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(54) Title: MATERIALS AND METHODS FOR DIAGNOSIS AND PROGNOSIS OF LIVER CANCER

(57) Abstract: The invention relates to materials and methods for diagnosing liver tumor types, and assessing patient prognosis. Specifically, but not exclusively, the invention concerns the determination of marker protein which enable primary liver tumors to be identified and classified according to the latest WHO classification. Particularly, the invention provides potential markers proteins which allow non- neoplastic and neoplastic hepatocytes and biliary epithelial cells to be distinguished. This allows grading of tumor differentiation to be refined and differential diagnosis of primary liver tumors and pathogenesis of sub-types of cholangiocarcinoma.

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Materials and Methods for Diagnosis and Prognosis of Liver Cancer

Field of the Invention

The invention relates to materials and methods for diagnosing tumor types, and assessing patient prognosis. In particular, the invention concerns the determination of marker proteins which enable primary liver tumors to be identified and classified.

Background of the Invention

The liver is a complex organ capable of regeneration after damage. It is highly structured with a number of specialised cells required to form amongst other features, the bile ducts and liver parenchyma. The most common cell type is the hepatocyte that forms the bulk of the liver parenchyma. Cholangiocytes are a much less common cell type forming the bile ducts of the intrahepatic biliary tree.

Primary liver tumors are classified into epithelial, mesenchymal, germ cell, lymphoid and of mixed or uncertain origin accordingly to the latest WHO classification [1]. Epithelial tumors are the commonest, and generally divided into hepatocellular and cholangiocellular due to their phenotypic similarity to hepatocytes and biliary epithelium, respectively and presumed derivation. Hepatocellular carcinoma (HCC) and cholangiocarcinoma (CC) are the most common malignant types. HCC is the fifth most common cancer worldwide, and usually develops in the context of chronic liver disease [2]. CC can arise from any portion of the intrahepatic biliary tree, and is classified into peripheral and hilar/perihilar based on the predominant location, probable different biological characteristics, and pathogenesis. This classification is supported by an association with risk factors such as viral hepatitis or alcoholic liver disease in peripheral CC. In contrast, multi-step carcinogenesis through intraepithelial neoplasia often in the context of a chronic cholangiopathy (e.g. primary sclerosing cholangitis (PSC)) appears to be behind the development of hilar/perihilar CC [3].

Some primary carcinomas show a mixed phenotype, with areas of hepatocellular differentiation alternating with areas of cholangiocellular differentiation.

An origin from hepatic progenitor cells has been proposed for these tumors, on the broader basis of the cancer stem cell theory that all primary liver tumors and in particular the epithelial ones may be part of a phenotypic spectrum with "pure" HCC and CC at either end, and mixed cancers somewhere in the middle [4, 5]. In this respect, we reported recently that local ablation therapy with transarterial chemoembolization (TACE) is associated with cholangiocellular differentiation in HCC [6]. A potential explanation for this observation is that TACE provides selection pressure in favor of a minor progenitor cell population that is resistant to TACE and capable of multipotent differentiation including biliary lineage. The hepatocellular and cholangiocellular/progenitor cell components were identified by single or double immunostainings or gene expression analysis (RT-PCR) from microdissected tissue, using a relatively limited number of known conventional markers [6]. More markers are required to help better define the details of the phenotype and pathogenesis of the different HCC/CC components of post-TACE tumors, their similarities to their normal and typical malignant counterparts, and aid in diagnosis, prognosis and potentially identify new selective therapeutic targets and predictive markers.

Liquid chromatography – mass spectrometry (LC-MS/MS) based proteomics has proven to be superior over conventional biochemical methods at identifying and quantifying thousands of marker proteins extracted from complex samples including cultured cells and clinical tissue [7-8]. Recently, the application of mass spectrometry based proteomic analysis on formalin fixed paraffin embedded (FFPE) tissue has gained particular focus because of the enormous collections of highly characterized FFPE tissue derived from both human and model organisms [9-10] and its compatibility with Laser Capture Microdissection to enrich tumor cell populations from heterogenous tissue sections.

Large scale global proteomic analysis of laser microdissected FFPE tissue has been successfully employed to discover differentially expressed marker proteins between histological tissue types that can serve as novel protein biomarkers of disease [10-13]. Many of these studies utilized label free quantitative proteomic strategies, such as spectral counting and signal intensities of peptide precursor ions. Both approaches benefit from reduced

spectral complexity, enhanced analytical depth and good linear dynamic range (over two orders of magnitude for spectral counting) and consequently provide a high level of quantitative proteome coverage [11-15].

Standard liver histology and immunohistochemistry for tumor marker marker proteins have provided some means of differentiating between HCC and CC but are prone to inter-operator variability and lack of sensitivity. There remains therefore, a need for more informative markers for characterising liver tumors in terms of the predominant cellular type – hepatocytes or cholangiocytes – and potentially incorporating molecular markers of drug responsiveness. Such biomarkers of tumor cell lineage can provide an aid to earlier diagnosis, prognostic monitoring of disease, optimised treatment selection and may potentially identify new selective therapeutic targets for future drug development.

Summary of the Invention

The present invention, therefore, provides for novel biomarkers for use in the classification of primary liver tumors and particularly distinction between hepatocellular carcinoma and cholangiocellular carcinoma. Such classification allows treatment regimens and prognosis to be specifically tailored to the patient.

In a first aspect, the present invention provides for a method of determining the cellular phenotype of a liver tissue sample said method comprising

(1) extracting marker proteins from said liver tissue sample;

(2) determining expression levels of a plurality of marker proteins in said sample, wherein said plurality of marker proteins are selected from a biomarker panel as represented by any one of Table 1A, Tables 2 to 11; optionally, repeating step (2) with a different plurality of marker proteins selected from a biomarker panel as represented by any one of Table 1A, Tables 2 to 11;

(3) comparing said determined expression levels with reference expression levels for said plurality of marker proteins in known cellular phenotypes, thereby determining the cellular phenotype of the liver tissue sample.

In a second aspect, there is provided a method of identifying the cellular phenotype of a liver cell, said method comprising

(1) determining expression levels of a plurality of marker proteins in said liver cell;

(2) comparing said expression levels with reference set of expression levels for said plurality of marker proteins, said reference levels representing a cellular phenotype;

(3) identifying the cellular phenotype of the liver cell based on the comparison between the expression levels of the marker proteins in the liver cell and the reference expression levels;

wherein the plurality of marker proteins are selected from a biomarker panel as represented by any one of Table 1A, Tables 2 to 10 or Table 11.

In embodiments of these aspects, the cellular phenotype is selected from normal liver epithelium cells (hepatocytes), normal biliary epithelium cells (cholangiocytes), hepatocellular carcinoma cells, peripheral cholangiocellular carcinoma cells or hilar cholangiocellular carcinoma cells.

In some other embodiments the methods further comprise comparing said expression levels with a second reference set of expression levels representing a second cellular phenotype.

In some embodiments, the liver cell is a liver tumor cell.

In some embodiments, the biomarker panel is represented by Table 5 and/or Table 7 and the cellular phenotype is selected from hepatocellular carcinoma cells and cholangiocellular carcinoma cells, preferably the plurality of marker proteins is selected from part A of Table 5.

In some other embodiments, the liver tumor cell is obtained from a liver tumor biopsy sample, preferably obtained from a patient having previously been treated with transarterial chemoembolization.

In yet some other embodiments, the plurality of marker proteins are selected from Table 7, preferably the plurality of marker proteins are selected from Table 7 part A.

In yet some other embodiments of these aspect, the step of determining the expression levels of a plurality of marker proteins comprises

(a) contacting the liver cell or the liver tissue sample with a plurality of binding members, wherein each binding member selectively binds to one of said plurality of marker proteins or nucleic acid sequences encoding said marker proteins; and

(b) detecting and/or quantifying a complex formed by said specific binding members and marker proteins or nucleic acid sequences encoding said marker proteins.

The specific binding member is an antibody or antibody fragment which selectively binds to one of said plurality of marker proteins or a nucleic acid sequence which selectively binds to nucleic acid encoding one of said plurality of marker proteins.

Optionally, the specific binding member is an aptamer or the binding member is immobilised on a solid support.

In some other embodiments of these aspects, the step of determining expression levels of a plurality of marker proteins is performed by mass spectrometry or by Selected Reaction Monitoring using one or more transitions for protein derived peptides; and comparing the peptide levels in the liver cell or the liver tissue sample under test with peptide levels previously determined to represent a cellular phenotype.

Preferably, comparing the peptide levels includes determining the amount of protein derived peptides from the liver cell or the liver tissue sample with known amounts of corresponding synthetic peptides, wherein the synthetic peptides are identical in sequence to the peptides obtained from the liver cell or the liver tissue sample except for a label. More preferably, the label is a tag of a different mass or a heavy isotope.

In a third aspect, the present invention provides for a method for the diagnosis or prognostic monitoring of a liver tumor in an individual, said method comprising

(a) determining the presence or level of expression of a plurality of marker proteins selected from a biomarker panel as represented by any one of Tables 2 to 11, in a liver tumor cell obtained from said individual;

(b) identifying the cellular phenotype of the liver tumor cell; and

(c) selecting a diagnosis or prognosis based on the cellular phenotype of the liver tumor cell.

In a fourth aspect, the present invention provides for a method for determining a treatment regimen for an individual having a liver tumor, said method comprising

(a) determining the presence or level of expression of a plurality of marker proteins selected from a biomarker panel as represented by any one of Tables 2 to 11, in a liver tumor cell obtained from said individual;

(b) identifying the cellular phenotype of the liver tumor cell; and

(c) selecting a treatment regimen based on the cellular phenotype of the liver tumor cell.

In some embodiments of these third and fourth aspects, the liver tumor cell is from a liver tumor biopsy.

In some other embodiments of these aspects, the biomarker panel is represented by Table 5, preferably by Part A of Table 5.

In some further embodiments of these aspects the individual had previously been treated with transarterial chemoembolization. Preferably, the biomarker panel is represented by Table 7, more preferably by Part A of Table 7.

In a fifth aspect, the present invention provides for a method of diagnosing liver cancer in an individual comprising detecting one or more marker proteins or fragments thereof selected from Table 1A, Tables 2 to 11 in a blood, tissue, saliva or urine sample obtained from said individual. Preferably, said one or more protein markers or fragments thereof are detecting using a specific binding member, more preferably said binding member is an antibody specific for said one or marker protein.

In some embodiments of all these aspects, the plurality of marker proteins are selected from any one of Collagen alpha 1 (XVIII) chain, Plastin-3, AKR1B10, Fibronectin, Beta 3 tubulin, Asporin, 14-3-3 protein eta or Dihydropyrimidinase-related protein 3 or combinations thereof, preferably the plurality of marker proteins comprises AKR1B10 and/or Beta 3 tubulin.

In another aspect, the present invention provides for the use of one or more marker proteins selected from Table 1A, Tables 2 to 11 as a diagnostic marker for liver

cancer.

In yet another aspect, the present invention provides for a method for diagnosing recurrent or primary liver tumor in a subject, the method comprising determining the presence or absence of one or more marker proteins selected from the group consisting of Collagen alpha 1 (XVIII) chain, Plastin-3, AKR1B10, Fibronectin, Beta 3 tubulin, Asporin, 14-3-3 protein eta, and Dihydropyrimidinase-related protein 3 in a sample. Prefereably, the liver tumor is selected from the group consisting of hepatocellular carcinoma, peripheral cholangiocellular carcinoma or hilar cholangiocellular carcinoma cells.

In one embodiment of this aspect the marker protein is Beta 3 tubulin and/or AKR1B10, preferably Beta 3 tubulin.

In another embodiment the sample is selected from any one of blood, plasma, serum, liver tissue, liver cells or combinations thereof, preferably the sample is liver tissue, optionally formalin-fixed paraffin-embedded liver tissue section.

In another embodiment, the determining the presence or absence of one or more marker proteins in the sample is performed by either Immunohistochemistry (IHC) or mass spectrometry.

In another aspect the invention provides for a kit for diagnosing recurrent or primary liver tumor in a subject, the kit comprising reagents for determining the presence or absence of one or more marker proteins selected from the group consisting of Collagen alpha 1 (XVIII) chain, Plastin-3, AKR1B10, Fibronectin, Beta 3 tubulin, Asporin, 14-3-3 protein eta, and Dihydropyrimidinase-related protein 3 in a sample. Preferably, the liver tumor is selected from the group consisting of hepatocellular carcinoma, peripheral cholangiocellular carcinoma or hilar cholangiocellular carcinoma cells.

In one embodiment, the marker protein is Beta 3 tubulin and/or AKR1B10, preferably Beta 3 tubulin.

In another embodiment, the kit comprises reagents suitable for preparing the sample, wherein the sample is selected from any one of blood, plasma, serum, liver tissue, liver cells or combinations thereof.

In yet another embodiment, the sample is liver tissue and the kit comprises reagents suitable for preparing liver tissue, optionally for preparing formalin-fixed

paraffin-embedded liver tissue sections.

In another embodiment, the determining the presence or absence of of one or more marker proteins in the sample is performed by either Immunohistochemistry.

In yet another aspect, the present invention provides for a kit for use in determining the cellular phenotype of a liver cell, said kit allowing the user to determine the presence or level of expression of a plurality of analytes selected from proteins or fragments thereof provided in biomarker panels as represented by any one of Table 1A, Tables 2 to 11, a plurality of antibodies against said marker proteins and a plurality of nucleic acid molecules encoding said marker proteins or fragments thereof, in a cell under test; the kit comprising

(a) a solid support having a plurality of binding members, each capable of binding to one of the analytes immobilised thereon;

(b) a developing agent comprising a label; and, optionally

(c) one or more components selected from the group consisting of washing solutions, diluents and buffers.

The present invention also provides for a kit for use in determining the cellular phenotype of a liver cell *in vitro*, said kit allowing the user to determine the presence or level of expression of a plurality of proteins or fragments thereof provided in biomarker panels represented by Table 1A, Tables 2 to 11, in a cell under test; the kit comprising

(a) a set of reference peptides in an assay compatible format wherein each peptide in the set is uniquely representative of one of the plurality of marker proteins provided in any one of Table 1A, Tables 2 to 11; and, optionally

(b) one or more components selected from the group consisting of washing solutions, diluents and buffers.

In yet a further aspect, the present invention provides for a kit for the diagnosis, prognostic monitoring of a liver tumor in an individual or for determining a treatment regimen for an individual having a liver tumor, the kit comprising

(a) a solid support having a plurality of binding members immobilised thereon, wherein each binding member selectively binds to a protein selected from a biomarker panel as represented by any one of Table 1A, Tables 2 to 11; or a nucleic acid encoding the protein or fragment thereof;

(b) a developing agent comprising a label; and

(c) one or more components selected from washing solutions, diluents and buffers.

Preferably, the biomarker panel is represented by Table 5 or by Part A of Table 4 or by by Table 7 or Part A of Table 7.

In yet a further aspect, the present invention provides for a plurality of synthetic peptides each having a sequence identical to a fragment of one of a plurality of proteins selected from a biomarker panel selected from any one of Table 1A, Tables 2 to 11, said fragment resulting from digestion of the protein by trypsin, ArgC, AspN or Lys-C digestion, wherein one or more of the plurality of synthetic peptides comprises a label, optionally for the use in Selective Reaction Monitoring. Preferably, the label is a heavy isotope.

The present invention also provides for a liver cellular classification system comprising a liver cellular classification apparatus and an information communication terminal apparatus, said liver cellular classification apparatus including a control component and a memory component, said apparatuses being communicatively connected to each other via a network;

(1) wherein the information communication terminal apparatus includes

(1a) a protein data sending unit that transmits the protein data derived from a liver tissue sample of a subject to the liver cellular classification apparatus;

(1b) a result-receiving unit that receives the result of the liver cellular classification of the subject transmitted from the liver cellular classification apparatus;

(2) wherein the liver cellular classification apparatus includes

(2a) a protein data-receiving unit that receives protein data derived from the liver tissue sample of the subject transmitted from the information communication terminal apparatus;

(2b) a data comparison unit which compares the data from the data-receiving unit with the data stored in the memory unit;

(2c) a classifier unit that determines the class (e.g. cellular phenotype) of the liver tissue of the subject, based on the results of the data comparison

unit; and

(2d) a classification result-sending unit that transmits the classification result of the subject obtained by the classifier unit to the information communication terminal apparatus; and

wherein the memory unit contains protein expression level data of at least one protein selected from any one or more of Table 1A, Tables 2 to 10 or Table 11.

Preferably, the memory unit contains data of a plurality of proteins selected from Table 5 or Table 11 and wherein the classification is between Hepatocellular carcinoma and peripheral cholangiocarcinoma; alternatively the memory unit contains data of a plurality of proteins selected from Table 7 or Table 11 and wherein the classification is between Hepatocellular carcinoma and cholangiocarcinoma in post-TACE liver tumors.

In some embodiments, the liver cellular classification system according to the invention is connected to an apparatus for determining the protein expression levels in a liver tissue sample, preferably the apparatus can process multiple samples using liquid chromatography-mass spectrometry (LC-MS/MS).

In yet a further aspect of the present invention, there is provided a liver tissue cellular classification program that makes an information processing apparatus including a control component and a memory component execute a method of determining and/or classifying the liver tissue of a subject, the method comprising:

(i) a comparing step of comparing data based on the protein expression levels of at least one (preferably a plurality) protein selected from any one of Table 1A, Tables 2 to 11 obtained of a subject with the protein expression level data stored in the memory component; and

(ii) a classifying step for classifying the liver tissue cells of said subject, based on the comparison calculated at the comparing step; and wherein said tissue is classified into phenotypes including normal (hepatocytes, cholangiocytes), hepatocellular carcinoma, truly mixed hepatocholangiocellular carcinoma (pre or post TACE therapy), peripheral cholangiocarcinoma, Hilar cholangiocarcinoma (with or without primary sclerosing cholangitis), or metastatic colo-rectal carcinoma. Preferably, the liver tissue cellular

classification program of claim 48 recorded thereon.

Brief Description of the Drawings

Figure 1. Overall workflow. Overall data analysis workflow; Spectrum files (0), Spectrum Selector (1), Sequest (2), Percolator (3), Mascot (4), Event Detector (5), Precursors Ions Area Detector (6), Peptide Area Quantified (7), Peptide Identification at 1%FDR + spectral counting (8), Peptide Matrix with Area under the Curve (AUC)(9), Peptide data matrix with spectral count information (10), Statistical validation (11; 12) and final list (13).

Figure 2. Venn-Diagram. The diagram shows comparison of the two quantitation methods (left: spectral count; right: Area under the Curve) for marker proteins with unique and shared peptides. The numbers shown the marker proteins found to be significantly modulated in each quantification method and those common to both, across all comparisons made in this study.

Figure 3. Principal component analysis (PCA) for identifying outliers and groups/clusters nested within the datasets (A) for the Area under the Curve (AUC) and (B) for the spectral counts. Each small triangle represents the PC score along the first two PC components for each of the samples. The naming convention of the samples is batch number_tissue type number.

Figure 4. Validation of protein up-regulation through Volcano plots. (a) Volcano plots for AKR1B10(upper left panel, normal liver parenchyma (1) *vs.* HCC (2); upper right panel, normal liver parenchyma (1) *vs.* normal bile duct (9)) and Tubulin-beta 3 chain (lower left panel, normal liver parenchyma (1) *vs.* peripheral CC (5); lower right panel, peripheral CC (5) *vs.* normal bile duct (9).

Figure 5. Validation of protein up-regulation through Immuno-hystochemical staining (IHC). (1): tissue type 1 (normal liver); (2) tissue type 2 (HCC); (3) tissue type 9 (Normal bile duct) and (4) tissue type 5 (peripheral CC). AKR1B10 is diffusely expressed in HCC, while its expression is only patchy or weak in normal liver parenchyma and peripheral CC. AKR1B10 is also diffusely positive in normal bile duct. Immunostaining for Tubulin-beta 3 chain on normal liver, HCC, normal bile duct, and peripheral CC. The expression of Tubulin-beta

3 chain appears to be specific for peripheral CC.

Figure 6. Normalised spectral counts for Collagen alpha 1 (XVIII) chain (1), Plastin-3 (2), AKR1B10 (3), Fibronectin (4), Beta 3 tubulin (5), Asporin (6) and Dihydropyrimidinase-related protein 3 (7).

Figure 7. Table 11 shows a list of marker proteins (467) with both unique and shared peptide sequences.

Definitions

The term "plurality of marker proteins" means at least two marker proteins as disclosed herein.

The term "marker protein" includes all biologically relevant forms of the protein identified, including post-translational modifications. For example, the marker protein can be present in a glycosylated, phosphorylated, multimeric, fragmented or precursor form. A marker protein fragment may be naturally occurring or, for example, enzymatically generated and the biologically active function of the full marker protein. Fragments will typically be at least about 10 amino acids, usually at least about 50 amino acids in length, and can be as long as 300 amino acids in length or longer.

The term "cellular phenotype" refers to the characteristics or traits of a cell or group of cells. Cellular phenotype refers to the cells anatomical location, morphology, development, biochemical or physiological properties, behaviour, and products of biochemistry/behaviour. Cellular phenotype results from the expression of cell genes as well as the influence of environmental factors and the interactions between the two.

The term "liver tissue sample" include, but is not limited to, a specimen of liver tissue removed by resection or core needle biopsy.

The term "expression level" refers to the relative amount of protein in a liver tissue sample, for example as determined by LC-MS/MS label free quantification approaches such as area under the curve and spectral counting.

The term "comparing" means measuring the relative amount of a protein or proteins in a sample relative to other samples (for example protein amounts stored in our database).

The term "reference set" refers to the samples (for example in our database) used as classifiers (e.g. classic examples or HCC, or CC). These classifiers can be used to help diagnosis of non-classic specimens from new cases.

The term "reference level", "reference set of expression level"; "reference expression level" and "reference amount" are used herein as synonyms and refers to a pre-determined level, which may, for example be provided in the form of an accessible data record from a public database.

The term "antibody" includes polyclonal antiserum, monoclonal antibodies, fragments of antibodies such as single chain and Fab fragments, and genetically engineered antibodies. The antibodies may be chimeric or of a single species.

The terms "marker protein" and "biomarker", which are used interchangeably herein, include all biologically relevant forms of the protein identified, including post-translational modifications. For example, the marker protein can be present in a glycosylated, phosphorylated, multimeric or precursor form.

The term "control" refers to a cultured cell line, primary culture of cells taken from a human or animal subject, or biopsy material taken from a human or animal subject that is free of HCC or CC.

The term "antibody array" or "antibody microarray" means an array of unique addressable elements on a continuous solid surface whereby at each unique addressable element an antibody with defined specificity for an antigen is immobilised in a manner allowing its subsequent capture of the target antigen and subsequent detection of the extent of such binding. Each unique addressable element is spaced from all other unique addressable elements on the solid surface so that the binding and detection of specific antigens does

not interfere with any adjacent such unique addressable element.

The term "bead suspension array" means an aqueous suspension of one or more identifiably distinct particles whereby each particle contains coding features relating to its size and colour or fluorescent signature and to which all of the beads of a particular combination of such coding features is coated with an antibody with a defined specificity for an antigen in a manner allowing its subsequent capture of the target antigen and subsequent detection of the extent of such binding. Examples of such arrays can be found at www.luminexcorp.com where application of the xMAP® bead suspension array on the Luminex® 100™ System is described.

The terms "selected reaction monitoring", "SRM" and "MRM" means a mass spectrometry assay whereby precursor ions of known mass-to-charge ratio representing known biomarkers are preferentially targeted for analysis by tandem mass spectrometry in an ion trap or triple quadrupole mass spectrometer. During the analysis the parent ion is fragmented and the number of daughter ions of a second predefined mass-to-charge ratio is counted. Typically, an equivalent precursor ion bearing a predefined number of stable isotope substitutions but otherwise chemically identical to the target ion is included in the method to act as a quantitative internal standard.

"Differential expression", as used herein, refers to at least one recognisable difference in protein expression. It may be a quantitatively measurable, semi-quantitatively estimable or qualitatively detectable difference in tissue protein expression. Thus, a differentially expressed protein may be strongly expressed in tissue in one cellular phenotype (e.g. HCC) and less strongly expressed or not expressed at all in another cellular phenotype (e.g. CC). Further, expression may be regarded as differential if the protein undergoes any recognisable change such as cleavage or post-translational modification between two cellular phenotypes under comparison.

The term "isolated" means throughout this specification, that the marker protein, antibody or polynucleotide, as the case may be, exists in a physical milieu distinct from that in which it may occur in nature.

As used herein, the term "subject" includes any human or non-human animal. The term "non-human animal" includes all vertebrates, e.g., mammals and non-mammals, such as non-human primates, sheep, dogs, cats, horses, cows, chickens, amphibians, reptiles, etc.

The term "treat", "treating", "treatment", "prevent", "preventing" or "prevention" includes therapeutic treatments, prophylactic treatments and applications in which one reduces the risk that a subject will develop a disorder or other risk factor. Treatment does not require the complete curing of a disorder and encompasses the reduction of the symptoms or underlying risk factors.

Abbreviations

LMD: laser microdissection; TACE: trans-arterial chemo-embolization; HCC: hepatocellular carcinoma; CC: cholangiocellular carcinoma
PSC: primary sclerosing cholangitis; FFPE: Formalin Fixed Paraffin embedded; AUC: area under the curve; PSM: peptide spectrum match.

Detailed Description

The inventors have identified marker proteins that demonstrate statistically significant differences in protein expression levels between different cellular phenotypes of liver cells, including liver tumor cells. In particular, the inventors have determined marker proteins having different expression levels between components (HCC and CC) of post-TACE HCC, Often cases diagnosed with HCC are then treated with transarterial chemoembolization (TACE), however tumors generally come back, but no longer show the classic HCC phenotype, having some regions that look classic HCC, some that look classic CC, and some which are undefinable. The present invention allows for the identification of marker proteins more specific for HCC than CC, or vice versa, in a patient that has already undergone TACE. The inventors have further explored their similarities or dissimilarities compared to their normal and typical malignant counterparts. The inventors also found significant differences in other tissue type comparisons. These differentially expressed marker proteins provide

useful biomarkers to help diagnosing tumor types, assessing patient prognosis and determining appropriate treatment regimens.

The identification of marker protein sets (or biomarker panels) specific to the hepatocellular and cholangiocellular phenotype of post-TACE mixed tumors, and their similarity to their normal and typical neoplastic counterparts confirms that the differentiation process is truly divergent, despite a probable origin from a common progenitor. Of equal importance is the identification by the inventors of marker proteins differentially expressed between normal and neoplastic hepatocytes and biliary epithelial cells, as they provide new markers of malignant transformation or tumor differentiation; and between HCC and peripheral CC, which often overlap in both clinical presentation, and appearance on imaging and histology (22, 23).

1. Marker proteins and methods of using thereof

The present invention provides herein marker proteins which are differentially expressed between two cell types tested and allow a particular cellular phenotype to be determined.

Table 1A shows the preferred marker proteins (including their synonyms) according to the invention, namely Beta 3 tubulin, AKR1B10, Collagen alpha 1 (XVIII) chain, Plastin-3, Fibronectin, Asporin, 14-3-3 protein eta and Dihydropyrimidinase-related protein 3.

Table 1A: Preferred marker proteins

Protein	Name	Abbreviation(s)/synonyms (Syn)	Tissue of upregulation
Q13509	Tubulin beta-3 chain	TUBB3 Syn: Beta-3 tubulin; β-3 tubulin; tubulin-β-3; TUBB4	peripheral CC
O60218	Aldo-keto reductase family 1 member B10	AKR1B10 Syn: AKR1B11	HCC
P39060	Collagen alpha-1(XVIII) chain	COL18A1	HCC

		Syn: Collagen α-1 (XVIII)	
P13797	Plastin-3	PLS3	Hilar CC
P02751	Fibronectin	FN1 Syn: FN	HCC
Q9BXN1	Asporin	Syn: PLAP1; SLRR1C	Hilar CC
Q04917	14-3-3 protein eta	YWHAH Syn: YWHA1; 14-3-3 protein ε	HCC pre-TACE
Q14195	Dihydropyrimidinase-related protein 3	DPYSL3 Syn: CRMP4; DRP3; ULIP; ULIP1	HCC without psc

Pre-TACE: pre-trans-arterial chemo-embolization; HCC: hepatocellular carcinoma; CC: cholangiocellular carcinoma; PSC: primary sclerosing cholangitis;

Table 1B indicates the numbers of proteins that showed statistically significant differential expression levels between two types of liver tissues (p-value <0.05 and Log2[fold change]≥2 or ≤-2) using shared and unique peptides. These numbers illustrate the number of differentially modulated proteins that were common to both area under the curve and spectral counting datasets per tissue type comparison (467 proteins common to both).

Table 1B: Number of proteins showing statistically significant differential expression between types of liver tissue.

Tissue Type	2	3	4	5	6	7	8	9
1	11	37	203	236	269	248	258	212
2		2	125	165	195	175	188	153
3			95	130	151	140	163	125
4				5	15	17	33	31
5					14	34	29	37
6						5	63	32
7							51	43
8							0	53

1: Normal liver; 2: HCC; 3: Post-TACE HCC, hepatocellular area; 4: post-TACE HCC, cholangiocellular area; 5: peripheral CC; 6: hilar CC without PSC; 7: hilar CC with PSC; 8: metastatic colorectal carcinoma.

The marker proteins indicated in the Tables 2 to 10 allow the following cell types to be distinguished:-

Table 2: Normal hepatocytes from HCC.
Table 3: Peripheral cholangiocarcinoma from normal bile duct.
Table 4: Hilar cholangiocarcinoma from normal bile duct.
Table 5: Hepatocellular carcinoma from peripheral cholangiocarcinoma.
Table 6: Hepatocytes from cholangiocytes.
Table 7: Hepatocellular carcinoma and cholangiocarcinoma in post-TACE liver tumors.
Table 8: Peripheral cholangiocarcinoma from metastatic colorectal cancer.
Table 9: Hilar cholangiocarcinoma from hilar cholangiocarcinoma with primary sclerosing cholangitis.
Table 10: Hilar cholangiocarcinoma from metastatic colorectal cancer.

This determination provides clinicians for the first time with knowledge of the cellular phenotype of the liver tumor and as a result, accurate decisions regarding type and assessment of treatment, and prognosis can be provided. For each Table, all negative values for effect size (g), relate to marker proteins that were present at a lower concentration in the first tissue type versus the second tissue type. All positive values for effect size (g), relate to marker proteins that were present in higher concentration in the first tissue type versus the second tissue type.

The statistical significance for each protein regulation is shown as a p-value calculated after performing an unrelated t-test comparing the number of spectral counts for each protein between the two named tissue types. Hedges' g unbiased standardized effect size estimates were calculated, along with 95% confidence intervals for these estimates. Values of $g < 0.2$ are regarded as very small differences, $g = 0.5$ average differences, $g > 0.8$ regarded as large differences. Unstandardized effect size estimates (i.e., differences in the mean spectral counts in two compared tissue types) were also calculated, along with 95% confidence intervals for these estimates. The tables displayed these unbiased standardized effect size estimates and the unstandardized effect size estimates. Q-values (adjusted p values) provide a more stringent measure of statistical significance than p-values and were computed using a direct False

Discovery Rate approach. Individual Q-values are not shown here but all marker proteins with q-values ≤0.05 are listed in section A of each tables 2 to 10, while all marker proteins with p-values ≤0.05 are displayed in section B of each table 2 to 10.

Protein expression levels for marker proteins shown in Tables 2 to 10 were determined using label free LC-MS/MS quantification based on spectral counting (shared and unique peptides) which is well known in the art. All marker proteins showing statistically significant differences in mean spectral counts between two tissue types are display in Tables 2-10. We have also used an alternate method of data analysis based on the area under the curve (AUC) of the MS1 peak of the three most intense peptides for each protein. All marker proteins in Table 11 (Figure 7) marker proteins (467 marker proteins) were found to be significantly regulated in at least one of the tissue comparisons that were common to both quantification methods (spectral counting and AUC of both shared and unique peptides). The Table contains tissue type comparison (Tissue type number versus tissue type number), uniprot ID, and protein names along with P-values, t-scores and $\log_2$ Fold-change values for both quantitative methods.

In Tables 2 to 10 the significantly modulated marker proteins were filtered by the stringent q-values (section A), then the less stringent p-values (section B). In Table 11 (Figure 7) the marker proteins were filtered on p-values and fold change (combined). In summary, Tables 2 to 10 only considered spectral counts for quantification, whereas Table 11 considered spectral counts and area under the curve.

Table 2 provides protein markers for use in distinguishing normal hepatocytes from hepatocellular carcinoma cells (HCC).

Table 2 - Proteins differentiating normal hepatocytes from hepatocellular carcinoma*

Protein	Name	P Value	Effect Size (g)	Magnitude of Effect Size (g)	Effect Size (Mean Dif)	Magnitude of Mean dif (Mean Dif)
PART A:						
P39060*	**Collagen alpha-1(XVIII) chain / Name=COL18A1**	**2.28E-07**	**-5.26**	**5.26**	**-6.71**	**6.71**
Q9H2A2	Aldehyde dehydrogenase	2.27E-05	3.39	3.39	7.71	7.71

	family 8 member A1 / Name=ALDH8A1; Synonyms=ALDH12					
P10632	Cytochrome P450 2C8 / Name=CYP2C8	3.25E-05	3.25	3.25	10.71	10.71
P00367	Glutamate dehydrogenase 1, mitochondrial / Name=GLUD1; Synonyms=GLUD	3.26E-05	3.52	3.52	34.86	34.86
P07355*	**Annexin A2 / Name=ANXA2; Synonyms=ANX2, ANX2L4, CAL1H, LPC2D**	**3.36E-05**	**-3.7**	**3.7**	**-10.57**	**10.57**
Q6IB77	Glycine N-acyltransferase / Name=GLYAT; Synonyms=ACGNAT, CAT, GAT	4.20E-05	3.14	3.14	10.29	10.29
P02751*	**Fibronectin / Name=FN1; Synonyms=FN**	**1.58E-04**	**-3.61**	**3.61**	**-19.43**	**19.43**
Q02338	D-beta-hydroxybutyrate dehydrogenase, mitochondrial / Name=BDH1; Synonyms=BDH	1.83E-04	2.68	2.68	7.86	7.86
P05091	Aldehyde dehydrogenase, mitochondrial / Name=ALDH2; Synonyms=ALDM	2.02E-04	2.65	2.65	27.86	27.86
P45954	Short/branched chain specific acyl-CoA dehydrogenase, mitochondrial / Name=ACADSB	2.95E-04	2.59	2.59	8.71	8.71
Q9Y617	Phosphoserine aminotransferase / Name=PSAT1; Synonyms=PSA	3.68E-04	3.41	3.41	5.43	5.43
P30084	Enoyl-CoA hydratase, mitochondrial / Name=ECHS1	3.85E-04	2.48	2.48	12.57	12.57
O75452	Retinol dehydrogenase 16 / Name=RDH16; Synonyms=RODH4	4.23E-04	2.41	2.41	8.71	8.71
P16219	Short-chain specific acyl-CoA dehydrogenase, mitochondrial / Name=ACADS	4.84E-04	2.61	2.61	12.14	12.14

P21695	Glycerol-3-phosphate dehydrogenase [NAD+], cytoplasmic / Name=GPD1	5.29E-04	2.36	2.36	6.71	6.71
P09467	Fructose-1,6-bisphosphatase 1 / Name=FBP1; Synonyms=FBP	6.24E-04	2.4	2.4	12.43	12.43
P00439	Phenylalanine-4-hydroxylase / Name=PAH	6.34E-04	2.32	2.32	4.71	4.71
O95954	Formimidoyltransferase-cyclodeaminase / Name=FTCD	7.19E-04	2.34	2.34	23.57	23.57
P34913	Epoxide hydrolase 2 / Name=EPHX2	8.34E-04	2.37	2.37	8	8
P01876*	**Ig alpha-1 chain C region / Name=IGHA1**	**1.03E-03**	**-2.16**	**2.16**	**-6.57**	**6.57**
PART B:						
P49189	4-trimethylaminobutyraldehyde dehydrogenase / Name=ALDH9A1; Synonyms=ALDH4, ALDH7, ALDH9	1.23E-03	2.21	2.21	3	3
P06737	Glycogen phosphorylase, liver form / Name=PYGL	1.30E-03	2.1	2.1	11	11
P62807	Histone H2B type 1-C/E/F/G/I / Name=HIST1H2BC; Synonyms=H2BFL	1.35E-03	-2.08	2.08	-10.57	10.57
P58876	Histone H2B type 1-D / Name=HIST1H2BD; Synonyms=H2BFB, HIRIP2	1.35E-03	-2.08	2.08	-10.57	10.57
Q93079	Histone H2B type 1-H / Name=HIST1H2BH; Synonyms=H2BFJ	1.35E-03	-2.08	2.08	-10.57	10.57
O60814	Histone H2B type 1-K / Name=HIST1H2BK; Synonyms=H2BFT, HIRIP1	1.35E-03	-2.08	2.08	-10.57	10.57
Q99880	Histone H2B type 1-L / Name=HIST1H2BL; Synonyms=H2BFC	1.35E-03	-2.08	2.08	-10.57	10.57
Q99879	Histone H2B type 1-M / Name=HIST1H2BM; Synonyms=H2BFE	1.35E-03	-2.08	2.08	-10.57	10.57
Q99877	Histone H2B type 1-N / Name=HIST1H2BN; Synonyms=H2BFD	1.35E-03	-2.08	2.08	-10.57	10.57

Q5QNW6	Histone H2B type 2-F / Name=HIST2H2BF	1.35E-03	-2.08	2.08	-10.57	10.57
P57053	Histone H2B type F-S / Name=H2BFS	1.35E-03	-2.08	2.08	-10.57	10.57
P16401	Histone H1.5 / Name=HIST1H1B; Synonyms=H1F5	1.39E-03	-2.29	2.29	-4.86	4.86
P27824	Calnexin / Name=CANX	1.56E-03	-2.04	2.04	-6.43	6.43
Q02928	Cytochrome P450 4A11 / Name=CYP4A11; Synonyms=CYP4A2	1.69E-03	2.02	2.02	5.43	5.43
Q9UL12	Sarcosine dehydrogenase, mitochondrial / Name=SARDH; Synonyms=DMGDH L1	1.85E-03	2.01	2.01	10	10
Q07020	60S ribosomal protein L18 / Name=RPL18	1.97E-03	-2.03	2.03	-3	3
P62269	40S ribosomal protein S18 / Name=RPS18; Synonyms=D6S218E	2.26E-03	-1.93	1.93	-5.71	5.71
Q68CK6	Acyl-coenzyme A synthetase ACSM2B, mitochondrial / Name=ACSM2B; Synonyms=ACSM2; ORFNames=HYST1 046	2.74E-03	1.92	1.92	14.71	14.71
P26599	Polypyrimidine tract-binding protein 1 / Name=PTBP1; Synonyms=PTB	2.75E-03	-2.01	2.01	-4	4
Q04837	Single-stranded DNA-binding protein, mitochondrial / Name=SSBP1; Synonyms=SSBP	2.93E-03	-2.41	2.41	-2.29	2.29
P35573	Glycogen debranching enzyme / Name=AGL; Synonyms=GDE	3.20E-03	2.13	2.13	12.43	12.43
Q16836	Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial / Name=HADH; Synonyms=HAD, HADHSC, SCHAD	3.20E-03	1.84	1.84	4.57	4.57
P01834	Ig kappa chain C region / Name=IGKC	3.49E-03	-1.93	1.93	-10	10
Q08AH3	Acyl-coenzyme A synthetase ACSM2A,	3.66E-03	1.83	1.83	15.14	15.14

	mitochondrial / Name=ACSM2A; Synonyms=ACSM2, MACS2					
P19105	Myosin regulatory light chain 12A / Name=MYL12A; Synonyms=MLCB, MRLC3, RLC	3.66E-03	-1.8	1.8	-2.14	2.14
O14950	Myosin regulatory light chain 12B / Name=MYL12B; Synonyms=MRLC2, MYLC2B	3.66E-03	-1.8	1.8	-2.14	2.14
P02649	Apolipoprotein E / Name=APOE	3.66E-03	-1.81	1.81	-7.43	7.43
Q9Y2P5	Bile acyl-CoA synthetase / Name=SLC27A5; Synonyms=ACSB, ACSVL6, FACVL3, FATP5	3.95E-03	1.78	1.78	11	11
P37802	Transgelin-2 / Name=TAGLN2; Synonyms=KIAA0120; ORFNames=CDABP0035	4.12E-03	-2.04	2.04	-5.29	5.29
Q86XE5	Probable 4-hydroxy-2-oxoglutarate aldolase, mitochondrial / Name=HOGA1; Synonyms=C10orf65, DHDPSL	4.84E-03	1.81	1.81	2	2
O43772	Mitochondrial carnitine/acylcarnitine carrier protein / Name=SLC25A20; Synonyms=CAC, CACT	4.92E-03	1.75	1.75	4.86	4.86
Q16134	Electron transfer flavoprotein-ubiquinone oxidoreductase, mitochondrial / Name=ETFDH	5.09E-03	1.72	1.72	4.86	4.86
Q7Z5P4	17-beta-hydroxysteroid dehydrogenase 13 / Name=HSD17B13; Synonyms=SCDR9; ORFNames=HMFN0376, UNQ497/PRO1014	5.15E-03	1.71	1.71	6.57	6.57
P09651	Heterogeneous nuclear ribonucleoprotein A1 / Name=HNRNPA1;	5.18E-03	-1.77	1.77	-3.14	3.14

	Synonyms=HNRPA1					
Q3LXA3	Bifunctional ATP-dependent dihydroxyacetone kinase/FAD-AMP lyase (cyclizing) / Name=DAK	5.25E-03	1.71	1.71	19.43	19.43
Q02878	60S ribosomal protein L6 / Name=RPL6; Synonyms=TXREB1	5.39E-03	-1.72	1.72	-4.29	4.29
P98160	Basement membrane-specific heparan sulfate proteoglycan core protein / Name=HSPG2	5.49E-03	-1.93	1.93	-11	11
P84103	Serine/arginine-rich splicing factor 3 / Name=SRSF3; Synonyms=SFRS3, SRP20	5.59E-03	-2.11	2.11	-2.14	2.14
P05177	Cytochrome P450 1A2 / Name=CYP1A2	5.93E-03	1.78	1.78	6.29	6.29
P62847	40S ribosomal protein S24 / Name=RPS24	5.97E-03	-1.72	1.72	-2.29	2.29
Q16851	UTP--glucose-1-phosphate uridylyltransferase / Name=UGP2; Synonyms=UGP1	6.19E-03	1.82	1.82	17	17
Q9UQ80	Proliferation-associated protein 2G4 / Name=PA2G4; Synonyms=EBP1	6.43E-03	-1.65	1.65	-2.86	2.86
P62937	Peptidyl-prolyl cis-trans isomerase A / Name=PPIA; Synonyms=CYPA	6.77E-03	-1.71	1.71	-7.57	7.57
P08238	Heat shock protein HSP 90-beta / Name=HSP90AB1; Synonyms=HSP90B, HSPC2, HSPCB	6.79E-03	-1.72	1.72	-8.57	8.57
Q9UI17	Dimethylglycine dehydrogenase, mitochondrial / Name=DMGDH	6.89E-03	1.64	1.64	7	7
O60218	Aldo-keto reductase family 1 member B10 / Name=AKR1B10; Synonyms=AKR1B11	6.95E-03	-1.97	1.97	-14.43	14.43
P00918	Carbonic anhydrase	7.02E-03	1.65	1.65	4.86	4.86

	2 / Name=CA2					
P36578	60S ribosomal protein L4 / Name=RPL4; Synonyms=RPL1	7.35E-03	-1.68	1.68	-3.71	3.71
P00915	Carbonic anhydrase 1 / Name=CA1	7.43E-03	1.61	1.61	5.14	5.14
P84077	ADP-ribosylation factor 1 / Name=ARF1	7.87E-03	-1.6	1.6	-3.86	3.86
P61204	ADP-ribosylation factor 3 / Name=ARF3	7.87E-03	-1.6	1.6	-3.86	3.86
P51857	3-oxo-5-beta-steroid 4-dehydrogenase / Name=AKR1D1; Synonyms=SRD5B1	8.04E-03	1.95	1.95	6.29	6.29
Q86UE4	Protein LYRIC / Name=MTDH; Synonyms=AEG1, LYRIC	8.40E-03	-1.58	1.58	-2	2
P63104	14-3-3 protein zeta/delta / Name=YWHAZ	8.55E-03	-1.73	1.73	-5.71	5.71
P02730	Band 3 anion transport protein / Name=SLC4A1; Synonyms=AE1, DI, EPB3	8.62E-03	1.92	1.92	3.71	3.71
Q9UBR1	Beta-ureidopropionase / Name=UPB1; Synonyms=BUP1	8.63E-03	1.61	1.61	7.43	7.43
P08319	Alcohol dehydrogenase 4 / Name=ADH4	8.79E-03	1.57	1.57	37.86	37.86
P00491	Purine nucleoside phosphorylase / Name=PNP; Synonyms=NP	9.05E-03	1.56	1.56	4.29	4.29
P61978	Heterogeneous nuclear ribonucleoprotein K / Name=HNRNPK; Synonyms=HNRPK	9.14E-03	-1.68	1.68	-5.57	5.57
P34896	Serine hydroxymethyltransferase, cytosolic / Name=SHMT1	9.87E-03	1.62	1.62	9	9
Q12905	Interleukin enhancer-binding factor 2 / Name=ILF2; Synonyms=NF45; ORFNames=PRO3063	9.90E-03	-1.54	1.54	-2.29	2.29

*Bold type indicates increased relative expression in hepatocellular carcinoma

compared to normal hepatocytes.

Table 2 provides information as to whether the marker proteins are relatively over-expressed (identified in bold) or under-expressed in HCC versus normal hepatocytes. Accordingly, by determining the presence, absence or change in expression levels of a plurality of these marker proteins and comparing these changes with a reference of known expression levels, one is able to determine whether the cells under test are HCC or normal hepatocytes. The plurality of marker proteins may be selected from Table 2 as a whole, or preferably from Part A which lists those marker proteins showing a higher statistically significant difference between the two cell types.

Table 3 provides information as to whether the marker proteins are relatively over-expressed (identified in bold) or under-expressed in peripheral cholangiocarcinoma versus normal cholangiocytes. Accordingly, by determining the presence, absence or change in expression levels of a plurality of these marker proteins and comparing these changes with a reference of known expression levels, one is able to determine whether the cells under test are peripheral cholangiocarcinoma or normal cholangiocytes.

Table 3 – Proteins differentiating peripheral cholangiocarcinoma from normal cholangiocytes*

Protein	Name	P Value	Effect Size (g)	Magnitude of Effect Size (g)	Effect Size (Mean Dif)	Magnitude of Mean dif (Mean Dif)
PART A:						
P04424	Argininosuccinate lyase / Name=ASL	5.71E-05	-3.6	3.6	-6.57	6.57
O95994	Anterior gradient protein 2 homolog / Name=AGR2; Synonyms=AG2; ORFNames=UNQ515/PRO1030	8.34E-05	-3.5	3.5	-10.55	10.55
P07327	Alcohol dehydrogenase 1A / Name=ADH1A; Synonyms=ADH1	9.97E-05	-5.06	5.06	-13.24	13.24
O94760	N(G),N(G)-dimethylarginine dimethylaminohydrolase 1 / Name=DDAH1; Synonyms=DDAH	1.17E-04	-6.1	6.1	-5.17	5.17
Q9NR45	Sialic acid synthase / Name=NANS; Synonyms=SAS	1.38E-04	-3.09	3.09	-3.43	3.43
P56470	Galectin-4 / Name=LGALS4	1.76E-04	-3.02	3.02	-14.74	14.74

P00352	Retinal dehydrogenase 1 / Name=ALDH1A1; Synonyms=ALDC, ALDH1, PUMB1	2.43E-04	-2.83	2.83	-27.55	27.55
P08263	Glutathione S-transferase A1 / Name=GSTA1	3.42E-04	-2.9	2.9	-8.14	8.14
O95154	Aflatoxin B1 aldehyde reductase member 3 / Name=AKR7A3; Synonyms=AFAR2	3.52E-04	-4.84	4.84	-8	8
P09211	Glutathione S-transferase P / Name=GSTP1; Synonyms=FAEES3, GST3	4.23E-04	-2.53	2.53	-22.02	22.02
P00918	Carbonic anhydrase 2 / Name=CA2	6.13E-04	-3.84	3.84	-18.71	18.71
Q13228	Selenium-binding protein 1 / Name=SELENBP1; Synonyms=SBP	6.18E-04	-2.81	2.81	-9.81	9.81
P20774	Mimecan / Name=OGN; Synonyms=OIF, SLRR3A	6.39E-04	-3.32	3.32	-18.76	18.76
O75489	NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial / Name=NDUFS3	7.45E-04	-2.4	2.4	-2.43	2.43
Q14914	Prostaglandin reductase 1 / Name=PTGR1; Synonyms=LTB4DH	7.50E-04	-3.54	3.54	-9.57	9.57
P21333*	**Filamin-A / Name=FLNA; Synonyms=FLN, FLN1**	**9.79E-04**	**2.3**	**2.3**	**37.69**	**37.69**
P00325	Alcohol dehydrogenase 1B / Name=ADH1B; Synonyms=ADH2	1.03E-03	-2.4	2.4	-14.33	14.33
PART B:						
P00326	Alcohol dehydrogenase 1C / Name=ADH1C; Synonyms=ADH3	1.33E-03	-3.63	3.63	-10	10
P09525	Annexin A4 / Name=ANXA4; Synonyms=ANX4	1.63E-03	-2.44	2.44	-34.64	34.64
P55083	Microfibril-associated glycoprotein 4 / Name=MFAP4	1.82E-03	-2.74	2.74	-8.67	8.67
Q14376	UDP-glucose 4-epimerase / Name=GALE	2.25E-03	-2.14	2.14	-3.12	3.12
P09467	Fructose-1,6-bisphosphatase 1 / Name=FBP1; Synonyms=FBP	2.32E-03	-3.21	3.21	-4.33	4.33
P13611	Versican core protein / Name=VCAN; Synonyms=CSPG2	3.00E-03	2.21	2.21	13.55	13.55
P21810	Biglycan / Name=BGN; Synonyms=SLRR1A	3.04E-03	-2.02	2.02	-17.88	17.88
P18283	Glutathione peroxidase 2 / Name=GPX2	3.21E-03	-2.98	2.98	-4.67	4.67
P23141	Liver carboxylesterase 1 / Name=CES1; Synonyms=CES2, SES1	3.26E-03	-2.88	2.88	-42.02	42.02
O60218	Aldo-keto reductase family 1 member B10 / Name=AKR1B10;	3.53E-03	-2.38	2.38	-18.83	18.83

	Synonyms=AKR1B11					
P12277	Creatine kinase B-type / Name=CKB; Synonyms=CKBB	3.53E-03	-2.11	2.11	-5.29	5.29
P42330	Aldo-keto reductase family 1 member C3 / Name=AKR1C3; Synonyms=DDH1, HSD17B5, KIAA0119, PGFS	4.39E-03	-2.11	2.11	-13.24	13.24
Q16762	Thiosulfate sulfurtransferase / Name=TST	4.70E-03	-1.81	1.81	-7.33	7.33
P12532	Creatine kinase U-type, mitochondrial / Name=CKMT1A; Synonyms=CKMT	4.72E-03	-2.72	2.72	-3.83	3.83
P01622	Ig kappa chain V-III region Ti /	4.82E-03	-2.07	2.07	-2.21	2.21
P04206	Ig kappa chain V-III region GOL /	4.82E-03	-2.07	2.07	-2.21	2.21
P13797	Plastin-3 / Name=PLS3	5.39E-03	1.76	1.76	8.38	8.38
O60664	Perilipin-3 / Name=PLIN3; Synonyms=M6PRBP1, TIP47	5.48E-03	1.75	1.75	4.26	4.26
P08311	Cathepsin G / Name=CTSG	5.54E-03	-1.82	1.82	-4.19	4.19
P17516	Aldo-keto reductase family 1 member C4 / Name=AKR1C4; Synonyms=CHDR	6.54E-03	-2.52	2.52	-8.83	8.83
P08238	Heat shock protein HSP 90-beta / Name=HSP90AB1; Synonyms=HSP90B, HSPC2, HSPCB	7.56E-03	1.71	1.71	8.76	8.76
P18206	Vinculin / Name=VCL	8.06E-03	1.94	1.94	5.86	5.86
Q13576	Ras GTPase-activating-like protein IQGAP2 / Name=IQGAP2	8.14E-03	-2.37	2.37	-14.38	14.38
Q13509	Tubulin beta-3 chain / Name=TUBB3; Synonyms=TUBB4	9.15E-03	1.8	1.8	28.57	28.57
P02751	Fibronectin / Name=FN1; Synonyms=FN	9.73E-03	1.62	1.62	36.02	36.02

*Bold type indicates increased relative expression in peripheral cholangiocarcinoma compared to normal cholangiocytes

Table 4 provides information as to whether the marker proteins are relatively over-expressed (identified in bold) or under-expressed in hilar cholangiocarcinoma versus normal cholangiocytes. Accordingly, by determining the presence, absence or change in expression levels of a plurality of these marker proteins and comparing these changes with a reference of known expression levels, one is able to determine whether the cells under test are hilar cholangiocarcinoma or normal cholangiocytes.

Table 4 - Proteins differentiating hilar cholangiocarcinoma from normal cholangiocytes*

Protein	Name	P Value	Effect Size (g)	Magnitude of Effect Size (g)	Effect Size (Mean Dif)	Magnitude of Mean dif (Mean Dif)
PART A:						
P05062	Fructose-bisphosphate aldolase B / Name=ALDOB; Synonyms=ALDB	2.36E-05	-3.85	3.85	-9.9	9.9
P49411	Elongation factor Tu, mitochondrial / Name=TUFM	5.80E-05	-3.23	3.23	-5.62	5.62
P04424	Argininosuccinate lyase / Name=ASL	7.38E-05	-3.22	3.22	-6.57	6.57
P30837	Aldehyde dehydrogenase X, mitochondrial / Name=ALDH1B1; Synonyms=ALDH5, ALDHX	7.57E-05	-3.11	3.11	-6.93	6.93
O94760	N(G),N(G)-dimethylarginine dimethylaminohydrolase 1 / Name=DDAH1; Synonyms=DDAH	7.84E-05	-3.13	3.13	-4.17	4.17
P42765	3-ketoacyl-CoA thiolase, mitochondrial / Name=ACAA2	3.45E-04	-2.71	2.71	-7.48	7.48
P09525	Annexin A4 / Name=ANXA4; Synonyms=ANX4	3.75E-04	-2.76	2.76	-43.5	43.5
P07327	Alcohol dehydrogenase 1A / Name=ADH1A; Synonyms=ADH1	4.00E-04	-2.54	2.54	-10.67	10.67
P08263	Glutathione S-transferase A1 / Name=GSTA1	5.04E-04	-3.5	3.5	-8.29	8.29
P13797*	**Plastin-3 / Name=PLS3**	**5.11E-04**	**2.68**	**2.68**	**8.52**	**8.52**
P00325	Alcohol dehydrogenase 1B / Name=ADH1B; Synonyms=ADH2	8.05E-04	-2.84	2.84	-14.76	14.76
Q14914	Prostaglandin reductase 1 / Name=PTGR1; Synonyms=LTB4DH	9.44E-04	-3.92	3.92	-10	10
PART B:						
P00352	Retinal dehydrogenase 1 / Name=ALDH1A1; Synonyms=ALDC, ALDH1, PUMB1	1.29E-03	-2.38	2.38	-21.26	21.26
P42330	Aldo-keto reductase family 1 member C3 / Name=AKR1C3; Synonyms=DDH1, HSD17B5, KIAA0119, PGFS	1.31E-03	-2.89	2.89	-16.81	16.81
Q96KP4	Cytosolic non-specific dipeptidase / Name=CNDP2; Synonyms=CN2, CPGL, PEPA	1.61E-03	-2.17	2.17	-10.48	10.48
P06396	Gelsolin / Name=GSN	1.80E-03	2.09	2.09	7.62	7.62
O95154	Aflatoxin B1 aldehyde reductase member 3 / Name=AKR7A3; Synonyms=AFAR2	1.83E-03	-2.07	2.07	-6	6

O75489	NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial / Name=NDUFS3	1.98E-03	-2.14	2.14	-2.57	2.57
P20774	Mimecan / Name=OGN; Synonyms=OIF, SLRR3A	2.05E-03	-2.53	2.53	-14.9	14.9
Q14195	Dihydropyrimidinase-related protein 3 / Name=DPYSL3; Synonyms=CRMP4, DRP3, ULIP, ULIP1	2.74E-03	2.33	2.33	6.29	6.29
P25787	Proteasome subunit alpha type-2 / Name=PSMA2; Synonyms=HC3, PSC3	2.97E-03	-1.94	1.94	-3.38	3.38
O60218	Aldo-keto reductase family 1 member B10 / Name=AKR1B10; Synonyms=AKR1B11	2.98E-03	-2.55	2.55	-19.69	19.69
P12277	Creatine kinase B-type / Name=CKB; Synonyms=CKBB	3.15E-03	-2.74	2.74	-5.71	5.71
P02545	Prelamin-A/C / Name=LMNA; Synonyms=LMN1	3.23E-03	1.95	1.95	10.24	10.24
P23141	Liver carboxylesterase 1 / Name=CES1; Synonyms=CES2, SES1	3.36E-03	-2.92	2.92	-42.17	42.17
Q13228	Selenium-binding protein 1 / Name=SELENBP1; Synonyms=SBP	3.37E-03	-1.96	1.96	-7.95	7.95
P27216	Annexin A13 / Name=ANXA13; Synonyms=ANX13	3.90E-03	-2.85	2.85	-8.33	8.33
Q16762	Thiosulfate sulfurtransferase / Name=TST	3.92E-03	-1.84	1.84	-8.76	8.76
P31930	Cytochrome b-c1 complex subunit 1, mitochondrial / Name=UQCRC1	3.94E-03	-1.97	1.97	-2.33	2.33
P00918	Carbonic anhydrase 2 / Name=CA2	4.75E-03	-1.79	1.79	-15	15
Q08257	Quinone oxidoreductase / Name=CRYZ	4.78E-03	-1.8	1.8	-4.93	4.93
P56470	Galectin-4 / Name=LGALS4	5.53E-03	-1.79	1.79	-9.45	9.45
P18283	Glutathione peroxidase 2 / Name=GPX2	5.82E-03	-1.82	1.82	-3.95	3.95
P00738	Haptoglobin / Name=HP	6.33E-03	1.73	1.73	7.64	7.64
P17516	Aldo-keto reductase family 1 member C4 / Name=AKR1C4; Synonyms=CHDR	6.54E-03	-2.52	2.52	-8.83	8.83
P23142	Fibulin-1 / Name=FBLN1; ORFNames=PP213	6.64E-03	1.93	1.93	8.14	8.14
P08670	Vimentin / Name=VIM	7.13E-03	1.68	1.68	15.83	15.83
Q9Y3Z3	SAM domain and HD domain-containing protein 1 / Name=SAMHD1; Synonyms=MOP5	7.45E-03	1.66	1.66	2.5	2.5
Q14376	UDP-glucose 4-epimerase / Name=GALE	7.68E-03	-1.75	1.75	-2.55	2.55
P09467	Fructose-1,6-bisphosphatase 1 / Name=FBP1; Synonyms=FBP	8.04E-03	-1.73	1.73	-3.19	3.19

Q12805	EGF-containing fibulin-like extracellular matrix protein 1 / Name=EFEMP1; Synonyms=FBLN3, FBNL	8.24E-03	1.84	1.84	5.71	5.71
P12429	Annexin A3 / Name=ANXA3; Synonyms=ANX3	8.25E-03	1.74	1.74	5.81	5.81
P60842	Eukaryotic initiation factor 4A-I / Name=EIF4A1; Synonyms=DDX2A, EIF4A	8.54E-03	-1.62	1.62	-5.95	5.95
Q13509	Tubulin beta-3 chain / Name=TUBB3; Synonyms=TUBB4	8.81E-03	1.82	1.82	27.86	27.86
Q9UBR2	Cathepsin Z / Name=CTSZ	8.92E-03	1.66	1.66	2.79	2.79
Q13576	Ras GTPase-activating-like protein IQGAP2 / Name=IQGAP2	8.98E-03	-2.28	2.28	-13.95	13.95
Q99536	Synaptic vesicle membrane protein VAT-1 homolog / Name=VAT1	9.04E-03	1.61	1.61	3.29	3.29
P13611	Versican core protein / Name=VCAN; Synonyms=CSPG2	9.26E-03	1.78	1.78	17.4	17.4

*Bold type indicates increased relative expression in hilar cholangiocarcinoma compared to normal cholangiocytes

Table 5 provides information as to whether the marker proteins are relatively over-expressed (identified in bold) or under-expressed in peripheral carcinoma versus hepatocellular carcinoma. Accordingly, by determining the presence, absence or change in expression levels of a plurality of these marker proteins and comparing these changes with a reference of known expression levels, one is able to determine whether the cells under test are hepatocellular carcinoma or peripheral carcinoma.

Table 5 – Proteins differentiating hepatocellular carcinoma from peripheral cholangiocarcinoma*

Protein	Name	P Value	Effect Size (g)	Magnitude of Effect Size (g)	Effect Size (Mean Dif)	Magnitude of Mean dif (Mean Dif)
PART A:						
P18206*	**Vinculin / Name=VCL**	**1.65E-08**	**-7.07**	**7.07**	**-13.14**	**13.14**
P15311*	**Ezrin / Name=EZR; Synonyms=VIL2**	**8.38E-07**	**-5.26**	**5.26**	**-11.14**	**11.14**
P51659	Peroxisomal multifunctional enzyme type 2 / Name=HSD17B4;	1.09E-06	5.92	5.92	40.43	40.43

	Synonyms=EDH17B4					
P00352	Retinal dehydrogenase 1 / Name=ALDH1A1; Synonyms=ALDC, ALDH1, PUMB1	1.55E-05	3.61	3.61	39.57	39.57
Q8NBX0	Probable saccharopine dehydrogenase / Name=SCCPDH; ORFNames=CGI-49	1.60E-05	3.47	3.47	5.71	5.71
P04040	Catalase / Name=CAT	2.67E-05	3.8	3.8	37	37
P07148	Fatty acid-binding protein, liver / Name=FABP1; Synonyms=FABPL	3.16E-05	3.4	3.4	20.29	20.29
P33121	Long-chain-fatty-acid--CoA ligase 1 / Name=ACSL1; Synonyms=FACL1, FACL2, LACS, LACS1, LACS2	3.20E-05	5.55	5.55	11.57	11.57
P63104*	**14-3-3 protein zeta/delta / Name=YWHAZ**	**3.33E-05**	**-3.22**	**3.22**	**-13.29**	**13.29**
P14618*	**Pyruvate kinase isozymes M1/M2 / Name=PKM2; Synonyms=OIP3, PK2, PK3, PKM**	**3.76E-05**	**-4.42**	**4.42**	**-39.86**	**39.86**
P09525*	**Annexin A4 / Name=ANXA4; Synonyms=ANX4**	**4.58E-05**	**-3.8**	**3.8**	**-33.14**	**33.14**
P31949*	**Protein S100-A11 / Name=S100A11; Synonyms=MLN70, S100C**	**4.81E-05**	**-5.17**	**5.17**	**-3.71**	**3.71**
O95831	Apoptosis-inducing factor 1, mitochondrial / Name=AIFM1; Synonyms=AIF, PDCD8	5.22E-05	3.15	3.15	9.43	9.43
P04075*	**Fructose-bisphosphate aldolase A / Name=ALDOA; Synonyms=ALDA**	**6.82E-05**	**-3.58**	**3.58**	**-25**	**25**
P00558*	**Phosphoglycerate kinase 1 / Name=PGK1; Synonyms=PGKA; ORFNames=MIG10, OK/SW-cl.110**	**7.65E-05**	**-3.1**	**3.1**	**-19.43**	**19.43**
P46940*	**Ras GTPase-activating-like protein IQGAP1 / Name=IQGAP1; Synonyms=KIAA0051**	**7.86E-05**	**-4.74**	**4.74**	**-14.29**	**14.29**
P34897	Serine hydroxymethyltransferase, mitochondrial / Name=SHMT2	8.07E-05	2.95	2.95	6.86	6.86
P10620	Microsomal glutathione S-transferase 1 / Name=MGST1; Synonyms=GST12, MGST	8.41E-05	3.47	3.47	4.57	4.57
Q15019*	**Septin-2 / Name=SEPT2; Synonyms=DIFF6, KIAA0158, NEDD5**	**8.46E-05**	**-4.68**	**4.68**	**-5**	**5**
O14756	17-beta-hydroxysteroid dehydrogenase type 6 / Name=HSD17B6;	8.58E-05	4.67	4.67	11.29	11.29

	Synonyms=RODH					
P07099	Epoxide hydrolase 1 / Name=EPHX1; Synonyms=EPHX, EPOX	8.96E-05	2.99	2.99	38.14	38.14
Q02338	D-beta-hydroxybutyrate dehydrogenase, mitochondrial / Name=BDH1; Synonyms=BDH	9.25E-05	4.61	4.61	8.86	8.86
P45954	Short/branched chain specific acyl-CoA dehydrogenase, mitochondrial / Name=ACADSB	9.70E-05	4.57	4.57	9.29	9.29
Q16822	Phosphoenolpyruvate carboxykinase [GTP], mitochondrial / Name=PCK2; Synonyms=PEPCK2	1.03E-04	4.29	4.29	30.86	30.86
P08238*	**Heat shock protein HSP 90-beta / Name=HSP90AB1; Synonyms=HSP90B, HSPC2, HSPCB**	**1.09E-04**	**-2.97**	**2.97**	**-12.71**	**12.71**
P50454*	**Serpin H1 / Name=SERPINH1; Synonyms=CBP1, CBP2, HSP47, SERPINH2; ORFNames=PIG14**	**1.10E-04**	**-3.45**	**3.45**	**-8.29**	**8.29**
P05062	Fructose-bisphosphate aldolase B / Name=ALDOB; Synonyms=ALDB	1.16E-04	3.47	3.47	50.71	50.71
P05091	Aldehyde dehydrogenase, mitochondrial / Name=ALDH2; Synonyms=ALDM	1.17E-04	2.86	2.86	28.86	28.86
P13010*	**X-ray repair cross-complementing protein 5 / Name=XRCC5; Synonyms=G22P2**	**1.20E-04**	**-2.91**	**2.91**	**-8.29**	**8.29**
P51649	Succinate-semialdehyde dehydrogenase, mitochondrial / Name=ALDH5A1; Synonyms=SSADH	1.28E-04	2.77	2.77	7.71	7.71
P27348*	**14-3-3 protein theta / Name=YWHAQ**	**1.30E-04**	**-2.99**	**2.99**	**-11.71**	**11.71**
P02649	Apolipoprotein E / Name=APOE	1.32E-04	2.93	2.93	13.86	13.86
P09467	Fructose-1,6-bisphosphatase 1 / Name=FBP1; Synonyms=FBP	1.44E-04	4.26	4.26	12.29	12.29
P21333*	**Filamin-A / Name=FLNA; Synonyms=FLN, FLN1**	**1.57E-04**	**-3.96**	**3.96**	**-55.43**	**55.43**
P08133	Annexin A6 / Name=ANXA6; Synonyms=ANX6	1.57E-04	2.72	2.72	23.14	23.14
Q9UJS0	Calcium-binding mitochondrial carrier protein Aralar2 / Name=SLC25A13; Synonyms=ARALAR2	1.62E-04	2.73	2.73	9.71	9.71
P61158*	**Actin-related protein 3 / Name=ACTR3;**	**1.66E-04**	**-2.74**	**2.74**	**-6.29**	**6.29**

	Synonyms=ARP3					
P55157	Microsomal triglyceride transfer protein large subunit / Name=MTTP; Synonyms=MTP	1.76E-04	4.11	4.11	7.57	7.57
P24752	Acetyl-CoA acetyltransferase, mitochondrial / Name=ACAT1; Synonyms=ACAT, MAT	1.97E-04	3.2	3.2	18	18
P52758	Ribonuclease UK114 / Name=HRSP12; Synonyms=PSP	1.99E-04	3.62	3.62	8.29	8.29
P16930	Fumarylacetoacetase / Name=FAH	2.11E-04	2.99	2.99	11.14	11.14
P00505	Aspartate aminotransferase, mitochondrial / Name=GOT2	2.16E-04	2.87	2.87	8.43	8.43
P12429*	**Annexin A3 / Name=ANXA3; Synonyms=ANX3**	**2.25E-04**	**-3.14**	**3.14**	**-4.57**	**4.57**
P68032*	**Actin, alpha cardiac muscle 1 / Name=ACTC1; Synonyms=ACTC**	**2.30E-04**	**-2.62**	**2.62**	**-55.86**	**55.86**
P00367	Glutamate dehydrogenase 1, mitochondrial / Name=GLUD1; Synonyms=GLUD	2.42E-04	2.61	2.61	18	18
P30038	Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial / Name=ALDH4A1; Synonyms=ALDH4, P5CDH	2.42E-04	3.04	3.04	16.43	16.43
Q12905*	**Interleukin enhancer-binding factor 2 / Name=ILF2; Synonyms=NF45; ORFNames=PRO3063**	**2.58E-04**	**-2.58**	**2.58**	**-3.86**	**3.86**
P21810*	**Biglycan / Name=BGN; Synonyms=SLRR1A**	**2.80E-04**	**-3.62**	**3.62**	**-21.57**	**21.57**
P78417	Glutathione S-transferase omega-1 / Name=GSTO1; Synonyms=GSTTLP28	2.87E-04	2.92	2.92	5.43	5.43
Q14032	Bile acid-CoA:amino acid N-acyltransferase / Name=BAAT	3.13E-04	3.7	3.7	6.43	6.43
Q9H8H3	Methyltransferase-like protein 7A / Name=METTL7A; ORFNames=PRO0066, UNQ1902/PRO4348	3.14E-04	2.6	2.6	3.86	3.86
Q9UJM8	Hydroxyacid oxidase 1 / Name=HAO1; Synonyms=GOX1, HAOX1	3.16E-04	3.69	3.69	20	20
P12956*	**X-ray repair cross-complementing protein 6 / Name=XRCC6; Synonyms=G22P1**	**3.17E-04**	**-2.71**	**2.71**	**-10.57**	**10.57**
O00264	Membrane-associated progesterone receptor component 1 / Name=PGRMC1;	3.42E-04	3.21	3.21	10.71	10.71

	Synonyms=HPR6.6, PGRMC					
P67936*	**Tropomyosin alpha-4 chain / Name=TPM4**	**3.48E-04**	**-2.88**	**2.88**	**-9.43**	**9.43**
P11498	Pyruvate carboxylase, mitochondrial / Name=PC	3.68E-04	3.54	3.54	20.14	20.14
Q9HDC9	Adipocyte plasma membrane-associated protein / Name=APMAP; Synonyms=C20orf3; ORFNames=UNQ1869/PRO4305	3.72E-04	2.45	2.45	5.14	5.14
P36871	Phosphoglucomutase-1 / Name=PGM1	3.85E-04	2.48	2.48	17.71	17.71
Q93099	Homogentisate 1,2-dioxygenase / Name=HGD; Synonyms=HGO	4.18E-04	2.64	2.64	12.14	12.14
Q969Z3	MOSC domain-containing protein 2, mitochondrial / Name=MOSC2	4.42E-04	3.47	3.47	6.14	6.14
P30084	Enoyl-CoA hydratase, mitochondrial / Name=ECHS1	4.53E-04	2.43	2.43	9.86	9.86
Q9Y2Q3	Glutathione S-transferase kappa 1 / Name=GSTK1; ORFNames=HDCMD47P	4.71E-04	2.46	2.46	10.57	10.57
Q16762	Thiosulfate sulfurtransferase / Name=TST	4.86E-04	2.54	2.54	14.29	14.29
P00480	Ornithine carbamoyltransferase, mitochondrial / Name=OTC	4.87E-04	3.41	3.41	14.71	14.71
O60664*	**Perilipin-3 / Name=PLIN3; Synonyms=M6PRBP1, TIP47**	**5.02E-04**	**-3.39**	**3.39**	**-6.43**	**6.43**
Q9P0Z9	Peroxisomal sarcosine oxidase / Name=PIPOX; Synonyms=LPIPOX, PSO	5.12E-04	3.38	3.38	13.14	13.14
Q4G0N4	NAD kinase domain-containing protein 1 / Name=NADKD1; Synonyms=C5orf33	5.57E-04	3.33	3.33	8.57	8.57
Q06520	Bile salt sulfotransferase / Name=SULT2A1; Synonyms=HST, STD	5.74E-04	3.31	3.31	14.43	14.43
P06396*	**Gelsolin / Name=GSN**	**6.42E-04**	**-2.49**	**2.49**	**-8.43**	**8.43**
P31327	Carbamoyl-phosphate synthase [ammonia], mitochondrial / Name=CPS1	6.50E-04	3	3	162.57	162.57
P04424	Argininosuccinate lyase / Name=ASL	6.65E-04	3.05	3.05	18	18
P11310	Medium-chain specific acyl-CoA dehydrogenase, mitochondrial / Name=ACADM	6.71E-04	2.65	2.65	7.43	7.43
Q9BPW8	Protein NipSnap homolog 1 / Name=NIPSNAP1	7.94E-04	2.28	2.28	6.71	6.71
P23141	Liver carboxylesterase 1 / Name=CES1; Synonyms=CES2, SES1	7.99E-04	3.05	3.05	57.14	57.14

P06737	Glycogen phosphorylase, liver form / Name=PYGL	8.18E-04	3.1	3.1	12.29	12.29
P50995*	**Annexin A11 / Name=ANXA11; Synonyms=ANX11**	**8.64E-04**	**-2.47**	**2.47**	**-6.57**	**6.57**
Q03154	Aminoacylase-1 / Name=ACY1	9.00E-04	3.04	3.04	16.71	16.71
P42765	3-ketoacyl-CoA thiolase, mitochondrial / Name=ACAA2	1.01E-03	2.26	2.26	18.71	18.71
PART B:						
O43399	Tumor protein D54 / Name=TPD52L2	1.06E-03	-2.34	2.34	-3.57	3.57
P07954	Fumarate hydratase, mitochondrial / Name=FH	1.12E-03	2.38	2.38	6.43	6.43
P80404	4-aminobutyrate aminotransferase, mitochondrial / Name=ABAT; Synonyms=GABAT	1.16E-03	2.83	2.83	24	24
P21549	Serine--pyruvate aminotransferase / Name=AGXT; Synonyms=AGT1, SPAT	1.18E-03	2.73	2.73	66.43	66.43
P34913	Epoxide hydrolase 2 / Name=EPHX2	1.23E-03	2.87	2.87	5	5
P04350	Tubulin beta-4 chain / Name=TUBB4; Synonyms=TUBB5	1.25E-03	-2.85	2.85	-50.43	50.43
O95479	GDH/6PGL endoplasmic bifunctional protein / Name=H6PD; Synonyms=GDH	1.27E-03	2.65	2.65	6.29	6.29
P00167	Cytochrome b5 / Name=CYB5A; Synonyms=CYB5	1.29E-03	2.76	2.76	10.86	10.86
Q08426	Peroxisomal bifunctional enzyme / Name=EHHADH; Synonyms=ECHD	1.29E-03	2.8	2.8	32.86	32.86
P61981	14-3-3 protein gamma / Name=YWHAG	1.33E-03	-2.15	2.15	-4.57	4.57
P05089	Arginase-1 / Name=ARG1	1.35E-03	2.81	2.81	22.14	22.14
P05455	Lupus La protein / Name=SSB	1.36E-03	-2.09	2.09	-4.57	4.57
P51884	Lumican / Name=LUM; Synonyms=LDC, SLRR2D	1.37E-03	-2.46	2.46	-12.71	12.71
P21399	Cytoplasmic aconitate hydratase / Name=ACO1; Synonyms=IREB1	1.45E-03	2.52	2.52	13.14	13.14
Q15436	Protein transport protein Sec23A / Name=SEC23A	1.47E-03	2.17	2.17	4.43	4.43
P60660	Myosin light polypeptide 6 / Name=MYL6	1.50E-03	-2.06	2.06	-5.29	5.29
P54868	Hydroxymethylglutaryl-CoA synthase, mitochondrial / Name=HMGCS2	1.51E-03	2.66	2.66	29.57	29.57
Q9NVS	Pyridoxine-5'-phosphate	1.52E-03	2.75	2.75	3.57	3.57

9	oxidase / Name=PNPO					
P23528	Cofilin-1 / Name=CFL1; Synonyms=CFL	1.67E-03	-2.02	2.02	-3.86	3.86
Q6NVY1	3-hydroxyisobutyryl-CoA hydrolase, mitochondrial / Name=HIBCH	1.74E-03	2.04	2.04	2.71	2.71
P28845	Corticosteroid 11-beta-dehydrogenase isozyme 1 / Name=HSD11B1; Synonyms=HSD11, HSD11L	1.78E-03	2.67	2.67	4.86	4.86
P30086	Phosphatidylethanolamine-binding protein 1 / Name=PEBP1; Synonyms=PBP, PEBP	1.87E-03	2.13	2.13	12.57	12.57
Q04828	Aldo-keto reductase family 1 member C1 / Name=AKR1C1; Synonyms=DDH, DDH1	1.96E-03	2.16	2.16	20.14	20.14
O43707	Alpha-actinin-4 / Name=ACTN4	1.98E-03	-2.12	2.12	-18.14	18.14
Q9Y490	Talin-1 / Name=TLN1; Synonyms=KIAA1027, TLN	2.03E-03	-2.09	2.09	-11.86	11.86
Q02252	Methylmalonate-semialdehyde dehydrogenase [acylating], mitochondrial / Name=ALDH6A1; Synonyms=MMSDH	2.03E-03	2.41	2.41	26.57	26.57
P09211	Glutathione S-transferase P / Name=GSTP1; Synonyms=FAEES3, GST3	2.12E-03	-2.51	2.51	-17.14	17.14
P32754	4-hydroxyphenylpyruvate dioxygenase / Name=HPD; Synonyms=PPD	2.17E-03	2.56	2.56	19.86	19.86
P07384	Calpain-1 catalytic subunit / Name=CAPN1; Synonyms=CANPL1; ORFNames=PIG30	2.20E-03	-1.99	1.99	-8.14	8.14
Q9H2A2	Aldehyde dehydrogenase family 8 member A1 / Name=ALDH8A1; Synonyms=ALDH12	2.23E-03	2.55	2.55	4.43	4.43
P30043	Flavin reductase (NADPH) / Name=BLVRB; Synonyms=FLR	2.27E-03	2.18	2.18	6	6
Q68CK6	Acyl-coenzyme A synthetase ACSM2B, mitochondrial / Name=ACSM2B; Synonyms=ACSM2; ORFNames=HYST1046	2.31E-03	2.53	2.53	15.57	15.57
P13611	Versican core protein / Name=VCAN; Synonyms=CSPG2	2.34E-03	-2.5	2.5	-14.43	14.43
P07237	Protein disulfide-isomerase / Name=P4HB; Synonyms=ERBA2L, PDI, PDIA1, PO4DB	2.40E-03	2	2	11.14	11.14
P22307	Non-specific lipid-transfer protein / Name=SCP2	2.42E-03	2.46	2.46	11.14	11.14

Q9Y265	RuvB-like 1 / Name=RUVBL1; Synonyms=INO80H, NMP238, TIP49, TIP49A	2.47E-03	-2.5	2.5	-4.71	4.71
P49419	Alpha-aminoadipic semialdehyde dehydrogenase / Name=ALDH7A1; Synonyms=ATQ1	2.47E-03	1.93	1.93	13	13
P62258	14-3-3 protein epsilon / Name=YWHAE	2.56E-03	-1.9	1.9	-6.86	6.86
P19105	Myosin regulatory light chain 12A / Name=MYL12A; Synonyms=MLCB, MRLC3, RLC	2.59E-03	-1.94	1.94	-2.86	2.86
O14950	Myosin regulatory light chain 12B / Name=MYL12B; Synonyms=MRLC2, MYLC2B	2.59E-03	-1.94	1.94	-2.86	2.86
O75367	Core histone macro-H2A.1 / Name=H2AFY; Synonyms=MACROH2A1	2.59E-03	-1.97	1.97	-9	9
P11216	Glycogen phosphorylase, brain form / Name=PYGB	2.60E-03	-1.89	1.89	-6.57	6.57
P16152	Carbonyl reductase [NADPH] 1 / Name=CBR1; Synonyms=CBR, CRN	2.61E-03	2.26	2.26	17	17
Q7Z4W1	L-xylulose reductase / Name=DCXR	2.69E-03	2.42	2.42	26.29	26.29
P07355	Annexin A2 / Name=ANXA2; Synonyms=ANX2, ANX2L4, CAL1H, LPC2D	2.85E-03	-2.38	2.38	-25.43	25.43
P78527	DNA-dependent protein kinase catalytic subunit / Name=PRKDC; Synonyms=HYRC, HYRC1	2.86E-03	-2.11	2.11	-13.71	13.71
Q15393	Splicing factor 3B subunit 3 / Name=SF3B3; Synonyms=KIAA0017, SAP130	2.91E-03	-2.42	2.42	-3.29	3.29
Q04917	14-3-3 protein eta / Name=YWHAH; Synonyms=YWHA1	2.97E-03	-1.99	1.99	-6.86	6.86
P38117	Electron transfer flavoprotein subunit beta / Name=ETFB; ORFNames=FP585	2.97E-03	2.01	2.01	8.43	8.43
P08729	Keratin, type II cytoskeletal 7 / Name=KRT7; Synonyms=SCL	3.10E-03	-2.39	2.39	-12	12
Q14914	Prostaglandin reductase 1 / Name=PTGR1; Synonyms=LTB4DH	3.21E-03	2.29	2.29	10.71	10.71
P17516	Aldo-keto reductase family 1 member C4 / Name=AKR1C4; Synonyms=CHDR	3.24E-03	2.36	2.36	11.43	11.43
P63261	Actin, cytoplasmic 2 / Name=ACTG1; Synonyms=ACTB, ACTG	3.35E-03	-2.22	2.22	-101.57	101.57
P16435	NADPH--cytochrome P450 reductase / Name=POR;	3.46E-03	2.28	2.28	12.86	12.86

	Synonyms=CYPOR					
Q15067	Peroxisomal acyl-coenzyme A oxidase 1 / Name=ACOX1; Synonyms=ACOX	3.54E-03	2.32	2.32	11	11
P35914	Hydroxymethylglutaryl-CoA lyase, mitochondrial / Name=HMGCL	3.55E-03	2.32	2.32	4.71	4.71
P30046	D-dopachrome decarboxylase / Name=DDT	3.63E-03	1.95	1.95	4.86	4.86
P30613	Pyruvate kinase isozymes R/L / Name=PKLR; Synonyms=PK1, PKL	3.63E-03	2.31	2.31	11.14	11.14
Q07960	Rho GTPase-activating protein 1 / Name=ARHGAP1; Synonyms=CDC42GAP, RHOGAP1	3.67E-03	-2.07	2.07	-3.43	3.43
Q6YN16	Hydroxysteroid dehydrogenase-like protein 2 / Name=HSDL2; Synonyms=C9orf99	3.67E-03	2.07	2.07	3.43	3.43
Q08AH3	Acyl-coenzyme A synthetase ACSM2A, mitochondrial / Name=ACSM2A; Synonyms=ACSM2, MACS2	3.69E-03	2.3	2.3	15.14	15.14
Q9UL12	Sarcosine dehydrogenase, mitochondrial / Name=SARDH; Synonyms=DMGDHL1	3.70E-03	2.3	2.3	7.29	7.29
O00299	Chloride intracellular channel protein 1 / Name=CLIC1; Synonyms=G6, NCC27	3.76E-03	-2	2	-7.71	7.71
Q13838	Spliceosome RNA helicase DDX39B / Name=DDX39B; Synonyms=BAT1, UAP56	3.79E-03	-1.85	1.85	-4.43	4.43
P09110	3-ketoacyl-CoA thiolase, peroxisomal / Name=ACAA1; Synonyms=ACAA, PTHIO	3.81E-03	2	2	14.71	14.71
P52907	F-actin-capping protein subunit alpha-1 / Name=CAPZA1	3.82E-03	-1.96	1.96	-3.29	3.29
P34896	Serine hydroxymethyltransferase, cytosolic / Name=SHMT1	3.85E-03	2.07	2.07	10.71	10.71
P00491	Purine nucleoside phosphorylase / Name=PNP; Synonyms=NP	3.87E-03	-1.84	1.84	-5.86	5.86
Q9P0M6	Core histone macro-H2A.2 / Name=H2AFY2; Synonyms=MACROH2A2	4.02E-03	-2.26	2.26	-6	6
Q01995	Transgelin / Name=TAGLN; Synonyms=SM22, WS3-10	4.04E-03	-2.16	2.16	-9.86	9.86
Q16851	UTP--glucose-1-phosphate uridylyltransferase / Name=UGP2; Synonyms=UGP1	4.09E-03	2.09	2.09	18.57	18.57
P05090	Apolipoprotein D /	4.10E-03	2.25	2.25	2.57	2.57

	Name=APOD					
P22033	Methylmalonyl-CoA mutase, mitochondrial / Name=MUT	4.20E-03	2.24	2.24	2.71	2.71
P31939	Bifunctional purine biosynthesis protein PURH / Name=ATIC; Synonyms=PURH; ORFNames=OK/SW-cl.86	4.22E-03	-2.01	2.01	-11.43	11.43
Q08380	Galectin-3-binding protein / Name=LGALS3BP; Synonyms=M2BP	4.25E-03	-1.98	1.98	-7.71	7.71
P07437	Tubulin beta chain / Name=TUBB; Synonyms=TUBB5; ORFNames=OK/SW-cl.56	4.34E-03	-1.76	1.76	-24.71	24.71
P07585	Decorin / Name=DCN; Synonyms=SLRR1B	4.35E-03	-2.22	2.22	-8	8
O75533	Splicing factor 3B subunit 1 / Name=SF3B1; Synonyms=SAP155	4.39E-03	-2.22	2.22	-3.71	3.71
P22310	UDP-glucuronosyltransferase 1-4 / Name=UGT1A4; Synonyms=GNT1, UGT1	4.46E-03	2.21	2.21	8.29	8.29
P07195	L-lactate dehydrogenase B chain / Name=LDHB	4.47E-03	-1.88	1.88	-9.43	9.43
P24298	Alanine aminotransferase 1 / Name=GPT; Synonyms=AAT1, GPT1	4.50E-03	2.21	2.21	8	8
Q9H9B4	Sideroflexin-1 / Name=SFXN1	4.52E-03	1.84	1.84	4.14	4.14
P14923	Junction plakoglobin / Name=JUP; Synonyms=CTNNG, DP3	4.73E-03	-2.01	2.01	-7.57	7.57
P11586	C-1-tetrahydrofolate synthase, cytoplasmic / Name=MTHFD1; Synonyms=MTHFC, MTHFD	4.73E-03	2.1	2.1	17.57	17.57
P28838	Cytosol aminopeptidase / Name=LAP3; Synonyms=LAPEP, PEPS	4.91E-03	1.86	1.86	9.29	9.29
P21291	Cysteine and glycine-rich protein 1 / Name=CSRP1; Synonyms=CSRP, CYRP	4.96E-03	-1.79	1.79	-3.29	3.29
P00441	Superoxide dismutase [Cu-Zn] / Name=SOD1	4.99E-03	2.03	2.03	7.43	7.43
Q9Y6C9	Mitochondrial carrier homolog 2 / Name=MTCH2; Synonyms=MIMP; ORFNames=HSPC032	5.15E-03	1.79	1.79	6	6
P23284	Peptidyl-prolyl cis-trans isomerase B / Name=PPIB; Synonyms=CYPB	5.21E-03	1.71	1.71	4.14	4.14
O60701	UDP-glucose 6-dehydrogenase / Name=UGDH	5.24E-03	1.96	1.96	6.86	6.86
P16422	Epithelial cell adhesion molecule / Name=EPCAM; Synonyms=GA733-2, M1S2,	5.30E-03	-2.13	2.13	-2.86	2.86

	M4S1, MIC18, TACSTD1, TROP1					
P07327	Alcohol dehydrogenase 1A / Name=ADH1A; Synonyms=ADH1	5.37E-03	2.12	2.12	38.86	38.86
Q9UIJ7	GTP:AMP phosphotransferase, mitochondrial / Name=AK3; Synonyms=AK3L1, AK6, AKL3L	5.41E-03	1.98	1.98	4	4
P61160	Actin-related protein 2 / Name=ACTR2; Synonyms=ARP2	5.48E-03	-1.86	1.86	-5.14	5.14
P06703	Protein S100-A6 / Name=S100A6; Synonyms=CACY	5.49E-03	-1.94	1.94	-3.43	3.43
Q96HR9	Receptor expression-enhancing protein 6 / Name=REEP6; Synonyms=C19orf32, DP1L1	5.56E-03	2.11	2.11	3.43	3.43
O75521	Enoyl-CoA delta isomerase 2, mitochondrial / Name=ECI2; Synonyms=DRS1, HCA88, PECI	5.59E-03	2.11	2.11	6.43	6.43
P13639	Elongation factor 2 / Name=EEF2; Synonyms=EF2	5.61E-03	-1.79	1.79	-12.43	12.43
P13804	Electron transfer flavoprotein subunit alpha, mitochondrial / Name=ETFA	5.64E-03	1.87	1.87	8	8
Q16698	2,4-dienoyl-CoA reductase, mitochondrial / Name=DECR1; Synonyms=DECR	5.68E-03	1.85	1.85	9	9
O95154	Aflatoxin B1 aldehyde reductase member 3 / Name=AKR7A3; Synonyms=AFAR2	5.77E-03	2.09	2.09	8.14	8.14
O14773	Tripeptidyl-peptidase 1 / Name=TPP1; Synonyms=CLN2; ORFNames=GIG1, UNQ267/PRO304	5.93E-03	1.69	1.69	7.29	7.29
P19338	Nucleolin / Name=NCL	6.02E-03	-1.7	1.7	-7.71	7.71
P07900	Heat shock protein HSP 90-alpha / Name=HSP90AA1; Synonyms=HSP90A, HSPC1, HSPCA	6.08E-03	-1.89	1.89	-19.71	19.71
Q9BWD1	Acetyl-CoA acetyltransferase, cytosolic / Name=ACAT2; Synonyms=ACTL	6.15E-03	1.99	1.99	5.57	5.57
Q07507	Dermatopontin / Name=DPT	6.20E-03	-1.98	1.98	-5.14	5.14
Q9Y2P5	Bile acyl-CoA synthetase / Name=SLC27A5; Synonyms=ACSB, ACSVL6, FACVL3, FATP5	6.22E-03	2.06	2.06	9.14	9.14

P17174	Aspartate aminotransferase, cytoplasmic / Name=GOT1	6.37E-03	1.8	1.8	23.14	23.14
P08727	Keratin, type I cytoskeletal 19 / Name=KRT19	6.49E-03	-2.04	2.04	-27.29	27.29
P51888	Prolargin / Name=PRELP; Synonyms=SLRR2A	6.58E-03	-2	2	-25.29	25.29
Q9UBQ7	Glyoxylate reductase/hydroxypyruvate reductase / Name=GRHPR; Synonyms=GLXR; ORFNames=MSTP035	6.71E-03	1.99	1.99	13.57	13.57
P34932	Heat shock 70 kDa protein 4 / Name=HSPA4; Synonyms=APG2	6.91E-03	-1.63	1.63	-3.71	3.71
Q15149	Plectin / Name=PLEC; Synonyms=PLEC1	6.91E-03	-1.95	1.95	-14	14
P00403	Cytochrome c oxidase subunit 2 / Name=MT-CO2; Synonyms=COII, COXII, MTCO2	6.92E-03	1.65	1.65	2.71	2.71
Q15274	Nicotinate-nucleotide pyrophosphorylase [carboxylating] / Name=QPRT	7.04E-03	2.01	2.01	3.86	3.86
Q14117	Dihydropyrimidinase / Name=DPYS	7.23E-03	1.99	1.99	3.57	3.57
P27695	DNA-(apurinic or apyrimidinic site) lyase / Name=APEX1; Synonyms=APE, APE1, APEX, APX, HAP1, REF1	7.51E-03	-1.64	1.64	-4.14	4.14
P51858	Hepatoma-derived growth factor / Name=HDGF; Synonyms=HMG1L2	7.54E-03	-1.7	1.7	-5.86	5.86
Q13228	Selenium-binding protein 1 / Name=SELENBP1; Synonyms=SBP	7.54E-03	1.89	1.89	16.57	16.57
P46783	40S ribosomal protein S10 / Name=RPS10	7.58E-03	1.63	1.63	3	3
Q00796	Sorbitol dehydrogenase / Name=SORD	7.61E-03	1.97	1.97	12.86	12.86
P00325	Alcohol dehydrogenase 1B / Name=ADH1B; Synonyms=ADH2	7.68E-03	1.91	1.91	37.57	37.57
P01024	Complement C3 / Name=C3; Synonyms=CPAMD1	7.77E-03	-1.77	1.77	-23.71	23.71
Q93088	Betaine--homocysteine S-methyltransferase 1 / Name=BHMT	7.81E-03	1.96	1.96	16.29	16.29
P17655	Calpain-2 catalytic subunit / Name=CAPN2; Synonyms=CANPL2	8.05E-03	-1.95	1.95	-5.29	5.29
Q13724	Mannosyl-oligosaccharide glucosidase / Name=MOGS; Synonyms=GCS1	8.22E-03	1.68	1.68	1.86	1.86
O75489	NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial /	8.27E-03	1.62	1.62	2.43	2.43

	Name=NDUFS3					
P50226	Sulfotransferase 1A2 / Name=SULT1A2; Synonyms=STP2	8.35E-03	1.73	1.73	4.14	4.14
P02790	Hemopexin / Name=HPX	8.37E-03	-1.63	1.63	-5.14	5.14
Q02318	Sterol 26-hydroxylase, mitochondrial / Name=CYP27A1; Synonyms=CYP27	8.51E-03	1.92	1.92	4.43	4.43
P30041	Peroxiredoxin-6 / Name=PRDX6; Synonyms=AOP2, KIAA0106	8.74E-03	1.58	1.58	9.86	9.86
P00966	Argininosuccinate synthase / Name=ASS1; Synonyms=ASS	8.90E-03	1.9	1.9	16.71	16.71
P02768	Serum albumin / Name=ALB	9.02E-03	-1.68	1.68	-69.14	69.14
P04632	Calpain small subunit 1 / Name=CAPNS1; Synonyms=CAPN4, CAPNS	9.08E-03	-1.84	1.84	-5.57	5.57
Q13509	Tubulin beta-3 chain / Name=TUBB3; Synonyms=TUBB4	9.15E-03	-1.89	1.89	-28.57	28.57
Q96FW1	Ubiquitin thioesterase OTUB1 / Name=OTUB1; Synonyms=OTB1, OTU1; ORFNames=HSPC263	9.17E-03	-1.55	1.55	-2.43	2.43
Q96QK1	Vacuolar protein sorting-associated protein 35 / Name=VPS35; Synonyms=MEM3; ORFNames=TCCCTA00141	9.26E-03	-1.67	1.67	-5	5
O00515	Ladinin-1 / Name=LAD1; Synonyms=LAD	9.35E-03	-1.88	1.88	-8.29	8.29
Q9Y678	Coatomer subunit gamma / Name=COPG; Synonyms=COPG1	9.47E-03	-1.88	1.88	-2.57	2.57
Q99424	Peroxisomal acyl-coenzyme A oxidase 2 / Name=ACOX2	9.52E-03	1.88	1.88	9.57	9.57
Q7Z6Z7	E3 ubiquitin-protein ligase HUWE1 / Name=HUWE1; Synonyms=KIAA0312, KIAA1578, UREB1; ORFNames=HSPC272	9.60E-03	-1.87	1.87	-2	2
Q9BUF5	Tubulin beta-6 chain / Name=TUBB6	9.62E-03	-1.87	1.87	-21	21
P02774	Vitamin D-binding protein / Name=GC	9.72E-03	-1.7	1.7	-3.29	3.29
P09417	Dihydropteridine reductase / Name=QDPR; Synonyms=DHPR	9.74E-03	1.87	1.87	5.57	5.57
P50225	Sulfotransferase 1A1 / Name=SULT1A1; Synonyms=STP, STP1; ORFNames=OK/SW-cl.88	9.79E-03	1.69	1.69	4.29	4.29
Q9NUI1	Peroxisomal 2,4-dienoyl-CoA reductase / Name=DECR2;	9.84E-03	1.86	1.86	4.71	4.71

	Synonyms=PDCR					
P31947	14-3-3 protein sigma / Name=SFN; Synonyms=HME1	9.95E-03	-1.86	1.86	-9.14	9.14

*Bold type indicates increased relative expression in peripheral cholangiocarcinoma compared to hepatocellular carcinoma

Table 6 provides information as to whether the marker proteins are relatively over-expressed (identified in bold) or under-expressed in normal cholangiocytes versus normal hepatocytes. Accordingly, by determining the presence, absence or change in expression levels of a plurality of these marker proteins and comparing these changes with a reference of known expression levels, one is able to determine whether the cells under test are normal cholangiocytes or normal hepatocytes.

Table 6 – Proteins differentiating normal hepatocytes from normal cholangiocytes*

Protein	Name	P Value	Effect Size (g)	Magnitude of Effect Size (g)	Effect Size (Mean Dif)	Magnitude of Mean dif (Mean Dif)
PART A:						
P07099	Epoxide hydrolase 1 / Name=EPHX1; Synonyms=EPHX, EPOX	1.21E-08	9.4	9.4	38.02	38.02
P22307	Non-specific lipid-transfer protein / Name=SCP2	3.92E-08	7.85	7.85	14.14	14.14
Q969Z3	MOSC domain-containing protein 2, mitochondrial / Name=MOSC2	9.34E-08	6.25	6.25	6.1	6.1
Q16851	UTP--glucose-1-phosphate uridylyltransferase / Name=UGP2; Synonyms=UGP1	1.06E-07	9.18	9.18	38.5	38.5
Q16822	Phosphoenolpyruvate carboxykinase [GTP], mitochondrial / Name=PCK2; Synonyms=PEPCK2	2.74E-07	7.02	7.02	39.67	39.67
P05091	Aldehyde dehydrogenase, mitochondrial / Name=ALDH2;	3.03E-07	5.98	5.98	49.64	49.64

	Synonyms=ALDM					
P30740*	**Leukocyte elastase inhibitor / Name=SERPINB1; Synonyms=ELANH2, MNEI, PI2**	**3.97E-07**	**-6.1**	**6.1**	**-9.9**	**9.9**
Q02252	Methylmalonate-semialdehyde dehydrogenase [acylating], mitochondrial / Name=ALDH6A1; Synonyms=MMSDH	4.15E-07	8.09	8.09	32.24	32.24
Q4G0N4	NAD kinase domain-containing protein 1 / Name=NADKD1; Synonyms=C5orf33	5.85E-07	10.45	10.45	12.14	12.14
P16435	NADPH--cytochrome P450 reductase / Name=POR; Synonyms=CYPOR	1.42E-06	4.81	4.81	7.79	7.79
P34896	Serine hydroxymethyltransferase, cytosolic / Name=SHMT1	1.90E-06	7.21	7.21	20.24	20.24
P50440	Glycine amidinotransferase, mitochondrial / Name=GATM; Synonyms=AGAT	2.14E-06	5.62	5.62	21.98	21.98
Q96QK1*	**Vacuolar protein sorting-associated protein 35 / Name=VPS35; Synonyms=MEM3; ORFNames=TCCCTA00141**	**2.15E-06**	**-5.61**	**5.61**	**-5.38**	**5.38**
P16930	Fumarylacetoacetase / Name=FAH	2.34E-06	6.04	6.04	17.38	17.38
P30084	Enoyl-CoA hydratase, mitochondrial / Name=ECHS1	2.90E-06	4.97	4.97	22.81	22.81
P27338	Amine oxidase [flavin-containing] B / Name=MAOB	3.06E-06	4.79	4.79	12.45	12.45
Q9H2A2	Aldehyde dehydrogenase family 8 member A1 / Name=ALDH8A1; Synonyms=ALDH12	3.20E-06	7.83	7.83	12.14	12.14
Q9UHD8*	**Septin-9 / Name=SEPT9; Synonyms=KIAA0991, MSF**	**3.32E-06**	**-5.38**	**5.38**	**-5.21**	**5.21**
P00367	Glutamate	3.36E-06	5.78	5.78	53.21	53.21

	dehydrogenase 1, mitochondrial / Name=GLUD1; Synonyms=GLUD					
O43175	D-3-phosphoglycerate dehydrogenase / Name=PHGDH; Synonyms=PGDH3	3.48E-06	4.35	4.35	8.43	8.43
O95831	Apoptosis-inducing factor 1, mitochondrial / Name=AIFM1; Synonyms=AIF, PDCD8	3.83E-06	4.5	4.5	13.74	13.74
P22760	Arylacetamide deacetylase / Name=AADAC; Synonyms=DAC	3.95E-06	7.56	7.56	8.29	8.29
P51659	Peroxisomal multifunctional enzyme type 2 / Name=HSD17B4; Synonyms=EDH17B4	4.43E-06	4.58	4.58	26.17	26.17
Q02338	D-beta-hydroxybutyrate dehydrogenase, mitochondrial / Name=BDH1; Synonyms=BDH	5.31E-06	7.19	7.19	16.71	16.71
P45954	Short/branched chain specific acyl-CoA dehydrogenase, mitochondrial / Name=ACADSB	5.84E-06	6.12	6.12	17.67	17.67
Q01995*	**Transgelin / Name=TAGLN; Synonyms=SM22, WS3-10**	**6.29E-06**	**-8.08**	**8.08**	**-13.71**	**13.71**
P21399	Cytoplasmic aconitate hydratase / Name=ACO1; Synonyms=IREB1	6.70E-06	4.62	4.62	12.4	12.4
O14756	17-beta-hydroxysteroid dehydrogenase type 6 / Name=HSD17B6; Synonyms=RODH	6.81E-06	6.89	6.89	14.43	14.43
P21397	Amine oxidase [flavin-containing] A / Name=MAOA	8.06E-06	6.69	6.69	7.43	7.43
P35914	Hydroxymethylglutaryl-CoA lyase, mitochondrial / Name=HMGCL	8.14E-06	4.03	4.03	6.79	6.79
Q16836	Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial / Name=HADH; Synonyms=HAD, HADHSC, SCHAD	8.65E-06	4.51	4.51	8.62	8.62

Q06520	Bile salt sulfotransferase / Name=SULT2A1; Synonyms=HST, STD	8.73E-06	6.6	6.6	15.86	15.86
Q9Y6C9	Mitochondrial carrier homolog 2 / Name=MTCH2; Synonyms=MIMP; ORFNames=HSPC032	8.80E-06	6.59	6.59	8	8
P30038	Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial / Name=ALDH4A1; Synonyms=ALDH4, P5CDH	9.19E-06	6.54	6.54	22.43	22.43
P06737	Glycogen phosphorylase, liver form / Name=PYGL	9.88E-06	6.46	6.46	23.29	23.29
P50995*	**Annexin A11 / Name=ANXA11; Synonyms=ANX11**	**1.11E-05**	**-9.87**	**9.87**	**-8.67**	**8.67**
Q07960*	**Rho GTPase-activating protein 1 / Name=ARHGAP1; Synonyms=CDC42GAP, RHOGAP1**	**1.15E-05**	**-9.79**	**9.79**	**-3.67**	**3.67**
Q68CK6	Acyl-coenzyme A synthetase ACSM2B, mitochondrial / Name=ACSM2B; Synonyms=ACSM2; ORFNames=HYST1046	1.17E-05	6.28	6.28	30.29	30.29
Q9Y2Q3	Glutathione S-transferase kappa 1 / Name=GSTK1; ORFNames=HDCMD47P	1.22E-05	3.82	3.82	6.93	6.93
O95954	Formimidoyltransferase-cyclodeaminase / Name=FTCD	1.27E-05	6.19	6.19	37.43	37.43
P17174	Aspartate aminotransferase, cytoplasmic / Name=GOT1	1.39E-05	4.69	4.69	19.57	19.57
P08670*	**Vimentin / Name=VIM**	**1.42E-05**	**-3.89**	**3.89**	**-33.31**	**33.31**
P21912	Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial / Name=SDHB; Synonyms=SDH, SDH1	1.44E-05	6.06	6.06	5.14	5.14

P51649	Succinate-semialdehyde dehydrogenase, mitochondrial / Name=ALDH5A1; Synonyms=SSADH	1.46E-05	4.81	4.81	9.95	9.95
Q9UJS0	Calcium-binding mitochondrial carrier protein Aralar2 / Name=SLC25A13; Synonyms=ARALAR2	1.52E-05	3.88	3.88	12.31	12.31
Q7Z4W1	L-xylulose reductase / Name=DCXR	1.60E-05	5.42	5.42	30.26	30.26
P10632	Cytochrome P450 2C8 / Name=CYP2C8	1.62E-05	5.94	5.94	13.57	13.57
P00480	Ornithine carbamoyltransferase, mitochondrial / Name=OTC	1.68E-05	5.9	5.9	15.71	15.71
P08758*	**Annexin A5 / Name=ANXA5; Synonyms=ANX5, ENX2, PP4**	**1.70E-05**	**-5.87**	**5.87**	**-18.48**	**18.48**
P30041	Peroxiredoxin-6 / Name=PRDX6; Synonyms=AOP2, KIAA0106	1.72E-05	4.32	4.32	11.26	11.26
P49189	4-trimethylaminobutyraldehyde dehydrogenase / Name=ALDH9A1; Synonyms=ALDH4, ALDH7, ALDH9	1.87E-05	3.76	3.76	6.1	6.1
P49419	Alpha-aminoadipic semialdehyde dehydrogenase / Name=ALDH7A1; Synonyms=ATQ1	1.89E-05	4.84	4.84	18.69	18.69
Q08AH3	Acyl-coenzyme A synthetase ACSM2A, mitochondrial / Name=ACSM2A; Synonyms=ACSM2, MACS2	1.99E-05	5.73	5.73	30.29	30.29
P32754	4-hydroxyphenylpyruvate dioxygenase / Name=HPD; Synonyms=PPD	1.99E-05	5.73	5.73	18.71	18.71
Q6IB77	Glycine N-acyltransferase / Name=GLYAT; Synonyms=ACGNAT, CAT, GAT	2.03E-05	5.71	5.71	13.57	13.57
Q13838*	**Spliceosome RNA helicase DDX39B / Name=DDX39B; Synonyms=BAT1, UAP56**	**2.36E-05**	**-3.75**	**3.75**	**-7.12**	**7.12**

P00439	Phenylalanine-4-hydroxylase / Name=PAH	2.40E-05	3.54	3.54	5.88	5.88
P28838	Cytosol aminopeptidase / Name=LAP3; Synonyms=LAPEP, PEPS	2.51E-05	3.63	3.63	13.05	13.05
P09211*	**Glutathione S-transferase P / Name=GSTP1; Synonyms=FAEES3, GST3**	**2.59E-05**	**-7.63**	**7.63**	**-39.45**	**39.45**
P50053	Ketohexokinase / Name=KHK	2.65E-05	5.45	5.45	5	5
O14979*	**Heterogeneous nuclear ribonucleoprotein D-like / Name=HNRPDL; Synonyms=JKTBP**	**2.78E-05**	**-8.18**	**8.18**	**-5.83**	**5.83**
P37802*	**Transgelin-2 / Name=TAGLN2; Synonyms=KIAA0120; ORFNames=CDABP0035**	**2.84E-05**	**-4.52**	**4.52**	**-7.26**	**7.26**
Q9UBQ7	Glyoxylate reductase/hydroxypyruvate reductase / Name=GRHPR; Synonyms=GLXR; ORFNames=MSTP035	2.99E-05	4.68	4.68	20.74	20.74
P09467	Fructose-1,6-bisphosphatase 1 / Name=FBP1; Synonyms=FBP	2.99E-05	4.33	4.33	20.38	20.38
P60660*	**Myosin light polypeptide 6 / Name=MYL6**	**3.13E-05**	**-3.8**	**3.8**	**-6.83**	**6.83**
P06396*	**Gelsolin / Name=GSN**	**3.33E-05**	**-5.01**	**5.01**	**-10.38**	**10.38**
P08729*	**Keratin, type II cytoskeletal 7 / Name=KRT7; Synonyms=SCL**	**3.41E-05**	**-7.85**	**7.85**	**-12.17**	**12.17**
P07954	Fumarate hydratase, mitochondrial / Name=FH	3.43E-05	3.46	3.46	10.88	10.88
O75452	Retinol dehydrogenase 16 / Name=RDH16; Synonyms=RODH4	3.53E-05	5.19	5.19	13.43	13.43
P08107*	**Heat shock 70 kDa protein 1A/1B / Name=HSPA1A; Synonyms=HSPA1**	**3.76E-05**	**-4.78**	**4.78**	**-22.98**	**22.98**
P80404	4-aminobutyrate	3.85E-05	5.02	5.02	38.81	38.81

	aminotransferase, mitochondrial / Name=ABAT; Synonyms=GABAT					
P00167	Cytochrome b5 / Name=CYB5A; Synonyms=CYB5	4.00E-05	3.42	3.42	9.81	9.81
P05181	Cytochrome P450 2E1 / Name=CYP2E1; Synonyms=CYP2E	4.19E-05	5.04	5.04	8	8
O00299*	**Chloride intracellular channel protein 1 / Name=CLIC1; Synonyms=G6, NCC27**	**4.23E-05**	**-4.64**	**4.64**	**-11.76**	**11.76**
Q9Y2S2	Lambda-crystallin homolog / Name=CRYL1; Synonyms=CRY	4.36E-05	5	5	6.43	6.43
P31943*	**Heterogeneous nuclear ribonucleoprotein H / Name=HNRNPH1; Synonyms=HNRPH, HNRPH1**	**4.37E-05**	**-3.33**	**3.33**	**-7.24**	**7.24**
P08684	Cytochrome P450 3A4 / Name=CYP3A4; Synonyms=CYP3A3	4.65E-05	4.95	4.95	12	12
Q05707*	**Collagen alpha-1(XIV) chain / Name=COL14A1; Synonyms=UND**	**4.98E-05**	**-7.27**	**7.27**	**-19.33**	**19.33**
P05089	Arginase-1 / Name=ARG1	5.04E-05	4.88	4.88	28.14	28.14
P05455*	**Lupus La protein / Name=SSB**	**5.30E-05**	**-3.69**	**3.69**	**-4.43**	**4.43**
P30086	Phosphatidylethanolamine-binding protein 1 / Name=PEBP1; Synonyms=PBP, PEBP	5.38E-05	3.67	3.67	17.29	17.29
Q14032	Bile acid-CoA:amino acid N-acyltransferase / Name=BAAT	6.14E-05	4.71	4.71	6.43	6.43
P68366*	**Tubulin alpha-4A chain / Name=TUBA4A; Synonyms=TUBA1**	**6.27E-05**	**-3.82**	**3.82**	**-40**	**40**
Q08426	Peroxisomal bifunctional enzyme / Name=EHHADH; Synonyms=ECHD	6.30E-05	4.69	4.69	41.29	41.29
Q8NBX0	Probable saccharopine dehydrogenase / Name=SCCPDH; ORFNames=CGI-49	6.32E-05	4.69	4.69	5.86	5.86

Q03154	Aminoacylase-1 / Name=ACY1	6.39E-05	4.68	4.68	16.71	16.71
Q08211*	**ATP-dependent RNA helicase A / Name=DHX9; Synonyms=DDX9, LKP, NDH2**	**6.61E-05**	**-5.12**	**5.12**	**-10.1**	**10.1**
O43390*	**Heterogeneous nuclear ribonucleoprotein R / Name=HNRNPR; Synonyms=HNRPR**	**6.75E-05**	**-3.34**	**3.34**	**-6.38**	**6.38**
P19105*	**Myosin regulatory light chain 12A / Name=MYL12A; Synonyms=MLCB, MRLC3, RLC**	**7.33E-05**	**-3.86**	**3.86**	**-5.64**	**5.64**
O14950*	**Myosin regulatory light chain 12B / Name=MYL12B; Synonyms=MRLC2, MYLC2B**	**7.33E-05**	**-3.86**	**3.86**	**-5.64**	**5.64**
Q99623	Prohibitin-2 / Name=PHB2; Synonyms=BAP, REA	7.56E-05	3.18	3.18	5.14	5.14
P26440	Isovaleryl-CoA dehydrogenase, mitochondrial / Name=IVD	7.76E-05	3.12	3.12	4.83	4.83
P61978*	**Heterogeneous nuclear ribonucleoprotein K / Name=HNRNPK; Synonyms=HNRPK**	**8.02E-05**	**-4.28**	**4.28**	**-12.88**	**12.88**
P67936*	**Tropomyosin alpha-4 chain / Name=TPM4**	**8.10E-05**	**-4.86**	**4.86**	**-7.21**	**7.21**
P21810*	**Biglycan / Name=BGN; Synonyms=SLRR1A**	**8.14E-05**	**-6.13**	**6.13**	**-39.6**	**39.6**
P04424	Argininosuccinate lyase / Name=ASL	8.16E-05	3.42	3.42	12.43	12.43
P24752	Acetyl-CoA acetyltransferase, mitochondrial / Name=ACAT1; Synonyms=ACAT, MAT	8.38E-05	4.3	4.3	34.83	34.83
O00748	Cocaine esterase / Name=CES2; Synonyms=ICE	8.46E-05	3.33	3.33	7.36	7.36
Q9Y2P5	Bile acyl-CoA synthetase / Name=SLC27A5; Synonyms=ACSB, ACSVL6, FACVL3, FATP5	8.48E-05	4.45	4.45	20.14	20.14

P31040	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial / Name=SDHA; Synonyms=SDH2, SDHF	8.68E-05	3.1	3.1	8.88	8.88
P11586	C-1-tetrahydrofolate synthase, cytoplasmic / Name=MTHFD1; Synonyms=MTHFC, MTHFD	8.73E-05	4.43	4.43	26	26
P36871	Phosphoglucomutase-1 / Name=PGM1	8.74E-05	3.43	3.43	26.21	26.21
Q9H8H3	Methyltransferase-like protein 7A / Name=METTL7A; ORFNames=PRO0066, UNQ1902/PRO4348	8.77E-05	4.42	4.42	5.14	5.14
Q9NVS9	Pyridoxine-5'-phosphate oxidase / Name=PNPO	9.05E-05	3.66	3.66	3.69	3.69
P21695	Glycerol-3-phosphate dehydrogenase [NAD+], cytoplasmic / Name=GPD1	9.12E-05	4.39	4.39	8.71	8.71
Q9UI17	Dimethylglycine dehydrogenase, mitochondrial / Name=DMGDH	9.49E-05	4.36	4.36	12.29	12.29
Q9UL12	Sarcosine dehydrogenase, mitochondrial / Name=SARDH; Synonyms=DMGDHL1	1.06E-04	4.28	4.28	17.29	17.29
P34913	Epoxide hydrolase 2 / Name=EPHX2	1.07E-04	4.27	4.27	13	13
O00571*	**ATP-dependent RNA helicase DDX3X / Name=DDX3X; Synonyms=DBX, DDX3**	**1.11E-04**	**-3.66**	**3.66**	**-4.93**	**4.93**
Q9UIJ7	GTP:AMP phosphotransferase, mitochondrial / Name=AK3; Synonyms=AK3L1, AK6, AKL3L	1.17E-04	3.16	3.16	5.45	5.45
P40926	Malate dehydrogenase, mitochondrial / Name=MDH2	1.21E-04	2.97	2.97	7.29	7.29
P13010*	**X-ray repair cross-complementing protein 5 / Name=XRCC5;**	**1.25E-04**	**-4.51**	**4.51**	**-8.6**	**8.6**

	Synonyms=G22P2					
P09525*	**Annexin A4 / Name=ANXA4; Synonyms=ANX4**	**1.30E-04**	**-5.9**	**5.9**	**-68.21**	**68.21**
P08727*	**Keratin, type I cytoskeletal 19 / Name=KRT19**	**1.31E-04**	**-5.96**	**5.96**	**-33**	**33**
Q86WU2	Probable D-lactate dehydrogenase, mitochondrial / Name=LDHD	1.32E-04	4.12	4.12	2.57	2.57
Q01105*	**Protein SET / Name=SET**	**1.33E-04**	**-2.98**	**2.98**	**-3.95**	**3.95**
Q99714	3-hydroxyacyl-CoA dehydrogenase type-2 / Name=HSD17B10; Synonyms=ERAB, HADH2, MRPP2, SCHAD, XH98G2	1.33E-04	3.03	3.03	9.55	9.55
Q9NQR4	Omega-amidase NIT2 / Name=NIT2; ORFNames=CUA002	1.34E-04	3.01	3.01	6.31	6.31
Q9NR45*	**Sialic acid synthase / Name=NANS; Synonyms=SAS**	**1.38E-04**	**-3.09**	**3.09**	**-3.43**	**3.43**
O75521	Enoyl-CoA delta isomerase 2, mitochondrial / Name=ECI2; Synonyms=DRS1, HCA88, PECI	1.41E-04	4.07	4.07	7.43	7.43
Q00839*	**Heterogeneous nuclear ribonucleoprotein U / Name=HNRNPU; Synonyms=HNRPU, SAFA, U21.1**	**1.43E-04**	**-4.08**	**4.08**	**-11.9**	**11.9**
P12111*	**Collagen alpha-3(VI) chain / Name=COL6A3**	**1.55E-04**	**-3.89**	**3.89**	**-57.57**	**57.57**
Q13263*	**Transcription intermediary factor 1-beta / Name=TRIM28; Synonyms=KAP1, RNF96, TIF1B**	**1.58E-04**	**-5.72**	**5.72**	**-5.67**	**5.67**
P21549	Serine--pyruvate aminotransferase / Name=AGXT; Synonyms=AGT1, SPAT	1.64E-04	3.96	3.96	68.43	68.43
O60506*	**Heterogeneous nuclear ribonucleoprotein Q / Name=SYNCRIP; Synonyms=HNRPQ,**	**1.70E-04**	**-2.89**	**2.89**	**-5.83**	**5.83**

	NSAP1					
P24298	Alanine aminotransferase 1 / Name=GPT; Synonyms=AAT1, GPT1	1.70E-04	3.93	3.93	13	13
P46952	3-hydroxyanthranilate 3,4-dioxygenase / Name=HAAO	1.71E-04	3.93	3.93	8.14	8.14
P43243*	**Matrin-3 / Name=MATR3; Synonyms=KIAA0723**	**1.80E-04**	**-2.85**	**2.85**	**-4.69**	**4.69**
O95994*	**Anterior gradient protein 2 homolog / Name=AGR2; Synonyms=AG2; ORFNames=UNQ515/PRO1030**	**1.83E-04**	**-5.55**	**5.55**	**-12.83**	**12.83**
P25325	3-mercaptopyruvate sulfurtransferase / Name=MPST; Synonyms=TST2	1.89E-04	3.74	3.74	12.05	12.05
P40121*	**Macrophage-capping protein / Name=CAPG; Synonyms=AFCP, MCP**	**1.91E-04**	**-5.5**	**5.5**	**-5.5**	**5.5**
P15311*	**Ezrin / Name=EZR; Synonyms=VIL2**	**1.93E-04**	**-5.49**	**5.49**	**-13.5**	**13.5**
P08133	Annexin A6 / Name=ANXA6; Synonyms=ANX6	1.94E-04	2.96	2.96	15.69	15.69
Q6YN16	Hydroxysteroid dehydrogenase-like protein 2 / Name=HSDL2; Synonyms=C9orf99	2.02E-04	2.8	2.8	4.43	4.43
P62258*	**14-3-3 protein epsilon / Name=YWHAE**	**2.02E-04**	**-2.96**	**2.96**	**-9.52**	**9.52**
Q16698	2,4-dienoyl-CoA reductase, mitochondrial / Name=DECR1; Synonyms=DECR	2.15E-04	3.08	3.08	13.31	13.31
P05062	Fructose-bisphosphate aldolase B / Name=ALDOB; Synonyms=ALDB	2.19E-04	3.73	3.73	71.67	71.67
Q04917*	**14-3-3 protein eta / Name=YWHAH; Synonyms=YWHA1**	**2.20E-04**	**-3.17**	**3.17**	**-10.83**	**10.83**
P53007	Tricarboxylate transport protein, mitochondrial / Name=SLC25A1;	2.24E-04	3.35	3.35	4.57	4.57

	Synonyms=SLC20A3					
P30613	Pyruvate kinase isozymes R/L / Name=PKLR; Synonyms=PK1, PKL	2.25E-04	3.74	3.74	14.43	14.43
Q16555*	**Dihydropyrimidinase -related protein 2 / Name=DPYSL2; Synonyms=CRMP2, ULIP2**	**2.26E-04**	**-4.73**	**4.73**	**-10.88**	**10.88**
P11712	Cytochrome P450 2C9 / Name=CYP2C9; Synonyms=CYP2C10	2.29E-04	3.73	3.73	17	17
Q00266	S-adenosylmethionine synthase isoform type-1 / Name=MAT1A; Synonyms=AMS1, MATA1	2.33E-04	3.72	3.72	10.14	10.14
Q9BPW8	Protein NipSnap homolog 1 / Name=NIPSNAP1	2.38E-04	3.7	3.7	7.86	7.86
P31930	Cytochrome b-c1 complex subunit 1, mitochondrial / Name=UQCRC1	2.38E-04	2.73	2.73	4.52	4.52
Q14117	Dihydropyrimidinase / Name=DPYS	2.41E-04	3.69	3.69	6.71	6.71
O75356	Ectonucleoside triphosphate diphosphohydrolase 5 / Name=ENTPD5; Synonyms=CD39L4, PCPH	2.43E-04	3.69	3.69	4.43	4.43
P35520	Cystathionine beta-synthase / Name=CBS	2.43E-04	3.69	3.69	4.43	4.43
P30039	Phenazine biosynthesis-like domain-containing protein / Name=PBLD; Synonyms=MAWBP	2.60E-04	3.64	3.64	9.43	9.43
Q93088	Betaine--homocysteine S-methyltransferase 1 / Name=BHMT	2.62E-04	3.64	3.64	29.86	29.86
Q3LXA3	Bifunctional ATP-dependent dihydroxyacetone kinase/FAD-AMP lyase (cyclizing) / Name=DAK	2.66E-04	3.47	3.47	31.83	31.83
Q9HDC9	Adipocyte plasma membrane-associated protein / Name=APMAP; Synonyms=C20orf3;	2.90E-04	2.65	2.65	4.26	4.26

	ORFNames=UNQ1869/PRO4305					
P78417	Glutathione S-transferase omega-1 / Name=GSTO1; Synonyms=GSTTLP28	3.10E-04	2.8	2.8	8.17	8.17
O75367*	**Core histone macro-H2A.1 / Name=H2AFY; Synonyms=MACROH2A1**	**3.15E-04**	**-4.24**	**4.24**	**-11.52**	**11.52**
P26599*	**Polypyrimidine tract-binding protein 1 / Name=PTBP1; Synonyms=PTB**	**3.31E-04**	**-3.17**	**3.17**	**-10.24**	**10.24**
P16662	UDP-glucuronosyltransferase 2B7 / Name=UGT2B7; Synonyms=UGTB2B9	3.34E-04	3.21	3.21	13.93	13.93
P56470*	**Galectin-4 / Name=LGALS4**	**3.40E-04**	**-2.63**	**2.63**	**-18.6**	**18.6**
Q9P0Z9	Peroxisomal sarcosine oxidase / Name=PIPOX; Synonyms=LPIPOX, PSO	3.41E-04	3.47	3.47	12.29	12.29
P00966	Argininosuccinate synthase / Name=ASS1; Synonyms=ASS	3.44E-04	2.93	2.93	15.98	15.98
P68371*	**Tubulin beta-2C chain / Name=TUBB2C**	**3.46E-04**	**-2.61**	**2.61**	**-42.24**	**42.24**
P16219	Short-chain specific acyl-CoA dehydrogenase, mitochondrial / Name=ACADS	3.46E-04	3.16	3.16	13.83	13.83
P33121	Long-chain-fatty-acid--CoA ligase 1 / Name=ACSL1; Synonyms=FACL1, FACL2, LACS, LACS1, LACS2	3.46E-04	3.46	3.46	22.29	22.29
P09110	3-ketoacyl-CoA thiolase, peroxisomal / Name=ACAA1; Synonyms=ACAA, PTHIO	3.48E-04	3.4	3.4	33.38	33.38
Q02928	Cytochrome P450 4A11 / Name=CYP4A11; Synonyms=CYP4A2	3.52E-04	3.45	3.45	7.14	7.14
O75891	Aldehyde dehydrogenase family 1 member L1 / Name=ALDH1L1;	3.59E-04	3.43	3.43	32	32

	Synonyms=FTHFD					
P31327	Carbamoyl-phosphate synthase [ammonia], mitochondrial / Name=CPS1	3.68E-04	3.4	3.4	228.5	228.5
P11509	Cytochrome P450 2A6 / Name=CYP2A6; Synonyms=CYP2A3	3.73E-04	3.41	3.41	22	22
P34897	Serine hydroxymethyltransferase, mitochondrial / Name=SHMT2	3.80E-04	2.84	2.84	9.95	9.95
Q9H9B4	Sideroflexin-1 / Name=SFXN1	3.86E-04	3.39	3.39	7.43	7.43
Q9Y617	Phosphoserine aminotransferase / Name=PSAT1; Synonyms=PSA	3.86E-04	3.39	3.39	5.57	5.57
Q9UBX3	Mitochondrial dicarboxylate carrier / Name=SLC25A10; Synonyms=DIC	3.86E-04	3.39	3.39	3.71	3.71
P00441	Superoxide dismutase [Cu-Zn] / Name=SOD1	4.11E-04	2.97	2.97	10.07	10.07
Q16775	Hydroxyacylglutathione hydrolase, mitochondrial / Name=HAGH; Synonyms=GLO2, HAGH1	4.35E-04	3.32	3.32	4.14	4.14
Q9Y3I0*	**tRNA-splicing ligase RtcB homolog / Name=C22orf28; ORFNames=HSPC117**	**4.35E-04**	**-4.63**	**4.63**	**-3**	**3**
Q15067	Peroxisomal acyl-coenzyme A oxidase 1 / Name=ACOX1; Synonyms=ACOX	4.40E-04	3.31	3.31	13.29	13.29
O00264	Membrane-associated progesterone receptor component 1 / Name=PGRMC1; Synonyms=HPR6.6, PGRMC	4.40E-04	2.52	2.52	7.57	7.57
P04083*	**Annexin A1 / Name=ANXA1; Synonyms=ANX1, LPC1**	**4.62E-04**	**-3.05**	**3.05**	**-9.62**	**9.62**
P08319	Alcohol dehydrogenase 4 / Name=ADH4	4.68E-04	3.27	3.27	62	62
P22314*	**Ubiquitin-like modifier-activating enzyme 1 /**	**4.70E-04**	**-2.74**	**2.74**	**-10.45**	**10.45**

	Name=UBA1; Synonyms=A1S9T, UBE1					
P07195*	**L-lactate dehydrogenase B chain / Name=LDHB**	**4.77E-04**	**-2.58**	**2.58**	**-7.24**	**7.24**
P43155	Carnitine O-acetyltransferase / Name=CRAT; Synonyms=CAT1	4.78E-04	3.26	3.26	3.14	3.14
P12956*	**X-ray repair cross-complementing protein 6 / Name=XRCC6; Synonyms=G22P1**	**4.80E-04**	**-3.94**	**3.94**	**-10.98**	**10.98**
Q16134	Electron transfer flavoprotein-ubiquinone oxidoreductase, mitochondrial / Name=ETFDH	4.85E-04	3.25	3.25	7.43	7.43
Q96PK6*	**RNA-binding protein 14 / Name=RBM14; Synonyms=SIP**	**4.93E-04**	**-4.5**	**4.5**	**-2.67**	**2.67**
P30046	D-dopachrome decarboxylase / Name=DDT	4.99E-04	2.54	2.54	6.67	6.67
P09417	Dihydropteridine reductase / Name=QDPR; Synonyms=DHPR	5.12E-04	3.22	3.22	9.14	9.14
P55786*	**Puromycin-sensitive aminopeptidase / Name=NPEPPS; Synonyms=PSA**	**5.70E-04**	**-3.16**	**3.16**	**-4.93**	**4.93**
P07384*	**Calpain-1 catalytic subunit / Name=CAPN1; Synonyms=CANPL1; ORFNames=PIG30**	**5.70E-04**	**-4.07**	**4.07**	**-14.43**	**14.43**
P04040	Catalase / Name=CAT	5.88E-04	3.06	3.06	50.98	50.98
P60842*	**Eukaryotic initiation factor 4A-I / Name=EIF4A1; Synonyms=DDX2A, EIF4A**	**6.15E-04**	**-2.67**	**2.67**	**-7.1**	**7.1**
P11498	Pyruvate carboxylase, mitochondrial / Name=PC	6.17E-04	3.11	3.11	31.71	31.71
P23528*	**Cofilin-1 / Name=CFL1; Synonyms=CFL**	**6.28E-04**	**-2.4**	**2.4**	**-4.81**	**4.81**
P00558*	**Phosphoglycerate kinase 1 / Name=PGK1; Synonyms=PGKA; ORFNames=MIG10,**	**6.29E-04**	**-2.61**	**2.61**	**-13.74**	**13.74**

	OK/SW-cl.110					
P07327	Alcohol dehydrogenase 1A / Name=ADH1A; Synonyms=ADH1	6.32E-04	2.98	2.98	52.05	52.05
Q9BTZ2	Dehydrogenase/reductase SDR family member 4 / Name=DHRS4; ORFNames=UNQ851/PRO1800	6.39E-04	3.09	3.09	3.86	3.86
P04632*	**Calpain small subunit 1 / Name=CAPNS1; Synonyms=CAPN4, CAPNS**	**6.42E-04**	**-3.26**	**3.26**	**-7.29**	**7.29**
P78329	Leukotriene-B(4) omega-hydroxylase 1 / Name=CYP4F2	6.50E-04	3.08	3.08	4.43	4.43
P06748*	**Nucleophosmin / Name=NPM1; Synonyms=NPM**	**6.64E-04**	**-2.89**	**2.89**	**-5.83**	**5.83**
Q13151*	**Heterogeneous nuclear ribonucleoprotein A0 / Name=HNRNPA0; Synonyms=HNRPA0**	**7.14E-04**	**-4.16**	**4.16**	**-4.83**	**4.83**
Q7Z5P4	17-beta-hydroxysteroid dehydrogenase 13 / Name=HSD17B13; Synonyms=SCDR9; ORFNames=HMFN0376, UNQ497/PRO1014	7.45E-04	3	3	8.57	8.57
O95479	GDH/6PGL endoplasmic bifunctional protein / Name=H6PD; Synonyms=GDH	7.49E-04	2.68	2.68	5.95	5.95
P50991*	**T-complex protein 1 subunit delta / Name=CCT4; Synonyms=CCTD, SRB**	**7.55E-04**	**-3.16**	**3.16**	**-4.21**	**4.21**
Q9UBR2	Cathepsin Z / Name=CTSZ	7.56E-04	2.42	2.42	3.36	3.36
Q15019*	**Septin-2 / Name=SEPT2; Synonyms=DIFF6, KIAA0158, NEDD5**	**7.71E-04**	**-4.09**	**4.09**	**-4.5**	**4.5**
P24539	ATP synthase subunit b, mitochondrial / Name=ATP5F1	7.76E-04	2.37	2.37	2.95	2.95
Q96I99	Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial / Name=SUCLG2	8.21E-04	2.56	2.56	6.14	6.14
P48735	Isocitrate	8.39E-04	2.49	2.49	16.29	16.29

	dehydrogenase [NADP], mitochondrial / Name=IDH2					
P54868	Hydroxymethylglutaryl-CoA synthase, mitochondrial / Name=HMGCS2	8.44E-04	2.92	2.92	59.1	59.1
P20774*	**Mimecan / Name=OGN; Synonyms=OIF, SLRR3A**	**8.69E-04**	**-3.99**	**3.99**	**-20.33**	**20.33**
P54578*	**Ubiquitin carboxyl-terminal hydrolase 14 / Name=USP14; Synonyms=TGT**	**8.82E-04**	**-3.97**	**3.97**	**-2.83**	**2.83**
P51888*	**Prolargin / Name=PRELP; Synonyms=SLRR2A**	**9.02E-04**	**-3.64**	**3.64**	**-30.1**	**30.1**
P09960*	**Leukotriene A-4 hydrolase / Name=LTA4H; Synonyms=LTA4**	**9.14E-04**	**-2.52**	**2.52**	**-4**	**4**
P52758	Ribonuclease UK114 / Name=HRSP12; Synonyms=PSP	9.24E-04	2.64	2.64	6.52	6.52
P27348*	**14-3-3 protein theta / Name=YWHAQ**	**9.53E-04**	**-2.97**	**2.97**	**-7.31**	**7.31**
Q969I3	Glycine N-acyltransferase-like protein 1 / Name=GLYATL1; Synonyms=GNAT	9.65E-04	2.86	2.86	1.71	1.71
Q9UBR1	Beta-ureidopropionase / Name=UPB1; Synonyms=BUP1	9.87E-04	2.84	2.84	11.43	11.43
Q93099	Homogentisate 1,2-dioxygenase / Name=HGD; Synonyms=HGO	1.01E-03	2.83	2.83	9	9
O43772	Mitochondrial carnitine/acylcarnitine carrier protein / Name=SLC25A20; Synonyms=CAC, CACT	1.03E-03	2.82	2.82	6.57	6.57
PART B:						
Q99424	Peroxisomal acyl-coenzyme A oxidase 2 / Name=ACOX2	1.05E-03	2.81	2.81	17.43	17.43
P19338	Nucleolin / Name=NCL	1.05E-03	-2.73	2.73	-6.88	6.88
P07585	Decorin / Name=DCN; Synonyms=SLRR1B	1.06E-03	-3.82	3.82	-9.17	9.17

P09651	Heterogeneous nuclear ribonucleoprotein A1 / Name=HNRNPA1; Synonyms=HNRPA1	1.08E-03	-3.49	3.49	-13.93	13.93
P55072	Transitional endoplasmic reticulum ATPase / Name=VCP	1.08E-03	-2.46	2.46	-13.43	13.43
P12429	Annexin A3 / Name=ANXA3; Synonyms=ANX3	1.09E-03	-3.8	3.8	-3.33	3.33
O43143	Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15 / Name=DHX15; Synonyms=DBP1, DDX15	1.09E-03	-3.8	3.8	-3.33	3.33
P31513	Dimethylaniline monooxygenase [N-oxide-forming] 3 / Name=FMO3	1.11E-03	2.78	2.78	17	17
P04075	Fructose-bisphosphate aldolase A / Name=ALDOA; Synonyms=ALDA	1.11E-03	-3.19	3.19	-18.79	18.79
P42765	3-ketoacyl-CoA thiolase, mitochondrial / Name=ACAA2	1.12E-03	2.71	2.71	44.1	44.1
P09327	Villin-1 / Name=VIL1; Synonyms=VIL	1.12E-03	-3.77	3.77	-7.67	7.67
Q15185	Prostaglandin E synthase 3 / Name=PTGES3; Synonyms=P23, TEBP	1.14E-03	-2.48	2.48	-2.38	2.38
P13716	Delta-aminolevulinic acid dehydratase / Name=ALAD	1.16E-03	2.76	2.76	10.14	10.14
Q13765	Nascent polypeptide-associated complex subunit alpha / Name=NACA; ORFNames=HSD48	1.21E-03	-2.32	2.32	-2.57	2.57
Q96AB3	Isochorismatase domain-containing protein 2, mitochondrial / Name=ISOC2	1.22E-03	2.44	2.44	5.07	5.07
P07437	Tubulin beta chain / Name=TUBB; Synonyms=TUBB5; ORFNames=OK/SW-cl .56	1.23E-03	-2.88	2.88	-28.74	28.74
Q92506	Estradiol 17-beta-dehydrogenase 8 / Name=HSD17B8; Synonyms=FABGL,	1.28E-03	2.7	2.7	3.14	3.14

	HKE6, RING2					
P13804	Electron transfer flavoprotein subunit alpha, mitochondrial / Name=ETFA	1.35E-03	2.29	2.29	12.43	12.43
P08238	Heat shock protein HSP 90-beta / Name=HSP90AB1; Synonyms=HSP90B, HSPC2, HSPCB	1.36E-03	-2.17	2.17	-12.52	12.52
P27144	Adenylate kinase isoenzyme 4, mitochondrial / Name=AK4; Synonyms=AK3, AK3L1	1.37E-03	2.67	2.67	6	6
P42330	Aldo-keto reductase family 1 member C3 / Name=AKR1C3; Synonyms=DDH1, HSD17B5, KIAA0119, PGFS	1.38E-03	-2.35	2.35	-16.24	16.24
Q86YB7	Enoyl-CoA hydratase domain-containing protein 2, mitochondrial / Name=ECHDC2	1.39E-03	2.66	2.66	5.57	5.57
Q00610	Clathrin heavy chain 1 / Name=CLTC; Synonyms=CLH17, CLTCL2, KIAA0034	1.40E-03	-2.4	2.4	-7.4	7.4
P62807	Histone H2B type 1-C/E/F/G/I / Name=HIST1H2BC; Synonyms=H2BFL	1.43E-03	-3.01	3.01	-28.57	28.57
P58876	Histone H2B type 1-D / Name=HIST1H2BD; Synonyms=H2BFB, HIRIP2	1.43E-03	-3.01	3.01	-28.57	28.57
Q93079	Histone H2B type 1-H / Name=HIST1H2BH; Synonyms=H2BFJ	1.43E-03	-3.01	3.01	-28.57	28.57
O60814	Histone H2B type 1-K / Name=HIST1H2BK; Synonyms=H2BFT, HIRIP1	1.43E-03	-3.01	3.01	-28.57	28.57
Q99880	Histone H2B type 1-L / Name=HIST1H2BL; Synonyms=H2BFC	1.43E-03	-3.01	3.01	-28.57	28.57
Q99879	Histone H2B type 1-M / Name=HIST1H2BM; Synonyms=H2BFE	1.43E-03	-3.01	3.01	-28.57	28.57
Q99877	Histone H2B type 1-N / Name=HIST1H2BN; Synonyms=H2BFD	1.43E-03	-3.01	3.01	-28.57	28.57
Q5QNW6	Histone H2B type 2-F /	1.43E-03	-3.01	3.01	-28.57	28.57

	Name=HIST2H2BF					
P57053	Histone H2B type F-S / Name=H2BFS	1.43E-03	-3.01	3.01	-28.57	28.57
P68032	Actin, alpha cardiac muscle 1 / Name=ACTC1; Synonyms=ACTC	1.46E-03	-2.43	2.43	-35.74	35.74
P35573	Glycogen debranching enzyme / Name=AGL; Synonyms=GDE	1.50E-03	2.62	2.62	15.14	15.14
Q96HR9	Receptor expression-enhancing protein 6 / Name=REEP6; Synonyms=C19orf32, DP1L1	1.57E-03	2.6	2.6	3.71	3.71
P62753	40S ribosomal protein S6 / Name=RPS6; ORFNames=OK/SW-cl .2	1.58E-03	-2.15	2.15	-2.81	2.81
P00325	Alcohol dehydrogenase 1B / Name=ADH1B; Synonyms=ADH2	1.60E-03	2.45	2.45	53.24	53.24
Q08257	Quinone oxidoreductase / Name=CRYZ	1.63E-03	2.1	2.1	6.21	6.21
Q00796	Sorbitol dehydrogenase / Name=SORD	1.66E-03	2.48	2.48	16.05	16.05
P14618	Pyruvate kinase isozymes M1/M2 / Name=PKM2; Synonyms=OIP3, PK2, PK3, PKM	1.66E-03	-3.37	3.37	-27.81	27.81
Q9BY49	Peroxisomal trans-2-enoyl-CoA reductase / Name=PECR; ORFNames=PRO1004	1.66E-03	2.57	2.57	5	5
P16152	Carbonyl reductase [NADPH] 1 / Name=CBR1; Synonyms=CBR, CRN	1.70E-03	3.2	3.2	8.24	8.24
Q15274	Nicotinate-nucleotide pyrophosphorylase [carboxylating] / Name=QPRT	1.77E-03	2.54	2.54	6.57	6.57
Q13011	Delta(3,5)-Delta(2,4)-di enoyl-CoA isomerase, mitochondrial / Name=ECH1	1.79E-03	2.08	2.08	8.33	8.33
P55083	Microfibril-associated glycoprotein 4 / Name=MFAP4	1.82E-03	-3.39	3.39	-9.67	9.67
Q96DG6	Carboxymethylenebut	1.86E-03	2.51	2.51	4.71	4.71

	enolidase homolog / Name=CMBL					
Q14749	Glycine N-methyltransferase / Name=GNMT	1.88E-03	2.51	2.51	7	7
P29401	Transketolase / Name=TKT	1.91E-03	-2.66	2.66	-13.76	13.76
Q1KMD3	Heterogeneous nuclear ribonucleoprotein U-like protein 2 / Name=HNRNPUL2; Synonyms=HNRPUL2	1.92E-03	-3.35	3.35	-5.83	5.83
P11216	Glycogen phosphorylase, brain form / Name=PYGB	1.92E-03	-3.35	3.35	-9.67	9.67
P35237	Serpin B6 / Name=SERPINB6; Synonyms=PI6, PTI	1.95E-03	-3.34	3.34	-4.17	4.17
P13929	Beta-enolase / Name=ENO3	1.96E-03	2.49	2.49	10.57	10.57
P52272	Heterogeneous nuclear ribonucleoprotein M / Name=HNRNPM; Synonyms=HNRPM, NAGR1	2.06E-03	-2.48	2.48	-12.19	12.19
Q96CX2	BTB/POZ domain-containing protein KCTD12 / Name=KCTD12; Synonyms=C13orf2, KIAA1778, PFET1	2.06E-03	-3.3	3.3	-4	4
P02649	Apolipoprotein E / Name=APOE	2.07E-03	2.13	2.13	7.6	7.6
P45974	Ubiquitin carboxyl-terminal hydrolase 5 / Name=USP5; Synonyms=ISOT	2.13E-03	-3.27	3.27	-3	3
P63104	14-3-3 protein zeta/delta / Name=YWHAZ	2.26E-03	-2.92	2.92	-13.14	13.14
P55084	Trifunctional enzyme subunit beta, mitochondrial / Name=HADHB; ORFNames=MSTP029	2.33E-03	2.11	2.11	15.31	15.31
P07900	Heat shock protein HSP 90-alpha / Name=HSP90AA1; Synonyms=HSP90A, HSPC1, HSPCA	2.33E-03	-2.22	2.22	-18.76	18.76
P30042	ES1 protein homolog, mitochondrial / Name=C21orf33;	2.33E-03	2.4	2.4	2.43	2.43

	Synonyms=HES1, KNPI					
P08311	Cathepsin G / Name=CTSG	2.38E-03	-2.23	2.23	-4.62	4.62
Q15149	Plectin / Name=PLEC; Synonyms=PLEC1	2.45E-03	-3.12	3.12	-16.21	16.21
P07858	Cathepsin B / Name=CTSB; Synonyms=CPSB	2.46E-03	2.13	2.13	8.14	8.14
P54819	Adenylate kinase 2, mitochondrial / Name=AK2; Synonyms=ADK2	2.57E-03	2.03	2.03	5.81	5.81
Q14651	Plastin-1 / Name=PLS1	2.58E-03	-3.13	3.13	-8	8
P01860	Ig gamma-3 chain C region / Name=IGHG3	2.61E-03	-2.28	2.28	-18.93	18.93
P50454	Serpin H1 / Name=SERPINH1; Synonyms=CBP1, CBP2, HSP47, SERPINH2; ORFNames=PIG14	2.62E-03	-3.12	3.12	-6.67	6.67
Q12905	Interleukin enhancer-binding factor 2 / Name=ILF2; Synonyms=NF45; ORFNames=PRO3063	2.69E-03	-2.59	2.59	-6.21	6.21
Q14974	Importin subunit beta-1 / Name=KPNB1; Synonyms=NTF97	2.78E-03	-2.16	2.16	-3.45	3.45
Q9ULC5	Long-chain-fatty-acid--CoA ligase 5 / Name=ACSL5; Synonyms=ACS5, FACL5; ORFNames=UNQ633/PRO1250	2.81E-03	2.32	2.32	4.71	4.71
P05177	Cytochrome P450 1A2 / Name=CYP1A2	2.81E-03	2.32	2.32	7.57	7.57
P00505	Aspartate aminotransferase, mitochondrial / Name=GOT2	2.88E-03	2.23	2.23	14.43	14.43
P25705	ATP synthase subunit alpha, mitochondrial / Name=ATP5A1; Synonyms=ATP5A, ATP5AL2, ATPM	2.90E-03	2	2	13.52	13.52
Q86XE5	Probable 4-hydroxy-2-oxoglutarate aldolase, mitochondrial / Name=HOGA1; Synonyms=C10orf65, DHDPSL	2.93E-03	2.3	2.3	2.29	2.29

Q15717	ELAV-like protein 1 / Name=ELAVL1; Synonyms=HUR	2.95E-03	-1.95	1.95	-3.26	3.26
O60218	Aldo-keto reductase family 1 member B10 / Name=AKR1B10; Synonyms=AKR1B11	2.98E-03	-2.93	2.93	-20.98	20.98
P31937	3-hydroxyisobutyrate dehydrogenase, mitochondrial / Name=HIBADH	2.99E-03	1.96	1.96	6.02	6.02
Q15493	Regucalcin / Name=RGN; Synonyms=SMP30	3.00E-03	2.28	2.28	5.43	5.43
Q06278	Aldehyde oxidase / Name=AOX1; Synonyms=AO	3.06E-03	2.27	2.27	27	27
P31150	Rab GDP dissociation inhibitor alpha / Name=GDI1; Synonyms=GDIL, OPHN2, RABGDIA, XAP4	3.07E-03	-3.01	3.01	-9.33	9.33
P18206	Vinculin / Name=VCL	3.11E-03	-2.28	2.28	-7	7
P12277	Creatine kinase B-type / Name=CKB; Synonyms=CKBB	3.11E-03	-3	3	-6	6
P11310	Medium-chain specific acyl-CoA dehydrogenase, mitochondrial / Name=ACADM	3.19E-03	2.1	2.1	10.33	10.33
P84243	Histone H3.3 / Name=H3F3A; Synonyms=H3.3A, H3F3; ORFNames=PP781	3.20E-03	-1.93	1.93	-4.26	4.26
P18283	Glutathione peroxidase 2 / Name=GPX2	3.21E-03	-2.98	2.98	-4.67	4.67
Q02318	Sterol 26-hydroxylase, mitochondrial / Name=CYP27A1; Synonyms=CYP27	3.22E-03	2.25	2.25	4	4
P40925	Malate dehydrogenase, cytoplasmic / Name=MDH1; Synonyms=MDHA	3.25E-03	1.9	1.9	3.33	3.33
P05787	Keratin, type II cytoskeletal 8 / Name=KRT8; Synonyms=CYK8	3.35E-03	-1.93	1.93	-23.17	23.17
Q9UJM8	Hydroxyacid oxidase 1 / Name=HAO1; Synonyms=GOX1, HAOX1	3.39E-03	2.23	2.23	21.71	21.71

P17655	Calpain-2 catalytic subunit / Name=CAPN2; Synonyms=CANPL2	3.47E-03	-2.93	2.93	-8.67	8.67
P98160	Basement membrane-specific heparan sulfate proteoglycan core protein / Name=HSPG2	3.48E-03	-2.5	2.5	-12.55	12.55
P05166	Propionyl-CoA carboxylase beta chain, mitochondrial / Name=PCCB	3.49E-03	2.21	2.21	7.71	7.71
P01620	Ig kappa chain V-III region SIE /	3.52E-03	-2.28	2.28	-2.71	2.71
P01623	Ig kappa chain V-III region WOL /	3.52E-03	-2.28	2.28	-2.71	2.71
Q14764	Major vault protein / Name=MVP; Synonyms=LRP	3.57E-03	-2.91	2.91	-8	8
P40939	Trifunctional enzyme subunit alpha, mitochondrial / Name=HADHA; Synonyms=HADH	3.79E-03	1.85	1.85	18.24	18.24
Q86VP6	Cullin-associated NEDD8-dissociated protein 1 / Name=CAND1; Synonyms=KIAA0829, TIP120, TIP120A	3.82E-03	-2.86	2.86	-4.5	4.5
P27216	Annexin A13 / Name=ANXA13; Synonyms=ANX13	3.90E-03	-2.85	2.85	-8.33	8.33
P23786	Carnitine O-palmitoyltransferase 2, mitochondrial / Name=CPT2; Synonyms=CPT1	3.93E-03	2.16	2.16	10.29	10.29
Q14103	Heterogeneous nuclear ribonucleoprotein D0 / Name=HNRNPD; Synonyms=AUF1, HNRPD	4.09E-03	-2.06	2.06	-3.5	3.5
P38117	Electron transfer flavoprotein subunit beta / Name=ETFB; ORFNames=FP585	4.26E-03	1.98	1.98	11.6	11.6
P01876	Ig alpha-1 chain C region / Name=IGHA1	4.48E-03	-2.01	2.01	-6.79	6.79
Q07507	Dermatopontin / Name=DPT	4.49E-03	-2.76	2.76	-7.83	7.83
P01834	Ig kappa chain C region / Name=IGKC	4.68E-03	-2.31	2.31	-14.74	14.74

P13639	Elongation factor 2 / Name=EEF2; Synonyms=EF2	4.71E-03	-2.32	2.32	-12.57	12.57
P00738	Haptoglobin / Name=HP	4.71E-03	1.8	1.8	7.21	7.21
P12532	Creatine kinase U-type, mitochondrial / Name=CKMT1A; Synonyms=CKMT	4.72E-03	-2.72	2.72	-3.83	3.83
Q14247	Src substrate cortactin / Name=CTTN; Synonyms=EMS1	4.72E-03	-2.72	2.72	-3.83	3.83
P01622	Ig kappa chain V-III region Ti /	4.82E-03	-2.07	2.07	-2.21	2.21
P04206	Ig kappa chain V-III region GOL /	4.82E-03	-2.07	2.07	-2.21	2.21
P28845	Corticosteroid 11-beta-dehydrogenase isozyme 1 / Name=HSD11B1; Synonyms=HSD11, HSD11L	4.98E-03	2.06	2.06	4	4
P14314	Glucosidase 2 subunit beta / Name=PRKCSH; Synonyms=G19P1	5.09E-03	2.04	2.04	3.33	3.33
P68363	Tubulin alpha-1B chain / Name=TUBA1B	5.15E-03	-2.45	2.45	-27.93	27.93
P04792	Heat shock protein beta-1 / Name=HSPB1; Synonyms=HSP27, HSP28	5.24E-03	-2.37	2.37	-7.45	7.45
P78527	DNA-dependent protein kinase catalytic subunit / Name=PRKDC; Synonyms=HYRC, HYRC1	5.25E-03	-2.29	2.29	-8.62	8.62
P14866	Heterogeneous nuclear ribonucleoprotein L / Name=HNRNPL; Synonyms=HNRPL; ORFNames=P/OKcl.14	5.43E-03	-2.06	2.06	-6.19	6.19
P27169	Serum paraoxonase/arylesterase 1 / Name=PON1; Synonyms=PON	5.56E-03	2.01	2.01	3.43	3.43
P17844	Probable ATP-dependent RNA helicase DDX5 / Name=DDX5; Synonyms=G17P1, HELR, HLR1	5.58E-03	-2.62	2.62	-7	7

P07355	Annexin A2 / Name=ANXA2; Synonyms=ANX2, ANX2L4, CAL1H, LPC2D	5.72E-03	-2.49	2.49	-30.07	30.07
P09382	Galectin-1 / Name=LGALS1	5.94E-03	-2	2	-3.24	3.24
P07148	Fatty acid-binding protein, liver / Name=FABP1; Synonyms=FABPL	6.00E-03	1.94	1.94	37.48	37.48
Q9H4A4	Aminopeptidase B / Name=RNPEP; Synonyms=APB	6.02E-03	-2.57	2.57	-3.67	3.67
P05165	Propionyl-CoA carboxylase alpha chain, mitochondrial / Name=PCCA	6.04E-03	1.97	1.97	6	6
Q15233	Non-POU domain-containing octamer-binding protein / Name=NONO; Synonyms=NRB54	6.08E-03	-1.79	1.79	-4.64	4.64
Q9BXN1	Asporin / Name=ASPN; Synonyms=PLAP1, SLRR1C; ORFNames=UNQ215/ PRO241	6.39E-03	-2.54	2.54	-7.83	7.83
P22392	Nucleoside diphosphate kinase B / Name=NME2; Synonyms=NM23B	6.41E-03	-1.7	1.7	-3.79	3.79
P21333	Filamin-A / Name=FLNA; Synonyms=FLN, FLN1	6.47E-03	-2.08	2.08	-18.31	18.31
P12694	2-oxoisovalerate dehydrogenase subunit alpha, mitochondrial / Name=BCKDHA	6.53E-03	1.94	1.94	5.14	5.14
Q86TX2	Acyl-coenzyme A thioesterase 1 / Name=ACOT1; Synonyms=CTE1	6.55E-03	1.94	1.94	5.86	5.86
Q14011	Cold-inducible RNA-binding protein / Name=CIRBP; Synonyms=A18HNRN P, CIRP	6.57E-03	-2.52	2.52	-2	2
Q9NUI1	Peroxisomal 2,4-dienoyl-CoA reductase / Name=DECR2; Synonyms=PDCR	6.57E-03	1.94	1.94	4.43	4.43

P09429	High mobility group protein B1 / Name=HMGB1; Synonyms=HMG1	6.59E-03	-1.75	1.75	-5.21	5.21
Q9HCC0	Methylcrotonoyl-CoA carboxylase beta chain, mitochondrial / Name=MCCC2; Synonyms=MCCB	6.63E-03	1.83	1.83	7.12	7.12
P42126	Enoyl-CoA delta isomerase 1, mitochondrial / Name=ECI1; Synonyms=DCI	6.78E-03	1.68	1.68	3.69	3.69
P05026	Sodium/potassium-transporting ATPase subunit beta-1 / Name=ATP1B1; Synonyms=ATP1B	6.78E-03	-2.5	2.5	-5.33	5.33
Q8N4T8	Carbonyl reductase family member 4 / Name=CBR4	6.78E-03	1.92	1.92	2.29	2.29
Q9Y5M8	Signal recognition particle receptor subunit beta / Name=SRPRB; ORFNames=PSEC0230	7.00E-03	1.68	1.68	1.67	1.67
Q96GK7	Fumarylacetoacetate hydrolase domain-containing protein 2A / Name=FAHD2A; ORFNames=CGI-105	7.04E-03	1.91	1.91	3.86	3.86
P63261	Actin, cytoplasmic 2 / Name=ACTG1; Synonyms=ACTB, ACTG	7.15E-03	-2.2	2.2	-70.62	70.62
P61160	Actin-related protein 2 / Name=ACTR2; Synonyms=ARP2	7.35E-03	-1.86	1.86	-3.64	3.64
P00390	Glutathione reductase, mitochondrial / Name=GSR; Synonyms=GLUR, GRD1	7.37E-03	-2.45	2.45	-3.67	3.67
P07737	Profilin-1 / Name=PFN1	7.41E-03	-1.95	1.95	-5.57	5.57
P22033	Methylmalonyl-CoA mutase, mitochondrial / Name=MUT	7.42E-03	1.89	1.89	4.71	4.71
P61158	Actin-related protein 3 / Name=ACTR3; Synonyms=ARP3	7.44E-03	-2.1	2.1	-6.07	6.07
P31153	S-adenosylmethionine synthase isoform type-2 /	7.49E-03	-2.44	2.44	-2.83	2.83

	Name=MAT2A; Synonyms=AMS2, MATA2					
Q12906	Interleukin enhancer-binding factor 3 / Name=ILF3; Synonyms=DRBF, MPHOSPH4, NF90	7.56E-03	-2.05	2.05	-5.64	5.64
P10620	Microsomal glutathione S-transferase 1 / Name=MGST1; Synonyms=GST12, MGST	7.60E-03	1.65	1.65	3.9	3.9
Q15436	Protein transport protein Sec23A / Name=SEC23A	7.63E-03	2.06	2.06	2.93	2.93
P12109	Collagen alpha-1(VI) chain / Name=COL6A1	7.80E-03	-2.03	2.03	-10.07	10.07
P01008	Antithrombin-III / Name=SERPINC1; Synonyms=AT3; ORFNames=PRO0309	7.88E-03	-1.93	1.93	-4.95	4.95
P51991	Heterogeneous nuclear ribonucleoprotein A3 / Name=HNRNPA3; Synonyms=HNRPA3	7.92E-03	-2.08	2.08	-8.57	8.57
O75874	Isocitrate dehydrogenase [NADP] cytoplasmic / Name=IDH1; Synonyms=PICD	7.94E-03	1.65	1.65	10.67	10.67
P51857	3-oxo-5-beta-steroid 4-dehydrogenase / Name=AKR1D1; Synonyms=SRD5B1	8.04E-03	1.85	1.85	6.29	6.29
Q16181	Septin-7 / Name=SEPT7; Synonyms=CDC10	8.17E-03	-2.39	2.39	-4.33	4.33
P51570	Galactokinase / Name=GALK1; Synonyms=GALK	8.24E-03	1.84	1.84	5	5
P49326	Dimethylaniline monooxygenase [N-oxide-forming] 5 / Name=FMO5	8.38E-03	1.84	1.84	7.43	7.43
P14550	Alcohol dehydrogenase [NADP+] / Name=AKR1A1; Synonyms=ALDR1, ALR	8.58E-03	1.65	1.65	4.38	4.38
P06703	Protein S100-A6 / Name=S100A6; Synonyms=CACY	8.63E-03	-2.36	2.36	-2.33	2.33
P31949	Protein S100-A11 / Name=S100A11;	8.63E-03	-2.36	2.36	-2.33	2.33

	Synonyms=MLN70, S100C					
P61163	Alpha-centractin / Name=ACTR1A; Synonyms=CTRN1	8.63E-03	-2.36	2.36	-2.33	2.33
Q96I15	Selenocysteine lyase / Name=SCLY; Synonyms=SCL	8.83E-03	1.81	1.81	3	3
P07910	Heterogeneous nuclear ribonucleoproteins C1/C2 / Name=HNRNPC; Synonyms=HNRPC	8.95E-03	-1.94	1.94	-5.24	5.24
Q02878	60S ribosomal protein L6 / Name=RPL6; Synonyms=TXREB1	9.27E-03	-1.6	1.6	-3.07	3.07
P30043	Flavin reductase (NADPH) / Name=BLVRB; Synonyms=FLR	9.29E-03	1.65	1.65	5.19	5.19
P01011	Alpha-1-antichymotrypsin / Name=SERPINA3; Synonyms=AACT; ORFNames=GIG24, GIG25	9.34E-03	-1.84	1.84	-4.98	4.98
P68133	Actin, alpha skeletal muscle / Name=ACTA1; Synonyms=ACTA	9.54E-03	1.78	1.78	25.43	25.43
O43809	Cleavage and polyadenylation specificity factor subunit 5 / Name=NUDT21; Synonyms=CFIM25, CPSF25, CPSF5	9.56E-03	-1.91	1.91	-2.38	2.38
Q7Z406	Myosin-14 / Name=MYH14; Synonyms=KIAA2034; ORFNames=FP17425	9.57E-03	-2.3	2.3	-8.33	8.33
P23381	Tryptophanyl-tRNA synthetase, cytoplasmic / Name=WARS; Synonyms=IFI53, WRS	9.94E-03	-2.27	2.27	-2.5	2.5

*Bold type indicates increased relative expression in normal cholangiocytes compared to normal hepatocytes

Table 7 provides information as to whether the marker proteins are relatively over-expressed (identified in bold) or under-expressed in hepatocellular

carcinoma versus cholangiocarcinoma in post-TACE liver tumours. Accordingly, by determining the presence, absence or change in expression levels of a plurality of these marker proteins and comparing these changes with a reference of known expression levels, one is able to determine whether the cells under test are hepatocellular carcinoma versus cholangiocarcinoma in post-TACE liver tumours.

