

Serum/Plasma Proteome

Analysis of the Human Serum Proteome

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Abstract

Changes in serum proteins that signal histopathological states, such as cancer, are useful diagnostic and prognostic biomarkers. Unfortunately, the large dynamic concentration range of proteins in serum makes it a challenging proteome to effectively characterize. Typically, methods to deplete highly abundant proteins to decrease this dynamic protein concentration range are employed, yet such depletion results in removal of important low abundant proteins.

A multi-dimensional peptide separation strategy utilizing conventional separation techniques combined with tandem mass spectrometry (MS/MS) was employed for a proteome analysis of human serum. Serum proteins were digested with trypsin and resolved into 20 fractions by ampholyte-free liquid phase isoelectric focusing. These 20 peptide fractions were further fractionated by strong cation-exchange chromatography,

each of which was analyzed by microcapillary reversed-phase liquid chromatography coupled online with MS/MS analysis.

This investigation resulted in the identification of 1444 unique proteins in serum. Proteins from all functional classes, cellular localization, and abundance levels were identified.

This study illustrates that a majority of lower abundance proteins identified in serum are present as secreted or shed species by cells as a result of signalling, necrosis, apoptosis, and hemolysis. These findings show that the protein content of serum is quite reflective of the overall profile of the human organism and a conventional multi-dimensional fractionation strategy combined with MS/MS is entirely capable of characterizing a significant fraction of the serum proteome. We have constructed a publicly available human serum proteomic database (<http://bpp.nci.nih.gov>) to provide a reference resource to facilitate future investigations of the vast archive of pathophysiological content in serum.

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Introduction

A major trend underlying current biological research is the development and application of analytical methods capable of making global measurements of entire biological systems. These advances have created unique opportunities in the field of medicine, where the results from gene expression studies are expected to help identify cellular alterations associated with disease diagnosis, etiology, progression, outcome, and response to therapy. A major goal is to obtain a greater understanding of the function of proteins in a cellular context, as well as their more conventionally delineated individual molecular function. This global view promises to provide a greater understanding of the cellular responses to events such as cell division, differentiation, respiration, hormonal signalling, and changes in homeostasis. The impetus for conducting global measurements of biological systems is to establish new diagnostic approaches and therapeutic targets for a host of maladies, including infectious diseases, behavioral disorders, developmental defects, neurodegenerative diseases, aging, and cancer.

Whereas the availability of complete genome sequences opens the door to important biological advances, much of the detailed understanding of cellular systems and the roles of its constituents will, by necessity, be based upon proteomics, which has classically been defined as the study of the entire complement of proteins, and their modifications, expressed by a cell. Typically, proteomic investigations are conducted using mass spectrometry (MS) as the core analytical technique for protein identification and relative quantitation (1). Current MS-based proteomic measurements rely heavily on databases of predicted proteins generated from genome sequence information

to correlate data obtained from tandem MS (MS/MS) measurements for protein identification. Because a potential archive of pathophysiological information is endowed to serum from its constant perfusion of tissues, particular focus has been given to developing methods to allow its facile investigation by proteomic technologies. Serum is a rather unique biological sample in that no specific cellular genomic expression *per se* contributes to its protein content, but rather it may be hypothesized that the protein content is contributed by the summation of all cellular genomic expression in the organism. It is therefore clear that the collection of histopathological information in serum is comprised not only of the expected circulatory proteins such as immunoglobulins, but also of peptides and proteins that are secreted into the blood and shed species from diseased, dying, or dead cells (2).

The importance of characterizing the protein content of serum is underscored by the fact that subtle changes of low abundance proteins have been shown to indicate development of different disease states such as ovarian (3,4), breast, (5) and prostate (6,7) cancer. Despite decades of research, however, only a few hundred proteins have been identified from either serum or plasma (8,9). Unfortunately, the large dynamic concentration range of proteins in serum renders this proteome cumbersome to effectively characterize. Most serum proteome studies have therefore removed high abundance proteins, such as albumin or immunoglobulins, prior to analysis. It is plausible that depletion of highly abundant proteins from serum may in fact result in concomitant depletion of the histopathological archive of potentially important peptides and proteins that may be present at low abundance. Hence, the multi-dimensional chromatographic-MS/MS method we have utilized in the present work does not rely on the depletion of any highly abundant proteins.

While the importance of studying the serum proteome is clear, its composition and complexity make it one of the most challenging proteome samples to characterize. Serum is composed of a wide variety of biomolecules ranging from large molecules such as proteins and lipids, to small metabolites such as peptides, amino acids, and electrolytes. Twenty-two proteins, such as albumin, immunoglobulins, haptoglobin, transferrin, and lipoproteins, account for 99% of the protein mass of serum (2). It is estimated that as many as 10,000 unique proteins are present within the human serum proteome that span a dynamic range of concentration estimated to be greater than 10^9 (2). This dynamic range of protein concentration is the primary factor that makes global characterization of the serum proteome so challenging and necessitates effective fractionation methods capable of separating high abundance proteins from low abundance species prior to MS or MS/MS analyses.

The most extensive characterization and cataloging of serum proteins to date is that reported by Adkins et al., in which 490 proteins were identified (8). Because the presence of high abundant proteins, such as albumin and immunoglobulins, in serum pose a serious problem for MS analysis, a common strategy is to deplete these proteins using affinity based methods as in the study by Adkins et al. (8). It has been proposed, however, that such a depletion may also result in the loss of pathophysiologically important low abundant proteins (10).

Here we show that a multidimensional peptide separation strategy utilizing conventional separation techniques combined with tandem mass spectrometry is capable of providing broad-scale identification of proteins in human serum without the need for prior depletion of highly abundant proteins. Our investigation resulted in the identification of 1444 proteins in serum. Proteins from all functional classes, cellular localization, and abundance levels

were identified, demonstrating the ability to conduct investigations of human serum using conventional proteomic technologies.

Materials

1. Pooled standard human serum, NH_4HCO_3 , NaHCO_2 , urea, formic acid, trifluoroacetic acid (TFA), and dithiothreitol (DTT) were purchased from Sigma (St. Louis, MO).
2. Porcine sequencing grade modified trypsin was purchased from Promega (Madison, WI).
3. High performance liquid chromatography (HPLC) grade acetonitrile was obtained from EMD Chemicals Inc. (Gibbstown, NJ).
4. All buffers and reagents were used as supplied from the manufacturer and prepared in double distilled water using a NANOPure Diamond water system (Barnstead International, Dubuque, IA).

Methods

Serum Tryptic Digestion

Two hundred microliters of a pooled standard human serum (approx 15 mg total protein, Sigma) was diluted 1:1 (v/v) with 100 mM NH_4HCO_3 , pH 8.2, and boiled for 5 min. Trypsin (Promega) was added to the denatured serum at a protein to enzyme ratio of 50:1 (w/w). Trypsin digestion was carried out at 37°C overnight. The digest was supplemented with the same amount of trypsin the following day and incubated for an additional 5 h. The entire digestion process was completed in 20 h.

Liquid-Phase Isoelectric Focusing

The serum tryptic digest was fractionated using a preparative-scale isoelectric focusing (IEF) device (Rotofor, Bio-Rad, Hercules, CA). The focusing cell, which is divided into 20 chambers by permeable membranes, was assembled, filled with 2M urea, 2 mM DTT and pre-run for 5 min at a constant power of 5 W to remove any residual ionic contaminants from the system. The tryptically digested serum sample was diluted to a total of 15 mL

in 2M urea, 2 mM DTT and loaded onto the focusing cell followed by a focusing step separating the entire peptide mixture into 20 fractions. The peptides in the different chambers, approx 625 μ L each, were aspirated simultaneously with vacuum into separate test tubes. The apparatus was kept at 10°C using a circulating refrigerated water bath. The focusing was conducted at 10 W for 2 h. Formation of a pH gradient was confirmed by measuring the pH of each fraction using pH indicator paper.

The IEF peptide fractions were desalted to remove urea by solid phase extraction (SPE) using C-18-bonded cartridges (Extract-Clean Columns, Alltech, Deerfield, IL). Each cartridge was equilibrated with 2 bed volumes of methanol and washed with 2 volumes of 0.1% (v/v) trifluoroacetic acid (TFA). The peptide fractions were applied to the columns and the cartridge was washed with 2 volumes of 0.1% (v/v) TFA. Peptides were eluted with 4 mL of acetonitrile: H₂O:TFA (80:19.9:0.1, v/v/v). The eluent was initially concentrated to 1 mL by evaporation under argon atmosphere at 37°C and to 300 μ L by vacuum centrifugation. The peptide fractions were stored at 4°C prior to microcapillary reversed-phase liquid chromatography (μ RPLC)-MS/MS analysis.

Strong Cation Exchange Fractionation

Typically, 250 μ L of each Rotofor fraction were injected onto a strong cation exchange liquid chromatography (SCXLC) column (Polysulfoethyl A, PolyLC Inc., Columbia, MD). An ammonium formate/acetonitrile multistep gradient was used to elute the peptides from the column at a flow rate of 1 mL/min: 2% solvent B for 2 min, followed by 30% B in 50 min, then 100% B in 28 min and maintained at 100% B for 16 min. Solvent A was 20% acetonitrile, and solvent B was 20% acetonitrile, 0.5M ammonium formate, pH 3.0. Six fractions from the SCXLC column were collected between minutes 10 and 51. The last (seventh) fraction was collected between minutes 52 and 76. Each SCXLC frac-

tion was lyophilized and reconstituted in 20 μ L of 0.1% formic acid prior to μ RPLC-MS/MS.

Microcapillary LC-MS/MS Analysis

Microcapillary RPLC was performed using an Agilent 1100 capillary LC system (Agilent Technologies, Palo Alto, CA) coupled online to an ion trap (IT) mass spectrometer (LCQ DecaXP, ThermoElectron, San Jose, CA) with the nanoelectrospray interface supplied by the manufacturer. Microcapillary RPLC separations of each sample were performed using 75 μ m id \times 360 μ m od \times 10 cm long fused silica capillary columns (Polymicro Technologies, Phoenix, AZ) that were slurry packed in house with 3 μ m, 300 Å pore size C-18 silica-bonded stationary phase (Vydac, Hysperia, CA). After injecting 7 μ L of sample, the column was washed for 20 min with 98% solvent A (0.1% formic acid in water, v/v) and peptides were eluted using a linear gradient of 2% solvent B (0.1% formic acid in 100% acetonitrile, v/v) to 85% solvent B in 160 min at a constant flow rate of 0.5 μ L/min.

The IT mass spectrometer was operated in a data dependent mode in which each full MS scan was followed by three MS/MS scans where the three most abundant peptide molecular ions were dynamically selected from the prior scan for collision-induced dissociation (CID) using a normalized collision energy of 38%. Dynamic exclusion was utilized to prevent redundant acquisition of peptides previously selected for MS/MS. The temperature of the heated capillary and electrospray voltage were 180°C and 1.5 kV, respectively.

Bioinformatic Analysis

Tandem MS spectra from the μ RPLC-MS/MS analyses were searched against the Expert Protein Analysis System's human proteomic database (<http://www.expasy.org>) with SEQUEST operating on an 18 node Beowulf cluster (ThermoElectron). For a peptide to be considered legitimately identified, it had to

Table 1
SEQUEST Filter Criteria for Peptide Identification

Charge State ^a	Xcorr ^b	Proteolytic Constraint
+1	≥ 1.9	Fully Tryptic
+1	≥ 2.1	Fully chymotryptic and/or elastic
+1	≥ 2.2	Partially tryptic, chymotryptic, and/or elastic
+1	≥ 2.2	No protease constraint
+2	≥ 2.2	Fully Tryptic
+2	≥ 2.2	Fully chymotryptic and/or elastic
+2	≥ 2.4	Partially tryptic, chymotryptic, and/or elastic
+2	≥ 3.0	No protease constraint
+3	≥ 3.5	Fully Tryptic
+3	≥ 3.5	Fully chymotryptic and/or elastic
+3	≥ 3.75	Partially tryptic, chymotryptic, and/or elastic
+3	≥ 3.75	No protease constraint

^aCharge state of the peptide molecular ion chosen for tandem MS.

^bSEQUEST cross correlation score.

achieve stringent charge state and proteolytic cleavage-dependent cross correlation (X_{corr}) scores similar to those previously reported (8,11) (Table 1) and a minimum delta correlation (DelCN) of 0.08.

Results

One of the primary focuses in the field of proteomics is to develop technologies to efficiently interrogate the pathophysiological state of an organism through the analysis of serum. A number of technologies have been developed toward achieving this goal and range from those designed to recognize a diagnostic proteomic pattern (3,5–7) (without the need to identify any of the components contributing to the diagnostic pattern) to those that identify a unique biomarker for a specific disease state (12). Disease biomarker identification is generally accomplished using one of two strategies: resolution of serum by two dimensional-polyacrylamide gel electrophoresis (2D-PAGE) followed by MS analysis of the stained protein spots, or multi-dimensional liquid chromatographic/electrophoretic separation coupled with MS analysis. Both of these approaches rely heavily on a high-resolution

separation/fractionation step prior to MS analysis to enable identification of greater numbers of proteins.

The presence of high abundant proteins, such as albumin and immunoglobulins, in serum pose a serious analytical challenge for MS-based proteomic analysis. A common strategy employed in serum proteomic investigations is depletion of the highly abundant proteins using affinity based methods. However, such depletion strategies likely result in loss of physiologically important low abundant proteins. The objective of this study was to determine if a three-dimensional fractionation based on liquid phase peptide IEF in the first dimension, strong cation exchange in the second dimension, and hydrophobicity in the third dimension prior to MS would allow for the identification of lower abundance proteins in serum in the presence of the more common highly abundant proteins.

Serum Proteome Analysis

The experimental procedure employed in this study (Fig. 1) utilized a tryptic digestate of 200 μL of a standard pooled human serum sample (approx 15 mg) that was fractionated

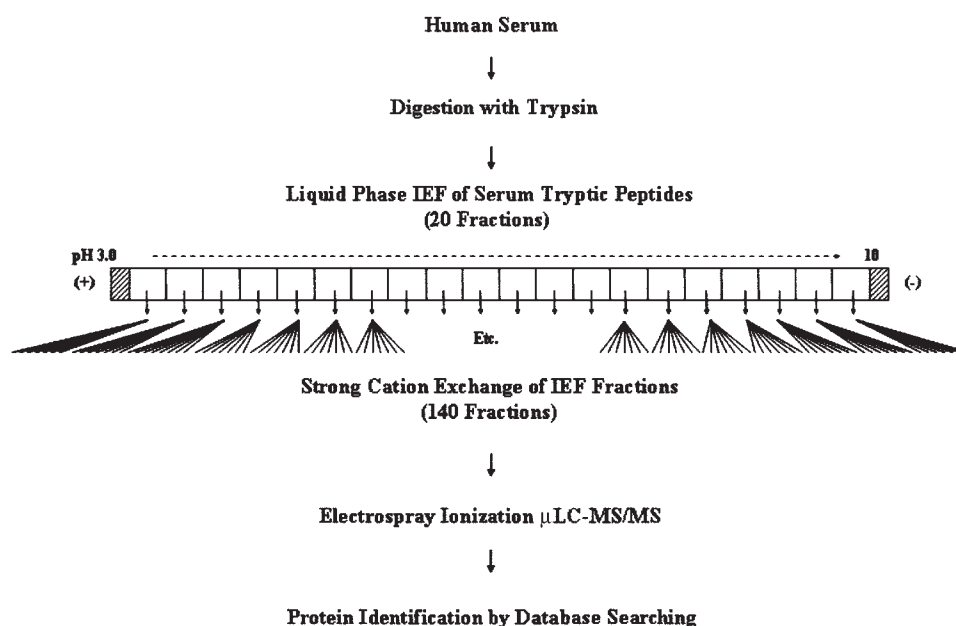


Fig. 1. Flowchart of the experimental strategy employed for the global analysis of the human serum proteome. Two hundred microliters of pooled human serum was digested with trypsin. The serum digestate was subjected to ampholyte-free IEF from which 20 fractions were collected. Each IEF fraction was further fractionated by SCX into seven fractions that were each analyzed by μ LC-MS/MS.

by liquid phase isoelectric focusing (IEF). Typically, preparative liquid phase IEF is employed for separating or fractionating proteins, not peptides. In the separation of proteins by IEF, the pH gradient is generated using ampholytes that must be removed prior to additional downstream separations and/or MS analysis (13). Arising from the amphoteric nature of complex peptide mixtures, it is possible to exploit peptide "auto focusing" for pH gradient generation in liquid phase IEF, enabling the separation of peptide mixtures without the use of ampholytes. The potential sample loss during the necessary ampholyte removal prior to subsequent separations or MS analysis is also eliminated. Twenty IEF fractions were collected with measured pH values ranging from 3.0 to 10.0 (data not shown), indicating that the peptides had successfully autofocused. A small aliquot of each of the 20 IEF fractions was desalted by solid phase extraction, concentrated and analyzed

by μ RPLC coupled online to a conventional IT-MS for peptide identification by MS/MS. Bioinformatic analysis of the MS/MS spectra from the 20 IEF serum peptide fractions resulted in the identification of 957 unique peptides corresponding to 473 proteins. In addition, the remaining aliquots of each of the 20 IEF fractions were further resolved by SCXLC into 7 fractions. Each of the 140 IEF-SCXLC serum peptide fractions was analyzed by μ RPLC-MS/MS. Analysis of the set of MS/MS spectra obtained from the 140 IEF/SCX/ μ RPLC fractions resulted in the identification of 2071 unique peptides corresponding to 1143 proteins. When combined, the μ RPLC-MS/MS analyses of the 20 IEF and the 140 IEF-SCXLC serum peptide fractions resulted in the total identification of 2646 unique peptides corresponding to 1444 unique proteins from the human serum proteome (Table 1, Supplemental).

