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Systematic assessment of protein profiles of primary and cultured human cells

Mag. Astrid Slany

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*Der Beginn aller Wissenschaften ist das Erstaunen, dass die Dinge
sind, wie sie sind...*

Aristoteles

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1 Summary

An important ambition of proteome research is the establishment of protein profiles of biological samples, providing insight in the protein expression pattern of investigated cells or tissues and thereby supporting the understanding of biological processes and contributing to the identification of biomarkers and novel drug targets.

The aim of this PhD-thesis was to generate reference maps of different cell types, such as normal primary cells, but also of immortalized or transformed cultured cells and cells at different functional states. The analysis of the resulting proteome profiles was done in order to identify cell type-specific and cell function-associated proteins. By means of a home-made SQL-database, the interpretation of proteome profiles, typically comprising more than 1000 proteins, was supported. In the course of these investigations, the following results were obtained.

The cytoplasmic fractions of four largely differing kinds of cells, namely human dendritic cells, endothelial cells, fibroblasts and keratinocytes were compared and proteins which occurred in each of the four cell types were isolated and identified. The list of these ubiquitously expressed proteins can now be used as internal standard for proteome profiling. Comparative proteome profiling of blood constituents such as lymphocytes, monocytes, neutrophils, erythrocytes and platelets, isolated from human peripheral blood mononuclear cells, was performed and specific proteins of each of the purified constituents were successfully identified. The assignment of proteins to their putative source of origin makes now comparative analyses easier to interpret.

Comparative proteome and secretome profiling was performed on primary human hepatocytes and on the well-established cell lines HepG2 and Hep3B, in order to assess the differentiation and functional states of these cells. HepG2 showed more features characteristic for hepatocytes than Hep3B, while Hep3B express proteins indicative for an epithelial-mesenchymal transition. Proteome profiling can thus serve to get a comprehensive assessment of functional cell states and cell differentiation states.

1 Zusammenfassung

Ein wichtiges Ziel der Proteom Forschung ist die Erstellung von Proteinprofilen von biologischen Proben, wodurch neue Erkenntnisse über die Expressionsmuster von Proteinen der untersuchten Zellen oder Geweben gewonnen werden und ein neues Verständnis für biologische Prozesse entsteht, was zur Ermittlung von Biomarkern und bisher unbekannten Angriffspunkten für Medikamente führen kann.

Das Ziel dieser Doktorarbeit war die Erstellung von Protein-Referenzlisten von unterschiedlichen Zelltypen, wie von normalen primären Zellen, aber auch von immortalisierten oder transformierten kultivierten Zellen und von Zellen in unterschiedlichen funktionellen Zuständen. Die Analyse der entsprechenden Proteinprofile wurde mit dem Ziel, zelltypspezifische und zellfunktionsassoziierte Proteine zu identifizieren, durchgeführt. Mit Hilfe einer selbstgebauten SQL-Datenbank konnte die Interpretation von Proteinprofilen, die normalerweise mehr als 1000 Proteine umfassen, unterstützt werden. Im Laufe dieser Untersuchungen wurden die folgenden Resultate erzielt.

Die zytoplasmatischen Fraktionen von vier sehr unterschiedlichen Zelltypen, nämlich humane dendritische Zellen, Endothelzellen, Fibroblasten und Keratinozyten, wurden verglichen. Proteine, die in allen vier Zelltypen vorkommen, wurden ermittelt und identifiziert. Die Liste dieser ubiquitär exprimierten Proteine kann nun als interner Standard für Proteom Analysen verwendet werden.

Proteinprofile von Blutkomponenten, wie Lymphozyten, Monozyten, Neutrophile, Erythrozyten und Blutplättchen, die aus humanen peripheren mononuklearen Blutzellen isoliert worden sind, wurden verglichen, und spezifische Proteine von jeder Komponente wurden erfolgreich identifiziert. Die Zuordnung von Proteinen zu ihrer Herkunftsquelle macht es nun einfacher, die Ergebnisse aus vergleichenden Analysen zu interpretieren.

Vergleichende Proteom- und Sekretomanalysen wurden an primären humanen Hepatozyten und den etablierten Zelllinien HepG2 und Hep3B durchgeführt, um die Differenzierungszustände und funktionellen Zustände dieser Zellen zu bestimmen. In HepG2 konnten mehr hepatozytenspezifische Proteine nachgewiesen werden als in Hep3B. Hep3B exprimieren Proteine, die auf einen epithelial-mesenchymalen Übergang hinweisen.

Proteomprofile können demnach dazu beitragen, Differenzierungszustände und funktionelle Zustände umfassend abzuschätzen.

2 List of abbreviations

1/2D-PAGE: ½-dimensional Polyacryamid Gel-electrophoresis

CPL/MUW: Clinical Proteomics Laboratories at the Medical University of Vienna

DC: Dendritic Cell

ESI: electrospray ionization

HaCaT: Human keratinocyte cell line

HUVEC: Human Umbilical Vein Endothelial Cell

IEF: isoelectric focusing

IPG: immobilized pH-gradient

MALDI: matrix assisted laser desorption/ionization

MGUS: monoclonal gammopathy of undetermined significance

MS/MS: tandem mass spectrometry

m/z ratio: mass-to-charge ratio

pI: isoelectric point

PRIDE: Proteomics Identifications Database (<http://www.ebi.ac.uk/pride>)

RuBPS: Ruthenium II tris (bathophenanthrolin disulfonate)

SDS: sodium dodecyl sulfate

SQL: Structured Query Language

3 Introduction

3.1 Aims

An important purpose of proteome research is the establishment of protein profiles of biological samples, in order to provide insight in the protein expression pattern of investigated cells or tissues. Subsequent comparative studies of the generated protein profiles can then support the understanding of biological processes, including pathophysiological mechanisms, and may contribute to the identification of biomarkers and novel molecular drug targets [1-11].

Comparative proteome profiling of different cell types and of cells at different functional states

The aim of this PhD-thesis was to generate reference maps of different cell types, such as fibroblasts, leukocytes, keratinocytes, endothelial cells, peripheral blood mononuclear cells and hepatocytes. These cells comprised normal primary cells in addition to immortalized or transformed cultured cells and cells at different functional states. The analysis of the resulting proteome profiles was done focusing on the identification of cell type-specific and cell function-associated proteins. Additionally, comparative studies of these protein profiles should enable the identification of ubiquitously expressed proteins, proteins present in nearly every cell type, which could be used as internal standard for quality control for subsequent proteomic experiments.

3.2 Background

Proteomics of individual cell types versus that of complex cellular samples

Proteomics has been established as one of the most important post-genomic techniques and should contribute to elucidate expression patterns in biological systems, under different developmental and physiological conditions, and under disease conditions [12-14].

Proteomics should thus enable the identification of biomarkers or marker proteins in general.

Nevertheless, success in clinical applications is still limited [15, 16]. This is partly due to the complexity of most biological systems. Clinical samples, such as blood or tissues, consist of a pool of different cells and fluids, and interpretation of resulting proteomics data is rather complex [17]. The availability of reference proteome profiles revealing marker proteins which are indicative for the individual cell types present in complex samples would facilitate data interpretation.

Proteomics of cells at different functional states:

Another challenge when elucidating pathophysiological mechanisms is the fact that not one simple phenomenon is investigated, but the overlap of multiple events [18]. The resulting proteome profile is not only the effect of the disease, but of the overlap of multiple epiphenomena, such as inflammation, infiltration of immunological cells, the activation of the complement system, fibrosation, activation of metalloproteins, neoangiogenesis or oxidative stress [19, 20]. Many kinds of disease-related protein alterations may be attributed to altered cell states, which may be causally related to the corresponding disease. Here again, proteome reference maps of different cell types present in complex samples would facilitate proteome analyses and even more, cell function-associated proteome profiles would contribute to the interpretability of complex data.

Proteomics of primary cells compared to that of cell cultures

One other important point in the field of elucidating (patho-) physiological mechanisms is the common use of cell lines as model systems, as for example HepG2 and Hep3B have been used to investigate functional features of liver cells [21-23]. Indeed, data are more reproducible when using cell lines instead of primary cells, which are more variable. Nevertheless, cells in culture are prone to genotypic and phenotypic drifting [24], arising from long-term cell cultures, immortalization or even processes of malignant transformation [25]. It is therefore advisable to determine functional and differentiation states of cell lines by comparing their proteome profiles with that of primary cells [24]. Definite expression of specific proteins of interest can then be confirmed before focusing on experiments dependent on specific functional capabilities.

3.3 Methods and limitations

Proteome analysis

Gene expression in a given cell type not only depends on transcription and mRNA stability, but also on mRNA processing, nuclear export, translation and protein modification [26, 27]. To define the cellular protein composition of a sample, it is therefore necessary to examine the proteome, which exhibits the complete set of proteins present in the given cell [28].

Proteins are also those who react to altered conditions. Indeed, cells that are involved in diseases express different proteins compared to cells under healthy conditions [29]. Proteins which indicate physiological and pathological changes can serve as biomarkers, allowing early detection of disease or therapy control [30].

However, due to the large number of diverse molecules in biological samples, protein analysis constitutes a big challenge. Thousands of proteins occur in concentration spanning up to 10 orders of magnitude [31]. For example, cytoskeletal proteins may be billion-fold more abundant compared to signaling proteins. Additionally, proteins are mixed with lipids, polysaccharides and nucleic acid. Potential biomarkers may be present at extremely low concentrations and their analysis can be impeded by the presence of high abundant proteins [31].

In order to get access to low abundant proteins of high biological relevance, sub-cellular protein fractions such as cytoplasmic and secreted proteins were enriched and isolated [32]. Cytoplasmic proteins encompasses proteins which are rather necessary for maintenance of vital functions, whereas secreted proteins may be more involved in cell-associated functions such as cell signaling [33].

Additionally, in order to assess a maximum of proteins, we focused on a combination of established proteome analysis methods. On the one hand, separation of proteins by two-dimensional polyacrylamide gel electrophoresis (2D- PAGE) was employed, which enables quantification by fluorescence detection or autoradiography. This approach allows quantitative analysis, but is limited with respect to sensitivity, molecular weight and molecular charge range of proteins. Therefore, shotgun proteomics employing prefractionation with one-dimensional polyacrylamide gel electrophoresis (1D-PAGE) was performed on the other hand. This shotgun approach is more sensitive, but rather semi-quantitative.

Post-translational modifications also contribute to the tremendous diversity and heterogeneity of gene products [34]. They also play an important role in the elucidation of biological and pathogenic processes [34]. Nevertheless, this field would exceed the scope of the present thesis. The present studies are therefore limited to protein identifications rather than post-translational modifications, as for example phosphorylation or glycosylation are not considered.

2D-Polyacrylamide gel-electrophoresis (2D-PAGE)

Two-dimensional polyacrylamide gel-electrophoresis (2D-PAGE) represents one of the most common techniques for proteome profiling [35]. At first, proteins migrate in an immobilized pH-gradient on a gel-matrix, according to their isoelectric point (pI) (1). In a second step, proteins are separated according to their different molecular weights (2). Thereafter, different methods enable visualization and quantification of proteins (3).

(1) First dimension: Separation according to the isoelectric point

Proteins are separated according to their different charges, whereas the state of their charge is determined by the amino acid composition. The pH at which the positive and negative charges of amino acids of a given protein are equal, is called the isoelectric point or pI-value (pI). At this pH, the protein becomes electrically neutral and stops to migrate in the gel-matrix, a process which is called isoelectric focusing [36, 37]. To generate an immobilized pH-gradient, different acrylamide derivatives, which are composed of amino- and carboxylgroups and a gel-matrix, are co-polymerized.

(2) Second dimension: Separation according to the molecular weight

Proteins are treated with sodium dodecyl sulphate (SDS), an anionic detergent, which binds to the protein and denatures it, giving a negative charge to the protein in proportion to its mass. This leads to an approximately uniform mass-to-charge (m/z) ratio for most proteins, so that the distance of migration through a polyacrylamide gel, after application of an electric field, can be assumed to be directly related to only the size of the protein.

(3) Protein quantification

The quantification of proteins can be achieved by different methods. Here, we used on the one hand fluorescence detection, where proteins are stained with Ruthenium II tris, after 2D-PAGE (Figure 1A) as described by Rabilloud et al. [38]. This enables to assess the amount of proteins. On the other hand, cell aliquots have been labeled with [^{35}S] methionine and [^{35}S] cysteine before protein extraction and 2D-PAGE. Autoradiographs of the resulting gels then reveal newly synthesized proteins (Figure 1B).

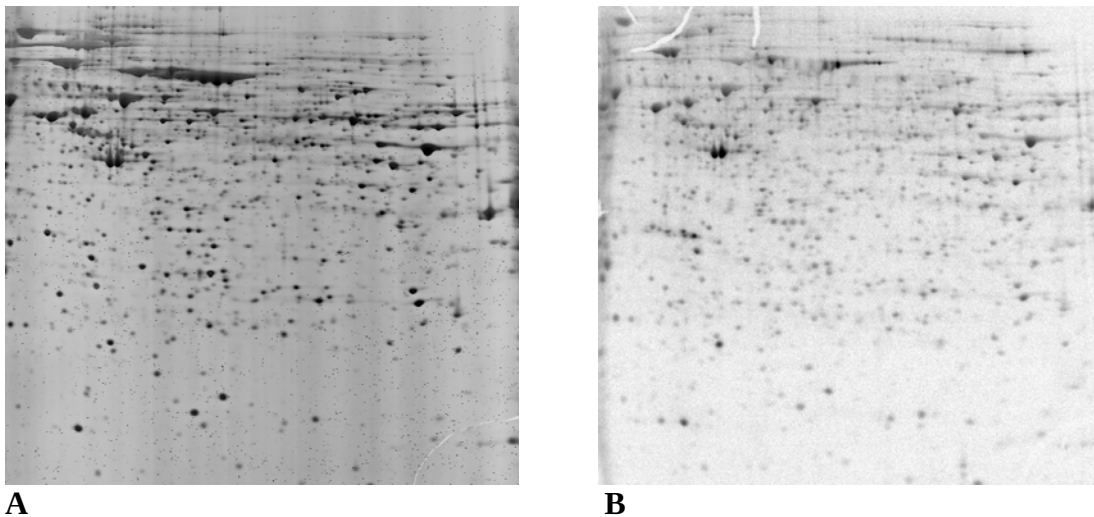


Figure 1: 2D-PAGE. First dimension: separation according to the isoelectric point, ranging from approximately 4 to 8 (from left to right). Second dimension: separation according to the molecular weight, ranging from approximately 10 to 180 kDa (from top to bottom).

A: Fluorescence detection of proteins after 2D-PAGE. Spots represent proteins which have been present in the sample. **B:** Autoradiographs. Cells have been labeled with [^{35}S] methionine/cysteine. Spots represent proteins which have been newly synthesized during labeling.

shotgun proteomics using prefractionation with 1D-Polyacrylamide gel-electrophoresis (1D-PAGE)

Another very powerful approach for proteome profiling is shotgun proteomics using prefractionation of proteins with 1D-Polyacrylamide gel-electrophoresis (1D-PAGE) followed by mass spectrometry. While 2D-PAGE is the method of choice for quantitative analysis, 1D-PAGE represents a rather qualitative technique with high protein identification rate. Complex protein mixtures are separated in 1D-PAGE according to their molecular weight. The gel is cut into several slices and digested with trypsin. Peptides are separated by nano-flow liquid chromatography and finally identified by mass spectrometry.

Protein Identification by Mass Spectrometry (MS)

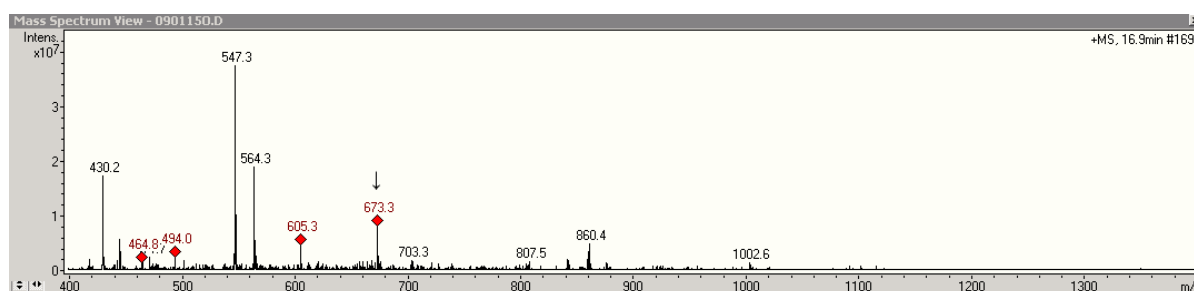
Reliable and sensitive identification of proteins and peptides is necessary for a comprehensive understanding of cellular functions [39]. Mass spectrometry represents the most important method therefor [40].

Mass spectrometry is made up basically of three principle components: an ion source, which ionizes the peptides under analysis; a mass analyzer, which sorts the ions by their masses by applying electric and magnetic fields; and an ion detector. The peptides have first to be charged and transferred into the gas phase by ionization, which can be accomplished for example by matrix assisted laser desorption/ionization (MALDI) or electrospray ionization (ESI). ESI is based on the electrically generation of a fine mist of ions which reaches the mass spectrometer [39, 41].

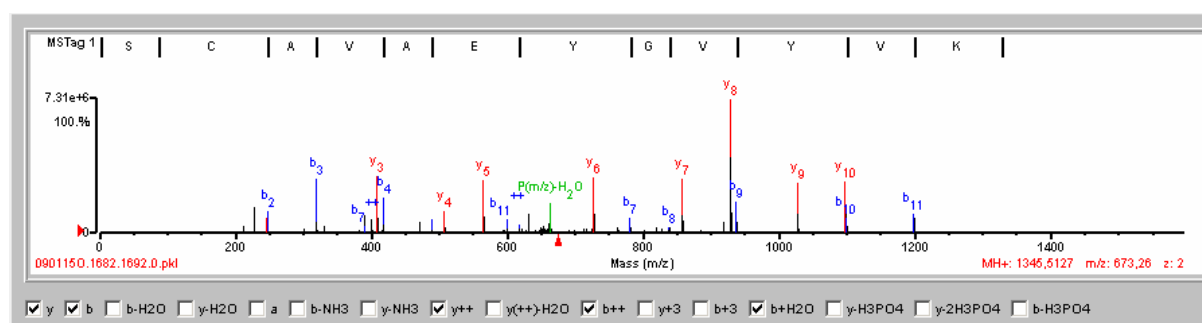
In a second step, the ionized peptides reach the mass analyzer, where the ions are separated due to their different mass-to-charge (m/z) ratio. For accumulation or selection of peptides, an ion trap can be used. Ions are accumulated for several milliseconds in the ion trap and are then released from low to high m/z to the detector [39, 41]. Scanning is accomplished by a photomultiplier, which results in a MS^1 spectrum or mass fingerprint which displays an overview of peptide masses (Figure 2A). Furthermore, the ion trap allows to isolate ions with defined m/z values, which then get fragmented by collision with helium particles. Thereby, single peptide bonds are broken and the resulting peptide fragments are displayed in the MS^2 (or MS/MS) spectrum [42].

There are different types of bonds that can be broken along the amino acid backbone. The most common cleavage sites are at the CO-NH bonds which give rise to the “b” and/or the

“y” ions. Each bond breakage gives rise to two fragments, one neutral and the other one charged. The charge can stay on either of the two fragments depending on their chemistry and relative proton affinity, b-ions having the charge retained on the N-terminal fragment, y-ions on the C-terminal fragment. Only the charged fragment is detected by the mass spectrometer. The mass difference between two adjacent b-ions, or y-ions, is representative for a particular amino acid. By combining the y- and the b-series, the amino acid sequence of the peptide, can be determined (Figure 2B). Because of the uniqueness of many amino acid sequences, some proteins can already be identified from one single peptide.



A



B

Figure 2: A: MS¹ spectrum or mass fingerprint of a primary human hepatocyte probe at the elution time 16.9min. **B:** Corresponding MS² spectra of a selected peptide (arrow in Fig 2A). The m/z difference between two adjacent b-ions, or y-ions, is indicative of a particular amino acid. y- and b-series differ in their starting points, one starts from the C-terminal and the other from the N-terminal end of the peptide sequence. The amino acid sequence of the peptide can be read by combining the y- and the b-series.

Construction of proteome reference maps

For the generation of the final protein list of different cell types, the following protein selection algorithm was applied. Peptide scores were considered to select appropriate sequence assignments. To assess the reliability of the peptide scores, searches were performed against the corresponding reversed database. 5.9% positive hits were found with peptides scoring >9.0, while 0.21% positive hits were found with peptides scoring >13.0. Only peptides scoring higher than 9.0 were considered for protein identification. Identification details for each protein including all identified peptides, sequence coverage, peptide scores and MS2 spectra are fully accessible via PRIDE database (<http://www.ebi.ac.uk/pride/>).[43, 44]

In the final protein list, the sums of all peptides related to the single proteins from the corresponding cell type are listed. Proteins derived from obvious contaminants such as fetal calf serum were deleted. Proteins were selected based on the expression of specific peptides. Selection of protein isoforms was performed as described by Zhang *et al* [45]. In case a definite assignment was not possible due to sequence homologies, the biologically most plausible candidate was selected. The derived data was further arranged and analyzed by a home made SQL-database, recently designed as database of the Clinical Proteomics Laboratories at the Medical University of Vienna (CPL/MUW-database, Wimmer H. et al, manuscript in preparation).

3.4 Significance of the established model systems

In this PhD-thesis, reference maps of different cell types, such as normal primary cells, but also of immortalized or transformed cultured cells and cells at different functional states were generated. The analysis of the resulting proteome profiles was done in order to identify cell type-specific and cell function-associated proteins, as well as commonly expressed proteins. By means of a home-made SQL-database, the interpretation of proteome profiles, typically comprising more than 1000 proteins, was supported. In the course of these investigations, the following results were obtained.

Commonly expressed proteins

In a first study (Slany *et al.*, Electrophoresis 2009, in press), proteome reference maps of dendritic cells as well as of human umbilical vein endothelial cells (HUVEC), fibroblasts and keratinocytes were presented. Comparative analysis of those different protein profiles enabled the identification of ubiquitously expressed proteins, proteins present in nearly every cell type, which could be used as internal standard for the quality control of subsequent proteomic experiments.

Interpretation of proteome profiling experiments largely relies on comparative analyses. One of the difficulties hereby are false positive identifications which may cause fatal misinterpretation of data. Otherwise, proteome analysis may also suffer from false negative results, when proteins which are actually present are not detected. This circumstance may be as fatal as false positive identifications and was hardly considered until now in the literature. One result of the present work was the generation of a positive control for proteome profiling experiments

Following a pragmatic experimental strategy, the cytoplasmic fractions of four largely differing kinds of cells were compared and proteins which occurred in each of those cell types were isolated and identified. These proteins were considered as common proteins and allowed the implementation of a new parameter for quality control of proteome profiling.

The resulting proteome reference maps of dendritic cells as well as of human umbilical vein endothelial cells (HUVEC), fibroblasts and keratinocytes will be as well considered with respect to the identification of cell type-specific and cell function-associated proteins.

Proteome profiles of different cell types

In a second study (Haudek, Slany *et al.*, J. Proteome Res., accepted with minor modifications), a comparative proteome profiling analysis of blood constituents was performed. It is clear that human blood represents on the one hand an optimal source for discovery of biomarkers [46], on the other hand it is a rather complex analytical sample because it consists of many different cell types such as lymphocytes, monocytes, neutrophils, erythrocytes and platelets. Furthermore, other clinical samples such as cells or tissues are often interspersed with blood constituents, which affect the results of proteome analyses [47]. Such contaminations cannot be avoided completely. As the extent of these contaminations may vary, the final proteome profiles may obscure many important disease-related proteome alterations. In order to allow the identification of the mentioned blood constituents, T cells, monocytes, neutrophils, erythrocytes and platelets were isolated from human peripheral blood mononuclear cells (PBMCs), and comparative protein profiling was performed. Specific proteins of each of the purified constituents were successfully identified. The assignment of proteins to their putative source of origin can now render comparative analyses searching for disease marker proteins easier to interpret.

Proteome profiles of primary cells and immortalized cultured cell lines

In a third study (Slany, Haudek *et al.*, submitted to J. Proteome Res.), comparative proteome and secretome profiling was performed on primary human hepatocytes and on the well-established cell lines HepG2 and Hep3B [48]. This led to a comprehensive assessment of the cell differentiation and functional cell states of these cells. Hepatocytes are known to express a large number of characteristic liver-specific proteins. Transformed and cultured hepatocytes proofed to maintain only part of this protein assortment, a fact that has drastic implications for appropriate data interpretation [49]. It is of fundamental help to know which features that are characteristic for hepatocytes are still present in the applied cell system. In general, it is helpful to use cell lines for functional studies because data of those are more reproducible than that of primary cells. Indeed, HepG2 and Hep3B cells have been used in many studies as model systems to investigate functional features of liver cells [21, 22, 50]. However, knowing which proteins are definitely expressed in or secreted by the cell line of interest is essential for the design of function-related experiments.

3.5 Conclusions

In summary, the present work allowed the implementation of new parameters for quality assurance and interpretability of proteome profiling experiments. On the one hand, the use of commonly expressed proteins as a positive control for proteome analyses has been demonstrated. On the other hand, proteome profiles of different cell types and cells at different functional states have been elucidated. Firstly, such protein profiles permit to recognize proteins derived from unwanted contaminations of samples. Secondly, they provide an insight into the definite protein content of cell lines, which is of fundamental importance.

Further investigations will be done with focus on clinical applications, including the analysis of multiple myeloma and its benign precursor monoclonal gammopathy of undetermined significance (MGUS). Protein profiles of cancer cells present in the corresponding bone marrow samples or stroma cells, like fibroblasts and endothelial cells, were already generated and compared to those of healthy cells. In further steps, characteristic functional states will be analyzed by applying different co-culture approaches, using cancer cells growing and differentiating in close contact with different stroma cells. Specificities of protein expression profiles can then be used to identify interesting marker proteins.

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4 Results and Discussion

Paper I

Introducing a New Parameter for Quality Control of Proteome Profiles: Consideration of Commonly Expressed Proteins

Astrid Slany, Verena J. Haudek, Nina C. Gundacker, Johannes Griss, Thomas Mohr, Helge Wimmer, Maria Eisenbauer, Leonilla Elbling, Christopher Gerner
Electrophoresis, in press

Paper II

Proteome Maps of the Main Human Peripheral Blood Constituents

Verena J. Haudek⁺, **Astrid Slany**⁺, Nina C. Gundacker, Helge Wimmer, Johannes Drach, Christopher Gerner (⁺contributed equally)
J. Proteome Res., accepted with minor modifications

Paper III

Cell Characterization by Proteome Profiling Applied to Primary Hepatocytes and Hepatocyte Cell Lines Hep-G2 and Hep-3B.

Astrid Slany⁺, **Verena J. Haudek**⁺, Hannes Zwickl, Michael Grusch, Nina C. Gundacker, Thomas Weiss, Katja Seir, Chantal Rodgarkia-Dara, Claus Hellerbrand, Christopher Gerner (⁺contributed equally)
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Introducing a New Parameter for Quality Control of Proteome Profiles: Consideration of Commonly Expressed Proteins

Astrid Slany¹, Verena J. Haudek¹, Nina C. Gundacker¹, Johannes Griss¹, Thomas Mohr¹,
Helge Wimmer², Maria Eisenbauer¹, Leonilla Elbling¹, Christopher Gerner¹

¹Department of Medicine I, Institute of Cancer Research, Medical University of Vienna,
Austria

²Section Biomedical Laboratory Science, University of Applied Sciences, Vienna, Austria

Correspondence: Christopher Gerner, Department of Medicine I, Institute of Cancer
Research, Medical University of Vienna, Austria

Email: Christopher.gerner@meduniwien.ac.at

Phone: +43-1-4277-65230

Keywords:

2D-PAGE, Shotgun Proteomics, Common Proteins, Quality Control, Proteome Profiling

Abbreviations:

ACN: Acetonitrile

CPL/MUW: Clinical Proteomics Laboratories at the Medical University of Vienna

DC: Dendritic Cell

DMEM: Dulbecco's Modified Eagle Medium

HaCaT: Human keratinocyte cell line

HUVEC: Human Umbilical Vein Endothelial Cell

MEM: minimal essential medium

PRIDE: Proteomics Identifications Database (<http://www.ebi.ac.uk/pride>)

RuBPS: Ruthenium II tris (bathophenanthroline disulfonate)

SPI: Scored Peak Intensity

SQL: Structured Query Language

SW-480: human colon adenocarcinoma cell line

Reviewer account for PRIDE-submissions (<http://www.ebi.ac.uk/pride/plainLogin.do>):

A: dendritic cells and HUVEC:

Username: review35774

Password: DAs-RfzP

B: fibroblasts and HaCaT:

Username: review89790

Password: mDsGF\$cf

Abstract

Interpretation of proteome profiling experiments largely relies on comparative analyses. False positive identifications may cause fatal misinterpretation of data. On the other hand, proteome analysis may also suffer from false negatives, when proteins which are actually present are not detected. This circumstance may be as fatal as false positive identifications and was hardly considered until now. Appropriate positive controls would facilitate quality assessment of proteome profiling experiments. Based on cell biology knowledge, our aim was to generate a list of commonly expressed proteins which may serve as positive control. Following a pragmatic experimental strategy, we compared the cytoplasmic fractions of four largely differing kinds of cells, which were human dendritic cells, endothelial cells, fibroblasts and keratinocytes. Proteome profiling was performed by 2D-PAGE in addition to shotgun analysis. By shotgun analysis, 665 proteins were identified which occurred in each of the four cells types, 360 proteins of those were also detectable in the corresponding 2D gels. We consider these proteins as common proteins. All shotgun analysis data, including mass fragmentation spectra of the corresponding peptides, are accessible via the PRIDE database. As expected, most of the common proteins could be clearly assigned to at least one of the following functional categories: chaperones, cytoskeleton, energy metabolism, redox regulation, nucleic acid processing, protein turnover, membrane transport, protein synthesis and signaling. We suggest that the present data may prove helpful for data assessment, quality control and interpretation of a large variety of experiments based on proteome profiling.

Introduction

One important ambition of proteome research is the establishment of protein profiles of biological systems, providing insight in the protein expression pattern of the investigated cells or tissues. Comparative studies of protein profiles may support the understanding of biological processes as well as the identification of biomarkers and novel molecular drug targets [1-3].

The comparison of protein profiles for biomedical interpretation relies on the robustness and sensitivity of the applied methods. Current concepts for quality control focus on the reliability of protein identification and the elimination of false positive results [4, 5]. Here, we introduce a new parameter for an improved quality assessment of proteome profiles: the positive identification of proteins that are ubiquitous present in any human nucleated cell type. Even though cells arise from different origin and exert diverse functions, they comprise essential, ubiquitous cell organelles and beside cell- and function-specific proteins they consist of a standard set of proteins. Positive identification of these commonly expressed proteins may serve as validation of analytical quality. Missing of such proteins indicates inadequate or incomplete analysis which may, as well as false positive identifications, lead to fatal misinterpretation of data.

To generate a reference list of commonly expressed proteins the following strategy was used. Cells representative for human leukocytes, endothelial cells, epithelial cells and fibroblasts were chosen, comprising normal primary cells in addition to immortalized cultured cells, proliferating as well as non-proliferating cells. A protein list was generated selecting only proteins identified in each of the four different cell types.

Due to the large number of diverse molecules present in biological samples, protein analysis represents a big challenge. Many thousands of proteins, occurring at highly different concentrations spanning up to eight orders of magnitude [6] with very different chemical properties are mixed with a broad variety of non-protein molecules, such as lipids, polysaccharides and nucleic acids, which may impede analysis.

The most usual proteome analysis methods are based either on the separation of proteins, as two-dimensional polyacrylamide electrophoresis (2D-PAGE) [7], or on the separation of peptides by nano flow liquid chromatography (nano-LC) as employed for shotgun proteomics [8]. Proteins may then be identified by mass spectrometric analysis of peptides generated by most usually tryptic digest [9]. Using 2D-PAGE, proteins can be quantified by fluorescence detection according to integrated staining intensities [10]. Shotgun proteomics is based on the

identification of peptide sequences by fragmentation analysis via mass spectrometry [11] and enables the identification of a larger number of proteins compared to 2D-PAGE. We have achieved very high accordance combining the two techniques, 2D-PAGE and shotgun, supporting our concept of optimal data reliability.

In this study, we present proteome reference maps of dendritic cells as well as of human umbilical vein endothelial cells (HUVEC), fibroblasts and keratinocytes. These reference maps will be again presented elsewhere with focus on the identification of cell type-specific and cell function-associated proteins. Here, we used these reference maps with another objective, namely to find out ubiquitous rather than specific proteins. The consideration of these data allowed the implementation of a new parameter which may prove useful for quality control for proteome profiling: the introduction of commonly expressed proteins as a kind of internal standard.

Materials and Methods

Monocyte-derived DC preparation and maturation

Peripheral blood mononuclear cells were isolated from heparinized whole blood of four different healthy donors by standard density gradient centrifugation with Ficoll-Paque (GE Healthcare Bio-Sciences AB, Uppsala, Sweden). Subsequently, monocytes were separated by magnetic sorting using the MACS technique (Miltenyi Biotec, Bergisch Gladbach, Germany) as previously described [12]. Monocytes were enriched by using the biotinylated CD14 mAb VIM13 (purity 95%) as previously described [12]. Dendritic cells (DC) were generated by culturing purified blood monocytes for 7 days with a combination of granulocyte-macrophage colony-stimulating factor (GM-CSF) (50 ng/ml) and interleukin-4 (IL-4) (100 U/ml).

Isolation and culture of HUVECs

Human umbilical vein endothelial cells (HUVECs) were isolated as described by Jaffe *et al.* [13]. Obtained cells were seeded into tissue culture flasks (Corning, Corning NY) coated with 0.5 µg/cm² human fibronectin (HFN, Chemicon, Temecula, CA, USA) and cultivated in EBM-2(MV) (Cambrex) supplemented with growth factors according to the instructions of the manufacturer and additionally with 10% FCS and 10 µg/ml ECGS (EBM-2MV complete).

Isolation and cultivation of fibroblasts

Fibroblasts were cultured as described by Frazier *et al.* [14], except that cells were isolated from normal skin punches and were cultured in RPMI supplemented with 10% FCS at standard cell culture conditions.

Isolation and cultivation of HaCaT

HaCaT are a spontaneously transformed human epithelial cell line, which maintain full epidermal differentiation capacity, as described by Boukamp *et al.* [15]. Cells were cultured in DMEM supplemented with 10% FCS at standard cell culture conditions.

Sub-cellular fractionation

The isolation of cytoplasmic proteins was performed as described by Gundacker *et al.* [16]. Cells were lysed in hypotonic lysis buffer (10 mM HEPES/NaOH, pH 7.4, 0.25 M sucrose, 10 mM NaCl, 3 mM MgCl₂, 0.5% Triton X-100) supplemented with protease inhibitors and

pressed through a 26 g syringe to induce cell lysis. The cytoplasmic fraction was separated from nuclei by centrifugation and precipitated by the addition of ethanol. Afterwards, all protein samples were dissolved in sample buffer (7.5 M urea, 1.5 M thiourea, 4% CHAPS, 0.5% SDS, 100 mM DDT).

2D polyacrylamid gel electrophoresis (2D-PAGE)

Proteins were loaded by passive rehydration on IPG strips pH 5–8, 17 cm (BioRad, Hercules, CA) at room temperature. Alternatively, IPG Immobiline™ strips (GE) were used and applied at similar conditions, which gave similar results (not shown). IEF was performed in a stepwise fashion (1 h 0– 500 V linear; 5 h 500 V; 5 h 500–3500 V linear; 12 h 3500 V). After IEF, the strips were equilibrated with 100 mM DTT and 2.5% iodacetamide according to the instructions of the manufacturer (BioRad). Tube gels with free ampholytes were prepared as described previously [17]. For SDS-PAGE using the Protean II xi electrophoresis system (BioRad), the IPG strips were placed on top of 1.5 mm 12% polyacrylamide slab gels and overlaid with 0.5% low-melting agarose. The gels were stained with a 400 nM solution of Ruthenium II tris (bathophenanthroline disulfonate) (RuBPS) as described [18]. Fluorography scanning was performed with the FluorImager 595 (GE Healthcare, Fairfield, CT) at a resolution of 100 µm. [19]. All 2D gel data were independently reproduced two times. Gels were warped to a reference gel with the TT900 S2S software (version 2006.0.2389, Nonlinear dynamics, Carlsbad, CA) and evaluated with the Progenesis software PG200 (version 2006, Nonlinear) using the “same spot” algorithm. Spot assignment, background correction, normalization and statistical calculations (analysis of variance, ANOVA) were performed using this software package. The synthetic 2D image of common proteins (Figure 3) was generated with the aid of the ImageMaster 2D Platinum software (Amersham). The web-page accessible via <http://www.meduniwien.ac.at/proteomics/Bilder/common-PG200A/gel.html> was created using the Progenesis software PG200 (version 2006, Nonlinear).

1D-PAGE for subsequent shotgun analysis

Cytoplasmic protein fractions were loaded on 12% polyacrylamid gels, electrophoresis was performed until complete separation of a pre-stained molecular marker (Dual Color, Biorad, Hercules, CA) was visible. Gels were fixed with 50% methanol/10% acetic acid and subsequently silver stained as described below. Gel lanes were cut out of the gel and were digested with trypsin as described below.

MS-compatible silver staining procedure

2D gels were fixed with 50% methanol, washed and sensitized with 0.02% Na₂S₂O₃. The gels were stained with 0.1% AgNO₃ ice cold for 20 minutes, rinsed with bi-distilled water and subsequently developed with 3% Na₂CO₃/0.05% formaldehyde as previously described [20].

Tryptic digest

Protein spots were cut out of the gel, the gel-pieces were de-stained with 15 mM K₃Fe(CN)₆/50 mM Na₂S₂O₃ and intensively washed with 50% methanol/10% acetic acid. The pH was adjusted with 50 mM NH₄HCO₃, proteins were reduced with 10 mM DTT/50 mM NH₄HCO₃ for 30 minutes at 56°C and alkylated with 50 mM iodacetamide/50 mM NH₄HCO₃ 20 minutes in the dark. Afterwards the gel-pieces were treated with acetonitril and dried in a speedvac. Between each step, the tubes were shaken 5-10 minutes (Eppendorf Thermomixer comfort). Dry gel-spots were treated with trypsin 0.1 mg/ml (Trypsin sequencing grade, Roche Diagnostics, Germany)/50 mM NH₄HCO₃, in a ratio of 1:8 for 20 minutes on ice, afterwards covered with 50 mM NH₄HCO₃ and were subsequently incubated over night at 37°C. The digested peptides were eluted by adding 50 mM NH₄HCO₃, the supernatant was transferred into silicon-coated tubes, and this procedure was repeated two times with 5% formic acid/50% acetonitril. Between each elution step the gel-spots were ultrasonicated for 10 minutes. Finally the peptide solution was concentrated in a speedvac to an appropriate volume.

Mass spectrometry analysis

For the identification of 2D spots, peptides were loaded on a Zorbax 300SB-C8 (5 µm, 0.3 mm, 5 mm) column and separated by nanoflow LC (1100 Series LC system, Agilent, Palo Alto, CA) with a Zorbax 300SB-C18 (5 µm, 75 mm, 150 mm) column at a flow rate of 250 nl/min using a gradient from 0.2% formic acid and 3% acetonitrile (ACN) to 0.2% formic acid and 45% ACN over 12 minutes. In case of shotgun analysis, peptides were separated by nano-flow LC (1100 Series LC system, Agilent, Palo Alto, CA) using the HPLC-Chip technology (Agilent) equipped with a 40 nl Zorbax 300SB-C18 trapping column and a 75 µm x 150 mm Zorbax 300SB-C18 separation column at a flow rate of 400 nl/min, using a gradient from 0.2% formic acid and 3% ACN to 0.2% formic acid and 50% ACN over 60 minutes. Peptide identification was accomplished by MS/MS fragmentation analysis with an iontrap mass spectrometer (XCT-Ultra, Agilent) equipped with an orthogonal nanospray ion source. The MS/MS data, including peak list-generation and search engine, were interpreted

by the Spectrum Mill MS Proteomics Workbench software (Version A.03.02, Agilent) allowing for two missed cleavages and searched against the SwissProt Database for human proteins (Version 20071025 containing 17 482 entries or alternatively Version 20080409 containing 19 038 entries) allowing for precursor mass deviation of 1.5 Da, a product mass tolerance of 0.7 Da and a minimum matched peak intensity (%SPI) of 70%. Due to previous chemical modification, carbamidomethylation of cysteine was set as fixed modification. No other modifications were considered here.

Construction of proteome reference maps

The following protein selection algorithm was applied for the generation of the final protein lists. Peptides scores were considered to select appropriate sequence assignments. To assess the reliability of the peptide scores, we performed searches against the corresponding reversed database. 5.9% positive hits were found with peptides scoring >9.0, while 0.21% positive hits were found with peptides scoring >13.0. Only peptides scoring higher than 9.0 were considered for protein identification. Identification details for each protein including all identified peptides, sequence coverage, peptide scores and MS² spectra are fully accessible via PRIDE database (<http://www.ebi.ac.uk/pride/>) [21, 22]. Dendritic cells: PRIDE accessions 3381-3884; HUVEC: PRIDE accessions 3718-3721, fibroblasts: PRIDE accessions 3860-3862; HaCat: PRIDE accessions 3863-3865. Each of the proteome reference maps listed in Tables S1 to S4 were generated by combining the corresponding independent shotgun experiments. These combinations list the sum of all peptides related to single proteins which were collected from all corresponding experiments. Proteins derived from obvious contaminants such as fetal calf serum were deleted. Proteins were selected based on the expression of specific peptides, identified in one protein only. Selection of protein isoforms was performed as described by Zhang *et al.* [23]. In case an unambiguous assignment was not possible due to sequence homologies, the biologically most plausible candidate based on gene expression data was selected.

Identification of common proteins

Final protein lists of dendritic cells and HUVEC, HaCaT and fibroblasts were compared and proteins present in each of these four cell types were determined using our own specially created SQL database (Clinical Proteomics Laboratories at the Medical University of Vienna, CPL/MUW-database, programmed by HW).

Results

Generation of proteome reference maps for human dendritic cells, endothelial cells, fibroblasts and keratinocytes

The use of sub-cellular fractions for protein profiling rather than whole cell lysates has been described previously to improve data reliability [16]. Therefore, the cytoplasmic protein fractions of four different kinds of human cells, namely dendritic cells, umbilical vein endothelial cells (HUVEC), cultured fibroblasts from skin punches and keratinocytes (HaCaT) were isolated and investigated by 2D-PAGE and shotgun analysis.

Immature DCs of four different donors were generated by *in vitro* cultivation and treatment of peripheral blood monocytes with GM-CSF and IL-4. Cytoplasmic proteins were isolated as described [16] and analyzed by shotgun proteomics and 2D-PAGE. The supplementary Table S1 lists all 1 347 distinct proteins assembled from the four independent shotgun experiments. The complete data generated by these experiments is accessible via PRIDE database (<http://www.ebi.ac.uk/pride/>) [21, 22], PRIDE accessions 3381-3384. 923 spots were reproducibly detected in 2D gels, cut out of silver-stained gels and subsequently analyzed by nano-LC-MS/MS. 768 spots were identified successfully, corresponding to 537 different proteins.

HUVEC were analyzed using the methods as described above. The supplementary Table S2 lists all 1 377 distinct proteins identified and assembled from four independent shotgun experiments, accessible via PRIDE accessions 3718-3721. 526 proteins were identified in 2D gels of these cells (Table S2).

Fibroblasts cultured from skin punches were analyzed similarly. The supplementary Table S3 lists all 1 262 distinct proteins identified and assembled from three independent shotgun experiments, accessible via PRIDE accessions 3860-3862. 715 spots were cut out of 2D gels from fibroblast cytoplasmic protein fractions, resulting in the identification of 512 different proteins.

1 460 different proteins were identified in three independent shotgun experiments with HaCaT keratinocyte cytoplasmic fractions (Table S4), accessible via PRIDE accessions 3381-3384. 745 spots were cut out of 2D gels derived from the same protein fractions, resulting in the identification of 539 different proteins.

Identification of common proteins

The analysis of the four reference proteome maps revealed 665 proteins to occur in all of these cell types (Figure 1). We designated these proteins as common proteins. 360 of those were also detectable in 2D gels in at least one of the four investigated cell types. 230 spots were detectable in each of the 2D gels of the four investigated cell types (Figure 2A-D). A synthetic 2D gel was created consisting only of those 230 spots, extracted from the 2D gels of dendritic cells. This fully annotated gel was made publicly available via

<http://www.meduniwien.ac.at/proteomics/Bilder/common-PG200A/gel.html>. The identified spots are listed in alphabetical order at

<http://www.meduniwien.ac.at/proteomics/Bilder/common-PG200A/summary.html>. Clicking on a spot displays the corresponding 2D gel sections of the four different kinds of cells to enable direct comparison of the spot environments. In addition to the presently applied IPG strips from BioRad we tested Immobiline™ strips from Pharmacia and tube gel-based isoelectric focusing with free ampholytes [17], which resulted in similar spot patterns at corresponding pI ranges including the presently described common spots (data not shown). The common protein pattern may thus prove useful for the fast assignment of commonly expressed proteins in a broad variety of cells.

In Figure 3 we demonstrate the feasibility of this strategy with a 2D gel generated from the cytoplasmic fraction of human colon carcinoma SW40 cells. The main part of the common proteins was clearly assigned. To verify these results, identification of each protein has been confirmed independently by mass-spectrometry as well (data not shown).

Characterization of common proteins

Many common proteins are represented as highly abundant spots on 2D gels, most obvious in case of several chaperons and cytoskeletal proteins. On average, the sum of integrated intensities of the spots comprising the common proteins exceeds more than 50% of the total integrated spot intensities of the analyzed 2D gels. We classified the identified common proteins into nine categories, namely: 1) chaperones 2) cytoskeleton 3) energy metabolism 4) redox regulation 5) nucleic acid processing 6) protein synthesis 7) protein turnover 8) membrane transport and 9) signaling (Table 1).

Discussion

Numerous studies rely on the analysis of proteins derived from clinical samples [1]. Classical assessment of the applicability as well as of the sensitivity of analytical methods is based on the primary analysis of samples of known composition. Such an approach is not conceivable in case of proteome profiling because the nature of the analyzed samples is thus complex that it could not be adequately represented by an artificial mixture. Therefore, alternative strategies are required for quality assessment.

Somatic cells comprise several organelles in common as for example mitochondria, ribosomes or proteasomes. The protein composition of organelles may vary to some extent but certain proteins are essential and must be present in all cell types [24]. In this study we chose a pragmatic approach in order to perform systematic evaluation of these proteins, which has not been realized in this way until now. We compared cells of quite different origin and function and identified their common proteins. Indeed, according to our primary concept, most of them could be clearly related to basic cellular functions. To systematically structure the data, we defined nine different functional categories. Table 1 lists all common proteins including the assignment to functional categories as well as the information whether these proteins were identified in 2D gels. More than 93% of all common proteins were assigned to at least one of these functional categories. The remaining 7% are related to basic cell functions too, but are more heterogeneous regarding potential classifications.

The common proteins can therefore be regarded as a set of internal standard proteins as they are expected to occur in any kind of cell. It is obvious, however, that common proteins may still be expressed at quite different concentrations, depending on cell type and functional state. We analyzed the cytoplasmic fraction of a variety of other human cells by shotgun proteomics as well as by 2D-PAGE. Considering our shotgun experiments, results of considerable quality typically list 1 200 to 1 500 proteins per cell type. Such lists of proteins usually comprise about 95% of the common proteins (data not shown).

In addition to the shotgun data, common proteins were identified on 2D gels. As the protein amounts vary considerably depending on the cell type, some spots were not detected in all 2D gels. Based on the common proteins detectable in all 2D gels, a synthetic spot pattern was generated. Remarkably, the total spot intensity of these common proteins was found to sum up to more than 50% of the total integrated spot intensity of all 2D gels analyzed. This finding suggested that the identification of this spot pattern may facilitate quick and reliable assignment of a large number of protein spots in 2D gels of cytoplasmic fractions of nearly

any kind of human cells. Presuming optimal protein solubilization and separation [16], the common spot pattern was detectable independent of the conditions applied for iso-electric focusing. The feasibility of this approach is demonstrated for human colon carcinoma SW-480 cells in Figure 3. In 2D gels of cytoplasmic fractions of different human cells, we typically detected about 90% of the protein spots classified as common (data not shown). The fully annotated synthetic gel was made publicly available via www.meduniwien.ac.at/proteomics. Clicking on a spot on the synthetic gel provides the spot identification and the local spot environment of the four different cell types including normalized spot volumes. The same information is accessible via clicking proteins from an alphabetic protein list.

As a conclusion, the detection of common proteins, whose existence is biologically evident, can be used in proteomic experiments as positive control. The application of two different proteome profiling methods supported the validity of the protein list which we generated by the comparison of highly differing cell types. The knowledge of identity, spot position and relative intensity of commonly expressed proteins will prove useful for data interpretation within proteome profiling experiments.

Acknowledgments

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Legend to Figures:

Figure 1: Schematic presentation of the number of proteins identified by shotgun and 2D-PAGE. Results obtained from dendritic cells, HUVEC, HaCaT and fibroblasts were compared, the number of proteins shared by two different cells respectively are indicated in the intersection areas. 672 proteins were common to all four cell types. 364 of those were also identified in each of the 2D gels.

Figure 2: Proteome profiling of human dendritic cells (A), HUVEC (B), HaCaT (C) and fibroblasts (D). Corresponding 2D gel sections of the four different cell types are shown. Protein detection was performed by fluorescence staining with RuBPS. Proteins were identified by mass spectrometric analysis of tryptic digests. Annotation: Swiss Prot accession numbers.

Figure 3: Application of a synthetic 2D gel of commonly expressed proteins for the assignment of spot identities. Based on a 2D gel of dendritic cells a synthetic gel was generated including only common protein spots (common). A 2D gel of the cytoplasmic fraction of human colon carcinoma SW-480 cells was warped to the synthetic gel for easy and quick assignment of common proteins (common on SW-480).

Legend to Tables:

Table 1: List of common proteins identified by shotgun analysis. Proteins were classified into nine categories according to their specific function. AccNo, Swiss Prot accession number. 2D, proteins as well identified in 2D gels (X).

Supplementary Tables:

Table S1: Proteome reference map of human dendritic cells. Proteins were identified by shotgun analysis from four independent samples. Proteins are sorted according to protein names and identified by their SwissProt accession numbers. Molecular weight, pI value, the number of distinct peptides identified per protein and the consequent sequence coverage are indicated. Furthermore, protein identifications which contain at least one peptide not identified in any other protein (row: SP; specific peptide) and proteins which were independently identified in 2D gels as well (row: 2D) are marked (X).

Table S2: Proteome reference map of HUVEC. Annotation as in Table S1.

Table S3: Proteome reference map of human fibroblasts. Annotation as in Table S1.

Table S4: Proteome reference map of human HaCaT cells. Annotation as in Table S1.

These lists will be available at <http://www3.interscience.wiley.com/journal/10008330/home>.

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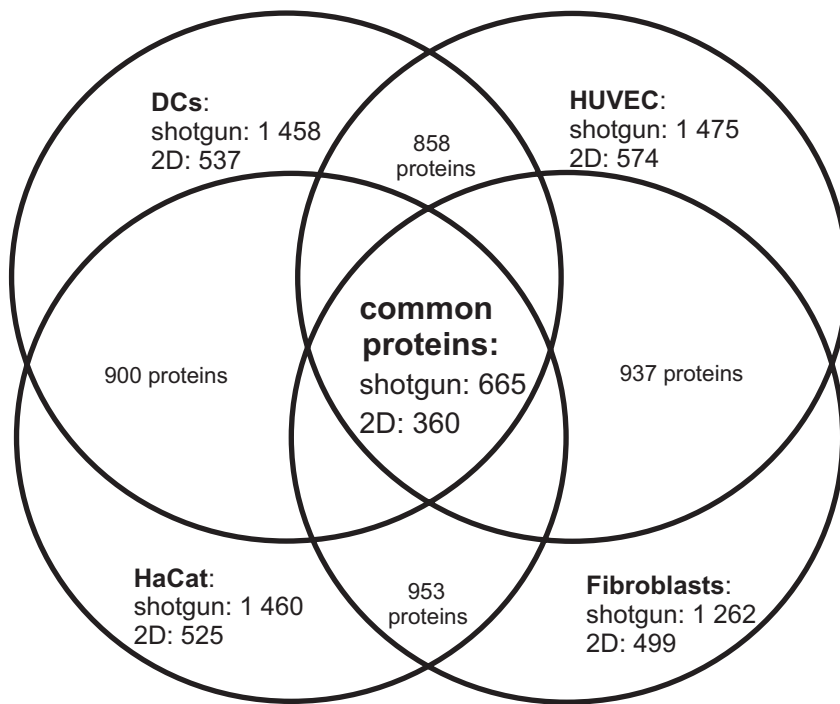


Figure 1

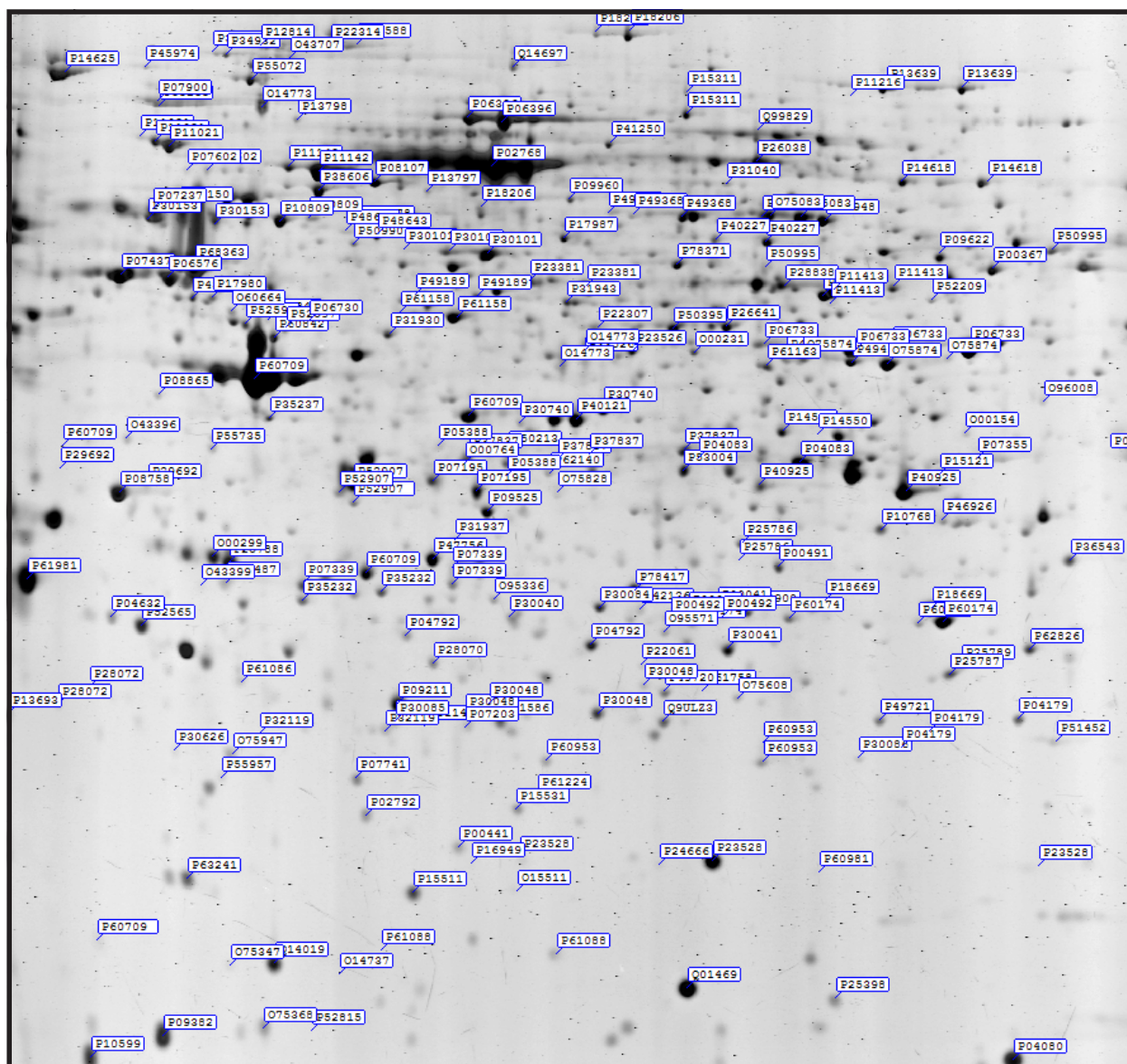


Figure 2a

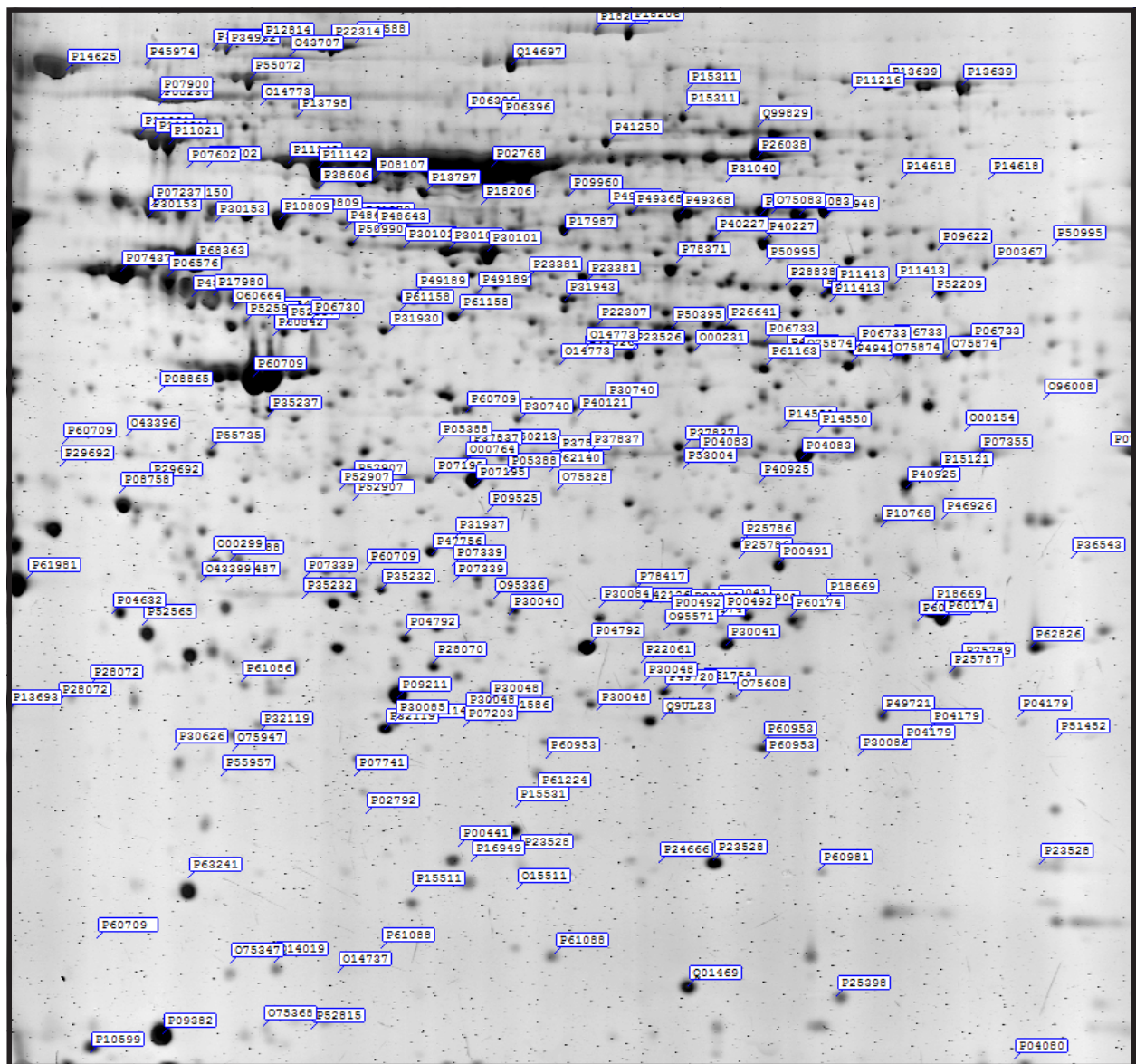
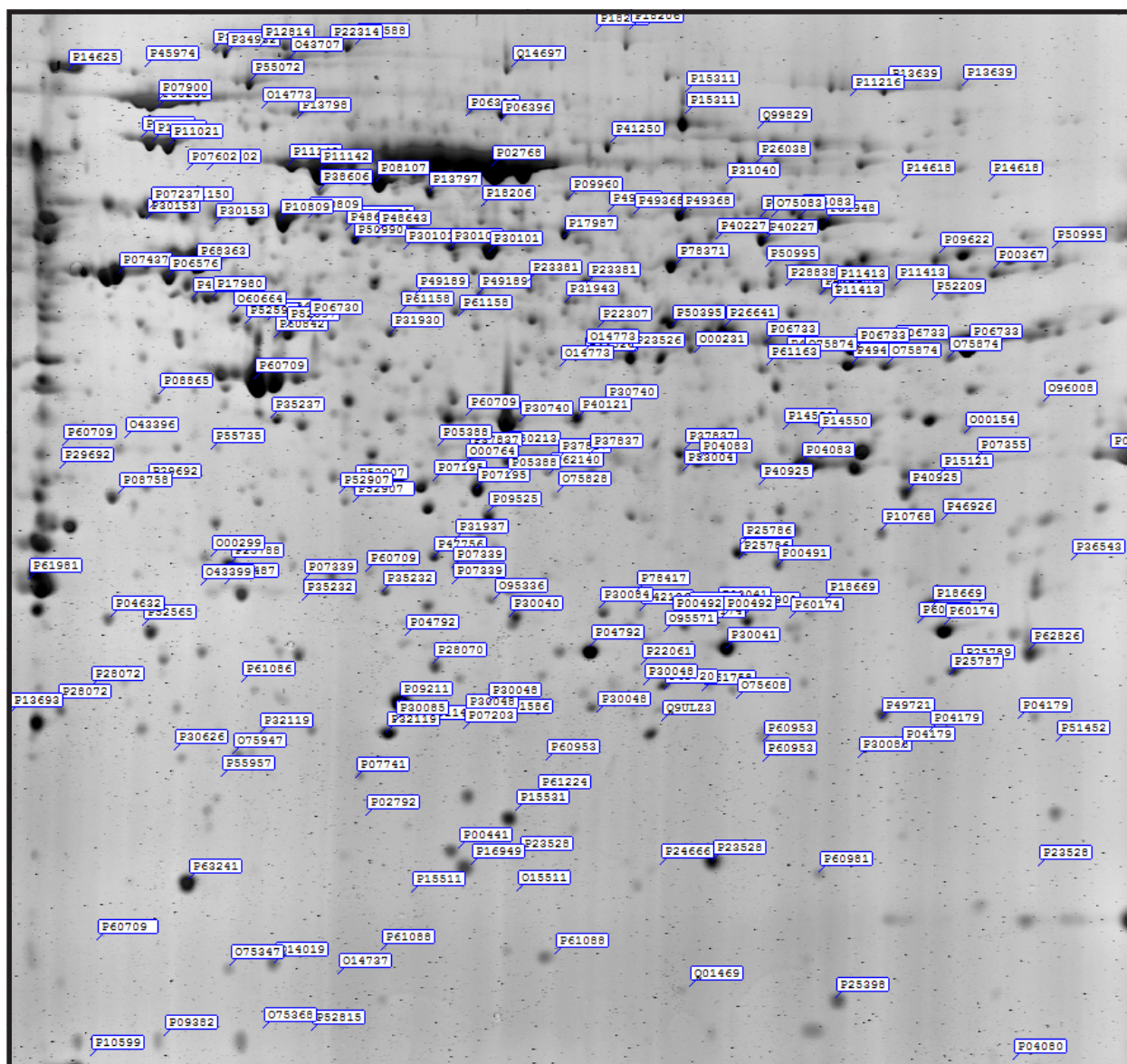
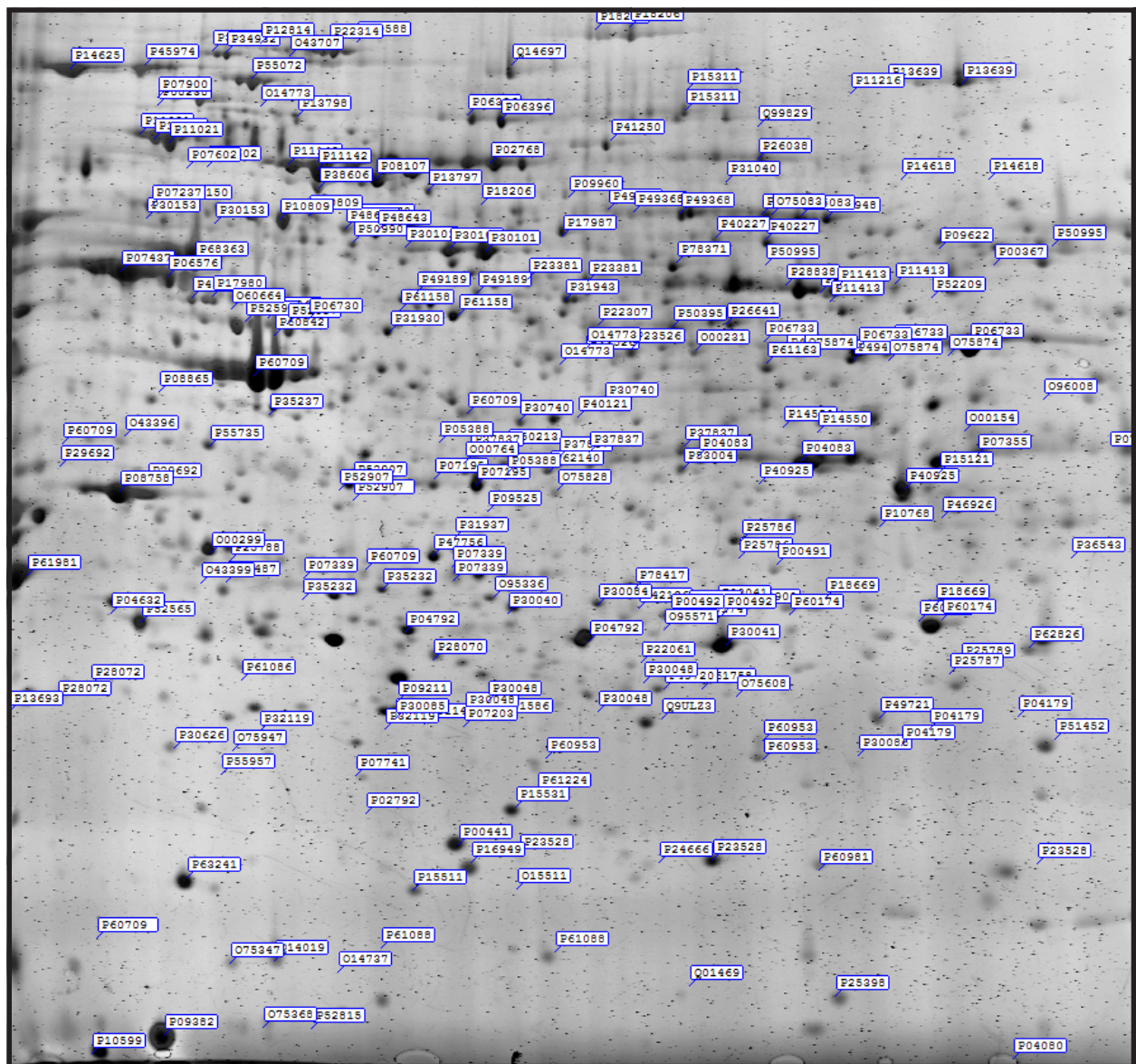


Figure 2b





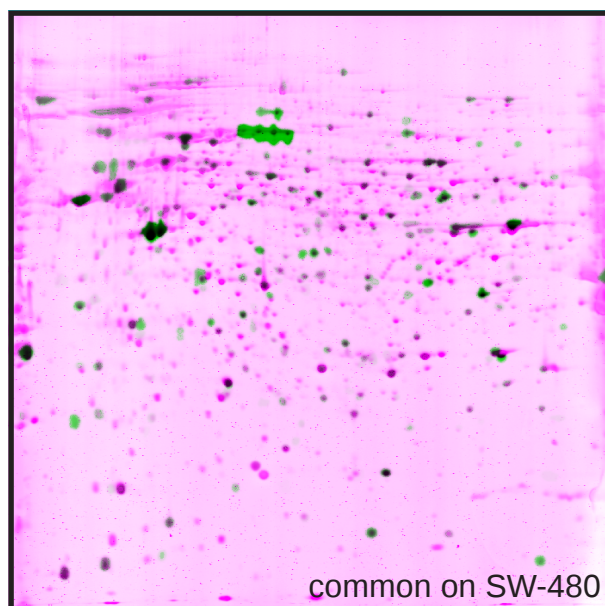
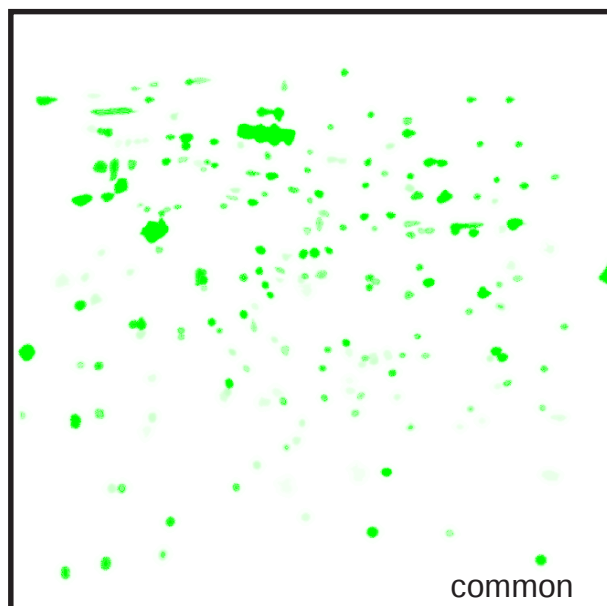


Figure 3

Table 1: List of common proteins identified by shotgun analysis.

AccNr	Protein	Chaperone	Energy metabolism	Membrane Transport	Nucleic acid processing	Protein turnover	Signal transduction	Cytoskeleton	Protein synthesis	Redox regulation	2D
P61604	10 kDa heat shock protein, mitochondrial (Hsp10) (10 kDa chaperon	X	-	-	-	-	-	-	-	-	-
P42704	130 kDa leucine-rich protein (LRP 130) (GP130) (Leucine-rich PPR	-	X	-	-	-	-	-	-	-	X
Q9NRX4	14 kDa phosphohistidine phosphatase (EC 3.1.3,-) (Phosphohistidin	-	-	-	-	-	X	-	-	-	-
P31946	14-3-3 protein beta/alpha (Protein kinase C inhibitor protein 1) (KCIF	-	-	X	-	-	-	-	-	-	-
P62258	14-3-3 protein epsilon (14-3-3E)	-	-	X	-	-	-	-	-	-	-
Q04917	14-3-3 protein eta (Protein AS1)	-	-	X	-	-	-	-	-	-	-
P61981	14-3-3 protein gamma (Protein kinase C inhibitor protein 1) (KCIP-1	-	-	X	-	-	-	-	-	-	X
P27348	14-3-3 protein theta (14-3-3 protein tau) (14-3-3 protein T-cell) (HS1	-	-	X	-	-	-	-	-	-	-
P63104	14-3-3 protein zeta/delta (Protein kinase C inhibitor protein 1) (KCIP	-	-	X	-	-	-	-	-	-	X
Q9Y4L1	150 kDa oxygen-regulated protein precursor (Orp150) (Hypoxia up-r	-	-	-	-	-	-	-	-	X	X
P17980	26S protease regulatory subunit 6A (TAT-binding protein 1) (TBP-1)	-	-	-	-	X	-	-	-	-	X
P43686	26S protease regulatory subunit 6B (MIP224) (MB67-interacting pro	-	-	-	-	X	-	-	-	-	X
P62195	26S protease regulatory subunit 8 (Proteasome subunit p45) (p45/S	-	-	-	-	X	-	-	-	-	X
P62333	26S protease regulatory subunit S10B (Proteasome subunit p42) (P	-	-	-	-	X	-	-	-	-	X
O00231	26S proteasome non-ATPase regulatory subunit 11 (26S proteasom	-	-	-	-	X	-	-	-	-	X
O00232	26S proteasome non-ATPase regulatory subunit 12 (26S proteasom	-	-	-	-	X	-	-	-	-	-
Q9UNM6	26S proteasome non-ATPase regulatory subunit 13 (26S proteasom	-	-	-	-	X	-	-	-	-	X
O00487	26S proteasome non-ATPase regulatory subunit 14 (26S proteasom	-	-	-	-	X	-	-	-	-	X
Q13200	26S proteasome non-ATPase regulatory subunit 2 (26S proteasome	-	-	-	-	X	-	-	-	-	-
P51665	26S proteasome non-ATPase regulatory subunit 7 (26S proteasome	-	-	-	-	X	-	-	-	-	X
P48556	26S proteasome non-ATPase regulatory subunit 8 (26S proteasome	-	-	-	-	X	-	-	-	-	X
P42126	3,2-trans-enoyl-CoA isomerase, mitochondrial precursor (EC 5.3.3.8	-	X	-	-	-	-	-	-	-	X
P52815	39S ribosomal protein L12, mitochondrial precursor (L12mt) (MRP-L	-	X	-	-	-	-	-	-	-	X
Q96EL3	39S ribosomal protein L53, mitochondrial precursor (L53mt) (MRP-L	-	X	-	-	-	-	-	-	-	-
Q99714	3-hydroxyacyl-CoA dehydrogenase type II (EC 1.1.1.35) (Type II HA	-	X	-	-	-	-	-	-	-	X
P31937	3-hydroxyisobutyrate dehydrogenase, mitochondrial precursor (EC 1	-	X	-	-	-	-	-	-	-	X
P09110	3-ketoacyl-CoA thiolase, peroxisomal precursor (EC 2.3.1.16) (Beta-	-	X	-	-	-	-	-	-	-	-
P46783	40S ribosomal protein S10	-	-	-	-	-	-	-	X	-	-
P62280	40S ribosomal protein S11 - Homo sapiens (Human)	-	-	-	-	-	-	-	X	-	-
P25398	40S ribosomal protein S12 - Homo sapiens (Human)	-	-	-	-	-	-	-	X	-	X
P62277	40S ribosomal protein S13	-	-	-	-	-	-	-	X	-	-
P62263	40S ribosomal protein S14	-	-	-	-	-	-	-	X	-	-
P62244	40S ribosomal protein S15a	-	-	-	-	-	-	-	X	-	-
P62249	40S ribosomal protein S16	-	-	-	-	-	-	-	X	-	-
P08708	40S ribosomal protein S17 - Homo sapiens (Human)	-	-	-	-	-	-	-	X	-	-
P62269	40S ribosomal protein S18 (Ke-3) (Ke3)	-	-	-	-	-	-	-	X	-	-
P39019	40S ribosomal protein S19	-	-	-	-	-	-	-	X	-	-
P15880	40S ribosomal protein S2 (S4) (LLRep3 protein) - Homo sapiens (H	-	-	-	-	-	-	-	X	-	-
P60866	40S ribosomal protein S20 - Homo sapiens (Human)	-	-	-	-	-	-	-	X	-	-
P63220	40S ribosomal protein S21	-	-	-	-	-	-	-	X	-	-
P62266	40S ribosomal protein S23 - Homo sapiens (Human)	-	-	-	-	-	-	-	X	-	-
P62847	40S ribosomal protein S24 - Homo sapiens (Human)	-	-	-	-	-	-	-	X	-	-
P62851	40S ribosomal protein S25	-	-	-	-	-	-	-	X	-	-
P62854	40S ribosomal protein S26	-	-	-	-	-	-	-	X	-	-
P62857	40S ribosomal protein S28	-	-	-	-	-	-	-	X	-	-
P23396	40S ribosomal protein S3 - Homo sapiens (Human)	-	-	-	-	-	-	-	X	-	-
P61247	40S ribosomal protein S3a - Homo sapiens (Human)	-	-	-	-	-	-	-	X	-	-
P62701	40S ribosomal protein S4, X isoform (Single copy abundant mRNA f	-	-	-	-	-	-	-	X	-	-
P46782	40S ribosomal protein S5	-	-	-	-	-	-	-	X	-	-
P62753	40S ribosomal protein S6 (Phosphoprotein NP33)	-	-	-	-	-	-	-	X	-	-
P62081	40S ribosomal protein S7	-	-	-	-	-	-	-	X	-	-
P62241	40S ribosomal protein S8	-	-	-	-	-	-	-	X	-	-
P46781	40S ribosomal protein S9 - Homo sapiens (Human)	-	-	-	-	-	-	-	X	-	-
P08865	40S ribosomal protein SA (p40) (34/67 kDa laminin receptor) (Colon	-	-	-	-	-	-	-	X	-	X
P49189	4-trimethylaminobutyraldehyde dehydrogenase (EC 1.2.1.47) (TMAI	-	-	-	-	-	-	-	-	X	X

P10809	60 kDa heat shock protein, mitochondrial precursor (Hsp60) (60 kDa	X	X	-	-	-	-	-	-	-	X
P10155	60 kDa SS-A/Ro ribonucleoprotein (60 kDa Ro protein) (60 kDa ribo	-	-	-	X	-	-	-	-	-	-
P05388	60S acidic ribosomal protein P0 (L10E)	-	-	-	-	-	-	-	X	-	X
P05387	60S acidic ribosomal protein P2	-	-	-	-	-	-	-	X	-	-
P27635	60S ribosomal protein L10 (QM protein) (Tumor suppressor QM) (L	-	-	-	-	-	-	-	X	-	-
P62913	60S ribosomal protein L11 (CLL-associated antigen KW-12)	-	-	-	-	-	-	-	X	-	-
P30050	60S ribosomal protein L12	-	-	-	-	-	-	-	X	-	-
P26373	60S ribosomal protein L13 (Breast basic conserved protein 1) - Horr	-	-	-	-	-	-	-	X	-	-
P50914	60S ribosomal protein L14 (CAG-ISL 7) - Homo sapiens (Human)	-	-	-	-	-	-	-	X	-	-
P61313	60S ribosomal protein L15 - Homo sapiens (Human)	-	-	-	-	-	-	-	X	-	-
P18621	60S ribosomal protein L17 (L23) - Homo sapiens (Human)	-	-	-	-	-	-	-	X	-	-
Q07020	60S ribosomal protein L18	-	-	-	-	-	-	-	X	-	-
Q02543	60S ribosomal protein L18a - Homo sapiens (Human)	-	-	-	-	-	-	-	X	-	-
P46778	60S ribosomal protein L21 - Homo sapiens (Human)	-	-	-	-	-	-	-	X	-	-
P35268	60S ribosomal protein L22 (Epstein-Barr virus small RNA-associated	-	-	-	-	-	-	-	X	-	-
P62829	60S ribosomal protein L23 (Ribosomal protein L17)	-	-	-	-	-	-	-	X	-	-
P62750	60S ribosomal protein L23a - Homo sapiens (Human)	-	-	-	-	-	-	-	X	-	-
P83731	60S ribosomal protein L24 (Ribosomal protein L30) - Homo sapiens	-	-	-	-	-	-	-	X	-	-
P61353	60S ribosomal protein L27 - Homo sapiens (Human)	-	-	-	-	-	-	-	X	-	-
P46776	60S ribosomal protein L27a - Homo sapiens (Human)	-	-	-	-	-	-	-	X	-	-
P47914	60S ribosomal protein L29 (Cell surface heparin-binding protein HIP	-	-	-	-	-	-	-	X	-	-
P62888	60S ribosomal protein L30	-	-	-	-	-	-	-	X	-	-
P42766	60S ribosomal protein L35 - Homo sapiens (Human)	-	-	-	-	-	-	-	X	-	-
P61513	60S ribosomal protein L37a - Homo sapiens (Human)	-	-	-	-	-	-	-	X	-	-
P63173	60S ribosomal protein L38 - Homo sapiens (Human)	-	-	-	-	-	-	-	X	-	-
Q02878	60S ribosomal protein L6 (TAX-responsive enhancer element-bindin	-	-	-	-	-	-	-	X	-	-
P18124	60S ribosomal protein L7 - Homo sapiens (Human)	-	-	-	-	-	-	-	X	-	-
P62424	60S ribosomal protein L7a (Surfeit locus protein 3) (PLA-X polypepti	-	-	-	-	-	-	-	X	-	-
P62917	60S ribosomal protein L8 - Homo sapiens (Human)	-	-	-	-	-	-	-	X	-	-
P32969	60S ribosomal protein L9 - Homo sapiens (Human)	-	-	-	-	-	-	-	X	-	-
P52209	6-phosphogluconate dehydrogenase, decarboxylating (EC 1,1,1,44)	-	-	-	-	-	-	-	-	X	X
O95336	6-phosphogluconolactonase (EC 3,1,1,31) (6PGL)	-	X	-	-	-	-	-	-	-	X
P11021	78 kDa glucose-regulated protein precursor (GRP 78) (Immunoglobuli	X	-	-	-	-	-	-	-	-	X
Q96IU4	Abhydrolase domain-containing protein 14B (CCG1-interacting facto	-	-	-	-	-	-	-	-	-	X
P24752	Acetyl-CoA acetyltransferase, mitochondrial precursor (EC 2,3,1,9) (	-	X	-	-	-	-	-	-	-	X
Q13510	Acid ceramidase precursor (EC 3,5,1,23) (Acylsphingosine deacylas	-	-	X	-	-	-	-	-	-	X
Q92688	Acidic leucine-rich nuclear phosphoprotein 32 family member B (PH	-	-	-	X	-	-	-	-	-	-
Q99798	Aconitate hydratase, mitochondrial precursor (EC 4,2,1,3) (Citrate h	-	X	-	-	-	-	-	-	-	X
P60709	Actin, cytoplasmic 1 (Beta-actin)	-	-	-	-	-	-	X	-	-	X
P61160	Actin-like protein 2 (Actin-related protein 2)	-	-	-	-	-	-	X	-	-	X
P61158	Actin-like protein 3 (Actin-related protein 3)	-	-	-	-	-	-	X	-	-	X
O15143	Actin-related protein 2/3 complex subunit 1B (ARP2/3 complex 41 kD	-	-	-	-	-	-	X	-	-	-
O15144	Actin-related protein 2/3 complex subunit 2 (ARP2/3 complex 34 kD	-	-	-	-	-	-	X	-	-	X
O15145	Actin-related protein 2/3 complex subunit 3 (ARP2/3 complex 21 kD	-	-	-	-	-	-	X	-	-	-
P59998	Actin-related protein 2/3 complex subunit 4 (ARP2/3 complex 20 kD	-	-	-	-	-	-	X	-	-	-
O15511	Actin-related protein 2/3 complex subunit 5 (ARP2/3 complex 16 kD	-	-	-	-	-	-	X	-	-	X
P53999	Activated RNA polymerase II transcriptional coactivator p15 (SUB1 I	-	-	-	X	-	-	-	-	-	-
O95433	Activator of 90 kDa heat shock protein ATPase homolog 1 (AHA1) (I	X	-	-	-	-	-	-	-	-	X
P07108	Acyl-CoA-binding protein (ACBP) (Diazepam-binding inhibitor) (DBI)	-	X	-	-	-	-	-	-	-	-
P07311	Acylphosphatase-1 (EC 3,6,1,7) (Acylphosphate phosphohydrolase	-	-	-	-	-	-	-	-	-	-
O75608	Acyl-protein thioesterase 1 (EC 3,1,2,-) (Lysophospholipase I)	-	-	-	-	-	-	-	-	-	X
O95372	Acyl-protein thioesterase 2 (EC 3,1,2,-) (Lysophospholipase II) (LPL	-	-	-	-	-	-	-	-	-	X
P07741	Adenine phosphoribosyltransferase (EC 2,4,2,7) (APRT)	-	-	-	X	-	-	-	-	-	X
P55263	Adenosine kinase (EC 2,7,1,20) (AK) (Adenosine 5'-phosphotransfe	-	-	-	X	-	-	-	-	-	X
P23526	Adenosylhomocysteinase (EC 3,3,1,1) (S-adenosyl-L-homocysteine	-	-	-	X	-	-	-	-	-	X
P54819	Adenylate kinase isoenzyme 2, mitochondrial (EC 2,7,4,3) (ATP-AM	-	-	-	X	-	-	-	-	-	X
Q01518	Adenylyl cyclase-associated protein 1 (CAP 1)	-	-	-	X	-	-	-	-	-	X
P05141	ADP/ATP translocase 2 (Adenine nucleotide translocator 2) (ANT 2)	-	-	-	X	-	-	-	-	-	-
P84077	ADP-ribosylation factor 1	-	-	-	X	-	-	-	-	-	-
P18085	ADP-ribosylation factor 4	-	-	-	X	-	-	-	-	-	-
P84085	ADP-ribosylation factor 5	-	-	-	X	-	-	-	-	-	-
P62330	ADP-ribosylation factor 6 - Homo sapiens (Human)	-	-	-	X	-	-	-	-	-	-
P36405	ADP-ribosylation factor-like protein 3 - Homo sapiens (Human)	-	-	-	X	-	-	-	-	-	-

Q9UUK9	ADP-sugar pyrophosphatase (EC 3,6,1,13) (EC 3,6,1,-) (Nucleoside	-	-	-	X	-	-	-	-	-	X
P49588	Alanyl-tRNA synthetase (EC 6,1,1,7) (Alanine--tRNA ligase) (AlaRS)	-	-	-	-	-	-	-	X	-	X
P14550	Alcohol dehydrogenase [NADP+] (EC 1,1,1,2) (Aldehyde reductase)	-	-	-	-	-	-	-	-	X	X
P15121	Aldose reductase (EC 1,1,1,21) (AR) (Aldehyde reductase)	-	-	-	-	-	-	-	-	X	X
P35221	Alpha-1 catenin (Cadherin-associated protein) (Alpha E-catenin)	-	-	-	-	-	-	X	-	-	-
P12814	Alpha-actinin-1 (Alpha-actinin cytoskeletal isoform) (Non-muscle alp	-	-	-	-	-	-	X	-	-	X
O43707	Alpha-actinin-4 (Non-muscle alpha-actinin 4) (F-actin cross linking p	-	-	-	-	-	-	X	-	-	X
P61163	Alpha-centractin (Centractin) (Centrosome-associated actin homolo	-	-	-	-	-	-	X	-	-	X
P06733	Alpha-enolase (EC 4,2,1,11) (2-phospho-D-glycerate hydro-lyase) (f	-	X	-	-	-	-	-	-	-	X
P04083	Annexin A1 (Annexin I) (Lipocortin I) (Calpactin II) (Chromobindin-9)	-	-	X	-	-	X	-	-	-	X
P50995	Annexin A11 (Annexin XI) (Calcyclin-associated annexin 50) (CAP-5	-	-	X	-	-	-	-	-	-	X
P07355	Annexin A2 (Annexin II) (Lipocortin II) (Calpactin I heavy chain) (Chr	-	-	X	-	-	-	-	-	-	X
P09525	Annexin A4 (Annexin IV) (Lipocortin IV) (Endonexin	-	-	X	-	-	-	-	-	-	X
P08758	Annexin A5 (Annexin V) (Lipocortin V) (Endonexin II) (Calphobindin	-	-	X	-	-	-	-	-	-	X
P20073	Annexin A7 (Annexin VII) (Synexin)	-	-	X	-	-	-	-	-	-	X
Q10567	AP-1 complex subunit beta-1 (Adapter-related protein complex 1 bet	-	-	-	-	-	-	-	-	-	-
Q9ULZ3	Apoptosis-associated speck-like protein containing a CARD (hASC)	-	-	-	-	-	X	-	-	-	X
P55145	ARMET protein precursor (Arginine-rich protein) - Homo sapiens (H	-	-	-	-	-	-	-	-	-	-
O43681	Arsenical pump-driving ATPase (EC 3,6,3,16) (Arsenite-translocatin	-	-	X	-	-	-	-	-	-	X
P00505	Aspartate aminotransferase, mitochondrial precursor (EC 2,6,1,1) (T	-	X	-	-	-	-	-	-	-	-
Q15121	Astrocytic phosphoprotein PEA-15 (Phosphoprotein enriched in diat	-	-	-	-	-	X	-	-	-	X
P25705	ATP synthase alpha chain, mitochondrial precursor (EC 3,6,3,14)	-	X	-	-	-	-	-	-	-	X
P24539	ATP synthase B chain, mitochondrial precursor (EC 3,6,3,14)	-	X	-	-	-	-	-	-	-	-
P06576	ATP synthase beta chain, mitochondrial precursor (EC 3,6,3,14)	-	X	-	-	-	-	-	-	-	X
O75947	ATP synthase D chain, mitochondrial (EC 3,6,3,14)	-	X	-	-	-	-	-	-	-	X
P30049	ATP synthase delta chain, mitochondrial precursor (EC 3,6,3,14)	-	X	-	-	-	-	-	-	-	X
P56385	ATP synthase e chain, mitochondrial (EC 3,6,3,14) - Homo sapiens	-	X	-	-	-	-	-	-	-	-
P56134	ATP synthase f chain, mitochondrial (EC 3,6,3,14)	-	X	-	-	-	-	-	-	-	-
P36542	ATP synthase gamma chain, mitochondrial precursor (EC 3,6,3,14)	-	X	-	-	-	-	-	-	-	-
P48047	ATP synthase O subunit, mitochondrial precursor (EC 3,6,3,14) (Oli	-	X	-	-	-	-	-	-	-	-
O75964	ATP synthase subunit g, mitochondrial (EC 3,6,3,14) (ATPase subu	-	X	-	-	-	-	-	-	-	-
P53396	ATP-citrate synthase (EC 2,3,3,8) (ATP-citrate (pro-S-)-lyase) (Citra	-	X	-	-	-	-	-	-	-	-
P12956	ATP-dependent DNA helicase 2 subunit 1 (EC 3,6,1,-) (ATP-depend	-	-	-	X	-	-	-	-	-	X
P13010	ATP-dependent DNA helicase 2 subunit 2 (EC 3,6,1,-) (ATP-depend	-	-	-	X	-	-	-	-	-	-
O00571	ATP-dependent RNA helicase DDX3X (EC 3,6,1,-) (DEAD box prote	-	-	-	X	-	-	-	-	-	X
O75531	Barrier-to-autointegration factor (Breakpoint cluster region protein 1)	-	-	-	X	-	-	-	-	-	-
P61769	Beta-2-microglobulin precursor [Contains: Beta-2-microglobulin vari	-	-	X	-	-	-	-	-	-	X
P07686	Beta-hexosaminidase beta chain precursor (EC 3,2,1,52) (N-acetyl-l	-	-	-	-	-	-	-	-	-	X
P55957	BH3 interacting domain death agonist (BID)	-	-	-	-	-	X	-	-	-	X
P31939	Bifunctional purine biosynthesis protein PURH [Includes: Phosphoril	-	-	-	X	-	-	-	-	-	X
P53004	Biliverdin reductase A precursor (EC 1,3,1,24) (Biliverdin-IX alpha-r	-	-	-	-	-	-	-	-	X	X
P78537	Biogenesis of lysosome-related organelles complex-1 subunit 1 (BL	-	-	-	-	X	-	-	-	-	-
P50583	Bis(5*-nucleosyl)-tetrphosphatase [asymmetrical] (EC 3,6,1,17) (Di	-	-	-	-	-	X	-	-	-	-
Q9H3K6	BolA-like protein 2	-	-	-	-	-	-	-	-	-	X
P11586	C-1-tetrahydrofolate synthase, cytoplasmic (C1-THF synthase) [Incl	-	X	-	-	-	-	-	-	-	-
P49593	Ca(2+)/calmodulin-dependent protein kinase phosphatase (EC 3,1,3	-	-	-	-	-	X	-	-	-	-
Q99653	Calcium-binding protein p22 (Calcium-binding protein CHP) (Calcine	-	-	X	-	-	-	-	-	-	-
P06703	Calcyclin (Prolactin receptor-associated protein) (PRA) (Growth fact	-	-	-	-	-	X	-	-	-	X
Q9HB71	Calcyclin-binding protein (CacyBP) (hCacyBP) (Siah-interacting prot	-	-	-	-	X	-	-	-	-	-
P31949	Calgizzarin (S100 calcium-binding protein A11) (S100C protein) (ML	-	-	-	-	-	X	-	-	-	-
P62158	Calmodulin (CaM)	-	-	-	-	-	X	-	-	-	-
P27824	Calnexin precursor (Major histocompatibility complex class I antigen	-	-	X	-	-	-	-	-	-	-
P60903	Calpactin I light chain (S100 calcium-binding protein A10) (p10 prote	-	-	X	-	-	-	-	-	-	X
P04632	Calpain small subunit 1 (CSS1) (Calcium-dependent protease small	-	-	-	-	X	-	-	-	-	X
P07384	Calpain-1 catalytic subunit (EC 3,4,22,52) (Calpain-1 large subunit)	-	-	-	-	X	-	-	-	-	-
P17655	Calpain-2 catalytic subunit precursor (EC 3,4,22,53) (Calpain-2 large	-	-	-	-	X	-	-	-	-	-
Q99439	Calponin-2 (Calponin H2, smooth muscle) (Neutral calponin)	-	-	-	-	-	-	X	-	-	X
P27797	Calreticulin precursor (CRP55) (Calregulin) (HACBP) (ERp60) (grp6	X	-	-	-	-	-	-	-	-	-
P16152	Carbonyl reductase [NADPH] 1 (EC 1,1,1,184) (NADPH-dependent	-	-	-	-	-	-	-	-	X	X
P42574	Caspase-3 precursor (EC 3,4,22,-) (CASP-3) (Apopain) (Cysteine pr	-	-	-	-	X	-	-	-	-	X
P21964	Catechol O-methyltransferase (EC 2,1,1,6)	-	-	X	-	-	-	-	-	-	X
P07858	Cathepsin B precursor (EC 3,4,22,1) (Cathepsin B1) (APP secretase	-	-	-	-	X	-	-	-	-	X
P07339	Cathepsin D precursor (EC 3,4,23,5) [Contains: Cathepsin D light ch	-	-	-	-	X	-	-	-	-	X

P16070	CD44 antigen precursor (Phagocytic glycoprotein I) (PGP-1) (HUTC	-	-	X	-	-	-	-	-	-	-
P13987	CD59 glycoprotein precursor (Membrane attack complex inhibition f	-	-	X	-	-	-	-	-	-	-
P60953	Cell division control protein 42 homolog precursor (G25K GTP-bindin	-	-	-	-	-	X	-	-	-	X
P62633	Cellular nucleic acid-binding protein (CNBP) (Zinc finger protein 9) -	-	-	-	X	-	-	-	-	-	-
O00299	Chloride intracellular channel protein 1 (Nuclear chloride ion channe	-	-	-	-	-	X	-	-	-	X
Q13185	Chromobox protein homolog 3 (Heterochromatin protein 1 homolog	-	-	-	X	-	-	-	-	-	X
O75390	Citrate synthase, mitochondrial precursor (EC 2,3,3,1)	-	X	-	-	-	-	-	-	-	-
Q00610	Clathrin heavy chain 1 (CLH-17)	-	-	-	-	-	-	X	-	-	-
P53675	Clathrin heavy chain 2 (CLH-22)	-	-	-	-	-	-	X	-	-	-
Q99417	C-Myc-binding protein (Associate of Myc 1) (AMY-1)	-	-	-	-	-	X	-	-	-	-
O43598	c-Myc-responsive protein Rcl	-	-	-	-	-	X	-	-	-	X
Q14019	Coactosin-like protein	-	-	-	-	-	-	X	-	-	X
P53618	Coatomer subunit beta (Beta-coat protein) (Beta-COP)	-	-	X	-	-	-	-	-	-	-
O14579	Coatomer subunit epsilon (Epsilon-coat protein) (Epsilon-COP)	-	-	X	-	-	-	-	-	-	X
Q9Y678	Coatomer subunit gamma (Gamma-coat protein) (Gamma-COP)	-	-	X	-	-	-	-	-	-	-
P61923	Coatomer subunit zeta-1 (Zeta-1 coat protein) (Zeta-1 COP) - Homo	-	-	X	-	-	-	-	-	-	-
P23528	Cofilin-1 (Cofilin, non-muscle isoform) (18 kDa phosphoprotein) (p18	-	-	-	-	-	-	X	-	-	X
Q9UBI1	COMM domain-containing protein 3 (Bup protein) (PIL protein)	-	-	-	-	-	-	-	-	-	X
Q9BT78	COP9 signalosome complex subunit 4 (Signalosome subunit 4) (SG	-	-	-	-	X	-	-	-	-	X
Q99627	COP9 signalosome complex subunit 8 (Signalosome subunit 8) (SG	-	-	-	-	X	-	-	-	-	X
Q99829	Copine-1 (Copine I)	-	-	X	-	-	-	-	-	-	X
Q86VP6	Cullin-associated NEDD8-dissociated protein 1 (Cullin-associated ar	-	-	-	-	X	-	-	-	-	-
P04080	Cystatin B (Liver thiol proteinase inhibitor) (CPI-B) (Stefin B)	-	-	-	-	-	-	-	-	-	X
P21291	Cysteine and glycine-rich protein 1 (Cysteine-rich protein 1) (CRP1)	-	-	-	-	-	-	-	-	-	X
P49589	Cysteinyl-tRNA synthetase, cytoplasmic (EC 6,1,1,16) (Cysteine--tR	-	-	-	-	-	-	-	X	-	-
O43169	Cytochrome b5 outer mitochondrial membrane isoform precursor	-	X	-	-	-	-	-	-	X	-
P99999	Cytochrome c	-	X	-	-	-	-	-	-	X	-
P20674	Cytochrome c oxidase polypeptide Va, mitochondrial precursor (EC	-	X	-	-	-	-	-	-	X	X
P00403	Cytochrome c oxidase subunit 2 (EC 1,9,3,1) (Cytochrome c oxidase	-	X	-	-	-	-	-	-	-	X
P28838	Cytosol aminopeptidase (EC 3,4,11,1) (Leucine aminopeptidase) (L	-	-	-	-	X	-	-	-	-	X
O00154	Cytosolic acyl coenzyme A thioester hydrolase (EC 3,1,2,2) (Long cl	-	X	-	-	-	-	-	-	-	X
Q96KP4	Cytosolic nonspecific dipeptidase (Glutamate carbo	-	-	-	-	X	-	-	-	-	X
P30046	D-dopachrome decarboxylase (EC 4,1,1,84) (D-dopachrome tautom	-	-	-	-	-	-	-	-	-	X
Q13011	Delta3,5-delta2,4-dienoyl-CoA isomerase, mitochondrial precursor (l	-	X	-	-	-	-	-	-	-	X
P60981	Destrin (Actin-depolymerizing factor) (ADF)	-	-	-	-	-	-	X	-	-	X
Q9NR28	Diablo homolog, mitochondrial precursor (Second mitochondria-deri	-	-	-	-	-	X	-	-	-	-
P09622	Dihydrolipoyl dehydrogenase, mitochondrial precursor (EC 1,8,1,4) (	-	X	-	-	-	-	-	-	-	X
Q16555	Dihydropyrimidinase-related protein 2 (DRP-2) (Collapsin response	-	-	-	-	-	X	-	-	-	X
P53634	Dipeptidyl-peptidase 1 precursor (EC 3,4,14,1) (Dipeptidyl-peptidase	-	-	-	-	X	-	-	-	-	-
P27695	DNA-(apurinic or apyrimidinic site) lyase (EC 4,2,99,18) (AP endonu	-	-	-	X	-	-	-	-	-	-
P04844	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 63 k	X	-	-	-	-	-	-	-	-	-
P04843	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 67 k	X	-	-	-	-	-	-	-	-	-
Q9C005	Dpy-30-like protein - Homo sapiens (Human)	-	-	-	-	-	-	-	-	-	-
P51452	Dual specificity protein phosphatase 3 (EC 3,1,3,48) (EC 3,1,3,16) (l	-	-	-	-	-	X	-	-	-	X
Q13561	Dynactin subunit 2 (Dynactin complex 50 kDa subunit) (50 kDa dyne	-	-	-	-	-	-	X	-	-	X
O75935	Dynactin subunit 3 (Dynactin complex subunit 22 kDa subunit) (p22)	-	-	-	-	-	-	X	-	-	X
Q14203	Dynactin-1 (150 kDa dynein-associated polypeptide) (DP-150) (DAF	-	-	-	-	-	-	X	-	-	-
P63167	Dynein light chain 1, cytoplasmic (Dynein light chain LC8-type 1) (8	-	-	-	-	-	-	X	-	-	-
Q9NP97	Dynein light chain 2A, cytoplasmic (Dynein-associated protein Km25	-	-	-	-	-	-	X	-	-	-
Q15075	Early endosome antigen 1 (Endosome-associated protein p162) (Zir	-	-	X	-	-	-	-	-	-	-
Q96C19	EF-hand domain-containing protein 2 (Swiprosin-1)	-	-	-	-	-	X	-	-	-	X
Q9H4M9	EH-domain-containing protein 1 (Testilin) (hPAST1)	-	-	-	-	-	-	-	-	-	X
P13804	Electron transfer flavoprotein alpha-subunit, mitochondrial precursor	-	X	-	-	-	-	-	-	-	X
P38117	Electron transfer flavoprotein beta-subunit (Beta-ETF)	-	X	-	-	-	-	-	-	-	-
P68104	Elongation factor 1-alpha 1 (EF-1-alpha-1) (Elongation factor 1 A-1)	-	-	-	-	-	-	-	X	-	X
P24534	Elongation factor 1-beta (EF-1-beta)	-	-	-	-	-	-	-	X	-	-
P29692	Elongation factor 1-delta (EF-1-delta) (Antigen NY-CO-4)	-	-	-	-	-	-	-	X	-	X
P26641	Elongation factor 1-gamma (EF-1-gamma) (eEF-1B gamma)	-	-	-	-	-	-	-	X	-	X
P13639	Elongation factor 2 (EF-2)	-	-	-	-	-	-	-	X	-	X
P49411	Elongation factor Tu, mitochondrial precursor (EF-Tu) (P43)	-	-	-	-	-	-	-	X	-	X
P30040	Endoplasmic reticulum protein ERp29 precursor (ERp31) (ERp28)	X	-	-	-	-	-	-	-	-	X
P14625	Endoplasmic precursor (94 kDa glucose-regulated protein) (GRP94)	X	-	-	-	-	-	-	-	-	X
P30084	Enoyl-CoA hydratase, mitochondrial precursor (EC 4,2,1,17) (Short	-	X	-	-	-	-	-	-	-	X