All the marker proteins in section A of Table 7 are proteins with q-values less than or equal to 0.05. Those marker proteins in bold text (and with –ve effect size (g)) were less abundant in the HCC regions of the post-TACE, relative to the CC regions of the post-TACE. All the marker proteins in Table 7B are marker proteins with p-values less than or equal to 0.05.

Table 7 – Proteins differentiating between hepatocellular carcinoma and cholangiocarcinoma in post-TACE liver tumors*

Protein	Name	P Value	Effect Size (g)	Magnitude of Effect Size (g)	Effect Size (Mean Dif)	Magnitude of Mean dif (Mean Dif)
PART A:						
P68032*	**Actin, alpha cardiac muscle 1 / Name=ACTC1; Synonyms=ACTC**	**5.30E-06**	**-5**	**5**	**-36.86**	**36.86**
P00491*	**Purine nucleoside phosphorylase / Name=PNP; Synonyms=NP**	**1.19E-05**	**-3.7**	**3.7**	**-6.71**	**6.71**
Q9UHD8*	**Septin-9 / Name=SEPT9; Synonyms=KIAA0991, MSF**	**4.03E-05**	**-3.18**	**3.18**	**-5.43**	**5.43**
P50440	Glycine amidinotransferase, mitochondrial / Name=GATM; Synonyms=AGAT	4.05E-05	3.16	3.16	12.43	12.43
Q04917*	**14-3-3 protein eta / Name=YWHAH; Synonyms=YWHA1**	**4.45E-05**	**-3.11**	**3.11**	**-10.71**	**10.71**
Q03154	Aminoacylase-1 / Name=ACY1	5.54E-05	4.05	4.05	11.29	11.29
Q02338	D-beta-hydroxybutyrate dehydrogenase, mitochondrial / Name=BDH1; Synonyms=BDH	8.10E-05	4.72	4.72	5.71	5.71
Q14974*	**Importin subunit beta-1 / Name=KPNB1; Synonyms=NTF97**	**1.01E-04**	**-3.14**	**3.14**	**-4.43**	**4.43**

Q9UBR2	Cathepsin Z / Name=CTSZ	1.85E-04	2.69	2.69	3.57	3.57
P00167	Cytochrome b5 / Name=CYB5A; Synonyms=CYB5	1.96E-04	2.99	2.99	5.86	5.86
Q08426	Peroxisomal bifunctional enzyme / Name=EHHADH; Synonyms=ECHD	1.97E-04	3.56	3.56	28	28
P07099	Epoxide hydrolase 1 / Name=EPHX1; Synonyms=EPHX, EPOX	2.05E-04	2.64	2.64	30.14	30.14
P17174	Aspartate aminotransferase, cytoplasmic / Name=GOT1	2.08E-04	2.9	2.9	18.71	18.71
O95831	Apoptosis-inducing factor 1, mitochondrial / Name=AIFM1; Synonyms=AIF, PDCD8	2.36E-04	2.89	2.89	9.71	9.71
P34896	Serine hydroxymethyltransferase, cytosolic / Name=SHMT1	2.50E-04	2.57	2.57	6	6
P00480	Ornithine carbamoyltransferase, mitochondrial / Name=OTC	2.86E-04	3.76	3.76	14.29	14.29
P08133	Annexin A6 / Name=ANXA6; Synonyms=ANX6	3.22E-04	2.64	2.64	14.71	14.71
Q93099	Homogentisate 1,2-dioxygenase / Name=HGD; Synonyms=HGO	4.38E-04	3.22	3.22	12.14	12.14
P16930	Fumarylacetoacetase / Name=FAH	4.52E-04	2.54	2.54	6.29	6.29
P78417	Glutathione S-transferase omega-1 / Name=GSTO1; Synonyms=GSTTLP28	4.68E-04	2.52	2.52	4.43	4.43
Q00839*	**Heterogeneous nuclear ribonucleoprotein U / Name=HNRNPU; Synonyms=HNRPU, SAFA, U21.1**	**5.13E-04**	**-2.36**	**2.36**	**-9.14**	**9.14**
Q16762	Thiosulfate sulfurtransferase / Name=TST	5.46E-04	2.69	2.69	16	16
P13010*	**X-ray repair cross-complementing protein 5 / Name=XRCC5; Synonyms=G22P2**	**5.80E-04**	**-2.36**	**2.36**	**-6**	**6**
P07737*	**Profilin-1 / Name=PFN1**	**6.04E-04**	**-2.52**	**2.52**	**-6.14**	**6.14**
Q4G0N4	NAD kinase domain-containing protein 1 / Name=NADKD1; Synonyms=C5orf33	6.39E-04	2.36	2.36	6.86	6.86
P04632*	**Calpain small subunit 1 / Name=CAPNS1; Synonyms=CAPN4, CAPNS**	**6.49E-04**	**-2.39**	**2.39**	**-3.71**	**3.71**
P52907*	**F-actin-capping protein subunit alpha-1 / Name=CAPZA1**	**6.74E-04**	**-2.41**	**2.41**	**-4.29**	**4.29**

P04040	Catalase / Name=CAT	7.26E-04	2.5	2.5	25.29	25.29
P52565*	**Rho GDP-dissociation inhibitor 1 / Name=ARHGDIA; Synonyms=GDIA1**	**7.34E-04**	**-2.28**	**2.28**	**-3.57**	**3.57**
Q9Y2Q3	Glutathione S-transferase kappa 1 / Name=GSTK1; ORFNames=HDCMD47P	8.67E-04	2.38	2.38	9	9
O15144*	**Actin-related protein 2/3 complex subunit 2 / Name=ARPC2; Synonyms=ARC34; ORFNames=PRO2446**	**8.69E-04**	**-2.59**	**2.59**	**-5.57**	**5.57**
Q9Y6C9	Mitochondrial carrier homolog 2 / Name=MTCH2; Synonyms=MIMP; ORFNames=HSPC032	8.73E-04	2.53	2.53	4.43	4.43
Q9UJM8	Hydroxyacid oxidase 1 / Name=HAO1; Synonyms=GOX1, HAOX1	8.77E-04	3.06	3.06	17.43	17.43
P63261*	**Actin, cytoplasmic 2 / Name=ACTG1; Synonyms=ACTB, ACTG**	**8.89E-04**	**-2.74**	**2.74**	**-93.86**	**93.86**
P23141	Liver carboxylesterase 1 / Name=CES1; Synonyms=CES2, SES1	9.00E-04	2.48	2.48	42.29	42.29
PART B:						
P12956	X-ray repair cross-complementing protein 6 / Name=XRCC6; Synonyms=G22P1	1.06E-03	-2.41	2.41	-6.86	6.86
P09651	Heterogeneous nuclear ribonucleoprotein A1 / Name=HNRNPA1; Synonyms=HNRPA1	1.08E-03	-2.23	2.23	-8.43	8.43
Q8NBX0	Probable saccharopine dehydrogenase / Name=SCCPDH; ORFNames=CGI-49	1.09E-03	2.15	2.15	5.57	5.57
P14618	Pyruvate kinase isozymes M1/M2 / Name=PKM2; Synonyms=OIP3, PK2, PK3, PKM	1.14E-03	-2.7	2.7	-29	29
Q9H8H3	Methyltransferase-like protein 7A / Name=METTL7A; ORFNames=PRO0066, UNQ1902/PRO4348	1.16E-03	2.9	2.9	4	4
P30086	Phosphatidylethanolamine-binding protein 1 / Name=PEBP1; Synonyms=PBP, PEBP	1.27E-03	2.16	2.16	9.14	9.14
P54868	Hydroxymethylglutaryl-CoA synthase, mitochondrial / Name=HMGCS2	1.35E-03	2.58	2.58	18.86	18.86
P13804	Electron transfer flavoprotein	1.37E-03	2.4	2.4	9.43	9.43

	subunit alpha, mitochondrial / Name=ETFA					
P38117	Electron transfer flavoprotein subunit beta / Name=ETFB; ORFNames=FP585	1.39E-03	2.28	2.28	9.86	9.86
P10620	Microsomal glutathione S-transferase 1 / Name=MGST1; Synonyms=GST12, MGST	1.43E-03	2.06	2.06	4.29	4.29
Q13228	Selenium-binding protein 1 / Name=SELENBP1; Synonyms=SBP	1.44E-03	2.14	2.14	10.57	10.57
O75521	Enoyl-CoA delta isomerase 2, mitochondrial / Name=ECI2; Synonyms=DRS1, HCA88, PECI	1.45E-03	2.13	2.13	4.29	4.29
P30084	Enoyl-CoA hydratase, mitochondrial / Name=ECHS1	1.49E-03	2.09	2.09	12	12
O00299	Chloride intracellular channel protein 1 / Name=CLIC1; Synonyms=G6, NCC27	1.50E-03	-2.19	2.19	-5.71	5.71
O14756	17-beta-hydroxysteroid dehydrogenase type 6 / Name=HSD17B6; Synonyms=RODH	1.55E-03	2.48	2.48	9.57	9.57
Q9P2E9	Ribosome-binding protein 1 / Name=RRBP1; Synonyms=KIAA1398	1.59E-03	2.35	2.35	18	18
P40121	Macrophage-capping protein / Name=CAPG; Synonyms=AFCP, MCP	1.65E-03	-2.06	2.06	-6.71	6.71
Q16698	2,4-dienoyl-CoA reductase, mitochondrial / Name=DECR1; Synonyms=DECR	1.66E-03	2.24	2.24	10.57	10.57
P21549	Serine--pyruvate aminotransferase / Name=AGXT; Synonyms=AGT1, SPAT	1.70E-03	2.36	2.36	38	38
Q9NVS9	Pyridoxine-5'-phosphate oxidase / Name=PNPO	1.80E-03	2.05	2.05	2.57	2.57
P61978	Heterogeneous nuclear ribonucleoprotein K / Name=HNRNPK; Synonyms=HNRPK	1.93E-03	-2.01	2.01	-7.29	7.29
P09525	Annexin A4 / Name=ANXA4; Synonyms=ANX4	1.97E-03	-2.26	2.26	-20.43	20.43
P02753	Retinol-binding protein 4 / Name=RBP4; ORFNames=PRO2222	2.01E-03	2.6	2.6	3.71	3.71
P32754	4-hydroxyphenylpyruvate dioxygenase / Name=HPD; Synonyms=PPD	2.09E-03	2.58	2.58	19.86	19.86
P00367	Glutamate dehydrogenase 1,	2.10E-03	2.05	2.05	22.29	22.29

	mitochondrial / Name=GLUD1; Synonyms=GLUD					
Q3LXA3	Bifunctional ATP-dependent dihydroxyacetone kinase/FAD-AMP lyase (cyclizing) / Name=DAK	2.12E-03	2.26	2.26	12.71	12.71
P61158	Actin-related protein 3 / Name=ACTR3; Synonyms=ARP3	2.26E-03	-2.29	2.29	-8.71	8.71
O43776	Asparaginyl-tRNA synthetase, cytoplasmic / Name=NARS	2.27E-03	-1.94	1.94	-2.71	2.71
P31947	14-3-3 protein sigma / Name=SFN; Synonyms=HME1	2.36E-03	-2.15	2.15	-10.29	10.29
P27348	14-3-3 protein theta / Name=YWHAQ	2.45E-03	-2.13	2.13	-8.43	8.43
O95479	GDH/6PGL endoplasmic bifunctional protein / Name=H6PD; Synonyms=GDH	2.45E-03	2.01	2.01	4.57	4.57
P05062	Fructose-bisphosphate aldolase B / Name=ALDOB; Synonyms=ALDB	2.49E-03	2.01	2.01	29.43	29.43
Q9H9B4	Sideroflexin-1 / Name=SFXN1	2.59E-03	1.9	1.9	3.29	3.29
Q16836	Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial / Name=HADH; Synonyms=HAD, HADHSC, SCHAD	2.59E-03	2.25	2.25	4.43	4.43
P51858	Hepatoma-derived growth factor / Name=HDGF; Synonyms=HMG1L2	2.60E-03	-1.91	1.91	-6.14	6.14
O14745	Na(+)/H(+) exchange regulatory cofactor NHE-RF1 / Name=SLC9A3R1; Synonyms=NHERF, NHERF1	2.63E-03	-2.01	2.01	-3.43	3.43
P07437	Tubulin beta chain / Name=TUBB; Synonyms=TUBB5; ORFNames=OK/SW-cl.56	2.66E-03	-1.94	1.94	-28.86	28.86
Q9UJS0	Calcium-binding mitochondrial carrier protein Aralar2 / Name=SLC25A13; Synonyms=ARALAR2	2.69E-03	1.89	1.89	9.14	9.14
P45954	Short/branched chain specific acyl-CoA dehydrogenase, mitochondrial / Name=ACADSB	2.71E-03	1.92	1.92	6.29	6.29
P49419	Alpha-aminoadipic semialdehyde	2.75E-03	1.88	1.88	7	7

	dehydrogenase / Name=ALDH7A1; Synonyms=ATQ1					
O00264	Membrane-associated progesterone receptor component 1 / Name=PGRMC1; Synonyms=HPR6.6, PGRMC	2.80E-03	2.07	2.07	7	7
P05089	Arginase-1 / Name=ARG1	2.82E-03	2.43	2.43	18.43	18.43
P28288	ATP-binding cassette sub-family D member 3 / Name=ABCD3; Synonyms=PMP70, PXMP1	2.82E-03	2.43	2.43	3	3
P04424	Argininosuccinate lyase / Name=ASL	2.84E-03	2.01	2.01	14.14	14.14
P22307	Non-specific lipid-transfer protein / Name=SCP2	2.91E-03	2.21	2.21	6.29	6.29
P60660	Myosin light polypeptide 6 / Name=MYL6	3.20E-03	-1.84	1.84	-4	4
P07954	Fumarate hydratase, mitochondrial / Name=FH	3.20E-03	2.12	2.12	6.57	6.57
P09417	Dihydropteridine reductase / Name=QDPR; Synonyms=DHPR	3.32E-03	2.35	2.35	4.57	4.57
Q02252	Methylmalonate-semialdehyde dehydrogenase [acylating], mitochondrial / Name=ALDH6A1; Synonyms=MMSDH	3.40E-03	2.29	2.29	15.43	15.43
P51659	Peroxisomal multifunctional enzyme type 2 / Name=HSD17B4; Synonyms=EDH17B4	3.85E-03	2.15	2.15	31.86	31.86
O00571	ATP-dependent RNA helicase DDX3X / Name=DDX3X; Synonyms=DBX, DDX3	3.93E-03	-1.88	1.88	-3.86	3.86
Q9BPW8	Protein NipSnap homolog 1 / Name=NIPSNAP1	3.94E-03	1.96	1.96	5.57	5.57
P06703	Protein S100-A6 / Name=S100A6; Synonyms=CACY	3.94E-03	-1.95	1.95	-2.57	2.57
P00403	Cytochrome c oxidase subunit 2 / Name=MT-CO2; Synonyms=COII, COXII, MTCO2	4.03E-03	1.78	1.78	3	3
P22760	Arylacetamide deacetylase / Name=AADAC; Synonyms=DAC	4.06E-03	2.26	2.26	5.86	5.86
P51991	Heterogeneous nuclear ribonucleoprotein A3 / Name=HNRNPA3; Synonyms=HNRPA3	4.11E-03	-1.81	1.81	-5.14	5.14
P55084	Trifunctional enzyme subunit beta, mitochondrial /	4.13E-03	1.77	1.77	7.43	7.43

	Name=HADHB; ORFNames=MSTP029					
Q12905	Interleukin enhancer-binding factor 2 / Name=ILF2; Synonyms=NF45; ORFNames=PRO3063	4.15E-03	-1.93	1.93	-5.43	5.43
Q68CK6	Acyl-coenzyme A synthetase ACSM2B, mitochondrial / Name=ACSM2B; Synonyms=ACSM2; ORFNames=HYST1046	4.16E-03	2.25	2.25	14.71	14.71
P27338	Amine oxidase [flavin-containing] B / Name=MAOB	4.32E-03	1.79	1.79	5.43	5.43
P47756	F-actin-capping protein subunit beta / Name=CAPZB	4.35E-03	-1.85	1.85	-2.71	2.71
P68371	Tubulin beta-2C chain / Name=TUBB2C	4.44E-03	-1.75	1.75	-26.71	26.71
P55157	Microsomal triglyceride transfer protein large subunit / Name=MTTP; Synonyms=MTP	4.60E-03	2.2	2.2	7.71	7.71
P16435	NADPH--cytochrome P450 reductase / Name=POR; Synonyms=CYPOR	4.65E-03	1.98	1.98	9.86	9.86
P07148	Fatty acid-binding protein, liver / Name=FABP1; Synonyms=FABPL	4.78E-03	1.92	1.92	16.43	16.43
P30153	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform / Name=PPP2R1A	4.81E-03	-1.73	1.73	-3	3
Q16822	Phosphoenolpyruvate carboxykinase [GTP], mitochondrial / Name=PCK2; Synonyms=PEPCK2	4.83E-03	1.97	1.97	16.57	16.57
O43707	Alpha-actinin-4 / Name=ACTN4	4.86E-03	-1.72	1.72	-15	15
Q13838	Spliceosome RNA helicase DDX39B / Name=DDX39B; Synonyms=BAT1, UAP56	5.28E-03	-1.74	1.74	-5.29	5.29
O95154	Aflatoxin B1 aldehyde reductase member 3 / Name=AKR7A3; Synonyms=AFAR2	5.39E-03	1.88	1.88	5.43	5.43
P24752	Acetyl-CoA acetyltransferase, mitochondrial / Name=ACAT1; Synonyms=ACAT, MAT	5.49E-03	1.93	1.93	14.86	14.86
P11498	Pyruvate carboxylase, mitochondrial / Name=PC	5.55E-03	2	2	16.29	16.29
Q9UI17	Dimethylglycine dehydrogenase, mitochondrial /	5.56E-03	2.11	2.11	3.43	3.43

	Name=DMGDH					
P11216	Glycogen phosphorylase, brain form / Name=PYGB	5.62E-03	-1.68	1.68	-4.86	4.86
P50995	Annexin A11 / Name=ANXA11; Synonyms=ANX11	5.63E-03	-1.73	1.73	-3.71	3.71
Q9NUI1	Peroxisomal 2,4-dienoyl-CoA reductase / Name=DECR2; Synonyms=PDCR	5.67E-03	1.73	1.73	3.57	3.57
Q99613	Eukaryotic translation initiation factor 3 subunit C / Name=EIF3C; Synonyms=EIF3S8	5.80E-03	-1.68	1.68	-2.71	2.71
Q15365	Poly(rC)-binding protein 1 / Name=PCBP1	6.00E-03	-1.74	1.74	-5.29	5.29
Q00796	Sorbitol dehydrogenase / Name=SORD	6.09E-03	1.83	1.83	5.29	5.29
P18754	Regulator of chromosome condensation / Name=RCC1; Synonyms=CHC1	6.15E-03	-1.79	1.79	-2.29	2.29
Q86VP6	Cullin-associated NEDD8-dissociated protein 1 / Name=CAND1; Synonyms=KIAA0829, TIP120, TIP120A	6.15E-03	-1.94	1.94	-4	4
P37802	Transgelin-2 / Name=TAGLN2; Synonyms=KIAA0120; ORFNames=CDABP0035	6.24E-03	-1.79	1.79	-8.86	8.86
P04075	Fructose-bisphosphate aldolase A / Name=ALDOA; Synonyms=ALDA	6.27E-03	-1.95	1.95	-23.57	23.57
P13667	Protein disulfide-isomerase A4 / Name=PDIA4; Synonyms=ERP70, ERP72	6.30E-03	1.73	1.73	13	13
P26599	Polypyrimidine tract-binding protein 1 / Name=PTBP1; Synonyms=PTB	6.69E-03	-1.66	1.66	-5.57	5.57
P09467	Fructose-1,6-bisphosphatase 1 / Name=FBP1; Synonyms=FBP	6.84E-03	1.86	1.86	9.71	9.71
P68363	Tubulin alpha-1B chain / Name=TUBA1B	6.88E-03	-1.67	1.67	-17.71	17.71
P05455	Lupus La protein / Name=SSB	6.91E-03	-1.71	1.71	-4	4
P09382	Galectin-1 / Name=LGALS1	7.15E-03	-1.62	1.62	-3.29	3.29
P10619	Lysosomal protective protein / Name=CTSA; Synonyms=PPGB	7.30E-03	1.62	1.62	2.57	2.57
Q9Y265	RuvB-like 1 / Name=RUVBL1; Synonyms=INO80H, NMP238, TIP49, TIP49A	7.46E-03	-1.98	1.98	-2.57	2.57

P31939	Bifunctional purine biosynthesis protein PURH / Name=ATIC; Synonyms=PURH; ORFNames=OK/SW-cl.86	7.52E-03	-1.9	1.9	-10	10
P52272	Heterogeneous nuclear ribonucleoprotein M / Name=HNRNPM; Synonyms=HNRPM, NAGR1	7.52E-03	-1.63	1.63	-7.57	7.57
P00441	Superoxide dismutase [Cu-Zn] / Name=SOD1	7.76E-03	1.63	1.63	2.86	2.86
Q9NTK5	Obg-like ATPase 1 / Name=OLA1; Synonyms=GTPBP9; ORFNames=PTD004, PRO2455	7.85E-03	-1.64	1.64	-1.71	1.71
P13797	Plastin-3 / Name=PLS3	7.99E-03	-1.62	1.62	-5.71	5.71
P30038	Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial / Name=ALDH4A1; Synonyms=ALDH4, P5CDH	8.31E-03	1.88	1.88	13.43	13.43
Q01518	Adenylyl cyclase-associated protein 1 / Name=CAP1; Synonyms=CAP	8.41E-03	-1.72	1.72	-7	7
P11586	C-1-tetrahydrofolate synthase, cytoplasmic / Name=MTHFD1; Synonyms=MTHFC, MTHFD	8.47E-03	1.87	1.87	9.43	9.43
P22314	Ubiquitin-like modifier-activating enzyme 1 / Name=UBA1; Synonyms=A1S9T, UBE1	8.69E-03	-1.63	1.63	-8.14	8.14
Q07954	Prolow-density lipoprotein receptor-related protein 1 / Name=LRP1; Synonyms=A2MR, APR	8.71E-03	1.68	1.68	2.14	2.14
P52758	Ribonuclease UK114 / Name=HRSP12; Synonyms=PSP	8.71E-03	1.72	1.72	4.14	4.14
Q9P0Z9	Peroxisomal sarcosine oxidase / Name=PIPOX; Synonyms=LPIPOX, PSO	8.79E-03	1.73	1.73	7.71	7.71
P31930	Cytochrome b-c1 complex subunit 1, mitochondrial / Name=UQCRC1	8.86E-03	1.7	1.7	6.57	6.57
P31513	Dimethylaniline monooxygenase [N-oxide-forming] 3 / Name=FMO3	8.91E-03	1.68	1.68	6	6
Q15233	Non-POU domain-containing octamer-binding protein / Name=NONO; Synonyms=NRB54	9.27E-03	-1.55	1.55	-4.14	4.14
P07858	Cathepsin B / Name=CTSB;	9.46E-03	1.55	1.55	4.71	4.71

	Synonyms=CPSB					
P23528	Cofilin-1 / Name=CFL1; Synonyms=CFL	9.69E-03	-1.66	1.66	-4.14	4.14
O00515	Ladinin-1 / Name=LAD1; Synonyms=LAD	9.73E-03	-1.87	1.87	-4.29	4.29

*Bold type indicates increased relative expression in cholangiocarcinoma compared to hepatocellular carcinoma post-TACE

Table 8 provides information as to whether the marker proteins are relatively over-expressed (identified in bold) or under-expressed in peripheral cholangiocarcinoma versus metastatic colorectal cancer in post-TACE liver tumours. Accordingly, by determining the presence, absence or change in expression levels of a plurality of these marker proteins and comparing these changes with a reference of known expression levels, one is able to determine whether the cells under test are peripheral cholangiocarcinoma or metastatic colorectal cancer.

Table 8 – Proteins differentiating peripheral cholangiocarcinoma from metastatic colorectal cancer*

Protein	Name	P Value	Effect Size (g)	Magnitude of Effect Size (g)	Effect Size (Mean Dif)	Magnitude of Mean dif (Mean Dif)
PART A:						
P17987*	**T-complex protein 1 subunit alpha / Name=TCP1; Synonyms=CCT1, CCTA**	**9.41E-05**	**-2.98**	**2.98**	**-5.29**	**5.29**
Q8NFW8*	**N-acylneuraminate cytidylyltransferase / Name=CMAS**	**1.05E-04**	**-2.91**	**2.91**	**-2.71**	**2.71**
P15374*	**Ubiquitin carboxyl-terminal hydrolase isozyme L3 / Name=UCHL3**	**2.53E-04**	**-2.61**	**2.61**	**-3.57**	**3.57**
P09525	Annexin A4 / Name=ANXA4; Synonyms=ANX4	2.77E-04	2.92	2.92	25.71	25.71
Q99829*	**Copine-1 / Name=CPNE1; Synonyms=CPN1**	**6.96E-04**	**-2.32**	**2.32**	**-3.29**	**3.29**
P08758	Annexin A5 / Name=ANXA5; Synonyms=ANX5, ENX2, PP4	8.30E-04	2.69	2.69	14.71	14.71
P48643*	**T-complex protein 1 subunit epsilon / Name=CCT5; Synonyms=CCTE, KIAA0098**	**9.45E-04**	**-2.27**	**2.27**	**-3.86**	**3.86**

PART B:						
P50990	T-complex protein 1 subunit theta / Name=CCT8; Synonyms=C21orf112, CCTQ, KIAA0002	1.52E-03	-2.25	2.25	-6.43	6.43
P23526	Adenosylhomocysteinase / Name=AHCY; Synonyms=SAHH	1.55E-03	-2.07	2.07	-5.43	5.43
Q14444	Caprin-1 / Name=CAPRIN1; Synonyms=GPIAP1, GPIP137, M11S1, RNG105	1.55E-03	-2.21	2.21	-1.86	1.86
Q8NE71	ATP-binding cassette sub-family F member 1 / Name=ABCF1; Synonyms=ABC50	1.57E-03	-2.73	2.73	-1.86	1.86
O60547	GDP-mannose 4,6 dehydratase / Name=GMDS	1.61E-03	-2.72	2.72	-2.29	2.29
P56470	Galectin-4 / Name=LGALS4	1.65E-03	-2.17	2.17	-8	8
P09429	High mobility group protein B1 / Name=HMGB1; Synonyms=HMG1	1.72E-03	-2.04	2.04	-7	7
P50991	T-complex protein 1 subunit delta / Name=CCT4; Synonyms=CCTD, SRB	1.76E-03	-2.01	2.01	-4.57	4.57
P12532	Creatine kinase U-type, mitochondrial / Name=CKMT1A; Synonyms=CKMT	1.87E-03	-2.64	2.64	-3.43	3.43
P06731	Carcinoembryonic antigen-related cell adhesion molecule 5 / Name=CEACAM5; Synonyms=CEA	1.98E-03	-2.35	2.35	-8.43	8.43
P26038	Moesin / Name=MSN	2.09E-03	2.11	2.11	10.14	10.14
O95994	Anterior gradient protein 2 homolog / Name=AGR2; Synonyms=AG2; ORFNames=UNQ515/PRO 1030	2.12E-03	-1.96	1.96	-5.43	5.43
Q9NR45	Sialic acid synthase / Name=NANS; Synonyms=SAS	2.37E-03	-1.94	1.94	-2.29	2.29
Q9H0W9	Ester hydrolase C11orf54 / Name=C11orf54; ORFNames=LP4947, PTD012	2.93E-03	2.41	2.41	2.29	2.29
Q92598	Heat shock protein 105 kDa / Name=HSPH1; Synonyms=HSP105, HSP110, KIAA0201	2.98E-03	-2.35	2.35	-9.14	9.14
Q9UKM9	RNA-binding protein Raly / Name=RALY; Synonyms=HNRPCL2, P542	3.02E-03	-1.86	1.86	-4.14	4.14

P08729	Keratin, type II cytoskeletal 7 / Name=KRT7; Synonyms=SCL	3.10E-03	2.39	2.39	12	12
Q14498	RNA-binding protein 39 / Name=RBM39; Synonyms=HCC1, RNPC2	3.30E-03	-1.88	1.88	-1.86	1.86
O76021	Ribosomal L1 domain-containing protein 1 / Name=RSL1D1; Synonyms=CATX11, CSIG, PBK1; ORFNames=L12	3.30E-03	-1.88	1.88	-1.86	1.86
Q08J23	tRNA (cytosine(34)-C(5))-methyltransferase / Name=NSUN2; Synonyms=SAKI, TRM4	3.30E-03	-1.88	1.88	-1.86	1.86
Q06210	Glucosamine--fructose-6-phosphate aminotransferase [isomerizing] 1 / Name=GFPT1; Synonyms=GFAT, GFPT	3.42E-03	-2.02	2.02	-8.29	8.29
Q12864	Cadherin-17 / Name=CDH17	3.45E-03	-2.33	2.33	-6.14	6.14
P01024	Complement C3 / Name=C3; Synonyms=CPAMD1	3.53E-03	2.04	2.04	27.43	27.43
Q96C19	EF-hand domain-containing protein D2 / Name=EFHD2; Synonyms=SWS1	3.76E-03	-2.29	2.29	-3	3
Q9H0D6	5'-3' exoribonuclease 2 / Name=XRN2	3.94E-03	-1.81	1.81	-1.71	1.71
P21333	Filamin-A / Name=FLNA; Synonyms=FLN, FLN1	3.97E-03	1.79	1.79	32.29	32.29
Q9Y6E2	Basic leucine zipper and W2 domain-containing protein 2 / Name=BZW2; ORFNames=HSPC028, MSTP017	3.98E-03	-1.9	1.9	-2.29	2.29
Q86V81	THO complex subunit 4 / Name=THOC4; Synonyms=ALY, BEF	4.10E-03	-1.77	1.77	-1.43	1.43
P34897	Serine hydroxymethyltransferase, mitochondrial / Name=SHMT2	4.31E-03	-1.76	1.76	-4.29	4.29
Q16822	Phosphoenolpyruvate carboxykinase [GTP], mitochondrial / Name=PCK2; Synonyms=PEPCK2	4.43E-03	-1.87	1.87	-4.71	4.71
Q92820	Gamma-glutamyl hydrolase / Name=GGH	5.13E-03	-2.15	2.15	-3.71	3.71
P21810	Biglycan / Name=BGN; Synonyms=SLRR1A	5.20E-03	1.71	1.71	13.43	13.43
P05556	Integrin beta-1 / Name=ITGB1; Synonyms=FNRB, MDF2,	5.34E-03	1.81	1.81	5	5

	MSK12					
P07585	Decorin / Name=DCN; Synonyms=SLRR1B	5.72E-03	1.88	1.88	7.29	7.29
Q6YN16	Hydroxysteroid dehydrogenase-like protein 2 / Name=HSDL2; Synonyms=C9orf99	5.79E-03	-1.79	1.79	-2.14	2.14
P16401	Histone H1.5 / Name=HIST1H1B; Synonyms=H1F5	5.98E-03	-1.67	1.67	-5.86	5.86
P18206	Vinculin / Name=VCL	6.58E-03	1.8	1.8	6.43	6.43
P30837	Aldehyde dehydrogenase X, mitochondrial / Name=ALDH1B1; Synonyms=ALDH5, ALDHX	6.65E-03	-1.66	1.66	-7.71	7.71
P14618	Pyruvate kinase isozymes M1/M2 / Name=PKM2; Synonyms=OIP3, PK2, PK3, PKM	7.11E-03	1.67	1.67	17.14	17.14
Q13148	TAR DNA-binding protein 43 / Name=TARDBP; Synonyms=TDP43	7.69E-03	-1.6	1.6	-2.14	2.14
O43488	Aflatoxin B1 aldehyde reductase member 2 / Name=AKR7A2; Synonyms=AFAR, AFAR1, AKR7	8.24E-03	-1.94	1.94	-1.43	1.43
P35659	Protein DEK / Name=DEK	8.93E-03	-1.72	1.72	-3.29	3.29
P11940	Polyadenylate-binding protein 1 / Name=PABPC1; Synonyms=PAB1, PABP1, PABPC2	9.11E-03	-1.6	1.6	-4.86	4.86
P56537	Eukaryotic translation initiation factor 6 / Name=EIF6; Synonyms=EIF3A, ITGB4BP; ORFNames=OK/SW-cl.27	9.52E-03	-1.65	1.65	-4.29	4.29
Q9BUF5	Tubulin beta-6 chain / Name=TUBB6	9.62E-03	1.87	1.87	21	21

*Bold type indicates increased relative expression in metastatic colorectal cancer compared to peripheral cholangiocarcinoma

Table 9 provides information as to whether the marker proteins are relatively over-expressed or under-expressed in hilar cholangiocarcinoma versus HCC plus primary sclerosis cholangitis in post-TACE liver tumours. Accordingly, by determining the presence, absence or change in expression levels of a plurality of these marker proteins and comparing these changes with a reference of known expression levels, one is able to determine whether the cells under test are

peripheral hilar cholangiocarcinoma or primary sclerosis cholangitis.

Table 9 – Proteins differentiating hilar cholangiocarcinoma from hilar cholangiocarcinoma with primary sclerosing cholangitis

Protein	Name	P Value	Effect Size (g)	Magnitude of Effect Size (g)	Effect Size (Mean Dif)	Magnitude of Mean dif (Mean Dif)
P08670	Vimentin / Name=VIM	2.45E-03	1.93	1.93	21.57	21.57
Q9Y3Z3	SAM domain and HD domain-containing protein 1 / Name=SAMHD1; Synonyms=MOP5	4.30E-03	1.79	1.79	2.57	2.57
Q07960	Rho GTPase-activating protein 1 / Name=ARHGAP1; Synonyms=CDC42GAP, RHOGAP1	4.43E-03	1.76	1.76	3.29	3.29
P13797	Plastin-3 / Name=PLS3	4.74E-03	1.76	1.76	6	6
Q9BXN1	Asporin / Name=ASPN; Synonyms=PLAP1, SLRR1C; ORFNames=UNQ215/PRO241	5.73E-03	1.92	1.92	5	5
P06396	Gelsolin / Name=GSN	9.95E-03	1.53	1.53	7	7

Table 10 provides information as marker proteins that showed significant difference between hilar cholangiocarcinoma and colorectal metastasis.

Table 10

Protein Name	P Value	Effect Size (g)	Magnitude of Effect Size (g)	Effect Size (Mean Dif)	Magnitude of Mean dif (Mean Dif)	Q Value
Hilar cholangiocarcinoma > Colorectal metastasis (3 proteins)						
P08758; Annexin A5 / Name=ANXA5; Synonyms=ANX5, ENX2, PP4	1.11E-04	3.24	3.24	12.86	12.86	0.0108085
P21980; Protein-glutamine gamma-glutamyltransferase 2 / Name=TGM2	1.51E-04	2.73	2.73	8.71	8.71	0.0134021
P05155; Plasma protease C1 inhibitor / Name=SERPING1; Synonyms=C1IN, C1NH	7.78E-04	3.13	3.13	3.57	3.57	0.04078436
Hilar cholangiocarcinoma < Colorectal metastasis (27 proteins)						
P17987; T-complex protein 1	3.21E-05	-3.82	3.82	-6.14	6.14	0.00485819

subunit alpha / Name=TCP1; Synonyms=CCT1, CCTA						
P31939; Bifunctional purine biosynthesis protein PURH / Name=ATIC; Synonyms=PURH; ORFNames=OK/SW-cl.86	4.25E-05	-3.13	3.13	-8.86	8.86	0.0056545
P50990; T-complex protein 1 subunit theta / Name=CCT8; Synonyms=C21orf112, CCTQ, KIAA0002	4.49E-05	-3.29	3.29	-7.43	7.43	0.00588578
P34897; Serine hydroxymethyltransferase, mitochondrial / Name=SHMT2	7.58E-05	-3.02	3.02	-6.43	6.43	0.00856843
Q99832; T-complex protein 1 subunit eta / Name=CCT7; Synonyms=CCTH, NIP7-1	8.76E-05	-2.89	2.89	-6.71	6.71	0.0091784
P22102; Trifunctional purine biosynthetic protein adenosine-3 / Name=GART; Synonyms=PGFT, PRGS	1.25E-04	-2.87	2.87	-2.71	2.71	0.01173283
P54136; Arginyl-tRNA synthetase, cytoplasmic / Name=RARS	1.26E-04	-2.91	2.91	-3.71	3.71	0.01177183
P23526; Adenosylhomocysteinase / Name=AHCY; Synonyms=SAHH	2.03E-04	-2.64	2.64	-5.71	5.71	0.0164932
P78371; T-complex protein 1 subunit beta / Name=CCT2; Synonyms=99D8.1, CCTB	2.09E-04	-2.71	2.71	-9.29	9.29	0.01687596
P10809; 60 kDa heat shock protein, mitochondrial / Name=HSPD1; Synonyms=HSP60	2.47E-04	-2.63	2.63	-27.86	27.86	0.01851074
P31948; Stress-induced-phosphoprotein 1 / Name=STIP1	2.83E-04	-2.87	2.87	-3.57	3.57	0.02052934
P15374; Ubiquitin carboxyl-terminal hydrolase isozyme L3 / Name=UCHL3	2.94E-04	-3.74	3.74	-4	4	0.02113147
P16422; Epithelial cell adhesion molecule / Name=EPCAM; Synonyms=GA733-2, M1S2, M4S1, MIC18, TACSTD1, TROP1	3.03E-04	-2.53	2.53	-2.86	2.86	0.02170325
Q9NSD9; Phenylalanyl-tRNA synthetase beta chain / Name=FARSB; Synonyms=FARSLB, FRSB; ORFNames=HSPC173	3.13E-04	-3.07	3.07	-4.86	4.86	0.02225712
P48643; T-complex protein 1	3.34E-04	-2.61	2.61	-4.43	4.43	0.023226731

subunit epsilon / Name=CCT5; Synonyms=CCTE, KIAA0098						

Table 11 (Figure 7)shows a list of marker proteins (467) with both unique and shared peptide sequences that were found to be significantly regulated in at least one of the tissue comparisons that were common to both quantification methods (spectral counting and area under the curve). Table 11 contains tissue type comparison (Tissue type number versus tissue type number), Uniprot ID, and protein names along with P-values, t-scores and log_2FoldChanges values for both quantitative methods. Positive Log2 Fold changes refer to proteins which were up-regulated in the second tissue type compared to the first tissue type, while negative Log2 Fold Changes refer to proteins which were down-regulated in the second tissue (e.g. In Tissue comparison 1_2, P51857 (AK1D1) gave a Log2 fold change of -3.0581 for Area under the curve and -2.6145 for spectral counts. This means P51857 went down in Tissue 2 (HCC) compared to Tissue 1 (normal liver)).

Accordingly, the invention provides for the first time marker proteins which, by determining their relative expression by any appropriate means, can distinguish between different liver cell phenotypes. The disclosure herein provides details of how such expression levels may be determined and/or quantified, but may be employed and the method of quantification itself is not a limiting component of the invention.

The invention provides for a method of determining the cellular phenotype of a liver tissue sample said method comprising

(1) extracting marker proteins from said liver tissue sample;

(2) determining expression levels of a plurality of marker proteins in said sample, wherein said plurality of marker proteins are selected from a biomarker panel as represented by any one of Tables 2 to 10 or the relevant section of Table 11; optionally, repeating step (2) with a different plurality of marker proteins selected from any one of Tables 2 to 11;

(3) comparing said determined expression levels with reference expression levels for said plurality of marker proteins in known cellular phenotypes, thereby determining the cellular phenotype of the liver tissue sample.

The invention also provides for a method of identifying the cellular phenotype of a liver cell, said method comprising

(1) determining expression levels of a plurality of marker proteins in said liver cell;

(2) comparing said determined expression levels with reference set of expression levels for said plurality of marker proteins, said reference levels representing a particular cellular phenotype;

(3) identifying the cellular phenotype of the liver cell based on the comparison between the expression levels of the marker proteins in the liver cell and the reference expression levels;

wherein the plurality of marker proteins are selected from a biomarker panel as represented by any one of Tables 2 to 11.

Preferably the known cellular phenotypes comprise normal liver epithelium cells (hepatocytes), normal biliary epithelium cells (cholangiocytes), hepatocellular carcinoma cells, peripheral cholangiocellular carcinoma cells and hilar cholangiocellular carcinoma cells.

In all cases, the plurality of marker proteins may be selected from a biomarker panel as represented by the relevant Table as a whole or from Part A of the Table which contains those marker proteins showing the highest statistically significant difference. Alternatively the plurality of marker proteins may be selected from those shown to be over-expressed (identified in bold) or under-expressed as compared to the two cell types from either the whole Table or part A.

Alternatively, the plurality of marker proteins may be selected from Table 11 for the relevant tissue comparison.

In all cases, the plurality of protein may comprises 2, 3, 5, 10, 20, 30, 40, 50, 60, 70, 80, 90, 100, 120 or more protein markers provided in the respective

Tables. With respect to Table 5, the plurality of marker proteins may comprise 2, 3, 5, 10, 20, 30, 40, 50, 60, 70, or more protein markers.

Alternatively, the method may comprises determining the presence or change in level of expression of at least 5%, 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90% of the protein markers provided in any one of Tables 2 to 10.

In one embodiment, the method may determine the presence or change in level of expression of 100% of the protein markers provided in any one of Tables 2 to 10 or Table 11 or the relevant section of Table 11.

Preferably, the plurality of marker proteins are selected from any one of Collagen alpha 1 (XVIII) chain, Plastin-3, AKR1B10, Fibronectin, Beta 3 tubulin, Asporin, 14-3-3 protein eta or Dihydropyrimidinase-related protein 3 or combinations thereof, preferably the plurality of marker proteins comprises AKR1B10 and/or Beta 3 tubulin.

The liver tissue sample may be a biopsy sample taken from an individual suspect of having a liver tumor. Alternatively, the biopsy may be taken from an individual having previously received treatment for a liver tumor such as surgery, transplantation with or without transarterial chemoembolization.

The step of determining expression levels of said plurality of marker proteins includes determining the presence or absence of the marker proteins in said sample as well as the degree of change in expression levels. When compared to a reference or standard of known expression levels for the cellular phenotype, the presence, absence or change in degree of expression will be indicative of the cellular phenotype.

For this and all other aspects of the invention, the reference or standard protein expression levels may be determined from non-tumor liver tissue from the same subject. In this way, the difference in protein expression levels may be used to determine the cellular phenotype of the liver tumor. Alternatively, the reference levels may be a database comprising data representing expression levels for the marker proteins of interest as selected from any one or more of Tables 2 to 10 or the relevant section of Table 11. Ideally, the reference levels are provided by a liver tumor classification

system, such as according to the present invention. The data representing expression levels may be a collection of data obtained from multiple liver samples and presented as an average or range. The data may relate to the levels of specific peptides each being unique to a protein of interest.

The biomarkers provided in Table 5 allow for the first time accurate and reliable distinction to be made between HCC and CC cells.
In particular the marker proteins selected from Table 5 or fragments thereof, or antibodies against said proteins or nucleic acids encoding said proteins or fragments thereof, can be used as a marker for the determination of cellular phenotype of a liver cell wherein said cellular phenotype is selected from HCC or CC.

Preferably, there is provided a method of determining the cellular phenotype of a liver tumor cell, said method comprising

(1) determining protein expression levels in said liver tumor cell of a plurality of marker proteins selected from Table 5;

(2) comparing said protein expression levels with a reference of expression levels for said plurality of marker proteins; and

(3) determining said cellular phenotype of said cell based on the comparison of expression levels of said plurality of marker proteins;

wherein said cellular phenotype of said liver tumor cell is selected from HCC or CC.

Where the liver tumor cell is from a biopsy taken from an individual having previously received treatment for a liver tumor such as surgery, transplantation with transarterial chemoembolization, it may be preferably to determine the protein expression levels of a plurality of marker proteins selected from Table 7, in addition to, or instead of, those selected from Table 5.
Hence, in one embodiment, the method of determining the cellular phenotype of a liver tumor cell, comprises:

(1) determining protein expression levels in said liver tumor cell of a plurality of marker proteins selected from

a) Table 5, or

b) Table 7, or
c) Table 5 and Table 7, or
d) Table 5A or
e) Table 7A, or
f) Table 5A and Table 7A;

(2) comparing said protein expression levels with a reference of expression levels for said plurality of marker proteins; and

(3) determining said cellular phenotype of said cell based on the comparison of expression levels of said plurality of marker proteins;

wherein said cellular phenotype of said liver tumor cell is selected from HCC or CC.

It will also be appreciated that the marker proteins determined herein may also be used as tumor antigens for the purpose of diagnostic and/or prognostic methods and/or for selecting or determining a treatment regimen for an individual based on determination of a cellular phenotype of the liver tumour cell. For example, the marker proteins or fragments thereof may be secreted or lost into the bloodstream as a result of cell death and may therefore be detected from blood, urine or saliva samples using standard techniques, e.g. antibodies. The detection of such protein markers (e.g. tumor antigens) will enable the clinician to determine whether the individual has liver cancer and the cellular classification of the tumor. Thus, it is envisaged that the same methods may be used to diagnose liver tumor at an early stage using samples, including but not exclusively, from blood, saliva or urine.

Hence, there is provided a method for the diagnosis or prognostic monitoring of a liver tumor in an individual, said method comprising

(a) determining the presence or level of expression of a plurality of marker proteins selected from a biomarker panel as represented by any one of Tables 2 to 10 or relevant section of Table 11, in a liver tumor cell obtained from said individual;

(b) identifying the cellular phenotype of the liver tumor cell; and

(c) selecting a diagnosis or prognosis based on the cellular phenotype of the liver tumor cell.

Furthermore, there is provided a method for determining a treatment regimen for an individual having a liver tumor, said method comprising

(a) determining the presence or level of expression of a plurality of marker proteins selected from a biomarker panel as represented by any one of Tables 2 to 10 or relevant section of Table 11, in a liver tumor cell obtained from said individual;

(b) identifying the cellular phenotype of the liver tumor cell; and

(c) selecting a treatment regimen based on the cellular phenotype of the liver tumor cell.

In particular, the methods according to the invention may be based on the determination of cellular phenotypes of the liver tumor cells based on the protein expression levels identified in respect of a plurality of protein markers provided in Table 5 and/or Table 7.

The method may comprise comparing the determined expression levels with a previously determined reference level for said plurality of marker proteins. The reference level is preferably a pre-determined level, which may, for example be provided in the form of an accessible data record. The reference level is preferable representative of the expression levels of a number of the biomarkers identified in Table 5 and/or Table 7, each one being the derived mean and range of values obtained from known cellular phenotypes. It will be appreciated that in other embodiments the reference level may be representative of the expression levels of marker proteins selected from other biomarker panels represented by the Tables provided herein depending on the cellular phenotype under investigation.

The liver tumor cell is preferably from a liver tumor biopsy from the individual and more preferably the biomarker panel is represented by Table 5, more preferably Table 5, Part A.

Still further, it is preferred that the plurality of marker proteins selected from the biomarker panel of Table 11 section 2_5.

Where the biopsy is from a patient having previously been treated with transarterial chemoembolization (TACE), it is preferred that the plurality

of marker proteins are selected from the biomarker panel of Table 7 or Table 7, Part A. More preferably, the plurality of marker proteins selected from Table 11 section 3_4.

For all methods provided herein, it is envisaged that a further step of determining expressions levels for a second set of marker proteins may be performed. The second set of marker proteins may be selected from the same biomarker panel as the first set, or may be selected from a different biomarker panel as represented by the Tables herein. For example, the method may include firstly determining the expression levels for a plurality of marker proteins selected from Table 5 or relevant section of Table 11, and then determining the expression levels of a plurality of marker proteins selected from Table 7 (or relevant section of Table 11). The expression levels for the first and second set of marker proteins may be measured sequentially or at the same time.

Determining the presence or change in expression level of the plurality of marker proteins may be achieved in many ways all of which are well within the capabilities of the skilled person.

The determination may involve direct quantification of marker protein levels, of nucleic acid encoding those marker proteins or it may involve indirect quantification, e.g. using an assay that provides a measure that is correlated with the amount of marker protein present.

Accordingly, determining the presence or level of expression of the plurality of marker proteins may comprise

(a) contacting the liver cell with a plurality of binding members, wherein each binding member selectively binds to one of said plurality of marker proteins or nucleic acid sequences encoding said marker proteins; and

(b) detecting and/or quantifying a complex formed by said specific binding members and marker proteins or nucleic acid sequences encoding said marker protein.

The binding member may be an antibody specific for a marker protein or a part thereof, or it may be a nucleic acid molecule which binds to a nucleic acid

molecule representing the presence, increase or decrease of expression of a marker protein, e.g. an mRNA sequence.

The antibodies raised against specific marker proteins may be anti- to any biologically relevant state of the marker protein. Thus, for example, they can be raised against the unglycosylated form of a protein which exists in the body in a glycosylated form, against a precursor form of the protein, or a more mature form of the precursor protein, e.g. minus its signal sequence, or against a peptide carrying a relevant epitope of the marker protein. The detection and/or quantification may include preparing a standard curve using standards of known expression levels of the one or more marker proteins and comparing to the level of complex obtained in step (b) above.

A variety of methods may be suitable for determining the presence or changes in level of the plurality of marker proteins: by way of a non-limiting example, these include Western blot, ELISA (Enzyme-Linked Immunosorbent Assay), RIA (Radioimmunoassay), Competitive EIA (Competitive Enzyme Immunoassay), DAS-ELISA (Double Antibody Sandwich-ELISA), Liquid Immunoarray technology), immunocytochemical or immunohistochemical techniques, techniques based on the use of protein microarrays that include specific antibodies, "dipstick" assays, affinity chromatography techniques and liquid binding assays.

Antibodies may be obtained using techniques which are standard in the art. Methods of producing antibodies include immunising a mammal (e.g. mouse, rat, rabbit, horse, goat, sheep or monkey) with the protein or a fragment thereof. Antibodies may be obtained from immunised animals using any of a variety of techniques known in the art, and screened, preferably using binding of antibody to antigen of interest. For instance, Western blotting techniques or immunoprecipitation may be used (Armitage et al, Nature, 357:80-82, 1992). Isolation of antibodies and/or antibody-producing cells from an animal may be accompanied by a step of sacrificing the animal. As an alternative or supplement to immunising a mammal with a peptide, an antibody specific for a protein may be obtained from a recombinantly produced library of expressed immunoglobulin variable domains, e.g. using lambda bacteriophage or filamentous bacteriophage which display functional immunoglobulin binding

domains on their surfaces; for instance see WO92/01047. The library may be naive, that is constructed from sequences obtained from an organism which has not been immunised with any of the proteins (or fragments), or may be one constructed using sequences obtained from an organism which has been exposed to the antigen of interest.

Antibodies according to the present invention may be modified in a number of ways that are well known in the art. Indeed the term "antibody" should be construed as covering any binding substance having a binding domain with the required specificity. Thus the invention covers antibody fragments, derivatives, functional equivalents and homologues of antibodies, including synthetic molecules and molecules whose shape mimics that of an antibody enabling it to bind an antigen or epitope. Humanised antibodies in which CDRs from a non-human source are grafted onto human framework regions, typically with the alteration of some of the framework amino acid residues, to provide antibodies which are less immunogenic than the parent non-human antibodies, are also included within the present invention.

A hybridoma producing a monoclonal antibody according to the present invention may be subject to genetic mutation or other changes. It will further be understood by those skilled in the art that a monoclonal antibody can be subjected to the techniques of recombinant DNA technology to produce other antibodies or chimeric molecules which retain the specificity of the original antibody. Such techniques may involve introducing DNA encoding the immunoglobulin variable region, or the complementarity determining regions (CDRs), of an antibody to the constant regions, or constant regions plus framework regions, of a different immunoglobulin. See, for instance, EP 0 184 187 A, GB 2 188 638 A or EP 0 239 400 A. Cloning and expression of chimeric antibodies are described in EP 0 120 694 A and EP 0 125 023 A.

Preferred antibodies for use in accordance with the methods disclosed herein are isolated, in the sense of being free from contaminants such as antibodies able to bind other polypeptides and/or free of serum components. Monoclonal antibodies are preferred for some purposes, though polyclonal antibodies are within the scope of the present invention. For example, the primary monoclonal

antibodies used herein were anti-AKR1B10 (clone 1A6; 1:500; Abcam, Cambridge, UK) and anti-tubulin beta 3 (clone TU20; 1:500; Abcam).

The binding of antibodies on a sample may be determined by any appropriate means. Tagging with individual reporter molecules is one possibility. The reporter molecules may directly or indirectly generate detectable, and preferably measurable, signals. The linkage of reporter molecules may be directly or indirectly, covalently, e.g. via a peptide bond or non-covalently. Linkage via a peptide bond may be as a result of recombinant expression of a gene fusion encoding antibody and reporter molecule. One favoured mode is by covalent linkage of each antibody with an individual fluorochrome, phosphor or laser exciting dye with spectrally isolated absorption or emission characteristics. Suitable fluorochromes include fluorescein, rhodamine, phycoerythrin and Texas Red. Suitable chromogenic dyes include diaminobenzidine.

Other reporters include macromolecular colloidal particles or particulate material such as latex beads that are coloured, magnetic or paramagnetic, and biologically or chemically active agents that can directly or indirectly cause detectable signals to be visually observed, electronically detected or otherwise recorded. These molecules may be enzymes which catalyse reactions that develop or change colours or cause changes in electrical properties, for example. They may be molecularly excitable, such that electronic transitions between energy states result in characteristic spectral absorptions or emissions. They may include chemical entities used in conjunction with biosensors. Biotin/avidin or biotin/streptavidin and alkaline phosphatase detection systems may be employed.

The determination of over expression of the one or more (or plurality) of marker proteins according to the present invention may be carried out in many different ways well known to those skilled in the art that include, by way of example, determining the presence or amount of expression of said marker protein, or a fragment thereof, in the sample (tissue or blood) obtained from the individual, or determining the expression of the marker protein gene, for example by examining the marker protein mRNA levels expressed from the marker

protein gene.

Preferably, the methods comprise detecting the expression levels of the marker proteins. Such detection may involve the step of contacting an antibody or antibody fragment capable of recognising said polypeptide, or fragment thereof, with said sample (tissue or blood).

The analysis may comprise a qualitative analysis, e.g. by monitoring the presence of the one or more marker proteins by microscopy, e.g. using immunohistochemical staining. Immunohistochemical analysis can be performed on either formalin-fixed, paraffin fixed samples or on frozen tissue samples.

Examples of possible IHC methods which could be used to detect and quantify the one or more marker proteins are as described in the present invention.

In one aspect, the present invention provides for a method for diagnosing recurrent or primary liver tumor in a subject, the method comprising determining the presence or absence of one or more marker proteins selected from the group consisting of Collagen alpha 1 (XVIII) chain, Plastin-3, AKR1B10, Fibronectin, Beta 3 tubulin, Asporin, 14-3-3 protein eta, and Dihydropyrimidinase-related protein 3 in a sample. Preferably, the liver tumor is selected from the group consisting of hepatocellular carcinoma, peripheral cholangiocellular carcinoma or hilar cholangiocellular carcinoma cells.

In one embodiment of this aspect the marker protein is Beta 3 tubulin and/or AKR1B10, preferably Beta 3 tubulin.

In another embodiment, the sample is selected from any one of blood, plasma, serum, liver tissue, liver cells or combinations thereof, preferably the sample is liver tissue, optionally formalin-fixed paraffin-embedded liver tissue section.

In another embodiment, the determining the presence or absence of one or more marker proteins in the sample is performed by either Immunohistochemistry (IHC) or mass-spectrometry.

In one preferred embodiment, the method for diagnosing recurrent or primary liver tumor in a subject comprises determining the presence or absence of Beta 3 tubulin, and optionally, AKR1B10, in a sample, wherein the liver tumor is selected from the group consisting of hepatocellular carcinoma, peripheral cholangiocellular carcinoma or hilar cholangiocellular carcinoma cells and wherein the sample is

liver tissue, optionally formalin-fixed paraffin-embedded liver tissue section and wherein determining the presence or absence of one or more marker proteins in the sample is performed by Immunohistochemistry (IHC).

More preferably, the method comprises determining Beta 3 tubulin with a primary antibody.

By way of further example a primary antibody that is capable of specifically binding to a marker protein, e.g. Beta 3 tubulin and/or AKR1B10 in a binding assay may be labelled with a detectable molecule such as, but not limited to, radioactive or fluorescent labels or to enzymes which utilise a chromogenic substrate. Examples of radiolabels of use in this technique are ^{32}P, ^{3}H or ^{14}C. Examples of fluorescent molecules of use in this technique are green fluorescent protein, Fluorescein IsoThioCyanate (FITC), Rhodamine IsoThioCyanate (TRICT) Cy3 and Cy5 Dyes. Examples of enzymes with chromagenic substrates of possible use in this technique are peroxidase, alkaline phosphatase or glucose oxidase.

Instead of detecting the signal from the primary antibody itself (as described above), a secondary antibody which binds to the primary antibody can be utilised. The secondary antibody may be labelled with a suitable molecule for detection purposes examples of which are described above.

In an alternative method of detection the primary or secondary antibody may be labelled with a biotin molecule which can then be bound by a streptavidin or avidin linked enzyme with a suitable chromogenic substrate for detection.

Additional variations of the above techniques exist that will be apparent to someone skilled in the art.
In the context of this invention antibodies which could be used in such a technique could be generated by standard techniques involving immunisation of animals or could be generated in vitro by recombinant techniques. Antibodies could in this context be whole immunoglobulins or fragments of antibodies (Fab fragments) that correspond to the anti-idiotype. Such antibodies can be readily produced by the skilled person as discussed above.

The invention demonstrates the use of histological analysis to detect marker proteins and from this the cellular phenotype may be determined and the appropriate diagnosis and prognosis for the individual

In one embodiment, the method comprises the measurement of a plurality of marker proteins, preferably including tubulin beta 3 and/or AKR1B10 proteins in a liver tumour tissue section. The section may be a fresh-frozen section or formalin-fixed, paraffin embedded section such as is routine in the art of histology. Staining of sections may require a step of antigen retrieval prior to detection with a primary antibody specific for the target protein. Accordingly, the invention provides a method of determining the expression level of one or more marker proteins (preferably a plurality) using a binding member such as an antibody. Materials and methods relating to such assays are described in more detail below.

Alternatively, antibodies to the plurality of marker proteins may be detected in the blood or saliva of patients suspected of having liver cancer, using the marker proteins or fragments thereof as a detection agent.

In a further embodiment, the determination of the one or more (or plurality) of marker proteins in a sample from the individual may comprise the detection and quantification of autoantibodies. The marker protein or fragment thereof must be capable of specifically binding to such an autoantibody. Techniques such as ELISA may be used. An altered concentration of the plurality of marker proteins maybe identified by detecting the presence or altered levels of autoantibody thereto, compared to the level in a reference or control sample.

The level of autoantibody may be detected by Western blot (from 1D or 2D electrophoresis) against liver cell or liver tumor cells obtained from a biopsy or cell lines grown in vitro; or by ELISA, protein microarray or bead suspension array using purified marker proteins.

By way of example, detection of autoantibodies to marker proteins in different liver cell phenotypes can be carried out as follows. Recombinant marker proteins are expressed in baculovirus infected insect cells and used to coat the surface of microtitre plates. A blood or saliva sample, preferably a blood

plasma sample and more preferably a blood serum sample is added to duplicate wells of each microtitre plate and incubated at 37 ° C for 1 hour. Plates are aspirated and washed prior to the addition of a horse-radish peroxidase (HRP) labelled anti-human IgG antiserum and incubated for 1 hour at 37 ° C. Finally, binding of the antihuman antiserum is revealed by aspirating the plates, washing, and then adding tetra-methylbenzidine (TMB) which in the presence of HRP produces a coloured product the intensity of which is measured by reading the plates at 450 nm. An identical set of plates is tested with the exception that the second antibody is a HRP labelled anti-human IgM antiserum. The levels of IgG, IgE, IgA, IgD and/or IgM autoantibodies to each of the liver cell or liver tumor cell marker marker proteins is altered when compared to the levels found in reference standards or control samples.

In other embodiments, autoantibodies to the plurality of protein markers may be detected using the Western blotting approach using cells from the liver tumor sample, and then detecting the presence of antibodies specific for the protein markers that are present in the tumor.

It is contemplated within the invention to use (i) an antibody chip or array of chips, or a bead suspension array capable of detecting the plurality of marker proteins that interact with that antibody; or (ii) a protein chip or array of chips, or bead suspension array capable of detecting one or more autoantibodies that interact with the marker proteins; or (iii) a combination of both antibody arrays and protein arrays.

A further class of specific binding members contemplated herein in accordance with any aspect of the invention comprise aptamers (including nucleic acid aptamers and peptide aptamers). Advantageously, an aptamer directed to a protein marker may be provided by a technique known as SELEX (Systematic Evolution of Ligands by Exponential Enrichment), described in US Patent Nos. 5,475,096 and 5,270,163.

Alternatively, differential expression of nucleic acids encoding marker proteins may be used as a detection method. Expression of nucleic acids may be detected by methods known in the art, such as RT-PCR, Northern blotting

or in situ hybridisation such as FISH.

Gene expression technologies such as reverse transcriptase – polymerase chain reaction (RT-PCR) can give accurate measurement of mRNA expression levels and the presence of the one or more marker proteins mRNA in a sample as opposed to its absence could also be used to provide the cellular phenotype classification. RT-PCR can be performed in a range of formats including quantitative versions and with sensitivities that enable the determination of mRNA levels in a single cell.

In one embodiment, the expression of the marker protein gene can be assessed by determining the presence or amount of marker protein mRNA in the sample and methods for doing this are well known to the skilled person. By way of example, they include determining the presence of marker protein mRNA in the sample (i) using a labelled probe capable of hybridising to the marker protein nucleic acid; and/or (ii) using PCR involving one or more primers based on a marker protein nucleic acid sequence to determine whether the marker protein transcript is present in a sample. The probe may also be immobilised as a sequence included in a microarray.

In accordance with these and other aspects of the invention, the the plurality of marker proteins are selected from any one of Collagen alpha 1 (XVIII) chain, Plastin-3, AKR1B10, Fibronectin, Beta 3 tubulin, Asporin, 14-3-3 protein eta or Dihydropyrimidinase-related protein 3 or combinations thereof, preferably the plurality of marker proteins comprises AKR1B10 and/or Beta 3 tubulin.

In some embodiments, the determination of the presence or amount of the plurality of protein markers comprises measuring the presence or amount of mRNA derived from the cell under test. The presence or level of mRNA encoding the protein marker in the liver cells under examination will allow the cell to be classified according to its phenotype.

Techniques suitable for measuring the level of protein marker encoding mRNA are readily available to the skilled person and include “real-time” reverse transcriptase PCR or Northern blots. The method of measuring the level of a protein marker encoding mRNA may comprise using a plurality of primers or probes

that are each independently directed to the sequence of one of the plurality of protein marker encoding genes or complement thereof. Each of the primers or probes may comprise a nucleotide sequence of at least 10, 15, 20, 25, 30 or 50 contiguous nucleotides that has at least 70%, 80%, 90%, 95%, 98%, 99% or 100% identity to a nucleotide sequence encoding the protein marker provided Table 5 (or any of Table 2 to 10 or relevant section of combined Table 11).

Preferably, the probes or primers according to the invention hybridise under stringent conditions to their specific protein marker encoding nucleic acid sequence.

The methods of the invention may comprise contacting the liver cell with a binding member as described above, but also includes contacting the binding member with cell lysate to increase contact directly or indirectly with the one or more of the marker proteins.

The binding members may be immobilised on a solid support. This may be in the form of an antibody array or a nucleic acid microarray. Arrays such as these are well known in the art. The solid support may be contacted with the cell lysate, thereby allowing the binding members to bind to the cell products representing the presence or amount of the one or more marker proteins.

In some embodiments, the binding member is an antibody or fragment thereof which is capable of binding to a marker protein or part thereof. In other embodiments, the binding member may be a nucleic acid molecule capable of binding (i.e. complementary to) the sequence of the nucleic acid to be detected.

The methods may further comprise contacting the solid support with a developing agent that is capable of binding to the one or more marker proteins, antibody or nucleic acid.

The developing agent may comprise a label and the method may comprise detecting the label to obtain a value representative of the presence or amount of the one or more marker proteins, antibody or nucleic acid in the cell, cell culture medium or cell lysate.

The label may be, for example, a radioactive label, a fluorophor, a phosphor, a laser dye, a chromogenic dye, a macromolecular colloidal particle, a latex bead which is coloured, magnetic or paramagnetic, an enzyme which catalyses a reaction producing a detectable result or the label is a tag.

The methods preferably comprise determining the presence or level of expression of a plurality of marker proteins or nucleic acids encoding said marker proteins in a single sample. For example, a plurality of binding members, each specific for one of a plurality of protein markers selected from Table 5 (or any one of Tables 2 to 10 or relevant section of combined Table 11), may be immobilised at predefined locations on the solid support. The number of binding members on the solid support may make up 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90% or 100% of the total number of binding members on the support.

Additional methodologies to detect the one or more marker protein gene expression will be apparent to those skilled in the art.

In some embodiments, the determination of the presence or the level of expression of one or more of the marker proteins may be performed by mass spectrometry. Techniques suitable for measuring the level of a protein marker selected from Table 5 (or any other of Table 2 to 10 or relevant section of combined Table 11) include, but are not limited to techniques related to Selected Reaction Monitoring (SRM) and Multiple Reaction Monitoring (MRM) isotope dilution mass spectrometry including SILAC, AQUA (as disclosed in WO 03/016861, the entire content of which is specifically incorporated herein by reference) and TMTcalibrator (as disclosed in WO 2008/110581; the entire content of which is specifically incorporated herein by reference).

WO 2008/110581 discloses a method using isobaric mass tags to label separate aliquots of all marker proteins in a reference sample which can, after labelling, be mixed in quantitative ratios to deliver a standard calibration curve. A test sample is then labelled with a further independent member of the same set of isobaric mass tags and mixed with the calibration curve. This mixture is the subjected to tandem mass spectrometry and peptides derived from specific

marker proteins can be identified and quantified based on the appearance of unique mass reported ions released from the isobaric mass tags in the MS/MS spectrum.

By way of a reference level, a known or predicted protein marker derived peptide may be created by trypsin, ArgC, AspN or Lys-C digestion of said protein marker. In some cases, when employing mass spectrometry based determination of protein markers, the methods of the invention comprises providing a calibration sample comprising at least two different aliquots comprising the protein marker and/or at least one protein marker derived peptide, each aliquot being of known quantity and wherein said biological sample and each of said aliquots are differentially labelled with one or more isobaric mass labels. Preferably, the isobaric mass labels each comprise a different mass spectrometrically distinct mass marker group.

Accordingly, the method of determining the cellular phenotype of a liver cell, wherein the method comprises determining the presence or expression level of one or more of the marker proteins selected from Table 5 (or from any one of Tables 2 to 10 or relevant section of combined Table 11 in a liver cell by Selected Reaction Monitoring using one or more determined transitions for known protein marker derived peptides; comparing the determined expression levels with reference set of expression levels previously determined to represent a particular cellular phenotype, e.g. HCC or CC; and determining or identifying the cellular phenotype based on changes in expression of said one or more, preferably plurality of marker proteins. The comparison step may include determining the amount of marker protein derived peptides from the liver cell with known amounts of corresponding synthetic peptides. The synthetic peptides are identical in sequence to the peptides obtained from the cell, but may be distinguished by a label such as a tag of a different mass or a heavy isotope.

More preferably, the determination and/or quantification is made by mass spectrometry.

One or more of these synthetic protein marker derived peptides with or without

label form a further aspect of the present invention. These synthetic peptides may be provided in the form of a kit for the purpose of determining the cellular phenotype of a liver cell, in particular HCC or CC phenotype.

Other suitable methods for determining levels of protein expression include surface-enhanced laser desorption ionization-time of flight (SELDI-TOF) mass spectrometry; matrix assisted laser desorption ionization-time of flight (MALDI-TOF) mass spectrometry, including LS/MS/MS; electrospray ionization (ESI) mass spectrometry; as well as the preferred SRM and TMT-SRM. Each of these methods may be preceded by a step of marker protein enrichment by immunoprecipitation or affinity chromatography performed in column or batch mode. Any binding agent with the required specificity for the marker proteins may be employed in such enrichment including but not limited to polyclonal antibodies, monoclonal antibodies and aptamers.

Liquid chromatography – mass spectrometry (LC-MS/MS) based proteomics has proven to be superior over conventional biochemical methods at identifying and precisely quantifying thousands of marker proteins from complex samples including cultured cells (prokaryotes/eukaryotes), and tissue (Fresh Frozen/formalin fixed paraffin embedded), leading to the identification of novel biomarkers in an unbiased manner [7, 8, 9]. The present inventors have used laser microdissection (LMD) of specific formalin fixed tissue types thereby allowing regions of archival tumor material enriched for normal hepatocytes, normal cholangiocytes, and their respective transformed equivalents to be independently analysed by LC-MS proteomics. Spectral counting was used for relative quantification due to its good linear dynamic range (two to three orders of magnitude) and high quantitative proteome coverage [10, 11].

Thus, as detailed above, a differentially expressed protein which is a member of the plurality of protein markers described herein and illustrated in Tables 1A and Tables 2 to 11 may qualitatively have its expression activated or completely inactivated in first cellular phenotype versus a second cellular phenotype. Such a qualitatively regulated protein will exhibit an expression pattern within a given cell type which is detectable in one phenotype, e.g. HCC or CC, but not detectable in both. 'Detectable', as used herein, refers

to a protein expression pattern, which is detectable using techniques described herein.

Alternatively, a differentially expressed protein which is a member of the plurality of marker proteins described herein may have its expression modulated, i.e. quantitatively increased or decreased, in a first cellular phenotype versus a second cellular phenotype. The degree to which expression differs between cellular phenotypes under comparison, e.g. HCC and CC, need only be large enough to be visualised via standard characterisation techniques, such as silver staining of 2D-electrophoretic gels. Other such standard characterisation techniques by which expression differences may be visualised are well known to those skilled in the art. These include successive chromatographic separations of fractions and comparisons of the peaks, capillary electrophoresis, separations using micro-channel networks, including on a micro-chip, SELDI analysis and qPST analysis.

Chromatographic separations can be carried out by high performance liquid chromatography as described in Pharmacia literature, the chromatogram being obtained in the form of a plot of absorbance of light at 280 nm against time of separation. The material giving incompletely resolved peaks is then re-chromatographed and so on.

Capillary electrophoresis is a technique described in many publications, for example in the literature "Total CE Solutions" supplied by Beckman with their P/ACE 5000 system. The technique depends on applying an electric potential across the sample contained in a small capillary tube. The tube has a charged surface, such as negatively charged silicate glass. Oppositely charged ions (in this instance, positive ions) are attracted to the surface and then migrate to the appropriate electrode of the same polarity as the surface (in this instance, the cathode). In this electroosmotic flow (EOF) of the sample, the positive ions move fastest, followed by uncharged material and negatively charged ions. Thus, marker proteins are separated essentially according to charge on them.

Micro-channel networks function somewhat like capillaries and can be formed

by photoablation of a polymeric material. In this technique, a UV laser is used to generate high energy light pulses that are fired in bursts onto polymers having suitable UV absorption characteristics, for example polyethylene terephthalate or polycarbonate. The incident photons break chemical bonds with a confined space, leading to a rise in internal pressure, mini-explosions and ejection of the ablated material, leaving behind voids which form micro-channels. The micro-channel material achieves a separation based on EOF, as for capillary electrophoresis. It is adaptable to micro-chip form, each chip having its own sample injector, separation column and electrochemical detector: see J.S.Rossier *et al.*, 1999, Electrophoresis *20:* pages 727-731.

Surface enhanced laser desorption ionisation time of flight mass spectrometry (SELDI-TOF-MS) combined with ProteinChip technology can also provide a rapid and sensitive means of profiling marker proteins and is used as an alternative to 2D gel electrophoresis in a complementary fashion. The ProteinChip system consists of aluminium chips to which protein samples can be selectively bound on the surface chemistry of the chip (eg. anionic, cationic, hydrophobic, hydrophilic etc). Bound marker proteins are then co-crystallised with a molar excess of small energy-absorbing molecules. The chip is then analysed by short intense pulses of N2 320nm UV laser with protein separation and detection being by time of flight mass spectrometry. Spectral profiles of each group within an experiment are compared and any peaks of interest can be further analysed using techniques as described below to establish the identity of the protein.

Isotopic or isobaric Tandem Mass Tags® (TMT®) (Thermo Scientific, Rockford, USA) technology may also be used to detect differentially expressed marker proteins which are members of a biomarker panel described herein. Briefly, the marker proteins in the samples for comparison are optionally digested, labelled with a stable isotope tag and quantified by mass spectrometry. In this way, expression of equivalent marker proteins in the different samples can be compared directly by comparing the intensities of their respective isotopic peaks or of reporter ions released from the TMT reagents during fragmentation in a tandem mass spectrometry experiment.

Differentially expressed marker proteins which are members of the plurality

of protein markers described herein may be further described as target marker proteins and/or fingerprint marker proteins. 'Fingerprint marker proteins', as used herein, refer to a differentially expressed protein whose expression pattern may be utilised as part of a prognostic or diagnostic cellular phenotype evaluation. A fingerprint protein may also have characteristics of a target protein or a pathway protein. For example, the one or more marker proteins described herein may be used as liver tumor markers as well as determining the cellular phenotype of the liver cell. For example, it is contemplated that any of the markers provided in Tables 2 to 11, but at least tubulin beta 3 and/or AKR1B10 proteins may be used as markers for liver tumor. The detection of these proteins in blood may well provide a diagnostic tool for liver cancer. The marker proteins may be secreted or lost into the blood stream following cell death and may serve as circulating tumor antigens.

As described above, the invention provides a number of methods by which the one or marker proteins may be determined in a liver tissue sample, blood or saliva sample from an individual. The method comprises detecting the expression levels of the one or more (preferably plurality) of marker proteins selected from any one of Tables 2 to 10 or the relevant section of Table 11.

Unless context dictates otherwise, the descriptions and definitions of the features set out above are not limited to any particular aspect or embodiment of the invention and apply equally to all aspects and embodiments which are described. Thus, the features set out above are disclosed in all combinations and permutations.

2. Kits

One or more of the marker proteins selected from table 2 to 11 may be used as diagnostic marker for liver cancer in the methods described above and kits for use in carrying out these methods, in particular determining the cellular phenotype of a liver cell, preferably a liver tumor cell, *in vitro*, are encompassed herein.

Preferably, the kit allows the determination/identification of a cellular

phenotype selected from normal liver epithelium cells (hepatocytes), normal biliary epithelium cells (cholangiocytes), hepatocellular carcinoma cells, peripheral cholangiocellular carcinoma cells and hilar cholangiocellular carcinoma cells.

More preferably, the kit allows the liver tumor cell to be identified as an HCC cell or a CC cell.

The kit allows the user to determine the presence or level of expression of a plurality of analytes selected from

a) a plurality of marker proteins or fragments thereof provided in Table 5 (or one of Tables 2 to 10 or relevant section of combined Table 11);

b) antibodies against said marker proteins and nucleic acid molecules encoding said marker proteins or fragments thereof, in a liver cell under test; the kit comprising:

(a) a solid support having a plurality of binding members, each being independently specific for one of said plurality of analytes immobilised thereon;

(b) a developing agent comprising a label; and, optionally

(c) one or more components selected from the group consisting of washing solutions, diluents and buffers.

Suitable binding members have been described herein. In particular, for detection of a marker protein or fragment thereof, the binding member may be an antibody which is capable of binding to one or more of the marker proteins selected from Table 5 (or any one of Tables 2 to 10 or relevant section of combined Table 11), or a combination thereof.

Kits according for the invention may be used for diagnosing recurrent or primary liver tumor in a subject by comprising reagents for determining the presence or absence of one or more marker proteins selected from the group consisting of Collagen alpha 1 (XVIII) chain, Plastin-3, AKR1B10, Fibronectin, Beta 3 tubulin, Asporin, 14-3-3 protein eta, and Dihydropyrimidinase-related protein 3 in a sample. Preferably, the liver tumor is selected from the group consisting of hepatocellular carcinoma, peripheral cholangiocellular carcinoma or hilar cholangiocellular carcinoma cells.

In one embodiment, the marker protein is Beta 3 tubulin and/or AKR1B10, preferably Beta 3 tubulin.

In another embodiment, the kit comprises reagents suitable for preparing the sample, wherein the sample is selected from any one of blood, plasma, serum, liver tissue, liver cells or combinations thereof.

In yet another embodiment, the sample is liver tissue and the kit comprises reagents suitable for preparing liver tissue, optionally for preparing formalin-fixed paraffin-embedded liver tissue sections.

In another embodiment, the determining the presence or absence of of one or more marker proteins in the sample is performed by either Immuno-hystochemistry.

In one preferred embodiment, the kit for diagnosing recurrent or primary liver tumor in a subject comprises reagents for determining the presence or absence of Beta 3 tubulin, and optionally, AKR1B10, in a sample, wherein the liver tumor is selected from the group consisting of hepatocellular carcinoma, peripheral cholangiocellular carcinoma or hilar cholangiocellular carcinoma cells and wherein the kit comprises reagents suitable for preparing liver tissue, optionally for preparing formalin-fixed paraffin-embedded liver tissue sections and wherein the kit is suitable for determining the presence or absence of one or more marker proteins in the sample by Immuno-hystochemistry (IHC).

More preferably, the kit comprises a primary antibody for Beta 3 tubulin.

As mentioned above, various methodologies are known in the art for determining the presence or amount of a marker protein, antibody or nucleic acid molecule in a sample. Various suitable assays are described below in more detail and each form embodiments of the invention.

The kit may additionally provide a standard or reference which provides a quantitative measure by which determination of an expression level of one or more marker proteins can be compared. The standard may indicate the levels of marker protein expression which indicate the cellular phenotype of the liver cell, e.g. HCC or CC

The kit may also comprise printed instructions for performing the method.

In one embodiment, the kit may be for performance of a mass spectrometry assay and may comprise a set of reference peptides (e.g. SRM peptides) in an assay compatible format wherein each peptide in the set is uniquely representative of each of the plurality of marker proteins provided in Table 5, (or any one of Tables 2 to 10 or relevant section of combined Table 11). Preferably two and more preferably three such unique peptides are used for each protein for which the kit is designed, and wherein each set of unique peptides are provided in known amounts which reflect the levels of such proteins in a standard preparation of said cell of known phenotype, e.g. HCC or CC cells. Optionally, the kit may also provide protocols and reagents for the isolation and extraction of proteins from a sample, a purified preparation of a proteolytic enzyme such as trypsin and a detailed protocol of the method including details of the precursor mass and specific transitions to be monitored. The peptides may be synthetic peptides and may comprise one or more heavy isotopes of carbon, nitrogen, oxygen and/or hydrogen.

Optionally, the kits of the present invention may also comprise appropriate cells, vessels, growth media and buffers.

The invention also includes the use of a plurality of binding members each capable of independently binding to one or more of a plurality of marker proteins or fragments thereof provided in Table 5, one or more antibodies against said marker proteins and one or more nucleic acid molecules encoding said marker proteins or fragments thereof, for the in vitro diagnosis or prognostic monitoring of an individual having or suspecting a liver tumor, or following treatment for a liver tumor.

The kit may comprise reagents for the detection of the plurality of protein markers in a liver tumor sample, wherein said plurality of protein markers are selected from Table 5 or part A of Table 5, or section 2_5 of Table 11.

A kit may comprise a plurality of primary antibodies, each antibody binding specifically to a different individual protein marker of the plurality of protein markers selected from Table 5 or section 2_5 of Table 11.

The antibodies may be immobilised on an assay plate, beads, microspheres or particles. Optionally, beads, microspheres or particles may be dyed, tagged or labelled.

A kit may further comprise one or more secondary antibodies which bind specifically bind to the primary antibodies. The secondary antibodies may be labelled, for example fluorescent labelled or tagged.

A kit may further comprise one or more detection reagents for detecting the presence of the tagged secondary antibodies.

Furthermore, the invention provides for a kit for classifying the cellular phenotype of a liver tumor cell or for determining a liver tumor in an individual in line with the methods described herein. Preferably, the kit comprises the reagents necessary for carrying out the determination of the presence or level of expression of one or more (preferably a plurality) of the marker proteins selected from one or more of Tables 2 to 11 on a sample (tissue or blood) and instructions for carrying out the test and interpreting the results. Preferred types of kit may comprise one or more of the following reagents:

(a) an antibody capable of recognising said one or more marker proteins or fragments thereof, for example for use in a binding assay such as an ELISA or in an immunohistochemical test. The antibody may be detected either by being directly labelled or through interaction with one or more other species, for example a labelled secondary antibody; and/or

(b) one or more primers based on the nucleic acid sequence of the one or more marker proteins, for example for detecting the presence and/or amount of the marker protein mRNA; and/or

(c) a probe based on the nucleic acid sequence of the one or more marker protein gene, for example for detecting the marker protein gene expression. As for antibody reagents, the probes may conveniently be directly or indirectly labelled to enable them to be detected.

3. Liver cellular classification system

The invention also provide for a liver cellular classification system comprising a liver cellular classification apparatus and an information communication terminal apparatus, said liver cellular classification apparatus including a control component and a memory component, said apparatuses being communicatively connected to each other via a network;

(1) wherein the information communication terminal apparatus includes

(1a) a protein data sending unit that transmits the protein data derived from a liver tissue sample of a subject to the liver cellular classification apparatus;

(1b) a result-receiving unit that receives the result of the liver cellular classification of the subject transmitted from the liver cellular classification apparatus;

(2) wherein the liver cellular classification apparatus includes

(2a) a protein data-receiving unit that receives protein data derived from the liver tissue sample of the subject transmitted from the information communication terminal apparatus;

(2b) a data comparison unit which compares the data from the data-receiving unit with the data stored in the memory unit;

(2c) a classifier unit that determines the class (e.g. cellular phenotype) of the liver tissue of the subject, based on the results of the data comparison unit; and

(2d) a classification result-sending unit that transmits the classification result of the subject obtained by the classifier unit to the information communication terminal apparatus; and

wherein the memory unit contains protein expression level data of at least one (preferably a plurality) proteins selected from any one or more of Tables 2 to 10 or Table 11.

The data derived from the liver tissue sample of the subject is preferably expression level data such as that obtained from methods described herein e.g. LC-MS/MS and other proteomic approaches. The data may be derived just from the tissue being either normal tissue of tumor (or suspected tumor) tissue sample.

The protein data received by the data-receiving unit may be the actual protein

levels, or it may be peptide levels from which the protein levels can be calculated. The peptide is unique to the at least one (preferably plurality) protein. In some embodiments it is preferable to use multiple, i.e. 2, 3, 4, or 5 peptides which are all unique to said protein. Where multiple peptides are used, data may be collated and optionally a median value used in the data comparison step.

The memory unit preferably includes data sets relating to protein expression levels representative of liver tissue or tumor sample. In a preferred embodiment, the protein expression levels are derived from actual peptide levels in the sample. This is particularly so if the data has been obtained using proteomic methods such as the LC-MS/MS method described herein. The data sets may provide a representative (e.g. average) level of protein expression levels found in liver tissue (normal or tumor) from a collection of data sets, e.g. as provided herein by Table 11. Alternatively, it may be preferable for the data sets to include a value representing a ratio of the protein expression level as compared to the protein expression level of a different cellular phenotype (e.g. HCC v peripheral CC) tissue obtained from the same source.

In this way, the system can compare the protein expression levels obtained from liver tissue samples (non-tumor or tumor) with protein expression levels representative of a particular liver cellular phenotype for the same protein and thereby classify the tissue by its cell type.

The system may further comprise the means to add the inputted data via the data sending unit to the stored data already held in the memory unit so that this new data can be included in the analysis performed by the determining unit. In this way the data representative of liver cellular phenotype (tumor or non-tumor) is constantly updated.

The liver tissue classification system may be connected to an apparatus for determining protein expression levels in a liver tissue (tumor or non-tumor) sample and feeding this data to the protein data sending unit.

Ideally the apparatus can process multiple samples using LC-MS/MS as described herein.

In accordance with this aspect of the invention, there is also provided a liver

tissue (tumor or non-tumor) cellular classification program that makes an information processing apparatus including a control component and a memory component execute a method of determining and/or classifying the liver tissue of a subject, the method comprising:

(i) a comparing step of comparing data based on the protein expression levels of at least one (preferably a plurality) protein selected from Tables 2 to 11 obtained of a subject with the protein expression level data stored in the memory component; and

(ii) a classifying step for classifying the liver tissue cells of said subject, based on the comparison calculated at the comparing step; and wherein said tissue is classified into phenotypes including normal (hepatocytes, cholangiocytes), hepatocellular carcinoma, hepatocholangiocellular carcinoma (pre or post TACE therapy), peripheral cholangiocarcinoma, Hilar cholangiocarcinoma (with or without primary sclerosing cholangitis), or metastatic colo-rectal carcinoma.

In accordance with this aspect of the invention, there is also provided a computer-readable recording medium, comprising the liver tissue cellular classification program described above recorded thereon.

The data representing protein expression levels may be derived from peptide levels in the sample where said peptides are each unique to a particular protein selected from any one of Tables 2 to 11. It will be appreciated that peptides may be designed which will be unique for the protein from which they are derived, e.g. by proteolytic enzyme digestion such as trypsin, aspN, gluC and other such enzymes well known in the art.

In accordance with all aspects and embodiments of the invention the plurality of marker proteins are selected from any one of Collagen alpha 1 (XVIII) chain, Plastin-3, AKR1B10, Fibronectin, Beta 3 tubulin, Asporin, 14-3-3 protein eta or Dihydropyrimidinase-related protein 3 or combinations thereof, preferably the plurality of marker protein comprises AKR1B10 and/or Beta 3 tubulin.

4. Examples

Certain aspects and embodiments of the invention will now be illustrated by way of example and with reference to the figures and tables described above.

All documents mentioned in this specification are incorporated herein by reference in their entirety for all purposes.

4.1 MATERIAL AND METHODS

Liver tissue

This study consists of 9 types of liver tissue taken from a total of 55 archived specimens: mixed HCC/CC after TACE (areas of HCC and areas of CC separately examined), non-treated HCC, normal liver parenchyma, normal bile duct, non-treated peripheral CC, non-treated hilar / perihilar CC, PSC-associated hilar CC, and metastatic colorectal cancer. All specimens were surgically resected or explanted livers from adult patients ranging from 27 to 80 years in age. Details of tissues in each group are as follows:

- **Mixed cancer after TACE** (n=7): Before the treatment with TACE, all nodules were radiologically diagnosed as HCC according to European Association for the Study of the Liver (EASL) criteria of concordant imaging of nodular arterialized lesions with portal venous washout [16]. Presence of features suggestive of combined HCC and CC and in particular hypoarterialization was a criterion of exclusion for TACE. In explanted livers, cholangiocellular differentiation in addition to HCC components was histologically suggested. HCC and CC components were separately examined.
- **HCC** (n=7): Well to moderately differentiated HCCs, which did not receive any treatment before transplantation, arranged in a trabecular or pseudoglandular pattern and developed in cirrhotic livers were examined. Etiologies of liver cirrhosis were viral hepatitis (n=3) and excessive alcoholic intake (n=4). One tumor was selected from each case when multiple tumors were present.
- **Normal liver tissue** (n=7): Histologically unremarkable liver tissues without steatosis, inflammation, or fibrosis were selected from specimens that were surgically resected for metastatic cancers.
- **Normal bile duct** (n=6): Histologically unremarkable hilar bile ducts are selected from liver specimens that were explanted for acute liver failure due to paracetamol overdose.
- **Peripheral CC** (n=7): All cases showed well to moderately differentiated tubular adenocarcinoma against the background of fibrotic stroma. Hilar or perihilar tissue was not involved in any cases. The background liver

was not cirrhotic in any cases, but two had early bridging fibrosis with moderate steatosis.

- **Hilar CC** (n=7): All were ductal adenocarcinoma predominantly involving hilar / perihilar bile ducts. No patients had histories of chronic hepatobiliary diseases.
- **PSC-associated CC** (n=7): Four cases were diagnosed to have CCs during treatment for PSC and underwent surgical resection, whereas three were incidentally found to have CC in explanted livers. All tumors were histologically adenocarcinoma, four associated with mucinous foci, which are sometimes seen in PSC-associated CC.
- **Metastatic colorectal cancer** (n=7): All were typical intestinal type adenocarcinoma.

Tissue sampling

Fresh liver specimens, which were surgically resected, were immediately received at our pathology laboratory. After macroscopic examination, samples were extensively taken, and were fixed in 10% formalin for at least 4 hours before being embedded in paraffin.

Microdissection of FFPE tissue

10µm thick sections were prepared from FFPE tissue blocks. After deparaffinization with xylene and alcohol, a target area of 1.5×10^7 μm^2 ($0.15 mm^3$) was selectively cut using the Laser Capture Microdissection System (LMD6500, Leica Microsystems, Wetzlar, Germany). Dissected tissues were directly immersed in 50 µL of Qproteome® FFPE Tissue Extraction Buffer (QIAGEN, Valencia, CA) and stored in -80°C until protein extraction. Samples were prepared in batches e.g. week 1 (batch 1) the 1^{st} biological replicate of each tissue/tumor type were prepared and analysed. At week 2 (batch 2), the 2^{nd} biological replicates of each tissue/tumor type were prepared and analysed. This process was continued up until week 7 (batch 7) where the 7^{th} biological replicate of each tissue/tumor type were prepared and analysed. Samples were prepared and analysed in this way to ensure that differences in protein expression levels between different tissue types were due to biology/pathology of the sample, rather than any sample preparation variability.

Protein extraction from FFPE liver tissue

Following storage at -80°C samples were thawed on ice then homogenised, vortexed and centrifuged. Samples were transferred to 1.5 ml collection tubes and sealed with collection tube sealing clip, as provided in the Qproteome® kit. Samples were incubated on a heating block at 100°C for 20 min, then for a further 2 hours at 80°C with agitation at 750 rpm. After heating, the sample tubes were placed on ice for 1 min and the collection tube sealing clip removed. Each tube was centrifuged for 15 min at 14,000g at 4°C. The supernatant were then transferred to a new siliconised collection tubes. The protein concentration of each sample were then determined using the Bradford protein assay and microplate luminometer.

1D electrophoresis gels

Stacking gels were constructed to comprise a 1cm height 4% w/v polyacrylamide matrix on top of a 20% w/v polyacrylamide matrix. Protein samples and pre-stained molecular weight markers were each prepared in Sigma 2 x Laemmli sample buffer (1:1) and run into the gels in Tris-glycine running buffer (Invitrogen, Loughborough, UK) for 20 min at 150 V, or until the protein sample and molecular weight markers were observed to concentrate at the 4-20% w/v gel interface. Each sample was loaded onto the gel at 100 µg/well. Following electrophoresis the gels were briefly stained with Imperial protein stain (Pierce, IL, USA) then de-stained in water to visualize the proteins and to confirm their migration as a homogeneous population. The protein band visible at the 4-20% w/v gel interface was excised from each lane.

For separation gels we used the 1 mm thick 10 well Nu-PAGE 4 to 12% Bis-Tris gels from Invitrogen, Carlsbad, CA, USA.

Reduction/Alkylation/trypsin digestion

Gel bands were chopped into small $1mm^3$ pieces then destained and dehydrated with ACN. Proteins were subsequently reduced with 10 mM dithiothreitol in 25 mM ammonium bicarbonate at 56 °C for 1 h and alkylated with 55 mM iodoacetamide in 25 mM ammonium bicarbonate at room temperature for 45 min. Gel pieces were then washed, dried, rehydrated on ice for 10 min in 2 µg of sequence grade trypsin, reconstituted in 100 µL of 25 mM ammonium bicarbonate, then covered with an additional 20 µL ammonium bicarbonate solution, and incubated overnight at 37 °C. The resulting proteolytic peptides were subjected to aqueous (30

µL ammonium bicarbonate, 20 min vortex) and two hydrophobic extractions (100 µL of 50% ACN, 5% formic acid, 20 min vortex, 10 min sonication). Samples were quickly vortexed and centrifuged then frozen to -80°C. The frozen sample were then concentrated under vacuum to ~20 µL, then topped up with 0.1% Formic acid to 70 µL, gel particulates filtered out using 30000MW filters (Millipore), and finally stored at -80 °C until used for LC-MS/MS.

Liquid Chromatography Mass spectrometry (LC-MS/MS).

After freeze/thaw, 10 µL of each sample were injected onto a Thermo pre-column (EASY-Column, 2cm, ID 100µm, 5µm C18-A1), using the Proxeon EASY-nLC II system (Thermo Fisher Scientific). Peptides were then resolved using an increasing gradient of 0.1% formic acid in acetonitirile (5 to 50% over 80 minute) through a Thermo analytical column (EASY-Column, 10cm, ID 75µm, 3µm C18-A2) at a flow rate of 300nL/min. Mass spectra were acquired on an LTQ-Orbitrap Velos (Thermo Fisher Scientific) throughout the chromatographic run (115 minutes), using 20 x CID scans following each FTMS scan (2 x µScans at 30000 resolving power @ 400 m/z). CID was carried out on 20 of the most intense ions from each FTMS scan then put on a dynamic exclusion list for 30 secs (20 ppm m/z window). AGC ion injection target for each FTMS scan were 1000000 (500 ms max injection time). AGC ion injection target for each MSA CID scan were 10000 (50 ms max ion injection time).

Data pre-processing

Peptide identification. Peak lists were extracted from Xcalibur Raw data file format using Proteome Discoverer 1.4 and searched using Mascot 2.2 and Sequest HT search engines. Figure 1 illustrates the overall data analysis workflow used for peptide identification and quantification prior to the statistical analysis. The spectrum files node (0) was used to select the raw data files of interest. Spectrum selector (1) node was set to its default values (data was not smoothed, no signal to noise threshold) and no charge state filtering or de-isotoping took place. Both Mascot (4) and Sequest Nodes (2), were set up to search data against the UniProtKB/Swiss-Prot database (uniprot_sprot.fasta, downloaded from http://www.uniprot.org/downloads 20th February 2013), taxonomy Homo-sapiens (human). These nodes (2; 4) were programmed to search for tryptic peptides with up to 2 missed cleavages (C-Term K/R restrict P), with static modifications set as carbamidomethyl (C). Dynamic

modifications were set to deamidation (N/Q), oxidation (M). Precursor mass tolerance was set to 10ppm and fragment mass tolerance 0.5 Da for both data base search engines. Following peptide identification their q-values were calculated based on target-decoy approach with a 1% false discovery rate (FDR) and filtered in the Percolator node (3). The protein filter 'Peptides per Protein' option was set to 2. Both 'Count only rank 1 peptides' and 'Count peptide only in top scored proteins' were set as active. This ensured the highest stringency at the Protein level. Node 5 represents the 'Event Detector' which clusters isotopes of precursor ions in MS1 spectra that elute during the same retention time, whilst removing noise and spike signals from the spectra used for further processing. It is used in precursor ion quantification and peak area quantification. Node 6 represents the Precursor ions area detector node, calculating the area of each precursor ion. For accuracy it uses an average of the three most abundant peptides rather than the actual peptides to calculate the proteins area. The two data quantification methods that were implemented; Area under the Curve (AUC) (9) and Spectral Counting (10) generated a data matrix (11; 12) that was used for further statistical analysis. The final list (13) was obtained for marker proteins that were common to both quantitation methods and showed differential regulation.

Protein quantification. For each of the 62 tissue specimen data files (n=7 for 8 of the tissue types, n=6 for normal bile duct), Proteome Discover 1.4 was used to export the list of identified proteins to excel. For quantification purposes we utilized the node 'The Precursor Ions Area Detector' (Figure 1 (6)) of Proteome Discoverer 1.4 which calculates the area under the curve (AUC) of each precursor ion using integration. For greater accuracy, it uses an average of the three most abundant peptides per protein rather than all peptides per protein to calculate the protein area. The number of PSMs for each protein in each sample was also used for quantification (spectral counting). Proteome Discoverer results were exported into an Excel sheet containing uniprot accession number, protein name, number of peptide spectrum matches and the protein area for each protein from each sample file. Both number of spectral counts and protein area estimates for each protein in each sample were used for further statistical validation.

Normalization: Both spectral counts and AUC for each protein from each sample

were normalized to compensate for any artifact differences between samples such as unequal loading of protein onto the gel, variable in-gel digestion and peptide extraction and variable injection volume into the LC-MS/MS system. The protein area estimates were $\log_{10}$ transformed prior to normalization. Normalization was done using the following equation;

$$N = \left[\frac{p}{\sum^{n}/_{\tilde{x}}} \right]$$

Where

- N is the normalized value for each protein in each sample
- p is the un-normalized value for each protein in each sample
- $\sum n$ is the total number of PSMs or the total $\log_{10}$ transformed protein area per LC-MS/MS analysis
- $\tilde{x}$ is the median value of $\sum n$ of all the LC-MS/MS analyses

Statistical Analysis

Principal component analysis (PCA) was performed to investigate the multivariate datasets and identify outliers and groups/clusters nested within the datasets. Normalized protein values were used for PCA, which was performed using Simca v. 11, MKS Umetrics AB, Sweden [17].

Hierarchical clustering to build a class hierarchy for tissue types in relation to normalized protein values, alongside statistical analyses to observe differential regulation of proteins between tissue-types were both carried out in MATLAB: The MathWorks Inc., (R2012a) [18]. Two types of hierarchical clustering were performed to group the normalized protein abundances using agglomerative based clustering. In the first approach Pearson's correlation coefficients were obtained by comparing all normalized protein levels in all the samples (62) across all other samples (62), which resulted in a square data matrix consisting of 62x62 r2 Pearson's correlation coefficients. The second clustering was performed using 'city-block' distance metric (also known as the Manhattan distance) with un-weighted average distance (UPGMA) linkage to generate a hierarchical tree. The process clustered all data points first along all the columns (producing row-clustered data), and then along all the rows in the data matrix where rows corresponded to marker proteins and columns corresponded to the samples.

For Tables 2 to 10; the statistical analyses were run using R and the following R packages: q value and MBESS. For each group comparison and each protein an unrelated t-tests was computed to obtain the p value. Then q values (adjusted p values) were computed using a direct False Discovery Rate approach proposed by Storey (A direct approach to false discovery rates. Journal of the Royal Statistical Society, 2002, Series B, 64: 479-498). Hedges' g unbiased standardized effect size estimates were calculated, along with 95% confidence intervals for these estimates (Hedges, L. V. & Olkin, I. (1985). Statistical methods for meta-analysis. New York: Academic press). g < 0.2 are regarded as very small differences, g = 0.5 average differences, g > 0.8 regarded as large differences. Unstandardized effect size estimates (i.e., mean difference) were calculated, along with 95% confidence intervals for these estimates.

For Table 11 (Figure 7) each of the between group (tissue type) comparisons unpaired t-tests were performed for each protein to obtain significance level estimates (p-values) from the protein expression data matrix that consisted of normalized protein areas or normalized Spectral Counts (number of PSMs). A protein was considered to be differentially modulated between the two tissue types when it had a p-value <0.05, $\log_2$ fold ratio > 2 or $\log_2$ fold ratio < -2 (representing fourfold up- and down-regulation respectively). Volcano plots were created using these p-values and $\log_2$ fold changes as described by Cui, X et al and Best, C.J.M et al [19-20].

Immunohistochemistry (IHC)

Four tissue types (normal liver (n=7), normal bile duct (n=6), HCC (n=7), and peripheral CC (n=7)) were used for validation IHC, as these are clinically most important to differentiate. One representative section selected from each case was used for immunostaining. Sections for IHC were taken from the same cases that were analysed by LC-MS. Immunostaining on FFPE specimens was performed using an autostainer Bond Max (Leica Microsystems, Wetzlar, Germany). The deparaffinized sections were heat-treated in a pH6.0 buffer for 10 mins. The primary monoclonal antibodies used were anti-AKR1B10 (clone 1A6; 1:500; Abcam, Cambridge, UK) and anti-tubulin beta 3 (clone TU20; 1:500; Abcam).

Tissue type number key; (as used in Table 11 first column)

1) = Normal liver epithelium (Hepatocytes).

2)= Hepatocellular carcinoma.Combined hepato-cholangiocellular carcinoma after TACE therapy i.e.

3) = areas of hepatocellular differentiation, and

4) = areas of cholangiocellular differentiation.

5) = Peripheral (intrahepatic) cholangiocarcinoma.

6) = Hilar cholangiocarcinoma originated in patients without primary sclerosing cholangitis.

7) = Hilar cholangiocarcinoma originated in patients with primary sclerosing cholangitis.

8) = Metastatic colo-rectal carcinoma.

9) = Normal biliary epithelium (Cholangiocytes).

4.2 RESULTS

Protein markers identification

In total 2864 proteins were identified using rank 1 peptides at 1 %FDR at peptide level (≥2 rank 1 peptides per protein ID). Of the 2864 proteins 2628 (92%) had at least 1 unique peptide sequence and 2009 (70%) proteins had only unique peptide sequences. It was further observed that 236 (8%) proteins out of 2864 proteins had only shared peptide sequences. Of the 619 proteins with unique and shared peptides the inventors performed quantification using only unique peptides and compared this quantification to using the unique&shared peptides and found a correlation of 0.99 when comparing the fold change values from the two datasets (0.992 for spectral counting and 0.999 for area under the curve). Thus, as there appears to be no detrimental effect on accuracy using the shared and unique peptides, compared to only unique peptides, and due to the additional coverage gained by using shared and unique peptides, the

inventors present results here obtained using shared and unique peptide sequences from both spectral counting and AUC forms of quantitation in the main text (Table 1, Table 11).

Protein quantification and hierarchical clustering

The inventors found 1072 proteins significantly regulated in at least one of the tissue type comparisons when using the area under the curve dataset, while 611 proteins were significantly regulated using the spectral counting dataset (in at least one of the tissue type comparisons). A total of 467 marker proteins were found to be significantly regulated in at least one of the tissue type comparisons, as observed in both quantification methods (e.g. common to both spectral counting (right) and AUC (left) in the Venn-Diagram in Figure 2). PCA bi-plots using area under the curve (AUC) dataset (Figure 3A) and spectral counting dataset (Figure 3B) for these 467 common marker proteins shows clear separation between tissue types/groups that consists of cells that have common origin. Tissue types 1, 2 and 3 (left side of the plot, outer ellipse in Figures 3A and 3B)were all hepatocellular in origin and tissue types 4 to 9 (ellipse at right side of the plot in Figures 3A and 3B)belonged to glandular epithelium which clearly separated across two planes of the Bi-plot. Within each bi-plot it can also be seen that all cases of normal liver parenchyma (tissue type -1) are close to each other (left side of the plot, inner ellipse in Figures 3A and 3B).

Hierarchal clustering of the same 467 common marker proteins also supported the results obtained using PCA which clusters hepatocellular tissue types from glandular epithelium. Clustering of these 467 marker proteins based on Pearson's correlation coefficients and on protein data matrix using normalized protein area values clustered samples that originated from tissue types 1, 8 and 9 within single nested sub-groups (data not shown). Although using spectral counting as a data matrix produced similar results, it was found that area under curve data matrix produced better separation between groups when hierarchical clustering was performed. Table 1 illustrates the number of differentially modulated marker proteins that were common to both area under the curve and spectral counting datasets per tissue type comparison.

Difference in protein expression profiling among 9 tissue types

Post-TACE mixed cancer: Although HCC and CC components of post-TACE cancer are theoretically same in origin, these two areas showed significantly different protein markers' profiles as clearly demonstrated by PCA (Figure 3) and hierarchal clustering (data not shown). In total 95 marker proteins were shown to be significantly modulated in the post-TACE HCC regions compared to the CC regions. Among the 95 marker proteins, 60 (63%) were overlapped with molecules that were identified in the comparison between normal liver parenchyma and bile duct (see below), in keeping with the hypothesis that post-TACE cancers can show bilineage differentiation. Seventy-eight marker proteins were found to be more abundant in HCC components, whereas 17 marker proteins were significantly up-regulated in CC areas. Two and five marker proteins showed significant difference between HCC components of post-TACE cancer and conventional HCC, and between CC components of post-TACE cancer and peripheral CC, respectively (Table 1). Names of those marker proteins are available in Table 11.

***Normal liver parenchyma vs. normal bile duct*:** (See Table 6) Over 200 marker proteins were expressed at significantly different levels between normal liver and bile duct (Table 1 and Table 6). About a half of those marker proteins were liver enzymes, which were more abundantly present in normal liver parenchyma. In contrast, marker proteins that were more strongly expressed in normal bile ducts were diverse, including keratins 7 and 19, annexins, and galectins (Table 11).

Normal liver parenchyma vs. HCC: (See Table 2) Among 11 marker proteins that showed statistically significant difference between normal liver parenchyma and HCC, 5 marker proteins (14-3-3 protein eta, Aldo-keto reductase family 1 member B10 [AKR1B10], Heterogeneous nuclear ribonucleoprotein R, Histone H1.5, Keratin type II cytoskeletal 6B) appeared overexpressed in the cancer tissue. The remaining six, which were less abundant in HCC, were mostly liver enzymes supposed to represent mature hepatocyte functions. In accordance with the invention the one or more, or plurality of marker marker proteins may be selected from the group consisting of 14-3-3 protein eta, Aldo-keto reductase family 1 member B10 [AKR1B10], Heterogeneous nuclear ribonucleoprotein R, Histone H1.5, Keratin type II cytoskeletal 6B.

Normal bile duct vs. peripheral or hilar CC: (See Tables 3 and 4) Numbers of marker proteins that showed statistically significant difference between normal and neoplastic bile ducts are 37 for peripheral CC and 32 for hilar CC (Table 1, Table 11). Six and eight marker proteins were significantly overexpressed in peripheral and hilar CC, respectively. Among them, 3 marker proteins (Tubulin-beta 3 chain, Periostin, Collagen alpha-1(XII) chain) were up-regulated in both types of CC. Fourteen marker proteins were significantly less abundant in both types of CCs. In accordance with the invention the one or more, or plurality of marker proteins may be selected from the group consisting of Tubulin-beta 3 chain, Periostin, and Collagen alpha-1(XII) chain.

The one or more, or plurality of marker proteins may also be selected from argininosuccinate lyase, N9G), N9G)-dimethylarginine dimethylaminohydrolase 1A and 1B, Filamin-A and plastin-3.

HCC vs. peripheral CC: (See Table 5) One hundred and sixty-five marker proteins showed statistically significant differences between these two types of cancers, which develop in the liver parenchyma (Table 1, Table 4 and Table 11). Most marker proteins that were overexpressed in HCC were liver enzymes or mitochondrial marker proteins, whereas marker proteins that were up-regulated in peripheral CC were diverse in function including cell-cell adhesion, cell migration, and signal transduction. Multi-functional marker proteins such as annexins and S100-A11 were also more abundantly present in peripheral CC. Ninety-six marker proteins (58%) were overlapped with marker proteins that were identified in the comparison between normal liver parenchyma and normal bile duct.

Peripheral CC vs. hilar CC: These two types of CC are both adenocarcinoma of the biliary epithelium in origin. Interestingly, 14 showed significant differences between peripheral and hilar CC. For example, MUC5AC, a gastric type mucin, was significantly more abundant in hilar CC, while Tenascin was upregulated in peripheral CC. In accordance with the present invention, the protein markers may include MUC5AC and Tenascin.

PSC-associated CC vs. hilar CC:*(Table 9)* These two types of CC are histologically indistinguishable. But 5 marker proteins

(Alpha-1B-glycoprotein, Asporin, Decorin, Methyl-CpG-binding protein 2, and Mimecan) were significantly different in abundance between PSC-associated and conventional hilar CC. All of these were more abundant in hilar CC unrelated to PSC. In accordance with the present invention, the one or more, or plurality of marker proteins may be selected from the group consisiting of Alpha-1B-glycoprotein, Asporin, Decorin, Methyl-CpG-binding protein 2, and Mimecan.

Peripheral or hilar CC vs. colorectal metastasis: (See Table 10) There were only 29 marker proteins expressed at significantly different levels in peripheral CC vs. colorectal metastasis and 63 marker proteins expressed at significantly different levels in hilar CC vs. colorectal metastasis (Table 1, Table 10, Table 11). Keratin 20, which is the most commonly used intestinal marker in routine pathological examination, did not reach statistical significance in this tissue comparison. Marker proteins that were significantly more abundant in CCs included annexins A4 and A5, protein-glutamine gamma-glutamyltransferase 2, and plasma protease C1 inhibitor.

AKR1B10 and Tubulin-beta 3 were investigated further by Volcano plots and Immuno-hystochemistry as a validation study. AKR1B10 was chosen as it is significantly upregulated in HCC than in normal liver or peripheral CC, suggesting that this may become a diagnostic marker specific to HCC. Tubulin-beta 3 was significantly up-regulated in peripheral CC than in either tissue type of normal liver, HCC, or normal bile duct, suggesting Tubulin-beta 3 to have a diagnostic value specific to peripheral CC. The inventors focused on four tissue types: normal liver parenchyma, HCC, normal bile duct, and peripheral CC, as they are clinically most important to differentiate.

AKR1B10 (O60218) is up-regulated in HCC (tissue type 2) (Figure 4, upper panels) as statistically significant (p-value 2.83E-02 and log 2 fold change 2.95) when compared to normal liver parenchyma (tissue type 1) using AUC data matrix for quantitation. Spectral counting data also demonstrates statistically significant increase of AKR1B10 in HCC versus normal tissue (p-value 7.93 E-04 and log 2 fold change 3.87). AKR1B10 was surprisingly found to be up-regulated in normal bile duct (tissue type 9) when compared to normal liver parenchyma.

On immunostaining, AKR1B10 was only focally expressed in normal liver, while this was more diffusely positive in HCC (Figure 5). AKR1B10 was also moderately expressed in cirrhotic liver (background of HCC), suggesting this to be up-regulated at the early stage of multi-step hepato-carcinogenesis. AKR1B10 was diffusely positive in normal bile duct, and patchily positive in peripheral CC, in keeping with the proteomics results (Table 1).

Tubulin-beta 3 chain (Q13509) was found to be up-regulated in peripheral CC (tissue type 5) when compared to normal liver parenchyma or normal bile duct. Tubulin-beta 3 chain was surprisingly completely negative in normal liver, HCC, and normal bile duct, while it was diffusely expressed in 5 of 7 cases of peripheral CC (Figure 5).

Finally, Figure 6 shows the spectral counts obtained with respect to the expression of the marker proteins indicated therein in tissue types under study.

4.3 DISCUSSION

The inventors have shown that the combination of laser microdissection and LC-MS/MS proteomics is a powerful approach which allows extensive profiling of protein expression in selected tumor sub-populations. This technique can be applied to FFPE histological archival material, a major advantage in the design of both prospective and retrospective tissue based studies. The identification of marker proteins already known to be specific to certain lineages (e.g. keratins 7 and 19 in biliary epithelium [21]), supports the robustness of the technique. The inventors have identified sets of marker proteins specific to well characterised hepato-biliary lineages and their neoplastic counterparts, and which could be used as biomarkers with diagnostic and prognostic potential, therapeutic targets or to understand the underlying carcinogenetic processes.

The identification of protein sets specific to the hepatocellular and cholangiocellular phenotype of post-TACE mixed tumors, and their similarity to their normal and typical neoplastic counterparts confirms that the differentiation process is truly divergent, despite a probable origin from a common progenitor. Of equal importance is the identification of marker

proteins differentially expressed between normal and neoplastic hepatocytes and biliary epithelial cells, as these provide markers of malignant transformation or tumor differentiation; and between HCC and peripheral CC, which often overlap in both clinical presentation, and appearance on imaging and histology [22-23]. Of note alpha-fetoprotein (AFP), a marker commonly increased in the serum of patients with HCC [2], was not identified in any tissue type in this study. This is probably due to expression levels in tissue samples being below the LC-MS/MS detection threshold. Serum AFP levels are known to be elevated in about 75% of patients with HCC, but its expression in tissue is detectable in than 40% of patients even by IHC [24-25].

Interestingly one (14-3-3 protein eta) of the five marker proteins (14-3-3 protein eta; AK1BA; H15 and K2C6B) shown to be significantly over-expressed in HCC compared to normal liver parenchyma is known to play a role in mechanisms known to contribute to the cancer phenotype, as the abnormal expression of 14-3-3 protein eta has been reported in some human neoplasms [26-27]. Another two (Heterogeneous nuclear ribonucleoprotein R and Histone H1.5) are involved in gene transcription through chromatin remodeling, DNA methylation, and processing of precursor mRNA in the nucleus. The inventors also identified AKR1B10 as a significantly upregulated protein in HCC, which was validated by additional IHC. This finding is in keeping with a previous study, where a random-based gene fishing approach identified AKR1B10 as a significantly up-regulated gene in HCC compared to non-neoplastic liver tissue [28].

The inventors were also interested in molecules that were specifically up-regulated in CCs. Three marker proteins (Tubulin-beta 3 chain, Periostin, Collagen alpha-1(XII) chain) were up-regulated in CC compared to normal bile duct. Tubulin-beta 3 is the major constituent of microtubules and plays a critical role in proper axon guidance and maintenance. Periostin induces cell attachment and spreading and plays a role in cell adhesion. Collagen alpha-1(XII) interacts with type I collagen-containing fibrils, which are known to be overexpressed in invasive breast carcinoma [11]. Increased deposition and aberrant cross-linking of collagen is associated with the development of invasive breast cancer, the result of which contributes to stiffening of the extracellular matrix and is a factor that has been shown to drive progression of in situ disease [11]. The overexpression of these three

marker proteins in CCs, and their known functional roles in biology and pathology means they will be useful markers of CC.

The three types of CCs are histologically very similar. Only a small number of markers that show significant difference in abundance between peripheral and hilar CCs have been identified [29]. The invention provides at least 5 such marker proteins, which may represent different underlying carcinogenetic processes. PSC-associated CC is supposedly different from conventional CC in underlying molecular events. However, these two types of CCs are histologically almost identical with no reliable molecular discriminators. No oncogenes or tumor suppressor genes specifically involved in PSC-associated carcinogenesis have been identified to the best of the inventors' knowledge. The inventors have identified 5 significantly modulated marker proteins between these two tissue types, all less abundant in PSC-associated CC.

In conclusion, the inventors have shown that the combination of laser microdissection and LC-MS/MS allows comprehensive proteomic profiling of tumor cell subpopulations and is applicable to FFPE archival tissue. The inventors have identified biomarkers, in particular Collagen alpha 1 (XVIII) chain, Plastin-3, AKR1B10, Fibronectin, Beta 3 tubulin, Asporin, 14-3-3 protein eta and Dihydropyrimidinase-related protein 3, to be used in the distinction between non-neoplastic and neoplastic hepatocytes and biliary epithelial cells, to refine grading of tumor differentiation, in the differential diagnosis of primary liver tumors, and to investigate the pathogenesis of sub-types of cholangiocarcinoma.

5. References

1. Bosman FT, Carneiro F, Hruban RH, Theise ND. WHO Classification of Tumors of the Digestive System, 4th Ed. Lyom: IARC; 2010.

2. El-Serag HB. Hepatocellular carcinoma. N Engl J Med. 2011:365;1118-27.

3. Blechacz B, Komuta M, Roskams T, Gores GJ. Clinical diagnosis and staging of cholangiocarcinoma. Nat Rev Gastroenterol Hepatol. 2011:8;512-22.

4. Alison MR. Liver stem cells: implications for hepatocarcinogenesis. Stem Cell Rev. 2005;1:253-60.

5. Marquardt JU, Factor VM, Thorgeirsson SS. Epigenetic regulation of cancer stem cells in liver cancer: current concepts and clinical implications. J Hepatol. 2010:53;568-77.

6. Zen C, Zen Y, Mitry RR, Corbeil D, Karbanová J, O'Grady J, Karani J, Kane P, Heaton N, Portmann BC, Quaglia A. Mixed phenotype hepatocellular carcinoma after transarterial chemoembolization and liver transplantation. Liver Transpl. 2011:17;943-54.

7. Aebersold R, Mann M. Mass spectrometry-based proteomics. Nature. 2003;422:198-207.

8. Ong SE, Mann M. Mass spectrometry-based proteomics turns quantitative. Nat Chem Biol. 2005;1:252-62.

9. Shi SR, Liu C, Balgley BM, Lee C, Taylor CR. Protein extraction from formalin-fixed, paraffin-embedded tissue sections: quality evaluation by mass spectrometry. J Histochem Cytochem. 2006;54:739-43.

10. Krizman DB & Burrows J. Use of Formalin-Fixed, Paraffin-Embedded Tissue for Proteomic Biomarker Discovery. Proteomics for Biomarker Discovery: Methods and Protocols, Methods in Molecular Biology. 2013: vol. 1002, p85-92.

11. Bateman NW, Sun M, Bhargava R, Hood BL, Darfler MM, Kovatich AJ, Hooke JA, Krizman DB, Conrads TP. Differential proteomic analysis of late-stage and recurrent breast cancer from formalin-fixed paraffin-embedded tissues. J Proteome Res. 2011:10(3):1323-32.

12. Patel V, Hood BL, Molinolo AA, Lee NH, Conrads TP, Braisted JC, Krizman DB, Veenstra TD, Gutkind JS. Proteomic analysis of laser-captured paraffin-embedded tissues: a molecular portrait of head and neck cancer progression. Clin Cancer Res. 2008. 14(4):1002-14.

13. Azimzadeh O, Scherthan H, Yentrapalli R, Barjaktarovic Z, Ueffing M, Conrad M, Neff F, Calzada-Wack J, Aubele M, Buske C, Atkinson MJ, Hauck SM, Tapio S. Label-free protein profiling of formalin-fixed paraffin-embedded (FFPE) heart tissue reveals immediate mitochondrial impairment after ionising radiation. J Proteomics. 2012;75(8):2384-95.

14. Bantscheff M, Schirle M, Sweetman G, Rick J, Kuster B. Quantitative mass spectrometry in proteomics: a critical review. Anal Bioanal Chem. 2007;389:1017-31.

15. Liu H, Sadygov RG, Yates JR. 3rd. A model for random sampling and estimation of relative protein abundance in shotgun proteomics. Anal Chem. 2004;76:4193-201.

16. Bruix J, Sherman M, Llovet JM, Beaugrand M, Lencioni R, Burroughs AK, Christensen E, Pagliaro L, Colombo M, Rodés J; EASL Panel of Experts on HCC. Clinical management of hepatocellular carcinoma. Conclusions of the Barcelona-2000 EASL conference. European Association for the Study of the Liver. J Hepatol. 2001;35:421-30.

17. Kettaneh, N., Berglund, S., and Wold, S., (2005), PCA and PLS with Very Large Data Sets, Computational Statistics & Data Analysis, 48, 69-85.

18. Bar-Joseph, Z., Gifford, D.K., and Jaakkola, T.S. (2001). Fast optimal leaf ordering for hierarchical clustering. Bioinformatics 17, Suppl 1:S22 – 9. PMID: 11472989.

19. Cui, X., Churchill, G.A. (2003). Statistical tests for differential expression in cDNA microarray experiments. Genome Biology 4, 210.

20. Best, C.J.M., Gillespie, J.W., Yi, Y., Chandramouli, G.V.R., Perlmutter, M.A., Gathright, Y., Erickson, H.S., Georgevich, L., Tangrea, M.A., Duray, P.H., Gonzalez, S., Velasco, A., Linehan, W.M., Matusik, R.J., Price, D.K., Figg, W.D., Emmert-Buck, M.R., and Chuaqui, R.F. (2005). Molecular alterations in primary prostate cancer after androgen ablation therapy. Clinical Cancer Research 11, 6823–6834.

21. Chu PG, Weiss LM. Keratin expression in human tissues and neoplasms. Histopathology 2002;40;403-39.

22. Vilana R, Forner A, Bianchi L, García-Criado A, Rimola J, de Lope CR, Reig M, Ayuso C, Brú C, Bruix J. Intrahepatic peripheral cholangiocarcinoma in cirrhosis patients may display a vascular pattern similar to hepatocellular carcinoma on contrast-enhanced ultrasound. Hepatology 2010;51;2020-9.

23. Sempoux C, Jibara G, Ward SC, Fan C, Qin L, Roayaie S, Fiel MI, Schwartz M, Thung SN. Intrahepatic cholangiocarcinoma: new insights in pathology. Semin Liver Dis. 2011;31;49-60.

24. Liu C, Xiao GQ, Yan LN, Li B, Jiang L, Wen TF, Wang WT, Xu MQ, Yang JY. Value of α-fetoprotein in association with clinicopathological features of hepatocellular carcinoma. World J Gastroenterol. 2013;19:1811-9.

25. Porcell AI, De Young BR, Proca DM, Frankel WL. Immunohistochemical analysis of hepatocellular and adenocarcinoma in the liver: MOC31 compares favorably with other putative markers. Mod Pathol. 2000;13:773-8.

26. Wang Z, Nesland JM, Suo Z, Trope CG, Holm R. The prognostic value of 14-3-3 isoforms in vulvar squamous cell carcinoma cases: 14-3-3β and ε are

independent prognostic factors for these tumors. PLoS One. 2011;6:e24843.

27. Yang X, Cao W, Lin H, Zhang W, Lin W, Cao L, Zhen H, Huo J, Zhang X. Isoform-specific expression of 14-3-3 proteins in human astrocytoma. J Neurol Sci. 2009;276:54-9.

28. Heringlake S, Hofdmann M, Fiebeler A, Manns MP, Schmiegel W, Tannapfel A. Identification and expression analysis of the aldo-ketoreductase1-B10 gene in primary malignant liver tumors. J Hepatol. 2010;52:220-7.

29. Guedj N, Zhan Q, Perigny M, Rautou PE, Degos F, Belghiti J, Farges O, Bedossa P, Paradis V. Comparative protein expression profiles of hilar and peripheral hepatic cholangiocarcinomas. J Hepatol. 2009;51;93-101.

What is claimed:

1. A method of determining the cellular phenotype of a liver tissue sample said method comprising:

(1) extracting marker proteins from said liver tissue sample;

(2) determining expression levels of a plurality of marker proteins in said liver tissue sample, wherein said plurality of marker proteins are selected from a biomarker panel as represented by any one of Table 1A, Tables 2 to 11; optionally, repeating step (2) with a different plurality of marker proteins selected from a biomarker panel as represented by any one of Table 1A, Tables 2 to 11;

(3) comparing said determined expression levels with reference set of expression levels for said plurality of marker proteins in known cellular phenotypes, thereby determining the cellular phenotype of the liver tissue sample.

2. A method of identifying the cellular phenotype of a liver cell, said method comprising:

(1) determining expression levels of a plurality of marker proteins in said liver cell;

(2) comparing said determined expression levels with reference set of expression levels for said plurality of marker proteins, said reference levels representing a cellular phenotype;

(3) identifying the cellular phenotype of the liver cell based on the comparison between the expression levels of the marker proteins in the liver cell and the reference expression levels;

wherein the plurality of marker proteins are selected from a biomarker panel as represented by any one of Table 1A, Tables 2 to 11.

3. A method according to claim 1 or claim 2 wherein the cellular phenotype is selected from normal liver epithelium cells (hepatocytes), normal biliary epithelium cells (cholangiocytes), hepatocellular carcinoma cells, peripheral cholangiocellular carcinoma cells or hilar cholangiocellular carcinoma cells.

4. A method according to any one of claims 1 to 3 further comprising comparing said expression levels with a second reference set of expression levels representing a second cellular phenotype.

5. A method according to any one of claims 2 to 4 wherein the liver cell is a liver tumor cell.

6. A method according to anyone of the preceding claims wherein the biomarker panel is represented by Table 5 and/or Table 7 and the cellular phenotype is selected from hepatocellular carcinoma cells and cholangiocellular carcinoma cells.

7. A method according to claim 6 wherein the plurality of marker proteins is selected from part A of Table 5.

8. A method according to any one of claims 5 to 7 wherein the liver tumor cell is obtained from a liver tumor biopsy sample.

9. A method according to claim 8 wherein the liver tumor biopsy was obtained from a patient having previously been treated with transarterial chemoembolization.

10. A method according to claim 6 wherein the plurality of marker proteins are selected from Table 7.

11. A method according to claim 10 wherein the plurality of marker proteins are selected from Table 7 part A.

12. A method according to any one of the preceding claims wherein the step of determining the expression levels of a plurality of marker proteins comprises:

(a) contacting the liver cell or the liver tissue sample with a plurality of binding members, wherein each binding member selectively binds to one of said plurality of marker proteins or nucleic acid sequences encoding said marker proteins; and

(b) detecting and/or quantifying a complex formed by said specific binding members and marker proteins or nucleic acid sequences encoding said marker proteins.

13. A method according to claim 12 wherein the specific binding member is an antibody or antibody fragment which selectively binds to one of said plurality of marker proteins.

14. A method according to claim 12 wherein the specific binding member is a nucleic acid sequence which selectively binds to nucleic acid encoding one of said plurality of marker proteins.

15. A method according to claim 12 wherein said specific binding member is an aptamer.

16. A method according to any one of claims 12 to 15 wherein the binding member is immobilised on a solid support.

17. A method according to any one of claims 1 to 11 wherein said step of determining expression levels of a plurality of marker proteins is performed by mass spectrometry.

18. A method according to any one of claims 1 to 11 wherein said step of determining expression levels of a plurality of proteins is performed by Selected Reaction Monitoring using one or more transitions for protein derived peptides; and comparing the peptide levels in the liver cell or the liver tissue sample under test with peptide levels previously determined to represent a cellular phenotype.

19. A method according to claim 18 wherein comparing the peptide levels includes determining the amount of protein derived peptides from the liver cell or the liver tissue sample with known amounts of corresponding synthetic peptides, wherein the synthetic peptides are identical in sequence to the peptides obtained from the liver cell or the liver tissue sample except for a label.

20. A method according to claim 19 wherein the label is a tag of a different mass or a heavy isotope.

21. A method for the diagnosis or prognostic monitoring of a liver tumor in an individual, said method comprising:

(a) determining the presence or level of expression of a plurality of marker proteins selected from a biomarker panel as represented by any one of Table 1A, Tables 2 to 11, in a liver tumor cell obtained from said individual;

(b) identifying the cellular phenotype of the liver tumor cell; and

(c) selecting a diagnosis or prognosis based on the cellular phenotype of the liver tumor cell.

22. A method for determining a treatment regimen for an individual having a liver tumor, said method comprising:

(a) determining the presence or level of expression of a plurality of marker proteins selected from a biomarker panel as represented by any one of Table 1A, Tables 2 to 11, in a liver tumor cell obtained from said individual;

(b) identifying the cellular phenotype of the liver tumor cell; and

(c) selecting a treatment regimen based on the cellular phenotype of the liver tumor cell.

23. A method according to claim 21 or claim 22 wherein the liver tumor cell is from a liver tumor biopsy.

24. A method according to any one of claims 21 to 23 wherein the biomarker panel is represented by Table 5.

25. A method according to claim 24 wherein the biomarker panel is represented by Part A of Table 5.

26. A method according to any one of claims 21 to 23 wherein said individual had previously been treated with transarterial chemoembolization.

27. A method according to claim 26 wherein the biomarker panel is represented by Table 7.

28. A method according to claim 27 wherein the biomarker panel is represented by Part A of Table 7.

29. A method of diagnosing liver cancer in an individual comprising detecting one or more marker proteins or fragments thereof selected from Table 1A, Tables 2 to 11 in a blood, tissue, saliva or urine sample obtained from said individual.

30. A method according to claim 29 wherein said one or more protein markers or fragments thereof are detecting using a specific binding member.

31. A method according to claim 30 wherein said binding member is an antibody specific for said one or marker protein.

32. A method according to any one of claims 1 to 31 wherein the plurality of marker proteins are selected from any one of Collagen alpha 1 (XVIII) chain, Plastin-3, AKR1B10, Fibronectin, Beta 3 tubulin, Asporin, 14-3-3 protein eta, Dihydropyrimidinase-related protein 3 or combinations thereof.

33. A method according to claim 32 wherein the plurality of marker proteins comprises AKR1B10 and/or Beta 3 tubulin.

34. Use of one or more marker proteins selected from Table 1A, Tables 2 to 11 as a diagnostic marker for liver cancer.

35. A method for diagnosing recurrent or primary liver tumor in a subject, the method comprising determining the presence or absence of one or more marker proteins selected from the group consisting of Collagen alpha 1 (XVIII) chain, Plastin-3, AKR1B10, Fibronectin, Beta 3 tubulin, Asporin, 14-3-3 protein eta, and Dihydropyrimidinase-related protein 3 in a sample.

36. The method according to claim 35, wherein the marker protein is Beta 3 tubulin and/or AKR1B10.

37. The method according to claim 35, wherein the marker proteins is Beta 3 tubulin.

38. The method according to any one of claims 35 to 37, wherein the sample is selected from any one of blood, plasma, serum, liver tissue, liver cells or combinations thereof.

39. The method according to claim 38, wherein the sample is liver tissue, optionally formalin-fixed paraffin-embedded liver tissue section.

40. The method according to any one of claims 35 to 39, wherein determining the presence or absence of one or more marker proteins in the sample is performed by either Immuno-hystochemistry (IHC) or mass-spectrometry.

41. The method according to any one of claims 35 to 40, wherein the liver tumor is selected from the group consisting of hepatocellular carcinoma, peripheral cholangiocellular carcinoma or hilar cholangiocellular carcinoma cells.

42. A kit for diagnosing recurrent or primary liver tumor in a subject, the kit comprising reagents for determining the presence or absence of one or more marker proteins selected from the group consisting of Collagen alpha 1 (XVIII) chain, Plastin-3, AKR1B10, Fibronectin, Beta 3 tubulin, Asporin, 14-3-3 protein eta, and Dihydropyrimidinase-related protein 3 in a sample.

43. The kit according to claim 41, wherein the marker protein is Beta 3 tubulin and/or AKR1B10.

44. The kit according to claim 43, wherein the marker proteins is Beta 3 tubulin.

45. The kit according to any one of claims 42 to 44, wherein the kit comprises reagents suitable for preparing the sample, wherein the sample is selected from any one of blood, plasma, serum, liver tissue, liver cells or combinations thereof.

46. The kit according to claim 45, wherein the sample is liver tissue and wherein the kit comprises reagents suitable for preparing liver tissue, optionally for preparing formalin-fixed paraffin-embedded liver tissue sections.

47. The kit according to any one of claims 42 to 46, wherein determining the presence or absence of of one or more marker proteins in the sample is performed by either Immuno-hystochemistry.

48. The kit according to any one of claims 42 to 47, wherein the liver tumor is selected from the group consisting of hepatocellular carcinoma, peripheral cholangiocellular carcinoma or hilar cholangiocellular carcinoma cells.

49. A kit for use in determining the cellular phenotype of a liver cell *in vitro*, said kit allowing the user to determine the presence or level of expression of a plurality of marker proteins or fragments thereof provided in biomarker panels represented by Tables 2 to 11, in a cell under test; the kit comprising:

(a) a set of reference peptides in an assay compatible format wherein each peptide in the set is uniquely representative of one of the plurality of marker proteins provided in any one of Table 1A, Tables 2 to 11; and, optionally

(b) one or more components selected from the group consisting of washing solutions, diluents and buffers.

50. A kit for the diagnosis or prognostic monitoring of a liver tumor in an individual, the kit comprising:

(a) a solid support having a plurality of binding members immobilised thereon, wherein each binding member selectively binds to a protein selected from a biomarker panel as represented by any one of Table 1A, Tables 2 to 11; or a nucleic acid encoding the protein or fragment thereof;

(b) a developing agent comprising a label; and

(c) one or more components selected from washing solutions, diluents and buffers.

51. A kit for determining a treatment regimen for an individual having a liver tumor, the kit comprising

(a) a solid support having a plurality of binding members immobilised thereon, wherein each binding member selectively binds to a protein selected from a biomarker panel as represented by any

one of Table 1A, Tables 2 to 11; or a nucleic acid encoding the protein or fragment thereof;

(b) a developing agent comprising a label; and

(c) one or more components selected from washing solutions, diluents and buffers.

52. A kit according to claim 51 wherein the biomarker panel is represented by Table 5 or Part A of Table 4.

53. A kit according to claim 51 wherein the biomarker panel is represented by Table 7 or Part A of Table 7.

54. A plurality of synthetic peptides each having a sequence identical to a fragment of one of a plurality of proteins selected from a biomarker panel selected from any one of Table 1A, Tables 2 to 11, said fragment resulting from digestion of the protein by trypsin, ArgC, AspN or Lys-C digestion, wherein one or more of the plurality of synthetic peptides comprises a label.

55. A plurality of synthetic peptides according to claim 54 wherein the label is a heavy isotope.

56. A plurality of synthetic peptides according to claim 54 or claim 55 for use in Selective Reaction Monitoring.

57. A liver cellular classification system comprising a liver cellular classification apparatus and an information communication terminal apparatus, said liver cellular classification apparatus including a control component and a memory component, said apparatuses being communicatively connected to each other via a network;

(1) wherein the information communication terminal apparatus includes

(1a) a protein data sending unit that transmits the protein data derived from a liver tissue sample of a subject to the liver cellular classification apparatus;

(1b) a result-receiving unit that receives the result of the liver cellular classification of the subject transmitted from the liver cellular classification apparatus;

(2) wherein the liver cellular classification apparatus includes

(2a) a protein data-receiving unit that receives protein data derived from the liver tissue sample of the subject transmitted from the information communication terminal apparatus;

(2b) a data comparison unit which compares the data from the data-receiving unit with the data stored in the memory unit;

(2c) a classifier unit that determines the class (e.g. cellular phenotype) of the liver tissue of the subject, based on the results of the data comparison unit; and

(2d) a classification result-sending unit that transmits the classification result of the subject obtained by the classifier unit to the information communication terminal apparatus; and

wherein the memory unit contains protein expression level data of at least one protein selected from any one or more of Table 1A, Tables 2 to 10 or Table 11.

58. A liver cellular classification system according to claim 57 wherein the memory unit contains data of a plurality of proteins selected from Table 5 or Table 11 and wherein the classification is between Hepatocellular carcinoma and peripheral cholangiocarcinoma.

59. A liver cellular classification system according to claim 57 wherein the memory unit contains data of a plurality of proteins selected from Table 7 or Table 11 and wherein the classification is between Hepatocellular carcinoma and cholangiocarcinoma in post-TACE liver tumors.

60. A liver cellular classification system according to any one of claims 57 to 59 connected to an apparatus for determining the protein expression levels in a liver tissue sample.

61. A liver cellular classification system according to claim 58 wherein said apparatus can process multiple samples using liquid chromatography-mass spectrometry (LC-MS/MS).

62. A liver tissue cellular classification program that makes an information processing apparatus including a control component and a memory component execute a method of determining and/or classifying the liver tissue of a subject, the method comprising:

(i) a comparing step of comparing data based on the protein expression levels of at least one (preferably a plurality) protein selected from any one of Table 1A, Tables 2 to 11 obtained of a subject with the protein expression level data stored in the memory component; and

(ii) a classifying step for classifying the liver tissue cells of said subject, based on the comparison calculated at the comparing step; and wherein said tissue is classified into phenotypes including normal (hepatocytes, cholangiocytes), hepatocellular carcinoma, hepatocholangiocellular carcinoma (pre or post TACE therapy), peripheral cholangiocarcinoma, Hilar cholangiocarcinoma (with or without primary sclerosing cholangitis), or metastatic colo-rectal carcinoma.

63. A computer-readable recording medium, comprising the liver tissue cellular classification program of claim 60 recorded thereon.