We sought to estimate the confidence interval of our bioinformatic results by searching the

MS/MS spectra of selected μ RPLC-MS/MS analyses against a proteomic database derived from *Archea* that possesses 12,038 "non-human" protein sequences. The number of peptides identified from the MS/MS spectra of the human-derived serum peptides when searched against this *Archea* database should give a reasonable measure of the false positive rate inherent in the data. We found the overall confidence interval of our analysis to be >90% using the present SEQUEST filtering criteria. For example, 624 identified human peptides were identified from one particularly rich μ RPLC-MS/MS run. When this same μ RPLC-MS/MS run was searched against the *Archea* database, only 60 peptides were identified, giving a confidence interval in the identifications when the data is searched against the appropriate human database of approx 90% of this specific run.

Serum contains thousands of proteins and peptides such as the common highly abundant proteins (such as albumin and immunoglobulins) to the extremely low abundant proteins that are present in a large dynamic concentration range (2). Indeed a single protein, albumin, comprises greater than 50% of the protein content (Fig. 2). A total of ten proteins constitute approx 90% of the protein content of serum and the remaining approx 9% is primarily made up of only twelve different proteins. Hence, it is potentially only the remaining approx 1% of the protein content of serum that is important to characterize in the search for potential biomarkers of disease states.

The Nature of the Human Serum Proteome

To identify biomarkers in serum, any given list of identified proteins must be reflective of the organism as a whole and not just contain the expected circulatory proteins. The proteins we have identified arise from a wide range of functional classes (Fig. 3). As anticipated all of the 22 highest abundant proteins, as illustrated in Fig. 2, were identified as were proteins com-

monly associated with serum, such as coagulation and complement factors, transport and binding proteins, cytokines, growth factors, and hormones. Quite remarkably, we find a number of proteins not commonly associated with serum, for example, intracellular and membrane associated proteins make up 39.6% and 32.1% of the identified proteins, respectively. Indeed, such proteins as transcription factors, nuclear proteins, channels, and receptors were identified, substantiating the notion that serum possesses an archive of potentially pathophysiological information arising from the fact that cellular proteins and peptides may be released into the bloodstream during necrosis, apoptosis, and hemolysis (2,8).

Detection and Identification of Low Abundant Proteins

Recent reports estimate that the dynamic concentration range separating the lowest abundant proteins (e.g., hormones and cytokines) from the most abundant proteins (e.g., albumin) in human serum to be more than nine orders of magnitude (2). Hence, if the average concentration of serum albumin is greater than 50 mg/mL, analytical technologies must be able to detect proteins present at or below the pg/mL level to enable comprehensive proteomic measurements. Indeed, this low concentration is a level at which many key proteins currently utilized as disease indicators are present, such as prostate-specific antigen (PSA) (14) and cancer antigen 125 (CA 125) (15) for prostate and ovarian cancer, respectively. Inspection of the proteins identified in our study demonstrates that the use of a conventional multi-dimensional separation strategy coupled with conventional MS detection successfully enables identification of proteins that span this dynamic concentration range. For example, we confidently identified interferon γ (<10 pg/mL) (2) and amyloid A4 (>10 ng/mL) (16) (Fig. 4), proteins known to be present in serum at low abundance,

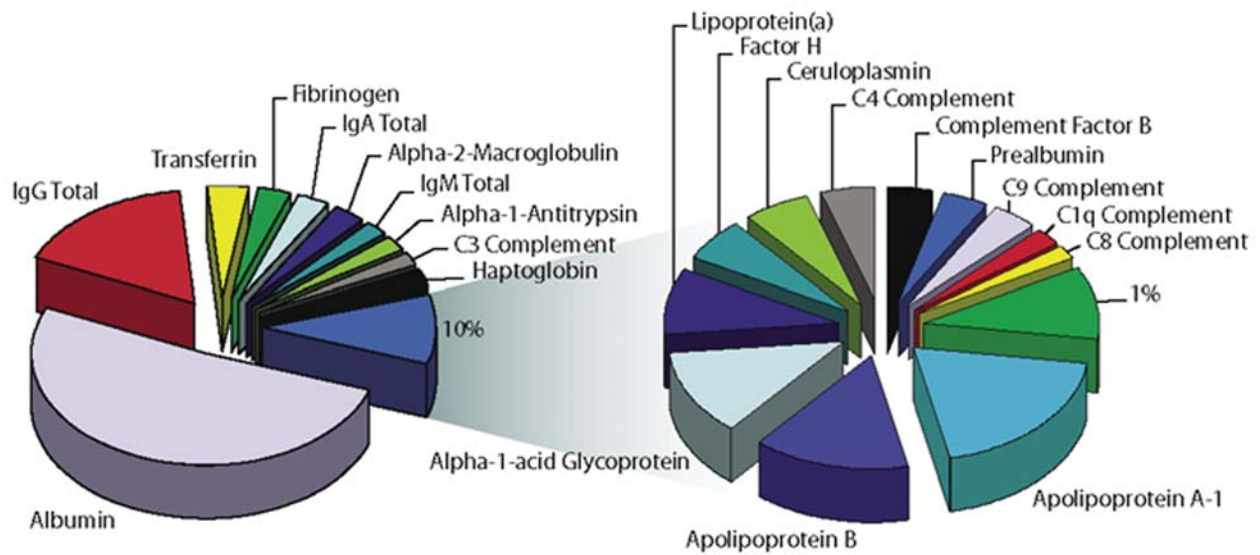


Fig. 2. Pie chart representing the relative contribution of proteins within the blood proteome. Twenty-two proteins constitute approx 99% of the protein content.

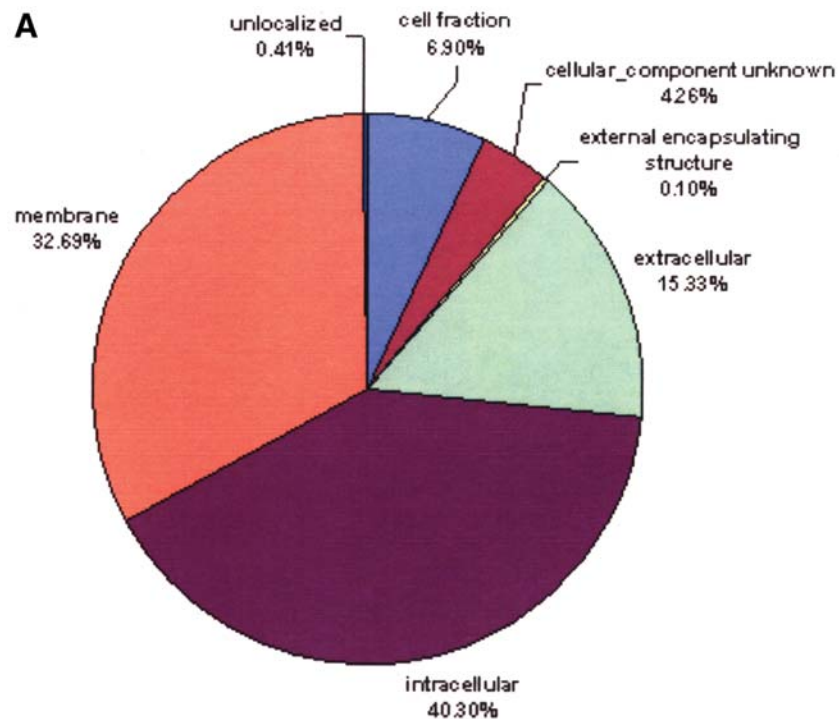
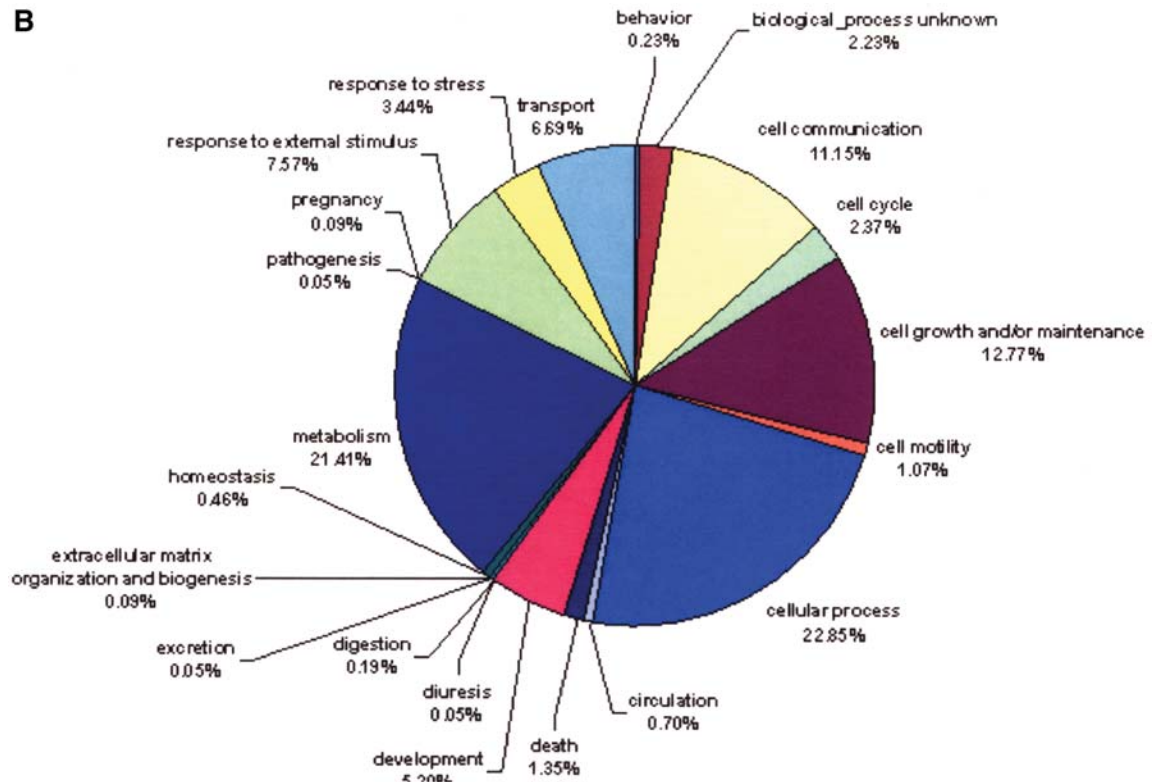
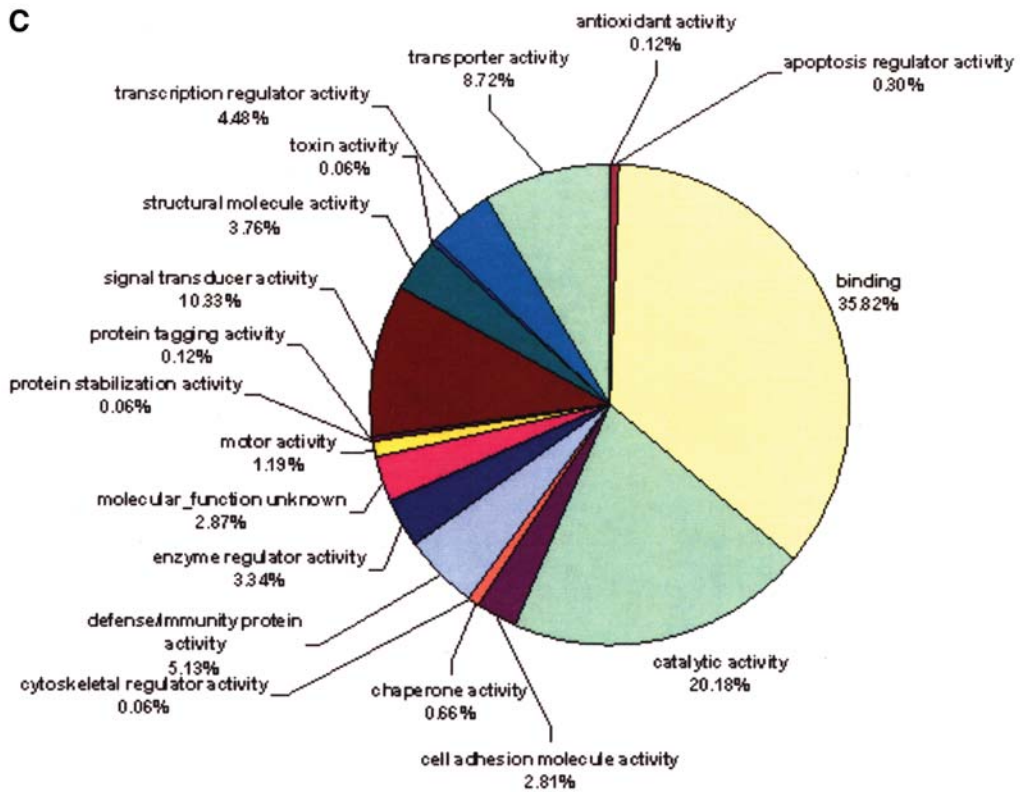


Fig. 3. Pie charts illustrating the classification of the proteins identified in human serum according to the three organizing principles of the gene ontology consortium (<http://www.geneontology.org>). **(A)** Cellular compartment, **(B)** biological process, and **(C)** molecular function.

B



C



without the need to deplete highly abundant proteins, such as albumin, the various immunoglobulins, and apolipoprotein, all of which are present at well above the mg/mL level.

A Serum Proteome Database

The development of new technologies promises new biomarker discoveries to aid in the diagnosis and prognosis of diseases. It is likely that the most successful strategies for biomarker discovery will employ methods that allow parallel characterization of proteins. Because serum possesses such a rich archive of potential histopathological information as demonstrated in this work, there exists great potential and benefit to "mine" serum for disease-specific biomarkers. To increase the success rate at which novel and more effective ensembles of biomarkers may be enumerated from serum requires the ability to comprehensively characterize such analytically challenging samples, as no targeted methods exist for their discovery. We have produced a benchmark serum proteome database (<http://bpp.nci.nih.gov>) that represents a three-fold increase in the number of proteins identified to date that will serve as a web-accessible resource to aid in serum biomarker investigations. In the future, this database will be sequentially updated and annotated as new proteins and their function are discovered. Presently, this reference resource should contribute substantially to the advancement of our understanding of the human serum proteome, to comparative biology, and to the isolation of human disease biomarkers, particularly those underlying complex disease states such as cancer.

Conclusions

A major thrust in proteomics aims at identification of biomarkers useful for early disease diagnosis, disease progression, or response to therapy. This task is obviously laborious as there are several levels of complexity that are counter to biomarker discovery. One such

level lies within the samples being assayed. For true utility, a biomarker should be assayable through protein-rich and readily obtainable biofluids, such as plasma or serum. Unfortunately, these samples are made up of a myriad of different biological molecules including proteins, peptides, carbohydrates, small molecules, and lipids that are present at extreme dynamic ranges of concentration. A second level of complexity arises from the organism itself with respect to the particular disease state. In the case of identifying a serum biomarker for the presence of cancer for example, such a biomarker is being used to indicate a malignancy within a patient that may comprise less than 0.1% of the body mass. In essence the search is on for analytical "needles in the haystack." A clear need exists for a more complete understanding of the matrix protein background of the "haystack" of serum and for public dissemination of such information as updatable databases of proteins, interpreted MS/MS spectra, and even raw MS data, as in the case of the publicly available database constructed from the present work (<http://bpp.nci.nih.gov>).

Although serum is one of the most analytically challenging proteome samples to characterize, the ability to do so promises rich information regarding the histopathological state of a patient and its analysis using proteomic techniques is being heavily relied upon for the discovery of reliable disease biomarkers. Fortunately, our study illustrates that a majority of lower abundance proteins identified in serum are present as secreted or shed species likely by cells as a result of signalling, necrosis, apoptosis and hemolysis. Taken together, these findings show that the protein content of serum is quite reflective of the overall profile of the human organism and that conventional multi-dimensional fractionation strategies combined with conventional MS analysis are entirely capable of characterizing a significant fraction of the serum proteome.

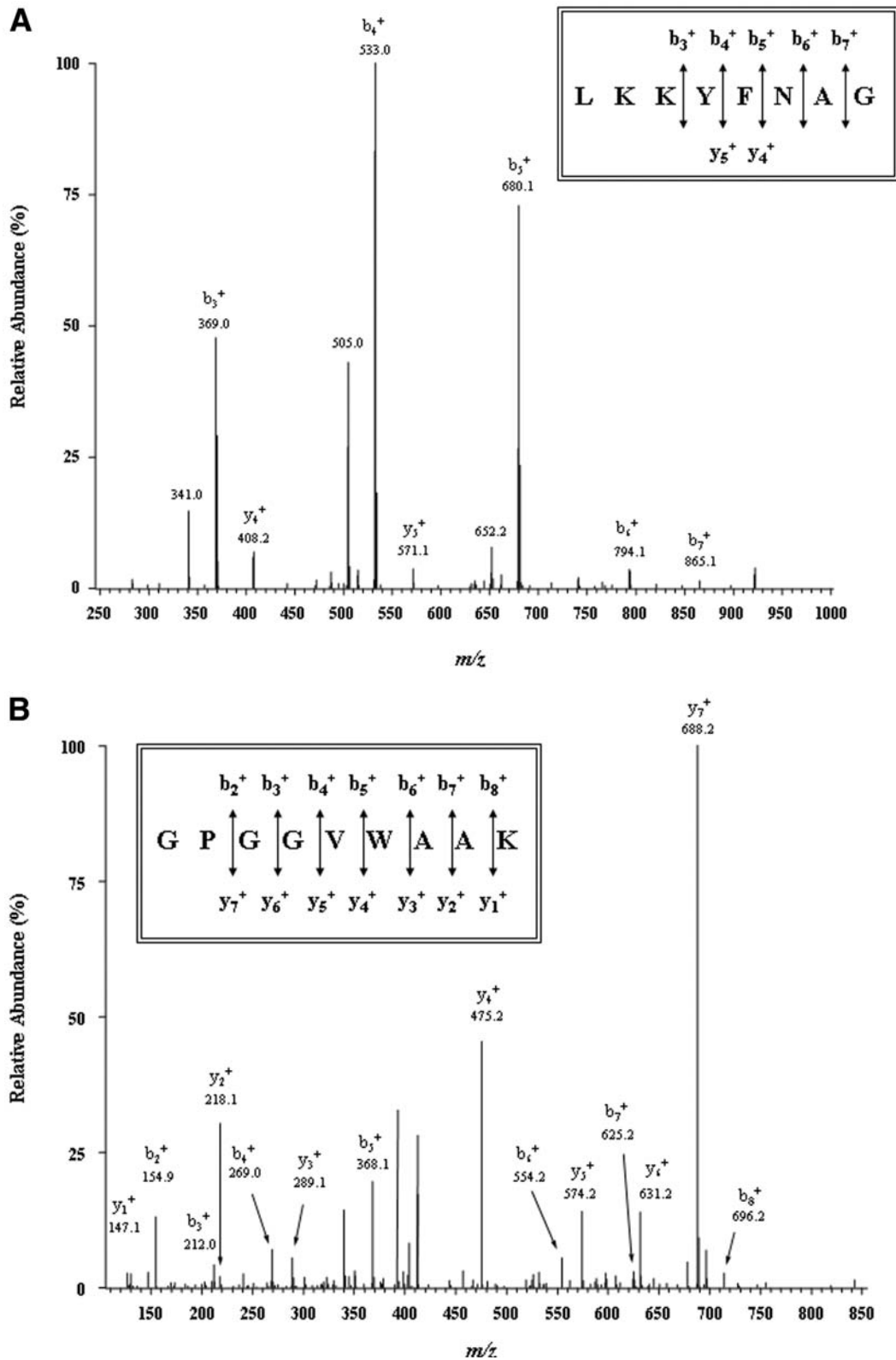


Fig. 4. Ion-trap MS/MS for the identification of human serum peptides. Shown for illustration are two peptides at m/z 421.8 (**A**) and 940.8 (**B**) that were selected for MS/MS and dissociated using collision-induced dissociation in the ion-trap MS. The resulting fragment ions detected in the MS/MS spectra unambiguously identify these peptides as N.LKKYFNAG.H (**A**) and R.GPGGVWAAK.L (**B**) that arise from serum amyloid A4 and interferon- γ , respectively.