P61916	Epididymal secretory protein E1 precursor (Niemann-Pick disease ty	-	-	X	-	-	-	-	-	-	X
Q96HE7	ERO1-like protein alpha precursor (EC 1,8,4,-) (ERO1-L-alpha) (Oxic	-	X	-	-	-	-	-	-	-	-
P10768	Esterase D (EC 3,1,1,1)	-	-	X	-	-	-	-	-	-	X
O95571	ETHE1 protein, mitochondrial precursor (EC 3,-,-,-) (Ethylmalonic er	-	X	-	-	-	-	-	-	-	X
P60842	Eukaryotic initiation factor 4A-I (EC 3,6,1,-) (ATP-dependent RNA h	-	-	-	-	-	-	-	X	-	X
Q14240	Eukaryotic initiation factor 4A-II (EC 3,6,1,-) (ATP-dependent RNA h	-	-	-	-	-	-	-	X	-	X
O43324	Eukaryotic translation elongation factor 1 epsilon-1 (Multisynthetase	-	-	-	-	-	-	-	X	-	-
P41567	Eukaryotic translation initiation factor 1 (eIF1) (Protein translation fa	-	-	-	-	-	-	-	X	-	X
P05198	Eukaryotic translation initiation factor 2 subunit 1 (Eukaryotic transla	-	-	-	-	-	-	-	X	-	X
O75822	Eukaryotic translation initiation factor 3 subunit 1 (eIF-3 alpha) (eIF3	-	-	-	-	-	-	-	X	-	-
Q14152	Eukaryotic translation initiation factor 3 subunit 10 (eIF-3 theta) (eIF	-	-	-	-	-	-	-	X	-	-
O00303	Eukaryotic translation initiation factor 3 subunit 5 (eIF-3 epsilon) (eIF	-	-	-	-	-	-	-	X	-	X
P55884	Eukaryotic translation initiation factor 3 subunit 9 (eIF-3 eta) (eIF3 p	-	-	-	-	-	-	-	X	-	-
Q04637	Eukaryotic translation initiation factor 4 gamma 1 (eIF-4-gamma 1) (	-	-	-	-	-	-	-	X	-	-
Q15056	Eukaryotic translation initiation factor 4H (eIF-4H) (Williams-Beuren	-	-	-	-	-	-	-	X	-	X
P55010	Eukaryotic translation initiation factor 5 (eIF-5)	-	-	-	-	-	-	-	X	-	X
P63241	Eukaryotic translation initiation factor 5A (eIF-5A) (eIF-4D) (Rev-bin	-	-	-	-	-	-	-	X	-	X
P56537	Eukaryotic translation initiation factor 6 (eIF-6) (B4 integrin interacto	-	-	-	-	-	-	-	X	-	-
P15311	Ezrin (p81) (Cytovillin) (Villin-2)	-	-	-	-	-	-	X	-	-	X
P52907	F-actin capping protein alpha-1 subunit (CapZ alpha-1)	-	-	-	-	-	-	X	-	-	X
P47756	F-actin capping protein beta subunit (CapZ beta),	-	-	-	-	-	-	X	-	-	X
Q92945	Far upstream element-binding protein 2 (FUSE-binding protein 2) (K	-	-	-	X	-	-	-	-	-	X
P14324	Farnesyl pyrophosphate synthetase (FPP synthetase) (FPS) (Farne	-	-	X	-	-	-	-	-	-	-
Q16658	Fascin (Singed-like protein) (55 kDa actin bundling protein) (p55)	-	-	-	-	-	-	X	-	-	X
P49327	Fatty acid synthase (EC 2,3,1,85) [Includes: [Acyl-carrier-protein] S-	-	X	-	-	-	-	-	-	-	-
Q01469	Fatty acid-binding protein, epidermal (E-FABP) (Psoriasis-associated	-	-	X	-	-	-	-	-	-	X
P02792	Ferritin light chain (Ferritin L subunit)	-	-	-	-	-	-	-	-	X	X
P21333	Filamin-A (Alpha-filamin) (Filamin-1) (Endothelial actin-binding prote	-	-	-	-	-	-	X	-	-	X
O75369	Filamin-B (FLN-B) (Beta-filamin) (Actin-binding-like protein) (Thyroid	-	-	-	-	-	-	X	-	-	-
P26885	FK506-binding protein 2 precursor (EC 5,2,1,8) (Peptidyl-prolyl cis-t	X	-	-	-	-	-	-	-	-	-
P30043	Flavin reductase (EC 1,5,1,30) (FR) (NADPH-dependent diaphorase	-	-	-	-	-	-	-	-	X	X
P04075	Fructose-bisphosphate aldolase A (EC 4,1,2,13) (Muscle-type aldol	-	X	-	-	-	-	-	-	-	X
P09972	Fructose-bisphosphate aldolase C (EC 4,1,2,13) (Brain-type aldolas	-	X	-	-	-	-	-	-	-	-
P07954	Fumarate hydratase, mitochondrial precursor (EC 4,2,1,2) (Fumaras	-	X	-	-	-	-	-	-	-	X
Q6P587	Fumarylacetoacetate hydrolase domain-containing protein 1 (EC 3,-	X	-	-	-	-	-	-	-	-	-
P09382	Galectin-1 (Beta-galactoside-binding lectin L-14-I) (Lactose-binding	-	-	-	-	-	X	-	-	-	X
P17931	Galectin-3 (Galactose-specific lectin 3) (Mac-2 antigen) (IgE-binding	-	-	-	-	-	X	-	-	-	-
P06396	Gelsolin precursor (Actin-depolymerizing factor) (ADF) (Brevin) (AGI	-	-	-	-	-	-	X	-	-	X
P60983	Glia maturation factor beta (GMF-beta)	-	-	-	-	-	X	-	-	-	X
P46926	Glucosamine-6-phosphate isomerase (EC 3,5,99,6) (Glucosamine-6	-	X	-	-	-	-	-	-	-	X
P11413	Glucose-6-phosphate 1-dehydrogenase (EC 1,1,1,49) (G6PD)	-	X	-	-	-	-	-	-	-	X
P06744	Glucose-6-phosphate isomerase (EC 5,3,1,9) (GPI) (Phosphoglucos	-	X	-	-	-	-	-	-	-	X
P14314	Glucosidase II beta subunit precursor (Protein kinase C substrate, 6	-	-	-	-	-	X	-	-	-	-
O94925	Glutaminase kidney isoform, mitochondrial precursor (EC 3,5,1,2) (C	-	X	-	-	-	-	-	-	-	X
P07203	Glutathione peroxidase 1 (EC 1,11,1,9) (GSHPx-1) (GPx-1) (Cellula	-	-	-	-	-	-	-	-	X	X
P00390	Glutathione reductase, mitochondrial precursor (EC 1,8,1,7) (GR) (C	-	-	-	-	-	-	-	-	X	-
Q9Y2Q3	Glutathione S-transferase kappa 1 (EC 2,5,1,18) (GST 13-13) (Gluta	-	-	-	-	-	-	-	-	X	-
P09211	Glutathione S-transferase P (EC 2,5,1,18) (GST class-pi) (GSTP1-1	-	-	-	-	-	-	-	-	X	X
P30711	Glutathione S-transferase theta-1 (EC 2,5,1,18) (GST class-theta-1)	-	-	-	-	-	-	-	-	X	-
P78417	Glutathione transferase omega-1 (EC 2,5,1,18) (GSTO 1-1)	-	-	-	-	-	-	-	-	X	X
P04406	Glyceraldehyde-3-phosphate dehydrogenase (EC 1,2,1,12) (GAPDH	-	X	-	-	-	-	-	-	-	X
P43304	Glycerol-3-phosphate dehydrogenase, mitochondrial precursor (EC	-	X	-	-	-	-	-	-	-	X
P11216	Glycogen phosphorylase, brain form (EC 2,4,1,1)	-	X	-	-	-	-	-	-	-	X
P41250	Glycyl-tRNA synthetase (EC 6,1,1,14) (Glycine--tRNA ligase) (GlyR	-	-	-	-	-	-	-	X	-	X
Q9HC38	Glyoxalase domain-containing protein 4 - Homo sapiens (Human)	-	X	-	-	-	-	-	-	-	-
Q9HAV7	GrpE protein homolog 1, mitochondrial precursor (Mt-GrpE#1) (HMC	-	X	-	-	-	-	-	-	-	X
Q9UIJ7	GTP:AMP phosphotransferase mitochondrial (EC 2,7,4,10) (Adenyl	-	X	-	-	-	-	-	-	-	-
P01112	GTPase HRas precursor (Transforming protein p21) (p21ras) (H-Ra	-	-	-	-	-	X	-	-	-	-
P01111	GTPase NRas precursor (Transforming protein N-Ras) - Homo sapi	-	-	-	-	-	X	-	-	-	-
P62826	GTP-binding nuclear protein Ran (GTPase Ran) (Ras-like protein T	-	-	-	X	-	-	-	-	-	X
Q9NR31	GTP-binding protein SAR1a (COPII-associated small GTPase)	-	-	-	X	-	-	-	-	-	X
Q9Y6B6	GTP-binding protein SAR1b (GTBPB)	-	-	-	X	-	-	-	-	-	X
P63244	Guanine nucleotide-binding protein beta subunit 2-like 1 (Guanine n	-	-	-	X	-	-	-	-	-	X

P62873	Guanine nucleotide-binding protein G(I)/G(S)/G(T) beta subunit 1 (T	-	X	-	X	-	-	-	-	-	X
P62879	Guanine nucleotide-binding protein G(I)/G(S)/G(T) beta subunit 2 (T	-	X	-	X	-	-	-	-	-	X
Q16774	Guanylate kinase (EC 2,7,4,8) (GMP kinase)	-	-	-	X	-	-	-	-	-	X
P08107	Heat shock 70 kDa protein 1 (HSP70,1) (HSP70-1/HSP70-2)	X	-	-	-	-	-	-	-	-	X
P34932	Heat shock 70 kDa protein 4 (Heat shock 70-related protein APG-2)	X	-	-	-	-	-	-	-	-	X
P11142	Heat shock cognate 71 kDa protein (Heat shock 70 kDa protein 8)	X	-	-	-	-	-	-	-	-	X
Q12931	Heat shock protein 75 kDa, mitochondrial precursor (HSP 75) (Tum	X	-	-	-	-	-	-	-	-	X
P07900	Heat shock protein HSP 90-alpha (HSP 86)	X	-	-	-	-	-	-	-	-	X
P08238	Heat shock protein HSP 90-beta (HSP 84) (HSP 90)	X	-	-	-	-	-	-	-	-	X
Q92598	Heat-shock protein 105 kDa (Heat shock 110 kDa protein) (Antigen	X	-	-	-	-	-	-	-	-	X
P04792	Heat-shock protein beta-1 (HspB1) (Heat shock 27 kDa protein) (HS	X	-	-	-	-	-	-	-	-	X
Q9NRV9	Heme-binding protein 1 (p22HBP)	-	-	-	-	-	-	-	-	-	X
Q9Y5Z4	Heme-binding protein 2 (Protein SOUL) (Placental protein 23) (PP2	-	-	-	-	-	-	-	-	-	-
Q99729	Heterogeneous nuclear ribonucleoprotein A/B (hnRNP A/B) (APOB	-	-	-	X	-	-	-	-	-	-
Q14103	Heterogeneous nuclear ribonucleoprotein D0 (hnRNP D0) (AU-rich	-	-	-	X	-	-	-	-	-	X
P52597	Heterogeneous nuclear ribonucleoprotein F (hnRNP F) (Nucleolin-lil	-	-	-	X	-	-	-	-	-	X
P61978	Heterogeneous nuclear ribonucleoprotein K (hnRNP K) (Transforma	-	-	-	X	-	-	-	-	-	X
O60506	Heterogeneous nuclear ribonucleoprotein Q (hnRNP Q) (hnRNP-Q)	-	-	-	X	-	-	-	-	-	-
Q00839	Heterogenous nuclear ribonucleoprotein U (hnRNP U) (Scaffold att	-	-	-	X	-	-	-	-	-	-
P19367	Hexokinase-1 (EC 2,7,1,1) (Hexokinase type I) (HK I) (Brain form he	-	X	-	-	-	-	-	-	-	-
P09429	High mobility group protein 1 (HMG-1) (High mobility group protein E	-	-	-	X	-	-	-	-	-	-
O15347	High mobility group protein B3 (High mobility group protein 4) (HMG	-	-	-	X	-	-	-	-	-	-
P49773	Histidine triad nucleotide-binding protein 1 (Adenosine 5'-monophos	-	-	-	X	-	-	-	-	-	X
Q9BX68	Histidine triad nucleotide-binding protein 2 (EC 3,-,-,-) (HINT-2) (HIN	-	-	-	X	-	-	-	-	-	X
P62805	Histone H4	-	-	-	X	-	-	-	-	-	-
P50502	Hsc70-interacting protein (Hip) (Putative tumor suppressor ST13) (P	X	-	-	-	-	-	-	-	-	X
P35914	Hydroxymethylglutaryl-CoA lyase, mitochondrial precursor (EC 4,1,3	-	X	-	-	-	-	-	-	-	-
P00492	Hypoxanthine-guanine phosphoribosyltransferase (EC 2,4,2,8) (HGI	-	-	-	X	-	-	-	-	-	X
O00629	Importin alpha-4 subunit (Karyopherin alpha-4 subunit) (Qip1 protei	-	-	-	X	-	-	-	-	-	-
Q14974	Importin beta-1 subunit (Karyopherin beta-1 subunit) (Nuclear factor	-	-	-	X	-	-	-	-	-	-
O00410	Importin beta-3 (Karyopherin beta-3) (Ran-binding protein 5) (RanB	-	-	-	X	-	-	-	-	-	-
O95373	Importin-7 (Imp7) (Ran-binding protein 7) (RanBP7) - Homo sapiens	-	-	-	X	-	-	-	-	-	-
P55060	Importin-alpha re-exporter (Chromosome segregation 1-like protein)	-	-	-	X	-	-	-	-	-	-
Q15181	Inorganic pyrophosphatase (EC 3,6,1,1) (Pyrophosphate phospho-h	-	-	-	-	-	X	-	-	-	X
Q9H2U2	Inorganic pyrophosphatase 2, mitochondrial precursor (EC 3,6,1,1) (	-	-	-	-	-	-	-	-	-	X
Q9BY32	Inosine triphosphate pyrophosphatase (EC 3,6,1,19) (ITPase) (Inosi	-	-	-	-	-	-	-	-	-	X
P05556	Integrin beta-1 precursor (Fibronectin receptor beta subunit) (Integri	-	-	X	-	-	-	-	-	-	-
P50213	Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial precu	-	X	-	-	-	-	-	-	-	X
O75874	Isocitrate dehydrogenase [NADP] cytoplasmic (EC 1,1,1,42) (Oxalos	-	X	-	-	-	-	-	-	-	X
P33176	Kinesin heavy chain (Ubiquitous kinesin heavy chain) (UKHC)	-	-	-	-	-	-	X	-	-	-
Q04760	Lactoylglutathione lyase (EC 4,4,1,5) (Methylglyoxalase) (Aldoketom	-	-	-	-	-	-	-	-	-	X
P46379	Large proline-rich protein BAT3 (HLA-B-associated transcript 3) (Pro	X	-	-	-	-	-	-	-	-	-
P30740	Leukocyte elastase inhibitor (LEI) (Serp1 B1) (Monocyte/neutrophil	-	-	-	-	X	-	-	-	-	X
P09960	Leukotriene A-4 hydrolase (EC 3,3,2,6) (LTA-4 hydrolase) (Leukotrie	-	-	-	-	X	-	-	-	-	X
Q14847	LIM and SH3 domain protein 1 (LASP-1) (MLN 50)	-	-	-	-	-	-	X	-	-	X
P00338	L-lactate dehydrogenase A chain (EC 1,1,1,27) (LDH-A) (LDH musc	-	X	-	-	-	-	-	-	-	-
P07195	L-lactate dehydrogenase B chain (EC 1,1,1,27) (LDH-B) (LDH heart	-	X	-	-	-	-	-	-	-	X
P24666	Low molecular weight phosphotyrosine protein phosphatase (EC 3,1	-	-	-	-	-	-	-	-	-	X
P05455	Lupus La protein (Sjogren syndrome type B antigen) (SS-B) (La ribo	-	-	-	X	-	-	-	-	-	X
P10619	Lysosomal protective protein precursor (EC 3,4,16,5) (Cathepsin A)	-	-	-	-	X	-	-	-	-	-
P11279	Lysosome-associated membrane glycoprotein 1 precursor (LAMP-1	-	-	-	-	X	-	-	-	-	-
Q15046	Lysyl-tRNA synthetase (EC 6,1,1,6) (Lysine--tRNA ligase) (LysRS) -	-	-	-	-	-	-	X	-	-	-
P40121	Macrophage capping protein (Actin-regulatory protein CAP-G)	-	-	-	-	-	-	X	-	-	X
P14174	Macrophage migration inhibitory factor (MIF) (Phenylpyruvate taut	-	-	-	-	-	X	-	-	-	X
Q14764	Major vault protein (MVP) (Lung resistance-related protein)	X	-	-	-	-	-	-	-	-	X
P40925	Malate dehydrogenase, cytoplasmic (EC 1,1,1,37) (Cytosolic malate	-	X	-	-	-	-	-	-	-	X
P40926	Malate dehydrogenase, mitochondrial precursor (EC 1,1,1,37)	-	X	-	-	-	-	-	-	-	-
O60664	Mannose-6-phosphate receptor-binding protein 1 (Cargo selection p	-	-	X	-	-	-	-	-	-	X
O15173	Membrane-associated progesterone receptor component 2 (Progest	-	-	X	-	-	-	-	-	-	-
Q14696	Mesoderm development candidate 2 (NY-REN-61 antigen) - Homo s	-	-	-	-	-	-	-	-	-	-
Q9NZL9	Methionine adenosyltransferase 2 subunit beta - Homo sapiens (Hui	-	-	-	-	-	-	-	X	-	-
O14880	Microsomal glutathione S-transferase 3 (EC 2,5,1,18) (Microsomal C	-	-	-	-	-	-	-	-	X	-
P27816	Microtubule-associated protein 4 (MAP 4)	-	-	-	-	-	-	X	-	-	-

Q15691	Microtubule-associated protein RP/EB family member 1 (APC-binding protein)	-	-	-	-	-	-	X	-	-	X
Q9Y2B0	MIR-interacting saposin-like protein precursor (Transmembrane protein)	-	-	X	-	-	-	-	-	-	X
Q9NS69	Mitochondrial import receptor subunit TOM22 homolog (Translocase of outer membrane)	-	-	X	-	-	-	-	-	-	-
O94826	Mitochondrial precursor proteins import receptor (Translocase of outer membrane)	-	-	X	-	-	-	-	-	-	X
P28482	Mitogen-activated protein kinase 1 (EC 2,7,1,37) (Extracellular signal-regulated kinase 1)	-	-	-	-	-	X	-	-	-	X
P27361	Mitogen-activated protein kinase 3 (EC 2,7,1,37) (Extracellular signal-regulated kinase 3)	-	-	-	-	-	X	-	-	-	X
Q9UHA4	Mitogen-activated protein kinase kinase 1-interacting protein 1 (MEK1)	-	-	-	-	-	X	-	-	-	X
Q9Y2Q5	Mitogen-activated protein-binding protein-interacting protein (Late endosome protein)	-	-	-	-	-	X	-	-	-	-
P26038	Moesin (Membrane-organizing extension spike protein)	-	-	-	-	-	-	X	-	-	X
Q7L9L4	Mps one binder kinase activator-like 1A (Mob1 homolog 1A) (Mob1A)	-	-	-	-	-	X	-	-	-	X
P22234	Multifunctional protein ADE2 [Includes: Phosphoribosylaminoimidazole succinyl transferase]	-	-	-	X	-	-	-	-	-	X
Q9NZM1	Myoferlin (Fer-1-like protein 3) - Homo sapiens (Human)	-	-	X	-	-	-	-	-	-	-
O00159	Myosin Ic (Myosin I beta) (MMI-beta) (MMIb) - Homo sapiens (Human)	-	-	-	-	-	-	X	-	-	-
P60660	Myosin light polypeptide 6 (Myosin light chain alkali 3) (Myosin light chain 3)	-	-	-	-	-	-	X	-	-	-
P19105	Myosin regulatory light chain 2, nonsarcomeric (Myosin RLC)	-	-	-	-	-	-	X	-	-	X
P35580	Myosin-10 (Myosin heavy chain, nonmuscle IIb) (Nonmuscle myosin IIb)	-	-	-	-	-	-	X	-	-	-
Q7Z406	Myosin-14 (Myosin heavy chain, nonmuscle IIc) (Nonmuscle myosin IIc)	-	-	-	-	-	-	X	-	-	-
P35579	Myosin-9 (Myosin heavy chain, nonmuscle IIa) (Nonmuscle myosin IIa)	-	-	-	-	-	-	X	-	-	-
P58546	Myotrophin (V-1 protein)	-	-	-	-	-	-	-	X	-	X
Q9UJ70	N-acetylglucosamine kinase (EC 2,7,1,59) (GlcNAc kinase)	-	-	-	-	-	-	-	-	-	X
O43678	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 2 (l)	-	X	-	-	-	-	-	-	X	-
O96000	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 10 (l)	-	X	-	-	-	-	-	-	X	-
P00387	NADH-cytochrome b5 reductase (EC 1,6,2,2) (B5R) (Diaphorase-1)	-	X	-	-	-	-	-	-	X	-
Q16718	NADH-ubiquinone oxidoreductase 13 kDa-B subunit (EC 1,6,5,3) (E)	-	X	-	-	-	-	-	-	X	X
O00217	NADH-ubiquinone oxidoreductase 23 kDa subunit, mitochondrial precursor	-	X	-	-	-	-	-	-	X	-
O75489	NADH-ubiquinone oxidoreductase 30 kDa subunit, mitochondrial precursor	-	X	-	-	-	-	-	-	X	X
P56556	NADH-ubiquinone oxidoreductase B14 subunit (EC 1,6,5,3) (EC 1,6,5,3)	-	X	-	-	-	-	-	-	X	-
Q13765	Nascent polypeptide-associated complex alpha subunit (NAC-alpha)	X	-	-	-	-	-	-	-	-	-
Q92597	NDRG1 protein (N-myc downstream-regulated gene 1 protein) (Differentially expressed in neuroblastoma)	X	-	-	-	-	-	-	-	-	X
Q15843	NEDD8 precursor (Ubiquitin-like protein Nedd8) (Neddylin) - Homo sapiens	-	-	-	-	X	-	-	-	-	-
P61081	NEDD8-conjugating enzyme Ubc12 (EC 6,3,2,-) (Ubiquitin-conjugating enzyme)	-	-	-	-	X	-	-	-	-	X
Q14697	Neutral alpha-glucosidase AB precursor (EC 3,2,1,84) (Glucosidase AB)	X	-	-	-	-	-	-	-	-	X
Q96TA1	Niban-like protein (Meg-3)	-	-	-	-	-	-	-	-	-	-
P43490	Nicotinamide phosphoribosyltransferase (EC 2,4,2,12) (NAMPTase)	-	-	-	X	-	-	-	-	-	X
Q86X76	Nitrilase homolog 1 (EC 3,5,-,-) - Homo sapiens (Human)	-	-	-	-	-	-	-	-	-	X
P22307	Nonspecific lipid-transfer protein, mitochondrial precursor (EC 2,3,1,1)	-	-	X	-	-	-	-	-	-	X
Q9UNZ2	NSFL1 cofactor p47 (p97 cofactor p47)	-	-	X	-	-	-	-	-	-	X
P61970	Nuclear transport factor 2 (NTF-2) (Placental protein 15) (PP15)	-	-	X	-	-	-	-	-	-	X
P15531	Nucleoside diphosphate kinase A (EC 2,7,4,6) (NDK A) (NDP kinase A)	-	-	-	X	-	-	-	-	-	X
P22392	Nucleoside diphosphate kinase B (EC 2,7,4,6) (NDK B) (NDP kinase B)	-	-	-	X	-	-	-	-	-	-
P55209	Nucleosome assembly protein 1-like 1 (NAP-1-related protein) (hNAP)	-	-	-	X	-	-	-	-	-	-
Q56VL3	OCIA domain-containing protein 2 - Homo sapiens (Human)	-	-	-	-	X	-	-	-	-	-
Q92882	Osteoclast-stimulating factor 1	-	-	-	-	-	X	-	-	-	X
P20962	Parathymosin - Homo sapiens (Human)	-	-	-	X	-	-	-	-	-	-
Q9UBV8	Peflin (PEF protein with a long N-terminal hydrophobic domain) (Peflin)	-	-	X	-	-	-	-	-	-	-
P62937	Peptidyl-prolyl cis-trans isomerase A (EC 5,2,1,8) (PPIase) (Rotamase)	X	-	-	-	-	-	-	-	-	X
P23284	Peptidyl-prolyl cis-trans isomerase B precursor (EC 5,2,1,8) (PPIase)	X	-	-	-	-	-	-	-	-	-
Q13526	Peptidyl-prolyl cis-trans isomerase NIMA-interacting 1 (EC 5,2,1,8) (PIN1)	X	-	-	-	-	-	-	-	-	-
Q9Y3E5	Peptidyl-tRNA hydrolase 2, mitochondrial precursor (EC 3,1,1,29) (F)	X	-	-	-	-	-	-	-	-	-
Q06830	Peroxisome oxidoreductin-1 (EC 1,11,1,15) (Thioredoxin peroxidase 2) (Thioredoxin)	-	-	-	-	-	-	-	-	X	X
P32119	Peroxisome oxidoreductin-2 (EC 1,11,1,15) (Thioredoxin peroxidase 1) (Thioredoxin)	-	-	-	-	-	-	-	-	X	X
Q13162	Peroxisome oxidoreductin-4 (EC 1,11,1,15) (Prx-IV) (Thioredoxin peroxidase AC)	-	-	-	-	-	-	-	-	X	X
P30044	Peroxisome oxidoreductin-5, mitochondrial precursor (EC 1,11,1,15) (Prx-V) (Pe)	-	-	-	-	-	-	-	-	X	X
P30041	Peroxisome oxidoreductin-6 (EC 1,11,1,15) (Antioxidant protein 2) (1-Cys peroxi)	-	-	-	-	-	-	-	-	X	X
Q00325	Phosphate carrier protein, mitochondrial precursor (PTP) (Solute carrier)	-	-	X	-	-	-	-	-	-	-
P30086	Phosphatidylethanolamine-binding protein (PEBP) (Prostatic binding protein)	-	-	-	-	-	X	-	-	-	X
P36871	Phosphoglucosyltransferase-1 (EC 5,4,2,2) (Glucose phosphomutase 1) (F)	-	X	-	-	-	-	-	-	-	X
Q96G03	Phosphoglucosyltransferase-2 (EC 5,4,2,2) (Glucose phosphomutase 2) (F)	-	X	-	-	-	-	-	-	-	-
P00558	Phosphoglycerate kinase 1 (EC 2,7,2,3) (Primer recognition protein)	-	X	-	-	-	-	-	-	-	X
P18669	Phosphoglycerate mutase 1 (EC 5,4,2,1) (EC 5,4,2,4) (EC 3,1,3,13)	-	X	-	-	-	-	-	-	-	X
Q15126	Phosphomevalonate kinase (EC 2,7,4,2) (PMKase)	-	-	-	-	-	-	-	-	-	X
O00625	Pirin - Homo sapiens (Human)	-	-	-	X	-	-	-	-	-	-
P35237	Placental thrombin inhibitor (Cytoplasmic antiproteinase) (CAP) (Prc)	-	-	-	-	X	-	-	-	-	X

P13797	Plastin-3 (T-plastin)	-	-	-	-	-	-	X	-	-	X
P43034	Platelet-activating factor acetylhydrolase IB alpha subunit (PAF acet	-	-	-	-	-	X	X	-	-	-
P68402	Platelet-activating factor acetylhydrolase IB beta subunit (EC 3,1,1,4	-	-	-	-	-	X	X	-	-	X
Q15102	Platelet-activating factor acetylhydrolase IB gamma subunit (EC 3,1,	-	-	-	-	-	X	X	-	-	X
Q15365	Poly(rC)-binding protein 1 (Alpha-CP1) (hnRNP-E1) (Nucleic acid-bi	-	-	-	X	-	-	-	-	-	X
Q15366	Poly(rC)-binding protein 2 (Alpha-CP2) (hnRNP-E2)	-	-	-	X	-	-	-	-	-	X
P11940	Polyadenylate-binding protein 1 (Poly(A)-binding protein 1) (PABP 1	-	-	-	X	-	-	-	-	-	-
Q96CX2	Potassium channel tetramerisation domain-containing protein 12 (Pf	X	-	-	-	-	-	-	-	-	X
Q9UHV9	Prefoldin subunit 2	X	-	-	-	-	-	-	-	-	X
P61758	Prefoldin subunit 3 (Von Hippel-Lindau-binding protein 1) (VHL-bind	X	-	-	-	-	-	-	-	-	X
Q99471	Prefoldin subunit 5 (C-myc-binding protein Mm-1) (Myc modulator 1)	X	-	-	-	-	-	-	-	-	X
P07602	Proactivator polypeptide precursor [Contains: Saposin A (Protein A);	-	-	X	-	-	-	-	-	-	X
Q9HA77	Probable cysteinyl-tRNA synthetase, mitochondrial precursor (EC 6,	-	-	-	-	-	-	-	X	-	-
O96008	Probable mitochondrial import receptor subunit TOM40 homolog (Tr	-	X	-	-	-	-	-	-	-	X
P07737	Profilin-1 (Profilin I)	-	-	-	-	-	-	X	-	-	X
Q8WUM4	Programmed cell death 6-interacting protein (PDCD6-interacting pro	-	-	-	-	-	X	-	-	-	X
Q9BUL8	Programmed cell death protein 10 (TF-1 cell apoptosis-related prote	-	-	-	-	-	X	-	-	-	-
O14737	Programmed cell death protein 5 (Protein TFAR19) (TF-1 cell apopt	-	-	-	-	-	X	-	-	-	X
O75340	Programmed cell death protein 6 (Probable calcium-binding protein .	-	-	-	-	-	X	-	-	-	X
P35232	Prohibitin,	-	-	-	X	-	-	-	-	-	X
Q99623	Prohibitin-2 (B-cell receptor-associated protein BAP37) (Repressor c	-	-	-	X	-	-	-	-	-	-
Q9UQ80	Proliferation-associated protein 2G4 (Cell cycle protein p38-2G4 hor	-	-	-	-	-	X	-	-	-	X
O94903	Proline synthetase co-transcribed bacterial homolog protein	-	-	-	-	-	-	-	-	-	-
P48147	Prolyl endopeptidase (EC 3,4,21,26) (Post-proline cleaving enzyme)	-	-	-	-	X	-	-	-	-	X
Q9H7Z7	Prostaglandin E synthase 2 (EC 5,3,99,3) (Microsomal prostaglandi	-	-	-	-	-	X	-	-	-	X
Q15185	Prostaglandin E synthase 3 (EC 5,3,99,3) (Cytosolic prostaglandin E	X	-	-	-	-	-	-	-	-	X
Q06323	Proteasome activator complex subunit 1 (Proteasome	-	-	-	-	X	-	-	-	-	X
Q9UL46	Proteasome activator complex subunit 2 (Proteasome activator 28-b	-	-	-	-	X	-	-	-	-	X
P25786	Proteasome subunit alpha type 1 (EC 3,4,25,1) (Proteasome compo	-	-	-	-	X	-	-	-	-	X
P25787	Proteasome subunit alpha type 2 (EC 3,4,25,1) (Proteasome compo	-	-	-	-	X	-	-	-	-	X
P25788	Proteasome subunit alpha type 3 (EC 3,4,25,1) (Proteasome compo	-	-	-	-	X	-	-	-	-	X
P25789	Proteasome subunit alpha type 4 (EC 3,4,25,1) (Proteasome compo	-	-	-	-	X	-	-	-	-	X
P28066	Proteasome subunit alpha type 5 (EC 3,4,25,1) (Proteasome zeta cl	-	-	-	-	X	-	-	-	-	-
P60900	Proteasome subunit alpha type 6 (EC 3,4,25,1) (Proteasome iota ch	-	-	-	-	X	-	-	-	-	X
O14818	Proteasome subunit alpha type 7 (EC 3,4,25,1) (Proteasome subuni	-	-	-	-	X	-	-	-	-	X
P20618	Proteasome subunit beta type 1 (EC 3,4,25,1) (Proteasome compor	-	-	-	-	X	-	-	-	-	-
P49721	Proteasome subunit beta type 2 (EC 3,4,25,1) (Proteasome compor	-	-	-	-	X	-	-	-	-	X
P49720	Proteasome subunit beta type 3 (EC 3,4,25,1) (Proteasome theta ch	-	-	-	-	X	-	-	-	-	X
P28070	Proteasome subunit beta type 4 precursor (EC 3,4,25,1) (Proteasom	-	-	-	-	X	-	-	-	-	X
P28072	Proteasome subunit beta type 6 precursor (EC 3,4,25,1) (Proteasom	-	-	-	-	X	-	-	-	-	X
P28062	Proteasome subunit beta type 8 precursor (EC 3,4,25,1) (Proteasom	-	-	-	-	X	-	-	-	-	-
P28065	Proteasome subunit beta type 9 precursor (EC 3,4,25,1) (Proteasom	-	-	-	-	X	-	-	-	-	X
Q9NQ88	Protein C12orf5	-	-	-	-	-	-	-	-	-	-
Q9Y224	Protein C14orf166	-	-	-	-	-	-	-	-	-	X
Q969H8	Protein C19orf10 precursor (Stromal cell-derived growth factor SF2C	-	-	-	-	-	-	-	-	-	X
Q9P1F3	Protein C6orf115	-	-	-	-	-	-	-	-	-	X
O75223	Protein C7orf24	-	-	X	-	-	-	-	-	-	X
O60888	Protein CutA precursor (Brain acetylcholinesterase putative membra	-	-	-	-	-	-	-	-	-	-
O60610	Protein diaphanous homolog 1 (Diaphanous-related formin-1) (DRF:	-	-	-	-	-	-	-	-	-	-
P30101	Protein disulfide-isomerase A3 precursor (EC 5,3,4,1) (Disulfide isor	X	-	-	-	-	-	-	-	-	X
P13667	Protein disulfide-isomerase A4 precursor (EC 5,3,4,1) (Protein ERp	X	-	-	-	-	-	-	-	-	-
Q15084	Protein disulfide-isomerase A6 precursor (EC 5,3,4,1) (Protein disulf	X	-	-	-	-	-	-	-	-	X
P07237	Protein disulfide-isomerase precursor (EC 5,3,4,1) (PDI) (Prolyl 4-hy	X	-	-	-	-	-	-	-	-	X
Q99497	Protein DJ-1 (Oncogene DJ1)	X	-	-	-	-	-	-	-	X	X
Q9BSJ8	Protein FAM62A (Membrane-bound C2 domain-containing protein) -	-	-	X	-	-	-	-	-	-	-
Q9BPW8	Protein NipSnap1 - Homo sapiens (Human)	-	-	-	-	-	-	-	-	-	-
Q9UFN0	Protein NipSnap3A (NipSnap4) (Target for Salmonella secreted prot	-	-	-	-	-	-	-	-	-	-
O94979	Protein transport protein Sec31A - Homo sapiens (Human)	-	-	X	-	-	-	-	-	-	-
P22061	Protein-L-isoaspartate(D-aspartate) O-methyltransferase (EC 2,1,1,1,	X	-	-	-	-	-	-	-	-	X
Q04941	Proteolipid protein 2 (Intestinal membrane A4 protein) (Differentiatio	-	-	X	-	-	-	-	-	-	-
P61457	Pterin-4-alpha-carbinolamine dehydratase (EC 4,2,1,96) (PHS) (4-al	-	-	-	X	-	-	-	-	-	-
P00491	Purine nucleoside phosphorylase (EC 2,4,2,1) (Inosine phosphoryla	-	-	-	X	-	-	-	-	-	X
P55786	Puromycin-sensitive aminopeptidase (EC 3,4,11,-) (PSA)	-	-	-	-	X	-	-	-	-	-

Q9NTK5	Putative GTP-binding protein PTD004	-	-	-	X	-	-	-	-	-	-
P98179	Putative RNA-binding protein 3 (RNA-binding motif protein 3) (RNPL	-	-	-	X	-	-	-	-	-	-
O00764	Pyridoxal kinase (EC 2,7,1,35) (Pyridoxine kinase)	-	-	-	-	-	-	-	-	-	X
P14618	Pyruvate kinase isozymes M1/M2 (EC 2,7,1,40) (Pyruvate kinase m	-	X	-	-	-	-	-	-	-	X
P31150	Rab GDP dissociation inhibitor alpha (Rab GDI alpha) (Guanosine d	-	-	-	-	-	X	-	-	-	X
P50395	Rab GDP dissociation inhibitor beta (Rab GDI beta) (Guanosine dipl	-	-	-	-	-	X	-	-	-	X
O60518	Ran-binding protein 6 (RanBP6)	-	-	-	X	-	-	-	-	-	-
P43487	Ran-specific GTPase-activating protein (Ran-binding protein 1) (Rar	-	-	-	X	-	-	-	-	-	X
P46940	Ras GTPase-activating-like protein IQGAP1 (p195)	-	-	-	-	-	X	-	-	-	-
Q15404	Ras suppressor protein 1 (Rsu-1) (RSP-1)	-	-	-	-	-	X	-	-	-	-
P63000	Ras-related C3 botulinum toxin substrate 1 precursor (p21-Rac1) (R	-	-	-	-	-	X	-	-	-	-
P15153	Ras-related C3 botulinum toxin substrate 2 precursor (p21-Rac2) (S	-	-	-	-	-	X	-	-	-	X
P61026	Ras-related protein Rab-10	-	-	X	-	-	-	-	-	-	-
P62491	Ras-related protein Rab-11A (Rab-11) (YL8)	-	-	X	-	-	-	-	-	-	-
P61106	Ras-related protein Rab-14	-	-	X	-	-	-	-	-	-	-
P59190	Ras-related protein Rab-15	-	-	X	-	-	-	-	-	-	-
Q9NP72	Ras-related protein Rab-18 - Homo sapiens (Human)	-	-	X	-	-	-	-	-	-	-
P62820	Ras-related protein Rab-1A (YPT1-related protein)	-	-	X	-	-	-	-	-	-	X
Q9H0U4	Ras-related protein Rab-1B	-	-	X	-	-	-	-	-	-	-
Q9UL25	Ras-related protein Rab-21 - Homo sapiens (Human)	-	-	X	-	-	-	-	-	-	-
P61019	Ras-related protein Rab-2A	-	-	X	-	-	-	-	-	-	-
Q9H082	Ras-related protein Rab-33B	-	-	X	-	-	-	-	-	-	-
Q15286	Ras-related protein Rab-35 (Rab-1C) (GTP-binding protein RAY)	-	-	X	-	-	-	-	-	-	-
Q14964	Ras-related protein Rab-39A (Rab-39)	-	-	X	-	-	-	-	-	-	-
P20339	Ras-related protein Rab-5A	-	-	X	-	-	-	-	-	-	-
P61020	Ras-related protein Rab-5B	-	-	X	-	-	-	-	-	-	-
P51148	Ras-related protein Rab-5C (RAB5L) (L1880)	-	-	X	-	-	-	-	-	-	-
P20340	Ras-related protein Rab-6A (Rab-6)	-	-	X	-	-	-	-	-	-	-
P51149	Ras-related protein Rab-7	-	-	X	-	-	-	-	-	-	X
P61006	Ras-related protein Rab-8A (Oncogene c-mel)	-	-	X	-	-	-	-	-	-	-
P62834	Ras-related protein Rap-1A precursor (GTP-binding protein smg-p2:	-	-	X	-	-	-	-	-	-	-
P61224	Ras-related protein Rap-1b precursor (GTP-binding protein smg p21	-	-	X	-	-	-	-	-	-	X
P61225	Ras-related protein Rap-2b precursor	-	-	X	-	-	-	-	-	-	-
P35244	Replication protein A 14 kDa subunit (RP-A) (RF-A) (Replication fac	-	-	-	X	-	-	-	-	-	-
Q9NQC3	Reticulon-4 (Neurite outgrowth inhibitor) (Nogo protein) (Foocen) (N	-	-	-	-	-	-	-	-	-	-
P52565	Rho GDP-dissociation inhibitor 1 (Rho GDI 1) (Rho-GDI alpha)	-	-	-	-	-	-	X	-	-	X
P52566	Rho GDP-dissociation inhibitor 2 (Rho GDI 2) (Rho-GDI beta) (Ly-G	-	-	-	-	-	-	X	-	-	X
P08134	Rho-related GTP-binding protein RhoC precursor (H9)	-	-	-	-	-	-	X	-	-	-
P84095	Rho-related GTP-binding protein RhoG precursor	-	-	-	-	-	-	X	-	-	-
P13489	Ribonuclease inhibitor (Ribonuclease/angiogenin inhibitor 1) (RAI) (I	-	-	-	X	-	-	-	-	-	-
P52758	Ribonuclease UK114 (EC 3,1,-,-) (14,5 kDa translational inhibitor pr	-	-	-	X	-	-	-	-	-	-
P11908	Ribose-phosphate pyrophosphokinase II (EC 2,7,6,1) (Phosphoribo	-	-	-	X	-	-	-	-	-	X
Q96AT9	Ribulose-phosphate 3-epimerase (EC 5,1,3,1) (Ribulose-5-phospha	-	-	-	X	-	-	-	-	-	X
P35637	RNA-binding protein FUS (Oncogene FUS) (Oncogene TLS) (Trans	-	-	-	X	-	-	-	-	-	-
P55735	SEC13-related protein (SEC13-like protein 1)	-	-	X	-	-	-	-	-	-	X
P35270	Sepiapterin reductase (EC 1,1,1,153) (SPR) - Homo sapiens (Huma	-	-	-	-	-	-	-	-	X	-
Q15019	Septin-2 (Protein NEDD5)	-	-	-	-	-	-	X	-	-	X
P62140	Serine/threonine protein phosphatase PP1-beta catalytic subunit (E	-	-	-	-	-	X	-	-	-	X
P30153	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit	-	-	-	-	-	X	-	-	-	X
P62136	Serine/threonine-protein phosphatase PP1-alpha catalytic subunit (E	-	-	-	-	-	X	-	-	-	X
Q9Y3F4	Serine-threonine kinase receptor-associated protein (UNR-interactin	-	-	-	-	-	X	-	-	-	X
P49591	Seryl-tRNA synthetase (EC 6,1,1,11) (Serine--tRNA ligase) (SerRS)	-	-	-	-	-	-	-	X	-	X
O75368	SH3 domain-binding glutamic acid-rich-like protein	-	-	-	-	-	-	-	-	-	X
Q9H299	SH3 domain-binding glutamic acid-rich-like protein 3 (SH3 domain-b	-	-	-	-	-	-	-	-	-	-
Q16836	Short chain 3-hydroxyacyl-CoA dehydrogenase, mitochondrial precu	-	X	-	-	-	-	-	-	-	-
Q9NR45	Sialic acid synthase (N-acetylneuraminase synthase) (EC 2,5,1,56) (	-	-	-	-	-	-	-	-	-	X
Q9BWM7	Sideroflexin-3 - Homo sapiens (Human)	-	-	-	-	-	-	-	-	-	-
P49458	Signal recognition particle 9 kDa protein (SRP9)	-	-	-	-	-	-	-	-	-	-
Q04837	Single-stranded DNA-binding protein, mitochondrial precursor (Mt-S	-	X	-	-	-	-	-	-	-	-
P62314	Small nuclear ribonucleoprotein Sm D1 (snRNP core protein D1) (S	-	-	-	X	-	-	-	-	-	-
Q13126	S-methyl-5-thioadenosine phosphorylase (EC 2,4,2,28) (5*-methylth	-	-	-	X	-	-	-	-	-	X
P05023	Sodium/potassium-transporting ATPase alpha-1 chain precursor (E	-	-	-	-	-	-	-	-	-	-
P30626	Sorcin (22 kDa protein) (CP-22) (V19)	-	-	-	-	-	X	-	-	-	X

O60493	Sorting nexin-3 (SDP3 protein)	-	-	X	-	-	-	-	-	-	-
Q7KZF4	Staphylococcal nuclease domain-containing protein 1 (p100 co-activator)	-	-	-	X	-	-	-	-	-	-
P16949	Stathmin (Phosphoprotein p19) (pp19) (Oncoprotein 18) (Op18) (Leukemia inhibitory factor-binding protein 1) (LIFBP1)	-	-	-	-	-	-	X	-	-	X
Q9UJZ1	Stomatin-like protein 2 (SLP-2) (EPB72-like 2)	-	-	X	-	-	-	-	-	-	X
P38646	Stress-70 protein, mitochondrial precursor (75 kDa glucose-regulated protein)	X	-	-	-	-	-	-	-	-	X
P31948	Stress-induced-phosphoprotein 1 (STI1) (Hsc70/Hsp90-organizing protein)	X	-	-	-	-	-	-	-	-	X
P31040	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial	-	X	-	-	-	-	-	-	X	X
Q9Y6N5	Sulfide:quinone oxidoreductase, mitochondrial precursor (EC 1,-,-,-)	-	X	-	-	-	-	-	-	X	-
P00441	Superoxide dismutase [Cu-Zn] (EC 1,15,1,1)	-	-	-	-	-	-	-	-	X	X
P04179	Superoxide dismutase [Mn], mitochondrial precursor (EC 1,15,1,1)	-	-	-	-	-	-	-	-	X	X
O15260	Surfeit locus protein 4	-	-	X	-	-	-	-	-	-	-
Q9UH65	Switch-associated protein 70 (SWAP-70) - Homo sapiens (Human)	-	-	X	-	-	-	-	-	-	-
Q99536	Synaptic vesicle membrane protein VAT-1 homolog (EC 1,-,-,-)	-	-	X	-	-	-	-	-	-	X
O95721	Synaptosomal-associated protein 29 (SNAP-29) (Vesicle-membrane-associated protein 29)	-	-	X	-	-	-	-	-	-	X
O00560	Syntenin-1 (Syndecan-binding protein 1) (Melanoma differentiation-associated protein 1)	-	-	-	-	-	-	X	-	-	-
Q9Y490	Talin-1	-	-	-	-	-	-	X	-	-	X
O14907	Tax1-binding protein 3 (Tax interaction protein 1) (TIP-1) (Glutaminase-binding protein 1)	-	-	-	-	-	X	-	-	-	-
P17987	T-complex protein 1 subunit alpha (TCP-1-alpha) (CCT-alpha)	X	-	-	-	-	-	-	-	-	X
P78371	T-complex protein 1 subunit beta (TCP-1-beta) (CCT-beta)	X	-	-	-	-	-	-	-	-	X
P50991	T-complex protein 1 subunit delta (TCP-1-delta) (CCT-delta) (Stimulin)	X	-	-	-	-	-	-	-	-	-
P48643	T-complex protein 1 subunit epsilon (TCP-1-epsilon) (CCT-epsilon)	X	-	-	-	-	-	-	-	-	X
Q99832	T-complex protein 1 subunit eta (TCP-1-eta) (CCT-eta) (HIV-1 Nef-interacting protein)	X	-	-	-	-	-	-	-	-	-
P49368	T-complex protein 1 subunit gamma (TCP-1-gamma) (CCT-gamma)	X	-	-	-	-	-	-	-	-	X
P50990	T-complex protein 1 subunit theta (TCP-1-theta) (CCT-theta)	X	-	-	-	-	-	-	-	-	X
P40227	T-complex protein 1 subunit zeta (TCP-1-zeta) (CCT-zeta) (CCT-zeta)	X	-	-	-	-	-	-	-	-	X
Q9Y3D6	Tetratricopeptide repeat protein 11 (TPR repeat protein 11) (Fis1 homolog)	-	-	X	-	-	-	-	-	-	-
P10599	Thioredoxin (ATL-derived factor) (ADF) (Surface-associated sulphhydryl oxidase)	-	-	-	-	-	-	-	-	X	X
O95881	Thioredoxin domain-containing protein 12 precursor (EC 1,8,4,2) (Thioredoxin)	-	-	-	-	-	-	-	-	X	-
Q9BS26	Thioredoxin domain-containing protein 4 precursor (Endoplasmic reticulum oxidoreductase)	-	-	-	-	-	-	-	-	X	X
P30048	Thioredoxin-dependent peroxide reductase, mitochondrial precursor	-	-	-	-	-	-	-	-	X	X
O43396	Thioredoxin-like protein 1 (32 kDa thioredoxin-related protein)	-	-	-	-	-	-	-	-	X	X
Q9BRA2	Thioredoxin-like protein 5 (14 kDa thioredoxin-related protein) (TRP)	-	-	-	-	-	-	-	-	X	-
P62328	Thymosin beta-4 (T beta 4) (Fx) [Contains: Hematopoietic system receptor]	-	-	-	-	-	-	X	-	-	-
Q9H0E2	Toll-interacting protein	-	-	-	-	-	X	-	-	-	X
O43617	Trafficking protein particle complex subunit 3 (BET3 homolog) - Homo sapiens	-	-	X	-	-	-	-	-	-	-
P37837	Transaldolase (EC 2,2,1,2)	-	X	-	-	-	-	-	-	-	X
Q15369	Transcription elongation factor B polypeptide 1 (RNA polymerase II subunit)	-	-	-	X	-	-	-	X	-	-
P20290	Transcription factor BTF3 (RNA polymerase B transcription factor 3)	-	-	-	X	-	-	-	-	-	X
Q96K17	Transcription factor BTF3 homolog 4 (Basic transcription factor 3-like)	-	-	-	X	-	-	-	-	-	X
P61586	Transforming protein RhoA precursor (H12)	-	-	-	-	-	-	X	-	-	X
P37802	Transgelin-2 (SM22-alpha homolog)	-	-	-	-	-	-	X	-	-	-
P55072	Transitional endoplasmic reticulum ATPase (TER ATPase) (15S Mg ATPase)	X	-	-	-	-	-	-	-	-	X
P29401	Transketolase (EC 2,2,1,1) (TK)	-	X	-	-	-	-	-	-	-	X
P13693	Translationally-controlled tumor protein (TCTP) (p23) (Histamine-releasing factor)	-	-	-	-	-	X	-	-	-	X
Q99598	Translin-associated protein X (Translin-associated factor X)	-	-	-	X	-	-	-	-	-	X
P51571	Translocon-associated protein delta subunit precursor (TRAP-delta)	X	-	-	-	-	-	-	-	-	-
Q15363	Transmembrane emp24 domain trafficking protein 2 precursor (Membrane protein 24)	-	-	X	-	-	-	-	-	-	-
Q9BVK6	Transmembrane emp24 domain-containing protein 9 precursor (Glycosylated)	-	-	X	-	-	-	-	-	-	-
Q9BVC6	Transmembrane protein 109 precursor (Mitsugumin-23) (Mg23)	-	-	X	-	-	-	-	-	-	-
P40939	Trifunctional enzyme alpha subunit, mitochondrial precursor (TP-alpha)	-	X	-	-	-	-	-	-	-	-
P55084	Trifunctional enzyme subunit beta, mitochondrial precursor (TP-beta)	-	X	-	-	-	-	-	-	-	-
P22102	Trifunctional purine biosynthetic protein adenosine-3 [Includes: Phosphoribosyl transferase]	-	-	-	X	-	-	-	-	-	X
P60174	Triosephosphate isomerase (EC 5,3,1,1) (TIM) (Triose-phosphate isomerase)	-	X	-	-	-	-	-	-	-	X
O14773	Tripeptidyl-peptidase I precursor (EC 3,4,14,9) (TPP-I) (Tripeptidyl aminopeptidase)	-	-	-	-	X	-	-	-	-	X
Q9UI30	TRM112-like protein - Homo sapiens (Human)	-	-	-	-	-	-	-	-	-	X
Q9NYL9	Tropomodulin-3 (Ubiquitous tropomodulin) (U-Tmod) - Homo sapiens	-	-	-	-	-	-	X	-	-	X
P09493	Tropomyosin 1 alpha chain (Alpha-tropomyosin)	-	-	-	-	-	-	X	-	-	X
P06753	Tropomyosin alpha-3 chain (Tropomyosin-3) (Tropomyosin gamma)	-	-	-	-	-	-	X	-	-	X
P67936	Tropomyosin alpha-4 chain (Tropomyosin-4) (TM30p1)	-	-	-	-	-	-	X	-	-	X
P23381	Tryptophanyl-tRNA synthetase (EC 6,1,1,2) (Tryptophan--tRNA ligase)	-	-	-	-	-	-	-	X	-	X
P68363	Tubulin alpha-ubiquitous chain (Alpha-tubulin ubiquitous) (Tubulin K)	-	-	-	-	-	-	X	-	-	X
P07437	Tubulin beta-2 chain	-	-	-	-	-	-	X	-	-	X
Q9BUF5	Tubulin beta-6 chain - Homo sapiens (Human)	-	-	-	-	-	-	X	-	-	-

O75347	Tubulin-specific chaperone A (Tubulin-folding cofactor A) (CFA) (TC	X	-	-	-	-	-	X	-	-	X
Q99426	Tubulin-specific chaperone B (Tubulin folding cofactor B) (Cytoskele	X	-	-	-	-	-	X	-	-	X
O43399	Tumor protein D54 (hD54) (Tumor protein D52-like 2)	-	-	-	-	-	-	-	-	-	X
Q12792	Twinfilin-1 (Protein A6) (Protein tyrosine kinase 9) - Homo sapiens (I	-	-	-	-	-	-	X	-	-	-
Q6IBS0	Twinfilin-2 (Twinfilin-1-like protein) (A6-related protein) (hA6RP) (Pro	-	-	-	-	-	-	X	-	-	X
P54577	Tyrosyl-tRNA synthetase, cytoplasmic (EC 6.1.1.1) (Tyrosyl-tRNA li	-	-	-	-	-	-	-	X	-	X
Q9Y333	U6 snRNA-associated Sm-like protein LSm2 (SnRNP core Sm-like p	-	-	-	X	-	-	-	-	-	-
P47985	Ubiquinol-cytochrome c reductase iron-sulfur subunit, mitochondrial	-	X	-	-	-	-	-	-	-	X
P22695	Ubiquinol-cytochrome-c reductase complex core protein 2, mitochor	-	X	-	-	-	-	-	-	-	-
P62988	Ubiquitin	-	-	-	-	X	-	-	-	-	X
P54578	Ubiquitin carboxyl-terminal hydrolase 14 (EC 3.1.2.15) (Ubiquitin thio	-	-	-	-	X	-	-	-	-	X
P45974	Ubiquitin carboxyl-terminal hydrolase 5 (EC 3.1.2.15) (Ubiquitin thiol	-	-	-	-	X	-	-	-	-	X
P15374	Ubiquitin carboxyl-terminal hydrolase isozyme L3 (EC 3.4.19.12) (U	-	-	-	-	X	-	-	-	-	X
Q96FW1	Ubiquitin thiolesterase protein OTUB1 (EC 3.4.-.-) (Otubain 1) (OTU	-	-	-	-	X	-	-	-	-	-
P22314	Ubiquitin-activating enzyme E1 (A1S9 protein)	-	-	-	-	X	-	-	-	-	X
P62837	Ubiquitin-conjugating enzyme E2 D2 (EC 6.3.2.19) (Ubiquitin-protein	-	-	-	-	X	-	-	-	-	-
P68036	Ubiquitin-conjugating enzyme E2 L3 (EC 6.3.2.19) (Ubiquitin-protein	-	-	-	-	X	-	-	-	-	-
O14933	Ubiquitin-conjugating enzyme E2 L6 (EC 6.3.2.19) (Ubiquitin-protein	-	-	-	-	X	-	-	-	-	-
P61088	Ubiquitin-conjugating enzyme E2 N (EC 6.3.2.19) (Ubiquitin-protein	-	-	-	-	X	-	-	-	-	X
Q13404	Ubiquitin-conjugating enzyme E2 variant 1 (UEV-1) (CROC-1) (Ubiqui	-	-	-	-	X	-	-	-	-	X
Q15819	Ubiquitin-conjugating enzyme E2 variant 2 (MMS2) (Enterocyte diffe	-	-	-	-	X	-	-	-	-	X
P61086	Ubiquitin-conjugating enzyme E2-25 kDa (EC 6.3.2.19) (Ubiquitin-pr	-	-	-	-	X	-	-	-	-	X
P61960	Ubiquitin-fold modifier 1 precursor - Homo sapiens (Human)	-	-	-	-	X	-	-	-	-	X
Q9UBT2	Ubiquitin-like 1-activating enzyme E1B (SUMO-1-activating enzyme	-	-	-	-	X	-	-	-	-	-
Q9NYU2	UDP-glucose:glycoprotein glucosyltransferase 1 precursor (EC 2.4.1	X	-	-	-	-	-	-	-	-	-
P30085	UMP-CMP kinase (EC 2.7.4.14) (Cytidylate kinase) (Deoxycytidylate	-	-	-	X	-	-	-	-	-	X
Q6IAA8	UPF0404 protein C11orf59 - Homo sapiens (Human)	-	-	-	-	-	-	-	-	-	-
P54727	UV excision repair protein RAD23 homolog B (hHR23B) (XP-C repa	-	-	-	X	-	-	-	-	-	-
P38606	Vacuolar ATP synthase catalytic subunit A, ubiquitous isoform (EC 3	-	X	-	-	-	-	-	-	-	X
P36543	Vacuolar ATP synthase subunit E (EC 3.6.3.14) (V-ATPase E subur	-	X	-	-	-	-	-	-	-	X
O75348	Vacuolar ATP synthase subunit G 1 (EC 3.6.3.14) (V-ATPase G sub	-	X	-	-	-	-	-	-	-	-
Q9UBQ0	Vacuolar protein sorting 29 (Vesicle protein sorting 29) (hVPS29) (P	-	-	X	-	-	-	-	-	-	X
Q96QK1	Vacuolar protein sorting 35 (Vesicle protein sorting 35) (hVPS35) (M	-	-	X	-	-	-	-	-	-	-
Q9BRG1	Vacuolar protein sorting-associated protein 25 (hVps25) (ELL-assoc	-	-	X	-	-	-	-	-	-	-
P63027	Vesicle-associated membrane protein 2 (VAMP-2) (Synaptobrevin-2	-	-	X	-	-	-	-	-	-	-
P46459	Vesicle-fusing ATPase (EC 3.6.4.6) (Vesicular-fusion protein NSF) (	-	-	X	-	-	-	-	-	-	X
Q00341	Vigilin (High density lipoprotein-binding protein) (HDL-binding protei	-	-	X	-	-	-	-	-	-	-
P18206	Vinculin (Metavinculin)	-	-	-	-	-	-	X	-	-	X
P21796	Voltage-dependent anion-selective channel protein 1 (VDAC-1) (hVI	-	-	X	-	-	-	-	-	-	-
P45880	Voltage-dependent anion-selective channel protein 2 (VDAC-2) (hVI	-	-	X	-	-	-	-	-	-	X
Q9Y277	Voltage-dependent anion-selective channel protein 3 (VDAC-3) (hVI	-	-	X	-	-	-	-	-	-	-
O75083	WD-repeat protein 1 (Actin-interacting protein 1) (AIP1) (NORI-1)	-	-	-	-	-	-	X	-	-	X
Q92558	Wiskott-Aldrich syndrome protein family member 1 (WASP-family pr	-	-	-	-	-	-	X	-	-	-

Proteome Maps of the Main Human Peripheral Blood Constituents

Verena J. Haudek¹⁺, Astrid Slany¹⁺, Nina C. Gundacker¹, Helge Wimmer², Johannes Drach³, Christopher Gerner^{1*}

¹Department of Medicine I, Institute of Cancer Research, Medical University of Vienna, Austria

²Section Biomedical Laboratory Science, University of Applied Science, Vienna, Austria

³Department of Medicine I, Department of Clinical Oncology, Medical University of Vienna, Austria

⁺ contributed equally

^{*} Correspondence: Christopher Gerner, Department of Medicine I, Institute of Cancer Research, Medical University of Vienna, Austria

Email: Christopher.Gerner@meduniwien.ac.at

Phone: 0043-1-4277-65230

Abstract

Clinical proteome analysis will almost inevitably be confronted with blood constituents. Purified plasma, serum, cell or tissue samples may easily be contaminated with some other constituents, affecting the final proteome analysis result. In order to recognize proteins which are potentially indicative for the presence of major blood constituents, we purified T cells, monocytes, neutrophils, erythrocytes, platelets and plasma and performed comparative proteome profiling employing 2D-PAGE in addition to shotgun proteomics. By mass analysis, 605 different proteins were identified in the 2D gels. Seven of those displayed a highly specific expression pattern. A total of 1889 proteins were identified by shotgun proteomics, including 34 proteins with highly specific expression patterns. Indeed, proteins specific for each of the constituents were successfully identified. The corresponding genes displayed compatible expression specificities as determined by the use of GENATLAS. The present protein maps of each of the constituents may serve as references for comparative analyses and will aid the interpretation of proteome profiles of clinical materials.

Keywords:

proteome profiling, peripheral blood mononuclear cells, 2D-PAGE, shotgun proteomics, plasma, platelets, T cells, monocytes, neutrophils, erythrocytes

Introduction

Human blood represents an optimal source for discovery and analysis of biomarker. Proteins derived from diseased tissue compartments may leak into lymph and blood, eventually becoming detectable in plasma and serum. Many diseases accompanied by e.g. inflammation may directly affect the protein expression profile of blood compartments such as immune cells or platelets.¹ Such characteristic alterations may as well give rise to clinical biomarkers. Another important approach for biomarker discovery is the comparison of tissue specimen derived from healthy and diseased organs.² Differences in the finally obtained protein lists, however, may be due to epiphenomena accompanying disease states such as leukocyte invasion, platelet and fibrin deposition³ or alterations of the blood supply. It is not trivial to recognize such events from differential analysis of proteome profiles.⁴ To support data interpretation of clinical proteome profiling results, reference proteome maps might be very helpful.⁵ The knowledge of proteins expressed in a healthy background and the assignment of proteins to their potential source of origin could render comparative analyses searching for disease marker proteins easier to interpret.

Much effort has already been spent on the establishment of proteome profiles of blood constituents. Amongst others, these include the analysis of peripheral blood mononuclear cells (PBMCs),^{6, 7} lymphocytes,⁸ monocytes,⁹ neutrophils,¹⁰ erythrocytes,^{5, 11} platelets,¹²⁻¹⁴ T cells,¹⁵ and plasma.¹⁶⁻¹⁸ Proteome studies of blood constituents were employed to investigate various diseases such as atopic dermatitis,¹⁹ rheumatoid arthritis,²⁰ or to perform *in vivo* intervention studies with soy isoflavones,²¹ Brussels sprouts,²² or vitamin C supplementation.²³ Despite the large number of studies already performed, there is still a lack of standardization and it is hard to conclude for specificities in protein expression by comparing results obtained from different research teams. Therefore, systematic comparative studies employing different laboratories have been performed.²⁴ Obviously, apparent differences are derived from variations in methods employed for the purification of constituents, for protein isolation, protein and peptide separation and protein identification. This may be not surprising, considering the large number of diverse molecules in biological samples. Thousands of different proteins occur in concentration spans up to 8-10 orders of magnitude,^{25, 26} and are mixed with metabolites, lipids, polysaccharides and nucleic acids. We have described recently that protein isolation strategies may be critical to obtain representative and reproducible results.²⁷

Here, we present a comparative proteome study of the most abundant blood constituents including plasma, lymphocytes, monocytes, platelets, neutrophils and erythrocytes. We purified each of those constituents and the analysis was confined to cytoplasmic proteins. The major aim was a reliable assignment of specific proteins to each of the different constituents. On one hand, we used 2D-PAGE and performed comparative pattern analysis. Spots were cut out and identified by mass spectrometry. On the other hand, we analyzed the same samples by shotgun proteomics^{28,29} resulting in many more protein identifications. Database-assisted analysis allowed us to identify several specifically expressed proteins which may serve as marker proteins for the respective blood constituents.

Experimental section

Isolation of PBMCs (peripheral blood mononuclear cells)

PBMCs were isolated from heparinized whole blood of different healthy donors by standard density gradient centrifugation with Ficoll-Paque (GE Healthcare Bio-Sciences AB, Uppsala, Sweden).^{8, 30} The cells were subsequently washed with HBSS (Hanks' Buffered Salt Solution, 1:1).

Isolation of plasma

2 ml of the heparinized whole blood were used for plasma isolation by centrifugation for 10 min at room temperature at 8000 g. The supernatant plasma was carefully isolated and stored at -80°C.

Monocyte and T cell separation

T cells and monocytes were separated by magnetic sorting using the MACS technique (Miltenyi Biotec, Bergisch Gladbach, Germany). Purified T cells were obtained through negative depletion of CD11b, CD14, CD16, CD19, CD33, and MHC class II-positive cells with the respective monoclonal antibody. Monocytes were enriched by using the biotinylated CD14 mAb VIM13 (achieving a cell purity 95 %) as previously described.³¹

Neutrophil and Erythrocyte separation

After standard density gradient centrifugation with Ficoll-Paque the resulting soft pellet was put on ice. 200 µl of the pellet were resuspended in 200 µl of sample buffer (7.5 M urea, 1.5 M thiourea, 4% CHAPS, 0.05% SDS, 100 mM DDT) to gain the erythrocytes. The rest of the pellet was resuspended in haemolysis buffer (0.16 M ammonium chloride, 0.01 M potassium hydrogen carbonate, 1 µM EDTA) to destroy erythrocytes and centrifuged to pellet neutrophils. The procedure was repeated two times to isolate the neutrophils.

Platelet separation

Whole blood of healthy donors was collected in Acid-Citrate-Dextrose-A tubes and was centrifuged at 110g for 30 minutes at room temperature. The supernatant was washed with RPMI 0 medium by centrifugation. Prostaglandin E1 (0.1 µg/ml) (98% (HPLC) Synthetic, Sigma, Steinheim, Germany) was added during all steps to keep the thrombocytes inactivated. The pellet was resuspended in RPMI 0, an aliquote was taken for control and another aliquote

was activated by Thrombin (1µg/ml) (Sigma, Steinheim, Germany). The platelets were then sonicated.

Sub-cellular fractionation

The isolation of cytoplasmic proteins was performed as described by Gundacker et al.²⁷ Cells were lysed in hypotonic lysis buffer (10 mM HEPES/NaOH, pH 7.4, 0.25 M sucrose, 10 mM NaCl, 3 mM MgCl₂, 0.5% Triton X-100) supplemented with protease inhibitors and pressed through a 26 g syringe to induce cell lysis. The cytoplasmic fraction was separated from nuclei by centrifugation and precipitated by addition of ethanol. Afterwards, all protein samples were dissolved in sample buffer (7.5 M urea, 1.5 M thiourea, 4% CHAPS, 0.05% SDS, 100 mM DDT).

2D polyacrylamid gel electrophoresis (2D-PAGE)

Proteins were loaded by passive rehydration on IPG strips pH 5–8, 17 cm (BioRad, Hercules, CA) at room temperature. Alternatively, IPG immobiline strips (GE) were used, which gave similar results (not shown). IEF was performed in a stepwise fashion (1 h 0– 500 V linear; 5 h 500 V; 5 h 500–3500 V linear; 12 h 3500 V). After IEF, the strips were equilibrated with 100 mM DTT and 2.5% iodacetamide according to the instructions of the manufacturer (BioRad). For SDS-PAGE using the Protean II xi electrophoresis system (BioRad), IPG strips were placed on top of 1.5 mm 12% polyacrylamide slab gels and overlaid with 0.5% low-melting agarose. The gels were stained with a 400 nM solution of Ruthenium II tris (bathophenanthroline disulfonate) (RuBPS) as described.³² Fluorography scanning was performed with the FluorImager 595 (GE Healthcare, Fairfield, CT) at a resolution of 100 µm.³³ All 2D gel data were independently reproduced two times. Gels were warped to a reference gel with the TT900 S2S software (version 2006.0.2389, Nonlinear dynamics, Carlsbad, CA) and evaluated with the Progenesis software PG200 (version 2006, Nonlinear) using the “same spot” algorithm.

1D-PAGE for subsequent shotgun analysis

Cytoplasmic protein fractions were loaded on 13% polyacrylamid gels, electrophoresis was performed until complete separation of a pre-stained molecular marker (Dual Color, Biorad, Hercules, CA) was visible. After fixation with 50% methanol/10% acetic acid and subsequent silver staining, gel lanes were cut out of the gel and digested with trypsin as described below.

MS-compatible silver staining procedure

2D gels were fixed with 50% methanol, washed and sensitized with 0.02% Na₂S₂O₃. The gels were stained with 0.1% AgNO₃ ice cold for 20 minutes, rinsed with bi-distilled water and subsequently developed with 3% Na₂CO₃/0.05% formaldehyde as previously described.³⁴

Tryptic digest

Protein spots were cut out of the gel, the gel-pieces were de-stained with 15 mM K₃Fe(CN)₆/50 mM Na₂S₂O₃ and intensively washed with 50% methanol/10% acetic acid. The pH was adjusted with 50 mM NH₄HCO₃, proteins were reduced with 10 mM DTT/50 mM NH₄HCO₃ for 30 minutes at 56°C and alkylated with 50 mM iodacetamide/50 mM NH₄HCO₃ 20 minutes in the dark. Afterwards the gel-pieces were treated with acetonitrile (ACN) and dried in a vacuum centrifuge. Between each step, the tubes were shaken for 5-10 minutes (Eppendorf Thermomixer comfort). Dry gel-spots were treated with trypsin 0.1 mg/ml (Trypsin sequencing grade, Roche Diagnostics, Germany)/50 mM NH₄HCO₃ for 20 minutes on ice, afterwards covered with 50 mM NH₄HCO₃ and subsequently incubated over night at 37°C. The digested peptides were eluted by adding 50 mM NH₄HCO₃, the supernatant was transferred into silicon-coated tubes, and this procedure was repeated two times with 5% formic acid/50% ACN. Between each elution step the gel-spots were ultrasonicated for 10 minutes. Finally the peptide solution was concentrated in a vacuum centrifuge to an appropriate volume.

Mass spectrometry analysis

For the identification of 2D spots, peptides were loaded on a Zorbax 300SB-C8 (5 µm, 0.3 mm, 5 mm) column and separated by nanoflow LC (1100 Series LC system, Agilent, Palo Alto, CA) with a Zorbax 300SB-C18 (5 µm, 75 mm, 150 mm) column at a flow rate of 250 nl/min using a gradient from 0.2% formic acid and 3% ACN to 0.2% formic acid and 45% ACN over 12 minutes. In case of shotgun analysis, peptides were also separated by nano-flow LC (1100 Series LC system, Agilent, Palo Alto, CA) using the HPLC-Chip technology (Agilent) equipped with a 40 nl Zorbax 300SB-C18 trapping column and a 75 µm x 150 mm Zorbax 300SB-C18 separation column at a flow rate of 400 nl/min, using a gradient from 0.2% formic acid and 3% ACN to 0.2% formic acid and 50% ACN over 80 minutes. Peptide identification was accomplished by MS/MS fragmentation analysis with an iontrap mass spectrometer (XCT-Ultra, Agilent) equipped with an orthogonal nanospray ion source. The MS/MS data, including peak list-generation and search engine, were interpreted

by the Spectrum Mill MS Proteomics Workbench software (Version A.03.02, Agilent) allowing for two missed cleavages and searched against the SwissProt Database for human proteins (Version 20080409 containing 19038 entries or, alternatively, version 14.3 containing 20328 entries) allowing for precursor mass deviation of 1.5 Da, a product mass tolerance of 0.7 Da and a minimum matched peak intensity (%SPI) of 70%. Due to previous chemical modification, carbamidomethylation of cysteine was set as fixed modification. No other modifications were considered here.

Construction of proteome reference maps

For the generation of the final protein list of all different cell types and plasma, the following protein selection algorithm was applied. Peptide scores were considered to select appropriate sequence assignments. To assess the reliability of the peptide scores, searches were performed against the corresponding reversed database. 5.9% positive hits were found with peptides scoring >9.0, while 0.21% positive hits were found with peptides scoring >13.0. Only peptides scoring higher than 9.0 were considered for protein identification. Identification details for each protein including all identified peptides, sequence coverage, peptide scores and MS2 spectra are fully accessible via PRIDE database (<http://www.ebi.ac.uk/pride/>).^{35, 36} In the final protein list (see supplementary data) the sums of all peptides related to the single proteins from the corresponding cell type are listed. Proteins derived from obvious contaminants such as fetal calf serum were deleted. Proteins were selected based on the expression of specific peptides. Selection of protein isoforms was performed as described by Zhang et al.³⁷ In case a definite assignment was not possible due to sequence homologies, the biologically most plausible candidate was selected. The derived data was further arranged and analyzed by a home made SQL-database, recently designed as database of the Clinical Proteomics Laboratories at the Medical University of Vienna (CPL/MUW-database, Wimmer H. et al, manuscript in preparation).

Results

2D-PAGE analysis of purified blood constituents

In order to assess the specificity of protein expression patterns, we employed 2D-PAGE to analyze the cytoplasmic protein fraction of three to six individual samples each of purified T cells, monocytes, neutrophils, erythrocytes and platelets in addition to blood plasma (Figure 1). Furthermore, we analyzed PBMCs which consist of lymphocytes (mainly T cells) and monocytes, interspersed to a varying degree with platelets, neutrophils, erythrocytes and plasma. Referring to previously published data, several commonly expressed proteins were readily identified.³⁸ Including proteins previously identified in PBMCs,⁷ a total of 1445 spots were cut out of the gels, resulting in the identification of 605 proteins (Table S1).

Shotgun analysis of purified blood constituents

All protein fractions analyzed by 2D-PAGE were also investigated by shotgun proteomics. Here, proteins were pre-fractionated via SDS-PAGE and the sliced gels digested with trypsin. Mass analysis was similar as applied for isolated 2D gel spots. A total of 1887 proteins were identified. All complete data analyzed in the present study is publicly accessible via PRIDE database (<http://www.ebi.ac.uk/pride/>),^{35, 36} PRIDE accessions 8884-8908. The number of proteins identified in the purified constituents is depicted in Figure 2.

In comparison, shotgun proteomics proved to be more sensitive than protein identification in 2D gels. All proteins identified in 2D gel spots were independently identified by shotgun proteomics as indicated in Table S1.

Comparative analysis searching for specifically expressed proteins

In order to find specifically expressed proteins, we compared 2D gel spot patterns of the purified constituents. It was our aim to identify proteins occurring in one, but not in any other of the purified blood constituents.

In T cells no specific protein was identified in 2D gels. Plasminogen activator inhibitor 2 (P05120) was found to be specific for monocytes; annexin A3 (P12429) for neutrophils; hemoglobin subunit beta (P68871) for erythrocytes and Integrin alpha-IIb (P08514) for platelets (Figure 1). Erythrocytes additionally displayed other specific proteins (Table 1). By means of shotgun analysis, these data were confirmed and extended. In Figure 2, the number of proteins which were only identified in the respective constituent, but not in any other, are indicated in brackets. The expression pattern of each identified protein can be

retrieved from Table S1. Comparative analysis was supported by a home-made SQL-database (CPL/MUW-database, Wimmer et al., manuscript in preparation). To further evaluate the specificity of these proteins, we referred to the gene expression databases GENATLAS (<http://genatlas.medecine.univ-paris5.fr/>). In Table 1 we listed only those 34 proteins whose gene expression has been described to be specific for the particular constituent.

Database-assisted interpretation of cell samples:

The presented protein specificities can be used to assess the presence or absence of blood constituents in any protein sample of interest. The identification of a specifically expressed protein may give a strong indication for the presence of the corresponding constituent. This is exemplified for PBMCs treated *in vitro* with hydrogen peroxide (Table S2). The purified leukocyte fraction contained integrin alpha-IIb and Hemoglobin subunit alpha and beta which indicate contamination with platelets and erythrocytes.

Discussion

Enormous effort has been spent on proteome profiling of blood constituents such as serum and plasma.³⁹ The value of that effort is not doubted, as it holds great promise for biomarker discovery. The proteome profile of plasma or other body fluids, however, may be affected by a large variety of contaminants, which may occur at varying degrees. Within serum or plasma, lysed erythrocytes or platelets may be considered as contaminants which may significantly affect the final proteome profile. Otherwise, plasma and other blood constituents may be considered as potential contaminants when analyzing primary cells or tissue specimen. According to our own experience, it is not trivial to recognize potential contaminants, which may render subsequent data interpretation inappropriate. Although a large number of proteome profiling studies have been performed on blood constituents, as mentioned above, clear specificities of protein expression can hardly be derived from these data. This is mainly due to the heterogeneity of study designs and methods.

Here, we performed a comprehensive comparative proteome profiling study of the purified blood constituents T cells, monocytes, neutrophils, erythrocytes and platelets in addition to blood plasma and PBMCs. We employed both 2D-PAGE and shotgun proteomics in order to make the final data applicable to a broad variety of proteome studies.

As expected, a large number of proteins were found to be expressed by more than one constituent (Table S1). Specific proteins of each of the purified constituents, however, were successfully identified (Table 1).

We have applied the same identification methodology to all constituents, ensuring optimal compatibility for comparative analysis. This allows as well comparison to other published data as follows.

PBMCs

Of the 174 different proteins identified in 2D gels of PBMCs by Vergara et al.,⁶ we also identified 156 proteins by shotgun analysis, representing 90% of these recently published results. In a formerly published reference 2D gel,⁷ we were able to detect 519 different proteins. 138 of these listed proteins correspond to the published data of Vergara et al..⁶

T cells

Till now, no proteome map of purified T cells has been published. We were able to detect 934 different proteins in primary human T cells by means of shotgun analysis. 95 of them were only found in this cell type. In Table 1, two specific T cell proteins are listed.

Monocytes

In a study using 2D gels for the investigation of the monocyte proteome, 231 protein spots have been identified, which corresponded to 164 different proteins.⁹ In 2D-gels we detected 391 different proteins, 108 overlap with the published data. By means of shotgun analysis, we were able to identify 837 different proteins, 85% of the 164 proteins were found in this data set. We listed three proteins as specific for monocytes (Table 1).

Platelets

2D gel platelet proteome profiles were established in several studies,^{12, 13} identifying about 800 different proteins. We detected 632 proteins by means of shotgun analysis and 328 proteins in 2D gels. In a further study, 10 potential biomarkers of platelet contaminations in PBMCs were presented.²⁴ Nine of these 10 proteins have been also found in our dataset not displaying the claimed specificity. Furthermore, their specificity for platelets could not be confirmed by means of the database GENATLAS. We listed nine other proteins as putative markers for platelet contamination (Table 1).

Erythrocytes

In an in-depth analysis of red blood cells, 587 different membrane and soluble proteins have been identified.¹¹ By shotgun analysis, we were able to identify 212 different proteins. The data overlap is about 15%. This may be mainly due to the fact that Pasini et al.¹¹ spent more effort on pre-fractionation and focused on membrane and cytoplasmic proteins, whereas we focussed only cytoplasmic proteins.

Neutrophils

In a 2D gel based study, 102 different spots were reproducibly detected in neutrophils, 22 of them were successfully identified.¹⁰ We were able to identify 326 in 2D gels and 542 different proteins by means of shotgun proteomics. Eleven of them were found specific for neutrophils (Table 1).

Plasma

We detected 203 different proteins in plasma. A recent manually validated human blood plasma protein reference set listed 679 proteins.¹⁶ The overlap was 167 different proteins representing about 24%.

Conclusion

By means of 2D-PAGE and shotgun analysis we were able to define a set of specifically expressed proteins, which may serve as markers for one of the main blood constituents T cells, monocytes, neutrophils, erythrocytes, platelets and blood plasma. Some proteins were detectable in 2D gels, but many more were identified by shotgun proteomics. The present data may serve as reference for proteome profiling studies dealing with materials potentially contaminated with blood constituents. Furthermore, pathologic events such as tissue invasion by lymphocytes, monocytes and neutrophils or platelet aggregation may be detected in tissue samples by the use of the presently identified marker proteins.

Acknowledgments

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Legend to the figures/tables

Figure 1:

Specific proteins indicated in 2D gel sections of PBMCs, monocytes, platelets, neutrophils, plasma and erythrocytes. For each constituent except T cells, one potential marker protein was exemplified to demonstrate specific expression. For orientation on the gels, actin (P60709) was marked with a pentagon. The following proteins, detected by fluorescence staining, were depicted on the 2D gel sections: plasminogen activator inhibitor 2, P05120 (monocytes), annexin A3, P12429 (neutrophils), hemoglobin subunit alpha, P69905 (erythrocytes), integrin alpha-IIb, P08514 (platelets) and serum albumin, P02768 (plasma). Full circles indicate expressed proteins, whereas dashed circles indicate the localization of the absent proteins.

Figure 2:

Number of proteins in PBMCs, T cells, monocytes, platelets, neutrophils, erythrocytes and plasma identified by shotgun proteomics. In total, 1887 proteins have been identified. In the figure the total number of identified proteins for each constituent is listed, the X-axis represents the corresponding percentage with respect to the total number of proteins. The dark gray bar represents ubiquitous proteins, the dashed bar represents the numbers of proteins which were only identified in the respective constituent, but not in any others. The corresponding number for each constituent is also indicated in brackets.

Table 1:

Proteins specifically occurring in the purified constituents as indicated. Proteins were identified by shotgun proteomics, the observed specificity was also found to apply to the corresponding genes according to gene expression data. Proteins which were also detectable on 2D gels are listed under “2D”.

Supporting Information Available

Table S1: List of all detected proteins in PBMCs and purified constituents.

This table represents the total list of identified proteins in PBMCs, T cells, monocytes, neutrophils, platelets, erythrocytes and plasma. Proteins are sorted according to protein names and identified by their SwissProt Accession numbers. The numbers listed in rows indicate the number of distinct peptides identified by mass spectrometry corresponding to each constituent. Proteins which were also identified in 2D gels are marked (X)

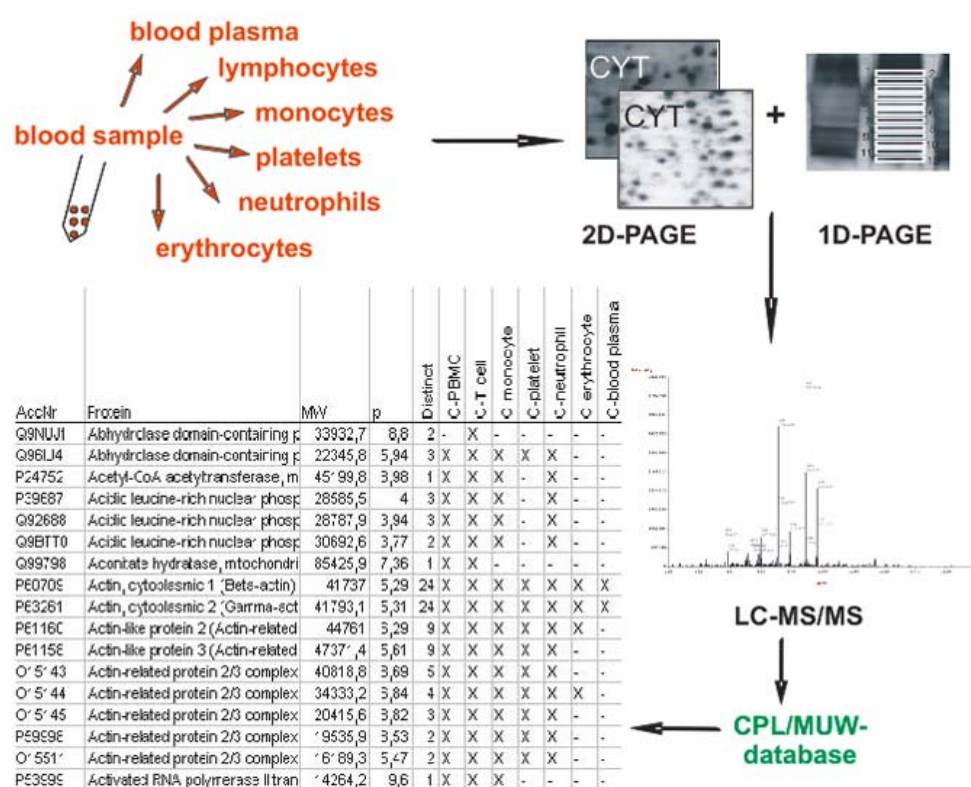
Table S2: Example of database-assisted interpretation of a single sample. The table lists all proteins identified in a sample of PBMCs treated *in vitro* with 100 μ M hydrogen peroxide. It

was chosen to show the use of database-assisted interpretation of cell samples. It is immediately possible to read the potential origins of each of the identified proteins with respect to the single constituents. This information may be used for the interpretation of differently regulated proteins in any kind of clinical sample.

This information is available free of charge via the internet at <http://pubs.arc.org>.

Synopsis:

Blood mainly consists of lymphocytes, monocytes, neutrophils, erythrocytes, platelets and plasma. We purified these constituents and applied 2D-PAGE in addition to shotgun proteomics, resulting in the identification of 1887 proteins. For each constituent we present specifically expressed marker proteins. These data provide validated reference proteome maps of each constituent and may aid the interpretation of clinical proteome data.