Fig. 1

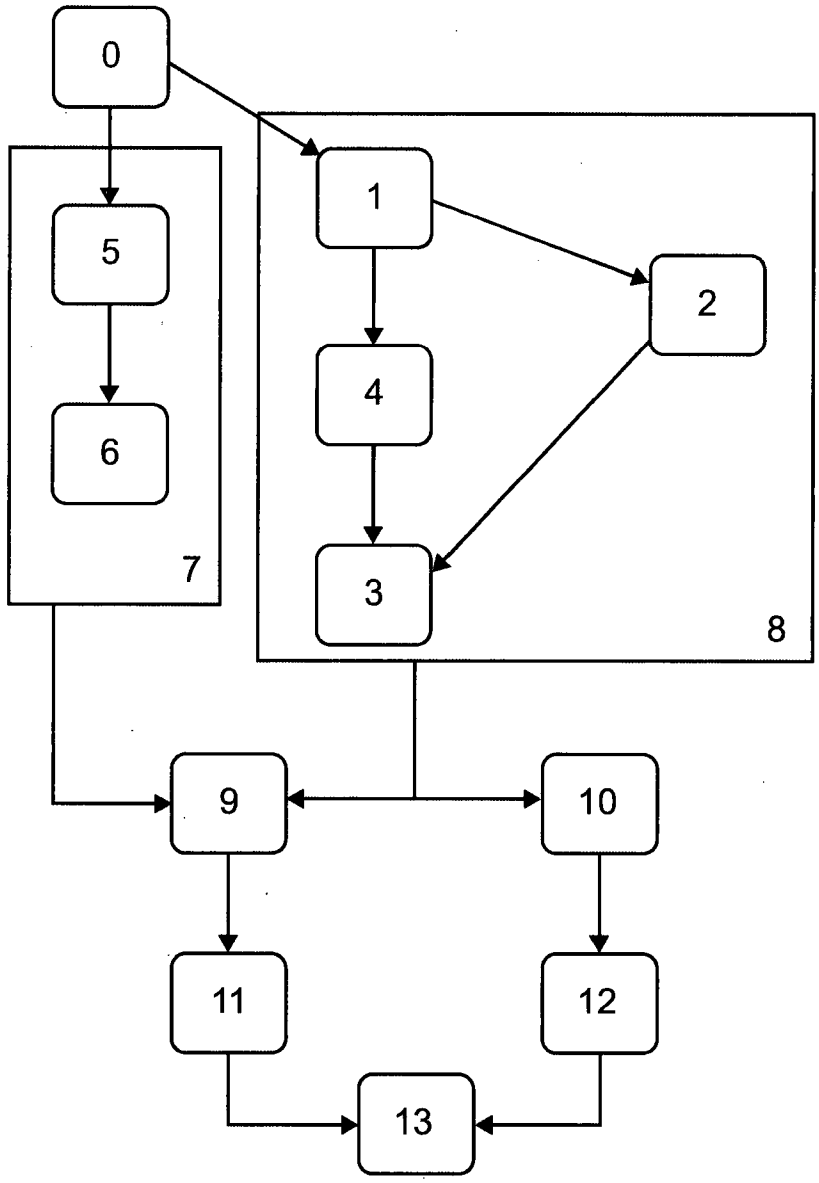
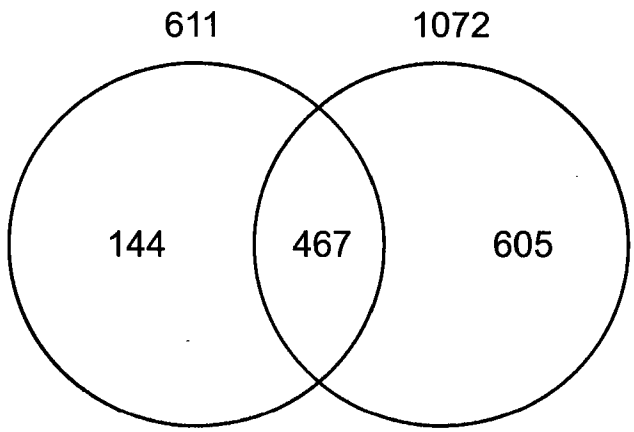


Fig. 2



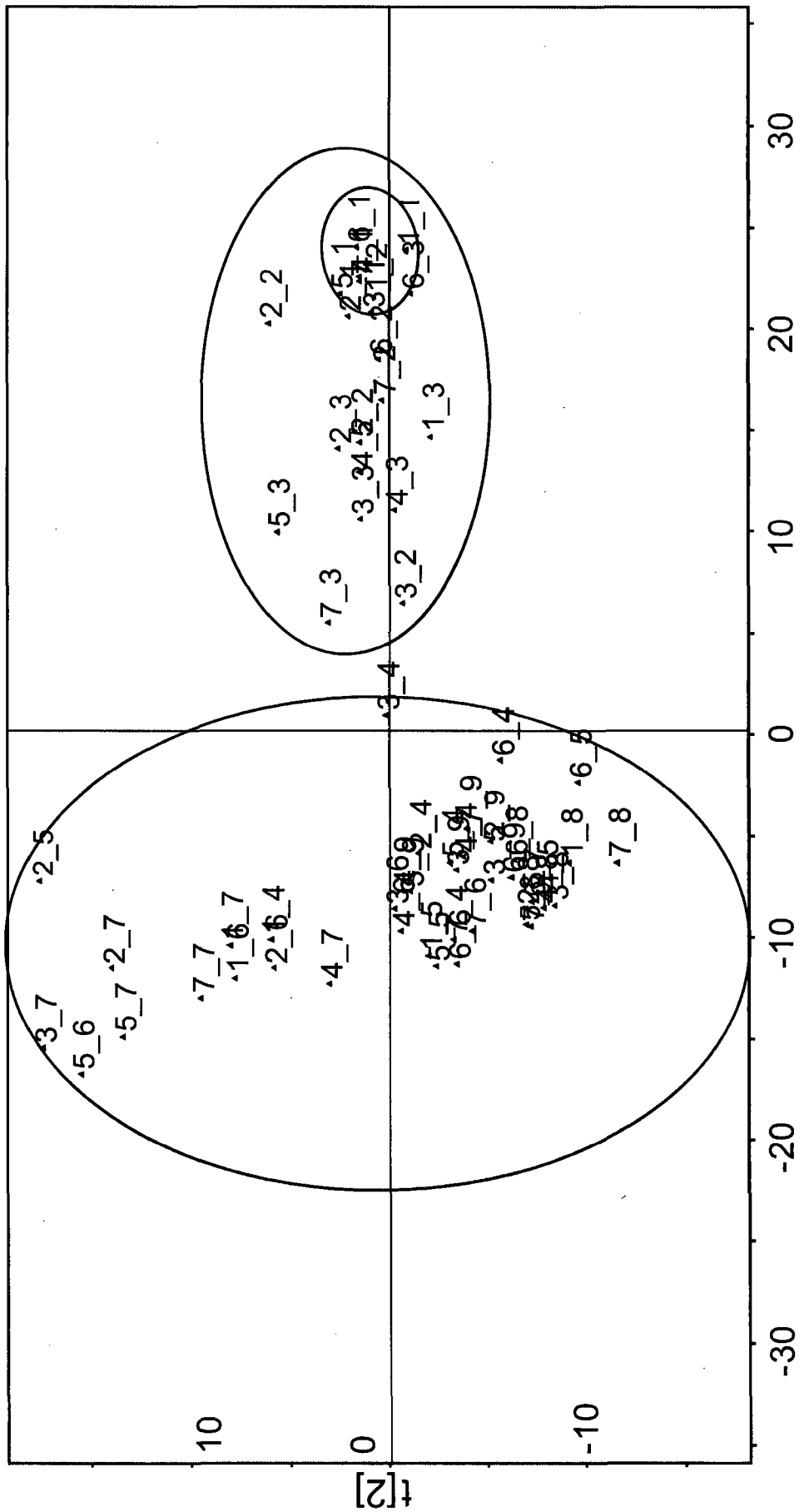


Fig. 3A

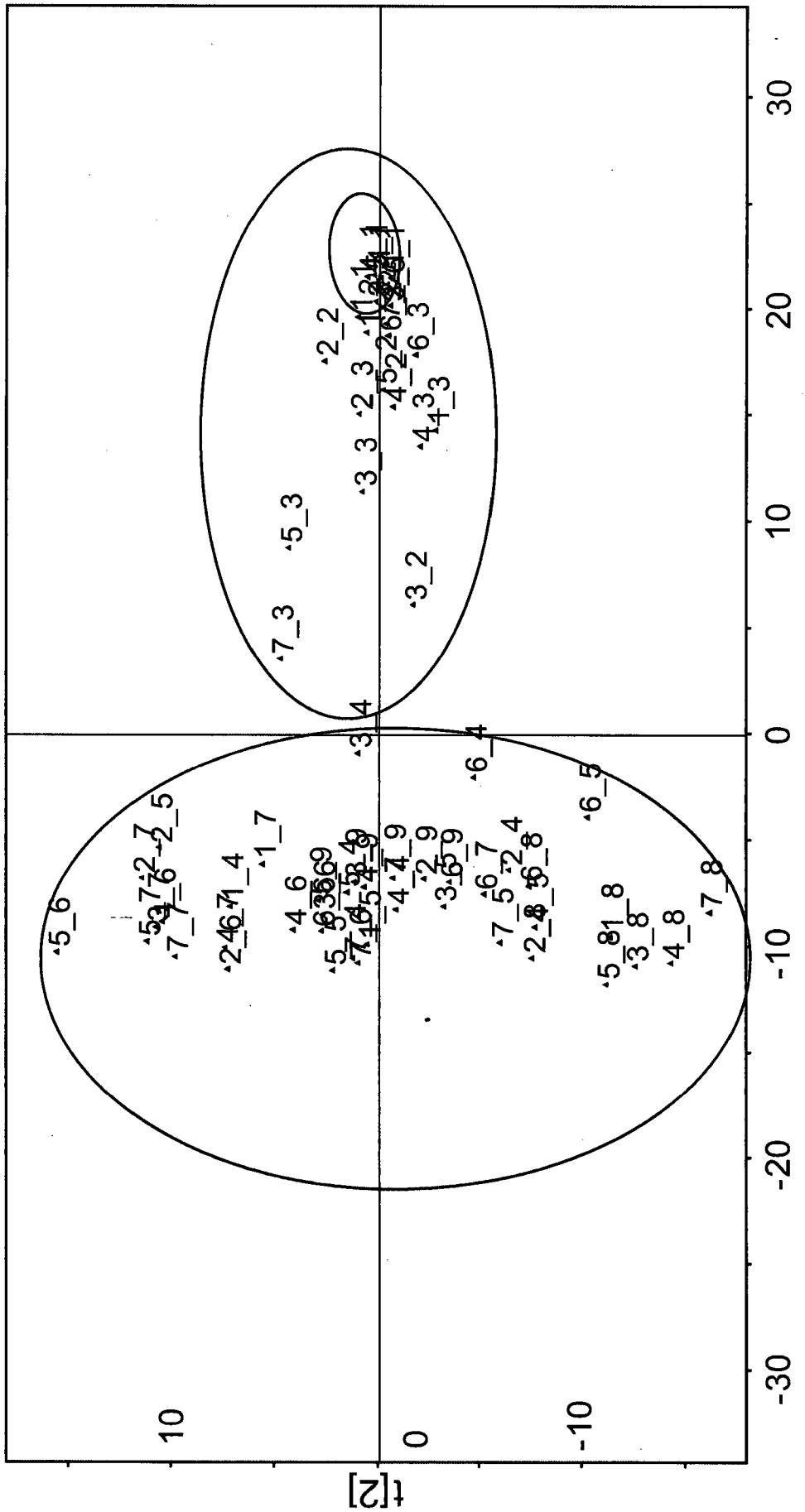
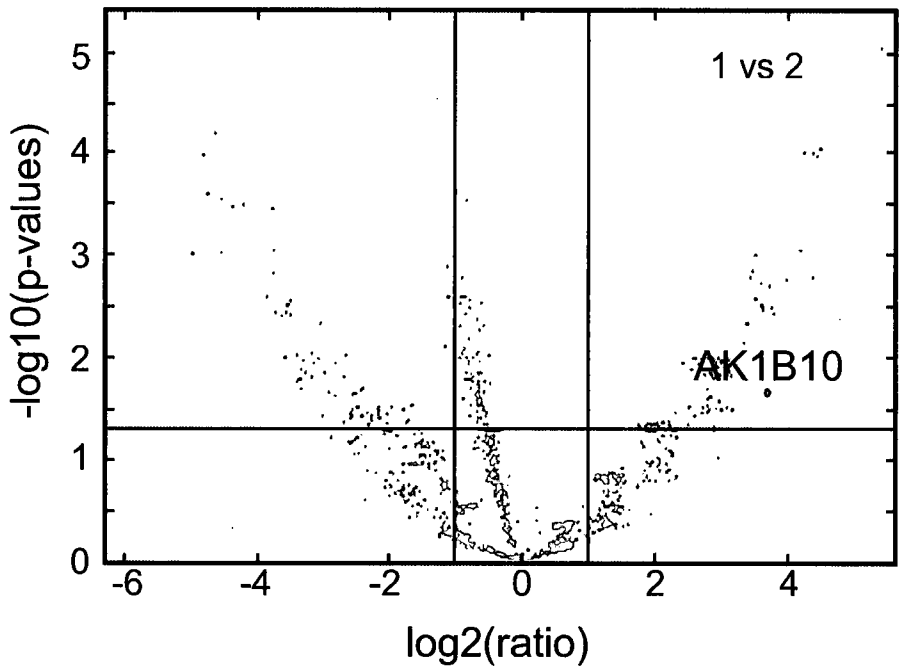


Fig. 3B

Fig. 4

AKR1B10



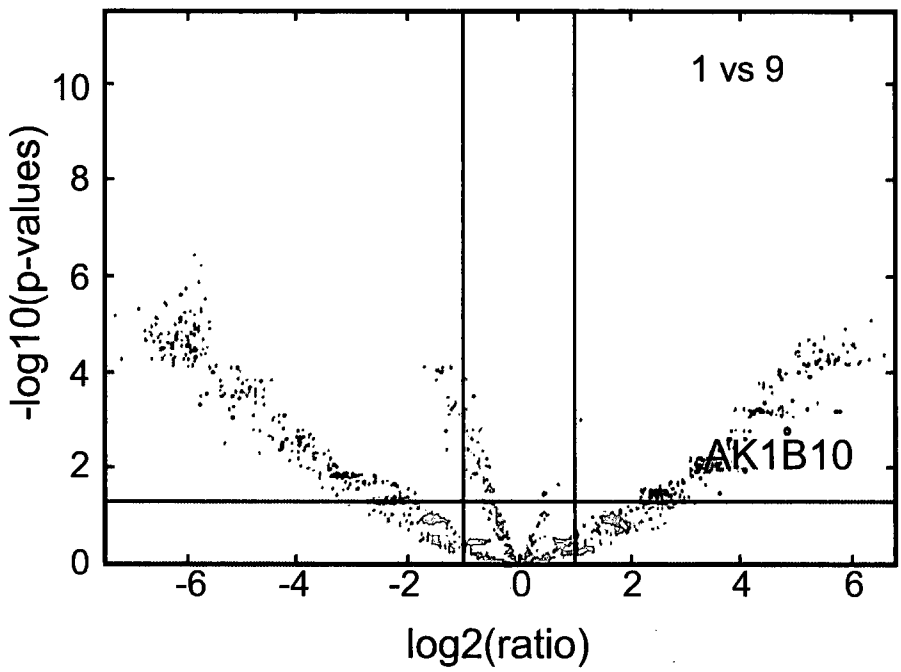


Fig. 4 continued

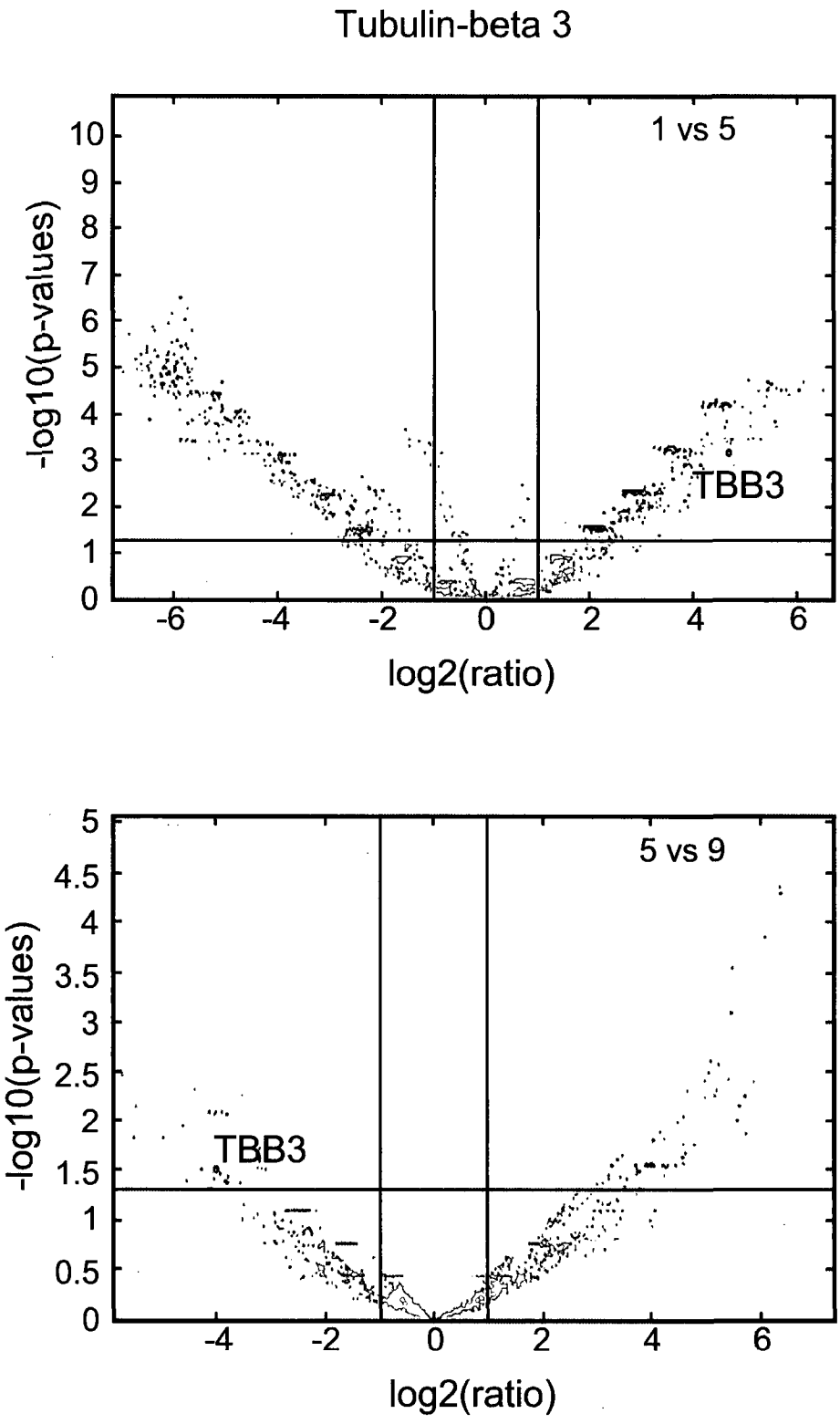


Fig. 5

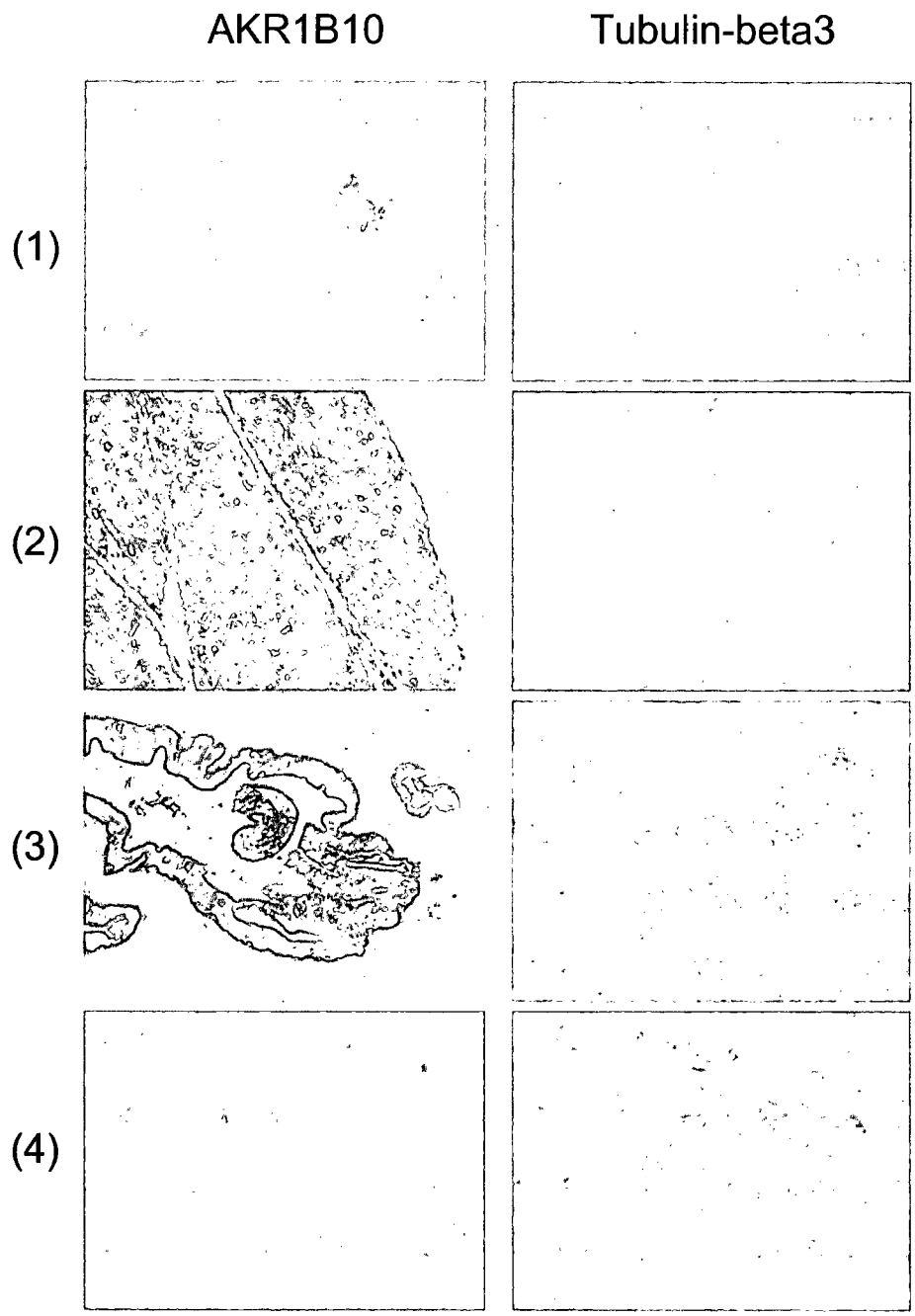


Fig. 6

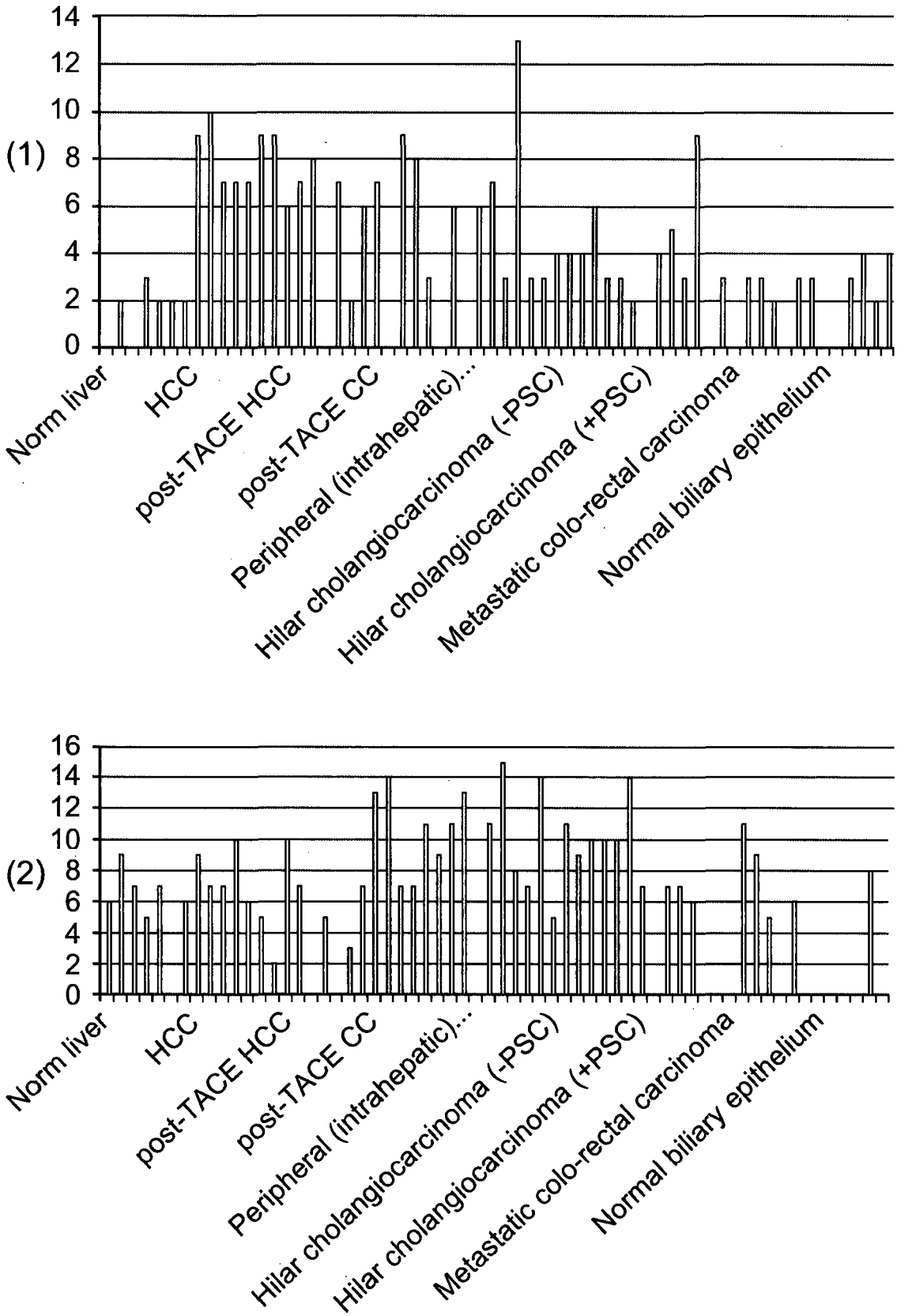
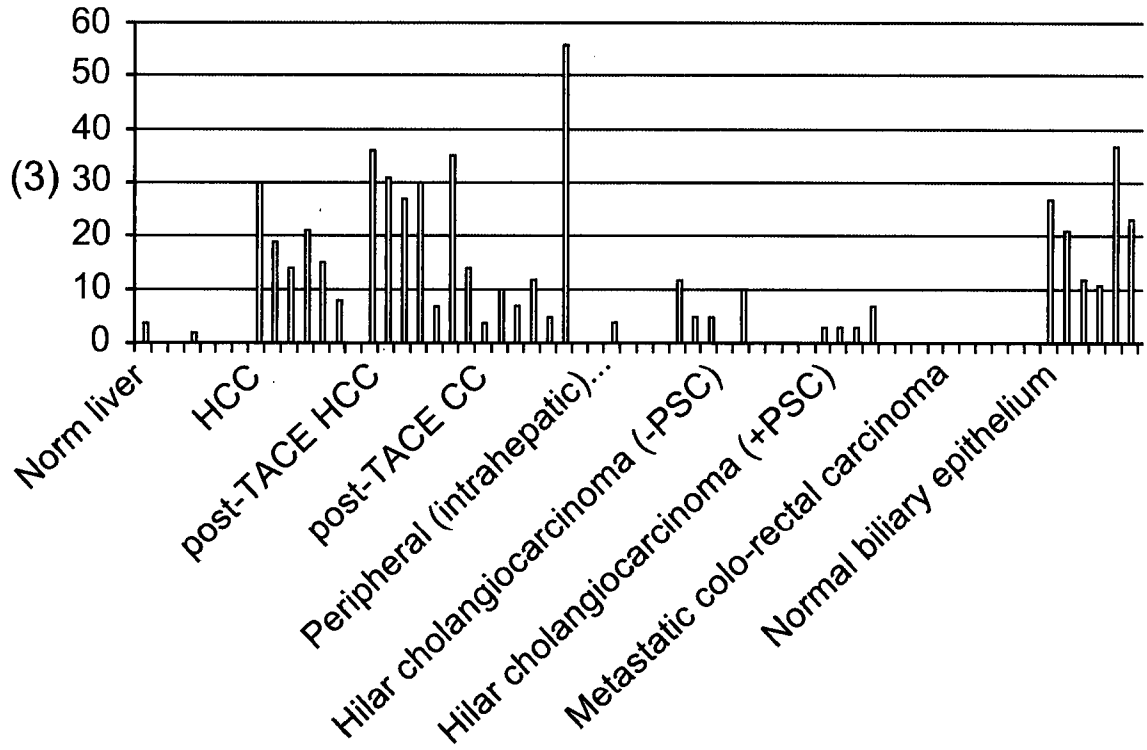

(1)
14
12
10
8
6
4
2
0
Norm liver
HCC
post-TACE HCC
post-TACE CC
Peripheral (intrahepatic)...
Hilar cholangiocarcinoma (-PSC)
Hilar cholangiocarcinoma (+PSC)
Metastatic colo-rectal carcinoma
Normal biliary epithelium
(2)
16
14
12
10
8
6
4
2
0
Norm liver
HCC
post-TACE HCC
post-TACE CC
Peripheral (intrahepatic)...
Hilar cholangiocarcinoma (-PSC)
Hilar cholangiocarcinoma (+PSC)
Metastatic colo-rectal carcinoma
Normal biliary epithelium

Fig. 6 continued



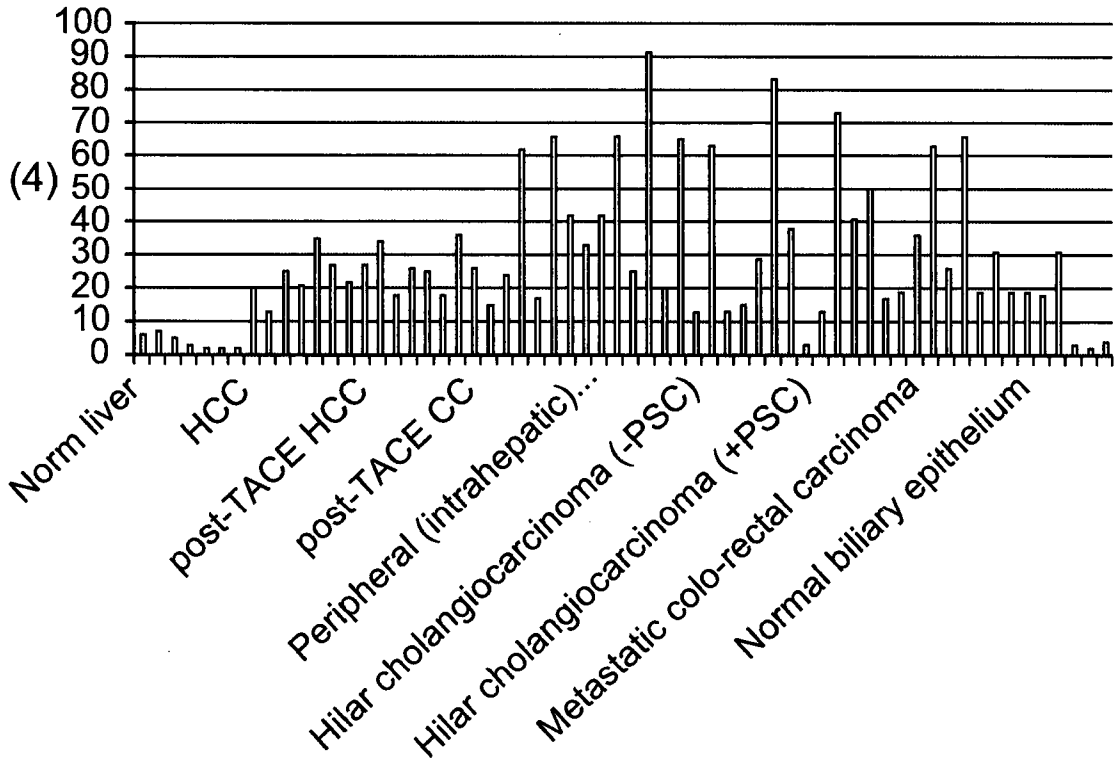


Fig. 6 continued

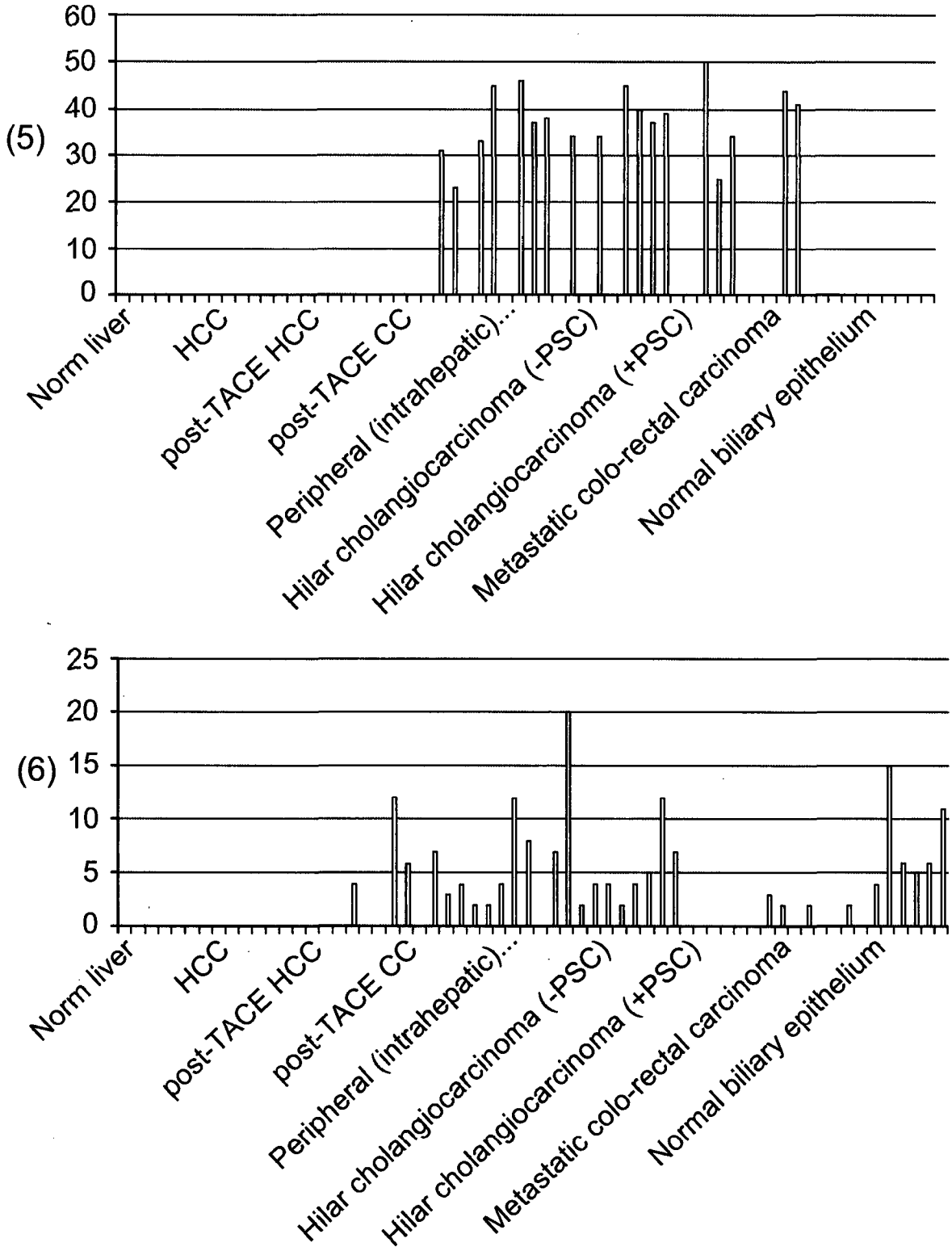


Fig. 6 continued

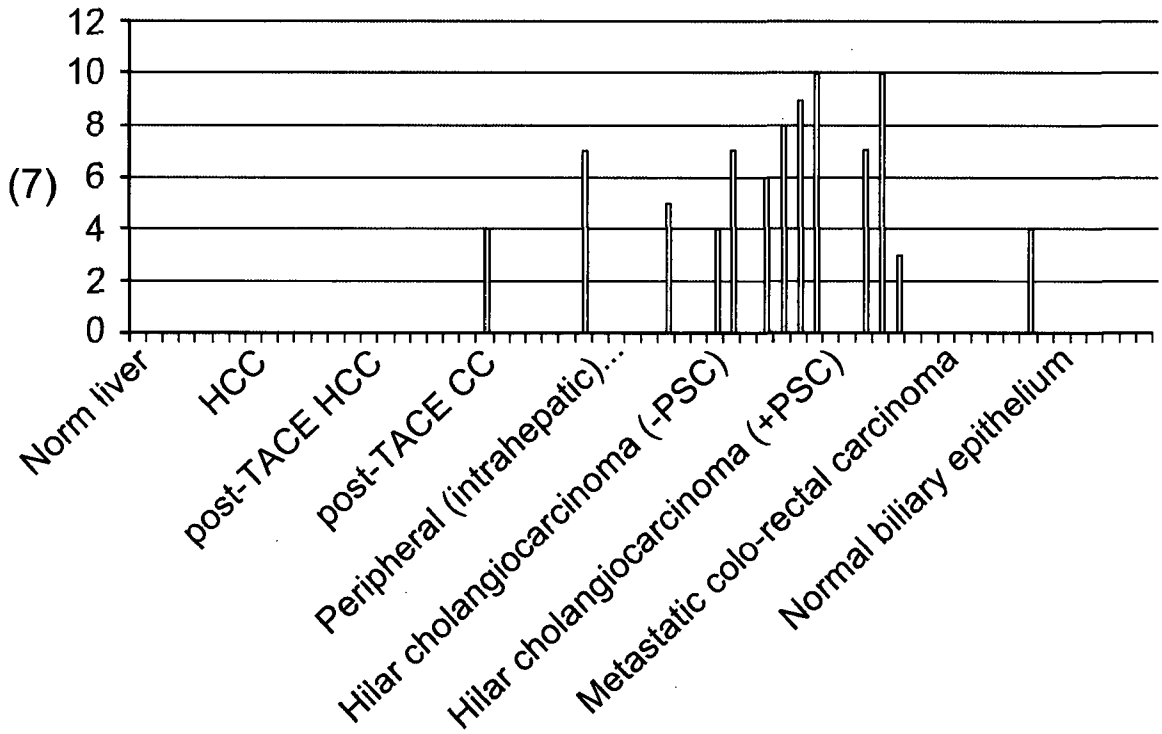


Fig. 7

Table 11

A	ID	ProtName	Area			Spectral Counting		
			Pvalues	tscores	log2 Fold Change	pvalues	tscores	log2 Fold Change
1_2	Q04917	14-3-3 protein eta OS=Homo sapiens GN=YWHAH PE=1 SV=4 - [1433F_HUMAN]	3.37E-02	2.1220	2.8718	1.73E-02	2.4306	2.7999
1_2	P51857	3-oxo-5-beta-steroid 4-dehydrogenase OS=Homo sapiens GN=AKR1D1 PE=1 SV=1 - [AK1D1_HUMAN]	1.16E-06	-18.5719	-3.0581	7.11E-03	-2.8413	-2.6145
1_2	O60218	Aldo-keto reductase family 1 member B10 OS=Homo sapiens GN=AKR1B10 PE=1 SV=2 - [AK1BA_HUMAN]	2.83E-02	2.2469	2.9501	7.93E-04	4.0407	3.8679
1_2	P05177	Cytochrome P450 1A2 OS=Homo sapiens GN=CYP1A2 PE=1 SV=3 - [CP1A2_HUMAN]	4.47E-04	-4.6985	-3.0235	1.87E-03	-3.5435	-3.2232
1_2	O43175	D-3-phosphoglycerate dehydrogenase OS=Homo sapiens GN=PHGDH PE=1 SV=4 - [SERA_HUMAN]	3.09E-03	-3.5953	-3.0089	2.99E-03	-3.2955	-3.3183
1_2	P23378	Glycine dehydrogenase [decarboxylating], mitochondrial OS=Homo sapiens GN=GLDC PE=1 SV=2 - [GCSP_HUMAN]	3.68E-04	-5.1197	-3.0836	4.93E-03	-3.0305	-4.1123
1_2	O43390	Heterogeneous nuclear ribonucleoprotein R OS=Homo sapiens GN=HNRNPR PE=1 SV=1 - [HNRPR_HUMAN]	1.22E-02	2.7708	2.8122	4.57E-02	1.9797	2.0606
1_2	P16401	Histone H1.5 OS=Homo sapiens GN=HIST1H1B PE=1 SV=3 - [H15_HUMAN]	2.54E-03	3.6915	2.8743	1.05E-03	3.8565	2.4391
1_2	P04259	Keratin, type II cytoskeletal 6B OS=Homo sapiens GN=KRT6B PE=1 SV=5 - [K2C6B_HUMAN]	2.93E-03	3.6310	2.9050	3.50E-02	2.0814	2.7219
1_2	O43772	Mitochondrial carnitine/acylcarnitine carrier protein OS=Homo sapiens GN=SLC25A20 PE=1 SV=1 - [MCAT_HUMAN]	1.08E-03	-3.9269	-2.9591	1.74E-02	-2.4267	-2.4681
1_2	Q9Y617	Phosphoserine aminotransferase OS=Homo sapiens GN=PSAT1 PE=1 SV=2 - [SERC_HUMAN]	5.30E-04	-4.4420	-3.0023	1.61E-03	-3.6307	-2.3735
1_3	Q7Z5P4	17-beta-hydroxysteroid dehydrogenase 13 OS=Homo sapiens GN=HSD17B13 PE=2 SV=1 - [DHB13_HUMAN]	6.77E-04	-4.2626	-3.1005	7.99E-04	-4.0198	-3.2567
1_3	P12694	2-oxoisovalerate dehydrogenase subunit alpha, mitochondrial OS=Homo sapiens GN=BCKDHA PE=1 SV=2 - [ODBA_HUMAN]	3.12E-02	-2.1335	-2.9176	1.94E-02	-2.3693	-2.6382
1_3	P51857	3-oxo-5-beta-steroid 4-dehydrogenase OS=Homo sapiens GN=AKR1D1 PE=1 SV=1 - [AK1D1_HUMAN]	6.53E-05	-6.2878	-3.0581	1.22E-02	-2.5826	-2.6145
1_3	Q9BSE5	Agmatinase, mitochondrial OS=Homo sapiens GN=AGMAT PE=1 SV=2 - [SPEB_HUMAN]	3.16E-02	-2.1255	-3.0674	5.59E-03	-2.9536	-2.0086
1_3	O60218	Aldo-keto reductase family 1 member B10 OS=Homo sapiens GN=AKR1B10 PE=1 SV=2 - [AK1BA_HUMAN]	4.53E-03	3.3008	3.0091	2.63E-05	5.9623	5.0151
1_3	Q9UBR1	Beta-ureidopropionase OS=Homo sapiens GN=UPB1 PE=1 SV=1 - [BUP1_HUMAN]	3.69E-05	-7.0719	-3.1074	2.61E-05	-5.9844	-3.6551
1_3	P02462	Collagen alpha-1(IV) chain OS=Homo sapiens GN=COL4A1 PE=1 SV=3 - [CO4A1_HUMAN]	1.07E-05	22.3057	2.8930	9.71E-05	5.3018	2.2905
1_3	P35520	Cystathionine beta-synthase OS=Homo sapiens GN=CBS PE=1 SV=2 - [CBS_HUMAN]	3.56E-03	-3.4985	-2.9856	4.36E-03	-3.0853	-2.0840
1_3	P05177	Cytochrome P450 1A2 OS=Homo sapiens GN=CYP1A2 PE=1 SV=3 - [CP1A2_HUMAN]	3.49E-05	-24.1947	-3.0235	1.73E-04	-4.9713	-3.2232
1_3	P10632	Cytochrome P450 2C8 OS=Homo sapiens GN=CYP2C8 PE=1 SV=2 - [CP2C8_HUMAN]	6.46E-04	-4.3052	-3.0569	2.80E-06	-7.8852	-3.9088
1_3	P08684	Cytochrome P450 3A4 OS=Homo sapiens GN=CYP3A4 PE=1 SV=4 - [CP3A4_HUMAN]	2.14E-07	-33.4351	-3.1061	1.09E-06	-8.6528	-3.8971
1_3	Q02928	Cytochrome P450 4A11 OS=Homo sapiens GN=CYP4A11 PE=1 SV=1 - [CP4AB_HUMAN]	1.77E-03	-3.8078	-3.0294	1.82E-03	-3.5448	-3.0008
1_3	Q96LJ7	Dehydrogenase/reductase SDR family member 1 OS=Homo sapiens GN=DHRS1 PE=1 SV=1 - [DHRS1_HUMAN]	4.06E-05	-6.9378	-2.9590	1.11E-02	-2.6287	-2.4681
1_3	P49326	Dimethylaniline monooxygenase [N-oxide-forming] 5 OS=Homo sapiens GN=FMO5 PE=2 SV=2 - [FMO5_HUMAN]	2.53E-03	-3.7225	-2.9711	5.19E-03	-2.9973	-3.4376
1_3	Q16134	Electron transfer flavoprotein-ubiquinone oxidoreductase, mitochondrial OS=Homo sapiens GN=ETFDH PE=1 SV=2 - [ETFD_HUMAN]	4.61E-03	-3.2885	-3.0460	1.70E-03	-3.5817	-2.8644
1_3	Q96YB7	Enoyl-CoA hydratase domain-containing protein 2, mitochondrial OS=Homo sapiens GN=ECHDC2 PE=2 SV=2 - [ECHD2_HUMAN]	2.93E-03	-3.6496	-3.0081	4.35E-04	-4.3818	-2.7619
1_3	P17931	Galectin-3 OS=Homo sapiens GN=LGALS3 PE=1 SV=5 - [LEG3_HUMAN]	8.09E-03	2.8112	2.5940	8.86E-03	2.7254	2.2426

Fig. 7 continued

1_3	P23378	Glycine dehydrogenase [decarboxylating], mitochondrial OS=Homo sapiens GN=GLDC PE=1 SV=2 - [GCSP_HUMAN]	2.64E-04	-5.4228	-3.0836	4.44E-03	-3.0789	-4.1123
1_3	Q6IB77	Glycine N-acyltransferase OS=Homo sapiens GN=GLYAT PE=1 SV=3 - [GLYAT_HUMAN]	7.67E-04	-4.1842	-3.1178	1.20E-05	-6.8151	-4.1035
1_3	Q14749	Glycine N-methyltransferase OS=Homo sapiens GN=GNMT PE=1 SV=3 - [GNMT_HUMAN]	3.15E-04	-5.1784	-2.9366	5.11E-03	-3.0064	-2.8276
1_3	P35573	Glycogen debranching enzyme OS=Homo sapiens GN=AGL PE=1 SV=3 - [GDE_HUMAN]	3.24E-03	-3.3821	-3.0393	2.65E-04	-4.7124	-4.4446
1_3	P16401	Histone H1.5 OS=Homo sapiens GN=HIST1H1B PE=1 SV=3 - [H15_HUMAN]	2.60E-02	2.2724	2.8149	5.70E-03	2.9441	2.5061
1_3	P01860	Ig gamma-3 chain C region OS=Homo sapiens GN=IGHG3 PE=1 SV=2 - [IGHG3_HUMAN]	1.45E-02	2.6946	2.9648	3.79E-02	2.0545	3.9344
1_3	Q9ULC5	Long-chain-fatty-acid--CoA ligase 5 OS=Homo sapiens GN=ACSL5 PE=1 SV=1 - [ACSL5_HUMAN]	2.11E-04	-5.6309	-3.0648	1.37E-03	-3.7113	-2.7091
1_3	P10619	Lysosomal protective protein OS=Homo sapiens GN=CTSA PE=1 SV=2 - [PPGB_HUMAN]	4.68E-03	3.2693	2.8071	9.62E-05	5.3232	2.0078
1_3	P40121	Macrophage-capping protein OS=Homo sapiens GN=CAPG PE=1 SV=2 - [CAPG_HUMAN]	1.69E-03	3.8172	2.5852	3.38E-03	3.2264	2.1275
1_3	O43708	Maleylacetoacetate isomerase OS=Homo sapiens GN=GSTZ1 PE=1 SV=3 - [MAAI_HUMAN]	2.15E-02	-2.4060	-2.9999	1.22E-02	-2.5800	-2.0086
1_3	O43772	Mitochondrial carnitine/acylcarnitine carrier protein OS=Homo sapiens GN=SLC25A20 PE=1 SV=1 - [MCAT_HUMAN]	6.40E-04	-4.3022	-2.9591	3.31E-02	-2.0991	-2.4661
1_3	Q9BY49	Peroxisomal trans-2-enoyl-CoA reductase OS=Homo sapiens GN=PECR PE=1 SV=2 - [PECR_HUMAN]	2.39E-03	-3.6374	-3.0006	1.11E-02	-2.6280	-2.0500
1_3	Q9Y617	Phosphoserine aminotransferase OS=Homo sapiens GN=PSAT1 PE=1 SV=2 - [SERC_HUMAN]	5.35E-04	-4.4608	-3.0023	2.45E-03	-3.3944	-2.3735
1_3	Q15149	Plectin OS=Homo sapiens GN=PLEC PE=1 SV=3 - [PLEC_HUMAN]	2.99E-04	5.2735	2.7534	1.02E-03	3.8882	3.1777
1_3	Q9UQ80	Proliferation-associated protein 2G4 OS=Homo sapiens GN=PA2G4 PE=1 SV=3 - [PA2G4_HUMAN]	1.83E-02	2.5251	2.8129	4.07E-03	3.1222	2.3297
1_3	Q01105	Protein SET OS=Homo sapiens GN=SET PE=1 SV=3 - [SET_HUMAN]	3.15E-03	3.6032	2.8321	2.59E-03	3.3592	2.1909
1_3	P14618	Pyruvate kinase isozymes M1/M2 OS=Homo sapiens GN=PKM PE=1 SV=4 - [KPYM_HUMAN]	4.85E-03	3.2351	2.8382	1.88E-03	3.5338	2.4280
1_3	P51149	Ras-related protein Rab-7a OS=Homo sapiens GN=RAB7A PE=1 SV=1 - [RAB7A_HUMAN]	2.90E-02	2.1908	2.7349	2.41E-02	2.2580	2.1385
1_3	O75452	Retinol dehydrogenase 16 OS=Homo sapiens GN=RDH16 PE=1 SV=2 - [RDH16_HUMAN]	3.80E-03	-3.4436	-3.1225	1.32E-03	-3.7293	-3.8444
1_3	P21912	Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial OS=Homo sapiens GN=SDHB PE=1 SV=3 - [DHSB_HUMAN]	4.39E-03	-3.3287	-2.9806	1.70E-02	-2.4268	-2.4158
1_4	Q04917	14-3-3 protein eta OS=Homo sapiens GN=YWHAH PE=1 SV=4 - [1433F_HUMAN]	5.84E-04	5.1157	2.9739	6.97E-05	6.7011	3.6309
1_4	P31947	14-3-3 protein sigma OS=Homo sapiens GN=SFN PE=1 SV=1 - [1433S_HUMAN]	4.39E-03	3.4718	2.9768	4.99E-05	7.4370	3.6322
1_4	Q7Z5P4	17-beta-hydroxysteroid dehydrogenase 13 OS=Homo sapiens GN=HSD17B13 PE=2 SV=1 - [DHB13_HUMAN]	4.17E-05	-19.0172	-3.1005	1.85E-04	-5.2191	-3.2567
1_4	O14756	17-beta-hydroxysteroid dehydrogenase type 6 OS=Homo sapiens GN=HSD17B6 PE=1 SV=1 - [HI17B6_HUMAN]	6.11E-05	-7.6136	-3.1163	4.81E-05	-7.4752	-3.9088
1_4	P12804	2-oxoisovalerate dehydrogenase subunit alpha, mitochondrial OS=Homo sapiens GN=BCKDHA PE=1 SV=2 - [ODBA_HUMAN]	1.51E-04	-5.9395	-2.9176	5.41E-04	-4.2558	-2.6382
1_4	P46952	3-hydroxyanthranilate 3,4-dioxygenase OS=Homo sapiens GN=HAAO PE=1 SV=2 - [3HAO_HUMAN]	7.76E-06	-25.2483	-3.0508	2.64E-05	-8.7071	-3.3183
1_4	P31937	3-hydroxyisobutyrate dehydrogenase, mitochondrial OS=Homo sapiens GN=HIBADH PE=1 SV=2 - [3HIDH_HUMAN]	6.93E-04	-4.5289	-3.0409	2.91E-03	-3.2819	-3.2360
1_4	Q6NVY1	3-hydroxyisobutyryl-CoA hydrolase, mitochondrial OS=Homo sapiens GN=HIBCH PE=1 SV=2 - [HIBCH_HUMAN]	6.63E-04	-4.6608	-3.0159	3.04E-03	-3.2530	-2.0500
1_4	P51857	3-oxo-5-beta-steroid 4-dehydrogenase OS=Homo sapiens GN=AKR1D1 PE=1 SV=1 - [AK1D1_HUMAN]	4.43E-05	-18.5719	-3.0581	6.74E-03	-2.8413	-2.6145
1_4	P80404	4-aminobutyrate aminotransferase, mitochondrial OS=Homo sapiens GN=ABAT PE=1 SV=3 - [GABT_HUMAN]	1.78E-05	-23.5269	-3.1594	6.18E-06	-11.7015	-5.3259
1_4	P32754	4-hydroxyphenylpyruvate dioxygenase OS=Homo sapiens GN=HPD PE=1 SV=2 - [HPPD_HUMAN]	2.39E-05	-22.1822	-3.1328	1.45E-05	-9.9568	-4.4376
1_4	Q9BWD1	Acetyl-CoA acetyltransferase, cytosolic OS=Homo sapiens GN=ACAT2 PE=1 SV=2 - [THIC_HUMAN]	5.82E-05	-8.0645	-3.0279	1.15E-03	-3.8120	-3.4294

Fig. 7 continued

1_4	P61160	Actin-related protein 2 OS=Homo sapiens GN=ACTR2 PE=1 SV=1 -	ARP2_HUMAN		2.37E-02	2.3684	2.0574	1.11E-04	5.7820	2.8424
1_4	O15144	Actin-related protein 2/3 complex subunit 2 OS=Homo sapiens GN=ARPC2 PE=1 SV=1 -	ARPC2_HUMAN		3.95E-03	3.5479	2.0364	1.65E-04	5.3202	2.6656
1_4	Q08AH3	Acyl-coenzyme A synthetase ACSM2A, mitochondrial OS=Homo sapiens GN=ACSM2A PE=1 SV=2 -	ACS2A_HUMAN		9.71E-06	-24.9514	-3.1313	1.74E-04	-5.2804	-5.0015
1_4	Q6ICK6	Acyl-coenzyme A synthetase ACSM2B, mitochondrial OS=Homo sapiens GN=ACSM2B PE=1 SV=2 -	ACS2B_HUMAN		5.67E-05	-9.5889	-3.1313	1.18E-05	-10.6014	-5.1339
1_4	P27144	Adenylate kinase isoenzyme 4, mitochondrial OS=Homo sapiens GN=AK4 PE=1 SV=1 -	KAD4_HUMAN		2.38E-02	-2.3653	-2.9842	7.83E-03	-2.7522	-2.7214
1_4	O95154	Aldehyde reductase member 3 OS=Homo sapiens GN=AKR1A3 PE=1 SV=2 -	AKR73_HUMAN		6.19E-04	-4.8918	-3.0662	2.08E-05	-9.0829	-3.8276
1_4	Q9BSE5	Agmatinase, mitochondrial OS=Homo sapiens GN=AGMAT PE=1 SV=2 -	SPEB_HUMAN		1.62E-04	-5.9240	-3.0674	1.88E-03	-3.5341	-2.0086
1_4	O00468	Agrin OS=Homo sapiens GN=AGRN PE=1 SV=4 -	AGRIN_HUMAN		3.10E-03	3.6914	2.6720	2.76E-02	2.1439	2.5021
1_4	P24298	Alanine aminotransferase 1 OS=Homo sapiens GN=GPT PE=1 SV=3 -	ALAT1_HUMAN		1.33E-05	-24.4015	-3.0208	3.15E-05	-8.3445	-3.9964
1_4	P07327	Alcohol dehydrogenase 1A OS=Homo sapiens GN=ADH1A PE=1 SV=2 -	ADH1A_HUMAN		1.43E-04	-5.9640	-3.2451	4.98E-04	-4.3406	-6.0582
1_4	P00326	Alcohol dehydrogenase 1C OS=Homo sapiens GN=ADH1C PE=1 SV=2 -	ADH1G_HUMAN		4.22E-04	-5.6069	-3.2398	1.43E-03	-3.8801	-4.9413
1_4	P08319	Alcohol dehydrogenase 4 OS=Homo sapiens GN=ADH4 PE=1 SV=5 -	ADH4_HUMAN		4.20E-05	-18.9978	-3.2128	9.65E-05	-5.9807	-5.9289
1_4	P28332	Alcohol dehydrogenase 6 OS=Homo sapiens GN=ADH6 PE=2 SV=2 -	ADH6_HUMAN		4.94E-04	-5.5097	-3.0225	6.63E-03	-2.8500	-3.3238
1_4	Q9H2A2	Aldehyde dehydrogenase family 8 member A1 OS=Homo sapiens GN=ALDH8A1 PE=1 SV=1 -	AL8A1_HUMAN		2.30E-05	-22.2723	-3.0403	1.34E-04	-5.5086	-3.5313
1_4	Q06278	Aldehyde oxidase OS=Homo sapiens GN=AOX1 PE=2 SV=2 -	ADO_HUMAN		4.01E-05	-19.3202	-3.0642	1.95E-03	-3.5143	-4.8209
1_4	P17516	Aldo-keto reductase family 1 member C4 OS=Homo sapiens GN=AKR1C4 PE=1 SV=3 -	AK1C4_HUMAN		1.20E-04	-6.1794	-3.0995	2.77E-02	-2.1431	-3.5814
1_4	P21397	Amine oxidase [flavin-containing] A OS=Homo sapiens GN=MAOA PE=1 SV=1 -	AOFA_HUMAN		6.27E-04	-4.8786	-3.0613	1.93E-11	-21.9394	-3.3301
1_4	Q03154	Aminoacylase-1 OS=Homo sapiens GN=ACY1 PE=1 SV=1 -	ACY1_HUMAN		5.74E-04	-5.1979	-3.1496	1.40E-05	-10.2366	-4.4905
1_4	P50995	Annexin A11 OS=Homo sapiens GN=ANXA11 PE=1 SV=1 -	ANX11_HUMAN		2.63E-05	21.8337	2.8192	1.69E-05	9.4429	2.8721
1_4	P12429	Annexin A3 OS=Homo sapiens GN=ANXA3 PE=1 SV=3 -	ANXA3_HUMAN		2.46E-03	3.7510	2.7599	3.44E-03	3.2011	2.4826
1_4	O95831	Apoptosis-inducing factor 1, mitochondrial OS=Homo sapiens GN=AIFM1 PE=1 SV=1 -	AIFM1_HUMAN		1.11E-03	-3.9221	-3.0900	6.70E-06	-11.2978	-3.9584
1_4	P05089	Arginase-1 OS=Homo sapiens GN=ARG1 PE=1 SV=2 -	ARGI1_HUMAN		7.32E-06	-25.2963	-3.1406	1.00E-05	-11.0155	-4.9801
1_4	P04424	Argininosuccinate lyase OS=Homo sapiens GN=ASL PE=1 SV=4 -	ARLY_HUMAN		6.91E-04	-4.5442	-3.1175	1.62E-05	-9.5700	-4.4990
1_4	P00966	Argininosuccinate synthase OS=Homo sapiens GN=ASS1 PE=1 SV=2 -	ASSY_HUMAN		6.51E-04	-4.7057	-3.1455	2.72E-04	-4.8410	-4.1123
1_4	P22760	Arylacetamide deacetylase OS=Homo sapiens GN=AADAC PE=1 SV=5 -	AAAD_HUMAN		1.95E-05	-23.4316	-3.0027	2.81E-06	-14.3418	-3.4125
1_4	Q08211	ATP-dependent RNA helicase A OS=Homo sapiens GN=DHX9 PE=1 SV=4 -	DHX9_HUMAN		5.49E-03	3.2579	2.7817	2.71E-03	3.3245	2.5447
1_4	O00571	ATP-dependent RNA helicase DDX3X OS=Homo sapiens GN=DDX3X PE=1 SV=3 -	DDX3X_HUMAN		2.04E-03	3.7651	2.8030	1.95E-05	9.2365	2.6209
1_4	P13929	Beta-enolase OS=Homo sapiens GN=ENO3 PE=1 SV=5 -	ENOB_HUMAN		1.50E-02	-2.6875	-3.0904	1.27E-03	-3.7418	-3.7619
1_4	Q93088	Betaine--homocysteine S-methyltransferase 1 OS=Homo sapiens GN=BHMT PE=1 SV=2 -	BHMT1_HUMAN		3.09E-05	-21.4499	-3.1673	5.82E-05	-6.9563	-4.8682
1_4	Q9UBR1	Beta-ureidopropionase OS=Homo sapiens GN=UPB1 PE=1 SV=1 -	BUP1_HUMAN		2.84E-05	-21.6121	-3.1074	9.25E-05	-6.0471	-3.6561
1_4	P34913	Bifunctional epoxide hydrolase 2 OS=Homo sapiens GN=EPHX2 PE=1 SV=2 -	HYES_HUMAN		1.37E-05	-24.3491	-3.0627	7.42E-05	-6.5741	-3.7851
1_4	P31939	Bifunctional purine biosynthesis protein PURH OS=Homo sapiens GN=ATIC PE=1 SV=3 -	PUR9_HUMAN		1.01E-03	4.0070	2.8384	5.43E-04	4.2508	3.3386

Fig. 7 continued

1_4	P21810	Biglycan OS=Homo sapiens GN=BGN PE=1 SV=2 - [PGS1_HUMAN]	3.60E-03	3.6129	2.8811	1.99E-04	5.1776	4.1264
1_4	Q14032	Bile acid-CoA:amino acid N-acyltransferase OS=Homo sapiens GN=BAAT PE=1 SV=1 - [BAAT_HUMAN]	2.71E-05	-21.6713	-3.0672	3.20E-04	-4.7041	-2.6382
1_4	Q9Y2P5	Bile acyl-CoA synthetase OS=Homo sapiens GN=SLC27A5 PE=1 SV=1 - [S27A5_HUMAN]	3.01E-05	-21.4856	-3.0863	3.16E-05	-8.3404	-4.4024
1_4	Q06520	Bile salt sulfotransferase OS=Homo sapiens GN=SULT2A1 PE=1 SV=3 - [ST2A1_HUMAN]	2.05E-05	-23.3737	-3.1402	4.98E-05	-11.8596	-4.0738
1_4	Q96CX2	BTB/POZ domain-containing protein KCTD12 OS=Homo sapiens GN=KCTD12 PE=1 SV=1 - [KCD12_HUMAN]	3.61E-05	20.4756	2.7434	1.19E-04	5.7045	2.9680
1_4	Q96DG6	Carboxymethylenebutenolidase homolog OS=Homo sapiens GN=CMBL PE=1 SV=1 - [CMBL_HUMAN]	6.02E-04	-5.0077	-3.0003	3.01E-03	-3.2609	-2.6745
1_4	P23786	Carnitine O-palmitoyltransferase 2, mitochondrial OS=Homo sapiens GN=CPT2 PE=1 SV=2 - [CPT2_HUMAN]	4.19E-04	-5.6114	-3.0257	5.01E-04	-4.3379	-3.1528
1_4	O00748	Cocaine esterase OS=Homo sapiens GN=CES2 PE=1 SV=1 - [EST2_HUMAN]	5.87E-05	-7.9572	-3.0621	2.86E-05	-8.5092	-3.3301
1_4	Q05707	Collagen alpha-1(XIV) chain OS=Homo sapiens GN=COL14A1 PE=1 SV=3 - [COEA1_HUMAN]	1.43E-02	2.7179	2.7220	9.71E-03	2.6568	4.1595
1_4	P31146	Coronin-1A OS=Homo sapiens GN=CORO1A PE=1 SV=4 - [COR1A_HUMAN]	5.93E-04	5.0700	2.7939	4.28E-03	3.0962	2.5501
1_4	P28845	Cortisone reductase 11-beta-dehydrogenase isozyme 1 OS=Homo sapiens GN=HSD11B1 PE=1 SV=3 - [DHI1_HUMAN]	2.89E-05	-21.5948	-2.9859	4.12E-03	-3.1190	-2.0008
1_4	P35520	Cystathionine beta-synthase OS=Homo sapiens GN=CBS PE=1 SV=2 - [CBS_HUMAN]	1.50E-08	-31.2554	-2.9856	6.20E-04	-4.1863	-2.0840
1_4	P32929	Cystathionine gamma-lyase OS=Homo sapiens GN=CTH PE=1 SV=3 - [CGL_HUMAN]	3.36E-04	-5.7178	-2.9700	2.51E-03	-3.3636	-2.5186
1_4	P00167	Cytochrome b5 OS=Homo sapiens GN=CYB5A PE=1 SV=2 - [CYB5_HUMAN]	5.47E-04	-5.3539	-3.1862	3.43E-04	-4.6624	-3.5936
1_4	P05177	Cytochrome P450 1A2 OS=Homo sapiens GN=CYP1A2 PE=1 SV=3 - [CP1A2_HUMAN]	1.42E-05	-24.1947	-3.0205	2.36E-04	-4.9713	-3.2232
1_4	P11509	Cytochrome P450 2A6 OS=Homo sapiens GN=CYP2A6 PE=1 SV=3 - [CP2A6_HUMAN]	5.57E-05	-8.9191	-3.0746	1.90E-04	-5.2001	-4.6052
1_4	P10632	Cytochrome P450 2C8 OS=Homo sapiens GN=CYP2C8 PE=1 SV=2 - [CP2C8_HUMAN]	1.47E-05	-24.1394	-3.0569	1.12E-05	-10.9282	-3.9088
1_4	P11712	Cytochrome P450 2C9 OS=Homo sapiens GN=CYP2C9 PE=1 SV=3 - [CP2C9_HUMAN]	5.72E-05	-8.5248	-3.0856	3.69E-05	-7.9942	-4.2291
1_4	P10635	Cytochrome P450 2D6 OS=Homo sapiens GN=CYP2D6 PE=1 SV=2 - [CP2D6_HUMAN]	2.17E-04	-5.8528	-2.9841	1.01E-02	-2.6392	-2.4158
1_4	P05181	Cytochrome P450 2E1 OS=Homo sapiens GN=CYP2E1 PE=1 SV=1 - [CP2E1_HUMAN]	6.98E-05	-7.1624	-3.0416	2.18E-05	-9.0366	-3.3879
1_4	P08684	Cytochrome P450 3A4 OS=Homo sapiens GN=CYP3A4 PE=1 SV=4 - [CP3A4_HUMAN]	5.77E-05	-8.1547	-3.1061	2.69E-05	-8.6528	-3.8971
1_4	Q02928	Cytochrome P450 4A11 OS=Homo sapiens GN=CYP4A11 PE=1 SV=1 - [CP4AB_HUMAN]	1.46E-06	-29.1359	-3.0294	1.17E-03	-3.8049	-3.0008
1_4	Q14204	Cytoplasmic dynein 1 heavy chain 1 OS=Homo sapiens GN=DYNC1H1 PE=1 SV=5 - [DYHC1_HUMAN]	1.76E-03	3.8120	2.6197	1.06E-02	2.6080	2.5529
1_4	O75891	Cytosolic 10-formyltetrahydrofolate dehydrogenase OS=Homo sapiens GN=ALDH1L1 PE=1 SV=2 - [AL1L1_HUMAN]	6.40E-05	-7.5304	-3.0944	2.27E-04	-5.0175	-5.1429
1_4	Q02338	D-beta-hydroxybutyrate dehydrogenase, mitochondrial OS=Homo sapiens GN=BDH1 PE=1 SV=3 - [BDH_HUMAN]	1.13E-05	-24.6173	-3.1312	4.23E-05	-7.7814	-4.1884
1_4	P07305	Decorin OS=Homo sapiens GN=DCN PE=1 SV=1 - [PGS2_HUMAN]	2.29E-03	3.7630	2.7217	1.44E-03	3.6760	2.1517
1_4	Q96LJ7	Dehydrogenase/reductase SDR family member 1 OS=Homo sapiens GN=DHRS1 PE=1 SV=1 - [DHRS1_HUMAN]	6.45E-05	-7.3945	-2.9580	7.55E-03	-2.7748	-2.4681
1_4	P13716	Delta-aminolevulinic acid dehydratase OS=Homo sapiens GN=ALAD PE=1 SV=1 - [HEM2_HUMAN]	5.40E-04	-5.3831	-3.0717	3.80E-04	-4.5459	-3.5645
1_4	P09417	Dihydropteridine reductase OS=Homo sapiens GN=QDPR PE=1 SV=2 - [DHPR_HUMAN]	5.52E-05	-9.2599	-3.0537	1.89E-04	-5.2022	-3.5579
1_4	Q14117	Dihydropyrimidinase OS=Homo sapiens GN=DPYS PE=1 SV=1 - [DPYS_HUMAN]	5.70E-04	-5.2259	-3.0297	1.05E-04	-5.8612	-2.9183
1_4	P31513	Dimethylaniline monooxygenase [N-oxide-forming] 3 OS=Homo sapiens GN=FMO3 PE=1 SV=5 - [FMO3_HUMAN]	3.39E-04	-5.7141	-3.1060	3.63E-04	-4.6015	-4.2567
1_4	P49326	Dimethylaniline monooxygenase [N-oxide-forming] 5 OS=Homo sapiens GN=FMO5 PE=2 SV=2 - [FMO5_HUMAN]	7.49E-05	-7.0442	-2.9711	1.43E-03	-3.6790	-3.4376

Fig. 7 continued

1_4	Q9UJ17	Dimethylglycine dehydrogenase, mitochondrial OS=Homo sapiens GN=DMGDH PE=1 SV=2 - [M2GD_HUMAN]	2.10E-05	-23.1845	-3.0665	1.91E-05	-9.2639	-4.0343
1_4	P78527	DNA-dependent protein kinase catalytic subunit OS=Homo sapiens GN=PRKDC PE=1 SV=3 - [PRKDC_HUMAN]	4.55E-03	3.4466	2.8052	1.45E-03	3.6716	4.4282
1_4	O75356	Ectonucleoside triphosphate diphosphohydrolase 5 OS=Homo sapiens GN=ENTPD5 PE=1 SV=1 - [ENTP5_HUMAN]	7.74E-05	-5.9705	-2.9465	9.51E-04	-3.9142	-2.6382
1_4	Q16134	Electron transfer flavoprotein-ubiquinone oxidoreductase, mitochondrial OS=Homo sapiens GN=ETFDH PE=1 SV=2 - [ETFD_HUMAN]	3.33E-05	-20.9402	-3.0460	6.68E-05	-6.7647	-2.8644
1_4	O75521	Enoyl-CoA delta isomerase 2, mitochondrial OS=Homo sapiens GN=ECI2 PE=1 SV=4 - [ECI2_HUMAN]	7.20E-05	-7.1371	-3.0291	3.51E-04	-4.6346	-3.1495
1_4	Q86Y87	Enoyl-CoA hydratase domain-containing protein 2, mitochondrial OS=Homo sapiens GN=ECHDC2 PE=2 SV=2 - [ECHD2_HUMAN]	1.95E-05	-23.4294	-3.0081	2.17E-04	-5.0804	-2.7619
1_4	Q96HE7	ERO1-like protein alpha OS=Homo sapiens GN=ERO1L PE=1 SV=2 - [ERO1A_HUMAN]	1.08E-05	24.6745	2.8391	8.90E-04	3.9583	2.5529
1_4	P15311	Ezrin OS=Homo sapiens GN=EZR PE=1 SV=4 - [EZRI_HUMAN]	3.87E-05	19.6556	2.9388	3.30E-04	4.6847	3.5140
1_4	P51648	Fatty aldehyde dehydrogenase OS=Homo sapiens GN=ALDH3A2 PE=1 SV=1 - [AL3A2_HUMAN]	8.71E-04	-4.1541	-3.0148	1.11E-03	-3.8299	-3.0343
1_4	O95954	Formimidoyltransferase-cyclodeaminase OS=Homo sapiens GN=FTCD PE=1 SV=2 - [FTCD_HUMAN]	5.91E-05	-7.9351	-3.1264	2.77E-05	-8.6009	-5.2716
1_4	P09467	Fructose-1,6-bisphosphatase 1 OS=Homo sapiens GN=FBP1 PE=1 SV=5 - [F16P1_HUMAN]	7.01E-04	-4.4925	-3.1701	4.49E-06	-12.0460	-4.7202
1_4	P51570	Galactokinase OS=Homo sapiens GN=GALK1 PE=1 SV=1 - [GALK1_HUMAN]	7.20E-03	-2.9402	-3.0024	4.10E-03	-3.1217	-2.4493
1_4	P09382	Galectin-1 OS=Homo sapiens GN=LGALS1 PE=1 SV=2 - [LEG1_HUMAN]	5.50E-04	5.3382	2.7975	1.09E-04	5.8153	2.3985
1_4	P17931	Galectin-3 OS=Homo sapiens GN=LGALS3 PE=1 SV=5 - [LEG3_HUMAN]	3.07E-03	3.6949	2.7358	7.74E-03	2.7588	2.1351
1_4	Q08380	Galectin-3-binding protein OS=Homo sapiens GN=LGALS3BP PE=1 SV=1 - [LG3BP_HUMAN]	4.75E-04	5.5468	2.8028	4.54E-03	3.0632	2.6016
1_4	O95479	GDH/6PGL endoplasmic bifunctional protein OS=Homo sapiens GN=H6PD PE=1 SV=2 - [G6PE_HUMAN]	9.51E-04	-4.0677	-2.9933	3.70E-03	-3.1663	-2.9964
1_4	P11413	Glucose-6-phosphate 1-dehydrogenase OS=Homo sapiens GN=G6PD PE=1 SV=4 - [G6PD_HUMAN]	4.91E-04	5.5198	2.8217	1.55E-02	2.4271	2.8646
1_4	P08211	Glutathione S-transferase P OS=Homo sapiens GN=GSTP1 PE=1 SV=2 - [GSTP1_HUMAN]	3.10E-03	3.6916	2.8533	2.84E-03	3.2962	2.8721
1_4	P21695	Glycerol-3-phosphate dehydrogenase [NAD(+)], cytoplasmic OS=Homo sapiens GN=GPD1 PE=1 SV=4 - [GPDA_HUMAN]	3.45E-05	-20.7786	-2.9811	7.96E-05	-6.4160	-3.1620
1_4	P23378	Glycine dehydrogenase (decarboxylating), mitochondrial OS=Homo sapiens GN=GLDC PE=1 SV=2 - [GCSP_HUMAN]	2.35E-05	-22.2182	-3.0836	2.76E-03	-3.3110	-4.1123
1_4	Q6IB77	Glycine N-acyltransferase OS=Homo sapiens GN=GLYAT PE=1 SV=3 - [GLYAT_HUMAN]	5.89E-06	-25.6978	-3.1178	1.68E-06	-17.1499	-4.1035
1_4	Q14749	Glycine N-methyltransferase OS=Homo sapiens GN=GNMT PE=1 SV=3 - [GNMT_HUMAN]	4.42E-06	-26.4860	-2.9966	1.96E-03	-3.5107	-2.8276
1_4	P35573	Glycogen debranching enzyme OS=Homo sapiens GN=AGL PE=1 SV=3 - [GDE_HUMAN]	3.81E-05	-19.8828	-3.0393	1.51E-04	-5.4231	-4.4446
1_4	P11216	Glycogen phosphorylase, brain form OS=Homo sapiens GN=PYGB PE=1 SV=5 - [PYGB_HUMAN]	6.77E-04	4.5931	2.8440	3.83E-04	4.5408	3.0586
1_4	Q9UIJ7	GTP:AMP phosphotransferase, mitochondrial OS=Homo sapiens GN=AK3 PE=1 SV=4 - [KAD3_HUMAN]	7.88E-04	-4.3030	-2.9904	2.91E-04	-4.8019	-2.8644
1_4	O14979	Heterogeneous nuclear ribonucleoprotein D-like OS=Homo sapiens GN=HNRPDL PE=1 SV=3 - [HNRDL_HUMAN]	1.64E-04	5.9225	2.8773	9.60E-06	11.0431	2.5140
1_4	O43390	Heterogeneous nuclear ribonucleoprotein R OS=Homo sapiens GN=HNRNPR PE=1 SV=1 - [HNRPR_HUMAN]	1.33E-02	2.7456	2.8542	1.64E-04	5.3284	2.8424
1_4	Q1KMD3	Heterogeneous nuclear ribonucleoprotein U-like protein 2 OS=Homo sapiens GN=HNRNPUL2 PE=1 SV=1 - [HNRL2_HUMAN]	1.27E-04	6.0959	2.8210	2.94E-03	3.2778	2.2839
1_4	P16401	Histone H1.5 OS=Homo sapiens GN=HIST1H1B PE=1 SV=3 - [H15_HUMAN]	1.18E-03	3.8880	2.9601	6.60E-05	6.7659	2.8646
1_4	Q71UI9	Histone H2A.V OS=Homo sapiens GN=H2AFV PE=1 SV=3 - [H2AV_HUMAN]	4.95E-04	5.5050	3.1084	3.67E-03	3.1712	3.6715
1_4	P0C0S5	Histone H2A.Z OS=Homo sapiens GN=H2AFZ PE=1 SV=2 - [H2AZ_HUMAN]	4.95E-04	5.5050	3.1084	3.67E-03	3.1712	3.6715
1_4	P01903	HLA class II histocompatibility antigen, DR alpha chain OS=Homo sapiens GN=HLA-DRA PE=1 SV=1 - [DRA_HUMAN]	1.39E-02	2.7305	2.8477	3.76E-03	3.1596	2.2871

Fig. 7 continued

1_4	Q93099	Homogentisate 1,2-dioxygenase OS=Homo sapiens GN=HGD PE=1 SV=2 - [HGD_HUMAN]	1.35E-04	-6.0421	-3.0396	6.30E-04	-4.1773	-3.6287
1_4	Q9UJM8	Hydroxyacid oxidase 1 OS=Homo sapiens GN=HAO1 PE=1 SV=1 - [HAOX1_HUMAN]	1.27E-05	-24.4661	-3.1053	2.34E-04	-4.9782	-4.4990
1_4	Q16836	Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial OS=Homo sapiens GN=HADH PE=1 SV=3 - [HCDH_HUMAN]	2.65E-04	-5.8105	-3.1087	2.81E-05	-8.5808	-3.4009
1_4	Q16775	Hydroxyacylglutathione hydrolase, mitochondrial OS=Homo sapiens GN=HAGH PE=1 SV=2 - [GLO2_HUMAN]	6.70E-05	-7.2904	-2.9897	5.71E-05	-7.0319	-2.4493
1_4	P35914	Hydroxymethylglutaryl-CoA lyase, mitochondrial OS=Homo sapiens GN=HMGCL PE=1 SV=2 - [HMGCL_HUMAN]	7.01E-04	-4.4927	-3.0761	2.22E-04	-5.0383	-2.9431
1_4	P54868	Hydroxymethylglutaryl-CoA synthase, mitochondrial OS=Homo sapiens GN=HMGCS2 PE=1 SV=1 - [HMCS2_HUMAN]	1.01E-03	-4.0061	-3.2672	1.10E-04	-5.8081	-6.0495
1_4	Q6YN16	Hydroxysteroid dehydrogenase-like protein 2 OS=Homo sapiens GN=HSDL2 PE=1 SV=1 - [HSDL2_HUMAN]	1.02E-04	-6.4491	-3.0249	1.21E-03	-3.7835	-2.3749
1_4	Q14974	Importin subunit beta-1 OS=Homo sapiens GN=KPNB1 PE=1 SV=2 - [IMB1_HUMAN]	3.35E-03	3.6563	2.7566	6.29E-05	6.8482	2.7204
1_4	Q12906	Interleukin enhancer-binding factor 3 OS=Homo sapiens GN=ILF3 PE=1 SV=3 - [ILF3_HUMAN]	1.25E-02	2.7628	2.8157	1.46E-03	3.6686	3.0834
1_4	P26440	Isovaleryl-CoA dehydrogenase, mitochondrial OS=Homo sapiens GN=IVD PE=1 SV=1 - [IVD_HUMAN]	7.85E-04	-4.3126	-2.9789	9.46E-04	-3.9194	-2.6745
1_4	P08727	Keratin, type I cytoskeletal 19 OS=Homo sapiens GN=KRT19 PE=1 SV=4 - [K1C19_HUMAN]	3.12E-03	3.6890	2.8178	5.62E-03	2.9394	4.2797
1_4	P08729	Keratin, type II cytoskeletal 7 OS=Homo sapiens GN=KRT7 PE=1 SV=5 - [K2C7_HUMAN]	2.94E-03	3.7067	2.7941	1.67E-02	2.3970	2.5501
1_4	O00515	Ladinin-1 OS=Homo sapiens GN=LAD1 PE=1 SV=2 - [LAD1_HUMAN]	1.82E-05	23.5174	2.7578	3.02E-03	3.2574	2.0675
1_4	Q9Y2S2	Lambda-crystallin homolog OS=Homo sapiens GN=CRYL1 PE=1 SV=3 - [CRYL1_HUMAN]	1.02E-05	-24.9065	-3.0232	1.43E-04	-5.4584	-2.8309
1_4	P09960	Leukotriene A-4 hydrolase OS=Homo sapiens GN=LTA4H PE=1 SV=2 - [LKHA4_HUMAN]	7.05E-03	2.9659	2.7898	8.80E-04	3.9646	3.0526
1_4	P33121	Long-chain-fatty-acid--CoA ligase 1 OS=Homo sapiens GN=ACSL1 PE=1 SV=1 - [ACSL1_HUMAN]	6.19E-05	-7.5903	-3.1446	2.21E-04	-5.0508	-4.5260
1_4	Q8ULC5	Long-chain-fatty-acid--CoA ligase 5 OS=Homo sapiens GN=ACSL5 PE=1 SV=1 - [ACSL5_HUMAN]	4.29E-05	-18.8499	-3.0648	1.33E-03	-3.7113	-2.7091
1_4	P05455	Lupus La protein OS=Homo sapiens GN=SSB PE=1 SV=2 - [LA_HUMAN]	6.11E-04	4.9743	2.7805	8.27E-05	6.3495	2.9420
1_4	P40121	Macrophage-capping protein OS=Homo sapiens GN=CAPG PE=1 SV=2 - [CAPG_HUMAN]	4.80E-05	17.8148	2.8374	3.04E-05	8.3848	3.2131
1_4	Q14764	Major vault protein OS=Homo sapiens GN=MVP PE=1 SV=4 - [MVP_HUMAN]	3.23E-04	5.7312	2.7013	1.53E-02	2.4182	2.6322
1_4	O43708	Maleylacetoacetate isomerase OS=Homo sapiens GN=GSTZ1 PE=1 SV=3 - [MAAI_HUMAN]	1.80E-03	-3.8104	-2.9899	1.12E-02	-2.5800	-2.0086
1_4	P43243	Matrin-3 OS=Homo sapiens GN=MATR3 PE=1 SV=2 - [MATR3_HUMAN]	1.90E-02	2.5127	2.8141	8.94E-03	2.6951	2.4246
1_4	O00264	Membrane-associated progesterone receptor component 1 OS=Homo sapiens GN=PGRMC1 PE=1 SV=3 - [PGRC1_HUMAN]	5.24E-04	-5.4550	-3.0713	5.56E-05	-7.1816	-3.6888
1_4	Q02252	Methylmalonate-semialdehyde dehydrogenase [acylating], mitochondrial OS=Homo sapiens GN=ALDH6A1 PE=1 SV=2 - [MMSA_HUMAN]	5.83E-04	-5.1258	-3.1940	1.12E-06	-19.7058	-5.1968
1_4	Q9H8R3	Methyltransferase-like protein 7A OS=Homo sapiens GN=METTL7A PE=1 SV=1 - [METTA_HUMAN]	4.84E-04	-5.5378	-3.1078	3.76E-04	-4.5558	-2.4125
1_4	P10620	Microsomal glutathione S-transferase 1 OS=Homo sapiens GN=MGST1 PE=1 SV=1 - [MGST1_HUMAN]	3.93E-03	-3.5514	-3.1164	3.22E-03	-3.2307	-2.4125
1_4	O43772	Mitochondrial carnitine/acylcarnitine carrier protein OS=Homo sapiens GN=SLC25A20 PE=1 SV=1 - [MCAT_HUMAN]	3.90E-06	-26.7650	-2.9591	7.82E-04	-4.0361	-2.4681
1_4	Q9Y6C9	Mitochondrial carrier homolog 2 OS=Homo sapiens GN=MTCH2 PE=1 SV=1 - [MTCH2_HUMAN]	8.44E-04	-4.1947	-3.0184	3.92E-06	-12.8298	-3.0840
1_4	Q969Z3	MOSC domain-containing protein 2, mitochondrial OS=Homo sapiens GN=MARC2 PE=1 SV=1 - [MOSC2_HUMAN]	6.53E-05	-7.3292	-2.9702	4.33E-05	-7.5966	-2.7020
1_4	Q4G0N4	NAD kinase domain-containing protein 1 OS=Homo sapiens GN=NADKD1 PE=1 SV=2 - [NAKD1_HUMAN]	6.00E-05	-7.9112	-3.0937	2.87E-04	-4.8098	-3.8160
1_4	P16435	NADPH--cytochrome P450 reductase OS=Homo sapiens GN=POR PE=1 SV=2 - [NCPR_HUMAN]	5.18E-04	-5.4768	-3.0231	5.66E-05	-7.0940	-3.3749
1_4	Q09666	Neuroblast differentiation-associated protein AHNAK OS=Homo sapiens GN=AHNAK PE=1 SV=2 - [AHNK_HUMAN]	2.95E-02	2.1886	2.7969	1.46E-02	2.4562	2.6947

Fig. 7 continued

1_4	Q15274	Nicotinate-nucleotide pyrophosphorylase [carboxylating] OS=Homo sapiens GN=QPRT PE=1 SV=3 - [NADC_HUMAN]	6.72E-04	-4.6212	-2.9935	4.89E-02	-1.9070	-2.4990
1_4	P22307	Non-specific lipid-transfer protein OS=Homo sapiens GN=SCP2 PE=1 SV=2 - [NLTP_HUMAN]	4.92E-04	-5.5157	-3.0822	2.24E-06	-15.4677	-4.0008
1_4	P00480	Ornithine carbamoyltransferase, mitochondrial OS=Homo sapiens GN=OTC PE=1 SV=3 - [OTC_HUMAN]	1.78E-05	-23.5268	-3.1288	5.55E-07	-20.1799	-4.1620
1_4	O60664	Perilipin-3 OS=Homo sapiens GN=PLIN3 PE=1 SV=3 - [PLIN3_HUMAN]	4.52E-04	5.5697	2.7383	2.27E-03	3.4214	2.2899
1_4	Q15063	Periostin OS=Homo sapiens GN=POSTN PE=1 SV=2 - [POSTN_HUMAN]	3.67E-05	20.3842	2.8242	8.93E-04	3.9561	3.2899
1_4	Q9NUI1	Peroxisomal 2,4-dienoyl-CoA reductase OS=Homo sapiens GN=DECR2 PE=1 SV=1 - [DECR2_HUMAN]	1.26E-03	-3.8555	-2.9838	9.02E-03	-2.6908	-2.5645
1_4	Q15067	Peroxisomal acyl-coenzyme A oxidase 1 OS=Homo sapiens GN=ACOX1 PE=1 SV=3 - [ACOX1_HUMAN]	1.13E-03	-3.9100	-3.0451	1.24E-03	-3.7563	-3.7712
1_4	Q9NP24	Peroxisomal acyl-coenzyme A oxidase 2 OS=Homo sapiens GN=ACOX2 PE=1 SV=1 - [ACOX2_HUMAN]	1.62E-05	-23.6363	-3.0730	1.00E-04	-5.8231	-4.0961
1_4	Q08426	Peroxisomal bifunctional enzyme OS=Homo sapiens GN=EHHADH PE=1 SV=3 - [ECHP_HUMAN]	4.99E-04	-5.5017	-3.1724	2.00E-05	-9.2181	-5.7091
1_4	Q9P0Z9	Peroxisomal sarcosine oxidase OS=Homo sapiens GN=PIPOX PE=2 SV=2 - [SOX_HUMAN]	5.81E-04	-5.1413	-3.0673	7.78E-05	-6.4434	-3.6145
1_4	Q9BY49	Peroxisomal trans-2-enoyl-CoA reductase OS=Homo sapiens GN=PECR PE=1 SV=2 - [PECR_HUMAN]	3.44E-06	-26.8861	-3.0006	3.63E-03	-3.1755	-2.0500
1_4	P30039	Phenazine biosynthesis-like domain-containing protein OS=Homo sapiens GN=PBLD PE=1 SV=2 - [PBLD_HUMAN]	6.06E-05	-7.7600	-3.0315	3.04E-04	-4.7480	-3.1863
1_4	P00439	Phenylalanine-4-hydroxylase OS=Homo sapiens GN=PAH PE=1 SV=1 - [PH4H_HUMAN]	2.61E-05	-21.8428	-3.0126	4.79E-04	-4.3598	-2.7619
1_4	Q9Y617	Phosphoserine aminotransferase OS=Homo sapiens GN=PSAT1 PE=1 SV=2 - [SERC_HUMAN]	8.06E-05	-6.8971	-3.0023	3.10E-03	-3.2442	-2.3735
1_4	Q15149	Plectin OS=Homo sapiens GN=PLEC PE=1 SV=3 - [PLEC_HUMAN]	4.88E-03	3.3793	2.7478	1.02E-02	2.6336	3.7927
1_4	Q9UQB0	Proliferation-associated protein 2G4 OS=Homo sapiens GN=PA2G4 PE=1 SV=3 - [PA2G4_HUMAN]	1.53E-02	2.6727	2.8473	2.84E-04	4.8159	2.7049
1_4	P05165	Propionyl-CoA carboxylase alpha chain, mitochondrial OS=Homo sapiens GN=PCCA PE=1 SV=4 - [PCCA_HUMAN]	6.25E-05	-7.5773	-2.9800	3.12E-03	-3.2421	-2.6745
1_4	P05166	Propionyl-CoA carboxylase beta chain, mitochondrial OS=Homo sapiens GN=PCCB PE=1 SV=3 - [PCCB_HUMAN]	8.27E-04	-4.2186	-3.0162	5.33E-03	-2.9735	-2.9964
1_4	Q14914	Prostaglandin reductase 1 OS=Homo sapiens GN=PTGR1 PE=1 SV=2 - [PTGR1_HUMAN]	8.19E-04	-4.2331	-3.0490	8.64E-03	-2.7134	-3.7662
1_4	Q07105	Protein SET OS=Homo sapiens GN=SET PE=1 SV=3 - [SET_HUMAN]	1.67E-03	3.8232	2.8584	3.87E-04	4.5349	2.3821
1_4	P55786	Puromycin-sensitive aminopeptidase OS=Homo sapiens GN=NPEPPS PE=1 SV=2 - [PSA_HUMAN]	8.19E-03	2.8276	2.7998	1.77E-02	2.3736	2.6522
1_4	A6ND91	Putative L-aspartate dehydrogenase OS=Homo sapiens GN=ASPDH PE=2 SV=2 - [ASPD_HUMAN]	2.19E-04	-5.8503	-2.9302	1.44E-02	-2.4630	-2.0086
1_4	Q9NVS9	Pyridoxine-5-phosphate oxidase OS=Homo sapiens GN=PNPO PE=1 SV=1 - [PNPO_HUMAN]	5.26E-03	-3.3019	-2.9789	6.00E-05	-6.8815	-2.1967
1_4	P11498	Pyruvate carboxylase, mitochondrial OS=Homo sapiens GN=PC PE=1 SV=2 - [PYC_HUMAN]	5.75E-04	-5.1910	-3.1278	8.51E-05	-6.2142	-5.0961
1_4	P14618	Pyruvate kinase isozymes M1/M2 OS=Homo sapiens GN=PKM PE=1 SV=4 - [KPYM_HUMAN]	1.42E-04	5.9851	2.9726	8.24E-05	6.3564	5.1377
1_4	P30613	Pyruvate kinase isozymes R/L OS=Homo sapiens GN=PKLR PE=1 SV=2 - [KPYR_HUMAN]	1.21E-04	-6.1642	-3.0488	6.01E-03	-2.8999	-4.1016
1_4	P31150	Rab GDP dissociation inhibitor alpha OS=Homo sapiens GN=GDI1 PE=1 SV=2 - [GDIA_HUMAN]	1.78E-02	2.5621	2.7718	2.10E-03	3.4731	2.7927
1_4	P46940	Ras GTPase-activating-like protein IQGAP1 OS=Homo sapiens GN=IQGAP1 PE=1 SV=1 - [IQGA1_HUMAN]	2.30E-02	2.1950	2.7745	4.26E-03	3.1002	3.4989
1_4	Q13576	Ras GTPase-activating-like protein IQGAP2 OS=Homo sapiens GN=IQGAP2 PE=1 SV=4 - [IQGA2_HUMAN]	6.19E-04	-4.8927	-2.9401	2.61E-02	-2.1729	-3.0343
1_4	Q96HR9	Receptor expression-enhancing protein 6 OS=Homo sapiens GN=REEP6 PE=1 SV=1 - [REEP6_HUMAN]	5.62E-05	-8.8752	-3.0203	5.83E-04	-4.2242	-2.1528
1_4	Q15493	Regucalcin OS=Homo sapiens GN=RGN PE=1 SV=1 - [RGN_HUMAN]	4.85E-07	-30.8468	-2.9930	3.97E-03	-3.1364	-2.5936
1_4	O75452	Retinol dehydrogenase 16 OS=Homo sapiens GN=RDH16 PE=1 SV=2 - [RDH16_HUMAN]	3.32E-05	-20.9445	-3.1225	1.62E-04	-5.3418	-3.8444

Fig. 7 continued

1_4	P52566	Rho GDP-dissociation inhibitor 2 OS=Homo sapiens GN=ARHGDIB PE=1 SV=3 - [GDIR2_HUMAN]	2.82E-03	3.7175	2.7592	3.58E-03	3.1825	2.2871
1_4	Q8NBX0	Saccharopine dehydrogenase-like oxidoreductase OS=Homo sapiens GN=SCCPDH PE=1 SV=1 - [SCPDL_HUMAN]	6.43E-04	-4.7371	-2.9965	9.20E-03	-2.6815	-2.6145
1_4	Q00266	S-adenosylmethionine synthase isoform type-1 OS=Homo sapiens GN=MAT1A PE=1 SV=2 - [METK1_HUMAN]	5.88E-04	-5.0906	-3.0877	3.90E-05	-7.8864	-3.5857
1_4	Q9UL12	Sarcosine dehydrogenase, mitochondrial OS=Homo sapiens GN=SARDH PE=1 SV=1 - [SARDH_HUMAN]	9.53E-06	-24.9611	-3.0485	1.28E-06	-10.3773	-4.1035
1_4	Q9UHD8	Septin-9 OS=Homo sapiens GN=SEPT9 PE=1 SV=2 - [SEPT9_HUMAN]	4.40E-04	5.5875	2.8187	2.24E-05	8.9297	2.9835
1_4	P34896	Serine hydroxymethyltransferase, cytosolic OS=Homo sapiens GN=SHMT1 PE=1 SV=1 - [GLYC_HUMAN]	8.78E-04	-4.1442	-3.1135	4.77E-05	-7.3267	-4.3879
1_4	Q07955	Serine/arginine-rich splicing factor 1 OS=Homo sapiens GN=SRSF1 PE=1 SV=2 - [SRSF1_HUMAN]	4.60E-05	18.4337	2.7671	6.52E-03	2.8599	2.5140
1_4	P62136	Serine/threonine-protein phosphatase PP1-alpha catalytic subunit OS=Homo sapiens GN=PPP1CA PE=1 SV=1 - [PP1A_HUMAN]	2.75E-02	2.2512	2.7753	5.08E-03	2.9981	2.2871
1_4	P62140	Serine/threonine-protein phosphatase PP1-beta catalytic subunit OS=Homo sapiens GN=PPP1CB PE=1 SV=3 - [PP1B_HUMAN]	1.97E-02	2.4891	2.7832	7.37E-03	2.7867	2.0675
1_4	P50454	Serpin H1 OS=Homo sapiens GN=SERPINH1 PE=1 SV=2 - [SERPH_HUMAN]	6.02E-03	3.1508	2.8080	7.77E-05	6.4468	2.8522
1_4	P27169	Serum paraoxonase/arylesterase 1 OS=Homo sapiens GN=PON1 PE=1 SV=3 - [PON1_HUMAN]	6.36E-06	-25.6833	-3.0375	3.23E-03	-3.2296	-2.0086
1_4	P45954	Short/branched chain specific acyl-CoA dehydrogenase, mitochondrial OS=Homo sapiens GN=ACADSB PE=1 SV=1 - [ACDSB_HUMAN]	3.02E-04	-5.7644	-3.1545	1.80E-04	-5.2557	-4.3301
1_4	P16219	Short-chain specific acyl-CoA dehydrogenase, mitochondrial OS=Homo sapiens GN=ACADS PE=1 SV=1 - [ACADS_HUMAN]	4.04E-04	-5.6498	-3.0990	2.68E-04	-4.8482	-3.7377
1_4	Q9H9B4	Sideroflexin-1 OS=Homo sapiens GN=SFXN1 PE=1 SV=4 - [SFXN1_HUMAN]	7.86E-04	-4.3105	-3.0416	1.65E-03	-3.6002	-3.0008
1_4	Q00796	Sorbitol dehydrogenase OS=Homo sapiens GN=SORD PE=1 SV=4 - [DHSO_HUMAN]	6.75E-04	-4.6020	-3.1283	5.27E-04	-4.2817	-4.1863
1_4	P31040	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial OS=Homo sapiens GN=SDHA PE=1 SV=2 - [DHSA_HUMAN]	5.35E-04	-5.4129	-3.0661	5.81E-05	-6.9581	-3.8160
1_4	P21912	Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial OS=Homo sapiens GN=SDHB PE=1 SV=3 - [DHSB_HUMAN]	8.29E-06	-25.1113	-2.9806	3.76E-05	-7.9800	-2.4158
1_4	P51649	Succinate-semialdehyde dehydrogenase, mitochondrial OS=Homo sapiens GN=ALDH5A1 PE=1 SV=2 - [SSDH_HUMAN]	8.42E-04	-4.1973	-3.0464	6.24E-04	-4.1831	-3.5313
1_4	P53597	Succinyl-CoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial OS=Homo sapiens GN=SUCLG1 PE=1 SV=4 - [SUCA_HUMAN]	7.60E-03	-2.8959	-2.9835	4.18E-03	-3.1111	-2.0343
1_4	P53985	Sulfotransferase 1A1 OS=Homo sapiens GN=SULT1A1 PE=1 SV=3 - [ST1A1_HUMAN]	8.93E-06	-24.9006	-3.1066	8.74E-05	-6.1862	-3.0840
1_4	Q99536	Synaptic vesicle membrane protein VAT-1 homolog OS=Homo sapiens GN=VAT1 PE=1 SV=2 - [VAT1_HUMAN]	1.40E-04	6.0086	2.8511	3.76E-03	3.1593	2.1297
1_4	P24821	Tenascin OS=Homo sapiens GN=TNC PE=1 SV=3 - [TENA_HUMAN]	2.29E-03	3.7639	2.7053	1.56E-02	2.4241	2.6322
1_4	Q01995	Transgelin OS=Homo sapiens GN=TAGLN PE=1 SV=4 - [TAGL_HUMAN]	5.60E-04	5.2949	2.8656	2.49E-04	4.9123	3.2058
1_4	P53007	Tricarboxylate transport protein, mitochondrial OS=Homo sapiens GN=SLC25A1 PE=1 SV=2 - [TXTP_HUMAN]	8.53E-04	-4.1774	-3.0340	2.41E-04	-4.9530	-2.6745
1_4	P09493	Tropomyosin alpha-1 chain OS=Homo sapiens GN=TPM1 PE=1 SV=2 - [TPM1_HUMAN]	2.35E-02	2.3755	2.8161	1.34E-02	2.4977	2.2797
1_4	P67936	Tropomyosin alpha-4 chain OS=Homo sapiens GN=TPM4 PE=1 SV=3 - [TPM4_HUMAN]	2.49E-04	5.8231	2.9284	3.53E-05	8.1100	2.6322
1_4	P22310	UDP-glucuronosyltransferase 1-4 OS=Homo sapiens GN=UGT1A4 PE=1 SV=1 - [UD14_HUMAN]	3.30E-04	-5.7263	-3.0442	7.37E-04	-4.0686	-2.9518
1_4	P06133	UDP-glucuronosyltransferase 2B4 OS=Homo sapiens GN=UGT2B4 PE=1 SV=2 - [UD2B4_HUMAN]	4.32E-04	-5.5968	-3.0069	7.27E-03	-2.7944	-3.2903
1_4	P16662	UDP-glucuronosyltransferase 2B7 OS=Homo sapiens GN=UGT2B7 PE=1 SV=1 - [UD2B7_HUMAN]	4.64E-05	-18.2245	-3.1155	2.55E-04	-4.8869	-3.5857
1_4	Q96CK1	Vacuolar protein sorting-associated protein 35 OS=Homo sapiens GN=VPS35 PE=1 SV=2 - [VPS35_HUMAN]	5.35E-03	3.2839	2.6788	1.88E-03	3.5346	2.4516
1_4	P13611	Versican core protein OS=Homo sapiens GN=VCAN PE=1 SV=3 - [CSPG2_HUMAN]	5.34E-04	5.4194	2.8142	5.12E-03	2.9930	3.1355

Fig. 7 continued

A	ID	ProtName	Pvalues	tscores	log2 Fold Change	pvalues	tscores	log2 Fold Change
1.5	Q04917	14-3-3 protein eta OS=Homo sapiens GN=YWHAH PE=1 SV=4 - [1433F_HUMAN]	5.87E-04	5.0500	3.0198	4.69E-06	9.3956	3.8567
1.5	P31947	14-3-3 protein sigma OS=Homo sapiens GN=SFN PE=1 SV=1 - [1433S_HUMAN]	1.89E-02	2.4449	3.0139	7.01E-04	4.0905	3.6959
1.5	Q17ZP4	17-beta-hydroxysteroid dehydrogenase 13 OS=Homo sapiens GN=HSD17B13 PE=2 SV=1 - [DHB13_HUMAN]	4.59E-05	-19.0172	-3.1005	1.26E-04	-5.2191	-3.2567
1.5	O14756	17-beta-hydroxysteroid dehydrogenase type 6 OS=Homo sapiens GN=HSD17B6 PE=1 SV=1 - [H17B6_HUMAN]	4.25E-05	-20.0852	-3.1163	1.11E-05	-8.1240	-3.9088
1.5	P12694	2-oxoisovalerate dehydrogenase subunit alpha, mitochondrial OS=Homo sapiens GN=BCKDHA PE=1 SV=2 - [ODBA_HUMAN]	1.64E-04	-5.9395	-2.9176	5.42E-04	-4.2558	-2.6382
1.5	P46952	3-hydroxyanthranilate 3,4-dioxygenase OS=Homo sapiens GN=HAAO PE=1 SV=2 - [3HAO_HUMAN]	1.26E-05	-25.2483	-3.0508	5.19E-06	-8.7071	-3.3183
1.5	P51857	3-oxo-5-beta-steroid 4-dehydrogenase OS=Homo sapiens GN=AKR1D1 PE=1 SV=1 - [AK1D1_HUMAN]	4.69E-05	-18.8719	-3.0581	6.10E-03	-2.8413	-2.6145
1.5	P80404	4-aminobutyrate aminotransferase, mitochondrial OS=Homo sapiens GN=ABAT PE=1 SV=3 - [GABT_HUMAN]	7.99E-04	-4.1292	-3.1594	1.03E-06	-11.4817	-5.3259
1.5	P32754	4-hydroxyphenylpyruvate dioxygenase OS=Homo sapiens GN=HPD PE=1 SV=2 - [HPPD_HUMAN]	3.02E-05	-22.1822	-3.1328	4.54E-06	-9.9588	-4.4376
1.5	Q01813	6-phosphofructokinase type C OS=Homo sapiens GN=PFKP PE=1 SV=2 - [K6PP_HUMAN]	1.45E-03	3.8212	2.7049	8.32E-03	2.7042	2.0637
1.5	Q9BWD1	Acetyl-CoA acetyltransferase, cytosolic OS=Homo sapiens GN=ACAT2 PE=1 SV=2 - [THIC_HUMAN]	6.75E-05	-7.8944	-3.0279	9.97E-04	-3.8675	-3.4294
1.5	P68133	Actin, alpha skeletal muscle OS=Homo sapiens GN=ACTA1 PE=1 SV=1 - [ACTS_HUMAN]	2.01E-03	-3.7789	-3.1987	6.76E-03	-2.7862	-5.0961
1.5	P61160	Actin-related protein 2 OS=Homo sapiens GN=ACTR2 PE=1 SV=1 - [ARP2_HUMAN]	1.62E-02	2.5191	2.8651	3.52E-04	4.5350	2.9462
1.5	O15144	Actin-related protein 2/3 complex subunit 2 OS=Homo sapiens GN=ARPC2 PE=1 SV=1 - [ARPC2_HUMAN]	2.02E-02	2.4043	2.7903	2.94E-02	2.1002	2.0637
1.5	Q08AH3	Acyl-coenzyme A synthetase ACSM2A, mitochondrial OS=Homo sapiens GN=ACSM2A PE=1 SV=2 - [ACS2A_HUMAN]	1.46E-05	-24.9514	-3.1313	1.11E-04	-5.2804	-5.0015
1.5	Q6ICK6	Acyl-coenzyme A synthetase ACSM2B, mitochondrial OS=Homo sapiens GN=ACSM2B PE=1 SV=2 - [ACS2B_HUMAN]	1.50E-05	-24.9362	-3.1313	2.91E-06	-10.6014	-5.1339
1.5	P27144	Adenylate kinase isoenzyme 4, mitochondrial OS=Homo sapiens GN=AK4 PE=1 SV=1 - [KAD4_HUMAN]	1.57E-04	-5.9493	-2.9842	6.56E-04	-4.1428	-2.7214
1.5	Q8IUX7	Adipocyte enhancer-binding protein 1 OS=Homo sapiens GN=AEBP1 PE=1 SV=1 - [AEBP1_HUMAN]	1.13E-03	3.8426	2.8321	2.17E-02	2.2468	2.3713
1.5	O43488	Aflatoxin B1 aldehyde reductase member 2 OS=Homo sapiens GN=AKR7A2 PE=1 SV=3 - [ARK72_HUMAN]	6.02E-03	-2.8309	-3.0229	4.53E-04	-4.3764	-2.3306
1.5	O95154	Aflatoxin B1 aldehyde reductase member 3 OS=Homo sapiens GN=AKR7A3 PE=1 SV=2 - [ARK73_HUMAN]	1.45E-05	-24.9555	-3.0862	4.49E-06	-10.0339	-3.8276
1.5	Q9BSE5	Agmatinase, mitochondrial OS=Homo sapiens GN=AGMAT PE=1 SV=2 - [SPEB_HUMAN]	9.66E-04	-3.8668	-3.0674	1.77E-03	-3.5341	-2.0086
1.5	P24298	Alanine aminotransferase 1 OS=Homo sapiens GN=GPT PE=1 SV=3 - [ALAT1_HUMAN]	1.97E-05	-24.4015	-3.0208	9.33E-06	-8.3445	-3.9964
1.5	P07327	Alcohol dehydrogenase 1A OS=Homo sapiens GN=ADH1A PE=1 SV=2 - [ADH1A_HUMAN]	3.63E-03	-3.4267	-3.2451	4.22E-04	-4.4272	-6.0582
1.5	P00325	Alcohol dehydrogenase 1B OS=Homo sapiens GN=ADH1B PE=1 SV=2 - [ADH1B_HUMAN]	5.47E-03	-2.9296	-3.2523	1.42E-04	-5.1686	-6.0932
1.5	P00326	Alcohol dehydrogenase 1C OS=Homo sapiens GN=ADH1C PE=1 SV=2 - [ADH1G_HUMAN]	4.62E-04	-5.6069	-3.2398	1.38E-03	-3.6801	-4.9413
1.5	P08319	Alcohol dehydrogenase 4 OS=Homo sapiens GN=ADH4 PE=1 SV=5 - [ADH4_HUMAN]	6.88E-04	-4.5477	-3.2128	5.30E-05	-5.9153	-5.9289
1.5	P28332	Alcohol dehydrogenase 6 OS=Homo sapiens GN=ADH6 PE=2 SV=2 - [ADH6_HUMAN]	5.08E-04	-5.5097	-3.0225	5.99E-03	-2.8500	-3.3238
1.5	Q9H2A2	Aldehyde dehydrogenase family 8 member A1 OS=Homo sapiens GN=ALDH8A1 PE=1 SV=1 - [AL8A1_HUMAN]	2.94E-05	-22.2723	-3.0403	7.84E-05	-5.5086	-3.5313
1.5	Q06278	Aldehyde oxidase OS=Homo sapiens GN=AOX1 PE=2 SV=2 - [AldO_HUMAN]	4.54E-05	-19.3202	-3.0642	1.84E-03	-3.5143	-4.8209

Fig. 7 continued

1_5	P52895	Aldo-keto reductase family 1 member C2 OS=Homo sapiens GN=AKR1C2 PE=1 SV=3 - [AK1C2_HUMAN]	4.37E-04	-5.6657	-3.0900	1.45E-03	-3.6421	-3.6287
1_5	P17516	Aldo-keto reductase family 1 member C4 OS=Homo sapiens GN=AKR1C4 PE=1 SV=3 - [AK1C4_HUMAN]	4.09E-05	-20.6989	-3.0995	1.70E-04	-5.0263	-3.3814
1_5	P21397	Amine oxidase [flavin-containing] A OS=Homo sapiens GN=MAOA PE=1 SV=1 - [AOFA_HUMAN]	9.10E-04	-3.9539	-3.0613	2.11E-05	-7.0348	-3.3301
1_5	Q03154	Aminoacylase-1 OS=Homo sapiens GN=ACY1 PE=1 SV=1 - [ACY1_HUMAN]	6.00E-05	-9.1930	-3.1496	2.91E-06	-10.6002	-4.4905
1_5	P50995	Annexin A11 OS=Homo sapiens GN=ANXA11 PE=1 SV=1 - [ANX11_HUMAN]	5.71E-05	9.4030	2.8601	2.03E-05	7.0738	3.0302
1_5	P12429	Annexin A3 OS=Homo sapiens GN=ANXA3 PE=1 SV=3 - [ANXA3_HUMAN]	5.53E-05	10.2215	2.8156	1.59E-03	3.5885	2.4937
1_5	P02649	Apolipoprotein E OS=Homo sapiens GN=APOE PE=1 SV=1 - [APOE_HUMAN]	1.33E-02	-2.6121	-2.9647	1.42E-02	-2.4597	-3.3183
1_5	O95831	Apoptosis-inducing factor 1, mitochondrial OS=Homo sapiens GN=AIFM1 PE=1 SV=1 - [AIFM1_HUMAN]	5.53E-03	-2.9211	-3.0900	4.68E-06	-9.5508	-3.9584
1_5	P05089	Arginase-1 OS=Homo sapiens GN=ARG1 PE=1 SV=2 - [ARGI1_HUMAN]	1.22E-05	-25.2963	-3.1406	2.34E-06	-11.0155	-4.9801
1_5	P04424	Argininosuccinate lyase OS=Homo sapiens GN=ASL PE=1 SV=4 - [ARLY_HUMAN]	7.25E-04	-4.3949	-3.1175	1.63E-05	-18.9351	-3.3838
1_5	P00966	Argininosuccinate synthase OS=Homo sapiens GN=ASS1 PE=1 SV=2 - [ASSY_HUMAN]	6.85E-05	-7.8186	-3.1455	2.31E-04	-4.8402	-4.1123
1_5	P22760	Arylacetamide deacetylase OS=Homo sapiens GN=AADAC PE=1 SV=5 - [AAAD_HUMAN]	2.39E-05	-23.4316	-3.0027	5.39E-07	-14.3418	-3.4125
1_5	O43776	Asparagine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=NARS PE=1 SV=1 - [SYNC_HUMAN]	3.43E-04	5.8033	2.7515	2.54E-03	3.3381	2.2012
1_5	Q9BXN1	Asporin OS=Homo sapiens GN=ASPN PE=1 SV=2 - [ASPN_HUMAN]	6.64E-04	4.6521	2.9156	7.24E-03	2.7612	2.7933
1_5	Q08211	ATP-dependent RNA helicase A OS=Homo sapiens GN=DHX9 PE=1 SV=4 - [DHX9_HUMAN]	2.42E-02	2.2769	2.8113	1.46E-04	5.1336	3.8377
1_5	O00571	ATP-dependent RNA helicase DDX3X OS=Homo sapiens GN=DDX3X PE=1 SV=3 - [DDX3X_HUMAN]	1.99E-02	2.4139	2.7327	7.29E-04	4.0652	2.5277
1_5	P13929	Beta-enolase OS=Homo sapiens GN=ENO3 PE=1 SV=5 - [ENOB_HUMAN]	3.10E-04	-5.8220	-3.0904	1.21E-03	-3.7418	-3.7619
1_5	Q93088	Betaine--homocysteine S-methyltransferase 1 OS=Homo sapiens GN=BHMT PE=1 SV=2 - [BHMT1_HUMAN]	3.67E-06	-21.4499	-3.1673	2.37E-05	-6.9563	-4.8682
1_5	Q9UBR1	Beta-ureidopropionase OS=Homo sapiens GN=UPB1 PE=1 SV=1 - [BUP1_HUMAN]	3.42E-05	-21.6121	-3.1074	4.60E-05	-6.0471	-3.6561
1_5	P34913	Bifunctional epoxide hydrolase 2 OS=Homo sapiens GN=EPHX2 PE=1 SV=2 - [HYES_HUMAN]	6.64E-05	-8.1044	-3.0627	3.14E-05	-6.5741	-3.7851
1_5	P31939	Bifunctional purine biosynthesis protein PURH OS=Homo sapiens GN=ATIC PE=1 SV=3 - [PURH_HUMAN]	6.79E-03	2.8065	2.8570	2.93E-04	4.6748	3.8090
1_5	P21810	Biglycan OS=Homo sapiens GN=BGN PE=1 SV=2 - [PGS1_HUMAN]	1.23E-03	3.8353	3.0256	2.10E-05	7.0388	4.7778
1_5	Q14032	Bile acid-CoA:amino acid N-acyltransferase OS=Homo sapiens GN=BAAT PE=1 SV=1 - [BAAT_HUMAN]	3.32E-05	-21.6713	-3.0672	2.73E-04	-4.7041	-2.6382
1_5	Q9Y2P5	Bile acyl-CoA synthetase OS=Homo sapiens GN=SLC27A5 PE=1 SV=1 - [S27A5_HUMAN]	3.60E-05	-21.4856	-3.0863	9.39E-06	-8.3404	-4.4024
1_5	Q06520	Bile salt sulfotransferase OS=Homo sapiens GN=SULT2A1 PE=1 SV=3 - [ST2A1_HUMAN]	2.49E-05	-23.3737	-3.1402	6.35E-07	-11.8596	-4.0738
1_5	P17655	Calpain-2 catalytic subunit OS=Homo sapiens GN=CAPN2 PE=1 SV=6 - [CAN2_HUMAN]	3.40E-04	5.8000	2.7473	2.61E-03	3.3268	2.3612
1_5	P31327	Carbamoyl-phosphate synthase [ammonia], mitochondrial OS=Homo sapiens GN=CPS1 PE=1 SV=2 - [CPSM_HUMAN]	3.38E-03	-3.4694	-3.3307	1.79E-05	-7.2204	-7.8140
1_5	P00918	Carbonic anhydrase 2 OS=Homo sapiens GN=CA2 PE=1 SV=2 - [CAH2_HUMAN]	1.31E-02	-2.6231	-3.0716	5.75E-04	-4.2256	-3.4990
1_5	Q96DG6	Carboxymethylenebutenolidase homolog OS=Homo sapiens GN=CMBL PE=1 SV=1 - [CMBL_HUMAN]	6.85E-05	-7.8198	-3.0003	6.10E-04	-4.1841	-2.6745
1_5	P23786	Carnitine O-palmitoyltransferase 2, mitochondrial OS=Homo sapiens GN=CPT2 PE=1 SV=2 - [CPT2_HUMAN]	5.69E-04	-5.1499	-3.0257	4.92E-04	-4.3063	-3.1528
1_5	O00748	Cocaine esterase OS=Homo sapiens GN=CES2 PE=1 SV=1 - [EST2_HUMAN]	3.76E-05	-21.1922	-3.0621	4.93E-06	-8.7904	-3.3301
1_5	P02462	Collagen alpha-1(IV) chain OS=Homo sapiens GN=COL4A1 PE=1 SV=3 - [CO4A1_HUMAN]	1.83E-04	5.9234	2.8022	2.38E-03	3.3633	2.6246

Fig. 7 continued

1_5	Q99715	Collagen alpha-1(XII) chain OS=Homo sapiens GN=COL12A1 PE=1 SV=2 - [COCA1_HUMAN]	2.42E-04	5.8617	2.7621	2.39E-02	2.2001	2.3351
1_5	Q05707	Collagen alpha-1(XIV) chain OS=Homo sapiens GN=COL14A1 PE=1 SV=3 - [COEA1_HUMAN]	6.89E-04	4.5392	2.9208	7.32E-03	2.7584	3.5311
1_5	P08572	Collagen alpha-2(IV) chain OS=Homo sapiens GN=COL4A2 PE=1 SV=4 - [CO4A2_HUMAN]	1.02E-02	2.7812	2.9100	9.32E-04	3.8946	2.8847
1_5	P00751	Complement factor B OS=Homo sapiens GN=CFB PE=1 SV=2 - [CFAB_HUMAN]	6.47E-04	4.7423	2.8293	2.53E-02	2.1726	2.0493
1_5	Q9P0M6	Core histone macro-H2A.2 OS=Homo sapiens GN=H2AFY2 PE=1 SV=3 - [H2AW_HUMAN]	2.82E-04	5.8368	2.8875	3.96E-04	4.4572	2.9562
1_5	P28845	Corticosteroid 11-beta-dehydrogenase isozyme 1 OS=Homo sapiens GN=HSD11B1 PE=1 SV=3 - [DHI1_HUMAN]	3.52E-05	-21.5846	-2.9659	3.68E-03	-3.1190	-2.0008
1_5	Q86YP6	Cullin-associated NEDD8-dissociated protein 1 OS=Homo sapiens GN=CAND1 PE=1 SV=2 - [CAND1_HUMAN]	3.37E-03	3.4721	2.7822	3.34E-03	3.1719	2.3993
1_5	P35520	Cystathionine beta-synthase OS=Homo sapiens GN=CBS PE=1 SV=2 - [CBS_HUMAN]	2.47E-06	-31.2554	-2.9856	6.09E-04	-4.1863	-2.0840
1_5	P32929	Cystathionine gamma-lyase OS=Homo sapiens GN=CTH PE=1 SV=3 - [CGL_HUMAN]	4.14E-04	-5.7178	-2.9700	2.38E-03	-3.3636	-2.5186
1_5	P00167	Cytochrome b5 OS=Homo sapiens GN=CYB5A PE=1 SV=2 - [CYB5_HUMAN]	4.42E-03	-3.2399	-3.1862	1.37E-04	-5.1888	-3.5936
1_5	P05177	Cytochrome P450 1A2 OS=Homo sapiens GN=CYP1A2 PE=1 SV=3 - [CP1A2_HUMAN]	2.15E-05	-24.1947	-3.0205	1.87E-04	-4.9713	-3.2232
1_5	P11509	Cytochrome P450 2A6 OS=Homo sapiens GN=CYP2A6 PE=1 SV=3 - [CP2A6_HUMAN]	4.08E-05	-20.6985	-3.0746	1.32E-04	-5.2001	-4.6052
1_5	P10632	Cytochrome P450 2C8 OS=Homo sapiens GN=CYP2C8 PE=1 SV=2 - [CP2C8_HUMAN]	2.20E-05	-24.1394	-3.0569	2.54E-06	-10.9282	-3.9088
1_5	P11712	Cytochrome P450 2C9 OS=Homo sapiens GN=CYP2C9 PE=1 SV=3 - [CP2C9_HUMAN]	2.29E-05	-23.7830	-3.0856	1.15E-05	-7.9942	-4.2291
1_5	P10635	Cytochrome P450 2D6 OS=Homo sapiens GN=CYP2D6 PE=1 SV=2 - [CP2D6_HUMAN]	2.54E-04	-5.8528	-2.9541	9.61E-03	-2.6392	-2.4158
1_5	P05181	Cytochrome P450 2E1 OS=Homo sapiens GN=CYP2E1 PE=1 SV=1 - [CP2E1_HUMAN]	4.89E-06	-27.9570	-3.0416	4.66E-06	-9.6735	-3.3879
1_5	P08684	Cytochrome P450 3A4 OS=Homo sapiens GN=CYP3A4 PE=1 SV=4 - [CP3A4_HUMAN]	1.46E-06	-33.4351	-3.1061	6.08E-06	-8.6528	-3.8971
1_5	Q02928	Cytochrome P450 4A11 OS=Homo sapiens GN=CYP4A11 PE=1 SV=1 - [CP4AB_HUMAN]	4.39E-06	-29.1359	-3.0294	1.08E-03	-3.8049	-3.0008
1_5	Q14204	Cytoplasmic dynein 1 heavy chain 1 OS=Homo sapiens GN=DYNC1H1 PE=1 SV=5 - [DYHC1_HUMAN]	2.19E-04	5.8871	2.7437	1.82E-03	3.5186	3.6977
1_5	O75891	Cytosolic 10-formyltetrahydrofolate dehydrogenase OS=Homo sapiens GN=ALDH1L1 PE=1 SV=2 - [AL1L1_HUMAN]	4.84E-05	-18.1426	-3.0944	1.72E-04	-5.0175	-5.1429
1_5	Q02338	D-beta-hydroxybutyrate dehydrogenase, mitochondrial OS=Homo sapiens GN=BDH1 PE=1 SV=3 - [BDH_HUMAN]	1.77E-05	-24.6173	-3.1312	1.27E-05	-7.7814	-4.1884
1_5	P07585	Decorin OS=Homo sapiens GN=DCN PE=1 SV=1 - [PGS2_HUMAN]	6.22E-05	8.9125	2.8707	9.37E-04	3.8928	2.9632
1_5	Q96LJ7	Dehydrogenase/reductase SDR family member 1 OS=Homo sapiens GN=DHRS1 PE=1 SV=1 - [DHRS1_HUMAN]	4.43E-05	-19.8630	-2.9590	7.00E-03	-2.7748	-2.4681
1_5	P30038	Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial OS=Homo sapiens GN=ALDH4A1 PE=1 SV=3 - [AL4A1_HUMAN]	5.28E-03	-2.9694	-3.1271	4.89E-06	-8.8352	-4.6287
1_5	P13716	Delta-aminolevulinic acid dehydratase OS=Homo sapiens GN=ALAD PE=1 SV=1 - [HEM2_HUMAN]	6.57E-04	-4.6955	-3.0717	2.49E-04	-4.7612	-3.5645
1_5	Q07507	Dermatopontin OS=Homo sapiens GN=DPT PE=2 SV=2 - [DERM_HUMAN]	6.51E-04	4.7126	2.9262	8.35E-03	2.7026	2.2357
1_5	P15924	Desmoplakin OS=Homo sapiens GN=DSP PE=1 SV=3 - [DESP_HUMAN]	6.07E-03	2.8254	2.7094	3.97E-02	1.9997	2.3351
1_5	P09417	Dihydropteridine reductase OS=Homo sapiens GN=QDPR PE=1 SV=2 - [DHPR_HUMAN]	8.67E-06	-26.4491	-3.0537	1.31E-04	-5.2022	-3.5579
1_5	Q14117	Dihydropyrimidinase OS=Homo sapiens GN=DPYS PE=1 SV=1 - [DPYS_HUMAN]	3.41E-05	-21.6167	-3.0297	3.89E-05	-6.2560	-2.9183
1_5	P31513	Dimethylaniline monooxygenase [N-oxide-forming] 3 OS=Homo sapiens GN=FMO3 PE=1 SV=5 - [FMO3_HUMAN]	4.40E-05	-19.6725	-3.1060	1.95E-04	-4.9392	-4.2567
1_5	P49326	Dimethylaniline monooxygenase [N-oxide-forming] 5 OS=Homo sapiens GN=FMO5 PE=2 SV=2 - [FMO5_HUMAN]	8.13E-05	-6.8306	-2.9711	1.95E-03	-3.4852	-3.4376
1_5	Q9UI17	Dimethylglycine dehydrogenase, mitochondrial OS=Homo sapiens GN=DMGDH PE=1 SV=2 - [MZGD_HUMAN]	2.54E-05	-23.1845	-3.0665	4.71E-06	-9.2639	-4.0343

Fig. 7 continued

1_5	P78527	DNA-dependent protein kinase catalytic subunit OS=Homo sapiens GN=PRKDC PE=1 SV=3 - [PRKDC_HUMAN]	1.90E-02	2.4431	2.8907	1.71E-04	5.0189	4.1338
1_5	O75356	Ectonucleoside triphosphate diphosphohydrolase 5 OS=Homo sapiens GN=ENTPD5 PE=1 SV=1 - [ENTP5_HUMAN]	1.02E-04	-6.4069	-2.9465	5.08E-02	-1.8860	-2.6382
1_5	Q16134	Electron transfer flavoprotein-ubiquinone oxidoreductase, mitochondrial OS=Homo sapiens GN=ETFDH PE=1 SV=2 - [ETFD_HUMAN]	3.87E-05	-20.9402	-3.0460	2.77E-05	-6.7647	-2.8644
1_5	O75521	Enoyl-CoA delta isomerase 2, mitochondrial OS=Homo sapiens GN=ECI2 PE=1 SV=4 - [ECI2_HUMAN]	1.77E-05	-24.7010	-3.0291	1.07E-04	-5.2911	-3.1495
1_5	Q86Y87	Enoyl-CoA hydratase domain-containing protein 2, mitochondrial OS=Homo sapiens GN=ECHDC2 PE=2 SV=2 - [ECHD2_HUMAN]	2.39E-05	-23.4294	-3.0081	1.53E-04	-5.0804	-2.7619
1_5	Q96HE7	ERO1-like protein alpha OS=Homo sapiens GN=ERO1L PE=1 SV=2 - [ERO1A_HUMAN]	2.93E-04	5.8312	2.8742	8.43E-04	3.9578	2.5088
1_5	P15311	Ezrin OS=Homo sapiens GN=EZR PE=1 SV=4 - [EZRI_HUMAN]	5.96E-05	9.2370	2.9018	8.36E-05	5.4557	3.6512
1_5	Q96AE4	Far upstream element-binding protein 1 OS=Homo sapiens GN=FUBP1 PE=1 SV=3 - [FUBP1_HUMAN]	1.83E-02	2.4629	2.7570	4.38E-03	3.0194	2.5088
1_5	P51648	Fatty aldehyde dehydrogenase OS=Homo sapiens GN=ALDH3A2 PE=1 SV=1 - [AL3A2_HUMAN]	3.40E-03	-3.4663	-3.0148	3.22E-03	-3.1909	-3.0343
1_5	O95954	Formimidoyltransferase-cyclodeaminase OS=Homo sapiens GN=FTCD PE=1 SV=2 - [FTCD_HUMAN]	3.57E-05	-21.5029	-3.1264	4.80E-06	-8.9810	-5.2716
1_5	P09467	Fructose-1,6-bisphosphatase 1 OS=Homo sapiens GN=FBP1 PE=1 SV=5 - [F16P1_HUMAN]	1.15E-04	-6.1991	-3.1701	6.01E-07	-14.4050	-4.7202
1_5	P05062	Fructose-bisphosphate aldolase B OS=Homo sapiens GN=ALDOB PE=1 SV=2 - [ALDOB_HUMAN]	4.53E-03	-3.1992	-3.2556	4.70E-06	-9.3016	-6.4059
1_5	P16930	Fumarylacetoacetase OS=Homo sapiens GN=FAH PE=1 SV=2 - [FAAA_HUMAN]	4.05E-03	-3.3478	-3.1257	4.60E-06	-9.8630	-4.4125
1_5	P51570	Galactokinase OS=Homo sapiens GN=GALK1 PE=1 SV=1 - [GALK1_HUMAN]	4.88E-03	-3.0740	-3.0024	3.00E-03	-3.2346	-2.4493
1_5	P09382	Galectin-1 OS=Homo sapiens GN=LGALS1 PE=1 SV=2 - [LEG1_HUMAN]	3.47E-03	3.4537	2.8706	2.99E-03	3.2349	2.5088
1_5	P17931	Galectin-3 OS=Homo sapiens GN=LGALS3 PE=1 SV=5 - [LEG3_HUMAN]	5.33E-05	10.9702	2.8752	7.20E-03	2.7637	2.0637
1_5	Q08380	Galectin-3-binding protein OS=Homo sapiens GN=LGALS3BP PE=1 SV=1 - [LG3BP_HUMAN]	6.06E-05	9.1350	2.8627	4.71E-04	4.3510	3.1856
1_5	O95479	GDH/6PGL endoplasmic bifunctional protein OS=Homo sapiens GN=H6PD PE=1 SV=2 - [G6PE_HUMAN]	6.46E-05	-8.4845	-2.9933	1.14E-03	-3.7786	-2.9964
1_5	P00390	Glutathione reductase, mitochondrial OS=Homo sapiens GN=GSR PE=1 SV=2 - [GSHR_HUMAN]	1.01E-02	2.7830	2.9352	5.63E-03	2.8790	2.6623
1_5	P08263	Glutathione S-transferase A1 OS=Homo sapiens GN=GSTA1 PE=1 SV=3 - [GSTA1_HUMAN]	2.45E-03	-3.6700	-3.2529	3.87E-03	-3.0961	-5.5464
1_5	P09211	Glutathione S-transferase P OS=Homo sapiens GN=GSTP1 PE=1 SV=2 - [GSTP1_HUMAN]	8.40E-04	4.0443	2.9716	2.34E-04	4.8257	4.4697
1_5	P21695	Glycerol-3-phosphate dehydrogenase [NAD(+)], cytoplasmic OS=Homo sapiens GN=GPD1 PE=1 SV=4 - [GPDA_HUMAN]	4.01E-05	-20.7786	-2.9811	3.49E-05	-6.4160	-3.1620
1_5	P23378	Glycine dehydrogenase [decarboxylating], mitochondrial OS=Homo sapiens GN=GLDC PE=1 SV=2 - [GCSP_HUMAN]	2.39E-05	-22.2182	-3.0836	2.69E-03	-3.3110	-4.1123
1_5	Q6IB77	Glycine N-acyltransferase OS=Homo sapiens GN=GLYAT PE=1 SV=3 - [GLYAT_HUMAN]	1.03E-05	-25.8978	-3.1178	7.21E-06	-17.1469	-4.1035
1_5	Q14749	Glycine N-methyltransferase OS=Homo sapiens GN=GNMT PE=1 SV=3 - [GNMT_HUMAN]	7.90E-06	-26.4860	-2.9966	1.85E-03	-3.5107	-2.8276
1_5	P35573	Glycogen debranching enzyme OS=Homo sapiens GN=AGL PE=1 SV=3 - [GDE_HUMAN]	4.39E-05	-19.8828	-3.0393	9.13E-05	-5.4231	-4.4446
1_5	P11216	Glycogen phosphorylase, brain form OS=Homo sapiens GN=PYGB PE=1 SV=5 - [PYGB_HUMAN]	6.84E-04	4.5548	2.8991	3.88E-05	6.2528	3.4937
1_5	P06737	Glycogen phosphorylase, liver form OS=Homo sapiens GN=PYGL PE=1 SV=4 - [PYGL_HUMAN]	3.71E-05	-21.4062	-3.0756	4.69E-06	-9.4541	-4.6954
1_5	Q9UJ07	GTP:AMP phosphotransferase, mitochondrial OS=Homo sapiens GN=AK3 PE=1 SV=4 - [KAD3_HUMAN]	7.43E-05	-7.1536	-2.9904	8.89E-05	-5.4336	-2.8644
1_5	P62879	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2 OS=Homo sapiens GN=GNB2 PE=1 SV=3 - [GBB2_HUMAN]	1.77E-02	2.4802	2.7538	1.04E-02	2.6000	2.0982
1_5	O14979	Heterogeneous nuclear ribonucleoprotein D-like OS=Homo sapiens GN=HNRPDL PE=1 SV=3 - [HNRDL_HUMAN]	1.71E-02	2.4977	2.8239	1.03E-02	2.6062	2.0982
1_5	Q1KMD3	Heterogeneous nuclear ribonucleoprotein U-like protein 2 OS=Homo sapiens GN=HNRNPUL2 PE=1 SV=1 - [HNRL2_HUMAN]	2.37E-03	3.6928	2.8978	1.04E-02	2.5947	2.1652

Fig. 7 continued

1_5	Q93099	Homogentisate 1,2-dioxygenase OS=Homo sapiens GN=HGD PE=1 SV=2 - [HGD_HUMAN]	8.55E-05	-6.6352	-3.0396	2.43E-03	-3.3548	-3.6287
1_5	Q9UJM8	Hydroxyacid oxidase 1 OS=Homo sapiens GN=HAO1 PE=1 SV=1 - [HAOX1_HUMAN]	1.86E-05	-24.4661	-3.1053	1.86E-04	-4.9782	-4.4990
1_5	Q16836	Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial OS=Homo sapiens GN=HADH PE=1 SV=3 - [HCDH_HUMAN]	6.54E-04	-4.7039	-3.1087	6.26E-05	-5.7171	-3.4009
1_5	Q16775	Hydroxyacylglutathione hydrolase, mitochondrial OS=Homo sapiens GN=HAGH PE=1 SV=2 - [GLO2_HUMAN]	6.99E-05	-7.6573	-2.9897	2.11E-05	-7.0319	-2.4493
1_5	P35914	Hydroxymethylglutaryl-CoA lyase, mitochondrial OS=Homo sapiens GN=HMGCL PE=1 SV=2 - [HMGCL_HUMAN]	1.66E-05	-24.7393	-3.0761	7.82E-05	-5.5207	-2.9431
1_5	P54868	Hydroxymethylglutaryl-CoA synthase, mitochondrial OS=Homo sapiens GN=HMGCS2 PE=1 SV=1 - [HMCS2_HUMAN]	2.66E-03	-3.6060	-3.2672	4.89E-05	-5.9487	-6.0495
1_5	Q6YN16	Hydroxysteroid dehydrogenase-like protein 2 OS=Homo sapiens GN=HSDL2 PE=1 SV=1 - [HSDL2_HUMAN]	8.44E-05	-6.6591	-3.0249	4.98E-04	-4.2974	-2.3749
1_5	Q14974	Importin subunit beta-1 OS=Homo sapiens GN=KPNB1 PE=1 SV=2 - [IMB1_HUMAN]	1.85E-02	2.4576	2.8059	2.35E-03	3.3706	3.2193
1_5	P05556	Integrin beta-1 OS=Homo sapiens GN=ITGB1 PE=1 SV=2 - [ITB1_HUMAN]	2.43E-03	3.6750	2.8239	3.89E-03	3.0848	2.1652
1_5	P19823	Inter-alpha-trypsin inhibitor heavy chain H2 OS=Homo sapiens GN=ITIH2 PE=1 SV=2 - [ITIH2_HUMAN]	5.72E-05	9.3946	2.8529	3.17E-03	3.2019	3.3993
1_5	P26440	Isovaleryl-CoA dehydrogenase, mitochondrial OS=Homo sapiens GN=IVD PE=1 SV=1 - [IVD_HUMAN]	7.26E-05	-7.3549	-2.9789	1.27E-03	-3.7261	-2.6745
1_5	P14923	Junction plakoglobin OS=Homo sapiens GN=JUP PE=1 SV=3 - [PLAK_HUMAN]	3.60E-03	3.4318	2.8074	7.44E-04	4.0482	2.9897
1_5	P08727	Keratin, type I cytoskeletal 19 OS=Homo sapiens GN=KRT19 PE=1 SV=4 - [K1C19_HUMAN]	6.16E-05	8.9687	3.0423	1.23E-03	3.7371	4.7762
1_5	P08729	Keratin, type II cytoskeletal 7 OS=Homo sapiens GN=KRT7 PE=1 SV=5 - [K2C7_HUMAN]	1.99E-04	5.9129	3.0068	2.48E-04	4.7647	3.8292
1_5	O00515	Ladinin-1 OS=Homo sapiens GN=LAD1 PE=1 SV=2 - [LAD1_HUMAN]	5.23E-05	11.8329	2.8060	1.62E-03	3.5811	2.7002
1_5	Q9Y2S2	Lambda-crystallin homolog OS=Homo sapiens GN=CRYL1 PE=1 SV=3 - [CRYL1_HUMAN]	1.59E-05	-24.9065	-3.0232	8.34E-05	-5.4584	-2.8309
1_5	P09960	Leukotriene A-4 hydrolase OS=Homo sapiens GN=LTA4H PE=1 SV=2 - [LKHA4_HUMAN]	5.17E-03	2.9954	2.8263	8.61E-04	3.9451	2.3612
1_5	P23141	Liver carboxylesterase 1 OS=Homo sapiens GN=CES1 PE=1 SV=2 - [EST1_HUMAN]	3.08E-03	-3.5200	-3.2803	7.34E-05	-5.5425	-5.9909
1_5	P07195	L-lactate dehydrogenase B chain OS=Homo sapiens GN=LDHB PE=1 SV=2 - [LDHB_HUMAN]	1.51E-02	2.5517	3.0324	5.39E-04	4.2594	3.3782
1_5	P33121	Long-chain-fatty-acid--CoA ligase 1 OS=Homo sapiens GN=ACSL1 PE=1 SV=1 - [ACSL1_HUMAN]	4.69E-05	-18.5806	-3.1446	1.46E-04	-5.1283	-4.5280
1_5	Q9ULC5	Long-chain-fatty-acid--CoA ligase 5 OS=Homo sapiens GN=ACSL5 PE=1 SV=1 - [ACSL5_HUMAN]	4.64E-05	-18.8499	-3.0648	1.32E-03	-3.7113	-2.7091
1_5	P05455	Lupus La protein OS=Homo sapiens GN=SSB PE=1 SV=2 - [LA_HUMAN]	6.29E-04	4.8868	2.8492	4.59E-05	6.0509	3.1152
1_5	Q7Z4W1	L-xylulose reductase OS=Homo sapiens GN=DCXR PE=1 SV=2 - [DCXR_HUMAN]	3.60E-03	-3.4319	-3.2214	2.63E-06	-10.8683	-5.2410
1_5	P40121	Macrophage-capping protein OS=Homo sapiens GN=CAPG PE=1 SV=2 - [CAPG_HUMAN]	3.54E-03	3.4409	2.8198	3.22E-03	3.1911	2.8292
1_5	Q14764	Major vault protein OS=Homo sapiens GN=MVP PE=1 SV=4 - [MVP_HUMAN]	1.67E-04	5.9364	2.8679	7.08E-04	4.0834	4.0027
1_5	O43708	Maleylacetoacetate isomerase OS=Homo sapiens GN=GSTZ1 PE=1 SV=3 - [MAAI_HUMAN]	1.65E-03	-3.8104	-2.9999	1.08E-02	-2.5800	-2.0086
1_5	P11310	Medium-chain specific acyl-CoA dehydrogenase, mitochondrial OS=Homo sapiens GN=ACADM PE=1 SV=1 - [ACADM_HUMAN]	5.30E-04	-5.4169	-3.0653	3.52E-03	-3.1425	-3.7091
1_5	Q02252	Methylmalonate-semialdehyde dehydrogenase [acylating], mitochondrial OS=Homo sapiens GN=ALDH6A1 PE=1 SV=2 - [MMSA_HUMAN]	7.22E-05	-7.3785	-3.1940	1.26E-06	-14.9249	-5.1968
1_5	Q9H8H3	Methyltransferase-like protein 7A OS=Homo sapiens GN=METTL7A PE=1 SV=1 - [MET7A_HUMAN]	7.90E-05	-6.9288	-3.1078	8.90E-04	-3.9186	-2.4125
1_5	P10620	Microsomal glutathione S-transferase 1 OS=Homo sapiens GN=MGST1 PE=1 SV=1 - [MGST1_HUMAN]	7.19E-05	-7.3936	-3.1164	2.64E-04	-4.7228	-2.4125
1_5	O43772	Mitochondrial carnitine/acylcarnitine carrier protein OS=Homo sapiens GN=SLC25A20 PE=1 SV=1 - [MCAT_HUMAN]	7.32E-06	-26.7650	-2.9591	7.53E-04	-4.0361	-2.4681
1_5	Q9Y6C9	Mitochondrial carrier homolog 2 OS=Homo sapiens GN=MTCH2 PE=1 SV=1 - [MTCH2_HUMAN]	9.07E-04	-3.9565	-3.0184	2.47E-05	-6.9376	-3.0840

Fig. 7 continued

1.5	Q969Z3	MOSC domain-containing protein 2, mitochondrial OS=Homo sapiens GN=MARC2 PE=1 SV=1 - [MOSC2_HUMAN]	2.83E-05	-22.6254	-2.9702	4.86E-06	-8.8723	-2.7020
1.5	Q4G0N4	NAD kinase domain-containing protein 1 OS=Homo sapiens GN=NADKD1 PE=1 SV=2 - [NAKD1_HUMAN]	9.74E-06	-26.1600	-3.0837	4.96E-05	-5.9437	-3.8160
1.5	P16435	NADPH--cytochrome P450 reductase OS=Homo sapiens GN=POR PE=1 SV=2 - [NCPR_HUMAN]	7.35E-05	-7.3305	-3.0231	6.07E-06	-8.6537	-3.3749
1.5	Q09666	Neuroblast differentiation-associated protein AHNAK OS=Homo sapiens GN=AHNAK PE=1 SV=2 - [AHNK_HUMAN]	2.19E-02	2.3562	2.8604	3.27E-02	2.0730	3.8497
1.5	Q15274	Nicotinate-nucleotide pyrophosphorylase [carboxylating] OS=Homo sapiens GN=QPRT PE=1 SV=3 - [NADC_HUMAN]	6.69E-05	-7.9961	-2.9335	1.89E-03	-3.9013	-2.4990
1.5	P22307	Non-specific lipid-transfer protein OS=Homo sapiens GN=SCP2 PE=1 SV=2 - [NLTP_HUMAN]	7.10E-04	-4.4658	-3.0822	2.82E-06	-15.7413	-4.0008
1.5	O00567	Nucleolar protein 56 OS=Homo sapiens GN=NOP56 PE=1 SV=4 - [NOP56_HUMAN]	6.20E-03	2.8146	2.7255	6.51E-03	2.8065	2.8656
1.5	P00480	Ornithine carbamoyltransferase, mitochondrial OS=Homo sapiens GN=OTC PE=1 SV=3 - [OTC_HUMAN]	7.03E-05	-7.5405	-3.1288	2.53E-05	-20.1799	-4.1620
1.5	O60664	Perilipin-3 OS=Homo sapiens GN=PLIN3 PE=1 SV=3 - [PLIN3_HUMAN]	5.47E-05	10.2596	2.8256	6.12E-05	5.8038	2.9562
1.5	Q15063	Periostin OS=Homo sapiens GN=POSTN PE=1 SV=2 - [POSTN_HUMAN]	5.33E-05	10.9638	3.0149	2.00E-03	3.4708	4.5277
1.5	Q9NUI1	Peroxisomal 2,4-dienoyl-CoA reductase OS=Homo sapiens GN=DECR2 PE=1 SV=1 - [DECR2_HUMAN]	2.97E-04	-5.8291	-2.9638	1.44E-03	-3.8454	-2.5645
1.5	Q15067	Peroxisomal acyl-coenzyme A oxidase 1 OS=Homo sapiens GN=ACOX1 PE=1 SV=3 - [ACOX1_HUMAN]	7.08E-05	-7.4793	-3.0451	4.64E-04	-4.3608	-3.7712
1.5	Q9Y4Z4	Peroxisomal acyl-coenzyme A oxidase 2 OS=Homo sapiens GN=ACOX2 PE=1 SV=1 - [ACOX2_HUMAN]	2.35E-05	-23.6363	-3.0730	5.83E-05	-5.8231	-4.0961
1.5	Q08426	Peroxisomal bifunctional enzyme OS=Homo sapiens GN=EHHADH PE=1 SV=3 - [ECHP_HUMAN]	7.25E-04	-4.3993	-3.1724	4.68E-06	-9.4939	-5.7091
1.5	Q9P0Z9	Peroxisomal sarcosine oxidase OS=Homo sapiens GN=PIPOX PE=2 SV=2 - [SOX_HUMAN]	1.91E-05	-24.4395	-3.0673	1.66E-05	-7.3762	-3.6145
1.5	Q9BY49	Peroxisomal trans-2-enoyl-CoA reductase OS=Homo sapiens GN=PECR PE=1 SV=2 - [PECR_HUMAN]	7.09E-05	-7.4863	-3.0006	3.32E-03	-3.1755	-2.0500
1.5	P30039	Phenazine biosynthesis-like domain-containing protein OS=Homo sapiens GN=PBLD PE=1 SV=2 - [PBLD_HUMAN]	2.70E-05	-22.8342	-3.0315	2.19E-04	-4.8794	-3.1863
1.5	P00439	Phenylalanine-4-hydroxylase OS=Homo sapiens GN=PAH PE=1 SV=1 - [PHAH_HUMAN]	6.54E-05	-8.3949	-3.0126	5.33E-04	-4.2671	-2.7619
1.5	Q16822	Phosphoenolpyruvate carboxykinase [GTP], mitochondrial OS=Homo sapiens GN=PCK2 PE=1 SV=3 - [PCKGM_HUMAN]	1.24E-04	-6.1344	-3.1994	4.49E-06	-16.3857	-5.5632
1.5	Q9Y617	Phosphoserine aminotransferase OS=Homo sapiens GN=PSAT1 PE=1 SV=2 - [SERC_HUMAN]	3.96E-05	-20.8837	-3.0023	1.38E-03	-3.8830	-2.3735
1.5	Q15149	Plectin OS=Homo sapiens GN=PLEC PE=1 SV=3 - [PLEC_HUMAN]	3.29E-03	3.4863	2.8085	6.86E-04	4.1126	4.2195
1.5	P51888	Prolargin OS=Homo sapiens GN=PRELP PE=1 SV=1 - [PRELP_HUMAN]	1.15E-02	2.7262	3.0463	1.10E-03	3.7944	4.4506
1.5	Q9UQ80	Proliferation-associated protein 2G4 OS=Homo sapiens GN=PA2G4 PE=1 SV=3 - [PA2G4_HUMAN]	5.40E-03	2.9413	2.8791	2.20E-04	4.8533	2.7498
1.5	P05165	Propionyl-CoA carboxylase alpha chain, mitochondrial OS=Homo sapiens GN=PCCA PE=1 SV=4 - [PCCA_HUMAN]	7.10E-04	-4.4656	-2.9800	3.00E-02	-2.0933	-2.6745
1.5	P05166	Propionyl-CoA carboxylase beta chain, mitochondrial OS=Homo sapiens GN=PCCB PE=1 SV=3 - [PCCB_HUMAN]	6.43E-04	-4.8035	-3.0162	1.88E-02	-2.3293	-2.9964
1.5	Q14914	Prostaglandin reductase 1 OS=Homo sapiens GN=PTGR1 PE=1 SV=2 - [PTGR1_HUMAN]	7.29E-05	-7.3423	-3.0490	2.88E-04	-4.6813	-3.7662
1.5	Q9BPW8	Protein NipSnap homolog 1 OS=Homo sapiens GN=NIPSNAP1 PE=1 SV=1 - [NIPS1_HUMAN]	1.01E-03	-3.8609	-3.0532	1.64E-04	-5.0462	-3.1967
1.5	P31949	Protein S100-A11 OS=Homo sapiens GN=S100A11 PE=1 SV=2 - [S10AB_HUMAN]	5.78E-04	5.0788	2.8796	1.19E-04	5.2427	2.0637
1.5	Q01105	Protein SET OS=Homo sapiens GN=SET PE=1 SV=3 - [SET_HUMAN]	2.55E-03	3.6351	2.8665	1.82E-03	3.5172	2.4022
1.5	Q15436	Protein transport protein Sec23A OS=Homo sapiens GN=SEC23A PE=1 SV=2 - [SC23A_HUMAN]	3.11E-03	-3.5155	-2.8620	2.27E-02	-2.2254	-2.3735
1.5	P55786	Puromycin-sensitive aminopeptidase OS=Homo sapiens GN=NPEPPS PE=1 SV=2 - [PSA_HUMAN]	4.94E-03	3.0601	2.8279	1.24E-02	2.5260	2.3612
1.5	A6ND91	Putative L-aspartate dehydrogenase OS=Homo sapiens GN=ASPDH PE=2 SV=2 - [ASPD_HUMAN]	2.57E-04	-5.8503	-2.9302	1.41E-02	-2.4630	-2.0086

Fig. 7 continued

1.5	Q9NVS9	Pyridoxine-5-phosphate oxidase OS=Homo sapiens GN=PNPO PE=1 SV=1 - [PNPO_HUMAN]	1.27E-05	-25.2404	-2.9789	8.13E-08	-13.6449	-2.1967
1.5	P11498	Pyruvate carboxylase, mitochondrial OS=Homo sapiens GN=PC PE=1 SV=2 - [PYC_HUMAN]	6.59E-05	-8.3156	-3.1278	3.36E-05	-6.4613	-5.0961
1.5	P14618	Pyruvate kinase isozymes M1/M2 OS=Homo sapiens GN=PKM PE=1 SV=4 - [KPYM_HUMAN]	4.20E-04	5.7071	3.0740	7.39E-07	11.7508	5.5615
1.5	P30613	Pyruvate kinase isozymes R/L OS=Homo sapiens GN=PKLR PE=1 SV=2 - [KPYR_HUMAN]	3.81E-05	-20.9736	-3.0488	5.51E-05	-5.8947	-4.1006
1.5	P46940	Ras GTPase-activating-like protein IQGAP1 OS=Homo sapiens GN=IQGAP1 PE=1 SV=1 - [IQGA1_HUMAN]	2.33E-03	3.7068	2.9488	1.92E-05	7.1304	4.0493
1.5	Q13576	Ras GTPase-activating-like protein IQGAP2 OS=Homo sapiens GN=IQGAP2 PE=1 SV=4 - [IQGA2_HUMAN]	1.02E-04	-6.4054	-2.9401	1.05E-02	-2.5924	-3.0343
1.5	Q96HR9	Receptor expression-enhancing protein 6 OS=Homo sapiens GN=REEP6 PE=1 SV=1 - [REEP6_HUMAN]	1.12E-05	-25.3477	-3.0203	3.59E-04	-4.5217	-2.1528
1.5	Q15493	Regucalcin OS=Homo sapiens GN=RGN PE=1 SV=1 - [RGN_HUMAN]	2.92E-06	-30.8468	-2.9930	3.56E-03	-3.1364	-2.5936
1.5	O75452	Retinol dehydrogenase 16 OS=Homo sapiens GN=RDH16 PE=1 SV=2 - [RDH16_HUMAN]	3.86E-05	-20.9445	-3.1225	9.95E-05	-5.3418	-3.8444
1.5	Q07960	Rho GTPase-activating protein 1 OS=Homo sapiens GN=ARHGAP1 PE=1 SV=1 - [RHG01_HUMAN]	2.36E-04	5.8673	2.7838	3.20E-04	4.6015	2.2357
1.5	P52758	Ribonuclease UK114 OS=Homo sapiens GN=HRSP12 PE=1 SV=1 - [UK114_HUMAN]	3.43E-04	-5.8032	-3.1335	1.93E-05	-7.1284	-2.8276
1.5	Q9Y265	RuvB-like 1 OS=Homo sapiens GN=RUVBL1 PE=1 SV=1 - [RUVB1_HUMAN]	3.48E-04	5.7997	2.7167	3.96E-04	4.4576	2.4022
1.5	Q8NBX0	Saccharopine dehydrogenase-like oxidoreductase OS=Homo sapiens GN=SCCPDH PE=1 SV=1 - [SCPDL_HUMAN]	2.62E-03	-3.6145	-2.9965	2.62E-03	-3.3251	-2.6145
1.5	Q00266	S-adenosylmethionine synthase isoform type-1 OS=Homo sapiens GN=MAT1A PE=1 SV=2 - [METK1_HUMAN]	3.27E-05	-21.9037	-3.0877	4.70E-06	-9.3090	-3.5857
1.5	Q9UL12	Sarcosine dehydrogenase, mitochondrial OS=Homo sapiens GN=SARDH PE=1 SV=1 - [SARDH_HUMAN]	1.43E-05	-24.9611	-3.0485	3.19E-06	-10.3773	-4.1035
1.5	Q13228	Selenium-binding protein 1 OS=Homo sapiens GN=SELENBP1 PE=1 SV=2 - [SBP1_HUMAN]	1.82E-02	-2.4660	-3.1481	4.70E-06	-9.2947	-4.4349
1.5	Q15019	Septin-2 OS=Homo sapiens GN=SEPT2 PE=1 SV=1 - [SEPT2_HUMAN]	2.79E-04	5.8383	2.8024	2.67E-04	4.7148	2.2193
1.5	Q8IUH03	Septin-9 OS=Homo sapiens GN=SEPT9 PE=1 SV=2 - [SEPT9_HUMAN]	3.26E-03	3.4910	2.8003	1.62E-03	3.5802	2.5491
1.5	P34896	Serine hydroxymethyltransferase, cytosolic OS=Homo sapiens GN=SHMT1 PE=1 SV=1 - [GLYC_HUMAN]	7.64E-05	-7.0147	-3.1135	1.22E-05	-7.8469	-4.3879
1.5	Q07955	Serine/arginine-rich splicing factor 1 OS=Homo sapiens GN=SRSF1 PE=1 SV=2 - [SRSF1_HUMAN]	6.08E-04	4.9807	2.8279	2.55E-03	3.3361	2.0493
1.5	P30153	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform OS=Homo sapiens GN=PPP2R1A PE=1 SV=4 - [2AAA_HUMAN]	2.59E-02	2.2206	2.7136	8.54E-04	3.9502	2.8292
1.5	P21549	Serine--pyruvate aminotransferase OS=Homo sapiens GN=AGXT PE=1 SV=1 - [SPYA_HUMAN]	3.32E-03	-3.4812	-3.2392	1.04E-05	-8.2032	-6.0039
1.5	P50454	Serpin H1 OS=Homo sapiens GN=SERPINH1 PE=1 SV=2 - [SERPH_HUMAN]	3.09E-03	3.5177	2.9251	4.68E-06	9.5452	3.4871
1.5	P27169	Serum paraoxonase/arylesterase 1 OS=Homo sapiens GN=PON1 PE=1 SV=3 - [PON1_HUMAN]	1.08E-05	-25.6833	-3.0375	3.03E-03	-3.2296	-2.0086
1.5	P45954	Short/branched chain specific acyl-CoA dehydrogenase, mitochondrial OS=Homo sapiens GN=ACADSB PE=1 SV=1 - [ACDSB_HUMAN]	2.25E-05	-23.9208	-3.1545	6.26E-05	-5.7184	-4.3301
1.5	P16219	Short-chain specific acyl-CoA dehydrogenase, mitochondrial OS=Homo sapiens GN=ACADS PE=1 SV=1 - [ACADS_HUMAN]	1.81E-05	-24.5669	-3.0990	1.89E-04	-4.9560	-3.7377
1.5	Q00796	Sorbitol dehydrogenase OS=Homo sapiens GN=SORD PE=1 SV=4 - [DHSO_HUMAN]	6.48E-05	-8.4766	-3.1283	3.55E-04	-4.5286	-4.1863
1.5	O75533	Splicing factor 3B subunit 1 OS=Homo sapiens GN=SF3B1 PE=1 SV=3 - [SF3B1_HUMAN]	2.14E-03	3.7591	2.7362	8.14E-04	3.9832	2.1652
1.5	Q14247	Src substrate cortactin OS=Homo sapiens GN=CTTN PE=1 SV=2 - [SRC8_HUMAN]	1.15E-03	3.8411	2.7452	5.10E-03	2.9286	2.1127
1.5	P21912	Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial OS=Homo sapiens GN=SDHB PE=1 SV=3 - [DHSB_HUMAN]	1.37E-05	-25.1113	-2.9806	1.15E-05	-7.9800	-2.4158
1.5	P51649	Succinate-semialdehyde dehydrogenase, mitochondrial OS=Homo sapiens GN=ALDH5A1 PE=1 SV=2 - [SSDH_HUMAN]	8.15E-05	-6.8162	-3.0464	9.93E-04	-3.8681	-3.5313
1.5	P52225	Sulfotransferase 1A1 OS=Homo sapiens GN=SULT1A1 PE=1 SV=3 - [ST1A1_HUMAN]	7.03E-04	-4.4988	-3.1066	5.48E-05	-5.8883	-3.0840

Fig. 7 continued

1_5	P24821	Tenascin OS=Homo sapiens GN=TNC PE=1 SV=3 - [TENA_HUMAN]	1.56E-03	3.8150	2.7562	1.74E-02	2.3657	3.3713
1_5	P07996	Thrombospondin-1 OS=Homo sapiens GN=THBS1 PE=1 SV=2 - [TSP1_HUMAN]	3.97E-03	3.3645	2.7621	5.49E-03	2.8909	2.2012
1_5	Q13263	Transcription intermediary factor 1-beta OS=Homo sapiens GN=TRIM28 PE=1 SV=5 - [TIF1B_HUMAN]	2.80E-04	5.8380	2.7646	2.20E-03	3.4092	2.9117
1_5	Q01995	Transgelin OS=Homo sapiens GN=TAGLN PE=1 SV=4 - [TAGL_HUMAN]	5.61E-04	5.2302	2.9333	6.24E-04	4.1694	3.4966
1_5	P67936	Tropomyosin alpha-4 chain OS=Homo sapiens GN=TPM4 PE=1 SV=3 - [TPM4_HUMAN]	4.93E-04	5.5606	2.9368	1.72E-05	7.2845	3.3612
1_5	Q13509	Tubulin beta-3 chain OS=Homo sapiens GN=TUBB3 PE=1 SV=2 - [TBB3_HUMAN]	1.55E-03	3.8165	2.9859	7.12E-03	2.7685	5.1341
1_5	P04350	Tubulin beta-4A chain OS=Homo sapiens GN=TUBB4A PE=1 SV=2 - [TBB4A_HUMAN]	5.16E-03	2.9887	3.0176	6.67E-05	5.6551	5.9834
1_5	Q9BUF5	Tubulin beta-6 chain OS=Homo sapiens GN=TUBB6 PE=1 SV=1 - [TBB6_HUMAN]	4.62E-02	2.0789	2.9867	1.27E-03	3.7252	4.9018
1_5	O43399	Tumor protein D54 OS=Homo sapiens GN=TPD52L2 PE=1 SV=2 - [TPD54_HUMAN]	5.31E-04	5.4130	2.8424	7.91E-04	4.0032	2.3713
1_5	P22310	UDP-glucuronosyltransferase 1-4 OS=Homo sapiens GN=UGT1A4 PE=1 SV=1 - [UD14_HUMAN]	4.11E-04	-5.7253	-3.0442	7.23E-04	-4.0686	-2.9518
1_5	P06133	UDP-glucuronosyltransferase 2B4 OS=Homo sapiens GN=UGT2B4 PE=1 SV=2 - [UD2B4_HUMAN]	4.69E-04	-5.5958	-3.0069	6.66E-03	-2.7944	-3.2903
1_5	P16662	UDP-glucuronosyltransferase 2B7 OS=Homo sapiens GN=UGT2B7 PE=1 SV=1 - [UD2B7_HUMAN]	4.79E-05	-18.2245	-3.1155	2.16E-04	-4.8869	-3.5857
1_5	O00159	Unconventional myosin-Ic OS=Homo sapiens GN=MYO1C PE=1 SV=4 - [MYO1C_HUMAN]	2.21E-02	2.3480	2.7065	2.43E-03	3.3545	2.2012
1_5	Q96QK1	Vacuolar protein sorting-associated protein 35 OS=Homo sapiens GN=VPS35 PE=1 SV=2 - [VPS35_HUMAN]	3.34E-03	3.4767	2.7386	3.70E-04	4.4968	2.7501
1_5	P13611	Versican core protein OS=Homo sapiens GN=VCAN PE=1 SV=3 - [CSPG2_HUMAN]	6.11E-05	9.0752	2.9521	8.31E-05	5.4631	3.7501
1_6	Q04917	14-3-3 protein eta OS=Homo sapiens GN=YWHAH PE=1 SV=4 - [1433F_HUMAN]	1.54E-04	5.7344	3.2807	4.33E-05	7.9230	3.5485
1_6	P31947	14-3-3 protein sigma OS=Homo sapiens GN=SFN PE=1 SV=1 - [1433S_HUMAN]	1.54E-02	2.6681	3.2798	2.52E-03	3.3927	3.1797
1_6	Q7Z5P4	17-beta-hydroxysteroid dehydrogenase 13 OS=Homo sapiens GN=HSD17B13 PE=2 SV=1 - [DHB13_HUMAN]	2.93E-06	-19.0172	-3.1005	1.80E-04	-5.2191	-3.2567
1_6	O14756	17-beta-hydroxysteroid dehydrogenase type 6 OS=Homo sapiens GN=HSD17B6 PE=1 SV=1 - [1H17B6_HUMAN]	2.87E-06	-20.0852	-3.1163	3.86E-05	-8.1240	-3.9088
1_6	P12694	2-oxoisovalerate dehydrogenase subunit alpha, mitochondrial OS=Homo sapiens GN=BCKDHA PE=1 SV=2 - [ODBA_HUMAN]	8.75E-05	-5.9395	-2.9176	5.54E-04	-4.2558	-2.6382
1_6	P46952	3-hydroxyanthranilate 3,4-dioxygenase OS=Homo sapiens GN=HAAO PE=1 SV=2 - [3HAO_HUMAN]	8.82E-08	-25.2483	-3.0508	2.92E-05	-8.7071	-3.3183
1_6	P31937	3-hydroxyisobutyrate dehydrogenase, mitochondrial OS=Homo sapiens GN=HIBADH PE=1 SV=2 - [3HIDH_HUMAN]	2.30E-04	-5.6261	-3.0409	3.22E-04	-4.6688	-3.2360
1_6	Q6NVY1	3-hydroxyisobutyryl-CoA hydrolase, mitochondrial OS=Homo sapiens GN=HIBCH PE=1 SV=2 - [HIBCH_HUMAN]	7.15E-04	-4.2380	-3.0159	3.21E-03	-3.2515	-2.0500
1_6	P42765	3-ketoacyl-CoA thiolase, mitochondrial OS=Homo sapiens GN=ACAA2 PE=1 SV=2 - [THIM_HUMAN]	4.53E-04	-4.8381	-3.2303	4.43E-05	-7.8429	-5.7830
1_6	P09110	3-ketoacyl-CoA thiolase, peroxisomal OS=Homo sapiens GN=ACAA1 PE=1 SV=2 - [THIK_HUMAN]	7.60E-05	-6.0806	-3.1528	4.92E-05	-7.5404	-5.1346
1_6	P51857	3-oxo-5-beta-steroid 4-dehydrogenase OS=Homo sapiens GN=AKR1D1 PE=1 SV=1 - [AK1D1_HUMAN]	2.99E-06	-18.5719	-3.0581	6.98E-03	-2.8413	-2.6145
1_6	P80404	4-aminobutyrate aminotransferase, mitochondrial OS=Homo sapiens GN=ABAT PE=1 SV=3 - [GABT_HUMAN]	4.92E-07	-23.5269	-3.1594	1.11E-05	-11.7015	-5.3259
1_6	P32754	4-hydroxyphenylpyruvate dioxygenase OS=Homo sapiens GN=HPD PE=1 SV=2 - [HPPD_HUMAN]	1.63E-06	-22.1822	-3.1328	1.92E-05	-9.9568	-4.4376
1_6	P49189	4-trimethylaminobutyraldehyde dehydrogenase OS=Homo sapiens GN=ALDH9A1 PE=1 SV=3 - [AL9A1_HUMAN]	3.62E-03	-3.6083	-3.0463	3.78E-03	-3.1787	-2.9224
1_6	Q9BWD1	Acetyl-CoA acetyltransferase, cytosolic OS=Homo sapiens GN=ACAT2 PE=1 SV=2 - [THIC_HUMAN]	1.58E-05	-8.0756	-3.0279	1.40E-03	-3.7103	-3.4294
1_6	P61160	Actin-related protein 2 OS=Homo sapiens GN=ACTR2 PE=1 SV=1 - [ARP2_HUMAN]	7.72E-03	2.9081	3.1370	6.31E-05	6.8070	3.3581
1_6	O15143	Actin-related protein 2/3 complex subunit 1B OS=Homo sapiens GN=ARPC1B PE=1 SV=3 - [ARC1B_HUMAN]	6.00E-03	3.2022	3.1098	3.32E-04	4.6453	2.0642

Fig. 7 continued

1_6	O15144	Actin-related protein 2/3 complex subunit 2 OS=Homo sapiens GN=ARPC2 PE=1 SV=1 - [ARPC2_HUMAN]	8.34E-04	4.0735	3.1408	7.70E-04	4.0553	2.4792
1_6	P59998	Actin-related protein 2/3 complex subunit 4 OS=Homo sapiens GN=ARPC4 PE=1 SV=3 - [ARPC4_HUMAN]	5.34E-03	3.3387	3.1919	2.70E-04	4.8711	2.0247
1_6	Q08AH3	Acyl-coenzyme A synthetase ACSM2A, mitochondrial OS=Homo sapiens GN=ACSM2A PE=1 SV=2 - [ACS2A_HUMAN]	1.28E-07	-24.9514	-3.1313	1.73E-04	-5.2804	-5.0015
1_6	Q6ICK6	Acyl-coenzyme A synthetase ACSM2B, mitochondrial OS=Homo sapiens GN=ACSM2B PE=1 SV=2 - [ACS2B_HUMAN]	1.31E-07	-24.9352	-3.1313	1.44E-05	-10.6014	-5.1339
1_6	P27144	Adenylate kinase isoenzyme 4, mitochondrial OS=Homo sapiens GN=AK4 PE=1 SV=1 - [KAD4_HUMAN]	8.54E-05	-5.9493	-2.9842	6.87E-04	-4.1428	-2.7214
1_6	Q8IUX7	Adipocyte enhancer-binding protein 1 OS=Homo sapiens GN=AEBP1 PE=1 SV=1 - [AEBP1_HUMAN]	2.52E-04	5.5874	3.0447	1.34E-02	2.5302	2.1194
1_6	P05141	ADP/ATP translocase 2 OS=Homo sapiens GN=SLC25A5 PE=1 SV=7 - [ADT2_HUMAN]	2.61E-02	-2.2333	-3.0057	2.75E-02	-2.1604	-2.2360
1_6	Q9BSE5	Agmatinase, mitochondrial OS=Homo sapiens GN=AGMAT PE=1 SV=2 - [SPEB_HUMAN]	9.03E-05	-5.9240	-3.0674	1.99E-03	-3.5341	-2.0086
1_6	P24298	Alanine aminotransferase 1 OS=Homo sapiens GN=GPT PE=1 SV=3 - [ALAT1_HUMAN]	2.32E-07	-24.4015	-3.0208	3.58E-05	-8.3445	-3.9964
1_6	P00326	Alcohol dehydrogenase 1C OS=Homo sapiens GN=ADH1C PE=1 SV=2 - [ADH1G_HUMAN]	2.06E-02	-2.4450	-3.2398	3.43E-03	-3.2318	-4.9413
1_6	P08319	Alcohol dehydrogenase 4 OS=Homo sapiens GN=ADH4 PE=1 SV=5 - [ADH4_HUMAN]	2.93E-06	-18.9978	-3.2128	9.06E-06	-5.9807	-5.9289
1_6	P28332	Alcohol dehydrogenase 6 OS=Homo sapiens GN=ADH6 PE=2 SV=2 - [ADH6_HUMAN]	2.94E-04	-5.8097	-3.0225	6.86E-03	-2.8500	-3.3238
1_6	Q9NR42	Aldehyde dehydrogenase family 8 member A1 OS=Homo sapiens GN=ALDH8A1 PE=1 SV=1 - [AL8A1_HUMAN]	1.61E-06	-22.2723	-3.0403	1.31E-04	-5.5086	-3.5313
1_6	P30837	Aldehyde dehydrogenase X, mitochondrial OS=Homo sapiens GN=ALDH1B1 PE=1 SV=3 - [AL1B1_HUMAN]	7.94E-04	-4.1237	-3.1642	1.51E-04	-5.3609	-3.8644
1_6	Q06278	Aldehyde oxidase OS=Homo sapiens GN=AOX1 PE=2 SV=2 - [AOX_HUMAN]	2.91E-06	-19.3202	-3.0642	2.06E-03	-3.5143	-4.8209
1_6	Q04828	Aldo-keto reductase family 1 member C1 OS=Homo sapiens GN=AKR1C1 PE=1 SV=1 - [AK1C1_HUMAN]	3.32E-03	-3.8402	-3.1311	6.84E-04	-4.1453	-3.8666
1_6	P52895	Aldo-keto reductase family 1 member C2 OS=Homo sapiens GN=AKR1C2 PE=1 SV=3 - [AK1C2_HUMAN]	1.96E-04	-5.6657	-3.0900	1.63E-03	-3.8421	-3.6287
1_6	P17516	Aldo-keto reductase family 1 member C4 OS=Homo sapiens GN=AKR1C4 PE=1 SV=3 - [AK1C4_HUMAN]	2.77E-06	-20.6989	-3.0995	2.23E-04	-5.0263	-3.5814
1_6	P21397	Amine oxidase [flavin-containing] A OS=Homo sapiens GN=MAOA PE=1 SV=1 - [AOFA_HUMAN]	1.57E-06	-22.5677	-3.0613	1.51E-11	-21.9394	-3.3301
1_6	Q03154	Aminoacylase-1 OS=Homo sapiens GN=ACY1 PE=1 SV=1 - [ACY1_HUMAN]	1.98E-07	-30.4245	-3.1496	1.45E-05	-10.6002	-4.4905
1_6	Q9H4A4	Aminopeptidase B OS=Homo sapiens GN=RNPEP PE=1 SV=2 - [AMPB_HUMAN]	1.45E-02	2.7082	2.8457	2.00E-03	3.5311	2.5883
1_6	P15144	Aminopeptidase N OS=Homo sapiens GN=ANPEP PE=1 SV=4 - [AMPN_HUMAN]	3.72E-05	-6.8231	-2.9516	6.21E-03	-2.8940	-2.5648
1_6	P50995	Annexin A11 OS=Homo sapiens GN=ANXA11 PE=1 SV=1 - [ANX11_HUMAN]	7.83E-06	16.7702	3.1058	5.01E-05	7.4947	3.0416
1_6	P12429	Annexin A3 OS=Homo sapiens GN=ANXA3 PE=1 SV=3 - [ANXA3_HUMAN]	1.43E-05	14.9937	3.1235	7.56E-05	6.3399	3.1797
1_6	O95394	Anterior gradient protein 2 homolog OS=Homo sapiens GN=AGR2 PE=1 SV=1 - [AGR2_HUMAN]	2.31E-04	5.6211	3.1957	2.65E-03	3.3658	3.6814
1_6	O95831	Apoptosis-inducing factor 1, mitochondrial OS=Homo sapiens GN=AIFM1 PE=1 SV=1 - [AIFM1_HUMAN]	3.93E-04	-5.2010	-3.0900	1.70E-05	-10.4416	-3.9584
1_6	P05089	Arginase-1 OS=Homo sapiens GN=ARG1 PE=1 SV=2 - [ARGI1_HUMAN]	8.26E-08	-25.2963	-3.1406	1.22E-05	-11.0155	-4.9801
1_6	P22760	Arylacetamide deacetylase OS=Homo sapiens GN=AADAC PE=1 SV=5 - [AAAD_HUMAN]	1.00E-06	-23.4316	-3.0027	5.85E-06	-14.3418	-3.4125
1_6	Q9BXN1	Asporin OS=Homo sapiens GN=ASPN PE=1 SV=2 - [ASPN_HUMAN]	1.45E-05	14.7798	3.1279	1.99E-04	5.1185	2.6491
1_6	P24539	ATP synthase subunit b, mitochondrial OS=Homo sapiens GN=ATP5F1 PE=1 SV=2 - [AT5F1_HUMAN]	1.26E-07	-24.9701	-3.0367	4.89E-04	-4.3422	-2.1765
1_6	O75947	ATP synthase subunit d, mitochondrial OS=Homo sapiens GN=ATP5H PE=1 SV=3 - [ATP5H_HUMAN]	2.93E-02	-2.1279	-3.0122	2.19E-02	-2.2841	-2.0086
1_6	Q08211	ATP-dependent RNA helicase A OS=Homo sapiens GN=DHX9 PE=1 SV=4 - [DHX9_HUMAN]	2.02E-02	2.4621	2.8670	2.25E-04	5.0154	3.7258

Fig. 7 continued

1.6	P13929	Beta-enolase OS=Homo sapiens GN=ENO3 PE=1 SV=5 - [ENOB_HUMAN]	1.19E-04	-5.8220	-3.0904	1.32E-03	-3.7418	-3.7619
1.6	P07686	Beta-hexosaminidase subunit beta OS=Homo sapiens GN=HEXB PE=1 SV=3 - [HEXB_HUMAN]	2.67E-02	2.2113	2.7027	1.55E-03	3.8585	2.1156
1.6	Q9Z0S8	Betaine--homocysteine S-methyltransferase 1 OS=Homo sapiens GN=BHMT PE=1 SV=2 - [BHMT1_HUMAN]	2.07E-06	-21.4499	-3.1673	5.89E-05	-6.9563	-4.8682
1.6	Q9UBR1	Beta-ureidopropionase OS=Homo sapiens GN=UPB1 PE=1 SV=1 - [BUP1_HUMAN]	1.87E-06	-21.6121	-3.1074	8.78E-05	-6.0471	-3.6561
1.6	P34913	Bifunctional epoxide hydrolase 2 OS=Homo sapiens GN=EPHX2 PE=1 SV=2 - [HYES_HUMAN]	2.44E-07	-24.3491	-3.0627	6.77E-05	-6.5741	-3.7851
1.6	P31939	Bifunctional purine biosynthesis protein PURH OS=Homo sapiens GN=ATIC PE=1 SV=3 - [PUR9_HUMAN]	8.09E-03	2.8635	2.8685	1.11E-03	3.8273	2.3766
1.6	P21810	Biglycan OS=Homo sapiens GN=BGN PE=1 SV=2 - [PGS1_HUMAN]	5.78E-04	4.4986	3.2174	5.68E-04	4.2420	4.6606
1.6	Q14032	Bile acid-CoA:amino acid N-acyltransferase OS=Homo sapiens GN=BAAT PE=1 SV=1 - [BAAT_HUMAN]	1.82E-06	-21.6713	-3.0672	3.12E-04	-4.7041	-2.6382
1.6	Q9Y2P5	Bile acyl-CoA synthetase OS=Homo sapiens GN=SLC27A5 PE=1 SV=1 - [S27A5_HUMAN]	1.98E-06	-21.4856	-3.0863	3.59E-05	-8.3404	-4.4024
1.6	Q06520	Bile salt sulfotransferase OS=Homo sapiens GN=SULT2A1 PE=1 SV=3 - [ST2A1_HUMAN]	1.09E-06	-23.3737	-3.1402	9.90E-06	-11.8596	-4.0738
1.6	Q96CX2	BTB/POZ domain-containing protein KCTD12 OS=Homo sapiens GN=KCTD12 PE=1 SV=1 - [KCD12_HUMAN]	1.25E-05	15.4303	2.9986	7.59E-04	4.0656	2.6814
1.6	P11586	C-1-tetrahydrofolate synthase, cytoplasmic OS=Homo sapiens GN=MTHFD1 PE=1 SV=3 - [C1TC_HUMAN]	6.99E-04	-4.2655	-3.1108	6.82E-05	-6.5332	-4.9364
1.6	Q9UJS0	Calcium-binding mitochondrial carrier protein Aralar2 OS=Homo sapiens GN=SLC25A13 PE=1 SV=2 - [CMC2_HUMAN]	4.59E-04	-4.8311	-3.0757	2.45E-05	-9.2116	-3.9518
1.6	P17655	Calpain-2 catalytic subunit OS=Homo sapiens GN=CAPN2 PE=1 SV=5 - [CAN2_HUMAN]	2.66E-04	5.5739	2.7966	2.08E-03	3.5107	3.2821
1.6	P31327	Carbamoyl-phosphate synthase [ammonia], mitochondrial OS=Homo sapiens GN=CPS1 PE=1 SV=2 - [CPSM_HUMAN]	4.43E-04	-4.8931	-3.3307	4.84E-05	-7.6142	-7.8140
1.6	Q96DG6	Carboxymethylenebutenolidase homolog OS=Homo sapiens GN=CMBL PE=1 SV=1 - [CMBL_HUMAN]	2.56E-05	-7.0491	-3.0003	9.43E-04	-3.9333	-2.6745
1.6	P23786	Carnitine O-palmitoyltransferase 2, mitochondrial OS=Homo sapiens GN=CPT2 PE=1 SV=2 - [CPT2_HUMAN]	2.60E-06	-21.1579	-3.0257	2.85E-04	-4.7884	-3.1528
1.6	P00450	Ceruloplasmin OS=Homo sapiens GN=CP PE=1 SV=1 - [CERU_HUMAN]	1.24E-02	2.7504	3.1911	6.86E-04	4.1440	3.4363
1.6	O00748	Cocaine esterase OS=Homo sapiens GN=CES2 PE=1 SV=1 - [EST2_HUMAN]	2.59E-06	-21.1922	-3.0821	2.86E-05	-8.7904	-3.3301
1.6	P02462	Collagen alpha-1(IV) chain OS=Homo sapiens GN=COL4A1 PE=1 SV=3 - [CO4A1_HUMAN]	3.03E-04	5.4947	2.8130	3.19E-03	3.2572	2.0033
1.6	Q99715	Collagen alpha-1(XII) chain OS=Homo sapiens GN=COL12A1 PE=1 SV=2 - [COCA1_HUMAN]	3.90E-04	5.2139	2.7725	2.07E-02	2.3219	3.8564
1.6	Q05707	Collagen alpha-1(XIV) chain OS=Homo sapiens GN=COL14A1 PE=1 SV=3 - [COEA1_HUMAN]	9.07E-06	16.3255	3.0884	2.29E-04	5.0039	4.4792
1.6	P00751	Complement factor B OS=Homo sapiens GN=CFB PE=1 SV=2 - [CFAB_HUMAN]	1.44E-04	5.7592	3.1180	1.56E-04	5.3435	3.2664
1.6	P31146	Coronin-1A OS=Homo sapiens GN=CORO1A PE=1 SV=4 - [COR1A_HUMAN]	5.07E-03	3.3881	2.8914	1.07E-03	3.8518	2.1194
1.6	P28845	Corticosteroid 11-beta-dehydrogenase isozyme 1 OS=Homo sapiens GN=HSD11B1 PE=1 SV=3 - [DHI1_HUMAN]	1.88E-06	-21.5848	-2.9859	4.16E-03	-3.1190	-2.0008
1.6	P12532	Creatine kinase U-type, mitochondrial OS=Homo sapiens GN=CKMT1A PE=1 SV=1 - [KCRU_HUMAN]	1.91E-03	3.7681	2.8880	5.88E-03	2.9246	2.1408
1.6	Q86VP6	Cullin-associated NEDD8-dissociated protein 1 OS=Homo sapiens GN=CAND1 PE=1 SV=2 - [CAND1_HUMAN]	2.09E-02	2.4319	2.7057	7.69E-03	2.7841	2.0361
1.6	P35520	Cystathionine beta-synthase OS=Homo sapiens GN=CBS PE=1 SV=2 - [CBS_HUMAN]	4.20E-07	-31.2554	-2.9856	6.28E-04	-4.1863	-2.0840
1.6	P32929	Cystathionine gamma-lyase OS=Homo sapiens GN=CTH PE=1 SV=3 - [CGL_HUMAN]	1.59E-04	-5.7178	-2.9700	2.66E-03	-3.3636	-2.5186
1.6	P21291	Cysteine and glycine-rich protein 1 OS=Homo sapiens GN=CSRP1 PE=1 SV=3 - [CSRP1_HUMAN]	6.84E-03	3.0341	3.1942	3.09E-03	3.2796	2.4941
1.6	P00167	Cytochrome b5 OS=Homo sapiens GN=CYB5A PE=1 SV=2 - [CYB5_HUMAN]	7.42E-04	-4.1956	-3.1862	1.52E-04	-5.3563	-3.5936
1.6	P05177	Cytochrome P450 1A2 OS=Homo sapiens GN=CYP1A2 PE=1 SV=3 - [CP1A2_HUMAN]	2.82E-07	-24.1947	-3.0205	2.38E-04	-4.9713	-3.2232