Supplementary Table 1
 Proteins/Peptides Identified From Human Serum

Protein	Peptide ^a	Swiss-Prot Accession ^b	Peptide Count ^c	Xcorr ^d	Charge State ^e
ABC transporter ABCA6	L.GNSPVLLDDEPS.T	Q8N139	1	2.644	2
Abnormal spindles	R.EKLNKTKKTDLSIFRT.P	Q8IZT6	1	2.4331	2
ABP125	I.DASQTEFEKKNVWS.F	Q9UM06	1	2.4392	2
Absent in melanoma 1 protein	I.YSKLKPNIVLDIKGGTQ.Y	Q9Y4K1	1	2.486	2
Acetylcholine receptor protein, β chain	I.DGPNRAVALLPEL.R	P11230	1	2.6529	2
Acetyl-CoA carboxylase 2 (EC 6.4.1.2) (ACC- β)	V.SIQCADHLEDEALVPIL.R	O00763	1	2.2843	2
	V.EVAVPADPANL.D	O00763	1	2.2644	2
Acidic leucine-rich nuclear phosphoprotein 32 family member	D.EEEGEEEE.D	P39687	1	2.224	1
Acidic leucine-rich nuclear phosphoprotein 32 family member	E.EFDEEDEDVE	Q92688	1	2.9979	2
Actin-related protein Arp11	V.KEFAYDVPQK.W	Q9C0K3	1	2.441	2
Activating signal cointegrator 1 (ASC-1)	L.MSGVENSGKVDJSTKDLLPHQELRIKSG.L	Q15650	1	2.9918	2
Acyl-coenzyme A oxidase 1, peroxisomal (EC 1.3.3.6)	L.FSEKLLKIQDKA.I	Q15067	1	2.537	2
AD036	P.ESLKIQFENVVNT.F	Q9H2L6	1	2.7828	1
ADAM 12	L.VTILCLLAAG.F	O43184	1	2.5405	2
ADAM 21	H.DFFIYSQ.S	Q9UKJ8	1	2.3327	1
ADAMTS-10	R.DVEQYVLAIMNIVAKL.F	Q9H324	1	2.8216	2
ADAMTS-9	S.FSGETDDDDNYLALSSSK.G	Q9P2N4	3	2.4151	2

Adapter-related protein complex 1 β 1 subunit	G.SYVAPKAVWLPAKAKGLE	Q10567	1	2.8714	2
Adapter-related protein complex 1 γ 1 subunit	L.DSCEPEFKADCAS.G	O43747	1	2.6335	2
Adapter-related protein complex 3 β 2 subunit	S.IQPPVGELMAPVFMSE.N	Q13367	1	2.3839	1
Adenomatous polyposis coli protein (APC protein)	E.CISSAMPKKKPSR.L	P25054	1	2.9705	2
Adenylate cyclase type I (EC 4.6.1.1) (Fragment)	-MAGAPRGGGGGGGAGEPQGAER.A	Q8NFM5	1	2.7466	2
Adenylate cyclase type III (EC 4.6.1.1)	Q.QENLMLSILPK.H	O60266	1	2.276	1
Adhesion regulating molecule 1	A.LITGGLASLLGSSGPPGSSS.S	Q16186	1	2.9009	2
Adlican	L.VEPEVTSTPLEEVVD.D	Q9NIR99	6	2.6423	2
	F.LKTKDDAINGD.K	Q9NIR99	3	2.631	2
	Q.LVCMARNEGGEAR.L	Q9NIR99	1	2.6167	2
AF-4 protein (Proto-oncogene AF4) (FEL protein)	Y.RQTFEKTDLKVPA.K	P51825	1	2.5416	2
Afamin (α -albumin) (α -Alb)	K.SDVGFLLPFPPTLD.P	P43652	1	2.2582	1
	K.LPNNVLQEK.I	P43652	1	2.7702	2
	K.DMVEYK.D	P43652	1	2.0797	1
	R.ESLLNHFLYEVAR.R	P43652	3	2.4602	2
	R.DADPDTFFAK.F	P43652	1	2.2087	2
Aggrecan core protein	A.EVSGESSRAEIGSLPSGA.Y	P16112	1	2.9114	2
A-kinase anchor protein 11	V.EGLGQDGKTL.L	Q9UKA4	1	3.3994	2
A-kinase anchor protein 9 (Protein kinase A anchoring protein)	K.SLKQEKQVSLRCRELE.I	Q99996	1	2.8081	2
	M.KLEFGEENLPKE.E	Q99996	3	3.3013	1
Aldehyde dehydrogenase 1A1	C.PFGGFKMSGNGREL.G	P00352	1	2.3626	1
ALMS1 protein	A.SVQVLITGDNLS.D	Q8TCU4	1	2.463	2

(continued)

Supplementary Table 1 (continued)

Protein	Peptide ^a	Swiss-Prot Accession ^b	Peptide Count ^c	Xcorr ^d	Charge State ^e	
α -(1,3)-fucosyltransferase	N.GSRFPDSTGTPAHSIPLILL.W	P51993	1	2.4898	2	
α -1-acid glycoprotein 1 (AGP 1)	K.NWGLSVYADKPETTK.E	P02763	2	4.6259	2	
	K.TEDTIFLR.E	P02763	5	2.975	2	
	G.LSVYADKPETTK.E	P02763	2	2.916	2	
	K.WFYIASAFR.N	P02763	1	3.1987	2	
	K.SDVVYTDWKK.D	P02763	2	2.547	2	
	K.SDVVYTDWKK.K	P02763	4	3.02	2	
	R.YVGGQEHFAHLLILR.D	P02763	1	4.1392	2	
	R.SDVMYTDWKK.K	P19652	1	2.6156	2	
	W.GLSFYADKPETTK.E	P19652	1	2.9649	2	
α -1-acid glycoprotein 2 (AGP 2)	K.AVLDFVEEGTEASAATAVK.I	P01011	2	5.7892	2	
	G.SEAFATDFQDSAAAK.K	P01011	1	3.0441	2	
	K.MEEVEAMLLPETLK.R	P01011	2	2.2959	2	
	K.ADLSGITGAR.N	P01011	6	2.6098	2	
	K.LINDYVK.N	P01011	2	2.6841	2	
	K.ITLLSALVETR.T	P01011	2	2.7783	2	
	R.LYGSEAFATDFQDSAAAK.K	P01011	13	4.3353	2	
	R.EIGELYLPK.F	P01011	5	2.202	2	
	R.NLAVSQVVK.A	P01011	12	2.9613	2	
	P.NSPLDEENLTQENQDR.G	P01011	4	3.838	2	
	α -1-antitrypsin (α -1 protease inhibitor)	K.LYHSEAFVNFQDTEEAKK.Q	P01009	6	5.1736	2
		L.SGVTEEAPLK.L	P01009	14	3.307	2
		K.FNKPFVFLMIEQNTK.S	P01009	4	4.6986	2
K.LYHSEAFVNFQDTEEAKK.Q		P01009	1	2.6451	2	
F.HVDQVTTVK.V		P01009	1	2.9002	2	
K.QINDYVEK.G		P01009	1	2.3965	2	
K.TDTSHHDDQDHPPTFNK.I		P01009	23	3.6922	3	
K.DTEEDFHVD.Q		P01009	1	2.4445	2	
G.VTEEAPLK.L		P01009	1	2.5992	1	
D.FHVDQVTTVK.V		P01009	2	2.5239	2	

K.WERPFEVK.D	P01009	7	2.2646	2
K.DTEEDDFHVDQVTTVK.V	P01009	23	3.6016	2
D.LSGVTEEAPLK.L	P01009	6	2.4237	2
K.VFSNGADLSGVTEEAPLK.L	P01009	42	5.0453	2
A.TAIFLPPDEGK.L	P01009	5	2.4793	2
L.ENELTHDIITK.F	P01009	4	2.4688	2
K.FLENEDRR.S	P01009	10	2.5207	2
K.SVLGQLGITK.V	P01009	28	2.2582	2
H.LENELTHDIITK.F	P01009	3	3.9513	2
K.SPLFMGK.V	P01009	11	1.9787	1
K.AVLTIDEK.G	P01009	30	2.0124	1
E.NELTHDIITK.F	P01009	6	2.8188	2
K.FLEDVKK.L	P01009	12	2.602	2
K.FLENEDR.R	P01009	5	2.2743	2
K.ELDRDTVFALVNYIFFK.G	P01009	1	3.6105	2
G.LFSEGLK.L	P01009	1	2.4399	2
K.LQHLENELTHD.I	P01009	9	3.3513	2
F.TVNFQDTEEAK.K	P01009	6	2.8353	2
K.LQHLENELTHDIITK.F	P01009	94	3.831	3
F.TVNFQDTEEAKK.Q	P01009	28	2.8769	2
K.LSITIGTYDLK.S	P01009	56	2.6557	2
K.LQHLENELTH.D	P01009	1	2.9785	2
K.KQINDYVEK.G	P01009	4	3.1848	2
K.ITPNLAEFAFSLYR.Q	P01009	3	2.2774	1
F.SNGADLSGVTEEAPLK.L	P01009	6	2.4139	2
G.ADLSGVTEEAPLK.L	P01009	15	3.5818	2
A.DLSGVTEEAPLK.L	P01009	6	2.829	2
L.TTGNGLFLSEGLK.L	P01009	2	2.6057	2
K.GKWERPFEVK.D	P01009	7	3.1221	2
K.LSSWVLLMK.Y	P01009	2	2.7493	2
R.SASLHLPK.L	P01009	38	2.5588	2
N.LAEFAFSLYR.Q	P01009	1	2.5092	2
N.GADLSGVTEEAPLK.L	P01009	9	3.5966	2
S.NGADLSGVTEEAPLK.L	P01009	4	2.6898	2
R.TLNQPSQLTTGNGLFLSEGLK.L	P01009	15	4.5806	2
T.VNFGDTEEAKK.Q	P01009	2	2.4483	2
Q.HLENELTHDIITK.F	P01009	1	3.935	2
Q.INDYVEK.G	P01009	2	2.7765	2

(continued)

Supplementary Table 1 (continued)

Protein	Peptide ^a	Swiss-Prot Accession ^b	Peptide Count ^c	Xcorr ^d	Charge State ^e	
α -1B-glycoprotein (α -1-B glycoprotein)	K.HQFLLTGDTQGR.Y	P04217	27	3.5625	2	
	A.PEFPEPESGR.A	P04217	1	2.4665	2	
	K.LLELTGPK.S	P04217	13	2.4429	2	
	K.NGVAQEPVHLDSPAIK.H	P04217	4	4.0614	2	
	E.TLPAPEFPEPESGR.A	P04217	1	2.9326	2	
	L.SDETLPAPEFPEPESGR.A	P04217	1	3.9795	2	
	P.TPGAAAANLELIFVGPQHAGNYR.C	P04217	23	5.0976	3	
	R.SWVPHTFESELS.D.P	P04217	1	3.6388	2	
	α -2 macroglobulin family protein VIP	P.AEGVTVQIKAE.L	Q8IZJ3	1	3.01	2
		T.VQIKAEELTPKDNITYTSEVVYVSRQ.G.L	Q8IZJ3	3	3.1897	2
α 2,3-sialyltransferase ST3GAL VI	K.PALNLIYK.P	Q9Y274	1	2.9461	2	
	W.REKLLQR.L	Q92186	4	2.9102	2	
α -2,8-sialyltransferase 8B (EC 2.4.99.-) (ST8Sia II)	K.HTLNQIDEVK.V	P02765	42	3.5955	2	
	G.SPSGEVSHPR.K	P02765	1	2.6556	2	
α -2-HS-glycoprotein (Fetuin-A)	K.FSVVYAK.C	P02765	5	2.5008	2	
	G.VVSLGPSGEVSHPR.K	P02765	3	3.2757	2	
	F.MGVVSLGPSGEVSHPR.K	P02765	1	3.6727	2	
	M.GVVSLGPSGEVSHPR.K	P02765	1	2.962	2	
	R.HTFMGVVSLGPSGEVSHPR.K	P02765	2	5.5066	3	
	P.HGPGLIYR.Q	P02765	10	2.4429	2	
	R.AQLVPLPSTYVEFTVSGTDCVAK.E	P02765	1	2.7098	2	
	α -2-macroglobulin (α -2-M)	K.LPPNVVEESAR.A	P01023	101	2.2359	2
		K.HYDGSYSTFGER.Y	P01023	32	3.2648	2
		K.VDLFSFSPSQSLPASHAH.L	P01023	8	3.2719	2
K.YGAATFTR.T		P01023	13	2.2899	2	
K.DTIVIKPLLVEPEG.L		P01023	1	2.5304	2	
L.SFSPSQSLPASHAH.L		P01023	1	2.5569	2	
D.SLVFVQTDK.S	P01023	1	2.4615	2		

A.SPAFLAVPEK.E	P01023	10	3.7168	2
K.SIYKPGQTVK.F	P01023	4	2.2077	2
L.PPNVVEESAR.A	P01023	4	3.1942	2
K.DTVIKPLLVEPEGLEKE	P01023	30	4.1965	2
H.PFTVEEFVLPK.F	P01023	1	3.146	2
K.DMYSFLEDMGLK.A	P01023	16	3.7441	2
K.YDVENCLANK.V	P01023	6	2.1307	1
A.SVSGKPOYMVLVPSLLHTTETEK.G	P01023	1	4.4279	3
K.ATVLNLYPK.C	P01023	17	2.2869	2
K.TAQEGDHGSHVYTK.A	P01023	3	3.7946	2
FSSTQDTVVALHALSK.Y	P01023	12	3.7274	2
G.TVVLTGR.Q	P01023	2	2.9096	2
G.FSSTQDTVVALHALSK.Y	P01023	1	3.9512	2
K.GHFSISIPVK.S	P01023	33	3.0319	2
K.FEVQVTVPK.I	P01023	4	2.4979	2
K.NEDSLVAVQTDK.S	P01023	49	3.1756	2
K.DNSVHWRPQKPK.A	P01023	4	3.3328	2
F.FVELTMPYSVIR.G	P01023	2	2.4262	2
K.SLNEEAVKK.D	P01023	4	2.6727	2
K.MVSGFIPLKPTVK.M	P01023	23	3.3094	2
K.LHTEAQIQEETVVVELTGR.Q	P01023	2	3.6176	2
M.VLVPSLLHTTETEK.G	P01023	4	2.7605	2
K.QFSFPLSSEPFQGSYK.V	P01023	5	4.0516	2
K.MVSGFIPLKPTV.K	P01023	1	2.8228	2
K.VDLSFSPSQSLPASH.A	P01023	2	2.8676	2
K.DNSVHWR.P	P01023	5	2.6082	2
K.VYDYYETDEFAIAEYNAPCSK.D	P01023	1	3.3003	2
D.TVVVALHALSK.Y	P01023	6	2.5027	2
K.FQVDNRR.L	P01023	2	2.4831	2
K.PLLVEPEGLEK.E	P01023	6	2.3542	2
L.EASPAFLAVPEK.E	P01023	1	3.1655	2
K.PQYMLVPSLLHTTETEK.G	P01023	4	4.4423	3
K.ALLAYAFALAGNQDK.R	P01023	2	4.4268	2
K.AAQVTIQSSGTFSSK.F	P01023	8	3.0378	2
K.AIGYLNTRYQR.Q	P01023	33	2.5474	2
R.TGTHGLVK.Q	P01023	11	2.5347	2
R.SLFTDLEAENDVLHCYAFVAPK.S	P01023	3	3.7014	2
R.SSGSLNNAIK.G	P01023	18	2.5526	2

(continued)

Supplementary Table 1 (continued)