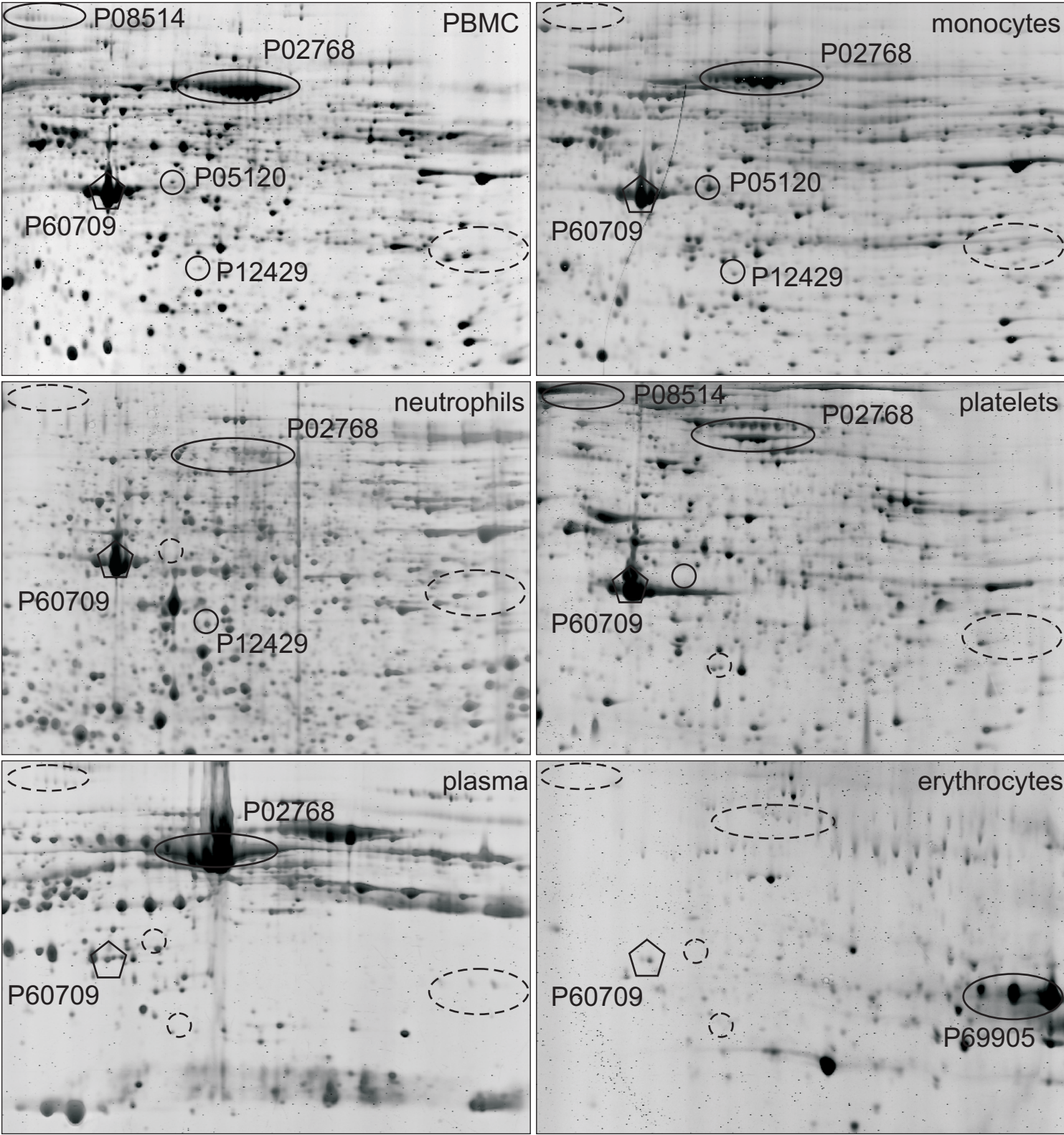


Figure 1

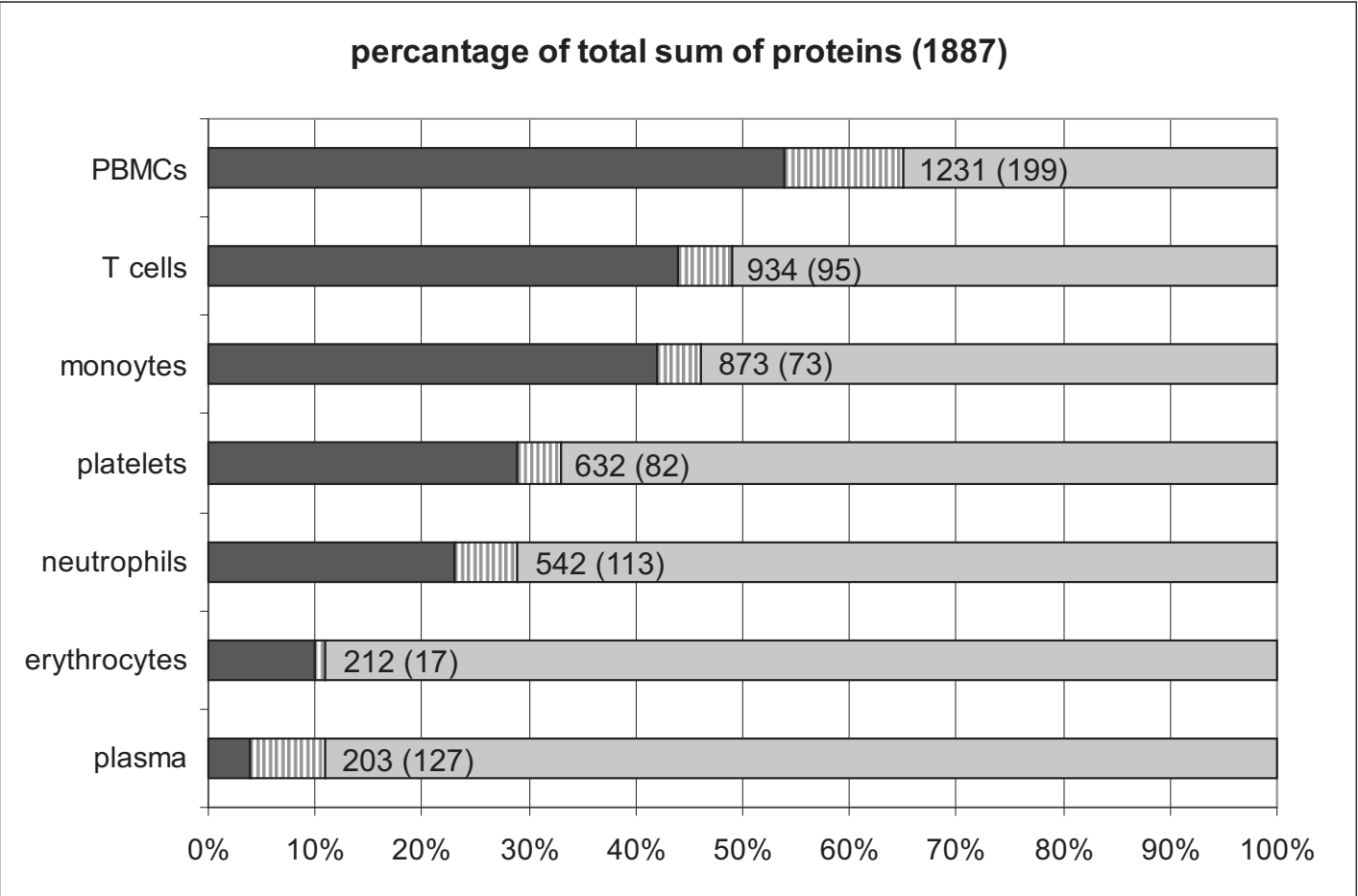


Figure 2

cell-specific proteins (without plasma)			
cell type	AccNr	Protein	2D
monocytes	P05120	Plasminogen activator inhibitor 2 precursor	x
	Q9Y336	Sialic acid-binding Ig-like lectin 9 precursor	
	O60603	Toll-like receptor 2 precursor	
T cells	P23743	Diacylglycerol kinase alpha	
	P14151	L-selectin precursor	
platelets	P08514	Integrin alpha-IIb precursor	x
	P22064	Latent-transforming growth factor beta-binding protein, isoform 1S precursor	
	Q14766	Latent-transforming growth factor beta-binding protein, isoform 1L precursor	
	Q13201	Multimerin-1 precursor	
	P02776	Platelet factor 4 precursor	
	P10720	Platelet factor 4 variant precursor	
	P07359	Platelet glycoprotein Ib alpha chain precursor	
	P40197	Platelet glycoprotein V precursor	
	P16109	P-selectin precursor	
neutrophils	P49913	Cathelicidin antimicrobial peptide precursor	
	P20061	Transcobalamin-1 precursor	
	P12429	Annexin A3	x
	P17213	Bactericidal permeability-increasing protein precursor	
	P59665	Neutrophil defensin 1 precursor	
	Q08477	Cytochrome P450 4F3	
	P22894	Neutrophil collagenase precursor	
	P11678	Eosinophil peroxidase precursor	
	O15389	Sialic acid-binding Ig-like lectin 5	
	O75015	Low affinity immunoglobulin gamma Fc region receptor III-B precursor	
erythrocytes	Q8N6Q3	CD177 antigen	
	P02730	Band 3 anion transport protein	x
	P16452	Erythrocyte membrane protein band 4.2	
	P69905	Hemoglobin subunit alpha (Alpha-globin)	x
	P68871	Hemoglobin subunit beta (Beta-globin)	
	P02042	Hemoglobin subunit delta (Delta-globin)	
	P69891	Hemoglobin subunit gamma-1	x
	P11171	Protein 4.1	
	P02549	Spectrin alpha chain, erythrocyte	
	P11277	Spectrin beta chain, erythrocyte	x

Table 1

Supplementary Table 1

	AccNr	Protein	plasma	erythrocytes	platelets	neutrophils	T cells	monocytes	PBMCs	2D
1	Q04446	1,4-alpha-glucan branching enzyme (EC 2,4,1,18) (Gly	-	-	-	3	-	-	-	-
2	P61604	10 kDa heat shock protein, mitochondrial (Hsp10) (10	-	-	2	2	2	5	6	X
3	P42704	130 kDa leucine-rich protein (LRP 130) (GP130) (Leuc	-	-	-	1	-	1	16	X
4	Q9NRX4	14 kDa phosphohistidine phosphatase (EC 3.1.3.-) (Ph	-	-	-	-	2	-	-	-
5	P31946	14-3-3 protein beta/alpha (Protein kinase C inhibitor pr	-	-	8	4	10	9	13	-
6	P62258	14-3-3 protein epsilon (14-3-3E)	-	3	13	3	10	10	12	-
7	Q04917	14-3-3 protein eta (Protein AS1)	-	-	10	6	11	4	7	-
8	P61981	14-3-3 protein gamma (Protein kinase C inhibitor prote	-	-	9	-	10	9	9	X
9	P27348	14-3-3 protein theta (14-3-3 protein tau) (14-3-3 protei	-	-	8	2	12	8	12	-
10	P63104	14-3-3 protein zeta/delta (Protein kinase C inhibitor pro	-	-	19	7	23	14	17	X
11	O60613	15 kDa selenoprotein precursor	-	-	-	-	-	-	2	-
12	Q9Y4L1	150 kDa oxygen-regulated protein precursor (Orp150)	-	-	-	-	1	-	4	X
13	Q99943	1-acyl-sn-glycerol-3-phosphate acyltransferase alpha	-	-	-	-	-	-	1	-
14	P09543	2*,3*-cyclic-nucleotide 3*-phosphodiesterase (EC 3,1,4	-	-	-	1	-	-	-	-
15	Q16698	2,4-dienoyl-CoA reductase, mitochondrial precursor (E	-	-	-	-	3	1	3	-
16	P62191	26S protease regulatory subunit 4 (P26s4) (Proteasom	-	1	-	-	-	-	-	X
17	P17980	26S protease regulatory subunit 6A (TAT-binding prote	-	-	-	-	2	-	3	X
18	P43686	26S protease regulatory subunit 6B (MIP224) (MB67-i	-	-	-	-	-	3	2	X
19	P62195	26S protease regulatory subunit 8 (Proteasome subun	-	-	-	-	1	1	2	X
20	P62333	26S protease regulatory subunit S10B (Proteasome su	-	1	-	-	3	1	5	X
21	Q99460	26S proteasome non-ATPase regulatory subunit 1 (26	-	1	-	-	-	1	3	-
22	O75832	26S proteasome non-ATPase regulatory subunit 10 (2	-	-	-	-	-	-	2	-
23	O00231	26S proteasome non-ATPase regulatory subunit 11 (2	-	-	1	-	1	1	1	X
24	O00232	26S proteasome non-ATPase regulatory subunit 12 (2	-	1	-	-	1	1	2	-
25	Q9UNM6	26S proteasome non-ATPase regulatory subunit 13 (2	-	-	1	-	2	1	1	X
26	O00487	26S proteasome non-ATPase regulatory subunit 14 (2	-	-	-	-	1	-	1	X
27	Q13200	26S proteasome non-ATPase regulatory subunit 2 (26	-	1	-	-	3	3	4	-
28	O43242	26S proteasome non-ATPase regulatory subunit 3 (26	-	-	-	-	2	10	3	-
29	Q15008	26S proteasome non-ATPase regulatory subunit 6 (26	-	-	-	-	-	2	-	-
30	P51665	26S proteasome non-ATPase regulatory subunit 7 (26	-	-	-	-	2	1	1	X
31	P48556	26S proteasome non-ATPase regulatory subunit 8 (26	-	-	-	-	1	2	1	X
32	Q13442	28 kDa heat- and acid-stable phosphoprotein (PDGF-a	-	-	-	-	-	-	2	-
33	Q02218	2-oxoglutarate dehydrogenase E1 component, mitoch	-	-	-	-	6	-	5	X
34	P42126	3,2-trans-enoyl-CoA isomerase, mitochondrial precurs	-	-	-	-	4	1	-	X
35	Q9Y3B7	39S ribosomal protein L11, mitochondrial precursor (L	-	-	-	-	-	-	2	-
36	P52815	39S ribosomal protein L12, mitochondrial precursor (L	-	-	-	-	1	1	-	X
37	Q7Z2W9	39S ribosomal protein L21, mitochondrial precursor (L	-	-	-	-	-	-	1	-
38	Q99714	3-hydroxyacyl-CoA dehydrogenase type II (EC 1.1.1.3	-	-	8	1	11	8	12	X
39	Q9BUT1	3-hydroxybutyrate dehydrogenase type 2 (EC 1.1.1.30	-	-	-	-	-	-	1	-
40	P31937	3-hydroxyisobutyrate dehydrogenase, mitochondrial pr	-	-	-	-	2	1	4	X
41	P42765	3-ketoacyl-CoA thiolase, mitochondrial (EC 2.3.1.16) (	-	-	-	-	2	-	1	-
42	P09110	3-ketoacyl-CoA thiolase, peroxisomal precursor (EC 2	-	-	-	1	-	-	-	-
43	P25325	3-mercaptopyruvate sulfurtransferase (EC 2.8.1.2) (M	-	-	1	1	1	-	-	X
44	P46783	40S ribosomal protein S10	-	-	-	-	6	1	5	-
45	P62280	40S ribosomal protein S11 - Homo sapiens (Human)	-	-	-	-	8	-	7	-
46	P25398	40S ribosomal protein S12 - Homo sapiens (Human)	-	-	-	-	1	-	4	X
47	P62277	40S ribosomal protein S13	-	-	-	-	5	-	6	-
48	P62263	40S ribosomal protein S14	-	-	-	-	7	1	9	-
49	P62841	40S ribosomal protein S15 (RIG protein) - Homo sapie	-	-	-	-	1	-	2	-
50	P62244	40S ribosomal protein S15a	-	-	-	-	3	2	7	-

51	P62249	40S ribosomal protein S16	-	-	-	-	7	1	8	-
52	P08708	40S ribosomal protein S17 - Homo sapiens (Human)	-	-	-	-	3	-	5	-
53	P62269	40S ribosomal protein S18 (Ke-3) (Ke3)	-	-	-	-	10	1	8	-
54	P39019	40S ribosomal protein S19	-	-	-	-	3	-	7	-
55	P15880	40S ribosomal protein S2 (S4) (LLRep3 protein) - Homo sapiens (Human)	-	-	-	-	3	1	5	-
56	P60866	40S ribosomal protein S20 - Homo sapiens (Human)	-	-	-	-	2	-	5	-
57	P63220	40S ribosomal protein S21	-	-	-	-	1	-	-	-
58	P62266	40S ribosomal protein S23 - Homo sapiens (Human)	-	-	-	-	1	-	-	-
59	P62847	40S ribosomal protein S24 - Homo sapiens (Human)	-	-	-	-	3	-	2	-
60	P62851	40S ribosomal protein S25	-	-	-	-	2	-	2	-
61	P62854	40S ribosomal protein S26	-	-	-	-	3	1	3	-
62	P62857	40S ribosomal protein S28	-	-	-	-	1	3	1	-
63	P23396	40S ribosomal protein S3 - Homo sapiens (Human)	-	2	-	-	9	1	12	-
64	P61247	40S ribosomal protein S3a - Homo sapiens (Human)	-	-	-	-	6	-	10	-
65	P62701	40S ribosomal protein S4, X isoform (Single copy abundant)	-	-	-	-	6	-	8	-
66	P46782	40S ribosomal protein S5	-	-	-	-	5	1	2	-
67	P62753	40S ribosomal protein S6 (Phosphoprotein NP33)	-	-	-	-	4	-	5	-
68	P62081	40S ribosomal protein S7	-	-	-	-	8	2	6	-
69	P62241	40S ribosomal protein S8	-	-	-	-	6	1	7	-
70	P46781	40S ribosomal protein S9 - Homo sapiens (Human)	-	-	-	-	4	-	3	-
71	P08865	40S ribosomal protein SA (p40) (34/67 kDa laminin receptor)	-	-	-	-	8	2	5	X
72	P08195	4F2 cell-surface antigen heavy chain (4F2hc) (Lymphocyte)	-	-	-	-	-	1	1	-
73	P49189	4-trimethylaminobutyraldehyde dehydrogenase (EC 1.4.1.1)	-	1	-	-	8	-	8	X
74	Q8TCD5	5*(3*)-deoxyribonucleotidase, cytosolic type (EC 3.1.3.1)	-	-	-	-	1	-	1	-
75	Q00013	55 kDa erythrocyte membrane protein (p55) (Membrane protein)	-	-	2	-	-	-	-	-
76	P10809	60 kDa heat shock protein, mitochondrial precursor (Hsp60)	-	-	15	1	26	15	21	X
77	P05388	60S acidic ribosomal protein P0 (L10E)	-	-	-	-	7	1	7	X
78	P05386	60S acidic ribosomal protein P1	-	-	-	-	-	1	1	-
79	P05387	60S acidic ribosomal protein P2	-	-	-	-	5	2	4	-
80	P27635	60S ribosomal protein L10 (QM protein) (Tumor suppressor)	-	-	-	-	1	-	5	-
81	P62906	60S ribosomal protein L10a (CSA-19) - Homo sapiens (Human)	-	-	-	-	1	-	1	-
82	P62913	60S ribosomal protein L11 (CLL-associated antigen KV)	-	-	-	-	6	1	5	-
83	P30050	60S ribosomal protein L12	-	-	-	-	6	3	5	-
84	P26373	60S ribosomal protein L13 (Breast basic conserved protein)	-	-	-	-	3	-	5	-
85	P50914	60S ribosomal protein L14 (CAG-ISL 7) - Homo sapiens (Human)	-	-	-	-	2	1	3	-
86	P61313	60S ribosomal protein L15 - Homo sapiens (Human)	-	-	-	-	2	-	2	-
87	P18621	60S ribosomal protein L17 (L23) - Homo sapiens (Human)	-	-	-	-	6	-	2	-
88	Q07020	60S ribosomal protein L18	-	-	-	-	1	-	3	-
89	Q02543	60S ribosomal protein L18a - Homo sapiens (Human)	-	-	-	-	4	-	3	-
90	P46778	60S ribosomal protein L21 - Homo sapiens (Human)	-	-	-	-	3	-	1	-
91	P35268	60S ribosomal protein L22 (Epstein-Barr virus small R protein)	-	-	-	-	1	1	5	-
92	P62829	60S ribosomal protein L23 (Ribosomal protein L17)	-	-	-	-	2	1	6	-
93	P62750	60S ribosomal protein L23a - Homo sapiens (Human)	-	-	-	-	5	1	2	-
94	P83731	60S ribosomal protein L24 (Ribosomal protein L30) - Homo sapiens (Human)	-	-	-	-	2	-	-	-
95	P61254	60S ribosomal protein L26	-	-	-	-	4	-	-	-
96	P61353	60S ribosomal protein L27 - Homo sapiens (Human)	-	-	-	-	3	-	-	-
97	P46776	60S ribosomal protein L27a - Homo sapiens (Human)	-	-	-	-	5	-	2	-
98	P46779	60S ribosomal protein L28 - Homo sapiens (Human)	-	-	-	-	3	-	2	-
99	P47914	60S ribosomal protein L29 (Cell surface heparin-binding protein)	-	-	-	-	2	-	1	-
100	P39023	60S ribosomal protein L3 (HIV-1 TAR RNA-binding protein)	-	-	-	-	4	-	7	-
101	P62888	60S ribosomal protein L30	-	-	-	-	3	1	3	-
102	P62910	60S ribosomal protein L32 - Homo sapiens (Human)	-	-	-	-	3	-	-	-
103	P42766	60S ribosomal protein L35 - Homo sapiens (Human)	-	-	-	-	3	1	-	-
104	P61513	60S ribosomal protein L37a - Homo sapiens (Human)	-	-	-	-	-	-	1	-
105	P63173	60S ribosomal protein L38 - Homo sapiens (Human)	-	-	-	-	2	2	4	-
106	P36578	60S ribosomal protein L4 (L1) - Homo sapiens (Human)	-	-	-	-	5	-	4	-

107	P46777	60S ribosomal protein L5 - Homo sapiens (Human)	-	1	-	-	2	-	5	-
108	Q02878	60S ribosomal protein L6 (TAX-responsive enhancer e	-	-	-	-	4	1	5	-
109	P18124	60S ribosomal protein L7 - Homo sapiens (Human)	-	-	-	-	2	-	5	-
110	P62424	60S ribosomal protein L7a (Surfeit locus protein 3) (PL	-	-	-	-	2	-	5	-
111	P62917	60S ribosomal protein L8 - Homo sapiens (Human)	-	-	-	-	4	-	2	-
112	P32969	60S ribosomal protein L9 - Homo sapiens (Human)	-	-	-	-	4	-	3	-
113	Q01813	6-phosphofructokinase type C (EC 2.7.1.11) (Phospho	-	3	3	-	-	-	1	-
114	P17858	6-phosphofructokinase, liver type (EC 2.7.1.11) (Phos	-	-	-	-	-	4	5	-
115	P52209	6-phosphogluconate dehydrogenase, decarboxylating	-	-	1	17	5	12	7	X
116	O95336	6-phosphogluconolactonase (EC 3.1.1.31) (6PGL)	-	-	4	8	7	10	9	X
117	P11021	78 kDa glucose-regulated protein precursor (GRP 78)	-	-	25	2	22	22	23	X
118	Q9NUJ1	Abhydrolase domain-containing protein 10, mitochond	-	-	-	-	1	-	-	-
119	Q8NFV4	Abhydrolase domain-containing protein 11 - Homo sap	-	-	3	1	-	1	1	-
120	Q96IU4	Abhydrolase domain-containing protein 14B (CCG1-in	-	-	2	2	6	5	6	X
121	P24752	Acetyl-CoA acetyltransferase, mitochondrial precursor	-	-	-	4	5	4	3	X
122	O00400	Acetyl-coenzyme A transporter 1 (AT-1) (Acetyl-CoA tr	-	-	-	-	-	-	1	-
123	Q13510	Acid ceramidase precursor (EC 3.5.1.23) (Acylsphingo	-	-	-	5	2	5	5	X
124	P39687	Acidic leucine-rich nuclear phosphoprotein 32 family m	-	-	-	1	5	5	7	X
125	Q92688	Acidic leucine-rich nuclear phosphoprotein 32 family m	-	-	-	1	3	5	3	-
126	O43423	Acidic leucine-rich nuclear phosphoprotein 32 family m	-	-	-	-	-	-	2	-
127	Q9BTT0	Acidic leucine-rich nuclear phosphoprotein 32 family m	-	-	-	-	4	5	5	-
128	Q99798	Aconitate hydratase, mitochondrial precursor (EC 4.2.1	-	-	-	-	6	-	13	X
129	P60709	Actin, cytoplasmic 1 (Beta-actin)	-	3	31	22	34	23	26	X
130	P63261	Actin, cytoplasmic 2 (Gamma-actin)	-	3	31	22	34	23	26	X
131	P61160	Actin-like protein 2 (Actin-related protein 2)	-	1	10	11	10	6	12	X
132	P61158	Actin-like protein 3 (Actin-related protein 3)	-	-	15	9	12	8	16	X
133	O15143	Actin-related protein 2/3 complex subunit 1B (ARP2/3	-	-	5	6	7	5	11	-
134	O15144	Actin-related protein 2/3 complex subunit 2 (ARP2/3 co	-	1	9	11	11	6	19	X
135	O15145	Actin-related protein 2/3 complex subunit 3 (ARP2/3 co	-	-	6	3	6	4	7	-
136	P59998	Actin-related protein 2/3 complex subunit 4 (ARP2/3 co	-	-	4	4	6	3	6	-
137	O15511	Actin-related protein 2/3 complex subunit 5 (ARP2/3 co	-	-	4	1	4	3	4	X
138	Q9BPX5	Actin-related protein 2/3 complex subunit 5-like protein	-	-	-	-	-	-	2	X
139	Q9P1U1	Actin-related protein 3B OS=Homo sapiens GN=ACTF	-	-	-	2	-	-	-	-
140	P53999	Activated RNA polymerase II transcriptional coactivator	-	-	-	-	3	4	5	-
141	O95433	Activator of 90 kDa heat shock protein ATPase homolog	-	-	1	-	-	1	-	X
142	P13798	Acylamino-acid-releasing enzyme (EC 3.4.19.1) (AAR	-	5	1	-	2	1	2	X
143	P45954	Acyl-CoA dehydrogenase, short/branched chain specif	-	-	-	-	2	-	-	X
144	P16219	Acyl-CoA dehydrogenase, short-chain specific, mitoch	-	-	1	-	3	1	-	X
145	P49748	Acyl-CoA dehydrogenase, very-long-chain specific, mi	-	-	-	-	-	8	2	X
146	P07108	Acyl-CoA-binding protein (ACBP) (Diazepam-binding i	-	-	-	2	2	2	4	-
147	O75608	Acyl-protein thioesterase 1 (EC 3.1.2.-) (Lysophospho	-	-	4	4	2	4	5	X
148	O95372	Acyl-protein thioesterase 2 (EC 3.1.2.-) (Lysophospho	-	-	-	-	2	-	4	X
149	Q7L5N7	Acyltransferase-like 1 (EC 2,3,1,-) - Homo sapiens (Hu	-	-	-	1	-	-	-	-
150	O14672	ADAM 10 precursor (EC 3.4.24.81) (A disintegrin and	-	-	3	-	-	-	-	-
151	O43184	ADAM 12 precursor - Homo sapiens (Human)	-	-	1	-	-	-	-	-
152	P07741	Adenine phosphoribosyltransferase (EC 2.4.2.7) (APR	-	2	7	7	10	9	10	X
153	P55263	Adenosine kinase (EC 2.7.1.20) (AK) (Adenosine 5*-p	-	1	-	-	2	-	2	X
154	P23526	Adenosylhomocysteinase (EC 3.3.1.1) (S-adenosyl-L-	-	1	-	3	2	1	4	X
155	P00568	Adenylate kinase isoenzyme 1 (EC 2.7.4.3) (ATP-AMF	-	6	5	-	4	-	1	-
156	P54819	Adenylate kinase isoenzyme 2, mitochondrial (EC 2.7.	-	-	7	4	9	11	11	X
157	P30566	Adenylosuccinate lyase (EC 4.3.2.2) (Adenylosuccinas	-	2	-	-	2	-	4	X
158	P30520	Adenylosuccinate synthetase isozyme 2 (EC 6.3.4.4) (	-	-	-	6	-	-	2	X
159	Q01518	Adenylyl cyclase-associated protein 1 (CAP 1)	-	-	12	17	17	15	22	X
160	Q9HDC9	Adipocyte plasma membrane-associated protein (BSC	-	-	-	7	1	-	5	X
161	Q9NZ08	Adipocyte-derived leucine aminopeptidase precursor (	-	-	-	2	3	7	8	-
162	Q15848	Adiponectin precursor (Adipocyte, C1q and collagen d	2	-	-	-	-	-	-	-

163	P12235	ADP/ATP translocase 1 (Adenine nucleotide translocase 1)	-	-	-	-	-	1	-	-
164	P05141	ADP/ATP translocase 2 (Adenine nucleotide translocase 2)	-	-	2	-	2	4	8	-
165	P12236	ADP/ATP translocase 3 (Adenine nucleotide translocase 3)	-	-	-	-	-	5	-	-
166	Q9BRR6	ADP-dependent glucokinase (EC 2.7.1.147) (ADPGK)	-	-	1	1	-	1	1	-
167	Q10588	ADP-ribosyl cyclase 2 precursor (EC 3.2.2.5) (Cyclic AMP 3-phosphatase)	-	-	-	1	-	-	-	-
168	P84077	ADP-ribosylation factor 1	-	3	12	-	12	9	11	-
169	P61204	ADP-ribosylation factor 3	-	-	-	-	-	-	10	-
170	P18085	ADP-ribosylation factor 4	-	-	7	-	6	4	5	-
171	P84085	ADP-ribosylation factor 5	-	-	-	-	7	4	-	-
172	P62330	ADP-ribosylation factor 6 - Homo sapiens (Human)	-	-	-	-	2	2	7	-
173	P40616	ADP-ribosylation factor-like protein 1	-	-	-	2	-	-	-	-
174	Q96BM9	ADP-ribosylation factor-like protein 8A (ADP-ribosylation factor-like protein 8A)	-	-	-	-	1	3	2	-
175	Q9NVJ2	ADP-ribosylation factor-like protein 8B (ADP-ribosylation factor-like protein 8B)	-	-	-	4	-	-	-	-
176	Q9UKK9	ADP-sugar pyrophosphatase (EC 3.6.1.13) (EC 3.6.1.13)	-	-	-	-	2	-	2	X
177	P43652	Afamin precursor (Alpha-albumin) (Alpha-Alb) - Homo sapiens	6	-	-	-	-	-	-	-
178	O43488	Aflatoxin B1 aldehyde reductase member 2 (EC 1.-.-.-) (Aflatoxin B1 aldehyde reductase member 2)	-	1	5	-	4	-	2	X
179	O00170	AH receptor-interacting protein (AIP) (Aryl-hydrocarbon receptor-interacting protein)	-	-	-	-	2	-	3	X
180	P49588	Alanyl-tRNA synthetase (EC 6.1.1.7) (Alanine--tRNA ligase)	-	1	-	-	2	-	4	X
181	P14550	Alcohol dehydrogenase [NADP+] (EC 1.1.1.2) (Aldehyde dehydrogenase)	-	-	-	-	5	-	3	X
182	P11766	Alcohol dehydrogenase class 3 chi chain (EC 1.1.1.1) (Alcohol dehydrogenase class 3 chi chain)	-	-	-	-	3	-	3	X
183	Q8IZ83	Aldehyde dehydrogenase family 16 member A1 - Homo sapiens	-	-	1	1	1	2	4	-
184	P05091	Aldehyde dehydrogenase, mitochondrial precursor (EC 1.2.1.29) (Aldehyde dehydrogenase, mitochondrial)	-	-	-	-	-	6	4	X
185	P15121	Aldose reductase (EC 1.1.1.21) (AR) (Aldehyde reductase)	-	1	1	-	8	2	6	X
186	P55008	Allograft inflammatory factor 1 (AIF-1) (Ionized calcium-binding adapter molecule 1)	-	-	-	1	1	1	-	X
187	P02763	Alpha-1-acid glycoprotein 1 precursor (AGP 1) (Orosomucoid)	5	-	-	2	-	-	1	-
188	P19652	Alpha-1-acid glycoprotein 2 precursor (AGP 2) (Orosomucoid)	3	-	-	-	-	-	-	-
189	P04217	Alpha-1B-glycoprotein precursor (Alpha-1-B glycoprotein)	11	-	-	-	-	-	1	-
190	P08697	Alpha-2-antiplasmin precursor (Alpha-2-plasmin inhibitor)	3	-	-	-	-	-	-	-
191	P02765	Alpha-2-HS-glycoprotein precursor (Fetuin-A) (Alpha-2-HS-glycoprotein)	1	-	-	-	-	-	1	-
192	P01023	Alpha-2-macroglobulin precursor (Alpha-2-M)	61	-	24	-	-	-	42	-
193	P12814	Alpha-actinin-1 (Alpha-actinin cytoskeletal isoform) (Non-muscle alpha-actinin)	-	13	56	7	18	21	41	X
194	P35609	Alpha-actinin-2 (Alpha actinin skeletal muscle isoform) (Muscle alpha-actinin)	-	-	-	-	-	-	4	-
195	O43707	Alpha-actinin-4 (Non-muscle alpha-actinin 4) (F-actin-binding protein)	-	15	23	-	14	24	33	X
196	P35611	Alpha-adducin (Erythrocyte adducin subunit alpha) - Homo sapiens	-	-	-	-	3	-	1	-
197	P61163	Alpha-centractin (Centractin) (Centrosome-associated protein)	-	-	4	-	-	1	1	X
198	P06733	Alpha-enolase (EC 4.2.1.11) (2-phospho-D-glycerate kinase)	-	4	17	16	30	25	27	X
199	P02771	Alpha-fetoprotein precursor (Alpha-fetoglobulin) (Alpha-fetoprotein)	-	-	-	1	-	2	1	X
200	P54920	Alpha-soluble NSF attachment protein (SNAP-alpha) (SNAP-25)	-	-	6	-	5	2	7	X
201	P37840	Alpha-synuclein (Non-A beta component of AD amyloid) (Synuclein)	-	6	6	-	6	-	1	X
202	Q8TCU4	Alstrom syndrome protein 1 - Homo sapiens (Human)	-	-	-	-	1	-	-	-
203	P02760	AMBIP protein precursor [Contains: Alpha-1-microglobulin]	10	-	-	-	-	-	2	-
204	Q9H4A4	Aminopeptidase B (EC 3.4.11.6) (Ap-B) (Arginyl aminopeptidase)	-	-	-	1	-	3	-	X
205	P15144	Aminopeptidase N (EC 3.4.11.2) (hAPN) (Alanyl aminopeptidase)	-	4	-	-	-	-	-	-
206	Q01432	AMP deaminase 3 (EC 3.5.4.6) (AMP deaminase isoform 3)	-	-	-	2	-	-	-	-
207	Q7Z5R6	Amyloid beta A4 precursor protein-binding family B member 1	-	-	-	-	-	-	2	-
208	P03950	Angiogenin precursor (EC 3.1.27.-) (Ribonuclease 5) (Angiogenin)	7	-	-	-	-	-	-	-
209	P01019	Angiotensinogen precursor [Contains: Angiotensin-1 (Angiotensinogen)]	3	-	-	-	1	-	4	X
210	P16157	Ankyrin-1 (Erythrocyte ankyrin) (Ankyrin-R) - Homo sapiens	-	29	6	-	9	-	-	-
211	P04083	Annexin A1 (Annexin I) (Lipocortin I) (Calpactin II) (Channellipin)	-	-	-	23	22	19	27	X
212	P50995	Annexin A11 (Annexin XI) (Calcyclin-associated annexin)	-	-	1	4	11	4	8	X
213	P07355	Annexin A2 (Annexin II) (Lipocortin II) (Calpactin I head)	-	5	-	-	18	19	27	X
214	P12429	Annexin A3 (Annexin III) (Lipocortin III) (Placental antileukemic factor)	-	-	4	24	-	5	-	X
215	P09525	Annexin A4 (Annexin IV) (Lipocortin IV) (Endonexin)	-	-	1	10	4	4	7	X
216	P08758	Annexin A5 (Annexin V) (Lipocortin V) (Endonexin II) (Placental antileukemic factor)	-	-	8	11	16	17	20	X
217	P08133	Annexin A6 (Annexin VI) (Lipocortin VI) (P68) (P70) (P71)	-	-	1	22	39	32	37	X
218	P20073	Annexin A7 (Annexin VII) (Synexin)	-	1	-	-	7	1	6	X

219	Q03518	Antigen peptide transporter 1 (APT1) (Peptide transpo	-	-	-	-	-	2	1	-
220	Q03519	Antigen peptide transporter 2 (APT2) (ATP-binding cas	-	-	-	-	-	-	2	-
221	P01008	Antithrombin-III precursor (ATIII) - Homo sapiens (Hun	8	-	-	-	-	-	1	-
222	Q10567	AP-1 complex subunit beta-1 (Adapter-related protein	-	-	3	-	-	2	4	-
223	O43747	AP-1 complex subunit gamma-1 (Adapter-related prote	-	-	-	-	-	-	1	-
224	P63010	AP-2 complex subunit beta-1 (Adapter-related protein	-	-	-	-	3	-	4	-
225	P02647	Apolipoprotein A-I precursor (Apo-AI) (ApoA-I) [Contai	31	-	-	-	-	1	27	X
226	Q8NCW5	Apolipoprotein A-I-binding protein precursor - Homo sa	-	-	-	-	-	-	2	-
227	P02652	Apolipoprotein A-II precursor (Apo-AII) (ApoA-II) [Cont	2	-	-	-	-	-	-	-
228	P06727	Apolipoprotein A-IV precursor (Apo-AIV) (ApoA-IV)	24	-	-	-	-	-	8	X
229	P04114	Apolipoprotein B-100 precursor (Apo B-100) [Contains	77	-	-	-	-	-	3	-
230	Q0VD83	Apolipoprotein B-100 receptor - Homo sapiens (Huma	-	1	-	2	-	2	4	-
231	P02656	Apolipoprotein C-III precursor (Apo-CIII) (ApoC-III) - H	1	-	-	-	-	2	3	-
232	P55056	Apolipoprotein C-IV precursor (Apo-CIV) (ApoC-IV) - H	3	-	-	-	-	-	-	-
233	P05090	Apolipoprotein D precursor (Apo-D) (ApoD) - Homo sa	5	-	-	-	-	-	-	X
234	P02649	Apolipoprotein E precursor (Apo-E) - Homo sapiens (H	16	-	-	-	-	-	5	-
235	Q13790	Apolipoprotein F precursor (Apo-F) (Lipid transfer inhib	2	-	-	-	-	-	-	-
236	O95445	Apolipoprotein M (Apo-M) (ApoM) (Protein G3a) - Hom	3	-	-	-	-	-	-	-
237	O14791	Apolipoprotein-L1 precursor (Apolipoprotein L-I) (Apoli	4	-	-	-	-	-	-	-
238	Q07812	Apoptosis regulator BAX, membrane isoform alpha	-	-	-	2	1	2	3	-
239	Q9ULZ3	Apoptosis-associated speck-like protein containing a C	-	-	-	7	4	12	9	X
240	O14727	Apoptotic protease-activating factor 1 (Apaf-1)	-	-	-	-	-	1	2	-
241	P18054	Arachidonate 12-lipoxygenase, 12S-type (EC 1.13.11.	-	-	2	-	-	-	-	-
242	P16050	Arachidonate 15-lipoxygenase (EC 1.13.11.33) (Arach	-	-	-	8	-	-	-	X
243	P09917	Arachidonate 5-lipoxygenase (EC 1.13.11.34) (5-lipox	-	-	-	-	-	2	-	-
244	P05089	Arginase-1 (EC 3.5.3.1) (Type I arginase) (Liver-type a	-	-	-	8	-	-	-	X
245	P55145	ARMET protein precursor (Arginine-rich protein) - Hom	-	-	3	-	1	4	4	-
246	O43681	Arsenical pump-driving ATPase (EC 3.6.3.16) (Arsenit	-	-	1	-	1	1	-	X
247	P17174	Aspartate aminotransferase, cytoplasmic (EC 2.6.1.1)	-	1	-	1	-	-	-	X
248	P00505	Aspartate aminotransferase, mitochondrial precursor (	-	-	1	1	4	2	8	-
249	Q9ULA0	Aspartyl aminopeptidase (EC 3.4.11.21) - Homo sapie	-	-	-	-	-	-	4	X
250	P14868	Aspartyl-tRNA synthetase (EC 6.1.1.12) (Aspartate--tF	-	-	2	-	3	-	-	X
251	Q6DD88	Atlantin-3 - Homo sapiens (Human)	-	-	-	-	-	5	1	-
252	P00846	ATP synthase a chain (EC 3.6.3.14) (ATPase protein 6	-	-	-	-	-	1	-	-
253	P25705	ATP synthase alpha chain, mitochondrial precursor (E	-	-	16	8	22	17	23	X
254	P24539	ATP synthase B chain, mitochondrial precursor (EC 3.	-	-	1	-	2	2	6	-
255	P06576	ATP synthase beta chain, mitochondrial precursor (EC	-	-	17	6	21	18	20	X
256	O75947	ATP synthase D chain, mitochondrial (EC 3.6.3.14)	-	-	3	-	9	7	9	X
257	P30049	ATP synthase delta chain, mitochondrial precursor (EC	-	-	2	1	1	2	1	X
258	P56385	ATP synthase e chain, mitochondrial (EC 3.6.3.14) - H	-	-	-	-	1	2	-	-
259	P56134	ATP synthase f chain, mitochondrial (EC 3.6.3.14)	-	-	-	-	1	2	2	-
260	P36542	ATP synthase gamma chain, mitochondrial precursor (	-	-	2	1	7	1	5	-
261	P48047	ATP synthase O subunit, mitochondrial precursor (EC	-	-	5	2	8	7	11	-
262	O75964	ATP synthase subunit g, mitochondrial (EC 3.6.3.14) (	-	-	3	-	1	5	4	-
263	Q8N139	ATP-binding cassette sub-family A member 6 - Homo	-	-	-	1	-	-	-	-
264	Q8NE71	ATP-binding cassette sub-family F member 1 (ATP-bir	-	-	-	-	1	-	-	-
265	P53396	ATP-citrate synthase (EC 2.3.3.8) (ATP-citrate (pro-S-	-	2	-	1	1	4	8	-
266	P12956	ATP-dependent DNA helicase 2 subunit 1 (EC 3.6.1.-)	-	-	-	-	19	1	23	X
267	P13010	ATP-dependent DNA helicase 2 subunit 2 (EC 3.6.1.-)	-	-	-	-	16	5	17	-
268	Q08211	ATP-dependent RNA helicase A (EC 3.6.1.-) (Nuclear	-	-	-	-	-	-	1	-
269	Q9NUU7	ATP-dependent RNA helicase DDX19A (EC 3,6,1,-) (D	-	-	-	-	-	1	-	X
270	O00148	ATP-dependent RNA helicase DDX39 (EC 3.6.1.-) (DE	-	-	-	-	-	-	2	-
271	O14497	AT-rich interactive domain-containing protein 1A (ARIL	-	-	-	1	-	-	-	-
272	O75882	Attractin precursor (Mahogany homolog) (DPPT-L) - H	7	-	-	-	-	-	-	-
273	Q9NT62	Autophagy-related protein 3 (APG3-like) (hApg3) (Prot	-	-	-	-	-	4	-	-
274	O95352	Autophagy-related protein 7 (APG7-like) (Ubiquitin-act	-	-	-	-	-	-	1	-

275	P20160	Azurocidin precursor (Cationic antimicrobial protein CA	-	-	-	3	-	2	1	-
276	P17213	Bactericidal permeability-increasing protein precursor	-	-	-	6	-	-	-	-
277	P02730	Band 3 anion transport protein (Anion exchange protei	-	12	-	-	12	-	-	-
278	O75531	Barrier-to-autointegration factor (Breakpoint cluster reg	-	-	-	-	2	3	2	-
279	P51572	B-cell receptor-associated protein 31 (BCR-associated	-	-	-	2	1	1	4	-
280	Q13884	Beta-1-syntrophin (59 kDa dystrophin-associated prote	-	-	-	-	-	-	1	-
281	P02749	Beta-2-glycoprotein 1 precursor (Beta-2-glycoprotein I	6	-	-	-	-	-	3	-
282	P61769	Beta-2-microglobulin precursor [Contains: Beta-2-micr	1	-	3	1	-	2	3	X
283	P25098	Beta-adrenergic receptor kinase 1 - Homo sapiens (Hu	-	-	-	-	-	-	1	-
284	Q96KN2	Beta-Ala-His dipeptidase precursor (EC 3.4.13.20) (Ca	4	-	-	-	-	-	-	-
285	P49407	Beta-arrestin-1 (Arrestin, beta 1)	-	-	1	-	-	-	1	-
286	P32121	Beta-arrestin-2 (Arrestin beta 2) - Homo sapiens (Hum	-	-	-	-	1	-	-	-
287	P42025	Beta-centractin (Actin-related protein 1B) (ARP1B)	-	-	3	-	-	-	-	X
288	P13929	Beta-enolase (EC 4.2.1.11) (2-phospho-D-glycerate hy	-	2	5	4	-	-	5	-
289	P16278	Beta-galactosidase precursor (EC 3.2.1.23) (Lactase)	-	-	-	-	-	3	1	-
290	P06865	Beta-hexosaminidase alpha chain precursor (EC 3.2.1	-	-	-	-	-	1	-	-
291	P07686	Beta-hexosaminidase beta chain precursor (EC 3.2.1.4	-	-	-	-	-	4	1	X
292	Q9HBI1	Beta-parvin (Affixin)	-	-	15	-	1	-	4	-
293	P55957	BH3 interacting domain death agonist (BID)	-	2	4	2	2	4	3	X
294	P07814	Bifunctional aminoacyl-tRNA synthetase [Includes: Glu	-	-	-	-	5	-	1	-
295	P31939	Bifunctional purine biosynthesis protein PURH [Include	-	3	-	-	5	-	4	X
296	P19835	Bile salt-activated lipase precursor - Homo sapiens (H	-	-	-	-	-	-	1	-
297	P53004	Biliverdin reductase A precursor (EC 1.3.1.24) (Biliver	-	-	1	1	4	3	1	X
298	P50583	Bis(5*-nucleosyl)-tetraphosphatase [asymmetrical] (EC	-	-	-	-	2	-	1	-
299	P07738	Bisphosphoglycerate mutase (EC 5.4.2.4) (2,3-bisphos	-	3	-	-	6	-	-	-
300	Q13867	Bleomycin hydrolase (EC 3.4.22.40) (BLM hydrolase)	-	1	-	-	-	-	1	X
301	Q9H3K6	BolA-like protein 2	-	-	-	-	2	3	2	X
302	P13727	Bone-marrow proteoglycan precursor (BMPG) (Proteo	-	-	-	5	-	1	-	-
303	P80723	Brain acid soluble protein 1 (BASP1 protein) (Neurona	-	-	-	1	-	-	1	-
304	Q9UBW5	Bridging integrator 2 (Breast cancer-associated protei	-	-	9	1	-	-	3	-
305	P11586	C-1-tetrahydrofolate synthase, cytoplasmic (C1-THF s	-	1	-	2	-	-	3	-
306	P04003	C4b-binding protein alpha chain precursor (C4bp) (Pro	9	-	-	-	-	-	-	-
307	P21730	C5a anaphylatoxin chemotactic receptor - Homo sapie	-	-	-	1	-	-	-	-
308	P49593	Ca(2+)/calmodulin-dependent protein kinase phosphat	-	-	2	-	1	1	1	-
309	P27708	CAD protein [Includes: Glutamine-dependent carbamo	-	-	-	-	-	1	-	-
310	P63098	Calcineurin subunit B isoform 1 (Protein phosphatase	-	-	-	-	1	-	-	-
311	O75746	Calcium-binding mitochondrial carrier protein Aralar1 (	-	-	-	-	2	-	-	-
312	Q6NUK1	Calcium-binding mitochondrial carrier protein SCA-MC-	-	-	-	1	-	2	3	-
313	Q9Y376	Calcium-binding protein 39 (Protein Mo25) - Homo sap	-	-	-	2	-	-	-	X
314	Q9ULU8	Calcium-dependent secretion activator 1 (Calcium-dep	-	-	-	-	-	-	1	-
315	Q9Y2V2	Calcium-regulated heat stable protein 1 (Calcium-regu	-	-	-	1	2	-	1	-
316	P06703	Calcyclin (Prolactin receptor-associated protein) (PRA	-	-	-	-	2	6	-	X
317	Q9HB71	Calcyclin-binding protein (CacyBP) (hCacyBP) (Siah-ir	-	-	1	-	3	2	1	-
318	Q05682	Caldesmon (CDM)	-	1	7	-	-	-	-	X
319	P31949	Calgizzarin (S100 calcium-binding protein A11) (S100	-	-	-	3	2	6	3	-
320	P05109	Calgranulin A (Migration inhibitory factor-related protei	-	1	1	13	3	15	12	X
321	P06702	Calgranulin B (Migration inhibitory factor-related protei	-	-	-	14	5	16	11	X
322	P62158	Calmodulin (CaM)	-	1	3	1	3	5	4	-
323	P27824	Calnexin precursor (Major histocompatibility complex c	-	-	5	-	2	8	10	-
324	P60903	Calpactin I light chain (S100 calcium-binding protein A	-	-	-	-	-	4	2	X
325	P04632	Calpain small subunit 1 (CSS1) (Calcium-dependent p	-	1	7	4	10	4	7	X
326	P07384	Calpain-1 catalytic subunit (EC 3.4.22.52) (Calpain-1 k	-	2	6	3	3	4	11	-
327	P17655	Calpain-2 catalytic subunit precursor (EC 3.4.22.53) (C	-	-	-	-	2	2	7	-
328	P20810	Calpastatin (Calpain inhibitor) (Sperm BS-17 compone	-	-	-	-	-	2	7	-
329	Q99439	Calponin-2 (Calponin H2, smooth muscle) (Neutral cal	-	-	10	6	10	1	8	X
330	P27797	Calreticulin precursor (CRP55) (Calregulin) (HACBP) (	-	-	7	3	4	7	5	X

331	P10644	cAMP-dependent protein kinase type I-alpha regulator	-	-	3	-	1	2	2	X
332	P31323	cAMP-dependent protein kinase type II-beta regulatory	-	-	2	-	-	-	-	-
333	P17612	cAMP-dependent protein kinase, alpha-catalytic subun	-	-	-	-	-	-	1	-
334	P22694	cAMP-dependent protein kinase, beta-catalytic subuni	-	-	-	-	-	-	1	-
335	Q6JBY9	Capz-interacting protein - Homo sapiens (Human)	-	-	-	-	-	-	1	-
336	P00915	Carbonic anhydrase 1 (EC 4.2.1.1) (Carbonic anhydra	-	11	6	-	16	5	1	X
337	P00918	Carbonic anhydrase 2 (EC 4.2.1.1) (Carbonic anhydra	-	7	9	-	12	2	4	X
338	P16152	Carbonyl reductase [NADPH] 1 (EC 1.1.1.184) (NADP	-	1	5	-	8	2	9	X
339	O75828	Carbonyl reductase [NADPH] 3 (EC 1.1.1.184) (NADP	-	-	-	-	-	-	3	X
340	Q96IY4	Carboxypeptidase B2 precursor (EC 3,4,17,20) (Carbo	2	-	-	-	-	-	-	-
341	P22792	Carboxypeptidase N subunit 2 precursor (Carboxypep	8	-	-	-	-	-	-	X
342	P13688	Carcinoembryonic antigen-related cell adhesion molec	-	-	-	2	-	-	-	-
343	P40199	Carcinoembryonic antigen-related cell adhesion molec	-	-	-	2	-	-	-	-
344	P31997	Carcinoembryonic antigen-related cell adhesion molec	-	-	-	2	-	-	-	-
345	Q8N3K9	Cardiomyopathy-associated protein 5 - Homo sapiens	-	-	-	-	-	-	2	-
346	P67870	Casein kinase II subunit beta (CK II beta) (Phosvitin) (	-	-	1	-	-	-	-	-
347	P29466	Caspase-1 precursor (EC 3.4.22.36) (CASP-1) (Interle	-	-	-	-	2	1	-	X
348	P42574	Caspase-3 precursor (EC 3.4.22.-) (CASP-3) (Apopair	-	-	2	-	-	-	1	X
349	Q9BXW7	Cat eye syndrome critical region protein 5 precursor -	-	-	-	-	-	-	1	-
350	P04040	Catalase (EC 1.11.1.6)	-	17	4	9	21	13	11	X
351	P21964	Catechol O-methyltransferase (EC 2.1.1.6)	-	-	-	-	2	6	3	X
352	P49913	Cathelicidin antimicrobial peptide precursor (18 kDa ca	-	-	-	5	-	1	-	-
353	P07858	Cathepsin B precursor (EC 3.4.22.1) (Cathepsin B1) (A	-	-	-	-	4	4	4	X
354	P07339	Cathepsin D precursor (EC 3.4.23.5) [Contains: Cathe	-	-	1	2	4	8	6	X
355	P08311	Cathepsin G precursor (EC 3.4.21.20) (CG) - Homo sa	-	-	-	6	-	1	-	-
356	P09668	Cathepsin H precursor (EC 3.4.22.16) [Contains: Cath	-	-	-	-	1	1	2	-
357	P25774	Cathepsin S precursor (EC 3.4.22.27)	-	-	-	3	3	7	6	X
358	Q9UBR2	Cathepsin Z precursor (EC 3.4.22.-) (Cathepsin X) (Ca	-	-	-	1	-	2	2	X
359	Q8N6Q3	CD177 antigen OS=Homo sapiens GN=CD177 PE=1	-	-	-	1	-	-	-	-
360	Q15762	CD226 antigen precursor (DNAX accessory molecule	-	-	1	-	-	-	-	-
361	P16070	CD44 antigen precursor (Phagocytic glycoprotein I) (P	-	1	-	-	1	3	3	-
362	O43866	CD5 antigen-like precursor (SP-alpha) (CT-2) (IgM-ass	1	-	-	-	-	-	-	-
363	P08962	CD63 antigen (Melanoma-associated antigen ME491)	-	-	-	2	-	-	-	-
364	P21926	CD9 antigen (p24) (Leukocyte antigen MIC3) (Motility-	-	-	2	-	-	-	2	-
365	P48960	CD97 antigen precursor (Leukocyte antigen CD97) - H	-	-	-	-	-	2	2	-
366	P14209	CD99 antigen precursor (T-cell surface glycoprotein E	-	-	1	-	1	-	-	-
367	Q9NV96	Cell cycle control protein 50A (Transmembrane protei	-	-	-	1	-	-	-	-
368	P60953	Cell division control protein 42 homolog precursor (G2	-	-	3	1	5	4	5	X
369	Q99741	Cell division control protein 6 homolog (CDC6-related	1	-	-	-	-	-	-	-
370	P62633	Cellular nucleic acid-binding protein (CNBP) (Zinc fing	-	-	-	-	2	4	5	-
371	Q15027	Centaurin-beta 1 (Cnt-b1) - Homo sapiens (Human)	-	1	2	-	4	-	1	-
372	Q96P48	Centaurin-delta 2 (Cnt-d2) (Arf-GAP, Rho-GAP, ankyri	-	-	-	-	-	2	4	-
373	P00450	Ceruloplasmin precursor (EC 1.16.3.1) (Ferroxidase)	39	-	-	-	-	-	13	X
374	O76074	cGMP-specific 3*,5*-cyclic phosphodiesterase (EC 3.1	-	-	1	-	-	-	-	-
375	Q9BY43	Charged multivesicular body protein 4a (Chromatin-mo	-	-	-	-	1	1	-	-
376	Q9H444	Charged multivesicular body protein 4b (Chromatin-mo	-	-	-	-	1	-	1	-
377	Q96FZ7	Charged multivesicular body protein 6 (Chromatin-mo	-	-	1	-	-	-	-	-
378	P36222	Chitinase-3-like protein 1 precursor (Cartilage glycopro	-	-	-	11	-	-	-	-
379	Q13231	Chitotriosidase-1 precursor (EC 3.2.1.14) (Chitinase-1	-	-	-	4	-	-	-	-
380	O00299	Chloride intracellular channel protein 1 (Nuclear chlorid	-	2	6	4	8	6	7	X
381	Q9Y696	Chloride intracellular channel protein 4 (Intracellular ch	-	-	6	-	-	-	1	X
382	Q9NZA1	Chloride intracellular channel protein 5 - Homo sapiens	-	-	-	-	-	1	-	-
383	Q8WWI5	Choline transporter-like protein 1 (Solute carrier family	-	-	-	-	-	1	1	-
384	Q8IWA5	Choline transporter-like protein 2 (Solute carrier family	-	-	-	3	-	-	-	-
385	P83916	Chromobox protein homolog 1 (Heterochromatin prote	-	-	-	-	1	-	-	-
386	Q13185	Chromobox protein homolog 3 (Heterochromatin prote	-	-	-	-	3	3	4	X

387	O75390	Citrate synthase, mitochondrial precursor (EC 2.3.3.1)	-	-	1	2	5	3	5	-
388	Q00610	Clathrin heavy chain 1 (CLH-17)	-	4	10	-	13	25	45	-
389	P53675	Clathrin heavy chain 2 (CLH-22)	-	-	-	-	-	-	11	-
390	Q14677	Clathrin interactor 1 (Epsin-4) (Epsin-related protein) (	-	-	-	-	1	-	1	-
391	O43809	Cleavage and polyadenylation specificity factor 5 (Clea	-	-	-	-	1	-	3	-
392	Q16630	Cleavage and polyadenylation specificity factor 6 (Clea	-	-	-	-	1	-	-	-
393	P10909	Clusterin precursor (Complement-associated protein S	17	-	7	-	-	-	7	X
394	Q99417	C-Myc-binding protein (Associate of Myc 1) (AMY-1)	-	-	-	-	-	1	1	-
395	O43598	c-Myc-responsive protein Rcl	-	-	-	-	3	1	1	X
396	Q14019	Coactosin-like protein	-	-	6	6	6	9	10	X
397	P00740	Coagulation factor IX precursor (EC 3,4,21,22) (Christ	4	-	-	-	-	-	-	-
398	P12259	Coagulation factor V precursor (Activated protein C co	3	-	7	-	-	-	-	-
399	P00742	Coagulation factor X precursor (EC 3,4,21,6) (Stuart fa	1	-	-	-	-	-	-	-
400	P00748	Coagulation factor XII precursor (EC 3,4,21,38) (Hage	4	-	-	-	-	-	-	-
401	P00488	Coagulation factor XIII A chain precursor (EC 2.3.2.13	-	-	29	-	4	6	14	X
402	P05160	Coagulation factor XIII B chain precursor (Protein-gluta	2	-	-	-	-	-	-	-
403	P53621	Coatomer subunit alpha (Alpha-coat protein) (Alpha-C	-	-	-	-	-	-	8	-
404	P53618	Coatomer subunit beta (Beta-coat protein) (Beta-COP)	-	-	-	-	3	4	5	-
405	O14579	Coatomer subunit epsilon (Epsilon-coat protein) (Epsil	-	-	-	-	-	-	1	X
406	Q9Y678	Coatomer subunit gamma (Gamma-coat protein) (Gan	-	-	-	1	1	1	5	-
407	Q9UBF2	Coatomer subunit gamma-2 (Gamma-2 coat protein) (	-	-	-	-	-	-	2	-
408	P61923	Coatomer subunit zeta-1 (Zeta-1 coat protein) (Zeta-1	-	-	-	-	1	2	1	-
409	P23528	Cofilin-1 (Cofilin, non-muscle isoform) (18 kDa phosph	1	4	14	11	16	17	18	X
410	Q9Y281	Cofilin-2 (Cofilin, muscle isoform)	-	-	-	-	-	-	7	X
411	Q96CT7	Coiled-coil domain-containing protein 124 - Homo sapi	-	-	-	-	1	-	-	-
412	Q9Y6H1	Coiled-coil-helix-coiled-coil-helix domain-containing pr	-	-	-	-	-	1	1	-
413	Q9BWP8	Collectin-11 precursor - Homo sapiens (Human)	1	-	-	-	-	-	-	-
414	Q8N668	COMM domain-containing protein 1 (Protein Murr1) - H	-	-	-	-	-	1	-	-
415	Q9UBI1	COMM domain-containing protein 3 (Bup protein) (PIL	-	-	-	-	-	2	1	X
416	Q9P000	COMM domain-containing protein 9	-	-	-	-	1	1	1	-
417	P02745	Complement C1q subcomponent subunit A precursor	1	-	-	-	-	-	-	-
418	P02746	Complement C1q subcomponent subunit B precursor	7	-	1	-	-	-	-	-
419	P02747	Complement C1q subcomponent subunit C precursor	4	-	-	-	-	-	-	-
420	P00736	Complement C1r subcomponent precursor (EC 3,4,21	3	-	-	-	-	-	-	X
421	P09871	Complement C1s subcomponent precursor (EC 3,4,21	2	-	-	-	-	-	-	X
422	P06681	Complement C2 precursor (EC 3,4,21,43) (C3/C5 com	3	-	-	-	-	-	-	-
423	P01024	Complement C3 precursor [Contains: Complement C3	89	-	5	-	-	-	27	X
424	P0C0L4	Complement C4-A precursor (Acidic complement C4)	48	-	-	-	-	-	5	X
425	P0C0L5	Complement C4-B precursor (Basic complement C4) [	50	-	-	-	-	-	-	X
426	P01031	Complement C5 precursor [Contains: Complement C5	16	-	-	-	-	-	-	-
427	Q07021	Complement component 1 Q subcomponent-binding p	-	-	1	-	2	-	1	-
428	P13671	Complement component C6 precursor - Homo sapiens	8	-	-	-	-	-	-	-
429	P10643	Complement component C7 precursor - Homo sapiens	2	-	-	-	-	-	-	-
430	P07357	Complement component C8 alpha chain precursor (Co	2	-	-	-	-	-	-	-
431	P07358	Complement component C8 beta chain precursor (Cor	2	-	-	-	-	-	-	-
432	P07360	Complement component C8 gamma chain precursor	7	-	-	-	-	-	-	-
433	P02748	Complement component C9 precursor [Contains: Com	7	-	-	-	-	-	-	-
434	P00751	Complement factor B precursor (EC 3.4.21.47) (C3/C5	18	-	-	-	-	-	1	X
435	P00746	Complement factor D precursor (EC 3,4,21,46) (C3 co	5	-	-	-	-	-	-	-
436	P08603	Complement factor H precursor (H factor 1) - Homo sa	36	-	1	-	-	-	3	-
437	Q03591	Complement factor H-related protein 1 precursor (FHR	5	-	-	-	-	-	-	-
438	P36980	Complement factor H-related protein 2 precursor (FHR	3	-	-	-	-	-	-	-
439	Q9BXR6	Complement factor H-related protein 5 precursor (FHR	2	-	-	-	-	-	-	-
440	P05156	Complement factor I precursor (EC 3.4.21.45) (C3B/C	9	-	-	-	-	-	-	X
441	P78357	Contactin-associated protein 1 precursor (Caspr) (Cas	-	-	-	1	-	-	-	-
442	P61201	COP9 signalosome complex subunit 2 (Signalosome s	-	-	-	-	2	-	-	-

443	Q9BT78	COP9 signalosome complex subunit 4 (Signalosome s	-	1	-	-	2	-	-	X
444	Q7L5N1	COP9 signalosome complex subunit 6 (Signalosome s	-	-	1	-	1	-	-	X
445	Q99627	COP9 signalosome complex subunit 8 (Signalosome s	-	-	1	-	2	2	-	X
446	Q99829	Copine-1 (Copine I)	-	-	1	2	4	4	5	X
447	Q96FN4	Copine-2 (Copine II) - Homo sapiens (Human)	-	-	-	2	-	-	-	-
448	O75131	Copine-3 (Copine III)	-	-	-	5	3	3	2	-
449	Q96A23	Copine-4 (Copine IV) (Copine-8) - Homo sapiens (Hur	-	-	-	1	-	-	-	-
450	Q9NTM9	Copper homeostasis protein cutC homolog - Homo sa	-	-	-	-	1	-	-	-
451	O75367	Core histone macro-H2A.1 (Histone macroH2A1) (mH	-	-	-	1	-	-	1	-
452	Q13951	Core-binding factor subunit beta (CBF-beta) (Polyoma	-	-	-	-	2	1	-	X
453	P31146	Coronin-1A (Coronin-like protein p57) (Coronin-like pro	-	-	3	9	14	3	12	X
454	Q9ULV4	Coronin-1C (Coronin-3) (hCRNN4)	-	-	8	-	-	-	-	X
455	P57737	Coronin-7 (70 kDa WD repeat tumor rejection antigen	-	-	-	2	2	2	3	X
456	P08185	Corticosteroid-binding globulin precursor (CBG) (Trans	4	-	-	-	-	-	-	-
457	P02741	C-reactive protein precursor [Contains: C-reactive prot	1	-	-	-	-	-	-	-
458	P46109	Crk-like protein	-	-	4	-	-	-	1	X
459	Q13363	C-terminal-binding protein 1 (EC 1.1.1.-) (CtBP1) - Hor	-	-	-	-	2	-	-	-
460	Q9Y240	C-type lectin domain family 11 member A precursor (S	-	-	1	-	-	-	-	-
461	Q13620	Cullin-4B - Homo sapiens (Human)	-	-	-	-	1	-	1	-
462	Q86VP6	Cullin-associated NEDD8-dissociated protein 1 (Cullin	-	7	-	-	7	3	16	-
463	P55273	Cyclin-dependent kinase 4 inhibitor D (p19-INK4d) - H	-	-	1	-	-	-	-	-
464	P01040	Cystatin A (Stefin A) (Cystatin AS)	-	-	-	2	1	3	1	-
465	P04080	Cystatin B (Liver thiol proteinase inhibitor) (CPI-B) (Ste	-	-	-	2	3	5	4	X
466	P01034	Cystatin C precursor (Neuroendocrine basic polypeptid	4	-	-	-	-	-	-	-
467	Q15828	Cystatin M precursor (Cystatin E) - Homo sapiens (Hu	1	-	-	-	-	-	-	-
468	P21291	Cysteine and glycine-rich protein 1 (Cysteine-rich prote	-	-	8	-	2	-	1	X
469	P49589	Cysteinyl-tRNA synthetase, cytoplasmic (EC 6.1.1.16)	-	-	-	-	-	-	2	-
470	P32320	Cytidine deaminase (EC 3.5.4.5) (Cytidine aminohydro	-	-	-	2	-	2	1	-
471	P04839	Cytochrome b-245 heavy chain (p22 phagocyte B-cyto	-	-	-	5	1	12	7	-
472	P13498	Cytochrome b-245 light chain (p22 phagocyte B-cyto	-	-	-	1	-	1	-	-
473	O43169	Cytochrome b5 outer mitochondrial membrane isoform	-	-	1	-	3	2	2	-
474	P99999	Cytochrome c	-	-	1	-	1	2	7	-
475	P20674	Cytochrome c oxidase polypeptide Va, mitochondrial p	-	-	-	-	2	3	3	X
476	P10606	Cytochrome c oxidase polypeptide Vb, mitochondrial p	-	-	-	-	1	3	2	-
477	P12074	Cytochrome c oxidase polypeptide VIa-liver, mitochon	-	-	-	-	-	2	-	-
478	P14406	Cytochrome c oxidase polypeptide VIIa-liver/heart, mit	-	-	-	-	-	2	-	-
479	P00403	Cytochrome c oxidase subunit 2 (EC 1.9.3.1) (Cytochr	-	-	-	-	4	3	5	-
480	P13073	Cytochrome c oxidase subunit IV isoform 1, mitochond	-	-	-	-	3	3	2	-
481	P14854	Cytochrome c oxidase subunit VIb isoform 1 (EC 1.9.3	-	-	-	-	1	3	-	-
482	P08574	Cytochrome c1, heme protein, mitochondrial precursor	-	-	-	-	-	1	4	-
483	Q9HBI6	Cytochrome P450 4F11 - Homo sapiens (Human)	-	-	-	1	-	-	-	-
484	P78329	Cytochrome P450 4F2 (EC 1.14.13.30) (CYPIVF2) (Le	-	-	-	1	-	-	-	-
485	Q08477	Cytochrome P450 4F3 - Homo sapiens (Human)	-	-	-	5	-	-	-	-
486	P98187	Cytochrome P450 4F8 OS=Homo sapiens GN=CYP4F	-	-	-	2	-	-	-	-
487	Q8IUI8	Cytokine receptor-like factor 3 - Homo sapiens (Huma	-	-	5	-	4	1	-	-
488	P50453	Cytoplasmic antiproteinase 3 (CAP3) (CAP-3) (Protea	-	-	1	-	7	4	11	X
489	O14576	Cytoplasmic dynein 1 intermediate chain 1 - Homo sap	-	1	-	-	-	-	-	-
490	Q13409	Cytoplasmic dynein 1 intermediate chain 2 (Dynein int	-	1	-	-	-	-	2	X
491	Q8NCM8	Cytoplasmic dynein 2 heavy chain 1 - Homo sapiens (	-	-	-	-	1	-	-	-
492	Q7L576	Cytoplasmic FMR1-interacting protein 1 - Homo sapier	-	-	-	-	-	3	1	-
493	Q96F07	Cytoplasmic FMR1-interacting protein 2 - Homo sapier	-	-	-	-	-	-	1	-
494	P28838	Cytosol aminopeptidase (EC 3.4.11.1) (Leucine amino	-	-	1	-	1	1	3	X
495	Q96KP4	Cytosolic nonspecific dipeptidase (Glutamate carbo	-	-	-	-	5	4	8	X
496	P47712	Cytosolic phospholipase A2 (cPLA2) (Phospholipase A	-	-	-	-	1	-	-	-
497	P49902	Cytosolic purine 5*-nucleotidase - Homo sapiens (Hum	-	-	-	1	-	-	-	-
498	Q8N465	D-2-hydroxyglutarate dehydrogenase, mitochondrial p	-	-	1	-	1	-	-	-

499	O43175	D-3-phosphoglycerate dehydrogenase (EC 1.1.1.95) (D-3-PGADH)	-	-	-	-	-	1	-	X
500	Q96EP5	DAZ-associated protein 1 (Deleted in azoospermia-associated gene X chromosome)	-	-	-	-	2	-	1	-
501	Q5TDH0	DDI1 homolog 2 - Homo sapiens (Human)	-	1	-	-	-	-	-	-
502	P30046	D-dopachrome decarboxylase (EC 4.1.1.84) (D-dopachrome decarboxylase)	-	-	-	3	2	3	3	X
503	Q92608	Dedicator of cytokinesis protein 2	-	-	-	-	-	1	2	-
504	Q9BTZ2	Dehydrogenase/reductase SDR family member 4 (EC 1.1.1.179)	-	-	-	-	-	-	2	-
505	Q9Y394	Dehydrogenase/reductase SDR family member 7 precursor	-	-	-	-	-	1	-	-
506	Q8NBQ5	Dehydrogenase/reductase SDR family member 8 precursor	-	-	-	1	-	1	-	-
507	P54886	Delta 1-pyrroline-5-carboxylate synthetase (P5CS) (Ala1)	-	-	-	-	-	-	1	-
508	Q13011	Delta3,5-delta2,4-dienoyl-CoA isomerase, mitochondrial	1	-	6	1	10	8	8	X
509	P13716	Delta-aminolevulinic acid dehydratase (EC 4.2.1.24) (F	-	4	10	-	9	-	-	X
510	P27707	Deoxycytidine kinase (EC 2.7.1.74) (dCK) - Homo sap	-	-	-	-	-	1	1	-
511	P32321	Deoxycytidylate deaminase (EC 3.5.4.12) (dCMP deami	-	-	2	-	-	1	1	X
512	P33316	Deoxyuridine 5'-triphosphate nucleotidohydrolase, mit	-	-	-	-	3	1	1	X
513	Q07507	Dermatopontin precursor - Homo sapiens (Human)	3	-	-	-	-	-	-	-
514	P60981	Destrin (Actin-depolymerizing factor) (ADF)	-	-	5	-	2	-	7	X
515	Q9Y295	Developmentally-regulated GTP-binding protein 1 (DR	-	-	-	-	-	1	1	-
516	Q9NR28	Diablo homolog, mitochondrial precursor (Second mito	-	-	2	-	2	2	3	-
517	P23743	Diacylglycerol kinase alpha (EC 2.7.1.107) (Diglycerid	-	-	-	-	3	-	4	-
518	P49619	Diacylglycerol kinase gamma - Homo sapiens (Human)	-	-	1	-	-	-	-	-
519	Q9H4E7	Differentially expressed in FDCP 6 - Homo sapiens (H	-	-	-	-	1	-	1	-
520	P09622	Dihydrolipoyl dehydrogenase, mitochondrial precursor	-	-	-	1	1	1	2	X
521	P36957	Dihydrolipoyllysine-residue succinyltransferase compo	-	-	-	-	3	-	-	X
522	P09417	Dihydropteridine reductase (EC 1.5.1.34) (HDHPR) (Q	-	-	-	-	1	-	1	X
523	Q16555	Dihydropyrimidinase-related protein 2 (DRP-2) (Collap	-	-	2	-	2	2	3	X
524	Q3LXA3	Dihydroxyacetone kinase (EC 2.7.1.29) (Glycerone kin	-	-	-	-	1	-	-	X
525	Q01459	Di-N-acetylchitobiase precursor - Homo sapiens (Hum	-	-	-	1	-	-	-	-
526	P53634	Dipeptidyl-peptidase 1 precursor (EC 3.4.14.1) (Dipep	-	-	1	4	1	2	4	-
527	Q9UHL4	Dipeptidyl-peptidase 2 precursor (EC 3.4.14.2) (Dipep	-	-	1	2	-	1	2	-
528	Q9NY33	Dipeptidyl-peptidase 3 (EC 3.4.14.4) (Dipeptidyl-peptid	-	-	-	-	-	1	2	-
529	Q95989	Diphosphoinositol polyphosphate phosphohydrolase 1	-	-	-	2	-	-	-	-
530	Q8NFP7	Diphosphoinositol polyphosphate phosphohydrolase 3	-	-	-	-	-	-	1	-
531	Q14689	Disco-interacting protein 2 homolog A - Homo sapiens	-	-	-	-	-	1	-	-
532	P26358	DNA (cytosine-5)-methyltransferase 1 (EC 2.1.1.37) (D	-	-	1	-	-	-	-	-
533	Q16531	DNA damage-binding protein 1 (Damage-specific DNA	-	-	-	-	1	2	3	-
534	Q9UBZ9	DNA repair protein REV1 - Homo sapiens (Human)	-	-	-	1	-	-	-	-
535	Q13472	DNA topoisomerase 3-alpha (EC 5.99.1.2) (DNA topoi	-	-	-	-	1	-	-	-
536	P27695	DNA-(apurinic or apyrimidinic site) lyase (EC 4.2.99.18	-	-	-	3	7	1	9	-
537	Q9UBS4	DnaJ homolog subfamily B member 11 precursor (ER-	-	-	1	-	-	1	-	X
538	P59910	DnaJ homolog subfamily B member 13 - Homo sapien	-	-	-	-	-	1	-	-
539	Q9NVM6	DnaJ homolog subfamily C member 17 - Homo sapien	-	-	-	-	-	1	-	-
540	Q9H3Z4	DnaJ homolog subfamily C member 5 (Cysteine string	-	-	-	2	-	1	1	-
541	O75937	DnaJ homolog subfamily C member 8 (Splicing proteir	-	-	-	-	3	-	6	-
542	O60496	Docking protein 2 (Downstream of tyrosine kinase 2) (	-	-	3	-	-	-	1	X
543	Q7L591	Docking protein 3 (Downstream of tyrosine kinase 3) -	-	-	2	1	-	-	-	-
544	O60762	Dolichol-phosphate mannosyltransferase (EC 2.4.1.83)	-	-	-	-	-	-	2	-
545	P39656	Dolichyl-diphosphooligosaccharide--protein glycosyltra	-	-	-	1	-	4	3	-
546	P04844	Dolichyl-diphosphooligosaccharide--protein glycosyltra	-	-	1	1	1	10	-	X
547	P04843	Dolichyl-diphosphooligosaccharide--protein glycosyltra	-	-	-	1	5	17	10	X
548	Q9C005	Dpy-30-like protein - Homo sapiens (Human)	-	-	-	-	-	1	1	-
549	Q16643	Drebrin (Developmentally-regulated brain protein) - Ho	-	-	2	-	-	-	-	-
550	Q9UJU6	Drebrin-like protein (SH3 domain-containing protein 7)	-	-	4	2	-	-	2	X
551	Q02750	Dual specificity mitogen-activated protein kinase kinas	-	-	-	-	-	-	2	-
552	P46734	Dual specificity mitogen-activated protein kinase kinas	-	-	-	1	2	-	-	-
553	P51452	Dual specificity protein phosphatase 3 (EC 3.1.3.48) (E	-	-	7	-	-	3	2	X
554	Q13561	Dynactin subunit 2 (Dynactin complex 50 kDa subunit)	-	-	3	-	-	-	1	X

555	Q14203	Dynactin-1 (150 kDa dynein-associated polypeptide) (I	-	-	1	-	-	-	2	-
556	O00429	Dynamamin-1-like protein (EC 3.6.5.5) (Dynamamin-like prot	-	-	10	-	-	1	4	-
557	P50570	Dynamamin-2 (EC 3,6,5,5)	-	-	-	-	-	2	-	-
558	Q14204	Dynein heavy chain, cytosolic (DYHC) (Cytoplasmic dy	-	-	-	-	-	6	-	-
559	Q96FJ2	Dynein light chain 2, cytoplasmic (Dynein light chain L	-	-	-	-	-	2	-	-
560	Q9NP97	Dynein light chain 2A, cytoplasmic (Dynein-associated	-	-	-	-	1	2	-	-
561	Q96C19	EF-hand domain-containing protein 2 (Swiprosin-1)	-	-	1	4	8	12	12	X
562	Q8N3D4	EH domain-binding protein 1-like protein 1 - Homo sap	-	-	-	-	-	1	-	-
563	Q9H4M9	EH-domain-containing protein 1 (Testilin) (hPAST1)	-	-	10	9	5	-	11	X
564	Q9NZN3	EH-domain-containing protein 3	-	-	14	-	-	-	-	-
565	Q15717	ELAV-like protein 1 (Hu-antigen R) (HuR) - Homo sapi	-	-	-	-	-	1	-	-
566	P13804	Electron transfer flavoprotein alpha-subunit, mitochond	-	-	7	-	8	4	13	X
567	P38117	Electron transfer flavoprotein beta-subunit (Beta-ETF)	-	-	1	-	8	5	5	-
568	P68104	Elongation factor 1-alpha 1 (EF-1-alpha-1) (Elongation	-	2	2	7	18	13	18	X
569	P24534	Elongation factor 1-beta (EF-1-beta)	-	-	2	-	2	3	3	-
570	P29692	Elongation factor 1-delta (EF-1-delta) (Antigen NY-CO	-	-	2	-	7	3	4	X
571	P26641	Elongation factor 1-gamma (EF-1-gamma) (eEF-1B ga	-	-	1	2	2	2	5	X
572	P13639	Elongation factor 2 (EF-2)	-	10	-	3	21	15	28	X
573	P49411	Elongation factor Tu, mitochondrial precursor (EF-Tu)	-	-	1	-	16	5	7	X
574	Q9Y6C2	EMILIN-1 precursor (Elastin microfibril interface-locate	-	-	3	-	-	-	-	-
575	Q9UI08	Ena/VASP-like protein (Ena/vasodilator-stimulated pho	-	-	-	-	1	-	2	-
576	O94919	Endonuclease domain-containing 1 protein precursor (	-	-	1	-	-	-	-	-
577	Q6P179	Endoplasmic reticulum aminopeptidase 2 - Homo sapi	-	-	-	-	-	-	1	-
578	P30040	Endoplasmic reticulum protein ERp29 precursor (ERp	-	-	6	2	6	8	8	X
579	P14625	Endoplasmin precursor (94 kDa glucose-regulated pro	-	3	14	-	14	19	23	X
580	Q96AP7	Endothelial cell-selective adhesion molecule precursor	-	-	2	-	-	-	-	-
581	O60869	Endothelial differentiation-related factor 1 (EDF-1) (Mu	-	-	-	-	-	1	2	-
582	Q9UHY7	Enolase-phosphatase E1 (EC 3.1.3.77) (2,3-diketo-5-r	-	-	1	-	1	1	-	-
583	Q9NTX5	Enoyl-CoA hydratase domain-containing protein 1 - Ho	-	-	-	-	-	-	2	-
584	P30084	Enoyl-CoA hydratase, mitochondrial precursor (EC 4.2	-	-	1	-	8	4	8	X
585	P12724	Eosinophil cationic protein precursor (EC 3.1.27.-) (EC	-	-	-	2	-	1	-	-
586	Q05315	Eosinophil lysophospholipase (EC 3.1.1.5) (Charcot-L	-	-	-	6	2	4	1	-
587	P11678	Eosinophil peroxidase precursor (EC 1.11.1.7) (EPO)	-	-	-	6	-	-	-	-
588	P61916	Epididymal secretory protein E1 precursor (Niemann-F	-	-	-	-	1	3	1	X
589	P12830	Epithelial-cadherin precursor (E-cadherin) (Uvomorulin	3	-	-	-	-	-	-	-
590	P07099	Epoxide hydrolase 1 (EC 3.3.2.9) (Microsomal epoxide	-	-	-	-	-	1	-	-
591	Q96HE7	ERO1-like protein alpha precursor (EC 1.8.4.-) (ERO1	-	-	-	-	2	4	1	-
592	P27105	Erythrocyte band 7 integral membrane protein (Stomat	-	5	13	2	6	1	8	-
593	P16452	Erythrocyte membrane protein band 4.2 (Erythrocyte p	-	14	-	-	1	-	-	-
594	P30042	ES1 protein homolog, mitochondrial precursor (Protein	-	-	2	-	4	-	4	X
595	P10768	Esterase D (EC 3.1.1.1)	-	1	4	2	4	3	6	X
596	Q92506	Estradiol 17-beta-dehydrogenase 8 (EC 1.1.1.62) (17-	-	-	-	-	1	-	-	X
597	O95571	ETHE1 protein, mitochondrial precursor (EC 3.-.-.-) (E	-	-	3	3	7	5	5	X
598	P60842	Eukaryotic initiation factor 4A-I (EC 3.6.1.-) (ATP-depe	-	1	3	-	8	4	7	X
599	Q14240	Eukaryotic initiation factor 4A-II (EC 3.6.1.-) (ATP-depe	-	-	-	-	5	-	5	X
600	O43324	Eukaryotic translation elongation factor 1 epsilon-1 (M	-	-	-	-	-	1	1	-
601	P41567	Eukaryotic translation initiation factor 1 (eIF1) (Protein	-	-	-	-	-	1	3	X
602	P47813	Eukaryotic translation initiation factor 1A, X-chromoso	-	-	-	-	3	-	-	X
603	P05198	Eukaryotic translation initiation factor 2 subunit 1 (Euk	-	-	1	-	2	-	2	X
604	O75822	Eukaryotic translation initiation factor 3 subunit 1 (eIF-	-	-	-	-	1	-	-	-
605	Q14152	Eukaryotic translation initiation factor 3 subunit 10 (eIF	-	-	-	-	3	-	14	-
606	Q9UBQ5	Eukaryotic translation initiation factor 3 subunit 12 (eIF	-	-	1	-	1	-	3	-
607	O15372	Eukaryotic translation initiation factor 3 subunit 3 (eIF-	-	-	-	-	-	-	1	X
608	O00303	Eukaryotic translation initiation factor 3 subunit 5 (eIF-	-	-	-	-	3	1	1	X
609	Q9Y262	Eukaryotic translation initiation factor 3 subunit 6-intera	-	-	-	-	-	4	1	-
610	P55884	Eukaryotic translation initiation factor 3 subunit 9 (eIF-	-	-	-	-	1	-	4	-

611	Q04637	Eukaryotic translation initiation factor 4 gamma 1 (eIF-4G1)	-	-	-	-	2	-	-	-
612	O43432	Eukaryotic translation initiation factor 4 gamma 3 (eIF-4G3)	-	-	-	-	-	-	1	-
613	P23588	Eukaryotic translation initiation factor 4B (eIF-4B)	-	-	-	-	1	-	-	X
614	P06730	Eukaryotic translation initiation factor 4E (eIF4E) (eIF-4E)	-	-	2	-	1	1	2	X
615	Q8N5X7	Eukaryotic translation initiation factor 4E type 3 - Homo sapiens	-	-	-	1	-	-	-	-
616	Q15056	Eukaryotic translation initiation factor 4H (eIF-4H) (Wilamowski factor)	-	-	1	-	3	1	2	X
617	P55010	Eukaryotic translation initiation factor 5 (eIF-5)	-	-	1	-	-	-	-	X
618	P63241	Eukaryotic translation initiation factor 5A (eIF-5A) (eIF-5A)	-	3	6	-	7	6	6	X
619	P56537	Eukaryotic translation initiation factor 6 (eIF-6) (B4 integrin)	-	-	-	1	1	1	3	-
620	P34910	EVI2B protein precursor (Ecotropic viral integration site 2B)	-	-	-	-	-	3	1	-
621	Q16394	Exostosin-1 - Homo sapiens (Human)	-	-	-	1	-	-	-	-
622	O14980	Exportin-1 (Chromosome region maintenance 1 protein)	-	-	-	-	-	3	3	-
623	Q9UIA9	Exportin-7 (Exp7) (Ran-binding protein 16) - Homo sapiens	-	-	-	-	1	1	-	-
624	P15311	Ezrin (p81) (Cytovillin) (Villin-2)	-	-	3	7	12	9	14	X
625	O14745	Ezrin-radixin-moesin-binding phosphoprotein 50 (EBP50)	-	-	4	2	6	1	3	-
626	P52907	F-actin capping protein alpha-1 subunit (CapZ alpha-1)	-	2	7	7	8	6	9	X
627	P47755	F-actin capping protein alpha-2 subunit (CapZ alpha-2)	-	2	8	1	5	7	5	X
628	P47756	F-actin capping protein beta subunit (CapZ beta)	-	-	12	8	10	9	14	X
629	Q13158	FADD protein (FAS-associating death domain-containing protein)	-	-	-	-	-	-	1	-
630	Q96AE4	Far upstream element-binding protein 1 (FUSE-binding protein 1)	-	-	-	-	4	2	9	X
631	Q92945	Far upstream element-binding protein 2 (FUSE-binding protein 2)	-	1	-	-	5	7	11	X
632	Q96124	Far upstream element-binding protein 3 (FUSE-binding protein 3)	-	-	-	-	2	-	-	-
633	P14324	Farnesyl pyrophosphate synthetase (FPP synthetase)	-	-	1	1	-	-	1	-
634	P49327	Fatty acid synthase (EC 2.3.1.85) [Includes: [Acyl-carrier protein]]	-	-	4	-	1	1	7	-
635	Q01469	Fatty acid-binding protein, epidermal (E-FABP) (Psoriasis)	-	-	-	1	1	4	4	X
636	P02794	Ferritin heavy chain (EC 1.16.3.1) (Ferritin H subunit) (L-type)	-	-	-	-	3	2	6	X
637	P02792	Ferritin light chain (Ferritin L subunit)	-	-	-	7	4	6	7	X
638	P02671	Fibrinogen alpha chain precursor [Contains: Fibrinopeptide A]	9	-	15	-	-	-	15	X
639	P02675	Fibrinogen beta chain precursor [Contains: Fibrinopeptide B]	16	1	27	-	1	-	23	X
640	P02679	Fibrinogen gamma chain precursor	11	-	12	-	-	-	15	X
641	P02751	Fibronectin precursor (FN) (Cold-insoluble globulin) (C1G)	33	2	6	-	-	-	4	-
642	P23142	Fibulin-1 precursor	2	-	-	-	-	-	-	-
643	O00602	Ficolin-1 precursor (Collagen/fibrinogen domain-containing)	-	-	-	-	-	3	-	X
644	Q15485	Ficolin-2 precursor (Ficolin-B) (Ficolin-beta) (L-ficolin)	3	-	-	-	-	-	-	-
645	O75636	Ficolin-3 precursor (Collagen/fibrinogen domain-containing)	7	-	-	-	-	-	-	-
646	P20930	Filaggrin - Homo sapiens (Human)	-	-	-	-	-	-	2	-
647	P21333	Filamin-A (Alpha-filamin) (Filamin-1) (Endothelial actin-binding protein)	1	17	94	12	56	65	103	X
648	O75369	Filamin-B (FLN-B) (Beta-filamin) (Actin-binding-like protein)	-	23	-	-	1	3	9	-
649	Q14315	Filamin-C (Gamma-filamin) (Filamin-2) (Protein FLNC)	-	8	-	-	-	-	4	-
650	P62942	FK506-binding protein 1A (EC 5.2.1.8) (Peptidyl-prolyl isomerase)	-	-	1	-	-	2	2	-
651	P26885	FK506-binding protein 2 precursor (EC 5.2.1.8) (Peptidyl-prolyl isomerase)	-	-	1	-	-	2	2	X
652	Q00688	FK506-binding protein 3 (EC 5.2.1.8) (Peptidyl-prolyl isomerase)	-	-	-	-	1	-	2	-
653	Q02790	FK506-binding protein 4 (EC 5.2.1.8) (Peptidyl-prolyl isomerase)	-	-	-	-	1	-	1	X
654	Q13451	FK506-binding protein 5 (EC 5.2.1.8) (Peptidyl-prolyl isomerase)	-	-	-	-	4	-	2	X
655	P30043	Flavin reductase (EC 1.5.1.30) (FR) (NADPH-dependent)	-	11	2	-	8	6	7	X
656	O75955	Flotillin-1 - Homo sapiens (Human)	-	3	1	-	-	-	-	-
657	Q14254	Flotillin-2 - Homo sapiens (Human)	-	1	1	-	-	-	-	-
658	P41439	Folate receptor gamma precursor (FR-gamma) (Folate receptor)	-	-	-	3	-	-	-	-
659	Q96RU3	Formin-binding protein 1 (Formin-binding protein 17) (Formin)	-	-	-	-	4	-	-	-
660	O95466	Formin-like 1 protein (Formin-like protein) (Leukocyte formin)	-	-	-	-	2	4	9	-
661	Q13642	Four and a half LIM domains protein 1 (FHL-1) (Skeletal)	-	-	2	-	1	-	2	-
662	P09467	Fructose-1,6-bisphosphatase 1 (EC 3.1.3.11) (D-fructose-1,6-bisphosphate)	-	-	-	1	2	2	5	X
663	P04075	Fructose-bisphosphate aldolase A (EC 4.1.2.13) (Muscle)	-	7	14	10	19	14	16	X
664	P09972	Fructose-bisphosphate aldolase C (EC 4.1.2.13) (Brain)	-	-	3	3	6	2	5	-
665	P07954	Fumarate hydratase, mitochondrial precursor (EC 4.2.1.2)	-	-	1	1	2	1	2	X
666	P16930	Fumarylacetoacetase (EC 3.7.1.2) (Fumarylacetoacetate hydrolase)	-	-	2	2	-	2	-	X

667	Q6P587	Fumarylacetoacetate hydrolase domain-containing pro	-	-	-	-	1	1	2	X
668	O15117	FYN-binding protein (FYN-T-binding protein) (FYB-120	-	-	3	-	-	-	-	-
669	O95866	G6b protein precursor - Homo sapiens (Human)	-	-	3	-	-	-	-	-
670	P09382	Galectin-1 (Beta-galactoside-binding lectin L-14-I) (Lac	-	-	-	-	3	6	5	X
671	P17931	Galectin-3 (Galactose-specific lectin 3) (Mac-2 antigen	-	-	-	4	-	4	2	-
672	Q08380	Galectin-3-binding protein precursor (Lectin galactosid	-	-	2	-	-	-	-	-
673	Q3ZCW2	Galectin-related protein - Homo sapiens (Human)	-	-	6	-	-	-	-	-
674	O95166	Gamma-aminobutyric acid receptor-associated protein	-	-	-	1	-	2	-	-
675	P09104	Gamma-enolase (EC 4.2.1.11) (2-phospho-D-glycerate	-	-	-	-	6	-	-	X
676	Q92820	Gamma-glutamyl hydrolase precursor (EC 3.4.19.9) (G	2	-	-	1	-	1	1	-
677	P13284	Gamma-interferon-inducible lysosomal thiol reductase	-	-	-	-	-	1	1	-
678	Q9HBI0	Gamma-parvin - Homo sapiens (Human)	-	-	-	2	-	1	1	-
679	P17900	Ganglioside GM2 activator precursor (GM2-AP) (Cere	-	-	-	-	-	1	-	-
680	Q9NS71	Gastrokine-1 precursor - Homo sapiens (Human)	1	-	-	-	-	-	-	-
681	O95479	GDH/6PGL endoplasmic bifunctional protein precursor	-	-	-	1	-	-	1	-
682	Q13630	GDP-L-fucose synthetase (EC 1.1.1.271) (Protein FX)	-	2	-	-	-	-	-	X
683	P06396	Gelsolin precursor (Actin-depolymerizing factor) (ADF)	9	4	18	14	5	6	16	X
684	Q9P107	GEM-interacting protein (GMIP)	-	-	-	-	-	1	1	-
685	O60763	General vesicular transport factor p115 (Transcytosis-	-	-	-	-	-	3	1	-
686	P60983	Glia maturation factor beta (GMF-beta)	-	-	2	-	3	2	2	X
687	O60234	Glia maturation factor gamma (GMF-gamma)	-	-	2	1	6	3	5	X
688	P46926	Glucosamine-6-phosphate isomerase (EC 3.5.99.6) (G	-	-	-	-	2	1	2	X
689	P11413	Glucose-6-phosphate 1-dehydrogenase (EC 1.1.1.49)	-	-	4	11	3	9	5	X
690	P06744	Glucose-6-phosphate isomerase (EC 5.3.1.9) (GPI) (P	-	1	4	12	8	12	9	X
691	P14314	Glucosidase II beta subunit precursor (Protein kinase	-	-	-	1	1	-	6	-
692	P00367	Glutamate dehydrogenase 1, mitochondrial precursor	-	-	-	-	8	2	10	X
693	P48506	Glutamate--cysteine ligase catalytic subunit (EC 6.3.2.	-	3	-	-	-	-	-	-
694	P48507	Glutamate--cysteine ligase regulatory subunit (EC 6.3.	-	-	3	-	1	-	-	X
695	O94925	Glutaminase kidney isoform, mitochondrial precursor (	-	-	-	-	1	-	1	X
696	P35754	Glutaredoxin-1 (Thioltransferase-1) (TTase-1)	-	-	-	2	-	3	-	-
697	P07203	Glutathione peroxidase 1 (EC 1.11.1.9) (GSHPx-1) (G	-	1	11	-	6	11	10	X
698	P22352	Glutathione peroxidase 3 precursor (EC 1.11.1.9) (GS	4	-	-	-	-	-	-	X
699	P00390	Glutathione reductase, mitochondrial precursor (EC 1.	-	1	2	3	9	2	5	-
700	Q9Y2Q3	Glutathione S-transferase kappa 1 (EC 2.5.1.18) (GST	-	-	5	-	8	4	11	-
701	P09488	Glutathione S-transferase Mu 1 (EC 2.5.1.18) (GSTM1	-	-	-	-	5	4	7	-
702	P28161	Glutathione S-transferase Mu 2 (EC 2.5.1.18) (GSTM2	-	-	1	-	5	-	4	-
703	P21266	Glutathione S-transferase Mu 3 (EC 2.5.1.18) (GSTM3	-	-	-	-	3	-	1	X
704	Q03013	Glutathione S-transferase Mu 4 (EC 2.5.1.18) (GSTM4	-	-	2	-	5	4	7	-
705	P09211	Glutathione S-transferase P (EC 2.5.1.18) (GST class-	-	-	8	8	6	9	8	X
706	P48637	Glutathione synthetase (EC 6.3.2.3) (Glutathione s	-	-	-	-	-	2	1	X
707	P78417	Glutathione transferase omega-1 (EC 2.5.1.18) (GSTC	-	-	9	5	5	4	6	X
708	P04406	Glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.	-	7	22	25	25	14	21	X
709	Q8N335	Glycerol-3-phosphate dehydrogenase 1-like protein - H	-	-	-	1	-	-	-	-
710	P43304	Glycerol-3-phosphate dehydrogenase, mitochondrial p	-	-	2	-	1	2	3	X
711	P35573	Glycogen debranching enzyme (Glycogen debrancher	-	-	-	1	-	-	2	-
712	P11216	Glycogen phosphorylase, brain form (EC 2.4.1.1)	-	-	2	-	5	-	9	X
713	P06737	Glycogen phosphorylase, liver form (EC 2.4.1.1) - Hon	-	-	-	28	-	4	4	-
714	P46976	Glycogenin-1 (EC 2.4.1.186) - Homo sapiens (Human)	-	-	-	1	-	-	-	-
715	P04921	Glycophorin C (PAS-2*) (Glycoprotein beta) (GLPC) (C	-	1	-	-	-	-	-	-
716	P30419	Glycylpeptide N-tetradecanoyltransferase 1 (EC 2.3.1.	-	-	-	-	-	-	1	-
717	P41250	Glycyl-tRNA synthetase (EC 6.1.1.14) (Glycine--tRNA	-	-	-	-	1	-	1	X
718	Q9HC38	Glyoxalase domain-containing protein 4 - Homo sapier	-	-	1	2	4	-	10	-
719	Q9UBQ7	Glyoxylate reductase/hydroxypyruvate reductase (EC	-	-	-	-	-	-	2	X
720	P36959	GMP reductase 1 (EC 1.7.1.7) (Guanosine 5*-monoph	-	-	1	-	1	-	-	-
721	Q9H4A6	Golgi phosphoprotein 3 (Coat-protein GPP34)	-	1	-	-	-	-	1	X
722	Q9H3P7	Golgi resident protein GCP60 (Acyl-CoA-binding doma	-	-	-	1	-	2	-	-

723	Q9H4G4	Golgi-associated plant pathogenesis-related protein 1	1	-	1	2	2	2	3	-
724	P28676	Grancalcin	-	-	1	4	3	5	3	X
725	P10144	Granzyme B precursor - Homo sapiens (Human)	-	-	-	-	-	-	1	-
726	O75791	GRB2-related adapter protein 2 (GADS protein) (Grow	-	-	1	-	1	-	-	-
727	Q12849	G-rich sequence factor 1 (GRSF-1)	-	-	-	-	1	1	1	X
728	Q4V328	GRIP1-associated protein 1 (GRASP-1) - Homo sapie	-	-	-	-	-	-	1	-
729	P62993	Growth factor receptor-bound protein 2 (Adapter prote	-	-	2	3	2	4	10	X
730	Q9UIJ7	GTP:AMP phosphotransferase mitochondrial (EC 2.7.4	-	-	2	-	2	1	1	-
731	P01112	GTPase HRas precursor (Transforming protein p21) (p	-	-	2	-	-	2	-	-
732	P01111	GTPase NRas precursor (Transforming protein N-Ras	-	-	2	-	1	-	-	-
733	Q8WWP7	GTPase, IMAP family member 1 (Immunity-associated	-	-	-	-	3	1	4	-
734	Q9NUV9	GTPase, IMAP family member 4 (Immunity-associated	-	-	-	-	7	1	5	-
735	P62826	GTP-binding nuclear protein Ran (GTPase Ran) (Ras-	-	4	4	4	10	10	12	X
736	P36406	GTP-binding protein ARD-1 (ADP-ribosylation factor d	-	-	-	-	1	-	-	-
737	Q15382	GTP-binding protein Rheb (Ras homolog enriched in b	-	-	2	-	-	-	-	-
738	Q9NR31	GTP-binding protein SAR1a (COPII-associated small G	-	-	8	3	2	2	4	X
739	Q9Y6B6	GTP-binding protein SAR1b (GTBPB)	-	-	-	-	-	-	2	X
740	Q03113	Guanine nucleotide-binding protein alpha-12 subunit (G	-	-	-	1	-	-	-	X
741	Q14344	Guanine nucleotide-binding protein alpha-13 subunit (G	-	-	-	-	-	-	2	-
742	P63244	Guanine nucleotide-binding protein beta subunit 2-like	-	1	-	-	11	3	13	X
743	P63096	Guanine nucleotide-binding protein G(i), alpha-1 subu	-	-	-	-	2	-	-	-
744	P04899	Guanine nucleotide-binding protein G(i), alpha-2 subu	-	-	8	8	7	8	9	X
745	P59768	Guanine nucleotide-binding protein G(l)/G(s)/G(o) sub	-	-	-	1	-	-	-	-
746	P62873	Guanine nucleotide-binding protein G(l)/G(s)/G(t) bet	-	-	6	-	5	2	-	X
747	P62879	Guanine nucleotide-binding protein G(l)/G(s)/G(t) bet	-	-	6	3	5	-	7	X
748	P09471	Guanine nucleotide-binding protein G(o) subunit alpha	-	-	-	2	-	-	-	-
749	P50148	Guanine nucleotide-binding protein G(q) subunit alpha	-	-	4	2	-	-	1	-
750	P19086	Guanine nucleotide-binding protein G(z) subunit alpha	-	-	3	-	-	-	-	-
751	Q16774	Guanylate kinase (EC 2.7.4.8) (GMP kinase)	-	-	-	-	2	-	2	X
752	Q9H0R5	Guanylate-binding protein 3 (GTP-binding protein 3) (G	-	-	-	-	2	-	-	-
753	Q96PP8	Guanylate-binding protein 5 (GTP-binding protein 5) (G	-	-	-	-	-	-	1	-
754	Q9H0R4	Haloacid dehalogenase-like hydrolase domain-contain	-	-	4	-	1	-	-	-
755	Q9BSH5	Haloacid dehalogenase-like hydrolase domain-contain	-	-	-	-	-	-	1	-
756	P00738	Haptoglobin precursor [Contains: Haptoglobin alpha ch	25	-	-	3	-	8	10	X
757	P00739	Haptoglobin-related protein precursor - Homo sapiens	18	1	-	-	-	5	-	-
758	Q7Z4H3	HD domain-containing protein 2 - Homo sapiens (Hum	-	-	-	-	1	-	1	-
759	Q8N4P3	HD domain-containing protein 3 - Homo sapiens (Hum	-	-	-	-	1	-	-	-
760	Q86WZ0	HEAT repeat-containing protein 4 - Homo sapiens (Hu	-	-	-	-	1	-	2	-
761	P08107	Heat shock 70 kDa protein 1 (HSP70.1) (HSP70-1/HS	-	1	8	16	12	13	16	X
762	P34931	Heat shock 70 kDa protein 1L (Heat shock 70 kDa pro	-	-	-	9	-	-	6	X
763	P34932	Heat shock 70 kDa protein 4 (Heat shock 70-related p	-	4	2	-	4	4	6	X
764	P17066	Heat shock 70 kDa protein 6 (Heat shock 70 kDa prote	-	-	-	5	-	2	4	X
765	P11142	Heat shock cognate 71 kDa protein (Heat shock 70 kD	-	7	16	8	24	15	25	X
766	Q12931	Heat shock protein 75 kDa, mitochondrial precursor (H	-	-	1	-	1	2	1	X
767	P07900	Heat shock protein HSP 90-alpha (HSP 86)	-	5	17	5	24	23	30	X
768	P08238	Heat shock protein HSP 90-beta (HSP 84) (HSP 90)	-	3	9	5	18	21	29	X
769	P54652	Heat shock-related 70 kDa protein 2 (Heat shock 70 k	-	-	-	-	-	-	6	X
770	Q92598	Heat-shock protein 105 kDa (Heat shock 110 kDa prot	-	1	-	-	-	-	-	X
771	P04792	Heat-shock protein beta-1 (HspB1) (Heat shock 27 kD	-	-	6	-	1	-	4	X
772	Q9NQ75	HEF-like protein - Homo sapiens (Human)	-	-	4	-	-	-	-	-
773	P14317	Hematopoietic lineage cell-specific protein (Hematopo	-	1	-	-	8	2	3	X
774	Q9NRV9	Heme-binding protein 1 (p22HBP)	-	1	-	1	2	2	1	X
775	Q9Y5Z4	Heme-binding protein 2 (Protein SOUL) (Placental pro	-	-	1	3	1	3	-	-
776	P69905	Hemoglobin subunit alpha (Hemoglobin alpha chain) (G	4	19	-	6	-	11	9	-
777	P68871	Hemoglobin subunit beta (Hemoglobin beta chain) (Be	6	21	-	11	-	17	15	X
778	P02042	Hemoglobin subunit delta (Hemoglobin delta chain) (D	-	15	-	4	-	12	12	-

779	P69891	Hemoglobin subunit gamma-1 (Hemoglobin gamma-1	-	7	-	-	-	-	-	-	-
780	P69892	Hemoglobin subunit gamma-2 (Hemoglobin gamma-2	4	-	-	-	-	-	-	-	-
781	P02790	Hemopexin precursor (Beta-1B-glycoprotein)	13	-	-	-	-	-	-	5	-
782	Q9Y251	Heparanase precursor (EC 3.2.-.-) (Heparanase-1) (H	-	-	1	-	-	-	-	-	-
783	P05546	Heparin cofactor 2 precursor (Heparin cofactor II) (HC	9	-	-	-	-	-	-	-	-
784	Q04756	Hepatocyte growth factor activator precursor (EC 3,4,2	1	-	-	-	-	-	-	-	-
785	P26927	Hepatocyte growth factor-like protein precursor (Macro	1	-	-	-	-	-	-	-	-
786	P51858	Hepatoma-derived growth factor (HDGF) (High-mobilit	-	-	-	1	2	-	-	5	-
787	Q13151	Heterogeneous nuclear ribonucleoprotein A0 (hnRNP	-	-	-	-	-	1	1	-	-
788	P09651	Heterogeneous nuclear ribonucleoprotein A1 (Helix-de	-	-	-	3	6	2	7	-	-
789	Q32P51	Heterogeneous nuclear ribonucleoprotein A1-like prote	-	-	-	-	-	-	8	-	-
790	P51991	Heterogeneous nuclear ribonucleoprotein A3 (hnRNP	-	-	-	-	1	-	2	-	-
791	O60812	Heterogeneous nuclear ribonucleoprotein C-like 1 (hnf	-	-	-	-	-	3	2	-	-
792	Q14103	Heterogeneous nuclear ribonucleoprotein D0 (hnRNP	-	-	-	1	6	4	8	X	-
793	P52597	Heterogeneous nuclear ribonucleoprotein F (hnRNP F	-	-	-	-	6	2	5	X	-
794	P38159	Heterogeneous nuclear ribonucleoprotein G (hnRNP G	-	-	-	-	1	2	-	-	-
795	P31943	Heterogeneous nuclear ribonucleoprotein H (hnRNP H	-	-	-	-	6	2	4	X	-
796	P31942	Heterogeneous nuclear ribonucleoprotein H3 (hnRNP	-	-	-	-	1	1	-	X	-
797	P61978	Heterogeneous nuclear ribonucleoprotein K (hnRNP K	-	-	3	2	12	14	11	X	-
798	O60506	Heterogeneous nuclear ribonucleoprotein Q (hnRNP Q	-	-	-	-	3	2	2	-	-
799	O43390	Heterogeneous nuclear ribonucleoprotein R (hnRNP R	-	-	-	-	1	-	2	-	-
800	Q9BUJ2	Heterogeneous nuclear ribonucleoprotein U-like protei	-	-	-	-	1	-	-	-	-
801	Q1KMD3	Heterogeneous nuclear ribonucleoprotein U-like protei	-	-	-	-	-	-	1	-	-
802	P22626	Heterogeneous nuclear ribonucleoproteins A2/B1 (hnF	-	2	-	3	6	6	10	X	-
803	P07910	Heterogeneous nuclear ribonucleoproteins C1/C2 (hnF	-	-	-	-	2	4	3	X	-
804	Q00839	Heterogenous nuclear ribonucleoprotein U (hnRNP U)	-	-	-	-	9	2	8	-	-
805	P19367	Hexokinase-1 (EC 2.7.1.1) (Hexokinase type I) (HK I)	-	3	3	-	4	-	6	-	-
806	P52790	Hexokinase-3 (EC 2.7.1.1) (Hexokinase type III) (HK II	-	-	-	13	-	10	10	-	-
807	P30273	High affinity immunoglobulin epsilon receptor gamma-	-	-	1	1	-	3	1	-	-
808	P09429	High mobility group protein 1 (HMG-1) (High mobility g	-	-	-	-	16	11	19	-	-
809	Q9UGV6	High mobility group protein 1-like 10 (HMG-1L10)	-	-	-	-	-	-	7	-	-
810	P26583	High mobility group protein 2 (HMG-2)	-	-	-	1	7	8	16	-	-
811	O15347	High mobility group protein B3 (High mobility group pro	-	-	-	-	-	2	-	-	-
812	P37235	Hippocalcin-like protein 1 (Visinin-like protein 3) (VILIP	-	-	-	-	4	-	-	X	-
813	P49773	Histidine triad nucleotide-binding protein 1 (Adenosine	-	-	2	-	3	4	4	X	-
814	P04196	Histidine-rich glycoprotein precursor (Histidine-proline-	10	-	-	-	-	-	-	-	-
815	P12081	Histidyl-tRNA synthetase (EC 6.1.1.21) (Histidine--tRN	-	-	-	-	2	-	-	X	-
816	Q96QV6	Histone H2A type 1-A - Homo sapiens (Human)	-	-	-	-	-	-	3	-	-
817	P33778	Histone H2B type 1-B (H2B,f) (H2B/f) (H2B,1) - Homo	-	-	-	-	-	-	2	-	-
818	P62805	Histone H4	-	-	3	-	4	1	11	-	-
819	P30443	HLA class I histocompatibility antigen, A-1 alpha chain	-	1	4	-	2	-	5	-	-
820	P13746	HLA class I histocompatibility antigen, A-11 alpha chai	-	-	-	-	-	-	4	-	-
821	P01892	HLA class I histocompatibility antigen, A-2 alpha chain	-	-	5	-	-	-	6	-	-
822	P18462	HLA class I histocompatibility antigen, A-25 alpha chai	-	-	-	-	-	-	4	-	-
823	P16188	HLA class I histocompatibility antigen, A-30 alpha chai	-	-	-	-	-	-	6	-	-
824	P30455	HLA class I histocompatibility antigen, A-36 alpha chai	-	-	-	-	-	-	5	-	-
825	P30464	HLA class I histocompatibility antigen, B-15 alpha chai	-	-	-	-	-	-	8	-	-
826	P30685	HLA class I histocompatibility antigen, B-35 alpha chai	-	-	-	-	-	-	6	-	-
827	P30481	HLA class I histocompatibility antigen, B-44 alpha chai	-	-	-	-	-	-	3	-	-
828	P30491	HLA class I histocompatibility antigen, B-53 alpha chai	-	-	-	-	-	-	5	-	-
829	P01889	HLA class I histocompatibility antigen, B-7 alpha chain	-	-	-	3	-	-	-	-	-
830	P30460	HLA class I histocompatibility antigen, B-8 alpha chain	-	-	-	-	-	-	5	-	-
831	P30499	HLA class I histocompatibility antigen, Cw-1 alpha cha	-	-	-	-	-	-	1	-	-
832	Q07000	HLA class I histocompatibility antigen, Cw-15 alpha ch	-	-	-	-	-	-	2	-	-
833	P30501	HLA class I histocompatibility antigen, Cw-2 alpha cha	-	-	-	-	-	-	1	-	-
834	P04233	HLA class II histocompatibility antigen gamma chain (H	-	-	-	-	-	2	2	-	-