Fig. 7 continued

1.6	P11509	Cytochrome P450 2A6 OS=Homo sapiens GN=CYP2A6 PE=1 SV=3 - [CP2A6_HUMAN]	2.77E-06	-20.6985	-3.0746	1.82E-04	-5.2001	-4.6052
1.6	P10632	Cytochrome P450 2C8 OS=Homo sapiens GN=CYP2C8 PE=1 SV=2 - [CP2C8_HUMAN]	2.97E-07	-24.1394	-3.0569	1.29E-05	-10.9282	-3.9088
1.6	P11712	Cytochrome P450 2C9 OS=Homo sapiens GN=CYP2C9 PE=1 SV=3 - [CP2C9_HUMAN]	4.02E-07	-23.7830	-3.0856	4.07E-05	-7.9942	-4.2291
1.6	P10635	Cytochrome P450 2D6 OS=Homo sapiens GN=CYP2D6 PE=1 SV=2 - [CP2D6_HUMAN]	1.01E-04	-5.8528	-2.9541	1.06E-02	-2.6392	-2.4158
1.6	P05181	Cytochrome P450 2E1 OS=Homo sapiens GN=CYP2E1 PE=1 SV=1 - [CP2E1_HUMAN]	3.82E-10	-27.9570	-3.0416	2.10E-05	-9.6735	-3.3879
1.6	P08684	Cytochrome P450 3A4 OS=Homo sapiens GN=CYP3A4 PE=1 SV=4 - [CP3A4_HUMAN]	1.66E-06	-33.4351	-3.1061	3.09E-05	-8.8528	-3.8971
1.6	Q02928	Cytochrome P450 4A11 OS=Homo sapiens GN=CYP4A11 PE=1 SV=1 - [CP4AB_HUMAN]	3.39E-08	-29.1359	-3.0294	1.17E-03	-3.8049	-3.0008
1.6	O75891	Cytosolic 10-formyltetrahydrofolate dehydrogenase OS=Homo sapiens GN=ALDH1L1 PE=1 SV=2 - [AL1L1_HUMAN]	3.04E-06	-18.1426	-3.0944	2.25E-04	-5.0175	-5.1429
1.6	O43175	D-3-phosphoglycerate dehydrogenase OS=Homo sapiens GN=PHGDH PE=1 SV=4 - [SERA_HUMAN]	2.04E-03	-3.7571	-3.0089	3.54E-05	-8.3556	-3.3183
1.6	Q02338	D-beta-hydroxybutyrate dehydrogenase, mitochondrial OS=Homo sapiens GN=BDH1 PE=1 SV=3 - [BDH_HUMAN]	1.87E-07	-24.6173	-3.1312	4.52E-05	-7.7814	-4.1884
1.6	P30046	D-dopachrome decarboxylase OS=Homo sapiens GN=DDT PE=1 SV=3 - [DOPD_HUMAN]	1.03E-03	-3.9366	-3.1796	5.72E-04	-4.2393	-2.7020
1.6	P07585	Decorin OS=Homo sapiens GN=DCN PE=1 SV=1 - [PGS2_HUMAN]	1.49E-05	13.5719	3.1399	1.12E-04	5.6942	3.3048
1.6	Q96LJ7	Dehydrogenase/reductase SDR family member 1 OS=Homo sapiens GN=DHRS1 PE=1 SV=1 - [DHRS1_HUMAN]	2.89E-06	-19.8630	-2.9590	7.89E-03	-2.7748	-2.4681
1.6	P30038	Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial OS=Homo sapiens GN=ALDH4A1 PE=1 SV=3 - [AL4A1_HUMAN]	1.56E-05	-8.5389	-3.1271	1.87E-05	-10.2586	-4.6287
1.6	P13716	Delta-aminolevulinic acid dehydratase OS=Homo sapiens GN=ALAD PE=1 SV=1 - [HEM2_HUMAN]	5.71E-04	-4.5170	-3.0717	1.75E-04	-5.2680	-3.5645
1.6	Q07507	Dermatopontin OS=Homo sapiens GN=DPT PE=2 SV=2 - [DERM_HUMAN]	1.49E-05	13.5815	3.1511	8.11E-05	6.1865	2.7366
1.6	P09417	Dihydropteridine reductase OS=Homo sapiens GN=QDPR PE=1 SV=2 - [DHPR_HUMAN]	8.36E-09	-26.4491	-3.0537	1.82E-04	-5.2022	-3.5579
1.6	Q14117	Dihydropyrimidinase OS=Homo sapiens GN=DPYS PE=1 SV=1 - [DPYS_HUMAN]	1.86E-06	-21.6167	-3.0297	7.87E-05	-6.2560	-2.9183
1.6	Q16555	Dihydropyrimidinase-related protein 2 OS=Homo sapiens GN=DPYSL2 PE=1 SV=1 - [DPYL2_HUMAN]	5.92E-03	3.2217	3.1073	3.30E-04	4.6521	3.2173
1.6	Q14195	Dihydropyrimidinase-related protein 3 OS=Homo sapiens GN=DPYSL3 PE=1 SV=1 - [DPYL3_HUMAN]	2.81E-04	5.5511	3.0468	6.68E-04	4.1575	2.8564
1.6	P31513	Dimethylaniline monooxygenase [N-oxide-forming] 3 OS=Homo sapiens GN=FMO3 PE=1 SV=5 - [FMO3_HUMAN]	2.90E-06	-19.6725	-3.1060	2.51E-04	-4.9392	-4.2567
1.6	P49326	Dimethylaniline monooxygenase [N-oxide-forming] 5 OS=Homo sapiens GN=FMO5 PE=2 SV=2 - [FMO5_HUMAN]	2.95E-06	-18.6809	-2.9711	1.49E-03	-3.6790	-3.4376
1.6	Q9UI17	Dimethylglycine dehydrogenase, mitochondrial OS=Homo sapiens GN=DMGDH PE=1 SV=2 - [DMGD_HUMAN]	1.29E-06	-23.1845	-3.0665	2.40E-05	-9.2639	-4.0343
1.6	O75356	Ectonucleoside triphosphate diphosphohydrolase 5 OS=Homo sapiens GN=ENTPD5 PE=1 SV=1 - [ENTP5_HUMAN]	1.32E-10	-27.7478	-2.9465	5.08E-04	-4.3124	-2.6382
1.6	Q12805	EGF-containing fibulin-like extracellular matrix protein 1 OS=Homo sapiens GN=EFEMP1 PE=1 SV=2 - [FBLN3_HUMAN]	3.41E-04	5.4096	2.7915	2.29E-03	3.4522	2.5392
1.6	Q16134	Electron transfer flavoprotein-ubiquinone oxidoreductase, mitochondrial OS=Homo sapiens GN=ETFDH PE=1 SV=2 - [ETFD_HUMAN]	2.69E-06	-20.9402	-3.0460	6.37E-05	-6.7647	-2.8644
1.6	O75521	Enoyl-CoA delta isomerase 2, mitochondrial OS=Homo sapiens GN=ECI2 PE=1 SV=4 - [ECI2_HUMAN]	1.71E-07	-24.7010	-3.0291	1.70E-04	-5.2911	-3.1495
1.6	Q86YB7	Enoyl-CoA hydratase domain-containing protein 2, mitochondrial OS=Homo sapiens GN=ECHDC2 PE=2 SV=2 - [ECHD2_HUMAN]	1.01E-06	-23.4294	-3.0081	2.06E-04	-5.0804	-2.7619
1.6	P07099	Epoxide hydrolase 1 OS=Homo sapiens GN=EPHX1 PE=1 SV=1 - [HYEP_HUMAN]	1.32E-04	-5.7899	-3.2331	1.17E-05	-11.3049	-5.4844
1.6	Q96HE7	ERO1-like protein alpha OS=Homo sapiens GN=ERO1L PE=1 SV=2 - [ERO1A_HUMAN]	1.50E-05	12.7342	3.1641	2.07E-03	3.5115	2.6814
1.6	Q9H0W9	Ester hydrolase C11orf54 OS=Homo sapiens GN=C11orf54 PE=1 SV=1 - [CK054_HUMAN]	3.60E-04	-5.3450	-3.0476	2.60E-03	-3.3772	-2.1785
1.6	P15311	Ezrin OS=Homo sapiens GN=EZR PE=1 SV=4 - [EZRI_HUMAN]	1.86E-04	5.6812	3.2246	2.38E-03	3.4249	4.0756

Fig. 7 continued

1_6	Q96AE4	Far upstream element-binding protein 1 OS=Homo sapiens GN=FUBP1 PE=1 SV=3 - [FUBP1_HUMAN]	3.34E-03	3.6384	2.7994	4.79E-03	3.0359	2.0642
1_6	P07148	Fatty acid-binding protein, liver OS=Homo sapiens GN=FABP1 PE=1 SV=1 - [FABPL_HUMAN]	4.63E-04	-4.8186	-3.2292	3.41E-04	-4.6147	-5.6382
1_6	P51648	Fatty aldehyde dehydrogenase OS=Homo sapiens GN=ALDH3A2 PE=1 SV=1 - [AL3A2_HUMAN]	2.69E-06	-20.9277	-3.0748	4.48E-04	-4.3921	-3.0343
1_6	P35555	Fibrillin-1 OS=Homo sapiens GN=FBN1 PE=1 SV=3 - [FBN1_HUMAN]	2.80E-02	2.1703	2.7787	4.66E-02	1.9406	3.5883
1_6	P23142	Fibulin-1 OS=Homo sapiens GN=FBLN1 PE=1 SV=4 - [FBLN1_HUMAN]	1.47E-05	14.1074	3.0170	1.59E-03	3.6488	2.7366
1_6	P30043	Flavin reductase (NADPH) OS=Homo sapiens GN=BLVRB PE=1 SV=3 - [BLVRB_HUMAN]	5.10E-03	-3.3847	-3.0674	7.06E-03	-2.8351	-2.5814
1_6	O95954	Formimidoyltransferase-cyclodeaminase OS=Homo sapiens GN=FTCD PE=1 SV=2 - [FTCD_HUMAN]	1.96E-06	-21.5029	-3.1264	2.63E-05	-8.9810	-5.2716
1_6	P16930	Fumarylacetoacetase OS=Homo sapiens GN=FAH PE=1 SV=2 - [FAAA_HUMAN]	8.48E-08	-25.2770	-3.1257	1.58E-05	-10.5232	-4.4125
1_6	P51570	Galactokinase OS=Homo sapiens GN=GALK1 PE=1 SV=1 - [GALK1_HUMAN]	8.15E-04	-4.0925	-3.0024	2.60E-03	-3.3770	-2.4493
1_6	P09382	Galectin-1 OS=Homo sapiens GN=LGALS1 PE=1 SV=2 - [LEG1_HUMAN]	3.01E-03	3.6783	2.9328	1.08E-03	3.8436	2.4956
1_6	P17931	Galectin-3 OS=Homo sapiens GN=LGALS3 PE=1 SV=5 - [LEG3_HUMAN]	1.43E-05	15.0115	3.2008	1.07E-04	5.7292	3.3861
1_6	Q08380	Galectin-3-binding protein OS=Homo sapiens GN=LGALS3BP PE=1 SV=1 - [LG3BP_HUMAN]	1.46E-05	14.5078	3.1195	3.15E-04	4.6882	3.4956
1_6	P56470	Galectin-4 OS=Homo sapiens GN=LGALS4 PE=1 SV=1 - [LEG4_HUMAN]	1.90E-02	2.5102	3.2233	3.76E-02	2.0372	4.1797
1_6	O95479	GDH/6PGL endoplasmic bifunctional protein OS=Homo sapiens GN=H6PD PE=1 SV=2 - [G6PE_HUMAN]	1.89E-05	-7.3454	-2.9933	2.95E-03	-3.3059	-2.9964
1_6	P08263	Glutathione S-transferase A1 OS=Homo sapiens GN=GSTA1 PE=1 SV=3 - [GSTA1_HUMAN]	5.06E-05	-6.4630	-3.2529	4.06E-03	-3.1366	-5.5464
1_6	P09211	Glutathione S-transferase P OS=Homo sapiens GN=GSTP1 PE=1 SV=2 - [GSTP1_HUMAN]	4.51E-04	4.8699	3.2108	6.03E-05	6.9256	4.9430
1_6	P21695	Glycerol-3-phosphate dehydrogenase [NAD(+)], cytoplasmic OS=Homo sapiens GN=GPD1 PE=1 SV=4 - [GPDA_HUMAN]	2.74E-06	-20.7786	-2.9811	7.26E-05	-6.4160	-3.1620
1_6	P50440	Glycine amidinotransferase, mitochondrial OS=Homo sapiens GN=GATM PE=1 SV=1 - [GATM_HUMAN]	9.39E-05	-5.8566	-3.1259	8.17E-06	-13.6109	-4.7469
1_6	P23378	Glycine dehydrogenase (decarboxylating), mitochondrial OS=Homo sapiens GN=GLDC PE=1 SV=2 - [GCSP_HUMAN]	1.62E-06	-22.2182	-3.0836	2.93E-03	-3.3110	-4.1123
1_6	Q6IB77	Glycine N-acyltransferase OS=Homo sapiens GN=GLYAT PE=1 SV=3 - [GLYAT_HUMAN]	3.11E-08	-25.8078	-3.1178	2.34E-06	-17.1499	-4.1035
1_6	Q14749	Glycine N-methyltransferase OS=Homo sapiens GN=GNMT PE=1 SV=3 - [GNMT_HUMAN]	7.49E-09	-26.4860	-2.9966	2.08E-03	-3.5107	-2.8276
1_6	P35573	Glycogen debranching enzyme OS=Homo sapiens GN=AGL PE=1 SV=3 - [GDE_HUMAN]	2.89E-06	-19.8828	-3.0393	1.43E-04	-5.4231	-4.4446
1_6	P11216	Glycogen phosphorylase, brain form OS=Homo sapiens GN=PYGB PE=1 SV=5 - [PYGB_HUMAN]	3.89E-04	5.2196	3.1286	3.46E-04	4.6008	3.7910
1_6	P06737	Glycogen phosphorylase, liver form OS=Homo sapiens GN=PYGL PE=1 SV=4 - [PYGL_HUMAN]	1.63E-05	-7.8355	-3.0756	2.22E-05	-9.4541	-4.6854
1_6	Q9UJX7	GTP:AMP phosphotransferase, mitochondrial OS=Homo sapiens GN=AK3 PE=1 SV=4 - [KAD3_HUMAN]	1.59E-04	-5.7179	-2.9904	1.32E-04	-5.5033	-2.8644
1_6	O14979	Heterogeneous nuclear ribonucleoprotein D-like OS=Homo sapiens GN=HNRPDL PE=1 SV=3 - [HNRDL_HUMAN]	4.57E-05	6.5506	3.1433	7.95E-03	2.7715	2.5392
1_6	O43390	Heterogeneous nuclear ribonucleoprotein R OS=Homo sapiens GN=HNRNPR PE=1 SV=1 - [HNRPR_HUMAN]	4.77E-03	3.4377	3.1793	2.93E-04	4.7535	2.9293
1_6	Q1KMD3	Heterogeneous nuclear ribonucleoprotein U-like protein 2 OS=Homo sapiens GN=HNRNPUL2 PE=1 SV=1 - [HNRL2_HUMAN]	3.73E-05	6.8194	3.1349	5.01E-05	7.4949	3.1156
1_6	P16401	Histone H1.5 OS=Homo sapiens GN=HIST1H1B PE=1 SV=3 - [H15_HUMAN]	1.66E-02	2.6087	3.0385	1.36E-03	3.7241	2.8011
1_6	Q7TUI9	Histone H2A.V OS=Homo sapiens GN=H2AFV PE=1 SV=3 - [H2AV_HUMAN]	3.66E-04	5.3336	3.2461	8.70E-03	2.7280	3.8564
1_6	P0C0S5	Histone H2A.Z OS=Homo sapiens GN=H2AFZ PE=1 SV=2 - [H2AZ_HUMAN]	3.66E-04	5.3336	3.2461	8.70E-03	2.7280	3.8564
1_6	P01903	HLA class II histocompatibility antigen, DR alpha chain OS=Homo sapiens GN=HLA-DRA PE=1 SV=1 - [DRA_HUMAN]	5.29E-03	3.3478	3.0973	9.79E-03	2.6700	3.2349

Fig. 7 continued

1_6	Q93099	Homogentisate 1,2-dioxygenase OS=Homo sapiens GN=HGD PE=1 SV=2 - [HGD_HUMAN]	1.56E-05	-8.5338	-3.0396	5.09E-04	-4.3107	-3.6287
1_6	Q9UJM8	Hydroxyacid oxidase 1 OS=Homo sapiens GN=HAO1 PE=1 SV=1 - [HAOX1_HUMAN]	2.18E-07	-24.4661	-3.1053	2.37E-04	-4.9782	-4.4990
1_6	Q16836	Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial OS=Homo sapiens GN=HADH PE=1 SV=3 - [HCDH_HUMAN]	2.93E-04	-5.5105	-3.1087	5.26E-05	-7.3286	-3.4009
1_6	Q16775	Hydroxyacylglutathione hydrolase, mitochondrial OS=Homo sapiens GN=HAGH PE=1 SV=2 - [GLO2_HUMAN]	4.38E-05	-6.8011	-2.9897	5.83E-05	-7.0319	-2.4493
1_6	P35914	Hydroxymethylglutaryl-CoA lyase, mitochondrial OS=Homo sapiens GN=HMGCL PE=1 SV=2 - [HMGCL_HUMAN]	1.64E-07	-24.7393	-3.0761	1.28E-04	-5.5207	-2.9431
1_6	P54868	Hydroxymethylglutaryl-CoA synthase, mitochondrial OS=Homo sapiens GN=HMGCS2 PE=1 SV=1 - [HMCS2_HUMAN]	1.77E-05	-7.5632	-3.2672	8.54E-05	-6.0842	-6.0495
1_6	Q6YN16	Hydroxysteroid dehydrogenase-like protein 2 OS=Homo sapiens GN=HSDL2 PE=1 SV=1 - [HSDL2_HUMAN]	1.61E-06	-22.3011	-3.0249	3.64E-04	-4.5544	-2.3749
1_6	P01871	Ig mu chain C region OS=Homo sapiens GN=IGHM PE=1 SV=3 - [IGHM_HUMAN]	1.71E-02	2.5892	2.8265	4.23E-03	3.1068	2.2173
1_6	P19827	Inter-alpha-trypsin inhibitor heavy chain H1 OS=Homo sapiens GN=ITIH1 PE=1 SV=3 - [ITIH1_HUMAN]	6.80E-03	3.0403	3.0907	5.64E-03	2.9504	3.0247
1_6	Q14624	Inter-alpha-trypsin inhibitor heavy chain H4 OS=Homo sapiens GN=ITIH4 PE=1 SV=4 - [ITIH4_HUMAN]	2.79E-03	3.7011	3.0728	7.96E-03	2.7711	2.2173
1_6	Q12906	Interleukin enhancer-binding factor 3 OS=Homo sapiens GN=ILF3 PE=1 SV=3 - [ILF3_HUMAN]	5.50E-03	3.3107	3.0335	2.18E-03	3.4612	3.1408
1_6	Q96AB3	Isochorismatase domain-containing protein 2, mitochondrial OS=Homo sapiens GN=ISOC2 PE=1 SV=1 - [ISOC2_HUMAN]	3.37E-04	-5.4246	-3.0074	9.55E-04	-3.9247	-2.4681
1_6	P26440	Isovaleryl-CoA dehydrogenase, mitochondrial OS=Homo sapiens GN=IVD PE=1 SV=1 - [IVD_HUMAN]	3.53E-04	-5.3820	-2.9789	7.43E-04	-4.0779	-2.6745
1_6	P14923	Junction plakoglobin OS=Homo sapiens GN=JUP PE=1 SV=3 - [PLAK_HUMAN]	4.40E-03	3.5006	2.7845	4.66E-04	4.3707	2.3581
1_6	P08727	Keratin, type I cytoskeletal 19 OS=Homo sapiens GN=KRT19 PE=1 SV=4 - [K1C19_HUMAN]	1.50E-05	13.1564	3.3319	8.10E-04	4.0219	5.1859
1_6	P04259	Keratin, type II cytoskeletal 6B OS=Homo sapiens GN=KRT6B PE=1 SV=5 - [K2C6B_HUMAN]	1.41E-02	2.7181	2.7619	2.07E-02	2.3240	3.0737
1_6	P08729	Keratin, type II cytoskeletal 7 OS=Homo sapiens GN=KRT7 PE=1 SV=5 - [K2C7_HUMAN]	2.43E-03	3.7284	2.9343	1.25E-02	2.5703	3.4941
1_6	P01042	Kininogen-1 OS=Homo sapiens GN=KNG1 PE=1 SV=2 - [KNG1_HUMAN]	3.56E-04	5.3735	2.7491	9.40E-04	3.9355	2.2866
1_6	Q9Y2S2	Lambda-crystallin homolog OS=Homo sapiens GN=CRYL1 PE=1 SV=3 - [CRYL1_HUMAN]	1.35E-07	-24.9065	-3.0232	1.39E-04	-5.4584	-2.8309
1_6	P09960	Leukotriene A-4 hydrolase OS=Homo sapiens GN=LTA4H PE=1 SV=2 - [LKHA4_HUMAN]	5.20E-03	3.3700	3.0449	1.16E-03	3.8085	2.1194
1_6	P23141	Liver carboxylesterase 1 OS=Homo sapiens GN=CES1 PE=1 SV=2 - [EST1_HUMAN]	5.19E-03	-3.3727	-3.2803	1.22E-04	-5.5654	-5.9909
1_6	P07195	L-lactate dehydrogenase B chain OS=Homo sapiens GN=LDHB PE=1 SV=2 - [LDHB_HUMAN]	1.31E-02	2.7390	3.2394	1.05E-04	5.7483	3.0737
1_6	P33121	Long-chain-fatty-acid--CoA ligase 1 OS=Homo sapiens GN=ACSL1 PE=1 SV=1 - [ACSL1_HUMAN]	2.96E-06	-18.5806	-3.1446	1.97E-04	-5.1283	-4.5280
1_6	Q9ULC5	Long-chain-fatty-acid--CoA ligase 5 OS=Homo sapiens GN=ACSL5 PE=1 SV=1 - [ACSL5_HUMAN]	2.94E-06	-18.8499	-3.0648	1.40E-03	-3.7113	-2.7091
1_6	P05455	Lupus La protein OS=Homo sapiens GN=SSB PE=1 SV=2 - [LA_HUMAN]	5.18E-03	3.3727	2.8789	3.57E-03	3.2140	2.5392
1_6	Q7Z4W1	L-xylulose reductase OS=Homo sapiens GN=DCXR PE=1 SV=2 - [DCXR_HUMAN]	1.11E-03	-3.8982	-3.2214	1.34E-05	-10.8744	-5.2410
1_6	P61626	Lysozyme C OS=Homo sapiens GN=LYZ PE=1 SV=1 - [LYSC_HUMAN]	2.65E-02	2.2190	3.1166	9.01E-03	2.7166	2.3418
1_6	P40121	Macrophage-capping protein OS=Homo sapiens GN=CAPG PE=1 SV=2 - [CAPG_HUMAN]	1.35E-05	15.2715	3.1677	9.37E-05	5.9300	3.5451
1_6	Q14764	Major vault protein OS=Homo sapiens GN=MVP PE=1 SV=4 - [MVP_HUMAN]	1.37E-05	15.1982	3.1330	6.92E-05	6.5008	3.4363
1_6	O43708	Maleylacetoacetate isomerase OS=Homo sapiens GN=GSTZ1 PE=1 SV=3 - [MAAI_HUMAN]	1.54E-03	-3.8104	-2.9899	1.20E-02	-2.5800	-2.0086
1_6	P11310	Medium-chain specific acyl-CoA dehydrogenase, mitochondrial OS=Homo sapiens GN=ACADM PE=1 SV=1 - [ACADM_HUMAN]	5.99E-04	-4.4413	-3.0653	1.60E-03	-3.6476	-3.7091
1_6	O00264	Membrane-associated progesterone receptor component 1 OS=Homo sapiens GN=PGRMC1 PE=1 SV=3 - [PGRC1_HUMAN]	1.07E-04	-5.8410	-3.0713	3.02E-05	-8.6752	-3.6888

Fig. 7 continued

1.6	Q9HCC0	Methylcrotonoyl-CoA carboxylase beta chain, mitochondrial OS=Homo sapiens GN=MCCC2 PE=1 SV=1 - MCCB_HUMAN	3.22E-04	-5.4574	-2.9659	6.34E-04	-4.1812	-3.2566
1.6	Q02252	Methylmalonate-semialdehyde dehydrogenase [acylating], mitochondrial OS=Homo sapiens GN=ALDH6A1 PE=1 SV=2 - MMSA_HUMAN	1.37E-07	-24.8938	-3.1940	1.16E-06	-19.8986	-5.1968
1.6	Q9H8H3	Methyltransferase-like protein 7A OS=Homo sapiens GN=METTL7A PE=1 SV=1 - MET7A_HUMAN	2.90E-06	-19.7644	-3.1078	2.37E-04	-4.9765	-2.4125
1.6	P55083	Microfibril-associated glycoprotein 4 OS=Homo sapiens GN=MFAP4 PE=1 SV=2 - MFAP4_HUMAN	1.82E-03	3.7763	2.8862	1.73E-02	2.4046	2.4941
1.6	P10620	Microsomal glutathione S-transferase 1 OS=Homo sapiens GN=MGST1 PE=1 SV=1 - MGST1_HUMAN	2.59E-06	-21.1889	-3.1164	3.07E-04	-4.7228	-2.4125
1.6	P20774	Mimecan OS=Homo sapiens GN=OGN PE=1 SV=1 - MIME_HUMAN	3.66E-04	5.3354	2.8528	2.57E-03	3.3825	2.2866
1.6	O43772	Mitochondrial carnitine/acylcarnitine carrier protein OS=Homo sapiens GN=SLC25A20 PE=1 SV=1 - MCAT_HUMAN	2.62E-09	-26.7650	-2.9591	7.93E-04	-4.0361	-2.4681
1.6	Q9Y6C9	Mitochondrial carrier homolog 2 OS=Homo sapiens GN=MTCH2 PE=1 SV=1 - MTCH2_HUMAN	1.59E-06	-22.4401	-3.0784	7.03E-06	-13.8061	-3.0840
1.6	Q969Z3	MOSC domain-containing protein 2, mitochondrial OS=Homo sapiens GN=MARC2 PE=1 SV=1 - MOSC2_HUMAN	1.56E-06	-22.6254	-2.9702	2.74E-05	-8.8723	-2.7020
1.6	P98088	Mucin-5AC (Fragments) OS=Homo sapiens GN=MUC5AC PE=1 SV=3 - MUC5A_HUMAN	1.12E-02	2.7770	2.8309	4.77E-02	1.9316	3.6767
1.6	Q7Z406	Myosin-14 OS=Homo sapiens GN=MYH14 PE=1 SV=2 - MYH14_HUMAN	1.18E-02	2.7610	2.8608	1.16E-02	2.5900	3.3581
1.6	Q4G0N4	NAD kinase domain-containing protein 1 OS=Homo sapiens GN=NADKD1 PE=1 SV=2 - NAKD1_HUMAN	1.79E-08	-26.1600	-3.0937	9.27E-05	-5.9437	-3.8160
1.6	P16435	NADPH--cytochrome P450 reductase OS=Homo sapiens GN=POR PE=1 SV=2 - NCPR_HUMAN	1.64E-06	-22.1096	-3.0231	2.22E-05	-9.4504	-3.3749
1.6	Q09666	Neuroblast differentiation-associated protein AHNAK OS=Homo sapiens GN=AHNAK PE=1 SV=2 - AHNK_HUMAN	1.94E-02	2.4917	2.8429	3.32E-02	2.0820	3.5597
1.6	P08246	Neutrophil elastase OS=Homo sapiens GN=ELANE PE=1 SV=1 - ELNE_HUMAN	5.98E-03	3.2071	3.1323	4.64E-02	1.9421	2.2664
1.6	Q15274	Nicotinate-nucleotide pyrophosphorylase [carboxylating] OS=Homo sapiens GN=QPRT PE=1 SV=3 - NADC_HUMAN	1.56E-06	-22.5176	-2.9935	2.11E-03	-3.5013	-2.4990
1.6	P22307	Non-specific lipid-transfer protein OS=Homo sapiens GN=SCP2 PE=1 SV=2 - NLTP_HUMAN	5.62E-05	-6.3966	-3.0822	3.49E-06	-16.3154	-4.0008
1.6	Q9NQR4	Omega-amidase NIT2 OS=Homo sapiens GN=NIT2 PE=1 SV=1 - NIT2_HUMAN	6.31E-04	-4.3907	-3.0391	1.09E-03	-3.8376	-2.9140
1.6	P00480	Ornithine carbamoyltransferase, mitochondrial OS=Homo sapiens GN=OTC PE=1 SV=3 - OTC_HUMAN	4.92E-07	-23.5268	-3.1288	5.77E-07	-20.1799	-4.1620
1.6	O60664	Perilipin-3 OS=Homo sapiens GN=PLIN3 PE=1 SV=3 - PLIN3_HUMAN	2.73E-03	3.7057	2.7541	3.01E-03	3.2955	2.3786
1.6	Q15063	Periostin OS=Homo sapiens GN=POSTN PE=1 SV=2 - POSTN_HUMAN	1.49E-05	13.9084	3.1496	1.85E-03	3.5761	4.0580
1.6	Q9NUJ1	Peroxisomal 2,4-dienoyl-CoA reductase OS=Homo sapiens GN=DECR2 PE=1 SV=1 - DECR2_HUMAN	1.15E-04	-5.8291	-2.9838	1.61E-03	-3.6454	-2.5645
1.6	Q15067	Peroxisomal acyl-coenzyme A oxidase 1 OS=Homo sapiens GN=ACOX1 PE=1 SV=3 - ACOX1_HUMAN	5.16E-08	-25.6091	-3.0451	4.31E-04	-4.4148	-3.7712
1.6	Q9Y424	Peroxisomal acyl-coenzyme A oxidase 2 OS=Homo sapiens GN=ACOX2 PE=1 SV=1 - ACOX2_HUMAN	4.52E-07	-23.6363	-3.0730	1.01E-04	-5.8231	-4.0961
1.6	Q08426	Peroxisomal bifunctional enzyme OS=Homo sapiens GN=EHHADH PE=1 SV=3 - ECHP_HUMAN	4.12E-05	-6.6556	-3.1724	2.16E-05	-9.5611	-5.7091
1.6	Q9P0Z9	Peroxisomal sarcosine oxidase OS=Homo sapiens GN=PIPOX PE=2 SV=2 - ISOX_HUMAN	2.24E-07	-24.4395	-3.0673	5.19E-05	-7.3762	-3.6145
1.6	Q9BY49	Peroxisomal trans-2-enoyl-CoA reductase OS=Homo sapiens GN=PECR PE=1 SV=2 - PECR_HUMAN	1.42E-09	-26.8861	-3.0006	3.80E-03	-3.1755	-2.0500
1.6	P30039	Phenazine biosynthesis-like domain-containing protein OS=Homo sapiens GN=PBLD PE=1 SV=2 - PBLD_HUMAN	1.49E-06	-22.8342	-3.0315	2.68E-04	-4.8794	-3.1863
1.6	P00439	Phenylalanine-4-hydroxylase OS=Homo sapiens GN=PAH PE=1 SV=1 - PHAH_HUMAN	1.73E-06	-21.8428	-3.0126	4.76E-04	-4.3598	-2.7619
1.6	Q16822	Phosphoenolpyruvate carboxykinase [GTP], mitochondrial OS=Homo sapiens GN=PCK2 PE=1 SV=3 - PCKGM_HUMAN	4.04E-05	-6.7026	-3.1994	2.93E-06	-16.5600	-5.5632
1.6	Q9Y617	Phosphoserine aminotransferase OS=Homo sapiens GN=PSAT1 PE=1 SV=2 - SERC_HUMAN	2.71E-06	-20.8837	-3.0023	1.47E-03	-3.6830	-2.3735
1.6	Q15149	Plectin OS=Homo sapiens GN=PLEC PE=1 SV=3 - PLEC_HUMAN	5.71E-05	6.3868	3.1588	7.27E-05	6.4148	5.4956

Fig. 7 continued

1_6	P01833	Polymeric immunoglobulin receptor OS=Homo sapiens GN=PIGR PE=1 SV=4 - [PIGR_HUMAN]	2.08E-03	3.7546	3.0703	1.85E-03	3.5768	3.4363
1_6	P51888	Prolargin OS=Homo sapiens GN=PRELP PE=1 SV=1 - [PRELP_HUMAN]	6.39E-03	3.1209	3.2154	1.84E-04	5.1902	5.1242
1_6	P05165	Propionyl-CoA carboxylase alpha chain, mitochondrial OS=Homo sapiens GN=PCCA PE=1 SV=4 - [PCCA_HUMAN]	3.75E-07	-23.8690	-2.9900	1.97E-03	-3.5393	-2.6745
1_6	P05166	Propionyl-CoA carboxylase beta chain, mitochondrial OS=Homo sapiens GN=PCCB PE=1 SV=3 - [PCCB_HUMAN]	1.77E-05	-7.5575	-3.0162	3.57E-03	-3.2133	-2.9964
1_6	Q14914	Prostaglandin reductase 1 OS=Homo sapiens GN=PTGR1 PE=1 SV=2 - [PTGR1_HUMAN]	1.59E-05	-7.9178	-3.0490	2.70E-04	-4.8697	-3.7662
1_6	Q9BPW8	Protein NipSnap homolog 1 OS=Homo sapiens GN=NIPSNAP1 PE=1 SV=1 - [NIPS1_HUMAN]	4.45E-04	-4.8872	-3.0532	4.60E-05	-7.7559	-3.1967
1_6	P29590	Protein PML OS=Homo sapiens GN=PML PE=1 SV=3 - [PML_HUMAN]	2.46E-03	3.7262	2.7478	2.18E-03	3.4809	2.6767
1_6	P31949	Protein S100-A11 OS=Homo sapiens GN=S100A11 PE=1 SV=2 - [S10AB_HUMAN]	3.75E-04	5.3180	2.8902	6.96E-04	4.1337	2.2531
1_6	P06703	Protein S100-A6 OS=Homo sapiens GN=S100A6 PE=1 SV=1 - [S10A6_HUMAN]	1.51E-05	11.7279	3.1658	2.64E-04	4.8935	2.7044
1_6	Q01105	Protein SET OS=Homo sapiens GN=SET PE=1 SV=3 - [SET_HUMAN]	6.08E-04	4.4233	3.1484	1.39E-03	3.7125	2.4792
1_6	P00734	Prothrombin OS=Homo sapiens GN=F2 PE=1 SV=2 - [THRB_HUMAN]	1.52E-02	2.6800	3.0942	7.52E-03	2.7953	2.2173
1_6	A6ND91	Putative L-aspartate dehydrogenase OS=Homo sapiens GN=ASPDH PE=2 SV=2 - [ASPD_HUMAN]	1.01E-04	-5.8503	-2.9302	1.54E-02	-2.4630	-2.0086
1_6	Q9NVS9	Pyridoxine-5-phosphate oxidase OS=Homo sapiens GN=PNPO PE=1 SV=1 - [PNPO_HUMAN]	8.91E-08	-25.2404	-2.9789	7.64E-06	-13.6449	-2.1967
1_6	P11498	Pyruvate carboxylase, mitochondrial OS=Homo sapiens GN=PC PE=1 SV=2 - [PYC_HUMAN]	1.39E-06	-23.0605	-3.1278	6.97E-05	-6.4805	-5.0961
1_6	P14618	Pyruvate kinase isozymes M1/M2 OS=Homo sapiens GN=PKM PE=1 SV=4 - [KPYM_HUMAN]	4.06E-05	6.6925	3.2827	5.72E-05	7.0458	5.5568
1_6	P30613	Pyruvate kinase isozymes R/L OS=Homo sapiens GN=PKLR PE=1 SV=2 - [KPYR_HUMAN]	2.66E-06	-20.9736	-3.0488	9.66E-05	-5.8847	-4.1006
1_6	P31150	Rab GDP dissociation inhibitor alpha OS=Homo sapiens GN=GDI1 PE=1 SV=2 - [GDIA_HUMAN]	7.76E-03	2.9033	2.8427	2.86E-04	4.7840	3.2173
1_6	P46940	Ras GTPase-activating-like protein IQGAP1 OS=Homo sapiens GN=IQGAP1 PE=1 SV=1 - [IQGA1_HUMAN]	8.35E-04	4.0725	3.1140	9.08E-04	3.9548	4.4285
1_6	Q13576	Ras GTPase-activating-like protein IQGAP2 OS=Homo sapiens GN=IQGAP2 PE=1 SV=4 - [IQGA2_HUMAN]	9.18E-04	-3.9972	-2.9401	1.35E-02	-2.5266	-3.0343
1_6	P51149	Ras-related protein Rab-7a OS=Homo sapiens GN=RAB7A PE=1 SV=1 - [RAB7A_HUMAN]	7.46E-04	4.1897	3.0135	1.99E-04	5.1179	2.5392
1_6	Q96HR9	Receptor expression-enhancing protein 6 OS=Homo sapiens GN=REEP6 PE=1 SV=1 - [REEP6_HUMAN]	7.66E-08	-25.3477	-3.0203	3.83E-04	-4.5217	-2.1528
1_6	Q15493	Regucalcin OS=Homo sapiens GN=RGN PE=1 SV=1 - [RGN_HUMAN]	2.97E-07	-30.8468	-2.9930	4.06E-03	-3.1364	-2.5936
1_6	O75452	Retinol dehydrogenase 16 OS=Homo sapiens GN=RDH16 PE=1 SV=2 - [RDH16_HUMAN]	2.69E-06	-20.9445	-3.1225	1.57E-04	-5.3418	-3.8444
1_6	Q07960	Rho GTPase-activating protein 1 OS=Homo sapiens GN=ARHGAP1 PE=1 SV=1 - [RHG01_HUMAN]	2.90E-04	5.5186	2.7972	1.48E-03	3.6817	2.0642
1_6	P52758	Ribonuclease UK114 OS=Homo sapiens GN=HRSP12 PE=1 SV=1 - [UK114_HUMAN]	1.54E-05	-9.1029	-3.1335	5.93E-05	-6.9421	-2.8276
1_6	Q8NBX0	Saccharopine dehydrogenase-like oxidoreductase OS=Homo sapiens GN=SCCPDH PE=1 SV=1 - [SCPDL_HUMAN]	2.33E-04	-5.6167	-2.9965	1.08E-03	-3.8426	-2.6145
1_6	Q00266	S-adenosylmethionine synthase isoform type-1 OS=Homo sapiens GN=MAT1A PE=1 SV=2 - [METK1_HUMAN]	1.70E-06	-21.9037	-3.0877	2.34E-05	-9.3090	-3.5857
1_6	Q9UL12	Sarcosine dehydrogenase, mitochondrial OS=Homo sapiens GN=SARDH PE=1 SV=1 - [SARDH_HUMAN]	1.27E-07	-24.9611	-3.0485	1.79E-05	-10.3773	-4.1035
1_6	Q15019	Septin-2 OS=Homo sapiens GN=SEPT2 PE=1 SV=1 - [SEPT2_HUMAN]	1.81E-03	3.7710	2.7704	1.27E-03	3.7615	2.2173
1_6	Q9UHD8	Septin-9 OS=Homo sapiens GN=SEPT9 PE=1 SV=2 - [SEPT9_HUMAN]	4.22E-03	3.5263	2.8028	6.45E-03	2.8772	2.1194
1_6	P34896	Serine hydroxymethyltransferase, cytosolic OS=Homo sapiens GN=SHMT1 PE=1 SV=1 - [GLYC_HUMAN]	2.84E-06	-20.3223	-3.1135	3.54E-05	-8.3563	-4.3879
1_6	P34897	Serine hydroxymethyltransferase, mitochondrial OS=Homo sapiens GN=SHMT2 PE=1 SV=3 - [GLYM_HUMAN]	1.09E-03	-3.9082	-3.0520	4.40E-05	-7.8624	-3.6382

Fig. 7 continued

1.6	Q07955	Serine/arginine-rich splicing factor 1 OS=Homo sapiens GN=SRSF1 PE=1 SV=2 - [SRSF1_HUMAN]	3.58E-04	5.3576	2.8458	8.42E-03	2.7440	2.5344
1.6	P30153	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform OS=Homo sapiens GN=PPP2R1A PE=1 SV=4 - [2AAA_HUMAN]	1.07E-03	3.9199	3.0735	9.17E-03	2.7072	2.3786
1.6	P21549	Serine--pyruvate aminotransferase OS=Homo sapiens GN=AGXT PE=1 SV=1 - [SPYA_HUMAN]	4.99E-05	-6.4817	-3.2392	2.93E-05	-8.7024	-6.0039
1.6	P35237	Serpin B6 OS=Homo sapiens GN=SERPINB6 PE=1 SV=3 - [SPB6_HUMAN]	2.01E-04	5.6611	3.0736	2.19E-02	2.2829	2.0642
1.6	P50454	Serpin H1 OS=Homo sapiens GN=SERPINH1 PE=1 SV=2 - [SERPH_HUMAN]	9.71E-04	3.9588	3.1927	6.91E-04	4.1389	3.3172
1.6	P27169	Serum paraoxonase/arylesterase 1 OS=Homo sapiens GN=PON1 PE=1 SV=3 - [PON1_HUMAN]	4.58E-08	-25.6833	-3.0375	3.45E-03	-3.2296	-2.0086
1.6	P45954	Short/branched chain specific acyl-CoA dehydrogenase, mitochondrial OS=Homo sapiens GN=ACADSB PE=1 SV=1 - [ACDSB_HUMAN]	3.59E-07	-23.9208	-3.1545	1.08E-04	-5.7184	-4.3301
1.6	P16219	Short-chain specific acyl-CoA dehydrogenase, mitochondrial OS=Homo sapiens GN=ACADS PE=1 SV=1 - [ACADS_HUMAN]	1.57E-05	-8.3477	-3.0990	2.45E-04	-4.9560	-3.7377
1.6	Q9H9B4	Sideroflexin-1 OS=Homo sapiens GN=SFXN1 PE=1 SV=4 - [SFXN1_HUMAN]	2.06E-04	-5.6558	-3.0416	1.04E-03	-3.8712	-3.0008
1.6	Q00796	Sorbitol dehydrogenase OS=Homo sapiens GN=SORD PE=1 SV=4 - [DHSO_HUMAN]	1.56E-05	-8.3906	-3.1283	3.79E-04	-4.5286	-4.1863
1.6	Q14247	Src substrate cortactin OS=Homo sapiens GN=CTTN PE=1 SV=2 - [SRC8_HUMAN]	2.26E-03	3.7393	2.7135	3.08E-03	3.2816	2.2061
1.6	P31040	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial OS=Homo sapiens GN=SDHA PE=1 SV=2 - [DHSA_HUMAN]	6.71E-04	-4.3188	-3.0661	3.99E-05	-8.0215	-3.8160
1.6	P21912	Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial OS=Homo sapiens GN=SDHB PE=1 SV=3 - [DHSB_HUMAN]	1.06E-07	-25.1113	-2.9806	4.18E-05	-7.9800	-2.4158
1.6	P51649	Succinate-semialdehyde dehydrogenase, mitochondrial OS=Homo sapiens GN=ALDH5A1 PE=1 SV=2 - [SSDH_HUMAN]	1.75E-05	-7.6226	-3.0464	1.62E-04	-5.3255	-3.5313
1.6	P53597	Succinyl-CoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial OS=Homo sapiens GN=SUCLG1 PE=1 SV=4 - [SUCA_HUMAN]	9.22E-05	-5.9134	-2.9835	3.15E-03	-3.2686	-2.0343
1.6	P50225	Sulfotransferase 1A1 OS=Homo sapiens GN=SULT1A1 PE=1 SV=3 - [ST1A1_HUMAN]	1.23E-07	-24.9906	-3.1066	8.11E-05	-6.1862	-3.0840
1.6	Q01995	Transgelin OS=Homo sapiens GN=TAGLN PE=1 SV=4 - [TAGL_HUMAN]	8.18E-05	6.0046	3.2470	2.63E-04	4.8960	3.9177
1.6	P53007	Tricarboxylate transport protein, mitochondrial OS=Homo sapiens GN=SLC25A1 PE=1 SV=2 - [TXTP_HUMAN]	2.35E-05	-7.1297	-3.0340	1.66E-04	-5.3045	-2.6745
1.6	P67936	Tropomyosin alpha-4 chain OS=Homo sapiens GN=TPM4 PE=1 SV=3 - [TPM4_HUMAN]	2.61E-03	3.7147	2.9449	3.23E-03	3.2487	2.7005
1.6	Q15661	Tryptase alpha/beta-1 OS=Homo sapiens GN=TPSAB1 PE=1 SV=1 - [TRYB1_HUMAN]	1.49E-05	13.8266	3.1732	1.70E-03	3.6298	3.6971
1.6	Q71U36	Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1 - [TBA1A_HUMAN]	2.24E-03	3.7421	3.0309	7.52E-03	2.7949	5.4652
1.6	Q13509	Tubulin beta-3 chain OS=Homo sapiens GN=TUBB3 PE=1 SV=2 - [TBB3_HUMAN]	2.54E-03	3.7205	2.9906	1.09E-03	3.8370	5.3253
1.6	O43399	Tumor protein D54 OS=Homo sapiens GN=TPD52L2 PE=1 SV=2 - [TPD54_HUMAN]	3.06E-03	3.6730	2.7959	3.64E-03	3.2024	2.3752
1.6	P22310	UDP-glucuronosyltransferase 1-4 OS=Homo sapiens GN=UGT1A4 PE=1 SV=1 - [UD14_HUMAN]	1.56E-04	-5.7253	-3.0442	7.56E-04	-4.0686	-2.9518
1.6	P06133	UDP-glucuronosyltransferase 2B4 OS=Homo sapiens GN=UGT2B4 PE=1 SV=2 - [UD2B4_HUMAN]	2.45E-04	-5.5958	-3.0069	7.53E-03	-2.7944	-3.2903
1.6	P16662	UDP-glucuronosyltransferase 2B7 OS=Homo sapiens GN=UGT2B7 PE=1 SV=1 - [UD2B7_HUMAN]	3.02E-06	-18.2245	-3.1155	2.66E-04	-4.8869	-3.5857
1.6	Q96QK1	Vacuolar protein sorting-associated protein 35 OS=Homo sapiens GN=VPS35 PE=1 SV=2 - [VPS35_HUMAN]	7.36E-05	6.1245	3.0105	2.92E-03	3.3127	2.7005
1.6	P13611	Versican core protein OS=Homo sapiens GN=VCAN PE=1 SV=3 - [CSPG2_HUMAN]	1.49E-05	13.2630	3.1785	1.27E-03	3.7645	4.0190
1.7	Q04917	14-3-3 protein eta OS=Homo sapiens GN=YWHAH PE=1 SV=4 - [1433F_HUMAN]	1.89E-03	3.7879	3.3175	2.04E-03	3.6205	3.2925
1.7	Q7Z5P4	17-beta-hydroxysteroid dehydrogenase 13 OS=Homo sapiens GN=HSD17B13 PE=2 SV=1 - [DHB13_HUMAN]	6.79E-05	-19.0172	-3.1005	3.15E-04	-5.2191	-3.2567
1.7	O14756	17-beta-hydroxysteroid dehydrogenase type 6 OS=Homo sapiens GN=HSD17B6 PE=1 SV=1 - [H17B6_HUMAN]	6.30E-05	-20.0852	-3.1163	8.24E-05	-8.1240	-3.9088
1.7	P12694	2-oxoisovalerate dehydrogenase subunit alpha, mitochondrial OS=Homo sapiens GN=BCKDHA PE=1 SV=2 - [ODBA_HUMAN]	1.96E-04	-5.9395	-2.9176	8.20E-04	-4.2558	-2.6382

Fig. 7 continued

1_7	P46952	3-hydroxyanthranilate 3,4-dioxygenase OS=Homo sapiens GN=HAAO PE=1 SV=2 - [3HAO_HUMAN]	1.73E-05	-25.2483	-3.0508	6.57E-05	-8.7071	-3.3183
1_7	P31937	3-hydroxyisobutyrate dehydrogenase, mitochondrial OS=Homo sapiens GN=HIBADH PE=1 SV=2 - [3HIDH_HUMAN]	5.71E-03	-3.2010	-3.0409	6.31E-04	-4.4844	-3.2360
1_7	Q6NVY1	3-hydroxyisobutyryl-CoA hydrolase, mitochondrial OS=Homo sapiens GN=HIBCH PE=1 SV=2 - [HIBCH_HUMAN]	6.45E-05	-20.0177	-3.0759	2.29E-03	-3.5445	-2.0500
1_7	P42765	3-ketoacyl-CoA thiolase, mitochondrial OS=Homo sapiens GN=ACAA2 PE=1 SV=2 - [THIM_HUMAN]	8.76E-04	-4.2029	-3.2303	8.50E-05	-7.9918	-5.7630
1_7	P09110	3-ketoacyl-CoA thiolase, peroxisomal OS=Homo sapiens GN=ACAA1 PE=1 SV=2 - [THIK_HUMAN]	9.65E-04	-4.0787	-3.1528	9.62E-05	-7.5312	-5.1346
1_7	P51857	3-oxo-5-beta-steroid 4-dehydrogenase OS=Homo sapiens GN=AKR1D1 PE=1 SV=1 - [AK1D1_HUMAN]	7.05E-05	-18.5719	-3.0581	7.27E-03	-2.8413	-2.6145
1_7	P62266	40S ribosomal protein S23 OS=Homo sapiens GN=RPS23 PE=1 SV=3 - [RS23_HUMAN]	2.45E-02	2.3428	3.3022	3.86E-03	3.2159	2.0745
1_7	P80404	4-aminobutyrate aminotransferase, mitochondrial OS=Homo sapiens GN=ABAT PE=1 SV=3 - [GABT_HUMAN]	3.33E-05	-23.5269	-3.1594	2.13E-05	-11.7015	-5.3259
1_7	P32754	4-hydroxyphenylpyruvate dioxygenase OS=Homo sapiens GN=HPD PE=1 SV=2 - [HPPD_HUMAN]	4.37E-05	-22.1822	-3.1328	4.31E-05	-9.9568	-4.4376
1_7	P49189	4-trimethylaminobutyraldehyde dehydrogenase OS=Homo sapiens GN=ALDH9A1 PE=1 SV=3 - [AL9A1_HUMAN]	1.57E-05	-25.4861	-3.0463	3.06E-04	-5.2556	-2.9224
1_7	Q9BWD1	Acetyl-CoA acetyltransferase, cytosolic OS=Homo sapiens GN=ACAT2 PE=1 SV=2 - [THIC_HUMAN]	7.65E-05	-16.9674	-3.0279	1.38E-03	-3.8675	-3.4294
1_7	P24752	Acetyl-CoA acetyltransferase, mitochondrial OS=Homo sapiens GN=ACAT1 PE=1 SV=1 - [THIL_HUMAN]	5.86E-04	-5.0734	-3.1956	6.41E-05	-8.8367	-5.4821
1_7	P61160	Actin-related protein 2 OS=Homo sapiens GN=ACTR2 PE=1 SV=1 - [ARP2_HUMAN]	3.33E-03	3.6229	3.2449	1.11E-04	6.9909	2.8192
1_7	O15144	Actin-related protein 2/3 complex subunit 2 OS=Homo sapiens GN=ARPC2 PE=1 SV=1 - [ARPC2_HUMAN]	6.00E-04	4.9831	3.2140	7.29E-03	2.8395	2.6550
1_7	Q09AH3	Acyl-coenzyme A synthetase ACSM2A, mitochondrial OS=Homo sapiens GN=ACSM2A PE=1 SV=2 - [ACS2A_HUMAN]	1.99E-05	-24.9514	-3.1313	3.00E-04	-5.2804	-5.0015
1_7	Q6ICX6	Acyl-coenzyme A synthetase ACSM2B, mitochondrial OS=Homo sapiens GN=ACSM2B PE=1 SV=2 - [ACS2B_HUMAN]	2.04E-05	-24.9352	-3.1313	3.63E-05	-10.6014	-5.1339
1_7	P54819	Adenylate kinase 2, mitochondrial OS=Homo sapiens GN=AK2 PE=1 SV=2 - [KAD2_HUMAN]	3.92E-03	-3.5307	-3.0512	2.10E-04	-5.7551	-2.9224
1_7	P27144	Adenylate kinase isoenzyme 4, mitochondrial OS=Homo sapiens GN=AK4 PE=1 SV=1 - [KAD4_HUMAN]	1.94E-04	-5.9493	-2.9842	9.72E-04	-4.1428	-2.7214
1_7	Q9BSE5	Agmatinase, mitochondrial OS=Homo sapiens GN=AGMAT PE=1 SV=2 - [SPEB_HUMAN]	2.04E-04	-5.9240	-3.0674	2.33E-03	-3.5341	-2.0086
1_7	P24298	Alanine aminotransferase 1 OS=Homo sapiens GN=GPT PE=1 SV=3 - [ALAT1_HUMAN]	2.61E-05	-24.4015	-3.0208	7.20E-05	-8.3445	-3.9984
1_7	P07327	Alcohol dehydrogenase 1A OS=Homo sapiens GN=ADH1A PE=1 SV=2 - [ADH1A_HUMAN]	1.67E-04	-6.1622	-3.2451	5.82E-04	-4.5699	-6.0592
1_7	P00325	Alcohol dehydrogenase 1B OS=Homo sapiens GN=ADH1B PE=1 SV=2 - [ADH1B_HUMAN]	1.66E-04	-6.1661	-3.2523	2.91E-04	-5.3230	-6.0932
1_7	P00326	Alcohol dehydrogenase 1C OS=Homo sapiens GN=ADH1C PE=1 SV=2 - [ADH1G_HUMAN]	9.89E-04	-4.0530	-3.2398	2.32E-03	-3.5368	-4.9413
1_7	P08319	Alcohol dehydrogenase 4 OS=Homo sapiens GN=ADH4 PE=1 SV=5 - [ADH4_HUMAN]	6.83E-05	-18.9978	-3.2128	1.81E-04	-5.9807	-5.9289
1_7	P28332	Alcohol dehydrogenase 6 OS=Homo sapiens GN=ADH6 PE=2 SV=2 - [ADH6_HUMAN]	4.52E-04	-5.5097	-3.0225	7.16E-03	-2.8500	-3.3238
1_7	Q9HZA2	Aldehyde dehydrogenase family 8 member A1 OS=Homo sapiens GN=ALDH8A1 PE=1 SV=1 - [AL8A1_HUMAN]	4.19E-05	-22.2723	-3.0403	2.52E-04	-5.5086	-3.5313
1_7	P30837	Aldehyde dehydrogenase X, mitochondrial OS=Homo sapiens GN=ALDH1B1 PE=1 SV=3 - [AL1B1_HUMAN]	4.18E-03	-3.4968	-3.1642	3.89E-04	-5.0020	-3.8644
1_7	Q06278	Aldehyde oxidase OS=Homo sapiens GN=AOX1 PE=2 SV=2 - [AOX_HUMAN]	6.72E-05	-19.3202	-3.0642	2.42E-03	-3.5143	-4.8209
1_7	Q04828	Aldo-keto reductase family 1 member C1 OS=Homo sapiens GN=AKR1C1 PE=1 SV=1 - [AK1C1_HUMAN]	2.10E-02	-2.4634	-3.1311	7.34E-04	-4.3484	-3.8666
1_7	P52895	Aldo-keto reductase family 1 member C2 OS=Homo sapiens GN=AKR1C2 PE=1 SV=3 - [AK1C2_HUMAN]	3.56E-04	-5.6657	-3.0900	1.94E-03	-3.6421	-3.6287
1_7	P17516	Aldo-keto reductase family 1 member C4 OS=Homo sapiens GN=AKR1C4 PE=1 SV=3 - [AK1C4_HUMAN]	5.82E-05	-20.6989	-3.0995	3.74E-04	-5.0263	-3.5814
1_7	Q96IU4	Alpha/beta hydrolase domain-containing protein 14B OS=Homo sapiens GN=ABHD14B PE=1 SV=1 - [ABHEB_HUMAN]	5.78E-03	-3.1825	-3.0113	2.32E-04	-5.5952	-2.7816

Fig. 7 continued

1_7	P49419	Alpha-aminoadipic semialdehyde dehydrogenase OS=Homo sapiens GN=ALDH7A1 PE=1 SV=5 - [AL7A1_HUMAN]	9.22E-05	-7.7182	-3.1379	2.39E-04	-5.5746	-4.6002
1_7	P21397	Amine oxidase [flavin-containing] A OS=Homo sapiens GN=MAOA PE=1 SV=1 - [AOFA_HUMAN]	5.23E-03	-3.3098	-3.0613	1.61E-04	-6.0918	-3.3301
1_7	P27338	Amine oxidase [flavin-containing] B OS=Homo sapiens GN=MAOB PE=1 SV=3 - [AOFB_HUMAN]	1.91E-05	-24.9681	-3.0750	1.38E-05	-14.0871	-3.9628
1_7	Q03154	Aminoacylase-1 OS=Homo sapiens GN=ACY1 PE=1 SV=1 - [ACY1_HUMAN]	1.62E-06	-30.4245	-3.1496	3.63E-05	-10.6002	-4.4905
1_7	P50995	Annexin A11 OS=Homo sapiens GN=ANXA11 PE=1 SV=1 - [ANX11_HUMAN]	6.31E-05	20.0804	3.1827	4.76E-04	4.7949	2.6576
1_7	P12429	Annexin A3 OS=Homo sapiens GN=ANXA3 PE=1 SV=3 - [ANXA3_HUMAN]	6.99E-05	18.5979	3.1575	5.07E-03	3.0486	2.8192
1_7	O95994	Anterior gradient protein 2 homolog OS=Homo sapiens GN=AGR2 PE=1 SV=1 - [AGR2_HUMAN]	4.02E-05	22.5617	3.3637	1.06E-04	7.2675	3.5751
1_7	P05089	Arginase-1 OS=Homo sapiens GN=ARG1 PE=1 SV=2 - [ARG1_HUMAN]	1.68E-05	-25.2963	-3.1406	3.10E-05	-11.0155	-4.9801
1_7	P04424	Argininosuccinate lyase OS=Homo sapiens GN=ASL PE=1 SV=4 - [ARLY_HUMAN]	6.35E-03	-3.0546	-3.1175	2.38E-05	-11.4652	-4.4990
1_7	P00966	Argininosuccinate synthase OS=Homo sapiens GN=ASS1 PE=1 SV=2 - [ASSY_HUMAN]	1.68E-04	-6.1384	-3.1455	5.13E-04	-4.7170	-4.1123
1_7	P22760	Arylacetamide deacetylase OS=Homo sapiens GN=AADAC PE=1 SV=5 - [AAAD_HUMAN]	3.43E-05	-23.4316	-3.0027	1.15E-05	-14.3418	-3.4125
1_7	P24539	ATP synthase subunit b, mitochondrial OS=Homo sapiens GN=ATP5F1 PE=1 SV=2 - [AT5F1_HUMAN]	4.45E-04	-5.5247	-3.0367	7.88E-03	-2.7905	-2.1785
1_7	O75947	ATP synthase subunit d, mitochondrial OS=Homo sapiens GN=ATP5H PE=1 SV=3 - [ATP5H_HUMAN]	4.48E-03	-3.4491	-3.0122	1.45E-02	-2.4868	-2.0086
1_7	Q08211	ATP-dependent RNA helicase A OS=Homo sapiens GN=DHX9 PE=1 SV=4 - [DHX9_HUMAN]	1.09E-02	2.7848	3.0459	1.85E-03	3.6648	2.5735
1_7	P13929	Beta-enolase OS=Homo sapiens GN=ENO3 PE=1 SV=5 - [ENOB_HUMAN]	2.44E-04	-5.8220	-3.0904	1.62E-03	-3.7418	-3.7619
1_7	Q93088	Betaine--homocysteine S-methyltransferase 1 OS=Homo sapiens GN=BHMT PE=1 SV=2 - [BHMT1_HUMAN]	5.21E-05	-21.4499	-3.1673	1.12E-04	-6.9563	-4.8692
1_7	Q9UBR1	Beta-ureidopropionase OS=Homo sapiens GN=UPB1 PE=1 SV=1 - [BUP1_HUMAN]	4.94E-05	-21.6121	-3.1074	1.65E-04	-6.0471	-3.6567
1_7	Q3LXA3	Bifunctional ATP-dependent dihydroxyacetone kinase/FAD-AMP lyase (cyclizing) OS=Homo sapiens GN=DAK PE=1 SV=2 - [DHAK_HUMAN]	6.69E-03	-2.9932	-3.1166	1.30E-04	-6.5735	-5.2650
1_7	P34913	Bifunctional epoxide hydrolase 2 OS=Homo sapiens GN=EPHX2 PE=1 SV=2 - [HYES_HUMAN]	1.89E-04	-5.9713	-3.0627	2.04E-04	-5.8423	-3.7851
1_7	P21810	Biglycan OS=Homo sapiens GN=BGN PE=1 SV=2 - [PGS1_HUMAN]	6.34E-03	3.0569	3.2970	1.68E-02	2.4182	3.4695
1_7	Q14032	Bile acid-CoA:amino acid N-acyltransferase OS=Homo sapiens GN=BAAT PE=1 SV=1 - [BAAT_HUMAN]	4.82E-05	-21.6713	-3.0672	5.21E-04	-4.7041	-2.6382
1_7	Q9Y2P5	Bile acyl-CoA synthetase OS=Homo sapiens GN=SLC27A5 PE=1 SV=1 - [S27A5_HUMAN]	5.14E-05	-21.4856	-3.0863	7.29E-05	-8.3404	-4.4024
1_7	Q06520	Bile salt sulfotransferase OS=Homo sapiens GN=SULT2A1 PE=1 SV=3 - [ST2A1_HUMAN]	3.58E-05	-23.3737	-3.1402	1.99E-05	-11.8596	-4.0738
1_7	Q96CX2	BTB/POZ domain-containing protein KCTD12 OS=Homo sapiens GN=KCTD12 PE=1 SV=1 - [KCD12_HUMAN]	7.45E-05	17.5224	3.2195	5.06E-04	4.7291	2.8115
1_7	P11586	C-1-tetrahydrofolate synthase, cytoplasmic OS=Homo sapiens GN=MTHFD1 PE=1 SV=3 - [C1TC_HUMAN]	1.41E-04	-6.4316	-3.1108	1.25E-04	-6.6924	-4.9364
1_7	Q9UJS0	Calcium-binding mitochondrial carrier protein Aralar2 OS=Homo sapiens GN=SLC25A13 PE=1 SV=2 - [CMC2_HUMAN]	2.11E-03	-3.7690	-3.0757	7.00E-05	-8.3887	-3.9518
1_7	Q96DG6	Carboxymethylenebutenolidase homolog OS=Homo sapiens GN=CMBL PE=1 SV=1 - [CMBL_HUMAN]	6.00E-04	-4.9823	-3.0003	9.16E-04	-4.1841	-2.6745
1_7	P06731	Carcinoembryonic antigen-related cell adhesion molecule 5 OS=Homo sapiens GN=CEACAM5 PE=1 SV=3 - [CEAM5_HUMAN]	9.63E-03	2.7946	3.1781	2.09E-02	2.3221	2.0701
1_7	P23786	Carnitine O-palmitoyltransferase 2, mitochondrial OS=Homo sapiens GN=CPT2 PE=1 SV=2 - [CPT2_HUMAN]	9.77E-05	-7.0173	-3.0257	5.43E-04	-4.6761	-3.1528
1_7	P00450	Ceruloplasmin OS=Homo sapiens GN=CP PE=1 SV=1 - [CERU_HUMAN]	4.81E-03	3.3945	3.2327	4.51E-04	4.8592	3.1881
1_7	O00748	Cocaine esterase OS=Homo sapiens GN=CES2 PE=1 SV=1 - [EST2_HUMAN]	3.66E-02	-2.0988	-3.0621	6.14E-03	-2.9335	-3.3301
1_7	Q05707	Collagen alpha-1(XIV) chain OS=Homo sapiens GN=COL14A1 PE=1 SV=3 - [COEA1_HUMAN]	1.68E-03	3.8077	3.2243	1.14E-02	2.6162	2.4695

Fig. 7 continued

1.7	P00751	Complement factor B OS=Homo sapiens GN=CFB PE=1 SV=2 - [CFAB_HUMAN]	1.12E-04	6.7417	3.1971	5.30E-04	4.6924	2.6576
1.7	P31146	Coronin-1A OS=Homo sapiens GN=CORO1A PE=1 SV=4 - [COR1A_HUMAN]	1.02E-04	6.9446	3.2122	1.79E-03	3.6885	2.2925
1.7	P28845	Corticosteroid 11-beta-dehydrogenase isozyme 1 OS=Homo sapiens GN=HSD11B1 PE=1 SV=3 - [DHI1_HUMAN]	5.04E-05	-21.5848	-2.9859	4.50E-03	-3.1190	-2.0008
1.7	P35520	Cystathionine beta-synthase OS=Homo sapiens GN=CBS PE=1 SV=2 - [CBS_HUMAN]	5.49E-07	-31.2654	-2.9856	9.12E-04	-4.1863	-2.0940
1.7	P32929	Cystathionine gamma-lyase OS=Homo sapiens GN=CTH PE=1 SV=3 - [CGL_HUMAN]	3.23E-04	-5.7178	-2.9700	3.01E-03	-3.3636	-2.5186
1.7	P00167	Cytochrome b5 OS=Homo sapiens GN=CYB5A PE=1 SV=2 - [CYB5_HUMAN]	1.47E-05	-25.6116	-3.1862	2.80E-04	-5.3563	-3.5936
1.7	P05177	Cytochrome P450 1A2 OS=Homo sapiens GN=CYP1A2 PE=1 SV=3 - [CP1A2_HUMAN]	2.67E-05	-24.1947	-3.0205	3.98E-04	-4.9713	-3.2232
1.7	P11509	Cytochrome P450 2A6 OS=Homo sapiens GN=CYP2A6 PE=1 SV=3 - [CP2A6_HUMAN]	5.83E-05	-20.6985	-3.0746	3.21E-04	-5.2001	-4.6052
1.7	P10632	Cytochrome P450 2C8 OS=Homo sapiens GN=CYP2C8 PE=1 SV=2 - [CP2C8_HUMAN]	2.83E-05	-24.1394	-3.0569	3.38E-05	-10.9282	-3.9088
1.7	P11712	Cytochrome P450 2C9 OS=Homo sapiens GN=CYP2C9 PE=1 SV=3 - [CP2C9_HUMAN]	3.14E-05	-23.7830	-3.0856	8.49E-05	-7.9942	-4.2291
1.7	P10635	Cytochrome P450 2D6 OS=Homo sapiens GN=CYP2D6 PE=1 SV=2 - [CP2D6_HUMAN]	2.26E-04	-5.8528	-2.9541	1.08E-02	-2.6392	-2.4156
1.7	P05181	Cytochrome P450 2E1 OS=Homo sapiens GN=CYP2E1 PE=1 SV=1 - [CP2E1_HUMAN]	5.98E-06	-27.9570	-3.0416	4.43E-05	-9.6735	-3.3879
1.7	P08684	Cytochrome P450 3A4 OS=Homo sapiens GN=CYP3A4 PE=1 SV=4 - [CP3A4_HUMAN]	8.53E-12	-33.4351	-3.1061	6.75E-05	-8.6528	-3.8971
1.7	Q02928	Cytochrome P450 4A11 OS=Homo sapiens GN=CYP4A11 PE=1 SV=1 - [CP4AB_HUMAN]	3.25E-06	-29.1359	-3.0294	1.49E-03	-3.8049	-3.0008
1.7	P21399	Cytoplasmic aconitate hydratase OS=Homo sapiens GN=ACO1 PE=1 SV=3 - [ACOC_HUMAN]	6.42E-03	-3.0405	-3.0773	5.02E-05	-9.4348	-4.3183
1.7	O75891	Cytosolic 10-formyltetrahydrofolate dehydrogenase OS=Homo sapiens GN=ALDH1L1 PE=1 SV=2 - [AL1L1_HUMAN]	7.21E-05	-18.1426	-3.0944	3.81E-04	-5.0175	-5.1429
1.7	O43175	D-3-phosphoglycerate dehydrogenase OS=Homo sapiens GN=PHGDH PE=1 SV=4 - [SERA_HUMAN]	5.05E-03	-3.3456	-3.0089	5.91E-04	-4.5539	-3.3183
1.7	Q02338	D-beta-hydroxybutyrate dehydrogenase, mitochondrial OS=Homo sapiens GN=BDH1 PE=1 SV=3 - [BDH_HUMAN]	2.39E-05	-24.6173	-3.1312	8.89E-05	-7.7814	-4.1884
1.7	P30046	D-dopachrome decarboxylase OS=Homo sapiens GN=DDT PE=1 SV=3 - [DOPD_HUMAN]	6.66E-03	-2.9985	-3.1798	3.71E-04	-5.0322	-2.7020
1.7	Q96LJ7	Dehydrogenase/reductase SDR family member 1 OS=Homo sapiens GN=DHRS1 PE=1 SV=1 - [DHRS1_HUMAN]	6.54E-05	-19.8630	-2.9590	8.11E-03	-2.7748	-2.4681
1.7	P30038	Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial OS=Homo sapiens GN=ALDH4A1 PE=1 SV=3 - [AL4A1_HUMAN]	2.32E-05	-24.6848	-3.1271	3.99E-05	-10.3124	-4.6287
1.7	P13716	Delta-aminolevulinic acid dehydratase OS=Homo sapiens GN=ALAD PE=1 SV=1 - [HEM2_HUMAN]	4.04E-04	-5.5855	-3.0717	2.27E-04	-5.6233	-3.5645
1.7	Q07507	Dermatopontin OS=Homo sapiens GN=DPT PE=2 SV=2 - [DERM_HUMAN]	1.36E-02	2.7369	3.0544	1.58E-02	2.4447	2.6550
1.7	P09622	Dihydrolipoyl dehydrogenase, mitochondrial OS=Homo sapiens GN=DLD PE=1 SV=2 - [DLDH_HUMAN]	2.31E-02	-2.3947	-3.0296	2.54E-02	-2.2040	-3.0040
1.7	P09417	Dihydropteridine reductase OS=Homo sapiens GN=QDPR PE=1 SV=2 - [DHPR_HUMAN]	1.07E-05	-26.4491	-3.0537	3.21E-04	-5.2022	-3.5579
1.7	Q14117	Dihydropyrimidinase OS=Homo sapiens GN=DPYS PE=1 SV=1 - [DPYS_HUMAN]	4.92E-05	-21.6167	-3.0297	1.46E-04	-6.2560	-2.9183
1.7	P31513	Dimethylaniline monooxygenase [N-oxide-forming] 3 OS=Homo sapiens GN=FMO3 PE=1 SV=5 - [FMO3_HUMAN]	6.66E-05	-19.6725	-3.1060	4.14E-04	-4.9392	-4.2567
1.7	P49326	Dimethylaniline monooxygenase [N-oxide-forming] 5 OS=Homo sapiens GN=FMO5 PE=2 SV=2 - [FMO5_HUMAN]	6.94E-05	-18.6809	-2.9711	1.81E-03	-3.6790	-3.4376
1.7	Q9UI17	Dimethylglycine dehydrogenase, mitochondrial OS=Homo sapiens GN=DMGDH PE=1 SV=2 - [DMGD_HUMAN]	3.69E-05	-23.1845	-3.0665	5.39E-05	-9.2639	-4.0343
1.7	O75356	Ectonucleoside triphosphate diphosphohydrolase 5 OS=Homo sapiens GN=ENTPD5 PE=1 SV=1 - [ENTP5_HUMAN]	7.04E-06	-27.7478	-2.9465	7.73E-04	-4.3124	-2.6382
1.7	Q12805	EGF-containing fibulin-like extracellular matrix protein 1 OS=Homo sapiens GN=EFEMP1 PE=1 SV=2 - [FBLN3_HUMAN]	2.20E-03	3.7598	3.1926	5.71E-03	2.9734	2.8070
1.7	Q16134	Electron transfer flavoprotein-ubiquinone oxidoreductase, mitochondrial OS=Homo sapiens GN=ETFDH PE=1 SV=2 - [ETFD_HUMAN]	5.60E-05	-20.9402	-3.0460	1.23E-04	-6.7647	-2.8644

Fig. 7 continued

1_7	P30040	Endoplasmic reticulum resident protein 29 OS=Homo sapiens GN=ERP29 PE=1 SV=4 - [ERP29_HUMAN]	7.48E-03	-2.8743	-3.0183	1.15E-04	-6.9268	-2.9431
1_7	O75521	Enoyl-CoA delta isomerase 2, mitochondrial OS=Homo sapiens GN=ECI2 PE=1 SV=4 - [ECI2_HUMAN]	2.29E-05	-24.7010	-3.0291	2.96E-04	-5.2911	-3.1485
1_7	Q86Y87	Enoyl-CoA hydratase domain-containing protein 2, mitochondrial OS=Homo sapiens GN=ECHDC2 PE=2 SV=2 - [ECHD2_HUMAN]	3.44E-05	-23.4294	-3.0081	3.60E-04	-5.0804	-2.7619
1_7	P30084	Enoyl-CoA hydratase, mitochondrial OS=Homo sapiens GN=ECHS1 PE=1 SV=4 - [ECHM_HUMAN]	2.60E-03	-3.7179	-3.1961	2.65E-05	-11.2609	-4.8186
1_7	P11678	Eosinophil peroxidase OS=Homo sapiens GN=EPX PE=1 SV=2 - [PERE_HUMAN]	8.17E-03	2.8097	3.1923	9.60E-03	2.6929	3.4580
1_7	P07099	Epoxide hydrolase 1 OS=Homo sapiens GN=EPHX1 PE=1 SV=1 - [HYEP_HUMAN]	8.48E-03	-2.8054	-3.2331	2.56E-05	-11.3004	-5.4844
1_7	Q96HE7	ERO1-like protein alpha OS=Homo sapiens GN=ERO1L PE=1 SV=2 - [ERO1A_HUMAN]	8.21E-03	2.8089	3.0146	2.06E-02	2.3262	2.6817
1_7	Q9H0W9	Ester hydrolase C11orf54 OS=Homo sapiens GN=C11orf54 PE=1 SV=1 - [CK054_HUMAN]	2.17E-06	-29.3991	-3.0476	2.30E-03	-3.5412	-2.1785
1_7	P15311	Ezrin OS=Homo sapiens GN=EZR PE=1 SV=4 - [EZRI_HUMAN]	7.37E-05	17.5594	3.3023	6.88E-05	8.5078	3.3965
1_7	Q96AE4	Far upstream element-binding protein 1 OS=Homo sapiens GN=FUBP1 PE=1 SV=3 - [FUBP1_HUMAN]	1.10E-02	2.7789	3.0892	1.60E-02	2.4405	2.2960
1_7	P51648	Fatty aldehyde dehydrogenase OS=Homo sapiens GN=ALDH3A2 PE=1 SV=1 - [AL3A2_HUMAN]	1.57E-04	-6.2282	-3.0148	6.94E-04	-4.3921	-3.0343
1_7	P23142	Fibulin-1 OS=Homo sapiens GN=FBLN1 PE=1 SV=4 - [FBLN1_HUMAN]	1.93E-03	3.7848	3.0299	1.05E-02	2.6560	2.9032
1_7	O95954	Formimidoyltransferase-cyclodeaminase OS=Homo sapiens GN=FTCD PE=1 SV=2 - [FTCD_HUMAN]	5.10E-05	-21.5029	-3.1264	5.85E-05	-8.9810	-5.2716
1_7	P09467	Fructose-1,6-bisphosphatase 1 OS=Homo sapiens GN=FBP1 PE=1 SV=5 - [F16P1_HUMAN]	1.30E-03	-3.8535	-3.1701	1.01E-05	-14.4935	-4.7202
1_7	P07954	Fumarate hydratase, mitochondrial OS=Homo sapiens GN=FH PE=1 SV=3 - [FUMH_HUMAN]	7.96E-04	-4.3218	-3.1322	5.63E-05	-9.0238	-3.9964
1_7	P16930	Fumarylacetoacetase OS=Homo sapiens GN=FAH PE=1 SV=2 - [FAAA_HUMAN]	4.13E-04	-5.5714	-3.1257	4.10E-05	-10.2764	-4.4125
1_7	P51570	Galactokinase OS=Homo sapiens GN=GALK1 PE=1 SV=1 - [GALK1_HUMAN]	3.32E-04	-5.7040	-3.0024	2.95E-03	-3.3770	-2.4493
1_7	P17931	Galectin-3 OS=Homo sapiens GN=LGALS3 PE=1 SV=5 - [LEG3_HUMAN]	7.26E-05	18.0886	3.3209	3.32E-04	5.1679	4.0087
1_7	Q08380	Galectin-3-binding protein OS=Homo sapiens GN=LGALS3BP PE=1 SV=1 - [LG3BP_HUMAN]	4.26E-04	5.5541	3.2972	6.01E-04	4.5415	3.8774
1_7	P56470	Galectin-4 OS=Homo sapiens GN=LGALS4 PE=1 SV=1 - [LEG4_HUMAN]	5.01E-03	3.3550	3.3321	7.08E-03	2.8563	4.4851
1_7	O95479	GDH/6PGL endoplasmic bifunctional protein OS=Homo sapiens GN=H6PD PE=1 SV=2 - [G6PE_HUMAN]	1.12E-04	-6.7608	-2.9933	1.77E-03	-3.6947	-2.9984
1_7	P09211	Glutathione S-transferase P OS=Homo sapiens GN=GSTP1 PE=1 SV=2 - [GSTP1_HUMAN]	2.81E-04	5.7816	3.3570	5.84E-05	8.9835	4.6817
1_7	P21695	Glycerol-3-phosphate dehydrogenase [NAD(+)], cytoplasmic OS=Homo sapiens GN=GPD1 PE=1 SV=4 - [GPDA_HUMAN]	4.95E-03	-3.3683	-2.9811	1.65E-04	-6.0479	-3.1620
1_7	P50440	Glycine amidinotransferase, mitochondrial OS=Homo sapiens GN=GATM PE=1 SV=1 - [GATM_HUMAN]	3.66E-05	-23.2006	-3.1259	1.26E-05	-14.3034	-4.7469
1_7	P23378	Glycine dehydrogenase (decarboxylating), mitochondrial OS=Homo sapiens GN=GLDC PE=1 SV=2 - [GCSP_HUMAN]	4.30E-05	-22.2182	-3.0836	3.30E-03	-3.3110	-4.1123
1_7	Q6IB77	Glycine N-acyltransferase OS=Homo sapiens GN=GLYAT PE=1 SV=3 - [GLYAT_HUMAN]	1.30E-05	-25.6978	-3.1178	2.50E-06	-17.1499	-4.1035
1_7	Q14749	Glycine N-methyltransferase OS=Homo sapiens GN=GNMT PE=1 SV=3 - [GNMT_HUMAN]	9.86E-06	-26.4860	-2.9966	2.43E-03	-3.5107	-2.8276
1_7	P35573	Glycogen debranching enzyme OS=Homo sapiens GN=AGL PE=1 SV=3 - [GDE_HUMAN]	6.50E-05	-19.8828	-3.0393	2.70E-04	-5.4231	-4.4446
1_7	P11216	Glycogen phosphorylase, brain form OS=Homo sapiens GN=PYGB PE=1 SV=5 - [PYGB_HUMAN]	3.49E-03	3.6012	3.1641	2.78E-03	3.4191	2.9490
1_7	P06737	Glycogen phosphorylase, liver form OS=Homo sapiens GN=PYGL PE=1 SV=4 - [PYGL_HUMAN]	5.25E-05	-21.4062	-3.0756	4.80E-05	-9.4541	-4.6954
1_7	Q9UBQ7	Glyoxylate reductase/hydroxypyruvate reductase OS=Homo sapiens GN=GRHPR PE=1 SV=1 - [GRHPR_HUMAN]	1.30E-03	-3.8553	-3.1694	2.89E-05	-11.1007	-4.5368
1_7	Q9UJU7	GTP:AMP phosphotransferase, mitochondrial OS=Homo sapiens GN=AK3 PE=1 SV=4 - [KAD3_HUMAN]	2.25E-04	-5.8588	-2.9904	1.95E-04	-5.9011	-2.8644

Fig. 7 continued

1_7	O43390	Heterogeneous nuclear ribonucleoprotein R OS=Homo sapiens GN=HNRNPR PE=1 SV=1 - [HNRPR_HUMAN]	2.08E-02	2.4678	3.1932	5.82E-03	2.9632	2.8096
1_7	Q1KMD3	Heterogeneous nuclear ribonucleoprotein U-like protein 2 OS=Homo sapiens GN=HNRNPUL2 PE=1 SV=1 - [HNRL2_HUMAN]	7.87E-03	2.8233	3.0910	2.71E-02	2.1666	2.0726
1_7	P16401	Histone H1.5 OS=Homo sapiens GN=HIST1H1B PE=1 SV=3 - [H15_HUMAN]	5.53E-04	5.2834	3.4126	7.69E-05	8.3009	3.0602
1_7	P68431	Histone H3.1 OS=Homo sapiens GN=HIST1H3A PE=1 SV=2 - [H31_HUMAN]	1.62E-02	2.6338	3.6119	3.78E-03	3.2300	2.6804
1_7	P01903	HLA class II histocompatibility antigen, DR alpha chain OS=Homo sapiens GN=HLA-DRA PE=1 SV=1 - [DRA_HUMAN]	2.41E-02	2.3594	3.0742	9.12E-03	2.7166	2.5735
1_7	Q93099	Homogentisate 1,2-dioxygenase OS=Homo sapiens GN=HGD PE=1 SV=2 - [HGD_HUMAN]	9.26E-06	-26.6151	-3.0396	6.89E-04	-4.4074	-3.8287
1_7	Q9UJM8	Hydroxyacid oxidase 1 OS=Homo sapiens GN=HAO1 PE=1 SV=1 - [HAOX1_HUMAN]	2.49E-05	-24.4661	-3.1053	3.96E-04	-4.9782	-4.4990
1_7	Q16836	Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial OS=Homo sapiens GN=HADH PE=1 SV=3 - [HCDH_HUMAN]	3.16E-04	-5.7283	-3.1087	8.32E-05	-8.1170	-3.4009
1_7	Q16775	Hydroxyacylglutathione hydrolase, mitochondrial OS=Homo sapiens GN=HAGH PE=1 SV=2 - [GLO2_HUMAN]	4.87E-04	-5.4656	-2.9897	1.10E-04	-7.0319	-2.4493
1_7	P35914	Hydroxymethylglutaryl-CoA lyase, mitochondrial OS=Homo sapiens GN=HMGCL PE=1 SV=2 - [HMGCL_HUMAN]	2.21E-05	-24.7393	-3.0761	2.49E-04	-5.5207	-2.9431
1_7	P54868	Hydroxymethylglutaryl-CoA synthase, mitochondrial OS=Homo sapiens GN=HMGCS2 PE=1 SV=1 - [HMCS2_HUMAN]	4.41E-04	-5.5342	-3.2672	1.64E-04	-6.0594	-6.0495
1_7	Q6YN16	Hydroxysteroid dehydrogenase-like protein 2 OS=Homo sapiens GN=HSDL2 PE=1 SV=1 - [HSDL2_HUMAN]	4.13E-05	-22.3011	-3.0249	5.91E-04	-4.5544	-2.3749
1_7	Q14974	Importin subunit beta-1 OS=Homo sapiens GN=KPNB1 PE=1 SV=2 - [IMB1_HUMAN]	6.70E-03	2.9756	3.0876	7.29E-03	2.8392	2.0430
1_7	Q96AB3	Isochorismatase domain-containing protein 2, mitochondrial OS=Homo sapiens GN=ISOC2 PE=1 SV=1 - [ISOC2_HUMAN]	2.74E-05	-24.1805	-3.0074	7.47E-04	-4.3350	-2.4681
1_7	P26440	Isovaleryl-CoA dehydrogenase, mitochondrial OS=Homo sapiens GN=IVD PE=1 SV=1 - [IVD_HUMAN]	6.13E-04	-4.9484	-2.9789	1.34E-03	-3.8885	-2.6745
1_7	P08727	Keratin, type I cytoskeletal 19 OS=Homo sapiens GN=KRT19 PE=1 SV=4 - [K1C19_HUMAN]	8.30E-05	13.1489	3.4319	1.83E-04	5.9579	5.5735
1_7	P08729	Keratin, type II cytoskeletal 7 OS=Homo sapiens GN=KRT7 PE=1 SV=5 - [K2C7_HUMAN]	1.40E-02	2.7266	3.1228	1.94E-02	2.3551	3.5726
1_7	Q9Y2S2	Lambda-crystallin homolog OS=Homo sapiens GN=CRYL1 PE=1 SV=3 - [CRYL1_HUMAN]	5.65E-03	-3.2176	-3.0232	5.28E-04	-4.6951	-2.8309
1_7	P23141	Liver carboxylesterase 1 OS=Homo sapiens GN=CES1 PE=1 SV=2 - [EST1_HUMAN]	1.95E-04	-5.9462	-3.2803	2.29E-04	-5.6146	-5.9909
1_7	P07195	L-lactate dehydrogenase B chain OS=Homo sapiens GN=LDHB PE=1 SV=2 - [LDHB_HUMAN]	3.74E-03	3.5636	3.3757	8.58E-04	4.2263	2.9447
1_7	P33121	Long-chain-fatty-acid--CoA ligase 1 OS=Homo sapiens GN=ACSL1 PE=1 SV=1 - [ACSL1_HUMAN]	7.04E-05	-18.5806	-3.1446	3.49E-04	-5.1283	-4.5280
1_7	Q9ULC5	Long-chain-fatty-acid--CoA ligase 5 OS=Homo sapiens GN=ACSL5 PE=1 SV=1 - [ACSL5_HUMAN]	6.62E-04	-4.6901	-3.0648	2.74E-03	-3.4358	-2.7091
1_7	P61626	Lysozyme C OS=Homo sapiens GN=LYZ PE=1 SV=1 - [LYSC_HUMAN]	6.81E-04	4.6253	3.2855	8.27E-03	2.7647	3.0187
1_7	P40121	Macrophage-capping protein OS=Homo sapiens GN=CAPG PE=1 SV=2 - [CAPG_HUMAN]	7.32E-05	17.8531	3.2766	2.06E-04	5.8145	3.0745
1_7	Q14764	Major vault protein OS=Homo sapiens GN=MVP PE=1 SV=4 - [MVP_HUMAN]	5.96E-05	20.6343	3.1790	1.57E-04	6.1423	3.3965
1_7	O43708	Maleylacetoacetate isomerase OS=Homo sapiens GN=GSTZ1 PE=1 SV=3 - [MAAI_HUMAN]	1.65E-03	-3.8104	-2.9899	1.22E-02	-2.5800	-2.0086
1_7	P11310	Medium-chain specific acyl-CoA dehydrogenase, mitochondrial OS=Homo sapiens GN=ACADM PE=1 SV=1 - [ACADM_HUMAN]	2.93E-05	-24.0591	-3.0653	1.58E-03	-3.7582	-3.7091
1_7	O00264	Membrane-associated progesterone receptor component 1 OS=Homo sapiens GN=PGRMC1 PE=1 SV=3 - [PGRC1_HUMAN]	2.70E-02	-2.2535	-3.0713	1.20E-04	-6.8593	-3.6888
1_7	Q9HCC0	Methylcrotonoyl-CoA carboxylase beta chain, mitochondrial OS=Homo sapiens GN=MCCC2 PE=1 SV=1 - [MCCB_HUMAN]	7.39E-04	-4.4396	-2.9659	6.41E-04	-4.4586	-3.2566
1_7	Q02252	Methylmalonate-semialdehyde dehydrogenase [acylating], mitochondrial OS=Homo sapiens GN=ALDH6A1 PE=1 SV=2 - [MMSA_HUMAN]	2.11E-05	-24.8938	-3.1940	2.95E-08	-20.5378	-5.1968
1_7	Q9H8H3	Methyltransferase-like protein 7A OS=Homo sapiens GN=METTL7A PE=1 SV=1 - [MET7A_HUMAN]	6.62E-05	-19.7644	-3.1078	3.96E-04	-4.9765	-2.4125
1_7	P10620	Microsomal glutathione S-transferase 1 OS=Homo sapiens GN=MGST1 PE=1 SV=1 - [MGST1_HUMAN]	5.36E-05	-21.1889	-3.1164	5.10E-04	-4.7228	-2.4125

Fig. 7 continued

1_7	O43772	Mitochondrial carnitine/acylcarnitine carrier protein OS=Homo sapiens GN=SLC25A20 PE=1 SV=1 - [MCAT_HUMAN]	8.65E-06	-26.7650	-2.9591	1.11E-03	-4.0361	-2.4681
1_7	Q9Y6C9	Mitochondrial carrier homolog 2 OS=Homo sapiens GN=MTCH2 PE=1 SV=1 - [MTCH2_HUMAN]	1.68E-02	-2.6105	-3.0184	3.50E-05	-10.7880	-3.0840
1_7	Q96I23	MOSC domain-containing protein 2, mitochondrial OS=Homo sapiens GN=MARC2 PE=1 SV=1 - [MOSC2_HUMAN]	3.96E-05	-22.6254	-2.9702	6.18E-05	-8.8723	-2.7020
1_7	P98088	Mucin-5AC (Fragments) OS=Homo sapiens GN=MUC5AC PE=1 SV=3 - [MUC5A_HUMAN]	1.25E-02	2.7512	3.2398	2.33E-02	2.2479	4.7330
1_7	P24158	Myeloblastin OS=Homo sapiens GN=PRTN3 PE=1 SV=3 - [PRTN3_HUMAN]	3.04E-02	2.1330	3.0919	2.88E-02	2.1366	2.9605
1_7	Q7Z406	Myosin-14 OS=Homo sapiens GN=MYH14 PE=1 SV=2 - [MYH14_HUMAN]	5.32E-05	21.2300	3.1729	3.77E-03	3.2310	3.3440
1_7	Q4G0N4	NAD kinase domain-containing protein 1 OS=Homo sapiens GN=NADKD1 PE=1 SV=2 - [NAKD1_HUMAN]	1.19E-05	-26.1600	-3.0937	1.86E-04	-5.9437	-3.8160
1_7	P16435	NADPH--cytochrome P450 reductase OS=Homo sapiens GN=POR PE=1 SV=2 - [NCPR_HUMAN]	4.56E-05	-22.1096	-3.0231	4.87E-05	-9.4504	-3.3749
1_7	Q09666	Neuroblast differentiation-associated protein AHNAK OS=Homo sapiens GN=AHNAK PE=1 SV=2 - [AHNK_HUMAN]	1.07E-02	2.7827	3.0836	2.26E-02	2.2716	2.5735
1_7	P80188	Neutrophil gelatinase-associated lipocalin OS=Homo sapiens GN=LCN2 PE=1 SV=2 - [NGAL_HUMAN]	5.61E-03	3.2274	3.1911	3.79E-02	2.0289	3.2251
1_7	Q15274	Nicotinate-nucleotide pyrophosphorylase [carboxylating] OS=Homo sapiens GN=QPRT PE=1 SV=3 - [NADC_HUMAN]	4.07E-05	-22.5176	-2.9935	2.48E-03	-3.5013	-2.4990
1_7	P22307	Non-specific lipid-transfer protein OS=Homo sapiens GN=SCP2 PE=1 SV=2 - [NLTP_HUMAN]	1.38E-04	-6.4637	-3.0822	4.98E-06	-16.3154	-4.0008
1_7	Q9NQR4	Omega-amidase NIT2 OS=Homo sapiens GN=NIT2 PE=1 SV=1 - [NIT2_HUMAN]	4.72E-05	-21.8438	-3.0391	7.49E-04	-4.3333	-2.9140
1_7	P00480	Ornithine carbamoyltransferase, mitochondrial OS=Homo sapiens GN=OTC PE=1 SV=3 - [OTC_HUMAN]	3.32E-05	-23.5268	-3.1288	1.24E-06	-20.1799	-4.1620
1_7	Q15063	Periostin OS=Homo sapiens GN=POSTN PE=1 SV=2 - [POSTN_HUMAN]	2.55E-04	5.8119	3.1524	8.40E-03	2.7566	3.0545
1_7	Q9NUJ1	Peroxisomal 2,4-dienoyl-CoA reductase OS=Homo sapiens GN=DECR2 PE=1 SV=1 - [DECR2_HUMAN]	2.38E-04	-5.8291	-2.9838	1.92E-03	-3.8454	-2.5645
1_7	Q15067	Peroxisomal acyl-coenzyme A oxidase 1 OS=Homo sapiens GN=ACOX1 PE=1 SV=3 - [ACOX1_HUMAN]	1.47E-05	-25.6091	-3.0451	6.63E-04	-4.4148	-3.7712
1_7	Q9NP24	Peroxisomal acyl-coenzyme A oxidase 2 OS=Homo sapiens GN=ACOX2 PE=1 SV=1 - [ACOX2_HUMAN]	3.20E-05	-23.6363	-3.0730	2.05E-04	-5.8231	-4.0961
1_7	Q08426	Peroxisomal bifunctional enzyme OS=Homo sapiens GN=EHHADH PE=1 SV=3 - [ECHP_HUMAN]	1.01E-04	-6.9714	-3.1724	4.62E-05	-9.6324	-5.7091
1_7	Q9P0Z9	Peroxisomal sarcosine oxidase OS=Homo sapiens GN=PIPOX PE=2 SV=2 - [SOX_HUMAN]	2.55E-05	-24.4395	-3.0673	1.03E-04	-7.3762	-3.6145
1_7	Q9BY49	Peroxisomal trans-2-enoyl-CoA reductase OS=Homo sapiens GN=PECR PE=1 SV=2 - [PECR_HUMAN]	8.15E-06	-26.8861	-3.0006	4.14E-03	-3.1755	-2.0500
1_7	P30039	Phenazine biosynthesis-like domain-containing protein OS=Homo sapiens GN=PBLD PE=1 SV=2 - [PBLD_HUMAN]	3.85E-05	-22.8342	-3.0315	4.39E-04	-4.8794	-3.1863
1_7	P00439	Phenylalanine-4-hydroxylase OS=Homo sapiens GN=PAH PE=1 SV=1 - [PAH_HUMAN]	4.72E-05	-21.8428	-3.0126	7.23E-04	-4.3598	-2.7619
1_7	Q16822	Phosphoenolpyruvate carboxykinase [GTP], mitochondrial OS=Homo sapiens GN=PCK2 PE=1 SV=3 - [PCKGM_HUMAN]	1.28E-03	-3.8611	-3.1994	7.53E-06	-15.0816	-5.5632
1_7	Q9Y617	Phosphoserine aminotransferase OS=Homo sapiens GN=PSAT1 PE=1 SV=2 - [SERC_HUMAN]	5.70E-05	-20.8837	-3.0023	1.80E-03	-3.6830	-2.3735
1_7	Q15149	Plectin OS=Homo sapiens GN=PLEC PE=1 SV=3 - [PLEC_HUMAN]	9.27E-05	7.5880	3.2421	3.97E-04	4.9739	5.3488
1_7	P51888	Prolargin OS=Homo sapiens GN=PRELP PE=1 SV=1 - [PRELP_HUMAN]	3.02E-03	3.6705	3.3467	6.52E-03	2.9009	4.4081
1_7	Q9UQB0	Proliferation-associated protein 2G4 OS=Homo sapiens GN=PA2G4 PE=1 SV=3 - [PA2G4_HUMAN]	8.75E-04	4.2040	3.2452	2.64E-03	3.4561	2.4695
1_7	P05165	Propionyl-CoA carboxylase alpha chain, mitochondrial OS=Homo sapiens GN=PCCA PE=1 SV=4 - [PCCA_HUMAN]	3.10E-05	-23.8690	-2.9900	2.31E-03	-3.5393	-2.6745
1_7	P05165	Propionyl-CoA carboxylase beta chain, mitochondrial OS=Homo sapiens GN=PCCB PE=1 SV=3 - [PCCB_HUMAN]	1.35E-05	-25.7011	-3.0162	2.56E-03	-3.4805	-2.9964
1_7	Q14914	Prostaglandin reductase 1 OS=Homo sapiens GN=PTGR1 PE=1 SV=2 - [PTGR1_HUMAN]	9.32E-05	-7.3974	-3.0490	4.43E-04	-4.8697	-3.7662
1_7	O95571	Protein ETHE1, mitochondrial OS=Homo sapiens GN=ETHE1 PE=1 SV=2 - [ETHE1_HUMAN]	1.95E-02	2.5162	3.0795	5.59E-03	2.9854	2.2950

Fig. 7 continued

1_7	Q99PW8	Protein NipSnap homolog 1 OS=Homo sapiens GN=NIPSNAP1 PE=1 SV=1 - /NIPS1_HUMAN/	5.43E-06	-28.1693	-3.0532	8.97E-05	-7.7559	-3.1967
1_7	P31949	Protein S100-A11 OS=Homo sapiens GN=S100A11 PE=1 SV=2 - /S10AB_HUMAN/	7.80E-05	16.5818	3.2807	4.62E-05	9.6329	2.1671
1_7	P06703	Protein S100-A6 OS=Homo sapiens GN=S100A6 PE=1 SV=1 - /S10A6_HUMAN/	7.70E-05	16.7873	3.4440	6.97E-04	4.3891	2.9471
1_7	Q01105	Protein SET OS=Homo sapiens GN=SET PE=1 SV=3 - /SET_HUMAN/	5.35E-04	5.3449	3.3135	1.56E-04	6.1570	2.4881
1_7	P55786	Puromycin-sensitive aminopeptidase OS=Homo sapiens GN=NPEPPS PE=1 SV=2 - /PSA_HUMAN/	2.15E-02	2.4474	3.0658	6.40E-03	2.9086	2.0745
1_7	A6NDG4	Putative L-aspartate dehydrogenase OS=Homo sapiens GN=ASPDH PE=2 SV=2 - /ASPD_HUMAN/	2.26E-04	-5.8503	-2.9302	1.51E-02	-2.4630	-2.0086
1_7	Q9NVS9	Pyridoxine-5-phosphate oxidase OS=Homo sapiens GN=PNPO PE=1 SV=1 - /PNPO_HUMAN/	1.59E-04	-6.2163	-2.9789	1.50E-05	-13.6449	-2.1967
1_7	P11498	Pyruvate carboxylase, mitochondrial OS=Homo sapiens GN=PC PE=1 SV=2 - /PYC_HUMAN/	5.14E-04	-5.4082	-3.1278	1.47E-04	-6.2550	-5.0961
1_7	P14618	Pyruvate kinase isozymes M1/M2 OS=Homo sapiens GN=PKM PE=1 SV=4 - /KPYM_HUMAN/	9.11E-05	7.9329	3.3495	9.62E-05	7.5306	4.9447
1_7	P30613	Pyruvate kinase isozymes R/L OS=Homo sapiens GN=PKLR PE=1 SV=2 - /KPYR_HUMAN/	5.53E-05	-20.9736	-3.0488	2.00E-04	-5.0847	-4.7006
1_7	Q08257	Quinone oxidoreductase OS=Homo sapiens GN=CRYZ PE=1 SV=1 - /QOR_HUMAN/	7.22E-03	-2.9116	-3.0579	3.27E-05	-10.9847	-3.9599
1_7	P46940	Ras GTPase-activating-like protein IQGAP1 OS=Homo sapiens GN=IQGAP1 PE=1 SV=1 - /IQGA1_HUMAN/	6.39E-04	4.8069	3.1593	1.33E-02	2.5404	2.5297
1_7	Q13576	Ras GTPase-activating-like protein IQGAP2 OS=Homo sapiens GN=IQGAP2 PE=1 SV=4 - /IQGA2_HUMAN/	5.11E-04	-5.4274	-2.9401	1.16E-02	-2.6069	-3.0943
1_7	P51149	Ras-related protein Rab-7a OS=Homo sapiens GN=RAB7A PE=1 SV=1 - /RAB7A_HUMAN/	5.79E-04	5.1114	3.2225	2.45E-03	3.5062	2.2969
1_7	Q96HR9	Receptor expression-enhancing protein 6 OS=Homo sapiens GN=REEP6 PE=1 SV=1 - /REEP6_HUMAN/	1.63E-05	-25.3477	-3.0203	6.15E-04	-4.5217	-2.1528
1_7	Q15493	Regucalcin OS=Homo sapiens GN=RGN PE=1 SV=1 - /RGN_HUMAN/	1.09E-06	-30.9468	-2.9930	4.40E-03	-3.1364	-2.5936
1_7	O75452	Retinol dehydrogenase 16 OS=Homo sapiens GN=RDH16 PE=1 SV=2 - /RDH16_HUMAN/	5.59E-05	-20.9445	-3.1225	2.85E-04	-5.3418	-3.8444
1_7	P52758	Ribonuclease UK114 OS=Homo sapiens GN=HRSP12 PE=1 SV=1 - /UK114_HUMAN/	2.06E-04	-5.9230	-3.1335	2.31E-04	-5.5998	-2.8276
1_7	Q9P2E9	Ribosome-binding protein 1 OS=Homo sapiens GN=RRBP1 PE=1 SV=4 - /RRBP1_HUMAN/	1.95E-02	-2.5150	-2.9840	2.49E-02	-2.2167	-4.1994
1_7	Q8NBX0	Saccharopine dehydrogenase-like oxidoreductase OS=Homo sapiens GN=SCCPDH PE=1 SV=1 - /SCPDL_HUMAN/	3.27E-05	-23.5505	-2.9965	8.67E-04	-4.2168	-2.6145
1_7	Q00266	S-adenosylmethionine synthase isoform type-1 OS=Homo sapiens GN=MAT1A PE=1 SV=2 - /METK1_HUMAN/	4.67E-05	-21.9037	-3.0877	5.25E-05	-9.3090	-3.5857
1_7	Q9UL12	Sarcosine dehydrogenase, mitochondrial OS=Homo sapiens GN=SARDH PE=1 SV=1 - /SARDH_HUMAN/	1.95E-05	-24.9611	-3.0485	3.86E-05	-10.3773	-4.1035
1_7	P34896	Serine hydroxymethyltransferase, cytosolic OS=Homo sapiens GN=SHMT1 PE=1 SV=1 - /GLYC_HUMAN/	6.15E-05	-20.3223	-3.1135	7.09E-05	-8.3563	-4.3879
1_7	P34897	Serine hydroxymethyltransferase, mitochondrial OS=Homo sapiens GN=SHMT2 PE=1 SV=3 - /GLYM_HUMAN/	1.83E-04	-6.0121	-3.0520	7.85E-05	-8.2576	-3.6382
1_7	Q07955	Serine/arginine-rich splicing factor 1 OS=Homo sapiens GN=SRSF1 PE=1 SV=2 - /SRSF1_HUMAN/	4.09E-04	5.5769	3.1465	2.44E-03	3.5094	2.4876
1_7	P62136	Serine/threonine-protein phosphatase PP1-alpha catalytic subunit OS=Homo sapiens GN=PPP1CA PE=1 SV=1 - /PP1A_HUMAN/	7.01E-03	2.9392	3.0850	2.86E-02	2.1395	2.1671
1_7	P21549	Serine--pyruvate aminotransferase OS=Homo sapiens GN=AGXT PE=1 SV=1 - /SPYA_HUMAN/	1.85E-04	-5.9961	-3.2392	6.34E-05	-8.8454	-6.0039
1_7	P35237	Serpin B6 OS=Homo sapiens GN=SERPINB6 PE=1 SV=3 - /SPB6_HUMAN/	3.75E-04	5.6362	3.1650	8.90E-04	4.1991	2.3598
1_7	P50454	Serpin H1 OS=Homo sapiens GN=SERPINH1 PE=1 SV=2 - /SERPH_HUMAN/	6.68E-04	4.6636	3.2122	2.63E-04	5.4676	3.4695
1_7	P27169	Serum paraoxonase/arylesterase 1 OS=Homo sapiens GN=PON1 PE=1 SV=3 - /PON1_HUMAN/	1.36E-05	-25.6833	-3.0375	3.70E-03	-3.2296	-2.0086
1_7	P45954	Short/branched chain specific acyl-CoA dehydrogenase, mitochondrial OS=Homo sapiens GN=ACADSB PE=1 SV=1 - /ACDSB_HUMAN/	3.05E-05	-23.9208	-3.1545	2.16E-04	-5.7184	-4.3301
1_7	P16219	Short-chain specific acyl-CoA dehydrogenase, mitochondrial OS=Homo sapiens GN=ACADS PE=1 SV=1 - /ACADS_HUMAN/	1.72E-04	-6.1025	-3.0990	4.57E-04	-4.8527	-3.7377

Fig. 7 continued

1_7	Q9H9B4	Sideroflexin-1 OS=Homo sapiens GN=SFXN1 PE=1 SV=4 - [SFXN1_HUMAN]	2.17E-05	-24.7870	-3.0416	8.51E-04	-4.2324	-3.0008
1_7	Q00796	Sorbitol dehydrogenase OS=Homo sapiens GN=SORD PE=1 SV=4 - [DHSO_HUMAN]	6.62E-04	-4.6915	-3.1283	8.63E-04	-4.2209	-4.1863
1_7	P31040	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial OS=Homo sapiens GN=SDHA PE=1 SV=2 - [DHSA_HUMAN]	1.67E-04	-6.1483	-3.0661	1.02E-04	-7.3906	-3.8160
1_7	P21912	Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial OS=Homo sapiens GN=SDHB PE=1 SV=3 - [DHSB_HUMAN]	1.79E-05	-25.1113	-2.9806	8.83E-05	-7.9800	-2.4158
1_7	P51649	Succinate-semialdehyde dehydrogenase, mitochondrial OS=Homo sapiens GN=ALDH5A1 PE=1 SV=2 - [SSDH_HUMAN]	1.20E-05	-26.1341	-3.0464	2.67E-04	-5.4418	-3.3313
1_7	P53597	Succinyl-CoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial OS=Homo sapiens GN=SUCLG1 PE=1 SV=4 - [SUCA_HUMAN]	2.12E-04	-5.9134	-2.9835	3.33E-03	-3.2686	-2.0343
1_7	Q96I99	Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial OS=Homo sapiens GN=SUCLG2 PE=1 SV=2 - [SUCB2_HUMAN]	2.01E-02	-2.4967	-3.0789	1.90E-04	-5.9288	-3.2903
1_7	P52225	Sulfotransferase 1A1 OS=Homo sapiens GN=SULT1A1 PE=1 SV=3 - [ST1A1_HUMAN]	1.86E-05	-24.9906	-3.1066	1.55E-04	-6.1862	-3.0840
1_7	P30048	Thioredoxin-dependent peroxide reductase, mitochondrial OS=Homo sapiens GN=PRDX3 PE=1 SV=3 - [PRDX3_HUMAN]	1.60E-02	-2.6433	-3.1004	7.40E-03	-2.8239	-2.6717
1_7	Q01995	Transgelin OS=Homo sapiens GN=TAGLN PE=1 SV=4 - [TAGL_HUMAN]	9.43E-05	7.2012	3.3116	1.49E-03	3.8054	3.8070
1_7	P53007	Tricarboxylate transport protein, mitochondrial OS=Homo sapiens GN=SLC25A1 PE=1 SV=2 - [TXTP_HUMAN]	4.74E-03	-3.4085	-3.0340	4.16E-04	-4.9316	-2.6745
1_7	P40939	Trifunctional enzyme subunit alpha, mitochondrial OS=Homo sapiens GN=HADHA PE=1 SV=2 - [ECHA_HUMAN]	1.58E-02	-2.6505	-3.1613	2.26E-04	-5.6630	-5.0141
1_7	P67936	Tropomyosin alpha-4 chain OS=Homo sapiens GN=TPM4 PE=1 SV=3 - [TPM4_HUMAN]	9.39E-05	7.2821	3.2483	4.71E-04	4.8106	2.4876
1_7	Q15661	Tryptase alpha/beta-1 OS=Homo sapiens GN=TPSAB1 PE=1 SV=1 - [TRYB1_HUMAN]	3.99E-04	5.5970	3.2103	1.09E-02	2.6329	2.4851
1_7	O43399	Tumor protein D54 OS=Homo sapiens GN=TPD52L2 PE=1 SV=2 - [TPD54_HUMAN]	9.16E-05	7.7667	3.2282	2.09E-03	3.6064	2.2065
1_7	P22310	UDP-glucuronosyltransferase 1-4 OS=Homo sapiens GN=UGT1A4 PE=1 SV=1 - [UD14_HUMAN]	3.18E-04	-5.7253	-3.0442	1.06E-03	-4.0686	-2.9518
1_7	P06133	UDP-glucuronosyltransferase 2B4 OS=Homo sapiens GN=UGT2B4 PE=1 SV=2 - [UD2B4_HUMAN]	3.99E-04	-5.8958	-3.0069	7.82E-03	-2.7944	-3.2903
1_7	P16662	UDP-glucuronosyltransferase 2B7 OS=Homo sapiens GN=UGT2B7 PE=1 SV=1 - [UD2B7_HUMAN]	7.16E-05	-18.2245	-3.1155	4.35E-04	-4.8869	-3.5857
1_7	Q16851	UTP--glucose-1-phosphate uridylyltransferase OS=Homo sapiens GN=UGP2 PE=1 SV=5 - [UGPA_HUMAN]	9.70E-04	-4.0730	-3.1823	8.74E-06	-14.5510	-5.4791
1_7	P13611	Versican core protein OS=Homo sapiens GN=VCAN PE=1 SV=3 - [CSPG2_HUMAN]	4.62E-04	5.4971	3.1761	1.08E-02	2.6388	2.8070
1_8	Q15029	116 kDa U5 small nuclear ribonucleoprotein component OS=Homo sapiens GN=EFTUD2 PE=1 SV=1 - [U5S1_HUMAN]	2.25E-04	5.8542	2.6748	1.12E-03	3.8379	2.4336
1_8	Q04917	14-3-3 protein eta OS=Homo sapiens GN=YWHAH PE=1 SV=4 - [1433F_HUMAN]	6.13E-04	4.9243	2.9218	6.49E-06	7.3559	3.8341
1_8	P31947	14-3-3 protein sigma OS=Homo sapiens GN=SFN PE=1 SV=1 - [1433S_HUMAN]	5.66E-03	3.2476	2.9218	4.63E-06	7.5997	3.7240
1_8	Q7Z5P4	17-beta-hydroxysteroid dehydrogenase 13 OS=Homo sapiens GN=HSD17B13 PE=2 SV=1 - [DHB13_HUMAN]	8.39E-05	-19.0172	-3.1005	1.02E-04	-5.2191	-3.2567
1_8	O14756	17-beta-hydroxysteroid dehydrogenase type 6 OS=Homo sapiens GN=HSD17B6 PE=1 SV=1 - [H17B6_HUMAN]	7.69E-05	-20.0852	-3.1163	2.47E-06	-8.1240	-3.9088
1_8	P12694	2-oxoisovalerate dehydrogenase subunit alpha, mitochondrial OS=Homo sapiens GN=BCKDHA PE=1 SV=2 - [ODBA_HUMAN]	7.23E-04	-4.4466	-2.9176	7.61E-04	-4.0428	-2.6382
1_8	P46952	3-hydroxyanthranilate 3,4-dioxygenase OS=Homo sapiens GN=HAAO PE=1 SV=2 - [3HAO_HUMAN]	2.56E-05	-25.2483	-3.0508	1.46E-06	-8.7071	-3.3183
1_8	P51857	3-oxo-5-beta-steroid 4-dehydrogenase OS=Homo sapiens GN=AKR1D1 PE=1 SV=1 - [AK1D1_HUMAN]	8.71E-05	-18.5719	-3.0581	7.23E-03	-2.8413	-2.6145
1_8	P80404	4-aminobutyrate aminotransferase, mitochondrial OS=Homo sapiens GN=ABAT PE=1 SV=3 - [GABT_HUMAN]	1.44E-04	-6.1452	-3.1594	2.03E-06	-11.1543	-5.3259
1_8	P32754	4-hydroxyphenylpyruvate dioxygenase OS=Homo sapiens GN=HPD PE=1 SV=2 - [HPPD_HUMAN]	5.49E-05	-22.1822	-3.1328	8.27E-08	-9.9568	-4.4376
1_8	P68133	Actin, alpha skeletal muscle OS=Homo sapiens GN=ACTA1 PE=1 SV=1 - [ACTS_HUMAN]	2.23E-03	-3.7789	-3.1987	8.13E-03	-2.7862	-5.0861
1_8	O15144	Actin-related protein 2/3 complex subunit 2 OS=Homo sapiens GN=ARPC2 PE=1 SV=1 - [ARPC2_HUMAN]	6.14E-03	3.1647	2.7747	5.94E-03	2.9552	2.0686

Fig. 7 continued

1_8	Q08AH3	Acyl-coenzyme A synthetase ACSM2A, mitochondrial OS=Homo sapiens GN=ACSM2A PE=1 SV=2 - |ACS2A_HUMAN|	2.74E-05	-24.9514	-3.1313	9.20E-05	-5.2804	-5.0015
1_8	Q68CK6	Acyl-coenzyme A synthetase ACSM2B, mitochondrial OS=Homo sapiens GN=ACSM2B PE=1 SV=2 - |ACS2B_HUMAN|	2.77E-05	-24.9352	-3.1313	2.60E-07	-10.6014	-5.1339
1_8	P27144	Adenylate kinase isoenzyme 4, mitochondrial OS=Homo sapiens GN=AK4 PE=1 SV=1 - |KAD4_HUMAN|	7.48E-03	-2.9613	-2.9842	7.98E-04	-4.0145	-2.7214
1_8	Q9BSE5	Agmatinase, mitochondrial OS=Homo sapiens GN=AGMAT PE=1 SV=2 - |SPEB_HUMAN|	1.42E-03	-3.8377	-3.0674	2.03E-03	-3.5341	-2.0085
1_8	P24298	Alanine aminotransferase 1 OS=Homo sapiens GN=GPT PE=1 SV=3 - |ALAT1_HUMAN|	3.14E-05	-24.4015	-3.0208	2.24E-06	-8.3445	-3.9964
1_8	P07327	Alcohol dehydrogenase 1A OS=Homo sapiens GN=ADH1A PE=1 SV=2 - |ADH1A_HUMAN|	1.07E-04	-7.4787	-3.2451	3.27E-04	-4.5638	-6.0582
1_8	P00325	Alcohol dehydrogenase 1B OS=Homo sapiens GN=ADH1B PE=1 SV=2 - |ADH1B_HUMAN|	1.08E-04	-7.4723	-3.2523	8.34E-05	-5.3180	-6.0932
1_8	P08326	Alcohol dehydrogenase 1C OS=Homo sapiens GN=ADH1C PE=1 SV=2 - |ADH1G_HUMAN|	4.08E-03	-3.4976	-3.2398	1.96E-03	-3.5554	-4.9413
1_8	P08319	Alcohol dehydrogenase 4 OS=Homo sapiens GN=ADH4 PE=1 SV=5 - |ADH4_HUMAN|	1.03E-04	-7.7179	-3.2128	3.34E-05	-5.9601	-5.9289
1_8	P28332	Alcohol dehydrogenase 6 OS=Homo sapiens GN=ADH6 PE=2 SV=2 - |ADH6_HUMAN|	4.85E-04	-5.5097	-3.0225	7.12E-03	-2.8500	-3.3238
1_8	Q9H2A2	Aldehyde dehydrogenase family 8 member A1 OS=Homo sapiens GN=ALDH8A1 PE=1 SV=1 - |AL8A1_HUMAN|	5.36E-05	-22.2723	-3.0403	6.06E-05	-5.5086	-3.3513
1_8	Q06278	Aldehyde oxidase OS=Homo sapiens GN=AOX1 PE=2 SV=2 - |ADO_HUMAN|	8.15E-05	-19.3202	-3.0642	2.11E-03	-3.5143	-4.8209
1_8	Q04828	Aldo-keto reductase family 1 member C1 OS=Homo sapiens GN=AKR1C1 PE=1 SV=1 - |AK1C1_HUMAN|	1.67E-04	-5.9304	-3.1311	5.00E-04	-4.3010	-3.8666
1_8	P52895	Aldo-keto reductase family 1 member C2 OS=Homo sapiens GN=AKR1C2 PE=1 SV=3 - |AK1C2_HUMAN|	4.17E-04	-5.6657	-3.0900	1.62E-03	-3.8421	-3.6287
1_8	P17516	Aldo-keto reductase family 1 member C4 OS=Homo sapiens GN=AKR1C4 PE=1 SV=3 - |AK1C4_HUMAN|	7.20E-05	-20.6989	-3.0995	1.55E-04	-5.0263	-3.5814
1_8	P21397	Amine oxidase [flavin-containing] A OS=Homo sapiens GN=MAOA PE=1 SV=1 - |AOFA_HUMAN|	6.07E-04	-4.9692	-3.0613	1.57E-04	-15.9782	-3.3301
1_8	P27338	Amine oxidase [flavin-containing] B OS=Homo sapiens GN=MAOB PE=1 SV=3 - |AOFB_HUMAN|	9.32E-05	-11.1029	-3.0750	4.25E-05	-13.6771	-3.9628
1_8	Q03154	Aminoacylase-1 OS=Homo sapiens GN=ACY1 PE=1 SV=1 - |ACY1_HUMAN|	9.74E-05	-8.8107	-3.1496	4.50E-08	-10.3597	-4.4905
1_8	Q9H4A4	Aminopeptidase B OS=Homo sapiens GN=RNPEP PE=1 SV=2 - |AMPB_HUMAN|	3.89E-03	3.5243	2.6784	5.64E-03	2.9891	2.1622
1_8	P15144	Aminopeptidase N OS=Homo sapiens GN=ANPEP PE=1 SV=4 - |AMPN_HUMAN|	3.73E-06	-31.9538	-2.9516	1.43E-03	-3.7063	-2.5648
1_8	P50995	Annexin A11 OS=Homo sapiens GN=ANXA11 PE=1 SV=1 - |ANX11_HUMAN|	2.34E-05	25.5259	2.7475	1.85E-07	9.6410	2.7914
1_8	P12429	Annexin A3 OS=Homo sapiens GN=ANXA3 PE=1 SV=3 - |ANXA3_HUMAN|	3.04E-04	5.7926	2.7772	2.29E-03	3.4818	2.8845
1_8	O95994	Anterior gradient protein 2 homolog OS=Homo sapiens GN=AGR2 PE=1 SV=1 - |AGR2_HUMAN|	5.64E-05	21.9349	2.8776	1.81E-05	6.4948	3.0799
1_8	P05089	Arginase-1 OS=Homo sapiens GN=ARG1 PE=1 SV=2 - |ARGI1_HUMAN|	2.51E-05	-25.2963	-3.1406	1.42E-06	-11.0155	-4.9801
1_8	P54136	Arginine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=RARS PE=1 SV=2 - |SYRC_HUMAN|	3.66E-05	23.8665	2.6671	6.72E-05	5.4315	2.2914
1_8	P22760	Arylacetamide deacetylase OS=Homo sapiens GN=AADAC PE=1 SV=5 - |AAAD_HUMAN|	4.23E-05	-23.4316	-3.0027	6.61E-05	-14.3418	-3.4125
1_8	P14868	Aspartate--tRNA ligase, cytoplasmic OS=Homo sapiens GN=DARS PE=1 SV=2 - |SYDC_HUMAN|	1.14E-03	3.9073	2.7269	1.66E-05	6.5838	2.6105
1_8	P24539	ATP synthase subunit b, mitochondrial OS=Homo sapiens GN=ATP5F1 PE=1 SV=2 - |AT5F1_HUMAN|	8.21E-04	-4.2139	-3.0367	4.68E-04	-4.3422	-2.1785
1_8	O75947	ATP synthase subunit d, mitochondrial OS=Homo sapiens GN=ATP5H PE=1 SV=3 - |ATP5H_HUMAN|	4.74E-03	-3.4010	-3.0122	3.77E-03	-3.2221	-2.0086
1_8	P53396	ATP-citrate synthase OS=Homo sapiens GN=ACLY PE=1 SV=3 - |ACLY_HUMAN|	2.19E-02	2.4272	2.6621	3.86E-03	3.2078	2.6394
1_8	Q08211	ATP-dependent RNA helicase A OS=Homo sapiens GN=DHX9 PE=1 SV=4 - |DHX9_HUMAN|	5.39E-03	3.3030	2.7977	1.62E-05	6.7082	3.9923
1_8	Q92499	ATP-dependent RNA helicase DDX1 OS=Homo sapiens GN=DDX1 PE=1 SV=2 - |DDX1_HUMAN|	3.59E-05	23.9764	2.6698	1.77E-03	3.5946	2.2914

Fig. 7 continued

1_8	O00571	ATP-dependent RNA helicase DDX3X OS=Homo sapiens GN=DDX3X PE=1 SV=3 - [DDX3X_HUMAN]	4.31E-03	3.4616	2.7108	3.30E-05	6.0115	2.6171
1_8	P13929	Beta-enolase OS=Homo sapiens GN=ENO3 PE=1 SV=5 - [ENOB_HUMAN]	2.71E-04	-5.8220	-3.0904	1.33E-03	-3.7418	-3.7619
1_8	Q93088	Betaine--homocysteine S-methyltransferase 1 OS=Homo sapiens GN=BHMT PE=1 SV=2 - [BHMT1_HUMAN]	6.53E-05	-21.4499	-3.1673	1.19E-05	-6.9563	-4.8682
1_8	Q9UBR1	Beta-ureidopropionase OS=Homo sapiens GN=UPB1 PE=1 SV=1 - [BUP1_HUMAN]	6.11E-05	-21.6121	-3.1074	3.25E-05	-6.0471	-3.6561
1_8	P34913	Bifunctional epoxide hydrolase 2 OS=Homo sapiens GN=EPHX2 PE=1 SV=2 - [HYES_HUMAN]	3.23E-05	-24.3491	-3.0627	1.67E-05	-6.5741	-3.7851
1_8	P07814	Bifunctional glutamate/proline--tRNA ligase OS=Homo sapiens GN=EPRS PE=1 SV=5 - [SYEP_HUMAN]	2.72E-02	2.2629	2.8527	1.05E-04	5.1944	2.6919
1_8	P31939	Bifunctional purine biosynthesis protein PURH OS=Homo sapiens GN=ATIC PE=1 SV=3 - [PURH_HUMAN]	1.16E-03	3.8960	2.8264	9.14E-04	21.2739	3.9166
1_8	P21810	Biglycan OS=Homo sapiens GN=BGN PE=1 SV=2 - [PGS1_HUMAN]	3.18E-02	2.1186	2.8100	4.86E-03	3.0665	3.1742
1_8	Q14032	Bile acid-CoA:amino acid N-acyltransferase OS=Homo sapiens GN=BAAT PE=1 SV=1 - [BAAT_HUMAN]	6.01E-05	-21.6713	-3.0672	2.73E-04	-4.7041	-2.6382
1_8	Q9Y2P5	Bile acyl-CoA synthetase OS=Homo sapiens GN=SLC27A5 PE=1 SV=1 - [S27A5_HUMAN]	6.47E-05	-21.4856	-3.0863	2.24E-06	-8.3404	-4.4024
1_8	Q06520	Bile salt sulfotransferase OS=Homo sapiens GN=SULT2A1 PE=1 SV=3 - [ST2A1_HUMAN]	4.33E-05	-23.3737	-3.1402	7.14E-06	-11.8596	-4.0738
1_8	Q12864	Cadherin-17 OS=Homo sapiens GN=CDH17 PE=1 SV=3 - [CAD17_HUMAN]	3.13E-04	5.7758	2.7688	3.42E-04	4.5434	3.2065
1_8	Q9UJS0	Calcium-binding mitochondrial carrier protein Aralar2 OS=Homo sapiens GN=SLC25A13 PE=1 SV=2 - [CMC2_HUMAN]	6.22E-04	-4.8752	-3.0757	9.21E-06	-7.1481	-3.9518
1_8	P31327	Carbamoyl-phosphate synthase [ammonia], mitochondrial OS=Homo sapiens GN=CPS1 PE=1 SV=2 - [CPSM_HUMAN]	5.09E-04	-5.4365	-3.3307	4.63E-06	-7.5986	-7.8140
1_8	P00915	Carbonic anhydrase 1 OS=Homo sapiens GN=CA1 PE=1 SV=2 - [CAH1_HUMAN]	9.37E-05	-10.5109	-3.0495	1.25E-06	-8.9182	-4.0008
1_8	P00918	Carbonic anhydrase 2 OS=Homo sapiens GN=CA2 PE=1 SV=2 - [CAH2_HUMAN]	1.00E-04	-8.3426	-3.0716	1.33E-04	-5.0921	-3.4990
1_8	Q96DG6	Carboxymethylenebutenolidase homolog OS=Homo sapiens GN=CMBL PE=1 SV=1 - [CMBL_HUMAN]	9.78E-05	-8.5513	-3.0003	5.97E-04	-4.1841	-2.6745
1_8	P06731	Carcinoembryonic antigen-related cell adhesion molecule 5 OS=Homo sapiens GN=CEACAM5 PE=1 SV=3 - [CEAM5_HUMAN]	8.40E-05	18.8897	2.8744	5.44E-04	4.2417	2.7240
1_8	P40199	Carcinoembryonic antigen-related cell adhesion molecule 6 OS=Homo sapiens GN=CEACAM6 PE=1 SV=3 - [CEAM6_HUMAN]	1.28E-03	3.8466	2.7790	3.22E-03	3.2987	2.0866
1_8	P23786	Carnitine O-palmitoyltransferase 2, mitochondrial OS=Homo sapiens GN=CPT2 PE=1 SV=2 - [CPT2_HUMAN]	9.46E-05	-9.4360	-3.0257	2.68E-04	-4.7134	-3.1528
1_8	P02462	Collagen alpha-1(IV) chain OS=Homo sapiens GN=COL4A1 PE=1 SV=3 - [COA1_HUMAN]	8.34E-05	19.1028	2.7088	3.75E-05	5.7829	2.2981
1_8	Q05707	Collagen alpha-1(XIV) chain OS=Homo sapiens GN=COL14A1 PE=1 SV=3 - [COEA1_HUMAN]	2.33E-03	3.7705	2.6759	1.33E-02	2.5505	2.8235
1_8	P08572	Collagen alpha-2(IV) chain OS=Homo sapiens GN=COL4A2 PE=1 SV=4 - [COA2_HUMAN]	3.10E-02	2.1893	2.7453	1.47E-03	3.6844	2.5221
1_8	Q99829	Copine-1 OS=Homo sapiens GN=CPNE1 PE=1 SV=1 - [CPNE1_HUMAN]	6.29E-05	21.5582	2.7256	7.18E-04	4.0780	2.2997
1_8	P28845	Corticosteroid 11-beta-dehydrogenase isozyme 1 OS=Homo sapiens GN=HSD11B1 PE=1 SV=3 - [DHI1_HUMAN]	6.20E-05	-21.5848	-2.9859	4.47E-03	-3.1190	-2.0008
1_8	P12277	Creatine kinase B-type OS=Homo sapiens GN=CKB PE=1 SV=1 - [KCRB_HUMAN]	8.84E-03	2.8213	2.7880	1.93E-02	2.3613	3.4402
1_8	Q86VP6	Cullin-associated NEDD8-dissociated protein 1 OS=Homo sapiens GN=CAND1 PE=1 SV=2 - [CAND1_HUMAN]	5.83E-04	5.1265	2.7095	9.20E-05	5.2804	2.3142
1_8	P35520	Cystathionine beta-synthase OS=Homo sapiens GN=CBS PE=1 SV=2 - [CBS_HUMAN]	4.69E-06	-31.2554	-2.9856	5.95E-04	-4.1863	-2.0840
1_8	P32929	Cystathionine gamma-lyase OS=Homo sapiens GN=CTH PE=1 SV=3 - [CGL_HUMAN]	3.85E-04	-5.7178	-2.9700	2.88E-03	-3.3636	-2.5186
1_8	P00167	Cytochrome b5 OS=Homo sapiens GN=CYB5 PE=1 SV=2 - [CYB5_HUMAN]	2.28E-05	-25.6116	-3.1862	7.66E-05	-5.3563	-3.5936
1_8	P05177	Cytochrome P450 1A2 OS=Homo sapiens GN=CYP1A2 PE=1 SV=3 - [CP1A2_HUMAN]	3.31E-05	-24.1947	-3.0205	1.75E-04	-4.9713	-3.2232
1_8	P11509	Cytochrome P450 2A6 OS=Homo sapiens GN=CYP2A6 PE=1 SV=3 - [CP2A6_HUMAN]	7.20E-05	-20.6985	-3.0746	1.04E-04	-5.2001	-4.6052

Fig. 7 continued

1_8	P10632	Cytochrome P450 2C8 OS=Homo sapiens GN=CYP2C8 PE=1 SV=2 - [CP2C8_HUMAN]	3.42E-05	-24.1394	-3.0569	1.10E-06	-10.9282	-3.9088
1_8	P11712	Cytochrome P450 2C9 OS=Homo sapiens GN=CYP2C9 PE=1 SV=3 - [CP2C9_HUMAN]	3.81E-05	-23.7830	-3.0856	2.69E-06	-7.9942	-4.2291
1_8	P10635	Cytochrome P450 2D6 OS=Homo sapiens GN=CYP2D6 PE=1 SV=2 - [CP2D6_HUMAN]	2.27E-04	-5.8528	-2.9541	1.11E-02	-2.6392	-2.4168
1_8	P05181	Cytochrome P450 2E1 OS=Homo sapiens GN=CYP2E1 PE=1 SV=1 - [CP2E1_HUMAN]	9.81E-06	-27.9570	-3.0416	1.49E-07	-9.6735	-3.3879
1_8	P08684	Cytochrome P450 3A4 OS=Homo sapiens GN=CYP3A4 PE=1 SV=4 - [CP3A4_HUMAN]	1.85E-06	-33.4351	-3.1061	1.53E-06	-8.6528	-3.8971
1_8	Q029928	Cytochrome P450 4A11 OS=Homo sapiens GN=CYP4A11 PE=1 SV=1 - [CP4AB_HUMAN]	6.52E-06	-29.1359	-3.0294	1.20E-03	-3.8049	-3.0008
1_8	Q14204	Cytoplasmic dynein 1 heavy chain 1 OS=Homo sapiens GN=DYNC1H1 PE=1 SV=5 - [DYHC1_HUMAN]	7.44E-05	20.3670	2.7153	2.01E-03	3.5409	3.9823
1_8	O75891	Cytosolic 10-formyltetrahydrofolate dehydrogenase OS=Homo sapiens GN=ALDH1L1 PE=1 SV=2 - [AL1L1_HUMAN]	9.70E-06	-8.8365	-3.0944	1.66E-04	-4.9909	-5.1429
1_8	Q02338	D-beta-hydroxybutyrate dehydrogenase, mitochondrial OS=Homo sapiens GN=BDH1 PE=1 SV=3 - [BDH_HUMAN]	7.05E-04	-4.5196	-3.1312	4.62E-06	-7.6041	-4.1884
1_8	Q96LJ7	Dehydrogenase/reductase SDR family member 1 OS=Homo sapiens GN=DHRS1 PE=1 SV=1 - [DHRS1_HUMAN]	7.84E-05	-19.0630	-2.9580	8.37E-03	-2.7748	-2.4681
1_8	P30038	Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial OS=Homo sapiens GN=ALDH4A1 PE=1 SV=3 - [AL4A1_HUMAN]	1.14E-04	-7.1904	-3.1271	2.45E-08	-9.8004	-4.6287
1_8	P54886	Delta-1-pyrroline-5-carboxylate synthase OS=Homo sapiens GN=ALDH18A1 PE=1 SV=2 - [P5CS_HUMAN]	3.66E-05	23.8624	2.6907	6.32E-03	2.9129	2.6394
1_8	P13716	Delta-aminolevulinic acid dehydratase OS=Homo sapiens GN=ALAD PE=1 SV=1 - [HEM2_HUMAN]	3.81E-05	-23.7821	-3.0717	5.07E-05	-5.6233	-3.5645
1_8	P15924	Desmoplakin OS=Homo sapiens GN=DSP PE=1 SV=3 - [DESP_HUMAN]	1.38E-03	3.8401	2.6089	2.91E-02	2.1512	2.1539
1_8	P09417	Dihydropteridine reductase OS=Homo sapiens GN=QDPR PE=1 SV=2 - [DHPR_HUMAN]	9.49E-05	-9.4078	-3.0537	2.20E-04	-4.8471	-3.5579
1_8	Q14117	Dihydropyrimidinase OS=Homo sapiens GN=DPYS PE=1 SV=1 - [DPYS_HUMAN]	6.10E-05	-21.6167	-3.0297	2.62E-05	-6.2560	-2.9183
1_8	P31513	Dimethylaniline monooxygenase [N-oxide-forming] 3 OS=Homo sapiens GN=FMO3 PE=1 SV=5 - [FMO3_HUMAN]	8.01E-05	-19.6725	-3.1060	1.86E-04	-4.9392	-4.2567
1_8	P49326	Dimethylaniline monooxygenase [N-oxide-forming] 5 OS=Homo sapiens GN=FMO5 PE=2 SV=2 - [FMO5_HUMAN]	8.57E-05	-18.6809	-2.9711	1.40E-03	-3.6790	-3.4376
1_8	Q9UI17	Dimethylglycine dehydrogenase, mitochondrial OS=Homo sapiens GN=DMGDH PE=1 SV=2 - [M2GD_HUMAN]	4.48E-05	-23.1945	-3.0685	7.25E-07	-9.2639	-4.0343
1_8	P11387	DNA topoisomerase 1 OS=Homo sapiens GN=TOP1 PE=1 SV=2 - [TOP1_HUMAN]	3.90E-04	5.7135	2.7446	2.61E-03	3.4055	2.3440
1_8	P78527	DNA-dependent protein kinase catalytic subunit OS=Homo sapiens GN=PRKDC PE=1 SV=3 - [PRKDC_HUMAN]	4.55E-03	3.4299	2.7749	1.62E-05	6.7098	5.1622
1_8	Q7Z6Z7	E3 ubiquitin-protein ligase HUWE1 OS=Homo sapiens GN=HUWE1 PE=1 SV=3 - [HUWE1_HUMAN]	6.80E-05	21.1366	2.6790	1.62E-03	3.6426	2.5850
1_8	O75356	Ectonucleoside triphosphate diphosphohydrolase 5 OS=Homo sapiens GN=ENTPD5 PE=1 SV=1 - [ENTP5_HUMAN]	1.09E-05	-27.7478	-2.9465	4.88E-04	-4.3124	-2.6382
1_8	Q16134	Electron transfer flavoprotein-ubiquinone oxidoreductase, mitochondrial OS=Homo sapiens GN=ETFDH PE=1 SV=2 - [ETFD_HUMAN]	6.92E-05	-20.9402	-3.0460	1.60E-05	-6.7647	-2.8644
1_8	O75521	Enoyl-CoA delta isomerase 2, mitochondrial OS=Homo sapiens GN=ECI2 PE=1 SV=4 - [ECI2_HUMAN]	2.98E-05	-24.7010	-3.0291	8.84E-05	-5.2911	-3.1495
1_8	Q96YB7	Enoyl-CoA hydratase domain-containing protein 2, mitochondrial OS=Homo sapiens GN=ECHDC2 PE=2 SV=2 - [ECHD2_HUMAN]	4.24E-05	-23.4294	-3.0081	1.35E-04	-5.0804	-2.7619
1_8	P58107	Epiplakin OS=Homo sapiens GN=EPPK1 PE=1 SV=2 - [EPIPL_HUMAN]	7.55E-05	20.2857	2.7065	1.21E-03	3.7977	2.4170
1_8	P07099	Epoxide hydrolase 1 OS=Homo sapiens GN=EPHX1 PE=1 SV=1 - [HYEP_HUMAN]	6.03E-04	-4.9627	-3.2331	2.73E-06	-11.2890	-5.4844
1_8	Q9H0W9	Ester hydrolase C11orf54 OS=Homo sapiens GN=C11orf54 PE=1 SV=1 - [CK054_HUMAN]	9.84E-05	-8.4645	-3.0476	2.00E-03	-3.5412	-2.1785
1_8	P56537	Eukaryotic translation initiation factor 6 OS=Homo sapiens GN=EIF6 PE=1 SV=1 - [IF6_HUMAN]	3.45E-04	5.7509	2.7654	2.22E-04	4.8352	2.6394
1_8	P55060	Exportin-2 OS=Homo sapiens GN=CSE1L PE=1 SV=3 - [XPO2_HUMAN]	7.44E-03	2.9653	2.9586	3.11E-03	3.3187	2.5016
1_8	P15311	Ezrin OS=Homo sapiens GN=EZR PE=1 SV=4 - [EZRI_HUMAN]	3.70E-05	23.8414	2.8640	7.15E-05	5.3793	3.3846

Fig. 7 continued

1_8	Q96AE4	Far upstream element-binding protein 1 OS=Homo sapiens GN=FUBP1 PE=1 SV=3 - [FUBP1_HUMAN]	5.31E-03	3.3166	2.6404	6.88E-04	4.1000	2.4517
1_8	P51648	Fatty aldehyde dehydrogenase OS=Homo sapiens GN=ALDH3A2 PE=1 SV=1 - [AL3A2_HUMAN]	6.97E-05	-20.9277	-3.0148	4.37E-04	-4.3921	-3.0343
1_8	P35555	Fibrillin-1 OS=Homo sapiens GN=FBN1 PE=1 SV=3 - [FBN1_HUMAN]	1.60E-02	2.6941	2.6635	1.40E-02	2.5224	3.4759
1_8	O95394	Formimidoyltransferase-cyclodeaminase OS=Homo sapiens GN=FTCD PE=1 SV=2 - [FTCD_HUMAN]	6.44E-05	-21.5029	-3.1264	1.19E-06	-8.9810	-5.2716
1_8	P05062	Fructose-bisphosphate aldolase B OS=Homo sapiens GN=ALDOB PE=1 SV=2 - [ALDOB_HUMAN]	1.04E-04	-7.5406	-3.2556	1.01E-07	-9.9880	-6.4059
1_8	P16930	Fumarylacetoacetase OS=Homo sapiens GN=FAH PE=1 SV=2 - [FAAA_HUMAN]	1.25E-04	-6.6236	-3.1257	1.26E-07	-10.1785	-4.4125
1_8	P51570	Galactokinase OS=Homo sapiens GN=GALK1 PE=1 SV=1 - [GALK1_HUMAN]	4.01E-04	-5.7040	-3.0024	2.82E-03	-3.3770	-2.4493
1_8	P17931	Galectin-3 OS=Homo sapiens GN=LGALS3 PE=1 SV=5 - [LEG3_HUMAN]	5.88E-05	21.8426	2.8939	2.87E-05	6.1451	3.6200
1_8	Q08380	Galectin-3-binding protein OS=Homo sapiens GN=LGALS3BP PE=1 SV=1 - [LG3BP_HUMAN]	2.42E-04	5.8417	2.7516	1.26E-02	2.5734	2.7240
1_8	O95479	GDH/6PGL endoplasmic bifunctional protein OS=Homo sapiens GN=H6PD PE=1 SV=2 - [G6PE_HUMAN]	5.96E-05	-21.7210	-2.9933	1.26E-03	-3.7786	-2.9964
1_8	Q06210	Glutamine--fructose-6-phosphate aminotransferase [isomerizing] 1 OS=Homo sapiens GN=GFPT1 PE=1 SV=3 - [GFPT1_HUMAN]	8.67E-05	18.6472	2.7907	5.02E-04	4.2983	3.2914
1_8	P08263	Glutathione S-transferase A1 OS=Homo sapiens GN=GSTA1 PE=1 SV=3 - [GSTA1_HUMAN]	4.51E-05	-23.1754	-3.2529	4.10E-03	-3.1714	-5.5464
1_8	P09211	Glutathione S-transferase P OS=Homo sapiens GN=GSTP1 PE=1 SV=2 - [GSTP1_HUMAN]	9.39E-04	4.0595	2.9457	5.58E-07	9.3581	4.9818
1_8	P48637	Glutathione synthetase OS=Homo sapiens GN=GSS PE=1 SV=1 - [GSHB_HUMAN]	2.46E-02	2.3476	2.6946	2.42E-03	3.4582	2.2914
1_8	P21695	Glycerol-3-phosphate dehydrogenase [NAD(+)], cytoplasmic OS=Homo sapiens GN=GPD1 PE=1 SV=4 - [GPDA_HUMAN]	7.10E-05	-20.7786	-2.9811	2.09E-05	-6.4160	-3.1620
1_8	P50440	Glycine amidinotransferase, mitochondrial OS=Homo sapiens GN=GATM PE=1 SV=1 - [GATM_HUMAN]	4.44E-05	-23.2006	-3.1259	6.45E-05	-14.3034	-4.7469
1_8	P23378	Glycine dehydrogenase (decarboxylating), mitochondrial OS=Homo sapiens GN=GLDC PE=1 SV=2 - [GCSP_HUMAN]	5.42E-05	-22.2182	-3.0836	3.15E-03	-3.3110	-4.1123
1_8	Q6IB77	Glycine N-acyltransferase OS=Homo sapiens GN=GLYAT PE=1 SV=3 - [GLYAT_HUMAN]	2.10E-05	-25.8978	-3.1178	2.56E-04	-17.1499	-4.1035
1_8	Q14749	Glycine N-methyltransferase OS=Homo sapiens GN=GNMT PE=1 SV=3 - [GNMT_HUMAN]	1.69E-05	-26.4860	-2.9966	2.13E-03	-3.5107	-2.8276
1_8	P41250	Glycine--tRNA ligase OS=Homo sapiens GN=GARS PE=1 SV=3 - [SYG_HUMAN]	3.95E-05	23.6470	2.7478	1.75E-06	8.5342	2.5324
1_8	P35573	Glycogen debranching enzyme OS=Homo sapiens GN=AGL PE=1 SV=3 - [GDE_HUMAN]	7.76E-05	-19.8828	-3.0393	6.76E-05	-5.4231	-4.4446
1_8	P11216	Glycogen phosphorylase, brain form OS=Homo sapiens GN=PYGB PE=1 SV=5 - [PYGB_HUMAN]	6.88E-04	4.5807	2.8001	2.88E-03	3.3630	4.7240
1_8	P06737	Glycogen phosphorylase, liver form OS=Homo sapiens GN=PYGL PE=1 SV=4 - [PYGL_HUMAN]	6.57E-05	-21.4062	-3.0756	4.22E-07	-9.4541	-4.6954
1_8	Q92598	Heat shock protein 105 kDa OS=Homo sapiens GN=HSPH1 PE=1 SV=1 - [HS105_HUMAN]	5.44E-05	22.2078	2.8188	1.70E-04	4.9833	3.2769
1_8	O14979	Heterogeneous nuclear ribonucleoprotein D-like OS=Homo sapiens GN=HNRPDL PE=1 SV=3 - [HNRDL_HUMAN]	4.50E-03	3.4370	2.7959	1.87E-04	4.9329	2.7914
1_8	P31942	Heterogeneous nuclear ribonucleoprotein H3 OS=Homo sapiens GN=HNRNPH3 PE=1 SV=2 - [HNRH3_HUMAN]	6.06E-03	3.1802	2.7145	1.41E-04	5.0525	2.4356
1_8	O43390	Heterogeneous nuclear ribonucleoprotein R OS=Homo sapiens GN=HNRNPR PE=1 SV=1 - [HNRPR_HUMAN]	1.72E-02	2.6135	2.8443	1.10E-05	7.0172	3.4356
1_8	Q9BUJ2	Heterogeneous nuclear ribonucleoprotein U-like protein 1 OS=Homo sapiens GN=HNRNPUL1 PE=1 SV=2 - [HNRL1_HUMAN]	2.11E-04	5.8668	2.6996	4.52E-03	3.1117	2.2997
1_8	Q1KMD3	Heterogeneous nuclear ribonucleoprotein U-like protein 2 OS=Homo sapiens GN=HNRNPUL2 PE=1 SV=1 - [HNRL2_HUMAN]	1.82E-04	5.8977	2.7958	1.20E-06	8.9746	3.3142
1_8	P26583	High mobility group protein B2 OS=Homo sapiens GN=HMGB2 PE=1 SV=2 - [HMGB2_HUMAN]	2.86E-04	5.8116	2.8017	2.82E-03	3.3754	2.5611
1_8	P16401	Histone H1.5 OS=Homo sapiens GN=HIST1H1B PE=1 SV=3 - [H15_HUMAN]	2.88E-03	3.7012	3.0096	3.72E-05	5.7925	3.3142
1_8	Q93099	Homogentisate 1,2-dioxygenase OS=Homo sapiens GN=HGD PE=1 SV=2 - [HGD_HUMAN]	1.64E-05	-26.6161	-3.0396	4.18E-04	-4.4074	-3.6287

Fig. 7 continued

1_8	Q9UJM8	Hydroxyacid oxidase 1 OS=Homo sapiens GN=HAO1 PE=1 SV=1 - [HAOX1_HUMAN]	3.03E-05	-24.4661	-3.1053	1.72E-04	-4.9782	-4.4990
1_8	Q16775	Hydroxyacylglutathione hydrolase, mitochondrial OS=Homo sapiens GN=HAGH PE=1 SV=2 - [GLO2_HUMAN]	3.54E-05	-24.0935	-2.9897	1.08E-05	-7.0319	-2.4493
1_8	P35914	Hydroxymethylglutaryl-CoA lyase, mitochondrial OS=Homo sapiens GN=HMGCL PE=1 SV=2 - [HMGCL_HUMAN]	2.99E-04	-5.8004	-3.0761	2.77E-04	-4.6974	-2.9431
1_8	Q14974	Importin subunit beta-1 OS=Homo sapiens GN=KPNB1 PE=1 SV=2 - [IMB1_HUMAN]	4.96E-03	3.3704	2.7187	9.12E-06	7.1555	2.9627
1_8	O00410	Importin-5 OS=Homo sapiens GN=IPO5 PE=1 SV=4 - [IPO5_HUMAN]	7.03E-05	20.8239	2.7315	1.53E-04	5.0298	2.6216
1_8	Q15181	Inorganic pyrophosphatase OS=Homo sapiens GN=PPA1 PE=1 SV=2 - [IPYR_HUMAN]	1.31E-05	27.2065	2.7286	2.21E-03	3.4962	2.2981
1_8	Q12906	Interleukin enhancer-binding factor 3 OS=Homo sapiens GN=ILF3 PE=1 SV=3 - [ILF3_HUMAN]	1.83E-02	2.5601	2.7849	6.23E-04	4.1574	3.5491
1_8	P26440	Isovaleryl-CoA dehydrogenase, mitochondrial OS=Homo sapiens GN=IVD PE=1 SV=1 - [IVD_HUMAN]	6.19E-04	-4.8911	-2.9789	2.21E-03	-3.4961	-2.6745
1_8	P14923	Junction plakoglobin OS=Homo sapiens GN=JUP PE=1 SV=3 - [PLAK_HUMAN]	5.56E-04	5.2915	2.7850	1.89E-07	10.8592	2.9761
1_8	P08727	Keratin, type I cytoskeletal 19 OS=Homo sapiens GN=KRT19 PE=1 SV=4 - [K1C19_HUMAN]	8.06E-05	19.5914	2.8580	3.93E-05	5.7526	4.7993
1_8	P09960	Leukotriene A-4 hydrolase OS=Homo sapiens GN=LTA4H PE=1 SV=2 - [LKHA4_HUMAN]	1.77E-02	2.5879	2.6756	2.25E-04	4.8277	2.6171
1_8	P23141	Liver carboxylesterase 1 OS=Homo sapiens GN=CES1 PE=1 SV=2 - [EST1_HUMAN]	5.99E-04	-5.0036	-3.2803	5.63E-05	-5.5409	-5.9909
1_8	P07195	L-lactate dehydrogenase B chain OS=Homo sapiens GN=LDHB PE=1 SV=2 - [LDHB_HUMAN]	4.51E-02	2.0833	2.9143	3.03E-06	7.9216	4.0041
1_8	P33121	Long-chain-fatty-acid--CoA ligase 1 OS=Homo sapiens GN=ACSL1 PE=1 SV=1 - [ACSL1_HUMAN]	8.71E-05	-18.5806	-3.1446	1.22E-04	-5.1283	-4.5280
1_8	P05455	Lupus La protein OS=Homo sapiens GN=SSB PE=1 SV=2 - [LA_HUMAN]	6.30E-04	4.8374	2.7756	4.34E-06	11.5360	3.5221
1_8	Q15046	Lysine--tRNA ligase OS=Homo sapiens GN=KARS PE=1 SV=3 - [SYK_HUMAN]	5.59E-06	29.4027	2.6871	4.77E-05	5.6829	2.2997
1_8	P10253	Lysosomal alpha-glucosidase OS=Homo sapiens GN=GAA PE=1 SV=4 - [LYAG_HUMAN]	7.10E-03	-3.0145	-2.9513	2.06E-02	-2.3318	-2.3749
1_8	P40121	Macrophage-capping protein OS=Homo sapiens GN=CAPG PE=1 SV=2 - [CAPG_HUMAN]	1.26E-05	27.2436	2.8149	2.23E-06	8.3484	3.0019
1_8	Q14764	Major vault protein OS=Homo sapiens GN=MVP PE=1 SV=4 - [MVP_HUMAN]	7.75E-05	19.8927	2.7809	4.41E-04	4.3861	3.6105
1_8	O43708	Maleylacetoacetate isomerase OS=Homo sapiens GN=GSTZ1 PE=1 SV=3 - [MAAI_HUMAN]	1.80E-03	-3.8104	-2.9999	1.24E-02	-2.5800	-2.0086
1_8	P43243	Matrin-3 OS=Homo sapiens GN=MATR3 PE=1 SV=2 - [MATR3_HUMAN]	2.16E-02	2.4373	2.7685	1.05E-04	5.1973	3.4517
1_8	P11310	Medium-chain specific acyl-CoA dehydrogenase, mitochondrial OS=Homo sapiens GN=ACADM PE=1 SV=1 - [ACADM_HUMAN]	9.56E-05	-9.2879	-3.0653	1.96E-03	-3.5535	-3.7091
1_8	Q002252	Methylmalonate-semialdehyde dehydrogenase [acylating], mitochondrial OS=Homo sapiens GN=ALDH6A1 PE=1 SV=2 - [MMSA_HUMAN]	3.06E-04	-5.7880	-3.1940	5.28E-04	-19.2760	-5.1968
1_8	Q9H8R3	Methyltransferase-like protein 7A OS=Homo sapiens GN=METTL7A PE=1 SV=1 - [MET7A_HUMAN]	7.94E-05	-19.7844	-3.1078	1.73E-04	-4.9765	-2.4125
1_8	P10620	Microsomal glutathione S-transferase 1 OS=Homo sapiens GN=MGST1 PE=1 SV=1 - [MGST1_HUMAN]	6.71E-05	-21.1889	-3.1164	2.68E-04	-4.7228	-2.4125
1_8	O43772	Mitochondrial carnitine/acylcarnitine carrier protein OS=Homo sapiens GN=SLC25A20 PE=1 SV=1 - [MCAT_HUMAN]	1.54E-05	-26.7650	-2.9591	7.69E-04	-4.0361	-2.4681
1_8	Q96GZ3	MOSC domain-containing protein 2, mitochondrial OS=Homo sapiens GN=MARC2 PE=1 SV=1 - [MOSC2_HUMAN]	5.13E-05	-22.6254	-2.9702	1.30E-06	-8.8723	-2.7020
1_8	Q7Z406	Myosin-14 OS=Homo sapiens GN=MYH14 PE=1 SV=2 - [MYH14_HUMAN]	7.14E-05	20.7491	2.8464	5.69E-04	4.2142	4.7862
1_8	Q4G0N4	NAD kinase domain-containing protein 1 OS=Homo sapiens GN=NADKD1 PE=1 SV=2 - [NAKD1_HUMAN]	1.99E-05	-26.1600	-3.0937	3.39E-05	-5.9437	-3.8160
1_8	P16435	NADPH--cytochrome P450 reductase OS=Homo sapiens GN=POR PE=1 SV=2 - [NCPR_HUMAN]	5.83E-04	-5.1327	-3.0231	4.27E-07	-9.4504	-3.3749
1_8	P22307	Non-specific lipid-transfer protein OS=Homo sapiens GN=SCP2 PE=1 SV=2 - [NLTP_HUMAN]	5.53E-04	-5.3108	-3.0822	1.48E-04	-15.8564	-4.0008
1_8	Q14980	Nuclear mitotic apparatus protein 1 OS=Homo sapiens GN=NUMA1 PE=1 SV=2 - [NUMA1_HUMAN]	7.76E-05	19.8780	2.6318	7.62E-03	2.8125	2.2386

Fig. 7 continued

1_8	O00567	Nucleolar protein 56 OS=Homo sapiens GN=NOP56 PE=1 SV=4 - [NOP56_HUMAN]	6.67E-05	21.2834	2.7320	7.10E-04	4.0829	2.3142
1_8	P00480	Ornithine carbamoyltransferase, mitochondrial OS=Homo sapiens GN=OTC PE=1 SV=3 - [OTC_HUMAN]	4.11E-05	-23.5268	-3.1288	6.85E-04	-20.1799	-4.1620
1_8	Q02790	Peptidyl-prolyl cis-trans isomerase FKBP4 OS=Homo sapiens GN=FKBP4 PE=1 SV=3 - [FKBP4_HUMAN]	1.58E-05	26.6876	2.6916	5.37E-04	4.2485	2.9627
1_8	Q15063	Periostin OS=Homo sapiens GN=POSTN PE=1 SV=2 - [POSTN_HUMAN]	9.04E-05	16.5373	2.7865	1.40E-02	2.5014	3.3474
1_8	Q9NUI1	Peroxisomal 2,4-dienoyl-CoA reductase OS=Homo sapiens GN=DECR2 PE=1 SV=1 - [DECR2_HUMAN]	2.61E-04	-5.8291	-2.9838	1.60E-03	-3.6454	-2.5645
1_8	Q15067	Peroxisomal acyl-coenzyme A oxidase 1 OS=Homo sapiens GN=ACOX1 PE=1 SV=3 - [ACOX1_HUMAN]	9.89E-05	-8.4511	-3.0451	4.13E-04	-4.4148	-3.7712
1_8	Q99424	Peroxisomal acyl-coenzyme A oxidase 2 OS=Homo sapiens GN=ACOX2 PE=1 SV=1 - [ACOX2_HUMAN]	3.97E-05	-23.6363	-3.0730	3.67E-05	-5.8231	-4.0961
1_8	Q08426	Peroxisomal bifunctional enzyme OS=Homo sapiens GN=EHHADH PE=1 SV=3 - [ECHP_HUMAN]	1.23E-04	-6.7555	-3.1724	3.36E-07	-9.5181	-5.7091
1_8	Q9P0Z9	Peroxisomal sarcosine oxidase OS=Homo sapiens GN=PIPOX PE=2 SV=2 - [SOX_HUMAN]	3.08E-05	-24.4395	-3.0673	6.13E-06	-7.3762	-3.6145
1_8	Q9BY49	Peroxisomal trans-2-enoyl-CoA reductase OS=Homo sapiens GN=PECR PE=1 SV=2 - [PECR_HUMAN]	1.46E-05	-26.8861	-3.0006	4.07E-03	-3.1755	-2.0500
1_8	P30039	Phenazine biosynthesis-like domain-containing protein OS=Homo sapiens GN=PBLD PE=1 SV=2 - [PBLD_HUMAN]	5.04E-05	-22.8342	-3.0315	2.05E-04	-4.8794	-3.1863
1_8	P00439	Phenylalanine-4-hydroxylase OS=Homo sapiens GN=PAH PE=1 SV=1 - [PH4H_HUMAN]	5.88E-05	-21.8428	-3.0126	4.56E-04	-4.3598	-2.7619
1_8	Q9Y285	Phenylalanine--tRNA ligase alpha subunit OS=Homo sapiens GN=FARSA PE=1 SV=3 - [SYFA_HUMAN]	5.05E-04	5.4530	2.6603	1.05E-03	3.8716	2.1622
1_8	Q9NSD9	Phenylalanine--tRNA ligase beta subunit OS=Homo sapiens GN=FARSB PE=1 SV=3 - [SYFB_HUMAN]	3.63E-05	23.8810	2.7077	1.59E-05	6.7926	2.5772
1_8	Q9Y617	Phosphoserine aminotransferase OS=Homo sapiens GN=PSAT1 PE=1 SV=2 - [SERC_HUMAN]	1.01E-04	-7.9253	-3.0023	2.14E-03	-3.5084	-2.3735
1_8	Q14651	Plastin-1 OS=Homo sapiens GN=PLS1 PE=1 SV=2 - [PLS1_HUMAN]	6.26E-05	21.5550	2.8071	1.97E-04	4.8977	2.7240
1_8	Q6P2Q9	Pre-mRNA-processing-splicing factor 8 OS=Homo sapiens GN=PRPF8 PE=1 SV=2 - [PRP8_HUMAN]	7.98E-05	19.7361	2.6754	4.74E-03	3.0790	2.3761
1_8	P17844	Probable ATP-dependent RNA helicase DDX5 OS=Homo sapiens GN=DDX5 PE=1 SV=1 - [DDX5_HUMAN]	3.30E-05	24.2039	2.7914	4.35E-04	4.3941	3.2734
1_8	Q8WUM4	Programmed cell death 6-interacting protein OS=Homo sapiens GN=PDCD6IP PE=1 SV=1 - [PDC6I_HUMAN]	6.08E-04	4.9673	2.7388	1.51E-03	3.6699	2.4695
1_8	P12004	Proliferating cell nuclear antigen OS=Homo sapiens GN=PCNA PE=1 SV=1 - [PCNA_HUMAN]	5.92E-05	21.8276	2.7851	2.52E-03	3.4334	3.0255
1_8	Q9UQB0	Proliferation-associated protein 2G4 OS=Homo sapiens GN=PA2G4 PE=1 SV=3 - [PA2G4_HUMAN]	1.94E-02	2.5126	2.8122	1.22E-05	6.9409	3.0797
1_8	Q14914	Prostaglandin reductase 1 OS=Homo sapiens GN=PTGR1 PE=1 SV=2 - [PTGR1_HUMAN]	4.03E-05	-23.6224	-3.0490	2.10E-04	-4.8697	-3.7662
1_8	Q9BPW8	Protein NipSnap homolog 1 OS=Homo sapiens GN=NIPSNAP1 PE=1 SV=1 - [NIPS1_HUMAN]	7.69E-04	-4.3486	-3.0532	2.81E-05	-6.2084	-3.1967
1_8	Q9P258	Protein RCC2 OS=Homo sapiens GN=RCC2 PE=1 SV=2 - [RCC2_HUMAN]	6.29E-05	21.5455	2.6566	9.20E-04	3.9381	2.4152
1_8	P06703	Protein S100-A6 OS=Homo sapiens GN=S100A6 PE=1 SV=1 - [S10A6_HUMAN]	4.65E-05	23.0590	2.8409	6.53E-04	4.1262	2.0545
1_8	Q01105	Protein SET OS=Homo sapiens GN=SET PE=1 SV=3 - [SET_HUMAN]	3.51E-03	3.5902	2.8432	1.61E-05	6.7282	2.7240
1_8	P55786	Puromycin-sensitive aminopeptidase OS=Homo sapiens GN=NPEPPS PE=1 SV=2 - [PSA_HUMAN]	1.97E-02	2.4994	2.6909	1.65E-05	6.6313	2.9627
1_8	A6ND91	Putative L-aspartate dehydrogenase OS=Homo sapiens GN=ASPDH PE=2 SV=2 - [ASPD_HUMAN]	2.30E-04	-5.8503	-2.9302	1.57E-02	-2.4630	-2.0086
1_8	O43143	Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15 OS=Homo sapiens GN=DHX15 PE=1 SV=2 - [DHX15_HUMAN]	1.21E-05	27.3948	2.7146	2.87E-05	6.1485	2.4356
1_8	Q9NVS9	Pyridoxine-5-phosphate oxidase OS=Homo sapiens GN=PNPO PE=1 SV=1 - [PNPO_HUMAN]	6.36E-04	-4.8229	-2.9789	3.29E-06	-11.3835	-2.1967
1_8	P11498	Pyruvate carboxylase, mitochondrial OS=Homo sapiens GN=PC PE=1 SV=2 - [PYC_HUMAN]	4.65E-05	-23.0605	-3.1278	1.82E-05	-6.4805	-5.0961
1_8	P14618	Pyruvate kinase isozymes M1/M2 OS=Homo sapiens GN=PKM PE=1 SV=4 - [KPYM_HUMAN]	4.19E-04	5.6620	2.9018	9.43E-07	10.8813	4.7146

