery capable of generating COPI vesicles from all parts of the Golgi stack. The current alternative model of direct tubular

connections between Golgi cisternae and the continuous Golgi apparatus donating secretory cargo at different rates may be operative but can only be in addition to the major role of free standing peri-Golgi COPI vesicles in maintaining the vectorial direction and processivity of cargo modification during cisternal progression within the stacked cisternae (Kartberg et al 2005). Further detailed analyses of the proteomics data generated here with those of the endoplasmic reticulum should give insight into the molecular mechanisms governing organelle identity and communication.

Tables

Table 2 – Proteins that increase in COPI GTP vesicles.

Proteins that increase in COPI GTP vesicles as compared to Golgi apparatus are shown as their fold increase over Golgi with standard deviation indicated for each protein. The column “protein name” contains the name of the protein as we assigned it in our Cell Map Base. The column “function” indicates to which of the 23 functional categories the protein belongs. The column “CMBSEQID” is the identification number for the protein in Cell Map Base. The last three columns indicate the fold increase as compared to Golgi for each of the three organelles.

Table 2 – Proteins that increase in COPI vesicles

Protein Identification			Fold Change $\pm$ SD		
PROTEIN NAME	FUNCTION	CMBSEQID	GOLGI	COPI	GTPgS
TYROSYLPROTEIN SULFOTRANSFERASE-1	PROT MOD	241393	1.00 $\pm$ 0.84	1.45 $\pm$ 0.11	0.63 $\pm$ 0.16
BETA 1,3-GALACTOSYLTRANSFERASE POLYPEPTIDE 1	PROT MOD	56042	1.00 $\pm$ 0.56	1.48 $\pm$ 0.26	0.63 $\pm$ 0.48
MANNOSIDASE 2, ALPHA 1	PROT MOD	196264 205526 212806 294051	1.00 $\pm$ 0.30	1.60 $\pm$ 0.13	0.45 $\pm$ 0.18
SIMILAR TO MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE	PROT MOD	273814	1.00 $\pm$ 0.51	2.29 $\pm$ 0.43	0.93 $\pm$ 0.01
GALACTOSYLGALACTOSYLXYLOSYLPROTEIN 3-BETA-GLUCURONOSYLTRANSFERASE 3	PROT MOD	228888	1.00 $\pm$ 0.60	2.89 $\pm$ 0.99	1.92 $\pm$ 0.06
UDP-N-ACETYL-ALPHA-D-GALACTOSAMINE:POLYPEPTIDE N-ACETYLGALACTOSAMINYLTRANSFERASE 2; PPGANTASE-T2	PROT MOD	307730	1.00 $\pm$ 0.81	3.71 $\pm$ 0.62	0.47 $\pm$ 0.22
POLYPEPTIDE N-ACETYLGALACTOSAMINYLTRANSFERASE	PROT MOD	68735	1.00 $\pm$ 0.15	4.96 $\pm$ 1.27	0.88 $\pm$ 0.27
ALPHA-1,3-MANNOSYL-GLYCOPROTEIN 2-BETA-N-ACETYLGALACTOSAMINYLTRANSFERASE	PROT MOD	2699	1.00 $\pm$ 1.39	12.72 $\pm$ 5.13	1.18 $\pm$ 0.87
P24 ALPHA 2	TRAFFIC	285748 170045	1.00 $\pm$ 0.42	1.92 $\pm$ 0.48	1.08 $\pm$ 0.13
NOVEL MEMBER OF P24 FAMILY (TIRAP3B)	TRAFFIC	204384	1.00 $\pm$ 0.47	2.16 $\pm$ 0.32	1.30 $\pm$ 0.26
SIMILAR TO GOLGI MEMBRANE PROTEIN GP73	TRAFFIC	231145	1.00 $\pm$ 1.41	2.82 $\pm$ 0.81	0.81 $\pm$ 0.55
ERGIC-53 PROTEIN	TRAFFIC	77835	1.00 $\pm$ 0.21	2.85 $\pm$ 0.12	1.71 $\pm$ 0.46
R, SEC22	TETH/DOCK/FUS	41516	1.00 $\pm$ 0.63	1.68 $\pm$ 0.78	2.07 $\pm$ 0.21
ALPHA-SOLUBLE NSF ATTACHMENT PROTEIN	TETH/DOCK/FUS	51376	1.00 $\pm$ 0.87	1.91 $\pm$ 0.83	1.93 $\pm$ 0.62
GOLGI AUTOANTIGEN, GOLGIN SUBFAMILY A MEMBER 2	TETH/DOCK/FUS	169300	1.00 $\pm$ 0.75	1.95 $\pm$ 0.24	0.38 $\pm$ 0.05
GPP130	TETH/DOCK/FUS	237211	1.00 $\pm$ 0.49	2.64 $\pm$ 0.15	0.47 $\pm$ 0.16
GOLGIN-84	TETH/DOCK/FUS	302868	1.00 $\pm$ 0.53	6.79 $\pm$ 1.22	1.85 $\pm$ 0.82
CCAAT DISPLACEMENT PROTEIN (CASP)	TETH/DOCK/FUS	280644	1.00 $\pm$ 1.37	10.22 $\pm$ 3.21	1.79 $\pm$ 0.20
NUCLEOBINDIN 2 (CALNUC 2)	CALCIUM TRANS/BIND	3157	1.00 $\pm$ 0.72	3.29 $\pm$ 1.13	2.09 $\pm$ 0.13
45 KDA CALCIUM-BINDING PROTEIN	CALCIUM TRANS/BIND	64664	1.00 $\pm$ 1.03	3.88 $\pm$ 1.70	1.22 $\pm$ 0.37
NUCLEOBINDIN 1 (CALNUC 1)	CALCIUM TRANS/BIND	60416	1.00 $\pm$ 0.83	4.46 $\pm$ 0.54	2.11 $\pm$ 0.54
ERP44 (SIMILAR TO THIOREDOXIN DOMAIN CONTAINING 4; ENDOPLASMIC RETICULUM RESIDENT PROTEIN 44KDA)	PROT SYN/FOLD	310568	1.00 $\pm$ 0.81	2.83 $\pm$ 0.87	2.31 $\pm$ 0.48
TRANSMEMBRANE 9 SUPERFAMILY MEMBER 4	UNKNOWN	260512	1.00 $\pm$ 1.67	1.86 $\pm$ 0.78	0.57 $\pm$ 0.18
TRANSMEMBRANE 9 SUPERFAMILY MEMBER 3	UNKNOWN	140307	1.00 $\pm$ 1.54	3.56 $\pm$ 0.81	0.52 $\pm$ 0.18
TRANSMEMBRANE 9 SUPERFAMILY MEMBER 1	UNKNOWN	211728	1.00 $\pm$ 1.73	5.09 $\pm$ 0.86	0.14 $\pm$ 0.25

Table 3 – Proteins that decrease in COPI vesicles.

Proteins that decrease in COPI GTP vesicles as compared to Golgi apparatus are shown as their fold decrease over Golgi with standard deviation indicated for each protein. The column “protein name” contains the name of the protein as we assigned it in our Cell Map Base. The column “function” indicates to which of the 23 functional categories the protein belongs. The column “CMBSEQID” is the identification number for the protein in Cell Map Base. The last three columns indicate the fold increase as compared to Golgi for each of the three organelles.

Table 3 – Proteins that decrease in COPI vesicles

Protein Identification			Fold Change $\pm$ SD		
PROTEIN NAME	FUNCTION	CMBSEQID	GOLGI	COPI	GTPgS
TRANS-GOLGI NETWORK INTEGRAL MEMBRANE PROTEIN (TGN38)	TRAFFIC	31491	1.00 $\pm$ 0.44	0.46 $\pm$ 0.18	1.49 $\pm$ 0.17
R-SLY1	TRAFFIC	80378	1.00 $\pm$ 0.78	0.35 $\pm$ 0.21	0.21 $\pm$ 0.13
RAB6, MEMBER RAS ONCOGENE FAMILY	GTPASE	290450	1.00 $\pm$ 0.29	0.26 $\pm$ 0.17	0.49 $\pm$ 0.08
CYCLOPHILIN B	PROT SYN/FOLD	80354	1.00 $\pm$ 0.33	0.51 $\pm$ 0.18	0.67 $\pm$ 0.28
COMPLEMENT COMPONENT 3	BIOSYNTHETIC CARGO	181406 221549	1.00 $\pm$ 0.29	0.55 $\pm$ 0.15	0.44 $\pm$ 0.01
TRANSFERRIN	BIOSYNTHETIC CARGO	37301 166319 166406	1.00 $\pm$ 0.05	0.50 $\pm$ 0.08	0.69 $\pm$ 0.13
ALPHA-1-MACROGLOBULIN	BIOSYNTHETIC CARGO	126488 41194	1.00 $\pm$ 0.19	0.43 $\pm$ 0.19	0.28 $\pm$ 0.09
SERUM ALBUMIN	BIOSYNTHETIC CARGO	120645 124397	1.00 $\pm$ 0.53	0.40 $\pm$ 0.04	0.61 $\pm$ 0.19
FIBRINOGEN ALPHA/ALPHA-E CHAIN	BIOSYNTHETIC CARGO	67713	1.00 $\pm$ 0.55	0.36 $\pm$ 0.02	0.11 $\pm$ 0.07
PLASMA RETINOL-BINDING PROTEIN	BIOSYNTHETIC CARGO	44322	1.00 $\pm$ 0.19	0.32 $\pm$ 0.15	0.34 $\pm$ 0.09
ANTITHROMBIN III	BIOSYNTHETIC CARGO	166246 207228	1.00 $\pm$ 0.57	0.30 $\pm$ 0.14	0.40 $\pm$ 0.03
ALPHA-1-ANTIPROTEINASE	BIOSYNTHETIC CARGO	11475	1.00 $\pm$ 0.32	0.28 $\pm$ 0.03	0.53 $\pm$ 0.13
FETUIN-B	BIOSYNTHETIC CARGO	145181	1.00 $\pm$ 0.49	0.27 $\pm$ 0.13	0.38 $\pm$ 0.18
VITAMIN D-BINDING PROTEIN	BIOSYNTHETIC CARGO	86608 3781	1.00 $\pm$ 0.68	0.24 $\pm$ 0.09	0.39 $\pm$ 0.19
APOLIPOPROTEIN A-IV	BIOSYNTHETIC CARGO	141420	1.00 $\pm$ 0.87	0.23 $\pm$ 0.07	0.60 $\pm$ 0.24
ALPHA-2-HS-GLYCOPROTEIN	BIOSYNTHETIC CARGO	3620 111646	1.00 $\pm$ 0.56	0.16 $\pm$ 0.06	0.50 $\pm$ 0.11
HAPTOGLOBIN	BIOSYNTHETIC CARGO	166334	1.00 $\pm$ 0.33	0.07 $\pm$ 0.03	0.36 $\pm$ 0.12
SIMILAR TO RIKEN CDNA 3110038B19	UNKNOWN	235525	1.00 $\pm$ 0.39	0.19 $\pm$ 0.04	0.63 $\pm$ 0.38

Figures

Figure 7.1. Maturation hypothesis and vesicular transport hypothesis.

This figure was adapted from Au et al. (Au et al 2007). Upper. The cisternal maturation model of biosynthetic cargo progression through the Golgi apparatus states that the cisternae themselves move the cargo forwards (upwards arrows), and peri-Golgi COPI vesicles (curved arrows) carry Golgi resident sugar transferase enzymes in a retrograde manner in order that they are not secreted to the cell surface. Lower. The vesicular transport model states that the cisternae are static and do not move. Cargo moves from cisternae to cisternae by way of peri-Golgi vesicles (curved arrows) and then is transported to the cell surface (upwards arrows) by secretory vesicles. The resident sugar transferases remain in the cisternae.

Figure 7.1

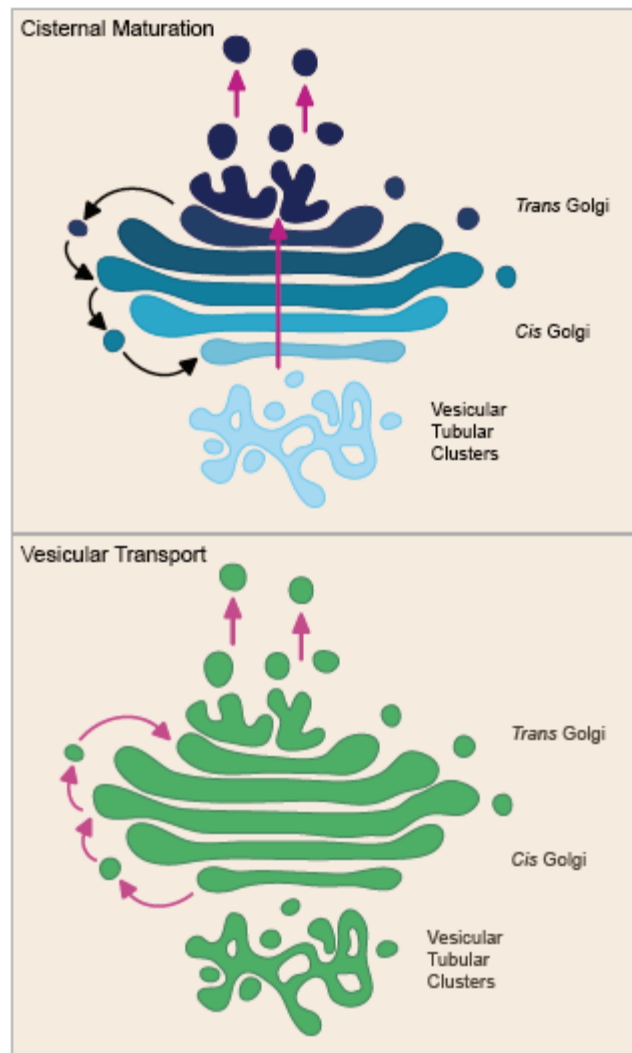


Figure 7.2. Enrichment of Golgi resident proteins over biosynthetic cargo in COPI vesicles.

Peptides of Golgi resident proteins (functional categories: Calcium Binding, Traffic, Tether/Dock/Fuse, and Protein Modification) are 1.9 fold higher in COPI GTP vesicles than in Golgi cisternae. Soluble biosynthetic cargo is decreased 2.5 fold in COPI GTP vesicles as compared to Golgi cisterna. Vesicles generated using GTP γ S have a cohort of Golgi resident proteins whose abundance is similar to those in the Golgi fraction; whereas biosynthetic cargo is diminished in both COPI vesicles isolated with hydrolysable and non-hydrolysable GTP.

Figure 7.2

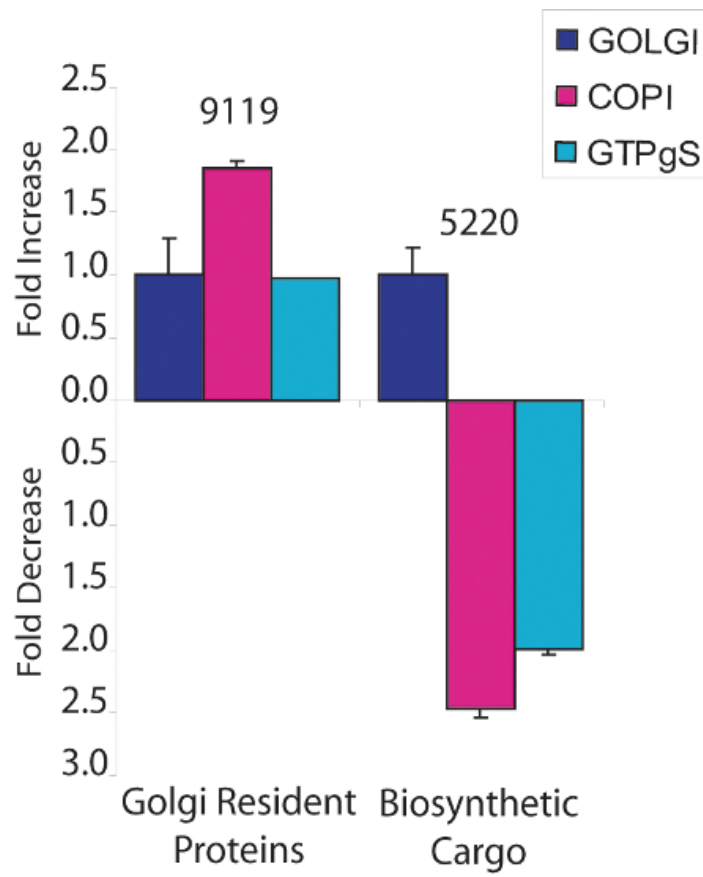


Figure 7.3. Characterization of abundant proteins which increase in COPI vesicles.

The data are from Table 2. Most proteins, except for ERp44 (asterisk) are known Golgi resident proteins. The number of tandem mass spectra assigned to a protein (peptide count) is indicated on top of each group of histograms. The table below links the number on the ordinate with the name of the protein.

#	PROTEIN NAME
1	TYROSYLPROTEIN SULFOTRANSFERASE-1
2	BETA 1,3-GALACTOSYLTRANSFERASE POLYPEPTIDE 1
3	MANNOSIDASE 2, ALPHA 1
4	SIMILAR TO MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE
5	GALACTOSYLGALACTOSYLXYLOSYLPROTEIN 3-BETA-GLUCURONOSYLTRANSFERASE 3
6	UDP-N-ACETYL-ALPHA-D-GALACTOSAMINE:POLYPEPTIDE N-
7	POLYPEPTIDE N-ACETYLGALACTOSAMINYLTRANSFERASE
8	ALPHA-1,3-MANNOSYL-GLYCOPROTEIN 2-BETA-N-ACETYLGLUCOSAMINYLTRANSFERASE
9	P24 ALPHA 2
10	NOVEL MEMBER OF P24 FAMILY (TIRAP3B)
11	SIMILAR TO GOLGI MEMBRANE PROTEIN GP73
12	ERGIC-53 PROTEIN
13	R, SEC22
14	ALPHA-SOLUBLE NSF ATTACHMENT PROTEIN
15	GOLGI AUTOANTIGEN, GOLGIN SUBFAMILY A MEMBER 2
16	GPP130
17	GOLGIN-84
18	CCAAT DISPLACEMENT PROTEIN (CASP)
19	NUCLEOBINDIN 2 (CALNUC 2)
20	45 KDA CALCIUM-BINDING PROTEIN
21	NUCLEOBINDIN 1 (CALNUC 1)
22	ERP44 (SIMILAR TO THIOREDOXIN DOMAIN CONTAINING 4; ENDOPLASMIC RETICULUM RESIDENT
23	TRANSMEMBRANE 9 SUPERFAMILY MEMBER 4
24	TRANSMEMBRANE 9 SUPERFAMILY MEMBER 3
25	TRANSMEMBRANE 9 SUPERFAMILY MEMBER 1

Figure 7.3

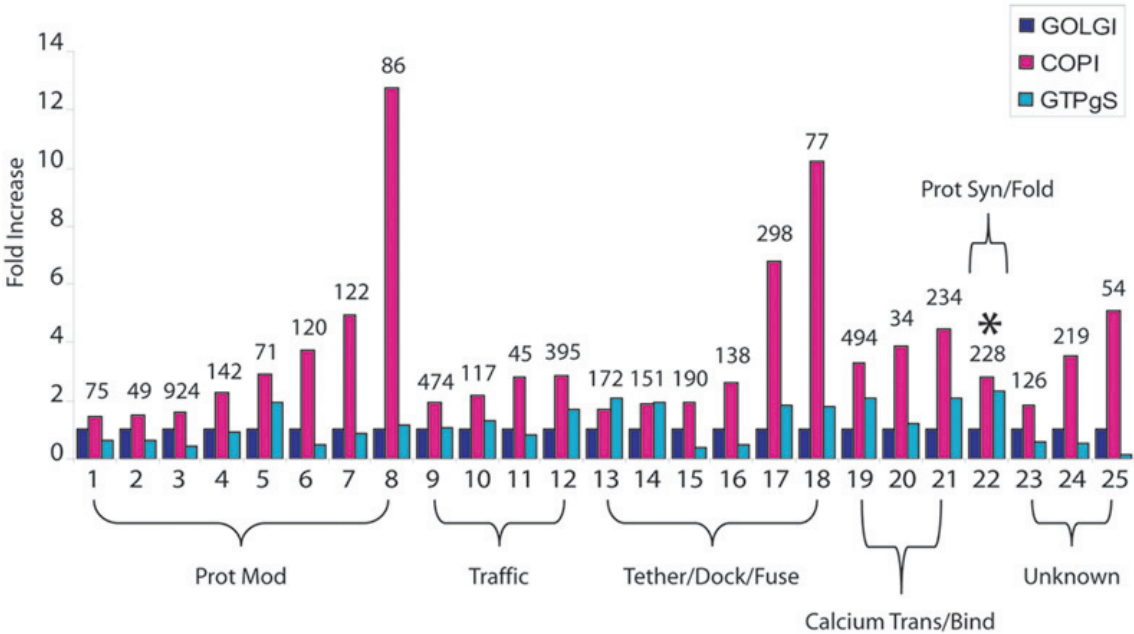
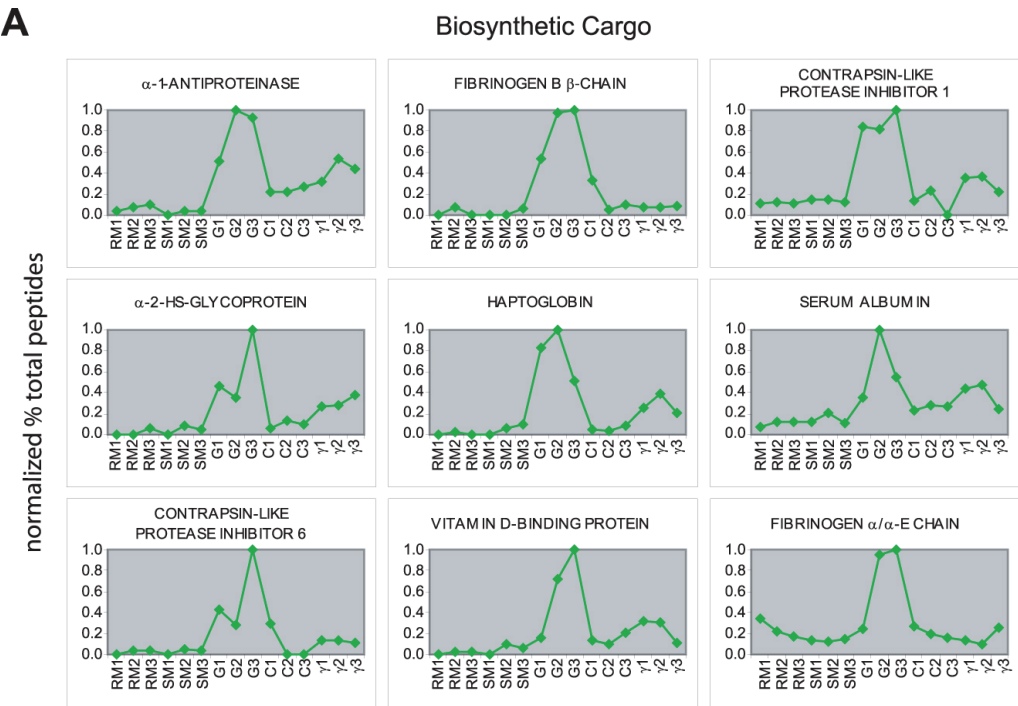


Figure 7.4. Cargo of COPI vesicles compared to RM, SM and Golgi fractions.

This figure was taken from Gilchrist et al. (Gilchrist et al 2006). A. Abundant biosynthetic cargo (9 proteins) were plotted over 3 biological replicates of rough and smooth microsomes (RM,SM), 3 Golgi (G), 3 COPI (C), and 3 COPI GTP γ S (γ) fractions as normalized peptide counts. In all cases proteins are greatly diminished in C vs. G fractions. B. Nine abundant Golgi resident proteins of the protein modification category are shown and plotted as in A. In all cases, their concentration increases in C vs. G fractions. Proteins with mean % total peptides $\geq 0.15\%$ over all replicates of RM, SM, G, C, γ fractions were selected for this figure. The maximal value (% total peptides) was set as 1.0, and all other % total peptides were normalized to the maximal value. Abbreviations: PPGANTASE-T2 = UDP-N-acetyl- α -D-galactosamine polypeptide N-acetylgalactosaminyltransferase 2; MGAT1 = α -1,3-mannosyl-glycoprotein 2-beta-N-acetylglucosaminyltransferase; SCAN-1 (UDPASE) = soluble calcium-activated nucleotidase.

Figure 7.4

A



B

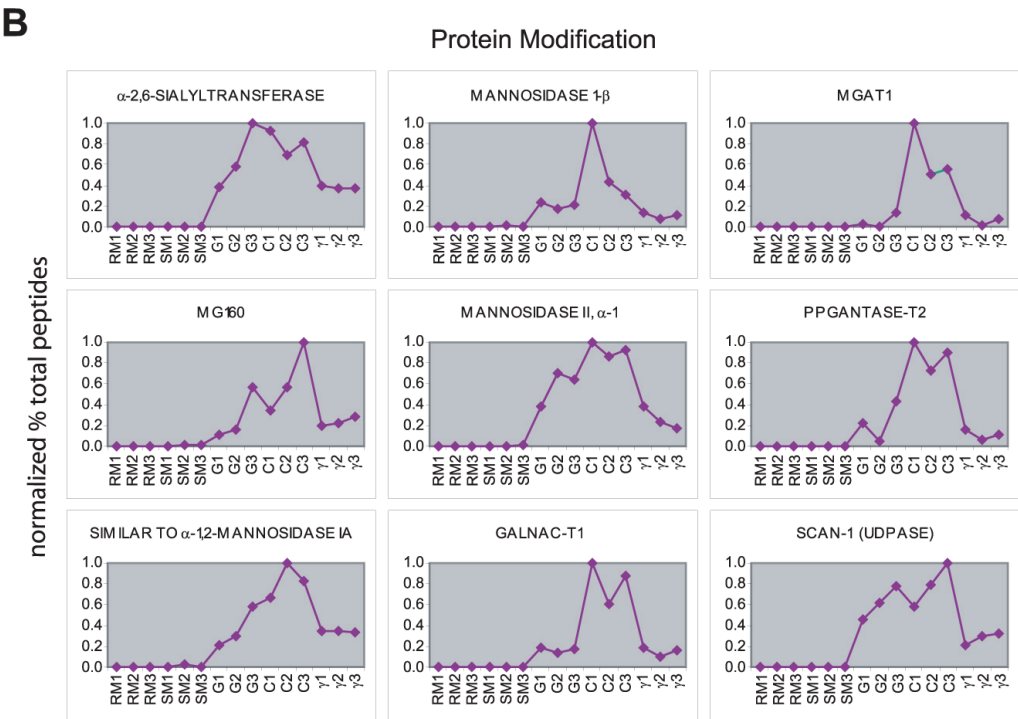


Figure 7.5. Two abundant soluble proteins in COPI vesicles.

Two abundant soluble luminal proteins were assessed for their behaviour in the COPI and COPI GTP γ S vesicles as compared to Golgi. Calnexin, a soluble Golgi resident protein increased almost 4-fold in the COPI GTP vesicles but not in the COPI GTP γ S vesicles. Serum albumin, a soluble biosynthetic cargo protein showed an almost 3-fold decrease in the COPI vesicles.

Figure 7.5

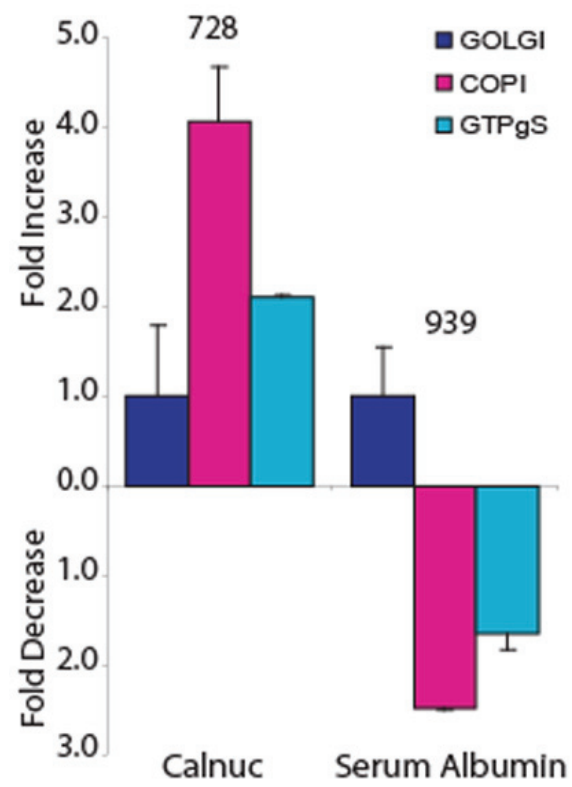
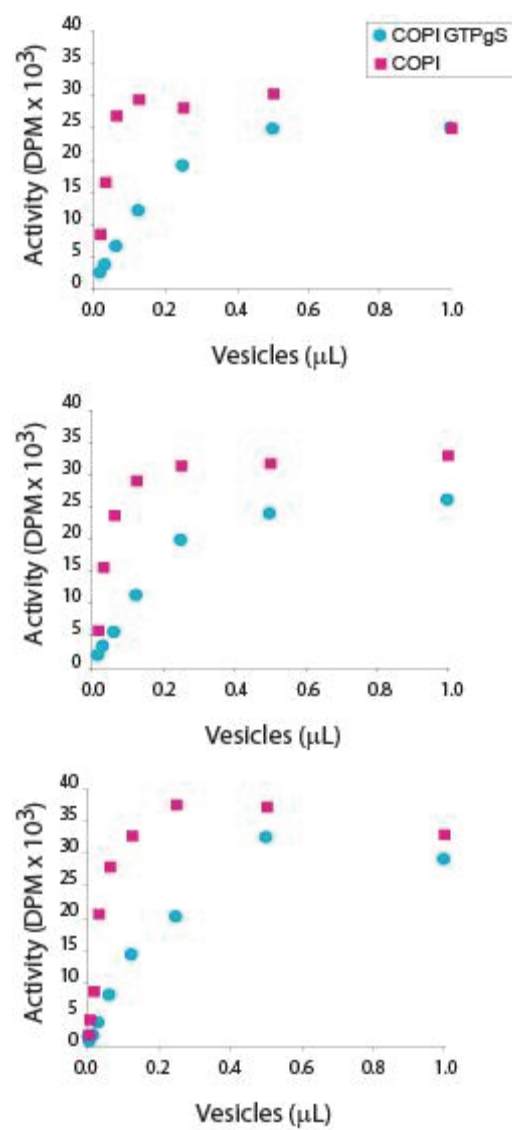


Figure 7.6. Retrograde transport assay.

Comparison of COPI vesicles and COPI GTP γ S vesicles as donors of N-acetylglucosaminyltransferase I in a cell free assay with lec1 Golgi (85 μ g/ml protein) containing VSVG substrate. Vesicles were purified as previously described, and subjected to intra-Golgi fusion assay to determine fusogenic activity (Ostermann 2001). Three separate experiments are shown, for COPI GTP vesicles generated with GTP (0.23 μ g/ml; pink squares) and COPI GTP γ S vesicles (0.14 μ g/ml; light blue circles). COPI vesicles generated with GTP were 3.5 ± 0.7 fold more fusogenic per unit protein than COPI vesicles generated with GTP γ S, by the comparison of Cvapp (concentration of vesicles that are fusogenic) using the method of Ostermann (Ostermann 2001).

Figure 7.6



Chapter 8 -- Novel proteins of the Golgi apparatus and COPI vesicles

8.1 Abstract

During our analysis of the data, we discovered over 100 novel proteins of the Golgi apparatus COPI vesicles, and COPI GTP γ S vesicles. We performed bioinformatics predictions on these proteins to determine the localization (lumen, transmembrane, or cytosolic membrane associated) as well as the presence of functional domains and motifs. These proteins may prove to be new players in membrane trafficking and secretion after further investigation.

8.2 Introduction

Proteins of unknown function are of major interest to investigators doing proteomics research. For most of the existence of the field of molecular biology, the paradigm has been 'one lab, one protein, one lifetime'. Proteomics has allowed the researcher to identify thousands of proteins in one experiment, and then pick and chose which of these proteins he or she wishes to investigate further. Every protein of unknown function is a potential jackpot. It could be a newly identified protein involved in cancer progression; of great interest to researchers and pharmaceutical companies alike. It could be a predicted component of a well known cellular process. The possibilities are endless.

One example of proteins of unknown function that were uncovered via proteomics is the seven novel proteins of clathrin coated vesicles identified in the study of Blondeau et al. (Blondeau et al 2004). These proteins were later confirmed to be new constituents of the clathrin and membrane trafficking machinery of clathrin coated vesicles (Blondeau et al 2004, Conner & Schmid 2005, McPherson 2007). Our proteins of unknown function may well lead to more discoveries in membrane trafficking.

8.3 Results

As for all current organellar proteomics efforts reviewed in (Au et al 2007, Yates et al 2005), several proteins of unknown function were identified (Figure 8.1 A-C, Table 4). Only a few of these have been localized by large scale efforts aimed at elucidating the location of predicted protein gene products (Simpson et al 2000). Those which have been observed in our ER fractions and are also present in our Golgi and COPI vesicles fractions at lower abundance (by peptide counting) are also indicated in Figure 8.1 (Gilchrist et al 2006). Several of the proteins identified here for the first time by tandem MS are predicted to be bona fide new constituents of Golgi cisternae and COPI vesicles. Curated predictions of the transmembrane domains for the proteins with unknown function as well as the known proteins have been described (Table S1c).

In our study of the early secretory pathway we identified over 100 proteins of unknown function that were found in the Golgi apparatus, COPI vesicles, or COPI GTP γ S vesicles, 53 of which were identified only in these three compartments (Table 4). Most of these proteins of unknown function were of low abundance. There were a few, however, of comparable abundance to highly abundant, well characterized Golgi resident proteins such as α -2,6-sialyltransferase and biosynthetic cargo proteins such as transferrin. Four proteins from the TMSF9 family fell into this category.

TMSF9 family members 1, 2, 3, and 4 are highly enriched in the COPI GTP vesicles. Identified by Schimmöller et al. in endosomal membrane fractions (Schimmoller et al 1998), these proteins are related to the *S. cerevisiae* EMP70 protein.

8.4 Discussion

The novel proteins identified in this effort need to be investigated in greater detail in order to elucidate their functional significance and verify their sub-cellular localization. At present, work has been performed on the ER localized proteins identified in this proteomics effort, but work on Golgi and COPI vesicle proteins is pending. A collaboration with another laboratory is attempting RNAi for the four members of the TMSF9 family.

Tables

Table 4 -- Unknown proteins.

Proteins of unknown function that were identified solely in the Golgi apparatus, COPI vesicles, and COPI GTPγS vesicles are shown in the following table with their percentage total peptide distributions in the three biological replicates of each of the organellar fractions. The first column contains the assigned protein name of the proteins. The second column contains the CMBSEQID(s) assigned to the indicated protein name. The rest of the columns indicated by “%TP” show the percentage total peptides in the indicated fraction (“G” represents Golgi, “C” represents COPI vesicles, and “γ” represents COPI GTPγS vesicles).

Table 4 -- Unknown proteins.

ASSIGNED PROT NAME	CMBSEQID LIST	% TP G1	% TP G2	% TP G3	% TP C1	% TP C2	% TP C3	% TP y1	% TP y2	% TP y3
(RCAS1) TYPE II RECEPTOR LIKE CANCER ASSOCIATED SURFACE ANTIGEN (RCAS1) TYPE II RECEPTOR LIKE CANCER ASSOCIATED SURFACE ANTIGEN	239738	0	0	0.0404	0.0471	0.1015	0.0717	0.0734	0.0327	0.0614
AB2-095	276652	0.1637	0.0277	0.2021	0.1885	0.1692	0.1793	0.1284	0.0654	0.1074
AC2-256	166247	0	0	0	0	0.0338	0	0	0.0163	0.0153
BAT3 (HLA-B ASSOCIATED TRANSCRIPT 3)	60486	0	0	0	0	0	0.0359	0	0	0
BC004044 (DENTIN MATRIX PROTEIN 4)	220519	0.0546	0	0	0	0	0.0359	0	0	0
BRAIN PROTEIN 44	80419	0	0.0277	0	0	0	0	0	0	0
BROMODOMAIN ADJACENT TO ZINC FINGER DOMAIN, 2A (PREDICTED)	316025	0	0	0	0	0.0338	0	0	0.0163	0
BTB (POZ) DOMAIN CONTAINING 7 (PREDICTED)	273407	0	0	0.0404	0	0	0	0	0	0
CELL GROWTH REGULATORY GENE 11 PROTEIN	38628	0	0	0	0	0	0	0.0183	0	0
COMM DOMAIN CONTAINING 10	211553	0	0	0.0404	0	0	0	0	0	0
D130038B21	270449	0	0.0277	0	0	0	0	0	0	0
DIAMINE OXIDASE-LIKE PROTEIN 1	216306	0	0	0	0	0	0	0	0.0163	0
DNAJC13	261337	0	0	0	0.0471	0	0	0	0	0.0153
DORZ1	203847	0	0.0277	0	0	0	0	0	0	0.0153
EMOPAMIL BINDING RELATED PROTEIN	245607	0	0	0	0	0	0	0	0	0.0153
FAM3C-LIKE PROTEIN	173223	0.1091	0.083	0.1213	0.1414	0.1353	0.1793	0.2018	0.2615	0.2456
HYPOTHETICAL PROTEIN D4ERTD765E	200143	0	0.0277	0	0	0	0	0	0	0
HYPOTHETICAL PROTEIN LOC298851	167119	0	0	0	0	0	0	0	0	0.0307
HYPOTHETICAL PROTEIN XP_215523	295192	0	0	0	0	0.1015	0.1076	0	0.0327	0.0153
HYPOTHETICAL PROTEIN XP_216137	345922	0	0	0	0	0	0	0	0.0163	0.0307
HYPOTHETICAL PROTEIN XP_238476	299198	0	0	0	0	0	0	0	0.0163	0
INTEGRAL MEMBRANE PROTEIN 2B	284296	0	0.1107	0	0	0	0	0.0367	0.049	0.0921
INTERFERON-INDUCIBLE PROTEIN	17165	0	0	0	0	0	0	0.0183	0.0327	0.0307
INTRAFLAGELLAR TRANSPORT PROTEIN 20-LIKE PROTEIN	239897	0	0	0	0	0	0	0.0183	0.0163	0
JTB PROTEIN	128391	0	0	0	0	0	0	0	0.0163	0.0307
LOC246208 PROTEIN	726783	0	0	0	0	0	0	0.0183	0.049	0.0153
OCIA DOMAIN CONTAINING 1	194680	0	0	0	0	0	0	0.0183	0	0
OXYSTEROL BINDING PROTEIN-LIKE 11	230365	0	0	0	0.0471	0	0	0.0183	0.0163	0
P55	54494	0	0	0	0	0	0.0359	0	0	0
PANCREATITIS-INDUCED PROTEIN 49	222783	0	0.0277	0.1213	0.0943	0.406	0.1793	0	0	0.0307
PQ LOOP REPEAT CONTAINING 1	197729	0	0.0277	0.0404	0	0	0.0359	0	0	0.0307
PROTEIN FAM18B (NPD008) (CGI-148)	303059	0	0	0	0	0	0	0	0.0327	0.0153
PROTEIN FAM20B PRECURSOR	309339	0.0546	0.0277	0.1213	0.2828	0.3045	0.2868	0.0734	0.0163	0.046
PROTEOLIPID PROTEIN 2	166582	0	0	0	0	0	0	0	0	0.0153
RECEPTOR-TRANSPORTING PROTEIN 4 (28 KDA INTERFERON	246358	0	0	0	0	0	0	0	0.0163	0.0153

Table 4 –Page 2

ASSIGNED PROT NAME	CMBSEQID LIST	% TP G1	% TP G2	% TP G3	% TP C1	% TP C2	% TP C3	% TP γ1	% TP γ2	% TP γ3
RING FINGER PROTEIN 121	241539	0	0	0.0808	0	0.1015	0.0717	0	0.0327	0.0614
SARCOMA AMPLIFIED SEQUENCE (PREDICTED)	260364	0	0	0	0	0	0	0	0	0.0614
SEROLOGICALLY DEFINED BREAST CANCER ANTIGEN NY-BR-84 HOMOLOG	275347	0	0.0553	0.2021	0.0943	0.5751	0.4303	0.2569	0.2778	0.4451
SIMILAR TO 9130011E15RIK PROTEIN	198410	0	0.0553	0.2021	0	0	0	0	0	0
SIMILAR TO AMYLOID BETA A4 PRECURSOR PROTEIN-BINDING FAMILY B MEMBER 2 (FE65-LIKE PROTEIN)	294691	0	0	0	0.0471	0.0677	0	0	0	0
SIMILAR TO ARMADILLO REPEAT-CONTAINING PROTEIN	302905	0	0	0	0	0	0	0.0183	0	0
SIMILAR TO CDNA SEQUENCE BC003322	204667	0	0	0	0	0.0338	0	0	0	0
SIMILAR TO CDNA SEQUENCE BC005632	265453	0	0	0	0	0	0	0	0	0.0153
SIMILAR TO CG11388-PA	241377	0	0	0	0	0	0	0	0.0163	0
SIMILAR TO CG17660-PA	293554	0	0	0	0	0	0	0	0	0.046
SIMILAR TO CG2144-PA	237985	0	0	0	0	0.1015	0.1076	0	0	0.0153
SIMILAR TO CHO FUNCTIONALLY UNKNOWN TYPE II TRANSMEMBRANE PROTEIN	235290	0.1091	0.0277	0	0	0.0338	0	0.0183	0.0163	0.0307
SIMILAR TO CHROMOSOME 13 OPEN READING FRAME 1	141958	0.1091	0.1107	0.1213	0.0471	0.1353	0.1076	0.0734	0.1961	0.2302
SIMILAR TO CHROMOSOME 14 OPEN READING FRAME 9	209283	0	0	0	0	0	0	0	0	0.0153
SIMILAR TO CHROMOSOME 20 OPEN READING FRAME 30	190070	0	0	0	0	0	0	0	0.0163	0
SIMILAR TO CHROMOSOME 9 OPEN READING FRAME 7	272157	0	0	0	0	0	0	0	0.0163	0.0153
SIMILAR TO DIVALENT CATION TOLERANT PROTEIN CUTA	281056	0	0	0	0.0471	0.0677	0.0359	0	0	0
SIMILAR TO DNA SEGMENT, CHR 1, ERATO DOI 578, EXPRESSED	262592	0	0	0	0	0.0338	0.0359	0	0	0.0153
SIMILAR TO DNA SEGMENT, CHR 12, ERATO DOI 551, EXPRESSED	300896	0	0.0277	0	0	0	0	0	0	0
SIMILAR TO EXPRESSED SEQUENCE AW556797	206392	0	0	0.0808	0	0	0	0	0	0.046
SIMILAR TO FLJ12716 PROTEIN	272431	0	0	0.0404	0	0	0	0	0	0
SIMILAR TO FLJ21963	243174	0	0.0277	0	0	0	0	0	0	0
SIMILAR TO FOLLICULAR LYMPHOMA VARIANT TRANSLOCATION 1	198248	0	0	0	0	0	0	0	0.0163	0
SIMILAR TO HTGN29 PROTEIN; KERATINOCYTES ASSOCIATED TRANSMEMBRANE PROTEIN 2	258441	0.0546	0	0.0404	0.0943	0.0677	0.1076	0	0.0163	0.0307
SIMILAR TO HYPOTHETICAL PROTEIN B230358A15	314842	0	0	0	0	0	0	0	0	0.0153

Table 4 –Page 3

ASSIGNED PROT NAME	CMBSEQID LIST	% TP G1	% TP G2	% TP G3	% TP C1	% TP C2	% TP C3	% TP γ1	% TP γ2	% TP γ3
SIMILAR TO HYPOTHETICAL PROTEIN B230358A15	314842	0	0	0	0	0	0	0	0	0.0153
SIMILAR TO HYPOTHETICAL PROTEIN FLJ12681	205672	0	0	0	0	0	0	0	0	0.0153
SIMILAR TO HYPOTHETICAL PROTEIN FLJ35794	166638	0	0	0	0	0	0	0	0.0163	0
SIMILAR TO HYPOTHETICAL PROTEIN MGC15523	304037	0	0	0	0.4241	0.3045	0.502	0	0	0.046
SIMILAR TO HYPOTHETICAL PROTEIN MGC40107	240868	0	0	0	0	0	0	0.0183	0.0163	0
SIMILAR TO KIAA0445 PROTEIN	256921	0	0	0	0	0	0	0.0183	0	0.0153
SIMILAR TO KIAA0963 PROTEIN	279597	0	0	0	0	0	0	0	0	0.0153
SIMILAR TO KIAA0980 PROTEIN	230119	0	0	0.0404	0	0	0	0	0	0.0153
SIMILAR TO KIAA1055 PROTEIN	211597	0	0	0	0	0	0	0	0.0163	0
SIMILAR TO KIAA1204 PROTEIN	309548	0	0	0	0	0	0	0	0	0.0153
SIMILAR TO KIAA1414 PROTEIN	207796	0	0	0	0	0	0	0	0	0.0153
SIMILAR TO MKIAA0493 PROTEIN	234949	0	0.0277	0.1617	0.0943	0	0	0	0	0
SIMILAR TO P3 PROTEIN	262782	0	0	0.1213	0.0943	0.0338	0.0717	0.0183	0.0327	0.0153
SIMILAR TO PROBABLE TRANSMEMBRANE PROTEIN FT27 - MOUSE	206786	0	0	0.0404	0.0943	0.0677	0.3944	0.0183	0.049	0.0767
SIMILAR TO PROTEIN HSPC163	225990	0	0	0	0	0	0.0359	0	0	0.0307
SIMILAR TO PROTEIN KINASE NJMU-R1	315828	0	0	0.0404	0	0	0	0	0	0
SIMILAR TO RECOMBINATION ACTIVATING GENE 1 GENE ACTIVATION	292043	0	0	0	0	0	0	0.0183	0.0163	0.0153
SIMILAR TO RETINOIC ACID EARLY INDUCIBLE PROTEIN 1 BETA PRECURSOR (RAE-1BETA)	367801	0	0	0	0	0	0	0	0.0163	0
SIMILAR TO RIKEN CDNA 1110020C03	233158	0	0	0	0	0	0	0	0.0163	0
SIMILAR TO RIKEN CDNA 1700025G04 GENE	318230	0	0	0	0	0	0	0	0.0163	0
SIMILAR TO RIKEN CDNA 1810037C20	200680	0.0546	0.0277	0.0404	0	0	0.0359	0	0.0327	0.0614
SIMILAR TO RIKEN CDNA 2010005O13	301426	0	0	0	0	0	0	0	0	0.0153
SIMILAR TO RIKEN CDNA 2510039O18	235860	0	0.083	0	0.1885	0.0677	0.0717	0.055	0	0.0307
SIMILAR TO RIKEN CDNA 8430437G11	191057	0	0	0.1213	0.6301	0.203	0.1434	0	0	0
SIMILAR TO RIKEN CDNA 9430083G14	218419	0	0.0277	0	0	0	0	0	0	0
SIMILAR TO RIKEN CDNA 9630046K23	228920	0	0	0	0	0	0	0.0183	0.0163	0.0153
SIMILAR TO RIKEN CDNA D430028G21	215394	0	0	0	0	0	0	0.0183	0	0.0153
SIMILAR TO SH3 DOMAIN PROTEIN D19	291964	0	0	0	0	0.0338	0	0	0	0
SIMILAR TO SIF AND TIAM1-LIKE EXCHANGE FACTOR	204958	0.0546	0	0	0	0	0	0	0	0

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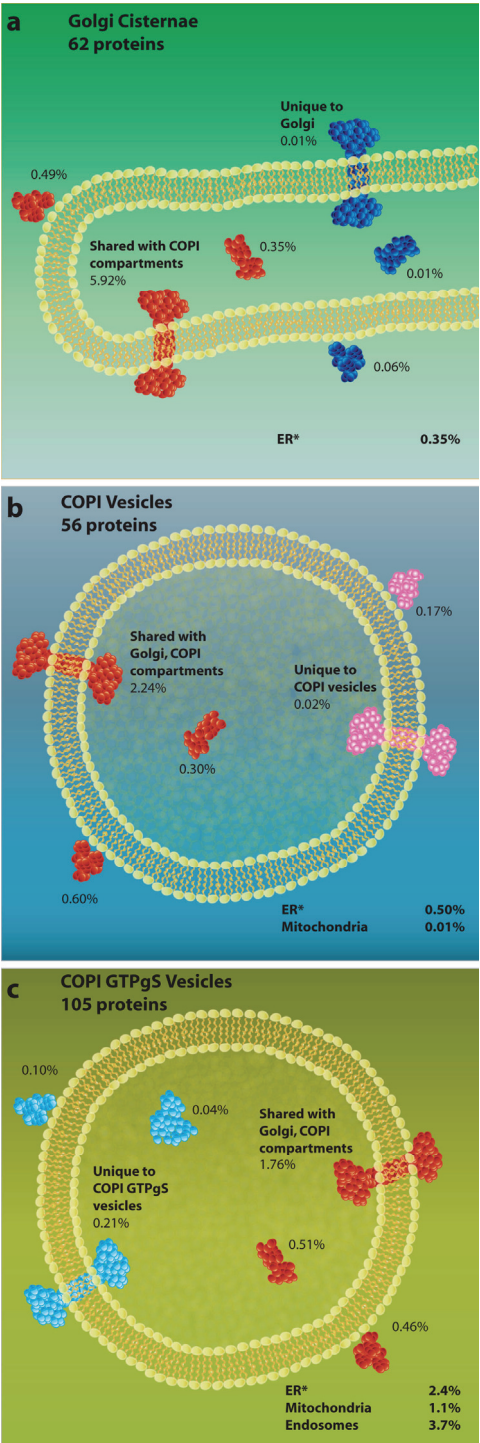
ASSIGNED PROT NAME	CMBSEQID LIST	% TP G1	% TP G2	% TP G3	% TP C1	% TP C2	% TP C3	% TP γ1	% TP γ2	% TP γ3
SIMILAR TO THYROID HORMONE RECEPTOR INTERACTOR 11; THYROID RECEPTOR INTERACTING PROTEIN 11	280942	0.0546	0	0	0	0.0338	0	0	0	0.0153
SIMILAR TO WD REPEAT DOMAIN 20 ISOFORM 2	289309	0.0546	0	0	0	0	0	0	0	0
SIMILAR TO ZINC TRANSPORTER 5	259074	0	0	0.0404	0.0471	0.0677	0.0717	0	0	0
SOLUTE CARRIER FAMILY 35, MEMBER B3 (PREDICTED)	247534	0	0	0.0404	0	0.1015	0.0717	0	0	0.0307
SOLUTE CARRIER FAMILY 39 (ZINC TRANSPORTER), MEMBER 9	272995	0	0	0	0	0	0	0	0	0.0307
SYNAPTIC VESICLE MEMBRANE PROTEIN VAT-1 HOMOLOG	312134	0	0	0	0.0943	0	0	0	0	0
TEA DOMAIN-CONTAINING TRANSCRIPTION FACTOR	267553	0	0	0	0	0	0	0.0183	0	0
TORID	161242	0	0	0	0	0.0338	0	0	0	0
TRANSMEMBRANE 9 SUPERFAMILY MEMBER 1	211728	0	0	0.3234	0.5184	0.4736	0.6454	0	0	0.046
TRANSMEMBRANE 9 SUPERFAMILY MEMBER 3	140307	0.0546	0.0553	1.3743	2.1678	1.6915	1.3984	0.2752	0.1634	0.3377
TRANSMEMBRANE PROTEIN 14C (P11)	30411	0	0	0	0	0	0	0.0183	0	0
TSGA10	7578	0	0	0	0	0	0	0.0183	0	0
WOLF-HIRSCHHORN SYNDROME CANDIDATE 1 PROTEIN ISOFORM 1; IL5 PROMOTER REII REGION-BINDING PROTEIN; TRITHORAX/ASH1-RELATED PROTEIN 5; MULTIPLE MYELOMA SET DOMAIN PROTEIN	214625	0	0	0	0	0	0.0359	0	0	0

Figures

Figure 8.1. Novel proteins identified in the Golgi apparatus, COPI vesicles, and COPI GTP γ S vesicles.

Using TMHMM (Sonnhammer et al 1998) and SignalP (Bendtsen et al 2004) results, the location of each protein of unknown function was predicted as either transmembrane, luminal, or cytosolic membrane associated. Each panel is a cartoon showing the percentage total peptides assigned to proteins of each of the three predicted localizations. Upper: unknown proteins identified in the Golgi apparatus. Proteins unique to the Golgi apparatus are shown in dark blue. Middle: unknown proteins identified in COPI vesicles. Proteins unique to the Golgi apparatus are shown in pink. Lower: unknown proteins identified in the COPI GTP γ S vesicles. Proteins unique to the COPI GTP γ S vesicles are shown in light blue. Proteins found in more than one compartment are shown in orange in each panel.

Figure 8.1



Chapter 9 – Discussion and Conclusions.

9.1 Discussion

9.1.1 Quantitation and proteomics.

During the course of the work developed in this thesis, proteomics underwent a change from a descriptive and qualitative compendium of tables with lists of proteins identified in the mass spectrometer, to a quantitative representation of the spectra characterized by this technology. Indeed, the application of quantitative methodologies to proteomics has now led to the claim that “proteomics is the new genomics” as a result of some of the publications which have emanated from the organellar proteomics field (including the publication associated with the work presented in this thesis) (Cox & Mann 2007, Gilchrist et al 2006). These approaches have led to the now globally accepted “gold standard” for the screening of protein abundance by high throughput proteomics. As outlined in a Nature Biotechnology News and Views article (Bergeron & Hallett 2007), the formal foundation of the peptide counting method is based on the best methodology thus far developed for quantifying mRNA abundance, namely SAGE (serial analysis of gene expression) (Velculescu et al 1995). The underlying logic behind this technique involves the isolation and cloning, and subsequent sequencing, of a set of sequence tags from a sample. Quantitation of the number of times a sequence tag is detected corresponds to the level of expression.

For peptide counting, the method employed here, its first large scale application was in the study of Blondeau et al. (Blondeau et al 2004), which itself was based largely on the efforts of the work presented in this thesis. With the simple counting of peptides which have been

characterized repeatedly by the tandem mass spectrometer, the analysis of clathrin coated vesicles from rat brain revealed a 1:1 stoichiometry of the clathrin heavy and light chain (Blondeau et al 2004). Never before had proteomics alone established the stoichiometry of a known molecular complex.

Tandem mass spectrometry involves two steps wherein “uncertainty” is part of the technology. The first consists of the chemical features of the tryptic peptide which enable it to be selected preferentially for electrospray ionization (ESI) for charge transfer and efficient presentation to the mass spectrometer. These so called proteotypic peptides (Mallick et al 2007), were seen in enormous abundance in the studies described here. The second is a consequence of the stochastic aspect of selection of mass spectra for fragmentation. It is tandem mass spectra resultant from the fragmentation of these selected peptides that are matched against protein databases. I believe that our use of highly enriched, homogenous organelle preparations in the studies described here, contribute to the high proportion of quality tandem mass spectra we collect. Using the micro QToF, greater than 50% of the collected tandem mass spectra were assigned with greater than 95% confidence to peptides in the database with a false positive rate of less than 1.5%. In my opinion, the combination of the use of highly enriched organelles, as well as extensive time on the mass spectrometer (greater than 5000 hours), assures a representative sampling of the peptides generated by tryptic digestion in proportion to the abundance of their cognate proteins in our samples. This is strikingly evident by principal component analysis of our proteomics data. An unbiased assignment of all peptides matched to proteins in each of the biological samples under study, clearly indicated how tightly grouped each of these biological samples were to each other, and how distinct they were as an organelle compared to other organelles. Only the isolated Golgi fractions showed a higher degree of variation (70%

of the variability was seen in the first two components) and this is due to the inherent difficulty of isolating this organelle (Blouin et al 1977). The tight clustering of the ER (RM and SM) is expected since it represents the majority of the membranes in the liver parenchymal cell (Blouin et al 1977), but the equally tight clustering of COPI GTP and COPI GTP γ S vesicles is unexpected. This is likely due to the cell free strategy used to generate these structures, which selects for a homogenous compartment under the conditions employed.

That our estimates of protein abundance by peptide counting were valid was also shown by its application to test samples of purified proteins, as well as its comparison to enzyme enrichment studies and quantitative western blotting as seen in Chapter 3. Although other methods for quantitation such as SILAC (Ong et al 2002), iCAT (Gygi et al 1999), and iTRAQ (Ross et al 2004) exist, these all necessitate the use of isotopically labeled modifications and this is not possible (except for iCAT and iTRAQ) for the *in vivo* studies discussed here. For iCAT and iTRAQ the high cost of the reagents make them impractical for the number of biological replicates and samples used here (over 2000 wells). As well, iCAT and iTRAQ limit the number of samples that can be compared to the number of isobaric tags available, which is at present four, insufficient for the 15 samples presented here.

9.1.2 High throughput proteomics.

The BSA standard curve seen in Chapter 3 indicated in a striking way the limited dynamic range and relatively low sensitivity of the tandem mass spectrometer. This was unexpected given the claims of the field (Corthals et al 2000). My interpretation of this result was that there was a need for homogenous samples to be loaded onto the mass spectrometer. Considerable attention was given to the preparation and documentation of

sample homogeneity as discussed in Chapter 4. Given the consideration of the BSA standard curve I believe that this aspect of the pipeline of proteomics can not be underestimated. In my experience the actual processing of the samples for peptide characterization is robust, reliable, and straightforward, hence its automation ensures the lack of human variation. The use of 1D-SDS page ensures size separation of a complex protein mixture in order to reduce the complexity of the sample. The robotic gel slicing and robotic in-gel tryptic digestion assures a lack of human variation, and the use of high quality HPLC columns in-line with the tandem mass spectrometer ensures a reproducible method for peptide separation and peptide entry into the tandem mass spectrometer. The quality of the tandem mass spectra generated is reflected in the high proportion of those matched with greater than 95% probability. The in house database, Cell Map Base, has been designed to accommodate all of the collected tandem mass spectra, and enable easy selection of the representative protein after Mascot spectra to peptide matching. It is the manual annotation and curation of these representative proteins which presented an unexpectedly heavy burden on the biologist. This is due to the remarkably poor quality of current rat database. In the studies described in this thesis, each and every protein initially indicated as the representative protein, required verification by literature and BLAST analysis to confirm the validity of the original database entry. This work alone consumed most of the biologists time for this proteomics effort. A detailed description of the hurdles of annotation is covered in Chapter 5.

9.1.3 Proteomes of the Golgi and COPI vesicles.

After all the work that went into accurate annotation of our compendium of proteins, we were finally able to look at the proteomes of the Golgi apparatus and COPI vesicles. For the first time, a global view of the total protein contents of these organelles was available. We identified 700

proteins in the Golgi apparatus, over 480 in the COPI GTP vesicles and over 900 in the COPI GTPyS vesicles.

Greater than 25% of the total peptides assigned in the Golgi apparatus were in the category of biosynthetic cargo. Given the role of liver parenchymal cells in the production of serum proteins and the Golgi's role in cargo concentration prior to secretion, this was an expected result. Not so expected was the enrichment of subunits of COPII coatamer in the Golgi apparatus as compared to the RM and SM fractions.

The COPI GTP vesicles were characterized by their enrichment in Golgi resident protein modification enzymes. Approximately 20% of the peptides assigned in the COPI GTP vesicles belonged to this functional group. Also seen was an enrichment of calcium transport and binding proteins such as Calnuc.

The COPI GTPyS vesicles were characterized by their enrichment in COPI coatamer subunits. This was expected because of the need for GTP hydrolysis in order for the coat to detach. These vesicles were otherwise nondescript in their protein complement, most likely due to the lack of selection for content which would normally be controlled by repeated cycles of GTP hydrolysis that were blocked by GTPyS.

9.1.4 Cisternal maturation versus vesicular transport.

We used proteomics to test the maturation hypothesis of Golgi transport, because we felt that proteomics exploited the limitations of cryoimmune electron microscopy, which was unable to resolve this problem (Martinez-Menarguez et al 2001, Orci et al 2000). Cryoimmune electron microscopy is hampered by the inability to study more than three proteins at the same time due to the limitations on the sizes of gold particles that can be linked

to antibodies. Also, identifying single black dots in extremely small structures involves large correction factors which complicate the interpretation of results. Proteomics analysis, on the other hand, is perfect for the analysis of small homogeneous structures.

The hypothesis of cisternal maturation requires that the Golgi cisternae are enriched in biosynthetic cargo and the peri Golgi COPI vesicles are enriched in resident proteins that are being returned to the Golgi cisternae. The vesicular transport hypothesis requires the peri Golgi COPI vesicles to be enriched in biosynthetic cargo that they carry between cisternae.

Our data support the cisternal maturation model, with our COPI GTP vesicles (representative of vesicles that are formed *in vivo*) enriched in both soluble and transmembrane Golgi resident proteins and depleted in biosynthetic cargo proteins.

9.1.5 Proteins of unknown function.

The over 100 proteins of unknown function that we identified in the Golgi apparatus and COPI vesicles are an interesting avenue of research that needs to be more fully explored. It is likely that some of these proteins will be involved in membrane traffic and content selection of COPI vesicles. Of great interest to me are members of the TMSF9 group. Three family members were identified as highly enriched in our COPI GTP vesicles, at abundances comparable to well known Golgi terminal glycosyl transferases.

9.2 Conclusions

In this thesis I have described the extension of the Golgi proteome to 246 proteins, as well as the first analysis of Golgi derived COPI GTP and COPI GTPyS vesicles. I show the first use of proteomics to test a cell biological hypothesis, namely the cisternal maturation hypothesis. This model of Golgi transport is supported by our proteomics data. Finally, I use bioinformatics software to predict the topology over 100 novel proteins identified in the Golgi apparatus and COPI vesicles.

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DATE	
DB	✓
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#: 1st 2nd

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
 Email: john.bergeron@mcgill.ca Phone: 514-398-1259 Fax: 514-398-5047
 Funding source: Canadian Institutes of Health Research 17016 4516
 Start of Funding: July 1, 2003 End of Funding: Sept. 30, 2008
 Emergency contact #1 + Ali Fazel, work 514-398-6352, home 514-684-8609
 work AND home phone #s:
 Emergency contact #2 + Pamela Cameron, work 514-398-6352, home 514-845-1086
 work AND home phone #s:

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

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 one) ① ② ③			
Principal Investigator/course director:		date: 12 MAY 2003 day month year	
Chairperson, Biohazards Committee:		date: 15-05-2003 day month year	
Approved for:		beginning 01-07-2003 ending 30-09-2008 day month year day month year	

* as defined in the "McGill Laboratory Biosafety manual"

3rd REVISION, JANUARY 1996

McGill University Internal Radioisotope Permit

20070194

McGill University Internal Radioisotope Permit Date Issued: 2006/09/01 Expiry Date: 2007/08/31	
PLEASE POST	Date Issued: 2006/09/01 Expiry Date: 2007/08/31

Department: ANATOMY AND CELL BIOLOGY
 Faculty: MEDICAL SCIENCES
 Building (Lab): 398-1259
 Room Number: 6400-6503
 Telephone: 398-1259
 Fax: 398-6352

PERSON(S) APPROVED TO WORK WITH RADIOISOTOPES

Name	Train.	Cond(s)	Class(es)	Radioisotope(s)
JOHN J.M. BERGERON, PROFESSOR	N	6		
ALL FAZEL, RESEARCH ASSISTANT	Y	1, 2, 4	2, 3, 4	C-14, H-3, I-125, P-32, S-35
MARKUS L. PORTER, GRADUATE STUDENT	Y	6		
MARY DELANEY, RESEARCH ASSISTANT	N	6		
PAMELA CANNON, 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 NAGATA, 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 CANS 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 food or drink and the application of cosmetics and contact with skin must be prohibited in the work area.
- 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 clothes are not contaminated.
- Procedures for the disposal of radioactive waste must be strictly followed and documented in a log book.
- For disposal of radioactive waste, consult the McGill Radiation Safety Policy Manual and/or McGill WAMP.
- 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 same and telephone number of the permit holder.
- Sealed sources must be stored in approved containers equal to or greater than 50 MBq (1.35 mCi).
- Extensive decontamination (i.e. ring or wrist badges) must be worn if 50 MBq or more of P-32, Sr-90, Sc-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 box (50 MBq) are used.

Approved Sealed Radioisotope(s) and Location(s)

Isotope	Activity	Isotope	Activity	Accessable Source(s)	Shielded Source(s)	Handled
P-32	< 1 GBq (27 mCi)	6500 / 03	6500 / 03	6500 / 03	6500 / 03	
I-125	< 400 MBq (11 mCi)	6500 / 03	6500 / 03	6500 / 03	6500 / 03	
Sr-90	< 4 GBq (108 mCi)	6500 / 03	6500 / 03	6500 / 03	6500 / 03	
C-14	< 40 MBq (1.1 mCi)	6500 / 03	6500 / 03	6500 / 03	6500 / 03	
H-3	< 1 GBq (27 mCi)	6500 / 03	6500 / 03	6500 / 03	6500 / 03	

Approved Unsealed Radioisotope(s) and Location(s)

Isotope	Activity	Isotope	Activity	Accessable Source(s)	Shielded Source(s)	Handled
P-32	< 1 GBq (27 mCi)	6500 / 03	6500 / 03	6500 / 03	6500 / 03	
I-125	< 400 MBq (11 mCi)	6500 / 03	6500 / 03	6500 / 03	6500 / 03	
Sr-90	< 4 GBq (108 mCi)	6500 / 03	6500 / 03	6500 / 03	6500 / 03	
C-14	< 40 MBq (1.1 mCi)	6500 / 03	6500 / 03	6500 / 03	6500 / 03	
H-3	< 1 GBq (27 mCi)	6500 / 03	6500 / 03	6500 / 03	6500 / 03	

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-90, Sc-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 < 10 MBq (270 uCi) of unsealed radioisotopes in open area.
- Work load < 10 MBq (270 uCi) of unsealed radioisotopes in a fume hood.
- Work load > 10 MBq (270 uCi) of unsealed radioisotopes in open area.
- 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.

For: Dr. Janusz Kozinski, Chair
Associate Vice-Principal (Research)

Joseph V. Vucelja, PHS & Radiation Safety Officer
McGill Environmental Health & Safety

Approved: 2006/09/01

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Appendix 2

Supplemental Table Legends

Table S1a. RM, SM, Golgi, COPI Vesicles, and COPI GTPyS Protein Identifications.

The following table has been adapted from Gilchrist et al. (Gilchrist et al 2006). Complete proteomes of RM, SM, Golgi, COPI vesicles, and COPI GTPyS vesicles, as determined by this study and presented according to the guidelines of Carr et al. (Carr et al 2004) with details for single peptide identifications in Supplementary Table 1B. This table reflects 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 for public access (<http://www.ebi.ac.uk/pride/>).

Table S1b. Proteins Identified by a Single Distinct Peptide.

The following table has been adapted from Gilchrist et al. (Gilchrist et al 2006). Details presented for proteins identified by 1 peptide according to the guidelines of Carr et al. (Carr et al 2004). In addition to the details in A, the following are presented: N-terminal flanking amino-acid (START indicates the N-terminal tryptic peptide, M indicates initiator methionine has been removed); peptide sequence; C-terminal flanking amino acid (END indicates the C-terminal tryptic peptide); m/z value in thomsons (Th); observed peptide charge, experimental peptide mass in Daltons (Da);

calculated peptide mass in Daltons (Da); experimental peptide mass in Daltons (Da); calculated peptide mass in Daltons (Da); delta value (the difference between the experimental and calculated peptide mass); Peptide MOWSE Score (<http://www.matrixscience.com>); and Mascot Identity Score (Perkins et al 1999) for the best peptide identification.

Table S1c. Curation of Protein Identifications.

The following table has been adapted from Gilchrist et al. (Gilchrist et al 2006). The protein identifications were curated into functional categories, annotated with representative assigned protein names based on primary literature, and both signal type and transmembrane topology were predicted, with membrane status including those proteins inserted via lipid anchors. Presented are: Assigned Protein Name, biochemical treatment; functional category; NCBI Description; calculated molecular weight (MW); NCBI gi number, CMBSEQID; subcellular fraction; repeat number which corresponds to biological repeat; membrane status (assigned based on TMHMM and literature search) (Sonnhammer et al 1998); signal type (SignalP prediction) (Bendtsen et al 2004); transmembrane (TM) prediction (TMHMM prediction: starting amino acid, length of the TMS, direction relative to the cytoplasm (IN = cytoplasmic) (Bendtsen et al 2004); TMHMM prediction (starting amino acid, length of the TMS, direction relative to the cytoplasm (IN = cytoplasmic) (Sonnhammer et al 1998)); UNIREF100 identifier (Apweiler et al 2004); NCBI REFSEQ identifier (Pruitt et al 2005).

Table S1d. Total Peptide Statistics by Assigned Protein Name.

The following table has been adapted from Gilchrist et al. (Gilchrist et al 2006). Redundant peptide counts (Total Peptides) were done exactly as described in Blondeau et al.(Blondeau et al 2004) and correspond to the spectral count method of Liu et al. (Liu et al 2004) Shown are total

peptides (equal to spectral counts (Liu et al 2004)) and normalized total peptide statistics for biological repeats $n=1, 2, 3$ with the mean and standard deviations for these measurements for all proteins. Proteins with the same assigned protein name in Table S1c have been grouped together and the Total Peptides (TP) summed and Percent Total Peptides calculated. All CMBSEQID numbers associated with an assigned protein name are listed in the CMBSEQID list.

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

NCBI DESCRIPTION	MW	ginumber	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:2610511I21 product:proteasome (prosome, macropain) subunit, alpha type 2, full insert sequence TIB-55 BB88 cDNA, RIKEN full-length enriched library, clone:I730006B17 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 (prosom	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-CI	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:I920072G18 product:ribosomal protein L21, full insert sequence TIB-55 BB88 cDNA, RIKEN full-length enriched library, clone:I730098C20 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')oligo(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 PRL receptor-associated protein PRAP	37370	8393576	708	3	3	15.8683
3-ketoacyl-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-methylpropionate 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	1	1	2.4
4-trimethylaminobutyraldehyde dehydrogenase TMABADH Aldehyde dehydrogenase 9A1	53650	78099320	104196	11	11	29.1498
40S ribosomal protein S11	18430	54039305	4834	14	14	60.7595
40S ribosomal protein S12	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-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: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	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 Trypstatin	38850	6978497	3629	8	8	28.9398
AP-1 complex subunit beta-1 Adapter-related protein complex 1 beta-1 subunit Beta-adaptin 1 Adaptor protein complex AP-1 beta-1 subunit Golgi adaptor HA1/AP1 adaptin beta subunit Clathrin assembly protein complex 1 beta large chain	104600	8392872	126513	15	28	39.0938
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 Ac1-060	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	199808	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 hydratase 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 Trihydroxycoprostanoyl-CoA oxidase THCCox THCA-CoA oxidase	76800	21955130	3086	24	24	40.6755
Acyl-coenzyme A oxidase 3, peroxisomal Pristanoyl-CoA oxidase Branched-chain acyl-CoA oxidase BRCAcox	78450	2498208	42129	19	19	40.7143
Acyl-protein thioesterase 1 Lysophospholipase 1 Lysophospholipase I	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:I920019I09 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-1 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:surfeit gene 4, full insert sequence Bone marrow macrophage cDNA, RIKEN full-length enriched library, clone:I830028A12 product:surfeit gene 4, full insert sequence Bone marrow macrophage cDNA, RIKEN full-length enriched library, clone:I830026D09 product:surfeit gene 4, full insert sequence Bone marrow macrophage cDNA, RIKEN full-length enriched library, clone:I830012C22 product:surfeit gene 4, full insert sequence Blastocyst blastocyst cDNA, RIKEN full-length enriched library, clone:I1C0027M05 product:surfeit 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:I830027D22 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	6.5574
Advanced glycosylation end product-specific receptor precursor Receptor for advanced glycosylation end products	42660	498034	128256	1	1	3.4826
Afadin Protein Af-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
AlF-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 mutarotase	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-antiproteinase 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 Angiotensin-3 Angiotensin III Ang III Des-Asp[1]-angiotensin II	51980	56585074	45123	8	8	26.4151
Anionic trypsin-1 precursor Anionic trypsin I Pretrypsinogen I	25960	6981420	75054	1	1	8.1301
Annexin A3	36360	71766	120574	11	11	50.6173
Annexin A4	35850	37999910	171244	8	8	31.0345
Annexin A5	35740	6978505	3633	15	15	50.4702
Antigen peptide transporter 1 APT1 Peptide transporter TAP1 ATP-binding cassette sub-family B member 2	79150	2506117	43654	2	2	3.5862
Ap2b1 protein	105700	73695330	59082	4	33	46.0568
Apoa5 protein	41430	6707431	114274	11	11	34.0599
Apolipoprotein A-I precursor	30060	6978515	3638	11	11	49.8069
Apolipoprotein A-II precursor	11440	91985	3639	1	1	10.7843
Apolipoprotein A-IV precursor	44460	60552712	141420	16	16	50.3836
Apolipoprotein C-IV precursor Apo-CIV ApoC-IV Apolipoprotein E-linked ECL	10250	2492915	136243	1	1	12.5
Apolipoprotein E precursor Apo-E	35750	55824759	126501	20	20	51.6026
Apolipoprotein M	21510	9506391	95121	3	3	18.4211

Apoptosis-inducing factor	66720	7619915	63059	19	19	45.7516
Arginase 1	34970	6573527	37797	28	28	82.0433
Argininosuccinate lyase	51550	551296	45085	12	12	33.4056
Argininosuccinate synthase Citrulline--aspartate ligase	46500	55767	45108	29	29	72.3301
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-acetylneuraminyI)-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]-glucosaminyl 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 Neuropep 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 MEMD 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-phosphatidyltransferase Phosphatidylinositol synthase PtdIns synthase PI synthase	23610	7674155	70677	5	5	27.23
CLIP-associating protein 2 Cytoplasmic linker-associated protein 2	140600	77416394	60531	2	2	1.3219
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	2	2	9.3093
CMP-N-acetylneuramine-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 CH1 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 Metalloprotease 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
Cct5 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
Clathrin heavy chain	191600	9506497	95154	63	63	49.194
Clathrin 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-coat protein 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 gC1qBP C1qBP GC1q-R protein	30740	9506435	80872	2	2	15.8273

Complement component C6 precursor	105100	61211276	240055	1	1	1.2848
Complement component C9 precursor	62280	2499467	43431	8	8	20.2166
Complement inhibitory factor H	140300	18426830	96883	10	10	10.5987
Complement regulatory protein Crry precursor Antigen 512	61680	9506513	35260	1	1	3.5778
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	0.5814
Contrapsin-like protease inhibitor 1 precursor	46520	57294	84230	2	20	52.8846
Contrapsin-like protease inhibitor 1 precursor	46480	220698	135016	1	19	50.4808
Contrapsin-like protease inhibitor 6 precursor CPI-26 Serine protease inhibitor 3 SPI-3 SPI-2.2	46650	50927309	88238	14	17	57.4163
Core binding factor beta	21520	61557239	2681	1	1	4.3956
Core1 UDP-galactose:N-acetylgalactosamine-alpha-R beta 1,3-galactosyltransferase	42310	8927166	55277	9	9	35.2617
Coronin-1B Coronin-2	53850	9506507	95157	3	3	9.5041
Cortactin isoform C	52630	2996044	57161	1	1	2.5478
Corticosteroid 11-beta-dehydrogenase isozyme 1 11-DH 11-beta-hydroxysteroid dehydrogenase 1 11-beta-HSD1	31880	78214365	95697	22	22	69.4444
Cp431	104600	3851160	7578	1	1	1.0022
Creatine kinase M-type Creatine kinase M chain M-CK	43020	6978661	3700	1	1	3.6745
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	4	4	3.4959
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 CRP2 Protein ESP1	22700	737713	46143	2	2	23.0769
Cysteine-sulfinate decarboxylase	55250	6685331	35923	2	2	7.3022
Cytidylate 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 CYP1IB2 P450E P450 PB4	55930	34855371	13404	4	13	37.4745
Cytochrome P450 2B3 CYP1IB3	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 CYP1IC70 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 CYP1IIIA18 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 CYP1IVA12 CYP1VA8 P450-KP1 P450-PP1	58520	203757	78089	1	6	10.0394
Cytochrome P450 4A14 precursor CYP1VA14 Lauric acid omega-hydroxylase P450-LA-omega 3	58230	28461155	21524	12	36	72.3866
Cytochrome P450 4F1 CYP1IVF1 P450-A3	59870	9665225	134595	11	17	45.0382
Cytochrome P450 4F4 CYP1IVF4	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 Cytochrom 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	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	52.381
Cytochrome oxidase subunit II	26010	829023	105670	1	7	26.4317
Cytochrome oxidase subunit II Cytochrome c oxidase subunit II	25930	58615680	142106	1	7	30.837
Cytokeratin type I	15550	55956	11221	1	1	5.3892
D-amino-acid oxidase DAMOX DAO DAAO	38820	56972124	60497	2	2	7.2254
DAD1 protein	12500	48428847	13029	3	3	26.5487
DAMP-1 protein	19670	37693510	116798	2	2	11.0465
DOPA/tyrosine sulfotransferase	34840	688032	74919	9	9	36.7893
Da1-24	124000	33086684	287107	8	8	8.7814
Damage-specific DNA binding protein 1	126900	9843869	111030	5	5	7.1053
Ddx5	69240	56090441	161883	7	9	18.6992
Dehydrogenase/reductase (SDR family) member 1	34020	56090381	240184	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	23.8462
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	14	16	60.0671
Delta-5 desaturase	52470	16758190	60408	2	2	6.9351
Delta-6 fatty acid desaturase Fatty acid desaturase 2	52380	7513959	36810	6	6	13.964
Delta-aminolevulinic acid dehydratase Porphobilinogen synthase ALADH	36030	6978483	3622	4	4	25.4545
Delta3,5-delta2,4-dienoyl-CoA isomerase, mitochondrial precursor	36200	478984	80356	10	10	34.8624
Dephospho-CoA kinase domain containing	27350	56090393	318309	2	2	10.4167
Derlin-1 Degradation in endoplasmic reticulum protein 1 Der1-like protein 1	28830	62652445	119910	4	4	18.7251
Destrin Actin-depolymerizing factor ADF	18390	7441446	123978	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	37.6022
Diaclylglycerol O-acyltransferase 1 Diglyceride acyltransferase	56870	9965432	145183	1	1	3.2129
Diamine oxidase-like protein 1	80090	40385889	216306	1	1	1.2857
Dihydrofolate reductase	21640	81871579	53424	2	2	13.9037
Dihydrolipoamide dehydrogenase E3 component of pyruvate dehydrogenase complex, 2-oxo-glutarate complex, branched chain keto acid dehydrogenase complex	54040	40786469	253447	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 Nucl	11960	10835705	108686	2	2	23.0769
Dimethylaniline monooxygenase [N-oxide-forming] 1 Hepatic flavin-containing monooxygenase 1 FMO 1 Dimethylaniline 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:I1C0041A13 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
Dynamin 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:ENSRNOP00000011183 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 Plasma-cell membrane glycoprotein PC-1 Alkaline phosphodiesterase I Nucleotide pyrophosphatase NPPase	102900	23396766	60453	15	15	26.6004
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 retuclum 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:I920165O08 product:eukaryotic translation initiation factor 4A1, full insert sequence 17 days embryo kidney cDNA, RIKEN full-length enriched library, clone:I920077H15 product:eukaryotic translation initiation factor 4A1, full insert sequence 16 days embryo heart cDNA, RIKEN full-length enriched library, clone:I920075M13 product:eukaryotic translation initiation factor 4A1, full insert sequence 17 days embryo heart cDNA, RIKEN full-length enriched library, clone:I920075G18 product:eukaryotic translation initiation factor 4A1, full insert sequence 17 days embryo kidney cDNA, RIKEN full-length enriched library, clone:I920054E16 product:eukaryotic translation initiation factor 4A1, full insert sequence CDNA, RIKEN full-length enriched library, clone:I730045F20 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 exostoses 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 3 member A 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	9.7368
GM2 activator protein	21520	27229316	157436	1	1	11.0553
GNB2 protein	37330	8927570	4326	3	7	27.3529
GPP34-related protein	32920	62644637	220058	2	3	12.9825
GTP cyclohydrolase 1 feedback regulatory protein GTP cyclohydrolase I feedback regulatory protein GFRP p35	9541	16975337	140831	2	2	31.3253
GTP-binding nuclear protein Ran GTPase Ran Ras-like protein TC4	24420	51338593	76611	2	2	11.1111
GTP-binding protein rab10 - rat	22610	420269	44648	9	12	59
GTPase HRas precursor Transforming protein p21 p21ras H-Ras-1 c-H-ras	21300	34861217	10323	1	3	19.0476
Galactokinase 1 Predicted	42380	56605662	206276	2	2	10.9694
Galactose-1-phosphate uridylyltransferase Gal-1-P uridylyltransferase UDP-glucose--hexose-1-phosphate uridylyltransferase	43310	68533665	71441	1	1	2.3747
Galectin-3	27200	57870645	71532	1	1	4.1985
Galectin-9	36320	1916610	18989	7	7	31.3665
Gamma-butyrobetaine dioxygenase Gamma-butyrobetaine,2-oxoglutarate dioxygenase Gamma-butyrobetaine hydroxylase Gamma-BBH	44550	5825482	139030	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	2.6224
Gap junction beta-1 protein Connexin-32 Cx32	32000	8393444	51463	5	5	14.4876
Gene,	48610	22775474	113271	1	1	2.6432
General vesicular transport factor p115 Transcytosis-associated protein TAP Vesicle docking protein	107200	538153	71574	14	14	19.3952
Genethonin-1	35490	62078705	169873	5	5	18.6186
Glia maturation factor beta GMF-beta	16610	111660	148966	1	1	16.3121
Glial fibrillary acidic protein alpha Gfap protein	49960	62657131	26394	3	4	10.2326
Glucose phosphate isomerase	62830	46485440	295907	5	5	13.9785

Glutamate dehydrogenase, mitochondrial precursor	61420	92090591	3897	42	42	67.5627
Glutamine fructose-6-phosphate transaminase 1	76830	54400724	277551	1	1	2.3495
Glutamine synthetase	42270	61098201	28251	12	12	33.5121
Glutamyl aminopeptidase	108000	7159085	62885	2	2	2.328
Glutathione S-transferase Yb-1	25920	204503	126642	2	26	89.4495
Glutathione S-transferase Yb-2	25700	66613	28291	4	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	81.448
Glutathione S-transferase alpha-4 Glutathione S-transferase Yk GST Yk GST 8-8 GST K GST A4-4	25510	5420030	28290	1	3	9.9099
Glutathione peroxidase	22260	121668	28283	11	11	55.7214
Glutathione transferase (EC 2.5.1.18) psi	3544	92300	84221	1	1	33.3333
Glutathione transferase omega 1	27670	12585231	55147	3	3	13.6929
Glyceraldehyde-3-phosphate dehydrogenase Gapd protein	35830	9798638	51456	2	17	63.6637
Glycerol kinase ATP:glycerol 3-phosphotransferase Glycerokinase GK ATP-stimulated glucocorticoid-receptor translocation promoter ASTP	57480	433211	18015	1	1	2.2901
Glycerol-3-phosphate acyltransferase, mitochondrial precursor GPAT	93710	8393466	51468	7	7	11.9565
Glycerol-3-phosphate dehydrogenase, mitochondrial precursor GPD-M GPDH-M	80970	6980978	3907	1	1	2.0633
Glycine N-methyltransferase	32420	6137382	19169	9	9	45.8904
Glycylpeptide N-tetradecanoyltransferase 1 Peptide N-myristoyltransferase 1 Myristoyl-CoA:protein N-myristoyltransferase 1 NMT 1 Type I N-myristoyltransferase	56860	81914601	229000	2	2	6.0484
Golgi SNAP receptor complex member 1 28 kDa Golgi SNARE protein 28 kDa cis-Golgi SNARE p28 GOS-28	28530	16758358	21695	15	15	61.2
Golgi apparatus protein 1 precursor Golgi sialoglycoprotein MG-160 E-selectin ligand 1 ESL-1	133600	8393450	51465	48	48	49.7011
Golgi phosphoprotein 3 Coat-protein GPP34 Trans-Golgi protein GMx33	33780	50400215	54283	11	12	40.2685
Golgi reassembly stacking protein 2	47310	56090463	288023	7	7	22.467
Golgin subfamily A member 2 Cis-Golgi matrix protein GM130	111400	7513936	169300	33	33	45.3347
Golgin subfamily A member 7	15780	81884637	199992	1	1	10.9489
Group specific component	53520	51260133	86608	17	17	41.3866
Growth factor receptor bound protein 2	25210	77539774	29315	1	1	5.53
Gstm7 protein	25680	529588	33791	1	10	39.9083
Guanidinoacetate N-Methyltransferase	22590	30750124	196203	2	2	14.0704
Guanine deaminase Guanase Guanine aminase Guanine aminohydrolase GAH	51020	9910706	42862	4	4	12.5551
Guanine nucleotide binding protein alpha inhibiting 2	40500	71089913	37194	7	13	48.4507
Guanine nucleotide binding protein, beta 2, related sequence 1 CRL-1722 L5178Y-R cDNA, RIKEN full-length enriched library, clone:I730096H10 product:guanine nucleotide binding protein, beta 2, related sequence 1, full insert sequence Blastocyst blastocyst cDNA, RIKEN full-length enriched library, clone:I1C0024M22 product:guanine nucleotide binding protein, beta 2, related sequence 1, full insert sequence Blastocyst blastocyst cDNA, RIKEN full-length enriched library, clone:I1C0014F18 product:guanine nucleotide binding protein, beta 2, related sequence 1, full insert sequence Blastocyst blastocyst cDNA, RIKEN full-length enriched library, clone:I1C0013E14 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	19	19	77.918
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 locus Ke4	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:I920176M04 product:heat shock protein 8, full insert sequence 16 days embryo kidney cDNA, RIKEN full-length enriched library, clone:I920096J24 product:heat shock protein 8, full insert sequence 16 days embryo kidney cDNA, RIKEN full-length enriched library, clone:I920087N17 product:heat shock protein 8, full insert sequence 16 days embryo kidney cDNA, RIKEN full-length enriched library, clone:I920079M09 product:heat shock protein 8, full insert sequence 17 days pregnant adult female amnion cDNA, RIKEN full-length enriched library, clone:I920066C08 product:heat shock protein 8, full insert sequence 16 days embryo kidney cDNA, RIKEN full-length enriched library, clone:I920062I24 product:heat shock protein 8, full insert sequence 17 days embryo stomach cDNA, RIKEN full-length enriched library, clone:I920052L10 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	27465521	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	8.5938
Hypothetical protein	37380	51338711	8648	2	6	20.2941
Hypothetical protein	24090	83415090	163993	2	7	41.8605
Hypothetical protein	40560	58477247	71440	5	5	25.2101
Hypothetical protein	14900	25282411	132369	2	2	18.9781
Hypothetical protein Ccdc51	42310	62078929	366853	1	1	2.6385
Hypothetical protein D10Wsu52e	55250	50926851	54494	9	9	23.5644
Hypothetical protein DKFZp468N1517	6677	6981490	4847	3	3	33.9286
Hypothetical protein FLJ20445 Ring finger protein 153	31230	34862676	49021	1	1	4.6763
Hypothetical protein MG87 MOCO sulphurase C-terminal domain containing 2	38250	38511548	161253	9	9	23.6686
Hypothetical protein MGC72560	17720	40018580	139384	1	1	8.0745
Hypothetical protein MGC72996	20710	38454298	220427	1	1	5.2632
Hypothetical protein MGC94464	19290	56090373	282775	1	1	4.8485
Hypothetical protein Mettl7b	27900	66730429	244225	11	11	50
Hypothetical protein Ndufc2	14360	57164133	164223	2	2	18.3333
Hypothetical protein RGD1305677	21660	58585236	209082	1	1	8.1633
Hypothetical protein RGD1310224	33690	57164137	208921	6	6	34.3234
Hypothetical protein RPL37A	10280	57123	4820	3	3	42.3913
Hypothetical protein Tmem97	20950	56605746	300133	3	3	13.0682
Hypoxanthine-guanine phosphoribosyltransferase HGPR HGPRase	24480	68534712	16980	3	3	15.1376
INSIG2 membrane protein Insulin induced gene 2	24970	55250700	200861	1	1	4.8889
ITI heavy chain-related protein	1809	1041915	40462	1	2	93.75
Ig gamma-2A chain C region	25220	13399989	62937	1	1	4.4444
IgG receptor FcRN large subunit P51 precursor	40170	56437	15418	1	1	3.0055
Implantation-associated protein precursor IAP	37990	6016303	128379	6	6	14.0299
Importin beta-1 subunit Karyopherin beta-1 subunit Nuclear factor P97	97120	8393610	51498	3	3	4.8
Injury-inducible-protein I-55	58100	24475405	154010	2	2	3.9139
Inosine monophosphate dehydrogenase 2	55800	40018566	231448	1	1	2.7237
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	2	2	1.1107

Insulin receptor precursor IR Insulin receptor subunit alpha Insulin receptor subunit beta	156800	8393621	51500	8	8	6.5799
Insulin-like growth factor binding 4 Insulin-like growth factor binding protein 4	27740	68534170	11776	2	2	11.4173
Insulin-like growth factor-binding protein complex acid labile chain precursor ALS	66810	71896592	11211	2	2	5.141
Integral membrane protein 2B	30310	81883760	284296	5	5	23.6842
Integrin alpha-1 precursor Laminin and collagen receptor VLA-1 CD49a antigen	130800	56494	37168	4	4	3.4746
Integrin beta-1 precursor Fibronectin receptor subunit beta Integrin VLA-4 subunit beta CD29 antigen	88490	8393636	51502	12	12	20.5257
Integrin beta3 subunit	86930	24308466	153869	7	7	10.4193
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
Iodotyrosine 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 Oxalosuccinate decarboxylase IDH NADP(+)-specific ICDH IDP	46730	627999	71492	12	12	44.9275
Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial precursor Isocitric dehydrogenase NAD(+)-specific ICDH	39610	68565369	60501	1	1	3.2787
Isovaleryl-CoA dehydrogenase, mitochondrial precursor IVD	46440	6981112	3955	3	3	9.434
KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 1 Predicted	24550	62821823	272716	4	5	32.5472
Kallistatin	48020	21490001	38912	2	2	6.6194
Keratin K6	3107	554464	66467	1	1	38.4615
Keratin, type II cytoskeletal 5 Cytokeratin-5 CK-5 Keratin-K5	61830	81170669	318877	6	12	15.1042
Keratin, type II cytoskeletal 8	54020	67678416	67836	33	38	70.8075
Ketohexokinase Hepatic fructokinase	32750	62650395	127122	4	4	18.1208
Kidney predominant protein NCU-G1	43870	51948424	169834	2	2	5.4455
Kinesin-like protein KIF15	159600	31745148	166145	3	3	1.444
Kynurenine 3-monooxygenase Kynurenine 3-hydroxylase	54350	81882198	70289	8	8	20.9205
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	3	3	11.5294
L-gulonolactone oxidase	50610	204150	104163	14	14	41.3636
L-lactate dehydrogenase A chain LDH-A LDH muscle subunit LDH-M	36450	8393706	51518	7	29	87.9518
L-serine dehydratase/L-threonine deaminase	38480	21617859	44348	3	3	15.427
L-xylulose reductase XR Dicarboxyl/L-xylulose reductase	25720	50400214	161241	3	3	18.0328
LEA_4 domain containing protein RGD1359600	31470	56090371	205582	1	1	3.663
LIM and SH3 domain protein 1 LASP-1	29970	71122452	19687	1	1	4.943
LIN-7 homolog C LIN-7C mLin7C Mammalian LIN-seven protein 3 MALS-3 Vertebrate LIN 7 homolog 3 Veli-3 protein	21830	59798059	29682	2	3	17.2589
LOC246208 protein	47340	44890246	726783	4	4	15
LOC362065 protein Transmembrane protein	62200	45680888	339290	1	1	2.0333
LOC495749 protein	14550	57702	103229	2	2	18.6992
LOC495860 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 Dri42	35320	45477000	82681	2	2	7.3718
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	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 Carboxyesterase ES-3 pI 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	61556986	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	1.3684
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	1.8576
Long-chain specific acyl-CoA dehydrogenase, mitochondrial precursor LCAD	47870	6978431	3599	13	13	30.6977
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	85756	38	42	67.8112
Long-chain-fatty-acid--CoA ligase 4 Long-chain acyl-CoA synthetase 4 LACS 4	74330	6016483	22152	4	4	8.9552
Long-chain-fatty-acid--CoA ligase 5 Long-chain acyl-CoA synthetase 5 LACS 5	76400	6016484	60485	29	33	57.8331
Long-chain-fatty-acid--CoA ligase 6	78180	417242	44475	3	3	3.7303
Low molecular mass ubiquinone-binding protein	9849	68341999	311481	1	1	15.8537
Low-density lipoprotein receptor precursor LDL receptor	96620	56570	106673	2	2	3.2992
Lupus La protein homolog La ribonucleoprotein La autoantigen homolog	47780	729919	37247	2	2	6.747
LysM, putative peptidoglycan-binding, domain containing	33700	57527470	204667	1	1	4.6667
Lysosomal acid lipase/cholesteryl ester hydrolase precursor LAL Acid cholesteryl ester hydrolase Sterol esterase Lipase A Cholesteryl esterase	45190	9653291	72321	1	1	3.2746
Lysosomal acid phosphatase precursor LAP	48320	8392842	144356	1	1	2.8369
Lysosome-associated membrane glycoprotein 1 precursor	43970	6981144	3967	5	5	14.742
Lysosome-associated membrane glycoprotein 2 precursor	43130	205169	44157	4	4	11.9593
Lysozyme	16730	7428180	39196	1	1	12.8378
Lysyl-tRNA synthetase	71620	55741637	269157	1	1	1.7572
MAL2A Mal, T-cell differentiation protein 2	19200	77157795	166255	1	1	6.25
MHC class II transactivator type I	127300	9931450	42953	1	1	0.69384
MOBILFERRIN	1917	300525	182793	1	1	41.1765
MYB binding protein 1a	144700	7514041	78121	3	3	3.3673
Macrophage migration inhibitory factor	12480	7514124	37207	3	3	23.4783
Major urinary protein precursor	20740	992637	69402	1	15	71.2707
Malate dehydrogenase, cytoplasmic Cytosolic malate dehydrogenase	36480	81861572	118982	9	9	36.5269
Malate dehydrogenase, mitochondrial	35680	42476181	339913	17	17	63.3136
Maleylacetoacetate isomerase MAAI Glutathione S-transferase zeta 1 GSTZ1-1	2943	11133293	36062	1	1	39.2857
Mannose 6-phosphate/insulin-like growth factor II receptor	273400	6981078	3946	24	24	12.6664
Mannose-binding protein A precursor	16550	1942287	19138	1	1	8.0537
Mannosidase 2, alpha B1	114300	40786505	338661	3	3	3.7661
Mannosyl-oligosaccharide glucosidase Glycoprotein-processing glucosidase I	91870	48427849	51409	29	29	46.8825
Medium-chain specific acyl-CoA dehydrogenase, mitochondrial precursor MCAD	46560	8392833	11499	4	4	15.9145
Membrane-associated progesterone receptor component 2	23400	62900631	274611	5	7	37.3272
Membrane-bound aminopeptidase P X-prolyl aminopeptidase (Aminopeptidase P) 2, membrane-bound	76080	49258142	140638	3	3	7.8635
Merlin Moesin-ezrin-radixin-like protein Neurofibromin-2 Schwannomin	68710	32363191	124359	1	1	2.7304
Mesenchymal stem cell protein DSCD75	23750	56090359	259160	1	1	5.314
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 Malonate-semialdehyde dehydrogenase [acylating]	57810	400269	37213	11	11	37.3832
Microsomal dipeptidase precursor	45520	47938984	23872	7	7	31.2195

Microsomal signal peptidase 18 kDa subunit SPase 18 kDa subunit SPC18 Endopeptidase SP18 SEC11-like 1 Sid 2895	20630	61889101	3224	7	7	44.6927
Mid-1-related chloride channel 2	57430	17736804	16130	2	2	7.2978
Migration-inducing protein 5 Ras-related C3 botulinum toxin substrate 1, isoform Rac1	21450	54607147	111212	4	6	39.0625
Mitochondrial 2-oxoglutarate/malate carrier protein	34150	1580888	77688	2	8	39.4904
Mitochondrial antiviral signaling protein Interferon-beta promoter stimulator protein 1 IPS-1 Virus-induced signaling adapter	53800	81170680	215394	2	2	6.1144
Mitochondrial carnitine/acylcarnitine carrier protein Carnitine/acylcarnitine translocase CAC Solute carrier family 25 member 20	33150	2497984	63382	8	8	27.907
Mitochondrial carrier homolog 2	31460	27702070	156740	11	11	51.4184
Mitochondrial dicarboxylate carrier Solute carrier family 25 (Mitochondrial carrier; dicarboxylate transporter), member 10	31450	51859428	140375	10	10	44.7552
Mitochondrial import inner membrane translocase subunit TIM13	10460	59800393	77128	4	4	36.8421
Mitochondrial import inner membrane translocase subunit TIM8 A Deafness dystonia protein 1 homolog	11040	5107153	12056	1	1	11.3402
Mitochondrial protein, 18 kDa	18370	55741522	220289	1	1	7.8313
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	3.2787
Mitogen-activated protein kinase kinase 1-interacting protein 1	13580	81883452	237355	1	1	8.871
Mitogen-activated protein-binding protein-interacting protein Late endosomal/lysosomal Mp1-interacting protein p14	13480	27692916	12815	3	3	36
Monocarboxylate transporter 1 MCT 1	53240	6981542	75090	4	4	9.7166
Monoclonal Antibody Against The Main Immunog	23340	6730147	73388	2	2	12.6761
Monocyte differentiation antigen CD14 precursor	40050	38197682	35920	1	1	2.957
Monoglyceride lipase MGL	33500	79158553	76956	5	5	23.4323
Mpg-1 protein	73330	5052048	176262	3	3	6.0423
Multidrug resistance-associated protein 6 ATP-binding cassette sub-family C member 6 MRP-like protein 1 MLP-1	165000	7514016	37180	4	4	3.1957
Multiple coagulation factor deficiency protein 2 homolog precursor Neural stem cell-derived neuronal survival protein	16150	49036094	216613	4	4	44.8276
Myelin basic protein S	21500	70166245	3277	1	1	7.1795
Myosin I heavy chain	118100	480659	6153	29	29	37.5486
Myosin Ib Myosin I alpha MMI-alpha MMIa Myosin heavy chain myr 1	131900	56733	63042	49	50	52.2007
Myosin Id Myosin heavy chain myr 4	116100	6981242	75002	37	37	42.8429
Myosin Ie Myosin heavy chain myr 3	126800	693995	105842	8	9	9.8464
Myosin VIIA	251100	23618899	217296	1	1	0.45935
Myosin, light polypeptide 6, alkali, smooth muscle and non-muscle, isoform 2	16960	34862212	69375	7	8	55.6291
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 glucosaminyl) 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 Dithiolethione-inducible gene 1 protein D3T-inducible gene 1 protein DIG-1	35720	6012071	1678	9	9	37.69
NADPH--cytochrome P450 reductase	76930	205660	44210	1	37	62.5369
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	6	13	68.5083
Na(+)/H(+) exchange regulatory co-factor NHE-RF2	34910	13925523	78016	1	1	4.4444
Nascent polypeptide-associated complex subunit alpha Alpha-NAC Alpha-NAC/1.9.2	23380	27710456	74102	5	5	32.5581
Nck-associated protein 1 NAP 1 p125Nap1 Membrane-associated protein HEM-2	128900	1708980	67879	11	11	12.766
Ndufa10 protein	40490	62531217	199168	11	11	45.3521
Neighbor of Cox4 Predicted	23410	62665359	215440	5	5	33.3333
Nesprin-1	325100	19705491	161237	2	2	0.66949
Neural-cadherin precursor N-cadherin Cadherin-2	99690	3983131	63008	11	11	20.5298
Neuronal myosin heavy chain	231500	111999	11249	10	49	27.8639

Nicastrin precursor	78400	37081094	116574	4	4	9.1808
Nicotinate phosphoribosyltransferase-like protein	58560	46485387	722226	1	1	3.5316
Non-POU domain-containing octamer-binding protein NonO protein	54930	67460593	219030	2	2	7.1429
Non-muscle caldesmon CDM L-caldesmon	60580	6978589	3674	1	1	2.2599
Nuclear pore membrane glycoprotein 210 precursor POM210 Nuclear pore protein gp210	204200	92557	111676	2	2	1.4846
Nucleobindin 2 precursor	50090	8515422	3157	17	18	51.1905
Nucleobindin-1 precursor CALNUC Bone 63 kDa calcium-binding protein	53510	871525	60416	36	37	77.7778
Nucleophosmin NPM Nucleolar phosphoprotein B23 Numatrin Nucleolar protein NO38	32560	7242160	44225	4	4	8.9041
Nucleoside diphosphate kinase B	17280	55926145	69495	6	6	53.2895
Nucleotide exchange factor SIL1 precursor	52350	81892269	318887	2	2	4.9462
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:I830081B01 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 Aip-5 Glutamate transporter EAAC1-interacting protein GTRAP3-18 Prenylated Rab acceptor protein 2 Protein JWa	21550	57012987	54281	1	1	10.6383
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	62654450	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 TCP1) 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 DKFZP586A0522 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	251068	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	27668745	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 slingshot-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 tetratricopeptide 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
Peptidylprolyl 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
Phospholemman 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 Phytanic acid oxidase	38590	6539658	55437	11	11	34.6154
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-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	21	21	45.6172
Polypeptide N-acetylgalactosaminyltransferase 11 Protein-UDP acetylgalactosaminyltransferase 11 UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase 1 Polypeptide GalNAc transferase 11 GalNAc-T11 pp-GaNTase 11	69040	51315700	319029	7	7	16.9408
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 kDa subunit homolog 38 kDa mitochondrial outer membrane protein OM38	37920	81864912	726780	3	3	16.8975
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: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	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 gamma 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	81885839	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 58 kDa microsomal protein p58 ERp57 HIP-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 protein Synaptic dynamin-associated protein II Syndapin Syndapin-II SdplI	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 c regenerating liver 1 PRL-1 PTP(CAAXI)	19820	68566099	4701	1	1	8.6705
Protein-glutamine gamma-glutamyltransferase K Transglutaminase K TGase K TGK 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-acyltransferase OACT5 O-acyltransferase 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 Epac2	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 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	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:I830091I21 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:I830025E19 product:ribosomal protein S24, full insert sequence Rps24 protein	15420	57858	4843	4	4	29.3233
Ribosomal protein S27 Metallopanstimulin 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:I920028E16 product:ribosomal protein S6, full insert sequence Blastocyst blastocyst cDNA, RIKEN full-length enriched library, clone:I1C0007K02 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:I920079C04 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:I920030G04 product:ribosomal protein L36a, full insert sequence Bone marrow macrophage cDNA, RIKEN full-length enriched library, clone:I830174F05 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:I730062K18 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 Squalene transfer protein	46170	21542226	60562	6	8	28.2878
SH3P13 SH3 domain protein 2 C1	35310	7109256	75738	1	1	2.5641
SIRR-1 precursor	44730	425789	100550	1	1	1.9512
SP120	87750	624918	140634	4	4	8.396
SWISS-PROT:P09811 REFSEQ_NP:NP_071604 ENSEMBL:ENSRNOP00000009183 Glycogen phosphorylase, liver form	97480	585688	104192	8	8	13.0588
SWISS-PROT:P12368 cAMP-dependent protein kinase type II-alpha regulatory subunit	41980	206150	168209	1	1	3.5135
SWISS-PROT:P24329 TREMBL:Q5I0D4 REFSEQ_NP:NP_036940 ENSEMBL:ENSRNOP00000000202 Thiosulfate sulfurtransferase	33410	83305808	299568	14	14	43.771
SWISS-PROT:P32755 TREMBL:O88655 REFSEQ_NP:NP_058929 ENSEMBL:ENSRNOP00000001809 4-hydroxyphenylpyruvate dioxygenase	45110	8393557	51489	10	10	35.369
SWISS-PROT:P38659 TREMBL:Q6P7S5 REFSEQ_NP:NP_446301 ENSEMBL:ENSRNOP00000008728 Protein disulfide-isomerase A4 precursor	72810	729436	60584	3	52	64.3857
SWISS-PROT:Q07936-1 TREMBL:Q8R513 ENSEMBL:ENSRNOP00000013988 REFSEQ:NP_063970 annexin A2	38680	9845234	109734	12	12	40.118
SWISS-PROT:Q62812 TREMBL:Q62704 REFSEQ_NP:NP_037326 ENSEMBL:ENSRNOP00000007398 Myosin-9	226300	967249	75000	43	84	45.589
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	109700	57303	84180	32	32	37.5125
Sarcosine dehydrogenase, mitochondrial precursor SarDH	101400	52000744	85749	1	1	2.7203
Scavenger receptor class B member 1 SRB1 SR-BI	56960	49904285	38864	6	6	18.2711
Sec1 family domain-containing protein 1 Syntaxin-binding protein 1-like 2 Vesicle transport-related protein Ra410 Sly1p	72260	9507019	47254	15	15	37.2057
Sec22 homolog	28540	16924008	35326	6	6	27.9528
Sec61 alpha subunit homolog	52260	63101555	75284	12	12	33.1933
Secreted phosphoprotein 24 precursor Spp-24 Secreted phosphoprotein 2	20690	2498940	43395	5	5	29.4444
Secretory carrier membrane protein 2	34340	10764633	150292	2	2	10.356
Secretory carrier membrane protein 3	38370	34857962	169836	5	5	19.1977
Secretory carrier-associated membrane protein 1 Secretory carrier membrane protein 1 SCAMP 37	38000	487057	46139	5	5	21.5976
Sel1 (suppressor of lin-12) 1 homolog	68660	29336095	213126	10	10	26.9919
Selenium binding protein 2	52530	49256633	111519	4	4	11.0169
Selenoprotein P precursor	41580	47939025	1271	1	1	5.7143
Sepiapterin reductase	28130	34856334	31392	2	2	13.7405
Septin-7 CDC10 protein homolog	50510	9789715	167832	4	4	13.7615
Septin-9 Eseptin eighth septin Septin-like protein SLP	63790	6090881	70797	2	2	4.4326
Sequestosome-1 Ubiquitin-binding protein p62 Protein kinase C-zeta-interacting protein PKC-zeta-interacting protein	47680	77416574	19107	1	1	3.6446
Serine (Or cysteine) proteinase inhibitor, clade D, member 1	54550	60551378	68739	2	2	5.8455
Serine (Or cysteine) proteinase inhibitor, clade F, member 2 Predicted	54890	58865362	341343	1	1	2.6477