835	P28068	HLA class II histocompatibility antigen, DM beta chain	-	-	-	-	-	-	1	-
836	P01908	HLA class II histocompatibility antigen, DQ(1) alpha chain	-	-	-	-	-	-	1	X
837	P01903	HLA class II histocompatibility antigen, DR alpha chain	-	-	-	-	-	3	-	-
838	P01912	HLA class II histocompatibility antigen, DR-1 beta chain	-	-	-	-	-	2	-	-
839	P13761	HLA class II histocompatibility antigen, DRB1-7 beta chain	-	-	-	-	-	-	4	X
840	P50502	Hsc70-interacting protein (Hip) (Putative tumor suppressor)	-	1	4	-	2	-	3	X
841	Q16543	Hsp90 co-chaperone Cdc37 (Hsp90 chaperone protein)	-	1	1	-	2	2	3	-
842	Q16775	Hydroxyacylglutathione hydrolase (EC 3.1.2.6) (Glyoxalase I)	-	-	-	-	1	-	-	X
843	P35914	Hydroxymethylglutaryl-CoA lyase, mitochondrial precursor	-	-	-	1	-	-	-	-
844	Q6YN16	Hydroxysteroid dehydrogenase-like protein 2 - Homo sapiens	-	-	-	2	-	-	-	-
845	P00492	Hypoxanthine-guanine phosphoribosyltransferase (EC 2.7.1.3)	-	1	5	3	3	6	4	X
846	P01876	Ig alpha-1 chain C region - Homo sapiens (Human)	11	-	-	-	-	-	8	X
847	P01877	Ig alpha-2 chain C region - Homo sapiens (Human)	7	-	-	-	-	-	5	-
848	P01857	Ig gamma-1 chain C region - Homo sapiens (Human)	14	-	-	-	-	-	14	-
849	P01859	Ig gamma-2 chain C region - Homo sapiens (Human)	10	-	-	-	-	-	7	-
850	P01860	Ig gamma-3 chain C region (Heavy chain disease protein)	9	-	-	-	-	-	4	-
851	P01861	Ig gamma-4 chain C region - Homo sapiens (Human)	8	-	-	-	-	-	-	-
852	P01742	Ig heavy chain V-I region EU - Homo sapiens (Human)	-	-	-	-	-	-	1	-
853	P01743	Ig heavy chain V-I region HG3 precursor - Homo sapiens	2	-	-	-	-	-	-	-
854	P06331	Ig heavy chain V-II region ARH-77 precursor - Homo sapiens	2	-	-	-	-	-	-	-
855	P01825	Ig heavy chain V-II region NEWM - Homo sapiens (Human)	1	-	-	-	-	-	-	-
856	P01824	Ig heavy chain V-II region WAH - Homo sapiens (Human)	1	-	-	-	-	-	-	-
857	P01766	Ig heavy chain V-III region BRO - Homo sapiens (Human)	3	-	-	-	-	-	-	-
858	P01767	Ig heavy chain V-III region BUT - Homo sapiens (Human)	1	-	-	-	-	-	-	-
859	P01781	Ig heavy chain V-III region GAL - Homo sapiens (Human)	4	-	-	-	-	-	-	-
860	P01771	Ig heavy chain V-III region HIL - Homo sapiens (Human)	2	-	-	-	-	-	-	-
861	P01777	Ig heavy chain V-III region TEI - Homo sapiens (Human)	-	-	-	-	-	-	1	-
862	P01779	Ig heavy chain V-III region TUR - Homo sapiens (Human)	2	-	-	-	-	-	-	-
863	P01764	Ig heavy chain V-III region VH26 precursor - Homo sapiens	4	-	-	-	-	-	-	-
864	P01834	Ig kappa chain C region - Homo sapiens (Human)	7	6	-	2	-	-	7	-
865	P01593	Ig kappa chain V-I region AG	2	-	-	-	-	-	-	X
866	P04430	Ig kappa chain V-I region BAN - Homo sapiens (Human)	1	-	-	-	-	-	-	-
867	P01596	Ig kappa chain V-I region CAR - Homo sapiens (Human)	2	-	-	-	-	-	-	-
868	P01602	Ig kappa chain V-I region HK102 precursor (Fragment)	1	-	-	-	-	-	-	-
869	P01613	Ig kappa chain V-I region Ni - Homo sapiens (Human)	1	-	-	-	-	-	-	-
870	P01609	Ig kappa chain V-I region Scw - Homo sapiens (Human)	2	-	-	-	-	-	-	-
871	P01611	Ig kappa chain V-I region Wes - Homo sapiens (Human)	1	-	-	-	-	-	-	-
872	P01614	Ig kappa chain V-II region Cum - Homo sapiens (Human)	2	-	-	-	-	-	-	-
873	P04206	Ig kappa chain V-III region GOL (Rheumatoid factor)	-	-	-	-	-	-	4	-
874	P18135	Ig kappa chain V-III region HAH precursor	4	-	-	-	-	-	-	-
875	P01622	Ig kappa chain V-III region Ti - Homo sapiens (Human)	3	-	-	-	-	-	-	-
876	P04433	Ig kappa chain V-III region VG precursor (Fragment)	-	-	-	-	-	-	1	-
877	P01625	Ig kappa chain V-IV region Len - Homo sapiens (Human)	3	-	-	-	-	-	2	-
878	P01842	Ig lambda chain C regions - Homo sapiens (Human)	5	-	-	-	2	-	4	-
879	P04208	Ig lambda chain V-I region WAH - Homo sapiens (Human)	-	-	-	-	-	-	2	-
880	P80748	Ig lambda chain V-III region LOI - Homo sapiens (Human)	1	-	-	-	-	-	-	X
881	P01714	Ig lambda chain V-III region SH - Homo sapiens (Human)	1	-	-	-	-	-	-	-
882	P01717	Ig lambda chain V-IV region Hil - Homo sapiens (Human)	1	-	-	-	-	-	-	-
883	P01871	Ig mu chain C region - Homo sapiens (Human)	8	-	-	-	-	-	9	-
884	P04220	Ig mu heavy chain disease protein (BOT) - Homo sapiens	-	-	-	-	-	-	4	-
885	P01591	Immunoglobulin J chain - Homo sapiens (Human)	3	-	-	-	-	-	-	-
886	O00629	Importin alpha-4 subunit (Karyopherin alpha-4 subunit)	-	-	-	-	1	1	1	-
887	Q14974	Importin beta-1 subunit (Karyopherin beta-1 subunit) (Importin beta-1)	-	-	3	4	4	4	10	-
888	O00410	Importin beta-3 (Karyopherin beta-3) (Ran-binding protein 4)	-	-	-	-	3	-	6	-
889	Q8TEX9	Importin-4 (Importin 4b) (Imp4b) (Ran-binding protein 4)	-	-	-	-	1	-	-	-
890	Q96P70	Importin-9 (Imp9) (Ran-binding protein 9) (RanBP9) - Homo sapiens	-	-	-	-	-	1	-	-

891	P55060	Importin-alpha re-exporter (Chromosome segregation	-	-	-	-	-	6	2	-
892	Q5TEJ8	Induced by contact to basement membrane 1 protein (I	-	-	-	1	-	1	1	-
893	O14920	Inhibitor of nuclear factor kappa-B kinase subunit beta	-	-	1	-	-	1	-	-
894	Q15181	Inorganic pyrophosphatase (EC 3.6.1.1) (Pyrophosphat	-	-	-	2	6	1	5	X
895	Q9H2U2	Inorganic pyrophosphatase 2, mitochondrial precursor	-	-	1	1	4	-	5	X
896	Q9BY32	Inosine triphosphate pyrophosphatase (EC 3.6.1.19) (I	-	-	-	-	2	2	2	X
897	P20839	Inosine-5*-monophosphate dehydrogenase 1 (EC 1.1.	-	-	-	-	1	1	-	X
898	P12268	Inosine-5*-monophosphate dehydrogenase 2 (EC 1.1.	-	-	-	-	1	1	2	X
899	P29218	Inositol monophosphatase (EC 3.1.3.25) (IMPase) (IM	-	-	2	-	2	1	4	X
900	O14732	Inositol monophosphatase 2 (EC 3.1.3.25) (IMPase 2)	-	-	-	-	-	1	-	-
901	P17936	Insulin-like growth factor-binding protein 3 precursor (I	1	-	-	-	-	-	-	-
902	P24593	Insulin-like growth factor-binding protein 5 precursor (I	1	-	-	-	-	-	-	-
903	P35858	Insulin-like growth factor-binding protein complex acid	7	-	-	-	-	-	-	-
904	P17301	Integrin alpha-2 precursor (Platelet membrane glycopr	-	-	1	-	-	-	-	-
905	P23229	Integrin alpha-6 precursor (VLA-6) (CD49f antigen) [C	-	-	8	-	-	-	-	-
906	P08514	Integrin alpha-IIb precursor (Platelet membrane glycop	-	-	31	3	-	-	21	X
907	P20701	Integrin alpha-L precursor (Leukocyte adhesion glycop	-	-	-	-	2	3	4	-
908	P11215	Integrin alpha-M precursor (Cell surface glycoprotein M	-	-	-	33	9	32	22	-
909	P20702	Integrin alpha-X precursor (Leukocyte adhesion glycop	-	-	-	3	-	3	-	-
910	P05556	Integrin beta-1 precursor (Fibronectin receptor beta su	-	4	4	-	-	-	1	-
911	P05107	Integrin beta-2 precursor (Cell surface adhesion glycop	-	-	-	13	2	14	11	-
912	P05106	Integrin beta-3 precursor (Platelet membrane glycopro	-	-	23	1	-	-	9	-
913	P18084	Integrin beta-5 precursor - Homo sapiens (Human)	-	-	-	1	-	1	-	-
914	Q13418	Integrin-linked protein kinase (EC 2.7.11.1) (ILK-1) (IL	-	-	8	-	1	-	7	X
915	P05362	Intercellular adhesion molecule 1 precursor (ICAM-1) (	-	1	-	-	-	1	-	-
916	P13598	Intercellular adhesion molecule 2 precursor (ICAM-2) (	-	-	2	-	-	-	-	-
917	P32942	Intercellular adhesion molecule 3 precursor (ICAM-3) (	-	-	-	-	-	1	2	-
918	P48551	Interferon-alpha/beta receptor beta chain precursor - H	-	-	-	-	-	-	1	-
919	P05161	Interferon-induced 17 kDa protein precursor [Contains	-	-	-	-	-	-	1	-
920	P80217	Interferon-induced 35 kDa protein (IFP 35)	-	-	-	-	-	-	1	X
921	P20591	Interferon-induced GTP-binding protein Mx1 (Interfero	-	-	-	-	2	-	3	X
922	P32455	Interferon-induced guanylate-binding protein 1 (GTP-b	-	-	-	-	1	-	-	-
923	P32456	Interferon-induced guanylate-binding protein 2 (GTP-b	-	-	-	-	2	-	1	X
924	P09914	Interferon-induced protein with tetratricopeptide repeat	-	-	-	-	2	-	-	-
925	P13164	Interferon-induced transmembrane protein 1 (Interfero	-	-	-	1	1	-	1	-
926	Q96AZ6	Interferon-stimulated gene 20 kDa protein (EC 3.1.13.1	-	-	-	-	3	-	2	-
927	Q12905	Interleukin enhancer-binding factor 2 (Nuclear factor o	-	-	-	-	-	-	1	X
928	P01584	Interleukin-1 beta precursor (IL-1 beta) (Catabolin)	-	-	-	-	-	-	3	-
929	P18510	Interleukin-1 receptor antagonist protein precursor (IL-	-	-	-	-	-	-	1	X
930	Q14005	Interleukin-16 precursor (IL-16) (Lymphocyte chemoat	-	-	-	-	6	-	9	-
931	Q27J81	Inverted formin-2 - Homo sapiens (Human)	-	-	4	-	-	-	1	-
932	Q96CN7	Isochorismatase domain-containing protein 1 - Homo s	-	-	3	-	-	-	2	-
933	Q96AB3	Isochorismatase domain-containing protein 2, mitoch	-	-	1	-	2	1	2	-
934	P50213	Isocitrate dehydrogenase [NAD] subunit alpha, mitoch	1	-	1	-	3	2	4	X
935	O43837	Isocitrate dehydrogenase [NAD] subunit beta, mitoch	-	-	-	-	-	-	1	-
936	O75874	Isocitrate dehydrogenase [NADP] cytoplasmic (EC 1.1	-	-	1	7	-	7	2	X
937	P48735	Isocitrate dehydrogenase [NADP], mitochondrial precu	-	-	6	5	7	6	8	-
938	P41252	Isoleucyl-tRNA synthetase, cytoplasmic (EC 6.1.1.5) (I	-	-	-	-	-	2	1	-
939	Q9NSE4	Isoleucyl-tRNA synthetase, mitochondrial precursor (E	-	-	-	-	4	1	1	-
940	Q13907	Isopentenyl-diphosphate delta-isomerase 1 (EC 5.3.3.	-	-	-	1	-	-	-	X
941	P26440	Isovaleryl-CoA dehydrogenase, mitochondrial precursor	-	-	1	-	1	-	1	X
942	Q9Y624	Junctional adhesion molecule A precursor (JAM-A) (Ju	-	-	3	-	-	-	-	-
943	O60229	Kalirin RhoGEF - Homo sapiens (Human)	-	-	1	-	-	-	-	-
944	P29622	Kallistatin precursor (Serpins A4) (Kallikrein inhibitor) (F	2	-	-	-	-	-	-	-
945	P33176	Kinesin heavy chain (Ubiquitous kinesin heavy chain) (	-	1	-	-	-	-	-	-
946	Q86VH2	Kinesin-like protein KIF27 - Homo sapiens (Human)	1	-	1	-	-	-	1	-

947	P01042	Kininogen-1 precursor (Alpha-2-thiol proteinase inhibitor)	5	-	-	-	-	-	-	-	X
948	Q14657	L antigen family member 3 (ITBA2 protein) (ESO-3 protein)	-	-	-	-	-	1	2	-	-
949	P02788	Lactotransferrin precursor (EC 3.4.21.-) (Lactoferrin) (Human)	-	-	-	45	12	19	-	-	-
950	Q04760	Lactoylglutathione lyase (EC 4.4.1.5) (Methylglyoxal lyase)	-	-	3	1	6	4	6	X	-
951	Q6P4A8	LAMA-like protein 1 precursor - Homo sapiens (Human)	-	-	-	8	-	4	2	-	-
952	Q8NHP8	LAMA-like protein 2 precursor - Homo sapiens (Human)	-	-	-	-	-	-	1	-	-
953	P42166	Lamina-associated polypeptide 2 isoform alpha (Thymocyte)	-	-	-	-	-	-	2	-	-
954	P42167	Lamina-associated polypeptide 2, isoforms beta/gamma	-	-	-	-	-	-	2	-	-
955	Q14739	Lamin-B receptor (Integral nuclear envelope inner membrane)	-	-	-	1	-	-	-	-	-
956	P24043	Laminin alpha-2 chain precursor (Laminin M chain) (Mammalian)	-	-	-	-	-	1	-	-	-
957	P46379	Large proline-rich protein BAT3 (HLA-B-associated transmembrane)	-	-	-	-	-	1	1	X	-
958	Q14766	Latent-transforming growth factor beta-binding protein	-	-	11	-	-	-	1	-	-
959	P22064	Latent-transforming growth factor beta-binding protein	-	-	12	-	-	-	-	-	-
960	Q9BS40	Latexin (Endogenous carboxypeptidase inhibitor) (EC 3.4.21.100)	-	1	-	1	-	-	-	-	-
961	Q6P5Q4	Leiomodin-2 - Homo sapiens (Human)	-	-	-	1	-	-	-	-	-
962	P02750	Leucine-rich alpha-2-glycoprotein precursor (LRG) - Human	5	-	-	-	-	-	-	-	-
963	Q32MZ4	Leucine-rich repeat flightless-interacting protein 1 (LRR-FLIP1)	-	-	2	-	4	4	9	-	-
964	Q8N1G4	Leucine-rich repeat-containing protein 47 - Homo sapiens	-	-	-	-	-	-	1	-	-
965	Q8N9N7	Leucine-rich repeat-containing protein 57 - Homo sapiens	-	-	-	1	-	-	2	-	-
966	Q96AG4	Leucine-rich repeat-containing protein 59 - Homo sapiens	-	-	1	-	-	-	1	-	-
967	Q9P2J5	Leucyl-tRNA synthetase, cytoplasmic (EC 6.1.1.4) (Leucyl-tRNA synthetase)	-	-	-	-	-	-	1	-	-
968	P08575	Leukocyte common antigen precursor (EC 3.1.3.48) (Leukocyte common antigen)	-	-	-	9	22	27	27	X	-
969	P30740	Leukocyte elastase inhibitor (LEI) (Serpine B1) (Monocyte)	-	1	10	16	10	14	11	X	-
970	P08246	Leukocyte elastase precursor (EC 3.4.21.37) (Elastase)	-	-	-	6	-	1	2	-	-
971	Q8N6C8	Leukocyte immunoglobulin-like receptor subfamily A member 1	-	-	-	2	-	-	-	-	-
972	Q8NHL6	Leukocyte immunoglobulin-like receptor subfamily B member 1	-	-	-	-	-	1	-	-	-
973	P09960	Leukotriene A-4 hydrolase (EC 3.3.2.6) (LTA-4 hydrolase)	-	-	-	14	8	15	11	X	-
974	Q15722	Leukotriene B4 receptor 1 (LTB4-R 1) (P2Y purinoceptor)	-	-	-	1	-	-	-	-	-
975	O60711	Leupaxin - Homo sapiens (Human)	-	-	-	-	1	-	-	X	-
976	P48059	LIM and senescent cell antigen-like-containing domain	-	-	10	-	-	-	8	-	-
977	Q14847	LIM and SH3 domain protein 1 (LASP-1) (MLN 50)	-	-	4	1	4	2	6	X	-
978	P18428	Lipopolysaccharide-binding protein precursor (LBP) - Human	1	-	-	-	-	-	-	-	-
979	P05451	Lithostathine 1 alpha precursor - Homo sapiens (Human)	1	-	-	-	-	-	-	-	-
980	P48304	Lithostathine 1 beta precursor - Homo sapiens (Human)	1	-	-	-	-	-	-	-	-
981	P23141	Liver carboxylesterase 1 precursor (EC 3.1.1.1) (Acyl coenzyme A esterase)	-	-	-	-	-	5	7	X	-
982	P00338	L-lactate dehydrogenase A chain (EC 1.1.1.27) (LDH-A)	-	1	14	14	18	9	20	-	-
983	Q9BYZ2	L-lactate dehydrogenase A-like 6B (EC 1.1.1.27) - Homo sapiens	-	-	-	-	-	1	1	-	-
984	P07195	L-lactate dehydrogenase B chain (EC 1.1.1.27) (LDH-B)	2	6	14	5	22	9	19	X	-
985	P36776	Lon protease homolog, mitochondrial precursor (EC 3.4.21.26)	-	-	-	-	-	-	3	X	-
986	P33121	Long-chain-fatty-acid--CoA ligase 1 (EC 6.2.1.3) (Long-chain-fatty-acid-CoA ligase)	-	-	-	1	-	-	-	-	-
987	P08637	Low affinity immunoglobulin gamma Fc region receptor 1	-	-	-	-	-	-	1	-	-
988	O75015	Low affinity immunoglobulin gamma Fc region receptor 1	-	-	-	1	-	-	-	-	-
989	P24666	Low molecular weight phosphotyrosine protein phosphatase	-	3	4	-	5	5	4	X	-
990	Q07954	Low-density lipoprotein receptor-related protein 1 precursor	-	-	-	-	-	3	-	-	-
991	P14151	L-selectin precursor (Lymph node homing receptor) (L-selectin)	-	-	-	-	1	-	-	-	-
992	P51884	Lumican precursor (Keratan sulfate proteoglycan lumican)	1	-	-	-	-	-	-	-	-
993	P05455	Lupus La protein (Sjogren syndrome type B antigen) (Sjogren syndrome type B antigen)	-	-	-	-	6	-	3	X	-
994	Q7Z4W1	L-xylulose reductase (EC 1.1.1.10) (XR) (Dicarbonyl/L-xylulose reductase)	-	-	2	-	4	-	3	-	-
995	Q13094	Lymphocyte cytosolic protein 2 (SH2 domain-containing)	-	-	1	-	2	4	2	-	-
996	P33241	Lymphocyte-specific protein 1 (Protein pp52) (52 kDa)	-	-	-	2	3	2	-	-	-
997	P10253	Lysosomal alpha-glucosidase precursor (EC 3.2.1.20) (Alpha-glucosidase)	-	-	-	-	-	5	1	X	-
998	O00754	Lysosomal alpha-mannosidase precursor (EC 3.2.1.24) (Alpha-mannosidase)	-	-	-	-	1	3	2	-	-
999	P10619	Lysosomal protective protein precursor (EC 3.4.16.5) (Protective protein)	-	-	1	3	-	2	3	-	-
1000	P42785	Lysosomal Pro-X carboxypeptidase precursor (EC 3.4.21.100)	-	-	-	2	-	2	-	-	-
1001	P11279	Lysosome-associated membrane glycoprotein 1 precursor	-	-	-	4	1	4	4	-	-
1002	P13473	Lysosome-associated membrane glycoprotein 2 precursor	-	-	-	-	-	2	-	X	-

1003	P61626	Lysozyme C precursor (EC 3.2.1.17) (1,4-beta-N-acetylglucosaminidase)	1	-	-	5	2	10	8	-
1004	Q15046	Lysyl-tRNA synthetase (EC 6.1.1.6) (Lysine--tRNA ligase)	-	-	-	-	-	-	1	-
1005	P40121	Macrophage capping protein (Actin-regulatory protein)	-	1	-	8	4	8	4	X
1006	P14174	Macrophage migration inhibitory factor (MIF) (Phenylphosphorylcholine hydrolase)	-	-	1	1	1	1	1	X
1007	P34810	Macrosialin precursor (GP110) (CD68 antigen)	-	-	1	-	-	-	1	-
1008	Q86V88	Magnesium-dependent phosphatase 1 (EC 3.1.3.-) (EC 3.1.3.1)	-	-	-	2	-	-	-	-
1009	Q14728	Major facilitator superfamily domain-containing protein	-	-	-	1	-	1	1	-
1010	P04156	Major prion protein precursor (PrP) (PrP27-30) (PrP33-36)	-	-	1	-	-	-	-	-
1011	Q14764	Major vault protein (MVP) (Lung resistance-related protein)	-	11	-	-	10	3	7	X
1012	P40925	Malate dehydrogenase, cytoplasmic (EC 1.1.1.37) (Cytoplasmic malate dehydrogenase)	-	3	6	5	12	3	10	X
1013	P40926	Malate dehydrogenase, mitochondrial precursor (EC 1.1.1.40)	-	-	11	6	16	10	16	-
1014	Q9ULC4	Malignant T cell amplified sequence 1 OS=Homo sapiens	-	-	-	1	-	-	-	-
1015	O43451	Maltase-glucoamylase, intestinal [Includes: Maltase (EC 3.2.1.20)]	-	-	-	5	-	-	-	-
1016	Q8NFP4	MAM domain-containing glycosylphosphatidylinositol anchor	-	-	-	-	-	1	-	-
1017	O00187	Mannan-binding lectin serine protease 2 precursor (EC 3.4.21.26)	3	-	-	-	-	-	-	-
1018	Q9Y5P6	Mannose-1-phosphate guanylttransferase subunit beta	-	-	-	-	-	-	1	-
1019	O60664	Mannose-6-phosphate receptor-binding protein 1 (Carbohydrate binding protein)	-	-	1	3	1	4	5	X
1020	P11226	Mannose-binding protein C precursor (MBP-C) (MBP1)	1	-	-	-	-	-	-	-
1021	Q96L34	MAP/microtubule affinity-regulating kinase 4 (EC 2.7.1.1)	-	-	1	-	-	1	-	-
1022	Q8IX19	Mast cell-expressed membrane protein 1 - Homo sapiens	-	-	-	1	-	1	-	-
1023	P43243	Matrin-3	-	-	-	-	-	-	3	-
1024	P08493	Matrix Gla-protein precursor (MGP) (Cell growth-inhibitory protein)	1	-	-	-	-	-	-	-
1025	P14780	Matrix metalloproteinase-9 precursor (EC 3.4.24.35) (Hs-MMP-9)	-	-	-	21	3	14	-	-
1026	Q9NVC6	Mediator of RNA polymerase II transcription subunit 17	-	-	-	2	-	-	-	-
1027	O00264	Membrane-associated progesterone receptor component 1	-	-	3	-	-	-	1	-
1028	O15173	Membrane-associated progesterone receptor component 2	-	-	-	-	-	-	1	-
1029	Q96N66	Membrane-bound O-acyltransferase domain-containing protein	-	-	-	-	-	3	-	-
1030	Q13255	Metabotropic glutamate receptor 1 precursor (mGluR1)	-	-	-	1	-	-	-	-
1031	P01033	Metalloproteinase inhibitor 1 precursor (TIMP-1) (Erythrin)	1	-	5	-	-	-	-	-
1032	P16035	Metalloproteinase inhibitor 2 precursor (TIMP-2) (Tissue inhibitor of metalloproteinases)	3	-	-	-	-	-	-	-
1033	Q2M296	Methenyltetrahydrofolate synthetase domain-containing protein	-	1	-	-	-	-	-	-
1034	Q9NZL9	Methionine adenosyltransferase 2 subunit beta - Homo sapiens	-	1	-	-	3	-	-	-
1035	P50579	Methionine aminopeptidase 2 (EC 3.4.11.18) (MetAP 2)	-	-	-	-	1	-	2	-
1036	Q9NZV6	Methionine-R-sulfoxide reductase B1 - Homo sapiens	-	-	-	1	-	-	-	-
1037	Q9H8H3	Methyltransferase-like protein 7A precursor (EC 2.1.1.1)	-	-	-	-	-	3	1	-
1038	O14880	Microsomal glutathione S-transferase 3 (EC 2.5.1.18)	-	-	-	1	-	-	-	-
1039	P67812	Microsomal signal peptidase 18 kDa subunit (EC 3.4.21.1)	-	-	-	-	-	2	2	-
1040	Q9UPN3	Microtubule-actin cross-linking factor 1, isoforms 1/2/3	-	1	-	-	-	-	-	-
1041	Q66K74	Microtubule-associated protein 1S - Homo sapiens (Ht)	-	-	-	-	-	-	1	-
1042	P27816	Microtubule-associated protein 4 (MAP 4)	-	1	-	-	-	-	-	-
1043	Q15691	Microtubule-associated protein RP/EB family member	-	-	6	-	6	4	4	X
1044	Q15555	Microtubule-associated protein RP/EB family member	-	-	9	-	-	-	-	-
1045	Q8TCT9	Minor histocompatibility antigen H13 (EC 3.4.99.-) (Signal peptide)	-	-	-	-	-	1	-	-
1046	Q9Y2B0	MIR-interacting saposin-like protein precursor (Transmembrane protein)	-	-	-	-	3	2	1	X
1047	Q02978	Mitochondrial 2-oxoglutarate/malate carrier protein (Oxoglutarate/malate carrier)	-	-	-	-	-	-	2	-
1048	Q16540	Mitochondrial 39S ribosomal protein L23 (L23mt) (MR)	-	-	-	-	-	-	1	-
1049	Q9Y6C9	Mitochondrial carrier homolog 2 (Met-induced mitochondrial carrier)	-	-	-	-	1	1	1	-
1050	Q9Y5J7	Mitochondrial import inner membrane translocase subunit	-	-	-	-	2	-	-	-
1051	Q9NS69	Mitochondrial import receptor subunit TOM22 homolog	-	-	1	-	1	1	2	-
1052	P28482	Mitogen-activated protein kinase 1 (EC 2.7.1.37) (Extracellular signal-regulated kinase)	-	-	-	3	2	1	1	X
1053	Q16539	Mitogen-activated protein kinase 14 (EC 2.7.11.24) (Mitogen-activated protein kinase)	-	-	-	1	1	-	-	-
1054	Q9UHA4	Mitogen-activated protein kinase kinase 1-interacting protein	-	-	-	1	1	2	2	X
1055	Q9Y2Q5	Mitogen-activated protein-binding protein-interacting protein	-	-	-	-	-	1	1	-
1056	Q96T76	MMS19-like protein (hMMS19) (MET18 homolog) - Homo sapiens	-	-	-	-	1	-	-	-
1057	P26038	Moesin (Membrane-organizing extension spike protein)	-	1	10	19	24	21	30	X
1058	O95396	Molybdenum cofactor synthesis protein 3 (Molybdopterin synthase)	-	-	1	1	1	-	1	-

1059	P50224	Monoamine-sulfating phenol sulfotransferase (EC 2.8.	-	-	4	-	-	-	1	X
1060	O15427	Monocarboxylate transporter 4 (MCT 4) (MCT 3) (Solu	-	-	-	-	-	2	2	-
1061	P08571	Monocyte differentiation antigen CD14 precursor (Myc	-	-	-	-	-	1	-	-
1062	Q99685	Monoglyceride lipase (EC 3.1.1.23) (MGL) (HU-K5) (L	-	-	10	1	-	-	-	-
1063	Q7L9L4	Mps one binder kinase activator-like 1A (Mob1 homolo	-	-	2	1	2	1	3	X
1064	Q9H8S9	Mps one binder kinase activator-like 1B (Mob1 homolo	-	-	-	-	-	-	4	-
1065	Q96BX8	Mps one binder kinase activator-like 2A (Mob1 homolo	-	-	-	-	1	-	1	-
1066	P22234	Multifunctional protein ADE2 [Includes: Phosphoribosy	-	-	1	-	3	-	2	X
1067	Q13201	Multimerin-1 precursor (Endothelial cell multimerin 1) (	-	-	15	-	-	-	5	-
1068	Q9H8L6	Multimerin-2 precursor (EMILIN-3) (Elastin microfibril i	5	-	-	-	-	-	-	-
1069	O00499	Myc box-dependent-interacting protein 1 (Bridging inte	-	-	-	-	1	-	1	-
1070	P24158	Myeloblastin precursor (EC 3.4.21.76) (Leukocyte prot	-	-	-	4	4	4	2	-
1071	P41218	Myeloid cell nuclear differentiation antigen	-	-	-	5	-	1	3	-
1072	P05164	Myeloperoxidase precursor (EC 1.11.1.7) (MPO) [Con	-	-	-	33	8	20	20	-
1073	Q9NZM1	Myoferlin (Fer-1-like protein 3) - Homo sapiens (Huma	1	-	-	-	-	-	-	-
1074	Q12965	Myosin Ie (Myosin Ic)	-	-	-	1	-	1	-	-
1075	O00160	Myosin If (Myosin-IE)	-	-	-	5	2	6	6	-
1076	P05976	Myosin light chain 1, skeletal muscle isoform (MLC1F)	-	-	-	-	-	-	1	-
1077	Q15746	Myosin light chain kinase, smooth muscle (EC 2.7.11.1	-	-	2	-	-	-	-	-
1078	P60660	Myosin light polypeptide 6 (Myosin light chain alkali 3)	-	-	10	1	8	8	8	-
1079	P19105	Myosin regulatory light chain 2, nonsarcomeric (Myosin	-	-	7	2	7	5	8	X
1080	P35580	Myosin-10 (Myosin heavy chain, nonmuscle IIb) (Nonm	-	-	-	-	8	-	20	-
1081	Q7Z406	Myosin-14 (Myosin heavy chain, nonmuscle IIc) (Nonm	-	1	-	3	5	3	-	-
1082	P35579	Myosin-9 (Myosin heavy chain, nonmuscle IIa) (Nonm	-	25	76	28	71	63	156	-
1083	P58546	Myotrophin (V-1 protein)	-	-	5	3	3	5	5	X
1084	P29966	Myristoylated alanine-rich C-kinase substrate (MARCK	-	-	-	-	-	-	3	-
1085	P20933	N(4)-(beta-N-acetylglucosaminy)-L-asparaginase prec	-	-	-	-	-	-	1	-
1086	Q9UJ70	N-acetylglucosamine kinase (EC 2.7.1.59) (GlcNAc kir	-	1	-	2	2	7	7	X
1087	P15586	N-acetylglucosamine-6-sulfatase precursor (EC 3.1.6.1	-	1	-	-	-	1	-	-
1088	Q96PD5	N-acetylmuramoyl-L-alanine amidase precursor (EC 3	4	-	-	-	-	-	-	-
1089	Q9GZZ1	N-acetyltransferase 13 - Homo sapiens (Human)	-	-	-	-	2	1	2	-
1090	Q02083	N-acyl ethanolamine-hydrolyzing acid amidase precurs	-	-	-	-	-	-	1	-
1091	Q13423	NAD(P) transhydrogenase, mitochondrial precursor (E	-	-	-	-	-	6	3	-
1092	P23368	NAD-dependent malic enzyme, mitochondrial precursor	-	-	1	-	2	-	4	X
1093	Q86Y39	NADH dehydrogenase [ubiquinone] 1 alpha subcomple	-	-	-	-	-	-	2	-
1094	O00483	NADH dehydrogenase [ubiquinone] 1 alpha subcomple	-	-	-	-	2	2	1	-
1095	O95182	NADH dehydrogenase [ubiquinone] 1 alpha subcomple	-	-	-	-	-	1	2	-
1096	Q16795	NADH dehydrogenase [ubiquinone] 1 alpha subcomple	-	-	-	-	2	2	2	-
1097	O96000	NADH dehydrogenase [ubiquinone] 1 beta subcomple	-	-	-	-	1	4	2	-
1098	O95168	NADH dehydrogenase [ubiquinone] 1 beta subcomple	-	-	-	-	-	-	3	-
1099	O43920	NADH dehydrogenase [ubiquinone] iron-sulfur protein	-	-	-	-	-	-	2	-
1100	O75251	NADH dehydrogenase [ubiquinone] iron-sulfur protein	-	-	-	-	1	-	3	-
1101	P00387	NADH-cytochrome b5 reductase (EC 1.6.2.2) (B5R) (E	-	-	6	-	2	-	1	-
1102	O75380	NADH-ubiquinone oxidoreductase 13 kDa-A subunit, r	-	-	-	-	-	-	1	-
1103	Q16718	NADH-ubiquinone oxidoreductase 13 kDa-B subunit (E	-	-	1	-	1	1	1	X
1104	O00217	NADH-ubiquinone oxidoreductase 23 kDa subunit, mit	-	-	-	-	2	1	2	-
1105	P19404	NADH-ubiquinone oxidoreductase 24 kDa subunit, mit	-	-	-	-	1	1	-	X
1106	O75489	NADH-ubiquinone oxidoreductase 30 kDa subunit, mit	-	-	-	-	5	3	7	X
1107	O95299	NADH-ubiquinone oxidoreductase 42 kDa subunit, mit	-	-	-	-	2	1	1	-
1108	P28331	NADH-ubiquinone oxidoreductase 75 kDa subunit, mit	-	-	-	-	3	1	3	X
1109	P56556	NADH-ubiquinone oxidoreductase B14 subunit (EC 1.6	-	-	-	-	-	-	2	-
1110	Q9P0J0	NADH-ubiquinone oxidoreductase B16.6 subunit (EC	-	-	-	-	-	1	3	-
1111	Q9Y5S8	NADPH oxidase homolog 1 (NOX-1) (NOH-1) (NADH/	-	-	-	-	-	1	1	-
1112	Q13765	Nascent polypeptide-associated complex alpha subun	-	-	1	-	6	2	4	X
1113	P49279	Natural resistance-associated macrophage protein 1 (N	-	-	-	-	-	1	-	-
1114	P55160	Nck-associated protein 1-like (Membrane-associated p	-	-	-	-	1	-	1	-

1115	Q92597	NDRG1 protein (N-myc downstream-regulated gene 1	-	-	-	-	2	-	2	X
1116	Q15843	NEDD8 precursor (Ubiquitin-like protein Nedd8) (Nedd	-	-	-	1	1	2	-	-
1117	P61081	NEDD8-conjugating enzyme Ubc12 (EC 6.3.2.-) (Ubiq	-	-	2	-	-	4	2	X
1118	P08473	Neprilysin (EC 3.4.24.11) (Neutral endopeptidase) (NE	-	-	-	1	-	-	-	-
1119	Q8WXH0	Nesprin-2 (Nuclear envelope spectrin repeat protein 2)	-	-	-	-	-	1	-	-
1120	Q09666	Neuroblast differentiation-associated protein AHNAK (	-	-	-	-	-	16	13	-
1121	Q14697	Neutral alpha-glucosidase AB precursor (EC 3.2.1.84)	-	7	10	4	13	19	21	X
1122	P22894	Neutrophil collagenase precursor (EC 3.4.24.34) (Matr	-	-	-	9	-	4	-	-
1123	P14598	Neutrophil cytosol factor 1 (NCF-1) (Neutrophil NADPH	-	-	-	6	-	3	1	-
1124	P19878	Neutrophil cytosol factor 2 (NCF-2) (Neutrophil NADPH	-	-	-	4	-	3	-	-
1125	Q15080	Neutrophil cytosol factor 4 (NCF-4) (Neutrophil NADPH	-	-	-	4	-	3	-	-
1126	P59665	Neutrophil defensin 1 precursor (HNP-1) (HP-1) (HP1)	-	-	-	3	-	-	-	-
1127	P80188	Neutrophil gelatinase-associated lipocalin precursor (N	3	-	-	13	5	6	-	-
1128	Q0ZGT2	Nexilin - Homo sapiens (Human)	-	-	3	-	-	-	-	-
1129	O95865	NG,NG-dimethylarginine dimethylaminohydrolase 2 (E	-	-	-	-	2	-	-	X
1130	P55769	NHP2-like protein 1 (High mobility group-like nuclear p	-	-	-	-	-	-	2	-
1131	Q9BZQ8	Niban protein	-	-	-	-	-	-	1	-
1132	Q96TA1	Niban-like protein (Meg-3)	-	4	-	-	-	2	-	-
1133	P43490	Nicotinamide phosphoribosyltransferase (EC 2.4.2.12)	-	-	-	11	1	-	-	X
1134	Q6XQN6	Nicotinate phosphoribosyltransferase - Homo sapiens	-	1	1	2	-	1	2	-
1135	P14543	Nidogen-1 precursor (Entactin) - Homo sapiens (Huma	-	-	6	-	-	-	-	-
1136	Q86X76	Nitrilase homolog 1 (EC 3.5.-.-) - Homo sapiens (Huma	-	-	-	1	-	-	-	X
1137	Q9NQR4	Nitrilase homolog 2 - Homo sapiens (Human)	-	-	-	1	-	4	3	-
1138	P05204	Nonhistone chromosomal protein HMG-17 (High-mobil	-	-	-	-	-	-	1	-
1139	P10153	Nonsecretory ribonuclease precursor (EC 3.1.27.5) (R	-	-	-	5	1	3	-	-
1140	P22307	Nonspecific lipid-transfer protein, mitochondrial precur	-	-	-	1	-	-	2	X
1141	Q9UNZ2	NSFL1 cofactor p47 (p97 cofactor p47)	-	1	-	-	4	-	2	X
1142	P41227	N-terminal acetyltransferase complex ARD1 subunit h	-	-	-	-	1	-	-	-
1143	P49321	Nuclear autoantigenic sperm protein (NASP) - Homo s	-	-	-	-	1	1	1	-
1144	P82979	Nuclear protein Hcc-1 (Proliferation-associated cytokin	-	-	-	-	-	-	1	-
1145	P61970	Nuclear transport factor 2 (NTF-2) (Placental protein 1	-	-	-	-	3	3	4	X
1146	P67809	Nuclease sensitive element-binding protein 1 (Y-box-b	-	-	-	-	1	-	1	-
1147	P19338	Nucleolin (Protein C23)	-	-	-	1	10	-	4	-
1148	P06748	Nucleophosmin (NPM) (Nucleolar phosphoprotein B23	-	-	-	-	2	1	4	X
1149	P52594	Nucleoporin-like protein RIP (HIV-1 Rev-binding protei	-	-	1	-	-	-	-	-
1150	P15531	Nucleoside diphosphate kinase A (EC 2.7.4.6) (NDK A	-	4	8	5	7	8	7	X
1151	P22392	Nucleoside diphosphate kinase B (EC 2.7.4.6) (NDK B	-	-	9	7	10	9	8	-
1152	Q96DE0	Nucleoside diphosphate-linked moiety X motif 16 (EC	-	-	-	-	-	3	1	X
1153	P55209	Nucleosome assembly protein 1-like 1 (NAP-1-related	-	-	5	-	-	2	-	-
1154	Q99733	Nucleosome assembly protein 1-like 4 (Nucleosome a	-	-	-	-	2	-	3	-
1155	Q9Y5Y2	Nucleotide-binding protein 2 (NBP 2)	-	-	-	-	1	-	1	X
1156	Q8WVJ2	NudC domain-containing protein 2 - Homo sapiens (Hu	-	-	-	-	1	1	-	-
1157	Q56VL3	OCIA domain-containing protein 2 - Homo sapiens (Hu	-	-	-	-	-	-	2	-
1158	Q6UX06	Olfactomedin-4 precursor - Homo sapiens (Human)	-	-	-	6	-	-	-	-
1159	Q9NZT2	Opioid growth factor receptor (OGFr) (Zeta-type opioi	-	-	-	-	-	-	1	-
1160	Q92882	Osteoclast-stimulating factor 1	-	-	2	4	4	5	5	X
1161	P78380	Oxidized low-density lipoprotein receptor 1 - Homo sag	-	-	-	1	-	-	-	-
1162	P50897	Palmitoyl-protein thioesterase 1 precursor (EC 3.1.2.2	-	-	-	-	-	-	1	-
1163	O95497	Pantetheinase precursor (EC 3.5.1.92) (Pantetheine h	-	-	-	1	-	-	-	-
1164	P20962	Parathymosin - Homo sapiens (Human)	-	-	-	-	-	-	1	-
1165	P49023	Paxillin	-	-	-	-	-	-	3	-
1166	O00151	PDZ and LIM domain protein 1 (Elfin) (LIM domain pro	-	-	21	-	2	-	6	X
1167	Q9UBV8	Peflin (PEF protein with a long N-terminal hydrophobic	-	-	-	2	-	-	-	-
1168	Q9UJ68	Peptide methionine sulfoxide reductase (EC 1.8.4.11)	-	-	-	2	-	-	-	-
1169	O75594	Peptidoglycan recognition protein precursor (PGRP-S)	-	-	-	4	-	2	-	-
1170	P62937	Peptidyl-prolyl cis-trans isomerase A (EC 5.2.1.8) (PPI	2	5	10	6	14	12	12	X

1171	P23284	Peptidyl-prolyl cis-trans isomerase B precursor (EC 5.2.1.8) (PPIB)	1	-	14	5	7	10	14	X
1172	Q9UNP9	Peptidyl-prolyl cis-trans isomerase E (EC 5.2.1.8) (PPIE)	-	-	-	-	-	-	1	X
1173	Q13526	Peptidyl-prolyl cis-trans isomerase NIMA-interacting 1 (PIN1)	-	-	-	-	1	-	-	X
1174	Q9Y237	Peptidyl-prolyl cis-trans isomerase NIMA-interacting 4 (PIN4)	-	-	-	-	-	-	2	-
1175	P30405	Peptidyl-prolyl cis-trans isomerase, mitochondrial precursor (PPIB)	-	-	5	-	-	1	-	-
1176	Q9Y3C6	Peptidyl-prolyl cis-trans isomerase-like 1 (EC 5.2.1.8) (PPIB)	-	1	-	-	-	-	2	-
1177	Q9H2H8	Peptidyl-prolyl cis-trans isomerase-like 3 (EC 5.2.1.8) (PPIB)	-	-	-	1	2	2	1	-
1178	Q9Y3E5	Peptidyl-tRNA hydrolase 2, mitochondrial precursor (EPT2)	-	-	-	-	-	1	-	X
1179	P14222	Perforin-1 precursor (P1) (Lymphocyte pore forming protein)	-	-	-	-	1	-	6	-
1180	Q06830	Peroxiredoxin-1 (EC 1.11.1.15) (Thioredoxin peroxidase)	-	5	7	2	17	15	19	X
1181	P32119	Peroxiredoxin-2 (EC 1.11.1.15) (Thioredoxin peroxidase)	-	16	5	5	15	12	11	X
1182	Q13162	Peroxiredoxin-4 (EC 1.11.1.15) (Prx-IV) (Thioredoxin peroxidase)	-	-	6	-	3	2	3	X
1183	P30044	Peroxiredoxin-5, mitochondrial precursor (EC 1.11.1.15) (Prx-V)	-	-	7	10	10	11	9	X
1184	P30041	Peroxiredoxin-6 (EC 1.11.1.15) (Antioxidant protein 2) (Prx-VI)	-	5	20	11	14	8	14	X
1185	P51659	Peroxisomal multifunctional enzyme type 2 (MFE-2) (PEX2)	-	-	2	-	-	1	1	-
1186	Q8WW12	PEST proteolytic signal-containing nuclear protein (PEST)	-	-	-	-	-	-	2	-
1187	Q00325	Phosphate carrier protein, mitochondrial precursor (PTC1)	-	-	-	-	1	2	6	-
1188	P30086	Phosphatidylethanolamine-binding protein (PEBP) (Protein)	-	6	5	5	13	10	14	X
1189	Q9NTJ5	Phosphatidylinositol phosphatase SAC1 - Homo sapiens	-	-	1	-	-	-	-	-
1190	Q8TCU6	Phosphatidylinositol 3,4,5-trisphosphate-dependent Rac guanine nucleotide exchange factor 1 (PHOEX)	-	-	-	-	-	1	1	-
1191	P27986	Phosphatidylinositol 3-kinase regulatory subunit alpha (PI3K)	-	-	-	-	-	-	1	-
1192	Q00169	Phosphatidylinositol transfer protein alpha isoform (PtdITP)	-	1	-	-	1	1	1	X
1193	P48739	Phosphatidylinositol transfer protein beta isoform (PtdITP)	-	-	-	-	1	-	1	X
1194	P48426	Phosphatidylinositol-4-phosphate 5-kinase type-2 alpha (PIP2K)	-	-	2	-	3	-	3	-
1195	P80108	Phosphatidylinositol-glycan-specific phospholipase D 2 (PLD2)	5	-	-	-	-	-	-	-
1196	Q16822	Phosphoenolpyruvate carboxykinase [GTP], mitochondrial	-	-	-	-	-	1	1	X
1197	P36871	Phosphoglucomutase-1 (EC 5.4.2.2) (Glucose phosphomutase)	-	-	5	6	5	-	4	X
1198	Q96G03	Phosphoglucomutase-2 (EC 5.4.2.2) (Glucose phosphomutase)	-	-	-	1	6	1	7	-
1199	P00558	Phosphoglycerate kinase 1 (EC 2.7.2.3) (Primer recognition)	-	8	16	20	21	15	23	X
1200	P18669	Phosphoglycerate mutase 1 (EC 5.4.2.1) (EC 5.4.2.4)	-	-	7	9	15	12	15	X
1201	P36969	Phospholipid hydroperoxide glutathione peroxidase, mitochondrial	-	-	2	-	4	2	3	-
1202	P55058	Phospholipid transfer protein precursor (Lipid transfer protein)	1	-	-	-	-	-	-	-
1203	Q9H008	Phospholysine phosphohistidine inorganic pyrophosphatase	-	-	-	1	2	-	3	-
1204	Q15126	Phosphomevalonate kinase (EC 2.7.4.2) (PMKase)	-	-	2	-	1	1	-	X
1205	O60256	Phosphoribosyl pyrophosphate synthetase-associated protein	-	-	-	-	1	-	-	-
1206	O15067	Phosphoribosylformylglycinamide synthase (EC 6.3.4.12)	-	-	-	-	-	-	2	X
1207	Q96BW5	Phosphotriesterase-related protein (Parathion hydrolase)	-	-	-	-	2	-	-	X
1208	P36955	Pigment epithelium-derived factor precursor (PEDF) (Secreted)	4	-	-	-	-	-	-	-
1209	P35237	Placental thrombin inhibitor (Cytoplasmic antiproteinasin)	-	-	3	2	2	6	3	X
1210	P03952	Plasma kallikrein precursor (EC 3.4.21.34) (Plasma prokallikrein)	5	-	-	-	-	-	-	-
1211	P23634	Plasma membrane calcium-transporting ATPase 4 - Homo sapiens	-	-	-	-	-	4	-	-
1212	P05155	Plasma protease C1 inhibitor precursor (C1 Inh) (C1In)	15	-	-	-	-	-	2	X
1213	P02753	Plasma retinol-binding protein precursor (PRBP) (RBP)	7	-	-	-	1	-	1	X
1214	P05121	Plasminogen activator inhibitor 1 precursor (PAI-1) (EPAI1)	-	-	2	-	-	-	-	X
1215	Q8NC51	Plasminogen activator inhibitor 1 RNA-binding protein	-	-	-	-	1	-	1	-
1216	P05120	Plasminogen activator inhibitor 2 precursor (PAI-2) (PI2)	-	-	-	-	-	1	1	X
1217	P00747	Plasminogen precursor (EC 3.4.21.7) [Contains: Plasminogen]	10	-	2	-	-	-	3	-
1218	Q02325	Plasminogen-related protein B precursor - Homo sapiens	1	-	-	-	-	-	-	-
1219	P13796	Plastin-2 (L-plastin) (Lymphocyte cytosolic protein 1) (LPL)	-	-	-	31	47	39	45	X
1220	P02775	Platelet basic protein precursor (PBP) (Small inducible)	2	-	9	2	-	-	6	-
1221	P16284	Platelet endothelial cell adhesion molecule precursor (PECAM-1)	-	5	5	-	-	1	2	-
1222	P02776	Platelet factor 4 precursor (PF-4) (CXCL4) (Oncostatin M)	1	-	6	-	-	-	6	-
1223	P10720	Platelet factor 4 variant precursor (PF4var1) (PF4alt) (PF4)	-	-	3	-	-	-	-	-
1224	P16671	Platelet glycoprotein 4 (Platelet glycoprotein IV) (GPVI)	-	-	5	-	-	1	1	-
1225	P07359	Platelet glycoprotein Ib alpha chain precursor (Glycoprotein Ib)	-	-	8	-	-	-	-	-
1226	P13224	Platelet glycoprotein Ib beta chain precursor (GP-Ib beta)	-	-	4	-	-	-	2	-

1227	P14770	Platelet glycoprotein IX precursor (GPIX) (CD42a antigen)	-	-	5	-	-	-	2	-
1228	P40197	Platelet glycoprotein V precursor (GPV) (CD42D antigen)	-	-	7	-	-	-	1	-
1229	Q9HCN6	Platelet glycoprotein VI precursor - Homo sapiens (Human)	-	-	1	-	-	-	-	-
1230	Q9H7M9	Platelet receptor Gi24 precursor - Homo sapiens (Human)	-	-	1	-	-	1	1	-
1231	P43034	Platelet-activating factor acetylhydrolase IB alpha subunit	-	1	1	-	4	2	2	-
1232	P68402	Platelet-activating factor acetylhydrolase IB beta subunit	-	-	4	-	2	2	2	X
1233	Q15102	Platelet-activating factor acetylhydrolase IB gamma subunit	-	-	-	-	3	1	2	X
1234	P08567	Pleckstrin (Platelet p47 protein)	-	-	16	3	2	-	11	-
1235	Q96S99	Pleckstrin homology domain-containing family F member 1	-	-	-	-	-	-	1	-
1236	O15031	Plexin-B2 precursor (MM1) - Homo sapiens (Human)	-	-	-	-	-	1	-	-
1237	Q9UKK3	Poly [ADP-ribose] polymerase 4 (EC 2.4.2.30) (PARP-1)	-	-	-	-	-	1	-	-
1238	Q9NX46	Poly(ADP-ribose) glycohydrolase ARH3 - Homo sapiens (Human)	-	1	-	-	1	-	1	-
1239	Q15365	Poly(rC)-binding protein 1 (Alpha-CP1) (hnRNP-E1) (Nucleophosmin 1)	-	-	5	3	9	5	7	X
1240	Q15366	Poly(rC)-binding protein 2 (Alpha-CP2) (hnRNP-E2) (Nucleophosmin 2)	-	-	1	-	5	6	6	X
1241	P11940	Polyadenylate-binding protein 1 (Poly(A)-binding protein 1)	-	-	1	-	3	1	2	-
1242	P26599	Polypyrimidine tract-binding protein 1 (PTB) (Heterogeneous nuclear ribonucleoprotein A)	-	-	1	-	3	5	7	-
1243	P08397	Porphobilinogen deaminase (EC 2.5.1.61) (Hydroxymethylglutaryl-CoA lyase)	-	-	-	-	2	-	-	-
1244	Q96CX2	Potassium channel tetramerisation domain-containing protein 1	-	-	-	2	-	12	6	X
1245	O75915	PRA1 family protein 3 (ARL-6-interacting protein 5) (ARL6IP5)	-	-	-	-	2	1	4	-
1246	Q9UHV9	Prefoldin subunit 2	-	-	1	-	4	2	1	X
1247	P61758	Prefoldin subunit 3 (Von Hippel-Lindau-binding protein 1)	-	-	1	-	1	-	1	X
1248	Q9NQP4	Prefoldin subunit 4 (Protein C-1) - Homo sapiens (Human)	-	-	-	-	1	-	-	-
1249	Q99471	Prefoldin subunit 5 (C-myc-binding protein Mm-1) (Myc-binding protein 1)	-	-	-	-	2	1	1	X
1250	P20742	Pregnancy zone protein precursor	10	-	-	-	-	3	14	-
1251	Q5JRX3	Presequence protease, mitochondrial precursor (EC 3.4.21.10)	-	1	-	-	1	-	-	-
1252	P07602	Proactivator polypeptide precursor [Contains: Saposin B]	-	-	-	4	-	6	2	X
1253	P38919	Probable ATP-dependent RNA helicase DDX48 (EC 3.6.4.12)	-	-	-	-	4	1	2	X
1254	Q9HA77	Probable cysteinyl-tRNA synthetase, mitochondrial precursor	-	-	-	1	-	-	-	-
1255	Q8TEA8	Probable D-tyrosyl-tRNA(Tyr) deacylase 1 (EC 3.1.1.15)	-	-	1	-	-	-	-	-
1256	Q86Y34	Probable G-protein coupled receptor 97 precursor (GPR97)	-	-	-	2	-	-	-	-
1257	O96008	Probable mitochondrial import receptor subunit TOM40	-	-	-	-	1	-	1	X
1258	Q8N0Y7	Probable phosphoglycerate mutase 4 (EC 5.4.2.1) (EC 5.4.2.1)	-	-	-	-	-	1	-	-
1259	P98196	Probable phospholipid-transporting ATPase 1H (EC 3.6.3.1)	-	-	-	-	-	1	-	-
1260	Q86YV0	Probable Ras GTPase-activating protein FLJ00412 - Homo sapiens	-	-	-	-	-	-	1	-
1261	P07737	Profilin-1 (Profilin I)	3	-	17	11	12	15	14	X
1262	Q8WUM4	Programmed cell death 6-interacting protein (PDCD6-interacting protein 1)	-	1	1	-	8	8	10	X
1263	Q9BUL8	Programmed cell death protein 10 (TF-1 cell apoptosis-inducing factor 10)	-	-	5	-	3	-	3	-
1264	Q53EL6	Programmed cell death protein 4 (Nuclear antigen H73)	-	-	-	-	2	-	1	-
1265	O75340	Programmed cell death protein 6 (Probable calcium-binding protein)	-	-	2	2	4	5	5	X
1266	P35232	Prohibitin	-	-	7	1	7	7	8	X
1267	Q99623	Prohibitin-2 (B-cell receptor-associated protein BAP37)	-	-	7	-	8	2	11	-
1268	Q9HCU5	Prolactin regulatory element-binding protein (Mammalian)	-	-	-	1	-	-	-	-
1269	P12273	Prolactin-inducible protein precursor (Secretory actin-binding protein)	2	-	-	-	-	-	-	X
1270	P12004	Proliferating cell nuclear antigen (PCNA) (Cyclin) - Homo sapiens	-	-	-	-	1	-	-	-
1271	Q9UQ80	Proliferation-associated protein 2G4 (Cell cycle protein 2G4)	-	-	1	-	2	-	2	X
1272	O94903	Proline synthetase co-transcribed bacterial homolog protein	-	-	1	1	5	1	4	-
1273	Q9H939	Proline-serine-threonine phosphatase-interacting protein	-	-	5	-	1	-	-	-
1274	P48147	Prolyl endopeptidase (EC 3.4.21.26) (Post-proline cleaving enzyme)	-	-	1	-	1	-	1	X
1275	P27918	Properdin precursor (Factor P) - Homo sapiens (Human)	-	-	-	1	-	-	-	-
1276	Q8NBP7	Proprotein convertase subtilisin/kexin type 9 precursor	2	-	-	-	-	-	-	-
1277	Q15185	Prostaglandin H synthase 3 (EC 5.3.99.3) (Cytosolic phospholipase A2)	-	-	2	1	5	4	5	X
1278	P41222	Prostaglandin-H2 D-isomerase precursor (EC 5.3.99.2)	1	-	-	-	-	-	-	-
1279	Q6S8J3	Prostate, ovary, testis-expressed protein on chromosome 1	-	-	-	8	-	-	9	-
1280	Q06323	Proteasome activator complex subunit 1 (Proteasome activator complex subunit 1)	-	-	7	6	16	11	16	X
1281	Q9UL46	Proteasome activator complex subunit 2 (Proteasome activator complex subunit 2)	-	1	6	5	12	9	11	X
1282	P61289	Proteasome activator complex subunit 3 (Proteasome activator complex subunit 3)	-	-	-	-	1	-	-	X

1283	Q92530	Proteasome inhibitor PI31 subunit (hPI31) - Homo sap	-	-	-	-	2	-	-	-
1284	P25786	Proteasome subunit alpha type 1 (EC 3.4.25.1) (Protea	-	-	2	1	7	3	9	X
1285	P25787	Proteasome subunit alpha type 2 (EC 3.4.25.1) (Protea	-	1	4	2	6	6	5	X
1286	P25788	Proteasome subunit alpha type 3 (EC 3.4.25.1) (Protea	-	1	3	-	8	4	8	X
1287	P25789	Proteasome subunit alpha type 4 (EC 3.4.25.1) (Protea	-	-	2	-	7	4	6	X
1288	P28066	Proteasome subunit alpha type 5 (EC 3.4.25.1) (Protea	-	-	2	-	3	3	7	-
1289	P60900	Proteasome subunit alpha type 6 (EC 3.4.25.1) (Protea	-	1	2	-	6	5	10	X
1290	O14818	Proteasome subunit alpha type 7 (EC 3.4.25.1) (Protea	-	-	3	1	10	6	8	X
1291	Q8TAA3	Proteasome subunit alpha type 7-like (EC 3.4.25.1)	-	-	-	-	-	-	4	-
1292	P20618	Proteasome subunit beta type 1 (EC 3.4.25.1) (Protea	-	-	5	1	9	8	10	-
1293	P40306	Proteasome subunit beta type 10 precursor (EC 3.4.25	-	-	-	-	4	1	3	X
1294	P49721	Proteasome subunit beta type 2 (EC 3.4.25.1) (Protea	-	-	3	-	6	5	8	X
1295	P49720	Proteasome subunit beta type 3 (EC 3.4.25.1) (Protea	-	-	4	1	6	5	8	X
1296	P28070	Proteasome subunit beta type 4 precursor (EC 3.4.25.	-	-	1	-	1	2	4	X
1297	P28074	Proteasome subunit beta type 5 precursor (EC 3.4.25.	-	3	-	-	1	-	-	-
1298	P28062	Proteasome subunit beta type 8 precursor (EC 3.4.25.	-	-	5	1	8	7	6	-
1299	P28065	Proteasome subunit beta type 9 precursor (EC 3.4.25.	-	-	1	-	7	5	6	X
1300	Q5VYK3	Proteasome-associated protein ECM29 homolog (Ecm	-	-	-	-	-	-	2	-
1301	P11171	Protein 4.1 (Band 4.1) (P4.1) (EPB4.1) (4.1R) - Homo	-	11	1	-	-	-	1	-
1302	Q99873	Protein arginine N-methyltransferase 1 (EC 2.1.1.-) (In	-	-	-	-	1	-	-	-
1303	Q562R1	Protein beta-actin-like - Homo sapiens (Human)	-	-	10	6	9	7	8	-
1304	Q9NQ88	Protein C12orf5	-	-	-	-	-	1	2	-
1305	Q9Y224	Protein C14orf166	-	-	-	-	5	-	1	X
1306	Q969H8	Protein C19orf10 precursor (Stromal cell-derived grow	-	-	-	-	3	4	3	X
1307	Q9NQG5	Protein C20orf77	-	-	-	-	-	-	3	X
1308	Q9P1F3	Protein C6orf115	-	-	-	2	1	1	2	X
1309	O75223	Protein C7orf24	-	-	-	1	1	1	2	X
1310	Q9NZB2	Protein C9orf10	-	-	-	-	1	-	-	-
1311	Q9UKY7	Protein CDV3 homolog - Homo sapiens (Human)	-	-	-	-	2	-	1	-
1312	Q8WUX9	Protein CHMP7 - Homo sapiens (Human)	-	-	-	-	2	1	-	-
1313	Q2KHT3	Protein CLEC16A - Homo sapiens (Human)	-	-	1	-	-	-	-	-
1314	O75629	Protein CREG1 precursor (Cellular repressor of E1A-s	-	-	-	1	1	2	-	-
1315	O60888	Protein CutA precursor (Brain acetylcholinesterase pu	-	-	-	-	1	1	1	-
1316	O60610	Protein diaphanous homolog 1 (Diaphanous-related fo	-	-	13	-	12	5	24	-
1317	Q9NSV4	Protein diaphanous homolog 3 (Diaphanous-related fo	-	-	1	-	-	-	-	-
1318	P30101	Protein disulfide-isomerase A3 precursor (EC 5.3.4.1)	-	-	12	5	16	17	20	X
1319	P13667	Protein disulfide-isomerase A4 precursor (EC 5.3.4.1)	-	-	-	-	2	3	8	X
1320	Q15084	Protein disulfide-isomerase A6 precursor (EC 5.3.4.1)	-	-	11	-	7	7	6	X
1321	P07237	Protein disulfide-isomerase precursor (EC 5.3.4.1) (PD	-	-	13	10	5	14	16	X
1322	Q99497	Protein DJ-1 (Oncogene DJ1)	-	3	7	6	7	7	12	X
1323	Q9H098	Protein FAM107B - Homo sapiens (Human)	-	-	-	-	3	-	-	-
1324	Q8IZP2	Protein FAM10A4	-	-	3	-	-	-	3	-
1325	Q9BUR5	Protein FAM121B precursor - Homo sapiens (Human)	-	-	-	-	-	1	2	-
1326	Q9H0Q0	Protein FAM49A	-	-	-	-	-	-	2	-
1327	Q9NUQ9	Protein FAM49B (L1)	-	-	-	10	4	8	12	-
1328	Q9BSJ8	Protein FAM62A (Membrane-bound C2 domain-contai	-	1	2	-	10	6	18	-
1329	P49354	Protein farnesyltransferase/geranylgeranyltransferase	-	-	-	1	-	-	-	X
1330	Q13045	Protein flightless-1 homolog	-	-	-	-	-	-	6	-
1331	Q6NYC8	Protein KIAA1949 - Homo sapiens (Human)	-	-	-	-	1	-	2	-
1332	Q8N163	Protein KIAA1967 (Deleted in breast cancer gene 1 pr	-	-	-	-	-	-	6	-
1333	P17252	Protein kinase C alpha type (EC 2.7.11.13) (PKC-alpha	-	-	1	-	1	2	-	-
1334	P05771	Protein kinase C beta type (EC 2.7.11.13) (PKC-beta)	-	-	-	-	-	-	3	-
1335	Q05655	Protein kinase C delta type (EC 2.7.11.13) (nPKC-delt	-	-	-	1	-	1	1	-
1336	Q86UE4	Protein LYRIC (Lysine-rich CEACAM1 co-isolated prot	-	-	-	-	1	-	-	-
1337	P61326	Protein mago nashi homolog	-	-	-	-	-	2	3	-
1338	Q96A72	Protein mago nashi homolog 2	-	-	-	-	-	-	4	X

1339	Q9BPW8	Protein NipSnap1 - Homo sapiens (Human)	-	-	-	-	-	-	5	-
1340	O75323	Protein NipSnap2 (Glioblastoma amplified sequence)	-	-	-	-	-	1	2	-
1341	Q9UFN0	Protein NipSnap3A (NipSnap4) (Target for Salmonella)	-	-	3	2	2	3	6	-
1342	Q96FA3	Protein pellino homolog 1 - Homo sapiens (Human)	-	-	1	-	-	-	1	-
1343	O14974	Protein phosphatase 1 regulatory subunit 12A (Myosin)	-	-	-	-	-	-	1	-
1344	Q15435	Protein phosphatase 1 regulatory subunit 7 (Protein ph	-	-	-	-	1	-	2	X
1345	P35813	Protein phosphatase 2C isoform alpha (EC 3.1.3.16) (	-	-	1	-	1	-	-	-
1346	O75688	Protein phosphatase 2C isoform beta (EC 3.1.3.16) (P	-	-	-	1	-	-	-	X
1347	Q96M27	Protein PPRC1 - Homo sapiens (Human)	-	-	-	-	1	-	-	-
1348	Q9P258	Protein RCC2 (Telophase disk protein of 60 kDa) (RC	-	-	-	-	1	-	1	-
1349	P80511	Protein S100-A12 (S100 calcium-binding protein A12)	-	-	-	3	-	3	-	X
1350	P25815	Protein S100-P (S100 calcium-binding protein P) - Hor	-	-	-	4	-	1	-	-
1351	Q01105	Protein SET (Phosphatase 2A inhibitor I2PP2A) (I-2PP	-	-	-	-	3	2	1	X
1352	Q15436	Protein transport protein Sec23A (SEC23-related prote	-	-	-	-	1	-	2	X
1353	O95486	Protein transport protein Sec24A (SEC24-related prote	-	-	-	-	-	1	-	-
1354	P53992	Protein transport protein Sec24C (SEC24-related prote	-	-	-	-	-	-	2	-
1355	O94979	Protein transport protein Sec31A - Homo sapiens (Hur	-	-	1	-	2	2	2	-
1356	P61619	Protein transport protein Sec61 subunit alpha isoform	-	-	-	-	1	1	-	-
1357	Q14761	Protein tyrosine phosphatase receptor type C-associat	-	-	-	-	1	-	3	-
1358	Q12974	Protein tyrosine phosphatase type IVA protein 2 (EC 3	-	-	1	-	1	-	2	-
1359	Q9BRP8	Protein wibg homolog - Homo sapiens (Human)	-	-	-	-	-	-	1	-
1360	Q9UK55	Protein Z-dependent protease inhibitor precursor (PZ-d	2	-	-	-	-	-	-	-
1361	Q9ULC6	Protein-arginine deiminase type-1 (EC 3.5.3.15) (Prote	-	-	1	-	1	1	1	-
1362	Q9Y2J8	Protein-arginine deiminase type-2 (EC 3.5.3.15) (Prote	-	-	-	1	-	1	-	-
1363	P21980	Protein-glutamine gamma-glutamyltransferase 2 (EC 2	-	5	-	-	-	-	-	X
1364	P22061	Protein-L-isoaspartate(D-aspartate) O-methyltransfera	-	1	3	2	6	3	9	X
1365	Q9Y2Y8	Proteoglycan 3 precursor (Eosinophil major basic prote	-	-	-	4	-	-	-	-
1366	Q92954	Proteoglycan-4 precursor (Lubricin) (Megakaryocyte-s	3	-	-	-	-	-	-	-
1367	Q04941	Proteolipid protein 2 (Intestinal membrane A4 protein)	-	-	2	1	1	2	1	-
1368	P00734	Prothrombin precursor (EC 3.4.21.5) (Coagulation fact	22	-	-	-	-	-	1	-
1369	P06454	Prothymosin alpha [Contains: Thymosin alpha-1]	-	-	-	-	-	1	-	-
1370	P01100	Proto-oncogene protein c-fos - Homo sapiens (Human)	-	-	-	-	-	1	-	-
1371	P09769	Proto-oncogene tyrosine-protein kinase FGR (EC 2.7.1	-	-	-	3	-	-	-	-
1372	P06241	Proto-oncogene tyrosine-protein kinase Fyn (EC 2.7.1	-	-	2	-	-	-	3	-
1373	P06239	Proto-oncogene tyrosine-protein kinase LCK (EC 2.7.1	-	-	-	-	1	-	2	-
1374	P12931	Proto-oncogene tyrosine-protein kinase Src (EC 2.7.10	-	-	7	-	-	-	5	-
1375	P15498	Proto-oncogene vav	-	-	-	-	-	-	1	-
1376	P16109	P-selectin precursor (Granule membrane protein 140)	-	-	6	-	-	1	1	-
1377	P61457	Pterin-4-alpha-carbinolamine dehydratase (EC 4.2.1.9	-	-	-	1	-	-	-	-
1378	P00491	Purine nucleoside phosphorylase (EC 2.4.2.1) (Inosine	-	4	17	14	16	11	16	X
1379	P55786	Puromycin-sensitive aminopeptidase (EC 3.4.11.-) (PS	-	1	-	-	1	3	5	-
1380	Q9NTK5	Putative GTP-binding protein PTD004	-	-	-	-	-	-	1	-
1381	Q14568	Putative heat shock protein HSP 90-alpha A2 - Homo	-	-	-	-	-	3	-	-
1382	Q6ZN80	Putative maltase-glucoamylase-like protein FLJ16351	-	-	-	3	-	-	-	-
1383	A6NI72	Putative neutrophil cytosol factor 1B OS=Homo sapier	-	-	-	2	-	-	-	-
1384	A8MVU1	Putative neutrophil cytosol factor 1C OS=Homo sapier	-	-	-	3	-	-	-	-
1385	O43143	Putative pre-mRNA-splicing factor ATP-dependent RN	-	-	-	-	-	-	3	-
1386	Q53FA7	Putative quinone oxidoreductase (EC 1.-.-.-) (Tumor p	-	-	-	2	-	-	-	-
1387	P98179	Putative RNA-binding protein 3 (RNA-binding motif pro	-	-	-	-	1	-	2	-
1388	Q9Y383	Putative RNA-binding protein Luc7-like 2 - Homo sapie	-	-	-	-	2	1	-	-
1389	Q8NFU3	Putative thiosulfate sulfurtransferase KAT (EC 2.8.1.1)	-	-	-	-	-	-	1	-
1390	Q9Y448	Putative TRAF4-associated factor 1 - Homo sapiens (H	-	-	-	-	-	-	1	-
1391	Q5T440	Putative transferase C1orf69, mitochondrial precursor	-	-	-	-	-	-	1	-
1392	Q9NTT1	Putative ubiquitin-conjugating enzyme E2 D3-like prote	-	-	2	-	-	2	2	-
1393	O00764	Pyridoxal kinase (EC 2.7.1.35) (Pyridoxine kinase)	-	-	-	3	3	2	3	X
1394	P08559	Pyruvate dehydrogenase E1 component alpha subunit	-	-	-	-	-	-	3	X

1395	P11177	Pyruvate dehydrogenase E1 component beta subunit	-	-	2	-	5	-	9	X
1396	Q8NCN5	Pyruvate dehydrogenase phosphatase regulatory subunit	-	-	-	-	1	-	-	-
1397	P14618	Pyruvate kinase isozymes M1/M2 (EC 2.7.1.40) (Pyruv	-	6	29	30	32	38	35	X
1398	Q08257	Quinone oxidoreductase (EC 1.6.5.5) (NADPH:quinon	-	1	-	-	2	-	2	-
1399	P31150	Rab GDP dissociation inhibitor alpha (Rab GDI alpha)	-	-	7	5	5	5	9	X
1400	P50395	Rab GDP dissociation inhibitor beta (Rab GDI beta) (G	-	4	10	11	13	13	21	X
1401	Q6WKZ4	Rab11 family-interacting protein 1 (Rab11-FIP1) (Rab-	-	-	-	1	-	-	-	-
1402	O60518	Ran-binding protein 6 (RanBP6)	-	-	-	-	-	-	1	-
1403	P43487	Ran-specific GTPase-activating protein (Ran-binding p	-	-	2	1	2	1	3	X
1404	P52306	Rap1 GTPase-GDP dissociation stimulator 1 (SMG P2	-	-	2	-	-	-	-	X
1405	Q8TB24	Ras and Rab interactor 3 (Ras interaction/interference	-	-	-	-	1	-	-	-
1406	Q14644	Ras GTPase-activating protein 3 (GAP1(IP4BP)) (Ins	-	-	2	-	-	-	1	-
1407	P46940	Ras GTPase-activating-like protein IQGAP1 (p195)	-	1	-	4	23	30	39	-
1408	Q13576	Ras GTPase-activating-like protein IQGAP2	-	-	3	-	7	2	19	-
1409	Q7LDG7	RAS guanyl-releasing protein 2 - Homo sapiens (Hum	-	-	-	-	-	-	1	-
1410	Q15404	Ras suppressor protein 1 (Rsu-1) (RSP-1)	-	-	13	2	3	-	10	-
1411	P63000	Ras-related C3 botulinum toxin substrate 1 precursor (	-	-	6	-	5	7	6	-
1412	P15153	Ras-related C3 botulinum toxin substrate 2 precursor (	-	-	7	4	10	7	10	X
1413	P61026	Ras-related protein Rab-10	-	-	4	2	5	5	4	-
1414	P62491	Ras-related protein Rab-11A (Rab-11) (YL8)	-	-	7	7	7	5	7	-
1415	Q15907	Ras-related protein Rab-11B (GTP-binding protein YP	-	-	-	-	8	5	8	-
1416	P61106	Ras-related protein Rab-14	-	-	10	3	4	8	9	-
1417	P59190	Ras-related protein Rab-15	-	-	2	-	2	2	2	-
1418	Q9NP72	Ras-related protein Rab-18 - Homo sapiens (Human)	-	-	-	3	-	5	3	-
1419	P62820	Ras-related protein Rab-1A (YPT1-related protein)	-	-	8	-	-	9	7	X
1420	Q9H0U4	Ras-related protein Rab-1B	-	-	10	5	7	10	9	-
1421	Q9UL25	Ras-related protein Rab-21 - Homo sapiens (Human)	-	-	-	3	1	2	3	-
1422	Q969Q5	Ras-related protein Rab-24 - Homo sapiens (Human)	-	-	-	1	-	-	-	-
1423	P51159	Ras-related protein Rab-27A (Rab-27) (GTP-binding p	-	-	-	6	2	5	3	-
1424	O00194	Ras-related protein Rab-27B (C25KG)	-	-	9	2	-	-	5	-
1425	P61019	Ras-related protein Rab-2A	-	-	2	5	5	9	6	-
1426	Q13636	Ras-related protein Rab-31 (Rab-22B)	-	-	-	5	-	4	-	-
1427	Q13637	Ras-related protein Rab-32 - Homo sapiens (Human)	-	-	1	2	-	3	-	-
1428	Q9H082	Ras-related protein Rab-33B	-	-	1	-	2	2	2	-
1429	Q15286	Ras-related protein Rab-35 (Rab-1C) (GTP-binding pr	-	-	2	1	2	2	2	-
1430	Q96AX2	Ras-related protein Rab-37	-	-	2	-	-	1	-	-
1431	Q14964	Ras-related protein Rab-39A (Rab-39)	-	-	-	-	2	2	2	-
1432	P20336	Ras-related protein Rab-3A	-	-	-	2	-	3	5	-
1433	P20337	Ras-related protein Rab-3B	-	-	-	1	-	-	-	-
1434	O95716	Ras-related protein Rab-3D	-	-	-	4	-	5	6	-
1435	P61018	Ras-related protein Rab-4B	-	-	-	-	-	-	2	-
1436	P20339	Ras-related protein Rab-5A	-	-	3	4	-	4	4	-
1437	P61020	Ras-related protein Rab-5B	-	-	3	4	2	-	-	-
1438	P51148	Ras-related protein Rab-5C (RAB5L) (L1880)	-	-	-	7	6	5	6	-
1439	P20340	Ras-related protein Rab-6A (Rab-6)	-	-	-	2	5	2	4	-
1440	Q9NRW1	Ras-related protein Rab-6B	-	-	9	-	-	-	-	-
1441	P51149	Ras-related protein Rab-7	-	-	11	10	10	10	10	X
1442	P61006	Ras-related protein Rab-8A (Oncogene c-mel)	-	-	5	3	6	6	6	-
1443	Q92930	Ras-related protein Rab-8B	-	-	-	3	4	4	7	-
1444	Q9NP90	Ras-related protein Rab-9B (Rab-9L) (RAB9-like prote	-	-	-	1	-	-	-	-
1445	P11233	Ras-related protein Ral-A - Homo sapiens (Human)	-	-	-	-	-	-	2	-
1446	P11234	Ras-related protein Ral-B - Homo sapiens (Human)	-	-	3	3	-	-	3	-
1447	P62834	Ras-related protein Rap-1A precursor (GTP-binding pr	-	-	-	-	8	8	11	-
1448	P61224	Ras-related protein Rap-1b precursor (GTP-binding pr	-	-	16	8	12	9	14	X
1449	A6NIZ1	Ras-related protein Rap-1b-like protein OS=Homo sap	-	-	-	9	-	-	-	-
1450	P61225	Ras-related protein Rap-2b precursor	-	-	2	-	2	2	-	-

1451	Q9Y3L5	Ras-related protein Rap-2c precursor	-	-	-	1	-	-	-	-
1452	Q00765	Receptor expression-enhancing protein 5 (Polyposis lo	-	-	-	1	-	-	1	-
1453	Q12913	Receptor-type tyrosine-protein phosphatase eta precu	-	-	-	1	-	2	-	-
1454	O43665	Regulator of G-protein signaling 10 (RGS10)	-	-	5	-	6	-	2	X
1455	Q9NS28	Regulator of G-protein signaling 18 (RGS18) - Homo s	-	-	4	-	-	-	-	-
1456	P49795	Regulator of G-protein signaling 19 OS=Homo sapiens	-	-	-	1	-	-	-	-
1457	P35244	Replication protein A 14 kDa subunit (RP-A) (RF-A) (R	-	-	-	-	2	-	4	-
1458	P15927	Replication protein A 32 kDa subunit (RP-A) (RF-A) (R	-	-	-	-	2	1	3	X
1459	P27694	Replication protein A 70 kDa DNA-binding subunit (RP	-	-	-	-	-	-	3	-
1460	Q9HD89	Resistin precursor (Cysteine-rich secreted protein FIZ2	-	-	-	3	-	2	-	X
1461	P30622	Restin (Cytoplasmic linker protein 170 alpha-2) (CLIP-	-	-	1	-	-	-	1	-
1462	O95197	Reticulon-3 (Neuroendocrine-specific protein-like 2) (N	-	-	-	2	-	2	-	-
1463	Q9NQC3	Reticulon-4 (Neurite outgrowth inhibitor) (Nogo protein	-	-	3	2	1	4	2	-
1464	P00352	Retinal dehydrogenase 1 (EC 1.2.1.36) (RdDH1) (RAI	-	6	-	-	-	-	-	X
1465	Q99969	Retinoic acid receptor responder protein 2 precursor (C	3	-	-	-	-	-	-	-
1466	Q9HB40	Retinoid-inducible serine carboxypeptidase precursor (	-	-	-	1	-	3	2	-
1467	Q8TC12	Retinol dehydrogenase 11 (EC 1.1.1.-) (Retinal reduct	-	-	4	-	-	-	1	-
1468	P52565	Rho GDP-dissociation inhibitor 1 (Rho GDI 1) (Rho-GI	-	-	4	5	6	5	7	X
1469	P52566	Rho GDP-dissociation inhibitor 2 (Rho GDI 2) (Rho-GI	-	-	10	13	17	13	18	X
1470	Q68EM7	Rho GTPase-activating protein 17 - Homo sapiens (Hu	-	-	-	-	-	-	1	-
1471	Q7Z616	Rho GTPase-activating protein 30 - Homo sapiens (Hu	-	-	-	-	1	-	2	-
1472	Q92888	Rho guanine nucleotide exchange factor 1 (p115-RhoG	-	-	-	-	7	-	5	-
1473	Q96PE2	Rho guanine nucleotide exchange factor 17 - Homo sa	-	-	-	-	2	-	-	-
1474	Q13464	Rho-associated protein kinase 1 (EC 2.7.11.1) (Rho-a	-	-	-	-	-	-	5	-
1475	Q07960	Rho-GTPase-activating protein 1 (GTPase-activating p	-	-	1	5	1	1	6	X
1476	Q8N392	Rho-GTPase-activating protein 18 (MacGAP) - Homo	-	-	1	-	-	-	-	-
1477	P42331	Rho-GTPase-activating protein 25 - Homo sapiens (Hu	-	-	-	-	1	-	1	-
1478	P98171	Rho-GTPase-activating protein 4 (Rho-GAP hematopo	-	-	-	-	5	4	4	-
1479	O43182	Rho-GTPase-activating protein 6 (Rho-type GTPase-a	-	-	1	-	-	-	-	-
1480	P62745	Rho-related GTP-binding protein RhoB precursor (H6)	-	-	-	3	-	-	-	X
1481	P08134	Rho-related GTP-binding protein RhoC precursor (H9)	-	-	7	-	-	-	9	-
1482	P84095	Rho-related GTP-binding protein RhoG precursor	-	-	2	7	6	8	8	-
1483	P34096	Ribonuclease 4 precursor (EC 3.1.27.-) (RNase 4) - H	1	-	-	-	-	-	-	-
1484	P13489	Ribonuclease inhibitor (Ribonuclease/angiogenesis inh	-	4	2	4	3	11	12	-
1485	O00584	Ribonuclease T2 precursor (EC 3.1.27.-) (Ribonucleas	-	-	-	1	1	-	1	-
1486	P49247	Ribose-5-phosphate isomerase (EC 5.3.1.6) (Phospho	-	-	1	2	3	-	1	X
1487	P60891	Ribose-phosphate pyrophosphokinase I (EC 2.7.6.1) (	-	5	-	-	5	-	1	X
1488	P11908	Ribose-phosphate pyrophosphokinase II (EC 2.7.6.1) (	-	-	-	-	-	-	2	X
1489	P51812	Ribosomal protein S6 kinase alpha-3 (EC 2.7.11.1) (S	-	-	-	-	1	2	5	-
1490	Q9P2E9	Ribosome-binding protein 1 (Ribosome receptor protei	-	-	-	-	-	-	1	-
1491	P16083	Ribosyl-dihydroxynicotinamide dehydrogenase [quinone]	-	-	-	2	-	-	-	X
1492	Q63HN8	RING finger protein 213 - Homo sapiens (Human)	-	-	-	-	-	2	-	-
1493	Q9Y5S9	RNA-binding protein 8A (RNA-binding motif protein 8A	-	-	1	-	2	-	1	X
1494	Q01844	RNA-binding protein EWS (EWS oncogene) (Ewing sar	-	-	-	-	-	-	1	-
1495	P35637	RNA-binding protein FUS (Oncogene FUS) (Oncogene	-	-	-	-	-	-	1	-
1496	Q96T51	RUN and FYVE domain-containing protein 1 (FYVE-fir	-	-	1	-	2	-	-	-
1497	Q9Y230	RuvB-like 2 (EC 3.6.1.-) (48-kDa TATA box-binding pr	-	1	-	-	1	-	1	X
1498	P26447	S100 calcium-binding protein A4 (Metastasin) (Mts1 pr	-	-	-	3	3	6	4	X
1499	Q9UH99	Sad1/unc-84-like protein 2 (Rab5-interacting protein) (	-	-	-	-	1	-	2	-
1500	P31153	S-adenosylmethionine synthetase isoform type-2 (EC	-	-	-	-	2	-	-	X
1501	Q9Y3Z3	SAM domain and HD domain-containing protein 1 (De	-	-	-	-	14	15	31	X
1502	Q9UPN7	SAPS domain family member 1	-	-	-	-	-	-	1	-
1503	P16615	Sarcoplasmic/endoplasmic reticulum calcium ATPase	-	-	-	-	-	1	6	-
1504	Q93084	Sarcoplasmic/endoplasmic reticulum calcium ATPase	-	-	7	3	3	1	8	-
1505	Q96C86	Scavenger mRNA decapping enzyme DcpS (EC 3.-.-.	-	-	-	-	4	1	-	X
1506	P55735	SEC13-related protein (SEC13-like protein 1)	-	-	1	-	-	-	1	X

1507	Q13103	Secreted phosphoprotein 24 precursor (Spp-24) (Secr	3	-	-	-	-	-	-	-	-
1508	Q96PL1	Secretoglobulin family 3A member 2 precursor - Homo s	1	-	-	-	-	-	-	-	-
1509	O15126	Secretory carrier-associated membrane protein 1 (Sec	-	-	-	-	-	1	-	-	-
1510	O15127	Secretory carrier-associated membrane protein 2 (Sec	-	-	-	-	-	2	-	-	-
1511	P49903	Selenide, water dikinase 1 (EC 2.7.9.3) (Selenophospi	-	-	-	-	1	-	-	-	X
1512	Q13228	Selenium-binding protein 1	-	6	-	-	6	-	-	-	X
1513	Q8IZQ5	Selenoprotein H - Homo sapiens (Human)	-	-	-	-	-	-	1	-	-
1514	P49908	Selenoprotein P precursor (SeP) - Homo sapiens (Hur	1	-	-	-	-	-	-	-	-
1515	Q8WYJ6	Septin-1 (LARP) (Serologically defined breast cancer a	-	-	-	-	-	-	3	X	-
1516	Q9NVA2	Septin-11	-	-	-	-	-	-	3	X	-
1517	Q15019	Septin-2 (Protein NEDD5)	-	-	4	-	2	1	3	X	-
1518	Q14141	Septin-6	-	-	1	-	4	-	6	X	-
1519	Q16181	Septin-7 (CDC10 protein homolog)	-	-	2	-	5	-	8	-	-
1520	Q9UHD8	Septin-9 (MLL septin-like fusion protein) (MLL septin-li	-	1	1	-	8	-	5	-	-
1521	P34897	Serine hydroxymethyltransferase, mitochondrial precu	-	-	-	-	1	3	-	-	-
1522	O15269	Serine palmitoyltransferase 1 (EC 2.3.1.50) (Long cha	-	-	-	-	-	2	-	-	-
1523	P62140	Serine/threonine protein phosphatase PP1-beta cataly	-	-	5	-	6	-	7	X	-
1524	O94804	Serine/threonine-protein kinase 10 (EC 2.7.1.37) (Lym	-	-	-	-	3	1	12	-	-
1525	Q9Y6E0	Serine/threonine-protein kinase 24 (EC 2.7.11.1) (STE	-	-	4	-	-	-	-	-	-
1526	O00506	Serine/threonine-protein kinase 25 (EC 2.7.11.1) (Ster	-	-	-	-	2	-	-	-	-
1527	Q13043	Serine/threonine-protein kinase 4 (EC 2.7.11.1) (STE2	-	-	-	1	-	-	2	X	-
1528	Q8TD19	Serine/threonine-protein kinase Nek9 (EC 2.7.11.1) (N	-	-	-	-	-	-	1	-	-
1529	O95747	Serine/threonine-protein kinase OSR1 (EC 2.7.1.37) (O	-	1	-	-	-	-	1	-	-
1530	Q13177	Serine/threonine-protein kinase PAK 2 (EC 2.7.1.37) (P	-	-	1	-	-	1	1	X	-
1531	Q96C45	Serine/threonine-protein kinase ULK4 (EC 2.7.11.1) (U	-	-	-	-	-	-	1	-	-
1532	P63151	Serine/threonine-protein phosphatase 2A 55 kDa regu	-	-	-	1	-	-	1	X	-
1533	P30153	Serine/threonine-protein phosphatase 2A 65 kDa regu	-	-	2	1	7	5	9	X	-
1534	P67775	Serine/threonine-protein phosphatase 2A catalytic sub	-	-	1	-	1	-	-	X	-
1535	Q15257	Serine/threonine-protein phosphatase 2A regulatory su	-	-	-	-	-	-	1	-	-
1536	P62136	Serine/threonine-protein phosphatase PP1-alpha cata	-	-	5	-	6	-	8	X	-
1537	P02787	Serotransferrin precursor (Transferrin) (Siderophilin) (E	35	-	5	-	-	-	29	X	-
1538	P48595	Serpin B10 (Bomapin) (Protease inhibitor 10) - Homo s	-	-	-	4	-	1	-	-	-
1539	P50452	Serpin B8 (Cytoplasmic antiproteinase 2) (CAP2) (CAI	-	-	-	-	-	5	2	X	-
1540	P02768	Serum albumin precursor	56	17	-	-	-	-	60	X	-
1541	P02735	Serum amyloid A protein precursor (SAA) [Contains: A	2	-	-	-	-	-	-	-	-
1542	P35542	Serum amyloid A-4 protein precursor (Constitutively ex	8	-	1	-	-	-	-	-	-
1543	P02743	Serum amyloid P-component precursor (SAP) (9.5S al	9	-	-	-	-	-	-	-	-
1544	O95810	Serum deprivation-response protein (Phosphatidylserin	-	-	9	-	1	-	2	-	-
1545	P27169	Serum paraoxonase/arylesterase 1 (EC 3.1.1.2) (EC 3	7	-	-	-	-	-	-	X	-
1546	Q15166	Serum paraoxonase/lactonase 3 (EC 3.1.1.-) - Homo s	1	-	-	-	-	-	-	-	-
1547	P49591	Seryl-tRNA synthetase (EC 6.1.1.11) (Serine--tRNA lig	-	-	-	-	4	-	5	X	-
1548	P04278	Sex hormone-binding globulin precursor (SHBG) (Sex	3	-	-	-	-	-	-	-	-
1549	O60880	SH2 domain protein 1A (Signaling lymphocyte activati	-	-	-	-	2	-	3	-	-
1550	O75368	SH3 domain-binding glutamic acid-rich-like protein	-	-	4	3	3	4	5	X	-
1551	Q9UJC5	SH3 domain-binding glutamic acid-rich-like protein 2 (f	-	-	2	-	-	-	1	-	-
1552	Q9H299	SH3 domain-binding glutamic acid-rich-like protein 3 (S	-	-	4	2	2	4	4	-	-
1553	Q9Y3L3	SH3 domain-binding protein 1 (3BP-1) - Homo sapiens	-	-	-	-	4	-	-	-	-
1554	O75995	SH3 protein expressed in lymphocytes homolog	-	-	-	-	1	-	-	-	-
1555	Q16836	Short chain 3-hydroxyacyl-CoA dehydrogenase, mitoc	-	-	8	-	9	1	8	-	-
1556	Q9Y3A5	Shwachman-Bodian-Diamond syndrome protein - Hom	-	-	1	-	1	-	-	-	-
1557	Q9NR45	Sialic acid synthase (N-acetylneuraminate synthase) (	-	-	-	1	1	1	1	X	-
1558	O15389	Sialic acid-binding Ig-like lectin 5 OS=Homo sapiens G	-	-	-	1	-	-	-	-	-
1559	Q9Y286	Sialic acid-binding Ig-like lectin 7 precursor (Siglec-7) (	-	-	-	-	-	1	-	-	-
1560	Q9Y336	Sialic acid-binding Ig-like lectin 9 precursor (Siglec-9) (	-	-	-	-	-	2	1	-	-
1561	Q9H9B4	Sideroflexin-1 (Tricarboxylate carrier protein) (TCC)	-	-	-	-	5	-	4	-	-
1562	Q9BWM7	Sideroflexin-3 - Homo sapiens (Human)	-	-	-	-	1	-	2	-	-

1563	Q15005	Signal peptidase complex subunit 2 (EC 3.4.-.-) (Micro	-	-	-	-	-	1	-	-
1564	P61009	Signal peptidase complex subunit 3 (EC 3.4.-.-) (Micro	-	-	-	-	-	1	-	-
1565	P37108	Signal recognition particle 14 kDa protein (SRP14) (18	-	-	-	-	3	1	2	-
1566	O76094	Signal recognition particle 72 kDa protein (SRP72) - H	-	-	-	-	1	-	-	-
1567	P49458	Signal recognition particle 9 kDa protein (SRP9)	-	-	-	-	1	2	2	-
1568	P42224	Signal transducer and activator of transcription 1-alpha	-	-	-	-	4	-	10	-
1569	P40763	Signal transducer and activator of transcription 3 (Acu	-	-	-	-	-	-	3	-
1570	P51692	Signal transducer and activator of transcription 5B - H	-	-	-	-	1	1	3	-
1571	Q9Y3P8	Signaling threshold-regulating transmembrane adapte	-	-	-	-	1	-	-	-
1572	Q04837	Single-stranded DNA-binding protein, mitochondrial pr	-	-	1	-	2	1	7	-
1573	Q9UIB8	SLAM family member 5 precursor (Signaling lymphocy	-	-	1	-	-	-	-	-
1574	O43765	Small glutamine-rich tetratricopeptide repeat-contain	-	-	1	-	-	-	-	-
1575	P62304	Small nuclear ribonucleoprotein E (snRNP-E) (Sm pro	-	-	-	-	1	-	1	-
1576	P62314	Small nuclear ribonucleoprotein Sm D1 (snRNP core p	-	-	-	-	-	-	1	-
1577	P62316	Small nuclear ribonucleoprotein Sm D2 (snRNP core p	-	-	-	-	1	-	-	-
1578	P62318	Small nuclear ribonucleoprotein Sm D3 (snRNP core p	-	-	-	-	2	-	-	-
1579	P61956	Small ubiquitin-related modifier 2 precursor (SUMO-2)	-	-	-	1	1	1	1	X
1580	P13501	Small-inducible cytokine A5 precursor - Homo sapiens	-	-	2	-	-	-	-	-
1581	Q13126	S-methyl-5-thioadenosine phosphorylase (EC 2.4.2.28	-	-	1	1	-	-	4	X
1582	O95295	SNARE-associated protein Snapin (Synaptosomal-ass	-	-	-	-	1	2	1	-
1583	P05023	Sodium/potassium-transporting ATPase alpha-1 chain	-	-	-	-	1	4	6	-
1584	P54709	Sodium/potassium-transporting ATPase beta-3 chain (	-	-	-	-	-	1	-	-
1585	P11166	Solute carrier family 2, facilitated glucose transporter r	-	1	-	-	3	-	-	-
1586	Q8TDB8	Solute carrier family 2, facilitated glucose transporter r	-	-	-	2	-	-	-	-
1587	P11169	Solute carrier family 2, facilitated glucose transporter r	-	-	1	3	-	-	3	-
1588	P01241	Somatotropin precursor - Homo sapiens (Human)	1	-	-	-	-	-	-	-
1589	P30626	Sorcin (22 kDa protein) (CP-22) (V19)	-	-	4	-	4	4	2	X
1590	Q99523	Sortilin precursor (Neurotensin receptor 3) (NTR3) (NT	-	-	-	-	-	1	-	-
1591	O60493	Sorting nexin-3 (SDP3 protein)	-	-	1	2	-	3	-	-
1592	P09486	SPARC precursor (Secreted protein acidic and rich in	2	-	4	-	-	-	-	-
1593	Q13813	Spectrin alpha chain, brain (Spectrin, non-erythroid alp	-	3	-	-	-	1	2	-
1594	P02549	Spectrin alpha chain, erythrocyte (Erythroid alpha-spe	-	57	8	-	-	-	-	-
1595	Q01082	Spectrin beta chain, brain 1 (Spectrin, non-erythroid be	1	-	1	-	-	-	-	-
1596	P11277	Spectrin beta chain, erythrocyte (Beta-I spectrin) - Hor	-	49	14	-	-	-	1	-
1597	P63208	S-phase kinase-associated protein 1A (Cyclin A/CDK2	-	2	-	-	4	2	2	-
1598	Q13838	Spliceosome RNA helicase BAT1 (EC 3.6.1.-) (DEAD	-	-	-	-	2	-	3	X
1599	P26368	Splicing factor U2AF 65 kDa subunit (U2 auxiliary fact	-	-	-	-	-	-	1	-
1600	P23246	Splicing factor, proline- and glutamine-rich (Polypyrim	-	-	-	-	-	-	1	-
1601	Q15020	Squamous cell carcinoma antigen recognized by T-cell	-	-	-	-	-	-	3	-
1602	O75563	Src kinase-associated phosphoprotein 2 - Homo sapie	-	-	1	3	-	4	-	-
1603	Q14247	Src substrate cortactin (Amplaxin) (Oncogene EMS1)	-	-	4	-	-	-	-	X
1604	Q7KZF4	Staphylococcal nuclease domain-containing protein 1	-	2	1	-	1	-	2	-
1605	P16949	Stathmin (Phosphoprotein p19) (pp19) (Oncoprotein 1	-	-	-	-	4	5	4	X
1606	Q9UJZ1	Stomatin-like protein 2 (SLP-2) (EPB72-like 2)	-	-	-	-	-	-	1	X
1607	P38646	Stress-70 protein, mitochondrial precursor (75 kDa glu	-	-	-	-	4	4	9	X
1608	P31948	Stress-induced-phosphoprotein 1 (STI1) (Hsc70/Hsp90	-	2	2	-	2	4	4	X
1609	Q9NRL3	Striatin-4 (Zinedin) - Homo sapiens (Human)	-	-	1	-	-	-	-	-
1610	Q9HCN8	Stromal cell-derived factor 2-like protein 1 precursor (S	-	-	-	-	-	1	1	-
1611	Q13586	Stromal interaction molecule 1 precursor - Homo sapie	-	-	1	-	-	-	-	-
1612	Q8WU79	Stromal membrane-associated protein 2 OS=Homo sa	-	-	-	2	-	-	-	-
1613	P31040	Succinate dehydrogenase [ubiquinone] flavoprotein su	-	-	-	-	2	1	4	X
1614	P21912	Succinate dehydrogenase [ubiquinone] iron-sulfur prot	-	-	-	-	5	3	3	-
1615	Q9P2R7	Succinyl-CoA ligase [ADP-forming] beta-chain, mitoch	-	-	-	-	1	-	-	X
1616	Q96199	Succinyl-CoA ligase [GDP-forming] beta-chain, mitoch	-	-	-	-	2	-	-	X
1617	P53597	Succinyl-CoA ligase [GDP-forming] subunit alpha, mit	-	-	-	-	3	-	2	-
1618	P55809	Succinyl-CoA:3-ketoacid-coenzyme A transferase 1, m	-	-	3	-	2	-	-	X