Protein	Peptide ^a	Swiss-Prot Accession ^b	Peptide Count ^c	Xcorr ^d	Charge State ^e
	R.AVDQSVLLMKPDAELSSASSVYNNLLPEK.D	P01023	3	3.8699	2
	Q.FSFPSSSEPFQGSYK.V	P01023	1	3.1744	2
	R.TEVSSNHVLLYLDK.V	P01023	1	4.3545	2
	S.STQDTVVVALHALSK.Y	P01023	1	2.7694	2
	N.GITYTPVSSSTNEK.D	P01023	5	3.2414	2
	R.VVSMDENFHLNELIPLVYIQDPK.G	P01023	4	3.2632	2
	R.SLFTDLEAENDVLH.C	P01023	1	3.4195	2
	R.SASNNMAIVDK.M	P01023	7	3.1983	2
	R.VTAAPOQSVCALR.A	P01023	7	2.2157	2
	T.VIKPLLVPEGLEK.E	P01023	1	3.2207	2
	R.VGFYESDVMGR.G	P01023	29	3.4185	2
	R.TEHPFTVBEFVLPK.F	P01023	26	4.1984	3
	R.LVHVEEPHTETVR.K	P01023	20	3.0381	2
	R.KDVIKPLLVPEGLEK.E	P01023	7	2.9462	2
	R.LLIYAVLPTGDVIGDSAK.Y	P01023	18	2.6208	2
	V.HVEEPHTETVR.K	P01023	1	2.5361	2
	P.PNVVEESAR.A	P01023	4	2.3505	1
	R.LVHVEEPHTETVR	P01023	2	3.1365	2
	V.SMDENFHLNELIPLVYIQDPK.G	P01023	2	3.3294	2
	R.IAQWQSFQLEGGLK.Q	P01023	7	2.7785	2
	R.NALFCLSAWK.T	P01023	3	2.4561	1
	R.NQGNWTWLFVFLK.T	P01023	2	3.3135	2
	Y.MVLVPSLLHTETTEK.G	P01023	1	2.4408	2
	R.HNVYINGITYTPVSSSTNEK.D	P01023	18	3.5073	2
	R.QTVSWAVTPK.S	P01023	2	2.6846	2
	Q.DTVVALHALSK.Y	P01023	4	2.989	2
	R.QGIPFFGQVR.L	P01023	1	2.549	2
α -catenin-like protein VR22	L.DTTVPLLLVIEAAKN.G	Q9UI47	1	3.128	2
α -s1 casein [Contains: Casoxin D]	S.DISNPTAHENYEKNNVMLQW.-	P47710	1	2.4844	2
ALR	P.GTSNHLLLA	O14686	1	2.5903	2
	N.EEMPLPPPEE.S	O14686	5	2.4816	1

Amino acid transporter hNAT3	W.YLNGNYLIIF.V	Q969I6	2	2.5468	2
Amplified in breast cancer 1	K.EDSCSGSDAGSAAAGST.Y	Q8TDM9	1	2.8712	2
Amyloid β A4 protein-binding family A member 1	A.EVEVTDEAAAGGEVNESVE.A	Q02410	3	2.4854	2
Amyloid β A4 protein (APP) (ABPP)	D.KFRGVEFVCCPLA.E	P05067	3	2.913	
Androgen-induced prostate proliferative shutoff associated	I.RKQLEVLVSPITCSCK.Q	Q9Y451	1	3.2163	2
Angiotensin-related protein 2 (Angiotensin-like 2)	Y.WLTNQGNKLLVVTMED.W	Q9UKU9	1	2.418	2
Angiotensin-related protein 5	L.LRELQRLLAAADGA.V	Q9BZZ0	1	2.2504	2
Angiotensin-converting enzyme, testis-specific isoform	F.DVYNQLQNTTIKR.I	P22966	1	2.8034	2
Angiotensinogen [Contains: Angiotensin I (Ang I)]	K.ALQDQLVLVAAK.L	P01019	1	2.5331	2
	K.QPFVQGLALYTPVVLPR.S	P01019	3	3.5813	2
	K.DPTFIPAPIQAK.T	P01019	7	2.2056	2
	R.LQAILGVVPWK.D	P01019	1	2.359	2
	R.SLDFTELDVAAEK.I	P01019	5	3.2971	2
Ankyrin 3 (ANK-3) (Ankyrin G)	Q.ECKTVQETIRGTFYTTR.Q	Q12955	1	2.7253	2
Ankyrin repeat domain protein 2 (Skeletal muscle ankyrin)	T.GPVDEETFLLK.A	Q9GZV1	1	2.8445	2
Antithrombin-III (ATIII) (PRO0309)	K.LPGIVAEGR.D	P01008	4	2.2544	2
	K.SKLPGIVAEGR.D	P01008	3	2.6239	2
	R.DDLVSDAFHK.A	P01008	8	2.633	2
AP-2-like protein	V.EAQCGILVNGQGGVIRRG.G	Q8IWX0	1	2.4971	2
Apolipoprotein A-I (Apo-AI)	L.GPVTQEFWDNLEK.E	P02647	6	3.5104	1
	K.LHELQEK.L	P02647	2	2.2824	1
	K.LLDNWDSDVSTFSK.L	P02647	81	3.778	2
	K.VSFLSALEEYTK.K	P02647	73	3.8248	2
	K.PALEDLR.Q	P02647	3	1.9462	1

(continued)

Supplementary Table 1 (continued)

Protein	Peptide ^a	Swiss-Prot Accession ^b	Peptide Count ^c	Xcorr ^d	Charge State ^e
	D.YVYQFEGSALGK.Q	P02647	3	2.922	2
	K.AKPALEDLR.Q	P02647	26	2.3827	2
	K.LREQQLGPPVTQEFWDNLEK.E	P02647	2	3.4443	2
	G.PVTQEFWDNLEK.E	P02647	11	3.4813	2
	K.VSFLSALEEYTKK.L	P02647	1	2.9771	2
	L.PVLESFK.V	P02647	2	2.4006	2
	K.ATEHLSTLSEK.A	P02647	63	3.2899	2
	L.DNWDSVTSTFSK.L	P02647	4	3.503	2
	A.PYSDELR.Q	P02647	1	2.3052	1
	K.VQPYLDDFQK.K	P02647	2	2.0188	1
	K.DLATVYVDVLK.D	P02647	18	2.2466	2
	D.NWDSVTSTFSK.L	P02647	3	2.4802	2
	L.LDNWDSVTSTFSK.L	P02647	1	2.8585	2
	R.AELQEGAR.Q	P02647	1	2.7327	2
	Q.GLLPVLESFK.V	P02647	4	2.4088	2
	Q.PYLDDFQK.K	P02647	5	2.2534	1
	Y.VSQFEGSALGK.Q	P02647	1	3.2428	2
	T.HLAPYSDELR.Q	P02647	8	2.8164	2
	N.WDSVTSTFSK.L	P02647	1	2.521	2
	V.TQEFWDNLEK.E	P02647	1	2.2243	1
	R.THLAPYSDEL	P02647	1	2.529	2
	R.LAEYHAK.A	P02647	1	2.2094	2
	R.QGLLPVLESFK.V	P02647	13	2.3848	2
	Q.DEPPQSPWDR.V	P02647	1	2.4812	2
	R.EQLGPPVTQEFWDNLEK.E	P02647	20	3.1572	2
	R.AHVDALR.T	P02647	2	1.9003	1
	R.THLAPYSDELR.Q	P02647	94	2.8903	2
	R.DYVYQFEGSALGK.Q	P02647	91	2.6133	2
	R.DYVYQFEG.S	P02647	1	2.3581	1
	R.VKDLATVYVDVLK.D	P02647	14	2.5871	2
Apolipoprotein A-II (Apo-AII)					
	K.SPELQAEAK.S	P02652	56	2.2975	2
	K.SKEQLTPLIK.K	P02652	58	3.1895	2
	K.VKSPELQAEAK.S	P02652	11	2.706	2

Apolipoprotein A-IV (Apo-AIV)							
S.KEQLTPLIK.K	P02652	1	2.5479	2			
Apolipoprotein B-100 (Apo B-100)							
K.LVFPATELHER.L	P06727	1	2.4198	2			
K.LGEVNTYAGDLQK.K	P06727	2	2.3551	2			
K.SVSLPSLDPASAK.I	P04114	1	2.3814	2			
K.FPEVDVLT.K.Y	P04114	18	2.4942	2			
K.MGLAFESTK.S	P04114	1	2.3956	2			
K.ALVEQQFTVPEIK.T	P04114	1	2.3459	2			
K.GNVATEISTER.D	P04114	5	3.1074	2			
K.SVSDGIAALDLNNAVANK.I	P04114	3	4.2328	2			
F.IEDVNFKFLDMLIKKLSFD.Y	P04114	1	2.7093	2			
K.TGLKEFLK.T	P04114	1	2.3911	2			
K.LTISEQNIQR.A	P04114	1	2.5093	2			
K.TEVIPPLIENR.Q	P04114	4	2.2401	2			
L.SGGNTLHLVSTTK.T	P04114	2	2.9646	2			
K.HINIDQFVR.K	P04114	1	2.4716	2			
A.GKLLKQHEAIDVR.V	P04114	1	2.7493	2			
K.SVGFHLPSR.E	P04114	9	2.621	2			
K.VLVDHFGYTK.D	P04114	6	2.8297	2			
G.GNTLHLVSTTK.T	P04114	1	2.5701	2			
K.FSVFAGVIPSQALTAR.F	P04114	3	2.3473	2			
K.EVYGFNPEGK.A	P04114	2	2.0261	1			
K.IISDYHQQFR.Y	P04114	1	2.3364	2			
K.SPFTDLHLR.Y	P04114	15	3.5189	2			
K.FVTQAEQAK.Q	P04114	4	2.2888	1			
K.GFEPTLEALFGK.Q	P04114	2	2.6842	2			
K.ATFQTPDFIVPLTDLR.I	P04114	2	3.6204	2			
K.YSQPEDSLIPFEITVPESQLTVSQFTLTK.S	P04114	2	3.0624	2			
K.ATGVLYDYVVK.Y	P04114	4	2.6852	2			
K.IEGNLIIFDPNNYLPK.E	P04114	2	3.4729	2			
K.LL.SGGNTLHLVSTTK.T	P04114	10	4.307	2			
R.TSSFALNLPVPEVK.F	P04114	3	2.3633	2			
R.VIGNMGQTMQLTPELK.S	P04114	2	3.3675	2			
R.TGISPLALIK.G	P04114	6	2.3031	2			
R.SEILAHWSPAK.L	P04114	4	3.2666	2			
R.VPSYTLILPSLELPLVHLVPR.N	P04114	7	5.4198	3			
R.LPYTHITTPPLKD.F	P04114	1	2.6241	2			

(continued)

Supplementary Table 1 (continued)

Protein	Peptide ^a	Swiss-Prot Accession ^b	Peptide Count ^c	Xcorr ^d	Charge State ^e
Apolipoprotein C-I (Apo-CI)	R.LPYTIITTPPLK.D	P04114	13	3.8202	2
	V.PESQLTVSQFTLPK.S	P04114	1	2.7832	1
	R.KGNVATEISTER.D	P04114	8	3.8081	2
	R.ITENDIQIALDDAK.I	P04114	2	2.9551	2
Apolipoprotein C-II (Apo-CII)	G.TPDVSSALDK.L	P02654	2	2.6324	2
	K.LKEFGNTLEDK.A	P02654	6	3.1292	2
Apolipoprotein C-III (Apo-CIII)	K.TAAQNLYEK.T	P02655	1	2.4772	2
Apolipoprotein D (Apo-D) (ApoD)	K.DALSSVQESQVAQQAR.G	P02656	2	3.9693	2
	R.GWVTDGFSSLK.D	P02656	9	2.4324	2
	K.VLNQELR.A	P05090	1	2.2702	2
Apolipoprotein E (Apo-E)	K.NILTSNNIDVKK.K	P05090	3	3.0569	2
	R.NPNLPPETVDSLK.N	P05090	1	2.8552	2
	A.KVEQAVETEPEPELR.Q	P02649	2	2.4094	2
Apolipoprotein E receptor 2 906	K.SELEEQITPVAEETR.A	P02649	1	2.8404	2
	A.AVIGIIVPIVVIALLCMS.G	Q99876	1	2.8511	2
Apolipoprotein L1 (Apolipoprotein L-I)	R.VQQNVPSGTDTPQSK.P	O14791	1	2.8038	2
	R.VTEPISAESGEQVER.V	O14791	2	2.7808	2
	R.NEDELK.A	O14791	2	2.551	2
Apolipoprotein L3 (Apolipoprotein L-III) (ApoL-III)	G.SGGQAERTIAGITTRAVSR.G	O95236	1	2.7241	2
	K.WIYHLTEGSTDLR.T	O95445	1	3.5798	2
Apoptosis related protein APR-5 (Fragment)	L.LQDLLLLGLQFRAELGLQGCLGRGAGM.H	Q9Y5L6	1	3.0424	2
	L.HGQPVSFLLK.E	P05089	2	2.6211	2
Arginase 1 (EC 3.5.3.1) (Liver-type arginase)	V.EALFQLWTAEPILDQAAA.S	Q9HAU8	1	2.2979	2

Arginyl-tRNA synthetase (EC 6.1.1.19) (Arginine—tRNA ligase)					
T.IFAAAQMGWYDPK.V					
ARL-6 interacting protein-1 (Aip-1)					
A.AETASLEEQQQ					
ASH1					
I.RSNVYVDVKPL.S					
R.EGATANVSEGEKK.T					
Aspartyl protease 3 (Fragment)					
S.EIPKLPVSLIIGVWF.N					
Ataxin-2 related domain protein					
P.VTSSVSDPGVGSI.S					
ATP(GTP)-binding protein					
D.FKGSDDDEESR.L					
ATP-binding cassette, sub-family A, member 1					
R.NNVKVVFNKKGWH.A					
ATP-binding cassette, sub-family A, member 3					
V.HHHVVPNATLESSAGA.E					
ATP-citrate synthase (EC 2.3.3.8) (ATP-citrate (pro-S)-lyase)					
S.FSESRADEVAPAK.K					
ATP-dependent RNA helicase A (Nuclear DNA helicase II)					
V.IEAEHTLRELDALDAN.D					
Attractin (Mahogany homolog) (DPPT-L)					
K.KVEFVLK.Q					
B cell RAG associated protein					
L.AAHQIHQGLQASSAK.E					
B7-H1 (PD-1-ligand)					
H.LLNAFTVTPK.D					
BA110H4.2 (Similar to membrane protein)					
A.SRDAGAREQQDALVLYQQ.D					
BA145L22.1.2 (Myelin/oligodendrocyte glycoprotein, MOG)					
L.RAEIENLHRTFGQFL.E					
BA93B14.2 (Novel protein) (Fragment)					
W.NARSFTAGREHGPR.C					
Baculoviral IAP repeat-containing protein 6					
L.MKVHLKFEINAYDPAL.V					
Baculoviral IAP repeat-containing protein 8					
A.VVFI PCGHLV.T.C					
BAF180					
N.ILEKEDVPVEMSNGEVPVCHYF.E					
P54136	1	2.6361	2		
Q15041	1	2.8104	2		
Q9NR48	2	2.436	1		
Q9NR48	1	2.3294	2		
Q9UHB3	1	2.4186	2		
Q8WWM7	1	2.6951	2		
Q96QE3	1	2.4684	2		
O95477	1	2.2257	1		
Q99758	1	2.3863	2		
P53396	1	2.4802	2		
Q08211	2	2.4785	2		
O75882	1	2.5028	2		
O60474	1	2.535	2		
Q9NZQ7	1	2.7083	2		
Q9H1S5	1	2.9715	2		
Q9NU64	1	2.7546	2		
Q9H4T6	1	2.4344	2		
Q9NR09	1	2.3275	2		
Q96P09	1	2.5654	2		
Q9H301	1	3.2829	2		

(continued)

Supplementary Table 1 (continued)

Protein	Peptide ^a	Swiss-Prot Accession ^b	Peptide Count ^c	Xcorr ^d	Charge State ^e
Band 4.1-like protein 2 (Generally expressed protein 4.1)	V.KTEMVTISDASQRTEIS.T	O43491	1	3.273	2
BarH-like 1 homeobox protein	L.SHRAGSPALPKGDPPLLGDCRS.P	Q9BZE3	1	2.4621	2
Basement membrane-specific heparan sulfate proteoglycan	V.VNLSVHGGPPTVSVLPE	P98160	4	2.7867	2
β crystallin B2 (BP)	K.ETGVVEKAGSVLVQAGPWVG.Y	P43320	1	2.5157	2
β -1 adrenergic receptor	A.ASDDDDDDV.V	P08588	1	2.1109	1
β 1,3-N-acetylglucosaminyltransferase 5	R.RSGIRRTWGNENY.V	Q9BYG0	1	2.5016	2
β -2-glycoprotein I (Apolipoprotein H) (Apo-H)	K.ATVYQGER.V	P02749	4	2.4423	2
	K.FICPLTGLWPINTLK.C	P02749	1	4.2545	2
	F.AGILENGAVR.Y	P02749	3	2.5211	2
	K.WSPELPYCAPIICPPPSIPTFATLR.V	P02749	3	2.8171	2
	R.VCFPAGILENGAVR.Y	P02749	1	3.4264	2
β -4-N-acetylgalactosaminyltransferase	R.KLLKHLQ.H	Q8NHY0	1	2.4102	2
β -adrenergic receptor kinase 1 (EC 2.7.1.126)	L.RGDVFKFIESDK.F	P25098	1	3.2741	2
BH3 interacting domain death agonist (BID)	Y.PRDMEKEKTMVLALLLAKKVASHTP.S	P55957	1	4.032	3
Bloom's syndrome protein (EC 3.6.1.-) (RecQ protein-like 3)	T.QPSYDIDNFD.I	P54132	1	2.2413	1
Blue-sensitive opsin (Blue cone photoreceptor pigment)	Q.FQACIMKMVCGK.A	P03999	1	2.5039	2
BOG25	H.YLLEYKKGDDGIALLSEE.R	Q9P0V3	1	3.0467	2
Bombesin receptor subtype-3 (BRS-3)	I.GCKVLSFIR.L	P32247	7	2.864	2
Brain acid soluble protein 1 (BASP1 protein)	A.EGKAEKEGE.K	P80723	5	2.8084	2