Serine (Or cysteine) proteinase inhibitor, clade G (C1 inhibitor), member 1, Angioedema, hereditary	55610	40018558	222317	4	4	13.8889
Serine protease hepsin Serine protease hepsin non-catalytic chain Serine protease hepsin catalytic chain	44930	8393560	51490	1	1	2.6442
Serine protease inhibitor, Kunitz type 2	21310	40018550	319145	1	1	6.2176
Serine--pyruvate aminotransferase, mitochondrial precursor SPT Alanine--glyoxylate aminotransferase AGT	45830	66655	31393	4	4	12.5604
Serine/threonine protein phosphatase	35580	8394021	41475	3	3	16.1812
Serine/threonine protein phosphatase PP1-beta catalytic subunit	37190	999343	4597	6	6	23.2416
Serine/threonine-protein kinase PLK1 Polo-like kinase 1 PLK-1	68310	497994	12071	1	1	2.4876
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	1	1	0.80275
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	1	1	3.0905
Serotransferrin precursor Transferrin Siderophilin Beta-1-metal-binding globulin	76360	6175089	37301	1	43	54.8711
Serpinh1 protein	46560	55824765	280024	7	7	25.1799
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 Opioid 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 MtSSB 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+I6	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) (Ip) (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 Sulfate/carbonate antiporter	75450	431453	104202	3	3	6.9701
Sulfated glycoprotein 1 precursor	61120	92782	75055	5	5	11.9134
Sulfite oxidase	54350	40254758	318917	6	6	18.4426
Sulfotransferase 1C1 N-hydroxyarylamine sulfotransferase HAST-I	35760	543420	78152	8	8	34.8684
Superoxide dismutase [Cu-Zn]	16020	1213217	35188	4	4	32.2581
Superoxide dismutase [Mn], mitochondrial precursor	24680	56691	111692	6	6	35.5856
Synaptic glycoprotein SC2	36120	37589607	33179	12	12	30.8442
Synaptogyrin-1 p29	25670	9507167	47308	1	1	5.1282
Synaptotjanin 2 binding protein	22560	5106930	36071	2	2	12.6214
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	5.4475
Synaptotagmin III	63340	14210270	19552	2	2	3.7415
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
TORID	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:XP_579556 ENSEMBL:ENSRNOP00000004864 Flavin containing monooxygenase 3	59980	62659523	246480	24	30	69.4915
TREMBL:Q6MG49;Q9WTN8 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:Q9R0T3;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	7.8236
Tax_Id=10116 Aldehyde dehydrogenase family 1, subfamily A4	54560	91935	83139	1	3	7.984
Tax_Id=10116 Aldo-keto reductase family 1, member A1	36510	399660	37172	8	8	32.3077
Tax_Id=10116 Aldolase A	39350	6978487	3624	4	5	12.6374
Tax_Id=10116 Amine oxidase (flavin-containing)	58390	91974	74982	22	22	54.2308
Tax_Id=10116 Annexin 1	38830	6978501	3631	6	7	28.6127
Tax_Id=10116 ArylAcetAmide deAcetylase	45690	8347733	5958	11	11	36.4322
Tax_Id=10116 Brain lipid Binding protein	14860	476082	71698	3	3	28.0303
Tax_Id=10116 CD36 antigen (collagen type I receptor, thrombospondin receptor)-like 2	54090	38197654	157248	8	8	26.569
Tax_Id=10116 Catalase	59760	6978607	3681	24	24	58.8235
Tax_Id=10116 Coatomer protein Complex, subunit beta 2 (beta prime)	102600	3023522	35931	40	40	60.442
Tax_Id=10116 Cofilin 1	18530	8393101	87332	4	6	48.7952
Tax_Id=10116 Complement Component 5	134400	34853897	205903	1	1	1.1745
Tax_Id=10116 Cysteine and glycine-rich protein 1	20610	8393206	51411	2	2	12.9534
Tax_Id=10116 D-beta-hydroxybutyrate dehydrogenase, mitochondrial precursor	38350	482346	141497	17	17	58.1395
Tax_Id=10116 D-dopachrome tautomerase	13130	895882	29986	7	7	76.2712
Tax_Id=10116 DEAD (Asp-Glu-Ala-Asp) box polypeptide 1	97470	34863163	240056	24	24	35.3075
Tax_Id=10116 Diazepam binding inhibitor	10030	54261671	4320	4	4	52.8736
Tax_Id=10116 Dihydrodipicolinate decarboxylase chain transacylase E2	53460	34859889	232730	1	1	2.8926
Tax_Id=10116 Dimethylarginine Dimethylaminohydroxylase 1	31430	6831527	104206	3	3	18.2456
Tax_Id=10116 Ensembl_locations(Chr-bp):1-95678925 ribosomal protein L13A	23480	548747	106718	14	14	46.798
Tax_Id=10116 Ensembl_locations(Chr-bp):10-40398095 annexin VI	75750	763181	127131	45	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	17.3469
Tax_Id=10116 Ensembl_locations(Chr-bp):11-64934053 similar to homogentisate 1, 2-dioxygenase	59620	34869194	303719	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	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	19.3548
Tax_Id=10116 Ensembl_locations(Chr-bp):14-37304188 similar to RIKEN cDNA 6030432N09	27020	34877284	194680	2	2	11.8852
Tax_Id=10116 Ensembl_locations(Chr-bp):14-70683054 similar to leucine aminopeptidase	64550	34878080	204743	2	2	5.1581
Tax_Id=10116 Ensembl_locations(Chr-bp):14-77957500 similar to Syntaxin 18	49850	34878414	291113	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	9.7969
Tax_Id=10116 Ensembl_locations(Chr-bp):15-56616580 similar to component of oligomeric golgi complex 2	72190	34874501	274159	7	7	15.109
Tax_Id=10116 Ensembl_locations(Chr-bp):16-1479259 similar to annexin A11	72140	34876896	205775	2	2	3.4226
Tax_Id=10116 Ensembl_locations(Chr-bp):16-73342360 similar to ankyrin	186300	34879099	195573	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	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 methylcrotonoyl-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	69538	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 Integrln, 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), Methenyltetrahydrofolate 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 PhosPhoglucomutase 1	61400	8393951	51568	8	8	25.9786
Tax_Id=10116 PhosPhoribosylaminoimidazole carboxylase, PhosPhoribosylaminoibosylaminoimidazole 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-acyltranSferaSe 2	31100	34853099	274486	4	4	23.0216
Tax_Id=10116 Similar to 1700013L23Rik 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 Subun (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 - mouS (fragment)	374300	34863265	267292	1	1	0.26178
Tax_Id=10116 Similar to Alpha enolaSe (2-phoSpho-D-glycerate hydro-lyaSe) (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 IIx (MannoSyl-oligoSaccharide 1,3-1,6-alpha-mannoSidaSe) (MAN IIx) (MannoSidaSe alpha claSS 2A member 2)	133000	34857364	209202	1	3	2.294
Tax_Id=10116 Similar to Amyloid beta A4 precurSor 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	2.4845
Tax_Id=10116 Similar to B aggreSSive lymphoma	106500	34869208	269562	4	4	6.9286
Tax_Id=10116 Similar to BC013491 protein	76140	34856101	235741	1	1	1.0294
Tax_Id=10116 Similar to Band 4.1-like protein 5	114300	34879408	300797	2	3	3.0978
Tax_Id=10116 Similar to CAD protein	245800	34862992	315461	5	7	3.6526
Tax_Id=10116 Similar to CENTROMERIC PROTEIN E (CENP-E PROTEIN)	313000	34860597	241018	1	1	0.25679
Tax_Id=10116 Similar to CG11388-PA	36250	34869404	241377	1	1	5.7402
Tax_Id=10116 Similar to CG17660-PA	52310	34857630	293554	2	2	6.5076
Tax_Id=10116 Similar to CG2144-PA	100600	34875840	237985	3	3	3.9301
Tax_Id=10116 Similar to CG31613-PA	101500	34876364	249977	6	9	10.4009
Tax_Id=10116 Similar to CG32774-PA	79590	34876775	221370	2	2	2.3192
Tax_Id=10116 Similar to CG33130-PA	132700	34853057	208493	1	1	1.0842
Tax_Id=10116 Similar to CG9346-PA	113900	34865480	232164	2	2	2.0263
Tax_Id=10116 Similar to CMP-Sialic acid tranSporter	36550	34867231	260011	1	1	3.5608
Tax_Id=10116 Similar to CUB and SuShi multiple domainS 3	213400	34866475	195940	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	24.9725
Tax_Id=10116 Similar to Cgn-pending protein	159200	34858031	242726	1	5	3.0561
Tax_Id=10116 Similar to Coatomer gamma-2 Subunit (Gamma-2 coat protein) (Gamma-2 COP)	84430	34855105	309005	14	16	30.429
Tax_Id=10116 Similar to Coatomer zeta-1 Subunit (Zeta-coat protein) (Zeta-1 COP) (CGI-120) (HSPC181)	23840	34868640	236737	7	7	46.4115
Tax_Id=10116 Similar to Complement C5 precurSor (Hemolytic complement)	42190	34853846	242533	1	1	4.244
Tax_Id=10116 Similar to Component of oligomeric golgi complex 4	91040	34851754	245295	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	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	11.9522
Tax_Id=10116 Similar to ConServed oligomeric Golgi complex component 8	70760	34851657	222168	5	5	12.776
Tax_Id=10116 Similar to Cox7a2I protein	12650	27716471	268354	1	1	10.6195
Tax_Id=10116 Similar to Cux/CDP(1B1)	157000	34873366	289275	2	21	14.2658
Tax_Id=10116 Similar to D-glucuronyl C5-epimeraSe	93260	34863951	299013	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	1.937
Tax_Id=10116 Similar to DEAH (ASp-Glu-Ala-HiS) box polypeptide 29	145700	34854165	249374	2	2	1.926
Tax_Id=10116 Similar to DNA Segment, Chr 12, ERATO Doi 551, expreSSed	130300	34865806	300896	1	1	0.94017
Tax_Id=10116 Similar to DNA-directed RNA polymeraSe II largeSt Subunit (RPB1)	197600	34871645	202233	1	1	0.61694
Tax_Id=10116 Similar to DeSmoplakin (DP) (250/210 kD paraneoplaStic pemphiguS antigen)	327800	34875216	219502	3	3	1.8362
Tax_Id=10116 Similar to Delta(14)-Sterol reductaSe (C-1 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	15.7518
Tax_Id=10116 Similar to DnaJ (HSp40) homolog, Subfamily B, member 12	40330	34882652	201409	5	5	20
Tax_Id=10116 Similar to ENSANGP00000013261	15620	27689183	197176	1	1	7.2993
Tax_Id=10116 Similar to Epithelial protein loSt in neoplaSm (mEPLIN)	94450	34868179	277610	14	14	22.7433
Tax_Id=10116 Similar to FERM, RhoGEF and pleckStrin domain protein 2	179800	34877686	293497	6	6	5.5556
Tax_Id=10116 Similar to FERM, RhoGEF, and pleckStrin domain protein 1	23830	34876611	304176	1	1	6.422
Tax_Id=10116 Similar to FLJ00343 protein	279400	34881882	282403	5	6	3.0845
Tax_Id=10116 Similar to FLJ00354 protein	155900	34861517	210125	1	2	1.1561
Tax_Id=10116 Similar to FYVE and coiled-coil domain containing 1	174100	34866719	308794	2	2	1.0975
Tax_Id=10116 Similar to Farp1 protein	195200	34876071	216529	5	5	3.303
Tax_Id=10116 Similar to G protein-coupled receptor 108	59750	34853540	214715	2	2	5.2731
Tax_Id=10116 Similar to GE36	76150	34880541	272300	1	1	1.8895
Tax_Id=10116 Similar to GTP binding protein	36860	34859732	225450	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	12.5926
Tax_Id=10116 Similar to Golgi phoSphoprotein 2	54350	34873592	231145	10	10	34.9896
Tax_Id=10116 Similar to Herc2	542900	34856238	254063	1	1	0.24125
Tax_Id=10116 Similar to Hypothetical protein 5031404N19	336600	34867996	239621	1	1	0.36089
Tax_Id=10116 Similar to Hypothetical protein 9030012M21	37150	34875719	205153	1	1	3.5608
Tax_Id=10116 Similar to Hypothetical protein FLJ35794	51380	27708530	166638	1	1	2.4775
Tax_Id=10116 Similar to Hypothetical protein KIAA0152	26440	34872654	268830	8	8	34.8548
Tax_Id=10116 Similar to Hypothetical protein KIAA0233	237700	34932058	265857	1	1	0.43394
Tax_Id=10116 Similar to IQ motif containing GTPaSe activating protein 1	193900	34857388	242453	2	4	3.4604
Tax_Id=10116 Similar to Integrin alpha 5 (fibronectin receptor alpha)	115500	34868649	259355	3	3	3.7843
Tax_Id=10116 Similar to Integrin beta-2 precuSor (Cell Surface adheSion glycoproteinS LFA-1/CR3/P150,95 beta Subunit) (CD18) (Complement receptor C3 beta-Subunit)	84530	34852369	241188	1	1	2.2164
Tax_Id=10116 Similar to KDEL containing protein 1	60890	34863399	261916	1	1	2.2814
Tax_Id=10116 Similar to KIAA0090 protein	91240	34872226	302513	26	26	39.2109
Tax_Id=10116 Similar to KIAA0315	211600	34867650	248510	16	16	12.11
Tax_Id=10116 Similar to KIAA0316 protein	140900	34879922	244528	1	1	1.0133
Tax_Id=10116 Similar to KIAA0342 protein	333800	34866451	266038	1	1	0.344
Tax_Id=10116 Similar to KIAA0372 gene product	169500	34852783	312697	8	8	7.7982
Tax_Id=10116 Similar to KIAA0635 gene product	147000	34877224	224112	2	2	1.1058
Tax_Id=10116 Similar to KIAA0695 protein	71450	34879447	314767	1	1	2.0934
Tax_Id=10116 Similar to KIAA0903-like protein	120900	34879170	275605	1	1	1.7658
Tax_Id=10116 Similar to KIAA0963 protein	162200	34862323	279597	1	1	0.68306
Tax_Id=10116 Similar to KIAA0970 protein	135200	34874472	295665	14	14	16.3934
Tax_Id=10116 Similar to KIAA0980 protein	221500	34858955	230119	3	3	2.2472
Tax_Id=10116 Similar to KIAA1055 protein	108500	34865572	211597	2	2	1.5856
Tax_Id=10116 Similar to KIAA1208 protein	154100	34864701	229899	5	5	4.3478
Tax_Id=10116 Similar to KIAA1407 protein	75980	34869160	295453	1	1	1.059
Tax_Id=10116 Similar to KIAA1414 protein	184500	34861977	207796	1	1	0.99707
Tax_Id=10116 Similar to KIAA1453 protein	119600	34875569	239514	1	1	0.73126
Tax_Id=10116 Similar to KIAA1509 protein	212500	34867549	239536	2	2	0.91104
Tax_Id=10116 Similar to KIAA1630 protein	148300	34876831	315956	1	1	1.1646
Tax_Id=10116 Similar to KIAA1724 protein	43370	34863046	197285	2	2	8.6842
Tax_Id=10116 Similar to KIAA1940 protein	82950	34856348	273209	1	1	1.4398
Tax_Id=10116 Similar to KIF13A	204000	34874048	266483	2	2	1.1501
Tax_Id=10116 Similar to Kinetochore-aSSociated protein 1 (Rough deal homolog) (hRod) (HSROD) (Rod)	222900	34872331	265212	1	1	0.61287
Tax_Id=10116 Similar to Leukotriene A-4 hydrolaSe (LTA-4 hydrolaSe) (Leukotriene A(4) hydrolaSe)	93570	34864937	286024	1	1	1.8116
Tax_Id=10116 Similar to MaltaSe-glucoamylaSe, inteStinal	494700	34855581	199085	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 claSS 1C member 1) (HMIC)	51490	34872059	315202	2	2	5.4945
Tax_Id=10116 Similar to Meningioma expreSSed antigen 6 (coiled-coil proline-rich)	57130	34865266	286300	3	3	8.9109
Tax_Id=10116 Similar to Myl9 protein	34570	34860268	240507	3	8	37.7419
Tax_Id=10116 Similar to Mylk protein	73330	34869218	268038	1	1	1.3867
Tax_Id=10116 Similar to MyoSin VI	167000	34865321	261550	10	10	9.022
Tax_Id=10116 Similar to N-acetylglucoSaminyltraSnferaSe IVb	71740	34870693	194890	15	15	34.4
Tax_Id=10116 Similar to NOD3	118900	34868757	253799	2	2	2.2018
Tax_Id=10116 Similar to Nebulette (Actin-binding Z-diSk protein)	121800	34877348	276942	1	1	1.4995
Tax_Id=10116 Similar to Nedd4 WW binding protein 4	32550	34860870	317802	1	1	3.413
Tax_Id=10116 Similar to Nit protein 2	34190	34868007	213226	8	8	26.2295
Tax_Id=10116 Similar to OligoSaccharyl tranSferaSe 3 CG7748-PA	141400	34866419	214259	2	7	7.2395
Tax_Id=10116 Similar to P3 protein	44450	27689253	262782	3	3	7.9602
Tax_Id=10116 Similar to PALS2-beta Splice variant	67230	34855859	233877	4	4	9.6506
Tax_Id=10116 Similar to POLYPOSIS LOCUS PROTEIN 1 HOMOLOG (TB2 PROTEIN HOMOLOG) (GP106)	21070	34878680	252129	4	4	16.2162
Tax_Id=10116 Similar to PTB-aSSociated Splicing factor	65140	34871066	310879	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	4.4771
Tax_Id=10116 Similar to Potential phoSpholipid-tranSporting ATPaSe IG (ATPaSe claSS I type 11C) (ATPaSe IQ)	131400	34881712	292511	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	7.218
Tax_Id=10116 Similar to Prolactin regulatory element-binding protein	45370	34863006	293599	5	5	13.6691
Tax_Id=10116 Similar to Protein Njmu-R1	44430	34872893	315828	1	1	4.0712
Tax_Id=10116 Similar to Protein diSulfide iSomeraSe-related	89320	34869214	276048	25	25	41.5929
Tax_Id=10116 Similar to Protein tranSport protein Sec24 (SEC24-related protein A)	105700	34870707	295725	17	17	22.9885
Tax_Id=10116 Similar to Protein tranSport protein Sec24D (SEC24-related protein D)	110300	34859959	219262	7	7	9.7126
Tax_Id=10116 Similar to RAB22, member RAS oncogene family	23730	34860889	296032	4	4	21.5962
Tax_Id=10116 Similar to RIKEN cDNA 0610008C08	18820	34880585	277830	2	2	15.8537
Tax_Id=10116 Similar to RIKEN cDNA 0610040B21	27040	34870174	239547	7	7	33.4694
Tax_Id=10116 Similar to RIKEN cDNA 0610041L09	37560	34855114	227312	2	2	7.8788
Tax_Id=10116 Similar to RIKEN cDNA 1110025H10	26400	34871118	269702	2	2	13.75
Tax_Id=10116 Similar to RIKEN cDNA 1110031I02	36810	34875673	300976	1	1	3.0581
Tax_Id=10116 Similar to RIKEN cDNA 1110055L24	27770	34854713	201498	1	1	7.6305
Tax_Id=10116 Similar to RIKEN cDNA 1200014J11	80090	34872727	249723	1	1	1.5603
Tax_Id=10116 Similar to RIKEN cDNA 1300006L01	34660	34865173	223033	5	5	16.4087
Tax_Id=10116 Similar to RIKEN cDNA 1300011P19	69740	34863012	258910	3	3	5.8085
Tax_Id=10116 Similar to RIKEN cDNA 1300013G12	59080	34879692	246703	2	2	6.5056
Tax_Id=10116 Similar to RIKEN cDNA 1300014E15	74920	34877442	203301	1	1	1.9288
Tax_Id=10116 Similar to RIKEN cDNA 1300017J02	74750	34865830	304054	17	18	32.5037
Tax_Id=10116 Similar to RIKEN cDNA 1700034M03 gene	122500	34854321	261953	1	1	0.94073
Tax_Id=10116 Similar to RIKEN cDNA 1810063B07 gene	31470	34868966	280249	2	2	11.5789
Tax_Id=10116 Similar to RIKEN cDNA 2010321J07	62770	27694215	169892	11	13	33.4545
Tax_Id=10116 Similar to RIKEN cDNA 2210404D11	57560	34873697	262247	4	4	16.2933
Tax_Id=10116 Similar to RIKEN cDNA 2310008M10	19420	34860558	316149	2	2	12.069
Tax_Id=10116 Similar to RIKEN cDNA 2310050P13	55910	34859909	271576	3	3	8.9286
Tax_Id=10116 Similar to RIKEN cDNA 2310079N02	20810	34851911	222133	3	3	26.0417
Tax_Id=10116 Similar to RIKEN cDNA 2410011G03	23970	34864767	297605	4	4	25.2427
Tax_Id=10116 Similar to RIKEN cDNA 2610020H15	71060	34872958	298062	1	1	1.9048
Tax_Id=10116 Similar to RIKEN cDNA 2610207I16	122600	34868438	250916	1	1	1.6901
Tax_Id=10116 Similar to RIKEN cDNA 2610318K02	17320	34856650	238667	2	2	18.125
Tax_Id=10116 Similar to RIKEN cDNA 2810025M15	71590	34880767	272641	1	1	4.0971
Tax_Id=10116 Similar to RIKEN cDNA 2810405J04	61290	34862460	198258	3	3	7.3214
Tax_Id=10116 Similar to RIKEN cDNA 3110038B19	46280	34879556	235525	9	9	38.149
Tax_Id=10116 Similar to RIKEN cDNA 4632417N05	35570	34851797	239422	1	1	6.4815
Tax_Id=10116 Similar to RIKEN cDNA 4732474A20 gene	70120	34862810	190227	1	3	5.7566
Tax_Id=10116 Similar to RIKEN cDNA 4921526O06	68350	34875183	247534	3	3	3.0744
Tax_Id=10116 Similar to RIKEN cDNA 4931400A14	231900	34878255	296181	2	2	0.9704
Tax_Id=10116 Similar to RIKEN cDNA 4932408F18	164100	34867309	293100	1	1	1.2943
Tax_Id=10116 Similar to RIKEN cDNA 4933412D19	51730	34858091	273635	1	1	2.6608
Tax_Id=10116 Similar to RIKEN cDNA 5630401D24	81090	34880803	213507	1	1	1.6667
Tax_Id=10116 Similar to RIKEN cDNA 5730406I15	24970	27678066	216144	8	8	46.9027
Tax_Id=10116 Similar to RIKEN cDNA 5730469M10	39980	34877094	208161	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 9630046K23	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-acetyleSteraSe	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-I interacting protein 5	183400	34862191	316025	1	1	0.72115
Tax_Id=10116 Similar to Tetratricopeptide repeat protein (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-acetylgalactoSaminyltranSferaSe 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 aSpartly 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 precurSor	357700	34877775	307227	3	3	1.1522
Tax_Id=10116 Similar to alpha glucoSidaSe 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	34880938	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 cyokeratin	47590	34855041	245216	4	18	45.1537
Tax_Id=10116 Similar to dJ14N1.2 (novel S-100/ICaBP 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 estradiol 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, Stomatin	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 translation initiation factor 4G I	175000	34869741	239406	6	6	4.2112
Tax_Id=10116 Similar to exostosin (multiple) 2	93370	34856569	247469	2	2	3.4063
Tax_Id=10116 Similar to expressed Sequence AI788959	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 D4Ertd765e	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	2.1635
Tax_Id=10116 Similar to hypothetical protein FLJ30373	29880	34855399	229721	1	1	2.9197
Tax_Id=10116 Similar to hypothetical protein FLJ30596	61060	34854388	283019	1	1	2.5641
Tax_Id=10116 Similar to hypothetical protein FLJ31657	64050	34855501	253349	1	1	2.385
Tax_Id=10116 Similar to hypothetical protein MGC15523	132100	34875626	304037	12	12	14.4608
Tax_Id=10116 Similar to hypothetical protein MGC23920	24660	34869196	243905	4	4	22.87
Tax_Id=10116 Similar to hypothetical protein MGC26706	19680	34880064	228294	4	4	28.6585
Tax_Id=10116 Similar to hypothetical protein MGC37818	19860	34861397	316589	3	3	20.9302
Tax_Id=10116 Similar to hypothetical protein MGC38524	121800	34877564	273384	12	12	12.2109
Tax_Id=10116 Similar to hypothetical protein from EUROIMAGE 2021883	75830	34862247	195586	13	13	18.5294
Tax_Id=10116 Similar to immunoglobulin 4G6 light chain variable region	17890	34855968	195860	1	1	9.3168
Tax_Id=10116 Similar to inner membrane protein, mitochondrial (mitofilin)	82360	34855983	247605	22	22	39.4879
Tax_Id=10116 Similar to integrin alpha v Subunit	114700	34856480	299926	3	3	3.3816
Tax_Id=10116 Similar to intracellular membrane-associated calcium-independent phospholipase A2 gamma	107800	34865151	313999	1	1	0.62435
Tax_Id=10116 Similar to kidney ankyrin repeat-containing protein	127000	34860436	261449	1	1	1.1036
Tax_Id=10116 Similar to kinesin family protein KIF1a	218300	34877667	265199	2	2	1.0808
Tax_Id=10116 Similar to IdIBp	110800	34875017	282341	2	2	2.4024
Tax_Id=10116 Similar to lectin, mannose-binding 2-like	44440	34875582	221907	3	3	8.9286
Tax_Id=10116 Similar to lipoprotein receptor-related protein	517200	34865759	268163	58	58	17.1815
Tax_Id=10116 Similar to lysosomal aspartase-like 1	40920	34874392	217901	1	1	2.5496
Tax_Id=10116 Similar to lymphocyte cytosolic protein 1	80290	34875362	272629	1	3	4.8679
Tax_Id=10116 Similar to mKIAA0384 protein	101400	34856482	193681	2	2	3.0837
Tax_Id=10116 Similar to mKIAA0678 protein	96130	34865848	276172	2	2	3.7166
Tax_Id=10116 Similar to mKIAA1402 protein	86520	34853978	259133	1	1	2.0619
Tax_Id=10116 Similar to macrophage hemoglobin Scavenger receptor CD163 precursor	119500	34858425	192759	2	2	2.3423
Tax_Id=10116 Similar to macrophage mannose receptor precursor	192400	34877265	296460	31	31	20.9166
Tax_Id=10116 Similar to malignant cell expression-enhanced gene/tumor progression-enhancer	33720	34854458	281230	1	1	7.1661
Tax_Id=10116 Similar to mannose 6-phosphate isomerase 1,2-mannosidase	31910	27705330	273814	12	12	42.953
Tax_Id=10116 Similar to medium-chain acyl-CoA synthetase	22360	34859067	258281	5	5	36
Tax_Id=10116 Similar to meiotic recombination protein REC14	28800	34863419	201803	1	1	6.2016
Tax_Id=10116 Similar to melanoma inhibitory activity protein 2	58930	34865264	225113	1	1	4
Tax_Id=10116 Similar to membrane receptor (5H375)	42380	34865609	318262	1	1	4.8649
Tax_Id=10116 Similar to methionyl aminopeptidase 1	53240	34860820	221417	1	1	2.3109
Tax_Id=10116 Similar to microtubule-associated protein 4	303100	34866431	264572	2	2	1.0892

Tax_Id=10116 Similar to mitochondria-associated granulocyte macrophage CSF Signaling molecule	13800	27667166	288315	2	2	33.6
Tax_Id=10116 Similar to modifier of cell adhesion	227300	34865889	203448	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 nonclathrin 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-hydroxylase	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 peptidylprolyl isomerase D (cyclophilin D)	69130	34873471	283106	1	1	1.9324
Tax_Id=10116 Similar to phosphatidylinositolglycan 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	268034	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 precursor	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 non-sense transcript 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 comparison to mTEF1 (accession # 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 toll-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 uridindiphosphoglucosylphosphorylase 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 1A4	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
Transthyretin precursor	15720	57425	31553	9	9	67.3469
Tricarboxylate transport protein, mitochondrial precursor Citrate transport protein CTP 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 UDPGTr-5 UDP-glucuronosyltransferase R-21 UDPGTr-21	60590	55925581	31603	11	21	55.4717
Ube2i-prov protein	18010	6981690	22316	1	1	7.5949
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 Timing protein clk-1 homolog	20140	7446711	30131	1	1	6.1453
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	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 rvps45	64890	51858559	19366	3	3	9.2982
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 Vacuolar proton pump subunit 1 Vacuolar adenosine triphosphatase subunit Ac116	96330	206430	11413	1	1	1.432
Vacuole membrane protein 1 Transmembrane protein 49	45900	38197344	31214	3	3	15.7635
Vascular endothelial cell specific protein 11 Septin 2	41590	51858574	140635	5	5	22.1607
Ventral midline antigen VEMA	21600	6647578	19913	12	14	66.1538
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	37	37	63.2258
Very-long-chain specific acyl-CoA dehydrogenase, mitochondrial precursor VLCAD	70750	6978435	3601	14	14	31.2977
Vesicle associated protein	135400	7514116	26418	11	11	12.5701
Vesicle transport protein SEC20	26170	81867205	111524	5	5	25.8772
Vesicle transport through interaction with t-SNAREs homolog 1A	25160	9719420	6158	5	5	23.0415
Vesicle-associated membrane 2	12690	6981614	38248	1	4	34.4828
Vesicle-associated membrane protein 3 VAMP-3 Synaptobrevin-3 Cellubrevin CEB	11480	56789137	23581	1	4	38.835
Vesicle-associated membrane protein 7	24780	9502258	3011	3	3	18.1818
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	8	9	42.562
Vesicle-trafficking protein SEC22b SEC22 vesicle-trafficking protein-like 1	24740	71043604	41516	18	18	65.1163
Vesicular integral-membrane protein VIP36 precursor	40390	27682691	139706	22	22	62.0112
Vigilin High density lipoprotein-binding protein HDL-binding protein	141600	46397078	26167	32	54	48.1073
Vitamin K epoxide reductase complex subunit 1 Vitamin K1 2,3-epoxide reductase subunit 1	17780	62511143	291525	1	1	11.1801
Vitamin K epoxide reductase complex subunit 1-like protein 1 VKORC1-like protein 1	19780	62511142	165266	1	1	6.25
Vitamin K-dependent gamma-carboxylase Gamma-glutamyl carboxylase Vitamin K gamma glutamyl carboxylase	87480	6136262	78166	7	7	11.4776
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	3	8.4599
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:I920191D06 product:voltage-dependent anion channel 1, full insert sequence 17 days embryo kidney cDNA, RIKEN full-length enriched library, clone:I920170K05 product:voltage-dependent anion channel 1, full insert sequence 17 days embryo stomach cDNA, RIKEN full-length enriched library, clone:I920087C06 product:voltage-dependent anion channel 1, full insert sequence 17 days pregnant adult female amnion cDNA, RIKEN full-length enriched library, clone:I920043H09 product:voltage-dependent anion channel 1, full insert sequence	30760	8810245	11037	17	17	77.7385
Voltage-dependent anion-selective channel protein 2 VDAC-2 Outer mitochondrial membrane protein porin 2 B36-VDAC	31750	8810247	5942	4	5	21.3559

Voltage-dependent anion-selective channel protein 3	30800	15214186	5943	7	8	42.7562
XLalphas protein	78230	14161099	72067	4	6	13.7063
Xanthine dehydrogenase/oxidase	146300	2144323	80445	1	1	0.90158
Xylosyltransferase 2 Xylosyltransferase II Peptide O-xylosyltransferase 2	96790	71164811	189334	5	5	7.9861
Yif1b protein	25210	38454214	262403	2	2	10.917
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 canalculus-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	9.6296
kynureninase (L-kynurenine hydrolase)	52450	3913969	157223	1	1	2.8017
lanosterol synthase	83330	13591981	37206	1	12	20.191
lin-7-Ba [Rattus norvegicus]	19930	3885830	158790	2	3	18.6813
lysozyme homolog AT-2, bone - rat (fragments)	3164	539969	130837	2	2	100
major vault protein - rat	99530	7514005	132766	1	24	41.8994
mannose-binding protein C (liver)	26100	205263	44167	4	4	20.082
null	12780	51702801	4817	7	10	72.1739
p105 coactivator	99330	1800307	177421	41	41	49.2045
peroxisome assembly factor-2 [Rattus norvegicus]	104300	2911135	169183	6	6	7.9755
phosphatidylethanolamine binding protein [Rattus norvegicus]	20800	8393910	51562	4	4	36.8984
proteasome (prosome, macropain) subunit, beta type 4	25790	310214	78104	2	2	8.1897
ribosomal protein L13	24240	510552	37239	6	10	37.9147
ribosomal protein L6	33570	2507315	42185	11	15	42.0875
roundabout (axon guidance receptor, Drosophila) homolog 2 [Rattus norvegicus]	176100	34867440	317126	1	1	0.43559
secreted frizzled-related protein 1	35350	34879084	271324	1	1	2.5559
senescence marker protein 2A	33200	32964821	69809	4	9	39.4366
sialyltransferase 1	25210	285193	41195	1	7	40.6542
similar to EST AA408438	42480	27713571	204725	10	10	36.3395
similar to 2310009N05Rik protein	30570	34932411	197729	2	2	7.3801
similar to 2310036I02Rik protein	89350	34932104	265519	1	1	1.995
similar to 40S RIBOSOMAL PROTEIN S17	15680	34853950	250506	10	10	62.5
similar to 40S ribosomal protein S2 [Rattus norvegicus]	28120	34868798	193682	1	12	41.9847
similar to 60S RIBOSOMAL PROTEIN L13	20290	27714695	312086	2	3	11.236
similar to 60S RIBOSOMAL PROTEIN L18	21470	34932167	248463	3	6	32.9787
similar to 60S ribosomal protein L15	23920	34869871	293440	1	7	33.0049
similar to 60S ribosomal protein L36	12250	34856346	214593	1	6	37.7358
similar to 9530008L14Rik protein [Rattus norvegicus]	11600	34875157	310564	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 contractin alpha	62980	34865224	222641	2	3	9.364
similar to ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9), isoform 2	14750	27685029	262837	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	20.3098
similar to Ab2-095 [Rattus norvegicus]	79240	34865464	276652	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	33.8266
similar to Apoptosis inhibitor 5	36870	34878251	281550	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) (Citrin)	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 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 (Carboxyesterase 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) (Phosphoglucomutase 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	1.8832
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 Sh3bgrl 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 REII 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 aspartly 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 cytokeratin	42970	34860580	202236	1	4	13.8381
similar to endonuclease G	32270	77917570	273385	1	1	4.4218
similar to enthoproting; 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	168139	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 GDH/6PG endoplasmic bifunctional protein	114800	34872615	251640	31	31	39.9417
similar to histocompatibility 13; presenilin-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 D4Ert89e	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	3.5813
similar to hypothetical protein MGC23280	35980	34872804	277215	1	1	3.6585
similar to immunoglobulin alpha heavy chain	48960	34935283	224861	2	2	10.8647
similar to inhibitor of growth family, member 3	56500	34855011	234073	1	1	1.7751
similar to inter-alpha trypsin inhibitor, heavy chain 1 [Rattus norvegicus]	99190	34877130	227779	5	5	11.6592
similar to keratin associated protein 11-1	18900	27670141	269756	1	1	6.0109
similar to keratin type II, hair (b4) - mouse	105900	34868202	262043	14	15	31.9749
similar to keratinocytes associated protein 2	27650	34857976	235658	1	1	6.6667
similar to liver regeneration-related protein LRRG07 [Rattus norvegicus]	35400	34876593	287183	8	11	49.3548
similar to lysosomal apyrase-like 1	49290	34874388	305737	2	2	7.0938
similar to mCASP	35060	34873372	194891	10	10	38.535
similar to mKIAA0493 protein	110600	34866514	234949	6	6	8.3
similar to male enhanced antigen 2/golgi autoantigen, golgin subfamily a, 3 [Rattus norvegicus]	166100	34873054	267138	1	1	0.81191
similar to mannosyl-oligosaccharide 1,3-1,6-alpha-mannosidase	87810	34877942	294051	11	22	36.4205
similar to microrchidia	55070	34869318	309715	1	1	1.8595
similar to mirror-image polydactyly gene 1	52780	34865613	265130	1	1	1.9397
similar to nonclathrin coat protein epsilon-COP	34650	34877816	259217	17	17	74.3506
similar to ornithine transporter	32800	27673563	205798	8	8	35.8804
similar to osteoclast stimulating factor 1	34620	34880977	297002	1	1	6.1093
similar to peroxisomal long chain acyl-CoA thioesterase la	46360	27667388	160562	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	8.7542
similar to proline dehydrogenase; PRODH	12130	27665096	305160	1	1	14.9533
similar to rab20	32660	34879665	240940	1	1	2.349
similar to receptor-interacting protein 2	60780	34867073	242276	1	1	1.8553
similar to recombination activating 1 activation	24690	27692967	292043	1	1	9.0498
similar to retinal short-chain dehydrogenase/reductase 4	38310	34865424	315286	3	4	13.3136
similar to ribosomal protein S12; 40S ribosomal protein S12	12210	34869042	285721	1	2	28.5714
similar to ribosomal protein S2	21310	34879560	317435	2	3	18.1818
similar to serine protease OMI	49090	34856275	218478	5	5	15.0655
similar to sorting nexin 2	58530	34879535	319162	3	3	6.9364
similar to splicing coactivator subunit SRm300; RNA binding protein; AT-rich element binding factor [Rattus norvegicus]	212600	34868816	290757	1	1	0.40589
similar to talin [Rattus norvegicus]	269500	34867875	230030	26	29	17.369
similar to thyroid hormone receptor interactor 11; thyroid receptor interacting protein 11	37170	34867559	280942	1	1	3.9039
similar to torsinB protein	17860	34853518	202385	1	1	8.642
similar to transducin (beta)-like 2	49610	34873382	294309	16	16	42.5339
similar to ubiquitin-protein ligase (EC 6.3.2.19) E1 - mouse	123600	34933178	317625	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	ginumber	CMBSEQID	UNIQUE PEPTIDES	DISTINCT PEPTIDES	% SEQUENCE COVERAGE	N-TERM AA	PEPTIDE SEQUENCE	C-TERM AA	m/z	+ CHARGE	Experimental peptide mass	DELTA	Calculated peptide mass	MASCOT SCORE	ID SCORE
(P08644) Isoform 2B of P08644	21490	495534	71624	1	3	20.7447	R	SYGIPFIE TSAK	T	656.8383	2	1311.6621	-0.008857	1311.670957	33.21	31
(Q810T5) Isoform 2 of Q810T5	66820	29650457	268104	1	1	1.5464	R	ASEDLEKL R	L	530.8598	2	1059.705	0.14898	1059.55602	36.08	32
(Q9ESC1) Isoform 2 of Q9ESC1	73800	11225481	129647	1	1	1.5106	R	RMVSASLHVR	L	578.3196	2	1154.6246	-0.009553	1154.634153	35	31
(Q9QUH6) Isoform 5 of Q9QUH6	127700	7514095	13883	1	1	0.60034	R	SQPMVLR	G	423.7283	2	845.442	-0.000858	845.442858	41.38	33
(Q9WVG6) Isoform 5 of Q9WVG6	63460	77539446	292598	1	1	2.5641	K	AGDTLSGTCLLIANK	R	767.2662	2	1532.5179	-0.26888	1532.78678	45.34	30
1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase beta 3	139400	32699414	166274	1	1	1.6207	R	DDLIASILSEVTPTPLEELR	S	1106.0898	2	2210.165	-0.003089	2210.168089	90.28	29
10 days embryo whole body cDNA, RIKEN full-length enriched library, clone:2610511121 product:proteasome (prosome, macropain) subunit, alpha type 2, full insert sequence TIB-55 BB88 cDNA, RIKEN full-length enriched library, clone:I730006B17 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,	25930	8394063	33375	1	1	5.9829	R	GYSFSLTTFSPSGK	L	739.9373	2	1477.8601	0.15126	1477.70884	98.05	30
10-Formyltetrahydrofolate Dehydrogenase	34040	42543697	723160	1	3	13.5484	K	AGLILFGNDDR	M	595.8397	2	1189.6649	0.055818	1189.609082	54.95	32
14-3-3 protein eta	28210	6981710	29710	1	3	15.0407	K	NSVVEASEAAYKEAFEISK	E	691.226	3	2070.6563	-0.35453	2071.01083	32.62	28
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	R	EGPPFISEAAVR	G	636.9036	2	1271.7926	0.14172	1271.65088	88.97	30
2',3' -cyclic-nucleotide 3' -phosphodiesterase CNP CNPase	47270	66912120	109735	1	1	3.0952	K	DFLPLYFGWFLTK	K	823.955	2	1645.8955	0.041143	1645.854357	48.65	30
4-aminobutyrate aminotransferase, mitochondria precursor (S)-3-amino-2-methylpropionate 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	1	1	2.4	K	NLLLAEVINI IK	R	676.9559	2	1351.8971	0.053337	1351.843763	62.96	31
49 kDa protein	2429	262199	124397	1	1	47.619	R	FKDLGEENFK	A	613.7819	2	1225.5493	-0.048536	1225.597836	63.68	31
5' -AMP-activated protein kinase catalytic subunit alpha-1 AMPK alpha-1 chain	62600	1703034	23444	1	1	3.1022	R	NHQDPLAVAYHLIIDNR	R	663.6699	3	1987.9879	-0.034879	1988.022779	40.04	29
60S ribosomal protein L36	12250	34849736	65711	1	6	37.1429	R	RAMLELLK	V	430.8147	2	859.6148	0.11987	859.49493	33.11	33
60S ribosomal protein L37	11080	57121	3029	1	1	7.2165	R	KYNWSAK	A	448.7545	2	895.4944	0.039294	895.455106	34.99	31
60S ribosomal protein L39	6407	6981484	4822	1	1	19.6078	K	QNRPI PQWIR	M	436.6048	3	1306.7924	0.066622	1306.725778	37.17	31
60S ribosomal protein L40 CEP52	6181	973178	77849	1	1	13.4615	START	IIIEPSLR	Q	414.2812	2	826.5478	0.056577	826.491223	40.48	31

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	6.5574K	ASVDELFAEIVR	Q	674.855	2	1347.6954	-0.007986	1347.703386	40.2	31
A-Raf proto-oncogene serine/threonine-protein kinase	67550	55757	90531	1	1	1.8212R	IGTGSFGTVFR	G	571.3198	2	1140.625	0.032326	1140.592674	35.45	31
ADP-ribosylation-like factor 6-interacting protein Arf6ip1 protein	23450	68534822	139514	1	1	3.9409K	WTTTEQQQR	F	538.7455	2	1075.4764	-0.028246	1075.504646	54.08	32
ARHG protein Ras homolog gene family, member G Rho G	21310	82524300	93024	1	1	9.9476K	EYIPTVFDNYSQAQSAVDGR	T	1066.5538	2	2131.093	0.10731	2130.98569	35.88	29
ATP synthase epsilon chain, mitochondrial	5636	258789	11887	1	1	16R	DALKTEFK	A	476.2603	2	950.506	-0.00124	950.50724	49.26	32
ATP-binding cassette, sub-family B (MDR/TAP), member 10 Predicted	77390	58865904	264038	1	1	3.4965K	ILLLDEATSALDAENEHLVQEALDR	L	926.8069	3	2777.3988	-0.009452	2777.408252	58.6	27
ATP-binding cassette, sub-family C (CFTR/MRP), member 3	169300	3242460	52680	1	1	0.72226R	SKILLALAEKG	I	571.8435	2	1141.6725	-0.034457	1141.706957	32.37	31
ATP-binding cassette, sub-family F (GCN20), member 1	92870	34852051	231492	1	1	1.348K	GAVIVVSHDAR	L	562.3095	2	1122.6044	-0.010099	1122.614499	43.62	31
ATPase, H+ transporting, V1 subunit C, isoform 1 Predicted	43900	62652340	311925	1	1	4.1885K	VGTLDLVLVGLSDELAK	L	814.9779	2	1627.9412	0.03804	1627.90316	45.69	30
ATPase, H+ transporting, lysosomal 34kDa, V1 subunit D	28310	40786463	160475	1	1	4.8583R	TLAYITELDER	E	718.8755	2	1435.7365	-0.019286	1435.755786	30.99	30
Aa1064	42690	111387	148924	1	12	36.3636R	LELANIQAELVAK	A	706.4379	2	1410.8612	0.053097	1410.808103	34.39	30
Ab2-225 Hypothetical protein RGD1306952	27900	56970828	244467	1	1	4.0816R	NLIEWLNKYI	END	653.2685	2	1304.5224	-0.19039	1304.71279	36.27	31
Ac1573	79140	32264637	263869	1	6	10.2857R	EGDYFTQQGEFR	V	738.8982	2	1475.7818	0.15019	1475.63161	84.28	31
Ac2-067	27970	34862605	166240	1	1	5.9289K	TPAGLQVLNDYLADK	S	809.2723	2	1616.5301	-0.31084	1616.84094	129.79	30
Ac2-155	102100	33086620	199808	1	1	1.0239K	DEQDPLLR	T	543.852	2	1085.6895	0.15425	1085.53525	31.16	31
Ac2-256	71830	62177146	166247	1	1	1.374K	TLTVLHPLR	A	525.3208	2	1048.6271	-0.012214	1048.639314	40.97	31
Acetyl-CoA carboxylase 1 ACC-alpha Biotin carboxylase	265200	202645	84141	1	1	0.59701R	IGSFGPQEDLLFLR	A	796.4442	2	1590.8739	0.033413	1590.840487	82.92	30
Acyl-protein thioesterase 1 Lysophospholipase 1 Lysophospholipase I	24710	6981362	75037	1	1	4.7826K	GLVNPANVTFK	V	580.3822	2	1158.7499	0.11026	1158.63964	47.69	32
Adenine phosphoribosyltransferase APRT	19550	61556832	126504	1	1	7.2222R	SFPDFPIPGVLFR	D	746.4668	2	1490.919	0.12685	1490.79215	46	31
Adenosine kinase	40100	7448824	3608	1	3	8.5873K	DIKEIAR	K	422.7955	2	843.5765	0.095119	843.481381	35.66	32
Adenosine kinase	37310	1373230	85486	1	3	10.1796R	TFTLNLAPFISQFFK	E	931.0958	2	1860.177	0.19489	1859.98211	109.74	30
Adenylate kinase isoenzyme 4, mitochondrial	25200	8392885	181389	1	1	5.3812R	IWPYVYTLFSNK	I	765.9618	2	1529.909	0.11721	1529.79179	39.61	31
Adenylate kinase 3-like 1 ATP-AMP transphosphorylase															

Adult male thymus cDNA, RIKEN full-length enriched library, clone:5830427H10 product:GL009 homolog Bone marrow macrophage cDNA, RIKEN full-length enriched library, clone:I830027D22 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	1	6.5574R	AAGTDGSDFFQHR	E	631.3118	2	1260.6091	0.060849	1260.548251	101.95	31
	42660	498034	128256	1	1	1	3.4826K	VLSPQGDPWDSVAR	I	763.733	2	1525.4514	-0.30103	1525.75243	74.6	30
	207700	7513996	3616	1	1	1	0.49207R	VTRSQEELR	E	559.3347	2	1116.6548	0.066084	1116.588716	44.67	32
	25490	40352787	270293	1	1	1	5.7269K	GVLETFSGTETNK	I	691.9997	2	1381.7849	0.11245	1381.67245	38.25	30
	33530	68341957	157070	1	4	4	15.7895K	ELILTGFTFMR	K	664.3456	2	1326.6767	-0.023858	1326.700558	45.58	31
	15520	62655914	114803	1	2	2	16.9014K	IGNHAAEIGAETIGR	L	755.0583	2	1508.1021	0.32791	1507.77419	68.74	30
	9484	92036	84182	1	1	1	14.6067R	NAGNEQDLGIQYR	A	739.399	2	1476.7834	0.08772	1476.69568	99.64	31
	23580	72091	11470	1	1	1	4.3902K	KPDLSPELR	K	527.8548	2	1053.6951	0.11325	1053.58185	65.44	31
	56480	57012547	155721	1	1	1	2.1442R	VLNQGFSPTR	D	616.3205	2	1230.6264	-0.045584	1230.671984	69.44	31
	15280	60688619	109334	1	11	11	75.3521K	IGGHGGEYGEEALQRMFAAFPTTK	T	856.3438	3	2566.0095	-0.21789	2566.22739	64	28
Alpha-2-globin chain Hba-a1 protein 2-alpha globin	20560	8307690	125352	1	8	8	34.8066R	IKENGVCTEFSLVADK	T	905.5263	2	1809.0381	0.14034	1808.89776	122.93	29
	42290	20138815	37085	1	1	1	3.7634K	VLIDWINDVLVGER	I	820.9622	2	1639.9098	0.016488	1639.893312	70.76	30
	86880	1703345	10860	1	1	1	1.9608R	VGGLEEEPDVSGPLR	E	777.4083	2	1552.8021	0.028859	1552.773241	30.68	30
	101600	75905813	256333	1	1	1	0.87623K	LKEHVIEK	E	498.2562	2	994.4978	-0.083242	994.581042	34.34	31
	25960	6981420	75054	1	1	1	8.1301R	LGEHNINVLGDEQFINAAK	I	737.593	3	2209.7573	-0.33936	2210.09666	65.82	29
	11440	91985	3639	1	1	1	10.7843R	TGTLNMDFLSR	L	635.7664	2	1269.5182	-0.084107	1269.602307	40.44	31
	10250	2492915	136243	1	1	1	12.5R	VMEWVEPLVTR	T	668.3118	2	1334.6091	-0.048221	1334.657321	46.33	31
	28230	55742817	243481	1	1	1	6.639K	NNDNTEEHVLETENKK	L	638.6746	3	1913.002	0.12584	1912.87616	39.86	29
	26230	456209	23753	1	1	1	3.8298R	KINFALLK	F	531.3262	2	1060.6379	0.009887	1060.628013	53.59	32
	82640	66730443	214565	1	1	1	0.82079R	IYKPLR	T	395.2123	2	788.41	-0.080766	788.490766	33.06	33
Brain protein 44-like protein	12450	66911415	92620	1	1	1	7.3394R	LINYEMSK	R	507.3054	2	1012.5963	0.10644	1012.48986	31.06	31
	61100	68533633	60545	1	1	1	2.3636R	GLEEAQSEIQALR	G	722.4679	2	1442.9213	0.18484	1442.73646	78.42	31
	62270	899380	3668	1	1	1	2.1505R	TQVTYECEGYR	L	767.9279	2	1533.8413	0.20081	1533.64049	31.21	30
	13790	6978635	3690	1	1	1	7.1429R	LEIANVQYR	C	553.2455	2	1104.4764	-0.11629	1104.59269	32.22	32
	22830	51948526	211553	1	1	1	6.9307K	LQSPQAVLQLGVSK	E	734.3381	2	1466.6617	-0.18388	1466.84558	51.63	30
	1978	111445	148937	1	1	1	88.8889	START	S	867.871	2	1733.7274	-0.020496	1733.747896	136.94	30
	28080	19864480	76638	1	1	1	9.0226R	ILGGVISAISEAAQYNPEPPPPR	S	816.4444	3	2446.3113	0.02576	2446.28554	56.57	28
	25290	55562775	166315	1	1	1	8.0508R	TMIQQGSGSVNVGSIIGLK	G	966.1051	2	1930.1956	0.13996	1930.05564	36.67	30
Cardiac alpha actin 1	2133	1478388	42034	1	1	1	60	START	G	644.1955	2	1286.3765	-0.31053	1286.68703	93.49	31
	42020	77993370	10199	1	17	17	40.8488K	YPIEHGIIWNDDMEK	I	980.9391	2	1959.8637	-0.039897	1959.903597	79.26	29
	34190	60688149	160297	1	1	1	3.9216R	NVNGVNYASVTR	N	647.4318	2	1292.8491	0.20186	1292.64724	61.34	30
	26270	27465583	31543	1	1	1	3.2389R	VSTVSLPR	S	429.802	2	857.5894	0.092423	857.496977	43.5	32

Cell growth regulator with EF hand domain 1 Cell growth regulatory gene 11 protein	30830	23396481	38628		1	1	3.9146K	VDALSPGEAR	G	572.2446	2	1142.4746	-0.082114	1142.556714	31.65	31
Cell surface protein CD36	52730	6707016	105482		1	1	3.6017R	TYLDVEPTGFTLQFAK	R	971.9707	2	1941.9269	-0.081805	1942.008705	82.28	29
Centaurin-alpha 2	43520	9910340	42770		1	1	4.5213K	LAFPDLPESELVPLITR	N	955.5699	2	1909.1253	0.069348	1909.055952	65.83	29
Ceramidase	83490	16758458	60505		1	1	1.7083K	SIDIAHTNLKPGK	V	697.3885	2	1392.7624	-0.010013	1392.772413	37.73	31
Ceramide glucosyltransferase Glucosylceramide synthase GCS UDP-glucose:N-acylsphingosine D-glucosyltransferase UDP-glucose ceramide glucosyltransferase GLCT-1	44820	62648957	85745		1	1	2.7919K	LPGVSLLKPLK	G	582.8677	2	1163.7209	-0.043186	1163.764086	74.59	31
Choline/ethanolamine phosphotransferase 1	46500	56090333	264754		1	1	2.6442K	LFQLPTPLSR	H	634.7167	2	1267.4188	-0.30997	1267.72877	56.9	31
Claithrin light chain B	25120	203359	60578		1	1	3.9301R	LQELDAASK	V	487.7515	2	973.4884	-0.019552	973.507952	42.55	32
Coagulation factor IX Christmas factor	31450	204146	149112		1	1	3.9007K	FGSGYVSGWGK	V	572.7609	2	1143.5072	-0.027633	1143.534833	58.67	31
Complement component C6 precursor	105100	61211276	240055		1	1	1.2848K	TTDLQLSDVFLK	A	690.3444	2	1378.6743	-0.060072	1378.734372	46.13	31
Complement regulatory protein Cry precursor Antigen 512	61680	9506513	35260		1	1	3.5778K	LPQDMSGFQK	G	575.8287	2	1149.6429	0.094055	1149.548845	44.62	31
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	0.5814K	LSFIKR	C	382.2522	2	762.4899	0.014729	762.475171	49.19	33
Contrapsin-like protease inhibitor 1 precursor	46480	220698	135016		1	19	50.4808K	IAELFSDLDER	T	654.3633	2	1306.712	0.071586	1306.640414	79.43	31
Core binding factor beta	21520	61557239	2681		1	1	4.3956K	LSRECEIK	Y	517.783	2	1033.5515	0.028925	1033.522575	45.37	32
Cortactin isoform C	52630	2996044	57161		1	1	2.5478R	YGLFPANYVELR	Q	721.2738	2	1440.533	-0.2071	1440.7401	52.42	30
Cp431	104600	3851160	7578		1	1	1.0022R	EELKCMLEK	Y	598.2923	2	1194.5701	0.007715	1194.562385	32.82	31
Creatine kinase M-type Creatine kinase M chain M-CK	43020	6978661	3700		1	1	3.6745K	LSVEALNSLTGEFK	G	754.3409	2	1506.6673	-0.12556	1506.79286	99.87	30
Cydylate kinase	25830	71043752	267331		1	1	8.8106R	IQTYLESTKPIDLYEEMGK	V	796.4611	3	2386.3616	0.16388	2386.19772	44.06	28
Cytochrome P450 2C11	57180	56971259	63780		1	38	84.4K	VQEEIER	V	451.8157	2	901.6168	0.16631	901.45049	66.08	32
Cytochrome P450 2C22	56210	203521	33163		1	23	61.7587K	TNGSPCDPSFLLACVPCNLISSVIFQHR	F	1063.8174	3	3188.4304	-0.090105	3188.520505	33.44	26
Cytochrome P450 2C70 CYP11C70 P-450Md P450 P49	56160	56827	63786		1	23	61.7587K	EYGPVFTMYLGMKPTVWLYGYEVLK	E	977.1417	3	2928.4034	-0.065831	2928.469231	29.8	27
Cytochrome P450 2c13	55840	71051773	84196		1	31	70.2041K	IISSPGIQVFNIFPILLDYCPGNHNIYLK	N	1116.0858	3	3345.2356	0.47254	3344.76306	37.37	26
Cytochrome P450 3A	57720	6978749	3731		1	9	24.3028R	LKEMFPVIEQYGDLVK	Y	680.0892	3	2037.2459	0.16037	2037.08553	38.01	29
Cytochrome P450 4A12 CYP1A12 CYP1VA8	58520	203757	78089		1	6	10.0394R	KAQLQDEEELQK	V	729.9482	2	1457.8819	0.14576	1457.73614	61.2	30
Cytochrome b5 outer mitochondrial membrane isoform precursor	15220	7427560	39173		1	5	60 START	DGGGSDPAVTTYR	L	714.8439	2	1427.6733	0.0416	1427.6317	81.34	30
Cytochrome c oxidase polypeptide VIlc, mitochondrial VIIIA	1117	1169069	71407		1	1	90 START	SHYEEGPGK	N	502.2178	2	1002.4209	-0.019665	1002.440566	49.83	32
Cytochrome c oxidase subunit 2	25940	5835181	98989		1	7	30.837R	LLEVDNRVVLPMELPIR	M	669.4313	3	2005.2722	0.13285	2005.13935	43.56	29
Cytochrome oxidase subunit II	26010	829023	105670		1	7	26.4317R	LNQATVTSNR	L	552.3412	2	1102.6678	0.094744	1102.573056	62.55	32
Cytochrome oxidase subunit II Cytochrome c oxidase subunit II	25930	58615680	142106		1	7	30.837R	MLISSEDVLHSAWVPSLGLK	T	733.4322	3	2197.2747	0.12946	2197.14524	84.88	28
Cytokeratin type I	15550	55956	11221		1	1	5.3892R	DYQELMNTK	L	571.2668	2	1140.519	0.008668	1140.512132	49.33	31
Diacylglycerol O-acyltransferase 1 Diglyceride acyltransferase	56870	9965432	145183		1	1	3.2129K	YGILVDPIQVVSFLK	D	902.6778	2	1803.341	0.28647	1803.05453	49.93	30
Diamine oxidase-like protein 1	80090	40385889	216306		1	1	1.2857R	HPVLGNTLK	K	489.7784	2	977.5423	-0.023497	977.565797	33.59	32
Dimethylglycine dehydrogenase, mitochondrial precursor ME2GLYDH	96050	56689	82662		1	1	1.9837R	NITDELGLVGAGPYAR	R	872.9316	2	1743.8487	-0.066783	1743.915483	109.37	30
Dipeptidyl peptidase IV	88000	6978773	3741		1	19	28.292K	IVSDKDGYK	H	512.7186	2	1023.4225	-0.10107	1023.52357	40.27	31
Dnaj-like protein	25760	9910322	42765		1	1	3.139R	TKEELIR	G	444.7019	2	887.3893	-0.11832	887.50762	32.01	32
Dnajc3 protein [Rattus norvegicus]	50240	38197558	318957		1	15	46.0137R	AEAYLIEEMYDEAIQDYEAQAQEQNENDQQIR	E	1240.392	3	3718.1542	-0.46742	3718.62162	138.18	25
EIF3S6 protein	52220	62652368	55867		1	1	2.9213R	HLVFPLEFLSVK	E	771.4475	2	1540.8804	-0.021289	1540.901689	35.34	30
ENSEMBL:ENSRNOP0000002163 REFSEQ:XP_342451 PREDICTED: similar to lunapark	47640	34855225	271473		1	1	1.8824R	TVAPALPR	R	412.7899	2	823.5653	0.073721	823.491579	31.83	31
Engulfment and cell motility protein 1	28740	34876182	4981		1	1	7.2874R	LLDLENIQIPDAPPIPK	E	991.9931	2	1981.9717	-0.13705	1982.10875	60.7	29
Epsin 1	60160	41016934	105332		1	1	2.087K	NIVHNYSEAIK	V	708.9066	2	1415.7985	0.094126	1415.704374	48.6	31

Estrogen sulfotransferase, isoform 1 EST-1 Sulfotransferase, estrogen-preferring Estrone sulfotransferase	35510	1711599	109266	1	7	31.1864K	YWEDIETFLARPDDLLIVTPK	S	899.7803	3	2696.319	-0.054721	2696.373721	71.84	27
Estrogen sulfotransferase, isoform 3 EST-3 Sulfotransferase, estrogen-preferring Estrone sulfotransferase	35420	6981594	75106	1	7	31.1864K	FMEGQVPYGSWYDHSV	S	653.6047	3	1957.7924	-0.074444	1957.866844	49.27	29
Estrogen sulfotransferase, isoform 6 EST-6 Sulfotransferase, estrogen-preferring Estrone sulfotransferase	35300	913357	62242	1	6	29.1525K	LIEFLERDPLAELVDK	I	950.5094	2	1899.0043	-0.03098	1899.03528	33.02	29
Estrogen-related receptor gamma Estrogen receptor-related protein 3	51310	50400205	17534	1	1	2.1834R	ELVVIIGWAK	H	564.2632	2	1126.5118	-0.16315	1126.67495	47.26	31
Eukaryotic translation initiation factor 4H	27320	55741853	295040	1	1	9.2742R	TVATPLNQVANPNSAIFGGARPR	E	784.2937	3	2349.8593	-0.3912	2350.2505	50.75	28
Evolutionarily conserved signaling intermediate in Toll pathway	49620	55741518	276570	1	1	3.2258R	DLSVYNLLLDVFPK	E	818.4932	2	1634.9719	0.080057	1634.891843	72.94	30
Exocyst complex component 2 Exocyst complex component Sec5 rSec5	104000	7513971	161256	1	1	1.6234R	ASNTADTLFQEVLR	K	811.458	2	1620.9014	0.090724	1620.810676	112.63	30
Exostosin-1 Glucuronosyl-N-acetylglucosaminyl-proteoglycan/N-acetylglucosaminyl-proteoglycan 4-alpha-N-acetylglucosaminyltransferase Multiple exostosins protein 1 homolog	86310	62652423	57456	1	1	2.1448K	IAESYQNILAAIEGSR	F	867.8508	2	1733.687	-0.2077	1733.8947	40.26	30
F-actin binding protein b-Nexilin	78390	40538878	173653	1	1	1.2195K	QAEEEARR	R	494.7741	2	987.5337	0.060416	987.473284	35.31	32
Ficolin-1 precursor Collagen/fibrinogen domain-containing protein 1 Ficolin-A Ficolin A M-Ficolin	36630	6714560	75919	1	1	5.0746K	LTLGQFLEGTAGDSLTK	H	875.8626	2	1749.7105	-0.20426	1749.91476	84.52	30
Fukutin related protein	54850	71043684	242747	1	1	3.0364R	GWAQVQLDLTFASAR	Q	824.5433	2	1647.0721	0.19409	1646.87801	30.74	30
Fumarate hydratase, mitochondrial precursor Fumarase	54460	8393358	45080	1	7	25.8383R	THTQDAVPLTLGQEFSGYVQVQYAMER	I	1066.3155	3	3195.9247	0.39524	3195.52946	110.17	27
Furin precursor Paired basic amino acid residue cleaving enzyme PACE Dibasic-processing enzyme Prohormone convertase 3	86650	9506955	47234	1	1	1.6393R	MLDGEVTDAREAR	S	711.377	2	1420.7395	0.089183	1420.650317	31.36	30
GM2 activator protein	21520	27229316	157436	1	1	11.0553K	SLTLQDPPIVPGDVIVSAEGK	T	1117.794	2	2233.5734	0.35297	2233.22043	51.89	29
GTPase HRas precursor Transforming protein p21 p21ras H-Ras-1 c-H-ras	21300	34861217	10323	1	3	19.0476R	TGEGFLCVFAINNTK	S	835.9179	2	1669.8213	0.007959	1669.813341	65.88	30
Galactose-1-phosphate uridylyltransferase Gal-1-P uridylyltransferase UDP-glucose--hexose-1-phosphate uridylyltransferase	43310	68533665	71441	1	1	2.3747R	LPELTPAER	D	513.2642	2	1024.5138	-0.041459	1024.555259	32.18	31
Galectin-3	27200	57870645	71532	1	1	4.1985K	GNDIAFHFNPR	F	644.3596	2	1286.7047	0.089153	1286.615547	35.1	31
Gamma-butyrobetaine dioxygenase Gamma-butyrobetaine,2-oxoglutarate dioxygenase Gamma-butyrobetaine hydroxylase Gamma-BBH	44550	5825482	139030	1	1	3.1008K	IDANNVAYTTGK	L	633.8896	2	1265.7646	0.13949	1265.62511	54.58	31
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	2.6224R	LPWAQLFQPTIALLR	E	883.915	2	1765.8155	-0.20875	1766.02423	53.51	30
Gene.	48610	22775474	113271	1	1	2.6432R	NVETMNYADIER	T	735.8648	2	1469.715	0.069389	1469.645611	84.99	30
Glia maturation factor beta GMF-beta	16610	111660	148966	1	1	16.3121R	LVVLDEELEGVSPDELKDELPER	Q	875.078	3	2622.2121	-0.11542	2622.32752	63.06	27
Glutamine fructose-6-phosphate transaminase 1	76830	54400724	277551	1	1	2.3495R	VIFLEDDDDVAADVDR	L	867.018	2	1732.0214	0.15352	1731.86788	87.84	30
Glutathione S-transferase alpha-4 Glutathione S-transferase Yk GST Yk GST 8-8 GST K GST A4	25510	5420030	28290	1	3	9.9099R	KPPPDGHYVDWR	T	739.9563	2	1477.8981	0.13043	1477.76767	36.84	30
Glutathione transferase (EC 2.5.1.18) psi	3544	92300	84221	1	1	33.3333START	PMILGYWDIR	G	640.3514	2	1278.6882	0.045132	1278.643068	37.27	31

Glycerol Kinase ATP:glycerol 3-phosphotransferase	57480	433211	18015	1	1	2.2901K	LGQLNIDISNIK	A	664.3273	2	1326.64	-0.11061	1326.75061	35.8	31
stimulated glucocorticoid-receptor translocation promoter ASTP															
Glycerol-3-phosphate dehydrogenase, mitochondrial precursor	80970	6980978	3907	1	1	2.0633R	LAFLNVQAAEEALPK	I	807.5073	2	1613.0001	0.11774	1612.88236	68.91	30
GPDH-M															
Golgin subfamily A member 7	15780	81884637	19992	1	1	10.9489K	IYAPQGLLLTDPIER	G	850.0647	2	1698.1149	0.17972	1697.93518	70.98	30
Growth factor receptor bound protein 2	25210	77539774	29315	1	1	5.53K	FNSLNELVDYHR	S	753.944	2	1505.8735	0.14726	1505.72624	34.01	30
Gstm7 protein	25680	529588	33791	1	10	39.9083R	VDILENQLMDNR	M	738.3807	2	1474.7469	0.038386	1474.708514	40.03	30
H2-K region expressed gene 4, rat orthologue	49500	62665667	219015	1	1	5.5556R	VSGYLNLAADLAHNFTDGLAIGASFR	G	898.4341	3	2692.2805	-0.080322	2692.360822	122.31	28
RT1 class I, locus Ke4															
H3 histone, family 3A H3 histone, family 3B	15330	56388767	16060	1	1	23.5294R	FQSAAGALQEASEAYLVGLFEDTNLCAIHAK	R	1146.5423	3	3436.6051	-0.092102	3436.697202	97.14	26
H3F3A protein															
Heat shock 27 kDa protein	22890	204665	71479	1	1	8.2524K	AVTQSAEITPVTFEAR	A	917.066	2	1832.1174	0.14952	1831.96788	44.86	29
Heme oxygenase 1	33010	6981032	3930	1	1	3.8062R	MNTLEMTPEVK	H	662.7934	2	1323.5721	-0.032848	1323.604948	36.77	31
Hemoglobin alpha-1 and alpha-2 chains	15330	6981010	3923	1	11	75.3521M	VLSADDDKTNIK	N	602.2018	2	1202.3891	-0.26149	1202.65059	87.36	31
Heterogeneous nuclear ribonucleoprotein D0	38190	9588096	47431	1	1	3.966K	IFVGGLSPTPEEK	I	744.7052	2	1487.3958	-0.35485	1487.75065	82.89	30
hnRNP D0 AU-rich element RNA-binding protein 1															
Hexokinase, type I	102400	6981022	3926	1	1	0.87146K	QTLMEVKK	R	488.855	2	975.6955	0.1532	975.5423	32.74	32
Histidine triad nucleotide binding protein	13780	34870743	82484	1	1	11.1111K	AQVAQPGGDTIFGK	I	694.9034	2	1387.7923	0.082765	1387.709535	61.31	31
Histidine triad protein 4	18890	21654864	153619	1	1	8.4337K	AGPEVSPGTSER	D	680.842	2	1359.6695	0.042976	1359.626524	46.23	31
Histidine-rich glycoprotein 1	59050	62657833	140379	1	4	7.619K	AENGDFASFR	V	557.2382	2	1112.4619	-0.026669	1112.488569	48	31
hnRNP protein	18280	3021529	57359	1	1	11.399R	SSGSPYGGYGSGGGSGGYGSR	R	955.9617	2	1909.9089	0.12632	1909.78258	30.49	29
Hypothetical protein Ccdc51	42310	62078929	366853	1	1	2.6385K	DLQNLMDLR	G	616.723	2	1231.4314	-0.19164	1231.62304	57.67	31
Hypothetical protein FLJ20445 Ring finger protein 153	31230	34862676	49021	1	1	4.6763K	LGPVVYVLDLADR	L	715.3615	2	1428.7085	-0.089104	1428.797604	51.28	30
Hypothetical protein MGC72560	17720	40018580	139384	1	1	8.0745R	TDEQALLSSILAK	T	694.7851	2	1387.5556	-0.20023	1387.75583	83.84	31
Hypothetical protein MGC72996	20710	38454298	220427	1	1	5.2632K	FLNDSEQVAR	A	589.8017	2	1177.5888	0.016155	1177.572645	63.61	31
Hypothetical protein MGC94464	19290	56090373	282775	1	1	4.8485K	AVVESLPR	T	435.818	2	869.6214	0.12442	869.49698	31.96	31
Hypothetical protein RGD1305677	21660	58585236	209082	1	1	8.1633R	GNIFNYWITISKPVFR	K	652.3782	3	1954.1129	0.066505	1954.046395	43.5	29
INSIG2 membrane protein Insulin induced gene 2	24970	55250700	200861	1	1	4.8889M	AEGETESPRPK	K	400.9239	3	1199.7497	0.17155	1199.57815	37.3	31
ITI heavy chain-related protein	1809	1041915	40462	1	2	93.75 START	EKNQIDNYSLTVDSR	V	855.3143	2	1708.6139	-0.24916	1708.86306	104.48	30
Ig gamma-2A chain C region	25220	13399989	62937	1	1	4.4444K	SISKPEGTPR	G	536.2457	2	1070.4769	-0.095088	1070.571988	37.72	32
IgG receptor FcRn large subunit P51 precursor	40170	56437	15418	1	1	3.0055K	SKEQLFLEAIR	T	667.3298	2	1332.645	-0.095114	1332.740114	87.42	31
Inosine monophosphate dehydrogenase 2	55800	40018566	231448	1	1	2.7237K	REDLVVAPAGVTLK	E	489.93	3	1466.7681	-0.077514	1466.845614	31.08	30
Ischemia responsive 94 kDa protein	94060	3360521	95874	1	1	1.0714R	FQESEERP	L	575.2915	2	1148.5685	0.022325	1148.546175	53.49	31
Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial precursor	39610	68565369	60501	1	1	3.2787K	TPYTDNVITIR	E	696.4075	2	1390.8004	0.054818	1390.745582	64.59	30
Isocitric dehydrogenase NAD(+)-specific ICDH															
Keratin K6	3107	554464	66467	1	1	38.4615K	YEELQITAGR	H	590.2647	2	1178.5149	-0.078166	1178.593066	83.78	31
LEA_4 domain containing protein RGD1359600	31470	56090371	205582	1	1	3.663K	KEEPDPLQDK	S	599.7824	2	1197.5502	-0.037524	1197.587724	34.75	31
LIM and SH3 domain protein 1 LASP-1	29970	71122452	19687	1	1	4.943K	GFSVWADTPELQR	I	709.9306	2	1417.8467	0.12659	1417.72011	49.36	31
LOC362065 protein Transmembrane protein	62200	45680888	339290	1	1	2.0333K	QSSLPAMSKVR	R	602.3882	2	1202.7618	0.11772	1202.64408	31.85	31
LRRGT00050	168800	66793366	286877	1	1	0.94213K	DQVDSAVQELLQLK	A	793.4454	2	1584.8763	0.040462	1584.835838	52.69	30
LRRGT00086	62990	37361858	209490	1	1	1.9784K	ERPGVYTNVAK	Y	617.4187	2	1232.8228	0.17151	1232.65129	32.45	31
LanC-like protein 1 40 kDa erythrocyte membrane protein p40	45240	6625487	126112	1	1	3.0075K	SLAENYFDSTGR	L	680.2895	2	1358.5645	-0.045711	1358.610211	36.55	31
Leucyl-cystinyl aminopeptidase	117200	20138455	5106	1	1	1.4634R	ANLNNIFELAGLKG	V	793.8726	2	1585.7305	-0.15214	1585.88264	70.08	30
Leukocyte common antigen variant 4 precursor	132600	56560	111680	1	1	0.93857R	LFLAEFQSIPR	V	660.8968	2	1319.779	0.055299	1319.723701	69	31
Liver NTE-related protein	75650	21314221	198073	1	1	2.4927R	ILTGNAIALVLGGGGAR	G	776.972	2	1551.9294	0.019887	1551.909513	106.36	30
Liver carboxylesterase 10 precursor	62140	56899	112141	1	35	65.8407R	AISESGVLTLSALITTSKPIAKIATLSGCK	T	1082.3855	3	3244.1347	0.33479	3243.79991	28.69	26
Liver carboxylesterase B-1 precursor	62490	562010	10945	1	29	56.328K	MAIMLLEK	F	490.8184	2	979.6221	0.11397	979.50813	39.23	31
Liver carboxylesterase															
microsomal carboxylesterase															
Liver regeneration-related protein 1	17130	28194393	52861	1	1	6.2893K	AASLHWTSE	V	579.3485	2	1156.6825	0.12004	1156.56246	44.2	31
Liver-specific transport protein	58710	529590	60454	1	1	2.243K	AQLPETIQDVER	K	699.8596	2	1397.7047	-0.010264	1397.714964	37.7	31
Lon	105800	19173766	140367	1	1	1.3684K	AQLSATVLTLLIK	Q	685.8934	2	1369.7722	-0.082213	1369.854413	50.95	30

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	1.8576K	VLASYAQPIFLR	L	689.3662	2	1376.7178	-0.063787	1376.781587	67.46	31
Low molecular mass ubiquinone-binding protein	9849	68341999	311481	1	1	15.8537R	HVISYSLSPFEQR	A	781.9603	2	1561.9061	0.11731	1561.78879	93.19	31
LysM, putative peptidoglycan-binding, domain containing 3	33700	57527470	204667	1	1	4.8667R	VNNLISDQDFFALR	S	826.3235	2	1650.6324	-0.20409	1650.83649	48.15	30
Lysosomal acid lipase/cholesteryl ester hydrolase precursor LAL Acid cholesteryl ester hydrolase Sterol esterase Lipase A Cholesteryl esterase	45190	9653291	72321	1	1	3.2746R	LPDLLLEDLFGQK	Q	750.8958	2	1499.777	-0.046438	1499.823438	98.6	30
Lysosomal acid phosphatase precursor LAP	48320	8392842	144356	1	1	2.8369R	LQGGVLLAQILK	N	626.8603	2	1251.706	-0.085334	1251.791334	93.51	31
Lysozyme	16730	7428180	39196	1	1	12.8378R	NYNPGDQSTDYGIFQINSR	Y	1094.8997	2	2187.7848	-0.19721	2187.98201	107.78	28
Lysyl-tRNA synthetase	71620	55741637	269157	1	1	1.7572R	YLDLILNDFVR	Q	690.8522	2	1379.6898	-0.055055	1379.744855	43.95	31
MAL2A Mai, T-cell differentiation protein 2	19200	77157795	166255	1	1	6.25R	ITLPAGPDILR	T	583.3827	2	1164.7509	0.064273	1164.686627	38.45	31
MHC class II transactivator type I	127300	9931450	42953	1	1	0.69384K	ISLTLEK	G	458.7124	2	915.4103	-0.15373	915.56403	32.21	32
MOBILFERRIN	1917	300525	182793	1	1	41.1765 START	DPAIYFK	E	427.2797	2	852.5448	0.1067	852.4381	59.59	31
Major urinary protein precursor	20740	992637	69402	1	15	71.2707K	NGETFQLMVLYGR	T	764.3592	2	1526.7039	-0.051133	1526.755033	117.48	30
Maleylacetacetate isomerase MAAI Glutathione S-transferase zeta 1 GSTZ1-1	2943	11133293	36062	1	1	39.2857K	AITSGFNALEK	I	575.7646	2	1149.5146	-0.088353	1149.602953	63.58	31
Mannose-binding protein A precursor	16550	1942287	19138	1	1	8.0537K	LANMEAEINTLK	S	681.8395	2	1361.6644	-0.021637	1361.686037	96.29	31
Merlin Moesin-ezrin-radixin-like protein Neurofibromin-2 Schwannomin	68710	32363191	124359	1	1	2.7304K	IAQDLEMYGVNYFIIR	N	967.0184	2	1932.0223	0.07726	1931.94504	76.39	29
Mesenchymal stem cell protein DSCD75	23750	56090359	259160	1	1	5.314R	DLLAEQLYAGR	V	624.8629	2	1247.7112	0.060308	1247.650892	33.54	31
Mitochondrial import inner membrane translocase subunit TIM8 A Deafness dystonia protein 1 homolog	11040	5107153	12056	1	1	11.3402R	FIDTSQFILNR	L	677.283	2	1352.5514	-0.15737	1352.70877	87.13	31
Mitochondrial protein, 18 kDa	18370	55741522	220289	1	1	7.8313R	YLYGANEVGEAFR	S	744.9229	2	1487.8313	0.12692	1487.70438	64.29	30
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	3.2787K	QDINKTAWELPK	T	721.8674	2	1441.7202	-0.036257	1441.756457	36.06	30
Mitogen-activated protein kinase kinase 1-interacting protein 1	13580	81883452	237355	1	1	8.871K	ELAPLFEELIK	V	651.3919	2	1300.7692	0.041465	1300.727735	51.3	30
Monocyte differentiation antigen CD14 precursor	40050	38197682	35920	1	1	2.957R	VPTQILFGTLR	V	622.8489	2	1243.6833	-0.045498	1243.728798	48.01	31
Myelin basic protein S	21500	70166245	3277	1	1	7.1795K	GAYDAQGTLISKIFK	L	749.828	2	1497.6415	-0.14114	1497.78264	31.87	30
Myosin VIIA	251100	23618899	217296	1	1	0.45935R	GETVSTPLSR	E	523.8373	2	1045.66	0.11968	1045.54032	36.94	32
N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 2 [Rattus norvegicus]	95740	34868948	210844	1	4	5.3635R	LGLYTFESLVR	F	649.3754	2	1296.7361	0.02843	1296.70767	56.33	30
NADH-ubiquinone oxidoreductase chain 4 NADH dehydrogenase subunit 4	51800	639984	98993	1	1	4.3573R	ELTLMALHIPLMLLTINPK	L	769.4469	3	2305.3188	0.003475	2305.315325	47.68	28
NADPH--cytochrome P450 reductase	76930	205660	44210	1	37	62.5369R	QYELVVHEDMDAAK	V	832.3084	2	1662.6021	-0.15373	1662.75583	43.58	30
Na(+)/H(+) exchange regulatory co-factor NHE-RF2	34910	13925523	78016	1	1	4.4444R	SVDPGSPASLSGLR	A	671.9285	2	1341.8424	0.15361	1341.68879	35.1	31
Nicotinate phosphoribosyltransferase-like protein	58560	46485387	722226	1	1	3.5316R	SGLPNFLAVALALGELGYR	A	980.9524	2	1959.8903	-0.18777	1960.07807	36.12	29
Non-muscle caldesmon CDM L-caldesmon	60580	6978589	3674	1	1	2.2599R	LEQYTNAIEGTK	A	683.9173	2	1365.82	0.14244	1365.67756	61.25	31
Oligoribonuclease, mitochondrial precursor Small fragment nuclease RNA exonuclease 2 homolog	26750	81910234	216886	1	1	3.3755M	LGVSLGAR	L	386.7593	2	771.5039	0.043728	771.460172	36.3	33
Ornithine aminotransferase	24280	206706	44333	1	1	8.9686R	IAIAALEVLEEHLAENADK	M	726.5971	3	2176.7696	-0.35188	2177.12148	28.46	28
PEF protein with a long N-terminal hydrophobic domain	30010	56090329	201603	1	1	4.5936R	LSFEDFVTMTASR	M	760.3165	2	1518.6185	-0.083865	1518.702365	55.6	30
PRA1 family protein 3 ARL-6-interacting protein 4 ADP-ribosylation-like factor 6-interacting protein Aip-5 Glutamate transporter EAAC1-interacting protein GTRAP3-18 Prenylated Rab acceptor protein 2 Protein JWa	21550	57012987	54281	1	1	10.6383K	KTPMGIIIDALEQQEDSINK	F	748.3589	3	2242.0548	-0.096691	2242.151491	38.53	28

PREDICTED: T-cell, immune regulator 1, ATPase, H+ transporting, lysosomal V0 protein a isoform 3	93210	62641689	274163	1	1	1.6787K	TTQNEIWQTFFGGR	Y	842.9633	2	1683.912	0.11157	1683.80043	41.98	30
PREDICTED: branched chain keto acid dehydrogenase E1, beta polypeptide	42820	34866350	151463	1	1	3.0769R	AAVEQVPVEPYK	I	665.3874	2	1328.7603	0.062768	1328.697532	48.04	31
PREDICTED: cadherin 11	88040	34851208	199319	1	1	1.3819K	VEAANVHIDPK	F	596.7627	2	1191.5108	-0.11396	1191.62476	34.53	31
PREDICTED: hypothetical protein XP_579502	83280	62665770	317748	1	12	20.191K	AQTAHEGALNGVTFYAK	L	889.4221	2	1776.8295	-0.049862	1776.879362	60.14	29
PREDICTED: mitogen-activated protein kinase kinase kinase 7 interacting protein 2 (predicted)	76330	90108450	226905	1	1	1.0101K	LRSSGPR	T	386.7335	2	771.4524	0.017279	771.435121	35.61	33
PREDICTED: peanut-like 2 (Drosophila) (predicted)	53080	62656738	223925	1	1	3.0501K	STLVNSLFLTDLYR	D	821.393	2	1640.7715	-0.10585	1640.87735	32.23	30
PREDICTED: pyrroline-5-carboxylate reductase-like (predicted)	28860	62652621	268213	1	1	4.0146R	MAEAIAGGLIR	A	594.7967	2	1187.5789	-0.054311	1187.633211	50.69	31
PREDICTED: similar to 1700001K19Rik protein	24610	34867823	299198	1	1	3.653R	NSPSYTLR	F	469.181	2	936.3474	-0.11907	936.46647	36.94	31
PREDICTED: similar to 3.5-cyclic-GMP phosphodiesterase; rod phosphodiesterase beta subunit	98490	34875832	283891	1	1	1.1682K	DEIQEILPTR	D	607.3453	2	1212.6761	0.041089	1212.635011	42.65	31
PREDICTED: similar to 60S acidic ribosomal protein P1	11560	27717711	214842	1	1	14.1593K	AAGVNVELFWPGLFAK	A	859.9982	2	1717.9818	0.062781	1717.919019	45.36	30
PREDICTED: similar to 60S acidic ribosomal protein P2	11760	62660456	201232	1	7	75.6522K	ILDSVGIEAEDER	L	723.414	2	1444.8135	0.10905	1444.70445	92.17	31
PREDICTED: similar to Aldose reductase (AR) (Aldehyde reductase)	35900	62648070	161456	1	2	6.962K	AIGSVNFNPLQIER	I	779.3983	2	1556.782	-0.048961	1556.830961	102.03	30
PREDICTED: similar to Apolipoprotein C2	10700	27676424	215733	1	1	9.2784K	AAAGELYQK	T	475.7132	2	949.4118	-0.075064	949.486864	35.61	31
PREDICTED: similar to BTB (POZ) domain containing 14A	63110	34853069	292782	1	1	1.3675K	RPLDTGPR	D	456.275	2	910.5354	0.03702	910.49838	34.69	31
PREDICTED: similar to Cab39 protein	39870	34877516	314871	1	1	3.2258K	DVAQIFNNILR	R	651.8518	2	1301.689	-0.020094	1301.709094	35.67	31
PREDICTED: similar to Coiled-coil-helix-coiled-coil-helix domain containing 6	35250	34856405	277277	1	1	4.4586K	FQQEQLAVQDELVK	V	837.9986	2	1673.9827	0.12035	1673.86235	38.87	30
PREDICTED: similar to Cysteine-rich with EGF-like domains 1	45700	81170413	208169	1	1	2.619R	LVEVLEGVCSK	S	616.8957	2	1231.7769	0.12876	1231.64814	37.36	31
PREDICTED: similar to DNA segment, Chr 13, Wayne State University 177, expressed	21120	95102018	253829	1	1	10.1124R	KPYVNDLEAEASLPEKK	G	677.2164	3	2028.6273	-0.44582	2029.07312	31.4	29
PREDICTED: similar to DXlmx39e protein	15360	34933457	246770	1	1	7.8014R	ALDDFVLGSAR	L	582.3163	2	1162.618	0.019813	1162.598187	44.13	31
PREDICTED: similar to Dual specificity phosphatase 14	22270	62644625	209194	1	1	10.6061R	MISEGDIGIAQITSSLFLGR	A	1091.0462	2	2180.0778	-0.036776	2180.114576	117.48	28
PREDICTED: similar to Emopamil-binding protein-like (Emopamil-binding related protein)	23410	34874266	245607	1	1	4.3689R	GHOEASLAR	K	484.7488	2	967.4831	-0.000422	967.483522	37.97	31
PREDICTED: similar to F-box protein 28	41070	27681007	262592	1	1	2.9891R	QEVTKLQQVK	T	664.9462	2	1327.8779	0.13204	1327.74586	39.12	31
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	2.5862R	AFPVLLDDAVPWYLR	L	887.0494	2	1772.0843	0.081867	1772.002433	32.66	30
PREDICTED: similar to LECT2	20890	34873621	209309	1	1	4.8128K	LGTLPLQK	V	491.8248	2	981.6351	0.012865	981.622235	41.63	31
PREDICTED: similar to MAP kinase kinase 3b	47090	34870816	238438	1	1	3.58K	IPEDILGEIAVSIVR	A	812.5398	2	1623.0649	0.14071	1622.92419	84.54	30
PREDICTED: similar to Metaxin 1, isoform 2	26260	34857966	262377	1	1	6.7227K	ISNPWQSPSGTLPALR	T	862.454	2	1722.8934	-0.011905	1722.905305	66.77	30
PREDICTED: similar to Protein HSPC163	16090	27679416	225990	1	1	14.3885R	FIMVPSGNMGVFDPTIEIHDR	G	765.0145	3	2292.0218	-0.044873	2292.066673	82.6	28
PREDICTED: similar to RCK	54310	34879288	208269	1	1	3.1056R	QILLYSATFPLSVQK	F	854.5399	2	1707.0652	0.10454	1706.96066	100.9	30
PREDICTED: similar to RIKEN cDNA 1110038M16	31550	34870283	246519	1	1	8.3333R	HLHVVGTFIDSGPGDSDLIGALR	A	792.7405	3	2375.1996	-0.023655	2375.223255	33.73	28
PREDICTED: similar to RIKEN cDNA 120009C21	25110	27730981	189964	1	1	6.422K	ENAYDLEANLAVLK	L	781.9909	2	1561.9671	0.16844	1561.79866	56.79	31
PREDICTED: similar to RIKEN cDNA 1700025G04	13890	27712468	318230	1	1	5.7851R	NOENLEK	S	437.7334	2	873.4523	0.033169	873.419131	40.77	32

PREDICTED: similar to RIKEN cDNA 170027N10	31220	34874480	246387	1	1	3.9855K	VFDEEVVVQIK	E	652.8805	2	1303.7465	0.044242	1303.702258	33.05	30
PREDICTED: similar to RIKEN cDNA 2610019P18	28380	34871484	194048	1	1	4.8583K	LLSMELQEELSR	T	732.3879	2	1462.7613	0.02758	1462.73372	52.37	31
PREDICTED: similar to RIKEN cDNA D930001I22	30110	62646328	359989	1	1	6.1069K	SFSPGLPPQSSSLTLK	Q	823.464	2	1644.9135	0.04125	1644.87225	42.69	30
PREDICTED: similar to RPP20 protein	15740	27663642	220097	1	1	10.7143R	GAIEAELDPVEYTLR	K	838.5001	2	1674.9857	0.13936	1674.84634	44.02	30
PREDICTED: similar to RS21-C6 protein	32140	34877104	218331	1	1	4.4983K	SESCPPSENPFVK	G	763.3654	2	1524.7163	0.060867	1524.655433	30.13	30
PREDICTED: similar to Ras-related protein R-Ras (P23)	23910	34856057	257746	1	2	12.844R	LNVDFAFEQLVR	T	716.9273	2	1431.84	0.10425	1431.73575	94.73	31
PREDICTED: similar to Ras-related protein Rab	23230	81887426	161420	1	2	10.4762K	LVLVGDA SVGK	T	529.2752	2	1056.5358	-0.08206	1056.61786	35.79	31
PREDICTED: similar to Retinoic acid early inducible protein 1 beta precursor (RAE-1beta)	27450	62638284	367801	1	1	5.4852K	VHTTKTSGHPTLR	V	478.9465	3	1433.8176	0.043732	1433.773868	32.75	30
PREDICTED: similar to Sfrs7 protein	20570	34862692	226986	1	2	14.2077K	VYVGNLGTGAGK	G	568.3593	2	1134.7041	0.1009	1134.6032	38.35	31
PREDICTED: similar to Smhs2 homolog	49210	34874232	269978	1	1	3.9443K	VATGQELSNLLD TVFK	I	925.0869	2	1848.1592	0.19641	1847.96279	32.53	29
PREDICTED: similar to Stromal cell-derived factor 2 precursor (SDF-2)	24060	27673471	232984	1	1	3.653R	LTHINTGR	N	456.2292	2	910.4438	-0.05462	910.49842	32.41	31
PREDICTED: similar to TOLLIP protein	30310	34861256	225945	1	1	5.1095R	GPVYIGELPQDFLR	I	802.402	2	1602.7895	-0.051047	1602.840547	53.91	30
PREDICTED: similar to Tripartite motif protein 47	70030	27690552	251068	1	1	1.7134R	GLGSGEDELQK	L	566.7482	2	1131.4819	-0.058782	1131.540682	31.62	31
PREDICTED: similar to alpha/beta hydrolase fold protein	48340	34857271	271294	1	1	5.8824R	IYVPLMLVNAADDPLVHESLLTIPK	S	921.1789	3	2760.5148	0.001338	2760.513462	62.25	28
PREDICTED: similar to armadillo repeat-containing protein	31200	34855505	302905	1	1	7.4468R	VGSHPEGGASWLSTAA NFLSR	S	715.2599	3	2142.7578	-0.28676	2143.04456	29.58	29
PREDICTED: similar to cathepsin 1 precursor	40980	27681673	266171	1	1	2.2284K	IPKTLDWR	D	514.8538	2	1027.693	0.11161	1027.58139	38.06	31
PREDICTED: similar to chromosome 9 open reading frame 7	18410	34853142	272157	1	1	5.2632K	KGDAISYAR	I	490.7538	2	979.4929	-0.015688	979.508588	62.25	31
PREDICTED: similar to evolutionarily conserved G-patch domain containing	100900	34855741	271140	1	1	1.2128K	AIVTTDDFASK	T	584.3668	2	1166.7191	0.13719	1166.58191	31.75	31
PREDICTED: similar to glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) (EC 1.2.1.12) - mouse	34590	34869386	306407	1	3	11.1111K	LVINGKPVTFQER	D	807.4097	2	1612.8048	-0.12518	1612.92998	35.01	30
PREDICTED: similar to hypothetical protein 6820428D13	64490	27688925	279415	1	1	1.9031R	DQGSFSFFLEK	D	652.8749	2	1303.7352	0.12681	1303.60839	35.61	30
PREDICTED: similar to hypothetical protein BC013949	25320	27668745	274768	1	1	5.9908R	AAFTAFEEVQLPR	L	739.8548	2	1477.695	-0.061486	1477.756486	55.04	30
PREDICTED: similar to hypothetical protein FLJ20254	76570	34863014	234260	1	1	1.7518K	SLSPFAIAYLDR	L	676.8341	2	1351.6536	-0.059899	1351.713499	33.16	31
PREDICTED: similar to immunoglobulin light chain	16750	62647397	161334	1	1	8.7248R	FSGSGSGTDFTLK	I	652.2633	2	1302.5121	-0.096983	1302.609083	63.9	31
PREDICTED: similar to mALDP	81940	34881747	306584	1	1	2.7137R	GPQVPAGESTQEASGATTAK	A	943.8514	2	1885.6882	-0.2135	1885.9017	70.76	29
PREDICTED: similar to mKIAA1311 protein	118700	34879262	281850	1	1	1.0377R	LSSGEDITELR	K	604.3165	2	1206.6185	0.045719	1206.572781	31.41	31
PREDICTED: similar to magnesium-dependent phosphatase-1	18610	27700106	272326	1	1	10.9756R	TSEIEGANQLLELFDLGK	Y	989.0144	2	1976.0143	0.004121	1976.010179	61.35	29
PREDICTED: similar to membrane progesterin receptor alpha	39280	27732829	204220	1	1	6.087R	SFQEVPSALAYALDISPVVHR	I	767.1476	3	2298.4209	0.22017	2298.20073	62.91	28
PREDICTED: similar to mitochondrial inner membrane translocase component Tim17b	18380	34933423	256607	1	1	8.7209R	NAPPFLEDPNQLTPK	E	840.9801	2	1679.9456	0.093751	1679.851849	55.23	30
PREDICTED: similar to novel protein of unknown function (DUF423) family member	11780	27672946	240868	1	1	24.7788R	LGALSGAGALSLATYGAHG A QFPDAYGK	E	888.6893	3	2663.0461	-0.28813	2663.33423	78.88	27
PREDICTED: similar to phosphoinositide 3-kinase, regulatory subunit 4, p150	152400	83288384	268833	1	1	1.1782R	LAYAENIALLAETALR	F	866.4817	2	1730.9488	-0.007756	1730.956556	33.84	30
PREDICTED: similar to polypeptide GalNAc transferase-T4	66710	77736615	167222	1	1	2.2491R	SPTMAGGLFAVSK	K	641.2776	2	1280.5407	-0.10271	1280.64341	92.83	31
PREDICTED: similar to protein tyrosine phosphatase-like (proline instead of catalytic arginine), member b	15720	34882969	201524	1	1	9.0909R	QAGLYSISLPNK	Y	645.8876	2	1289.7607	0.062837	1289.697863	85.48	31

PREDICTED: similar to ribosomal protein L10a	24720	27665840	215516	1	4	23.5023K	KYDVFLASESLIK	Q	756.9743	2	1511.934	0.1105	1511.8235	48.66	30
PREDICTED: similar to seven transmembrane domain protein	25290	84042519	227176	1	1	7.5893K	ASVDVADLIGLNLVMSR	N	894.9816	2	1787.9487	0.003635	1787.945065	95.26	29
PREDICTED: similar to signal peptidase 12kDa	11750	27667224	307512	1	1	11.7647K	WLPVQDSGTEDK	K	687.875	2	1373.7354	0.089137	1373.646263	45.57	31
PREDICTED: similar to signal recognition particle 19kDa	16140	27683535	219536	1	1	9.7222K	QEDGSLCLVQFPSR	K	818.5063	2	1634.9981	0.22595	1634.77215	35.64	30
PREDICTED: similar to slingshot-2L	159400	34873212	264614	1	1	1.6073K	AVSELVSPDIIMQSHSENAISVK	E	818.6183	3	2452.8332	-0.41392	2453.24712	29.81	28
PREDICTED: similar to vesicle associated membrane protein 4	16370	62659601	164208	1	1	8.5106R	HLNDDDDVTGSVK	S	650.2713	2	1298.528	-0.082246	1298.610246	91.12	31
PREDICTED: similar to zinc binding alcohol dehydrogenase, domain containing 2	40480	34932585	231239	1	1	3.9788R	FVGINASDINYSAGR	Y	792.4118	2	1582.809	0.035168	1582.773832	33.23	30
Peptidyl-prolyl cis-trans isomerase, mitochondria precursor PPIase Rotamase Cyclophilin F	21810	56268806	88229	1	1	4.3689R	FPDENFTLK	H	555.7968	2	1109.579	0.039772	1109.539228	47.15	30
Peroxisomal biogenesis factor 3 Peroxin-3	42210	8926847	12072	1	1	2.957K	HSLSLLDLEQK	L	641.8343	2	1281.654	-0.038837	1281.692837	63.37	30
Peroxisomal assembly protein PEX3	24730	8393922	51565	1	1	5.6075R	LLDQSTGLYEYK	V	715.3687	2	1428.7228	0.00922	1428.71358	56.09	30
Phosphatidylcholine transfer protein	22490	6981348	69787	1	1	6.5327R	SHCFTQAMMSQPK	M	792.8426	2	1583.6706	0.017582	1583.653018	50.91	30
Phosphatidylethanolamine N-methyltransferase	10470	1916012	78112	1	1	13.0435R	TGEPDEEEGTFR	S	683.8603	2	1365.706	0.13764	1365.56836	108.05	31
Phospholemmann precursor	161100	2696236	82680	1	1	1.3793R	GHAEMAIALWNNMLEVPVGKK	T	747.707	3	2240.0993	-0.008831	2240.108131	30.8	28
Phospholipase B	40590	29692074	249141	1	1	2.973K	LPYSVLLEIQK	Q	651.8403	2	1301.666	-0.093442	1301.759442	51.84	31
Phosphoserine aminotransferase	32180	57164095	304888	1	1	4.1237K	MLDPFLLFDEFK	G	765.9509	2	1529.8872	0.13964	1529.74756	65.7	31
Pirin	58880	57667	63679	1	1	1.6981R	SSYLPTPHR	A	353.1837	3	1056.5294	-0.005825	1056.535225	39.7	31
Potassium voltage-gated channel subfamily A member 6	52790	6174931	37272	1	1	4.0598R	AAVQELSGSILTSDEPEER	G	1015.9663	2	2029.918	-0.062268	2029.980268	29.46	29
Presenilin 1	15810	62651081	178365	1	1	9.2857R	TFGIWTLLSSVIR	C	746.9729	2	1491.9313	0.086434	1491.844866	85.08	31
Probable ergosterol biosynthetic protein 28	18720	34862186	25274	1	1	8.125K	LTFSCLGSDNFK	H	723.9937	2	1444.7728	0.10718	1444.66562	50.92	31
Prostaglandin E synthase 3 Cytosolic prostaglandin E2 synthase cPGES Telomerase-binding protein p23 Hsp90 co-chaperone Progesterone receptor complex p23 Sid 3177															
Prostaglandin G/H synthase 1 precursor	69030	603052	103863	1	1	2.99K	IIIEEYVQHLSGYFLQLK	F	731.805	3	2192.3931	0.205	2192.1881	36.53	28
Proteasome (Prosome, macropain) 26S subunit, ATPase 3	49550	38304011	71853	1	1	3.6199K	LAGPQLVQMFIGDGAK	L	823.0124	2	1644.0103	0.13987	1643.87043	32.6	30
Proteasome (Prosome, macropain) subunit, beta type 1	26410	37231712	233720	1	1	7.5R	FFPYVYVNIIGLDEEGK	G	1062.5058	2	2122.997	-0.027992	2123.024992	44.71	29
Proteasome subunit alpha type 7 Proteasome subunit RC6-1	28330	2118151	72897	1	1	5.9055K	NYTDDAIEITDDLTIK	L	863.9064	2	1725.7982	0.003784	1725.794416	47.67	30
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	4.6414R	LAAIQQSVER	Q	556.365	2	1170.7154	0.079768	1170.635632	62.3	31
Protein C2orf18 homolog precursor	41090	81883393	167119	1	1	4.0323R	GYLEDALDAFCQVGR	Q	825.3882	2	1648.7619	-0.025899	1648.787799	61.86	30
Protein C6orf89 homolog	39570	40786457	205305	1	1	3.7356R	ELFPVFTQLPFPK	D	781.9985	2	1561.9825	0.12808	1561.85442	44.15	31
Protein JTB precursor	16390	6016410	128391	1	1	8.9041K	TTPECGSTGYVEK	I	714.8542	2	1427.6938	0.070038	1427.623762	89.34	30
Protein LRP16	28640	32129697	214491	1	1	3.876K	VDLSTSTDWK	E	576.3015	2	1150.5885	0.03791	1150.55059	56.59	31
Protein kinase C, alpha type	76790	56914	44893	1	1	1.7857K	LTDNFNLMVLGK	G	707.3809	2	1412.7473	0.010003	1412.737297	37.08	30
Protein tyrosine phosphatase type IVA protein 1 Protein-tyrosine phosphatase 4a1 Protein-tyrosin phosphatase of regenerating liver 1 PRL-1 PTP(CAAXI)	19820	68566099	4701	1	1	8.6705R	APVLVALALIEGGMK	Y	749.473	2	1496.9314	0.067907	1496.863493	54.7	30
Protein-tyrosine phosphatase-like N precursor	105200	1113923	11137	1	1	1.1329START	CGGSEGGGLR	L	518.8038	2	1035.593	0.15271	1035.44029	32.74	31
Proteolipid protein 2	16560	62286961	166582	1	1	7.947R	HTAAPTDPTDGP	END	590.2621	2	1178.5096	-0.010802	1178.520402	56.96	31
Proto-oncogene C-crk P38 Adapter molecule crk	33840	9506515	95160	1	1	5.5921R	IGDQEFDSLPALEFYK	I	992.9824	2	1983.9502	-0.032692	1983.982892	95.22	29
Putative SKAP55 Src family associated phosphoprotein 2	40720	47482120	15613	1	1	4.1899R	NLLADVETFVADTLK	G	825.0391	2	1648.0636	0.19168	1647.87192	60.16	30

Putative secreted protein ZS1G11	33770	56090363	262914	1	1	4.5307R	ETSATPFSPGASNR	A	711.2112	2	1420.4078	-0.25037	1420.65817	50.55	30
RAB6-interacting protein 2 ERC protein 1 ERC1 CAZ-associated structural protein 2 CAST2	108800	51701367	165980	1	1	1.1603K	LSSTQQSLAEK	E	596.3446	2	1190.6746	0.060365	1190.614236	70.51	31
RAT liver glutathione S-transferase YA subunit mRNA	15290	2117744	72819	1	7	51.8797R	KLPVDAK	Q	385.7816	2	769.5486	0.078886	769.469714	43.64	31
RGPR-p117	116800	16758344	60469	1	1	1.0397R	VLEPDWLVLQR	R	684.4029	2	1366.7912	0.030354	1366.760846	40.95	30
RNA terminal phosphate cyclase domain 1	39310	51948426	319337	1	1	3.8251K	VGIEAAEMLLANLR	H	758.4513	2	1514.888	0.075392	1514.812608	42.6	30
RNA-dependent initiation factor-2 Kinase	58260	9506993	47246	1	1	2.1442K	LAVEILDNENK	V	629.3733	2	1256.732	0.070865	1256.661136	68.77	31
RT1.A1(F) protein	39250	1483574	42127	1	4	13.2565R	YISVGYYDHTFEVR	F	562.2311	3	1693.6716	-0.154	1683.8256	45.05	30
Rab GDP dissociation inhibitor alpha	50540	71534276	67742	1	3	11.1857R	KFDLGQDVDFIGHALALYR	T	760.3104	3	2277.9095	-0.26501	2278.17451	96.55	29
Rab-related GTP-binding protein Rab38, member of RAS oncogene family	23780	47125439	44313	1	1	5.2133R	LQLWDIAGQER	F	664.8723	2	1327.7301	0.041668	1327.688432	52.31	31
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	2.5229K	EQLAELEKTVK	Q	644.2027	2	1286.3908	-0.31733	1286.70813	31.46	31
Ras-related C3 botulinum toxin substrate 2 precursor p21-Rac2 EN-7 protein	21440	56605840	8458	1	3	16.6667K	LAPITYPQGLALAK	D	728.3608	2	1454.707	-0.14265	1454.84965	36.98	30
Ras-related protein Rab-11A Rab-11	24390	55249677	41486	1	10	54.1667R	ENDMSPSNVVIHVPPPTTENKPK	V	665.8661	4	2659.4354	0.14431	2659.29109	30.79	28
Ras-related protein Rab-13	22900	46577668	169821	1	3	15.7635K	SSNVNDEAFSSLAR	D	741.4209	2	1480.8273	0.11161	1480.71569	32.09	31
Ras-related protein Rab-1B	22180	56605816	166705	1	17	85.5721K	IDSTPVK	S	380.1765	2	758.3385	-0.078881	758.417381	44.37	33
Ras-related protein Rab-35 Rab-1C GTP-binding protein RAY	23030	62900797	35585	1	2	12.9353K	FAGQMIGIQLFETSAK	E	822.4275	2	1642.8405	0.038114	1642.802386	61.22	30
Ras-related protein Rap-1A	20990	54114993	4747	1	6	35.3261R	VKDTEDVPMILVGNK	C	829.4734	2	1656.9323	0.056753	1656.875547	47.62	30
Rat alpha(1)-inhibitor 3, variant I precursor	165300	91949	6160	1	49	46.2677K	SPLPKEPPR	K	510.7496	2	1019.4847	-0.091612	1019.576312	42.8	32
Ratg1	40610	18266700	111523	1	1	4.5699R	STGEAFVQFASQEIAEK	A	921.5228	2	1841.0311	0.14691	1840.88419	50.32	30
Retinol-binding protein I, cellular Cellular retinol-binding protein CRBP	15700	809309	105881	1	1	8.9552K	MLSNENFEELYR	A	780.8504	2	1559.6863	-0.006227	1559.692527	93.53	30
Rh blood group protein RH30	46580	3445506	90519	1	1	4.2654R	ATISTLPLLIISAGAVLGK	V	863.0218	2	1724.029	-0.015645	1724.044645	55.26	30
Rho guanine nucleotide exchange factor 7 PAK-interacting exchange factor beta Beta-Pix	73140	2865596	2120	1	1	2.1672R	KESAPQVLLPEEEK	I	798.8085	2	1595.6024	-0.23819	1595.84059	37.41	30
Rho-related GTP-binding protein RhoB precursor H6	22120	51338594	113828	1	3	25.5102K	DEFPEVYVPTVFENYVADIEVDGK	Q	925.5009	3	2773.481	0.18009	2773.30091	54.66	27
Ribonuclease 4 precursor RNase 4 RL3	16900	9910536	42830	1	1	8.8435R	FNTFIHEDIWNIR	S	852.8478	2	1703.681	-0.16095	1703.84195	59.66	30
Ribosomal protein S27 Metallopanstimulin 1	9461	5924385	4845	1	4	39.2857K	DLLHPSPEEEK	R	647.3616	2	1292.7086	0.083786	1292.624814	83.89	30
S-arrestin	44990	92737	84325	1	1	3.2258K	AFATDITDAEEDK	I	713.1802	2	1424.3458	-0.28489	1424.63069	34.24	31
S15 ribosomal protein	13360	40287237	337119	1	5	55.2632START	RGVDLDQLDMSYEQLMQLYSAR	Q	926.1673	3	2775.4802	0.15947	2775.32073	54.25	27
SH3P13 SH3 domain protein 2 C1	35310	7109256	75738	1	1	2.5641K	AVAEILSK	A	415.7921	2	829.5697	0.078848	829.490852	45.4	33
SIRR-1 precursor	44730	425789	100550	1	1	1.9512R	SEVTELRR	L	495.2648	2	988.515	-0.015098	988.530098	38.5	32
SWISS-PROT:P12368 cAMP-dependent protein kinase type II-alpha regulatory subunit	41980	206150	168209	1	1	3.5135K	MFESFIESVPLFK	S	795.4111	2	1588.8077	0.023031	1588.784669	42.13	30
Sarcosine dehydrogenase, mitochondrial precursor SarDH	101400	52000744	85749	1	1	2.7203R	DILQDVLADLSNEAFFPSTHQLVR	A	948.4267	3	2842.2584	-0.15527	2842.41367	71.08	27
Selenoprotein P precursor	41580	47939025	1271	1	1	5.7143R	LVYHLGLPYSFLTFPYVEEAIK	I	867.1588	3	2598.4546	0.077313	2598.377287	49.07	27
Sequestosome-1 Ubiquitin-binding protein p62 Protein kinase C-zeta-interacting protein PKC-zeta-interacting protein	47680	77416574	19107	1	1	3.6446R	LTPTSAESSSTGTEDK	S	805.8938	2	1609.773	0.041151	1609.731849	44.76	30
Serine (Or cysteine) proteinase inhibitor, clade F member 2 Predicted	54890	58865362	341343	1	1	2.6477K	LGLQDLFQSPDLR	G	751.4627	2	1500.9108	0.11717	1500.79363	91.9	31
Serine protease hepsin Serine protease hepsin non-catalytic chain Serine protease hepsin catalytic chain	44930	8393560	51490	1	1	2.6442R	IVGGQDSSLGR	W	544.7971	2	1087.5795	0.017429	1087.562071	34.31	32
Serine protease inhibitor, Kunitz type 2	21310	40018550	319145	1	1	6.2176R	SSDGASALSVP	K	573.7886	2	1145.5626	-0.005024	1145.567624	37.03	31
Serine/threonine-protein kinase PLK1 Polo-like kinase 1 PLK-1	68310	497994	12071	1	1	2.4876R	LILYNDGDSLQYIER	D	906.5876	2	1811.1607	0.25064	1810.91006	30.37	30

Serine/threonine-protein phosphatase 1 regulatory subunit 10 Phosphatase 1 nuclear targeting subunit Protein PNUITS MHC class I region proline-rich protein CAT53	92830	61214571	55278	1	1	0.80275K	LVKQLSK	S	408.3245	2	814.6345	0.10692	814.52758	32.28	32
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	1	1	3.0905R	SFFSEIISISDVK	F	779.9089	2	1557.8032	0.010596	1557.792604	58.7	30
Serotransferrin precursor Transferrin Siderophilin Beta-1 metal-binding globulin	76360	6175089	37301	1	43	54.8711R	EGVCPEASIDSA PVK	W	779.9286	2	1557.8426	0.10816	1557.73444	41.85	30
Serum amyloid A 4 Predicted	14970	57164089	301225	1	1	9.2308R	DHGLSQSTQK	A	671.795	2	1341.5754	-0.076972	1341.652372	70.15	31
Serum paraoxonase/arylesterase 1	38460	1945471	19325	1	12	58.2609START	GLVLALYKNHR	S	642.4152	2	1282.8158	0.064932	1282.750868	98.12	30
Short/branched chain specific acyl-CoA dehydrogenase, mitochondrial precursor SBCAD	47820	6978433	3600	1	1	5.0926R	IFDFQGLQHQA VHA VTA QL EAAR	L	827.0623	3	2478.165	-0.11166	2478.27666	55.94	28
2-methyl branched chain acyl-CoA dehydrogenase 2-MEBCAD 2-methylbutyryl-coenzyme A dehydrogenase 2-methylbutyryl-CoA dehydrogenase															
Shwachman-Bodian-Diamond syndrome Predicted	28750	56605652	227484	1	1	4K	GEVQVSDKER	H	573.8598	2	1145.7051	0.13751	1145.56759	64.94	31
Sideroflexin 1	38560	545998	80422	1	9	37.2549R	SGDAPLTVNELGTAYVSATTGAVATAGLNLTK	H	1083.2095	3	3246.6067	-0.091555	3246.698255	53.88	26
Signal recognition particle 14 kDa protein SRP14	12510	27731985	38099	1	1	12.7273M	VLLESEQFLTELTR	L	839.3813	2	1676.748	-0.15041	1676.89841	46.49	30
Similar to interferon-inducible GTPase	48190	62664492	237237	1	4	14.8681R	DIDGTPLNVAVTGESGAGK	S	900.8925	2	1799.7704	-0.1196	1799.89	33.75	29
Similar to phospholysine phosphorhistidine inorganic pyrophosphate phosphata 5M590	29190	57528359	221017	1	1	7.7778R	ADGYVDNLAEAVDLLLQHMDK	END	782.7123	3	2345.115	-0.005868	2345.120868	61.88	28
Single-stranded DNA-binding protein, mitochondrial precursor Mt-SSB MtSSB P16	17450	423723	44190	1	1	6.6225R	SLNRVQLLGR	V	578.3557	2	1154.6969	0.008604	1154.688296	31.59	31
Small nuclear ribonucleoprotein Sm D1 snRNP core protein D1 Sm-D1 Sm-D autoantigen	13280	34877889	3858	1	1	16.8067R	YFILPDLSPLDTLLVDVEPK	V	1144.1941	2	2286.3736	0.13381	2286.23979	33.7	28
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	0.35879R	LKNISSK	Y	395.2252	2	788.4359	-0.039687	788.475587	35.63	33
Sodium/calcium exchanger 1 precursor	108100	57209	44653	1	1	0.72091R	EMARILK	E	430.7267	2	859.4389	-0.055971	859.494871	34.76	33
Solute carrier family 10, member 1	39300	8394279	11254	1	1	3.8674K	AAATEDATPAALEK	G	679.8021	2	1357.5895	-0.082922	1357.672422	85.8	31
Solute carrier family 21 member 4	62970	19071449	198521	1	3	6.338START	MGPDALPR	S	428.8248	2	855.6351	0.20782	855.42728	34.13	31
Son protein	12550	34849639	313065	1	1	8.8496R	SLPNEEIVQK	I	578.8297	2	1155.6449	0.031393	1155.613507	33.78	31
Sorting nexin 3	18760	79152346	75350	1	1	4.321K	TNLPIFK	L	416.7642	2	831.5138	0.028411	831.485389	42.47	33
Splicing factor, arginine/serine-rich 3	19330	62665747	4905	1	2	12.8049R	NPPGFAFVEFEDPRDAADAVR	E	774.116	3	2319.3261	0.23415	2319.09195	42.92	28
Squalene monooxygenase Squalene epoxidase SE	64020	8394354	137571	1	1	2.0942R	GVLLGDAYNLR	H	652.4264	2	1302.8383	0.10876	1302.72954	62.25	31
Sterol 12-alpha hydroxylase	57520	4587057	129969	1	4	10.02K	DGISNWLGFMLR	F	704.7827	2	1407.5508	-0.14605	1407.69685	44.16	30
Sterol 12alpha-hydroxylase P450	57590	5360891	75741	1	4	10.02K	VLDFVTYAR	E	542.337	2	1082.6595	0.083519	1082.575981	37.64	31
Stonin	81920	33636736	277960	1	1	0.95759K	IDRLPDK	N	428.7544	2	855.4942	0.012824	855.481376	39.17	31
Stromal cell-derived factor-1 gamma	13550	76563910	209385	1	1	11.7647K	ILNTPNCALQIVAR	L	791.9137	2	1581.8129	-0.053115	1581.866015	83.14	30
Synaptogyrin-1 p29	25670	9507167	47308	1	1	5.1282K	AGGAFDPYTLVR	Q	633.8406	2	1265.6667	0.026342	1265.640358	78.11	31
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	5.4475K	IDSNLDELSVGLGR	L	744.2637	2	1486.5129	-0.2498	1486.7627	107.13	30
Syndecan-1 precursor	33210	6981518	75082	1	1	6.0703R	NQSPVDEGATGASQGLLDR	K	958.031	2	1914.0475	0.13967	1913.90783	107.13	29
Syntaxin 6	29060	51858907	78119	1	1	9.8039R	IGGELEEQA VMLDDF SHELESTQSR	L	946.0789	3	2835.2148	-0.071947	2835.286747	30.45	27

Syntaxin-8	26910	3834382	78117	1	1	7.6271K	IIIEQDAGLDALSSIISR	Q	965.0954	2	1928.1763	0.15492	1928.02138	103.96	30
TREMBL:O35234 Diphor-1	52250	2331224	80899	1	13	35.654K	NNDLVVAVNGESVEALDHDGVVEMIR	N	937.5396	3	2809.597	0.24187	2809.35513	52.95	27
TREMBL:Q6MG49;Q9WTN8 REFSEQ_NP:NP_446061 ENSEMBL:ENSRNOP0000001129 BAT3	114900	4587081	60486	1	1	1.184R	LLGNITFVLSDLR	C	709.8459	2	1417.6772	-0.1156	1417.7928	33.82	31
TREMBL:Q9EPH2 REFSEQ_NP:NP_110489 ENSEMBL:ENSRNOP00000012663 Mac-MARCKS protein	19850	76363234	71714	1	1	7.5377R	GDVTAAEEAAGASPAK	A	687.3173	2	1372.62	-0.026949	1372.646949	62.72	31
TSH receptor suppressor element-binding protein 1	35530	9653686	93202	1	3	18.323R	SVGDGETVEFDVVEGEK	G	898.4817	2	1794.9489	0.13303	1794.81587	88.81	29
Target of myb1 homolog	54090	56605806	200982	1	1	2.6423K	VLNLIQSWADAFR	S	766.879	2	1531.7434	-0.071243	1531.814643	37.31	30
Tax_Id=10116 2-oxoglutarate carrier	34250	2497985	23402	1	7	28.3439K	TSFHALTSILK	A	609.3841	2	1216.7537	0.072174	1216.681526	70.62	31
Tax_Id=10116 33 kDa protein	33300	34872473	212891	1	1	4.0678R	KMDEADASSAVK	V	634.2444	2	1266.4742	-0.1019	1266.5761	42.38	31
Tax_Id=10116 Aldehyde dehydrogenase family 1, subfamily A4	54560	91935	83139	1	3	7.984R	ANNTPYGLAAGVFTK	D	762.4825	2	1522.9504	0.17254	1522.77786	93.47	30
Tax_Id=10116 Complement Component 5	134400	34853897	205903	1	1	1.1745K	GLLIGEFLSTVLSK	E	738.8831	2	1475.7517	-0.10816	1475.85986	100.93	31
Tax_Id=10116 Dihydrolipamide branched chain transacylase E2	53460	34859889	232730	1	1	2.8926K	SYLENPAFMILLDLK	END	835.5105	2	1669.0065	0.16324	1668.84326	51.53	30
Tax_Id=10116 Ensembl_locations(Chr-bp):16-73342360 similar to ankyrin	186300	34879099	195573	1	1	0.58685K	HGVTVDATTR	M	528.748	2	1055.4815	-0.054426	1055.535926	37.82	31
Tax_Id=10116 Ensembl_locations(Chr-bp):17-77022236 similar to aldo-keto reductase family 1 member C12	32180	34876320	221880	1	4	15.1408R	SSAQIALR	Y	423.2294	2	844.4443	-0.032336	844.476636	33.13	33
Tax_Id=10116 Ensembl_locations(Chr-bp):2-120296304 similar to fragile-X-related protein 1 isoform e	68720	34856814	266426	1	1	2.2913R	GFLEFVEDFIQVPR	N	848.4714	2	1694.9282	0.061454	1694.866746	86.88	30
Tax_Id=10116 Ensembl_locations(Chr-bp):2-252454876 similar to crystallin, zeta	37130	34860973	210117	1	1	2.5714START	MATGQKLMR	A	534.1603	2	1066.3061	-0.22014	1066.52624	31.62	31
Tax_Id=10116 Ensembl_locations(Chr-bp):2-2908047 glutaredoxin 1 (thioltransferase)	11880	38181944	246362	1	1	10.2804K	TQEILSQLPFK	R	652.4083	2	1302.8021	0.083821	1302.718279	61.39	31
Tax_Id=10116 Ensembl_locations(Chr-bp):3-141766859 FK506 binding protein 2	11920	501064	43461	1	1	12.037M	GVQVETISSGDGR	T	652.7463	2	1303.4781	-0.15865	1303.63675	41.37	30
Tax_Id=10116 Ensembl_locations(Chr-bp):4-160981651 Serine protease	77790	7435632	13085	1	1	2.0173K	IQSPFWQVYFESPR	G	892.3701	2	1782.7257	-0.14715	1782.87285	77.6	30
Tax_Id=10116 Ensembl_locations(Chr-bp):4-56330652 similar to Impdh1 protein	60730	34855047	190455	1	1	1.4109K	LVGIVTSR	D	422.828	2	843.6415	0.12376	843.51774	34.77	32
Tax_Id=10116 Ensembl_locations(Chr-bp):4-97148803 Hypothetical RNA binding protein RDA288	43010	18041977	114376	1	1	2.8061R	RPDQQLQGDGK	I	621.1814	2	1240.3482	-0.26778	1240.61598	60.42	31
Tax_Id=10116 Ensembl_locations(Chr-bp):6-93096989;10-64690010 proteasome (prosome, macropain) subunit, alpha type 3	28420	8394066	45012	1	1	4.7059K	AVENSSSTAIGIR	C	609.3848	2	1216.7551	0.11401	1216.64109	37.96	31
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	4.2705R	GVVQDLQQAISK	L	643.3357	2	1284.6568	-0.046897	1284.703697	39.62	31
Tax_Id=10116 Ensembl_locations(Chr-bp):7-120740849 similar to alpha-N-acetyl-galactosaminidase	54520	34867288	202900	1	1	3.5197R	TISPNIDILQNPLLIK	I	960.5403	2	1919.066	-0.043128	1919.109128	43.56	29
Tax_Id=10116 Ensembl_locations(Chr-bp):8-46234308 similar to RIKEN cDNA D130038B21	40890	34863198	270449	1	1	3.2698R	GVDSVFEPLLK	E	645.8893	2	1289.764	0.077402	1289.686598	35.74	31
Tax_Id=10116 Ensembl_locations(Chr-bp):None similar to CLCP	25370	34852289	287945	1	1	5.1724K	NSNPALNDNLEK	G	664.884	2	1327.7534	0.11668	1327.63672	60.22	31
Tax_Id=10116 Ensembl_locations(Chr-bp):None similar to betaine-homocysteine methyltransferase 2	46420	34861318	247159	1	1	4.0094R	AGADVLQITFSAADR	M	899.944	2	1797.8735	0.020197	1797.853303	80.56	30
Tax_Id=10116 Glutathione S-transferase theta 1	27470	56265	111659	1	1	5K	DLFLEAHEVILK	V	713.8975	2	1425.7804	-0.006289	1425.786689	82.67	30

Tax_Id=101116 HypotHetical protein XP_213403	19700	34872851	239897	1	1	8.1871K	IVGGLIELVDQLAK	E		734.36	2	1466.7054	-0.16537	1466.87077	74.04	30
Tax_Id=101116 HypotHetical protein XP_215523	21540	34854965	295192	1	1	4.6632K	TKIDSLGR	L		501.7512	2	1001.4878	-0.099071	1001.586871	59.46	32
Tax_Id=101116 HypotHetical protein XP_235050	101800	34864725	191344	1	1	1.31K	NACLQTSSLAVR	V		660.3511	2	1318.6876	0.021298	1318.666302	33.73	31
Tax_Id=101116 HypotHetical protein XP_342343	17520	34860574	313817	1	1	9.9379K	SSAGNVLLGSADFYSR	F		822.3948	2	1642.7751	-0.019885	1642.794985	63.39	30
Tax_Id=101116 HypotHetical protein XP_346991	26610	34857419	273429	1	1	2.9046R	VLESRIR	E		436.7579	2	871.5012	-0.022707	871.523907	33.63	32
Tax_Id=101116 Integrln, alpha 6	141300	34855181	306780	1	1	1.1067K	SEDEVGSLIEYEFR	V		836.8288	2	1671.643	-0.11974	1671.76274	54.42	30
Tax_Id=101116 Lactate dehydrogenase B	36610	6981146	3968	1	4	12.5749K	SLADELALVDVLEDK	L		815.4046	2	1628.7946	-0.056247	1628.850847	71.03	30
Tax_Id=101116 M4 protein	74540	16124253	136387	1	1	1.8651R	LGSTVFVANLDYK	V		713.8933	2	1425.772	0.021723	1425.750277	66.53	30
Tax_Id=101116 Major vault protein	95800	49256645	395977	1	24	45.7607K	SLTIDGSSPINLFSTAFGLLGLGSDGQPPAQK	END		1097.3122	3	3288.9148	0.22709	3288.68771	45.76	26
Tax_Id=101116 P450 (cytochrome) oxidoreductase	76960	66118	78074	1	37	62.5369R	AKEPAGENGGR	A		543.23	2	1084.4454	-0.080619	1084.526019	37.18	31
Tax_Id=101116 PDZ domain-containing protein	56890	8439549	78142	1	13	30.9751R	IMFLLVDKETAR	C		718.3032	2	1434.5918	-0.19865	1434.79045	30.61	30
Tax_Id=101116 Similar to 1700013L23Rik protein	22400	34853020	251303	1	1	7.4257R	TLPVSDSALNAFEER	V		824.8641	2	1647.7137	-0.096621	1647.810321	100.15	30
Tax_Id=101116 Similar to 25 kDa brain-Specific protein (p25-alpha)	30720	34853331	206115	1	1	5.6338R	TITFEQFQEALEELAK	K		949.0633	2	1896.1121	0.16052	1895.95158	32.41	29
Tax_Id=101116 Similar to 60S riboSomal protein L10 (QM protein homolog)	11450	34853952	238486	1	8	62R	IHIGQVIMSIR	T		641.9205	2	1281.8264	0.10374	1281.72266	45.7	30
Tax_Id=101116 Similar to 60S riboSomal protein L7a (Surfeit locuS protein 3) (PLA-X polypeptide)	26160	34869696	200139	1	10	33.0435K	KVWNPLYEK	G		545.3787	2	1088.7429	0.11996	1088.62294	52.3	32
Tax_Id=101116 Similar to 9630010P11Rik protein	161100	34855819	234438	1	1	0.54018R	EELDRHIR	I		534.2118	2	1066.409	-0.14292	1066.55192	32.22	31
Tax_Id=101116 Similar to A-kinase anchor protein 9 iSoform 2	441400	34854301	223472	1	1	0.23438K	QEKEQLLR	C		578.8407	2	1155.6668	0.00565	1155.66115	31.15	31
Tax_Id=101116 Similar to ALY	21140	34875658	307156	1	1	5.5838R	SLGTADVHFER	K		616.1626	2	1230.3106	-0.28865	1230.59925	45.9	31
Tax_Id=101116 Similar to Actin monomer-binding protein	204100	34866518	244260	1	1	0.58824R	QGGENTFCLPK	T		625.8949	2	1249.7752	0.19914	1249.57606	34.79	31
Tax_Id=101116 Similar to Alanyl-tRNA SynthetaseS (Alanine--tRNA ligaSe) (AlaRS)	108200	34851760	253193	1	1	1.9388K	EIADLGEVLATAVIPQWQK	D		1041.1431	2	2080.2716	0.15127	2080.12033	30.7	29
Tax_Id=101116 Similar to Ali-1 protein +GTE form mouSe (fragment)	374300	34863265	267292	1	1	0.26178K	KIIPAPKPK	G		496.1893	2	990.364	-0.29489	990.65889	36.12	32
Tax_Id=101116 Similar to Alpha enolaSe (2-phospho-D-glycerate hydro-lyase) (Non-neural enolaSe) (NNE) (EnolaSe 1)	39350	34875256	313683	1	8	29.3296K	IDQLMIK	M		438.7653	2	875.516	0.037361	875.478639	37.22	33
Tax_Id=101116 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	2.294R	LSWSLLVNSPR	V		642.3401	2	1282.6656	-0.09517	1282.76077	43.15	30
Tax_Id=101116 Similar to Amyloid beta A4 precuSor protein-binding family B member 2 (Fe65-like protein)	53090	34877353	294691	1	1	2.7368K	VRPPPPPADSVTR	R		694.9203	2	1387.826	0.068892	1387.757108	47.63	31
Tax_Id=101116 Similar to Arginine-tRNA-protein tranSferaSe 1	51870	34859415	229620	1	1	1.5086R	YQMIIHK	D		466.9106	2	931.8066	0.31171	931.49489	33.94	32
Tax_Id=101116 Similar to BC013491 protein	76140	34856101	235741	1	1	1.0294K	MGMLOER	A		440.7833	2	879.5521	0.15788	879.39422	62.24	32
Tax_Id=101116 Similar to CENTROMERIC PROTEIN E (CENP-E PROTEIN)	313000	34860597	241018	1	1	0.25679K	QEQLNIK	E		436.7311	2	871.4476	-0.0287	871.4763	35.04	32
Tax_Id=101116 Similar to CG11388-PA	36250	34869404	241377	1	1	5.7402R	ELFEEFDNFLPGAVIGIAR	E		1069.0252	2	2136.0358	-0.053187	2136.088987	38.25	28
Tax_Id=101116 Similar to CG33130-PA	132700	34853057	208493	1	1	1.0842K	TPTPSVETLPHSR	S		711.4732	2	1420.9318	0.20079	1420.73101	33.65	30
Tax_Id=101116 Similar to CMP-Sialic acid tranSporter	36550	34867231	260011	1	1	3.5608K	ASLSENVLGSPK	E		601.3059	2	1200.5972	-0.037741	1200.634941	75.43	31
Tax_Id=101116 Similar to CUB and SuShi multipledomain 3	213400	34866475	195940	1	1	0.6208R	SGSSELSTVIGR	L		596.8293	2	1191.644	0.034501	1191.609499	36.74	31