1619	P14410	Sucrase-isomaltase, intestinal OS=Homo sapiens GN	-	-	-	1	-	-	-	-
1620	Q9Y6N5	Sulfide:quinone oxidoreductase, mitochondrial precurs	-	-	-	-	4	5	4	-
1621	P50225	Sulfotransferase 1A1 (EC 2.8.2.1) (Aryl sulfotransferas	-	-	4	1	-	2	-	X
1622	P63279	SUMO-conjugating enzyme UBC9 (EC 6.3.2.-) (SUMO	-	-	-	-	2	2	5	-
1623	P00441	Superoxide dismutase [Cu-Zn] (EC 1.15.1.1)	2	5	5	4	8	6	8	X
1624	P04179	Superoxide dismutase [Mn], mitochondrial precursor (E	-	-	10	5	8	6	9	X
1625	Q9Y2Z0	Suppressor of G2 allele of SKP1 homolog (Sgt1) (Put	-	-	1	-	-	-	1	X
1626	Q8TF42	Suppressor of T-cell receptor signaling 1 (Sts-1) (Cbl-i	-	-	2	-	-	-	-	-
1627	O15260	Surfeit locus protein 4	-	-	-	1	1	1	2	-
1628	Q99536	Synaptic vesicle membrane protein VAT-1 homolog (E	-	-	-	11	3	2	2	X
1629	O15056	Synaptojanin-2 (EC 3.1.3.36) (Synaptic inositol-1,4,5-t	-	1	-	-	1	-	-	-
1630	O00161	Synaptosomal-associated protein 23 (SNAP-23) (Vesi	-	-	3	-	-	-	1	-
1631	O95721	Synaptosomal-associated protein 29 (SNAP-29) (Vesi	-	-	2	-	-	-	-	X
1632	Q96C24	Synaptotagmin-like protein 4 (Exophilin-2) (Granuphilin	-	-	2	-	-	-	-	-
1633	Q9NX95	Syntabulin - Homo sapiens (Human)	-	-	-	-	1	-	-	-
1634	O75558	Syntaxin-11 - Homo sapiens (Human)	-	-	4	-	-	-	1	-
1635	Q12846	Syntaxin-4 (NY-REN-31 antigen) - Homo sapiens (Hur	-	-	1	-	-	-	-	-
1636	O15400	Syntaxin-7 - Homo sapiens (Human)	-	-	2	-	-	1	1	-
1637	Q15833	Syntaxin-binding protein 2 (Unc-18 homolog 2) (Unc-1	-	-	7	1	-	-	-	X
1638	O00560	Syntenin-1 (Syndecan-binding protein 1) (Melanoma d	-	-	-	2	-	1	-	-
1639	Q9Y490	Talin-1	-	17	135	42	75	53	136	X
1640	Q9Y4G6	Talin-2 - Homo sapiens (Human)	-	-	-	-	-	-	8	-
1641	O15533	Tapasin precursor - Homo sapiens (Human)	-	-	1	-	1	1	1	-
1642	Q13148	TAR DNA-binding protein 43 (TDP-43)	-	-	-	-	-	-	2	X
1643	O60784	Target of Myb protein 1 - Homo sapiens (Human)	-	-	-	1	-	-	-	-
1644	Q6SJ96	TATA box-binding protein-like protein 2 - Homo sapien	-	-	-	1	-	-	-	-
1645	Q66K14	TBC1 domain family member 9B - Homo sapiens (Hur	-	-	-	-	-	1	-	-
1646	P56279	T-cell leukemia/lymphoma protein 1A (P14 TCL1 prote	-	-	-	-	-	-	2	-
1647	P04234	T-cell surface glycoprotein CD3 delta chain precursor	-	-	-	-	2	-	1	-
1648	P07766	T-cell surface glycoprotein CD3 epsilon chain precurs	-	-	-	-	1	-	-	-
1649	P20963	T-cell surface glycoprotein CD3 zeta chain precursor	-	-	-	-	1	-	-	-
1650	P06127	T-cell surface glycoprotein CD5 precursor (Lymphocyt	-	-	-	-	1	-	1	-
1651	P17987	T-complex protein 1 subunit alpha (TCP-1-alpha) (CC	-	2	2	-	6	2	8	X
1652	P78371	T-complex protein 1 subunit beta (TCP-1-beta) (CCT-l	-	-	6	-	12	1	6	X
1653	P50991	T-complex protein 1 subunit delta (TCP-1-delta) (CCT	-	2	2	1	6	4	5	X
1654	P48643	T-complex protein 1 subunit epsilon (TCP-1-epsilon) (C	-	1	2	-	5	1	5	X
1655	Q99832	T-complex protein 1 subunit eta (TCP-1-eta) (CCT-eta	-	3	2	1	5	1	8	X
1656	P49368	T-complex protein 1 subunit gamma (TCP-1-gamma) (C	-	1	4	-	8	-	8	X
1657	P50990	T-complex protein 1 subunit theta (TCP-1-theta) (CCT	-	2	6	-	8	4	10	X
1658	P40227	T-complex protein 1 subunit zeta (TCP-1-zeta) (CCT-z	-	1	4	1	10	6	11	X
1659	Q92526	T-complex protein 1 subunit zeta-2 (TCP-1-zeta-2) (C	-	-	2	-	-	-	-	-
1660	Q9UGI8	Testin (TESS)	-	-	-	-	-	-	3	-
1661	P05452	Tetranectin precursor (TN) (C-type lectin domain famil	5	-	-	-	-	-	-	-
1662	Q8NG11	Tetraspanin-14 (Tspan-14) (Transmembrane 4 superf	-	-	-	-	-	1	-	-
1663	Q9Y3D6	Tetratricopeptide repeat protein 11 (TPR repeat protei	-	-	-	-	1	2	2	-
1664	Q9BU02	Thiamine-triphosphatase (EC 3.6.1.28) (ThTPase) - H	-	-	-	-	1	-	-	-
1665	Q9NPJ3	Thioesterase superfamily member 2 - Homo sapiens (	-	-	-	-	2	-	-	-
1666	P10599	Thioredoxin (ATL-derived factor) (ADF) (Surface-assor	-	-	2	5	1	4	3	X
1667	Q9H3N1	Thioredoxin domain-containing protein 1 precursor (Tr	-	-	-	1	-	2	3	-
1668	O95881	Thioredoxin domain-containing protein 12 precursor (E	-	-	-	2	-	-	-	-
1669	Q9BS26	Thioredoxin domain-containing protein 4 precursor (Er	-	-	-	-	-	1	-	X
1670	Q8NBS9	Thioredoxin domain-containing protein 5 precursor (Th	-	-	-	-	1	-	-	X
1671	Q16881	Thioredoxin reductase 1, cytoplasmic precursor (EC 1	-	-	-	1	-	-	-	X
1672	Q9NNW7	Thioredoxin reductase 2, mitochondrial precursor (EC	-	-	-	-	1	-	-	-
1673	P30048	Thioredoxin-dependent peroxide reductase, mitochond	-	-	6	2	4	8	8	X
1674	O43396	Thioredoxin-like protein 1 (32 kDa thioredoxin-related	-	1	6	-	-	-	-	X

1675	Q9BRA2	Thioredoxin-like protein 5 (14 kDa thioredoxin-related	-	-	-	2	1	3	-	-
1676	Q16762	Thiosulfate sulfurtransferase (EC 2.8.1.1) (Rhodanese	-	-	3	-	-	-	-	X
1677	P26639	Threonyl-tRNA synthetase, cytoplasmic (EC 6.1.1.3) (	-	-	-	-	-	1	3	-
1678	P07996	Thrombospondin-1 precursor	7	-	30	-	-	-	27	-
1679	P35443	Thrombospondin-4 precursor - Homo sapiens (Human	3	-	-	-	-	-	-	-
1680	P24557	Thromboxane-A synthase (EC 5.3.99.5) (TXA synthas	-	-	-	-	-	4	-	-
1681	P19971	Thymidine phosphorylase precursor (EC 2.4.2.4) (TdR	-	-	5	2	5	5	7	X
1682	P23919	Thymidylate kinase (EC 2.7.4.9) (dTMP kinase)	-	-	-	-	2	-	-	-
1683	P63313	Thymosin beta-10	-	-	-	-	-	1	1	-
1684	P62328	Thymosin beta-4 (T beta 4) (Fx) [Contains: Hematopo	-	-	-	1	-	3	2	-
1685	P05543	Thyroxine-binding globulin precursor (T4-binding globu	3	-	-	-	-	-	-	-
1686	Q9BVW5	TIMELESS-interacting protein - Homo sapiens (Human	-	-	-	2	-	-	-	-
1687	Q8WZ42	Titin (EC 2.7.11.1) (Connectin) (Rhabdomyosarcoma a	2	-	-	-	-	-	-	-
1688	Q9H0E2	Toll-interacting protein	-	-	1	-	-	3	-	X
1689	O60603	Toll-like receptor 2 precursor (Toll/interleukin 1 recept	-	-	-	-	-	4	-	-
1690	Q6ZVM7	TOM1-like protein 2 - Homo sapiens (Human)	-	-	1	-	-	-	-	-
1691	O14656	Torsin A precursor (Torsin family 1 member A) (Dystor	-	-	-	1	-	-	1	-
1692	Q5JTV8	Torsin-1A-interacting protein 1	-	-	-	1	-	1	2	X
1693	Q9Y3C4	TP53RK-binding protein - Homo sapiens (Human)	-	-	-	-	1	-	1	-
1694	Q9Y228	TRAF3-interacting JNK-activating modulator (TRAF3-i	-	-	-	-	1	-	3	-
1695	O43617	Trafficking protein particle complex subunit 3 (BET3 ho	-	-	1	-	4	2	3	-
1696	P37837	Transaldolase (EC 2.2.1.2)	-	-	9	16	17	17	15	X
1697	P20061	Transcobalamin-1 precursor (Transcobalamin I) (TCI)	-	-	-	2	-	-	-	-
1698	P23193	Transcription elongation factor A protein 1 (Transcripti	-	-	-	-	-	-	2	-
1699	Q15369	Transcription elongation factor B polypeptide 1 (RNA p	-	-	2	-	-	-	1	-
1700	Q15370	Transcription elongation factor B polypeptide 2 (RNA p	-	-	-	2	-	-	1	-
1701	Q00059	Transcription factor A, mitochondrial precursor (mtTFA	-	-	-	-	-	-	2	-
1702	P20290	Transcription factor BTF3 (RNA polymerase B transcri	-	-	-	-	3	3	3	X
1703	Q96K17	Transcription factor BTF3 homolog 4 (Basic transcripti	-	-	-	-	1	-	1	X
1704	P17947	Transcription factor PU.1 (31 kDa transforming protein	-	-	-	-	-	1	-	-
1705	P13984	Transcription initiation factor IIF subunit beta - Homo s	-	-	-	-	1	-	-	-
1706	Q13263	Transcription intermediary factor 1-beta (TIF1-beta) (T	-	-	-	-	1	-	3	X
1707	P11308	Transcriptional regulator ERG (Transforming protein E	-	-	-	-	-	1	1	-
1708	P02786	Transferrin receptor protein 1 (TfR1) (TR) (TfR) (Trfr) (	-	-	-	-	1	-	-	-
1709	Q9Y6A5	Transforming acidic coiled-coil-containing protein 3 (Ei	-	-	-	-	-	-	1	-
1710	P01137	Transforming growth factor beta-1 precursor (TGF-beta	1	-	6	-	-	-	-	-
1711	O43294	Transforming growth factor beta-1-induced transcript 1	-	-	4	-	-	-	-	-
1712	P61586	Transforming protein RhoA precursor (H12)	-	1	7	7	10	6	12	X
1713	Q01995	Transgelin (Smooth muscle protein 22-alpha) (SM22-a	-	-	-	-	-	-	4	-
1714	P37802	Transgelin-2 (SM22-alpha homolog)	1	-	22	9	16	15	19	-
1715	P55072	Transitional endoplasmic reticulum ATPase (TER ATP	-	13	14	-	20	14	23	X
1716	P29401	Transketolase (EC 2.2.1.1) (TK)	-	2	2	23	16	21	23	X
1717	P13693	Translationally-controlled tumor protein (TCTP) (p23) (	-	-	3	1	4	2	4	X
1718	Q15631	Translin - Homo sapiens (Human)	-	-	-	-	4	6	2	-
1719	Q99598	Translin-associated protein X (Translin-associated fac	-	-	-	1	3	1	3	X
1720	P51571	Translocon-associated protein delta subunit precursor	-	-	-	-	3	2	2	X
1721	Q9UM00	Transmembrane and coiled-coil domain-containing pro	-	-	-	-	-	-	1	-
1722	Q15363	Transmembrane emp24 domain trafficking protein 2 pr	-	-	-	-	3	1	2	-
1723	P49755	Transmembrane emp24 domain-containing protein 10	-	-	-	-	4	5	5	-
1724	Q9Y3B3	Transmembrane emp24 domain-containing protein 7 p	-	-	1	-	-	-	-	-
1725	Q9BVK6	Transmembrane emp24 domain-containing protein 9 p	-	-	3	-	1	3	4	-
1726	Q9BVC6	Transmembrane protein 109 precursor (Mitsugumin-23	-	-	-	-	-	1	-	-
1727	Q4KMQ2	Transmembrane protein 16F - Homo sapiens (Human)	-	-	-	-	-	-	1	-
1728	Q86WV6	Transmembrane protein 173 - Homo sapiens (Human)	-	-	-	-	-	5	-	-
1729	Q6UW68	Transmembrane protein 205 - Homo sapiens (Human)	-	-	-	-	-	1	1	-
1730	P57088	Transmembrane protein 33 (DB83 protein) - Homo sap	-	-	-	-	-	1	1	-

1731	Q9BTV4	Transmembrane protein 43 - Homo sapiens (Human)	-	-	-	-	-	1	1	-
1732	Q92973	Transportin-1 (Importin beta-2) (Karyopherin beta-2) (H	-	-	-	-	1	-	2	-
1733	P02766	Transthyretin precursor (Prealbumin) (TBPA) (TTR) (A	15	1	2	-	-	6	6	-
1734	Q86YW5	Trem-like transcript 1 protein precursor (TLT-1) (Trigge	-	-	5	-	1	-	1	-
1735	P40939	Trifunctional enzyme alpha subunit, mitochondrial prec	6	-	-	-	2	1	17	-
1736	P55084	Trifunctional enzyme subunit beta, mitochondrial precu	-	-	1	-	2	3	5	-
1737	P60174	Triosephosphate isomerase (EC 5.3.1.1) (TIM) (Triose	-	4	16	11	20	16	21	X
1738	P29144	Tripeptidyl-peptidase 2 (EC 3.4.14.10) (Tripeptidyl-pep	-	-	2	-	-	-	2	-
1739	O14773	Tripeptidyl-peptidase I precursor (EC 3.4.14.9) (TPP-I)	-	-	1	2	1	4	3	X
1740	Q9UI30	TRM112-like protein - Homo sapiens (Human)	-	-	-	-	1	-	1	X
1741	Q9NZR1	Tropomodulin-2 (Neuronal tropomodulin) (N-Tmod) - H	-	-	-	1	-	-	-	-
1742	Q9NYL9	Tropomodulin-3 (Ubiquitous tropomodulin) (U-Tmod) -	-	-	6	3	-	-	-	X
1743	P09493	Tropomyosin 1 alpha chain (Alpha-tropomyosin)	-	-	11	-	7	6	9	X
1744	P06753	Tropomyosin alpha-3 chain (Tropomyosin-3) (Tropomy	-	-	14	-	16	12	16	X
1745	P67936	Tropomyosin alpha-4 chain (Tropomyosin-4) (TM30p1	-	-	25	-	14	9	19	X
1746	P07951	Tropomyosin beta chain (Tropomyosin 2) (Beta-tropon	-	-	11	-	7	7	8	X
1747	P23381	Tryptophanyl-tRNA synthetase (EC 6.1.1.2) (Tryptoph	-	-	-	2	1	5	5	X
1748	Q9Y3Q8	TSC22 domain family protein 4 - Homo sapiens (Huma	-	-	1	-	-	-	-	-
1749	Q8TAP9	TTD non-photosensitive 1 protein - Homo sapiens (Hu	-	-	-	-	-	-	1	-
1750	P68366	Tubulin alpha-1 chain (Alpha-tubulin 1) (Testis-specific	-	-	-	-	-	7	16	-
1751	Q13748	Tubulin alpha-2 chain (Alpha-tubulin 2)	-	-	-	-	-	5	-	-
1752	Q71U36	Tubulin alpha-3 chain (Alpha-tubulin 3) (Tubulin B-alph	-	-	-	10	-	9	17	X
1753	Q9BQE3	Tubulin alpha-6 chain (Alpha-tubulin 6)	-	-	17	-	-	-	-	X
1754	Q9NY65	Tubulin alpha-8 chain (Alpha-tubulin 8)	-	-	-	-	-	-	10	-
1755	P68363	Tubulin alpha-ubiquitous chain (Alpha-tubulin ubiquito	-	-	-	-	15	12	17	X
1756	Q9H4B7	Tubulin beta-1 chain - Homo sapiens (Human)	-	-	29	-	-	-	16	-
1757	P07437	Tubulin beta-2 chain	-	2	27	-	22	16	24	X
1758	Q13885	Tubulin beta-2A chain - Homo sapiens (Human)	-	-	-	-	-	-	16	-
1759	P68371	Tubulin beta-2C chain (Tubulin beta-2 chain)	-	-	-	14	-	7	21	-
1760	P04350	Tubulin beta-4 chain (Tubulin 5 beta)	-	-	-	-	-	-	15	-
1761	Q9BUF5	Tubulin beta-6 chain - Homo sapiens (Human)	-	-	7	-	-	-	6	-
1762	O75347	Tubulin-specific chaperone A (Tubulin-folding cofactor	-	-	1	1	2	3	2	X
1763	Q99426	Tubulin-specific chaperone B (Tubulin folding cofactor	-	-	2	-	3	-	2	X
1764	Q14166	Tubulin--tyrosine ligase-like protein 12	-	-	-	-	-	-	2	X
1765	Q6EMB2	Tubulin--tyrosine ligase-like protein 5 (SRC1 and TIF2	-	-	-	-	-	1	-	-
1766	O95379	Tumor necrosis factor, alpha-induced protein 8 - Homo	-	-	-	-	1	-	3	-
1767	Q6P589	Tumor necrosis factor, alpha-induced protein 8-like pro	-	-	-	1	2	1	3	-
1768	O43399	Tumor protein D54 (hD54) (Tumor protein D52-like 2)	-	-	2	-	2	4	3	X
1769	Q6IBS0	Twinfilin-2 (Twinfilin-1-like protein) (A6-related protei	-	-	6	4	3	2	5	X
1770	O43914	TYRO protein tyrosine kinase-binding protein precursor	-	-	-	-	-	2	1	-
1771	P41240	Tyrosine-protein kinase CSK (EC 2.7.1.112) (C-SRC k	-	-	2	-	4	3	6	X
1772	P08631	Tyrosine-protein kinase HCK (EC 2.7.10.2) (p59-HCK/	-	-	-	-	-	1	-	-
1773	P43405	Tyrosine-protein kinase SYK (EC 2.7.10.2) (Spleen tyr	-	-	-	-	-	4	-	-
1774	P43403	Tyrosine-protein kinase ZAP-70 (EC 2.7.1.112) (70 kD	-	-	-	-	1	-	4	-
1775	P18031	Tyrosine-protein phosphatase non-receptor type 1 (EC	-	-	1	-	1	-	-	-
1776	P29350	Tyrosine-protein phosphatase non-receptor type 6 (EC	-	-	2	5	6	11	20	-
1777	P35236	Tyrosine-protein phosphatase non-receptor type 7 - Ho	-	-	-	-	1	-	-	-
1778	P78324	Tyrosine-protein phosphatase non-receptor type subst	-	-	-	1	-	-	-	-
1779	P54577	Tyrosyl-tRNA synthetase, cytoplasmic (EC 6.1.1.1) (Ty	-	-	1	-	-	-	1	X
1780	Q8WWY3	U4/U6 small nuclear ribonucleoprotein Prp31 - Homo s	-	-	-	-	1	-	-	-
1781	Q9Y333	U6 snRNA-associated Sm-like protein LSm2 (SnRNP	-	-	-	-	3	3	2	-
1782	Q9Y4Z0	U6 snRNA-associated Sm-like protein LSm4 (Glycine-	-	-	-	-	-	-	1	-
1783	P62312	U6 snRNA-associated Sm-like protein LSm6 (Sm prote	-	-	-	-	1	-	-	-
1784	O95777	U6 snRNA-associated Sm-like protein LSm8	-	-	-	-	-	-	1	-
1785	P14927	Ubiquinol-cytochrome c reductase complex 14 kDa pro	-	-	-	-	1	1	-	-
1786	P47985	Ubiquinol-cytochrome c reductase iron-sulfur subunit,	-	-	1	-	2	-	3	X

1787	P22695	Ubiquinol-cytochrome-c reductase complex core prote	-	-	1	-	2	1	6	-
1788	P31930	Ubiquinol-cytochrome-c reductase complex core prote	-	-	1	-	4	4	8	X
1789	P62988	Ubiquitin	-	1	3	5	6	7	6	X
1790	P54578	Ubiquitin carboxyl-terminal hydrolase 14 (EC 3.1.2.15)	-	1	2	-	3	1	5	X
1791	Q9Y4E8	Ubiquitin carboxyl-terminal hydrolase 15 (EC 3.1.2.15)	-	-	-	-	-	-	1	-
1792	P45974	Ubiquitin carboxyl-terminal hydrolase 5 (EC 3.1.2.15)	-	4	-	-	6	2	9	X
1793	Q93009	Ubiquitin carboxyl-terminal hydrolase 7 (EC 3.1.2.15)	-	-	-	-	2	3	5	-
1794	P15374	Ubiquitin carboxyl-terminal hydrolase isozyme L3 (EC	-	-	-	-	1	-	2	X
1795	Q96FW1	Ubiquitin thiolesterase protein OTUB1 (EC 3.4.-.-) (Otu	-	-	2	2	5	1	7	-
1796	P22314	Ubiquitin-activating enzyme E1 (A1S9 protein)	-	6	5	6	18	14	25	X
1797	P41226	Ubiquitin-activating enzyme E1 homolog (D8) - Homo	-	-	3	-	1	1	-	-
1798	P62837	Ubiquitin-conjugating enzyme E2 D2 (EC 6.3.2.19) (Ubi	-	-	-	-	1	-	3	-
1799	P62256	Ubiquitin-conjugating enzyme E2 H (EC 6.3.2.19) (Ubi	-	-	-	-	-	-	1	-
1800	P68036	Ubiquitin-conjugating enzyme E2 L3 (EC 6.3.2.19) (Ubi	-	-	2	4	4	5	4	-
1801	O14933	Ubiquitin-conjugating enzyme E2 L6 (EC 6.3.2.19) (Ubi	-	-	-	-	-	3	1	-
1802	P61088	Ubiquitin-conjugating enzyme E2 N (EC 6.3.2.19) (Ubi	-	1	3	2	6	7	9	X
1803	Q9C0C9	Ubiquitin-conjugating enzyme E2 O - Homo sapiens (H	-	-	1	-	2	1	1	-
1804	Q13404	Ubiquitin-conjugating enzyme E2 variant 1 (UEV-1) (C	-	3	5	-	5	6	6	X
1805	Q15819	Ubiquitin-conjugating enzyme E2 variant 2 (MMS2) (E	-	2	3	3	5	-	4	X
1806	P61086	Ubiquitin-conjugating enzyme E2-25 kDa (EC 6.3.2.19	-	-	2	-	2	-	3	X
1807	Q9UBE0	Ubiquitin-like 1-activating enzyme E1A (SUMO-activat	-	-	-	-	2	-	1	X
1808	Q9UBT2	Ubiquitin-like 1-activating enzyme E1B (SUMO-1-activ	-	-	-	-	3	2	2	-
1809	Q9NYU2	UDP-glucose:glycoprotein glucosyltransferase 1 precu	-	-	1	-	-	10	14	X
1810	Q9Y3C8	Ufm1-conjugating enzyme 1 (Ubiquitin-fold modifier-co	-	-	2	-	2	-	-	-
1811	P30085	UMP-CMP kinase (EC 2.7.4.14) (Cytidylate kinase) (D	-	-	6	2	5	-	5	X
1812	Q86UX7	Unc-112-related protein 2 (Kindlin-3) (MIG2-like)	-	-	25	1	6	9	21	X
1813	Q70J99	Unc-13 homolog D (Munc13-4)	-	-	2	-	2	1	2	-
1814	Q9H1C4	UNC93 homolog B1 (UNC-93B protein) (hUNC93B1)	-	-	-	-	-	1	1	-
1815	Q9BRF8	Uncharacterized metallophosphoesterase CSTP1 - Hc	-	-	-	1	-	-	-	-
1816	Q8IXM2	Uncharacterized potential DNA-binding protein C17orf	-	-	-	-	3	2	3	-
1817	Q53FT3	Uncharacterized protein C11orf73 - Homo sapiens (Hu	-	-	1	-	1	-	1	-
1818	Q9BQ61	Uncharacterized protein C19orf43 - Homo sapiens (Hu	-	-	-	-	1	3	2	-
1819	Q6PJW8	Uncharacterized protein C1orf71 - Homo sapiens (Hur	-	-	-	-	1	-	-	-
1820	Q96HY6	Uncharacterized protein C20orf116 precursor - Homo	-	-	-	-	-	-	1	-
1821	Q7Z570	Uncharacterized protein C2orf10 - Homo sapiens (Hur	-	-	-	1	-	1	-	-
1822	Q9GZY8	Uncharacterized protein C2orf33 - Homo sapiens (Hur	-	-	1	-	-	-	-	-
1823	Q9BU61	Uncharacterized protein C3orf60 - Homo sapiens (Hur	-	-	-	-	1	-	-	-
1824	Q5VWP3	Uncharacterized protein C6orf142 - Homo sapiens (Hu	-	1	-	-	-	-	-	-
1825	Q86YL5	Uncharacterized protein C8orf42 - Homo sapiens (Hur	-	-	2	-	-	-	-	-
1826	Q9BUH6	Uncharacterized protein C9orf142 - Homo sapiens (Hu	-	-	-	-	5	2	5	-
1827	Q9Y3I0	UPF0027 protein C22orf28 - Homo sapiens (Human)	-	-	-	-	2	-	-	-
1828	Q9NRG7	UPF0105 protein C14orf124 - Homo sapiens (Human)	-	-	-	-	1	-	1	-
1829	Q9BVM4	UPF0131 protein - Homo sapiens (Human)	-	-	1	-	-	-	-	-
1830	Q9H993	UPF0364 protein C6orf211 - Homo sapiens (Human)	-	-	-	1	-	-	-	-
1831	Q6IAA8	UPF0404 protein C11orf59 - Homo sapiens (Human)	-	-	3	-	2	3	2	-
1832	Q9GZP4	UPF0424 protein C1orf128 - Homo sapiens (Human)	-	1	-	-	4	-	3	-
1833	Q4G0N4	UPF0465 protein C5orf33 - Homo sapiens (Human)	-	-	-	1	-	-	-	-
1834	Q9H1C7	UPF0467 protein C5orf32 - Homo sapiens (Human)	-	-	-	1	-	-	-	-
1835	Q9NRP0	UPF0527 membrane protein - Homo sapiens (Human)	-	-	-	-	-	1	1	-
1836	P06132	Uroporphyrinogen decarboxylase (EC 4.1.1.37) (URO	-	-	-	-	2	-	1	X
1837	Q96QR1	Uteroglobin-related protein 2 precursor (Cytokine HIN	2	-	-	-	-	-	-	-
1838	Q16851	UTP--glucose-1-phosphate uridylyltransferase 2 (EC 2	-	-	1	5	4	1	2	X
1839	P54727	UV excision repair protein RAD23 homolog B (hHR23B	-	-	-	1	-	-	-	-
1840	Q9P2Y5	UV radiation resistance-associated gene protein - Homo	-	-	-	-	-	-	1	-
1841	Q9BZF9	Uveal autoantigen with coiled-coil domains and ankyrin	-	-	1	-	-	-	-	-
1842	P38606	Vacuolar ATP synthase catalytic subunit A, ubiquitous	-	-	1	-	-	3	6	X

1843	P21281	Vacuolar ATP synthase subunit B, brain isoform (EC 3.6.3.14) (V-ATPase)	-	-	1	-	1	2	2	X
1844	P36543	Vacuolar ATP synthase subunit E (EC 3.6.3.14) (V-ATPase)	-	-	1	-	-	2	2	X
1845	O75348	Vacuolar ATP synthase subunit G 1 (EC 3.6.3.14) (V-ATPase)	-	-	-	1	-	1	1	-
1846	Q9UBQ0	Vacuolar protein sorting 29 (Vesicle protein sorting 29)	-	-	1	-	-	4	3	X
1847	Q96QK1	Vacuolar protein sorting 35 (Vesicle protein sorting 35)	-	-	-	-	1	2	5	-
1848	Q9BRG1	Vacuolar protein sorting-associated protein 25 (hVps25)	-	-	-	-	-	2	-	-
1849	O75436	Vacuolar protein sorting-associated protein 26A (Vesicle protein sorting 26A)	-	-	-	-	-	-	1	-
1850	Q9UK41	Vacuolar protein sorting-associated protein 28 homolog (Vesicle protein sorting 28)	-	-	1	-	-	-	-	-
1851	O75351	Vacuolar protein sorting-associated protein 4B (Suppression of vacuolar protein sorting 4B)	-	-	1	-	2	2	2	-
1852	P26640	Valyl-tRNA synthetase (EC 6.1.1.9) (Valine--tRNA ligase)	-	-	-	-	1	2	7	-
1853	O95498	Vascular non-inflammatory molecule 2 precursor (Vascular non-inflammatory molecule 2)	-	-	-	1	-	-	-	-
1854	Q9NY84	Vascular non-inflammatory molecule 3 precursor - Homo sapiens	-	-	-	1	-	-	-	-
1855	P50552	Vasodilator-stimulated phosphoprotein (VASP) - Homo sapiens	-	-	5	6	1	1	-	-
1856	O75396	Vesicle trafficking protein SEC22b (SEC22 vesicle trafficking protein)	-	-	-	2	-	4	5	-
1857	P63027	Vesicle-associated membrane protein 2 (VAMP-2) (Synaptic vesicle-associated membrane protein 2)	-	-	2	-	-	-	-	-
1858	Q15836	Vesicle-associated membrane protein 3 (VAMP-3) (Synaptic vesicle-associated membrane protein 3)	-	-	3	-	-	-	-	-
1859	Q9BV40	Vesicle-associated membrane protein 8 (VAMP-8) (Endosomal vesicle-associated membrane protein 8)	-	-	1	-	-	2	3	-
1860	Q9POL0	Vesicle-associated membrane protein-associated protein 1 (VAMP-Associated Protein 1)	-	-	1	-	-	-	-	-
1861	P46459	Vesicle-fusing ATPase (EC 3.6.4.6) (Vesicular-fusion ATPase)	-	-	-	-	-	-	1	X
1862	Q12907	Vesicular integral-membrane protein VIP36 precursor	-	-	1	-	2	-	1	-
1863	Q00341	Vigilin (High density lipoprotein-binding protein) (HDL-binding protein)	-	1	-	-	-	-	-	-
1864	P08670	Vimentin	-	-	-	1	-	1	14	X
1865	P18206	Vinculin (Metavinculin)	-	8	51	7	12	18	37	X
1866	P02774	Vitamin D-binding protein precursor (DBP) (Group-specific component of vitamin D-binding protein)	10	-	1	-	-	-	2	X
1867	P04070	Vitamin K-dependent protein C precursor (EC 3.4.21.6) (Protein C)	3	-	-	-	-	-	-	-
1868	P07225	Vitamin K-dependent protein S precursor - Homo sapiens	2	-	3	-	-	-	-	-
1869	P04004	Vitronectin precursor (Serum spreading factor) (S-protein)	5	-	1	-	-	-	6	X
1870	P21796	Voltage-dependent anion-selective channel protein 1 (VDAC1)	-	-	9	-	6	3	9	-
1871	P45880	Voltage-dependent anion-selective channel protein 2 (VDAC2)	-	-	5	-	4	2	5	X
1872	Q9Y277	Voltage-dependent anion-selective channel protein 3 (VDAC3)	-	-	11	2	-	4	6	-
1873	O00305	Voltage-dependent L-type calcium channel subunit beta 1 (L-type voltage-dependent calcium channel subunit beta 1)	-	-	-	1	-	-	-	-
1874	P04275	Von Willebrand factor precursor (vWF) [Contains: Von Willebrand factor type A domain]	-	-	34	-	-	-	5	-
1875	Q5JSH3	WD repeat protein 44 (Rabphilin-11) - Homo sapiens	-	-	2	-	-	-	-	-
1876	Q9GZS3	WD repeat protein 61 (Meiotic recombination REC14 protein)	-	-	-	-	1	-	-	-
1877	O75083	WD-repeat protein 1 (Actin-interacting protein 1) (AIP1)	-	2	15	7	15	5	12	X
1878	P42768	Wiskott-Aldrich syndrome protein (WASp)	-	-	-	1	-	-	4	-
1879	Q92558	Wiskott-Aldrich syndrome protein family member 1 (WASF1)	-	-	-	1	-	-	-	-
1880	O43516	Wiskott-Aldrich syndrome protein-interacting protein (WASP-interacting protein)	-	-	-	-	1	-	2	-
1881	Q969T9	WW domain-binding protein 2 (WBP-2) - Homo sapiens	-	1	1	-	1	1	-	X
1882	Q9NQW7	Xaa-Pro aminopeptidase 1 (EC 3.4.11.9) (X-Pro aminopeptidase)	-	-	-	-	-	-	1	-
1883	P12955	Xaa-Pro dipeptidase (EC 3.4.13.9) (X-Pro dipeptidase)	-	-	-	-	2	-	-	X
1884	O15231	Zinc finger protein 185 (LIM-domain protein ZNF185) (Zinc finger protein 185)	-	-	1	-	-	-	-	-
1885	Q5T4S7	Zinc finger UBR1-type protein 1 - Homo sapiens (Human)	-	-	-	1	-	2	-	-
1886	P25311	Zinc-alpha-2-glycoprotein precursor (Zn-alpha-2-glycoprotein)	11	-	-	-	-	-	-	X
1887	Q15942	Zyxin (Zyxin-2)	-	-	9	-	-	3	5	X

Supplementary Table 2

	AccNr	Protein	MW	pI	Distinct	C-PBMC	C-T cell	C-monocyte	C-platelet	C-neutrophil	C-erythrocyte	C-blood plasma
1	P61604	10 kDa heat shock protein, mitochondria	10800.5	8.91	3	X	X	X	X	X	-	-
2	P42704	130 kDa leucine-rich protein (LRP 130) (	145202.1	5.5	1	X	-	X	-	-	-	-
3	P31946	14-3-3 protein beta/alpha (Protein kinase	27951.3	4.76	5	X	X	X	X	X	-	-
4	P62258	14-3-3 protein epsilon (14-3-3E)	29174.1	4.63	6	X	X	X	X	X	X	-
5	Q04917	14-3-3 protein eta (Protein AS1)	28087.7	4.76	4	X	X	X	X	X	-	-
6	P61981	14-3-3 protein gamma (Protein kinase C	28171.5	4.8	6	X	X	X	X	X	-	-
7	P27348	14-3-3 protein theta (14-3-3 protein tau) (	27764.4	4.68	8	X	X	X	X	X	-	-
8	P63104	14-3-3 protein zeta/delta (Protein kinase	27745.3	4.73	14	X	X	X	X	X	-	-
9	Q9Y4L1	150 kDa oxygen-regulated protein precu	111335.9	5.16	1	X	X	-	-	-	-	-
10	P62191	26S protease regulatory subunit 4 (P26s	49184.8	5.87	1	-	-	-	-	-	X	-
11	P17980	26S protease regulatory subunit 6A (TAT	49203.8	5.13	1	X	X	-	-	-	-	-
12	P35998	26S protease regulatory subunit 7 (MSS	48502.9	5.72	1	-	-	-	-	-	-	-
13	P62333	26S protease regulatory subunit S10B (P	44173.2	7.09	2	X	X	X	-	-	X	-
14	O75832	26S proteasome non-ATPase regulatory	24428	5.72	1	X	-	-	-	-	-	-
15	Q9UNM6	26S proteasome non-ATPase regulatory	42918.7	5.53	1	X	X	X	X	-	-	-
16	Q13200	26S proteasome non-ATPase regulatory	100200.3	5.08	1	X	X	X	-	-	X	-
17	O43242	26S proteasome non-ATPase regulatory	60977.9	8.47	1	X	X	X	-	-	-	-
18	P51665	26S proteasome non-ATPase regulatory	37025.6	6.29	1	X	X	X	-	-	-	-
19	Q02218	2-oxoglutarate dehydrogenase E1 compo	113476.1	6.62	1	X	X	-	-	-	-	-
20	P42126	3,2-trans-enoyl-CoA isomerase, mitochol	32816.2	8.8	2	-	X	X	-	X	-	-
21	Q9H9J2	39S ribosomal protein L44, mitochondria	37535.6	8.65	1	X	-	-	-	-	-	-
22	Q99714	3-hydroxyacyl-CoA dehydrogenase type	26792	7.87	2	X	X	X	X	X	-	-
23	P42765	3-ketoacyl-CoA thiolase, mitochondrial (E	41924.4	8.32	6	X	X	-	-	-	-	-
24	P62263	40S ribosomal protein S14	16141.6	9.99	1	X	X	X	-	-	-	-
25	P62269	40S ribosomal protein S18 (Ke-3) (Ke3)	17718.8	9.99	2	X	X	X	-	-	-	-
26	P39019	40S ribosomal protein S19	15929.4	9.99	2	X	X	-	-	-	-	-
27	P15880	40S ribosomal protein S2 (S4) (LLRep3 p	31324.6	9.99	3	X	X	X	-	-	-	-
28	P60866	40S ribosomal protein S20 - Homo sapie	13372.8	9.95	4	X	X	-	-	-	-	-
29	P62854	40S ribosomal protein S26	12884.3	9.99	2	X	X	X	-	-	-	-
30	P62857	40S ribosomal protein S28	7841.1	9.99	1	X	X	X	-	-	-	-
31	P62701	40S ribosomal protein S4, X isoform (Sin	29466.7	9.99	2	X	X	-	-	-	-	-
32	P46782	40S ribosomal protein S5	22745.3	9.73	1	X	X	X	-	-	-	-
33	P08865	40S ribosomal protein SA (p40) (34/67 k	32723	4.79	3	X	X	X	-	X	-	-
34	P10809	60 kDa heat shock protein, mitochondria	61055	5.7	14	X	X	X	X	X	-	-
35	P05388	60S acidic ribosomal protein P0 (L10E)	34273.7	5.72	4	X	X	X	-	-	-	-
36	P05386	60S acidic ribosomal protein P1	11514	4.26	1	-	X	X	-	-	-	-
37	P05387	60S acidic ribosomal protein P2	11665	4.42	4	X	X	X	-	-	-	-
38	P62913	60S ribosomal protein L11 (CLL-associat	20121.3	9.64	2	X	X	X	-	X	-	-
39	P30050	60S ribosomal protein L12	17818.7	9.48	3	X	X	X	-	-	-	-
40	P35268	60S ribosomal protein L22 (Epstein-Barr	14655.9	9.22	1	X	X	X	-	-	-	-
41	P62888	60S ribosomal protein L30	12652.9	9.66	3	X	X	X	-	-	-	-
42	Q02878	60S ribosomal protein L6 (TAX-responsi	32596.9	9.99	2	X	X	X	-	-	-	-
43	P52209	6-phosphogluconate dehydrogenase, de	53009.1	6.88	10	X	X	X	X	X	-	-
44	O95336	6-phosphogluconolactonase (EC 3.1.1.3	27547	5.7	5	X	X	X	X	X	-	-
45	P11021	78 kDa glucose-regulated protein precurs	72333.3	5.07	6	X	X	X	X	X	-	-
46	Q9NUJ1	Abhydrolase domain-containing protein 1	33932.7	8.8	2	-	X	-	-	-	-	-
47	Q96IU4	Abhydrolase domain-containing protein 1	22345.8	5.94	3	X	X	X	X	X	-	-
48	P24752	Acetyl-CoA acetyltransferase, mitochond	45199.8	8.98	1	X	X	X	-	X	-	-
49	P39687	Acidic leucine-rich nuclear phosphoprote	28585.5	4	3	X	X	X	-	X	-	-

50	Q92688	Acidic leucine-rich nuclear phosphoprote	28787.9	3.94	3	X	X	X	-	X	-	-
51	Q9BTT0	Acidic leucine-rich nuclear phosphoprote	30692.6	3.77	2	X	X	X	-	X	-	-
52	Q99798	Aconitate hydratase, mitochondrial precu	85425.9	7.36	1	X	X	-	-	-	-	-
53	P60709	Actin, cytoplasmic 1 (Beta-actin)	41737	5.29	24	X	X	X	X	X	X	X
54	P63261	Actin, cytoplasmic 2 (Gamma-actin)	41793.1	5.31	24	X	X	X	X	X	X	X
55	P61160	Actin-like protein 2 (Actin-related protein	44761	6.29	9	X	X	X	X	X	X	-
56	P61158	Actin-like protein 3 (Actin-related protein	47371.4	5.61	9	X	X	X	X	X	-	-
57	O15143	Actin-related protein 2/3 complex subunit	40818.8	8.69	5	X	X	X	X	X	-	-
58	O15144	Actin-related protein 2/3 complex subunit	34333.2	6.84	4	X	X	X	X	X	X	-
59	O15145	Actin-related protein 2/3 complex subunit	20415.6	8.82	3	X	X	X	X	X	-	-
60	P59998	Actin-related protein 2/3 complex subunit	19535.9	8.53	2	X	X	X	X	X	-	-
61	O15511	Actin-related protein 2/3 complex subunit	16189.3	5.47	2	X	X	X	X	X	-	-
62	P53999	Activated RNA polymerase II transcriptio	14264.2	9.6	1	X	X	X	-	-	-	-
63	O95433	Activator of 90 kDa heat shock protein A	38274.5	5.41	1	-	-	X	X	-	-	-
64	P45954	Acyl-CoA dehydrogenase, short/branche	47485.7	6.53	1	-	X	-	-	-	-	-
65	P49748	Acyl-CoA dehydrogenase, very-long-cha	70390.5	8.92	4	X	-	X	-	-	-	-
66	P07741	Adenine phosphoribosyltransferase (EC	19476.7	5.79	4	X	X	X	X	X	X	-
67	P23526	Adenosylhomocysteinase (EC 3.3.1.1) (S	47585.2	5.92	4	X	X	X	-	X	X	-
68	P54819	Adenylate kinase isoenzyme 2, mitochon	26346.7	7.85	7	X	X	X	X	X	-	-
69	P30566	Adenylosuccinate lyase (EC 4.3.2.2) (Ad	54889.6	6.68	1	X	X	-	-	-	X	-
70	Q01518	Adenylyl cyclase-associated protein 1 (C	51542.1	8.13	15	X	X	X	X	X	-	-
71	Q9HDC9	Adipocyte plasma membrane-associated	46480.6	5.82	2	X	X	-	-	X	-	-
72	P05141	ADP/ATP translocase 2 (Adenine nucleo	32764.2	9.76	5	X	X	X	X	-	-	-
73	P84077	ADP-ribosylation factor 1	20565.7	6.36	5	X	X	X	X	X	X	-
74	P61204	ADP-ribosylation factor 3	20469.7	7.03	5	-	-	-	X	-	-	-
75	P84085	ADP-ribosylation factor 5	20398.6	6.36	3	-	X	X	-	-	-	-
76	Q12802	A-kinase anchor protein 13 - Homo sapie	307552	5.12	1	-	-	-	-	-	-	-
77	P14550	Alcohol dehydrogenase [NADP+] (EC 1.1	36442	6.35	1	X	X	-	-	X	-	-
78	P15121	Aldose reductase (EC 1.1.1.21) (AR) (Al	35722.4	6.56	2	X	X	X	X	-	X	-
79	P02763	Alpha-1-acid glycoprotein 1 precursor (A	23511.7	4.93	1	X	-	-	-	X	-	X
80	P02765	Alpha-2-HS-glycoprotein precursor (Fetu	39324.9	5.43	2	X	-	-	-	-	-	X
81	P01023	Alpha-2-macroglobulin precursor (Alpha-	163278.8	6	6	X	-	-	X	-	-	X
82	P12814	Alpha-actinin-1 (Alpha-actinin cytoskele	103058.1	5.25	2	X	X	X	X	X	X	-
83	P06733	Alpha-enolase (EC 4.2.1.11) (2-phospho	47038	6.99	22	X	X	X	X	X	X	-
84	P04083	Annexin A1 (Annexin I) (Lipocortin I) (Ca	38583.3	6.64	15	X	X	X	-	X	-	-
85	P50995	Annexin A11 (Annexin XI) (Calcylin-ass	54390	7.53	4	X	X	X	X	X	-	-
86	P07355	Annexin A2 (Annexin II) (Lipocortin II) (C	38473.1	7.56	15	X	X	X	-	X	X	-
87	P09525	Annexin A4 (Annexin IV) (Lipocortin IV) (	35751.7	5.85	2	X	X	X	X	X	-	-
88	P08758	Annexin A5 (Annexin V) (Lipocortin V) (E	35805.7	4.94	8	X	X	X	X	X	-	-
89	P08133	Annexin A6 (Annexin VI) (Lipocortin VI) (	75742.5	5.42	20	X	X	X	X	X	-	-
90	P20073	Annexin A7 (Annexin VII) (Synexin)	52739.5	5.52	2	X	X	X	-	X	X	-
91	P02647	Apolipoprotein A-I precursor (Apo-AI) (Ap	30778	5.56	12	X	-	X	-	-	-	X
92	Q8NCW5	Apolipoprotein A-I-binding protein precu	31674.8	7.56	3	X	-	-	-	-	-	-
93	P06727	Apolipoprotein A-IV precursor (Apo-AIV)	45399.3	5.28	11	X	-	-	-	-	-	X
94	P02656	Apolipoprotein C-III precursor (Apo-CIII)	10852.4	5.23	2	X	-	X	-	-	-	X
95	P02649	Apolipoprotein E precursor (Apo-E) - Hor	36154.3	5.65	3	X	-	-	-	-	-	X
96	Q07812	Apoptosis regulator BAX, membrane isof	21184.5	5.08	2	X	X	X	-	X	-	-
97	P10415	Apoptosis regulator Bcl-2	26266	6.75	1	-	-	-	-	-	-	-
98	Q9ULZ3	Apoptosis-associated speck-like protein c	21626.9	5.95	2	X	X	X	-	X	-	-
99	P55145	ARMET protein precursor (Arginine-rich p	20256.7	8.69	1	X	X	X	X	X	-	-
100	P00505	Aspartate aminotransferase, mitochondrial	47475.8	9.13	6	X	X	X	X	X	-	-
101	P25705	ATP synthase alpha chain, mitochondrial	59750.9	9.16	21	X	X	X	X	X	-	-
102	P24539	ATP synthase B chain, mitochondrial pre	28908.8	9.37	4	X	X	X	X	X	-	-
103	P06576	ATP synthase beta chain, mitochondrial	56560.2	5.26	17	X	X	X	X	X	-	-
104	O75947	ATP synthase D chain, mitochondrial (EC	18360.1	5.22	2	X	X	X	X	X	-	-
105	P30049	ATP synthase delta chain, mitochondrial	17490	5.38	2	X	X	X	X	X	-	-

106	P56134	ATP synthase f chain, mitochondrial (EC	10786.7	9.7	2	X	X	X	-	-	-	-
107	P36542	ATP synthase gamma chain, mitochondr	32996.2	9.23	2	X	X	X	X	-	-	-
108	P48047	ATP synthase O subunit, mitochondrial p	23277.4	9.97	7	X	X	X	X	X	-	-
109	Q86UK0	ATP-binding cassette sub-family A mem	293252.3	7.89	1	-	-	-	-	-	-	-
110	P53396	ATP-citrate synthase (EC 2.3.3.8) (ATP-c	120825.9	6.95	1	X	X	X	-	X	X	-
111	P12956	ATP-dependent DNA helicase 2 subunit	69712.2	6.23	2	X	X	X	-	-	-	-
112	P13010	ATP-dependent DNA helicase 2 subunit	82573.8	5.55	1	X	X	X	-	-	-	-
113	P20160	Azurocidin precursor (Cationic antimicrob	26885.8	9.75	1	X	-	X	-	X	-	-
114	P51572	B-cell receptor-associated protein 31 (BC	27860.6	8.44	2	X	X	X	-	X	-	-
115	P61769	Beta-2-microglobulin precursor [Contains	13714.6	6.06	1	X	-	X	X	X	-	X
116	P13929	Beta-enolase (EC 4.2.1.11) (2-phospho-l	46855.9	7.73	4	X	-	-	X	X	X	-
117	P07686	Beta-hexosaminidase beta chain precurs	63111.7	6.29	1	X	-	X	-	-	-	-
118	P31939	Bifunctional purine biosynthesis protein F	64616.2	6.27	2	X	X	-	-	-	X	-
119	P53004	Biliverdin reductase A precursor (EC 1.3.	33428.7	6.06	2	X	X	X	X	X	-	-
120	P49593	Ca(2+)/calmodulin-dependent protein kin	49831.1	4.99	1	X	X	X	X	X	-	-
121	P31949	Calgizzarin (S100 calcium-binding protei	11740.5	6.56	1	X	X	X	-	X	-	X
122	P05109	Calgranulin A (Migration inhibitory factor-	10834.6	6.51	8	X	X	X	X	X	X	X
123	P06702	Calgranulin B (Migration inhibitory factor-	13242.1	5.71	7	X	X	X	-	X	-	X
124	P62158	Calmodulin (CaM)	16706.5	4.09	3	X	X	X	X	X	X	-
125	P27824	Calnexin precursor (Major histocompatib	67568.6	4.47	6	X	X	X	X	X	-	-
126	P04632	Calpain small subunit 1 (CSS1) (Calcium	28315.9	5.05	4	X	X	X	X	X	X	-
127	Q99439	Calponin-2 (Calponin H2, smooth muscle	33566.1	6.92	1	X	X	X	X	X	-	-
128	P27797	Calreticulin precursor (CRP55) (Calregul	48141.8	4.29	8	X	X	X	X	X	-	-
129	P10644	cAMP-dependent protein kinase type I- α	42981.9	5.27	1	X	X	X	X	X	-	-
130	P16152	Carbonyl reductase [NADPH] 1 (EC 1.1.1.	30243.9	8.55	4	X	X	X	X	X	X	-
131	O75828	Carbonyl reductase [NADPH] 3 (EC 1.1.1.	30719.2	5.82	2	X	-	-	-	-	-	-
132	P04040	Catalase (EC 1.11.1.6)	59625.3	6.95	6	X	X	X	X	X	X	-
133	P07339	Cathepsin D precursor (EC 3.4.23.5) [Co	44552.5	6.1	3	X	X	X	X	X	-	-
134	P25774	Cathepsin S precursor (EC 3.4.22.27)	37495.9	8.61	5	X	X	X	-	X	-	-
135	P60953	Cell division control protein 42 homolog p	21310.7	5.77	1	X	X	X	X	X	-	-
136	P62633	Cellular nucleic acid-binding protein (CNI	19462.9	8	1	X	X	X	-	-	-	-
137	O00299	Chloride intracellular channel protein 1 (N	26791.7	5.09	5	X	X	X	X	X	X	-
138	O75390	Citrate synthase, mitochondrial precursor	51712.7	8.45	5	X	X	X	X	X	-	-
139	Q00610	Clathrin heavy chain 1 (CLH-17)	191484.5	5.48	18	X	X	X	X	X	X	-
140	O43809	Cleavage and polyadenylation specificity	26227.4	8.85	1	X	X	-	-	-	-	-
141	P10909	Clusterin precursor (Complement-associ	52494.9	5.89	6	X	-	-	X	X	-	X
142	Q14019	Coactosin-like protein	15813.9	5.55	9	X	X	X	X	X	-	-
143	P23528	Cofilin-1 (Cofilin, non-muscle isoform) (1	18371.4	8.27	9	X	X	X	X	X	X	X
144	P01024	Complement C3 precursor [Contains: Co	187149.1	6.02	4	X	-	-	X	-	-	X
145	P31146	Coronin-1A (Coronin-like protein p57) (C	51026.6	6.25	11	X	X	X	X	X	-	-
146	P57737	Coronin-7 (70 kDa WD repeat tumor reje	100575.6	5.51	1	X	X	X	-	X	-	-
147	Q86VP6	Cullin-associated NEDD8-dissociated pro	136376.5	5.52	2	X	X	X	-	X	X	-
148	Q8ND76	Cyclin-Y - Homo sapiens (Human)	39336.9	6.76	1	-	-	-	-	-	-	-
149	P04080	Cystatin B (Liver thiol proteinase inhibitor	11139.6	6.96	1	X	X	X	-	X	-	-
150	P04839	Cytochrome b-245 heavy chain (p22 pha	65205.1	8.9	2	X	X	X	-	X	-	-
151	P13498	Cytochrome b-245 light chain (p22 phag	20827.3	9.61	1	-	-	X	-	X	-	-
152	P99999	Cytochrome c	11617.6	9.59	2	X	X	X	X	-	-	-
153	P00403	Cytochrome c oxidase subunit 2 (EC 1.9.	25565.2	4.67	5	X	X	X	-	-	-	-
154	P13073	Cytochrome c oxidase subunit IV isoform	19576.8	9.52	2	X	X	X	-	-	-	-
155	Q81UI8	Cytokine receptor-like factor 3 - Homo sa	49766.2	5.01	1	-	X	X	X	-	-	-
156	P50453	Cytoplasmic antiproteinase 3 (CAP3) (CA	42403.9	5.61	4	X	X	X	X	X	-	-
157	Q7L576	Cytoplasmic FMR1-interacting protein 1-	145183.3	6.46	1	X	-	X	-	-	-	-
158	P28838	Cytosol aminopeptidase (EC 3.4.11.1) (L	52640.4	6.28	1	X	X	X	X	-	-	-
159	Q96KP4	Cytosolic nonspecific dipeptidase (Glutar	52878.8	5.66	3	X	X	X	-	-	-	-
160	Q96EP5	DAZ-associated protein 1 (Deleted in azo	43383.6	8.73	2	X	X	-	-	-	-	-
161	P30046	D-dopachrome decarboxylase (EC 4.1.1.	12580.6	7.25	1	X	X	X	-	X	-	-

162	Q13011	Delta3,5-delta2,4-dienoyl-CoA isomerase	35816.4	8.16	5	X	X	X	X	X	-	-
163	P60981	Destrin (Actin-depolymerizing factor) (AD	18374.7	8.12	1	X	X	-	X	X	-	-
164	P09622	Dihydrolipoyl dehydrogenase, mitochond	54150.5	7.59	1	X	X	X	-	-	-	-
165	Q16555	Dihydropyrimidinase-related protein 2 (D	62294	5.95	1	X	X	X	X	X	-	-
166	P27695	DNA-(apurinic or apyrimidinic site) lyase	35423.5	8.42	6	X	X	X	-	X	-	-
167	O75937	DnaJ homolog subfamily C member 8 (S	29841.8	9.04	1	X	X	-	-	-	-	-
168	P39656	Dolichyl-diphosphooligosaccharide--prote	48809.7	5.43	1	X	-	X	-	X	-	-
169	P04844	Dolichyl-diphosphooligosaccharide--prote	69284.3	5.44	5	-	X	X	X	-	-	-
170	P04843	Dolichyl-diphosphooligosaccharide--prote	68569.7	5.96	4	X	X	X	-	X	-	-
171	Q9UJU6	Drebrin-like protein (SH3 domain-contain	48207.5	5.02	1	X	-	-	X	X	-	-
172	Q14203	Dynactin-1 (150 kDa dynein-associated p	141695.6	5.61	1	X	-	-	X	-	-	-
173	Q9HC35	Echinoderm microtubule-associated prot	108903.7	5.88	1	-	-	-	-	-	-	-
174	Q96C19	EF-hand domain-containing protein 2 (Sv	26697.4	5.15	1	X	X	X	X	X	-	-
175	Q9H4M9	EH-domain-containing protein 1 (Testilin)	60627.2	6.35	3	X	X	-	X	X	-	-
176	P13804	Electron transfer flavoprotein alpha-subu	35079.8	8.62	3	X	X	X	X	X	-	-
177	P38117	Electron transfer flavoprotein beta-subun	27843.8	8.25	3	X	X	X	X	-	-	-
178	P68104	Elongation factor 1-alpha 1 (EF-1-alpha-1	50141.1	9.1	13	X	X	X	X	X	X	-
179	P29692	Elongation factor 1-delta (EF-1-delta) (Ar	30990.8	4.9	3	X	X	X	X	-	-	-
180	P26641	Elongation factor 1-gamma (EF-1-gamma)	49987.9	6.27	3	X	X	X	X	X	-	-
181	P13639	Elongation factor 2 (EF-2)	95207.5	6.42	8	X	X	X	-	X	X	-
182	P49411	Elongation factor Tu, mitochondrial precu	49541.8	7.26	7	X	X	X	X	-	-	-
183	P30040	Endoplasmic reticulum protein ERp29 pr	28993.6	6.77	5	X	X	X	X	X	-	-
184	P14625	Endoplasmin precursor (94 kDa glucose-	92469.3	4.76	2	X	X	X	X	X	X	-
185	P10768	Esterase D (EC 3.1.1.1)	31463	6.54	2	X	X	X	X	X	X	-
186	P60842	Eukaryotic initiation factor 4A-I (EC 3.6.1	46154.2	5.32	2	X	X	X	X	X	X	-
187	Q14240	Eukaryotic initiation factor 4A-II (EC 3.6.1	46402.5	5.33	2	X	X	-	-	-	-	-
188	Q14152	Eukaryotic translation initiation factor 3 s	166570.2	6.38	4	X	X	-	-	-	-	-
189	Q15056	Eukaryotic translation initiation factor 4H	27254	6.92	1	X	X	X	X	-	-	-
190	P63241	Eukaryotic translation initiation factor 5A	16701.2	5.08	3	X	X	X	X	X	X	-
191	O14980	Exportin-1 (Chromosome region mainten	123386.6	5.71	1	X	-	X	-	-	-	-
192	P15311	Ezrin (p81) (Cytovillin) (Villin-2)	69267.9	5.95	8	X	X	X	-	X	-	-
193	O14745	Ezrin-radixin-moesin-binding phosphop	38737.4	5.55	2	X	X	X	X	X	-	-
194	P52907	F-actin capping protein alpha-1 subunit (f	32922.9	5.45	5	X	X	X	X	X	X	-
195	P47755	F-actin capping protein alpha-2 subunit (f	32818.1	5.58	1	X	X	X	X	X	X	-
196	P47756	F-actin capping protein beta subunit (Cap	31219.5	5.36	2	X	X	X	X	X	-	-
197	Q96AE4	Far upstream element-binding protein 1 (f	67473.6	7.18	1	X	X	X	-	-	-	-
198	Q01469	Fatty acid-binding protein, epidermal (E-f	15033.3	6.82	2	X	X	X	-	X	-	-
199	P02792	Ferritin light chain (Ferritin L subunit)	19888.6	5.51	4	X	X	X	-	X	-	-
200	P02671	Fibrinogen alpha chain precursor [Contai	94973.5	5.7	5	X	-	-	X	-	-	X
201	P02675	Fibrinogen beta chain precursor [Contain	55928.5	8.54	9	X	X	-	X	X	X	X
202	P02679	Fibrinogen gamma chain precursor	51511.9	5.37	6	X	-	-	X	-	-	X
203	P21333	Filamin-A (Alpha-filamin) (Filamin-1) (En	280631.3	5.73	47	X	X	X	X	X	X	-
204	P30043	Flavin reductase (EC 1.5.1.30) (FR) (NA	21988.3	7.31	2	X	X	X	X	X	X	-
205	O95466	Formin-like 1 protein (Formin-like protein	121828.2	5.56	4	X	X	X	-	-	-	-
206	P09467	Fructose-1,6-bisphosphatase 1 (EC 3.1.3	36683.5	6.61	1	X	X	X	-	X	-	-
207	P04075	Fructose-bisphosphate aldolase A (EC 4	39289	8.39	10	X	X	X	X	X	X	-
208	P09972	Fructose-bisphosphate aldolase C (EC 4	39324.9	6.46	1	X	X	X	X	X	-	-
209	P09382	Galectin-1 (Beta-galactoside-binding lect	14584.6	5.34	4	X	X	X	-	-	-	-
210	P17931	Galectin-3 (Galactose-specific lectin 3) (N	26057.3	8.61	1	X	-	X	-	X	-	-
211	P09104	Gamma-enolase (EC 4.2.1.11) (2-phosph	47137.6	4.91	4	-	X	-	-	X	-	-
212	Q9P107	GEM-interacting protein (GMIP)	106733.5	5.5	1	X	-	X	-	-	-	-
213	P60983	Glia maturation factor beta (GMF-beta)	16582.1	5.19	1	X	X	X	X	-	-	-
214	O60234	Glia maturation factor gamma (GMF-gam	16801.4	5.18	3	X	X	X	X	X	-	-
215	P11413	Glucose-6-phosphate 1-dehydrogenase	59134.9	6.44	4	X	X	X	X	X	-	-
216	P06744	Glucose-6-phosphate isomerase (EC 5.3	63016.3	8.44	8	X	X	X	X	X	X	-
217	P00367	Glutamate dehydrogenase 1, mitochondr	61398.2	7.66	5	X	X	X	-	-	-	-

218	O94925	Glutaminase kidney isoform, mitochondri	73461.5	7.85	1	X	X	-	-	-	-	-
219	P07203	Glutathione peroxidase 1 (EC 1.11.1.9) (	21899.2	6.15	5	X	X	X	X	X	X	-
220	P00390	Glutathione reductase, mitochondrial pre	56257.4	8.74	5	X	X	X	X	X	X	-
221	Q9Y2Q3	Glutathione S-transferase kappa 1 (EC 2	25365.8	8.53	4	X	X	X	X	-	-	-
222	P09211	Glutathione S-transferase P (EC 2.5.1.18	23224.8	5.44	4	X	X	X	X	X	-	-
223	P78417	Glutathione transferase omega-1 (EC 2.5	27566	6.24	2	X	X	X	X	X	-	-
224	P04406	Glyceraldehyde-3-phosphate dehydrogen	35922.2	8.58	17	X	X	X	X	X	X	X
225	Q9HC38	Glyoxalase domain-containing protein 4 -	34793.7	5.4	3	X	X	-	X	X	-	-
226	Q9UBQ7	Glyoxylate reductase/hydroxypyruvate re	35668.5	7.01	1	X	-	-	-	-	-	-
227	Q9H4G4	Golgi-associated plant pathogenesis-rela	17087.2	9.44	2	X	X	X	X	X	-	X
228	P28676	Grancalcin	24010.2	5.02	2	X	X	X	X	X	-	-
229	P62993	Growth factor receptor-bound protein 2 (	25206.5	5.89	3	X	X	X	X	X	-	-
230	Q9NUV9	GTPase, IMAP family member 4 (Immun	37534	7.66	3	X	X	X	-	-	-	-
231	P62826	GTP-binding nuclear protein Ran (GTPas	24292	7.2	6	X	X	X	X	X	X	-
232	Q03113	Guanine nucleotide-binding protein alpha	44148.3	9.84	1	-	-	X	-	X	-	-
233	P63244	Guanine nucleotide-binding protein beta	35076.9	7.6	8	X	X	X	-	-	X	-
234	P04899	Guanine nucleotide-binding protein G(i),	40319.9	5.34	5	X	X	X	X	X	-	-
235	P62873	Guanine nucleotide-binding protein G(i)/G	37246	5.6	3	-	X	X	X	X	-	-
236	P62879	Guanine nucleotide-binding protein G(i)/G	37200.1	5.6	3	X	X	-	X	X	-	-
237	P08107	Heat shock 70 kDa protein 1 (HSP70.1) (	70052.6	5.48	6	X	X	X	X	X	X	-
238	P11142	Heat shock cognate 71 kDa protein (Hea	70898.4	5.38	12	X	X	X	X	X	X	-
239	Q12931	Heat shock protein 75 kDa, mitochondria	80110.4	8.3	1	X	X	X	X	X	-	-
240	P07900	Heat shock protein HSP 90-alpha (HSP 8	84543	4.94	11	X	X	X	X	X	X	-
241	P08238	Heat shock protein HSP 90-beta (HSP 8	83133.4	4.97	10	X	X	X	X	X	X	-
242	P14317	Hematopoietic lineage cell-specific prote	53998.3	4.74	1	X	X	X	-	-	X	-
243	Q9Y5Z4	Heme-binding protein 2 (Protein SOUL) (	22875.5	4.58	1	-	X	X	X	X	-	-
244	P69905	Hemoglobin subunit alpha (Hemoglobin a	15126.4	8.73	3	X	-	X	-	X	X	X
245	P68871	Hemoglobin subunit beta (Hemoglobin be	15867.3	6.81	9	X	-	X	-	X	X	X
246	P51858	Hepatoma-derived growth factor (HDGF)	26788.4	4.7	2	X	X	-	-	-	-	-
247	Q99729	Heterogeneous nuclear ribonucleoprotein	36612.7	9.04	1	-	-	-	-	-	-	-
248	P09651	Heterogeneous nuclear ribonucleoprotein	38714.8	9.26	6	X	X	X	-	X	-	-
249	Q14103	Heterogeneous nuclear ribonucleoprotein	38434.4	7.61	6	X	X	X	-	X	-	-
250	P52597	Heterogeneous nuclear ribonucleoprotein	45540.9	5.38	5	X	X	X	-	X	-	-
251	P31943	Heterogeneous nuclear ribonucleoprotein	49098.5	5.89	5	X	X	X	-	-	-	-
252	P55795	Heterogeneous nuclear ribonucleoprotein	49263.9	5.89	2	-	-	-	-	-	-	-
253	P61978	Heterogeneous nuclear ribonucleoprotein	50976.5	5.39	4	X	X	X	X	X	-	-
254	P22626	Heterogeneous nuclear ribonucleoprotein	37429.9	8.97	7	X	X	X	-	X	X	-
255	P07910	Heterogeneous nuclear ribonucleoprotein	33688.2	4.95	2	X	X	X	-	-	-	-
256	Q00839	Heterogenous nuclear ribonucleoprotein	90479.8	5.76	1	X	X	X	-	-	-	-
257	P09429	High mobility group protein 1 (HMG-1) (H	24762.7	5.62	7	X	X	X	-	-	-	-
258	P26583	High mobility group protein 2 (HMG-2)	23902.7	7.77	4	X	X	X	-	-	-	-
259	P49773	Histidine triad nucleotide-binding protein	13670.8	6.46	1	X	X	X	X	X	-	-
260	P0C0S8	Histone H2A type 1 (H2A.1) - Homo sapi	13960.3	9.99	3	-	-	-	-	-	-	-
261	P62805	Histone H4	11236.2	9.99	1	X	X	X	X	-	-	-
262	P13746	HLA class I histocompatibility antigen, A-	40937	5.77	3	-	-	-	X	-	-	-
263	P01892	HLA class I histocompatibility antigen, A-	40922.1	6.5	3	X	-	-	X	-	-	-
264	P01908	HLA class II histocompatibility antigen, D	28105.3	5.12	1	X	-	-	-	-	-	-
265	P50502	Hsc70-interacting protein (Hip) (Putative	41331.9	5.18	1	X	X	-	X	-	X	-
266	P00492	Hypoxanthine-guanine phosphoribosyltra	24448.3	6.24	2	X	X	X	X	X	X	-
267	P01876	Ig alpha-1 chain C region - Homo sapien	37654.9	6.08	4	X	X	-	-	-	-	X
268	P01857	Ig gamma-1 chain C region - Homo sapien	36106.1	8.46	6	X	-	-	-	-	X	X
269	P01859	Ig gamma-2 chain C region - Homo sapien	35884.8	7.66	5	X	-	-	-	-	-	X
270	P01834	Ig kappa chain C region - Homo sapiens	11608.9	5.58	3	X	-	-	-	X	X	X
271	P01842	Ig lambda chain C regions - Homo sapien	11236.6	6.91	2	X	X	-	-	X	-	X
272	Q9H2U2	Inorganic pyrophosphatase 2, mitochond	37962.5	7.06	2	X	X	-	X	X	-	-
273	P29218	Inositol monophosphatase (EC 3.1.3.25)	30189	5.16	1	X	X	X	X	X	-	-

274	Q16270	Insulin-like growth factor-binding protein	29130.5	8.25	2	-	-	-	-	-	-	-
275	P08514	Integrin alpha-IIb precursor (Platelet mem	113391.5	5.21	8	X	-	-	X	X	-	-
276	P20701	Integrin alpha-L precursor (Leukocyte ad	128770.3	5.4	3	X	X	X	-	-	-	-
277	P11215	Integrin alpha-M precursor (Cell surface	127179.2	6.88	12	X	X	X	-	X	-	-
278	P13164	Interferon-induced transmembrane prote	13938.5	7.78	1	X	X	-	-	X	-	-
279	Q2TAA2	Isoamyl acetate-hydrolyzing esterase 1 h	27598.9	5.13	1	-	-	-	-	-	-	-
280	P50213	Isocitrate dehydrogenase [NAD] subunit	39592	6.47	1	X	X	X	X	-	-	-
281	O43837	Isocitrate dehydrogenase [NAD] subunit	42212	8.64	1	X	-	-	-	-	-	-
282	O75874	Isocitrate dehydrogenase [NADP] cytopla	46659.6	6.53	2	X	-	X	X	X	-	-
283	P48735	Isocitrate dehydrogenase [NADP], mitocl	50909.6	8.88	10	X	X	X	X	X	-	-
284	Q86Y91	Kinesin-like protein LOC146909 - Homo	92195	8.73	1	-	-	-	-	-	-	-
285	Q04760	Lactoylglutathione lyase (EC 4.4.1.5) (Me	20588.6	5.25	3	X	X	X	X	X	-	-
286	P42166	Lamina-associated polypeptide 2 isoform	75361.2	7.8	1	-	-	-	-	-	-	-
287	P42167	Lamina-associated polypeptide 2, isoform	50539.3	9.39	1	X	-	-	-	-	-	-
288	Q32MZ4	Leucine-rich repeat flightless-interacting	89253.5	4.59	7	X	X	X	X	-	-	-
289	P08575	Leukocyte common antigen precursor (E	147255	5.77	16	X	X	X	-	X	-	-
290	P30740	Leukocyte elastase inhibitor (LEI) (Serp	42742	5.9	10	X	X	X	X	X	X	-
291	P09960	Leukotriene A-4 hydrolase (EC 3.3.2.6) (	69154.4	5.8	5	X	X	X	-	X	-	-
292	Q14847	LIM and SH3 domain protein 1 (LASP-1)	29717.3	6.61	3	X	X	X	X	X	-	-
293	P23141	Liver carboxylesterase 1 precursor (EC 3	62521.4	6.15	3	X	-	X	-	-	-	-
294	P00338	L-lactate dehydrogenase A chain (EC 1.1	36557.7	8.46	10	X	X	X	X	X	X	X
295	Q9BYZ2	L-lactate dehydrogenase A-like 6B (EC 1	41943.2	8.88	1	-	-	-	X	-	-	-
296	P07195	L-lactate dehydrogenase B chain (EC 1.1	36507.5	5.72	14	X	X	X	X	X	X	X
297	Q9NZR2	Low-density lipoprotein receptor-related	515501.7	5.09	1	-	-	-	-	-	-	-
298	P05455	Lupus La protein (Sjogren syndrome type	46837.3	6.68	6	X	X	-	-	-	-	-
299	Q7Z4W1	L-xylulose reductase (EC 1.1.1.10) (XR)	25913.2	8.33	1	X	X	-	X	X	-	-
300	Q13094	Lymphocyte cytosolic protein 2 (SH2 dom	60188.5	5.89	2	X	X	X	X	X	-	-
301	P42785	Lysosomal Pro-X carboxypeptidase prec	55800.1	6.76	2	-	-	X	-	X	-	-
302	P11279	Lysosome-associated membrane glycop	44773.3	9.22	2	X	X	X	-	X	-	-
303	P61626	Lysozyme C precursor (EC 3.2.1.17) (1,4	16537.1	9.38	3	X	X	X	-	X	-	X
304	P40121	Macrophage capping protein (Actin-regul	38517.8	5.89	4	X	X	X	-	X	X	-
305	P14174	Macrophage migration inhibitory factor (M	12345.2	8.24	1	X	X	X	X	X	-	-
306	P40925	Malate dehydrogenase, cytoplasmic (EC	36295.1	6.89	7	X	X	X	X	X	X	-
307	P40926	Malate dehydrogenase, mitochondrial pr	35531.5	8.92	11	X	X	X	X	X	-	-
308	Q5VYJ5	MAM and LDL-receptor class A domain-c	136444.6	5.7	1	-	-	-	-	-	-	-
309	Q96IJ6	Mannose-1-phosphate guanylttransferase	46291.4	6.74	1	-	-	-	-	-	-	-
310	Q96T17	MAP7 domain-containing protein 2 - Hom	81961.8	8.95	1	X	X	-	X	-	-	-
311	O15173	Membrane-associated progesterone rece	23818.6	4.76	1	-	X	-	-	-	-	-
312	Q15691	Microtubule-associated protein RP/EB fa	29868	5.02	1	X	X	X	X	X	-	-
313	Q02978	Mitochondrial 2-oxoglutarate/malate carri	33930.7	9.92	1	X	-	-	-	-	-	-
314	Q9NS69	Mitochondrial import receptor subunit TO	15390.5	4.27	1	X	X	X	X	-	-	-
315	P28482	Mitogen-activated protein kinase 1 (EC 2	41258.7	6.53	3	X	X	X	-	X	-	-
316	Q16539	Mitogen-activated protein kinase 14 (EC	41162.3	5.48	1	-	X	-	-	X	-	-
317	P26038	Moesin (Membrane-organizing extension	67689.2	6.09	17	X	X	X	X	X	X	-
318	Q7L9L4	Mps one binder kinase activator-like 1A (	24959.8	6.24	1	X	X	X	X	-	-	-
319	P22234	Multifunctional protein ADE2 [Includes: P	46948.3	7.09	2	X	X	-	X	-	-	-
320	O00499	Myc box-dependent-interacting protein 1	64699.7	4.97	1	X	X	-	-	-	-	-
321	P24158	Myeloblastin precursor (EC 3.4.21.76) (L	27807.2	8.71	1	X	X	X	-	X	-	-
322	P05164	Myeloperoxidase precursor (EC 1.11.1.7	83869.1	9.19	9	X	X	X	-	X	-	-
323	P60660	Myosin light polypeptide 6 (Myosin light c	16799	4.56	8	X	X	X	X	X	-	-
324	P19105	Myosin regulatory light chain 2, nonsarco	19663	4.67	2	X	X	X	X	X	-	-
325	Q7Z406	Myosin-14 (Myosin heavy chain, nonmus	228002.9	5.77	3	-	X	X	-	X	X	-
326	P35579	Myosin-9 (Myosin heavy chain, nonmusc	226402.2	5.5	53	X	X	X	X	X	X	-
327	P58546	Myotrophin (V-1 protein)	12763.7	5.28	1	X	X	X	X	X	-	-
328	P20933	N(4)-(beta-N-acetylglucosaminy)-L-aspa	37194.5	5.86	1	X	-	-	-	X	-	-
329	Q9UJ70	N-acetylglucosamine kinase (EC 2.7.1.5)	37244.7	5.82	4	X	X	X	-	X	X	-

330	Q13423	NAD(P) transhydrogenase, mitochondria	113896.3	8.31	3	X	-	X	-	-	-	-
331	O95168	NADH dehydrogenase [ubiquinone] 1 be	15077.5	9.85	1	X	-	-	-	-	-	-
332	O00217	NADH-ubiquinone oxidoreductase 23 kD	23705.3	6	1	X	X	X	-	-	-	-
333	P19404	NADH-ubiquinone oxidoreductase 24 kD	27391.7	8.21	1	-	X	X	-	-	-	-
334	O75489	NADH-ubiquinone oxidoreductase 30 kD	30241.7	6.98	1	X	X	X	-	-	-	-
335	O95299	NADH-ubiquinone oxidoreductase 42 kD	40750.8	8.67	1	X	X	X	-	-	-	-
336	Q9P0J0	NADH-ubiquinone oxidoreductase B16.6	16567.2	8.24	1	X	-	X	-	-	-	-
337	Q13765	Nascent polypeptide-associated complex	23384	4.52	1	X	X	X	X	-	-	-
338	Q14697	Neutral alpha-glucosidase AB precursor	106874.5	5.73	3	X	X	X	X	X	X	-
339	P43490	Nicotinamide phosphoribosyltransferase	55521.4	6.69	1	-	X	-	-	X	-	-
340	P49321	Nuclear autoantigenic sperm protein (NA	85238.1	4.26	1	X	X	X	-	-	-	-
341	P19338	Nucleolin (Protein C23)	76483.5	4.6	1	X	X	-	-	X	-	-
342	P15531	Nucleoside diphosphate kinase A (EC 2.	17148.8	5.83	2	X	X	X	X	X	X	-
343	P22392	Nucleoside diphosphate kinase B (EC 2.	17298.1	8.52	5	X	X	X	X	X	-	-
344	Q56VL3	OCIA domain-containing protein 2 - Hom	16953.6	9.24	1	X	-	-	-	-	-	-
345	Q92882	Osteoclast-stimulating factor 1	23798.9	5.19	1	X	X	X	X	X	-	-
346	Q9UBV8	Peflin (PEF protein with a long N-termina	30381.1	6.1	1	X	-	-	-	X	-	-
347	Q9UJ68	Peptide methionine sulfoxide reductase (	26132.6	8.22	1	-	-	-	-	X	-	-
348	P62937	Peptidyl-prolyl cis-trans isomerase A (EC	17881.4	7.82	12	X	X	X	X	X	X	X
349	P23284	Peptidyl-prolyl cis-trans isomerase B pre	22742.5	9.33	5	X	X	X	X	X	-	X
350	Q9H2H8	Peptidyl-prolyl cis-trans isomerase-like 3	18154.6	6.29	1	X	X	X	-	X	-	-
351	Q06830	Peroxiredoxin-1 (EC 1.11.1.15) (Thioredd	22110.5	8.27	8	X	X	X	X	X	X	-
352	P32119	Peroxiredoxin-2 (EC 1.11.1.15) (Thioredd	21760.8	5.67	3	X	X	X	X	X	X	-
353	P30044	Peroxiredoxin-5, mitochondrial precursor	22026.5	8.85	2	X	X	X	X	X	-	-
354	P30041	Peroxiredoxin-6 (EC 1.11.1.15) (Antioxid	24903.9	6.03	6	X	X	X	X	X	X	-
355	Q00325	Phosphate carrier protein, mitochondrial	40095.1	9.45	2	X	X	X	-	-	-	-
356	O95674	Phosphatidate cytidyltransferase 2 (EC	51418.3	6.64	1	-	X	X	-	-	-	-
357	P30086	Phosphatidylethanolamine-binding protei	20925.7	7.43	5	X	X	X	X	X	X	-
358	P36871	Phosphoglucomutase-1 (EC 5.4.2.2) (Glu	61318.2	6.32	1	X	X	-	X	X	-	-
359	Q96G03	Phosphoglucomutase-2 (EC 5.4.2.2) (Glu	68210.6	6.18	1	X	X	X	-	X	-	-
360	P00558	Phosphoglycerate kinase 1 (EC 2.7.2.3)	44483.8	8.3	19	X	X	X	X	X	X	-
361	P18669	Phosphoglycerate mutase 1 (EC 5.4.2.1)	28672.9	6.75	10	X	X	X	X	X	-	-
362	P36969	Phospholipid hydroperoxide glutathione p	22128	8.65	1	X	X	X	X	-	-	-
363	Q9H008	Phospholysine phosphohistidine inorgani	29165.5	5.8	1	X	X	-	-	X	-	-
364	P35237	Placental thrombin inhibitor (Cytoplasmic	42590.1	5.19	1	X	X	X	X	X	-	-
365	Q14651	Plastin-1 (I-plastin) (Intestine-specific pla	70353	5.33	5	-	-	-	-	-	-	-
366	P13796	Plastin-2 (L-plastin) (Lymphocyte cytosol	70289.7	5.2	44	X	X	X	-	X	-	-
367	P02775	Platelet basic protein precursor (PBP) (S	13894.3	9.04	1	X	-	-	X	X	-	X
368	P68402	Platelet-activating factor acetylhydrolase	25569.4	5.57	2	X	X	X	X	-	-	-
369	Q15102	Platelet-activating factor acetylhydrolase	25734.4	6.33	2	X	X	X	-	-	-	-
370	P08567	Pleckstrin (Platelet p47 protein)	40097.1	8.5	3	X	X	-	X	X	-	-
371	Q9UUK3	Poly [ADP-ribose] polymerase 4 (EC 2.4.	192589.6	5.43	1	-	-	X	-	-	-	-
372	Q15365	Poly(rC)-binding protein 1 (Alpha-CP1) (I	37498	6.66	5	X	X	X	X	X	-	-
373	Q15366	Poly(rC)-binding protein 2 (Alpha-CP2) (I	38580.3	6.33	5	X	X	X	X	-	-	-
374	Q3KNV8	Polycomb group RING finger protein 3 - I	28115.7	8.53	1	-	-	-	-	-	-	-
375	Q96CX2	Potassium channel tetramerisation doma	35701	5.51	5	X	-	X	-	X	-	-
376	O75915	PRA1 family protein 3 (ARL-6-interacting	21614.8	9.77	3	X	X	X	-	X	-	-
377	O96008	Probable mitochondrial import receptor s	37893.3	6.79	1	X	X	-	-	-	-	-
378	P07737	Profilin-1 (Profilin I)	14923.1	8.47	11	X	X	X	X	X	-	X
379	P35232	Prohibitin.	29804.2	5.57	6	X	X	X	X	X	-	-
380	Q99623	Prohibitin-2 (B-cell receptor-associated p	33296.5	9.83	5	X	X	X	X	-	-	-
381	O94903	Proline synthetase co-transcribed bacteri	30344.1	7.09	1	X	X	X	X	-	-	-
382	Q15185	Prostaglandin E synthase 3 (EC 5.3.99.3	18697.5	4.34	1	X	X	X	X	-	-	-
383	Q6S8J3	Prostate, ovary, testis-expressed protein	80753.2	5.64	10	-	-	-	-	X	-	-
384	Q06323	Proteasome activator complex subunit 1	28723.3	5.78	7	X	X	X	X	X	-	-
385	Q9UL46	Proteasome activator complex subunit 2	27230.6	5.44	8	X	X	X	X	X	X	-

386	P25786	Proteasome subunit alpha type 1 (EC 3.4.21.10)	29555.8	6.15	3	X	X	X	X	-	-	-
387	P25788	Proteasome subunit alpha type 3 (EC 3.4.21.10)	28302.2	5.19	4	X	X	X	X	X	X	-
388	P25789	Proteasome subunit alpha type 4 (EC 3.4.21.10)	29484	7.58	3	X	X	X	X	-	-	-
389	P28066	Proteasome subunit alpha type 5 (EC 3.4.21.10)	26411.2	4.74	3	X	X	X	X	-	-	-
390	P60900	Proteasome subunit alpha type 6 (EC 3.4.21.10)	27399.6	6.35	4	X	X	X	X	X	X	-
391	O14818	Proteasome subunit alpha type 7 (EC 3.4.21.10)	27887	8.6	8	X	X	X	X	X	-	-
392	P20618	Proteasome subunit beta type 1 (EC 3.4.21.10)	26489.5	8.27	5	X	X	X	X	X	-	-
393	P49721	Proteasome subunit beta type 2 (EC 3.4.21.10)	22836.4	6.52	3	X	X	X	X	X	-	-
394	P49720	Proteasome subunit beta type 3 (EC 3.4.21.10)	22949.1	6.14	2	X	X	X	X	X	-	-
395	P28062	Proteasome subunit beta type 8 precursor (EC 3.4.21.10)	30354.5	7.63	3	X	X	X	X	X	-	-
396	P28065	Proteasome subunit beta type 9 precursor (EC 3.4.21.10)	23264.4	4.93	3	X	X	X	X	-	-	-
397	Q969H8	Protein C19orf10 precursor (Stromal cell)	18795.3	6.2	3	X	X	X	-	X	-	-
398	Q9Y426	Protein C21orf25 precursor	75533.6	6.47	1	-	-	-	-	-	-	-
399	O75223	Protein C7orf24	21007.8	5.07	1	X	X	X	-	X	-	-
400	O60888	Protein CutA precursor (Brain acetylcholinesterase)	19116.4	5.42	1	X	X	X	-	-	-	-
401	O60610	Protein diaphanous homolog 1 (Diaphanous)	138979.4	5.31	18	X	X	X	X	X	-	-
402	P30101	Protein disulfide-isomerase A3 precursor	56782.7	5.99	11	X	X	X	X	X	-	-
403	Q15084	Protein disulfide-isomerase A6 precursor	48121.6	4.95	4	X	X	X	X	X	-	-
404	P07237	Protein disulfide-isomerase precursor (EC 1.8.1.7)	57116.6	4.76	9	X	X	X	X	X	-	-
405	Q99497	Protein DJ-1 (Oncogene DJ1)	19891.2	6.33	3	X	X	X	X	X	X	-
406	Q9H0Q0	Protein FAM49A	37313.1	5.71	2	X	X	-	-	-	-	-
407	Q9NUQ9	Protein FAM49B (L1)	36748.2	5.76	3	X	X	X	-	X	-	-
408	Q9BSJ8	Protein FAM62A (Membrane-bound C2 domain)	122857	5.57	7	X	X	X	X	-	X	-
409	Q8N163	Protein KIAA1967 (Deleted in breast cancer)	102902.1	5.14	2	X	-	-	-	-	-	-
410	P61326	Protein mago nashi homolog	17163.7	5.74	1	X	-	X	-	-	-	-
411	Q9UFN0	Protein NipSnap3A (NipSnap4) (Target for ubiquitination)	28466.8	9.21	4	X	X	X	X	X	-	-
412	Q15435	Protein phosphatase 1 regulatory subunit 14	41564.4	4.84	1	X	X	-	-	-	-	-
413	Q9P258	Protein RCC2 (Telophase disk protein of Drosophila)	56084.8	9.02	1	X	X	-	-	-	-	-
414	Q01105	Protein SET (Phosphatase 2A inhibitor 12)	33489	4.23	3	X	X	X	-	-	-	-
415	O94979	Protein transport protein Sec31A - Homo sapiens	133015.4	6.43	1	X	X	X	X	-	-	-
416	P61619	Protein transport protein Sec61 subunit alpha	52133.9	8.33	1	-	X	X	-	-	-	-
417	Q9ULC6	Protein-arginine deiminase type-1 (EC 3.5.1.15)	74666	6.07	1	X	X	X	X	-	-	-
418	P22061	Protein-L-isoaspartate(D-aspartate) O-methyltransferase	24519.4	6.78	5	X	X	X	X	X	X	-
419	P00491	Purine nucleoside phosphorylase (EC 2.4.1.1)	32148.1	6.45	3	X	X	X	X	X	X	-
420	Q9NTK5	Putative GTP-binding protein PTD004	44743.8	7.64	1	X	X	X	X	-	-	-
421	Q9NTT1	Putative ubiquitin-conjugating enzyme E2	16905.5	8.81	1	X	-	X	X	-	-	-
422	Q6ZW7	Putative uncharacterized protein FLJ413	23948.7	9.99	1	-	-	-	-	-	-	-
423	P08559	Pyruvate dehydrogenase E1 component	43295.9	8.35	1	X	-	-	-	-	-	-
424	P11177	Pyruvate dehydrogenase E1 component	39219.6	6.21	3	X	X	-	X	-	-	-
425	P14618	Pyruvate kinase isozymes M1/M2 (EC 2.7.1.40)	57806	7.95	30	X	X	X	X	X	X	-
426	Q08257	Quinone oxidoreductase (EC 1.6.5.5) (NADH dehydrogenase)	35206.8	8.56	3	X	X	-	-	-	X	-
427	P31150	Rab GDP dissociation inhibitor alpha (RabGDI)	50583	5	5	X	X	X	X	X	-	-
428	P50395	Rab GDP dissociation inhibitor beta (RabGDI2)	50663.5	6.11	14	X	X	X	X	X	X	-
429	P43487	Ran-specific GTPase-activating protein (RanGAP1)	23310.2	5.19	1	X	X	X	X	X	-	-
430	Q15404	Ras suppressor protein 1 (Rsu-1) (RSP-1)	31409.3	8.57	3	X	X	-	X	X	-	-
431	P63000	Ras-related C3 botulinum toxin substrate 1	21450.2	8.77	4	X	X	X	X	X	-	-
432	P15153	Ras-related C3 botulinum toxin substrate 2	21428.9	7.52	8	X	X	X	X	X	-	-
433	P62491	Ras-related protein Rab-11A (Rab-11) (YPT1-related)	24262.4	6.14	2	X	X	X	X	X	-	-
434	P61106	Ras-related protein Rab-14	23765.9	5.86	5	X	X	X	X	X	-	-
435	P59190	Ras-related protein Rab-15	24390.8	5.53	2	X	X	X	X	X	-	-
436	P62820	Ras-related protein Rab-1A (YPT1-related)	22546.7	5.93	3	X	-	X	X	X	-	-
437	Q9H0U4	Ras-related protein Rab-1B	22171.3	5.55	4	X	X	X	X	X	-	-
438	Q9UL25	Ras-related protein Rab-21 - Homo sapiens	24216.5	8.16	2	X	X	X	-	X	-	-
439	P61019	Ras-related protein Rab-2A	23545.7	6.08	1	X	X	X	X	X	-	-
440	Q13637	Ras-related protein Rab-32 - Homo sapiens	24866.2	6.1	1	-	-	X	X	X	-	-
441	Q9H082	Ras-related protein Rab-33B	25717.7	6.71	1	X	X	X	X	-	-	-

442	Q15286	Ras-related protein Rab-35 (Rab-1C) (G	23025.3	8.53	2	X	X	X	X	X	-	-
443	P61018	Ras-related protein Rab-4B	23586.9	5.8	2	-	-	-	-	-	-	-
444	P61020	Ras-related protein Rab-5B	23706.9	8.29	2	-	X	-	X	X	-	-
445	P51148	Ras-related protein Rab-5C (RAB5L) (L1	23482.7	8.64	4	X	X	X	-	X	-	-
446	P20340	Ras-related protein Rab-6A (Rab-6)	23461.7	5.42	1	X	X	X	-	X	-	-
447	P51149	Ras-related protein Rab-7	23489.9	6.39	7	X	X	X	X	X	-	-
448	P62834	Ras-related protein Rap-1A precursor (G	20987.3	6.39	3	X	X	X	-	X	-	-
449	P61224	Ras-related protein Rap-1b precursor (G	20824.9	5.65	5	X	X	X	X	X	-	-
450	P52565	Rho GDP-dissociation inhibitor 1 (Rho G	23207.2	5.02	4	X	X	X	X	X	-	-
451	P52566	Rho GDP-dissociation inhibitor 2 (Rho G	22988.1	5.1	6	X	X	X	X	X	-	-
452	Q07960	Rho-GTPase-activating protein 1 (GTPas	50436	5.85	3	X	X	X	X	X	-	-
453	P13489	Ribonuclease inhibitor (Ribonuclease/an	49842.6	4.71	10	X	X	X	X	X	X	-
454	P49247	Ribose-5-phosphate isomerase (EC 5.3.	26091.2	6.97	1	X	X	-	X	X	-	-
455	P60891	Ribose-phosphate pyrophosphokinase I	34703.3	6.56	1	X	X	-	-	-	X	-
456	P35637	RNA-binding protein FUS (Oncogene FU	53426.1	9.4	1	X	-	-	-	-	-	-
457	P26447	S100 calcium-binding protein A4 (Metast	11728.6	5.85	4	X	X	X	-	X	-	-
458	P31153	S-adenosylmethionine synthetase isoform	43660.9	6.02	1	-	X	-	-	-	-	-
459	Q9Y3Z3	SAM domain and HD domain-containing	72200.9	6.7	19	X	X	X	-	-	-	-
460	Q93084	Sarcoplasmic/endoplasmic reticulum cal	113978.1	5.42	2	X	X	X	X	X	-	-
461	Q96C86	Scavenger mRNA decapping enzyme Dc	38681	5.84	1	-	X	X	-	-	-	-
462	Q15019	Septin-2 (Protein NEDD5)	41487.7	6.15	1	X	X	X	X	-	-	-
463	Q14141	Septin-6	49585.7	6.25	4	X	X	-	X	-	-	-
464	Q16181	Septin-7 (CDC10 protein homolog)	50680.2	8.77	4	X	X	-	X	-	-	-
465	Q9UHD8	Septin-9 (MLL septin-like fusion protein)	65369.7	9.05	3	X	X	-	X	-	X	-
466	O94804	Serine/threonine-protein kinase 10 (EC 2	112135.9	6.52	6	X	X	X	-	-	-	-
467	P63151	Serine/threonine-protein phosphatase 2A	51692.4	5.82	1	-	X	-	-	X	-	-
468	P30153	Serine/threonine-protein phosphatase 2A	65092.7	4.97	4	X	X	X	X	X	-	-
469	P62136	Serine/threonine-protein phosphatase PF	37512.3	5.94	3	X	X	-	X	X	-	-
470	P02768	Serum albumin precursor	69367.1	5.92	54	X	-	-	-	-	X	X
471	P49591	Seryl-tRNA synthetase (EC 6.1.1.11) (Se	58646.4	6.06	2	X	X	-	-	-	-	-
472	O60880	SH2 domain protein 1A (Signaling lymph	14187.3	8.74	1	X	X	-	-	-	-	-
473	O75368	SH3 domain-binding glutamic acid-rich-li	12774.3	5.22	3	X	X	X	X	X	-	-
474	Q9H299	SH3 domain-binding glutamic acid-rich-li	10437.8	4.82	1	X	X	X	X	X	-	-
475	Q16836	Short chain 3-hydroxyacyl-CoA dehydrog	34277.7	8.88	4	X	X	X	X	X	-	-
476	Q9H9B4	Sideroflexin-1 (Tricarboxylate carrier prot	35488.4	9.22	2	X	X	-	-	-	-	-
477	Q04837	Single-stranded DNA-binding protein, mi	17259.8	9.59	3	X	X	X	X	-	-	-
478	P62304	Small nuclear ribonucleoprotein E (snRN	10803.7	9.46	1	X	X	-	-	-	-	-
479	P62316	Small nuclear ribonucleoprotein Sm D2 (	13527	9.92	1	-	X	-	-	-	-	-
480	Q13126	S-methyl-5-thioadenosine phosphorylase	31250.3	6.75	1	X	-	-	X	X	-	-
481	Q4G0N8	Sodium/hydrogen exchanger 10 - Homo	135206.8	6.72	2	-	-	-	-	-	-	-
482	P30626	Sorcin (22 kDa protein) (CP-22) (V19)	21676.5	5.32	1	X	X	X	X	X	-	-
483	O60493	Sorting nexin-3 (SDP3 protein)	18631.2	8.73	1	-	-	X	X	X	-	-
484	Q13838	Spliceosome RNA helicase BAT1 (EC 3.	48991.6	5.44	3	X	X	-	-	-	-	-
485	P84103	Splicing factor, arginine/serine-rich 3 (Pre	19329.7	9.99	1	-	-	-	-	-	-	-
486	P31948	Stress-induced-phosphoprotein 1 (STI1)	62639.6	6.4	2	X	X	X	X	-	X	-
487	P21912	Succinate dehydrogenase [ubiquinone] in	31629.9	9.03	5	X	X	X	-	-	-	-
488	Q96I99	Succinyl-CoA ligase [GDP-forming] beta-	46510.9	6.15	1	-	X	-	-	-	-	-
489	Q9Y6N5	Sulfide:quinone oxidoreductase, mitocho	49961	9.18	1	X	X	X	-	X	-	-
490	P63279	SUMO-conjugating enzyme UBC9 (EC 6	18006.9	8.87	2	X	X	X	-	-	-	-
491	P00441	Superoxide dismutase [Cu-Zn] (EC 1.15.	15804.6	5.7	1	X	X	X	X	X	X	X
492	P04179	Superoxide dismutase [Mn], mitochondria	24722.2	8.34	2	X	X	X	X	X	-	-
493	O15260	Surfeit locus protein 4	30394.2	7.64	1	X	X	X	-	X	-	-
494	Q15833	Syntaxin-binding protein 2 (Unc-18 hom	66438.9	6.11	1	-	-	-	X	X	-	-
495	Q9Y490	Talin-1	269768.5	5.78	56	X	X	X	X	X	X	-
496	P78371	T-complex protein 1 subunit beta (TCP-1	57357.3	6.02	9	X	X	X	X	-	-	-
497	P50991	T-complex protein 1 subunit delta (TCP-1	57793.4	8.13	4	X	X	X	X	X	X	-

498	P48643	T-complex protein 1 subunit epsilon (TCP-1)	59671.4	5.45	2	X	X	X	X	X	X	-
499	Q99832	T-complex protein 1 subunit eta (TCP-1)	59367	7.55	2	X	X	X	X	X	X	-
500	P49368	T-complex protein 1 subunit gamma (TCP-1)	60534.3	6.1	5	X	X	-	X	-	X	-
501	P50990	T-complex protein 1 subunit theta (TCP-1)	59489.7	5.42	7	X	X	X	X	X	X	-
502	P40227	T-complex protein 1 subunit zeta (TCP-1)	57893.3	6.25	4	X	X	X	X	X	X	-
503	Q9UGI8	Testin (TESS)	47996.8	7.96	5	X	-	-	-	-	-	-
504	Q9Y3D6	Tetratricopeptide repeat protein 11 (TPR)	16937.8	8.84	1	X	X	X	-	X	-	-
505	P10599	Thioredoxin (ATL-derived factor) (ADF) (	11606.4	4.82	1	X	X	X	X	X	-	-
506	Q9H3N1	Thioredoxin domain-containing protein 1	31791.4	4.92	1	X	-	X	-	-	-	-
507	Q8NBS9	Thioredoxin domain-containing protein 5	47629.1	5.63	2	-	X	-	-	-	-	-
508	P30048	Thioredoxin-dependent peroxide reducta	27692.8	7.67	2	X	X	X	X	X	-	-
509	P19971	Thymidine phosphorylase precursor (EC	49955.8	5.36	4	X	X	X	X	X	-	-
510	Q5JTV8	Torsin-1A-interacting protein 1	66248.7	8.21	1	X	-	X	-	X	-	-
511	P37837	Transaldolase (EC 2.2.1.2)	37540.3	6.36	12	X	X	X	X	X	-	-
512	P61586	Transforming protein RhoA precursor (H	21768.3	5.83	5	X	X	X	X	X	X	-
513	P37802	Transgelin-2 (SM22-alpha homolog)	22260.4	8.45	8	X	X	X	X	X	-	X
514	P29401	Transketolase (EC 2.2.1.1) (TK)	67878	7.58	18	X	X	X	X	X	X	-
515	P13693	Translationally-controlled tumor protein (	19595.5	4.84	2	X	X	X	X	X	-	-
516	P51571	Translocon-associated protein delta subu	18998.7	5.76	2	X	X	X	-	X	-	-
517	P49755	Transmembrane emp24 domain-containi	24976.1	6.98	1	X	X	X	-	X	-	-
518	P55084	Trifunctional enzyme subunit beta, mitoc	51294.8	9.44	3	X	X	X	X	-	-	-
519	P60174	Triosephosphate isomerase (EC 5.3.1.1)	26538.4	6.51	13	X	X	X	X	X	X	-
520	P29144	Tripeptidyl-peptidase 2 (EC 3.4.14.10) (T	138219.4	5.9	2	X	-	-	X	-	-	-
521	O14773	Tripeptidyl-peptidase I precursor (EC 3.4	61229.2	5.97	1	X	X	X	X	X	-	-
522	P06753	Tropomyosin alpha-3 chain (Tropomyosi	32818.9	4.68	8	X	X	X	X	X	-	-
523	P67936	Tropomyosin alpha-4 chain (Tropomyosi	28390.8	4.67	7	X	X	X	X	X	-	-
524	P07951	Tropomyosin beta chain (Tropomyosin 2	32850.9	4.66	4	X	X	X	X	-	-	-
525	P23381	Tryptophanyl-tRNA synthetase (EC 6.1.1	53165.7	5.83	3	X	X	X	-	X	-	-
526	P68366	Tubulin alpha-1 chain (Alpha-tubulin 1) (	49924.7	4.95	13	X	-	-	X	-	-	-
527	P07437	Tubulin beta-2 chain	49671.1	4.78	19	X	X	X	X	X	X	-
528	P68371	Tubulin beta-2C chain (Tubulin beta-2 ch	49831.3	4.79	17	X	-	-	-	X	-	-
529	P04350	Tubulin beta-4 chain (Tubulin 5 beta)	49631.2	4.81	15	X	-	-	-	-	-	-
530	O75347	Tubulin-specific chaperone A (Tubulin-fo	12723.7	5.25	1	X	X	X	X	X	-	-
531	Q6IBS0	Twinfilin-2 (Twinfilin-1-like protein) (A6-re	39548.2	6.37	4	X	X	X	X	X	-	-
532	P41240	Tyrosine-protein kinase CSK (EC 2.7.1.1	50704.6	6.62	1	X	X	X	X	-	-	-
533	P29350	Tyrosine-protein phosphatase non-recep	67561.5	7.65	11	X	X	X	X	X	-	-
534	P22695	Ubiquinol-cytochrome-c reductase comp	48443.2	8.74	3	X	X	X	X	-	-	-
535	P62988	Ubiquitin	8564.9	6.56	5	X	X	X	X	X	X	-
536	Q93009	Ubiquitin carboxyl-terminal hydrolase 7 (	128272.7	5.33	3	X	X	X	-	-	-	-
537	Q96FW1	Ubiquitin thiolesterase protein OTUB1 (E	31284.2	4.85	2	X	X	X	X	X	-	-
538	P22314	Ubiquitin-activating enzyme E1 (A1S9 pr	117849.6	5.49	1	X	X	X	X	X	X	-
539	P62837	Ubiquitin-conjugating enzyme E2 D2 (EC	16735.4	7.69	1	X	X	-	-	X	-	-
540	P68036	Ubiquitin-conjugating enzyme E2 L3 (EC	17861.7	8.68	2	X	X	X	X	X	-	-
541	P61088	Ubiquitin-conjugating enzyme E2 N (EC	17137.9	6.13	10	X	X	X	X	X	X	-
542	Q13404	Ubiquitin-conjugating enzyme E2 variant	25796.9	8.55	4	X	X	X	X	X	X	-
543	Q15819	Ubiquitin-conjugating enzyme E2 variant	16231.7	8.05	3	X	X	-	X	X	X	-
544	Q9UBE0	Ubiquitin-like 1-activating enzyme E1A (S	38450.1	5.17	1	X	X	-	-	-	-	-
545	Q9NYU2	UDP-glucose:glycoprotein glucosyltransf	174977.9	5.4	7	X	-	X	X	-	-	-
546	Q86UX7	Unc-112-related protein 2 (Kindlin-3) (M	75953.2	6.52	5	X	X	X	X	X	-	-
547	Q9BUH6	Uncharacterized protein C9orf142 - Homo	21639.7	5.39	1	X	X	X	-	-	-	-
548	Q6IAA8	UPF0404 protein C11orf59 - Homo sapie	17744.9	5.01	2	X	X	X	X	-	-	-
549	Q16851	UTP--glucose-1-phosphate uridylyltransf	56809.3	8.15	7	X	X	X	X	X	-	-
550	Q9UBQ0	Vacuolar protein sorting 29 (Vesicle prote	20505.8	6.28	2	X	-	X	X	-	-	-
551	O75396	Vesicle trafficking protein SEC22b (SEC2	24609.5	8.68	2	X	-	X	-	X	-	-
552	Q9BV40	Vesicle-associated membrane protein 8 (	11438.3	6.73	2	X	-	X	X	-	-	-
553	P08670	Vimentin	53520.7	5.06	4	X	-	X	-	X	-	-

554	P18206	Vinculin (Metavinculin)	123668.8	5.51	4	X	X	X	X	X	X	-
555	P21796	Voltage-dependent anion-selective chan	30641.5	8.63	3	X	X	X	X	X	-	-
556	P45880	Voltage-dependent anion-selective chan	38092.9	6.32	3	X	X	X	X	-	-	-
557	Q9Y277	Voltage-dependent anion-selective chan	30658.8	8.84	5	X	-	X	X	X	-	-
558	Q6ZS11	VPS9 domain-containing protein FLJ459	50053.3	5.69	1	-	-	-	-	-	-	-
559	O75083	WD-repeat protein 1 (Actin-interacting pr	66062.7	6.18	9	X	X	X	X	X	X	-
560	P42768	Wiskott-Aldrich syndrome protein (WASp	52781.7	6.18	2	X	-	-	-	-	-	-
561	Q9H171	Z-DNA-binding protein 1 - Homo sapiens	46343.1	6.29	1	-	-	-	-	-	-	-
562	Q5T4S7	Zinc finger UBR1-type protein 1 - Homo s	573844.3	5.7	1	-	-	-	-	X	-	-
563	Q15942	Zyxin (Zyxin-2)	61277.7	6.22	3	X	-	X	X	X	-	-

Cell Characterization by Proteome Profiling Applied to Primary Hepatocytes and Hepatocyte Cell Lines Hep-G2 and Hep-3B

Astrid Slany¹⁺, Verena J. Haudek¹⁺, Hannes Zwickl¹, Nina C. Gundacker¹, Michael Grusch¹, Thomas Weiss³, Katja Seir², Chantal Rodgarkia-Dara¹, Claus Hellerbrand³, Christopher Gerner¹

¹Internal Medicine Clinic I, Dept.: Institute of Cancer Research, Medical University of Vienna, Austria

²Section Biomedical Laboratory Science, University of Applied Sciences, Vienna, Austria

³University Hospital Regensburg ,Department of Internal Medicine I, Regensburg, Germany

⁺ contributed equally

Running Title: Proteome profiling of human hepatocytes

Correspondence: Christopher Gerner, Department of Medicine I, Institute of Cancer Research, Medical University of Vienna, Austria

Email: Christopher.gerner@meduniwien.ac.at

Phone: +43-1-4277-65230

Reviewer account for PRIDE-submissions (<http://www.ebi.ac.uk/pride/plainLogin.do>):

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Abbreviations:

1D/2D-PAGE: one/two dimensional polyacrylamid gel electrophoresis

ACN: Acetonitrile

CPL/MUW: Clinical Proteomics Laboratories at the Medical University of Vienna

DC: Dendritic cells

EMT: epithelial to mesenchymal transition

FCS: fetal calf serum

HUVEC: Human Umbilical Vein Endothelial Cell

MEME: Minimal Essential Medium Eagle

PHH: primary human hepatocytes

PRIDE: Proteomics Identifications Database (<http://www.ebi.ac.uk/pride>)

RuBPS: Ruthenium II tris (bathophenanthroline disulfonate)

SPI: Scored Peak Intensity

Abstract

Hepatocytes are known to express a large number of characteristic proteins. Transformed and cultured hepatocytes only partially maintain functional cell differentiation characteristics, which can be assessed by proteome profiling. Here, we applied 2D-PAGE analysis in addition to shotgun proteomics to assess the functional cell state of primary human hepatocytes (PHH), HepG2 and Hep3B cells. Out of a total of 1995 proteins identified in the cytoplasm of these cells, we filtered 116 proteins which are characteristic for hepatocytes. 114 of those were identified in primary human hepatocytes, 20 in HepG2 and only 6 in Hep3B. 46 out of 65 proteins identified in the secretome of PHH, 55 out of 139 in HepG2 and only 24 out of 72 in Hep3B were plasma proteins characteristic for hepatocytes. Beside other biomarker candidates presently identified, eleven proteins of the HepG2 secretome have been described previously as biomarkers for hepatocellular carcinoma. Due to indications that epithelial to mesenchymal transition (EMT) may have occurred in the cultured hepatoma cells, we included the analysis of fibroblasts representative for mesenchymal cells. Hep3B, but not HepG2, secreted five proteins including follistatin-related protein 1 which are characteristic for mesenchymal cells and may be marker proteins for EMT. Our data demonstrate that HepG2 show more features characteristic for hepatocytes than Hep3B, while Hep3B express more mesenchymal proteins indicative for EMT. Proteome profiling thus proved to enable comprehensive assessment of functional cell states and cell differentiation states of cultured hepatocytes and enabled the identification of numerous biomarkers for hepatocellular carcinoma and EMT.