Fig. 7 continued

1_8	P30613	Pyruvate kinase isozymes R/L OS=Homo sapiens GN=PKLR PE=1 SV=2 - [KPYR_HUMAN]	6.85E-05	-20.9736	-3.0488	3.53E-05	-5.8847	-4.1006
1_8	Q13283	Ras GTPase-activating protein-binding protein 1 OS=Homo sapiens GN=G3BP1 PE=1 SV=1 - [G3BP1_HUMAN]	1.75E-04	5.9099	2.6861	1.04E-04	5.2012	2.0866
1_8	P46940	Ras GTPase-activating-like protein IQGAP1 OS=Homo sapiens GN=IQGAP1 PE=1 SV=1 - [IQGA1_HUMAN]	5.93E-03	3.2062	2.7990	2.32E-05	6.2912	4.1954
1_8	Q13576	Ras GTPase-activating-like protein IQGAP2 OS=Homo sapiens GN=IQGAP2 PE=1 SV=4 - [IQGA2_HUMAN]	8.99E-05	-17.2089	-2.9401	1.03E-02	-2.6716	-3.0343
1_8	Q96HR9	Receptor expression-enhancing protein 6 OS=Homo sapiens GN=REEP6 PE=1 SV=1 - [REEP6_HUMAN]	2.47E-05	-25.3477	-3.0203	3.54E-04	-4.5217	-2.1528
1_8	Q15493	Regucalcin OS=Homo sapiens GN=RGN PE=1 SV=1 - [RGN_HUMAN]	5.12E-06	-30.8468	-2.9930	4.33E-03	-3.1864	-2.5936
1_8	O75452	Retinol dehydrogenase 16 OS=Homo sapiens GN=RDH16 PE=1 SV=2 - [RDH16_HUMAN]	6.90E-05	-20.9445	-3.1225	8.01E-05	-5.3418	-3.8444
1_8	P52758	Ribonuclease UK114 OS=Homo sapiens GN=HRSP12 PE=1 SV=1 - [UK114_HUMAN]	4.02E-13	-38.8462	-3.1335	5.50E-06	-7.4385	-2.8276
1_8	Q9UKM9	RNA-binding protein Raly OS=Homo sapiens GN=RALY PE=1 SV=1 - [RALY_HUMAN]	3.84E-05	23.7616	2.7958	2.96E-07	9.5495	2.6927
1_8	Q9Y265	RuvB-like 1 OS=Homo sapiens GN=RUVBL1 PE=1 SV=1 - [RUVB1_HUMAN]	2.83E-05	24.9007	2.7000	1.34E-06	8.8226	2.4517
1_8	Q8NBX0	Saccharopine dehydrogenase-like oxidoreductase OS=Homo sapiens GN=SCCPDH PE=1 SV=1 - [SCPDL_HUMAN]	9.65E-05	-9.2103	-2.9965	6.67E-04	-4.1168	-2.6145
1_8	Q00266	S-adenosylmethionine synthase isoform type-1 OS=Homo sapiens GN=MAT1A PE=1 SV=2 - [METK1_HUMAN]	5.69E-05	-21.9037	-3.0877	6.40E-07	-9.3090	-3.5857
1_8	Q9UL12	Sarcosine dehydrogenase, mitochondrial OS=Homo sapiens GN=SARDH PE=1 SV=1 - [SARDH_HUMAN]	2.72E-05	-24.9611	-3.0485	3.00E-08	-10.3773	-4.1035
1_8	Q15019	Septin-2 OS=Homo sapiens GN=SEPT2 PE=1 SV=1 - [SEPT2_HUMAN]	4.84E-05	22.9491	2.7322	1.62E-05	6.7151	2.4356
1_8	Q16181	Septin-7 OS=Homo sapiens GN=SEPT7 PE=1 SV=2 - [SEPT7_HUMAN]	6.61E-05	21.3532	2.6803	3.68E-05	5.8184	2.0255
1_8	Q9UHD8	Septin-9 OS=Homo sapiens GN=SEPT9 PE=1 SV=2 - [SEPT9_HUMAN]	6.26E-03	3.1439	2.6779	1.28E-02	2.5677	2.0367
1_8	P34896	Serine hydroxymethyltransferase, cytosolic OS=Homo sapiens GN=SHMT1 PE=1 SV=1 - [GLYC_HUMAN]	7.51E-05	-20.3223	-3.1135	2.22E-06	-8.3563	-4.3879
1_8	Q07955	Serine/arginine-rich splicing factor 1 OS=Homo sapiens GN=SRSF1 PE=1 SV=2 - [SRSF1_HUMAN]	1.89E-05	26.3344	2.7417	8.90E-06	7.1720	3.0636
1_8	P30153	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform OS=Homo sapiens GN=PPP2R1A PE=1 SV=4 - [2AAA_HUMAN]	6.79E-03	3.0555	2.6901	1.77E-04	4.9658	2.4170
1_8	P62136	Serine/threonine-protein phosphatase PP1-alpha catalytic subunit OS=Homo sapiens GN=PPP1CA PE=1 SV=1 - [PP1A_HUMAN]	4.98E-03	3.3675	2.7546	2.08E-03	3.5217	3.1539
1_8	P21549	Serine--pyruvate aminotransferase OS=Homo sapiens GN=AGXT PE=1 SV=1 - [SPYA_HUMAN]	9.41E-05	-9.7163	-3.2392	1.26E-06	-8.9156	-6.0039
1_8	P35237	Serpin B6 OS=Homo sapiens GN=SERPINB6 PE=1 SV=3 - [SPB6_HUMAN]	3.21E-04	5.7672	2.7966	1.28E-03	3.7643	2.5772
1_8	P50454	Serpin H1 OS=Homo sapiens GN=SERPINH1 PE=1 SV=2 - [SERPH_HUMAN]	7.37E-03	2.9736	2.8429	2.16E-04	4.8593	2.8329
1_8	P27169	Serum paraoxonase/arylesterase 1 OS=Homo sapiens GN=PON1 PE=1 SV=3 - [PON1_HUMAN]	2.22E-05	-25.6833	-3.0375	3.71E-03	-3.2296	-2.0086
1_8	P45954	Short/branched chain specific acyl-CoA dehydrogenase, mitochondrial OS=Homo sapiens GN=ACADSB PE=1 SV=1 - [ACDSB_HUMAN]	1.04E-04	-7.5977	-3.1545	4.15E-05	-5.7184	-4.3301
1_8	P16219	Short-chain specific acyl-CoA dehydrogenase, mitochondrial OS=Homo sapiens GN=ACADS PE=1 SV=1 - [ACADS_HUMAN]	1.33E-04	-6.3488	-3.0990	2.46E-04	-4.7689	-3.7377
1_8	Q9H9B4	Sideroflexin-1 OS=Homo sapiens GN=SFXN1 PE=1 SV=4 - [SFXN1_HUMAN]	1.43E-04	-6.2018	-3.0416	6.78E-04	-4.1086	-3.0008
1_8	O75533	Splicing factor 3B subunit 1 OS=Homo sapiens GN=SF3B1 PE=1 SV=3 - [SF3B1_HUMAN]	1.40E-04	6.1822	2.6708	2.35E-03	3.4236	2.5221
1_8	Q15393	Splicing factor 3B subunit 3 OS=Homo sapiens GN=SF3B3 PE=1 SV=4 - [SF3B3_HUMAN]	2.09E-05	25.9167	2.7124	1.71E-04	4.9817	2.3761
1_8	P26368	Splicing factor U2AF 65 kDa subunit OS=Homo sapiens GN=U2AF2 PE=1 SV=4 - [U2AF2_HUMAN]	2.60E-05	25.1705	2.7538	4.34E-04	4.3948	2.1460
1_8	Q14247	Src substrate cortactin OS=Homo sapiens GN=CTTN PE=1 SV=2 - [SRC8_HUMAN]	5.56E-05	22.0572	2.7471	2.79E-05	6.2168	2.4356
1_8	P21912	Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial OS=Homo sapiens GN=SDHB PE=1 SV=3 - [DHSB_HUMAN]	9.56E-05	-9.2832	-2.9806	8.01E-06	-7.2486	-2.4158

Fig. 7 continued

1_8	P50225	Sulfotransferase 1A1 OS=Homo sapiens GN=SULT1A1 PE=1 SV=3 - [ST1A1_HUMAN]	2.67E-05	-24.9906	-3.1066	2.84E-05	-6.1862	-3.0840
1_8	P48643	T-complex protein 1 subunit epsilon OS=Homo sapiens GN=CCT5 PE=1 SV=1 - [TCPE_HUMAN]	4.81E-05	22.9667	2.7078	2.86E-05	6.1554	2.2997
1_8	Q99832	T-complex protein 1 subunit eta OS=Homo sapiens GN=CCT7 PE=1 SV=2 - [TCPH_HUMAN]	4.76E-02	2.0741	2.7803	1.20E-07	10.0568	3.0799
1_8	P40227	T-complex protein 1 subunit zeta OS=Homo sapiens GN=CCT6A PE=1 SV=3 - [TCPZ_HUMAN]	7.41E-05	20.3818	2.7717	5.21E-06	7.4754	2.4356
1_8	P29821	Tenascin OS=Homo sapiens GN=TNC PE=1 SV=3 - [TENA_HUMAN]	8.87E-05	18.2425	2.7745	4.62E-03	3.0935	3.3556
1_8	P19971	Thymidine phosphorylase OS=Homo sapiens GN=TYMP PE=1 SV=2 - [TYPH_HUMAN]	6.70E-04	-4.6632	-2.9355	1.85E-02	-2.3833	-2.3749
1_8	Q13263	Transcription intermediary factor 1-beta OS=Homo sapiens GN=TRIM28 PE=1 SV=5 - [TIF1B_HUMAN]	2.43E-05	25.3652	2.7771	1.11E-04	5.1592	3.4696
1_8	Q01995	Transgelin OS=Homo sapiens GN=TAGLN PE=1 SV=4 - [TAGL_HUMAN]	5.84E-04	5.1183	2.8150	2.10E-05	6.3577	3.3684
1_8	P53007	Tricarboxylate transport protein, mitochondrial OS=Homo sapiens GN=SLC25A1 PE=1 SV=2 - [TXTP_HUMAN]	1.92E-03	-3.8009	-3.0340	8.53E-05	-5.3045	-2.6745
1_8	Q9Y310	tRNA-splicing ligase RtcB homolog OS=Homo sapiens GN=C22orf28 PE=1 SV=1 - [RTCB_HUMAN]	9.36E-06	27.9841	2.7233	2.92E-05	6.1069	2.0545
1_8	P67936	Tropomyosin alpha-4 chain OS=Homo sapiens GN=TPM4 PE=1 SV=3 - [TPM4_HUMAN]	5.30E-04	5.3848	2.8272	4.81E-06	7.5426	2.8320
1_8	Q9BQE3	Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 - [TBA1C_HUMAN]	1.50E-03	3.8333	2.9913	9.13E-03	2.7314	5.3684
1_8	P68366	Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A PE=1 SV=1 - [TBA4A_HUMAN]	3.13E-02	2.1283	3.0127	3.70E-06	7.8408	5.5599
1_8	O43399	Tumor protein D54 OS=Homo sapiens GN=TPD52L2 PE=1 SV=2 - [TPD54_HUMAN]	5.08E-04	5.4398	2.6755	2.12E-03	3.5127	2.0545
1_8	P15374	Ubiquitin carboxyl-terminal hydrolase isozyme L3 OS=Homo sapiens GN=UCHL3 PE=1 SV=1 - [UCHL3_HUMAN]	4.93E-03	3.3745	2.6997	8.43E-06	7.2085	2.1742
1_8	P22310	UDP-glucuronosyltransferase 1-4 OS=Homo sapiens GN=UGT1A4 PE=1 SV=1 - [UD14_HUMAN]	3.76E-04	-5.7253	-3.0442	7.32E-04	-4.0686	-2.9518
1_8	P06133	UDP-glucuronosyltransferase 2B4 OS=Homo sapiens GN=UGT2B4 PE=1 SV=2 - [UD2B4_HUMAN]	4.48E-04	-5.5958	-3.0069	7.97E-03	-2.7944	-3.2903
1_8	P16662	UDP-glucuronosyltransferase 2B7 OS=Homo sapiens GN=UGT2B7 PE=1 SV=1 - [UD2B7_HUMAN]	8.90E-06	-18.2245	-3.1155	2.02E-04	-4.8869	-3.5857
1_8	O94832	Unconventional myosin-Id OS=Homo sapiens GN=MYO1D PE=1 SV=2 - [MYO1D_HUMAN]	1.25E-03	3.8490	2.6680	1.68E-02	2.4275	2.4170
1_8	Q96CX1	Vacuolar protein sorting-associated protein 35 OS=Homo sapiens GN=VPS35 PE=1 SV=2 - [VPS35_HUMAN]	5.80E-04	5.1477	2.6981	2.88E-06	7.9472	2.7259
1_8	P13611	Versican core protein OS=Homo sapiens GN=VCAN PE=1 SV=3 - [CSPG2_HUMAN]	4.04E-04	5.7009	2.7352	8.74E-03	2.7547	2.0255
1_8	P09327	Villin-1 OS=Homo sapiens GN=VIL1 PE=1 SV=4 - [VILI_HUMAN]	4.36E-05	23.3591	2.7640	1.72E-06	8.5474	3.6394
1_9	Q04917	14-3-3 protein eta OS=Homo sapiens GN=YWHAH PE=1 SV=4 - [1433F_HUMAN]	7.14E-04	5.4251	3.1114	2.86E-04	5.4521	3.5304
1_9	Q72SP4	17-beta-hydroxysteroid dehydrogenase 13 OS=Homo sapiens GN=HSD17B13 PE=2 SV=1 - [DHB13_HUMAN]	3.83E-05	-19.0172	-3.1005	3.97E-04	-5.2191	-3.2567
1_9	O14756	17-beta-hydroxysteroid dehydrogenase type 6 OS=Homo sapiens GN=HSD17B6 PE=1 SV=1 - [DH17B6_HUMAN]	3.18E-05	-20.0852	-3.1163	1.93E-05	-8.1240	-3.9088
1_9	P12694	2-oxoisovalerate dehydrogenase subunit alpha, mitochondrial OS=Homo sapiens GN=BCKDHA PE=1 SV=2 - [ODBA_HUMAN]	2.36E-04	-5.9395	-2.9176	1.17E-03	-4.2538	-2.6382
1_9	P46952	3-hydroxyanthranilate 3,4-dioxygenase OS=Homo sapiens GN=HAAO PE=1 SV=2 - [3HAO_HUMAN]	8.54E-06	-25.2483	-3.0508	9.77E-06	-8.7071	-3.3183
1_9	P51857	3-oxo-5-beta-steroid 4-dehydrogenase OS=Homo sapiens GN=AKR1D1 PE=1 SV=1 - [AK1D1_HUMAN]	4.04E-06	-18.5719	-3.0581	1.00E-02	-2.8413	-2.6145
1_9	P80404	4-aminobutyrate aminotransferase, mitochondrial OS=Homo sapiens GN=ABAT PE=1 SV=3 - [GABT_HUMAN]	9.31E-05	-6.4554	-3.1594	1.40E-06	-11.6193	-5.3259
1_9	P32754	4-hydroxyphenylpyruvate dioxygenase OS=Homo sapiens GN=HPD PE=1 SV=2 - [HPPD_HUMAN]	2.16E-05	-22.1822	-3.1328	2.71E-06	-9.9568	-4.4376
1_9	P17858	6-phosphofructokinase, liver type OS=Homo sapiens GN=PFKL PE=1 SV=5 - [K6PL_HUMAN]	3.40E-02	2.2060	2.8732	5.27E-03	3.2283	2.5825
1_9	P24752	Acetyl-CoA acetyltransferase, mitochondrial OS=Homo sapiens GN=ACAT1 PE=1 SV=1 - [THIL_HUMAN]	7.33E-04	-5.2990	-3.1966	7.92E-06	-8.9260	-4.7963

Fig. 7 continued

1_9	P68133	Actin, alpha skeletal muscle OS=Homo sapiens GN=ACTA1 PE=1 SV=1 - [ACTS_HUMAN]	2.42E-03	-3.7789	-3.1987	1.11E-02	-2.7862	-5.0961
1_9	P61160	Actin-related protein 2 OS=Homo sapiens GN=ACTR2 PE=1 SV=1 - [ARP2_HUMAN]	2.20E-02	2.4205	2.9006	5.33E-04	4.9858	2.2639
1_9	O15144	Actin-related protein 2/3 complex subunit 2 OS=Homo sapiens GN=ARPC2 PE=1 SV=1 - [ARPC2_HUMAN]	3.30E-03	3.6061	2.8756	3.57E-03	3.4744	2.4277
1_9	Q8IA1F3	Acyl-coenzyme A synthetase ACSM2A, mitochondrial OS=Homo sapiens GN=ACSM2A PE=1 SV=2 - [ACS2A_HUMAN]	9.80E-06	-24.9514	-3.1313	3.75E-04	-5.2804	-5.0015
1_9	Q6BCK6	Acyl-coenzyme A synthetase ACSM2B, mitochondrial OS=Homo sapiens GN=ACSM2B PE=1 SV=2 - [ACS2B_HUMAN]	9.86E-06	-24.9352	-3.1313	1.68E-06	-10.6014	-5.1339
1_9	P27144	Adenylate kinase isoenzyme 4, mitochondrial OS=Homo sapiens GN=AK4 PE=1 SV=1 - [KAD4_HUMAN]	1.83E-03	-3.8845	-2.9842	1.37E-03	-4.1428	-2.7214
1_9	Q9BSE5	Agmatinase, mitochondrial OS=Homo sapiens GN=AGMAT PE=1 SV=2 - [SPEB_HUMAN]	2.44E-04	-5.9240	-3.0674	3.25E-03	-3.5341	-2.0086
1_9	P24298	Alanine aminotransferase 1 OS=Homo sapiens GN=GPT PE=1 SV=3 - [ALAT1_HUMAN]	1.25E-05	-24.4015	-3.0208	1.54E-05	-8.3445	-3.9864
1_9	P08319	Alcohol dehydrogenase 4 OS=Homo sapiens GN=ADH4 PE=1 SV=5 - [ADH4_HUMAN]	3.83E-05	-18.9978	-3.2128	1.51E-04	-5.9807	-5.9289
1_9	P28332	Alcohol dehydrogenase 6 OS=Homo sapiens GN=ADH6 PE=2 SV=2 - [ADH6_HUMAN]	6.84E-04	-5.5097	-3.0225	9.87E-03	-2.8500	-3.3238
1_9	Q9H2A2	Aldehyde dehydrogenase family 8 member A1 OS=Homo sapiens GN=ALDH8A1 PE=1 SV=1 - [AL8A1_HUMAN]	2.13E-05	-22.2723	-3.0403	2.61E-04	-5.5086	-3.5313
1_9	P30838	Aldehyde dehydrogenase, dimeric NADP-preferring OS=Homo sapiens GN=ALDH3A1 PE=1 SV=3 - [AL3A1_HUMAN]	1.76E-02	2.6173	2.9253	2.19E-02	2.4303	2.6514
1_9	Q06278	Aldehyde oxidase OS=Homo sapiens GN=AOX1 PE=2 SV=2 - [ADO_HUMAN]	3.77E-05	-19.3202	-3.0642	3.32E-03	-3.5143	-4.8209
1_9	O60218	Aldo-keto reductase family 1 member B10 OS=Homo sapiens GN=AKR1B10 PE=1 SV=2 - [AK1BA_HUMAN]	3.34E-03	3.5894	3.1370	1.51E-04	5.9782	4.6421
1_9	Q03154	Aminoacylase-1 OS=Homo sapiens GN=ACY1 PE=1 SV=1 - [ACY1_HUMAN]	5.47E-04	-5.6343	-3.1496	1.71E-06	-10.5293	-4.4905
1_9	Q9H4A4	Aminopeptidase B OS=Homo sapiens GN=RNPEP PE=1 SV=2 - [AMPB_HUMAN]	1.59E-03	4.1040	2.8914	1.34E-03	4.1629	2.3040
1_9	P50995	Annexin A11 OS=Homo sapiens GN=ANXA11 PE=1 SV=1 - [ANX11_HUMAN]	5.05E-05	16.3072	2.9430	3.63E-02	18.3200	3.0952
1_9	P27216	Annexin A13 OS=Homo sapiens GN=ANXA13 PE=1 SV=3 - [ANX13_HUMAN]	5.38E-05	15.3326	2.9618	7.27E-04	4.6796	3.3431
1_9	O95394	Anterior gradient protein 2 homolog OS=Homo sapiens GN=AGR2 PE=1 SV=1 - [AGR2_HUMAN]	4.53E-05	17.4246	3.1376	7.84E-06	9.0460	3.9199
1_9	O95831	Apoptosis-inducing factor 1, mitochondrial OS=Homo sapiens GN=AIFM1 PE=1 SV=1 - [AIFM1_HUMAN]	2.06E-03	-3.8253	-3.0900	9.63E-07	-13.2685	-3.9584
1_9	P05089	Arginase-1 OS=Homo sapiens GN=ARG1 PE=1 SV=2 - [ARGI1_HUMAN]	8.40E-06	-25.2963	-3.1406	1.53E-06	-11.0155	-4.9801
1_9	P22760	Arylacetamide deacetylase OS=Homo sapiens GN=AADAC PE=1 SV=5 - [AAAD_HUMAN]	1.81E-05	-23.4316	-3.0027	5.28E-05	-14.3418	-3.4125
1_9	Q9BXN1	Asporin OS=Homo sapiens GN=ASPN PE=1 SV=2 - [ASPN_HUMAN]	5.36E-05	15.2567	3.0403	8.59E-04	4.5521	2.9255
1_9	Q08211	ATP-dependent RNA helicase A OS=Homo sapiens GN=DHX9 PE=1 SV=4 - [DHX9_HUMAN]	3.33E-03	3.6075	2.8907	9.62E-06	8.7161	3.7477
1_9	O00571	ATP-dependent RNA helicase DDX3X OS=Homo sapiens GN=DDX3X PE=1 SV=3 - [DDX3X_HUMAN]	1.57E-03	4.1136	2.8669	3.19E-05	7.5464	2.4677
1_9	P13929	Beta-enolase OS=Homo sapiens GN=ENO3 PE=1 SV=5 - [ENOB_HUMAN]	3.36E-04	-5.8220	-3.0904	2.37E-03	-3.7418	-3.7619
1_9	Q93088	Betaine--homocysteine S-methyltransferase 1 OS=Homo sapiens GN=BHMT PE=1 SV=2 - [BHMT1_HUMAN]	5.90E-05	-8.4811	-3.1673	6.58E-05	-6.9257	-4.8682
1_9	Q9UBR1	Beta-ureidopropionase OS=Homo sapiens GN=UPB1 PE=1 SV=1 - [BUP1_HUMAN]	2.36E-05	-21.6121	-3.1074	1.45E-04	-6.0471	-3.6561
1_9	P34913	Bifunctional epoxide hydrolase 2 OS=Homo sapiens GN=EPHX2 PE=1 SV=2 - [HYES_HUMAN]	1.28E-05	-24.3491	-3.0627	9.09E-05	-6.5741	-3.7851
1_9	P31939	Bifunctional purine biosynthesis protein PURH OS=Homo sapiens GN=ATIC PE=1 SV=3 - [PUR9_HUMAN]	1.61E-03	4.0812	2.9075	5.74E-03	3.1712	2.2593
1_9	P21810	Biglycan OS=Homo sapiens GN=BGN PE=1 SV=2 - [PGS1_HUMAN]	1.37E-03	4.3878	3.1510	1.73E-06	10.4956	5.5185
1_9	Q14032	Bile acid-CoA:amino acid N-acyltransferase OS=Homo sapiens GN=BAAT PE=1 SV=1 - [BAAT_HUMAN]	2.35E-05	-21.6713	-3.0672	7.11E-04	-4.7041	-2.6382

Fig. 7 continued

1_9	Q9Y2P5	Bile acyl-CoA synthetase OS=Homo sapiens GN=SLC27A5 PE=1 SV=1 - [S27A5_HUMAN]	2.44E-05	-21.4856	-3.0863	1.54E-05	-8.3404	-4.4024
1_9	Q06520	Bile salt sulfotransferase OS=Homo sapiens GN=SULT2A1 PE=1 SV=3 - [ST2A1_HUMAN]	1.82E-05	-23.3737	-3.1402	1.35E-05	-11.8596	-4.0738
1_9	Q96CX2	BTB/POZ domain-containing protein KCTD12 OS=Homo sapiens GN=KCTD12 PE=1 SV=1 - [KCD12_HUMAN]	5.05E-05	16.5401	2.9172	5.58E-05	7.0815	2.3377
1_9	P11586	C-1-tetrahydrofolate synthase, cytoplasmic OS=Homo sapiens GN=MTHFD1 PE=1 SV=3 - [C1TC_HUMAN]	7.64E-05	-6.7457	-3.1108	8.57E-05	-6.6421	-4.9364
1_9	P17655	Calpain-2 catalytic subunit OS=Homo sapiens GN=CAPN2 PE=1 SV=6 - [CAN2_HUMAN]	5.28E-05	15.7356	2.9337	2.94E-04	5.4397	3.1575
1_9	Q96DG6	Carboxymethylenebutenolidase homolog OS=Homo sapiens GN=CMBL PE=1 SV=1 - [CMBL_HUMAN]	3.13E-03	-3.6680	-3.0003	2.74E-03	-3.6443	-2.6745
1_9	P23786	Carnitine O-palmitoyltransferase 2, mitochondrial OS=Homo sapiens GN=CPT2 PE=1 SV=2 - [CPT2_HUMAN]	9.17E-05	-6.4753	-3.0257	6.65E-04	-4.7884	-3.1528
1_9	P35222	Catenin beta-1 OS=Homo sapiens GN=CTNNB1 PE=1 SV=1 - [CTNB1_HUMAN]	2.58E-02	2.3199	2.8628	5.32E-03	3.2212	2.3529
1_9	P02462	Collagen alpha-1(IV) chain OS=Homo sapiens GN=COL4A1 PE=1 SV=3 - [CO4A1_HUMAN]	7.94E-03	3.0867	2.6884	1.06E-02	2.8117	2.1352
1_9	Q05707	Collagen alpha-1(XIV) chain OS=Homo sapiens GN=COL14A1 PE=1 SV=3 - [CO5A1_HUMAN]	4.70E-05	17.1962	3.0033	1.85E-06	10.2995	4.4065
1_9	P26845	Corticosteroid 11-beta-dehydrogenase isozyme 1 OS=Homo sapiens GN=HSD11B1 PE=1 SV=3 - [DHI1_HUMAN]	2.36E-05	-21.5848	-2.9859	6.21E-03	-3.1190	-2.0008
1_9	P12277	Creatine kinase B-type OS=Homo sapiens GN=CKB PE=1 SV=1 - [KCRB_HUMAN]	5.38E-05	15.3291	2.9996	3.07E-03	3.5718	2.6691
1_9	P12532	Creatine kinase U-type, mitochondrial OS=Homo sapiens GN=CKMT1A PE=1 SV=1 - [KCRU_HUMAN]	5.05E-05	16.3138	3.0081	6.93E-04	4.7443	2.2888
1_9	Q86YP6	Cullin-associated NEDD8-dissociated protein 1 OS=Homo sapiens GN=CAND1 PE=1 SV=2 - [CAND1_HUMAN]	5.28E-04	5.6501	2.8567	7.81E-04	4.6297	2.2739
1_9	P35520	Cystathionine beta-synthase OS=Homo sapiens GN=CBS PE=1 SV=2 - [CBS_HUMAN]	5.13E-06	-31.2554	-2.9866	1.30E-03	-4.1863	-2.0840
1_9	P32929	Cystathionine gamma-lyase OS=Homo sapiens GN=CTH PE=1 SV=3 - [CGL_HUMAN]	4.41E-04	-5.7178	-2.9700	4.24E-03	-3.3636	-2.5186
1_9	P21291	Cysteine and glycine-rich protein 1 OS=Homo sapiens GN=CSRP1 PE=1 SV=3 - [CSRP1_HUMAN]	1.84E-02	2.5693	2.9083	3.24E-03	3.5351	2.3377
1_9	P05177	Cytochrome P450 1A2 OS=Homo sapiens GN=CYP1A2 PE=1 SV=3 - [CP1A2_HUMAN]	1.42E-06	-24.1947	-3.0205	5.41E-04	-4.9713	-3.2232
1_9	P11509	Cytochrome P450 2A6 OS=Homo sapiens GN=CYP2A6 PE=1 SV=3 - [CP2A6_HUMAN]	3.01E-05	-20.6985	-3.0746	4.06E-04	-5.2001	-4.6052
1_9	P10632	Cytochrome P450 2C8 OS=Homo sapiens GN=CYP2C8 PE=1 SV=2 - [CP2C8_HUMAN]	1.48E-05	-24.1394	-3.0569	1.55E-06	-10.9282	-3.9088
1_9	P11712	Cytochrome P450 2C9 OS=Homo sapiens GN=CYP2C9 PE=1 SV=3 - [CP2C9_HUMAN]	1.73E-05	-23.7830	-3.0856	2.37E-05	-7.9942	-4.2291
1_9	P10635	Cytochrome P450 2D6 OS=Homo sapiens GN=CYP2D6 PE=1 SV=2 - [CP2D6_HUMAN]	3.09E-04	-5.8528	-2.9541	1.50E-02	-2.6392	-2.4158
1_9	P05181	Cytochrome P450 2E1 OS=Homo sapiens GN=CYP2E1 PE=1 SV=1 - [CP2E1_HUMAN]	6.36E-06	-27.9570	-3.0416	4.34E-06	-9.6735	-3.3879
1_9	P08684	Cytochrome P450 3A4 OS=Homo sapiens GN=CYP3A4 PE=1 SV=4 - [CP3A4_HUMAN]	4.25E-06	-33.4351	-3.1061	1.07E-05	-8.6528	-3.8971
1_9	Q02928	Cytochrome P450 4A11 OS=Homo sapiens GN=CYP4A11 PE=1 SV=1 - [CP4AB_HUMAN]	6.20E-06	-29.1359	-3.0294	2.16E-03	-3.8049	-3.0008
1_9	Q14204	Cytoplasmic dynein 1 heavy chain 1 OS=Homo sapiens GN=DYNC1H1 PE=1 SV=5 - [DYHC1_HUMAN]	1.16E-03	4.6396	2.7291	3.91E-03	3.4058	3.2759
1_9	O75891	Cytosolic 10-formyltetrahydrofolate dehydrogenase OS=Homo sapiens GN=ALDH1L1 PE=1 SV=2 - [AL1L1_HUMAN]	4.15E-05	-18.1426	-3.0944	5.19E-04	-5.0175	-5.1429
1_9	Q02338	D-beta-hydroxybutyrate dehydrogenase, mitochondrial OS=Homo sapiens GN=BDH1 PE=1 SV=3 - [BDH_HUMAN]	1.15E-05	-24.6173	-3.1312	2.92E-05	-7.7814	-4.1884
1_9	P07585	Decorin OS=Homo sapiens GN=DCN PE=1 SV=1 - [PGS2_HUMAN]	4.04E-05	18.5712	3.0320	2.22E-04	5.6256	3.5142
1_9	Q96LJ7	Dehydrogenase/reductase SDR family member 1 OS=Homo sapiens GN=DHRS1 PE=1 SV=1 - [DHRS1_HUMAN]	3.23E-05	-19.8630	-2.9590	1.14E-02	-2.7748	-2.4681
1_9	P30038	Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial OS=Homo sapiens GN=ALDH4A1 PE=1 SV=3 - [AL4A1_HUMAN]	1.11E-05	-24.6848	-3.1271	1.84E-06	-10.3124	-4.6287
1_9	P13716	Delta-aminolevulinic acid dehydratase OS=Homo sapiens GN=ALAD PE=1 SV=1 - [HEM2_HUMAN]	1.73E-05	-23.7821	-3.0717	2.23E-04	-5.6233	-3.5645

Fig. 7 continued

1_9	Q07507	Dermatopontin OS=Homo sapiens GN=DPT PE=2 SV=2 - [DERM_HUMAN]	4.06E-05	18.4098	3.0288	6.55E-04	4.8022	2.8244
1_9	P09417	Dihydropteridine reductase OS=Homo sapiens GN=QDPR PE=1 SV=2 - [DHPR_HUMAN]	6.60E-06	-26.4491	-3.0537	4.04E-04	-5.2022	-3.5579
1_9	Q14117	Dihydropyrimidinase OS=Homo sapiens GN=DPYS PE=1 SV=1 - [DPYS_HUMAN]	2.36E-05	-21.6167	-3.0297	1.21E-04	-5.2560	-2.9183
1_9	Q16555	Dihydropyrimidinase-related protein 2 OS=Homo sapiens GN=DPYSL2 PE=1 SV=1 - [DPYL2_HUMAN]	9.76E-03	2.9805	2.9514	1.47E-04	6.0106	3.5974
1_9	P31513	Dimethylaniline monooxygenase [N-oxide-forming] 3 OS=Homo sapiens GN=FMO3 PE=1 SV=5 - [FMO3_HUMAN]	3.45E-05	-19.6725	-3.1060	5.60E-04	-4.9392	-4.2567
1_9	P49326	Dimethylaniline monooxygenase [N-oxide-forming] 5 OS=Homo sapiens GN=FMO5 PE=2 SV=2 - [FMO5_HUMAN]	3.96E-05	-18.6809	-2.9711	2.61E-03	-3.6790	-3.4376
1_9	Q9UI17	Dimethylglycine dehydrogenase, mitochondrial OS=Homo sapiens GN=DMGDH PE=1 SV=2 - [DMGD_HUMAN]	1.82E-05	-23.1845	-3.0665	7.76E-06	-9.2639	-4.0343
1_9	P78527	DNA-dependent protein kinase catalytic subunit OS=Homo sapiens GN=PRKDC PE=1 SV=3 - [PRKDC_HUMAN]	2.97E-03	3.7055	2.9078	1.04E-03	4.3686	3.5856
1_9	O75356	Ectonucleoside triphosphate diphosphohydrolase 5 OS=Homo sapiens GN=ENTPD5 PE=1 SV=1 - [ENTP5_HUMAN]	6.39E-06	-27.7478	-2.9465	1.10E-03	-4.3124	-2.6382
1_9	Q16134	Electron transfer flavoprotein-ubiquinone oxidoreductase, mitochondrial OS=Homo sapiens GN=ETFDH PE=1 SV=2 - [ETFD_HUMAN]	2.91E-05	-20.9402	-3.0460	7.80E-05	-6.7647	-2.8644
1_9	O75521	Enoyl-CoA delta isomerase 2, mitochondrial OS=Homo sapiens GN=ECI2 PE=1 SV=4 - [ECI2_HUMAN]	1.11E-05	-24.7010	-3.0291	3.66E-04	-5.2911	-3.1495
1_9	Q86Y87	Enoyl-CoA hydratase domain-containing protein 2, mitochondrial OS=Homo sapiens GN=ECHDC2 PE=2 SV=2 - [ECHD2_HUMAN]	1.81E-05	-23.4294	-3.0081	4.82E-04	-5.0804	-2.7619
1_9	P08294	Extracellular superoxide dismutase [Cu-Zn] OS=Homo sapiens GN=SOD3 PE=1 SV=2 - [SOD3_HUMAN]	1.06E-03	4.7506	2.7472	2.34E-03	3.7493	2.2501
1_9	P15311	Ezrin OS=Homo sapiens GN=EZR PE=1 SV=4 - [EZRI_HUMAN]	5.40E-05	15.1736	3.0292	3.96E-06	9.7189	3.9079
1_9	Q96AE4	Far upstream element-binding protein 1 OS=Homo sapiens GN=FUBP1 PE=1 SV=3 - [FUBP1_HUMAN]	7.76E-03	3.0944	2.7377	6.71E-03	3.0742	2.1681
1_9	O95954	Formimidoyltransferase-cyclodeaminase OS=Homo sapiens GN=FTCD PE=1 SV=2 - [FTCD_HUMAN]	2.43E-05	-21.5029	-3.1264	7.87E-06	-8.9810	-5.2716
1_9	P51570	Galactokinase OS=Homo sapiens GN=GALK1 PE=1 SV=1 - [GALK1_HUMAN]	4.60E-04	-5.7040	-3.0024	4.15E-03	-3.3770	-2.4493
1_9	P17931	Galectin-3 OS=Homo sapiens GN=LGALS3 PE=1 SV=5 - [LEG3_HUMAN]	3.21E-05	19.9165	3.0360	2.32E-03	3.7546	2.9642
1_9	P56470	Galectin-4 OS=Homo sapiens GN=LGALS4 PE=1 SV=1 - [LEG4_HUMAN]	1.88E-02	2.5519	3.1450	4.81E-04	5.0837	4.7460
1_9	O95479	GDH/6PGL endoplasmic bifunctional protein OS=Homo sapiens GN=H6PD PE=1 SV=2 - [G6PE_HUMAN]	1.00E-02	-2.9537	-2.9933	3.03E-03	-3.5802	-2.9964
1_9	P11413	Glucose-6-phosphate 1-dehydrogenase OS=Homo sapiens GN=G6PD PE=1 SV=4 - [G6PD_HUMAN]	5.30E-05	15.3179	2.9598	2.26E-03	3.7702	3.5061
1_9	Q06210	Glutamine--fructose-6-phosphate aminotransferase [isomerizing] 1 OS=Homo sapiens GN=GFPT1 PE=1 SV=3 - [GFPT1_HUMAN]	4.11E-05	18.2475	2.8408	1.03E-02	2.8248	2.7338
1_9	P18283	Glutathione peroxidase 2 OS=Homo sapiens GN=GPX2 PE=1 SV=3 - [GPX2_HUMAN]	5.38E-05	15.3382	2.9965	7.04E-04	4.7174	2.6529
1_9	P09211	Glutathione S-transferase P OS=Homo sapiens GN=GSTP1 PE=1 SV=2 - [GSTP1_HUMAN]	1.02E-03	4.7781	3.1756	1.37E-06	11.7661	5.5137
1_9	P21695	Glycerol-3-phosphate dehydrogenase [NAD(+)], cytoplasmic OS=Homo sapiens GN=GPD1 PE=1 SV=4 - [GPDA_HUMAN]	2.96E-05	-20.7765	-2.9811	9.95E-05	-6.4160	-3.1620
1_9	P23378	Glycine dehydrogenase (decarboxylating), mitochondrial OS=Homo sapiens GN=GLDC PE=1 SV=2 - [GCSP_HUMAN]	2.14E-05	-22.2182	-3.0836	4.60E-03	-3.3110	-4.1123
1_9	Q6IB77	Glycine N-acyltransferase OS=Homo sapiens GN=GLYAT PE=1 SV=3 - [GLYAT_HUMAN]	6.82E-06	-25.8978	-3.1178	1.47E-02	-17.1499	-4.1035
1_9	Q14749	Glycine N-methyltransferase OS=Homo sapiens GN=GNMT PE=1 SV=3 - [GNMT_HUMAN]	6.59E-06	-26.4860	-2.9966	3.34E-03	-3.5107	-2.8276
1_9	P35573	Glycogen debranching enzyme OS=Homo sapiens GN=AGL PE=1 SV=3 - [GDE_HUMAN]	3.22E-05	-19.8828	-3.0393	3.02E-04	-5.4231	-4.4446
1_9	P11216	Glycogen phosphorylase, brain form OS=Homo sapiens GN=PYGB PE=1 SV=5 - [PYGB_HUMAN]	8.29E-04	4.9429	2.9366	4.43E-05	7.3236	3.5675
1_9	P06737	Glycogen phosphorylase, liver form OS=Homo sapiens GN=PYGL PE=1 SV=4 - [PYGL_HUMAN]	2.46E-05	-21.4062	-3.0756	6.90E-06	-9.4541	-4.6954
1_9	P62879	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2 OS=Homo sapiens GN=GNB2 PE=1 SV=3 - [GBB2_HUMAN]	2.28E-04	5.9723	2.9336	8.20E-03	2.9627	2.3418

Fig. 7 continued

1_9	Q13151	Heterogeneous nuclear ribonucleoprotein A0 OS=Homo sapiens GN=HNRNPA0 PE=1 SV=1 - [ROA0_HUMAN]	5.05E-05	16.5947	2.9579	1.07E-06	12.9407	2.3251
1_9	O43390	Heterogeneous nuclear ribonucleoprotein R OS=Homo sapiens GN=HNRNPR PE=1 SV=1 - [HNRPR_HUMAN]	6.90E-03	3.1922	2.9865	8.18E-05	6.7315	3.1737
1_9	Q1KMD3	Heterogeneous nuclear ribonucleoprotein U-like protein 2 OS=Homo sapiens GN=HNRNPUL2 PE=1 SV=1 - [HNRL2_HUMAN]	8.99E-05	6.5210	3.0612	8.22E-05	6.7239	2.9008
1_9	Q9UJM8	Hydroxyacid oxidase 1 OS=Homo sapiens GN=HAO1 PE=1 SV=1 - [HAOX1_HUMAN]	1.22E-05	-24.4661	-3.1053	5.37E-04	-4.9782	-4.4990
1_9	Q16775	Hydroxyacylglutathione hydrolase, mitochondrial OS=Homo sapiens GN=HAGH PE=1 SV=2 - [GLO2_HUMAN]	1.50E-05	-24.0835	-2.9897	6.00E-05	-7.0319	-2.4493
1_9	P35914	Hydroxymethylglutaryl-CoA lyase, mitochondrial OS=Homo sapiens GN=HMGCL PE=1 SV=2 - [HMGCL_HUMAN]	6.13E-05	-7.7000	-3.0761	5.68E-04	-4.9301	-2.9431
1_9	P54868	Hydroxymethylglutaryl-CoA synthase, mitochondrial OS=Homo sapiens GN=HMGCS2 PE=1 SV=1 - [HMCS2_HUMAN]	7.84E-04	-5.0083	-3.2672	1.45E-04	-6.0436	-6.0495
1_9	P01860	Ig gamma-3 chain C region OS=Homo sapiens GN=IGHG3 PE=1 SV=2 - [IGHG3_HUMAN]	9.89E-03	2.9693	3.0748	1.81E-03	3.9379	4.4383
1_9	Q14974	Importin subunit beta-1 OS=Homo sapiens GN=KPNB1 PE=1 SV=2 - [IMB1_HUMAN]	1.79E-03	3.9172	2.8565	8.16E-03	2.9659	2.2373
1_9	Q12906	Interleukin enhancer-binding factor 3 OS=Homo sapiens GN=ILF3 PE=1 SV=3 - [ILF3_HUMAN]	9.89E-03	2.9693	2.9318	3.05E-03	3.5746	3.0713
1_9	Q96AB3	Isochorismatase domain-containing protein 2, mitochondrial OS=Homo sapiens GN=ISOC2 PE=1 SV=1 - [ISOC2_HUMAN]	9.76E-04	-4.8154	-3.0074	1.50E-03	-4.0756	-2.4661
1_9	P08727	Keratin, type I cytoskeletal 19 OS=Homo sapiens GN=KRT19 PE=1 SV=4 - [K1C19_HUMAN]	5.05E-05	16.3086	3.0791	1.72E-06	10.5084	5.2600
1_9	P08729	Keratin, type II cytoskeletal 7 OS=Homo sapiens GN=KRT7 PE=1 SV=5 - [K2C7_HUMAN]	4.20E-05	17.9159	2.9851	3.91E-06	9.7253	3.7312
1_9	Q9Y2S2	Lambda-crystallin homolog OS=Homo sapiens GN=CRYL1 PE=1 SV=3 - [CRYL1_HUMAN]	9.99E-06	-24.9065	-3.0232	2.83E-04	-5.4584	-2.8309
1_9	P09960	Leukotriene A-4 hydrolase OS=Homo sapiens GN=LTA4H PE=1 SV=2 - [LKHA4_HUMAN]	6.19E-03	3.1842	2.8673	1.01E-04	6.4010	2.5986
1_9	P07195	L-lactate dehydrogenase B chain OS=Homo sapiens GN=LDHB PE=1 SV=2 - [LDHB_HUMAN]	1.84E-02	2.5663	3.0791	8.64E-05	6.6312	3.4949
1_9	P33121	Long-chain-fatty-acid--CoA ligase 1 OS=Homo sapiens GN=ACSL1 PE=1 SV=1 - [ACSL1_HUMAN]	4.03E-05	-18.5806	-3.1446	4.46E-04	-5.1283	-4.5280
1_9	Q9ULC5	Long-chain-fatty-acid--CoA ligase 5 OS=Homo sapiens GN=ACSL5 PE=1 SV=1 - [ACSL5_HUMAN]	3.87E-05	-18.8499	-3.0648	2.49E-03	-3.7113	-2.7091
1_9	P05455	Lupus La protein OS=Homo sapiens GN=SSB PE=1 SV=2 - [LA_HUMAN]	6.66E-04	5.5402	2.9832	7.09E-05	6.8416	2.6028
1_9	P10253	Lysosomal alpha-glucosidase OS=Homo sapiens GN=GAA PE=1 SV=4 - [LYAG_HUMAN]	3.19E-02	-2.2167	-2.9513	2.78E-02	-2.2854	-2.3749
1_9	P40121	Macrophage-capping protein OS=Homo sapiens GN=CAPG PE=1 SV=2 - [CAPG_HUMAN]	5.05E-05	16.4692	2.9948	1.74E-05	8.1952	2.8842
1_9	Q14764	Major vault protein OS=Homo sapiens GN=MVP PE=1 SV=4 - [MVP_HUMAN]	5.38E-05	15.2562	2.9291	2.79E-04	5.4686	3.0605
1_9	O43708	Maleylacetoacetate isomerase OS=Homo sapiens GN=GSTZ1 PE=1 SV=3 - [MAAI_HUMAN]	2.16E-03	-3.8104	-2.9999	1.67E-02	-2.5800	-2.0086
1_9	P43243	Matrin-3 OS=Homo sapiens GN=MATR3 PE=1 SV=2 - [MATR3_HUMAN]	9.89E-03	2.9692	2.9280	6.43E-05	6.9591	2.8708
1_9	Q9H8R3	Methyltransferase-like protein 7A OS=Homo sapiens GN=METTL7A PE=1 SV=1 - [METTA_HUMAN]	3.38E-05	-19.7644	-3.1078	5.38E-04	-4.9765	-2.4125
1_9	P55083	Microfibril-associated glycoprotein 4 OS=Homo sapiens GN=MFAP4 PE=1 SV=2 - [MFAP4_HUMAN]	4.04E-05	18.5724	2.9582	2.39E-04	5.5674	3.3874
1_9	P10620	Microsomal glutathione S-transferase 1 OS=Homo sapiens GN=MGST1 PE=1 SV=1 - [MGST1_HUMAN]	8.16E-04	-4.9545	-3.1164	2.57E-03	-3.6892	-2.4125
1_9	P28774	Mimecan OS=Homo sapiens GN=OGN PE=1 SV=1 - [MIME_HUMAN]	3.11E-05	20.5281	3.0821	9.84E-05	6.4233	4.4171
1_9	O43772	Mitochondrial carnitine/acylcarnitine carrier protein OS=Homo sapiens GN=SLC25A20 PE=1 SV=1 - [MCAT_HUMAN]	6.52E-06	-26.7650	-2.9591	1.60E-03	-4.0361	-2.4681
1_9	Q9HC84	Mucin-5B OS=Homo sapiens GN=MUC5B PE=1 SV=3 - [MUC5B_HUMAN]	4.22E-05	17.8357	2.9423	1.26E-03	4.2058	3.8016
1_9	Q7Z406	Myosin-14 OS=Homo sapiens GN=MYH14 PE=1 SV=2 - [MYH14_HUMAN]	1.15E-03	4.6815	2.9542	1.85E-03	3.9225	3.3017
1_9	Q4G0N4	NAD kinase domain-containing protein 1 OS=Homo sapiens GN=NADKD1 PE=1 SV=2 - [NAKD1_HUMAN]	6.70E-06	-26.1600	-3.0937	1.54E-04	-5.9437	-3.8160

Fig. 7 continued

1_9	P15559	NAD(P)H dehydrogenase [quinone] 1 OS=Homo sapiens GN=NQO1 PE=1 SV=1 - [NQO1_HUMAN]	5.50E-05	14.9712	3.0085	4.65E-03	3.3057	2.8346
1_9	P16435	NADPH--cytochrome P450 reductase OS=Homo sapiens GN=POR PE=1 SV=2 - [NCPR_HUMAN]	6.15E-05	-7.4966	-3.0231	6.94E-06	-9.4504	-3.3749
1_9	Q09666	Neuroblast differentiation-associated protein AHNAK OS=Homo sapiens GN=AHNAK PE=1 SV=2 - [AHNK_HUMAN]	3.39E-03	3.5711	2.8447	3.65E-03	3.4594	2.8074
1_9	Q967A1	Niban-like protein 1 OS=Homo sapiens GN=FAM129B PE=1 SV=3 - [NIBL1_HUMAN]	1.21E-03	4.6003	2.7488	8.24E-03	2.9595	2.1683
1_9	Q15274	Nicotinate-nucleotide pyrophosphorylase [carboxylating] OS=Homo sapiens GN=QPRT PE=1 SV=3 - [NADC_HUMAN]	2.05E-05	-22.5176	-2.9935	3.39E-03	-3.5013	-2.4990
1_9	Q9NQR4	Omega-amidase NIT2 OS=Homo sapiens GN=NIT2 PE=1 SV=1 - [NIT2_HUMAN]	7.14E-04	-5.4233	-3.0391	1.96E-03	-3.8849	-2.9140
1_9	Q9NUI1	Peroxisomal 2,4-dienoyl-CoA reductase OS=Homo sapiens GN=DECR2 PE=1 SV=1 - [DECR2_HUMAN]	3.30E-04	-5.8291	-2.9838	2.73E-03	-3.6454	-2.5645
1_9	Q15067	Peroxisomal acyl-coenzyme A oxidase 1 OS=Homo sapiens GN=ACOX1 PE=1 SV=3 - [ACOX1_HUMAN]	6.99E-06	-25.6091	-3.0451	9.76E-04	-4.4148	-3.7712
1_9	Q99424	Peroxisomal acyl-coenzyme A oxidase 2 OS=Homo sapiens GN=ACOX2 PE=1 SV=1 - [ACOX2_HUMAN]	1.79E-05	-23.6363	-3.0730	1.83E-04	-5.8231	-4.0961
1_9	Q08426	Peroxisomal bifunctional enzyme OS=Homo sapiens GN=EHHADH PE=1 SV=3 - [ECHP_HUMAN]	1.84E-05	-22.9393	-3.1724	4.93E-06	-9.6324	-5.7091
1_9	Q9P0Z9	Peroxisomal sarcosine oxidase OS=Homo sapiens GN=PIPOX PE=2 SV=2 - [SOX_HUMAN]	1.23E-05	-24.4395	-3.0673	3.82E-05	-7.3762	-3.6145
1_9	Q9BY49	Peroxisomal trans-2-enoyl-CoA reductase OS=Homo sapiens GN=PECR PE=1 SV=2 - [PECR_HUMAN]	6.49E-06	-26.8861	-3.0006	5.71E-03	-3.1755	-2.0500
1_9	P30039	Phenazine biosynthesis-like domain-containing protein OS=Homo sapiens GN=PBLD PE=1 SV=2 - [PBLD_HUMAN]	1.86E-05	-22.8342	-3.0315	5.93E-04	-4.8794	-3.1863
1_9	P00439	Phenylalanine-4-hydroxylase OS=Homo sapiens GN=PAH PE=1 SV=1 - [PH4H_HUMAN]	7.78E-04	-5.0448	-3.0126	2.21E-03	-3.7859	-2.7619
1_9	Q9Y617	Phosphoserine aminotransferase OS=Homo sapiens GN=PSAT1 PE=1 SV=2 - [SERC_HUMAN]	2.93E-05	-20.8837	-3.0023	2.60E-03	-3.6830	-2.3735
1_9	Q14651	Plastin-1 OS=Homo sapiens GN=PLS1 PE=1 SV=2 - [PLS1_HUMAN]	5.33E-05	15.3306	2.9693	3.41E-03	3.4981	2.7130
1_9	Q15149	Plectin OS=Homo sapiens GN=PLEC PE=1 SV=3 - [PLEC_HUMAN]	2.76E-04	5.8955	2.9496	1.45E-04	6.0325	3.9620
1_9	Q9NZI2	Polymerase I and transcript release factor OS=Homo sapiens GN=PTRF PE=1 SV=1 - [PTRF_HUMAN]	1.16E-03	4.6743	2.8027	5.02E-03	3.2622	2.3674
1_9	P01833	Polymeric immunoglobulin receptor OS=Homo sapiens GN=PIGR PE=1 SV=4 - [PIGR_HUMAN]	3.00E-05	20.7088	2.8741	2.76E-03	3.6563	2.4873
1_9	P17844	Probable ATP-dependent RNA helicase DDX5 OS=Homo sapiens GN=DDX5 PE=1 SV=1 - [DDX5_HUMAN]	1.01E-03	4.7870	2.9867	6.08E-03	3.1311	3.2097
1_9	P51888	Prolargin OS=Homo sapiens GN=PRELP PE=1 SV=1 - [PRELP_HUMAN]	1.03E-02	2.9234	3.1249	1.24E-04	6.2414	5.0590
1_9	P05165	Propionyl-CoA carboxylase alpha chain, mitochondrial OS=Homo sapiens GN=PCCA PE=1 SV=4 - [PCCA_HUMAN]	1.66E-05	-23.8690	-2.9900	3.22E-03	-3.5393	-2.6745
1_9	P05166	Propionyl-CoA carboxylase beta chain, mitochondrial OS=Homo sapiens GN=PCCB PE=1 SV=3 - [PCCB_HUMAN]	1.62E-03	-4.0712	-3.0162	3.79E-03	-3.4280	-2.9964
1_9	Q9BPW8	Protein NipSnap homolog 1 OS=Homo sapiens GN=NIPSNAP1 PE=1 SV=1 - [NIPS1_HUMAN]	6.34E-06	-28.1693	-3.0532	3.00E-05	-7.7559	-3.1967
1_9	Q01105	Protein SET OS=Homo sapiens GN=SET PE=1 SV=3 - [SET_HUMAN]	1.63E-03	4.0638	2.9943	2.19E-04	5.6430	2.4629
1_9	P55786	Puromycin-sensitive aminopeptidase OS=Homo sapiens GN=NPEPPS PE=1 SV=2 - [PSA_HUMAN]	8.03E-03	3.0809	2.9162	3.34E-05	7.4925	2.6078
1_9	A6ND91	Putative L-aspartate dehydrogenase OS=Homo sapiens GN=ASPDH PE=2 SV=2 - [ASPD_HUMAN]	3.11E-04	-5.8503	-2.9302	2.07E-02	-2.4630	-2.0086
1_9	O43143	Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15 OS=Homo sapiens GN=DHX15 PE=1 SV=2 - [DHX15_HUMAN]	4.48E-05	17.5414	2.8379	1.30E-04	6.1436	2.0605
1_9	Q9NVS9	Pyridoxine-5-phosphate oxidase OS=Homo sapiens GN=PNPO PE=1 SV=1 - [PNPO_HUMAN]	8.45E-05	-6.6201	-2.9789	1.11E-06	-12.4286	-2.1967
1_9	P11498	Pyruvate carboxylase, mitochondrial OS=Homo sapiens GN=PC PE=1 SV=2 - [PYC_HUMAN]	1.83E-05	-23.0605	-3.1278	9.46E-05	-6.4805	-5.0961
1_9	P14618	Pyruvate kinase isozymes M1/M2 OS=Homo sapiens GN=PKM PE=1 SV=4 - [KPYM_HUMAN]	1.69E-04	6.1385	3.0694	9.33E-05	6.5495	4.7997
1_9	P30613	Pyruvate kinase isozymes R/L OS=Homo sapiens GN=PKLR PE=1 SV=2 - [KPYR_HUMAN]	2.89E-05	-20.9736	-3.0488	1.68E-04	-5.8847	-4.1006

Fig. 7 continued

1_9	P31150	Rab GDP dissociation inhibitor alpha OS=Homo sapiens GN=GDI1 PE=1 SV=2 - [GDIA_HUMAN]	1.50E-03	4.2178	2.9283	1.88E-04	5.7617	3.2951
1_9	P46940	Ras GTPase-activating-like protein IQGAP1 OS=Homo sapiens GN=IQGAP1 PE=1 SV=1 - [IQGA1_HUMAN]	2.55E-03	3.7638	2.9168	1.81E-03	3.9373	4.6006
1_9	Q96HR9	Receptor expression-enhancing protein 6 OS=Homo sapiens GN=REEP6 PE=1 SV=1 - [REEP6_HUMAN]	7.17E-06	-25.3477	-3.0203	8.89E-04	-4.5217	-2.1528
1_9	Q15493	Regucalcin OS=Homo sapiens GN=RGN PE=1 SV=1 - [RGN_HUMAN]	5.37E-06	-30.8468	-2.9930	6.02E-03	-3.1364	-2.5936
1_9	O94788	Retinal dehydrogenase 2 OS=Homo sapiens GN=ALDH1A2 PE=1 SV=3 - [AL1A2_HUMAN]	1.07E-03	4.7414	2.8083	1.01E-02	2.8383	2.0931
1_9	O75452	Retinol dehydrogenase 16 OS=Homo sapiens GN=RDH16 PE=1 SV=2 - [RDH16_HUMAN]	2.91E-05	-20.9445	-3.1225	3.36E-04	-5.3418	-3.8444
1_9	P52758	Ribonuclease UK114 OS=Homo sapiens GN=HRSP12 PE=1 SV=1 - [UK114_HUMAN]	1.27E-03	-4.5276	-3.1335	6.32E-05	-6.9690	-2.8276
1_9	Q9UKN9	RNA-binding protein Raly OS=Homo sapiens GN=RALY PE=1 SV=1 - [RALY_HUMAN]	3.84E-05	18.9590	2.9546	5.00E-03	3.2648	2.0161
1_9	Q8NBX0	Saccharopine dehydrogenase-like oxidoreductase OS=Homo sapiens GN=SCCPDH PE=1 SV=1 - [SCPDL_HUMAN]	1.80E-05	-23.8505	-2.9965	1.24E-03	-4.2168	-2.6145
1_9	Q00266	S-adenosylmethionine synthase isoform type-1 OS=Homo sapiens GN=MAT1A PE=1 SV=2 - [METK1_HUMAN]	2.34E-05	-21.9037	-3.0877	7.71E-06	-9.3090	-3.5857
1_9	Q9UL12	Sarcosine dehydrogenase, mitochondrial OS=Homo sapiens GN=SARDH PE=1 SV=1 - [SARDH_HUMAN]	9.77E-06	-24.9611	-3.0485	1.80E-06	-10.3773	-4.1035
1_9	Q15019	Septin-2 OS=Homo sapiens GN=SEPT2 PE=1 SV=1 - [SEPT2_HUMAN]	4.50E-05	17.5184	2.9199	2.23E-04	5.6199	2.3040
1_9	Q16181	Septin-7 OS=Homo sapiens GN=SEPT7 PE=1 SV=2 - [SEPT7_HUMAN]	5.36E-06	15.4554	2.8447	2.16E-03	3.7990	2.1733
1_9	Q9UH03	Septin-9 OS=Homo sapiens GN=SEPT9 PE=1 SV=2 - [SEPT9_HUMAN]	5.07E-04	5.6699	2.8386	3.87E-05	7.3668	2.3974
1_9	P34896	Serine hydroxymethyltransferase, cytosolic OS=Homo sapiens GN=SHMT1 PE=1 SV=1 - [GLYC_HUMAN]	1.65E-03	-4.0421	-3.1135	1.69E-05	-8.2560	-4.3879
1_9	Q07955	Serine/arginine-rich splicing factor 1 OS=Homo sapiens GN=SRSF1 PE=1 SV=2 - [SRSF1_HUMAN]	1.11E-03	4.7163	2.7176	3.40E-02	2.1591	2.0240
1_9	P30153	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform OS=Homo sapiens GN=PPP2R1A PE=1 SV=4 - [2AAA_HUMAN]	4.30E-02	2.1207	2.7937	4.09E-02	2.0777	2.0853
1_9	P62140	Serine/threonine-protein phosphatase PP1-beta catalytic subunit OS=Homo sapiens GN=PPP1CB PE=1 SV=3 - [PP1B_HUMAN]	2.11E-04	6.0126	2.9134	1.22E-02	2.7430	2.2593
1_9	P21549	Serine--pyruvate aminotransferase OS=Homo sapiens GN=AGXT PE=1 SV=1 - [SPYA_HUMAN]	6.67E-06	-26.2334	-3.2392	7.99E-06	-8.9156	-6.0039
1_9	P35237	Serpin B6 OS=Homo sapiens GN=SERPINB6 PE=1 SV=3 - [SPB6_HUMAN]	5.05E-05	16.5873	2.9194	2.36E-04	5.5758	2.2888
1_9	P50454	Serpin H1 OS=Homo sapiens GN=SERPINH1 PE=1 SV=2 - [SERPH_HUMAN]	3.67E-03	3.4946	2.9479	8.44E-05	6.6617	2.8674
1_9	P27169	Serum paraoxonase/arylesterase 1 OS=Homo sapiens GN=PON1 PE=1 SV=3 - [PON1_HUMAN]	6.94E-06	-25.6833	-3.0375	5.26E-03	-3.2296	-2.0086
1_9	P45954	Short/branched chain specific acyl-CoA dehydrogenase, mitochondrial OS=Homo sapiens GN=ACADSB PE=1 SV=1 - [ACDSB_HUMAN]	5.90E-05	-8.3340	-3.1545	2.11E-04	-5.6698	-4.3301
1_9	Q9NR45	Sialic acid synthase OS=Homo sapiens GN=NANS PE=1 SV=2 - [SIAS_HUMAN]	9.35E-03	3.0189	2.9690	2.32E-06	10.0677	2.3935
1_9	Q9H9B4	Sideroflexin-1 OS=Homo sapiens GN=SFXN1 PE=1 SV=4 - [SFXN1_HUMAN]	1.06E-05	-24.7870	-3.0416	1.22E-03	-4.2324	-3.0008
1_9	P05023	Sodium/potassium-transporting ATPase subunit beta-1 OS=Homo sapiens GN=ATP1B1 PE=1 SV=1 - [AT1B1_HUMAN]	1.18E-03	4.6421	2.8045	1.22E-03	4.2274	2.8074
1_9	Q14247	Src substrate cortactin OS=Homo sapiens GN=CTTN PE=1 SV=2 - [SRC8_HUMAN]	3.94E-05	18.7484	2.8312	1.64E-03	4.0115	2.1006
1_9	P21912	Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial OS=Homo sapiens GN=SDHB PE=1 SV=3 - [DHSB_HUMAN]	8.80E-06	-25.1113	-2.9806	2.40E-05	-7.9800	-2.4158
1_9	P51649	Succinate-semialdehyde dehydrogenase, mitochondrial OS=Homo sapiens GN=ALDH5A1 PE=1 SV=2 - [SSDH_HUMAN]	6.17E-05	-7.3717	-3.0464	4.10E-04	-5.1938	-3.5313
1_9	P50225	Sulfotransferase 1A1 OS=Homo sapiens GN=SULT1A1 PE=1 SV=3 - [ST1A1_HUMAN]	6.86E-05	-7.1556	-3.1065	1.33E-04	-6.1662	-3.0840
1_9	Q13263	Transcription intermediary factor 1-beta OS=Homo sapiens GN=TRIM28 PE=1 SV=5 - [TIF1B_HUMAN]	4.76E-05	17.0870	2.8980	1.23E-05	8.5508	2.6278
1_9	Q01995	Transgelin OS=Homo sapiens GN=TAGLN PE=1 SV=4 - [TAGL_HUMAN]	3.27E-04	5.8325	3.0173	1.83E-06	10.3287	3.8235

Fig. 7 continued

1_9	P53007	Tricarboxylate transport protein, mitochondrial OS=Homo sapiens GN=SLC25A1 PE=1 SV=2 - [TXTP_HUMAN]	9.69E-04	-4.8230	-3.0340	1.36E-03	-4.1490	-2.6745
1_9	P67936	Tropomyosin alpha-4 chain OS=Homo sapiens GN=TPM4 PE=1 SV=3 - [TPM4_HUMAN]	2.31E-04	5.9676	2.9885	1.69E-05	8.2687	2.9730
1_9	Q15561	Tryptase alpha/beta-1 OS=Homo sapiens GN=TPSAB1 PE=1 SV=1 - [TRYB1_HUMAN]	5.62E-05	14.7977	2.9718	8.51E-04	4.5605	3.5929
1_9	P68366	Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A PE=1 SV=1 - [TBA4A_HUMAN]	1.70E-02	2.6583	3.1784	1.81E-03	3.9385	5.3380
1_9	P22310	UDP-glucuronosyltransferase 1-4 OS=Homo sapiens GN=UGT1A4 PE=1 SV=1 - [UD14_HUMAN]	4.32E-04	-5.7253	-3.0442	1.52E-03	-4.0686	-2.9518
1_9	P06133	UDP-glucuronosyltransferase 2B4 OS=Homo sapiens GN=UGT2B4 PE=1 SV=2 - [UD2B4_HUMAN]	5.94E-04	-5.5958	-3.0069	1.10E-02	-2.7944	-3.2803
1_9	P16662	UDP-glucuronosyltransferase 2B7 OS=Homo sapiens GN=UGT2B7 PE=1 SV=1 - [UD2B7_HUMAN]	1.06E-04	-6.3582	-3.1155	7.56E-04	-4.6595	-3.5857
1_9	O00159	Unconventional myosin-Ic OS=Homo sapiens GN=MYO1C PE=1 SV=4 - [MYO1C_HUMAN]	8.19E-03	3.0758	2.8796	2.18E-03	3.7942	2.2377
1_9	Q96QK1	Vacuolar protein sorting-associated protein 35 OS=Homo sapiens GN=VPS35 PE=1 SV=2 - [VPS35_HUMAN]	4.19E-04	5.7373	2.8249	3.99E-05	7.3529	2.5543
1_9	P09327	Villin-1 OS=Homo sapiens GN=VIL1 PE=1 SV=4 - [VILI_HUMAN]	5.05E-05	16.4186	2.8983	1.82E-04	5.8302	2.8579
2_3	Q9UBR1	Beta-ureidopropionase OS=Homo sapiens GN=UPB1 PE=1 SV=1 - [BUP1_HUMAN]	5.23E-03	-3.2913	-2.7768	3.22E-03	-3.2520	-2.3236
2_3	P40121	Macrophage-capping protein OS=Homo sapiens GN=CAPG PE=1 SV=2 - [CAPG_HUMAN]	2.02E-02	2.4660	2.5852	9.35E-03	2.7362	2.1275
2_4	P31947	14-3-3 protein sigma OS=Homo sapiens GN=SFN PE=1 SV=1 - [1433S_HUMAN]	2.55E-04	5.6485	2.9768	4.21E-06	8.2333	3.6322
2_4	O14756	17-beta-hydroxysteroid dehydrogenase type 6 OS=Homo sapiens GN=HSD17B6 PE=1 SV=1 - [1H17B6_HUMAN]	7.84E-05	-6.2007	-2.8648	5.54E-06	-7.5923	-3.5460
2_4	P12694	2-oxoisovalerate dehydrogenase subunit alpha, mitochondrial OS=Homo sapiens GN=BCKDHA PE=1 SV=2 - [ODBA_HUMAN]	1.66E-03	-3.7847	-2.6657	2.10E-02	-2.2920	-2.1159
2_4	P31937	3-hydroxyisobutyrate dehydrogenase, mitochondrial OS=Homo sapiens GN=HIBADH PE=1 SV=2 - [3HIDH_HUMAN]	2.76E-03	-3.6142	-2.7853	3.79E-03	-3.1465	-3.3175
2_4	P80404	4-aminobutyrate aminotransferase, mitochondrial OS=Homo sapiens GN=ABAT PE=1 SV=3 - [GABT_HUMAN]	2.32E-05	-13.2667	-2.8460	5.49E-05	-5.6401	-4.6929
2_4	P32754	4-hydroxyphenylpyruvate dioxygenase OS=Homo sapiens GN=HPD PE=1 SV=2 - [HPPD_HUMAN]	2.46E-05	-12.6416	-2.8898	2.04E-04	-4.7439	-4.7268
2_4	Q9BWD1	Acetyl-CoA acetyltransferase, cytosolic OS=Homo sapiens GN=ACAT2 PE=1 SV=2 - [THIC_HUMAN]	1.84E-03	-3.7556	-2.7071	1.37E-03	-3.6605	-2.6394
2_4	Q08AH3	Acyl-coenzyme A synthetase ACSM2A, mitochondrial OS=Homo sapiens GN=ACSM2A PE=1 SV=2 - [ACS2A_HUMAN]	1.18E-05	-16.0532	-2.8285	1.86E-04	-4.8093	-4.3789
2_4	Q6ICK6	Acyl-coenzyme A synthetase ACSM2B, mitochondrial OS=Homo sapiens GN=ACSM2B PE=1 SV=2 - [ACS2B_HUMAN]	3.63E-05	-6.8222	-2.8285	5.24E-05	-5.6594	-4.4100
2_4	O95154	Aflatoxin B1 aldehyde reductase member 3 OS=Homo sapiens GN=AKR7A3 PE=1 SV=2 - [AKR73_HUMAN]	2.21E-03	-3.7123	-2.8542	1.73E-03	-3.5258	-3.4373
2_4	O00468	Agrin OS=Homo sapiens GN=AGRN PE=1 SV=4 - [AGRIN_HUMAN]	4.76E-02	2.0486	2.6120	4.26E-02	1.9754	2.5021
2_4	P24298	Alanine aminotransferase 1 OS=Homo sapiens GN=GPT PE=1 SV=3 - [ALAT1_HUMAN]	3.77E-04	-5.3706	-2.7134	4.57E-04	-4.2661	-3.5153
2_4	P07327	Alcohol dehydrogenase 1A OS=Homo sapiens GN=ADH1A PE=1 SV=2 - [ADH1A_HUMAN]	4.28E-04	-4.7922	-2.9492	1.34E-03	-3.6729	-4.8261
2_4	P00326	Alcohol dehydrogenase 1C OS=Homo sapiens GN=ADH1C PE=1 SV=2 - [ADH1G_HUMAN]	2.61E-03	-3.6506	-2.9342	8.94E-03	-2.7016	-4.0606
2_4	P08319	Alcohol dehydrogenase 4 OS=Homo sapiens GN=ADH4 PE=1 SV=5 - [ADH4_HUMAN]	2.41E-05	-12.7969	-2.8967	5.41E-03	-2.9601	-4.8219
2_4	Q9H2A2	Aldehyde dehydrogenase family 8 member A1 OS=Homo sapiens GN=ALDH8A1 PE=1 SV=1 - [AL8A1_HUMAN]	2.71E-04	-5.6224	-2.7885	1.42E-04	-4.9419	-2.3323
2_4	Q06278	Aldehyde oxidase OS=Homo sapiens GN=AOX1 PE=2 SV=2 - [AL DO_HUMAN]	2.16E-03	-3.7191	-2.7288	2.08E-02	-2.2971	-3.3236
2_4	P17516	Aldo-keto reductase family 1 member C4 OS=Homo sapiens GN=AKR1C4 PE=1 SV=3 - [AK1C4_HUMAN]	3.44E-03	-3.4151	-2.9196	6.51E-03	-2.8632	-3.9866
2_4	Q03154	Aminoacylase-1 OS=Homo sapiens GN=ACY1 PE=1 SV=1 - [ACY1_HUMAN]	6.96E-04	-4.1357	-2.9370	9.43E-05	-5.2749	-4.3069
2_4	P12429	Annexin A3 OS=Homo sapiens GN=ANXA3 PE=1 SV=3 - [ANXA3_HUMAN]	1.35E-02	2.6461	2.7599	3.39E-03	3.2011	2.4826

Fig. 7 continued

2_4	O95831	Apoptosis-inducing factor 1, mitochondrial OS=Homo sapiens GN=AIFM1 PE=1 SV=1 - [AIFM1_HUMAN]	5.06E-03	-3.0297	-2.8141	2.51E-05	-6.3940	-3.7008
2_4	P05089	Arginase-1 OS=Homo sapiens GN=ARG1 PE=1 SV=2 - [ARGI1_HUMAN]	2.17E-05	-13.6063	-2.9120	9.44E-05	-5.2734	-4.5199
2_4	P04424	Argininosuccinate lyase OS=Homo sapiens GN=ASL PE=1 SV=4 - [ARLY_HUMAN]	2.95E-03	-3.5733	-2.8761	1.33E-04	-4.9667	-4.2799
2_4	P00966	Argininosuccinate synthase OS=Homo sapiens GN=ASS1 PE=1 SV=2 - [ASSY_HUMAN]	2.49E-03	-3.6733	-2.8669	3.67E-03	-3.1622	-3.6929
2_4	P22760	Arylacetamide deacetylase OS=Homo sapiens GN=AADAC PE=1 SV=5 - [AAAD_HUMAN]	2.67E-04	-5.6321	-2.8962	6.97E-03	-2.8267	-2.6394
2_4	P20160	Azurocidin OS=Homo sapiens GN=AZU1 PE=1 SV=3 - [CAP7_HUMAN]	1.33E-02	2.6533	2.8499	4.91E-02	1.9119	2.2730
2_4	Q93088	Betaine--homocysteine S-methyltransferase 1 OS=Homo sapiens GN=BHMT PE=1 SV=2 - [BHMT1_HUMAN]	3.72E-04	-5.3788	-2.8536	1.24E-03	-3.7147	-3.9443
2_4	Q9UBR1	Beta-ureidopropionase OS=Homo sapiens GN=UPB1 PE=1 SV=1 - [BUP1_HUMAN]	3.43E-04	-5.4570	-2.7768	2.50E-03	-3.3534	-2.3236
2_4	P34913	Bifunctional epoxide hydrolase 2 OS=Homo sapiens GN=EPHX2 PE=1 SV=2 - [HYES_HUMAN]	9.91E-06	-16.8141	-2.7439	3.87E-05	-6.0466	-2.0114
2_4	P31939	Bifunctional purine biosynthesis protein PURH OS=Homo sapiens GN=ATIC PE=1 SV=3 - [PUR9_HUMAN]	5.30E-03	2.9839	2.8384	1.71E-03	3.5315	3.3386
2_4	P21810	Biglycan OS=Homo sapiens GN=BGN PE=1 SV=2 - [PGS1_HUMAN]	4.44E-04	4.6856	2.8811	8.53E-05	5.3816	4.1264
2_4	Q14032	Bile acid-CoA:amino acid N-acyltransferase OS=Homo sapiens GN=BAAT PE=1 SV=1 - [BAAT_HUMAN]	2.22E-05	-13.5177	-2.8539	1.80E-05	-6.5942	-2.6218
2_4	Q9Y2P5	Bile acyl-CoA synthetase OS=Homo sapiens GN=SLC27A5 PE=1 SV=1 - [S27A5_HUMAN]	3.46E-04	-5.4430	-2.7777	8.99E-04	-3.8922	-3.5460
2_4	Q06520	Bile salt sulfotransferase OS=Homo sapiens GN=SULT2A1 PE=1 SV=3 - [ST2A1_HUMAN]	1.72E-05	-14.7411	-2.9192	1.55E-05	-6.9258	-4.0747
2_4	P23786	Carnitine O-palmitoyltransferase 2, mitochondrial OS=Homo sapiens GN=CPT2 PE=1 SV=2 - [CPT2_HUMAN]	4.97E-04	-4.5295	-2.7694	5.76E-03	-2.9261	-3.0755
2_4	P08311	Cathepsin G OS=Homo sapiens GN=CTSG PE=1 SV=2 - [CATG_HUMAN]	1.66E-02	2.5354	2.8700	2.40E-02	2.2257	2.7725
2_4	O00748	Cocaine esterase OS=Homo sapiens GN=CES2 PE=1 SV=1 - [EST2_HUMAN]	4.67E-05	-6.5404	-2.8874	2.52E-03	-3.3496	-3.3789
2_4	P31146	Coronin-1A OS=Homo sapiens GN=CORO1A PE=1 SV=4 - [COR1A_HUMAN]	8.48E-06	6.1466	2.7939	3.65E-03	3.1659	2.5601
2_4	P28845	Corticosteroid 11-beta-dehydrogenase isozyme 1 OS=Homo sapiens GN=HSD11B1 PE=1 SV=3 - [DHI1_HUMAN]	3.33E-04	-5.4732	-2.7739	1.56E-04	-4.8962	-2.2673
2_4	P32929	Cystathionine gamma-lyase OS=Homo sapiens GN=CTH PE=1 SV=3 - [CGL_HUMAN]	3.63E-04	-5.3886	-2.7750	9.09E-03	-2.6944	-2.7316
2_4	P00167	Cytochrome b5 OS=Homo sapiens GN=CYB5A PE=1 SV=2 - [CYB5_HUMAN]	5.61E-04	-4.3660	-2.9940	2.27E-04	-4.6778	-3.5964
2_4	P11509	Cytochrome P450 2A6 OS=Homo sapiens GN=CYP2A6 PE=1 SV=3 - [CP2A6_HUMAN]	2.83E-05	-7.2318	-2.8972	3.16E-03	-3.2368	-3.6597
2_4	P11712	Cytochrome P450 2C9 OS=Homo sapiens GN=CYP2C9 PE=1 SV=3 - [CP2C9_HUMAN]	1.84E-03	-3.7554	-2.8364	3.12E-03	-3.2410	-3.7909
2_4	P05181	Cytochrome P450 2E1 OS=Homo sapiens GN=CYP2E1 PE=1 SV=1 - [CP2E1_HUMAN]	1.72E-02	-2.5166	-2.7621	2.16E-02	-2.2800	-2.9678
2_4	O75891	Cytosolic 10-formyltetrahydrofolate dehydrogenase OS=Homo sapiens GN=ALDH1L1 PE=1 SV=2 - [AL1L1_HUMAN]	2.00E-03	-3.7372	-2.8376	6.43E-03	-2.8688	-4.2534
2_4	Q02338	D-beta-hydroxybutyrate dehydrogenase, mitochondrial OS=Homo sapiens GN=BDH1 PE=1 SV=3 - [BDH_HUMAN]	1.61E-05	-14.9205	-2.8298	4.14E-06	-8.2936	-3.0118
2_4	P07585	Decorin OS=Homo sapiens GN=DCN PE=1 SV=1 - [PGS2_HUMAN]	1.79E-03	3.7650	2.7217	1.34E-03	3.6760	2.1517
2_4	P09417	Dihydropteridine reductase OS=Homo sapiens GN=QDPR PE=1 SV=2 - [DHPR_HUMAN]	7.66E-04	-4.0375	-2.7510	1.71E-03	-3.5306	-2.5460
2_4	Q14117	Dihydropyrimidinase OS=Homo sapiens GN=DPYS PE=1 SV=1 - [DPYS_HUMAN]	1.62E-02	-2.5481	-2.8922	1.60E-03	-3.5713	-2.1159
2_4	P31513	Dimethylaniline monooxygenase [N-oxide-forming] 3 OS=Homo sapiens GN=FMO3 PE=1 SV=5 - [FMO3_HUMAN]	5.03E-04	-4.5106	-2.8470	8.99E-03	-2.6993	-2.4253
2_4	Q9UI17	Dimethylglycine dehydrogenase, mitochondrial OS=Homo sapiens GN=DMGDH PE=1 SV=2 - [DMGD_HUMAN]	2.59E-04	-5.6442	-2.7582	4.81E-03	-3.0281	-2.3323
2_4	P78527	DNA-dependent protein kinase catalytic subunit OS=Homo sapiens GN=PRKDC PE=1 SV=3 - [PRKDC_HUMAN]	2.74E-03	3.6264	2.8052	3.71E-03	3.1546	4.4282

Fig. 7 continued

2_4	O75521	Enoyl-CoA delta isomerase 2, mitochondrial OS=Homo sapiens GN=ECI2 PE=1 SV=4 - [ECI2_HUMAN]	3.09E-03	-3.5273	-2.7705	3.63E-03	-3.1685	-2.7939
2_4	P15311	Ezrin OS=Homo sapiens GN=EZR PE=1 SV=4 - [EZRI_HUMAN]	6.04E-04	4.2761	2.9388	9.93E-04	3.8310	3.5140
2_4	O95954	Formimidoyltransferase-cyclodeaminase OS=Homo sapiens GN=FTCD PE=1 SV=2 - [FTCD_HUMAN]	1.08E-04	-5.9573	-2.8156	4.96E-03	-3.0091	-4.0241
2_4	P09467	Fructose-1,6-bisphosphatase 1 OS=Homo sapiens GN=FBP1 PE=1 SV=5 - [F16P1_HUMAN]	3.65E-03	-3.3633	-2.8730	1.70E-05	-6.6557	-3.7148
2_4	P09382	Galectin-1 OS=Homo sapiens GN=LGALS1 PE=1 SV=2 - [LEG1_HUMAN]	6.72E-04	4.1653	2.7975	1.34E-04	4.9653	2.3985
2_4	O95479	GDH/6PGL endoplasmic bifunctional protein OS=Homo sapiens GN=H6PD PE=1 SV=2 - [G6PE_HUMAN]	3.39E-03	-3.2706	-2.7628	8.00E-04	-3.9522	-2.9678
2_4	P11413	Glucose-6-phosphate 1-dehydrogenase OS=Homo sapiens GN=G6PD PE=1 SV=4 - [G6PD_HUMAN]	1.95E-03	3.7418	2.8217	1.81E-02	2.3651	2.8646
2_4	P09211	Glutathione S-transferase P OS=Homo sapiens GN=GSTP1 PE=1 SV=2 - [GSTP1_HUMAN]	1.08E-02	2.7439	2.8533	3.04E-03	3.2520	2.8721
2_4	P11216	Glycogen phosphorylase, brain form OS=Homo sapiens GN=PYGB PE=1 SV=5 - [PYGB_HUMAN]	1.02E-03	3.8583	2.8440	1.29E-02	2.5275	3.0586
2_4	Q9UJJ7	GTP:AMP phosphotransferase, mitochondrial OS=Homo sapiens GN=AK3 PE=1 SV=4 - [KAD3_HUMAN]	2.72E-02	-2.2018	-2.8197	2.14E-03	-3.4266	-2.4373
2_4	P04899	Guanine nucleotide-binding protein G(i) subunit alpha-2 OS=Homo sapiens GN=GNAI2 PE=1 SV=3 - [GNAI2_HUMAN]	9.76E-03	2.7721	2.7782	4.54E-03	3.0572	2.0675
2_4	O14979	Heterogeneous nuclear ribonucleoprotein D-like OS=Homo sapiens GN=HNRPDL PE=1 SV=3 - [HNRDL_HUMAN]	6.19E-03	2.8541	2.8773	2.39E-05	6.2819	2.5140
2_4	Q99098	Homogentisate 1,2-dioxygenase OS=Homo sapiens GN=HGD PE=1 SV=2 - [HGD_HUMAN]	4.21E-04	-4.9213	-2.8230	3.46E-05	-6.1415	-4.0222
2_4	Q9UJM8	Hydroxyacid oxidase 1 OS=Homo sapiens GN=HAO1 PE=1 SV=1 - [HAOX1_HUMAN]	1.84E-05	-14.5838	-2.9012	8.79E-06	-7.2034	-4.6766
2_4	Q16836	Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial OS=Homo sapiens GN=HADH PE=1 SV=3 - [HCDH_HUMAN]	4.48E-04	-4.6598	-2.7695	4.97E-05	-5.7240	-2.4843
2_4	P35914	Hydroxymethylglutaryl-CoA lyase, mitochondrial OS=Homo sapiens GN=HMGCL PE=1 SV=2 - [HMGCL_HUMAN]	2.82E-02	-2.1734	-2.7659	5.26E-04	-4.1728	-2.4944
2_4	P54868	Hydroxymethylglutaryl-CoA synthase, mitochondrial OS=Homo sapiens GN=HMGCS2 PE=1 SV=1 - [HMCS2_HUMAN]	5.10E-03	-3.0220	-2.9989	1.52E-04	-4.9124	-4.6936
2_4	P26440	Isovaleryl-CoA dehydrogenase, mitochondrial OS=Homo sapiens GN=IVD PE=1 SV=1 - [IVD_HUMAN]	2.77E-02	-2.1810	-2.7571	3.69E-03	-3.1588	-2.0747
2_4	P08727	Keratin, type I cytoskeletal 19 OS=Homo sapiens GN=KRT19 PE=1 SV=4 - [K1C19_HUMAN]	2.41E-03	3.6890	2.8178	5.59E-03	2.9394	4.2797
2_4	P08729	Keratin, type II cytoskeletal 7 OS=Homo sapiens GN=KRT7 PE=1 SV=5 - [K2C7_HUMAN]	2.26E-03	3.7067	2.7941	1.70E-02	2.3970	2.5501
2_4	O00515	Ladinin-1 OS=Homo sapiens GN=LAD1 PE=1 SV=2 - [LAD1_HUMAN]	7.06E-07	23.5174	2.7578	3.01E-03	3.2574	2.0675
2_4	P33121	Long-chain-fatty-acid--CoA ligase 1 OS=Homo sapiens GN=ACSL1 PE=1 SV=1 - [ACSL1_HUMAN]	7.32E-05	-6.2587	-2.8078	7.34E-07	-9.5330	-3.7481
2_4	P51884	Lumican OS=Homo sapiens GN=LUM PE=1 SV=2 - [LUM_HUMAN]	9.14E-03	2.7669	2.8626	9.58E-04	3.8537	3.8302
2_4	P40121	Macrophage-capping protein OS=Homo sapiens GN=CAPG PE=1 SV=2 - [CAPG_HUMAN]	3.35E-05	6.8624	2.8374	5.16E-06	7.8764	3.2131
2_4	Q14764	Major vault protein OS=Homo sapiens GN=MVP PE=1 SV=4 - [MVP_HUMAN]	1.22E-02	2.7023	2.7013	4.55E-02	1.9496	2.6322
2_4	O00264	Membrane-associated progesterone receptor component 1 OS=Homo sapiens GN=PGRMC1 PE=1 SV=3 - [PGRC1_HUMAN]	4.96E-04	-4.5333	-2.8734	4.45E-05	-5.8925	-3.9095
2_4	Q02252	Methylmalonate-semialdehyde dehydrogenase [acylating], mitochondrial OS=Homo sapiens GN=ALDH6A1 PE=1 SV=2 - [MMSA_HUMAN]	8.15E-04	-3.9825	-2.8877	9.93E-05	-5.2848	-4.8374
2_4	Q9H8H3	Methyltransferase-like protein 7A OS=Homo sapiens GN=METTL7A PE=1 SV=1 - [META_HUMAN]	4.69E-04	-4.5880	-2.8084	1.55E-04	-4.9003	-2.0616
2_4	P10620	Microsomal glutathione S-transferase 1 OS=Homo sapiens GN=MGST1 PE=1 SV=1 - [MGST1_HUMAN]	6.18E-03	-2.8552	-2.8540	5.05E-04	-4.1991	-2.4391
2_4	P55157	Microsomal triglyceride transfer protein large subunit OS=Homo sapiens GN=MTTP PE=1 SV=1 - [MTP_HUMAN]	2.55E-05	-11.4288	-2.7437	4.55E-06	-8.1044	-3.0747
2_4	Q9Y6C9	Mitochondrial carrier homolog 2 OS=Homo sapiens GN=MTCH2 PE=1 SV=1 - [MTCH2_HUMAN]	3.68E-03	-3.3538	-2.8105	3.71E-04	-4.4035	-2.9678
2_4	Q969Z3	MOSC domain-containing protein 2, mitochondrial OS=Homo sapiens GN=MARC2 PE=1 SV=1 - [MOSC2_HUMAN]	9.68E-05	-6.0043	-2.7157	4.84E-04	-4.2358	-2.5520

Fig. 7 continued

2_4	P41218	Myeloid cell nuclear differentiation antigen OS=Homo sapiens GN=MNDA PE=1 SV=1 - [MNDA_HUMAN]	1.52E-02	2.5791	2.8067	1.32E-02	2.5114	2.4246
2_4	P05164	Myeloperoxidase OS=Homo sapiens GN=MPO PE=1 SV=1 - [PERM_HUMAN]	8.77E-05	6.0914	2.9238	4.54E-03	3.0577	4.1746
2_4	Q4G0N4	NAD kinase domain-containing protein 1 OS=Homo sapiens GN=NADKD1 PE=1 SV=2 - [NAKD1_HUMAN]	6.02E-05	-6.3811	-2.8631	6.74E-04	-4.0423	-2.7939
2_4	P16435	NADPH--cytochrome P450 reductase OS=Homo sapiens GN=POR PE=1 SV=2 - [NCPR_HUMAN]	4.59E-04	-4.6255	-2.8868	3.83E-04	-4.3932	-3.5681
2_4	P22307	Non-specific lipid-transfer protein OS=Homo sapiens GN=SCP2 PE=1 SV=2 - [NLTP_HUMAN]	4.80E-04	-4.5718	-2.8208	4.84E-04	-4.2352	-3.3548
2_4	P00480	Ornithine carbamoyltransferase, mitochondrial OS=Homo sapiens GN=OTC PE=1 SV=3 - [OTC_HUMAN]	1.65E-05	-14.8728	-2.9020	5.09E-06	-7.9404	-4.1166
2_4	O60664	Perilipin-3 OS=Homo sapiens GN=PLIN3 PE=1 SV=3 - [PLIN3_HUMAN]	2.85E-04	5.5697	2.7383	2.16E-03	3.4214	2.2899
2_4	Q15063	Periostin OS=Homo sapiens GN=POSTN PE=1 SV=2 - [POSTN_HUMAN]	8.04E-06	20.3842	2.8242	7.95E-04	3.9561	3.2899
2_4	Q15067	Peroxisomal acyl-coenzyme A oxidase 1 OS=Homo sapiens GN=ACOX1 PE=1 SV=3 - [ACOX1_HUMAN]	4.78E-03	-3.0792	-2.7623	1.19E-03	-3.7414	-3.6013
2_4	Q9BWG4	Peroxisomal acyl-coenzyme A oxidase 2 OS=Homo sapiens GN=ACOX2 PE=1 SV=1 - [ACOX2_HUMAN]	2.03E-05	-14.7095	-2.7478	2.34E-03	-3.3885	-3.1310
2_4	Q08426	Peroxisomal bifunctional enzyme OS=Homo sapiens GN=EHHADH PE=1 SV=3 - [ECHP_HUMAN]	5.20E-04	-4.4630	-2.9160	8.86E-05	-5.3515	-5.2498
2_4	Q9P0Z9	Peroxisomal sarcosine oxidase OS=Homo sapiens GN=PIPOX PE=2 SV=2 - [SOX_HUMAN]	5.82E-04	-4.3120	-2.8337	4.38E-05	-5.9094	-3.9173
2_4	Q99424	Peroxisomal acyl-coenzyme A oxidase 2 OS=Homo sapiens GN=ACOX2 PE=1 SV=1 - [ACOX2_HUMAN]	2.03E-05	-14.7095	-2.7478	2.34E-03	-3.3885	-3.1310
2_4	Q08426	Peroxisomal bifunctional enzyme OS=Homo sapiens GN=EHHADH PE=1 SV=3 - [ECHP_HUMAN]	5.20E-04	-4.4630	-2.9160	8.86E-05	-5.3515	-5.2498
2_4	Q9P0Z9	Peroxisomal sarcosine oxidase OS=Homo sapiens GN=PIPOX PE=2 SV=2 - [SOX_HUMAN]	5.82E-04	-4.3120	-2.8337	4.38E-05	-5.9094	-3.9173
2_4	P05165	Propionyl-CoA carboxylase alpha chain, mitochondrial OS=Homo sapiens GN=PCCA PE=1 SV=4 - [PCCA_HUMAN]	2.37E-03	-3.6944	-2.7099	5.07E-03	-2.9991	-2.2462
2_4	Q14914	Prostaglandin reductase 1 OS=Homo sapiens GN=PTGR1 PE=1 SV=2 - [PTGR1_HUMAN]	3.84E-03	-3.3090	-2.8204	1.09E-02	-2.6105	-3.3166
2_4	P55786	Puromycin-sensitive aminopeptidase OS=Homo sapiens GN=NPEPPS PE=1 SV=2 - [PSA_HUMAN]	4.98E-04	4.5271	2.7998	2.09E-02	2.2945	2.6322
2_4	Q9NVS9	Pyridoxine-5-phosphate oxidase OS=Homo sapiens GN=PNPO PE=1 SV=1 - [PNPO_HUMAN]	1.25E-02	-2.6905	-2.8059	7.16E-04	-4.0180	-2.4373
2_4	P11498	Pyruvate carboxylase, mitochondrial OS=Homo sapiens GN=PC PE=1 SV=2 - [PYC_HUMAN]	7.17E-04	-4.0985	-2.8449	4.30E-05	-5.9560	-4.8219
2_4	P46940	Ras GTPase-activating-like protein IQGAP1 OS=Homo sapiens GN=IQGAP1 PE=1 SV=1 - [IQGA1_HUMAN]	2.13E-04	5.7335	2.7745	2.93E-03	3.2762	3.4989
2_4	Q13576	Ras GTPase-activating-like protein IQGAP2 OS=Homo sapiens GN=IQGAP2 PE=1 SV=4 - [IQGA2_HUMAN]	1.44E-02	-2.6144	-2.6976	4.03E-02	-1.9920	-2.7148
2_4	O75452	Retinol dehydrogenase 16 OS=Homo sapiens GN=RDH16 PE=1 SV=2 - [RDH16_HUMAN]	3.53E-04	-5.4067	-2.7982	1.53E-03	-3.5966	-2.3593
2_4	P02753	Retinol-binding protein 4 OS=Homo sapiens GN=RBP4 PE=1 SV=3 - [RET4_HUMAN]	1.32E-05	-15.3927	-2.8141	1.79E-04	-4.8337	-2.4944
2_4	P52566	Rho GDP-dissociation inhibitor 2 OS=Homo sapiens GN=ARHGDIB PE=1 SV=3 - [GDIR2_HUMAN]	1.34E-02	2.6505	2.7592	4.25E-03	3.0879	2.2871
2_4	Q9NBX0	Saccharopine dehydrogenase-like oxidoreductase OS=Homo sapiens GN=SCCPDH PE=1 SV=1 - [SCPDL_HUMAN]	7.11E-04	-4.1129	-2.8219	3.93E-04	-4.3780	-2.7268
2_4	Q00266	S-adenosylmethionine synthase isoform type-1 OS=Homo sapiens GN=MAT1A PE=1 SV=2 - [METK1_HUMAN]	8.52E-04	-3.9485	-2.8606	4.86E-03	-3.0213	-2.8628
2_4	Q9UU12	Sarcosine dehydrogenase, mitochondrial OS=Homo sapiens GN=SARDH PE=1 SV=1 - [SARDH_HUMAN]	2.46E-04	-5.6627	-2.7893	4.00E-04	-4.3623	-3.1624
2_4	Q9UHD8	Septin-9 OS=Homo sapiens GN=SEPT9 PE=1 SV=2 - [SEPT9_HUMAN]	5.08E-05	6.5044	2.8187	3.95E-06	8.5556	2.9835
2_4	P34896	Serine hydroxymethyltransferase, cytosolic OS=Homo sapiens GN=SHMT1 PE=1 SV=1 - [GLYC_HUMAN]	4.22E-03	-3.2082	-2.8595	1.21E-03	-3.7307	-3.6455
2_4	P45954	Short/branched chain specific acyl-CoA dehydrogenase, mitochondrial OS=Homo sapiens GN=ACADSB PE=1 SV=1 - [ACDSB_HUMAN]	5.35E-04	-4.4192	-2.8717	2.41E-05	-6.4404	-3.3069
2_4	Q9H9B4	Sideroflexin-1 OS=Homo sapiens GN=SFXN1 PE=1 SV=4 - [SFXN1_HUMAN]	3.69E-03	-3.3506	-2.7687	2.25E-04	-4.6832	-2.4391
2_4	Q00796	Sorbitol dehydrogenase OS=Homo sapiens GN=SORD PE=1 SV=4 - [DHSO_HUMAN]	2.53E-03	-3.6648	-2.8382	1.52E-03	-3.6006	-3.5460
2_4	Q02318	Sterol 26-hydroxylase, mitochondrial OS=Homo sapiens GN=CYP27A1 PE=1 SV=1 - [CP27A_HUMAN]	7.23E-05	-6.2669	-2.7763	9.21E-04	-3.8776	-2.4391
2_4	P37040	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial OS=Homo sapiens GN=SDHA PE=1 SV=2 - [DHSA_HUMAN]	5.35E-04	-4.4216	-2.7491	9.16E-03	-2.6915	-2.4944

Fig. 7 continued

2.4	P51649	Succinate-semialdehyde dehydrogenase, mitochondrial OS=Homo sapiens GN=ALDH5A1 PE=1 SV=2 - [SSDH_HUMAN]	3.92E-03	-3.2868	-2.7755	1.00E-04	-5.1939	-3.2534
2.4	Q99536	Synaptic vesicle membrane protein VAT-1 homolog OS=Homo sapiens GN=VAT1 PE=1 SV=2 - [VAT1_HUMAN]	3.51E-05	6.8479	2.8511	4.46E-03	3.0680	2.1297
2.4	P24821	Tenascin OS=Homo sapiens GN=TNC PE=1 SV=3 - [TENA_HUMAN]	1.37E-02	2.6387	2.7053	1.69E-02	2.3985	2.6322
2.4	P53007	Tricarboxylate transport protein, mitochondrial OS=Homo sapiens GN=SLC25A1 PE=1 SV=2 - [TXTP_HUMAN]	3.92E-03	-3.2884	-2.7448	1.99E-03	-3.4588	-2.1981
2.4	P22310	UDP-glucuronosyltransferase 1-4 OS=Homo sapiens GN=UGT1A4 PE=1 SV=1 - [UD14_HUMAN]	3.17E-04	-5.4923	-2.8845	5.90E-04	-4.1140	-2.9086
2.4	P06133	UDP-glucuronosyltransferase 2B4 OS=Homo sapiens GN=UGT2B4 PE=1 SV=2 - [UD2B4_HUMAN]	2.06E-05	-14.0468	-2.7905	6.82E-04	-4.0358	-2.7008
2.4	P16662	UDP-glucuronosyltransferase 2B7 OS=Homo sapiens GN=UGT2B7 PE=1 SV=1 - [UD2B7_HUMAN]	3.50E-04	-5.4286	-2.7992	2.88E-03	-3.2828	-2.7316
2.4	Q96QK1	Vacuolar protein sorting-associated protein 35 OS=Homo sapiens GN=VPS35 PE=1 SV=2 - [VPS35_HUMAN]	2.74E-02	2.1953	2.6788	3.09E-03	3.2448	2.4516
2.4	P13611	Versican core protein OS=Homo sapiens GN=VCAN PE=1 SV=3 - [CSPG2_HUMAN]	1.40E-03	3.8059	2.8142	5.37E-03	2.9654	3.1355
2.5	P31947	14-3-3 protein sigma OS=Homo sapiens GN=SFN PE=1 SV=1 - [1433S_HUMAN]	3.03E-03	3.4608	3.0139	5.81E-04	4.3343	3.6959
2.5	O14756	17-beta-hydroxysteroid dehydrogenase type 6 OS=Homo sapiens GN=HSD17B6 PE=1 SV=1 - [H17B6_HUMAN]	2.84E-06	-14.5723	-2.8648	9.59E-06	-8.8102	-3.5460
2.5	P12694	2-oxoisovalerate dehydrogenase subunit alpha, mitochondrial OS=Homo sapiens GN=BCKDHA PE=1 SV=2 - [ODBA_HUMAN]	1.52E-03	-3.7847	-2.6657	2.12E-02	-2.2920	-2.1159
2.5	P80404	4-aminobutyrate aminotransferase, mitochondrial OS=Homo sapiens GN=ABAT PE=1 SV=3 - [GABT_HUMAN]	3.51E-03	-3.3258	-2.8460	1.07E-04	-5.5095	-4.6929
2.5	P32754	4-hydroxyphenylpyruvate dioxygenase OS=Homo sapiens GN=HPD PE=1 SV=2 - [HPPD_HUMAN]	2.89E-06	-12.6416	-2.8898	3.30E-04	-4.7439	-4.7268
2.5	Q01813	6-phosphofructokinase type C OS=Homo sapiens GN=PFKP PE=1 SV=2 - [K6PP_HUMAN]	1.25E-03	3.8212	2.7049	9.25E-03	2.7042	2.0637
2.5	Q96WD1	Acetyl-CoA acetyltransferase, cytosolic OS=Homo sapiens GN=ACAT2 PE=1 SV=2 - [THIC_HUMAN]	2.04E-03	-3.7056	-2.7071	1.15E-03	-3.8469	-2.6394
2.5	Q08AH3	Acyl-coenzyme A synthetase ACSM2A, mitochondrial OS=Homo sapiens GN=ACSM2A PE=1 SV=2 - [ACS2A_HUMAN]	2.79E-06	-16.0532	-2.8285	2.78E-04	-4.8093	-4.3789
2.5	Q6ICK6	Acyl-coenzyme A synthetase ACSM2B, mitochondrial OS=Homo sapiens GN=ACSM2B PE=1 SV=2 - [ACS2B_HUMAN]	2.80E-06	-15.8889	-2.8285	8.85E-05	-5.6594	-4.4100
2.5	Q8IUX7	Adipocyte enhancer-binding protein 1 OS=Homo sapiens GN=AEBP1 PE=1 SV=1 - [AEBP1_HUMAN]	1.10E-03	3.9426	2.8321	2.30E-02	2.2468	2.3713
2.5	O95154	Aflatoxin B1 aldehyde reductase member 3 OS=Homo sapiens GN=AKR7A3 PE=1 SV=2 - [ARK73_HUMAN]	2.86E-06	-13.4494	-2.8542	1.24E-03	-3.7898	-3.4373
2.5	P24298	Alanine aminotransferase 1 OS=Homo sapiens GN=GPT PE=1 SV=3 - [ALAT1_HUMAN]	3.52E-04	-5.3706	-2.7134	6.26E-04	-4.2661	-3.5153
2.5	P07327	Alcohol dehydrogenase 1A OS=Homo sapiens GN=ADH1A PE=1 SV=2 - [ADH1A_HUMAN]	1.12E-02	-2.6933	-2.9492	1.26E-03	-3.7790	-4.8261
2.5	P00325	Alcohol dehydrogenase 1B OS=Homo sapiens GN=ADH1B PE=1 SV=2 - [ADH1B_HUMAN]	2.36E-02	-2.2160	-2.9536	1.25E-03	-3.7864	-4.7789
2.5	P00326	Alcohol dehydrogenase 1C OS=Homo sapiens GN=ADH1C PE=1 SV=2 - [ADH1G_HUMAN]	2.37E-03	-3.6506	-2.9342	9.30E-03	-2.7016	-4.0606
2.5	P08319	Alcohol dehydrogenase 4 OS=Homo sapiens GN=ADH4 PE=1 SV=5 - [ADH4_HUMAN]	2.94E-03	-3.4903	-2.8967	6.25E-03	-2.8765	-4.8219
2.5	Q9H2A2	Aldehyde dehydrogenase family 8 member A1 OS=Homo sapiens GN=ALDH8A1 PE=1 SV=1 - [AL8A1_HUMAN]	2.80E-04	-5.6224	-2.7885	2.32E-04	-4.9419	-2.3323
2.5	Q06278	Aldehyde oxidase OS=Homo sapiens GN=AOX1 PE=2 SV=2 - [AIDO_HUMAN]	1.95E-03	-3.7191	-2.7288	2.11E-02	-2.2971	-3.3236
2.5	O60218	Aldo-keto reductase family 1 member B10 OS=Homo sapiens GN=AKR1B10 PE=1 SV=2 - [AK1BA_HUMAN]	4.37E-02	-2.0511	-2.9501	6.63E-03	-2.8524	-3.8679
2.5	P52895	Aldo-keto reductase family 1 member C2 OS=Homo sapiens GN=AKR1C2 PE=1 SV=3 - [AK1C2_HUMAN]	2.03E-03	-3.7077	-2.9553	9.60E-03	-2.6872	-4.3506
2.5	P17516	Aldo-keto reductase family 1 member C4 OS=Homo sapiens GN=AKR1C4 PE=1 SV=3 - [AK1C4_HUMAN]	3.03E-04	-5.5171	-2.9196	2.98E-04	-4.7877	-3.9866
2.5	Q03154	Aminoacylase-1 OS=Homo sapiens GN=ACY1 PE=1 SV=1 - [ACY1_HUMAN]	8.06E-06	-7.2584	-2.9370	1.15E-04	-5.4332	-4.3069
2.5	P12429	Annexin A3 OS=Homo sapiens GN=ANXA3 PE=1 SV=3 - [ANXA3_HUMAN]	5.47E-05	6.1636	2.8156	1.70E-03	3.5885	2.4937

Fig. 7 continued

2_5	P02649	Apolipoprotein E OS=Homo sapiens GN=APOE PE=1 SV=1 - [APOE_HUMAN]	1.74E-02	-2.4393	-2.8548	8.02E-05	-5.7323	-4.2498
2_5	O95831	Apoptosis-inducing factor 1, mitochondrial OS=Homo sapiens GN=AIFM1 PE=1 SV=1 - [AIFM1_HUMAN]	2.31E-02	-2.2319	-2.8141	9.39E-05	-5.6306	-3.7008
2_5	P05089	Arginase-1 OS=Homo sapiens GN=ARG1 PE=1 SV=2 - [ARG1_HUMAN]	2.86E-06	-13.6063	-2.9120	1.44E-04	-5.2734	-4.5199
2_5	P04424	Argininosuccinate lyase OS=Homo sapiens GN=ASL PE=1 SV=4 - [ARLY_HUMAN]	3.04E-03	-3.4537	-2.8761	5.40E-05	-6.1362	-3.1647
2_5	P00966	Argininosuccinate synthase OS=Homo sapiens GN=ASS1 PE=1 SV=2 - [ASSY_HUMAN]	5.10E-05	-6.1884	-2.8669	3.73E-03	-3.1615	-3.6829
2_5	P22760	Arylacetamide deacetylase OS=Homo sapiens GN=AADAC PE=1 SV=5 - [AAAD_HUMAN]	2.77E-04	-5.6321	-2.6962	6.92E-03	-2.8267	-2.6394
2_5	O43776	Asparagine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=NARS PE=1 SV=1 - [SYNC_HUMAN]	5.41E-03	2.8333	2.7515	8.12E-03	2.7511	2.2012
2_5	Q9BXN1	Asporin OS=Homo sapiens GN=ASPN PE=1 SV=2 - [ASPN_HUMAN]	4.56E-04	4.6521	2.9156	7.89E-03	2.7612	2.7933
2_5	P13929	Beta-enolase OS=Homo sapiens GN=ENO3 PE=1 SV=5 - [ENOB_HUMAN]	9.77E-03	-2.7577	-2.8908	1.64E-02	-2.4241	-2.5460
2_5	Q93088	Betaine--homocysteine S-methyltransferase 1 OS=Homo sapiens GN=BHMT PE=1 SV=2 - [BHMT1_HUMAN]	3.47E-04	-5.3788	-2.8536	1.40E-03	-3.7147	-3.9443
2_5	Q9UBR1	Beta-ureidopropionase OS=Homo sapiens GN=UPB1 PE=1 SV=1 - [BUP1_HUMAN]	3.21E-04	-5.4510	-2.7768	2.70E-03	-3.3534	-2.3236
2_5	P34913	Bifunctional epoxide hydrolase 2 OS=Homo sapiens GN=EPHX2 PE=1 SV=2 - [HYES_HUMAN]	4.37E-05	-6.2820	-2.7439	6.13E-05	-6.0466	-2.0114
2_5	P31939	Bifunctional purine biosynthesis protein PURH OS=Homo sapiens GN=ATIC PE=1 SV=3 - [PUR9_HUMAN]	4.88E-02	1.9686	2.8570	1.01E-03	3.9427	3.8090
2_5	P21810	Biglycan OS=Homo sapiens GN=BGN PE=1 SV=2 - [PGS1_HUMAN]	4.61E-04	4.6397	3.0256	2.47E-05	7.1805	4.7778
2_5	Q14032	Bile acid-CoA:amino acid N-acyltransferase OS=Homo sapiens GN=BAAT PE=1 SV=1 - [BAAT_HUMAN]	2.86E-06	-13.5177	-2.8539	4.14E-05	-6.5942	-2.6218
2_5	Q9Y2P5	Bile acyl-CoA synthetase OS=Homo sapiens GN=SLC27A5 PE=1 SV=1 - [S27A5_HUMAN]	3.24E-04	-5.4430	-2.7777	1.07E-03	-3.8922	-3.5460
2_5	Q06520	Bile salt sulfotransferase OS=Homo sapiens GN=SULT2A1 PE=1 SV=3 - [ST2A1_HUMAN]	2.83E-06	-14.7411	-2.9192	3.07E-05	-6.9258	-4.0747
2_5	P17655	Calpain-2 catalytic subunit OS=Homo sapiens GN=CAPN2 PE=1 SV=6 - [CAN2_HUMAN]	1.71E-04	5.8000	2.7473	2.82E-03	3.3268	2.3612
2_5	P31327	Carbamoyl-phosphate synthase [ammonia], mitochondrial OS=Homo sapiens GN=CPS1 PE=1 SV=2 - [CPSM_HUMAN]	9.62E-03	-2.7643	-3.0320	7.52E-05	-5.7893	-7.5266
2_5	P23786	Carnitine O-palmitoyltransferase 2, mitochondrial OS=Homo sapiens GN=CPT2 PE=1 SV=2 - [CPT2_HUMAN]	6.18E-04	-4.1734	-2.7694	6.07E-03	-2.8904	-3.0755
2_5	P35222	Catenin beta-1 OS=Homo sapiens GN=CTNNB1 PE=1 SV=1 - [CTNB1_HUMAN]	4.47E-02	2.0377	2.7214	1.79E-02	2.3804	2.2357
2_5	O00748	Cocaine esterase OS=Homo sapiens GN=CES2 PE=1 SV=1 - [EST2_HUMAN]	2.86E-06	-13.4498	-2.8874	2.42E-03	-3.4057	-3.3789
2_5	Q99715	Collagen alpha-1(XII) chain OS=Homo sapiens GN=COL12A1 PE=1 SV=2 - [COCA1_HUMAN]	1.25E-04	5.8617	2.7621	2.52E-02	2.2001	2.3351
2_5	Q05707	Collagen alpha-1(XIV) chain OS=Homo sapiens GN=COL14A1 PE=1 SV=3 - [COEA1_HUMAN]	5.27E-03	2.8579	2.9208	8.00E-03	2.7564	3.5311
2_5	P00751	Complement factor B OS=Homo sapiens GN=CFB PE=1 SV=2 - [CFAB_HUMAN]	3.22E-03	3.4012	2.8233	4.39E-02	1.9739	2.0493
2_5	Q9P0M6	Core histone macro-H2A.2 OS=Homo sapiens GN=H2AFY2 PE=1 SV=3 - [H2AW_HUMAN]	6.96E-04	4.0200	2.8875	4.77E-04	4.4572	2.9562
2_5	P28845	Corticosteroid 11-beta-dehydrogenase isozyme 1 OS=Homo sapiens GN=HSD11B1 PE=1 SV=3 - [DHI1_HUMAN]	3.16E-04	-5.4732	-2.7739	2.49E-04	-4.8962	-2.2673
2_5	Q86VP6	Cullin-associated NEDD8-dissociated protein 1 OS=Homo sapiens GN=CAND1 PE=1 SV=2 - [CAND1_HUMAN]	1.39E-02	2.5707	2.7822	1.23E-02	2.5731	2.3993
2_5	P32929	Cystathionine gamma-lyase OS=Homo sapiens GN=CTH PE=1 SV=3 - [CGL_HUMAN]	3.43E-04	-5.3896	-2.7750	9.45E-03	-2.6944	-2.7316
2_5	P00167	Cytochrome b5 OS=Homo sapiens GN=CYB5A PE=1 SV=2 - [CYB5_HUMAN]	1.28E-02	-2.6132	-2.9940	1.83E-04	-5.1527	-3.5984
2_5	P11509	Cytochrome P450 2A6 OS=Homo sapiens GN=CYP2A6 PE=1 SV=3 - [CP2A6_HUMAN]	2.81E-06	-15.4599	-2.8972	3.29E-03	-3.2368	-3.6597
2_5	P11712	Cytochrome P450 2C9 OS=Homo sapiens GN=CYP2C9 PE=1 SV=3 - [CP2C9_HUMAN]	3.66E-04	-5.2236	-2.8364	3.26E-03	-3.2410	-3.7909

Fig. 7 continued

2_5	P05181	Cytochrome P450 2E1 OS=Homo sapiens GN=CYP2E1 PE=1 SV=1 - [CP2E1_HUMAN]	2.38E-03	-3.6489	-2.7621	1.79E-02	-2.3803	-2.9678
2_5	Q14204	Cytoplasmic dynein 1 heavy chain 1 OS=Homo sapiens GN=DYNC1H1 PE=1 SV=5 - [DYHC1_HUMAN]	5.43E-03	2.8294	2.7437	2.88E-03	3.3155	3.6977
2_5	O75891	Cytosolic 10-formyltetrahydrofolate dehydrogenase OS=Homo sapiens GN=ALDH1L1 PE=1 SV=2 - [AL1L1_HUMAN]	3.02E-04	-5.5195	-2.8376	6.38E-03	-2.8688	-4.2534
2_5	O43175	D-3-phosphoglycerate dehydrogenase OS=Homo sapiens GN=PHGDH PE=1 SV=4 - [SERA_HUMAN]	4.46E-02	2.0381	2.9203	3.66E-02	2.0565	3.1368
2_5	Q02338	D-beta-hydroxybutyrate dehydrogenase, mitochondrial OS=Homo sapiens GN=BDH1 PE=1 SV=3 - [BDH_HUMAN]	2.83E-06	-14.9205	-2.8298	1.32E-05	-8.2936	-3.0118
2_5	P07585	Decorin OS=Homo sapiens GN=DCN PE=1 SV=1 - [PGS2_HUMAN]	4.31E-06	8.9125	2.8707	1.07E-03	3.8928	2.9632
2_5	P30038	Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial OS=Homo sapiens GN=ALDH4A1 PE=1 SV=3 - [AL4A1_HUMAN]	1.99E-02	-2.3472	-2.8957	5.62E-05	-6.1102	-4.3593
2_5	Q07507	Dermatopontin OS=Homo sapiens GN=DPT PE=2 SV=2 - [DERM_HUMAN]	4.83E-03	2.9495	2.9262	1.10E-02	2.6271	2.2257
2_5	P09417	Dihydropteridine reductase OS=Homo sapiens GN=QDPR PE=1 SV=2 - [DHPR_HUMAN]	3.20E-04	-5.4556	-2.7510	1.88E-03	-3.5306	-2.5460
2_5	Q14117	Dihydropyrimidinase OS=Homo sapiens GN=DPYS PE=1 SV=1 - [DPYS_HUMAN]	2.64E-04	-5.6984	-2.6922	8.70E-04	-4.0569	-2.1159
2_5	Q16555	Dihydropyrimidinase-related protein 2 OS=Homo sapiens GN=DPYSL2 PE=1 SV=1 - [DPYL2_HUMAN]	5.95E-03	2.8147	2.8193	4.07E-03	3.1105	3.5311
2_5	P31513	Dimethylaniline monooxygenase [N-oxide-forming] 3 OS=Homo sapiens GN=FMO3 PE=1 SV=5 - [FMO3_HUMAN]	2.84E-06	-14.1915	-2.8470	4.34E-03	-3.0686	-2.4253
2_5	Q9UI17	Dimethylglycine dehydrogenase, mitochondrial OS=Homo sapiens GN=DMGDH PE=1 SV=2 - [M2GD_HUMAN]	2.75E-04	-5.6442	-2.7582	4.67E-03	-3.0281	-2.3323
2_5	P78527	DNA-dependent protein kinase catalytic subunit OS=Homo sapiens GN=PRKDC PE=1 SV=3 - [PRKDC_HUMAN]	1.82E-02	2.4059	2.8907	7.63E-04	4.1544	4.1338
2_5	O75521	Enoyl-CoA delta isomerase 2, mitochondrial OS=Homo sapiens GN=ECI2 PE=1 SV=4 - [ECI2_HUMAN]	1.59E-04	-5.8171	-2.7705	1.68E-03	-3.5966	-2.7939
2_5	P15311	Ezrin OS=Homo sapiens GN=EZR PE=1 SV=4 - [EZRI_HUMAN]	6.77E-04	4.0608	2.9018	6.96E-04	4.2104	3.6512
2_5	O95954	Formimidoyltransferase-cyclodeaminase OS=Homo sapiens GN=FTCD PE=1 SV=2 - [FTCD_HUMAN]	2.87E-06	-13.2613	-2.8156	3.10E-03	-3.2713	-4.0241
2_5	P09467	Fructose-1,6-bisphosphatase 1 OS=Homo sapiens GN=FBP1 PE=1 SV=5 - [F16P1_HUMAN]	4.33E-04	-4.7487	-2.8730	9.10E-06	-8.8251	-3.7148
2_5	P05062	Fructose-bisphosphate aldolase B OS=Homo sapiens GN=ALDOB PE=1 SV=2 - [ALDOB_HUMAN]	1.54E-02	-2.5178	-3.0577	1.95E-05	-7.4667	-5.9960
2_5	P16930	Fumarylacetoacetase OS=Homo sapiens GN=FAH PE=1 SV=2 - [FAAA_HUMAN]	1.15E-02	-2.6855	-2.8819	5.59E-05	-6.1146	-3.7219
2_5	P09382	Galectin-1 OS=Homo sapiens GN=LGALS1 PE=1 SV=2 - [LEG1_HUMAN]	5.24E-03	2.8627	2.8706	4.52E-03	3.0486	2.5088
2_5	Q08380	Galectin-3-binding protein OS=Homo sapiens GN=LGALS3BP PE=1 SV=1 - [LG3BP_HUMAN]	3.67E-03	3.2809	2.8627	1.75E-03	3.5693	3.1856
2_5	Q92820	Gamma-glutamyl hydrolase OS=Homo sapiens GN=GGH PE=1 SV=2 - [GGH_HUMAN]	1.32E-04	-5.8547	-2.7954	7.91E-03	-2.7605	-2.2462
2_5	O95479	GDH/6PGL endoplasmic bifunctional protein OS=Homo sapiens GN=H6PD PE=1 SV=2 - [G6PE_HUMAN]	1.24E-05	-6.8300	-2.7628	3.67E-04	-4.6537	-2.9678
2_5	P08263	Glutathione S-transferase A1 OS=Homo sapiens GN=GSTA1 PE=1 SV=3 - [GSTA1_HUMAN]	6.63E-03	-2.8094	-3.0048	3.19E-03	-3.2516	-4.5966
2_5	P09211	Glutathione S-transferase P OS=Homo sapiens GN=GSTP1 PE=1 SV=2 - [GSTP1_HUMAN]	3.86E-03	3.2244	2.9716	2.82E-04	4.8013	4.4697
2_5	P11216	Glycogen phosphorylase, brain form OS=Homo sapiens GN=PYGB PE=1 SV=5 - [PYGB_HUMAN]	7.56E-04	3.9378	2.8991	1.02E-03	3.9317	3.4937
2_5	P06737	Glycogen phosphorylase, liver form OS=Homo sapiens GN=PYGL PE=1 SV=4 - [PYGL_HUMAN]	2.76E-06	-16.2063	-2.8466	3.97E-05	-6.6799	-3.9678
2_5	Q9UJU7	GTP:AMP phosphotransferase, mitochondrial OS=Homo sapiens GN=AK3 PE=1 SV=4 - [KAD3_HUMAN]	2.58E-03	-3.5944	-2.8197	9.23E-04	-4.0081	-2.4373
2_5	P02790	Hemopexin OS=Homo sapiens GN=HPX PE=1 SV=2 - [HEMO_HUMAN]	4.95E-04	4.4974	2.9469	1.06E-03	3.8948	2.6432
2_5	Q93099	Homogentisate 1,2-dioxygenase OS=Homo sapiens GN=HGD PE=1 SV=2 - [HGD_HUMAN]	3.19E-04	-5.4588	-2.8230	1.93E-04	-5.0966	-4.0222
2_5	Q8IUM8	Hydroxyacid oxidase 1 OS=Homo sapiens GN=HAO1 PE=1 SV=1 - [HAOX1_HUMAN]	2.84E-06	-14.5838	-2.9012	2.38E-05	-7.2034	-4.6766

Fig. 7 continued

2.5	Q16836	Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial OS=Homo sapiens GN=HADH PE=1 SV=3 - [HCDH_HUMAN]	1.83E-03	-3.7518	-2.7695	7.33E-03	-2.7954	-2.4843
2.5	P35914	Hydroxymethylglutaryl-CoA lyase, mitochondrial OS=Homo sapiens GN=HMGCL PE=1 SV=2 - [HMGCL_HUMAN]	2.81E-04	-5.6212	-2.7659	2.78E-04	-4.8069	-2.4944
2.5	P54868	Hydroxymethylglutaryl-CoA synthase, mitochondrial OS=Homo sapiens GN=HMGCS2 PE=1 SV=1 - [HMCS2_HUMAN]	7.60E-03	-2.8001	-2.9989	1.76E-04	-5.1722	-4.6936
2.5	P19823	Inter-alpha-trypsin inhibitor heavy chain H2 OS=Homo sapiens GN=ITIH2 PE=1 SV=2 - [ITIH2_HUMAN]	1.96E-03	3.7189	2.8529	6.44E-03	2.8659	3.3993
2.5	P26440	Isovaleryl-CoA dehydrogenase, mitochondrial OS=Homo sapiens GN=IVD PE=1 SV=1 - [IVD_HUMAN]	2.40E-03	-3.6460	-2.7571	5.20E-03	-2.9721	-2.0747
2.5	P14923	Junction plakoglobin OS=Homo sapiens GN=JUP PE=1 SV=3 - [PLAK_HUMAN]	1.94E-03	3.7211	2.8074	1.04E-03	3.9160	2.9897
2.5	P08727	Keratin, type I cytoskeletal 19 OS=Homo sapiens GN=KRT19 PE=1 SV=4 - [K1C19_HUMAN]	4.03E-06	8.9687	3.0423	1.33E-03	3.7371	4.7762
2.5	P08729	Keratin, type II cytoskeletal 7 OS=Homo sapiens GN=KRT7 PE=1 SV=5 - [K2C7_HUMAN]	9.74E-05	5.9129	3.0068	3.17E-04	4.7647	3.8292
2.5	O00515	Ladinin-1 OS=Homo sapiens GN=LAD1 PE=1 SV=2 - [LAD1_HUMAN]	2.94E-06	11.8329	2.8060	1.73E-03	3.5811	2.7002
2.5	P23141	Liver carboxylesterase 1 OS=Homo sapiens GN=CES1 PE=1 SV=2 - [EST1_HUMAN]	4.79E-03	-2.9568	-3.0234	5.45E-05	-6.1940	-5.7751
2.5	P07195	L-lactate dehydrogenase B chain OS=Homo sapiens GN=LDHB PE=1 SV=2 - [LDHB_HUMAN]	6.66E-04	4.0882	3.0324	1.09E-03	3.8770	3.3782
2.5	P33121	Long-chain-fatty-acid--CoA ligase 1 OS=Homo sapiens GN=ACSL1 PE=1 SV=1 - [ACSL1_HUMAN]	2.83E-06	-15.0296	-2.8078	3.23E-06	-10.1533	-3.7481
2.5	P51884	Lumican OS=Homo sapiens GN=LUM PE=1 SV=2 - [LUM_HUMAN]	4.70E-04	4.6022	3.0183	1.90E-04	5.1086	4.3746
2.5	Q7Z4W1	L-xylulose reductase OS=Homo sapiens GN=DCXR PE=1 SV=2 - [DCXR_HUMAN]	9.65E-03	-2.7629	-2.9913	4.29E-04	-4.5359	-5.1500
2.5	P40121	Macrophage-capping protein OS=Homo sapiens GN=CAPG PE=1 SV=2 - [CAPG_HUMAN]	1.18E-02	2.6592	2.8198	5.01E-03	2.9906	2.8292
2.5	Q14764	Major vault protein OS=Homo sapiens GN=MVP PE=1 SV=4 - [MVP_HUMAN]	5.20E-03	2.8693	2.8679	1.57E-03	3.6360	4.0027
2.5	P11310	Medium-chain specific acyl-CoA dehydrogenase, mitochondrial OS=Homo sapiens GN=ACADM PE=1 SV=1 - [ACADM_HUMAN]	5.47E-04	-4.3493	-2.8628	1.44E-04	-5.2711	-3.1863
2.5	Q02252	Methylmalonate-semialdehyde dehydrogenase [acylating], mitochondrial OS=Homo sapiens GN=ALDH6A1 PE=1 SV=2 - [MMSA_HUMAN]	1.51E-04	-5.8342	-2.8877	2.29E-04	-4.9506	-4.8374
2.5	Q9H8H3	Methyltransferase-like protein 7A OS=Homo sapiens GN=METTL7A PE=1 SV=1 - [META_HUMAN]	1.31E-04	-5.8552	-2.8084	9.71E-04	-3.9741	-2.0606
2.5	P10620	Microsomal glutathione S-transferase 1 OS=Homo sapiens GN=MGST1 PE=1 SV=1 - [MGST1_HUMAN]	5.49E-05	-6.1495	-2.8540	2.05E-05	-7.3877	-2.4391
2.5	P55157	Microsomal triglyceride transfer protein large subunit OS=Homo sapiens GN=MTTP PE=1 SV=1 - [MTP_HUMAN]	2.98E-06	-11.4288	-2.7437	1.45E-05	-8.1044	-3.0747
2.5	Q9Y6C9	Mitochondrial carrier homolog 2 OS=Homo sapiens GN=MTCH2 PE=1 SV=1 - [MTCH2_HUMAN]	4.08E-03	-3.1536	-2.8105	2.99E-03	-3.2936	-2.9678
2.5	Q969Z3	MOSC domain-containing protein 2, mitochondrial OS=Homo sapiens GN=MARC2 PE=1 SV=1 - [MOSC2_HUMAN]	2.85E-06	-14.1039	-2.7157	2.62E-04	-4.8655	-2.5520
2.5	P05164	Myeloperoxidase OS=Homo sapiens GN=MPO PE=1 SV=1 - [PERM_HUMAN]	3.18E-03	3.4126	2.7845	1.83E-02	2.3674	2.5836
2.5	Q4G0N4	NAD kinase domain-containing protein 1 OS=Homo sapiens GN=NADKD1 PE=1 SV=2 - [NAKD1_HUMAN]	2.83E-06	-14.9263	-2.8631	1.09E-04	-5.4860	-2.7939
2.5	P16435	NADPH--cytochrome P450 reductase OS=Homo sapiens GN=POR PE=1 SV=2 - [NCPR_HUMAN]	5.53E-05	-6.1236	-2.8868	3.79E-04	-4.6316	-3.5681
2.5	Q15274	Nicotinate-nucleotide pyrophosphorylase [carboxylating] OS=Homo sapiens GN=QPRT PE=1 SV=3 - [NADC_HUMAN]	3.61E-05	-6.4119	-2.7679	7.00E-04	-4.2072	-2.3236
2.5	P22307	Non-specific lipid-transfer protein OS=Homo sapiens GN=SCP2 PE=1 SV=2 - [NLTP_HUMAN]	2.51E-03	-3.6115	-2.8208	6.26E-04	-4.2663	-3.3548
2.5	O00567	Nucleolar protein 56 OS=Homo sapiens GN=NOP56 PE=1 SV=4 - [NOP56_HUMAN]	5.97E-03	2.8146	2.7255	7.17E-03	2.8065	2.8656
2.5	P00480	Ornithine carbamoyltransferase, mitochondrial OS=Homo sapiens GN=OTC PE=1 SV=3 - [OTC_HUMAN]	4.09E-05	-6.3085	-2.9020	1.51E-05	-7.9484	-4.1166
2.5	O60664	Perilipin-3 OS=Homo sapiens GN=PLIN3 PE=1 SV=3 - [PLIN3_HUMAN]	3.14E-06	10.2596	2.8256	7.29E-05	5.8038	2.9562
2.5	Q15063	Periostin OS=Homo sapiens GN=POSTN PE=1 SV=2 - [POSTN_HUMAN]	3.03E-06	10.9638	3.0149	2.11E-03	3.4708	4.5277

Fig. 7 continued

2_5	Q15067	Peroxisomal acyl-coenzyme A oxidase 1 OS=Homo sapiens GN=ACOX1 PE=1 SV=3 - [ACOX1_HUMAN]	7.54E-05	-5.9522	-2.7623	5.64E-04	-4.3588	-3.6013
2_5	Q99424	Peroxisomal acyl-coenzyme A oxidase 2 OS=Homo sapiens GN=ACOX2 PE=1 SV=1 - [ACOX2_HUMAN]	2.83E-06	-14.1095	-2.7478	2.50E-03	-3.3885	-3.1310
2_5	Q08426	Peroxisomal bifunctional enzyme OS=Homo sapiens GN=EHHADH PE=1 SV=3 - [ECHP_HUMAN]	2.30E-03	-3.6617	-2.9160	1.07E-04	-5.5170	-5.2498
2_5	Q9P0Z9	Peroxisomal sarcosine oxidase OS=Homo sapiens GN=PIPOX PE=2 SV=2 - [SOX_HUMAN]	2.84E-06	-14.4133	-2.8337	3.93E-05	-6.7133	-3.9173
2_5	Q16822	Phosphoenolpyruvate carboxykinase [GTP], mitochondrial OS=Homo sapiens GN=PCK2 PE=1 SV=3 - [PCKGM_HUMAN]	4.15E-04	-4.8068	-2.9075	5.41E-06	-9.2966	-5.1253
2_5	P05165	Propionyl-CoA carboxylase beta chain, mitochondrial OS=Homo sapiens GN=PCCB PE=1 SV=3 - [PCCB_HUMAN]	1.72E-02	-2.4477	-2.7141	1.85E-02	-2.3604	-3.0118
2_5	Q14914	Prostaglandin reductase 1 OS=Homo sapiens GN=PTGR1 PE=1 SV=2 - [PTGR1_HUMAN]	1.25E-04	-5.8611	-2.8204	4.41E-04	-4.5049	-3.3166
2_5	Q9BPW8	Protein NipSnap homolog 1 OS=Homo sapiens GN=NIPSNAP1 PE=1 SV=1 - [NPS1_HUMAN]	4.28E-03	-3.0873	-2.8331	5.43E-04	-4.3811	-2.9866
2_5	P31949	Protein S100-A11 OS=Homo sapiens GN=S100A11 PE=1 SV=2 - [S10AB_HUMAN]	3.80E-04	5.0788	2.8796	1.53E-04	5.2427	2.0637
2_5	Q15436	Protein transport protein Sec23A OS=Homo sapiens GN=SEC23A PE=1 SV=2 - [SC23A_HUMAN]	4.45E-03	-3.0412	-2.7214	7.41E-04	-4.1705	-2.6394
2_5	P55786	Puromycin-sensitive aminopeptidase OS=Homo sapiens GN=NPEPPS PE=1 SV=2 - [PSA_HUMAN]	4.83E-04	4.5460	2.8279	1.75E-02	2.3938	2.3612
2_5	Q9NVS9	Pyridoxine-5-phosphate oxidase OS=Homo sapiens GN=PNPO PE=1 SV=1 - [PNPO_HUMAN]	2.88E-06	-12.8665	-2.8059	1.74E-04	-5.1757	-2.4373
2_5	P11498	Pyruvate carboxylase, mitochondrial OS=Homo sapiens GN=PC PE=1 SV=2 - [PYC_HUMAN]	3.24E-05	-6.4744	-2.8449	4.62E-05	-6.3967	-4.8219
2_5	P30613	Pyruvate kinase isozymes R/L OS=Homo sapiens GN=PKLR PE=1 SV=2 - [KPYR_HUMAN]	2.56E-06	-18.3184	-2.8332	7.49E-04	-4.1686	-3.3175
2_5	P46940	Ras GTPase-activating-like protein IQGAP1 OS=Homo sapiens GN=IQGAP1 PE=1 SV=1 - [IQGA1_HUMAN]	2.97E-06	11.5570	2.9488	1.73E-05	7.6272	4.0493
2_5	Q13576	Ras GTPase-activating-like protein IQGAP2 OS=Homo sapiens GN=IQGAP2 PE=1 SV=4 - [IQGA2_HUMAN]	3.07E-03	-3.4433	-2.6976	4.34E-03	-3.0693	-2.7148
2_5	O75452	Retinol dehydrogenase 16 OS=Homo sapiens GN=RDH16 PE=1 SV=2 - [RDH16_HUMAN]	3.39E-04	-5.4067	-2.7982	1.68E-03	-3.5966	-2.3593
2_5	P02753	Retinol-binding protein 4 OS=Homo sapiens GN=RBP4 PE=1 SV=3 - [RET4_HUMAN]	2.82E-06	-15.3927	-2.8141	2.75E-04	-4.8337	-2.4944
2_5	Q07960	Rho GTPase-activating protein 1 OS=Homo sapiens GN=ARHGAP1 PE=1 SV=1 - [RHG01_HUMAN]	7.93E-04	3.9075	2.7838	3.94E-04	4.6015	2.2357
2_5	P52758	Ribonuclease UK114 OS=Homo sapiens GN=HRSP12 PE=1 SV=1 - [UK114_HUMAN]	4.29E-04	-4.7551	-2.9118	9.79E-05	-5.5891	-3.3825
2_5	Q9Y265	RuvB-like 1 OS=Homo sapiens GN=RUVBL1 PE=1 SV=1 - [RUVB1_HUMAN]	1.72E-04	5.7997	2.7167	4.76E-04	4.4576	2.4022
2_5	Q6NBX0	Saccharopine dehydrogenase-like oxidoreductase OS=Homo sapiens GN=SCCPDH PE=1 SV=1 - [SCPDL_HUMAN]	4.30E-03	-3.0792	-2.8219	5.16E-05	-6.2207	-2.7268
2_5	Q00266	S-adenosylmethionine synthase isoform type-1 OS=Homo sapiens GN=MAT1A PE=1 SV=2 - [METK1_HUMAN]	2.86E-06	-13.5038	-2.8606	1.34E-03	-3.7415	-2.8628
2_5	Q9UL12	Sarcosine dehydrogenase, mitochondrial OS=Homo sapiens GN=SARDH PE=1 SV=1 - [SARDH_HUMAN]	2.71E-04	-5.6627	-2.7883	5.60E-04	-4.3623	-3.1624
2_5	Q15019	Septin-2 OS=Homo sapiens GN=SEPT2 PE=1 SV=1 - [SEPT2_HUMAN]	7.99E-04	3.9018	2.8024	3.43E-04	4.7148	2.2193
2_5	Q9UHD8	Septin-9 OS=Homo sapiens GN=SEPT9 PE=1 SV=2 - [SEPT9_HUMAN]	1.22E-03	3.8253	2.8003	2.14E-03	3.4649	2.5491
2_5	P34896	Serine hydroxymethyltransferase, cytosolic OS=Homo sapiens GN=SHMT1 PE=1 SV=1 - [GLYC_HUMAN]	2.36E-04	-5.7514	-2.8595	8.85E-04	-4.0341	-3.6455
2_5	P21549	Serine--pyruvate aminotransferase OS=Homo sapiens GN=AGXT PE=1 SV=1 - [SPYA_HUMAN]	4.91E-03	-2.9321	-3.0092	1.23E-04	-5.3808	-6.0079
2_5	P45954	Short/branched chain specific acyl-CoA dehydrogenase, mitochondrial OS=Homo sapiens GN=ACADSB PE=1 SV=1 - [ACDSB_HUMAN]	2.84E-06	-14.5552	-2.8717	8.03E-06	-8.9809	-3.3069
2_5	Q00796	Sorbitol dehydrogenase OS=Homo sapiens GN=SORD PE=1 SV=4 - [DHSO_HUMAN]	9.00E-06	-6.9697	-2.8382	1.03E-03	-3.9261	-3.5460
2_5	O75533	Splicing factor 3B subunit 1 OS=Homo sapiens GN=SF3B1 PE=1 SV=3 - [SF3B1_HUMAN]	4.54E-03	3.0127	2.7362	9.56E-04	3.9832	2.1652
2_5	Q14247	Src substrate cortactin OS=Homo sapiens GN=CTTN PE=1 SV=2 - [SRC8_HUMAN]	1.08E-03	3.8411	2.7452	1.08E-02	2.6370	2.1127

Fig. 7 continued

2_5	Q02318	Sterol 26-hydroxylase, mitochondrial OS=Homo sapiens GN=CYP27A1 PE=1 SV=1 - [CP27A_HUMAN]	2.83E-06	-14.8968	-2.7763	7.99E-04	-4.1259	-2.4391
2_5	P51649	Succinate-semialdehyde dehydrogenase, mitochondrial OS=Homo sapiens GN=ALDH5A1 PE=1 SV=2 - [SSDH_HUMAN]	2.88E-04	-5.5947	-2.7755	4.76E-04	-4.4576	-3.2534
2_5	P24821	Tenascin OS=Homo sapiens GN=TNC PE=1 SV=3 - [TENA_HUMAN]	1.15E-02	2.6838	2.7562	1.91E-02	2.3448	3.3713
2_5	P07996	Thrombospondin-1 OS=Homo sapiens GN=THBS1 PE=1 SV=2 - [TSP1_HUMAN]	3.34E-03	3.3645	2.7621	6.07E-03	2.8909	2.2012
2_5	Q13263	Transcription intermediary factor 1-beta OS=Homo sapiens GN=TRIM28 PE=1 SV=5 - [TIF1B_HUMAN]	1.49E-04	5.8380	2.7946	2.41E-03	3.4092	2.9117
2_5	Q13509	Tubulin beta-3 chain OS=Homo sapiens GN=TUBB3 PE=1 SV=2 - [TBB3_HUMAN]	1.29E-03	3.8155	2.9858	7.76E-03	2.7685	5.1341
2_5	P04350	Tubulin beta-4A chain OS=Homo sapiens GN=TUBB4A PE=1 SV=2 - [TBB4A_HUMAN]	1.33E-04	5.8533	3.0176	8.88E-05	5.6851	5.9854
2_5	Q9BUF5	Tubulin beta-6 chain OS=Homo sapiens GN=TUBB6 PE=1 SV=1 - [TBB6_HUMAN]	1.30E-03	3.8146	2.9867	1.37E-03	3.7252	4.9018
2_5	O43399	Tumor protein D54 OS=Homo sapiens GN=TPD52L2 PE=1 SV=2 - [TPD54_HUMAN]	2.43E-03	3.6388	2.8424	8.49E-04	4.0721	2.3713
2_5	P22310	UDP-glucuronosyltransferase 1-4 OS=Homo sapiens GN=UGT1A4 PE=1 SV=1 - [UD14_HUMAN]	3.10E-04	-5.4923	-2.8845	8.06E-04	-4.1140	-2.9086
2_5	P06133	UDP-glucuronosyltransferase 2B4 OS=Homo sapiens GN=UGT2B4 PE=1 SV=2 - [UD2B4_HUMAN]	2.85E-06	-14.0468	-2.7905	8.84E-04	-4.0358	-2.7008
2_5	P16662	UDP-glucuronosyltransferase 2B7 OS=Homo sapiens GN=UGT2B7 PE=1 SV=1 - [UD2B7_HUMAN]	3.29E-04	-5.4286	-2.7992	3.05E-03	-3.2828	-2.7316
2_5	Q96QK1	Vacuolar protein sorting-associated protein 35 OS=Homo sapiens GN=VPS35 PE=1 SV=2 - [VPS35_HUMAN]	1.88E-02	2.3834	2.7386	6.44E-04	4.2556	2.7501
2_5	P13611	Versican core protein OS=Homo sapiens GN=VCAN PE=1 SV=3 - [CSPG2_HUMAN]	5.77E-05	6.0836	2.9521	1.16E-04	5.4294	3.7501
2_6	P31947	14-3-3 protein sigma OS=Homo sapiens GN=SFN PE=1 SV=1 - [1433S_HUMAN]	2.02E-03	3.7849	3.2798	1.44E-03	3.6117	3.1797
2_6	O14756	17-beta-hydroxysteroid dehydrogenase type 6 OS=Homo sapiens GN=RSDT7B6 PE=1 SV=1 - [H17B6_HUMAN]	1.90E-05	-14.5723	-2.8648	2.61E-06	-8.8102	-3.5460
2_6	P12694	2-oxoisovalerate dehydrogenase subunit alpha, mitochondrial OS=Homo sapiens GN=BCKDHA PE=1 SV=2 - [ODBA_HUMAN]	2.02E-03	-3.7847	-2.6657	2.08E-02	-2.2920	-2.7159
2_6	P31937	3-hydroxyisobutyrate dehydrogenase, mitochondrial OS=Homo sapiens GN=HIBADH PE=1 SV=2 - [3HIDH_HUMAN]	7.92E-04	-4.5690	-2.7853	3.07E-04	-4.4768	-3.3175
2_6	P42765	3-ketoacyl-CoA thiolase, mitochondrial OS=Homo sapiens GN=ACAA2 PE=1 SV=2 - [THIM_HUMAN]	3.12E-03	-3.6728	-2.9265	9.81E-06	-7.2673	-5.0277
2_6	P09110	3-ketoacyl-CoA thiolase, peroxisomal OS=Homo sapiens GN=ACAA1 PE=1 SV=2 - [THIK_HUMAN]	7.77E-04	-4.5905	-2.9069	9.92E-05	-5.1622	-4.5886
2_6	P80404	4-aminobutyrate aminotransferase, mitochondrial OS=Homo sapiens GN=ABAT PE=1 SV=3 - [GABT_HUMAN]	3.22E-05	-13.2667	-2.9460	4.72E-05	-5.6401	-4.6929
2_6	P32754	4-hydroxyphenylpyruvate dioxygenase OS=Homo sapiens GN=HPD PE=1 SV=2 - [HPPD_HUMAN]	3.68E-05	-12.6416	-2.8898	1.93E-04	-4.7439	-4.7268
2_6	P49189	4-trimethylaminobutyraldehyde dehydrogenase OS=Homo sapiens GN=ALDH9A1 PE=1 SV=3 - [AL9A1_HUMAN]	1.50E-02	-2.6776	-2.7721	7.15E-03	-2.7955	-2.1159
2_6	Q9BWD1	Acetyl-CoA acetyltransferase, cytosolic OS=Homo sapiens GN=ACAT2 PE=1 SV=2 - [THIC_HUMAN]	2.19E-03	-3.7621	-2.7071	2.87E-03	-3.2615	-2.6394
2_6	O15143	Actin-related protein 2/3 complex subunit 1B OS=Homo sapiens GN=ARPC1B PE=1 SV=3 - [ARC1B_HUMAN]	6.01E-04	4.8978	3.1098	1.53E-03	3.5720	2.0642
2_6	Q08AH3	Acyl-coenzyme A synthetase ACSM2A, mitochondrial OS=Homo sapiens GN=ACSM2A PE=1 SV=2 - [ACS2A_HUMAN]	6.71E-06	-16.0532	-2.8285	1.70E-04	-4.8093	-4.3769
2_6	Q6BCK6	Acyl-coenzyme A synthetase ACSM2B, mitochondrial OS=Homo sapiens GN=ACSM2B PE=1 SV=2 - [ACS2B_HUMAN]	8.71E-06	-15.6889	-2.8285	4.58E-05	-5.6594	-4.4100
2_6	Q8IUX7	Adipocyte enhancer-binding protein 1 OS=Homo sapiens GN=AEBP1 PE=1 SV=1 - [AEBP1_HUMAN]	3.21E-04	5.5874	3.0447	1.29E-02	2.5302	2.1194
2_6	P24298	Alanine aminotransferase 1 OS=Homo sapiens GN=GPT PE=1 SV=3 - [ALAT1_HUMAN]	4.22E-04	-5.3706	-2.7134	4.51E-04	-4.2661	-3.5153
2_6	P08319	Alcohol dehydrogenase 4 OS=Homo sapiens GN=ADH4 PE=1 SV=5 - [ADH4_HUMAN]	3.58E-05	-12.7989	-2.8967	5.14E-03	-2.9601	-4.8219
2_6	Q9H2A2	Aldehyde dehydrogenase family 8 member A1 OS=Homo sapiens GN=ALDH8A1 PE=1 SV=1 - [AL8A1_HUMAN]	2.99E-04	-5.6224	-2.7885	1.40E-04	-4.9419	-2.3323
2_6	Q06278	Aldehyde oxidase OS=Homo sapiens GN=AOX1 PE=2 SV=2 - [ADO_HUMAN]	2.59E-03	-3.7191	-2.7288	2.06E-02	-2.2971	-3.3236

Fig. 7 continued

2.6	Q04828	Aldo-keto reductase family 1 member C1 OS=Homo sapiens GN=AKR1C1 PE=1 SV=1 - [AK1C1_HUMAN]	5.81E-03	-3.0995	-2.9553	6.67E-04	-4.0541	-4.7056
2.6	P52895	Aldo-keto reductase family 1 member C2 OS=Homo sapiens GN=AKR1C2 PE=1 SV=3 - [AK1C2_HUMAN]	2.77E-03	-3.7077	-2.9553	8.97E-03	-2.6872	-4.3506
2.6	P17516	Aldo-keto reductase family 1 member C4 OS=Homo sapiens GN=AKR1C4 PE=1 SV=3 - [AK1C4_HUMAN]	3.54E-04	-5.5171	-2.9196	1.80E-04	-4.7877	-3.9866
2.6	P04217	Alpha-1B-glycoprotein OS=Homo sapiens GN=A1BG PE=1 SV=4 - [A1BG_HUMAN]	2.12E-03	3.7715	3.1231	1.73E-02	2.3856	2.8011
2.6	Q03154	Aminoacylase-1 OS=Homo sapiens GN=ACY1 PE=1 SV=1 - [ACY1_HUMAN]	1.04E-05	-15.5149	-2.9370	6.14E-05	-5.4332	-4.3069
2.6	P12429	Annexin A3 OS=Homo sapiens GN=ANXA3 PE=1 SV=3 - [ANXA3_HUMAN]	4.96E-05	7.5070	3.1295	1.99E-05	6.3399	3.1797
2.6	O95994	Anterior gradient protein 2 homolog OS=Homo sapiens GN=AGR2 PE=1 SV=1 - [AGR2_HUMAN]	1.19E-03	4.1536	3.1957	3.68E-03	3.1348	3.6814
2.6	O95831	Apoptosis-inducing factor 1, mitochondrial OS=Homo sapiens GN=AIFM1 PE=1 SV=1 - [AIFM1_HUMAN]	1.20E-03	-4.1415	-2.8141	2.30E-05	-6.1899	-3.7008
2.6	P05089	Arginase-1 OS=Homo sapiens GN=ARG1 PE=1 SV=2 - [ARG1_HUMAN]	2.66E-05	-13.8063	-2.9120	7.87E-05	-5.2734	-4.5199
2.6	P22760	Arylacetamide deacetylase OS=Homo sapiens GN=AADAC PE=1 SV=5 - [AAAD_HUMAN]	2.90E-04	-5.6321	-2.6962	6.79E-03	-2.8267	-2.6394
2.6	Q9BXN1	Asporin OS=Homo sapiens GN=ASPN PE=1 SV=2 - [ASPN_HUMAN]	1.65E-05	14.7798	3.1279	1.05E-04	5.1185	2.6491
2.6	P13929	Beta-enolase OS=Homo sapiens GN=ENO3 PE=1 SV=5 - [ENOB_HUMAN]	1.13E-02	-2.7577	-2.8908	1.60E-02	-2.4241	-2.5460
2.6	Q93088	Betaine--homocysteine S-methyltransferase 1 OS=Homo sapiens GN=BHMT PE=1 SV=2 - [BHMT1_HUMAN]	4.17E-04	-5.3788	-2.8536	1.17E-03	-3.7147	-3.9443
2.6	Q9UBR1	Beta-ureidopropionase OS=Homo sapiens GN=UPB1 PE=1 SV=1 - [BUP1_HUMAN]	3.79E-04	-5.4510	-2.7768	2.45E-03	-3.3534	-2.3236
2.6	P34913	Bifunctional epoxide hydrolase 2 OS=Homo sapiens GN=EPHX2 PE=1 SV=2 - [HYES_HUMAN]	3.98E-06	-16.8141	-2.7439	2.85E-05	-6.0466	-2.0114
2.6	P31939	Bifunctional purine biosynthesis protein PURH OS=Homo sapiens GN=ATIC PE=1 SV=3 - [PURH_HUMAN]	4.73E-02	2.0547	2.8685	3.32E-02	2.0700	2.3786
2.6	P21810	Biglycan OS=Homo sapiens GN=BGN PE=1 SV=2 - [PGS1_HUMAN]	2.66E-04	5.6548	3.2174	4.20E-04	4.3061	4.6606
2.6	Q14032	Bile acid-CoA:amino acid N-acyltransferase OS=Homo sapiens GN=BAAT PE=1 SV=1 - [BAAT_HUMAN]	2.73E-05	-13.5177	-2.8539	1.76E-05	-6.5942	-2.6218
2.6	Q9Y2P5	Bile acyl-CoA synthetase OS=Homo sapiens GN=SLC27A5 PE=1 SV=1 - [S27A5_HUMAN]	3.82E-04	-5.4430	-2.7777	8.49E-04	-3.8922	-3.5460
2.6	Q06520	Bile salt sulfotransferase OS=Homo sapiens GN=SULT2A1 PE=1 SV=3 - [ST2A1_HUMAN]	1.69E-05	-14.7411	-2.9192	1.09E-05	-6.9258	-4.0747
2.6	P11586	C-1-tetrahydrofolate synthase, cytoplasmic OS=Homo sapiens GN=MTHFD1 PE=1 SV=3 - [C1TC_HUMAN]	4.76E-03	-3.3233	-2.8443	2.51E-04	-4.5837	-4.6455
2.6	Q9UJS0	Calcium-binding mitochondrial carrier protein Aralar2 OS=Homo sapiens GN=SLC25A13 PE=1 SV=2 - [CMC2_HUMAN]	1.41E-03	-3.9605	-2.8168	6.74E-06	-7.7701	-3.6813
2.6	P17655	Calpain-2 catalytic subunit OS=Homo sapiens GN=CAPN2 PE=1 SV=6 - [CAN2_HUMAN]	3.28E-04	5.5739	2.7966	1.83E-03	3.5107	3.2821
2.6	P31327	Carbamoyl-phosphate synthase [ammonia], mitochondrial OS=Homo sapiens GN=CPS1 PE=1 SV=2 - [CPSM_HUMAN]	1.53E-03	-3.8952	-3.0320	2.26E-05	-6.2273	-7.5266
2.6	P23786	Carnitine O-palmitoyltransferase 2, mitochondrial OS=Homo sapiens GN=CPT2 PE=1 SV=2 - [CPT2_HUMAN]	3.53E-05	-12.8369	-2.7694	2.19E-03	-3.4185	-3.0755
2.6	P35221	Catenin alpha-1 OS=Homo sapiens GN=CTNNA1 PE=1 SV=1 - [CTNA1_HUMAN]	2.32E-02	2.3663	2.7404	2.46E-02	2.2652	2.6767
2.6	P08311	Cathepsin G OS=Homo sapiens GN=CTSG PE=1 SV=2 - [CATG_HUMAN]	5.27E-03	3.2070	3.1916	2.10E-02	2.2669	2.9939
2.6	P00450	Ceruloplasmin OS=Homo sapiens GN=CP PE=1 SV=1 - [CERU_HUMAN]	9.54E-04	4.3841	3.1911	6.78E-04	4.0415	2.5624
2.6	O00748	Cocaine esterase OS=Homo sapiens GN=CES2 PE=1 SV=1 - [EST2_HUMAN]	2.95E-05	-13.4498	-2.8874	2.26E-03	-3.4057	-3.3789
2.6	Q99715	Collagen alpha-1(XII) chain OS=Homo sapiens GN=COL12A1 PE=1 SV=2 - [COCA1_HUMAN]	5.01E-04	5.2139	2.7725	1.98E-02	2.3219	3.8564
2.6	Q05707	Collagen alpha-1(XIV) chain OS=Homo sapiens GN=COL14A1 PE=1 SV=3 - [COEA1_HUMAN]	3.17E-04	5.5956	3.0884	1.26E-04	5.0039	4.4792
2.6	P00751	Complement factor B OS=Homo sapiens GN=CFB PE=1 SV=2 - [CFAB_HUMAN]	1.05E-03	4.2805	3.1180	9.60E-05	5.1731	3.2664