Tax_Id=10116 Similar to Cgn-pending protein	159200	34858031	242726	1	5	3.0561R	LQELLEK	R	436.8391	2	871.6636	0.16215	871.50145	47.62	32
Tax_Id=10116 Similar to Complement C5 precursor (Hemolytic complement)	42190	34853846	242533	1	1	4.244R	ALVEGV DQLLT DYQIK	D	903.023	2	1804.0314	0.069607	1803.961793	33.75	30
Tax_Id=10116 Similar to Cox7a2l protein	12650	27716471	268354	1	1	10.6195R	EAPPIIFATPTK	L	642.9253	2	1283.836	0.12347	1283.71253	55.46	31
Tax_Id=10116 Similar to DEAD/H (ASp-Glu-Ala-ASp/His) box polypeptide RIG-I	94370	34867138	315303	1	1	1.937K	IESFVEDIESGVQNR	H	911.0774	2	1820.1402	0.24514	1819.89506	40.42	30
Tax_Id=10116 Similar to DNA Segment, Chr 12, ERATO D01 551, expresSed	130300	34865806	300896	1	1	0.94017K	ELGKVLIDL SK	Q	607.8991	2	1213.7837	0.055609	1213.728091	39.47	31
Tax_Id=10116 Similar to DNA-directed RNA polymerase II largeSt Subunit (RPB1)	197600	34871645	202233	1	1	0.61694K	LLVDSNNPKIK	D	620.7996	2	1239.5846	-0.13404	1239.71864	32.08	31
Tax_Id=10116 Similar to ENSANGP00000013261	15620	27689183	197176	1	1	7.2993K	DPAKPVVAQK	T	526.8282	2	1051.6417	0.039209	1051.602491	40.92	31
Tax_Id=10116 Similar to FERM, RhoGEF, and pleckStrin domain protein 1	23830	34876611	304176	1	1	6.422R	LGAPENSIGSTLER	G	722.4089	2	1442.8031	0.066698	1442.736402	110.25	31
Tax_Id=10116 Similar to FLJ00354 protein	155900	34861517	210125	1	2	1.1561R	TVEQENRTL R	G	623.3532	2	1244.6919	0.044645	1244.647255	32.16	31
Tax_Id=10116 Similar to GE36	76150	34880541	272300	1	1	1.8895K	KYYEIVMLCGLLK	M	823.466	2	1644.9174	0.055561	1644.861839	33.5	30
Tax_Id=10116 Similar to Herc2	542900	34856238	254063	1	1	0.24125R	VIGELGEDGWIR	V	672.473	2	1342.9315	0.24351	1342.68799	43.8	31
Tax_Id=10116 Similar to Hypothetical protein 5031404N19	336600	34867996	239621	1	1	0.36089K	SSSISEMEELR	L	634.4375	2	1266.8605	0.28437	1266.57613	37.22	31
Tax_Id=10116 Similar to Hypothetical protein 9030012M21	37150	34875719	205153	1	1	3.5608R	EALGLWSALQLK	I	664.9237	2	1327.8328	0.082924	1327.749876	44.73	31
Tax_Id=10116 Similar to Hypothetical protein FLJ35794	51380	27708530	166638	1	1	2.4775K	QLLAKELEEEK	M	665.2834	2	1328.5523	-0.16639	1328.71869	31.64	31
Tax_Id=10116 Similar to Hypothetical protein KIAA0233	237700	34932058	265857	1	1	0.43394R	DDELEESEK	F	547.2541	2	1092.4937	0.047897	1092.445803	33.64	32
Tax_Id=10116 Similar to Integrin beta-2 precursor (Cell Surface adhesion glycoproteinSLFA-1/CR3/P150,95 beta-Subunit) (CD18) (Complement receptor C3 beta-Subunit)	84530	34852369	241188	1	1	2.2164K	LGGDLLQALNEITESGR	I	893.5945	2	1785.1744	0.24765	1784.92675	36.37	30
Tax_Id=10116 Similar to KDEL containing protein 1	60890	34863399	261916	1	1	2.2814R	YFFLQSV DSDGR	N	717.3451	2	1432.6757	0.013437	1432.662263	52.21	31
Tax_Id=10116 Similar to KIAA0316 protein	140900	34879922	244528	1	1	1.0133R	SLLTSLSGPDTLKK	A	686.8436	2	1371.6726	-0.12466	1371.79726	35.09	31
Tax_Id=10116 Similar to KIAA0342 protein	333800	34866451	266038	1	1	0.344K	NHVL CQEVQR	N	641.8058	2	1281.597	-0.027728	1281.624728	32.62	30
Tax_Id=10116 Similar to KIAA0695 protein	71450	34879447	314767	1	1	2.0934R	SLLSMLS DLQVYK	D	748.9104	2	1495.8063	0.01071	1495.79559	48.05	30
Tax_Id=10116 Similar to KIAA0903-like protein	120900	34879170	275605	1	1	1.7658R	AHFSGQELNVVQIEENSSK	S	1058.4557	2	2114.8968	-0.12632	2115.02312	36.73	29
Tax_Id=10116 Similar to KIAA0963 protein	162200	34862323	279597	1	1	0.68306R	GMKWEEAFTR	S	627.7642	2	1253.5139	-0.072315	1253.586215	31.78	31
Tax_Id=10116 Similar to KIAA1407 protein	75980	34869160	295453	1	1	1.059K	KMDELLK	A	438.7809	2	875.5472	0.068561	875.478639	34.63	33
Tax_Id=10116 Similar to KIAA1414 protein	184500	34861977	207796	1	1	0.99707R	SFATFLSHVLDLVSHPR	A	642.6429	3	1924.9068	-0.10906	1925.01586	40.53	29
Tax_Id=10116 Similar to KIAA1453 protein	119600	34875569	239514	1	1	0.73126K	SPEGPVSR	V	414.8052	2	827.5959	0.18219	827.41371	33.85	32
Tax_Id=10116 Similar to KIAA1630 protein	148300	34876831	315956	1	1	1.1646K	LLLESQEFDFHLATK	F	895.9361	2	1789.8576	-0.06742	1789.92502	34.83	29
Tax_Id=10116 Similar to KIAA1940 protein	82950	34856348	273209	1	1	1.4398R	SNEVISPEILK	M	614.9249	2	1227.8353	0.16426	1227.67104	41.51	31
Tax_Id=10116 Similar to KinetochoresAssociated protein 1 (Rough deal homolog) (hRod) (HSROD (Rod))	222900	34872331	265212	1	1	0.61287R	GYGIREVNLLNK	E	688.3583	2	1374.702	-0.059888	1374.761888	35.47	31
Tax_Id=10116 Similar to Leukotriene A-4 hydrolase (LTA-4 hydrolase) (Leukotriene A(4) hydrolase)	93570	34864937	286024	1	1	1.8116K	DVDPDVAYSSIPYEK	G	849.5094	2	1697.0043	0.22115	1696.78315	33.7	30
Tax_Id=10116 Similar to MaltaSe-glucosaminylaseinteStinal	494700	34855581	199085	1	1	0.90048R	YTLLPYLYTLMYK	A	849.4736	2	1696.9326	0.053997	1696.878603	33.85	30
Tax_Id=10116 Similar to Mylk protein	73330	34869218	268038	1	1	1.3867R	RLNAGSLK	V	494.3432	2	986.6719	0.12104	986.55086	33.02	32
Tax_Id=10116 Similar to Nebulette (Actin-binding Z-diSk protein)	121800	34877348	276942	1	1	1.4995K	KDLENEIK	G	494.7817	2	987.5489	0.025287	987.523613	54.28	32
Tax_Id=10116 Similar to Nedd4 WW binding protein 4	32550	34860870	317802	1	1	3.413R	DPEQQLELNR	E	621.3888	2	1240.7631	0.15837	1240.60473	38.3	31
Tax_Id=10116 Similar to PTB-aSSociated Splicing factor	65140	34871066	310879	1	1	2.6891R	LFVGNLPADITEDEFK	R	904.4217	2	1806.8288	-0.075112	1806.903912	35.03	29
Tax_Id=10116 Similar to Protein Njmu-R1	44430	34872893	315828	1	1	4.0712K	GAFFEGLGNVASVELR	I	833.3019	2	1664.5893	-0.26277	1664.85207	76.6	30
Tax_Id=10116 Similar to RIKEN cDNA 111003102	36810	34875673	300976	1	1	3.0581R	VPEGNSAAER	R	515.3525	2	1028.6905	0.20189	1028.48861	42.75	32

Tax_Id=10116 Similar to RIKEN cDNA 1110055L24	27770	34854713	201498	1	1	7.6305K	GPDDLGLGMFYDTDDASFK	W	1060.4786	2	2118.9426	-0.002893	2118.945493	62.96	29
Tax_Id=10116 Similar to RIKEN cDNA 1200014J11	80090	34872727	249723	1	1	1.5603R	SSNRNSAVLYR	C	633.9231	2	1265.8316	0.18404	1265.64756	33.35	31
Tax_Id=10116 Similar to RIKEN cDNA 1300014E15	74920	34877442	203301	1	1	1.9288R	GSLNEQIALVLIR	L	713.4754	2	1424.9362	0.10117	1424.83503	83.15	31
Tax_Id=10116 Similar to RIKEN cDNA 1700034M03 gene	122500	34854321	261953	1	1	0.94073R	IWQDVQLKVK	T	628.7619	2	1255.5093	-0.2195	1255.7288	35.61	31
Tax_Id=10116 Similar to RIKEN cDNA 2610020H15	71060	34872958	298062	1	1	1.9048R	STGVNVNVS DLK	Y	616.755	2	1231.4955	-0.14521	1231.64071	39.3	31
Tax_Id=10116 Similar to RIKEN cDNA 2610207I16	122600	34868438	250916	1	1	1.6901K	LLGTIYTAEEIEAAGGK	A	904.0862	2	1806.1578	0.21685	1805.94095	73.61	29
Tax_Id=10116 Similar to RIKEN cDNA 2810025M15	71590	34880767	272641	1	1	4.0971R	IPENVSLQDAAVLPVSYGTAILAVDHR	A	950.1097	3	2847.3072	-0.20577	2847.51297	39.21	27
Tax_Id=10116 Similar to RIKEN cDNA 4632417N05	35570	34851797	239422	1	1	6.4815R	VILFDIIEPAQNLP EGITFVR	G	1192.4636	2	2382.9126	-0.40238	2383.31498	64.25	28
Tax_Id=10116 Similar to RIKEN cDNA 4732474A20 gene	70120	34862810	190227	1	3	5.7566R	TENGLWLNVEPLPSR	A	862.8559	2	1723.6971	-0.19212	1723.88922	55.77	30
Tax_Id=10116 Similar to RIKEN cDNA 4933412D19	164100	34867309	293100	1	1	1.2943R	TVLIAADVL PDGGLPQDEK	L	996.1077	2	1990.2009	0.13872	1990.06218	57.17	29
Tax_Id=10116 Similar to RIKEN cDNA 4932408F18	51730	34858091	273635	1	1	2.6608R	INVTDTDILALER	R	680.3453	2	1358.6761	-0.028049	1358.704149	80.34	31
Tax_Id=10116 Similar to RIKEN cDNA 5730507E09	81090	34880803	213507	1	1	1.6667R	FSLPVF AFVMTK	F	701.9706	2	1401.9266	0.19006	1401.73654	51.95	31
Tax_Id=10116 Similar to RIKEN cDNA 5630401D24	131000	34867616	273407	1	1	0.68435R	DLDMEELR	E	518.6503	2	1035.2861	-0.16815	1035.45425	33.38	31
Tax_Id=10116 Similar to RIKEN cDNA 5730507E09	89840	34881696	266670	1	1	0.86634R	RGVCGPR	A	401.2242	2	800.4338	0.026282	800.407518	39.86	32
Tax_Id=10116 Similar to RIKEN cDNA 6430520C02	73500	34851643	224054	1	1	2.1962K	NLVLPTD TFFSYDLR	R	924.0269	2	1846.0393	0.10924	1845.93006	35.53	29
Tax_Id=10116 Similar to RIKEN cDNA 9530027K23	41350	34869346	228920	1	1	3.9886K	TDLSDVQELLQFVK	A	818.0168	2	1634.0191	0.16282	1633.85628	129.29	30
Tax_Id=10116 Similar to RIKEN cDNA 9630046K23	238800	34853214	288172	1	1	0.5717R	IVGLSTALANAR	D	593.3464	2	1184.6782	-0.009485	1184.687685	33.75	31
Tax_Id=10116 Similar to Rab24 protein	26250	34873657	250158	1	1	4.721K	TGQSVDEL FQK	V	626.3621	2	1250.7097	0.095441	1250.614259	45.38	31
Tax_Id=10116 Similar to SH3 domain protein D19	125000	34857900	291964	1	1	0.69869R	LSNSDRTR	N	474.6934	2	947.3722	-0.10626	947.47846	39.62	32
Tax_Id=10116 Similar to Semaphorin SubclaSS member G	128000	34863455	222218	1	1	0.94991R	EEGSSSF TQSR	S	607.7974	2	1213.5801	0.059091	1213.521009	48.22	31
Tax_Id=10116 Similar to Serine/threonine kinaSe	179600	34874060	212247	1	1	0.4914K	TYSQMKEK	M	507.7771	2	1013.5396	0.054475	1013.485125	32.84	31
Tax_Id=10116 Similar to Sialic-acid O-acetylcSteraSe	56760	34863093	198275	1	1	2.3483K	ELSDTAAYQSVR	I	670.3304	2	1338.6462	0.004698	1338.641502	50.22	30
Tax_Id=10116 Similar to Sidekick 2	185200	34875033	275767	1	1	0.59737K	TLFLAENSVK	L	561.3678	2	1120.7211	0.10837	1120.61273	33.93	32
Tax_Id=10116 Similar to Sif and Tiam1-like exchange factor	155900	34853702	204958	1	1	0.78684R	RFSDWTGSLSR	K	656.2482	2	1310.4818	-0.15488	1310.63668	34.89	31
Tax_Id=10116 Similar to Solute carrier family 30 (zinc tranSporter), member 6	51480	34862482	294808	1	1	3.4483R	SLCGIIPGLSSIFLPR	M	865.4609	2	1728.9072	-0.052387	1728.959587	70.06	30
Tax_Id=10116 Similar to Structural maintenance of chromoSomaS 1beta	147300	34867523	216707	1	1	1.1032K	SNVMDALSFVMGEK	T	772.3794	2	1542.7442	0.038478	1542.705722	32.22	30
Tax_Id=10116 Similar to Sulfide quinone reductaSe-like	78570	34856819	285775	1	1	2.3121K	ANIIFNTALGTIFGVK	K	839.971	2	1677.9275	-0.017749	1677.945249	88.56	30
Tax_Id=10116 Similar to T-box 1	54510	34861377	314802	1	1	2.0576R	GV PALLYTLR	S	551.8151	2	1101.6156	-0.038944	1101.654544	32.85	32
Tax_Id=10116 Similar to TAFII140 protein	85530	34876351	313782	1	1	1.3072R	EPLSSINPQK	I	556.8441	2	1111.6736	0.086312	1111.587288	36.22	31
Tax_Id=10116 Similar to TTF-I interacting protein 5	183400	34862191	316025	1	1	0.72115K	SSFPLTFTEEDR	L	714.7942	2	1427.5738	-0.082982	1427.656782	36.35	30
Tax_Id=10116 Similar to Trm26 protein	47090	34852035	264888	1	1	4.6229R	EQHLLDQLATLEQLL TEGR	E	736.413	3	2206.2173	0.05802	2206.15928	89.46	28
Tax_Id=10116 Similar to TyroSine-protein kinaSe JAK1 (JanuS kinaSe 1) (JAK-1)	150400	34869913	290958	1	1	1.1459R	TTFQNLIEGFEALLK	END	862.529	2	1723.0435	0.12431	1722.91919	50.3	30
Tax_Id=10116 Similar to UDP-glucuronate decarboxylaSe 1	20220	34881188	201012	1	1	4.4944K	AAPILSPR	H	412.7144	2	823.4142	-0.077319	823.491519	42.08	31

Tax_Id=10116 Similar to UNR-interacting protein (Serine-threonine kinaSe receptor-aSSociated protein)	48180	34858563	269251	1	1	1.5909R	DPRSPLR	V		420.8165	2	839.6184	0.15707	839.46133	32.18	31
Tax_Id=10116 Similar to WAVE2	41650	34871786	222802	1	2	8.5561K	FYTNPSYFFDLWK	E		864.4714	2	1726.9283	0.1252	1726.8031	53.1	30
Tax_Id=10116 Similar to WD repeat domain 9 iSoform A	225200	34881323	312923	1	1	0.55276K	AAKIVTDVLLR	F		599.9475	2	1197.8805	0.13608	1197.74442	37.24	31
Tax_Id=10116 Similar to actin - Hydra attenuata	13310	34871187	219221	1	1	5.7851M	PACAPSR	T		379.676	2	757.3374	-0.016652	757.354052	48.1	33
Tax_Id=10116 Similar to acyltranSferaSe family member (5G933)	33640	34862502	237775	1	1	3.4843R	TTGFTFVDR	L		571.7155	2	1141.4163	-0.16037	1141.57667	78.91	31
Tax_Id=10116 Similar to alpha-2u-globulin	61070	34868545	210822	1	7	9.8148R	VFMQHINVLENSLGFK	F		631.4844	3	1891.4314	0.46532	1890.96608	68.94	29
Tax_Id=10116 Similar to alpha-catenin-like protein	21080	34852606	311543	1	1	5.8824K	NLMNAVVTVK	M		608.8389	2	1215.6633	-0.001202	1215.664502	61.91	32
Tax_Id=10116 Similar to aminoadipate-Semialdehyde Synthase	92010	34855019	258586	1	1	2.0507K	SIGPLTFVFTGTGNVSK	G		862.9113	2	1723.808	-0.10643	1723.91443	50.26	30
Tax_Id=10116 Similar to amyIo-1,6-glucosidaSe 4-alpha-glucanotranSferaSe iSoform 1	180900	34859913	208010	1	1	1.192K	GFIQVYVDQVDEDIVAVTR	H		1083.5612	2	2165.1078	0.007491	2165.100309	39.41	28
Tax_Id=10116 Similar to apoA-I binding protein	78970	34857927	303449	1	1	2.5035K	GNPSGIQPDLLISLTAPK	K		910.9997	2	1819.9848	-0.019535	1820.004335	78.16	30
Tax_Id=10116 Similar to archvillin	236900	34876218	258828	1	1	0.61205K	VPAGDSSLDSPSK	T		630.3223	2	1258.6301	0.026003	1258.604097	85.69	31
Tax_Id=10116 Similar to autocrine motility factor receptor	68280	34851252	285136	1	1	3.1457R	TYTGLSGLALLGTIVSAYR	A		978.5678	2	1955.121	0.048315	1955.072685	53.6	29
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	1.6269R	ATGFGVALLLALFGR	A		753.4647	2	1504.9149	0.038388	1504.876512	31.2	30
Tax_Id=10116 Similar to beta1-Syntrophin	48920	34866568	190168	1	1	5.2506K	DSATAQAWFSAIHNVGDLLVR	V		786.6261	3	2356.8565	-0.3198	2357.1763	84.77	28
Tax_Id=10116 Similar to breakpoint cluSter region protein	177200	34852435	289382	1	1	0.50441R	AEWRESIR	E		523.8292	2	1045.6437	0.11331	1045.53039	33.9	32
Tax_Id=10116 Similar to bromodomain-containing protein BRD4 Short variant	159800	34862361	292562	1	1	0.62805R	LAELQEQLK	A		536.334	2	1070.6535	0.056366	1070.597134	44.84	32
Tax_Id=10116 Similar to bullouS pemphigoid antigen 1-b	1087000	34874618	233230	1	1	0.083005K	SPASKLDK	S		423.1348	2	844.255	-0.21035	844.46535	35.44	33
Tax_Id=10116 Similar to chromoSome 14 open reading frame 9	34520	34869712	209283	1	1	3.3846R	VCQSPINVEGK	M		615.8246	2	1229.6347	0.027307	1229.607393	43.41	31
Tax_Id=10116 Similar to chromoSome 17 open reading frame 27	668500	34875599	199223	1	1	0.20315R	VPFNINFDSLPR	H		709.8594	2	1417.7042	-0.031148	1417.735348	51.14	31
Tax_Id=10116 Similar to coiled-coil protein	148900	34869656	304228	1	1	1.2298R	TVEELLETGLIQVATR	E		886.6491	2	1771.2836	0.31095	1770.97265	30.5	30
Tax_Id=10116 Similar to complement component 8 alpha Subunit	62090	34869994	295319	1	1	5.1376K	YNPVVIDFEMQPIYQLLQHTNLGPLETK	R		1106.1719	3	3315.4939	-0.19099	3315.68489	55.79	26
Tax_Id=10116 Similar to copine IV	96010	34865971	245798	1	1	0.81301K	QNIPSTR	G		408.2984	2	814.5823	0.15264	814.42966	33.33	32
Tax_Id=10116 Similar to dJ14N1.2 (novel S-100/CaBP type calcium binding domain protein, Similar to trichohyalin)	133800	34858169	280707	1	1	0.96154R	LDFTEFILMVFK	L		759.9577	2	1517.9008	0.11689	1517.78391	86.15	30
Tax_Id=10116 Similar to dedicator of cyto-kineSiS 2	113200	34861140	200712	1	1	1.417K	GEADFVESLLQLFR	S		812.3713	2	1622.7279	-0.10239	1622.83029	129.4	30
Tax_Id=10116 Similar to development- and differentiation-enhancing factor 2	119200	34863212	230447	1	1	0.74697K	EIISEVQR	M		487.3155	2	972.6164	0.092432	972.523968	46.98	32
Tax_Id=10116 Similar to embryonic biaStocoelar extracellular matrix protein precuSor	242800	34851569	303538	1	1	0.59199K	LAEAVGEFLVPVR	R		700.4502	2	1398.8859	0.098885	1398.787015	43.77	31
Tax_Id=10116 Similar to eukaryotic tranSlation initiation factor 3, Subunit 5 epSiIon, 47kDa	35120	34858904	213255	1	1	5.7576R	IQDALSTVLQYAEDVLSGK	V		1025.44	2	2048.8654	-0.19748	2049.06288	119.51	29
Tax_Id=10116 Similar to ferrochelatase	71200	34932061	313806	1	1	1.9139R	VMEQLGYPNPYR	L		741.8265	2	1481.6385	-0.058747	1481.697247	78.61	30
Tax_Id=10116 Similar to heterogeneous nuclear ribonucleoprotein D-like	58310	34876235	191966	1	2	4.1431K	DAASVDKYLELK	E		644.3552	2	1286.6959	-0.012247	1286.708147	35.44	31
Tax_Id=10116 Similar to hiStidyl-tRNA Synthetase-like	82680	34878791	223302	1	1	0.96286R	LFGIADK	I		382.2187	2	762.4228	-0.004748	762.427548	37.02	33

Tax_Id=10116 Similar to hyaluronan receptor for endocytosis HARE precursor	58970	34868786	260956	1	4	9.6296K	GLTGS LPSLLTR	L		607.871	2	1213.7275	0.0245	1213.703	49.19	31
Tax_Id=10116 Similar to hypothetical protein	390800	34865159	241253	1	1	0.17361R	HSVQDR	S		371.244	2	740.4735	0.11695	740.35655	35.91	30
Tax_Id=10116 Similar to hypothetical protein	125800	34878417	272431	1	1	1.5233K	SLFVLPHTDHLVGYIIR	L		660.6016	3	1978.7829	-0.31632	1979.09922	33.25	29
Tax_Id=10116 Similar to hypothetical protein	141900	34854842	233766	1	1	0.99923R	QDHLTG HMLTHQK	T		781.5132	2	1561.0119	0.26522	1560.74668	31.69	30
Tax_Id=10116 Similar to hypothetical protein BC002942	96350	34867679	290052	1	1	1.4134R	LIQNQVANYPFR	E		732.0012	2	1461.9879	0.21509	1461.77281	74.19	30
Tax_Id=10116 Similar to hypothetical protein FLJ10375	107600	34866614	302504	1	1	1.7895K	ETLENQNLYLVGASNIR	L		967.5939	2	1933.1732	0.18283	1932.99037	48.96	29
Tax_Id=10116 Similar to hypothetical protein FLJ10737	91330	34872498	233304	1	1	1.7073K	AGFFGTIVEYGAER	K		758.9073	2	1515.8	0.064321	1515.735679	48.65	31
Tax_Id=10116 Similar to hypothetical protein FLJ10900	93700	34872027	198580	1	1	1.8072K	AVTSLDLPVAIINLK	E		783.987	2	1565.9595	0.02031	1565.93919	56.34	30
Tax_Id=10116 Similar to hypothetical protein FLJ11274	34120	34866189	272995	1	1	5.5901K	APAAFGLVSFLMHAGLER	N		629.6642	3	1885.9708	-0.016411	1885.987211	43.88	29
Tax_Id=10116 Similar to hypothetical protein FLJ12681	90650	34870562	205672	1	1	2.4814K	LLADDAEALSLLALNPFEGR	A		1064.4595	2	2126.9044	-0.21665	2127.12105	37.13	29
Tax_Id=10116 Similar to hypothetical protein FLJ14681	65310	34858680	304442	1	1	1.2153R	LGTVMHR	V		415.2767	2	828.5389	0.11134	828.42756	61.09	33
Tax_Id=10116 Similar to hypothetical protein FLJ20531	57240	34871405	217607	1	1	1.938K	FLLDRLGAER	D		595.391	2	1188.7674	0.10595	1188.66145	45.34	31
Tax_Id=10116 Similar to hypothetical protein FLJ21665	52020	34876595	213091	1	4	8.4233R	LIAQVLSSITASLR	F		736.4615	2	1470.9084	0.031525	1470.876875	61.71	30
Tax_Id=10116 Similar to hypothetical protein FLJ21820	32850	34863103	317090	1	1	6.2284R	APELPVVHTLLFPPTIER	M		693.7561	3	2078.2465	0.0901	2078.1564	61.42	29
Tax_Id=10116 Similar to hypothetical protein FLJ21963	91790	34865010	243174	1	1	2.1635R	VLAHEGVAALFTAPT AIR	A		613.0399	3	1836.0977	0.072041	1836.025659	34.85	29
Tax_Id=10116 Similar to hypothetical protein FLJ30373	29880	34855399	229721	1	1	2.9197R	YLQEARSR	E		511.8091	2	1021.6036	0.073147	1021.530453	37.23	31
Tax_Id=10116 Similar to hypothetical protein FLJ30596	61060	34854388	283019	1	1	2.5641R	VAAQAVEDVLI NAR	R		734.9181	2	1467.8216	0.017149	1467.804451	91.62	30
Tax_Id=10116 Similar to hypothetical protein FLJ31657	64050	34855501	253349	1	1	2.385K	HTTSIFDDFAHYEK	R		570.9744	3	1709.9014	0.13289	1709.76851	36.98	29
Tax_Id=10116 Similar to immunoglobulin 4G6 light chain variable region	17890	34855968	195860	1	1	9.3168R	FSGSGSGTDFTLTIR	S		773.3759	2	1544.7373	-0.009757	1544.747057	47.44	30
Tax_Id=10116 Similar to intracellular membrane-associated calcium-independent phospholipase A2 gamma	107800	34865151	313999	1	1	0.62435K	FPSLRR	A		388.268	2	774.5214	0.071436	774.449964	50.21	33
Tax_Id=10116 Similar to kidney ankyrin repeat-containing protein	127000	34860436	261449	1	1	1.1036K	TQDDIDITLQLFR	L		789.4549	2	1576.8953	0.085606	1576.809694	70.33	31
Tax_Id=10116 Similar to lysosomal aspartate-like 1	40920	34874392	217901	1	1	2.5496R	GTGDFDLOR	E		520.6973	2	1039.3801	-0.059187	1039.439287	45.04	31
Tax_Id=10116 Similar to lymphocyte cytosolic protein 1	80290	34875362	272629	1	3	4.8679K	VNDDIIVNWNVNTLK	E		872.3513	2	1742.688	-0.23225	1742.92025	54.23	30
Tax_Id=10116 Similar to mKIAA1402 protein	86520	34853978	259133	1	1	2.0619R	ADVGD AVDTALEQLNR	R		844.0205	2	1686.0265	0.20455	1685.82195	37.34	30
Tax_Id=10116 Similar to malignant cell expression-enhanced gene/tumor progression enhancer	33720	34854458	281230	1	1	7.1661R	TYLDWLEQFPPEAVPSLRPLLR	R		880.9235	3	2639.7487	0.33761	2639.41109	38.09	27
Tax_Id=10116 Similar to meiotic recombination protein REC14	28800	34863419	201803	1	1	6.2016K	ENIETVWTGSLDDL VK	V		866.5213	2	1731.028	0.13429	1730.89371	66.54	30
Tax_Id=10116 Similar to melanoma inhibitory activity protein 2	58930	34865264	225113	1	1	4K	FFDNPWG FQNRPEDTELPFSK	Q		857.8044	3	2570.3913	0.20479	2570.18651	50.94	28
Tax_Id=10116 Similar to membrane receptor (5H375)	42380	34865609	318262	1	1	4.8649R	WDEV PDDFVECFILSGYR	R		1124.1398	2	2246.265	0.2661	2245.9989	57.14	29
Tax_Id=10116 Similar to methionyl aminopeptidase 1	53240	34860820	221417	1	1	2.3109K	HAQANGFSVVR	S		593.3512	2	1184.6879	0.082888	1184.605012	54.09	31
Tax_Id=10116 Similar to myosin X	251600	34855017	249318	1	1	0.27347K	IVVDER	E		365.6345	2	729.2544	-0.14765	729.40205	33.79	33

Tax_Id=10116 Similar to nonclathrin coat protein zeta2-COP	18220	34873491	273036	1	1	6.0241R	FQEPSLYTIK	A	613.3153	2	1224.616	-0.022964	1224.638964	46.08	31
Tax_Id=10116 Similar to oSmotic StreSS protein	148000	34856875	290180	1	4	2.9456K	QVYVDKLQELK	K	681.8933	2	1361.772	0.016626	1361.755374	31.19	31
Tax_Id=10116 Similar to oSteoclaSt inhibitory lectin	23540	34858508	255984	1	1	5.7971R	FDTEELNFLSR	Y	750.4496	2	1498.8846	0.1907	1498.6939	48.4	30
Tax_Id=10116 Similar to p140mDia	140200	34878815	217100	1	1	1.0293K	TAQNLSIFLGSFR	M	727.403	2	1452.7915	0.019062	1452.772438	48.54	30
Tax_Id=10116 Similar to peptidylprolyl iSomeraS D (cyclophilin D)	69130	34873471	283106	1	1	1.9324R	IVLELFADIVPK	T	678.8605	2	1355.7064	-0.099958	1355.806358	31.87	31
Tax_Id=10116 Similar to phoSphatidyInoSitolglycan claSS N	89310	34878866	217052	1	1	2.0356K	AESMFTNAVQILEQFK	E	928.3787	2	1854.7429	-0.17565	1854.91855	100.98	29
Tax_Id=10116 Similar to poliovirus receptor homolog	76950	34855325	279332	1	1	1.6925R	ITWISSLGGEAR	D	645.3344	2	1288.6543	-0.023202	1288.677502	38.98	31
Tax_Id=10116 Similar to protein RAKc	41260	34876322	249119	1	2	8.9136K	LNDGNLMPVLGFGTFASK	E	949.0657	2	1896.1169	0.17183	1895.94507	62.79	29
Tax_Id=10116 Similar to protein tyroSine phoSphataSe, receptor type, D iSoform 3	203600	34869007	215340	1	1	0.82827R	SPQGLGASTAEISAR	T	722.915	2	1443.8154	0.083683	1443.731717	41.71	31
Tax_Id=10116 Similar to putative mannoSyIttranSferaSe	59900	34867585	231757	1	1	2.0638K	VPPFDVSLQTK	L	615.8736	2	1229.7327	0.067205	1229.665495	31.86	31
Tax_Id=10116 Similar to putative zinc finger tranScription factor OVO1	37260	27661858	294340	1	1	2.1407R	LPELDLR	E	428.271	2	854.5275	0.041358	854.486142	34.63	30
Tax_Id=10116 Similar to retinal Short-chain dehydrogenaSe/reductaSe	43630	34872444	294993	1	1	3.7783R	FPNLPPLKPETVAR	R	576.0104	3	1725.0095	0.048158	1724.961342	46.73	30
Tax_Id=10116 Similar to riboSomal protein L27	22160	34875503	301863	1	1	10.8808K	IIDDGTSDRPYSHALVAGIDR	Y	757.8636	3	2270.5688	0.43976	2270.12904	50.76	28
Tax_Id=10116 Similar to riboSomal protein S15	50300	34851670	224899	1	1	2.6316K	VPPMEKPEVVK	T	676.419	2	1350.8235	0.065447	1350.758053	45.39	30
Tax_Id=10116 Similar to riboSomal protein S6 kinaSe, 52kDa, polypeptide 1	40530	34881360	216365	1	1	2.4064R	SSRESLDIK	E	517.7621	2	1033.5096	-0.030716	1033.540316	40.97	32
Tax_Id=10116 Similar to riboSomal protein S6 kinaSe, polypeptide 4	86910	34935429	292778	1	1	1.5524K	TNQAFAVKIISK	R	660.1745	2	1318.3345	-0.42633	1318.76083	35.97	31
Tax_Id=10116 Similar to ring finger protein 20	122200	34868389	236982	1	1	0.66794K	AELEDLR	Q	423.2296	2	844.4446	0.015567	844.429033	37.75	33
Tax_Id=10116 Similar to teSHS protein TEX15	282400	34866738	211558	1	1	0.67891R	YDLASGATEQLPLSGLR	A	895.9894	2	1789.9643	0.043369	1789.920931	36.07	29
Tax_Id=10116 Similar to the firSt amino acid was determined to be iSoleucine rather than methionine by compariSon to mTEF1 (aScSeSSio # L13853)	78480	34858488	267553	1	1	1.1065K	LKMALSVR	S	467.2436	2	932.4726	-0.07504	932.54764	32.71	32
Tax_Id=10116 Similar to tolloid-like 2	23740	34883204	298591	1	1	5.5556K	KTCEVETVPLEK	E	716.8288	2	1431.6431	-0.084767	1431.727867	45.04	31
Tax_Id=10116 Similar to tranSthyretin (4L369)	16010	34861187	199559	1	1	11.3475K	FHVPLLLSPWSYTTYR	G	660.5983	3	1978.773	-0.25746	1979.03046	42.37	29
Tax_Id=10116 Similar to tricarboxylate carrier	40660	34873877	278396	1	9	34.1463R	ASHFFTVDPR	N	639.2702	2	1276.5259	-0.094127	1276.620027	39.81	31
Tax_Id=10116 Similar to tubulin, alpha 6	63060	34868254	298819	1	19	46.4664K	EDAAANNYAR	G	512.2225	2	1022.4305	-0.011133	1022.441633	69.17	31
Tax_Id=10116 Similar to ubiquitin lgaSe E3 alpha-II	175300	34874398	274677	1	1	0.71244R	LLAGLHVLLSK	S	582.3272	2	1162.6399	-0.1038	1162.7437	33.9	31
Tax_Id=10116 Similar to ubiquitous tetratricopeptide containing protein RoXaN	111900	34867257	230656	1	1	1.407K	LVQNLFAGENDLFR	E	818.4677	2	1634.9209	0.07932	1634.84158	42.17	30
Tax_Id=10116 Similar to vaScular endothelial zinc finger 1	82930	34872980	252804	1	1	3.0144R	GGPPFAFVEFEDPRDAEDAVYGR	D	847.8827	3	2540.6264	0.46567	2540.16073	41.94	28
Tax_Id=10116 Similar to villin-like protein	99190	34866628	253969	1	1	1.2458K	LGESNVYNVQR	L	639.8634	2	1277.7122	0.075911	1277.636289	34.46	31
Tax_Id=10116 Similar to xylulokinaSe homolog	66490	34866669	229118	1	1	2.6016K	VVAFGDNPASLAGMR	L	803.3534	2	1604.6923	-0.10566	1604.79796	81.46	30
Tax_Id=10116 Similar to zinc finger protein, Subfamily 1A, 4	64460	34862217	313581	1	1	1.528START	MTAVPLTSR	N	488.26	2	974.5055	-0.016333	974.521833	35.81	32
Tax_Id=10116 Solute carrier family 25, member 5	32900	728810	117684	1	16	50K	GTDIMYTGTLDCWR	K	852.904	2	1703.7935	0.065171	1703.728329	54.08	30
Telomerase protein component 1 rTLP1 Telomerase-associated protein 1 protein 1 p240 p230 p80 telomerase homolog	291700	47606056	169376	1	1	0.38037R	YPSTLELFSR	S	606.9016	2	1211.7886	0.17002	1211.61858	53.96	31

Tetraspanin-31 Tspan-31 Sarcoma amplified sequence homolog	22660	62900748	260364	1	1	6.1905R	SSPCQMCGETFLK	H	772.8108	2	1543.607	-0.039928	1543.646928	56.65	30
Thioredoxin-related transmembrane protein 2	33870	56090369	227628	1	1	4.0678K	QLPTLILFQGGK	E	657.8585	2	1313.7025	-0.068152	1313.770652	31.64	31
Trafficking protein particle complex subunit 3 BET3 homolog	20300	71153350	145735	1	1	7.2222R	GALEMVQMAVEAK	F	696.779	2	1391.5435	-0.13529	1391.67879	38.23	30
Transaldolase	37480	17433174	50402	1	1	2.9674K	LGGPQEEQIK	N	549.7916	2	1097.5687	-0.002937	1097.571637	60.57	31
Transcobalamin-2 precursor Transcobalamin II TCII TC II	47420	5910985	90533	1	1	3.2787K	ISGGSIALYLLALR	A	723.9165	2	1445.8184	-0.042131	1445.860531	108.82	30
Transmembrane protein 14C p11	11780	27734399	30411	1	1	25.2174K	AGSVPSLAAGLFFGGLAGLGAYQLSQDPR	N	940.722	3	2819.1441	-0.31643	2819.46053	53.98	27
Transmembrane protein induced by tumor necrosis factor alpha	40660	58219512	260939	1	1	4.9563R	NWEDLQDFQGIQETHR	L	715.4072	3	2143.1998	0.22792	2142.97188	34.74	29
Tripeptidyl-peptidase 1 precursor Tripeptidyl-peptidase I TPP-I Tripeptidyl aminopeptidase	61330	20140356	75921	1	1	2.4867R	LFGSSFAHQASVAR	V	739.321	2	1476.6274	-0.11984	1476.74724	70.08	31
Tryptophan 2,3-dioxygenase	47860	59809151	11402	1	1	3.6946K	VFVDLFLNLSSYLVR	H	884.9868	2	1767.9591	0.003216	1767.955894	48.88	30
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	4.7138R	ILGIPVIITEQYPK	G	792.5446	2	1583.0746	0.1412	1582.9334	72.65	30
Type I keratin KA17	48120	71682170	301880	1	7	13.6259R	LEQEIATYR	R	561.7799	2	1121.5452	-0.026472	1121.571672	61.26	31
Type I keratin KA22	50210	57012446	161849	1	4	10.6195R	GQVGDDVNVEMDAAPGVDLSR	I	1051.4724	2	2100.9302	-0.044239	2100.974439	109.4	29
Type II keratin Kb15	57610	46485029	222258	1	8	11.2782R	AEAESWYQTK	Y	606.7504	2	1211.4862	-0.059614	1211.545814	44.9	31
Tyrosine-protein kinase LYN	58660	294583	71712	1	2	4.6875K	VNTLETEEWFFK	D	771.8775	2	1541.7404	0.000285	1541.740115	47.67	30
UDP glycosyltransferase 1 family polypeptide A7 UDP glycosyltransferase 1 family, polypeptide A6	60240	89276780	205347	1	22	51.6981R	SFGNNHFAASSPLMAPLR	E	645.0316	3	1932.0729	0.1418	1931.9311	70.55	29
UDP-glucuronosyltransferase 1A6	60250	1890306	53068	1	22	51.6981K	LPSIYLFR	G	504.8216	2	1007.6286	0.048275	1007.580325	49.98	31
UDP-glucuronosyltransferase 2B12 precursor, microsomal	60920	458397	127236	1	15	40.9434R	FVSVWTYELPR	D	698.8648	2	1395.7151	-0.00356	1395.71866	70.29	30
Ube2i-prov protein	18010	6981690	22316	1	1	7.5949K	DHPFGFVA/PTK	N	657.8871	2	1313.7597	0.08295	1313.67675	40.98	31
Ubiquinone biosynthesis protein COQ7 homolog Coenzyme Q biosynthesis protein 7 homolog Timing protein clk-1 homolog	20140	7446711	30131	1	1	6.1453R	IYAGQMAVLGR	T	589.8149	2	1177.6152	-0.012493	1177.627693	35.27	31
Ubiquitin specific protease 1 Predicted	87330	62543525	282121	1	1	1.0204K	HLFNIISR	K	500.252	2	998.4893	-0.076753	998.566053	40.96	32
Ubiquitin-conjugating enzyme E2 G2 Ubiquitin-protein ligase G2 Ubiquitin carrier protein G2	18570	62665819	58922	1	1	14.5455K	ILLSVWSMLAEPNDESGANVDASK	M	1238.0709	2	2474.1272	-0.093684	2474.220884	43.6	28
Uncharacterized protein C20orf30 homolog	13200	81882492	190070	1	1	9.1667R	TNLATGIPSSK	V	544.8175	2	1087.6204	0.033092	1087.587308	38.85	32
Uncharacterized protein family UPF0227 member RGD1359682	33990	55741536	265453	1	1	4.5161K	NLYADIDAAWQALR	T	810.4144	2	1618.8143	0.004045	1618.810255	34.73	30
Urinary protein 1 precursor RUP-1 Liver regeneration-related protein LRRG05	10960	6537316	37481	1	1	10.8911R	OESLDSTGLCR	V	649.3146	2	1296.6146	0.0708	1296.5438	36.04	30
Uroporphyrinogen decarboxylase	40450	5524747	44446	1	1	6.044R	LRDPAAVASELGYVFQAITLIR	Q	797.8476	3	2390.5209	0.22521	2390.29569	62.83	29
Vacuolar protein sorting 26 Vesicle protein sortin 26	38110	78099277	276682	1	1	3.9755R	LFLAGYDPTPTMR	D	741.231	2	1480.4474	-0.291	1480.7384	57.01	31
Vacuolar protein sorting 33A	67510	23396893	55286	1	1	3.5176R	EFTGSQNSVFPVFDNLLLLDR	N	1206.1587	2	2410.3028	0.086066	2410.216734	63.65	28
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 Vacuolar proton pump subunit 1 Vacuolar adenosine triphosphatase subunit Ac116	96330	206430	11413	1	1	1.432R	MQTNQTPPTYNK	T	719.858	2	1437.7014	0.045561	1437.655839	34.81	30
Vesicle-associated membrane 2	12690	6981614	38248	1	4	34.4828R	LQQTQAQVDEVVDIMR	V	936.8723	2	1871.73	-0.21108	1871.94108	77.16	29
Vesicle-associated membrane protein 3 VAMP-3 Synaptobrevin-3 Cellubrevin CEB	11480	56789137	23581	1	4	38.835R	LQQTQNQVDEVVDIMR	V	958.3339	2	1914.6533	-0.29354	1914.94684	133.6	29
Vitamin K epoxide reductase complex subunit 1 Vitamin K1 2,3-epoxide reductase subunit 1	17780	62511143	291525	1	1	11.1801R	LALCLAGLALSLYALHVK	A	642.7691	3	1925.2854	0.1683	1925.1171	104.32	29

Vitamin K epoxide reductase complex subunit 1-like protein 1 VKORC1-like protein 1	19780	62511142	165266	1	1	6.25R	GFGLLSIFGK	D	548.3042	2	1094.5938	-0.018507	1094.612307	52.58	31
Xanthine dehydrogenase/oxidase alpha-1-inhibitor III precursor	146300	2144323	80445	1	1	0.90158K	IPAFGSIPIEFR	V	673.9016	2	1345.7887	0.049319	1345.739381	61.5	31
apolipoprotein C-III precursor - rat	19360	554401	66447	1	6	54.4379K	NLHPLNELPLAYIED	END	949.4346	2	1896.8546	-0.10749	1896.96209	75.05	30
bile canalculus-specific membrane glycoprotein precursor	11030	91990	84170	1	1	19K	TVQDALSSMQESDIAVVAR	G	1018.5001	2	2034.9856	-0.003472	2034.989072	144.87	29
cAMP-dependent protein kinase, alpha-catalytic subunit (PKA C-alpha)	90930	204464	11237	1	19	24.8737R	RTYTLADYLK	N	622.3908	2	1242.767	0.10617	1242.66083	41.02	31
cathepsin J peak 2 [rats, liver, Peptide Partial, 34 aa]	40620	125207	168211	1	4	11.396R	FPSHFSSDLK	D	582.8023	2	1163.59	0.028907	1163.561093	45.21	31
claudin 1	3838	245685	79044	1	1	58.8235START	DPFNPFELTNHAVLLVGYGK	D	744.3846	3	2230.1321	-0.010029	2230.142129	63.2	29
cytochrome P450	22870	61889099	318701	1	1	7.5829K	VFDSLNLNLSTLQATR	A	896.5674	2	1791.1202	0.16758	1790.95262	84.32	30
cytochrome P450, family 2, subfamily c, polypeptide 23	57160	203695	126560	1	38	85.2K	GTNVV/SLSSILHDDK	E	849.432	2	1696.8495	-0.050018	1696.899518	49.88	30
cytochrome-c oxidase (EC 1.9.3.1) chain VIIa, hepatic - rat (fragment)	56490	56825	78212	1	28	60.9312R	VQEEAWCLVEELQK	T	880.7808	2	1759.547	-0.29803	1759.84503	99.96	30
divalent cation tolerant protein CUTA	1246	7513957	80282	1	1	80START	FENKVPEK	Q	495.7712	2	989.5278	0.009701	989.518099	47.76	32
ezrin, p81 [Rattus norvegicus]	16410	61212255	281056	1	1	5.8442M	PALLPVASR	L	462.2738	2	922.533	-0.026984	922.559984	36.65	31
fibrinopeptide A	18790	56126	85113	1	1	5.625K	QRIDEFEAM	END	577.8013	2	1153.5881	0.080764	1153.507336	40.27	31
fibrinopeptide B	1740	229210	22617	1	1	100START	ADTGTTFSEIDEGAGIR	END	870.51	2	1739.0055	0.20464	1738.80086	99.76	29
fumarase	1492	229196	22616	1	1	100START	ATTDSKVDISLAR	END	746.2426	2	1490.4707	-0.28695	1490.75765	145.82	31
hemoglobin beta chain, minor - rat	54460	227665	168825	1	7	25.8383K	LNDHFFLVVWQTGSGTQTNMNVNEISNR	A	1096.3061	3	3285.8965	0.3129	3285.5836	73.45	26
hypothetical protein XP_347087	15990	92362	84237	1	17	89.7959K	EFTPSAQAAFQKVAGVASALAHK	Y	810.0231	3	2427.0474	-0.24354	2427.29094	65.51	29
hypothetical protein XP_343009	87580	34862025	301974	1	1	1.0256R	LLACLEGK	E	452.2644	2	902.5143	0.024801	902.489499	41.61	33
hypothetical protein XP_343478	31580	34865907	203844	1	1	4.7138K	VSSVCGVEPMATLR	G	761.3429	2	1520.6713	-0.061307	1520.732607	33.7	30
hypothetical protein XP_344851	48260	34854602	287423	1	1	3.2483K	SQGGVQIPSQGGK	L	670.3776	2	1338.7406	0.051466	1338.689134	46.24	30
immunoglobulin kappa-chain	13870	34866914	300655	1	1	7.1429K	MSLHFQMLK	R	583.8669	2	1165.7193	0.15698	1165.56232	32.28	31
inureninase (L-kynurenine hydrolase)	14860	204835	126680	1	1	9.6296R	FSGSGSGTQYSLK	I	659.818	2	1317.6214	0.001422	1317.619978	49.37	31
lanosterol synthase	52450	3913969	157223	1	1	2.8017K	SILLTGYLEYLLK	H	763.3715	2	1524.7284	-0.15182	1524.88022	78.64	30
major vault protein - rat	83330	13591981	37206	1	12	20.191R	LYDAVAVLLSMR	N	683.8143	2	1365.6141	-0.11849	1365.73259	85.59	31
roundabout (axon guidance receptor, Drosophila homolog 2 [Rattus norvegicus])	99530	7514005	132766	1	24	41.8994R	IPPYHYIHVLDQNSNVSR	V	718.0447	3	2151.1122	0.026167	2151.086033	30.01	29
secreted frizzled-related protein 1	176100	34867440	317126	1	1	0.43559START	MFGRRLR	Q	441.7843	2	881.5541	0.10001	881.45409	32.12	31
sigalytransferase 1	35350	34879084	271324	1	1	2.5559START	MGVGRNAR	G	438.7953	2	875.5759	0.13645	875.43945	33.76	33
similar to 2310036102Rik protein	25210	285193	41195	1	7	40.6542K	FFDSACIMGAYHPLLFEK	N	717.2117	3	2148.6132	-0.3516	2148.9648	83.73	29
similar to 40S ribosomal protein S2 [Rattus norvegicus]	89350	34932104	265519	1	1	1.995R	NLETLQOELGIEGENR	V	922.0351	2	1842.0557	0.14387	1841.91183	76.23	29
similar to 60S ribosomal protein L15	28120	34868798	193682	1	12	41.9847K	AIGDYDGHVGLGVK	C	700.8433	2	1399.672	-0.03748	1399.70948	58.28	31
similar to 60S ribosomal protein L36	23920	34869871	293440	1	7	33.0049R	NPDTQWITK	F	551.716	2	1101.4175	-0.12791	1101.54541	65.45	32
similar to 9530008L14Rik protein [Rattus norvegicus]	12250	34856346	214593	1	6	37.7358R	QREELSNVLAAMR	K	506.3295	3	1515.9666	0.18388	1515.78272	65.53	31
similar to ATP synthase, H+-transporting, mitochondrial F0 complex, subunit c (subunit 9), isoform 2	11600	34875157	310564	1	1	7.9208K	WGATVTKPR	M	457.7685	2	913.5224	0.009112	913.513288	43.03	31
similar to Apoptosis inhibitor 5	14750	27685029	262837	1	1	5.7554R	SASQLPSR	L	423.2726	2	844.5307	0.090481	844.440219	37.62	33
similar to Asparaginyl-tRNA synthetase, cytoplasmic (Asparagine--tRNA ligase) (AsnRS)	36870	34878251	281550	1	1	5.4545K	GTLGGLFSQILQGEDIVR	E	951.9896	2	1901.9647	-0.056273	1902.020973	86.83	29
similar to BLOCK 23	64130	34932063	238208	1	1	2.6882K	SPVASIVYDLNPNFK	A	832.5356	2	1663.0567	0.19506	1662.86164	36.3	30
similar to CG33130-PA	30630	34869320	240773	1	2	6.2963K	TLGIATNISR	G	523.3183	2	1044.622	0.029316	1044.592684	34.34	32
similar to CG8014-PA	125000	34870072	215152	1	1	0.86207K	LSAALSSLQR	D	523.3128	2	1044.6111	0.018396	1044.592704	32.12	32
similar to CGI-90 protein	55190	34865850	245025	1	1	2.3158R	SYEFFNELYHR	F	752.9421	2	1503.8696	0.1914	1503.6782	39.75	30
similar to Conserved oligomeric Golgi complex subunit 5 (13S Golgi transport complex 90 kDa subunit) (GTC-90) (Golgi transport complex 1)	52100	34867201	258588	1	1	2.1598K	ESEDVELLWR	L	638.4117	2	1274.8088	0.19462	1274.61418	31.39	31
similar to DNA (cytosine-5)-methyltransferase 3A (Dnmt3a) (DNA methyltransferase MmullIA) (DNA MTase MmullIA) (M.MmullIA)	23020	34864266	295519	1	1	8.4906K	TYTSQSIHQAVIAEQLAK	L	663.2112	3	1986.6117	-0.42569	1987.03739	29.02	29
similar to DNA (cytosine-5)-methyltransferase 3A (Dnmt3a) (DNA methyltransferase MmullIA) (DNA MTase MmullIA) (M.MmullIA)	59410	34871224	241066	1	1	1.3133R	DNGLLAR	Q	379.7185	2	757.4224	0.014185	757.408215	36.67	33

similar to Dysferlin (Dystrophy associated fer-1 like protein) (Fer-1 like protein 1) [Rattus norvegicus]	224600	34856330	229917	1	1	0.55923R	TAIEILAWGLR	N	621.9494	2	1241.8842	0.17106	1241.71314	44.09	31
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	21.0402K	SGDAAIVDMVPGK	A	638.2748	2	1274.535	-0.082576	1274.617576	36.74	31
similar to Exocyst complex component Sec6 (rSec6)	72270	34855314	276511	1	1	1.0819R	RLPLADR	Y	420.7588	2	839.503	0.005292	839.497708	34.99	31
similar to Fc fragment of IgG binding protein; IgG Fc binding protein	583400	34855405	285938	1	1	0.16587R	ISVINGGSK	A	437.75	2	873.4854	-0.006525	873.491925	33.59	32
similar to Glyceraldehyde 3-phosphate dehydrogenase (GAPDH) (38 kDa BFA-dependent ADP-ribosylation substrate) (BARS-38)	13770	34858500	247025	1	1	12.8788K	IVSNASCTTKCLAPLAK	V	917.2406	2	1832.4667	-0.4821	1832.9488	58.22	29
similar to Glycine decarboxylase [Rattus norvegicus]	111900	34862790	260747	1	1	1.6882R	EMLQALGLASIDELIEK	T	936.9937	2	1871.9727	-0.0186	1871.9913	54.89	29
similar to HTPAP protein	29160	34879054	255469	1	1	3.8462R	IQPEELWLVR	N	673.7541	2	1345.4936	-0.2094	1345.703	33.09	31
similar to Heat shock cognate 71 kDa protein	64610	34855549	236971	1	18	30.5461K	SINPNEAVAYGAAVQAAIISGDK	S	753.865	3	2258.5731	0.41898	2258.15412	50.54	28
similar to Histone H2A.o (H2A/o) (H2A.2) (H2a-615)	21070	34858256	279473	1	2	24.7423R	VGAGAPVYMAAVLEYLTAEILELAGNAAR	D	983.824	3	2948.4501	-0.081474	2948.531574	117.75	27
similar to Hypothetical protein KIAA0379	41000	27732065	190049	1	1	3.3333K	VHLARFVLDALDR	S	762.9013	2	1523.7881	-0.06911	1523.85721	36.35	31
similar to KIAA0946 protein	84730	34864845	282355	1	1	4.3127K	NTALHWAVLAGNTTVISLILLEAGGNVDAQNVK	G	1097.3943	3	3289.1611	0.41457	3288.74653	32.51	25
similar to LDL receptor adaptor protein	60620	34872138	266460	1	1	1.9713K	APLSTVSANTK	N	544.8085	2	1087.6025	0.015252	1087.587248	58.26	32
similar to Liver carboxylesterase 1 precursor (Carboxylesterase ES-1) (E1) (ES-THET)	26910	34882067	308005	1	2	8.8353R	HPSSPPVVDDTTK	G	632.8507	2	1263.6869	0.041039	1263.645861	95.41	31
similar to N-acetylneuraminic acid synthase (sialic acid synthase)	40050	27714479	225772	1	1	7.7994K	LFPDIPIGYSGHETGIAISVAAVALGAK	V	923.2601	3	2766.7584	0.2629	2766.4955	34.38	27
similar to NADH dehydrogenase (ubiquinone) 1 beta subcomplex 3	11280	34876452	287362	1	1	11K	IEGTPLEAMQK	K	616.8727	2	1231.7309	0.11908	1231.61182	56.32	31
similar to NADH:ubiquinone oxidoreductase B15 subunit	15060	82617686	192715	1	1	19.3798K	YKPAPLAALPNTLDPAEYDVSPETR	K	910.1728	3	2727.4966	0.1211	2727.37549	78.5	27
similar to NADP+-specific isocitrate dehydrogenase	14720	34857317	195949	1	1	9.5588K	TIEAEAAHGTVTR	H	678.2954	2	1354.5762	-0.10781	1354.68401	35.98	30
similar to PKR-associating protein RAX	34390	34856450	191003	1	1	6.0703R	SLLSLPNTDYIQLLSEIAK	E	1059.5651	2	2117.1156	-0.046278	2117.161878	45.92	29
similar to PalBH [Rattus norvegicus]	90550	34876995	233624	1	1	1.1292R	INSPHYLTK	I	536.8444	2	1071.6742	0.10293	1071.57127	37.9	32
similar to Phosphoacetylglucosamine mutase (PAGM) (Acetylglucosamine phosphomutase) (N-acetylglucosamine-phosphate mutase) (Phosphoglucumutase 3) [Rattus norvegicus]	50750	34865378	202185	1	1	2.1786R	MGLLAVLRSK	Q	552.3812	2	1102.7478	0.094625	1102.653175	40.55	32
similar to Proteasome activator complex subunit (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	3.7915K	DPHVMDYR	A	516.7392	2	1031.4639	0.0145	1031.4494	32.01	32
similar to Pyruvate kinase, M2 isozyme	57960	34875446	288218	1	1	1.8832K	KGDVVIVLTR	X	550.278	2	1098.5414	-0.13464	1098.67604	31.29	31
similar to RIKEN cDNA 1810003N24	31780	34873957	230313	1	1	3.5088K	DTKDVSTLTk	A	554.3588	2	1106.703	0.12115	1106.58185	32.51	31
similar to RIKEN cDNA 1810045K17	10150	34857339	270299	1	1	16.129K	VLSVPESTPFTAVLK	F	794.4249	2	1586.8353	-0.056583	1586.891883	54.09	30
similar to RIKEN cDNA 2010005O13 [Rattus norvegicus]	15020	34880819	301426	1	1	7.4074K	VLSGQDTEDR	S	560.2575	2	1118.5004	-0.019912	1118.520312	66.17	32
similar to RIKEN cDNA 2410002O22 gene [Rattus norvegicus]	22220	34853743	269534	1	1	5.9701K	LDVWKTNLGER	G	722.4076	2	1442.8006	0.012487	1442.788113	31.69	31
similar to RIKEN cDNA 2810409H07 [Rattus norvegicus]	42320	34855205	260021	1	1	4.0214K	IPAFLNVDIAGLVK	G	784.9261	2	1567.8376	-0.096102	1567.933702	82.5	30
similar to RIKEN cDNA 9430097N02 [Rattus norvegicus]	81520	34869388	230365	1	1	1.5068R	SVILHLLSQLK	L	625.8919	2	1249.7693	-0.006469	1249.775769	85.79	31
similar to RIKEN cDNA C920006C10	16670	27718855	264993	1	1	9.4595K	IAESLGGSGYSVER	L	712.8732	2	1423.7318	0.037559	1423.694241	45.57	30
similar to RNA-binding protein isoform G3BP-2a	54070	34876568	211028	1	1	3.527K	LPNFGVVFDSEPVQR	I	983.5374	2	1965.0602	0.097033	1964.963167	79.34	29

similar to Rap2c protein	13510	34881637	197399	1	1	10.2564K	SMVDELF AEIVR	Q	712.9085	2	1423.8024	0.10076	1423.70164	80.58	30
similar to SLIT-ROBO Rho GTPase-activating protein 3; WAVE-associated Rac GTPase activating protein	35530	34879743	229135	1	1	3.7855R	VQLQLDQDFFR	K	761.4231	2	1520.8316	0.032952	1520.798648	47.06	30
similar to SSC2	59620	34875179	315186	1	1	3.2075K	AFDNEVNAFLDNMFGR	D	979.0146	2	1956.0147	0.13123	1955.88347	32.96	29
similar to Sh3bgrl protein	12800	27706424	198937	1	1	15.7895R	ENNAVYAFGLTAPPGSK	E	924.9838	2	1847.9531	0.011482	1847.941618	72.8	29
similar to Swiprosin 1	26760	72255531	250786	1	1	4.6025K	LGAPQTHLGLK	S	567.82	2	1133.6255	-0.030112	1133.655612	36.44	31
similar to T-cell activation leucine repeat-rich protein	92210	34876057	221702	1	1	1.7435K	QINLNNEWTVEKLIK	S	864.9696	2	1727.9247	0.004105	1727.920595	41.36	29
similar to Txndc1 protein	31430	67078422	283888	1	1	4.3165K	VDVTEQTGLSGR	F	631.37	2	1260.7254	0.094432	1260.630968	93.19	31
similar to UDP-galactose transporter	38530	34933455	208424	1	1	3.8251K	ILTTALFVLMNLR	S	804.4568	2	1606.899	-0.012543	1606.911543	57.55	30
similar to WD repeat domain 20 isoform 1	68240	34935498	289309	1	1	1.6807K	LFNEERLIDK	S	638.8066	2	1275.5986	-0.083648	1275.682248	32.57	31
similar to Wdr1 protein [Rattus norvegicus]	48550	34878397	292693	1	1	3.6117K	YAPSGFYIASGDISGK	L	816.8129	2	1631.6112	-0.17184	1631.78304	47.51	30
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	1	1	1.0989K	AIEAASSLKSQAATK	N	738.3632	2	1474.7119	-0.087189	1474.799089	31.08	30
similar to adaptor-related protein complex 2, beta 1 subunit	105700	34876358	254285	1	16	17.5975K	LQNDSVYTIAR	R	640.3038	2	1278.593	-0.063761	1278.656761	33.14	31
similar to adenine nucleotide translocase	32800	34866578	257029	1	8	23.8255R	AAYYGIYDTAK	G	618.316	2	1234.6175	0.030563	1234.586937	39.86	31
similar to apoptosis-inducing factor (AIF)-homologous mitochondrial-associated inducer of death; p53-responsive gene 3 [Rattus norvegicus]	14880	34852510	209377	1	1	10.2941R	NDGVGQISGFYVGR	L	734.8517	2	1467.6889	-0.021633	1467.710533	83.43	30
similar to aspartyl beta-hydroxylase	53800	34866148	285481	1	1	3.6961K	LGVYDADGDGDFVD DAK	V	943.896	2	1885.7774	-0.007941	1885.785341	68.95	29
similar to butyrate-induced transcript 1	28810	34864679	236762	1	1	4.0486R	FSFTLPYPLR	M	620.9054	2	1239.7963	0.13116	1239.66514	42.93	31
similar to cAMP-dependent protein kinase, beta-2 catalytic subunit (PKA C-beta-2)	73330	34861056	256498	1	4	6.135R	ILQAVEFFLVR	L	716.372	2	1430.7294	-0.099103	1430.828503	46.76	31
similar to cDNA sequence BC003251	53180	34871409	253866	1	1	2.714K	EGLSGQEWRVLVK	G	750.9822	2	1499.9497	0.14021	1499.80949	33.99	30
similar to chromosome 20 open reading frame 169	20950	34860687	214268	1	1	11.5789R	SSPSLDQMFD AEILGFSTPPGR	L	1184.5304	2	2367.0462	-0.058961	2367.105161	44.02	28
similar to endo B cyokeratin	42970	34860580	202236	1	4	13.8381R	STTFSTNYR	S	538.7758	2	1075.5371	0.04372	1075.49338	41.75	32
similar to endonuclease G	32270	77917570	273385	1	1	4.4218R	ASGLLFVPNILAR	A	685.9757	2	1369.9368	0.12868	1369.80812	32.9	30
similar to ethanol induced 6	15850	27686507	168139	1	1	16.2338R	RAPAAQPPATAAAPS AVGSPAAAPR	Q	751.9566	3	2252.8479	-0.34981	2253.19771	69.03	28
similar to glyceraldehyde-3-phosphate dehydrogenase	36450	34852715	210943	1	3	13.4731K	VNHDFGIVEGLMTTVHAITATQK	T	866.2229	3	2595.6469	0.33548	2595.31142	50.34	28
similar to glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) (EC 1.2.1.12) - mouse	31550	34864978	296252	1	3	16.8919K	VLISAPSANAPMFVMGVNHEK	Y	743.5205	3	2227.5398	0.42697	2227.11283	37.49	28
similar to glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) (EC 1.2.1.12) - mouse	27870	27699577	156654	1	1	5.4475K	GLMTTVHAITATQK	S	744.4846	2	1486.9547	0.17334	1486.78136	105.85	30
similar to glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) (EC 1.2.1.12) - mouse	46820	34856839	252379	1	1	3.5545R	GAAENIIPASTGAAK	A	685.9309	2	1369.8473	0.12721	1369.72009	31.78	30
similar to golgi-associated microtubule-binding protein HOOK3; hook3 protein [Rattus norvegicus]	83230	34879033	220378	1	1	1.6506K	TTEELNEALS AK	E	653.2043	2	1304.394	-0.25193	1304.64593	35.8	31
similar to heat shock protein 105 kDa alpha	82350	34870188	195465	1	1	1.2295R	FQEAEEERPR	V	581.2886	2	1160.5627	0.005355	1160.557345	31.18	31
similar to hepatocellular carcinoma autoantigen	13340	34869447	272734	1	1	4.918R	LPKPTR	S	356.2361	2	710.4577	0.01379	710.44391	36.01	30
similar to hypothetical protein A	36410	34869364	193827	1	1	3.4921K	TLEDEEEELFK	M	691.3137	2	1380.6128	-0.016785	1380.629585	53.6	31
similar to hypothetical protein D4Ert089e	46520	34868399	231118	1	1	2.3641R	QQQQFSLSEK	K	611.8244	2	1221.6342	0.035305	1221.598895	41.58	31
similar to hypothetical protein FLJ14675	21510	34873570	196884	1	1	5.8824R	EGLKGSWPSPR	H	607.2761	2	1212.5377	-0.087373	1212.625073	40.91	31
similar to hypothetical protein FLJ20331 [Rattus norvegicus]	48370	34861003	248047	1	1	3.7471R	LATVPADFALLSNLLR	L	857.5268	2	1713.039	0.056551	1712.982449	43.49	30
similar to hypothetical protein FLJ22625	35090	34865046	243991	1	1	3.7267R	VAEPSEASLGRPR	G	606.7806	2	1211.5466	-0.06792	1211.61452	82.54	31
similar to hypothetical protein FLJ22865	33930	34872934	263071	1	1	2.5559K	MAERIEER	I	517.3084	2	1032.6023	0.10011	1032.50219	32.9	32
similar to hypothetical protein MGC10084	42080	34851552	202821	1	1	3.5813K	QWADIGFQGDDPK	T	738.9959	2	1475.7772	0.10917	1475.66803	34.65	31
similar to hypothetical protein MGC23280	35980	34872804	277215	1	1	3.6585R	APSSLSAPSPEK	T	585.7126	2	1169.4106	-0.18213	1169.59273	37.94	31

similar to inhibitor of growth family, member 3	56500	34855011	234073	1	1	1.7751R	EEQMASIKK	D	532.3543	2	1062.6941	0.15618	1062.53792	31.33	31
similar to keratin associated protein 11-1	18900	27670141	269756	1	1	6.0109R	TYQQSCVSSCR	R	688.2818	2	1374.5491	-0.016485	1374.565585	61.57	31
similar to keratinocytes associated protein 2	27650	34857976	235658	1	1	6.6667K	ISSTLYQATAPALTPAK	V	867.0371	2	1732.0596	0.11891	1731.94069	89.24	30
similar to male enhanced antigen 2/golgi autoantigen, golgin subfamily a, 3 [Rattus norvegicus]	166100	34873054	267138	1	1	0.81191K	VLEDELQESR	G	730.3044	2	1458.5943	-0.12585	1458.72015	44.99	31
similar to microorchidia	55070	34869318	309715	1	1	1.8595K	QEDSAQIIR	R	530.333	2	1058.6515	0.11595	1058.53555	34.06	32
similar to mirror-image polydactyly gene 1	52780	34865613	265130	1	1	1.9397R	MKHMESLKL	M	583.8165	2	1165.6184	0.089065	1165.529335	32.75	31
similar to osteoclast stimulating factor 1	34620	34880977	297002	1	1	6.1093K	DIVEVLTQPNVELNQNK	L	1114.6785	2	2227.3424	0.19407	2227.14833	36.8	29
similar to peroxisomal long chain acyl-CoA thioesterase la	46360	27667388	160562	1	1	3.0879K	VAFSGILDIVDIR	N	709.4531	2	1416.8916	0.094036	1416.797564	31.97	31
similar to proline dehydrogenase; PRODH	12130	27665096	305160	1	1	14.9533K	YYPYGPVMEVLPYLSR	R	941.9669	2	1881.9192	-0.05063	1881.96983	82.36	29
similar to rab20	32660	34879665	240940	1	1	2.349K	YKMILDER	E	485.774	2	969.5334	0.074465	969.458935	38.29	31
similar to receptor-interacting protein 2	60780	34867073	242276	1	1	1.8553K	CLIELEPVLR	T	621.3195	2	1240.6244	-0.060463	1240.684863	37.52	31
similar to recombination activating 1 activation	24690	27692967	292043	1	1	9.0498R	LKDPYITVPNLPGILTG FIR	L	743.0534	3	2226.1384	-0.13917	2226.27757	59.21	29
similar to ribosomal protein S12; 40S ribosomal protein S12	12210	34869042	285721	1	2	28.5714START	MAEGGVAAAGVMDVNTALQEVLK	T	1145.5963	2	2289.178	0.043694	2289.134306	28.79	28
similar to splicing coactivator subunit SRm300; RNA binding protein; AT-rich element binding factor [Rattus norvegicus]	212600	34866816	290757	1	1	0.40589K	VKAVISPR	R	435.2562	2	868.4978	-0.051589	868.549389	31.64	31
similar to thyroid hormone receptor interactor 11; thyroid receptor interacting protein 11	37170	34867559	280942	1	1	3.9039R	LDEANAALDSASR	L	666.7835	2	1331.5523	-0.07932	1331.63162	105.45	31
similar to torsinB protein	17860	34853518	202385	1	1	8.642K	NFVSQIVAENLYPK	G	811.3079	2	1620.6012	-0.24983	1620.85103	63.36	30
similar to ubiquitin-protein ligase (EC 6.3.2.19) E - mouse	123600	34933178	317625	1	1	1.3489R	LAGTQPLEVLEAVQR	S	812.4913	2	1622.9681	0.068974	1622.899128	55.62	30
synaptogyrin 2	25710	6685963	60460	1	1	4.2735R	YVSQPQVVTR	L	588.7967	2	1175.5789	-0.050894	1175.629794	70.76	32
unknown	84160	34880715	314842	1	1	1.4966R	DYSGDHVQQAQ	Y	624.2342	2	1246.4539	-0.10388	1246.55778	67.3	31
unknown	26610	84781644	345922	1	1	5.7613R	VPASASTQSQGSSR	V	681.8869	2	1361.7593	0.10586	1361.65344	55.11	31
unknown	167300	34869344	309548	1	1	0.65147K	IAGLEEKALK	A	536.2893	2	1070.5641	-0.069376	1070.633476	38.18	32
unknown	111800	34872548	263673	1	1	1.3374R	IENSLASLLELLK	G	721.9996	2	1441.9847	0.14558	1441.83912	31.39	30

Table S1C. Curation of protein identifications

ASSIGNED PROT NAME	FUNCTIONAL CATEGORY	NCBI DESCRIPTION	MW	gnumber	CMBSEQID	MEMBRANE STATUS	SIGNAL TYPE	TMD	UNIREF100	REFSEQ
CHAPERONIN 10	PROT SYN/FOLD	10 kDa heat shock protein, mitochondrial	10770	400542	121548	SOLUBLE			P26772	
14-3-3 PROTEIN EPSILON	SIGNALING	14-3-3 protein epsilon	29170	61216932	35616	SOLUBLE			P42655 P62260	
14-3-3 PROTEIN ZETA/Delta	SIGNALING	14-3-3 protein zeta/delta Protein kinase C inhibitor protein 1 KCIP-1 SEZ-2	27770	68085421	29712	SOLUBLE			P63102 Q52KK1 Q6IRF4	
15 KDA SELENOPROTEIN	PROT MOD	15 kDa selenoprotein precursor	17780	20139870	129368	SOLUBLE	cleavable signal peptide		Q923V8	
ALCOHOL DEHYDROGENASE PAN1B-LIKE PROTEIN	METABOLISM	17-beta hydroxysteroid dehydrogenase 13 precursor Short-chain dehydrogenase/reductase 9	33490	77416416	169811	SOLUBLE	cleavable signal peptide		Q5M875	
2,4-DIENOYL-COA REDUCTASE, MITOCHONDRIAL	MITOCHONDRIA	2,4-dienoyl-CoA reductase, mitochondrial precursor	36130	67476443	148907	SOLUBLE	cleavable signal peptide		Q64591 Q6PCV4	
2-HYDROXYPHYTYNANOYL-COA LYASE	PEROXISOME	2-hydroxyphytanoyl-CoA lyase 2-hydroxyphytanoyl-Coenzyme A lyase	63620	50926767	187564	SOLUBLE			Q8CHM7	
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	SOLUBLE			P23965	
3-ALPHA-HYDROXYSTEROID DEHYDROGENASE	DETOXIFICATION	3-alpha-hydroxysteroid dehydrogenase	37030	6708142	19230	SOLUBLE			P23457 Q5BKC8 Q6LDE6 Q6LDE7	
3-HYDROXYACYL-COA DEHYDROGENASE TYPE II (TYPE	DETOXIFICATION	3-hydroxyacyl-CoA dehydrogenase type II	27250	7387724	83190	SOLUBLE	cleavable signal peptide		O70351	
3-KETOACYL-COA THIOLASE, MITOCHONDRIAL	MITOCHONDRIA	3-ketoacyl-CoA thiolase, mitochondrial Beta-ketothiolase Acetyl-CoA acyltransferase Mitochondrial 3-oxoacyl-CoA thiolase	41870	55544	96895	SOLUBLE			P13437	
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	SOLUBLE			P31210	
40S RIBOSOMAL PROTEIN S11	PROT SYN/FOLD	40S ribosomal protein S11	18430	54039305	4834	SOLUBLE				
40S RIBOSOMAL PROTEIN S12	PROT SYN/FOLD	40S ribosomal protein S12	14510	78126139	132206	SOLUBLE			Q6PDW1	
40S RIBOSOMAL PROTEIN S13	PROT SYN/FOLD	40S ribosomal protein S13	17220	57730	4835	SOLUBLE				
40S RIBOSOMAL PROTEIN S14	PROT SYN/FOLD	40S ribosomal protein S14	16270	37231722	98434	SOLUBLE			Q6PDV6	
40S RIBOSOMAL PROTEIN S16	PROT SYN/FOLD	40S ribosomal protein S16	16450	57714	4837	SOLUBLE				
40S RIBOSOMAL PROTEIN S18	PROT SYN/FOLD	40S ribosomal protein S18	17720	50403620	60848	SOLUBLE			P25232 P62271	XP_215328.1
40S RIBOSOMAL PROTEIN S19	PROT SYN/FOLD	40S ribosomal protein S19	16090	82654220	122667	SOLUBLE				
40S RIBOSOMAL PROTEIN S20	PROT SYN/FOLD	40S ribosomal protein S20	13370	57720	4840	SOLUBLE			P60868	XP_233622.1
40S RIBOSOMAL PROTEIN S21	PROT SYN/FOLD	40S ribosomal protein S21	9127	483517	37243	SOLUBLE			P05765	
40S RIBOSOMAL PROTEIN S23	PROT SYN/FOLD	40S ribosomal protein S23	15810	730647	4842	SOLUBLE				
40S RIBOSOMAL PROTEIN S25	PROT SYN/FOLD	40S ribosomal protein S25	13740	74355904	4844	SOLUBLE			P62853 Q3SYP7	XP_217121.1
40S RIBOSOMAL PROTEIN S26	PROT SYN/FOLD	40S ribosomal protein S26	13020	6981488	75074	SOLUBLE				
40S RIBOSOMAL PROTEIN S27	PROT SYN/FOLD	40S ribosomal protein S27-like protein	9477	57741	120488	SOLUBLE				
40S RIBOSOMAL PROTEIN S28	PROT SYN/FOLD	40S ribosomal protein S28	7841	57726	1344	SOLUBLE			P62859	
40S RIBOSOMAL PROTEIN S3	PROT SYN/FOLD	40S ribosomal protein S3	26670	57728	60850	SOLUBLE			P17073 P62909	XP_341889.1
40S RIBOSOMAL PROTEIN S30	PROT SYN/FOLD	40S ribosomal protein S30	6648	51338625	106720	SOLUBLE			P62864	
40S RIBOSOMAL PROTEIN S3A	PROT SYN/FOLD	40S ribosomal protein S3a	29940	8394221	51618	SOLUBLE			P49242	
40S RIBOSOMAL PROTEIN S7	PROT SYN/FOLD	40S ribosomal protein S7	22130	66730357	4853	SOLUBLE			P23821 P62083	
40S RIBOSOMAL PROTEIN S9	PROT SYN/FOLD	40S ribosomal protein S9	22590	52788199	142294	SOLUBLE				

40S RIBOSOMAL PROTEIN SA	PROT SYN/FOLD	40S ribosomal protein SA	32820	8393693	51515	SOLUBLE			P38983	
60 KDA HEAT SHOCK PROTEIN,MITOCHONDRIAL (HSP60)	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	SOLUBLE			P63039	
60S RIBOSOMAL PROTEIN P0	PROT SYN/FOLD	60S acidic ribosomal protein P0 L10E	34220	730581	23405	SOLUBLE			P19945	
60S RIBOSOMAL PROTEIN P1	PROT SYN/FOLD	60S acidic ribosomal protein P1	11500	57710	144430	SOLUBLE			P19944	XP_343404.1
60S RIBOSOMAL PROTEIN P2	PROT SYN/FOLD	60S acidic ribosomal protein P2	11690	71795613	144431	SOLUBLE	cleavable signal peptide		P02401 Q499W9	
60S RIBOSOMAL PROTEIN L12	PROT SYN/FOLD	60S ribosomal protein L12	17850	57680	144419	SOLUBLE			P23358	
60S RIBOSOMAL PROTEIN L18A	PROT SYN/FOLD	60S ribosomal protein L18a	20730	50403587	71631	SOLUBLE			P62718	XP_214302.1
60S RIBOSOMAL PROTEIN L24	PROT SYN/FOLD	60S ribosomal protein L24	17780	560493	4812	SOLUBLE			P83732	
60S RIBOSOMAL PROTEIN L36	PROT SYN/FOLD	60S ribosomal protein L36	12250	34849736	65711	SOLUBLE			Q6PDV5	
60S RIBOSOMAL PROTEIN L4	PROT SYN/FOLD	60S ribosomal protein L4	47310	1363989	85424	SOLUBLE			P50878	
60S RIBOSOMAL PROTEIN L5	PROT SYN/FOLD	60S ribosomal protein L5	34460	57125	37237	SOLUBLE			P09895	
BIP	PROT SYN/FOLD	78 kDa glucose-regulated protein precursor GRP 78 Immunoglobulin heavy chain-binding protein BIP Steroidogenesis-activator polypeptide	72350	38303969	28269	SOLUBLE	cleavable signal peptide		P06761	
NAD+ ADP-RIBOSYL TRANSFERASE 3 PARP-3	NUCLEUS	ADP-ribosyltransferase NAD+, poly (ADP-ribose polymerase)-like 3 (Predicted)	58870	56605734	298279	SOLUBLE			Q5U2U3	XP_217264.2
ALPHA-1-MICROGLOBULIN	BIOSYNTHETIC CARGO	AMBP protein precursor Alpha-1-microglobulin Inter- alpha-trypsin inhibitor light chain ITI-LC Bikunin HI-30 Trypstatin	38850	6978497	3629	SOLUBLE	cleavable signal peptide		P19603 Q63336 Q64240	
ARP3 ACTIN-RELATED PROTEIN 3 HOMOLOG	CYTOSKELETON	ARP3 actin-related protein 3 homolog	47360	70912366	71751	SOLUBLE			Q4V7C7	
ATP SYNTHASE B CHAIN, MITOCHONDRIAL	MITOCHONDRIA	ATP synthase B chain, mitochondrial precursor	28870	39645769	141484	SOLUBLE	cleavable signal peptide		P19511	
ATP SYNTHASE D CHAIN, MITOCHONDRIAL	MITOCHONDRIA	ATP synthase D chain, mitochondrial	18760	9506411	21505	SOLUBLE			P31399	
ATP SYNTHASE OLIGOMYCIN SENSITIVITY CONFERRAL	MITOCHONDRIA	ATP synthase O subunit, mitochondrial precursor Oligomycin sensitivity conferral protein OSCP	23400	543880	142437	SOLUBLE			Q06647	
ATP SYNTHASE ALPHA CHAIN, MITOCHONDRIAL	MITOCHONDRIA	ATP synthase alpha chain, mitochondrial precursor	55280	6729934	73367	MEMBRANE			P15999	
ATP SYNTHASE BETA CHAIN, MITOCHONDRIAL	MITOCHONDRIA	ATP synthase beta chain, mitochondrial precursor	56350	71681130	141479	SOLUBLE	cleavable signal peptide		P10719 Q499W0	
ATP SYNTHASE COUPLING FACTOR 6, MITOCHONDRIAL	MITOCHONDRIA	ATP synthase coupling factor 6, mitochondrial precursor ATPase subunit F6	12490	599963	60480	SOLUBLE			P21571	
ATP SYNTHASE DELTA CHAIN, MITOCHONDRIAL	MITOCHONDRIA	ATP synthase delta chain, mitochondrial precursor	17600	457929	21504	SOLUBLE	cleavable signal peptide		P35434	
ATP SYNTHASE EPSILON CHAIN, MITOCHONDRIAL	MITOCHONDRIA	ATP synthase epsilon chain, mitochondrial	5636	258789	11887	SOLUBLE			P29418	
ATP SYNTHASE GAMMA CHAIN, MITOCHONDRIAL	MITOCHONDRIA	ATP synthase gamma chain, mitochondrial	29930	6729936	69786	SOLUBLE			P35435 UPI000011257C	
ATP CITRATE LYASE	METABOLISM	ATP-citrate synthase ATP-citrate (pro-S-)lyase Citrate cleavage enzyme	120600	8392839	126543	SOLUBLE			P16638	
VITRONECTIN	BIOSYNTHETIC CARGO	Aa1018	55960	32492572	302124	SOLUBLE	cleavable signal peptide		Q7TQ11	
APOLIPOPROTEIN B	BIOSYNTHETIC CARGO	Aa1064	42690	111387	148924	SOLUBLE			Q7TMA5	
CCG1-INTERACTING FACTOR B	UNKNOWN	Abhydrolase domain containing 14b	22620	56090461	151517	SOLUBLE			Q6DGG1	XP_217255.1
FIBRINOGEN B BETA CHAIN	BIOSYNTHETIC CARGO	Act1-581 Ab1-216 Ab1-181	56610	33086484	166238	SOLUBLE			Q7TME5	

SIMILAR TO OLIGOSACCHARYL TRANSFERASE 3	PROT MOD	Ac1573		79140	32264637	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-OUT	Q7TQ74	
FIBRINOGEN ALPHA/ALPHA-E CHAIN	BIOSYNTHETIC CARGO	Ac1873		86660	62643670	173317	SOLUBLE	cleavable signal peptide		Q7TQ70	XP_342268.1
MURINE COAGULATION FACTOR V	BIOSYNTHETIC CARGO	Ac2-120		237300	62659617	166242	SOLUBLE			Q7TPK2	
Ac2-155	UNKNOWN	Ac2-155		102100	33086620	199808	SOLUBLE			Q7TP30	
ACETYL-CoA ACETYLTRANSFERASE, MITOCHONDRIAL	MITOCHONDRIA	Acetyl-CoA acetyltransferase, mitochondrial precursor		44690	66502	31496	SOLUBLE			P17764	
LYSOPHOSPHATIDIC ACID PHOSPHATASE	METABOLISM	Acid phosphatase 6, lysophosphatidic		47280	72255521	193296	SOLUBLE	cleavable signal peptide		Q4FZU0	
PROLIFERATION RELATED ACIDIC LEUCINE RICH PROTEIN	NUCLEUS	Acidic leucine-rich nuclear phosphoprotein 32 family member B Proliferation-related acidic leucine-rich protein PAL31		31060	9971212	3001	SOLUBLE			Q9EST6	
MITOCHONDRIAL ACONITASE	MITOCHONDRIA	Aconitate hydratase, mitochondrial precursor Citrate hydro-lyase Aconitase		85430	60391194	338228	SOLUBLE			Q6P6V3 Q9ER34	
ACTIN, GAMMA	CYTOSKELETON	Actin, cytoplasmic 2		41790	62645364	120792	SOLUBLE			P63259	
ACTIN-LIKE PROTEIN 2 ACTIN-RELATED PROTEIN 2	CYTOSKELETON	Actin-like protein 2 Actin-related protein 2		44730	62899645	156591	SOLUBLE			Q5M7U6	
ACYL-COENZYME A OXIDASE 1, PEROXISOMAL	PEROXISOME	Acyl-coenzyme A oxidase 1, peroxisomal		74680	8394149	51604	SOLUBLE			P07872 P11354	
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	SOLUBLE			P97562	
ACYL-COENZYME A OXIDASE 3, PEROXISOMAL	PEROXISOME	Acyl-coenzyme A oxidase 3, peroxisomal Pristanoyl-CoA oxidase Branched-chain acyl-CoA oxidase BRCACoX		78450	2498208	42129	SOLUBLE			Q63448	
ADENOSYLMOCYSTEINASE	METABOLISM	Adenosylhomocysteinase		47420	24158803	54409	SOLUBLE			P10760 UPI0000110EC7	
ADENYLATE KINASE 2	MITOCHONDRIA	Adenylate kinase 2, isoform b		25530	77020256	340217	SOLUBLE			Q6P7C6	
ADIPOCYTE-DERIVED LEUCINE AMINOPEPTIDASE	PROT MOD	Adipocyte-derived leucine aminopeptidase precursor		100700	8131852	605	SOLUBLE	cleavable signal peptide		Q9J22 Q9JU22-2	
AFAMIN	BIOSYNTHETIC CARGO	Afamin precursor Alpha-albumin Alpha-Alb		69340	543793	23759	SOLUBLE	cleavable signal peptide		P36953	
AFLATOXIN B1 ALDEHYDE REDUCTASE MEMBER 1	DETOXIFICATION	Aflatoxin B1 aldehyde reductase member 1		36740	433611	100616	SOLUBLE			P38918	
ALDEHYDE DEHYDROGENASE	METABOLISM	Aldehyde dehydrogenase		48270	16073616	7845	SOLUBLE			Q91ZD7	
ESTRADIOL 17BETA-DEHYDROGENASE (EC 1.1.1.62), A-S	DETOXIFICATION	Aldo-keto reductase family 1, member C6		37000	76096330	217551	SOLUBLE			Q3MHS3	
ALPHA-ACTININ 4	CYTOSKELETON	Alpha actinin 4		104900	77539778	319018	SOLUBLE			Q6P786	
ALPHA GLOBIN	BLOOD + OTHER CELLS	Alpha globin		15520	62655914	114803	SOLUBLE			Q63910	
ALPHA-1-ANTIPEPTINASE	BIOSYNTHETIC CARGO	Alpha-1-antipeptinase precursor		46140	112889	11475	SOLUBLE	cleavable signal peptide		P17475 Q6AYZ5	
ALPHA-1 PROTEINASE INHIBITOR III	BIOSYNTHETIC CARGO	Alpha-1-inhibitor III precursor		163800	83816939	11478	SOLUBLE	cleavable signal peptide	7 18 IN-OUT	P14046 Q6LDP2	
ALPHA-1-MACROGLOBULIN	BIOSYNTHETIC CARGO	Alpha-1-macroglobulin		167100	739596	126488	SOLUBLE	cleavable signal peptide		Q63041	
ALPHA-2-HS-GLYCOPROTEIN	BIOSYNTHETIC CARGO	Alpha-2-HS-glycoprotein		37980	60552688	111646	SOLUBLE	cleavable signal peptide		P24090 Q5BKD2	
HEMOGLOBIN ALPHA-1 AND ALPHA-2 CHAINS	BLOOD + OTHER CELLS	Alpha-2-globin chain Hba-a1 protein 2-alpha globin		15280	60688619	109334	SOLUBLE			Q91V15	
ALPHA-2U GLOBULIN	BIOSYNTHETIC CARGO	Alpha-2U globulin		20560	8307690	125352	SOLUBLE	cleavable signal peptide		Q63022 Q63213	

ALPHA-2U-GLOBULIN	BIOSYNTHETIC CARGO	Alpha-2u globulin PGCL2	20710	56269668	161585	SOLUBLE	cleavable signal peptide		Q8K1Q6	XP_216422.1
ELECTRON TRANSFER FLAVOPROTEIN ALPHA-SUBUNIT	MITOCHONDRIA	Alpha-ETF	34950	57527204	151400	SOLUBLE	cleavable signal peptide		Q5M7W0	
ALPHA-ACTININ 1	CYTOSKELETON	Alpha-actinin-1 Alpha-actinin cytoskeletal isoform Non-muscle alpha-actinin-1 F-actin cross linking protein	103000	4210985	37175	SOLUBLE			Q9Z1P2	
ALPHA-METHYLACYL-COA RACEMASE	PEROXISOME	Alpha-methylacyl-CoA racemase	41830	13637497	76476	SOLUBLE			P70473	
ALPHA-SOLUBLE NSF ATTACHMENT PROTEIN (ALPHA SUBUNIT)	TETH/DOCK/FUS	Alpha-soluble NSF attachment protein SNAP-alpha N-ethylmaleimide-sensitive factor attachment protein, alpha	33190	6094309	51376	SOLUBLE			P54921	
ANGIOTENSINOGEN	BIOSYNTHETIC CARGO	Angiotensinogen precursor Angiotensin-1 Angiotensin I Ang I Angiotensin-2 Angiotensin II Ang II Angiotensin-3 Angiotensin III Ang III Des-Asp[1]-angiotensin II	51980	56585074	45123	SOLUBLE	cleavable signal peptide		P01015	
TRYPSIN I, ANIONIC	TRYPSIN	Anionic trypsin-1 precursor Anionic trypsin I Pretrypsinogen I	25960	6981420	75054	SOLUBLE	cleavable signal peptide		P00762	
ANNEXIN A3	TETH/DOCK/FUS	Annexin A3	36360	71766	120574	SOLUBLE			P14669 Q642C2	
ANNEXIN 5	TETH/DOCK/FUS	Annexin A5	35740	6978505	3633	SOLUBLE			P14668	
APOLIPOPROTEIN A-I	BIOSYNTHETIC CARGO	Apolipoprotein A-I precursor	30060	6978515	3638	SOLUBLE	cleavable signal peptide		P04639 Q5EBB2	
APOLIPOPROTEIN A-IV	BIOSYNTHETIC CARGO	Apolipoprotein A-IV precursor	44460	60552712	141420	SOLUBLE	cleavable signal peptide		P02651 Q5BK92	
APOLIPOPROTEIN E	BIOSYNTHETIC CARGO	Apolipoprotein E precursor Apo-E	35750	55824759	126501	SOLUBLE	cleavable signal peptide		P02650	
PROGRAMMED CELL DEATH PROTEIN 8, MITOCHONDRIAL	MITOCHONDRIA	Apoptosis-inducing factor	66720	7619915	63059	SOLUBLE			Q548E3 Q9JM53	
ARGINASE 1	METABOLISM	Arginase 1	34970	6573527	37797	SOLUBLE			P07824 Q5BK93	
ARGININOSUCCINATE SYNTHASE	METABOLISM	Argininosuccinate synthase Citrulline--aspartate ligase	46500	55767	45108	SOLUBLE			P09034	
ASPARTATE TRANSAMINASE	MITOCHONDRIA	Aspartate aminotransferase, cytoplasmic	46430	91997	84171	SOLUBLE			P13221	
ASPARTATE AMINOTRANSFERASE, MITOCHONDRIAL	MITOCHONDRIA	Aspartate aminotransferase, mitochondrial precursor Transaminase A Glutamate oxaloacetate transaminase 2	47310	6980972	3905	SOLUBLE	cleavable signal peptide		P00507 Q64551	
SIMILAR TO BCS1-LIKE	UNKNOWN	BCS1-like	47390	56090628	232734	SOLUBLE			Q5XIM0	XP_217434.2
ERP44 (SIMILAR TO THIOREDOXIN DOMAIN CONTAINING)	PROT SYN/FOLD	BWK4	46880	62648953	310568	SOLUBLE	cleavable signal peptide		Q5VLR5	XP_216396.2
HAPTOGLOBIN	BIOSYNTHETIC CARGO	Bat -647	42470	33086640	166334	SOLUBLE	cleavable signal peptide		Q7TP23	
SIMILAR TO BETA-2-GLYCOPROTEIN I	BIOSYNTHETIC CARGO	Beta-2-glycoprotein 1 precursor Beta-2-glycoprotein I Apolipoprotein H Apo-H B2GPI Beta(2)GPI	33200	57525	21485	SOLUBLE	cleavable signal peptide		P26644	
BETA-2-MICROGLOBULIN	BIOSYNTHETIC CARGO	Beta-2-microglobulin precursor	11640	999862	27803	SOLUBLE			P07151	
BETA-GLUCURONIDASE	LYSOSOME	Beta-glucuronidase precursor	73270	758260	21055	SOLUBLE	cleavable signal peptide		P06760	
BETAINE--HOMOCYSTEINE S-METHYLTRANSFERASE	MITOCHONDRIA	Betaine--homocysteine S-methyltransferase	44980	3913156	71708	SOLUBLE			O09171	
BILE ACID COA LIGASE	DETOXIFICATION	Bile acyl-CoA synthetase BACS Bile acid CoA ligase Bile acid CoA ligase BAL Chololate--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	SOLUBLE	cleavable signal peptide	7 23 IN-OUT	Q9ES38	
BILIVERDIN REDUCTASE A PRECURSOR	DETOXIFICATION	Biliverdin reductase A precursor Biliverdin-IX alpha-reductase BVR A	33570	285208	54374	SOLUBLE			P46844	

C-REACTIVE PROTEIN	BIOSYNTHETIC CARGO	C-reactive protein, petaxin related	25470	8393197	126549	SOLUBLE	cleavable signal peptide		P48199 Q5BK94	
CDK5 REGULATORY SUBUNIT ASSOCIATED PROTEIN 3	SIGNALING	CDK5 regulatory subunit-associated protein 3 CDK5 activator-binding protein C53	57040	7330736	18021	SOLUBLE			Q9JLH7	
CDP-DIACYLGLYCEROL--INOSITOL 3-PHOSPHATIDYLTRANSFERASE	PROT MOD	CDP-diacylglycerol--inositol 3-phosphatidyltransferase Phosphatidylinositol synthase PtdIns synthase PI synthase	23610	7674155	70677	MEMBRANE		20 23 OUT-IN 141 20 IN-OUT 175 23 OUT-IN	P70500	
ENDOPLASMIN PRECURSOR (ENDOPLASMIC RETICULUM)	PROT SYN/FOLD	Calcium-binding protein 4	1978	111445	148937	SOLUBLE			Q7M079	
CALNEXIN	PROT SYN/FOLD	Calnexin precursor	67250	543922	69775	MEMBRANE	cleavable signal peptide	484 23 OUT-IN	P35565	
CALRETICULIN	PROT SYN/FOLD	Calreticulin precursor CRP55 Calregulin HACBP Erp60 CALBP Calcium-binding protein 3 CABP3	48000	55855	23403	SOLUBLE	cleavable signal peptide		P10452 P18418	
CARBAMOYL-PHOSPHATE SYNTHASE [AMMONIA], MITOCHONDRIA	MITOCHONDRIA	Carbamoyl-phosphate synthase [ammonia], mitochondrial precursor Carbamoyl-phosphate synthetase I CPSase I	164600	8393186	45074	SOLUBLE			P07756	
CARBONIC ANHYDRASE III	METABOLISM	Carbonic anhydrase III	29420	10120584	5972	SOLUBLE			P14141	
CARBOXYLESTERASE B-1	DETOXIFICATION	Carboxylesterase RL1	62310	14331129	158916	SOLUBLE	cleavable signal peptide		Q924V9	
CARBOXYLESTERASE ESNA3	DETOXIFICATION	Carboxylesterase isoenzyme	61800	21426807	157137	SOLUBLE	cleavable signal peptide		Q8K3R0	
CARBOXYLESTERASE 10	DETOXIFICATION	Carboxylesterase isozyme	2133	1478388	42034	SOLUBLE			Q9QUX7	
CARBOXYLESTERASE ESNA2	DETOXIFICATION	Carboxylesterase precursor	62040	2641992	182047	SOLUBLE	cleavable signal peptide		O35535	
CARBOXYLESTERASE 2	DETOXIFICATION	Carboxylesterase precursor	62240	3062827	13000	SOLUBLE	cleavable signal peptide	7 20 IN-OUT	O70177	
ACTIN, ALPHA CARDIAC	CYTOSKELETON	Cardiac alpha actin 1	42020	77993370	10199	SOLUBLE			P68035	
CARNITINE O-PALMITOYLTRANSFERASE 1, MITOCHONDRIA	MITOCHONDRIA	Carnitine O-palmitoyltransferase I, mitochondrial liver isoform	88130	48735405	63443	MEMBRANE		104 23 IN-OUT	P32198 Q6IMZ4	
CATHEPSIN B	LYSOSOME	Cathepsin B precursor	35600	1942646	19199	SOLUBLE			P00787 UPI0000112628	
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	SOLUBLE	cleavable signal peptide		P07154 Q9QV07	
CC1-9	UNKNOWN	Cc1-9	62860	62641625	194016	SOLUBLE	cleavable signal peptide		Q7TP14	
CERAMIDASE	LYSOSOME	Ceramidase	83490	16758458	60505	SOLUBLE	signal anchor	12 23 IN-OUT	Q91XT9	
CHOLINE DEHYDROGENASE, MITOCHONDRIAL	MITOCHONDRIA	Choline dehydrogenase	66390	55250736	160551	SOLUBLE	cleavable signal peptide		Q6UPE0	
CLATHRIN HEAVY CHAIN	COAT	Clathrin heavy chain	191600	9506497	95154	SOLUBLE			P11442	
COAGULATION FACTOR IX	BIOSYNTHETIC CARGO	Coagulation factor IX Christmas factor	31450	204146	149112	SOLUBLE			P16296	
COFILIN, MUSCLE ISOFORM	CYTOSKELETON	Cofilin-2 Cofilin, muscle isoform	18710	62650690	74438	SOLUBLE				
COMPLEMENT C4	BIOSYNTHETIC CARGO	Complement C4 precursor Complement C4 beta chain Complement C4 alpha chain C4a anaphylatoxin Complement C4 gamma chain	192200	29789265	162301	SOLUBLE	cleavable signal peptide		P08649 Q62895 Q8R403	
COMPLEMENT COMPONENT C9	BIOSYNTHETIC CARGO	Complement component C9 precursor	62280	2499467	43431	SOLUBLE	cleavable signal peptide		Q62930 Q62957	
CONTRAPSIN-LIKE PROTEASE INHIBITOR 1	BIOSYNTHETIC CARGO	Contrapsin-like protease inhibitor 1 precursor	46520	57294	84230	SOLUBLE	cleavable signal peptide		P05545	
CONTRAPSIN-LIKE PROTEASE INHIBITOR 3	BIOSYNTHETIC CARGO	Contrapsin-like protease inhibitor 3 precursor	45280	57231	84327	SOLUBLE	cleavable signal peptide		P05544	
CONTRAPSIN-LIKE PROTEASE INHIBITOR 6	BIOSYNTHETIC CARGO	Contrapsin-like protease inhibitor 6 precursor CPI-26 Serine protease inhibitor 3 SPI-3 SPI-2.2	46650	50927309	88238	SOLUBLE	cleavable signal peptide		P09006 Q03312	
HYDROXYSTEROID 11-BETA DEHYDROGENASE 1	DETOXIFICATION	Corticosteroid 11-beta-dehydrogenase isozyme 1 11-D 11-beta-hydroxysteroid dehydrogenase 1 11-beta-HSD1	31880	78214365	95697	SOLUBLE	cleavable signal peptide		O09170 P16232 Q6LDH6	

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	SOLUBLE				P97536	
CYCLOPHILIN B	PROT SYN/FOLD	Cyclophilin B	20310	2143900	80354	SOLUBLE				Q88541	
CYTOCHROME P450 4A2	DETOXIFICATION	Cyp4a14 protein	57970	71051108	63760	MEMBRANE	cleavable signal peptide	15 18 OUT-IN		P20816 Q4G071	
CYSTATHIONINE GAMMA-LYASE	METABOLISM	Cystathionine gamma-lyase CTL target antigen	43580	51261011	62524	SOLUBLE				Q9EQS4	
CYTOCHROME P450 1A2	DETOXIFICATION	Cytochrome P450 1A2	58290	203832	3724	MEMBRANE	cleavable signal peptide	7 23 IN-OUT		P04799 Q64588	
CYTOCHROME P450 27A1	DETOXIFICATION	Cytochrome P450 27, mitochondrial precursor	60730	62655087	63757	MEMBRANE				P17178 Q64615 Q64639	
CYTOCHROME P450 2B2	DETOXIFICATION	Cytochrome P450 2B2 CYP11B2 P450E P450 PB4	55930	34855371	13404	MEMBRANE	cleavable signal peptide	5 18 IN-OUT		P04167 Q64579 Q64582	
CYTOCHROME P450 2B3	DETOXIFICATION	Cytochrome P450 2B3 CYP11B3	56380	28849945	63770	MEMBRANE	cleavable signal peptide	5 20 IN-OUT		P13107 Q64585	
CYTOCHROME P450 2C11	DETOXIFICATION	Cytochrome P450 2C11	57180	56971259	63780	MEMBRANE	cleavable signal peptide			P08683 Q63141 Q64554	
CYTOCHROME P450 2C13	DETOXIFICATION	Cytochrome P450 2C13, male-specific	55860	205935	63782	MEMBRANE	cleavable signal peptide	5 18 IN-OUT		P20814 P22693 Q64587	
CYTOCHROME P450 2C22	DETOXIFICATION	Cytochrome P450 2C22	56210	203521	33163	MEMBRANE	cleavable signal peptide	2 19 IN-OUT		P19225 UPI000016796B	
CYTOCHROME P450 2C23	DETOXIFICATION	Cytochrome P450 2C23	56430	6166042	72763	MEMBRANE	cleavable signal peptide	3 23 IN-OUT		P24470 Q63914 Q64534	
CYTOCHROME P450 2C6	DETOXIFICATION	Cytochrome P450 2C6	56000	117223	63778	MEMBRANE	cleavable signal peptide			P05178	
CYTOCHROME P450 2C7	DETOXIFICATION	Cytochrome P450 2C7	56190	482947	45873	MEMBRANE	cleavable signal peptide			P05179	
CYTOCHROME P450 2D2	DETOXIFICATION	Cytochrome P450 2D2	56680	57812	63788	MEMBRANE	signal anchor	9 18 IN-OUT		P10634	
CYTOCHROME P450 2D5	DETOXIFICATION	Cytochrome P450 2D5	57080	57818	63790	MEMBRANE	signal anchor	4 23 OUT-IN 301 23 IN-OUT		P12939	
CYTOCHROME P450 2E1	DETOXIFICATION	Cytochrome P450 2E1	56630	51980637	21526	MEMBRANE	cleavable signal peptide	2 22 IN-OUT		P05182	
CYTOCHROME P450 3A1	DETOXIFICATION	Cytochrome P450 3A	57720	6978749	3731	MEMBRANE	cleavable signal peptide	4 23 OUT-IN 217 23 IN-OUT		Q6LEQ2	
CYTOCHROME P450 3A18	DETOXIFICATION	Cytochrome P450 3A18 CYP11A18 P450(6)beta-2	57310	5921916	104898	MEMBRANE	signal anchor	7 23 IN-OUT 219 23 OUT-IN		Q64581	
CYTOCHROME P450 3A2	DETOXIFICATION	Cytochrome P450 3A2	57730	515799	87425	MEMBRANE	cleavable signal peptide	4 23 OUT-IN 219 23 IN-OUT 301 23 OUT-IN		P05183	
CYTOCHROME P450 4A3	DETOXIFICATION	Cytochrome P450 4A14 precursor CYP11A14 Lauric acid omega-hydroxylase P450-LA-omega 3	58230	28461155	21524	MEMBRANE	cleavable signal peptide	15 18 OUT-IN 113 20 IN-OUT		P20817	
CYTOCHROME P450 2D3	DETOXIFICATION	Cytochrome P450, family 2, subfamily d, polypeptide 13	56640	58477687	103927	MEMBRANE	signal anchor	4 23 OUT-IN 305 23 IN-OUT		Q35106 P12938 Q5FVU3	
CYTOCHROME P450 2D4	DETOXIFICATION	Cytochrome P450, family 2, subfamily d, polypeptide 22	56680	62471444	33164	MEMBRANE	signal anchor	7 20 IN-OUT		Q566D3 Q64680	
CYTOCHROME C OXIDASE POLYPEPTIDE VA, MITOCHONDRIAL PRECURSOR	MITOCHONDRIA	Cytochrome c oxidase polypeptide Va, mitochondrial precursor	16130	55971	63743	SOLUBLE	cleavable signal peptide			P11240	

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:cytochrom 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	SOLUBLE				
D-AMINO ACID OXIDASE	PEROXISOME	D-amino-acid oxidase DAMOX DAO DAAO	38820	56972124	60497	SOLUBLE	cleavable signal peptide	O35078		
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	SOLUBLE		Q8VID1		
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	SOLUBLE	cleavable signal peptide	Q6AYS8	XP_213994.2	
DELTA-AMINOLEVULINIC ACID DEHYDRATASE	DETOXIFICATION	Delta-aminolevulinic acid dehydratase Porphobilinogen synthase ALADH	36030	6978483	3622	SOLUBLE		P06214		
DELTA3,5-DELTA2,4-DIENOYL-COA ISOMERASE, MITOCH	PEROXISOME	Delta3,5-delta2,4-dienoyl-CoA isomerase, mitochondrial precursor	36200	478984	80356	SOLUBLE		Q62651 UPI0000167964		
DIHYDROPTERIDINE REDUCTASE	METABOLISM	Dihydropteridine reductase HDHPR Quinoid dihydropteridine reductase	25550	576089	23398	SOLUBLE		P11348		
DIMETHYLANILINE MONOOXYGENASE [N-OXIDE FORMING]	DETOXIFICATION	Dimethylaniline monooxygenase [N-oxide-forming] 1 Hepatic flavin-containing monooxygenase 1 FMO 1 Dimethylaniline oxidase 1	59830	78099773	339248	MEMBRANE	cleavable signal peptide	P36365 Q6P7Q5		
DNAJ HOMOLOG SUBFAMILY A MEMBER 1	PROT SYN/FOLD	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	SOLUBLE		P63036		
PROTEIN KINASE INHIBITOR P58	SIGNALING	Dnajc3 protein [Rattus norvegicus]	50240	38197558	318957	SOLUBLE	cleavable signal peptide			
RIBOPHORIN 2	PROT MOD	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 63 kDa subunit precursor Ribophorin II RPN-II	69080	62512124	193923	MEMBRANE	cleavable signal peptide	P25235 Q6P9X0		
SIMILAR TO NADH DEHYDROGENASE (UBIQUINONE) 1 A	MITOCHONDRIA	ENSEMBL:ENSRNOP00000023811 REFSEQ:XP_214570 PREDICTED: similar to NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 2	10840	27682913	250139	SOLUBLE				

ERGIC-53 PROTEIN	TRAFFIC	ERGIC-53 protein precursor ER-Golgi intermediate compartment 53 kDa protein Lectin, mannose-binding 1 p58	57960	29611707	77835	MEMBRANE	cleavable signal peptide	483 23 OUT-IN	Q62902	
OXIDOREDUCTASE ERO1-L	PROT SYN/FOLD	ERO1-like	54120	19924061	33170	SOLUBLE	cleavable signal peptide		UPI00000E73E1	
ES1 PROTEIN	MITOCHONDRIA	ES1 protein homolog, mitochondrial precursor	28170	83302472	214426	SOLUBLE	cleavable signal peptide		P56571 Q68FS5	XP_215368.1
EZRIN	CYTOSKELETON	EZRIN [Rattus norvegicus]	54170	17902245	145232	SOLUBLE				
ECTONUCLEOSIDE TRIPHOSPHATE DIPHOSPHOHYDROLASE 5	PLASMA MB	Ectonucleoside triphosphate diphosphohydrolase 5	47370	40786479	318787	MEMBRANE	cleavable signal peptide	5 18 OUT-IN 29 23 IN-OUT	Q6P6S9	
ELECTRON TRANSFER FLAVOPROTEIN BETA SUBUNIT	MITOCHONDRIA	Electron transfer flavoprotein subunit beta Beta-ETF	27690	81884360	189992	SOLUBLE				XP_214922.1
ELONGATION FACTOR 1-ALPHA 1 (EF-1-ALPHA-1)	PROT SYN/FOLD	Elongation factor EF-1 alpha	50110	85057089	140182	SOLUBLE			P62630 Q5BJW8 Q64718 Q78ED4	XP_215242.2
ENDOPLASMIC RETICULUM PROTEIN ERP29	PROT SYN/FOLD	Endoplasmic reticulum protein 29	28570	60688521	157237	SOLUBLE	cleavable signal peptide	7 23 IN-OUT	P52555 P80749 Q5BKC2	
ALPHA ENOLASE	METABOLISM	Eno1 protein [Rattus norvegicus]	51260	38649320	338764	SOLUBLE				
ENOYL-COA HYDRATASE, MITOCHONDRIAL	MITOCHONDRIA	Enoyl-CoA hydratase, mitochondrial precursor	31520	56072	15873	SOLUBLE			P14604	
PEROXISOMAL BIFUNCTIONAL ENZYME	PEROXISOME	Enoyl-Coenzyme A, hydratase/3-hydroxyacyl Coenzyme A dehydrogenase	78660	59809132	149061	SOLUBLE			Q5EBD2	
ESTROGEN SULFOTRANSFERASE	DETOXIFICATION	Estrogen sulfotransferase, isoform 1 EST-1 Sulfotransferase, estrogen-preferring Estrone sulfotransferase	35510	1711599	109266	SOLUBLE			P52844	
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	SOLUBLE				
F-ACTIN CAPPING PROTEIN ALPHA-2 SUBUNIT	CYTOSKELETON	F-actin capping protein alpha-2 subunit	32970	74355722	74410	SOLUBLE			Q3T1K5	
PEPTIDYL-PROLYL CIS-TRANS ISOMERASE	PROT SYN/FOLD	FK506-binding protein 2 precursor	15390	27661294	170945	SOLUBLE	cleavable signal peptide		UPI00001820BB	
FATTY-ACID AMIDE HYDROLASE	PROT MOD	Faah protein	63360	6225312	29993	MEMBRANE	cleavable signal peptide	7 23 IN-OUT	P97612 Q5BKA3	
FATTY ACID SYNTHASE	PROT MOD	Fatty acid synthase	272600	57890	43659	MEMBRANE			O09187 O09190 P12785 Q63577 Q64717	
FATTY ACID-BINDING PROTEIN, LIVER	PROT MOD	Fatty acid-binding protein, liver	14270	6978825	3760	SOLUBLE			P02692	
ALDEHYDE DEHYDROGENASE FAMILY 3 MEMBER A2	DETOXIFICATION	Fatty aldehyde dehydrogenase Aldehyde dehydrogenase, microsomal Aldehyde dehydrogenase family 3 member A2 Aldehyde dehydrogenase 10	54080	399362	78151	MEMBRANE		463 18 OUT-IN	P30839	
FERRITIN LIGHT CHAIN	METABOLISM	Ferritin light chain 1	20750	84000579	277663	SOLUBLE			Q6P7T1	
FETUIN-B	BIOSYNTHETIC CARGO	Fetuin-B precursor IRL685	41530	6562849	145181	SOLUBLE	cleavable signal peptide		Q9QX79	
FIBRINOGEN GAMMA CHAIN	BIOSYNTHETIC CARGO	Fibrinogen gamma chain precursor	49650	1183937	3766	SOLUBLE	cleavable signal peptide		P02680 P02680-2	
FIBRONECTIN 1	BIOSYNTHETIC CARGO	Fibronectin precursor FN	272500	9506703	95208	SOLUBLE	cleavable signal peptide		P04937 Q6LDX9	
FIBRINOGEN	BIOSYNTHETIC CARGO	Fibrinogen-like protein	30750	25282415	181007	SOLUBLE	cleavable signal peptide		Q8K583	
FORMIMIDOYLTRANSFERASE-CYCLODEAMINASE	METABOLISM	Fcd protein	58910	60688163	39875	SOLUBLE			O88618 Q5BKB7	
FUMARATE HYDRATASE, MITOCHONDRIAL	MITOCHONDRIA	Fumarate hydratase, mitochondrial precursor Fumarase	54460	8393358	45080	SOLUBLE	cleavable signal peptide		P14408	

FUMARYLACETOACETASE	MITOCHONDRIA	Fumarylacetoacetase Fumarylacetoacetate hydrolase Beta-diketonase FAA	45980	8393349	51443	SOLUBLE			P25093	
GTP CYCLOHYDROLASE I FEEDBACK REGULATORY PROTEIN	SIGNALING	GTP cyclohydrolase 1 feedback regulatory protein GTP cyclohydrolase I feedback regulatory protein GFRP p35	9541	16975337	140831	SOLUBLE			P70552	
RAB10	GTPASE	GTP-binding protein rab10 - rat	22610	420269	44648	MEMBRANE				
DLST DIHYDROLIPOAMIDE SUCCINYLTRANSFERASE, EX	MITOCHONDRIA	Gene,	48610	22775474	113271	SOLUBLE			Q8CJG5	
GLIAL FIBRILLARY ACIDIC PROTEIN ALPHA	CYTOSKELETON	Glial fibrillary acidic protein alpha Gfap protein	49960	62657131	26394	SOLUBLE			Q9R1Q3	XP_346411.1
GLUTAMATE DEHYDROGENASE, MITOCHONDRIAL	MITOCHONDRIA	Glutamate dehydrogenase, mitochondrial precursor	61420	92090591	3897	SOLUBLE	cleavable signal peptide		P10860 Q66HI8 Q6LC16	
GLUTAMINE SYNTHETASE	METABOLISM	Glutamine synthetase	42270	61098201	28251	SOLUBLE			P09606	
GLUTATHIONE S-TRANSFERASE YA-1	DETOXIFICATION	Glutathione S-transferase Ya-1	25640	66611	146667	SOLUBLE			P00502	
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	SOLUBLE				
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	SOLUBLE			P14942	
GLUTATHIONE S-TRANSFERASE YC-2	DETOXIFICATION	Glutathione S-transferase alpha-5 Glutathione S-transferase Yc-2 GST Yc2 GST A5-5	25350	58331159	63272	SOLUBLE				
GLUTATHIONE PEROXIDASE	DETOXIFICATION	Glutathione peroxidase	22260	121668	28283	SOLUBLE	cleavable signal peptide		O08946 P04041 Q4PIY2	
GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE	METABOLISM	Glyceraldehyde-3-phosphate dehydrogenase Gapd protein	35830	9798638	51456	SOLUBLE			Q9QWU4	XP_216453.1
VITAMIN D-BINDING PROTEIN	BIOSYNTHETIC CARGO	Group specific component	53520	51260133	86608	SOLUBLE	cleavable signal peptide		Q68FY4	
GLUTATHIONE S-TRANSFERASE YB-3	DETOXIFICATION	Gstm7 protein	25680	529588	33791	SOLUBLE				
GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT	SIGNALING	Guanine nucleotide binding protein, beta 2, related sequence 1 CRL-1722 L5178Y-R cDNA, RIKEN full-length enriched library, clone:I730096H10 product:guanine nucleotide binding protein, beta 2, related sequence 1, full insert sequence Blastocyst cDNA, RIKEN full-length enriched library, clone:I1C0024M22 product:guanine nucleotide binding protein, beta 2, related sequence 1, full insert sequence Blastocyst cDNA, RIKEN full-length enriched library, clone:I1C0014F18 product:guanine nucleotide binding protein, beta 2, related sequence 1, full insert sequence Blastocyst cDNA, RIKEN full-length enriched library, clone:I1C0013E14 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	SOLUBLE				
VIGILIN (HIGH DENSITY LIPOPROTEIN-BINDING PROTEIN)	METABOLISM	Hdlbp protein	41290	38649090	338318	SOLUBLE			Q6P513	
HEAT SHOCK 70 KDA PROTEIN 1/2	PROT SYN/FOLD	Heat shock 70 kDa protein 1/2	70090	396270	85008	SOLUBLE			Q07439	

HEAT-SHOCK COGNATE 70KD PROTEIN (44KD ATPASE N	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	68722	SOLUBLE			P63018 Q4FZY7	
HEAT SHOCK PROTEIN 86; HSP86	PROT SYN/FOLD	Heat shock protein 86 Heat shock protein 1, alpha	84810	54673763	82698	SOLUBLE			Q91XW0	
HEMOGLOBIN BETA CHAIN	BLOOD + OTHER CELLS	Hemoglobin beta chain, major-form	15980	55823	28543	SOLUBLE			P02091	
HEMOPEXIN	BIOSYNTHETIC CARGO	Hemopexin precursor	51290	204621	16936	SOLUBLE	cleavable signal peptide	5 18 IN-OUT	P20059	
HISTIDINE-RICH GLYCOPROTEIN HRG	UNKNOWN	Histidine-rich glycoprotein 1	59050	62657833	140379	SOLUBLE	cleavable signal peptide		Q99PS8	
CARBOXYLESTERASE 4	DETOXIFICATION	Hydrolase A	3058	807108	105537	SOLUBLE			Q9QV19	
HYDROXYACID OXIDASE 3	PEROXISOME	Hydroxyacid oxidase 3	39200	50925465	100475	SOLUBLE			Q07523	
HYDROXYACYLGLUTATHIONE HYDROLASE	MITOCHONDRIA	Hydroxyacylglutathione hydrolase Glyoxalase II Glx II Round spermatid protein RSP29	28900	3913728	15417	SOLUBLE			O35962	
HYDROXYMETHYLGLUTARYL-COA SYNTHASE, MITOCHONDRIAL	MITOCHONDRIA	Hydroxymethylglutaryl-CoA synthase, mitochondrial precursor HMG-CoA synthase 3-hydroxy-3-methylglutaryl coenzyme A synthase	56910	27465521	16963	SOLUBLE			P22791	
GRP170 (HYPOXIA UP-REGULATED 1)	PROT SYN/FOLD	Hyou1 protein	111200	77404380	395638	SOLUBLE	cleavable signal peptide	13 23 IN-OUT	Q6P136	
PROSTAGLANDIN E SYNTHASE 2	METABOLISM	Hypothetical glutaredoxin/glutathione S-transferase C terminus containing protein	43450	27706734	166503	SOLUBLE	cleavable signal peptide		UPI000017FFAE	
RAB2B	GTPASE	Hypothetical protein	24090	83415090	163993	MEMBRANE			Q3B7V5	
40S RIBOSOMAL PROTEIN S29	PROT SYN/FOLD	Hypothetical protein DKFZp468N1517	6677	6981490	4847	SOLUBLE				
SIMILAR TO RIKEN CDNA 0610006F02	UNKNOWN	Hypothetical protein Mettl7b	27900	66730429	244225	SOLUBLE	cleavable signal peptide	10 23 OUT-IN	Q562C4	
SIMILAR TO PECI PROTEIN	PEROXISOME	Hypothetical protein RGD1310224	33690	57164137	208921	SOLUBLE			Q5M884	XP_214465.2
60S RIBOSOMAL PROTEIN L37A	PROT SYN/FOLD	Hypothetical protein RPL37A	10280	57123	4820	SOLUBLE				
OPTINEURIN	UNKNOWN	Injury-inducible-protein I-55	58100	24475405	154070	SOLUBLE			Q8CJH5	
INTER-ALPHA-INHIBITOR H4 HEAVY CHAIN	BIOSYNTHETIC CARGO	Inter-alpha-inhibitor H4 heavy chain	103600	9506819	47186	SOLUBLE	cleavable signal peptide	7 20 IN-OUT	O35802	
INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H3	BIOSYNTHETIC CARGO	Inter-alpha-trypsin inhibitor heavy chain H3 precursor 1 heavy chain H3 Inter-alpha-inhibitor heavy chain 3	99100	8393899	38418	SOLUBLE	cleavable signal peptide		Q63416	
ISOCITRATE DEHYDROGENASE [NADP] CYTOPLASMIC	METABOLISM	Isocitrate dehydrogenase [NADP] cytoplasmic Cytosolic NADP-isocitrate dehydrogenase Oxalosuccinate decarboxylase IDH NADP (+)-specific ICDH IDP	46730	627999	71492	SOLUBLE			P41562 P80300	