Brain carboxylesterase hBr2	V.VVTIQRLGIWGFSTGDEHGRGN.W	Q8TDZ9	1	2.4089	2
Brain specific membrane-anchored protein	V.LEAPSGALSLLDLFSTLCNDLVN.S	Q9UK28	1	2.5122	2
Brain-cadherin (BR-cadherin) (Cadherin-12)	I.VILLAIVVLYV.A	P55289	6	2.3064	1
Brain-specific angiogenesis inhibitor 2	Y.RYLYLSLRE	O60241	1	2.4837	2
Brain-specific Na-dependent inorganic phosphate	S.GFAISGFNVNHLIDIA.P	Q9P2U7	1	2.6642	2
BRCA1 associated protein 1 (BRCA1 associated protein-1)	C.LKEEVEKRRKFK	Q92560	1	3.1534	2
BRCA1-binding helicase-like protein BACH1	A.KDLFEIRTIKE.V	Q9BX63	1	2.9589	2
BRDT	Y.IKTDITE.T	O14789	2	2.5388	1
Breast cancer type 2 susceptibility protein	A.SGYLTDENEVGFRRG	P51587	1	2.8909	2
	S.VTDSSENTINQREAAASHGFG	P51587	1	2.5041	2
	S.LKAAVGGQ.V	P51587	1	2.3265	1
Breast carcinoma-associated antigen (Fragment)	S.GAEVTRTAGGAVEPGAGLLSGAEVTRTAGGAV.E	Q14127	1	2.8363	2
Brix domain containing protein 1	S.KLQTRKMKGLKK.R	Q9H7B2	1	3.0236	2
Bromodomain adjacent to zinc finger domain 2A	G.EKVSEIPLTR.D	Q9UIF9	1	2.9498	2
Bromodomain-containing protein 1 (BRI40-like protein)	A.QEMSECNSNKE.N	O95696	1	2.7016	2
Bullous pemphigoid antigen 1, isoforms 6/9/10	L.NEVSSALLELVWWRARE.G	O94833	1	2.4983	2
	P.DKPIVKKSIDE.L	O94833	2	2.3235	1
C-4 methyl sterol oxidase (EC 1.-.-.-)	A.IYFLFCLPGFLFQ.F	Q15800	1	2.4194	2
C4b-binding protein α chain (C4bp)	K.GYILVGGQAK.L	P04003	1	2.4154	2
	K.LNNGEITQHR.K	P04003	4	2.3276	2
	R.GSSVIHCDADSK.W	P04003	1	3.1372	2
	R.KPELVNGR.L	P04003	2	2.3665	2

(continued)

Supplementary Table 1 (continued)

Protein	Peptide ^e	Swiss-Prot Accession ^b	Peptide Count ^f	Xcorr ^d	Charge State ^e
C5a anaphylatoxin chemotactic receptor (C5a-R)	L.IILNMYASILLLA	P21730	2	2.2779	2
Cadherin EGF LAG seven-pass G-type receptor 1	R.FNEKHDFIALEIVDE.Q	Q9NYQ6	3	3.3684	2
Cadherin-7	K.IQDINDNEPK.F	Q9ULB5	1	2.282	2
Cadherin-related tumor suppressor homolog	H.SPVVHVQANSPEGLK.V	Q14517	2	2.7667	2
	H.EMVASVDVSIQVK.D	Q14517	2	2.4434	2
	Y.AIVTVDDCDQGANGLIASLSIVAGDLL	Q14517	1	3.2841	2
Calcium channel α 1.2.2 subunit (Fragment)	G.ERYRLGGNVLDLESQAE.G	Q9HAT3	2	3.4537	2
Calcium/calmodulin-dependent protein kinase type II β	E.SSDSANTTIEDEDAKAPR.V	Q13554	1	2.4545	2
Calcium-binding protein CaBP1 (Calbrain)	N.CMRTMGYMPTEMELIEL.S	Q9NZU7	1	3.8169	3
Calcium-transporting ATPase type 2C, member 1 (EC)	K.YISQFKNPLIM.L	P98194	1	2.7841	2
Calponin homology domain containing protein 1 (Fragment)	F.TIRRKMEQMREEKEL.V	Q9Y2L9	1	2.8398	1
Calreticulin 3 (Calreticulin 2)	L.TSLKKETSPAESKDWE.Q	Q96L12	1	2.5547	2
Calsynenin-2	K.ESEMDWDDSAITITVNPMEKHE.G	Q9H4D0	1	3.8028	3
	P.SIHLETCDGA.V	Q9H4D0	2	2.4341	2
Canalicular multispecific organic anion transporter 1	K.LIKKEFIETGK.V	Q92887	9	2.4517	2
Candidate tumor suppressor protein DICE1	L.KGQDEQVHSVPQAQM.G	Q9UL03	1	2.8302	2
CAP-binding protein complex interacting protein 1 (Fragment)	F.KNIKTVMKAFE	Q9NQ18	4	2.1034	1
Carbonic anhydrase VA, mitochondrial (EC 4.2.1.1)	A.VVGENGLAVIGV.F	P35218	1	2.4335	2
Carboxypeptidase D (EC 3.4.17.-) (gp180)	L.ESLMLRS.S	O75976	1	2.7435	2
	N.HPIIMKTGEPHCPGDEDETF.K	O75976	1	3.0889	2

Carboxypeptidase N 83 kDa chain	K.LSNNALSGLPQGVFGK.L R.LFQLPLHLK.T	1 1	3.196 2.2958	2 2
Cask-interacting protein 1	A.KPPGTPPSLGASPAK.P	1	2.4718	2
Cask-interacting protein 2 (Hypothetical protein KIAA1139)	L.IALLLEAQATVDIKD.S	1	2.7645	2
Caspase recruitment domain protein 14	L.DVSESGVLMRRRR.P	3	2.5863	2
Cationic amino acid transporter-4 (CAT-4) (CAT4)	F.AHVHPRIQVPVAGT.L	1	2.7712	2
Cation-independent mannose-6-phosphate receptor	V.FASSSKCGKDKTK.S	4	3.2816	2
C-C chemokine receptor type 7 (C-C CKR-7)	L.FKLFKDLGCL.S	1	2.3545	1
CD180 antigen (Lymphocyte antigen 64)	K.TNLLQTVGSLEVLIL.S	2	2.774	2
CD2-associated protein (Cas ligand with multiple SH3)	F.AYEGTNEDELTF.K	2	2.8094	2
CD46	L.NMPLTRLNQLQQS.R	1	2.8726	2
CD5 antigen-like (SP- α) (CT-2)	G.TPSGILYEPPAEK.E	1	2.9673	2
Cdc42 guanine nucleotide exchange factor zizimin 1	A.QYQFTDSETDVE.G	1	2.606	2
CDC42-binding protein kinase β	Q.FPAQVTDVSENAKDPI.R	1	2.9172	2
CDV-1R	L.KAEFGLLQ.R	4	2.9411	2
Cell cycle checkpoint protein	D.FCSTNVINKIILQSEGL.R	1	3.0582	2
Cell surface glycoprotein MUC18	V.SDVVRVSPAAPERQ.E	1	2.923	2
Centaurin β 5 (Cnt-b5)	A.WGLADVRELHPGLLAH.R	1	2.5926	2
Centaurin γ 1	D.RNLARALSTDCTPSGDLSPLSREPPSP.M A.SSPRVVGDARARALCADM.K	1 1	3.2548 2.8958	2 2

(continued)

Supplementary Table 1 (continued)

Protein	Peptide ^a	Swiss-Prot Accession ^b	Peptide Count ^c	Xcorr ^d	Charge State ^e
Centromere protein C (CENP-C) (Centromere autoantigen C)	I.SSRNINDHH.S	Q03188	1	2.4284	2
	Q.EKIQELKANE.H	Q02224	2	2.5254	1
Centrosome-associated protein 350	K.AERGS HQGKSGTSSKLSVKDFEQ.T	Q8WY20	1	2.4347	2
Ceruloplasmin (EC 1.16.3.1) (Ferroxidase)	K.MYYSAVDPTK.D	P00450	5	2.5961	2
	K.ERGP EEEHLGILGPVIWA EVGDTIR.V	P00450	1	4.6581	3
	K.DIFTGLIGPMK.I	P00450	19	2.2282	2
	L.GPQLHADVGDK.V	P00450	1	2.6795	2
	K.EVGPTNADPVCLAK.M	P00450	2	3.4912	2
	K.ALYLQYTD EFR.T	P00450	1	3.1961	2
	K.VNKDDEEFIESNK.M	P00450	44	4.2563	2
	K.DVDKEFYLPFTVFDENESLLEDNIR.M	P00450	1	4.1304	2
	K.VDKDNEDFQESNR.M	P00450	1	3.1031	2
	K.NNEGTYYS PNYNPQS.R	P00450	1	2.4743	2
	K.GAYPLSIEPIGVR.F	P00450	26	3.1325	2
	K.LISVDTEHSNIYLQNGPDR.I	P00450	3	3.1481	2
	R.TTIEKPVWLGFGLPIIK.A	P00450	3	3.2893	2
	R.GPEEEHLGILGPVIWA EVGDTIR.V	P00450	3	5.6504	2
	R.SVPPSASHVAPTEFTYEWTVPK.E	P00450	6	2.4653	2
	R.DTANLFPQTSLLH.M	P00450	2	2.8672	2
	R.MFTTAPDQVDKED.E	P00450	1	2.4251	2
R.GVYSSDVDFIPGTYQTLEMFPFR.T	P00450	4	3.4632	2	
R.MFTTAPDQVDKED EDFQESNK.M	P00450	7	4.0216	2	
R.EYTDASFTNR.K	P00450	3	2.306	2	
R.KAEEHLGILGPQLHADVGDK.V	P00450	1	3.7408	3	
Q.SEDSTFYLGER.T	P00450	1	2.9725	2	
R.IYHSHIDAPK.D	P00450	8	2.7255	2	
CGI-118 protein	K.ARPELEE.L	Q96GC5	1	2.6653	1
Cholinephosphotransferase 1	L.III LAIMYKKSATDVF.E	Q8WUD6	1	2.5755	2

Chondroitin sulfate proteoglycan BEHAB/brevican V.TPSQRCGGGLPGV.K	Q96GW7	1	2.6023	2
Chordin L.LLLGLLLLSRPAR.G	Q9H2X0	1	2.4964	2
Chorein (Chorea-acanthocytosis protein) I.RNHFSVPLSVYEG.D	Q96RL7	1	2.5277	2
Chromodomain-helicase-DNA-binding protein 2 (CHD-2) K.QVNIYRLVTKGTVEEIIIRA.K	O14647	1	2.558	2
Chromodomain-helicase-DNA-binding protein 5 (CHD-5) R.AILEKNFSLTKGANQHNMNP.N.L	Q8TD26	3	2.4874	2
Ciliary dynein heavy chain 11 E.EEAAAARRARSAQDA.R	Q96DT5	1	2.5977	2
Cingulin G.FPAPSQSSTSDEEPGA.Y	Q9P2M7	5	2.9358	2
Circadian locomotor output cycles kaput protein (hCLOCK) C.SKMSIVDR.D	O15516	1	2.4089	2
Cisplatin resistance related protein CRR9p A.FKNDISFWKKK.K	Q96KA5	3	2.4677	2
Class I cytokine receptor (CRL1 protein) F.WLWPLPKLALLPLLV.L	O60624	1	2.4653	2
Class II cytokine receptor ZCYTOR7 T.LLESQAALAV.L	Q9UHF4	26	3.2839	2
Clathrin heavy chain 2 (CLH-22) G.YFEELILLE.A	P53675	2	2.625	1
Clusterin K.TLLSNLEEAKK.K	P10909	11	2.8565	2
K.FMETVAEK.A	P10909	2	2.1842	1
D.PITVTVPEVSR.K	P10909	6	2.4485	2
K.TLLSNLEEAK.K	P10909	6	2.4298	2
K.LFDSDPITVTVPEVSR.K	P10909	2	4.7358	2
R.KTLLSNLEEAK.K	P10909	1	3.3445	2
R.VTTVASHTSDDVPSGVTEVVVK.L	P10909	11	3.634	2
R.ASSIIDELFQDR.F	P10909	1	2.5528	2
R.IDSLENDR.Q	P10909	3	2.5579	2
Coagulation factor XI (EC 3.4.21.27) K.MAESGYDIALLK.L	P03951	1	2.6059	2
Coagulation factor XIII (B chain) S.FTEMEKNLLLK.W	P05160	1	2.5062	2

(continued)

Supplementary Table 1 (continued)

Protein	Peptide ^a	Swiss-Prot Accession ^b	Peptide Count ^c	Xcorr ^d	Charge State ^e
Cofactor of BRCA1	L.QPVVMCVMKHLPKVP.E	Q8WX92	1	2.7555	2
Collagen α 1(I) chain	G.FQGLPGAGPPGEAGKPGEQGV.P	P02452	1	2.904	2
	T.ALLTHGQEEGQVEGGQDEDEPPITCVQNG	P02452	1	3.0983	2
Collagen α 1(X) chain	P.GLPGPPGPSAVGK.P	Q03692	1	2.4213	2
Collagen α 1(XI) chain	G.EKGAKGEAG.AEG.P	P12107	4	3.0303	2
Collagen α 1(XIX) chain	P.GPPGKDGLP.PPG.D	Q14993	1	2.3793	1
Collagen α 2(XI) chain	K.GPQGGDDGPKGNPG.PV	P13942	1	2.6128	2
Collagen α 4(IV) chain	P.GGRGALPGGGPLGHPGEGKKGNSVFI.L	P53420	3	2.8053	2
Colon carcinoma related protein	G.DMDLEPLFYLQQL.V	Q9UKZ7	2	2.4156	2
Complement C1q subcomponent, B chain	R.FDHVITNMNNNNYEPR.S	P02746	2	3.5548	3
Complement C1q subcomponent, C chain	K.TNQVNSGGVLLR.L	P02747	2	2.2661	2
	R.FNAVLTNPQGDYDTSTGK.F	P02747	4	4.1056	2
Complement C1r component (EC 3.4.21.41)	K.VLNYYVDWIK.K	P00736	1	2.3732	2
	K.LFGEVTSPLFPK.P	P00736	1	2.9637	2
Complement C1s component (EC 3.4.21.42) (C1)	K.EDTPNSVWEPK.A	P09871	3	2.8012	2
Complement C2 (EC 3.4.21.43) (C3/C5 convertase)	R.HAFILQDTK.A	P06681	1	2.7998	2
	R.HAILLTDGK.S	P06681	1	3.287	2
Complement C3 [Contains: C3a anaphylatoxin]	K.TIYTPGSTVLYR.I	P01024	11	2.3738	2
	I.PPADLSDQVPDTESETR.I	P01024	2	2.6694	2
	I.PIVTSPYQIHFTK.T	P01024	5	2.7953	2
	K.GYTQQQLAFR.Q	P01024	12	2.2316	2

K.SLSVPYVIVPLK.T	P01024	19	2.7553	2
K.SGSDEVQVGQQR.T	P01024	8	3.7153	2
K.TGLQEVEVK.A	P01024	10	3.274	2
G.SGEVLSR.K	P01024	1	2.46	2
D.VPVTVTVHDFPGK.K	P01024	2	3.5905	2
D.TVQSLTQGDGVAK.L	P01024	1	2.794	2
K.GVFVLNK.K	P01024	4	1.9376	1
K.PGMPFDLMVFTNPDGSPAYR.V	P01024	1	3.3407	2
G.EDTVQSLTQGDGVAK.L	P01024	1	2.6133	2
K.LSINTHPSQKPLSITVR.T	P01024	3	2.9305	2
K.AGFLEANYMNLQRS	P01024	4	4.3759	2
L.SITTFIPSR.L	P01024	2	2.4352	2
K.FYYINEK.G	P01024	2	2.7441	2
H.YLDETEQWEK.F	P01024	1	3.2252	2
K.IWDVVEK.A	P01024	9	2.2257	1
K.GQGTLVVTMYHAK.A	P01024	8	3.0788	2
K.AAVYHHFI	P01024	4	2.4465	2
L.PLSITTFIPSR.L	P01024	1	2.547	1
K.SDDKVLEER.L	P01024	31	3.2001	2
K.QELSEAFQATR.T	P01024	7	3.2493	2
K.KQELSEAFQATR.T	P01024	19	3.88	2
K.LMNIFLK.D	P01024	2	3.0209	2
G.NSNNYLHLSVLR.T	P01024	1	3.5111	2
G.DVPVTVTVHDFPGK.K	P01024	11	3.1498	2
K.LSINTHPSQK.P	P01024	1	2.2019	2
K.AAVYHHFISDGV.R.K	P01024	8	3.8402	2
K.EVVLPSFEVIVEPTEK.F	P01024	8	2.8204	1
L.PSFEVIVEPTEK.F	P01024	1	3.1425	1
K.YFKPGMPFDLMVFTNPDGSPAYR.V	P01024	3	4.0167	2
G.TPVAQMTEDAVDAER.L	P01024	1	5.1231	2
K.VQLSNDFDEYIMAEQTIK.S	P01024	5	2.6527	2
K.QDSLSSQNQLGVPLSWDIPELVNMGMQWK.I	P01024	2	2.7869	2
G.TLSVVTMYHAK.A	P01024	1	2.5064	2
K.VTIKPAPETEK.R	P01024	22	2.6495	2
K.DYAGVFS DAGLFTFTSSGQQT.AQR.A	P01024	4	4.876	2
K.DYAGVFS DA.G	P01024	2	2.2306	1
K.VLLDGVQNL.R.A	P01024	1	2.4432	2
R.FYHPEKEDGK.L	P01024	6	2.5705	2

(continued)

Supplementary Table 1 (continued)