Fig. 7 continued

2 6	P31146	Coronin-1A OS=Homo sapiens GN=CORO1A PE=1 SV=4 - [COR1A_HUMAN]	2.11E-03	3.7736	2.8914	7.45E-04	3.9837	2.1194
2 6	P28845	Corticosteroid 11-beta-dehydrogenase isozyme 1 OS=Homo sapiens GN=HSD11B1 PE=1 SV=3 - [DHI1_HUMAN]	3.72E-04	-5.4732	-2.7739	1.49E-04	-4.8962	-2.2673
2 6	P12532	Creatine kinase U-type, mitochondrial OS=Homo sapiens GN=CKMT1A PE=1 SV=1 - [KCRU_HUMAN]	2.74E-03	3.7681	2.8880	5.56E-03	2.9246	2.1408
2 6	P32929	Cystathionine gamma-lyase OS=Homo sapiens GN=CTH PE=1 SV=3 - [CGL_HUMAN]	4.07E-04	-5.3896	-2.7750	8.87E-03	-2.6944	-2.7316
2 6	P21291	Cysteine and glycine-rich protein 1 OS=Homo sapiens GN=CSRP1 PE=1 SV=3 - [CSRP1_HUMAN]	2.33E-03	3.7485	3.1342	4.36E-03	3.0437	2.4941
2 6	P00167	Cytochrome b5 OS=Homo sapiens GN=CYB5A PE=1 SV=2 - [CYB5_HUMAN]	4.59E-03	-3.3760	-2.9940	7.58E-05	-5.3045	-3.5964
2 6	P11509	Cytochrome P450 2A6 OS=Homo sapiens GN=CYP2A6 PE=1 SV=3 - [CP2A6_HUMAN]	1.11E-05	-15.4599	-2.8972	3.04E-03	-3.2368	-3.6597
2 6	P11712	Cytochrome P450 2C9 OS=Homo sapiens GN=CYP2C9 PE=1 SV=3 - [CP2C9_HUMAN]	4.98E-04	-5.2236	-2.8364	3.01E-03	-3.2410	-3.7909
2 6	P05181	Cytochrome P450 2E1 OS=Homo sapiens GN=CYP2E1 PE=1 SV=1 - [CP2E1_HUMAN]	3.27E-03	-3.6489	-2.7621	1.74E-02	-2.3803	-2.9678
2 6	O75891	Cytosolic 10-formyltetrahydrofolate dehydrogenase OS=Homo sapiens GN=ALDH1L1 PE=1 SV=2 - [AL1L1_HUMAN]	3.53E-04	-5.5195	-2.8376	6.26E-03	-2.8688	-4.2534
2 6	Q02338	D-beta-hydroxybutyrate dehydrogenase, mitochondrial OS=Homo sapiens GN=BDH1 PE=1 SV=3 - [BDH_HUMAN]	1.38E-05	-14.9205	-2.8298	3.80E-06	-8.2936	-3.0118
2 6	P30046	D-dopachrome decarboxylase OS=Homo sapiens GN=DDT PE=1 SV=3 - [DOPD_HUMAN]	6.26E-03	-3.0233	-2.8921	6.26E-03	-2.8689	-2.7219
2 6	P07585	Decorin OS=Homo sapiens GN=DCN PE=1 SV=1 - [PGS2_HUMAN]	2.74E-05	13.5119	3.1399	4.36E-05	5.6942	3.3048
2 6	P30038	Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial OS=Homo sapiens GN=ALDH4A1 PE=1 SV=3 - [AL4A1_HUMAN]	6.91E-05	-6.8662	-2.8957	1.01E-05	-7.1752	-4.3593
2 6	Q07507	Dermatopontin OS=Homo sapiens GN=DPT PE=2 SV=2 - [DERM_HUMAN]	4.26E-04	5.3666	3.1511	2.84E-05	6.0481	2.7366
2 6	P09417	Dihydropteridine reductase OS=Homo sapiens GN=QDPR PE=1 SV=2 - [DHPR_HUMAN]	3.77E-04	-5.4556	-2.7510	1.75E-03	-3.5306	-2.5460
2 6	Q14117	Dihydropyrimidinase OS=Homo sapiens GN=DPYS PE=1 SV=1 - [DPYS_HUMAN]	2.48E-04	-5.6984	-2.8922	6.64E-04	-4.0569	-2.1159
2 6	Q16555	Dihydropyrimidinase-related protein 2 OS=Homo sapiens GN=DPYSL2 PE=1 SV=1 - [DPYL2_HUMAN]	5.26E-04	5.1013	3.1073	4.17E-04	4.3075	3.2173
2 6	Q14195	Dihydropyrimidinase-related protein 3 OS=Homo sapiens GN=DPYSL3 PE=1 SV=1 - [DPYL3_HUMAN]	3.36E-04	5.5511	3.0468	5.52E-04	4.1575	2.8564
2 6	P31513	Dimethylaniline monooxygenase [N-oxide-forming] 3 OS=Homo sapiens GN=FMO3 PE=1 SV=5 - [FMO3_HUMAN]	2.18E-05	-14.1915	-2.8470	4.14E-03	-3.0686	-2.4253
2 6	Q9UI17	Dimethylglycine dehydrogenase, mitochondrial OS=Homo sapiens GN=DMGDH PE=1 SV=2 - [M2GD_HUMAN]	2.77E-04	-5.6442	-2.7582	4.52E-03	-3.0281	-2.3323
2 6	Q12805	EGF-containing fibulin-like extracellular matrix protein 1 OS=Homo sapiens GN=EFEMP1 PE=1 SV=2 - [FBLN3_HUMAN]	1.40E-03	3.9645	2.7915	2.34E-03	3.3818	2.5392
2 6	O75521	Enoyl-CoA delta isomerase 2, mitochondrial OS=Homo sapiens GN=ECI2 PE=1 SV=4 - [ECI2_HUMAN]	2.19E-04	-5.8171	-2.7705	1.40E-03	-3.5966	-2.7939
2 6	P07099	Epoxide hydrolase 1 OS=Homo sapiens GN=EPHX1 PE=1 SV=1 - [HYEP_HUMAN]	5.63E-04	-4.9976	-3.0464	2.57E-06	-8.8593	-5.5825
2 6	Q9H0W9	Ester hydrolase C11orf54 OS=Homo sapiens GN=C11orf54 PE=1 SV=1 - [CK054_HUMAN]	9.92E-04	-4.3366	-2.7939	3.67E-04	-4.3709	-2.0627
2 6	P15311	Ezrin OS=Homo sapiens GN=EZR PE=1 SV=4 - [EZRI_HUMAN]	5.85E-03	3.0910	3.2246	4.84E-03	2.9900	4.0756
2 6	P07148	Fatty acid-binding protein, liver OS=Homo sapiens GN=FABP1 PE=1 SV=1 - [FABPL_HUMAN]	1.57E-03	-3.8809	-3.0514	2.37E-06	-9.0649	-4.8550
2 6	P23142	Fibulin-1 OS=Homo sapiens GN=FBLN1 PE=1 SV=4 - [FBLN1_HUMAN]	2.34E-05	14.1074	3.0170	1.34E-03	3.6488	2.7366
2 6	P30043	Flavin reductase (NADPH) OS=Homo sapiens GN=BLVRB PE=1 SV=3 - [BLVRB_HUMAN]	1.20E-02	-2.7474	-2.8100	9.25E-05	-5.1845	-3.0419
2 6	O95954	Formimidoyltransferase-cyclodeaminase OS=Homo sapiens GN=FTCD PE=1 SV=2 - [FTCD_HUMAN]	3.24E-05	-13.2613	-2.8156	2.81E-03	-3.2713	-4.0241
2 6	P16930	Fumarylacetoacetase OS=Homo sapiens GN=FAH PE=1 SV=2 - [FAAA_HUMAN]	2.23E-05	-14.1385	-2.8819	1.59E-05	-6.6758	-3.7219
2 6	P51570	Galactokinase OS=Homo sapiens GN=GALK1 PE=1 SV=1 - [GALK1_HUMAN]	1.71E-02	-2.6090	-2.7893	6.46E-03	-2.8634	-2.2554

Fig. 7 continued

2_6	P09382	Galectin-1 OS=Homo sapiens GN=LGALS1 PE=1 SV=2 - [LEG1_HUMAN]	6.18E-03	3.0357	2.9328	1.47E-03	3.6040	2.4956
2_6	Q08380	Galectin-3-binding protein OS=Homo sapiens GN=LGALS3BP PE=1 SV=1 - [LG3BP_HUMAN]	3.20E-03	3.6609	3.1195	6.34E-04	4.0824	3.4956
2_6	Q92820	Gamma-glutamyl hydrolase OS=Homo sapiens GN=GGH PE=1 SV=2 - [GGH_HUMAN]	2.13E-04	-5.8547	-2.7954	7.65E-03	-2.7605	-2.2462
2_6	O95479	GDH/6PGL endoplasmic bifunctional protein OS=Homo sapiens GN=H6PD PE=1 SV=2 - [G6PE_HUMAN]	1.79E-04	-6.0083	-2.7628	5.99E-04	-4.1135	-2.9678
2_6	Q13630	GDP-L-fucose synthase OS=Homo sapiens GN=TSTA3 PE=1 SV=1 - [FCL_HUMAN]	1.19E-03	4.1488	3.0881	8.40E-04	3.8986	2.0247
2_6	P08263	Glutathione S-transferase A1 OS=Homo sapiens GN=GSTA1 PE=1 SV=3 - [GSTA1_HUMAN]	5.39E-04	-4.9028	-3.0048	2.60E-03	-3.3192	-4.5966
2_6	P09488	Glutathione S-transferase Mu 1 OS=Homo sapiens GN=GSTM1 PE=1 SV=3 - [GSTM1_HUMAN]	1.65E-03	-3.8523	-2.8124	3.90E-03	-3.1062	-3.0118
2_6	P09211	Glutathione S-transferase P OS=Homo sapiens GN=GSTP1 PE=1 SV=2 - [GSTP1_HUMAN]	1.50E-03	3.8782	3.2108	1.15E-05	6.8998	4.9430
2_6	P50440	Glycine amidinotransferase, mitochondrial OS=Homo sapiens GN=GATM PE=1 SV=1 - [GATM_HUMAN]	6.30E-04	-4.8125	-2.9650	1.09E-03	-3.7561	-4.5520
2_6	P11216	Glycogen phosphorylase, brain form OS=Homo sapiens GN=PYGB PE=1 SV=5 - [PYGB_HUMAN]	8.31E-04	4.5294	3.1286	1.25E-03	3.6860	3.7910
2_6	P06737	Glycogen phosphorylase, liver form OS=Homo sapiens GN=PYGL PE=1 SV=4 - [PYGL_HUMAN]	9.42E-05	-6.5054	-2.8466	1.57E-05	-6.6799	-3.9678
2_6	Q9UJ7	GTP:AMP phosphotransferase, mitochondrial OS=Homo sapiens GN=AK3 PE=1 SV=4 - [KAD3_HUMAN]	6.85E-03	-2.9451	-2.8197	6.42E-04	-4.0748	-2.4373
2_6	P02790	Hemopexin OS=Homo sapiens GN=HPX PE=1 SV=2 - [HEMO_HUMAN]	4.78E-04	5.2821	3.2150	1.46E-04	4.9141	3.7044
2_6	O14979	Heterogeneous nuclear ribonucleoprotein D-like OS=Homo sapiens GN=HNRPDL PE=1 SV=3 - [HNRDL_HUMAN]	4.13E-03	3.5052	3.1433	2.69E-02	2.1662	2.5392
2_6	Q1KMD3	Heterogeneous nuclear ribonucleoprotein U-like protein 2 OS=Homo sapiens GN=HNRNPUL2 PE=1 SV=1 - [HNRL2_HUMAN]	5.03E-04	5.2050	3.1349	6.01E-04	4.1115	3.1156
2_6	Q7U1I9	Histone H2A.V OS=Homo sapiens GN=H2AFV PE=1 SV=3 - [H2AV_HUMAN]	2.90E-02	2.1800	3.2461	2.95E-02	2.1127	3.8564
2_6	P0C0S5	Histone H2A.Z OS=Homo sapiens GN=H2AFZ PE=1 SV=2 - [H2AZ_HUMAN]	2.90E-02	2.1800	3.2461	2.95E-02	2.1127	3.8564
2_6	Q93099	Homogentisate 1,2-dioxygenase OS=Homo sapiens GN=HGD PE=1 SV=2 - [HGD_HUMAN]	7.30E-05	-6.7962	-2.8230	2.11E-05	-6.2958	-4.0222
2_6	Q9UJM8	Hydroxyacid oxidase 1 OS=Homo sapiens GN=HAO1 PE=1 SV=1 - [HAOX1_HUMAN]	1.82E-05	-14.5838	-2.9012	9.99E-06	-7.2034	-4.6766
2_6	Q16836	Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial OS=Homo sapiens GN=HADH PE=1 SV=3 - [HCDH_HUMAN]	9.27E-04	-4.4150	-2.7695	4.57E-04	-4.2610	-2.4843
2_6	P35914	Hydroxymethylglutaryl-CoA lyase, mitochondrial OS=Homo sapiens GN=HMGCL PE=1 SV=2 - [HMGCL_HUMAN]	3.01E-04	-5.6212	-2.7659	1.70E-04	-4.8069	-2.4944
2_6	P54868	Hydroxymethylglutaryl-CoA synthase, mitochondrial OS=Homo sapiens GN=HMGCS2 PE=1 SV=1 - [HMCS2_HUMAN]	1.80E-04	-6.0038	-2.9989	6.37E-05	-5.4155	-4.6936
2_6	P19827	Inter-alpha-trypsin inhibitor heavy chain H1 OS=Homo sapiens GN=ITIH1 PE=1 SV=3 - [ITIH1_HUMAN]	5.18E-03	3.2237	3.0907	4.90E-03	2.9863	3.0247
2_6	Q96AB3	Isochorismatase domain-containing protein 2, mitochondrial OS=Homo sapiens GN=ISOC2 PE=1 SV=1 - [ISOC2_HUMAN]	6.93E-03	-2.9364	-2.8366	1.98E-03	-3.4769	-2.5520
2_6	P26440	Isovaleryl-CoA dehydrogenase, mitochondrial OS=Homo sapiens GN=IVD PE=1 SV=1 - [IVD_HUMAN]	8.49E-03	-2.8101	-2.7571	2.58E-03	-3.3231	-2.0747
2_6	P14923	Junction plakoglobin OS=Homo sapiens GN=JUP PE=1 SV=3 - [PLAK_HUMAN]	2.23E-03	3.7581	2.7845	6.92E-04	4.0287	2.3581
2_6	P08727	Keratin, type I cytoskeletal 19 OS=Homo sapiens GN=KRT19 PE=1 SV=4 - [K1C19_HUMAN]	3.43E-05	13.1564	3.3319	7.00E-04	4.0219	5.1859
2_6	P08729	Keratin, type II cytoskeletal 7 OS=Homo sapiens GN=KRT7 PE=1 SV=5 - [K2C7_HUMAN]	2.49E-03	3.7284	2.9343	1.20E-02	2.5703	3.4941
2_6	P02788	Lactotransferrin OS=Homo sapiens GN=LTF PE=1 SV=6 - [TRFL_HUMAN]	4.17E-03	3.4942	3.1986	5.16E-03	2.9590	5.0502
2_6	P23141	Liver carboxylesterase 1 OS=Homo sapiens GN=CES1 PE=1 SV=2 - [EST1_HUMAN]	1.16E-02	-2.7545	-3.0234	2.37E-05	-6.1649	-5.7751
2_6	P07195	L-lactate dehydrogenase B chain OS=Homo sapiens GN=LDHB PE=1 SV=2 - [LDHB_HUMAN]	7.78E-04	4.5894	3.2394	2.96E-04	4.5020	3.0737
2_6	P33121	Long-chain-fatty-acid--CoA ligase 1 OS=Homo sapiens GN=ACSL1 PE=1 SV=1 - [ACSL1_HUMAN]	1.31E-05	-15.0296	-2.8078	7.12E-07	-10.1533	-3.7481

Fig. 7 continued

2_6	P51884	Lumican OS=Homo sapiens GN=LUM PE=1 SV=2 - [LUM_HUMAN]	4.99E-04	5.2205	3.1354	1.39E-04	4.9469	4.4375
2_6	Q7Z4W1	L-xylulose reductase OS=Homo sapiens GN=DCXR PE=1 SV=2 - [DCXR_HUMAN]	6.13E-03	-3.0441	-2.9913	2.87E-04	-4.5181	-5.1500
2_6	P10253	Lysosomal alpha-glucosidase OS=Homo sapiens GN=GAA PE=1 SV=4 - [LYAG_HUMAN]	2.62E-02	-2.2656	-2.8348	7.25E-03	-2.7899	-2.7219
2_6	P61626	Lysozyme C OS=Homo sapiens GN=LYZ PE=1 SV=1 - [LYSC_HUMAN]	5.66E-03	3.1245	3.1166	7.59E-03	2.7657	2.3418
2_6	P40121	Macrophage-capping protein OS=Homo sapiens GN=CAPG PE=1 SV=2 - [CAPG_HUMAN]	4.70E-05	7.5409	3.1677	4.50E-05	5.6723	3.5451
2_6	Q14764	Major vault protein OS=Homo sapiens GN=MVP PE=1 SV=4 - [MVP_HUMAN]	5.32E-04	5.0825	3.1330	7.71E-05	5.2904	3.4363
2_6	P11310	Medium-chain specific acyl-CoA dehydrogenase, mitochondrial OS=Homo sapiens GN=ACADM PE=1 SV=1 - [ACADM_HUMAN]	3.83E-03	-3.5683	-2.8628	2.29E-09	-122106	-3.1863
2_6	O00264	Membrane-associated progesterone receptor component 1 OS=Homo sapiens GN=PGRMC1 PE=1 SV=3 - [PGRC1_HUMAN]	6.25E-04	-4.8378	-2.8734	1.67E-05	-6.6224	-3.9095
2_6	P51608	Methyl-CpG-binding protein 2 OS=Homo sapiens GN=MECP2 PE=1 SV=1 - [MECP2_HUMAN]	2.55E-02	2.2885	2.7403	2.19E-03	3.4186	2.0642
2_6	Q9HCC0	Methylcrotonoyl-CoA carboxylase beta chain, mitochondrial OS=Homo sapiens GN=MCCC2 PE=1 SV=1 - [MCCB_HUMAN]	1.38E-02	-2.7152	-2.7212	3.60E-03	-3.1467	-2.9866
2_6	Q02252	Methylmalonate-semialdehyde dehydrogenase [acylating], mitochondrial OS=Homo sapiens GN=ALDH6A1 PE=1 SV=2 - [MMSA_HUMAN]	3.01E-05	-13.3627	-2.8877	7.25E-05	-5.3301	-4.8374
2_6	Q9H8H3	Methyltransferase-like protein 7A OS=Homo sapiens GN=METTL7A PE=1 SV=1 - [METTA_HUMAN]	4.37E-06	-16.7897	-2.8084	5.68E-05	-5.4891	-2.0606
2_6	P55083	Microfibril-associated glycoprotein 4 OS=Homo sapiens GN=MFAP4 PE=1 SV=2 - [MFAP4_HUMAN]	1.29E-02	2.7317	2.8862	1.79E-02	2.3666	2.4941
2_6	P10620	Microsomal glutathione S-transferase 1 OS=Homo sapiens GN=MGST1 PE=1 SV=1 - [MGST1_HUMAN]	1.84E-05	-14.5806	-2.8540	8.03E-06	-7.3877	-2.4391
2_6	P55157	Microsomal triglyceride transfer protein large subunit OS=Homo sapiens GN=MTTP PE=1 SV=1 - [MTP_HUMAN]	4.12E-05	-11.4288	-2.7437	4.11E-06	-8.1044	-3.0747
2_6	P20774	Mimecan OS=Homo sapiens GN=OGN PE=1 SV=1 - [MIME_HUMAN]	4.38E-04	5.3354	2.8528	2.34E-03	3.3825	2.2866
2_6	Q9Y6C9	Mitochondrial carrier homolog 2 OS=Homo sapiens GN=MTCH2 PE=1 SV=1 - [MTCH2_HUMAN]	1.27E-05	-15.0542	-2.8105	2.29E-04	-4.6340	-2.9678
2_6	Q969Z3	MOSC domain-containing protein 2, mitochondrial OS=Homo sapiens GN=MARC2 PE=1 SV=1 - [MOSC2_HUMAN]	2.39E-05	-14.1039	-2.7157	1.58E-04	-4.8655	-2.5520
2_6	P98088	Mucin-5AC (Fragments) OS=Homo sapiens GN=MUC5AC PE=1 SV=3 - [MUC5A_HUMAN]	1.02E-02	2.7770	2.8309	4.64E-02	1.9316	3.6767
2_6	P05164	Myeloperoxidase OS=Homo sapiens GN=MPO PE=1 SV=1 - [PERM_HUMAN]	1.01E-04	6.4509	3.2360	1.77E-02	2.3728	3.6096
2_6	Q7Z406	Myosin-14 OS=Homo sapiens GN=MYH14 PE=1 SV=2 - [MYH14_HUMAN]	1.11E-02	2.7610	2.8608	1.13E-02	2.5900	3.3581
2_6	Q4G0N4	NAD kinase domain-containing protein 1 OS=Homo sapiens GN=NADKD1 PE=1 SV=2 - [NAKD1_HUMAN]	1.38E-05	-14.9263	-2.8631	5.70E-05	-5.4860	-2.7939
2_6	P16435	NADPH--cytochrome P450 reductase OS=Homo sapiens GN=POR PE=1 SV=2 - [NCPR_HUMAN]	3.04E-05	-13.3563	-2.8868	1.84E-04	-4.7781	-3.5681
2_6	P08246	Neutrophil elastase OS=Homo sapiens GN=ELANE PE=1 SV=1 - [ELNE_HUMAN]	6.19E-04	4.8521	3.1323	3.88E-02	2.0038	2.2664
2_6	Q15274	Nicotinate-nucleotide pyrophosphorylase [carboxylating] OS=Homo sapiens GN=QPRT PE=1 SV=3 - [NADC_HUMAN]	2.27E-05	-14.1170	-2.7679	5.04E-04	-4.2072	-2.3236
2_6	P22307	Non-specific lipid-transfer protein OS=Homo sapiens GN=SCP2 PE=1 SV=2 - [NLTP_HUMAN]	4.14E-04	-5.3823	-2.8208	3.75E-04	-4.3609	-3.3548
2_6	Q9NQR4	Omega-amidase NIT2 OS=Homo sapiens GN=NIT2 PE=1 SV=1 - [NIT2_HUMAN]	3.00E-02	-2.1541	-2.7870	5.04E-03	-2.9686	-2.2554
2_6	P00480	Ornithine carbamoyltransferase, mitochondrial OS=Homo sapiens GN=OTC PE=1 SV=3 - [OTC_HUMAN]	1.60E-05	-14.8728	-2.9020	4.91E-06	-7.9484	-4.1166
2_6	O60664	Perilipin-3 OS=Homo sapiens GN=PLIN3 PE=1 SV=3 - [PLIN3_HUMAN]	2.80E-03	3.7057	2.7541	2.69E-03	3.2955	2.3786
2_6	Q15063	Periostin OS=Homo sapiens GN=POSTN PE=1 SV=2 - [POSTN_HUMAN]	2.54E-05	13.9064	3.1496	1.57E-03	3.5761	4.0580
2_6	Q15067	Peroxisomal acyl-coenzyme A oxidase 1 OS=Homo sapiens GN=ACOX1 PE=1 SV=3 - [ACOX1_HUMAN]	2.89E-05	-13.4645	-2.7623	3.35E-04	-4.4140	-3.6013
2_6	Q9NP24	Peroxisomal acyl-coenzyme A oxidase 2 OS=Homo sapiens GN=ACOX2 PE=1 SV=1 - [ACOX2_HUMAN]	2.31E-05	-14.1095	-2.7478	2.32E-03	-3.3885	-3.1310

Fig. 7 continued

2_6	Q08426	Peroxisomal bifunctional enzyme OS=Homo sapiens GN=EHHADH PE=1 SV=3 - [ECHP_HUMAN]	3.81E-04	-5.4461	-2.9160	5.21E-05	-5.5574	-5.2498
2_6	Q9P0Z9	Peroxisomal sarcosine oxidase OS=Homo sapiens GN=PIPOX PE=2 SV=2 - [SOX_HUMAN]	2.03E-05	-14.4133	-2.8337	1.45E-05	-6.7133	-3.9173
2_6	Q16822	Phosphoenolpyruvate carboxykinase [GTP], mitochondrial OS=Homo sapiens GN=PCK2 PE=1 SV=3 - [PCKGM_HUMAN]	4.45E-04	-5.3308	-2.9075	1.24E-06	-9.3924	-5.1253
2_6	P01833	Polymeric immunoglobulin receptor OS=Homo sapiens GN=PIGR PE=1 SV=4 - [PIGR_HUMAN]	6.52E-03	2.9880	3.0703	1.56E-03	3.5768	3.4363
2_6	P05165	Propionyl-CoA carboxylase alpha chain, mitochondrial OS=Homo sapiens GN=PCCA PE=1 SV=4 - [PCCA_HUMAN]	1.90E-04	-5.8775	-2.7089	2.14E-03	-3.4346	-2.2462
2_6	P05166	Propionyl-CoA carboxylase beta chain, mitochondrial OS=Homo sapiens GN=PCCB PE=1 SV=3 - [PCCB_HUMAN]	3.21E-03	-3.6605	-2.7141	4.73E-04	-4.2436	-3.0118
2_6	Q14914	Prostaglandin reductase 1 OS=Homo sapiens GN=PTGR1 PE=1 SV=2 - [PTGR1_HUMAN]	1.29E-04	-6.2689	-2.8204	2.07E-04	-4.6878	-3.3166
2_6	Q9BPW8	Protein NipSnap homolog 1 OS=Homo sapiens GN=NIPSNAP1 PE=1 SV=1 - [NPS1_HUMAN]	1.36E-03	-4.0076	-2.8331	1.82E-05	-6.4347	-2.9866
2_6	P29590	Protein PML OS=Homo sapiens GN=PML PE=1 SV=3 - [PML_HUMAN]	2.51E-03	3.7262	2.7478	1.96E-03	3.4809	2.6767
2_6	P31949	Protein S100-A11 OS=Homo sapiens GN=S100A11 PE=1 SV=2 - [S10AB_HUMAN]	4.54E-04	5.3180	2.8902	5.83E-04	4.1337	2.2531
2_6	P06703	Protein S100-A6 OS=Homo sapiens GN=S100A6 PE=1 SV=1 - [S10A6_HUMAN]	5.73E-05	7.0941	3.1658	2.29E-04	4.6348	2.7044
2_6	P07737	Profilin-1 OS=Homo sapiens GN=PFN1 PE=1 SV=2 - [PROF1_HUMAN]	7.45E-03	2.8769	3.0942	2.56E-02	2.1857	2.2173
2_6	Q9NVS9	Pyridoxine-5-phosphate oxidase OS=Homo sapiens GN=PNPO PE=1 SV=1 - [PNPO_HUMAN]	3.49E-05	-12.8685	-2.8059	9.49E-05	-5.1757	-2.4373
2_6	P11498	Pyruvate carboxylase, mitochondrial OS=Homo sapiens GN=PC PE=1 SV=2 - [PYC_HUMAN]	3.11E-05	-13.3228	-2.8449	1.83E-05	-6.4269	-4.8219
2_6	P30613	Pyruvate kinase isozymes R/L OS=Homo sapiens GN=PKLR PE=1 SV=2 - [KPYR_HUMAN]	4.65E-07	-18.3184	-2.8332	5.41E-04	-4.1686	-3.3175
2_6	P31150	Rab GDP dissociation inhibitor alpha OS=Homo sapiens GN=GDI1 PE=1 SV=2 - [GDIA_HUMAN]	1.49E-02	2.6823	2.8427	1.07E-02	2.6128	3.2173
2_6	P46940	Ras GTPase-activating-like protein IQGAP1 OS=Homo sapiens GN=IQGAP1 PE=1 SV=1 - [IQGA1_HUMAN]	5.33E-06	16.2604	3.1140	6.34E-04	4.0826	4.4285
2_6	O75462	Retinol dehydrogenase 16 OS=Homo sapiens GN=RDH16 PE=1 SV=2 - [RDH16_HUMAN]	4.01E-04	-5.4067	-2.7982	1.48E-03	-3.5966	-2.3593
2_6	P02753	Retinol-binding protein 4 OS=Homo sapiens GN=RBP4 PE=1 SV=3 - [RET4_HUMAN]	5.54E-04	-5.0213	-2.8141	1.64E-04	-4.8337	-2.4944
2_6	Q07960	Rho GTPase-activating protein 1 OS=Homo sapiens GN=ARHGAP1 PE=1 SV=1 - [RHG01_HUMAN]	1.46E-03	3.9328	2.7972	1.26E-03	3.6817	2.0642
2_6	P52758	Ribonuclease UK114 OS=Homo sapiens GN=HRSP12 PE=1 SV=1 - [UK114_HUMAN]	5.74E-05	-7.0931	-2.9118	5.54E-05	-5.5102	-3.3825
2_6	Q8NBX0	Saccharopine dehydrogenase-like oxidoreductase OS=Homo sapiens GN=SCCPDH PE=1 SV=1 - [SCPDL_HUMAN]	5.86E-04	-4.9275	-2.8219	5.74E-06	-7.8651	-2.7268
2_6	Q00266	S-adenosylmethionine synthase isoform type-1 OS=Homo sapiens GN=MAT1A PE=1 SV=2 - [METK1_HUMAN]	2.79E-05	-13.5038	-2.8606	1.12E-03	-3.7415	-2.8628
2_6	Q8IUL12	Sarcosine dehydrogenase, mitochondrial OS=Homo sapiens GN=SARDH PE=1 SV=1 - [SARDH_HUMAN]	2.62E-04	-5.6627	-2.7883	3.74E-04	-4.3623	-3.1624
2_6	Q15019	Septin-2 OS=Homo sapiens GN=SEPT2 PE=1 SV=1 - [SEPT2_HUMAN]	1.41E-02	2.7066	2.7704	1.08E-03	3.7615	2.2173
2_6	Q9UHD8	Septin-9 OS=Homo sapiens GN=SEPT9 PE=1 SV=2 - [SEPT9_HUMAN]	1.72E-03	3.8404	2.8028	7.84E-03	2.7479	2.1194
2_6	P34896	Serine hydroxymethyltransferase, cytosolic OS=Homo sapiens GN=SHMT1 PE=1 SV=1 - [GLYC_HUMAN]	9.21E-06	-15.7261	-2.8595	3.17E-04	-4.4546	-3.6455
2_6	P34897	Serine hydroxymethyltransferase, mitochondrial OS=Homo sapiens GN=SHMT2 PE=1 SV=3 - [GLYM_HUMAN]	5.54E-03	-3.1479	-2.8161	9.56E-07	-9.7790	-3.4589
2_6	P21549	Serine--pyruvate aminotransferase OS=Homo sapiens GN=AGXT PE=1 SV=1 - [SPYA_HUMAN]	4.04E-04	-5.3953	-3.0092	5.17E-05	-5.5824	-6.0079
2_6	P35237	Serpin B6 OS=Homo sapiens GN=SERPINB6 PE=1 SV=3 - [SPB6_HUMAN]	5.00E-03	3.2627	3.0736	4.78E-02	1.9176	2.0642
2_6	P45954	Short/branched chain specific acyl-CoA dehydrogenase, mitochondrial OS=Homo sapiens GN=ACADSB PE=1 SV=1 - [ACDSB_HUMAN]	1.90E-05	-14.5552	-2.8717	2.48E-06	-8.9809	-3.3069
2_6	Q9H9B4	Sideroflexin-1 OS=Homo sapiens GN=SFXN1 PE=1 SV=4 - [SFXN1_HUMAN]	7.77E-04	-4.5970	-2.7687	9.26E-05	-5.1839	-2.4391

Fig. 7 continued

2_6	Q00796	Sorbitol dehydrogenase OS=Homo sapiens GN=SORD PE=1 SV=4 - [DHSO_HUMAN]	6.71E-05	-6.9022	-2.8392	8.13E-04	-3.9261	-3.5460
2_6	Q14247	Src substrate cortactin OS=Homo sapiens GN=CTTN PE=1 SV=2 - [SRC8_HUMAN]	2.42E-03	3.7393	2.7135	5.03E-03	2.9698	2.2061
2_6	Q02318	Sterol 26-hydroxylase, mitochondrial OS=Homo sapiens GN=CYP27A1 PE=1 SV=1 - [CP27A_HUMAN]	1.52E-05	-14.8968	-2.7763	5.90E-04	-4.1259	-2.4391
2_6	P31040	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial OS=Homo sapiens GN=SDHA PE=1 SV=2 - [DHSA_HUMAN]	4.16E-03	-3.4981	-2.7491	3.42E-03	-3.1738	-2.4944
2_6	P51649	Succinate-semialdehyde dehydrogenase, mitochondrial OS=Homo sapiens GN=ALDH5A1 PE=1 SV=2 - [SSDH_HUMAN]	1.37E-04	-6.2183	-2.7755	7.41E-06	-7.4581	-3.2534
2_6	P53007	Tricarboxylate transport protein, mitochondrial OS=Homo sapiens GN=SLC25A1 PE=1 SV=2 - [TXTP_HUMAN]	2.13E-04	-5.8546	-2.7448	1.20E-03	-3.7011	-2.1981
2_6	Q15661	Tryptase alpha/beta-1 OS=Homo sapiens GN=TPSAB1 PE=1 SV=1 - [TRYB1_HUMAN]	5.46E-05	7.1720	3.1732	1.58E-03	3.5735	3.6971
2_6	Q71U36	Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1 - [TBA1A_HUMAN]	2.40E-03	3.7421	3.0309	7.16E-03	2.7949	5.4652
2_6	Q13509	Tubulin beta-3 chain OS=Homo sapiens GN=TUBB3 PE=1 SV=2 - [TBB3_HUMAN]	2.57E-03	3.7205	2.9906	9.17E-04	3.8370	5.3253
2_6	O43399	Tumor protein D54 OS=Homo sapiens GN=TPD52L2 PE=1 SV=2 - [TPD54_HUMAN]	2.09E-02	2.4579	2.7959	2.89E-03	3.2583	2.3752
2_6	P22310	UDP-glucuronosyltransferase 1-4 OS=Homo sapiens GN=UGT1A4 PE=1 SV=1 - [UD14_HUMAN]	3.61E-04	-5.4923	-2.8845	5.99E-04	-4.1140	-2.9086
2_6	O60656	UDP-glucuronosyltransferase 1-9 OS=Homo sapiens GN=UGT1A9 PE=1 SV=1 - [UD19_HUMAN]	9.85E-03	-2.7835	-2.8097	9.94E-03	-2.6519	-2.4391
2_6	P06133	UDP-glucuronosyltransferase 2B4 OS=Homo sapiens GN=UGT2B4 PE=1 SV=2 - [UD2B4_HUMAN]	2.47E-05	-14.0468	-2.7905	6.84E-04	-4.0358	-2.7008
2_6	P16662	UDP-glucuronosyltransferase 2B7 OS=Homo sapiens GN=UGT2B7 PE=1 SV=1 - [UD2B7_HUMAN]	3.88E-04	-5.4286	-2.7992	2.75E-03	-3.2828	-2.7316
2_6	Q96QK1	Vacuolar protein sorting-associated protein 35 OS=Homo sapiens GN=VPS35 PE=1 SV=2 - [VPS35_HUMAN]	8.56E-04	4.4902	3.0105	3.95E-03	3.1003	2.7005
2_6	P13611	Versican core protein OS=Homo sapiens GN=VCAN PE=1 SV=3 - [CSPG2_HUMAN]	4.79E-05	7.5253	3.1785	1.11E-03	3.7471	4.0190
2_6	P02774	Vitamin D-binding protein OS=Homo sapiens GN=GC PE=1 SV=1 - [VTDB_HUMAN]	2.43E-02	2.3257	3.0926	4.77E-03	2.9986	2.1825
2_7	P31947	14-3-3 protein sigma OS=Homo sapiens GN=SFN PE=1 SV=1 - [1433S_HUMAN]	1.14E-02	2.7619	3.3175	8.87E-03	2.6728	3.0745
2_7	O14756	17-beta-hydroxysteroid dehydrogenase type 6 OS=Homo sapiens GN=HSD17B6 PE=1 SV=1 - [H17B6_HUMAN]	2.03E-05	-14.5723	-2.8648	8.23E-06	-8.8102	-3.5460
2_7	P12694	2-oxoisovalerate dehydrogenase subunit alpha, mitochondrial OS=Homo sapiens GN=BCKDHA PE=1 SV=2 - [ODBA_HUMAN]	1.83E-03	-3.7847	-2.6657	2.05E-02	-2.2920	-2.1159
2_7	P31937	3-hydroxyisobutyrate dehydrogenase, mitochondrial OS=Homo sapiens GN=HIBADH PE=1 SV=2 - [3HIDH_HUMAN]	2.00E-02	-2.5190	-2.7853	4.12E-04	-4.2941	-3.3175
2_7	P42765	3-ketoacyl-CoA thiolase, mitochondrial OS=Homo sapiens GN=ACAA2 PE=1 SV=2 - [THIM_HUMAN]	4.87E-03	-3.2709	-2.9265	1.54E-05	-7.6012	-5.0277
2_7	P09110	3-ketoacyl-CoA thiolase, peroxisomal OS=Homo sapiens GN=ACAA1 PE=1 SV=2 - [THIK_HUMAN]	5.90E-03	-3.0810	-2.9069	1.25E-04	-5.1504	-4.5886
2_7	P80404	4-aminobutyrate aminotransferase, mitochondrial OS=Homo sapiens GN=ABAT PE=1 SV=3 - [GABT_HUMAN]	3.38E-05	-13.2667	-2.8460	7.07E-05	-5.6401	-4.6929
2_7	P32754	4-hydroxyphenylpyruvate dioxygenase OS=Homo sapiens GN=HPD PE=1 SV=2 - [HPPD_HUMAN]	3.97E-05	-12.6416	-2.8898	2.16E-04	-4.7439	-4.7268
2_7	P49189	4-trimethylaminobutyraldehyde dehydrogenase OS=Homo sapiens GN=ALDH9A1 PE=1 SV=3 - [AL9A1_HUMAN]	7.13E-06	-16.1914	-2.7721	1.06E-05	-8.2976	-2.1159
2_7	Q9BWD1	Acetyl-CoA acetyltransferase, cytosolic OS=Homo sapiens GN=ACAT2 PE=1 SV=2 - [THIC_HUMAN]	2.73E-04	-5.5810	-2.7071	8.87E-04	-3.8469	-2.6394
2_7	P24752	Acetyl-CoA acetyltransferase, mitochondrial OS=Homo sapiens GN=ACAT1 PE=1 SV=1 - [THIL_HUMAN]	1.08E-03	-4.0843	-2.9105	1.00E-05	-8.5257	-4.6597
2_7	Q08AH3	Acyl-coenzyme A synthetase ACSM2A, mitochondrial OS=Homo sapiens GN=ACSM2A PE=1 SV=2 - [ACS2A_HUMAN]	7.64E-06	-16.0532	-2.8285	1.99E-04	-4.8093	-4.3789
2_7	Q86CK6	Acyl-coenzyme A synthetase ACSM2B, mitochondrial OS=Homo sapiens GN=ACSM2B PE=1 SV=2 - [ACS2B_HUMAN]	9.19E-06	-15.8809	-2.8285	6.91E-05	-5.6594	-4.4100
2_7	P24298	Alanine aminotransferase 1 OS=Homo sapiens GN=GPT PE=1 SV=3 - [ALAT1_HUMAN]	4.31E-04	-5.3706	-2.7134	4.27E-04	-4.2661	-3.5153
2_7	P07327	Alcohol dehydrogenase 1A OS=Homo sapiens GN=ADH1A PE=1 SV=2 - [ADH1A_HUMAN]	6.06E-04	-5.0332	-2.9492	7.36E-04	-3.9546	-4.8261

Fig. 7 continued

2_7	P00325	Alcohol dehydrogenase 1B OS=Homo sapiens GN=ADH1B PE=1 SV=2 - [ADH1B_HUMAN]	5.94E-04	-5.0633	-2.9536	6.64E-04	-4.0175	-4.7789
2_7	P00326	Alcohol dehydrogenase 1C OS=Homo sapiens GN=ADH1C PE=1 SV=2 - [ADH1G_HUMAN]	1.81E-02	-2.5888	-2.9342	1.15E-02	-2.5679	-4.0606
2_7	P08319	Alcohol dehydrogenase 4 OS=Homo sapiens GN=ADH4 PE=1 SV=5 - [ADH4_HUMAN]	3.72E-05	-12.7889	-2.8967	4.71E-03	-2.9601	-4.8219
2_7	Q9H2A2	Aldehyde dehydrogenase family 8 member A1 OS=Homo sapiens GN=ALDH8A1 PE=1 SV=1 - [ALDA1_HUMAN]	2.54E-04	-5.6224	-2.7885	1.62E-04	-4.9419	-2.3323
2_7	Q06278	Aldehyde oxidase OS=Homo sapiens GN=AOX1 PE=2 SV=2 - [ADO_HUMAN]	2.54E-03	-3.7191	-2.7288	2.04E-02	-2.2971	-3.3236
2_7	Q04828	Aldo-keto reductase family 1 member C1 OS=Homo sapiens GN=AKR1C1 PE=1 SV=1 - [AK1C1_HUMAN]	4.61E-02	-2.0612	-2.9553	5.12E-04	-4.1546	-4.7066
2_7	P52895	Aldo-keto reductase family 1 member C2 OS=Homo sapiens GN=AKR1C2 PE=1 SV=3 - [AK1C2_HUMAN]	2.67E-03	-3.7077	-2.9553	8.59E-03	-2.6872	-4.3506
2_7	P17516	Aldo-keto reductase family 1 member C4 OS=Homo sapiens GN=AKR1C4 PE=1 SV=3 - [AK1C4_HUMAN]	3.21E-04	-5.5171	-2.9196	2.05E-04	-4.7877	-3.9866
2_7	Q96IU4	Alpha/beta hydrolase domain-containing protein 14B OS=Homo sapiens GN=ABHD14B PE=1 SV=1 - [ABHEB_HUMAN]	1.80E-02	-2.5941	-2.7936	2.76E-03	-3.2247	-2.2534
2_7	P49419	Alpha-aminoadipic semialdehyde dehydrogenase OS=Homo sapiens GN=ALDH7A1 PE=1 SV=5 - [AL7A1_HUMAN]	1.11E-04	-6.2977	-2.8631	2.43E-05	-6.8282	-4.2498
2_7	P27338	Amine oxidase [flavin-containing] B OS=Homo sapiens GN=MAOB PE=1 SV=3 - [AOFB_HUMAN]	1.74E-05	-14.7432	-2.8185	7.62E-05	-5.5721	-3.7939
2_7	Q03154	Aminoacylase-1 OS=Homo sapiens GN=ACY1 PE=1 SV=1 - [ACY1_HUMAN]	1.17E-05	-15.5149	-2.9370	8.83E-05	-5.4332	-4.3069
2_7	P12429	Annexin A3 OS=Homo sapiens GN=ANXA3 PE=1 SV=3 - [ANXA3_HUMAN]	5.12E-05	8.8222	3.1575	3.85E-03	3.0486	2.8192
2_7	O95994	Anterior gradient protein 2 homolog OS=Homo sapiens GN=AGR2 PE=1 SV=1 - [AGR2_HUMAN]	4.95E-05	9.2116	3.3637	3.97E-05	6.3696	3.5751
2_7	P05089	Arginase-1 OS=Homo sapiens GN=ARG1 PE=1 SV=2 - [ARGI1_HUMAN]	2.86E-05	-13.6063	-2.9120	1.06E-04	-5.2734	-4.5199
2_7	P04424	Argininosuccinate lyase OS=Homo sapiens GN=ASL PE=1 SV=4 - [ARLY_HUMAN]	2.15E-02	-2.4569	-2.8761	1.09E-04	-5.2433	-4.2799
2_7	P00966	Argininosuccinate synthase OS=Homo sapiens GN=ASS1 PE=1 SV=2 - [ASSY_HUMAN]	6.27E-04	-4.9677	-2.8669	3.77E-03	-3.0680	-3.6929
2_7	P22760	Arylacetamide deacetylase OS=Homo sapiens GN=AADAC PE=1 SV=5 - [AAAD_HUMAN]	2.43E-04	-5.6321	-2.6962	6.28E-03	-2.8267	-2.6394
2_7	P28160	Azurocidin OS=Homo sapiens GN=AZU1 PE=1 SV=3 - [CAP7_HUMAN]	6.40E-03	3.0163	3.1358	1.27E-02	2.5133	3.1256
2_7	P13929	Beta-enolase OS=Homo sapiens GN=ENO3 PE=1 SV=5 - [ENOB_HUMAN]	1.16E-02	-2.7577	-2.8908	1.52E-02	-2.4241	-2.5460
2_7	Q93088	Betaine--homocysteine S-methyltransferase 1 OS=Homo sapiens GN=BHMT PE=1 SV=2 - [BHMT1_HUMAN]	4.22E-04	-5.3788	-2.8536	1.09E-03	-3.7147	-3.9443
2_7	Q8IUBR1	Beta-ureidopropionase OS=Homo sapiens GN=UPB1 PE=1 SV=1 - [BUP1_HUMAN]	3.64E-04	-5.4570	-2.7768	2.21E-03	-3.3534	-2.3236
2_7	Q3LXA3	Bifunctional ATP-dependent dihydroxyacetone kinase/FAD-AMP lyase (cyclizing) OS=Homo sapiens GN=DAK PE=1 SV=2 - [DHAK_HUMAN]	4.93E-02	-2.0395	-2.8765	5.59E-03	-2.8849	-3.5681
2_7	P34913	Bifunctional epoxide hydrolase 2 OS=Homo sapiens GN=EPHX2 PE=1 SV=2 - [HYES_HUMAN]	7.70E-04	-4.6297	-2.7439	3.40E-03	-3.1149	-2.0114
2_7	P21810	Biglycan OS=Homo sapiens GN=BGN PE=1 SV=2 - [PGS1_HUMAN]	3.87E-03	3.5296	3.2970	1.24E-02	2.5230	3.4695
2_7	Q14032	Bile acid-CoA:amino acid N-acyltransferase OS=Homo sapiens GN=BAAT PE=1 SV=1 - [BAAT_HUMAN]	2.95E-05	-13.5177	-2.8539	3.30E-05	-6.5942	-2.6218
2_7	Q9Y2P5	Bile acyl-CoA synthetase OS=Homo sapiens GN=SLC27A5 PE=1 SV=1 - [S27A5_HUMAN]	3.70E-04	-5.4430	-2.7777	8.15E-04	-3.8922	-3.5460
2_7	Q06520	Bile salt sulfotransferase OS=Homo sapiens GN=SULT2A1 PE=1 SV=3 - [ST2A1_HUMAN]	1.74E-05	-14.7411	-2.9192	2.15E-05	-6.9258	-4.0747
2_7	P11586	C-1-tetrahydrofolate synthase, cytoplasmic OS=Homo sapiens GN=MTHFD1 PE=1 SV=3 - [C1TC_HUMAN]	5.31E-04	-5.2158	-2.8443	2.29E-04	-4.7280	-4.6455
2_7	Q9UJS0	Calcium-binding mitochondrial carrier protein Aralar2 OS=Homo sapiens GN=SLC25A13 PE=1 SV=2 - [CMC2_HUMAN]	6.13E-03	-3.0541	-2.8168	2.13E-05	-6.9227	-3.6813
2_7	P06731	Carcinoembryonic antigen-related cell adhesion molecule 5 OS=Homo sapiens GN=CEACAM5 PE=1 SV=3 - [CEAM5_HUMAN]	9.66E-03	2.7946	3.1781	1.94E-02	2.3921	2.0701
2_7	P23786	Carnitine O-palmitoyltransferase 2, mitochondrial OS=Homo sapiens GN=CPT2 PE=1 SV=2 - [CPT2_HUMAN]	2.12E-04	-5.6776	-2.7694	2.48E-03	-3.2923	-3.0755

Fig. 7 continued

2_7	P08311	Cathepsin G OS=Homo sapiens GN=CTSG PE=1 SV=2 - [CATG_HUMAN]	8.23E-04	4.5082	3.2985	2.27E-02	2.2408	3.9032
2_7	P00450	Ceruloplasmin OS=Homo sapiens GN=CP PE=1 SV=1 - [CERU_HUMAN]	4.48E-04	5.3548	3.2327	2.04E-04	4.7905	2.3142
2_7	Q05707	Collagen alpha-1(XIV) chain OS=Homo sapiens GN=COL14A1 PE=1 SV=3 - [COEA1_HUMAN]	2.25E-02	2.4087	3.2243	1.02E-02	2.6162	2.4695
2_7	P00751	Complement factor B OS=Homo sapiens GN=CFB PE=1 SV=2 - [CFAB_HUMAN]	5.64E-04	5.1425	3.1971	3.56E-04	4.4021	2.6576
2_7	P31146	Coronin-1A OS=Homo sapiens GN=CORO1A PE=1 SV=4 - [COR1A_HUMAN]	5.46E-05	8.2555	3.2122	9.43E-04	3.7983	2.2925
2_7	P28845	Corticosteroid 11-beta-dehydrogenase isozyme 1 OS=Homo sapiens GN=HSD11B1 PE=1 SV=3 - [DHI1_HUMAN]	3.46E-04	-5.4732	-2.7739	1.73E-04	-4.8862	-2.2673
2_7	P32929	Cystathionine gamma-lyase OS=Homo sapiens GN=CTH PE=1 SV=3 - [CGL_HUMAN]	4.12E-04	-5.3896	-2.7750	8.45E-03	-2.6944	-2.7316
2_7	P00167	Cytochrome b5 OS=Homo sapiens GN=CYB5A PE=1 SV=2 - [CYB5_HUMAN]	3.25E-05	-13.3535	-2.9940	1.05E-04	-5.3045	-3.5964
2_7	P11509	Cytochrome P450 2A6 OS=Homo sapiens GN=CYP2A6 PE=1 SV=3 - [CP2A6_HUMAN]	1.22E-05	-15.4599	-2.8972	2.73E-03	-3.2368	-3.6597
2_7	P11712	Cytochrome P450 2C9 OS=Homo sapiens GN=CYP2C9 PE=1 SV=3 - [CP2C9_HUMAN]	5.26E-04	-5.2236	-2.8364	2.71E-03	-3.2410	-3.7909
2_7	P05181	Cytochrome P450 2E1 OS=Homo sapiens GN=CYP2E1 PE=1 SV=1 - [CP2E1_HUMAN]	3.17E-03	-3.6489	-2.7621	1.69E-02	-2.3803	-2.9678
2_7	P21399	Cytoplasmic aconitate hydratase OS=Homo sapiens GN=ACO1 PE=1 SV=3 - [ACOC_HUMAN]	2.24E-02	-2.4133	-2.8526	6.67E-05	-5.7254	-4.0606
2_7	O75891	Cytosolic 10-formyltetrahydrofolate dehydrogenase OS=Homo sapiens GN=ALDH1L1 PE=1 SV=2 - [AL1L1_HUMAN]	3.20E-04	-5.5195	-2.8376	5.77E-03	-2.8688	-4.2534
2_7	Q02338	D-beta-hydroxybutyrate dehydrogenase, mitochondrial OS=Homo sapiens GN=BDH1 PE=1 SV=3 - [BDH_HUMAN]	1.52E-05	-14.9205	-2.8298	1.09E-05	-8.2936	-3.0118
2_7	P30046	D-dopachrome decarboxylase OS=Homo sapiens GN=DDT PE=1 SV=3 - [DOPD_HUMAN]	2.55E-02	-2.3044	-2.8921	1.45E-03	-3.5732	-2.7219
2_7	P30038	Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial OS=Homo sapiens GN=ALDH4A1 PE=1 SV=3 - [AL4A1_HUMAN]	1.73E-05	-14.7538	-2.8957	1.77E-05	-7.2220	-4.3593
2_7	P09417	Dihydropteridine reductase OS=Homo sapiens GN=QDPR PE=1 SV=2 - [DHPR_HUMAN]	3.60E-04	-5.4556	-2.7510	1.56E-03	-3.5306	-2.5460
2_7	Q14117	Dihydropyrimidinase OS=Homo sapiens GN=DPYS PE=1 SV=1 - [DPYS_HUMAN]	1.91E-04	-5.6984	-2.6922	6.16E-04	-4.0569	-2.1159
2_7	P31513	Dimethylaniline monooxygenase [N-oxide-forming] 3 OS=Homo sapiens GN=FMO3 PE=1 SV=5 - [FMO3_HUMAN]	2.35E-05	-14.1915	-2.8470	3.72E-03	-3.0686	-2.4253
2_7	Q9UI17	Dimethylglycine dehydrogenase, mitochondrial OS=Homo sapiens GN=DMGDH PE=1 SV=2 - [M2GD_HUMAN]	2.33E-04	-5.6442	-2.7582	4.07E-03	-3.0281	-2.3323
2_7	Q12805	EGF-containing fibulin-like extracellular matrix protein 1 OS=Homo sapiens GN=EFEMP1 PE=1 SV=2 - [FBLN3_HUMAN]	6.53E-03	2.9995	3.1926	5.17E-03	2.9215	2.8070
2_7	P30040	Endoplasmic reticulum resident protein 29 OS=Homo sapiens GN=ERP29 PE=1 SV=4 - [ERP29_HUMAN]	2.61E-02	-2.2822	-2.7682	5.26E-03	-2.9140	-2.1159
2_7	O75521	Enoyl-CoA delta isomerase 2, mitochondrial OS=Homo sapiens GN=ECI2 PE=1 SV=4 - [ECI2_HUMAN]	1.62E-04	-5.8171	-2.7705	1.39E-03	-3.5966	-2.7939
2_7	P30084	Enoyl-CoA hydratase, mitochondrial OS=Homo sapiens GN=ECHS1 PE=1 SV=4 - [ECHM_HUMAN]	7.84E-03	-2.8724	-2.9018	2.83E-05	-6.7083	-3.7268
2_7	P11678	Eosinophil peroxidase OS=Homo sapiens GN=EPX PE=1 SV=2 - [PERE_HUMAN]	6.09E-03	3.0606	3.1923	8.03E-03	2.7143	3.4580
2_7	P07099	Epoxide hydrolase 1 OS=Homo sapiens GN=EPHX1 PE=1 SV=1 - [HYEP_HUMAN]	2.49E-02	-2.3227	-3.0464	7.63E-06	-8.8512	-5.5825
2_7	Q9H0W9	Ester hydrolase C11orf54 OS=Homo sapiens GN=C11orf54 PE=1 SV=1 - [CK054_HUMAN]	4.07E-06	-17.0764	-2.7939	2.27E-04	-4.7189	-2.0627
2_7	P15311	Ezrin OS=Homo sapiens GN=EZR PE=1 SV=4 - [EZRI_HUMAN]	2.04E-04	5.6860	3.3023	7.37E-05	5.6042	3.3965
2_7	P23142	Fibulin-1 OS=Homo sapiens GN=FBLN1 PE=1 SV=4 - [FBLN1_HUMAN]	1.83E-03	3.7848	3.0299	9.34E-03	2.6560	2.9032
2_7	O95954	Formimidoyltransferase-cyclodeaminase OS=Homo sapiens GN=FTCD PE=1 SV=2 - [FTCD_HUMAN]	3.41E-05	-13.2613	-2.8156	2.56E-03	-3.2713	-4.0241
2_7	P09467	Fructose-1,6-bisphosphatase 1 OS=Homo sapiens GN=FBP1 PE=1 SV=5 - [F16P1_HUMAN]	6.88E-03	-2.9621	-2.8730	7.03E-06	-8.9154	-3.7148
2_7	P07954	Fumarate hydratase, mitochondrial OS=Homo sapiens GN=FH PE=1 SV=3 - [FUMH_HUMAN]	3.43E-03	-3.6185	-2.9025	4.16E-06	-9.2304	-3.7789

Fig. 7 continued

2_7	P16930	Fumarylacetoacetase OS=Homo sapiens GN=FAH PE=1 SV=2 - [FAAA_HUMAN]	8.11E-04	-4.5376	-2.8819	3.72E-05	-6.4598	-3.7219
2_7	P51570	Galactokinase OS=Homo sapiens GN=GALK1 PE=1 SV=1 - [GALK1_HUMAN]	1.97E-03	-3.7728	-2.7883	5.97E-03	-2.8534	-2.2554
2_7	Q08380	Galectin-3-binding protein OS=Homo sapiens GN=LGALS3BP PE=1 SV=1 - [LG3BP_HUMAN]	7.53E-03	2.8963	3.2972	7.55E-04	3.9330	3.8774
2_7	Q92820	Gamma-glutamyl hydrolase OS=Homo sapiens GN=GGH PE=1 SV=2 - [GGH_HUMAN]	1.54E-04	-5.8547	-2.7954	7.16E-03	-2.7605	-2.2462
2_7	O95479	GDH/6PGL endoplasmic bifunctional protein OS=Homo sapiens GN=H6PD PE=1 SV=2 - [G6PE_HUMAN]	2.85E-04	-5.5703	-2.7628	2.83E-04	-4.5606	-2.9678
2_7	P09488	Glutathione S-transferase Mu 1 OS=Homo sapiens GN=GSTM1 PE=1 SV=3 - [GSTM1_HUMAN]	1.43E-03	-3.8523	-2.8124	3.46E-03	-3.1062	-3.0118
2_7	P09211	Glutathione S-transferase P OS=Homo sapiens GN=GSTP1 PE=1 SV=2 - [GSTP1_HUMAN]	7.24E-04	4.7299	3.3570	6.45E-06	8.9291	4.6817
2_7	P50440	Glycine amidinotransferase, mitochondrial OS=Homo sapiens GN=GATM PE=1 SV=1 - [GATM_HUMAN]	8.80E-06	-15.9405	-2.9650	8.54E-04	-3.8646	-4.5520
2_7	P11216	Glycogen phosphorylase, brain form OS=Homo sapiens GN=PYGB PE=1 SV=5 - [PYGB_HUMAN]	5.40E-03	3.1665	3.1641	3.35E-02	2.0659	2.9490
2_7	P06737	Glycogen phosphorylase, liver form OS=Homo sapiens GN=PYGL PE=1 SV=4 - [PYGL_HUMAN]	6.75E-06	-16.2053	-2.8466	2.94E-05	-6.6799	-3.9678
2_7	Q9UBQ7	Glyoxylate reductase/hydroxypyruvate reductase OS=Homo sapiens GN=GRHPR PE=1 SV=1 - [GRHPR_HUMAN]	6.70E-03	-2.9804	-2.9034	3.47E-04	-4.4138	-4.0747
2_7	Q9UJ07	GTP:AMP phosphotransferase, mitochondrial OS=Homo sapiens GN=AK3 PE=1 SV=4 - [KAD3_HUMAN]	5.28E-03	-3.1881	-2.8197	3.11E-04	-4.4738	-2.4373
2_7	P02790	Hemopexin OS=Homo sapiens GN=HPX PE=1 SV=2 - [HEMO_HUMAN]	4.00E-03	3.4900	3.1551	1.40E-02	2.4519	2.6401
2_7	Q99099	Homogentisate 1,2-dioxygenase OS=Homo sapiens GN=HGD PE=1 SV=2 - [HGD_HUMAN]	2.71E-05	-13.9676	-2.8230	3.87E-05	-6.3987	-4.0222
2_7	Q9UJM8	Hydroxyacid oxidase 1 OS=Homo sapiens GN=HAO1 PE=1 SV=1 - [HAOX1_HUMAN]	1.95E-05	-14.5838	-2.9012	1.95E-05	-7.2034	-4.6766
2_7	Q16836	Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial OS=Homo sapiens GN=HADH PE=1 SV=3 - [HCDH_HUMAN]	7.50E-04	-4.6763	-2.7695	1.24E-04	-5.1510	-2.4843
2_7	P35914	Hydroxymethylglutaryl-CoA lyase, mitochondrial OS=Homo sapiens GN=HMGCL PE=1 SV=2 - [HMGCL_HUMAN]	2.55E-04	-5.6212	-2.7659	1.99E-04	-4.8069	-2.4944
2_7	P54868	Hydroxymethylglutaryl-CoA synthase, mitochondrial OS=Homo sapiens GN=HMGCS2 PE=1 SV=1 - [HMCS2_HUMAN]	8.61E-04	-4.4297	-2.9389	9.24E-05	-5.3704	-4.6936
2_7	Q96AB3	Isochorismatase domain-containing protein 2, mitochondrial OS=Homo sapiens GN=ISOC2 PE=1 SV=1 - [ISOC2_HUMAN]	3.01E-04	-5.5456	-2.8366	1.12E-03	-3.7046	-2.5520
2_7	P26440	Isovaleryl-CoA dehydrogenase, mitochondrial OS=Homo sapiens GN=IVD PE=1 SV=1 - [IVD_HUMAN]	8.51E-03	-2.8223	-2.7571	3.28E-03	-3.1324	-2.0747
2_7	P08727	Keratin, type I cytoskeletal 19 OS=Homo sapiens GN=KRT19 PE=1 SV=4 - [K1C19_HUMAN]	3.52E-05	13.1409	3.4319	5.27E-05	5.9579	5.5735
2_7	P08729	Keratin, type II cytoskeletal 7 OS=Homo sapiens GN=KRT7 PE=1 SV=5 - [K2C7_HUMAN]	1.38E-02	2.7266	3.1228	1.79E-02	2.3551	3.5726
2_7	P02788	Lactotransferrin OS=Homo sapiens GN=LTF PE=1 SV=5 - [TRFL_HUMAN]	8.01E-04	4.5598	3.2803	1.44E-02	2.4487	6.0575
2_7	P23141	Liver carboxylesterase 1 OS=Homo sapiens GN=CES1 PE=1 SV=2 - [ES11_HUMAN]	5.78E-04	-5.1169	-3.0234	4.29E-05	-6.2247	-5.7751
2_7	P07195	L-lactate dehydrogenase B chain OS=Homo sapiens GN=LDHB PE=1 SV=2 - [LDHB_HUMAN]	2.61E-04	5.6154	3.3757	1.63E-03	3.5136	2.9447
2_7	P33121	Long-chain-fatty-acid--CoA ligase 1 OS=Homo sapiens GN=ACSL1 PE=1 SV=1 - [ACSL1_HUMAN]	1.38E-05	-15.0296	-2.8078	2.36E-06	-10.1533	-3.7481
2_7	P51884	Lumican OS=Homo sapiens GN=LUM PE=1 SV=2 - [LUM_HUMAN]	1.17E-04	6.2294	3.2994	2.03E-02	2.2994	2.4695
2_7	P61626	Lysozyme C OS=Homo sapiens GN=LYZ PE=1 SV=1 - [LYSC_HUMAN]	9.19E-05	6.4680	3.2855	6.45E-03	2.8111	3.0187
2_7	P40121	Macrophage-capping protein OS=Homo sapiens GN=CAPG PE=1 SV=2 - [CAPG_HUMAN]	5.20E-05	8.7575	3.2766	8.43E-05	5.4854	3.0745
2_7	Q14764	Major vault protein OS=Homo sapiens GN=MVP PE=1 SV=4 - [MVP_HUMAN]	1.26E-04	6.1636	3.1790	2.19E-04	4.7382	3.3865
2_7	P11310	Medium-chain specific acyl-CoA dehydrogenase, mitochondrial OS=Homo sapiens GN=ACADM PE=1 SV=1 - [ACADM_HUMAN]	1.89E-05	-14.6532	-2.9628	2.23E-10	-14.1718	-3.1863
2_7	Q9HCC0	Methylcrotonoyl-CoA carboxylase beta chain, mitochondrial OS=Homo sapiens GN=MCCC2 PE=1 SV=1 - [MCCB_HUMAN]	2.64E-02	-2.2732	-2.7212	2.27E-03	-3.3433	-2.9866

Fig. 7 continued

2_7	Q02252	Methylmalonate-semialdehyde dehydrogenase [acylating], mitochondrial OS=Homo sapiens GN=ALDH6A1 PE=1 SV=2 - [MMSA_HUMAN]	3.20E-05	-13.3627	-2.8877	8.96E-05	-5.4088	-4.8374
2_7	Q9H8H3	Methyltransferase-like protein 7A OS=Homo sapiens GN=METTL7A PE=1 SV=1 - [META_HUMAN]	5.11E-06	-16.7897	-2.8084	8.38E-05	-5.4891	-2.0606
2_7	P10620	Microsomal glutathione S-transferase 1 OS=Homo sapiens GN=MGST1 PE=1 SV=1 - [MGST1_HUMAN]	1.98E-05	-14.5806	-2.8540	1.66E-05	-7.3877	-2.4391
2_7	P55157	Microsomal triglyceride transfer protein large subunit OS=Homo sapiens GN=MTTP PE=1 SV=1 - [MTP_HUMAN]	4.65E-05	-11.4288	-2.7437	1.22E-05	-8.1044	-3.0747
2_7	Q969Z3	MOSC domain-containing protein 2, mitochondrial OS=Homo sapiens GN=MARC2 PE=1 SV=1 - [MOSC2_HUMAN]	2.47E-05	-14.1039	-2.7157	1.81E-04	-4.8635	-2.5520
2_7	P98088	Mucin-5AC (Fragments) OS=Homo sapiens GN=MUC5AC PE=1 SV=3 - [MUC5A_HUMAN]	1.16E-02	2.7572	3.2398	2.24E-02	2.2479	4.7330
2_7	P24158	Myeloblastin OS=Homo sapiens GN=PRTN3 PE=1 SV=3 - [PRTN3_HUMAN]	1.24E-02	2.7442	3.0919	2.49E-02	2.1912	2.9605
2_7	P05164	Myeloperoxidase OS=Homo sapiens GN=MPO PE=1 SV=1 - [PERM_HUMAN]	5.32E-05	8.5801	3.2965	2.57E-02	2.1766	5.7276
2_7	Q77406	Myosin-14 OS=Homo sapiens GN=MYH14 PE=1 SV=2 - [MYH14_HUMAN]	1.53E-06	21.2300	3.1729	2.75E-03	3.2310	3.3440
2_7	Q4G0N4	NAD kinase domain-containing protein 1 OS=Homo sapiens GN=NADKD1 PE=1 SV=2 - [NAKD1_HUMAN]	1.49E-05	-14.9263	-2.8631	8.42E-05	-5.4860	-2.7939
2_7	P16435	NADPH--cytochrome P450 reductase OS=Homo sapiens GN=POR PE=1 SV=2 - [NCPR_HUMAN]	3.24E-05	-13.3563	-2.8868	2.08E-04	-4.7781	-3.5681
2_7	P08246	Neutrophil elastase OS=Homo sapiens GN=ELANE PE=1 SV=1 - [ELNE_HUMAN]	1.96E-02	2.5378	3.2179	1.17E-02	2.5555	4.4277
2_7	P80188	Neutrophil gelatinase-associated lipocalin OS=Homo sapiens GN=LCN2 PE=1 SV=2 - [NGAL_HUMAN]	9.67E-04	4.2429	3.1911	3.82E-02	2.0171	3.2251
2_7	Q15274	Nicotinate-nucleotide pyrophosphorylase [carboxylating] OS=Homo sapiens GN=QPRT PE=1 SV=3 - [NADC_HUMAN]	2.44E-05	-14.1170	-2.7679	4.69E-04	-4.2072	-2.3236
2_7	P22307	Non-specific lipid-transfer protein OS=Homo sapiens GN=SCP2 PE=1 SV=2 - [NLTP_HUMAN]	3.74E-04	-5.4381	-2.8208	3.80E-04	-4.3609	-3.3548
2_7	Q9NQR4	Omega-amidase NIT2 OS=Homo sapiens GN=NIT2 PE=1 SV=1 - [NIT2_HUMAN]	3.47E-04	-5.4715	-2.7870	1.29E-03	-3.6500	-2.2554
2_7	P00480	Ornithine carbamoyltransferase, mitochondrial OS=Homo sapiens GN=OTC PE=1 SV=3 - [OTC_HUMAN]	1.68E-05	-14.8728	-2.9020	1.30E-05	-7.9484	-4.1165
2_7	Q15063	Periostin OS=Homo sapiens GN=POSTN PE=1 SV=2 - [POSTN_HUMAN]	1.63E-04	5.8119	3.1524	7.22E-03	2.7566	3.0545
2_7	Q15067	Peroxisomal acyl-coenzyme A oxidase 1 OS=Homo sapiens GN=ACOX1 PE=1 SV=3 - [ACOX1_HUMAN]	3.12E-05	-13.4645	-2.7623	3.46E-04	-4.4140	-3.6013
2_7	Q9Y424	Peroxisomal acyl-coenzyme A oxidase 2 OS=Homo sapiens GN=ACOX2 PE=1 SV=1 - [ACOX2_HUMAN]	2.45E-05	-14.1095	-2.7478	2.10E-03	-3.3885	-3.1310
2_7	Q08426	Peroxisomal bifunctional enzyme OS=Homo sapiens GN=EHHADH PE=1 SV=3 - [ECHP_HUMAN]	2.06E-04	-5.6944	-2.9160	7.35E-05	-5.6064	-5.2498
2_7	Q9P0Z9	Peroxisomal sarcosine oxidase OS=Homo sapiens GN=PIPOX PE=2 SV=2 - [SOX_HUMAN]	2.19E-05	-14.4133	-2.8337	2.77E-05	-6.7133	-3.9173
2_7	Q16822	Phosphoenolpyruvate carboxykinase [GTP], mitochondrial OS=Homo sapiens GN=PCK2 PE=1 SV=3 - [PCKGM_HUMAN]	6.20E-03	-3.0437	-2.9075	8.84E-06	-8.6903	-5.1253
2_7	P05165	Propionyl-CoA carboxylase alpha chain, mitochondrial OS=Homo sapiens GN=PCCA PE=1 SV=4 - [PCCA_HUMAN]	1.50E-04	-5.8775	-2.7099	1.93E-03	-3.4346	-2.2462
2_7	P05166	Propionyl-CoA carboxylase beta chain, mitochondrial OS=Homo sapiens GN=PCCB PE=1 SV=3 - [PCCB_HUMAN]	1.67E-04	-5.8027	-2.7141	1.81E-04	-4.8662	-3.0118
2_7	Q14914	Prostaglandin reductase 1 OS=Homo sapiens GN=PTGR1 PE=1 SV=2 - [PTGR1_HUMAN]	1.47E-04	-5.9006	-2.8204	2.41E-04	-4.6878	-3.3166
2_7	Q9BPW8	Protein NipSnap homolog 1 OS=Homo sapiens GN=NIPSNAP1 PE=1 SV=1 - [NIPS1_HUMAN]	1.04E-05	-15.5652	-2.8331	3.77E-05	-6.4347	-2.9865
2_7	P31949	Protein S100-A11 OS=Homo sapiens GN=S100A11 PE=1 SV=2 - [S10AB_HUMAN]	5.63E-06	16.5818	3.2807	2.95E-06	9.6329	2.1671
2_7	P06703	Protein S100-A6 OS=Homo sapiens GN=S100A6 PE=1 SV=1 - [S10A6_HUMAN]	5.01E-05	9.1427	3.4440	4.61E-04	4.2168	2.9471
2_7	P55786	Puromycin-sensitive aminopeptidase OS=Homo sapiens GN=NPEPPS PE=1 SV=2 - [PSA_HUMAN]	4.32E-03	3.4001	3.0658	1.22E-02	2.5330	2.0745
2_7	Q9NVS9	Pyridoxine-5-phosphate oxidase OS=Homo sapiens GN=PNPO PE=1 SV=1 - [PNPO_HUMAN]	5.69E-04	-5.1318	-2.8059	1.21E-04	-5.1757	-2.4373
2_7	P11498	Pyruvate carboxylase, mitochondrial OS=Homo sapiens GN=PC PE=1 SV=2 - [PYC_HUMAN]	8.89E-04	-4.3629	-2.8449	4.91E-05	-6.0310	-4.8219

Fig. 7 continued

2_7	P30613	Pyruvate kinase isozymes R/L OS=Homo sapiens GN=PKLR PE=1 SV=2 - [KPYR_HUMAN]	2.04E-06	-18.3184	-2.8332	4.97E-04	-4.1686	-3.3175
2_7	Q00257	Quinone oxidoreductase OS=Homo sapiens GN=CRYZ PE=1 SV=1 - [QOR_HUMAN]	2.40E-02	-2.3529	-2.8399	9.01E-05	-5.3999	-3.9687
2_7	P46940	Ras GTPase-activating-like protein IQGAP1 OS=Homo sapiens GN=IQGAP1 PE=1 SV=1 - [IQGA1_HUMAN]	1.03E-06	21.3826	3.1593	8.51E-03	2.6911	2.5297
2_7	Q13576	Ras GTPase-activating-like protein IQGAP2 OS=Homo sapiens GN=IQGAP2 PE=1 SV=4 - [IQGA2_HUMAN]	6.26E-03	-3.0357	-2.6976	3.46E-03	-3.1060	-2.7148
2_7	Q15907	Ras-related protein Rab-11B OS=Homo sapiens GN=RAB11B PE=1 SV=4 - [RB11B_HUMAN]	1.69E-03	3.8005	3.2846	1.23E-02	2.5282	2.6919
2_7	O75452	Retinol dehydrogenase 16 OS=Homo sapiens GN=RDH16 PE=1 SV=2 - [RDH16_HUMAN]	3.95E-04	-5.4067	-2.7982	1.39E-03	-3.5966	-2.3593
2_7	P02753	Retinol-binding protein 4 OS=Homo sapiens GN=RBP4 PE=1 SV=3 - [RET4_HUMAN]	1.28E-05	-15.3927	-2.8141	1.96E-04	-4.8337	-2.4944
2_7	P52758	Ribonuclease UK114 OS=Homo sapiens GN=HRSP12 PE=1 SV=1 - [UK114_HUMAN]	6.43E-04	-4.9394	-2.9118	1.65E-04	-4.9297	-3.3825
2_7	Q9P2E9	Ribosome-binding protein 1 OS=Homo sapiens GN=RRBP1 PE=1 SV=4 - [RRBP1_HUMAN]	3.13E-02	-2.1290	-2.8193	1.20E-03	-3.6812	-3.9782
2_7	Q8NBX0	Saccharopine dehydrogenase-like oxidoreductase OS=Homo sapiens GN=SCCPDH PE=1 SV=1 - [SCPDL_HUMAN]	6.12E-06	-16.2503	-2.8219	4.70E-06	-9.1961	-2.7268
2_7	Q00266	S-adenosylmethionine synthase isoform type-1 OS=Homo sapiens GN=MAT1A PE=1 SV=2 - [METK1_HUMAN]	2.39E-05	-13.5638	-2.8606	1.04E-03	-3.7415	-2.8628
2_7	Q8IUL12	Sarcosine dehydrogenase, mitochondrial OS=Homo sapiens GN=SARDH PE=1 SV=1 - [SARDH_HUMAN]	2.22E-04	-5.6627	-2.7883	3.79E-04	-4.3623	-3.1624
2_7	P34896	Serine hydroxymethyltransferase, cytosolic OS=Homo sapiens GN=SHMT1 PE=1 SV=1 - [GLYC_HUMAN]	9.71E-06	-15.7261	-2.8595	3.24E-04	-4.4546	-3.6455
2_7	P34897	Serine hydroxymethyltransferase, mitochondrial OS=Homo sapiens GN=SHMT2 PE=1 SV=3 - [GLYM_HUMAN]	6.40E-04	-4.9475	-2.8161	1.19E-06	-10.6767	-3.4589
2_7	P21549	Serine--pyruvate aminotransferase OS=Homo sapiens GN=AGXT PE=1 SV=1 - [SPYA_HUMAN]	6.08E-04	-5.0259	-3.0092	6.97E-05	-5.6492	-6.0079
2_7	P36237	Serpin B6 OS=Homo sapiens GN=SERPINB6 PE=1 SV=3 - [SPB6_HUMAN]	3.72E-03	3.5694	3.1650	2.05E-03	3.4004	2.3598
2_7	P45954	Short/branched chain specific acyl-CoA dehydrogenase, mitochondrial OS=Homo sapiens GN=ACADSB PE=1 SV=1 - [ACDSB_HUMAN]	2.08E-05	-14.5552	-2.8717	5.89E-06	-8.9809	-3.3069
2_7	Q9NR84	Sideroflexin-1 OS=Homo sapiens GN=SFXN1 PE=1 SV=4 - [SFXN1_HUMAN]	2.61E-05	-14.0677	-2.7687	4.83E-05	-6.0414	-2.4391
2_7	Q00796	Sorbitol dehydrogenase OS=Homo sapiens GN=SORD PE=1 SV=4 - [DHSO_HUMAN]	1.59E-03	-3.8156	-2.8382	1.61E-03	-3.5187	-3.5460
2_7	Q02318	Sterol 26-hydroxylase, mitochondrial OS=Homo sapiens GN=CYP27A1 PE=1 SV=1 - [CP27A_HUMAN]	1.62E-05	-14.8968	-2.7763	5.38E-04	-4.1259	-2.4391
2_7	P31040	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial OS=Homo sapiens GN=SDHA PE=1 SV=2 - [DHSA_HUMAN]	5.80E-04	-5.1140	-2.7491	5.13E-03	-2.9240	-2.4944
2_7	P51649	Succinate-semialdehyde dehydrogenase, mitochondrial OS=Homo sapiens GN=ALDH5A1 PE=1 SV=2 - [SSDH_HUMAN]	4.56E-06	-16.9681	-2.7755	1.41E-05	-7.6780	-3.2534
2_7	P30048	Thioredoxin-dependent peroxide reductase, mitochondrial OS=Homo sapiens GN=PRDX3 PE=1 SV=3 - [PRDX3_HUMAN]	2.86E-02	-2.2005	-2.9242	4.22E-04	-4.2735	-3.1369
2_7	P53007	Tricarboxylate transport protein, mitochondrial OS=Homo sapiens GN=SLC25A1 PE=1 SV=2 - [TXTP_HUMAN]	1.38E-02	-2.7227	-2.7448	1.89E-03	-3.4452	-2.1981
2_7	Q15661	Tryptase alpha/beta-1 OS=Homo sapiens GN=TPSAB1 PE=1 SV=1 - [TRYB1_HUMAN]	9.82E-04	4.2243	3.2103	1.19E-02	2.5474	2.4851
2_7	O43399	Tumor protein D54 OS=Homo sapiens GN=TPD52L2 PE=1 SV=2 - [TPD54_HUMAN]	5.00E-04	5.2871	3.2282	1.26E-03	3.6520	2.2065
2_7	P22310	UDP-glucuronosyltransferase 1-4 OS=Homo sapiens GN=UGT1A4 PE=1 SV=1 - [UD14_HUMAN]	3.35E-04	-5.4923	-2.8845	5.47E-04	-4.1140	-2.9086
2_7	O60656	UDP-glucuronosyltransferase 1-9 OS=Homo sapiens GN=UGT1A9 PE=1 SV=1 - [UD19_HUMAN]	1.03E-02	-2.7835	-2.8097	9.44E-03	-2.8519	-2.4391
2_7	P06133	UDP-glucuronosyltransferase 2B4 OS=Homo sapiens GN=UGT2B4 PE=1 SV=2 - [UD2B4_HUMAN]	2.66E-05	-14.0468	-2.7905	6.32E-04	-4.0358	-2.7008
2_7	P16662	UDP-glucuronosyltransferase 2B7 OS=Homo sapiens GN=UGT2B7 PE=1 SV=1 - [UD2B7_HUMAN]	3.81E-04	-5.4286	-2.7992	2.51E-03	-3.2828	-2.7316
2_7	Q16851	UTP--glucose-1-phosphate uridylyltransferase OS=Homo sapiens GN=UGP2 PE=1 SV=5 - [UGPA_HUMAN]	5.23E-03	-3.1973	-2.9566	1.33E-04	-5.1058	-4.3718
2_7	P13611	Versican core protein OS=Homo sapiens GN=VCAN PE=1 SV=3 - [CSPG2_HUMAN]	9.05E-04	4.3329	3.1761	1.01E-02	2.6196	2.8070

Fig. 7 continued

2_8	Q15029	116 kDa U5 small nuclear ribonucleoprotein component OS=Homo sapiens GN=EFTUD2 PE=1 SV=1 - [U5S1_HUMAN]	1.38E-04	5.8542	2.6748	1.09E-03	3.8379	2.4356
2_8	P31947	14-3-3 protein sigma OS=Homo sapiens GN=SFN PE=1 SV=1 - [1433S_HUMAN]	3.45E-04	5.4750	2.9218	3.70E-06	8.4216	3.7240
2_8	O14756	17-beta-hydroxysteroid dehydrogenase type 6 OS=Homo sapiens GN=HSD17B6 PE=1 SV=1 - [1H1786_HUMAN]	8.52E-06	-14.5723	-2.8648	3.17E-06	-8.8102	-3.5460
2_8	P12694	2-oxoisovalerate dehydrogenase subunit alpha, mitochondrial OS=Homo sapiens GN=BCKDHA PE=1 SV=2 - [ODBA_HUMAN]	7.01E-03	-2.8168	-2.6857	2.86E-02	-2.1598	-2.1159
2_8	P80404	4-aminobutyrate aminotransferase, mitochondrial OS=Homo sapiens GN=ABAT PE=1 SV=3 - [GABT_HUMAN]	4.55E-04	-4.7806	-2.8460	1.01E-04	-5.3153	-4.6929
2_8	P32754	4-hydroxyphenylpyruvate dioxygenase OS=Homo sapiens GN=HPD PE=1 SV=2 - [HPPD_HUMAN]	9.40E-06	-12.6416	-2.8898	2.69E-04	-4.7439	-4.7268
2_8	Q08AH3	Acyl-coenzyme A synthetase ACSM2A, mitochondrial OS=Homo sapiens GN=ACSM2A PE=1 SV=2 - [ACS2A_HUMAN]	8.33E-06	-16.0532	-2.8285	2.43E-04	-4.8093	-4.3789
2_8	Q6ICX6	Acyl-coenzyme A synthetase ACSM2B, mitochondrial OS=Homo sapiens GN=ACSM2B PE=1 SV=2 - [ACS2B_HUMAN]	8.34E-06	-15.8889	-2.8285	6.15E-05	-5.6594	-4.4100
2_8	P24298	Alanine aminotransferase 1 OS=Homo sapiens GN=GPT PE=1 SV=3 - [ALAT1_HUMAN]	3.80E-04	-5.3706	-2.7134	5.43E-04	-4.2661	-3.5153
2_8	P07327	Alcohol dehydrogenase 1A OS=Homo sapiens GN=ADH1A PE=1 SV=2 - [ADH1A_HUMAN]	5.90E-05	-6.0941	-2.9492	9.16E-04	-3.9471	-4.8261
2_8	P00325	Alcohol dehydrogenase 1B OS=Homo sapiens GN=ADH1B PE=1 SV=2 - [ADH1B_HUMAN]	5.65E-05	-6.1326	-2.9536	8.23E-04	-4.0099	-4.7789
2_8	P00326	Alcohol dehydrogenase 1C OS=Homo sapiens GN=ADH1C PE=1 SV=2 - [ADH1G_HUMAN]	2.86E-02	-2.1334	-2.9342	1.21E-02	-2.5831	-4.0606
2_8	P08319	Alcohol dehydrogenase 4 OS=Homo sapiens GN=ADH4 PE=1 SV=5 - [ADH4_HUMAN]	1.22E-04	-5.8884	-2.8967	5.87E-03	-2.9329	-4.8219
2_8	Q9H2A2	Aldehyde dehydrogenase family 8 member A1 OS=Homo sapiens GN=ALDH8A1 PE=1 SV=1 - [AL8A1_HUMAN]	2.95E-04	-5.6224	-2.7885	1.90E-04	-4.9419	-2.3323
2_8	Q06278	Aldehyde oxidase OS=Homo sapiens GN=AOX1 PE=2 SV=2 - [ADO_HUMAN]	2.24E-03	-3.7191	-2.7288	2.21E-02	-2.2971	-3.3236
2_8	O60218	Aldo-keto reductase family 1 member B10 OS=Homo sapiens GN=AKR1B10 PE=1 SV=2 - [AK1BA_HUMAN]	3.60E-04	-5.4239	-2.9501	7.32E-04	-4.0780	-3.8679
2_8	Q04828	Aldo-keto reductase family 1 member C1 OS=Homo sapiens GN=AKR1C1 PE=1 SV=1 - [AK1C1_HUMAN]	4.21E-04	-5.1281	-2.9553	6.55E-04	-4.1378	-4.7056
2_8	P52895	Aldo-keto reductase family 1 member C2 OS=Homo sapiens GN=AKR1C2 PE=1 SV=3 - [AK1C2_HUMAN]	2.30E-03	-3.7077	-2.9553	9.69E-03	-2.6872	-4.3506
2_8	P17516	Aldo-keto reductase family 1 member C4 OS=Homo sapiens GN=AKR1C4 PE=1 SV=3 - [AK1C4_HUMAN]	3.33E-04	-5.5171	-2.9196	2.55E-04	-4.7877	-3.9866
2_8	P27338	Amine oxidase [flavin-containing] B OS=Homo sapiens GN=MAOB PE=1 SV=3 - [AOFB_HUMAN]	1.12E-05	-8.5794	-2.8185	7.72E-05	-5.4794	-3.7939
2_8	Q03154	Aminoacylase-1 OS=Homo sapiens GN=ACY1 PE=1 SV=1 - [ACY1_HUMAN]	2.24E-05	-6.9990	-2.9370	9.73E-05	-5.3344	-4.3069
2_8	P12429	Annexin A3 OS=Homo sapiens GN=ANXA3 PE=1 SV=3 - [ANXA3_HUMAN]	1.80E-03	3.7859	2.7772	2.07E-03	3.4818	2.8845
2_8	O95994	Anterior gradient protein 2 homolog OS=Homo sapiens GN=AGR2 PE=1 SV=1 - [AGR2_HUMAN]	4.77E-05	6.2278	2.8776	1.16E-04	5.2298	3.0799
2_8	P05089	Arginase-1 OS=Homo sapiens GN=ARG1 PE=1 SV=2 - [ARG1_HUMAN]	9.32E-06	-13.6063	-2.9120	1.09E-04	-5.2734	-4.5199
2_8	P54136	Arginine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=RARS PE=1 SV=2 - [SYRC_HUMAN]	7.64E-05	5.9876	2.6671	1.89E-04	4.9448	2.2914
2_8	P22760	Arylacetamide deacetylase OS=Homo sapiens GN=AADAC PE=1 SV=5 - [AAAD_HUMAN]	2.89E-04	-5.6321	-2.6962	7.13E-03	-2.8267	-2.6394
2_8	P14868	Aspartate--tRNA ligase, cytoplasmic OS=Homo sapiens GN=DARS PE=1 SV=2 - [SYDC_HUMAN]	8.59E-05	5.9365	2.7269	1.06E-04	5.2941	2.6105
2_8	P53396	ATP-citrate synthase OS=Homo sapiens GN=ACLY PE=1 SV=3 - [ACLY_HUMAN]	2.02E-03	3.7566	2.6621	1.19E-02	2.5905	2.6394
2_8	Q92499	ATP-dependent RNA helicase DDX1 OS=Homo sapiens GN=DDX1 PE=1 SV=2 - [DDX1_HUMAN]	5.69E-08	23.9764	2.6698	1.63E-03	3.5946	2.2914
2_8	P13929	Beta-enolase OS=Homo sapiens GN=ENO3 PE=1 SV=5 - [ENOB_HUMAN]	1.19E-02	-2.7577	-2.8908	1.68E-02	-2.4241	-2.5460
2_8	Q93088	Betaine--homocysteine S-methyltransferase 1 OS=Homo sapiens GN=BHMT PE=1 SV=2 - [BHMT1_HUMAN]	3.77E-04	-5.3788	-2.8536	1.32E-03	-3.7147	-3.9443
2_8	Q9UBR1	Beta-ureidopropionase OS=Homo sapiens GN=UPB1 PE=1 SV=1 - [BUP1_HUMAN]	3.52E-04	-5.4510	-2.7768	2.69E-03	-3.3534	-2.3236

Fig. 7 continued

2_8	P34913	Bifunctional epoxide hydrolase 2 OS=Homo sapiens GN=EPHX2 PE=1 SV=2 - [HYES_HUMAN]	8.29E-06	-16.8141	-2.7439	4.17E-05	-6.0466	-2.0114
2_8	P31939	Bifunctional purine biosynthesis protein PURH OS=Homo sapiens GN=ATIC PE=1 SV=3 - [PUR9_HUMAN]	5.97E-03	2.8542	2.8264	9.07E-07	10.8750	3.9166
2_8	P21810	Biglycan OS=Homo sapiens GN=BGN PE=1 SV=2 - [PGS1_HUMAN]	1.35E-02	2.6704	2.8100	3.43E-03	3.2189	3.1742
2_8	Q14032	Bile acid-CoA:amino acid N-acyltransferase OS=Homo sapiens GN=BAAT PE=1 SV=1 - [BAAT_HUMAN]	9.33E-06	-13.5177	-2.8539	1.97E-05	-6.5942	-2.6218
2_8	Q9Y2P5	Bile acyl-CoA synthetase OS=Homo sapiens GN=SLC27A5 PE=1 SV=1 - [S27A5_HUMAN]	3.55E-04	-5.4430	-2.7777	1.01E-03	-3.8922	-3.5460
2_8	Q06520	Bile salt sulfotransferase OS=Homo sapiens GN=SULT2A1 PE=1 SV=3 - [ST2A1_HUMAN]	8.40E-06	-14.7411	-2.9192	1.68E-05	-6.9258	-4.0747
2_8	Q12864	Cadherin-17 OS=Homo sapiens GN=CDH17 PE=1 SV=3 - [CAD17_HUMAN]	2.00E-04	5.7758	2.7688	3.64E-04	4.5434	3.2065
2_8	Q9UJS0	Calcium-binding mitochondrial carrier protein Aralar2 OS=Homo sapiens GN=SLC25A13 PE=1 SV=2 - [CMC2_HUMAN]	7.78E-04	-3.9943	-2.8168	5.71E-05	-5.7103	-3.6813
2_8	P31327	Carbamoyl-phosphate synthase [ammonia], mitochondrial OS=Homo sapiens GN=CPS1 PE=1 SV=2 - [CPSM_HUMAN]	5.99E-04	-4.2301	-3.0320	3.42E-05	-6.2094	-7.5266
2_8	P00915	Carbonic anhydrase 1 OS=Homo sapiens GN=CA1 PE=1 SV=2 - [CAH1_HUMAN]	6.19E-04	-4.1931	-2.7555	1.01E-03	-3.8949	-2.5520
2_8	P00918	Carbonic anhydrase 2 OS=Homo sapiens GN=CA2 PE=1 SV=2 - [CAH2_HUMAN]	4.09E-05	-6.3546	-2.7679	2.48E-03	-3.3964	-2.2554
2_8	P06731	Carcinoembryonic antigen-related cell adhesion molecule 5 OS=Homo sapiens GN=CEACAM5 PE=1 SV=3 - [CEAM5_HUMAN]	7.06E-06	18.8897	2.8744	5.53E-04	4.2417	2.7240
2_8	P40199	Carcinoembryonic antigen-related cell adhesion molecule 6 OS=Homo sapiens GN=CEACAM6 PE=1 SV=3 - [CEAM6_HUMAN]	1.11E-03	3.8466	2.7790	2.96E-03	3.2087	2.0666
2_8	P23786	Carnitine O-palmitoyltransferase 2, mitochondrial OS=Homo sapiens GN=CPT2 PE=1 SV=2 - [CPT2_HUMAN]	1.65E-05	-7.3358	-2.7694	2.80E-03	-3.3335	-3.0755
2_8	P35221	Catenin alpha-1 OS=Homo sapiens GN=CTNNA1 PE=1 SV=1 - [CTNA1_HUMAN]	4.20E-03	3.2280	2.6880	9.89E-04	3.9084	2.7389
2_8	P35222	Catenin beta-1 OS=Homo sapiens GN=CTNNB1 PE=1 SV=1 - [CTNB1_HUMAN]	4.31E-03	3.1920	2.8094	2.66E-05	6.4045	3.4997
2_8	O60716	Catenin delta-1 OS=Homo sapiens GN=CTNND1 PE=1 SV=1 - [CTND1_HUMAN]	1.22E-02	2.7278	2.7073	1.51E-02	2.4800	2.8992
2_8	Q9UBR2	Cathepsin Z OS=Homo sapiens GN=CTSZ PE=1 SV=1 - [CATZ_HUMAN]	2.60E-05	-6.7793	-2.8622	4.53E-04	-4.3897	-2.0627
2_8	Q9BQB9	Copine-1 OS=Homo sapiens GN=CPNE1 PE=1 SV=1 - [CPNE1_HUMAN]	4.05E-05	6.3572	2.7256	9.66E-04	3.9218	2.2997
2_8	P28845	Corticosteroid 11-beta-dehydrogenase isozyme 1 OS=Homo sapiens GN=HSD11B1 PE=1 SV=3 - [DHI1_HUMAN]	3.46E-04	-5.4732	-2.7739	2.11E-04	-4.8962	-2.2673
2_8	P12277	Creatine kinase B-type OS=Homo sapiens GN=CKB PE=1 SV=1 - [KCRB_HUMAN]	6.73E-03	2.8213	2.7880	1.92E-02	2.3613	3.4402
2_8	Q86VP6	Cullin-associated NEDD8-dissociated protein 1 OS=Homo sapiens GN=CAND1 PE=1 SV=2 - [CAND1_HUMAN]	3.07E-03	3.5428	2.7095	4.41E-03	3.0879	2.3142
2_8	P32929	Cystathionine gamma-lyase OS=Homo sapiens GN=CTH PE=1 SV=3 - [CGL_HUMAN]	3.72E-04	-5.3896	-2.7750	9.55E-03	-2.6944	-2.7316
2_8	P00167	Cytochrome b5 OS=Homo sapiens GN=CYB5A PE=1 SV=2 - [CYB5_HUMAN]	9.36E-06	-13.3535	-2.9940	1.04E-04	-5.3045	-3.5964
2_8	P11509	Cytochrome P450 2A6 OS=Homo sapiens GN=CYP2A6 PE=1 SV=3 - [CP2A6_HUMAN]	8.37E-06	-15.4599	-2.8972	3.33E-03	-3.2388	-3.6597
2_8	P11712	Cytochrome P450 2C9 OS=Homo sapiens GN=CYP2C9 PE=1 SV=3 - [CP2C9_HUMAN]	4.11E-04	-5.2236	-2.8364	3.31E-03	-3.2410	-3.7909
2_8	P05181	Cytochrome P450 2E1 OS=Homo sapiens GN=CYP2E1 PE=1 SV=1 - [CP2E1_HUMAN]	2.59E-03	-3.6489	-2.7621	1.84E-02	-2.3803	-2.9678
2_8	Q14204	Cytoplasmic dynein 1 heavy chain 1 OS=Homo sapiens GN=DYNC1H1 PE=1 SV=5 - [DYHC1_HUMAN]	6.93E-04	4.0847	2.7153	2.64E-03	3.3631	3.9923
2_8	O75891	Cytosolic 10-formyltetrahydrofolate dehydrogenase OS=Homo sapiens GN=ALDH1L1 PE=1 SV=2 - [AL1L1_HUMAN]	6.87E-04	-4.0903	-2.8376	6.98E-03	-2.8391	-4.2534
2_8	Q02338	D-beta-hydroxybutyrate dehydrogenase, mitochondrial OS=Homo sapiens GN=BDH1 PE=1 SV=3 - [BDH_HUMAN]	3.64E-03	-3.3831	-2.8298	6.59E-06	-7.7049	-3.0118
2_8	P30038	Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial OS=Homo sapiens GN=ALDH4A1 PE=1 SV=3 - [AL4A1_HUMAN]	1.26E-04	-5.8792	-2.8957	1.89E-05	-6.8353	-4.3593
2_8	P54886	Delta-1-pyrroline-5-carboxylate synthase OS=Homo sapiens GN=ALDH18A1 PE=1 SV=2 - [P5CS_HUMAN]	1.42E-08	23.8624	2.6807	6.12E-03	2.9129	2.6394

Fig. 7 continued

2_8	P09417	Dihydropteridine reductase OS=Homo sapiens GN=QDPR PE=1 SV=2 - [DHPR_HUMAN]	7.14E-04	-4.0663	-2.7510	3.61E-03	-3.1917	-2.5460
2_8	Q14117	Dihydropyrimidinase OS=Homo sapiens GN=DPYS PE=1 SV=1 - [DPYS_HUMAN]	2.47E-04	-5.6884	-2.8922	7.62E-04	-4.0569	-2.7159
2_8	P31513	Dimethylaniline monooxygenase [N-oxide-forming] 3 OS=Homo sapiens GN=FMO3 PE=1 SV=5 - [FMO3_HUMAN]	8.90E-06	-14.1915	-2.8470	4.55E-03	-3.0686	-2.4253
2_8	Q9UI17	Dimethylglycine dehydrogenase, mitochondrial OS=Homo sapiens GN=DMGDH PE=1 SV=2 - [M2GD_HUMAN]	2.84E-04	-5.6442	-2.7582	4.88E-03	-3.0281	-2.3323
2_8	P11387	DNA topoisomerase 1 OS=Homo sapiens GN=TOP1 PE=1 SV=2 - [TOP1_HUMAN]	9.56E-04	3.8714	2.7446	2.83E-03	3.3291	2.3440
2_8	P78527	DNA-dependent protein kinase catalytic subunit OS=Homo sapiens GN=PRKDC PE=1 SV=3 - [PRKDC_HUMAN]	2.74E-03	3.6070	2.7749	3.46E-05	6.1940	5.1622
2_8	Q72627	E3 ubiquitin-protein ligase HUWE1 OS=Homo sapiens GN=HUWE1 PE=1 SV=3 - [HUWE1_HUMAN]	1.28E-05	7.3015	2.6790	1.50E-03	3.6426	2.3850
2_8	O75521	Enoyl-CoA delta isomerase 2, mitochondrial OS=Homo sapiens GN=ECI2 PE=1 SV=4 - [ECI2_HUMAN]	1.71E-04	-5.8171	-2.7705	1.63E-03	-3.5966	-2.7939
2_8	P56107	Ephrin OS=Homo sapiens GN=EPPK1 PE=1 SV=2 - [EPIPL_HUMAN]	5.12E-06	20.2857	2.7065	1.16E-03	3.7977	2.4170
2_8	P07099	Epoxide hydrolase 1 OS=Homo sapiens GN=EPHX1 PE=1 SV=1 - [HYEP_HUMAN]	6.04E-04	-4.2226	-3.0464	3.10E-06	-8.8458	-5.5825
2_8	Q9H0W9	Ester hydrolase C11orf54 OS=Homo sapiens GN=C11orf54 PE=1 SV=1 - [CK054_HUMAN]	2.52E-05	-6.8487	-2.7939	2.82E-04	-4.7189	-2.0627
2_8	P55060	Exportin-2 OS=Homo sapiens GN=CSE1L PE=1 SV=3 - [XPO2_HUMAN]	1.04E-05	10.7992	2.9586	2.88E-03	3.3187	2.5016
2_8	P15311	Ezrin OS=Homo sapiens GN=EZR PE=1 SV=4 - [EZRI_HUMAN]	1.84E-03	3.7820	2.8640	5.51E-04	4.2547	3.3846
2_8	O95954	Formimidoyltransferase-cyclodeaminase OS=Homo sapiens GN=FTCD PE=1 SV=2 - [FTCD_HUMAN]	9.37E-06	-13.2613	-2.8156	3.12E-03	-3.2713	-4.0241
2_8	P05062	Fructose-bisphosphate aldolase B OS=Homo sapiens GN=ALDOB PE=1 SV=2 - [ALDOB_HUMAN]	5.34E-05	-6.1562	-3.0577	3.70E-06	-8.4206	-5.9960
2_8	P16930	Fumarylacetoacetase OS=Homo sapiens GN=FAH PE=1 SV=2 - [FAAA_HUMAN]	4.08E-04	-5.2397	-2.8819	2.81E-05	-6.3696	-3.7219
2_8	P51570	Galactokinase OS=Homo sapiens GN=GALK1 PE=1 SV=1 - [GALK1_HUMAN]	1.92E-03	-3.7728	-2.7893	6.80E-03	-2.8534	-2.2554
2_8	O95479	GDH/6PGL endoplasmic bifunctional protein OS=Homo sapiens GN=H6PD PE=1 SV=2 - [G6PE_HUMAN]	9.32E-06	-13.5715	-2.7628	3.00E-04	-4.6537	-2.9678
2_8	Q06210	Glutamine--fructose-6-phosphate aminotransferase [isomerizing] 1 OS=Homo sapiens GN=GFPT1 PE=1 SV=3 - [GFPT1_HUMAN]	5.07E-05	6.1989	2.7907	1.17E-03	3.7897	3.2914
2_8	P08263	Glutathione S-transferase A1 OS=Homo sapiens GN=GSTA1 PE=1 SV=3 - [GSTA1_HUMAN]	9.41E-06	-12.9711	-3.0048	2.59E-03	-3.3745	-4.5966
2_8	P09488	Glutathione S-transferase Mu 1 OS=Homo sapiens GN=GSTM1 PE=1 SV=3 - [GSTM1_HUMAN]	1.50E-02	-2.5967	-2.8124	4.27E-03	-3.1062	-3.0118
2_8	P09211	Glutathione S-transferase P OS=Homo sapiens GN=GSTP1 PE=1 SV=2 - [GSTP1_HUMAN]	4.81E-03	3.0625	2.9457	2.34E-06	9.3207	4.9818
2_8	P50440	Glycine amidinotransferase, mitochondrial OS=Homo sapiens GN=GATM PE=1 SV=1 - [GATM_HUMAN]	8.33E-06	-15.9405	-2.9650	1.04E-03	-3.8646	-4.5520
2_8	P41250	Glycine--tRNA ligase OS=Homo sapiens GN=GARS PE=1 SV=3 - [SYG_HUMAN]	6.21E-04	4.1884	2.7478	6.67E-05	5.5713	2.5324
2_8	P11216	Glycogen phosphorylase, brain form OS=Homo sapiens GN=PYGB PE=1 SV=5 - [PYGB_HUMAN]	1.06E-03	3.8518	2.8001	4.14E-03	3.1239	4.7240
2_8	P06737	Glycogen phosphorylase, liver form OS=Homo sapiens GN=PYGL PE=1 SV=4 - [PYGL_HUMAN]	8.32E-06	-16.2053	-2.9466	1.95E-05	-6.6799	-3.9678
2_8	Q92598	Heat shock protein 105 kDa OS=Homo sapiens GN=HSPH1 PE=1 SV=1 - [HS105_HUMAN]	2.51E-06	22.2078	2.8188	1.76E-04	4.9863	3.2769
2_8	P02790	Hemopexin OS=Homo sapiens GN=HPX PE=1 SV=2 - [HEMO_HUMAN]	7.00E-04	4.0782	2.7585	1.59E-02	2.4540	2.3474
2_8	Q9BUJ2	Heterogeneous nuclear ribonucleoprotein U-like protein 1 OS=Homo sapiens GN=HNRNPUL1 PE=1 SV=2 - [HNRL1_HUMAN]	2.74E-03	3.6091	2.6996	5.39E-03	2.9829	2.2997
2_8	Q1KMD3	Heterogeneous nuclear ribonucleoprotein U-like protein 2 OS=Homo sapiens GN=HNRNPUL2 PE=1 SV=1 - [HNRL2_HUMAN]	6.26E-04	4.1819	2.7958	1.39E-04	5.1458	3.3142
2_8	P26583	High mobility group protein B2 OS=Homo sapiens GN=HMGB2 PE=1 SV=2 - [HMGB2_HUMAN]	1.86E-02	2.4667	2.8017	6.09E-03	2.9157	2.3611
2_8	Q93099	Homogentisate 1,2-dioxygenase OS=Homo sapiens GN=HGD PE=1 SV=2 - [HGD_HUMAN]	9.19E-06	-13.9676	-2.8230	2.71E-05	-6.3987	-4.0222

Fig. 7 continued

2_8	Q9UJM8	Hydroxyacid oxidase 1 OS=Homo sapiens GN=HAO1 PE=1 SV=1 - [HAOX1_HUMAN]	8.52E-06	-14.5838	-2.90112	1.26E-05	-7.2034	-4.6766
2_8	P35914	Hydroxymethylglutaryl-CoA lyase, mitochondrial OS=Homo sapiens GN=HMGCL PE=1 SV=2 - [HMGCL_HUMAN]	5.64E-03	-2.8978	-2.77659	1.27E-03	-3.7411	-2.4944
2_8	O00410	Importin-5 OS=Homo sapiens GN=IPO5 PE=1 SV=4 - [IPO5_HUMAN]	4.54E-05	6.2742	2.73315	1.64E-04	5.0298	2.6216
2_8	Q15181	Inorganic pyrophosphatase OS=Homo sapiens GN=PPA1 PE=1 SV=2 - [IPYR_HUMAN]	5.70E-04	4.2929	2.72686	5.09E-03	3.0054	2.2981
2_8	P26440	Isovaleryl-CoA dehydrogenase, mitochondrial OS=Homo sapiens GN=IVD PE=1 SV=1 - [IVD_HUMAN]	1.96E-02	-2.4334	-2.7571	8.91E-03	-2.7250	-2.0747
2_8	P14923	Junction plakoglobin OS=Homo sapiens GN=JUP PE=1 SV=3 - [PLAK_HUMAN]	6.53E-05	6.0610	2.7850	1.62E-06	9.6513	2.9761
2_8	P08727	Keratin, type I cytoskeletal 19 OS=Homo sapiens GN=KRT19 PE=1 SV=4 - [K1C19_HUMAN]	6.49E-06	19.5914	2.8580	5.36E-05	5.7526	4.7993
2_8	P04259	Keratin, type II cytoskeletal 6B OS=Homo sapiens GN=KRT6B PE=1 SV=5 - [K2C6B_HUMAN]	2.03E-02	-2.4060	-2.9050	3.45E-02	-2.0814	-2.7219
2_8	P23141	Liver carboxylesterase 1 OS=Homo sapiens GN=CES1 PE=1 SV=2 - [EST1_HUMAN]	6.30E-04	-4.1765	-3.0234	3.74E-05	-6.1356	-5.7751
2_8	P07195	L-lactate dehydrogenase B chain OS=Homo sapiens GN=LDHB PE=1 SV=2 - [LDHB_HUMAN]	9.00E-04	3.8989	2.9143	1.97E-05	6.5988	4.0041
2_8	P33121	Long-chain-fatty-acid--CoA ligase 1 OS=Homo sapiens GN=ACSL1 PE=1 SV=1 - [ACSL1_HUMAN]	8.42E-06	-15.0296	-2.8078	1.07E-06	-10.1533	-3.7481
2_8	Q15046	Lysine--tRNA ligase OS=Homo sapiens GN=KARS PE=1 SV=3 - [SYK_HUMAN]	7.53E-03	2.8095	2.6871	2.78E-04	4.7273	2.2997
2_8	P10253	Lysosomal alpha-glucosidase OS=Homo sapiens GN=GAA PE=1 SV=4 - [LYAG_HUMAN]	1.14E-05	-7.7728	-2.8348	2.03E-03	-3.4882	-2.7219
2_8	P40121	Macrophage-capping protein OS=Homo sapiens GN=CAPG PE=1 SV=2 - [CAPG_HUMAN]	2.64E-05	6.7720	2.8149	6.59E-06	7.7005	3.0019
2_8	Q14764	Major vault protein OS=Homo sapiens GN=MVP PE=1 SV=4 - [MVP_HUMAN]	6.36E-04	4.1678	2.7809	1.15E-03	3.8081	3.6105
2_8	P11310	Medium-chain specific acyl-CoA dehydrogenase, mitochondrial OS=Homo sapiens GN=ACADM PE=1 SV=1 - [ACADM_HUMAN]	1.66E-05	-7.3199	-2.8628	1.07E-06	-10.1427	-3.1863
2_8	Q02252	Methylmalonate-semialdehyde dehydrogenase [acylating], mitochondrial OS=Homo sapiens GN=ALDH6A1 PE=1 SV=2 - [MMSA_HUMAN]	4.82E-04	-4.5804	-2.8877	1.09E-04	-5.2804	-4.8374
2_8	Q9H8H3	Methyltransferase-like protein 7A OS=Homo sapiens GN=METTL7A PE=1 SV=1 - [METTA_HUMAN]	8.29E-06	-16.7897	-2.8084	7.59E-05	-5.4891	-2.0606
2_8	P10620	Microsomal glutathione S-transferase 1 OS=Homo sapiens GN=MGST1 PE=1 SV=1 - [MGST1_HUMAN]	8.52E-06	-14.5806	-2.8540	9.59E-06	-7.3877	-2.4391
2_8	P55157	Microsomal triglyceride transfer protein large subunit OS=Homo sapiens GN=MTTP PE=1 SV=1 - [MTP_HUMAN]	1.01E-05	-11.4288	-2.7437	4.45E-06	-8.1044	-3.0747
2_8	Q969Z3	MOSC domain-containing protein 2, mitochondrial OS=Homo sapiens GN=MARC2 PE=1 SV=1 - [MOSC2_HUMAN]	9.11E-06	-14.1039	-2.7157	2.23E-04	-4.8655	-2.5520
2_8	P05164	Myeloperoxidase OS=Homo sapiens GN=MPO PE=1 SV=1 - [PERM_HUMAN]	7.60E-05	5.9660	2.7651	3.92E-03	3.1571	3.2914
2_8	Q72406	Myosin-14 OS=Homo sapiens GN=MYH14 PE=1 SV=2 - [MYH14_HUMAN]	4.16E-06	20.7491	2.8464	5.76E-04	4.2142	4.7662
2_8	Q4G0N4	NAD kinase domain-containing protein 1 OS=Homo sapiens GN=NADKD1 PE=1 SV=2 - [NAKD1_HUMAN]	8.44E-06	-14.9263	-2.8631	7.62E-05	-5.4880	-2.7939
2_8	P16435	NADPH--cytochrome P450 reductase OS=Homo sapiens GN=POR PE=1 SV=2 - [NCPR_HUMAN]	5.79E-04	-4.2709	-2.8868	2.59E-04	-4.7781	-3.5681
2_8	P22307	Non-specific lipid-transfer protein OS=Homo sapiens GN=SCP2 PE=1 SV=2 - [NLTP_HUMAN]	5.27E-04	-4.4014	-2.8208	5.32E-04	-4.2804	-3.3548
2_8	Q14980	Nuclear mitotic apparatus protein 1 OS=Homo sapiens GN=NUMA1 PE=1 SV=2 - [NUMA1_HUMAN]	5.92E-06	19.8780	2.6318	7.34E-03	2.8125	2.2386
2_8	O00567	Nucleolar protein 56 OS=Homo sapiens GN=NOP56 PE=1 SV=4 - [NOP56_HUMAN]	3.25E-06	21.2834	2.7320	7.25E-04	4.0829	2.3142
2_8	P00480	Ornithine carbamoyltransferase, mitochondrial OS=Homo sapiens GN=OTC PE=1 SV=3 - [OTC_HUMAN]	8.45E-06	-14.8728	-2.9020	5.52E-06	-7.9484	-4.1166
2_8	Q02790	Peptidyl-prolyl cis-trans isomerase FKBP4 OS=Homo sapiens GN=FKBP4 PE=1 SV=3 - [FKBP4_HUMAN]	4.33E-05	6.3252	2.6916	7.40E-04	4.0729	2.9627
2_8	Q15063	Periostin OS=Homo sapiens GN=POSTN PE=1 SV=2 - [POSTN_HUMAN]	8.30E-06	16.5373	2.7865	1.45E-02	2.5014	3.3474
2_8	Q15067	Peroxisomal acyl-coenzyme A oxidase 1 OS=Homo sapiens GN=ACOX1 PE=1 SV=3 - [ACOX1_HUMAN]	2.91E-05	-6.6094	-2.7623	4.32E-04	-4.4140	-3.6013

Fig. 7 continued

2_8	Q99424	Peroxisomal acyl-coenzyme A oxidase 2 OS=Homo sapiens GN=ACOX2 PE=1 SV=1 - [ACOX2_HUMAN]	9.11E-06	-14.1095	-2.7478	2.52E-03	-3.3885	-3.1310
2_8	Q08426	Peroxisomal bifunctional enzyme OS=Homo sapiens GN=EHHADH PE=1 SV=3 - [ECHP_HUMAN]	3.60E-04	-5.4257	-2.9160	7.00E-05	-5.5311	-5.2498
2_8	Q9P0Z9	Peroxisomal sarcosine oxidase OS=Homo sapiens GN=PIPOX PE=2 SV=2 - [SOX_HUMAN]	8.57E-06	-14.4133	-2.8337	1.94E-05	-6.7133	-3.9173
2_8	Q9Y285	Phenylalanine--tRNA ligase alpha subunit OS=Homo sapiens GN=FARSA PE=1 SV=3 - [SYFA_HUMAN]	1.90E-03	3.7758	2.6603	2.89E-03	3.3170	2.1622
2_8	Q9NSD9	Phenylalanine--tRNA ligase beta subunit OS=Homo sapiens GN=FARSB PE=1 SV=3 - [SYFB_HUMAN]	7.61E-05	5.9928	2.7077	3.79E-04	4.5204	2.5772
2_8	Q14651	Plastin-1 OS=Homo sapiens GN=PLS1 PE=1 SV=2 - [PLS1_HUMAN]	3.49E-05	6.4525	2.8071	2.10E-04	4.8977	2.7240
2_8	Q6P2Q9	Pre-mRNA-processing-splicing factor 8 OS=Homo sapiens GN=PRPF8 PE=1 SV=2 - [PRP8_HUMAN]	6.22E-06	19.7361	2.6754	4.48E-03	3.0790	2.3761
2_8	P17844	Probable ATP-dependent RNA helicase DDX5 OS=Homo sapiens GN=DDX5 PE=1 SV=1 - [DDX5_HUMAN]	2.81E-04	5.6507	2.7914	4.50E-04	4.3941	3.2734
2_8	P12004	Proliferating cell nuclear antigen OS=Homo sapiens GN=PCNA PE=1 SV=1 - [PCNA_HUMAN]	3.40E-04	5.4932	2.7851	4.83E-02	1.9450	3.0255
2_8	Q14914	Prostaglandin reductase 1 OS=Homo sapiens GN=PTGR1 PE=1 SV=2 - [PTGR1_HUMAN]	9.31E-06	-13.6123	-2.8204	2.92E-04	-4.6878	-3.3166
2_8	Q9BPW8	Protein NipSnap homolog 1 OS=Homo sapiens GN=NIPSNAP1 PE=1 SV=1 - [NIPS1_HUMAN]	3.27E-03	-3.4906	-2.8331	1.09E-04	-5.2752	-2.9866
2_8	Q9P258	Protein RCC2 OS=Homo sapiens GN=RCC2 PE=1 SV=2 - [RCC2_HUMAN]	3.05E-06	21.5455	2.6566	9.32E-04	3.9381	2.4152
2_8	P06703	Protein S100-A6 OS=Homo sapiens GN=S100A6 PE=1 SV=1 - [S10A6_HUMAN]	2.86E-05	6.6820	2.8409	1.27E-03	3.7427	2.0545
2_8	P55786	Puromycin-sensitive aminopeptidase OS=Homo sapiens GN=NPEPPS PE=1 SV=2 - [PSA_HUMAN]	6.13E-04	4.2053	2.6909	4.59E-05	5.9334	2.9627
2_8	O43143	Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15 OS=Homo sapiens GN=DHX15 PE=1 SV=2 - [DHX15_HUMAN]	5.57E-04	4.3274	2.7146	1.37E-04	5.1649	2.4356
2_8	Q9NVS9	Pyridoxine-5-phosphate oxidase OS=Homo sapiens GN=PNPO PE=1 SV=1 - [PNPO_HUMAN]	8.39E-04	-3.8991	-2.8059	2.28E-04	-4.8804	-2.4373
2_8	P11498	Pyruvate carboxylase, mitochondrial OS=Homo sapiens GN=PC PE=1 SV=2 - [PYC_HUMAN]	9.37E-06	-13.3228	-2.8449	2.63E-05	-6.4269	-4.8219
2_8	P30613	Pyruvate kinase isozymes R/L OS=Homo sapiens GN=PKLR PE=1 SV=2 - [KPYR_HUMAN]	8.00E-06	-18.3184	-2.8332	6.28E-04	-4.1686	-3.3175
2_8	Q13283	Ras GTPase-activating protein-binding protein 1 OS=Homo sapiens GN=G3BP1 PE=1 SV=1 - [G3BP1_HUMAN]	1.61E-02	2.5554	2.6861	4.45E-04	4.4010	2.0866
2_8	P46940	Ras GTPase-activating-like protein IQGAP1 OS=Homo sapiens GN=IQGAP1 PE=1 SV=1 - [IQGA1_HUMAN]	3.67E-06	20.9268	2.7990	2.01E-05	6.5511	4.1954
2_8	Q13576	Ras GTPase-activating-like protein IQGAP2 OS=Homo sapiens GN=IQGAP2 PE=1 SV=4 - [IQGA2_HUMAN]	1.74E-04	-5.8141	-2.6976	3.23E-03	-3.2562	-2.7148
2_8	O75452	Retinol dehydrogenase 16 OS=Homo sapiens GN=RDH16 PE=1 SV=2 - [RDH16_HUMAN]	3.63E-04	-5.4067	-2.7982	1.63E-03	-3.5866	-2.3593
2_8	P02753	Retinol-binding protein 4 OS=Homo sapiens GN=RBP4 PE=1 SV=3 - [RET4_HUMAN]	8.37E-06	-15.3927	-2.8141	2.33E-04	-4.8337	-2.4944
2_8	P52758	Ribonuclease UK114 OS=Homo sapiens GN=HRSP12 PE=1 SV=1 - [UK114_HUMAN]	8.62E-06	-14.2705	-2.9118	5.51E-05	-5.7379	-3.3825
2_8	Q9UKM9	RNA-binding protein Raly OS=Homo sapiens GN=RALY PE=1 SV=1 - [RALY_HUMAN]	4.56E-03	3.1222	2.7958	3.72E-06	8.4100	2.6927
2_8	Q9Y265	RuvB-like 1 OS=Homo sapiens GN=RUVBL1 PE=1 SV=1 - [RUVB1_HUMAN]	1.30E-06	24.9007	2.7000	3.14E-06	8.8226	2.4517
2_8	Q8NBX0	Saccharopine dehydrogenase-like oxidoreductase OS=Homo sapiens GN=SCCPDH PE=1 SV=1 - [SCPDL_HUMAN]	1.14E-05	-7.8377	-2.8219	2.92E-06	-8.9206	-2.7268
2_8	Q00266	S-adenosylmethionine synthase isoform type-1 OS=Homo sapiens GN=MAT1A PE=1 SV=2 - [METK1_HUMAN]	9.34E-06	-13.5038	-2.8606	1.27E-03	-3.7415	-2.8628
2_8	Q9UL12	Sarcosine dehydrogenase, mitochondrial OS=Homo sapiens GN=SARDH PE=1 SV=1 - [SARDH_HUMAN]	2.71E-04	-5.6627	-2.7893	4.71E-04	-4.3623	-3.1624
2_8	Q15019	Septin-2 OS=Homo sapiens GN=SEPT2 PE=1 SV=1 - [SEPT2_HUMAN]	3.60E-05	6.4174	2.7322	1.94E-05	6.7151	2.4356
2_8	Q16181	Septin-7 OS=Homo sapiens GN=SEPT7 PE=1 SV=2 - [SEPT7_HUMAN]	4.35E-03	3.1783	2.6803	1.35E-03	3.7002	2.0255
2_8	Q9UHD8	Septin-9 OS=Homo sapiens GN=SEPT9 PE=1 SV=2 - [SEPT9_HUMAN]	3.31E-03	3.4796	2.6779	1.60E-02	2.4512	2.0367

Fig. 7 continued

2_8	P34896	Serine hydroxymethyltransferase, cytosolic OS=Homo sapiens GN=SHMT1 PE=1 SV=1 - [GLYC_HUMAN]	8.35E-06	-15.7261	-2.8595	4.15E-04	-4.4546	-3.6455
2_8	P21549	Serine--pyruvate aminotransferase OS=Homo sapiens GN=AGXT PE=1 SV=1 - [SPYA_HUMAN]	1.16E-05	-7.6270	-3.0092	5.91E-05	-5.6886	-6.0079
2_8	P35237	Serpin B6 OS=Homo sapiens GN=SERPINB6 PE=1 SV=3 - [SPB6_HUMAN]	8.98E-03	2.7949	2.7966	4.68E-03	3.0501	2.5772
2_8	P45954	Short/branched chain specific acyl-CoA dehydrogenase, mitochondrial OS=Homo sapiens GN=ACADSB PE=1 SV=1 - [ACDSB_HUMAN]	1.16E-04	-5.8944	-2.8717	2.79E-06	-8.9809	-3.3069
2_8	Q9H9B4	Sideroflexin-1 OS=Homo sapiens GN=SFXN1 PE=1 SV=4 - [SFXN1_HUMAN]	4.42E-04	-4.9106	-2.7687	5.24E-05	-5.7792	-2.4391
2_8	O75533	Splicing factor 3B subunit 1 OS=Homo sapiens GN=SF3B1 PE=1 SV=3 - [SF3B1_HUMAN]	4.60E-04	4.7214	2.6708	2.33E-03	3.4236	2.5221
2_8	Q15393	Splicing factor 3B subunit 3 OS=Homo sapiens GN=SF3B3 PE=1 SV=4 - [SF3B3_HUMAN]	4.44E-05	6.2881	2.7124	1.76E-04	4.9817	2.3761
2_8	P26368	Splicing factor U2AF 65 kDa subunit OS=Homo sapiens GN=U2AF2 PE=1 SV=4 - [U2AF2_HUMAN]	5.15E-03	2.9817	2.7558	8.60E-04	3.9804	2.1460
2_8	Q14247	Src substrate cortactin OS=Homo sapiens GN=CTTN PE=1 SV=2 - [SRC8_HUMAN]	2.70E-06	22.0572	2.7471	5.27E-05	5.7713	2.4366
2_8	Q02318	Sterol 26-hydroxylase, mitochondrial OS=Homo sapiens GN=CYP27A1 PE=1 SV=1 - [CP27A_HUMAN]	8.45E-06	-14.8968	-2.7763	6.69E-04	-4.1259	-2.4391
2_8	P40643	T-complex protein 1 subunit epsilon OS=Homo sapiens GN=CCT5 PE=1 SV=1 - [TCPE_HUMAN]	1.88E-03	3.7779	2.7078	5.73E-05	5.7071	2.2997
2_8	P24821	Tenascin OS=Homo sapiens GN=TNC PE=1 SV=3 - [TENA_HUMAN]	5.97E-05	6.0885	2.7745	4.65E-03	3.0541	3.3556
2_8	P19971	Thymidine phosphorylase OS=Homo sapiens GN=TYMP PE=1 SV=2 - [TYPH_HUMAN]	1.51E-03	-3.8123	-2.8089	2.90E-02	-2.1544	-2.8628
2_8	Q13263	Transcription intermediary factor 1-beta OS=Homo sapiens GN=TRIM28 PE=1 SV=5 - [TIF1B_HUMAN]	2.40E-06	25.3652	2.7771	1.39E-04	5.1592	3.4696
2_8	P53007	Tricarboxylate transport protein, mitochondrial OS=Homo sapiens GN=SLC25A1 PE=1 SV=2 - [TXTP_HUMAN]	5.20E-03	-2.9721	-2.7448	1.35E-03	-3.7011	-2.1981
2_8	Q9BQE3	Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 - [TBA1C_HUMAN]	1.26E-03	3.8333	2.9913	8.80E-03	2.7314	5.3684
2_8	P68366	Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A PE=1 SV=1 - [TBA4A_HUMAN]	1.83E-02	2.4763	3.0127	1.09E-04	5.2803	5.5599
2_8	Q3ZCM7	Tubulin beta-8 chain OS=Homo sapiens GN=TUBB8 PE=1 SV=2 - [TBB8_HUMAN]	1.46E-02	2.6164	2.9105	7.31E-03	2.8145	4.7672
2_8	O43399	Tumor protein D54 OS=Homo sapiens GN=TPD52L2 PE=1 SV=2 - [TPD54_HUMAN]	4.13E-03	3.2413	2.6755	1.78E-03	3.5607	2.0545
2_8	P15374	Ubiquitin carboxyl-terminal hydrolase isozyme L3 OS=Homo sapiens GN=UCHL3 PE=1 SV=1 - [UCHL3_HUMAN]	5.88E-04	4.2518	2.6997	3.04E-05	6.3342	2.1742
2_8	P22310	UDP-glucuronosyltransferase 1-4 OS=Homo sapiens GN=UGT1A4 PE=1 SV=1 - [UD14_HUMAN]	3.41E-04	-5.4923	-2.8845	6.78E-04	-4.1140	-2.9086
2_8	O60656	UDP-glucuronosyltransferase 1-9 OS=Homo sapiens GN=UGT1A9 PE=1 SV=1 - [UD19_HUMAN]	9.95E-03	-2.7835	-2.8097	1.05E-02	-2.6519	-2.4391
2_8	P06133	UDP-glucuronosyltransferase 2B4 OS=Homo sapiens GN=UGT2B4 PE=1 SV=2 - [UD2B4_HUMAN]	9.15E-06	-14.0468	-2.7905	7.92E-04	-4.0338	-2.7008
2_8	P16662	UDP-glucuronosyltransferase 2B7 OS=Homo sapiens GN=UGT2B7 PE=1 SV=1 - [UD2B7_HUMAN]	3.59E-04	-5.4286	-2.7992	3.05E-03	-3.2828	-2.7316
2_8	O94832	Unconventional myosin-Id OS=Homo sapiens GN=MYO1D PE=1 SV=2 - [MYO1D_HUMAN]	1.08E-03	3.8490	2.6680	1.67E-02	2.4275	2.4170
2_8	Q96QK1	Vacuolar protein sorting-associated protein 35 OS=Homo sapiens GN=VPS35 PE=1 SV=2 - [VPS35_HUMAN]	3.35E-03	3.4671	2.6981	1.13E-05	7.3191	2.7259
2_8	P13611	Versican core protein OS=Homo sapiens GN=VCAN PE=1 SV=3 - [CSPG2_HUMAN]	2.46E-03	3.6819	2.7352	9.52E-03	2.6960	2.0255
2_8	P09327	Villin-1 OS=Homo sapiens GN=VIL1 PE=1 SV=4 - [VIL1_HUMAN]	1.83E-07	23.3591	2.7640	3.54E-06	8.5474	3.6394
2_9	P31947	14-3-3 protein sigma OS=Homo sapiens GN=SFN PE=1 SV=1 - [1433S_HUMAN]	4.42E-02	2.1161	2.9592	2.63E-02	2.2394	2.9563
2_9	O14756	17-beta-hydroxysteroid dehydrogenase type 6 OS=Homo sapiens GN=HSD17B6 PE=1 SV=1 - [H17B6_HUMAN]	4.32E-05	-14.5723	-2.8648	2.18E-05	-8.8102	-3.5460
2_9	P12694	2-oxoisovalerate dehydrogenase subunit alpha, mitochondrial OS=Homo sapiens GN=BCKDHA PE=1 SV=2 - [ODBA_HUMAN]	2.41E-03	-3.7847	-2.6657	2.40E-02	-2.2920	-2.1159
2_9	P80404	4-aminobutyrate aminotransferase, mitochondrial OS=Homo sapiens GN=ABAT PE=1 SV=3 - [GABT_HUMAN]	6.24E-04	-5.1111	-2.8460	1.95E-04	-5.5847	-4.6929

Fig. 7 continued

2_9	P32754	4-hydroxyphenylpyruvate dioxygenase OS=Homo sapiens GN=HPD PE=1 SV=2 - [HPPD_HUMAN]	4.99E-05	-12.6416	-2.8898	4.69E-04	-4.7439	-4.7268
2_9	P24752	Acetyl-CoA acetyltransferase, mitochondrial OS=Homo sapiens GN=ACAT1 PE=1 SV=1 - [THIL_HUMAN]	1.36E-03	-4.2385	-2.9105	2.19E-05	-8.7635	-3.9739
2_9	Q08AH3	Acyl-coenzyme A synthetase ACSM2A, mitochondrial OS=Homo sapiens GN=ACSM2A PE=1 SV=2 - [ACS2A_HUMAN]	2.88E-05	-16.0532	-2.8285	4.37E-04	-4.8093	-4.3789
2_9	Q6BCX6	Acyl-coenzyme A synthetase ACSM2B, mitochondrial OS=Homo sapiens GN=ACSM2B PE=1 SV=2 - [ACS2B_HUMAN]	2.99E-05	-16.8809	-2.8285	1.75E-04	-5.6594	-4.4100
2_9	P24298	Alanine aminotransferase 1 OS=Homo sapiens GN=GPT PE=1 SV=3 - [ALAT1_HUMAN]	5.41E-04	-5.3706	-2.7134	8.25E-04	-4.2661	-3.5153
2_9	P08319	Alcohol dehydrogenase 4 OS=Homo sapiens GN=ADH4 PE=1 SV=5 - [ADH4_HUMAN]	4.96E-05	-12.7989	-2.8967	6.66E-03	-2.9801	-4.8219
2_9	Q9H2A2	Aldehyde dehydrogenase family 8 member A1 OS=Homo sapiens GN=ALDH8A1 PE=1 SV=1 - [AL8A1_HUMAN]	3.90E-04	-5.6224	-2.7885	3.80E-04	-4.9419	-2.3323
2_9	Q06278	Aldehyde oxidase OS=Homo sapiens GN=AOX1 PE=2 SV=2 - [AOX_HUMAN]	2.94E-03	-3.7191	-2.7288	2.38E-02	-2.2971	-3.3236
2_9	P52895	Aldo-keto reductase family 1 member C2 OS=Homo sapiens GN=AKR1C2 PE=1 SV=3 - [AK1C2_HUMAN]	2.02E-02	-2.4633	-2.9553	4.94E-02	-1.9526	-4.3506
2_9	Q03154	Aminoacylase-1 OS=Homo sapiens GN=ACY1 PE=1 SV=1 - [ACY1_HUMAN]	1.13E-03	-4.5626	-2.9370	2.32E-04	-5.3985	-4.3069
2_9	P27216	Annexin A13 OS=Homo sapiens GN=ANXA13 PE=1 SV=3 - [ANX13_HUMAN]	3.39E-05	15.3326	2.9618	4.98E-04	4.6796	3.3431
2_9	O95994	Anterior gradient protein 2 homolog OS=Homo sapiens GN=AGR2 PE=1 SV=1 - [AGR2_HUMAN]	5.59E-05	7.3537	3.1376	3.32E-05	8.0290	3.9199
2_9	O95831	Apoptosis-inducing factor 1, mitochondrial OS=Homo sapiens GN=AIFM1 PE=1 SV=1 - [AIFM1_HUMAN]	8.74E-03	-3.0369	-2.8141	4.64E-05	-7.4023	-3.7008
2_9	P05089	Arginase-1 OS=Homo sapiens GN=ARG1 PE=1 SV=2 - [ARGI1_HUMAN]	4.75E-05	-13.8063	-2.9120	2.74E-04	-5.2734	-4.5199
2_9	P22760	Arylacetamide deacetylase OS=Homo sapiens GN=AADAC PE=1 SV=5 - [AAAD_HUMAN]	3.79E-04	-5.6321	-2.6962	8.54E-03	-2.8267	-2.6394
2_9	Q9BXN1	Asporin OS=Homo sapiens GN=ASPN PE=1 SV=2 - [ASPN_HUMAN]	3.43E-05	15.2567	3.0403	5.85E-04	4.5521	2.9255
2_9	P13929	Beta-enolase OS=Homo sapiens GN=ENO3 PE=1 SV=5 - [ENOB_HUMAN]	1.36E-02	-2.7577	-2.8908	1.88E-02	-2.4241	-2.5460
2_9	P16278	Beta-galactosidase OS=Homo sapiens GN=GLB1 PE=1 SV=2 - [BGAL_HUMAN]	3.30E-02	-2.2163	-2.7440	4.86E-03	-3.1261	-2.3236
2_9	Q93088	Betaine--homocysteine S-methyltransferase 1 OS=Homo sapiens GN=BHMT PE=1 SV=2 - [BHMT1_HUMAN]	2.04E-03	-3.8421	-2.8536	1.94E-03	-3.6845	-3.9443
2_9	Q9UBR1	Beta-ureidopropionase OS=Homo sapiens GN=UPB1 PE=1 SV=1 - [BUP1_HUMAN]	5.09E-04	-5.4510	-2.7768	3.29E-03	-3.3534	-2.3236
2_9	P34913	Bifunctional epoxide hydrolase 2 OS=Homo sapiens GN=EPHX2 PE=1 SV=2 - [HYES_HUMAN]	1.71E-05	-16.8141	-2.7439	1.26E-04	-6.0466	-2.0114
2_9	P21810	Biglycan OS=Homo sapiens GN=BGN PE=1 SV=2 - [PGS1_HUMAN]	4.17E-04	5.5836	3.1510	9.51E-06	10.6300	5.5185
2_9	Q14032	Bile acid-CoA:amino acid N-acyltransferase OS=Homo sapiens GN=BAAT PE=1 SV=1 - [BAAT_HUMAN]	4.76E-05	-13.5177	-2.8539	7.71E-05	-6.5942	-2.6218
2_9	Q9Y2P5	Bile acyl-CoA synthetase OS=Homo sapiens GN=SLC27A5 PE=1 SV=1 - [S27A5_HUMAN]	5.14E-04	-5.4430	-2.7777	1.41E-03	-3.8922	-3.5460
2_9	Q06520	Bile salt sulfotransferase OS=Homo sapiens GN=SULT2A1 PE=1 SV=3 - [ST2A1_HUMAN]	4.04E-05	-14.7411	-2.9192	6.27E-05	-6.9258	-4.0747
2_9	P11586	C-1-tetrahydrofolate synthase, cytoplasmic OS=Homo sapiens GN=MTHFD1 PE=1 SV=3 - [C1TC_HUMAN]	5.05E-04	-5.4569	-2.8443	4.99E-04	-4.6788	-4.6455
2_9	P17655	Calpain-2 catalytic subunit OS=Homo sapiens GN=CAPN2 PE=1 SV=5 - [CAN2_HUMAN]	3.16E-05	15.7356	2.9337	2.27E-04	5.4397	3.1575
2_9	P23786	Carnitine O-palmitoyltransferase 2, mitochondrial OS=Homo sapiens GN=CPT2 PE=1 SV=2 - [CPT2_HUMAN]	5.73E-04	-5.2779	-2.7694	2.93E-03	-3.4185	-3.0755
2_9	P35221	Catenin alpha-1 OS=Homo sapiens GN=CTNNA1 PE=1 SV=1 - [CTNA1_HUMAN]	1.88E-03	3.9055	2.8648	9.83E-04	4.1458	3.3156
2_9	P35222	Catenin beta-1 OS=Homo sapiens GN=CTNNB1 PE=1 SV=1 - [CTNB1_HUMAN]	4.23E-03	3.4532	2.8628	2.29E-02	2.3159	2.3529
2_9	O60716	Catenin delta-1 OS=Homo sapiens GN=CTNND1 PE=1 SV=1 - [CTND1_HUMAN]	7.73E-04	4.8325	2.8941	7.25E-03	2.9184	2.5825
2_9	P08311	Cathepsin G OS=Homo sapiens GN=CTSG PE=1 SV=2 - [CATG_HUMAN]	1.01E-02	2.8951	2.9910	6.91E-03	2.9410	2.7459

Fig. 7 continued

2_9	Q9UBR2	Cathepsin Z OS=Homo sapiens GN=CTSZ PE=1 SV=1 - [CATZ_HUMAN]	1.73E-03	-3.9945	-2.8622	8.36E-04	-4.2551	-2.0627
2_9	Q05707	Collagen alpha-1(XIV) chain OS=Homo sapiens GN=COL14A1 PE=1 SV=3 - [COEA1_HUMAN]	5.75E-04	5.2704	3.0033	1.01E-05	10.2985	4.4065
2_9	P28845	Corticosteroid 11-beta-dehydrogenase isozyme 1 OS=Homo sapiens GN=HSD11B1 PE=1 SV=3 - [DHI1_HUMAN]	4.95E-04	-5.4732	-2.7739	4.04E-04	-4.8962	-2.2673
2_9	P12277	Creatine kinase B-type OS=Homo sapiens GN=CKB PE=1 SV=1 - [KCRB_HUMAN]	3.39E-05	15.3291	2.9996	2.31E-03	3.5718	2.6691
2_9	P12532	Creatine kinase U-type, mitochondrial OS=Homo sapiens GN=CKMT1A PE=1 SV=1 - [KCRU_HUMAN]	2.63E-05	16.3138	3.0081	4.68E-04	4.7443	2.2888
2_9	Q86VP6	Cullin-associated NEDD8-dissociated protein 1 OS=Homo sapiens GN=CAND1 PE=1 SV=2 - [CAND1_HUMAN]	1.50E-03	4.1435	2.8567	4.37E-03	3.1874	2.2739
2_9	P32929	Cystathionine gamma-lyase OS=Homo sapiens GN=CTH PE=1 SV=3 - [CGL_HUMAN]	5.32E-04	-5.3886	-2.7750	1.11E-02	-2.6944	-2.7316
2_9	P21291	Cysteine and glycine-rich protein 1 OS=Homo sapiens GN=CSRP1 PE=1 SV=3 - [CSRP1_HUMAN]	6.14E-03	3.2212	2.9083	4.55E-03	3.1641	2.3377
2_9	P11509	Cytochrome P450 2A6 OS=Homo sapiens GN=CYP2A6 PE=1 SV=3 - [CP2A6_HUMAN]	3.32E-05	-15.4599	-2.8972	4.00E-03	-3.2368	-3.6597
2_9	P11712	Cytochrome P450 2C9 OS=Homo sapiens GN=CYP2C9 PE=1 SV=3 - [CP2C9_HUMAN]	5.87E-04	-5.2236	-2.8364	3.97E-03	-3.2410	-3.7909
2_9	P05181	Cytochrome P450 2E1 OS=Homo sapiens GN=CYP2E1 PE=1 SV=1 - [CP2E1_HUMAN]	3.44E-03	-3.6489	-2.7621	2.04E-02	-2.3803	-2.9678
2_9	Q14204	Cytoplasmic dynein 1 heavy chain 1 OS=Homo sapiens GN=DYNC1H1 PE=1 SV=5 - [DYHC1_HUMAN]	1.78E-02	2.5585	2.7291	4.89E-03	3.1239	3.2759
2_9	O75891	Cytosolic 10-formyltetrahydrofolate dehydrogenase OS=Homo sapiens GN=ALDH1L1 PE=1 SV=2 - [AL1L1_HUMAN]	4.67E-04	-5.5195	-2.8376	7.88E-03	-2.8688	-4.2534
2_9	Q02338	D-beta-hydroxybutyrate dehydrogenase, mitochondrial OS=Homo sapiens GN=BDH1 PE=1 SV=3 - [BDH_HUMAN]	3.61E-05	-14.9205	-2.8298	2.79E-05	-8.2936	-3.0118
2_9	P07585	Decorin OS=Homo sapiens GN=DCN PE=1 SV=1 - [PGS2_HUMAN]	1.09E-05	18.5712	3.0320	1.87E-04	5.6256	3.5142
2_9	P30038	Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial OS=Homo sapiens GN=ALDH4A1 PE=1 SV=3 - [AL4A1_HUMAN]	4.03E-05	-14.7538	-2.8957	5.30E-05	-7.2220	-4.3593
2_9	Q07507	Dermatopontin OS=Homo sapiens GN=DPT PE=2 SV=2 - [DERM_HUMAN]	5.94E-04	5.2092	3.0288	4.75E-04	4.7308	2.8244
2_9	P09417	Dihydropteridine reductase OS=Homo sapiens GN=QDPR PE=1 SV=2 - [DHPR_HUMAN]	5.06E-04	-5.4556	-2.7510	2.47E-03	-3.5306	-2.5460
2_9	Q14117	Dihydropyrimidinase OS=Homo sapiens GN=DPYS PE=1 SV=1 - [DPYS_HUMAN]	3.04E-04	-5.6984	-2.8922	1.12E-03	-4.0569	-2.1159
2_9	Q16555	Dihydropyrimidinase-related protein 2 OS=Homo sapiens GN=DPYSL2 PE=1 SV=1 - [DPYL2_HUMAN]	8.03E-04	4.7970	2.9514	1.99E-04	5.5996	3.5974
2_9	P31513	Dimethylaniline monooxygenase [N-oxide-forming] 3 OS=Homo sapiens GN=FMO3 PE=1 SV=5 - [FMO3_HUMAN]	4.39E-05	-14.1915	-2.8470	5.41E-03	-3.0686	-2.4253
2_9	Q9UI17	Dimethylglycine dehydrogenase, mitochondrial OS=Homo sapiens GN=DMGDH PE=1 SV=2 - [M2GD_HUMAN]	3.64E-04	-5.6442	-2.7582	5.82E-03	-3.0281	-2.3323
2_9	P78527	DNA-dependent protein kinase catalytic subunit OS=Homo sapiens GN=PRKDC PE=1 SV=3 - [PRKDC_HUMAN]	1.91E-03	3.8934	2.9078	4.36E-03	3.1891	3.5656
2_9	Q9UJU6	Drebrin-like protein OS=Homo sapiens GN=DBNL PE=1 SV=1 - [DBNL_HUMAN]	3.38E-02	2.2123	2.8073	1.47E-02	2.5589	2.0327
2_9	O75521	Enoyl-CoA delta isomerase 2, mitochondrial OS=Homo sapiens GN=ECI2 PE=1 SV=4 - [ECI2_HUMAN]	2.33E-04	-5.8171	-2.7705	2.22E-03	-3.5966	-2.7939
2_9	P08294	Extracellular superoxide dismutase [Cu-Zn] OS=Homo sapiens GN=SOD3 PE=1 SV=2 - [SODE_HUMAN]	8.88E-04	4.7506	2.7472	1.77E-03	3.7493	2.2501
2_9	P15311	Ezrin OS=Homo sapiens GN=EZR PE=1 SV=4 - [EZRI_HUMAN]	1.20E-03	4.4685	3.0292	5.39E-05	7.2160	3.9079
2_9	O95954	Formimidoyltransferase-cyclodeaminase OS=Homo sapiens GN=FTCD PE=1 SV=2 - [FTCD_HUMAN]	4.83E-05	-13.2613	-2.8156	3.77E-03	-3.2713	-4.0241
2_9	P51570	Galactokinase OS=Homo sapiens GN=GALK1 PE=1 SV=1 - [GALK1_HUMAN]	2.52E-03	-3.7728	-2.7883	8.10E-03	-2.8534	-2.2554
2_9	O95479	GDH/6PGL endoplasmic bifunctional protein OS=Homo sapiens GN=H6PD PE=1 SV=2 - [G6PE_HUMAN]	2.18E-02	-2.4081	-2.7628	6.76E-04	-4.4271	-2.9678
2_9	P11413	Glucose-6-phosphate 1-dehydrogenase OS=Homo sapiens GN=G6PD PE=1 SV=4 - [G6PD_HUMAN]	6.61E-05	6.8095	2.9598	2.00E-03	3.6650	3.5061
2_9	Q06210	Glutamine--fructose-6-phosphate aminotransferase [isomerizing] 1 OS=Homo sapiens GN=GFPT1 PE=1 SV=3 - [GFPT1_HUMAN]	6.98E-05	6.6747	2.8408	1.81E-02	2.4425	2.7338

Fig. 7 continued

2_9	P18283	Glutathione peroxidase 2 OS=Homo sapiens GN=GPX2 PE=1 SV=3 - [GPX2_HUMAN]	5.64E-04	5.2983	2.9965	6.31E-04	4.4949	2.6529
2_9	P09211	Glutathione S-transferase P OS=Homo sapiens GN=GSTP1 PE=1 SV=2 - [GSTP1_HUMAN]	2.42E-03	3.7842	3.1756	3.67E-06	11.7302	5.5137
2_9	P11216	Glycogen phosphorylase, brain form OS=Homo sapiens GN=PYGB PE=1 SV=5 - [PYGB_HUMAN]	1.40E-03	4.2219	2.9366	5.83E-04	4.5569	3.5675
2_9	P06737	Glycogen phosphorylase, liver form OS=Homo sapiens GN=PYGL PE=1 SV=4 - [PYGL_HUMAN]	2.70E-05	-16.2053	-2.9466	7.09E-05	-6.6799	-3.9678
2_9	P02790	Hemopexin OS=Homo sapiens GN=HPX PE=1 SV=2 - [HEMO_HUMAN]	6.91E-04	4.9389	2.9763	9.30E-03	2.7824	3.0810
2_9	Q13151	Heterogeneous nuclear ribonucleoprotein A0 OS=Homo sapiens GN=HNRNPA0 PE=1 SV=1 - [ROA0_HUMAN]	5.50E-05	7.5850	2.9579	1.68E-06	12.9407	2.3251
2_9	O14979	Heterogeneous nuclear ribonucleoprotein D-like OS=Homo sapiens GN=HNRPDL PE=1 SV=3 - [HNRDL_HUMAN]	6.19E-03	3.2148	3.0087	1.32E-05	9.6738	2.7575
2_9	Q1KMD3	Heterogeneous nuclear ribonucleoprotein U-like protein 2 OS=Homo sapiens GN=HNRNPUL2 PE=1 SV=1 - [HNRL2_HUMAN]	6.98E-04	4.9327	3.0612	2.47E-03	3.5323	2.9008
2_9	Q9UJM8	Hydroxyacid oxidase 1 OS=Homo sapiens GN=HAO1 PE=1 SV=1 - [HAOX1_HUMAN]	4.31E-05	-14.5838	-2.9012	5.39E-05	-7.2034	-4.6766
2_9	P35914	Hydroxymethylglutaryl-CoA lyase, mitochondrial OS=Homo sapiens GN=HMGCL PE=1 SV=2 - [HMGCL_HUMAN]	3.03E-03	-3.7075	-2.7659	1.17E-03	-4.0315	-2.4944
2_9	P54868	Hydroxymethylglutaryl-CoA synthase, mitochondrial OS=Homo sapiens GN=HMGCS2 PE=1 SV=1 - [HMCS2_HUMAN]	1.86E-03	-3.9134	-2.9989	2.40E-04	-5.3454	-4.6936
2_9	Q96AB3	Isochorismatase domain-containing protein 2, mitochondrial OS=Homo sapiens GN=ISOC2 PE=1 SV=1 - [ISOC2_HUMAN]	1.57E-02	-2.6795	-2.8366	2.40E-03	-3.5553	-2.5520
2_9	P08727	Keratin, type I cytoskeletal 19 OS=Homo sapiens GN=KRT19 PE=1 SV=4 - [K1C19_HUMAN]	2.64E-05	16.3066	3.0791	9.66E-06	10.5084	5.2600
2_9	P08729	Keratin, type II cytoskeletal 7 OS=Homo sapiens GN=KRT7 PE=1 SV=5 - [K2C7_HUMAN]	1.23E-05	17.9159	2.9851	1.25E-05	9.7253	3.7312
2_9	P07195	L-lactate dehydrogenase B chain OS=Homo sapiens GN=LDHB PE=1 SV=2 - [LDHB_HUMAN]	1.22E-03	4.4531	3.0791	2.29E-04	5.4249	3.4949
2_9	P33121	Long-chain-fatty-acid--CoA ligase 1 OS=Homo sapiens GN=ACSL1 PE=1 SV=1 - [ACSL1_HUMAN]	3.52E-05	-15.0296	-2.8078	1.05E-05	-10.1533	-3.7461
2_9	P51884	Lumican OS=Homo sapiens GN=LUM PE=1 SV=2 - [LUM_HUMAN]	5.87E-04	5.2441	3.1011	1.16E-03	4.0418	4.1373
2_9	P10253	Lysosomal alpha-glucosidase OS=Homo sapiens GN=GAA PE=1 SV=4 - [LYAG_HUMAN]	1.30E-03	-4.3525	-2.8348	2.92E-03	-3.4207	-2.7219
2_9	P40121	Macrophage-capping protein OS=Homo sapiens GN=CAPG PE=1 SV=2 - [CAPG_HUMAN]	5.83E-05	7.0893	2.9948	5.39E-05	7.1930	2.8842
2_9	Q14764	Major vault protein OS=Homo sapiens GN=MVP PE=1 SV=4 - [MVP_HUMAN]	9.47E-04	4.7180	2.9291	1.25E-03	3.9945	3.0605
2_9	Q9H8H3	Methyltransferase-like protein 7A OS=Homo sapiens GN=METTL7A PE=1 SV=1 - [METTA_HUMAN]	1.74E-05	-16.7897	-2.8084	2.15E-04	-5.4891	-2.0606
2_9	P55083	Microfibril-associated glycoprotein 4 OS=Homo sapiens GN=MFAP4 PE=1 SV=2 - [MFAP4_HUMAN]	5.63E-05	7.2005	2.9582	2.09E-04	5.5043	3.3874
2_9	P10620	Microsomal glutathione S-transferase 1 OS=Homo sapiens GN=MGST1 PE=1 SV=1 - [MGST1_HUMAN]	1.56E-03	-4.1010	-2.8540	3.70E-04	-4.9648	-2.4391
2_9	P55157	Microsomal triglyceride transfer protein large subunit OS=Homo sapiens GN=MTTP PE=1 SV=1 - [MTTP_HUMAN]	5.26E-05	-11.4288	-2.7437	3.09E-05	-8.1044	-3.0747
2_9	P20774	Mimecan OS=Homo sapiens GN=OGN PE=1 SV=1 - [MIME_HUMAN]	6.33E-06	20.5281	3.0821	9.29E-05	6.4233	4.4171
2_9	Q9HC84	Mucin-5B OS=Homo sapiens GN=MUC5B PE=1 SV=3 - [MUC5B_HUMAN]	1.29E-05	17.8357	2.9423	8.97E-04	4.2058	3.8016
2_9	P05164	Myeloperoxidase OS=Homo sapiens GN=MPO PE=1 SV=1 - [PERM_HUMAN]	8.32E-05	6.4583	2.9632	3.26E-02	2.1376	2.7070
2_9	Q7Z406	Myosin-14 OS=Homo sapiens GN=MYH14 PE=1 SV=2 - [MYH14_HUMAN]	9.90E-04	4.6815	2.9542	1.36E-03	3.9225	3.3017
2_9	Q4G0N4	NAD kinase domain-containing protein 1 OS=Homo sapiens GN=NADKD1 PE=1 SV=2 - [NAKD1_HUMAN]	3.60E-05	-14.9263	-2.8631	2.14E-04	-5.4880	-2.7939
2_9	P15559	NAD(P)H dehydrogenase [quinone] 1 OS=Homo sapiens GN=NQO1 PE=1 SV=1 - [NQO1_HUMAN]	8.30E-05	6.4592	3.0085	4.74E-03	3.1420	2.8346
2_9	P16435	NADPH--cytochrome P450 reductase OS=Homo sapiens GN=POR PE=1 SV=2 - [NCPR_HUMAN]	1.20E-04	-6.2448	-2.8868	4.55E-04	-4.7781	-3.5681
2_9	Q9BTA1	Niban-like protein 1 OS=Homo sapiens GN=FAM129B PE=1 SV=3 - [NIBL1_HUMAN]	1.09E-03	4.6003	2.7488	6.67E-03	2.9595	2.7683

Fig. 7 continued

2_9	Q15274	Nicotinate-nucleotide pyrophosphorylase [carboxylating] OS=Homo sapiens GN=QPRT PE=1 SV=3 - [NADC_HUMAN]	4.40E-05	-14.1170	-2.7679	8.95E-04	-4.2072	-2.3236
2_9	Q9NQR4	Omega-amidase NIT2 OS=Homo sapiens GN=NIT2 PE=1 SV=1 - [NIT2_HUMAN]	9.49E-03	-2.9619	-2.7870	5.82E-03	-3.0284	-2.2554
2_9	P00480	Ornithine carbamoyltransferase, mitochondrial OS=Homo sapiens GN=OTC PE=1 SV=3 - [OTC_HUMAN]	3.74E-05	-14.8728	-2.9020	3.42E-05	-7.9484	-4.1166
2_9	Q15067	Peroxisomal acyl-coenzyme A oxidase 1 OS=Homo sapiens GN=ACOX1 PE=1 SV=3 - [ACOX1_HUMAN]	4.77E-05	-13.4645	-2.7623	6.86E-04	-4.4140	-3.6073
2_9	Q9Y424	Peroxisomal acyl-coenzyme A oxidase 2 OS=Homo sapiens GN=ACOX2 PE=1 SV=1 - [ACOX2_HUMAN]	4.41E-05	-14.7085	-2.7478	3.07E-03	-3.3885	-3.1310
2_9	Q08426	Peroxisomal bifunctional enzyme OS=Homo sapiens GN=EHHADH PE=1 SV=3 - [ECHP_HUMAN]	4.53E-05	-13.9642	-2.9160	1.92E-04	-5.6064	-5.2498
2_9	Q9P0Z9	Peroxisomal sarcosine oxidase OS=Homo sapiens GN=PIPOX PE=2 SV=2 - [SOX_HUMAN]	4.33E-05	-14.4133	-2.8337	7.01E-05	-6.7133	-3.9173
2_9	Q14651	Plastin-1 OS=Homo sapiens GN=PLS1 PE=1 SV=2 - [PLS1_HUMAN]	5.98E-05	7.0119	2.9693	2.59E-03	3.4981	2.7130
2_9	Q6NZI2	Polymerase I and transcript release factor OS=Homo sapiens GN=PTRF PE=1 SV=1 - [PTRF_HUMAN]	9.96E-04	4.6743	2.8027	3.83E-03	3.2622	2.3674
2_9	P01833	Polymeric immunoglobulin receptor OS=Homo sapiens GN=PIGR PE=1 SV=4 - [PIGR_HUMAN]	5.48E-05	7.8046	2.8741	2.03E-03	3.6563	2.4873
2_9	P17844	Probable ATP-dependent RNA helicase DDX5 OS=Homo sapiens GN=DDX5 PE=1 SV=1 - [DDX5_HUMAN]	5.11E-03	3.3304	2.9867	4.82E-03	3.1311	3.2097
2_9	P05165	Propionyl-CoA carboxylase alpha chain, mitochondrial OS=Homo sapiens GN=PCCA PE=1 SV=4 - [PCCA_HUMAN]	2.08E-04	-5.8775	-2.7099	2.85E-03	-3.4346	-2.2462
2_9	P05166	Propionyl-CoA carboxylase beta chain, mitochondrial OS=Homo sapiens GN=PCCB PE=1 SV=3 - [PCCB_HUMAN]	4.84E-02	-2.0921	-2.7141	4.61E-04	-4.7627	-3.0118
2_9	Q9BPW8	Protein NipSnap homolog 1 OS=Homo sapiens GN=NIPSNAP1 PE=1 SV=1 - [NIPS1_HUMAN]	3.28E-05	-15.5652	-2.8331	9.29E-05	-6.4347	-2.9866
2_9	P55786	Puromycin-sensitive aminopeptidase OS=Homo sapiens GN=NPEPPS PE=1 SV=2 - [PSA_HUMAN]	8.64E-04	4.7609	2.9162	1.26E-04	6.0757	2.6078
2_9	O43143	Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15 OS=Homo sapiens GN=DHX15 PE=1 SV=2 - [DHX15_HUMAN]	9.03E-04	4.7435	2.8379	7.29E-04	4.3693	2.0605
2_9	Q9NVS9	Pyridoxine-5-phosphate oxidase OS=Homo sapiens GN=PNPO PE=1 SV=1 - [PNPO_HUMAN]	5.23E-04	-5.4244	-2.8059	3.55E-04	-5.0006	-2.4373
2_9	P11498	Pyruvate carboxylase, mitochondrial OS=Homo sapiens GN=PC PE=1 SV=2 - [PYC_HUMAN]	4.80E-05	-13.3228	-2.8449	9.26E-05	-6.4269	-4.8219
2_9	P30613	Pyruvate kinase isozymes R/L OS=Homo sapiens GN=PKLR PE=1 SV=2 - [KPYR_HUMAN]	1.12E-05	-18.3184	-2.8332	9.65E-04	-4.1686	-3.3175
2_9	P31150	Rab GDP dissociation inhibitor alpha OS=Homo sapiens GN=GDI1 PE=1 SV=2 - [GDIA_HUMAN]	1.62E-03	4.0653	2.9283	2.09E-03	3.6388	3.2951
2_9	P46940	Ras GTPase-activating-like protein IQGAP1 OS=Homo sapiens GN=IQGAP1 PE=1 SV=1 - [IQGA1_HUMAN]	4.03E-05	14.7547	2.9168	1.14E-03	4.0519	4.6006
2_9	O94788	Retinal dehydrogenase 2 OS=Homo sapiens GN=ALDH1A2 PE=1 SV=3 - [AL1A2_HUMAN]	9.08E-04	4.7414	2.8083	8.33E-03	2.8383	2.0831
2_9	O75452	Retinol dehydrogenase 16 OS=Homo sapiens GN=RDH16 PE=1 SV=2 - [RDH16_HUMAN]	5.27E-04	-5.4067	-2.7982	2.22E-03	-3.5966	-2.3593
2_9	P02753	Retinol-binding protein 4 OS=Homo sapiens GN=RBP4 PE=1 SV=3 - [RET4_HUMAN]	1.83E-03	-3.9221	-2.8141	6.67E-04	-4.4412	-2.4944
2_9	P52758	Ribonuclease UK114 OS=Homo sapiens GN=HRSP12 PE=1 SV=1 - [UK114_HUMAN]	2.50E-03	-3.7757	-2.9118	2.06E-04	-5.5214	-3.3825
2_9	Q9UKM9	RNA-binding protein Raly OS=Homo sapiens GN=RALY PE=1 SV=1 - [RALY_HUMAN]	3.40E-03	3.6386	2.9546	8.27E-03	2.8417	2.0161
2_9	Q6NBX0	Saccharopine dehydrogenase-like oxidoreductase OS=Homo sapiens GN=SCCPDH PE=1 SV=1 - [SCPDL_HUMAN]	2.68E-05	-16.2503	-2.8219	2.00E-05	-9.1961	-2.7268
2_9	Q00266	S-adenosylmethionine synthase isoform type-1 OS=Homo sapiens GN=MAT1A PE=1 SV=2 - [METK1_HUMAN]	4.76E-05	-13.5038	-2.8606	1.74E-03	-3.7415	-2.8628
2_9	Q9UJJ2	Sarcosine dehydrogenase, mitochondrial OS=Homo sapiens GN=SARDH PE=1 SV=1 - [SARDH_HUMAN]	3.44E-04	-5.6627	-2.7893	7.36E-04	-4.3623	-3.1624
2_9	Q15019	Septin-2 OS=Homo sapiens GN=SEPT2 PE=1 SV=1 - [SEPT2_HUMAN]	6.15E-05	6.9617	2.9199	1.88E-04	5.6199	2.3040
2_9	Q16181	Septin-7 OS=Homo sapiens GN=SEPT7 PE=1 SV=2 - [SEPT7_HUMAN]	2.98E-03	3.7134	2.8447	1.22E-02	2.6483	2.1733
2_9	Q9UHD8	Septin-9 OS=Homo sapiens GN=SEPT9 PE=1 SV=2 - [SEPT9_HUMAN]	7.91E-05	6.5206	2.8386	6.28E-05	6.9236	2.3974