ISOVALERYL-COA DEHYDROGENASE, MITOCHONDRIAL	MITOCHONDRIA	Isovaleryl-CoA dehydrogenase, mitochondrial precursor IVD	46440	6981112	3955	SOLUBLE	cleavable signal peptide		P12007	
KERATIN K6	LIKELY CONTAMINANTS	Keratin K6	3107	554464	66467	SOLUBLE			Q63282	
CYTOKERATIN 15	LIKELY CONTAMINANTS	Keratin, type I cytoskeletal 15 Cytokeratin-15 CK-15 Keratin-15 K15 Type I keratin Ka15	48370	81891677	210892	SOLUBLE			Q6IFV3	XP_213482.2
KERATIN 5	LIKELY CONTAMINANTS	Keratin, type II cytoskeletal 5 Cytokeratin-5 CK-5 Keratin 5 K5	61830	81170669	318877	SOLUBLE			Q6P6Q2 Q7TN97	
KERATIN, TYPE II CYTOSKELETAL 8	LIKELY CONTAMINANTS	Keratin, type II cytoskeletal 8	54020	67678416	67836	SOLUBLE	signal anchor		Q10758	
KETOHEXOKINASE	METABOLISM	Ketohexokinase Hepatic fructokinase	32750	62650395	127122	SOLUBLE			P97550 Q02974	
L-LACTATE DEHYDROGENASE	METABOLISM	L-lactate dehydrogenase A chain LDH-A LDH muscle subunit LDH-M	36450	8393706	51518	SOLUBLE			P04642	
HEAT SHOCK PROTEIN 90; HSP90	PROT SYN/FOLD	LOC495860 protein	83280	51243735	139643	SOLUBLE			Q68GV5	XP_217339.1
MICROSOMAL GLUTATHIONE S-TRANSFERASE 1	DETOXIFICATION	LOC496117 protein	17470	38649092	28295	MEMBRANE		12 23 IN-OUT 131 OUT-IN		
ARP2/3 COMPLEX 20 KDA SUBUNIT	CYTOSKELETON	LOC496278 protein	19670	34858314	32844	SOLUBLE	cleavable signal peptide			
LRRGT00057	UNKNOWN	LRRGT00057	268200	37654330	203325	SOLUBLE	cleavable signal peptide		Q6TXE2	
DNAJ (HSP40) HOMOLOG, SUBFAMILY B, MEMBER 11	PROT SYN/FOLD	LRRGT00084 DnaJ (Hsp40) homolog, subfamily B, member 11 Predicted	40490	62543491	295796	SOLUBLE	cleavable signal peptide	5 23 IN-OUT	Q6TUG0	
LACTATE DEHYDROGENASE A-LIKE PROTEIN	METABOLISM	Lactate dehydrogenase A-like	42050	50927335	224451	SOLUBLE			Q7TNA8	
LEUCINE ZIPPER-EF-HAND CONTAINING TRANSMEMBRANE PROTEIN 1, MITOCHONDRIAL PRECURSOR	MITOCHONDRIA	Leucine zipper-EF-hand-containing transmembrane protein 1, mitochondrial precursor	83060	62510718	296680	MEMBRANE		205 23 IN-OUT	Q5XIN6	XP_223541.2
CARBOXYLESTERASE 1	DETOXIFICATION	Liver carboxylesterase 1 precursor	60170	2506388	43686	SOLUBLE	cleavable signal peptide		P10959 Q63106 Q64626	
CARBOXYLESTERASE 3	DETOXIFICATION	Liver carboxylesterase 3 precursor Carboxylesterase ES-3 pl 5.5 esterase ES-HTEL	61710	550147	78070	SOLUBLE	cleavable signal peptide		Q63108	
SERINE PROTEASE INHIBITOR 2A; LIVER REGENERATION INHIBITOR	BIO SYNTHETIC CARGO	Liver regeneration protein Iryvan Ab1-021	68220	33086444	166149	SOLUBLE			Q7TMB9	
TRANSFERIN	BIO SYNTHETIC CARGO	Liver regeneration-related protein LRRG03 Transferin	76400	61556986	166406	SOLUBLE	cleavable signal peptide		Q7TNX0	
ACYL-COA DEHYDROGENASE, LONG-CHAIN SPECIFIC, MITOCHONDRIAL	MITOCHONDRIA	Long-chain specific acyl-CoA dehydrogenase, mitochondrial precursor LCAD	47870	6978431	3599	SOLUBLE	cleavable signal peptide		P15650	
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	85756	MEMBRANE		21 23 IN-OUT	P18163	
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	MEMBRANE	signal anchor	7 23 IN-OUT	O88813	
LONG-CHAIN-FATTY-ACID--COA LIGASE 6	PROT MOD	Long-chain-fatty-acid--CoA ligase 6	78180	417242	44475	MEMBRANE	signal anchor	21 23 IN-OUT	P33124 Q63835	
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	SOLUBLE	cleavable signal peptide		Q64194	
MACROPHAGE MIGRATION INHIBITORY FACTOR	BLOOD + OTHER CELLS	Macrophage migration inhibitory factor	12480	7514124	37207	SOLUBLE			P30904	
MALATE DEHYDROGENASE, MITOCHONDRIAL	MITOCHONDRIA	Malate dehydrogenase, mitochondrial	35680	42476181	339913	SOLUBLE			Q6GSM4	
MANNOSE-BINDING PROTEIN A	BIO SYNTHETIC CARGO	Mannose-binding protein A precursor	16550	1942287	19138	SOLUBLE			P19999 UPI00001121CE	
MANNOSIDASE 2, ALPHA B1	PROT MOD	Mannosidase 2, alpha B1	114300	40786505	338661	MEMBRANE	cleavable signal peptide	20 23 IN-OUT	Q6F762	
GLYCOPROTEIN PROCESSING GLUCOSIDASE I	PROT MOD	Mannosyl-oligosaccharide glucosidase Glycoprotein-processing glucosidase I	91870	48427849	51409	MEMBRANE	signal anchor	40 23 IN-OUT	O88941	
BOCA	PROT SYN/FOLD	Mesoderm development candidate 2	25220	81883487	280160	SOLUBLE	cleavable signal peptide		Q5U2R7	XP_218854.1

METHYLMALONATE-SEMIALDEHYDE DEHYDROGENASE	MITOCHONDRIA	Methylmalonate-semialdehyde dehydrogenase [acylating], mitochondrial precursor MMSDH Malonate-semialdehyde dehydrogenase [acylating]	57810	400269	37213	MEMBRANE	cleavable signal peptide	174 23 IN-OUT	Q02253	
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	MEMBRANE		21 23 IN-OUT	Q6F9X2	
MITOCHONDRIAL 2-OXOGLUTARATE/MALATE CARRIER	MITOCHONDRIA	Mitochondrial 2-oxoglutarate/malate carrier protein	34150	1580888	77688	SOLUBLE				
MITOCHONDRIAL IMPORT INNER MEMBRANE TRANSLOCATOR	MITOCHONDRIA	Mitochondrial import inner membrane translocase subunit TIM13	10460	59800393	77128	SOLUBLE			P62076	
MITOCHONDRIAL IMPORT INNER MEMBRANE TRANSLOCATOR	MITOCHONDRIA	Mitochondrial import inner membrane translocase subunit TIM8 A Deafness dystonia protein 1 homolog	11040	5107153	12056	MEMBRANE			Q9WVA1	
SIMILAR TO PUTATIVE NAD(P)H STEROID DEHYDROGENASE	UNKNOWN	NAD(P) dependent steroid dehydrogenase-like	40410	57164113	228858	MEMBRANE		288 23 IN-OUT	Q5PPL3	XP_219730.2
NADH DEHYDROGENASE (UBIQUINONE) FE-S PROTEIN	MITOCHONDRIA	NADH dehydrogenase (Ubiquinone) Fe-S protein 1, 75kDa	79410	53850628	229389	SOLUBLE			Q66HF1	XP_217417.2
SIMILAR TO NADH DEHYDROGENASE (UBIQUINONE) FE-S PROTEIN	MITOCHONDRIA	NADH dehydrogenase (Ubiquinone) Fe-S protein 7 Predicted	23950	56606108	213294	SOLUBLE	cleavable signal peptide		Q5RJN0	XP_343166.1
SIMILAR TO NADH DEHYDROGENASE (UBIQUINONE) FLAVOPROTEIN	MITOCHONDRIA	NADH dehydrogenase (Ubiquinone) flavoprotein 1, 51kDa	50730	55741424	243054	SOLUBLE			Q5XIH3	XP_215176.2
NADH-UBIQUINONE OXIDOREDUCTASE 24 KDA SUBUNIT	MITOCHONDRIA	NADH-ubiquinone oxidoreductase 24 kDa subunit, mitochondrial precursor	27380	83305118	291031	SOLUBLE			P19234 Q6PDU9	XP_343639.1
NADPH-CYTOCHROME P450 REDUCTASE	DETOXIFICATION	NADPH--cytochrome P450 reductase	76930	205660	44210	MEMBRANE		20 23 IN-OUT	P00388	
NADH DEHYDROGENASE 1 ALPHA SUBCOMPLEX 10-LIKE	MITOCHONDRIA	Ndufa10 protein	40490	62531217	199168	SOLUBLE	cleavable signal peptide		Q561S0	XP_234089.2
NESPRIN-1	NUCLEUS	Nesprin-1	325100	19705491	161237	SOLUBLE			Q8VHJ9	NP_599208.1
NON-POU-DOMAIN-CONTAINING, OCTAMER BINDING PROTEIN	NUCLEUS	Non-POU domain-containing octamer-binding protein NonO protein	54930	67460593	219030	SOLUBLE			Q5FVM4	
NUCLEAR PORE PROTEIN GP210 PRECURSOR	NUCLEUS	Nuclear pore membrane glycoprotein 210 precursor POM210 Nuclear pore protein gp210	204200	92557	111676	MEMBRANE	cleavable signal peptide	1809 23 OUT-IN	P11654	
NUCLEOBINDIN 2 (CALNUC 2)	CALCIUM TRANS/BIND	Nucleobindin 2 precursor	50090	8515422	3157	SOLUBLE	cleavable signal peptide		Q9JH5	
NUCLEOSIDE DIPHOSPHATE KINASE B	MITOCHONDRIA	Nucleoside diphosphate Kinase B	17280	55926145	69495	SOLUBLE			P19804	
SIMILAR TO ENDOPLASMIC RETICULUM CHAPERONE SUBUNIT	PROT SYN/FOLD	Nucleotide exchange factor SIL1 precursor	52350	81892269	318887	SOLUBLE	cleavable signal peptide		Q6P6S4	
ORNITHINE TRANS-CARBAMYLASE; ORNITHINE CARBAMYLTRANSFERASE	MITOCHONDRIA	Ornithine carbamoyltransferase, mitochondrial precursor	39890	6981312	75019	SOLUBLE			P00481 Q63407	
OXIDATIVE 17 BETA HYDROXYSTEROID DEHYDROGENASE	DETOXIFICATION	Oxidative 17 beta hydroxysteroid dehydrogenase type 6	37140	27545384	102628	MEMBRANE	signal anchor	10 18 OUT-IN	Q54753	
CERULOPLASMIN	BIOSYNTHETIC CARGO	PREDICTED: hypothetical protein XP_215541	120700	34855491	219134	SOLUBLE	cleavable signal peptide		UPI00001CEDA C	
COMPLEMENT COMPONENT 3	BIOSYNTHETIC CARGO	PREDICTED: hypothetical protein XP_579384	186300	62718645	221549	SOLUBLE	cleavable signal peptide	9 23 IN-OUT	UPI00001D1A63	
ALPHA-2-MACROGLOBULIN RECEPTOR-ASSOCIATED PROTEIN	BIOSYNTHETIC CARGO	PREDICTED: low density lipoprotein receptor-related protein associated protein 1	47360	34878475	237675	SOLUBLE			UPI00001D0C4B	
ACIDIC RIBOSOMAL PROTEIN P1	PROT SYN/FOLD	PREDICTED: similar to 60S acidic ribosomal protein P1	11560	27717711	214842	SOLUBLE			UPI00001C9D52	
ACIDIC RIBOSOMAL PROTEIN P2, CYTOSOLIC	PROT SYN/FOLD	PREDICTED: similar to 60S acidic ribosomal protein P2	11760	62660456	201232	SOLUBLE	cleavable signal peptide		UPI000019B6E0	
60S RIBOSOMAL PROTEIN L27A	PROT SYN/FOLD	PREDICTED: similar to 60S ribosomal protein L27a	16590	62639430	273222	SOLUBLE			UPI00001C705B	
NADH:UBIQUINONE OXIDOREDUCTASE PGIV SUBUNIT	MITOCHONDRIA	PREDICTED: similar to Aa2-258	19970	27706932	292254	SOLUBLE			UPI000017E147	
SIMILAR TO ACYL-COA DEHYDROGENASE FAMILY MEMBER	MITOCHONDRIA	PREDICTED: similar to Acyl-CoA dehydrogenase family member 8, mitochondrial precursor (ACAD-8) (Isobutyryl-CoA dehydrogenase)	14960	34860605	288262	SOLUBLE			UPI00001CFEE5	

CCT (CHAPERONIN CONTAINING TCP-1) ZETA SUBUNIT	PROT SYN/FOLD	PREDICTED: similar to CCT (chaperonin containing TCP-1) zeta subunit	58020	76253725	288751	SOLUBLE			Q3MHS9 UPI000017E18D	
SIMILAR TO MICROSOMAL TRIGLYCERIDE TRANSFER PROTEIN	PROT SYN/FOLD	PREDICTED: similar to Microsomal triglyceride transfer protein	99190	34860789	198793	SOLUBLE	cleavable signal peptide		UPI0000182984	
SIMILAR TO NADH DEHYDROGENASE (UBIQUINONE) 1 A	MITOCHONDRIA	PREDICTED: similar to NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 6 (B14)	15220	27663138	280728	SOLUBLE			UPI0000180449	
NADH DEHYDROGENASE:UBIQUINONE FE-S PROTEIN 8	MITOCHONDRIA	PREDICTED: similar to NADH dehydrogenase (ubiquinone) Fe-S protein 8	23970	27661165	313497	SOLUBLE			UPI000017E24F	
SIMILAR TO NADH OXIDOREDUCTASE	MITOCHONDRIA	PREDICTED: similar to NADH oxidoreductase	12500	27717677	167188	SOLUBLE			UPI000017EC12	
SIMILAR TO NADH-UBIQUINONE OXIDOREDUCTASE 30 KDa	MITOCHONDRIA	PREDICTED: similar to NADH-ubiquinone oxidoreductase 30 kDa subunit, mitochondrial precursor (Complex I-30KD) (CI-30KD)	30230	27702072	256004	SOLUBLE	cleavable signal peptide		UPI0000180F4C	
SIMILAR TO PM5 PROTEIN; DNA SEGMENT, CHR 7, ERAT	UNKNOWN	PREDICTED: similar to Nodal modulator 1	133400	34856103	215096	SOLUBLE	cleavable signal peptide		UPI00001CE8C3	
POLY(A) BINDING PROTEIN	PROT SYN/FOLD	PREDICTED: similar to Poly(A) binding protein, cytoplasmic 4, isoform 1	72410	34870953	206311	SOLUBLE			UPI00001CF7C4	
PRE-MRNA SPLICING FACTOR RNA HELICASE (DEAH BOX)	PROT SYN/FOLD	PREDICTED: similar to Putative pre-mRNA splicing factor RNA helicase (DEAH box protein 15)	90980	34878065	276202	SOLUBLE			UPI00001D0BF1	
SIMILAR TO RIKEN CDNA 0610010D20	UNKNOWN	PREDICTED: similar to RIKEN cDNA 0610010D20	34460	34865395	220359	SOLUBLE			UPI0000180E7B	
CARBOXYLESTERASE ESNA1	DETOXIFICATION	PREDICTED: similar to RIKEN cDNA 2210023G05	62910	27658990	227817	SOLUBLE	cleavable signal peptide	7 20 IN-OUT	UPI00001CD14E	
HYPOTHETICAL PROTEIN MGC40499	UNKNOWN	PREDICTED: similar to RIKEN cDNA 2610019P18	28380	34871484	194048	SOLUBLE	cleavable signal peptide		UPI00001D08D1	
BETA-ACTIN	CYTOSKELETON	PREDICTED: similar to RIKEN cDNA 4732495G21 gene	41960	27687455	161693	SOLUBLE			UPI00001C79D9	
SIMILAR TO SEC63	PROT SYN/FOLD	PREDICTED: similar to SEC63-like	87720	34863169	209405	MEMBRANE	signal anchor	13 23 IN-OUT 69 23 OUT-IN 191 23 IN-OUT	UPI00001D1639	
SPFH DOMAIN FAMILY, MEMBER 2	UNKNOWN	PREDICTED: similar to SPFH domain family, member 2	37710	34879021	249650	SOLUBLE	cleavable signal peptide		UPI00001D1016	
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	SOLUBLE	cleavable signal peptide		UPI00001D1120	
CARBOXYLESTERASE ESNA4	DETOXIFICATION	PREDICTED: similar to carboxylesterase isoenzyme gene	60750	34864823	286563	SOLUBLE	cleavable signal peptide		UPI00001CEC61	
CYTOCHROME P450 2C18	DETOXIFICATION	PREDICTED: similar to cytochrome P450 2C66; CYP2C66	56170	34862902	260440	MEMBRANE	cleavable signal peptide	2 19 IN-OUT	UPI00001CEBD2	
SIMILAR TO CYTOCHROME C-1	MITOCHONDRIA	PREDICTED: similar to cytochrome c-1	35430	34866853	271135	SOLUBLE	cleavable signal peptide		UPI00001CFD4B	
P63	TRAFFIC	PREDICTED: similar to cytoskeleton-associated protein 4	63550	34862422	306304	MEMBRANE		86 23 IN-OUT	UPI00001CFC2F	
SIMILAR TO DOLICHOL-PHOSPHATE-MANNOSE SYNTHASE	PROT MOD	PREDICTED: similar to dolichol-phosphate-mannose synthase	29250	34860748	191580	SOLUBLE			UPI00001CF3A2	
DERMATOPONTIN	BIOSYNTHETIC CARGO	PREDICTED: similar to early quiescence protein-1	24200	27677818	208059	SOLUBLE	cleavable signal peptide		UPI00001CBC39	
SIMILAR TO ARYLACETYL ACYL-COA N-ACYLTRANSFERASE	PROT MOD	PREDICTED: similar to glycine-N-acyltransferase isoform a	33990	27681359	139592	SOLUBLE			UPI00001C7619	
GLYCOLATE OXIDASE; SHORT-CHAIN ALPHA-HYDROXY	PEROXISOME	PREDICTED: similar to glycolate oxidase, short-chain alpha-hydroxy acid oxidase	40970	34859262	270415	SOLUBLE			UPI0000181D12	
SIMILAR TO PURINE-NUCLEOSIDE PHOSPHORYLASE; PUM	METABOLISM	PREDICTED: similar to purine-nucleoside phosphorylase	32300	34869683	209477	SOLUBLE			UPI00001D0D54	
60S RIBOSOMAL PROTEIN L10A	PROT SYN/FOLD	PREDICTED: similar to ribosomal protein L10a	24720	27665840	215516	SOLUBLE			UPI00001CA225	
SIMILAR TO SERINE BETA LACTAMASE-LIKE PROTEIN LA	MITOCHONDRIA	PREDICTED: similar to serine beta lactamase-like protein LACT-1	60420	34864295	314386	SOLUBLE	cleavable signal peptide		UPI00001CFF0B	

SERINE PROTEASE INHIBITOR 2.4 PRECURSOR	BIOSYNTHETIC CARGO	PREDICTED: similar to serine protease inhibitor 2.4	46840	34867677	195578	SOLUBLE	cleavable signal peptide		UPI00001CFA7C	
SOLUTE CARRIER FAMILY 25 (MITOCHONDRIAL CARRIER)	MITOCHONDRIA	PREDICTED: similar to solute carrier family 25 (mitochondrial carrier, Aralar), member 12	27180	34854800	195681	SOLUBLE	cleavable signal peptide		UPI00001CF14D	
STOMATIN-LIKE PROTEIN 2	CYTOSKELETON	PREDICTED: similar to stomatin-like protein 2	38410	72255527	299358	SOLUBLE	cleavable signal peptide		Q4FZT0 UPI00001811E2	
SIMILAR TO ZINC BINDING ALCOHOL DEHYDROGENASE	UNKNOWN	PREDICTED: similar to zinc binding alcohol dehydrogenase, domain containing 2	40480	34932585	231239	SOLUBLE			UPI00001D137B	
PROTEIN DISULFIDE ISOMERASE A6	PROT SYN/FOLD	PREDICTED: thioredoxin domain containing 7	48760	62651585	278868	SOLUBLE	cleavable signal peptide	7 20 IN-OUT	UPI00001CFB6B	XP_343129.1
PRX III	MITOCHONDRIA	PRx III	28320	4336877	90537	SOLUBLE	cleavable signal peptide		Q9Z0V6	
PRX IV	PEROXISOME	PRx IV Peroxiredoxin 4	31010	4336879	60442	SOLUBLE	cleavable signal peptide		Q9Z0V5	
PARAOXONASE 1	BIOSYNTHETIC CARGO	Paraoxonase 1	39360	60551577	198556	SOLUBLE	cleavable signal peptide		Q5BJN6	XP_342640.1
PEPTIDYL-PROLYL CIS-TRANS ISOMERASE A	PROT SYN/FOLD	Peptidylprolyl isomerase A	17870	951425	45089	SOLUBLE			Q5BK98	
PEROXIREDOXIN 1	PEROXISOME	Peroxiredoxin 1	22110	56789700	43433	SOLUBLE			Q63716	
PEROXIREDOXIN 5, MITOCHONDRIAL	MITOCHONDRIA	Peroxiredoxin-5, mitochondrial precursor Prx-V Peroxisomal antioxidant enzyme P1P Thioredoxin reductase Thioredoxin peroxidase PMP20 Antioxidant enzyme B166 AOEB166	22180	6103726	60487	SOLUBLE	cleavable signal peptide		Q9R063	
PUTATIVE PEROXISOMAL 2,4-DIENOYL-COA REDUCTASE	PEROXISOME	Peroxisomal 2,4-dienoyl-CoA reductase 2,4-dienoyl-CoA reductase 2 DCR-AKL pVI-AKL	31290	90109768	176638	SOLUBLE			Q9Z2M4	
PEROXISOMAL MEMBRANE ANCHOR PROTEIN	PEROXISOME	Peroxisomal membrane anchor protein	40970	4126962	155718	SOLUBLE			Q9Z2Z4	
PEROXISOMAL MULTIFUNCTIONAL ENZYME TYPE 2 (MF1)	PEROXISOME	Peroxisomal multifunctional enzyme type 2	79430	2492741	108354	SOLUBLE	cleavable signal peptide		P97852	
PUTATIVE SHORT-CHAIN DEHYDROGENASE/REDUCTASE	PEROXISOME	Peroxisomal trans-2-enoyl-CoA reductase RLF98 Peroxisomal 2,4-dienoyl CoA reductase px-2,4-DCR1	32430	6491860	34787	SOLUBLE	cleavable signal peptide		Q9WVK3	
SIMILAR TO PHENYLALANYL-TRNA SYNTHETASE BETA (PHE)	PROT SYN/FOLD	Phenylalanine-tRNA synthetase-like, beta subunit	65650	51948478	254493	SOLUBLE			Q68FT7	XP_217455.2
PHOSPHATE CARRIER PROTEIN, MITOCHONDRIAL	MITOCHONDRIA	Phosphate carrier protein, mitochondrial precursor PTP Solute carrier family 25 member 3	39450	20806141	69383	MEMBRANE		256 23 OUT-IN 308 20 IN-OUT	P16036	
PHYTANOYL-COA DIOXYGENASE, PEROXISOMAL	PEROXISOME	Phytanoyl-CoA dioxygenase, peroxisomal precursor Phytanoyl-CoA alpha-hydroxylase PhyH Phytanic acid oxidase	38590	6539658	55437	SOLUBLE			P57093 Q9QY64	
PLASMA RETINOL-BINDING PROTEIN	BIOSYNTHETIC CARGO	Plasma retinol-binding protein precursor PRBP RBP	23220	27685035	144413	SOLUBLE	cleavable signal peptide		P04916	
PLASMINOGEN	BIOSYNTHETIC CARGO	Plasminogen	90540	62638541	60419	SOLUBLE	cleavable signal peptide		Q01177 Q5BKB6 Q9R0W3	NP_445943.1
PROCOLLAGEN-LYSINE,2-OXOGLUTARATE 5-DIOXYGENASE	PROT MOD	Procollagen-lysine,2-oxoglutarate 5-dioxygenase 1 precursor Lysyl hydroxylase 1 LH1	83610	6093729	60574	SOLUBLE	cleavable signal peptide		Q63321	
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	SOLUBLE				
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	SOLUBLE	cleavable signal peptide		P67779 Q4V8M6	

PROPIONYL-COA CARBOXYLASE ALPHA CHAIN, MITOCH	MITOCHONDRIA	Propionyl-CoA carboxylase alpha chain, mitochondrial precursor PCCase subunit alpha Propanoyl-CoA:carbo dioxide ligase subunit alpha	77710	129684	69597	SOLUBLE			P14882	
SIMILAR TO GI:13385412-LIKE PROTEIN SPLICE FORM I	UNKNOWN	Protein C6orf89 homolog	39570	40786457	205305	MEMBRANE		57 23 IN-OUT	Q6P6G2	
GLUT4 VESICLE PROTEIN	UNKNOWN	Protein FAM62A Membrane-bound C2 domain-containing protein vp115	121200	8393755	51531	MEMBRANE		54 23 IN-OUT	Q3T1L3 Q9Z1X1	
PROTEIN DISULFIDE ISOMERASE	PROT SYN/FOLD	Protein disulfide isomerase precursor	56950	38197382	69606	SOLUBLE	cleavable signal peptide		P04785 P13700	
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	21556	SOLUBLE	cleavable signal peptide		P11598	
PROTEIN DISULFIDE ISOMERASE A4	PROT SYN/FOLD	Protein disulfide-isomerase A4 precursor Protein ERp-72 ERp72 Calcium-binding protein 2 CaBP2	72720	78099786	227664	SOLUBLE	cleavable signal peptide		P38659 Q6P7S5	
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	SOLUBLE	cleavable signal peptide		P18292	
PROTON-TRANSLOCATING ATPASE D SUBUNIT ISOFORM I	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	SOLUBLE			Q5M7T6	
PYRUVATE CARBOXYLASE, MITOCHONDRIAL	MITOCHONDRIA	Pyruvate carboxylase, mitochondrial precursor	129800	7438124	40425	SOLUBLE			P52873 Q5RKM0 XP_346578.1	
RAB1A	GTPASE	RAB1A, member RAS oncogene family RAB1A protein	22680	51338716	21122	MEMBRANE				
RAB7	GTPASE	RAB7	23500	9837359	111003	MEMBRANE			P09527 Q4AEF6	
60S RIBOSOMAL PROTEIN L34	PROT SYN/FOLD	RPL34 protein Ribosomal protein L34	13290	34860562	136355	SOLUBLE				
RAB GDI BETA	TRAFFIC	Rab GDP dissociation inhibitor beta Rab GDI beta Guanosine diphosphate dissociation inhibitor 2 GDI-2 GDI-3	50540	40254781	8623	SOLUBLE			Q6P797	
CAMP-REGULATED GUANINE NUCLEOTIDE EXCHANGE I	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	SOLUBLE			Q9Z1C7	
RAB2A	GTPASE	Ras-related protein Rab-2A	23540	92340	78145	MEMBRANE			P05712	
CYTOCHROME P450 2C12	DETOXIFICATION	Rat female-specific cytochrome P450 15-beta CYP2C12 Cytochrome P450 2C12	55890	59808903	3729	MEMBRANE	cleavable signal peptide	5 18 IN-OUT	Q04648	
REGUCALCIN	METABOLISM	Regucalcin RC Senescence marker protein 30 SMP-30	33390	6970313	3576	SOLUBLE			Q03336 Q63496 Q925W3	
RETICULON 3 PROTEIN ISOFORM B	UNKNOWN	Reticulon 3 protein isoform b RTN3-A1 Reticulon 3 protein isoform a	25370	57977317	64492	MEMBRANE		68 23 IN-OUT 170 23 OUT-IN	Q8VBU0	NP_543185.1
RETINOL DEHYDROGENASE TYPE II	DETOXIFICATION	Retinol dehydrogenase 2 Retinol dehydrogenase type II RODH II 29 k-protein	35600	50926989	80376	SOLUBLE	cleavable signal peptide		P50170	
RETINOL DEHYDROGENASE TYPE I	DETOXIFICATION	Retinol dehydrogenase 7 Retinol dehydrogenase type II RODH III	35740	68534258	35165	MEMBRANE	cleavable signal peptide		P55006 Q4KMB6	
RIBOPHORIN I	PROT MOD	Ribophorin I Ribophorin1	68400	71891579	337611	MEMBRANE	cleavable signal peptide	439 20 OUT-IN	Q6P7A7	

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	SOLUBLE			P62755	
40S RIBOSOMAL PROTEIN S8	PROT SYN/FOLD	Ribosomal protein S8	24210	62078585	4854	SOLUBLE				
60S RIBOSOMAL PROTEIN L11	PROT SYN/FOLD	Rpl11 protein	19020	71043900	2378	SOLUBLE			Q4V8I6	
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	SOLUBLE			Q99MS0	
THIOSULFATE SULFURTRANSFERASE (RHODANASE)	MITOCHONDRIA	SWISS-PROT:P24329 TREMBL:Q5I0D4 REFSEQ_NP:NP_036940 ENSEMBL:ENSRNOP000000000202 Thiosulfate sulfurtransferase	33410	83305808	299568	SOLUBLE				
SARCOPLASMIC CA2+/MG2+ ATPASE	CALCIUM TRANS/BIND	Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	109700	57303	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	
PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT	PROT SYN/FOLD	Sec61 alpha subunit homolog	52260	63101555	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	
SEL1L	TRANSCRIPTION	Sel1 (suppressor of lin-12) 1 homolog	68660	29336095	213126	MEMBRANE			UPI0000005CD43	
SEPIAPTERIN REDUCTASE	METABOLISM	Sepiapterin reductase	28130	34856334	31392	SOLUBLE	cleavable signal peptide		P18297	
HEPARIN COFACTOR II	BIOSYNTHETIC CARGO	Serine (Or cysteine) proteinase inhibitor, clade D, member 1	54550	60551378	68739	SOLUBLE	cleavable signal peptide		Q5BKA6 Q64268	
ALPHA-2-ANTIPLASMIN	BIOSYNTHETIC CARGO	Serine (Or cysteine) proteinase inhibitor, clade F, member 2 Predicted	54890	58865362	341343	SOLUBLE	cleavable signal peptide		Q68FT8	
SERINE--PYRUVATE AMINOTRANSFERASE; MITOCHONDRIA	MITOCHONDRIA	Serine--pyruvate aminotransferase, mitochondrial precursor SPT Alanine--glyoxylate aminotransferase AGT	45830	66655	31393	SOLUBLE			P09139 Q9R2C7	
HEAT SHOCK PROTEIN 47 PRECURSOR	PROT SYN/FOLD	Serpinh1 protein	46560	55824765	280024	SOLUBLE	cleavable signal peptide		Q5RJR9	
SERUM ALBUMIN	BIOSYNTHETIC CARGO	Serum albumin precursor	68720	72101	120645	SOLUBLE	cleavable signal peptide		P02770 P11382	
SERUM AMYLOID P-COMPONENT	BIOSYNTHETIC CARGO	Serum amyloid P-component precursor	26180	3183550	52390	SOLUBLE	cleavable signal peptide		P23680 Q63539	

SHORT CHAIN 3-HYDROXYACYL-COA DEHYDROGENASE	MITOCHONDRIA	Short chain 3-hydroxyacyl-CoA dehydrogenase, mitochondrial precursor HCDH Medium and short chain L-3-hydroxyacyl-coenzyme A dehydrogenase	34450	7387725	70622	SOLUBLE	cleavable signal peptide		Q9WVK7	
SIDEROFLEXIN 1 (TRICARBOXYLATE CARRIER PROTEIN)	MITOCHONDRIA		38560	545998	80422	MEMBRANE		264 23 IN-OUT 301 23 OUT-IN	Q63965	
SRP RECEPTOR BETA	PROT SYN/FOLD	Signal recognition particle receptor subunit beta SR-beta	29580	null (6678137)	38101	SOLUBLE	signal anchor	34 23 IN-OUT		
F1FO-ATP SYNTHASE G SUBUNIT	MITOCHONDRIA	Similar to CG6105-PA	11460	47058994	288462	SOLUBLE			Q6PDU7	
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	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 599 23 IN-OUT	O35913 O55224	
SORBITOL DEHYDROGENASE	METABOLISM	Sorbitol dehydrogenase	42830	2506157	43660	SOLUBLE	cleavable signal peptide		P27867	
SPHINGOSINE-1-PHOSPHATE LYASE 1	PROT MOD	Sphingosine-1-phosphate lyase 1 SP-lyase SPL Sphingosine-1-phosphate aldolase	63760	37999349	269681	SOLUBLE			Q8CHN6	
FARNESYL-DIPHOSPHATE FARNESYLTRANSFERASE	PROT MOD	Squalene synthetase SQS SS Farnesyl-diphosphate farnesyltransferase FPP:FPP farnesyltransferase	48110	9506591	85115	MEMBRANE			Q02769	
GRP75	PROT SYN/FOLD	Stress-70 protein, mitochondrial precursor	73740	62664205	36413	SOLUBLE	cleavable signal peptide		P48721 UPI0000170CC4	
FLAVOPROTEIN SUBUNIT OF SUCCINATE-UBIQUINONE	MITOCHONDRIA	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial precursor Fp Flavoprotein subunit of complex II	71620	52782765	96892	SOLUBLE			Q920L2	
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	SOLUBLE			UPI00001C9571	
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	SOLUBLE			P13086	
SULFITE OXIDASE	MITOCHONDRIA	Sulfite oxidase	54350	40254758	318917	SOLUBLE	cleavable signal peptide		Q6P6W0	
SUPEROXIDE DISMUTASE [CU-ZN]	MITOCHONDRIA	Superoxide dismutase [Cu-Zn]	16020	1213217	35188	SOLUBLE			P07632	
SUPEROXIDE DISMUTASE [Mn], MITOCHONDRIAL	MITOCHONDRIA	Superoxide dismutase [Mn], mitochondrial precursor	24680	56691	111692	SOLUBLE			P07895	
SYNAPTIC GLYCOPROTEIN SC2	PLASMA MB	Synaptic glycoprotein SC2	36120	37589607	33179	MEMBRANE		85 23 IN-OUT 165 20 OUT-IN 196 20 IN-OUT 253 23 OUT-IN	Q64232	
T-KININOGEN I	BIOSYNTHETIC CARGO	T-kininogen I precursor	47700	6981138	3965	SOLUBLE	cleavable signal peptide		P01048 UPI0000163B79	
MITOCHONDRIAL PRECURSOR PROTEINS IMPORT RECEPTOR	MITOCHONDRIA	TOM70 Translocase of outer mitochondrial membrane 70 homolog A	67440	68534716	726503	SOLUBLE	cleavable signal peptide		Q75Q39	
KERATIN 14	LIKELY CONTAMINANTS	TREMBL:Q35813 Keratin 14	25680	2443314	22440	SOLUBLE				
FLAVIN-CONTAINING MONOOXYGENASE 3	DETOXIFICATION	TREMBL:Q5PQV6 REFSEQ_XP:XP_579556 ENSEMBL:ENSRNOP000000004864 Flavin containing monooxygenase 3	59980	62659523	246480	SOLUBLE	cleavable signal peptide			
URATE OXIDASE	PEROXISOME	Tax_Id=10116 35 kDa protein	34930	57463	31609	SOLUBLE				

ATP SYNTHASE E CHAIN, MITOCHONDRIAL	MITOCHONDRIA	Tax_Id=10116 ATP synthase, H+ transporting, mitochondrial F0 complex, subunit e	8255	461587	11888	MEMBRANE			
FRUCTOSE-BISPHOSPHATE ALDOLASE A	METABOLISM	Tax_Id=10116 Aldolase A	39350	6978487	3624	SOLUBLE			
CATALASE	PEROXISOME	Tax_Id=10116 Catalase	59760	6978607	3681	SOLUBLE			
COFILIN, NON-MUSCLE ISOFORM	CYTOSKELETON	Tax_Id=10116 Cofilin 1	18530	8393101	87332	SOLUBLE			
3-HYDROXYBUTYRATE DEHYDROGENASE (EC 1.1.1.30)	MITOCHONDRIA	Tax_Id=10116 D-beta-hydroxybutyrate dehydrogenase mitochondrial precursor	38350	482346	141497	SOLUBLE			NP_446447.1
D-DOPACHROME TAUTOMERASE	METABOLISM	Tax_Id=10116 D-dopachrome tautomerase	13130	895882	29986	SOLUBLE			
ACYL-COA-BINDING PROTEIN	METABOLISM	Tax_Id=10116 Diazepam binDing inhibitor	10030	54261671	4320	SOLUBLE		Q2V4X5	
60S RIBOSOMAL PROTEIN L13A	PROT SYN/FOLD	Tax_Id=10116 Ensembl_locations(Chr-bp):1-95678925 ribosomal protein L13A	23480	548747	106718	SOLUBLE			
ANNEXIN A6	TETH/DOCK/FUS	Tax_Id=10116 Ensembl_locations(Chr-bp):10-40398095 annexin VI	75750	763181	127131	SOLUBLE			
PROCOLLAGEN-LYSINE,2-OXOGLUTARATE 5-DIOXYGEN	PROT MOD	Tax_Id=10116 Ensembl_locations(Chr-bp):12-20846400 Procollagen-lysine, 2-oxoglutarate 5-dioxygenase 3	84910	30017429	286288	SOLUBLE	cleavable signal peptide		
SIMILAR TO NADH DEHYDROGENASE (UBIQUINONE) FE-	MITOCHONDRIA	Tax_Id=10116 Ensembl_locations(Chr-bp):13-87313501 similar to NADH dehydrogenase (ubiquinone Fe-S protein 2	38440	34880923	216920	SOLUBLE	cleavable signal peptide		
PROTECTIVE PROTEIN	LYSOSOME	Tax_Id=10116 Ensembl_locations(Chr-bp):3-155772538 similar to protective protein precursor - mouse	57110	34860773	247133	SOLUBLE	cleavable signal peptide		
PARAOXONASE 2	BIOSYNTHETIC CARGO	Tax_Id=10116 Ensembl_locations(Chr-bp):4-30073201;4-30073201 similar to Pon2 protein	27380	34854947	217377	SOLUBLE	cleavable signal peptide		
SIMILAR TO OLIGOSACCHARYLTRANSFERASE	PROT MOD	Tax_Id=10116 Ensembl_locations(Chr-bp):5-157093377 similar to oligosaccharyltransferase	53840	34872203	206351	MEMBRANE	cleavable signal peptide	40 23 IN-OUT 453 23 OUT-IN	
DEHYDROGENASE/REDUCTASE (SDR FAMILY) MEMBER	DETOXIFICATION	Tax_Id=10116 Ensembl_locations(Chr-bp):6-94917824 similar to CGI-86 protein	36250	34865689	214468	SOLUBLE	cleavable signal peptide	5 23 IN-OUT	
DP1L1 PROTEIN	UNKNOWN	Tax_Id=10116 Ensembl_locations(Chr-bp):None similar to Dp1l1 protein	20580	34862308	288307	MEMBRANE	signal anchor	43 23 IN-OUT 89 23 OUT-IN 118 23 IN-OUT	
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	SOLUBLE	cleavable signal peptide	13 20 IN-OUT	
FLAVIN-CONTAINING MONOOXYGENASE 5	DETOXIFICATION	Tax_Id=10116 Flavin-containing monooxygenase 5	60060	62286643	187298	MEMBRANE	cleavable signal peptide	510 23 OUT-IN	
HYPOTHETICAL PROTEIN XP_234496	BIOSYNTHETIC CARGO	Tax_Id=10116 Hypothetical protein XP_234496	43990	34935467	262615	SOLUBLE	cleavable signal peptide		
KAN-1	PEROXISOME	Tax_Id=10116 Kan-1	46500	8392962	80318	SOLUBLE			
L-LACTATE DEHYDROGENASE B CHAIN	METABOLISM	Tax_Id=10116 Lactate dehydrogenase B	36610	6981146	3968	SOLUBLE			
MAJOR VAULT PROTEIN	PROT SYN/FOLD	Tax_Id=10116 Major vault protein	95800	49256645	395977	SOLUBLE			
C-1-TETRAHYDROFOLATE SYNTHASE, CYTOPLASMIC	METABOLISM	Tax_Id=10116 Methylene tetrahydrofolate dehydrogenase (NADP+ dependent), Methenyltetrahydrofolate cyclohydrolase, forMyltetrahydrofolate synthase	101000	901850	62122	SOLUBLE			
MOESIN	CYTOSKELETON	Tax_Id=10116 Moesin	67740	32363196	71715	SOLUBLE			
PHOSPHOGLUCOMUTASE	METABOLISM	Tax_Id=10116 Phosphoglucumutase 1	61400	8393951	51568	SOLUBLE			
MULTIFUNCTIONAL PROTEIN ADE2	METABOLISM	Tax_Id=10116 Phosphoribosylaminoimidazole carboxylase, PhosPhoribosylaminoribosylaminoimidazole succinocarboxamide synthetase	47100	976252	111533	SOLUBLE			
60S RIBOSOMAL PROTEIN L14	PROT SYN/FOLD	Tax_Id=10116 Ribosomal pRotein L14	23340	2500360	43519	SOLUBLE			
60S RIBOSOMAL PROTEIN L18	PROT SYN/FOLD	Tax_Id=10116 Ribosomal pRotein L18	21660	54261673	37240	SOLUBLE			
60S RIBOSOMAL PROTEIN L3	PROT SYN/FOLD	Tax_Id=10116 Ribosomal pRotein L3	46140	57698	144426	SOLUBLE			
SIMILAR TO 5730439E10RIK PROTEIN	PROT MOD	Tax_Id=10116 Similar to 5730439E10Rik protein	88550	34865846	303924	SOLUBLE			
ANTITHROMBIN III	BIOSYNTHETIC CARGO	Tax_Id=10116 Similar to Ac2-248	97230	34880787	207228	SOLUBLE			
SIMILAR TO ALDH8A1 PROTEIN	DETOXIFICATION	Tax_Id=10116 Similar to Aldh8a1 protein	72630	34852829	197702	SOLUBLE			

CARBAMOYL-PHOSPHATE SYNTHETASE 2, ASPARTATE	MITOCHONDRIA	Tax_Id=10116 Similar to CAD protein	245800	34862992	315461	SOLUBLE			
U2-ASSOCIATED SR140 PROTEIN	UNKNOWN	Tax_Id=10116 Similar to CG9346-PA	113900	34865480	232164	SOLUBLE			
SIMILAR TO CALCIUM-BINDING MITOCHONDRIAL CARRIER	MITOCHONDRIA	Tax_Id=10116 Similar to Calcium-binding mitochondria carrier protein Arai1a2 (Solute carrier family 25, member 13) (Citrin)	101200	34854954	309822	MEMBRANE	cleavable signal peptide		
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	SOLUBLE			
SIMILAR TO KDEL CONTAINING PROTEIN 1; ENDOPLASM	TRAFFIC	Tax_Id=10116 Similar to KDEL containing protein 1	60890	34863399	261916	SOLUBLE	cleavable signal peptide		
SIMILAR TO KIAA0090 PROTEIN	UNKNOWN	Tax_Id=10116 Similar to KIAA0090 protein	91240	34872226	302513	SOLUBLE	cleavable signal peptide		
SIMILAR TO KIAA0316 PROTEIN	UNKNOWN	Tax_Id=10116 Similar to KIAA0316 protein	140900	34879922	244528	SOLUBLE			
SIMILAR TO KIAA0372 GENE PRODUCT	UNKNOWN	Tax_Id=10116 Similar to KIAA0372 gene product	169500	34852783	312697	SOLUBLE			
SIMILAR TO KIAA0635 GENE PRODUCT	UNKNOWN	Tax_Id=10116 Similar to KIAA0635 gene product	147000	34877224	224112	SOLUBLE			
SIMILAR TO FIBRONECTIN TYPE III DOMAIN CONTAINING	UNKNOWN	Tax_Id=10116 Similar to KIAA0970 protein	135200	34874472	295665	MEMBRANE		1197 23 OUT-IN	
KINESIN FAMILY PROTEIN 13A	CYTOSKELETON	Tax_Id=10116 Similar to KIF13A	204000	34874048	266483	SOLUBLE			
SIMILAR TO KINETOCHORE-ASSOCIATED PROTEIN 1 (RO	CYTOSKELETON	Tax_Id=10116 Similar to Kinetochore-aSSociated protein 1 (Rough deal homolog) (hRod) (HSROD) (Rod)	222900	34872331	265212	SOLUBLE			
SIMILAR TO MENINGIOMA EXPRESSED ANTIGEN 6 (COIL	UNKNOWN	Tax_Id=10116 Similar to Meningioma expreSSed antigen 6 (coiled-coil proline-rich)	57130	34865266	286300	SOLUBLE			
SIMILAR TO NEBULETTE (ACTIN-BINDING Z-DISK PROTE	CYTOSKELETON	Tax_Id=10116 Similar to Nebulette (Actin-binding Z-disk protein)	121800	34877348	276942	SOLUBLE			
SIMILAR TO NIT PROTEIN 2	UNKNOWN	Tax_Id=10116 Similar to Nit protein 2	34190	34868007	213226	SOLUBLE			
POLYPOSIS LOCUS PROTEIN 1 HOMOLOG (TB2 PROTEIN	UNKNOWN	Tax_Id=10116 Similar to POLYPOSIS LOCUS PROTEIN 1 HOMOLOG (TB2 PROTEIN HOMOLOG) (GP106)	21070	34878680	252129	MEMBRANE	signal anchor	31 23 IN-OUT 94 23 OUT-IN	
SIMILAR TO PROTEIN DISULFIDE ISOMERASE-RELATED	PROT SYN/FOLD	Tax_Id=10116 Similar to Protein disulfide iSomeraSe-related	89320	34869214	276048	SOLUBLE			
SIMILAR TO ENDOPLASMIC RETICULUM THIOREDOXIN S	PROT SYN/FOLD	Tax_Id=10116 Similar to RIKEN cDNA 0610040B21	27040	34870174	239547	SOLUBLE			
SIMILAR TO RIKEN CDNA 1200014J11	UNKNOWN	Tax_Id=10116 Similar to RIKEN cDNA 1200014J11	80090	34872727	249723	SOLUBLE			
SIMILAR TO TRANSFERRIN	BIOSYNTHETIC CARGO	Tax_Id=10116 Similar to RIKEN cDNA 1300017J02	74750	34865830	304054	SOLUBLE	cleavable signal peptide		
UDP-GLUCURONOSYLTRANSFERASE GTNA2	DETOXIFICATION	Tax_Id=10116 Similar to RIKEN cDNA 2010321J07	62770	27694215	169892	MEMBRANE	cleavable signal peptide	7 23 IN-OUT 509 23 OUT-IN	
SIMILAR TO RIKEN CDNA 2310008M10	UNKNOWN	Tax_Id=10116 Similar to RIKEN cDNA 2310008M10	19420	34860558	316149	MEMBRANE	signal anchor	57 23 IN-OUT 107 23 OUT-IN 142 23 IN-OUT	
SIMILAR TO NADH:UBIQUINONE OXIDOREDUCTASE B17	MITOCHONDRIA	Tax_Id=10116 Similar to RIKEN cDNA 2410011G03	23970	34864767	297605	SOLUBLE			
SIGNAL PEPTIDASE COMPLEX 25 KDA SUBUNIT	PROT SYN/FOLD	Tax_Id=10116 Similar to RIKEN cDNA 5730406I15	24970	27678066	216144	MEMBRANE		80 23 IN-OUT 112 23 OUT-IN	
SIMILAR TO RIKEN CDNA 5730469M10	UNKNOWN	Tax_Id=10116 Similar to RIKEN cDNA 5730469M10	39980	34877094	208161	MEMBRANE		135 23 OUT-IN	
SIMILAR TO RIKEN CDNA 9630046K23	UNKNOWN	Tax_Id=10116 Similar to RIKEN cDNA 9630046K23	41350	34869346	228920	SOLUBLE			
SIMILAR TO SIALIC-ACID O-ACETYLESTERASE	PROT MOD	Tax_Id=10116 Similar to Sialic-acid O-acetyl-eSteraSe	56760	34863093	198275	SOLUBLE	cleavable signal peptide		
TOB3	MITOCHONDRIA	Tax_Id=10116 Similar to TOB3	70420	34873064	239142	SOLUBLE			
UDP-GLUCURONATE DECARBOXYLASE 1	METABOLISM	Tax_Id=10116 Similar to UDP-glucuronate decarboxylaSe 1	20220	34881188	201012	SOLUBLE			
SIMILAR TO ASPARTLY BETA-HYDROXYLASE	METABOLISM	Tax_Id=10116 Similar to aSpartly beta-hydroxylaSe	60560	34866138	213158	MEMBRANE			
SIMILAR TO ALPHA GLUCOSIDASE II, BETA SUBUNIT	PROT MOD	Tax_Id=10116 Similar to alpha glucoSidaSe II, beta Subunit	59240	34860445	208522	SOLUBLE	cleavable signal peptide		

SIMILAR TO ALPHA-2U-GLOBULIN	BIOSYNTHETIC CARGO	Tax_Id=10116 Similar to alpha-2u-globulin	61070	34868545	210822	SOLUBLE	cleavable signal peptide			
ARMET PROTEIN	UNKNOWN	Tax_Id=10116 Similar to arginine-rich, mutated in early Stage tumors	26400	34865887	195759	MEMBRANE	signal anchor			
BAND 7 PROTEIN (35.3 KD) (4N53)	UNKNOWN	Tax_Id=10116 Similar to band 7 protein (35.3 kD) (4N53)	39270	34863101	288335	SOLUBLE	cleavable signal peptide	7 20 IN-OUT		
SIMILAR TO BILE ACID COENZYME A: AMINO ACID N-ACYLTRANSFERRASE	PEROXISOME	Tax_Id=10116 Similar to bile acid Coenzyme A: amino acid N-acyltransferase	47980	34868484	273878	SOLUBLE				
BIOTINIDASE	PLASMA MB	Tax_Id=10116 Similar to biotinidase	62250	34877005	196365	MEMBRANE	signal anchor			
SIMILAR TO COMPLEMENT COMPONENT 8 BETA SUBUNIT	BIOSYNTHETIC CARGO	Tax_Id=10116 Similar to complement component 8 beta Subunit	64810	34869943	204172	SOLUBLE				
SIMILAR TO EMBRYONIC BLASTOCOELAR EXTRACELLULAR MATRIX PROTEIN PRECURSOR	UNKNOWN	Tax_Id=10116 Similar to embryonic blastocoelar extracellular matrix protein precursor	242800	34851569	303538	SOLUBLE	cleavable signal peptide			
ENDOPLASMIC OXIDOREDUCTASE 1 BETA	PROT SYN/FOLD	Tax_Id=10116 Similar to endoplasmic oxidoreductase beta	57800	34876487	282876	SOLUBLE				
UDP-GLUCURONOSYLTRANSFERASE GTNA1	DETOXIFICATION	Tax_Id=10116 Similar to expressed Sequence A1788959	65670	34876789	217594	MEMBRANE	cleavable signal peptide	538 23 OUT-IN		
SIMILAR TO GLYOXYLATE REDUCTASE/HYDROXYPYRUVATE REDUCTASE	PEROXISOME	Tax_Id=10116 Similar to glyoxylate reductase/hydroxypyruvate reductase	34140	34935094	265523	SOLUBLE	cleavable signal peptide			
TPA: SENATAXIN; DEAXQ-BOX HELICASE; TRNA SPLICIN	TRANSCRIPTION	Tax_Id=10116 Similar to hypothetical protein	390800	34853159	241253	SOLUBLE				
HYPOTHETICAL PROTEIN (1)	UNKNOWN	Tax_Id=10116 Similar to hypothetical protein	141900	34854842	233766	SOLUBLE				
HYPOTHETICAL PROTEIN D4ERTD765E	UNKNOWN	Tax_Id=10116 Similar to hypothetical protein D4ERTd765e	42320	34870159	200143	SOLUBLE				
SIMILAR TO HYPOTHETICAL PROTEIN FLJ30596	UNKNOWN	Tax_Id=10116 Similar to hypothetical protein FLJ30596	61060	34854388	263019	SOLUBLE				
GLYCOSYLTRANSFERASE 25 DOMAIN CONTAINING 1	UNKNOWN	Tax_Id=10116 Similar to hypothetical protein MGC38524	121800	34877564	273384	SOLUBLE				
NICALIN HOMOLOG	SIGNALING	Tax_Id=10116 Similar to hypothetical protein from EUROMAGE 2021883	75530	34862247	195586	MEMBRANE	signal anchor	12 23 IN-OUT 638 23 OUT-IN		
SIMILAR TO INTRACELLULAR MEMBRANE-ASSOCIATED LIPOPROTEIN RECEPTOR	METABOLISM	Tax_Id=10116 Similar to intracellular membrane-associated calcium-independent phospholipase A2 gamma	107800	34865151	313999	SOLUBLE				
LIPOPROTEIN RECEPTOR-RELATED PROTEIN	PLASMA MB	Tax_Id=10116 Similar to lipoprotein receptor-related protein	517200	34865759	268163	MEMBRANE	cleavable signal peptide	4540 23 OUT-IN		
SIMILAR TO MEDIUM-CHAIN ACYL-COA SYNTHETASE	MITOCHONDRIA	Tax_Id=10116 Similar to medium-chain acyl-CoA Synthetase	22360	34859067	258281	SOLUBLE				
OSMOTIC STRESS PROTEIN	MITOCHONDRIA	Tax_Id=10116 Similar to osmotic stress protein	148000	34856875	290180	MEMBRANE		183 20 IN-OUT 222 23 OUT-IN 280 23 IN-OUT 312 23 OUT-IN 482 23 IN-OUT		
REPRESSOR OF ESTROGEN RECEPTOR ACTIVITY; B-CES	MITOCHONDRIA	Tax_Id=10116 Similar to repressor of estrogen receptor activity	33420	34858436	262284	SOLUBLE	cleavable signal peptide			
40S RIBOSOMAL PROTEIN S5	PROT SYN/FOLD	Tax_Id=10116 Similar to ribosomal protein S5	29840	34854534	278725	SOLUBLE	cleavable signal peptide			
TUBULIN ALPHA 6	CYTOSKELETON	Tax_Id=10116 Similar to tubulin, alpha 6	63060	34868254	298819	SOLUBLE				
ADENINE NUCLEOTIDE TRANSLOCATOR 2	MITOCHONDRIA	Tax_Id=10116 Solute carrier family 25, member 5	32900	728810	117684	MEMBRANE		112 23 IN-OUT 209 23 OUT-IN		
THIOREDOXIN	PROT SYN/FOLD	Tax_Id=10116 Thioredoxin	11670	57386	12218	SOLUBLE				
P97 (TRANSITIONAL ENDOPLASMIC RETICULUM ATPASE)	TETH/DOCK/FUS	Tax_Id=10116 Transitional endoplasmic reticulum ATPase	89350	641973	125172	SOLUBLE				

SIMILAR TO BC032271 PROTEIN	UNKNOWN	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	MEMBRANE	cleavable signal peptide	5 23 IN-OUT 42 23 OUT-IN		
UNKNOWN (PROTEIN FOR MGC:72610)	UNKNOWN	Torsin-1A-interacting protein 2	61700	81885310	313574	SOLUBLE			Q6P752	
TRANSKETOLASE	METABOLISM	Transketolase	67640	1729977	38668	SOLUBLE			P50137	
TRANSLOCON-ASSOCIATED PROTEIN ALPHA	PROT SYN/FOLD	Translocon-associated protein subunit alpha precursor TRAP-alpha Signal sequence receptor subunit alpha SSR-alpha Liver regeneration-related protein LRRG137	35630	71162390	166245	MEMBRANE	cleavable signal peptide	208 23 OUT-IN	Q7TPJ0	XP_341516.1
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	MEMBRANE	cleavable signal peptide	146 20 OUT-IN	Q07984	
COP-COATED VESICLE MEMBRANE PROTEIN P24 BETA	TRAFFIC	Transmembrane emp24 domain-containing protein 2 precursor Membrane protein p24A RNP21.4	22730	3914232	78146	MEMBRANE	cleavable signal peptide	4 20 OUT-IN 169 23 IN-OUT	Q63524	
30 KDA PROTEIN	UNKNOWN	Transmembrane protein 111	29980	71153386	63169	MEMBRANE	signal anchor	15 23 OUT-IN 115 23 IN-OUT		XP_232272.2
TRANSTHYRETIN	BIOSYNTHETIC CARGO	Transthyretin precursor	15720	57425	31553	SOLUBLE	cleavable signal peptide		P02767 Q547K9	
TRICARBOXYLATE TRANSPORT PROTEIN, MITOCHONDRIAL	MITOCHONDRIA	Tricarboxylate transport protein, mitochondrial precursor Citrate transport protein CTP Tricarboxylate carrier protein Solute carrier family 25 member 1	33840	8394297	69776	SOLUBLE	cleavable signal peptide		P32089 Q498T8	
TRIFUNCTIONAL ENZYME ALPHA SUBUNIT, MITOCHONDRIAL	MITOCHONDRIA	Trifunctional enzyme subunit alpha, mitochondrial precursor TP-alpha Long-chain enoyl-CoA hydratase Long chain 3-hydroxyacyl-CoA dehydrogenase	82510	510108	82392	SOLUBLE	cleavable signal peptide		Q64428	
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	SOLUBLE			Q60587	
TUBULIN ALPHA 1	CYTOSKELETON	Tubulin alpha-1 chain Alpha-tubulin 1 Alpha-tubulin I	50150	55976173	31423	SOLUBLE			Q6P9V9	
TUBULIN ALPHA 4	CYTOSKELETON	Tubulin alpha-1 chain Alpha-tubulin 1 Testis-specific alpha-tubulin Tubulin H2-alpha	49920	55741524	31436	SOLUBLE			Q5XIF6	XP_237302.1
TUBULIN BETA 5	CYTOSKELETON	Tubulin, beta polypeptide Beta 5-tubulin TUBB protein	49670	56754676	62620	SOLUBLE			P69897	
SIMILAR TO KERATIN, TYPE II CYTOSKELETAL 5 (CYTOKERATIN 5)	LIKELY CONTAMINANTS	Type II keratin Kb15	57610	46485029	222258	SOLUBLE			Q6IFZ4	
UDP-GLUCURONOSYLTRANSFERASE 1A1	DETOXIFICATION	UDP glucosyltransferase 1 family polypeptide A1 UDP-glucuronosyltransferase 1A1	59660	695162	43597	MEMBRANE	cleavable signal peptide	7 23 IN-OUT 493 23 OUT-IN	Q5DT04 Q64550 Q64635	
UDP-GLUCURONOSYLTRANSFERASE 1A6	DETOXIFICATION	UDP glucosyltransferase 1 family polypeptide A7 UDP glucosyltransferase 1 family, polypeptide A6	60240	89276780	205347	MEMBRANE	cleavable signal peptide	488 23 OUT-IN	Q6T5E9	
UDP-GLUCURONOSYLTRANSFERASE 2B12	DETOXIFICATION	UDP glucosyltransferase 2 family, polypeptide B4	61030	51948510	221298	MEMBRANE	cleavable signal peptide	494 23 OUT-IN	Q68G19	XP_346460.1
UDP-GLUCOSE GLYCOPROTEIN:GLUCOSYLTRANSFERASE 1	PROT MOD	UDP-glucose:glycoprotein glucosyltransferase 1 precursor UDP-glucose ceramide glucosyltransferase-like 1 UDP--Glc:glycoprotein glucosyltransferase RUGT	174000	7677176	171823	SOLUBLE	cleavable signal peptide		Q3JLA3	
UDP-GLUCURONOSYLTRANSFERASE 1A5	DETOXIFICATION	UDP-glucuronosyltransferase 1A5	60010	18308168	53066	MEMBRANE	cleavable signal peptide	489 23 OUT-IN	Q8VD45	

UDP-GLUCURONOSYLTRANSFERASE 1A7	DETOXIFICATION	UDP-glucuronosyltransferase 1A7	59610	18308176	53069	MEMBRANE	cleavable signal peptide	489 23 OUT-IN	Q8VD43	
UDP-GLUCURONOSYLTRANSFERASE 2A1	DETOXIFICATION	UDP-glucuronosyltransferase 2A1, microsomal (EC 2.4.1.17) (UDPGT) (UGT-OLF)	59860	112467	11410	SOLUBLE	cleavable signal peptide	492 23 OUT-IN	UPI0000178B8E	
UDP-GLUCURONOSYLTRANSFERASE 2B1	DETOXIFICATION	UDP-glucuronosyltransferase 2B1 precursor, microsomal	60480	27545358	31600	MEMBRANE	cleavable signal peptide	494 23 OUT-IN	P09875	
UDP-GLUCURONOSYLTRANSFERASE 2B2	DETOXIFICATION	UDP-glucuronosyltransferase 2B2 precursor, microsomal	60990	207583	78055	MEMBRANE	cleavable signal peptide	495 23 OUT-IN	P08541	
UDP-GLUCURONOSYLTRANSFERASE 2B3	DETOXIFICATION	UDP-glucuronosyltransferase 2B3 precursor UDPGT Testosterone, dihydrotestosterone, and beta-estradiol specific 17-beta-hydroxysteroid specific UDPGTR-3 RLUG38	60520	31543923	31602	MEMBRANE	cleavable signal peptide	495 23 OUT-IN	P08542 P16915	
UDP-GLUCURONOSYLTRANSFERASE 2B5	DETOXIFICATION	UDP-glucuronosyltransferase 2B5 precursor UDPGT 17-beta-hydroxysteroid specific UDPGTTr-5 UDP-glucuronosyltransferase R-21 UDPGTTr-21	60590	55925581	31603	MEMBRANE	cleavable signal peptide	495 23 OUT-IN	P19488 P19489	
UDP-GLUCURONOSYLTRANSFERASE 2B8	DETOXIFICATION	UDP-glucuronosyltransferase 2B8 precursor UDPGT UGT2B-RH4	60090	6136101	125219	MEMBRANE	cleavable signal peptide	496 23 OUT-IN	Q62789	
UBIQUITIN-CONJUGATING ENZYME E2L 3	PROTEASOME/UBIQUITIN	Ube2l3 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	SOLUBLE				
SIMILAR TO UBIQUINOL-CYTOCHROME C REDUCTASE C	MITOCHONDRIA	Ubiquinol-cytochrome c reductase core protein I	52850	51948476	220138	SOLUBLE	cleavable signal peptide		Q68FY0	XP_217267.2
UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX CO	MITOCHONDRIA	Ubiquinol-cytochrome c reductase core protein II	48400	55741544	139461	SOLUBLE			Q5XIR3	XP_215042.1
UBIQUINOL-CYTOCHROME C REDUCTASE IRON-SULFUR	MITOCHONDRIA	Ubiquinol-cytochrome c reductase iron-sulfur subunit, mitochondrial precursor Rieske iron-sulfur protein RISP Liver regeneration-related protein LRRGT00195	29450	57114330	230682	SOLUBLE	cleavable signal peptide		P20788 Q6Q113	XP_214457.2
MEMBRANE ASSOCIATED PROGESTERONE RECEPTOR VERY-LONG-CHAIN ACYL-COA SYNTHETASE (VERY-LON	DETOXIFICATION PEROXISOME	Ventral midline antigen VEMA 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	21600 70690	6647578 3183199	19913 78154	MEMBRANE MEMBRANE	cleavable signal peptide	20 23 OUT-IN 5 23 OUT-IN 266 23 IN-OUT	Q549C4 P97524	
VIGILIN	PROT SYN/FOLD	Vigilin High density lipoprotein-binding protein HDL-binding protein	141600	46397078	26167	SOLUBLE			Q9Z1A6	
VITAMIN K-DEPENDENT GAMMA-CARBOXYLASE	PROT MOD	Vitamin K-dependent gamma-carboxylase Gamma-glutamyl carboxylase Vitamin K gamma glutamyl carboxylase	87480	6136262	78166	MEMBRANE		116 23 IN-OUT 160 23 OUT-IN 195 20 IN-OUT 249 23 OUT-IN 278 23 IN-OUT	O88496	
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	SOLUBLE	cleavable signal peptide		P31394	
3-KETOACYL-COA THIOLASE A, PEROXISOMAL	PEROXISOME	acetyl-CoA acyltransferase, 3-oxo acyl-CoA thiolase A, peroxisomal	44780	6978429	3598	SOLUBLE	cleavable signal peptide		UPI000016852C	
FRUCTOSE-BISPHOSPHATE ALDOLASE B	IMETABOLISM	aldolase B [Rattus norvegicus]	39600	1619606	116234	SOLUBLE				
BETA 2 GLOBIN	BLOOD + OTHER CELLS	beta 2 globin [rats, Sprague-Dawley, Peptide, 146 aa]	15860	8048915	371	SOLUBLE				
CATHEPSIN C	LYSOSOME	cathepsin C	52240	8393218	51414	SOLUBLE	cleavable signal peptide		UPI0000049A8F	

CYTOCHROME P450 2D1	DETOXIFICATION	cytochrome P450	57190	203803	126576	MEMBRANE	signal anchor	4 23 OUT-IN 301 23 IN-OUT		
FERRITIN HEAVY CHAIN	METABOLISM	ferritin, heavy polypeptide 1	21100	6978859	3774	SOLUBLE			UPI0000163C2E	
FIBRINOPEPTIDE A	BIOSYNTHETIC CARGO	fibrinopeptide A	1740	229210	22617	SOLUBLE				
GLYCEROL-3-PHOSPHATE DEHYDROGENASE [NAD+], C1	METABOLISM	glycerol-3-phosphate dehydrogenase 1 (soluble) [Rattus norvegicus]	37400	3023880	80790	SOLUBLE				
HEAT RESPONSIVE PROTEIN 12	PROT SYN/FOLD	heat-responsive protein 12	14290	2425030	153343	SOLUBLE			UPI00001679A7	
HYPERTENSION-INDUCED PROTEIN S-2	UNKNOWN	hypertension-induced protein S-2 - rat (fragment)	11250	539959	130834	SOLUBLE				
MANNOSE-BINDING PROTEIN C PRECURSOR	BIOSYNTHETIC CARGO	mannose-binding protein C (liver)	26100	205263	44167	SOLUBLE	cleavable signal peptide		UPI0000168267	
60S RIBOSOMAL PROTEIN L30	PROT SYN/FOLD	null	12780	51702801	4817	SOLUBLE				
P105 COACTIVATOR	NUCLEUS	p105 coactivator	99330	1800307	177421	SOLUBLE			UPI000000E741D	
PHOSPHATIDYLETHANOLAMINE-BINDING PROTEIN	PROT MOD	phosphatidylethanolamine binding protein [Rattus norvegicus]	20800	8393910	51562	SOLUBLE				
60S RIBOSOMAL PROTEIN L13	PROT SYN/FOLD	ribosomal protein L13	24240	510552	37239	SOLUBLE			UPI00001679E1	
60S RIBOSOMAL PROTEIN L6	PROT SYN/FOLD	ribosomal protein L6	33570	2507315	42185	SOLUBLE			UPI00001679A0	
40S RIBOSOMAL PROTEIN S17	PROT SYN/FOLD	similar to 40S RIBOSOMAL PROTEIN S17	15680	34853950	250506	SOLUBLE			UPI00001CF113	
60S RIBOSOMAL PROTEIN L7A (SURFEIT LOCUS PROTEIN)	PROT SYN/FOLD	similar to 60S ribosomal protein L7a (Surfeit locus protein 3) (PLA-X polypeptide)	26720	34855926	208919	SOLUBLE			UPI00001CF4E6	
60S RIBOSOMAL PROTEIN L7A (SURFEIT LOCUS PROTEIN)	PROT SYN/FOLD	similar to 60S ribosomal protein L7a (Surfeit locus protein 3) (PLA-X polypeptide)	35790	34857405	311989	SOLUBLE			UPI00001CEE0A	
CG33130-PA	UNKNOWN	similar to CG33130-PA	125000	34870072	215152	SOLUBLE	cleavable signal peptide		UPI00001D081E	
UNNAMED PROTEIN	UNKNOWN	similar to CGI-90 protein	52100	34867201	258588	SOLUBLE	cleavable signal peptide		UPI00001CF684	
CALCIUM-BINDING MITOCHONDRIAL CARRIER PROTEIN	MITOCHONDRIA	similar to Calcium-binding mitochondrial carrier protein Aralar2 (Solute carrier family 25, member 13) (Citrim)	15470	27708576	166641	SOLUBLE			UPI00001C8924	
F-ACTIN CAPPING PROTEIN ALPHA-1 SUBUNIT	CYTOSKELETON	similar to Cappa1 protein	32910	34859736	230796	SOLUBLE			UPI00001CEF4D	
CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR	UNKNOWN	similar to Cleavage and polyadenylation specificity factor, 73 kDa subunit (CPSF 73 kDa subunit)	74350	34858109	240505	SOLUBLE			UPI00001CEE92	
G1 TO PHASE TRANSITION 2	SIGNALING	similar to G1 to phase transition 2	76550	27663980	171140	SOLUBLE	cleavable signal peptide		UPI00001C98FC	
AMPHOTERIN	NUCLEUS	similar to High mobility group protein 1 (HMG-1) (Amphoterin) (Heparin-binding protein p30)	48030	34861695	293750	SOLUBLE			UPI00001CEA7A	
SIMILAR TO NADH DEHYDROGENASE (UBIQUINONE) 1 A	MITOCHONDRIA	similar to NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 9	42560	34858473	215768	SOLUBLE	cleavable signal peptide		UPI00001CF5B3	
TRINUCLEOTIDE REPEAT CONTAINING 5 (PREDICTED)	UNKNOWN	similar to RIKEN cDNA 1600025D17	39820	34874446	296070	SOLUBLE			UPI00001D0171	
YEAST-44.2 PROTEIN	UNKNOWN	similar to RIKEN cDNA 2810409H07 [Rattus norvegicus]	42320	34855205	260021	SOLUBLE	cleavable signal peptide			
SDF2 LIKE PROTEIN 1	PROT MOD	similar to SDF2 like protein 1 [Rattus norvegicus]	23400	34869825	263376	SOLUBLE	cleavable signal peptide			
SMILAR TO ACTIN-RELATED PROTEIN 2	CYTOSKELETON	similar to actin-related protein 2	42030	34878017	194947	SOLUBLE			UPI00001D0BF6	
2610204L23RIK PROTEIN	UNKNOWN	similar to adipocyte-specific protein 4 [Rattus norvegicus]	55200	34873948	240031	SOLUBLE	cleavable signal peptide			
ALPHA GLUCOSIDASE II, ALPHA SUBUNIT	PROT MOD	similar to alpha glucosidase II, alpha subunit [Rattus norvegicus]	89880	34861580	192728	SOLUBLE				

COPROPORPHYRINOGEN OXIDASE	MITOCHONDRIA	similar to coproporphyrinogen oxidase	49280	79749365	160701	SOLUBLE			Q3B7D0 UPI000017ED67	
SIMILAR TO GLYCERALDEHYDE-3-PHOSPHATE DEHYDR	METABOLISM	similar to glyceraldehyde-3-phosphate dehydrogenase	41920	34854562	287450	SOLUBLE			UPI00001CE72B	
SIMILAR TO GLYCERALDEHYDE-3-PHOSPHATE DEHYDR	METABOLISM	similar to glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) (EC 1.2.1.12) - mouse	31550	34864978	296252	SOLUBLE	cleavable signal peptide		UPI00001CFC83	
SIMILAR TO HEXOSE-6-PHOSPHATE DEHYDROGENASE; INTER-ALPHA TRYPSIN INHIBITOR; HEAVY CHAIN 1	METABOLISM	similar to hexose-6-phosphate dehydrogenase GDH/6PGL endoplasmic bifunctional protein	114800	34872615	251640	SOLUBLE			UPI00001CF8A5	
	BIOSYNTHETIC CARGO	similar to inter-alpha trypsin inhibitor, heavy chain 1 [Rattus norvegicus]	99190	34877130	227779	SOLUBLE	cleavable signal peptide			
MIRROR-IMAGE POLYDACTYLY GENE 1	UNKNOWN	similar to mirror-image polydactyly gene 1	52780	34865613	265130	SOLUBLE			UPI00001CF9EA	
ORNITHINE TRANSPORTER	MITOCHONDRIA	similar to ornithine transporter	32800	27673563	205798	SOLUBLE	cleavable signal peptide		UPI00001CC87E	
SIMILAR TO RIBOSOMAL PROTEIN L10A	PROT SYN/FOLD	similar to ribosomal protein L10a	47220	34878384	298856	SOLUBLE			UPI00001D014B	
SIMILAR TO SERINE PROTEASE OMI	PROT MOD	similar to serine protease OMI	49090	34856275	218478	MEMBRANE	cleavable signal peptide	106 20 IN-OUT	UPI00001CF4FA	
SIMILAR TO SPLICING COACTIVATOR SUBUNIT SRM300; TALIN	NUCLEUS	similar to splicing coactivator subunit SRm300; RNA binding protein; AT-rich element binding factor [Rattus norvegicus]	212600	34868816	290757	SOLUBLE				
	CYTOSKELETON	similar to talin [Rattus norvegicus]	269500	34867875	230030	SOLUBLE				
TASTE RECEPTOR, TYPE 1, MEMBER 2	PLASMA MB	taste receptor, type 1, member 2	202100	34872230	217700	MEMBRANE		1612 23 OUT-IN 1647 23 IN-OUT 1684 23 OUT-IN 1719 23 IN-OUT 1745 23 OUT-IN	UPI00001CF880	
SIMILAR TO PEROXISOMAL LON PROTEASE	PEROXISOME	unknown	94390	34851379	292730	SOLUBLE			UPI0000181D18	
SIMILAR TO HYPOTHETICAL PROTEIN CGI-99	CYTOSKELETON	unknown	28170	27722175	195164	SOLUBLE			UPI00001CDC62	
TROPOMYOSIN ALPHA	CYTOSKELETON	(P04692) Isoform 5 of P04692	28340	112443	11396	SOLUBLE			P04692-5	
CLATHRIN LIGHT CHAIN A	COAT	(P08081) Isoform Non-brain of P08081	23570	56269651	126525	SOLUBLE			P08081-2 Q5PPP1	
H-RAS-1/P21	GTPASE	(P08644) Isoform 2B of P08644	21490	495534	71624	SOLUBLE			P08644-2	
SH3P7R2	UNKNOWN	(Q9JHL4) Isoform 3 of Q9JHL4	48250	7248379	18910	SOLUBLE			Q9JHL4-3	
SOLUTE CARRIER FAMILY 21 MEMBER 10	PLASMA MB	(Q9QZX8) Isoform 2 of Q9QZX8	76770	9624356	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	
COACTIVATOR-ASSOCIATED ARGININE METHYL TRANSF	NUCLEUS	(Q9WVG6) Isoform 2 of Q9WVG6	63460	77539446	292598	SOLUBLE	cleavable signal peptide		Q4AE68	
1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPH	SIGNALING	1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase beta 3	139400	32699414	166274	SOLUBLE			Q62887 Q99JE6 Q9QW29	

PROTEASOME SUBUNIT ALPHA TYPE 2	PROTEASOME/UBIQUITIN	10 days embryo whole body cDNA, RIKEN full-length enriched library, clone:2610511121 product:proteasome (prosome, macropain) subunit, alpha type 2, full insert sequence TIB-55 BB88 cDNA, RIKEN full-length enriched library, clone:I730006B17 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: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 (prosom	25930	8394063	33375	SOLUBLE			
10-FORMYLTETRAHYDROFOLATE DEHYDROGENASE	METABOLISM	10-Formyltetrahydrofolate Dehydrogenase	34040	42543697	723160	SOLUBLE			UPI0000237CD3
14-3-3 PROTEIN ETA	SIGNALING	14-3-3 protein eta	28210	6981710	29710	SOLUBLE			P11576
14-3-3 PROTEIN TAU	SIGNALING	14-3-3 protein theta	27780	6981712	29711	SOLUBLE			P68255
230 KDA PHOSPHATIDYLINOSITOL 4-KINASE	SIGNALING	230 kDa phosphatidylinositol 4-kinase	231300	25742825	19300	SOLUBLE			O08662
3-HYDROXYANTHRANILATE 3,4-DIOXYGENASE	METABOLISM	3-hydroxyanthranilate 3,4-dioxygenase 3-HAO 3-hydroxyanthranilic acid dioxygenase 3-hydroxyanthranilate oxygenase	32580	9910256	42736	SOLUBLE			P46953 P70474 Q5RKK0 Q64556
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	MEMBRANE	cleavable signal peptide		Q62904
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	MEMBRANE		15 20 OUT-IN 113 18 IN-OUT 145 23 OUT-IN	P24008
4- TRIMETHYLAMINOBUTYRALDEHYDE DEHYDROGENAS	METABOLISM	4-trimethylaminobutyraldehyde dehydrogenase TMABADH Aldehyde dehydrogenase 9A1	53650	78099320	104196	SOLUBLE			Q6GMM4 Q9JLJ3
5'-NUCLEOTIDASE	PLASMA MB	5' -nucleotidase precursor Ecto-5' -nucleotidase 5' -N CD73 antigen	63970	202551	11455	MEMBRANE	cleavable signal peptide	553 23 OUT-IN	P21588
5'-AMP-ACTIVATED PROTEIN KINASE, GAMMA-1 SUBUNIT	SIGNALING	5'-AMP-activated protein kinase, gamma-1 subunit	36670	1335860	68651	SOLUBLE			P80385
60S RIBOSOMAL PROTEIN L22	PROT SYN/FOLD	60S ribosomal protein L22	14760	52221202	4392	SOLUBLE			Q6PDV8
60S RIBOSOMAL PROTEIN L26	PROT SYN/FOLD	60S ribosomal protein L26	17260	27672824	4813	SOLUBLE			

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 Osteodlast-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	SOLUBLE			
ADP-RIBOSYLATION FACTOR 4	GTPASE	ADP-ribosylation factor 4	20400	543844	10609	MEMBRANE			
CLATHRIN ADAPTIN-1, BETA 1	COAT	AP-1 complex subunit beta-1 Adapter-related protein complex 1 beta-1 subunit Beta-adaptin 1 Adaptor protein complex AP-1 beta-1 subunit Golgi adaptor HA1/AP1 adaptin beta subunit Clathrin assembly protein complex 1 beta large chain	104600	8392872	126513	SOLUBLE	P52303		
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	SOLUBLE			
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	17020	56961624	65700	SOLUBLE	P62744	XP_346535.1	
ADP-RIBOSYLATION FACTOR 6	GTPASE	ARF6 protein ADP-ribosylation factor 6	20080	60552411	120856	MEMBRANE	Q5BKA5		
ARP2/3 COMPLEX 21 KDA SUBUNIT	CYTOSKELETON	ARP2/3 complex 21 kDa subunit	19650	27665454	160418	SOLUBLE			
ATPASE, H+ TRANSPORTING, V1 SUBUNIT E ISOFORM 1	LYSOSOME	ATPase, H+ transporting, V1 subunit E isoform 1	26130	38454230	261145	SOLUBLE	Q6PCU2		
VACUOLAR ATPASE	LYSOSOME	ATPase, H+ transporting, lysosomal 34kDa, V1 subunit D	28310	40786463	160475	SOLUBLE	Q6P503		
ACETYL-COENZYME A ACETYLTRANSFERASE 3-LIKE	UNKNOWN	Ab2-076	103300	33086552	166325	SOLUBLE	Q7TP61		
SIMILAR TO GLYCINE-N-ACYLTRANSFERASE	PROT MOD	Ab2-132	39450	33086562	261456	SOLUBLE	Q7TP56		
AB2-225	UNKNOWN	Ab2-225 Hypothetical protein RGD1306952	27900	56970828	244467	SOLUBLE	Q7TP52	XP_226908.2	
EUKARYOTIC TRANSLATION ELONGATION FACTOR 1 BETA	PROT SYN/FOLD	Ac2-067	27970	34862605	166240	SOLUBLE	Q7TPK5		
ACETYL-COA CARBOXYLASE 1	MITOCHONDRIA	Acetyl-CoA carboxylase 1 ACC-alpha Biotin carboxylase	265200	202645	84141	SOLUBLE	P11497 P97902		
SUPPRESSOR OF PROFILIN/P41 OF ACTIN-RELATED COMPLEX	CYTOSKELETON	Actin-related protein 2/3 complex subunit 1A	41600	59797636	168831	SOLUBLE	Q99PD4		

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	SOLUBLE			P84092	
ADENINE PHOSPHORIBOSYLTRANSFERASE	METABOLISM		Adenine phosphoribosyltransferase APRT	19550	61556832	126504	SOLUBLE			P36972	
ADENOSINE KINASE	METABOLISM		Adenosine kinase	40100	7448824	3608	SOLUBLE			Q64640	NP_037027.1
AFLATOXIN B1 ALDEHYDE REDUCTASE MEMBER 2	DETOXIFICATION		Akr7a2 protein	37600	6815049	161251	SOLUBLE			Q6P765	
HYDROXYSTEROID SULFOTRANSFERASE	DETOXIFICATION		Alcohol sulfotransferase	33080	204671	148916	SOLUBLE			P15709	
ALDEHYDE DEHYDROGENASE FAMILY 1 MEMBER A1	DETOXIFICATION		Aldehyde dehydrogenase 1A1	54460	38494348	72216	SOLUBLE			P51647	
ALDEHYDE OXIDASE	DETOXIFICATION		Aldehyde oxidase	146900	4324710	95119	SOLUBLE			Q9R240	Q9Z0U5
ALDOSE1-EPIMERASE	METABOLISM		Aldose 1-epimerase Galactose mutarotase	37890	84028322	290544	SOLUBLE			Q66HG4	XP_233806.2
ALPHA ISOFORM OF REGULATORY SUBUNIT A, PROTEIN	SIGNALING		Alpha isoform of regulatory subunit A, protein phosphatase 2	65320	55926139	36803	SOLUBLE			Q5X134	XP_341765.1
ALPHA-1 CATENIN	CYTOSKELETON		Alpha-1 catenin	9484	92036	84182	SOLUBLE		cleavable signal peptide	P02764	
ALPHA-1-ACID GLYCOPROTEIN PRECURSOR	BIOSYNTHETIC CARGO		Alpha-1-acid glycoprotein precursor Orosomucoid OMD	23580	72091	11470	SOLUBLE				
ALPHA-2 ANTIPLASMIN	BIOSYNTHETIC CARGO		Alpha-2 antiplasmin Serine (Or cysteine) proteinase inhibitor, clade F, member 1	46470	51261124	317738	SOLUBLE		cleavable signal peptide	Q80ZA3	
ALPHA-PARVIN	CYTOSKELETON		Alpha-parvin Actopaxin	42290	20138815	37085	SOLUBLE			Q9HB97	
ANNEXIN A4	TETH/DOCK/FUS		Annexin A4	35850	37999910	171244	SOLUBLE			P55260	NP_077069.2
CLATHRIN ADAPTIN-2, BETA 1	COAT		Ap2b1 protein	105700	73695330	59082	SOLUBLE			P62944-2	
ARGININOSUCCINATE LYASE	METABOLISM		Argininosuccinate lyase	51550	551296	45085	SOLUBLE			Q3ZB97	
AROMATIC-L-AMINO-ACID DECARBOXYLASE	METABOLISM		Aromatic-L-amino-acid decarboxylase AADC DOPA decarboxylase DDC	54050	6978759	3735	SOLUBLE			P14173	Q6LEG4
ARYL SULFOTRANSFERASE	DETOXIFICATION		Aryl sulfotransferase	33910	55761	69784	SOLUBLE			P17988	Q548D2
ASIALOGLYCOPROTEIN RECEPTOR 1	PLASMA MB		Asialoglycoprotein receptor 1	32850	7705290	120624	MEMBRANE	signal anchor	40 23 IN-OUT	P02706	
BETA-CATENIN	CYTOSKELETON		Beta-catenin	85470	16758082	74416	SOLUBLE				
BETA-UREIDOPROPIONASE	MITOCHONDRIA		Beta-ureidopropionase Beta-alanine synthase N-carbamoyl-beta-alanine amidohydrolase	44040	51259277	44431	SOLUBLE			Q03248	
BILE SALT EXPORT PUMP (ATP-BINDING CASSETTE, SUB	PLASMA MB		Bile salt export pump ATP-binding cassette sub-family member 11 Sister of P-glycoprotein	146300	3075422	13065	MEMBRANE		61 23 IN-OUT 143 23 OUT-IN 242 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	O70127	
ADENYLYL CYCLASE-ASSOCIATED PROTEIN 1	SIGNALING		CAP, adenylate cyclase-associated protein 1	51590	59709467	130827	SOLUBLE			Q5FVS8	
CADHERIN-17 PRECURSOR	PLASMA MB		Cadherin-17 precursor Liver-intestine-cadherin Li-cadherin	91860	628001	127670	MEMBRANE	cleavable signal peptide	784 23 OUT-IN	P55281	
CALCIUM-BINDING PROTEIN P22	SIGNALING		Calcium-binding protein p22 Calcium-binding protein CHP Calceineurin homologous protein Sid 470	22430	46577577	25354	SOLUBLE				

CALCIUM-INDEPENDENT ALPHA-LATROTOXIN RECEPTOR	PLASMA MB	Calcium-independent alpha-latrotoxin receptor 2 precursor	161100	3695131	70058	MEMBRANE	cleavable signal peptide	854 23 OUT-IN 889 18 IN-OUT 921 23 OUT-IN 956 20 IN-OUT 995 23 OUT-IN 1055 23 IN-OUT 1082 23 OUT-IN	O88923	
CALMODULIN	PROT SYN/FOLD	Cam protein Calm2a-prov protein	16940	8394168	55585	SOLUBLE				
CATECHOL O-METHYLTRANSFERASE, MEMBRANE-BOUND	DETOXIFICATION	Catechol O-methyltransferase, membrane-bound form	29600	6978681	3708	SOLUBLE	cleavable signal peptide	2 23 IN-OUT	P22734	
6-PHOSPHOGLUCONATE DEHYDROGENASE, DECARBOXYLATING	METABOLISM	Cc2-27	120500	33086672	166337	SOLUBLE			Q7TP11	
CC15 PROTEIN	PROT SYN/FOLD	Cct5 protein	31980	37590247	252047	SOLUBLE			Q6PCT4	
CDC42	GTPASE	Cell division cycle 42	21260	61889112	85184	MEMBRANE			Q6P9Y3	
CHAPERONIN CONTAINING TCP-1 BETA SUBUNIT	PROT SYN/FOLD	Chaperonin containing TCP1, subunit 2 Beta	57460	54400730	292700	SOLUBLE			Q5XIM9	XP_216891.2
CHAPERONIN CONTAINING TCP1, SUBUNIT 3 (GAMMA)	PROT SYN/FOLD	Chaperonin containing TCP1, subunit 3 Gamma	60650	40018616	169833	SOLUBLE			Q6P502	
CHLORIDE INTRACELLULAR CHANNEL PROTEIN 4	PLASMA MB	Chloride intracellular channel protein 4 Intracellular chloride ion channel protein p64H1	28630	6685295	78195	MEMBRANE				
COPI COATOMER BETA SUBUNIT	COAT	Coatomer subunit beta Beta-coat protein Beta-COP	107000	55819	63721	SOLUBLE			P23514	
COMPLEMENT COMPONENT 1, Q SUBCOMPONENT BINDING	MITOCHONDRIA	Complement component 1 Q subcomponent-binding protein, mitochondrial precursor Glycoprotein gC1qBP C1qBP GC1q-R protein	30740	9506435	80872	SOLUBLE	cleavable signal peptide		O35796	
CORONIN 1B	SIGNALING	Coronin-1B Coronin-2	53850	9506507	95157	SOLUBLE			O89046	
CORTACTIN ISOFORM C	CYTOSKELETON	Cortactin isoform C	52630	2996044	57161	SOLUBLE			O70419	
CYSTATHIONINE BETA-SYNTHASE	METABOLISM	Cystathionine beta-synthase	61450	543960	41205	SOLUBLE			P32232	
CYSTEINE-RICH PROTEIN 2	UNKNOWN	Cysteine-rich protein 2 CRP2 Protein ESP1	22700	737713	46143	SOLUBLE			P36201	
CYSTEINE SULFINIC ACID DECARBOXYLASE	METABOLISM	Cysteine-sulfinic decarboxylase	55250	6685331	35923	SOLUBLE			Q546T1 Q64577 Q64611 Q9R1F6	
SIMILAR TO UMP-CMP KINASE	SIGNALING	Cytidylate kinase	25830	71043752	267331	SOLUBLE	cleavable signal peptide		Q4KM73 UPI00001CF786	
CYTOCHROME P450 17A1	DETOXIFICATION	Cytochrome P450 17A1 CYPXVII P450-C17 P450c17 Steroid 17-alpha-hydroxylase/17,20 lyase	57250	940818	3722	MEMBRANE	cleavable signal peptide		P11715 Q68FY2 Q6LAE5	
DOPA/TYROSINE SULFOTRANSFERASE	DETOXIFICATION	DOPA/tyrosine sulfotransferase	34840	688032	74919	SOLUBLE			P52847	
B-FACTOR, PROPERDIN, ALTERNATIVE-COMPLEMENT PROTEIN 1	BIOSYNTHETIC CARGO	Da1-24	124000	33086684	287107	SOLUBLE	cleavable signal peptide		Q7TP05	
DAMAGE-SPECIFIC DNA BINDING PROTEIN 1	NUCLEUS	Damage-specific DNA binding protein 1	126900	9843869	111030	SOLUBLE			Q9ESW0	
DEHYDROGENASE/REDUCTASE SDR FAMILY MEMBER 1	UNKNOWN	Dehydrogenase/reductase (SDR family) member 1	34020	56090381	240184	SOLUBLE			Q6AXY8	XP_214194.2
DESTRIN	CYTOSKELETON	Destrin Actin-depolymerizing factor ADF	18390	7441446	123978	SOLUBLE			Q7M0E3	
DIHYDROFOLATE REDUCTASE	METABOLISM	Dihydrofolate reductase	21640	81871579	53424	SOLUBLE				
PTERIN-4-ALPHA-CARBINOLAMINE DEHYDRATASE	METABOLISM	Dimerization Cofactor Of Hepatocyte Nuclei	11960	10835705	108686	SOLUBLE			UPI000011156C	
DIPEPTIDYLPEPTIDASE 4	PLASMA MB	Dipeptidyl peptidase IV	88000	6978773	3741	MEMBRANE	signal anchor	7 23 IN-OUT	P14740 UPI0000129841	
PRESYNAPTIC PROTEIN SAP97	BIOSYNTHETIC CARGO	Disks large homolog 1 Synapse-associated protein 97 SAP-97	100600	6978763	3737	SOLUBLE			Q62696	
DYNEIN HEAVY CHAIN, CYTOSOLIC	CYTOSKELETON	Dynein heavy chain, cytosolic	532000	294543	95169	SOLUBLE			P38650	
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	SOLUBLE			Q78P75	
EH-DOMAIN-CONTAINING PROTEIN 1 (MPAST1)	UNKNOWN	EH-domain containing 1	60600	58865448	2280	SOLUBLE			Q641Z6	

EH-DOMAIN CONTAINING PROTEIN 3	UNKNOWN	EH-domain containing protein 2	60790	34536836	244145	SOLUBLE			Q8R491	
ECTO-NUCLEOTIDE PYROPHOSPHATASE/PHOSPHODIESTERASE 1	PLASMA MB	Ectonucleotide pyrophosphatase/phosphodiesterase 1	102900	23396766	60453	MEMBRANE	57 23 IN-OUT		Q91XQ3 Q920C8 Q924C3	
		1 Plasma-cell membrane glycoprotein PC-1 Alkaline phosphodiesterase 1 Nucleotide pyrophosphatase NPPase								
EPIDERMAL GROWTH FACTOR RECEPTOR	PLASMA MB	Epidermal growth factor receptor	134900	6478868	85744	MEMBRANE	647 23 OUT-IN 774 23 IN-OUT	cleavable signal peptide	Q9QX70	
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	MEMBRANE	713 23 OUT-IN	cleavable signal peptide	O35794 Q9JIV9 Q9ROT4	
EPOXIDE HYDROLASE	DETOXIFICATION	Epoxide hydrolase 1 Microsomal epoxide hydrolase Epoxide hydratase	52580	77539448	17081	MEMBRANE		cleavable signal peptide	P07687	
EPSIN 1	COAT	Epsin 1	60160	41016934	105332	SOLUBLE			O88339	
ESTROGEN SULFOTRANSFERASE, ISOFORM 2	PROT MOD	Estrogen sulfotransferase, isoform 2 EST-2 Sulfotransferase, estrogen-preferring Estrone sulfotransferase	35360	1711600	109267	SOLUBLE			P52845	
ESTROGEN SULFOTRANSFERASE, ISOFORM 6	METABOLISM	Estrogen sulfotransferase, isoform 6 EST-6 Sulfotransferase, estrogen-preferring Estrone sulfotransferase	35300	913357	62242	SOLUBLE			P49890	
ESTROGEN RECEPTOR-RELATED RECEPTOR GAMMA-1	TRANSCRIPTION	Estrogen-related receptor gamma Estrogen receptor-related protein 3	51310	50400205	17534	SOLUBLE			P62510 Q5QJE4 Q75T51 Q75T52	
TRANSLATION INITIATION FACTOR EIF-4A	PROT SYN/FOLD	Eukaryotic translation initiation factor 4A1 16 days embryo kidney cDNA, RIKEN full-length enriched library, clone:I920165O08 product:eukaryotic translation initiation factor 4A1, full insert sequence 17 days embryo kidney cDNA, RIKEN full-length enriched library, clone:I920077H15 product:eukaryotic translation initiation factor 4A1, full insert sequence 16 days embryo heart cDNA, RIKEN full-length enriched library, clone:I920075M13 product:eukaryotic translation initiation factor 4A1, full insert sequence 17 days embryo heart cDNA, RIKEN full-length enriched library, clone:I920075G18 product:eukaryotic translation initiation factor 4A1, full insert sequence 17 days embryo kidney cDNA, RIKEN full-length enriched library, clone:I920054E16 product:eukaryotic translation initiation factor 4A1, full insert sequence CDNA, RIKEN full-length enriched library, clone:I730045F20 product:eukaryotic translation initiation factor 4A1, full insert sequence Blastocyst blastocyst cDNA, RIKEN full-length enriched library, clone:I730045F20	46150	40786436	55871	SOLUBLE			Q6P3V8	
SIMILAR TO WBSCR1	UNKNOWN	Eukaryotic translation initiation factor 4H	27320	55741853	295040	SOLUBLE			Q5X172	XP_213755.2 XP_347155.1
EXOCYST COMPLEX COMPONENT SEC5	TRAFFIC	Exocyst complex component 2 Exocyst complex component Sec5 rSec5	104000	7513971	161256	SOLUBLE			O54921	
CAPPING PROTEIN (ACTIN FILAMENT) MUSCLE Z-LINE; BETA	CYTOSKELETON	F-actin capping protein beta subunit	30630	54400732	83668	SOLUBLE			Q5X132	XP_216562.2
SIMILAR TO GALACTOKINASE 1	METABOLISM	Galactokinase 1 Predicted	42380	56605662	206276	SOLUBLE			Q5RKH2	XP_213528.2

GALECTIN-9	PLASMA MB	Galectin-9	36320	1916610	18989	MEMBRANE			P97840 P97840-2	
GAMMA-BUTYROBETAINE,2-OXOGLUTARATE DIOXYGEN	METABOLISM	Gamma-butyrobetaine dioxygenase Gamma-butyrobetaine,2-oxoglutarate dioxygenase Gamma-butyrobetaine hydroxylase Gamma-BBH	44550	5825482	139030	SOLUBLE			Q9QZU7	
GLUCOSE-6-PHOSPHATE ISOMERASE	METABOLISM	Glucose phosphate isomerase	62830	46485440	295907	SOLUBLE			Q6P6V0	XP_214908.2
GLUTATHIONE TRANSFERASE (EC 2.5.1.18) PSI	DETOXIFICATION	Glutathione transferase (EC 2.5.1.18) psi	3544	92300	84221	SOLUBLE			Q7M0B7	
GLUTATHIONE TRANSFERASE OMEGA 1	DETOXIFICATION	Glutathione transferase omega 1	27670	12585231	55147	SOLUBLE			Q9Z339	
GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE, MITOCH	MITOCHONDRIA	Glycerol-3-phosphate acyltransferase, mitochondrial precursor GPAT	93710	8393466	51468	SOLUBLE			O35349 P97564 P97565 P97566	
GLYCINE N-METHYLTRANSFERASE	PROT MOD	Glycine N-methyltransferase	32420	6137382	19169	SOLUBLE			P13255	
GROWTH FACTOR RECEPTOR-BOUND PROTEIN 2	SIGNALING	Growth factor receptor bound protein 2	25210	77539774	29315	SOLUBLE			P62994 Q5BKA7	
GUANIDINOACETATE N-METHYLTRANSFERASE	METABOLISM	Guanidinoacetate N-Methyltransferase	22590	30750124	196203	SOLUBLE			UPI0000190F9E	
GUANINE DEAMINASE	METABOLISM	Guanine deaminase Guanase Guanine aminase Guanine aminohydrolase GAH	51020	9910706	42862	SOLUBLE	cleavable signal peptide		Q9WTT6	
GUANINE NUCLEOTIDE-BINDING PROTEIN G(I), ALPHA-2	SIGNALING	Guanine nucleotide binding protein alpha inhibiting 2	40500	71089913	37194	SOLUBLE			Q45QN0	
GUANINE NUCLEOTIDE-BINDING PROTEIN, ALPHA-11 SU	SIGNALING	Guanine nucleotide-binding protein alpha-11 subunit	42030	8925964	37192	SOLUBLE			Q9JID2	
HISTIDINE AMMONIA-LYASE	METABOLISM	Histidine ammonia lyase	72280	8393522	51482	SOLUBLE			P21213 Q5EBB8	
HISTIDINE TRIAD NUCLEOTIDE-BINDING PROTEIN 1	NUCLEUS	Histidine triad nucleotide binding protein	13780	34870743	82484	SOLUBLE				
SMOOTH MUSCLE-SPECIFIC 17BETA-HYDROXYSTEROID	DETOXIFICATION	Hsd17b12 protein	34840	38494210	337296	MEMBRANE	cleavable signal peptide	7 18 IN-OUT	Q6P7R8	
HYPOXANTHINE-GUANINE PHOSPHORIBOSYLTRANSFER	METABOLISM	Hypoxanthine-guanine phosphoribosyltransferase HGPRT HGPRtase	24480	68534712	16980	SOLUBLE			P27605 P70469 Q4KMC5 Q62926	
IMPORTIN BETA-1 SUBUNIT	NUCLEUS	Importin beta-1 subunit Karyopherin beta-1 subunit Nuclear factor P97	97120	8393610	51498	SOLUBLE			P52296	
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	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	P29995 Q99P56	
INSULIN RECEPTOR	PLASMA MB	Insulin receptor precursor IR Insulin receptor subunit alpha Insulin receptor subunit beta	156800	8393621	51500	MEMBRANE	cleavable signal peptide	958 23 OUT-IN	P15127 P97681	
INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN COM	BIOSYNTHETIC CARGO	Insulin-like growth factor-binding protein complex acid labile chain precursor ALS	66810	71896592	11211	SOLUBLE	cleavable signal peptide		P35859	
INTEGRIN BETA-1	PLASMA MB	Integrin beta-1 precursor Fibronectin receptor subunit beta Integrin VLA-4 subunit beta CD29 antigen	88490	8393636	51502	MEMBRANE	cleavable signal peptide	730 23 OUT-IN	P49134	
IRON-RESPONSIVE ELEMENT BINDING PROTEIN 1 (IRE-B	PROT SYN/FOLD	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	SOLUBLE			Q63270	
ISCHEMIA RESPONSIVE 94 KDA PROTEIN	PROT SYN/FOLD	Ischemia responsive 94 kDa protein	94060	3360521	95874	SOLUBLE			O88600	
KALLISTATIN	BIOSYNTHETIC CARGO	Kallistatin	48020	21490001	38912	SOLUBLE	cleavable signal peptide		P97569	NP_659565.1
DIACETYL/L-XYLULOSE REDUCTASE	METABOLISM	L-xylulose reductase XR Dicarboxyl/L-xylulose reductase	25720	50400214	161241	SOLUBLE	cleavable signal peptide		Q920P0	
LIM AND SH3 DOMAIN PROTEIN 1	CYTOSKELETON	LIM and SH3 domain protein 1 LASP-1	29970	71122452	19687	SOLUBLE			Q499R9 Q99MZ8	

LIN-7 HOMOLOG C	SIGNALING	LIN-7 homolog C LIN-7C mLIn7C Mammalian LIN-seven protein 3 MALS-3 Vertebrate LIN 7 homolog 3 Veli-3 protein	21830	59798059	29682	SOLUBLE			Q79210	
PHOSPHOGLYCERATE MUTASE	METABOLISM	LOC495903 protein	28830	41350889	11293	SOLUBLE			Q6P0K6	
14-3-3 PROTEIN GAMMA	SIGNALING	LOC495922 protein	28300	9507245	47332	SOLUBLE				
SIMILAR TO SERINE HYDROXYMETHYL TRANSFERASE 1	MITOCHONDRIA	LRRGT00032	75370	62656183	216194	SOLUBLE			Q6TXG7	
LACTOYLGLUTATHIONE LYASE	PEROXISOME	Lactoylglutathione lyase Methyglyoxalase Aldoketomutase Glyoxalase I Gix I Ketone-aldehyde mutase S-D-lactoylglutathione methylglyoxal lyase	20820	81885359	251837	SOLUBLE				XP_215365.1
PUTATIVE TRANSCRIPTION FACTOR LUZP	UNKNOWN	Leucine zipper protein 1 Leucine zipper motif-containing protein	117200	9931329	42949	SOLUBLE			Q9ESV1	
LEUKOCYTE COMMON ANTIGEN VARIANT 4 PRECURSOR	SIGNALING	Leukocyte common antigen variant 4 precursor	132600	56560	111680	MEMBRANE		446 22 OUT-IN 709 23 IN-OUT	P04157 4	
LIPID PHOSPHATE PHOSPHOHYDROLASE 3	PROT MOD	Lipid phosphate phosphohydrolase 3 Phosphatidic acid phosphatase 2b Phosphatidate phosphohydrolase type 2b PAP2b PAP-2b PAP2-beta Differentially expressed in rat intestine 42 Dri42	35320	45477000	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	
PLASMA GLUTAMATE CARBOXYPEPTIDASE	BIOSYNTHETIC CARGO	Liver annexin-like protein	52010	7108713	62757	SOLUBLE	cleavable signal peptide		Q9JLV0	
LONG-CHAIN-FATTY-ACID--COA LIGASE 4	METABOLISM	Long-chain-fatty-acid--CoA ligase 4 Long-chain acyl-CoA synthetase 4 LACS 4	74330	6016483	22152	SOLUBLE			Q35547	
MHC CLASS II TRANSACTIVATOR TYPE I	TRANSCRIPTION	MHC class II transactivator type I	127300	9931450	42953	SOLUBLE	cleavable signal peptide		Q9GJE0	
CYTOSOLIC MALATE DEHYDROGENASE	METABOLISM	Malate dehydrogenase, cytoplasmic Cytosolic malate dehydrogenase	36480	81861572	118982	SOLUBLE				
MALEYLACETOACETATE ISOMERASE	DETOXIFICATION	Maleylacetoacetate isomerase MAAI Glutathione S-transferase zeta 1 GSTZ1-1	2943	11133293	36062	SOLUBLE			P57113	
MANNOSE 6-PHOSPHATE/INSULIN-LIKE GROWTH FACTOR RECEPTOR	PLASMA MB	Mannose 6-phosphate/insulin-like growth factor II receptor	273400	6981078	3946	MEMBRANE	cleavable signal peptide	2291 23 OUT-IN	Q63002 Q63757	
PROGESTERONE RECEPTOR MEMBRANE COMPONENT	DETOXIFICATION	Membrane-associated progesterone receptor component 2	23400	62900631	274611	MEMBRANE		40 23 OUT-IN	Q5XIU9	XP_342240.1
MERLIN	UNKNOWN	Merlin Moesin-ezrin-radixin-like protein Neurofibromin-2 Schwannomin	68710	32363191	124359	SOLUBLE			Q63648	
MITOCHONDRIAL CARNITINE/ACYLCARNITINE CARRIER	MITOCHONDRIA	Mitochondrial carnitine/acylcarnitine carrier protein Carnitine/acylcarnitine translocase CAC Solute carrier family 25 member 20	33150	2497984	63382	MEMBRANE	signal anchor	13 19 IN-OUT 74 23 OUT-IN 108 23 IN-OUT	P97521	NP_446417.1
MITOCHONDRIAL CARRIER HOMOLOG 2	MITOCHONDRIA	Mitochondrial carrier homolog 2	31460	27702070	156740	MEMBRANE				
MONOCARBOXYLATE TRANSPORTER 1	PLASMA MB	Monocarboxylate transporter 1 MCT 1	53240	6981542	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	

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	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	
MYOSIN IB	CYTOSKELETON	Myosin Ib Myosin I alpha MMI-alpha MMla Myosin heavy chain myr 1	131900	56733	63042	SOLUBLE			Q05096	
MYOSIN HEAVY CHAIN, NONMUSCLE TYPE B	CYTOSKELETON	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	SOLUBLE			Q9JLT0	
N-ETHYLMALIMIDE SENSITIVE FACTOR	TETH/DOCK/FUS	N-ethylmaleimide sensitive factor	82650	6007811	9479	SOLUBLE			Q9QUL6	
NADP-DEPENDENT LEUKOTRIENE B4 12-HYDROXYDEHYDROGENASE	DETOXIFICATION	NADP-dependent leukotriene B4 12-hydroxydehydrogenase 15-oxoprostaglandin 13-reductase Dithiolethione-inducible gene 1 protein D3T-inducible gene 1 protein DIG-1	35720	6012071	1678	SOLUBLE			P97584 Q5EBD3	
ADP-RIBOSYLATION FACTOR 3	GTPASE	NOD-derived CD11c +ve dendritic cells cDNA, RIKEN full-length enriched library, clone:F630112117 product:ADP-ribosylation factor 3, full insert sequence	20600	57033190	20922	MEMBRANE				
NA(+)/H(+) EXCHANGE REGULATORY CO-FACTOR NHE-RF	CYTOSKELETON	Na(+)/H(+) exchange regulatory co-factor NHE-RF2	34910	13925523	78016	SOLUBLE			Q920G2	
NCK-ASSOCIATED PROTEIN 1	UNKNOWN	Nck-associated protein 1 NAP 1 p125Nap1 Membrane-associated protein HEM-2	128900	1708980	67879	SOLUBLE			P55161	
NEURAL-CADHERIN	PLASMA MB	Neural-cadherin precursor N-cadherin Cadherin-2	99690	3983131	63008	MEMBRANE	cleavable signal peptide	724 23 OUT-IN	Q9ROT5 Q9Z1Y3	
NEURONAL MYOSIN HEAVY CHAIN	CYTOSKELETON	Neuronal myosin heavy chain	231500	111999	11249	SOLUBLE			Q63731	
NON-MUSCLE CALDESMON	CYTOSKELETON	Non-muscle caldesmon CDM L-caldesmon	60580	6978589	3674	SOLUBLE			Q62736	
NUCLEOBINDIN 1 (CALNUC 1)	CALCIUM TRANS/BIND	Nucleobindin-1 precursor CALNUC Bone 63 kDa calcium-binding protein	53510	871525	60416	SOLUBLE	cleavable signal peptide		P97623 Q497A4 Q63083	
SIMILAR TO PEF PROTEIN WITH A LONG N-TERMINAL HY	UNKNOWN	PEF protein with a long N-terminal hydrophobic domain	30010	56090329	201603	SOLUBLE			Q641Z8	XP_238392.2
T-CELL, IMMUNE REGULATOR 1, ATPASE, H+ TRANSPORTING, LYSOSOMAL V0 PROTEIN A ISOFORM 3	LYSOSOME	PREDICTED: T-cell, immune regulator 1, ATPase, H+ transporting, lysosomal V0 protein a isoform 3	93210	62641689	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	
VACUOLAR SORTING PROTEIN 35	TRAFFIC	PREDICTED: maternal embryonic message 3	91730	34851395	206594	SOLUBLE			UPI00001D13DB	
H5	GTPASE	PREDICTED: peanut-like 2 (Drosophila) (predicted)	53080	62656738	223925	SOLUBLE			UPI00001D04F2	
SIMILAR TO 6-PHOSPHOGLUCONOLACTONASE	METABOLISM	PREDICTED: similar to 6-phosphogluconolactonase	30820	34877556	315711	SOLUBLE			UPI00001D0F55	
ATPASE, H+ TRANSPORTING, V1 SUBUNIT A, ISOFORM 1	LYSOSOME	PREDICTED: similar to ATPase, H+ transporting, V1 subunit A, isoform 1	68270	34869154	264901	SOLUBLE			UPI00001D0792	
ALDOSE REDUCTASE	METABOLISM	PREDICTED: similar to Aldose reductase (AR) (Aldehyde reductase)	35900	62648070	161456	SOLUBLE			UPI000017F39F	
SIMILAR TO BILIVERDIN REDUCTASE B (FLAVIN REDUCTASE)	DETOXIFICATION	PREDICTED: similar to Blvrb protein	22090	34855391	272510	SOLUBLE	cleavable signal peptide		UPI00001CE7A7	
SIMILAR TO MO25 PROTEIN	UNKNOWN	PREDICTED: similar to Cab39 protein	39870	34877516	314871	SOLUBLE			UPI0000183016	

COACTOSIN-LIKE 1	CYTOSKELETON	PREDICTED: similar to Chain A, Solution Structure Of Coactosin-Like Protein (Cofilin Family) From Mus Musculus	22140	34851815	211193	SOLUBLE	signal anchor		UPI00001D14D3	
DKFZP586A0522 PROTEIN	UNKNOWN	PREDICTED: similar to DKFZP586A0522 protein	21900	27664990	263674	SOLUBLE	cleavable signal peptide	10 23 OUT-IN	UPI00001CA1B5	
SIMILAR TO ER-RESIDENT PROTEIN ERDJ5	PROT SYN/FOLD	PREDICTED: similar to ER-resident protein ERdj5	90750	34856469	269276	MEMBRANE	signal anchor	21 23 IN-OUT	UPI00001CF190	
SIMILAR TO EPIDERMAL GROWTH FACTOR RECEPTOR	SIGNALING	PREDICTED: similar to Epidermal growth factor receptor pathway substrate 8-like protein 2	82280	34861230	276611	SOLUBLE			UPI00001CEB27	
SIMILAR TO FK506-BINDING PROTEIN 38	SIGNALING	PREDICTED: similar to FK506-binding protein 38	43560	81295379	221624	MEMBRANE		381 20 OUT-IN	Q3B7U9 UPI00001D0F5D	
SIMILAR TO PHENYLALANINE-TRNA SYNTHETASE-LIKE	PROT SYN/FOLD	PREDICTED: similar to Farslia protein	57720	66730413	312741	SOLUBLE			Q505J8 UPI000018073F	
SIMILAR TO NADH DEHYDROGENASE (UBIQUINONE) FE-	MITOCHONDRIA	PREDICTED: similar to NADH dehydrogenase (ubiquinone) Fe-S protein 5	12700	72086149	306807	SOLUBLE			UPI000018157F	
PLASTIN 1 (I ISOFORM)	CYTOSKELETON	PREDICTED: similar to PLS1 protein	70390	34865784	207221	SOLUBLE			UPI00001D0083	
SIMILAR TO RIKEN CDNA 1810074P20	UNKNOWN	PREDICTED: similar to RIKEN cDNA 1810074P20	89590	34867100	217843	SOLUBLE			UPI00001CF65A	
PROTEIN KIAA0103 HOMOLOG	UNKNOWN	PREDICTED: similar to RIKEN cDNA 4921631G14	34870	34866113	263127	SOLUBLE			UPI00001CFD06	
SIMILAR TO RIKEN CDNA 9430083G14	UNKNOWN	PREDICTED: similar to RIKEN cDNA 9430083G14	29550	34881196	218419	MEMBRANE	cleavable signal peptide	138 23 IN-OUT	UPI00001D17A5	
RAB33B	GTPASE	PREDICTED: similar to Rab33B	25750	34857303	281147	MEMBRANE			UPI000017EEFD	
R-RAS (P23)	GTPASE	PREDICTED: similar to Ras-related protein R-Ras (P23)	23910	34856057	257746	MEMBRANE			UPI0000181911	
RAB43	GTPASE	PREDICTED: similar to Ras-related protein Rab	23230	81887426	161420	SOLUBLE			Q53B90 UPI00001C8CE8	
SIMILAR TO SMHS2 HOMOLOG	UNKNOWN	PREDICTED: similar to Smhs2 homolog	49210	34874232	269978	SOLUBLE	cleavable signal peptide		UPI000019BC70	
SIMILAR TO GLYCERALDEHYDE-3-PHOSPHATE DEHYDR	METABOLISM	PREDICTED: similar to glyceraldehyde-3-phosphate dehydrogenase	35260	34875521	264061	SOLUBLE			UPI00001D0E0B	
SIMILAR TO GLYCERALDEHYDE-3-PHOSPHATE DEHYDR	METABOLISM	PREDICTED: similar to glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) (EC 1.2.1.12) - mouse	34590	34869386	306407	SOLUBLE			UPI00001D076A	
CCTTHETA, THETA SUBUNIT OF THE CHAPERONIN CON	PROT SYN/FOLD	PREDICTED: similar to mKIAA0002 protein	59590	34867525	249893	SOLUBLE			UPI00001D06BF	
MAGNESIUM DEPENDENT PHOSPHATASE -1	SIGNALING	PREDICTED: similar to magnesium-dependent phosphatase-1	18610	27700106	272326	SOLUBLE			UPI00001810E3	
SIMILAR TO MICROSOMAL GLUTATHIONE S-TRANSFER	DETOXIFICATION	PREDICTED: similar to microsomal glutathione S-transferase 3	16730	27678076	164232	MEMBRANE	cleavable signal peptide	10 18 OUT-IN 64 18 IN-OUT 85 20 OUT-IN 117 23 IN-OUT	UPI0000181D94	
SIMILAR TO NOVEL CELL DEATH-REGULATORY PROTEIN	NUCLEUS	PREDICTED: similar to novel cell death-regulatory protein GRIM19	16780	27668839	160674	MEMBRANE	signal anchor	29 23 IN-OUT	UPI00001CC6CB	
SIMILAR TO PROTEIN PHOSPHATASE 2C EPSILON	SIGNALING	PREDICTED: similar to protein phosphatase 1 (former 2C)-like	41040	34857062	230767	MEMBRANE	signal anchor		UPI000017E6E6	
INORGANIC DIPHOSPHATASE	SIGNALING	PREDICTED: similar to pyrophosphatase	32770	34852506	276601	SOLUBLE			UPI00001D15CC	
PERIPHERAL PLASMA MEMBRANE PROTEIN CASK	SIGNALING	Peripheral plasma membrane protein CASK Calcium/calmodulin-dependent serine protein kinase	103300	2497510	104145	SOLUBLE			Q62915	
PEROXIREDOXIN 2	PEROXISOME	Peroxisoredoxin 2 (EC 1.11.1.-) (Thioredoxin peroxidase (Thioredoxin- dependent peroxide reductase 1) (Thiol-specific antioxidant protein) (TSA).	21800	34849738	269931	SOLUBLE			UPI000019B77D	