Protein	Peptide ^a	Swiss-Prot Accession ^b	Peptide Count ^c	Xcorr ^d	Charge State ^e
	R.SGIPIVTSYQIHFTK.T	P01024	13	3.8726	2
	V.PYVIVPLK.T	P01024	3	2.559	1
	R.LKGPLLNK.F	P01024	1	2.3518	2
	R.APSTWLTAYVVK.V	P01024	1	3.0801	2
	R.VPVAVQGEDTVQSLTQGDGVAK.L	P01024	8	3.3679	2
	R.TFISPIK.C	P01024	7	2.241	1
	Q.PSSAFAAFVK.R	P01024	1	3.1185	2
	R.SGIPIVTSYQIHFT	P01024	5	2.6277	2
	R.LPYSVVR.N	P01024	1	2.2632	2
	W.GEKPNSYIIGK.D	P01024	1	2.9463	2
	R.EPGQDLVPLSITTDIFPSFR.L	P01024	2	3.5572	2
	R.LVAYYTLIGASGQRE	P01024	4	3.8479	2
	R.YYTYLIMNK.G	P01024	4	2.4523	1
	R.VVLYAVDK.G	P01024	6	1.9507	1
	R.SEPESWLWNVEDLKE	P01024	3	3.5286	2
	R.EVVADSVWVDVK.D	P01024	4	2.0769	1
	R.NTLIYLDK.V	P01024	4	2.242	1
	Y.STVGNNSNYLHLSVLR.T	P01024	3	3.8014	2
	R.SGIPIVTSYQIH.F	P01024	1	2.62	2
	R.IPIEDGSGEVVLSR.K	P01024	92	3.8576	2
	R.TVMVNIENPEGIPVK.Q	P01024	10	2.5193	2
	R.VELLHNPAFCSLAATK.R	P01024	1	3.7676	2
	R.HQQTVTIPPK.S	P01024	66	2.6705	2
	R.EALKLEEK.K	P01024	4	2.5509	2
	N.SNNYLHLSVLR.T	P01024	1	2.5302	2
	R.TMQALPYSTVGNNSNYLHLSVLR.T	P01024	2	3.5062	2
	R.SNLDEIIAEENIVSR.S	P01024	12	4.8268	2
	R.TELRPGETLNVNFLLR.M	P01024	2	2.689	2
	R.SVQLTEK.R	P01024	1	1.9184	1
	Q.GDVPVTVTVHDFPGK.K	P01024	2	3.4315	2
Complement C4 [Contains: C4A anaphylatoxin]					
	K.YVLPNFEVK.I	P01028	1	2.2999	2
	K.LGQYASPTAK.R	P01028	3	2.5413	2
	K.LELSVDGAK.Q	P01028	3	2.3268	2
	K.LHLETDSLALVALGALDTALYAAAGSK.S	P01028	2	5.7793	3

G.ALSPGGVASLLR.L	P01028	2	2.5173	2
K.ITQVLHFTK.D	P01028	10	2.6133	2
K.KYVLPNFEVK.I	P01028	1	2.3535	2
K.ADGSYAAWLSR.D	P01028	1	2.3694	2
K.ITPGKPYILTVPGHLDDEMQLDIQAR.Y	P01028	1	2.3723	2
K.LNMGITDLQGLR.L	P01028	4	3.7404	2
K.AEFQDALEKL	P01028	9	1.9015	1
K.VLQIEK.E	P01028	1	2.0926	1
K.VLSLAQEQVGGSPK.L	P01028	16	3.0274	2
L.SVSAGSPHPAIA.R.L	P01028	2	2.5536	2
K.PVQGVAYVRF	P01028	1	2.2721	2
K.LVNGQSHISL.K.A	P01028	12	2.9044	2
K.EVYMPSSIFQDDFVIPDISEPGTWK.I	P01028	4	3.483	2
K.VDFTLSSER.D	P01028	4	2.5931	2
G.SEGALSPGGVASLLR.L	P01028	3	2.5801	2
K.DHAVDLIQK.G	P01028	26	3.2355	2
R.EELVYELNPLDHR	P01028	7	3.4035	2
R.KADGSYAAWLSR.D	P01028	2	3.9674	2
R.LTVAAPPSPGGPFLSIER.P	P01028	1	3.5154	2
R.DFALLSLQVPLK.D	P01028	1	2.3949	1
R.TYNVLDMK.N	P01028	2	2.3154	1
R.LLLFSPSVVHLGVPLSVGVQLQDVPR.G	P01028	1	3.8368	3
R.DFALLSLQVPLKDAK.S	P01028	2	2.846	2
R.YYGGKPVQGVAYVRF	P01028	6	3.6262	2
R.VGDTLNLNLR.A	P01028	6	3.2146	2
R.FGLLDEDEGKK.T	P01028	17	2.8166	2
R.NVNFQK.A	P01028	1	2.1602	1
R.EMSGSPASGIPVK.V	P01028	2	2.2813	2
R.GPEVQLVAHSPWLK.D	P01028	8	3.7467	2
R.TTNIQGINLLFSSR.R	P01028	4	3.1061	2
R.GLQDEDEGYR.M	P01028	4	2.693	2
R.VTASDPLDTLGSEGALSPGGVASLLR.L	P01028	6	3.1882	2
R.GHLFLQTDQPIYNPQQR.V	P01028	2	3.6101	3
R.STQDVTIALDALSAWIAASHITTEER.G	P01028	5	3.891	3
R.PVAFSVVPTAAAASVSLK.V	P01028	2	4.0718	2
R.GSFEFPVGDVAVSK.V	P01028	16	2.9325	2
Complement C5 [Contains: C5a anaphylatoxin]				
K.LNLVATPLFLKPGIPYPIK.V	P01031	2	4.3531	2

(continued)

Supplementary Table 1 (continued)

Protein	Peptide ^a	Swiss-Prot Accession ^b	Peptide Count ^c	Xcorr ^d	Charge State ^e
Complement component C6	K.TLLPVSKPEIR.S	P01031	6	2.6767	2
	K.KIEEIAAK.Y	P01031	1	2.3225	2
	K.IDTQDIEASHYR.G	P01031	1	2.9317	2
	K.DSEITFIK.K	P01031	1	2.4918	2
	K.TDAPDLPEENQAR.E	P01031	2	2.3406	2
	R.YGMWTK.A	P01031	1	2.4396	2
	R.VYSLNDDDLKPAK.R	P01031	6	2.9785	2
	P.EGVKRESYSGVTLDPK.G	P01031	1	2.7207	2
	R.IPLDLVPK.T	P01031	1	2.4103	2
	Complement component C7	K.HEGSFIQGAEK.S	P13671	1	2.8464
K.MEILHPGK.C		P13671	2	2.5188	2
Complement component C8 α chain	T.PLYELVK.E	P10643	1	2.6771	2
	R.HTSLGPLLEAK.R	P07357	7	3.2061	2
Complement component C8 β chain	R.SDLEVAHYK.L	P07358	3	3.0505	2
	R.LPLEYSYGEYR.D	P07358	2	3.2865	2
Complement component C8 γ chain	R.RPASPISTIQPK.A	P07360	1	2.7071	2
	K.LSPIYNLVPVK.M	P02748	4	2.2413	2
Complement component C9	S.PIYNLVPVK.M	P02748	1	2.4517	2
	R.RPWNVASLIYETK.G	P02748	5	3.335	2
	R.DGNTLTYR.R	P02748	1	2.4076	2
	R.GTVIDVTFVNWASSINDAPVLISQK.L	P02748	2	3.8251	2
	R.AIEDYINFEYSR.K	P02748	2	3.1027	2
	R.VVESELAR.T	P02748	2	2.2974	2
	K.EAGIPEFYDYDVALIK.L	P00751	2	2.7504	2
	D.SGGPLIVHK.R	P00751	1	3.1641	2
	K.KDNEQHVFK.V	P00751	1	2.5118	2
	K.EELLPAQDIK.A	P00751	1	2.3281	2
Complement factor B	K.VASYGVKPR.Y	P00751	3	2.3782	2
	K.VKDISEVVTPR.F	P00751	6	3.7009	2

K.DISEVVTPR.F	P00751	8	2.929	2
K.DNEQHVFK.V	P00751	1	2.0972	1
K.ISVIRPSK.G	P00751	1	2.4795	2
K.ALfVSEEEKK.L	P00751	16	2.7728	2
K.VSEADSSNADWVTK.Q	P00751	26	3.3877	2
K.QLNEINVEDHK.L	P00751	2	2.7017	2
Q.LNEINVEDHK.L	P00751	4	3.4909	2
R.LPPTTTCQQQK.E	P00751	1	2.6828	2
R.DAQYAPGYDK.V	P00751	4	2.62	2
R.PHDFENGGEYWPR.S	P00751	1	3.2673	2
R.GDSGGPLIVHK.R	P00751	13	2.8478	2
R.LEDSVTYHCSR.G	P00751	1	3.4477	2
R.YGLVTYATYPK.I	P00751	18	3.2602	2
Complement factor H (H factor 1)				
K.EFDHNSNIR.Y	P08603	3	2.2884	2
K.SPPEISHGVVAH.M	P08603	22	3.7585	2
K.SIDVACHIPGYALPK.A	P08603	2	3.3067	2
K.SPDVINGSPISQK.I	P08603	11	2.3132	2
K.WSSPPQCEGLPCK.S	P08603	1	3.2118	2
K.GEWVALNPLR.K	P08603	3	2.9386	2
K.IDVHLVPPDR.K	P08603	14	2.7979	2
K.SSNLIILEEHLK.N	P08603	18	3.7921	3
R.RPYFPVAVGK.Y	P08603	21	3.0302	2
R.SSQESYAHGTK.L	P08603	1	2.5866	2
R.EIMENYNIALR.W	P08603	1	2.906	2
R.NTEILTGSWSDQTYPEGTQAIYK.C	P08603	4	3.2054	2
R.KGEWVALNPLR.K	P08603	10	2.2205	2
R.EYHFGQAVR.F	P08603	3	2.551	2
Complement factor H-related protein 1				
K.INHGILYDEEK.Y	Q03591	4	4.1175	2
Complement factor I (EC 3.4.21.45)				
K.HGNTDSEGIVEVK.L	P05156	8	4.3404	2
K.VTYTSQEDLVEK.K	P05156	1	2.6967	2
Complement-c1q tumor necrosis factor-related protein 1				
H.YYQIVIFDTE	Q9BXJ1	1	2.2641	1
Complement-c1q tumor necrosis factor-related protein 2				
P.KGKAGAIGRAGPRGPKGVNGTPGKHGTPGKK.G	Q9BXJ5	1	4.3781	3
Complement-c1q tumor necrosis factor-related protein 6				
F.QTLLFERVFNLDGCF.D	Q9BXI9	1	2.316	2

(continued)

Supplementary Table 1 (continued)

Protein	Peptide ^a	Swiss-Prot Accession ^b	Peptide Count ^c	Xcorr ^d	Charge State ^e
Condensin subunit 1	F.SSESEEDLSAEMTEDETPK.K	Q15021	1	4.1533	3
Conserved oligomeric Golgi complex component 7	K.SRMQLAAESLQE.A	P83436	1	3.0161	2
Contactin (Glycoprotein gP135)	L.DSNGELLIRNAQLKHAG.R	Q12860	3	3.005	2
Copper-transporting ATPase 1 (EC 3.6.3.4) (Copper pump 1)	R.SPSYTNDSSTATFIIDGMHCKSCVS.N	Q04656	1	2.744	2
Corticosteroid-binding globulin (CBG) (Transcortin)	K.HLVALSPPK.K	P08185	3	2.7278	2
Crumbs protein homolog 1	W.VKSGSVTTKGSVCNIALR.F	P82279	1	2.4323	2
C-terminal tensin-like protein	G.SFGLALKVQEVPAQAQR.P	Q81ZW8	1	2.2963	1
Cyclic-nucleotide-gated cation channel $\alpha 3$	K.EMYIINEGKLAVVADDG.V	Q16281	1	2.4106	2
Cyclin A1	Y.LCVSLMEPPAVLL.L	P78396	1	2.4801	2
Cyclin-dependent kinase 6 inhibitor (p18-INK6)	A.RAGFLDTLQTLLE	P42773	1	2.7742	2
Cystathionine β -synthase (EC 4.2.1.22)	A.VKAAQELQEGQ.R	P35520	1	2.3807	1
Cysteine-rich repeat-containing protein S52	L.SRNNSVPPNYCKN.I.D	Q9NZV1	1	2.7154	2
Cytochrome P450 11A1, mitochondrial (EC)	K.ADIYTQNFYWE.L	P05108	1	2.4613	2
Cytochrome P450 19A1 (Aromatase) (EC 1.14.14.1)	L.EFFPKPNEFTL.E	P11511	1	2.2896	2
Cytochrome P450 39A1 (EC 1.14.13.-) -	I.LNYIIPSGDLLML.S	Q9NYL5	1	2.4257	2
Cytochrome P450 4A11 (EC 1.14.15.3)	Q.LYDPPDYMKVI.L	Q02928	1	2.4671	1
Cytochrome P450 4F12 (EC 1.14.14.1) (CYPIV12)	H.RRMLTPAFHFNILKSYI.T	Q9HCS2	1	3.8916	3
	G.GLWLRVEPLNVGLQ.-	Q9HCS2	4	3.0699	2

Cytochrome P450 8B1 (EC 1.14.-.-) (CYPVIII B1) M.SSGQEYLF.R	Q9UNU6	1	2.4775	2
Cytohesin 1 (SEC7 homolog B2-1) G.EGLNKTAIG	Q15438	1	2.5683	2
Cytosolic phospholipase A2- γ G.LWGSALGNTE.V	O75457	1	2.2107	1
Cytosolic purine 5'-nucleotidase (EC 3.1.3.5) E.NLEKYVVKDGKLP LLLSRMKEVGK.V	P49902	1	2.6414	2
Dead ringer like-1 protein (B-cell regulator of IgH transcription) E.QFKQLYELDGDPK.R	Q99856	1	2.8137	2
Ded protein (Apoptosis antagonizing transcription factor) E.DEESGMEEGDDAEDSQGESEEDR.A	Q9NY61	1	2.9923	2
Densin-180 G.FLRRADSLVSATEM.A	Q96NW7	1	3.1557	2
Diacylglycerol acyltransferase 2-like protein V.FQYNFGLM.T	Q96PD6	1	2.2373	1
Dimethylglycine dehydrogenase, mitochondrial (EC) L.DRIMEHIKAAEMV PVLKKADIINVV.V	Q9UII7	1	2.2669	2
DJ1024N4.1 (Novel sodium:solute symporter family member) L.FPDEVGCVDPDVC.Q	Q9NPZ7	1	2.4438	2
DJ202D23.2 (Novel protein similar to C21ORF5 [KIAA0933]) C.LLVDFLLDIVSLEYIEIQTEHL.P	Q9NTT5	1	2.4515	2
DJ756N5.1.1 (Continues in Em:AL133324 as dj1161H23.3) L.NPSAIPDDTF.M	Q9H430	1	2.4177	2
DJ776F14.1 (ORTHOLOG of mouse P47) E.LEELRAALEQGER.S	Q9H430	1	2.7813	2
DJ842G6.1.2 (Novel protein) (Fragment) L.DNGELRSY.Q	Q9H102	1	2.4766	2
DJ8B1.3 (Similar to plasma-cell membrane glycoprotein PC- FSPHISPFTAVNDLGHLLG.R V.FFVIFIKHLIHSQIP.A	Q9BQM4	1	2.4743	2
DJ947L8.1.7 (Novel CUB domain protein) (Fragment) I.SLTVFYFLSEKQYDEFEIFDGPSP.L	Q9UJA9	1	2.5835	2
DJ967N21.6 (Novel CDP-alcohol phosphatidyltransferase Y.ADLIPVPLTYM.I	Q9H4W3	1	3.8984	3
DNA ligase I E.ARFIARSLSGRL.R S.EVLKRFEAAFTCEYK.Y	Q9UJA2	2	3.2709	2
	P18858	1	2.5389	2
	P18858	1	2.93	2

(continued)

Supplementary Table 1 (continued)

Protein	Peptide ^a	Swiss-Prot Accession ^b	Peptide Count ^c	Xcorr ^d	Charge State ^e
DNA mismatch repair protein Mlh3 (MutL protein homolog 3)	R.ACSETEESNTCC.S	Q9UHC1	1	2.4471	2
DNA mismatch repair protein Msh2	Y.MKLDIAAVRALNLFQGSVE.D	P43246	1	3.4995	2
DNA replication licensing factor MCM4 (CDC21 homolog)	L.YMQRLGEINVI.G	P33991	3	2.1488	1
DNA replication licensing factor MCM5 (CDC46 homolog)	A.CLLFGGSR.K	P33992	10	2.4689	2
DNA strand-exchange protein SEP1	L.FDEEFPGGLTIRCSPGRGY.R	Q8IZH2	1	2.7869	2
DNA topoisomerase III α (EC 5.99.1.2)	D.KFVVLRQ.Q	Q13472	1	2.448	1
DNA-binding protein RFX3	E.FGEVEISSLP.D	P48380	5	3.0035	2
DNA-dependent protein kinase catalytic subunit (EC 2.7.1.37)	E.PLVMQLIHW.F.T	P78527	1	2.6599	2
DNA-directed RNA polymerase, mitochondrial (EC)	L.QAESVSEVVVNRVDV.A	O00411	1	2.3162	2
DNA-directed RNA polymerases III 39 kDa polypeptide (EC)	P.PDADPVE.I	Q9H1D9	2	2.3972	1
DnaJ homolog subfamily C member 1	P.DKNKDENAETQFRQLVAIYEVLKDD.E	Q96KC8	1	3.039	2
DNA-repair protein complementing XP-G cells (Xeroderma)	Y.QLKGLLKKNYLN.Q	P28715	1	2.5338	2
DRIM protein	N.STYSEQDPLLK.N	O75691	1	2.2725	1
dTDP-D-glucose 4,6-dehydratase (EC 4.2.1.46)	W.GLPGGFQAKRVLVTGGAG.F.I	O95455	1	2.4086	2
Dual specificity mitogen-activated protein kinase kinase 1	L.EFQDFVKNKCLIK.N	Q02750	1	2.7179	2
Dynamitin 3 (EC 3.6.1.50) (Dynamitin, testicular) (T-dynamitin)	G.VYPDKSVAENDENGQAE.N	Q9UQ16	1	3.1389	2
Dynamitin-like 120 kDa protein, mitochondrial	A.IPSPGPHSGAPPVFRPGPLPPFPSS.D	Q9UQ16	1	2.5505	2
	V.RKNLESRGVEVDPSL.I	O60313	1	2.4064	2