Fig. 7 continued

2_9	P34896	Serine hydroxymethyltransferase, cytosolic OS=Homo sapiens GN=SHMT1 PE=1 SV=1 - [GLYC_HUMAN]	6.32E-03	-3.1992	-2.8595	7.40E-04	-4.3589	-3.6455
2_9	P21549	Serine--pyruvate aminotransferase OS=Homo sapiens GN=AGXT PE=1 SV=1 - [SPYA_HUMAN]	4.50E-05	-14.0091	-3.0092	1.69E-04	-5.6886	-6.0079
2_9	P35237	Serpin B6 OS=Homo sapiens GN=SERPINB6 PE=1 SV=3 - [SPB6_HUMAN]	6.12E-04	5.1489	2.9194	9.67E-04	4.1671	2.2888
2_9	P45954	Short/branched chain specific acyl-CoA dehydrogenase, mitochondrial OS=Homo sapiens GN=ACADSB PE=1 SV=1 - [ACDSB_HUMAN]	8.67E-05	-6.4231	-2.8717	2.18E-05	-8.7868	-3.3069
2_9	Q9NR45	Sialic acid synthase OS=Homo sapiens GN=NANS PE=1 SV=2 - [SIAS_HUMAN]	1.72E-03	4.0043	2.9690	3.92E-05	7.7657	2.3935
2_9	Q9H9B4	Sideroflexin-1 OS=Homo sapiens GN=SFXN1 PE=1 SV=4 - [SFXN1_HUMAN]	4.42E-05	-14.0677	-2.7687	1.27E-04	-6.0414	-2.4391
2_9	Q14247	Src substrate cortactin OS=Homo sapiens GN=CTTN PE=1 SV=2 - [SRC8_HUMAN]	1.04E-05	18.7484	2.8312	1.88E-03	3.7047	2.1006
2_9	Q02318	Sterol 26-hydroxylase, mitochondrial OS=Homo sapiens GN=CYP27A1 PE=1 SV=1 - [CP27A_HUMAN]	3.67E-05	-14.8968	-2.7763	1.01E-03	-4.1259	-2.4391
2_9	P51649	Succinate-semialdehyde dehydrogenase, mitochondrial OS=Homo sapiens GN=ALDH5A1 PE=1 SV=2 - [SSDH_HUMAN]	1.61E-04	-6.0225	-2.7755	5.49E-05	-7.1668	-3.2534
2_9	Q13263	Transcription intermediary factor 1-beta OS=Homo sapiens GN=TRIM28 PE=1 SV=5 - [TIF1B_HUMAN]	1.62E-05	17.0870	2.8980	2.42E-05	8.5508	2.6278
2_9	P53007	Tricarboxylate transport protein, mitochondrial OS=Homo sapiens GN=SLC25A1 PE=1 SV=2 - [TXTP_HUMAN]	1.30E-03	-3.8975	-2.7448	7.41E-03	-2.9080	-2.1961
2_9	Q15561	Tryptase alpha/beta-1 OS=Homo sapiens GN=TPSAB1 PE=1 SV=1 - [TRYB1_HUMAN]	7.15E-05	6.6539	2.9718	6.64E-04	4.4458	3.5929
2_9	P68366	Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A PE=1 SV=1 - [TBA4A_HUMAN]	8.88E-03	3.0254	3.1784	1.04E-02	2.7313	5.3380
2_9	P22310	UDP-glucuronosyltransferase 1-4 OS=Homo sapiens GN=UGT1A4 PE=1 SV=1 - [UD14_HUMAN]	4.86E-04	-5.4923	-2.8845	1.03E-03	-4.1140	-2.9086
2_9	O60656	UDP-glucuronosyltransferase 1-9 OS=Homo sapiens GN=UGT1A9 PE=1 SV=1 - [UD19_HUMAN]	1.27E-02	-2.7835	-2.8097	1.21E-02	-2.6519	-2.4391
2_9	P06133	UDP-glucuronosyltransferase 2B4 OS=Homo sapiens GN=UGT2B4 PE=1 SV=2 - [UD2B4_HUMAN]	4.44E-05	-14.0468	-2.7905	1.17E-03	-4.0368	-2.7008
2_9	P16662	UDP-glucuronosyltransferase 2B7 OS=Homo sapiens GN=UGT2B7 PE=1 SV=1 - [UD2B7_HUMAN]	5.18E-03	-3.3225	-2.7992	5.36E-03	-3.0738	-2.7316
2_9	O00159	Unconventional myosin-Ic OS=Homo sapiens GN=MYO1C PE=1 SV=4 - [MYO1C_HUMAN]	1.59E-02	2.6595	2.8796	4.06E-03	3.2263	2.2377
2_9	Q96QK1	Vacuolar protein sorting-associated protein 35 OS=Homo sapiens GN=VPS35 PE=1 SV=2 - [VPS35_HUMAN]	1.58E-03	4.0895	2.8249	7.07E-05	6.6867	2.5543
2_9	P09327	Villin-1 OS=Homo sapiens GN=VIL1 PE=1 SV=4 - [VILI_HUMAN]	2.54E-05	16.4186	2.8983	1.47E-04	5.8302	2.8579
2_9	P02774	Vitamin D-binding protein OS=Homo sapiens GN=GC PE=1 SV=1 - [VTDB_HUMAN]	4.27E-03	3.4478	2.8817	8.02E-03	2.8594	2.2696
3_4	Q04917	14-3-3 protein eta OS=Homo sapiens GN=YWHAH PE=1 SV=4 - [1433F_HUMAN]	4.08E-04	4.8001	2.9739	5.89E-05	5.8765	3.6309
3_4	P31947	14-3-3 protein sigma OS=Homo sapiens GN=SFN PE=1 SV=1 - [1433S_HUMAN]	6.34E-03	2.9145	2.9768	3.25E-05	6.4413	3.6322
3_4	O14756	17-beta-hydroxysteroid dehydrogenase type 6 OS=Homo sapiens GN=HSD17B6 PE=1 SV=1 - [HI17B6_HUMAN]	9.17E-05	-6.0406	-2.8892	2.30E-04	-4.8182	-3.2054
3_4	P31937	3-hydroxyisobutyrate dehydrogenase, mitochondrial OS=Homo sapiens GN=HIBADH PE=1 SV=2 - [3HIDH_HUMAN]	3.92E-03	-3.3469	-2.8185	1.42E-02	-2.4933	-2.6690
3_4	P80404	4-aminobutyrate aminotransferase, mitochondrial OS=Homo sapiens GN=ABAT PE=1 SV=3 - [GABT_HUMAN]	2.77E-05	-12.9166	-2.8695	4.31E-03	-3.0874	-3.4280
3_4	P32754	4-hydroxyphenylpyruvate dioxygenase OS=Homo sapiens GN=HPD PE=1 SV=2 - [HPPD_HUMAN]	2.73E-05	-12.9628	-2.9576	2.85E-04	-4.6765	-4.0978
3_4	Q08AH3	Acyl-coenzyme A synthetase ACSM2A, mitochondrial OS=Homo sapiens GN=ACSM2A PE=1 SV=2 - [ACS2A_HUMAN]	2.82E-04	-5.4960	-2.8194	1.16E-02	-2.5891	-3.6690
3_4	Q6ZCK6	Acyl-coenzyme A synthetase ACSM2B, mitochondrial OS=Homo sapiens GN=ACSM2B PE=1 SV=2 - [ACS2B_HUMAN]	7.64E-05	-6.2153	-2.8202	1.90E-03	-3.5317	-3.7082
3_4	O95154	Aflatoxin B1 aldehyde reductase member 3 OS=Homo sapiens GN=AKR7A3 PE=1 SV=2 - [ARK73_HUMAN]	3.53E-03	-3.4392	-2.8131	1.03E-03	-3.8749	-2.5535
3_4	P24298	Alanine aminotransferase 1 OS=Homo sapiens GN=GPT PE=1 SV=3 - [ALAT1_HUMAN]	2.90E-04	-5.4824	-2.8800	6.45E-03	-2.8831	-2.0078
3_4	P07327	Alcohol dehydrogenase 1A OS=Homo sapiens GN=ADH1A PE=1 SV=2 - [ADH1A_HUMAN]	5.06E-04	-4.4588	-2.9589	3.04E-03	-3.2628	-4.3663

Fig. 7 continued

3_4	P08319	Alcohol dehydrogenase 4 OS=Homo sapiens GN=ADH4 PE=1 SV=5 - [ADH4_HUMAN]	2.96E-05	-11.2379	-2.8303	6.10E-03	-2.9109	-3.8151
3_4	Q06278	Aldehyde oxidase OS=Homo sapiens GN=AOX1 PE=2 SV=2 - [AOX_HUMAN]	3.08E-05	-10.7701	-2.7162	9.20E-03	-2.7026	-2.4672
3_4	P17516	Aldo-keto reductase family 1 member C4 OS=Homo sapiens GN=AKR1C4 PE=1 SV=3 - [AK1C4_HUMAN]	3.60E-03	-3.4206	-2.9828	9.84E-03	-2.6687	-3.4921
3_4	P21397	Amine oxidase [flavin-containing] A OS=Homo sapiens GN=MAOA PE=1 SV=1 - [AOFA_HUMAN]	1.86E-03	-3.7743	-2.8433	9.43E-03	-2.6901	-2.3906
3_4	Q03154	Aminoacylase-1 OS=Homo sapiens GN=ACY1 PE=1 SV=1 - [ACY1_HUMAN]	1.52E-03	-3.8185	-2.9365	2.47E-05	-6.6601	-3.3608
3_4	P12429	Annexin A3 OS=Homo sapiens GN=ANXA3 PE=1 SV=3 - [ANXA3_HUMAN]	2.00E-03	3.7510	2.7599	3.46E-03	3.2011	2.4826
3_4	O95831	Apoptosis-inducing factor 1, mitochondrial OS=Homo sapiens GN=AIFM1 PE=1 SV=1 - [AIFM1_HUMAN]	6.17E-03	-2.9443	-2.8474	8.90E-05	-5.6336	-3.8056
3_4	P05089	Arginase-1 OS=Homo sapiens GN=ARG1 PE=1 SV=2 - [ARGI1_HUMAN]	2.39E-05	-14.4515	-2.9788	1.70E-04	-5.0827	-4.3292
3_4	P04424	Argininosuccinate lyase OS=Homo sapiens GN=ASL PE=1 SV=4 - [ARLY_HUMAN]	3.34E-03	-3.4899	-2.9437	8.50E-04	-3.9894	-4.2165
3_4	P00966	Argininosuccinate synthase OS=Homo sapiens GN=ASS1 PE=1 SV=2 - [ASSY_HUMAN]	3.93E-03	-3.3451	-2.8519	2.07E-02	-2.3145	-2.6503
3_4	P22760	Arylacetamide deacetylase OS=Homo sapiens GN=AADAC PE=1 SV=5 - [AAAD_HUMAN]	1.62E-05	-16.1155	-2.7673	2.55E-05	-6.6513	-2.8640
3_4	Q93088	Betaine--homocysteine S-methyltransferase 1 OS=Homo sapiens GN=BHMT PE=1 SV=2 - [BHMT1_HUMAN]	3.40E-04	-5.2976	-2.9078	3.22E-02	-2.0917	-3.2794
3_4	P21810	Biglycan OS=Homo sapiens GN=BGN PE=1 SV=2 - [PGS1_HUMAN]	3.89E-03	3.3540	2.8811	4.32E-03	3.0660	4.1264
3_4	Q9Y2P5	Bile acyl-CoA synthetase OS=Homo sapiens GN=SLC27A5 PE=1 SV=1 - [S27A5_HUMAN]	2.35E-03	-3.7096	-2.6951	3.29E-03	-3.2288	-2.5061
3_4	Q06520	Bile salt sulfotransferase OS=Homo sapiens GN=SULT2A1 PE=1 SV=3 - [ST2A1_HUMAN]	2.44E-05	-14.3652	-2.9030	1.28E-03	-3.7370	-2.8466
3_4	P23786	Carnitine O-palmitoyltransferase 2, mitochondrial OS=Homo sapiens GN=CPT2 PE=1 SV=2 - [CPT2_HUMAN]	6.15E-04	-4.2774	-2.8192	7.33E-03	-2.8140	-2.1909
3_4	O00748	Cocaine esterase OS=Homo sapiens GN=CES2 PE=1 SV=1 - [EST2_HUMAN]	4.87E-05	-6.8159	-2.8885	1.96E-03	-3.5193	-2.9344
3_4	P31146	Coronin-1A OS=Homo sapiens GN=CORO1A PE=1 SV=4 - [COR1A_HUMAN]	3.51E-03	3.4438	2.7939	6.67E-03	2.8654	2.5501
3_4	P00167	Cytochrome b5 OS=Homo sapiens GN=CYB5A PE=1 SV=2 - [CYB5_HUMAN]	7.55E-04	-4.0933	-3.0069	2.04E-04	-4.9155	-3.0531
3_4	P11509	Cytochrome P450 2A6 OS=Homo sapiens GN=CYP2A6 PE=1 SV=3 - [CP2A6_HUMAN]	1.68E-03	-3.7961	-2.8057	3.47E-03	-3.1991	-2.8754
3_4	P11712	Cytochrome P450 2C9 OS=Homo sapiens GN=CYP2C9 PE=1 SV=3 - [CP2C9_HUMAN]	1.10E-04	-5.8944	-2.7039	7.20E-03	-2.8247	-2.1275
3_4	P10635	Cytochrome P450 2D6 OS=Homo sapiens GN=CYP2D6 PE=1 SV=2 - [CP2D6_HUMAN]	2.05E-03	-3.7456	-2.6731	3.06E-03	-3.2589	-2.1385
3_4	O75891	Cytosolic 10-formyltetrahydrofolate dehydrogenase OS=Homo sapiens GN=ALDH1L1 PE=1 SV=2 - [AL1L1_HUMAN]	3.36E-04	-5.3051	-2.8507	2.57E-02	-2.1987	-3.8154
3_4	Q02338	D-beta-hydroxybutyrate dehydrogenase, mitochondrial OS=Homo sapiens GN=BDH1 PE=1 SV=3 - [BDH_HUMAN]	2.21E-05	-15.3212	-2.8436	1.89E-05	-7.0629	-2.5424
3_4	P09417	Dihydropteridine reductase OS=Homo sapiens GN=QDPR PE=1 SV=2 - [DHPR_HUMAN]	4.60E-05	-6.9169	-2.8151	5.05E-04	-4.3148	-2.2905
3_4	P31513	Dimethylaniline monooxygenase [N-oxide-forming] 3 OS=Homo sapiens GN=FMO3 PE=1 SV=5 - [FMO3_HUMAN]	1.32E-02	-2.7224	-2.8163	2.60E-03	-3.3448	-2.9344
3_4	Q9UI17	Dimethylglycine dehydrogenase, mitochondrial OS=Homo sapiens GN=DMGDH PE=1 SV=2 - [M2GD_HUMAN]	3.12E-04	-5.4111	-2.7015	1.56E-03	-3.6258	-2.0015
3_4	O75356	Ectonucleoside triphosphate diphosphohydrolase 5 OS=Homo sapiens GN=ENTPD5 PE=1 SV=1 - [ENTP5_HUMAN]	3.63E-03	-3.4126	-2.7192	1.46E-02	-2.4821	-2.1777
3_4	O75521	Enoyl-CoA delta isomerase 2, mitochondrial OS=Homo sapiens GN=ECI2 PE=1 SV=4 - [ECI2_HUMAN]	3.42E-04	-5.2935	-2.6864	2.33E-03	-3.4063	-2.5424
3_4	P15311	Ezrin OS=Homo sapiens GN=EZR PE=1 SV=4 - [EZRI_HUMAN]	3.04E-03	3.5597	2.9388	2.51E-03	3.3659	3.5140
3_4	P51648	Fatty aldehyde dehydrogenase OS=Homo sapiens GN=ALDH3A2 PE=1 SV=1 - [AL3A2_HUMAN]	5.14E-03	-3.0903	-2.7786	1.39E-02	-2.5049	-2.3161
3_4	O95954	Formimidoyltransferase-cyclodeaminase OS=Homo sapiens GN=FTCD PE=1 SV=2 - [FTCD_HUMAN]	1.55E-04	-5.7829	-2.8579	1.34E-02	-2.5216	-2.8931

Fig. 7 continued

3_4	P09467	Fructose-1,6-bisphosphatase 1 OS=Homo sapiens GN=FBP1 PE=1 SV=5 - [F16P1_HUMAN]	4.57E-03	-3.2095	-2.9303	1.41E-03	-3.6770	-4.0129
3_4	P09382	Galectin-1 OS=Homo sapiens GN=LGALS1 PE=1 SV=2 - [LEG1_HUMAN]	4.49E-03	3.2279	2.7975	2.15E-03	3.4597	2.3985
3_4	O95479	GDH/6PGL endoplasmic bifunctional protein OS=Homo sapiens GN=H6PD PE=1 SV=2 - [G6PE_HUMAN]	5.01E-03	-3.1193	-2.8183	9.18E-04	-3.9411	-2.6130
3_4	P11413	Glucose-6-phosphate 1-dehydrogenase OS=Homo sapiens GN=G6PD PE=1 SV=4 - [G6PD_HUMAN]	6.54E-03	2.8944	2.8217	1.71E-02	2.4047	2.8646
3_4	Q9UJJ7	GTP:AMP phosphotransferase, mitochondrial OS=Homo sapiens GN=AK3 PE=1 SV=4 - [KAD3_HUMAN]	3.96E-03	-3.3361	-2.8578	5.29E-03	-2.9885	-2.4280
3_4	P04899	Guanine nucleotide-binding protein G(i) subunit alpha-2 OS=Homo sapiens GN=GNAI2 PE=1 SV=3 - [GNAI2_HUMAN]	1.70E-02	2.5531	2.7782	8.90E-03	2.7195	2.0675
3_4	Q1KMD3	Heterogeneous nuclear ribonucleoprotein U-like protein 2 OS=Homo sapiens GN=HNRNPUL2 PE=1 SV=1 - [HNRL2_HUMAN]	3.52E-03	3.4423	2.8210	6.56E-03	2.8741	2.2899
3_4	Q93099	Homogentisate 1,2-dioxygenase OS=Homo sapiens GN=HGD PE=1 SV=2 - [HGD_HUMAN]	4.12E-04	-4.7680	-2.8389	6.35E-05	-5.8327	-4.0042
3_4	Q9UJM8	Hydroxyacid oxidase 1 OS=Homo sapiens GN=HAO1 PE=1 SV=1 - [HAOX1_HUMAN]	1.16E-05	-16.4212	-2.8892	1.79E-05	-7.1383	-4.1274
3_4	Q16836	Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial OS=Homo sapiens GN=HADH PE=1 SV=3 - [HCDH_HUMAN]	5.23E-04	-4.4107	-2.8237	4.32E-04	-4.4132	-2.4169
3_4	P35914	Hydroxymethylglutaryl-CoA lyase, mitochondrial OS=Homo sapiens GN=HMGCL PE=1 SV=2 - [HMGCL_HUMAN]	4.39E-02	-2.0141	-2.7459	3.50E-03	-3.1925	-2.1275
3_4	P54868	Hydroxymethylglutaryl-CoA synthase, mitochondrial OS=Homo sapiens GN=HMGCS2 PE=1 SV=1 - [HMCS2_HUMAN]	1.25E-02	-2.7380	-2.9618	2.35E-04	-4.8016	-4.5313
3_4	P08727	Keratin, type I cytoskeletal 19 OS=Homo sapiens GN=KRT19 PE=1 SV=4 - [K1C19_HUMAN]	2.49E-02	2.2730	2.8178	1.06E-02	2.6339	4.2797
3_4	O00515	Ladinin-1 OS=Homo sapiens GN=LAD1 PE=1 SV=2 - [LAD1_HUMAN]	1.42E-06	23.5174	2.7578	3.07E-03	3.2574	2.0675
3_4	P33121	Long-chain-fatty-acid--CoA ligase 1 OS=Homo sapiens GN=ACSL1 PE=1 SV=1 - [ACSL1_HUMAN]	1.79E-04	-5.7300	-2.8373	3.20E-03	-3.2328	-3.3292
3_4	O00264	Membrane-associated progesterone receptor component 1 OS=Homo sapiens GN=PGRMC1 PE=1 SV=3 - [PGRC1_HUMAN]	5.39E-04	-4.2947	-2.8885	1.77E-03	-3.5605	-2.9344
3_4	Q02252	Methylmalonate-semialdehyde dehydrogenase [acylating], mitochondrial OS=Homo sapiens GN=ALDH6A1 PE=1 SV=2 - [MMSA_HUMAN]	2.89E-03	-3.6023	-2.8851	7.61E-04	-4.0638	-4.0977
3_4	Q9H8H3	Methyltransferase-like protein 7A OS=Homo sapiens GN=METTL7A PE=1 SV=1 - [ME7A_HUMAN]	5.60E-04	-4.3553	-2.8687	1.20E-04	-5.3364	-2.1385
3_4	P10620	Microsomal glutathione S-transferase 1 OS=Homo sapiens GN=MGST1 PE=1 SV=1 - [MGST1_HUMAN]	9.92E-03	-2.7871	-2.9236	1.16E-03	-3.8007	-2.2794
3_4	P55157	Microsomal triglyceride transfer protein large subunit OS=Homo sapiens GN=MTTP PE=1 SV=1 - [MTP_HUMAN]	2.59E-05	-13.6236	-2.7434	2.61E-04	-4.7269	-2.8913
3_4	Q9Y6C9	Mitochondrial carrier homolog 2 OS=Homo sapiens GN=MTCH2 PE=1 SV=1 - [MTCH2_HUMAN]	5.01E-03	-3.1194	-2.7947	7.51E-04	-4.0703	-2.3906
3_4	Q4G0N4	NAD kinase domain-containing protein 1 OS=Homo sapiens GN=NADKD1 PE=1 SV=2 - [NAKD1_HUMAN]	8.55E-05	-6.0889	-2.8105	8.40E-04	-3.9869	-2.8644
3_4	Q13423	NAD(P) transhydrogenase, mitochondrial OS=Homo sapiens GN=NNT PE=1 SV=3 - [NNTM_HUMAN]	2.99E-03	-3.5729	-2.7910	3.56E-03	-3.1659	-2.7758
3_4	P16435	NADPH--cytochrome P450 reductase OS=Homo sapiens GN=POR PE=1 SV=2 - [NCPR_HUMAN]	5.00E-04	-4.4729	-2.8486	8.30E-04	-4.0059	-3.6130
3_4	P22307	Non-specific lipid-transfer protein OS=Homo sapiens GN=SCP2 PE=1 SV=2 - [NLTP_HUMAN]	5.78E-04	-4.3233	-2.8858	2.01E-04	-4.9235	-2.6130
3_4	P00480	Ornithine carbamoyltransferase, mitochondrial OS=Homo sapiens GN=OTC PE=1 SV=3 - [OTC_HUMAN]	2.15E-05	-15.4513	-2.9239	1.21E-05	-7.5783	-4.0449
3_4	O60664	Perilipin-3 OS=Homo sapiens GN=PLIN3 PE=1 SV=3 - [PLIN3_HUMAN]	2.61E-02	2.2335	2.7383	5.07E-03	3.0114	2.2899
3_4	Q15063	Periostin OS=Homo sapiens GN=POSTN PE=1 SV=2 - [POSTN_HUMAN]	3.56E-03	3.4327	2.8242	1.63E-02	2.4254	3.2899
3_4	Q15067	Peroxisomal acyl-coenzyme A oxidase 1 OS=Homo sapiens GN=ACOX1 PE=1 SV=3 - [ACOX1_HUMAN]	1.22E-02	-2.7424	-2.6944	1.04E-02	-2.6443	-2.9862
3_4	Q9NUQ4	Peroxisomal acyl-coenzyme A oxidase 2 OS=Homo sapiens GN=ACOX2 PE=1 SV=1 - [ACOX2_HUMAN]	1.25E-02	-2.7385	-2.6299	1.92E-02	-2.3496	-2.2794
3_4	Q08426	Peroxisomal bifunctional enzyme OS=Homo sapiens GN=EHHADH PE=1 SV=3 - [ECHP_HUMAN]	5.84E-04	-4.3145	-2.9060	1.46E-05	-7.3782	-5.0344
3_4	Q9P0Z9	Peroxisomal sarcosine oxidase OS=Homo sapiens GN=PIPOX PE=2 SV=2 - [SOX_HUMAN]	8.88E-04	-3.9881	-2.8545	1.65E-03	-3.5989	-2.8754

Fig. 7 continued

3_4	P05165	Propionyl-CoA carboxylase beta chain, mitochondrial OS=Homo sapiens GN=PCCB PE=1 SV=3 - [PCCB_HUMAN]	5.50E-03	-3.0376	-2.7284	9.23E-03	-2.7007	-2.3297
3_4	Q14914	Prostaglandin reductase 1 OS=Homo sapiens GN=PTGR1 PE=1 SV=2 - [PTGR1_HUMAN]	4.94E-03	-3.1333	-2.7764	1.30E-02	-2.5326	-3.4672
3_4	P55786	Puromycin-sensitive aminopeptidase OS=Homo sapiens GN=NPEPPS PE=1 SV=2 - [PSA_HUMAN]	1.00E-03	3.9069	2.7998	2.22E-02	2.2803	2.6322
3_4	Q9NVS9	Pyridoxine-5-phosphate oxidase OS=Homo sapiens GN=PNPO PE=1 SV=1 - [PNPO_HUMAN]	1.72E-02	-2.5450	-2.8728	2.06E-04	-4.9096	-2.1274
3_4	P11498	Pyruvate carboxylase, mitochondrial OS=Homo sapiens GN=PC PE=1 SV=2 - [PYC_HUMAN]	9.97E-04	-3.9086	-2.8168	1.02E-03	-3.8802	-3.9982
3_4	P46940	Ras GTPase-activating-like protein IQGAP1 OS=Homo sapiens GN=IQGAP1 PE=1 SV=1 - [IQGA1_HUMAN]	7.14E-03	2.8387	2.7745	3.43E-03	3.2071	3.4989
3_4	P02753	Retinol-binding protein 4 OS=Homo sapiens GN=RBP4 PE=1 SV=3 - [RET4_HUMAN]	2.00E-05	-15.7175	-2.8475	2.98E-05	-6.5738	-2.2794
3_4	Q8NBX0	Saccharopine dehydrogenase-like oxidoreductase OS=Homo sapiens GN=SCCPDH PE=1 SV=1 - [SCPDL_HUMAN]	9.87E-04	-3.9159	-2.8469	7.58E-04	-4.0656	-2.5927
3_4	Q00266	S-adenosylmethionine synthase isoform type-1 OS=Homo sapiens GN=MAT1A PE=1 SV=2 - [METK1_HUMAN]	1.14E-03	-3.8576	-2.8581	7.64E-03	-2.7887	-2.7125
3_4	P34896	Serine hydroxymethyltransferase, cytosolic OS=Homo sapiens GN=SHMT1 PE=1 SV=1 - [GLYC_HUMAN]	6.37E-03	-2.9097	-2.8267	3.04E-04	-4.6465	-2.9536
3_4	P45954	Short/branched chain specific acyl-CoA dehydrogenase, mitochondrial OS=Homo sapiens GN=ACADSB PE=1 SV=1 - [ACDSB_HUMAN]	7.62E-04	-4.0860	-2.8646	6.32E-04	-4.1553	-3.1275
3_4	Q9Y6B4	Sideroflexin-1 OS=Homo sapiens GN=SFXN1 PE=1 SV=4 - [SFXN1_HUMAN]	4.78E-03	-3.1645	-2.8282	1.86E-04	-4.9926	-2.1777
3_4	Q00796	Sorbitol dehydrogenase OS=Homo sapiens GN=SORD PE=1 SV=4 - [DHSO_HUMAN]	4.27E-03	-3.2714	-2.8262	5.44E-03	-2.9704	-2.7312
3_4	Q02318	Sterol 26-hydroxylase, mitochondrial OS=Homo sapiens GN=CYP27A1 PE=1 SV=1 - [CP27A_HUMAN]	2.02E-03	-3.7479	-2.7775	3.20E-03	-3.2323	-2.0078
3_4	P51649	Succinate-semialdehyde dehydrogenase, mitochondrial OS=Homo sapiens GN=ALDH5A1 PE=1 SV=2 - [SSDH_HUMAN]	6.25E-03	-2.9331	-2.7413	1.16E-02	-2.5875	-2.4672
3_4	Q99536	Synaptic vesicle membrane protein VAT-1 homolog OS=Homo sapiens GN=VAT1 PE=1 SV=2 - [VAT1_HUMAN]	4.53E-04	4.5890	2.8511	6.42E-03	2.8852	2.1297
3_4	P22310	UDP-glucuronosyltransferase 1-4 OS=Homo sapiens GN=UGT1A4 PE=1 SV=1 - [UD14_HUMAN]	3.21E-04	-5.3717	-2.8417	1.36E-02	-2.5112	-2.8056
3_4	O60656	UDP-glucuronosyltransferase 1-9 OS=Homo sapiens GN=UGT1A9 PE=1 SV=1 - [UD19_HUMAN]	3.03E-03	-3.5621	-2.8416	3.70E-02	-2.0473	-2.0078
3_4	P06133	UDP-glucuronosyltransferase 2B4 OS=Homo sapiens GN=UGT2B4 PE=1 SV=2 - [UD2B4_HUMAN]	2.49E-05	-14.2817	-2.9014	4.76E-03	-3.0413	-2.9536
3_4	P16662	UDP-glucuronosyltransferase 2B7 OS=Homo sapiens GN=UGT2B7 PE=1 SV=1 - [UD2B7_HUMAN]	2.06E-05	-15.6905	-2.8565	1.52E-03	-3.6440	-2.8754
3_5	Q04917	14-3-3 protein eta OS=Homo sapiens GN=YWHAH PE=1 SV=4 - [1433F_HUMAN]	4.37E-04	4.7567	3.0198	2.37E-06	7.9009	3.8567
3_5	P31947	14-3-3 protein sigma OS=Homo sapiens GN=SFN PE=1 SV=1 - [1433S_HUMAN]	4.49E-02	2.0449	3.0139	1.47E-03	3.6175	3.6959
3_5	O14756	17-beta-hydroxysteroid dehydrogenase type 6 OS=Homo sapiens GN=HSD17B6 PE=1 SV=1 - [HI7B6_HUMAN]	1.70E-05	-14.8936	-2.8892	8.18E-05	-5.3332	-3.2064
3_5	P80404	4-aminobutyrate aminotransferase, mitochondrial OS=Homo sapiens GN=ABAT PE=1 SV=3 - [GABT_HUMAN]	3.99E-03	-3.0448	-2.8695	5.05E-03	-2.9844	-3.4280
3_5	P32754	4-hydroxyphenylpyruvate dioxygenase OS=Homo sapiens GN=HPD PE=1 SV=2 - [HPPD_HUMAN]	2.37E-05	-12.9628	-2.9576	2.27E-04	-4.6765	-4.0978
3_5	Q01813	6-phosphofructokinase type C OS=Homo sapiens GN=PFKP PE=1 SV=2 - [KGPP_HUMAN]	1.29E-03	3.8212	2.7049	8.74E-03	2.7042	2.0637
3_5	P68133	Actin, alpha skeletal muscle OS=Homo sapiens GN=ACTA1 PE=1 SV=1 - [ACTS_HUMAN]	7.62E-03	-2.7904	-3.0521	6.67E-03	-2.8215	-5.3557
3_5	Q09AH3	Acyl-coenzyme A synthetase ACSM2A, mitochondrial OS=Homo sapiens GN=ACSM2A PE=1 SV=2 - [ACS2A_HUMAN]	2.87E-04	-5.4960	-2.8194	1.11E-02	-2.5891	-3.6690
3_5	Q68CK6	Acyl-coenzyme A synthetase ACSM2B, mitochondrial OS=Homo sapiens GN=ACSM2B PE=1 SV=2 - [ACS2B_HUMAN]	2.46E-05	-12.8526	-2.8202	1.77E-03	-3.5317	-3.7082
3_5	Q8IUX7	Adipocyte enhancer-binding protein 1 OS=Homo sapiens GN=AEBP1 PE=1 SV=1 - [AEBP1_HUMAN]	5.13E-03	2.8330	2.8321	2.48E-02	2.2088	2.3713
3_5	O95154	Aflatoxin B1 aldehyde reductase member 3 OS=Homo sapiens GN=AKR7A3 PE=1 SV=2 - [AKR73_HUMAN]	1.94E-05	-14.5801	-2.8131	3.05E-04	-4.4711	-2.5535
3_5	P24298	Alanine aminotransferase 1 OS=Homo sapiens GN=GPT PE=1 SV=3 - [ALAT1_HUMAN]	2.93E-04	-5.4824	-2.6800	6.01E-03	-2.8831	-2.0078

Fig. 7 continued

3_5	P07327	Alcohol dehydrogenase 1A OS=Homo sapiens GN=ADH1A PE=1 SV=2 - [ADH1A_HUMAN]	1.51E-02	-2.4859	-2.9589	2.20E-03	-3.4049	-4.3653
3_5	P00325	Alcohol dehydrogenase 1B OS=Homo sapiens GN=ADH1B PE=1 SV=2 - [ADH1B_HUMAN]	4.77E-02	-1.9938	-2.9589	3.45E-03	-3.1685	-4.5623
3_5	P08319	Alcohol dehydrogenase 4 OS=Homo sapiens GN=ADH4 PE=1 SV=5 - [ADH4_HUMAN]	3.60E-03	-3.1728	-2.8303	7.60E-03	-2.7656	-3.8151
3_5	Q06278	Aldehyde oxidase OS=Homo sapiens GN=AOX1 PE=2 SV=2 - [ALDO_HUMAN]	2.74E-05	-10.7701	-2.7162	8.77E-03	-2.7026	-2.4672
3_5	O60218	Aldo-keto reductase family 1 member B10 OS=Homo sapiens GN=AKR1B10 PE=1 SV=2 - [AK1BA_HUMAN]	3.56E-03	-3.1856	-3.0091	1.67E-04	-4.8468	-5.0151
3_5	P52895	Aldo-keto reductase family 1 member C2 OS=Homo sapiens GN=AKR1C2 PE=1 SV=3 - [AK1C2_HUMAN]	3.22E-04	-5.3966	-3.0055	1.76E-02	-2.3773	-3.4921
3_5	P17516	Aldo-keto reductase family 1 member C4 OS=Homo sapiens GN=AKR1C4 PE=1 SV=3 - [AK1C4_HUMAN]	2.62E-04	-5.5674	-2.9828	2.83E-04	-4.5120	-3.4921
3_5	P21397	Amine oxidase [flavin-containing] A OS=Homo sapiens GN=MAOA PE=1 SV=1 - [AOFA_HUMAN]	4.39E-03	-2.9481	-2.8433	4.59E-02	-1.9576	-2.3906
3_5	Q03154	Aminoacylase-1 OS=Homo sapiens GN=ACY1 PE=1 SV=1 - [ACY1_HUMAN]	4.45E-05	-7.0427	-2.9365	1.16E-05	-7.0203	-3.3608
3_5	P12429	Annexin A3 OS=Homo sapiens GN=ANXA3 PE=1 SV=3 - [ANXA3_HUMAN]	2.79E-05	10.2215	2.8156	1.57E-03	3.5885	2.4937
3_5	P05090	Apolipoprotein D OS=Homo sapiens GN=APOD PE=1 SV=1 - [APOD_HUMAN]	1.16E-03	-3.8341	-2.6908	3.55E-03	-3.1519	-2.0015
3_5	P02649	Apolipoprotein E OS=Homo sapiens GN=APOE PE=1 SV=1 - [APOE_HUMAN]	1.83E-02	-2.3697	-2.9092	5.35E-05	-5.6328	-4.0078
3_5	O95831	Apoptosis-inducing factor 1, mitochondrial OS=Homo sapiens GN=AIFM1 PE=1 SV=1 - [AIFM1_HUMAN]	2.47E-02	-2.1550	-2.8474	1.13E-04	-5.1047	-3.8056
3_5	P05089	Arginase-1 OS=Homo sapiens GN=ARG1 PE=1 SV=2 - [ARGI1_HUMAN]	1.99E-05	-14.4515	-2.9788	1.16E-04	-5.0927	-4.3292
3_5	P04424	Argininosuccinate lyase OS=Homo sapiens GN=ASL PE=1 SV=4 - [ARLY_HUMAN]	2.93E-03	-3.3621	-2.9437	1.87E-04	-4.7842	-3.1013
3_5	P00966	Argininosuccinate synthase OS=Homo sapiens GN=ASS1 PE=1 SV=2 - [ASSY_HUMAN]	1.40E-04	-5.8411	-2.8519	2.02E-02	-2.3140	-2.6503
3_5	P22760	Arylacetamide deacetylase OS=Homo sapiens GN=AADAC PE=1 SV=5 - [AAAD_HUMAN]	1.37E-05	-16.1155	-2.7673	1.54E-05	-6.6513	-2.8640
3_5	P16278	Beta-galactosidase OS=Homo sapiens GN=GLB1 PE=1 SV=2 - [BGAL_HUMAN]	1.14E-02	-2.6604	-2.7926	1.36E-03	-3.6559	-2.2650
3_5	Q93088	Betaine--homocysteine S-methyltransferase 1 OS=Homo sapiens GN=BHMT PE=1 SV=2 - [BHMT1_HUMAN]	3.49E-04	-5.2976	-2.9078	3.20E-02	-2.0917	-3.2794
3_5	P21810	Biglycan OS=Homo sapiens GN=BGN PE=1 SV=2 - [PGS1_HUMAN]	2.28E-03	3.6010	3.0256	7.91E-05	5.3523	4.7778
3_5	Q9Y2P5	Bile acyl-CoA synthetase OS=Homo sapiens GN=SLC27A5 PE=1 SV=1 - [S27A5_HUMAN]	1.92E-03	-3.7096	-2.6951	3.13E-03	-3.2268	-2.5061
3_5	Q06520	Bile salt sulfotransferase OS=Homo sapiens GN=SULT2A1 PE=1 SV=3 - [ST2A1_HUMAN]	2.04E-05	-14.3652	-2.9030	1.17E-03	-3.7370	-2.8466
3_5	P17655	Calpain-2 catalytic subunit OS=Homo sapiens GN=CAPN2 PE=1 SV=5 - [CAN2_HUMAN]	1.58E-04	5.8000	2.7473	2.57E-03	3.3268	2.3612
3_5	P31327	Carbamoyl-phosphate synthase [ammonia], mitochondrial OS=Homo sapiens GN=CPS1 PE=1 SV=2 - [CPSM_HUMAN]	1.11E-02	-2.6799	-3.0534	3.11E-03	-3.2324	-7.2123
3_5	P23786	Carnitine O-palmitoyltransferase 2, mitochondrial OS=Homo sapiens GN=CPT2 PE=1 SV=2 - [CPT2_HUMAN]	8.38E-04	-3.9172	-2.8192	7.66E-03	-2.7629	-2.1909
3_5	P35222	Catenin beta-1 OS=Homo sapiens GN=CTNNB1 PE=1 SV=1 - [CTNB1_HUMAN]	3.83E-03	3.0871	2.7214	4.23E-03	3.0693	2.2357
3_5	O00748	Cocaine esterase OS=Homo sapiens GN=CES2 PE=1 SV=1 - [EST2_HUMAN]	5.68E-06	-20.4017	-2.8885	1.50E-03	-3.6108	-2.9344
3_5	Q99715	Collagen alpha-1(XII) chain OS=Homo sapiens GN=COL12A1 PE=1 SV=2 - [COCA1_HUMAN]	6.20E-04	4.1429	2.7621	2.51E-02	2.2001	2.3351
3_5	Q9P0M6	Core histone macro-H2A.2 OS=Homo sapiens GN=H2AFY2 PE=1 SV=3 - [H2AW_HUMAN]	7.59E-04	3.9847	2.8875	7.72E-04	3.9532	2.9562
3_5	Q86VP6	Cullin-associated NEDD8-dissociated protein 1 OS=Homo sapiens GN=CAND1 PE=1 SV=2 - [CAND1_HUMAN]	7.09E-04	4.0281	2.7822	3.90E-03	3.1060	2.3993
3_5	P00167	Cytochrome b5 OS=Homo sapiens GN=CYB5A PE=1 SV=2 - [CYB5_HUMAN]	1.95E-02	-2.3264	-3.0069	2.44E-05	-6.2894	-3.0531
3_5	P11509	Cytochrome P450 2A6 OS=Homo sapiens GN=CYP2A6 PE=1 SV=3 - [CP2A6_HUMAN]	3.42E-04	-5.3604	-2.8057	3.28E-03	-3.1991	-2.8754

Fig. 7 continued

3.5	P11712	Cytochrome P450 2C9 OS=Homo sapiens GN=CYP2C9 PE=1 SV=3 - [CP2C9_HUMAN]	2.60E-05	-12.1941	-2.7039	6.62E-03	-2.8247	-2.1275
3.5	P10635	Cytochrome P450 2D6 OS=Homo sapiens GN=CYP2D6 PE=1 SV=2 - [CP2D6_HUMAN]	1.73E-03	-3.7456	-2.6731	2.95E-03	-3.2589	-2.1385
3.5	Q14204	Cytoplasmic dynein 1 heavy chain 1 OS=Homo sapiens GN=DYNC1H1 PE=1 SV=5 - [DYHC1_HUMAN]	3.98E-03	3.0427	2.7437	1.81E-03	3.5186	3.6977
3.5	O75891	Cytosolic 10-formyltetrahydrofolate dehydrogenase OS=Homo sapiens GN=ALDH1L1 PE=1 SV=2 - [AL1L1_HUMAN]	2.84E-05	-10.0651	-2.8507	2.52E-02	-2.1987	-3.8154
3.5	Q02338	D-beta-hydroxybutyrate dehydrogenase, mitochondrial OS=Homo sapiens GN=BDH1 PE=1 SV=3 - [BDH_HUMAN]	1.66E-05	-15.3212	-2.8436	1.15E-05	-7.0629	-2.5424
3.5	P07585	Decorin OS=Homo sapiens GN=DCN PE=1 SV=1 - [PGS2_HUMAN]	2.77E-03	3.4084	2.8707	1.88E-02	2.3460	2.9632
3.5	P30038	Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial OS=Homo sapiens GN=ALDH4A1 PE=1 SV=3 - [AL4A1_HUMAN]	2.44E-02	-2.1642	-2.9501	1.04E-03	-3.7874	-3.7648
3.5	P09417	Dihydropteridine reductase OS=Homo sapiens GN=QDPR PE=1 SV=2 - [DHPR_HUMAN]	1.61E-05	-15.5209	-2.8151	4.18E-04	-4.3148	-2.2905
3.5	Q16555	Dihydropyrimidinase-related protein 2 OS=Homo sapiens GN=DPYSL2 PE=1 SV=1 - [DPYL2_HUMAN]	3.42E-02	2.0991	2.8193	3.43E-03	3.1720	3.5311
3.5	P31513	Dimethylaniline monooxygenase [N-oxide-forming] 3 OS=Homo sapiens GN=FMO3 PE=1 SV=5 - [FMO3_HUMAN]	2.85E-04	-5.5060	-2.8163	5.42E-04	-4.1361	-2.9344
3.5	Q9UI17	Dimethylglycine dehydrogenase, mitochondrial OS=Homo sapiens GN=DMGDH PE=1 SV=2 - [DMGD_HUMAN]	3.13E-04	-5.4111	-2.7015	1.45E-03	-3.6258	-2.0015
3.5	O75521	Enoyl-CoA delta isomerase 2, mitochondrial OS=Homo sapiens GN=ECI2 PE=1 SV=4 - [ECI2_HUMAN]	2.64E-05	-12.0565	-2.6864	6.48E-04	-4.0499	-2.5424
3.5	P15311	Ezrin OS=Homo sapiens GN=EZR PE=1 SV=4 - [EZRI_HUMAN]	2.64E-03	3.4639	2.9018	1.48E-03	3.6144	3.6512
3.5	O95954	Formimidoyltransferase-cyclodeaminase OS=Homo sapiens GN=FTCD PE=1 SV=2 - [FTCD_HUMAN]	1.94E-05	-14.7716	-2.8579	4.97E-03	-2.9921	-2.8931
3.5	P09467	Fructose-1,6-bisphosphatase 1 OS=Homo sapiens GN=FBP1 PE=1 SV=5 - [F16P1_HUMAN]	4.72E-04	-4.6109	-2.9303	3.91E-04	-4.3369	-4.0129
3.5	P05062	Fructose-bisphosphate aldolase B OS=Homo sapiens GN=ALDOB PE=1 SV=2 - [ALDOB_HUMAN]	1.90E-02	-2.3447	-3.0905	1.07E-04	-5.1492	-5.5231
3.5	P16930	Fumarylacetoacetase OS=Homo sapiens GN=FAH PE=1 SV=2 - [FAAA_HUMAN]	1.53E-02	-2.4702	-2.9440	1.54E-05	-6.6694	-3.0078
3.5	P08382	Galectin-1 OS=Homo sapiens GN=LGALS1 PE=1 SV=2 - [LEG1_HUMAN]	2.02E-02	2.3037	2.8706	1.21E-02	2.5484	2.5088
3.5	O95479	GDH/6PGL endoplasmic bifunctional protein OS=Homo sapiens GN=H6PD PE=1 SV=2 - [G6PE_HUMAN]	5.01E-05	-6.8695	-2.8183	1.52E-04	-4.8940	-2.6130
3.5	P08263	Glutathione S-transferase A1 OS=Homo sapiens GN=GSTA1 PE=1 SV=3 - [GSTA1_HUMAN]	1.06E-02	-2.7151	-3.0465	3.96E-04	-4.3348	-3.3608
3.5	P06737	Glycogen phosphorylase, liver form OS=Homo sapiens GN=PYGL PE=1 SV=4 - [PYGL_HUMAN]	9.92E-06	-18.0733	-2.9005	7.19E-04	-4.0002	-3.5535
3.5	Q9UJU7	GTP:AMP phosphotransferase, mitochondrial OS=Homo sapiens GN=AK3 PE=1 SV=4 - [KAD3_HUMAN]	1.96E-04	-5.7303	-2.8578	2.73E-03	-3.2955	-2.4280
3.5	Q1KMD3	Heterogeneous nuclear ribonucleoprotein U-like protein 2 OS=Homo sapiens GN=HNRNPUL2 PE=1 SV=1 - [HNRL2_HUMAN]	2.42E-02	2.1693	2.8978	2.19E-02	2.2734	2.1652
3.5	Q93099	Homogentisate 1,2-dioxygenase OS=Homo sapiens GN=HGD PE=1 SV=2 - [HGD_HUMAN]	3.47E-04	-5.3132	-2.8389	1.31E-04	-4.9789	-4.0042
3.5	Q9UJM8	Hydroxyacid oxidase 1 OS=Homo sapiens GN=HAO1 PE=1 SV=1 - [HAOX1_HUMAN]	1.23E-05	-16.4212	-2.8892	1.13E-05	-7.1383	-4.1274
3.5	Q16836	Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial OS=Homo sapiens GN=HADH PE=1 SV=3 - [HCDH_HUMAN]	2.39E-03	-3.5546	-2.8237	1.59E-02	-2.4300	-2.4169
3.5	P35914	Hydroxymethylglutaryl-CoA lyase, mitochondrial OS=Homo sapiens GN=HMGCL PE=1 SV=2 - [HMGCL_HUMAN]	3.26E-04	-5.3902	-2.7459	1.18E-03	-3.7310	-2.1275
3.5	P54868	Hydroxymethylglutaryl-CoA synthase, mitochondrial OS=Homo sapiens GN=HMGCS2 PE=1 SV=1 - [HMCS2_HUMAN]	1.36E-02	-2.5527	-2.9618	8.20E-05	-5.3306	-4.5313
3.5	P19823	Inter-alpha-trypsin inhibitor heavy chain H2 OS=Homo sapiens GN=ITIH2 PE=1 SV=2 - [ITIH2_HUMAN]	2.72E-03	3.4318	2.8529	1.49E-02	2.4656	3.3993
3.5	P14923	Junction plakoglobin OS=Homo sapiens GN=JUP PE=1 SV=3 - [PLAK_HUMAN]	1.33E-04	5.8600	2.8074	5.48E-04	4.1320	2.9897
3.5	P08727	Keratin, type I cytoskeletal 19 OS=Homo sapiens GN=KRT19 PE=1 SV=4 - [K1C19_HUMAN]	3.99E-04	4.9800	3.0423	1.88E-03	3.4985	4.7762
3.5	P08729	Keratin, type II cytoskeletal 7 OS=Homo sapiens GN=KRT7 PE=1 SV=5 - [K2C7_HUMAN]	2.21E-03	3.6363	3.0068	9.50E-04	3.8301	3.8292

Fig. 7 continued

3.5	O00515	Ladinin-1 OS=Homo sapiens GN=LAD1 PE=1 SV=2 - [LAD1_HUMAN]	2.69E-05	11.8329	2.8060	1.62E-03	3.5811	2.7002
3.5	P23141	Liver carboxylesterase 1 OS=Homo sapiens GN=CES1 PE=1 SV=2 - [EST1_HUMAN]	4.78E-03	-2.8757	-3.0504	2.61E-05	-6.2299	-5.7364
3.5	P33121	Long-chain-fatty-acid--CoA ligase 1 OS=Homo sapiens GN=ACSL1 PE=1 SV=1 - [ACSL1_HUMAN]	2.55E-05	-12.2483	-2.8373	2.54E-03	-3.3330	-3.3292
3.5	Q7Z4W1	L-xylulose reductase OS=Homo sapiens GN=DCXR PE=1 SV=2 - [DCXR_HUMAN]	1.51E-02	-2.4838	-3.0187	2.89E-03	-3.2691	-4.1274
3.5	P10619	Lysosomal protective protein OS=Homo sapiens GN=CTSA PE=1 SV=2 - [PPGB_HUMAN]	5.30E-04	-4.3704	-2.8071	3.39E-05	-6.0640	-2.0078
3.5	P11310	Medium-chain specific acyl-CoA dehydrogenase, mitochondrial OS=Homo sapiens GN=ACADM PE=1 SV=1 - [ACADM_HUMAN]	6.00E-04	-4.1675	-2.8732	1.70E-03	-3.5508	-3.0560
3.5	Q02252	Methylmalonate-semialdehyde dehydrogenase [acylating], mitochondrial OS=Homo sapiens GN=ALDH6A1 PE=1 SV=2 - [MMSA_HUMAN]	3.11E-04	-5.4190	-2.8851	1.53E-03	-3.5987	-4.0977
3.5	Q9H8H3	Methyltransferase-like protein 7A OS=Homo sapiens GN=METTL7A PE=1 SV=1 - [META_HUMAN]	2.59E-04	-5.5771	-2.8687	5.72E-04	-4.1054	-2.1385
3.5	P10620	Microsomal glutathione S-transferase 1 OS=Homo sapiens GN=MGST1 PE=1 SV=1 - [MGST1_HUMAN]	7.20E-05	-6.1017	-2.9236	3.29E-05	-6.0920	-2.2794
3.5	P55157	Microsomal triglyceride transfer protein large subunit OS=Homo sapiens GN=MTTP PE=1 SV=1 - [MTP_HUMAN]	2.22E-05	-13.6236	-2.7434	1.98E-04	-4.7269	-2.8913
3.5	Q9Y6C9	Mitochondrial carrier homolog 2 OS=Homo sapiens GN=MTCH2 PE=1 SV=1 - [MTCH2_HUMAN]	4.49E-03	-2.9302	-2.7947	1.16E-02	-2.5677	-2.3906
3.5	Q4G0N4	NAD kinase domain-containing protein 1 OS=Homo sapiens GN=NADKD1 PE=1 SV=2 - [NAKD1_HUMAN]	1.11E-05	-17.6699	-2.8105	5.61E-05	-5.5697	-2.8644
3.5	P16435	NADPH--cytochrome P450 reductase OS=Homo sapiens GN=POR PE=1 SV=2 - [NCPR_HUMAN]	7.82E-05	-5.9800	-2.8486	4.25E-04	-4.2991	-3.6130
3.5	P22307	Non-specific lipid-transfer protein OS=Homo sapiens GN=SCP2 PE=1 SV=2 - [NLTP_HUMAN]	2.88E-03	-3.3750	-2.8858	1.27E-04	-5.0217	-2.6130
3.5	P00480	Ornithine carbamoyltransferase, mitochondrial OS=Homo sapiens GN=OTC PE=1 SV=3 - [OTC_HUMAN]	6.87E-05	-6.1339	-2.9239	3.26E-06	-7.5783	-4.0449
3.5	O60664	Perilipin-3 OS=Homo sapiens GN=PLIN3 PE=1 SV=3 - [PLIN3_HUMAN]	1.35E-03	3.8090	2.8256	1.01E-04	5.1771	2.9562
3.5	Q15063	Periostin OS=Homo sapiens GN=POSTN PE=1 SV=2 - [POSTN_HUMAN]	7.14E-04	4.0246	3.0149	3.84E-03	3.1132	4.5277
3.5	Q15067	Peroxisomal acyl-coenzyme A oxidase 1 OS=Homo sapiens GN=ACOX1 PE=1 SV=3 - [ACOX1_HUMAN]	3.30E-04	-5.3846	-2.6944	3.79E-03	-3.1195	-2.9962
3.5	O99424	Peroxisomal acyl-coenzyme A oxidase 2 OS=Homo sapiens GN=ACOX2 PE=1 SV=1 - [ACOX2_HUMAN]	1.00E-02	-2.7385	-2.6239	1.86E-02	-2.3496	-2.2794
3.5	Q08426	Peroxisomal bifunctional enzyme OS=Homo sapiens GN=EHHADH PE=1 SV=3 - [ECHP_HUMAN]	2.44E-03	-3.5374	-2.9060	2.67E-06	-7.6974	-5.0344
3.5	Q9P0Z9	Peroxisomal sarcosine oxidase OS=Homo sapiens GN=PIPOX PE=2 SV=2 - [SOX_HUMAN]	2.27E-05	-13.2807	-2.8545	4.99E-04	-4.1917	-2.8754
3.5	Q16822	Phosphoenolpyruvate carboxykinase [GTP], mitochondrial OS=Homo sapiens GN=PCK2 PE=1 SV=3 - [PCKGM_HUMAN]	5.05E-04	-4.4685	-2.9462	2.14E-04	-4.6985	-4.2539
3.5	Q14914	Prostaglandin reductase 1 OS=Homo sapiens GN=PTGR1 PE=1 SV=2 - [PTGR1_HUMAN]	2.65E-04	-5.5529	-2.7764	1.29E-03	-3.6888	-3.4672
3.5	Q9BPW8	Protein NipSnap homolog 1 OS=Homo sapiens GN=NIPSNAP1 PE=1 SV=1 - [NIPS1_HUMAN]	4.69E-03	-2.8932	-2.8440	1.40E-03	-3.6441	-3.0560
3.5	P31949	Protein S100-A11 OS=Homo sapiens GN=S100A11 PE=1 SV=2 - [S10AB_HUMAN]	3.78E-04	5.0768	2.8796	9.12E-05	5.2427	2.0637
3.5	P55786	Puromycin-sensitive aminopeptidase OS=Homo sapiens GN=NPEPPS PE=1 SV=2 - [PSA_HUMAN]	7.39E-04	4.0031	2.8279	1.79E-02	2.3780	2.3612
3.5	Q9NVS9	Pyridoxine-5-phosphate oxidase OS=Homo sapiens GN=PNPO PE=1 SV=1 - [PNPO_HUMAN]	1.18E-05	-16.4862	-2.8728	2.31E-06	-7.9449	-2.1274
3.5	P11498	Pyruvate carboxylase, mitochondrial OS=Homo sapiens GN=PC PE=1 SV=2 - [PYC_HUMAN]	6.44E-05	-6.2633	-2.8168	5.21E-04	-4.1577	-3.9862
3.5	P30613	Pyruvate kinase isozymes R/L OS=Homo sapiens GN=PKLR PE=1 SV=2 - [KPYR_HUMAN]	1.04E-05	-17.8985	-2.8740	5.91E-04	-4.0802	-3.4485
3.5	P46940	Ras GTPase-activating-like protein IQGAP1 OS=Homo sapiens GN=IQGAP1 PE=1 SV=1 - [IQGA1_HUMAN]	4.23E-04	4.8199	2.9488	4.58E-06	7.4661	4.0493
3.5	Q13576	Ras GTPase-activating-like protein IQGAP2 OS=Homo sapiens GN=IQGAP2 PE=1 SV=4 - [IQGA2_HUMAN]	3.12E-03	-3.3167	-2.7576	4.29E-02	-1.9845	-2.3161
3.5	P02763	Retinol-binding protein 4 OS=Homo sapiens GN=RBP4 PE=1 SV=3 - [RET4_HUMAN]	1.51E-05	-15.7175	-2.8475	1.59E-05	-6.5738	-2.2794

Fig. 7 continued

3 5	P52758	Ribonuclease UK114 OS=Homo sapiens GN=HRSP12 PE=1 SV=1 - [UK114_HUMAN]	4.88E-04	-4.5400	-2.9999	1.80E-04	-4.8157	-3.1385
3 5	Q97265	RuvB-like 1 OS=Homo sapiens GN=RUVBL1 PE=1 SV=1 - [RUVB1_HUMAN]	3.00E-03	3.3269	2.7167	3.12E-04	4.4576	2.4022
3 5	Q8N8X0	Saccharopine dehydrogenase-like oxidoreductase OS=Homo sapiens GN=SCCPDH PE=1 SV=1 - [SCPDL_HUMAN]	4.62E-03	-2.9016	-2.9469	1.17E-04	-5.0839	-2.5927
3 5	Q00266	S-adenosylmethionine synthase isoform type-1 OS=Homo sapiens GN=MAT1A PE=1 SV=2 - [METK1_HUMAN]	2.31E-05	-13.1193	-2.8581	2.48E-03	-3.3468	-2.7125
3 5	P34896	Serine hydroxymethyltransferase, cytosolic OS=Homo sapiens GN=SHMT1 PE=1 SV=1 - [GLYC_HUMAN]	3.42E-04	-5.3599	-2.8267	7.73E-05	-5.3687	-2.9536
3 5	P21549	Serine--pyruvate aminotransferase OS=Homo sapiens GN=AGXT PE=1 SV=1 - [SPYA_HUMAN]	1.08E-02	-2.7028	-3.0303	1.12E-04	-5.1086	-5.2723
3 5	P45954	Short/branched chain specific acyl-CoA dehydrogenase, mitochondrial OS=Homo sapiens GN=ACADSB PE=1 SV=1 - [ACDSB_HUMAN]	2.17E-05	-13.7468	-2.8646	5.68E-05	-5.5525	-3.1275
3 5	Q00796	Sorbitol dehydrogenase OS=Homo sapiens GN=SORD PE=1 SV=4 - [DHSO_HUMAN]	6.14E-05	-6.4104	-2.8262	1.16E-03	-3.7463	-2.7312
3 5	O75533	Splicing factor 3B subunit 1 OS=Homo sapiens GN=SF3B1 PE=1 SV=3 - [SF3B1_HUMAN]	1.13E-02	2.6668	2.7362	1.21E-03	3.7219	2.1652
3 5	Q14247	Src substrate cortactin OS=Homo sapiens GN=CTTN PE=1 SV=2 - [SRC8_HUMAN]	4.43E-02	2.0524	2.7452	3.54E-02	2.0583	2.1127
3 5	Q02318	Sterol 26-hydroxylase, mitochondrial OS=Homo sapiens GN=CYP27A1 PE=1 SV=1 - [CP27A_HUMAN]	2.50E-04	-5.6078	-2.7775	1.65E-03	-3.5792	-2.0078
3 5	P51649	Succinate-semialdehyde dehydrogenase, mitochondrial OS=Homo sapiens GN=ALDH5A1 PE=1 SV=2 - [SSDH_HUMAN]	3.90E-04	-5.0398	-2.7413	1.71E-02	-2.3916	-2.4672
3 5	P07996	Thrombospondin-1 OS=Homo sapiens GN=THBS1 PE=1 SV=2 - [TSP1_HUMAN]	4.69E-02	2.0125	2.7621	1.29E-02	2.5202	2.2012
3 5	Q13263	Transcription intermediary factor 1-beta OS=Homo sapiens GN=TRIM28 PE=1 SV=5 - [TIF1B_HUMAN]	1.41E-04	5.8380	2.7646	2.19E-03	3.4092	2.9117
3 5	Q13509	Tubulin beta-3 chain OS=Homo sapiens GN=TUBB3 PE=1 SV=2 - [TBB3_HUMAN]	1.30E-03	3.8155	2.9858	7.54E-03	2.7685	5.1341
3 5	P04350	Tubulin beta-4A chain OS=Homo sapiens GN=TUBB4A PE=1 SV=2 - [TBB4A_HUMAN]	1.35E-04	5.8533	3.0176	5.09E-05	5.6551	5.9854
3 5	Q9BUF5	Tubulin beta-6 chain OS=Homo sapiens GN=TUBB6 PE=1 SV=1 - [TBB6_HUMAN]	1.31E-03	3.8146	2.9867	1.19E-03	3.7252	4.9018
3 5	P22310	UDP-glucuronosyltransferase 1-4 OS=Homo sapiens GN=UGT1A4 PE=1 SV=1 - [UD14_HUMAN]	3.37E-04	-5.3717	-2.8417	1.32E-02	-2.5112	-2.8065
3 5	P19224	UDP-glucuronosyltransferase 1-6 OS=Homo sapiens GN=UGT1A6 PE=1 SV=2 - [UD16_HUMAN]	3.27E-04	-5.3891	-2.8261	2.21E-02	-2.2707	-2.0015
3 5	O60656	UDP-glucuronosyltransferase 1-9 OS=Homo sapiens GN=UGT1A9 PE=1 SV=1 - [UD19_HUMAN]	2.21E-03	-3.6353	-2.8416	4.95E-02	-1.9293	-2.0078
3 5	P06133	UDP-glucuronosyltransferase 2B4 OS=Homo sapiens GN=UGT2B4 PE=1 SV=2 - [UD2B4_HUMAN]	2.09E-05	-14.2817	-2.9014	4.47E-03	-3.0413	-2.9536
3 5	P16662	UDP-glucuronosyltransferase 2B7 OS=Homo sapiens GN=UGT2B7 PE=1 SV=1 - [UD2B7_HUMAN]	1.56E-05	-15.6905	-2.8565	1.40E-03	-3.6440	-2.8754
3 6	Q04917	14-3-3 protein eta OS=Homo sapiens GN=YWHAH PE=1 SV=4 - [1433F_HUMAN]	4.23E-04	5.4428	3.2807	3.86E-05	6.6794	3.5485
3 6	P31947	14-3-3 protein sigma OS=Homo sapiens GN=SFN PE=1 SV=1 - [1433S_HUMAN]	2.69E-02	2.2514	3.2798	5.71E-03	2.9411	3.1797
3 6	O14756	17-beta-hydroxysteroid dehydrogenase type 6 OS=Homo sapiens GN=HSD17B6 PE=1 SV=1 - [HI7B6_HUMAN]	1.37E-05	-14.8936	-2.8892	1.32E-04	-5.3332	-3.2054
3 6	P31937	3-hydroxyisobutyrate dehydrogenase, mitochondrial OS=Homo sapiens GN=HIBADH PE=1 SV=2 - [3HIDH_HUMAN]	9.59E-04	-4.2885	-2.8185	2.15E-04	-4.9294	-2.6690
3 6	P42765	3-ketoacyl-CoA thiolase, mitochondrial OS=Homo sapiens GN=ACAA2 PE=1 SV=2 - [THIM_HUMAN]	2.67E-02	-2.2613	-2.9668	7.09E-03	-2.8113	-4.0910
3 6	P09110	3-ketoacyl-CoA thiolase, peroxisomal OS=Homo sapiens GN=ACAA1 PE=1 SV=2 - [THIK_HUMAN]	9.72E-04	-4.2485	-2.7809	7.10E-03	-2.8112	-4.0977
3 6	P80404	4-aminobutyrate aminotransferase, mitochondrial OS=Homo sapiens GN=ABAT PE=1 SV=3 - [GABT_HUMAN]	2.83E-05	-12.9166	-2.8695	4.43E-03	-3.0874	-3.4280
3 6	P32754	4-hydroxyphenylpyruvate dioxygenase OS=Homo sapiens GN=HPD PE=1 SV=2 - [HPPD_HUMAN]	2.76E-05	-12.9628	-2.9576	2.86E-04	-4.6765	-4.0978
3 6	Q08AH3	Acyl-coenzyme A synthetase ACSM2A, mitochondrial OS=Homo sapiens GN=ACSM2A PE=1 SV=2 - [ACS2A_HUMAN]	3.82E-04	-5.4960	-2.8194	1.16E-02	-2.5891	-3.6690
3 6	Q8ICX6	Acyl-coenzyme A synthetase ACSM2B, mitochondrial OS=Homo sapiens GN=ACSM2B PE=1 SV=2 - [ACS2B_HUMAN]	2.94E-05	-12.8526	-2.8202	1.93E-03	-3.5317	-3.7082

Fig. 7 continued

3_6	Q8IUX7	Adipocyte enhancer-binding protein 1 OS=Homo sapiens GN=AEBP1 PE=1 SV=1 - [AEBP1_HUMAN]	9.97E-04	4.2256	3.0447	1.47E-02	2.4746	2.1194
3_6	P24298	Alanine aminotransferase 1 OS=Homo sapiens GN=GPT PE=1 SV=3 - [ALAT1_HUMAN]	3.91E-04	-5.4824	-2.6800	6.28E-03	-2.8831	-2.0078
3_6	P08319	Alcohol dehydrogenase 4 OS=Homo sapiens GN=ADH4 PE=1 SV=5 - [ADH4_HUMAN]	3.78E-05	-11.2379	-2.8303	5.97E-03	-2.9109	-3.8151
3_6	P30837	Aldehyde dehydrogenase X, mitochondrial OS=Homo sapiens GN=ALDH1B1 PE=1 SV=3 - [AL1B1_HUMAN]	5.82E-03	-3.0736	-2.8918	6.49E-03	-2.8670	-3.1860
3_6	Q06278	Aldehyde oxidase OS=Homo sapiens GN=AOX1 PE=2 SV=2 - [AOX_HUMAN]	3.93E-05	-10.7701	-2.7162	9.03E-03	-2.7026	-2.4672
3_6	O60218	Aldo-keto reductase family 1 member B10 OS=Homo sapiens GN=AKR1B10 PE=1 SV=2 - [AK1BA_HUMAN]	1.62E-02	-2.6573	-3.0091	1.87E-04	-5.0247	-5.0151
3_6	Q04828	Aldo-keto reductase family 1 member C1 OS=Homo sapiens GN=AKR1C1 PE=1 SV=1 - [AK1C1_HUMAN]	6.34E-03	-3.0066	-3.0089	2.31E-03	-3.4365	-4.0151
3_6	P52895	Aldo-keto reductase family 1 member C2 OS=Homo sapiens GN=AKR1C2 PE=1 SV=3 - [AK1C2_HUMAN]	4.45E-04	-5.3956	-3.0055	1.76E-02	-2.3773	-3.4921
3_6	P17516	Aldo-keto reductase family 1 member C4 OS=Homo sapiens GN=AKR1C4 PE=1 SV=3 - [AK1C4_HUMAN]	3.22E-04	-5.5674	-2.9828	3.94E-04	-4.5120	-3.4921
3_6	P21397	Amine oxidase [flavin-containing] A OS=Homo sapiens GN=MAOA PE=1 SV=1 - [AOFA_HUMAN]	2.15E-05	-13.7361	-2.8433	9.30E-03	-2.6901	-2.3906
3_6	Q03154	Aminoacylase-1 OS=Homo sapiens GN=ACY1 PE=1 SV=1 - [ACY1_HUMAN]	9.82E-07	-17.9308	-2.9365	1.76E-05	-7.0203	-3.3608
3_6	P15144	Aminopeptidase N OS=Homo sapiens GN=ANPEP PE=1 SV=4 - [AMPN_HUMAN]	3.68E-03	-3.4705	-2.7082	3.20E-02	-2.0803	-2.1909
3_6	P12429	Annexin A3 OS=Homo sapiens GN=ANXA3 PE=1 SV=3 - [ANXA3_HUMAN]	1.28E-05	14.9937	3.1295	4.74E-05	6.3399	3.1797
3_6	O95994	Anterior gradient protein 2 homolog OS=Homo sapiens GN=AGR2 PE=1 SV=1 - [AGR2_HUMAN]	2.76E-04	5.6211	3.1957	2.59E-03	3.3658	3.6814
3_6	O95831	Apoptosis-inducing factor 1, mitochondrial OS=Homo sapiens GN=AIFM1 PE=1 SV=1 - [AIFM1_HUMAN]	1.18E-03	-4.0588	-2.8474	1.03E-04	-5.5512	-3.8066
3_6	P05089	Arginase-1 OS=Homo sapiens GN=ARG1 PE=1 SV=2 - [ARGI1_HUMAN]	1.62E-05	-14.4515	-2.9788	1.76E-04	-5.0927	-4.3292
3_6	P22760	Arylacetamide deacetylase OS=Homo sapiens GN=AADAC PE=1 SV=5 - [AAAD_HUMAN]	6.37E-06	-16.1155	-2.7673	3.71E-05	-6.6513	-2.8640
3_6	P36542	ATP synthase subunit gamma, mitochondrial OS=Homo sapiens GN=ATP5C1 PE=1 SV=1 - [ATPG_HUMAN]	4.54E-03	-3.2942	-2.8975	5.56E-07	-10.2392	-2.3161
3_6	Q93088	Betaine--homocysteine S-methyltransferase 1 OS=Homo sapiens GN=BHMT PE=1 SV=2 - [BHMT1_HUMAN]	5.19E-04	-5.2976	-2.9078	3.11E-02	-2.0917	-3.2794
3_6	P21810	Biglycan OS=Homo sapiens GN=BGN PE=1 SV=2 - [PGS1_HUMAN]	9.51E-04	4.2852	3.2174	2.36E-03	3.4252	4.6606
3_6	Q9Y2P5	Bile acyl-CoA synthetase OS=Homo sapiens GN=SLC27A5 PE=1 SV=1 - [S27A5_HUMAN]	2.36E-03	-3.7096	-2.6951	3.41E-03	-3.2268	-2.5061
3_6	Q06520	Bile salt sulfotransferase OS=Homo sapiens GN=SULT2A1 PE=1 SV=3 - [ST2A1_HUMAN]	1.72E-05	-14.3652	-2.9030	1.34E-03	-3.7370	-2.8466
3_6	P11586	C-1-tetrahydrofolate synthase, cytoplasmic OS=Homo sapiens GN=MTHFD1 PE=1 SV=3 - [C1TC_HUMAN]	6.29E-03	-3.0134	-2.8294	9.59E-04	-3.9240	-3.8644
3_6	Q9UJS0	Calcium-binding mitochondrial carrier protein Aralar2 OS=Homo sapiens GN=SLC25A13 PE=1 SV=2 - [CMC2_HUMAN]	1.60E-03	-3.8316	-2.8629	1.88E-05	-7.0086	-3.6690
3_6	P17655	Calpain-2 catalytic subunit OS=Homo sapiens GN=CAPN2 PE=1 SV=5 - [CAN2_HUMAN]	3.15E-04	5.5739	2.7966	2.01E-03	3.5107	3.2821
3_6	P31327	Carbamoyl-phosphate synthase [ammonia], mitochondrial OS=Homo sapiens GN=CPS1 PE=1 SV=2 - [CPSM_HUMAN]	1.77E-03	-3.7960	-3.0534	2.52E-03	-3.3894	-7.2123
3_6	P23786	Carnitine O-palmitoyltransferase 2, mitochondrial OS=Homo sapiens GN=CPT2 PE=1 SV=2 - [CPT2_HUMAN]	1.68E-05	-14.4234	-2.8192	1.76E-03	-3.5883	-2.1909
3_6	P35221	Catenin alpha-1 OS=Homo sapiens GN=CTNNA1 PE=1 SV=1 - [CTNA1_HUMAN]	1.15E-02	2.7626	2.7404	1.66E-02	2.4099	2.6767
3_6	O00748	Cocaine esterase OS=Homo sapiens GN=CES2 PE=1 SV=1 - [EST2_HUMAN]	2.88E-09	-20.4017	-2.8885	1.66E-03	-3.6108	-2.9344
3_6	Q99715	Collagen alpha-1(XII) chain OS=Homo sapiens GN=COL12A1 PE=1 SV=2 - [COCA1_HUMAN]	1.13E-03	4.0908	2.7725	1.99E-02	2.3219	3.8564
3_6	P00751	Complement factor B OS=Homo sapiens GN=CFB PE=1 SV=2 - [CFAB_HUMAN]	1.17E-03	4.0624	3.1180	1.65E-03	3.6171	2.4608
3_6	P31146	Coronin-1A OS=Homo sapiens GN=CORO1A PE=1 SV=4 - [COR1A_HUMAN]	2.41E-02	2.3588	2.8914	2.52E-03	3.3876	2.1194

Fig. 7 continued

3_6	P12532	Creatine kinase U-type, mitochondrial OS=Homo sapiens GN=CKMT1A PE=1 SV=1 - [KCRU_HUMAN]	1.90E-03	3.7681	2.8880	5.84E-03	2.9246	2.1408
3_6	Q86VP6	Cullin-associated NEDD8-dissociated protein 1 OS=Homo sapiens GN=CAND1 PE=1 SV=2 - [CAND1_HUMAN]	1.21E-02	2.7488	2.7057	9.22E-03	2.6935	2.0361
3_6	P00167	Cytochrome b5 OS=Homo sapiens GN=CYB5A PE=1 SV=2 - [CYB5_HUMAN]	5.80E-03	-3.0765	-3.0069	3.39E-05	-6.7295	-3.0631
3_6	P11509	Cytochrome P450 2A6 OS=Homo sapiens GN=CYP2A6 PE=1 SV=3 - [CP2A6_HUMAN]	4.83E-04	-5.3604	-2.8057	3.60E-03	-3.1991	-2.8754
3_6	P11712	Cytochrome P450 2C9 OS=Homo sapiens GN=CYP2C9 PE=1 SV=3 - [CP2C9_HUMAN]	3.19E-05	-12.1941	-2.7039	6.93E-03	-2.8247	-2.1275
3_6	P10635	Cytochrome P450 2D6 OS=Homo sapiens GN=CYP2D6 PE=1 SV=2 - [CP2D6_HUMAN]	1.99E-03	-3.7456	-2.6731	3.19E-03	-3.2589	-2.1385
3_6	O75891	Cytosolic 10-formyltetrahydrofolate dehydrogenase OS=Homo sapiens GN=ALDH1L1 PE=1 SV=2 - [AL1L1_HUMAN]	3.99E-05	-10.0651	-2.8507	2.48E-02	-2.1987	-3.8154
3_6	Q02338	D-beta-hydroxybutyrate dehydrogenase, mitochondrial OS=Homo sapiens GN=BDH1 PE=1 SV=3 - [BDH_HUMAN]	1.13E-05	-15.3212	-2.8436	1.67E-05	-7.0629	-2.5424
3_6	P07585	Decorin OS=Homo sapiens GN=DCN PE=1 SV=1 - [PGS2_HUMAN]	1.00E-03	4.2222	3.1399	1.91E-03	3.5380	3.3048
3_6	P30038	Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial OS=Homo sapiens GN=ALDH4A1 PE=1 SV=3 - [AL4A1_HUMAN]	8.75E-05	-6.4859	-2.9501	4.51E-04	-4.4182	-3.7648
3_6	P09417	Dihydropteridine reductase OS=Homo sapiens GN=QDPR PE=1 SV=2 - [DHPR_HUMAN]	9.40E-06	-15.5209	-2.8151	5.07E-04	-4.3148	-2.2905
3_6	Q16555	Dihydropyrimidinase-related protein 2 OS=Homo sapiens GN=DPYSL2 PE=1 SV=1 - [DPYL2_HUMAN]	1.39E-03	3.9488	3.1073	4.45E-04	4.4290	3.2173
3_6	Q14195	Dihydropyrimidinase-related protein 3 OS=Homo sapiens GN=DPYSL3 PE=1 SV=1 - [DPYL3_HUMAN]	3.36E-04	5.5611	3.0468	6.55E-04	4.1575	2.8564
3_6	P31513	Dimethylaniline monooxygenase [N-oxide-forming] 3 OS=Homo sapiens GN=FMO3 PE=1 SV=5 - [FMO3_HUMAN]	3.78E-04	-5.5050	-2.8163	6.85E-04	-4.1361	-2.9344
3_6	Q9UI17	Dimethylglycine dehydrogenase, mitochondrial OS=Homo sapiens GN=DMGDH PE=1 SV=2 - [DMGD_HUMAN]	4.36E-04	-5.4111	-2.7015	1.63E-03	-3.6258	-2.0015
3_6	O75356	Ectonucleoside triphosphate diphosphohydrolase 5 OS=Homo sapiens GN=ENTPD5 PE=1 SV=1 - [ENTP5_HUMAN]	2.97E-04	-5.5849	-2.7192	8.23E-03	-2.7447	-2.1777
3_6	O75521	Enoyl-CoA delta isomerase 2, mitochondrial OS=Homo sapiens GN=ECI2 PE=1 SV=4 - [ECI2_HUMAN]	3.44E-05	-12.0565	-2.6864	7.85E-04	-4.0499	-2.5424
3_6	P07099	Epoxide hydrolase 1 OS=Homo sapiens GN=EPHX1 PE=1 SV=1 - [HYEP_HUMAN]	6.71E-04	-4.7722	-3.0661	1.12E-06	-9.4980	-5.3436
3_6	P15311	Ezrin OS=Homo sapiens GN=EZR PE=1 SV=4 - [EZRI_HUMAN]	1.73E-02	2.6155	3.2246	8.97E-03	2.7056	4.0756
3_6	P07148	Fatty acid-binding protein, liver OS=Homo sapiens GN=FABP1 PE=1 SV=1 - [FABPL_HUMAN]	1.63E-03	-3.8246	-3.1027	6.08E-04	-4.2022	-4.7829
3_6	P51648	Fatty aldehyde dehydrogenase OS=Homo sapiens GN=ALDH3A2 PE=1 SV=1 - [AL3A2_HUMAN]	2.94E-05	-12.8553	-2.7786	4.12E-03	-3.1237	-2.3161
3_6	P23142	Fibulin-1 OS=Homo sapiens GN=FBLN1 PE=1 SV=4 - [FBLN1_HUMAN]	7.69E-05	6.6094	3.0170	2.02E-03	3.5079	2.7366
3_6	P30043	Flavin reductase (NADPH) OS=Homo sapiens GN=BLVRB PE=1 SV=3 - [BLVRB_HUMAN]	2.09E-02	-2.4733	-2.8775	6.62E-03	-2.8559	-2.4169
3_6	O95954	Formimidoyltransferase-cyclodeaminase OS=Homo sapiens GN=FTCD PE=1 SV=2 - [FTCD_HUMAN]	1.42E-05	-14.7716	-2.8579	5.29E-03	-2.9921	-2.8831
3_6	P16930	Fumarylacetoacetase OS=Homo sapiens GN=FAH PE=1 SV=2 - [FAAA_HUMAN]	2.47E-06	-17.1807	-2.9440	5.57E-06	-8.4371	-3.0078
3_6	P09382	Galectin-1 OS=Homo sapiens GN=LGALS1 PE=1 SV=2 - [LEG1_HUMAN]	2.19E-02	2.4380	2.9328	5.29E-03	2.9932	2.4956
3_6	Q08380	Galectin-3-binding protein OS=Homo sapiens GN=LGALS3BP PE=1 SV=1 - [LG3BP_HUMAN]	1.99E-03	3.7462	3.1195	4.55E-02	1.9456	3.4966
3_6	O95479	GDH/6PGL endoplasmic bifunctional protein OS=Homo sapiens GN=H6PD PE=1 SV=2 - [G6PE_HUMAN]	1.69E-04	-5.9679	-2.8183	6.55E-04	-4.1576	-2.6130
3_6	Q13630	GDP-L-fucose synthase OS=Homo sapiens GN=TSTA3 PE=1 SV=1 - [FCL_HUMAN]	2.97E-02	2.1733	3.0881	5.35E-03	2.9856	2.0247
3_6	P08263	Glutathione S-transferase A1 OS=Homo sapiens GN=GSTA1 PE=1 SV=3 - [GSTA1_HUMAN]	6.23E-04	-4.9405	-3.1465	3.21E-04	-4.6051	-3.3608
3_6	P09210	Glutathione S-transferase A2 OS=Homo sapiens GN=GSTA2 PE=1 SV=4 - [GSTA2_HUMAN]	6.56E-03	-2.9831	-3.0379	3.76E-02	-2.0144	-3.2054
3_6	P50440	Glycine amidinotransferase, mitochondrial OS=Homo sapiens GN=GATM PE=1 SV=1 - [GATM_HUMAN]	7.31E-04	-4.6251	-2.9324	1.54E-12	-12.9759	-4.1568

Fig. 7 continued

3_6	P06737	Glycogen phosphorylase, liver form OS=Homo sapiens GN=PYGL PE=1 SV=4 - [PYGL_HUMAN]	9.82E-05	-6.4013	-2.9005	8.44E-04	-4.0002	-3.5535
3_6	Q9UJ07	GTP:AMP phosphotransferase, mitochondrial OS=Homo sapiens GN=AK3 PE=1 SV=4 - [KAD3_HUMAN]	7.75E-04	-4.5428	-2.8578	2.77E-03	-3.3303	-2.4280
3_6	Q12931	Heat shock protein 75 kDa, mitochondrial OS=Homo sapiens GN=TRAP1 PE=1 SV=3 - [TRAP1_HUMAN]	2.46E-02	-2.3394	-2.7964	2.56E-03	-3.3760	-2.3297
3_6	Q7KMD3	Heterogeneous nuclear ribonucleoprotein U-like protein 2 OS=Homo sapiens GN=HNRNPUL2 PE=1 SV=1 - [HNRL2_HUMAN]	9.52E-04	4.2834	3.1349	3.11E-05	6.8764	3.1156
3_6	Q8N3D9	Homogentisate 1,2-dioxygenase OS=Homo sapiens GN=HGD PE=1 SV=2 - [HGD_HUMAN]	7.43E-05	-6.6723	-2.8389	6.51E-05	-5.9596	-4.0042
3_6	Q9UJM8	Hydroxyacid oxidase 1 OS=Homo sapiens GN=HAO1 PE=1 SV=1 - [HAOX1_HUMAN]	5.48E-06	-16.4212	-2.8892	1.45E-05	-7.1383	-4.1274
3_6	Q16836	Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial OS=Homo sapiens GN=HADH PE=1 SV=3 - [HCDH_HUMAN]	1.04E-03	-4.1807	-2.8237	2.06E-03	-3.4983	-2.4169
3_6	P35914	Hydroxymethylglutaryl-CoA lyase, mitochondrial OS=Homo sapiens GN=HMGCL PE=1 SV=2 - [HMGCL_HUMAN]	4.49E-04	-5.3902	-2.7459	1.36E-03	-3.7310	-2.1275
3_6	P54868	Hydroxymethylglutaryl-CoA synthase, mitochondrial OS=Homo sapiens GN=HMGCS2 PE=1 SV=1 - [HMCS2_HUMAN]	2.15E-04	-5.7503	-2.9618	8.40E-05	-5.8111	-4.5313
3_6	P01871	Ig mu chain C region OS=Homo sapiens GN=IGHM PE=1 SV=3 - [IGHM_HUMAN]	1.04E-02	2.7855	2.8266	2.74E-03	3.3385	2.2173
3_6	P19827	Inter-alpha-trypsin inhibitor heavy chain H1 OS=Homo sapiens GN=ITIH1 PE=1 SV=3 - [ITIH1_HUMAN]	3.39E-04	5.4806	3.0907	4.17E-03	3.1148	3.0247
3_6	Q96AB3	Isochorismatase domain-containing protein 2, mitochondrial OS=Homo sapiens GN=ISOC2 PE=1 SV=1 - [ISOC2_HUMAN]	1.56E-02	-2.6795	-2.7266	1.94E-03	-3.5269	-2.3297
3_6	P14923	Junction plakoglobin OS=Homo sapiens GN=JUP PE=1 SV=3 - [PLAK_HUMAN]	3.50E-04	5.5346	2.7845	3.66E-04	4.5612	2.3581
3_6	P08727	Keratin, type I cytoskeletal 19 OS=Homo sapiens GN=KRT19 PE=1 SV=4 - [K1C19_HUMAN]	1.72E-04	5.9454	3.3319	1.10E-03	3.8416	5.1859
3_6	P08729	Keratin, type II cytoskeletal 7 OS=Homo sapiens GN=KRT7 PE=1 SV=5 - [K2C7_HUMAN]	1.97E-02	2.5226	2.9343	2.41E-02	2.2138	3.4941
3_6	P23141	Liver carboxylesterase 1 OS=Homo sapiens GN=CES1 PE=1 SV=2 - [EST1_HUMAN]	1.60E-02	-2.6655	-3.0504	5.09E-05	-6.2706	-5.7364
3_6	P33121	Long-chain-fatty-acid--CoA ligase 1 OS=Homo sapiens GN=ACSL1 PE=1 SV=1 - [ACSL1_HUMAN]	3.15E-05	-12.2433	-2.8373	2.76E-03	-3.3330	-3.3292
3_6	Q7Z4W1	L-xylulose reductase OS=Homo sapiens GN=DCXR PE=1 SV=2 - [DCXR_HUMAN]	1.40E-02	-2.7192	-3.0187	3.30E-03	-3.2468	-4.1274
3_6	P10619	Lysosomal protective protein OS=Homo sapiens GN=CTSA PE=1 SV=2 - [PPGB_HUMAN]	1.53E-02	-2.6910	-2.8071	1.30E-04	-5.3641	-2.0078
3_6	P61626	Lysozyme C OS=Homo sapiens GN=LYZ PE=1 SV=1 - [LYSC_HUMAN]	2.24E-02	2.4175	3.1166	2.06E-02	2.3014	2.3418
3_6	P11310	Medium-chain specific acyl-CoA dehydrogenase, mitochondrial OS=Homo sapiens GN=ACADM PE=1 SV=1 - [ACADM_HUMAN]	4.05E-03	-3.3971	-2.8732	9.73E-05	-5.6294	-3.0560
3_6	O00264	Membrane-associated progesterone receptor component 1 OS=Homo sapiens GN=PGRMC1 PE=1 SV=3 - [PGRC1_HUMAN]	7.37E-04	-4.6078	-2.8885	7.67E-04	-4.0634	-2.9344
3_6	Q9HCC0	Methylcrotonoyl-CoA carboxylase beta chain, mitochondrial OS=Homo sapiens GN=MCCC2 PE=1 SV=1 - [MCCB_HUMAN]	1.10E-02	-2.7742	-2.7451	7.94E-03	-2.7622	-2.1274
3_6	Q02252	Methylmalonate-semialdehyde dehydrogenase [acylating], mitochondrial OS=Homo sapiens GN=ALDH6A1 PE=1 SV=2 - [MMSA_HUMAN]	2.90E-05	-12.8683	-2.8851	6.99E-04	-4.1272	-4.0977
3_6	Q9H8H3	Methyltransferase-like protein 7A OS=Homo sapiens GN=METTL7A PE=1 SV=1 - [ME17A_HUMAN]	1.13E-05	-15.3364	-2.8687	5.72E-05	-6.1096	-2.1385
3_6	P10620	Microsomal glutathione S-transferase 1 OS=Homo sapiens GN=MGST1 PE=1 SV=1 - [MGST1_HUMAN]	1.23E-05	-15.1365	-2.9236	5.89E-05	-6.0920	-2.2794
3_6	P55157	Microsomal triglyceride transfer protein large subunit OS=Homo sapiens GN=MTTP PE=1 SV=1 - [MTP_HUMAN]	2.26E-05	-13.6236	-2.7434	2.64E-04	-4.7269	-2.8913
3_6	P20774	Mimecan OS=Homo sapiens GN=OGN PE=1 SV=1 - [MIME_HUMAN]	1.37E-03	3.9576	2.8528	8.41E-03	2.7348	2.2666
3_6	Q8IYB3	Mitochondrial carrier homolog 2 OS=Homo sapiens GN=MTCH2 PE=1 SV=1 - [MTCH2_HUMAN]	2.50E-05	-13.3569	-2.7947	4.61E-04	-4.3869	-2.3906
3_6	P98088	Mucin-5AC (Fragments) OS=Homo sapiens GN=MUC5AC PE=1 SV=3 - [MUC5A_HUMAN]	1.08E-02	2.7770	2.8309	4.71E-02	1.9316	3.6767
3_6	Q7Z406	Myosin-14 OS=Homo sapiens GN=MYH14 PE=1 SV=2 - [MYH14_HUMAN]	1.15E-02	2.7610	2.8608	1.16E-02	2.5900	3.3581
3_6	Q4G0N4	NAD kinase domain-containing protein 1 OS=Homo sapiens GN=NADKD1 PE=1 SV=2 - [NAKD1_HUMAN]	1.97E-06	-17.6699	-2.8105	1.02E-04	-5.5697	-2.8644

Fig. 7 continued

3_6	Q13423	NAD(P) transhydrogenase, mitochondrial OS=Homo sapiens GN=NNT PE=1 SV=3 - [NNTM_HUMAN]	3.25E-04	-5.5640	-2.7910	3.71E-03	-3.1859	-2.7758
3_6	P16435	NADPH--cytochrome P450 reductase OS=Homo sapiens GN=POR PE=1 SV=2 - [NCPR_HUMAN]	2.20E-05	-13.7153	-2.8486	4.16E-04	-4.4774	-3.6130
3_6	P40261	Nicotinamide N-methyltransferase OS=Homo sapiens GN=NNMT PE=1 SV=1 - [NNMT_HUMAN]	7.02E-03	-2.9386	-2.9062	1.11E-02	-2.6099	-2.1777
3_6	P22307	Non-specific lipid-transfer protein OS=Homo sapiens GN=SCP2 PE=1 SV=2 - [NLTP_HUMAN]	5.80E-04	-5.1269	-2.8858	1.37E-04	-5.2826	-2.6130
3_6	P00480	Ornithine carbamoyltransferase, mitochondrial OS=Homo sapiens GN=OTC PE=1 SV=3 - [OTC_HUMAN]	9.81E-06	-15.4513	-2.9239	1.34E-05	-7.5783	-4.0449
3_6	Q15063	Periostin OS=Homo sapiens GN=POSTN PE=1 SV=2 - [POSTN_HUMAN]	9.41E-04	4.3004	3.1496	5.52E-03	2.9665	4.0580
3_6	Q15067	Peroxisomal acyl-coenzyme A oxidase 1 OS=Homo sapiens GN=ACOX1 PE=1 SV=3 - [ACOX1_HUMAN]	3.69E-05	-11.2872	-2.6944	3.85E-03	-3.1634	-2.9982
3_6	Q9NP24	Peroxisomal acyl-coenzyme A oxidase 2 OS=Homo sapiens GN=ACOX2 PE=1 SV=1 - [ACOX2_HUMAN]	1.30E-02	-2.7385	-2.6299	1.86E-02	-2.3496	-2.2794
3_6	Q08426	Peroxisomal bifunctional enzyme OS=Homo sapiens GN=EHHADH PE=1 SV=3 - [ECHP_HUMAN]	5.21E-04	-5.2935	-2.9060	1.10E-05	-7.7758	-5.0344
3_6	Q9P0Z9	Peroxisomal sarcosine oxidase OS=Homo sapiens GN=PIPOX PE=2 SV=2 - [SOX_HUMAN]	2.56E-05	-13.2807	-2.8545	6.18E-04	-4.1917	-2.8754
3_6	Q00325	Phosphate carrier protein, mitochondrial OS=Homo sapiens GN=SLC25A3 PE=1 SV=2 - [MPCP_HUMAN]	3.50E-03	-3.5165	-2.9181	3.07E-03	-3.2799	-2.4672
3_6	Q16822	Phosphoenolpyruvate carboxykinase [GTP], mitochondrial OS=Homo sapiens GN=PCK2 PE=1 SV=3 - [PCKGM_HUMAN]	6.10E-04	-4.9992	-2.9462	2.58E-04	-4.7570	-4.2539
3_6	P01833	Polymeric immunoglobulin receptor OS=Homo sapiens GN=PIGR PE=1 SV=4 - [PIGR_HUMAN]	2.72E-02	2.2417	3.0703	4.77E-02	1.9247	3.4263
3_6	P05166	Propionyl-CoA carboxylase beta chain, mitochondrial OS=Homo sapiens GN=PCCB PE=1 SV=3 - [PCCB_HUMAN]	2.77E-04	-5.6236	-2.7284	5.12E-03	-3.0143	-2.3297
3_6	Q14914	Prostaglandin reductase 1 OS=Homo sapiens GN=PTGR1 PE=1 SV=2 - [PTGR1_HUMAN]	1.76E-04	-5.9228	-2.7764	1.20E-03	-3.8022	-3.4672
3_6	Q9BPW8	Protein NipSnap homolog 1 OS=Homo sapiens GN=NIPSNAP1 PE=1 SV=1 - [NIPS1_HUMAN]	1.75E-03	-3.8010	-2.8440	6.27E-05	-6.0027	-3.0560
3_6	P29590	Protein PML OS=Homo sapiens GN=PML PE=1 SV=3 - [PML_HUMAN]	2.22E-03	3.7262	2.7478	2.12E-03	3.4809	2.6767
3_6	P31949	Protein S100-A11 OS=Homo sapiens GN=S100A11 PE=1 SV=2 - [S10AB_HUMAN]	5.06E-04	5.3180	2.8902	6.89E-04	4.1837	2.2531
3_6	P06703	Protein S100-A6 OS=Homo sapiens GN=S100A6 PE=1 SV=1 - [S10A6_HUMAN]	5.10E-05	7.1721	3.1658	2.68E-04	4.7192	2.7044
3_6	Q9NVS9	Pyridoxine-5-phosphate oxidase OS=Homo sapiens GN=PNPO PE=1 SV=1 - [PNPO_HUMAN]	4.96E-06	-16.4862	-2.8728	8.01E-06	-7.9449	-2.1274
3_6	P11498	Pyruvate carboxylase, mitochondrial OS=Homo sapiens GN=PC PE=1 SV=2 - [PYC_HUMAN]	2.45E-05	-13.3912	-2.8168	6.33E-04	-4.1811	-3.9962
3_6	P30613	Pyruvate kinase isozymes R/L OS=Homo sapiens GN=PKLR PE=1 SV=2 - [KPYR_HUMAN]	1.39E-06	-17.8985	-2.8740	7.33E-04	-4.0902	-3.4495
3_6	P31150	Rab GDP dissociation inhibitor alpha OS=Homo sapiens GN=GDI1 PE=1 SV=2 - [GDIA_HUMAN]	6.90E-03	2.9503	2.8427	1.37E-02	2.5071	3.2173
3_6	P46940	Ras GTPase-activating-like protein IQGAP1 OS=Homo sapiens GN=IQGAP1 PE=1 SV=1 - [IQGA1_HUMAN]	4.44E-04	5.3967	3.1140	8.01E-04	4.0322	4.4285
3_6	P62753	Retinol-binding protein 4 OS=Homo sapiens GN=RBP4 PE=1 SV=3 - [RET4_HUMAN]	6.85E-04	-4.7350	-2.8475	4.02E-05	-6.5738	-2.2794
3_6	P52758	Ribonuclease UK114 OS=Homo sapiens GN=HRSP12 PE=1 SV=1 - [UK114_HUMAN]	5.86E-05	-6.9836	-2.9899	2.67E-04	-4.7208	-3.1385
3_6	Q8NBX0	Saccharopine dehydrogenase-like oxidoreductase OS=Homo sapiens GN=SCCPDH PE=1 SV=1 - [SCPDL_HUMAN]	6.91E-04	-4.7180	-2.8469	8.13E-05	-5.8487	-2.5927
3_6	Q00266	S-adenosylmethionine synthase isoform type-1 OS=Homo sapiens GN=MAT1A PE=1 SV=2 - [METK1_HUMAN]	2.63E-05	-13.1193	-2.8581	2.70E-03	-3.3468	-2.7125
3_6	P34896	Serine hydroxymethyltransferase, cytosolic OS=Homo sapiens GN=SHMT1 PE=1 SV=1 - [GLYC_HUMAN]	1.53E-05	-14.6252	-2.8267	2.95E-05	-6.9286	-2.9536
3_6	P34897	Serine hydroxymethyltransferase, mitochondrial OS=Homo sapiens GN=SHMT2 PE=1 SV=3 - [GLYM_HUMAN]	4.35E-02	-2.0779	-2.8563	2.58E-03	-3.3701	-3.0560
3_6	P21549	Serine--pyruvate aminotransferase OS=Homo sapiens GN=AGXT PE=1 SV=1 - [SPYA_HUMAN]	5.69E-04	-5.1744	-3.0303	1.12E-04	-5.4973	-5.2723
3_6	P45954	Short/branched chain specific acyl-CoA dehydrogenase, mitochondrial OS=Homo sapiens GN=ACADSB PE=1 SV=1 - [ACDSB_HUMAN]	2.12E-05	-13.7468	-2.8646	1.03E-04	-5.5525	-3.1275

Fig. 7 continued

3_6	Q9H9B4	Sideroflexin-1 OS=Homo sapiens GN=SFXN1 PE=1 SV=4 - [SFXN1_HUMAN]	8.54E-04	-4.4221	-2.8292	8.09E-05	-5.8582	-2.1777
3_6	Q00796	Sorbitol dehydrogenase OS=Homo sapiens GN=SORD PE=1 SV=4 - [DHSO_HUMAN]	1.02E-04	-6.3478	-2.8262	1.32E-03	-3.7453	-2.7312
3_6	Q14247	Src substrate cortactin OS=Homo sapiens GN=CTTN PE=1 SV=2 - [SRC8_HUMAN]	3.80E-02	2.0965	2.7135	1.86E-02	2.3484	2.2061
3_6	Q02318	Sterol 26-hydroxylase, mitochondrial OS=Homo sapiens GN=CYP27A1 PE=1 SV=1 - [CP27A_HUMAN]	2.83E-04	-5.6078	-2.7775	1.79E-03	-3.5792	-2.0078
3_6	P31040	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial OS=Homo sapiens GN=SDHA PE=1 SV=2 - [DHSA_HUMAN]	2.62E-02	-2.2797	-2.7295	4.86E-02	-1.9166	-2.6130
3_6	P51649	Succinate-semialdehyde dehydrogenase, mitochondrial OS=Homo sapiens GN=ALDH5A1 PE=1 SV=2 - [SSDH_HUMAN]	3.14E-04	-5.5743	-2.7413	1.40E-03	-3.7096	-2.4672
3_6	Q71U36	Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1 - [TBA1A_HUMAN]	2.03E-03	3.7421	3.0309	7.29E-03	2.7949	5.4652
3_6	Q13509	Tubulin beta-3 chain OS=Homo sapiens GN=TUBB3 PE=1 SV=2 - [TBB3_HUMAN]	2.27E-03	3.7205	2.9806	1.11E-03	3.8370	5.3253
3_6	P22310	UDP-glucuronosyltransferase 1-4 OS=Homo sapiens GN=UGT1A4 PE=1 SV=1 - [UD14_HUMAN]	4.70E-04	-5.3717	-2.8417	1.36E-02	-2.5112	-2.8056
3_6	P19224	UDP-glucuronosyltransferase 1-6 OS=Homo sapiens GN=UGT1A6 PE=1 SV=2 - [UD16_HUMAN]	4.50E-04	-5.3891	-2.8261	2.18E-02	-2.2707	-2.0015
3_6	O60656	UDP-glucuronosyltransferase 1-9 OS=Homo sapiens GN=UGT1A9 PE=1 SV=1 - [UD19_HUMAN]	4.33E-04	-5.4205	-2.8416	1.40E-02	-2.4092	-2.0078
3_6	P06133	UDP-glucuronosyltransferase 2B4 OS=Homo sapiens GN=UGT2B4 PE=1 SV=2 - [UD2B4_HUMAN]	1.79E-05	-14.2817	-2.9014	4.80E-03	-3.0413	-2.9536
3_6	P16662	UDP-glucuronosyltransferase 2B7 OS=Homo sapiens GN=UGT2B7 PE=1 SV=1 - [UD2B7_HUMAN]	7.85E-06	-15.6905	-2.8565	1.53E-03	-3.6440	-2.8754
3_7	Q04917	14-3-3 protein eta OS=Homo sapiens GN=YWHAH PE=1 SV=4 - [1433F_HUMAN]	3.43E-03	3.5246	3.3175	3.22E-03	3.1157	3.2925
3_7	O14756	17-beta-hydroxysteroid dehydrogenase type 6 OS=Homo sapiens GN=HSD17B6 PE=1 SV=1 - [H17B6_HUMAN]	6.16E-06	-14.8936	-2.8892	7.17E-05	-5.3332	-3.2054
3_7	P31937	3-hydroxyisobutyrate dehydrogenase, mitochondrial OS=Homo sapiens GN=HIBADH PE=1 SV=2 - [3HIDH_HUMAN]	2.40E-02	-2.3112	-2.8185	2.06E-04	-4.6405	-2.6690
3_7	P42765	3-ketoacyl-CoA thiolase, mitochondrial OS=Homo sapiens GN=ACAA2 PE=1 SV=2 - [THIM_HUMAN]	2.85E-02	-2.1668	-2.9668	4.53E-03	-2.9507	-4.0910
3_7	P09110	3-ketoacyl-CoA thiolase, peroxisomal OS=Homo sapiens GN=ACAA1 PE=1 SV=2 - [THIK_HUMAN]	7.53E-03	-2.8555	-2.7809	5.89E-03	-2.8062	-4.0977
3_7	P60866	40S ribosomal protein S20 OS=Homo sapiens GN=RPS20 PE=1 SV=1 - [RS20_HUMAN]	2.10E-02	2.4116	3.2882	3.43E-03	3.0809	2.1256
3_7	P80404	4-aminobutyrate aminotransferase, mitochondrial OS=Homo sapiens GN=ABAT PE=1 SV=3 - [GABT_HUMAN]	1.18E-05	-12.9166	-2.8695	3.33E-03	-3.0874	-3.4280
3_7	P32754	4-hydroxyphenylpyruvate dioxygenase OS=Homo sapiens GN=HPD PE=1 SV=2 - [HPPD_HUMAN]	1.17E-05	-12.9628	-2.9576	1.93E-04	-4.6765	-4.0978
3_7	P49189	4-trimethylaminobutyraldehyde dehydrogenase OS=Homo sapiens GN=ALDH9A1 PE=1 SV=3 - [AL9A1_HUMAN]	1.54E-04	-5.6232	-2.7732	8.23E-04	-3.8161	-2.6130
3_7	P24752	Acetyl-CoA acetyltransferase, mitochondrial OS=Homo sapiens GN=ACAT1 PE=1 SV=1 - [THIL_HUMAN]	1.35E-03	-3.9228	-2.9392	5.80E-05	-5.3949	-4.2557
3_7	Q08AH3	Acyl-coenzyme A synthetase ACSM2A, mitochondrial OS=Homo sapiens GN=ACSM2A PE=1 SV=2 - [ACS2A_HUMAN]	2.31E-04	-5.4960	-2.8194	9.86E-03	-2.5891	-3.6690
3_7	Q8ICK6	Acyl-coenzyme A synthetase ACSM2B, mitochondrial OS=Homo sapiens GN=ACSM2B PE=1 SV=2 - [ACS2B_HUMAN]	1.19E-05	-12.9526	-2.8202	1.49E-03	-3.5317	-3.7082
3_7	P54819	Adenylate kinase 2, mitochondrial OS=Homo sapiens GN=AK2 PE=1 SV=2 - [KAD2_HUMAN]	1.43E-02	-2.6689	-2.7823	2.23E-03	-3.3159	-2.6503
3_7	P24298	Alanine aminotransferase 1 OS=Homo sapiens GN=GPT PE=1 SV=3 - [ALAT1_HUMAN]	2.38E-04	-5.4824	-2.6800	5.06E-03	-2.8831	-2.0078
3_7	P07327	Alcohol dehydrogenase 1A OS=Homo sapiens GN=ADH1A PE=1 SV=2 - [ADH1A_HUMAN]	5.95E-04	-4.7113	-2.9589	1.16E-03	-3.6414	-4.3653
3_7	P00325	Alcohol dehydrogenase 1B OS=Homo sapiens GN=ADH1B PE=1 SV=2 - [ADH1B_HUMAN]	5.96E-04	-4.7088	-2.9589	1.61E-03	-3.4907	-4.5623
3_7	P08319	Alcohol dehydrogenase 4 OS=Homo sapiens GN=ADH4 PE=1 SV=5 - [ADH4_HUMAN]	1.92E-05	-11.2379	-2.8303	4.88E-03	-2.9109	-3.8151
3_7	P30837	Aldehyde dehydrogenase X, mitochondrial OS=Homo sapiens GN=ALDH1B1 PE=1 SV=3 - [AL1B1_HUMAN]	1.44E-02	-2.6673	-2.8918	8.35E-03	-2.6548	-3.1860
3_7	Q06278	Aldehyde oxidase OS=Homo sapiens GN=AOX1 PE=2 SV=2 - [AOXO_HUMAN]	1.93E-05	-10.7701	-2.7162	7.52E-03	-2.7026	-2.4672

Fig. 7 continued

3.7	P52895	Aldo-keto reductase family 1 member C2 OS=Homo sapiens GN=AKR1C2 PE=1 SV=3 - [AK1C2_HUMAN]	2.91E-04	-5.3956	-3.0055	1.52E-02	-2.3773	-3.4921
3.7	P17516	Aldo-keto reductase family 1 member C4 OS=Homo sapiens GN=AKR1C4 PE=1 SV=3 - [AK1C4_HUMAN]	1.99E-04	-5.5674	-2.9828	2.47E-04	-4.5120	-3.4921
3.7	Q96IU4	Alphabeta hydrolase domain-containing protein 14B OS=Homo sapiens GN=ABHD14B PE=1 SV=1 - [ABHEB_HUMAN]	2.03E-02	-2.4460	-2.8387	1.17E-03	-3.6361	-2.2650
3.7	P49419	Alpha-aminoadipic semialdehyde dehydrogenase OS=Homo sapiens GN=ALDH7A1 PE=1 SV=5 - [AL7A1_HUMAN]	1.20E-04	-5.7870	-2.9481	1.04E-05	-7.1033	-3.3608
3.7	P27338	Amine oxidase [flavin-containing] B OS=Homo sapiens GN=MAOB PE=1 SV=3 - [AOFB_HUMAN]	4.48E-06	-15.7485	-2.8910	1.15E-06	-8.4594	-3.8154
3.7	Q03154	Aminoacylase-1 OS=Homo sapiens GN=ACY1 PE=1 SV=1 - [ACY1_HUMAN]	1.19E-07	-17.9308	-2.9365	1.09E-05	-7.0203	-3.3608
3.7	P01019	Angiotensinogen OS=Homo sapiens GN=AGT PE=1 SV=1 - [ANGT_HUMAN]	2.72E-02	-2.2052	-2.6321	2.75E-03	-3.1954	-2.1909
3.7	P12429	Annexin A3 OS=Homo sapiens GN=ANXA3 PE=1 SV=3 - [ANXA3_HUMAN]	2.86E-08	18.5979	3.1575	3.66E-03	3.0486	2.8192
3.7	O95994	Anterior gradient protein 2 homolog OS=Homo sapiens GN=AGR2 PE=1 SV=1 - [AGR2_HUMAN]	4.79E-07	22.5617	3.3637	8.78E-06	7.2675	3.5751
3.7	P05090	Apolipoprotein D OS=Homo sapiens GN=APOD PE=1 SV=1 - [APOD_HUMAN]	2.30E-02	-2.3459	-2.6908	4.28E-03	-2.9809	-2.0015
3.7	P05089	Arginase-1 OS=Homo sapiens GN=ARG1 PE=1 SV=2 - [ARGI1_HUMAN]	7.40E-06	-14.4515	-2.9788	1.12E-04	-5.0927	-4.3292
3.7	P04424	Arginosuccinate lyase OS=Homo sapiens GN=ASL PE=1 SV=4 - [ARLY_HUMAN]	2.35E-02	-2.3286	-2.9437	4.38E-04	-4.1528	-4.2165
3.7	P00966	Argininosuccinate synthase OS=Homo sapiens GN=ASS1 PE=1 SV=2 - [ASSY_HUMAN]	6.42E-04	-4.6411	-2.8519	2.11E-02	-2.2307	-2.6503
3.7	P22760	Arylacetamide deacetylase OS=Homo sapiens GN=AADAC PE=1 SV=5 - [AAAD_HUMAN]	1.94E-06	-16.1155	-2.7673	1.49E-05	-6.6513	-2.8640
3.7	P36542	ATP synthase subunit gamma, mitochondrial OS=Homo sapiens GN=ATP5C1 PE=1 SV=1 - [ATPG_HUMAN]	1.03E-02	-2.7651	-2.8975	2.26E-04	-4.5762	-2.3161
3.7	Q93088	Betaine--homocysteine S-methyltransferase 1 OS=Homo sapiens GN=BHMT PE=1 SV=2 - [BHMT1_HUMAN]	3.40E-04	-5.2976	-2.9078	2.96E-02	-2.0917	-3.2794
3.7	Q9Y2P5	Bile acyl-CoA synthetase OS=Homo sapiens GN=SLC27A5 PE=1 SV=1 - [S27A5_HUMAN]	2.14E-03	-3.7096	-2.6951	2.53E-03	-3.2288	-2.5061
3.7	Q06520	Bile salt sulfotransferase OS=Homo sapiens GN=SULT2A1 PE=1 SV=3 - [ST2A1_HUMAN]	7.50E-06	-14.3652	-2.9030	9.53E-04	-3.7370	-2.8466
3.7	P11586	C-1-tetrahydrofolate synthase, cytoplasmic OS=Homo sapiens GN=MTHFD1 PE=1 SV=3 - [C1TC_HUMAN]	5.25E-04	-4.8604	-2.8294	4.01E-04	-4.2028	-3.8644
3.7	Q9UJS0	Calcium-binding mitochondrial carrier protein Aralar2 OS=Homo sapiens GN=SLC25A13 PE=1 SV=2 - [CMC2_HUMAN]	6.43E-03	-2.9546	-2.8629	1.76E-05	-6.4383	-3.6690
3.7	P06731	Carcinoembryonic antigen-related cell adhesion molecule 5 OS=Homo sapiens GN=CEACAM5 PE=1 SV=3 - [CEAM5_HUMAN]	9.05E-03	2.7946	3.1761	1.72E-02	2.3221	2.0701
3.7	P23786	Carnitine O-palmitoyltransferase 2, mitochondrial OS=Homo sapiens GN=CPT2 PE=1 SV=2 - [CPT2_HUMAN]	2.52E-04	-5.4648	-2.8192	1.93E-03	-3.3913	-2.1909
3.7	P31146	Coronin-1A OS=Homo sapiens GN=CORO1A PE=1 SV=4 - [COR1A_HUMAN]	3.86E-04	5.2651	3.2122	2.24E-03	3.3125	2.2925
3.7	P00167	Cytochrome b5 OS=Homo sapiens GN=CYB5A PE=1 SV=2 - [CYB5_HUMAN]	1.34E-06	-16.4428	-3.0069	1.44E-05	-6.7295	-3.0531
3.7	P11509	Cytochrome P450 2A6 OS=Homo sapiens GN=CYP2A6 PE=1 SV=3 - [CP2A6_HUMAN]	3.15E-04	-5.3604	-2.8057	2.70E-03	-3.1991	-2.8754
3.7	P11712	Cytochrome P450 2C9 OS=Homo sapiens GN=CYP2C9 PE=1 SV=3 - [CP2C9_HUMAN]	1.52E-05	-12.1941	-2.7039	5.68E-03	-2.8247	-2.1275
3.7	P10635	Cytochrome P450 2D6 OS=Homo sapiens GN=CYP2D6 PE=1 SV=2 - [CP2D6_HUMAN]	1.92E-03	-3.7456	-2.6731	2.45E-03	-3.2589	-2.1385
3.7	P21399	Cytoplasmic aconitate hydratase OS=Homo sapiens GN=ACO1 PE=1 SV=3 - [ACOC_HUMAN]	2.67E-02	-2.2201	-2.8891	4.30E-04	-4.1619	-3.5535
3.7	O75891	Cytosolic 10-formyltetrahydrofolate dehydrogenase OS=Homo sapiens GN=ALDH1L1 PE=1 SV=2 - [AL1L1_HUMAN]	2.09E-05	-10.0651	-2.8507	2.29E-02	-2.1987	-3.8154
3.7	Q02338	D-beta-hydroxybutyrate dehydrogenase, mitochondrial OS=Homo sapiens GN=BDH1 PE=1 SV=3 - [BDH_HUMAN]	5.56E-06	-15.3212	-2.8436	1.09E-05	-7.0629	-2.5424
3.7	P30038	Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial OS=Homo sapiens GN=ALDH4A1 PE=1 SV=3 - [AL4A1_HUMAN]	1.00E-05	-13.7022	-2.9501	2.74E-04	-4.4517	-3.7648
3.7	P09417	Dihydropteridine reductase OS=Homo sapiens GN=QDPR PE=1 SV=2 - [DHPR_HUMAN]	5.26E-06	-15.5209	-2.8151	3.34E-04	-4.3148	-2.2905

Fig. 7 continued

3_7	P31513	Dimethylaniline monooxygenase [N-oxide-forming] 3 OS=Homo sapiens GN=FMO3 PE=1 SV=5 - [FMO3_HUMAN]	2.29E-04	-5.5060	-2.8163	4.59E-04	-4.1361	-2.9344
3_7	Q9UI17	Dimethylglycine dehydrogenase, mitochondrial OS=Homo sapiens GN=DMGDH PE=1 SV=2 - [DMGD_HUMAN]	2.81E-04	-5.4111	-2.7015	1.19E-03	-3.8258	-2.0015
3_7	O75356	Ectonucleoside triphosphate diphosphohydrolase 5 OS=Homo sapiens GN=ENTPD5 PE=1 SV=1 - [ENTP5_HUMAN]	1.76E-04	-5.5849	-2.7192	6.82E-03	-2.7447	-2.1777
3_7	P30040	Endoplasmic reticulum resident protein 29 OS=Homo sapiens GN=ERP29 PE=1 SV=4 - [ERP29_HUMAN]	3.37E-02	-2.1023	-2.7800	1.41E-03	-3.5589	-2.9147
3_7	O75521	Enoyl-CoA delta isomerase 2, mitochondrial OS=Homo sapiens GN=ECI2 PE=1 SV=4 - [ECI2_HUMAN]	1.54E-05	-12.0565	-2.6864	5.53E-04	-4.0499	-2.5424
3_7	P30084	Enoyl-CoA hydratase, mitochondrial OS=Homo sapiens GN=ECHS1 PE=1 SV=4 - [ECHM_HUMAN]	1.15E-02	-2.7374	-2.9086	1.40E-05	-6.7721	-4.0151
3_7	P11678	Eosinophil peroxidase OS=Homo sapiens GN=EPX PE=1 SV=2 - [PERE_HUMAN]	1.62E-02	2.6141	3.1923	8.26E-03	2.6598	3.4580
3_7	P07099	Epoxide hydrolase 1 OS=Homo sapiens GN=EPHX1 PE=1 SV=1 - [HYEP_HUMAN]	2.85E-02	-2.1678	-3.0661	4.29E-07	-9.4909	-5.3436
3_7	Q9BSJ8	Extended synaptotagmin-1 OS=Homo sapiens GN=ESYT1 PE=1 SV=1 - [ESYT1_HUMAN]	4.69E-03	-3.2237	-2.7140	2.94E-02	-2.0937	-2.1275
3_7	P15311	Ezrin OS=Homo sapiens GN=EZR PE=1 SV=4 - [EZRI_HUMAN]	4.88E-04	4.9660	3.3023	2.08E-04	4.6407	3.3965
3_7	P51648	Fatty aldehyde dehydrogenase OS=Homo sapiens GN=ALDH3A2 PE=1 SV=1 - [AL3A2_HUMAN]	5.16E-04	-4.8797	-2.7786	3.17E-03	-3.1237	-2.3161
3_7	P23142	Fibulin-1 OS=Homo sapiens GN=FBLN1 PE=1 SV=4 - [FBLN1_HUMAN]	8.92E-03	2.7975	3.0239	1.25E-02	2.4699	2.9032
3_7	O95954	Formimidoyltransferase-cyclodeaminase OS=Homo sapiens GN=FTCD PE=1 SV=2 - [FTCD_HUMAN]	7.21E-06	-14.7716	-2.8579	4.14E-03	-2.9921	-2.8931
3_7	P09467	Fructose-1,6-bisphosphatase 1 OS=Homo sapiens GN=FBP1 PE=1 SV=5 - [F16P1_HUMAN]	8.07E-03	-2.8221	-2.9303	2.99E-04	-4.3790	-4.0129
3_7	P07954	Fumarate hydratase, mitochondrial OS=Homo sapiens GN=FH PE=1 SV=3 - [FUMH_HUMAN]	3.65E-03	-3.4670	-2.8837	3.09E-05	-5.9300	-3.4388
3_7	P16930	Fumarylacetoacetase OS=Homo sapiens GN=FAH PE=1 SV=2 - [FAAA_HUMAN]	8.24E-04	-4.3243	-2.9440	4.95E-06	-7.7380	-3.0078
3_7	O95479	GDH/6PGL endoplasmic bifunctional protein OS=Homo sapiens GN=H6PD PE=1 SV=2 - [G6PE_HUMAN]	2.30E-04	-5.4988	-2.8183	1.67E-04	-4.7697	-2.6130
3_7	P50440	Glycine amidinotransferase, mitochondrial OS=Homo sapiens GN=GATM PE=1 SV=1 - [GATM_HUMAN]	1.32E-06	-16.5025	-2.9324	2.52E-03	-14.3632	-4.1568
3_7	P06737	Glycogen phosphorylase, liver form OS=Homo sapiens GN=PYGL PE=1 SV=4 - [PYGL_HUMAN]	9.22E-08	-18.0733	-2.9005	5.98E-04	-4.0002	-3.5535
3_7	Q9UBQ7	Glyoxylate reductase/hydroxypyruvate reductase OS=Homo sapiens GN=GRHPR PE=1 SV=1 - [GRHPR_HUMAN]	1.65E-02	-2.5978	-2.8986	2.52E-03	-3.2437	-2.4672
3_7	Q9UJJ7	G1P3 AMP phosphotransferase, mitochondrial OS=Homo sapiens GN=AK3 PE=1 SV=4 - [KAD3_HUMAN]	5.76E-04	-4.7486	-2.8578	1.42E-03	-3.5544	-2.4260
3_7	Q8IUW5	Homogentisate 1,2-dioxygenase OS=Homo sapiens GN=HGD PE=1 SV=2 - [HGD_HUMAN]	7.42E-06	-14.5976	-2.8389	2.72E-05	-6.0475	-4.0042
3_7	Q9UJM8	Hydroxyacid oxidase 1 OS=Homo sapiens GN=HAO1 PE=1 SV=1 - [HAOX1_HUMAN]	1.35E-06	-16.4212	-2.8892	9.92E-06	-7.1383	-4.1274
3_7	Q16836	Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial OS=Homo sapiens GN=HADH PE=1 SV=3 - [HCDH_HUMAN]	7.51E-04	-4.4501	-2.8237	5.06E-04	-4.0929	-2.4169
3_7	P35914	Hydroxymethylglutaryl-CoA lyase, mitochondrial OS=Homo sapiens GN=HMGCL PE=1 SV=2 - [HMGCL_HUMAN]	2.95E-04	-5.3902	-2.7459	9.74E-04	-3.7310	-2.1275
3_7	P54868	Hydroxymethylglutaryl-CoA synthase, mitochondrial OS=Homo sapiens GN=HMGCS2 PE=1 SV=1 - [HMCS2_HUMAN]	9.61E-04	-4.1600	-2.9618	4.36E-05	-5.7265	-4.5313
3_7	P01871	Ig mu chain C region OS=Homo sapiens GN=IGHM PE=1 SV=3 - [IGHM_HUMAN]	2.79E-02	2.1850	3.0497	4.86E-02	1.8956	2.6401
3_7	Q96AB3	Isochorismatase domain-containing protein 2, mitochondrial OS=Homo sapiens GN=ISOC2 PE=1 SV=1 - [ISOC2_HUMAN]	3.27E-04	-5.3394	-2.7266	6.99E-04	-3.9028	-2.3297
3_7	P08727	Keratin, type I cytoskeletal 19 OS=Homo sapiens GN=KRT19 PE=1 SV=4 - [K1C19_HUMAN]	5.29E-05	6.7689	3.4319	4.78E-05	5.6604	5.5735
3_7	P08729	Keratin, type II cytoskeletal 7 OS=Homo sapiens GN=KRT7 PE=1 SV=5 - [K2C7_HUMAN]	4.85E-02	2.0383	3.1228	2.56E-02	2.1425	3.5726
3_7	P23141	Liver carboxylesterase 1 OS=Homo sapiens GN=CES1 PE=1 SV=2 - [EST1_HUMAN]	4.84E-04	-4.9757	-3.0504	1.83E-05	-6.3436	-5.7364
3_7	P33121	Long-chain-fatty-acid--CoA ligase 1 OS=Homo sapiens GN=ACSL1 PE=1 SV=1 - [ACSL1_HUMAN]	1.51E-05	-12.2433	-2.8373	2.15E-03	-3.3330	-3.3292

Fig. 7 continued

3.7	P61626	Lysozyme C OS=Homo sapiens GN=LYZ PE=1 SV=1 - [LYSC_HUMAN]	4.39E-04	5.0767	3.2855	1.52E-02	2.3780	3.0187
3.7	P11310	Medium-chain specific acyl-CoA dehydrogenase, mitochondrial OS=Homo sapiens GN=ACADM PE=1 SV=1 - [ACADM_HUMAN]	5.53E-06	-15.3434	-2.8732	2.73E-05	-6.0401	-3.0560
3.7	Q9HCC0	Methylcrotonoyl-CoA carboxylase beta chain, mitochondrial OS=Homo sapiens GN=MCCC2 PE=1 SV=1 - [MCCB_HUMAN]	2.28E-02	-2.3513	-2.7451	3.98E-03	-3.0129	-2.1274
3.7	Q02252	Methylmalonate-semialdehyde dehydrogenase [acylating], mitochondrial OS=Homo sapiens GN=ALDH6A1 PE=1 SV=2 - [MMSA_HUMAN]	1.19E-05	-12.8683	-2.8851	3.85E-04	-4.2385	-4.0977
3.7	Q9H8H3	Methyltransferase-like protein 7A OS=Homo sapiens GN=METTL7A PE=1 SV=1 - [META_HUMAN]	5.54E-06	-15.3364	-2.8687	2.44E-05	-6.1096	-2.1385
3.7	P10620	Microsomal glutathione S-transferase 1 OS=Homo sapiens GN=MGST1 PE=1 SV=1 - [MGST1_HUMAN]	5.81E-06	-15.1365	-2.9236	2.52E-05	-6.0920	-2.2794
3.7	P55157	Microsomal triglyceride transfer protein large subunit OS=Homo sapiens GN=MTTP PE=1 SV=1 - [MTP_HUMAN]	1.03E-05	-13.6236	-2.7434	1.78E-04	-4.7269	-2.8913
3.7	P98088	Mucin-5AC (Fragments) OS=Homo sapiens GN=MUC5AC PE=1 SV=3 - [MUC5A_HUMAN]	1.05E-02	2.7572	3.2398	2.04E-02	2.2479	4.7330
3.7	P24844	Myosin regulatory light polypeptide 9 OS=Homo sapiens GN=MYL9 PE=1 SV=4 - [MYL9_HUMAN]	3.02E-02	2.1292	2.9568	9.91E-03	2.5871	3.0701
3.7	Q7Z406	Myosin-14 OS=Homo sapiens GN=MYH14 PE=1 SV=2 - [MYH14_HUMAN]	7.07E-08	21.2300	3.1729	2.56E-03	3.2310	3.3440
3.7	Q4G0N4	NAD kinase domain-containing protein 1 OS=Homo sapiens GN=NADKD1 PE=1 SV=2 - [NAKD1_HUMAN]	1.79E-07	-17.6609	-2.8105	5.10E-05	-5.5697	-2.8644
3.7	Q13423	NAD(P) transhydrogenase, mitochondrial OS=Homo sapiens GN=NNT PE=1 SV=3 - [NNTM_HUMAN]	2.00E-04	-5.5940	-2.7910	2.82E-03	-3.1859	-2.7758
3.7	P28331	NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial OS=Homo sapiens GN=NDUFS1 PE=1 SV=3 - [NDUS1_HUMAN]	2.86E-02	-2.1638	-2.6896	1.26E-02	-2.4625	-2.2794
3.7	P16435	NADPH--cytochrome P450 reductase OS=Homo sapiens GN=POR PE=1 SV=2 - [NCPR_HUMAN]	9.95E-06	-13.7153	-2.9486	2.69E-04	-4.4774	-3.6130
3.7	P08246	Neutrophil elastase OS=Homo sapiens GN=ELANE PE=1 SV=1 - [ELNE_HUMAN]	2.61E-02	2.2388	3.2179	1.33E-02	2.4414	4.4277
3.7	P80188	Neutrophil gelatinase-associated lipocalin OS=Homo sapiens GN=LCN2 PE=1 SV=2 - [NGAL_HUMAN]	4.22E-03	3.3342	3.1911	4.18E-02	1.9557	3.2251
3.7	P40261	Nicotinamide N-methyltransferase OS=Homo sapiens GN=NNMT PE=1 SV=1 - [NNMT_HUMAN]	3.22E-03	-3.5653	-2.9062	4.43E-03	-2.9623	-2.1777
3.7	P22307	Non-specific lipid-transfer protein OS=Homo sapiens GN=SCP2 PE=1 SV=2 - [NLTP_HUMAN]	3.97E-04	-5.1810	-2.8858	7.87E-05	-5.2826	-2.6130
3.7	P00480	Ornithine carbamoyltransferase, mitochondrial OS=Homo sapiens GN=OTC PE=1 SV=3 - [OTC_HUMAN]	5.37E-06	-15.4513	-2.9239	5.03E-06	-7.5783	-4.0449
3.7	Q15067	Peroxisomal acyl-coenzyme A oxidase 1 OS=Homo sapiens GN=ACOX1 PE=1 SV=3 - [ACOX1_HUMAN]	1.91E-05	-11.2872	-2.6944	2.93E-03	-3.1654	-2.9982
3.7	Q9Y4Z4	Peroxisomal acyl-coenzyme A oxidase 2 OS=Homo sapiens GN=ACOX2 PE=1 SV=1 - [ACOX2_HUMAN]	1.14E-02	-2.7365	-2.6299	1.61E-02	-2.3496	-2.2794
3.7	Q08426	Peroxisomal bifunctional enzyme OS=Homo sapiens GN=EHHADH PE=1 SV=3 - [ECHP_HUMAN]	2.20E-04	-5.5317	-2.9060	4.42E-06	-7.8597	-5.0344
3.7	Q9P0Z9	Peroxisomal sarcosine oxidase OS=Homo sapiens GN=PIPOX PE=2 SV=2 - [SOX_HUMAN]	1.11E-05	-13.2807	-2.8545	4.06E-04	-4.1917	-2.8754
3.7	Q00325	Phosphate carrier protein, mitochondrial OS=Homo sapiens GN=SLC25A3 PE=1 SV=2 - [MPCP_HUMAN]	2.30E-02	-2.3431	-2.9181	5.19E-04	-4.0834	-2.4672
3.7	Q16822	Phosphoenolpyruvate carboxykinase [GTP], mitochondrial OS=Homo sapiens GN=PCK2 PE=1 SV=3 - [PCKGM_HUMAN]	1.01E-02	-2.7706	-2.9462	3.10E-04	-4.3540	-4.2539
3.7	P05165	Propionyl-CoA carboxylase beta chain, mitochondrial OS=Homo sapiens GN=PCCB PE=1 SV=3 - [PCCB_HUMAN]	1.40E-05	-12.6404	-2.7284	1.99E-03	-3.3811	-2.3297
3.7	Q14914	Prostaglandin reductase 1 OS=Homo sapiens GN=PTGR1 PE=1 SV=2 - [PTGR1_HUMAN]	1.71E-04	-5.5888	-2.7764	8.47E-04	-3.8022	-3.4672
3.7	Q9BPW8	Protein NipSnap homolog 1 OS=Homo sapiens GN=NIPSNAP1 PE=1 SV=1 - [NIPS1_HUMAN]	5.81E-06	-15.1394	-2.8440	2.76E-05	-6.0027	-3.0560
3.7	P31949	Protein S100-A11 OS=Homo sapiens GN=S100A11 PE=1 SV=2 - [S10AB_HUMAN]	1.28E-06	16.5818	3.2807	3.29E-07	9.6329	2.1671
3.7	P06703	Protein S100-A6 OS=Homo sapiens GN=S100A6 PE=1 SV=1 - [S10A6_HUMAN]	2.16E-05	9.2555	3.4440	3.63E-04	4.2708	2.9471
3.7	P55786	Puromycin-sensitive aminopeptidase OS=Homo sapiens GN=NPEPPS PE=1 SV=2 - [PSA_HUMAN]	5.94E-03	3.0078	3.0658	1.08E-02	2.5440	2.0745
3.7	Q9NVS9	Pyridoxine-5-phosphate oxidase OS=Homo sapiens GN=PNPO PE=1 SV=1 - [PNPO_HUMAN]	4.28E-04	-5.1013	-2.8728	3.38E-06	-7.9449	-2.1274

Fig. 7 continued

3_7	P11498	Pyruvate carboxylase, mitochondrial OS=Homo sapiens GN=PC PE=1 SV=2 - PYC_HUMAN	9.43E-04	-4.1806	-2.8168	6.81E-04	-3.9242	-3.9982
3_7	P11498	Pyruvate carboxylase, mitochondrial OS=Homo sapiens GN=PC PE=1 SV=2 - PYC_HUMAN	9.43E-04	-4.1806	-2.8168	6.81E-04	-3.9242	-3.9982
3_7	P30613	Pyruvate kinase isozymes R/L OS=Homo sapiens GN=PKLR PE=1 SV=2 - KPYR_HUMAN	1.25E-07	-17.8985	-2.8740	5.10E-04	-4.0902	-3.4485
3_7	Q00257	Quinone oxidoreductase OS=Homo sapiens GN=CRYZ PE=1 SV=1 - QOR_HUMAN	2.52E-02	-2.2704	-2.9242	1.86E-04	-4.7039	-3.4963
3_7	P46940	Ras GTPase-activating-like protein IQGAP1 OS=Homo sapiens GN=IQGAP1 PE=1 SV=1 - IQGA1_HUMAN	7.37E-05	6.3594	3.1593	8.80E-03	2.6305	2.5297
3_7	Q13576	Ras GTPase-activating-like protein IQGAP2 OS=Homo sapiens GN=IQGAP2 PE=1 SV=4 - IQGA2_HUMAN	6.42E-03	-2.9559	-2.7576	3.77E-02	-1.9990	-2.3161
3_7	P02753	Retinol-binding protein 4 OS=Homo sapiens GN=RBP4 PE=1 SV=3 - RET4_HUMAN	4.62E-06	-15.7175	-2.8475	1.52E-05	-6.5738	-2.2794
3_7	P52758	Ribonuclease UK114 OS=Homo sapiens GN=HRSP12 PE=1 SV=1 - UK114_HUMAN	5.83E-04	-4.7336	-2.9999	5.57E-04	-4.0442	-3.1385
3_7	Q9P2E9	Ribosome-binding protein 1 OS=Homo sapiens GN=RRBP1 PE=1 SV=4 - RRBP1_HUMAN	3.59E-02	-2.0929	-2.8367	2.47E-04	-4.5113	-4.7758
3_7	Q6NBX0	Saccharopine dehydrogenase-like oxidoreductase OS=Homo sapiens GN=SCCPDH PE=1 SV=1 - SCPDL_HUMAN	5.37E-06	-15.4555	-2.8469	1.79E-05	-6.3913	-2.5827
3_7	Q00266	S-adenosylmethionine synthase isoform type-1 OS=Homo sapiens GN=MAT1A PE=1 SV=2 - IMET1_HUMAN	1.14E-05	-13.1193	-2.8581	2.09E-03	-3.3468	-2.7125
3_7	P34896	Serine hydroxymethyltransferase, cytosolic OS=Homo sapiens GN=SHMT1 PE=1 SV=1 - GLYC_HUMAN	7.40E-06	-14.6252	-2.8267	1.11E-05	-6.9286	-2.9536
3_7	P34897	Serine hydroxymethyltransferase, mitochondrial OS=Homo sapiens GN=SHMT2 PE=1 SV=3 - GLYM_HUMAN	4.99E-03	-3.1642	-2.8563	1.50E-03	-3.5289	-3.0560
3_7	P21549	Serine--pyruvate aminotransferase OS=Homo sapiens GN=AGXT PE=1 SV=1 - SPYA_HUMAN	5.62E-04	-4.7962	-3.0303	4.92E-05	-5.6194	-5.2723
3_7	P45954	Short/branched chain specific acyl-CoA dehydrogenase, mitochondrial OS=Homo sapiens GN=ACADSB PE=1 SV=1 - ACDSB_HUMAN	9.78E-06	-13.7468	-2.8646	5.14E-05	-5.5525	-3.1275
3_7	Q9H9B4	Sideroflexin-1 OS=Homo sapiens GN=SFXN1 PE=1 SV=4 - SFXN1_HUMAN	5.60E-06	-15.2902	-2.8292	3.35E-06	-7.9625	-2.1777
3_7	Q00796	Sorbitol dehydrogenase OS=Homo sapiens GN=SORD PE=1 SV=4 - DHSO_HUMAN	3.74E-03	-3.4464	-2.8262	6.77E-03	-2.7478	-2.7312
3_7	Q02318	Sterol 26-hydroxylase, mitochondrial OS=Homo sapiens GN=CYP27A1 PE=1 SV=1 - CP27A_HUMAN	1.63E-04	-5.6078	-2.7775	1.34E-03	-3.5792	-2.0078
3_7	P51649	Succinate-semialdehyde dehydrogenase, mitochondrial OS=Homo sapiens GN=ALDH5A1 PE=1 SV=2 - SSDH_HUMAN	1.21E-05	-12.8035	-2.7413	8.04E-04	-3.8335	-2.4672
3_7	P30048	Thioredoxin-dependent peroxide reductase, mitochondrial OS=Homo sapiens GN=PRDX3 PE=1 SV=3 - PRDX3_HUMAN	3.09E-02	-2.1208	-2.9383	2.47E-04	-4.5129	-2.9575
3_7	P22310	UDP-glucuronosyltransferase 1-4 OS=Homo sapiens GN=UGT1A4 PE=1 SV=1 - UD14_HUMAN	3.07E-04	-5.3717	-2.8417	1.16E-02	-2.5112	-2.8066
3_7	P19224	UDP-glucuronosyltransferase 1-6 OS=Homo sapiens GN=UGT1A6 PE=1 SV=2 - UD16_HUMAN	2.71E-03	-3.6458	-2.8261	2.18E-02	-2.2147	-2.0015
3_7	O60656	UDP-glucuronosyltransferase 1-9 OS=Homo sapiens GN=UGT1A9 PE=1 SV=1 - UD19_HUMAN	2.78E-04	-5.4205	-2.8416	1.18E-02	-2.4092	-2.0078
3_7	P06133	UDP-glucuronosyltransferase 2B4 OS=Homo sapiens GN=UGT2B4 PE=1 SV=2 - UD2B4_HUMAN	7.51E-06	-14.2817	-2.9014	3.74E-03	-3.0413	-2.9536
3_7	P16662	UDP-glucuronosyltransferase 2B7 OS=Homo sapiens GN=UGT2B7 PE=1 SV=1 - UD2B7_HUMAN	4.74E-06	-15.6905	-2.8565	1.15E-03	-3.6440	-2.8754
3_7	Q16851	UTP--glucose-1-phosphate uridylyltransferase OS=Homo sapiens GN=UGP2 PE=1 SV=5 - UGPA_HUMAN	5.30E-03	-3.1022	-2.9673	4.40E-05	-5.7211	-4.6124
3_8	Q15029	116 kDa U5 small nuclear ribonucleoprotein component OS=Homo sapiens GN=EFTUD2 PE=1 SV=1 - U5S1_HUMAN	1.34E-04	5.8542	2.6748	9.09E-04	3.8379	2.4356
3_8	Q04917	14-3-3 protein eta OS=Homo sapiens GN=YWHAH PE=1 SV=4 - 1433F_HUMAN	4.61E-04	4.5965	2.9218	1.78E-05	6.4947	3.8341
3_8	P31947	14-3-3 protein sigma OS=Homo sapiens GN=SFN PE=1 SV=1 - 1433S_HUMAN	1.43E-02	2.6792	2.9218	1.74E-05	6.5836	3.7240
3_8	O14756	17-beta-hydroxysteroid dehydrogenase type 6 OS=Homo sapiens GN=HSD17B6 PE=1 SV=1 - DH17B6_HUMAN	1.33E-05	-14.8936	-2.8892	8.53E-05	-5.3332	-3.2054
3_8	P80404	4-aminobutyrate aminotransferase, mitochondrial OS=Homo sapiens GN=ABAT PE=1 SV=3 - GABT_HUMAN	5.34E-04	-4.3979	-2.8695	6.17E-03	-2.8317	-3.4280
3_8	P32754	4-hydroxyphenylpyruvate dioxygenase OS=Homo sapiens GN=HPD PE=1 SV=2 - HPPD_HUMAN	1.43E-05	-12.9628	-2.9576	2.10E-04	-4.6765	-4.0978

Fig. 7 continued

3_8	P17858	6-phosphofructokinase, liver type OS=Homo sapiens GN=PFKL PE=1 SV=6 - [K6PL_HUMAN]	3.18E-04	5.4684	2.7283	1.70E-03	3.5127	2.7389
3_8	P68133	Actin, alpha skeletal muscle OS=Homo sapiens GN=ACTA1 PE=1 SV=1 - [ACTS_HUMAN]	1.00E-02	-2.7904	-3.0521	6.28E-03	-2.8215	-5.3557
3_8	Q08AH3	Acyl-coenzyme A synthetase ACSM2A, mitochondrial OS=Homo sapiens GN=ACSM2A PE=1 SV=2 - [ACS2A_HUMAN]	3.06E-04	-5.4960	-2.8194	1.06E-02	-2.5891	-3.6690
3_8	Q8IC36	Acyl-coenzyme A synthetase ACSM2B, mitochondrial OS=Homo sapiens GN=ACSM2B PE=1 SV=2 - [ACS2B_HUMAN]	1.44E-05	-12.8526	-2.8202	1.63E-03	-3.5317	-3.7092
3_8	P24298	Alanine aminotransferase 1 OS=Homo sapiens GN=GPT PE=1 SV=3 - [ALAT1_HUMAN]	3.13E-04	-5.4824	-2.6800	5.63E-03	-2.8831	-2.0078
3_8	P07327	Alcohol dehydrogenase 1A OS=Homo sapiens GN=ADH1A PE=1 SV=2 - [ADH1A_HUMAN]	2.30E-04	-5.7071	-2.9589	1.33E-03	-3.6314	-4.3653
3_8	P00325	Alcohol dehydrogenase 1B OS=Homo sapiens GN=ADH1B PE=1 SV=2 - [ADH1B_HUMAN]	2.36E-04	-5.6959	-2.9589	1.83E-03	-3.4802	-4.5623
3_8	P08319	Alcohol dehydrogenase 4 OS=Homo sapiens GN=ADH4 PE=1 SV=5 - [ADH4_HUMAN]	3.43E-04	-5.3466	-2.8303	5.83E-03	-2.8651	-3.8151
3_8	Q06278	Aldehyde oxidase OS=Homo sapiens GN=AOX1 PE=2 SV=2 - [ADO_HUMAN]	1.47E-05	-10.7701	-2.7162	8.30E-03	-2.7026	-2.4672
3_8	O60218	Aldo-keto reductase family 1 member B10 OS=Homo sapiens GN=AKR1B10 PE=1 SV=2 - [AK1BA_HUMAN]	1.37E-05	-13.9606	-3.0091	3.09E-05	-5.9931	-5.0151
3_8	Q04828	Aldo-keto reductase family 1 member C1 OS=Homo sapiens GN=AKR1C1 PE=1 SV=1 - [AK1C1_HUMAN]	3.87E-04	-4.9526	-3.0089	1.79E-03	-3.4961	-4.0151
3_8	P52895	Aldo-keto reductase family 1 member C2 OS=Homo sapiens GN=AKR1C2 PE=1 SV=3 - [AK1C2_HUMAN]	3.28E-04	-5.3956	-3.0055	1.66E-02	-2.3773	-3.4921
3_8	P17516	Aldo-keto reductase family 1 member C4 OS=Homo sapiens GN=AKR1C4 PE=1 SV=3 - [AK1C4_HUMAN]	2.79E-04	-5.5674	-2.9828	2.67E-04	-4.5120	-3.4921
3_8	P21397	Amine oxidase [flavin-containing] A OS=Homo sapiens GN=MAOA PE=1 SV=1 - [AOFA_HUMAN]	1.19E-03	-3.8451	-2.8433	1.53E-02	-2.4124	-2.3906
3_8	P27338	Amine oxidase [flavin-containing] B OS=Homo sapiens GN=MAOB PE=1 SV=3 - [AOFB_HUMAN]	1.48E-05	-8.6392	-2.8910	3.68E-06	-8.2256	-3.8154
3_8	Q03154	Aminoacylase-1 OS=Homo sapiens GN=ACY1 PE=1 SV=1 - [ACY1_HUMAN]	3.31E-05	-6.7663	-2.9365	1.57E-05	-6.7860	-3.3608
3_8	P15144	Aminopeptidase N OS=Homo sapiens GN=ANPEP PE=1 SV=4 - [AMPN_HUMAN]	1.12E-04	-5.8896	-2.7082	1.54E-02	-2.4098	-2.1909
3_8	P01019	Angiotensinogen OS=Homo sapiens GN=AGT PE=1 SV=1 - [ANGT_HUMAN]	2.06E-04	-5.7444	-2.6321	2.04E-04	-4.7134	-2.1909
3_8	P12429	Annexin A3 OS=Homo sapiens GN=ANXA3 PE=1 SV=3 - [ANXA3_HUMAN]	1.91E-04	5.7926	2.7772	1.83E-03	3.4818	2.8845
3_8	O95994	Anterior gradient protein 2 homolog OS=Homo sapiens GN=AGR2 PE=1 SV=1 - [AGR2_HUMAN]	5.81E-06	21.9349	2.8776	1.78E-05	6.4948	3.0799
3_8	P05090	Apolipoprotein D OS=Homo sapiens GN=APOD PE=1 SV=1 - [APOD_HUMAN]	1.29E-03	-3.8341	-2.6908	3.32E-03	-3.1519	-2.0015
3_8	P05089	Arginase-1 OS=Homo sapiens GN=ARG1 PE=1 SV=2 - [ARGI1_HUMAN]	1.36E-05	-14.4515	-2.9788	1.24E-04	-5.0927	-4.3292
3_8	P54136	Arginine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=RARS PE=1 SV=2 - [SYRC_HUMAN]	4.62E-03	3.1966	2.6671	5.47E-04	4.1129	2.2914
3_8	P22760	Arylacetamide deacetylase OS=Homo sapiens GN=AADAC PE=1 SV=5 - [AAAD_HUMAN]	1.05E-05	-16.1155	-2.7673	1.71E-05	-6.6513	-2.8640
3_8	P14868	Aspartate--tRNA ligase, cytoplasmic OS=Homo sapiens GN=DARS PE=1 SV=2 - [SYDC_HUMAN]	1.21E-02	2.7537	2.7269	7.55E-05	5.4279	2.6105
3_8	Q92499	ATP-dependent RNA helicase DDX1 OS=Homo sapiens GN=DDX1 PE=1 SV=2 - [DDX1_HUMAN]	7.65E-04	4.0739	2.6698	2.26E-03	3.3651	2.2914
3_8	Q93088	Betaine--homocysteine S-methyltransferase 1 OS=Homo sapiens GN=BHMT PE=1 SV=2 - [BHMT1_HUMAN]	3.47E-04	-5.2976	-2.9078	3.04E-02	-2.0917	-3.2794
3_8	Q9Y2P5	Bile acyl-CoA synthetase OS=Homo sapiens GN=SLC27A5 PE=1 SV=1 - [S27A5_HUMAN]	2.32E-03	-3.7096	-2.6951	2.94E-03	-3.2268	-2.5061
3_8	Q06520	Bile salt sulfotransferase OS=Homo sapiens GN=SULT2A1 PE=1 SV=3 - [ST2A1_HUMAN]	1.36E-05	-14.3652	-2.9030	1.07E-03	-3.7370	-2.8466
3_8	Q12864	Cadherin-17 OS=Homo sapiens GN=CDH17 PE=1 SV=3 - [CAD17_HUMAN]	1.90E-04	5.7758	2.7688	2.55E-04	4.5434	3.2065
3_8	Q9UJS0	Calcium-binding mitochondrial carrier protein Aralar2 OS=Homo sapiens GN=SLC25A13 PE=1 SV=2 - [CMC2_HUMAN]	1.10E-03	-3.8635	-2.8629	6.49E-05	-5.5921	-3.6890
3_8	P31327	Carbamoyl-phosphate synthase [ammonia], mitochondrial OS=Homo sapiens GN=CPS1 PE=1 SV=2 - [CPSM_HUMAN]	7.27E-04	-4.1224	-3.0534	2.20E-03	-3.3811	-7.2123

Fig. 7 continued

3_8	P06731	Carcinoembryonic antigen-related cell adhesion molecule 5 OS=Homo sapiens GN=CEACAM5 PE=1 SV=3 - [CEAM5_HUMAN]	8.43E-06	18.8897	2.8744	4.46E-04	4.2417	2.7240
3_8	P40199	Carcinoembryonic antigen-related cell adhesion molecule 6 OS=Homo sapiens GN=CEACAM6 PE=1 SV=3 - [CEAM6_HUMAN]	1.18E-03	3.8466	2.7790	2.59E-03	3.2987	2.0866
3_8	P23786	Carnitine O-palmitoyltransferase 2, mitochondrial OS=Homo sapiens GN=CPT2 PE=1 SV=2 - [CPT2_HUMAN]	2.22E-05	-7.2577	-2.8192	1.91E-03	-3.4577	-2.1909
3_8	P35221	Catenin alpha-1 OS=Homo sapiens GN=CTNNA1 PE=1 SV=1 - [CTNA1_HUMAN]	2.14E-03	3.7379	2.6880	5.09E-04	4.1499	2.7389
3_8	P35222	Catenin beta-1 OS=Homo sapiens GN=CTNNB1 PE=1 SV=1 - [CTNB1_HUMAN]	3.70E-04	5.0637	2.8094	9.90E-06	7.3339	3.4097
3_8	Q9UBR2	Cathepsin Z OS=Homo sapiens GN=CTSZ PE=1 SV=1 - [CATZ_HUMAN]	2.37E-05	-7.2165	-2.3318	1.76E-06	-9.0013	-2.4169
3_8	Q99829	Copine-1 OS=Homo sapiens GN=CPNE1 PE=1 SV=1 - [CPNE1_HUMAN]	6.03E-06	21.5582	2.7256	5.82E-04	4.0780	2.2997
3_8	P12277	Creatine kinase B-type OS=Homo sapiens GN=CKB PE=1 SV=1 - [KCRB_HUMAN]	7.53E-03	2.8213	2.7880	1.72E-02	2.3613	3.4402
3_8	Q86VP6	Cullin-associated NEDD8-dissociated protein 1 OS=Homo sapiens GN=CAND1 PE=1 SV=2 - [CAND1_HUMAN]	3.49E-05	6.7155	2.7095	1.27E-04	5.0798	2.3142
3_8	P00167	Cytochrome b5 OS=Homo sapiens GN=CYB5A PE=1 SV=2 - [CYB5_HUMAN]	1.04E-05	-16.4428	-3.0069	1.68E-05	-6.7295	-3.0531
3_8	P11509	Cytochrome P450 2A6 OS=Homo sapiens GN=CYP2A6 PE=1 SV=3 - [CP2A6_HUMAN]	3.39E-04	-5.3604	-2.8057	3.07E-03	-3.1991	-2.8754
3_8	P11712	Cytochrome P450 2C9 OS=Homo sapiens GN=CYP2C9 PE=1 SV=3 - [CP2C9_HUMAN]	1.46E-05	-12.1941	-2.7039	6.24E-03	-2.8247	-2.1275
3_8	P10635	Cytochrome P450 2D6 OS=Homo sapiens GN=CYP2D6 PE=1 SV=2 - [CP2D6_HUMAN]	2.07E-03	-3.7456	-2.6731	2.80E-03	-3.2589	-2.1385
3_8	Q14204	Cytoplasmic dynein 1 heavy chain 1 OS=Homo sapiens GN=DYNC1H1 PE=1 SV=5 - [DYHC1_HUMAN]	4.85E-04	4.5182	2.7153	1.69E-03	3.5409	3.9923
3_8	O75891	Cytosolic 10-formyltetrahydrofolate dehydrogenase OS=Homo sapiens GN=ALDH1L1 PE=1 SV=2 - [AL1L1_HUMAN]	7.07E-05	-6.0713	-2.8507	2.53E-02	-2.1684	-3.8154
3_8	Q02338	D-beta-hydroxybutyrate dehydrogenase, mitochondrial OS=Homo sapiens GN=BDH1 PE=1 SV=3 - [BDH_HUMAN]	4.93E-03	-3.1352	-2.8436	2.24E-05	-6.3291	-2.5424
3_8	P30038	Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial OS=Homo sapiens GN=ALDH4A1 PE=1 SV=3 - [AL4A1_HUMAN]	2.83E-04	-5.5380	-2.9501	4.62E-04	-4.2211	-3.7648
3_8	P54886	Delta-1-pyrroline-5-carboxylate synthase OS=Homo sapiens GN=ALDH18A1 PE=1 SV=2 - [P5CS_HUMAN]	4.89E-06	23.8624	2.6907	5.33E-03	2.9129	2.6394
3_8	P09417	Dihydropteridine reductase OS=Homo sapiens GN=QDPR PE=1 SV=2 - [DHPR_HUMAN]	2.75E-05	-7.0181	-2.8151	1.32E-03	-3.6319	-2.2905
3_8	P31513	Dimethylaniline monooxygenase [N-oxide-forming] 3 OS=Homo sapiens GN=FMO3 PE=1 SV=5 - [FMO3_HUMAN]	3.01E-04	-5.5050	-2.8163	5.21E-04	-4.1361	-2.9344
3_8	Q9UI17	Dimethylglycine dehydrogenase, mitochondrial OS=Homo sapiens GN=DMGDH PE=1 SV=2 - [DMGD_HUMAN]	3.25E-04	-5.4111	-2.7015	1.34E-03	-3.6258	-2.0015
3_8	P11387	DNA topoisomerase 1 OS=Homo sapiens GN=TOP1 PE=1 SV=2 - [TOP1_HUMAN]	1.59E-02	2.6078	2.7446	2.03E-02	2.2863	2.3440
3_8	Q7Z6Z7	E3 ubiquitin-protein ligase HUWE1 OS=Homo sapiens GN=HUWE1 PE=1 SV=3 - [HUWE1_HUMAN]	6.33E-06	21.1366	2.6790	1.29E-03	3.6426	2.5850
3_8	O75356	Ectonucleoside triphosphate diphosphohydrolase 5 OS=Homo sapiens GN=ENTPD5 PE=1 SV=1 - [ENTP5_HUMAN]	2.67E-04	-5.5849	-2.7192	7.41E-03	-2.7447	-2.1777
3_8	O75521	Enoyl-CoA delta isomerase 2, mitochondrial OS=Homo sapiens GN=ECI2 PE=1 SV=4 - [ECI2_HUMAN]	1.46E-05	-12.0565	-2.6864	6.17E-04	-4.0499	-2.5424
3_8	P54107	Ephrin OS=Homo sapiens GN=EPPK1 PE=1 SV=2 - [EPPL_HUMAN]	1.52E-05	7.6885	2.7065	9.68E-04	3.7977	2.4170
3_8	P07099	Epoxide hydrolase 1 OS=Homo sapiens GN=EPHX1 PE=1 SV=1 - [HYEP_HUMAN]	8.43E-04	-4.0053	-3.0661	1.41E-06	-9.4819	-5.3436
3_8	P55060	Exportin-2 OS=Homo sapiens GN=CSE1L PE=1 SV=3 - [XPO2_HUMAN]	1.47E-05	10.7992	2.9586	2.46E-03	3.3187	2.5016
3_8	Q9BSJ8	Extended synaptotagmin-1 OS=Homo sapiens GN=ESYT1 PE=1 SV=1 - [ESYT1_HUMAN]	3.02E-02	-2.1398	-2.7140	1.40E-03	-3.6064	-2.1275
3_8	P15311	Ezrin OS=Homo sapiens GN=EZR PE=1 SV=4 - [EZRI_HUMAN]	5.34E-03	3.0649	2.8640	1.16E-03	3.6963	3.3846
3_8	P51648	Fatty aldehyde dehydrogenase OS=Homo sapiens GN=ALDH3A2 PE=1 SV=1 - [AL3A2_HUMAN]	1.44E-05	-12.8558	-2.7786	3.54E-03	-3.1237	-2.3161
3_8	O95954	Formimidoyltransferase-cyclodeaminase OS=Homo sapiens GN=FTCD PE=1 SV=2 - [FTCD_HUMAN]	1.34E-05	-14.7716	-2.8579	4.65E-03	-2.9921	-2.8931

Fig. 7 continued

3_8	P05062	Fructose-bisphosphate aldolase B OS=Homo sapiens GN=ALDOB PE=1 SV=2 - [ALDOB_HUMAN]	7.18E-05	-6.0595	-3.0905	3.48E-05	-5.8930	-5.5231
3_8	P09972	Fructose-bisphosphate aldolase C OS=Homo sapiens GN=ALDOC PE=1 SV=2 - [ALDOC_HUMAN]	5.46E-03	3.0402	2.8104	5.87E-06	7.6721	3.4517
3_8	P16930	Fumarylacetoacetase OS=Homo sapiens GN=FAH PE=1 SV=2 - [FAAA_HUMAN]	3.72E-04	-5.0496	-2.9440	8.29E-06	-7.4933	-3.0078
3_8	O95479	GDH/6PGL endoplasmic bifunctional protein OS=Homo sapiens GN=H6PD PE=1 SV=2 - [G6PE_HUMAN]	1.05E-05	-15.9028	-2.8183	1.59E-04	-4.8940	-2.6130
3_8	Q06210	Glutamine--fructose-6-phosphate aminotransferase [isomerizing] 1 OS=Homo sapiens GN=GFPT1 PE=1 SV=3 - [GFPT1_HUMAN]	7.27E-05	6.0493	2.7907	5.01E-04	4.1622	3.2914
3_8	P08263	Glutathione S-transferase A1 OS=Homo sapiens GN=GSTA1 PE=1 SV=3 - [GSTA1_HUMAN]	1.00E-05	-17.2116	-3.0465	1.83E-04	-4.7846	-3.3608
3_8	P09210	Glutathione S-transferase A2 OS=Homo sapiens GN=GSTA2 PE=1 SV=4 - [GSTA2_HUMAN]	2.88E-04	-5.5472	-3.0379	2.76E-02	-2.1253	-3.2084
3_8	P50440	Glycine amidinotransferase, mitochondrial OS=Homo sapiens GN=GATM PE=1 SV=1 - [GATM_HUMAN]	1.04E-05	-16.5025	-2.9324	9.26E-09	-14.3632	-4.1568
3_8	P06737	Glycogen phosphorylase, liver form OS=Homo sapiens GN=PYGL PE=1 SV=4 - [PYGL_HUMAN]	9.16E-06	-18.0733	-2.9005	6.75E-04	-4.0002	-3.5535
3_8	Q92598	Heat shock protein 105 kDa OS=Homo sapiens GN=HSPH1 PE=1 SV=1 - [HS105_HUMAN]	5.68E-06	22.2078	2.8188	1.41E-04	4.9853	3.2769
3_8	P31942	Heterogeneous nuclear ribonucleoprotein H3 OS=Homo sapiens GN=HNRNPH3 PE=1 SV=2 - [HNRH3_HUMAN]	4.43E-03	3.2367	2.7145	4.27E-03	3.0343	2.4356
3_8	Q9BUJ2	Heterogeneous nuclear ribonucleoprotein U-like protein 1 OS=Homo sapiens GN=HNRNPUL1 PE=1 SV=2 - [HNRL1_HUMAN]	1.92E-03	3.7677	2.6996	3.62E-03	3.1117	2.2997
3_8	Q1KMD3	Heterogeneous nuclear ribonucleoprotein U-like protein 2 OS=Homo sapiens GN=HNRNPUL2 PE=1 SV=1 - [HNRL2_HUMAN]	4.46E-03	3.2321	2.7958	3.08E-06	8.3515	3.3142
3_8	P26583	High mobility group protein B2 OS=Homo sapiens GN=HMGB2 PE=1 SV=2 - [HMGB2_HUMAN]	1.73E-02	2.5479	2.8017	1.99E-02	2.2933	2.5611
3_8	Q93099	Homogentisate 1,2-dioxygenase OS=Homo sapiens GN=HGD PE=1 SV=2 - [HGD_HUMAN]	1.35E-05	-14.5976	-2.8389	2.82E-05	-6.0475	-4.0042
3_8	Q9UJM8	Hydroxyacid oxidase 1 OS=Homo sapiens GN=HAO1 PE=1 SV=1 - [HAOX1_HUMAN]	1.04E-05	-16.4212	-2.8892	1.27E-05	-7.1383	-4.1274
3_8	P35914	Hydroxymethylglutaryl-CoA lyase, mitochondrial OS=Homo sapiens GN=HMGCL PE=1 SV=2 - [HMGCL_HUMAN]	1.30E-02	-2.7292	-2.7459	5.99E-03	-2.8498	-2.1275
3_8	O00410	Importin-5 OS=Homo sapiens GN=IPO5 PE=1 SV=4 - [IPO5_HUMAN]	1.49E-05	8.0680	2.7315	1.35E-04	5.0298	2.6216
3_8	P14923	Junction plakoglobin OS=Homo sapiens GN=JUP PE=1 SV=3 - [PLAK_HUMAN]	2.17E-06	27.0828	2.7850	7.65E-07	10.9458	2.9761
3_8	P08727	Keratin, type I cytoskeletal 19 OS=Homo sapiens GN=KRT19 PE=1 SV=4 - [K1C19_HUMAN]	3.98E-04	4.8838	2.8580	9.91E-05	5.2382	4.7993
3_8	P23141	Liver carboxylesterase 1 OS=Homo sapiens GN=CES1 PE=1 SV=2 - [EST1_HUMAN]	8.03E-04	-4.0424	-3.0504	2.32E-05	-6.2354	-5.7364
3_8	P33121	Long-chain-fatty-acid--CoA ligase 1 OS=Homo sapiens GN=ACSL1 PE=1 SV=1 - [ACSL1_HUMAN]	1.48E-05	-12.2433	-2.8373	2.41E-03	-3.3330	-3.3292
3_8	Q15046	Lysine--tRNA ligase OS=Homo sapiens GN=KARS PE=1 SV=3 - [SYK_HUMAN]	3.35E-05	6.7513	2.6871	1.76E-04	4.7998	2.2997
3_8	P10253	Lysosomal alpha-glucosidase OS=Homo sapiens GN=GAA PE=1 SV=4 - [LYAG_HUMAN]	6.79E-04	-4.1831	-2.8273	1.12E-02	-2.5660	-2.8754
3_8	P10619	Lysosomal protective protein OS=Homo sapiens GN=CTSA PE=1 SV=2 - [PPGB_HUMAN]	4.62E-04	-4.5910	-2.8071	1.83E-05	-6.4690	-2.0078
3_8	P11310	Medium-chain specific acyl-CoA dehydrogenase, mitochondrial OS=Homo sapiens GN=ACADM PE=1 SV=1 - [ACADM_HUMAN]	2.45E-05	-7.1695	-2.8732	1.04E-04	-5.1982	-3.0560
3_8	Q02252	Methylmalonate-semialdehyde dehydrogenase [acylating], mitochondrial OS=Homo sapiens GN=ALDH6A1 PE=1 SV=2 - [MMSA_HUMAN]	6.67E-04	-4.1988	-2.8851	6.10E-04	-4.0565	-4.0977
3_8	Q9H8R3	Methyltransferase-like protein 7A OS=Homo sapiens GN=METTL7A PE=1 SV=1 - [METTA_HUMAN]	1.26E-05	-15.3364	-2.8687	2.70E-05	-6.1096	-2.1385
3_8	P10620	Microsomal glutathione S-transferase 1 OS=Homo sapiens GN=MGST1 PE=1 SV=1 - [MGST1_HUMAN]	1.31E-05	-15.1365	-2.9236	2.71E-05	-6.0920	-2.2794
3_8	P55157	Microsomal triglyceride transfer protein large subunit OS=Homo sapiens GN=MTTP PE=1 SV=1 - [MTP_HUMAN]	1.38E-05	-13.8236	-2.7434	1.99E-04	-4.7269	-2.8913
3_8	Q7Z406	Myosin-14 OS=Homo sapiens GN=MYH14 PE=1 SV=2 - [MYH14_HUMAN]	6.83E-06	20.7491	2.8464	4.68E-04	4.2142	4.7862
3_8	Q4G0N4	NAD kinase domain-containing protein 1 OS=Homo sapiens GN=NADKD1 PE=1 SV=2 - [NAKD1_HUMAN]	9.30E-06	-17.6899	-2.8105	6.72E-05	-5.5697	-2.8644