PEROXISOMAL ASSEMBLY PROTEIN PEX3	PEROXISOME	Peroxisomal biogenesis factor 3 Peroxin-3 Peroxisomal assembly protein PEX3	42210	8926847	12072	SOLUBLE	signal anchor		Q9JJK4	
CALM	COAT	Phosphatidylinositol-binding clathrin assembly protein Clathrin assembly lymphoid myeloid leukemia protein rCALM	69290	44888251	60461	SOLUBLE			O55011 O55012	
PHOSPHOENOLPYRUVATE CARBOXYKINASE, CYTOSOL	METABOLISM	Phosphoenolpyruvate carboxykinase, cytosolic [GTP] Phosphoenolpyruvate carboxylase PEPCK-C	69420	51859488	144363	SOLUBLE			P07379	
PHOSPHOGLYCERATE KINASE, TESTIS SPECIFIC	METABOLISM	Phosphoglycerate kinase 1	44540	56585024	340218	SOLUBLE			Q5M945	
PHOSPHOSERINE AMINOTRANSFERASE	METABOLISM	Phosphoserine aminotransferase	40590	29692074	249141	SOLUBLE			Q80YG1	
PIRIN	NUCLEUS	Pirin	32180	57164095	304888	SOLUBLE			Q5M827	XP_343785.1
PLAKOGLOBIN	CYTOSKELETON	Plakoglobin	81780	1497985	37204	SOLUBLE			P70565	
T-PLASTIN	CYTOSKELETON	Plastin-3 T-plastin	70300	57381	136274	SOLUBLE			Q63598	
POLYMERIC-IMMUNOGLOBULIN RECEPTOR	PLASMA MB	Polymeric-immunoglobulin receptor precursor Poly-Ig receptor PIgR Secretory component	84800	56465	128586	MEMBRANE	cleavable signal peptide	644 23 OUT-IN	P15083	
MAWDBP	UNKNOWN	Probable isomerase MAWBP	31720	19743770	33171	SOLUBLE				NP_612539.1
HSP90 CO-CHAPERONE,P23	NUCLEUS	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	SOLUBLE				
PROSTAGLANDIN F2 RECEPTOR NEGATIVE REGULATOR	SIGNALING	Prostaglandin F2 receptor negative regulator precursor Prostaglandin F2-alpha receptor regulatory protein Prostaglandin F2-alpha receptor-associated protein CD315 antigen	98730	9507007	47252	MEMBRANE	cleavable signal peptide	831 23 OUT-IN	Q62786	
PROTEASOME ACTIVATOR 28-ALPHA SUBUNIT	PROTEASOME/UBIQUITIN	Protease (Prosome, macropain) 28 subunit, alpha	28630	61098214	227267	SOLUBLE			Q6P9V7	
PROTEASOME (PROSOME, MACROPAIN) SUBUNIT, BETA	PROTEASOME/UBIQUITIN	Proteasome (Prosome, macropain) subunit, beta type 1	26410	37231712	233720	SOLUBLE			Q6PDW4	
26S PROTEASOME NON-ATPASE REGULATORY SUBUNIT	PROTEASOME/UBIQUITIN	Proteasome 26S non-ATPase subunit 12	52940	54400716	317815	SOLUBLE			Q5XIC6	XP_213502.2
PROTEASOME ACTIVATOR COMPLEX SUBUNIT 2	PROTEASOME/UBIQUITIN	Proteasome activator subunit 2	26860	8394091	51596	SOLUBLE			Q4QR96	
PROTEASOME SUBUNIT ALPHA TYPE 6	PROTEASOME/UBIQUITIN	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	SOLUBLE			P60901	
PROTEASOME SUBUNIT ALPHA TYPE 7	PROTEASOME/UBIQUITIN	Proteasome subunit alpha type 7 Proteasome subunit RC6-1	28330	2118151	72897	SOLUBLE			P48004	
PROTEASOME SUBUNIT BETA TYPE 3	PROTEASOME/UBIQUITIN	Proteasome subunit beta type 3 Proteasome theta chain Proteasome chain 13 Proteasome component C10-II	22960	8394082	51593	SOLUBLE			P40112	
PROTEASOME SUBUNIT BETA TYPE 6	PROTEASOME/UBIQUITIN	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	SOLUBLE				
DJ-1 PROTEIN	UNKNOWN	Protein DJ-1 Contraception-associated protein 1 Protein CAP1 Fertility protein SP22	19970	56404680	20683	SOLUBLE			Q88767	
NDRG1 RELATED PROTEIN NDRG2B1	SIGNALING	Protein NDRG2 NDRG1-related protein Antidepressant-related protein ADRG123	40780	81867103	123716	SOLUBLE			Q8VBU2 Q8VBW2 Q8V100 Q8V101	
PROTEIN KINASE C AND CASEIN KINASE SUBSTRATE IN	SIGNALING	Protein kinase C and casein kinase substrate in neuron 2 protein Synaptic dynamin-associated protein II Syndapin 2 Syndapin-II Sdpl	55980	6651163	74255	SOLUBLE			Q9QY17 Q9QY18 Q9QY19 Q9QY20	
PROTEIN TRANSPORT PROTEIN SEC23A	COAT	Protein transport protein Sec23A SEC23-related protein A	86160	34867969	141679	SOLUBLE				
PROTO-ONCOGENE C-CRK	SIGNALING	Proto-oncogene C-crk P38 Adapter molecule crk	33840	9506515	95160	SOLUBLE			Q63768	

PUTATIVE N-ACETYLTTRANSFERASE CAMELLO 4	PROT MOD	Putative N-acetyltransferase Camello 4	24890	6651436	176270	MEMBRANE	signal anchor	33 23 IN-OUT 60 20 OUT-IN	Q9QXT3	
PUTATIVE SKAP55	SIGNALING	Putative SKAP55 Src family associated phosphoprotein 2	40720	47482120	15613	SOLUBLE			Q920G0	
INTEGRAL MEMBRANE TRANSPORT PROTEIN UST5R	UNKNOWN	Putative integral membrane transport protein	62420	19705489	161236	MEMBRANE		179 23 OUT-IN 229 23 IN-OUT 261 20 OUT-IN 355 20 IN-OUT 378 23 OUT-IN 407 20 IN-OUT 432 23 OUT-IN 466 23 IN-OUT 498 18 OUT-IN	Q8VDA8	
INTEGRAL MEMBRANE TRANSPORT PROTEIN UST4R	UNKNOWN	Putative integral membrane transport protein	62210	19705487	161235	MEMBRANE	signal anchor	15 23 OUT-IN 229 23 IN-OUT 261 20 OUT-IN 350 23 IN-OUT 382 23 OUT-IN 470 23 IN-OUT 496 20 OUT-IN	Q8VDA7	
PYRUVATE DEHYDROGENASE E1 COMPONENT BETA SUBUNIT	MITOCHONDRIA	Pyruvate dehydrogenase (Lipoamide) beta	38980	56090293	203734	SOLUBLE			Q6AY95	XP_214142.2
PYRUVATE KINASE, ISOZYMES R/L	METABOLISM	Pyruvate kinase, isozymes R/L	62300	206213	44273	SOLUBLE			P12928	
RAB4A	GTPASE	RAB4A, member RAS oncogene family	23920	6981454	75065	SOLUBLE			UPI0000167A58	
RAB GDI ALPHA	TRAFFIC	Rab GDP dissociation inhibitor alpha	50540	71534276	67742	SOLUBLE			P50398 Q499U0 Q9R274	
RAB-RELATED GTP-BINDING PROTEIN	GTPASE	Rab-related GTP-binding protein Rab38, member of RAS oncogene family	23780	47125439	44313	MEMBRANE			Q63483	
RAB14	GTPASE	Ras-related protein Rab-14	23930	46577632	34567	MEMBRANE				
RAB18	GTPASE	Ras-related protein Rab-18	22980	81909560	161691	MEMBRANE			Q5EB77	
RAB1B	GTPASE	Ras-related protein Rab-1B	22180	56605816	166705	MEMBRANE			P10536 Q5U4F1 XP_341991.1	
RAB30	GTPASE	Ras-related protein Rab-30	23060	27678162	64372	MEMBRANE				
RAB35	GTPASE	Ras-related protein Rab-35 Rab-1C GTP-binding protein RAY	23030	62900797	35585	SOLUBLE			Q5U316	
RAB4B	GTPASE	Ras-related protein Rab-4B	23630	929830	51602	MEMBRANE			P51146	
RAB8A	GTPASE	Ras-related protein Rab-8A Oncogene c-mel	23670	82592520	33705	SOLUBLE			P35280 Q3B8Q4 Q6DKL2	
RAB8B	GTPASE	Ras-related protein Rab-8B	23600	2500066	43492	MEMBRANE			P70550	
RAP1A	GTPASE	Ras-related protein Rap-1A	20990	54114993	4747	MEMBRANE			P10113 P62836 XP_215669.1	
RAP1B	GTPASE	Ras-related protein Rap-1b precursor GTP-binding protein smg p21B	20800	539995	130852	MEMBRANE			Q62636 Q6J167	
GIA NTIN	TETH/DOCK/FUS	Rat GCP360	364300	7441640	124005	MEMBRANE		3164 23 OUT-IN	Q63714	
R-RAS2	GTPASE	Related RAS viral (R-ras) oncogene homolog 2 Predicted	23400	61740635	86161	MEMBRANE			Q5BJU0	
RETINOL-BINDING PROTEIN I, CELLULAR	METABOLISM	Retinol-binding protein I, cellular Cellular retinol-binding protein CRBP	15700	809309	105581	SOLUBLE			P02696	

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	SOLUBLE			Q5X173	XP_340951.1
S-ADENOSYLMETHIONINE SYNTHETASE ALPHA AND BETA FORMS	PROT MOD	S-adenosylmethionine synthetase alpha and beta forms	43700	92483	69363	SOLUBLE			P13444 Q5FVU2	
GLYCOGEN PHOSPHORYLASE	METABOLISM	SWISS-PROT:P09811 REFSEQ_NP:NP_071604 ENSEMBL:ENSRNOP00000009183 Glycogen phosphorylase, liver form	97480	565688	104192	SOLUBLE				
4-HYDROXYPHENYLPYRUVATE DIOXYGENASE	METABOLISM	SWISS-PROT:P32755 TREMBL:Q88655 REFSEQ_NP:NP_058929 ENSEMBL:ENSRNOP00000001809 4-hydroxyphenylpyruvate dioxygenase	45110	8393557	51489	SOLUBLE				
ANNEXIN A2	TETH/DOCK/FUS	SWISS-PROT:Q07936-1 TREMBL:Q8R513 ENSEMBL:ENSRNOP00000013988 REFSEQ:NP_063970 annexin A2	38680	9845234	109734	SOLUBLE				
MYOSIN HEAVY CHAIN, NONMUSCLE TYPE A	CYTOSKELETON	SWISS-PROT:Q62812 TREMBL:Q62704 REFSEQ_NP:NP_037326 ENSEMBL:ENSRNOP00000007398 Myosin-9	226300	967249	75000	SOLUBLE				
RSLY1P	TRAFFIC	Sec1 family domain-containing protein 1 Syntaxin-binding protein 1-like 2 Vesicle transport-related protein Ra410 Sly1p	72260	9507019	47264	SOLUBLE			Q62843 Q62991	
SELENIUM-BINDING PROTEIN	UNKNOWN	Selenium binding protein 2	52530	49256633	111519	SOLUBLE			Q8VIF7	
SEPTIN 7	GTPASE	Septin-7 CDC10 protein homolog	50510	9789715	167832	MEMBRANE			Q9WVC0	
SERINE (OR CYSTEINE) PROTEINASE INHIBITOR, CLADE G	BIOSYNTHETIC CARGO	Serine (Or cysteine) proteinase inhibitor, clade G (C1 inhibitor), member 1, Angioedema, hereditary	55610	40018558	222317	SOLUBLE	cleavable signal peptide		Q6P734	
SERINE/THREONINE PROTEIN PHOSPHATASE 2A, CATALYTIC SUBUNIT	SIGNALING	Serine/threonine protein phosphatase	35580	8394021	41475	SOLUBLE			P62716 Q6LDK0	
SERINE/THREONINE PROTEIN PHOSPHATASE PP1-BETA	SIGNALING	Serine/threonine protein phosphatase PP1-beta catalytic subunit	37190	999343	4597	SOLUBLE			P37140	
SERINE PROTEASE INHIBITOR 6	BIOSYNTHETIC CARGO	Similar to SPI6	42300	56090431	224458	SOLUBLE			Q6AYF8	XP_341523.1
SIMILAR TO PHOSPHOLYSINE PHOSPHOHISTIDINE INORGANIC PYROPHOSPHATE PHOSPHATA 5M590	METABOLISM	Similar to phospholysine phosphohistidine inorganic pyrophosphate phosphata 5M590	29190	57528359	221017	SOLUBLE			Q5I0D5	

SODIUM/POTASSIUM-TRANSPORTING ATPASE ALPHA-1	PLASMA MB	Sodium/potassium-transporting ATPase alpha-1 chain precursor Sodium pump 1 Na+/K+ ATPase 1	113100	6978543	3651	MEMBRANE		95 23 IN-OUT 130 OUT-OUT 290 23 IN-OUT 322 23 OUT-OUT 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	
SODIUM/POTASSIUM-TRANSPORTING ATPASE BETA-1	PLASMA MB	Sodium/potassium-transporting ATPase beta-1 chain	35230	6978549	3654	MEMBRANE	signal anchor	35 23 IN-OUT	P07340 UPI0000167A69	
SODIUM/POTASSIUM-TRANSPORTING ATPASE BETA-3	PLASMA MB	Sodium/potassium-transporting ATPase subunit beta-3 Sodium/potassium-dependent ATPase beta-3 subunit ATPB-3 CD298 antigen	31830	6978553	3656	MEMBRANE	signal anchor	38 23 IN-OUT	Q63377	
SODIUM/BILE ACID COTRANSPORTER	PLASMA MB	Solute carrier family 10, member 1	39300	8394279	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	
ORGANIC ANION TRANSPORTER K8	PLASMA MB	Solute carrier family 21 member 4	62970	19071449	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	
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	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	
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 moatp1	74210	9622206	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	
SON PROTEIN	UNKNOWN	Son protein	12550	34849639	313065	SOLUBLE			Q6PDU3	
SPECTRIN ALPHA CHAIN, BRAIN	CYTOSKELETON	Spectrin alpha chain, brain	284600	62644670	3340	SOLUBLE			Q88663 P16086 P70477	
SPECTRIN BETA CHAIN, BRAIN 2	CYTOSKELETON	Spectrin beta chain, brain 2	271100	3550975	3158	SOLUBLE			Q88197 Q9ES68 Q9QWN8	
STABILIN-2	PLASMA MB	Stabilin-2 precursor Hyaluronan receptor for endocytosis 175 kDa stabilin-2 175 kDa hyaluronan receptor for endocytosis	155900	50401220	153825	MEMBRANE		1325 23 OUT-IN	Q8CFM6	

NONSPECIFIC LIPID-TRANSFER PROTEIN, MITOCHONDRIA	MITOCHONDRIA	Sterol carrier protein 2	58790	51980631	33159	SOLUBLE			Q642G0	NP_612517.1
N-HYDROXYARYLAMINE SULFOTRANSFERASE	PROT MOD	Sulfotransferase 1C1 N-hydroxyarylamine sulfotransferase HAST-1	35760	543420	78152	SOLUBLE			P50237 Q5M8B5	
T-COMPLEX PROTEIN 1, ALPHA SUBUNIT	PROT SYN/FOLD	T-complex protein 1 subunit alpha TCP-1-alpha CCT-alpha	60360	6981642	75118	SOLUBLE			P28480	
PDZ DOMAIN-CONTAINING PROTEIN (DIPHOR 1)	BIOSYNTHETIC CARGO	TREMBL:Q35234 Diphor-1	52250	2331224	80899	SOLUBLE				
PROTEASOME 26S ATPASE SUBUNIT 6	PROTEASOME/UBIQUITIN	TREMBL:Q32PW9 ENSEMBL:ENSRNOP00000009649 REFSEQ:XP_214147 PREDICTED: similar to Psmc6 protein	45800	34869622	309670	SOLUBLE				
3-MERCAPTOPYRUVATE SULFURTRANSFERASE	MITOCHONDRIA	Tax_Id=10116 3-mercaptopyruvate sulfurtransferase	32940	62652539	13392	SOLUBLE	cleavable signal peptide			
ADP-RIBOSYLATION FACTOR 5	GTPASE	Tax_Id=10116 ADP-ribosylation factor 5	20530	56388751	10610	MEMBRANE				
ATP-BINDING CASSETTE, SUB-FAMILY D, MEMBER 3	PEROXISOME	Tax_Id=10116 ATP-binding cassette, sub-family D (ALD), member 3	75320	6981450	75063	MEMBRANE	cleavable signal peptide	125 23 IN-OUT 225 23 OUT-IN 306 23 IN-OUT		
ALDEHYDE DEHYDROGENASE (NAD)	METABOLISM	Tax_Id=10116 Aldehyde dehydrogenase fAmily 1, subFamily A4	54560	91935	83139	SOLUBLE				
ALCOHOL DEHYDROGENASE [NADP+]	METABOLISM	Tax_Id=10116 Aldo-keto reductase fAmily 1, member A1	36510	399660	37172	SOLUBLE				
AMINE OXIDASE [FLAVIN-CONTAINING] B	MITOCHONDRIA	Tax_Id=10116 Amine oxidase (flAvin-containing)	58390	91974	74982	MEMBRANE		489 23 OUT-IN		
ANNEXIN A1 (ANNEXIN I) (LIPOCORTIN I) (CALPACTIN II)	TETH/DOCK/FUS	Tax_Id=10116 Annexin 1	38830	6978501	3631	SOLUBLE				
FATTY ACID-BINDING PROTEIN, BRAIN	PROT MOD	Tax_Id=10116 Brain lipid Binding protein	14860	476082	71698	SOLUBLE				
COPI COATOMER BETA' SUBUNIT	COAT	Tax_Id=10116 Coatomer protein Complex, subunit beta 2 (beta prime)	102600	3023522	35931	SOLUBLE				
COMPLEMENT COMPONENT 5	BIOSYNTHETIC CARGO	Tax_Id=10116 Complement Component 5	134400	34853897	205903	SOLUBLE	cleavable signal peptide			
CYSTEINE-RICH PROTEIN 1	UNKNOWN	Tax_Id=10116 Cysteine and glycine-rich protein 1	20610	8393206	51411	SOLUBLE				
DEAD BOX PROTEIN 1	PROT SYN/FOLD	Tax_Id=10116 DEAD (Asp-Glu-Ala-Asp) box polypeptide 1	97470	34863163	240056	SOLUBLE				
DIHYDROLIPOAMIDE BRANCHED CHAIN TRANSACYLASE	MITOCHONDRIA	Tax_Id=10116 Dihydrolipoamide branched chain transacylase E2	53460	34859889	232730	SOLUBLE				
NG,NG-DIMETHYLARGININE DIMETHYLAMINOHYDROLASE	METABOLISM	Tax_Id=10116 Dimethylarginine Dimethylaminohydrolase 1	31430	6831527	104206	SOLUBLE				
SIMILAR TO HOMOGENTISATE 1, 2-DIOXYGENASE	METABOLISM	Tax_Id=10116 Ensembl_locations(Chr-bp):11-64934053 similar to homogentisate 1, 2-dioxygenase	59620	34869194	303719	SOLUBLE				
SIMILAR TO LEUCINE AMINOPEPTIDASE	METABOLISM	Tax_Id=10116 Ensembl_locations(Chr-bp):14-70683054 similar to leucine aminopeptidase	64550	34878080	204743	SOLUBLE				
SIMILAR TO MITOGEN INDUCIBLE GENE MIG-2	UNKNOWN	Tax_Id=10116 Ensembl_locations(Chr-bp):15-21359488 similar to mitogen inducible gene mig-2	95210	34869626	211833	SOLUBLE				
ANNEXIN A11	TETH/DOCK/FUS	Tax_Id=10116 Ensembl_locations(Chr-bp):16-1479259 similar to annexin A11	72140	34876896	205775	SOLUBLE				
SIMILAR TO ALDO-KETO REDUCTASE FAMILY 1, MEMBER 1	DETOXIFICATION	Tax_Id=10116 Ensembl_locations(Chr-bp):17-77022236 similar to aldo-keto reductase family 1, member C12	32180	34876320	221880	SOLUBLE				
FK506-BINDING PROTEIN 1A	PROT SYN/FOLD	Tax_Id=10116 Ensembl_locations(Chr-bp):3-141766859 FK506 binding protein 2	11920	501064	43461	SOLUBLE				
SIMILAR TO DYSTROBREVIN B	CYTOSKELETON	Tax_Id=10116 Ensembl_locations(Chr-bp):6-26565039 similar to dystrobrevin B (mD.TN-B)	82140	34863056	279256	SOLUBLE				
PROTEASOME SUBUNIT ALPHA TYPE 3	PROTEASOME/UBIQUITIN	Tax_Id=10116 Ensembl_locations(Chr-bp):6-93096989;10-64690010 proteasome (prosome, macropain) subunit, alpha type 3	28420	8394066	45012	SOLUBLE				
SIMILAR TO RIKEN CDNA 4931406C07	UNKNOWN	Tax_Id=10116 Ensembl_locations(Chr-bp):8-12086308 similar to RIKEN cDNA 4931406C07	19160	34860352	266321	SOLUBLE				

NUCLEAR CHLORIDE ION CHANNEL PROTEIN	NUCLEUS	Tax_Id=101116 Ensembl_locations(Chr-bp):None similar to GLCP	25370	34852289	287945	SOLUBLE				
SIMILAR TO INTERFERON-G INDUCED GTPASE	GTPASE	Tax_Id=101116 Ensembl_locations(Chr-bp):None similar to LRG-47	44620	27670133	160756	MEMBRANE				
BETAINE-HOMOCYSTEINE METHYLTRANSFERASE 2	MITOCHONDRIA	Tax_Id=101116 Ensembl_locations(Chr-bp):None similar to betaine-homocysteine methyltransferase 2	46420	34861318	247159	SOLUBLE				
ELONGATION FACTOR 2	PROT SYN/FOLD	Tax_Id=101116 Eukaryotic translation Elongation factor 2	95280	8393296	51432	SOLUBLE				
EZRIN-RADIXIN-MOESIN BINDING PHOSPHOPROTEIN 50	CYTOSKELETON	Tax_Id=101116 Ezrin-radixin-moesin binding phosphoprotein 50	38830	8132349	644	SOLUBLE				
FRUCTOSE-1,6-BISPHOSPHATASE	METABOLISM	Tax_Id=101116 Fructose-1,6- biphosphatase 1	39610	623562	149105	SOLUBLE				
GLUTATHIONE S-TRANSFERASE 5	DETOXIFICATION	Tax_Id=101116 Glutathione S-transferase theta 1	27470	56265	111659	SOLUBLE				
GLUTATHIONE S-TRANSFERASE P	DETOXIFICATION	Tax_Id=101116 Glutathione S-transferase, pi	23440	56336	28297	SOLUBLE				
GLUTATHIONE S-TRANSFERASE YRS-YRS (GST 12-12) (G	DETOXIFICATION	Tax_Id=101116 Glutathione S-transferase, theta 2	27440	769703	3914	SOLUBLE				
GUANINE NUCLEOTIDE-BINDING PROTEIN G(K), ALPHA S	SIGNALING	Tax_Id=101116 Guanine nucleotide binding protein, alpha inhibiting 3	40520	71899	3901	SOLUBLE				
NADH-UBIQUINONE OXIDOREDUCTASE 13 KDA-B SUBUNIT	MITOCHONDRIA	Tax_Id=101116 NADH dehydrogenase (ubiquinone) 1 alpha subcomplex 5	13410	6981260	75004	SOLUBLE				
PDZ AND LIM DOMAIN PROTEIN 1	UNKNOWN	Tax_Id=101116 PDZ and LIM domain protein 1	35530	8393153	40336	SOLUBLE				
PEROXIREDOXIN 6	PEROXISOME	Tax_Id=101116 Peroxiredoxin 6	24820	5902791	60471	SOLUBLE				
PHENYLALANINE-4-HYDROXYLASE	METABOLISM	Tax_Id=101116 Phenylalanine-4-hydroxylase	51820	6981330	75026	SOLUBLE				
SEC14-LIKE PROTEIN 3	UNKNOWN	Tax_Id=101116 Secretory protein, 45kD	100300	34878986	235129	SOLUBLE				
COMPLEMENT COMPONENT C8 GAMMA SUBUNIT	BIOSYNTHETIC CARGO	Tax_Id=101116 Similar to 17000013L23Rik protein	22400	34853020	251303	SOLUBLE	cleavable signal peptide			
SIMILAR TO GLYCEROL-3-PHOSPHATE DEHYDROGENASE	METABOLISM	Tax_Id=101116 Similar to 2210409H23Rik protein	47190	34866415	232409	SOLUBLE				
CLATHRIN AP47 PROTEIN	COAT	Tax_Id=101116 Similar to AP47 protein - mouse	61590	34877759	223265	SOLUBLE				
ARP2/3 COMPLEX 16 KDA SUBUNIT (P16-ARC) (ACTIN-RELATED SUBUNIT 5)	CYTOSKELETON	Tax_Id=101116 Similar to ARP2/3 complex 16 kDa Subunit (P16-ARC) (Actin-related protein 2/3 complex Subunit 5)	34540	34880487	318590	SOLUBLE				
SIMILAR TO ATP SULFURYLASE/APS KINASE 2	METABOLISM	Tax_Id=101116 Similar to ATP Sulfurylase/APS kinase 2	80990	34862615	219419	SOLUBLE				
SIMILAR TO ATP-BINDING CASSETTE TRANSPORTER SUBUNIT 2	PLASMA MB	Tax_Id=101116 Similar to ATP-binding cassette transporter Sub-family A member 6	191500	34875258	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		
SIMILAR TO ATP-BINDING CASSETTE TRANSPORTER SUBUNIT 8A	PLASMA MB	Tax_Id=101116 Similar to ATP-binding cassette transporter Sub-family A member 8a	187500	34875001	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-OUT		
SIMILAR TO ACTIN MONOMER-BINDING PROTEIN	CYTOSKELETON	Tax_Id=101116 Similar to Actin monomer-binding protein	204100	34866518	244260	SOLUBLE				

SIMILAR TO ALANYL-TRNA SYNTHETASE (ALANINE--TRN	PROT SYN/FOLD	Tax_Id=10116 Similar to Alanyl-tRNA Synthetase (Alanine--tRNA ligase) (AlaRS)	108200	34851760	253193	SOLUBLE			
SIMILAR TO ALPHA-2 CATENIN	CYTOSKELETON	Tax_Id=10116 Similar to Alpha-2 catenin (Alpha-catenin related protein) (Alpha N-catenin)	51430	34856264	258471	SOLUBLE			
ARMADILLO REPEAT GENE DELETED IN VELO-CARDIO-P	CYTOSKELETON	Tax_Id=10116 Similar to Arvcf protein	122400	34869778	246886	SOLUBLE			
SIMILAR TO CG32774-PA	UNKNOWN	Tax_Id=10116 Similar to CG32774-PA	79590	34876775	221370	SOLUBLE			
HC PROTEIN	BIOSYNTHETIC CARGO	Tax_Id=10116 Similar to Complement C5 precursor (Hemolytic complement)	42190	34853846	242533	SOLUBLE			
EPLIN	CYTOSKELETON	Tax_Id=10116 Similar to Epithelial protein lost in neoplasia (mEPLIN)	94450	34866179	277610	SOLUBLE			
SIMILAR TO FERM, RHOGEF AND PLECKSTRIN DOMAIN 1	UNKNOWN	Tax_Id=10116 Similar to FERM, RhoGEF and pleckStrin domain protein 2	179800	34877686	293497	SOLUBLE			
SIMILAR TO FERM, RHOGEF, AND PLECKSTRIN DOMAIN	UNKNOWN	Tax_Id=10116 Similar to FERM, RhoGEF, and pleckStrin domain protein 1	23830	34876611	304176	SOLUBLE			
FILAMIN, ALPHA	CYTOSKELETON	Tax_Id=10116 Similar to FLJ00343 protein	279400	34881882	282403	SOLUBLE			
SIMILAR TO GE36	UNKNOWN	Tax_Id=10116 Similar to GE36	76150	34880541	272300	SOLUBLE			
GAMMA-SOLUBLE NSF ATTACHMENT PROTEIN (GAMMA	TETH/DOCK/FUS	Tax_Id=10116 Similar to Gamma-Soluble NSF attachment protein (SNAP-gamma) (N-ethylmaleimide-Sensitive factor attachment protein, gamma)	45610	34932055	316372	SOLUBLE			
IQ MOTIF CONTAINING GTPASE ACTIVATING PROTEIN 1	SIGNALING	Tax_Id=10116 Similar to IQ motif containing GTPase activating protein 1	193900	34857388	242453	SOLUBLE			
SIMILAR TO PLEXIN	SIGNALING	Tax_Id=10116 Similar to KIAA0315	211600	34867650	248510	MEMBRANE	signal anchor	40 23 IN-OUT	
LEUKOTRIENE A-4 HYDROLASE	METABOLISM	Tax_Id=10116 Similar to Leukotriene A-4 hydrolase (LTA-4 hydrolase) (Leukotriene A(4) hydrolase)	93570	34864937	286024	SOLUBLE			
SIMILAR TO MALTASE-GLUCOAMYLASE, INTESTINAL	PLASMA MB	Tax_Id=10116 Similar to Maltase-glucoamylase, intestinal	494700	34855581	199085	MEMBRANE		208 23 IN-OUT	
MYOSIN LIGHT CHAIN KINASE	SIGNALING	Tax_Id=10116 Similar to Mylk protein	73330	34869218	268038	SOLUBLE			
SIMILAR TO NEDD4 WW BINDING PROTEIN 4	UNKNOWN	Tax_Id=10116 Similar to Nedd4 WW binding protein 4	32550	34860870	317802	MEMBRANE	signal anchor	54 23 IN-OUT	
PALS2-BETA SPLICE VARIANT	BIOSYNTHETIC CARGO	Tax_Id=10116 Similar to PALS2-beta Splice variant	67230	34855859	233877	SOLUBLE			
SIMILAR TO POTENTIAL PHOSPHOLIPID-TRANSPORTING	UNKNOWN	Tax_Id=10116 Similar to Potential phospholipid-transporting ATPase IG (ATPase class I type 11C) (ATPase IG)	131400	34881712	292511	MEMBRANE		369 23 OUT-IN 422 20 IN-OUT 1034 23 OUT-IN	
PROTEIN TRANSPORT PROTEIN SEC24A (SEC24-RELATE	COAT	Tax_Id=10116 Similar to Protein transport protein Sec24A (SEC24-related protein A)	105700	34870707	295725	SOLUBLE			
MITOCHONDRIAL GLUTAMATE CARRIER 1	MITOCHONDRIA	Tax_Id=10116 Similar to RIKEN cDNA 1300006L01	34660	34865173	223033	MEMBRANE		12 20 IN-OUT	
ETEA: EXPRESSED IN T-CELLS AND EOSINOPHILS IN AT	UNKNOWN	Tax_Id=10116 Similar to RIKEN cDNA 2210404D11	57560	34873697	262247	SOLUBLE			
SIMILAR TO RIKEN CDNA 3110038B19	UNKNOWN	Tax_Id=10116 Similar to RIKEN cDNA 3110038B19	46280	34879556	235525	SOLUBLE			
SIMILAR TO RIKEN CDNA C920006C10	UNKNOWN	Tax_Id=10116 Similar to RIKEN cDNA C920006C10	66760	34866542	287440	SOLUBLE			
SIMILAR TO ALPHA 3 TYPE VI COLLAGEN ISOFORM 4	BIOSYNTHETIC CARGO	Tax_Id=10116 Similar to RIKEN cDNA E330026B02	279300	34865864	264571	SOLUBLE			
SIMILAR TO START DOMAIN CONTAINING 10; SEROLOG	UNKNOWN	Tax_Id=10116 Similar to START domain containing 10	53820	34856808	195138	SOLUBLE			
CYTOPLASMIC FMR1 INTERACTING PROTEIN 1	UNKNOWN	Tax_Id=10116 Similar to Selective hybridizing clone	164100	34856144	203612	SOLUBLE			
SIDEROFLEXIN 2	MITOCHONDRIA	Tax_Id=10116 Similar to Sideroflexin 2	38820	34863716	229993	MEMBRANE		170 23 OUT-IN 252 23 IN-OUT 289 23 OUT-IN	
SLINGSHOT 1L	SIGNALING	Tax_Id=10116 Similar to SlingShot 1	178100	34872826	271907	SOLUBLE			

SPECTRIN BETA-II CHAIN, BRAIN 1 (SPECTRIN, NON-ERY	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	SOLUBLE				
STABILIN-1	PLASMA MB	Tax_Id=10116 Similar to Stabilin-1	285900	34876981	262547	MEMBRANE	58 23 IN-OUT 2565 23 OUT-IN			
SIMILAR TO STABILIN-2	PLASMA MB	Tax_Id=10116 Similar to Stabilin-2	93660	34864902	206065	MEMBRANE	cleavable signal peptide			
TRANSFERRIN RECEPTOR PROTEIN 2 (TFR2)	PLASMA MB	Tax_Id=10116 Similar to Transferrin receptor protein 2 (TFR2)	89250	34871536	315288	MEMBRANE	102 23 IN-OUT			
SIMILAR TO UROPLAKIN IA	PLASMA MB	Tax_Id=10116 Similar to Uroplakin Ia (UPIa) (UPKa)	52100	34855791	301709	MEMBRANE	87 23 IN-OUT 197 23 OUT-IN 231 23 IN-OUT			
SIMILAR TO VINCULIN (METAVINCULIN)	CYTOSKELETON	Tax_Id=10116 Similar to Vinculin (Metavinculin)	135500	34868946	268838	SOLUBLE				
WAVE2	CYTOSKELETON	Tax_Id=10116 Similar to WAVE2	41650	34871786	222802	SOLUBLE				
SIMILAR TO BETA ACTIN	CYTOSKELETON	Tax_Id=10116 Similar to actin - Hydra attenuata	13310	34871187	219221	SOLUBLE				
ARP2/3 COMPLEX 34 KDA SUBUNIT	CYTOSKELETON	Tax_Id=10116 Similar to actin related protein 2/3 complex Subunit 2	34350	34876797	205076	SOLUBLE				
FILAMIN B, BETA	CYTOSKELETON	Tax_Id=10116 Similar to actin-binding protein homolog ABP-278	284700	34869526	231012	SOLUBLE				
ALDEHYDE DEHYDROGENASE 7A1	DETOXIFICATION	Tax_Id=10116 Similar to aldehyde dehydrogenase family 7, member A1	57290	34879551	245155	SOLUBLE	cleavable signal peptide			
GLYCOGEN DEBRANCHING ENZYME	METABOLISM	Tax_Id=10116 Similar to amylo-1,6-glucosidase, 4-alpha-glucanotransferase isoform 1	180900	34859913	208010	SOLUBLE				
SIMILAR TO APOA-I	BIOSYNTHETIC CARGO	Tax_Id=10116 Similar to apoA-I binding protein	78970	34857927	303449	SOLUBLE				
SIMILAR TO BETA1-SYNTROPHIN	CYTOSKELETON	Tax_Id=10116 Similar to beta1-Syntrophin	46920	34866568	190168	SOLUBLE				
CHOREIN, VPS13P	TRAFFIC	Tax_Id=10116 Similar to chorein isoform B	254800	34861677	218802	SOLUBLE				
SIMILAR TO CHROMOSOME 20 OPEN READING FRAME 1	UNKNOWN	Tax_Id=10116 Similar to chromosome 20 open reading frame 116	36120	34858705	275755	SOLUBLE	cleavable signal peptide	4 18 OUT-IN		
COPI COATOMER ALPHA SUBUNIT	COAT	Tax_Id=10116 Similar to coatomer protein complex Subunit alpha	139100	34880938	293534	SOLUBLE				
CORDON-BLEU RELATED 1	UNKNOWN	Tax_Id=10116 Similar to cbl-related 1	135100	34854739	289448	SOLUBLE				
SIMILAR TO COMPLEMENT COMPONENT 8 ALPHA SUBUNIT	BIOSYNTHETIC CARGO	Tax_Id=10116 Similar to complement component 8 alpha Subunit	62090	34869994	295319	SOLUBLE	cleavable signal peptide			
SIMILAR TO ESTERASE 10; ESTERASE D	UNKNOWN	Tax_Id=10116 Similar to eSteraSe 10	42940	34874491	305590	SOLUBLE				
SIMILAR TO EUKARYOTIC TRANSLATION INITIATION FACTOR	PROT SYN/FOLD	Tax_Id=10116 Similar to eukaryotic translation initiation factor 3, Subunit 5 epSilon, 47kDa	35120	34858904	213255	SOLUBLE	cleavable signal peptide			
1,4-ALPHA-GLUCAN BRANCHING ENZYME	METABOLISM	Tax_Id=10116 Similar to glucan (1,4-alpha-), branching enzyme 1	43080	34867430	216271	SOLUBLE				
SIMILAR TO GLYCERALDEHYDE-3-PHOSPHATE DEHYDRATASE	METABOLISM	Tax_Id=10116 Similar to glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) (EC 1.2.1.12) - mouse	36190	34873236	316038	SOLUBLE				
GPP130	TETH/DOCK/FUS	Tax_Id=10116 Similar to golgi phosphoprotein 4	73200	34857091	237211	MEMBRANE				
SORTILIN-RELATED RECEPTOR/LDL RECEPTOR MOSAIC	TRAFFIC	Tax_Id=10116 Similar to gp250 precursor	209000	34863171	283274	MEMBRANE	1791 23 OUT-IN			
SIMILAR TO HYPOTHETICAL PROTEIN CL25084	UNKNOWN	Tax_Id=10116 Similar to hypothetical protein CL25084	60710	34879636	242521	MEMBRANE	65 23 IN-OUT			
SIMILAR TO DISHEVELLED-ASSOCIATED ACTIVATOR OF KINASE	UNKNOWN	Tax_Id=10116 Similar to hypothetical protein E130308H01	113900	34865376	283779	SOLUBLE				
TETRAPTRICOPEPTIDE REPEAT DOMAIN 17	UNKNOWN	Tax_Id=10116 Similar to hypothetical protein FLJ10890	138100	34856577	278036	SOLUBLE	cleavable signal peptide			
UNKNOWN ZINC FINGER PROTEIN	UNKNOWN	Tax_Id=10116 Similar to hypothetical protein FLJ20531	57240	34871405	217607	SOLUBLE				
SIMILAR TO HYPOTHETICAL PROTEIN FLJ20627	UNKNOWN	Tax_Id=10116 Similar to hypothetical protein FLJ20627	40260	34853516	295521	MEMBRANE	332 23 OUT-IN			
SIMILAR TO UROCANATE HYDRATASE	METABOLISM	Tax_Id=10116 Similar to hypothetical protein MGC37818	19860	34861397	316589	SOLUBLE				
IMMUNOGLOBULIN 4G6 LIGHT CHAIN	BLOOD + OTHER CELLS	Tax_Id=10116 Similar to immunoglobulin 4G6 light chain variable region	17890	34855968	195860	SOLUBLE				

LYMPHOCYTE CYTOSOLIC PROTEIN 1	CYTOSKELETON	Tax_Id=10116 Similar to lymphocyte cytoSolic protein 1	80290	34875362	272629	SOLUBLE				
P120 CATENIN ISOFORM 2B	CYTOSKELETON	Tax_Id=10116 Similar to mKIAA0384 protein	101400	34856482	193681	SOLUBLE				
SIMILAR TO MACROPHAGE MANNOSE RECEPTOR	BLOOD + OTHER CELLS	Tax_Id=10116 Similar to macrophage mannoSe receptor precurSor	192400	34877265	296460	MEMBRANE	signal anchor	7 23 IN-OUT 1634 23 OUT-IN		
MELANOMA INHIBITORY ACTIVITY PROTEIN 2(MIA2)	UNKNOWN	Tax_Id=10116 Similar to melanoma inhibitory activity protein 2	58930	34865264	225113	SOLUBLE	cleavable signal peptide			
SIMILAR TO MYOSIN HEAVY CHAIN	CYTOSKELETON	Tax_Id=10116 Similar to myoSin heavy chain	229700	34869316	230006	SOLUBLE				
SIMILAR TO O-METHYLTRANSFERASE FAMILY MEMBER	UNKNOWN	Tax_Id=10116 Similar to o-methyltranSeraSe family member (5C530)	24490	34868938	291365	SOLUBLE	cleavable signal peptide	10 23 OUT-IN		
P53 INDUCIBLE PROTEIN	SIGNALING	Tax_Id=10116 Similar to p53 inducible protein	164400	34870680	289228	SOLUBLE				
PEPTIDYLPROLYL ISOMERASE D (CYCLOPHILIN D)	PROT SYN/FOLD	Tax_Id=10116 Similar to peptidyprolyl iSomeraSe D (cyclophilin D)	69130	34873471	283106	MEMBRANE	cleavable signal peptide	525 20 OUT-IN		
SIMILAR TO PROBABLE NOCTURNIN PROTEIN	TRANSCRIPTION	Tax_Id=10116 Similar to probable nocturnin protein	16650	34861866	309047	SOLUBLE				
SIMILAR TO PROTEIN 4.1, P4.1 - MOUSE	UNKNOWN	Tax_Id=10116 Similar to protein 4.1, P4.1 - mouSe	105500	34871764	306783	SOLUBLE				
PROTEIN RAKC	DETOXIFICATION	Tax_Id=10116 Similar to protein RAKc	41260	34876322	249119	SOLUBLE				
PROTEIN TYROSINE PHOSPHATASE, RECEPTOR TYPE,	SIGNALING	Tax_Id=10116 Similar to protein tyroSine phoSphataSe, receptor type, D iSoform 3 precurSor	203600	34869007	215340	MEMBRANE		1167 23 OUT-IN		
TALIN 2	CYTOSKELETON	Tax_Id=10116 Similar to talin 2	284500	34864297	199727	SOLUBLE				
SIMILAR TO TESTIS PROTEIN TEX15	UNKNOWN	Tax_Id=10116 Similar to teSiS protein TEX15	282400	34866738	211558	SOLUBLE				
TRANSGELIN 2 (PREDICTED)	UNKNOWN	Tax_Id=10116 Similar to tranSgelin 2	29970	34880944	266044	SOLUBLE				
SIMILAR TO TRANSTHYRETIN (4L369)	BIOSYNTHETIC CARGO	Tax_Id=10116 Similar to tranSthyretin (4L369)	16010	34861187	199559	SOLUBLE				
SIMILAR TO UBIQUITIN LIGASE E3 ALPHA-II	PROTEASOME/UBIQUITIN	Tax_Id=10116 Similar to ubiquitin lgaSe E3 alpha-II	175300	34874398	274677	MEMBRANE		1520 23 OUT-IN		
SIMILAR TO URIDINDIPHOSPHOGLUCOSEPYROPHOSPHATASE	METABOLISM	Tax_Id=10116 Similar to uridindiphoSphoGlucoSepyrophoSphorylaSe 2	89950	34879163	225159	SOLUBLE				
SIMILAR TO VILLIN-LIKE PROTEIN	CYTOSKELETON	Tax_Id=10116 Similar to villin-like protein	99190	34866628	253969	SOLUBLE				
SIMILAR TO ZINC FINGER PROTEIN, SUBFAMILY 1A, 4	TRANSCRIPTION	Tax_Id=10116 Similar to zinc finger protein, Subfamily 1A, 4	64460	34862217	313581	SOLUBLE				
CHAPERONIN DELTA SUBUNIT	PROT SYN/FOLD	Tax_Id=10116 T-complex protein 1, delta subunit	58100	52000745	166356	SOLUBLE				
TROPOMYOSIN ALPHA 4 CHAIN	CYTOSKELETON	Tax_Id=10116 Tropomyosin 4	28510	763182	44422	SOLUBLE				
14-3-3 PROTEIN BETA/ALPHA	SIGNALING	Tax_Id=10116 Tyrosine 3-monooxygenase/TrypTophan monooxygenase acTivaTion proTein, beTa polyepTide	28050	9507243	47331	SOLUBLE				
VESICLE-ASSOCIATED MEMBRANE PROTEIN-ASSOCIATED	TRAFFIC	Tax_Id=10116 Vesicle-associated membrane protein-associated protein B	26920	4240464	57726	MEMBRANE		220 23 OUT-IN		
TELOMERASE PROTEIN COMPONENT 1	NUCLEUS	Telomerase protein component 1 rTLP1 Telomerase-associated protein 1 p240 p230 p80 telomerase homolog	291700	47606056	169376	SOLUBLE			O08653	
FARNESYL PYROPHOSPHATE SYNTHETASE	PROT MOD	Testis-specific farnesyl pyrophosphate synthetase	40800	37590777	78213	MEMBRANE			Q6GT82	
TISSUE-TYPE TRANSGLUTAMINASE	SIGNALING	Tissue-type transglutaminase	76930	9507185	47311	SOLUBLE			Q9WVJ6	
TORSINA	PROT SYN/FOLD	TorsinA	37980	22651450	188125	SOLUBLE	cleavable signal peptide		Q8K3L8	NP_695215.1
TRIOSEPHOSPHATE ISOMERASE	METABOLISM	Tpi1 protein	26720	38512111	340135	SOLUBLE			Q6P793	
RHOA	GTPASE	Transforming protein RhoA precursor	21780	47605935	76408	MEMBRANE			P61589	
P24 GAMMA 3	TRAFFIC	Transmembrane emp24 domain-containing protein 5 precursor	26140	62287552	228279	MEMBRANE	cleavable signal peptide	5 23 OUT-IN 195 23 IN-OUT	Q6AXN3	XP_214123.2
TROPOMYOSIN ISOFORM 6	CYTOSKELETON	Tropomyosin 5	28950	9653293	93198	SOLUBLE			P97726	

SIMILAR TO TRANSLATIONALLY CONTROLLED TUMOR PROTEIN	UNKNOWN	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:IO00031O13 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	SOLUBLE			P63029	
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	SOLUBLE	cleavable signal peptide	7 23 IN-OUT		
SIMILAR TO UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX III	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	SOLUBLE			Q5M9I5	XP_3455569.1
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	SOLUBLE			Q9EQX9	
UBIQUITIN-CONJUGATING ENZYME E2 VARIANT 1 UEV-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	SOLUBLE				
URINARY PROTEIN 1	BIOSYNTHETIC CARGO	Urinary protein 1 precursor RUP-1 Liver regeneration-related protein LRRG05	10960	6537316	37481	SOLUBLE	cleavable signal peptide		P81827 Q53ZD7	
UROPORPHYRINOGEN DECARBOXYLASE	DETOXIFICATION	Uroporphyrinogen decarboxylase	40450	5524747	44446	SOLUBLE			P32362	
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	SOLUBLE			P62815	
SEPTIN 2	GTPASE	Vascular endothelial cell specific protein 11 Septin 2	41590	51858574	140635	MEMBRANE			Q91Y81	
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	MEMBRANE		219 23 OUT-IN	Q6P723 Q9Z270	
R, SEC22	TETH/DOCK/FUS	Vesicle-trafficking protein SEC22b SEC22 vesicle-trafficking protein-like 1	24740	71043604	41516	MEMBRANE		191 23 IN-OUT	Q4KM74	

GUANINE NUCLEOTIDE-BINDING PROTEIN G-S ALPHA	SIGNALING	XLalphas protein	78230	14161099	72067	SOLUBLE			Q63803	
XANTHINE DEHYDROGENASE/OXIDASE	PEROXISOME	Xanthine dehydrogenase/oxidase	146300	2144323	80445	SOLUBLE			P22985	
ADAPTOR-RELATED PROTEIN COMPLEX 2 ALPHA 2 SUBUNIT	COAT	adaptor protein complex AP-2, alpha 2 subunit [Rattus norvegicus]	104000	55729	37177	SOLUBLE				
CAMP-DEPENDENT PROTEIN KINASE C ALPHA	SIGNALING	CAMP-dependent protein kinase, alpha-catalytic subunit (PKA C-alpha)	40620	125207	168211	SOLUBLE				
DIHYDROPYRIMIDINASE	METABOLISM	dihydropyrimidinase	56830	3122039	78138	SOLUBLE			UPI0000129870	
SEC24C	COAT	hypothetical protein XP_223792	115600	34868956	241419	SOLUBLE			UPI00001D0CDF	
KYNURENINASE	METABOLISM	kynureninase (L-kynurenine hydrolase)	52450	3913969	157223	SOLUBLE			UPI000012E177	
LIN-7 PROTEIN	SIGNALING	lin-7-Ba [Rattus norvegicus]	19930	3885830	158790	SOLUBLE				
LYSOZYME HOMOLOG AT-2, BINE - RAT (FRAGMENTS)	BIOSYNTHETIC CARGO	lysozyme homolog AT-2, bone - rat (fragments)	3164	539969	130837	SOLUBLE				
PROTEASOME SUBUNIT BETA TYPE 4	PROTEASOME/UBIQUITIN	proteasome (prosome, macropain) subunit, beta type 4	25790	310214	78104	SOLUBLE			UPI0000167973	
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	SOLUBLE				
SIMILAR TO ASPARAGINYL-TRNA SYNTHETASE, CYTOPLASMIC	PROT SYN/FOLD	similar to Asparaginyl-tRNA synthetase, cytoplasmic (Asparagine--tRNA ligase) (AsnRS)	64130	34932063	238208	SOLUBLE			UPI00001D1315	
CCTETA, ETA SUBUNIT OF THE CHAPERONIN CONTAINING TCP-1 (CCT)	PROT SYN/FOLD	similar to CCTeta, eta subunit of the chaperonin containing TCP-1 (CCT)	59660	27712178	161408	SOLUBLE			UPI00001C8C99	
SIMILAR TO CG4241-PA	MITOCHONDRIA	similar to CG4241-PA	35190	34877651	194839	MEMBRANE		186 23 IN-OUT	UPI00001D0F77	
RSEC6	TRAFFIC	similar to Exocyst complex component Sec6 (rSec6)	72270	34855314	276511	SOLUBLE			UPI00001CE7DD	
SIMILAR TO GLUTATHIONE S-TRANSFERASE, THETA 3	DETOXIFICATION	similar to Glutathione S-transferase, theta 3	44270	34852398	225794	SOLUBLE			UPI00001D15AC	
SIMILAR TO GROWTH-ARREST-SPECIFIC PROTEIN 2 (GAS-2)	SIGNALING	similar to Growth-arrest-specific protein 2 (GAS-2)	61200	34856132	300461	SOLUBLE			UPI00001CE8AA	
SIMILAR TO HYPOTHETICAL PROTEIN KIAA0379	UNKNOWN	similar to Hypothetical protein KIAA0379	41000	27732065	190049	SOLUBLE			UPI00001C83AC	
N-ACETYLNEURAMINIC ACID SYNTHASE (SIALIC ACID SYNTHASE)	METABOLISM	similar to N-acetylneuraminic acid synthase (sialic acid synthase)	40050	27714479	225772	SOLUBLE			UPI000018096E	
NEUROBLASTOMA AMPLIFIED GENE, NAG	UNKNOWN	similar to Nag-pending protein	60300	34863173	240310	SOLUBLE			UPI00001CF9A0	
PROTEIN TRANSPORT PROTEIN SEC23B (SEC23-RELATED PROTEIN B) [Rattus norvegicus]	COAT	similar to Protein transport protein Sec23B (SEC23-related protein B) [Rattus norvegicus]	86090	34858849	260808	SOLUBLE				
RAB6	GTPASE	similar to RAB6, member RAS oncogene family	26610	34859460	290450	MEMBRANE			UPI00001CEA56	
SIMILAR TO RIKEN CDNA 4732463H20	UNKNOWN	similar to RIKEN cDNA 4732463H20 [Rattus norvegicus]	52510	34857987	192449	SOLUBLE				
SIMILAR TO RAS GTPASE-ACTIVATING-LIKE PROTEIN IQGAP2	GTPASE	similar to Ras GTPase-activating-like protein IQGAP2	140700	34853552	197696	MEMBRANE			UPI00001CECE0	
SIMILAR TO RAS SUPPRESSOR PROTEIN 1 (RSU-1) (RSP-1)	GTPASE	similar to Ras suppressor protein 1 (Rsu-1) (RSP-1)	34760	34877253	195351	SOLUBLE			UPI00001D1212	
SH3-BINDING DOMAIN GLUTAMIC ACID-RICH PROTEIN L	UNKNOWN	similar to Sh3bglr protein	12800	27706424	198937	SOLUBLE			UPI00001CD5D	
UNNAMED PROTEIN PRODUCT2	UNKNOWN	similar to Swiprosin 1	26760	72255531	250786	SOLUBLE			Q4FZY0 UPI00001808E0	
SIMILAR TO WDR1 PROTEIN	UNKNOWN	similar to Wdr1 protein [Rattus norvegicus]	48550	34878397	292693	SOLUBLE				
TUBULIN ALPHA CHAIN	CYTOSKELETON	similar to alpha-tubulin	45060	34872542	234717	SOLUBLE			UPI00001CF88C	
SIMILAR TO ANCIENT UBIQUITOUS 46 KDA PROTEIN AUP46	UNKNOWN	similar to ancient ubiquitous 46 kDa protein AUP46	46200	34856277	205068	MEMBRANE	signal anchor	23 23 OUT-IN	UPI000017FDCE	

SIMILAR TO CDNA SEQUENCE BC003251	UNKNOWN	similar to cDNA sequence BC003251	53180	34871409	253866	SOLUBLE			UPI00001D04B6	
SIMILAR TO ENDONUCLEASE G	NUCLEUS	similar to endonuclease G	32270	77917570	273385	SOLUBLE	cleavable signal peptide		Q3V5X8 UPI0000182170	
SIMILAR TO SEPTIN 10	UNKNOWN	similar to ethanol induced 6	15850	27686507	168139	SOLUBLE	cleavable signal peptide		UPI000017FFE4	
SIMILAR TO GLUCAN (1,4-ALPHA-), BRANCHING ENZYME	PROT MOD	similar to glucan (1,4-alpha-), branching enzyme 1; DN segment, Chr 16, ERATO Doi 536, expressed	32500	34867432	299017	SOLUBLE			UPI00001D06E4	
SIMILAR TO GLYCERALDEHYDE-3-PHOSPHATE DEHYDR	METABOLISM	similar to glyceraldehyde-3-phosphate dehydrogenase	36450	34852715	210943	SOLUBLE			UPI00001D15EC	
SIMILAR TO GLYCERALDEHYDE-3-PHOSPHATE DEHYDR	METABOLISM	similar to glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) (EC 1.2.1.12) - mouse	27870	27699577	156654	SOLUBLE			UPI00001C810A	
HEAT SHOCK PROTEIN 105 KDA ALPHA	PROT SYN/FOLD	similar to heat shock protein 105 kDa alpha	82350	34870188	195465	SOLUBLE			UPI00001D084A	
RAN BINDING PROTEIN 1	NUCLEUS	similar to hypothetical protein A	36410	34869364	193827	SOLUBLE			UPI00001D0766	
MYOSIN HEAD DOMAIN CONTAINING 1	CYTOSKELETON	similar to hypothetical protein FLJ22865	33930	34872934	263071	SOLUBLE	signal anchor		UPI00001D056C	
LIVER REGENERATION-RELATED PROTEIN	DETOXIFICATION	similar to liver regeneration-related protein LRRG07 [Rattus norvegicus]	35400	34876593	287183	SOLUBLE				
LYSOSOMAL APYRASE-LIKE 1	LYSOSOME	similar to lysosomal apyrase-like 1	49290	34874388	305737	MEMBRANE		162 23 OUT-IN	UPI00001D0E3A	
SIMILAR TO OSTEOCLAST STIMULATING FACTOR 1	UNKNOWN	similar to osteoclast stimulating factor 1	34620	34880977	297002	SOLUBLE	cleavable signal peptide		UPI00001D0A8A	
CREG	TRANSCRIPTION	similar to placenta-specific 3 isoform 1; pregnancy-associated plasma protein-E; pregnancy-associated plasma preproprotein-A2	33400	34877698	287571	SOLUBLE			UPI00001D1232	
SIMILAR TO PROLINE DEHYDROGENASE; PRODH	METABOLISM	similar to proline dehydrogenase; PRODH	12130	27665096	305160	SOLUBLE			UPI00001CB397	
RICK	SIGNALING	similar to receptor-interacting protein 2	60780	34867073	242276	SOLUBLE			UPI0000181DE1	
UBIQUITIN-ACTIVATING ENZYME E1 1	PROTEASOME/UBIQUITIN	similar to ubiquitin-protein ligase (EC 6.3.2.19) E1 - mouse	123600	34933178	317625	SOLUBLE	cleavable signal peptide		UPI00001D16AF	
ER-GOLGI INTERMEDIATE COMPARTMENT 32 KDA PROT	TRAFFIC	unknown	35170	34870624	209664	MEMBRANE	signal anchor	42 23 OUT-IN 271 23 IN-OUT	UPI00001D03B5	
SEC13 LIKE 1 PROTEIN	COAT	1110003H02Rik protein	35550	55741774	161453	SOLUBLE			Q5XFW8	XP_216257.1
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	SOLUBLE	cleavable signal peptide	13 23 IN-OUT	Q91ZS3	
ARF-RELATED PROTEIN	GTPASE	ARF-related protein 1	22660	2492928	52078	MEMBRANE			Q63055	
ALPHA-1,6-MANNOSYL-GLYCOPROTEIN 2-BETA-N-ACET	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	MEMBRANE	signal anchor	12 18 IN-OUT	Q09326	
ALPHA 2,6-SIALYLTRANSFERASE	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	MEMBRANE	signal anchor	9 18 IN-OUT	P13721	
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	SOLUBLE			Q6P6R2	

MG160	PROT MOD	Golgi apparatus protein 1 precursor Golgi sialoglycoprotein MG-160 E-selectin ligand 1 ESL-1	133600	8393450	51465	MEMBRANE	cleavable signal peptide	1138 23 OUT-IN	Q62638	
TRANS-GOLGI PROTEIN GMX33	TETH/DOCK/FUS	Golgi phosphoprotein 3 Coat-protein GPP34 Trans-Golgi protein GMx33	33780	50400215	54283	SOLUBLE			Q9ERE4	
GRASP55_65	TETH/DOCK/FUS	Golgi reassembly stacking protein 2	47310	56090463	288023	SOLUBLE			Q68G33	XP_346654.1
GOLGI AUTOANTIGEN, GOLGIN SUBFAMILY A MEMBER 2	TETH/DOCK/FUS	Golgin subfamily A member 2 Cis-Golgi matrix protein GM130	111400	7513936	169300	MEMBRANE			Q62839	
HYDROXYMETHYLGLUTARYL-COA LYASE, MITOCHONDRIAL	MITOCHONDRIA	Hydroxymethylglutaryl-CoA lyase, mitochondrial precursor HMG-CoA lyase HL 3-hydroxy-3-methylglutarate-CoA lyase	34190	38511566	68742	SOLUBLE	cleavable signal peptide		P97519	
ACYL-COA DEHYDROGENASE, MEDIUM-CHAIN SPECIFIC	MITOCHONDRIA	Medium-chain specific acyl-CoA dehydrogenase, mitochondrial precursor MCAD	46560	8392833	11499	SOLUBLE			P08503	
ORNITHINE AMINOTRANSFERASE, MITOCHONDRIAL PRECURSOR	MITOCHONDRIA	Ornithine aminotransferase	24280	206706	44333	SOLUBLE			Q6LDF6	
GOLGI PERIPHERAL MEMBRANE PROTEIN P65	TETH/DOCK/FUS	PREDICTED: hypothetical protein XP_579439	47620	62654450	225098	SOLUBLE			UPI00001D0130	
SIMILAR TO DNA SEGMENT, CHR 1, ERATO DOI 578, EXP	UNKNOWN	PREDICTED: similar to F-box protein 28	41070	27681007	262592	SOLUBLE			UPI00001CBDD B	
GOLGIN-84	TETH/DOCK/FUS	PREDICTED: similar to RET-II	82410	34867583	302868	MEMBRANE		693 23 OUT-IN	UPI000017F5A9	
P24 ALPHA 2	TRAFFIC	PREDICTED: similar to Transmembrane emp24 protein transport domain containing 4	26120	27697481	170045	MEMBRANE	cleavable signal peptide	10 23 OUT-IN 195 20 IN-OUT	UPI0000182A1D	
SIMILAR TO BETA-1,3-GALACTOSYLTRANSFERASE-6	PROT MOD	PREDICTED: similar to beta-1,3-galactosyltransferase-6	37150	27663478	210144	MEMBRANE	cleavable signal peptide	12 19 IN-OUT	UPI0000180178	
SIMILAR TO HTGN29 PROTEIN; KERATINOCYTES ASSOCIATED	UNKNOWN	PREDICTED: similar to chromosome 5 open reading frame 15	28260	34870715	258441	MEMBRANE	cleavable signal peptide	190 20 OUT-IN	UPI00001D040D	
GALACTOSYL GALACTOSYLXYLOSYLPROTEIN 3-BETA-GALACTOSYL N-ACETYL GALACTOSAMINYLTRANSFERASE	PROT MOD	PREDICTED: similar to glucuronosyltransferase I	37070	34861582	228888	MEMBRANE	cleavable signal peptide	7 23 IN-OUT	UPI0000180E75	
	PROT MOD	Polypeptide N-acetylgalactosaminyltransferase 1 Protein UDP acetylgalactosaminyltransferase 1 UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase 1 Polypeptide GalNAc transferase 1 GalNAc-T1 pp-GalNTase 1 Polypeptide N-acetylgalactosaminyltransferase 1 soluble form	64230	1709559	68735	MEMBRANE	cleavable signal peptide	7 23 IN-OUT	Q10473	
R, YKT6	TETH/DOCK/FUS	Prenylated SNARE protein Ykt6p	22310	2642348	78131	SOLUBLE			O35487	
RAB5C	GTPASE	Ras-related protein Rab-5C	23430	27689505	161834	MEMBRANE			UPI000017ED6D	
SIMILAR TO GOLGI RESIDENT PROTEIN GCP60	TETH/DOCK/FUS	Tax_id=10116 Golgi resident protein GCP60	60480	51315724	295490	SOLUBLE				
KERATIN 18	LIKELY CONTAMINANTS	Tax_id=10116 Keratin 18	16960	587518	108078	SOLUBLE				
SIMILAR TO GOLGI MEMBRANE PROTEIN GP73	TRAFFIC	Tax_id=10116 Similar to Golgi phoSphoprotein 2	54350	34873592	231145	SOLUBLE	cleavable signal peptide	13 23 IN-OUT		
SIMILAR TO EH DOMAIN BINDING PROTEIN 1	TRAFFIC	Tax_id=10116 Similar to KIAA0903-like protein	120900	34879170	275605	SOLUBLE				
DVL-BINDING PROTEIN DAPLE	SIGNALING	Tax_id=10116 Similar to KIAA1509 protein	212500	34867549	239536	SOLUBLE	cleavable signal peptide			
SIMILAR TO N-ACETYLGLUCOSAMINYLTRANSFERASE IV	PROT MOD	Tax_id=10116 Similar to N-acetylglucosaminyltrasnferase IVb	71740	34870693	194890	MEMBRANE	cleavable signal peptide	7 23 IN-OUT		
SIMILAR TO RIKEN CDNA 4931400A14	UNKNOWN	Tax_id=10116 Similar to RIKEN cDNA 4931400A14	231900	34878255	296181	SOLUBLE				
MANNOSIDASE 1-BETA	PROT MOD	Tax_id=10116 Similar to alpha-mannoSidaSe	45930	34860045	248855	MEMBRANE				
SIMILAR TO COMPLEMENT COMPONENT FACTOR H	BIOSYNTHETIC CARGO	Tax_id=10116 Similar to complement component factor h	43820	34880509	275354	SOLUBLE	cleavable signal peptide			
TYROSYLPROTEIN SULFOTRANSFERASE-1	PROT MOD	Tpst1 protein	42140	76779364	241393	MEMBRANE	cleavable signal peptide		Q3KR92	
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	MEMBRANE	cleavable signal peptide	15 23 OUT-IN 186 23 IN-OUT	Q63584 Q9R0W6	

CDA14 (PTX1)	TRAFFIC	similar to EST AA408438	42480	27713571	204725	MEMBRANE	signal anchor		UPI00001C8F2F	
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 (yeast); Arp1 contractin alpha; Arp1 contractin alpha	62980	34865224	222641	SOLUBLE			UPI00001CE61F	
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	MEMBRANE	cleavable signal peptide	12 23 IN-OUT		
NOVEL MEMBER OF P24 FAMILY (TIRAP3B)	TRAFFIC	similar to Hypothetical protein CGI-109 precursor	20460	34879511	204384	MEMBRANE	cleavable signal peptide	148 23 IN-OUT	UPI00001D12FE	
MANNOSIDASE 2, ALPHA 1	PROT MOD	similar to Man9-mannosidase	57920	34852693	212806	MEMBRANE			UPI00001D15F6	
SIMILAR TO CYTOKERATIN	LIKELY CONTAMINANTS	similar to cytokeratin	46840	34873210	190628	SOLUBLE			UPI00001D0520	
SIMILAR TO ENDO B CYTOKERATIN	LIKELY CONTAMINANTS	similar to endo B cytokeratin	42970	34860580	202236	SOLUBLE			UPI00001CFEB9	
GBF1	TRAFFIC	similar to golgi-specific brefeldin A-resistance guanine nucleotide exchange factor 1	208100	34865240	218235	SOLUBLE			UPI00001CE622	
SIMILAR TO HEPARAN SULFATE 2-SULFOTRANSFERASE	PROT MOD	similar to heparan sulfate 2-sulfotransferase	41850	34860929	259411	MEMBRANE	signal anchor		UPI000017F21B	
SIMILAR TO MKIAA0493 PROTEIN	UNKNOWN	similar to mKIAA0493 protein	110600	34866514	234949	SOLUBLE			UPI00001CFD3D	
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	MEMBRANE	signal anchor	46 23 OUT-IN 85 23 IN-OUT		
2'-5'-OLIGOADENYLATE SYNTHETASE 1	SIGNALING	2'-5'-oligoadenylate synthetase 1 (2-5'-oligo(A) synthetase 1 2-5A synthetase 1	41670	56790	134570	SOLUBLE			Q05961	
Qb, MEMBRIN	TETH/DOCK/FUS	27 kDa Golgi SNARE protein	24650	2316090	55435	MEMBRANE		192 20 IN-OUT	O08566 O35165	
7-DEHYDROCHOLESTEROL REDUCTASE	DETOXIFICATION	7-dehydrocholesterol reductase 7-DHC reductase Steroid delta-7-reductase	54160	81882109	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	Q9Z2Z8	
MHC CLASS I RT1.AB HEAVY CHAIN PRECURSOR	PLASMA MB	A1b	39310	5912594	104733	MEMBRANE		286 23 OUT-IN	Q9QYP8	
AB2-305	UNKNOWN	Ab2-305	43570	33086580	166327	MEMBRANE	cleavable signal peptide		Q7TP48	
ABHYDROLASE DOMAIN CONTAINING 6	UNKNOWN	Abhydrolase domain containing 6	38310	56090644	309746	MEMBRANE	signal anchor	7 23 IN-OUT	Q5X164	XP_223871.2
ACETYL-COA TRANSPORTER	PROT MOD	Acetyl-coenzyme A transporter 1 AT-1 Acetyl-CoA transporter Solute carrier family 33 member 1	61190	7768591	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

ACYLCOA:CHOLESTEROL ACYLTRANSFERASE 2	PROT MOD	AcylCoA:Cholesterol Acyltransferase 2	60480	21392392	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	
SURFEIT LOCUS PROTEIN 4 (ERV29)	TRAFFIC	Adult male lung cDNA, RIKEN full-length enriched library, clone:1200010H03 product:surfeit gene 4, full insert sequence Bone marrow macrophage cDNA, RIKEN full-length enriched library, clone:l830028A12 product:surfeit gene 4, full insert sequence Bone marrow macrophage cDNA, RIKEN full-length enriched library, clone:l830026D09 product:surfeit gene 4, full insert sequence Bone marrow macrophage cDNA, RIKEN full-length enriched library, clone:l830012C22 product:surfeit gene 4, full insert sequence Blastocyst blastocyst cDNA, RIKEN full-length enriched library, clone:l1C0027M05 product:surfeit gene 4, full insert sequence	30380	76443685	60957	SOLUBLE		63 23 OUT-IN 92 23 IN-OUT 177 23 OUT-IN 206 20 IN-OUT 240 23 OUT-IN		
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	SOLUBLE	cleavable signal peptide	2 23 IN-OUT	Q8VHE9	
AMINE OXIDASE [FLAVIN-CONTAINING] A	MITOCHONDRIA	Amine oxidase [flavin-containing] A	58870	8170739	101201	SOLUBLE			P21396	
BAP31 (B-CELL RECEPTOR-ASSOCIATED PROTEIN 31)	TRAFFIC	B-cell receptor-associated protein 31	27910	51948420	139656	MEMBRANE	signal anchor	7 23 IN-OUT 44 20 OUT-IN 102 20 IN-OUT	Q6AY58	XP_215226.1
IGD B-CELL RECEPTOR-ASSOCIATED PROTEIN (BAP) 29	TRAFFIC	B-cell receptor-associated protein BAP29	28230	55742817	243481	MEMBRANE	signal anchor	7 23 IN-OUT 44 20 OUT-IN 103 20 IN-OUT	Q5XIU4	XP_216681.1
Qc, RBET1	TETH/DOCK/FUS	BET1 homolog Golgi vesicular membrane-trafficking protein p18 rBET1	13230	9506425	35327	MEMBRANE		96 20 IN-OUT	Q62896	
BAX INHIBITOR-1	SIGNALING	Bax inhibitor-1	26230	456209	23753	MEMBRANE	signal anchor	29 20 IN-OUT 52 20 OUT-IN 84 23 IN-OUT 111 23 OUT-IN 140 23 IN-OUT 166 20 OUT-IN	P55062	
BCL-2 INHIBITOR OF TRANSCRIPTION,	MITOCHONDRIA	Bcl-2 inhibitor of transcription	19530	62078455	215739	SOLUBLE	cleavable signal peptide		Q5XI86	
BRAIN PROTEIN 44	UNKNOWN	Brain protein 44 0-44 protein	14260	730248	80419	SOLUBLE			P38718	
CHOLINE/ETHANOLAMINEPHOSPHOTRANSFERASE 1	PROT MOD	Choline/ethanolamine phosphotransferase 1	46500	56090333	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
CORE BINDING FACTOR BETA SUBUNIT	TRANSCRIPTION	Core binding factor beta	21520	61557239	2681	SOLUBLE			Q66HA7	
CYTOCHROME P450 4A1	DETOXIFICATION	Cytochrome P450 4A1	58210	56047	51420	MEMBRANE	cleavable signal peptide	10 23 OUT-IN 117 23 IN-OUT	P08516	
CYTOCHROME P450 4A8	DETOXIFICATION	Cytochrome P450 4A12 CYP1A12 CYP1A8 P450-KP1 P450-PP1	58520	203757	78089	MEMBRANE	signal anchor	10 23 OUT-IN 116 23 IN-OUT		NP_113793.1
CYTOCHROME P450 4F1	DETOXIFICATION	Cytochrome P450 4F1 CYP1VF1 P450-A3	59870	9665225	134595	MEMBRANE	cleavable signal peptide		P33274	NP_062569.1

CYTOCHROME P450 4F4	DETOXIFICATION	Cytochrome P450 4F4 CYP1VF4	60050	27465575	80281	MEMBRANE	cleavable signal peptide	15 21 OUT-IN 80 23 IN-OUT	P51869	
CYTOCHROME P450 4F6	DETOXIFICATION	Cytochrome P450 4F6 CYP1VF6	61540	23463319	127733	MEMBRANE	cleavable signal peptide		P51871	
CYTOCHROME P450 51A1	DETOXIFICATION	Cytochrome P450 51A1	56710	870754	3732	MEMBRANE	cleavable signal peptide	21 23 IN-OUT	Q64549 Q64654	
CYTOCHROME P450 2A1	DETOXIFICATION	Cytochrome P450 1IA1 (Hepatic steroid hydroxylase 1IA1) gene	56000	51980506	126566	MEMBRANE	cleavable signal peptide	5 20 IN-OUT	Q642C5	
CYTOCHROME P450 2T1	DETOXIFICATION	Cytochrome P450 monooxygenase CYP2T1	55880	19705467	161231	MEMBRANE	cleavable signal peptide	7 18 IN-OUT	Q91Y29	
CYTOCHROME P450 2J3	DETOXIFICATION	Cytochrome P450, family 2, subfamily j, polypeptide 9	57970	59809108	125135	MEMBRANE	cleavable signal peptide	10 23 OUT-IN 75 23 IN-OUT	P51590 Q5EBD7	
CYTOCHROME P450 20A1	DETOXIFICATION	Cytochrome P450, family 20, subfamily A, polypeptide 1	52000	40786491	337678	MEMBRANE	cleavable signal peptide	5 20 IN-OUT	Q6P7D4	
CYTOCHROME P450 2A2	DETOXIFICATION	Cytochrome P450, subfamily 2A, polypeptide 1	56350	6978741	3727	MEMBRANE	cleavable signal peptide	5 20 IN-OUT	P15149 Q5EBB3	
CYTOCHROME B5	DETOXIFICATION	Cytochrome b5	10800	6980893	3890	MEMBRANE			P00173	
CYTOCHROME B5, MITOCHONDRIAL ISOFORM	MITOCHONDRIA	Cytochrome b5 outer mitochondrial membrane isoform precursor	16260	48735409	32875	MEMBRANE		119 23 IN-OUT	P04166 Q9QWG1	
CYTOCHROME C OXIDASE POLYPEPTIDE VB, MITOCHONDRIAL ISOFORM I	MITOCHONDRIA	Cytochrome c oxidase polypeptide Vb, mitochondrial precursor VIa*	13910	53237117	21518	SOLUBLE	cleavable signal peptide		P12075	
CYTOCHROME OXIDASE SUBUNIT II	MITOCHONDRIA	Cytochrome c oxidase subunit 2	25940	5835181	98989	MEMBRANE	signal anchor	26 23 IN-OUT 63 23 OUT-IN	P00406 Q37738 Q5UAJ6 Q80WI7	
CYTOCHROME C OXIDASE SUBUNIT IV ISOFORM 1, MITOCHONDRIAL ISOFORM I	MITOCHONDRIA	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	MEMBRANE		103 18 IN-OUT	P10888	
DAD1 (DEFENDER AGAINST CELL DEATH 1)	PROT MOD	DAD1 protein	12500	48428847	13029	MEMBRANE	signal anchor	29 23 OUT-IN 56 23 IN-OUT 93 20 OUT-IN		
DELTA-5 DESATURASE	PROT MOD	Delta-5 desaturase	52470	16758190	60408	MEMBRANE		134 23 OUT-IN 268 23 IN-OUT 310 23 OUT-IN	Q9EPV4	
DELTA-6 FATTY ACID DESATURASE	METABOLISM	Delta-6 fatty acid desaturase Fatty acid desaturase 2	52380	7513959	36810	MEMBRANE		132 23 OUT-IN 265 20 IN-OUT 304 23 OUT-IN	Q9Z122	
DERLIN-1 (DEGRADATION IN ENDOPLASMIC RETICULUM PROTEIN 1)	PROT SYN/FOLD	Derlin-1 Degradation in endoplasmic reticulum protein Der1-like protein 1	28830	62652445	119910	MEMBRANE		20 23 IN-OUT 57 23 OUT-IN 99 18 IN-OUT 120 18 OUT-IN 157 23 IN-OUT	Q5RKH9	
SIMILAR TO NEURONAL PROTEIN 15.6	UNKNOWN	ENSEMBL:ENSRNOP00000011183 REFSEQ:XP_216785 PREDICTED: similar to neuronal protein 15.6	17630	27669100	192375	MEMBRANE	cleavable signal peptide	85 23 OUT-IN		
ELECTRON TRANSFERRING FLAVOPROTEIN, DEHYDROGENASE 2	MITOCHONDRIA	Electron transfer flavoprotein-ubiquinone oxidoreductase, mitochondrial precursor ETF-QO ETF-ubiquinone oxidoreductase ETF dehydrogenase Electron-transferring-flavoprotein dehydrogenase	68200	52000614	258013	SOLUBLE			Q6UPE1	NP_942037.1
ESTRADIOL 17 BETA-DEHYDROGENASE 2	DETOXIFICATION	Estradiol 17-beta-dehydrogenase 2 17-beta-HSD 2 17-beta-hydroxysteroid dehydrogenase 2	41970	3334165	68349	MEMBRANE	signal anchor	10 20 OUT-IN 41 23 IN-OUT	Q6Z730	
GLYCEROL-3-PHOSPHATE DEHYDROGENASE, MITOCHONDRIAL ISOFORM I	MITOCHONDRIA	Glycerol-3-phosphate dehydrogenase, mitochondrial precursor GPD-M GPDH-M	80970	6980978	3907	MEMBRANE	cleavable signal peptide	7 23 IN-OUT	P35571	
HEME OXYGENASE 2	DETOXIFICATION	Heme oxygenase 2 HO-2	35760	501035	68743	MEMBRANE		295 20 OUT-IN	P23711	

GLUCOSE-6-PHOSPHATASE	METABOLISM	Hypothetical protein	40560	58477247	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	
MG87 PROTEIN	UNKNOWN	Hypothetical protein MG87 MOCO sulphurase C-terminal domain containing 2	38250	38511548	161253	SOLUBLE	cleavable signal peptide	20 20 OUT-IN	O88994		
SIMILAR TO NADH-UBIQUINONE OXIDOREDUCTASE B14	MITOCHONDRIA	Hypothetical protein Ndurf2	14360	57164133	164223	MEMBRANE	signal anchor	57 20 OUT-IN	Q5PQZ9	XP_214989.1	
SIMILAR TO RIKEN CDNA 1810020E01	UNKNOWN	Hypothetical protein RGD1305677	21660	58585236	209082	MEMBRANE		32 23 OUT-IN 66 23 IN-OUT 108 23 OUT-IN	Q5HZA9		
SIMILAR TO RIKEN CDNA 1810014L12	UNKNOWN	Hypothetical protein Tmem97	20950	56605746	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	
IMPLANTATION-ASSOCIATED PROTEIN	UNKNOWN	Implantation-associated protein precursor IAP	37990	6016303	128379	MEMBRANE	cleavable signal peptide	186 20 OUT-IN 212 23 IN-OUT 269 23 OUT-IN 304 18 IN-OUT	O35777		
IODOTYROSINE DEHALOGENASE PROTEIN	UNKNOWN	Iodotyrosine dehalogenase 1 precursor IYD-1	32850	81882575	258458	MEMBRANE	signal anchor	2 19 IN-OUT	Q5BK17		
KINESIN-LIKE PROTEIN KIF15	CYTOSKELETON	Kinesin-like protein KIF15	159600	31745148	166145	SOLUBLE			Q7TN17		
L-GULONOLACTONE OXIDASE	METABOLISM	L-gulonolactone oxidase	50610	204150	104163	MEMBRANE		251 23 IN-OUT	P10867		
RETINOL DEHYDROGENASE 11 (PREDICTED)	DETOXIFICATION	LRRGT00111	44780	62650915	238730	MEMBRANE	signal anchor	41 23 IN-OUT	Q6TUD3		
P34 PROTEIN	PROT SYN/FOLD	Leucine-rich repeat-containing protein 59 Protein p34	34870	81910029	152512	MEMBRANE		244 23 OUT-IN	Q5RJR8 Q63742	XP_213436.1	
LOW MOLECULAR MASS UBIQUINONE-BINDING PROTEIN	PROTEASOME/UBIQUITIN	Low molecular mass ubiquinone-binding protein	9849	68341999	311481	MEMBRANE	signal anchor	46 18 IN-OUT	Q7TQ16		
LYSOSOMAL ACID PHOSPHATASE	LYSOSOME	Lysosomal acid phosphatase precursor LAP	48320	8392842	144356	MEMBRANE	cleavable signal peptide	7 23 IN-OUT 382 23 OUT-IN	P20611		
LYSOSOMAL MEMBRANE GLYCOPROTEIN 1; LYSOSOMA	LYSOSOME	Lysosome-associated membrane glycoprotein 1 precursor	43970	6981144	3967	MEMBRANE	cleavable signal peptide	374 23 OUT-IN	P14562 P97620		
LYSOSOMAL MEMBRANE GLYCOPROTEIN-TYPE B	LYSOSOME	Lysosome-associated membrane glycoprotein 2 precursor	43130	205169	44157	MEMBRANE		361 23 OUT-IN	P17046		
SIMILAR TO MESENCHYMAL STEM CELL PROTEIN DSCD	UNKNOWN	Mesenchymal stem cell protein DSCD75	23750	56090359	259160	SOLUBLE	cleavable signal peptide	5 23 IN-OUT	Q5XIE1	XP_235418.1	
MID-1-RELATED CHLORIDE CHANNEL 2	PLASMA MB	Mid-1-related chloride channel 2	57430	17736804	16130	MEMBRANE	cleavable signal peptide	2 18 IN-OUT 151 23 OUT-IN 182 23 IN-OUT 298 23 OUT-IN	Q8VIF1		
MITOCHONDRIAL DICARBOXYLATE CARRIER	MITOCHONDRIA	Mitochondrial dicarboxylate carrier Solute carrier family 25 (Mitochondrial carrier; dicarboxylate transporter), member 10	31450	51859428	140375	SOLUBLE	cleavable signal peptide		O89035		
MONOGLYCERIDE LIPASE	METABOLISM	Monoglyceride lipase MGL	33500	79158553	76956	SOLUBLE			Q32PZ2 Q8R431		
MYOSIN VIIA	CYTOSKELETON	Myosin VIIA	251100	23618899	217296	SOLUBLE			Q8CJE3		
N-ACYLSPHINGOSINE AMIDOHYDROLASE (ACID CERAM	PROT MOD	N-acylsphingosine amidohydrolase 1	44440	40254747	338609	MEMBRANE	cleavable signal peptide		Q6P7S1		
RE70703P-LIKE PROTEIN	MITOCHONDRIA	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 11 NADH-ubiquinone oxidoreductase subunit B14.7 Complex 1-B14.7 Cl-B14.7	14850	52000746	204895	MEMBRANE		21 23 IN-OUT 58 23 OUT-IN	Q80W89		
NADH-CYTOCHROME B5 REDUCTASE	DETOXIFICATION	NADH-cytochrome b5 reductase	34170	38303959	69488	MEMBRANE	cleavable signal peptide		P20070		
SIMILAR TO HYPOTHETICAL PROTEIN COX4AL	UNKNOWN	Neighbor of Cox4 Predicted	23410	62665359	215440	SOLUBLE			Q5FVL2		

NICASTRIN	PROT MOD	Nicastrin precursor	78400	37081094	116574	MEMBRANE	cleavable signal peptide	669 23 OUT-IN	Q8CGU6 Q8CH12	
SIMILAR TO HYPOTHETICAL PROTEIN MGC18837	UNKNOWN	PREDICTED: hypothetical protein XP_217094	21180	27719651	278444	MEMBRANE	signal anchor	15 23 OUT-IN 57 23 IN-OUT 84 23 OUT-IN 164 23 IN-OUT	UPI000017E10A	
LANOSTEROL SYNTHASE	METABOLISM	PREDICTED: hypothetical protein XP_579502	83280	62665770	317748	SOLUBLE			UPI000019B5F2	
SIMILAR TO PEROXISOME BIOGENESIS FACTOR 16	PEROXISOME	PREDICTED: peroxisome biogenesis factor 16 (predicted)	38600	62645408	235341	SOLUBLE			UPI000017F003	
SIMILAR TO 3,5-CYCLIC-GMP PHOSPHODIESTERASE; RC	SIGNALING	PREDICTED: similar to 3,5-cyclic-GMP phosphodiesterase; rod phosphodiesterase beta subunit	98490	34875832	283891	SOLUBLE			UPI00001D0B24	
RECEPTOR-TRANSPORTING PROTEIN 4 (28 KDA INTERF	UNKNOWN	PREDICTED: similar to 5830458K16Rik protein	27750	34869300	246358	MEMBRANE		222 23 OUT-IN	UPI00001D07A4	
ALPHA-1,3-MANNOSYLTRANSFERASE ALG2	PROT MOD	PREDICTED: similar to Alg2 protein	47320	62648970	161569	SOLUBLE			UPI000017EC6D	
SIMILAR TO CLEFT LIP AND PALATE ASSOCIATED TRANS	PLASMA MB	PREDICTED: similar to Ciptm1 protein	75280	27676422	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	
SIMILAR TO CYSTEINE-RICH WITH EGF-LIKE DOMAINS 1	UNKNOWN	PREDICTED: similar to Cysteine-rich with EGF-like domains 1	45700	81170413	208169	MEMBRANE	cleavable signal peptide	363 20 OUT-IN 387 20 IN-OUT	Q4V7F2 UPI0000180F07	
SIMILAR TO INTERFERON-INDUCIBLE GTPASE	GTPASE	PREDICTED: similar to MGC108823 protein	48270	67846046	244814	MEMBRANE			Q4V797 UPI00001801ED	
SIMILAR TO MANNOSE-P-DOLICHOL UTILIZATION DEFEC	UNKNOWN	PREDICTED: similar to Mannose-P-dolichol utilization defect 1	26550	27673096	252753	MEMBRANE		45 23 OUT-IN 74 23 IN-OUT 106 18 OUT-IN 130 23 IN-OUT 213 23 OUT-IN	UPI000017EAB8	
SIMILAR TO NADH DEHYDROGENASE	MITOCHONDRIA	PREDICTED: similar to NADH dehydrogenase	15640	27660847	304373	MEMBRANE		64 23 OUT-IN	UPI00001C9183	
SIMILAR TO NADH DEHYDROGENASE (UBIQUINONE) 1 B	MITOCHONDRIA	PREDICTED: similar to NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 5	21660	34856800	235872	MEMBRANE	cleavable signal peptide	73 23 IN-OUT	UPI00001CEDC8	
SIMILAR TO NADH DEHYDROGENASE (UBIQUINONE) 1 B	MITOCHONDRIA	PREDICTED: similar to NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 7	16570	34851467	298146	SOLUBLE			UPI00001D141A	
26S PROTEASOME NON-ATPASE REGULATORY SUBUNIT	PROTEASOME/UBIQUITIN	PREDICTED: similar to Proteasome 26S non-ATPase subunit 2	100200	72255509	255113	SOLUBLE			Q4FZT9 UPI00001D07C8	
RAB5A	GTPASE	PREDICTED: similar to RAB5B protein	34900	34862219	218278	MEMBRANE			UPI00001CFB7E	
RAB9-LIKE PROTEIN	GTPASE	PREDICTED: similar to RAB9B, member RAS oncogene family	22720	34881545	240722	MEMBRANE	cleavable signal peptide		UPI000017FB23	
SIMILAR TO RIKEN CDNA 1500009M05	UNKNOWN	PREDICTED: similar to RIKEN cDNA 1500009M05	15290	27696657	235838	MEMBRANE	signal anchor	38 23 OUT-IN	UPI00001805B1	
PREDICTED E3 UBIQUITIN LIGASE	UNKNOWN	PREDICTED: similar to Zinc finger protein 364 (Rabrin	33870	34856089	298059	SOLUBLE			UPI00001827EE	
SIMILAR TO CATHEPSIN 1 PRECURSOR	LYSOSOME	PREDICTED: similar to cathepsin 1 precursor	40980	27681673	266171	SOLUBLE	cleavable signal peptide		UPI00001CC96D	
SIMILAR TO FOLLICULAR LYMPHOMA VARIANT TRANSLC	UNKNOWN	PREDICTED: similar to follicular lymphoma variant translocation 1	36040	34878781	198248	SOLUBLE	cleavable signal peptide	2 23 IN-OUT	UPI00001D09A7	
SIMILAR TO AAQ88810	UNKNOWN	PREDICTED: similar to hypothetical protein	26440	34856654	302143	MEMBRANE	cleavable signal peptide	159 23 OUT-IN	UPI00001831B1	
SIMILAR TO HYPOTHETICAL PROTEIN FLJ20254	UNKNOWN	PREDICTED: similar to hypothetical protein FLJ20254	76570	34863014	234260	MEMBRANE		563 23 OUT-IN	UPI00001CF998	
ILVB (BACTERIAL ACETOLACTATE SYNTHASE)-LIKE ISO	MITOCHONDRIA	PREDICTED: similar to iivB (bacterial acetolactate synthase)-like	68020	34862359	299827	SOLUBLE	cleavable signal peptide	12 23 IN-OUT	UPI00001CFC25	

SIMILAR TO KERATIN COMPLEX 2, BASIC, GENE 7	LIKELY CONTAMINANTS	PREDICTED: similar to keratin complex 2, basic, gene 7	50810	34868200	246071	SOLUBLE				UPI000017FE76	
UNKNOWN3	UNKNOWN	PREDICTED: similar to leucine rich repeat containing 27	17070	34861166	264583	SOLUBLE				UPI00001CEB24	
ATP-BINDING CASSETTE, SUB-FAMILY D (ALD), MEMBER	MITOCHONDRIA	PREDICTED: similar to mALDP	81940	34881747	306584	SOLUBLE	cleavable signal peptide			UPI0000180310	
SIMILAR TO MITOCHONDRIAL INNER MEMBRANE TRANS	MITOCHONDRIA	PREDICTED: similar to mitochondrial inner membrane translocase component Tim17b	18380	34933423	256607	MEMBRANE		111 23 OUT-IN		UPI00001D16C6	
SIMILAR TO HYPOTHETICAL PROTEIN MGC40107	UNKNOWN	PREDICTED: similar to novel protein of unknown function (DUF423) family member	11780	27672946	240888	MEMBRANE	cleavable signal peptide	65 23 IN-OUT 92 20 OUT-IN		UPI0000181FBE	
SIMILAR TO PROTEIN TYROSINE PHOSPHATASE-LIKE PR	SIGNALING	PREDICTED: similar to protein tyrosine phosphatase-like (proline instead of catalytic arginine), member b	15720	34882969	201524	MEMBRANE		15 23 OUT-IN 50 23 IN-OUT 92 23 OUT-IN		UPI00001D1A6E	
SIMILAR TO SEVEN TRANSMEMBRANE DOMAIN PROTEIN	UNKNOWN	PREDICTED: similar to seven transmembrane domain protein	25290	84042519	227176	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		
TETRATRICOPEPTIDE REPEAT PROTEIN 11	UNKNOWN	PREDICTED: similar to tetratricopeptide repeat domain 11	16990	94711371	171146	MEMBRANE		122 23 IN-OUT	P84817 UPI00001CB823		
UBIQUINOL-CYTOCHROME C REDUCTASE BINDING PRO	MITOCHONDRIA	PREDICTED: similar to ubiquinol-cytochrome c reductase binding protein	13560	34866011	293181	SOLUBLE			UPI0000180B5B		
SIMILAR TO NON-CANONICAL UBQUITIN CONJUGATING	PROTEASOME/UBIQUITIN	PREDICTED: similar to ubiquitin-conjugating enzyme E2, J1	30880	34867116	250662	MEMBRANE		246 23 OUT-IN	UPI00001CF637		
ZMPSTE24 METALLOPROTEINASE	PROT MOD	PREDICTED: similar to zinc metalloproteinase, STE24 homolog	54850	34870924	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		
PHOSPHATIDYLETHANOLAMINE N-METHYLTRANSFERAS	PROT MOD	Phosphatidylethanolamine N-methyltransferase	22490	6981348	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		
PHOSPHOINOSITIDE PHOSPHATASE SAC1	PROT MOD	Phosphoinositide phosphatase SAC1	67040	62654523	60561	MEMBRANE		521 23 OUT-IN 550 20 IN-OUT	Q9ES21		
CHLORIDE ION PUMP-ASSOCIATED 55 KDA PROTEIN	PEROXISOME	Prenylcysteine oxidase precursor Chloride ion pump-associated 55 kDa protein	56290	62286984	68714	SOLUBLE	cleavable signal peptide		Q99ML5		
PROSTAGLANDIN G/H SYNTHASE 1 PRECURSOR	BIOSYNTHETIC CARGO	Prostaglandin G/H synthase 1 precursor	69030	603052	103863	SOLUBLE	cleavable signal peptide		Q62731 Q63684 Q63921		
LYRIC	UNKNOWN	Protein LYRIC Lysine-rich CEACAM1 co-isolated protein Metastasis adhesion protein Metadherin	63970	56748899	118984	MEMBRANE	signal anchor	50 23 IN-OUT	Q9Z1W6		
PROTEIN TRANSPORT PROTEIN SEC61 BETA SUBUNIT	PROT SYN/FOLD	Protein transport protein SEC61 beta subunit	9988	27714473	161564	MEMBRANE		68 23 OUT-IN	UPI00001C91F7		
GLUCOSE-6-PHOSPHATASE, TRANSPORT PROTEIN 1	METABOLISM	Putative glycogen storage disease type 1b protein	46310	3929215	78079	MEMBRANE		7 20 IN-OUT 49 23 OUT-IN 78 23 IN-OUT 134 23 OUT-IN 169 20 IN-OUT 220 20 OUT-IN 260 23 IN-OUT 302 21 OUT-IN 329 23 IN-OUT 366 23 OUT-IN 395 23 IN-OUT	Q9Z296		
RAB21	GTPASE	RAB21, member RAS oncogene family	24160	51948448	311263	MEMBRANE	cleavable signal peptide		Q6AXT5		XP_216895.2

RAB9A	GTPASE	RAB9, member RAS oncogene family	22870	16758200	60413	MEMBRANE				UPI0000133184	
SELENOPROTEIN T	UNKNOWN	RIKEN cDNA 2810407C02 gene	15840	62643492	13862	SOLUBLE			22 23 IN-OUT	Q5PQZ8	
MHC CLASS I RT1.AW3 PROTEIN	PLASMA MB	RT1.A1(F) protein	39250	1483574	42127	MEMBRANE			288 23 OUT-IN	Q31257	
RAB11A	GTPASE	Ras-related protein Rab-11A Rab-11	24390	55249677	41486	MEMBRANE					
RAB11B	GTPASE	Ras-related protein Rab-11B	24490	9837357	19693	MEMBRANE					
GTP-BINDING PROTEIN RAB13	GTPASE	Ras-related protein Rab-13	22900	46577668	169821	MEMBRANE				P35286 Q8K3X5	
RAT MHC CLASS I CELL SURFACE ANTIGEN MRNA PREC	PLASMA MB	Rat MHC class I cell surface antigen mRNA. precursor	42090	420280	44652	MEMBRANE	cleavable signal peptide		309 23 OUT-IN	Q31265	
UTROPHIN	CYTOSKELETON	Rattus norvegicus utrophin	391100	6981696	75129	SOLUBLE				O55147	
SIDEROFLEXIN 3	MITOCHONDRIA	Sideroflexin-3	35430	8650526	55276	MEMBRANE			228 23 IN-OUT 265 23 OUT-IN	Q9JHY2	
BRAIN SIGMA RECEPTOR	PLASMA MB	Sigma1 receptor Opioid receptor, sigma 1	25270	6434855	78339	MEMBRANE	cleavable signal peptide		9 23 IN-OUT	Q9R0C9	
ZINC FINGER PROTEIN 183	UNKNOWN	Similar to RIKEN cDNA 2810428C21	38330	62339353	305856	SOLUBLE				Q5PPN1	
RAB5	GTPASE	Small GTP-binding protein rab5	23610	3309068	177419	MEMBRANE				O88565	
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	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	
SQUALENE MONOOXYGENASE	DETOXIFICATION	Squalene monooxygenase Squalene epoxidase SE	64020	8394354	137571	MEMBRANE	cleavable signal peptide		21 23 IN-OUT 517 18 OUT-IN 546 20 IN-OUT	P52020 Q4V8L3	
CYTOCHROME P450 8B1	DETOXIFICATION	Sterol 12-alpha hydroxylase	57520	4587057	129969	MEMBRANE	cleavable signal peptide			Q9WTN7	
3-BETA-HYDROXYSTEROID-DELTA(8),DELTA(7)-ISOMERASE	DETOXIFICATION	Sterol 8-isomerase	26740	8388884	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	
STERYL-SULFATASE	DETOXIFICATION	Steryl-sulfatase precursor Steroid sulfatase Steryl-sulfate sulfohydrolase Arylsulfatase C ASC	62680	6981598	75108	MEMBRANE	cleavable signal peptide		183 23 OUT-IN 212 23 IN-OUT	P15589	
SULFATED GLYCOPROTEIN 1	BIOSYNTHETIC CARGO	Sulfated glycoprotein 1 precursor	61120	92782	75055	SOLUBLE	cleavable signal peptide			P10960 Q62841 Q64190	
SYNAPTOTAGMIN III	TETH/DOCK/FUS	Synaptotagmin III	63340	14210270	19552	MEMBRANE	signal anchor		52 23 IN-OUT	P40748 UPI00000E760E	
TAPASIN	PROT SYN/FOLD	Tapasin Tap-binding protein	50040	46237539	140838	MEMBRANE	cleavable signal peptide		416 23 OUT-IN	Q99JC6	
ARYLACETAMIDE DEACETYLASE	DETOXIFICATION	Tax_Id=10116 ArylAcetAmide deAcetylase	45690	8347733	5958	MEMBRANE	cleavable signal peptide		5 18 IN-OUT 32 23 OUT-IN 105 20 IN-OUT		
LYSOSOME MEMBRANE PROTEIN II	LYSOSOME	Tax_Id=10116 CD36 antigen (collagen type I receptor, thrombospondin receptor)-like 2	54090	38197654	157248	MEMBRANE	cleavable signal peptide		7 23 IN-OUT 434 23 OUT-IN		
GTP-BINDING REGULATORY PROTEIN ALPHA-13 CHAIN	SIGNALING	Tax_Id=10116 Ensembl_locations(Chr-bp):10-98947600 similar to GTP-binding regulatory protein alpha-13 chain - mouse	45080	34875240	194129	SOLUBLE					

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	SOLUBLE			
3 BETA-HYDROXYSTEROID DEHYDROGENASE TYPE III	DETOXIFICATION	Tax_Id=10116 Hydroxy-delta-5-steroid deHydrogenase 3 beta- and steroid delta-isomerase	42210	6981050	3937	SOLUBLE	cleavable signal peptide		
HYPOTHETICAL PROTEIN XP_224972	UNKNOWN	Tax_Id=10116 Hypothetical protein XP_224972	34770	34879125	265270	SOLUBLE		20 23 OUT-IN 54 23	
PROTEIN FAM34A	UNKNOWN	Tax_Id=10116 Hypothetical protein XP_341172	45130	34881421	311586	MEMBRANE		IN-OUT 144 23 OUT-IN 357 23 IN-OUT	
PEROXISOMAL MEMBRANE PROTEIN 2	PEROXISOME	Tax_Id=10116 Peroxisomal membrane Protein 2	22580	585703	11779	MEMBRANE		31 23 OUT-IN 74 23 IN-OUT 111 23 OUT-IN 163 23 IN-OUT	
SIMILAR TO 1-ACYLGLYCEROL-3-PHOSPHATE O-ACYLTRANSFERASE	PROT MOD	Tax_Id=10116 Similar to 1-acylglycerol-3-phosphatase O-acyltransferase 2	31100	34853099	274486	MEMBRANE	cleavable signal peptide	4 18 OUT-IN 28 23 IN-OUT 123 20 OUT-IN	
24-DEHYDROCHOLESTEROL REDUCTASE	DETOXIFICATION	Tax_Id=10116 Similar to 24-dehydrocholesterol reductase	78850	34869959	290771	MEMBRANE	cleavable signal peptide	4 23 OUT-IN 183 18 IN-OUT 210 23 OUT-IN 390 23 IN-OUT	
ARL6IP2	UNKNOWN	Tax_Id=10116 Similar to ARL6IP2	79450	34861996	265779	MEMBRANE		595 23 OUT-IN 619 23 IN-OUT	
ATP-BINDING CASSETTE TRANSPORTER ABCG3 (1)	UNKNOWN	Tax_Id=10116 Similar to ATP-binding cassette transporter ABCG3	95680	34876022	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	
SIMILAR TO ATP-BINDING CASSETTE TRANSPORTER ABCG3	UNKNOWN	Tax_Id=10116 Similar to ATP-binding cassette transporter ABCG3	67490	34879726	242256	MEMBRANE		403 23 OUT-IN 437 23 IN-OUT 495 23 OUT-IN	
SIMILAR TO ARGININE-TRNA-PROTEIN TRANSFERASE 1	PROT SYN/FOLD	Tax_Id=10116 Similar to Arginine-tRNA-protein transferase 1	51870	34859415	229620	SOLUBLE			
SIMILAR TO BC013491 PROTEIN	UNKNOWN	Tax_Id=10116 Similar to BC013491 protein	76140	34856101	235741	SOLUBLE			
SIMILAR TO CG7744-PA	UNKNOWN	Tax_Id=10116 Similar to CG7744-PA	73420	27662674	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 647 23 IN-OUT	
SIMILAR TO DNA SEGMENT, CHR 16, BRIGHAM & WOMEN	UNKNOWN	Tax_Id=10116 Similar to DNA Segment, Chr 16, Brigham & Women's Genetics 1547 expressed	98700	34869279	294937	MEMBRANE		741 23 OUT-IN 776 20 IN-OUT 799 23 OUT-IN	
SIMILAR TO DNA-BINDING PROTEIN RFX1	TRANSCRIPTION	Tax_Id=10116 Similar to DNA-binding protein RFX1	109200	34851453	226741	SOLUBLE			
SIMILAR TO DUB-1	PROTEASOME/UBIQUITIN	Tax_Id=10116 Similar to DUB-1	82370	34859762	228869	SOLUBLE			
DELTA(14)-STEROL REDUCTASE (C-14 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	MEMBRANE		103 23 IN-OUT 129 23 OUT-IN 256 23 IN-OUT 288 18 OUT-IN 356 23 IN-OUT	
SIMILAR TO DNAJ (HSP40) HOMOLOG, SUBFAMILY B, MEMBER 12	PROT SYN/FOLD	Tax_Id=10116 Similar to DnaJ (HSP40) homolog, Subfamily B, member 12	40330	34882652	201409	MEMBRANE		243 23 IN-OUT	
DOWN SYNDROME CELL ADHESION MOLECULE DSCAM1	CYTOSKELETON	Tax_Id=10116 Similar to Down Syndrome cell adhesion molecule DSCAM1	211000	34863302	224702	SOLUBLE			
SIMILAR TO FLJ00354 PROTEIN	UNKNOWN	Tax_Id=10116 Similar to FLJ00354 protein	155900	34861517	210125	SOLUBLE			
HERC2	TRAFFIC	Tax_Id=10116 Similar to Herc2	542900	34856238	254063	SOLUBLE			

SIMILAR TO HYPOTHETICAL PROTEIN 5031404N19	UNKNOWN	Tax_Id=10116 Similar to Hypothetical protein 5031404N19	336600	34867996	239621	SOLUBLE			
SIMILAR TO HOLOCENTRIC CHROMOSOME BINDING PROTEIN 5031404N19	CYTOSKELETON	Tax_Id=10116 Similar to Hypothetical protein KIAA0056	130300	34860470	247233	SOLUBLE			
SIMILAR TO HYPOTHETICAL PROTEIN KIAA0152	UNKNOWN	Tax_Id=10116 Similar to Hypothetical protein KIAA0152	26440	34872654	268830	SOLUBLE	cleavable signal peptide		
INTEGRIN BETA-2 PRECURSOR (CELL SURFACE ADHESION MOLECULE)	CYTOSKELETON	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	MEMBRANE		699 23 OUT-IN	
SIMILAR TO KIAA0303	UNKNOWN	Tax_Id=10116 Similar to KIAA0303	247700	34853530	229044	SOLUBLE	cleavable signal peptide	20 23 IN-OUT	
SIMILAR TO KIAA0980 PROTEIN	UNKNOWN	Tax_Id=10116 Similar to KIAA0980 protein	221500	34858955	230119	SOLUBLE			
SIMILAR TO YEAST NOT1 PROTEIN	UNKNOWN	Tax_Id=10116 Similar to KIAA1007 protein	262700	34851212	247833	SOLUBLE			
SIMILAR TO UBIQUITIN SPECIFIC PROTEASE 36	PROTEASOME/UBIQUITIN	Tax_Id=10116 Similar to KIAA1453 protein	119600	34875569	239514	SOLUBLE			
SELENOPROTEIN 1	PROT MOD	Tax_Id=10116 Similar to KIAA1724 protein	43370	34863046	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	
SIMILAR TO KIAA2019 PROTEIN	UNKNOWN	Tax_Id=10116 Similar to KIAA2019 protein	887700	34935525	217059	SOLUBLE	cleavable signal peptide		
SIMILAR TO M-PHASE PHOSPHOPROTEIN 9; M PHASE PHOSPHOPROTEIN 9	SIGNALING	Tax_Id=10116 Similar to M-phase phosphoprotein 9	48800	34872316	229197	SOLUBLE			
MNT (MYC ANTAGONIST)	TRANSCRIPTION	Tax_Id=10116 Similar to Myc antagonist Mnt	73510	34872745	286820	SOLUBLE			
NOD3	UNKNOWN	Tax_Id=10116 Similar to NOD3	118900	34868757	253799	SOLUBLE			
SIMILAR TO PLU1	UNKNOWN	Tax_Id=10116 Similar to PLU1	129000	34880236	194762	SOLUBLE			
DNA-BINDING PROTEIN PROLACTIN REGULATORY ELEMENT	TRANSCRIPTION	Tax_Id=10116 Similar to Prolactin regulatory element-binding protein	45370	34863006	293599	MEMBRANE		313 20 OUT-IN 391 23 IN-OUT	
SIMILAR TO RIKEN CDNA 0610008C08	UNKNOWN	Tax_Id=10116 Similar to RIKEN cDNA 0610008C08	18820	34880585	277830	MEMBRANE		75 20 OUT-IN	
COILED-COIL-HELIX-COILED-COIL-HELIX DOMAIN CONTAINING	UNKNOWN	Tax_Id=10116 Similar to RIKEN cDNA 0610041L09	37560	34855114	227312	MEMBRANE	cleavable signal peptide	12 23 IN-OUT	
SIMILAR TO RIKEN CDNA 1110007C09	UNKNOWN	Tax_Id=10116 Similar to RIKEN cDNA 1110007C09	22850	34874030	191708	SOLUBLE			
SIMILAR TO ACYL-COA BINDING PROTEIN DOMAIN 5	UNKNOWN	Tax_Id=10116 Similar to RIKEN cDNA 1300014E15	74920	34877442	203301	MEMBRANE		647 23 OUT-IN	
SIMILAR TO RIKEN CDNA 1810063B07 GENE	UNKNOWN	Tax_Id=10116 Similar to RIKEN cDNA 1810063B07 gene	31470	34868966	280249	MEMBRANE		208 23 OUT-IN	
SIMILAR TO RIKEN CDNA 2610318K02	UNKNOWN	Tax_Id=10116 Similar to RIKEN cDNA 2610318K02	17320	34856650	238667	MEMBRANE		70 23 IN-OUT 107 20 OUT-IN	
CYTOCHROME P450 NA2	DETOXIFICATION	Tax_Id=10116 Similar to RIKEN cDNA 4732474A20 gene	70120	34862810	190227	SOLUBLE	signal anchor	21 20 IN-OUT	
SIMILAR TO RIKEN CDNA 4930539I12	UNKNOWN	Tax_Id=10116 Similar to RIKEN cDNA 4930539I12	25260	34932978	295383	SOLUBLE			
SIMILAR TO ARL6IP2	UNKNOWN	Tax_Id=10116 Similar to RIKEN cDNA 5730596K20	61690	34861548	267475	MEMBRANE		456 23 OUT-IN 480 23 IN-OUT	
TC1A	UNKNOWN	Tax_Id=10116 Similar to RIKEN cDNA 9130410M22	23060	34932902	287769	MEMBRANE		147 20 IN-OUT	
SIMILAR TO RIKEN CDNA C330023F11	UNKNOWN	Tax_Id=10116 Similar to RIKEN cDNA C330023F11	105000	34881052	274975	MEMBRANE		821 23 OUT-IN	
SIMILAR TO RIKEN CDNA E330009P21 GENE	UNKNOWN	Tax_Id=10116 Similar to RIKEN cDNA E330009P21 gene	67850	34866429	300320	SOLUBLE			

SLC26A9 ANION TRANSPORTER/EXCHANGE	PLASMA MB	Tax_Id=10116 Similar to Solute carrier family 26, member 9	150000	34879705	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		
SUPT6H	UNKNOWN	Tax_Id=10116 Similar to Supt6h	203400	34872813	219162	SOLUBLE				
TATA BOX BINDING PROTEIN ASSOCIATED FACTOR 148	TRANSCRIPTION	Tax_Id=10116 Similar to TAF148 protein	28070	34881098	248521	SOLUBLE				
SIMILAR TO TAFI140 PROTEIN	PROT SYN/FOLD	Tax_Id=10116 Similar to TAFI140 protein	85530	34876351	313782	SOLUBLE				
SIMILAR TO WD REPEAT MEMBRANE PROTEIN	UNKNOWN	Tax_Id=10116 Similar to WD repeat membrane protein	148000	34877378	284704	SOLUBLE				
SIMILAR TO AXONEMAL HEAVY CHAIN DYNEIN TYPE 3	CYTOSKELETON	Tax_Id=10116 Similar to axonemal heavy chain dynein type 3	258100	34860087	203193	SOLUBLE	signal anchor			
SIMILAR TO BREAKPOINT CLUSTER REGION PROTEIN	NUCLEUS	Tax_Id=10116 Similar to breakpoint cluSier region protein	177200	34852435	289382	SOLUBLE				
CELL PROLIFERATION RELATED PROTEIN CAP	NUCLEUS	Tax_Id=10116 Similar to bromodomain-containing protein BRD4 Short variant	159800	34862361	292562	SOLUBLE				
SIMILAR TO CDNA SEQUENCE BC017158	UNKNOWN	Tax_Id=10116 Similar to cDNA Sequence BC017158	51280	34859365	318242	SOLUBLE				
SIMILAR TO DOLICHYL-PHOSPHATE BETA-GLUCOSYLTRANSFERASE	PROT MOD	Tax_Id=10116 Similar to dolichyl-phoSphate beta-glucoSyltranSferaSe-like	47020	34856938	304061	MEMBRANE	cleavable signal peptide	7 23 IN-OUT		
SIMILAR TO EEA1	TRAFFIC	Tax_Id=10116 Similar to endoSomal protein	204800	34864971	310739	SOLUBLE				
STOMATIN	PLASMA MB	Tax_Id=10116 Similar to erthyrocyte band 7 integral membrane protein, protein 7.2B, Stomatin	61240	34853860	265569	MEMBRANE		291 23 OUT-IN		
LIPOMA HMGIC FUSION PARTNER-LIKE 2 (LHFP12)	UNKNOWN	Tax_Id=10116 Similar to expreSSed Sequence A1447312	40980	34853130	301089	MEMBRANE		169 23 IN-OUT 246 23 OUT-IN 281 23 IN-OUT 329 23 OUT-IN		
CYTOCHROME P450 4V3	DETOXIFICATION	Tax_Id=10116 Similar to family 4 cytochrome P450	66360	34878473	250367	MEMBRANE	cleavable signal peptide	13 23 IN-OUT		
SIMILAR TO GROUP XIII SECRETED PHOSPHOLIPASE A2	BIOSYNTHETIC CARGO	Tax_Id=10116 Similar to group XIII Secreted phoSpholipaSe A2	25660	34882179	272967	SOLUBLE	cleavable signal peptide			
SIMILAR TO HISTIDYL-TRNA SYNTHETASE-LIKE	PROT SYN/FOLD	Tax_Id=10116 Similar to hiStidyl-tRNA SynthetaSe-like	82680	34878791	223302	SOLUBLE				
UNKNOWN PROTEIN (1)	UNKNOWN	Tax_Id=10116 Similar to hypothetical protein	97420	34861994	213193	MEMBRANE		64 20 IN-OUT		
SIMILAR TO SMILE PROTEIN	UNKNOWN	Tax_Id=10116 Similar to hypothetical protein	103500	34864996	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		
SIMILAR TO HYPOTHETICAL PROTEIN BC002942	UNKNOWN	Tax_Id=10116 Similar to hypothetical protein BC002942	96350	34867679	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		

SIMILAR TO HYPOTHETICAL PROTEIN FLJ14681	UNKNOWN	Tax_Id=10116 Similar to hypothetical protein FLJ14681	65310	34856680	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	
SIMILAR TO HYPOTHETICAL PROTEIN FLJ21820	UNKNOWN	Tax_Id=10116 Similar to hypothetical protein FLJ21820	32850	34863103	317090	SOLUBLE			
SIMILAR TO HYPOTHETICAL PROTEIN FLJ32934	UNKNOWN	Tax_Id=10116 Similar to hypothetical protein FLJ32934	110800	34868139	294206	MEMBRANE	signal anchor	21 23 IN-OUT 48 23 OUT-IN 320 23 IN-OUT	
RAB13	GTPASE	Tax_Id=10116 Similar to hypothetical protein MGC23920	24660	34869196	243905	MEMBRANE			
SIMILAR TO HYPOTHETICAL PROTEIN MGC26706	UNKNOWN	Tax_Id=10116 Similar to hypothetical protein MGC26706	19680	34880064	228294	SOLUBLE			
SIMILAR TO INNER MEMBRANE PROTEIN, MITOCHONDRIAL (mitofilin)	MITOCHONDRIA	Tax_Id=10116 Similar to inner membrane protein, mitochondrial (mitofilin)	82360	34855983	247605	SOLUBLE	signal anchor		
SIMILAR TO NUCLEOLAR TRANSCRIPTION FACTOR 1	TRANSCRIPTION	Tax_Id=10116 Similar to methyl-CpG binding domain protein 3-like protein 2	82120	34860516	220741	SOLUBLE			
SIMILAR TO NEUROBLASTOMA-AMPLIFIED PROTEIN	UNKNOWN	Tax_Id=10116 Similar to neuroblastoma-amplified protein	163800	34863169	193119	SOLUBLE			
SIMILAR TO NICOTINAMIDE NUCLEOTIDE TRANSHYDROLYASE	MITOCHONDRIA	Tax_Id=10116 Similar to nicotinamide nucleotide transhydrogenase	120200	34854180	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	
CYTOCHROME P450 NA1	DETOXIFICATION	Tax_Id=10116 Similar to oxySterol 7alpha-hydroxylase	61430	34874781	201379	MEMBRANE	signal anchor		
SIMILAR TO P66 ALPHA HOMOLOG	TRANSCRIPTION	Tax_Id=10116 Similar to p66 alpha homolog	66700	34877681	207944	SOLUBLE			
SIMILAR TO POLYBROMO-1D	NUCLEUS	Tax_Id=10116 Similar to polybromo-1D	197500	34876969	310191	SOLUBLE			
PUTATIVE MANNOSYLTRANSFERASE	PROT MOD	Tax_Id=10116 Similar to putative mannosyltransferase	59900	34867585	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	
SIMILAR TO PUTATIVE PROTEIN, WITH AT LEAST 6 TRANSMEMBRANE DOMAINS, OF ANCIENT ORIGIN (58.5 kD)	UNKNOWN	Tax_Id=10116 Similar to putative protein, with at least 6 transmembrane domains, of ancient origin (58.5 kD) (3N884)	65350	34865136	269355	MEMBRANE		44 18 IN-OUT 114 18 OUT-IN 168 23 IN-OUT	
SIMILAR TO RETINAL SHORT-CHAIN DEHYDROGENASE/REDUCTASE	DETOXIFICATION	Tax_Id=10116 Similar to retinal short-chain dehydrogenase/reductase	43630	34872444	294993	SOLUBLE	cleavable signal peptide	7 23 IN-OUT	
SIMILAR TO VERY LONG-CHAIN ACYL-COA SYNTHETASE	METABOLISM	Tax_Id=10116 Similar to very long-chain acyl-CoA synthetase homolog 1	77170	34932120	234511	SOLUBLE			
VANIN 1	PLASMA MB	Tax_Id=10116 Vanin 1	107100	34852937	310121	MEMBRANE			

TRAM1	PROT SYN/FOLD	Translocation-associated membrane protein 1	43030	81883693	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
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	MEMBRANE		29 23 IN-OUT 55 23 OUT-IN 138 20 IN-OUT 162 23 OUT-IN	Q08013 Q6P6U5	
MEG-2-LIKE PROTEIN	UNKNOWN	Transmembrane and coiled-coil domain-containing protein 1	21170	81882981	91768	MEMBRANE	cleavable signal peptide	10 22 OUT-IN 90 20 IN-OUT	Q5I0H4 Q71DI0	
MITSUGUMIN 23	UNKNOWN	Transmembrane protein 109 precursor Mitsugumin-23 Mg23	26240	81884639	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	Q6AYQ4	XP_342026.1
DB83 PROTEIN	UNKNOWN	Transmembrane protein 33 DB83 protein	27980	4579688	137142	MEMBRANE		27 23 OUT-IN 96 23 IN-OUT 170 23 OUT-IN	Q9Z142	
FIBROUS SHEATH PROTEIN	UNKNOWN	Tsga10 interacting protein	61460	51948361	252663	SOLUBLE			Q66MI6	XP_341992.1
TUMOR NECROSIS FACTOR RECEPTOR TYPE II	PLASMA MB	Tumor necrosis factor receptor type II	45720	16225900	143647	MEMBRANE		243 23 OUT-IN	Q91ZM6	
TYPE I HAIR KERATIN	LIKELY CONTAMINANTS	Type I hair keratin KA27	45970	62656979	230035	SOLUBLE	cleavable signal peptide		Q6IFW1	XP_220966.2
TYPE I HAIR KERATIN KA28	LIKELY CONTAMINANTS	Type I hair keratin KA28	45840	57012440	161846	SOLUBLE	cleavable signal peptide		Q6IFW0	
CYTOKERATIN 17	LIKELY CONTAMINANTS	Type I keratin KA17	48120	71682170	301880	SOLUBLE			Q6IFU8	XP_213478.2
UNCHARACTERIZED HEMATOPOIETIC STEM/PROGENITOR	UNKNOWN	Uncharacterized hematopoietic stem/progenitor cells protein MDS029 homolog	12100	27675590	164032	SOLUBLE	cleavable signal peptide	13 19 OUT-IN	UPI000017E541	
DAPIT PROTEIN	UNKNOWN	Up-regulated during skeletal muscle growth protein 5 Diabetes-associated protein in insulin-sensitive tissues	6408	81868653	171802	MEMBRANE		23 23 OUT-IN	Q9JJW3	
UNCORTIN II	BIOSYNTHETIC CARGO	Urocortin-2 precursor Urocortin II Ucn II	11920	20532276	64824	SOLUBLE	cleavable signal peptide		Q91TWW1	
VACUOLE MEMBRANE PROTEIN 1	UNKNOWN	Vacuole membrane protein 1 Transmembrane protein 49	45900	38197344	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	
ACYL-COA DEHYDROGENASE, VERY-LONG-CHAIN SPEC	MITOCHONDRIA	Very-long-chain specific acyl-CoA dehydrogenase, mitochondrial precursor VLCAD	70750	6978435	3601	SOLUBLE			P45953	
BNIP1 PROTEIN	SIGNALING	Vesicle transport protein SEC20	26170	81867205	111524	MEMBRANE		203 18 IN-OUT	Q8VHI8	
VESICULAR INTEGRAL-MEMBRANE PROTEIN VIP36	TRAFFIC	Vesicular integral-membrane protein VIP36 precursor	40390	27682691	139706	MEMBRANE	cleavable signal peptide	325 23 OUT-IN	UPI0000182448	
VITAMIN K EPOXIDE REDUCTASE COMPLEX SUBUNIT 1	METABOLISM	Vitamin K epoxide reductase complex subunit 1 Vitamin K1 2,3-epoxide reductase subunit 1	17780	62511143	291525	MEMBRANE	cleavable signal peptide	10 20 OUT-IN 101 23 IN-OUT 127 23 OUT-IN	Q6TEK4	
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	MEMBRANE	cleavable signal peptide	17 20 IN-OUT 89 23 OUT-IN 118 18 IN-OUT 140 23 OUT-IN	Q6TEK3	