Dynein heavy chain, cytosolic (DYHC)	H.TVLVERSTLKEDVGD.E.G	Q14204	1	3.0782	2
	L.SGSEERVQVALEELQDL.K	Q14204	1	2.8861	2
	N.PGYAGRSNLPDNLK.K	Q14204	1	2.4943	2
Dynein intermediate chain 1, axonemal	A.QDFKYYDDAADE.Y	Q9UI46	1	2.8685	2
Dynein intermediate chain 1, cytosolic (DH IC-1)	Y.SGRELEEKDGDVQAGAN.L	O14576	1	2.7692	2
Dystroglycan (Dystrophin-associated glycoprotein)	A.GTTVPGQIRPTMTI.P	Q14118	1	2.2736	2
Dystrophin	T.ENIPGGAEIESEVLD.S	P11532	1	2.4451	1
EAF1	Q.VYARKEALKGGLEKTVSLQKDL.S.E	P11532	2	4.4343	3
Early growth response protein 2 (EGR-2) (Krox-20 protein)	K.LSSSIQVKKTRAEGSSKIQ.A	Q96JC9	1	2.4514	2
	A.STTASSSVTSAFPNPLATGPL.G	P11161	1	2.2978	2
	R.NFTLGGPSAGMTGPGAS.G	P11161	1	2.4338	2
EDIE protein	V.SQPQPANSNNGTSTATST.N	Q8NDV7	1	2.4694	2
EIF4GII	L.VSSTNLININEINGVSEKLSAT.E	O43432	1	2.4901	2
Elastin (Tropoelastin)	G.AAAGLVPGGPFGVGVPGAGVPGVPGA.G	P15502	5	2.9085	2
Ells2 (Fragment)	L.LVRSISLGGAVGSVSGARAA.Q	Q8NEX1	1	2.2572	2
Elongation factor 1- α 1 (EF-1- α -1)	K.IGGIGTVPVGR.V	P04720	2	2.3929	2
Endocytosis protein HSTNB	T.SVNGAEVEVQ.S	Q96RI7	1	2.3057	1
Endogenous retrovirus HERV-K10 putative pol polyprotein	R.NRVSLGAVTVEPPK.P	P10266	1	2.3795	1
Endothelial cell multimerin	F.EDLHIQE.S	Q13201	1	2.7637	2
	I.KELEVKQTHLEGA.L	Q13201	1	2.5078	2
Endothelin-converting enzyme 1 (EC 3.4.24.71) (ECE-1)	L.AAGLVACLAALGI.Q	P42892	3	2.8259	2
Ephrin type-A receptor 5 (EC 2.7.1.112)	K.RELPVAIKTLKVGYTE.K	P54756	1	2.4487	2

(continued)

Supplementary Table 1 (continued)

Protein	Peptide ^e	Swiss-Prot Accession ^b	Peptide Count ^f	Xcorr ^d	Charge State ^e
Ephrin type-A receptor 7 (EC 2.7.1.112)	I.DTIAADESFTIQDL.G	Q15375	1	2.3523	2
	V.TYRILCKRCSWEQGEVPCGSNIGYMPQQITGL.E	Q15375	1	2.2024	2
Ephrin type-B receptor 3 (EC 2.7.1.112) (Tyrosine- V.VAVVVVIAIVCLRK.Q	V.VAVVVVIAIVCLRK.Q	P54753	1	2.662	2
	L.AADDPEVRVLSI.G	P20827	1	2.3379	2
ETAA16 protein	S.CTKPEPETS NKYIDAF.T	Q9NY74	1	2.7888	2
Eukaryotic initiation factor 4A-1 (eIF4A-1)	S.SRVLTITD L LARGID.V	P04765	1	3.0417	2
Eukaryotic translation initiation factor 3 subunit 8 (eIF3 p110)	D.HKQGTGGYFR.D	Q99613	1	2.6721	2
EVI-5 homolog	L.SPDRVLELLAKLE.E	O60447	1	2.4354	2
Excitatory amino acid transporter 5	Y.LWTTFM AVIVGIFMVSIIHPGSA.A.Q	O00341	1	3.114	2
Exocyst complex component Sec10 (hSec10)	G.MLAICDVAEYRK.C	O00471	1	2.8493	2
Extracellular sulfatase SULF-1	C.SCRESGYRASRSQR.K	Q8IWU6	1	2.8941	2
Extracellular superoxide dismutase [Cu-Zn]	D.MYAKVTEIWQEVMMQR.R	P08294	1	2.5427	2
Eyes absent homolog 4	G.AFPIENIYSATKIGKE.S	O95677	2	3.4668	2
F25965_3	G.RSLRPHLPLLL.R	O14560	1	2.5722	2
Fanconi anemia complementation group D2 protein, isoform	D.TRLTQHVPLLKK.T	Q9BXW9	1	2.4038	2
Fatty acid transport protein	V.FKKGDQAYLTGDV.L	O95186	2	2.3191	2
Ferritin light chain (Ferritin L subunit)	K.KLNQALLDLHALGSAR.T	P02792	1	2.2528	2
Fetal brain protein 239 (239FB)	Q.GKVTITVDEYSSNPTQA.F	Q15777	4	2.843	2

Fetuin-B (JRL685) (16G2)

Fibrinogen α / α -E chain

Fibrinogen β chain [Contains: Fibrinopeptide B]

Fibrinogen γ chain (PRO2061)

Fibroblast growth factor-23 (FGF-23)

Fibronectin (FN) (Cold-insoluble globulin) (CIG)

K.KIYMTCPDCPS.S	Q9UGM5	1	2.4988	2
K.VQHIQLLQK.N	P02671	5	2.4138	2
K.ESSSHHPGIAEPPS.R	P02671	1	2.5937	2
R.EVDLKDYEDQK.Q	P02671	1	2.6038	2
R.GGTSYGTGSETESPR.N	P02671	1	2.8677	2
K.GGETSEMYLIQPDSSVKPYR.V	P02675	5	3.7406	2
K.AHYGGFTVQNEANK.Y	P02675	8	3.6279	2
K.DNENVVNEYSSELEKH	P02675	1	4.558	2
K.YQISVNK.Y	P02675	3	2.0031	1
R.TPCTVSCNIPVVS GK.E	P02675	2	3.0189	2
R.EEAPSLRPAPPPIISGG.G	P02675	1	2.4296	2
R.DNDGWLTSDPR.K	P02675	1	2.4716	2
K.QSGLYFIKPLK.A	P02679	1	2.706	2
K.MLEEIMK.Y	P02679	2	2.6501	2
K.YEASILTHDSSIR.Y	P02679	23	3.5925	2
R.VELEDWNGR.T	P02679	1	2.23	2
R.LDGSVDFK.K	P02679	1	2.2951	2
R.YLQEIYNSNNQK.I	P02679	2	4.3201	2
Q.SGLYFIKPLK.A	P02679	1	2.8861	2
G.MNPPPYSQLSRRNEL.P	Q9GZV9	1	2.8888	2
K.TPFVTHPGYDTG.N	P02751	1	2.4835	2
K.TYHVGEQWQKE	P02751	3	2.644	2
K.HYQINQQWER.T	P02751	1	2.3483	2
K.WLPSSPVTGYR.V	P02751	1	2.3004	2
K.EATIPGHLNSYTIK.G	P02751	6	2.8305	2
K.IYLYTLNDNAR.S	P02751	6	2.8349	2
D.SPASSKPISINYR.T	P02751	2	2.7738	2
K.LGVRPSQGGEAPRE	P02751	6	3.7013	3
G.TSTSATLTGLTR.G	P02751	1	2.4302	2
R.GATYNIIVEALK.D	P02751	2	2.2258	2
R.EESPLLIGQQSTVSDVPR.D	P02751	2	4.0035	2
R.DAPIVNK.V	P02751	1	1.9595	1

(continued)

Supplementary Table 1 (continued)

Protein	Peptide ^a	Swiss-Prot Accession ^b	Peptide Count ^c	Xcorr ^d	Charge State ^e
	R.NLQASEYTVSLVAIK.G	P02751	1	3.8221	2
	R.ESKPLTAQQTTK.L	P02751	1	2.2801	2
	R.SSPVVVIDASTAIDAPSNLR.F	P02751	3	3.9583	2
	R.VTWAPPPSIDLTNFLVR.Y	P02751	1	3.0002	2
	R.STTPDITGYR.I	P02751	1	2.2454	2
	R.GDSPASSKPIISIN.YR.T	P02751	8	3.5151	2
	R.VPGTSTSATLIGLTR.G	P02751	23	2.6938	2
	R.VGDIYERPK.D	P02751	5	2.8814	2
	R.HTSVQITSSGSGP.F	P02751	1	2.8058	2
	R.SYTIITGLQPGTDYK.I	P02751	12	3.5552	2
Filamin A (α -filamin) (Filamin 1) (Endothelial actin-binding					
	A.DFKVYTKGAGSGEL.K	P21333	1	2.2533	2
FK506-binding protein 5 (EC 5.2.1.8) (Peptidyl-prolyl cis-trans					
	L.AAFLNLAMCYLKLREY.T	Q13451	1	2.7367	2
FKSG16					
	L.LLFTVITYFFVVIGIAPIFILY.E	Q96QA1	1	2.6214	2
FKSG72					
	G.FYIAVQEVLALEVS	Q9BWW2	2	2.4473	2
FL cytokine receptor (EC 2.7.1.112)					
	G.AFGKVMNATAYGISK.T	P36888	1	2.7227	2
Flavin reductase (EC 1.5.1.30) (FR)					
	R.LQAVTDDHIR.M	P30043	1	2.5936	2
Flightless-I protein homolog					
	G.KLTNLEEF	Q13045	1	2.343	1
FLJ00034 protein (Fragment)					
	A.TSTAAAAPSTAPSAGSTAGDSG.A	Q9H7N4	1	2.4096	2
	K.KTKGKTKGKTK.P	Q9H7N4	1	2.1376	1
FLJ00070 protein (Fragment)					
	S.PGAPGPLLPSGAGSPRPG.A	Q9H7K2	1	2.484	1
FLJ00086 protein (Fragment)					
	T.LLPQPPPTTCPPGA.L	Q9H7J3	1	3.1311	2
FLJ00155 protein (Fragment)					
	V.RSTQPQQNNEELPTY.E	Q8TEN8	1	2.4103	2
FLJ00156 protein (Fragment)					
	A.WRAPEFLQTLA.I	Q8TEN7	3	2.6827	2
	P.RNAEAAHQALIPK.L	Q8TEN7	1	2.4001	2

FLJ00158 protein (Fragment)	V.WSAWYGKCVKGGKGS.L	Q8TEN5	1	2.6935	2
FLJ00225 protein (Fragment)	L.RTVFGTTPLPMACPA.L	Q8TEH2	1	2.2603	2
FLJ00238 protein (Fragment)	V.RSSTYSLIPITVAEAGL.T	Q8TEF9	1	2.5518	2
FMI protein	A.EAERFLL.Q	Q92735	1	2.3667	2
Folypolyglutaminate synthase, mitochondrial	V.VCGVSSLGIDHTSLL.G	Q05932	1	2.3424	2
Forkhead box protein O3A -	R.SELMDADG.L	O43524	3	2.5501	2
Fos-related antigen 1 (FRA-1)	Q.KFHLYPSINTMSGSELQWWMV.Q	P15407	1	2.5355	2
FRAP-related protein (Protein kinase ATR)	K.MLKKLVEEATFSEILPL.Q	Q13535	1	2.5184	2
	L.KETLYKNOEKL.I	Q13535	2	2.4427	2
FREB (FCRLa) (Fc receptor related protein X)	P.FHILVSYDWLILQGPAPKVPFEGDLL	Q8WXH3	1	3.7714	3
Fumarylacetoacetase (EC 3.7.1.2)	G.DGYRIGFGQCAGKVLPA.LL.P	P16930	1	2.3997	1
G antigen family D 2 protein (XAGE-1 protein)	Q.LKVGIHLGSRQKK.I	Q9HD64	1	2.7411	2
G protein-coupled receptor	H.AVVASVPVFAVTNVADIYATST.C	Q14439	1	3.2774	2
	V.WLPKVSLLANPV	Q14439	1	2.4889	2
G protein-coupled receptor kinase GRK7 (EC 2.7.1.-)	L.EKEILEKVSPP.F	Q8WTQ7	1	2.4976	2
	G.SREKSDDDPR.K	Q8WTQ7	1	2.7559	2
G1 to S phase transition protein 1 homolog	F.TLRDEGKTTAIGKVLLKLP	P15170	1	2.4176	2
G2/mitotic-specific cyclin F	S.FLCELSLLHTLSA.Y	P41002	1	2.4248	2
Gab2 (Hypothetical protein KIAA0571)	R.TFYLVAETEEDMKNK.W	Q9UQC2	1	2.2368	2
Galactoside 2- α -L-fucosyltransferase 1 (EC 2.4.1.69)	S.QGDVTFAGDGGQEATP.W	P19526	1	3.0188	2
Gamma-aminobutyric acid type B receptor, subunit 1	P.SINCTVDEMT.EA.V	Q9UBS5	1	2.693	2

(continued)

Supplementary Table 1 (continued)

Protein	Peptide ^a	Swiss-Prot Accession ^b	Peptide Count ^c	Xcorr ^d	Charge State ^e
Gamma-aminobutyric acid type B receptor, subunit 2	P.AILKLLKH.Y	O75899	1	2.4531	1
Gamma-aminobutyric-acid receptor pi subunit	R.GLEHLRLAQYTIERYFTL.V	O00591	1	2.4493	2
Gastric cancer-related protein GCYS-20	R.CVAAVSSVPKIVDWM DN.F	Q9UH48	1	2.6477	2
GCP170	S.TDSPLEK.E	O43241	2	2.4993	2
Gelsolin , plasma (Actin-depolymerizing factor)	K.HVVPNEVVVQR.L	P06396	1	3.1985	2
	K.AGALNSNDAFVLK.T	P06396	13	3.7006	2
	K.PALPAGTEDTAK.E	P06396	4	2.8072	2
	K.TGAQELLR.V	P06396	1	2.614	2
	F.FTGDAYVILK.T	P06396	1	2.6815	2
	K.DSQEEEKTEALTSAK.R	P06396	9	2.3629	2
	K.TPSAAAYLWVGTGASEAEK.T	P06396	3	2.377	2
	R.DPDQIDTDLGLSYLSSH.I	P06396	1	2.5308	2
	N.SMVVEHPEFLK.A	P06396	1	2.505	2
	R.PNSMVVEHPEFLK.A	P06396	1	3.882	2
Glioma tumor suppressor candidate region gene 1 protein	L.QGVTLPPSAVAMLNTPDGLVQPATPA.A	Q9NZM4	1	2.8757	2
Glutathione S-transferase, mitochondrial (EC 2.5.1.18)	P.KDFLSVMLEK.G	Q9Y2Q3	1	2.679	2
Glyceraldehyde 3-phosphate dehydrogenase, testis-specific	N.IVSNASCTTNCLAPLAK.V	O14556	2	2.5814	2
Glycerol kinase, testis specific 1 (EC 2.7.1.30)	R.WLLDNVR.K	Q14409	1	2.2752	2
Glycine dehydrogenase [decarboxylating], mitochondrial	P.RVNPLKMSPHSL.T	P23378	1	2.4462	2
Glycogen [starch] synthase, muscle (EC 2.4.1.11)	T.KAKVTGDEWGDNYF.L	P13807	1	2.7616	2
Glycogen phosphorylase, brain form (EC 2.4.1.1)	F.YELEPEKFN	P11216	1	2.284	1
	D.LQIPPPNIPR.D	P11216	1	2.5961	2

Glycogen phosphorylase, liver form (EC 2.4.1.1)	I.IGGKAAPGYHMA.K	1	2.2104	2
Glycogenin-interacting protein 1	A.LQLNGGQYWAVTSPER.S	5	2.483	2
Glycosyl-phosphatidylinositol-MAM	L.WGPMAlFLALQR-	1	2.6332	2
Glycylpeptide <i>N</i> -tetradecanoyltransferase 2 (EC 2.3.1.97)	S.DALILAKSKGFDVFNAL.D	1	2.7849	2
Glycyl-tRNA synthetase (EC 6.1.1.14) (Glycine-tRNA ligase)	I.EPSFGLGRIMYTVFE.H	1	2.2917	1
Golgi autoantigen, golgin subfamily B member 1 (Giantin)	K.DQLTDLNSLEK.C	1	2.9274	2
	L.QELLKEK.Q	1	3.0693	2
Golgin-160 (Fragment)	L.REHNSILETAL.A	1	2.2617	2
GPI transamidase component PIG-S	V.PILLSLVKIFLETRKS.W	2	3.3987	2
GPI-anchored protein p137 (p137GPI)	R.REQLMREEAEQ.K	3	2.7813	2
Graf2	V.KEEKKKFKETEKNYSLLID	1	2.6956	2
GREB1a (Fragment)	C.PEGDIDILLDKFH	1	2.349	1
Growth/differentiation factor 9 (GDF-9)	L.CFPISLGSQASGGEAQJAAS.A	1	2.9543	2
GTX	R.PVGAAGGGLLGGGLPR.L	1	2.2203	2
Guanine exchange factor MCG7 isoform 1	I.SLFNSVSQ.W	8	2.2712	1
Guanine nucleotide exchange factor DBS (DBL's big sister)	H.SVLESLRELQAEFGSEPSV.N	1	3.008	2
Guanine nucleotide-binding protein G(I)/G(S)/G(O) γ -10	N.ACKDALLVGV.P	5	3.3705	2
H-2K binding factor-2	F.YGNGGDDIGVFLS	1	2.4738	2
Haptoglobin-1	K.LRTEGDGVYTLNNE.K	1	3.3611	2
	K.DYAEVGR.V	18	2.795	2

(continued)

Supplementary Table 1 (continued)