Introduction

The cell state and functionality of cultured cells may substantially differ from the corresponding primary cells, with far reaching implications for appropriate data interpretation.¹ The assessment of cell differentiation and functional cell states of cell culture model systems is an important requirement but not easy to accomplish. Proteome profiling is a valuable approach for that purpose.^{2,3} Here, we applied proteome profiling to the well-established hepatoma cell lines HepG2 and Hep3B.⁴ The use and proper assessment of hepatocyte cell lines may be of great relevance e.g. for drug metabolism studies.⁵ HepG2 and Hep3B cells have been used in many studies as model systems to investigate functional features of liver cells.⁶⁻⁸ Transcription profiling has already been performed to assess the functional state of primary and cultured cells.⁹ Protein expression, however, may more directly reflect the differentiation state and functional capabilities. Accordingly, several studies have already been undertaken applying proteome profiling to hepatocytes and hepatocyte cell lines for functional characterization.¹⁰⁻¹² Gene and protein expression analysis was applied to primary rat hepatocytes to assess how they sustain their characteristic properties during *in vitro* culture.¹³ Secretome analysis of HepG2 cells by mass spectrometry already demonstrated that these cells secrete plasma proteins in addition to some other, previously unrecognized proteins.¹² A comprehensive study of the proteome profile of mouse hepatocytes compared to corresponding cultured cells was published quite recently.¹⁴ The present study comprises both cytoplasmic and secreted proteins and employs both 2D-PAGE and shotgun proteomics. For appropriate interpretation of the protein expression data, we applied a dual comparison strategy. During hepatocarcinogenesis, hepatocytes may eventually undergo epithelial to mesenchymal transition (EMT),¹⁵ thereby gaining cell properties characteristic for fibroblasts.¹⁶ Cultured hepatoma cells may thus not only lose features of hepatocytes, but as well gain functional properties of fibroblasts. For the functional assessment of the two hepatocyte cell lines, we therefore considered the following two reference cell systems. In accordance to other studies, highly differentiated primary human hepatocytes known to express many liver-specific proteins were considered here to represent fully functional hepatocytes. We supposed that the more liver-specific proteins we find expressed by the cultured cell lines, the more they will have maintained a functional state characteristic for hepatocytes. On the other hand, we supposed that EMT will be accompanied by a gain of protein expression properties characteristic for fibroblasts. Human skin fibroblasts display a proteome profile quite different from hepatocytes. We, therefore,

considered these cells as reference cell system for the identification of mesenchymal properties of the cultured cell lines. Considering the plasma protein secretion capability of hepatocytes,¹⁷ we focused our analysis strategy also on secreted proteins. The secretome is defined as the complete set of secreted proteins.^{18, 19} Secreted proteins may determine, control and coordinate many biological processes such as growth, cell division and differentiation. Their key roles makes them good candidates for biomarkers for diagnosis and prognosis. Application of this strategy allowed us to clearly recognize features of HepG2 and Hep3B cells related to hepatocyte functionality or, alternatively, to the acquisition of mesenchymal properties.

Material and Methods

Isolation and cultivation of Primary Human Hepatocytes (PHH)

Primary human hepatocytes (PHH) were isolated and cultured as previously described.²⁰ Human liver tissue for cell isolation was obtained from and experimental procedures were performed according to the guidelines of the charitable state controlled foundation HTCR, with the informed patient's consent.

Cultivation of HepG2 and Hep3B

HepG2 and Hep3B are two well-established cell lines derived from liver biopsies of two children with primary hepatoblastoma and hepatocellular carcinoma.⁴ Cells of these two cell lines were acquired from ATCC (ATCC-Number HB-8065 and HB-8064). Cells were cultured at standard cell culture conditions: HepG2 in RPMI and Hep3B in MEME medium.

Isolation and cultivation of fibroblasts

Fibroblasts were cultured as described by Frazier *et al.*²¹ Cells were isolated from normal skin punches and were cultured in RPMI supplemented with 10% FCS at standard cell culture conditions.

Sub-cellular fractionation

Isolation of cytoplasm and cell supernatant fractions: Cells were washed after treatment and further incubated in serum-free specialized media formulations supplemented with L-glutamine for 24 h at 37°C. For isolation of the secreted protein fraction, the cell supernatant was collected, sterile filtrated to remove cellular debris and precipitated by the addition of ethanol. The isolation of cytoplasmic proteins was performed as described by Gundacker *et al.*²² Cells were lysed in hypotonic lysis buffer (10 mM HEPES/NaOH, pH 7.4, 0.25 M sucrose, 10 mM NaCl, 3 mM MgCl₂, 0.5% Triton X-100) supplemented with protease inhibitors and pressed through a 26 g syringe to induce cell lysis. The cytoplasmic fraction was separated from nuclei by centrifugation and precipitated by the addition of ethanol. Afterwards, all protein samples were dissolved in sample buffer (7.5 M urea, 1.5 M thiourea, 4% CHAPS, 0.5% SDS, 100 mM DDT).

³⁵S-metabolic labeling

Cells were routinely cultivated in RPMI-1640 supplemented with 10% FCS. During metabolic labeling, cells were incubated in serum-free, methionine- and cysteine-free RPMI-1640 medium (MP Biomedicals, Solon, Ohio) supplemented with L-glutamine in the presence of ³⁵S- methionine and cysteine (Trans35label, Biomedica, MP Biomedicals) for 4 h at 37°C.

Real-time PCR

Real-time PCR was performed as previously described.²³ In brief, total RNA was isolated from logarithmically growing HepG2 and Hep3B cells with Trizol reagent (Invitrogen) and reverse transcribed using MMLV reverse transcriptase (Promega) and random hexamer primers (Fermentas). Taqman assays for follistatin-like 1 and 18s RNA (Applied Biosystems) were performed in duplicates on an ABI Prism 7000 sequence detection system using the amplification protocol suggested by the manufacturer. 18s RNA was used for normalization and the follistatin-like 1 expression level in normal liver tissue (mean of three mRNA preparations from commercial sources) was set as 1.

Western blot

HepG2 and Hep3B cells were grown to about 70% confluence and either lysed in protein lysis buffer (150 mM NaCl, 50 mM Tris pH 8, 1% Triton X 100, 1 mM EGTA, 1 mM Na₃VO₄, 10 mM NaF, 1 tablet of Complete protease inhibitor cocktail (Roche)) or switched to serum free medium. Serum free supernatants were collected 24 hours later and centrifuged briefly to remove cellular debris. Secreted proteins were precipitated from the medium with four volumes of ethanol at -20°C and resuspended in protein lysis buffer. Protein concentrations were determined with Bradford assay (Biorad) and 25 µg per lane were separated by SDS page and immunoblotted as previously described.²⁴ A goat polyclonal antibody to follistatin-like 1 (Abcam, ab11805, 1:1000) and a HRP coupled rabbit anti goat antibody (Dako, 1:10000) were used for immunodetection. Bioluminescence signals were developed with Immun-Star Western C kit (Biorad) and recorded with Chemismart 5100 detection system (Vilber Loumart) .

2D polyacrylamid gel electrophoresis (2D-PAGE)

Proteins were loaded by passive rehydration on IPG strips pH 5–8, 17 cm (BioRad, Hercules, CA) at room temperature. IEF was performed in a stepwise fashion (1 h 0– 500 V linear; 5 h 500 V; 5 h 500–3500 V linear; 12 h 3500 V). After isoelectric focusing, the strips were

equilibrated with 100 mM DTT and 2.5% iodacetamide according to the instructions of the manufacturer (BioRad). For SDS-PAGE using the Protean II xi electrophoresis system (BioRad), the IPG strips were placed on top of 1.5 mm 12% polyacrylamide slab gels and overlaid with 0.5% low-melting agarose. The gels were stained with a 400 nM solution of Ruthenium II tris (bathophenanthroline disulfonate) (RuBPS) as described by Rabilloud *et al.*²⁵ Fluorography scanning was performed with the FluorImager 595 (GE Healthcare, Fairfield, CT) at a resolution of 100 μm .²⁶ All 2D gel data were independently reproduced for at least three times.

1D-PAGE for subsequent shotgun analysis

Cytoplasmic protein fractions were loaded on 12% polyacrylamide gels, electrophoresis was performed until complete separation of a pre-stained molecular marker (Dual Color, Biorad, Hercules, CA) was visible. Gels were fixed with 50% methanol/10% acetic acid and subsequently silver stained as described below. Gel lanes were cut out of the gel and were digested with trypsin as described below.

MS-compatible silver staining procedure

2D gels were fixed with 50% methanol, washed and sensitized with 0.02% $\text{Na}_2\text{S}_2\text{O}_3$. The gels were stained with 0.1% AgNO_3 ice cold for 20 minutes, rinsed with bi-distilled water and subsequently developed with 3% Na_2CO_3 /0.05% formaldehyde as previously described.²⁷

Tryptic digest

Protein spots were cut out of the gel, the gel-pieces were de-stained with 15 mM $\text{K}_3\text{Fe}(\text{CN})_6$ /50 mM $\text{Na}_2\text{S}_2\text{O}_3$ and intensively washed with 50% methanol/10% acetic acid. The pH was adjusted with 50 mM NH_4HCO_3 , proteins were reduced with 10 mM DTT/50 mM NH_4HCO_3 for 30 minutes at 56°C and alkylated with 50 mM iodacetamide/50 mM NH_4HCO_3 20 minutes in the dark. Afterwards the gel-pieces were treated with acetonitril and dried in a speedvac. Between each step, the tubes were shaken 5-10 minutes (Eppendorf Thermomixer comfort). Dry gel-spots were treated with trypsin 0.1 mg/ml (Trypsin sequencing grade, Roche Diagnostics, Germany)/50 mM NH_4HCO_3 , in a ratio of 1:8 for 20 minutes on ice, afterwards covered with 50 mM NH_4HCO_3 and were subsequently incubated over night at 37°C. The digested peptides were eluted by adding 50 mM NH_4HCO_3 , the supernatant was transferred into silicon-coated tubes, and this procedure was repeated two times with 5% formic acid/50% acetonitril. Between each elution step the gel-spots were ultrasonicated for

10 minutes. Finally the peptide solution was concentrated in a speedvac to an appropriate volume.

Mass spectrometry analysis

For the identification of 2D spots, peptides were loaded on a Zorbax 300SB-C8 (5 μ m, 0.3 mm, 5 mm) column and separated by nanoflow LC (1100 Series LC system, Agilent, Palo Alto, CA) with a Zorbax 300SB-C18 (5 μ m, 75 mm, 150 mm) column at a flow rate of 250 nl/min using a gradient from 0.2% formic acid and 3% acetonitrile (ACN) to 0.2% formic acid and 45% ACN over 12 minutes. In case of shotgun analysis, peptides were separated by nano-flow LC (1100 Series LC system, Agilent, Palo Alto, CA) using the HPLC-Chip technology (Agilent) equipped with a 40 nl Zorbax 300SB-C18 trapping column and a 75 μ m x 150 mm Zorbax 300SB-C18 separation column at a flow rate of 400 nl/min, using a gradient from 0.2% formic acid and 3% ACN to 0.2% formic acid and 50% ACN over 60 minutes. Peptide identification was accomplished by MS/MS fragmentation analysis with an iontrap mass spectrometer (XCT-Ultra, Agilent) equipped with an orthogonal nanospray ion source. The MS/MS data, including peak list-generation and search engine, were interpreted by the Spectrum Mill MS Proteomics Workbench software (Version A.03.03, Agilent) allowing for two missed cleavages and searched against the SwissProt Database for human proteins (Version 14.3 containing 20 328 protein entries) allowing for precursor mass deviation of 1.5 Da, a product mass tolerance of 0.7 Da and a minimum matched peak intensity (%SPI) of 70%. Due to previous chemical modification, carbamidomethylation of cysteine was set as fixed modification. No other modifications were considered here.

Construction of proteome reference maps

The following protein selection algorithm was applied for the generation of the final protein lists. Peptides scores were considered to select appropriate sequence assignments. To assess the reliability of the peptide scores, we performed searches against the corresponding reversed database. 5.9% positive hits were found with peptides scoring >9.0, while 0.21% positive hits were found with peptides scoring >13.0. Only peptides scoring higher than 9.0 were considered for protein identification. Identification details for each protein including all identified peptides, sequence coverage, peptide scores and MS² spectra are fully accessible via PRIDE database (<http://www.ebi.ac.uk/pride/>)^{28, 29}: PHH, cytoplasmic fraction: PRIDE accessions 8971-8974; HepG2, cytoplasmic fraction: PRIDE accessions 8963-8966; HepG2, secreted protein fraction: PRIDE accessions 8967-8970; Hep3B, cytoplasmic fraction: PRIDE

accessions 8959-8960; Hep3B, secreted protein fraction: PRIDE accessions 8961-8962. Each of the proteome reference maps listed in Table S1 was generated by combining the corresponding independent shotgun experiments. These combinations list the sum of all peptides related to single proteins which were collected from all corresponding experiments. Proteins derived from obvious contaminants such as fetal calf serum were deleted. Proteins were selected based on the expression of specific peptides, identified in one protein only. Selection of protein isoforms was performed as described by Zhang *et al.*³⁰

Results

Primary human hepatocytes (PHH) were freshly obtained by liver reperfusion. The cytoplasmic and secreted protein fraction was analyzed by 2D-PAGE and shotgun proteomics. HepG2 and Hep3B were cultured at standard conditions. Cells were metabolically labeled with ^{35}S methionine/cysteine for secretome analysis by 2D-PAGE as described previously.²⁶ Both the cytoplasmic and secreted protein fractions of these cultured cells were analyzed by 2D-PAGE and shotgun proteomics. Assuming that epithelial to mesenchymal transition may occur in cultured tumor cells, we included a comparison to human skin fibroblast proteome analysis data, which were presented previously.³¹ To include cells unrelated to hepatocytes, we drew comparisons to human umbilical vein endothelial cells (HUVEC) and dendritic cells.^{32, 33} All protein identification data presented here including peptide sequences, peptide identification scores, MS² spectra and protein sequence coverages are fully accessible via the PRIDE database^{28, 29} at www.ebi.ac.uk/pride/ and CPL/MUW-database at www.meduniwien.ac.at/proteomics/database/.

2D-PAGE analysis of cytoplasmic proteins

Cytoplasmic proteins of PHH, HepG2 and Hep3B were analyzed by 2D-PAGE and subsequent LC-MS/MS analysis of isolated gel spots. In 2D gels of the cytoplasm of PHH we identified a total of 400 different proteins (Table S1). In 2D gels of the cytoplasm of HepG2 cells we identified a total of 578 different proteins, of Hep3B cells 541 different proteins. 301 were identified in all three different cells. Comparative analysis revealed 16 proteins identified only in PHH and not in HepG2 and Hep3B, 10 of those are described to be characteristic for the liver according to the uniprot database (Table 1, Figure 1).³⁴ Only one of those 16 proteins was found in 2D gels of human fibroblasts. In HepG2, 12 proteins appeared to be specifically expressed (Table 1, Figure 1), actually none of those is a protein characteristic for the liver. Four of those, however, were identified as well in human fibroblasts. In Hep3B, 20 proteins appeared to be specifically expressed (Table 1, Figure 1). Again, none of those is a protein characteristic for the liver. Intriguingly, 16 of those were identified as well in human fibroblasts (Table 1, Figure 1). Of those, caldesmon, plastin-3 and vimentin are characteristic for mesenchymal cells. 55 spots were found expressed in both PHH and HepG2 but not in Hep3B, 15 of those are characteristic for the liver (Table 1). 16 proteins were found expressed in PHH and Hep3B but not in HepG2, four of those were found to be characteristic for the liver (Table 1). These findings suggested that HepG2 are

more closely related to PHH than Hep3B. Furthermore, Hep3B apparently express a proteome profile more closely related to fibroblasts than that of HepG2 or PHH, respectively.

2D-PAGE analysis of secretomes

Secretome analysis of HepG2 and Hep3B by means of 2D-PAGE displayed substantial differences between these two cells (Figure 2). Comparison of the integrated autoradiograph intensities of spots (corrected for cell numbers) suggested a more than twenty-fold higher secretion performance of HepG2 compared to Hep3B cells. As described below in more detail, HepG2 cells secreted many more plasma proteins than Hep3B. Hep3B cells secreted few and relative small amounts of plasma proteins, but other proteins not characteristic for liver cells such as follistatin-related protein 1 (Figure 2).

Shotgun analysis of cytoplasmic proteins

913 proteins were identified by shotgun proteomics of cytoplasmic fractions of PHH (Table S1). By comparison of the protein composition of PHH to various leukocytes, endothelial cells, fibroblasts and keratinocytes³¹ and consultation of the uniprot database,³⁴ we filtered 113 proteins to be characteristic for hepatocytes (Figure 3A, Table 2). This list comprises specific proteins, i.e. not expressed by other cells, as well as proteins characteristic for liver functions which may be expressed at lower levels in other cells as well.

In the cytoplasm of HepG2 cells, we identified 1523 proteins. 20 of those were found characteristic for the liver, three of those were not detectable in PHH (Figure 3A, Table 2). In the cytoplasm of Hep3B cells, we identified 1192 proteins. Only six of those were characteristic for the liver (Figure 3A, Table 2). By comparing these results to those of other cells which are not related to hepatocytes, we determined two out of 1239 proteins identified in fibroblasts, two out of 1346 in immature human dendritic cells and one out of 1660 in HUVEC to be characteristic for the liver (Figure 3A). These findings suggested that HepG2 have lost many, and Hep3B most of the functional protein expression characteristics of hepatocytes.

Shotgun analysis of the secretome

Secretion of plasma proteins is a characteristic function of hepatocytes.¹⁷ The assessment of the secretome may thus serve as an important indicator of functional liver cell differentiation. To specify the secretome of cells, however, the protein list determined from analysis of cell supernatants was corrected for potential contaminants as follows. Plasma proteins were

included only when identified with human-specific amino acid sequences which are not present in bovine proteins (Figure 4). Consequently, we ruled out proteins potentially derived from residual fetal calf serum which was used for culturing the cells. The list of proteins identified in the cell supernatant including contaminants from the cytoplasm are fully accessible via the PRIDE database. Furthermore, only proteins displaying a signal sequence or described to be secreted by non classical pathways were included in Table 3 to remove proteins potentially derived from cytoplasm leaking from dead cells. As a result, we identified 65 proteins in the secretome of PHH cells (Figure 2B, Table 3). 46 of those were plasma proteins. 139 proteins were identified in the secretome of HepG2 cells (Table 3). 55 proteins of those were plasma proteins (Figure 2B, Table 3). The following proteins, all of them presently identified in the secretome of HepG2 (Table 3), have been described previously as biomarkers for hepatocellular carcinoma (HCC). Gastricsin (PGC) was identified by suppression subtractive hybridization,³⁵ and midkine by RT-PCR³⁶ to be associated with HCC. Expression of EXT1 (exostosin-1) was described to be specific for moderately and poorly differentiated liver tumors.³⁷ Expression of connective tissue growth factor, determined by RT-PCR, plays a role in hepatocarcinogenesis and correlates with recurrence and metastasis of HCC.³⁸ The mitogenic action as well as anti-apoptotic potential of IGF-II may be relevant for tumor cell survival and drug resistance.³⁹⁻⁴¹ Alpha-fetoprotein and glypican-3 are already well-established marker proteins for HCC.^{42, 43} Dickkopf-related protein 1 (Dkk-1) is involved in the regulation of proliferation and migration of HCC cells during the metastasis process.⁴⁴ Laminin alpha 5 was described to mediate ectopic adhesion of hepatocellular carcinoma cells involving lutheran,⁴⁵ both proteins were presently identified in HepG2. A pathophysiological role of osteopontin in liver inflammation and cancer was described recently.⁴⁶ Overexpression of vascular endothelial growth factor was found associated with adverse outcomes in HCC.⁴⁷ In addition to those known biomarkers, we identified two other proteins in the secretome of HepG2 cells, which show very restricted expression patterns and may thus be considered as biomarker candidates. Only few data exist about bactericidal/permeability-increasing protein-like 1 was identified otherwise by a bioinformatic approach as a secreted protein.⁴⁸ Stanniocalcin-2 was described to be stimulated by hypoxia and is epigenetically regulated in various cancer cells.⁴⁹

In the secretome of Hep3B cells, we identified 72 proteins, 24 of those were also plasma proteins (Figure 2B, Table 3). For comparison, 19 out of 54 proteins in the secretome of skin fibroblasts, 14 out of 132 in immature dendritic cells, and 9 out of 141 in HUVECs were plasma proteins (Figure 2B). These findings again corroborated the previous notion that

Hep3B have lost not all, but most of the functional protein expression characteristics of hepatocytes. Hep3B as well secreted some proteins which are described to be characteristic for HCC, including neuroserpin,³⁶ protein cyr61³⁸ and ephrin-A1.⁵⁰ Mesothelin (Table 3), however, was found highly expressed in different kinds of carcinomas, but not in the liver.⁵¹ Epilysin (MMP-28, Table 3) has been described to mediate epithelial to mesenchymal transition,⁵² pointing to an autocrine enhancement of EMT. Intriguingly, almost all proteins abundantly secreted by Hep3B only, including collagen alpha-1(XII), EGF-containing fibulin-like extracellular matrix protein 1, follistatin-related protein 1, insulin-like growth factor-binding protein 7 and procollagen C-endopeptidase enhancer 1 were found secreted as well by fibroblasts. The specificity of gene and protein expression of follistatin-related protein 1 was confirmed independently by RT-PCR and Western analysis (Figure 5). These findings again supported the notion that Hep3B lost properties of hepatocytes but gained properties of mesenchymal cells.

Discussion

In this study we demonstrated that proteome profiling can be successfully applied to characterize hepatoma cell lines. Cultured cells may substantially differ from the cells they are derived from.¹ This may be due to the way they got immortalized or transformed and it may also be a consequence of *in vitro* culturing conditions. For some *in vitro* applications it can be essential to know the exact differentiation state and functionality of the employed cells.¹⁴ This is most evident in case of cultured hepatocytes to be used for e.g. toxicological assessments.¹³

Functional assays may be applied to test whether the cultured cells actually fulfill the necessary requirements. Assessment of the expression of a single enzyme, however, does not allow to draw more generalized conclusions. A more comprehensive evaluation of cell functionality can be achieved by proteome profiling. Positive identification of cell type-specific proteins such as liver enzymes, may clearly proof the suitability of cultured cells as cell model systems for specific studies. Furthermore, a protein expression profile of a cell line may provide rich informations about the differentiation state of the cells and may reveal uncharacteristic cell phenotypes which are often observed in transformed cells. One challenge thereby is that a large number of proteins needs to be clearly related to specific functions and cell-specific expression patterns.^{53, 54}

Proteome profiling was already applied to assess cultured hepatocytes including HepG2 and Hep3B.^{6, 7} Here, we again analyzed these cells, focusing on cytoplasmic and secreted proteins. Identification of a large number of proteins was a first step of analysis. In a second step, we applied multiple comparisons to adequate reference cell systems, which allowed appropriate data interpretation. On the one hand, proteins characteristic for hepatocytes were recognized by comparing the proteome profile of primary hepatocytes to those of other cells and confirmation of candidates was performed using data from the literature (Table 2). We supposed that the more proteins characteristic for the primary hepatocytes we find expressed in the cultured cells, the more these cells would have retained properties of the primary cells. Consequently, we assessed the maintenance of hepatocyte features of the cell lines by determination of expression of proteins found to be characteristic for hepatocytes (Figure 2). On the other hand, transformation of hepatocytes and de-differentiation of cells may be accompanied by EMT.¹⁵ Here, we assumed that acquisition of mesenchymal properties would consequently mean that cells would express proteins characteristic for mesenchymal cells. Therefore, we compared the proteome profiles of the cultured hepatoma cells to those of

human fibroblasts. Intriguingly, this approach provided very clear and consistent data, indicating that especially Hep3B cells have gained mesenchymal properties. As a conclusion, we suggest that the interpretation of proteome profiles may be greatly supported by comparisons to appropriate reference cell systems.

The application of two different methodologies resulted in very similar conclusions. The protein expression data determined by 2D-PAGE clearly indicated the differing degree of de-differentiation of HepG2 and Hep3B. HepG2 retaining far more hepatocyte-related characteristics than Hep3B, whereas Hep3B displayed many more commonalities to skin fibroblasts (Figure 1, Table 1). The apparent difference between HepG2 and Hep3B cells was even more pronounced in the secreted protein fraction (Figure 2 and 3). While HepG2 cells were found to secrete a quite considerable amount of plasma proteins characteristic for hepatocytes, Hep3B cells secreted few and relative small amounts of plasma proteins, but other proteins not characteristic for liver cells such as follistatin-related protein 1 (Figure 2). We interpret this finding as a clear indication that Hep3B underwent de-differentiation to a greater extent than HepG2. This demonstrated that 2D-PAGE is a suitable method to determine (de-) differentiation states of cells. In contrast to shotgun proteomics, 2D-PAGE enables quite accurate quantification of selected marker proteins. This feature may prove useful when more subtle differences between cells need to be determined.

Generally, similar observations were made using shotgun proteomics, providing more comprehensive protein identification data which relate to the differentiation state and functionality of cultured cells. Here again, protein expression data clearly indicated different extent of de-differentiation of HepG2 and Hep3B, respectively (Figure 3A, Table 2). The differences between HepG2 and Hep3B cells were even more pronounced in the secreted protein fraction (Figure 3B). HepG2 were found to secrete a quite considerable amount of plasma proteins characteristic for hepatocytes. Beside many other proteins, eleven proteins previously described as biomarkers for HCC were found secreted by these cells (Table 3). The high coincidence of our data with so many previously established observations with respect to tumor biomarkers identification may be interpreted as indirect assurance of the high reliability of the presently applied proteome analysis methods and interpretation strategies. In contrast, Hep3B secreted less plasma proteins or proteins known as HCC biomarkers, but several proteins which were found secreted as well by fibroblasts. This observation supported the notion that Hep3B underwent EMT. As a conclusion, the present proteome profiling data clearly indicate that HepG2 cells are a more suitable model for hepatocellular carcinoma cells than Hep3B cells.

Conclusions

The presently applied proteome analysis methodology focusing on secreted proteins combined with a biology-based comparison strategy enabled a clear characterization of the hepatocyte cell lines HepG2 and Hep3B with respect to liver-specific features and EMT.

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Legends to Figures

Figure 1: Comparative proteome analysis of PHH, HepG2, Hep3B and of human fibroblasts. The cytoplasmic fraction of PHH, HepG2, Hep3B and of human fibroblasts were investigated by 2D-PAGE, protein detection was performed by fluorescence staining with RuBPS. Proteins were identified by mass spectrometric analysis of tryptic digests. Proteins characteristic for hepatocytes are indicated on 2D-gels of PHH and HepG2 cells. Proteins characteristic for fibroblasts are indicated on 2D-gels of fibroblasts and Hep3B cells.

Figure 2: Comparative secretome analysis of HepG2 and Hep3B by 2D-PAGE. Cells were metabolically labeled with ^{35}S -methionine/cysteine, cell supernatant proteins were separated by 2D-PAGE and detected by ^{35}S -autoradiography. Protein spots were identified from unlabeled protein fractions analyzed in parallel. SwissProt accession numbers of proteins identified by mass spectrometry are indicated. While all proteins identified in HepG2 cells were plasma proteins, Hep3B were found to express follistatin-related protein 1 (Q12841) which is characteristic for mesenchymal cells.

Figure 3: Comparison of expression of proteins characteristic for hepatocytes in hepatocyte-related and non related cell types. Grey bars indicate total numbers of proteins identified by shotgun proteomics per cell type, black bars indicate the number of proteins characteristic for hepatocytes. A) Cytoplasmic fractions of PHH, HepG2, Hep3B, fibroblasts, HUVEC and DCs B) Secretomes of PHH, HepG2, Hep3B, fibroblasts, HUVEC and DCs.

Figure 4: Identification of human alpha-fetoprotein in Hep3B cells. Expression of human plasma proteins, as for example alpha-fetoprotein, was confirmed by identifying human-specific amino acid sequences which are not present in bovine proteins. Analyzed cell supernatant fractions from cultured cells are contaminated with residual fetal calf serum. A mass analysis raw data set from Hep3B cells was searched against the bovine and human database, respectively. To give an example, the results for alpha-fetoprotein are shown. Reflecting relative abundances, many more peptides were found corresponding to bovine compared to human alpha-fetoprotein. Identification of a human-specific amino acid sequence, which is not present in the bovine protein, proofs the presence of the human protein and consequently the secretion of this protein by Hep3B cells. The MS^2 -spectra of the

indicated human peptides are shown. Following this strategy, proteins potentially derived from residual fetal calf serum were ruled out.

Figure 5: Identification of FSTL1 in Hep3B cells. A) Real-time PCR: Total RNA was isolated from logarithmically growing HepG2 and Hep3B and reverse transcribed. Taqman assays for FSTL1 and 18s RNA were performed. 18s RNA was used for normalization and the FSTL1 expression level in normal liver tissue (NML) was set as 1.

B) Western blot: Cell lysates or supernatants from HepG2 and Hep3B were collected. For immunodetection, a goat polyclonal antibody to FSTL1 and a HRP coupled rabbit anti goat antibody were used.

Legend to Tables

Table 1: List of proteins which were specifically identified in 2D-gels of PHH, HepG2 or Hep3B. Proteins are identified by their SwissProt accession numbers. They are sorted according to cell type-specific expression and within this classification according to protein names. The numbers listed in rows indicate the number of distinct peptides identified by mass spectrometry. Accession numbers of proteins characteristic for hepatocytes are highlighted (bold), as well as proteins which were also detected in fibroblasts (*italic*).

Table 2: List of cytoplasmic proteins characteristic for hepatocytes identified by shotgun proteomics. Proteins are sorted according to protein names and identified by their SwissProt accession numbers. The numbers listed in rows indicate the number of distinct peptides identified by mass spectrometry. Specific: hepatocyte-specific proteins which are not expressed by other cells; Carbohydrate, Lipid, Detox (detoxification), Mitochondrial, Aminoacid, Pyrimidin, Purin, Hormone refer to protein classification or the metabolical pathways in which proteins are involved.

Table 3: List of proteins secreted by PHH, HepG2 and Hep3B identified by shotgun proteomics. Proteins are identified by their SwissProt accession numbers. They are sorted depending on whether they are plasma proteins or according to their specific expression in PHH; HepG2 or Hep3B. Within this classification proteins are sorted according to protein names. The numbers listed in rows indicate the number of distinct peptides identified by mass spectrometry. Proteins which have been described previously as biomarkers for hepatocellular

carcinoma (HCC) or other cancers, as well as novel biomarker candidates are highlighted (bold). Proteins which were found secreted as well by fibroblasts are highlighted in the Hep3B-specific protein list (italic).

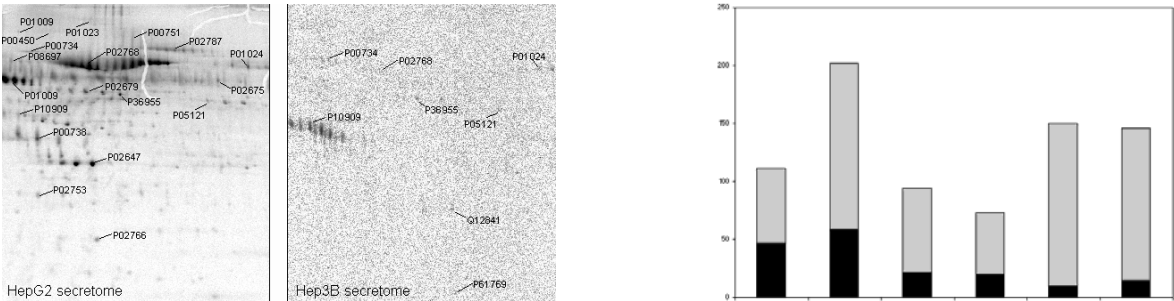
Supporting Information Available

Table S1: List of all proteins identified in the cytoplasmic fraction of PHH, HepG2 and Hep3B by shotgun proteomics. Proteins are sorted according to protein names and identified by their SwissProt accession numbers. The numbers listed in rows indicate the number of distinct peptides identified by mass spectrometry in the corresponding cells. This provides a semi-quantitative measure for protein abundance as the higher the relative protein concentration, the higher the peptide count. Proteins which were also identified in 2D gels of the indicated cell types are listed under “2D”.

Synopsis

Cultured hepatocytes may resemble their primary counterparts or rather acquire features of cancer cells. We assessed expression of liver-specific proteins and identified proteins indicative for epithelial to mesenchymal transition in HepG2 and Hep3B cells in comparison to primary human hepatocytes. Proteome profiling of cytoplasmic and secreted proteins was performed by 2D-PAGE and shotgun proteomics.

Secretom profiling of hepatoma cell lines → Proteins characteristic for hepatocytes



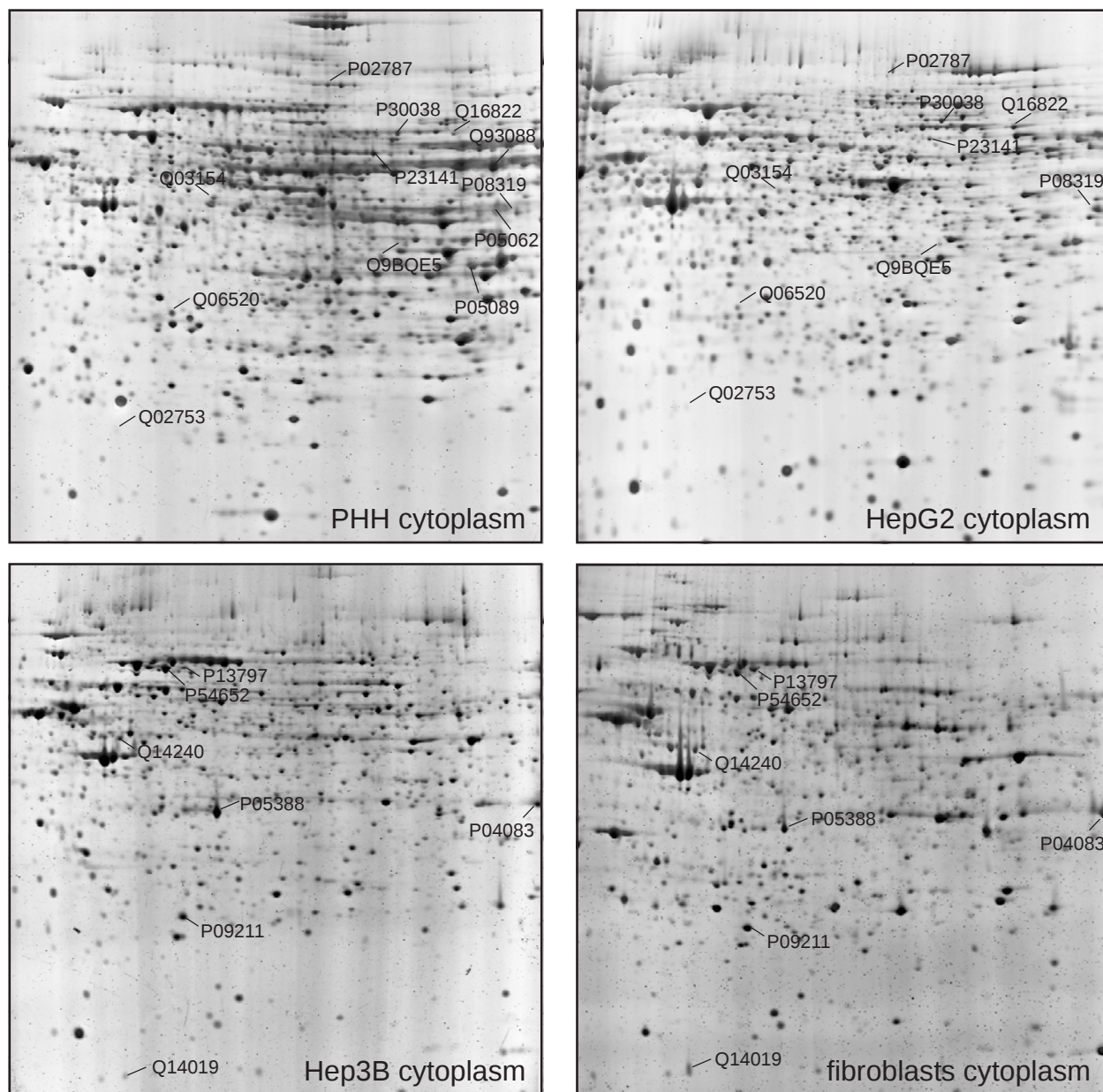


Figure 1

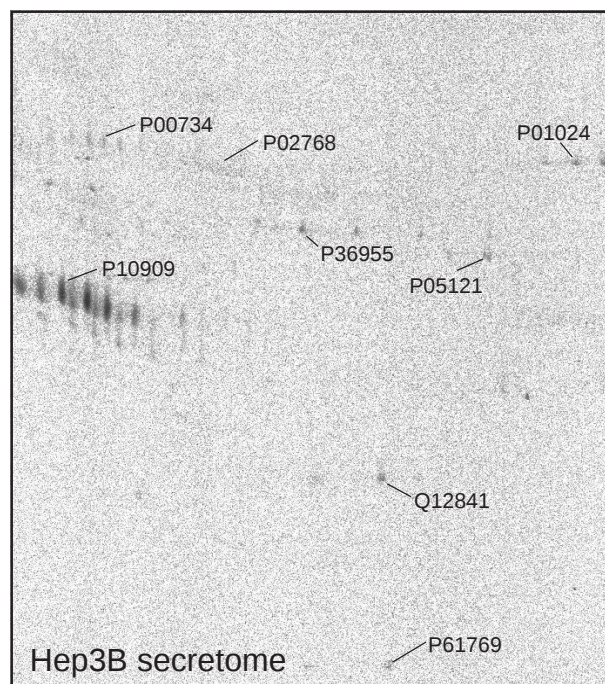
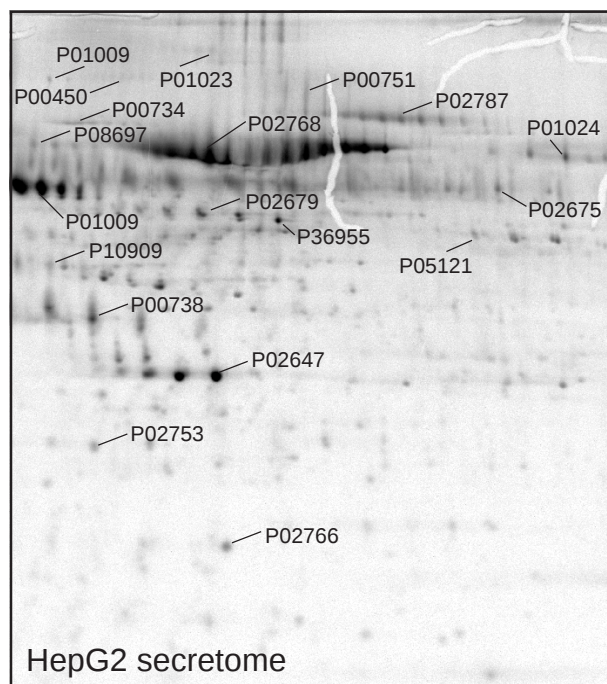


Figure 2

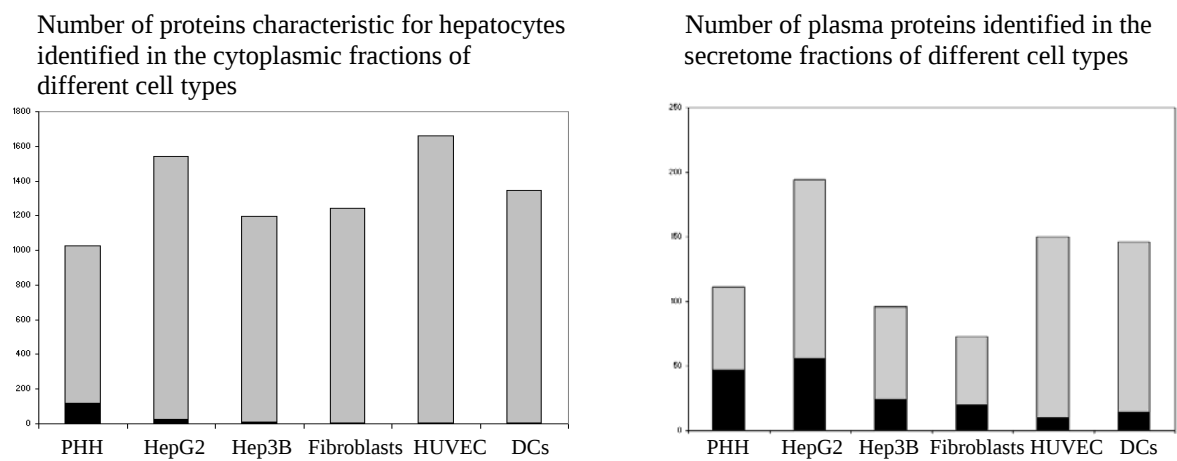


Figure 3

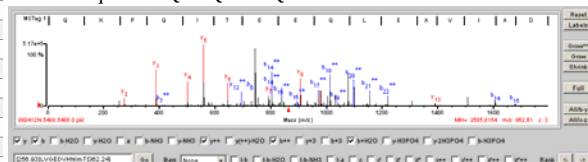
Bovine:

#	Filename	z	Score	SPI (%)	Spectrum Intensity	Sequence	MH* Matched (Da)
1	080412N.4348.4370.2	2	22.00	100.0	1.63e+008	(K) LGEYLLQNAFLVAYTK (K)	1892.979
2	080412N.1956.1956.0	3	21.01	95.5	6.68e+007	(R) HEENFIPNGVDQCCTSSYSNR (R)	2464.025
3	080412N.3333.3343.0	4	20.37	90.4	2.60e+008	(K) LVMDVAHIHEECCKGNVLECLQDGER (V)	3111.412
4	080412N.5228.5228.0	3	19.58	94.7	9.99e+007	(K) QKQITEEQLETVVADFSGLLEK (C)	2602.361
5	080412N.2294.2303.2	2	17.90	97.8	5.97e+008	(K) GTQELLEK (C)	979.510
6	080412N.3031.3048.2	2	17.87	93.3	2.18e+008	(R) ESSLLNQHICAVMGK (F)	1686.830
7	080412N.3358.3358.0	3	17.80	89.4	5.27e+008	(K) KAPQLTSPELMALTR (K)	1655.915
8	080412N.4664.4664.0	3	17.56	92.2	9.07e+007	(K) QLACGEGVADLIIGHLCIR (H)	2095.079
9	080412N.2975.3005.2	2	17.38	95.7	3.17e+008	(K) DLCCQVGVFLQTHK (Q)	1616.814
10	080412N.3045.3064.2	2	17.07	92.5	4.21e+008	(R) VHSYICQQDILSR (Q)	1699.814
11	080412N.1679.1688.2	2	16.01	95.5	4.36e+008	(K) YIQESQALAK (R)	1150.610
12	080412N.3984.4006.0	3	15.40	73.1	1.89e+008	(K) KAAEASIPFPFVLEPVISCK (S)	2109.141
13	080412N.2999.3008.0	2	15.21	94.6	3.53e+008	(K) DVLITIEKPTGSK (Q)	1400.800
14	080412N.4154.4154.0	3	14.19	89.6	1.81e+008	(K) LGEYLLQNAFLVAYTKK (A)	2021.074
15	080412N.4776.4799.0	3	13.90	87.3	5.21e+007	(K) QPAGCLENQVSAFLEEICREK (E)	2478.175
16	080412N.2644.2688.3	3	13.63	94.2	1.18e+009	(R) FLGDRDFNQLSSR (D)	1554.766
17	080412N.1961.1961.2	2	13.07	84.6	6.58e+007	(K) EIPERYGLSDCCSR (T)	1713.757
18	080412N.3611.3619.2	2	13.02	77.6	1.92e+008	(K) APQLTSPELMALTR (K)	1527.820
19	080412N.1500.1503.2	2	12.98	77.3	1.48e+008	(K) YGLSDCCSR (T)	1117.440
20	080412N.1774.1785.2	2	12.93	87.8	3.03e+008	(K) VTSITKELR (E)	1046.620
21	080412N.2285.2300.0	3	12.30	74.6	3.70e+008	(K) LVMDVAHIHEECCK (G)	1740.787
22	080412N.2280.2308.0	4	11.30	70.1	4.07e+008	(K) LVMDVAHIHEECCK (G)	1740.787
23	080412N.3673.3683.0	2	11.17	91.6	7.93e+008	(K) QQFLINLVK (Q)	1102.662
24	080412N.2655.2664.2	2	10.92	83.3	2.59e+008	(R) FLGDRDFNQLSSR (D)	1554.766
25	080412N.4189.4255.3	3	9.81	73.0	1.77e+008	(K) AAPASIPFPFVLEPVISCK (S)	1981.046
26	080412N.1794.1803.2	2	9.57	92.6	4.53e+008	(R) FTIYEYSR (R)	965.436
27	080412N.2249.2258.2	2	9.16	95.8	1.72e+009	(R) YIYEIAR (R)	927.493

Human:

#	Filename	z	Score	SPI (%)	Spectrum Intensity	Sequence	MH* Matched (Da)
1	080412N.4348.4370.2	2	22.00	100.0	1.63e+008	(K) LGEYLLQNAFLVAYTK (K)	1892.979
2	080412N.2294.2303.2	2	17.90	97.8	5.97e+008	(K) GTQELLEK (C)	979.510
3	080412N.5488.5488.0	3	17.28	85.7	3.76e+007	(K) QKQITEEQLEAVIADFSGLLEK (C)	2586.366
4	080412N.1679.1688.2	2	16.01	95.5	4.36e+008	(K) YIQESQALAK (R)	1150.610
5	080412N.4154.4154.0	3	14.19	89.6	1.81e+008	(K) LGEYLLQNAFLVAYTKK (A)	2021.074
6	080412N.3673.3683.0	2	10.35	96.0	7.93e+008	(K) QQFLINLVK (Q)	1103.646

human sequence: QKQITEEQLEAVIADFSGLLEK



bovine sequence: QKQITEEQLETVVADFSGLLEK

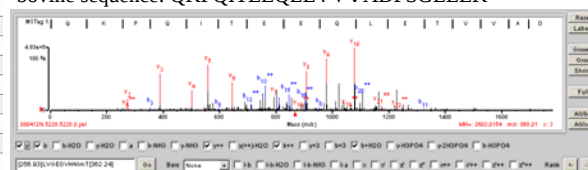
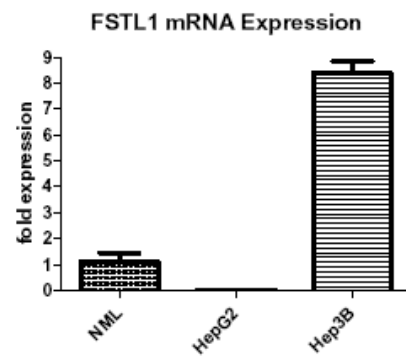
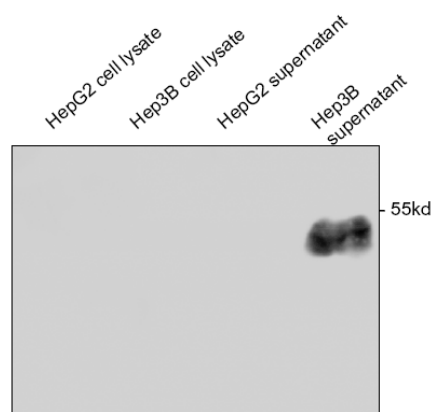


Figure 4

Figure 5



A)



B)

Table 1:

AccNr	Protein	PHH	HepG2	Hep3B
proteins expressed in only one cell type				
P46952	3-hydroxyanthranilate 3,4-dioxygenase	5		
P49189	4-trimethylaminobutyraldehyde dehydrogenase	6		
P24298	Alanine aminotransferase	5		
P05089	Arginase-1	12		
Q93088	Betaine--homocysteine S-methyltransferase	14		
P00918	Carbonic anhydrase 2	8		
P09467	Fructose-1,6-bisphosphatase 1	12		
P05062	Fructose-bisphosphate aldolase B	19		
P46439	Glutathione S-transferase Mu 5	4		
P00738	Haptoglobin precursor	10		
P54868	Hydroxymethylglutaryl-CoA synthase	19		
Q9Y2S2	Lambda-crystallin homolog	5		
P00439	Phenylalanine-4-hydroxylase	4		
P30613	Pyruvate kinase isozymes R/L	5		
Q00266	S-adenosylmethionine synthetase isoform type-1	6		
P50226	Sulfotransferase 1A2	5		
Q13510	<i>Acid ceramidase precursor</i>		4	
Q15417	<i>Calponin-3</i>		5	
O14618	Copper chaperone for superoxide dismutase		4	
P04844	<i>Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 63 kDa subunit</i>		3	
P07910	Heterogeneous nuclear ribonucleoproteins C1/C2		4	
Q8WZA9	Immunity-related GTPase family Q protein		3	
P09455	Retinol-binding protein I, cellular		3	
P62745	Rho-related GTP-binding protein RhoB precursor		3	
P49247	Ribose-5-phosphate isomerase		3	
Q96C86	Scavenger mRNA decapping enzyme DcpS		3	
Q8WVM8	Sec1 family domain-containing protein 1		4	
Q96K17	<i>Transcription factor BTF3 homolog 4</i>		3	
Q16401	26S proteasome non-ATPase regulatory subunit 5			4
O00233	<i>26S proteasome non-ATPase regulatory subunit 9</i>			3
P04083	<i>Annexin A1</i>			19
P06703	<i>Calcyclin</i>			4
Q05682	<i>Caldesmon</i>			3
P11802	<i>Cell division protein kinase 4</i>			5
Q14019	<i>Coactosin-like protein</i>			5
P21291	<i>Cysteine and glycine-rich protein 1</i>			4
Q14240	<i>Eukaryotic initiation factor 4A-II</i>			6
P09211	<i>Glutathione S-transferase P</i>			9
P43304	<i>Glycerol-3-phosphate dehydrogenase</i>			5
P54652	<i>Heat shock-related 70 kDa protein 2</i>			9
P55795	Heterogeneous nuclear ribonucleoprotein H*			3
P48163	<i>NADP-dependent malic enzyme</i>			4
P13797	<i>Plastin-3</i>			14
Q99584	<i>S100 calcium-binding protein A13</i>			3
P26447	<i>S100 calcium-binding protein A4</i>			7
P36873	Serine/threonine-protein phosphatase PP1-gamma catalytic subunit			5
Q9UMX0	Ubiquilin-1			3
P08670	<i>Vimentin</i>			4
proteins expressed in PHH and HepG2				
Q9BV57	1,2-dihydroxy-3-keto-5-methylthiopentene dioxygenase	4	6	

O95861	3*(2*),5*-bisphosphate nucleotidase 1	1	2
P45954	Acyl-CoA dehydrogenase, short/branched chain specific	8	5
P16219	Acyl-CoA dehydrogenase, short-chain specific	5	3
Q9HDC9	Adipocyte plasma membrane-associated protein	1	1
O43488	Aflatoxin B1 aldehyde reductase member 2	3	3
P08319	Alcohol dehydrogenase 4	18	1
P11766	Alcohol dehydrogenase class 3 chi chain	1	1
P05091	Aldehyde dehydrogenase	17	6
Q03154	Aminoacylase-1	6	5
P01019	Angiotensinogen precursor	1	4
Q9BQE5	Apolipoprotein-L2	1	1
Q06520	Bile-salt sulfotransferase	8	7
P07858	Cathepsin B precursor	5	6
P00450	Ceruloplasmin precursor	1	1
P01024	Complement C3 precursor	1	1
P0C0L4	Complement C4-A precursor	1	2
P30038	Delta-1-pyrroline-5-carboxylate dehydrogenase	8	5
P13716	Delta-aminolevulinic acid dehydratase	6	1
P32321	Deoxycytidylate deaminase	1	1
P09417	Dihydropteridine reductase	2	5
Q3LXA3	Dihydroxyacetone kinase	16	12
P04843	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 67 kDa subunit	1	4
Q9H0W9	Ester hydrolase C11orf54	2	2
Q92506	Estradiol 17-beta-dehydrogenase 8	4	3
Q99447	Ethanolamine-phosphate cytidyltransferase	2	2
P07148	Fatty acid-binding protein	17	7
P02794	Ferritin heavy chain	2	1
P51570	Galactokinase	4	4
P00367	Glutamate dehydrogenase 1	22	21
P11216	Glycogen phosphorylase	1	8
Q9UBQ7	Glyoxylate reductase/hydroxypyruvate reductase	8	5
P50135	Histamine N-methyltransferase	1	2
Q9BX68	Histidine triad nucleotide-binding protein 2	5	2
Q16775	Hydroxyacylglutathione hydrolase	3	2
P23141	Liver carboxylesterase 1 precursor	26	6
P10253	Lysosomal alpha-glucosidase precursor	4	7
P50224	Monoamine-sulfating phenol sulfotransferase	3	13
P19404	NADH-ubiquinone oxidoreductase 24 kDa subunit	2	2
P28331	NADH-ubiquinone oxidoreductase 75 kDa subunit	1	7
Q15274	Nicotinate-nucleotide pyrophosphorylase	3	6
Q9Y365	PCTP-like protein	1	1
Q16822	Phosphoenolpyruvate carboxykinase	24	17
Q96BW5	Phosphotriesterase-related protein	1	1
P02753	Plasma retinol-binding protein precursor	3	4
P21980	Protein-glutamine gamma-glutamyltransferase 2	2	1
P62820	Ras-related protein Rab-1A	3	4
P00352	Retinal dehydrogenase 1	15	13
P02787	Serotransferrin precursor	6	14
Q8WW5			
9	SPRY domain-containing protein 4	6	2
Q96I99	Succinyl-CoA ligase [GDP-forming] beta-chain	5	3
Q16762	Thiosulfate sulfurtransferase	4	1
P19971	Thymidine phosphorylase precursor	2	1
Q9H0E2	Toll-interacting protein	1	1
Q9NYU2	UDP-glucose:glycoprotein glucosyltransferase 1	1	2

proteins expressed in PHH and Hep3B

P61769	Beta-2-microglobulin precursor	2	2
P05109	Calgranulin A	2	1
P06702	Calgranulin B	1	1
P31327	Carbamoyl-phosphate synthase	80	53
P10909	Clusterin precursor	1	3
P35520	Cystathionine beta-synthase	1	1
P48507	Glutamate--cysteine ligase regulatory subunit	1	4
Q9Y2T3	Guanine deaminase	4	3
Q01581	Hydroxymethylglutaryl-CoA synthase	2	4
P07195	L-lactate dehydrogenase B chain	1	18
P40261	Nicotinamide N-methyltransferase	2	2
P16083	Ribosyldihydronicotinamide dehydrogenase	3	4
Q13228	Selenium-binding protein 1	9	1
O75368	SH3 domain-binding glutamic acid-rich-like protein	1	3
P09493	Tropomyosin 1 alpha chain	2	9
P07951	Tropomyosin beta chain	2	8

Table 2:

AccNr	Protein	PHH	HepG2	Hep3B	Specific	Carbohydrate	Lipid	Detox	Mitochondrial	Aminoacid	Pyrimidin-Purin	Hormone
O75891	10-formyltetrahydrofolate dehydrogenase	36	1					✓				
Q7Z5P4	17-beta hydroxysteroid dehydrogenase 13	11			✓			✓				
O75600	2-amino-3-ketobutyrate coenzyme A ligase	1							✓	✓		
Q9UJ83	2-hydroxyacyl-CoA lyase 1	1					✓					
P12694	2-oxoisovalerate dehydrogenase alpha subunit	2							✓	✓		
P51857	3-oxo-5-beta-steroid 4-dehydrogenase	5	1				✓					
P80404	4-aminobutyrate aminotransferase	22	9						✓			
P32754	4-hydroxyphenylpyruvate dioxygenase	12								✓		
P49914	5-formyltetrahydrofolate cyclo-ligase	1	1									
Q08AH3	Acyl-coenzyme A synthetase ACSM2A	12					✓		✓			
Q68CK6	Acyl-coenzyme A synthetase ACSM2B	11			✓		✓		✓			
O95154	Aflatoxin B1 aldehyde reductase member 3	12						✓				
Q9BSE5	Agmatinase, mitochondrial precursor	4	6						✓			
P24298	Alanine aminotransferase	9								✓		
P07327	Alcohol dehydrogenase 1A	30						✓				
P00325	Alcohol dehydrogenase 1B	32						✓				
P00326	Alcohol dehydrogenase 1C	21						✓				
P08319	Alcohol dehydrogenase 4	23	3		✓			✓				
P28332	Alcohol dehydrogenase 6	6						✓				
Q9H2A2	Aldehyde dehydrogenase family 8 member A1	6						✓				
Q06278	Aldehyde oxidase	3						✓				
P52895	Aldo-keto reductase family 1 member C2	6	13	10			✓	✓				
P42330	Aldo-keto reductase family 1 member C3	8	18	13			✓	✓				
P17516	Aldo-keto reductase family 1 member C4	13			✓		✓	✓				
Q9UDR5	Alpha-aminoacidic semialdehyde synthase	14	1						✓	✓		
Q03154	Aminoacylase-1	9	6							✓		
P05089	Arginase-1	20			✓					✓		
P04424	Argininosuccinate lyase	8								✓		
P00966	Argininosuccinate synthase	17		12	✓					✓		
P08236	Beta-glucuronidase precursor	1				✓						
Q93088	Betaine-homocysteine S-methyltransferase	21								✓		
Q9H2M3	Betaine-homocysteine S-methyltransferase 2	2								✓		
Q9UBR1	Beta-ureidopropionase	3								✓		
Q14032	Bile acid CoA:amino acid N-acyltransferase	4					✓					
Q9Y2P5	Bile acyl-CoA synthetase	5								✓		
Q06520	Bile-salt sulfotransferase	9	8									✓
Q9UJS0	Calcium-binding mitochondrial carrier protein Aralar2	7	4						✓			
P31327	Carbamoyl-phosphate synthase	105		67				✓	✓			

Table 3:

AccNr	Protein	PHH	HepG2	Hep3B
Plasma Proteins				
P02763	Alpha-1-acid glycoprotein 1 precursor	6	5	
P19652	Alpha-1-acid glycoprotein 2 precursor	2	3	
P01011	Alpha-1-antichymotrypsin precursor	9	4	
P01009	Alpha-1-antitrypsin precursor		12	
P04217	Alpha-1B-glycoprotein precursor	5	5	
P08697	Alpha-2-antiplasmin precursor		8	1
P02765	Alpha-2-HS-glycoprotein precursor		9	
P01023	Alpha-2-macroglobulin precursor		57	6
P02771	Alpha-fetoprotein precursor	1	31	6
P02760	AMBIP protein precursor	9		
P01008	Antithrombin-III precursor	2	5	
P02647	Apolipoprotein A-I precursor	22	40	1
P02652	Apolipoprotein A-II precursor	1	5	
P02656	Apolipoprotein C-III precursor	2		
P04114	Apolipoprotein B-100 precursor		3	
P02656	Apolipoprotein C-III precursor		1	
P02649	Apolipoprotein E precursor	16	20	
O95445	Apolipoprotein M		4	
P02749	Beta-2-glycoprotein 1 precursor	3	11	
P22792	Carboxypeptidase N subunit 2 precursor	3		
P00450	Ceruloplasmin precursor		20	
P10909	Clusterin precursor	11	7	18
P12259	Coagulation factor V precursor	1	2	
P00736	Complement C1r subcomponent precursor	3		
P06681	Complement C2 precursor		12	
P01024	Complement C3 precursor	15	71	4
P0C0L4	Complement C4-A precursor	12	49	1
P01031	Complement C5 precursor		4	
P00751	Complement factor B precursor	4	9	
P07360	Complement component C8 gamma chain	5		
P08603	Complement factor H precursor		1	
P05156	Complement factor I precursor		8	
P01034	Cystatin C precursor	3	11	1
P02675	Fibrinogen beta chain precursor	1	6	
P02679	Fibrinogen gamma chain precursor	7	7	
Q08830	Fibrinogen-like protein 1 precursor	2	10	
P02751	Fibronectin precursor	4	79	7
P00738	Haptoglobin precursor	18	20	
P02790	Hemopexin precursor (Beta-1B-glycoprotein)	1		
P19827	Inter-alpha-trypsin inhibitor heavy chain H1 precursor	2	1	2
P19823	Inter-alpha-trypsin inhibitor heavy chain H2 precursor	1	14	4
Q06033	Inter-alpha-trypsin inhibitor heavy chain H3 precursor	1	1	1
Q14624	Inter-alpha-trypsin inhibitor heavy chain H4 precursor	2		2
P02750	Leucine-rich alpha-2-glycoprotein precursor (LRG)	2		
P18428	Lipopolysaccharide-binding protein precursor (LBP)	1		
P61626	Lysozyme C precursor		11	
P01033	Metalloproteinase inhibitor 1 precursor		2	4
P16035	Metalloproteinase inhibitor 2 precursor		2	8
P36955	Pigment epithelium-derived factor precursor		5	6

P05155	Plasma protease C1 inhibitor precursor	12	1	
P02753	Plasma retinol-binding protein precursor	5	8	1
P05154	Plasma serine protease inhibitor precursor		8	
P05121	Plasminogen activator inhibitor 1 precursor	1	18	4
P20742	Pregnancy zone protein precursor		6	3
P00734	Prothrombin precursor		14	1
P02787	Serotransferrin precursor	3	48	2
P02768	Serum albumin precursor	41	56	23
P02743	Serum amyloid P-component precursor	2		
P02787	Serum amyloid A protein precursor (SAA)	5		
P35542	Serum amyloid A-4 protein		2	
P27169	Serum paraoxonase/arylesterase 1 (EC 3.1.1.2)	1		
P05452	Tetranectin precursor		2	1
P07996	Thrombospondin-1	1	12	13
P02766	Transthyretin precursor	8	9	
P02774	Vitamin D-binding protein precursor	5	4	
P04004	Vitronectin precursor	3	4	
P25311	Zinc-alpha-2-glycoprotein precursor	9	6	
Proteins secreted by PHH, HepG2 and/or Hep3B				
P03950	Angiogenin precursor	1	6	
P08758	Annexin A5		8	13
Q9H6X2	Anthrax toxin receptor 1 precursor		5	1
P98160	Basement membrane-specific heparan sulfate proteoglycan core protein	1	1	
P61769	Beta-2-microglobulin precursor	4	1	2
P19022	Cadherin-2 precursor		3	5
O94985	Calsyntenin-1 precursor		2	1
P07339	Cathepsin D precursor	1	6	5
P07711	Cathepsin L precursor		3	2
Q14118	Dystroglycan precursor		1	2
P61916	Epididymal secretory protein E1 precursor		3	5
Q08380	Galectin-3-binding protein precursor		1	2
Q92820	Gamma-glutamyl hydrolase precursor		8	7
P07093	Glia-derived nexin precursor		1	4
Q99988	Growth/differentiation factor 15 precursor	3	12	
P18065	Insulin-like growth factor-binding protein 2 precursor	2	1	
P24043	Laminin alpha-2 chain precursor	1	6	1
P11047	Laminin gamma-1 chain precursor		1	1
O15230	Laminin subunit alpha-5 precursor		5	12
P07942	Laminin subunit beta-1 precursor		5	9
Q02809	Procollagen-lysine,2-oxoglutarate 5-dioxygenase 1 precursor		2	3
O60568	Procollagen-lysine,2-oxoglutarate 5-dioxygenase 3 precursor		3	2
P34096	Ribonuclease 4 precursor	1	3	
P10599	Thioredoxin	1	4	
Proteins secreted by PHH only				
O00182	Galectin-9 (HOM-HD-21) (Ecalectin)	1		
P25391	Laminin subunit alpha-1 precursor (Laminin A chain)	1		
Q8TF66	Leucine-rich repeat-containing protein 15 precursor	5		
P14174	Macrophage migration inhibitory factor (MIF)	1		
O75095	Multiple epidermal growth factor-like domains 6 precursor	1		
P80188	Neutrophil gelatinase-associated lipocalin precursor (NGAL)	3		
P36955	Pigment epithelium-derived factor precursor (PEDF)	1		
Q15238	Pregnancy-specific beta-1-glycoprotein 5 precursor	1		
Q92954	Proteoglycan-4 precursor (Lubricin)	1		
Proteins secreted by HepG2 only				
P31947	14-3-3 protein sigma (Stratifin)		17	

O00468	Agrin precursor	2
P02760	AMBP protein precursor	2
P05067	Amyloid beta A4 protein precursor	15
Q06481	Amyloid-like protein 2 precursor	2
P01019	Angiotensinogen precursor	6
P55145	ARMET protein precursor	2
Q8N4F0	Bactericidal/permeability-increasing protein-like 1	3
P06865	Beta-hexosaminidase alpha chain precursor	1
P16870	Carboxypeptidase E precursor	3
P22792	Carboxypeptidase N subunit 2 precursor	2
P07858	Cathepsin B precursor	7
P09668	Cathepsin H precursor	1
Q9BWS9	Chitinase domain-containing protein 1	1
O00299	Chloride intracellular channel protein 1	4
P12109	Collagen alpha-1(VI) chain precursor	2
Q14050	Collagen alpha-3(IX) chain precursor	1
P50454	Collagen-binding protein 2 precursor	2
P29279	Connective tissue growth factor precursor	3
Q02413	Desmoglein-1 precursor	1
O94907	Dickkopf-related protein 1 precursor	1
P12830	Epithelial-cadherin precursor	1
Q16394	Exostosin-1 (EXT1)	1
P19883	Follistatin precursor	3
P20142	Gastricsin precursor (PGC)	2
P28161	Glutathione S-transferase Mu 2	1
P51654	Glypican-3 precursor	12
Q9HAV7	GrpE protein homolog 1	2
P05546	Heparin cofactor 2 precursor	8
P01344	Insulin-like growth factor II precursor	3
P08833	Insulin-like growth factor-binding protein 1 precursor	9
P05362	Intercellular adhesion molecule 1 precursor	1
P05161	Interferon-induced 17 kDa protein precursor	1
Q86UP2	Kinectin	2
P02788	Lactotransferrin precursor	1
P51884	Lumican precursor	1
P50895	Lutheran blood group glycoprotein precursor	3
P14174	Macrophage migration inhibitory factor	1
O15232	Matrilin-3 precursor	6
P21741	Midkine precursor	2
P80188	Neutrophil gelatinase-associated lipocalin precursor	2
P14543	Nidogen-1 precursor	10
P10451	Osteopontin precursor	1
P07602	Proactivator polypeptide precursor	2
Q8NBP7	Proprotein convertase subtilisin/kexin type 9 precursor	2
Q969H8	Protein C19orf10 precursor	2
O60888	Protein CutA precursor	1
P78509	Reelin precursor	4
Q99969	Retinoic acid receptor responder protein 2 precursor	2
P34096	Ribonuclease 4 precursor	1 3
O00584	Ribonuclease T2 precursor	2
O75830	Serpin I2 precursor	1
O76061	Stanniocalcin-2 precursor	2
P22105	Tenascin-X precursor	1
P05543	Thyroxine-binding globulin precursor	3
P10646	Tissue factor pathway inhibitor precursor	4
Q15582	Transforming growth factor-beta-induced protein ig-h3 precursor	10

P06132	Uroporphyrinogen decarboxylase	1
P15692	Vascular endothelial growth factor A precursor	1
Q6EMK4	Vasorin precursor	3
Proteins secreted by Hep3B only		
P06280	Alpha-galactosidase A precursor	2
P05109	Calgranulin A	1
P49747	Cartilage oligomeric matrix protein precursor	1
Q9UBR2	Cathepsin Z precursor	4
P02452	Collagen alpha-1(I) chain precursor	1
P02462	Collagen alpha-1(IV) chain precursor	1
P20908	Collagen alpha-1(V) chain precursor	3
Q02388	Collagen alpha-1(VII) chain precursor	1
Q99715	<i>Collagen alpha-1(XII) chain precursor</i>	7
Q12805	<i>EGF-containing fibulin-like extracellular matrix protein 1 precursor</i>	5
P20827	Ephrin-A1 precursor	1
P35555	Fibrillin-1 precursor	1
P35556	Fibrillin-2 precursor	1
P23142	Fibulin-1 precursor	2
Q12841	<i>Follistatin-related protein 1 precursor</i>	9
P13284	Gamma-interferon-inducible lysosomal thiol reductase precursor	1
P08581	Hepatocyte growth factor receptor precursor	1
P24592	Insulin-like growth factor-binding protein 6 precursor	1
Q16270	<i>Insulin-like growth factor-binding protein 7 precursor</i>	12
Q9H239	Matrix metalloproteinase-28 precursor (MMP-28, Epilysin)	1
Q13421	Mesothelin precursor	2
P55001	Microfibrillar-associated protein 2 precursor	3
Q99574	Neuroserpin precursor	1
O95497	Pantetheinase precursor	1
Q92626	Peroxidasin homolog precursor	5
Q15113	<i>Procollagen C-endopeptidase enhancer 1 precursor</i>	12
O00622	Protein CYR61 precursor	3
O75787	Renin receptor precursor	3
O00391	Sulfhydryl oxidase 1 precursor	2
Q7Z2Q7	Synleurin	1

AccNr	Protein	Cov	PHH	HepG2	Hep3B	2D
O14874	[3-methyl-2-oxobutanoate dehydrogenase [lipoamide]] kinase,	4.1	1	1		-
Q9BV57	1,2-dihydroxy-3-keto-5-methylthiopentene dioxygenase (EC 1,1	69.8	4	6		X
P61604	10 kDa heat shock protein, mitochondrial (Hsp10) (10 kDa chap	93.1	10	13	7	X
O75891	10-formyltetrahydrofolate dehydrogenase (EC 1,5,1,6) (10-FTHF	57.8	24	1		-
P42704	130 kDa leucine-rich protein (LRP 130) (GP130) (Leucine-rich PP	50.1	6	46	9	X
Q9NRX4	14 kDa phosphohistidine phosphatase (EC 3,1,3,-) (Phosphohist	28.8		1		-
P31946	14-3-3 protein beta/alpha (Protein kinase C inhibitor protein 1)	58.5	3	7	10	-
P62258	14-3-3 protein epsilon (14-3-3E)	71.4	6	11	16	-
Q04917	14-3-3 protein eta (Protein AS1)	50.4		6	7	-
P61981	14-3-3 protein gamma (Protein kinase C inhibitor protein 1) (KC	54.3	3	6	10	X
P31947	14-3-3 protein sigma (Stratifin) (Epithelial cell marker protein 1)	59.3		4	9	X
P27348	14-3-3 protein theta (14-3-3 protein tau) (14-3-3 protein T-cell)	58.8	2	8	12	-
P63104	14-3-3 protein zeta/delta (Protein kinase C inhibitor protein 1) (	64.5	3	11	14	X
Q9Y4L1	150 kDa oxygen-regulated protein precursor (Orp150) (Hypoxia	47.3	4	22	2	X
P15428	15-hydroxyprostaglandin dehydrogenase [NAD+] (EC 1,1,1,141)	20.3	2			-
Q7Z5P4	17-beta hydroxysteroid dehydrogenase 13 precursor (EC 1,1,-,-)	38.7	10			-
Q9C0C2	182 kDa tankyrase 1-binding protein - Homo sapiens (Human)	2.1	1		1	-
P19174	1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase gai	1		1		-
P09543	2*,3*-cyclic-nucleotide 3*-phosphodiesterase (EC 3,1,4,37) (CN	14.5		3	1	-
Q16698	2,4-dienoyl-CoA reductase, mitochondrial precursor (EC 1,3,1,3.	39.7	8			-
P62191	26S protease regulatory subunit 4 (P26s4) (Proteasome 26S sub	25.5	2	4	4	X
P17980	26S protease regulatory subunit 6A (TAT-binding protein 1) (TBI	34.2	1	8	5	X
P43686	26S protease regulatory subunit 6B (MIP224) (MB67-interacting	23.7	1	6	5	X
P35998	26S protease regulatory subunit 7 (MSS1 protein)	14.1		2	2	X
P62195	26S protease regulatory subunit 8 (Proteasome subunit p45) (p.	34.7		5	4	X
P62333	26S protease regulatory subunit S10B (Proteasome subunit p42	39.8		9	9	X
Q99460	26S proteasome non-ATPase regulatory subunit 1 (26S proteasc	5.5		2		-
O75832	26S proteasome non-ATPase regulatory subunit 10 (26S protea	16.8		1	2	-
O00231	26S proteasome non-ATPase regulatory subunit 11 (26S protea	12.8	1	3	3	X
Q9UNM6	26S proteasome non-ATPase regulatory subunit 13 (26S protea	32.2		3	7	X
O00487	26S proteasome non-ATPase regulatory subunit 14 (26S protea	22.6		3	1	X
Q13200	26S proteasome non-ATPase regulatory subunit 2 (26S proteasc	15.2		5	3	-
P55036	26S proteasome non-ATPase regulatory subunit 4 (26S proteasc	7.4			1	-
Q16401	26S proteasome non-ATPase regulatory subunit 5 (26S proteasc	17.7			4	X
P51665	26S proteasome non-ATPase regulatory subunit 7 (26S proteasc	17.3		3	1	X
P48556	26S proteasome non-ATPase regulatory subunit 8 (26S proteasc	13.2		1	3	X
O00233	26S proteasome non-ATPase regulatory subunit 9 (26S proteasc	21.1			3	X
Q13442	28 kDa heat- and acid-stable phosphoprotein (PDGF-associated	13.3		1	2	-
O15235	28S ribosomal protein S12, mitochondrial precursor (S12mt) (M	8.7		1		-
Q9Y3D3	28S ribosomal protein S16, mitochondrial precursor (S16mt) (M	29.9		3		-
Q9NVS2	28S ribosomal protein S18a, mitochondrial precursor (MRP-S18	8.2		1		-
Q9Y676	28S ribosomal protein S18b, mitochondrial precursor (MRP-S18	7.4		1		-
Q9BYN8	28S ribosomal protein S26, mitochondrial precursor (MRP-S26)	8.8		1		-
Q92665	28S ribosomal protein S31, mitochondrial precursor (S31mt) (M	5.6		2		-
P82673	28S ribosomal protein S35, mitochondrial precursor (S35mt) (M	3.1		1	1	-
Q9Y2R9	28S ribosomal protein S7, mitochondrial precursor - Homo sapi	17.4		2		-
P82933	28S ribosomal protein S9, mitochondrial precursor (S9mt) (MRF	3.3		1		-
Q9UJ83	2-hydroxyacyl-CoA lyase 1 (EC 4,1,-,-) (2-hydroxyphytanoyl-CoA	2.1	1			-
Q8N543	2-oxoglutarate and iron-dependent oxygenase domain-containi	7.4		1	2	-

Q02218	2-oxoglutarate dehydrogenase E1 component, mitochondrial pr	7.2	4	2	3	X
Q9ULD0	2-oxoglutarate dehydrogenase E1 component-like, mitochondri	4.9	2			-
P12694	2-oxoisovalerate dehydrogenase alpha subunit, mitochondrial p	9	2			-
O95861	3*(2*),5*-bisphosphate nucleotidase 1 (EC 3,1,3,7) (Bisphospha	8.8	1	2		X
Q9Y3B2	3*-5* exoribonuclease CSL4 homolog (EC 3,1,13,-) (Exosome co	8.2		1		-
P42126	3,2-trans-enoyl-CoA isomerase, mitochondrial precursor (EC 5,3	37.1	6	6	5	X
Q7Z7H8	39S ribosomal protein L10, mitochondrial precursor - Homo sap	7.3		1	1	-
Q9Y3B7	39S ribosomal protein L11, mitochondrial precursor (L11mt) (M	59.4		7	2	-
P52815	39S ribosomal protein L12, mitochondrial precursor (L12mt) (M	44.4	1	9	2	X
Q9BYD1	39S ribosomal protein L13, mitochondrial (L13mt) (MRP-L13) - t	71.3		6	3	-
Q6P1L8	39S ribosomal protein L14, mitochondrial precursor (L14mt) (M	10.3		2		-
Q9P015	39S ribosomal protein L15, mitochondrial precursor (L15mt) (M	10.8		1	1	-
Q9NRX2	39S ribosomal protein L17, mitochondrial precursor (L17mt) (M	26.3	1	4	3	-
Q9H0U6	39S ribosomal protein L18, mitochondrial precursor (L18mt) (M	14.4		2		-
P49406	39S ribosomal protein L19, mitochondrial precursor (L19mt) (M	11		2	3	-
Q9BYC9	39S ribosomal protein L20, mitochondrial precursor (L20mt) (M	21.5		2		-
Q7Z2W9	39S ribosomal protein L21, mitochondrial precursor (L21mt) (M	29.2		3		-
Q9NWU5	39S ribosomal protein L22, mitochondrial precursor (L22mt) (M	18		3		-
Q96A35	39S ribosomal protein L24, mitochondrial precursor - Homo sap	6		1		-
Q13084	39S ribosomal protein L28, mitochondrial precursor (L28mt) (M	18		1	2	-
Q9NQ50	39S ribosomal protein L40, mitochondrial precursor (L40mt) (M	15		2		-
Q8N983	39S ribosomal protein L43, mitochondrial precursor (L43mt) (M	10.2		2	2	-
Q9H9J2	39S ribosomal protein L44, mitochondrial precursor (EC 3,1,26,-	8.4		2	1	-
Q9BRJ2	39S ribosomal protein L45, mitochondrial precursor (L45mt) (M	6.5		1	1	-
Q9H2W6	39S ribosomal protein L46, mitochondrial precursor (L46mt) (M	35.8		3		-
Q9HD33	39S ribosomal protein L47, mitochondrial precursor (L47mt) (M	9.1		2		-
Q96EL3	39S ribosomal protein L53, mitochondrial precursor (L53mt) (M	36.6		2	2	-
Q7Z7F7	39S ribosomal protein L55, mitochondrial precursor - Homo sap	11.7		1		-
Q99714	3-hydroxyacyl-CoA dehydrogenase type II (EC 1,1,1,35) (Type II	91.2	12	10	10	X
P46952	3-hydroxyanthranilate 3,4-dioxygenase (EC 1,13,11,6) (3-HAO) (	37.1	5			X
Q9BUT1	3-hydroxybutyrate dehydrogenase type 2 (EC 1,1,1,30) (R-beta-	13.5	2	1	1	-
P31937	3-hydroxyisobutyrate dehydrogenase, mitochondrial precursor	54.2	8	4	3	X
Q6NVY1	3-hydroxyisobutyryl-CoA hydrolase, mitochondrial precursor - t	36.8	9	3		-
P42765	3-ketoacyl-CoA thiolase, mitochondrial (EC 2,3,1,16) (Beta-keto	62	12	3	4	-
P09110	3-ketoacyl-CoA thiolase, peroxisomal precursor (EC 2,3,1,16) (B	30.4	6	1	1	-
P25325	3-mercaptopyruvate sulfurtransferase (EC 2,8,1,2) (MST)	58.9	6	6	1	X
P51857	3-oxo-5-beta-steroid 4-dehydrogenase (EC 1,3,1,3) (Delta(4)-3-t	18.4	4	1		-
Q08752	40 kDa peptidyl-prolyl cis-trans isomerase (EC 5,2,1,8) (PPIase) (	15.9		5	1	X
P46783	40S ribosomal protein S10	57	3	6	7	-
P62280	40S ribosomal protein S11 - Homo sapiens (Human)	55.7	2	5	7	-
P25398	40S ribosomal protein S12 - Homo sapiens (Human)	37.9	3	7	3	X
P62277	40S ribosomal protein S13	39.7	3	7	5	-
P62263	40S ribosomal protein S14	70.2	3	7	8	-
P62841	40S ribosomal protein S15 (RIG protein) - Homo sapiens (Huma	40.7	2	4	2	-
P62244	40S ribosomal protein S15a	39.2	1	4	4	-
P62249	40S ribosomal protein S16	52.1	7	5	8	-
P08708	40S ribosomal protein S17 - Homo sapiens (Human)	71.1	1	6	4	-
P62269	40S ribosomal protein S18 (Ke-3) (Ke3)	55.9	6	7	12	-
P39019	40S ribosomal protein S19	58.6	4	5	9	-
P15880	40S ribosomal protein S2 (S4) (LLRep3 protein) - Homo sapiens	28		4	6	-

P60866	40S ribosomal protein S20 - Homo sapiens (Human)	41.2	4	4	4	-
P63220	40S ribosomal protein S21	66.3	2	5	4	-
P62266	40S ribosomal protein S23 - Homo sapiens (Human)	43.4	1	5	3	-
P62847	40S ribosomal protein S24 - Homo sapiens (Human)	28.6	2	2	2	-
P62851	40S ribosomal protein S25	25.6	2	4	3	-
P62854	40S ribosomal protein S26	31.3	2	2	3	-
P62979	40S ribosomal protein S27a - Homo sapiens (Human)	23.8		1	1	-
P62857	40S ribosomal protein S28	66.7	1	5	2	-
P62273	40S ribosomal protein S29 - Homo sapiens (Human)	14.3	1		1	-
P23396	40S ribosomal protein S3 - Homo sapiens (Human)	65	3	7	7	-
P61247	40S ribosomal protein S3a - Homo sapiens (Human)	60.2		11	8	-
P62701	40S ribosomal protein S4, X isoform (Single copy abundant mRNA)	47.5	1	5	10	-
P46782	40S ribosomal protein S5	43.6	3	6	4	-
P62753	40S ribosomal protein S6 (Phosphoprotein NP33)	34.5		5	6	-
P62081	40S ribosomal protein S7	67.5	6	10	8	-
P62241	40S ribosomal protein S8	44.7	2	6	4	-
P46781	40S ribosomal protein S9 - Homo sapiens (Human)	27.8		6	4	-
P08865	40S ribosomal protein SA (p40) (34/67 kDa laminin receptor) (C	58.6	1	7	11	X
Q9BRK5	45 kDa calcium-binding protein precursor (Cab45) (Stromal cell-	7.7		1		-
P80404	4-aminobutyrate aminotransferase, mitochondrial precursor (Ei	52.6	19	6		-
P08195	4F2 cell-surface antigen heavy chain (4F2hc) (Lymphocyte activi	32.9		7	10	-
P32754	4-hydroxyphenylpyruvate dioxygenase (EC 1,13,11,27) (4HPPD)	36.4	8			-
P49189	4-trimethylaminobutyraldehyde dehydrogenase (EC 1,2,1,47) (T	20.6	6			X
Q8TCD5	5*(3*)-deoxyribonucleotidase, cytosolic type (EC 3,1,3,-) (Cytos	32.3	1	2	1	-
O14841	5-oxoprolinase (EC 3,5,2,9) (5-oxo-L-prolinase) (Pyroglutamase)	5.7		3		-
P10809	60 kDa heat shock protein, mitochondrial precursor (Hsp60) (60	80.3	26	47	31	X
P10155	60 kDa SS-A/Ro ribonucleoprotein (60 kDa Ro protein) (60 kDa r	2.4		1		-
P05388	60S acidic ribosomal protein P0 (L10E)	55.2	1	11	8	X
Q8NHW5	60S acidic ribosomal protein P0-like OS=Homo sapiens PE=2 SV=	28.1		7		-
P05387	60S acidic ribosomal protein P2	82.6	3	6	4	-
P27635	60S ribosomal protein L10 (QM protein) (Tumor suppressor QM	48.1		7	4	-
Q96L21	60S ribosomal protein L10-like - Homo sapiens (Human)	17.3		1		-
P62913	60S ribosomal protein L11 (CLL-associated antigen KW-12)	46.1	2	5	6	-
P30050	60S ribosomal protein L12	66.1	3	6	7	-
P26373	60S ribosomal protein L13 (Breast basic conserved protein 1) - H	35.5	2	5	5	-
P40429	60S ribosomal protein L13a (23 kDa highly basic protein) - Homo	17.2	1	3	1	-
P50914	60S ribosomal protein L14 (CAG-ISL 7) - Homo sapiens (Human)	21.1	1	4	4	-
P61313	60S ribosomal protein L15 - Homo sapiens (Human)	30.9		4	2	-
P18621	60S ribosomal protein L17 (L23) - Homo sapiens (Human)	34.2	1	5	3	-
Q07020	60S ribosomal protein L18	30.9		4	4	-
Q02543	60S ribosomal protein L18a - Homo sapiens (Human)	34.7		6		-
P84098	60S ribosomal protein L19 - Homo sapiens (Human)	9.2		2	2	-
P46778	60S ribosomal protein L21 - Homo sapiens (Human)	36.3	1	3	2	-
P35268	60S ribosomal protein L22 (Epstein-Barr virus small RNA-associ	50.8	3	2	5	-
P62829	60S ribosomal protein L23 (Ribosomal protein L17)	40.7	2	4	4	-
P62750	60S ribosomal protein L23a - Homo sapiens (Human)	44.2	1	4	3	-
P83731	60S ribosomal protein L24 (Ribosomal protein L30) - Homo sapi	30.6	1	5	5	-
P61254	60S ribosomal protein L26	44.8		4	3	-
P61353	60S ribosomal protein L27 - Homo sapiens (Human)	36	1	3	2	-
P46776	60S ribosomal protein L27a - Homo sapiens (Human)	45.9	2	4	4	-

P46779	60S ribosomal protein L28 - Homo sapiens (Human)	29.9		2	5	-
P47914	60S ribosomal protein L29 (Cell surface heparin-binding protein	9.4		1	1	-
P39023	60S ribosomal protein L3 (HIV-1 TAR RNA-binding protein B) (TA	12.7		1	1	-
P62888	60S ribosomal protein L30	58.3	3	4	4	-
P62899	60S ribosomal protein L31 - Homo sapiens (Human)	33.6	1		3	-
P62910	60S ribosomal protein L32 - Homo sapiens (Human)	29.6	2	4	2	-
P49207	60S ribosomal protein L34 - Homo sapiens (Human)	7.7		1	2	-
P42766	60S ribosomal protein L35 - Homo sapiens (Human)	22		3	2	-
P18077	60S ribosomal protein L35a - Homo sapiens (Human)	16.4		1	1	-
Q9Y3U8	60S ribosomal protein L36 - Homo sapiens (Human)	30.5		2	2	-
P61513	60S ribosomal protein L37a - Homo sapiens (Human)	32.6		2	1	-
P63173	60S ribosomal protein L38 - Homo sapiens (Human)	50	1	2	3	-
P36578	60S ribosomal protein L4 (L1) - Homo sapiens (Human)	25.8		6	4	-
P46777	60S ribosomal protein L5 - Homo sapiens (Human)	29.3		3	4	-
Q02878	60S ribosomal protein L6 (TAX-responsive enhancer element-bi	35.8		5	7	-
P18124	60S ribosomal protein L7 - Homo sapiens (Human)	46	2	8	11	-
P62424	60S ribosomal protein L7a (Surfeit locus protein 3) (PLA-X polyp	47		8	6	-
P62917	60S ribosomal protein L8 - Homo sapiens (Human)	18.3	2	3	3	-
P32969	60S ribosomal protein L9 - Homo sapiens (Human)	45.8		5	4	-
Q01813	6-phosphofructokinase type C (EC 2,7,1,11) (Phosphofructokina	11.4			6	-
P52209	6-phosphogluconate dehydrogenase, decarboxylating (EC 1,1,1,	30.8		1	8	X
O95336	6-phosphogluconolactonase (EC 3,1,1,31) (6PGL)	58.5	2	4	6	X
P11021	78 kDa glucose-regulated protein precursor (GRP 78) (Immunog	59.8	14	38	25	X
Q92667	A kinase anchor protein 1, mitochondrial precursor (Protein kin	2.7	1	1		-
Q9NUJ1	Abhydrolase domain-containing protein 10, mitochondrial precu	11.8		1	2	-
Q8NFV4	Abhydrolase domain-containing protein 11 - Homo sapiens (Hui	17.1	1	2	2	-
Q96IU4	Abhydrolase domain-containing protein 14B (CCG1-interacting	51.9	5	6	3	X
Q8IZP0	Abl interactor 1 - Homo sapiens (Human)	2.2		1		-
Q9BWD1	Acetyl-CoA acetyltransferase, cytosolic (EC 2,3,1,9) (Cytosolic ac	45.6	3	6	2	X
P24752	Acetyl-CoA acetyltransferase, mitochondrial precursor (EC 2,3,1	53.2	13	8	3	X
Q13510	Acid ceramidase precursor (EC 3,5,1,23) (Acylsphingosine deacy	17.5		4		X
P39687	Acidic leucine-rich nuclear phosphoprotein 32 family member A	36.5	1	8	5	X
Q92688	Acidic leucine-rich nuclear phosphoprotein 32 family member B	27.9	1	7	4	-
O43423	Acidic leucine-rich nuclear phosphoprotein 32 family member C	12		1	2	-
Q9BTT0	Acidic leucine-rich nuclear phosphoprotein 32 family member E	18.3		3	2	-
Q99798	Aconitate hydratase, mitochondrial precursor (EC 4,2,1,3) (Citra	41.4	8	12	3	X
P60709	Actin, cytoplasmic 1 (Beta-actin)	70.4	10	18	25	X
P63261	Actin, cytoplasmic 2 (Gamma-actin)	70.4	10	18	25	X
P61158	Actin-like protein 3 (Actin-related protein 3)	31.1	2	4	5	X
O15143	Actin-related protein 2/3 complex subunit 1B (ARP2/3 complex	4.8			1	-
O15144	Actin-related protein 2/3 complex subunit 2 (ARP2/3 complex 3	39.7	2	2	4	X
O15145	Actin-related protein 2/3 complex subunit 3 (ARP2/3 complex 2	25.3	3	3	4	-
P59998	Actin-related protein 2/3 complex subunit 4 (ARP2/3 complex 2	17.3		1	2	-
O15511	Actin-related protein 2/3 complex subunit 5 (ARP2/3 complex 1	20.5	1	2	1	X
Q9BPX5	Actin-related protein 2/3 complex subunit 5-like protein - Homc	7.8	1	1	1	X
P53999	Activated RNA polymerase II transcriptional coactivator p15 (SU	33.1		4	3	-
O95433	Activator of 90 kDa heat shock protein ATPase homolog 1 (AHA	11.2		2	1	X
Q13705	Activin receptor type-2B precursor - Homo sapiens (Human)	7.2		1		-
P13798	Acylamino-acid-releasing enzyme (EC 3,4,19,1) (AARE) (Acyl-pep	13.3	2	5	3	X
P11310	Acyl-CoA dehydrogenase, medium-chain specific, mitochondria	27.8	7	4	3	X

P45954	Acyl-CoA dehydrogenase, short/branched chain specific, mitochondr	50.5	8	5		X
P16219	Acyl-CoA dehydrogenase, short-chain specific, mitochondrial pr	26.2	5	3		X
P49748	Acyl-CoA dehydrogenase, very-long-chain specific, mitochondri	20.5	7	4	3	X
Q4G176	Acyl-CoA synthetase family member 3, mitochondrial precursor	2.3	1	1		-
Q9H6R3	Acyl-CoA synthetase short-chain family member 3, mitochondri	9	1	2		-
P07108	Acyl-CoA-binding protein (ACBP) (Diazepam-binding inhibitor) (I	70.1	8	3	2	-
Q08AH3	Acyl-coenzyme A synthetase ACSM2A, mitochondrial precursor	26.5	10			-
Q68CK6	Acyl-coenzyme A synthetase ACSM2B, mitochondrial precursor	31.2	10			-
Q6NUN0	Acyl-coenzyme A synthetase MACS3, mitochondrial precursor -	7.1	3			-
Q86TX2	Acyl-coenzyme A thioesterase 1 (EC 3,1,2,2) (Acyl-CoA thioester	21.1	5	3		-
P49753	Acyl-coenzyme A thioesterase 2 (EC 3,1,2,2) (Acyl-CoA thioester	24.6	5	4		-
O75608	Acyl-protein thioesterase 1 (EC 3,1,2,-) (Lysophospholipase I)	46.5	4	5	4	X
O95372	Acyl-protein thioesterase 2 (EC 3,1,2,-) (Lysophospholipase II) (L	26.8		3	2	X
Q9UKF5	ADAM 29 precursor - Homo sapiens (Human)	2.7			1	-
P07741	Adenine phosphoribosyltransferase (EC 2,4,2,7) (APRT)	70.6	6	10	7	X
P55263	Adenosine kinase (EC 2,7,1,20) (AK) (Adenosine 5*-phosphotrar	20.7	4	3	1	X
P23526	Adenosylhomocysteinase (EC 3,3,1,1) (S-adenosyl-L-homocystei	35.9	6	8	8	X
P00568	Adenylate kinase isoenzyme 1 (EC 2,7,4,3) (ATP-AMP transphos	50	3	5	5	-
P54819	Adenylate kinase isoenzyme 2, mitochondrial (EC 2,7,4,3) (ATP-	75.3	7	9	7	X
P27144	Adenylate kinase isoenzyme 4, mitochondrial (EC 2,7,4,3) (Ader	72.6	3	6		-
Q9Y6K8	Adenylate kinase isoenzyme 5 (EC 2,7,4,3) (ATP-AMP transphos	4.5			1	-
P30566	Adenylosuccinate lyase (EC 4,3,2,2) (Adenylosuccinase) (ASL) (A	11.6		1	2	X
P30520	Adenylosuccinate synthetase isozyme 2 (EC 6,3,4,4) (Adenylosu	12.5		2	4	X
Q01518	Adenylyl cyclase-associated protein 1 (CAP 1)	34.3	1	5	6	X
P40123	Adenylyl cyclase-associated protein 2 (CAP 2)	4.4		1		X
Q9HDC9	Adipocyte plasma membrane-associated protein (BSCv protein)	10.6	1	1		X
Q99541	Adipophilin (Adipose differentiation-related protein) (ADRP) - H	25.2		4		-
P12235	ADP/ATP translocase 1 (Adenine nucleotide translocator 1) (AN	6.7		1		-
P05141	ADP/ATP translocase 2 (Adenine nucleotide translocator 2) (AN	14.8		1	3	-
P12236	ADP/ATP translocase 3 (Adenine nucleotide translocator 2) (AN	11.1			2	-
P84077	ADP-ribosylation factor 1	70.7	7	10	4	-
P61204	ADP-ribosylation factor 3	70.7			4	-
P18085	ADP-ribosylation factor 4	65.6	4	8	3	-
P84085	ADP-ribosylation factor 5	47.8	4	5		-
P62330	ADP-ribosylation factor 6 - Homo sapiens (Human)	38.9	6	1		-
Q9UJY4	ADP-ribosylation factor-binding protein GGA2 (Golgi-localized, ξ	4.6		1		-
P40616	ADP-ribosylation factor-like protein 1	22.7		3		-
P36404	ADP-ribosylation factor-like protein 2	25		3	1	X
Q9Y2Y0	ADP-ribosylation factor-like protein 2-binding protein - Homo sa	17.2		1	1	-
P36405	ADP-ribosylation factor-like protein 3 - Homo sapiens (Human)	6		1	1	-
Q9UKK9	ADP-sugar pyrophosphatase (EC 3,6,1,13) (EC 3,6,1,-) (Nucleosic	34.2	3	5	6	X
P10109	Adrenodoxin, mitochondrial precursor (Adrenal ferredoxin) (Fer	26.1	2	1		-
O75366	Advillin (p92) - Homo sapiens (Human)	1.2		1		-
P55196	Afadin (Protein AF-6) - Homo sapiens (Human)	0.9		1		-
O43488	Aflatoxin B1 aldehyde reductase member 2 (EC 1,-,-,-) (AFB1-AR	23.7	3	3		X
O95154	Aflatoxin B1 aldehyde reductase member 3 (EC 1,-,-,-) (AFB1-AR	39.6	8			-
Q8NHP1	Aflatoxin B1 aldehyde reductase member 4 (EC 1,-,-,-) (Fragmer	12.4	2			-
Q9BSE5	Agmatinase, mitochondrial precursor (EC 3,5,3,11) (Agmatine u	21.9	4	6		-
O00468	Agrin precursor	1.4		1		-
O00170	AH receptor-interacting protein (AIP) (Aryl-hydrocarbon recept	19.7		4	3	X