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:I920191D06 product:voltage-dependent anion channel 1, full insert sequence 17 days embryo kidney cDNA, RIKEN full-length enriched library, clone:I920170K05 product:voltage-dependent anion channel 1, full insert sequence 17 days embryo stomach cDNA, RIKEN full-length enriched library, clone:I920087C06 product:voltage-dependent anion channel 1, full insert sequence 17 days pregnant adult female amnion cDNA, RIKEN full-length enriched library, clone:I920043H09 product:voltage-dependent anion channel 1, full insert sequence	30760	8810245	11037	MEMBRANE				
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	MEMBRANE			P81155 Q9JI32	
VOLTAGE-DEPENDENT ANION-SELECTIVE CHANNEL PROTEIN 3	MITOCHONDRIA	Voltage-dependent anion-selective channel protein 3	30800	15214186	5943	MEMBRANE			Q9ESR2 Q9JI31 Q9R1Z0 Q9WTU2	
[PYRUVATE DEHYDROGENASE [LIPOAMIDE]] KINASE ISOFORM 4	MITOCHONDRIA	[Pyruvate dehydrogenase [lipoamide]] kinase isozyme 4, mitochondrial precursor Pyruvate dehydrogenase kinase isoform 4	46880	2772938	55158	SOLUBLE			O54937	
CYTOCHROME C OXIDASE SUBUNIT VIC	MITOCHONDRIA	cytochrome c oxidase subunit V1c	8455	203519	63749	SOLUBLE	cleavable signal peptide	20 23 OUT-IN		
2,3-OXIDOSQUALENE:LANOSTEROL CYCLASE	DETOXIFICATION	lanosterol synthase	83330	13591981	37206	SOLUBLE			UPI00000E8107	
OLFACTORY RECEPTOR MOR189-2	PLASMA MB	olfactory receptor Olr502	35720	47577533	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	UPI00001C81C9 XP_230110.1	
ROUNDAABOUT (AXON GUIDANCE RECEPTOR, DROSOPHILA) HOMOLOG 2 [RATTUS NORVEGICUS]	BIOSYNTHETIC CARGO	roundabout (axon guidance receptor, Drosophila) homolog 2 [Rattus norvegicus]	176100	34867440	317126	SOLUBLE				
DYSFERLIN (DYSTROPHY ASSOCIATED FER-1 LIKE PROTEIN) (FER-1 LIKE PROTEIN 1) [RATTUS NORVEGICUS]	CALCIUM TRANSBIND	similar to Dysferlin (Dystrophy associated fer-1 like protein) (Fer-1 like protein 1) [Rattus norvegicus]	224600	34856330	229917	MEMBRANE		1905 23 OUT-IN		
SIMILAR TO FK506 BINDING PROTEIN 11	UNKNOWN	similar to FK506 binding protein 11	22190	27664728	316692	MEMBRANE	cleavable signal peptide	155 23 OUT-IN	UPI0000180296	
SIMILAR TO FC FRAGMENT OF IGG BINDING PROTEIN; IGH G Fc BINDING PROTEIN	BIOSYNTHETIC CARGO	similar to Fc fragment of IgG binding protein; IgG Fc binding protein	583400	34855405	285938	SOLUBLE			UPI00001D1AB2	
SIMILAR TO NADH DEHYDROGENASE (UBIQUINONE) 1 BETA SUBCOMPLEX 3	MITOCHONDRIA	similar to NADH dehydrogenase (ubiquinone) 1 beta subcomplex 3	11280	34876452	287362	MEMBRANE		63 23 OUT-IN	UPI00001D11D7	
SIMILAR TO NADH DEHYDROGENASE (UBIQUINONE) 1 BETA SUBCOMPLEX 8	MITOCHONDRIA	similar to NADH dehydrogenase (ubiquinone) 1 beta subcomplex 8	23240	34865197	292854	SOLUBLE	cleavable signal peptide		UPI00001CE61B	
SIMILAR TO NADH DEHYDROGENASE (UBIQUINONE) 1 BETA SUBCOMPLEX, 10, 22KDa; NADH DEHYDROGENASE (UBIQUINONE) 1 BETA SUBCOMPLEX, 10 (22kD, PDSW)	MITOCHONDRIA	similar to NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 10, 22kDa; NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 10 (22kD, PDSW)	20860	27667934	291828	SOLUBLE			UPI0000180E3B	
SIMILAR TO NADH-UBIQUINONE OXIDOREDUCTASE B9 SUBUNIT (COMPLEX I-B9) (CI-B9)	MITOCHONDRIA	similar to NADH-ubiquinone oxidoreductase B9 subunit (Complex I-B9) (CI-B9)	11480	34854466	318196	MEMBRANE	signal anchor	36 23 OUT-IN	UPI00001CE77F	
SIMILAR TO NADH-UBIQUINONE OXIDOREDUCTASE B15 SUBUNIT	MITOCHONDRIA	similar to NADH-ubiquinone oxidoreductase B15 subunit	15060	82617686	192715	MEMBRANE		88 18 OUT-IN	UPI000018052B	

SIMILAR TO PALBH	METABOLISM	similar to PalBH [Rattus norvegicus]	90550	34876995	233624	SOLUBLE				
PROTO-ONCOGENE TYROSINE-PROTEIN KINASE ABL1 (p150) (c-ABL)	SIGNALING	similar to Proto-oncogene tyrosine-protein kinase ABL1 (p150) (c-ABL)	129900	34861357	196976	SOLUBLE			UPI00001CF058	
SIMILAR TO RHBDF1 PROTEIN	PLASMA MB	similar to Rhbdf1 protein	96150	34875782	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	
SIMILAR TO SSC2	UNKNOWN	similar to SSC2	59620	34875179	315186	MEMBRANE		243 23 OUT-IN 277 23 IN-OUT 331 20 OUT-IN 400 23 IN-OUT 466 23 OUT-IN	UPI00001D1137	
LAG1 LONGEVITY ASSURANCE HOMOLOG 2 (TRANSLOC)	UNKNOWN	similar to TRH3	44950	27693564	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	
THIOREDOXIN DOMAIN CONTAINING PROTEIN 1	UNKNOWN	similar to Txndc1 protein	31430	67078422	263888	MEMBRANE	cleavable signal peptide	4 23 OUT-IN 139 23 IN-OUT 181 23 OUT-IN	Q52KJ9 UPI00001CFA1C	
SIMILAR TO B-IND1	SIGNALING	similar to butyrate-induced transcript 1	28810	34864679	236762	MEMBRANE		85 23 IN-OUT 127 20 OUT-IN 167 23 IN-OUT 209 20 OUT-IN	UPI00001CFF0A	
SIMILAR TO CARCINOMA RELATED GENE	UNKNOWN	similar to carcinoma related gene	29600	34871082	257012	MEMBRANE		74 23 IN-OUT 133 20 OUT-IN 173 23 IN-OUT	UPI00001D043F	
ATPASE TYPE 13A1	MITOCHONDRIA	similar to cation-transporting atpase	131900	34877696	273691	MEMBRANE		61 23 IN-OUT 93 23 OUT-IN 439 20 IN-OUT 1042 23 OUT-IN 1090 23 IN-OUT 1127 18 OUT-IN	UPI00001828EA	
SIMILAR TO HISTOCOMPATIBILITY 13; PRESENILIN-LIKE	PLASMA MB	similar to histocompatibility 13; presenilin-like protein 3	41780	34858994	305736	MEMBRANE	signal anchor	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	
SIMILAR TO DISULFIDE ISOMERASE	UNKNOWN	similar to hypothetical protein FLJ22625	35090	34865046	243991	MEMBRANE		283 23 OUT-IN	UPI00001CFC94	
SIMILAR TO HYPOTHETICAL PROTEIN MGC10084	UNKNOWN	similar to hypothetical protein MGC10084	42080	34851552	202821	SOLUBLE			UPI00001D1434	
KERATIN TYPE II, HAIR (B4) - MOUSE	LIKELY CONTAMINANTS	similar to keratin type II, hair (b4) - mouse	105900	34868202	262043	SOLUBLE			UPI00001CFE3A	
SIMILAR TO KERATINOCYTES ASSOCIATED PROTEIN 2	UNKNOWN	similar to keratinocytes associated protein 2	27650	34857976	235658	MEMBRANE		120 23 OUT-IN 154 23 IN-OUT 191 23 OUT-IN	UPI00001CEE83	
SIMILAR TO PEPTIDYLPROLYL ISOMERASE A (CYCLOPHILIN A)	PROT SYN/FOLD	similar to peptidylprolyl isomerase A (cyclophilin A)	9589	34864413	268823	SOLUBLE			UPI00001CFFFF	
RAB20	GTPASE	similar to rab20	32660	34879665	240940	MEMBRANE			UPI00001D1073	
RETINAL SHORT-CHAIN DEHYDROGENASE/REDUCTASE	DETOXIFICATION	similar to retinal short-chain dehydrogenase/reductase 4	38310	34865424	315286	SOLUBLE	cleavable signal peptide	5 18 IN-OUT	UPI00001CF9D7	
TRANSDUCIN (BETA)-LIKE 2	SIGNALING	similar to transducin (beta)-like 2	49610	34873382	294309	SOLUBLE	cleavable signal peptide	9 23 IN-OUT	UPI00001D0815	

MICROSOMAL STRESS 70 PROTEIN ATPASE CORE	PROT SYN/FOLD	stress 70 protein chaperone, microsome-associated, 60kD human homolog	51830	9507149	47300	cleavable signal peptide	7 20 IN-OUT	UPI00000E791F	
SIMILAR TO RIKEN CDNA C230094B15	UNKNOWN	unknown	100200	68051948	301870	cleavable signal peptide		P84551 UPI000001CFF92	
SIMILAR TO RIKEN CDNA 2010107G23	UNKNOWN	unknown	13190	27705930	166454	MEMBRANE	92 23 IN-OUT	UPI0000017E25A	
PANCREATITIS-INDUCED PROTEIN 49	UNKNOWN	unknown	53820	34875854	222783	MEMBRANE	71 23 IN-OUT	UPI000001D0B3C	
5-HYDROXYTRYPTAMINE 6 RECEPTOR	BLOOD + OTHER CELLS	5-hydroxytryptamine 6 receptor	46920	385709	68729	MEMBRANE	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	
ATP-BINDING CASSETTE, SUB-FAMILY B, MEMBER 10	UNKNOWN	ATP-binding cassette, sub-family B (MDR/TAP), member 10 Predicted	77390	58865904	264038	MEMBRANE	136 23 OUT-IN 179 23 IN-OUT 279 23 OUT-IN 358 23 IN-OUT 395 23 OUT-IN	Q5FVL8	
SIMILAR TO MYO-INOSITOL MONOPHOSPHATASE A3	SIGNALING	Ac2-190	60820	34866106	305592	SOLUBLE	7 23 IN-OUT	Q7TPJ5	XP_232655.2
ALPHA-3 TYPE IV COLLAGEN	CYTOSKELETON	Alpha-3 type IV collagen	25400	4481745	120736	SOLUBLE		Q63122	
ALPHA-TOCOPHEROL TRANSFER PROTEIN	METABOLISM	Alpha-tocopherol transfer protein Alpha-TTP	31850	731023	75128	SOLUBLE		P41034	
AMINOPEPTIDASE N	PLASMA MB	Aminopeptidase N	109400	205109	11241	MEMBRANE	12 23 IN-OUT	P15684	
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	MEMBRANE	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	
BASIGIN	PLASMA MB	Basigin precursor	29590	7709992	141056	MEMBRANE	210 23 OUT-IN	P26453 P26453-2 Q6GT74	
BRAIN PROTEIN 44-LIKE PROTEIN	UNKNOWN	Brain protein 44-like protein	12450	66911415	92620	SOLUBLE		P63031 Q4V8N5	
BRAIN SPECIFIC NA+-DEPENDENT INORGANIC PHOSPHATASE	PLASMA MB	Brain specific Na+-dependent inorganic phosphate cotransporter	61670	507415	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	
3 BETA-HYDROXY-DELTA 5-C27-STEROID OXIDOREDUCTASE	DETOXIFICATION	CCA2 protein	37780	2563999	86059	MEMBRANE	252 23 OUT-IN 281 23 IN-OUT	O35048	
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	MEMBRANE	528 23 OUT-IN	O35112 O55172	
CLASP2	CYTOSKELETON	CLIP-associated protein 2 Cytoplasmic linker-associated protein 2	140600	77416394	60531	SOLUBLE		Q99JD4	
CARCINOEMBRYONIC ANTIGEN-RELATED CELL ADHESION MOLECULE	BIOSYNTHETIC CARGO	Carcinoembryonic antigen-related cell adhesion molecule, secreted isoform CEACAM1a-4C2 precursor	51410	76496479	39119	SOLUBLE	cleavable signal peptide	Q9JHL6	
CARNITINE O-PALMITOYLTRANSFERASE II, MITOCHONDRIAL	MITOCHONDRIA	Carnitine O-palmitoyltransferase II, mitochondrial precursor	74110	6978705	3716	SOLUBLE	cleavable signal peptide	P18886 P97781	
MANNOSE 6-PHOSPHATE RECEPTOR	PLASMA MB	Cation-dependent mannose-6-phosphate receptor	31100	56090485	161476	MEMBRANE	189 23 OUT-IN	Q6AY20	XP_232335.1

CD81 PROTEIN	PLASMA MB	CD81 protein	25900	62641476	228910	MEMBRANE	signal anchor	13 23 IN-OUT 62 23 OUT-IN 91 23 IN-OUT 204 23 OUT-IN	Q6F9V1	
PLATELET GLYCOPROTEIN IV	BLOOD + OTHER CELLS	Cell surface protein CD36	52730	6707016	105482	MEMBRANE	signal anchor	7 23 IN-OUT 441 23 OUT-IN	Q925W0	
CYTOCHROME C OXIDASE SUBUNIT I	MITOCHONDRIA	Cytochrome c oxidase subunit I	56980	1332384	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	
DIHYDROOROTATE DEHYDROGENASE, MITOCHONDRIA	MITOCHONDRIA	Dihydroorotate dehydrogenase, mitochondrial precursor	42660	62665239	43490	SOLUBLE	signal anchor	13 20 IN-OUT	Q63707	
DIHYDROXYACETONE KINASE FAMILY PROTEIN	METABOLISM	Dihydroxyacetone kinase Glycerone kinase DHA kinase	59440	85718638	223736	SOLUBLE			Q4KLZ6 UPI00001CEB5D	
ER LUMEN PROTEIN RETAINING RECEPTOR 2 (KDEL RECEPTOR 2)	TRAFFIC	ER lumen protein retaining receptor 2 KDEL receptor 2 KDEL endoplasmic reticulum protein retention receptor 2	24450	61557025	4394	MEMBRANE	cleavable signal peptide	56 23 IN-OUT 116 23 OUT-IN 151 18 IN-OUT 178 23 OUT-IN	Q5U305	
ECTONUCLEOTIDE PYROPHOSPHATASE/PHOSPHODIESTERASE 3	PLASMA MB	Ectonucleotide pyrophosphatase/phosphodiesterase 3	99090	806379	85379	MEMBRANE	signal anchor	23 23 IN-OUT	P97675	
G PROTEIN BETA 2 SUBUNIT	SIGNALING	GNB2 protein	37330	8927570	4326	MEMBRANE				
SIMILAR TO GENETHONIN 1	UNKNOWN	Genethonin-1	35490	62078705	169873	SOLUBLE	cleavable signal peptide	2 23 IN-OUT	Q5FVN1	
GLUTAMYL AMINOPEPTIDASE	PLASMA MB	Glutamyl aminopeptidase	108000	7159085	62885	MEMBRANE	signal anchor	20 20 IN-OUT	P50123 Q64200 Q9JLQ7 Q9JLQ9	
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	MEMBRANE		230 20 IN-OUT	Q62931	
SIMILAR TO RIKEN CDNA C130038N16	UNKNOWN	Golgin subfamily A member 7	15780	81884637	199992	SOLUBLE			Q6AYQ1	XP_341458.1
GUANINE NUCLEOTIDE BINDING PROTEIN (G PROTEIN) 1	SIGNALING	Guanine nucleotide binding protein alpha 12	44070	71089929	37193	SOLUBLE			Q45QM2	
GUANINE NUCLEOTIDE-BINDING PROTEIN G(Q), ALPHA 1	SIGNALING	Guanine nucleotide-binding protein G(q), alpha subunit	42140	7329187	37195	SOLUBLE			P82471 UPI0000167970	
SIMILAR TO KE4	UNKNOWN	H2-K region expressed gene 4, rat orthologue RT1 class I, locus Ke4	49500	62665667	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	Q6MGB4	XP_215320.2
HISTIDINE TRIAD PROTEIN 4	NUCLEUS	Histidine triad protein 4	18890	21654864	153619	SOLUBLE			Q8K3P7	
G PROTEIN BETA 1 SUBUNIT	SIGNALING	Hypothetical protein	37380	51338711	8648	SOLUBLE				
SIMILAR TO RIKEN CDNA 5730568A12	UNKNOWN	Hypothetical protein Ccdc51	42310	62078929	366853	MEMBRANE		354 23 OUT-IN	Q5PPN7	
2400001E08RIK PROTEIN	UNKNOWN	Hypothetical protein MGC72560	17720	40018580	139384	SOLUBLE			Q6P791	
INTEGRIN ALPHA-1 (LAMININ AND COLLAGEN RECEPTOR 1)	PLASMA MB	Integrin alpha-1 precursor Laminin and collagen receptor VLA-1 CD49a antigen	130800	56494	37168	MEMBRANE	cleavable signal peptide	7 23 IN-OUT 1143 23 OUT-IN	P18614	
INTEGRIN BETA3 SUBUNIT	PLASMA MB	Integrin beta3 subunit	86930	24308466	153869	MEMBRANE	cleavable signal peptide	718 23 OUT-IN	Q8R2H2	

INTERCELLULAR ADHESION MOLECULE-1 PRECURSOR	CYTOSKELETON	Intercellular adhesion molecule 1 precursor ICAM-1	60140	6981068	3942	MEMBRANE	cleavable signal peptide	12 20 IN-OUT 493 23 OUT-IN	Q00238	
INTERFERON-INDUCIBLE PROTEIN	UNKNOWN	Interferon-inducible protein	14970	57605	17165	MEMBRANE		58 23 OUT-IN 108 23 IN-OUT	P26376	
JUNCTIONAL ADHESION MOLECULE 1	PLASMA MB	Junctional adhesion molecule A precursor JAM-A Junctional adhesion molecule 1 JAM-1 CD321 antigen	32370	8650528	24909	MEMBRANE	cleavable signal peptide	239 23 OUT-IN	Q9JHY1	
KDEL RECEPTOR	TRAFFIC	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 1 Predicted	24550	62821823	272716	MEMBRANE	cleavable signal peptide	56 23 IN-OUT 116 23 OUT-IN 151 18 IN-OUT 178 23 OUT-IN	Q569A6	
F-BOX ONLY PROTEIN 41	UNKNOWN	Kidney predominant protein NCU-G1	43870	51948424	169834	MEMBRANE	cleavable signal peptide	370 23 OUT-IN	Q68FV6	XP_215623.1
SIMILAR TO PROBABLE POLYPROTEIN-RELATED PROTEIN	UNKNOWN	LRRGT00021	27510	62639574	274007	MEMBRANE		208 23 IN-OUT	Q6TXH8	
SUCCINATE DEHYDROGENASE COMPLEX, SUBUNIT D, IMMEDIATE	MITOCHONDRIA	Liver regeneration-related protein 1	17130	28194393	52861	SOLUBLE	cleavable signal peptide		Q812B0	
LIVER-SPECIFIC TRANSPORT PROTEIN	PLASMA MB	Liver-specific transport protein	58710	529590	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	
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	SOLUBLE	cleavable signal peptide	13 23 IN-OUT	P97849	NP_446032.1
SIMILAR TO KARS PROTEIN	PROT SYN/FOLD	Lysyl-tRNA synthetase	71620	55741637	269157	SOLUBLE			Q5XIM7	XP_214694.2
MAL2A	UNKNOWN	MAL2A Mal, T-cell differentiation protein 2	19200	77157795	166255	MEMBRANE		32 23 IN-OUT 69 23 OUT-IN 103 23 IN-OUT 148 23 OUT-IN	Q7TPB7	
SIMILAR TO METAXIN 2	MITOCHONDRIA	Metaxin 2 Predicted	29720	56605654	203309	SOLUBLE			Q5U1Z9	XP_213632.2
RAC1	GTPASE	Migration-inducing protein 5 Ras-related C3 botulinum toxin substrate 1, isoform Rac1	21450	54607147	111212	MEMBRANE			Q6RUV5	
HSPC242	UNKNOWN	Mitochondrial protein, 18 kDa	18370	55741522	220289	SOLUBLE			Q5XIG9	XP_214075.1
MITOGEN-ACTIVATED PROTEIN KINASE KINASE 1 INTERACTING PROTEIN 1	SIGNALING	Mitogen-activated protein kinase kinase 1-interacting protein 1	13580	81883452	237355	SOLUBLE			Q5UJ204	XP_342348.1
MYOSIN ID	CYTOSKELETON	Myosin Id Myosin heavy chain myr 4	116100	6981242	75002	SOLUBLE				NP_037115.1
NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4	MITOCHONDRIA	NADH-ubiquinone oxidoreductase chain 4 NADH dehydrogenase subunit 4	51800	633984	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	

SIMILAR TO ALG-2	PROT MOD	PREDICTED: similar to ALG-2	21900	34853323	296012	SOLUBLE			UPI0000181133	
BTB (POZ) DOMAIN CONTAINING 14A	UNKNOWN	PREDICTED: similar to BTB (POZ) domain containing 14A	63110	34853069	292782	SOLUBLE			UPI000017F463	
SIMILAR TO METAXIN 1	MITOCHONDRIA	PREDICTED: similar to Metaxin 1, isoform 2	26260	34857966	262377	SOLUBLE			UPI00001CEEAF	
SIMILAR TO MICROSOMAL GLUTATHIONE S-TRANSFERASE 2 (Microsomal GST-II)	DETOXIFICATION	PREDICTED: similar to Microsomal glutathione S-transferase 2 (Microsomal GST-2) (Microsomal GST-II)	16740	27690924	285736	MEMBRANE	cleavable signal peptide	64 23 OUT-IN 106 23 IN-OUT	UPI000017FA90	
SIMILAR TO EVOLUTIONARILY CONSERVED G-PATCH DOMAIN	NUCLEUS	PREDICTED: similar to evolutionarily conserved G-patch domain containing	100900	34855741	271140	SOLUBLE			UPI00001CE817	
SIMILAR TO HYPOTHETICAL PROTEIN FLJ34922	UNKNOWN	PREDICTED: similar to schlafen 5	95800	34872914	315377	SOLUBLE			UPI00001D052F	
PHOSPHOLEMMAN	PLASMA MB	Phospholemman precursor	10470	1916012	78112	MEMBRANE	cleavable signal peptide	2 19 IN-OUT 35 23 OUT-IN	O08589 UPI0000167BB7	
PHOSPHOLIPASE B	PROT MOD	Phospholipase B	161100	2696236	82680	MEMBRANE	cleavable signal peptide	1421 23 OUT-IN	O54728	
PHOSPHOLIPID HYDROPEROXIDE GLUTATHIONE PEROXIDASE	NUCLEUS	Phospholipid hydroperoxide glutathione peroxidase, nuclear	29400	14971097	1198	SOLUBLE			Q91XR8	
SIMILAR TO PROBABLE MITOCHONDRIAL IMPORT RECEPTOR	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	SOLUBLE			Q75Q40	
BARENTSZ- STAUFFEN LIKE	PROT SYN/FOLD	Protein CASC3 Cancer susceptibility candidate gene 3 protein homolog Barentsz protein Btz	75900	46395568	186570	SOLUBLE			Q8K3X0	
GENE RICH CLUSTER, C3F GENE (PREDICTED)	UNKNOWN	Putative O-acyltransferase OAC15 O-acyltransferase domain-containing protein 5	56020	81882826	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	Q5FVN0	
TEX264 PROTEIN	UNKNOWN	Putative secreted protein ZSIG11	33770	56090363	262914	SOLUBLE	cleavable signal peptide	5 23 IN-OUT	Q5XIF0	XP_217261.2
RER1	TRAFFIC	RER1 protein	22990	84781666	32618	MEMBRANE		39 23 OUT-IN 63 23 IN-OUT 140 23 OUT-IN	Q498C8	
RAS-RELATED PROTEIN RAL-A	GTPASE	Ras-related protein Ral-A	23550	54038996	37231	SOLUBLE			P63322	
RHO B	GTPASE	Rho-related GTP-binding protein RhoB precursor H6	22120	51338594	113828	SOLUBLE			P62747	
SCAVENGER RECEPTOR CLASS B MEMBER 1	PLASMA MB	Scavenger receptor class B member 1 SRB1 SR-BI	56960	49904285	38864	MEMBRANE	signal anchor	9 23 IN-OUT 440 23 OUT-IN	P97943	
SECRETORY CARRIER MEMBRANE PROTEIN 3	TRAFFIC	Secretory carrier membrane protein 3	38370	34857962	169836	MEMBRANE		171 23 IN-OUT 198 23 OUT-IN 233 23 IN-OUT 275 23 OUT-IN	UPI00001C7DDF	
SECRETORY CARRIER-ASSOCIATED MEMBRANE PROTEIN 1	TRAFFIC	Secretory carrier-associated membrane protein 1 Secretory carrier membrane protein 1 SCAMP 37	38000	487057	46139	MEMBRANE		154 23 IN-OUT 181 23 OUT-IN 216 23 IN-OUT 258 23 OUT-IN	P56603	
MEGF5	BIOSYNTHETIC CARGO	Slit homolog 3 protein precursor Slit-3 Multiple epidermal growth factor-like domains 5	167800	45477220	75902	SOLUBLE	cleavable signal peptide		O88280	

SOLUTE CARRIER FAMILY 2, FACILITATED GLUCOSE TRANSPORTER 2	PLASMA MB	Solute carrier family 2, facilitated glucose transporter member 2 Glucose transporter type 2, liver	57090	92281	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	
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	MEMBRANE		68 23 IN-OUT 94 23 OUT-IN 184 23 IN-OUT 260 20 OUT-IN 291 23 IN-OUT 346 23 OUT-IN 381 23 IN-OUT 416 23 OUT-IN 476 23 IN-OUT	P45380	
SYNAPTOJANIN 2 BINDING PROTEIN	MITOCHONDRIA	Synaptojanin 2 binding protein	22560	5106930	36071	MEMBRANE		178 23 OUT-IN	Q9WVJ4	
Qa, SYNTAXIN 4	TETH/DOCK/FUS	Syntaxin-4	34210	349321	37252	MEMBRANE		274 23 IN-OUT	Q08850	
NIPSNAP1 PROTEIN (SNAP25-LIKE)	TETH/DOCK/FUS	ENSEMBL:Q5EBA4 ENSEMBL:ENSRNOP00000011158 REFSEQ:XP_001067526;XP_341250 PREDICTED: similar to Protein NipSnap1	33350	34879019	217815	SOLUBLE				
OCIA DOMAIN CONTAINING 1	UNKNOWN	Tax_Id=10116 Ensembl_locations(Chr-bp):14-37304188 similar to RIKEN cDNA 6030432N09	27020	34877284	194680	SOLUBLE				
SIMILAR TO SYNTAXIN 18	TETH/DOCK/FUS	Tax_Id=10116 Ensembl_locations(Chr-bp):14-77957500 similar to Syntaxin 18	49850	34878414	291113	MEMBRANE		410 23 IN-OUT		
PANTOPHYSIN	TRAFFIC	Tax_Id=10116 Ensembl_locations(Chr-bp):6-51287726 similar to synaptophysin-like protein	29400	34864274	311134	MEMBRANE		103 23 OUT-IN 213 23 IN-OUT		
GLUCOKINASE REGULATORY PROTEIN	METABOLISM	Tax_Id=10116 Glucokinase reGulatory protein	68920	6978884	3782	SOLUBLE				
ZINC FINGER PROTEIN 536	UNKNOWN	Tax_Id=10116 Similar to 9630010P11Rik protein	161100	34855819	234438	SOLUBLE	cleavable signal peptide			
TRIBBLES HOMOLOG 2	SIGNALING	Tax_Id=10116 Similar to AW319517 protein	61480	34863190	252701	SOLUBLE				
CYTOCHROME C OXIDASE	MITOCHONDRIA	Tax_Id=10116 Similar to Cox7a2l protein	12650	27716471	268354	MEMBRANE		85 23 IN-OUT		
SIMILAR TO FLJ00375 PROTEIN	UNKNOWN	Tax_Id=10116 Similar to FLJ00375 protein	151500	34867944	192966	SOLUBLE				
INTEGRIN ALPHA 5	PLASMA MB	Tax_Id=10116 Similar to Integrin alpha 5 (fibronectin receptor alpha)	115500	34868649	259355	MEMBRANE	cleavable signal peptide	1007 23 OUT-IN		
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	SOLUBLE				
MYOSIN, HEAVY POLYPEPTIDE 7B, CARDIAC MUSCLE; B	CYTOSKELETON	Tax_Id=10116 Similar to KIAA1512 protein	248700	34859107	211488	SOLUBLE				
UBX DOMAIN CONTAINING 2 (PREDICTED)	UNKNOWN	Tax_Id=10116 Similar to RIKEN cDNA 1300013G12	59080	34879692	246703	SOLUBLE	cleavable signal peptide			
SIMILAR TO RIKEN CDNA 2610020H15	UNKNOWN	Tax_Id=10116 Similar to RIKEN cDNA 2610020H15	71060	34872958	298062	MEMBRANE	signal anchor	4 23 OUT-IN 516 23 IN-OUT		
SIMILAR TO NAD(P) DEPENDENT STEROID DEHYDROGENASE	UNKNOWN	Tax_Id=10116 Similar to RIKEN cDNA 4632417N05	35570	34851797	239422	MEMBRANE		297 23 OUT-IN		
SIMILAR TO RIKEN CDNA 5330415H22	UNKNOWN	Tax_Id=10116 Similar to RIKEN cDNA 5330415H22	44840	34874131	314793	SOLUBLE				
RAB24	GTPASE	Tax_Id=10116 Similar to Rab24 protein	26250	34873657	250158	MEMBRANE				
RIBOSOME-BINDING PROTEIN 1 (RIBOSOME RECEPTOR)	PROT SYN/FOLD	Tax_Id=10116 Similar to RiboSome-binding protein 1 (RiboSome receptor protein) (mRRp)	143300	34856829	244957	SOLUBLE				

SIMILAR TO SPINSTER-LIKE PROTEIN	PLASMA MB	Tax_id=10116 Similar to SpinSter-like protein	115400	34872719	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		
SIMILAR TO ACYLTRANSFERASE FAMILY MEMBER (5G93)	PROT MOD	Tax_id=10116 Similar to acyltranSferaSe family member (5G933)	33640	34862502	237775	MEMBRANE	signal anchor	7 23 IN-OUT		
SIMILAR TO LECTIN, MANNOSE-BINDING 2-LIKE; VIP36-L	TRAFFIC	Tax_id=10116 Similar to lectin, mannoSe-binding 2-like	44440	34875582	221907	MEMBRANE	cleavable signal peptide	358 23 OUT-IN		
SIMILAR TO LEUCINE RICH REPEAT CONTAINING 16	UNKNOWN	Tax_id=10116 Similar to leucine rich repeat containing 16	120700	34876156	290606	SOLUBLE				
SIMILAR TO MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-	PROT MOD	Tax_id=10116 Similar to mannoSyl-oligoSaccharide alpha-1,2-mannoSidaSe	31910	27705330	273814	MEMBRANE	signal anchor	5 23 OUT-IN 44 23 IN-OUT		
SIMILAR TO MITOCHONDRIA-ASSOCIATED GRANULOCY	MITOCHONDRIA	Tax_id=10116 Similar to mitochondria-aSSociated granulocyte macrophage CSF Signaling molecule	13800	27667166	288315	SOLUBLE	cleavable signal peptide			
MYOSIN HEAVY CHAIN 2B	CYTOSKELETON	Tax_id=10116 Similar to myoSin heavy chain 2b	230900	34870888	198855	SOLUBLE		172 20 IN-OUT		
POMFIL1; NEURON NAVIGATOR 3	NUCLEUS	Tax_id=10116 Similar to neuron navigator 3	186800	34864833	278518	SOLUBLE				
NECT1; POLIOVIRUS RELATED RECEPTOR	PLASMA MB	Tax_id=10116 Similar to polioviruS receptor homolog	76950	34855325	279332	MEMBRANE	cleavable signal peptide	351 23 OUT-IN 529 23 IN-OUT		
SIMILAR TO PROLINE DEHYDROGENASE (OXIDASE) 2	METABOLISM	Tax_id=10116 Similar to proline dehydrogenaSe (oxidaSe) 2	51070	34855688	268034	SOLUBLE	cleavable signal peptide			
PUTATIVE PHEROMONE RECEPTOR	PLASMA MB	Tax_id=10116 Similar to putative pheromone receptor	169800	34856154	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		
TORSIN FAMILY 2, MEMBER A	PROT SYN/FOLD	Torsin-2A precursor Torsin family 2 member A	35870	81884643	231792	SOLUBLE	cleavable signal peptide	7 23 IN-OUT	Q6AYR4	XP_342416.1
SIMILAR TO UBIQUITIN CARBOXYL-TERMINAL HYDROLA	PROTEASOME/UBIQUITIN	Ubiquitin specific protease 1 Predicted	87330	62543525	282121	SOLUBLE			Q569C3	

VASOPRESSIN V1B RECEPTOR	PLASMA MB	Vasopressin V1b receptor	47090	968900	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	
APOLIPOPROTEIN C-III	BIOSYNTHETIC CARGO	apolipoprotein C-III precursor - rat	11030	91990	84170	SOLUBLE	cleavable signal peptide			
CLAUDIN-1	PLASMA MB	claudin 1	22870	61889099	318701	MEMBRANE	cleavable signal peptide	5 23 IN-OUT 77 23 OUT-IN 119 23 IN-OUT 161 23 OUT-IN	UPI000021C5DA	
OLFACTORY RECEPTOR OLR406	PLASMA MB	olfactory receptor Olr406	34910	47577295	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
RAP2C	GTPASE	similar to Rap2c protein	13510	34881637	197399	MEMBRANE			UPI00001D184B	
SPINDLIN-LIKE PROTEIN 2	UNKNOWN	similar to Spindlin-like protein 2 (SPIN-2)	32010	34882053	222106	SOLUBLE			UPI00001D18FD	
SIMILAR TO T-CELL ACTIVATION LEUCINE REPEAT-RICH	UNKNOWN	similar to T-cell activation leucine repeat-rich protein	92210	34876057	221702	MEMBRANE	signal anchor	26 20 OUT-IN 120 23 IN-OUT 262 23 OUT-IN 305 23 IN-OUT	UPI000017FFDA	
SIMILAR TO ACTIVATING TRANSCRIPTION FACTOR 7 INT	TRANSCRIPTION	similar to activating transcription factor 7 interacting protein 2	32900	34868272	243423	SOLUBLE			UPI00001D035C	
CONTAINS TRANSMEMBRANE (TM) REGION	UNKNOWN	similar to contains transmembrane (TM) region	30350	34855994	257142	SOLUBLE	cleavable signal peptide	7 20 IN-OUT	UPI00001CE8B6	
ENVOPLAKIN	CYTOSKELETON	similar to envoplakin [Rattus norvegicus]	230800	34875366	316366	SOLUBLE				
INTEGRIN ALPHA2B	PLASMA MB	similar to glycoprotein IIb - rat	274100	34873959	220383	MEMBRANE		2459 23 OUT-IN	UPI00001D060E	
SIMILAR TO HYPOTHETICAL PROTEIN MGC23280	UNKNOWN	similar to hypothetical protein MGC23280	35980	34872804	277215	SOLUBLE	signal anchor	5 23 IN-OUT	UPI00001D0500	
TORSINB PROTEIN	PROT SYN/FOLD	similar to torsinB protein	17860	34853518	202385	SOLUBLE	cleavable signal peptide	13 23 IN-OUT	UPI00001CF0D7	
UNKNOWN EXPRESSED AFTER PARTIAL HEPATICTOMY	UNKNOWN	Ab2-183	51860	33086568	194122	MEMBRANE		196 23 OUT-IN	Q7TP53	
INTERFERON GAMMA INDUCED GTPASE	GTPASE	Ac2-233	161600	34870762	223700	MEMBRANE	cleavable signal peptide		Q7TPJ1	
ALPHA-1,3-MANNOSYL-GLYCOPROTEIN 2-BETA-N-ACETYL	PROT MOD	Alpha-1,3-mannosyl-glycoprotein 2-beta-N-acetylglucosaminyltransferase N-glycosyl-oligosaccharide-glycoprotein N-acetylglucosaminyltransferase I GNT-I GlcNAc-T I	51590	740930	2699	MEMBRANE	cleavable signal peptide	7 23 IN-OUT	Q09325	
AMYLOID-LIKE PROTEIN 2 PRECURSOR	PLASMA MB	Amyloid-like protein 2 precursor	86880	1703345	10860	MEMBRANE	cleavable signal peptide	12 23 IN-OUT 696 23 OUT-IN	P15943	
APOLIPOPROTEIN C-IV PRECURSOR	BIOSYNTHETIC CARGO	Apolipoprotein C-IV precursor Apo-CIV ApoC-IV Apolipoprotein E-linked ECL	10250	2492915	136243	SOLUBLE	cleavable signal peptide		P55797	
BETA-1,4 N-ACETYLGALACTOSAMINYLTRANSFERASE	PROT MOD	Beta-1,4 N-acetylgalactosaminyltransferase 1 (N-acetylneuraminy)-galactosylglucosylceramide GM2/GD synthase GalNAc-T	59280	51858903	137529	MEMBRANE	cleavable signal peptide	7 20 IN-OUT	Q10468	

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	MEMBRANE	signal anchor	19 23 IN-OUT	Q02353	
CCAAT DISPLACEMENT PROTEIN (CASP)	TETH/DOCK/FUS	CCAAT displacement protein	175300	34871708	280644	MEMBRANE			UPI00001D08E2	
CARBOXYPEPTIDASE D	PROT MOD	Carboxypeptidase D precursor Metalloboxypeptidase D gp180	152600	6978699	3713	MEMBRANE	cleavable signal peptide	1298 23 OUT-IN	O35850 Q9JHW1	
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	SOLUBLE			Q5M7T2	
CORE1 UDP-GALACTOSE:N-ACETYLGALACTOSAMINE-ALPHA-1,3-GALACTOSYLTRANSFERASE	PROT MOD	Core1 UDP-galactose:N-acetylgalactosamine-alpha-R beta 1,3-galactosyltransferase	42310	8927166	55277	MEMBRANE	cleavable signal peptide	7 23 IN-OUT	Q8JU05	
DAMP-1 PROTEIN	PLASMA MB	DAMP-1 protein	19670	37693510	116798	MEMBRANE	signal anchor	27 23 OUT-IN 148 23 IN-OUT	Q811A2	
ENDO-ALPHA-D-MANNOSIDASE	PROT MOD	Endo-alpha-D-mannosidase	51670	2642187	133253	MEMBRANE			O35390	
EXOCYST COMPLEX COMPONENT SEC8	TRAFFIC	Exocyst complex component 4 Exocyst complex component Sec8 rSec8	110600	24418659	80377	SOLUBLE			Q62824	
FURIN PRECURSOR	PROT MOD	Furin precursor Paired basic amino acid residue cleaving enzyme PACE Dibasic-processing enzyme Prohormone convertase 3	86650	9506955	47234	MEMBRANE	cleavable signal peptide	5 18 IN-OUT 713 23 OUT-IN	P23377	
GD3 ALPHA 2,8-SIALYLTRANSFERASE	PROT MOD	GD3 alpha 2,8-sialyltransferase	44010	6981540	75089	MEMBRANE	signal anchor	9 23 IN-OUT	P97877	
GPP34 RELATED PROTEIN	TETH/DOCK/FUS	GPP34-related protein	32920	62644637	220058	SOLUBLE			Q66H74	XP_227445.1
TRANSCYTOSIS ASSOCIATED PROTEIN/P115	TETH/DOCK/FUS	General vesicular transport factor p115 Transcytosis-associated protein TAP Vesicle docking protein	107200	538153	71574	SOLUBLE			P41542	
HEME OXYGENASE 1	DETOXIFICATION	Heme oxygenase 1	33010	6981032	3930	MEMBRANE		266 23 OUT-IN	P06762 Q5BK87	
MPS1 PROTEIN	BLOOD + OTHER CELLS	Mpg-1 protein	73330	5052048	176262	SOLUBLE	cleavable signal peptide		Q9WV57	
N-DEACETYLASE/N-SULFOTRANSFERASE (HEPARAN GLUCOSAMINYL) 2 [Rattus norvegicus]	PROT MOD	N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 2 [Rattus norvegicus]	95740	34868948	210844	MEMBRANE	signal anchor	19 23 IN-OUT		
GLYCOPROTEIN-4-BETA-GALACTOSYLTRANSFERASE 2	PROT MOD	PREDICTED: Glycoprotein-4-beta-galactosyltransferase 2	44480	34867143	229568	MEMBRANE	signal anchor		UPI00001CF67C	
SIMILAR TO PL6 PROTEIN	SIGNALING	PREDICTED: similar to PL6 protein	38050	34865897	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	
SIMILAR TO RIKEN CDNA 2510039018	UNKNOWN	PREDICTED: similar to RIKEN cDNA 2510039018	69480	34872456	235860	MEMBRANE	cleavable signal peptide	21 20 IN-OUT 592 23 OUT-IN	UPI00001CF8AF	
SIMILAR TO N-ACETYLLACTOSAMINIDE BETA-1,3-N-ACETYLGLUCOSAMINYLTRANSFERASE bGnT-6	PROT MOD	PREDICTED: similar to beta-1,3-N-acetylglucosaminyltransferase bGnT-6	47470	34861816	304110	MEMBRANE	cleavable signal peptide	7 23 IN-OUT	UPI00001CEB09	
PRENYLATED RAB ACCEPTOR 1	GTPASE	Prenylated Rab acceptor protein 1 PRA1 family protein 1	20640	56404679	78175	MEMBRANE		78 35 IN-OUT 142 23 OUT-IN	O35394	
NATURAL KILLER CELL-SPECIFIC ANTIGEN KLIP1	BLOOD + OTHER CELLS	Protein YIPF3 YIP1 family member 3 Liver regeneration-related protein LRRGT00110	37970	81885839	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
RGPR-P117	UNKNOWN	RGPR-p117	116800	16758344	60469	SOLUBLE			Q925T1	

RHO-GEF 7	GTPASE	Rho guanine nucleotide exchange factor 7 PAK-interacting exchange factor beta Beta-Pix	73140	2865596	2120	SOLUBLE			O55043	
SAR1 HOMOLOG	GTPASE	SAR1A protein promoting vesicle budding from the endoplasmic reticulum	22410	57528164	160782	MEMBRANE			Q5HZY2	
SEC22 HOMOLOG	TETH/DOCK/FUS	Sec22 homolog	28540	16924008	35326	MEMBRANE		188 23 IN-OUT 225 23 OUT-IN	Q62891	
SERINE PROTEASE HEPSIN	PLASMA MB	Serine protease hepsin Serine protease hepsin non-catalytic chain Serine protease hepsin catalytic chain	44930	8393560	51490	MEMBRANE	signal anchor	20 23 IN-OUT	Q05511	
KUNITZ TYPE SERINE PROTEINASE INHIBITOR	BIOSYNTHETIC CARGO	Serine protease inhibitor, Kunitz type 2	21310	40018550	319145	MEMBRANE	cleavable signal peptide	12 18 IN-OUT 139 23 OUT-IN	Q6P796	
SIMILAR TO HPS5 PROTEIN	TRAFFIC	Serum amyloid A 4 Predicted	14970	57164089	301225	SOLUBLE	cleavable signal peptide		Q5M878	XP_344894.1
SOLUBLE CALCIUM-ACTIVATED NUCLEOTIDASE SCAN-1	PROT MOD	Soluble calcium-activated nucleotidase 1 SCAN-1 Apyrase homolog	45660	71153846	231548	MEMBRANE	signal anchor		Q4V8N9 Q8K4Y7	
Qa, SYNTAXIN 5	TETH/DOCK/FUS	Syntaxin-5	34120	631892	78137	MEMBRANE		280 20 IN-OUT	Q08851	
TORID	UNKNOWN	TORID	28490	37590771	161242	MEMBRANE		58 23 OUT-IN 87 23 IN-OUT 124 23 OUT-IN 196 23 IN-OUT	Q925D4	
DENSIN 180	CYTOSKELETON	Tax_Id=10116 Ensembl_locations(Chr-lp):2-256243836 Densin-180 variant D	32790	8570180	24769	SOLUBLE				
SIMILAR TO AMYLOID BETA A4 PRECURSOR PROTEIN-B	UNKNOWN	Tax_Id=10116 Similar to Amyloid beta A4 precursor protein-binding family B member 2 (Fe65-like protein)	53090	34877353	294691	SOLUBLE				
COG5	TETH/DOCK/FUS	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	SOLUBLE				
D-GLUCURONYL C5-EPIMERASE	PROT MOD	Tax_Id=10116 Similar to D-glucuronyl C5-epimeraSe	93260	34863951	299013	MEMBRANE				
SIMILAR TO DNA SEGMENT, CHR 12, ERATO DOI 551, EX	UNKNOWN	Tax_Id=10116 Similar to DNA Segment, Chr 12, ERATO Doi 551, expresSed	130300	34865806	300896	MEMBRANE	signal anchor	54 23 IN-OUT		
GROWTH ARREST SPECIFIC 2	SIGNALING	Tax_Id=10116 Similar to GAS2-related protein	94280	27674275	209378	SOLUBLE			Q08851	
SIMILAR TO KIELIN	SIGNALING	Tax_Id=10116 Similar to Kielin	222300	34855063	263135	SOLUBLE				
FAM13C1	UNKNOWN	Tax_Id=10116 Similar to RIKEN cDNA 1200015N20	81340	34852453	252381	SOLUBLE				
SEROLOGICALLY DEFINED BREAST CANCER ANTIGEN N	UNKNOWN	Tax_Id=10116 Similar to Serologically defined breaSt cancer antigen 84	49120	34860248	275347	MEMBRANE		395 23 OUT-IN		
TRANSCRIPTIONAL CO-ACTIVATOR CRSP7 HOMOLOG	TRANSCRIPTION	Tax_Id=10116 Similar to Transcriptional co-activator CRSP7 homolog	114600	34877464	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		
UDP-N-ACETYL-ALPHA-D-GALACTOSAMINE:POLYPEPTID	PROT MOD	Tax_Id=10116 Similar to UDP-N-acetyl-alpha-D-galactoSamine:polypeptide N-acetylGalactoSaminyltranSferaSe 2	82140	34851891	307730	MEMBRANE				
QUIESCIN Q6-LIKE 1	MITOCHONDRIA	Tax_Id=10116 Similar to cDNA Sequence BC030934	81010	34853075	266866	MEMBRANE	cleavable signal peptide	653 23 OUT-IN		
EXOSTOSES (MULTIPLE) 2	PROT SYN/FOLD	Tax_Id=10116 Similar to exoStoSeS (multiple) 2	93370	34856569	247469	MEMBRANE	signal anchor	24 23 IN-OUT		
SIMILAR TO HYPOTHETICAL PROTEIN DJ667H12.2	UNKNOWN	Tax_Id=10116 Similar to hypothetical protein DJ667H12.2	57230	34865452	195844	SOLUBLE				
PRESENILIN-BINDING PROTEIN	SIGNALING	Tax_Id=10116 Similar to modifier of cell adheSion	227300	34865889	203448	SOLUBLE				
Qb, VTI 1B	TETH/DOCK/FUS	Tax_Id=10116 Similar to veSicle transPort through interaction with t-SNARES 1B homolog	35940	34866243	241548	MEMBRANE				

TRANS-GOLGI NETWORK INTEGRAL MEMBRANE PROTEIN	TRAFFIC	Trans-golgi network protein 1	38300	71051654	31491	MEMBRANE	cleavable signal peptide	304 20 OUT-IN	P19814 Q4G0B6	
TRANSMEMBRANE 9 SUPERFAMILY MEMBER 3	UNKNOWN	Transmembrane 9 superfamily protein member 3 precursor	67540	34862730	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		
INTEGRAL TYPE I PROTEIN P24 GAMMA4	TRAFFIC	Transmembrane emp24 domain-containing protein 3 precursor	25510	62901119	305262	MEMBRANE	cleavable signal peptide	5 19 OUT-IN 183 23 IN-OUT	Q6AY25	XP_217216.2
Qb, VTI 1A	TETH/DOCK/FUS	Vesicle transport through interaction with t-SNAREs homolog 1A	25160	9719420	6158	MEMBRANE		193 23 IN-OUT	Q9JI51 Q9JI51-2	
R, VAMP 3	TETH/DOCK/FUS	Vesicle-associated membrane protein 3 VAMP-3 Synaptobrevin-3 Cellubrevin CEB	11480	56789137	23581	MEMBRANE		83 20 IN-OUT	P63025	
XYLOSYLTRANSFERASE II	PROT MOD	Xylosyltransferase 2 Xylosyltransferase II Peptide O-xylosyltransferase 2	96790	71164811	189334	MEMBRANE	cleavable signal peptide	13 23 IN-OUT	Q9EP10	
AB2-095	UNKNOWN	similar to Ab2-095 [Rattus norvegicus]	79240	34865464	276652	SOLUBLE	cleavable signal peptide			
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	MEMBRANE		122 20 IN-OUT	UPI00001CF09A	
GOLGI COILED COIL PROTEIN GCC185 (GOLGIN FAMILY	TETH/DOCK/FUS	similar to Golgi coiled coil protein GCC185	245100	34852562	311145	SOLUBLE			UPI00001D15EE	
SIMILAR TO KIAA0802 PROTEIN	UNKNOWN	similar to KIAA0802 protein	105700	34878269	270395	SOLUBLE			UPI00001D0324	
ENHANCER FACTOR-1-ALPHA	TRANSCRIPTION	similar to Nuclease sensitive element binding protein 1 (Y box binding protein-1) (Y'-box transcription factor) (Y 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	SOLUBLE			UPI00001D04B3	
SIMILAR TO RIKEN CDNA 1810037C20	UNKNOWN	similar to RIKEN cDNA 1810037C20	39480	34881760	200680	MEMBRANE	signal anchor	7 23 IN-OUT	UPI00001D186F	
TRANSMEMBRANE 9 SUPERFAMILY MEMBER 4	UNKNOWN	similar to Transmembrane 9 superfamily protein member 4	74800	34859018	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	UPI00001CF2C4	
SIMILAR TO WD REPEAT DOMAIN 20 ISOFORM 2	UNKNOWN	similar to WD repeat domain 20 isoform 1	65240	34935498	289309	SOLUBLE			UPI00001CFAC8	
COG2	TETH/DOCK/FUS	similar to component of oligomeric golgi complex 2	41580	34851895	298383	SOLUBLE			UPI00001D14E3	
UDP-GALACTOSE:N-ACETYLGALACTOSAMINEALPHA-1,6-PHOSPHOTRANSFERASE	PROT MOD	similar to contains transmembrane (TM) region and ATP binding region [Rattus norvegicus]	13790	27707476	281048	MEMBRANE				
AXONEMAL DYNEIN HEAVY CHAIN 9	CYTOSKELETON	similar to mKIAA0357 protein	119700	34870863	302855	SOLUBLE			UPI00001D0488	
SYNAPTOGYRIN 2	TETH/DOCK/FUS	synaptogyrin 2	25710	6685963	60460	MEMBRANE		37 23 IN-OUT 79 23 OUT-IN 113 23 IN-OUT 155 23 OUT-IN	UPI0000135B31	

PROBABLE RNA-DEPENDENT HELICASE P68 (DEAD-BOX)	PROT SYN/FOLD	Ddx5	69240	56090441	161883	SOLUBLE				Q6AY11	XP_213508.1
DEVELOPMENTALLY REGULATED GTP-BINDING PROTEIN 1	GTPASE	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	SOLUBLE				Q5I0F0	
DIMETHYLGLYCINE DEHYDROGENASE, MITOCHONDRIA	MITOCHONDRIA	Dimethylglycine dehydrogenase, mitochondrial precursor ME2GLYDH	96050	56689	82662	SOLUBLE	signal anchor			Q63342	NP_620802.1
DNAJ HOMOLOG SUBFAMILY A MEMBER 2	PROT SYN/FOLD	DnaJ homolog subfamily A member 2 RDJ2	45770	2281451	1106	SOLUBLE				O35824	NP_114468.1
EUKARYOTIC TRANSLATION INITIATION FACTOR 2 SUBUNIT 1	PROT SYN/FOLD	EIF2S1 protein	36110	9506571	103	SOLUBLE					
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	SOLUBLE				P04646	
EUKARYOTIC PEPTIDE CHAIN RELEASE FACTOR SUBUNIT 1	PROT SYN/FOLD	Eukaryotic peptide chain release factor subunit 1 eRF1 Eukaryotic release factor 1	49030	68565348	41501	SOLUBLE					
FICOLIN 1 PRECURSOR	BIOSYNTHETIC CARGO	Ficolin-1 precursor Collagen/fibrinogen domain-containing protein 1 Ficolin-A Ficolin A M-Ficolin	36630	6714560	75919	SOLUBLE	cleavable signal peptide			Q9WTS8	NP_112638.1
GLYCEROL KINASE	SIGNALING	Glycerol Kinase ATP:glycerol 3-phosphotransferase Glycerokinase GK ATP-stimulated glucocorticoid-receptor translocation promoter ASTP	57480	433211	18015	SOLUBLE	cleavable signal peptide			Q63060	
HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN K	NUCLEUS	HNRPK protein Heterogeneous nuclear ribonucleoprotein K	51030	38197650	72151	SOLUBLE				Q5D059	
RIBONUCLEOPROTEIN F	NUCLEUS	Heterogeneous nuclear ribonucleoprotein F	45730	82546819	17327	SOLUBLE				Q794E4	
HISTONE H1.2	NUCLEUS	Histone H1.2	21990	444788	72598	SOLUBLE				P15865	
HYALURONAN SYNTHASE 1	PROT MOD	Hyaluronan synthase 1	65730	27229296	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	
P55	UNKNOWN	Hypothetical protein D10Wsu52e	55250	50926851	54494	SOLUBLE				Q6AYT3	XP_343186.1
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	SOLUBLE				Q5M7V2 Q63279 Q6S6J4	
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	SOLUBLE				Q64602	
60S RIBOSOMAL PROTEIN L35	PROT SYN/FOLD	LOC495749 protein	14550	57702	103229	SOLUBLE					XP_216052.1
PUTATIVE RNA BINDING PROTEIN 1	NUCLEUS	LRRGT00079	70520	37361844	231196	SOLUBLE				Q6TUG5	
MITOCHONDRIAL LON PROTEASE HOMOLOG	MITOCHONDRIA	Lon	105800	19173766	140367	SOLUBLE	cleavable signal peptide			Q924S5	
MYELIN BASIC PROTEIN S	BIOSYNTHETIC CARGO	Myelin basic protein S	21500	70166245	3277	SOLUBLE				P02688	

MYOSIN LIGHT CHAIN ALKALI, SMOOTH-MUSCLE ISOFORM 2	CYTOSKELETON	Myosin, light polypeptide 6, alkali, smooth muscle and non-muscle, isoform 2	16960	34862212	69375	SOLUBLE				
SIMILAR TO MITOGEN-ACTIVATED PROTEIN KINASE KINASE 7	SIGNALING	PREDICTED: mitogen-activated protein kinase kinase kinase 7 interacting protein 2 (predicted)	76330	90108450	226905	SOLUBLE			Q5U303 UPI0000182B91	
60S RIBOSOMAL PROTEIN L7	PROT SYN/FOLD	PREDICTED: similar to 60S ribosomal protein L7	30310	27660180	154516	SOLUBLE			UPI00001C8FA0	
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	SOLUBLE			UPI0000182BFD	
DEAD/H BOX POLYPEPTIDE 36 PROTEIN	UNKNOWN	PREDICTED: similar to DEAD/H box polypeptide 36 protein	113800	34856989	204574	SOLUBLE			UPI00001CEE14	
SIMILAR TO MAP KINASE KINASE 3B	SIGNALING	PREDICTED: similar to MAP kinase kinase 3b	47090	34870816	238438	SOLUBLE	cleavable signal peptide		UPI00001D045A	
SIMILAR TO RIKEN CDNA 1700027N10	UNKNOWN	PREDICTED: similar to RIKEN cDNA 1700027N10	31220	34874480	246387	SOLUBLE	cleavable signal peptide		UPI000017FF69	
HYPOTHETICAL PROTEIN FLJ14494	UNKNOWN	PREDICTED: similar to RNA pseudouridylyate synthase domain containing 4	52220	34863026	266306	SOLUBLE			UPI00001CFF23	
SPLICING FACTOR, ARGININE/SERINE-RICH 7, 35 kDa	PROT SYN/FOLD	PREDICTED: similar to Sfrs7 protein	20570	34862692	226986	SOLUBLE			UPI00001CFC47	
SIMILAR TO KIAA1074 PROTEIN	UNKNOWN	PREDICTED: similar to ankyrin repeat domain 26	80070	34877470	202835	MEMBRANE		674 20 OUT-IN	UPI00001D1223	
PHOSPHOFRUCTOKINASE, LIVER, B-TYPE	METABOLISM	Phosphofructokinase, liver, B-type	85300	38197562	318741	SOLUBLE			Q6P783	
POLY(RC)-BINDING PROTEIN 2 ALPHA-CP2 HNRNP-E2	NUCLEUS	Poly(RC)-binding protein 2 Alpha-CP2 hnRNP-E2	38580	61557337	2515	SOLUBLE			Q6AYU5	
ALG-2 INTERACTING PROTEIN 1	SIGNALING	Programmed cell death 6-interacting protein ALG-2-interacting protein 1	44060	6319138	157870	SOLUBLE			Q9QZA2	
RECEPTOR-TYPE PROTEIN-TYROSINE PHOSPHATASE V PRECURSOR	SIGNALING	Receptor-type tyrosine-protein phosphatase V precursor Embryonic stem cell protein-tyrosine phosphatase ES cell phosphatase Osteotesticular protein-tyrosine phosphatase OST-PTP	187300	725329	59236	SOLUBLE	cleavable signal peptide		Q64612	
60S RIBOSOMAL PROTEIN L17	PROT SYN/FOLD	Ribosomal protein L17	21400	71051098	139425	SOLUBLE			Q4G093	
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	SOLUBLE			P84100	
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	SOLUBLE			P62902	
60S RIBOSOMAL PROTEIN L32	PROT SYN/FOLD	Ribosomal protein L32	15860	6981482	4819	SOLUBLE			Q63ZV8	
RYANODINE RECEPTOR TYPE II	CALCIUM TRANS/BIND	Ryanodine receptor type II	62520	1930136	19063	MEMBRANE		174 20 IN-OUT 247 23 OUT-IN 386 23 IN-OUT 443 23 OUT-IN 524 20 IN-OUT	Q08661	
SMALL NUCLEAR RIBONUCLEOPROTEIN SM D1	NUCLEUS	Small nuclear ribonucleoprotein Sm D1 snRNP core protein D1 Sm-D1 Sm-D autoantigen	13280	34877889	3858	SOLUBLE				
SODIUM/CALCIUM EXCHANGER 1 PRECURSOR	CALCIUM TRANS/BIND	Sodium/calcium exchanger 1 precursor	108100	57209	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	
SYNAPTOTAGMIN X	TETH/DOCK/FUS	Synaptotagmin X	56410	7441534	2110	MEMBRANE		55 23 IN-OUT	Q08625	

GLUTAREDOXIN	PROT SYN/FOLD	Tax_Id=10116 Ensembl_locations(Chr-bp):2-2908047 glutaredoxin 1 (thioltransferase)	11880	38181944	246362	SOLUBLE			
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	SOLUBLE			
GLUTATHIONE S-TRANSFERASE, MITOCHONDRIAL	MITOCHONDRIA	Tax_Id=10116 Glutathione S-transferase, mitochondria	25490	42543496	110024	SOLUBLE			
HYPOTHETICAL PROTEIN XP_231157	UNKNOWN	Tax_Id=10116 Hypothetical protein XP_231157	115700	34853657	209125	SOLUBLE	cleavable signal peptide		
SIMILAR TO 60S RIBOSOMAL PROTEIN L19	PROT SYN/FOLD	Tax_Id=10116 Similar to 60S ribosomal protein L19	24360	34881946	232570	SOLUBLE			
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	SOLUBLE			
SIMILAR TO B AGGRESSIVE LYMPHOMA	UNKNOWN	Tax_Id=10116 Similar to B aggressive lymphoma	106500	34869208	269562	SOLUBLE			
HISTONE H3	NUCLEUS	Tax_Id=10116 Similar to CG31613-PA	101500	34876364	249977	SOLUBLE			
SIMILAR TO DNA SEGMENT ON CHROMOSOME X AND Y	UNKNOWN	Tax_Id=10116 Similar to DNA Segment on chromosome X and Y (unique) 155 expressed Sequence	112100	34932999	262653	SOLUBLE			
SIMILAR TO ERA G-PROTEIN-LIKE 1; GTPASE, HUMAN HOMOLOG	GTPASE	Tax_Id=10116 Similar to Era G-protein-like 1	52770	34873187	218788	SOLUBLE			
SIMILAR TO ADIPONUTRIN	UNKNOWN	Tax_Id=10116 Similar to GS2 like	50130	34867787	278047	SOLUBLE			
SIMILAR TO GTP BINDING PROTEIN	UNKNOWN	Tax_Id=10116 Similar to GTP binding protein	36860	34859732	225450	SOLUBLE			
SIMILAR TO IDN3 PROTEIN ISOFORM A	UNKNOWN	Tax_Id=10116 Similar to IDN3 protein isoform A	297800	34854352	234794	SOLUBLE			
RIKEN CDNA 2410066K11	UNKNOWN	Tax_Id=10116 Similar to KIAA1992 protein	132600	34854749	269290	SOLUBLE			
MYOSIN BINDING PROTEIN C, FAST-TYPE	CYTOSKELETON	Tax_Id=10116 Similar to MyoSin binding protein C, fast-type	81100	34856029	217827	SOLUBLE			
NUCLEAR FACTOR OF ACTIVATED T-CELLS, CYTOPLASMIC	TRANSCRIPTION	Tax_Id=10116 Similar to NFAT1-A	124800	34860796	295712	SOLUBLE			
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	SOLUBLE			
PROBABLE RNA-DEPENDENT HELICASE P72 (DEAD-BOX)	PROT SYN/FOLD	Tax_Id=10116 Similar to Probable RNA-dependent helicase p72 (DEAD-box protein p72) (DEAD-box protein 17)	73940	34866944	195895	SOLUBLE			
SIMILAR TO HOMOPROTOPORTECHUATE CATABOLISM B	METABOLISM	Tax_Id=10116 Similar to RIKEN cDNA 1110025H10	26400	34871118	269702	SOLUBLE			
PHTF1 PROTEIN	UNKNOWN	Tax_Id=10116 Similar to RIKEN cDNA 1110054G21	101700	34854019	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		
PROBABLE UPF0334 KINASE-LIKE PROTEIN	UNKNOWN	Tax_Id=10116 Similar to RIKEN cDNA 2310079N02	20810	34851911	222133	SOLUBLE			
SIMILAR TO RIKEN CDNA 2610207116	UNKNOWN	Tax_Id=10116 Similar to RIKEN cDNA 2610207116	122600	34868438	250916	SOLUBLE	cleavable signal peptide		
SIMILAR TO RIKEN CDNA 2810405J04	UNKNOWN	Tax_Id=10116 Similar to RIKEN cDNA 2810405J04	61290	34862460	198258	SOLUBLE			
SIMILAR TO EXOCYST COMPLEX COMPONENT SEC6	TRAFFIC	Tax_Id=10116 Similar to RIKEN cDNA E430013E20 gene	81050	34851597	259373	SOLUBLE			
GCN1 GENERAL CONTROL OF AMINO-ACID SYNTHESIS	PROT SYN/FOLD	Tax_Id=10116 Similar to RIKEN cDNA G431004K08	303100	34872627	241842	SOLUBLE	cleavable signal peptide		
RNA HELICASE	NUCLEUS	Tax_Id=10116 Similar to RNA helicase	80570	34933204	287882	SOLUBLE			
SIMILAR TO RNA HELICASE FAMILY	NUCLEUS	Tax_Id=10116 Similar to RNA helicase family	238800	34853214	288172	SOLUBLE			
SIMILAR TO SPECTRIN BETA CHAIN, BRAIN 4 (SPECTRIN)	CYTOSKELETON	Tax_Id=10116 Similar to Spectrin beta chain, brain 4 (Spectrin, non-erythroid beta chain 4) (Beta-V Spectrin) (BSPECV)	402100	34856723	275665	SOLUBLE			

PALLIDIN	TRAFFIC	Tax_Id=10116 Similar to Sulfide quinone reductase-like	78570	34856819	285775	SOLUBLE			
SIMILAR TO ALPHA 3 TYPE VI COLLAGEN ISOFORM 1 PRECURSOR	BIOSYNTHETIC CARGO	Tax_Id=10116 Similar to alpha 3 type VI collagen isoform 1 precursor	357700	34877775	307227	SOLUBLE	cleavable signal peptide		
SIMILAR TO ALPHA-TUBULIN	CYTOSKELETON	Tax_Id=10116 Similar to alpha-tubulin	45240	34852918	268840	SOLUBLE			
SIMILAR TO BULLOUS PEMPHIGOID ANTIGEN 1-B	CYTOSKELETON	Tax_Id=10116 Similar to bullous pemphigoid antigen 1-b	1087000	34874618	233230	SOLUBLE			
CARBOHYDRATE (CHONDROITIN) SYNTHASE 2	PROT MOD	Tax_Id=10116 Similar to carbohydrate (chondroitin) synthase 2	65060	27681143	278143	MEMBRANE			
SIMILAR TO CHROMOSOME 17 OPEN READING FRAME 2	UNKNOWN	Tax_Id=10116 Similar to chromosome 17 open reading frame 27	668500	34875599	199223	SOLUBLE			
COLLAGEN ALPHA1 TYPE VI-PRECURSOR	BIOSYNTHETIC CARGO	Tax_Id=10116 Similar to collagen alpha1 type VI-precursor	112800	34852376	201969	SOLUBLE	cleavable signal peptide		
SIMILAR TO DEVELOPMENT- AND DIFFERENTIATION-ENHANCING FACTOR 2	SIGNALING	Tax_Id=10116 Similar to development- and differentiation-enhancing factor 2	119200	34863212	230447	SOLUBLE			
SIMILAR TO FORMIN-LIKE PROTEIN	CYTOSKELETON	Tax_Id=10116 Similar to formin-like protein	123000	34873916	239048	SOLUBLE			
GLUTARYL-COA DEHYDROGENASE	MITOCHONDRIA	Tax_Id=10116 Similar to glutaryl-CoA dehydrogenase precursor	49330	34851534	270372	SOLUBLE			
SIMILAR TO ALPHA TUBULIN	CYTOSKELETON	Tax_Id=10116 Similar to hypothetical protein FLJ21665	52020	34876595	213091	SOLUBLE			
SIMILAR TO HYPOTHETICAL PROTEIN FLJ32784	UNKNOWN	Tax_Id=10116 Similar to hypothetical protein FLJ32784	138000	34872260	228083	SOLUBLE			
SIMILAR TO INTERLEUKIN-1 RECEPTOR ASSOCIATED KINASE 4	SIGNALING	Tax_Id=10116 Similar to interleukin-1 receptor associated kinase 4	57750	34867776	244001	SOLUBLE			
SIMILAR TO MYOCARDIN-RELATED TRANSCRIPTION FACTOR A	TRANSCRIPTION	Tax_Id=10116 Similar to myocardin-related transcription factor A	123400	34867047	275363	SOLUBLE			
SIMILAR TO NUCLEAR DOMAIN 10 PROTEIN	NUCLEUS	Tax_Id=10116 Similar to nuclear domain 10 protein	85380	34873520	275895	SOLUBLE			
PROCOLLAGEN, TYPE VI, ALPHA 2	BIOSYNTHETIC CARGO	Tax_Id=10116 Similar to procollagen, type VI, alpha 2	122100	34852378	258657	SOLUBLE	cleavable signal peptide		
SIMILAR TO XYLULOKINASE HOMOLOG; XYLULOKINASE	METABOLISM	Tax_Id=10116 Similar to xylulokinase homolog	66490	34866669	229118	SOLUBLE			
TITIN	UNKNOWN	Tax_Id=10116 Titin	1375000	34856454	293312	SOLUBLE			
VON WILLEBRAND FACTOR	BIOSYNTHETIC CARGO	Tax_Id=10116 Von Willebrand factor	289700	34858467	251407	SOLUBLE			
TRANSLATION INITIATION FACTOR EIF-2B BETA SUBUNIT	PROT SYN/FOLD	Translation initiation factor eIF-2B beta subunit	38880	2494306	112447	SOLUBLE		O08956 Q62818	
TRYPTOPHAN 2,3-DIOXYGENASE	METABOLISM	Tryptophan 2,3-dioxygenase	47860	59809151	11402	SOLUBLE		P21643 Q5EBC2 Q6LBW3	
TYPE I KERATIN KA22	LIKELY CONTAMINANTS	Type I keratin KA22	50210	57012446	161849	SOLUBLE		Q6IFU7	
UDP-GLUCOSE 6-DEHYDROGENASE	METABOLISM	UDP-glucose 6-dehydrogenase UDP-Glc dehydrogenase UDP-GlcDH UDPGDH	54890	6136118	75904	SOLUBLE		O70199	
60S RIBOSOMAL PROTEIN L38	PROT SYN/FOLD	Zgc:92860	8218	74354458	4821	SOLUBLE		Q3T1G5	
HYPOTHETICAL PROTEIN XP_343009	UNKNOWN	hypothetical protein XP_343009	87580	34862025	301974	SOLUBLE		UPI00001CF92A	
HYPOTHETICAL PROTEIN XP_347082	UNKNOWN	hypothetical protein XP_347082	10270	34862408	222136	SOLUBLE		UPI00001CFC5E	
PEROXISOME ASSEMBLY FACTOR-2	PEROXISOME	peroxisome assembly factor-2 [Rattus norvegicus]	104300	2911135	169183	SOLUBLE	cleavable signal peptide		
PROSTAGLANDIN E RECEPTOR 3; RAT KIDNEY PROSTATE	BIOSYNTHETIC CARGO	prostaglandin E receptor 3 (subtype EP3)	39630	6981434	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
SIMILAR TO 3000004C01RIK PROTEIN	UNKNOWN	similar to 3000004C01Rik protein	31860	34881333	281752	SOLUBLE	cleavable signal peptide	UPI00001D17BB	
SIMILAR TO 60S RIBOSOMAL PROTEIN L7	PROT SYN/FOLD	similar to 60S RIBOSOMAL PROTEIN L7	50520	34877407	254343	SOLUBLE	cleavable signal peptide	UPI00001D0BC3	

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	SOLUBLE				
SIMILAR TO APOPTOSIS INHIBITOR 5	SIGNALING	similar to Apoptosis inhibitor 5	36870	34878251	281550	SOLUBLE			UPI00001D125A	
EUKARYOTIC TRANSLATION INITIATION FACTOR 3 SUBUNIT 6	PROT SYN/FOLD	similar to Eukaryotic translation initiation factor 3 subunit 6 interacting protein (HSPC021/HSPC025)	66710	34866934	266163	SOLUBLE			UPI00001CFD5A	
RABCONNECTIN	TRAFFIC	similar to KIAA0856 protein	278000	34863411	215246	SOLUBLE			UPI00001CFF74	
SIMILAR TO POTENTIAL HELICASE MOV-10	NUCLEUS	similar to Potential helicase MOV-10 [Rattus norvegicus]	73800	27660592	154542	SOLUBLE				
SIMILAR TO RAS PROTEIN ACTIVATOR LIKE 2 ISOFORM 1	GTPASE	similar to RAS protein activator like 2 isoform 2; Ras GTPase activating protein-like; Ras protein activator like 1	34760	34880852	276474	SOLUBLE			UPI00001D0A7E	
PUTATIVE RNA BINDING PROTEIN, PARTNER TO NOB1	UNKNOWN	similar to RIKEN cDNA 1810003N24	31780	34873957	230313	SOLUBLE			UPI00001D0622	
SIMILAR TO RIKEN CDNA 2410002O22 GENE	UNKNOWN	similar to RIKEN cDNA 2410002O22 gene [Rattus norvegicus]	22220	34853743	269534	SOLUBLE				
DEOXYRIBOSE-PHOSPHATE ALDOLASE-LIKE	METABOLISM	similar to RIKEN cDNA 2500002K03 gene	36950	34858565	307749	SOLUBLE			UPI00001CF5C0	
SIMILAR TO RIKEN CDNA A930015D22	UNKNOWN	similar to RIKEN cDNA A930015D22	48920	34861327	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	
METHIONINE ADENOSYL TRANSFERASE II ALPHA SUBUNIT	METABOLISM	similar to RIKEN cDNA D630045P18	37180	34853482	239818	SOLUBLE			UPI00001CF419	
SUCCINYL-COA LIGASE [ADP-FORMING] BETA-CHAIN, MITOCHONDRIA	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	SOLUBLE				
SUCCINYL-COA LIGASE [GDP-FORMING] BETA-CHAIN, MITOCHONDRIA	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	SOLUBLE			UPI00001CF541	
SIMILAR TO APOPTOSIS-INDUCING FACTOR (AIF)-HOMOLOGOUS MITOCHONDRION-ASSOCIATED INDUCER OF DEATH; p53-RESPONSIVE GENE 3	MITOCHONDRIA	similar to apoptosis-inducing factor (AIF)-homologous mitochondrion-associated inducer of death; p53-responsive gene 3 [Rattus norvegicus]	14880	34852510	209377	SOLUBLE				
PROLINE DEHYDROGENASE	METABOLISM	similar to brain and kidney proline oxidase 2	30660	34869794	301508	SOLUBLE			UPI00001D07EC	
SIMILAR TO CYTOKERATIN ENDOA - MOUSE	LIKELY CONTAMINANTS	similar to cytokeratin EndoA - mouse	53620	34881863	292930	SOLUBLE			UPI00001D186E	
SIMILAR TO EXPRESSED SEQUENCE AU041483	UNKNOWN	similar to expressed sequence AU041483	63520	34869200	245616	MEMBRANE	172 23 IN-OUT		UPI00001D0769	
SIMILAR TO RNA BINDING PROTEINS	UNKNOWN	similar to hepatocellular carcinoma autoantigen	13340	34869447	272734	SOLUBLE			UPI00001D07B9	
SIMILAR TO HYPOTHETICAL PROTEIN MGC7793	UNKNOWN	similar to hypothetical protein MGC7793	139600	34855606	249584	SOLUBLE			UPI00001CF4A5	
SIMILAR TO MICROCHIDIA (ZINC FINGER CW-TYPE COILED COIL) PROTEIN	NUCLEUS	similar to microchidia	55070	34869318	309715	SOLUBLE			UPI00001D0784	

SIMILAR TO PUTATIVE ODORANT RECEPTOR	PLASMA MB	similar to putative odorant receptor	137500	34854788	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	
SIMILAR TO RIBOSOMAL PROTEIN L7, CYTOSOLIC [VALID]	PROT SYN/FOLD	similar to ribosomal protein L7, cytosolic [validated] - rat	28840	34866562	206770	SOLUBLE			UPI00001CFD27	
SIMILAR TO SORTING NEXIN 17	TRAFFIC	similar to sorting nexin 17 [Rattus norvegicus]	16590	27716735	167115	SOLUBLE				
SIMILAR TO RIKEN CDNA 1110020C03	UNKNOWN	unknown	29280	34870857	233158	SOLUBLE			UPI00001CF7D6	
2' 3' CYCLIC NUCLEOTIDE 3' PHOSPHODIESTERASE	SIGNALING	2' 3' -cyclic-nucleotide 3' -phosphodiesterase CNPase	47270	66912120	109735	SOLUBLE			P13233 Q4V796 Q64575	
5'-AMP-ACTIVATED PROTEIN KINASE, CATALYTIC ALPHA	SIGNALING	5' -AMP-activated protein kinase catalytic subunit alpha-1 AMPK alpha-1 chain	62600	1703034	23444	SOLUBLE			P54645	
5'-AMP-ACTIVATED PROTEIN KINASE, CATALYTIC ALPHA	SIGNALING	5'-AMP-activated protein kinase, catalytic alpha-2 chain	62260	728758	54292	SOLUBLE			Q09137	
60S RIBOSOMAL PROTEIN L37	PROT SYN/FOLD	60S ribosomal protein L37	11080	57121	3029	SOLUBLE				
ADP-RIBOSYLATION FACTOR-LIKE 1	GTPASE	ADP-ribosylation factor-like protein 1	20410	728889	23396	MEMBRANE			P61212	
RHO-RELATED GTP-BINDING PROTEIN RHOG	GTPASE	ARHG protein Ras homolog gene family, member G Rho G	21310	82524300	93024	SOLUBLE			Q32PX6	
ADRENOLEUKODYSTROPHY RELATED PROTEIN	PEROXISOME	ATP-binding cassette sub-family D member 2 Adrenoleukodystrophy-related protein	83370	81917721	15419	SOLUBLE	cleavable signal peptide		Q9QY44	
ATP-BINDING CASSETTE, SUB-FAMILY F (GCN20), MEMB	PROT SYN/FOLD	ATP-binding cassette, sub-family F (GCN20), member 1	92870	34852051	231492	SOLUBLE			UPI00001D152D	
SIMILAR TO VACUOLAR ATP SYNTHASE SUBUNIT C (V-A)	MITOCHONDRIA	ATPase, H+ transporting, V1 subunit C, isoform 1 Predicted	43900	62652340	311925	SOLUBLE			Q5FV16	
TUMOR NECROSIS FACTOR ALPHA-INDUCED ADIPOSE-F	PLASMA MB	Ab1-219	52040	62646756	201751	MEMBRANE		202 23 IN-OUT 246 23 OUT-IN 293 23 IN-OUT 348 23 OUT-IN	Q7TP88	
ADENYLATE CYCLASE, TYPE VIII	SIGNALING	Adenylate cyclase type 8 Adenylate cyclase type VIII ATP pyrophosphate-lyase 8 Ca(2+)/calmodulin-activate adenyllyl cyclase	139800	8392852	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	
ADENYLATE KINASE ISOENZYM 4, MITOCHONDRIAL	MITOCHONDRIA	Adenylate kinase isoenzyme 4, mitochondrial Adenylate kinase 3-like 1 ATP-AMP transphosphorylase	25200	8392885	181389	SOLUBLE	cleavable signal peptide		Q9WU50	
O-GLCNAC TRANSFERASE-INTERACTING PROTEIN OF 9	PROT MOD	Amyotrophic lateral sclerosis 2 chromosomal region candidate gene protein 3 homolog	101600	75905813	256333	SOLUBLE			Q8R2H6 Q8R2H7 Q8R4G3	

CALCIUM CHANNEL ISOFORM ALPHA1E7	CALCIUM TRANS/BIND	Calcium channel isoform alpha1E7	259200	14578563	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 1524 18 IN-OUT 1588 20 OUT-IN 1682 23 IN-OUT	Q923K6	
CALPAIN SMALL SUBUNIT 1	BIOSYNTHETIC CARGO	Calpain small subunit 1	28080	19864480	76638	SOLUBLE			Q64537	
CARBOXYPEPTIDASE A1 PRECURSOR	PROT MOD	Carboxypeptidase A1 precursor	47150	8393183	111631	SOLUBLE	cleavable signal peptide		P00731 UPI00001432A8	
CLATHRIN LIGHT CHAIN B	COAT	Clathrin light chain B	25120	203359	60578	SOLUBLE			P08082	
CLAUDIN-3	PLASMA MB	Claudin-3	23310	82617586	33971	MEMBRANE	cleavable signal peptide	7 23 IN-OUT 78 23 OUT-IN 121 23 IN- OUT 163 23 OUT-IN	Q63400	
COPI COATOMER DELTA SUBUNIT	COAT	Coatomer subunit delta Delta-coat protein Delta-COP Archain	57200	81884175	221177	SOLUBLE	cleavable signal peptide		Q66H80	XP_217133.2
COLORECTAL TUMOR SUPPRESSOR	CYTOSKELETON	Colorectal tumor suppressor	157900	6978755	3733	MEMBRANE	cleavable signal peptide	5 23 IN-OUT 1099 23 OUT-IN	Q63155	
KERATIN, TYPE II CYTOSKELETAL 1 (CYTOKERATIN 1) (6	LIKELY CONTAMINANTS	Cytokeratin type I	15550	55956	11221	SOLUBLE			Q63115	
DNA POLYMERASE BETA	NUCLEUS	DNA polymerase beta	36540	206276	44281	SOLUBLE			P06766	
DEATH EFFECTOR DOMAIN-CONTAINING PROTEIN	SIGNALING	Death effector domain-containing protein Death effector domain-containing testicular molecule	36850	3930224	54966	SOLUBLE			Q9Z2K0	
DYNAMIN 2	CYTOSKELETON	Dynamain 2	98230	729380	3740	SOLUBLE			P39052	
DYNAMIN-1	CYTOSKELETON	Dynamain-1 D100 Dynamain, brain B-dynamain	95930	56054	67605	SOLUBLE			P21575	
EUKARYOTIC TRANSLATION INITIATION FACTOR 3 SUBU	PROT SYN/FOLD	EIF3S6 protein	52220	62652368	55867	SOLUBLE			Q641X8	
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	SOLUBLE				
ERYTHROID SPECTRIN ALPHA	CYTOSKELETON	Erythroid spectrin alpha	276600	58865394	725563	SOLUBLE			Q6XDA1	
ERYTHROID SPECTRIN BETA	CYTOSKELETON	Erythroid spectrin beta	246300	47058982	726511	SOLUBLE			Q6XDA0	
FATTY ACID BINDING PROTEIN FABP-1	METABOLISM	Fatty acid binding protein FABP-1	3929	452977	23674	SOLUBLE			Q9QV50	
FLOTILIN-2	PLASMA MB	Flotillin-2 Reggie-1 REG-1	47040	4079709	101676	MEMBRANE			Q9QX33 Q9Z2S8 Q9Z2S9	
GRIP-ASSOCIATED PROTEIN 1 LONG FORM	SIGNALING	GRIP1-associated protein 1 GRASP-1	96070	8980841	60564	SOLUBLE			Q9JHZ3 Q9JHZ4	
GTPASE	GTPASE	GTP-binding nuclear protein Ran GTPase Ran Ras-like protein TC4	24420	51338593	76611	SOLUBLE				

GAP JUNCTION BETA-1 PROTEIN (CONNEXIN 32) (CX32)	PLASMA MB	Gap junction beta-1 protein Connexin-32 Cx32	32000	8393444	51463	MEMBRANE	cleavable signal peptide	23 23 IN-OUT 76 20 OUT-IN 131 23 IN-OUT 192 23 OUT-IN	P08033	
HEPATOMA-DERIVED GROWTH FACTOR 3	SIGNALING	Hepatoma-derived growth factor 3	74000	19424218	171803	SOLUBLE			Q925G1	
L-SERINE DEHYDRATASE/L-THREONINE DEAMINASE	METABOLISM	L-serine dehydratase/L-threonine deaminase	38480	21617859	44348	SOLUBLE			P09367 UPI00001684FB	
LAMININ-5 ALPHA 3 CHAIN	BIOSYNTHETIC CARGO	Laminin-5 alpha 3 chain	190400	27545378	116280	SOLUBLE	cleavable signal peptide		P70570	
2810002D13RIK PROTEIN	UNKNOWN	Leucine-rich repeat-containing protein 57	26720	81909634	240594	SOLUBLE			Q5FVI3	
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	SOLUBLE			Q6P2A7	
LIVER NTE-RELATED PROTEIN	UNKNOWN	Liver NTE-related protein	75650	21314221	198073	SOLUBLE			Q8K3H9	
MEMBRANE-BOUND AMINOPEPTIDASE P	PLASMA MB	Membrane-bound aminopeptidase P X-prolyl aminopeptidase (Aminopeptidase P) 2, membrane-bound	76080	49258142	140638	MEMBRANE	cleavable signal peptide		Q99MA2	
MICROSOMAL DIPEPTIDASE	PROT MOD	Microsomal dipeptidase precursor	45520	47938984	23872	SOLUBLE	cleavable signal peptide		P31430 Q6IN35	
SYNTROPHIN-ASSOCIATED SERINE/THREONINE KINASE	SIGNALING	Microtubule-associated serine/threonine-protein kinase Syntrophin-associated serine/threonine-protein kinase	171000	60389868	200842	SOLUBLE			Q810W7 Q810W8	
MONOCYTE DIFFERENTIATION ANTIGEN CD14 PRECURSOR	BIOSYNTHETIC CARGO	Monocyte differentiation antigen CD14 precursor	40050	38197682	35920	SOLUBLE	cleavable signal peptide		Q63691 Q6GT04	
MYOSIN I HEAVY CHAIN	CYTOSKELETON	Myosin I heavy chain	118100	480659	6153	SOLUBLE			Q63355	
MYOSIN IE	CYTOSKELETON	Myosin Ie Myosin heavy chain myr 3	126800	693995	105842	SOLUBLE			Q63356	
S-PHASE KINASE-ASSOCIATED PROTEIN 1A	SIGNALING	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:I830081B01 product:S-phase kinase-associated protein 1A, full insert sequence	18670	56090475	62616	SOLUBLE				XP_213290.1
P20-CGGBP	NUCLEUS	P20-CGGBP CGGBP1 protein CGG triplet repeat binding protein 1 Trinucleotide repeat DNA binding protein p20-CGGBP	18820	27672382	55652	SOLUBLE				
MKIAA0523 PROTEIN	UNKNOWN	PREDICTED: similar to CDNA sequence BC030477	64790	66730417	255746	SOLUBLE	cleavable signal peptide	17 20 IN-OUT	Q505J3 UPI00001CB000	
SIMILAR TO CELL DEATH-INDUCING DNA FRAGMENTATION FACTOR	NUCLEUS	PREDICTED: similar to Cell death-inducing DNA fragmentation factor, alpha subunit-like effector B	24750	34875073	235633	SOLUBLE			UPI000018133C	
EH-DOMAIN CONTAINING 2; EH DOMAIN CONTAINING 2	UNKNOWN	PREDICTED: similar to EH-domain containing 2	61240	67846074	287406	SOLUBLE			Q4V8H8 UPI00001CE791	
EMILIN	CYTOSKELETON	PREDICTED: similar to Elastin microfibril interfacer 1	107600	34863280	233953	SOLUBLE	cleavable signal peptide		UPI0000180741	
SIMILAR TO M PHASE PHOSPHOPROTEIN 6	PROT SYN/FOLD	PREDICTED: similar to M phase phosphoprotein 6	18880	34866285	221944	SOLUBLE			UPI00001CFA4A	
SIMILAR TO RIKEN CDNA 1110038M16	UNKNOWN	PREDICTED: similar to RIKEN cDNA 1110038M16	31550	34870283	246519	MEMBRANE		166 23 IN-OUT	UPI00001CF7A0	

SIMILAR TO RIKEN CDNA 2010002A20	UNKNOWN	PREDICTED: similar to RIKEN cDNA 2010002A20	29160	34873218	255476	MEMBRANE	cleavable signal peptide	217 23 OUT-IN	UPI00001D0587	
SIMILAR TO DJ881L22.2 (NOVEL PROTEIN)	UNKNOWN	PREDICTED: similar to RIKEN cDNA D930001I22	30110	62646328	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	
SIMILAR TO TOLLIP PROTEIN	SIGNALING	PREDICTED: similar to TOLLIP protein	30310	34861256	225945	SOLUBLE			UPI00001CEB28	
ABHYDROLASE DOMAIN CONTAINING PROTEIN 2	UNKNOWN	PREDICTED: similar to alpha/beta hydrolase fold protein	48340	34857271	271294	SOLUBLE			UPI000017E212	
SIMILAR TO KIAA1311 PROTEIN	UNKNOWN	PREDICTED: similar to mKIAA1311 protein	118700	34879262	281850	SOLUBLE			UPI00001D12DF	
PHOSPHOINOSITIDE-3-KINASE, REGULATORY SUBUNIT	TRAFFIC	PREDICTED: similar to phosphoinositide-3-kinase, regulatory subunit 4, p150	152400	83288384	268833	SOLUBLE			UPI00001D00B2	
SIMILAR TO MKIAA3002 PROTEIN	UNKNOWN	PREDICTED: similar to round spermatid basic protein 1 like	92310	34854016	266462	SOLUBLE			UPI00001CF433	
SIMILAR TO SEROLOGICALLY DEFINED COLON CANCER	TRANSCRIPTION	PREDICTED: similar to serologically defined colon cancer antigen 1 isoform a	118600	34855476	218537	SOLUBLE			UPI00001CE7BA	
TESTIS-SPECIFIC SERINE KINASE 4	SIGNALING	PREDICTED: similar to testis-specific serine kinase 4	37430	27700101	197055	SOLUBLE			UPI0000180DEE	
PHOSPHATIDYLCHOLINE TRANSFER PROTEIN	PROT MOD	Phosphatidylcholine transfer protein	24730	8393922	51565	SOLUBLE			P53809 Q9Z2N9	
PLECTIN 10	CYTOSKELETON	Plectin 10	518400	40849904	699022	SOLUBLE			Q6S396	
POTASSIUM VOLTAGE-GATED CHANNEL SUBFAMILY A MEMBER 6	PLASMA MB	Potassium voltage-gated channel subfamily A member 6	58880	57667	63679	MEMBRANE		171 23 OUT-IN 255 23 IN-OUT 290 23 OUT-IN 377 23 IN-OUT 438 23 OUT-IN	P17659 P19025	
PROTEIN LRP16	UNKNOWN	Protein LRP16	28640	32129697	214491	SOLUBLE	cleavable signal peptide		Q8K4G6	
PROTEIN KINASE C ALPHA	SIGNALING	Protein kinase C, alpha type	76790	56914	44893	SOLUBLE			P05696	
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	SOLUBLE			Q4QRA5 Q78EG7 Q8VH48	
PROTEIN-GLUTAMINE GAMMA-GLUTAMYLTRANSFERASE	PROT MOD	Protein-glutamine gamma-glutamyltransferase K Transglutaminase K TGase K TGK TG(K) Transglutaminase-1 Epidermal TGase	90770	67677918	31490	MEMBRANE			P23606 Q4QRA6	
CAST2	TRAFFIC	RAB6-interacting protein 2 ERC protein 1 ERC1 CAZ-associated structural protein 2 CAST2	108800	51701367	165980	SOLUBLE			Q811U3 Q8C1Y9	
MOMO	TRANSCRIPTION	RING finger protein 34 RING finger protein MOMO	42680	76363370	273497	SOLUBLE	cleavable signal peptide		Q6AYH3 Q8CIP0	XP_341083.1
RSB-11-77	UNKNOWN	RSB-11-77	42090	32996717	166313	SOLUBLE			Q80WN5	
RAB PROTEINS GERANYLGERANYLTRANSFERASE COMPONENT A1	PROT MOD	Rab proteins geranylgeranyltransferase component A1 Rab escort protein 1 REP-1 Choroideraemia protein homolog	72480	8393110	86616	SOLUBLE			P37727	
RAC2	GTPASE	Ras-related C3 botulinum toxin substrate 2 precursor p21-Rac2 EN-7 protein	21440	56605840	8458	MEMBRANE			Q5U1Y2	XP_345855.1
RETINOL DEHYDROGENASE 10	DETOXIFICATION	Retinol dehydrogenase 10	38060	31324556	227390	MEMBRANE	cleavable signal peptide	5 23 OUT-IN 34 20 IN-OUT	Q80ZF7	
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	SOLUBLE			Q63531	
RAT INSULIN RECEPTOR RELATED RECEPTOR 1 (SIRR-1)	PLASMA MB	SIRR-1 precursor	44730	425789	100550	MEMBRANE	cleavable signal peptide		Q63720	
SMPTB	NUCLEUS	SMPTB	63720	33414511	185761	SOLUBLE			Q80XZ1	

SP120	NUCLEUS	SP120	87750	624918	140634	SOLUBLE			Q63555	
CAMP-DEPENDENT PROTEIN KINASE TYPE II-ALPHA REGULATOR	SIGNALING	SWISS-PROT:P12368 cAMP-dependent protein kinase type II-alpha regulatory subunit	41980	206150	168209	SOLUBLE				
SCAFFOLDING PROTEIN SLIPR	CYTOSKELETON	Scaffolding protein SLIPR	129400	7650497	138308	SOLUBLE			Q9JK71	
SEMINAL VESICLE SECRETORY PROTEIN II PRECURSOR	BIOSYNTHETIC CARGO	Seminal vesicle secretory protein 2 precursor Seminal vesicle secretory protein II SVS II	45540	207115	11343	SOLUBLE	cleavable signal peptide		P22006	
PKC-ZETA-INTERACTING PROTEIN	SIGNALING	Sequestosome-1 Ubiquitin-binding protein p62 Protein kinase C-zeta-interacting protein PKC-zeta-interacting protein	47680	77416574	19107	SOLUBLE			O08623 Q8CH59	
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	SOLUBLE			P56932 Q66HR7	
2'-5'-OLIGOADENYLATE SYNTHETASE-LIKE 9	PROT SYN/FOLD	Solute carrier family 30 (Zinc transporter), member 4	47660	56268809	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	Q5PQX4	
Sorting nexin 3	BIOSYNTHETIC CARGO	Sorting nexin 3	18760	79152346	75350	SOLUBLE			Q5U211	
SPLICING FACTOR, ARGININE/SERINE-RICH 3	NUCLEUS	Splicing factor, arginine/serine-rich 3	19330	62665747	4905	SOLUBLE				
NEURAL ZINC FINGER FACTOR 3	TRANSCRIPTION	Suppression of tumorigenicity protein 18 Neural zinc finger factor 3 NZF-3 C2-HC type zinc finger protein r-MYT3	113500	7514025	169317	SOLUBLE				
SYNDECAN-2 PRECURSOR	PLASMA MB	Syndecan 2	23220	6981520	41211	MEMBRANE	cleavable signal peptide	157 23 OUT-IN	Q6IRK3	
SYNDECAN-1 PRECURSOR	PLASMA MB	Syndecan-1 precursor	33210	6981518	75082	MEMBRANE	cleavable signal peptide	257 23 OUT-IN	P26260	
SYNDECAN-4 PRECURSOR	PLASMA MB	Syndecan-4 precursor SYND4 Ryudocan core protein	21960	6981522	75083	MEMBRANE	cleavable signal peptide	152 23 OUT-IN	P34901	
ADAPTOR PROTEIN COMPLEX AP-1, GAMMA 1 SUBUNIT	COAT	Tax_Id=10116 AdAptor protein complex AP-1, gAmmA 1 subunit	77880	34851742	198626	SOLUBLE				
CADHERIN 7	PLASMA MB	Tax_Id=10116 Cadherin 7	91340	34878884	214165	MEMBRANE	cleavable signal peptide	642 23 OUT-IN		
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	SOLUBLE		542 23 OUT-IN		
SIMILAR TO FRAGILE-X-RELATED PROTEIN 1 ISOFORM B	UNKNOWN	Tax_Id=10116 Ensembl_locations(Chr-bp):2-120296304 similar to fragile-X-related protein 1 isoform e	68720	34856814	266426	SOLUBLE	cleavable signal peptide			
SIMILAR TO CALGIZZARIN	CALCIUM TRANS/BIND	Tax_Id=10116 Ensembl_locations(Chr-bp):2-186570454 similar to endothelial monocyte-activating polypeptide	16840	34856021	215128	SOLUBLE				
SIMILAR TO HYPOTHETICAL PROTEIN FLJ10579	UNKNOWN	Tax_Id=10116 Ensembl_locations(Chr-bp):3-105548427 similar to hypothetical protein FLJ10579	57210	34856697	285691	SOLUBLE				
3-HYDROXYISOBUTYRYL-COENZYME A HYDROLASE	METABOLISM	Tax_Id=10116 Ensembl_locations(Chr-bp):9-45566723 similar to RIKEN cDNA 261050915	47870	34875828	251780	SOLUBLE				
GLYPICAN 4	BIOSYNTHETIC CARGO	Tax_Id=10116 Ensembl_locations(Chr-bp):X-139040465 similar to glypican 4	62280	34881641	253728	SOLUBLE				
UNKNOWN1	UNKNOWN	Tax_Id=10116 Hypothetical protein XP_235050	101800	34864725	191344	SOLUBLE				
HYPOTHETICAL PROTEIN XP_342343	UNKNOWN	Tax_Id=10116 Hypothetical protein XP_342343	17520	34860574	313817	SOLUBLE				
M4 PROTEIN	UNKNOWN	Tax_Id=10116 M4 protein	74540	16124253	136387	SOLUBLE				
MYOSIN LIGHT CHAIN 1, SLOW-TWITCH MUSCLE B/VENTRICULAR	CYTOSKELETON	Tax_Id=10116 Myosin, light polypeptide 3	22160	763179	21125	SOLUBLE				
DHM1 PROTEIN	TRANSCRIPTION	Tax_Id=10116 Similar to 5-3 exoribonucleaSe 2	128500	34858884	242779	SOLUBLE				
SIMILAR TO AFADIN	CYTOSKELETON	Tax_Id=10116 Similar to AF-6 protein	16820	34853794	305979	SOLUBLE	signal anchor			

SIMILAR TO ATP BINDING CASSETTE GENE, SUB-FAMILY	UNKNOWN	Tax_Id=10116 Similar to ATP binding caSSette gene, Sub-family A (ABC1), member 13	646000	34879278	202444	MEMBRANE	21 23 IN-OUT 3143 23 OUT-IN 3172 23 IN-OUT 3209 23 OUT-IN 3288 23 IN- OUT 3305 18 OUT- IN 3350 18 IN-OUT 4100 23 OUT-IN 4143 23 IN-OUT 4175 23 OUT-IN 4204 23 IN-OUT 4236 23 OUT-IN 4279 23 IN-OUT 4821 23 OUT-IN 5041 23 IN-OUT 5093 23 OUT-IN 5120 23 IN-OUT 5157 23 OUT-IN 5238 23 IN-OUT		
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	SOLUBLE	cleavable signal peptide		
SIMILAR TO CDT1 PROTEIN	UNKNOWN	Tax_Id=10116 Similar to CDT1 protein	68840	34851851	203175	SOLUBLE			
SIMILAR TO CENTROMERIC PROTEIN E (CENP-E PROTEIN)	CYTOSKELETON	Tax_Id=10116 Similar to CENTROMERIC PROTEIN E (CENP-E PROTEIN)	313000	34860597	241018	SOLUBLE	cleavable signal peptide		
DEAD-BOX PROTEIN ABSTRAKT HOMOLOG	PROT SYN/FOLD	Tax_Id=10116 Similar to DEAD-box protein abStrakt homolog	165600	34873643	261560	SOLUBLE	cleavable signal peptide		
DEAH (ASP-GLU-ALA-HIS) BOX POLYPEPTIDE 29; NUCLE	PROT SYN/FOLD	Tax_Id=10116 Similar to DEAH (ASP-Glu-Ala-His) box polypeptide 29	145700	34854165	249374	SOLUBLE			
DESMOPLAKIN (DP) (250/210 KDA PARANEOPLASTIC PE	CYTOSKELETON	Tax_Id=10116 Similar to DeSmoplakin (DP) (250/210 kDa paraneoplaStic pemphiguS antigen)	327800	34875216	219502	SOLUBLE			
SIMILAR TO ENSANGP00000013261	UNKNOWN	Tax_Id=10116 Similar to ENSANGP00000013261	15620	27689183	197176	SOLUBLE			
FARP1 PROTEIN	UNKNOWN	Tax_Id=10116 Similar to Farp1 protein	195200	34876071	216529	SOLUBLE			
SIMILAR TO HYPOTHETICAL PROTEIN KIAA0233	UNKNOWN	Tax_Id=10116 Similar to Hypothetical protein KIAA0233	237700	34932058	265857	MEMBRANE	90 23 IN-OUT 132 20 OUT-IN 264 23 IN-OUT 290 18 OUT- IN 320 23 IN-OUT 368 23 OUT-IN 442 20 IN-OUT 465 23 OUT-IN 500 23 IN- OUT 1160 23 OUT- IN 1187 20 IN-OUT 1216 23 OUT-IN 1440 23 IN-OUT 1482 22 OUT-IN 1510 23 IN-OUT 1542 18 OUT-IN 1724 23 IN-OUT 1982 23 OUT-IN		
CULLIN 4A	PROTEASOME/UBIQUITIN	Tax_Id=10116 Similar to KIAA0695 protein	71450	34879447	314767	SOLUBLE			
SIMILAR TO KIAA1407 PROTEIN	UNKNOWN	Tax_Id=10116 Similar to KIAA1407 protein	75980	34869160	295453	SOLUBLE			
SIMILAR TO LEK1	CYTOSKELETON	Tax_Id=10116 Similar to LEK1	337700	34881142	192027	SOLUBLE			
GUANINE NUCLEOTIDE EXCHANGE FACTOR GEF-H1	SIGNALING	Tax_Id=10116 Similar to Lbc11 protein	113100	34857950	264247	SOLUBLE			
SIMILAR TO LEUCINE-RICH REPEAT-CONTAINING PROTE	UNKNOWN	Tax_Id=10116 Similar to Leucine-rich repeat-containing protein 2	45980	34866388	316728	SOLUBLE			
SIMILAR TO MYOSIN VI	CYTOSKELETON	Tax_Id=10116 Similar to MyoSin VI	167000	34865321	261550	SOLUBLE			

SIMILAR TO NBL4	SIGNALING	Tax_Id=10116 Similar to NBL4	95230	34878636	198264	SOLUBLE			
PHF3	UNKNOWN	Tax_Id=10116 Similar to PHD finger protein 3	226400	34874598	295897	SOLUBLE			
SIMILAR TO PROLYL 4-HYDROXYLASE ALPHA IIA SUBUNIT	PROT MOD	Tax_Id=10116 Similar to Prolyl 4-hydroxyLaSe alpha Ila Subunit	66900	34870735	212585	SOLUBLE	cleavable signal peptide		
SRP RECEPTOR ALPHA SUBUNIT	PROT SYN/FOLD	Tax_Id=10116 Similar to RIKEN cDNA 1300011P19	69740	34863012	258910	SOLUBLE	cleavable signal peptide		
UNNAMED PROTEIN PRODUCT3	UNKNOWN	Tax_Id=10116 Similar to RIKEN cDNA 1600013K19	91910	34867853	282761	SOLUBLE			
DEAD (ASP-GLU-ALA-ASP) BOX POLYPEPTIDE 42	PROT SYN/FOLD	Tax_Id=10116 Similar to RIKEN cDNA 1810047H21 gene	103600	27690029	238446	SOLUBLE			
SIMILAR TO CAP-BINDING PROTEIN COMPLEX INTERACT	NUCLEUS	Tax_Id=10116 Similar to RIKEN cDNA 4931407K02	161300	34867357	282579	SOLUBLE			
SIMILAR TO RIKEN CDNA 5730519E19 GENE	UNKNOWN	Tax_Id=10116 Similar to RIKEN cDNA 5730519E19 gene	118100	34862241	222795	SOLUBLE			
SB:CB404 PROTEIN	UNKNOWN	Tax_Id=10116 Similar to RIKEN cDNA 9530027K23	73500	34851643	224054	SOLUBLE			
SIMILAR TO RIKEN CDNA C730036B14 GENE	UNKNOWN	Tax_Id=10116 Similar to RIKEN cDNA C730036B14 gene	216400	34865292	282808	MEMBRANE	cleavable signal peptide	90 23 IN-OUT	
SIMILAR TO RHO GTPASE ACTIVATING PROTEIN 2	SIGNALING	Tax_Id=10116 Similar to Rho GTPaSe activating protein 2	89740	34877029	276572	SOLUBLE			
SIMILAR TO SEMAPHORIN SUBCLASS 4 MEMBER G	PLASMA MB	Tax_Id=10116 Similar to Semaphorin Subclass 4 member G	128000	34863455	222218	MEMBRANE		998 23 OUT-IN	
SHORT CHAIN DEHYDROGENASE REDUCTASE 9	DETOXIFICATION	Tax_Id=10116 Similar to Short chain dehydrogenase reductaSe 9	40410	34866289	268103	SOLUBLE			
SIMILAR TO SIGNAL RECOGNITION PARTICLE 68KDA	PROT SYN/FOLD	Tax_Id=10116 Similar to Signal recognition particle 68kDa	73120	34875372	300246	SOLUBLE			
SIMILAR TO STRUCTURAL MAINTENANCE OF CHROMOS	NUCLEUS	Tax_Id=10116 Similar to Structural maintenance of chromoSomeS 1beta	147300	34867523	216707	SOLUBLE			
SIMILAR TO TETRATRICOPEPTIDE REPEAT PROTEIN 7 (	UNKNOWN	Tax_Id=10116 Similar to Tetratricopeptide repeat protein 7 (TPR repeat protein 7)	102100	34862046	196091	SOLUBLE			
SIMILAR TO TRIM26 PROTEIN	UNKNOWN	Tax_Id=10116 Similar to Trim26 protein	47090	34852035	264688	SOLUBLE			
ARCHVILLIN	CYTOSKELETON	Tax_Id=10116 Similar to archvillin	236900	34876218	258828	SOLUBLE			
AUTOCRINE MOTILITY FACTOR RECEPTOR	PROTEASOME/UBIQUITIN	Tax_Id=10116 Similar to autocrine motility factor receptor	68280	34851252	285136	MEMBRANE	cleavable signal peptide	83 20 OUT-IN 122 20 IN-OUT 145 18 OUT-IN 187 23 IN-OUT	
SIMILAR TO BN280G18.3 (NOVEL PROTEIN)	UNKNOWN	Tax_Id=10116 Similar to bN280G18.3 (novel protein)	38950	34868997	199323	MEMBRANE		312 23 OUT-IN	
SIMILAR TO CENTROMERE/KINETOCHORE PROTEIN ZW	CYTOSKELETON	Tax_Id=10116 Similar to centromere/kinetochore protein zw10 homolog	88170	34863346	192125	SOLUBLE			
SIMILAR TO CHROMOSOME 2 OPEN READING FRAME 3;	NUCLEUS	Tax_Id=10116 Similar to chromoSome 2 open reading frame 3	83470	34856267	196107	SOLUBLE			
COPI COATOMER GAMMA-1 SUBUNIT	COAT	Tax_Id=10116 Similar to coat protein gamma-cop	138100	34856387	267886	SOLUBLE			
DJ1070B1.1 (KIAA0316 AND KIAA0967 PROTEINS)	UNKNOWN	Tax_Id=10116 Similar to dJ1070B1.1 (Similar to KIAA0316 and KIAA0967 proteins)	233200	34881575	253851	SOLUBLE			
SIMILAR TO EXPRESSED SEQUENCE C87860	UNKNOWN	Tax_Id=10116 Similar to expreSSed Sequence C87860	54690	34857072	242229	SOLUBLE			
SIMILAR TO HYPOTHETICAL PROTEIN 4932411E22	UNKNOWN	Tax_Id=10116 Similar to hypothetical protein 4932411E22	69500	34873297	232623	SOLUBLE			
SIMILAR TO HYPOTHETICAL PROTEIN 5832424M12	UNKNOWN	Tax_Id=10116 Similar to hypothetical protein 5832424M12	89010	34853466	213390	SOLUBLE			
SIMILAR TO SEPTIN 6	GTPASE	Tax_Id=10116 Similar to hypothetical protein FLJ10849	58770	34876531	204932	MEMBRANE			
SIMILAR TO HYPOTHETICAL PROTEIN FLJ10900	UNKNOWN	Tax_Id=10116 Similar to hypothetical protein FLJ10900	93700	34872027	198580	MEMBRANE	signal anchor	20 23 OUT-IN 96 20 IN-OUT	
SIMILAR TO HYPOTHETICAL PROTEIN FLJ30373	UNKNOWN	Tax_Id=10116 Similar to hypothetical protein FLJ30373	29880	34855399	229721	SOLUBLE	cleavable signal peptide		

SIMILAR TO KIDNEY ANKYRIN REPEAT-CONTAINING PROTEIN	UNKNOWN	Tax_Id=10116 Similar to kidney ankyrin repeat-containing protein	127000	34860436	261449	SOLUBLE				
SIMILAR TO KINESIN FAMILY PROTEIN KIF1A	CYTOSKELETON	Tax_Id=10116 Similar to kinesin family protein KIF1a	218300	34877667	265199	SOLUBLE				
KINESIN FAMILY MEMBER 5C	CYTOSKELETON	Tax_Id=10116 Similar to mKIAA0531 protein	114400	34854278	296600	SOLUBLE				
SIMILAR TO MYELOID/LYMPHOID OR MIXED-LINEAGE LEUKEMIA 2	UNKNOWN	Tax_Id=10116 Similar to myeloid/lymphoid or mixed-lineage leukemia 2	561200	34868150	316308	SOLUBLE				
HEMATOPOIETIC GROWTH FACTOR RECEPTOR	BIOSYNTHETIC CARGO	Tax_Id=10116 Similar to myeloproliferative leukemia virus oncogene	60890	34871078	277020	SOLUBLE	cleavable signal peptide			
P140MDIA	SIGNALING	Tax_Id=10116 Similar to p140mDia	140200	34878815	217100	SOLUBLE				
SIMILAR TO CELL-CYCLE AND APOPTOSIS REGULATORY PROTEIN 1	SIGNALING	Tax_Id=10116 Similar to p30 DBC protein	76270	34852526	276810	SOLUBLE				
RENT1 PROTEIN	NUCLEUS	Tax_Id=10116 Similar to regulator of nonSenSen transcripts 1	47750	34877805	234739	SOLUBLE				
RETINOBLASTOMA-ASSOCIATED FACTOR 600	TRANSCRIPTION	Tax_Id=10116 Similar to retinoblastoma-associated factor 600	577500	34872228	271261	SOLUBLE				
ROOTLETIN	UNKNOWN	Tax_Id=10116 Similar to rootletin	234800	34872243	290689	SOLUBLE				
TROPOMODULIN 3	CYTOSKELETON	Tax_Id=10116 Similar to tropomodulin 3	46420	34864364	261414	SOLUBLE				
SIMILAR TO UBIQUITIN SPECIFIC PROTEASE 28	PROTEASOME/UBIQUITIN	Tax_Id=10116 Similar to ubiquitin specific protease 28	135800	34863342	319220	SOLUBLE				
SIMILAR TO UBIQUITOUS TETRATRICOPEPTIDE CONTAINING PROTEIN	UNKNOWN	Tax_Id=10116 Similar to ubiquitously tetratricopeptide containing protein RoXan	111900	34867257	230656	SOLUBLE				
VIMENTIN	CYTOSKELETON	Tax_Id=10116 Vimentin	53730	57480	82925	SOLUBLE				
TRANSALDOLASE	METABOLISM	Transaldolase	37480	17433174	50402	SOLUBLE				
SIMILAR TO ESTROGEN-RESPONSIVE FINGER PROTEIN 1	TRANSCRIPTION	Tripartite motif protein 25	71950	57164029	318709	SOLUBLE			Q6P7B3	
TYROSINE-PROTEIN KINASE LYN	SIGNALING	Tyrosine-protein kinase LYN	58660	294583	71712	SOLUBLE			Q07014	
RING FINGER TRANSCRIPTION FACTOR	TRANSCRIPTION	Ubiquitin ligase protein RING2 RING finger protein 2 RING finger protein 1B RING1b	37620	27712522	33698	SOLUBLE				
MUNC13-4 PROTEIN	TETH/DOCK/FUS	Unc-13 homolog D Munc13-4	123500	5524667	20725	SOLUBLE			Q9R189	
VACUOLAR PROTEIN SORTING 33A	TRAFFIC	Vacuolar protein sorting 33A	67510	23396893	55286	SOLUBLE			Q63615	
VACUOLAR PROTON TRANSLOCATING ATPASE 116 KDa	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 Vacuolar proton pump subunit 1 Vacuolar adenosine triphosphatase subunit Ac116	96330	206430	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	
ZINC FINGER	TRANSCRIPTION	Zinc finger protein	130500	7514121	134827	SOLUBLE			Q63681	
HYPOTHETICAL PROTEIN XP_344851	UNKNOWN	hypothetical protein XP_344851	46260	34854602	287423	SOLUBLE			UPI00001CE797	
OLFACTORY RECEPTOR MOR164-2	PLASMA MB	olfactory receptor Olr1265	35790	47577731	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	UPI0000182E24	XP_236114.1
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	MEMBRANE		78 23 IN-OUT 115 23 OUT-IN	UPI00001CAB0E	
DNAJC13	UNKNOWN	similar to CG8014-PA	126100	34865967	261337	SOLUBLE			UPI00001D008C	
SIMILAR TO HYPOTHETICAL PROTEIN KIAA0586	UNKNOWN	similar to Hypothetical protein KIAA0586	39910	34865368	294179	SOLUBLE			UPI00001CFA1E	
IMMUNOGLOBULIN HEAVY CHAIN CONSTANT REGION M	BLOOD + OTHER CELLS	similar to Igh-6 protein	79080	34935297	225182	SOLUBLE			UPI00001CFA84	
SIMILAR TO KIAA0789 PROTEIN	UNKNOWN	similar to KIAA0789 protein	40750	34872839	235178	SOLUBLE			UPI00001D0976	
SIMILAR TO DEDICATOR OF CYTOKINESIS PROTEIN 6	SIGNALING	similar to KIAA1771 protein	233300	34869877	199377	SOLUBLE			UPI00001CF764	

SIMILAR TO LDL RECEPTOR ADAPTOR PROTEIN	SIGNALING		similar to LDL receptor adaptor protein	60620	34872138	266460	SOLUBLE			UPI00001CF868	
PRKRA PROTEIN KINASE, INTERFERON-INDUCIBLE DOU	SIGNALING		similar to PKR-associating protein RAX	34390	34856450	191003	SOLUBLE			UPI000017E04D	
SIMILAR TO RIKEN CDNA 1810045K17	UNKNOWN		similar to RIKEN cDNA 1810045K17	10150	34857339	270299	SOLUBLE			UPI00001CEE65	
UNKNOWN4	UNKNOWN		similar to RIKEN cDNA C920006C10	16670	27718855	264993	SOLUBLE	cleavable signal peptide		UPI00001C9F63	
RNA HELICASE A	NUCLEUS		similar to RNA helicase A	150200	34880497	203449	SOLUBLE			UPI00001D0A2F	
SIMILAR TO SLIT-ROBO RHO GTPASE-ACTIVATING PRO	SIGNALING		similar to SLIT-ROBO Rho GTPase-activating protein 3 WAVE-associated Rac GTPase activating protein	35530	34879743	229135	SOLUBLE			UPI00001D09D8	
SIMILAR TO TRAV8-1	UNKNOWN		similar to TRAV8-1	14930	27699808	236003	SOLUBLE	cleavable signal peptide		UPI00001CC370	
B-IND1	SIGNALING		similar to butyrate-induced transcript 1	20610	34880723	260591	MEMBRANE		149 23 IN-OUT	UPI00001D1798	
SIMILAR TO PKA C-BETA-2	SIGNALING		similar to cAMP-dependent protein kinase, beta-2-catalytic subunit (PKA C-beta-2)	73330	34861056	256498	SOLUBLE			UPI00001CF013	
SIMILAR TO CYCLIN G-ASSOCIATED KINASE	SIGNALING		similar to cyclin G-associated kinase	29950	34879280	254251	SOLUBLE			UPI00001D09AF	
SIMILAR TO CYTOPLASMIC BETA-ACTIN	CYTOSKELETON		similar to cytoplasmic beta-actin	27270	34881817	287459	SOLUBLE			UPI00001D1884	
ENTHOPROTEIN	COAT		similar to enthoprotin; epsin 4; clathrin interacting prote localized in the trans-Golgi region	64680	34880606	203525	SOLUBLE			UPI00001D1757	
EPIPLAKIN	CYTOSKELETON		similar to epiplakin	368200	34867002	318405	SOLUBLE			UPI00001CFDB4	
SIMILAR TO HYPOTHETICAL PROTEIN C230069C04 (1)	UNKNOWN		similar to hypothetical protein C230069C04	54880	34862585	263392	MEMBRANE	cleavable signal peptide	475 23 OUT-IN	UPI00001CFC44	
SIMILAR TO HYPOTHETICAL PROTEIN FLJ20331	UNKNOWN		similar to hypothetical protein FLJ20331 [Rattus norvegicus]	48370	34861003	248047	SOLUBLE				
SIMILAR TO HYPOTHETICAL PROTEIN MGC22776	UNKNOWN		similar to hypothetical protein MGC22776	19210	34875293	302017	SOLUBLE	cleavable signal peptide		UPI00001D0EAE	
SERINE (OR CYSTEINE) PROTEINASE INHIBITOR, CLADE	PROT SYN/FOLD		similar to serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 9	46840	34935459	300510	SOLUBLE	cleavable signal peptide		UPI00001CFAC6	
SIMILAR TO SOLUTE CARRIER FAMILY 22 MEMBER 6 ISO	PLASMA MB		similar to solute carrier family 22 member 6 isoform b; renal organic anion transporter 1; para-aminohippurate transporter	60990	34861829	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	
SORTING NEXIN 2	TRAFFIC		similar to sorting nexin 2	58530	34879535	319162	SOLUBLE			UPI00001D12EA	
ACTIN RELATED PROTEIN 2/3 COMPLEX, SUBUNIT 5-LIKE	CYTOSKELETON		unknown	17010	27707156	199239	SOLUBLE			UPI0000182CC0	
SIMILAR TO RIKEN CDNA 2010315L10	UNKNOWN		unknown	30510	34877499	258690	MEMBRANE		243 23 OUT-IN	UPI00001D0F57	
TRANSCRIPTION FACTOR BTF3	TRANSCRIPTION		(P20290) Isoform 2 of P20290	17700	56605700	33279	SOLUBLE			Q5U3Y8	XP_215460.1
EGF, LATROPHILIN AND SEVEN TRANSMEMBRANE DOM	PLASMA MB		(Q9ESC1) Isoform 2 of Q9ESC1	73800	11225481	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	