Fig. 7 continued

3_8	Q13423	NAD(P) transhydrogenase, mitochondrial OS=Homo sapiens GN=NNT PE=1 SV=3 - [NNTM_HUMAN]	3.84E-03	-3.3704	-2.7910	3.67E-03	-3.1069	-2.7758
3_8	P16435	NADPH--cytochrome P450 reductase OS=Homo sapiens GN=POR PE=1 SV=2 - [NCPR_HUMAN]	7.39E-04	-4.1112	-2.8486	3.02E-04	-4.4774	-3.6130
3_8	P40261	Nicotinamide N-methyltransferase OS=Homo sapiens GN=NNMT PE=1 SV=1 - [NNMT_HUMAN]	1.38E-05	-13.7154	-2.9062	4.88E-03	-2.9623	-2.1777
3_8	P22307	Non-specific lipid-transfer protein OS=Homo sapiens GN=SCP2 PE=1 SV=2 - [NLTP_HUMAN]	6.97E-04	-4.1589	-2.8858	1.29E-04	-5.0651	-2.6130
3_8	Q14980	Nuclear mitotic apparatus protein 1 OS=Homo sapiens GN=NUMA1 PE=1 SV=2 - [NUMA1_HUMAN]	8.30E-06	19.8780	2.6318	6.40E-03	2.8125	2.2386
3_8	O00567	Nucleolar protein 56 OS=Homo sapiens GN=NOP56 PE=1 SV=4 - [NOP56_HUMAN]	2.36E-02	2.3390	2.7320	1.14E-02	2.5613	2.3142
3_8	P00480	Ornithine carbamoyltransferase, mitochondrial OS=Homo sapiens GN=OTC PE=1 SV=3 - [OTC_HUMAN]	1.09E-05	-15.4513	-2.9239	7.46E-06	-7.5783	-4.0449
3_8	Q02790	Peptidyl-prolyl cis-trans isomerase FKBP4 OS=Homo sapiens GN=FKBP4 PE=1 SV=3 - [FKBP4_HUMAN]	3.16E-05	6.8099	2.6916	5.01E-04	4.1630	2.9627
3_8	Q15063	Periostin OS=Homo sapiens GN=POSTN PE=1 SV=2 - [POSTN_HUMAN]	4.82E-03	3.1567	2.7865	3.97E-02	1.9977	3.3474
3_8	Q15067	Peroxisomal acyl-coenzyme A oxidase 1 OS=Homo sapiens GN=ACOX1 PE=1 SV=3 - [ACOX1_HUMAN]	8.63E-05	-5.9485	-2.6944	3.24E-03	-3.1654	-2.9982
3_8	Q9Y274	Peroxisomal acyl-coenzyme A oxidase 2 OS=Homo sapiens GN=ACOX2 PE=1 SV=1 - [ACOX2_HUMAN]	1.27E-02	-2.7385	-2.6209	1.78E-02	-2.3496	-2.2794
3_8	Q08426	Peroxisomal bifunctional enzyme OS=Homo sapiens GN=EHHADH PE=1 SV=3 - [ECHP_HUMAN]	3.55E-04	-5.2673	-2.9060	5.68E-06	-7.7255	-5.0344
3_8	Q9P0Z9	Peroxisomal sarcosine oxidase OS=Homo sapiens GN=PIPOX PE=2 SV=2 - [SOX_HUMAN]	1.40E-05	-13.2807	-2.8545	4.79E-04	-4.1917	-2.8754
3_8	Q9Y285	Phenylalanine--tRNA ligase alpha subunit OS=Homo sapiens GN=FARSA PE=1 SV=3 - [SYFA_HUMAN]	5.95E-04	4.2936	2.6603	2.31E-03	3.3563	2.1622
3_8	Q9NSD9	Phenylalanine--tRNA ligase beta subunit OS=Homo sapiens GN=FARSB PE=1 SV=3 - [SYFB_HUMAN]	4.84E-06	23.8810	2.7077	2.32E-05	6.2460	2.5772
3_8	Q14651	Plastin-1 OS=Homo sapiens GN=PLS1 PE=1 SV=2 - [PLS1_HUMAN]	4.22E-05	6.4640	2.8071	3.20E-04	4.4299	2.7240
3_8	Q6P2Q9	Pre-mRNA-processing-splicing factor 8 OS=Homo sapiens GN=PRPF8 PE=1 SV=2 - [PRP8_HUMAN]	8.33E-06	19.7361	2.6754	3.87E-03	3.0790	2.3761
3_8	P07602	Proactivator polypeptide OS=Homo sapiens GN=PSAP PE=1 SV=2 - [SAP_HUMAN]	2.42E-03	-3.6954	-2.9204	1.96E-04	-4.7402	-2.3297
3_8	P17844	Probable ATP-dependent RNA helicase DDX5 OS=Homo sapiens GN=DDX5 PE=1 SV=1 - [DDX5_HUMAN]	3.42E-06	24.2039	2.7914	3.44E-04	4.3941	3.2734
3_8	Q8WUM4	Programmed cell death 6-interacting protein OS=Homo sapiens GN=PDCD6IP PE=1 SV=1 - [PDC6I_HUMAN]	6.43E-04	4.2373	2.7388	4.52E-03	3.0068	2.4695
3_8	P12004	Proliferating cell nuclear antigen OS=Homo sapiens GN=PCNA PE=1 SV=1 - [PCNA_HUMAN]	1.66E-05	7.5305	2.7851	1.99E-03	3.4334	3.0255
3_8	Q14914	Prostaglandin reductase 1 OS=Homo sapiens GN=PTGR1 PE=1 SV=2 - [PTGR1_HUMAN]	1.48E-05	-12.0259	-2.7764	9.59E-04	-3.8022	-3.4672
3_8	Q9BPW8	Protein NipSnap homolog 1 OS=Homo sapiens GN=NIPSNAP1 PE=1 SV=1 - [NIPS1_HUMAN]	4.22E-03	-3.2834	-2.8440	2.26E-04	-4.6264	-3.0560
3_8	Q9P258	Protein RCC2 OS=Homo sapiens GN=RCC2 PE=1 SV=2 - [RCC2_HUMAN]	2.42E-05	7.1809	2.6566	1.00E-03	3.7761	2.4152
3_8	P06703	Protein S100-A6 OS=Homo sapiens GN=S100A6 PE=1 SV=1 - [S10A6_HUMAN]	3.19E-05	6.7982	2.8409	8.61E-04	3.8686	2.0545
3_8	P55786	Puromycin-sensitive aminopeptidase OS=Homo sapiens GN=NPEPPS PE=1 SV=2 - [PSA_HUMAN]	3.03E-03	3.5639	2.6909	2.70E-05	6.1001	2.9627
3_8	O43143	Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15 OS=Homo sapiens GN=DHX15 PE=1 SV=2 - [DHX15_HUMAN]	4.61E-04	4.5947	2.7146	1.32E-04	5.0454	2.4356
3_8	Q9NVS9	Pyridoxine-5-phosphate oxidase OS=Homo sapiens GN=PNPO PE=1 SV=1 - [PNPO_HUMAN]	1.65E-03	-3.7997	-2.8728	1.31E-05	-7.0924	-2.1274
3_8	P11498	Pyruvate carboxylase, mitochondrial OS=Homo sapiens GN=PC PE=1 SV=2 - [PYC_HUMAN]	1.40E-05	-13.3912	-2.8168	4.92E-04	-4.1811	-3.9982
3_8	P30613	Pyruvate kinase isozymes R/L OS=Homo sapiens GN=PKLR PE=1 SV=2 - [KPYR_HUMAN]	9.23E-06	-17.8985	-2.8740	5.69E-04	-4.0892	-3.4495
3_8	P46940	Ras GTPase-activating-like protein IQGAP1 OS=Homo sapiens GN=IQGAP1 PE=1 SV=1 - [IQGA1_HUMAN]	5.19E-04	4.4298	2.7990	1.85E-05	6.4594	4.1954
3_8	Q13576	Ras GTPase-activating-like protein IQGAP2 OS=Homo sapiens GN=IQGAP2 PE=1 SV=4 - [IQGA2_HUMAN]	3.52E-04	-5.2783	-2.7576	3.29E-02	-2.0650	-2.3161

Fig. 7 continued

3_8	P02753	Retinol-binding protein 4 OS=Homo sapiens GN=RBP4 PE=1 SV=3 - [RET4_HUMAN]	1.07E-05	-15.7175	-2.8475	1.74E-05	-6.5738	-2.2794
3_8	P52758	Ribonuclease UK114 OS=Homo sapiens GN=HRSP12 PE=1 SV=1 - [UK114_HUMAN]	1.05E-05	-16.1444	-2.9999	1.39E-04	-4.9851	-3.1385
3_8	Q9Y265	RuvB-like 1 OS=Homo sapiens GN=RUVBL1 PE=1 SV=1 - [RUVB1_HUMAN]	3.90E-04	4.9281	2.7000	1.93E-06	8.8226	2.4517
3_8	Q9NBX0	Saccharopine dehydrogenase-like oxidoreductase OS=Homo sapiens GN=SCCPDH PE=1 SV=1 - [SCPDL_HUMAN]	1.70E-05	-7.5081	-2.9469	2.31E-05	-6.2617	-2.5927
3_8	Q00266	S-adenosylmethionine synthase isoform type-1 OS=Homo sapiens GN=MAT1A PE=1 SV=2 - [METK1_HUMAN]	1.41E-05	-13.1193	-2.8581	2.35E-03	-3.3468	-2.7125
3_8	P34896	Serine hydroxymethyltransferase, cytosolic OS=Homo sapiens GN=SHMT1 PE=1 SV=1 - [GLYC_HUMAN]	1.35E-05	-14.8252	-2.8267	1.40E-05	-6.9286	-2.9536
3_8	P21549	Serine--pyruvate aminotransferase OS=Homo sapiens GN=AGXT PE=1 SV=1 - [SPYA_HUMAN]	1.62E-05	-7.5863	-3.0303	5.33E-05	-5.6859	-5.2723
3_8	P45954	Short/branched chain specific acyl-CoA dehydrogenase, mitochondrial OS=Homo sapiens GN=ACADSB PE=1 SV=1 - [ACDSB_HUMAN]	3.00E-04	-5.5071	-2.8646	6.85E-05	-5.5525	-3.1275
3_8	Q9H9B4	Sideroflexin-1 OS=Homo sapiens GN=SFXN1 PE=1 SV=4 - [SFXN1_HUMAN]	4.25E-04	-4.7379	-2.8292	9.90E-06	-7.3334	-2.1777
3_8	O75533	Splicing factor 3B subunit 1 OS=Homo sapiens GN=SF3B1 PE=1 SV=3 - [SF3B1_HUMAN]	8.41E-04	4.0072	2.6708	2.47E-03	3.3216	2.5221
3_8	Q15393	Splicing factor 3B subunit 3 OS=Homo sapiens GN=SF3B3 PE=1 SV=4 - [SF3B3_HUMAN]	2.53E-06	25.9167	2.7124	1.41E-04	4.9817	2.3761
3_8	P26368	Splicing factor U2AF 65 kDa subunit OS=Homo sapiens GN=U2AF2 PE=1 SV=4 - [U2AF2_HUMAN]	3.45E-03	3.4645	2.7558	1.73E-03	3.5074	2.1460
3_8	Q14247	Src substrate cortactin OS=Homo sapiens GN=CTTN PE=1 SV=2 - [SRC8_HUMAN]	4.65E-04	4.5803	2.7471	1.68E-04	4.8501	2.4356
3_8	Q02318	Sterol 26-hydroxylase, mitochondrial OS=Homo sapiens GN=CYP27A1 PE=1 SV=1 - [CP27A_HUMAN]	2.62E-04	-5.6078	-2.7775	1.49E-03	-3.5792	-2.0078
3_8	P40227	T-complex protein 1 subunit zeta OS=Homo sapiens GN=CCT6A PE=1 SV=3 - [TCPZ_HUMAN]	7.88E-05	5.9851	2.7717	9.36E-06	7.4754	2.4356
3_8	P24821	Tenascin OS=Homo sapiens GN=TNC PE=1 SV=3 - [TENA_HUMAN]	1.55E-03	3.8084	2.7745	1.65E-02	2.3830	3.3556
3_8	P19971	Thymidine phosphorylase OS=Homo sapiens GN=TYMP PE=1 SV=2 - [TYPH_HUMAN]	2.48E-02	-2.2985	-2.7286	3.98E-03	-3.0646	-3.2054
3_8	Q13263	Transcription intermediary factor 1-beta OS=Homo sapiens GN=TRIM28 PE=1 SV=5 - [TIF1B_HUMAN]	2.66E-06	25.3652	2.7771	1.10E-04	5.1592	3.4696
3_8	Q9Y310	tRNA-splicing ligase RtcB homolog OS=Homo sapiens GN=C22orf28 PE=1 SV=1 - [RTCB_HUMAN]	8.18E-07	27.9841	2.7233	2.70E-05	6.1069	2.0545
3_8	Q9BQE3	Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 - [TBA1C_HUMAN]	1.28E-03	3.8333	2.9913	7.70E-03	2.7314	5.3684
3_8	Q3ZCM7	Tubulin beta-8 chain OS=Homo sapiens GN=TUBB8 PE=1 SV=2 - [TBB8_HUMAN]	1.77E-03	3.7866	2.9105	6.37E-03	2.8145	4.7612
3_8	P15374	Ubiquitin carboxyl-terminal hydrolase isozyme L3 OS=Homo sapiens GN=UCHL3 PE=1 SV=1 - [UCHL3_HUMAN]	5.02E-04	4.4754	2.6997	4.14E-06	7.9795	2.1742
3_8	P22310	UDP-glucuronosyltransferase 1-4 OS=Homo sapiens GN=UGT1A4 PE=1 SV=1 - [UD14_HUMAN]	3.34E-04	-5.3717	-2.8417	1.25E-02	-2.5112	-2.8066
3_8	P19224	UDP-glucuronosyltransferase 1-5 OS=Homo sapiens GN=UGT1A6 PE=1 SV=2 - [UD16_HUMAN]	3.33E-04	-5.3891	-2.8261	2.09E-02	-2.2707	-2.0015
3_8	O60656	UDP-glucuronosyltransferase 1-9 OS=Homo sapiens GN=UGT1A9 PE=1 SV=1 - [UD19_HUMAN]	3.24E-04	-5.4205	-2.8416	1.28E-02	-2.4892	-2.0078
3_8	P06133	UDP-glucuronosyltransferase 2B4 OS=Homo sapiens GN=UGT2B4 PE=1 SV=2 - [UD2B4_HUMAN]	1.36E-05	-14.2817	-2.9014	4.19E-03	-3.0413	-2.9536
3_8	P16662	UDP-glucuronosyltransferase 2B7 OS=Homo sapiens GN=UGT2B7 PE=1 SV=1 - [UD2B7_HUMAN]	1.07E-05	-15.6905	-2.8565	1.28E-03	-3.6440	-2.8754
3_8	O94832	Unconventional myosin-Id OS=Homo sapiens GN=MYO1D PE=1 SV=2 - [MYO1D_HUMAN]	1.17E-03	3.8490	2.6680	1.47E-02	2.4275	2.4170
3_8	P09327	Villin-1 OS=Homo sapiens GN=VIL1 PE=1 SV=4 - [VILI_HUMAN]	3.59E-05	6.6911	2.7640	2.36E-06	8.5474	3.6394
3_9	Q04917	14-3-3 protein eta OS=Homo sapiens GN=YWHAH PE=1 SV=4 - [1433F_HUMAN]	7.69E-04	5.1191	3.1114	3.52E-04	4.8172	3.5304
3_9	O14756	17-beta-hydroxysteroid dehydrogenase type 6 OS=Homo sapiens GN=HSD17B6 PE=1 SV=1 - [HV17B6_HUMAN]	4.92E-05	-14.8936	-2.8892	1.98E-04	-5.3332	-3.2054
3_9	P80404	4-aminobutyrate aminotransferase, mitochondrial OS=Homo sapiens GN=ABAT PE=1 SV=3 - [GABT_HUMAN]	1.03E-03	-4.7390	-2.8685	5.75E-03	-3.0412	-3.4280

Fig. 7 continued

3_9	P32754	4-hydroxyphenylpyruvate dioxygenase OS=Homo sapiens GN=HPD PE=1 SV=2 - /HPPD_HUMAN/	7.84E-05	-12.9628	-2.9576	4.30E-04	-4.6765	-4.0978
3_9	P17858	6-phosphofructokinase, liver type OS=Homo sapiens GN=PFKL PE=1 SV=6 - /K6PL_HUMAN/	2.49E-04	6.0097	2.8732	2.29E-03	3.5852	2.5825
3_9	P24752	Acetyl-CoA acetyltransferase, mitochondrial OS=Homo sapiens GN=ACAT1 PE=1 SV=1 - /THIL_HUMAN/	1.71E-03	-4.0808	-2.9392	1.76E-04	-5.4754	-3.5699
3_9	P68133	Actin, alpha skeletal muscle OS=Homo sapiens GN=ACTA1 PE=1 SV=1 - /ACTS_HUMAN/	1.17E-02	-2.7904	-3.0521	8.60E-03	-2.8215	-5.3557
3_9	Q08AH3	Acyl-coenzyme A synthetase ACSM2A, mitochondrial OS=Homo sapiens GN=ACSM2A PE=1 SV=2 - /ACS2A_HUMAN/	5.70E-04	-5.4960	-2.8194	1.38E-02	-2.5891	-3.6690
3_9	Q6ICK6	Acyl-coenzyme A synthetase ACSM2B, mitochondrial OS=Homo sapiens GN=ACSM2B PE=1 SV=2 - /ACS2B_HUMAN/	7.99E-05	-12.8526	-2.8202	2.50E-03	-3.5317	-3.7082
3_9	P24298	Alanine aminotransferase 1 OS=Homo sapiens GN=GPT PE=1 SV=3 - /ALAT1_HUMAN/	5.85E-04	-5.4824	-2.6800	7.68E-03	-2.8831	-2.0078
3_9	P08319	Alcohol dehydrogenase 4 OS=Homo sapiens GN=ADH4 PE=1 SV=5 - /ADH4_HUMAN/	9.13E-05	-11.2379	-2.8303	7.31E-03	-2.9109	-3.8151
3_9	Q06278	Aldehyde oxidase OS=Homo sapiens GN=AOX1 PE=2 SV=2 - /ADO_HUMAN/	9.19E-05	-10.7701	-2.7162	1.10E-02	-2.7026	-2.4672
3_9	P21397	Amine oxidase [flavin-containing] A OS=Homo sapiens GN=MAOA PE=1 SV=1 - /AOFA_HUMAN/	6.49E-05	-13.7361	-2.8433	1.12E-02	-2.6901	-2.3906
3_9	Q03154	Aminoacylase-1 OS=Homo sapiens GN=ACY1 PE=1 SV=1 - /ACY1_HUMAN/	1.55E-03	-4.2593	-2.9365	3.30E-05	-6.9469	-3.3608
3_9	P27216	Annexin A13 OS=Homo sapiens GN=ANXA13 PE=1 SV=3 - /ANX13_HUMAN/	4.50E-05	15.3326	2.9618	4.29E-04	4.6796	3.3431
3_9	O95994	Anterior gradient protein 2 homolog OS=Homo sapiens GN=AGR2 PE=1 SV=1 - /AGR2_HUMAN/	2.21E-05	17.4246	3.1376	4.66E-06	9.0460	3.9199
3_9	O95831	Apoptosis-inducing factor 1, mitochondrial OS=Homo sapiens GN=AIFM1 PE=1 SV=1 - /AIFM1_HUMAN/	8.95E-03	-2.9581	-2.8474	6.10E-05	-6.3768	-3.8056
3_9	P05089	Arginase-1 OS=Homo sapiens GN=ARG1 PE=1 SV=2 - /ARGI1_HUMAN/	5.72E-05	-14.4515	-2.9788	2.63E-04	-5.0927	-4.3292
3_9	P22760	Arylacetamide deacetylase OS=Homo sapiens GN=AADAC PE=1 SV=5 - /AAAD_HUMAN/	3.09E-05	-16.1155	-2.7673	4.53E-05	-6.6513	-2.8640
3_9	Q9BXN1	Asporin OS=Homo sapiens GN=ASPN PE=1 SV=2 - /ASPN_HUMAN/	7.03E-04	5.2988	3.0403	1.40E-02	2.5839	2.9255
3_9	P16278	Beta-galactosidase OS=Homo sapiens GN=GLB1 PE=1 SV=2 - /BGAL_HUMAN/	5.88E-03	-3.1448	-2.7926	1.41E-03	-3.8895	-2.2650
3_9	Q93088	Betaine--homocysteine S-methyltransferase 1 OS=Homo sapiens GN=BHMT PE=1 SV=2 - /BHMT1_HUMAN/	3.01E-03	-3.6877	-2.9078	3.83E-02	-2.0647	-3.2794
3_9	P21810	Biglycan OS=Homo sapiens GN=BGN PE=1 SV=2 - /PGS1_HUMAN/	1.63E-03	4.1688	3.1510	6.07E-06	8.7987	5.5185
3_9	Q9Y2P5	Bile acyl-CoA synthetase OS=Homo sapiens GN=SLC27A5 PE=1 SV=1 - /S27A5_HUMAN/	2.83E-03	-3.7096	-2.6951	4.12E-03	-3.2268	-2.5061
3_9	Q06520	Bile salt sulfotransferase OS=Homo sapiens GN=SULT2A1 PE=1 SV=3 - /ST2A1_HUMAN/	5.78E-05	-14.3652	-2.9030	1.81E-03	-3.7370	-2.8466
3_9	P11586	C-1-tetrahydrofolate synthase, cytoplasmic OS=Homo sapiens GN=MTHFD1 PE=1 SV=3 - /C1TC_HUMAN/	7.77E-04	-5.0869	-2.8294	9.46E-04	-4.1147	-3.8644
3_9	P17655	Calpain-2 catalytic subunit OS=Homo sapiens GN=CAPN2 PE=1 SV=6 - /CAN2_HUMAN/	3.33E-05	15.7356	2.9337	1.79E-04	5.4397	3.1575
3_9	P23786	Carnitine O-palmitoyltransferase 2, mitochondrial OS=Homo sapiens GN=CPT2 PE=1 SV=2 - /CPT2_HUMAN/	7.92E-04	-5.0496	-2.8192	2.29E-03	-3.5883	-2.1909
3_9	P35221	Catenin alpha-1 OS=Homo sapiens GN=CTNNA1 PE=1 SV=1 - /CTNA1_HUMAN/	1.43E-03	4.3955	2.8648	6.25E-04	4.4009	3.3156
3_9	P35222	Catenin beta-1 OS=Homo sapiens GN=CTNNB1 PE=1 SV=1 - /CTNB1_HUMAN/	7.44E-04	5.1915	2.8628	6.20E-03	2.9997	2.3529
3_9	Q9UBR2	Cathepsin Z OS=Homo sapiens GN=CTSZ PE=1 SV=1 - /CATZ_HUMAN/	1.71E-03	-4.0930	-2.9318	6.34E-06	-8.6987	-2.4169
3_9	P12277	Creatine kinase B-type OS=Homo sapiens GN=CKB PE=1 SV=1 - /KCRB_HUMAN/	4.52E-05	15.3291	2.9996	2.35E-03	3.5718	2.6691
3_9	P12532	Creatine kinase U-type, mitochondrial OS=Homo sapiens GN=CKMT1A PE=1 SV=1 - /KCRU_HUMAN/	2.89E-05	16.3138	3.0081	3.90E-04	4.7443	2.2888
3_9	Q86YP6	Cullin-associated NEDD8-dissociated protein 1 OS=Homo sapiens GN=CAND1 PE=1 SV=2 - /CAND1_HUMAN/	1.37E-04	7.0274	2.8567	5.52E-04	4.4964	2.2739
3_9	P11509	Cytochrome P450 2A6 OS=Homo sapiens GN=CYP2A6 PE=1 SV=3 - /CP2A6_HUMAN/	6.79E-04	-5.3604	-2.8057	4.33E-03	-3.1991	-2.8754

Fig. 7 continued

3_9	P11712	Cytochrome P450 2C9 OS=Homo sapiens GN=CYP2C9 PE=1 SV=3 - [CP2C9_HUMAN]	8.66E-05	-12.1941	-2.7039	8.55E-03	-2.8247	-2.1275
3_9	P10635	Cytochrome P450 2D6 OS=Homo sapiens GN=CYP2D6 PE=1 SV=2 - [CP2D6_HUMAN]	2.49E-03	-3.7456	-2.6731	3.89E-03	-3.2569	-2.1385
3_9	Q14204	Cytoplasmic dynein 1 heavy chain 1 OS=Homo sapiens GN=DYNC1H1 PE=1 SV=5 - [DYHC1_HUMAN]	1.48E-02	2.7199	2.7291	3.02E-03	3.4068	3.2759
3_9	O75891	Cytosolic 10-formyltetrahydrofolate dehydrogenase OS=Homo sapiens GN=ALDH1L1 PE=1 SV=2 - [AL1L1_HUMAN]	9.29E-05	-10.0851	-2.8507	2.91E-02	-2.1987	-3.8154
3_9	Q02338	D-beta-hydroxybutyrate dehydrogenase, mitochondrial OS=Homo sapiens GN=BDH1 PE=1 SV=3 - [BDH_HUMAN]	4.56E-05	-15.3212	-2.8436	2.88E-05	-7.0629	-2.5424
3_9	P07585	Decorin OS=Homo sapiens GN=DCN PE=1 SV=1 - [PGS2_HUMAN]	1.76E-03	4.0531	3.0320	2.61E-03	3.5051	3.5142
3_9	P30038	Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial OS=Homo sapiens GN=ALDH4A1 PE=1 SV=3 - [AL4A1_HUMAN]	6.62E-05	-13.7022	-2.9501	5.88E-04	-4.4517	-3.7648
3_9	P09417	Dihydropteridine reductase OS=Homo sapiens GN=QDPR PE=1 SV=2 - [DHPR_HUMAN]	3.85E-05	-15.5209	-2.8151	7.09E-04	-4.3148	-2.2905
3_9	Q16555	Dihydropyrimidinase-related protein 2 OS=Homo sapiens GN=DPYSL2 PE=1 SV=1 - [DPYL2_HUMAN]	3.13E-03	3.6758	2.9514	1.27E-04	5.7493	3.5974
3_9	P31513	Dimethylaniline monooxygenase [N-oxide-forming] 3 OS=Homo sapiens GN=FMO3 PE=1 SV=5 - [FMO3_HUMAN]	5.56E-04	-5.5050	-2.8163	9.09E-04	-4.1361	-2.9344
3_9	Q9UI17	Dimethylglycine dehydrogenase, mitochondrial OS=Homo sapiens GN=DMGDH PE=1 SV=2 - [M2GD_HUMAN]	6.39E-04	-5.4111	-2.7015	2.18E-03	-3.6258	-2.0015
3_9	Q9UJU6	Drebrin-like protein OS=Homo sapiens GN=DBNL PE=1 SV=1 - [DBNL_HUMAN]	1.70E-02	2.6065	2.8073	3.11E-03	3.3916	2.0327
3_9	O75356	Ectonucleoside triphosphate diphosphohydrolase 5 OS=Homo sapiens GN=ENTPD5 PE=1 SV=1 - [ENTP5_HUMAN]	4.85E-04	-5.5849	-2.7192	1.00E-02	-2.7447	-2.1777
3_9	O75521	Enoyl-CoA delta isomerase 2, mitochondrial OS=Homo sapiens GN=ECI2 PE=1 SV=4 - [ECI2_HUMAN]	8.91E-05	-12.0565	-2.6864	1.08E-03	-4.0499	-2.5424
3_9	Q9BSJ8	Extended synaptotagmin-1 OS=Homo sapiens GN=ESYT1 PE=1 SV=1 - [ESYT1_HUMAN]	5.22E-04	-5.5468	-2.7140	4.72E-04	-4.5977	-2.1275
3_9	P08294	Extracellular superoxide dismutase [Cu-Zn] OS=Homo sapiens GN=SOD3 PE=1 SV=2 - [SODE_HUMAN]	1.00E-03	4.7596	2.7472	1.76E-03	3.7493	2.2501
3_9	P15311	Ezrin OS=Homo sapiens GN=EZR PE=1 SV=4 - [EZRI_HUMAN]	2.33E-03	3.7757	3.0292	6.31E-05	6.2929	3.9079
3_9	O95954	Formimidoyltransferase-cyclodeaminase OS=Homo sapiens GN=FTCD PE=1 SV=2 - [FTCD_HUMAN]	5.04E-05	-14.7716	-2.8579	6.33E-03	-2.9921	-2.8931
3_9	O95479	GDH/6PGL endoplasmic bifunctional protein OS=Homo sapiens GN=H6PD PE=1 SV=2 - [G6PE_HUMAN]	2.79E-02	-2.2679	-2.8183	4.81E-04	-4.5819	-2.6130
3_9	P11413	Glucose-6-phosphate 1-dehydrogenase OS=Homo sapiens GN=G6PD PE=1 SV=4 - [G6PD_HUMAN]	7.85E-04	5.0683	2.9598	1.82E-03	3.7340	3.5061
3_9	Q06210	Glutamine--fructose-6-phosphate aminotransferase [isomerizing] 1 OS=Homo sapiens GN=GFPT1 PE=1 SV=3 - [GFPT1_HUMAN]	1.79E-04	6.5199	2.8408	1.08E-02	2.7130	2.7338
3_9	P18283	Glutathione peroxidase 2 OS=Homo sapiens GN=GPX2 PE=1 SV=3 - [GPX2_HUMAN]	7.22E-04	5.2421	2.9965	5.00E-04	4.5584	2.6529
3_9	P06737	Glycogen phosphorylase, liver form OS=Homo sapiens GN=PYGL PE=1 SV=4 - [PYGL_HUMAN]	1.68E-05	-18.0733	-2.9005	1.18E-03	-4.0002	-3.5535
3_9	P62879	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2 OS=Homo sapiens GN=GNB2 PE=1 SV=3 - [GBB2_HUMAN]	3.40E-03	3.5665	2.9336	5.41E-03	3.0775	2.3418
3_9	Q13151	Heterogeneous nuclear ribonucleoprotein A0 OS=Homo sapiens GN=HNRNPA0 PE=1 SV=1 - [ROA0_HUMAN]	1.01E-04	7.5655	2.9579	3.96E-06	9.8133	2.3251
3_9	Q1KMD3	Heterogeneous nuclear ribonucleoprotein U-like protein 2 OS=Homo sapiens GN=HNRNPUL2 PE=1 SV=1 - [HNRL2_HUMAN]	1.80E-03	4.0212	3.0612	8.97E-05	6.0947	2.9008
3_9	Q9UJM8	Hydroxyacid oxidase 1 OS=Homo sapiens GN=HAO1 PE=1 SV=1 - [HAOX1_HUMAN]	2.81E-05	-16.4212	-2.8892	2.67E-05	-7.1383	-4.1274
3_9	P35914	Hydroxymethylglutaryl-CoA lyase, mitochondrial OS=Homo sapiens GN=HMGCL PE=1 SV=2 - [HMGCL_HUMAN]	3.60E-03	-3.5249	-2.7459	5.22E-03	-3.0984	-2.1275
3_9	P54868	Hydroxymethylglutaryl-CoA synthase, mitochondrial OS=Homo sapiens GN=HMGCS2 PE=1 SV=1 - [HMCS2_HUMAN]	3.30E-03	-3.6315	-2.9618	1.40E-04	-5.6831	-4.5313
3_9	Q96AB3	Isochorismatase domain-containing protein 2, mitochondrial OS=Homo sapiens GN=ISOC2 PE=1 SV=1 - [ISOC2_HUMAN]	2.16E-02	-2.4284	-2.7266	2.05E-03	-3.6824	-2.3297
3_9	P08727	Keratin, type I cytoskeletal 19 OS=Homo sapiens GN=KRT19 PE=1 SV=4 - [K1C19_HUMAN]	5.09E-04	5.5682	3.0791	4.31E-06	9.3204	5.2600
3_9	P08729	Keratin, type II cytoskeletal 7 OS=Homo sapiens GN=KRT7 PE=1 SV=5 - [K2C7_HUMAN]	2.72E-04	5.9040	2.9851	8.83E-05	6.1136	3.7312

Fig. 7 continued

3 9	P33121	Long-chain-fatty-acid--CoA ligase 1 OS=Homo sapiens GN=ACSL1 PE=1 SV=1 - [ACSL1_HUMAN]	8.61E-05	-12.2433	-2.8373	3.42E-03	-3.3330	-3.3292
3 9	P10253	Lysosomal alpha-glucosidase OS=Homo sapiens GN=GAA PE=1 SV=4 - [LYAG_HUMAN]	1.15E-02	-2.7949	-2.8273	1.53E-02	-2.5339	-2.8754
3 9	P10619	Lysosomal protective protein OS=Homo sapiens GN=CTSA PE=1 SV=2 - [PPGB_HUMAN]	3.97E-06	-21.0581	-2.8071	3.82E-05	-6.8255	-2.0078
3 9	Q9H8H3	Methyltransferase-like protein 7A OS=Homo sapiens GN=METTL7A PE=1 SV=1 - [ME7TA_HUMAN]	4.47E-05	-15.3364	-2.8687	8.84E-05	-6.1096	-2.1365
3 9	P53083	Microfibril-associated glycoprotein 4 OS=Homo sapiens GN=MFAP4 PE=1 SV=2 - [MFAP4_HUMAN]	1.17E-03	4.6606	2.9582	4.15E-04	4.7021	3.3874
3 9	P10620	Microsomal glutathione S-transferase 1 OS=Homo sapiens GN=MGST1 PE=1 SV=1 - [MGST1_HUMAN]	1.78E-03	-4.0351	-2.9236	6.04E-04	-4.4212	-2.2794
3 9	P55157	Microsomal triglyceride transfer protein large subunit OS=Homo sapiens GN=MTTP PE=1 SV=1 - [MTP_HUMAN]	6.95E-05	-13.6236	-2.7434	4.00E-04	-4.7269	-2.8913
3 9	P20774	Mimecan OS=Homo sapiens GN=OGN PE=1 SV=1 - [MIME_HUMAN]	9.35E-05	8.0640	3.0821	7.68E-05	6.2269	4.4171
3 9	Q9HC84	Mucin-5B OS=Homo sapiens GN=MUC5B PE=1 SV=3 - [MUC5B_HUMAN]	1.83E-05	17.8357	2.9423	8.10E-04	4.2058	3.8016
3 9	Q72406	Myosin-14 OS=Homo sapiens GN=MYH14 PE=1 SV=2 - [MYH14_HUMAN]	1.14E-03	4.6815	2.9542	1.35E-03	3.9225	3.3017
3 9	O94760	N(G),N(G)-dimethylarginine dimethylaminohydrolase 1 OS=Homo sapiens GN=DDAH1 PE=1 SV=3 - [DDAH1_HUMAN]	1.72E-03	4.0815	2.9141	2.22E-04	5.1901	2.5246
3 9	Q4G0N4	NAD kinase domain-containing protein 1 OS=Homo sapiens GN=NADKD1 PE=1 SV=2 - [NAKD1_HUMAN]	1.92E-05	-17.6699	-2.8105	1.62E-04	-5.5697	-2.8644
3 9	Q13423	NAD(P) transhydrogenase, mitochondrial OS=Homo sapiens GN=NNT PE=1 SV=3 - [NNTM_HUMAN]	5.12E-04	-5.5640	-2.7910	4.42E-03	-3.1859	-2.7758
3 9	P15559	NAD(P)H dehydrogenase [quinone] 1 OS=Homo sapiens GN=NQO1 PE=1 SV=1 - [NQO1_HUMAN]	1.03E-04	7.4250	3.0085	3.59E-03	3.3057	2.8346
3 9	P16435	NADPH--cytochrome P450 reductase OS=Homo sapiens GN=POR PE=1 SV=2 - [NCPR_HUMAN]	2.33E-04	-6.1025	-2.8486	5.69E-04	-4.4774	-3.6130
3 9	Q9677A1	Niban-like protein 1 OS=Homo sapiens GN=FAM129B PE=1 SV=3 - [NIBL1_HUMAN]	1.25E-03	4.6003	2.7488	6.75E-03	2.9695	2.1683
3 9	P40261	Nicotinamide N-methyltransferase OS=Homo sapiens GN=NNMT PE=1 SV=1 - [NNMT_HUMAN]	6.54E-05	-13.7154	-2.9062	6.72E-03	-2.9623	-2.1777
3 9	P00480	Ornithine carbamoyltransferase, mitochondrial OS=Homo sapiens GN=OTC PE=1 SV=3 - [OTC_HUMAN]	4.04E-05	-15.4513	-2.9239	1.84E-05	-7.5783	-4.0449
3 9	Q13162	Peroxiredoxin-4 OS=Homo sapiens GN=PRDX4 PE=1 SV=1 - [PRDX4_HUMAN]	1.10E-03	-4.7103	-2.8745	3.35E-04	-4.8766	-2.0015
3 9	Q15067	Peroxisomal acyl-coenzyme A oxidase 1 OS=Homo sapiens GN=ACOX1 PE=1 SV=3 - [ACOX1_HUMAN]	9.08E-05	-11.2872	-2.6944	4.56E-03	-3.1654	-2.9982
3 9	Q9Y424	Peroxisomal acyl-coenzyme A oxidase 2 OS=Homo sapiens GN=ACOX2 PE=1 SV=1 - [ACOX2_HUMAN]	1.40E-02	-2.7365	-2.6239	2.19E-02	-2.3496	-2.2794
3 9	Q08426	Peroxisomal bifunctional enzyme OS=Homo sapiens GN=EHHADH PE=1 SV=3 - [ECHP_HUMAN]	6.15E-05	-14.0638	-2.9060	1.26E-05	-7.8597	-5.0344
3 9	Q9P0Z9	Peroxisomal sarcosine oxidase OS=Homo sapiens GN=PIPOX PE=2 SV=2 - [SOX_HUMAN]	7.47E-05	-13.2807	-2.8545	8.31E-04	-4.1917	-2.8754
3 9	Q00325	Phosphate carrier protein, mitochondrial OS=Homo sapiens GN=SLC25A3 PE=1 SV=2 - [MPCP_HUMAN]	5.96E-04	-5.4693	-2.9181	2.99E-03	-3.4129	-2.4672
3 9	Q14651	Plastin-1 OS=Homo sapiens GN=PLS1 PE=1 SV=2 - [PLS1_HUMAN]	1.38E-04	7.0223	2.9693	3.54E-03	3.3114	2.7130
3 9	Q6NZI2	Polymerase I and transcript release factor OS=Homo sapiens GN=PTRF PE=1 SV=1 - [PTRF_HUMAN]	3.74E-03	3.4929	2.8027	1.11E-02	2.6983	2.3674
3 9	P17844	Probable ATP-dependent RNA helicase DDX5 OS=Homo sapiens GN=DDX5 PE=1 SV=1 - [DDX5_HUMAN]	9.61E-04	4.7870	2.9867	4.89E-03	3.1311	3.2097
3 9	P05165	Propionyl-CoA carboxylase beta chain, mitochondrial OS=Homo sapiens GN=PCCB PE=1 SV=3 - [PCCB_HUMAN]	8.12E-03	-3.0306	-2.7284	3.54E-03	-3.3112	-2.3297
3 9	Q9BPW8	Protein NipSnap homolog 1 OS=Homo sapiens GN=NIPSNAP1 PE=1 SV=1 - [NIPS1_HUMAN]	4.72E-05	-15.1394	-2.8440	9.26E-05	-6.0027	-3.0560
3 9	P55786	Puromycin-sensitive aminopeptidase OS=Homo sapiens GN=NPEPPS PE=1 SV=2 - [PSA_HUMAN]	1.64E-03	4.1599	2.9162	5.49E-05	6.5038	2.6078
3 9	O43143	Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15 OS=Homo sapiens GN=DHX15 PE=1 SV=2 - [DHX15_HUMAN]	8.06E-04	5.0073	2.8379	8.29E-04	4.1938	2.0685
3 9	Q9NVS9	Pyridoxine-5-phosphate oxidase OS=Homo sapiens GN=PNPO PE=1 SV=1 - [PNPO_HUMAN]	6.34E-04	-5.4235	-2.8728	2.03E-05	-7.4728	-2.1274

Fig. 7 continued

3_9	P11498	Pyruvate carboxylase, mitochondrial OS=Homo sapiens GN=PC PE=1 SV=2 - [PYC_HUMAN]	7.24E-05	-13.3912	-2.8168	8.45E-04	-4.1811	-3.9982
3_9	P30613	Pyruvate kinase isozymes R/L OS=Homo sapiens GN=PKLR PE=1 SV=2 - [KPYR_HUMAN]	1.78E-05	-17.8985	-2.8740	9.97E-04	-4.0902	-3.4495
3_9	P31150	Rab GDP dissociation inhibitor alpha OS=Homo sapiens GN=GDI1 PE=1 SV=2 - [GDIA_HUMAN]	1.21E-03	4.6296	2.9283	2.52E-03	3.5286	3.2951
3_9	P46940	Ras GTPase-activating-like protein IQGAP1 OS=Homo sapiens GN=IQGAP1 PE=1 SV=1 - [IQGA1_HUMAN]	8.07E-04	5.0021	2.9168	1.17E-03	4.0063	4.6006
3_9	O94788	Retinal dehydrogenase 2 OS=Homo sapiens GN=ALDH1A2 PE=1 SV=3 - [AL1A2_HUMAN]	1.02E-03	4.7414	2.8083	8.31E-03	2.8383	2.0931
3_9	P02753	Retinol-binding protein 4 OS=Homo sapiens GN=RBP4 PE=1 SV=3 - [RET4_HUMAN]	3.16E-03	-3.6718	-2.8475	1.80E-04	-5.4327	-2.2794
3_9	P52758	Ribonuclease UK114 OS=Homo sapiens GN=HRSP12 PE=1 SV=1 - [UK114_HUMAN]	3.50E-03	-3.5538	-2.9999	3.97E-04	-4.7343	-3.1385
3_9	Q8NBX0	Saccharopine dehydrogenase-like oxidoreductase OS=Homo sapiens GN=SCCPDH PE=1 SV=1 - [SCPDL_HUMAN]	4.03E-05	-15.4555	-2.9469	6.08E-05	-6.3913	-2.5927
3_9	Q00266	S-adenosylmethionine synthase isoform type-1 OS=Homo sapiens GN=MAT1A PE=1 SV=2 - [METK1_HUMAN]	7.76E-05	-13.1193	-2.8581	3.35E-03	-3.3468	-2.7125
3_9	P34896	Serine hydroxymethyltransferase, cytosolic OS=Homo sapiens GN=SHMT1 PE=1 SV=1 - [GLYC_HUMAN]	9.23E-03	-2.9280	-2.8267	4.71E-05	-6.6332	-2.9536
3_9	P21549	Serine--pyruvate aminotransferase OS=Homo sapiens GN=AGXT PE=1 SV=1 - [SPYA_HUMAN]	3.15E-05	-16.0904	-3.0303	1.39E-04	-5.6859	-5.2723
3_9	P45954	Short/branched chain specific acyl-CoA dehydrogenase, mitochondrial OS=Homo sapiens GN=ACADSB PE=1 SV=1 - [ACDSB_HUMAN]	2.50E-04	-6.0072	-2.8646	1.80E-04	-5.4241	-3.1275
3_9	Q9NR45	Sialic acid synthase OS=Homo sapiens GN=NANS PE=1 SV=2 - [SIAS_HUMAN]	3.40E-03	3.5871	2.9690	3.79E-06	10.2745	2.3935
3_9	Q9H9B4	Sideroflexin-1 OS=Homo sapiens GN=SFXN1 PE=1 SV=4 - [SFXN1_HUMAN]	4.67E-05	-15.2902	-2.8292	9.83E-06	-7.9625	-2.1777
3_9	Q14247	Src substrate cortactin OS=Homo sapiens GN=CTTN PE=1 SV=2 - [SRC8_HUMAN]	7.64E-04	5.1265	2.8312	5.40E-03	3.0784	2.1006
3_9	Q00218	Sterol 26-hydroxylase, mitochondrial OS=Homo sapiens GN=CYP27A1 PE=1 SV=1 - [CP27A_HUMAN]	4.59E-04	-5.6078	-2.7775	2.31E-03	-3.5792	-2.0078
3_9	P51649	Succinate-semialdehyde dehydrogenase, mitochondrial OS=Homo sapiens GN=ALDH5A1 PE=1 SV=2 - [SSDH_HUMAN]	6.40E-04	-5.4104	-2.7413	2.32E-03	-3.5768	-2.4672
3_9	Q13263	Transcription intermediary factor 1-beta OS=Homo sapiens GN=TRIM28 PE=1 SV=5 - [TIF1B_HUMAN]	2.36E-05	17.0870	2.8980	6.85E-06	8.5508	2.6278
3_9	P22310	UDP-glucuronosyltransferase 1-4 OS=Homo sapiens GN=UGT1A4 PE=1 SV=1 - [UD14_HUMAN]	6.71E-04	-5.3717	-2.8417	1.61E-02	-2.5112	-2.8056
3_9	P19224	UDP-glucuronosyltransferase 1-6 OS=Homo sapiens GN=UGT1A6 PE=1 SV=2 - [UD16_HUMAN]	6.60E-04	-5.3891	-2.8261	2.54E-02	-2.2707	-2.0015
3_9	O60656	UDP-glucuronosyltransferase 1-9 OS=Homo sapiens GN=UGT1A9 PE=1 SV=1 - [UD19_HUMAN]	6.35E-04	-5.4205	-2.8416	1.64E-02	-2.4992	-2.0078
3_9	P06133	UDP-glucuronosyltransferase 2B4 OS=Homo sapiens GN=UGT2B4 PE=1 SV=2 - [UD2B4_HUMAN]	5.94E-05	-14.2817	-2.9014	5.74E-03	-3.0413	-2.9536
3_9	P16662	UDP-glucuronosyltransferase 2B7 OS=Homo sapiens GN=UGT2B7 PE=1 SV=1 - [UD2B7_HUMAN]	7.66E-04	-5.1244	-2.8565	3.21E-03	-3.3743	-2.8754
3_9	O00159	Unconventional myosin-Ic OS=Homo sapiens GN=MYO1C PE=1 SV=4 - [MYO1C_HUMAN]	2.71E-02	2.2885	2.8796	2.14E-02	2.3608	2.2377
3_9	P09327	Villin-1 OS=Homo sapiens GN=VIL1 PE=1 SV=4 - [VILI_HUMAN]	1.33E-04	7.0508	2.8983	1.16E-04	5.8302	2.8579
3_9	P02774	Vitamin D-binding protein OS=Homo sapiens GN=GC PE=1 SV=1 - [VTDB_HUMAN]	6.66E-03	3.0938	2.8817	3.18E-02	2.1534	2.2696
4_5	Q01813	6-phosphofructokinase type C OS=Homo sapiens GN=PFKP PE=1 SV=2 - [K6PP_HUMAN]	1.04E-02	2.6188	2.7049	1.34E-02	2.4498	2.0637
4_5	P02649	Apolipoprotein E OS=Homo sapiens GN=APOE PE=1 SV=1 - [APOE_HUMAN]	3.93E-02	-2.0653	-2.7900	3.48E-02	-2.0212	-3.3830
4_5	P35222	Catenin beta-1 OS=Homo sapiens GN=CTNNB1 PE=1 SV=1 - [CTNB1_HUMAN]	3.50E-02	2.0947	2.7214	1.81E-02	2.3216	2.2357
4_5	P07859	Ig gamma-2 chain C region OS=Homo sapiens GN=IGHG2 PE=1 SV=2 - [IGHG2_HUMAN]	2.35E-03	-3.5002	-2.9074	6.24E-03	-2.7905	-3.7147
4_5	P04350	Tubulin beta-4A chain OS=Homo sapiens GN=TUBB4A PE=1 SV=2 - [TBB4A_HUMAN]	1.74E-02	2.3130	3.0176	6.39E-03	2.7792	5.9854
4_6	P04217	Alpha-1B-glycoprotein OS=Homo sapiens GN=A1BG PE=1 SV=4 - [A1BG_HUMAN]	4.13E-04	5.0892	3.1231	1.25E-02	2.4940	2.8011

Fig. 7 continued

4_6	P15144	Aminopeptidase N OS=Homo sapiens GN=ANPEP PE=1 SV=4 - [AMPN_HUMAN]	2.52E-03	-3.6438	-2.8700	7.15E-03	-2.7712	-3.0683
4_6	P12532	Creatine kinase U-type, mitochondrial OS=Homo sapiens GN=CKMT1A PE=1 SV=1 - [KCRU_HUMAN]	1.80E-03	3.7681	2.8880	5.29E-03	2.9246	2.1408
4_6	P30038	Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial OS=Homo sapiens GN=ALDH4A1 PE=1 SV=3 - [AL4A1_HUMAN]	2.17E-03	-3.6965	-2.8111	5.83E-04	-4.1390	-2.0675
4_6	Q14195	Dihydropyrimidinase-related protein 3 OS=Homo sapiens GN=DPYSL3 PE=1 SV=1 - [DPYL3_HUMAN]	2.27E-02	2.2760	3.0468	8.09E-03	2.7035	2.8564
4_6	P07099	Epoxide hydrolase 1 OS=Homo sapiens GN=EPHX1 PE=1 SV=1 - [HYEP_HUMAN]	1.74E-02	-2.4626	-2.7365	5.06E-02	-1.8589	-2.1297
4_6	Q13630	GDP-L-fucose synthase OS=Homo sapiens GN=FSTA3 PE=1 SV=1 - [FCL_HUMAN]	1.86E-02	2.4198	3.0881	2.32E-02	2.1901	2.0247
4_6	Q12931	Heat shock protein 75 kDa, mitochondrial OS=Homo sapiens GN=TRAP1 PE=1 SV=3 - [TRAP1_HUMAN]	1.66E-02	-2.4907	-2.9151	2.79E-03	-3.2510	-2.3830
4_6	P01871	Ig mu chain C region OS=Homo sapiens GN=IGHM PE=1 SV=3 - [IGHM_HUMAN]	4.90E-02	2.0338	2.8266	1.74E-02	2.3349	2.2173
4_6	P19827	Inter-alpha-trypsin inhibitor heavy chain H1 OS=Homo sapiens GN=ITIH1 PE=1 SV=3 - [ITIH1_HUMAN]	9.60E-04	4.0301	3.0907	9.06E-03	2.6536	3.0247
4_6	P98088	Mucin-5AC (Fragments) OS=Homo sapiens GN=MUC5AC PE=1 SV=3 - [MUC5A_HUMAN]	9.13E-03	2.7770	2.8309	4.38E-02	1.9316	3.6767
4_6	P01833	Polymeric immunoglobulin receptor OS=Homo sapiens GN=PIGR PE=1 SV=4 - [PIGR_HUMAN]	1.81E-02	2.4388	3.0703	2.39E-03	3.3339	3.4363
4_6	P29590	Protein PML OS=Homo sapiens GN=PML PE=1 SV=3 - [PML_HUMAN]	2.77E-02	2.1349	2.7478	2.91E-02	2.0893	2.6767
4_6	P00734	Prothrombin OS=Homo sapiens GN=F2 PE=1 SV=2 - [THRB_HUMAN]	3.83E-02	2.0807	3.0942	2.37E-02	2.1805	2.2173
4_6	P24821	Tenascin OS=Homo sapiens GN=TNC PE=1 SV=3 - [TENA_HUMAN]	4.73E-02	-2.0461	-2.7053	1.94E-02	-2.2830	-2.6322
4_7	O00468	Agrin OS=Homo sapiens GN=AGRN PE=1 SV=4 - [AGRIN_HUMAN]	4.84E-02	-2.0425	-2.6120	2.44E-02	-2.1439	-2.5021
4_7	P27338	Amine oxidase [flavin-containing] B OS=Homo sapiens GN=MAOB PE=1 SV=3 - [AOFB_HUMAN]	2.01E-06	-20.0177	-2.8071	4.01E-04	-4.2963	-2.9010
4_7	P31939	Bifunctional purine biosynthesis protein PURH OS=Homo sapiens GN=ATIC PE=1 SV=3 - [PUR9_HUMAN]	3.78E-03	-3.4019	-2.8384	4.79E-03	-2.9204	-3.3386
4_7	P06731	Carcinoembryonic antigen-related cell adhesion molecule 5 OS=Homo sapiens GN=CEACAM5 PE=1 SV=3 - [CEAM5_HUMAN]	9.10E-03	2.7946	3.1781	1.74E-02	2.3221	2.0701
4_7	P30038	Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial OS=Homo sapiens GN=ALDH4A1 PE=1 SV=3 - [AL4A1_HUMAN]	2.81E-04	-5.6360	-2.8111	3.63E-04	-4.3501	-2.0675
4_7	P11678	Eosinophil peroxidase OS=Homo sapiens GN=EPX PE=1 SV=2 - [PERE_HUMAN]	1.81E-02	2.5237	3.1923	1.33E-02	2.4548	3.4580
4_7	P07954	Fumarate hydratase, mitochondrial OS=Homo sapiens GN=FH PE=1 SV=3 - [FUMH_HUMAN]	5.05E-03	-3.1443	-2.8612	1.01E-02	-2.5878	-2.4516
4_7	Q9UBQ7	Glyoxylate reductase/hydroxypyruvate reductase OS=Homo sapiens GN=GRHPR PE=1 SV=1 - [GRHPR_HUMAN]	2.31E-02	-2.3339	-2.8497	5.77E-03	-2.8178	-2.0042
4_7	P23141	Liver carboxylesterase 1 OS=Homo sapiens GN=CES1 PE=1 SV=2 - [EST1_HUMAN]	2.89E-02	-2.1514	-2.9022	2.51E-02	-2.1269	-2.5140
4_7	P98088	Mucin-5AC (Fragments) OS=Homo sapiens GN=MUC5AC PE=1 SV=3 - [MUC5A_HUMAN]	1.08E-02	2.7572	3.2398	2.00E-02	2.2479	4.7330
4_7	P24844	Myosin regulatory light polypeptide 9 OS=Homo sapiens GN=MYL9 PE=1 SV=4 - [MYL9_HUMAN]	1.15E-02	2.7446	2.9568	1.01E-02	2.5871	3.0701
4_7	Q7Z406	Myosin-14 OS=Homo sapiens GN=MYH14 PE=1 SV=2 - [MYH14_HUMAN]	2.82E-05	7.3945	3.1729	2.57E-03	3.2310	3.3440
4_7	O95571	Protein ETHE1, mitochondrial OS=Homo sapiens GN=ETHE1 PE=1 SV=2 - [ETHE1_HUMAN]	6.80E-03	2.9215	3.0795	4.92E-03	2.9072	2.2950
4_7	Q00257	Quinone oxidoreductase OS=Homo sapiens GN=CRYZ PE=1 SV=1 - [QOR_HUMAN]	2.83E-02	-2.1678	-2.8824	3.16E-03	-3.1257	-2.8424
4_7	P34897	Serine hydroxymethyltransferase, mitochondrial OS=Homo sapiens GN=SHMT2 PE=1 SV=3 - [GLYM_HUMAN]	5.31E-03	-3.1015	-2.8152	6.68E-03	-2.7563	-2.4826
4_7	P09493	Tropomyosin alpha-1 chain OS=Homo sapiens GN=TPM1 PE=1 SV=2 - [TPM1_HUMAN]	2.34E-03	-3.7016	-2.8161	1.19E-02	-2.4977	-2.2797
4_7	P06753	Tropomyosin alpha-3 chain OS=Homo sapiens GN=TPM3 PE=1 SV=1 - [TPM3_HUMAN]	2.02E-03	-3.7422	-2.8873	1.51E-03	-3.5217	-2.4246
4_8	P31937	3-hydroxyisobutyrate dehydrogenase, mitochondrial OS=Homo sapiens GN=HIBADH PE=1 SV=2 - [3HIDH_HUMAN]	4.39E-03	3.0228	2.7043	2.01E-02	2.2980	2.8022

Fig. 7 continued

4_8	P27338	Amine oxidase [flavin-containing] B OS=Homo sapiens GN=MAOB PE=1 SV=3 - [AOFB_HUMAN]	1.97E-05	-8.7190	-2.8071	5.49E-04	-4.1177	-2.9010
4_8	P15144	Aminopeptidase N OS=Homo sapiens GN=ANPEP PE=1 SV=4 - [AMPN_HUMAN]	1.52E-04	-5.7780	-2.8700	3.61E-03	-3.0969	-3.0683
4_8	P01019	Angiotensinogen OS=Homo sapiens GN=AGT PE=1 SV=1 - [ANGT_HUMAN]	1.86E-03	-3.7343	-2.7183	1.90E-03	-3.4629	-2.3985
4_8	Q12864	Cadherin-17 OS=Homo sapiens GN=CDH17 PE=1 SV=3 - [CAD17_HUMAN]	1.54E-04	5.7758	2.7688	2.63E-04	4.5434	3.2065
4_8	P31327	Carbamoyl-phosphate synthase [ammonia], mitochondrial OS=Homo sapiens GN=CPS1 PE=1 SV=2 - [CPSM_HUMAN]	4.52E-02	-2.0119	-2.8477	2.33E-02	-2.2218	-3.5700
4_8	P06731	Carcinoembryonic antigen-related cell adhesion molecule 5 OS=Homo sapiens GN=CEACAM5 PE=1 SV=3 - [CEAM5_HUMAN]	1.33E-05	18.8897	2.8744	4.23E-04	4.2417	2.7240
4_8	P40199	Carcinoembryonic antigen-related cell adhesion molecule 6 OS=Homo sapiens GN=CEACAM6 PE=1 SV=3 - [CEAM6_HUMAN]	9.14E-04	3.8466	2.7790	2.52E-03	3.2987	2.0866
4_8	P35222	Catenin beta-1 OS=Homo sapiens GN=CTNNB1 PE=1 SV=1 - [CTNB1_HUMAN]	3.30E-03	3.3094	2.8094	2.17E-05	6.3843	3.4997
4_8	Q99829	Copine-1 OS=Homo sapiens GN=CPNE1 PE=1 SV=1 - [CPNE1_HUMAN]	4.07E-03	3.0965	2.7256	2.52E-02	2.1762	2.2997
4_8	P12277	Creatine kinase B-type OS=Homo sapiens GN=CKB PE=1 SV=1 - [KCRB_HUMAN]	5.99E-03	2.8213	2.7880	1.78E-02	2.3613	3.4402
4_8	P30038	Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial OS=Homo sapiens GN=ALDH4A1 PE=1 SV=3 - [AL4A1_HUMAN]	3.31E-03	-3.3071	-2.8111	1.00E-02	-2.6424	-2.0675
4_8	P54886	Delta-1-pyrroline-5-carboxylate synthase OS=Homo sapiens GN=ALDH18A1 PE=1 SV=2 - [P5CS_HUMAN]	5.50E-06	23.8624	2.6907	5.26E-03	2.9129	2.6394
4_8	P15924	Desmoplakin OS=Homo sapiens GN=DSP PE=1 SV=3 - [DESP_HUMAN]	1.59E-02	2.4643	2.6089	2.65E-02	2.1512	2.1539
4_8	P58107	Epiplakin OS=Homo sapiens GN=EPPK1 PE=1 SV=2 - [EPIPL_HUMAN]	4.20E-05	6.5574	2.7065	1.50E-03	3.5929	2.4170
4_8	P27105	Erythrocyte band 7 integral membrane protein OS=Homo sapiens GN=STOM PE=1 SV=3 - [STOM_HUMAN]	4.54E-05	-6.4811	-2.8059	7.92E-05	-5.4137	-2.7822
4_8	P55060	Exportin-2 OS=Homo sapiens GN=CSE1L PE=1 SV=3 - [XPO2_HUMAN]	5.75E-05	6.2883	2.9586	3.38E-03	3.1335	2.5016
4_8	P05062	Fructose-bisphosphate aldolase B OS=Homo sapiens GN=ALDOB PE=1 SV=2 - [ALDOB_HUMAN]	2.92E-04	-5.1676	-2.9519	9.17E-03	-2.6724	-3.0615
4_8	Q06210	Glutamine--fructose-6-phosphate aminotransferase [isomerizing] 1 OS=Homo sapiens GN=GFPT1 PE=1 SV=3 - [GFPT1_HUMAN]	2.95E-05	7.1219	2.7907	3.84E-04	4.2983	3.2914
4_8	P04899	Guanine nucleotide-binding protein G(i) subunit alpha-2 OS=Homo sapiens GN=GNAI2 PE=1 SV=3 - [GNAI2_HUMAN]	2.40E-03	-3.6158	-2.7782	1.25E-02	-2.5322	-2.0675
4_8	Q92598	Heat shock protein 105 kDa OS=Homo sapiens GN=HSPH1 PE=1 SV=1 - [HS105_HUMAN]	8.70E-06	22.2078	2.8188	1.36E-04	4.9853	3.2769
4_8	P08729	Keratin, type II cytoskeletal 7 OS=Homo sapiens GN=KRT7 PE=1 SV=5 - [K2C7_HUMAN]	2.54E-02	-2.1516	-2.7941	1.63E-02	-2.3970	-2.5501
4_8	P36776	Lon protease homolog, mitochondrial OS=Homo sapiens GN=LONP1 PE=1 SV=2 - [LONM_HUMAN]	3.20E-03	3.3424	2.6863	3.69E-02	2.0286	2.0255
4_8	Q15046	Lysine--tRNA ligase OS=Homo sapiens GN=KARS PE=1 SV=3 - [SYK_HUMAN]	3.83E-03	3.1630	2.6871	1.33E-04	5.0204	2.2997
4_8	P10253	Lysosomal alpha-glucosidase OS=Homo sapiens GN=GAA PE=1 SV=4 - [LYAG_HUMAN]	4.80E-04	-4.1905	-2.8727	6.23E-03	-2.8260	-2.5112
4_8	P41218	Myeloid cell nuclear differentiation antigen OS=Homo sapiens GN=MNDA PE=1 SV=1 - [MNDA_HUMAN]	4.76E-02	-1.9654	-2.8067	1.64E-02	-2.3957	-2.4246
4_8	Q7Z406	Myosin-14 OS=Homo sapiens GN=MYH14 PE=1 SV=2 - [MYH14_HUMAN]	2.76E-04	5.3784	2.8464	4.45E-04	4.2142	4.7862
4_8	P40261	Nicotinamide N-methyltransferase OS=Homo sapiens GN=NNMT PE=1 SV=1 - [NNMT_HUMAN]	9.41E-03	-2.7581	-2.7015	6.39E-03	-2.8119	-2.5021
4_8	P52566	Rho GDP-dissociation inhibitor 2 OS=Homo sapiens GN=ARHGDIB PE=1 SV=3 - [GDIR2_HUMAN]	1.26E-02	-2.5843	-2.7592	6.26E-03	-2.8233	-2.2871
4_8	P19971	Thymidine phosphorylase OS=Homo sapiens GN=TYMP PE=1 SV=2 - [TYPH_HUMAN]	6.25E-04	-3.9793	-2.7915	2.41E-04	-4.6129	-3.0834
4_8	P15374	Ubiquitin carboxyl-terminal hydrolase isozyme L3 OS=Homo sapiens GN=UCHL3 PE=1 SV=1 - [UCHL3_HUMAN]	3.13E-04	4.8883	2.6897	1.04E-06	8.2390	2.1742
4_8	Q94832	Unconventional myosin-Id OS=Homo sapiens GN=MYO1D PE=1 SV=2 - [MYO1D_HUMAN]	7.39E-03	2.7990	2.6680	1.66E-02	2.3904	2.4170
4_8	P09327	Villin-1 OS=Homo sapiens GN=VIL1 PE=1 SV=4 - [VILI_HUMAN]	4.70E-03	2.9636	2.7640	2.22E-04	4.6507	3.6394

Fig. 7 continued

4_9	P00326	Alcohol dehydrogenase 1C OS=Homo sapiens GN=ADH1C PE=1 SV=2 - [ADH1G_HUMAN]	2.72E-05	15.0083	3.0221	4.43E-05	6.0660	3.3012
4_9	P30838	Aldehyde dehydrogenase, dimeric NADP-preferring OS=Homo sapiens GN=ALDH3A1 PE=1 SV=3 - [AL3A1_HUMAN]	7.65E-04	4.7280	2.9253	1.74E-02	2.4303	2.6514
4_9	P17516	Aldo-keto reductase family 1 member C4 OS=Homo sapiens GN=AKR1C4 PE=1 SV=3 - [AK1C4_HUMAN]	3.77E-04	5.4551	2.9851	3.32E-02	2.1013	3.3738
4_9	P27216	Annexin A13 OS=Homo sapiens GN=ANXA13 PE=1 SV=3 - [ANX13_HUMAN]	8.66E-04	4.6417	2.9618	5.72E-03	2.9806	3.3431
4_9	P04424	Argininosuccinate lyase OS=Homo sapiens GN=ASL PE=1 SV=4 - [ARLY_HUMAN]	3.35E-03	3.4940	2.9844	6.21E-03	2.9401	3.1717
4_9	P35222	Catenin beta-1 OS=Homo sapiens GN=CTNNB1 PE=1 SV=1 - [CTNB1_HUMAN]	3.10E-03	3.5665	2.8628	2.41E-02	2.2564	2.3529
4_9	P12277	Creatine kinase B-type OS=Homo sapiens GN=CKB PE=1 SV=1 - [KCRB_HUMAN]	2.41E-05	15.3291	2.9996	1.85E-03	3.5718	2.6691
4_9	P12532	Creatine kinase U-type, mitochondrial OS=Homo sapiens GN=CKMT1A PE=1 SV=1 - [KCRU_HUMAN]	1.86E-05	16.3138	3.0081	2.48E-04	4.7443	2.2888
4_9	P30038	Delta-1-pyrroline-5-carboxylate dehydrogenase, mitochondrial OS=Homo sapiens GN=ALDH4A1 PE=1 SV=3 - [AL4A1_HUMAN]	2.73E-04	-5.6360	-2.8111	4.70E-04	-4.3501	-2.0675
4_9	P08294	Extracellular superoxide dismutase [Cu-Zn] OS=Homo sapiens GN=SOD3 PE=1 SV=2 - [SODE_HUMAN]	1.43E-02	2.6562	2.7472	1.15E-02	2.6309	2.2501
4_9	P09467	Fructose-1,6-bisphosphatase 1 OS=Homo sapiens GN=FBP1 PE=1 SV=5 - [F16P1_HUMAN]	5.20E-03	3.1846	2.9524	2.69E-02	2.1986	2.1612
4_9	Q06210	Glutamine--fructose-6-phosphate aminotransferase [isomerizing] 1 OS=Homo sapiens GN=GFPT1 PE=1 SV=3 - [GFPT1_HUMAN]	3.75E-05	7.6236	2.8408	7.65E-03	2.8248	2.7338
4_9	P18283	Glutathione peroxidase 2 OS=Homo sapiens GN=GPX2 PE=1 SV=3 - [GPX2_HUMAN]	1.45E-04	5.8938	2.9965	4.25E-04	4.4079	2.6529
4_9	P10253	Lysosomal alpha-glucosidase OS=Homo sapiens GN=GAA PE=1 SV=4 - [LYAG_HUMAN]	8.43E-03	-2.9387	-2.8727	8.14E-03	-2.7931	-2.6112
4_9	P20774	Mimecan OS=Homo sapiens GN=OGN PE=1 SV=1 - [MIME_HUMAN]	4.05E-03	3.3513	3.0821	7.66E-05	5.6210	4.4171
4_9	Q9HC84	Mucin-5B OS=Homo sapiens GN=MUC5B PE=1 SV=3 - [MUC5B_HUMAN]	5.55E-04	4.9289	2.9423	8.18E-04	4.0411	3.8016
4_9	P41218	Myeloid cell nuclear differentiation antigen OS=Homo sapiens GN=MNDA PE=1 SV=1 - [MNDA_HUMAN]	2.51E-02	-2.2593	-2.8067	1.54E-02	-2.4865	-2.4246
4_9	Q7Z406	Myosin-14 OS=Homo sapiens GN=MYH14 PE=1 SV=2 - [MYH14_HUMAN]	5.11E-03	3.1988	2.9542	1.01E-03	3.9225	3.3017
4_9	O94760	N(G),N(G)-dimethylarginine dimethylaminohydrolase 1 OS=Homo sapiens GN=DDAH1 PE=1 SV=3 - [DDAH1_HUMAN]	4.09E-05	7.1069	2.9141	1.25E-05	7.6211	2.5246
4_9	P15559	NAD(P)H dehydrogenase [quinone] 1 OS=Homo sapiens GN=NQO1 PE=1 SV=1 - [NQO1_HUMAN]	2.47E-04	5.6659	3.0085	1.38E-02	2.5382	2.8346
4_9	Q9BTA1	Niban-like protein 1 OS=Homo sapiens GN=FAM129B PE=1 SV=3 - [NIBL1_HUMAN]	3.92E-03	3.3709	2.7488	1.55E-02	2.4843	2.1683
4_9	P40261	Nicotinamide N-methyltransferase OS=Homo sapiens GN=NNMT PE=1 SV=1 - [NNMT_HUMAN]	1.20E-02	-2.7581	-2.7015	7.82E-03	-2.8119	-2.5021
4_9	P01833	Polymeric immunoglobulin receptor OS=Homo sapiens GN=PIGR PE=1 SV=4 - [PIGR_HUMAN]	6.04E-04	4.8620	2.8741	3.68E-03	3.2092	2.4873
4_9	Q14914	Prostaglandin reductase 1 OS=Homo sapiens GN=PTGR1 PE=1 SV=2 - [PTGR1_HUMAN]	3.00E-03	3.6027	3.0090	6.11E-03	2.9482	3.6958
4_9	Q13576	Ras GTPase-activating-like protein IQGAP2 OS=Homo sapiens GN=IQGAP2 PE=1 SV=4 - [IQGA2_HUMAN]	7.65E-04	4.7280	2.9098	1.88E-03	3.5609	4.2634
4_9	O94788	Retinal dehydrogenase 2 OS=Homo sapiens GN=ALDH1A2 PE=1 SV=3 - [AL1A2_HUMAN]	7.56E-04	4.7414	2.8083	7.49E-03	2.8383	2.0931
4_9	P24821	Tenascin OS=Homo sapiens GN=TNC PE=1 SV=3 - [TENA_HUMAN]	2.55E-02	-2.2494	-2.7053	2.59E-02	-2.2147	-2.6322
4_9	P09327	Villin-1 OS=Homo sapiens GN=VIL1 PE=1 SV=4 - [VILI_HUMAN]	3.51E-03	3.4475	2.8983	1.32E-02	2.5604	2.8579
5_6	P42765	3-ketoacyl-CoA thiolase, mitochondrial OS=Homo sapiens GN=ACAA2 PE=1 SV=2 - [THIM_HUMAN]	4.93E-02	-1.9798	-2.8246	8.21E-03	-2.7194	-3.1685
5_6	P04217	Alpha-1B-glycoprotein OS=Homo sapiens GN=A1BG PE=1 SV=4 - [A1BG_HUMAN]	5.14E-04	4.3317	3.1231	8.68E-03	2.6928	2.8011
5_6	P00450	Ceruloplasmin OS=Homo sapiens GN=CP PE=1 SV=1 - [CERU_HUMAN]	1.30E-03	3.7860	3.1911	2.33E-03	3.3619	2.3870
5_6	P12532	Creatine kinase U-type, mitochondrial OS=Homo sapiens GN=CKMT1A PE=1 SV=1 - [KCRU_HUMAN]	1.44E-03	3.7681	2.8880	5.51E-03	2.9246	2.1408

Fig. 7 continued

5_6	O43175	D-3-phosphoglycerate dehydrogenase OS=Homo sapiens GN=PHGDH PE=1 SV=4 - [SERA_HUMAN]	2.74E-02	-2.1208	-2.9203	4.95E-03	-2.9751	-3.1368
5_6	Q14195	Dihydropyrimidinase-related protein 3 OS=Homo sapiens GN=DPYSL3 PE=1 SV=1 - [DPYL3_HUMAN]	4.43E-02	2.0540	3.0468	2.28E-03	3.3740	2.8564
5_6	P01859	Ig gamma-2 chain C region OS=Homo sapiens GN=IGHG2 PE=1 SV=2 - [IGHG2_HUMAN]	1.48E-02	2.5351	2.9054	2.17E-02	2.2573	3.7824
5_6	P516U8	Methyl-CpG-binding protein 2 OS=Homo sapiens GN=MECP2 PE=1 SV=1 - [MECP2_HUMAN]	4.16E-02	2.0723	2.7403	5.37E-03	2.9407	2.0642
5_6	Q9HCC0	Methylcrotonoyl-CoA carboxylase beta chain, mitochondrial OS=Homo sapiens GN=MCCC2 PE=1 SV=1 - [MCCB_HUMAN]	8.54E-03	-2.7596	-2.7703	1.93E-02	-2.3213	-2.6006
5_6	P55083	Microfibril-associated glycoprotein 4 OS=Homo sapiens GN=MFAP4 PE=1 SV=2 - [MFAP4_HUMAN]	1.81E-02	2.4183	2.8862	1.97E-02	2.3094	2.4941
5_6	P98088	Mucin-5AC (Fragments) OS=Homo sapiens GN=MUC5AC PE=1 SV=3 - [MUC5A_HUMAN]	7.93E-03	2.7770	2.8309	4.53E-02	1.9316	3.6767
5_6	P29590	Protein PML OS=Homo sapiens GN=PML PE=1 SV=3 - [PML_HUMAN]	7.93E-03	2.7770	2.7478	3.56E-03	3.1295	2.6767
5_6	P24821	Tenascin OS=Homo sapiens GN=TNC PE=1 SV=3 - [TENA_HUMAN]	3.91E-02	-2.0838	-2.7562	2.19E-02	-2.2531	-3.3713
5_6	Q15661	Tryptase alpha/beta-1 OS=Homo sapiens GN=TPSAB1 PE=1 SV=1 - [TRYB1_HUMAN]	1.02E-05	7.3645	3.1732	1.44E-03	3.6298	3.6971
5_7	P24752	Acetyl-CoA acetyltransferase, mitochondrial OS=Homo sapiens GN=ACAT1 PE=1 SV=1 - [THIL_HUMAN]	2.39E-02	-2.2739	-2.7517	1.04E-02	-2.5834	-2.2647
5_7	P54819	Adenylate kinase 2, mitochondrial OS=Homo sapiens GN=AK2 PE=1 SV=2 - [KAD2_HUMAN]	1.11E-02	-2.7580	-2.8767	4.72E-02	-1.9044	-2.0774
5_7	P49419	Alpha-aminoadipic semialdehyde dehydrogenase OS=Homo sapiens GN=ALDH7A1 PE=1 SV=5 - [AL7A1_HUMAN]	2.71E-03	-3.5658	-2.8181	1.66E-02	-2.3643	-2.3782
5_7	P27338	Amine oxidase [flavin-containing] B OS=Homo sapiens GN=MAOB PE=1 SV=3 - [AOFB_HUMAN]	3.16E-03	-3.4732	-2.8429	3.09E-03	-3.1700	-3.4022
5_7	P01019	Angiotensinogen OS=Homo sapiens GN=AGT PE=1 SV=1 - [ANGT_HUMAN]	1.71E-02	-2.5307	-2.7775	2.66E-02	-2.1244	-2.3612
5_7	Q9BXN1	Asporin OS=Homo sapiens GN=ASPN PE=1 SV=2 - [ASPN_HUMAN]	4.95E-02	-2.0019	-2.9156	1.27E-02	-2.4936	-2.7933
5_7	P31939	Bifunctional purine biosynthesis protein PURH OS=Homo sapiens GN=ATIC PE=1 SV=3 - [PUR9_HUMAN]	2.23E-02	-2.3335	-2.8570	2.34E-03	-3.3043	-3.8090
5_7	P06731	Carcinoembryonic antigen-related cell adhesion molecule 5 OS=Homo sapiens GN=CEACAM5 PE=1 SV=3 - [CEAM5_HUMAN]	9.00E-03	2.7946	3.1781	4.03E-02	1.9695	2.0701
5_7	P35222	Catenin beta-1 OS=Homo sapiens GN=CTNNB1 PE=1 SV=1 - [CTNB1_HUMAN]	4.88E-03	-3.0874	-2.7214	4.59E-03	-2.9885	-2.2357
5_7	P00450	Ceruloplasmin OS=Homo sapiens GN=CP PE=1 SV=1 - [CERU_HUMAN]	5.23E-04	4.6272	3.2327	2.26E-03	3.3174	2.1387
5_7	Q9P0M6	Core histone macro-H2A.2 OS=Homo sapiens GN=H2AFY2 PE=1 SV=3 - [H2AW_HUMAN]	3.61E-03	-3.3727	-2.8875	1.36E-03	-3.5859	-2.9562
5_7	O43175	D-3-phosphoglycerate dehydrogenase OS=Homo sapiens GN=PHGDH PE=1 SV=4 - [SERA_HUMAN]	4.42E-02	-2.0574	-2.9203	1.24E-02	-2.5094	-3.1368
5_7	P07585	Decorin OS=Homo sapiens GN=DCN PE=1 SV=1 - [PGS2_HUMAN]	4.47E-02	-2.0533	-2.8707	2.67E-02	-2.1236	-2.9632
5_7	P11678	Eosinophil peroxidase OS=Homo sapiens GN=EPX PE=1 SV=2 - [PERE_HUMAN]	1.80E-03	3.7558	3.1923	7.99E-03	2.7143	3.4580
5_7	P07954	Fumarate hydratase, mitochondrial OS=Homo sapiens GN=FH PE=1 SV=3 - [FUMH_HUMAN]	2.29E-02	-2.3116	-2.9328	1.56E-02	-2.4002	-2.4422
5_7	P00390	Glutathione reductase, mitochondrial OS=Homo sapiens GN=GSR PE=1 SV=2 - [GSHR_HUMAN]	2.39E-02	-2.2765	-2.9352	1.14E-02	-2.5442	-2.6623
5_7	P34932	Heat shock 70 kDa protein 4 OS=Homo sapiens GN=HSPA4 PE=1 SV=4 - [HSP74_HUMAN]	2.15E-02	-2.3657	-2.8468	3.59E-03	-3.0883	-2.9428
5_7	P01859	Ig gamma-2 chain C region OS=Homo sapiens GN=IGHG2 PE=1 SV=2 - [IGHG2_HUMAN]	7.83E-04	4.0619	3.3129	1.93E-02	2.2849	3.9175
5_7	P05556	Integrin beta-1 OS=Homo sapiens GN=ITGB1 PE=1 SV=2 - [ITB1_HUMAN]	2.94E-03	-3.5145	-2.8299	8.06E-03	-2.7106	-2.1652
5_7	Q9HCC0	Methylcrotonoyl-CoA carboxylase beta chain, mitochondrial OS=Homo sapiens GN=MCCC2 PE=1 SV=1 - [MCCB_HUMAN]	2.28E-02	-2.3143	-2.7703	1.08E-02	-2.5623	-2.6006
5_7	P98088	Mucin-5AC (Fragments) OS=Homo sapiens GN=MUC5AC PE=1 SV=3 - [MUC5A_HUMAN]	1.11E-02	2.7572	3.2398	2.09E-02	2.2479	4.7330
5_7	P80188	Neutrophil gelatinase-associated lipocalin OS=Homo sapiens GN=LCN2 PE=1 SV=2 - [NGAL_HUMAN]	3.22E-03	3.4616	3.1911	3.61E-02	2.0148	3.2251

Fig. 7 continued

5 7	O00567	Nucleolar protein 56 OS=Homo sapiens GN=NOP56 PE=1 SV=4 -	NOP56_HUMAN		7.38E-03	-2.8146	-2.7255	6.42E-03	-2.8065	-2.8656
5 7	Q08257	Quinone oxidoreductase OS=Homo sapiens GN=CRYZ PE=1 SV=1 -	QOR_HUMAN		1.87E-02	-2.4674	-2.9043	7.19E-04	-3.9454	-3.7304
5 7	Q9Y265	RuvB-like 1 OS=Homo sapiens GN=RUVBL1 PE=1 SV=1 -	RUVB1_HUMAN		4.42E-03	-3.1787	-2.7167	5.79E-04	-4.0697	-2.4022
5 7	P30153	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform OS=Homo sapiens GN=PPP2R1A PE=1 SV=4 -	2AAA_HUMAN		2.83E-02	-2.1377	-2.7136	1.05E-02	-2.5776	-2.8292
5 7	P30048	Thioredoxin-dependent peroxide reductase, mitochondrial OS=Homo sapiens GN=PRDX3 PE=1 SV=3 -	PRDX3_HUMAN		2.80E-02	-2.1473	-2.9549	1.39E-02	-2.4591	-2.0082
5 7	P40939	Trifunctional enzyme subunit alpha, mitochondrial OS=Homo sapiens GN=HADHA PE=1 SV=2 -	ECHA_HUMAN		4.53E-02	-2.0488	-2.9682	8.68E-03	-2.6782	-3.6959
5 7	P06753	Tropomyosin alpha-3 chain OS=Homo sapiens GN=TPM3 PE=1 SV=1 -	TPM3_HUMAN		1.43E-02	-2.6324	-2.8987	1.30E-02	-2.4816	-2.5491
5 7	Q15661	Tryptase alpha/beta-1 OS=Homo sapiens GN=TPSAB1 PE=1 SV=1 -	TRYB1_HUMAN		6.47E-04	4.2829	3.2103	9.44E-03	2.6329	2.4851
5 7	Q13885	Tubulin beta-2A chain OS=Homo sapiens GN=TUBB2A PE=1 SV=1 -	TBB2A_HUMAN		1.96E-02	-2.4328	-2.9887	4.95E-03	-2.9475	-5.9200
5 7	P04350	Tubulin beta-4A chain OS=Homo sapiens GN=TUBB4A PE=1 SV=2 -	TBB4A_HUMAN		2.61E-02	-2.2011	-3.0176	3.15E-04	-4.4338	-5.9854
5 7	Q9BUF5	Tubulin beta-6 chain OS=Homo sapiens GN=TUBB6 PE=1 SV=1 -	TBB6_HUMAN		2.72E-02	-2.1669	-2.9867	7.06E-03	-2.7620	-4.9018
5 7	O00159	Unconventional myosin-Ic OS=Homo sapiens GN=MYO1C PE=1 SV=4 -	MYO1C_HUMAN		1.88E-02	-2.4648	-2.7056	2.82E-03	-3.2141	-2.2012
5 8	Q15029	116 kDa U5 small nuclear ribonucleoprotein component OS=Homo sapiens GN=EFTUD2 PE=1 SV=1 -	U5S1_HUMAN		1.69E-02	2.3376	2.6748	3.55E-03	3.1533	2.4556
5 8	P27338	Amine oxidase [flavin-containing] B OS=Homo sapiens GN=MAOB PE=1 SV=3 -	AOFB_HUMAN		4.18E-03	-2.9154	-2.8429	4.06E-03	-3.0784	-3.4022
5 8	P15144	Aminopeptidase N OS=Homo sapiens GN=ANPEP PE=1 SV=4 -	AMPN_HUMAN		1.06E-02	-2.6336	-2.7349	1.57E-02	-2.4119	-2.0774
5 8	P01019	Angiotensinogen OS=Homo sapiens GN=AGT PE=1 SV=1 -	ANGT_HUMAN		2.56E-04	-5.5745	-2.7775	1.97E-02	-2.2993	-2.3612
5 8	Q9BXN1	Asporin OS=Homo sapiens GN=ASPN PE=1 SV=2 -	ASPN_HUMAN		1.77E-02	-2.3013	-2.9156	1.15E-02	-2.5743	-2.7933
5 8	Q12864	Cadherin-17 OS=Homo sapiens GN=CDH17 PE=1 SV=3 -	CAD17_HUMAN		1.81E-04	5.7758	2.7688	2.95E-04	4.5434	3.2065
5 8	P17655	Calpain-2 catalytic subunit OS=Homo sapiens GN=CAPN2 PE=1 SV=6 -	CAN2_HUMAN		3.47E-02	-2.0869	-2.7473	9.29E-03	-2.6787	-2.3612
5 8	P06731	Carcinoembryonic antigen-related cell adhesion molecule 5 OS=Homo sapiens GN=CEACAM5 PE=1 SV=3 -	CEAM5_HUMAN		1.28E-05	18.8897	2.8744	8.46E-04	3.9247	2.7240
5 8	P40199	Carcinoembryonic antigen-related cell adhesion molecule 6 OS=Homo sapiens GN=CEACAM6 PE=1 SV=3 -	CEAM6_HUMAN		4.56E-02	1.9264	2.7790	4.12E-03	3.0690	2.0666
5 8	Q99829	Copine-1 OS=Homo sapiens GN=CPNE1 PE=1 SV=1 -	CPNE1_HUMAN		1.24E-02	2.5267	2.7256	2.86E-03	3.2810	2.2997
5 8	P07585	Decorin OS=Homo sapiens GN=DCN PE=1 SV=1 -	PGS2_HUMAN		7.50E-04	-3.8092	-2.8707	2.29E-03	-3.4024	-2.9632
5 8	P54886	Delta-1-pyrroline-5-carboxylate synthase OS=Homo sapiens GN=ALDH18A1 PE=1 SV=2 -	P5CS_HUMAN		4.92E-05	6.1550	2.6907	6.00E-03	2.8685	2.6394
5 8	P11387	DNA topoisomerase 1 OS=Homo sapiens GN=TOP1 PE=1 SV=2 -	TOP1_HUMAN		1.44E-02	2.4396	2.7446	3.46E-03	3.1700	2.3440
5 8	P58107	Epiplakin OS=Homo sapiens GN=EPPK1 PE=1 SV=2 -	EPIPL_HUMAN		3.74E-03	3.0409	2.7065	2.67E-02	2.1399	2.4170
5 8	Q06210	Glutamine--fructose-6-phosphate aminotransferase [isomerizing] 1 OS=Homo sapiens GN=GFPT1 PE=1 SV=3 -	GFPT1_HUMAN		2.46E-04	5.6422	2.7907	1.34E-03	3.6944	3.2914
5 8	P41250	Glycine--tRNA ligase OS=Homo sapiens GN=GARS PE=1 SV=3 -	SYG_HUMAN		1.02E-02	2.6679	2.7478	8.04E-04	3.9499	2.5324
5 8	Q92598	Heat shock protein 105 kDa OS=Homo sapiens GN=HSPH1 PE=1 SV=1 -	HS105_HUMAN		7.35E-05	5.9322	2.8188	1.83E-04	4.8398	3.2769
5 8	P31942	Heterogeneous nuclear ribonucleoprotein H3 OS=Homo sapiens GN=HNRNPH3 PE=1 SV=2 -	HNRH3_HUMAN		1.90E-02	2.2471	2.7145	1.72E-02	2.3643	2.4356
5 8	Q15181	Inorganic pyrophosphatase OS=Homo sapiens GN=PPA1 PE=1 SV=2 -	IPYR_HUMAN		9.23E-03	2.7421	2.7286	2.54E-02	2.1640	2.2981
5 8	P05556	Integrin beta-1 OS=Homo sapiens GN=ITGB1 PE=1 SV=2 -	ITB1_HUMAN		3.24E-03	-3.2126	-2.8299	1.11E-02	-2.5925	-2.1652

Fig. 7 continued

5_8	P08729	Keratin, type II cytoskeletal 7 OS=Homo sapiens GN=KRT7 PE=1 SV=5 - [K2C7_HUMAN]	3.20E-03	-3.2272	-3.0068	2.13E-04	-4.7647	-3.8292
5_8	Q15046	Lysine--tRNA ligase OS=Homo sapiens GN=KARS PE=1 SV=3 - [SYK_HUMAN]	2.51E-03	3.4604	2.6871	2.81E-03	3.2903	2.2997
5_8	Q16822	Phosphoenolpyruvate carboxykinase [GTP], mitochondrial OS=Homo sapiens GN=PCK2 PE=1 SV=3 - [PCKGM_HUMAN]	1.70E-03	3.7468	2.7546	1.79E-03	3.5326	3.1539
5_8	P17844	Probable ATP-dependent RNA helicase DDX5 OS=Homo sapiens GN=DDX5 PE=1 SV=1 - [DDX5_HUMAN]	1.32E-03	3.8076	2.7914	3.07E-03	3.2411	3.2734
5_8	Q9P258	Protein RCC2 OS=Homo sapiens GN=RCC2 PE=1 SV=2 - [RCC2_HUMAN]	8.95E-03	2.7536	2.6566	1.22E-02	2.5420	2.4152
5_8	P19971	Thymidine phosphorylase OS=Homo sapiens GN=TYMP PE=1 SV=2 - [TYPH_HUMAN]	1.92E-03	-3.6922	-2.8302	3.72E-02	-2.0259	-2.4022
5_8	Q9BUF5	Tubulin beta-6 chain OS=Homo sapiens GN=TUBB6 PE=1 SV=1 - [TBB6_HUMAN]	1.25E-03	-3.8146	-2.9867	1.25E-03	-3.7252	-4.9018
5_8	P15374	Ubiquitin carboxyl-terminal hydrolase isozyme L3 OS=Homo sapiens GN=UCHL3 PE=1 SV=1 - [UCHL3_HUMAN]	4.81E-05	6.1778	2.6997	4.30E-05	5.9735	2.1742
5_8	O00159	Unconventional myosin-Ic OS=Homo sapiens GN=MYO1C PE=1 SV=4 - [MYO1C_HUMAN]	4.18E-02	-1.9839	-2.7056	2.41E-02	-2.1932	-2.2012
5_9	Q01813	6-phosphofructokinase type C OS=Homo sapiens GN=PFKP PE=1 SV=2 - [K6PP_HUMAN]	1.68E-02	-2.3655	-2.7049	2.00E-02	-2.3124	-2.0637
5_9	O95154	Aflatoxin B1 aldehyde reductase member 3 OS=Homo sapiens GN=AKR7A3 PE=1 SV=2 - [ARK73_HUMAN]	2.14E-05	15.8587	3.0557	5.75E-05	5.8499	3.1644
5_9	P07327	Alcohol dehydrogenase 1A OS=Homo sapiens GN=ADH1A PE=1 SV=2 - [ADH1A_HUMAN]	1.22E-02	2.5927	3.0186	2.63E-03	3.3127	3.8402
5_9	P00325	Alcohol dehydrogenase 1B OS=Homo sapiens GN=ADH1B PE=1 SV=2 - [ADH1B_HUMAN]	3.55E-02	2.1065	3.0213	4.26E-03	3.0643	4.0875
5_9	P00326	Alcohol dehydrogenase 1C OS=Homo sapiens GN=ADH1C PE=1 SV=2 - [ADH1G_HUMAN]	2.18E-05	15.0083	3.0221	4.94E-05	6.0660	3.3012
5_9	P30838	Aldehyde dehydrogenase, dimeric NADP-preferring OS=Homo sapiens GN=ALDH3A1 PE=1 SV=3 - [AL3A1_HUMAN]	7.27E-04	4.7280	2.9253	1.57E-02	2.4303	2.6514
5_9	O60218	Aldo-keto reductase family 1 member B10 OS=Homo sapiens GN=AKR1B10 PE=1 SV=2 - [AK1BA_HUMAN]	2.32E-03	3.5009	3.1370	2.91E-04	4.6719	4.6421
5_9	P17516	Aldo-keto reductase family 1 member C4 OS=Homo sapiens GN=AKR1C4 PE=1 SV=3 - [AK1C4_HUMAN]	1.02E-05	18.4615	2.9851	4.55E-04	4.3734	3.3738
5_9	P27216	Annexin A13 OS=Homo sapiens GN=ANXA13 PE=1 SV=3 - [ANX13_HUMAN]	6.54E-03	2.9228	2.9618	4.68E-02	1.9265	3.3431
5_9	P04424	Argininosuccinate lyase OS=Homo sapiens GN=ASL PE=1 SV=4 - [ARLY_HUMAN]	2.83E-03	3.3704	2.9844	1.67E-05	7.4212	2.0565
5_9	P00918	Carbonic anhydrase 2 OS=Homo sapiens GN=CA2 PE=1 SV=2 - [CAH2_HUMAN]	1.30E-02	2.5382	3.1049	1.25E-05	7.8389	4.5844
5_9	Q99715	Collagen alpha-1(XII) chain OS=Homo sapiens GN=COL12A1 PE=1 SV=2 - [COCA1_HUMAN]	1.33E-04	-5.8617	-2.7621	2.49E-02	-2.2001	-2.3351
5_9	P12277	Creatine kinase B-type OS=Homo sapiens GN=CKB PE=1 SV=1 - [KCRB_HUMAN]	8.01E-05	6.2812	2.9996	5.45E-03	2.9373	2.6691
5_9	P12532	Creatine kinase U-type, mitochondrial OS=Homo sapiens GN=CKMT1A PE=1 SV=1 - [KCRU_HUMAN]	1.93E-05	16.3138	3.0081	2.60E-04	4.7443	2.2888
5_9	P08294	Extracellular superoxide dismutase [Cu-Zn] OS=Homo sapiens GN=SOD3 PE=1 SV=2 - [SODE_HUMAN]	7.01E-04	4.7506	2.7472	1.21E-03	3.7493	2.2501
5_9	P09467	Fructose-1,6-bisphosphatase 1 OS=Homo sapiens GN=FBP1 PE=1 SV=5 - [F16P1_HUMAN]	8.04E-04	4.5399	2.9524	2.84E-04	4.6881	2.1812
5_9	P05062	Fructose-bisphosphate aldolase B OS=Homo sapiens GN=ALDOB PE=1 SV=2 - [ALDOB_HUMAN]	2.02E-02	2.2624	3.0339	3.87E-03	3.1121	3.7003
5_9	Q06210	Glutamine--fructose-6-phosphate aminotransferase [isomerizing] 1 OS=Homo sapiens GN=GFPT1 PE=1 SV=3 - [GFPT1_HUMAN]	9.68E-05	6.0970	2.8408	1.75E-02	2.3764	2.7338
5_9	P18283	Glutathione peroxidase 2 OS=Homo sapiens GN=GPX2 PE=1 SV=3 - [GPX2_HUMAN]	2.77E-05	15.3382	2.9965	2.72E-04	4.7174	2.6529
5_9	P08263	Glutathione S-transferase A1 OS=Homo sapiens GN=GSTA1 PE=1 SV=3 - [GSTA1_HUMAN]	8.09E-03	2.8038	3.0833	5.06E-03	2.9785	3.3590
5_9	P01859	Ig gamma-2 chain C region OS=Homo sapiens GN=IGHG2 PE=1 SV=2 - [IGHG2_HUMAN]	3.59E-03	3.2418	3.0412	6.15E-03	2.8842	4.1675
5_9	P23141	Liver carboxylesterase 1 OS=Homo sapiens GN=CES1 PE=1 SV=2 - [EST1_HUMAN]	4.63E-03	3.1246	3.1571	1.33E-04	5.2469	5.8487
5_9	P55083	Microfibril-associated glycoprotein 4 OS=Homo sapiens GN=MFAP4 PE=1 SV=2 - [MFAP4_HUMAN]	2.36E-04	5.7322	2.9582	1.07E-04	5.3918	3.3874

Fig. 7 continued

5 9	Q9HC84	Mucin-5B OS=Homo sapiens GN=MUC5B PE=1 SV=3 - [MUC5B_HUMAN]	1.41E-05	17.8357	2.9423	5.84E-04	4.2058	3.8016
5 9	O94760	N(G),N(G)-dimethylarginine dimethylaminohydrolase 1 OS=Homo sapiens GN=DDAH1 PE=1 SV=3 - [DDAH1_HUMAN]	1.67E-05	16.7724	2.9141	1.79E-06	12.5322	2.5246
5 9	P15559	NAD(P)H dehydrogenase [quinone] 1 OS=Homo sapiens GN=NQO1 PE=1 SV=1 - [NQO1_HUMAN]	4.37E-05	6.9634	3.0085	3.87E-03	3.1124	2.8346
5 9	Q967A1	Ntaln-like protein 1 OS=Homo sapiens GN=FAM129B PE=1 SV=3 - [NIBL1_HUMAN]	3.40E-02	2.1097	2.7488	5.22E-03	2.9595	2.1683
5 9	Q15063	Periostin OS=Homo sapiens GN=POSTN PE=1 SV=2 - [POSTN_HUMAN]	4.09E-04	-5.1842	-3.0149	4.57E-03	-3.0250	-4.5277
5 9	Q13162	Peroxiredoxin-4 OS=Homo sapiens GN=PRDX4 PE=1 SV=1 - [PRDX4_HUMAN]	5.74E-03	-3.0480	-2.8226	8.66E-03	-2.7152	-2.0493
5 9	P17844	Probable ATP-dependent RNA helicase DDX5 OS=Homo sapiens GN=DDX5 PE=1 SV=1 - [DDX5_HUMAN]	1.30E-02	2.5413	2.9867	3.17E-02	2.0937	3.2097
5 9	Q14914	Prostaglandin reductase 1 OS=Homo sapiens GN=PTGR1 PE=1 SV=2 - [PTGR1_HUMAN]	7.66E-05	6.3380	3.0090	3.32E-05	6.5451	3.6958
5 9	Q13576	Ras GTPase-activating-like protein IQGAP2 OS=Homo sapiens GN=IQGAP2 PE=1 SV=4 - [IQGA2_HUMAN]	8.77E-05	6.1717	2.9098	6.77E-04	4.1136	4.2634
5 9	O94788	Retinal dehydrogenase 2 OS=Homo sapiens GN=ALDH1A2 PE=1 SV=3 - [AL1A2_HUMAN]	3.43E-03	3.2646	2.8083	2.42E-02	2.2128	2.0931
5 9	Q9NR45	Sialic acid synthase OS=Homo sapiens GN=NANS PE=1 SV=2 - [SIAS_HUMAN]	9.18E-04	4.2584	2.9690	1.03E-05	8.1210	2.3935
5 9	P24821	Tenascin OS=Homo sapiens GN=TNC PE=1 SV=3 - [TENA_HUMAN]	1.92E-02	-2.2911	-2.7562	2.49E-02	-2.1997	-3.3713
5 9	Q15561	Tryptase alpha/beta-1 OS=Homo sapiens GN=TPSAB1 PE=1 SV=1 - [TRYB1_HUMAN]	4.66E-05	6.8570	2.9718	3.31E-04	4.5605	3.5929
5 9	Q13509	Tubulin beta-3 chain OS=Homo sapiens GN=TUBB3 PE=1 SV=2 - [TBB3_HUMAN]	1.46E-03	-3.8155	-2.9858	7.76E-03	-2.7685	-5.1341
6 7	P04217	Alpha-1B-glycoprotein OS=Homo sapiens GN=A1BG PE=1 SV=4 - [A1BG_HUMAN]	2.71E-02	-2.1497	-3.1231	5.10E-02	-1.8728	-2.8011
6 7	Q9BXN1	Asporin OS=Homo sapiens GN=ASPN PE=1 SV=2 - [ASPN_HUMAN]	4.20E-03	-3.1234	-3.1279	6.62E-04	-4.0865	-2.6491
6 7	P07585	Decorin OS=Homo sapiens GN=DCN PE=1 SV=1 - [PGS2_HUMAN]	1.57E-02	-2.5308	-3.1399	2.57E-03	-3.3096	-3.3048
6 7	P51608	Methyl-CpG-binding protein 2 OS=Homo sapiens GN=MECP2 PE=1 SV=1 - [MECP2_HUMAN]	2.20E-02	-2.2901	-2.7403	2.35E-02	-2.2128	-2.0642
6 7	P20774	Mimecan OS=Homo sapiens GN=OGN PE=1 SV=1 - [MIME_HUMAN]	4.56E-02	-2.0455	-2.8528	3.99E-03	-3.0918	-2.2866
6 8	Q15029	116 kDa U5 small nuclear ribonucleoprotein component OS=Homo sapiens GN=EFTUD2 PE=1 SV=1 - [U5S1_HUMAN]	1.68E-02	2.4746	2.6748	6.24E-03	2.9120	2.4356
6 8	P31937	3-hydroxyisobutyrate dehydrogenase, mitochondrial OS=Homo sapiens GN=HIBADH PE=1 SV=2 - [3HIDH_HUMAN]	7.55E-04	3.9870	2.7043	3.35E-03	3.2531	2.8022
6 8	P42765	3-ketoacyl-CoA thiolase, mitochondrial OS=Homo sapiens GN=ACAA2 PE=1 SV=2 - [THIM_HUMAN]	6.06E-03	2.8549	2.7744	1.25E-03	3.7784	3.4170
6 8	P17858	6-phosphofructokinase, liver type OS=Homo sapiens GN=PFKL PE=1 SV=6 - [K6PL_HUMAN]	2.45E-02	2.2064	2.7283	3.34E-02	2.0871	2.7389
6 8	P30837	Aldehyde dehydrogenase X, mitochondrial OS=Homo sapiens GN=ALDH1B1 PE=1 SV=3 - [AL1B1_HUMAN]	1.14E-02	2.7078	2.7940	1.17E-04	5.3617	3.7389
6 8	P04217	Alpha-1B-glycoprotein OS=Homo sapiens GN=A1BG PE=1 SV=4 - [A1BG_HUMAN]	1.47E-05	-12.4553	-3.1231	4.34E-03	-3.1065	-2.8011
6 8	P54136	Arginine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=RARS PE=1 SV=2 - [SYRC_HUMAN]	2.59E-02	2.1684	2.6671	3.49E-04	4.5717	2.2914
6 8	P14868	Aspartate--tRNA ligase, cytoplasmic OS=Homo sapiens GN=DARS PE=1 SV=2 - [SYDC_HUMAN]	1.79E-02	2.4325	2.7269	6.02E-05	5.9427	2.6105
6 8	Q9BXN1	Asporin OS=Homo sapiens GN=ASPN PE=1 SV=2 - [ASPN_HUMAN]	6.82E-04	-4.0453	-3.1279	3.99E-04	-4.4921	-2.6491
6 8	Q12864	Cadherin-17 OS=Homo sapiens GN=CDH17 PE=1 SV=3 - [CAD17_HUMAN]	1.36E-04	5.7758	2.7688	3.70E-04	4.5434	3.2065
6 8	P17655	Calpain-2 catalytic subunit OS=Homo sapiens GN=CAPN2 PE=1 SV=6 - [CAN2_HUMAN]	1.93E-02	-2.3809	-2.7966	4.50E-03	-3.0858	-3.2821
6 8	P00915	Carbonic anhydrase 1 OS=Homo sapiens GN=CA1 PE=1 SV=2 - [CAH1_HUMAN]	4.98E-03	-2.9936	-2.8205	2.75E-02	-2.1694	-2.2173
6 8	P00450	Ceruloplasmin OS=Homo sapiens GN=CP PE=1 SV=1 - [CERU_HUMAN]	5.02E-04	-4.2979	-3.1911	1.62E-03	-3.6359	-3.4363

Fig. 7 continued

6_8	Q99715	Collagen alpha-1(XII) chain OS=Homo sapiens GN=COL12A1 PE=1 SV=2 - [COCA1_HUMAN]	1.39E-02	-2.5898	-2.7725	2.68E-02	-2.1841	-3.8564
6_8	P07585	Decorin OS=Homo sapiens GN=DCN PE=1 SV=1 - [PGS2_HUMAN]	3.56E-04	-4.7618	-3.1399	1.84E-04	-5.0196	-3.3048
6_8	P54886	Delta-1-pyrroline-5-carboxylate synthase OS=Homo sapiens GN=ALDH18A1 PE=1 SV=2 - [P5CS_HUMAN]	7.34E-04	4.0077	2.6907	6.23E-03	2.9129	2.6394
6_8	Q14195	Dihydropyrimidinase-related protein 3 OS=Homo sapiens GN=DPYSL3 PE=1 SV=1 - [DPYL3_HUMAN]	5.05E-04	-4.2928	-3.0468	2.77E-03	-3.3501	-2.8564
6_8	P11387	DNA topoisomerase 1 OS=Homo sapiens GN=TOP1 PE=1 SV=2 - [TOP1_HUMAN]	1.51E-04	5.7135	2.7446	2.43E-03	3.4055	2.3440
6_8	Q7Z6Z7	E3 ubiquitin-protein ligase HUWE1 OS=Homo sapiens GN=HUWE1 PE=1 SV=3 - [HUWE1_HUMAN]	8.22E-06	5.9512	2.6790	1.99E-03	3.5107	2.5850
6_8	Q12805	EGF-containing fibulin-like extracellular matrix protein 1 OS=Homo sapiens GN=EFEMP1 PE=1 SV=2 - [FBLN3_HUMAN]	1.31E-02	-2.6311	-2.7915	1.00E-02	-2.6439	-2.5392
6_8	P55060	Exportin-2 OS=Homo sapiens GN=CSE1L PE=1 SV=3 - [XPO2_HUMAN]	7.67E-05	6.0446	2.9586	6.05E-03	2.9273	2.5016
6_8	Q06210	Glutamine--fructose-6-phosphate aminotransferase [isomerizing] 1 OS=Homo sapiens GN=GFPT1 PE=1 SV=3 - [GFPT1_HUMAN]	3.81E-03	3.2349	2.7907	2.25E-03	3.4497	3.2914
6_8	P48637	Glutathione synthetase OS=Homo sapiens GN=GSS PE=1 SV=1 - [GSHB_HUMAN]	5.29E-03	2.9492	2.6846	1.81E-04	5.0251	2.2914
6_8	Q92598	Heat shock protein 105 kDa OS=Homo sapiens GN=HSPH1 PE=1 SV=1 - [HS105_HUMAN]	3.55E-04	4.7806	2.8188	2.40E-04	4.8019	3.2769
6_8	Q12931	Heat shock protein 75 kDa, mitochondrial OS=Homo sapiens GN=TRAP1 PE=1 SV=3 - [TRAP1_HUMAN]	2.06E-02	2.3326	2.9512	9.52E-04	3.9255	2.9627
6_8	P33778	Histone H2B type 1-B OS=Homo sapiens GN=HIST1H2BB PE=1 SV=2 - [H2B1B_HUMAN]	2.61E-02	-2.1629	-3.2646	4.54E-02	-1.9574	-4.6767
6_8	P06899	Histone H2B type 1-J OS=Homo sapiens GN=HIST1H2BJ PE=1 SV=3 - [H2B1J_HUMAN]	2.61E-02	-2.1629	-3.2646	4.54E-02	-1.9574	-4.6767
6_8	P23527	Histone H2B type 1-O OS=Homo sapiens GN=HIST1H2BO PE=1 SV=3 - [H2B1O_HUMAN]	2.61E-02	-2.1629	-3.2646	4.54E-02	-1.9574	-4.6767
6_8	Q16778	Histone H2B type 2-E OS=Homo sapiens GN=HIST2H2BE PE=1 SV=3 - [H2B2E_HUMAN]	2.61E-02	-2.1629	-3.2646	4.54E-02	-1.9574	-4.6767
6_8	P54868	Hydroxymethylglutaryl-CoA synthase, mitochondrial OS=Homo sapiens GN=HMGCS2 PE=1 SV=1 - [HMCS2_HUMAN]	3.86E-03	3.2242	2.8125	7.77E-04	4.0352	2.6105
6_8	P01871	Ig mu chain C region OS=Homo sapiens GN=IGHM PE=1 SV=3 - [IGHM_HUMAN]	4.32E-02	-2.0515	-2.8266	1.06E-02	-2.6508	-2.2173
6_8	O00410	Importin-5 OS=Homo sapiens GN=IPO5 PE=1 SV=4 - [IPO5_HUMAN]	1.54E-02	2.5268	2.7315	1.77E-04	5.0298	2.6216
6_8	Q14624	Inter-alpha-trypsin inhibitor heavy chain H4 OS=Homo sapiens GN=ITIH4 PE=1 SV=4 - [ITIH4_HUMAN]	2.69E-05	-7.2534	-3.0728	9.78E-03	-2.6873	-2.2173
6_8	P08729	Keratin, type II cytoskeletal 7 OS=Homo sapiens GN=KRT7 PE=1 SV=5 - [K2C7_HUMAN]	2.20E-02	-2.2824	-2.9343	1.24E-02	-2.5703	-3.4941
6_8	P01042	Kininogen-1 OS=Homo sapiens GN=KNG1 PE=1 SV=2 - [KNG1_HUMAN]	1.45E-02	-2.5683	-2.7491	1.76E-03	-3.5909	-2.2866
6_8	P42704	Leucine-rich PPR motif-containing protein, mitochondrial OS=Homo sapiens GN=LRPPRC PE=1 SV=3 - [LPPRC_HUMAN]	1.52E-02	2.5365	2.7558	1.00E-03	3.8571	4.4961
6_8	P36776	Lon protease homolog, mitochondrial OS=Homo sapiens GN=LONP1 PE=1 SV=2 - [LONM_HUMAN]	1.41E-04	5.7542	2.6863	1.12E-02	2.6255	2.0255
6_8	Q15046	Lysine--tRNA ligase OS=Homo sapiens GN=KARS PE=1 SV=3 - [SYK_HUMAN]	4.68E-03	3.0472	2.6871	3.03E-04	4.6540	2.2997
6_8	P51608	Methyl-CpG-binding protein 2 OS=Homo sapiens GN=MECP2 PE=1 SV=1 - [MECP2_HUMAN]	6.76E-04	-4.0495	-2.7403	2.82E-03	-3.3376	-2.0642
6_8	P55083	Microfibril-associated glycoprotein 4 OS=Homo sapiens GN=MFAP4 PE=1 SV=2 - [MFAP4_HUMAN]	5.41E-03	-2.9313	-2.8862	2.59E-02	-2.2039	-2.4941
6_8	P20774	Mimecan OS=Homo sapiens GN=OGN PE=1 SV=1 - [MIME_HUMAN]	5.50E-04	-4.2076	-2.8528	2.53E-03	-3.3825	-2.2866
6_8	P98088	Mucin-5AC (Fragments) OS=Homo sapiens GN=MUC5AC PE=1 SV=3 - [MUC5A_HUMAN]	9.11E-03	-2.7770	-2.8309	4.82E-02	-1.9316	-3.6767
6_8	Q14980	Nuclear mitotic apparatus protein 1 OS=Homo sapiens GN=NUMA1 PE=1 SV=2 - [NUMA1_HUMAN]	1.41E-04	5.7515	2.6318	2.50E-02	2.2215	2.2386
6_8	O00567	Nucleolar protein 56 OS=Homo sapiens GN=NOP56 PE=1 SV=4 - [NOP56_HUMAN]	4.03E-03	3.1847	2.7320	1.30E-03	3.7687	2.3142
6_8	Q02790	Peptidyl-prolyl cis-trans isomerase FKBP4 OS=Homo sapiens GN=FKBP4 PE=1 SV=3 - [FKBP4_HUMAN]	2.12E-02	2.3124	2.6916	4.83E-03	3.0486	2.9627

Fig. 7 continued

6_8	Q9Y285	Phenylalanine--tRNA ligase alpha subunit OS=Homo sapiens GN=FARSA PE=1 SV=3 - [SYFA_HUMAN]	3.58E-03	3.2979	2.6603	2.95E-03	3.3183	2.1622
6_8	Q9NSD9	Phenylalanine--tRNA ligase beta subunit OS=Homo sapiens GN=FARSB PE=1 SV=3 - [SYFB_HUMAN]	5.94E-05	6.2359	2.7077	6.32E-05	5.9115	2.5772
6_8	Q16822	Phosphoenolpyruvate carboxykinase [GTP], mitochondrial OS=Homo sapiens GN=PCK2 PE=1 SV=3 - [PCKGM_HUMAN]	4.99E-04	4.3035	2.7546	1.33E-03	3.7526	3.1539
6_8	Q6P2Q9	Pre-mRNA-processing-splicing factor 8 OS=Homo sapiens GN=PRPF8 PE=1 SV=2 - [PRP8_HUMAN]	7.51E-04	3.9804	2.6754	9.61E-03	2.6965	2.3761
6_8	P12004	Proliferating cell nuclear antigen OS=Homo sapiens GN=PCNA PE=1 SV=1 - [PCNA_HUMAN]	1.02E-04	5.8706	2.7851	2.77E-03	3.3444	3.0255
6_8	P29590	Protein PML OS=Homo sapiens GN=PML PE=1 SV=3 - [PML_HUMAN]	2.29E-02	-2.2505	-2.7478	3.40E-03	-3.2458	-2.6767
6_8	P00734	Prothrombin OS=Homo sapiens GN=F2 PE=1 SV=2 - [THRB_HUMAN]	5.94E-03	-2.8680	-3.0942	1.61E-02	-2.4463	-2.2173
6_8	P34897	Serine hydroxymethyltransferase, mitochondrial OS=Homo sapiens GN=SHMT2 PE=1 SV=3 - [GLYM_HUMAN]	1.31E-02	2.6354	2.7760	9.70E-05	5.5019	2.9627
6_8	P17987	T-complex protein 1 subunit alpha OS=Homo sapiens GN=TCP1 PE=1 SV=1 - [TCPA_HUMAN]	2.70E-02	2.1421	2.8101	2.64E-05	6.4922	2.9627
6_8	P48643	T-complex protein 1 subunit epsilon OS=Homo sapiens GN=CCT5 PE=1 SV=1 - [TCPE_HUMAN]	4.12E-02	2.0703	2.7078	1.29E-04	5.2552	2.2997
6_8	P40227	T-complex protein 1 subunit zeta OS=Homo sapiens GN=CCT6A PE=1 SV=3 - [TCPZ_HUMAN]	2.26E-02	2.2611	2.7717	1.78E-03	3.5815	2.4556
6_8	P24821	Tenascin OS=Homo sapiens GN=TNC PE=1 SV=3 - [TENA_HUMAN]	8.02E-04	3.9539	2.7745	6.92E-03	2.8595	3.3556
6_8	P19971	Thymidine phosphorylase OS=Homo sapiens GN=TYMP PE=1 SV=2 - [TYPH_HUMAN]	4.62E-04	-4.3996	-3.0961	1.04E-02	-2.6568	-2.5883
6_8	Q15661	Tryptase alpha/beta-1 OS=Homo sapiens GN=TPSAB1 PE=1 SV=1 - [TRYB1_HUMAN]	2.12E-05	-8.0815	-3.1732	1.63E-03	-3.6298	-3.6971
6_8	Q9BQE3	Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 - [TBA1C_HUMAN]	1.12E-03	3.8333	2.9913	8.88E-03	2.7314	5.3684
6_8	Q3ZCM7	Tubulin beta-8 chain OS=Homo sapiens GN=TUBB8 PE=1 SV=2 - [TBB8_HUMAN]	1.67E-02	2.4752	2.9105	4.06E-02	2.0115	4.7612
6_8	P15374	Ubiquitin carboxyl-terminal hydrolase isozyme L3 OS=Homo sapiens GN=UCHL3 PE=1 SV=1 - [UCHL3_HUMAN]	8.14E-05	5.9587	2.6997	3.34E-06	8.5007	2.1742
6_8	P09327	Villin-1 OS=Homo sapiens GN=VIL1 PE=1 SV=4 - [VILI_HUMAN]	1.47E-02	2.5563	2.7640	4.34E-04	4.4303	3.6394
6_9	P42765	3-ketoacyl-CoA thiolase, mitochondrial OS=Homo sapiens GN=ACAA2 PE=1 SV=2 - [THIM_HUMAN]	3.31E-03	3.4890	2.9786	1.71E-04	5.2348	3.4571
6_9	P17858	6-phosphofructokinase, liver type OS=Homo sapiens GN=PFKL PE=1 SV=6 - [K6PL_HUMAN]	1.19E-02	2.7593	2.8732	2.77E-02	2.2229	2.5825
6_9	Q8IUX7	Adipocyte enhancer-binding protein 1 OS=Homo sapiens GN=AEBP1 PE=1 SV=1 - [AEBP1_HUMAN]	1.95E-02	-2.4656	-3.0447	1.56E-02	-2.5302	-2.1194
6_9	P00326	Alcohol dehydrogenase 1C OS=Homo sapiens GN=ADH1C PE=1 SV=2 - [ADH1G_HUMAN]	6.85E-03	3.0554	3.0221	3.99E-03	3.2541	3.3012
6_9	P30837	Aldehyde dehydrogenase X, mitochondrial OS=Homo sapiens GN=ALDH1B1 PE=1 SV=3 - [AL1B1_HUMAN]	4.65E-03	3.2531	2.9815	6.96E-06	8.0250	3.2111
6_9	P30838	Aldehyde dehydrogenase, dimeric NADP-preferring OS=Homo sapiens GN=ALDH3A1 PE=1 SV=3 - [AL3A1_HUMAN]	1.67E-02	2.5713	2.9253	3.14E-02	2.1571	2.6514
6_9	O60218	Aldo-keto reductase family 1 member B10 OS=Homo sapiens GN=AKR1B10 PE=1 SV=2 - [AK1BA_HUMAN]	8.37E-03	2.9371	3.1370	2.78E-04	4.8792	4.6421
6_9	Q04828	Aldo-keto reductase family 1 member C1 OS=Homo sapiens GN=AKR1C1 PE=1 SV=1 - [AK1C1_HUMAN]	4.99E-03	3.2032	3.0690	1.70E-04	5.2530	4.3834
6_9	P17516	Aldo-keto reductase family 1 member C4 OS=Homo sapiens GN=AKR1C4 PE=1 SV=3 - [AK1C4_HUMAN]	2.55E-06	18.4615	2.9851	6.17E-04	4.3734	3.3738
6_9	P15144	Aminopeptidase N OS=Homo sapiens GN=ANPEP PE=1 SV=4 - [AMPN_HUMAN]	1.19E-04	6.2313	2.8915	8.07E-03	2.8589	2.2684
6_9	P27216	Annexin A13 OS=Homo sapiens GN=ANXA13 PE=1 SV=3 - [ANX13_HUMAN]	2.01E-05	15.3326	2.9618	3.78E-04	4.6796	3.3431
6_9	Q99715	Collagen alpha-1(XII) chain OS=Homo sapiens GN=COL12A1 PE=1 SV=2 - [COCA1_HUMAN]	5.70E-04	-5.2139	-2.7725	2.30E-02	-2.3219	-3.8564
6_9	P12277	Creatine kinase B-type OS=Homo sapiens GN=CKB PE=1 SV=1 - [KCRB_HUMAN]	1.41E-02	2.6985	2.9996	2.69E-03	3.4743	2.6691
6_9	Q12805	EGF-containing fibulin-like extracellular matrix protein 1 OS=Homo sapiens GN=EFEMP1 PE=1 SV=2 - [FBLN3_HUMAN]	4.81E-04	-5.4086	-2.7915	2.79E-03	-3.4522	-2.5392

Fig. 7 continued

6 9	P07099	Epoxide hydrolase 1 OS=Homo sapiens GN=EPHX1 PE=1 SV=1 - [HYEP_HUMAN]	1.25E-03	4.1935	2.9616	8.09E-03	2.8571	2.3168
6 9	P51648	Fatty aldehyde dehydrogenase OS=Homo sapiens GN=ALDH3A2 PE=1 SV=1 - [AL3A2_HUMAN]	8.16E-04	4.7462	2.9085	6.65E-03	2.9613	2.3810
6 9	P23142	Fibulin-1 OS=Homo sapiens GN=FBLN1 PE=1 SV=4 - [FBLN1_HUMAN]	2.74E-05	-14.1074	-3.0170	1.95E-03	-3.6488	-2.7366
6 9	Q06210	Glutamine--fructose-6-phosphate aminotransferase [isomerizing] 1 OS=Homo sapiens GN=GFPT1 PE=1 SV=3 - [GFPT1_HUMAN]	2.86E-03	3.5963	2.8408	3.10E-02	2.1652	2.7338
6 9	P18283	Glutathione peroxidase 2 OS=Homo sapiens GN=GPX2 PE=1 SV=3 - [GPX2_HUMAN]	8.23E-03	2.9503	2.9865	3.40E-03	3.3422	2.6529
6 9	P08263	Glutathione S-transferase A1 OS=Homo sapiens GN=GSTA1 PE=1 SV=3 - [GSTA1_HUMAN]	6.29E-04	5.0685	3.0833	3.74E-03	3.2889	3.3590
6 9	P19827	Inter-alpha-trypsin inhibitor heavy chain H1 OS=Homo sapiens GN=ITIH1 PE=1 SV=3 - [ITIH1_HUMAN]	2.15E-02	-2.4017	-3.0907	2.01E-02	-2.3913	-3.0247
6 9	P23141	Liver carboxylesterase 1 OS=Homo sapiens GN=CES1 PE=1 SV=2 - [EST1_HUMAN]	8.36E-03	2.9379	3.1571	1.62E-04	5.2832	5.8487
6 9	O94760	N(G),N(G)-dimethylarginine dimethylaminohydrolase 1 OS=Homo sapiens GN=DDAH1 PE=1 SV=3 - [DDAH1_HUMAN]	1.92E-03	3.7678	2.9141	5.13E-06	9.7305	2.5246
6 9	P15559	NAD(P)H dehydrogenase [quinone] 1 OS=Homo sapiens GN=NQO1 PE=1 SV=1 - [NQO1_HUMAN]	1.01E-02	2.8073	3.0085	2.86E-02	2.2060	2.8346
6 9	Q15063	Periostin OS=Homo sapiens GN=POSTN PE=1 SV=2 - [POSTN_HUMAN]	3.92E-04	-5.5508	-3.1496	9.66E-03	-2.7612	-4.0560
6 9	Q14914	Prostaglandin reductase 1 OS=Homo sapiens GN=PTGR1 PE=1 SV=2 - [PTGR1_HUMAN]	8.05E-05	6.7992	3.0090	1.88E-05	6.9182	3.6958
6 9	P29590	Protein PML OS=Homo sapiens GN=PML PE=1 SV=3 - [PML_HUMAN]	4.89E-02	-2.0544	-2.7478	3.35E-03	-3.3476	-2.6767
6 9	Q13576	Ras GTPase-activating-like protein IQGAP2 OS=Homo sapiens GN=IQGAP2 PE=1 SV=4 - [IQGA2_HUMAN]	1.58E-03	3.8570	2.9098	1.05E-03	4.0409	4.2634
6 9	O94788	Retinal dehydrogenase 2 OS=Homo sapiens GN=ALDH1A2 PE=1 SV=3 - [AL1A2_HUMAN]	8.20E-04	4.7414	2.8083	8.33E-03	2.8383	2.0931
6 9	P10768	S-formylglutathione hydrolase OS=Homo sapiens GN=ESD PE=1 SV=2 - [ESTD_HUMAN]	4.66E-03	3.2499	2.8585	2.48E-02	2.2825	2.0784
6 9	Q13509	Tubulin beta-3 chain OS=Homo sapiens GN=TUBB3 PE=1 SV=2 - [TBB3_HUMAN]	2.26E-03	-3.7205	-2.9806	1.41E-03	-3.8370	-5.3253
6 9	P09327	Villin-1 OS=Homo sapiens GN=VIL1 PE=1 SV=4 - [VILI_HUMAN]	7.42E-03	3.0206	2.8983	1.60E-02	2.5165	2.8579
7 8	Q15029	116 kDa U5 small nuclear ribonucleoprotein component OS=Homo sapiens GN=EFTUD2 PE=1 SV=1 - [U5S1_HUMAN]	1.53E-04	5.8542	2.6748	1.09E-03	3.8379	2.4356
7 8	P42765	3-ketoacyl-CoA thiolase, mitochondrial OS=Homo sapiens GN=ACAA2 PE=1 SV=2 - [THIM_HUMAN]	1.80E-02	2.5477	2.7744	3.88E-04	4.5211	3.4170
7 8	P17858	6-phosphofructokinase, liver type OS=Homo sapiens GN=PFKL PE=1 SV=6 - [K6PL_HUMAN]	6.80E-03	2.9454	2.7263	4.63E-02	1.9438	2.7369
7 8	P24752	Acetyl-CoA acetyltransferase, mitochondrial OS=Homo sapiens GN=ACAT1 PE=1 SV=1 - [THIL_HUMAN]	5.98E-03	3.0398	2.6705	8.24E-03	2.7388	2.6171
7 8	P54819	Adenylate kinase 2, mitochondrial OS=Homo sapiens GN=AK2 PE=1 SV=2 - [KAD2_HUMAN]	2.24E-02	2.3853	2.7654	1.39E-02	2.4978	2.4695
7 8	P30837	Aldehyde dehydrogenase X, mitochondrial OS=Homo sapiens GN=ALDH1B1 PE=1 SV=3 - [AL1B1_HUMAN]	2.41E-02	2.3289	2.7940	3.04E-04	4.6736	3.7389
7 8	P49419	Alpha-aminoadipic semialdehyde dehydrogenase OS=Homo sapiens GN=ALDH7A1 PE=1 SV=5 - [AL7A1_HUMAN]	4.28E-03	3.3292	2.6932	7.03E-04	4.1257	2.0019
7 8	P54136	Arginine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=RARS PE=1 SV=2 - [SYRC_HUMAN]	1.20E-03	4.1941	2.6671	5.93E-04	4.2317	2.2914
7 8	P14868	Aspartate--tRNA ligase, cytoplasmic OS=Homo sapiens GN=DARS PE=1 SV=2 - [SYDC_HUMAN]	1.52E-02	2.6551	2.7269	2.97E-05	6.5838	2.6105
7 8	P53396	ATP-citrate synthase OS=Homo sapiens GN=ACLY PE=1 SV=3 - [ACLY_HUMAN]	7.46E-03	2.8855	2.6821	7.02E-03	2.8103	2.6394
7 8	Q92499	ATP-dependent RNA helicase DDX1 OS=Homo sapiens GN=DDX1 PE=1 SV=2 - [DDX1_HUMAN]	1.09E-03	4.3518	2.6698	5.69E-03	2.9319	2.2914
7 8	P31939	Bifunctional purine biosynthesis protein PURH OS=Homo sapiens GN=ATIC PE=1 SV=3 - [PURH_HUMAN]	4.49E-03	3.2810	2.8264	2.72E-05	6.6514	3.9166
7 8	P35222	Catenin beta-1 OS=Homo sapiens GN=CTNNB1 PE=1 SV=1 - [CTNB1_HUMAN]	9.12E-04	4.6869	2.8094	1.69E-05	7.1821	3.4997
7 8	P00450	Ceruloplasmin OS=Homo sapiens GN=CP PE=1 SV=1 - [CERU_HUMAN]	5.14E-04	-5.2499	-3.2327	1.16E-03	-3.7824	-3.1881

Fig. 7 continued

7_8	P54886	Delta-1-pyrroline-5-carboxylate synthase OS=Homo sapiens GN=ALDH18A1 PE=1 SV=2 - [P5CS_HUMAN]	1.92E-02	2.5008	2.6907	7.26E-03	2.7949	2.6394
7_8	P11387	DNA topoisomerase 1 OS=Homo sapiens GN=TOP1 PE=1 SV=2 - [TOP1_HUMAN]	2.36E-04	5.7135	2.7446	2.27E-03	3.4055	2.3440
7_8	Q7Z6Z7	E3 ubiquitin-protein ligase HUWE1 OS=Homo sapiens GN=HUWE1 PE=1 SV=3 - [HUWE1_HUMAN]	1.26E-03	4.1383	2.6790	2.03E-03	3.4666	2.5850
7_8	Q12805	EGF-containing fibulin-like extracellular matrix protein 1 OS=Homo sapiens GN=EFEMP1 PE=1 SV=2 - [FBLN3_HUMAN]	4.14E-02	-2.0801	-3.1926	1.71E-02	-2.3953	-2.8070
7_8	P68107	Epiplakin OS=Homo sapiens GN=EPPK1 PE=1 SV=2 - [EPIPL_HUMAN]	1.49E-02	2.6650	2.7065	4.72E-02	1.9332	2.4170
7_8	P55060	Exportin-2 OS=Homo sapiens GN=CSE1L PE=1 SV=3 - [XPO2_HUMAN]	1.77E-05	10.7992	2.9586	2.81E-03	3.3187	2.5016
7_8	P05062	Fructose-bisphosphate aldolase B OS=Homo sapiens GN=ALDOB PE=1 SV=2 - [ALDOB_HUMAN]	2.07E-03	-3.7768	-3.1196	1.87E-02	-2.3578	-2.9490
7_8	P09972	Fructose-bisphosphate aldolase C OS=Homo sapiens GN=ALDOC PE=1 SV=2 - [ALDOC_HUMAN]	9.01E-03	2.8059	2.8104	1.07E-02	2.6142	3.4517
7_8	Q92598	Heat shock protein 105 kDa OS=Homo sapiens GN=HSPH1 PE=1 SV=1 - [HS105_HUMAN]	8.50E-04	4.7538	2.8188	2.09E-04	4.9863	3.2769
7_8	P54868	Hydroxymethylglutaryl-CoA synthase, mitochondrial OS=Homo sapiens GN=HMGCS2 PE=1 SV=1 - [HMCS2_HUMAN]	1.98E-02	2.4773	2.8125	1.35E-03	3.6919	2.6105
7_8	O00410	Importin-5 OS=Homo sapiens GN=IPO5 PE=1 SV=4 - [IPO5_HUMAN]	4.46E-06	20.8239	2.7315	1.94E-04	5.0298	2.6216
7_8	P36776	Lon protease homolog, mitochondrial OS=Homo sapiens GN=LONP1 PE=1 SV=2 - [LONM_HUMAN]	2.05E-04	5.7542	2.6863	1.05E-02	2.6255	2.0255
7_8	Q15046	Lysine--tRNA ligase OS=Homo sapiens GN=KARS PE=1 SV=3 - [SYK_HUMAN]	1.07E-03	4.3821	2.6871	8.17E-04	4.0320	2.2997
7_8	P10253	Lysosomal alpha-glucosidase OS=Homo sapiens GN=GAA PE=1 SV=4 - [LYAG_HUMAN]	2.78E-02	-2.2210	-2.9030	1.25E-02	-2.5464	-2.0701
7_8	P98088	Mucin-5AC (Fragments) OS=Homo sapiens GN=MUC5AC PE=1 SV=3 - [MUC5A_HUMAN]	1.16E-02	-2.7572	-3.2398	2.30E-02	-2.2479	-4.7330
7_8	P24844	Myosin regulatory light polypeptide 9 OS=Homo sapiens GN=MYL9 PE=1 SV=4 - [MYL9_HUMAN]	3.77E-02	-2.0942	-2.9568	1.14E-02	-2.5871	-3.0701
7_8	Q14980	Nuclear mitotic apparatus protein 1 OS=Homo sapiens GN=NUMA1 PE=1 SV=2 - [NUMA1_HUMAN]	9.53E-04	4.5862	2.6318	6.98E-03	2.8125	2.2386
7_8	O00567	Nucleolar protein 56 OS=Homo sapiens GN=NOP56 PE=1 SV=4 - [NOP56_HUMAN]	3.97E-06	21.2834	2.7320	7.40E-04	4.0829	2.3142
7_8	Q02790	Peptidyl-prolyl cis-trans isomerase FKBP4 OS=Homo sapiens GN=FKBP4 PE=1 SV=3 - [FKBP4_HUMAN]	1.82E-02	2.5382	2.6916	1.71E-02	2.3942	2.9627
7_8	Q9Y285	Phenylalanine--tRNA ligase alpha subunit OS=Homo sapiens GN=FARSA PE=1 SV=3 - [SYFA_HUMAN]	1.37E-03	4.0534	2.6603	3.15E-03	3.2551	2.1622
7_8	Q9NSD9	Phenylalanine--tRNA ligase beta subunit OS=Homo sapiens GN=FARSB PE=1 SV=3 - [SYFB_HUMAN]	1.17E-03	4.2365	2.7077	8.14E-03	2.7442	2.5772
7_8	Q16822	Phosphoenolpyruvate carboxykinase [GTP], mitochondrial OS=Homo sapiens GN=PCK2 PE=1 SV=3 - [PCKGM_HUMAN]	2.99E-02	2.1678	2.7546	1.64E-02	2.4150	3.1539
7_8	Q6P2Q9	Pre-mRNA-processing-splicing factor 8 OS=Homo sapiens GN=PRPF8 PE=1 SV=2 - [PRP8_HUMAN]	1.02E-03	4.4613	2.6754	4.30E-03	3.0790	2.3761
7_8	P17844	Probable ATP-dependent RNA helicase DDX5 OS=Homo sapiens GN=DDX5 PE=1 SV=1 - [DDX5_HUMAN]	3.62E-02	2.1001	2.7914	1.44E-02	2.4809	3.2734
7_8	Q9Y265	RuvB-like 1 OS=Homo sapiens GN=RUVBL1 PE=1 SV=1 - [RUVB1_HUMAN]	9.49E-04	4.5963	2.7000	5.86E-06	7.6700	2.4517
7_8	P34897	Serine hydroxymethyltransferase, mitochondrial OS=Homo sapiens GN=SHMT2 PE=1 SV=3 - [GLYM_HUMAN]	1.04E-03	4.4256	2.7760	5.30E-05	6.0947	2.9627
7_8	P30153	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform OS=Homo sapiens GN=PPP2R1A PE=1 SV=4 - [2AAA_HUMAN]	7.08E-03	2.9157	2.6801	1.17E-02	2.5778	2.4170
7_8	Q15393	Splicing factor 3B subunit 3 OS=Homo sapiens GN=SF3B3 PE=1 SV=4 - [SF3B3_HUMAN]	5.20E-03	3.1604	2.7124	4.32E-04	4.4411	2.3761
7_8	P26368	Splicing factor U2AF 65 kDa subunit OS=Homo sapiens GN=U2AF2 PE=1 SV=4 - [U2AF2_HUMAN]	2.25E-02	2.3820	2.7558	1.86E-03	3.5097	2.1460
7_8	P17987	T-complex protein 1 subunit alpha OS=Homo sapiens GN=TCP1 PE=1 SV=1 - [TCPA_HUMAN]	1.09E-03	4.3620	2.8101	7.11E-04	4.1128	2.9627
7_8	P48643	T-complex protein 1 subunit epsilon OS=Homo sapiens GN=CCT5 PE=1 SV=1 - [TCPE_HUMAN]	2.12E-02	2.4266	2.7078	1.26E-03	3.7366	2.2997
7_8	Q99832	T-complex protein 1 subunit eta OS=Homo sapiens GN=CCT7 PE=1 SV=2 - [TCPH_HUMAN]	5.40E-03	3.1289	2.7803	3.63E-05	6.3897	3.0799

Fig. 7 continued

7_8	P40227	T-complex protein 1 subunit zeta OS=Homo sapiens GN=CCT6A PE=1 SV=3 - [TCPZ_HUMAN]	2.25E-02	2.3821	2.7717	5.49E-04	4.2879	2.4356
7_8	Q15661	Tryptase alpha/beta-1 OS=Homo sapiens GN=TPSAB1 PE=1 SV=1 - [TRYB1_HUMAN]	1.01E-03	-4.4847	-3.2103	1.04E-02	-2.6329	-2.4851
7_8	Q9BQE3	Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1 - [TBA1C_HUMAN]	2.63E-02	2.2628	2.9913	8.34E-03	2.7314	5.3684
7_8	Q3ZCM7	Tubulin beta-8 chain OS=Homo sapiens GN=TUBB8 PE=1 SV=2 - [TBB8_HUMAN]	2.00E-03	3.7866	2.9105	6.96E-03	2.8145	4.7672
7_8	P15374	Ubiquitin carboxyl-terminal hydrolase isozyme L3 OS=Homo sapiens GN=UCHL3 PE=1 SV=1 - [UCHL3_HUMAN]	4.09E-03	3.3737	2.6997	2.58E-05	6.6826	2.1742
7_9	Q02218	2-oxoglutarate dehydrogenase, mitochondrial OS=Homo sapiens GN=OGDH PE=1 SV=3 - [ODO1_HUMAN]	2.78E-02	2.2711	2.8169	3.99E-03	3.2389	2.0904
7_9	P42765	3-ketoacyl-CoA thiolase, mitochondrial OS=Homo sapiens GN=ACAA2 PE=1 SV=2 - [THIM_HUMAN]	7.15E-03	3.0962	2.9786	6.09E-05	6.3197	3.4571
7_9	P17858	6-phosphofructokinase, liver type OS=Homo sapiens GN=PFKL PE=1 SV=6 - [K6PL_HUMAN]	4.28E-03	3.4952	2.8732	3.75E-02	2.0746	2.5825
7_9	P07327	Alcohol dehydrogenase 1A OS=Homo sapiens GN=ADH1A PE=1 SV=2 - [ADH1A_HUMAN]	5.97E-04	4.9452	3.0186	7.17E-04	4.2777	3.8402
7_9	P00325	Alcohol dehydrogenase 1B OS=Homo sapiens GN=ADH1B PE=1 SV=2 - [ADH1B_HUMAN]	6.08E-04	4.9286	3.0213	1.71E-03	3.7002	4.0875
7_9	P00326	Alcohol dehydrogenase 1C OS=Homo sapiens GN=ADH1C PE=1 SV=2 - [ADH1C_HUMAN]	1.57E-04	6.0824	3.0221	2.49E-04	5.0469	3.3012
7_9	P30837	Aldehyde dehydrogenase X, mitochondrial OS=Homo sapiens GN=ALDH1B1 PE=1 SV=3 - [AL1B1_HUMAN]	1.14E-02	2.7981	2.9815	2.05E-04	5.2328	3.2111
7_9	Q04828	Aldo-keto reductase family 1 member C1 OS=Homo sapiens GN=AKR1C1 PE=1 SV=1 - [AK1C1_HUMAN]	4.05E-02	2.1236	3.0690	1.55E-04	5.4113	4.3834
7_9	P17516	Aldo-keto reductase family 1 member C4 OS=Homo sapiens GN=AKR1C4 PE=1 SV=3 - [AK1C4_HUMAN]	5.29E-06	18.4615	2.9851	6.15E-04	4.3734	3.3738
7_9	Q96IU4	Abhydrolase domain-containing protein 14B OS=Homo sapiens GN=ABHD14B PE=1 SV=1 - [ABHEB_HUMAN]	1.57E-02	2.6837	2.9301	9.96E-03	2.7317	2.4590
7_9	P27216	Annexin A13 OS=Homo sapiens GN=ANXA13 PE=1 SV=3 - [ANX13_HUMAN]	3.29E-05	15.3326	2.9618	3.88E-04	4.6796	3.3431
7_9	P04424	Argininosuccinate lyase OS=Homo sapiens GN=ASL PE=1 SV=4 - [ARLY_HUMAN]	2.41E-02	2.3611	2.9844	2.32E-03	3.5427	3.1717
7_9	Q9BXN1	Asporin OS=Homo sapiens GN=ASPN PE=1 SV=2 - [ASPN_HUMAN]	6.71E-03	3.1265	3.0403	9.42E-04	4.0961	2.9255
7_9	P20160	Azurocidin OS=Homo sapiens GN=AZU1 PE=1 SV=3 - [CAP7_HUMAN]	3.81E-02	-2.1536	-3.1358	2.93E-02	-2.1782	-3.1256
7_9	P17655	Calpain-2 catalytic subunit OS=Homo sapiens GN=CAPN2 PE=1 SV=5 - [CAN2_HUMAN]	1.51E-02	2.7100	2.9337	1.02E-03	4.0322	3.1575
7_9	P35221	Catenin alpha-1 OS=Homo sapiens GN=CTNNA1 PE=1 SV=1 - [CTNA1_HUMAN]	1.93E-02	2.5256	2.8648	4.09E-04	4.6333	3.3156
7_9	P35222	Catenin beta-1 OS=Homo sapiens GN=CTNNB1 PE=1 SV=1 - [CTNB1_HUMAN]	6.49E-04	4.8655	2.8628	7.00E-03	2.9204	2.3529
7_9	O60716	Catenin delta-1 OS=Homo sapiens GN=CTNND1 PE=1 SV=1 - [CTND1_HUMAN]	1.73E-02	2.6135	2.8941	4.71E-03	3.1312	2.5825
7_9	P12277	Creatine kinase B-type OS=Homo sapiens GN=CKB PE=1 SV=1 - [KCRB_HUMAN]	5.01E-04	5.2035	2.9996	6.36E-03	2.9718	2.6691
7_9	P21399	Cytoplasmic aconitate hydratase OS=Homo sapiens GN=ACO1 PE=1 SV=3 - [ACOC_HUMAN]	2.72E-02	2.2851	2.9054	3.65E-03	3.2897	2.7844
7_9	P07585	Decorin OS=Homo sapiens GN=DCN PE=1 SV=1 - [PGS2_HUMAN]	2.63E-02	2.3066	3.0320	3.72E-03	3.2775	3.5142
7_9	Q12805	EGF-containing fibulin-like extracellular matrix protein 1 OS=Homo sapiens GN=EFEMP1 PE=1 SV=2 - [FBLN3_HUMAN]	2.63E-03	-3.7598	-3.1926	6.34E-03	-2.9734	-2.8070
7_9	P51648	Fatty aldehyde dehydrogenase OS=Homo sapiens GN=ALDH3A2 PE=1 SV=1 - [AL3A2_HUMAN]	8.24E-03	3.0429	2.9085	6.40E-03	2.9613	2.3810
7_9	P23142	Fibulin-1 OS=Homo sapiens GN=FBLN1 PE=1 SV=4 - [FBLN1_HUMAN]	2.50E-03	-3.7848	-3.0299	1.15E-02	-2.6580	-2.9032
7_9	P09467	Fructose-1,6-bisphosphatase 1 OS=Homo sapiens GN=FBP1 PE=1 SV=5 - [F16P1_HUMAN]	1.10E-02	2.8138	2.9524	3.14E-04	4.8449	2.1812
7_9	P18283	Glutathione peroxidase 2 OS=Homo sapiens GN=GPX2 PE=1 SV=3 - [GPX2_HUMAN]	3.69E-03	3.6171	2.9965	8.56E-04	4.1683	2.6529
7_9	Q9UBQ7	Glyoxylate reductase/hydroxypyruvate reductase OS=Homo sapiens GN=GRHPR PE=1 SV=1 - [GRHPR_HUMAN]	1.54E-02	2.6999	2.9724	5.23E-04	4.4841	2.0324

Fig. 7 continued

7_9	P62879	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2 OS=Homo sapiens GN=GNB2 PE=1 SV=3 - [GBB2_HUMAN]	3.53E-02	2.1800	2.9336	2.60E-02	2.2275	2.3418
7_9	Q13151	Heterogeneous nuclear ribonucleoprotein A0 OS=Homo sapiens GN=HNRNPA0 PE=1 SV=1 - [ROA0_HUMAN]	1.75E-04	5.9396	2.9579	2.70E-05	7.2155	2.3251
7_9	P68431	Histone H3.1 OS=Homo sapiens GN=HIST1H3A PE=1 SV=2 - [H31_HUMAN]	1.13E-02	-2.8022	-3.6119	2.67E-02	-2.2170	-2.6804
7_9	P23141	Liver carboxylesterase 1 OS=Homo sapiens GN=CES1 PE=1 SV=2 - [EST1_HUMAN]	4.50E-04	5.3265	3.1571	1.75E-04	5.3535	5.8487
7_9	P55083	Microfibril-associated glycoprotein 4 OS=Homo sapiens GN=MFAP4 PE=1 SV=2 - [MFAP4_HUMAN]	2.60E-02	2.3148	2.9582	2.13E-03	3.5846	3.3874
7_9	P20774	Mimecan OS=Homo sapiens GN=OGN PE=1 SV=1 - [MIME_HUMAN]	5.47E-03	3.2936	3.0821	5.91E-05	6.3352	4.4171
7_9	P98088	Mucin-5AC (Fragments) OS=Homo sapiens GN=MUC5AC PE=1 SV=3 - [MUC5A_HUMAN]	1.32E-02	-2.7572	-3.2398	2.50E-02	-2.2479	-4.7330
7_9	O94760	N(G),N(G)-dimethylarginine dimethylaminohydrolase 1 OS=Homo sapiens GN=DDAH1 PE=1 SV=3 - [DDAH1_HUMAN]	2.55E-05	16.7724	2.9141	9.53E-09	12.5322	2.5246
7_9	P15559	NAD(P)H dehydrogenase [quinone] 1 OS=Homo sapiens GN=NQO1 PE=1 SV=1 - [NQO1_HUMAN]	8.97E-04	4.6853	3.0085	5.81E-03	3.0255	2.8346
7_9	Q6NZI2	Polymerase I and transcript release factor OS=Homo sapiens GN=PTRF PE=1 SV=1 - [PTRF_HUMAN]	4.11E-02	2.1147	2.8027	6.68E-03	2.9435	2.3674
7_9	Q14914	Prostaglandin reductase 1 OS=Homo sapiens GN=PTGR1 PE=1 SV=2 - [PTGR1_HUMAN]	1.29E-04	6.3825	3.0090	3.41E-05	6.9182	3.6958
7_9	Q08257	Quinone oxidoreductase OS=Homo sapiens GN=CRYZ PE=1 SV=1 - [QOR_HUMAN]	2.04E-02	2.4839	2.9942	3.38E-04	4.7784	3.1892
7_9	Q13576	Ras GTPase-activating-like protein IQGAP2 OS=Homo sapiens GN=IQGAP2 PE=1 SV=4 - [IQGA2_HUMAN]	4.85E-04	5.2530	2.9098	8.96E-04	4.1307	4.2634
7_9	O94788	Retinal dehydrogenase 2 OS=Homo sapiens GN=ALDH1A2 PE=1 SV=3 - [AL1A2_HUMAN]	8.07E-04	4.7414	2.8083	8.04E-03	2.8383	2.0931
7_9	P10768	S-formylglutathione hydrolase OS=Homo sapiens GN=ESD PE=1 SV=2 - [ESTD_HUMAN]	4.11E-03	3.5333	2.8585	6.67E-04	4.3291	2.0784
7_9	O00159	Unconventional myosin-Ic OS=Homo sapiens GN=MYO1C PE=1 SV=4 - [MYO1C_HUMAN]	6.04E-03	3.2089	2.8796	1.91E-03	3.6332	2.2377
8_9	P07327	Alcohol dehydrogenase 1A OS=Homo sapiens GN=ADH1A PE=1 SV=2 - [ADH1A_HUMAN]	1.39E-04	6.0443	3.0186	6.88E-04	4.2403	3.8402
8_9	P00325	Alcohol dehydrogenase 1B OS=Homo sapiens GN=ADH1B PE=1 SV=2 - [ADH1B_HUMAN]	1.44E-04	5.9823	3.0213	1.74E-03	3.6799	4.0875
8_9	P00326	Alcohol dehydrogenase 1C OS=Homo sapiens GN=ADH1C PE=1 SV=2 - [ADH1G_HUMAN]	5.16E-04	4.9575	3.0221	1.45E-04	5.2959	3.3012
8_9	P30838	Aldehyde dehydrogenase, dimeric NADP-preferring OS=Homo sapiens GN=ALDH3A1 PE=1 SV=3 - [AL3A1_HUMAN]	7.40E-04	4.7280	2.9253	1.83E-02	2.4303	2.6514
8_9	O60218	Aldo-keto reductase family 1 member B10 OS=Homo sapiens GN=AKR1B10 PE=1 SV=2 - [AK1BA_HUMAN]	4.75E-05	15.5571	3.1370	6.77E-05	6.0135	4.6421
8_9	Q04828	Aldo-keto reductase family 1 member C1 OS=Homo sapiens GN=AKR1C1 PE=1 SV=1 - [AK1C1_HUMAN]	4.17E-04	5.3391	3.0690	1.33E-04	5.3748	4.3834
8_9	P17516	Aldo-keto reductase family 1 member C4 OS=Homo sapiens GN=AKR1C4 PE=1 SV=3 - [AK1C4_HUMAN]	3.00E-05	18.4615	2.9851	5.58E-04	4.3734	3.3738
8_9	P15144	Aminopeptidase N OS=Homo sapiens GN=ANPEP PE=1 SV=4 - [AMPN_HUMAN]	3.09E-05	18.4472	2.8915	6.49E-04	4.2714	2.2684
8_9	P27216	Annexin A13 OS=Homo sapiens GN=ANXA13 PE=1 SV=3 - [ANX13_HUMAN]	7.89E-05	6.9815	2.9618	3.53E-04	4.6796	3.3431
8_9	O95831	Apoptosis-inducing factor 1, mitochondrial OS=Homo sapiens GN=AIFM1 PE=1 SV=1 - [AIFM1_HUMAN]	2.42E-02	-2.3303	-2.6760	1.09E-02	-2.6885	-2.1742
8_9	P14868	Aspartate--tRNA ligase, cytoplasmic OS=Homo sapiens GN=DARS PE=1 SV=2 - [SYDC_HUMAN]	2.92E-04	-5.6413	-2.7269	6.75E-05	-6.0148	-2.6105
8_9	Q9BXN1	Asporin OS=Homo sapiens GN=ASPN PE=1 SV=2 - [ASPN_HUMAN]	1.22E-03	4.0579	3.0403	6.71E-04	4.2561	2.9255
8_9	Q12864	Cadherin-17 OS=Homo sapiens GN=CDH17 PE=1 SV=3 - [CAD17_HUMAN]	1.69E-02	-2.6248	-2.7688	5.80E-04	-4.3465	-3.2065
8_9	P17655	Calpain-2 catalytic subunit OS=Homo sapiens GN=CAPN2 PE=1 SV=5 - [CAN2_HUMAN]	1.64E-03	3.8324	2.9337	3.11E-04	4.7921	3.1575
8_9	P00915	Carbonic anhydrase 1 OS=Homo sapiens GN=CA1 PE=1 SV=2 - [CAH1_HUMAN]	5.98E-05	8.4335	2.9651	3.89E-04	4.6136	3.1269
8_9	P00918	Carbonic anhydrase 2 OS=Homo sapiens GN=CA2 PE=1 SV=2 - [CAH2_HUMAN]	6.29E-05	7.5306	3.1049	8.88E-06	8.4464	4.5844

Fig. 7 continued

8_9	P06731	Carcinoembryonic antigen-related cell adhesion molecule 5 OS=Homo sapiens GN=CEACAM5 PE=1 SV=3 - [CEAM5_HUMAN]	2.08E-03	-3.7746	-2.8744	9.15E-03	-2.7772	-2.7240
8_9	P40199	Carcinoembryonic antigen-related cell adhesion molecule 6 OS=Homo sapiens GN=CEACAM6 PE=1 SV=3 - [CEAM6_HUMAN]	1.54E-03	-3.8466	-2.7790	3.50E-03	-3.2987	-2.0866
8_9	P07585	Decorin OS=Homo sapiens GN=DCN PE=1 SV=1 - [PGS2_HUMAN]	8.36E-04	4.6255	3.0320	2.45E-04	4.9630	3.5142
8_9	P54886	Delta-1-pyrroline-5-carboxylate synthase OS=Homo sapiens GN=ALDH18A1 PE=1 SV=2 - [P5CS_HUMAN]	4.21E-04	-5.3109	-2.6907	9.00E-03	-2.7851	-2.6394
8_9	P11387	DNA topoisomerase 1 OS=Homo sapiens GN=TOP1 PE=1 SV=2 - [TOP1_HUMAN]	2.28E-04	-5.7135	-2.7446	2.81E-03	-3.4055	-2.3440
8_9	Q7Z6Z7	E3 ubiquitin-protein ligase HUWE1 OS=Homo sapiens GN=HUWE1 PE=1 SV=3 - [HUWE1_HUMAN]	1.53E-05	-21.1366	-2.6790	1.85E-03	-3.6426	-2.5850
8_9	P53107	Epiplakin OS=Homo sapiens GN=EPPK1 PE=1 SV=2 - [EPIPL_HUMAN]	1.96E-05	-20.2857	-2.7065	1.41E-03	-3.7977	-2.4170
8_9	P07099	Epoxide hydrolase 1 OS=Homo sapiens GN=EPHX1 PE=1 SV=1 - [HYEP_HUMAN]	3.73E-03	3.4345	2.9616	8.71E-03	2.8021	2.3168
8_9	P55060	Exportin-2 OS=Homo sapiens GN=CSE1L PE=1 SV=3 - [XPO2_HUMAN]	2.17E-02	-2.4024	-2.9586	5.41E-03	-3.0565	-2.5016
8_9	P08294	Extracellular superoxide dismutase [Cu-Zn] OS=Homo sapiens GN=SOD3 PE=1 SV=2 - [SODE_HUMAN]	7.01E-04	4.7506	2.7472	1.51E-03	3.7493	2.2501
8_9	P51648	Fatty aldehyde dehydrogenase OS=Homo sapiens GN=ALDH3A2 PE=1 SV=1 - [AL3A2_HUMAN]	7.06E-04	4.7462	2.9065	6.54E-03	2.9613	2.3810
8_9	P05062	Fructose-bisphosphate aldolase B OS=Homo sapiens GN=ALDOB PE=1 SV=2 - [ALDOB_HUMAN]	1.47E-04	5.9529	3.0339	1.07E-09	15.1510	3.7003
8_9	P08263	Glutathione S-transferase A1 OS=Homo sapiens GN=GSTA1 PE=1 SV=3 - [GSTA1_HUMAN]	3.72E-05	16.8994	3.0833	2.36E-03	3.5063	3.3590
8_9	P09210	Glutathione S-transferase A2 OS=Homo sapiens GN=GSTA2 PE=1 SV=4 - [GSTA2_HUMAN]	3.85E-05	16.7462	3.0691	4.00E-02	2.0562	2.2365
8_9	Q92598	Heat shock protein 105 kDa OS=Homo sapiens GN=HSPH1 PE=1 SV=1 - [HS105_HUMAN]	3.53E-04	-5.5441	-2.8188	2.38E-04	-4.9863	-3.2769
8_9	P26583	High mobility group protein B2 OS=Homo sapiens GN=HMGB2 PE=1 SV=2 - [HMGB2_HUMAN]	3.52E-02	-2.1828	-2.8017	2.03E-02	-2.3734	-2.5611
8_9	O00410	Importin-5 OS=Homo sapiens GN=IPO5 PE=1 SV=4 - [IPO5_HUMAN]	3.12E-04	-5.6162	-2.7315	2.29E-04	-5.0238	-2.6216
8_9	P08729	Keratin, type II cytoskeletal 7 OS=Homo sapiens GN=KRT7 PE=1 SV=5 - [K2C7_HUMAN]	5.13E-04	4.9589	2.9851	2.97E-06	9.7253	3.7312
8_9	P23141	Liver carboxylesterase 1 OS=Homo sapiens GN=CES1 PE=1 SV=2 - [EST1_HUMAN]	9.72E-04	4.3968	3.1571	1.61E-04	5.2488	5.8487
8_9	P36776	Lon protease homolog, mitochondrial OS=Homo sapiens GN=LONP1 PE=1 SV=2 - [LONM_HUMAN]	8.51E-03	-3.0205	-2.6863	1.24E-02	-2.6255	-2.0255
8_9	Q15046	Lysine--tRNA ligase OS=Homo sapiens GN=KARS PE=1 SV=3 - [SYK_HUMAN]	4.86E-03	-3.2548	-2.6871	1.70E-04	-5.2184	-2.2997
8_9	P55083	Microfibril-associated glycoprotein 4 OS=Homo sapiens GN=MFAP4 PE=1 SV=2 - [MFAP4_HUMAN]	5.98E-05	8.4325	2.9582	1.94E-04	5.1489	3.3874
8_9	P20774	Mimecan OS=Homo sapiens GN=OGN PE=1 SV=1 - [MIME_HUMAN]	5.88E-05	9.2904	3.0821	4.42E-05	6.4233	4.4171
8_9	Q9HC84	Mucin-5B OS=Homo sapiens GN=MUC5B PE=1 SV=3 - [MUC5B_HUMAN]	9.07E-05	6.9465	2.9423	1.88E-03	3.6338	3.8016
8_9	P15559	NAD(P)H dehydrogenase [quinone] 1 OS=Homo sapiens GN=NQO1 PE=1 SV=1 - [NQO1_HUMAN]	1.10E-03	4.1795	3.0085	4.65E-03	3.1334	2.8346
8_9	Q14980	Nuclear mitotic apparatus protein 1 OS=Homo sapiens GN=NUMA1 PE=1 SV=2 - [NUMA1_HUMAN]	1.74E-02	-2.5913	-2.6318	1.64E-02	-2.4857	-2.2386
8_9	O00567	Nucleolar protein 56 OS=Homo sapiens GN=NOP56 PE=1 SV=4 - [NOP56_HUMAN]	1.24E-03	-4.0432	-2.7320	1.39E-03	-3.8030	-2.3142
8_9	Q6NZI2	Polymerase I and transcript release factor OS=Homo sapiens GN=PTRF PE=1 SV=1 - [PTRF_HUMAN]	7.77E-04	4.6743	2.8027	3.73E-03	3.2622	2.3674
8_9	Q6P2Q9	Pre-mRNA-processing-splicing factor 8 OS=Homo sapiens GN=PRPF8 PE=1 SV=2 - [PRP8_HUMAN]	1.68E-02	-2.6303	-2.6754	2.68E-02	-2.2291	-2.3761
8_9	Q14914	Prostaglandin reductase 1 OS=Homo sapiens GN=PTGR1 PE=1 SV=2 - [PTGR1_HUMAN]	4.46E-05	16.1660	3.0090	2.68E-05	6.9182	3.6958
8_9	Q9P258	Protein RCC2 OS=Homo sapiens GN=RCC2 PE=1 SV=2 - [RCC2_HUMAN]	1.14E-03	-4.1329	-2.6566	2.24E-03	-3.5270	-2.4152
8_9	Q13576	Ras GTPase-activating-like protein IQGAP2 OS=Homo sapiens GN=IQGAP2 PE=1 SV=4 - [IQGA2_HUMAN]	4.96E-05	15.2774	2.9098	7.27E-04	4.2033	4.2634

Fig. 7 continued

8_9	O94788	Retinal dehydrogenase 2 OS=Homo sapiens GN=ALDH1A2 PE=1 SV=3 - [AL1A2_HUMAN]	7.16E-04	4.7414	2.8083	8.15E-03	2.8383	2.0931
8_9	Q99832	T-complex protein 1 subunit eta OS=Homo sapiens GN=CCT7 PE=1 SV=2 - [TCPH_HUMAN]	2.99E-03	-3.6150	-2.7803	1.30E-05	-8.0441	-2.6081
8_9	P24821	Tenascin OS=Homo sapiens GN=TNC PE=1 SV=3 - [TENA_HUMAN]	8.85E-04	-4.5676	-2.7745	9.91E-03	-2.7375	-3.3556
8_9	Q15661	Tryptase alpha/beta-1 OS=Homo sapiens GN=TPSAB1 PE=1 SV=1 - [TRYB1_HUMAN]	6.19E-05	7.6294	2.9718	4.26E-04	4.5615	3.5929
8_9	O00159	Unconventional myosin-Ic OS=Homo sapiens GN=MYO1C PE=1 SV=4 - [MYO1C_HUMAN]	1.54E-02	2.7169	2.8796	1.77E-02	2.4464	2.2377