Q9UKA4	A-kinase anchor protein 11 - Homo sapiens (Human)	1	1			-
O43823	A-kinase anchor protein 8 - Homo sapiens (Human)	2.9		1		-
P24298	Alanine aminotransferase (EC 2,6,1,2) (Glutamic--pyruvic transa	29.4	5			X
Q8TD30	Alanine aminotransferase 2 (EC 2,6,1,2) (ALT2) (Glutamic--pyruv	8		2		-
P49588	Alanyl-tRNA synthetase (EC 6,1,1,7) (Alanine--tRNA ligase) (AlaF	42.5	4	18	16	X
P14550	Alcohol dehydrogenase [NADP+] (EC 1,1,1,2) (Aldehyde reducta	56	6	7	1	X
P07327	Alcohol dehydrogenase 1A (EC 1,1,1,1) (Alcohol dehydrogenase	61.6	23			-
P00325	Alcohol dehydrogenase 1B (EC 1,1,1,1) (Alcohol dehydrogenase	79.2	32			-
P00326	Alcohol dehydrogenase 1C (EC 1,1,1,1) (Alcohol dehydrogenase	57.6	21			-
P08319	Alcohol dehydrogenase 4 (EC 1,1,1,1) (Alcohol dehydrogenase c	81.8	18	1		X
P28332	Alcohol dehydrogenase 6 (EC 1,1,1,1) - Homo sapiens (Human)	32.9	5			-
P11766	Alcohol dehydrogenase class 3 chi chain (EC 1,1,1,1) (Alcohol de	25.1	1	1		X
Q8IZ83	Aldehyde dehydrogenase family 16 member A1 - Homo sapiens	4.6	2	3	2	-
P49419	Aldehyde dehydrogenase family 7 member A1 (EC 1,2,1,3) (Anti	39.3	6	9	6	X
Q9H2A2	Aldehyde dehydrogenase family 8 member A1 - Homo sapiens (	28.7	6			-
P30837	Aldehyde dehydrogenase X, mitochondrial precursor (EC 1,2,1,3)	40	8	11	1	X
P05091	Aldehyde dehydrogenase, mitochondrial precursor (EC 1,2,1,3)	54.9	17	6		X
Q06278	Aldehyde oxidase (EC 1,2,3,1) - Homo sapiens (Human)	3.9	2			-
O60218	Aldo-keto reductase family 1 member B10 (EC 1,1,1,-) (Aldose r	24.1		5		-
Q04828	Aldo-keto reductase family 1 member C1 (EC 1,1,1,-) (20-alpha-	87.9	7	21	9	-
P52895	Aldo-keto reductase family 1 member C2 (EC 1,-,-,-) (Trans-1,2-c	85.4	6	13	10	-
P42330	Aldo-keto reductase family 1 member C3 (EC 1,-,-,-) (Trans-1,2-c	70.9	5	14	11	-
P17516	Aldo-keto reductase family 1 member C4 (EC 1,1,1,-) (Chlordecc	65.3	9			-
Q96JD6	Aldo-keto reductase family 1 member C-like protein 2 - Homo s	2.5		1		-
Q96C23	Aldose 1-epimerase (EC 5,1,3,3) (Galactose mutarotase) (BLOCK	11.4		2		X
P15121	Aldose reductase (EC 1,1,1,21) (AR) (Aldehyde reductase)	48.7		4	8	X
P05186	Alkaline phosphatase, tissue-nonspecific isozyme precursor (EC	16.4			5	-
P35221	Alpha-1 catenin (Cadherin-associated protein) (Alpha E-catenin]	6.6			4	-
P02763	Alpha-1-acid glycoprotein 1 precursor (AGP 1) (Orosomuroid-1)	11.9	2			-
P02765	Alpha-2-HS-glycoprotein precursor (Fetuin-A) (Alpha-2-Z-globul	5.4		1		-
P01023	Alpha-2-macroglobulin precursor (Alpha-2-M)	5.3	1	3		-
P30533	Alpha-2-macroglobulin receptor-associated protein precursor (A	9		3		-
P12814	Alpha-actinin-1 (Alpha-actinin cytoskeletal isoform) (Non-muscl	45.3	5	19	19	X
P35609	Alpha-actinin-2 (Alpha actinin skeletal muscle isoform 2) (F-acti	11.1			8	-
O43707	Alpha-actinin-4 (Non-muscle alpha-actinin 4) (F-actin cross linki	68.9	9	26	39	X
Q9UDR5	Alpha-aminoacidic semialdehyde synthase, mitochondrial precu	24.9	10	1		-
P61163	Alpha-centractin (Centractin) (Centrosome-associated actin hor	20.2		2	2	X
P06733	Alpha-enolase (EC 4,2,1,11) (2-phospho-D-glycerate hydro-lyase	85.9	16	32	26	X
P02771	Alpha-fetoprotein precursor (Alpha-fetoglobulin) (Alpha-1-feto	20.5		7	1	X
P17050	Alpha-N-acetylgalactosaminidase precursor (EC 3,2,1,49) (Alpha	4.9		1		X
P54920	Alpha-soluble NSF attachment protein (SNAP-alpha) (N-ethylma	22.7	3	1	3	X
P40222	Alpha-taxilin - Homo sapiens (Human)	3.5		1		-
P02760	AMBP protein precursor [Contains: Alpha-1-microglobulin (Prot	9.1	1	1		-
P21397	Amine oxidase [flavin-containing] A (EC 1,4,3,4) (Monoamine ox	2.3	2			-
P27338	Amine oxidase [flavin-containing] B (EC 1,4,3,4) (Monoamine ox	16.2	4			-
Q8IYS1	Aminoacylase 1-like protein 2 - Homo sapiens (Human)	6		1		-
Q03154	Aminoacylase-1 (EC 3,5,1,14) (N-acyl-L-amino-acid amidohydrol	40.7	6	5		X
Q9H4A4	Aminopeptidase B (EC 3,4,11,6) (Ap-B) (Arginyl aminopeptidase	5.8			2	X
P15144	Aminopeptidase N (EC 3,4,11,2) (hAPN) (Alanyl aminopeptidase	8.4		4		-
Q06481	Amyloid-like protein 2 precursor (Amyloid protein homolog) (Af	2.6		1		-

Q6FI81	Anamorsin (Cytokine-induced apoptosis inhibitor 1) (CUA001) -	20.2		3	2	-
Q13685	Angio-associated migratory cell protein - Homo sapiens (Humar	5.5		2		-
P01019	Angiotensinogen precursor [Contains: Angiotensin-1 (Angiotens	20	1	4		X
Q9NXR5	Ankyrin repeat domain-containing protein 10 - Homo sapiens (H	2.6		1		-
P04083	Annexin A1 (Annexin I) (Lipocortin I) (Calpactin II) (Chromobindi	69.1			19	X
P50995	Annexin A11 (Annexin XI) (Calcyclin-associated annexin 50) (CAI	6.3			2	X
P07355	Annexin A2 (Annexin II) (Lipocortin II) (Calpactin I heavy chain) (	74.3	1	1	30	X
P12429	Annexin A3 (Annexin III) (Lipocortin III) (Placental anticoagulant	35		5	7	X
P09525	Annexin A4 (Annexin IV) (Lipocortin IV) (Endonexin	58.6	6	8	6	X
P08758	Annexin A5 (Annexin V) (Lipocortin V) (Endonexin II) (Calphobin	57.2	6	14	17	X
P08133	Annexin A6 (Annexin VI) (Lipocortin VI) (P68) (P70) (Protein III) (	52.6	19	9	15	X
P20073	Annexin A7 (Annexin VII) (Synexin)	12.9	2	2	1	X
Q10567	AP-1 complex subunit beta-1 (Adapter-related protein complex	5.2		3	2	-
P63010	AP-2 complex subunit beta-1 (Adapter-related protein complex	2.9		1		-
Q9NQ94	APOBEC1 complementation factor (APOBEC1-stimulating protei	4	1	1		-
P02647	Apolipoprotein A-I precursor (Apo-AI) (ApoA-I) [Contains: Apoli	40.4	6	10	1	X
Q8NCW5	Apolipoprotein A-I-binding protein precursor - Homo sapiens (H	22.6	3	3	2	-
P02656	Apolipoprotein C-III precursor (Apo-CIII) (ApoC-III) - Homo sapie	19.2	1			-
P02649	Apolipoprotein E precursor (Apo-E) - Homo sapiens (Human)	59.6	5	12		-
Q9BQE5	Apolipoprotein-L2 (Apolipoprotein L-II) (ApoL-II)	6.5	1	1		X
Q07812	Apoptosis regulator BAX, membrane isoform alpha	6.8		1		-
Q9ULZ3	Apoptosis-associated speck-like protein containing a CARD (hAS	12.8		2		X
O95831	Apoptosis-inducing factor 1, mitochondrial precursor (EC 1,-,-,-)	31.3	3	3	1	-
Q9UKV3	Apoptotic chromatin condensation inducer in the nucleus - Hon	1.4		1		-
P05089	Arginase-1 (EC 3,5,3,1) (Type I arginase) (Liver-type arginase)	71.7	12			X
P04424	Argininosuccinate lyase (EC 4,3,2,1) (Arginosuccinase) (ASAL) - H	19.2	6			-
P00966	Argininosuccinate synthase (EC 6,3,4,5) (Citrulline--aspartate lig	59.2	17		12	-
P55145	ARMET protein precursor (Arginine-rich protein) - Homo sapien	46.4	3	6	5	-
Q9BXP5	Arsenite-resistance protein 2 - Homo sapiens (Human)	2.7		1		-
P08243	Asparagine synthetase [glutamine-hydrolyzing] (EC 6,3,5,4) (Glu	4.1		1	1	-
Q9NWL6	Asparagine synthetase domain-containing protein 1 - Homo sap	2.5		1		-
O43776	Asparaginyl-tRNA synthetase, cytoplasmic (EC 6,1,1,22) (Aspara	2.6		1		-
P17174	Aspartate aminotransferase, cytoplasmic (EC 2,6,1,1) (Transami	58.4	7	8	6	X
P00505	Aspartate aminotransferase, mitochondrial precursor (EC 2,6,1,	56	10	8	6	-
Q9ULA0	Aspartyl aminopeptidase (EC 3,4,11,21) - Homo sapiens (Humar	2.5			1	X
P14868	Aspartyl-tRNA synthetase (EC 6,1,1,12) (Aspartate--tRNA ligase)	19.6	1	7	2	X
Q8WWM7	Ataxin-2-like protein (Ataxin-2 domain protein) (Ataxin-2-relate	2		1		-
P25705	ATP synthase alpha chain, mitochondrial precursor (EC 3,6,3,14	58.8	16	18	22	X
P24539	ATP synthase B chain, mitochondrial precursor (EC 3,6,3,14)	18.4	2	2		-
P06576	ATP synthase beta chain, mitochondrial precursor (EC 3,6,3,14)	70.3	16	26	19	X
P18859	ATP synthase coupling factor 6, mitochondrial precursor (EC 3,6	40.7	3			-
O75947	ATP synthase D chain, mitochondrial (EC 3,6,3,14)	80.1	7	8	6	X
P30049	ATP synthase delta chain, mitochondrial precursor (EC 3,6,3,14)	19	3	2	1	X
P56385	ATP synthase e chain, mitochondrial (EC 3,6,3,14) - Homo sapie	49.3	3	2	2	-
P56134	ATP synthase f chain, mitochondrial (EC 3,6,3,14)	25.5		2	1	-
P36542	ATP synthase gamma chain, mitochondrial precursor (EC 3,6,3,1	37.2	8	4	5	-
P48047	ATP synthase O subunit, mitochondrial precursor (EC 3,6,3,14) (	78.9	11	15	8	-
O75964	ATP synthase subunit g, mitochondrial (EC 3,6,3,14) (ATPase sul	58.3	4	3	4	-
Q99766	ATP synthase subunit s, mitochondrial precursor (ATP synthase	5.1		1		-
Q9NVI7	ATPase family AAA domain-containing protein 3A - Homo sapie	2.2		1	1	-

Q9UII2	ATPase inhibitor, mitochondrial precursor - Homo sapiens (Hurr	7.5			1	-
Q96S55	ATPase WRNIP1 (Werner helicase-interacting protein 1) - Homo	2.7		1		-
P61221	ATP-binding cassette sub-family E member 1 (RNase L inhibitor)	6.5			2	-
P53396	ATP-citrate synthase (EC 2,3,3,8) (ATP-citrate (pro-S)-lyase) (Cit	30.2		9	11	-
O76031	ATP-dependent Clp protease ATP-binding subunit ClpX-like, mit	7.9		2	1	-
P12956	ATP-dependent DNA helicase 2 subunit 1 (EC 3,6,1,-) (ATP-depe	42.2		12	7	X
P13010	ATP-dependent DNA helicase 2 subunit 2 (EC 3,6,1,-) (ATP-depe	35.8	1	11	2	-
Q08211	ATP-dependent RNA helicase A (EC 3,6,1,-) (Nuclear DNA helica	3.6		3		-
Q92499	ATP-dependent RNA helicase DDX1 (EC 3,6,1,-) (DEAD box prote	26.6		4	5	-
Q9NUU7	ATP-dependent RNA helicase DDX19A (EC 3,6,1,-) (DEAD box pr	9.8		1	2	X
Q9UHL0	ATP-dependent RNA helicase DDX25 - Homo sapiens (Human)	2.3			1	-
O00148	ATP-dependent RNA helicase DDX39 (EC 3,6,1,-) (DEAD box pro	8.4		1		-
O00571	ATP-dependent RNA helicase DDX3X (EC 3,6,1,-) (DEAD box pro	23.6		6	7	X
O15523	ATP-dependent RNA helicase DDX3Y (EC 3,6,1,-) (DEAD box pro	18.8		4	4	X
Q86XP3	ATP-dependent RNA helicase DDX42 - Homo sapiens (Human)	6.1		2		-
Q99856	AT-rich interactive domain-containing protein 3A - Homo sapier	7.8		3		-
Q8IVW6	AT-rich interactive domain-containing protein 3B - Homo sapier	2.9		1		-
O95816	BAG family molecular chaperone regulator 2 (BCL2-associated a	53.6		5	4	-
O43491	Band 4,1-like protein 2 (Generally expressed protein 4,1) (4,1G)	6.2		3		-
O75531	Barrier-to-autointegration factor (Breakpoint cluster region pro	62.9		2	3	-
P11362	Basic fibroblast growth factor receptor 1 precursor - Homo sapi	1			1	-
P35613	Basigin precursor (Leukocyte activation antigen M6) (Collagena	25.7		5	2	-
Q13884	Beta-1-syntrophin (59 kDa dystrophin-associated protein A1 ba	3.5		1		-
P02749	Beta-2-glycoprotein 1 precursor (Beta-2-glycoprotein I) (Apolip	4.3		1		-
P61769	Beta-2-microglobulin precursor [Contains: Beta-2-microglobulin	46.2	2		2	X
P13929	Beta-enolase (EC 4,2,1,11) (2-phospho-D-glycerate hydro-lyase)	32.7	7	6	5	-
P16278	Beta-galactosidase precursor (EC 3,2,1,23) (Lactase) (Acid beta-	18.9	1	5	1	-
P08236	Beta-glucuronidase precursor (EC 3,2,1,31) (Beta-G1) - Homo sa	1.2	1			-
P06865	Beta-hexosaminidase alpha chain precursor (EC 3,2,1,52) (N-ace	3.6		1		-
P07686	Beta-hexosaminidase beta chain precursor (EC 3,2,1,52) (N-ace	18.2	1	6	1	X
Q93088	Betaine--homocysteine S-methyltransferase (EC 2,1,1,5)	54.9	14			X
Q9H2M3	Betaine--homocysteine S-methyltransferase 2 - Homo sapiens (	8.5	2			-
Q9H115	Beta-soluble NSF attachment protein (SNAP-beta) (N-ethylmale	11.4	1		1	-
Q9UBR1	Beta-ureidopropionase (EC 3,5,1,6) (Beta-alanine synthase) (N-c	2.3	1			-
P55957	BH3 interacting domain death agonist (BID)	34.9	4	3	1	X
O43252	Bifunctional 3*-phosphoadenosine 5*-phosphosulfate syntheta	9.3		3	1	-
O95340	Bifunctional 3*-phosphoadenosine 5*-phosphosulfate syntheta	28.2		1	6	-
P07814	Bifunctional aminoacyl-tRNA synthetase [Includes: Glutamyl-tRI	20.2		9	6	-
Q13057	Bifunctional coenzyme A synthase (CoA synthase) (NBP) (POV-2	15.6		2	2	X
P13995	Bifunctional methylenetetrahydrofolate dehydrogenase/cyclohe	25.4		2		-
P31939	Bifunctional purine biosynthesis protein PURH [Includes: Phosp	56.8	1	20	11	X
Q14032	Bile acid CoA:amino acid N-acyltransferase (EC 2,3,1,65) (BAT) (	8.1	3			-
Q9Y2P5	Bile acyl-CoA synthetase (EC 6,2,1,7) (BACS) (Bile acid CoA ligase	11.2	4			-
Q06520	Bile-salt sulfotransferase (EC 2,8,2,14) (Hydroxysteroid Sulfotra	38.2	8	7		X
P53004	Biliverdin reductase A precursor (EC 1,3,1,24) (Biliverdin-IX alph	33.4		4	3	X
Q9H3K6	BolA-like protein 2	69.8		2	4	X
P80723	Brain acid soluble protein 1 (BASP1 protein) (Neuronal axonal n	44.9			3	-
Q9Y5U8	Brain protein 44-like protein - Homo sapiens (Human)	19.3	1			-
P54687	Branched-chain-amino-acid aminotransferase, cytosolic (EC 2,6,	5.4			2	-
Q9UIG0	Bromodomain adjacent to zinc finger domain protein 1B (Willia	3.8		2		-

Q9P203	BTB/POZ domain-containing protein 7 - Homo sapiens (Human)	1.8		1		-
P11586	C-1-tetrahydrofolate synthase, cytoplasmic (C1-THF synthase) [	52.2	21	16	13	-
P49593	Ca(2+)/calmodulin-dependent protein kinase phosphatase (EC 3	2.2		1		-
P27708	CAD protein [Includes: Glutamine-dependent carbamoyl-phosp	0.5	1			-
Q99828	Calcium and integrin-binding protein 1 (Calmyrin) (DNA-PKcs-in	7.9		1		-
O75746	Calcium-binding mitochondrial carrier protein Aralar1 (Mitocho	3.7	2	2		-
Q9UJS0	Calcium-binding mitochondrial carrier protein Aralar2 (Mitocho	14.7	4	3		-
Q6NUK1	Calcium-binding mitochondrial carrier protein SCaMC-1 - Homo	3.4		1	1	-
Q9Y2V2	Calcium-regulated heat stable protein 1 (Calcium-regulated hea	51	2	2		-
P06703	Calcyclin (Prolactin receptor-associated protein) (PRA) (Growth	30			4	X
Q9HB71	Calcyclin-binding protein (CacyBP) (hCacyBP) (Siah-interacting p	49.1		2	7	-
Q05682	Caldesmon (CDM)	6.3			3	X
P31949	Calgizzarin (S100 calcium-binding protein A11) (S100C protein) i	56.2		2	8	-
P05109	Calgranulin A (Migration inhibitory factor-related protein 8) (MI	24.7	2		1	X
P06702	Calgranulin B (Migration inhibitory factor-related protein 14) (M	13.2	1		1	X
P62158	Calmodulin (CaM)	45.6	4	4	1	-
P27824	Calnexin precursor (Major histocompatibility complex class I an	22.8		6	3	-
P60903	Calpactin I light chain (S100 calcium-binding protein A10) (p10 p	27.8			2	X
P04632	Calpain small subunit 1 (CSS1) (Calcium-dependent protease sr	52.6	2	5	6	X
Q9Y6Q1	Calpain-6 - Homo sapiens (Human)	4.2	1			-
Q99439	Calponin-2 (Calponin H2, smooth muscle) (Neutral calponin)	22.3		6	3	X
Q15417	Calponin-3 (Calponin, acidic isoform)	21.9		5		X
P27797	Calreticulin precursor (CRP55) (Calregulin) (HACBP) (ERp60) (gr	46	5	6	6	X
O43852	Calumenin precursor (Crocabin) (IEF SSP 9302) - Homo sapiens	22.9		2	2	-
P10644	cAMP-dependent protein kinase type I-alpha regulatory subunit	4.7			1	X
P13861	cAMP-dependent protein kinase type II-alpha regulatory subuni	2.7	1			-
P56211	cAMP-regulated phosphoprotein 19 (ARPP-19) - Homo sapiens i	9.8		1		-
P31327	Carbamoyl-phosphate synthase [ammonia], mitochondrial prec	73.1	80		53	X
Q9UHH6	Carbohydrate kinase-like protein (EC 2,7,1,-) - Homo sapiens (H	12.8	1	4		-
P00918	Carbonic anhydrase 2 (EC 4,2,1,1) (Carbonic anhydrase II) (Carb	48.5	8			X
P16152	Carbonyl reductase [NADPH] 1 (EC 1,1,1,184) (NADPH-depende	57.4	9	10	11	X
O75828	Carbonyl reductase [NADPH] 3 (EC 1,1,1,184) (NADPH-depende	21.7	3	2	5	X
Q8N4T8	Carbonyl reductase 4 - Homo sapiens (Human)	5.1	1	1		-
O00748	Carboxylesterase 2 precursor (EC 3,1,1,1) (CE-2) (hCE-2) - Homo	9.3	2			-
Q96DG6	Carboxymethylenebutenolidase homolog - Homo sapiens (Hum	31.8	3		2	-
P13688	Carcinoembryonic antigen-related cell adhesion molecule 1 pre	10.6		2		-
P43155	Carnitine O-acetyltransferase (EC 2,3,1,7) (Carnitine acetylase) (	2.4	1			-
P23786	Carnitine O-palmitoyltransferase 2, mitochondrial precursor (EC	14.9	4	1	1	-
P68400	Casein kinase II subunit alpha (EC 2,7,11,1) (CK II) - Homo sapie	13.3		3	1	-
P19784	Casein kinase II subunit alpha* (EC 2,7,11,1) (CK II) - Homo sapie	4.6			1	-
P67870	Casein kinase II subunit beta (CK II beta) (Phosvitin) (G5a)	16.7		1	1	-
P42574	Caspase-3 precursor (EC 3,4,22,-) (CASP-3) (Apopain) (Cysteine p	7.9		1		X
P55212	Caspase-6 precursor (EC 3,4,22,-) (CASP-6) (Apoptotic protease	2.7		1		-
Q9BXW7	Cat eye syndrome critical region protein 5 precursor - Homo sa	9.7			2	-
P04040	Catalase (EC 1,11,1,6)	59.2	17	6	4	X
P21964	Catechol O-methyltransferase (EC 2,1,1,6)	55	6	5	1	X
Q86VU5	Catechol-O-methyltransferase domain-containing protein 1 (EC	10.3	1	1	1	-
P35222	Catenin beta-1 (Beta-catenin) - Homo sapiens (Human)	1.5		1		-
O60716	Catenin delta-1 (p120 catenin) (p120(ctn)) (Cadherin-associated	9.1		4	1	-
P07858	Cathepsin B precursor (EC 3,4,22,1) (Cathepsin B1) (APP secreta	33.3	5	6		X

P07339	Cathepsin D precursor (EC 3,4,23,5) [Contains: Cathepsin D light	41.3	7	9	5	X
P09668	Cathepsin H precursor (EC 3,4,22,16) [Contains: Cathepsin H mi	5.1		1		-
Q9UBR2	Cathepsin Z precursor (EC 3,4,22,-) (Cathepsin X) (Cathepsin P)	7.6	1			X
P11717	Cation-independent mannose-6-phosphate receptor precursor	0.5		1		-
P16070	CD44 antigen precursor (Phagocytic glycoprotein I) (PGP-1) (HU	3			1	-
P13987	CD59 glycoprotein precursor (Membrane attack complex inhibi	28.1		3	2	-
P48960	CD97 antigen precursor (Leukocyte antigen CD97) - Homo sapie	5.1			2	-
Q15642	Cdc42-interacting protein 4 (Thyroid receptor-interacting prote	4.2			1	-
Q8N5K1	CDGSH iron sulfur domain-containing protein 2 - Homo sapiens	19.3	2	2		-
Q8TDN4	CDK5 and ABL1 enzyme substrate 1 - Homo sapiens (Human)	3.8	1			-
Q9BY67	Cell adhesion molecule 1 precursor - Homo sapiens (Human)	10.6		1		-
Q8IZL9	Cell cycle-related kinase - Homo sapiens (Human)	2.3			1	-
P06493	Cell division control protein 2 homolog (EC 2,7,11,22) (EC 2,7,11	48.8			10	-
P60953	Cell division control protein 42 homolog precursor (G25K GTP-b	16.8	1	2	2	X
Q9NYV4	Cell division cycle 2-related protein kinase 7 - Homo sapiens (Hu	0.5			1	-
O75794	Cell division cycle protein 123 homolog - Homo sapiens (Human	7.4			2	-
P24941	Cell division protein kinase 2 (EC 2,7,11,22) (p33 protein kinase)	15.8			3	-
Q00526	Cell division protein kinase 3 (EC 2,7,1,37)	10.8			3	-
P11802	Cell division protein kinase 4 (EC 2,7,1,37) (Cyclin-dependent kir	26.7			5	X
P43121	Cell surface glycoprotein MUC18 precursor (Melanoma-associa	3.3		1	1	-
P62633	Cellular nucleic acid-binding protein (CNBP) (Zinc finger protein	57.6		4	5	-
Q1MSJ5	Centrosome and spindle pole-associated protein 1 - Homo sapie	1.3		1	1	-
Q01850	Cerebellar degeneration-related protein 2 - Homo sapiens (Hun	2.2		1		-
P00450	Ceruloplasmin precursor (EC 1,16,3,1) (Ferroxidase)	3.1	1	1		X
Q8NI60	Chaperone-activity of bc1 complex-like, mitochondrial precursor	4.6	1	1		-
Q9BY43	Charged multivesicular body protein 4a (Chromatin-modifying p	11.3		3		-
Q9H444	Charged multivesicular body protein 4b (Chromatin-modifying p	21.4		3	1	-
Q9NZZ3	Charged multivesicular body protein 5 (Chromatin-modifying pr	7.3		1		-
A5A3E0	Chimeric POTE-actin protein - Homo sapiens (Human)	8.3		6		-
O00299	Chloride intracellular channel protein 1 (Nuclear chloride ion ch	77.2	1	10	9	X
Q9Y696	Chloride intracellular channel protein 4 (Intracellular chloride io	33.6		3	2	X
Q9NZA1	Chloride intracellular channel protein 5 - Homo sapiens (Humar	6.3		2	1	-
Q8NE62	Choline dehydrogenase, mitochondrial precursor (EC 1,1,99,1) (	5.1	2			-
P49585	Choline-phosphate cytidylyltransferase A (EC 2,7,7,15) (Phospho	7.9		1		-
P83916	Chromobox protein homolog 1 (Heterochromatin protein 1 hon	8.6			1	-
Q13185	Chromobox protein homolog 3 (Heterochromatin protein 1 hon	42.6		5	5	X
Q8TD26	Chromodomain-helicase-DNA-binding protein 6 - Homo sapiens	0.8		1		-
Q8N0X4	Citrate lyase subunit beta-like protein, mitochondrial precursor	30	7			-
O75390	Citrate synthase, mitochondrial precursor (EC 2,3,3,1)	42.3		4	5	-
P09496	Clathrin light chain A (Lca) - Homo sapiens (Human)	5.2		1		-
P09497	Clathrin light chain B (Lcb) - Homo sapiens (Human)	4.4			1	-
O43809	Cleavage and polyadenylation specificity factor 5 (Cleavage and	46.7		4	2	-
Q16630	Cleavage and polyadenylation specificity factor 6 (Cleavage and	7.1		2		-
P10909	Clusterin precursor (Complement-associated protein SP-40,40)	14.9	1		3	X
Q99417	C-Myc-binding protein (Associate of Myc 1) (AMY-1)	19.4			1	-
O43598	c-Myc-responsive protein Rcl	25.3	2	4	1	X
Q14019	Coactosin-like protein	37.3			5	X
P00742	Coagulation factor X precursor (EC 3,4,21,6) (Stuart factor) (Stu	3.1			1	-
P53618	Coatomer subunit beta (Beta-coat protein) (Beta-COP)	8		4		-
P48444	Coatomer subunit delta (Delta-coat protein) (Delta-COP) (Arch	6.3		2	2	X

O14579	Coatomer subunit epsilon (Epsilon-coat protein) (Epsilon-COP)	43.2	1	3	3	X
Q9Y678	Coatomer subunit gamma (Gamma-coat protein) (Gamma-COP)	1.4		1		-
P61923	Coatomer subunit zeta-1 (Zeta-1 coat protein) (Zeta-1 COP) - Homo sapiens	15.3		1	1	-
Q96EY8	Cob(I)yrinic acid a,c-diamide adenosyltransferase, mitochondrial	10.4	2	1	1	-
P23528	Cofilin-1 (Cofilin, non-muscle isoform) (18 kDa phosphoprotein)	84.3	6	13	16	X
Q9Y281	Cofilin-2 (Cofilin, muscle isoform)	68.1	4	8	11	X
Q96CT7	Coiled-coil domain-containing protein 124 - Homo sapiens (Human)	10.3		2	1	-
Q9BSH4	Coiled-coil domain-containing protein 44 - Homo sapiens (Human)	3.4	1			-
Q4VC31	Coiled-coil domain-containing protein 58 - Homo sapiens (Human)	41	1	4	2	-
Q9Y6H1	Coiled-coil-helix-coiled-coil-helix domain-containing protein 2 (Hs)	18.5		1	1	-
Q9NX63	Coiled-coil-helix-coiled-coil-helix domain-containing protein 3 - Homo sapiens	12.3		2	1	-
O75534	Cold shock domain-containing protein E1 (UNR protein) (N-ras u)	4.8	1	1	2	X
Q14011	Cold-inducible RNA-binding protein (Glycine-rich RNA-binding p	22.7		2		-
P02462	Collagen alpha-1(IV) chain precursor	0.9			1	-
Q17RW2	Collagen alpha-1(XXIV) chain precursor - Homo sapiens (Human)	3.7		1		-
P50454	Collagen-binding protein 2 precursor (Colligin 2) (Rheumatoid a	48.1		9	11	-
Q9UBI1	COMM domain-containing protein 3 (Bup protein) (PIL protein)	23.6		1	2	X
P01024	Complement C3 precursor [Contains: Complement C3 beta chain]	1.9	1	1		X
P0C0L4	Complement C4-A precursor (Acidic complement C4) [Contains:	2.9	1	2		X
P0C0L5	Complement C4-B precursor (Basic complement C4) [Contains:	2.9	1			X
Q07021	Complement component 1 Q subcomponent-binding protein, r	42.2	1	4	2	-
P08174	Complement decay-accelerating factor precursor - Homo sapiens	12.1			2	-
P00751	Complement factor B precursor (EC 3,4,21,47) (C3/C5 convertase	4.2	1			X
P17927	Complement receptor type 1 precursor - Homo sapiens (Human)	1.3		1		-
Q6PUV4	Complexin-2 (Complexin II) (CPX II) (Synaphin-1) - Homo sapiens	20.1		1		-
Q15003	Condensin complex subunit 2 (Non-SMC condensin I complex sub	8.2		1	2	-
Q96JB2	Conserved oligomeric Golgi complex component 3 (Vesicle dock	5		2		-
P61201	COP9 signalosome complex subunit 2 (Signalosome subunit 2) (	10.2			1	-
Q9BT78	COP9 signalosome complex subunit 4 (Signalosome subunit 4) (	12.1		1	2	X
Q9UBW8	COP9 signalosome complex subunit 7a (Signalosome subunit 7a	5.1			1	-
Q99627	COP9 signalosome complex subunit 8 (Signalosome subunit 8) (	30.1		4	3	X
Q99829	Copine-1 (Copine I)	25.7		6	8	X
O75131	Copine-3 (Copine III)	6		1	2	-
O14618	Copper chaperone for superoxide dismutase (Superoxide dismutase	16.4		4		X
Q9NTM9	Copper homeostasis protein cutC homolog - Homo sapiens (Human)	8.1			1	-
P36551	Coproporphyrinogen III oxidase, mitochondrial precursor (EC 1, 3	13.7		3	1	X
Q13951	Core-binding factor subunit beta (CBF-beta) (Polyomavirus enhancer	5.5		1	1	X
P28845	Corticosteroid 11-beta-dehydrogenase isozyme 1 (EC 1,1,1,146)	15.1	4			-
P12277	Creatine kinase, B chain (EC 2,7,3,2) (B-CK),	47		7	8	X
P17812	CTP synthase (EC 6,3,4,2) (UTP--ammonia ligase) (CTP synthetase	29.4		3	12	X
Q9NRF8	CTP synthase 2 - Homo sapiens (Human)	6			1	-
Q86VP6	Cullin-associated NEDD8-dissociated protein 1 (Cullin-associated	3.7		2		-
P42772	Cyclin-dependent kinase 4 inhibitor B (p14-INK4b) (p15-INK4b)	8.7			1	-
P42771	Cyclin-dependent kinase inhibitor 2A, isoforms 1/2/3 (Cyclin-dependent	29.5			3	-
Q96P16	Cyclin-dependent kinase inhibitor 2B-related protein - Homo sapiens	12.2		3		-
P61024	Cyclin-dependent kinases regulatory subunit 1 (CKS-1) - Homo sapiens	12.7			1	-
P35520	Cystathionine beta-synthase (EC 4,2,1,22) (Serine sulfhydrylase) (	4.4	1		1	X
P32929	Cystathionine gamma-lyase (EC 4,4,1,1) (Gamma-cystathionase	16	4	1	1	-
P01040	Cystatin A (Stefin A) (Cystatin AS)	26.5	2			-
P04080	Cystatin B (Liver thiol proteinase inhibitor) (CPI-B) (Stefin B)	55.1	3	4	2	X

P21291	Cysteine and glycine-rich protein 1 (Cysteine-rich protein 1) (CR	24.9			4	X
Q9UHD1	Cysteine and histidine-rich domain-containing protein 1 - Homo	4.5			1	-
P49589	Cysteinyl-tRNA synthetase, cytoplasmic (EC 6,1,1,16) (Cysteine-	7.6		2	2	-
P00167	Cytochrome b5 - Homo sapiens (Human)	60.4	7	3	1	-
O43169	Cytochrome b5 outer mitochondrial membrane isoform precursor	36.3	2	4	1	-
P0C7P4	Cytochrome b-c1 complex subunit Rieske-like protein 1 OS=Homo	18.7		3		-
P99999	Cytochrome c	61.9	5	6	8	-
P20674	Cytochrome c oxidase polypeptide Va, mitochondrial precursor	46.7	3	2	3	X
P10606	Cytochrome c oxidase polypeptide Vb, mitochondrial precursor	39.5	3	4	1	-
P00403	Cytochrome c oxidase subunit 2 (EC 1,9,3,1) (Cytochrome c oxid	27.8	2	3		-
P14854	Cytochrome c oxidase subunit VIb isoform 1 (EC 1,9,3,1) (COX V	38.4	2	2		-
P08574	Cytochrome c1, heme protein, mitochondrial precursor (Cytoch	12.6	1	1	2	-
P11509	Cytochrome P450 2A6 (EC 1,14,14,1) (CYP1A6) (Coumarin 7-hydr	6.9	2			-
P20853	Cytochrome P450 2A7 (EC 1,14,14,1) (CYP1A7) (P450-IIA4) - Homo	6.9	2			-
P33261	Cytochrome P450 2C19 - Homo sapiens (Human)	5.7	2			-
P11712	Cytochrome P450 2C9 (EC 1,14,13,80) ((R)-limonene 6-monooxygen	13.9	3			-
P08684	Cytochrome P450 3A4 - Homo sapiens (Human)	2.6	1			-
P20815	Cytochrome P450 3A5 (EC 1,14,14,1) (CYP1A5) (P450-PCN3) (H	2.6	1			-
Q02928	Cytochrome P450 4A11 precursor (EC 1,14,15,3) (CYP1A11) (Fa	9.2	3			-
Q5TCH4	Cytochrome P450 4A22 OS=Homo sapiens GN=CYP4A22 PE=1 S	2.3	1			-
P50453	Cytoplasmic antiproteinase 3 (CAP3) (CAP-3) (Protease inhibitor	5.9			2	X
Q07065	Cytoskeleton-associated protein 4 (63 kDa membrane protein) (	11.5		3		-
P28838	Cytosol aminopeptidase (EC 3,4,11,1) (Leucine aminopeptidase)	51.1	8	11	4	X
O00154	Cytosolic acyl coenzyme A thioester hydrolase (EC 3,1,2,2) (Long	14.5		1	2	X
Q96KP4	Cytosolic nonspecific dipeptidase (Glutamate carboxypeptidase	34.5	1	4	2	X
O43175	D-3-phosphoglycerate dehydrogenase (EC 1,1,1,95) (3-PGDH)	56.3	7	9	15	X
Q96EP5	DAZ-associated protein 1 (Deleted in azoospermia-associated p	9.1		2		-
Q02338	D-beta-hydroxybutyrate dehydrogenase, mitochondrial precursor	42.9	9			-
P30046	D-dopachrome decarboxylase (EC 4,1,1,84) (D-dopachrome tau	43.2	4	3	3	X
P78560	Death domain-containing protein CRADD (Caspase and RIP adapt	7	1			-
Q96LJ7	Dehydrogenase/reductase SDR family member 1 (EC 1,1,-,-) - Homo	34.2	5	2		-
Q13268	Dehydrogenase/reductase SDR family member 2 (EC 1,1,-,-) (HE	72.1		15		-
Q9BTZ2	Dehydrogenase/reductase SDR family member 4 (EC 1,1,1,184)	15.4	3	3		-
Q8NBQ5	Dehydrogenase/reductase SDR family member 8 precursor (EC	5.3	1			-
P54886	Delta 1-pyrroline-5-carboxylate synthetase (P5CS) (Aldehyde de	26.3	1	11	1	-
P30038	Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial	28.1	8	5		X
Q13011	Delta3,5-delta2,4-dienoyl-CoA isomerase, mitochondrial precursor	50.6	13	7	6	X
P13716	Delta-aminolevulinic acid dehydratase (EC 4,2,1,24) (Porphobil	35.2	6	1		X
O43583	Density-regulated protein (DRP) (Protein DRP1) (Smooth muscle	10.1			1	-
P32321	Deoxycytidylate deaminase (EC 3,5,4,12) (dCMP deaminase) - H	6.2	1	1		X
Q5QJE6	Deoxynucleotidyltransferase terminal-interacting protein 2 - Homo	2.4		1		-
P33316	Deoxyuridine 5'-triphosphate nucleotidohydrolase, mitochond	39.7		7	7	X
Q8WVC6	Dephospho-CoA kinase domain-containing protein - Homo sapi	5.6		1		-
P15924	Desmoplakin (DP) (250/210 kDa paraneoplastic pemphigus anti	5.2		5	1	X
P60981	Destrin (Actin-depolymerizing factor) (ADF)	70.3	2	5	11	X
Q9BW61	DET1- and DDB1-associated protein 1 - Homo sapiens (Human)	15.7		1		-
Q9NR28	Diablo homolog, mitochondrial precursor (Second mitochondria	25.5	1	5		-
Q96F10	Diamine acetyltransferase 2 (EC 2,3,1,57) (Spermidine/spermin	55.9	5			-
Q86XE5	Dihydrodipicolinate synthase-like, mitochondrial precursor - Ho	14.4	2			-
P00374	Dihydrofolate reductase (EC 1,5,1,3) - Homo sapiens (Human)	23		3	1	-

P09622	Dihydrolipoyl dehydrogenase, mitochondrial precursor (EC 1,8,1,4)	28.7	7	5	2	X
P10515	Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex	7.7		1	2	X
P36957	Dihydrolipoyllysine-residue succinyltransferase component of pyruvate dehydrogenase complex	11.3	2	1	1	X
P09417	Dihydropteridine reductase (EC 1,5,1,34) (HDHPR) (Quinoid dihydropteridine reductase)	36.9	2	5		X
Q14117	Dihydropyrimidinase (EC 3,5,2,2) (DHPase) (Hydantoinase) (DHPase)	21.6	5			-
Q14194	Dihydropyrimidinase-related protein 1 (DRP-1) (Collapsin response element-binding protein)	6.8			2	-
Q16555	Dihydropyrimidinase-related protein 2 (DRP-2) (Collapsin response element-binding protein)	44.1	1	8	2	X
Q3LXA3	Dihydroxyacetone kinase (EC 2,7,1,29) (Glycerone kinase) (DHA kinase)	66.3	16	12		X
P31513	Dimethylaniline monooxygenase [N-oxide-forming] 3 (EC 1,14,1,1)	23.9	6			-
P49326	Dimethylaniline monooxygenase [N-oxide-forming] 5 (EC 1,14,1,1)	2.8	1			-
Q9UI17	Dimethylglycine dehydrogenase, mitochondrial precursor (EC 1,5,1,3)	31.8	13			-
P27487	Dipeptidyl peptidase 4 (EC 3,4,14,5) (Dipeptidyl peptidase IV) (CD133)	7.6		3		-
P53634	Dipeptidyl-peptidase 1 precursor (EC 3,4,14,1) (Dipeptidyl-peptidase I)	19.2		5	1	-
Q9UHL4	Dipeptidyl-peptidase 2 precursor (EC 3,4,14,2) (Dipeptidyl-peptidase II)	4.1	1		1	-
Q9NY33	Dipeptidyl-peptidase 3 (EC 3,4,14,4) (Dipeptidyl-peptidase III) (CD133)	2.2		1	1	-
P98082	Disabled homolog 2 (Differentially expressed protein 2) (DOC-2)	19.2			9	-
Q16531	DNA damage-binding protein 1 (Damage-specific DNA-binding protein)	8.9		5	1	-
P43246	DNA mismatch repair protein Msh2 (MutS protein homolog 2) - Homo sapiens (Human)	3		2		-
P52701	DNA mismatch repair protein MSH6 (MutS-alpha 160 kDa subunit) - Homo sapiens (Human)	0.9		1		-
P28340	DNA polymerase delta catalytic subunit (EC 2,7,7,7) (DNA polymerase delta)	1.3			1	-
Q9NRF9	DNA polymerase epsilon subunit 3 (EC 2,7,7,7) (DNA polymerase epsilon)	11.6		1		-
Q9NR33	DNA polymerase epsilon subunit 4 - Homo sapiens (Human)	18.8		1		-
P49643	DNA primase large subunit - Homo sapiens (Human)	7.7			2	-
Q9UBZ9	DNA repair protein REV1 - Homo sapiens (Human)	1.4		1		-
Q9Y248	DNA replication complex GINS protein PSF2 - Homo sapiens (Human)	13.5		1		-
P49736	DNA replication licensing factor MCM2 (Minichromosome maintenance complex component 2)	6			5	-
P33991	DNA replication licensing factor MCM4 (CDC21 homolog) (P1-Clp1)	23.4		3	10	-
Q14566	DNA replication licensing factor MCM6 (p105MCM) - Homo sapiens (Human)	13			7	-
P33993	DNA replication licensing factor MCM7 (CDC47 homolog) (P1-Clp1)	15.9		1	7	-
P27695	DNA-(apurinic or apyrimidinic site) lyase (EC 4,2,99,18) (AP endonuclease)	30.5		5	2	-
P16989	DNA-binding protein A (Cold shock domain-containing protein A)	13.7		1	1	-
P19387	DNA-directed RNA polymerase II 33 kDa polypeptide (EC 2,7,7,6)	6.9		1		-
O15160	DNA-directed RNA polymerases I and III subunit RPAC1 - Homo sapiens (Human)	8.4		1		-
Q9Y2S0	DNA-directed RNA polymerases I and III subunit RPAC2 - Homo sapiens (Human)	8.3		1		-
P31689	DnaJ homolog subfamily A member 1 (Heat shock 40 kDa protein)	22.2		3	1	X
O60884	DnaJ homolog subfamily A member 2 (HIRA-interacting protein)	15		3	1	-
P25685	DnaJ homolog subfamily B member 1 (Heat shock 40 kDa protein)	25.6		8		-
Q9UBS4	DnaJ homolog subfamily B member 11 precursor (ER-associated protein)	7.8		2	1	X
Q9Y5T4	DnaJ homolog subfamily C member 15 - Homo sapiens (Human)	11.3			1	-
Q9NVM6	DnaJ homolog subfamily C member 17 - Homo sapiens (Human)	6.9		1		-
Q99615	DnaJ homolog subfamily C member 7 (Tetratricopeptide repeat domain)	7.1		2	1	-
O75937	DnaJ homolog subfamily C member 8 (Splicing protein spf31) - Homo sapiens (Human)	4.7		1		-
Q8WXX5	DnaJ homolog subfamily C member 9 (DnaJ protein SB73)	18.8		2		X
P04844	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase	8.2		3		X
P04843	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase	13.3	1	4		X
O95793	Double-stranded RNA-binding protein Staufen homolog 1 - Homo sapiens (Human)	4.7		2		-
Q9C005	Dpy-30-like protein - Homo sapiens (Human)	36.4	1	2	2	-
Q14919	Dr1-associated corepressor (Dr1-associated protein 1) (Negative regulator of Dr1)	5.4			1	-
Q16643	Drebrin (Developmentally-regulated brain protein) - Homo sapiens (Human)	4.9			2	-
Q9BVJ7	Dual specificity protein phosphatase 23 (EC 3,1,3,48) (EC 3,1,3,1)	7.3	1			-

P51452	Dual specificity protein phosphatase 3 (EC 3,1,3,48) (EC 3,1,3,16)	52.4	4	6	1	X
Q99956	Dual specificity protein phosphatase 9 (EC 3,1,3,48) (EC 3,1,3,16)	8.3		2		-
Q13561	Dynactin subunit 2 (Dynactin complex 50 kDa subunit) (50 kDa c	13.5		2	2	X
Q14203	Dynactin-1 (150 kDa dynein-associated polypeptide) (DP-150) (I	4.7		4		-
O00429	Dynammin-1-like protein (EC 3,6,5,5) (Dynammin-like protein) (Dnn	3.7			2	-
Q9NP97	Dynein light chain 2A, cytoplasmic (Dynein-associated protein K	29.2		1	2	-
Q14118	Dystroglycan precursor (Dystrophin-associated glycoprotein 1)	1.5		1		-
Q9ULT8	E3 ubiquitin-protein ligase HECTD1 - Homo sapiens (Human)	0.7			1	-
Q6UWE0	E3 ubiquitin-protein ligase LRSAM1 (EC 6,3,2,-) (Leucine-rich rep	1.7			1	-
Q15075	Early endosome antigen 1 (Endosome-associated protein p162)	9.6		7		-
Q9HC35	Echinoderm microtubule-associated protein-like 4 (EMAP-4) (Re	6.4	1	5		-
O75356	Ectonucleoside triphosphate diphosphohydrolase 5 precursor (I	5.6	2			-
Q9NQZ7	Ectonucleoside triphosphate diphosphohydrolase 7 - Homo sap	5.5	1			-
P22413	Ectonucleotide pyrophosphatase/phosphodiesterase 1 (E-NPP 1	1.3		1		-
Q9BUP0	EF-hand domain-containing protein 1 (Swiprosin-2)	8.8			2	-
Q96C19	EF-hand domain-containing protein 2 (Swiprosin-1)	29.6		1	5	X
Q9GZT9	Egl nine homolog 1 (EC 1,14,11,-) (Hypoxia-inducible factor prol	5.6		1		-
Q9H4M9	EH-domain-containing protein 1 (Testilin) (hPAST1)	9.4			2	X
Q15717	ELAV-like protein 1 (Hu-antigen R) (HuR) - Homo sapiens (Huma	10.7		2		-
Q9BY07	Electrogenic sodium bicarbonate cotransporter 4 - Homo sapier	0.9			1	-
P13804	Electron transfer flavoprotein alpha-subunit, mitochondrial pre	77.5	15	13	12	X
P38117	Electron transfer flavoprotein beta-subunit (Beta-ETF)	57.6	10	10	8	-
Q16134	Electron transfer flavoprotein-ubiquinone oxidoreductase, mito	7.5	3			-
P68104	Elongation factor 1-alpha 1 (EF-1-alpha-1) (Elongation factor 1 A	55.4	6	14	15	X
Q05639	Elongation factor 1-alpha 2 (EF-1-alpha-2) (Elongation factor 1 A	37.1	4		12	-
P24534	Elongation factor 1-beta (EF-1-beta)	35.6	2	4	3	-
P29692	Elongation factor 1-delta (EF-1-delta) (Antigen NY-CO-4)	49.5	2	9	6	X
P26641	Elongation factor 1-gamma (EF-1-gamma) (eEF-1B gamma)	16.9	1	4	7	X
P13639	Elongation factor 2 (EF-2)	56.3	14	23	28	X
Q96RP9	Elongation factor G 1, mitochondrial precursor (mEF-G 1) (Elong	11.1	2	1	5	X
Q969S9	Elongation factor G 2, mitochondrial precursor - Homo sapiens	2.4		1		-
P43897	Elongation factor Ts, mitochondrial precursor (EF-Ts) (EF-TsMt)	4	1			X
P49411	Elongation factor Tu, mitochondrial precursor (EF-Tu) (P43)	55.8	6	11	11	X
P50402	Emerin - Homo sapiens (Human)	6.7			1	-
P30040	Endoplasmic reticulum protein ERp29 precursor (ERp31) (ERp28	42.1	7	9	7	X
P14625	Endoplasmin precursor (94 kDa glucose-regulated protein) (GRF	57	21	32	20	X
O60869	Endothelial differentiation-related factor 1 (EDF-1) (Multiprotei	31.8		1	2	-
Q96F86	Enhancer of mRNA-decapping protein 3 - Homo sapiens (Huma	3.3			1	-
Q9NPA8	Enhancer of yellow 2 transcription factor homolog - Homo sapie	8.9		1		-
Q9UHY7	Enolase-phosphatase E1 (EC 3,1,3,77) (2,3-diketo-5-methylthio-	13.4	1	1	1	-
Q9NTX5	Enoyl-CoA hydratase domain-containing protein 1 - Homo sapie	15	2			-
Q86YB7	Enoyl-CoA hydratase domain-containing protein 2, mitochondri	46.9	9			-
Q96DC8	Enoyl-CoA hydratase domain-containing protein 3, mitochondri	19.8	3			-
P30084	Enoyl-CoA hydratase, mitochondrial precursor (EC 4,2,1,17) (Sh	79.3	19	8	8	X
Q9H6S3	Epidermal growth factor receptor kinase substrate 8-like protei	2.5		1		-
P61916	Epididymal secretory protein E1 precursor (Niemann-Pick disea	40.4	1	3	1	X
P58107	Epiplakin (450 kDa epidermal antigen) - Homo sapiens (Human)	2.2		1		-
P07099	Epoxide hydrolase 1 (EC 3,3,2,9) (Microsomal epoxide hydrolase	21.3	4			-
P34913	Epoxide hydrolase 2 (EC 3,3,2,10) (Soluble epoxide hydrolase) (S	21.8	6			-
Q96HE7	ERO1-like protein alpha precursor (EC 1,8,4,-) (ERO1-Lalpha) (O	9	1	3	1	-

P27105	Erythrocyte band 7 integral membrane protein (Stomatin) (Prot	18.1	1	2	1	-
P30042	ES1 protein homolog, mitochondrial precursor (Protein KNP-I) (	64.6	8	1	1	X
Q9H0W9	Ester hydrolase C11orf54 (EC 3,1,-,-) - Homo sapiens (Human)	15.9	2	2		X
P10768	Esterase D (EC 3,1,1,1)	48.6	4	5	3	X
Q92506	Estradiol 17-beta-dehydrogenase 8 (EC 1,1,1,62) (17-beta-HSD 8	31	4	3		X
Q99447	Ethanolamine-phosphate cytidylyltransferase (EC 2,7,7,14) (Phc	11.1	2	2		X
O95571	ETHE1 protein, mitochondrial precursor (EC 3,-,-,-) (Ethylmaloni	69.3	3	7	2	X
P60842	Eukaryotic initiation factor 4A-I (EC 3,6,1,-) (ATP-dependent RN	40.4	2	7	12	X
Q14240	Eukaryotic initiation factor 4A-II (EC 3,6,1,-) (ATP-dependent RN	22.1			6	X
Q8IYD1	Eukaryotic peptide chain release factor GTP-binding subunit ERI	6.8		1		-
P62495	Eukaryotic peptide chain release factor subunit 1 (eRF1) (Eukary	9.8		1	3	X
O43324	Eukaryotic translation elongation factor 1 epsilon-1 (Multisynth	28.7	1	2	2	-
P41567	Eukaryotic translation initiation factor 1 (eIF1) (Protein translati	33.6		2	1	X
P47813	Eukaryotic translation initiation factor 1A, X-chromosomal (eIF-	50.7	1	6	5	X
P05198	Eukaryotic translation initiation factor 2 subunit 1 (Eukaryotic tr	34.6		2	5	X
P20042	Eukaryotic translation initiation factor 2 subunit 2 (Eukaryotic tr	12.9		1	1	X
P41091	Eukaryotic translation initiation factor 2 subunit 3 (Eukaryotic tr	14.8		1	3	-
Q2VIR3	Eukaryotic translation initiation factor 2 subunit 3-like protein C	11.9			2	-
O75822	Eukaryotic translation initiation factor 3 subunit 1 (eIF-3 alpha)	14.3		2		-
Q14152	Eukaryotic translation initiation factor 3 subunit 10 (eIF-3 theta)	12		9	7	-
Q9UBQ5	Eukaryotic translation initiation factor 3 subunit 12 (eIF-3 p25) (	20.2		3		-
Q13347	Eukaryotic translation initiation factor 3 subunit 2 (eIF-3 beta) (u	19.1	1	1	1	X
O00303	Eukaryotic translation initiation factor 3 subunit 5 (eIF-3 epsilon	34.2	1	5	6	X
Q99613	Eukaryotic translation initiation factor 3 subunit 8 (eIF3 p110) (e	5.3		1		-
P55884	Eukaryotic translation initiation factor 3 subunit 9 (eIF-3 eta) (el	23.8		5	8	-
Q04637	Eukaryotic translation initiation factor 4 gamma 1 (eIF-4-gamma)	1.6	1	2		-
P23588	Eukaryotic translation initiation factor 4B (eIF-4B)	6.7	1	1	2	X
P06730	Eukaryotic translation initiation factor 4E (eIF4E) (eIF-4E) (mRN	11.5	1	2	2	X
Q15056	Eukaryotic translation initiation factor 4H (eIF-4H) (Williams-Ber	42.7		4	2	X
P55010	Eukaryotic translation initiation factor 5 (eIF-5)	12.8		2	3	X
P63241	Eukaryotic translation initiation factor 5A (eIF-5A) (eIF-4D) (Rev	61.7	7	6	8	X
Q6IS14	Eukaryotic translation initiation factor 5A-1-like OS=Homo sapien	35.7	4			-
O60841	Eukaryotic translation initiation factor 5B (eIF-5B) (Translation i	6.1		2		-
P56537	Eukaryotic translation initiation factor 6 (eIF-6) (B4 integrin inte	58.8		7	4	-
Q5RKV6	Exosome complex exonuclease MTR3 - Homo sapiens (Human)	18.8		3	2	-
Q13868	Exosome complex exonuclease RRP4 (EC 3,1,13,-) (Ribosomal R	7.2		1	1	-
O14980	Exportin-1 (Chromosome region maintenance 1 protein homolo	4.2		3		-
P15311	Ezrin (p81) (Cytovillin) (Villin-2)	34.5	1	7	15	X
O14745	Ezrin-radixin-moesin-binding phosphoprotein 50 (EBP50) (Na(+)	24.3		4		-
P52907	F-actin capping protein alpha-1 subunit (CapZ alpha-1)	32.9	1	4	4	X
P47755	F-actin capping protein alpha-2 subunit (CapZ alpha-2)	21		2	2	X
P47756	F-actin capping protein beta subunit (CapZ beta),	57	1	4	7	X
Q96AE4	Far upstream element-binding protein 1 (FUSE-binding protein	35.2	1	9	15	X
Q92945	Far upstream element-binding protein 2 (FUSE-binding protein	24.9	1	11	8	X
Q96I24	Far upstream element-binding protein 3 (FUSE-binding protein	24.3		5	5	-
P14324	Farnesyl pyrophosphate synthetase (FPP synthetase) (FPS) (Farr	13.3		1	1	-
Q16658	Fascin (Singed-like protein) (55 kDa actin bundling protein) (p55	36.9		4	10	X
P49327	Fatty acid synthase (EC 2,3,1,85) [Includes: [Acyl-carrier-protein	42.5	22	35	26	-
Q01469	Fatty acid-binding protein, epidermal (E-FABP) (Psoriasis-associ	49.6		6		X
P07148	Fatty acid-binding protein, liver (L-FABP)	93.7	17	7		X

P51648	Fatty aldehyde dehydrogenase (EC 1,2,1,3) (Aldehyde dehydrogenase)	2.5	1			-
Q9UK22	F-box only protein 2 - Homo sapiens (Human)	13.9		3		-
P02794	Ferritin heavy chain (EC 1,16,3,1) (Ferritin H subunit) (Proliferation)	36.1	2	1		X
P02792	Ferritin light chain (Ferritin L subunit)	46.3	6	4	1	X
P22830	Ferrochelatase, mitochondrial precursor (EC 4,99,1,1) (Protoheme	12.1	1		1	-
P02671	Fibrinogen alpha chain precursor [Contains: Fibrinopeptide A] -	2.1	1			X
P22455	Fibroblast growth factor receptor 4 precursor - Homo sapiens (H	1			1	-
P02751	Fibronectin precursor (FN) (Cold-insoluble globulin) (CIG)	14.4		22		-
P21333	Filamin-A (Alpha-filamin) (Filamin-1) (Endothelial actin-binding p	29		15	47	X
O75369	Filamin-B (FLN-B) (Beta-filamin) (Actin-binding-like protein) (Th	11.3	5	11	10	-
Q96AY3	FK506-binding protein 10 precursor (EC 5,2,1,8) (Peptidyl-prolyl	8.9		3	1	X
P62942	FK506-binding protein 1A (EC 5,2,1,8) (Peptidyl-prolyl cis-trans i	67.6		3	1	-
P26885	FK506-binding protein 2 precursor (EC 5,2,1,8) (Peptidyl-prolyl c	35.9	5	2	2	X
Q00688	FK506-binding protein 3 (EC 5,2,1,8) (Peptidyl-prolyl cis-trans is	24.6		4		-
Q02790	FK506-binding protein 4 (EC 5,2,1,8) (Peptidyl-prolyl cis-trans is	31.2		1	6	X
Q13451	FK506-binding protein 5 (EC 5,2,1,8) (Peptidyl-prolyl cis-trans is	4.6		1		X
P39748	Flap endonuclease 1 (EC 3,1,-,-) (Flap structure-specific endonu	5.8			2	-
P30043	Flavin reductase (EC 1,5,1,30) (FR) (NADPH-dependent diaphora	74.3	7	2	4	X
O75955	Flotillin-1 - Homo sapiens (Human)	3.5	1	1		-
O95954	Formimidoyltransferase-cyclodeaminase (Formiminotransferase)	37	11	1		-
P15408	Fos-related antigen 2 - Homo sapiens (Human)	7.1		1		-
Q13642	Four and a half LIM domains protein 1 (FHL-1) (Skeletal muscle	3.7	1		1	-
Q14192	Four and a half LIM domains protein 2 (FHL-2) (Skeletal muscle	10.4			1	-
Q16595	Frataxin, mitochondrial precursor (Friedreich ataxia protein) (Fr	5.7	1	1		-
Q9H479	Fructosamine-3-kinase - Homo sapiens (Human)	12.9		3		-
P09467	Fructose-1,6-bisphosphatase 1 (EC 3,1,3,11) (D-fructose-1,6-bis	47	12			X
O00757	Fructose-1,6-bisphosphatase isozyme 2 (EC 3,1,3,11) (D-fructos	7.7	2			-
P04075	Fructose-bisphosphate aldolase A (EC 4,1,2,13) (Muscle-type ald	77.2	1	21	14	X
P05062	Fructose-bisphosphate aldolase B (EC 4,1,2,13) (Liver-type aldol	67	19			X
P09972	Fructose-bisphosphate aldolase C (EC 4,1,2,13) (Brain-type aldo	33.5	2	7	2	-
P07954	Fumarate hydratase, mitochondrial precursor (EC 4,2,1,2) (Fum	32.4	7	4	4	X
P16930	Fumarylacetoacetase (EC 3,7,1,2) (Fumarylacetoacetate hydroly	31.7	7	6	1	X
Q6P587	Fumarylacetoacetate hydrolase domain-containing protein 1 (E	29.5	4	3	1	X
Q96GK7	Fumarylacetoacetate hydrolase domain-containing protein 2A -	16.2	3	1		-
P15170	G1 to S phase transition protein 1 homolog (GTP-binding protei	16.4		3	4	-
P51570	Galactokinase (EC 2,7,1,6) (Galactose kinase),	35.5	4	4		X
P07902	Galactose-1-phosphate uridylyltransferase - Homo sapiens (Hur	3.7	1			-
P22466	Galanin precursor [Contains: Galanin; Galanin message-associat	9.8			1	-
P09382	Galectin-1 (Beta-galactoside-binding lectin L-14-I) (Lactose-bind	61.5	2	4	5	X
P17931	Galectin-3 (Galactose-specific lectin 3) (Mac-2 antigen) (IgE-bin	35.2		4	5	-
P56470	Galectin-4 (Lactose-binding lectin 4) (L-36 lactose-binding prote	4.3	1			-
P09104	Gamma-enolase (EC 4,2,1,11) (2-phospho-D-glycerate hydro-ly	28.6		8	4	X
Q92820	Gamma-glutamyl hydrolase precursor (EC 3,4,19,9) (Gamma-Gl	11.9		2		-
O95479	GDH/6PGL endoplasmic bifunctional protein precursor [Include	19.1	6	1		-
Q9H488	GDP-fucose protein O-fucosyltransferase 1 precursor (EC 2,4,1,1	22.2	1	4	1	-
Q13630	GDP-L-fucose synthetase (EC 1,1,1,271) (Protein FX) (Red cell N	16.8			2	X
O60547	GDP-mannose 4,6 dehydratase (EC 4,2,1,47) (GDP-D-mannose c	5.4		1		-
P06396	Gelsolin precursor (Actin-depolymerizing factor) (ADF) (Brevi	3.6		1		X
O75496	Geminin - Homo sapiens (Human)	6.2		1		-
O60763	General vesicular transport factor p115 (Transcytosis-associat	2.1		1		-

Q9NQX3	Gephyrin - Homo sapiens (Human)	2.7		1		-
O95749	Geranylgeranyl pyrophosphate synthetase - Homo sapiens (Hur	6		1		-
P60983	Glia maturation factor beta (GMF-beta)	37.3	2	3	2	X
O60234	Glia maturation factor gamma (GMF-gamma)	6.3			1	X
Q96EK6	Glucosamine 6-phosphate N-acetyltransferase (EC 2,3,1,4) (Pho	22.8	2	2	1	-
P46926	Glucosamine-6-phosphate isomerase (EC 3,5,99,6) (Glucosamin	4.2			1	X
Q06210	Glucosamine--fructose-6-phosphate aminotransferase [isomeri	23.3	1	5	2	-
P11413	Glucose-6-phosphate 1-dehydrogenase (EC 1,1,1,49) (G6PD)	45.8		4	13	X
P06744	Glucose-6-phosphate isomerase (EC 5,3,1,9) (GPI) (Phosphogluc	37.6	3	6	10	X
P14314	Glucosidase II beta subunit precursor (Protein kinase C substrat	21.2	3	6	6	-
P00367	Glutamate dehydrogenase 1, mitochondrial precursor (EC 1,4,1,	64.9	22	21		X
P49448	Glutamate dehydrogenase 2, mitochondrial precursor (EC 1,4,1,	34.1	14	12		-
P48507	Glutamate--cysteine ligase regulatory subunit (EC 6,3,2,2) (Gam	21.2	1		4	X
Q9BQ67	Glutamate-rich WD repeat-containing protein 1 - Homo sapiens	9		1	2	-
O94925	Glutaminase kidney isoform, mitochondrial precursor (EC 3,5,1,	11.7		2	1	X
Q9UI32	Glutaminase liver isoform, mitochondrial precursor - Homo sap	10.1	2			-
P15104	Glutamine synthetase (EC 6,3,1,2) (Glutamate--ammonia ligase]	5.6	1			X
P47897	Glutamyl-tRNA synthetase (EC 6,1,1,18) (Glutamine--tRNA lig	12.8		3	2	-
P35754	Glutaredoxin-1 (Thioltransferase-1) (TTase-1)	31.1	2		2	-
Q86SX6	Glutaredoxin-related protein 5 - Homo sapiens (Human)	40.1	4	2		-
Q92947	Glutaryl-CoA dehydrogenase, mitochondrial precursor (EC 1,3,9	29	5			-
P07203	Glutathione peroxidase 1 (EC 1,11,1,9) (GSHPx-1) (GPx-1) (Cellu	65.7	7	1	1	X
P18283	Glutathione peroxidase 2 (EC 1,11,1,9) (GSHPx-2) (GPx-2) (Gluta	8.9	1	1		-
P00390	Glutathione reductase, mitochondrial precursor (EC 1,8,1,7) (GF	36.8		6	5	-
P08263	Glutathione S-transferase A1 (EC 2,5,1,18) (GTH1) (HA subunit 1	48.2	12			-
P09210	Glutathione S-transferase A2 (EC 2,5,1,18) (GTH2) (HA subunit 2	45	11			-
Q16772	Glutathione S-transferase A3 (EC 2,5,1,18) (Glutathione S-transf	24.8	6			-
Q7RTV2	Glutathione S-transferase A5 (EC 2,5,1,18) (Glutathione S-transf	13.5	4			-
Q9Y2Q3	Glutathione S-transferase kappa 1 (EC 2,5,1,18) (GST 13-13) (Gli	56.6	7	5	4	-
P09488	Glutathione S-transferase Mu 1 (EC 2,5,1,18) (GSTM1-1) (GST cl	54.1	12		4	-
P28161	Glutathione S-transferase Mu 2 (EC 2,5,1,18) (GSTM2-2) (GST cl	23.9	3			-
P21266	Glutathione S-transferase Mu 3 (EC 2,5,1,18) (GSTM3-3) (GST cl	74.2	1	7	17	X
Q03013	Glutathione S-transferase Mu 4 (EC 2,5,1,18) (GSTM4-4) (GST cl	70.2	7		9	-
P46439	Glutathione S-transferase Mu 5 (EC 2,5,1,18) (GSTM5-5) (GST cl	21.1	4			X
P09211	Glutathione S-transferase P (EC 2,5,1,18) (GST class-pi) (GSTP1-	61.9			9	X
P30711	Glutathione S-transferase theta-1 (EC 2,5,1,18) (GST class-theta	29.6	2	2	1	-
P30712	Glutathione S-transferase theta-2 (EC 2,5,1,18) (GST class-theta	16	2			-
P48637	Glutathione synthetase (EC 6,3,2,3) (Glutathione s	18.1	1	5	3	X
P78417	Glutathione transferase omega-1 (EC 2,5,1,18) (GSTO 1-1)	37.3	5	5	5	X
P04406	Glyceraldehyde-3-phosphate dehydrogenase (EC 1,2,1,12) (GAP	88.7	10	24	16	X
Q8IVS8	Glycerate kinase - Homo sapiens (Human)	8.4	2	1		-
P21695	Glycerol-3-phosphate dehydrogenase [NAD+], cytoplasmic (EC :	39.8	8	3		-
P43304	Glycerol-3-phosphate dehydrogenase, mitochondrial precursor	14.9			5	X
P50440	Glycine amidinotransferase, mitochondrial precursor (EC 2,1,4,-	49.9	15			-
P23434	Glycine cleavage system H protein, mitochondrial precursor - H	17.3	2	1		-
P23378	Glycine dehydrogenase [decarboxylating], mitochondrial precu	27.8	11	1		-
Q6IB77	Glycine N-acyltransferase - Homo sapiens (Human)	51.4	8			-
Q969I3	Glycine N-acyltransferase-like protein 1 - Homo sapiens (Humar	5	1			-
Q14749	Glycine N-methyltransferase (EC 2,1,1,20) - Homo sapiens (Hur	30.5	4			-
P35573	Glycogen debranching enzyme (Glycogen debrancher) [Includes	4.6	3			-

P11216	Glycogen phosphorylase, brain form (EC 2,4,1,1)	15.4	1	8		X
P06737	Glycogen phosphorylase, liver form (EC 2,4,1,1) - Homo sapiens	42.4	25	3	2	-
P30419	Glycylpeptide N-tetradecanoyltransferase 1 (EC 2,3,1,97) (Pepti	6.7		1		-
P41250	Glycyl-tRNA synthetase (EC 6,1,1,14) (Glycine--tRNA ligase) (Gly	31.1		4	8	X
Q9HC38	Glyoxalase domain-containing protein 4 - Homo sapiens (Huma	43.1	3	12	2	-
Q9UBQ7	Glyoxylate reductase/hydroxypyruvate reductase (EC 1,1,1,79)	39	8	5		X
P51654	Glypican-3 precursor (Intestinal protein OCI-5) (GTR2-2) (MXR7	18.4		4		-
P49915	GMP synthase [glutamine-hydrolyzing] (EC 6,3,5,2) (Glutamine :	21.8		5	5	X
Q9H4A6	Golgi phosphoprotein 3 (Coat-protein GPP34)	17.8		3	1	X
Q9H8Y8	Golgi reassembly-stacking protein 2 (GRS2) (Golgi reassembly-si	15.5		2		-
Q9H3P7	Golgi resident protein GCP60 (Acyl-CoA-binding domain-contair	8			2	-
Q08379	Golgin subfamily A member 2 (Cis-Golgi matrix protein GM130)	1		1	1	-
Q14444	GPI-anchored protein p137 (p137GPI) (Membrane component c	14.5		4	4	X
Q12849	G-rich sequence factor 1 (GRSF-1)	16.8		2	3	X
Q9BX93	Group XIIb secretory phospholipase A2-like protein precursor -	6.7	1	1		-
Q8TAE8	Growth arrest and DNA-damage-inducible proteins-interacting	27		4		-
O43903	Growth arrest-specific protein 2 - Homo sapiens (Human)	3.5		1		-
P62993	Growth factor receptor-bound protein 2 (Adapter protein GRB2	16.6		2		X
Q14451	Growth factor receptor-bound protein 7 - Homo sapiens (Huma	2.1		1		-
Q9HAV7	GrpE protein homolog 1, mitochondrial precursor (Mt-GrpE#1)	60.8	2	9	3	X
P30047	GTP cyclohydrolase 1 feedback regulatory protein (GTP cyclohy	28.6	2			-
Q9UIJ7	GTP:AMP phosphotransferase mitochondrial (EC 2,7,4,10) (Ade	63.4	6	9	1	-
P01112	GTPase HRas precursor (Transforming protein p21) (p21ras) (H-	33.9	1	3		-
P01111	GTPase NRas precursor (Transforming protein N-Ras) - Homo sa	54		4	3	-
P62826	GTP-binding nuclear protein Ran (GTPase Ran) (Ras-like protein	41.7	2	8	11	X
O00178	GTP-binding protein 1 - Homo sapiens (Human)	1.6		1		-
P36406	GTP-binding protein ARD-1 (ADP-ribosylation factor domain prc	1.7	1			-
Q9NR31	GTP-binding protein SAR1a (COPII-associated small GTPase)	64.6	2	5	3	X
Q9Y6B6	GTP-binding protein SAR1b (GTBPB)	31.3	3	2	2	X
Q14353	Guanidinoacetate N-methyltransferase (EC 2,1,1,2)	45.8	6	4	3	X
Q9Y2T3	Guanine deaminase (EC 3,5,4,3) (Guanase) (Guanine aminase) (	14.1	4		3	X
P63244	Guanine nucleotide-binding protein beta subunit 2-like 1 (Guan	70.3	4	10	15	X
P62873	Guanine nucleotide-binding protein G(I)/G(S)/G(T) beta subunit	23.8	2	3	3	X
P62879	Guanine nucleotide-binding protein G(I)/G(S)/G(T) beta subunit	18.8	2	2	4	X
Q16774	Guanylate kinase (EC 2,7,4,8) (GMP kinase)	5.6		1	1	X
Q9NX24	H/ACA ribonucleoprotein complex subunit 2 (Nucleolar protein	12.4		1		-
Q08623	Haloacid dehalogenase-like hydrolase domain-containing prote	13.6		2		-
Q9BSH5	Haloacid dehalogenase-like hydrolase domain-containing prote	36.3	3	2		-
P00738	Haptoglobin precursor [Contains: Haptoglobin alpha chain; Hap	43.6	10			X
Q96BR5	Hcp beta-lactamase-like protein C1orf163 - Homo sapiens (Hurr	6.9		1		-
Q15004	HCV NS5A-transactivated protein 9 (L5)	16.2			1	-
Q7Z4H3	HD domain-containing protein 2 - Homo sapiens (Human)	19.6		2		-
Q8N4P3	HD domain-containing protein 3 - Homo sapiens (Human)	27.4	1	2		-
P08107	Heat shock 70 kDa protein 1 (HSP70,1) (HSP70-1/HSP70-2)	49.8	6	18	24	X
O43301	Heat shock 70 kDa protein 12A - Homo sapiens (Human)	4.1		1		-
Q96MM6	Heat shock 70 kDa protein 12B - Homo sapiens (Human)	3.5		1		-
P34931	Heat shock 70 kDa protein 1L (Heat shock 70 kDa protein 1-like)	19	5	8	8	X
P34932	Heat shock 70 kDa protein 4 (Heat shock 70-related protein APC	27.7	1	11	13	X
O95757	Heat shock 70 kDa protein 4L (Osmotic stress protein 94) (Heat	18.6		3	7	X
P17066	Heat shock 70 kDa protein 6 (Heat shock 70 kDa protein B*)	12.6	2	8	7	X

P11142	Heat shock cognate 71 kDa protein (Heat shock 70 kDa protein	54.3	9	27	25	X
Q00613	Heat shock factor protein 1 (HSF 1) (Heat shock transcription fa	3.2		1		-
Q12931	Heat shock protein 75 kDa, mitochondrial precursor (HSP 75) (T	31.3	3	6	10	X
P07900	Heat shock protein HSP 90-alpha (HSP 86)	50.5	11	25	27	X
P08238	Heat shock protein HSP 90-beta (HSP 84) (HSP 90)	56.2	8	31	34	X
P54652	Heat shock-related 70 kDa protein 2 (Heat shock 70 kDa proteir	14.4			9	X
Q92598	Heat-shock protein 105 kDa (Heat shock 110 kDa protein) (Antiğ	42.7		8	17	X
P04792	Heat-shock protein beta-1 (HspB1) (Heat shock 27 kDa protein)	72.2	4	4	9	X
Q9UK76	Hematological and neurological expressed 1 protein (Androgen-	13		2	1	-
Q9H910	Hematological and neurological expressed 1-like protein (HN1-l	14.7		2	2	-
Q9NRV9	Heme-binding protein 1 (p22HBP)	20.6	2	1	2	X
Q9Y5Z4	Heme-binding protein 2 (Protein SOUL) (Placental protein 23) (F	19.5	1	2		-
P69905	Hemoglobin subunit alpha (Hemoglobin alpha chain) (Alpha-glo	87.3	7	2	4	-
P68871	Hemoglobin subunit beta (Hemoglobin beta chain) (Beta-globin	89.8	11	1	8	X
P02042	Hemoglobin subunit delta (Hemoglobin delta chain) (Delta-glob	51	7			-
O14792	Heparan sulfate glucosamine 3-O-sulfotransferase 1 precursor -	6.5	1			-
O14964	Hepatocyte growth factor-regulated tyrosine kinase substrate (	3.7		1	2	-
P20823	Hepatocyte nuclear factor 1-alpha (HNF-1A) (Liver-specific trans	3		1		-
P51858	Hepatoma-derived growth factor (HDGF) (High-mobility group p	32.1		5	3	-
Q99729	Heterogeneous nuclear ribonucleoprotein A/B (hnRNP A/B) (AP	13.9		4	3	-
Q13151	Heterogeneous nuclear ribonucleoprotein A0 (hnRNP A0) - Homo	5.2		1		-
P09651	Heterogeneous nuclear ribonucleoprotein A1 (Helix-destabilizin	42.5		9	4	-
P51991	Heterogeneous nuclear ribonucleoprotein A3 (hnRNP A3) - Homo	27.5		5		-
Q14103	Heterogeneous nuclear ribonucleoprotein D0 (hnRNP D0) (AU-r	24.8	1	6	4	X
O14979	Heterogeneous nuclear ribonucleoprotein D-like - Homo sapien	17.6		6	4	-
P52597	Heterogeneous nuclear ribonucleoprotein F (hnRNP F) (Nucleol	34.2		9	6	X
P31943	Heterogeneous nuclear ribonucleoprotein H (hnRNP H)	37.4		7	6	X
P55795	Heterogeneous nuclear ribonucleoprotein H* (hnRNP H*) (FTP-	10.9			3	X
P31942	Heterogeneous nuclear ribonucleoprotein H3 (hnRNP H3) (hnRI	15.3		3	1	X
P61978	Heterogeneous nuclear ribonucleoprotein K (hnRNP K) (Transfo	41.7	5	11	12	X
P14866	Heterogeneous nuclear ribonucleoprotein L (hnRNP L) - Homo s	14.5		3		-
Q8WVV9	Heterogeneous nuclear ribonucleoprotein L-like (Stromal RNA-r	3.5		1		-
P52272	Heterogeneous nuclear ribonucleoprotein M (hnRNP M) - Homo	8.5		3		-
O60506	Heterogeneous nuclear ribonucleoprotein Q (hnRNP Q) (hnRNP	25.2	1	8	6	-
O43390	Heterogeneous nuclear ribonucleoprotein R (hnRNP R) - Homo	19.3	1	6	3	-
Q9BUJ2	Heterogeneous nuclear ribonucleoprotein U-like protein 1 (Ade	9.3		2	1	-
Q1KMD3	Heterogeneous nuclear ribonucleoprotein U-like protein 2 - Ho	8.2		3		-
P22626	Heterogeneous nuclear ribonucleoproteins A2/B1 (hnRNP A2 /	52.7		8	6	X
P07910	Heterogeneous nuclear ribonucleoproteins C1/C2 (hnRNP C1 / I	13.7		4		X
Q00839	Heterogenous nuclear ribonucleoprotein U (hnRNP U) (Scaffold	26.5		12	6	-
Q9BW72	HIG1 domain family member 2A - Homo sapiens (Human)	19.8		1		-
P09429	High mobility group protein 1 (HMG-1) (High mobility group prc	43.7		7	9	-
Q9UGV6	High mobility group protein 1-like 10 (HMG-1L10)	21.8			4	-
P26583	High mobility group protein 2 (HMG-2)	27.3		2		-
O15347	High mobility group protein B3 (High mobility group protein 4) (	25.5		2	2	-
P50135	Histamine N-methyltransferase (EC 2,1,1,8) (HMT)	32.5	1	2		X
P42357	Histidine ammonia-lyase (EC 4,3,1,3) (Histidase) - Homo sapiens	4.6	2			-
P49773	Histidine triad nucleotide-binding protein 1 (Adenosine 5*-mon	81.7	4	6	5	X
Q9BX68	Histidine triad nucleotide-binding protein 2 (EC 3,-,-,-) (HINT-2)	57.1	5	2		X
P12081	Histidyl-tRNA synthetase (EC 6,1,1,21) (Histidine--tRNA ligase) (	16.9		1	5	X

Q9UBN7	Histone deacetylase 6 (HD6) - Homo sapiens (Human)	0.9	1			-
P0C0S8	Histone H2A type 1 (H2A,1) - Homo sapiens (Human)	26.9		3	2	-
Q6FI13	Histone H2A type 2-A (H2A,2)	26.9		3		-
P62805	Histone H4	41.7		1	4	-
Q09028	Histone-binding protein RBBP4 (Retinoblastoma-binding protein)	20.5		1	3	X
Q16576	Histone-binding protein RBBP7 (Retinoblastoma-binding protein)	29.6		1	4	-
Q93099	Homogentisate 1,2-dioxygenase (EC 1,13,11,5) (Homogentisicase)	18.2	5	1		-
O00165	HS1-associating protein X-1 (HAX-1) (HS1-binding protein) - Homo sapiens	8.6		1	1	-
P50502	Hsc70-interacting protein (Hip) (Putative tumor suppressor ST11)	19	3	7	4	X
Q9NZL4	Hsp70-binding protein 1 (HspBP1) (Heat shock protein-binding protein)	2.8			1	-
Q16543	Hsp90 co-chaperone Cdc37 (Hsp90 chaperone protein kinase-activating)	11.6	1	2	2	-
Q9NX55	Huntingtin-interacting protein HYPK - Homo sapiens (Human)	8.6			1	-
Q9UJM8	Hydroxyacid oxidase 1 (EC 1,1,3,15) (HAOX1) (Glycolate oxidase)	39.2	11			-
Q16775	Hydroxyacylglutathione hydrolase (EC 3,1,2,6) (Glyoxalase II) (Glyoxalase)	26.5	3	2		X
P35914	Hydroxymethylglutaryl-CoA lyase, mitochondrial precursor (EC 2,3,3,10)	31.7	9	2		-
Q01581	Hydroxymethylglutaryl-CoA synthase, cytoplasmic (EC 2,3,3,10)	21	2		4	X
P54868	Hydroxymethylglutaryl-CoA synthase, mitochondrial precursor (EC 2,3,3,10)	57.5	19			X
O14756	Hydroxysteroid 17-beta dehydrogenase 6 precursor - Homo sapiens	11	3			-
Q6YN16	Hydroxysteroid dehydrogenase-like protein 2 - Homo sapiens (Human)	24.4	4	5		-
P00492	Hypoxanthine-guanine phosphoribosyltransferase (EC 2,4,2,8) (HGPRT)	39	3	5	6	X
P01880	Ig delta chain C region - Homo sapiens (Human)	13.1	2			-
P01834	Ig kappa chain C region - Homo sapiens (Human)	22.6	2			-
Q14197	Immature colon carcinoma transcript 1 protein precursor (Digestion)	21.8		2		-
Q8WZA9	Immunity-related GTPase family Q protein - Homo sapiens (Human)	7.4		3		X
O43615	Import inner membrane translocase subunit TIM44, mitochondrial precursor	2.9			1	-
Q3ZCQ8	Import inner membrane translocase subunit TIM50, mitochondrial precursor	21.2		5	2	-
P52292	Importin alpha-2 subunit (Karyopherin alpha-2 subunit) (SRP1-a)	14.4		3	3	X
O00505	Importin alpha-3 subunit (Karyopherin alpha-3 subunit) (SRP1-g)	7.5			2	-
O00629	Importin alpha-4 subunit (Karyopherin alpha-4 subunit) (Qip1 p)	8.3		1	2	-
O60684	Importin alpha-7 subunit (Karyopherin alpha-6) - Homo sapiens	9.3			3	-
Q14974	Importin beta-1 subunit (Karyopherin beta-1 subunit) (Nuclear import)	31.3		9	9	-
O00410	Importin beta-3 (Karyopherin beta-3) (Ran-binding protein 5) (RanBP5)	11.5		5	3	-
Q8TEX9	Importin-4 (Importin 4b) (Imp4b) (Ran-binding protein 4) (RanBP4)	13.8		7	1	-
O95373	Importin-7 (Imp7) (Ran-binding protein 7) (RanBP7) - Homo sapiens	1.5		1		-
P55060	Importin-alpha re-exporter (Chromosome segregation 1-like protein)	7.1		3		-
Q9UKY3	Inactive carboxylesterase 4 precursor - Homo sapiens (Human)	19.1	5	1		-
O14920	Inhibitor of nuclear factor kappa-B kinase subunit beta (EC 2,7,1,1)	2.1		1		-
Q15181	Inorganic pyrophosphatase (EC 3,6,1,1) (Pyrophosphate phosphatase)	59.9	2	9	11	X
Q9H2U2	Inorganic pyrophosphatase 2, mitochondrial precursor (EC 3,6,1,1)	23.1	2	1	4	X
Q9BY32	Inosine triphosphate pyrophosphatase (EC 3,6,1,19) (ITPase) (Inositol)	40.2		5	2	X
P20839	Inosine-5*-monophosphate dehydrogenase 1 (EC 1,1,1,205) (IMDH1)	15.8		1	6	X
P12268	Inosine-5*-monophosphate dehydrogenase 2 (EC 1,1,1,205) (IMDH2)	48.1		6	10	X
P29218	Inositol monophosphatase (EC 3,1,3,25) (IMPase) (IMP) (Inositol)	7.9		1	1	X
Q9NPH2	Inositol-3-phosphate synthase - Homo sapiens (Human)	9.5		3		-
P14735	Insulin-degrading enzyme (EC 3,4,24,56) (Insulysin) (Insulinase)	5.2			3	-
Q9NZI8	Insulin-like growth factor 2 mRNA-binding protein 1 - Homo sapiens	34.7		12	1	-
Q9Y6M1	Insulin-like growth factor 2 mRNA-binding protein 2 (IGF-II mRNA)	24.1		6	1	-
O00425	Insulin-like growth factor 2 mRNA-binding protein 3 - Homo sapiens	18.8		6	2	-
P08833	Insulin-like growth factor-binding protein 1 precursor (IGFBP-1)	11.6		2		-
Q16270	Insulin-like growth factor-binding protein 7 precursor (IGFBP-7)	5.7			1	-

P56199	Integrin alpha-1 (Laminin and collagen receptor) (VLA-1) (CD49a)	3.6	1		1	-
P17301	Integrin alpha-2 precursor (Platelet membrane glycoprotein Ia)	2.5		2		-
P05556	Integrin beta-1 precursor (Fibronectin receptor beta subunit) (Ib)	14.8	1	4	2	-
P18084	Integrin beta-5 precursor - Homo sapiens (Human)	1.8		1		-
Q13418	Integrin-linked protein kinase (EC 2,7,11,1) (ILK-1) (ILK-2) (59 kD)	10.8	1	1	3	X
P05362	Intercellular adhesion molecule 1 precursor (ICAM-1) (Major gr	2.6		1		-
P48551	Interferon-alpha/beta receptor beta chain precursor - Homo sa	3.3		1		-
P05161	Interferon-induced 17 kDa protein precursor [Contains: Ubiquit	37			4	-
P19525	Interferon-induced, double-stranded RNA-activated protein kin	2.2		1	1	-
Q12905	Interleukin enhancer-binding factor 2 (Nuclear factor of activat	10.3		1		X
Q12906	Interleukin enhancer-binding factor 3 (Nuclear factor of activat	20.9		8		-
P18510	Interleukin-1 receptor antagonist protein precursor (IL-1ra) (IRA	10.7		1		X
Q14116	Interleukin-18 precursor (IL-18) (Interferon-gamma-inducing fac	17.6			3	-
P21399	Iron-responsive element-binding protein 1 (IRE-BP 1) (Iron regu	36.6	14	5	6	X
Q2TAA2	Isoamyl acetate-hydrolyzing esterase 1 homolog - Homo sapien	4.8		1		-
Q96CN7	Isochorismatase domain-containing protein 1 - Homo sapiens (I	26.2	5	1		-
Q96AB3	Isochorismatase domain-containing protein 2, mitochondrial pr	81.5	6	4	1	-
P50213	Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial p	26.8	1	5	6	X
O43837	Isocitrate dehydrogenase [NAD] subunit beta, mitochondrial pr	8.6		2		-
O75874	Isocitrate dehydrogenase [NADP] cytoplasmic (EC 1,1,1,42) (Ox	70	11	26	14	X
P48735	Isocitrate dehydrogenase [NADP], mitochondrial precursor (EC	33	6	7	2	-
P41252	Isoleucyl-tRNA synthetase, cytoplasmic (EC 6,1,1,5) (Isoleucine-	2.3		2		-
Q9NSE4	Isoleucyl-tRNA synthetase, mitochondrial precursor (EC 6,1,1,5)	13.8	3	2	5	-
Q13907	Isopentenyl-diphosphate delta-isomerase 1 (EC 5,3,3,2) (IPP iso	43.6	1	3	5	X
P26440	Isovaleryl-CoA dehydrogenase, mitochondrial precursor (EC 1,3	19.1	4	1	1	X
Q7Z4H8	KDEL motif-containing protein 2 precursor - Homo sapiens (Hun	3.4		1		-
P05783	Keratin, type I cytoskeletal 18 (Cytokeratin-18) (CK-18) (Keratin-	16		5		-
P35527	Keratin, type I cytoskeletal 9 (Cytokeratin-9) (CK-9) (Keratin-9) (	2.7		1		-
P05787	Keratin, type II cytoskeletal 8 (Cytokeratin-8) (CK-8) (Keratin-8) (	13		4		-
P50053	Ketohexokinase (EC 2,7,1,3) (Hepatic fructokinase) - Homo sapi	40.6	5			-
Q86UP2	Kinectin (Kinesin receptor) (CG-1 antigen)	3.2		1		-
P33176	Kinesin heavy chain (Ubiquitous kinesin heavy chain) (UKHC)	17.8		6	6	-
Q07866	Kinesin light chain 1 (KLC 1) - Homo sapiens (Human)	9		3		-
Q9H0B6	Kinesin light chain 2 - Homo sapiens (Human)	5		1	1	-
Q9NSK0	Kinesin light chain 4 (KLC 4) (Kinesin-like protein 8) - Homo sapi	9.4		3		-
O15066	Kinesin-like protein KIF3B - Homo sapiens (Human)	2.5		1		-
Q86Y91	Kinesin-like protein LOC146909 - Homo sapiens (Human)	3.2	1		1	-
Q8N5Z0	Kynurenine/alpha-aminoadipate aminotransferase mitochondri	4.2	1			-
Q16773	Kynurenine--oxoglutarate transaminase 1 (EC 2,6,1,7) (Kynuren	10.9		1	1	X
Q14657	L antigen family member 3 (ITBA2 protein) (ESO-3 protein)	26.6	1	1		-
Q04760	Lactoylglutathione lyase (EC 4,4,1,5) (Methylglyoxalase) (Aldoke	55.4	5	7	7	X
Q9Y2S2	Lambda-crystallin homolog	28.8	5			X
P02545	Lamin-A/C (70 kDa lamin)	13		3	3	X
P24043	Laminin alpha-2 chain precursor (Laminin M chain) (Merosin he	0.5			1	-
P11047	Laminin gamma-1 chain precursor (Laminin B2 chain)	4.5		5		-
P25391	Laminin subunit alpha-1 precursor (Laminin A chain) - Homo sa	0.9			1	-
P07942	Laminin subunit beta-1 precursor (Laminin B1 chain) - Homo sa	2		1		-
P55268	Laminin subunit beta-2 precursor (S-laminin) (Laminin B1s chair	1.1		1		-
Q92615	La-related protein 5 OS=Homo sapiens GN=LARP5 PE=1 SV=3	2.6		1		-
Q01650	Large neutral amino acids transporter small subunit 1 (L-type ar	3.6		1	1	-

P48634	Large proline-rich protein BAT2 (HLA-B-associated transcript 2)	1.1		1		-
P46379	Large proline-rich protein BAT3 (HLA-B-associated transcript 3)	1.1		1		X
Q9UIC8	Leucine carboxyl methyltransferase 1 - Homo sapiens (Human)	6.6			1	-
O95202	Leucine zipper-EF-hand-containing transmembrane protein 1, n	14.1		4	1	-
Q32MZ4	Leucine-rich repeat flightless-interacting protein 1 (LRR FLII-inte	15.8	1	2	2	-
Q86VH4	Leucine-rich repeat transmembrane neuronal protein 4 precurs	1.9	1			-
Q8N1G4	Leucine-rich repeat-containing protein 47 - Homo sapiens (Hum	9.8		4	1	-
Q96AG4	Leucine-rich repeat-containing protein 59 - Homo sapiens (Hum	28.7		5	3	-
Q9P2J5	Leucyl-tRNA synthetase, cytoplasmic (EC 6,1,1,4) (Leucine--trN	1.5			2	-
P30740	Leukocyte elastase inhibitor (LEI) (Serpin B1) (Monocyte/neutro	26.1	4	2	3	X
P09960	Leukotriene A-4 hydrolase (EC 3,3,2,6) (LTA-4 hydrolase) (Leuko	16.4	2	3	4	X
P48059	LIM and senescent cell antigen-like-containing domain protein :	3.7			1	-
Q14847	LIM and SH3 domain protein 1 (LASP-1) (MLN 50)	44.4	1	4	4	X
Q9UHB6	LIM domain and actin-binding protein 1 (Epithelial protein lost i	7.5		1	2	-
Q9NUP9	Lin-7 homolog C (Lin-7C) (Mammalian lin-seven protein 3) (MAL	18.8		2	2	-
P11182	Lipoamide acyltransferase component of branched-chain alpha-	6.4	2			-
Q93052	Lipoma-preferred partner (LIM domain-containing preferred tra	6.2		1		X
P23141	Liver carboxylesterase 1 precursor (EC 3,1,1,1) (Acyl coenzyme /	67.5	26	6		X
P00338	L-lactate dehydrogenase A chain (EC 1,1,1,27) (LDH-A) (LDH mu	84.3	11	17	23	-
Q9BYZ2	L-lactate dehydrogenase A-like 6B (EC 1,1,1,27) - Homo sapiens	4.5	1	1	1	-
P07195	L-lactate dehydrogenase B chain (EC 1,1,1,27) (LDH-B) (LDH hea	62.3	1		18	X
P36776	Lon protease homolog, mitochondrial precursor (EC 3,4,21,-) (Li	21.6	5	8	5	X
P28330	Long-chain specific acyl-CoA dehydrogenase, mitochondrial pre	3	1			-
P33121	Long-chain-fatty-acid--CoA ligase 1 (EC 6,2,1,3) (Long-chain acyl	25.8	8			-
O60488	Long-chain-fatty-acid--CoA ligase 4 (EC 6,2,1,3) (Long-chain acyl	9.4		3		-
Q9ULC5	Long-chain-fatty-acid--CoA ligase 5 (EC 6,2,1,3) (Long-chain acyl	1.8	1			-
P24666	Low molecular weight phosphotyrosine protein phosphatase (E	55.1	4	6	6	X
P20132	L-serine dehydratase (EC 4,3,1,17) (L-serine deaminase) - Homo	4.3	1			-
Q9BX40	LSM14 protein homolog B - Homo sapiens (Human)	6.8		1		-
P05455	Lupus La protein (Sjogren syndrome type B antigen) (SS-B) (La ri	37.5		7	3	X
Q7Z4W1	L-xylulose reductase (EC 1,1,1,10) (XR) (Dicarbonyl/L-xylulose re	86.9	12	5		-
Q5U5X0	LYR motif-containing protein 7 - Homo sapiens (Human)	24			1	-
Q5VWZ2	Lysophospholipase-like protein 1 (EC 3,1,2,-) - Homo sapiens (H	8	1			-
P10253	Lysosomal alpha-glucosidase precursor (EC 3,2,1,20) (Acid malta	18.8	4	7		X
O00754	Lysosomal alpha-mannosidase precursor (EC 3,2,1,24) (Mannos	7.3		3		-
P10619	Lysosomal protective protein precursor (EC 3,4,16,5) (Cathepsir	7.7		3		-
P42785	Lysosomal Pro-X carboxypeptidase precursor (EC 3,4,16,2) (Prol	3.8		1		-
P11279	Lysosome-associated membrane glycoprotein 1 precursor (LAM	6.5		1	1	-
P13473	Lysosome-associated membrane glycoprotein 2 precursor (LAM	4.1		1		X
P61626	Lysozyme C precursor (EC 3,2,1,17) (1,4-beta-N-acetylmuramid	35.1		3		-
Q15046	Lysyl-tRNA synthetase (EC 6,1,1,6) (Lysine--tRNA ligase) (LysRS)	27.5		3	10	-
P40121	Macrophage capping protein (Actin-regulatory protein CAP-G)	7.5			1	X
P14174	Macrophage migration inhibitory factor (MIF) (Phenylpyruvate i	23.5	1	4	1	X
Q86V88	Magnesium-dependent phosphatase 1 (EC 3,1,3,-) (EC 3,1,3,48)	17.6		1		-
Q9NZW5	MAGUK p55 subfamily member 6 (Veli-associated MAGUK 1) (V	1.9		1		-
Q8NHS3	Major facilitator superfamily domain-containing protein 8 - Hon	1.7		1		-
P04156	Major prion protein precursor (PrP) (PrP27-30) (PrP33-35C) (ASI	4.7		1		-
P40925	Malate dehydrogenase, cytoplasmic (EC 1,1,1,37) (Cytosolic ma	58.7	5	14	5	X
P40926	Malate dehydrogenase, mitochondrial precursor (EC 1,1,1,37)	75.4	14	29	12	-
O43708	Maleylacetoacetate isomerase (EC 5,2,1,2) (MAAI) (Glutathione	35.6	4			-