3' EXONUCLEASE	NUCLEUS	3' histone mRNA exonuclease 1 3' -5' exonuclease ERI1	39580	78098993	241027	SOLUBLE			Q5FVR4	
ALF-C1	NUCLEUS	AIF-C1	36210	3377279	75909	SOLUBLE			O88311	
SIMILAR TO BLOCK OF PROLIFERATION 1	UNKNOWN	Block of proliferation 1 Predicted	82640	66730443	214565	SOLUBLE			Q562C2	
BRAIN ZN-FINGER PROTEIN	TRANSCRIPTION	Brain Zn-finger protein Brain zinc finger protein	48300	58219528	307560	SOLUBLE			Q6U6G5	
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	MEMBRANE	signal anchor	45 23 IN-OUT	P10716 Q4KMB0	
CATHEPSIN D	LYSOSOME	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	SOLUBLE	cleavable signal peptide		P24268	
CATHEPSIN Z	LYSOSOME	Cathepsin Z precursor	34190	60688149	160297	SOLUBLE	cleavable signal peptide		Q5BKD9 Q9R1T3	
CENTAURIN-ALPHA2 PROTEIN	GTPASE	Centaurin-alpha 2	43520	9910340	42770	SOLUBLE			Q9JK15	
SIMILAR TO COMPLEMENT COMPONENT 1, Q SUBCOMP	BIOSYNTHETIC CARGO	Complement C1q subcomponent subunit A precursor	25920	62906846	355419	SOLUBLE	cleavable signal peptide		P31720 Q5RJK1	
COMPLEMENT INHIBITORY FACTOR H	BIOSYNTHETIC CARGO	Complement inhibitory factor H	140300	18426830	96863	SOLUBLE	cleavable signal peptide		Q91YB6	
MEMBRANE-ASSOCIATED GUANYLATE KINASE-INTERAC	SIGNALING	Connector enhancer of kinase suppressor of ras 2 Connector enhancer of KSR2 CNK2 Membrane-associated guanylate kinase-interacting protein MAGUIN	117400	50400225	169306	SOLUBLE			Q9R093 Q9Z1T4	
EDF-1 PROTEIN	SIGNALING	Endothelial differentiation-related factor 1 EDF-1 Multiprotein-bridging factor 1 MBF1 Calmodulin-associated peptide 19 CAP-19	16370	62510525	98538	SOLUBLE			P69736	
GM2 ACTIVATOR PROTEIN	LYSOSOME	GM2 activator protein	21520	27229316	157436	SOLUBLE	cleavable signal peptide	5 23 IN-OUT	Q8CJH4	NP_758838.1
GLUTAMATE--CYSTEINE LIGASE REGULATORY SUBUNIT	METABOLISM	Glutamate--cysteine ligase regulatory subunit Gamma-glutamyl/cysteine synthetase Gamma-ECS GCS light chain Glutamate--cysteine ligase modifier subunit	30550	8393446	51464	SOLUBLE			P48508	
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	SOLUBLE			Q8K1Q0	
HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN D0	NUCLEUS	Heterogeneous nuclear ribonucleoprotein D0 hnRNP D AU-rich element RNA-binding protein 1	38190	9588096	47431	SOLUBLE	cleavable signal peptide		Q9JU51 Q9JU52 Q9JU53 Q9JU54	
HYPOTHETICAL PROTEIN YGEH	UNKNOWN	Hypothetical protein ygeH	95100	2143952	80375	SOLUBLE				
INTERFERON-INDUCED 35 KDA PROTEIN	SIGNALING	Interferon-induced protein 35 Predicted	31760	57526854	315195	SOLUBLE			Q5M849	
LANTHIONINE SYNTHETASE C-LIKE PROTEIN 1	SIGNALING	LanC-like protein 1 40 kDa erythrocyte membrane protein p40	45240	6625487	126112	SOLUBLE			Q9ER29 Q9QX69	
LUPUS LA PROTEIN HOMOLOG	TRANSCRIPTION	Lupus La protein homolog La ribonucleoprotein La autoantigen homolog	47780	729919	37247	SOLUBLE			P38656	NP_112381.1
LYSOZYME C, TYPE 1 PRECURSOR	LYSOSOME	Lysozyme	16730	7428180	39196	SOLUBLE	cleavable signal peptide		Q6PDV1	
PAR INTERACTING PROTEIN	NUCLEUS	MYB binding protein 1a	144700	7514041	78121	SOLUBLE			UPI00000E85AB	
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	SOLUBLE			Q9WTY9	
NASCENT POLYPEPTIDE-ASSOCIATED COMPLEX ALPHA	PROT SYN/FOLD	Nascent polypeptide-associated complex subunit alpha Alpha-NAC Alpha-NAC/1.9.2	23380	27710456	74102	SOLUBLE				
NUCLEOPHOSMIN	NUCLEUS	Nucleophosmin NPM Nucleolar phosphoprotein B23 Numatrin Nucleolar protein NO38	32560	7242160	44225	SOLUBLE			P13084 Q63698 Q64269	

CADHERIN-11	PLASMA MB	PREDICTED: cadherin 11	88040	34851208	199319	MEMBRANE	cleavable signal peptide	618 23 OUT-IN	UPI000019BDF0	
FK506-BINDING PROTEIN 3	PROT SYN/FOLD	PREDICTED: similar to 25 kDa FK506-binding protein	25180	27664664	289953	SOLUBLE			UPI000018229C	
CLATHRIN AP-3, BETA 3B	COAT	PREDICTED: similar to AP-3 complex beta3B subunit	119100	34857415	191978	SOLUBLE			UPI00001CE91A	
AU-BINDING ENOYL-COA HYDRATASE	PEROXISOME	PREDICTED: similar to Auh protein	33340	34873875	242939	SOLUBLE	cleavable signal peptide		UPI00001D10E4	
SIMILAR TO CDNA SEQUENCE BC003236	UNKNOWN	PREDICTED: similar to BC003236 protein	70080	34859748	277682	SOLUBLE			UPI00001CEF50	
SIMILAR TO PROBABLE RNA HELICASE	NUCLEUS	PREDICTED: similar to RCK	54310	34879288	208269	SOLUBLE			UPI00001D09B7	
SIMILAR TO APOLIPOPROTEIN L3 (APOLIPOPROTEIN L-II)	BIOSYNTHETIC CARGO	PREDICTED: similar to RIKEN cDNA 2210421G13	39900	27662274	245688	SOLUBLE			UPI00001CA071	
RIBONUCLEASE P PROTEIN SUBUNIT P20	NUCLEUS	PREDICTED: similar to RPP20 protein	15740	27663642	220097	SOLUBLE			UPI000017F661	
SIMILAR TO EUKARYOTIC TRANSLATION INITIATION FACTOR 2, subunit 3, structural gene X-linked	PROT SYN/FOLD	PREDICTED: similar to eukaryotic translation initiation factor 2, subunit 3, structural gene X-linked	51080	34880581	267441	SOLUBLE			UPI000017E138	
SIMILAR TO H3 HISTONE FAMILY, MEMBER I	NUCLEUS	PREDICTED: similar to histone 1, H3g	33280	34876396	213604	SOLUBLE			UPI00001D117C	
SIMILAR TO KIAA0363	UNKNOWN	PREDICTED: similar to mKIAA0363 protein	138500	34879082	246047	SOLUBLE			UPI00001D0C60	
SLINGSHOT-2L	SIGNALING	PREDICTED: similar to slingshot-2L	159400	34873212	264614	SOLUBLE			UPI00001D0521	
PEPTIDYL-PROLYL CIS-TRANS ISOMERASE, MITOCHONDRIAL PRECURSOR PP1ase Rotamase Cyclophilin F	MITOCHONDRIA	Peptidyl-prolyl cis-trans isomerase, mitochondrial precursor PP1ase Rotamase Cyclophilin F	21810	56268806	88229	SOLUBLE	cleavable signal peptide		P29117	
SIMILAR TO PROLIFERATION-ASSOCIATED PROTEIN 1	NUCLEUS	Proliferation-associated 2G4, 38kDa	43660	51948384	304663	SOLUBLE			Q6AYD3	XP_213828.2
RNA-DEPENDENT INITIATION FACTOR-2 KINASE	PROT SYN/FOLD	RNA-dependent initiation factor-2 kinase	58260	9506993	47246	SOLUBLE			Q63184	
RATSG1	NUCLEUS	Ratg1	40610	18266700	111523	SOLUBLE			Q8VHV7	
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:l830174F05 product:ribosomal protein L36a-like, full insert sequence	12440	62643486	111202	SOLUBLE				
SH3 AND MULTIPLE ANKYRIN REPEAT DOMAINS PROTEIN 2	CYTOSKELETON	SH3 and multiple ankyrin repeat domains protein 2	134300	7513954	13148	SOLUBLE			Q9QX74 UPI000017086F	
PNUTS-PUTATIVE PROTEIN PHOSPHATASE 1 NUCLEAR	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	SOLUBLE			O55000 Q8M/G09	
SERUM DEPRIVATION RESPONSE GENE	UNKNOWN	Serum deprivation-response protein Phosphatidylserine-binding protein	46390	81884184	272310	SOLUBLE				XP_237121.2
SHWACHMAN-BODIAN-DIAMOND SYNDROME PROTEIN H	UNKNOWN	Shwachman-Bodian-Diamond syndrome Predicted	28750	56605652	227484	SOLUBLE			Q5RK30	XP_213759.1
RNA-BINDING PROTEIN STAUFEN	PROT SYN/FOLD	Staufen isoform Stau+I6	54800	9754866	60405	SOLUBLE			Q9ET50	
STRESS-INDUCED-PHOSPHOPROTEIN 1 (STI1)	SIGNALING	Stress-induced-phosphoprotein 1 STI1 Hsc70/Hsp90-organizing protein Hop	62570	54036435	82685	SOLUBLE			O35814	
TSH RECEPTOR SUPPRESSOR ELEMENT-BINDING PROTEIN-1	TRANSCRIPTION	TSH receptor suppressor element-binding protein-1	35530	9663686	93202	SOLUBLE			P97752	
SIMILAR TO TARDBP PROTEIN	UNKNOWN	Tax_id=101116 33 kDa protein	33300	34872473	212891	SOLUBLE				
NUCLEOLIN	NUCLEUS	Tax_id=101116 Ensembl_locations(Chr-bp):9-85296295 nucleolin	77150	6981248	69538	SOLUBLE				

SIMILAR TO 60S RIBOSOMAL PROTEIN L29	PROT SYN/FOLD	Tax_Id=10116 Similar to 60S RIBOSOMAL PROTEIN L29 (P23)	16820	34880973	233078	SOLUBLE			
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 Subunit) (Beta-3A-adaptin)	129800	34853134	203467	SOLUBLE			
CD83 ANTIGEN	PLASMA MB	Tax_Id=10116 Similar to CD83 antigen	29030	34875124	281345	MEMBRANE	204 23 IN-OUT		
SIMILAR TO (RETINAL SHORT-CHAIN DEHYDROGENASE) BOX POLYPEPTIDE	DETOXIFICATION	Tax_Id=10116 Similar to Cgn-pending protein	159200	34858031	242726	SOLUBLE			
SIMILAR TO DEAD (ASP-GLU-ALA-ASP) BOX POLYPEPTIDE	PROT SYN/FOLD	Tax_Id=10116 Similar to DEAD (ASP-Glu-Ala-ASP) box polypeptide 28	64620	34851714	284837	SOLUBLE			
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 RIG-I	94370	34867138	315303	SOLUBLE			
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	SOLUBLE			
SIMILAR TO HYPOTHETICAL PROTEIN KIAA0555	UNKNOWN	Tax_Id=10116 Similar to Hypothetical protein KIAA0555	108700	34879361	286232	SOLUBLE			
SIMILAR TO KIAA0342 PROTEIN	UNKNOWN	Tax_Id=10116 Similar to KIAA0342 protein	333800	34866451	266038	SOLUBLE			
NEBULIN	CYTOSKELETON	Tax_Id=10116 Similar to Nebulin	913200	34854661	287849	SOLUBLE			
SIMILAR TO QUINONE-REDUCTASE PROTEIN	UNKNOWN	Tax_Id=10116 Similar to RIKEN cDNA 2810025M15	71590	34880767	272641	SOLUBLE			
SIMILAR TO RIKEN CDNA 5630401D24	UNKNOWN	Tax_Id=10116 Similar to RIKEN cDNA 5630401D24	81090	34880803	213507	SOLUBLE			
SIMILAR TO RIKEN CDNA 5730409F24	UNKNOWN	Tax_Id=10116 Similar to RIKEN cDNA 5730409F24	38500	34861617	317744	SOLUBLE			
ZDHHC9 PROTEIN	UNKNOWN	Tax_Id=10116 Similar to RIKEN cDNA 9530098M12	30200	34881592	267183	MEMBRANE	36 20 IN-OUT 59 23 OUT-IN 184 23 IN-OUT		
SIMILAR TO RHO-RELATED BTB DOMAIN-CONTAINING PROTEIN 3	SIGNALING	Tax_Id=10116 Similar to Rho-related BTB domain-containing protein 3	77710	34852777	300892	SOLUBLE			
SIDEKICK 2; DROSOPHILA SIDEKICK-LIKE; CHICKEN SIDEKICK	PLASMA MB	Tax_Id=10116 Similar to Sidekick 2	185200	34875033	275767	MEMBRANE	524 23 IN-OUT 1363 23 OUT-IN		
SIMILAR TO ZINC FINGER PROTEIN 35 (ZFP-35)	UNKNOWN	Tax_Id=10116 Similar to Zinc finger protein 35 (Zfp-35)	87610	34878337	217979	SOLUBLE			
ASH1 (ABSENT, SMALL, OR HOMEOTIC)-LIKE	UNKNOWN	Tax_Id=10116 Similar to aSh1 (absent, small, or homeotic)-like	336900	34857960	247038	SOLUBLE			
SIMILAR TO ACYL-COENZYME A DEHYDROGENASE FAMILY	MITOCHONDRIA	Tax_Id=10116 Similar to acyl-Coenzyme A dehydrogenase family, member 8	28470	34866733	288241	SOLUBLE	cleavable signal peptide		
COILED-COIL PROTEIN	TRAFFIC	Tax_Id=10116 Similar to coiled-coil protein	148900	34869656	304228	MEMBRANE	signal anchor	7 23 IN-OUT	
COLLAGEN TYPE XIV	BIOSYNTHETIC CARGO	Tax_Id=10116 Similar to collagen type XIV	169900	34866496	308317	SOLUBLE	cleavable signal peptide	12 20 IN-OUT	
COPINE III	TRAFFIC	Tax_Id=10116 Similar to copine III	59690	34867199	274130	SOLUBLE			
EUKARYOTIC TRANSLATION INITIATION FACTOR 4 GAMMA	PROT SYN/FOLD	Tax_Id=10116 Similar to eukaryotic translation initiation factor 4 gamma, 3	181400	34872195	316191	SOLUBLE			
EUKARYOTIC TRANSLATION INITIATION FACTOR 4G I	PROT SYN/FOLD	Tax_Id=10116 Similar to eukaryotic translation initiation factor 4G I	175000	34869741	239406	SOLUBLE			
HYDROCEPHALUS-INDUCING PROTEIN	UNKNOWN	Tax_Id=10116 Similar to hydrocephalus-inducing protein	144600	34851748	250307	SOLUBLE			
SIMILAR TO HIGH GLUCOSE-REGULATED PROTEIN 8	UNKNOWN	Tax_Id=10116 Similar to hypothetical protein FLJ31657	64050	34855501	253349	SOLUBLE			
MEIOTIC RECOMBINATION PROTEIN REC14	NUCLEUS	Tax_Id=10116 Similar to meiotic recombination protein REC14	28800	34863419	201803	SOLUBLE			
SIMILAR TO METHIONYL AMINOPEPTIDASE 1	PROT MOD	Tax_Id=10116 Similar to methionyl aminopeptidase 1	53240	34860820	221417	SOLUBLE			
MICROTUBULE-ASSOCIATED PROTEIN 4	CYTOSKELETON	Tax_Id=10116 Similar to microtubule-associated protein 4	303100	34866431	264572	SOLUBLE			
GOLGI-ASSOCIATED MICROTUBULE-BINDING PROTEIN	CYTOSKELETON	Tax_Id=10116 Similar to thyroid hormone receptor interactor 11	115700	34867565	247636	SOLUBLE			
SIMILAR TO VASCULAR ENDOTHELIAL ZINC FINGER 1	TRANSCRIPTION	Tax_Id=10116 Similar to vascular endothelial zinc finger 1	82930	34872980	252804	SOLUBLE			

TRANSCRIPTIONAL ACTIVATOR PROTEIN PUR-ALPHA	NUCLEUS		Transcriptional activator protein PUR-alpha Purine-rich single-stranded DNA-binding protein alpha	34880	34878862	81816	SOLUBLE				
TROPONIN T, FAST SKELETAL MUSCLE ISOFORMS BETA	CYTOSKELETON		Troponin T, fast skeletal muscle isoforms beta/alpha	30750	78883516	31540	SOLUBLE			P09739 Q304F4	
UBIQUITIN-LIKE PROTEIN SUMO-1 CONJUGATING ENZYME	PROTEASOME/UBIQUITIN		Ube2l-prov protein	18010	6981690	22316	SOLUBLE			P63281	
HISTONE H2B	NUCLEUS		histone H2B	13770	223096	135066	SOLUBLE				
HISTONE H2A	NUCLEUS		similar to Histone H2A.o (H2A.o) (H2A.2) (H2a-615)	21070	34858256	279473	SOLUBLE			UPI00001CEF1B	
NADP+-SPECIFIC ISOCITRATE DEHYDROGENASE	MITOCHONDRIA		similar to NADP+-specific isocitrate dehydrogenase	14720	34857317	195949	SOLUBLE			UPI00001CE8EE	
(HNRNP-Q) (SYNAPTOTAGMIN BINDING, CYTOPLASMIC)	NUCLEUS		similar to Nsap1-pending protein [Rattus norvegicus]	82690	34865422	221070	SOLUBLE				
BIPHENYL HYDROLASE-LIKE (SERINE HYDROLASE, BIPHENYL HYDROLASE-LIKE)	DETOXIFICATION		similar to RIKEN cDNA 2010012D11	22040	34875339	204593	SOLUBLE	cleavable signal peptide		UPI00001D113E	
NUDT16 PROTEIN	UNKNOWN		similar to RIKEN cDNA 2310041H06 [Rattus norvegicus]	21700	34865854	267421	SOLUBLE				
XPA BINDING PROTEIN 1	NUCLEUS		similar to RIKEN cDNA 2410004J02	40230	34862639	270236	SOLUBLE	cleavable signal peptide		UPI00001CF964	
TUBBY RELATED PROTEIN 2	TRANSCRIPTION		similar to Tubby related protein 2 (Tubby-like protein 2) (P4-6 protein) [Rattus norvegicus]	48750	34856083	256460	SOLUBLE				
PEROXISOMAL ACYL-COA THIOESTERASE 2B; LIKELY OXALACETATE	PEROXISOME		similar to peroxisomal long chain acyl-CoA thioesterase la	46360	27667388	160562	SOLUBLE			UPI00001822A8	
RB BINDING PROTEIN	NUCLEUS		similar to retinoblastoma-binding protein 1 isoform l; retinoblastoma-binding protein 1	158900	34865364	211734	SOLUBLE			UPI00001CF9FE	
TELOMERIC AND TETRAPLEX DNA BINDING PROTEIN Q1	NUCLEUS		telomeric and tetraplex DNA binding protein qTBP42 V rat (fragment)	4079	7446334	72931	SOLUBLE				
MITOCHONDRIAL TRANSCRIPTION FACTOR A	MITOCHONDRIA		transcription factor A, mitochondrial	28140	4877353	75905	SOLUBLE			UPI0000167962	
SIMILAR TO HYPOTHETICAL PROTEIN FLJ13089	UNKNOWN		unknown	111800	34872548	263673	SOLUBLE			UPI00001D095C	
BICAUDAL D PROTEIN	UNKNOWN		Bicaudal D protein	93420	38454268	223054	SOLUBLE			Q712J3	
GALECTIN-3	TRANSCRIPTION		Galectin-3	27200	57870645	71532	SOLUBLE			P08699	
HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1	NUCLEUS		Heterogeneous nuclear ribonucleoprotein A1	34200	70819	29410	SOLUBLE			Q5I0M7	
HOMEODOMAIN PROTEIN OTX2	NUCLEUS		Homeobox protein OTX2	31640	27699029	44484	SOLUBLE				
HYDROXYSTEROID (17-BETA) DEHYDROGENASE 8	DETOXIFICATION		Hydroxysteroid (17-beta) dehydrogenase 8	26790	47087119	301041	SOLUBLE	cleavable signal peptide		Q6MGB5	XP_342097.1
N-MYC PROTO-ONCOGENE PROTEIN	TRANSCRIPTION		N-myc proto-oncogene protein	49690	61556942	103852	SOLUBLE			Q63379	
RAS-GTPASE-ACTIVATING PROTEIN SH3-DOMAIN BINDING	TRAFFIC		PREDICTED: Ras-GTPase-activating protein SH3-domain binding protein	51790	34870749	252580	SOLUBLE			UPI000017F395	
SIMILAR TO PROTEIN CGI-117 (PROTEIN HSPC111)	UNKNOWN		PREDICTED: similar to DNA segment, Chr 13, Wayne State University 177, expressed	21120	95102018	253829	SOLUBLE			Q1RP77	
SYNAPTIC VESICLE MEMBRANE PROTEIN VAT-1 HOMOLOG	UNKNOWN		PREDICTED: similar to Vesicle amine transport protein 1 homolog (T californica)	43120	76096306	312134	SOLUBLE			UPI0000183039	
SIMILAR TO HYPOTHETICAL PROTEIN BC013949	UNKNOWN		PREDICTED: similar to hypothetical protein BC013949	25320	27668745	274768	SOLUBLE			Q3MIE4	
PEROXISOME PROLIFERATOR-ACTIVATED RECEPTOR G	PEROXISOME		Peroxisome proliferator-activated receptor gamma coactivator 1-beta PPAR gamma coactivator-1beta PPARGC-1-beta PGC-1-beta	109400	28570176	279034	SOLUBLE			UPI0000180D5D	
SIGNAL RECOGNITION PARTICLE 14 KDA PROTEIN	PROT SYN/FOLD		Signal recognition particle 14 kDa protein SRP14	12510	27731985	38099	SOLUBLE			UPI000017FC64	
SPHINGOSINE 1-PHOSPHATE RECEPTOR EDG-1	PLASMA MB		Sphingosine 1-phosphate receptor Edg-1 Sphingosine phosphate receptor 1 S1P1	42750	8393290	51431	MEMBRANE			Q811R2-2	
									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	

ZETA-CRYSTALLIN	CYTOSKELETON	Tax_Id=10116 Ensembl_locations(Chr-bp):2-252454876 similar to crystallin, zeta	37130	34860973	210117	SOLUBLE				
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	SOLUBLE				
SIMILAR TO ALY	TRANSCRIPTION	Tax_Id=10116 Similar to ALY	21140	34875658	307156	SOLUBLE				
SIMILAR TO ATP-BINDING CASSETTE TRANSPORTER SUBUNIT 3	UNKNOWN	Tax_Id=10116 Similar to Abca3 protein	108000	34860091	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			
SIMILAR TO B CELL PHOSPHOINOSITIDE 3-KINASE ADAPTOR	UNKNOWN	Tax_Id=10116 Similar to B cell phosphoinositide 3-kinase adaptor	103600	34862928	233246	SOLUBLE				
SIMILAR TO CALMODULIN 4 (CALCIUM-BINDING PROTEIN)	PROT SYN/FOLD	Tax_Id=10116 Similar to Calmodulin 4 (Calcium-binding protein Dd112)	16820	34876599	290493	SOLUBLE				
FLASH	SIGNALING	Tax_Id=10116 Similar to FLASH	219700	34867106	267985	SOLUBLE				
PTB-ASSOCIATED SPLICING FACTOR	TRANSCRIPTION	Tax_Id=10116 Similar to PTB-associated Splicing factor	65140	34871066	310879	SOLUBLE				
PROTEIN TRANSPORT PROTEIN SEC24D (SEC24-RELATED PROTEIN)	COAT	Tax_Id=10116 Similar to Protein transport protein Sec24D (SEC24-related protein D)	110300	34859959	219262	SOLUBLE				
SIMILAR TO RIKEN CDNA 1700034M03 GENE	UNKNOWN	Tax_Id=10116 Similar to RIKEN cDNA 1700034M03 gene	122500	34854321	261953	SOLUBLE	cleavable signal peptide			
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	SOLUBLE				
CYTOCHROME P450 NA5	DETOXIFICATION	Tax_Id=10116 Similar to cytochrome P450RAL-2	95320	34862888	279884	SOLUBLE				
FERROCHELATASE	MITOCHONDRIA	Tax_Id=10116 Similar to ferrochelatase	71200	34932061	313806	SOLUBLE				
SPLICING FACTOR 3B, SUBUNIT 1, 155KD	NUCLEUS	Tax_Id=10116 Splicing factor 3b, Subunit 1, 155kD	146000	34875872	194817	SOLUBLE				
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	SOLUBLE			O08887 Q63619	
SIMILAR TO NEURONAL APOPTOSIS INHIBITORY PROTEIN	SIGNALING	similar to neuronal apoptosis inhibitory protein	158900	34853608	241983	SOLUBLE			UPI00001CECF0	
SIMILAR TO PUTATIVE ZN-FINGER PROTEIN C47S	UNKNOWN	similar to putative Zn-finger protein C47S	31790	34874602	251444	SOLUBLE			UPI00001D01B3	
NUCLEOLAR TRANSCRIPTION FACTOR 1 (UPSTREAM BINDING PROTEIN)	TRANSCRIPTION	(P25977) Isoform UBF2 of P25977	84970	112465	11409	SOLUBLE			P25977-2	
AMILORIDE-SENSITIVE CATION CHANNEL 1, NEURONAL	PLASMA MB	(Q62962) Isoform 2 of Q62962	63120	35902696	106925	SOLUBLE			Q62962-2	
60S RIBOSOMAL PROTEIN L39	PROT SYN/FOLD	60S ribosomal protein L39	6407	6981484	4822	SOLUBLE			P02404	
60S RIBOSOMAL PROTEIN L40	PROT SYN/FOLD	60S ribosomal protein L40 CEP52	6181	973178	77849	SOLUBLE			P62986	
CANALICULAR MULTISPECIFIC ORGANIC ANION TRANSPORTER	PLASMA MB	ATP-binding cassette, sub-family C (CFTR/MRP), member 3	169300	3242460	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		UPI000016797E	
SHORT CHAIN ACYL-COA DEHYDROGENASE	MITOCHONDRIA	Acyl-coenzyme A dehydrogenase, short chain	44970	48734846	84143	SOLUBLE	cleavable signal peptide		Q6IMX3	

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:I830027D22 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	SOLUBLE	signal anchor	40 23 IN-OUT 97 23 OUT-IN 139 23 IN-OUT	Q4KM64	
ADENYLATE KINASE 3 ALPHA-LIKE 1	MITOCHONDRIA	Ak3 protein	25490	40352787	270293	SOLUBLE	cleavable signal peptide		Q6F2A5	
AMYLOID BETA A4 PRECURSOR PROTEIN-BINDING FAMILY MEMBER 3 FE65-LIKE PROTEIN 2 FE65L2	BIOSYNTHETIC CARGO	Amyloid beta A4 precursor protein-binding family B member 3 Fe65-like protein 2 Fe65L2	54910	2293387	157236	SOLUBLE			O35827	
C-4 METHYL STEROL OXIDASE	DETOXIFICATION	C-4 methylsterol oxidase Methylsterol monooxygenase Neurolep 1 RANP-1	34960	38649308	807	MEMBRANE	cleavable signal peptide	55 23 OUT-IN 101 23 IN-OUT 194 23 OUT-IN	O35532	
C4B-BINDING PROTEIN ALPHA CHAIN	BIOSYNTHETIC CARGO	C4b-binding protein alpha chain precursor C4bp	62270	899380	3668	SOLUBLE	cleavable signal peptide		Q63514	
CARBONYL REDUCTASE 4	DETOXIFICATION	Carbonyl reductase 4	25290	55562775	166315	SOLUBLE			Q7TS56	
CATHEPSIN H	LYSOSOME	Cathepsin H precursor	37100	6978721	3719	SOLUBLE	cleavable signal peptide		P00786	
CYTOCHROME C OXIDASE POLYPEPTIDE VIIC, MITOCHONDRIAL	MITOCHONDRIA	Cytochrome c oxidase polypeptide VIic, mitochondrial VIIIA	1117	1169069	71407	SOLUBLE			P80432	
DIACYLGLYCEROL O-ACYLTRANSFERASE 1	PROT MOD	Diacylglycerol O-acyltransferase 1 Diglyceride acyltransferase	56870	9965432	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	
HEXOKINASE, TYPE I	METABOLISM	Hexokinase, type I	102400	6981022	3926	SOLUBLE			P05708	
HNRNP PROTEIN	NUCLEUS	HnRNP protein	18280	3021529	57359	SOLUBLE			O70592	
SIMILAR TO RIKEN CDNA 5730470L24	UNKNOWN	Hypothetical protein RGD1311316	23580	62644110	229302	SOLUBLE			Q5FWT9	
INSIG2 MEMBRANE PROTEIN (INSULIN INDUCED GENE 2)	PROT SYN/FOLD	INSIG2 membrane protein Insulin induced gene 2	24970	55250700	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	
INOSITOL 1,4,5-TRISPHOSPHATE RECEPTOR TYPE 1	CALCIUM TRANS/BIND	Inositol 1,4,5-trisphosphate receptor type 1	19180	204967	126700	SOLUBLE			P29994	
CARNITINE DEFICIENCY-ASSOCIATED GENE EXPRESSED IN VENTRICLE 1 CDV-1	UNKNOWN	Intraflagellar transport 81 Carnitine deficiency-associated protein expressed in ventricle 1 CDV-1 protein	79030	48474223	282022	SOLUBLE			P83829	
CG6210-LIKE	UNKNOWN	LOC362065 protein Transmembrane protein	62200	45680888	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	Q6F689	
LRRGT00033	UNKNOWN	LRRGT00033	230300	37654282	223419	SOLUBLE			Q6TXG6	
SIMILAR TO COAGULATION FACTOR XI; PLASMA THROMBIN	BIOSYNTHETIC CARGO	LRRGT00086	62990	37361858	209490	SOLUBLE			Q6TUF8	
MYOSIN HEAVY CHAIN, CARDIAC MUSCLE ALPHA ISOFORM	CYTOSKELETON	Myosin heavy chain, cardiac muscle alpha isoform MyHC-alpha	223500	8393804	51542	SOLUBLE			P02563 Q63351	
SIMILAR TO SMFN PROTEIN	NUCLEUS	Oligoribonuclease, mitochondrial precursor Small fragment nuclease RNA exonuclease 2 homolog	26750	81910234	216886	SOLUBLE			Q5U1X1	XP_217137.1

SIMILAR TO CD7 PROTEIN	PLASMA MB	PREDICTED: similar to Cd7 protein	22880	27690996	222889	MEMBRANE	cleavable signal peptide	146 23 OUT-IN	UPI00001CB348	
NEDD8 ULTIMATE BUSTER-1	PROTEASOME/UBIQUITIN	PREDICTED: similar to NEDD8 ultimate buster-1 (BS4 protein)	73130	34853974	279528	SOLUBLE			UPI00001CF42E	
EUKARYOTIC TRANSLATION INITIATION FACTOR 3, SUBUNIT 1	PROT SYN/FOLD	PREDICTED: similar to RIKEN cDNA 1200009C21	25110	27730981	189964	SOLUBLE			UPI00001816CA	
SIMILAR TO RS21-C6 PROTEIN	UNKNOWN	PREDICTED: similar to RS21-C6 protein	32140	34877104	218331	SOLUBLE			UPI00001D0F20	
STROMAL CELL-DERIVED FACTOR 2 (SDF-2)	BLOOD + OTHER CELLS	PREDICTED: similar to Stromal cell-derived factor 2 precursor (SDF-2)	24060	27673471	232984	SOLUBLE	cleavable signal peptide	12 23 IN-OUT	UPI00001CB008	
SIMILAR TO HYPOTHETICAL PROTEIN FLJ31364	NUCLEUS	PREDICTED: similar to hypothetical protein 6820428D13	64490	27688925	279415	SOLUBLE	cleavable signal peptide		UPI00001CB15C	
MEMBRANE PROGESTIN RECEPTOR ALPHA	DETOXIFICATION	PREDICTED: similar to membrane progesterin receptor alpha	39280	27732829	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	UPI00001830B3	
SIMILAR TO REGULATOR OF G-PROTEIN SIGNALING RGS18	SIGNALING	PREDICTED: similar to regulator of G-protein signaling RGS18	27660	34880519	259576	SOLUBLE			UPI000018124E	
SIMILAR TO SEX-DETERMINATION PROTEIN HOMOLOG 1	UNKNOWN	PREDICTED: similar to sex-determination protein homolog Fem1b	70240	27720561	314220	SOLUBLE	cleavable signal peptide		UPI000017E95E	
SP12	PROT SYN/FOLD	PREDICTED: similar to signal peptidase 12kDa	11750	27667224	307512	MEMBRANE	signal anchor	20 23 OUT-IN 47 23 IN-OUT	UPI00001CC60E	
SIMILAR TO ZINEDIN	SIGNALING	PREDICTED: similar to zinedin	81440	34855229	315735	SOLUBLE	cleavable signal peptide		UPI0000182C93	
SIMILAR TO HSPC288	UNKNOWN	Probable ergosterol biosynthetic protein 28	15810	62651081	178365	MEMBRANE	cleavable signal peptide	5 23 IN-OUT 47 23 OUT-IN 76 23 IN-OUT 108 23 OUT-IN		
RNA 3'-TERMINAL PHOSPHATE CYCLASE	NUCLEUS	RNA terminal phosphate cyclase domain 1	39310	51948426	319337	SOLUBLE			Q68FS8	XP_215694.2
SH3P13	UNKNOWN	SH3P13 SH3 domain protein 2 C1	35310	7109256	75738	SOLUBLE			Q9JKT0	
POLYCOMB-GROUP PROTEIN	UNKNOWN	Scm-like with four mbt domains 1	97510	8100077	78111	SOLUBLE			UPI00000E7DFC	
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	SOLUBLE	cleavable signal peptide			
INOSINE MONOPHOSPHATE DEHYDROGENASE 1	METABOLISM	Tax_Id=10116 Ensembl_locations(Chr-bp):4-56330652 similar to Impdh1 protein	60730	34855047	190455	SOLUBLE	cleavable signal peptide			
SIMILAR TO 2810022L02RIK PROTEIN	UNKNOWN	Tax_Id=10116 Ensembl_locations(Chr-bp):9-56745024 similar to 2810022L02Rik protein	31270	34877015	195304	SOLUBLE				
GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE (CYTOSOLIC)	(CYTOSOLIC) METABOLISM	Tax_Id=10116 HypoHetical protein XP_340782	19430	34870634	206459	SOLUBLE	signal anchor	43 23 OUT-IN		
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	SOLUBLE	cleavable signal peptide			
SIMILAR TO OTTHUMP00000028696	UNKNOWN	Tax_Id=10116 Similar to A1428795 protein	225500	34872984	229208	SOLUBLE				
SIMILAR TO CALMODULIN REGULATED SPECTRIN-ASSOCIATED PROTEIN 1	UNKNOWN	Tax_Id=10116 Similar to CG33130-PA	132700	34853057	208493	SOLUBLE				
FRUCTOSAMINE-3-KINASE-RELATED PROTEIN	SIGNALING	Tax_Id=10116 Similar to Hypothetical protein 9030012M21	37150	34875719	205153	SOLUBLE				
SIMILAR TO KIAA1208 PROTEIN	UNKNOWN	Tax_Id=10116 Similar to KIAA1208 protein	154100	34864701	229899	MEMBRANE	signal anchor	20 23 IN-OUT 1314 23 OUT-IN		
HYPOTHETICAL PROTEIN LOC303749	UNKNOWN	Tax_Id=10116 Similar to RIKEN cDNA 1110031I02	36810	34875673	300976	SOLUBLE	signal anchor	39 23 IN-OUT		

UDP-N-ACETYLGUCOSAMINE (UDP-GLCNAC) TRANSPO	PROT MOD	Tax_Id=10116 Similar to RIKEN cDNA 2310050P13	55910	34859909	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		
SIMILAR TO RIKEN CDNA 4932408F18	UNKNOWN	Tax_Id=10116 Similar to RIKEN cDNA 4932408F18	164100	34867309	293100	SOLUBLE				
SIMILAR TO RIBONUCLEASE III (RNASE III) (P241)	NUCLEUS	Tax_Id=10116 Similar to RibonucleaSe III (RNase III) (p241)	170500	34854376	206108	SOLUBLE				
SIMILAR TO SHORT TRANSIENT RECEPTOR POTENTIAL	PLASMA MB	Tax_Id=10116 Similar to Short tranSient receptor potential channel 3 (TrpC3) (Htrp-3) (Htrp3)	118800	34873770	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		
SIMILAR TO SULFATASE MODIFYING FACTOR 2	PROT MOD	Tax_Id=10116 Similar to SulfataSe modifying factor 2	25680	34872061	221314	SOLUBLE	cleavable signal peptide			
COPINE IV	TRAFFIC	Tax_Id=10116 Similar to copine IV	96010	34865971	245798	SOLUBLE				
SIMILAR TO DJ545L17.1 (NOVEL PROTEIN SIMILAR TO RAD21)	UNKNOWN	Tax_Id=10116 Similar to dJ545L17.1 (novel protein Similar to RAD21 (S. pombe) homolog (KIAA0078))	23480	34858963	293085	SOLUBLE				
SIMILAR TO ENDOPHILIN B1B	PROT MOD	Tax_Id=10116 Similar to endophilin B1b	47410	34860931	263938	SOLUBLE				
FIDGETIN	UNKNOWN	Tax_Id=10116 Similar to fidgetin	84370	34854854	247355	SOLUBLE				
HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN D-L	NUCLEUS	Tax_Id=10116 Similar to heterogeneouS nuclear ribonucleoprotein D-like	58310	34876235	191966	SOLUBLE				
SIMILAR TO HYPOTHETICAL PROTEIN FLJ32785	UNKNOWN	Tax_Id=10116 Similar to hypothetical protein FLJ32785	89490	34858137	311347	SOLUBLE				
LENG8_PREDICTED PROTEIN	UNKNOWN	Tax_Id=10116 Similar to leukocyte receptor cluSter (LRC) member 8	103400	34854521	313918	SOLUBLE				
LUNG ALPHA/BETA HYDROLASE FOLD PROTEIN 3	UNKNOWN	Tax_Id=10116 Similar to lung alpha/beta hydrolaSe fold protein 3	50090	34877891	224186	MEMBRANE	signal anchor	26 23 IN-OUT		
RHO8TB2	GTPASE	Tax_Id=10116 Similar to mKIAA0717 protein	79880	34874404	284812	SOLUBLE				
SIMILAR TO MKIAA1707 PROTEIN	UNKNOWN	Tax_Id=10116 Similar to mKIAA1707 protein	124200	34868019	273598	SOLUBLE				
MEMBRANE BOUND O-ACYL TRANSFERASE	PROT MOD	Tax_Id=10116 Similar to malignant cell expreSSion-enhanced gene/tumor progreSSion-enhanc	33720	34854458	281230	MEMBRANE	signal anchor	5 18 OUT-IN 35 23 IN-OUT 72 23 OUT- IN 245 23 IN-OUT		
SIMILAR TO MEMBRANE RECEPTOR (5H375)	UNKNOWN	Tax_Id=10116 Similar to membrane receptor (5H375)	42380	34865609	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		
SIMILAR TO TOLLOID-LIKE 2	SIGNALING	Tax_Id=10116 Similar to tolloid-like 2	23740	34883204	298591	SOLUBLE				
TRANSMEMBRANE PROTEIN INDUCED BY TUMOR NECROSIS FACTOR ALPHA	UNKNOWN	Transmembrane protein induced by tumor necrosis factor alpha	40660	58219512	260939	MEMBRANE		138 19 OUT-IN 163 20 IN-OUT 192 23 OUT-IN 266 20 IN- OUT 305 20 OUT-IN	Q5HZE2	
CYTOCHROME-C OXIDASE (EC 1.9.3.1) CHAIN VIIA, HEPATIC-RAT (FRAGMENT)	MITOCHONDRIA	cytochrome-c oxidase (EC 1.9.3.1) chain VIIa, hepatic-rat (fragment)	1246	7513957	80282	SOLUBLE				
HYPOTHETICAL PROTEIN XP_347087	UNKNOWN	hypothetical protein XP_347087	13870	34866914	300655	SOLUBLE	cleavable signal peptide		UPI00001CFDC3	
SIMILAR TO GLYCINE DECARBOXYLASE	MITOCHONDRIA	similar to Glycine decarboxylase [Rattus norvegicus]	111900	34862790	260747	SOLUBLE				

SIMILAR TO KIAA0445 PROTEIN	UNKNOWN	similar to KIAA0445 protein	19800	34877826	256921	SOLUBLE			UPI00001D02CB	
SIMILAR TO PHOSPHOACETYLGUCOSAMINE MUTASE (METABOLISM)		similar to Phosphoacetylglucosamine mutase (PAGM) (Acetylglucosamine phosphomutase) (N-acetylglucosamine-phosphate mutase) (Phosphoglucmutase 3) [Rattus norvegicus]	50750	34865378	202185	SOLUBLE				
RNA-BINDING PROTEIN ISOFORM G3BP-2A	SIGNALING	similar to RNA-binding protein isoform G3BP-2a	54070	34876568	211028	SOLUBLE			UPI000017FB84	
HEAT SHOCK PROTEIN 60 (LIVER); HEAT SHOCK 60KD PROTEIN 1 (CHAPERONIN)	PROT SYN/FOLD	similar to heat shock protein 60 (liver); heat shock 60kD protein 1 (chaperonin)	30730	34860223	220421	SOLUBLE	cleavable signal peptide		UPI00001CEF75	
SIMILAR TO HYPOTHETICAL PROTEIN MGC27616	UNKNOWN	similar to hypothetical protein MGC27616	108100	34871738	239371	SOLUBLE			UPI00001D08E6	
SIMILAR TO INHIBITOR OF GROWTH FAMILY, MEMBER 3	TRANSCRIPTION	similar to inhibitor of growth family, member 3	56500	34855011	234073	SOLUBLE			UPI000001CF470	
SIMILAR TO OOCYTE-TESTIS GENE 1	UNKNOWN	similar to oocyte-testis gene 1 [Rattus norvegicus]	99590	34864546	279578	SOLUBLE				
AA2-020	UNKNOWN	(Q5M828) Isoform 2 of Q5M828	19640	33086520	284155	MEMBRANE		7 18 IN-OUT 114 23 OUT-IN	Q5M828-2	
HISTONE ACETYLTRANSFERASE	NUCLEUS	(Q810T5) Isoform 2 of Q810T5	66820	29650457	268104	SOLUBLE			Q810T5-2	
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	SOLUBLE			O35817	
ADP-RIBOSYLATION FACTOR-LIKE 6 INTERACTING PROTEIN	UNKNOWN	ADP-ribosylation-like factor 6-interacting protein Arh6ip1 protein	23450	68534822	139514	MEMBRANE	signal anchor	42 20 IN-OUT 66 23 OUT-IN 136 18 IN-OUT 158 23 OUT-IN	Q7TMZ5	NP_942032.1
ATP-BINDING CASSETTE PROTEIN C12 VARIANT A	UNKNOWN	ATP-binding cassette protein C12 variant A	144200	37778161	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	
BAND 3 ANION TRANSPORT PROTEIN	PLASMA MB	Band 3 anion transport protein	103200	20141169	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 868 23 IN-OUT	P23562	
CLUSTERIN	BIOSYNTHETIC CARGO	Clusterin	24930	11127974	36009	SOLUBLE			Q9ERD1	
COMPLEMENT REGULATORY PROTEIN	PLASMA MB	Complement regulatory protein Crry precursor Antigen 5/2	61680	9506513	35260	MEMBRANE	cleavable signal peptide	483 23 OUT-IN	Q63135 Q63612	
CYTOCHROME C OXIDASE POLYPEPTIDE VIA-LIVER/HHE	MITOCHONDRIA	Cytochrome c oxidase polypeptide VIIa-liver/heart, mitochondrial precursor Cytochrome c oxidase subunit VIIa-L	9353	56025	90517	MEMBRANE		53 23 IN-OUT	P35171	
SIMILAR TO RIKEN CDNA 6720485C15	UNKNOWN	Dephospho-CoA kinase domain containing	27350	56090393	318309	MEMBRANE		202 23 OUT-IN	Q6AY55	XP_340918.1
R_VAMP8	TETH/DOCK/FUS	Endobrevin	7348	18655558	37566	MEMBRANE			UPI0000111953	
EVOLUTIONARILY CONSERVED SIGNALING INTERMEDIA	SIGNALING	Evolutionarily conserved signaling intermediate in Toll pathway	49620	55741518	276570	SOLUBLE			Q5XIC2	XP_217092.2
F-ACTIN BINDING PROTEIN B-NEXILIN	CYTOSKELETON	F-actin binding protein b-Nexilin	78390	40538878	173653	SOLUBLE			Q9Z2J4	
N-RAS	GTPASE	GTPase NRas precursor Transforming protein N-Ras	21240	68534734	41163	SOLUBLE			Q04970 Q4KMB1	

GLIA MATURATION FACTOR BETA	CYTOSKELETON	GLIA maturation factor beta GMF-beta	16610	111660	148966	SOLUBLE			Q63228	
UNKNOWN (PROTEIN FOR MGC:72996)	UNKNOWN	Hypothetical protein MGC72996	20710	38454298	220427	MEMBRANE		135 23 OUT-IN 164 23 IN-OUT	Q6FCT6	
SIMILAR TO RIKEN CDNA 4933403F05	UNKNOWN	LEA_4 domain containing protein RGD1359600	31470	56090371	205582	MEMBRANE		134 23 IN-OUT	Q5XIJ4	XP_225853.1
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	SOLUBLE	cleavable signal peptide		Q8K5B3	
NEURONAL NICOTINIC ACETYLCHOLINE RECEPTOR SUBUNIT	PLASMA MB	Neuronal acetylcholine receptor protein subunit alpha-1 precursor Nicotinic acetylcholine receptor subunit alpha 10 NACHR alpha 10	49820	68051992	176273	MEMBRANE	cleavable signal peptide	238 23 OUT-IN 267 20 IN-OUT 301 23 OUT-IN 426 20 IN-OUT	Q9JLB5	
OBSCURIN	GTPASE	Obscurin	88460	28273604	261258	SOLUBLE			Q80ZF5	
SIMILAR TO GLUCOKINASE	UNKNOWN	PREDICTED: similar to ATP-dependent glucokinase	53920	34863772	279185	SOLUBLE	cleavable signal peptide		UPI0000180ED9	
SIMILAR TO BCL2-LIKE 13	MITOCHONDRIA	PREDICTED: similar to BCL2-like 13	46730	34858394	258284	MEMBRANE		409 23 OUT-IN	UPI00001CF567	
CDNA SEQUENCE BC023105	UNKNOWN	PREDICTED: similar to CDNA sequence BC023105	47510	34932132	297879	SOLUBLE			UPI00001D1329	
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	SOLUBLE			UPI00001CF504	
GPI TRANSAMIDASE COMPONENT PIG-T PRECURSOR (POTASSIUM VOLTAGE-GATED CHANNEL SUBFAMILY KQT MEMBER 2)	(F) METABOLISM	PREDICTED: similar to GPI transamidase component PIG-T precursor (Phosphatidylinositol-glycan biosynthesis, class T protein) (Neuronal development-associated protein 7)	65550	34860689	195113	MEMBRANE	cleavable signal peptide	524 23 OUT-IN	UPI00001CF398	
GOA	SIGNALING	PREDICTED: similar to Tripartite motif protein 47	70030	27690552	251068	SOLUBLE			UPI00001CB2BF	
POTASSIUM VOLTAGE-GATED CHANNEL SUBFAMILY KQT MEMBER 2	PLASMA MB	Potassium voltage-gated channel subfamily KQT member 2 Voltage-gated potassium channel subunit Kv7.2 Potassium channel subunit alpha KvLQT2 KQT-like 2	93950	3641300	51393	MEMBRANE		93 23 IN-OUT 125 23 OUT-IN 168 20 IN-OUT 232 23 OUT-IN 290 23 IN-OUT	O88943	
PRESENILIN 1	SIGNALING	Presenilin 1	52790	6174931	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	
SERINE/THREONINE-PROTEIN KINASE PLK	SIGNALING	Serine/threonine-protein kinase PLK1 Polo-like kinase 1	68310	497994	12071	SOLUBLE			Q62673	
SIMILAR TO CDNA SEQUENCE BC003324	UNKNOWN	Similar to cDNA sequence BC003324	22440	51948382	314265	SOLUBLE			Q6AYA0	XP_213771.2
SIMILAR TO PROTEIN CGI-51	UNKNOWN	Sorting and assembly machinery component 50 homolog	51960	51948454	255631	SOLUBLE			Q6AXV4	XP_217005.2
SYNTAXIN BINDING PROTEIN MUNC18-3	TETH/DOCK/FUS	Syntaxin binding protein Munc18-3 Syntaxin binding protein 3	68020	71051327	157267	SOLUBLE			Q99PV2	
HYPOTHETICAL PROTEIN XP_346991	UNKNOWN	Tax_Id=101116 Hypothetical protein XP_346991	26610	34857419	273429	SOLUBLE				
SIMILAR TO 60S RIBOSOMAL PROTEIN L29 (P23)	PROT SYN/FOLD	Tax_Id=101116 Similar to 60S RIBOSOMAL PROTEIN L29 (P23)	16860	34860240	261531	SOLUBLE				
SIMILAR TO A-KINASE ANCHOR PROTEIN 9 ISOFORM 2;	SIGNALING	Tax_Id=101116 Similar to A-kinase anchor protein 9 isoform 2	441400	34854301	223472	SOLUBLE				
SIMILAR TO BRCA1 INTERACTING PROTEIN C-TERMINAL	UNKNOWN	Tax_Id=101116 Similar to BRCA1 interacting protein C-terminal helicaSe 1	114500	34872948	221550	SOLUBLE				
CUB AND SUSHI MULTIPLE DOMAINS 3	UNKNOWN	Tax_Id=101116 Similar to CUB and SuShi multiple domainS 3	213400	34866475	195940	MEMBRANE		1856 23 OUT-IN		

SIMILAR TO FYVE AND COILED-COIL DOMAIN CONTAININ	SIGNALING	Tax_Id=10116 Similar to FYVE and coiled-coil domain containing 1	174100	34866719	308794	SOLUBLE				
SIMILAR TO KIAA0528 PROTEIN	UNKNOWN	Tax_Id=10116 Similar to KIAA0528 protein	131100	34858585	263505	SOLUBLE				
SIMILAR TO MYOSIN HEAVY CHAIN A (MHC A)	CYTOSKELETON	Tax_Id=10116 Similar to MyoSin heavy chain A (MHC A)	92190	34878271	241434	SOLUBLE				
SIMILAR TO PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHAT	SIGNALING	Tax_Id=10116 Similar to PhoSphatidyInoSitol-4,5-biSphoSphate 3-kinase catalytic Subunit, delta iSoform (PI3-kinase p110 Subunit delta) (PtdInS-3-kinase p110 (PI3K) (p110delta)	111000	34872607	194716	SOLUBLE				
TYPE I TRANSMEMBRANE C-TYPE LECTIN RECEPTOR D	UNKNOWN	Tax_Id=10116 Similar to RIKEN cDNA 1110055L24	27770	34854713	201498	MEMBRANE	cleavable signal peptide	187 23 IN-OUT		
SIMILAR TO RIKEN CDNA 3000003F02	UNKNOWN	Tax_Id=10116 Similar to RIKEN cDNA 3000003F02	80990	34867913	317953	SOLUBLE				
SIMILAR TO RIKEN CDNA 4930548H24	UNKNOWN	Tax_Id=10116 Similar to RIKEN cDNA 4930548H24	50800	34881177	287094	SOLUBLE				
INTRAMEMBRANE PROTEASE	PROT MOD	Tax_Id=10116 Similar to SPPL2b	87570	34873981	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		
SIMILAR TO SERINE/THREONINE KINASE	SIGNALING	Tax_Id=10116 Similar to Serine/threonine kinase	179600	34874060	212247	SOLUBLE				
T-BOX TRANSCRIPTION FACTOR TBX10 (T-BOX PROTEIN	TRANSCRIPTION	Tax_Id=10116 Similar to T-box 1	54510	34861377	314602	SOLUBLE				
SIMILAR TO TYROSINE-PROTEIN KINASE JAK1 (JANUS K	SIGNALING	Tax_Id=10116 Similar to TyroSine-protein kinase JAK1 (JanuS kinase 1) (JAK-1)	150400	34869913	290958	SOLUBLE				
ANGIOMOTIN LIKE 1; JUNCTION-ENRICHED AND ASSOCI	UNKNOWN	Tax_Id=10116 Similar to angiominotin like 1	88040	34860492	250115	SOLUBLE				
SIMILAR TO BA261P9.2 (PUTATIVE NOVEL PROTEIN SIMI	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	SOLUBLE				
SIMILAR TO BUTYROPHILIN-LIKE PROTEIN	BIOSYNTHETIC CARGO	Tax_Id=10116 Similar to butyrophilin-like protein	56340	34862769	204977	SOLUBLE	cleavable signal peptide			
SIMILAR TO HOOK HOMOLOG 2	UNKNOWN	Tax_Id=10116 Similar to hook homolog 2	70280	34851423	289211	SOLUBLE				
SIMILAR TO HYPOTHETICAL PROTEIN FLJ10375	UNKNOWN	Tax_Id=10116 Similar to hypothetical protein FLJ10375	107600	34866614	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		
SIMILAR TO HYPOTHETICAL PROTEIN FLJ10737	UNKNOWN	Tax_Id=10116 Similar to hypothetical protein FLJ10737	91330	34872498	233304	SOLUBLE				
SIMILAR TO INTEGRIN ALPHA V SUBUNIT	PLASMA MB	Tax_Id=10116 Similar to integrin alpha v Subunit	114700	34856480	299926	MEMBRANE		981 23 OUT-IN		
NAKED CUTICLE-2	UNKNOWN	Tax_Id=10116 Similar to naked cuticle homolog 2	50280	34853337	310990	SOLUBLE				
SIMILAR TO PUTATIVE ZINC FINGER TRANSCRIPTION FA	TRANSCRIPTION	Tax_Id=10116 Similar to putative zinc finger tranScription factor OVO1	37260	27661858	294340	SOLUBLE				
RIG-1 PROTEIN	BIOSYNTHETIC CARGO	Tax_Id=10116 Similar to rig-1 protein	152300	34863083	191924	SOLUBLE				
THIOREDOXIN-RELATED TRANSMEMBRANE PROTEIN 2	UNKNOWN	Thioredoxin-related transmembrane protein 2	33870	56090369	227628	MEMBRANE	cleavable signal peptide	20 20 OUT-IN 103 23 IN-OUT	Q5XIK2	XP_230274.1
SIMILAR TO UBIQUITIN-CONJUGATING ENZYME E2G 2; U	PROTEASOME/UBIQUITIN	Ubiquitin-conjugating enzyme E2 G2 Ubiquitin-protein ligase G2 Ubiquitin carrier protein G2	18570	62665819	58922	SOLUBLE				
WD-REPEAT PROTEIN 13	UNKNOWN	WD repeat protein 13	53660	34933412	65960	SOLUBLE				
UNKNOWN (PROTEIN FOR MGC:72987)	UNKNOWN	Yf1fb protein	25210	38454214	262403	MEMBRANE		124 20 OUT-IN 156 23 IN-OUT 206 23 OUT-IN	Q8PEC3	

AXIN 1 PROTEIN	SIGNALING	axin 1	92860	7513916	68755	SOLUBLE			UPI00001679D2	
HYPOTHETICAL PROTEIN XP_343478	UNKNOWN	hypothetical protein XP_343478	31580	34865907	203844	SOLUBLE			UPI00001D00BC	
SECRETED FRIZZLED-RELATED PROTEIN 1	SIGNALING	secreted frizzled-related protein 1	36350	34879084	271324	SOLUBLE	cleavable signal peptide	12 20 IN-OUT	UPI00001D1029	
AFG3 ATPASE FAMILY GENE 3-LIKE 2	PROT MOD	similar to 2310036I02RIk protein	89350	34932104	265519	MEMBRANE		145 18 OUT-IN 251 20 IN-OUT	UPI000017F121	
SIMILAR TO 2610042L04RIK PROTEIN	UNKNOWN	similar to 2610042L04RIk protein	35150	34882725	237032	SOLUBLE			UPI00001D1A11	
SIMILAR TO 9530008L14RIK PROTEIN	UNKNOWN	similar to 9530008L14RIk protein [Rattus norvegicus]	11600	34875157	310564	MEMBRANE		25 20 IN-OUT 59 23 OUT-IN		
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	SOLUBLE			UPI00001D015C	
ALPHA-CATENIN RELATED PROTEIN	CYTOSKELETON	similar to alpha-catenin related protein	81630	34868416	257171	SOLUBLE			UPI00001CF6BA	
SIMILAR TO HYPOTHETICAL PROTEIN D4ERTD89E	UNKNOWN	similar to hypothetical protein D4ErtD89e	46520	34868399	231118	SOLUBLE	cleavable signal peptide		UPI00001CF6EF	
SIMILAR TO HYPOTHETICAL PROTEIN MGC45873	UNKNOWN	unknown	57950	34873128	290208	SOLUBLE			UPI00001CF8F1	
3-HYDROXYISOBUTYRATE DEHYDROGENASE, MITOCHONDRIAL	MITOCHONDRIA	3-hydroxyisobutyrate dehydrogenase, mitochondrial precursor	35300	83977457	55185	SOLUBLE	cleavable signal peptide		P29266	
BETA-ALANINE OXOGLUTARATE AMINOTRANSFERASE	MITOCHONDRIA	4-aminobutyrate aminotransferase, mitochondrial precursor (S)-3-amino-2-methylpropionate 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	SOLUBLE			O70539 P50554	
ATP-BINDING CASSETTE, SUB-FAMILY B, MEMBER 9 PRECURSOR	PREPROT 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	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	
DORZ1	UNKNOWN	Abhydrolase domain containing 14A	26760	57528269	203847	SOLUBLE	cleavable signal peptide	7 18 IN-OUT	Q5I0C4	
ALPHA-AMYLASE	BIOSYNTHETIC CARGO	Alpha-amylase	58830	58293772	106479	SOLUBLE	cleavable signal peptide	13 20 IN-OUT	Q99N59	
ANKYRIN G107	SIGNALING	Ankyrin G107	106900	18376635	53239	SOLUBLE			Q8VDA0	
APOLIPOPROTEIN A-V	BIOSYNTHETIC CARGO	Apoa5 protein	41430	6707431	114274	SOLUBLE	cleavable signal peptide		Q5FVT8 Q9QUH3	
APOLIPOPROTEIN A-II	BIOSYNTHETIC CARGO	Apolipoprotein A-II precursor	11440	91985	3639	SOLUBLE	cleavable signal peptide		P04638	
APOLIPOPROTEIN M	BIOSYNTHETIC CARGO	Apolipoprotein M	21510	9506391	95121	SOLUBLE	cleavable signal peptide		P14630 Q5EBB9 Q9QXI9	
ASIALOGLYCOPROTEIN RECEPTOR (RHL2)	PLASMA MB	Asialoglycoprotein receptor R2/3	34860	206649	44327	MEMBRANE		59 23 IN-OUT	P08290	
Qc, GS15	TETH/DOCK/FUS	BET1-like protein Vesicle transport protein GOS15 Golgi SNARE with a size of 15 kDa GS15 GOS-15	12410	61889075	315291	MEMBRANE		87 20 IN-OUT		
COMM DOMAIN CONTAINING 10	UNKNOWN	COMM domain containing 10	22830	51948526	211553	SOLUBLE			Q68FS9	XP_341612.1
DYNACTIN COMPLEX 50 KDA SUBUNIT	CYTOSKELETON	Dynactin 2	44150	51948450	260733	SOLUBLE			Q6AYH5	XP_216906.2

Qa, SYNTAXIN 2	TETH/DOCK/FUS	Epimorphin	33360	349313	11925	MEMBRANE		267 23 IN-OUT	P50279 Q08846 Q08847 Q08848	
FAM3C-LIKE PROTEIN	UNKNOWN	FAM3C-like protein	24710	38454280	173223	SOLUBLE	cleavable signal peptide	7 23 IN-OUT	Q810F4	
GRAB PROTEIN	TRAFFIC	GRAB	41910	19705545	161254	SOLUBLE			Q99NH3	
SIMILAR TO GENERAL TRANSCRIPTION FACTOR IIF POL	TRANSCRIPTION	General transcription factor IIF, polypeptide 1, 74kDa	57180	56090552	219560	SOLUBLE			Q6AY96	XP_236789.2
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	SOLUBLE	cleavable signal peptide		P21744 Q68J74	XP_340898.1
INTEGRAL MEMBRANE PROTEIN 2B	UNKNOWN	Integral membrane protein 2B	30310	81883760	284296	MEMBRANE		52 23 IN-OUT	Q5XIE8	XP_214228.1
P24 GAMMA 1	TRAFFIC	Interleukin 1 receptor-like 1 ligand Predicted	25210	61740631	194234	MEMBRANE	cleavable signal peptide	193 23 IN-OUT	Q3BK85	
NAD+-SPECIFIC ISOCITRATE DEHYDROGENASE A-SUBU	MITOCHONDRIA	Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial precursor Isocitric dehydrogenase NAD(+)-specific ICDH	39610	68565369	60501	SOLUBLE			Q99NA5	
APOLIPOPROTEIN C-I	BIOSYNTHETIC CARGO	Liver regeneration-related protein LRRG04 Apolipoprotein C-I	9861	91989	3640	SOLUBLE	cleavable signal peptide		P19939 Q53ZD8	
METABOTROPIC GLUTAMATE RECEPTOR 7 PRECURSOR	PLASMA MB	Metabotropic glutamate receptor 7 precursor mGluR7	102200	547904	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	
LATE ENDOSOMAL/LYSOSOMAL MP1 INTERACTING PRO	LYSOSOME	Mitogen-activated protein-binding protein-interacting protein Late endosomal/lysosomal Mp1-interacting protein p14	13480	27692916	12815	SOLUBLE				
BRANCHED CHAIN KETO ACID DEHYDROGENASE E1, BE	MITOCHONDRIA	PREDICTED: branched chain keto acid dehydrogenase E1, beta polypeptide	42820	34865350	151463	SOLUBLE	cleavable signal peptide		UPI00001CA61E	
CALCIUM CHANNEL BETA 4 SUBUNIT	CALCIUM TRANS/BIND	PREDICTED: calcium channel beta 4 subunit	57960	423788	100500	SOLUBLE			UPI000017956B	
SIMILAR TO RING FINGER PROTEIN 10	UNKNOWN	PREDICTED: ring finger protein 10 (predicted)	88540	62659003	265735	SOLUBLE			UPI00001D0942	
PHOSPHOPANTOTHENOYLCYSTEINE SYNTHETASE	METABOLISM	PREDICTED: similar to 6330579B17Rik protein	33910	34870890	191085	SOLUBLE			UPI00001CF7CB	
SIMILAR TO EXPRESSED SEQUENCE AW556797	UNKNOWN	PREDICTED: similar to D15Mgj27 protein	49680	27665476	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	
SIMILAR TO LECT2	SIGNALING	PREDICTED: similar to LECT2	20890	34873621	209309	SOLUBLE	cleavable signal peptide		UPI00001D10CC	
PROTEIN FAM18B (NPD008) (CGI-148).	UNKNOWN	PREDICTED: similar to RIKEN cDNA 1810036I24	22620	34861791	303059	MEMBRANE		53 23 OUT-IN 122 23 IN-OUT 149 20 OUT-IN	UPI00001823C0	
SIMILAR TO ECOTROPIC VIRAL INTEGRATION SITE 5	UNKNOWN	PREDICTED: similar to ecotropic viral integration site 5-like	83090	34870058	316795	SOLUBLE			UPI00001D0830	
R, VAMP 4	TETH/DOCK/FUS	PREDICTED: similar to vesicle associated membrane protein 4	16370	62659601	164208	SOLUBLE		118 20 OUT-IN	UPI00001803AD	
PERIPHERIN	CYTOSKELETON	Peripherin	53550	92597	75052	SOLUBLE			P21807	

PXF PROTEIN	PEROXISOME	Peroxisomal biogenesis factor 19 Peroxin-19 Peroxisomal farnesylated protein	32500	62903182	1659	SOLUBLE			Q9QYU1	
UDP-N-ACETYL-ALPHA-D-GALACTOSAMINE:POLYPEPTIDE	PROT MOD	Polypeptide N-acetylgalactosaminyltransferase 11 Protein-UDP acetylgalactosaminyltransferase 11 UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase 11 Polypeptide GalNAc transferase 11 GalNAc-T11 pp-GaNTase 11	69040	51315700	319029	MEMBRANE	signal anchor	7 23 IN-OUT	Q6P6V1	
YIP1	GTPASE	Protein YIPF4 YIP1 family member 4	27280	81883039	227072	MEMBRANE		117 20 IN-OUT 140 23 OUT-IN 169 23 IN-OUT 195 23 OUT-IN 226 20 IN-OUT	Q5M7T4	
PROTEIN-TYROSINE PHOSPHATASE-LIKE N	SIGNALING	Protein-tyrosine phosphatase-like N precursor	105200	1113923	11137	MEMBRANE	cleavable signal peptide	569 23 OUT-IN	Q63259	
BC004044 (DENTIN MATRIX PROTEIN 4)	UNKNOWN	Putative secreted protein	65610	59676599	220519	SOLUBLE	cleavable signal peptide	9 23 IN-OUT	Q5FV72 UPI00001D08A6	
(RCAS1) TYPE II RECEPTOR LIKE CANCER ASSOCIATED	UNKNOWN	Receptor-binding cancer antigen expressed on SiSo cells Estrogen receptor-binding fragment-associated gene 9 protein	24190	81883249	239738	MEMBRANE	cleavable signal peptide		Q5PQP2	
SIMILAR TO CHO FUNCTIONALLY UNKNOWN TYPE II TRA	UNKNOWN	Retinoic acid receptor responder (Tazarotene induced) Predicted	18500	61740621	235290	SOLUBLE	cleavable signal peptide		Q5BK77	
RETINOID-INDUCIBLE SERINE CARBOXYPEPTIDASE	PROT MOD	Retinoid-inducible serine carboxypeptidase precursor Serine carboxypeptidase 1	51170	48474727	140359	MEMBRANE	cleavable signal peptide	7 23 IN-OUT	Q920A6	
S-ARRESTIN	SIGNALING	S-arrestin	44990	92737	84325	SOLUBLE			P15887	
SARCOSINE DEHYDROGENASE	MITOCHONDRIA	Sarcosine dehydrogenase, mitochondrial precursor SarDH	101400	52000744	85749	SOLUBLE			O88499 Q64380	
SECRETED PHOSPHOPROTEIN 24	BIOSYNTHETIC CARGO	Secreted phosphoprotein 24 precursor Spp-24 Secreted phosphoprotein 2	20690	2498940	43395	SOLUBLE				
SELENOPROTEIN P	BIOSYNTHETIC CARGO	Selenoprotein P precursor	41580	47939025	1271	SOLUBLE	cleavable signal peptide		P25236 UPI000016794E	
ACYL-COA DEHYDROGENASE, SHORT/BRANCHED CHAIN	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	SOLUBLE			P70584	
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	SOLUBLE			Q9Z2P6	
TATA ELEMENT MODULATORY FACTOR	TRANSCRIPTION	TATA element modulatory factor	90260	6650548	60512	SOLUBLE			Q9QYA5	
COG3	TETH/DOCK/FUS	Tax_id=10116 Ensembl_locations(Chr-bp):15-56616580 similar to component of oligomeric golgi complex 2	72190	34874501	274159	SOLUBLE				
SERINE PROTEASE	BIOSYNTHETIC CARGO	Tax_id=10116 Ensembl_locations(Chr-bp):4-160981651 Serine protease	77790	7435632	13085	SOLUBLE	cleavable signal peptide			
SIMILAR TO RIKEN CDNA 8430437G11	UNKNOWN	Tax_id=10116 Ensembl_locations(Chr-bp):4-39132345 similar to RIKEN cDNA 8430437G11	61370	34854982	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		
D130038B21	UNKNOWN	Tax_id=10116 Ensembl_locations(Chr-bp):8-46234308 similar to RIKEN cDNA D130038B21	40890	34863198	270449	SOLUBLE				
SERINE/THREONINE PROTEIN KINASE 16	SIGNALING	Tax_id=10116 Serine/threonine kinaSe 16	34410	27465615	105853	SOLUBLE				

RING FINGER PROTEIN 121	UNKNOWN	Tax_Id=10116 Similar to 4930544L10Rik protein	37000	34858831	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		
SIMILAR TO 9130011E15RIK PROTEIN	UNKNOWN	Tax_Id=10116 Similar to 9130011E15Rik protein	79550	34863517	198410	SOLUBLE			
SIMILAR TO APOPTOTIC CHROMATIN CONDENSATION IN	NUCLEUS	Tax_Id=10116 Similar to Apoptotic chromatin condensator inducer in the nucleus (Acinus)	156800	34874127	238120	SOLUBLE			
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	SOLUBLE			
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	SOLUBLE			
COG4	TETH/DOCK/FUS	Tax_Id=10116 Similar to Component of oligomeric golgi complex 4	91040	34851754	245295	SOLUBLE			
SIMILAR TO CONSERVED OLIGOMERIC GOLGI COMPLEX	COAT	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	SOLUBLE			
COG8	TETH/DOCK/FUS	Tax_Id=10116 Similar to Conserved oligomeric Golgi complex component 8	70760	34851657	222168	SOLUBLE	cleavable signal peptide		
SIMILAR TO DNA-DIRECTED RNA POLYMERASE II LARGE	TRANSCRIPTION	Tax_Id=10116 Similar to DNA-directed RNA polymerase II large subunit (RPB1)	197600	34871645	202233	SOLUBLE			
SIMILAR TO G PROTEIN-COUPLED RECEPTOR 108	SIGNALING	Tax_Id=10116 Similar to G protein-coupled receptor 108	59750	34853540	214715	MEMBRANE	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		
SIMILAR TO G-PROTEIN COUPLED RECEPTOR 113	SIGNALING	Tax_Id=10116 Similar to G-protein coupled receptor 113	105200	34863284	309118	MEMBRANE	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		
SIMILAR TO HYPOTHETICAL PROTEIN KIAA0645	UNKNOWN	Tax_Id=10116 Similar to Hypothetical protein KIAA0645	153700	34878957	300384	SOLUBLE			
DEHYDROGENASE E1 AND TRANSKETOLASE DOMAIN C	METABOLISM	Tax_Id=10116 Similar to KIAA1630 protein	148300	34876831	315956	SOLUBLE			
SIMILAR TO P3 PROTEIN	UNKNOWN	Tax_Id=10116 Similar to P3 protein	44450	27689253	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		
SIMILAR TO PROTEIN KINASE NJMU-R1	UNKNOWN	Tax_Id=10116 Similar to Protein Njmu-R1	44430	34872893	315828	SOLUBLE			
UNNAMED PROTEIN PRODUCT1	UNKNOWN	Tax_Id=10116 Similar to RIKEN cDNA 1200002K10 gene	98650	34853708	249884	SOLUBLE			
SIMILAR TO RIKEN CDNA 4921513O20; CDNA SEQUENCE	UNKNOWN	Tax_Id=10116 Similar to RIKEN cDNA 4921513O20	282700	34867735	191004	SOLUBLE			

SOLUTE CARRIER FAMILY 35, MEMBER B3 (PREDICTED)	UNKNOWN	Tax_Id=10116 Similar to RIKEN cDNA 4921526O06	68350	34875183	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		
SIMILAR TO RIKEN CDNA 4921529O18	UNKNOWN	Tax_Id=10116 Similar to RIKEN cDNA 4921529O18	153300	34865399	221195	SOLUBLE			
BTB (POZ) DOMAIN CONTAINING 7 (PREDICTED)	UNKNOWN	Tax_Id=10116 Similar to RIKEN cDNA 5730507E09	131000	34867616	273407	SOLUBLE	cleavable signal peptide		
SIMILAR TO SIF AND TIAM1-LIKE EXCHANGE FACTOR	UNKNOWN	Tax_Id=10116 Similar to Sif and Tiam1-like exchange factor	155900	34853702	204958	SOLUBLE			
TRANSMEMBRANE 9 SUPERFAMILY MEMBER 1	UNKNOWN	Tax_Id=10116 Similar to Tm9Sf1 protein	89670	34874167	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		
SIMILAR TO TRIPLE FUNCTIONAL DOMAIN PROTEIN (PTP)	SIGNALING	Tax_Id=10116 Similar to Triple functional domain protein (PTPRF interacting protein)	352100	34854901	310374	SOLUBLE			
SIMILAR TO WD REPEAT DOMAIN 9 ISOFORM A; CAMP R	SIGNALING	Tax_Id=10116 Similar to WD repeat domain 9 iSoform A	225200	34881323	312923	SOLUBLE			
SIMILAR TO AMINOADIPATE-SEMIALDEHYDE SYNTHASE	METABOLISM	Tax_Id=10116 Similar to aminoadipate-Semialdehyde Synthase	92010	34855019	258586	SOLUBLE			
SIMILAR TO BETA-1,4-GALACTOSYLTRANSFERASE V	PROT MOD	Tax_Id=10116 Similar to beta-1,4-galactoSyltranSferase V	33110	34860732	275497	MEMBRANE	cleavable signal peptide	13 23 IN-OUT	
FBXL4 PROTEIN	UNKNOWN	Tax_Id=10116 Similar to expreSSed Sequence A1836810	71160	34867089	218543	SOLUBLE			
SIMILAR TO FERTILIZATION ANTIGEN-1; FA-1	UNKNOWN	Tax_Id=10116 Similar to fertilization antigen-1	11520	34872581	319241	SOLUBLE	cleavable signal peptide		
SIMILAR TO FLJ12716 PROTEIN	UNKNOWN	Tax_Id=10116 Similar to hypothetical protein	125800	34878417	272431	SOLUBLE			
UNKNOWN5	UNKNOWN	Tax_Id=10116 Similar to hypothetical protein A930013K19	71010	34878581	285571	SOLUBLE			
SIMILAR TO HYPOTHETICAL PROTEIN DKFZP547C176	UNKNOWN	Tax_Id=10116 Similar to hypothetical protein DKFZp547C176	41180	34863409	227549	SOLUBLE			
SIMILAR TO FLJ21963	UNKNOWN	Tax_Id=10116 Similar to hypothetical protein FLJ21963	91790	34865010	243174	SOLUBLE			
KINESIN-RELATED MITOTIC MOTOR PROTEIN	CYTOSKELETON	Tax_Id=10116 Similar to kineSin-related mitotic motor protein	129800	34862680	209577	SOLUBLE			
COG1	TETH/DOCK/FUS	Tax_Id=10116 Similar to ldlBp	110800	34875017	282341	SOLUBLE			
OSTEOCLAST INHIBITORY LECTIN	PROT SYN/FOLD	Tax_Id=10116 Similar to oSteoclaSt inhibitory lectin	23540	34858508	255984	MEMBRANE	signal anchor	42 23 IN-OUT	
SIMILAR TO PROBABLE TRANSMEMBRANE PROTEIN FT2	UNKNOWN	Tax_Id=10116 Similar to probable transMembrane protein FT27 - mouSe	39180	34877387	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	
RING FINGER PROTEIN 20; HOMOLOG OF S. CEREVISIAE	PROTEASOME/UBIQUITIN	Tax_Id=10116 Similar to ring finger protein 20	122200	34868389	236982	SOLUBLE			

SIMILAR TO ZINC TRANSPORTER 5	UNKNOWN	Tax_id=10116 Similar to zinc transPorter 5	71030	34853639	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			
SIMILAR TO ZINC TRANSPORTER LIKE 2	CALCIUM TRANS/BIND	Tax_id=10116 Similar to zinc transPorter like 2	57350	34859877	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			
BET3	TETH/DOCK/FUS	Trafficking protein particle complex subunit 3 BET3 homolog	20300	71153350	145735	MEMBRANE		Q5U1Z2	XP_342918.1	
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	MEMBRANE	5 23 IN-OUT	P61943		
BETA 1,3-GALACTOSYLTRANSFERASE POLYPEPTIDE 1	PROT MOD	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 1	37990	34854866	56042	MEMBRANE	7 20 IN-OUT			
UDP-GLUCURONATE DECARBOXYLASE	METABOLISM	UDP-glucuronic acid decarboxylase 1 UDP-glucuronate decarboxylase 1 UGD UXS-1	47500	21326465	86062	SOLUBLE	20 19 IN-OUT			
SIMILAR TO VACUOLAR PROTEIN SORTING 26, VACUOLE	TRAFFIC	Vacuolar protein sorting 26 Vesicle protein sorting 26	38110	78099277	276682	SOLUBLE		Q6AY86	XP_342141.1	
VESICLE ASSOCIATED PROTEIN	COAT	Vesicle associated protein	135400	7514116	26418	SOLUBLE		Q9Z2Q1		
DIHYDROPYRIDINE-SENSITIVE L-TYPE, CALCIUM CHANN	CALCIUM TRANS/BIND	Voltage-dependent L-type calcium channel subunit beta-3 CAB3 Calcium channel voltage-dependent subunit beta 3	54560	6978583	3671	SOLUBLE		P54287		
ZINC-ALPHA-2-GLYCOPROTEIN	BIOSYNTHETIC CARGO	Zinc-alpha-2-glycoprotein precursor	34020	6978565	3662	SOLUBLE	cleavable signal peptide	Q63523 Q63678		
PQ LOOP REPEAT CONTAINING 1	UNKNOWN	similar to 2310009N05Rik protein	30570	34932411	197729	MEMBRANE	15 23 OUT-IN 49 20 IN-OUT 78 23 OUT-IN 146 20 IN-OUT 169 23 OUT-IN	UPI0000183329		
SIMILAR TO APG16L BETA ISOFORM	UNKNOWN	similar to APG16L beta isoform [Rattus norvegicus]	36440	34858802	281500	SOLUBLE				
VACUOLAR PROTON-TRANSLOCATING ATPASE 100 KDA	LYSOSOME	similar to Cc1-3 [Rattus norvegicus]	162200	34872293	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			
GAG	LIKELY CONTAMINANTS	similar to Gag	67670	34869861	216646	SOLUBLE		UPI00001D07E2		
PUTATIVE PHOSPHATIDIC ACID PHOSPHATASE	METABOLISM	similar to HTPAP protein	29160	34879054	255469	MEMBRANE	cleavable signal peptide	UPI00001D1035		
ALDEHYDE DEHYDROGENASE 1 FAMILY, MEMBER L2	DETOXIFICATION	similar to RIKEN cDNA D330038109 [Rattus norvegicus]	96960	34862428	302704	SOLUBLE				
GOLGI-ASSOCIATED MICROTUBULE-BINDING PROTEIN H	CYTOSKELETON	similar to golgi-associated microtubule-binding protein HOOK3; hook3 protein [Rattus norvegicus]	83230	34879033	220378	SOLUBLE				

MALE ENHANCED ANTIGEN 2/GOLGI AUTOANTIGEN, GOLGIN SUBFAMILY A, 3 [Rattus norvegicus]	TETH/DOCK/FUS	similar to male enhanced antigen 2/golgi autoantigen, golgin subfamily a, 3 [Rattus norvegicus]	166100	34873054	267138	SOLUBLE				
SIMILAR TO NESPRIN-2	CYTOSKELETON	similar to nesprin-2	152400	34865470	310579	SOLUBLE			UPI00001CF9D8	
COPI COATOMER EPSILON SUBUNIT	COAT	similar to nonclathrin coat protein epsilon-COP	34650	34877816	259217	SOLUBLE			UPI0000180AD2	
SIMILAR TO THYROID HORMONE RECEPTOR INTERACTING RECEPTOR	UNKNOWN	similar to thyroid hormone receptor interactor 11; thyroid receptor interacting protein 11	37170	34867559	280942	SOLUBLE			UPI00001CFB06	
SIMILAR TO HYPOTHETICAL PROTEIN FLJ22419	UNKNOWN	unknown	99380	34873842	308914	SOLUBLE			UPI00001D05E1	
FOR PROTEASOMAL ATPASE (SUG1)	PROTEASOME/UBIQUITIN	26S protease regulatory subunit 8 Proteasome subunit p45 p45/SUG Proteasome 26S subunit ATPase 5 mSUG1	45630	49065782	62820	SOLUBLE			P62198	
AC2-256	UNKNOWN	Ac2-256	71830	62177146	166247	MEMBRANE			Q7TP18	
ACTIVATING SIGNAL COINTEGRATOR 1 COMPLEX SUBUNIT	NUCLEUS	Activating signal cointegrator 1 complex subunit 1	41180	56090367	229337	SOLUBLE		557 23 OUT-IN	Q5X11	XP_215419.2
ALPHA 1-B GLYCOPROTEIN	BIOSYNTHETIC CARGO	Alpha-1B-glycoprotein precursor Liver regeneration-related protein 1 C44	56480	57012547	155721	SOLUBLE	cleavable signal peptide			
CALCIUM-TRANSPORTING ATPASE TYPE 2C, MEMBER 1	CALCIUM TRANS/BIND	Calcium-transporting ATPase type 2C member 1 ATPase 2C1 ATP-dependent Ca(2+) pump PMR1	100500	8134332	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
COMPLEMENT FACTOR 6	BIOSYNTHETIC CARGO	Complement component C6 precursor	105100	61211276	240055	SOLUBLE	cleavable signal peptide		Q811M5	
COPPER-TRANSPORTING ATPASE 1	PROT MOD	Copper-transporting ATPase 1 Copper pump 1 Menkes disease-associated protein homolog	162100	16258817	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	
CYTOCHROME P450 11B3	DETOXIFICATION	Cytochrome P-450 11-beta hydroxylase	57180	595823	108087	MEMBRANE			Q64539	
DNAJ-LIKE PROTEIN	PROT SYN/FOLD	Dnaj-like protein	25760	9910322	42765	SOLUBLE			Q9QZW8	
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	SOLUBLE	cleavable signal peptide	7 20 IN-OUT		
SIMILAR TO FUKUTIN-RELATED PROTEIN	PROT MOD	Fukutin related protein	54850	71043684	242747	MEMBRANE	cleavable signal peptide	7 23 IN-OUT	Q4KLJ4 UPI00001C6FCF	
GLUCOSAMINE--FRUCTOSE-6-PHOSPHATE AMINOTRANSFERASE	METABOLISM	Glutamine fructose-6-phosphate transaminase 1	76830	54400724	277551	SOLUBLE			Q5X108	XP_216205.2
HEPCIDIN	BIOSYNTHETIC CARGO	Hepcidin precursor	9286	21542070	108861	SOLUBLE	cleavable signal peptide	4 23 OUT-IN	Q99MH3	
RING FINGER PROTEIN 153	PROTEASOME/UBIQUITIN	Hypothetical protein FLJ20445 Ring finger protein 153	31230	34862676	49021	MEMBRANE		97 23 IN-OUT 139 23 OUT-IN 209 20 IN-OUT 238 19 OUT-IN		
IGG RECEPTOR FCRN LARGE SUBUNIT P51	BLOOD + OTHER CELLS	IgG receptor FcRN large subunit P51 precursor	40170	56437	15418	MEMBRANE	cleavable signal peptide	299 23 OUT-IN	P13599	
KYNURENINE 3-HYDROXYLASE	METABOLISM	Kynurenine 3-monooxygenase Kynurenine 3-hydroxylase	54350	81882198	70269	MEMBRANE		386 23 OUT-IN 421 23 IN-OUT	O88867	
GLUTAMYL-PROLYL-TRNA SYNTHETASE	PROT SYN/FOLD	LRRGT00050	166800	66793366	286877	SOLUBLE			Q61XE9	

LEUKEMIA INHIBITOR FACTOR RECEPTOR ALPHA-CHAIN	PLASMA MB	Leukemia inhibitory factor receptor precursor LIF receptor LIF-R CD118 antigen	122400	81870502	37205	MEMBRANE	cleavable signal peptide	831 23 OUT-IN	O70535	
LOW-DENSITY LIPOPROTEIN RECEPTOR	PLASMA MB	Low-density lipoprotein receptor precursor LDL receptor	96620	56570	106673	MEMBRANE	cleavable signal peptide	806 23 OUT-IN	P35952	
SIMILAR TO CDNA SEQUENCE BC003322	UNKNOWN	LysM, putative peptidoglycan-binding, domain containing 3	33700	57527470	204667	MEMBRANE		217 23 OUT-IN	Q5M836	
HYPOTHETICAL PROTEIN XP_238476	UNKNOWN	PREDICTED: similar to 1700001K19Rik protein	24610	34867823	299198	SOLUBLE			UPI00001CF9F9	
PRA1 FAMILY PROTEIN 2 (JM4 PROTEIN)	GTPASE	PREDICTED: similar to DXImx39e protein	15360	34933457	246770	MEMBRANE		49 23 IN-OUT 76 23 OUT-IN	UPI00001D16D8	
VPS26	TRAFFIC	PREDICTED: similar to Dera	29720	34867703	287732	SOLUBLE			UPI00001D06F0	
SIMILAR TO MAGEB3	UNKNOWN	PREDICTED: similar to MAGEB3	38250	67846038	291571	SOLUBLE			Q4V8D8 UPI00001CD667	
SIMILAR TO MITOCHONDRIAL CARRIER TRIPLE REPEAT	MITOCHONDRIA	PREDICTED: similar to Mitochondrial carrier triple repeat 1	34420	34877540	303709	SOLUBLE		173 23 IN-OUT 215 23 OUT-IN	UPI00001802E6	
SIMILAR TO PROTEIN HSPC163	UNKNOWN	PREDICTED: similar to Protein HSPC163	16090	27679416	225990	MEMBRANE	cleavable signal peptide	5 23 IN-OUT 56 23 OUT-IN 118 20 IN-OUT	UPI00001CBD1A	
SIMILAR TO RIKEN CDNA 2810428115	UNKNOWN	PREDICTED: similar to RIKEN cDNA 2810428115	18770	27668986	291986	SOLUBLE			UPI000018042A	
SIMILAR TO SPECKLE-TYPE POZ PROTEIN-LIKE 1; POZ 5	UNKNOWN	PREDICTED: similar to TDPOZ2	40870	27692515	169806	SOLUBLE			UPI00001C7D93	
UDP-N-ACETYL-ALPHA-D-GALACTOSAMINE:POLYPEPTIDE T4	PROT MOD	PREDICTED: similar to polypeptide GalNAc transferase T4	66710	77736615	167222	MEMBRANE	cleavable signal peptide	13 23 IN-OUT	Q3KR95 UPI0000182D08	
SIMILAR TO SIGNAL RECOGNITION PARTICLE 19KDA; SIG	(PROT SYN/FOLD	PREDICTED: similar to signal recognition particle 19kDa	16140	27683535	219536	SOLUBLE			UPI00001CCF1F	
UDP-GALNAC:POLYPEPTIDE N-ACETYL GALACTOSAMINYL	PROT MOD	Polypeptide N-acetylgalactosaminyltransferase 10 Protein-UDP acetylgalactosaminyltransferase 10 UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase 10 Polypeptide GalNAc transferase 10 GalNAc-T10 pp-GaNTase 10	69120	51315730	72049	MEMBRANE	cleavable signal peptide	12 20 IN-OUT	Q925R7	
26S PROTEASE REGULATORY SUBUNIT 6A	PROTEASOME/UBIQUITIN	Proteasome (Prosome, macropain) 26S subunit, ATPase 3	49550	38304011	71853	SOLUBLE			Q6P6U2	
SIMILAR TO O-MANNOSYL N-ACETYLGLUCOSAMINYLTR	PROT MOD	Protein O-linked-mannose beta-1,2-N-acetylglucosaminyltransferase 1 POMGnT1	75150	73621412	285106	MEMBRANE	signal anchor		Q5XIN7	XP_342886.1
FAMILY WITH SEQUENCE SIMILARITY 20, MEMBER A (PR	BIOSYNTHETIC CARGO	Putative secreted protein	61440	59676595	271057	SOLUBLE	cleavable signal peptide	9 20 IN-OUT	Q5FV73 UPI00001812BB	
REG RECEPTOR	PROT MOD	Reg receptor	104400	9910530	42827	MEMBRANE	signal anchor	29 23 IN-OUT	Q9JMA8	
SECRETORY CARRIER MEMBRANE PROTEIN 2	TRAFFIC	Secretory carrier membrane protein 2	34340	10764633	150292	SOLUBLE		134 23 IN-OUT 161 23 OUT-IN 196 23 IN-OUT 241 23 OUT-IN	Q9ERM7	
SEPTIN-LIKE PROTEIN	GTPASE	Septin-9 Eseptin eighth septin Septin-like protein SLP	63790	6090881	70797	MEMBRANE			Q9QZJ7 Q9QZJ8 Q9QZP9 Q9QZR6	
PROTEIN KINASE (EC 2.7.1.37), MYOTONIC DYSTROPHY-	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	SOLUBLE			O54874	

SHORT TRANSIENT RECEPTOR POTENTIAL CHANNEL 2	PLASMA MB	Short transient receptor potential channel 2 TrpC2 rTRP2	99610	4877836	138976	MEMBRANE		343 23 OUT-IN 378 23 IN-OUT 450 23 OUT-IN 550 23 IN- OUT 611 23 OUT-IN	Q9R283	
STONIN	COAT	Stonin	81920	33636736	277960	SOLUBLE			Q7TNJ9	NP_891999.1
BAT3 (HLA-B ASSOCIATED TRANSCRIPT 3)	UNKNOWN	TREMBL:Q6MG49;Q9WTN8 REFSEQ_NP:NP_446061 ENSEMBL:ENSRNOP00000001129 BAT3	114900	4587081	60486	SOLUBLE				
SIMILAR TO MITOGEN ACTIVATED PROTEIN KINASE KIN	SIGNALING	Tax_Id=10116 Ensembl_locations(Chr-bp):11- 81385238 similar to mitogen-activated protein kinase kinase kinase 13	62180	27665594	259662	SOLUBLE				
SIMILAR TO RIKEN CDNA 2810002I04	UNKNOWN	Tax_Id=10116 Ensembl_locations(Chr-bp):6- 109338222 similar to RIKEN cDNA 2810002I04	45290	34935370	313692	SOLUBLE				
HYPOTHETICAL PROTEIN XP_215523	UNKNOWN	Tax_Id=10116 HypoHetical protein XP_215523	21540	34854965	295192	SOLUBLE				
HYPOTHETICAL PROTEIN XP_343384	UNKNOWN	Tax_Id=10116 HypoHetical protein XP_343384	69230	34863314	308477	SOLUBLE				
SIGNAL RECOGNITION PARTICLE 54 KDA	PROT SYN/FOLD	Tax_Id=10116 Signal recognition particle 54 kDa	79610	34865216	263863	SOLUBLE				
ATP-DEPENDENT ZINC METALLOPROTEASE	PROT MOD	Tax_Id=10116 Similar to ATP-dependent zinc metalloproteaseSe	85690	34851878	314287	SOLUBLE				
SIMILAR TO ALPHA-MANNOSIDASE IIX (MANNOSYL-OLIG	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	SOLUBLE	signal anchor	7 20 IN-OUT		
SIMILAR TO CG2144-PA	UNKNOWN	Tax_Id=10116 Similar to CG2144-PA	100600	34875840	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 852 23 IN-OUT 889 20 OUT-IN		
SIMILAR TO CMP-SIALIC ACID TRANSPORTER	PROT MOD	Tax_Id=10116 Similar to CMP-Sialic acid tranSporter	36550	34867231	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		
ALPHA N-CATENIN	SIGNALING	Tax_Id=10116 Similar to ENSANGP00000019826	159200	27732405	221731	SOLUBLE				
SIMILAR TO ETHANOLAMINE KINASE (EKI)	SIGNALING	Tax_Id=10116 Similar to Ethanolamine kinaSe (EKI)	43710	34856587	250733	SOLUBLE				
FORMIN HOMOLOGY 2 DOMAIN CONTAINING 1	UNKNOWN	Tax_Id=10116 Similar to FH1/FH2 domainS-containing protein (Formin homolog overexpresSed in Spleen) (FHOS) (Formin homology 2 domain containing 1)	68180	34851604	317496	SOLUBLE				
SIMILAR TO KDEL (LYS-ASP-GLU-LEU) ENDOPLASMIC RE	TRAFFIC	Tax_Id=10116 Similar to KDEL (LYS-ASp-Glu-Leu) endoplaSmic reticulum protein retention receptor 3	27420	34867041	283557	SOLUBLE		43 23 IN-OUT 80 19 OUT-IN 105 20 IN- OUT 134 20 OUT-IN 166 20 IN-OUT		
SIMILAR TO KIAA1055 PROTEIN	UNKNOWN	Tax_Id=10116 Similar to KIAA1055 protein	108500	34865572	211597	SOLUBLE				
SIMILAR TO RAB6IP1	UNKNOWN	Tax_Id=10116 Similar to KIAA1091 protein	38000	34861343	274376	SOLUBLE				

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) (HMIC)	51490	34872059	315202	SOLUBLE				
SIMILAR TO RIKEN CDNA C330027C09	UNKNOWN	Tax_Id=10116 Similar to RIKEN cDNA C330027C09	101300	34869119	273781	SOLUBLE				
SIMILAR TO SH3 DOMAIN PROTEIN D19	UNKNOWN	Tax_Id=10116 Similar to SH3 domain protein D19	125000	34857900	291964	SOLUBLE				
SPIR-1	TRAFFIC	Tax_Id=10116 Similar to Spic-1 protein	66730	34932106	284460	SOLUBLE				
TRS85 HOMOLOG	TRAFFIC	Tax_Id=10116 Similar to TRS85 homolog	150900	34878190	194979	SOLUBLE				
BROMODOMAIN ADJACENT TO ZINC FINGER DOMAIN, 2A	UNKNOWN	Tax_Id=10116 Similar to TTF-I interacting protein 5	183400	34862191	316025	SOLUBLE				
UDP-N-ACETYL-ALPHA-D-GALACTOSAMINE:POLYPEPTIDE GALACTO-4-EPIMERASE	PROT MOD	Tax_Id=10116 Similar to UDP-N-acetyl-alpha-D-galactoSamine:polypeptide N-acetylGalactoSaminyltranSferaSe 3	74480	34854862	247675	MEMBRANE				
SORTING NEXIN 23	TRAFFIC	Tax_Id=10116 Similar to chromoSome 20 open reading frame 23	177300	34859296	313987	SOLUBLE				
HYPOTHETICAL PROTEIN (3)	UNKNOWN	Tax_Id=10116 Similar to hypothetical protein	166900	34872142	230780	SOLUBLE				
SIMILAR TO HYPOTHETICAL PROTEIN C230030N03	UNKNOWN	Tax_Id=10116 Similar to hypothetical protein C230030N03	133800	34874915	193616	SOLUBLE				
SIMILAR TO HYPOTHETICAL PROTEIN MGC15523	UNKNOWN	Tax_Id=10116 Similar to hypothetical protein MGC15523	132100	34875626	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		
SIMILAR TO HYPOTHETICAL PROTEIN MGC19022	UNKNOWN	Tax_Id=10116 Similar to hypothetical protein MGC19022	626600	34862645	250792	SOLUBLE				
SIMILAR TO RME-8	TRAFFIC	Tax_Id=10116 Similar to mKIAA0678 protein	96130	34865848	276172	SOLUBLE				
CHONDROITIN SULFATE GLUCURONYLTRANSFERASE	PROT MOD	Tax_Id=10116 Similar to mKIAA1402 protein	86520	34853978	259133	MEMBRANE	cleavable signal peptide	13 23 IN-OUT		
SIMILAR TO MACROPHAGE HEMOGLOBIN SCAVENGER RECEPTOR CD163	BLOOD + OTHER CELLS	Tax_Id=10116 Similar to macrophage hemoglobin Scavenger receptor CD163 precuSor	119500	34858425	192759	MEMBRANE	cleavable signal peptide	20 23 IN-OUT 1047 23 OUT-IN		
SIMILAR TO MATRILIN-4 PRECURSOR	BIOSYNTHETIC CARGO	Tax_Id=10116 Similar to matrilin-4 precuSor	68970	34860683	276968	SOLUBLE	cleavable signal peptide			
SIMILAR TO PANCREATITIS INDUCED PROTEIN 49	UNKNOWN	Tax_Id=10116 Similar to pancreatitis-induced protein 49	54860	34853103	232078	SOLUBLE	cleavable signal peptide	87 23 IN-OUT		
POLYCYSTIC KIDNEY DISEASE 1-LIKE 3	PLASMA MB	Tax_Id=10116 Similar to polycyStic kidney diSeaSe 1-like 3	150800	34851921	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		
SIMILAR TO POLYCYSTIC KIDNEY DISEASE-LIKE 2 PROTEIN	PLASMA MB	Tax_Id=10116 Similar to polycyStic kidney diSeaSe-like 2 protein	68780	34878682	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		
SIMILAR TO TEKTN 3; TESTICULAR MICROTUBULES-RELATED PROTEIN 3	CYTOSKELETON	Tax_Id=10116 Similar to tektin 3	57610	34870851	284187	SOLUBLE				
SIMILAR TO TRIPARTITE MOTIF PROTEIN 8; RING FINGER PROTEIN 8	UNKNOWN	Tax_Id=10116 Similar to tripartite motif protein 8	102500	34863676	250614	SOLUBLE				
VACUOLE 14 PROTEIN; VAC14 PROTEIN; HYDIN	CYTOSKELETON	VAC14	88070	29293817	173122	SOLUBLE			Q80W92	
VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN 4	TRAFFIC	Vacuolar protein sorting-associated protein 45 rvps45	64890	51858559	19366	SOLUBLE			O08700	

R, VAMP 2	TETH/DOCK/FUS	Vesicle-associated membrane 2	12690	6981614	38248	SOLUBLE		93 23 IN-OUT		
R, VAMP 7	TETH/DOCK/FUS	Vesicle-associated membrane protein 7	24780	9502258	3011	MEMBRANE	cleavable signal peptide	192 23 IN-OUT	Q9JHW5	
SIMILAR TO DIVALENT CATION TOLERANT PROTEIN CUTA	UNKNOWN	divalent cation tolerant protein CUTA	16410	61212255	281056	SOLUBLE	cleavable signal peptide		UPI0000183321	XP_215338.2
HYPOTHETICAL PROTEIN XP_219683	UNKNOWN	hypothetical protein XP_219683	100200	34861395	198827	SOLUBLE			UPI00001CEB04	
SIMILAR TO 40S RIBOSOMAL PROTEIN S2	PROT SYN/FOLD	similar to 40S ribosomal protein S2	25730	34879332	271484	SOLUBLE		43 23 OUT-IN	UPI00001D0C7E	
DNAJ (HSP40) HOMOLOG, SUBFAMILY C, MEMBER 13	PROT SYN/FOLD	similar to CG8014-PA	55190	34865850	245025	SOLUBLE			UPI00001D00AF	
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-Asp/His) box polypeptide 37 [Rattus norvegicus]	125500	34872286	239799	SOLUBLE				
SIMILAR TO DKFZP586G1517 PROTEIN	UNKNOWN	similar to DKFZP586G1517 protein	50150	34853508	234819	SOLUBLE			UPI00001CE6BE	
SIMILAR TO DNA (CYTOSINE-5)-METHYLTRANSFERASE 3A (Dnmt3a) (DNA methyltransferase Mmullia) (DNA MTase Mmullia) (M.Mmullia)	NUCLEUS	similar to DNA (cytosine-5)-methyltransferase 3A (Dnmt3a) (DNA methyltransferase Mmullia) (DNA MTase Mmullia) (M.Mmullia)	59410	34871224	241066	SOLUBLE			UPI00001D03F9	
SIMILAR TO HYPOTHETICAL PROTEIN KIAA1383	UNKNOWN	similar to Hypothetical protein KIAA1383	96280	34851995	212350	SOLUBLE	cleavable signal peptide		UPI00001D14B9	
HUNTINGTIN INTERACTING PROTEIN 14 (HIP 14)	TETH/DOCK/FUS	similar to KIAA0946 protein	84730	34864845	282355	MEMBRANE		416 20 OUT-IN 467 23 IN-OUT 494 20 OUT-IN 594 23 IN-OUT 650 23 OUT-IN	UPI00001CFCA8	
SIMILAR TO RIKEN CDNA 1200014P05	UNKNOWN	similar to RIKEN cDNA 1200014P05	97320	34859177	239276	SOLUBLE			UPI00001CF34F	
OXYSTEROL BINDING PROTEIN-LIKE 11	UNKNOWN	similar to RIKEN cDNA 9430097N02 [Rattus norvegicus]	81520	34869388	230365	SOLUBLE				
WOLF-HIRSCHHORN SYNDROME CANDIDATE 1 PROTEIN	UNKNOWN	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	SOLUBLE			UPI0000182C44	
SIMILAR TO COMPONENT OF OLIGOMERIC GOLGI COMPLEX	COAT	similar to component of oligomeric golgi complex 2	41480	34851897	272329	SOLUBLE			UPI00001D148F	
SYNAPTIC RAS-GAP 1	GTPASE	(Q9QUH6) Isoform 5 of Q9QUH6	127700	7514095	13883	SOLUBLE			Q9QUH6-5	
55 KDA TYPE II PHOSPHATIDYLINOSITOL 4-KINASE	SIGNALING	55 kDa type II phosphatidylinositol 4-kinase	54300	16758554	60536	SOLUBLE			Q99M64	
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	32753	MEMBRANE			P61227	
A-RAF PROTO-ONCOGENE SERINE/THREONINE-PROTEIN	SIGNALING	A-Raf proto-oncogene serine/threonine-protein kinase	67550	55757	90531	SOLUBLE			P14056	

ATPase 7B	PROT MOD	ATPase 7B	156000	6006306	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	
ALDO-KETO REDUCTASE FAMILY 1 MEMBER E1	DETOXIFICATION	Aldo-keto reductase family 1, member E1	34500	56605762	218884	SOLUBLE			Q5U1Y4	XP_225536.2
MEMBRANE ATTACK COMPLEX INHIBITION FACTOR	BLOOD + OTHER CELLS	CD59 glycoprotein precursor Membrane attack complex inhibition factor MAC1F MAC-inhibitory protein MAC-IP Protectin	13790	6978635	3690	MEMBRANE	cleavable signal peptide	7 20 IN-OUT 103 20 OUT-IN	P27274	
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, ST SIAT4-C	38040	57870642	722827	MEMBRANE	cleavable signal peptide	7 20 IN-OUT	P61131	
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	SOLUBLE	signal anchor	20 19 IN-OUT	Q9QZL2	
CELL GROWTH REGULATORY GENE 11 PROTEIN	UNKNOWN	Cell growth regulator with EF hand domain 1 Cell growth regulatory gene 11 protein	30830	23396481	38628	SOLUBLE	cleavable signal peptide		P97586	
CERAMIDE GLUCOSYLTRANSFERASE	PROT MOD	Ceramide glucosyltransferase Glucosylceramide synthase GCS UDP-glucose:N-acylsphingosine D-glucosyltransferase UDP-glucose ceramide glucosyltransferase GLCT-1	44820	62648957	85745	MEMBRANE	signal anchor	10 23 OUT-IN 283 23 IN-OUT 310 20 OUT-IN	O55149 Q9R0E0	
CHAIN L, 1.9A STRUCTURE OF THE THERAPEUTIC ANTIBODY Campath-1h Fab In Complex With A Synthetic Peptide Antigen	BLOOD + OTHER CELLS	Chain L, 1.9a Structure Of The Therapeutic Antibody Campath-1h Fab In Complex With A Synthetic Peptide Antigen	23280	5542160	20841	SOLUBLE				
TSGA10	UNKNOWN	Cp431	104600	3851160	7578	SOLUBLE			Q9Z220	
CREATINE KINASE, M CHAIN	METABOLISM	Creatine kinase M-type Creatine kinase M chain M-CK	43020	6978661	3700	SOLUBLE			P00564	
DIAMINE OXIDASE-LIKE PROTEIN 1	UNKNOWN	Diamine oxidase-like protein 1	80090	40385889	216306	SOLUBLE	cleavable signal peptide		Q8IMK6	
EYES ABSENT 2 HOMOLOG	UNKNOWN	Drosophila-type eyes absent 2-like protein	58060	61097896	242823	SOLUBLE			Q6UN47	
SIMILAR TO RIKEN CDNA 2810433K01	UNKNOWN	ENSEMBL:ENSRNOP00000020637 REFSEQ:XP_214527 PREDICTED: similar to RIKEN cDNA 2810433K01	29420	27679138	190728	SOLUBLE				
ENGULFMENT AND CELL MOTILITY PROTEIN 1	CYTOSKELETON	Engulfment and cell motility protein 1	28740	34876182	4981	SOLUBLE				
GALACTOSE-1-PHOSPHATE URIDYLYLTRANSFERASE	METABOLISM	Galactose-1-phosphate uridylyltransferase Gal-1-P uridylyltransferase UDP-glucose--hexose-1-phosphate uridylyltransferase	43310	68533665	71441	SOLUBLE			P43424 Q4KM61	
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	SOLUBLE	signal anchor	7 23 IN-OUT	Q9QWE9	NP_062108.1
HEAT SHOCK 27 KDA PROTEIN	PROT SYN/FOLD	Heat shock 27 kDa protein	22890	204665	71479	SOLUBLE			P42930 Q63922 Q9QWA8	
HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR	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	SOLUBLE	cleavable signal peptide	24 23 OUT-IN	P20411	
HISTONE DEACETYLASE 4	NUCLEUS	Histone deacetylase 4	18710	12963266	122642	SOLUBLE			Q99P99	
YIP1P-INTERACTING FACTOR; LIVER PROTEIN	TETH/DOCK/FUS	Hypothetical protein	14900	25282411	132369	SOLUBLE			O35946	

IG GAMMA-2A CHAIN C REGION	BLOOD + OTHER CELLS	Ig gamma-2A chain C region	25220	13399989	62937	SOLUBLE			P20760 UPI000011CCD		
IMP (INOSINE MONOPHOSPHATE) DEHYDROGENASE 2	METABOLISM	Inosine monophosphate dehydrogenase 2	55800	40018566	231448	SOLUBLE			Q6P9U9		
INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 5 PRECURSOR	BIOSYNTHETIC CARGO	Insulin-like growth factor-binding protein 5 precursor IGFBP-5 IBP-5 IGF-binding protein 5	30300	6981088	3949	SOLUBLE	cleavable signal peptide		P24594		
LOC246208 PROTEIN	UNKNOWN	LOC246208 protein	47340	44890246	726783	SOLUBLE			Q6NYB8		
LAMIN B RECEPTOR	NUCLEUS	Lamin-B receptor Integral nuclear envelope inner membrane protein NBP60	70720	81861075	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	O08984		
LEUCYL-CYSTINYL AMINOPEPTIDASE	PROT MOD	Leucyl-cystinyl aminopeptidase	117200	20138455	5106	?		110 23 IN-OUT	P97629 Q11009		
SIMILAR TO MHC CLASS I PROTEIN	BIOSYNTHETIC CARGO	MHC class I protein RT1 class I, CE7	39930	62665606	290515	SOLUBLE	cleavable signal peptide	311 23 OUT-IN	Q861P9		
MHC CLASS II ANTIGEN RT1.B BETA CHAIN	PLASMA MB	MHC class II antigen RT1.B beta chain	22020	1762640	38923	MEMBRANE		150 23 IN-OUT	P79590		
MICROTUBULE ASSOCIATED PROTEIN 1A	CYTOSKELETON	Microtubule associated protein 1A	155800	56619	111687	SOLUBLE			Q63330		
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	SOLUBLE			Q66HG9	XP_230537.2	
CHAIN A, THE CRYSTAL STRUCTURE OF THE FAB FRAGMENT	PLASMA MB	Monoclonal Antibody Against The Main Immunog	23340	6730147	73388	SOLUBLE			UPI0000110B4C		
MYOSIN VA	CYTOSKELETON	Myosin-5A Myosin Va Dilute myosin heavy chain, non-muscle	211800	6577099	63044	SOLUBLE			Q9QYF3		
MARCKS	CYTOSKELETON	Myristoylated alanine-rich C-kinase substrate (MARCKS) (Protein kinase C substrate 80 kDa protein)	29780	27705710	166436	SOLUBLE			UPI00001CD470		
NICOTINATE PHOSPHORIBOSYLTRANSFERASE-LIKE PROTEIN	METABOLISM	Nicotinate phosphoribosyltransferase-like protein	58560	46485387	722226	SOLUBLE			Q6XQN1		
OLFACTORY RECEPTOR MOR263-6	PLASMA MB	Olfactory receptor 7, rat orthologue of mouse MOR263-3	34210	47834335	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	
PRA1 FAMILY PROTEIN 3 (ADP-RIBOSYLATION-LIKE FACTOR 3)	GTPASE	PRA1 family protein 3 ARL-6-interacting protein 5 ADP-ribosylation-like factor 6-interacting protein 5 Aip-5 Glutamate transporter EAAC1-interacting protein GTRAP3-18 Prenylated Rab acceptor protein 2 Protein JWa	21550	57012987	54281	MEMBRANE		36 23 IN-OUT 62 23 OUT-IN 97 18 IN-OUT 119 23 OUT-IN	Q9ES40 Q9JKD1		
DELTA 1-PYRROLINE-5-CARBOXYLATE REDUCTASE	METABOLISM	PREDICTED: pyrroline-5-carboxylate reductase-like (predicted)	28860	62652621	268213	SOLUBLE			UPI00001CFD51		
APOLIPOPROTEIN C2	BIOSYNTHETIC CARGO	PREDICTED: similar to Apolipoprotein C2	10700	27676424	215733	SOLUBLE	cleavable signal peptide		UPI000017F6A9		
SIMILAR TO DUAL SPECIFICITY PHOSPHATASE 14	SIGNALING	PREDICTED: similar to Dual specificity phosphatase 14	22270	62644625	209194	SOLUBLE			UPI00001804E3		
EMOPAMIL BINDING RELATED PROTEIN	UNKNOWN	PREDICTED: similar to Emopamil-binding protein-like (Emopamil-binding related protein)	23410	34874266	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		
SIMILAR TO CGI-35 PROTEIN	UNKNOWN	PREDICTED: similar to Protein C14orf111 homolog	23360	95102022	234912	SOLUBLE			Q1RP75 UPI00001CFA6C		

SIMILAR TO RIKEN CDNA 1700025G04 GENE	UNKNOWN	PREDICTED: similar to RIKEN cDNA 1700025G04	13890	27712468	318230	SOLUBLE			UPI00001CBB9B	
SIMILAR TO RIKEN CDNA 1700045I19	UNKNOWN	PREDICTED: similar to RIKEN cDNA 1700045I19	28360	27708820	208800	SOLUBLE			UPI00001815D9	
SIMILAR TO RETINOIC ACID EARLY INDUCIBLE PROTEIN	UNKNOWN	PREDICTED: similar to Retinoic acid early inducible protein 1 beta precursor (RAE-1beta)	27450	62638284	367801	SOLUBLE	cleavable signal peptide		UPI00001C6D86	
SIMILAR TO RIKEN CDNA A730063F07 GENE	UNKNOWN	PREDICTED: similar to SUMO/sentrin specific protease 5	85750	34869267	243468	SOLUBLE			UPI00001D0754	
SIMILAR TO ABNORMAL SPINDLE	CYTOSKELETON	PREDICTED: similar to abnormal spindle	364500	34880454	243295	SOLUBLE			UPI00001D0A15	
SIMILAR TO ARMADILLO REPEAT-CONTAINING PROTEIN	UNKNOWN	PREDICTED: similar to armadillo repeat-containing protein	31200	34855505	302905	SOLUBLE			UPI000017FFE4	
SIMILAR TO CHROMOSOME 9 OPEN READING FRAME 7	UNKNOWN	PREDICTED: similar to chromosome 9 open reading frame 7	18410	34853142	272157	MEMBRANE	cleavable signal peptide	32 23 IN-OUT 59 23 OUT-IN 101 23 IN-OUT	UPI00001CF064	
HIST3H3	NUCLEUS	PREDICTED: similar to histone 1, H3g	15430	27671651	163757	SOLUBLE				
IMMUNOGLOBULIN LIGHT CHAIN	BLOOD + OTHER CELLS	PREDICTED: similar to immunoglobulin light chain	16750	62647397	161334	SOLUBLE	cleavable signal peptide		UPI00001C8BAD	
SIMILAR TO RIKEN CDNA 1810015P03	TRAFFIC	PREDICTED: similar to transmembrane emp24 protein transport domain containing 6	27610	34851659	275967	MEMBRANE	cleavable signal peptide	201 23 OUT-IN	UPI00001813CD	
PLASMA MEMBRANE CALCIUM-TRANSPORTING ATPASE	PLASMA MB	Plasma membrane calcium-transporting ATPase 4	133100	14285346	39788	MEMBRANE		366 23 OUT-IN 409 23 IN-OUT 843 23 OUT-IN 919 20 IN-OUT 958 20 OUT-IN 990 23 IN-OUT 1027 23 OUT-IN	Q63127 Q63445 Q64542 Q64543 Q64544 Q64545	
HYPOTHETICAL PROTEIN LOC298851	UNKNOWN	Protein C2orf18 homolog precursor	41090	81883393	167119	MEMBRANE	cleavable signal peptide	9 23 IN-OUT 46 23 OUT-IN 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	
JTB PROTEIN	UNKNOWN	Protein JTB precursor	16390	6016410	128391	MEMBRANE	cleavable signal peptide	104 23 OUT-IN	O88823	
PROTEOLIPID PROTEIN 2	UNKNOWN	Proteolipid protein 2	16560	62286961	166582	MEMBRANE	signal anchor	25 18 OUT-IN 49 20 IN-OUT 83 23 OUT-IN 112 23 IN-OUT	Q6P742	XP_217597.1
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	SOLUBLE			Q31286	
RH BLOOD GROUP PROTEIN RH30	BLOOD + OTHER CELLS	Rh blood group protein RH30	46580	3445506	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	O88298	
RIBONUCLEASE 4	BLOOD + OTHER CELLS	Ribonuclease 4 precursor RNase 4 RL3	16900	9910536	42830	SOLUBLE	cleavable signal peptide	9 20 IN-OUT	O55004	

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	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	
STROMAL CELL DERIVED FACTOR 1 GAMMA	BLOOD + OTHER CELLS		13550	76563910	209385	SOLUBLE	cleavable signal peptide		Q80YV8	
SYNAPTOGYRIN 1	TETH/DOCK/FUS		25670	9507167	47308	SOLUBLE		27 18 IN-OUT 70 23 OUT-IN 105 23 IN-OUT 147 23 OUT-IN	Q62876	
Qa, SYNTAXIN 13	TETH/DOCK/FUS		30470	3184552	52412	SOLUBLE		244 23 IN-OUT	O70319	
Qc, SYNTAXIN 6	TETH/DOCK/FUS		29060	51858907	78119	SOLUBLE		235 20 IN-OUT	Q63635	
Qc, SYNTAXIN 8	TETH/DOCK/FUS		26910	3834382	78117	SOLUBLE		211 23 IN-OUT	Q9Z2Q7	
B-TOMOSYN ISOFORM	TETH/DOCK/FUS	Syntaxin-binding protein 5 Tomosyn-1 Lethal(2) giant larvae protein homolog 3	127700	81917877	21456	SOLUBLE			Q9WU70 Q9WU71 Q9Z152	
T-CELL SURFACE GLYCOPROTEIN CD1D	BLOOD + OTHER CELLS	T-cell surface glycoprotein CD1d precursor CD1d antigen	38540	8393070	12016	MEMBRANE	cleavable signal peptide	303 23 OUT-IN	Q63493	
TOM22 PROTEIN	MITOCHONDRIA	TOM22	15490	71051674	171046	SOLUBLE		84 18 IN-OUT	Q75Q41	
MAC-MARCKS PROTEIN	CYTOSKELETON	TREMBL:Q9EPH2 REFSEQ_NP:NP_110489 ENSEMBL:ENSRNOP0000012663 Mac-MARCKS protein	19850	76363234	71714	SOLUBLE				
MEMBRANE ASSOCIATED GUANYLATE KINASE INTERAC	UNKNOWN	Tax_id=101116 Ensembl_locations(Chr-bp):1-37869999 similar to hypothetical protein 6820402C05	60130	34853572	231037	SOLUBLE				
SIMILAR TO MENA PROTEIN	CYTOSKELETON	Tax_id=101116 Ensembl_locations(Chr-bp):13-98108982 similar to mena protein	88490	34881078	196358	SOLUBLE				
ANKYRIN	CYTOSKELETON	Tax_id=101116 Ensembl_locations(Chr-bp):16-73342360 similar to ankyrin	186300	34879099	195573	SOLUBLE				
SIMILAR TO TRANSLATION ELONGATION FACTOR 1 DEL	PROT SYN/FOLD	Tax_id=101116 Ensembl_locations(Chr-bp):7-113905923 similar to eukaryotic translation elongation factor 1 delta (guanine nucleotide exchange protein)	31330	27662108	302099	SOLUBLE				
SIMILAR TO ALPHA-N-ACETYL-GALACTOSAMINIDASE	PROT MOD	Tax_id=101116 Ensembl_locations(Chr-bp):7-120740849 similar to alpha-N-acetyl-galactosaminidase	54520	34867288	202900	SOLUBLE	cleavable signal peptide			
SIMILAR TO SP140 PROTEIN	UNKNOWN	Tax_id=101116 Ensembl_locations(Chr-bp):9-84465266 similar to Sp140 protein	104400	34877740	306790	SOLUBLE				
INTRAFLAGELLAR TRANSPORT PROTEIN 20-LIKE PROTE	UNKNOWN	Tax_id=101116 Hypothetical protein XP_213403	19700	34872851	239897	SOLUBLE				
HYPOTHETICAL PROTEIN XP_235398	UNKNOWN	Tax_id=101116 Hypothetical protein XP_235398	98020	34866792	248288	SOLUBLE				
SIMILAR TO 4631428G15 PROTEIN	UNKNOWN	Tax_id=101116 Similar to 4631428G15 protein	146800	34878459	250964	SOLUBLE				
SIMILAR TO A530083I02RIK PROTEIN	UNKNOWN	Tax_id=101116 Similar to A530083I02Rik protein	184100	34876687	308809	SOLUBLE				

SIMILAR TO CG11388-PA	UNKNOWN	Tax_Id=10116 Similar to CG11388-PA	36250	34869404	241377	MEMBRANE	cleavable signal peptide	69 23 IN-OUT		
SIMILAR TO CG17660-PA	UNKNOWN	Tax_Id=10116 Similar to CG17660-PA	52310	34857630	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		
SIMILAR TO COLORECTAL MUTANT CANCER PROTEIN (MCC protein)	UNKNOWN	Tax_Id=10116 Similar to Colorectal mutant cancer protein (MCC protein)	126800	34879375	199763	SOLUBLE	cleavable signal peptide			
SIMILAR TO DNA MISMATCH REPAIR PROTEIN MLH3 (MutL protein homolog 3)	NUCLEUS	Tax_Id=10116 Similar to DNA mismatch repair protein Mlh3 (MutL protein homolog 3)	157700	34867420	219867	SOLUBLE				
DNA-DEPENDENT PROTEIN KINASE CATALYTIC SUBUNIT	NUCLEUS	Tax_Id=10116 Similar to DNA-dependent protein kinase catalytic Subunit	470400	34870011	251203	SOLUBLE				
SIMILAR TO HYPOTHETICAL PROTEIN FLJ35794	UNKNOWN	Tax_Id=10116 Similar to Hypothetical protein FLJ35794	51380	27708530	166638	SOLUBLE				
SIMILAR TO HYPOTHETICAL PROTEIN KIAA0934	UNKNOWN	Tax_Id=10116 Similar to Hypothetical protein KIAA0934	194300	34876285	253215	SOLUBLE				
INHIBITOR OF GROWTH PROTEIN 1	SIGNALING	Tax_Id=10116 Similar to ING1 protein	31190	34879659	227451	SOLUBLE				
SIMILAR TO KIAA0963 PROTEIN	UNKNOWN	Tax_Id=10116 Similar to KIAA0963 protein	162200	34862323	279597	SOLUBLE				
SIMILAR TO B-TOMOSYN ISOFORM	TETH/DOCK/FUS	Tax_Id=10116 Similar to KIAA1006 protein	106300	34869352	253264	SOLUBLE				
SIMILAR TO KIAA1414 PROTEIN	UNKNOWN	Tax_Id=10116 Similar to KIAA1414 protein	184500	34861977	207796	SOLUBLE				
SIMILAR TO LIV-1 PROTEIN, ESTROGEN REGULATED	PLASMA MB	Tax_Id=10116 Similar to LIV-1 protein, estrogen regulated	85430	34878347	277425	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		
SIMILAR TO NMII PROTEIN	UNKNOWN	Tax_Id=10116 Similar to Nmi protein	31120	34854824	192515	SOLUBLE				
RAB22A	GTPASE	Tax_Id=10116 Similar to RAB22, member RAS oncogene family	23730	34860889	296032	MEMBRANE				
SIMILAR TO RBP1-LIKE PROTEIN ISOFORM 1	UNKNOWN	Tax_Id=10116 Similar to RBP1-like protein iSoform 1	67150	27682805	167845	SOLUBLE				
G PROTEIN-COUPLED RECEPTOR 89	SIGNALING	Tax_Id=10116 Similar to RIKEN cDNA 4933412D19	51730	34858091	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		
SIMILAR TO SOLUTE CARRIER FAMILY 9 (SODIUM/HYDRIUM) MITOCHONDRIA		Tax_Id=10116 Similar to RIKEN cDNA 6430520C02	89840	34881696	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		
SIMILAR TO RIKEN CDNA C820004H04	UNKNOWN	Tax_Id=10116 Similar to RIKEN cDNA C820004H04	111800	34869133	272177	SOLUBLE				
SIMILAR TO RIKEN CDNA D930036F22 GENE	UNKNOWN	Tax_Id=10116 Similar to RIKEN cDNA D930036F22 gene	12830	27662972	294302	SOLUBLE				
RAP1 GUANINE NUCLEOTIDE-EXCHANGE FACTOR PDZ-GTPASE	GTPASE	Tax_Id=10116 Similar to Rap1 guanine nucleotide-exchange factor PDZ-GEF2B	252400	34870741	252747	SOLUBLE				

SMC4 STRUCTURAL MAINTENANCE OF CHROMOSOMES	NUCLEUS	Tax_Id=10116 Similar to SMC4 protein	163900	34857050	301164	SOLUBLE			
SIMILAR TO SEC23-INTERACTING PROTEIN P125	UNKNOWN	Tax_Id=10116 Similar to Sec23-interacting protein p125	107800	34859392	284142	SOLUBLE			
SIMILAR TO SECRETED GEL FORMING MUCIN	BIOSYNTHETIC CARGO	Tax_Id=10116 Similar to Secreted gel-forming mucin	293900	34861766	270223	SOLUBLE	cleavable signal peptide		
SMYD1	TRANSCRIPTION	Tax_Id=10116 Similar to Skm-BOP2	57130	34855974	276020	SOLUBLE			
SIMILAR TO SOLUTE CARRIER FAMILY 30 (ZINC TRANSPORTER), member 6	PLASMA MB	Tax_Id=10116 Similar to Solute carrier family 30 (zinc transporter), member 6	51480	34862482	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	
SIMILAR TO STOMATIN RELATED OLFACTORY PROTEIN	UNKNOWN	Tax_Id=10116 Similar to Stomatin related olfactory protein SRO	36800	34857327	207620	SOLUBLE		67 23 IN-OUT	
Qa, SYNTAXIN 16	TETH/DOCK/FUS	Tax_Id=10116 Similar to Syntaxin 16 (Syn16)	41580	34860874	234670	SOLUBLE		345 20 IN-OUT	
SIMILAR TO TRANSCRIPTION FACTOR E3	TRANSCRIPTION	Tax_Id=10116 Similar to Transcription factor E3	61600	34933434	287807	SOLUBLE			
RLBP1 PROTEIN	UNKNOWN	Tax_Id=10116 Similar to cellular retinaldehyde-binding protein	43870	34857275	269045	SOLUBLE			
SIMILAR TO CHROMOSOME 10 OPEN READING FRAME 3	UNKNOWN	Tax_Id=10116 Similar to chromoSome 10 open reading frame 3	90190	34862686	216923	SOLUBLE			
SIMILAR TO CHROMOSOME 14 OPEN READING FRAME 9	UNKNOWN	Tax_Id=10116 Similar to chromoSome 14 open reading frame 9	34520	34869712	209283	MEMBRANE		260 23 IN-OUT 292 23 OUT-IN	
MEMBRALIN SPLICE VARIANT 2	UNKNOWN	Tax_Id=10116 Similar to chromoSome 19 open reading frame 6	60460	34862329	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	
SIMILAR TO CHROMOBX HOMOLOG 2 (DROSOPHILA P1)	NUCLEUS	Tax_Id=10116 Similar to chromobox homolog 2 (Drosophila Pc clasS)	55490	34882763	317761	SOLUBLE			
CORONIN 2A	CYTOSKELETON	Tax_Id=10116 Similar to coronin, actin binding protein, 2A	60470	34868360	191842	SOLUBLE			
SIMILAR TO CALCIUM BINDING DOMAIN PROTEIN, SIMILAR TO CALCIUM BINDING DOMAIN PROTEIN, Similar to type calcium binding domain protein, Similar to trichohyalin)	LIKELY CONTAMINANTS	Tax_Id=10116 Similar to dJ14N1.2 (novel S-100/CaBP type calcium binding domain protein, Similar to trichohyalin)	133800	34858169	280707	SOLUBLE			
SIMILAR TO DEDICATOR OF CYTO-KINESIS 2	SIGNALING	Tax_Id=10116 Similar to dedicator of cyto-kineSis 2	113200	34861140	200712	SOLUBLE			
MITOGEN-ACTIVATED PROTEIN KINASE KINASE	SIGNALING	Tax_Id=10116 Similar to hypothetical protein	74350	34873993	286816	SOLUBLE			
SIMILAR TO VACUOLAR PROTEIN SORTING 13D	TRAFFIC	Tax_Id=10116 Similar to hypothetical protein	465500	34872448	294934	SOLUBLE			
ENGULFMENT AND CELL MOTILITY PROTEIN 3	CYTOSKELETON	Tax_Id=10116 Similar to hypothetical protein 9930107J06	79800	34851601	290038	SOLUBLE			
SIMILAR TO HYPOTHETICAL PROTEIN C230069C04 (2)	UNKNOWN	Tax_Id=10116 Similar to hypothetical protein C230069C04	88310	34858101	286208	SOLUBLE			
SOLUTE CARRIER FAMILY 39 (ZINC TRANSPORTER), MEMBER 6	UNKNOWN	Tax_Id=10116 Similar to hypothetical protein FLJ11274	34120	34866189	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	
SIMILAR TO HYPOTHETICAL PROTEIN FLJ12681	UNKNOWN	Tax_Id=10116 Similar to hypothetical protein FLJ12681	90650	34870562	205672	MEMBRANE	signal anchor	24 23 IN-OUT 102 23 OUT-IN 520 23 IN-OUT 594 23 OUT-IN	
SIMILAR TO HYPOTHETICAL PROTEIN FLJ13511	UNKNOWN	Tax_Id=10116 Similar to hypothetical protein FLJ13511	152600	34861042	205697	SOLUBLE			
SIMILAR TO HYPOTHETICAL PROTEIN FLJ32000	UNKNOWN	Tax_Id=10116 Similar to hypothetical protein FLJ32000	118000	34870861	275469	SOLUBLE			

SIMILAR TO LOW AFFINITY SODIUM-GLUCOSE COTRANSPORTER	METABOLISM	Tax_Id=10116 Similar to low affinity Sodium-glucose cotransporter	67850	34852422	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		
SIMILAR TO LYSOSOMAL APYRASE-LIKE 1	LYSOSOME	Tax_Id=10116 Similar to lysoSomal apyrase-like 1	40920	34874392	217901	SOLUBLE		301 23 OUT-IN		
TRANSCRIPTION FACTOR 20 (STROMELYSIN 1 PDGF-RELATED)	TRANSCRIPTION	Tax_Id=10116 Similar to mKIAA0292 protein	199400	34867313	311710	SOLUBLE				
SIMILAR TO MKIAA0515 PROTEIN	UNKNOWN	Tax_Id=10116 Similar to mKIAA0515 protein	172900	34853592	286188	SOLUBLE				
SIMILAR TO MITOTIC KINESIN RELATED PROTEIN	CYTOSKELETON	Tax_Id=10116 Similar to mitotic kinesin-related protein	229600	34862643	291449	SOLUBLE	cleavable signal peptide			
SIMILAR TO MYOSIN X	CYTOSKELETON	Tax_Id=10116 Similar to myoSin X	251600	34855017	249318	SOLUBLE				
COPI COATOMER ZETA-2 SUBUNIT	COAT	Tax_Id=10116 Similar to nonclathrin coat protein zeta2 COP	18220	34873491	273036	SOLUBLE				
SIMILAR TO PARANEOPLASTIC ANTIGEN LIKE 5	UNKNOWN	Tax_Id=10116 Similar to paraneoplastic antigen like 5	49680	27682149	207724	SOLUBLE				
SIMILAR TO PHOSPHATIDYLINOSITOL GLYCAN CLASS N	PLASMA MB	Tax_Id=10116 Similar to phosphatidylinositol glycan class N	89310	34878866	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		
SIMILAR TO PLEXIN 1	SIGNALING	Tax_Id=10116 Similar to plexin 1	204500	34856403	308345	SOLUBLE	cleavable signal peptide			
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 (aScSSion # L13853)	78480	34858488	267553	SOLUBLE				
Qa, SYNTAXIN 7	TETH/DOCK/FUS	Tax_Id=10116 Syntaxin-7	29790	3152727	109585	SOLUBLE		237 23 IN-OUT	NP_068641.1	
SARCOMA AMPLIFIED SEQUENCE (PREDICTED)	UNKNOWN	Tetraspanin-31 Tspan-31 Sarcoma amplified sequence homolog	22660	62900748	260364	MEMBRANE	signal anchor	12 23 IN-OUT 44 23 OUT-IN 73 20 IN-OUT 174 20 OUT-IN	Q5U1V9	XP_343218.1
TRANSCOBALAMIN II	BIOSYNTHETIC CARGO	Transcobalamin-2 precursor Transcobalamin II TCII TCII	47420	5910985	90533	SOLUBLE	cleavable signal peptide		Q9R0D6	
TRANSMEMBRANE PROTEIN 14C (P11)	UNKNOWN	Transmembrane protein 14C p11	11780	27734399	30411	MEMBRANE		7 23 IN-OUT 34 23 OUT-IN 63 20 IN-OUT 87 20 OUT-IN	Q924P2	
TRIPEPTIDYL-PEPTIDASE I	LYSOSOME	Tripeptidyl-peptidase 1 precursor Tripeptidyl-peptidase TPP-I Tripeptidyl aminopeptidase	61330	20140356	75921	SOLUBLE	cleavable signal peptide		Q9EQV6	
SIMILAR TO CHROMOSOME 20 OPEN READING FRAME 3	UNKNOWN	Uncharacterized protein C20orf30 homolog	13200	81882492	190070	MEMBRANE	signal anchor	45 23 OUT-IN 80 23 IN-OUT	Q5BJP5	
SIMILAR TO CDNA SEQUENCE BC005632	UNKNOWN	Uncharacterized protein family UPF0227 member RGD1359682	33990	55741536	265453	SOLUBLE	cleavable signal peptide		Q5XUJ5	XP_216853.2
X-LINKED INTERLEUKIN-1 RECEPTOR ACCESSORY PROTEIN	BIOSYNTHETIC CARGO	X-linked interleukin-1 receptor accessory protein-like 1 precursor IL1RAPL-1	79770	34222486	241488	SOLUBLE	cleavable signal peptide		P59824	

GLUTAMATE RECEPTOR KA1 SUBUNIT	PLASMA MB	glutamate receptor, ionotropic, kainate 4 precursor	107300	475546	119817	MEMBRANE	cleavable signal peptide	544 23 OUT-IN 587 23 IN-OUT 624 23 OUT-IN 805 23 IN-OUT	UPI0000167F6F	
CHAIN H, 1.9A STRUCTURE OF THE THERAPEUTIC ANTIBODY	BLOOD + OTHER CELLS	immunoglobulin heavy chain [Rattus sp.]	51460	243866	79012	SOLUBLE	cleavable signal peptide			
IMMUNOGLOBULIN KAPPA-CHAIN	BLOOD + OTHER CELLS	immunoglobulin kappa-chain	14860	204835	126680	SOLUBLE				
OLFACTORY RECEPTOR OLR1063	PLASMA MB	olfactory receptor Olf1063	35540	47578031	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
BCL-2-ASSOCIATED TRANSCRIPTION FACTOR	TRANSCRIPTION	similar to Bcl-2-associated transcription factor [Rattus norvegicus]	92060	34852810	216315	SOLUBLE				
PYRUVATE KINASE, M2 ISOZYME	METABOLISM	similar to Pyruvate kinase, M2 isozyme	57960	34875446	288218	SOLUBLE			UPI00001D0DFC	
SIMILAR TO RIKEN CDNA 1500016H10	PROT SYN/FOLD	similar to RIKEN cDNA 1500016H10	14000	34882737	231235	SOLUBLE			UPI00001D1A15	
SIMILAR TO RIKEN CDNA 2010005O13	UNKNOWN	similar to RIKEN cDNA 2010005O13 [Rattus norvegicus]	15020	34880819	301426	MEMBRANE	signal anchor	36 23 OUT-IN 63 23 IN-OUT 95 23 OUT-IN		
UDP-GALACTOSE TRANSPORTER	METABOLISM	similar to UDP-galactose transporter	38530	34933455	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	
PROTEIN SYS1 HOMOLOG	TRAFFIC	similar to chromosome 20 open reading frame 169	20950	34860687	214268	SOLUBLE		48 23 IN-OUT 100 20 OUT-IN 126 20 IN-OUT 150 23 OUT-IN	UPI00001CF39A	
KRUPPEL-LIKE ZINC FINGER PROTEIN GLIS3	UNKNOWN	similar to hypothetical protein E230012L24	47320	34862740	246776	SOLUBLE	cleavable signal peptide		UPI00001CEBC1	
AMINOPEPTIDASE O (AP-O)	METABOLISM	similar to hypothetical protein FLJ14675	21510	34873570	196884	SOLUBLE	cleavable signal peptide		UPI00001D10C8	
SIMILAR TO IMMUNOGLOBULIN ALPHA HEAVY CHAIN	BLOOD + OTHER CELLS	similar to immunoglobulin alpha heavy chain	48960	34935283	224861	SOLUBLE			UPI00001CFAD8	
SIMILAR TO KERATIN ASSOCIATED PROTEIN 11-1	LIKELY CONTAMINANTS	similar to keratin associated protein 11-1	18900	27670141	269756	SOLUBLE			UPI00001CB5EB	
SERINE/THREONINE PROTEIN PHOSPHATASE WITH EF-H	SIGNALING	similar to protein phosphatase with EF-hands-2 [Rattus norvegicus]	84100	34876562	308740	SOLUBLE				
SIMILAR TO PUTATIVE PROTEIN AT THE X CHROMOSOMAL LOCUS	UNKNOWN	similar to putative protein at the X chromosomal L1cam locus	64310	34864432	293919	SOLUBLE			UPI00001CFF2C	
SIMILAR TO RECOMBINATION ACTIVATING GENE 1 GENE	UNKNOWN	similar to recombination activating 1 activation	24690	27692967	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	UPI0000181987	
SIMILAR TO TRANSMEMBRANE GAMMA-CARBOXYGLUTAMATE	PROT MOD	similar to transmembrane gamma-carboxyglutamic acid protein 4	45410	34856617	203605	SOLUBLE	signal anchor	23 23 IN-OUT 318 23 OUT-IN	UPI00001CF251	
HYPOTHETICAL PROTEIN XP_216137	UNKNOWN	unknown	26610	84781644	345922	MEMBRANE		62 23 IN-OUT 94 19 OUT-IN 121 23 IN-OUT 202 23 OUT-IN	Q4G068 UPI00001C8AC0	
SIMILAR TO KIAA1204 PROTEIN	UNKNOWN	unknown	167300	34869344	309548	SOLUBLE			UPI00001D0773	

SIMILAR TO HYPOTHETICAL PROTEIN MDS025	UNKNOWN	unknown		37550	34875130	276318	SOLUBLE		313 23 OUT-IN	UPI00001D1108	
SIMILAR TO HYPOTHETICAL PROTEIN B230358A15	UNKNOWN	unknown		84160	34880715	314842	MEMBRANE		584 23 OUT-IN	UPI00001D1772	

Table S1D. Peptide statistics by assigned protein name

FUNCTION	CMBSEQID LIST	glnumber	ASSIGNED PROT NAME	MEMBRANE STATUS	TP N=1 RM TOT	TP N=2 RM TOT	TP N=3 RM TOT	TP N=1 SM TOT	TP N=2 SM TOT	TP N=3 SM TOT	TP N=1 G TOT	TP N=2 G TOT	TP N=3 G TOT	% TP N=1 C TOT	% TP N=2 C TOT	% TP N=3 C TOT	% TP N=1 V TOT	% TP N=2 V TOT	% TP N=3 V TOT
BIOSYNTHETIC CARGO	319145	40018550	KUNITZ TYPE SERINE PROTEINASE INHIBITOR	MEMBRANE	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
BIOSYNTHETIC CARGO	23759	543793	AFAMIN	SOLUBLE	0	0	2	0	0	0	1	1	1	0	0	0	0	0	0
BIOSYNTHETIC CARGO	155721	57012547	ALPHA-1-B GLYCOPROTEIN	SOLUBLE	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
BIOSYNTHETIC CARGO	6160	6160 11478 66447 84131 256838 296398	ALPHA-1 PROTEINASE INHIBITOR III	SOLUBLE	3	34	41	39	45	22	38	59	35	38	45.978	40.93	54.871	53	84.785
BIOSYNTHETIC CARGO	11470	72091	ALPHA-1-ACID GLYCOPROTEIN PRECURSOR	SOLUBLE	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
BIOSYNTHETIC CARGO	11475	11475	ALPHA-1-ANTIPROTEINASE	SOLUBLE	1	4	6	0	2	2	20	20.333	25	5	7	8	19	36	31
BIOSYNTHETIC CARGO	126488	126488	ALPHA-1-MACROGLOBULIN	SOLUBLE	7	9	17	13	26	19	17	32	31	5	19	13	10	22	21
BIOSYNTHETIC CARGO	3629	3629	ALPHA-1-MICROGLOBULIN	SOLUBLE	0	0	0	0	0	1	2	4	1	0	0	1	0	1	3
BIOSYNTHETIC CARGO	317738	317738	ALPHA-2-ANTIPLASMIN	SOLUBLE	0	0	0	0	0	0	3	3	3	0	1	3	3	3	5
BIOSYNTHETIC CARGO	341343	341343	ALPHA-2-ANTIPLASMIN	SOLUBLE	0	0	0	0	1	0	0	1	0	0	0	0	0	0	0
BIOSYNTHETIC CARGO	111646	111646	ALPHA-2-HS-GLYCOPROTEIN	SOLUBLE	0	0	3	0	4	2	5	13	19	1	3	2	11	13	19
BIOSYNTHETIC CARGO	237675	237675	ALPHA-2-MACROGLOBULIN RECEPTOR-ASSOCIATED PROTEIN	SOLUBLE	0	2	3	0	1	2	0	0	0	0	0	2	0	2	12
BIOSYNTHETIC CARGO	69402	36387 69402 125352	ALPHA-2U GLOBULIN	SOLUBLE	8	21	14	31	25	25	26	32	0	0	0	0	0	0	0
BIOSYNTHETIC CARGO	106479	106479	ALPHA-AMYLASE	SOLUBLE	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0
BIOSYNTHETIC CARGO	45123	45123	ANGIOTENSINOGEN	SOLUBLE	0	0	0	0	0	0	3	2	4	0	0	0	0	1	0
BIOSYNTHETIC CARGO	207228	207228	ANTITHROMBIN III	SOLUBLE	0	1	0	1	1	1	3	10	13	1	4	3	7	8.8889	8
BIOSYNTHETIC CARGO	3638	3638	APOLIPOPROTEIN A-I	SOLUBLE	0	2	0	0	3	0	7	1	5	0	0	0	4	1	3
BIOSYNTHETIC CARGO	3639	3639	APOLIPOPROTEIN A-II	SOLUBLE	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
BIOSYNTHETIC CARGO	141420	141420	APOLIPOPROTEIN A-IV	SOLUBLE	1	5	3	0	5	4	6	0	8	1	2	1	10	8	5
BIOSYNTHETIC CARGO	114274	114274	APOLIPOPROTEIN A-V	SOLUBLE	0	0	0	0	0	0	3	2	6	1	0	4	5	2	8
BIOSYNTHETIC CARGO	166227	148924 166227	APOLIPOPROTEIN B	SOLUBLE	0	22.476	31	14.539	25	28	26	23	0	2	6	24	9	2	13.696
BIOSYNTHETIC CARGO	3640	3640	APOLIPOPROTEIN C-I	SOLUBLE	0	0	0	0	0	0	1	0	0	0	0	0	1	3	0
BIOSYNTHETIC CARGO	84170	84170	APOLIPOPROTEIN C-III	SOLUBLE	0	0	1	0	0	0	0	3	0	0	2	2	1	0	1
BIOSYNTHETIC CARGO	136243	136243	APOLIPOPROTEIN C-IV	SOLUBLE	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
BIOSYNTHETIC CARGO	215733	215733	PRECURSOR	SOLUBLE	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
BIOSYNTHETIC CARGO	126501	5824759	APOLIPOPROTEIN C2	SOLUBLE	4	2	10	9	7	9	30	7	42	2	19	29	74	71	56.932
BIOSYNTHETIC CARGO	95121	95121	APOLIPOPROTEIN E	SOLUBLE	0	0	0	0	0	0	0	0	2	0	0	0	1	3	1
BIOSYNTHETIC CARGO	268287	268287	ATP-BINDING CASSETTE, SUB- FAMILY F (GCN20), MEMBER 2	SOLUBLE	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
BIOSYNTHETIC CARGO	287107	287107	B-FACTOR, PROPERDIN, ALTERNATIVE-COMPLEMENT PATHWAY C3/C5 CONVERTASE	SOLUBLE	0	1	0	0	0	0	1	6	1	0	1	2	0	1	1
BIOSYNTHETIC CARGO	27803	27803	BETA-2-MICROGLOBULIN	SOLUBLE	0	0	0	2	1	2	3	3	0	0	2	2	4	2	1
BIOSYNTHETIC CARGO	126549	126549	C-REACTIVE PROTEIN	SOLUBLE	0	4	3	3	6	4	7	10	3	0	2	0	4	4	10
BIOSYNTHETIC CARGO	3668	3668	C4B-BINDING PROTEIN ALPHA CHAIN	SOLUBLE	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
BIOSYNTHETIC CARGO	76638	76638	CALPAIN SMALL SUBUNIT 1	SOLUBLE	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
BIOSYNTHETIC CARGO	39119	39119	CARCINOEMBRYONIC ANTIGEN- RELATED CELL ADHESION MOLECULE, SECRETED ISOFORM CEACAM1A-4C2	SOLUBLE	0	0	0	0	1	0	0	6	0	0	0	0	0	0	0
BIOSYNTHETIC CARGO	219134	219134	CERULOPLASMIN	SOLUBLE	0	5	4	5	4	11	7	9	2	0	2	5	6	4	1
BIOSYNTHETIC CARGO	36009	36009	CLUSTERIN	SOLUBLE	0	0	0	1	0	0	0	1	3	0	0	0	0	1	0
BIOSYNTHETIC CARGO	149112	149112	COAGULATION FACTOR IX	SOLUBLE	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
BIOSYNTHETIC CARGO	201969	201969	COLLAGEN ALPHA1 TYPE VI- PRECURSOR	SOLUBLE	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
BIOSYNTHETIC CARGO	308317	308317	COLLAGEN TYPE XIV	SOLUBLE	0	4	0	0	1	0	0	0	0	0	0	0	0	0	0
BIOSYNTHETIC CARGO	162301	162301	COMPLEMENT C4	SOLUBLE	0	1	3	4	2	4	0	2	1	1	12	9	3	12	8
BIOSYNTHETIC CARGO	221549	221549	COMPLEMENT COMPONENT 3	SOLUBLE	4	16	27	18	20	19	31	41	52	14	27	32	39	46	46
BIOSYNTHETIC CARGO	205903	205903	COMPLEMENT COMPONENT 5	SOLUBLE	0	0	1	0	2	0	0	0	0	0	0	0	2	1	1
BIOSYNTHETIC CARGO	251303	251303	COMPLEMENT COMPONENT C8 GAMMA SUBUNIT	SOLUBLE	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0

BIOSYNTHETIC CARGO	43431	43431	2499467	COMPLEMENT COMPONENT C9	SOLUBLE		0	2	0	0	0	1	0	0	1	1	6	0	2	1	0	0	1		0	0.0369	0	0	0.017	0	0.0546	0.0277	0.2425	0	0.0677	0.0359	0	0	0.0153
BIOSYNTHETIC CARGO							0	0	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	0.0359	0	0	0	
BIOSYNTHETIC CARGO	240055	240055	61211276	COMPLEMENT FACTOR 6	SOLUBLE		0	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	0.0359	0	0	0	
BIOSYNTHETIC CARGO	96883	96883	18426830	COMPLEMENT INHIBITORY FACTOR H	SOLUBLE		0	1	4	0	0	0	0	0	0	1	1	0	0	0	0	1	1		0	0.0185	0.0669	0	0	0	0	0.0277	0.0404	0	0	0	0.0163	0.0153	
BIOSYNTHETIC CARGO	84230	84230 135016	57294	CONTRAPSIN-LIKE PROTEASE INHIBITOR 1	SOLUBLE		5	12	12	8	15	11	26	53	43	5	12	0	34	39	25	0.1942	0.2214	0.2008	0.2459	0.2553	0.2198	1.4184	1.4661	1.7381	0.2356	0	0.406	0	0.6239	0.6374	0.3837		
BIOSYNTHETIC CARGO	88238	88238	50927309	CONTRAPSIN-LIKE PROTEASE INHIBITOR 6	SOLUBLE		0	2	2.0385	0	3	2	5	15	24	6	0	0	7	8	7	0	0.0369	0.0341	0	0.0511	0.04	0.2728	0.4149	0.9701	0.2828	0	0	0.1284	0.1307	0.1074			
BIOSYNTHETIC CARGO	208059	208059	27677818	DERMATOPONTIN	SOLUBLE		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.0277	0	0	0	0	0	0	0	0		
BIOSYNTHETIC CARGO	271057	271057	59676595	FAMILY WITH SEQUENCE SIMILARITY 20, MEMBER A (PREDICTED)	SOLUBLE		0	0	0	0	0	0	0	0	0	2	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0.0943	0	0	0	0	0.0153		
BIOSYNTHETIC CARGO	145181	145181	6662849	FETUIN-B	SOLUBLE		0	0	0	0	1	0	7	7	4	2	1	2	6	8	3	0	0	0	0	0.017				0.1936	0.1617	0.0943	0.0338	0.0717	0.1101	0.1307	0.046		
BIOSYNTHETIC CARGO	181007	181007	25282415	FIBRINOGEN	SOLUBLE		0	0	0	0	0	0	0	1	2	0	0	0	1	1	3		0	0	0	0	0	0.0277	0.0808	0	0	0	0.0183	0.0163	0.046				
BIOSYNTHETIC CARGO	173317	173317	62643670	FIBRINOGEN ALPHA/ALPHA-E CHAIN	SOLUBLE		6	8	7	3	5	5	12	6	17	4	3	5	4	11.588	0.233	0.1476	0.1172	0.0922	0.0851	0.0999	0.6547	0.166	0.6872	0.1885	0.1353	0.1076	0.0917	0.0654	0.1779				
BIOSYNTHETIC CARGO	166238	166238	33086484	FIBRINOGEN B BETA CHAIN	SOLUBLE		0	3	0	0	0	2	13	14	18	5	1	2	3	3	4		0	0	0	0	0.0554	0	0	0.0792	0.3873	0.7276	0.2356	0.0338	0.0717	0.055	0.049	0.0614	
BIOSYNTHETIC CARGO	3766	3766	1783937	FIBRINOGEN GAMMA CHAIN	SOLUBLE		0	3	2	0	0	3	7	8	15	4	1	0	6	8	3	0	0.0554	0.0335	0	0	0.06	0.3819	0.2213	0.6063	0.1885	0.0338	0	0.1101	0.1307	0.046			
BIOSYNTHETIC CARGO	22617	22617	229210	FIBRINOPEPTIDE A	SOLUBLE		0	1	1	0	1	0	0	1	1	0	2	2	0	0	1	0	0.0185	0.0167	0	0.017	0	0.0277	0.0404	0	0.0677	0.0717	0	0	0.0153				
BIOSYNTHETIC CARGO	95208	95208	9506703	FIBRONECTIN 1	SOLUBLE		0	0	2	0	1	0	4	0	0	0	4	7	1	2	8	0	0	0.0335	0	0.017	0	0.2182	0	0	0.1353	0.251	0.0183	0.0327	0.1228				
BIOSYNTHETIC CARGO	75919	75919	6714560	FICOLIN 1 PRECURSOR	SOLUBLE		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
BIOSYNTHETIC CARGO	8548	8548	40352785	FLOTILIN-1	SOLUBLE		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
BIOSYNTHETIC CARGO	253728	253728	34881641	GLYPLICAN 4	SOLUBLE		0	0	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	0.0153		
BIOSYNTHETIC CARGO	166334	166334	33086640	HAPTOGLOBIN	SOLUBLE		0	1	0	0	3	4	16	26	11	1	2	12	21	12	12	0.0185	0	0.0511	0.0799	0.8729	0.7192	0.4446	0.0471	0.0338	0.0717	0.2202	0.3432	0.1842					
BIOSYNTHETIC CARGO	242533	242533	34853846	HC PROTEIN	SOLUBLE		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
BIOSYNTHETIC CARGO	16936	16936	204621	HEMOPEXIN	SOLUBLE		0	3	0	0	7	0	7	25	12	6	1	8	16	22	19	0	0.0554	0	0.1191	0	0.3819	0.6916	0.485	0.2828	0.0338	0.2868	0.2936	0.3595	0.2916				
BIOSYNTHETIC CARGO	68739	68739	60551378	HEPARIN COFACTOR II	SOLUBLE		0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0.0185	0.0167	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
BIOSYNTHETIC CARGO	108861	108861	21542070	HEPCIDIN	SOLUBLE		0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0.0338	0.1434	0	0	0.0153			
BIOSYNTHETIC CARGO	18186	18186 140379	13358878	HISTIDINE-RICH GLYCOPROTEIN HRG	SOLUBLE		0	1	0	0	0	0	1	2	1	0	0	0	0	0	0	0	0.0185	0	0	0	0.0546	0.0553	0.0404	0	0	0	0	0	0	0	0	0	
BIOSYNTHETIC CARGO	11776	11776	68634170	INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 4	SOLUBLE		0	0	0	0	0	0	0	0	1	0	0	0	1	1	1	0	0	0	0	0	0	0	0.0404	0	0	0.0404	0	0	0.0183	0.0163	0.0153		
BIOSYNTHETIC CARGO	11211	11211	71896592	INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN COMPLEX ACID LABILE CHAIN PRECURSOR	SOLUBLE		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
BIOSYNTHETIC CARGO	227779	227779	34877130	INTER-ALPHA TRYPSIN INHIBITOR, HEAVY CHAIN 1	SOLUBLE		0	0	0	0	0	0	3	1	0	0	0	0	0	1	0	0	0	0	0	0	0.1637	0.0277	0	0	0	0	0	0	0	0.0163	0		
BIOSYNTHETIC CARGO	47186	47186	9506819	INTER-ALPHA-INHIBITOR H4 HEAVY CHAIN	SOLUBLE		0	2	1	0	1	1	7	11	8	2	12	13	12	9	12	0	0.0369	0.0167	0	0.017	0.02	0.3819	0.3043	0.3234	0.0943	0.406	0.4661	0.2202	0.1471	0.1842			
BIOSYNTHETIC CARGO	38418	38418	8393899	INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H3	SOLUBLE		0	0	0	0	0	0	5	7	4	0	1	3	5	13	15	0	0	0	0	0	0.2728	0.1936	0.1617	0	0.0338	0.1076	0.0917	0.2125	0.2302				
BIOSYNTHETIC CARGO	38912	38912	21490001	KALLISTATIN	SOLUBLE		0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0.0277	0	0	0	0	0	0	0	0	0		
BIOSYNTHETIC CARGO	60472	60472	2492888	LONG-CHAIN FATTY ACID TRANSPORT PROTEIN	SOLUBLE		0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0.0307	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
BIOSYNTHETIC CARGO	130837	130837	539969	LYSOZYME HOMOLOG AT-2, BINE RAT (FRAGMENTS)	SOLUBLE		0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.0185	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
BIOSYNTHETIC CARGO	19138	19138	1942287	MANNOSE-BINDING PROTEIN A	SOLUBLE		0	0	0	1	0	1	0	1	1	0	0	0	0	0	1	0	0	0	0.0307	0	0.02	0	0.0277	0.0404	0	0	0	0	0	0	0	0.0153	
BIOSYNTHETIC CARGO	44167	44167	205263	MANNOSE-BINDING PROTEIN C PRECURSOR	SOLUBLE		0	1	1	0	1	1	1	0	0	0	0	0	0	1	0	0	0.0185	0.0167	0	0.017	0.02	0.0546	0	0	0	0	0	0	0	0.0163	0		
BIOSYNTHETIC CARGO	35920	35920	38197682	MONOCYTE DIFFERENTIATION ANTIGEN CD14 PRECURSOR	SOLUBLE		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
BIOSYNTHETIC CARGO	166242	166242	62659617	MURINE COAGULATION FACTOR V	SOLUBLE		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
BIOSYNTHETIC CARGO	3277	3277	70166245	MYELIN BASIC PROTEIN S	SOLUBLE		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
BIOSYNTHETIC CARGO	233877	233877	34855859	PAL-S2-BETA SPLICE VARIANT	SOLUBLE		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
BIOSYNTHETIC CARGO	198556	19325 198556	60551377	PARAOXONASE 1	SOLUBLE		11	23	18	8	26	28	5	22	9	9	10	6	23	36	25	0.4272	0.4244	0.3013	0.2459	0.4425	0.5596	0.2728	0.6086	0.3638	0.4241	0.3383	0.2151	0.422	0.5883	0.3837			
BIOSYNTHETIC CARGO	217377	217377	34854947	PARAOXONASE 2	SOLUBLE		2	6	4	4	5	4	0	3	0	0	0	0	3	2	3	0.0777	0.1107	0.0669	0.123	0.0851	0.0799	0	0.083	0	0	0	0.055	0.0327	0.046				
BIOSYNTHETIC CARGO	62757	62757	7108713	PLASMA GLUTAMATE CARBOXYPEPTIDASE	SOLUBLE		0	0	0	0	0	0	0	1	0	1	0	0	0	1	0	0	0	0	0	0	0.0546	0	0.0404	0	0	0	0.0183	0	0	0	0		
BIOSYNTHETIC CARGO	144413	144413	27685035	PLASMA RETINOL-BINDING PROTEIN	SOLUBLE		1	3	4	3	4	4	5	9	9	1	4	3	5	8	5	0.0388	0.0554	0.0669	0.0922	0.0681	0.0799	0.2728	0.249	0.3638	0.0471	0.1353	0.1076	0.0917	0.1307	0.0767			
BIOSYNTHETIC CARGO	60419	60419 124523	62638541	PLASMINOGEN	SOLUBLE		5	5	12	3	4.1905	3	4	4																									

CALCIUM TRANS/BIND	268188	85740	268188	76559925	CALUMENIN	SOLUBLE	0	1	0	0	0	0	0	0	0	1	2	0	1	4	2	0	0.0185	0	0	0	0	0	0	0.0471	0.0677	0	0.0183	0.0654	0.0307			
CALCIUM TRANS/BIND	60416		60416	871525	NUCLEOBINDIN 1 (CALNUC 1)	SOLUBLE	0	0	0	3	0	17	1	22	53	93.726	72.648	74	81.322	79.631	0	0	0.9274	0.0277	0.8893	2.4976	3.1707	2.6048	1.3578	1.329	1.2223	0	0.0183	0.0654	0.0307			
CALCIUM TRANS/BIND	3157	3157		8515422	NUCLEOBINDIN 2 (CALNUC 2)	SOLUBLE	0	7	5	1	9	2	8	2	12	14	35.274	38.343	35	41.678	47.361	0	0.1292	0.0837	0.0307	0.1532	0.04	0.4364	0.0553	0.485	0.6598	1.1933	1.3748	0.6422	0.6811	0.727		
COAT	74369	74369		34871704	ADAPTER-RELATED PROTEIN COMPLEX 1 SIGMA 1A SUBUNIT	SOLUBLE	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0.0307			
COAT	198626	198626		34851742	ADAPTOR PROTEIN COMPLEX AP1, GAMMA 1 SUBUNIT	SOLUBLE	0	0	0	0	0	0	0	0	0	0	0	0	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0.0367	0.0327	0			
COAT	37177	37177		55729	ADAPTOR-RELATED PROTEIN COMPLEX 2 ALPHA 2 SUBUNIT	SOLUBLE	0	0	0	5	5.8333	0	0	0	0	9	0	0	3.1667	1	0	0	0	0.0851	0.1166	0	0	0	0.4241	0	0	0.0581	0.0163	0	0			
COAT	73521	73521		73536275	ADAPTOR-RELATED PROTEIN COMPLEX 2, MU 1 SUBUNIT	SOLUBLE	0	0	0	0	1	1	0	0	0	2	1	0	1	0	3	0	0	0	0	0	0	0.017	0.02	0	0	0.0943	0.0338	0	0.0183	0	0.046	
COAT	60461	60461		44888251	CALM	SOLUBLE	0	1	5	2	4	1	0	0	0	0	0	0	0	0	0	0	0.0185	0.0837	0.0615	0.0681	0.02	0	0	0	0	0	0	0	0	0		
COAT	126513	126513		8392872	CLATHRIN ADAPTIN-1, BETA 1	SOLUBLE	0	0	0	5.25	6.404	4.5	0	0	0	6	0	0	4	14.329	14.216	0	0	0.1614	0.109	0.0899	0	0	0.2828	0	0	0.0734	0.2342	0.2182	0	0		
COAT	219335	219335		34856047	CLATHRIN ADAPTIN-2, ALPHA 1	SOLUBLE	0	0	0	0	0	1.1667	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.0233	0	0	0	0	0	0	0	0	0	
COAT	59082	59082		73695330	CLATHRIN ADAPTIN-2, BETA 1	SOLUBLE	0	1	2	0	15.005	6.5	0	0	0	2	0	0	2.3026	4.1591	0	0	0.0185	0.0335	0	0.2554	0.1299	0	0	0	0	0.0677	0	0.0376	0.0638	0		
COAT	223265	223265		34877759	CLATHRIN AP47 PROTEIN	SOLUBLE	0	0	0	0	1	0	0	0	1	0	0	0	4	1	4	0	0	0	0	0	0.017	0	0	0.0404	0	0	0.0734	0.0163	0.0614	0		
COAT	65700	65700		56961624	CLATHRIN COAT ASSEMBLY PROTEIN AP17	SOLUBLE	0	0	0	0	1	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0.017	0.02	0	0	0	0	0	0.0163	0	0		
COAT	95154	95154		9506497	CLATHRIN HEAVY CHAIN	SOLUBLE	0	0	0	10	12	5	7	5	20	8	0	0	6	1	6	0	0	0.3074	0.2042	0.0999	0.3819	0.1383	0.8084	0.377	0	0.1101	0.0163	0.0921	0			
COAT	126525	126525		56269651	CLATHRIN LIGHT CHAIN A	SOLUBLE	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.017	0	0	0	0	0	0	0	0	0		
COAT	60578	60578		203359	CLATHRIN LIGHT CHAIN B	SOLUBLE	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
COAT	293534	293534		34880938	COPI COATOMER ALPHA SUBUNIT	SOLUBLE	0	0	0	1	0	0	0	0	12	60	41	20	119.98	185.94	143.96	0	0	0	0	0.0307	0	0	0.485	2.8275	1.387	0.7171	2.2015	3.0388	2.2096	0		
COAT	63721	63721		55819	COPI COATOMER BETA SUBUNIT	SOLUBLE	0	0	0	0	0	0	0	0	13	74	18	12	118	189	118	0	0	0	0	0	0	0	0.5255	3.4873	0.6089	0.4303	2.1651	3.0887	1.8112	0		
COAT	35931	35931		3023522	COPI COATOMER BETA' SUBUNIT	SOLUBLE	0	0	0	0	0	0	2	1	19.826	49	19	6	78	138	69	0	0	0	0	0	0	0.1091	0.0277	0.8014	2.3091	0.6428	0.2151	1.4312	2.2553	1.0591	0	
COAT	221177	221177		81884175	COPI COATOMER DELTA SUBUNIT	SOLUBLE	0	0	0	0	0	0	0	0	8	20	16	13	63	126	69	0	0	0	0	0	0	0	0.3234	0.9425	0.5413	0.4661	1.156	2.0592	1.0591	0		
COAT	259217	259217		34877816	COPI COATOMER EPSILON SUBUNIT	SOLUBLE	0	0	0	0	0	0	0	1	6	18.818	3	4	38	35	61	0	0	0	0	0	0	0	0.0277	0.2425	0.8868	0.1015	0.1434	0.6973	0.572	0.9363	0	
COAT	267886	267886		34856387	COPI COATOMER GAMMA-1 SUBUNIT	SOLUBLE	0	0	0	0	0	0	0	2	20	35.048	29.76	13.75	90.833	145.71	113.14	0	0	0	0	0	0	0.0553	0.8084	1.6516	1.0068	0.493	1.6667	2.3813	1.7366	0		
COAT	309005	309005		34855105	COPI COATOMER GAMMA-2 SUBUNIT	SOLUBLE	0	0	0	0	0	0	0	0	0	11.952	1.24	1.25	18.167	17.288	15.474	0	0	0	0	0	0	0	0	0	0	0.5633	0.0419	0.0448	0.3333	0.2825	0.2375	0
COAT	236737	236737		34868640	COPI COATOMER ZETA-1 SUBUNIT	SOLUBLE	0	0	0	0	0	0	3	0	1	4	0	0	6	11	10	0	0	0	0	0	0	0.1637	0	0.0404	0.1885	0	0.1101	0.1798	0.1535	0		
COAT	273036	273036		34873491	COPI COATOMER ZETA-2 SUBUNIT	SOLUBLE	0	0	0	0	0	0	0	0	0	0	0	0	0	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0.0327	0.0153	0		
COAT	203525	203525		34880606	ENTHOPROTEIN	SOLUBLE	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
COAT	105332	105332		41016934	EPSIN 1	SOLUBLE	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
COAT	141679	141679		34867969	PROTEIN TRANSPORT PROTEIN SEC23A	SOLUBLE	0	3	3	3	8	5	13	29.808	38.182	6	9	7	58	81	34.758	0	0.0554	0.0502	0.0922	0.1362	0.0999	0.7092	0.8246	1.5433	0.2828	0.3045	0.251	1.0642	1.3237	0.5335	0	
COAT	260808	260808		34858849	PROTEIN TRANSPORT PROTEIN SEC23B (SEC23-RELATED PROTEIN B)	SOLUBLE	0	0	0	0	0	0	0	1.1923	3.8182	0	0	0	0	0	2.2424	0	0	0	0	0	0	0	0.033	0.1543	0	0	0	0	0	0.0344	0	
COAT	295725	295725		34870707	PROTEIN TRANSPORT PROTEIN SEC24A (SEC24-RELATED PROTEIN A)	SOLUBLE	0	1	0	0	2	0	0	1	8	0	0	0	23	39	25.387	0	0.0185	0	0	0.034	0	0	0.0277	0.3234	0	0	0.422	0.6374	0.3897	0		
COAT	219262	219262		34859959	PROTEIN TRANSPORT PROTEIN SEC24D (SEC24-RELATED PROTEIN D)	SOLUBLE	0	0	0	0	1	0	2	0	8	0	0	0	5	0	3	0	0	0	0	0	0.017	0	0.1091	0	0.3234	0	0.0917	0	0.046	0		
COAT	161453	161453		55741774	SEC13 LIKE 1 PROTEIN	SOLUBLE	0	0	0	0	0	0	4	5	11	1	0	0	0	0	0	0	0	0	0	0	0	0.2182	0.1383	0.4446	0.0471	0	0	0	0	0	0	
COAT	241419	241419		34868956	SEC24C	SOLUBLE	0	0	0	0	1	2	17	7	32	1	0	0	23	9	11	0	0	0	0	0.017	0.04	0.9274	0.1936	1.2935	0.0471	0	0	0.422	0.1471	0.1688	0	
COAT	272329	272329		34851897	SIMILAR TO COMPONENT OF OLIGOMERIC G.COMPLEX 2	SOLUBLE	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0														

DETOXIFICATION	3724	3724	203832	CYTOCHROME P450 1A2	MEMBRANE	7	11	10	0	6	5	3	6	2	1	2	2	6	7	12	0.2718	0.203	0.1674	0	0.1021	0.0999	0.1637	0.166	0.0808	0.0471	0.0677	0.0717	0.1101	0.1144	0.184	
DETOXIFICATION	337678	337678	40786491	CYTOCHROME P450 20A1	MEMBRANE	0	0	0	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0.0307	0	0	0	0	0	0	0	0	0	0.0153		
DETOXIFICATION	63757	63757	62655087	CYTOCHROME P450 27A1	MEMBRANE	0	2	3	0	3	3	0	2	0	0	0	0	1	0	0	0	0	0.0369	0.0502	0	0.0511	0.06	0	0.0553	0	0	0	0.0183	0	0	
DETOXIFICATION	126566	126566	51980506	CYTOCHROME P450 2A1	MEMBRANE	8.75	6.5455	17.286	17.417	22.12	14.8	3.5	4.3333	0	0	11	10	17	35	59	0.3398	0.1208	0.2893	0.5354	0.3765	0.2958	0.1909	0.1199	0	0.3721	0.3586	0.3119	0.572	0.9056		
DETOXIFICATION	3727	3727	6978741	CYTOCHROME P450 2A2	MEMBRANE	5.25	11.455	15.714	20.583	11.88	22.2	3.5	8.6667	5	0	0	0	0	0	0	0	0.2039	0.2114	0.263	0.6328	0.2022	0.4437	0.1909	0.2397	0.2021	0	0	0	0	0	
DETOXIFICATION	13404	13404	34855371	CYTOCHROME P450 2B2	MEMBRANE	0	0	7.0749	0	0	4.0702	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.0813	0	0	0	0	0	0	0	0	0	
DETOXIFICATION	63770	63770	28849945	CYTOCHROME P450 2B3	MEMBRANE	11	17	31.964	3	29	23	1	2	4	1	2	1	1	3.75	7	0.4272	0.3137	0.535	0.0922	0.4935	0.4596	0.0546	0.0553	0.1617	0.0471	0.0677	0.0359	0.0183	0.1074		
DETOXIFICATION	126560	63780	126560	CYTOCHROME P450 2C11	MEMBRANE	21.667	70.188	58.556	14	81.15	66.625	10	27.08	14	0	0	0	0	0	0	0	0.8414	1.2952	0.98	0.4304	1.381	1.3314	0.5456	0.7491	0.5659	0	0	0	0	0	
DETOXIFICATION	3729	3729	59808903	CYTOCHROME P450 2C12	MEMBRANE	1.3922	2.6058	2.4775	3.9	1.2637	2.6632	0	0	0	4	24.833	16	34.757	36.829	60.8	0.0541	0.0481	0.0415	0.1199	0.0215	0.0532	0	0	0.1885	0.8401	0.5737	0.6377	0.6019	0.9332		
DETOXIFICATION	63782	63782	205935	CYTOCHROME P450 2C13	MEMBRANE	14.637	37.808	43.491	29.989	59.836	45.69	10.455	23.337	13.8	0	0	0	0	0	0	0	0.5684	0.6977	0.7279	0.9219	1.0183	0.9131	0.5704	0.6456	0.5578	0	0	0	0	0	
DETOXIFICATION	260440	260440	34862902	CYTOCHROME P450 2C18	MEMBRANE	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
DETOXIFICATION	63786	33163	63786	56827	CYTOCHROME P450 2C22	MEMBRANE	8.8667	10	19.826	10	13	19.387	3	5.3571	11	1	1	1	0	1	1	0.3443	0.1845	0.3318	0.3074	0.2212	0.3874	0.1637	0.1482	0.4446	0.0471	0.0338	0.0359	0	0.0163	0.0153
DETOXIFICATION	72763	72763	78212	6166042	CYTOCHROME P450 2C23	MEMBRANE	15	25.264	21.275	13	30.196	19	5	14	18	8	7	1	15	29	35	0.5825	0.4662	0.3561	0.3996	0.5139	0.3797	0.2728	0.3873	0.7276	0.377	0.2368	0.0359	0.2752	0.4739	0.5372
DETOXIFICATION	63778	63778	231660	117223	CYTOCHROME P450 2C6	MEMBRANE	6.1538	14.806	22.426	0	21.057	27.836	3.5455	15.705	2	0	1.5	1.3333	3.1818	10.528	9.7368	0.239	0.2732	0.3753	0	0.3584	0.5563	0.1934	0.4345	0.0808	0	0.0507	0.0478	0.0584	0.1721	0.1495
DETOXIFICATION	45873	45873	482947	CYTOCHROME P450 2C7	MEMBRANE	11.817	32.118	17.87	1.1111	34.986	12.628	1	13.52	2.2	2	1.6667	2.6667	10.061	17.643	14.463	0.4589	0.5927	0.2991	0.0342	0.5954	0.2524	0.0546	0.374	0.0889	0.0943	0.0564	0.0956	0.1846	0.2883	0.222	
DETOXIFICATION	126576	126576	203803	CYTOCHROME P450 2D1	MEMBRANE	7.8286	15.617	15.443	2	22.082	22.77	0	12.075	8	2	0	0	7.1401	11.956	15.474	0.304	0.2882	0.2585	0.0615	0.3758	0.455	0	0.334	0.3234	0.0943	0	0	0.131	0.1954	0.2375	
DETOXIFICATION	63788	63788	57812	CYTOCHROME P450 2D2	MEMBRANE	2.619	15.376	18.267	0	29.495	27.752	0	9.475	9	0	7	4	18.843	16.121	31.779	0.1017	0.2837	0.3057	0	0.502	0.5546	0	0.2621	0.3638	0	0.2368	0.1434	0.3458	0.2635	0.4878	
DETOXIFICATION	103927	103927	58477687	CYTOCHROME P450 2D3	MEMBRANE	7.3333	7.883	9.7861	0	16.624	7.5472	0	5.45	0	0	0	1	8.0168	5.6982	9.7468	0.2848	0.1455	0.1638	0	0.2829	0.1508	0	0.1508	0	0	0.0359	0.1471	0.0931	0.1496		
DETOXIFICATION	63790	63790	57818	CYTOCHROME P450 2D5	MEMBRANE	5.219	8.124	8.5044	0	11.798	10.931	0	0	0	0	0	0	0	2.2246	0	0.2027	0.1499	0.1423	0	0.2008	0.2184	0	0	0	0	0	0	0.0364	0	0	
DETOXIFICATION	21526	21526	51980637	CYTOCHROME P450 2E1	MEMBRANE	4	17.21	12	7	17.172	27	2	4	3	3	2.0217	4.0698	9	13	24.917	0.1553	0.3176	0.2008	0.2152	0.2922	0.5396	0.1091	0.1107	0.1213	0.1414	0.0684	0.1459	0.1651	0.2125	0.3825	
DETOXIFICATION	125135	125135	59809108	CYTOCHROME P450 2J3	MEMBRANE	0	1	2	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0.0185	0.0335	0.0307	0.017	0.02	0	0	0	0	0	0	0	0	0
DETOXIFICATION	161231	161231	19705467	CYTOCHROME P450 2T1	MEMBRANE	1	1	1	1	4.2	6	1	0	0	0	0	0	0	1	0	0.0388	0.0185	0.0167	0.0307	0.0715	0.1199	0.0546	0	0	0	0	0	0.0163	0	0	
DETOXIFICATION	63758	3731	63758	27465619	CYTOCHROME P450 3A1	MEMBRANE	0	0	0	0	0	1.233	0	0	0	0	0	0	0	0	0	0	0	0	0	0.0246	0	0	0	0	0	0	0	0	0	0
DETOXIFICATION	104898	104898	5921916	CYTOCHROME P450 3A18	MEMBRANE	0	13.957	8.375	0	16	7.2727	0	2.25	0	0	0	0	0	0	0	0	0.2576	0.1402	0	0.2723	0.1453	0	0.0622	0	0	0	0	0	0	0	0
DETOXIFICATION	87425	87425	515799	CYTOCHROME P450 3A2	MEMBRANE	5	18.431	15.625	2	19	18.494	1	5.75	0	0	0	0	0	0	0	0.1942	0.3401	0.2615	0.0615	0.3234	0.3696	0.0546	0.1591	0	0	0	0	0	0	0	0
DETOXIFICATION	51420	51420	46048525	CYTOCHROME P450 4A1	MEMBRANE	0	4.5	2.1667	0	1.1	4.8812	0	0	0	0	0	0	0	2	0	0	0.083	0.0363	0	0.0187	0.0975	0	0	0	0	0	0	0	0	0.0307	
DETOXIFICATION	63760	63760	71051108	CYTOCHROME P450 4A2	MEMBRANE	18.6	23.667	20.796	26.375	24.3	30.213	3	11	8.25	0	0	0	0	0	0	0.7223	0.4367	0.348	0.8108	0.4136	0.6038	0.1637	0.3043	0.3335	0	0	0	0	0	0	0
DETOXIFICATION	21524	21524	28461155	CYTOCHROME P450 4A3	MEMBRANE	12.4	11.833	30.038	14.625	15.6	21.906	0	0	2.75	0	0	0	0	4	0.4816	0.2184	0.5027	0.4496	0.2655	0.4378</											

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	3	0	2	6	1	0	0	0	0	0	0	0	1	0	2	5	0	0.0554	0	0.0615	0.1021	0.02	0	0	0	0	0.0359	0	0.0327	0.0767			
DETOXIFICATION		17081	17081	77539448	EPOXIDE HYDROLASE	MEMBRANE	14.65	19.419	31.439	22.26	33.524	40.459	5.1724	8.6667	7	0	10	8	16.667	35.333	45.696					0.5689	0.3583	0.5262	0.6843	0.5705	0.8085	0.2822	0.2397	0.2829	0	0.3383	0.2868	0.3058	0.5774	0.7014
DETOXIFICATION		68349	68349	3334165	ESTRADIOL 17 BETA-DEHYDROGENASE 2	MEMBRANE	0	1	8	3	0	14	0	0	0	0	0	0	0	0	0	1			0	0.0185	0.1339	0.0922	0	0.2798	0	0	0	0	0	0	0	0	0.0153	
DETOXIFICATION		708	708	8393576	ESTRADIOL 17 BETA-DEHYDROGENASE 7	MEMBRANE	1	1	1	2	1	2	0	0	0	0	0	0	0	0	0	0			0.0388	0.0185	0.0167	0.0615	0.017	0.04	0	0	0	0	0	0	0	0	0	
DETOXIFICATION		187298	187298	62286643	FLAVIN-CONTAINING MONOOXYGENASE 5	MEMBRANE	7	12	9	17	18	26	0	2	0	0	0	0	7	9	7				0.2718	0.2214	0.1506	0.5226	0.3063	0.5196	0	0.0553	0	0	0	0	0.1284	0.1471	0.1074	
DETOXIFICATION		3930	3930	6981032	HEME OXYGENASE 1	MEMBRANE	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			0	0	0	0	0	0	0	0	0	0	0	0	0	0		
DETOXIFICATION		68743	68743	501035	HEME OXYGENASE 2	MEMBRANE	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	1			0	0	0	0	0.034	0	0	0	0	0	0	0	0	0.0153		
DETOXIFICATION		19913	19913	6647578	MEMBRANE ASSOCIATED PROGESTERONE RECEPTOR COMPONENT 1	MEMBRANE	8.8889	22	18.7	13	21.667	16.762	4	4.8	4	0	8	2	6	6.6667	11.688				0.3452	0.406	0.313	0.3996	0.3687	0.335	0.2182	0.1328	0.1617	0	0.2706	0.0717	0.1101	0.109	0.1794	
DETOXIFICATION		204220	204220	27732829	MEMBRANE PROGESTIN RECEPTOR ALPHA	MEMBRANE	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0			0	0	0.0167	0	0	0.02	0	0	0	0	0	0	0	0	0	
DETOXIFICATION		28295	28295	38649092	MICROSOMAL GLUTATHIONE S-TRANSFERASE 1	MEMBRANE	8	18	31.583	16	34	23	8	15	5	1	16	18	40	29	16				0.3107	0.3322	0.5286	0.4919	0.5786	0.4596	0.4364	0.4149	0.2021	0.0471	0.5413	0.6454	0.7339	0.4739	0.2456	
DETOXIFICATION		69488	69488	38303959	NADH-CYTOCHROME B5 REDUCTASE	MEMBRANE	8	11	18	12	17	15	5	4	2	2	2	5	19	9	29				0.3107	0.203	0.3013	0.3689	0.2893	0.2998	0.2728	0.1107	0.0808	0.0943	0.0677	0.1793	0.3486	0.1471	0.4451	
DETOXIFICATION		78074	44210 78074	66118	NADPH-CYTOCHROME P450 REDUCTASE	MEMBRANE	18	34	49	28	50	47	3	12	0	1	4	3	18	14	16				0.699	0.6274	0.8201	0.8607	0.8509	0.9393	0.1637	0.332	0	0.0471	0.1353	0.1076	0.3303	0.2288	0.2456	
DETOXIFICATION		102628	102628	27545384	OXIDATIVE 17 BETA HYDROXYSTEROID DEHYDROGENASE TYPE 6	MEMBRANE	0	5.7895	2.1053	2.4	11.75	4.8235	0	0	0	0	1.5	2	0	0	5.5415				0	0.1068	0.0352	0.0738	0.2	0.0964	0	0	0	0.0507	0.0717	0	0	0.0851		
DETOXIFICATION		274611	274611	62900631	PROGESTERONE RECEPTOR MEMBRANE COMPONENT 2	MEMBRANE	1.1111	3	3.3	1	4.3333	5.2381	1	1.2	0	0	0	0	3.3333	5.3125					0.0432	0.0554	0.0552	0.0307	0.0737	0.1047	0.0546	0.0332	0	0	0	0	0.0545	0.0815		
DETOXIFICATION		227390	227390	31324556	RETINOL DEHYDROGENASE 10 (PREDICTED)	MEMBRANE	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0				0	0	0	0	0.0307	0	0	0	0	0	0	0	0	0		
DETOXIFICATION		238730	238730	62650915	RETINOL DEHYDROGENASE 11 (PREDICTED)	MEMBRANE	1	1	2	3	3	5	0	2	0	0	0	0	0	0	0	2			0.0388	0.0185	0.0335	0.0922	0.0511	0.0999	0	0.0553	0	0	0	0	0	0	0.0307	
DETOXIFICATION		105752	35165 105752	841197	RETINOL DEHYDROGENASE TYPE I	MEMBRANE	9	25.038	25.443	31.487	39.591	37.224	0	14.4	0	0	2.5	0	18	26	33.526				0.3495	0.462	0.4258	0.9679	0.6738	0.7439	0	0.3983	0	0.0846	0	0.3303	0.4249	0.5146		
DETOXIFICATION		285736	285736	27690924	SIMILAR TO MICROSOMAL GLUTATHIONE S-TRANSFERASE 2 (MICROSOMAL GST-2) (MICROSOMAL GST-II)	MEMBRANE	0	1	1	1	1	3	0	0	0	1	1	0	0	2	0				0	0.0185	0.0167	0.0307	0.017	0.06	0	0	0.0471	0.0338	0	0	0.0327	0		
DETOXIFICATION		164232	164232	27678076	SIMILAR TO MICROSOMAL GLUTATHIONE S-TRANSFERASE 3	MEMBRANE	0	0	1	0	0	0	0	1	0	0	0	1	6	2	3				0	0	0.0167	0	0	0	0	0.0277	0	0	0.0359	0.1101	0.0327	0.046		
DETOXIFICATION		337296	337296	81892292	SMOOTH MUSCLE-SPECIFIC 17BETA-HYDROXYSTEROID DEHYDROGENASE TYPE 3	MEMBRANE	1	11	8	7	13	6	1	2	0	0	0	0	1	0	3				0.0388	0.203	0.1339	0.2152	0.2212	0.1199	0.0546	0.0553	0	0	0	0.0183	0	0.046		
DETOXIFICATION		137571	137571	8394354	SQUALENE MONOOXYGENASE	MEMBRANE	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0				0	0	0	0	0	0	0	0	0	0	0	0	0	0		
DETOXIFICATION		75108	75108	6981598	STERYL-SULFATASE	MEMBRANE	0	3	4	4	4	2	0	0	0	0	0	0	0	0	0				0	0.0554	0.0669	0.123	0.0681	0.04	0	0	0	0	0	0	0	0	0	
DETOXIFICATION		43597	43597	695162	UDP-GLUCURONOSYL TRANSFERASE 1A1	MEMBRANE	23.066	22.629	35.433	31.297	24.824	29.538	0	16.211	5	0	3.1818	2.25	17.491	14.821	24.543				0.8958	0.4176	0.593	0.9621	0.4225	0.5903	0	0.4484	0.2021	0	0.1076	0.0807	0.3209	0.2422	0.3767	
DETOXIFICATION		53066	53066	18308168	UDP-GLUCURONOSYL TRANSFERASE 1A5	MEMBRANE	1.5377	11.314	5.9055	1.956	5.5501	13.034	0	4.0526	0	0	0	0	2.4702	2.2312				0.0597	0.2088	0.0988	0.0601	0.0945	0.2605	0	0.1121	0	0	0	0	0	0.0404	0.0342		
DETOXIFICATION		205347	53068 205347	89276780	UDP-GLUCURONOSYL TRANSFERASE 1A6	MEMBRANE	10.764	25.514	29.528	7.8242	15.958	6.3295	1	10.132	1.6667	0	0	0	0	0	0				0.418	0.4708	0.4942	0.2405	0.2716	0.1265	0.0546	0.2803	0.0674	0	0	0	0	0	0	
DETOXIFICATION		53069	53069	18308176	UDP-GLUCURONOSYL TRANSFERASE 1A7	MEMBRANE	1.5377	7.5429	1.9685	0	0	2.1098	0	0	0	0	0	0	0	0	0				0.0597	0.1392	0.0329	0	0	0.0422	0	0	0	0	0	0	0	0	0	
DETOXIFICATION		31600	31600	27545358	UDP-GLUCURONOSYL TRANSFERASE 2B1	MEMBRANE	4.4524	20.384	16.269	4.5128	10.37	6.4684	1	4.391	0	0	1.0909	0	2.2519	4.6828	6.8371				0.1729	0.3762	0.2723	0.1387	0.1765	0.1293	0.0546	0.1215	0	0.0369	0	0.0413	0.0765	0.1049		

DETOXIFICATION	80303	80303 127236 221298	549157	UDP- GLUCURONOSYL TRANSFERASE 2B12	13.81	28.963	14.883	1.1282	19.667	19.076	5	3.2932	0	1	0	1.25	6.7558	24.585	19.372	0.5363	0.5345	0.2491	0.0347	0.3347	0.3812	0.2728	0.0911	0	0.0471	0	0.0448	0.124	0.4018	0.2973	
DETOXIFICATION	78055	78055 146466	207583	UDP- GLUCURONOSYL TRANSFERASE 2B2	18.347	36.021	10.602	3.1026	27.578	9.6667	4	7.5865	7	5	10.502	6.5	44.911	80.144	53.785	0.7125	0.6647	0.1774	0.0954	0.4693	0.1932	0.2182	0.2099	0.2829	0.2356	0.3553	0.2331	0.8241	1.3098	0.8256	
DETOXIFICATION	31602	31602 84217	31543923	UDP- GLUCURONOSYL TRANSFERASE 2B3	17.819	31.721	34.504	0	22.234	28.829	3.3333	8.9709	4.5	0	2.4004	0	8.6738	8.9295	16.425	0.692	0.5854	0.5775	0	0.3784	0.5761	0.1819	0.2482	0.1819	0	0.0812	0	0.1592	0.1459	0.2521	
DETOXIFICATION	31603	31603	55925581	UDP- GLUCURONOSYL TRANSFERASE 2B5	13.929	24.049	30.746	11.359	22.519	21.248	1.6667	5.1682	3.8333	0	1.7338	0	3.6646	9.0255	5.6154	0.5409	0.4438	0.5146	0.3492	0.3832	0.4246	0.0909	0.143	0.1549	0	0.0587	0	0.0672	0.1475	0.0862	
DETOXIFICATION	217594	217594	34876789	UDP- GLUCURONOSYL TRANSFERASE GTNA1	3.4524	4.6114	12.983	4.5128	3.4567	9.3601	0	2.1955	0	0	1.0909	0	2.2519	2.3414	9.1161	0.1341	0.0851	0.2173	0.1387	0.0588	0.1871	0	0.0607	0	0	0.0369	0	0.0413	0.0383	0.1399	
DETOXIFICATION	169892	169892	27694215	UDP- GLUCURONOSYL TRANSFERASE GTNA2	5.2857	6.2513	14.178	5.3077	3.2143	8.7161	0	0	0	0	0	0	0	0	1.075	0.2053	0.1154	0.2373	0.1632	0.0547	0.1742	0	0	0	0	0	0	0	0	0.0165	
DETOXIFICATION	37206	37206	13591981	2,3- OXIDOSQUALENE:LANOSTEROL CYCLASE	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	
DETOXIFICATION	3937	3937	6981050	3 BETA-HYDROXYSTEROID DEHYDROGENASE TYPE III	13	15	13	10	13	15	0	0	2	0	0	0	0	0	0	0.5049	0.2768	0.2176	0.3074	0.2212	0.2998	0	0	0.0808	0	0	0	0	0	0	0
DETOXIFICATION	19230	19230	6708142	3-ALPHA-HYDROXYSTEROID DEHYDROGENASE	0	2	0	2	8.875	3	0	0	0	0	0	0	8.875	4	8	0	0.0369	0	0.0615	0.151	0.06	0	0	0	0	0	0	0.1628	0.0654	0.1228	
DETOXIFICATION	83190	83190	7387724	3-HYDROXYACYL-COA DEHYDROGENASE TYPE II (TYPE II HADH) (ENDOPLASMIC RETICULUM-ASSOCIATED AMYLOID BETA-PEPTIDE BINDING PROTEIN)	0	7	8	2	16	4	2	14	0	0	0	0	1	2	3	0	0.1292	0.1339	0.0615	0.2723	0.0799	0.1091	0.3873	0	0	0	0.0183	0.0327	0.046		
DETOXIFICATION	23758	23758	456303	3-OXO-5-BETA-STEROID 4- DEHYDROGENASE	0	0	0	2	3	1	0	0	0	0	0	0	0	0	2	0	0	0	0.0615	0.0511	0.02	0	0	0	0	0	0	0	0	0.0307	
DETOXIFICATION	100616	100616	433611	AF1ATOXIN B1 ALDEHYDE REDUCTASE MEMBER 1	0	1	0	0	3	2	0	0	0	0	0	0	0	1	1	0	0.0185	0	0	0.0511	0.04	0	0	0	0	0	0	0	0.0163	0.0153	
DETOXIFICATION	161251	161251	6815049	AF1ATOXIN B1 ALDEHYDE REDUCTASE MEMBER 2	0	0	0	0	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0.017	0	0	0	0	0	0	0	0.0183	0	0	
DETOXIFICATION	302704	302704	34862428	ALDEHYDE DEHYDROGENASE 1 FAMILY MEMBER L2	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.083	0	0	0	0	0	0	
DETOXIFICATION	245155	245155	34879551	ALDEHYDE DEHYDROGENASE 7A1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.0546	0	0	0	0	0	0	0	0	
DETOXIFICATION	72216	72216	38494348	ALDEHYDE DEHYDROGENASE FAMILY 1 MEMBER A1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
DETOXIFICATION	95119	95119	4324710	ALDEHYDE OXIDASE	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0.0183	0	0.0153	
DETOXIFICATION	27636	27636	81871478	ALL-TRANS-13,14- DIHYDRORETINOL SATURASE	3	5	6	12	10.769	10.625	0	0	3	0	0	0	3	2	3	0.1165	0.0923	0.1004	0.3689	0.1833	0.2123	0	0	0.1213	0	0	0	0.055	0.0327	0.046	
DETOXIFICATION	69784	69784	55761	ARYL SULFOTRANSFERASE	0	0	0	0	0	2	0	0	0	0	0	0	3	0	2	0	0	0	0	0.034	0	0	0	0	0	0	0	0.055	0	0.0307	
DETOXIFICATION	30001	30001	9963930	BILE ACID COA LIGASE	8.35	25.581	38.561	29.58	31.476	48.541	0	4.3333	1	3	5	0	8.3333	16.667	32.304	0.3243	0.4721	0.6454	0.9093	0.5357	0.9701	0	0.1199	0.0404	0.1414	0.1692	0	0.1529	0.2724	0.4959	
DETOXIFICATION	54374	54374	285208	BILIVERDIN REDUCTASE A PRECURSOR	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
DETOXIFICATION	204593	204593	34875339	BIPHENYL HYDROLASE-LIKE (SERINE HYDROLASE, BREAST EPITHELIAL MUCIN-ASSOCIATED ANTIGEN)	0	0	1	0	0	1	0	2	0	0	0	0	0	0	0	0	0	0	0	0.0167	0	0	0.0553	0	0	0	0	0	0	0	0
DETOXIFICATION	166315	166315	55562775	CARBONYL REDUCTASE 4	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.0185	0	0	0	0	0	0	0	0	0	0	0	0	0	
DETOXIFICATION	43686	43686	2506388	CARBOXYLESTERASE 1	0	7.3333	5.3426	9.5	8.2308	8.7692	4	9	8	0	0	0	6	4.3333	5.6667	0	0.1353	0.0894	0.292	0.1401	0.1752	0.2182	0.249	0.3234	0	0	0	0.1101	0.0708	0.087	
DETOXIFICATION	84186	42034 84186 112141 146478	92053	CARBOXYLESTERASE 10	25.091	34.391	31.622	33.735	56.078	39.924	4.3636	20.182	11.741	5.8333	15	8	21.769	20.333	29.455	0.9744	0.6346	0.5292	1.0371	0.9544	0.7978	0.2381	0.5583	0.4746	0.2749	0.5074	0.2868	0.3994	0.3323	0.4521	
DETOXIFICATION	12999	12999 13000	56541525	CARBOXYLESTERASE 2	0	1.4111	4	0	0	1.2222	0	0	0	0	1.452	0	0	0	3.0833	0	0.026	0.0669	0	0	0.0244	0	0	0	0	0	0.0491	0	0	0.0473	
DETOXIFICATION	78070	78070	550147	CARBOXYLESTERASE 3	9.8312	10.754	22.491	7.4817	19.512	16.593	0	2.1879	0	0	0	0	3.2312	7.1948	9.6043	0.3818	0.1985	0.3764	0.23	0.3321	0.3316	0	0	0	0	0	0.0593	0.1176	0.1474		
DETOXIFICATION	77793	77793 105537	550418	CARBOXYLESTERASE 4	24.862	36.117	26.208	40.453	37.849	38.114	6.1688	20.255	10.571	3.1667	11	6	12.437	10.724	14.679	0.9655	0.6665	0.4386	1.2436	0.6441	0.7617	0.3365	0.5603	0.4273	0.1492	0.3721	0.2151	0.2282	0.1753	0.2253	
DETOXIFICATION	10945	10945 123735 158916	562010	CARBOXYLESTERASE B-1	6.2156	11.405	16.38	15.83	26.33	11.6	2.4675	3.3758	0	0	0	0	7.1065	4.5961	3.262	0.2414	0.2105	0.2741	0.4866	0.4481	0.2318	0.1346	0.0934	0	0	0	0.1304	0.0751	0.0501		
DETOXIFICATION	227817	227817	27658990	CARBOXYLESTERASE ESNA1	0	1.3	0	0	0	0	0																								

MITOCHONDRIA	40425	40425	7438124	PYRUVATE CARBOXYLASE, MITOCHONDRIAL	SOLUBLE	0	2	1	0	0	1	6	10	0	0	0	0	0	0	0	0.0369	0.0167	0	0	0.02	0.3273	0.2766	0	0	0	0	0	0	0	0	0	0
MITOCHONDRIA	203734	203734	56090293	PYRUVATE DEHYDROGENASE E1 COMPONENT BETA SUBUNIT, MITOCHONDRIAL	SOLUBLE	0	0	1	0	0	0	1	5	0	0	0	0	0	0	0	0	0.0167	0	0	0	0.0546	0.1383	0	0	0	0	0	0	0	0	0	0
MITOCHONDRIA	262284	262284	34858436	REPRESSOR OF ESTROGEN RECEPTOR ACTIVITY; B-CELL ASSOCIATED PROTEIN	SOLUBLE	0	15	19	10	16	13	0	7	0	0	0	0	4	9	8	0	0.2768	0.318	0.3074	0.2723	0.2598	0	0.1936	0	0	0	0	0	0.0734	0.1471	0.1228	
MITOCHONDRIA	85749	85749	52000744	SARCOSINE DEHYDROGENASE	SOLUBLE	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0.0277	0	0	0	0	0	0	0	0	0	0	
MITOCHONDRIA	31393	31393	66655	SERINE-PYRUVATE AMINOTRANSFERASE, MITOCHONDRIAL	SOLUBLE	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0.0185	0.0167	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MITOCHONDRIA	70622	70622	7387725	SHORT CHAIN 3-HYDROXYACYL-COA DEHYDROGENASE, MITOCHONDRIAL	SOLUBLE	1	14	24	4	8	6	5	10	0	0	0	0	0	0	0	0.0388	0.2584	0.4017	0.123	0.1362	0.1199	0.2728	0.2766	0	0	0	0	0	0	0	0	0
MITOCHONDRIA	84143	84143	48734846	SHORT CHAIN ACYL-COA DEHYDROGENASE	SOLUBLE	0	0	1	0	0	0	0	7.35	0	0	0	0	0	0	0	0	0	0.0167	0	0	0	0.2033	0	0	0	0	0	0	0	0	0	0
MITOCHONDRIA	288262	288262	34860605	SIMILAR TO ACYL-COA DEHYDROGENASE FAMILY MEMBER 8, MITOCHONDRIAL	SOLUBLE	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0.0185	0.0167	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MITOCHONDRIA	288241	288241	34866733	SIMILAR TO ACYL-COENZYME A DEHYDROGENASE FAMILY, MEMBER 8	SOLUBLE	0	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0.0369	0.0167	0	0	0	0	0	0	0	0	0	0	0	0	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	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
MITOCHONDRIA	271135	271135	34866853	SIMILAR TO CYTOCHROME C-1	SOLUBLE	1	4	8	3	9	6	0	0	0	0	0	0	0	0	2	0.0388	0.0738	0.1339	0.0922	0.1532	0.1199	0	0	0	0	0	0	0	0	0	0.0307	
MITOCHONDRIA	260747	260747	34862790	SIMILAR TO GLYCINE DECARBOXYLASE	SOLUBLE	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.0185	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MITOCHONDRIA	247605	247605	34855983	SIMILAR TO INNER MEMBRANE PROTEIN, MITOCHONDRIAL (MITOFILIN); MOTOR PROTEIN	SOLUBLE	0	4	2	1	6	5	0	0	0	0	0	0	0	0	0	0	0.0738	0.0335	0.0307	0.1021	0.0999	0	0	0	0	0	0	0	0	0	0	
MITOCHONDRIA	258281	258281	34859067	SIMILAR TO MEDIUM-CHAIN ACYL-COA SYNTHETASE	SOLUBLE	0	0	1	1	0	1	0	3	0	2	1	1	1	4	0	0	0.0167	0.0307	0	0.02	0	0.083	0	0.0943	0.0677	0.0359	0.0183	0.0163	0.0614			
MITOCHONDRIA	262377	262377	34857966	SIMILAR TO METAXIN 1	SOLUBLE	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
MITOCHONDRIA	203309	203309	56605654	SIMILAR TO METAXIN 2	SOLUBLE	0	1	0	0	4	0	0	0	0	0	0	0	0	0	0	0	0.0185	0	0	0.0681	0	0	0	0	0	0	0	0	0	0	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	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	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	2	0	0	1	1	0	0	0	0	0	0	0	1	0	0.0185	0.0335	0	0	0.02	0.0546	0	0	0	0	0	0	0	0	0	0.0153
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	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.017	0	0	0	0	0	0	0	0	0	0	0	0
MITOCHONDRIA	215768	215768	34858473	SIMILAR TO NADH DEHYDROGENASE (UBIQUINONE) 1 ALPHA SUBCOMPLEX, 9	SOLUBLE	0	3	5	1	7	2	0	4	0	0	0	0	0	1	0	0.0554	0.0837	0.0307	0.1191	0.04	0	0.1107	0	0	0	0	0	0	0	0	0.0153	

PEROXISOME	68714	68714	62286984	CHLORIDE ION PUMP-ASSOCIATED 55 KDA PROTEIN	SOLUBLE	2	0	0	2	1	3	0	0	1	0	0	0	0	0	0	0.0777	0	0	0.0615	0.017	0.06	0	0	0.0404	0	0	0	0	0	0			
PEROXISOME	60497	60497	56972124	D-AMINO ACID OXIDASE	SOLUBLE	0	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0.0185	0	0	0	0	0	0	0.0277	0	0	0	0	0	0			
PEROXISOME	131621	131621	48474726	DEHYDROGENASE/REDUCTASE SDR FAMILY MEMBER 4	SOLUBLE	0	0	1	1	2.3333	3	0	1	1	0	0	0	0	0	0	0	0	0.0167	0.0307	0.0397	0.06	0	0.0277	0.0404	0	0	0	0	0	0			
PEROXISOME	80356	80356	478984	DELTA3,5-DELTA2,4-DIENOYL-COA ISOMERASE, MITOCHONDRIAL	SOLUBLE	1	4	5	0	0	1	0	1	0	1	0	0	0	0	0	0.0388	0.0738	0.0837	0	0	0.02	0	0.0277	0	0	0	0	0	0	0	0		
PEROXISOME	270415	270415	34859262	GLYCOLATE OXIDASE; SHORT-CHAIN ALPHA-HYDROXY ACID OXIDASE	SOLUBLE	8	12	12	0	0	0	0	0	1	0	0	0	0	0	0	0.3107	0.2214	0.2008	0	0	0	0	0.0277	0	0	0	0	0	0	0	0		
PEROXISOME	100475	100475	50925465	HYDROXYACID OXIDASE 3	SOLUBLE	1	4	2	1	1	0	1	0	2	0	0	0	0	0	0.0388	0.0738	0.0335	0.0307	0	0.02	0	0.0553	0	0	0	0	0	0	0	0	0		
PEROXISOME	80318	80318	8392962	KAN-1	SOLUBLE	10	13	20	2	1	10	1	1	1	1	0	0	0	1	2	0.3884	0.2399	0.3347	0.0615	0.017	0.1998	0.0546	0.0277	0.0404	0	0	0	0.0163	0.0307	0	0		
PEROXISOME	251837	251837	81885359	LACTOYLGLUTATHIONE LYASE	SOLUBLE	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
PEROXISOME	43433	43433	56789700	PEROXIREDOXIN 1	SOLUBLE	18.333	16.25	15	11.077	16.667	16.235	0	0	2.5	0	0	3	1.3333	1.1667	0.712	0.2999	0.2511	0.3405	0.2836	0.3245	0	0	0.1011	0	0	0	0.055	0.0218	0.0179	0	0		
PEROXISOME	269931	269931	34849738	PEROXIREDOXIN 2	SOLUBLE	0	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	0.0153	0	0		
PEROXISOME	60471	60471	5902791	PEROXIREDOXIN 6	SOLUBLE	0	0	0	1	1	1	0	0	0	0	0	1	0	1	0	0	0	0.0307	0.017	0.02	0	0	0	0	0	0	0	0.0183	0	0.0153	0	0	
PEROXISOME	160562	160562	27667388	PEROXISOMAL ACYL-COA THIOESTERASE 2B; LIKELY ORTHOLOG OF MOUSE PEROXISOMAL ACYL-COA THIOESTERASE 2B	SOLUBLE	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
PEROXISOME	12072	12072	8926847	PEROXISOMAL ASSEMBLY PROTEIN PEX3	SOLUBLE	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
PEROXISOME	149061	149061	59809132	PEROXISOMAL BIFUNCTIONAL ENZYME	SOLUBLE	39	35	51	19	24	27	0	1	7	0	0	1	1	1	1.5146	0.6459	0.8536	0.5841	0.4084	0.5396	0	0.0277	0.2829	0	0	0	0.0183	0.0163	0.0153	0	0		
PEROXISOME	155718	155718	4126962	PEROXISOMAL MEMBRANE ANCHOR PROTEIN	SOLUBLE	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.017	0	0	0	0	0	0	0	0	0	0	0	0	
PEROXISOME	108354	108354	2492741	PEROXISOMAL MULTIFUNCTIONAL ENZYME TYPE 2 (MFE-2) (D-BIFUNCTIONAL PROTEIN) (DBP) (17-BETA-HYDROXYSTEROID DEHYDROGENASE 4)	SOLUBLE	32.667	49	71.903	9	8	14	1	7	1	1	0	0	0	1	1.2686	0.9042	1.2034	0.2767	0.1362	0.2798	0.0546	0.1936	0.0404	0.0471	0	0	0	0	0.0153	0	0		
PEROXISOME	169183	169183	2911135	PEROXISOME ASSEMBLY FACTOR-2	SOLUBLE	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.02	0	0	0	0	0	0	0	0	0	0		
PEROXISOME	55437	55437	6539668	PHYTANOYL-COA DIOXYGENASE, PEROXISOMAL	SOLUBLE	3	2	5	0	2	0	0	1	3	0	0	0	0	0	0.1165	0.0369	0.0837	0	0.034	0	0	0.0277	0.1213	0	0	0	0	0	0	0	0		
PEROXISOME	60442	60442	4336879	PRX IV	SOLUBLE	2.6667	8.75	10	4.9231	8.3333	6.7647	2	7	2.5	0	0	1	2.6667	5.8333	0.1036	0.1615	0.1674	0.1513	0.1418	0.1352	0.1091	0.1936	0.1011	0	0	0	0.0183	0.0436	0.0895	0	0		
PEROXISOME	176638	176638	90109768	PUTATIVE PEROXISOMAL 2,4-DIENOYL-COA REDUCTASE	SOLUBLE	0	2	8	0	2	1	0	2	3	0	0	0	0	0	0	0.0369	0.1339	0	0.034	0.02	0	0.0553	0.1213	0	0	0	0	0	0	0	0		
PEROXISOME	34787	34787	6491860	PUTATIVE SHORT-CHAIN DEHYDROGENASE/REDUCTASE MRNA, COMPLETE CDS	SOLUBLE	9	16	16	1	7	7	1	6	6	1	0	0	0	0	0.3495	0.2953	0.2678	0.0307	0.1191	0.1399	0.0546	0.166	0.2425	0.0471	0	0	0	0	0	0	0		
PEROXISOME	273878	273878	34868484	SIMILAR TO BILE ACID COENZYME A; AMINO ACID N-ACYLTRANSFERASE; GLYCINE N-CHOLYLTRANSFERASE	SOLUBLE	0	0	2	0	0	0	1	0	2	0	0	0	0	0	0	0	0	0.0335	0	0	0.0546	0	0.0808	0	0	0	0	0	0	0	0		
PEROXISOME	265523	265523	34935094	SIMILAR TO GLYOXYLATE REDUCTASE/HYDROXYPYRUVATE REDUCTASE	SOLUBLE	1	2	2	2	1	2	0	0	0	0	0	0	0	0	0.0388	0.0369	0.0335	0.0615	0.017	0.04	0	0	0	0	0	0	0	0	0	0	0		
PEROXISOME	208921	208921	57164137	SIMILAR TO PEGI PROTEIN	SOLUBLE	2	2	5	1	0	0	0	0	0	0	0	0	0	0	0.0777	0.0369	0.0837	0.0307	0	0	0	0	0	0	0	0	0	0	0	0	0		
PEROXISOME	292730	292730	34851379	SIMILAR TO PEROXISOMAL LON PROTEASE	SOLUBLE	2	2	4	1	0	1	0	2	0	0	0	0	0	0	0.0777	0.0369	0.0669	0.0307	0	0.02	0	0.0553	0	0	0	0	0	0	0	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	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0.0185	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
PEROXISOME	235341	235341	62645408	SIMILAR TO PEROXISOME BIOGENESIS FACTOR 16	SOLUBLE	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
PEROXISOME	31609	31609	56971244	URATE OXIDASE	SOLUBLE	22	34	52	0	2	0	36	47.938	29	0	0	1	0	0	0.8544	0.6274	0.8703	0	0.034	0	1.964	1.3261	1.1722	0	0	0	0.0183	0	0	0	0		
PEROXISOME	80445	80445	2144323	XANTHINE DEHYDROGENASE/OXIDASE	SOLUBLE	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0.02	0	0	0	0	0	0	0	0	0	0	0	0	
PLASMA MB	11455	11455	202551	5'-NUCLEOTIDASE	MEMBRANE	0	0	0	0	1	1	1	0	2	0	0	1	10	4	8	0	0	0	0.017	0.02	0	0.0553	0	0	0	0.0359	0.1835	0.0654	0.1228	0	0		
PLASMA MB	11241	11241	205109	AMINOPEPTIDASE N	MEMBRANE	0	0	0	1	3	2	1	5	0	0	0	0	0	1	0	0	0	0	0.0307	0.0511	0.04	0.0546	0.1383	0	0	0	0	0	0	0	0.0153	0	0
PLASMA MB	10860	10860	1703345	AMYLOID-LIKE PROTEIN 2 PRECURSOR	MEMBRANE	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		

PLASMA MB	299926	299926	34856480	SIMILAR TO INTEGRIN ALPHA V SUBUNIT	MEMBRANE	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.0163	0.0153					
PLASMA MB	199085	199085	34855581	SIMILAR TO MALTASE-GLUCOAMYLASE, INTESTINAL	MEMBRANE	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
PLASMA MB	217052	217052	34878866	SIMILAR TO PHOSPHATIDYLINOSITOLGLYCAN CLASS N	MEMBRANE	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.0307	0	0.0307		
PLASMA MB	222218	222218	34863455	SIMILAR TO SEMAPHORIN SUBCLASS 4 MEMBER G	MEMBRANE	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
PLASMA MB	294808	294808	34862482	SIMILAR TO SOLUTE CARRIER FAMILY 30 (ZINC TRANSPORTER), MEMBER 6	MEMBRANE	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.0307				
PLASMA MB	206065	206065	34864902	SIMILAR TO STABILIN-2	MEMBRANE	0	0	0	0	1	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	0.0307	0.017	0	0	0	0	0	0	0	0	0	0	0.0153				
PLASMA MB	301709	301709	34855791	SIMILAR TO UROPLAKIN 1A	MEMBRANE	0	1	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.0185	0	0.034	0	0	0	0	0	0	0	0	0	0	0.0153				
PLASMA MB	268665	268665	34879705	SLC26A9 ANION TRANSPORTER/EXCHANGE	MEMBRANE	2	3	2	4	2	5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.0777	0.0554	0.0335	0.123	0.034	0.0999	0	0	0	0	0	0	0	0.049	0.0307				
PLASMA MB	75080	75080	6981510	SODIUM CHANNEL PROTEIN TYPE III ALPHA SUBUNIT	MEMBRANE	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.0163	0			
PLASMA MB	11254	11254	8394279	SODIUMBILE ACID COTRANSPORTER	MEMBRANE	0	0	0	0	1	3	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	0.0307	0.0511	0.02	0	0.0277	0	0	0	0	0	0	0.0153				
PLASMA MB	3651	3651	6978543	SODIUM/POTASSIUM-TRANSPORTING ATPASE ALPHA-1 CHAIN	MEMBRANE	0	0	2	8	19	12	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.0335	0.2459	0.3234	0.2398	0	0	0	0	0	0	0	0	0	0	0			
PLASMA MB	3654	3654	6978549	SODIUM/POTASSIUM-TRANSPORTING ATPASE BETA-1 CHAIN	MEMBRANE	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	0.0307	0	0	0	0	0	0	0	0	0	0	0	0				
PLASMA MB	3656	3656	6978553	SODIUM/POTASSIUM-TRANSPORTING ATPASE BETA-3 CHAIN	MEMBRANE	0	0	0	0	1	1	0	0	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.0307	0.017	0	0	0.0553	0.0404	0	0	0	0	0	0	0.0183	0	0		
PLASMA MB	75093	75093	92281	SOLUTE CARRIER FAMILY 2, FACILITATED GLUCOSE TRANSPORTER, MEMBER 2	MEMBRANE	0	0	0	4	15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.123	0.2553	0	0	0	0	0	0	0	0	0	0	0.0163	0			
PLASMA MB	78114	78114	9624356	SOLUTE CARRIER FAMILY 21 MEMBER 1C	MEMBRANE	0	0	0	0	0	1	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	0.017	0.0799	0	0	0	0	0	0	0	0	0	0	0.0367	0	0.046	
PLASMA MB	152150	152150	8394294	SOLUTE CARRIER FAMILY 21 MEMBER 3	MEMBRANE	0	0	0	2	6	6.4	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	0.0615	0.1021	0.1279	0	0	0	0	0	0	0	0	0	0	0.0307		
PLASMA MB	43622	43622	3914190	SOLUTE CARRIER FAMILY 21 MEMBER 5	MEMBRANE	0	0	4	4.75	16.591	10.6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.0669	0.146	0.2824	0.2118	0	0	0	0	0	0	0	0	0	0	0.0307		
PLASMA MB	47477	47477	9622206	SOLUTE CARRIER FAMILY 21 MEMBER 9	MEMBRANE	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
PLASMA MB	262547	262547	34876981	STABILIN-1	MEMBRANE	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
PLASMA MB	153825	153825	50401220	STABILIN-2	MEMBRANE	0	0	0	1	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.0307	0.034	0	0	0	0	0	0	0	0	0	0	0.0367	0	0.0921		
PLASMA MB	265569	265569	34853860	STOMATIN	MEMBRANE	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.0359	0.0367	0	0.0921
PLASMA MB	104202	104202	431453	SULFATE ANION TRANSPORTER 1	MEMBRANE	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	0	0	0	0	0	0	0	0	0	0		
PLASMA MB	33179	33179	37589607	SYNAPTIC GLYCOPROTEIN SC2	MEMBRANE	4	8	17	4	7	11	1	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.1553	0.1476	0.2845	0.123	0.1191	0.2198	0.0546	0.0277	0.0404	0	0.0338	0	0.0183	0.0327	0.0767			
PLASMA MB	75082	75082	6981518	SYNDECAN-1 PRECURSOR	MEMBRANE	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
PLASMA MB	41211	41211	6981520	SYNDECAN-2 PRECURSOR	MEMBRANE	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
PLASMA MB	75083	75083	6981522	SYNDECAN-4 PRECURSOR	MEMBRANE	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
PLASMA MB	217700	217700	34872230	TASTE RECEPTOR, TYPE 1, MEMBER 2	MEMBRANE	0	2.8889	3.1111	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0																							

PROT SYN/FOLD	310568	310568	62648953	ERP44 (SIMILAR TO THIOREDOXIN DOMAIN CONTAINING 4; ENDOPLASMIC RETICULUM RESIDENT PROTEIN 44KDA)	SOLUBLE	0	1	2	1	2	1	3	6	15	12	31	29	30	51	51	0	0.0185	0.0335	0.0307	0.034	0.02	0.1637	0.166	0.6063	0.5655	1.0487	1.0398	0.5505	0.8335	0.7828	
PROT SYN/FOLD	41501	41501	68565348	EUKARYOTIC PEPTIDE CHAIN RELEASE FACTOR SUBUNIT 1 (ERF1) (EUKARYOTIC RELEASE FACTOR 1) (TB3-1) (C11 PROTEIN)	SOLUBLE	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	0	0	0	0	0	
PROT SYN/FOLD	166240	166240	34862605	EUKARYOTIC TRANSLATION ELONGATION FACTOR 1 BETA 2	SOLUBLE	0	0	0	0	0	0	0	0	1	1	0	0	1	0	0	0	0	0	0	0	0	0	0.0404	0.0471	0	0	0.0183	0	0	0	
PROT SYN/FOLD	103	103	9506571	EUKARYOTIC TRANSLATION INITIATION FACTOR 2 SUBUNIT 1	SOLUBLE	1	6	4	0	3	0	0	0	0	0	0	0	0	0	0	0.0388	0.1107	0.0669	0	0.0511	0	0	0	0	0	0	0	0	0	0	
PROT SYN/FOLD	55867	55867	62652368	EUKARYOTIC TRANSLATION INITIATION FACTOR 3 SUBUNIT 6	SOLUBLE	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
PROT SYN/FOLD	266163	266163	34866934	EUKARYOTIC TRANSLATION INITIATION FACTOR 3 SUBUNIT 6 INTERACTING PROTEIN	SOLUBLE	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
PROT SYN/FOLD	189964	189964	27730981	EUKARYOTIC TRANSLATION INITIATION FACTOR 3, SUBUNIT 12 [MUS MUSCULUS]	SOLUBLE	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.0167	0	0	0	0	0	0	0	0	0	0	0	0	0
PROT SYN/FOLD	239406	239406	34868741	EUKARYOTIC TRANSLATION INITIATION FACTOR 4G1	SOLUBLE	0	5	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0.0923	0.0335	0	0	0	0	0	0	0	0	0	0	0	0	0
PROT SYN/FOLD	23682	23682	91207082	EUKARYOTIC TRANSLATION INITIATION FACTOR 5A	SOLUBLE	2	1	6	0	3	1	0	0	0	0	0	0	0	0	0	0.0777	0.0185	0.1004	0	0.0511	0.02	0	0	0	0	0	0	0	0	0	0
PROT SYN/FOLD	43461	43461	501064	FK506-BINDING PROTEIN 1A	SOLUBLE	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
PROT SYN/FOLD	289953	289953	27684684	FK506-BINDING PROTEIN 3	SOLUBLE	0	5	2	1	0	0	0	0	0	0	0	0	0	0	0	0.0923	0.0335	0.0307	0	0	0	0	0	0	0	0	0	0	0	0	0
PROT SYN/FOLD	241842	241842	34872627	GCN1 GENERAL CONTROL OF AMINO-ACID SYNTHESIS 1-LIKE 1	SOLUBLE	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0.0471	0	0	0	0	0	0	
PROT SYN/FOLD	286877	286877	66793366	GLUTAMYL-PROLYL-TRNA SYNTHETASE	SOLUBLE	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0.0471	0	0	0	0	0	0	
PROT SYN/FOLD	246362	246362	38181944	GLUTAREDOXIN	SOLUBLE	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.0185	0	0	0	0	0	0	0	0	0	0	0	0	0	
PROT SYN/FOLD	395638	395638	77404380	GRP170 (HYPOXIA UP-REGULATED 1)	SOLUBLE	8	24.889	17	17	11	27	1	2	2	0	4	2	4	10	15	0.3107	0.4593	0.2845	0.5226	0.1872	0.5396	0.0546	0.0553	0.0808	0	0.1353	0.0717	0.0734	0.1634	0.2302	
PROT SYN/FOLD	36413	36413	62684205	HEAT RESPONSIVE PROTEIN 12	SOLUBLE	0	2	0	0	0	1	0	9	0	0	0	0	0	0	0	0	0	0.0369	0	0	0	0.02	0	0.249	0	0	0	0	0	0	0
PROT SYN/FOLD	153343	153343	2425030	HEAT RESPONSIVE PROTEIN 47 PRECURSOR	SOLUBLE	0	1	1	2	7	4	0	2	0	0	1	0	4	5	0	0	0.0185	0.0167	0.0615	0.1191	0.0799	0	0.0553	0	0.0338	0	0.0734	0.0817	0	0	
PROT SYN/FOLD	71479	71479	204665	HEAT SHOCK 27 KDA PROTEIN	SOLUBLE	0	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	0.0163	0	0	
PROT SYN/FOLD	195465	195465	34870188	HEAT SHOCK PROTEIN 105 KDA ALPHA	SOLUBLE	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
PROT SYN/FOLD	280024	280024	55824765	HEAT SHOCK PROTEIN 47 PRECURSOR	SOLUBLE	0	0	2	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0.0335	0	0	0.02	0	0	0.0404	0	0	0	0	0	0	0
PROT SYN/FOLD	82698	82698	54673763	HEAT SHOCK PROTEIN 86; HSP86	SOLUBLE	0	1.6667	0	0	2.6	3.2	0	0	0	0	0	0	4.7143	0	5.5	0	0.0308	0	0	0.0442	0.0639	0	0	0	0	0	0	0.0865	0	0.0844	
PROT SYN/FOLD	139643	139643	51243735	HEAT SHOCK PROTEIN 90; HSP90	SOLUBLE	0	3.4271	2	6.1304	10.611	4.9224	0	0	0	0	0	0	6.8857	0	5.6154	0	0.0632	0.0335	0.1885	0.1806	0.0984	0	0	0	0	0	0.1263	0	0.0862		
PROT SYN/FOLD	68722	68722	71051777	HEAT-SHOCK COGNATE 70KD PROTEIN (44KD ATPASE N-TERMINAL FRAGMENT)	SOLUBLE	16.836	26.627	28.655	39.358	24.769	31	1.2	14.218	10	1	5.6944	1.125	18.633	10.529	13.186	0.6538	0.4914	0.4796	1.2099	0.4215	0.6195	0.0655	0.3933	0.4042	0.0471	0.1926	0.0403	0.3419	0.1721	0.2024	
PROT SYN/FOLD	200861	200861	55250700	INSIG2 MEMBRANE PROTEIN (INSULIN INDUCED GENE 2)	SOLUBLE	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.0388	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
PROT SYN/FOLD	51607	51607	8394162	IRON-RESPONSIVE ELEMENT BINDING PROTEIN 1 (IRE-BP 1) (IRON REGULATORY PROTEIN 1) (IRP1) (FERRITIN REPRESSOR PROTEIN) (ACONITATE HYDRATASE)	SOLUBLE	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.04	0	0	0	0	0	0	0	0	0	
PROT SYN/FOLD	95874	95874	3360521	ISCHEMIA RESPONSIVE 94 KDA PROTEIN	SOLUBLE	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
PROT SYN/FOLD	132766	132766	7514005	MAJOR VAULT PROTEIN	SOLUBLE	0	2	3	0	3	2	0	0	0	0	0	0	0	0	0	0	0.0369	0.0502	0	0.0511	0.04	0	0	0	0	0	0	0	0	0	
PROT SYN/FOLD	47300	47300	9507149	MICROSOMAL STRESS																																

PROT SYN/FOLD	170945	170945	27661294	0	2	3	0	2	2	1	0	1	1	1	0	2	3	1	0	0.0369	0.0502	0	0.034	0.04	0.0546	0	0.0404	0.0471	0.0338	0	0.0367	0.049	0.0153			
PROT SYN/FOLD			951425	6	7	5	3	7	8	0	2	0	0	1	1	5	3	6		0.233	0.1292	0.0837	0.0922	0.1191	0.1599	0	0.0553	0	0	0.0338	0.0359	0.0917	0.0921			
PROT SYN/FOLD			52789215	0	3	0	0	3	0	0	0	0	0	0	0	0	0	0		0	0.0554	0	0	0.0511	0	0	0	0	0	0	0	0	0			
PROT SYN/FOLD			34878065	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0	0	0	0	0	0	0	0	0	0	0			
PROT SYN/FOLD			56090441	0	3	2	0	0	0	0	0	0	0	0	0	0	0	0		0	0.0554	0.0335	0	0	0	0	0	0	0	0	0	0	0			
PROT SYN/FOLD			34866944	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0	0	0	0	0	0	0	0	0	0	0			
PROT SYN/FOLD			38197382	51	35	36	66	47	48	13	37	22.688	20	41	21	44	89.819	46		1.9806	0.6459	0.6025	2.0289	0.7999	0.9592	0.7092	1.0235	0.917	0.9425	1.387	0.753	0.8073	1.4679	0.7061		
PROT SYN/FOLD			38382858	48	61	56	68	69	70	9	32	12	4	27	10	31	36	35		1.8641	1.1257	0.9372	2.0904	1.1743	1.3989	0.491	0.8852	0.485	0.1885	0.9134	0.3586	0.5883	0.5372			
PROT SYN/FOLD			729436	15.333	44	50	23	51	36	2	6	0	0	3	1	3	21.263	29.372		0.5955	0.812	0.8368	0.707	0.8679	0.7194	0.1091	0.166	0	0	0.1015	0.0359	0.055	0.3475	0.4508		
PROT SYN/FOLD			62651585	24	16	24	21	20	21	5	6	5.5556	2	8	4.1739	11.611	20	16		0.932	0.2953	0.4017	0.6456	0.3404	0.4197	0.2728	0.166	0.2246	0.0943	0.2706	0.1497	0.2131	0.3269	0.2456		
PROT SYN/FOLD			34858829	9.4667	14	18.85	3	3	2.1	0	0	0	0	0	0	0	0	0		0.3676	0.2584	0.3155	0.0922	0.0511	0.042	0	0	0	0	0	0	0	0	0		
PROT SYN/FOLD																																				
PROT SYN/FOLD			34870116	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
PROT SYN/FOLD			9754866	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0.0369	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
PROT SYN/FOLD			9506993	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0.0185	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
PROT SYN/FOLD			27731985	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
PROT SYN/FOLD			34865216	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0		0	0	0	0	0	0	0	0	0	0	0	0.1414	0	0	0	0	
PROT SYN/FOLD			34875539	0	1	2	0	1	0	0	0	0	0	0	0	0	0	0		0	0.0185	0.0335	0	0.017	0	0	0	0	0	0	0	0	0	0	0	0
PROT SYN/FOLD			34851760	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
PROT SYN/FOLD																																				
PROT SYN/FOLD			34859415	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
PROT SYN/FOLD			34932063	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
PROT SYN/FOLD																																				
PROT SYN/FOLD	315303	315303	34867138	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
PROT SYN/FOLD																																				
PROT SYN/FOLD	318887	318887	81892269	0	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	0.0163	0	0	
PROT SYN/FOLD																																				
PROT SYN/FOLD	239547	239547	34870174	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0		0	0.0185	0.0167	0	0	0	0	0	0	0	0	0	0	0	0	0	
PROT SYN/FOLD																																				
PROT SYN/FOLD	267441	267441	34880581	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
PROT SYN/FOLD																																				
PROT SYN/FOLD	213255	213255	34858904	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0		0	0.0185	0	0	0.017	0	0	0	0	0	0	0	0	0	0	0	0
PROT SYN/FOLD																																				
PROT SYN/FOLD	223302	223302	34878791	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0		0	0	0.0167	0	0	0	0	0	0	0	0	0	0	0	0	0	0
PROT SYN/FOLD																																				
PROT SYN/FOLD	269157	269157	55741637	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	0.0471	0	0	0	0	0	

PROT SYN/FOLD	198793	198793	198793	34860789	SIMILAR TO MICROSOMAL TRIGLYCERIDE TRANSFER PROTEIN	SOLUBLE	27	43	55	36	51	50	25	45	19	24	33	56	58	71	61	1.0485	0.7935	0.9205	1.1067	0.8679	0.9992	1.3639	1.2448	0.768	1.131	1.1164	2.0079	1.0642	1.1603	0.9363			
PROT SYN/FOLD	312741	312741	312741	66730413	SIMILAR TO PHENYLALANINE-TRNA SYNTHETASE-LIKE	SOLUBLE	3	3	5	1	0	1	0	0	0	0	0	0	0	0	0	0	0.1165	0.0554	0.0837	0.0307	0	0.02	0	0	0	0	0	0	0	0			
PROT SYN/FOLD	254493	254493	254493	51948478	SIMILAR TO PHENYLALANYL-TRNA SYNTHETASE BETA CHAIN (PHENYLALANINE--TRNA LIGASE BETA CHAIN) (PHERS)	SOLUBLE	9	5	6	2	3	0	0	0	0	0	0	0	0	0	0	0	0.3495	0.0923	0.1004	0.0615	0.0511	0	0	0	0	0	0	0	0	0			
PROT SYN/FOLD	276048	276048	276048	34869214	SIMILAR TO PROTEIN DISULFIDE ISOMERASE-RELATED	SOLUBLE	7	21	10	3	9	3	0	1	0	1	0	0	0	0	0	0	0.2718	0.3875	0.1674	0.0922	0.1532	0.06	0	0.0277	0	0.0471	0	0	0	0	0		
PROT SYN/FOLD	219536	219536	219536	27683535	SIMILAR TO SIGNAL RECOGNITION PARTICLE 19KDA; SIGNAL RECOGNITION PARTICLE 19KD	SOLUBLE	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0.0471	0	0	0	0	0			
PROT SYN/FOLD	300246	300246	300246	34875372	SIMILAR TO SIGNAL RECOGNITION PARTICLE 68KDA	SOLUBLE	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0.0943	0	0	0	0	0	0			
PROT SYN/FOLD	313782	313782	313782	34876351	SIMILAR TO TAFII140 PROTEIN	SOLUBLE	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0			
PROT SYN/FOLD	302099	302099	302099	27662108	SIMILAR TO TRANSLATION ELONGATION FACTOR 1 DELTA (GUANINE NUCLEOTIDE EXCHANGE PROTEIN)	SOLUBLE	0	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	0	0		
PROT SYN/FOLD	226986	226986	226986	34862692	SPLICING FACTOR, ARGININE/SERINE-RICH 7, 35 kDa	SOLUBLE	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
PROT SYN/FOLD	258910	258910	258910	34863012	SRP RECEPTOR ALPHA SUBUNIT	SOLUBLE	0	0	1	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0.0167	0	0.017	0.02	0	0	0	0	0	0	0	0	0	0	0	
PROT SYN/FOLD	38101	38101	38101	null	SRP RECEPTOR BETA	SOLUBLE	1	3	6	3	7	3	1	0	0	0	0	0	0	2	1	0.0388	0.0554	0.1004	0.0922	0.1191	0.06	0.0546	0	0	0	0	0	0	0	0.0327	0.0153		
PROT SYN/FOLD	75118	75118	75118	6981642	T-COMPLEX PROTEIN 1, ALPHA SUBUNIT	SOLUBLE	0	0	0	1	2	0	0	0	0	0	0	0	0	0	0	0	0	0.0307	0.034	0	0	0	0	0	0	0	0	0	0	0	0	0	
PROT SYN/FOLD	12218	12218	12218	34849734	THIOREDOXIN	SOLUBLE	0	0	0	1	1	0	0	0	0	0	0	0	1	0	1	0	0	0.0307	0.017	0	0	0	0	0	0	0	0.0183	0	0.0153	0	0.0153		
PROT SYN/FOLD	231792	231792	231792	81884643	TORSIN FAMILY 2, MEMBER F	SOLUBLE	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
PROT SYN/FOLD	188125	188125	188125	22651450	TORSINA	SOLUBLE	0	2	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0.0369	0	0.0307	0.017	0	0	0	0	0	0	0	0	0	0	0	0	
PROT SYN/FOLD	202385	202385	202385	34853518	TORSINB PROTEIN	SOLUBLE	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
PROT SYN/FOLD	55871	55871	55871	40786436	TRANSLATION INITIATION FACTOR EIF-4A	SOLUBLE	0	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	0.0163	0	0	
PROT SYN/FOLD	98326	98326	98326	62906894	TRANSLOCIN-ASSOCIATED PROTEIN, GAMMA SUBUNIT	MEMBRANE	2	2	2	0	0	1	0	0	0	0	1	0	0	0	0	0	0.0777	0.0369	0.0335	0	0	0.02	0	0	0	0	0.0338	0	0	0	0	0	
PROT SYN/FOLD	26167	26167	26167	46397078	VIGILIN	SOLUBLE	30.667	65.604	81.009	6	3	16.297	0	0	0	0	0	0	0	0	0	1.1909	1.2106	1.3558	0.1845	0.0511	0.3257	0	0	0	0	0	0	0	0	0	0		
PROTEASOME/UBIQUITIN	285136	285136	285136	34851252	AUTOCRINE MOTILITY FACTOR RECEPTOR	MEMBRANE	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
PROTEASOME/UBIQUITIN	311481	311481	311481	68341999	LOW MOLECULAR MASS UBIQUINONE-BINDING PROTEIN	MEMBRANE	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0		
PROTEASOME/UBIQUITIN	49021	49021	49021	34862676	RING FINGER PROTEIN 153	MEMBRANE	0	0	0	0	0	0	0	0	0	0	1	0	2	0	1	0	0	0	0	0	0	0	0	0	0	0.0338	0	0.0367	0	0.0153			
PROTEASOME/UBIQUITIN	250662	250662	250662	34867116	SIMILAR TO NON-CANONICAL UBIQUITIN CONJUGATING ENZYME 1	MEMBRANE	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.0369	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
PROTEASOME/UBIQUITIN	274677	274677	274677	34874398	SIMILAR TO UBIQUITIN LIGASE E3 ALPHA-II	MEMBRANE	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0.0167	0	0.017	0	0	0	0	0	0	0	0	0	0	0	0	
PROTEASOME/UBIQUITIN	71853	71853	71853	38304011	26S PROTEASE REGULATORY SUBUNIT 6A	SOLUBLE	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.0471	0	0	0	0	0	0	0	
PROTEASOME/UBIQUITIN	85752	85752	85752	38970025	26S PROTEASE REGULATORY SUBUNIT 6B	SOLUBLE	0	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	0.0163	0	0	
PROTEASOME/UBIQUITIN	317815	317815	317815	54400716	26S PROTEASOME NON-ATPASE REGULATORY SUBUNIT 12	SOLUBLE	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
PROTEASOME/UBIQUITIN	255113	255113	255113	72255509	26S PROTEASOME NON-ATPASE REGULATORY SUBUNIT 2	SOLUBLE	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.0471	0	0	0	0	0	0	0	
PROTEASOME/UBIQUITIN	12328	12328	12328	77417616	BENDLESS PROTEIN	SOLUBLE	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0.0307	0	0	0	0	0	0	0	0	0	0	0	0	0.0153	
PROTEASOME/UBIQUITIN	314767	314767	314767	34879447	CULLIN 4A	SOLUBLE	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
PROTEASOME/UBIQUITIN	62820	62820	62820	49065782	FOR PROTEASOMAL ATPASE (SUG1)	SOLUBLE	0	0	0	0	0	0	0	0	0	1	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0.0471	0	0.0359	0	0.0153				
PROTEASOME/UBIQUITIN	233720	233720	233720	37231712	PROTEASOME (PROSOME, MACROPAIN) SUBUNIT, BETA TYPE 1	SOLUBLE	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	

UNKNOWN	274975	274975	34881052	SIMILAR TO RIKEN CDNA C330023F11	MEMBRANE	1	0	0	4	2	9	3	1	0	0	0	1	4	18	4	11	0.0388	0	0.0669	0.0615	0.1532	0.06	0.0546	0	0	0	0.0338	0.1434	0.3303	0.0654	0.1688	
UNKNOWN	227176	227176	84042519	SIMILAR TO SEVEN TRANSMEMBRANE DOMAIN PROTEIN	MEMBRANE	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0.0167	0	0.02	0	0	0	0	0	0	0	0	0	0	
UNKNOWN	301836	301836	34864996	SIMILAR TO SMILE PROTEIN	MEMBRANE	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.0185	0	0	0	0	0	0	0	0	0	0	0	0	
UNKNOWN	315186	315186	34875179	SIMILAR TO SSC2	MEMBRANE	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.0167	0	0	0	0	0	0	0	0	0	0	0	0	
UNKNOWN	221702	221702	34876057	SIMILAR TO T-CELL ACTIVATION LEUCINE REPEAT-RICH PROTEIN	MEMBRANE	0	0	0	0	0	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0.017	0	0	0	0	0	0	0	0.0183	0	0	
UNKNOWN	259074	259074	34853639	SIMILAR TO ZINC TRANSPORTER 5	MEMBRANE	0	0	0	0	0	0	0	0	1	1	2	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0.0404	0.0471	0.0677	0.0717	0	0	
UNKNOWN	274007	274007	62639574	SIMILAR TO PROBABLE POLYPROTEIN-RELATED PROTEIN 4	MEMBRANE	0	0	0	0	1	1	1	0	0	0	0	1	0	0	1	1	1	0	0	0.0307	0.017	0.02	0	0	0	0	0.0338	0	0	0.0163	0.0153	
UNKNOWN	247534	247534	34875183	SOLUTE CARRIER FAMILY 35, MEMBER B3 (PREDICTED)	MEMBRANE	0	0	0	0	0	0	0	0	0	0	1	0	3	2	0	0	2	0	0	0	0	0	0	0	0.0404	0	0.1015	0.0717	0	0.0307		
UNKNOWN	272995	272995	34866189	SOLUTE CARRIER FAMILY 39 (ZINC TRANSPORTER), MEMBER 9	MEMBRANE	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0.0307		
UNKNOWN	171146	171146	94711371	TETRATRICOPEPTIDE REPEAT PROTEIN 11	MEMBRANE	0	0	1	2	5	2	0	0	0	0	0	1	4	2	1	0	0	0	0.0167	0.0615	0.0851	0.04	0	0	0	0.0338	0.0359	0.0734	0.0327	0.0153		
UNKNOWN	283888	283888	67078422	THIOREDOXIN DOMAIN CONTAINING PROTEIN 1	MEMBRANE	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.02	0	0	0	0	0	0	0	0	0	
UNKNOWN	227628	227628	56090369	THIOREDOXIN-RELATED TRANSMEMBRANE PROTEIN 2	MEMBRANE	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.0307	0	0	0	0	0	0	0	0	0	0	0	
UNKNOWN	161242	161242	37590771	TORID	MEMBRANE	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	0.0338	0	0	0	0	0	
UNKNOWN	211728	211728	34874167	TRANSMEMBRANE 9 SUPERFAMILY MEMBER 1	MEMBRANE	0	0	0	0	0	0	0	0	0	8	11	14	18	0	0	3	0	0	0	0	0	0	0	0	0.3234	0.5184	0.4736	0.6454	0	0.046		
UNKNOWN	140307	140307	34862730	TRANSMEMBRANE 9 SUPERFAMILY MEMBER 3	MEMBRANE	0	0	0	0	0	0	0	1	2	34	46	50	39	15	10	22	0	0	0	0	0	0.0546	0.0553	1.3743	2.1678	1.6915	1.3984	0.2752	0.1634	0.3377		
UNKNOWN	260512	260512	34859018	TRANSMEMBRANE 9 SUPERFAMILY MEMBER 4	MEMBRANE	0	0	0	0	0	0	1	0	1	29	23	17	16	12	10.345	21	0	0	0	0	0	0.02	0	0.0277	1.1722	1.0839	0.5751	0.5737	0.2202	0.1691	0.3223	
UNKNOWN	30411	30411	27734399	TRANSMEMBRANE PROTEIN 14C (P11)	MEMBRANE	0	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	0.0183	0	0	0	
UNKNOWN	260939	260939	58219512	TRANSMEMBRANE PROTEIN INDUCED BY TUMOR NECROSIS FACTOR ALPHA	MEMBRANE	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.0167	0	0	0	0	0	0	0	0	0	0	0	0	0
UNKNOWN	201498	201498	34854713	TYPE I TRANSMEMBRANE C-TYPE LECTIN RECEPTOR DCL-1	MEMBRANE	0	0	0	0	0	1	0	0	0	1	0	0	0	0	0	1	0	0	0	0	0.017	0	0	0.0277	0	0	0	0	0	0	0.0153	
UNKNOWN	262403	262403	38454214	UNKNOWN (PROTEIN FOR MGC:72987)	MEMBRANE	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0.02	0	0	0	0	0	0	0	0	0.0153	
UNKNOWN	220427	220427	38454298	UNKNOWN (PROTEIN FOR MGC:72996)	MEMBRANE	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.017	0	0	0	0	0	0	0	0	0	0	
UNKNOWN	213193	213193	34861994	UNKNOWN PROTEIN (1)	MEMBRANE	0	1	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0.0185	0	0.0307	0	0.02	0	0	0	0	0	0	0	0	0
UNKNOWN	31214	31214	38197344	VACUOLE MEMBRANE PROTEIN 1	MEMBRANE	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
UNKNOWN	139384	139384	40018580	2400001E08RIK PROTEIN	SOLUBLE	0	0	0	0	1	0	0	0	0	0	0	2	1	1	0	0	0	0	0	0.0307	0	0	0	0	0	0	0.0677	0.0359	0.0183	0	0	
UNKNOWN	240031	240031	34873948	2610204L23RIK PROTEIN	SOLUBLE	1	5	7	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0.0388	0.0923	0.1172	0	0.017	0.02	0	0	0	0	0	0	0	0	0
UNKNOWN	240594	240594	81909634	2810002D13RIK PROTEIN	SOLUBLE	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
UNKNOWN	276652	276652	34865464	AB2-095	SOLUBLE	0	0	0	0	0	0	0	3	1	5	4	5	7	4	7	0	0	0	0	0	0	0.1637	0.0277	0.2021	0.1885	0.1692	0.1793	0.1284	0.0654	0.1074		
UNKNOWN	244467	244467	56970828	AB2-225	SOLUBLE	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
UNKNOWN	271294	271294	34857271	ABHYDROLASE DOMAIN CONTAINING PROTEIN 2	SOLUBLE	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0.017	0.02	0	0	0	0	0	0	0	0	0	0
UNKNOWN	199808	199808	33086620	AC2-155	SOLUBLE	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
UNKNOWN	166325	166325	33086552	ACETYL-COENZYME A ACETYLTRANSFERASE 3-LIKE	SOLUBLE	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
UNKNOWN	265779	265779	34861996	ARL6IP2	MEMBRANE	1	2	1	5	13.143	8	1	1	4	0	0	0	0	2	1	1	0.0388	0.0369	0.0167	0.1537	0.2237	0.1599	0.0546	0.0277	0.1617	0	0	0.0367	0.0163	0.0153		
UNKNOWN	288335	288335	34863101	BAND 7 PROTEIN (35.3 KD) (4N63)	SOLUBLE	0	4.7273	2.6667	1.75	3.6	4.7273	0	2	0	0	0	0	0	0	2	6	0	0.0872	0.0446	0.0538	0.0613	0.0945	0	0.0553	0	0	0	0	0	0.0327	0.0921	
UNKNOWN	60486	60486	4587081	BAT3 (HLA-B ASSOCIATED TRANSCRIPT 3)	SOLUBLE	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	0.0359	0	0	0	0	
UNKNOWN	220519	220519	59676599	BC004044 (DENTIN MATRIX PROTEIN 4)	SOLUBLE	0	0	0	0	0	0	0	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0.0546	0	0	0	0.0359	0	0	0	0	
UNKNOWN	80419	80419	730248	BRAIN PROTEIN 44	SOLUBLE	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0.0277	0	0	0	0	0	0	0	0