Q9ULC4	Malignant T cell amplified sequence 1 OS=Homo sapiens GN=M	9.4	1		1	-
Q9UM22	Mammalian endymin-related protein 1 precursor (MERP-1) (I	8.9		1		-
O60664	Mannose-6-phosphate receptor-binding protein 1 (Cargo select	58.1		12	7	X
Q96T17	MAP7 domain-containing protein 2 - Homo sapiens (Human)	1.5		1	1	-
P49006	MARCKS-related protein (MARCKS-like protein 1) (Macrophage	7.7		1		-
P43243	Matrin-3	9.9		2		-
O00264	Membrane-associated progesterone receptor component 1 (m	33.8	3	5	2	-
O15173	Membrane-associated progesterone receptor component 2 (Pr	18.8	1	3		-
Q14696	Mesoderm development candidate 2 (NY-REN-61 antigen) - Hor	32.9	2	3		-
P01033	Metalloproteinase inhibitor 1 precursor (TIMP-1) (Erythroid pot	5.8			1	-
O43312	Metastasis suppressor protein 1 OS=Homo sapiens GN=MTSS1	3.2	1			-
O94776	Metastasis-associated protein MTA2 - Homo sapiens (Human)	3.4		1		-
Q9NZL9	Methionine adenosyltransferase 2 subunit beta - Homo sapiens	29.3		3	4	-
P53582	Methionine aminopeptidase 1 - Homo sapiens (Human)	7.8			1	-
P56192	Methionyl-tRNA synthetase, cytoplasmic (EC 6,1,1,10) (Methior	6.4		2	1	-
Q9HCC0	Methylcrotonoyl-CoA carboxylase beta chain, mitochondrial pre	32.9	8	5	1	X
Q96RQ3	Methylcrotonoyl-CoA carboxylase subunit alpha, mitochondrial	7.9	3			-
P42898	Methylenetetrahydrofolate reductase (EC 1,5,1,20) - Homo sap	2.7			1	-
Q02252	Methylmalonate-semialdehyde dehydrogenase [acylating], mitc	37	14	2		-
Q96PE7	Methylmalonyl-CoA epimerase, mitochondrial precursor (EC 5,1	28.4	4			-
P22033	Methylmalonyl-CoA mutase, mitochondrial precursor (EC 5,4,9	37.5	11			-
Q9BQA1	Methylosome protein 50 (MEP50 protein) (WD-repeat protein	12		2	1	X
P54105	Methylosome subunit pICln (Chloride conductance regulatory p	21.5		2	2	-
Q9H8H3	Methyltransferase-like protein 7A precursor (EC 2,1,1,-) (Protei	6.1	1			-
P10620	Microsomal glutathione S-transferase 1 (EC 2,5,1,18) (Microson	27.1	4			-
P55157	Microsomal triglyceride transfer protein large subunit precurs	16.4	7			-
Q9UPN3	Microtubule-actin cross-linking factor 1, isoforms 1/2/3/5 (Actir	0.7	1		1	-
P27816	Microtubule-associated protein 4 (MAP 4)	15.1		5		-
Q15691	Microtubule-associated protein RP/EB family member 1 (APC-b	59.7		4	8	X
O15021	Microtubule-associated serine/threonine-protein kinase 4 - Hor	0.7		1		-
Q8N183	Mimitin, mitochondrial precursor (Myc-induced mitochondrial	16.6		2		-
Q9Y2B0	MIR-interacting saposin-like protein precursor (Transmembran	60.4	5	7	3	X
Q8N4C8	Misshapen-like kinase 1 (EC 2,7,11,1) (Mitogen-activated protei	1		1		-
P82664	Mitochondrial 28S ribosomal protein S10 (S10mt) (MRP-S10) -	13.4		2		-
O60783	Mitochondrial 28S ribosomal protein S14 (S14mt) (MRP-S14) -	21.9	1	2		-
P82921	Mitochondrial 28S ribosomal protein S21 (S21mt) (MRP-S21) -	13.8		1		-
P82650	Mitochondrial 28S ribosomal protein S22 (S22mt) (MRP-S22)	3.3		1		X
P82663	Mitochondrial 28S ribosomal protein S25 (S25mt) (MRP-S25) -	28.9		3		-
Q9Y2Q9	Mitochondrial 28S ribosomal protein S28 (S28mt) (MRP-S28) (M	29.9	1	3	2	-
P51398	Mitochondrial 28S ribosomal protein S29 (S29mt) (MRP-S29) (D	3.8		1		-
Q9NP92	Mitochondrial 28S ribosomal protein S30 (S30mt) (MRP-S30) (P	7.5		1		-
P82930	Mitochondrial 28S ribosomal protein S34 (S34mt) (MRP-S34) -	13.8		1	1	-
P82909	Mitochondrial 28S ribosomal protein S36 (S36mt) (MRP-S36) -	15.5	1			-
P82932	Mitochondrial 28S ribosomal protein S6 (S6mt) (MRP-S6) - Hom	10.4			1	-
Q16540	Mitochondrial 39S ribosomal protein L23 (L23mt) (MRP-L23) (L	24.2		1		-
Q9P0M9	Mitochondrial 39S ribosomal protein L27 (L27mt) (MRP-L27) - H	24.3		2	1	-
Q9NYK5	Mitochondrial 39S ribosomal protein L39 (L39mt) (MRP-L39) (M	8		1	2	X
Q9BYD3	Mitochondrial 39S ribosomal protein L4 (L4mt) (MRP-L4) - Hom	10.6		2		-
Q13405	Mitochondrial 39S ribosomal protein L49 (L49mt) (MRP-L49) (P	23.5	1	3	1	-
Q8N5N7	Mitochondrial 39S ribosomal protein L50 (L50mt) (MRP-L50) - H	27.2		2		-

O43772	Mitochondrial carnitine/acylcarnitine carrier protein (Carnitine/	11.3	3			-
Q9Y6C9	Mitochondrial carrier homolog 2 (Met-induced mitochondrial p	12.2	1	1		-
Q8WVM0	Mitochondrial dimethyladenosine transferase 1, mitochondrial	4		1		-
Q9H936	Mitochondrial glutamate carrier 1 (GC-1) (Glutamate/H(+) sym	14.6	1			-
Q9H1K4	Mitochondrial glutamate carrier 2 (GC-2) (Glutamate/H(+) sym	11.1	2			-
Q9Y5L4	Mitochondrial import inner membrane translocase subunit Tim	36.8	2	1		-
O60220	Mitochondrial import inner membrane translocase subunit Tim	40.2	3	2		-
Q9Y5J6	Mitochondrial import inner membrane translocase subunit Tim	15.5		1		-
Q9NS69	Mitochondrial import receptor subunit TOM22 homolog (Transl	33.8		3	2	-
Q15785	Mitochondrial import receptor subunit TOM34 (Translocase of	26.5		4		-
Q9Y619	Mitochondrial ornithine transporter 1 - Homo sapiens (Human)	9.3	1			-
O94826	Mitochondrial precursor proteins import receptor (Translocase	18.6	1	4	5	X
Q9Y3D9	Mitochondrial ribosomal protein S23 (S23mt) (MRP-S23) - Hom	27.4		3	1	-
Q10713	Mitochondrial-processing peptidase alpha subunit, mitochondri	11.8	1	2	1	X
O75439	Mitochondrial-processing peptidase beta subunit, mitochondria	7.2		2		X
P28482	Mitogen-activated protein kinase 1 (EC 2,7,1,37) (Extracellular s	8.3		1	1	X
Q16539	Mitogen-activated protein kinase 14 (EC 2,7,11,24) (Mitogen-ac	5.6		1		-
P27361	Mitogen-activated protein kinase 3 (EC 2,7,1,37) (Extracellular s	4.2			1	X
Q9UHA4	Mitogen-activated protein kinase kinase 1-interacting protein 1	49.2		2	2	X
O43684	Mitotic checkpoint protein BUB3	10.1		1	1	X
Q96T76	MMS19-like protein (hMMS19) (MET18 homolog) - Homo sapie	3.1		2		-
P26038	Moesin (Membrane-organizing extension spike protein)	41.4	1	2	19	X
Q96EN8	Molybdenum cofactor sulfurase - Homo sapiens (Human)	3		1	1	-
P50224	Monoamine-sulfating phenol sulfotransferase (EC 2,8,2,1) (Aryl	44.4	3	13		X
Q6UB35	Monofunctional C1-tetrahydrofolate synthase, mitochondrial O	2.5		1		-
Q99685	Monoglyceride lipase (EC 3,1,1,23) (MGL) (HU-K5) (Lysophosph	11.6	1			-
Q14149	MORC family CW-type zinc finger protein 3 - Homo sapiens (Hui	5.2		1	1	-
Q7L9L4	Mps one binder kinase activator-like 1A (Mob1 homolog 1A) (M	5.1			1	X
P78406	mRNA-associated protein mrnp 41 (Rae1 protein homolog) - Ho	4.1		1		-
P22234	Multifunctional protein ADE2 [Includes: Phosphoribosylaminoin	47.3	2	4	14	X
Q8NI22	Multiple coagulation factor deficiency protein 2 precursor (Neu	11.6		1		-
Q9UNW1	Multiple inositol polyphosphate phosphatase 1 precursor (EC 3,	2.3		1		-
Q13155	Multisynthetase complex auxiliary component p38 (Protein JTV	20.9		2	3	-
Q12904	Multisynthetase complex auxiliary component p43 [Contains: E	31.7		4	4	-
O00499	Myc box-dependent-interacting protein 1 (Bridging integrator 1	3.2			1	-
Q9HB07	MYG1 protein	14.9		2	5	-
P60660	Myosin light polypeptide 6 (Myosin light chain alkali 3) (Myosin	58.3	5	3	7	-
P19105	Myosin regulatory light chain 2, nonsarcomeric (Myosin RLC)	28.1	2	2	2	X
P58546	Myotrophin (V-1 protein)	74.6	1	3	3	X
P29966	Myristoylated alanine-rich C-kinase substrate (MARCKS) (Protei	16.6		1	1	-
P20933	N(4)-(beta-N-acetylglucosaminyl)-L-asparaginase precursor (EC	3.5		1		-
P15586	N-acetylglucosamine-6-sulfatase precursor (EC 3,1,6,14) (G6S) (	4.7		2		-
Q9GZZ1	N-acetyltransferase 13 - Homo sapiens (Human)	46.2		2	1	-
Q8TBE9	N-acylneuraminate-9-phosphatase (EC 3,1,3,29) (Neu5Ac-9-Pas	10.1		1		-
P15559	NAD(P)H dehydrogenase [quinone] 1 (EC 1,6,5,2) (Quinone red	48.2		5	6	-
Q9NXA8	NAD-dependent deacetylase sirtuin-5 (EC 3,5,1,-) (SIR2-like prot	4.5	1			-
Q86Y39	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subuni	10.6		1		-
O43678	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subuni	10.1	1	1		-
O00483	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subuni	27.2		2	2	-
O95182	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subuni	16.8	1			-

Q16795	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit	8.8	1	2		-
O96000	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit	33.1	2	4	1	-
O95168	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit	7.8	1	1		-
Q9Y6M9	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit	10.6		1		-
O43920	NADH dehydrogenase [ubiquinone] iron-sulfur protein 5 (EC 1,6,2,2)	32.1	1	1		-
O75251	NADH dehydrogenase [ubiquinone] iron-sulfur protein 7, mitochondrial	10.8		1		-
P00387	NADH-cytochrome b5 reductase (EC 1,6,2,2) (B5R) (Diaphorase)	46.2	4	4	1	-
O75380	NADH-ubiquinone oxidoreductase 13 kDa-A subunit, mitochondrial	20.2	1	1		-
Q16718	NADH-ubiquinone oxidoreductase 13 kDa-B subunit (EC 1,6,5,3)	50	3	3	4	X
P51970	NADH-ubiquinone oxidoreductase 19 kDa subunit (EC 1,6,5,3) (I)	33.1		1		-
O00217	NADH-ubiquinone oxidoreductase 23 kDa subunit, mitochondrial	20.5	1	3	1	-
P19404	NADH-ubiquinone oxidoreductase 24 kDa subunit, mitochondrial	9.2	2	2		X
O75489	NADH-ubiquinone oxidoreductase 30 kDa subunit, mitochondrial	44.3	3	9	5	X
O95299	NADH-ubiquinone oxidoreductase 42 kDa subunit, mitochondrial	9.6	2	2		-
P28331	NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	22.8	1	7		X
P56556	NADH-ubiquinone oxidoreductase B14 subunit (EC 1,6,5,3) (EC :)	35.2		3		-
Q9P0J0	NADH-ubiquinone oxidoreductase B16,6 subunit (EC 1,6,5,3) (E)	16.7	1	1		-
Q14914	NADP-dependent leukotriene B4 12-hydroxydehydrogenase (EC	53.5	7		9	-
P48163	NADP-dependent malic enzyme (EC 1,1,1,40) (NADP-ME) (Malic	18.2			4	X
P22570	NADPH:adrenodoxin oxidoreductase, mitochondrial precursor (	35	1	8		-
P16435	NADPH--cytochrome P450 reductase (EC 1,6,2,4) (CPR) (P450R)	41.5	5	11	6	-
Q13765	Nascent polypeptide-associated complex alpha subunit (NAC-al	35.8		6	5	X
Q9BZK3	Nascent polypeptide-associated complex subunit alpha-like pro	15		2		-
Q92597	NDRG1 protein (N-myc downstream-regulated gene 1 protein) (	7.9			2	X
Q15843	NEDD8 precursor (Ubiquitin-like protein Nedd8) (Neddylin) - Hc	40.7		2	2	-
P61081	NEDD8-conjugating enzyme Ubc12 (EC 6,3,2,-) (Ubiquitin-conju	37.7		4	6	X
O43402	Neighbor of COX4 - Homo sapiens (Human)	4.3		1		-
Q9UMX5	Neudesin precursor (Neuron-derived neurotrophic factor) (Secr	8.7		1		-
Q09666	Neuroblast differentiation-associated protein AHNK (Desmoye	2	3	3	2	-
A2RRP1	Neuroblastoma-amplified gene protein - Homo sapiens (Human	1.1			1	-
Q14697	Neutral alpha-glucosidase AB precursor (EC 3,2,1,84) (Glucosida	39.4	15	16	21	X
Q15758	Neutral amino acid transporter B(0) (ATB(0)) (Sodium-depende	8.1		3	2	-
Q9NYR9	NF-kappa-B inhibitor-interacting Ras-like protein 2 (I-kappa-B-ir	12		1		-
O94760	NG,NG-dimethylarginine dimethylaminohydrolase 1 (EC 3,5,3,1	17.5	1	2	1	X
Q96TA1	Niban-like protein (Meg-3)	26.3			11	-
P40261	Nicotinamide N-methyltransferase (EC 2,1,1,1)	23.1	2		2	X
P43490	Nicotinamide phosphoribosyltransferase (EC 2,4,2,12) (NAmPR	25.9	2	1	3	X
Q6XQN6	Nicotinate phosphoribosyltransferase - Homo sapiens (Human)	21.4	8		2	-
Q15274	Nicotinate-nucleotide pyrophosphorylase [carboxylating] (EC 2,	38.4	3	6		X
Q9GZT8	NIF3-like protein 1 (Amyotrophic lateral sclerosis 2 chromosom	6.9		2		-
Q86X76	Nitrilase homolog 1 (EC 3,5,-,-) - Homo sapiens (Human)	15.3	2	1	1	X
Q9NQR4	Nitrilase homolog 2 - Homo sapiens (Human)	48.6	6	2	1	-
Q15155	Nodal modulator 1 precursor (pM5)	3.4		2		-
Q15233	Non-POU domain-containing octamer-binding protein (NonO pr	7.2		1	1	-
P22307	Nonspecific lipid-transfer protein, mitochondrial precursor (EC :	35.5	16	5	4	X
O60443	Non-syndromic hearing impairment protein 5 (Inversely correla	2.8		1		-
Q9UNZ2	NSFL1 cofactor p47 (p97 cofactor p47)	33		4	1	X
P41227	N-terminal acetyltransferase complex ARD1 subunit homolog A	11.5		1	1	-
P49321	Nuclear autoantigenic sperm protein (NASP) - Homo sapiens (H	18.7		6	6	-
Q9Y266	Nuclear migration protein nudC (Nuclear distribution protein C	14.2		2	1	X

Q99567	Nuclear pore complex protein Nup88 (Nucleoporin Nup88) (88	3.9			1	-
P82979	Nuclear protein Hcc-1 (Proliferation-associated cytokine-inducib	9.5		2		-
P61970	Nuclear transport factor 2 (NTF-2) (Placental protein 15) (PP15)	55.9	1	3	2	X
P67809	Nuclease sensitive element-binding protein 1 (Y-box-binding pr	20.4		2	1	-
Q02818	Nucleobindin-1 precursor (CALNUC)	8.9		1	2	X
O60936	Nucleolar protein 3 - Homo sapiens (Human)	8.7			1	-
P19338	Nucleolin (Protein C23)	32.5		21	17	-
P06748	Nucleophosmin (NPM) (Nucleolar phosphoprotein B23) (Numat	35.4		4	5	X
O75607	Nucleoplasmin-3 - Homo sapiens (Human)	32		2		-
P52594	Nucleoporin-like protein RIP (HIV-1 Rev-binding protein) (Rev-ir	6.6		2		-
P15531	Nucleoside diphosphate kinase A (EC 2,7,4,6) (NDK A) (NDP kin	75	8	8	8	X
P22392	Nucleoside diphosphate kinase B (EC 2,7,4,6) (NDK B) (NDP kina	79.6	9	11	9	-
Q96DE0	Nucleoside diphosphate-linked moiety X motif 16 (EC 3,6,1,-) (N	6.7	1			X
P55209	Nucleosome assembly protein 1-like 1 (NAP-1-related protein) (	22.5		4	6	-
Q99733	Nucleosome assembly protein 1-like 4 (Nucleosome assembly p	23.7		5	4	-
Q9Y5Y2	Nucleotide-binding protein 2 (NBP 2)	29.5		2	3	X
Q8TB37	Nucleotide-binding protein-like - Homo sapiens (Human)	11.6	1	3		-
Q8WVJ2	NudC domain-containing protein 2 - Homo sapiens (Human)	19.1		1	3	-
Q9NX40	OCIA domain-containing protein 1 - Homo sapiens (Human)	7.3		1	1	-
Q56VL3	OCIA domain-containing protein 2 - Homo sapiens (Human)	27.3	3			-
Q9Y3B8	Oligoribonuclease, mitochondrial precursor (EC 3,1,-,-) (Small fr	19.8		2	1	X
P04181	Ornithine aminotransferase, mitochondrial precursor (EC 2,6,1,	21.9		1	5	X
P00480	Ornithine carbamoyltransferase, mitochondrial precursor (EC 2,	61.6	9			-
Q92882	Osteoclast-stimulating factor 1	5.6		1	1	X
Q8WZ82	Ovarian cancer-associated gene 2 protein - Homo sapiens (Hum	11.5			2	-
Q96B49	Overexpressed breast tumor protein - Homo sapiens (Human)	18.9		1		-
Q9BUP3	Oxidoreductase HTATIP2 (EC 1,1,1,-) (HIV-1 TAT-interactive pro	23.1			4	-
P50897	Palmitoyl-protein thioesterase 1 precursor (EC 3,1,2,22) (Palmit	15.4		2	1	-
P20962	Parathymosin - Homo sapiens (Human)	13.7	2	2	1	-
Q9GZU2	Paternally-expressed gene 3 protein - Homo sapiens (Human)	6		3		-
Q9Y365	PCTP-like protein (PCTP-L) (StAR-related lipid transfer protein 1	4.5	1	1		X
O00151	PDZ and LIM domain protein 1 (Elfin) (LIM domain protein CLP-3	56.5		9	2	X
Q96HC4	PDZ and LIM domain protein 5 (Enigma homolog) (Enigma-like F	3	1			-
Q9UBV8	Peflin (PEF protein with a long N-terminal hydrophobic domain)	12		1	3	-
Q9HBH1	Peptide deformylase, mitochondrial precursor - Homo sapiens (	5.3		1		-
Q9UJ68	Peptide methionine sulfoxide reductase (EC 1,8,4,11) (Protein-r	20	2			-
P62937	Peptidyl-prolyl cis-trans isomerase A (EC 5,2,1,8) (PPIase) (Rotar	92.1	11	14	13	X
P23284	Peptidyl-prolyl cis-trans isomerase B precursor (EC 5,2,1,8) (PPI	73.1	10	15	9	X
O43447	Peptidyl-prolyl cis-trans isomerase H (EC 5,2,1,8) (PPIase H) (Ro	13	1	1	1	-
Q13526	Peptidyl-prolyl cis-trans isomerase NIMA-interacting 1 (EC 5,2,1	31.3	1	3	1	X
Q9Y237	Peptidyl-prolyl cis-trans isomerase NIMA-interacting 4 (EC 5,2,1	10.7	1	1	1	-
P30405	Peptidyl-prolyl cis-trans isomerase, mitochondrial precursor (EC	71	6	6	3	-
Q9Y3C6	Peptidyl-prolyl cis-trans isomerase-like 1 (EC 5,2,1,8) (PPIase) (R	16.3		1	2	-
Q9H2H8	Peptidyl-prolyl cis-trans isomerase-like 3 (EC 5,2,1,8) (PPIase) (R	18.6	1	2	1	-
Q9Y3E5	Peptidyl-tRNA hydrolase 2, mitochondrial precursor (EC 3,1,1,2)	40.2		3	1	X
Q92626	Peroxidasin homolog precursor - Homo sapiens (Human)	1.6			1	-
Q06830	Peroxiredoxin-1 (EC 1,11,1,15) (Thioredoxin peroxidase 2) (Thio	73.4	14	19	23	X
P32119	Peroxiredoxin-2 (EC 1,11,1,15) (Thioredoxin peroxidase 1) (Thio	53.5	10	13	14	X
Q13162	Peroxiredoxin-4 (EC 1,11,1,15) (Prx-IV) (Thioredoxin peroxidase	64.2	8	10	12	X
P30044	Peroxiredoxin-5, mitochondrial precursor (EC 1,11,1,15) (Prx-V)	58.4	11	10	7	X

P30041	Peroxiredoxin-6 (EC 1,11,1,15) (Antioxidant protein 2) (1-Cys pe	75	13	14	18	X
O75521	Peroxisomal 3,2-trans-enoyl-CoA isomerase (EC 5,3,3,8) (Dodec	25.3	2	5		-
Q08426	Peroxisomal bifunctional enzyme (PBE) (PBFE) [Includes: Enoyl-l	32.9	10			-
P51659	Peroxisomal multifunctional enzyme type 2 (MFE-2) (D-bifuncti	17.3	4	2	4	-
Q9P0Z9	Peroxisomal sarcosine oxidase (EC 1,5,3,1) (PSO) (L-pipecolate c	10.8	3			-
P50542	Peroxisomal targeting signal 1 receptor - Homo sapiens (Humar	2		1		-
Q9BY49	Peroxisomal trans-2-enoyl-CoA reductase (EC 1,3,1,38) (TERP) (I	4	1			-
Q5VV67	Peroxisome proliferator-activated receptor gamma coactivator-	1.5	1			-
Q6Y7W6	PERQ amino acid-rich with GYF domain-containing protein 2 - H	1.7		1		-
Q8WW12	PEST proteolytic signal-containing nuclear protein (PEST-contair	36		7	2	-
Q7RTV0	PHD finger-like domain-containing protein 5A (PHD finger-like d	11.8		1		-
P00439	Phenylalanine-4-hydroxylase (EC 1,14,16,1) (PAH) (Phe-4-mono	18.4	4			X
Q9Y285	Phenylalanyl-tRNA synthetase alpha chain (EC 6,1,1,20) (Phenyl	12.2		1	3	-
Q9NSD9	Phenylalanyl-tRNA synthetase beta chain (EC 6,1,1,20) (Phenyla	8.1			3	-
P30086	Phosphatidylethanolamine-binding protein (PEBP) (Prostatic bir	85.6	17	13	5	X
P48739	Phosphatidylinositol transfer protein beta isoform (PtdIns trans	5.2		1		X
O00329	Phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic subuni	1.1	1			-
Q8TBX8	Phosphatidylinositol-5-phosphate 4-kinase type-2 gamma - Hon	4.3			1	-
O95394	Phosphoacetylglucosamine mutase (EC 5,4,2,3) (PAGM) (Acetyl	3.7		1		-
Q16822	Phosphoenolpyruvate carboxykinase [GTP], mitochondrial preci	53.1	24	17		X
P35558	Phosphoenolpyruvate carboxykinase, cytosolic [GTP] (EC 4,1,1,3	4.2	2	1		-
P36871	Phosphoglucomutase-1 (EC 5,4,2,2) (Glucose phosphomutase 1	63.7	18	13	5	X
Q96G03	Phosphoglucomutase-2 (EC 5,4,2,2) (Glucose phosphomutase 2	2.9		1	1	-
P00558	Phosphoglycerate kinase 1 (EC 2,7,2,3) (Primer recognition prot	77.7	8	22	17	X
P18669	Phosphoglycerate mutase 1 (EC 5,4,2,1) (EC 5,4,2,4) (EC 3,1,3,1	67.3	7	11	11	X
A6NDG6	Phosphoglycolate phosphatase - Homo sapiens (Human)	28.7		5	3	-
O00168	Phospholemman precursor - Homo sapiens (Human)	13	1			-
P36969	Phospholipid hydroperoxide glutathione peroxidase, mitochond	12.7	2			-
Q9H008	Phospholysine phosphohistidine inorganic pyrophosphate phos	7.8	1			-
O15305	Phosphomannomutase 2 (EC 5,4,2,8) (PMM 2)	15.4		1		X
Q15126	Phosphomevalonate kinase (EC 2,7,4,2) (PMKase)	17.7	1	1	2	X
O15067	Phosphoribosylformylglycinamide synthase (EC 6,3,5,3) (FGAM	29.7		11	16	X
Q9Y617	Phosphoserine aminotransferase (EC 2,6,1,52) (PSAT) - Homo sa	56.2	5	14	10	-
P78330	Phosphoserine phosphatase (EC 3,1,3,3) (PSP) (O-phosphoserin	40.9		5	5	X
Q96BW5	Phosphotriesterase-related protein (Parathion hydrolase-relate	3.2	1	1		X
Q5SRE7	Phytanoyl-CoA dioxygenase domain-containing protein 1 OS=Hu	4.1	1			-
O14832	Phytanoyl-CoA dioxygenase, peroxisomal precursor - Homo sap	3.3	1			-
P36955	Pigment epithelium-derived factor precursor (PEDF) (Serp-F1)	13.2		3		-
O00625	Pirin - Homo sapiens (Human)	26.9		2	6	-
P35237	Placental thrombin inhibitor (Cytoplasmic antiproteinase) (CAP)	26.3	1	1	7	X
Q5JTB6	Placenta-specific protein 9 precursor - Homo sapiens (Human)	21.6		1		-
P02753	Plasma retinol-binding protein precursor (PRBP) (RBP) [Contain	49.8	3	4		X
P13797	Plastin-3 (T-plastin)	36.4			14	X
P43034	Platelet-activating factor acetylhydrolase IB alpha subunit (PAF	3.7		1		-
P68402	Platelet-activating factor acetylhydrolase IB beta subunit (EC 3,:	31.4		4	2	X
Q15102	Platelet-activating factor acetylhydrolase IB gamma subunit (EC	18.2		2	1	X
Q86W56	Poly(ADP-ribose) glycohydrolase - Homo sapiens (Human)	3.4			1	-
Q15365	Poly(rC)-binding protein 1 (Alpha-CP1) (hnRNP-E1) (Nucleic acid	60.1		9	7	X
Q15366	Poly(rC)-binding protein 2 (Alpha-CP2) (hnRNP-E2)	41.9		4	6	X
P57721	Poly(rC)-binding protein 3 (Alpha-CP3)	20.9		4	3	X

P11940	Polyadenylate-binding protein 1 (Poly(A)-binding protein 1) (PA	42.8		14	16	-
Q4VXU2	Polyadenylate-binding protein 1-like - Homo sapiens (Human)	7.3		2	3	-
Q13310	Polyadenylate-binding protein 4 (Poly(A)-binding protein 4) (PA	22		5	11	X
Q96DU9	Polyadenylate-binding protein 5 - Homo sapiens (Human)	2.6			2	-
P26599	Polypyrimidine tract-binding protein 1 (PTB) (Heterogeneous nu	23.9		4	4	-
Q8TCS8	Polyribonucleotide nucleotidyltransferase 1, mitochondrial prec	2.9			1	-
P08397	Porphobilinogen deaminase (EC 2,5,1,61) (Hydroxymethylbilan	11.4		2	1	-
Q96RN5	Positive cofactor 2 glutamine/Q-rich-associated protein (PC2 gl	2.3			1	-
O60925	Prefoldin subunit 1	17.2		1	2	X
Q9UHV9	Prefoldin subunit 2	52.6	2	5	5	X
P61758	Prefoldin subunit 3 (Von Hippel-Lindau-binding protein 1) (VHL-	46.2		6	3	X
Q9NQP4	Prefoldin subunit 4 (Protein C-1) - Homo sapiens (Human)	20.1		1	2	-
Q99471	Prefoldin subunit 5 (C-myc-binding protein Mm-1) (Myc modul	49.4	1	2	5	X
O15212	Prefoldin subunit 6 (Protein Ke2) - Homo sapiens (Human)	29.5		1	3	-
Q15007	Pre-mRNA-splicing regulator WTAP - Homo sapiens (Human)	5.1		1		-
Q5JRX3	Presequence protease, mitochondrial precursor (EC 3,4,24,-) (h	5.4	1	1	1	-
P07602	Proactivator polypeptide precursor [Contains: Saposin A (Protei	14.9	3	6	3	X
Q3SY69	Probable 10-formyltetrahydrofolate dehydrogenase ALDH1L2 -	4.2	1			-
Q96HY7	Probable 2-oxoglutarate dehydrogenase E1 component DHKTD	16.1	4			-
Q5JTZ9	Probable alanyl-tRNA synthetase, mitochondrial precursor (EC	4.1		2		-
Q63HM1	Probable arylformamidase (EC 3,5,1,9) (Kynurenine formamidas	3.9	1			-
Q92841	Probable ATP-dependent RNA helicase DDX17 (EC 3,6,1,-) (DEA	13.1		4	4	-
P38919	Probable ATP-dependent RNA helicase DDX48 (EC 3,6,1,-) (DEA	15.8		2	2	X
P17844	Probable ATP-dependent RNA helicase DDX5 (EC 3,6,1,-) (DEAD	16		4	4	-
Q9HA77	Probable cysteinyl-tRNA synthetase, mitochondrial precursor (E	3.2	1	1	1	-
Q86WU2	Probable D-lactate dehydrogenase, mitochondrial precursor (EC	6.1	2			-
Q8TEA8	Probable D-tyrosyl-tRNA(Tyr) deacylase 1 (EC 3,1,-,-) - Homo sa	12.9		1		-
O75592	Probable E3 ubiquitin-protein ligase MYCBP2 (EC 6,3,2,-) (Myc-k	0.4		1		-
Q96NU7	Probable imidazolonepropionase - Homo sapiens (Human)	20	3			-
P30039	Probable isomerase MAWBP (EC 5,1,-,-) (MAWD-binding protei	84	12			-
O96008	Probable mitochondrial import receptor subunit TOM40 homol	19.7		3	5	X
Q8N0Y7	Probable phosphoglycerate mutase 4 (EC 5,4,2,1) (EC 5,4,2,4) (E	28.7		2		-
Q9H3G5	Probable serine carboxypeptidase CPVL precursor (EC 3,4,16,-) (	5.5		2		-
Q8WWH5	Probable tRNA pseudouridine synthase 1 (EC 5,4,99,-) - Homo s	6		1		-
Q9BSD7	Probable UPF0334 kinase-like protein C1orf57 - Homo sapiens (	20		1		-
O00469	Procollagen-lysine,2-oxoglutarate 5-dioxygenase 2 precursor (E	1.9		1	1	X
P07737	Profilin-1 (Profilin I)	78.6	9	8	11	X
P35080	Profilin-2 (Profilin II)	27.1	1	2	3	-
Q8WUM4	Programmed cell death 6-interacting protein (PDCD6-interactin	22.9	2	4	10	X
Q9BRP1	Programmed cell death protein 2-like - Homo sapiens (Human)	4.2			1	-
Q53EL6	Programmed cell death protein 4 (Nuclear antigen H731-like) (N	5.5			2	-
O14737	Programmed cell death protein 5 (Protein TFAR19) (TF-1 cell ap	29.6		3	3	X
O75340	Programmed cell death protein 6 (Probable calcium-binding pr	23		2	4	X
P35232	Prohibitin,	78.7	7	15	10	X
Q99623	Prohibitin-2 (B-cell receptor-associated protein BAP37) (Repres	53.5	6	9	8	-
P12004	Proliferating cell nuclear antigen (PCNA) (Cyclin) - Homo sapien	49.4		13	5	-
Q9UQ80	Proliferation-associated protein 2G4 (Cell cycle protein p38-2G4	38.3	1	6	5	X
O94903	Proline synthetase co-transcribed bacterial homolog protein	39.6	2	4		-
Q32P28	Prolyl 3-hydroxylase 1 precursor (EC 1,14,11,7) (Leucine- and pr	9.6		1	5	-
Q8IVL6	Prolyl 3-hydroxylase 3 precursor (EC 1,14,11,7) (Leprecan-like p	3.3			1	-

P13674	Prolyl 4-hydroxylase alpha-1 subunit precursor (EC 1,14,11,2) (4	9.6		3	1	X
P48147	Prolyl endopeptidase (EC 3,4,21,26) (Post-proline cleaving enzy	2.4		1	1	X
P05165	Propionyl-CoA carboxylase alpha chain, mitochondrial precursor	9.5	2			-
P05166	Propionyl-CoA carboxylase beta chain, mitochondrial precursor	14.5	4	4		-
Q9H7Z7	Prostaglandin E synthase 2 (EC 5,3,99,3) (Microsomal prostaglai	42.2		2	7	X
Q15185	Prostaglandin E synthase 3 (EC 5,3,99,3) (Cytosolic prostaglandi	36.9	1	4	1	X
Q06323	Proteasome activator complex subunit 1 (Proteasome	60.2	8	11	5	X
Q9UL46	Proteasome activator complex subunit 2 (Proteasome activator	72	9	10	9	X
P61289	Proteasome activator complex subunit 3 (Proteasome activator	24.4		3	5	X
Q5JS54	Proteasome assembly chaperone 4 OS=Homo sapiens GN=PSM	13			1	-
Q92530	Proteasome inhibitor PI31 subunit (hPI31) - Homo sapiens (Hun	14		1	1	-
P25786	Proteasome subunit alpha type 1 (EC 3,4,25,1) (Proteasome cor	67.3	2	6	8	X
P25787	Proteasome subunit alpha type 2 (EC 3,4,25,1) (Proteasome cor	38.5	3	5	4	X
P25788	Proteasome subunit alpha type 3 (EC 3,4,25,1) (Proteasome cor	34.5	3	6	6	X
P25789	Proteasome subunit alpha type 4 (EC 3,4,25,1) (Proteasome cor	53.6	2	5	7	X
P28066	Proteasome subunit alpha type 5 (EC 3,4,25,1) (Proteasome zet	34.4	2	4	3	-
P60900	Proteasome subunit alpha type 6 (EC 3,4,25,1) (Proteasome iot	43.5	2	7	7	X
O14818	Proteasome subunit alpha type 7 (EC 3,4,25,1) (Proteasome suk	64.5	5	8	7	X
P20618	Proteasome subunit beta type 1 (EC 3,4,25,1) (Proteasome com	61.4	6	7	8	-
P49721	Proteasome subunit beta type 2 (EC 3,4,25,1) (Proteasome com	62.2	2	5	6	X
P49720	Proteasome subunit beta type 3 (EC 3,4,25,1) (Proteasome thet	48.3	5	5	5	X
P28070	Proteasome subunit beta type 4 precursor (EC 3,4,25,1) (Protea	34.1		4	2	X
P28074	Proteasome subunit beta type 5 precursor (EC 3,4,25,1) (Protea	60.1	1	6	7	-
P28072	Proteasome subunit beta type 6 precursor (EC 3,4,25,1) (Protea	38.9	2	5	5	X
Q99436	Proteasome subunit beta type 7 precursor (EC 3,4,25,1) (Protea	30	1	2	4	X
P28062	Proteasome subunit beta type 8 precursor (EC 3,4,25,1) (Protea	12.7	2			-
P28065	Proteasome subunit beta type 9 precursor (EC 3,4,25,1) (Protea	11	1			X
P11171	Protein 4,1 (Band 4,1) (P4,1) (EPB4,1) (4,1R) - Homo sapiens (Hu	1.4	1	1		-
Q99873	Protein arginine N-methyltransferase 1 (EC 2,1,1,-) (Interferon r	7.5		1	1	-
Q562R1	Protein beta-actin-like - Homo sapiens (Human)	19.4	3	5		-
Q9NQ88	Protein C12orf5	13		2	2	-
Q9Y224	Protein C14orf166	57.4	1	7	6	X
Q969H8	Protein C19orf10 precursor (Stromal cell-derived growth factor	32.9	3	3	3	X
Q9NWU2	Protein C20orf11 (Two-hybrid associated protein 1 with RanBP1	25.4		2		-
Q9NQG5	Protein C20orf77	34.4		6	2	X
Q9P1F3	Protein C6orf115	16			1	X
O75223	Protein C7orf24	23.4		2	1	X
Q9UKY7	Protein CDV3 homolog - Homo sapiens (Human)	24.4		1		-
Q8WUX9	Protein CHMP7 - Homo sapiens (Human)	3.8			1	-
O75629	Protein CREG1 precursor (Cellular repressor of E1A-stimulated g	9.5		1		-
O60888	Protein CutA precursor (Brain acetylcholinesterase putative me	33	2	3	2	-
O60610	Protein diaphanous homolog 1 (Diaphanous-related formin-1) (	5.3	1	4		-
P30101	Protein disulfide-isomerase A3 precursor (EC 5,3,4,1) (Disulfide	64	12	24	16	X
P13667	Protein disulfide-isomerase A4 precursor (EC 5,3,4,1) (Protein E	39.7	7	16	2	X
Q15084	Protein disulfide-isomerase A6 precursor (EC 5,3,4,1) (Protein d	45	6	14	8	X
P07237	Protein disulfide-isomerase precursor (EC 5,3,4,1) (PDI) (Prolyl 4	72.2	17	30	11	X
Q99497	Protein DJ-1 (Oncogene DJ1)	82	7	11	7	X
Q9NX18	Protein EMI5 homolog, mitochondrial precursor - Homo sapiens	8.4			1	-
Q96BN8	Protein FAM105B - Homo sapiens (Human)	10.5			2	-
Q8IZP2	Protein FAM10A4	17.1			3	-

Q8NFI4	Protein FAM10A5 - Homo sapiens (Human)	15.2		4	3	-
Q9BUR5	Protein FAM121B precursor - Homo sapiens (Human)	13.6	1		2	-
Q96C01	Protein FAM136A - Homo sapiens (Human)	23.2		2		-
Q5RI15	Protein FAM36A - Homo sapiens (Human)	19.5			1	-
Q9BSJ8	Protein FAM62A (Membrane-bound C2 domain-containing prot	3.7	1	2		-
Q9Y3D0	Protein FAM96B - Homo sapiens (Human)	13.5		1		-
P49354	Protein farnesyltransferase/geranylgeranyltransferase type I al	4.7		1		X
Q9C0B1	Protein fatso - Homo sapiens (Human)	7.5		2	2	-
A2VDF0	Protein fucU homolog - Homo sapiens (Human)	29.9	3			-
O94992	Protein HEXIM1 - Homo sapiens (Human)	4.7		1		-
Q14165	Protein KIAA0152 precursor	8.9	1			X
Q8N163	Protein KIAA1967 (Deleted in breast cancer gene 1 protein) (DB	19.6		9		-
Q9UNF0	Protein kinase C and casein kinase substrate in neurons protein	4.5		2	1	X
Q14160	Protein LAP4 (Protein scribble homolog) (hScrib) - Homo sapien	1.3			1	-
Q9BQ69	Protein LRP16 - Homo sapiens (Human)	17.8	2	1	2	-
Q3MHD2	Protein LSM12 homolog - Homo sapiens (Human)	19		1	2	-
Q8WZAO	Protein LZIC (Leucine zipper and ICAT homologous domain-cont	25.3		2		-
P61326	Protein mago nashi homolog	24.7		1	3	-
Q9Y316	Protein memo (Mediator of ErbB2-driven cell motility) (C21orf1	23.9		1	2	-
Q9UN36	Protein NDRG2 (Protein Syld709613) - Homo sapiens (Human)	33.4	2	2		-
Q9BPW8	Protein NipSnap1 - Homo sapiens (Human)	48.6	6	5	1	-
O75323	Protein NipSnap2 (Glioblastoma amplified sequence) - Homo sa	22.7		3	2	-
Q9UFN0	Protein NipSnap3A (NipSnap4) (Target for Salmonella secreted	14.6	2			-
Q8IWE2	Protein NOXP20 - Homo sapiens (Human)	9.4	1	1	1	-
Q96C90	Protein phosphatase 1 regulatory subunit 14B (Phospholipase C	42.2		2	2	-
Q15435	Protein phosphatase 1 regulatory subunit 7 (Protein phosphata:	5		1	1	X
P35813	Protein phosphatase 2C isoform alpha (EC 3,1,3,16) (PP2C-alpha	3.1	1			-
O15355	Protein phosphatase 2C isoform gamma (EC 3,1,3,16) (PP2C-gar	14.1		2	3	-
P41236	Protein phosphatase inhibitor 2 (IPP-2) - Homo sapiens (Human	12.7		2		-
Q6NXS1	Protein phosphatase inhibitor 2-like protein 3 - Homo sapiens (I	12.7		2		-
Q9Y570	Protein phosphatase methylesterase 1 (EC 3,1,1,-) (PME-1)	9.1			2	X
Q96M27	Protein PPRC1 - Homo sapiens (Human)	10.1		2	2	-
P23297	Protein S100-A1 - Homo sapiens (Human)	26.6		2		-
Q96FQ6	Protein S100-A16 (S100 calcium-binding protein A16) (Protein S	10.7		1	1	-
P25815	Protein S100-P (S100 calcium-binding protein P) - Homo sapiens	62.1		2	4	-
Q01105	Protein SET (Phosphatase 2A inhibitor I2PP2A) (I-2PP2A) (Temp	28.3		3	5	X
Q92734	Protein TFG (TRK-fused gene protein) - Homo sapiens (Human)	7.5		1	2	-
Q15436	Protein transport protein Sec23A (SEC23-related protein A)	10.8	2	4	1	X
Q15437	Protein transport protein Sec23B (SEC23-related protein B) - Ho	1.6			1	-
O95486	Protein transport protein Sec24A (SEC24-related protein A) (Fra	1	1	1	1	-
O94979	Protein transport protein Sec31A - Homo sapiens (Human)	19.8	1	8	4	-
Q93096	Protein tyrosine phosphatase type IVA protein 1 (EC 3,1,3,48) (F	15.6		2		-
Q9UKW4	Protein vav-3 - Homo sapiens (Human)	3.8	1			-
Q9BRP8	Protein wibg homolog - Homo sapiens (Human)	16.2		2		-
P21980	Protein-glutamine gamma-glutamyltransferase 2 (EC 2,3,2,13) (	8	2	1		X
P22061	Protein-L-isoaspartate(D-aspartate) O-methyltransferase (EC 2,	63	2	4	3	X
P06454	Prothymosin alpha [Contains: Thymosin alpha-1]	9			1	-
Q8TAB3	Protocadherin-19 precursor - Homo sapiens (Human)	1.1	1			-
P46108	Proto-oncogene C-crk (P38) (Adapter molecule crk)	10.2		1	1	X
P09769	Proto-oncogene tyrosine-protein kinase FGR (EC 2,7,10,2) (P55-	1.5			1	-

P06239	Proto-oncogene tyrosine-protein kinase LCK (EC 2,7,10,2) (p56-	3.5		1		-
Q96PZ0	Pseudouridylate synthase 7 homolog (EC 5,4,99,-) - Homo sapie	2.7			1	-
P61457	Pterin-4-alpha-carbinolamine dehydratase (EC 4,2,1,96) (PHS) (4	57.7	5	4		-
Q9H0N5	Pterin-4-alpha-carbinolamine dehydratase 2 (EC 4,2,1,96) (PHS	8.7		1		-
P00491	Purine nucleoside phosphorylase (EC 2,4,2,1) (Inosine phosphor	54	6	3	6	X
P55786	Puromycin-sensitive aminopeptidase (EC 3,4,11,-) (PSA)	5.3		4	2	-
A6NMY6	Putative annexin A2-like protein OS=Homo sapiens GN=ANXA2F	47.5			21	-
Q16740	Putative ATP-dependent Clp protease proteolytic subunit, mitot	9.7		2	1	X
Q99622	Putative C10 protein - Homo sapiens (Human)	14.3			1	-
Q9NTK5	Putative GTP-binding protein PTD004	31.3	1	5	6	-
Q58FF8	Putative heat shock protein HSP 90-beta 2 OS=Homo sapiens Gl	19.4			7	-
Q58FF7	Putative heat shock protein HSP 90-beta-3 OS=Homo sapiens G	21.8			13	-
Q9HCE1	Putative helicase MOV-10 (EC 3,6,1,-) (Moloney leukemia virus	1.4		1		-
A6ND91	Putative L-aspartate dehydrogenase - Homo sapiens (Human)	10.2	2			-
O43143	Putative pre-mRNA-splicing factor ATP-dependent RNA helicase	7.5		2	2	-
Q53FA7	Putative quinone oxidoreductase (EC 1,-,-,-) (Tumor protein p53	9.6		1		-
P98179	Putative RNA-binding protein 3 (RNA-binding motif protein 3) (f	11.5		1	1	-
Q9NQ29	Putative RNA-binding protein Luc7-like 1 (SR+89) (Putative SR p	12.7		2		-
Q9Y383	Putative RNA-binding protein Luc7-like 2 - Homo sapiens (Huma	12		3	1	-
Q9Y448	Putative TRAF4-associated factor 1 - Homo sapiens (Human)	6		1	1	-
A6NL28	Putative tropomyosin alpha-3 chain-like protein OS=Homo sapi	14.8		2	4	-
Q9NTT1	Putative ubiquitin-conjugating enzyme E2 D3-like protein - Hom	23.8	1	2		-
O00764	Pyridoxal kinase (EC 2,7,1,35) (Pyridoxine kinase)	36.2	3	4	6	X
Q96GD0	Pyridoxal phosphate phosphatase (EC 3,1,3,74) (PLP phosphata	4.7		1		-
Q6P996	Pyridoxal-dependent decarboxylase domain-containing protein	3.3		2		-
Q9NVS9	Pyridoxine-5*-phosphate oxidase (EC 1,4,3,5) (Pyridoxamine-ph	49.4	1	5	1	X
Q9NXJ5	Pyroglutamyl-peptidase I (EC 3,4,19,3) (Pyrrolidone-carboxylate	7.7		1		X
P32322	Pyrroline-5-carboxylate reductase 1 (EC 1,5,1,2) (P5CR 1) (P5C r	44.2		9	1	-
Q96C36	Pyrroline-5-carboxylate reductase 2 (EC 1,5,1,2) (P5CR 2) (P5C r	20.9	1	3		-
P11498	Pyruvate carboxylase, mitochondrial precursor (EC 6,4,1,1) (Pyr	49.6	26	11	4	-
P08559	Pyruvate dehydrogenase E1 component alpha subunit, somatic	13.8		3	4	X
P11177	Pyruvate dehydrogenase E1 component beta subunit, mitochor	45.4	1	9	5	X
Q8NCN5	Pyruvate dehydrogenase phosphatase regulatory subunit, mitot	2.7		1		-
P14618	Pyruvate kinase isozymes M1/M2 (EC 2,7,1,40) (Pyruvate kinase	75.9		21	38	X
P30613	Pyruvate kinase isozymes R/L (EC 2,7,1,40) (R-type/L-type pyruv	22.5	5			X
Q08257	Quinone oxidoreductase (EC 1,6,5,5) (NADPH:quinone reductas	52.3	5	4		-
P31150	Rab GDP dissociation inhibitor alpha (Rab GDI alpha) (Guanosin	16.3		3	5	X
P50395	Rab GDP dissociation inhibitor beta (Rab GDI beta) (Guanosine	57.8	6	8	11	X
Q15042	Rab3 GTPase-activating protein catalytic subunit (RAB3 GTPase-	1.8		1		-
P35241	Radixin	36.7		5	11	X
P46060	Ran GTPase-activating protein 1	6.1		1		X
O60518	Ran-binding protein 6 (RanBP6)	3		1	1	-
P43487	Ran-specific GTPase-activating protein (Ran-binding protein 1) (	39.3		4	3	X
P52306	Rap1 GTPase-GDP dissociation stimulator 1 (SMG P21	3.5		1		X
P46940	Ras GTPase-activating-like protein IQGAP1 (p195)	5.8		2	2	-
Q13576	Ras GTPase-activating-like protein IQGAP2	5.8	3	3		-
Q15404	Ras suppressor protein 1 (Rsu-1) (RSP-1)	41.2		2	5	-
Q13283	Ras-GTPase-activating protein-binding protein 1 (EC 3,6,1,-) (AT	36.1		5	8	X
Q9UN86	Ras-GTPase-activating protein-binding protein 2 (GAP SH3-dom	4.6			1	-
P63000	Ras-related C3 botulinum toxin substrate 1 precursor (p21-Rac1	31.3		5		-

P62491	Ras-related protein Rab-11A (Rab-11) (YL8)	28.7	2	2	4	-
Q15907	Ras-related protein Rab-11B (GTP-binding protein YPT3)	28.4		3		-
P61106	Ras-related protein Rab-14	31.2	2	1	5	-
P59190	Ras-related protein Rab-15	10.4	2	2	2	-
Q9NP72	Ras-related protein Rab-18 - Homo sapiens (Human)	31.1	1	3		-
P62820	Ras-related protein Rab-1A (YPT1-related protein)	26.8	3	4		X
Q9H0U4	Ras-related protein Rab-1B	18.9		3	2	-
Q9UL25	Ras-related protein Rab-21 - Homo sapiens (Human)	5.3		1		-
P61019	Ras-related protein Rab-2A	24.1	3	3		-
Q9H082	Ras-related protein Rab-33B	4.8	1	1	1	-
Q15286	Ras-related protein Rab-35 (Rab-1C) (GTP-binding protein RAY)	10.9	2	2	2	-
Q14964	Ras-related protein Rab-39A (Rab-39)	5.1		1		-
P51148	Ras-related protein Rab-5C (RAB5L) (L1880)	28.7		3	2	-
P20340	Ras-related protein Rab-6A (Rab-6)	23.1		4	1	-
P51149	Ras-related protein Rab-7	50.7	7	8	8	X
P61006	Ras-related protein Rab-8A (Oncogene c-mel)	10.6	2			-
P11233	Ras-related protein Ral-A - Homo sapiens (Human)	11.2		2		-
P62834	Ras-related protein Rap-1A precursor (GTP-binding protein smg	19	3	3	3	-
P61224	Ras-related protein Rap-1b precursor (GTP-binding protein smg	19	2	4	3	X
P61225	Ras-related protein Rap-2b precursor	42.1		3	2	-
Q9Y3L5	Ras-related protein Rap-2c precursor	26.8		2	1	-
Q96HR9	Receptor expression-enhancing protein 6 (Polyposis locus prote	12.5	2	1		-
P23469	Receptor-type tyrosine-protein phosphatase epsilon precursor	2.9		1		-
Q15493	Regucalcin (RC) (Senescence marker protein 30) (SMP-30) - Hon	25.4	4			-
Q9UJD0	Regulating synaptic membrane exocytosis protein 3 (Nim3) (Ral	3.9	1	1		-
P18754	Regulator of chromosome condensation (Chromosome conden	4.5		1	1	-
O95758	Regulator of differentiation 1 (Rod1) - Homo sapiens (Human)	5.6		1		-
Q92900	Regulator of nonsense transcripts 1 (EC 3,6,1,-) (ATP-dependen	2.6		1	1	-
Q9NZ71	Regulator of telomere elongation helicase 1 - Homo sapiens (Hu	4.4		2		-
Q8WUF5	RelA-associated inhibitor (Inhibitor of ASPP protein) (Protein iA	3.7			1	-
P35244	Replication protein A 14 kDa subunit (RP-A) (RF-A) (Replication	55.4	1	2	3	-
P15927	Replication protein A 32 kDa subunit (RP-A) (RF-A) (Replication	14.4			2	X
Q15293	Reticulocalbin-1 precursor - Homo sapiens (Human)	18.1	1	1	1	-
P00352	Retinal dehydrogenase 1 (EC 1,2,1,36) (RALDH1) (RALDH 1) (Alde	54.7	15	13		X
O75884	Retinoblastoma-binding protein 9 (RBBP-9) (Retinoblastoma-bir	28		3		-
P28702	Retinoic acid receptor RXR-beta (Retinoid X receptor beta) - Ho	3.8	1			-
Q9HB40	Retinoid-inducible serine carboxypeptidase precursor (EC 3,4,16	3.1		1	1	-
Q8TC12	Retinol dehydrogenase 11 (EC 1,1,1,-) (Retinal reductase 1) (Ral	5.3	2			-
Q8NBN7	Retinol dehydrogenase 13 (EC 1,1,1,-) - Homo sapiens (Human)	9.1		1		-
O75452	Retinol dehydrogenase 16 - Homo sapiens (Human)	18.9	3			-
P09455	Retinol-binding protein I, cellular (Cellular retinol-binding prote	32.6		3		X
P82980	Retinol-binding protein III, cellular (CRBP-III) (HRBPiso) - Homo	6.7	1			-
Q86TG7	Retrotransposon-derived protein PEG10 - Homo sapiens (Huma	4.5		2		-
P52565	Rho GDP-dissociation inhibitor 1 (Rho GDI 1) (Rho-GDI alpha)	28.4	1	3	2	X
Q68EM7	Rho GTPase-activating protein 17 - Homo sapiens (Human)	2.8		1		-
O75116	Rho-associated protein kinase 2 (EC 2,7,11,1) (Rho-associated, c	8.9	1	3		-
Q07960	Rho-GTPase-activating protein 1 (GTPase-activating protein rho	3.2	1			X
P62745	Rho-related GTP-binding protein RhoB precursor (H6)	27		3		X
P08134	Rho-related GTP-binding protein RhoC precursor (H9)	37.8	2	5		-
P84095	Rho-related GTP-binding protein RhoG precursor	20.9		1	1	-

Q969G6	Riboflavin kinase (EC 2,7,1,26) (ATP:riboflavin 5*-phosphotransf	13			1	-
O75792	Ribonuclease H2 subunit A (EC 3,1,26,4) (RNase H2 subunit A) (I	5.4			1	X
P13489	Ribonuclease inhibitor (Ribonuclease/angiogenin inhibitor 1) (R	35.6		2	7	-
O00584	Ribonuclease T2 precursor (EC 3,1,27,-) (Ribonuclease 6) - Homo	18.4	3	3		-
P52758	Ribonuclease UK114 (EC 3,1,-,-) (14,5 kDa translational inhibitor	75.9	11	2		-
P23921	Ribonucleoside-diphosphate reductase large subunit (EC 1,17,4	23.2			8	-
P49247	Ribose-5-phosphate isomerase (EC 5,3,1,6) (Phosphoriboisomer	21.1		3		X
P60891	Ribose-phosphate pyrophosphokinase I (EC 2,7,6,1) (Phosphori	34.6	1	2	6	X
P11908	Ribose-phosphate pyrophosphokinase II (EC 2,7,6,1) (Phosphori	17.3		2		X
Q15418	Ribosomal protein S6 kinase alpha-1 (EC 2,7,11,1) (S6K-alpha 1)	3.4		2		-
Q15349	Ribosomal protein S6 kinase alpha-2 (EC 2,7,11,1) (S6K-alpha 2)	6.3		1		-
P51812	Ribosomal protein S6 kinase alpha-3 (EC 2,7,11,1) (S6K-alpha 3)	25.8		9		-
Q9P2E9	Ribosome-binding protein 1 (Ribosome receptor protein) (180 k	23.6	12	18		-
P16083	Ribosyldihydronicotinamide dehydrogenase [quinone] (EC 1,10,	42	3		4	X
Q96AT9	Ribulose-phosphate 3-epimerase (EC 5,1,3,1) (Ribulose-5-phosp	17.5		2		X
Q9NTZ6	RNA-binding protein 12 (RNA-binding motif protein 12) (SH3/W	9.5		4	1	-
Q9Y5S9	RNA-binding protein 8A (RNA-binding motif protein 8A) (Ribon	17.2		2		X
Q01844	RNA-binding protein EWS (EWS oncogene) (Ewing sarcoma brea	4.7		2		-
P35637	RNA-binding protein FUS (Oncogene FUS) (Oncogene TLS) (Tran	9.7		2		-
Q96DH6	RNA-binding protein Musashi homolog 2 (Musashi-2) - Homo sa	4.9		1		-
Q5TZA2	Rootletin (Ciliary rootlet coiled-coil protein) - Homo sapiens (Hu	0.4			1	-
Q9Y265	RuvB-like 1 (EC 3,6,1,-) (49-kDa TATA box-binding protein-intera	29.4		3	8	X
Q9Y230	RuvB-like 2 (EC 3,6,1,-) (48-kDa TATA box-binding protein-intera	22.7		3	6	X
Q99584	S100 calcium-binding protein A13	33.7			3	X
P26447	S100 calcium-binding protein A4 (Metastasin) (Mts1 protein) (P	45.5			7	X
Q00266	S-adenosylmethionine synthetase isoform type-1 (EC 2,5,1,6) (M	16.2	6			X
P31153	S-adenosylmethionine synthetase isoform type-2 (EC 2,5,1,6) (M	17.5	3	1	2	X
Q9Y3Z3	SAM domain and HD domain-containing protein 1 (Dendritic ce	4.2		2	1	X
Q9UPN7	SAPS domain family member 1	2		1		-
Q9UL12	Sarcosine dehydrogenase, mitochondrial precursor (EC 1,5,99,1	24.3	13	2		-
Q96C86	Scavenger mRNA decapping enzyme DcpS (EC 3,-,-,-) (DCS-1) (H	15.1		3		X
O75880	SCO1 protein homolog, mitochondrial precursor - Homo sapien	12		1	1	-
Q8WVM8	Sec1 family domain-containing protein 1 (Syntaxin-binding prot	16.7		4		X
P55735	SEC13-related protein (SEC13-like protein 1)	8.7	1	1	2	X
O76054	SEC14-like protein 2 (Alpha-tocopherol-associated protein) (TAI	8.7	1			-
Q9Y6Y8	SEC23-interacting protein (p125)	6.4		1		-
P49903	Selenide, water dikinase 1 (EC 2,7,9,3) (Selenophosphate synthe	16.3		4	1	X
Q13228	Selenium-binding protein 1	29	9		1	X
Q96I15	Selenocysteine lyase - Homo sapiens (Human)	6.3	1	1		-
P35270	Sepiapterin reductase (EC 1,1,1,153) (SPR) - Homo sapiens (Hun	43.7	5	6	5	-
Q15019	Septin-2 (Protein NEDD5)	21.9		2	3	X
Q16181	Septin-7 (CDC10 protein homolog)	10.8			2	-
Q9UHD8	Septin-9 (MLL septin-like fusion protein) (MLL septin-like fusion	11.6		2	1	-
P34896	Serine hydroxymethyltransferase, cytosolic (EC 2,1,2,1) (Serine	16.4	6	2		-
P34897	Serine hydroxymethyltransferase, mitochondrial precursor (EC :	41.9	7	10	9	-
O43464	Serine protease HTRA2, mitochondrial precursor (EC 3,4,21,-) (F	8.3		2		X
P62140	Serine/threonine protein phosphatase PP1-beta catalytic subun	34.9		5	7	X
Q9Y6E0	Serine/threonine-protein kinase 24 (EC 2,7,11,1) (STE20-like kin	6.8		2		-
Q9UPZ9	Serine/threonine-protein kinase ICK - Homo sapiens (Human)	1.3			1	-
Q9NRM7	Serine/threonine-protein kinase LATS2 - Homo sapiens (Human	1.3	1			-

O95747	Serine/threonine-protein kinase OSR1 (EC 2,7,1,37) (Oxidative s	7.4			2	-
Q9BXM7	Serine/threonine-protein kinase PINK1, mitochondrial precursor	4.3		1		-
P63151	Serine/threonine-protein phosphatase 2A 55 kDa regulatory sul	6.7		1	1	X
Q14738	Serine/threonine-protein phosphatase 2A 56 kDa regulatory sul	5		1	1	-
P30153	Serine/threonine-protein phosphatase 2A 65 kDa regulatory sul	41.3	2	6	12	X
P30154	Serine/threonine-protein phosphatase 2A 65 kDa regulatory sul	13.1	1	4	4	X
Q15257	Serine/threonine-protein phosphatase 2A regulatory subunit B*	2.8			1	-
P62136	Serine/threonine-protein phosphatase PP1-alpha catalytic subu	33.3		2	6	X
P36873	Serine/threonine-protein phosphatase PP1-gamma catalytic sul	34.1			5	X
P21549	Serine--pyruvate aminotransferase (EC 2,6,1,51) (SPT) (Alanine-	54.6	15			-
Q9Y3F4	Serine-threonine kinase receptor-associated protein (UNR-inter	28.9		1	7	X
P02787	Serotransferrin precursor (Transferrin) (Siderophilin) (Beta-1-m	38.1	6	14		X
P36952	Serpin B5 precursor (Maspin) (Protease inhibitor 5) - Homo sapi	3.5			1	-
P50452	Serpin B8 (Cytoplasmic antiproteinase 2) (CAP2) (CAP-2) (Protea	5.9			2	X
O75830	Serpin I2 precursor (Myoepithelium-derived serine protease inh	2.5			1	-
P02768	Serum albumin precursor	59.9	18	17	12	X
P02743	Serum amyloid P-component precursor (SAP) (9,5S alpha-1-glyc	9.4	1			-
Q15165	Serum paraoxonase/arylesterase 2 (EC 3,1,1,2) (EC 3,1,8,1) (POI	4.5		1	1	X
P49591	Seryl-tRNA synthetase (EC 6,1,1,11) (Serine--tRNA ligase) (SerRS	28		6	5	X
Q9NP81	Seryl-tRNA synthetase, mitochondrial precursor (EC 6,1,1,11) (S	3.1		1		-
O75368	SH3 domain-binding glutamic acid-rich-like protein	36.8	1		3	X
Q16836	Short chain 3-hydroxyacyl-CoA dehydrogenase, mitochondrial p	65.6	7	5	4	-
Q9Y3A5	Shwachman-Bodian-Diamond syndrome protein - Homo sapien	21.6	1		2	-
Q9NR45	Sialic acid synthase (N-acetylneuraminase synthase) (EC 2,5,1,5)	37		5	2	X
Q99519	Sialidase-1 precursor (EC 3,2,1,18) (Lysosomal sialidase) (N-acet	2.7		1		-
Q9H9B4	Sideroflexin-1 (Tricarboxylate carrier protein) (TCC)	30.4	3	2	4	-
Q9BWM7	Sideroflexin-3 - Homo sapiens (Human)	8.7			1	-
Q8TD22	Sideroflexin-5 - Homo sapiens (Human)	5.9	1			-
P37108	Signal recognition particle 14 kDa protein (SRP14) (18 kDa Alu R	38.2		3	1	-
P09132	Signal recognition particle 19 kDa protein (SRP19) - Homo sapie	26.4		2		-
O76094	Signal recognition particle 72 kDa protein (SRP72) - Homo sapie	5.5		2		-
P49458	Signal recognition particle 9 kDa protein (SRP9)	36		2	2	-
Q9Y5M8	Signal recognition particle receptor subunit beta (SR-beta) (Prot	5.2		1		-
P40763	Signal transducer and activator of transcription 3 (Acute-phase	2.3		1		-
Q92783	Signal transducing adapter molecule 1 - Homo sapiens (Human)	6.3		2		-
Q04837	Single-stranded DNA-binding protein, mitochondrial precursor (	55.4	4	4	5	-
O75044	SLIT-ROBO Rho GTPase-activating protein 2 - Homo sapiens (Hu	2.2	1			-
O43765	Small glutamine-rich tetratricopeptide repeat-containing protei	24.6		7	2	-
Q96EQ0	Small glutamine-rich tetratricopeptide repeat-containing protei	6.6		1		-
P62304	Small nuclear ribonucleoprotein E (snRNP-E) (Sm protein E) (Sm	12		1	1	-
P62306	Small nuclear ribonucleoprotein F (snRNP-F) (Sm protein F) (Sm	15.1		1		-
P62314	Small nuclear ribonucleoprotein Sm D1 (snRNP core protein D1]	16.8		1		-
P62316	Small nuclear ribonucleoprotein Sm D2 (snRNP core protein D2]	33.1		2	1	-
P62318	Small nuclear ribonucleoprotein Sm D3 (snRNP core protein D3]	24.6		2	1	-
P14678	Small nuclear ribonucleoprotein-associated proteins B and B* (s	3.8		2		-
P61956	Small ubiquitin-related modifier 2 precursor (SUMO-2) (Ubiquit	12.6	1	1	1	X
Q13126	S-methyl-5-thioadenosine phosphorylase (EC 2,4,2,28) (5*-metl	31.8		4	4	X
P05023	Sodium/potassium-transporting ATPase alpha-1 chain precursor	5	1	2	2	-
P05026	Sodium/potassium-transporting ATPase subunit beta-1 (Sodium	8.3		2		-
P11166	Solute carrier family 2, facilitated glucose transporter member :	7.1		2		-

Q9Y694	Solute carrier family 22 member 7 OS=Homo sapiens GN=SLC22	3.6	1			-
Q00796	Sorbitol dehydrogenase (EC 1,1,1,14) (L-iditol 2-dehydrogenase	54.9	11	6	2	-
P30626	Sorcin (22 kDa protein) (CP-22) (V19)	17.2			2	X
Q13596	Sorting nexin-1 - Homo sapiens (Human)	4.8			1	-
Q9UMY4	Sorting nexin-12 - Homo sapiens (Human)	26.7			2	-
O60749	Sorting nexin-2 (Transformation-related gene 9 protein) (TRG-9	7.9			2	X
O60493	Sorting nexin-3 (SDP3 protein)	16.7	1	1	1	-
Q9UNH7	Sorting nexin-6 (TRAF4-associated factor 2)	10.1		2		X
Q8N0X7	Spartin - Homo sapiens (Human)	2.7			1	-
Q9NUQ6	SPATS2-like protein - Homo sapiens (Human)	2.3		2		-
Q13813	Spectrin alpha chain, brain (Spectrin, non-erythroid alpha chain	15	2	8	11	-
Q9H254	Spectrin beta chain, brain 3 (Spectrin, non-erythroid beta chain	0.4			1	-
Q96SI9	Spermatid perinuclear RNA-binding protein - Homo sapiens (Hu	3.1		2		-
Q8NB90	Spermatogenesis-associated protein 5 OS=Homo sapiens GN=SI	3.7			2	-
P19623	Spermidine synthase (EC 2,5,1,16) (Putrescine aminopropyltran	26.8		2	5	X
O94905	SPFH domain-containing protein 2 precursor	3.2	1			X
P63208	S-phase kinase-associated protein 1A (Cyclin A/CDK2-associatec	53.4		7	2	-
Q13838	Spliceosome RNA helicase BAT1 (EC 3,6,1,-) (DEAD box protein I	8.4		1	2	X
Q15637	Splicing factor 1 (Zinc finger protein 162) (Transcription factor Z	14.2		3	2	-
Q13435	Splicing factor 3B subunit 2 (Spliceosome-associated protein 14	2.1		1		-
Q15427	Splicing factor 3B subunit 4 (Spliceosome-associated protein 49	5.4		1		-
P26368	Splicing factor U2AF 65 kDa subunit (U2 auxiliary factor 65 kDa :	3.8		1		-
P84103	Splicing factor, arginine/serine-rich 3 (Pre-mRNA-splicing factor	14		2	2	-
P23246	Splicing factor, proline- and glutamine-rich (Polypyrimidine trac	15.1		2	1	-
Q8WW59	SPRY domain-containing protein 4 - Homo sapiens (Human)	39.1	6	2		X
Q15020	Squamous cell carcinoma antigen recognized by T-cells 3 (SART-	8.9		3		-
Q9GZT3	SRA stem-loop-interacting RNA-binding protein, mitochondrial	78	3	7	5	-
Q14247	Src substrate cortactin (Amplixin) (Oncogene EMS1)	4.7		2	2	X
Q7KZF4	Staphylococcal nuclease domain-containing protein 1 (p100 co-	17.9	2	7	7	-
Q14849	StAR-related lipid transfer protein 3 (StARD3) (START domain-co	3.6	1	1		-
P16949	Stathmin (Phosphoprotein p19) (pp19) (Oncoprotein 18) (Op18	52.3		8	8	X
Q93045	Stathmin-2 (SCG10 protein) (Superior cervical ganglion-10 prote	15.1			3	-
Q9UNE7	STIP1 homology and U box-containing protein 1 (EC 6,3,2,-) (STI	12.5		3	1	X
Q9UJZ1	Stomatin-like protein 2 (SLP-2) (EPB72-like 2)	21.6	2	5	4	X
P38646	Stress-70 protein, mitochondrial precursor (75 kDa glucose-regu	51	11	24	23	X
P31948	Stress-induced-phosphoprotein 1 (STI1) (Hsc70/Hsp90-organizir	47		11	10	X
O43815	Striatin - Homo sapiens (Human)	2.7			1	-
Q9HCN8	Stromal cell-derived factor 2-like protein 1 precursor (SDF2-like	9		1		-
O14521	Succinate dehydrogenase [ubiquinone] cytochrome b small sub	16.4	1			-
P31040	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mi	20.5	4	3	5	X
P21912	Succinate dehydrogenase [ubiquinone] iron-sulfur protein, mitc	33.2	5	4		-
P51649	Succinate semialdehyde dehydrogenase, mitochondrial precurs	15.9	5			-
Q9P2R7	Succinyl-CoA ligase [ADP-forming] beta-chain, mitochondrial pr	8.4	1	1	1	X
Q96I99	Succinyl-CoA ligase [GDP-forming] beta-chain, mitochondrial pr	34	5	3		X
P53597	Succinyl-CoA ligase [GDP-forming] subunit alpha, mitochondrial	27.9	3	4		-
P55809	Succinyl-CoA:3-ketoacid-coenzyme A transferase 1, mitochondr	6.9			2	X
Q8NBJ7	Sulfatase-modifying factor 2 precursor (C-alpha-formylglycine-g	16.3	1	2	2	-
O00391	Sulfhydryl oxidase 1 precursor (EC 1,8,3,2) (Quiescin Q6) (hQSO	2.4			1	-
Q9Y6N5	Sulfide:quinone oxidoreductase, mitochondrial precursor (EC 1,	8	2	1		-
Q9BYN0	Sulfiredoxin-1 (EC 1,8,98,2) - Homo sapiens (Human)	46.7		2	2	-

P51687	Sulfite oxidase, mitochondrial precursor (EC 1,8,3,1) - Homo sapiens	14.1	3	1		-
P50225	Sulfotransferase 1A1 (EC 2,8,2,1) (Aryl sulfotransferase 1) (Phe)	65.4	7	10	1	X
P50226	Sulfotransferase 1A2 (EC 2,8,2,1) (Aryl sulfotransferase 2) (Phe)	40.7	5			X
P63279	SUMO-conjugating enzyme UBC9 (EC 6,3,2,-) (SUMO-protein ligase)	22.8		1	3	-
P00441	Superoxide dismutase [Cu-Zn] (EC 1,15,1,1)	79.9	9	5	4	X
P04179	Superoxide dismutase [Mn], mitochondrial precursor (EC 1,15,1,1)	65.3	9	10	2	X
Q9Y2Z0	Suppressor of G2 allele of SKP1 homolog (Sgt1) (Putative 40-6-3 protein)	24.7		4	2	X
O15260	Surfeit locus protein 4	4.8		1		-
Q92922	SWI/SNF-related matrix-associated actin-dependent regulator c	1.7		1		-
Q96A49	Synapse-associated protein 1 - Homo sapiens (Human)	9.9			1	-
Q99536	Synaptic vesicle membrane protein VAT-1 homolog (EC 1,-,-,-)	8.7		2		X
P57105	Synaptojanin-2-binding protein (Mitochondrial outer membrane protein)	14.5	2			-
O00161	Synaptosomal-associated protein 23 (SNAP-23) (Vesicle-membrane protein)	14.7		2		-
O95721	Synaptosomal-associated protein 29 (SNAP-29) (Vesicle-membrane protein)	13.2		1	2	X
P34741	Syndecan-2 precursor (SYND2) (Fibroglycan) (Heparan sulfate proteoglycan)	10	1	1		-
O00560	Syntenin-1 (Syndecan-binding protein 1) (Melanoma differentiation-associated protein)	7.7			1	-
Q9Y490	Talin-1	32.3	6	28	32	X
Q9Y4G6	Talin-2 - Homo sapiens (Human)	2.2			4	-
O15533	Tapasin precursor - Homo sapiens (Human)	5.8	1			-
Q13148	TAR DNA-binding protein 43 (TDP-43)	11.6		3	1	X
P17987	T-complex protein 1 subunit alpha (TCP-1-alpha) (CCT-alpha)	32.6	1	9	8	X
P78371	T-complex protein 1 subunit beta (TCP-1-beta) (CCT-beta)	58.9	4	9	17	X
P50991	T-complex protein 1 subunit delta (TCP-1-delta) (CCT-delta) (Sti)	31.2	1	7	8	X
P48643	T-complex protein 1 subunit epsilon (TCP-1-epsilon) (CCT-epsilon)	38.1	2	8	10	X
Q99832	T-complex protein 1 subunit eta (TCP-1-eta) (CCT-eta) (HIV-1 Nucleocapsid protein)	25.6	1	6	6	X
P49368	T-complex protein 1 subunit gamma (TCP-1-gamma) (CCT-gamma)	47.7	2	10	13	X
P50990	T-complex protein 1 subunit theta (TCP-1-theta) (CCT-theta)	51.5	3	14	14	X
P40227	T-complex protein 1 subunit zeta (TCP-1-zeta) (CCT-zeta) (CCT-zeta)	46	5	14	13	X
Q9UGI8	Testin (TESS)	7.4			1	-
Q9BZE9	Tether containing UBX domain for GLUT4 (Alveolar soft part sarcomere)	6.5		2		-
Q99614	Tetratricopeptide repeat protein 1 (TPR repeat protein 1) - Homo sapiens	12.3		1	1	-
Q9Y3D6	Tetratricopeptide repeat protein 11 (TPR repeat protein 11) (Fis)	34.9	5	2	4	-
A6NLP5	Tetratricopeptide repeat protein 36 OS=Homo sapiens GN=TTC1	32.3	4			-
Q8N5M4	Tetratricopeptide repeat protein 9C - Homo sapiens (Human)	17		2	2	-
P52888	Thimet oligopeptidase (EC 3,4,24,15) (Endopeptidase 24,15) (Metalloprotease)	5.4			2	-
Q9NPJ3	Thioesterase superfamily member 2 - Homo sapiens (Human)	32.9	4	3	3	-
P10599	Thioredoxin (ATL-derived factor) (ADF) (Surface-associated sulphhydryl oxidase)	65.7	3	4	5	X
O95881	Thioredoxin domain-containing protein 12 precursor (EC 1,8,4,2)	33.7		3	2	-
Q9BS26	Thioredoxin domain-containing protein 4 precursor (Endoplasmic reticulum)	24.9	2	3	3	X
Q8NBS9	Thioredoxin domain-containing protein 5 precursor (Thioredoxin domain)	34	3	10	7	X
Q16881	Thioredoxin reductase 1, cytoplasmic precursor (EC 1,8,1,9) (TR)	37.5		2	7	X
Q9NNW7	Thioredoxin reductase 2, mitochondrial precursor (EC 1,8,1,9) (TR)	6.3	1			-
P30048	Thioredoxin-dependent peroxide reductase, mitochondrial precursor	52.3	10	7	6	X
O43396	Thioredoxin-like protein 1 (32 kDa thioredoxin-related protein)	11.4		4	2	X
O76003	Thioredoxin-like protein 2 (PKC-interacting cousin of thioredoxin)	16.4		1	2	X
Q9BRA2	Thioredoxin-like protein 5 (14 kDa thioredoxin-related protein)	40.7	2	3	2	-
Q16762	Thiosulfate sulfurtransferase (EC 2,8,1,1) (Rhodanese)	40.1	4	1		X
Q8IYQ7	Threonine synthase-like 1 - Homo sapiens (Human)	3.1	1			-
P26639	Threonyl-tRNA synthetase, cytoplasmic (EC 6,1,1,3) (Threonine-tRNA synthetase)	23.7		4	8	-
O00142	Thymidine kinase 2, mitochondrial precursor (EC 2,7,1,21) (Mt-1)	4.9	1			-

P04183	Thymidine kinase, cytosolic (EC 2,7,1,21) - Homo sapiens (Human)	22.2			2	-
P19971	Thymidine phosphorylase precursor (EC 2,4,2,4) (TdRPase) (TP)	11.8	2	1		X
P23919	Thymidylate kinase (EC 2,7,4,9) (dTMP kinase)	60.4		12	9	-
P04818	Thymidylate synthase (EC 2,1,1,45) (TS) (TSase)	7.7		1	1	-
Q07157	Tight junction protein ZO-1 (Zonula occludens 1 protein) (Zona occludens 1 protein)	2.2			1	-
Q9UDY2	Tight junction protein ZO-2 (Zonula occludens 2 protein) (Zona occludens 2 protein)	2.4		1	1	-
P10646	Tissue factor pathway inhibitor precursor (TFPI) (Lipoprotein-associated phospholipase A2 inhibitor)	9.5		2		-
Q96KB5	T-lymphokine-activated killer cell-originated protein kinase (EC 2,7,1,2)	3.4			1	X
Q9H0E2	Toll-interacting protein	5.1	1	1		X
Q5JTV8	Torsin-1A-interacting protein 1	4.3		1		X
Q9Y3C4	TP53RK-binding protein - Homo sapiens (Human)	21.1		2		-
O43617	Trafficking protein particle complex subunit 3 (BET3 homolog) - Homo sapiens (Human)	20		2	2	-
Q9BV79	Trans-2-enoyl-CoA reductase, mitochondrial precursor - Homo sapiens (Human)	2.9	1			-
P37837	Transaldolase (EC 2,2,1,2)	50.7	3	8	12	X
P23193	Transcription elongation factor A protein 1 (Transcription elongation factor A protein 1)	11.6		3	2	-
Q15369	Transcription elongation factor B polypeptide 1 (RNA polymerase II transcription elongation factor B polypeptide 1)	24.1	1		3	-
Q15370	Transcription elongation factor B polypeptide 2 (RNA polymerase II transcription elongation factor B polypeptide 2)	50.8		1	3	-
P63272	Transcription elongation factor SPT4 (hSPT4) (DRB sensitivity-inducing factor)	13.7			1	-
Q00059	Transcription factor A, mitochondrial precursor (mtTFA) (Mitochondrial transcription factor A)	4.1		1		-
P20290	Transcription factor BTF3 (RNA polymerase B transcription factor 3) (BTF3)	35.4	1	5	2	X
Q96K17	Transcription factor BTF3 homolog 4 (Basic transcription factor 3 homolog 4)	22.8		3		X
Q9BYE0	Transcription factor HES-7 - Homo sapiens (Human)	8	1			-
Q04206	Transcription factor p65 (Nuclear factor NF-kappa-B p65 subunit) (NF-kappa-B p65 subunit)	2.5		1		X
Q13263	Transcription intermediary factor 1-beta (TIF1-beta) (Tripartite factor 1-beta)	28.9		9	13	X
P02786	Transferrin receptor protein 1 (TfR1) (TR) (TfR) (Trfr) (CD71 anti-transferrin receptor)	2			1	-
Q8WUH2	Transforming growth factor-beta receptor-associated protein 1	2.3			1	-
P61586	Transforming protein RhoA precursor (H12)	59.1	2	7	5	X
Q01995	Transgelin (Smooth muscle protein 22-alpha) (SM22-alpha) (WSN)	63.2		8		-
P37802	Transgelin-2 (SM22-alpha homolog)	78.9	2	5	18	-
P55072	Transitional endoplasmic reticulum ATPase (TER ATPase) (15S Nucleotide Phosphate Phosphatase)	66.9	9	35	26	X
P29401	Transketolase (EC 2,2,1,1) (TK)	57.9	4	13	26	X
Q9BV20	Translation initiation factor eIF-2B subunit alpha/beta/delta-like 1	11.1			2	-
P13693	Translationally-controlled tumor protein (TCTP) (p23) (Histamine release-inducing factor)	31.4	2	5	7	X
Q99598	Translin-associated protein X (Translin-associated factor X)	14.1	1	2	2	X
P51571	Translocon-associated protein delta subunit precursor (TRAP-delta)	24.9	1	2	1	X
P49755	Transmembrane emp24 domain-containing protein 10 precursor	12.8		2		-
Q9BVK6	Transmembrane emp24 domain-containing protein 9 precursor	14	2	3		-
Q9BVC6	Transmembrane protein 109 precursor (Mitsugumin-23) (Mg23)	4.9		1	1	-
Q9H061	Transmembrane protein 126A - Homo sapiens (Human)	14.9		2		-
Q5H9S7	Transmembrane protein C2orf37 - Homo sapiens (Human)	2.9	1			-
P02766	Transthyretin precursor (Prealbumin) (TBPA) (TTR) (ATTR) - Homo sapiens (Human)	57.1	4			-
P53007	Tricarboxylate transport protein, mitochondrial precursor (Citra)	7.7		1		-
P40939	Trifunctional enzyme alpha subunit, mitochondrial precursor (T)	49.8	20	13	11	-
P55084	Trifunctional enzyme subunit beta, mitochondrial precursor (TP)	41.6	4	5	2	-
P22102	Trifunctional purine biosynthetic protein adenosine-3 [Includes adenylosuccinyl-CoA synthetase]	13.9		3	3	X
P60174	Triosephosphate isomerase (EC 5,3,1,1) (TIM) (Triose-phosphate isomerase)	94	16	17	20	X
O14773	Tripeptidyl-peptidase I precursor (EC 3,4,14,9) (TPP-I) (Tripeptidyl-peptidase I)	12.3	1	4	1	X
Q9UI30	TRM112-like protein - Homo sapiens (Human)	80.8		3	5	X
Q08J23	tRNA - Homo sapiens (Human)	33.9		5	14	-
Q9UBP6	tRNA (guanine-N(7)-)-methyltransferase (EC 2,1,1,33) (tRNA(m7G) methyltransferase)	5.4		1		-

Q9NZR1	Tropomodulin-2 (Neuronal tropomodulin) (N-Tmod) - Homo sapiens	3.1			1	-
Q9NYL9	Tropomodulin-3 (Ubiquitous tropomodulin) (U-Tmod) - Homo sapiens	15.6			2	X
P09493	Tropomyosin 1 alpha chain (Alpha-tropomyosin)	30.6	2		9	X
P06753	Tropomyosin alpha-3 chain (Tropomyosin-3) (Tropomyosin gamma)	40.1	3	8	13	X
P67936	Tropomyosin alpha-4 chain (Tropomyosin-4) (TM30p1)	68.5		8	12	X
P07951	Tropomyosin beta chain (Tropomyosin 2) (Beta-tropomyosin)	25.4	2		8	X
P23381	Tryptophanyl-tRNA synthetase (EC 6,1,1,2) (Tryptophan--tRNA ligase)	15.5		2	1	X
P68366	Tubulin alpha-1 chain (Alpha-tubulin 1) (Testis-specific alpha-tubulin)	52.5			16	-
Q6PEY2	Tubulin alpha-3E chain - Homo sapiens (Human)	37.8			10	-
Q9BQE3	Tubulin alpha-6 chain (Alpha-tubulin 6)	72.2		18	20	X
P68363	Tubulin alpha-ubiquitous chain (Alpha-tubulin ubiquitous) (Tubulin alpha-2)	67.8	3	19	21	X
P07437	Tubulin beta-2 chain	73.9	14	27	27	X
Q13885	Tubulin beta-2A chain - Homo sapiens (Human)	55.1	11	23	22	-
Q9BVA1	Tubulin beta-2B chain - Homo sapiens (Human)	52.4			22	-
P68371	Tubulin beta-2C chain (Tubulin beta-2 chain)	67.6	8	26	26	-
Q13509	Tubulin beta-3 chain (Tubulin beta-III) (Tubulin beta-4)	52.9		16	15	-
Q99867	Tubulin beta-4q chain - Homo sapiens (Human)	15.9			4	-
Q9BUF5	Tubulin beta-6 chain - Homo sapiens (Human)	21.5		8	8	-
O75347	Tubulin-specific chaperone A (Tubulin-folding cofactor A) (CFA)	43.5	4	5	4	X
Q99426	Tubulin-specific chaperone B (Tubulin folding cofactor B) (Cytosolic)	13.1			2	X
Q15813	Tubulin-specific chaperone E (Tubulin-folding cofactor E)	3.2			1	X
Q14166	Tubulin--tyrosine ligase-like protein 12	25.3		6	5	X
P55327	Tumor protein D52 (N8 protein) - Homo sapiens (Human)	37		2	6	-
O43399	Tumor protein D54 (hD54) (Tumor protein D52-like 2)	42.2	1	5	5	X
Q12792	Twinfilin-1 (Protein A6) (Protein tyrosine kinase 9) - Homo sapiens	3.5		1		-
Q6IBS0	Twinfilin-2 (Twinfilin-1-like protein) (A6-related protein) (hA6RF)	19.8	1	2	2	X
Q06124	Tyrosine-protein phosphatase non-receptor type 11 (EC 3,1,3,4)	3.2		1		-
P54577	Tyrosyl-tRNA synthetase, cytoplasmic (EC 6,1,1,1) (Tyrosyl--tRNA ligase)	35.8		5	7	X
P09661	U2 small nuclear ribonucleoprotein A* (U2 snRNP-A*)	7.8			2	-
O15116	U6 snRNA-associated Sm-like protein LSm1 (Small nuclear ribonucleoprotein)	9.8		1		-
Q9Y333	U6 snRNA-associated Sm-like protein LSm2 (SnRNP core Sm-like protein)	48.4		1	2	-
P62310	U6 snRNA-associated Sm-like protein LSm3	13.7			2	-
O95777	U6 snRNA-associated Sm-like protein LSm8	16.7		1	1	-
Q9UMX0	Ubiquilin-1 (Protein linking IAP with cytoskeleton 1) (PLIC-1) (hPLIC-1)	7.1			3	X
Q9UHD9	Ubiquilin-2 (Protein linking IAP with cytoskeleton 2) (PLIC-2) (hPLIC-2)	4			2	-
Q9NRR5	Ubiquilin-4 - Homo sapiens (Human)	4.5			2	-
P07919	Ubiquinol-cytochrome c reductase complex 11 kDa protein, mitochondrial	34.1	1	1	1	-
P14927	Ubiquinol-cytochrome c reductase complex 14 kDa protein (EC 1,1,1,1)	43.2	2	2		-
P47985	Ubiquinol-cytochrome c reductase iron-sulfur subunit, mitochondrial	27.4	1	3	1	X
P22695	Ubiquinol-cytochrome-c reductase complex core protein 2, mitochondrial	24.1	2	4	1	-
P31930	Ubiquinol-cytochrome-c reductase complex core protein I, mitochondrial	23.5	4	4	1	X
Q5HYK3	Ubiquinone biosynthesis methyltransferase COQ5, mitochondrial	6.7	1			-
Q99807	Ubiquinone biosynthesis protein COQ7 homolog (Coenzyme Q1 synthase)	17.5		2		-
O75208	Ubiquinone biosynthesis protein COQ9, mitochondrial precursor	10.1	1	1		-
P62988	Ubiquitin	94.7	3	9	8	X
Q14694	Ubiquitin carboxyl-terminal hydrolase 10 (EC 3,1,2,15) (Ubiquitin-specific protease 10)	3.8		2	2	-
P51784	Ubiquitin carboxyl-terminal hydrolase 11 (EC 3,1,2,15) (Ubiquitin-specific protease 11)	1.6	1			-
P54578	Ubiquitin carboxyl-terminal hydrolase 14 (EC 3,1,2,15) (Ubiquitin-specific protease 14)	18	2	2	3	X
P45974	Ubiquitin carboxyl-terminal hydrolase 5 (EC 3,1,2,15) (Ubiquitin-specific protease 5)	20.6		5	7	X
Q93009	Ubiquitin carboxyl-terminal hydrolase 7 (EC 3,1,2,15) (Ubiquitin-specific protease 7)	14.7		8	1	-

P15374	Ubiquitin carboxyl-terminal hydrolase isozyme L3 (EC 3,4,19,12]	51.7	1	4	2	X
Q9Y5K5	Ubiquitin carboxyl-terminal hydrolase isozyme L5 (EC 3,4,19,12]	5.8		2	2	X
O14562	Ubiquitin domain-containing protein UBFD1 - Homo sapiens (H	5.6		2		-
Q92890	Ubiquitin fusion degradation protein 1 homolog (UB fusion prot	3.5		1		-
Q96FW1	Ubiquitin thiolesterase protein OTUB1 (EC 3,4,-,-) (Otubain 1) (C	26.9		4	2	-
P22314	Ubiquitin-activating enzyme E1 (A1S9 protein)	47.7	4	16	27	X
Q14157	Ubiquitin-associated protein 2-like (Protein NICE-4) - Homo sap	7.6		5	1	-
P49459	Ubiquitin-conjugating enzyme E2 A (EC 6,3,2,19) (Ubiquitin-proi	6.6			1	-
P62837	Ubiquitin-conjugating enzyme E2 D2 (EC 6,3,2,19) (Ubiquitin-pr	42.9	1	2	3	-
P60604	Ubiquitin-conjugating enzyme E2 G2 (EC 6,3,2,19) (Ubiquitin-pr	9.1	1			-
P68036	Ubiquitin-conjugating enzyme E2 L3 (EC 6,3,2,19) (Ubiquitin-prc	50	3	3	3	-
O14933	Ubiquitin-conjugating enzyme E2 L6 (EC 6,3,2,19) (Ubiquitin-prc	22.4		2		-
P61088	Ubiquitin-conjugating enzyme E2 N (EC 6,3,2,19) (Ubiquitin-pro	79.6	5	7	6	X
Q9C0C9	Ubiquitin-conjugating enzyme E2 O - Homo sapiens (Human)	2.8		1		-
Q9NPD8	Ubiquitin-conjugating enzyme E2 T (EC 6,3,2,19) (Ubiquitin-prot	14.2			2	-
Q13404	Ubiquitin-conjugating enzyme E2 variant 1 (UEV-1) (CROC-1) (U	26.7	4	5	5	X
Q15819	Ubiquitin-conjugating enzyme E2 variant 2 (MMS2) (Enterocyte	32.4	4	5	5	X
P61086	Ubiquitin-conjugating enzyme E2-25 kDa (EC 6,3,2,19) (Ubiquiti	56		5	4	X
P61960	Ubiquitin-fold modifier 1 precursor - Homo sapiens (Human)	17.6		1		X
Q9UBE0	Ubiquitin-like 1-activating enzyme E1A (SUMO-activating enzym	19.4		3	1	X
Q9UBT2	Ubiquitin-like 1-activating enzyme E1B (SUMO-1-activating enzy	25		4	7	-
Q14376	UDP-glucose 4-epimerase (EC 5,1,3,2) (Galactowaldenase) (UDF	22.4	1	1	2	-
O60701	UDP-glucose 6-dehydrogenase (EC 1,1,1,22) (UDP-Glc dehydrog	77.9	9	34	12	X
Q9NYU2	UDP-glucose:glycoprotein glucosyltransferase 1 precursor (EC 2	3.5	1	2		X
P22310	UDP-glucuronosyltransferase 1-4 precursor (EC 2,4,1,17) (UDP-ξ	6.9	1			-
Q9HAW7	UDP-glucuronosyltransferase 1-7 precursor (EC 2,4,1,17) (UDP-ξ	3.4	1			-
O75310	UDP-glucuronosyltransferase 2B11 precursor - Homo sapiens (H	4.3		1		-
P54855	UDP-glucuronosyltransferase 2B15 precursor (EC 2,4,1,17) (UDF	1.7	1			-
Q9Y3C8	Ufm1-conjugating enzyme 1 (Ubiquitin-fold modifier-conjugatir	11.4			2	-
P30085	UMP-CMP kinase (EC 2,7,4,14) (Cytidylate kinase) (Deoxycytidyl	65.8	10	14	6	X
Q9BRF8	Uncharacterized metallophosphoesterase CSTP1 - Homo sapien	36.3		5		-
Q9BRX8	Uncharacterized protein C10orf58 precursor - Homo sapiens (H	8.3	2			-
Q53FT3	Uncharacterized protein C11orf73 - Homo sapiens (Human)	11.2		1		-
Q9NSK7	Uncharacterized protein C19orf12 - Homo sapiens (Human)	7.1	1			-
Q9BQ61	Uncharacterized protein C19orf43 - Homo sapiens (Human)	14.8		2		-
Q3KP66	Uncharacterized protein C1orf106 - Homo sapiens (Human)	2.1		1		-
Q5JTJ3	Uncharacterized protein C1orf31 - Homo sapiens (Human)	11.2	1			-
Q9GZY8	Uncharacterized protein C2orf33 - Homo sapiens (Human)	3.5			1	-
Q9BT73	Uncharacterized protein C7orf48 - Homo sapiens (Human)	23			2	-
Q9BUH6	Uncharacterized protein C9orf142 - Homo sapiens (Human)	11.8		2	1	-
A2RU67	Uncharacterized protein KIAA1467 - Homo sapiens (Human)	3.9		1		-
Q8IWB1	Uncharacterized protein KIAA1754 precursor - Homo sapiens (H	1.3			1	-
Q6GMV3	Uncharacterized protein LOC391356 - Homo sapiens (Human)	55	1	3	1	-
Q96C11	Uncharacterized sugar kinase FLJ10986 - Homo sapiens (Human)	2.4	1			-
Q9Y3I0	UPF0027 protein C22orf28 - Homo sapiens (Human)	10.9		2	1	-
Q9NRG7	UPF0105 protein C14orf124 - Homo sapiens (Human)	5.3	2	2		-
Q9BVM4	UPF0131 protein - Homo sapiens (Human)	7.8	1			-
Q9P032	UPF0240 protein C6orf66 - Homo sapiens (Human)	26.3		2		-
Q9H7C9	UPF0366 protein C11orf67 - Homo sapiens (Human)	16.4	1			-
Q9BVG4	UPF0368 protein Cxorf26 - Homo sapiens (Human)	5.6		1		-

Q4G0N4	UPF0465 protein C5orf33 - Homo sapiens (Human)	9.3	2			-
Q9NRP0	UPF0527 membrane protein - Homo sapiens (Human)	8.1		1		-
Q5R3I4	UPF0530 protein - Homo sapiens (Human)	7.2	2			-
Q6P1X6	UPF0598 protein C8orf82 OS=Homo sapiens GN=C8orf82 PE=2	25	4	2		-
P11172	Uridine 5*-monophosphate synthase (UMP synthase) [Includes	8.1		1		X
Q9BZX2	Uridine-cytidine kinase 2 (EC 2,7,1,48) (UCK 2) (Uridine monoph	34.1			5	-
Q5DID0	Uromodulin-like 1 precursor - Homo sapiens (Human)	1.8		1		-
P06132	Uroporphyrinogen decarboxylase (EC 4,1,1,37) (URO-D) (UPD)	26.4		2	2	X
Q16851	UTP--glucose-1-phosphate uridylyltransferase 2 (EC 2,7,7,9) (UC	42.1	13	2	2	X
P54727	UV excision repair protein RAD23 homolog B (hHR23B) (XP-C re	24.9		4	3	-
P38606	Vacuolar ATP synthase catalytic subunit A, ubiquitous isoform (I	26.4		5	8	X
P21281	Vacuolar ATP synthase subunit B, brain isoform (EC 3,6,3,14) (V	13.9		2	1	X
P36543	Vacuolar ATP synthase subunit E (EC 3,6,3,14) (V-ATPase E subu	40.7		7	3	X
O75348	Vacuolar ATP synthase subunit G 1 (EC 3,6,3,14) (V-ATPase G su	41.5	1	2	1	-
Q9UBQ0	Vacuolar protein sorting 29 (Vesicle protein sorting 29) (hVPS29	29.7	1	2	2	X
Q96QK1	Vacuolar protein sorting 35 (Vesicle protein sorting 35) (hVPS35	5.7	1	3	1	-
Q7Z7G8	Vacuolar protein sorting-associated protein 13B OS=Homo sapi	0.9			1	-
Q9BRG1	Vacuolar protein sorting-associated protein 25 (hVps25) (ELL-as	16.5		1	1	-
Q86WA6	Valacyclovir hydrolase precursor (EC 3,1,-,-) (VACVase) (Bipheny	26.8	7	2		-
P26640	Valyl-tRNA synthetase (EC 6,1,1,9) (Valine--tRNA ligase) (ValRS)	8.8		3	3	-
P50552	Vasodilator-stimulated phosphoprotein (VASP) - Homo sapiens	3.7			1	-
Q6EMK4	Vasorin precursor (Protein Slit-like 2) - Homo sapiens (Human)	8		1		-
O75396	Vesicle trafficking protein SEC22b (SEC22 vesicle trafficking prot	5.6		1		-
P63027	Vesicle-associated membrane protein 2 (VAMP-2) (Synaptobrev	28.4		2		-
P46459	Vesicle-fusing ATPase (EC 3,6,4,6) (Vesicular-fusion protein NSF	6.7	1	1	2	X
Q12907	Vesicular integral-membrane protein VIP36 precursor (GP36b g	9		1	1	-
Q00341	Vigilin (High density lipoprotein-binding protein) (HDL-binding p	30.6	3	12	7	-
P09327	Villin-1 - Homo sapiens (Human)	24.5		9		-
P08670	Vimentin	14.2			4	X
P18206	Vinculin (Metavinculin)	43.6	1	8	36	X
P62760	Visinin-like protein 1 (VILIP) (Hippocalcin-like protein 3) (HLP3) -	20.4		2		-
P02774	Vitamin D-binding protein precursor (DBP) (Group-specific com	7.8	2			X
P21796	Voltage-dependent anion-selective channel protein 1 (VDAC-1)	55.8	5	9	8	-
P45880	Voltage-dependent anion-selective channel protein 2 (VDAC-2)	32.6	1	6	5	X
Q9Y277	Voltage-dependent anion-selective channel protein 3 (VDAC-3)	26.9	2	3	4	-
Q9H7D7	WD repeat protein 26 - Homo sapiens (Human)	3.7			1	-
Q9GZS3	WD repeat protein 61 (Meiotic recombination REC14 protein hc	6.6		1	1	-
O75083	WD-repeat protein 1 (Actin-interacting protein 1) (AIP1) (NORI-	29.5	1	5	5	X
Q92558	Wiskott-Aldrich syndrome protein family member 1 (WASP-fam	1.6	1	1		-
Q9NQW7	Xaa-Pro aminopeptidase 1 (EC 3,4,11,9) (X-Pro aminopeptidase	1.8			1	-
P12955	Xaa-Pro dipeptidase (EC 3,4,13,9) (X-Pro dipeptidase) (Proline d	16.6	1	3	1	X
Q9H773	XTP3-transactivated gene A protein - Homo sapiens (Human)	32.9		4		-
Q9UPT8	Zinc finger CCCH domain-containing protein 4 - Homo sapiens (I	1.2		1		-
Q9NUD5	Zinc finger CCHC domain-containing protein 3 - Homo sapiens (I	3.2		1		-
Q96B54	Zinc finger protein 428 - Homo sapiens (Human)	9		1		-
Q15942	Zyxin (Zyxin-2)	18.5		2	4	X

5 Curriculum Vitae

Personal data

Name: Astrid Slany

Nationality: Austrian

Date of birth: 11.06.1968

Private Address: Lascygasse 24/3/9; 1170 Wien

Education:

Primary and secondary school: Lycee Francais de Vienne

baccalaureate: 1986, French and Austrian

Study at the University of Vienna: Chemistry/ Biochemistry; 1986-1995

Diploma-thesis: Psychiatric-Biochemical Institute/ AKH; 1993-1995

Research work:

- Children Cancer Research Institute; 1995-2003
- Institute of Cancer Research/ Medical University of Vienna; since 2005