Protein	Peptide ^a	Swiss-Prot Accession ^b	Peptide Count ^c	Xcorr ^d	Charge State ^e
	K-AVGDKLPECEAVCGKPK.N	P00737	1	3.5565	2
	K-VLHPNYSQVDIGLIK.L	P00737	4	3.6348	3
	K-LPECEAVCGKPK.N	P00737	1	3.9034	2
	K-LPECEAVCGK.P	P00737	1	2.1871	1
	G.DGVYTLNNE.K	P00737	1	3.0942	2
	K-AVGDKLPECEAVCGK.P	P00737	1	2.7706	2
	K-SCAAEYGVYK.V	P00737	9	2.6394	1
	K.VTSIQDWWQK.T	P00737	31	2.2246	2
	G.DGVYTLNNEK.Q	P00737	4	2.5794	2
	K-SPVGVQPILNEHTFC	P00737	29	3.8496	2
	K-LRTEGDGVYTLNNEK.Q	P00737	1	3.8851	2
	K-GSFPWQAK.M	P00737	17	2.5038	2
	K-PPEIAHGYVEHSVR.Y	P00737	1	3.5875	3
	H.GYVEHSVR.Y	P00737	1	2.5362	2
	K-DIAPTLTLYVGKK.Q	P00737	4	2.6556	2
	K-NPANPVQ.R	P00737	3	2.3159	1
	K-DIAPTLTLYVGK.K	P00737	61	2.4193	2
	K-SPVGVQPIL.N	P00737	1	2.3265	1
	K-SPVGVQPILNEH.T	P00737	14	3.6468	2
	K-YVMLPVADQDQCIR.H	P00737	9	2.9424	2
	K-SPVGVQPILNEHTFCAGMSK.Y	P00737	5	3.6784	3
	K-SPVGVQPILNEHT.F	P00737	4	2.7975	2
	Q.PILNEHTFCAGMSK.Y	P00737	1	3.6047	1
	R.TEGDGVYTLNNEK.Q	P00737	87	3.2547	2
	R.TEGDGVYTLNNE.K	P00737	13	3.5205	2
	R.ILGGHLDK.G	P00737	46	2.7723	2
	R.HYEGSTVPEKK.T	P00737	7	3.1812	2
	R.HYEGSTVPEK.K	P00737	37	2.2078	2
	R.VGYVSGWGR.N	P00737	38	3.2308	2
	K-LRTEGDGVYTLNDK.K	P00738	4	4.6631	2
	G.DGVYTLNDKK.Q	P00738	3	2.4752	2
	K-LPECEADDGCPKPEIAHGYVEHSVR.Y	P00738	1	5.2132	3
	K-AVGDKLPECEADDGCPKPEIAHGYVEHSVR.Y	P00738	1	4.0167	3
	G.DGVYTLNDK.K	P00738	3	3.1704	2

Haptoglobin-2

Haptoglobin-related protein	D.GVYTLNDKK.Q	P00738	1	2.937	2
	R.TEGDGVYTLNDK.K	P00738	105	2.8057	2
	R.TEGDGVYTLNDKK.Q	P00738	81	3.2237	2
HDCMC04P	K.VVLHPNYHQVDIGLIK.L	P00739	1	2.4709	2
	R.VGYVSGWGQSDNFK.L	P00739	7	4.0885	2
Heat shock cognate 71 kDa protein	D.DGYMICCDK.C	Q9NS29	1	2.2315	1
	K.DAGTIAGLNLRLI	P11142	5	3.1295	2
Heat shock factor protein 1 (HSF 1)	I.ISDITELAPASPMASPGG.S	Q00613	2	2.7146	2
	Q.PTLPTPPALGEVPELQS.P	Q8NG67	1	3.0924	2
HECT domain protein LASU1	S.LISIALPENK.V	Q8NG67	1	2.4666	2
	V.PRAGKQQQHAVS	Q9NZ71	1	2.2894	1
Helicase-like protein NHL	HemK protein homolog (EC 2.1.1.-) (M.HsaHemKP)	Q9Y5R4	1	2.6693	2
	G.RMLWALLSGPGRRGSTR.G				
Hemoglobin α chain	-V.LSPADKTNV.K.A	P01922	9	2.7209	2
	K.VGAHAGEYGAEALER.M	P01922	22	3.6518	3
Hemoglobin β chain	G.AHAGEYGAEALER.M	P01922	1	3.7523	2
	W.GKVGAHAGEYGAEALER.M	P01922	2	4.049	3
Hemoglobin zeta chain (HBAZ)	K.VNVDEVGGEALGR.L	P02023	27	4.0625	2
	K.SAVTALWGK.V	P02023	1	2.4949	2
Hemopexin (β -1B-glycoprotein)	G.AFSDGLAHLNLIK.G	P02023	2	2.9683	2
	-VHLTPEEK.S	P02023	3	2.5311	2
Hemoglobin zeta chain (HBAZ)	K.VVAGVANALAHK.Y	P02023	16	2.7082	2
	FSDGLAHLNLIK.G	P02023	1	3.0574	2
Hemopexin (β -1B-glycoprotein)	K.VLGAFSDDLHLNLIK.G	P02023	3	4.6803	2
	R.LLVVYPWTQRF	P02023	1	2.4235	2
Hemoglobin zeta chain (HBAZ)	W.GKVNVDVGVGGEALGR.L	P02023	2	4.5473	2
	I.LLRVDPVNFK.L	P02008	4	2.8083	2
Hemopexin (β -1B-glycoprotein)	H.GNVAEGETKPPDPVTER.C	P02790	2	3.2595	2
	K.GGYTLVSGYPK.R	P02790	20	2.7084	2

(continued)

Supplementary Table 1 (continued)

Protein	Peptide ^a	Swiss-Prot Accession ^b	Peptide Count ^c	Xcorr ^d	Charge State ^e
	K.SLGNCSANGPLYLIHGPNLYCYSDVEK.L	P02790	1	2.9118	2
	K.VWVYPPEK.K	P02790	3	2.4217	2
	K.VWVYPPEK.E	P02790	2	2.2546	2
	K.EVGTPHGIILDSVD.A	P02790	2	3.4031	2
	G.HNSVFLIK.G	P02790	1	2.8246	2
	K.EVGTPHGIILDSVDAAFICPGSSR.L	P02790	1	4.4389	2
	D.PVRGEVPPR.Y	P02790	1	3.0371	2
	F.PSPVDAAFR.Q	P02790	1	2.6462	1
	G.NVAEGETKPPDVTER.C	P02790	1	2.9036	2
	K.SGAQATWTELPWPHEK.V	P02790	17	4.8058	3
	K.NFSPVDAAFR.Q	P02790	5	2.2169	2
	K.GDKVWVYPPEK.K	P02790	1	2.3765	2
	P.TSAHGNVAEGETKPD.P	P02790	1	4.5025	2
	R.LHIMAGR.R	P02790	1	2.0483	1
	N.VAEGETKPPDVTER.C	P02790	3	3.2258	2
	R.YYCFQGNQFLR.F	P02790	2	3.5206	2
	Q.GHNSVFLIK.G	P02790	1	2.5141	2
	R.EWFWDLATGTMKE	P02790	11	3.2395	2
Heparin cofactor II (HC-II) (Protease inhibitor)					
	K.TLEAQLTPR.V	P05546	5	2.546	2
	K.FAFNLYR.V	P05546	2	2.48	2
	K.NYNLVESLK.L	P05546	2	2.6494	1
	K.YEITTIHNLFR.K	P05546	4	2.5139	2
Hepatocellular carcinoma-associated protein HCA2					
	P.PQGPPKISPPQPPQSPQS.P	Q8TD91	1	3.7006	2
Hepatocyte growth factor (Scatter factor) (SF)					
	R.PAVLDDFVSTIDLPN.Y	P14210	1	2.81	2
Hepatocyte growth factor receptor (EC 2.7.1.112)					
	V.QPDQNFITGLIAGVVS.I	P08581	1	2.6197	2
Hermansky-Pudlak syndrome 5 protein					
	S.HLSLISVERCV.E	Q9UPZ3	3	2.4266	2
Heterogeneous nuclear ribonucleoprotein A3 (hnRNP A3)					
	N.FGGGGNFRDGNF.G	P51991	1	2.6149	2
Hexokinase, type I (EC 2.7.1.1) (HK I) (Brain form hexokinase)					
	H.IDLVEGDEGR.M	P19367	5	3.2456	2

HGF activator like protein (Hyaluronan binding protein 2)	R.DEIPHNDIALLK.L	1	2.5987	2
High mobility group protein-R	S.STCALJTTTLHSTPAAA.G	1	2.4382	2
High-affinity cAMP-specific and IBMX-insensitive 3',5'-cyclic G.FNRRRFMENSSI.I	G.FNRRRFMENSSI.I	12	2.8346	2
Histidine decarboxylase (EC 4.1.1.22) (HDC)	V.KLWVFVIRSFVKNLQ.A	4	2.9676	2
Histidine-rich glycoprotein (Histidine-proline rich)	K.ALDLINKR.R	3	2.6832	2
	K.SGFPQVSMFFTHFPK.-	1	2.5977	2
	K.YKEENDDDFASFR.V	5	2.9198	2
	K.ALDLINK.R	1	1.9613	1
	R.ADLFYDVEALDLESPK.N	2	5.0052	2
	R.IADAHLDR.V	2	2.8101	2
	R.KGEVLPPLPEANFSPFPLPH.H	4	4.1708	3
Histidine-rich membrane protein Ke4	A.LLTEGGAVGSEIAGGAGPGWVLPFTAGGFI.Y	1	2.5372	2
Histone deacetylase 6 (HD6)	I.GRAAGTGFTVNVV.W	1	2.3972	2
Histone deacetylase 9 (HD9) (HD7B) (HD7)	L.LGNELEPLAEDILHQ.S	1	3.0823	2
Histone H1.1	S.GSFKLNKK.A	1	2.4731	2
Histone H2A.a (H2A / a) (H2A.2)	R.VGAGAPVYLAADVLEYLTAEILELAGNAAR.D	3	5.0718	2
Histone RNA hairpin-binding protein	I.KLWKVALHFWDPPAE.E	1	2.4426	2
Histone-lysine N-methyltransferase, H3 lysine-9 specific 3	R.YMVQRGGCVYSK.E	1	2.3359	2
Homeobox even-skipped homolog protein 1 (EVX-1)	A.LVGSPPNGGSETPKSN.G	1	2.9071	2
Homeobox even-skipped homolog protein 2 (EVX-2)	A.AAAAAAGAAA.A	1	2.1173	1
	G.GGGGGGGGGGGGAGAGGGSDFGCSAA.A	1	2.5463	2
Homeobox protein HB9	L.DQWLRASTAGMILPKM.P	1	2.5005	2
Homeobox protein Hox-C10	E.NTTGNWLTAKSGR.K	1	2.7168	2

(continued)

Supplementary Table 1 (continued)

Protein	Peptide ^a	Swiss-Prot Accession ^b	Peptide Count ^c	Xcorr ^d	Charge State ^e
Homeobox protein Hox-C8 (Hox-3A)	V.VQYDPDCKSSANT.N	P31273	2	2.4897	2
Homeobox protein Hox-D8 (Hox-4E) (Hox-5.4)	Y.K.A.A.A.A.A.A.A.A.A.A.A.A.G.E	P13378	1	2.4063	1
Homeobox protein Meis2 (Meis1-related protein 1)	A.QRYDELPHYGGM.D	O14770	1	2.5709	2
Homeobox protein MOX-2 (Mesenchyme homeobox 2)	R.HSLCLQPDGGPPPELGSSPP	P50222	1	2.4828	2
Homeotic protein HB9 (Fragment)	Q.FKLNKYLSPK.R	Q9Y648	2	2.8032	2
Homer-2b	S.LKTDIEE.S	O95349	1	2.4532	1
Homolog of the aspergillus nidulans sudD gene product	I.GKGKDITTKHDEVVCG.R	O14730	1	2.4096	2
HSNF2H	E.EIFDDASPGKQKE.I	O60264	1	3.1664	2
HSPC263 (Fragment)	K.KYSYIRKTRPDGNCFYR.A	Q9P0B8	1	2.7274	2
HSPC280 (Fragment)	M.NVDHEVNLLVE	Q9P0A1	19	2.5998	2
HSPC300 (Fragment)	G.QEDPVQREIHQDW.A	Q9P082	1	2.7438	1
Huntingtin interacting protein 1 (HIP-1)	L.ETSAQSEANWAAE.F	O00291	1	2.6925	2
HUPF2	E.DYQEMQLSLA.Q	Q9H1J2	1	2.5293	2
Hypothetical FRG1-like protein c20orf80	K.ISKEESKILKK.A	Q9BZ01	2	2.6246	2
Hypothetical p38 protein	R.NVPIIVFVQDKG	Q8N0V3	2	2.3496	2
Hypothetical protein	P.KVTQLYK.C	O95568	1	2.5526	2
Hypothetical protein	N.FEFEDLQVTFR.G	Q8IV20	1	2.6495	2

Hypothetical protein	R.NYSVASGIQSSLDEGQSVG.F	Q8IXU4	1	2.7555	2
Hypothetical protein	R.ATWSGAVLAGR.D	Q8IYJ6	7	2.869	2
Hypothetical protein	Y.LYCEPSQLQEYA.K	Q8IZG0	1	2.4993	2
Hypothetical protein	R.VRLAEAEETAR.T	Q8N163	1	2.0744	1
Hypothetical protein	S.YVLTQPPSVSVAPGQTAR.I	Q8N355	2	3.3694	2
Hypothetical protein	S.YVLTQPPSVSVAPGQ.T	Q8N355	8	3.1509	2
Hypothetical protein	P.KFAKAPFLSCILSPG.E	Q8N371	1	2.5397	1
Hypothetical protein	A.GCTGGFLQA.Y	Q8N413	1	2.2455	2
Hypothetical protein	K.GTTVTVSSASPTSPK.V	Q8N5K4	17	3.9123	2
Hypothetical protein	T.EAEFVFPVLNIKRS	Q8N654	2	3.0269	2
Hypothetical protein	P.VREPVDNLSPEERDA.R	Q8ND16	1	2.6866	2
Hypothetical protein	M.EPTFVQVPTLKK.P	Q8ND61	1	2.6039	2
Hypothetical protein	R.NDQRPSGVPDR.F	Q8NEJ1	1	2.6961	2
Hypothetical protein	K.LQETKEKVSFKK.K	Q8TBL3	1	2.5113	2
Hypothetical protein	K.EEEEEPNPNYKEVEDPQQ.E	Q8TBY9	2	3.3833	2
Hypothetical protein	T.YLCELGFSILTR.L	Q8TCP9	1	2.4316	2
Hypothetical protein	N.KKKEEKKGK.G	Q8WTQ4	1	2.2496	1
Hypothetical protein	C.EVQLVESGGGLVQPGRS	Q8WU38	4	4.5022	2
Hypothetical protein	Q.LVESGGGLVQPGRS	Q8WU38	1	2.6193	2
Hypothetical protein	E.LLKGNETIARLQALA.K	Q8WUC8	1	2.4825	2

(continued)

Supplementary Table 1 (continued)

Protein	Peptide ^a	Swiss-Prot Accession ^b	Peptide Count ^c	Xcorr ^d	Charge State ^e
Hypothetical protein	K.LTVLGQPK.A	Q8WUK4	21	2.2198	2
Hypothetical protein	A.RLYQSVLRVWQ.V	Q8WUY4	1	2.444	2
Hypothetical protein	M.TGTPKTQEGAKDLEVDMNK.T	Q8WW03	1	2.6201	2
Hypothetical protein	A.DVEDVTEEDC.A	Q8WYY9	3	2.9394	2
Hypothetical protein	L.GWGRERELCVKCL.L	Q96AR0	1	2.3784	2
Hypothetical protein	V.KDLNGIDLTPVQD.T	Q96BJ3	1	2.4953	2
Hypothetical protein	H.MPQPVNPELTAGPITGLV.Y	Q96BQ3	1	3.8355	3
Hypothetical protein	H.SPPSAVLLR.A	Q96BT6	1	2.5522	2
Hypothetical protein	L.EAAGRFLLP	Q96C12	1	2.3887	2
Hypothetical protein	K.FDAKILHLPTYSDVK.L	Q96C45	1	2.6998	2
Hypothetical protein	P.KISSTKNISIK.Q	Q96CB8	1	2.4415	2
Hypothetical protein	Q.QGRELEAECPVCW.N	Q96D59	1	2.5543	2
Hypothetical protein	K.LGDSWDVVKLGA.L	Q96DA0	1	2.6438	2
Hypothetical protein	L.CGLLEASGGRALPQ.L	Q96DZ1	1	2.5704	2
Hypothetical protein	T.ICVTCKECEDLGV.E	Q96E18	1	2.5068	2
Hypothetical protein	I.ELTEMESMKTTLKEEVNELQY.R	Q96EA4	2	2.6952	2
Hypothetical protein	G.FYHLRIAYYASK.G	Q96ES2	1	2.4674	2
Hypothetical protein	A.EPTAAPHPVVKQV.I	Q96F28	1	2.2739	2

Hypothetical protein	H.NSWSSSRHPNPQATPKK.S	Q96F86	2	3.058	2
Hypothetical protein	A.IVLA VGGGGLLAGVVAGLLELV.G	Q96GA7	1	2.4513	2
Hypothetical protein	I.YAKLEEIEADKA.P	Q96GS8	1	2.524	2
Hypothetical protein	S.SEDAKIHEKTSR.T	Q96GV0	1	2.5182	2
Hypothetical protein	L..ALAPDLSTEQRRRR.R	Q96HB5	1	2.5643	2
Hypothetical protein	I.VKESLTEEDV LNCQKT.I	Q96HM2	1	2.2343	1
Hypothetical protein	Y.KIDGSLEVPLERAK.D	Q96HM2	1	2.5623	2
Hypothetical protein	K.AGVETTKPSK.Q	Q96I69	19	2.9767	2
Hypothetical protein	Q.VTVLGQPK.A	Q96I69	1	2.5323	2
Hypothetical protein	H.SEEPLTIFSGA.L	Q96IH6	1	2.3929	1
Hypothetical protein	V.SVSLSLGEAPGGGLFLPPP.S	Q96IQ8	1	2.4053	2
Hypothetical protein	E.LEQEVQRLKKE.Q	Q96J23	1	3.0091	2
Hypothetical protein	S.TVQVCNSILCPKTGR.E	Q96QE5	1	3.1605	2
Hypothetical protein	R.IHLMAGR.V	Q96S83	1	2.0391	1
Hypothetical protein	K.GDTFSCMVGHEALPLAFTQE.T	Q9BRV0	4	4.9399	2
Hypothetical protein	M.VGHEALPLAFTQE.T	Q9BRV0	2	3.442	2
Hypothetical protein	G.HEALPLAFTQE.T	Q9BRV0	5	3.4416	2
Hypothetical protein	E.SWVTDMCKVGASSDPC	Q9BS82	1	3.4029	2
Hypothetical protein	M.QHCNLLCLPENYQMKYYLYHGLSWP.Q	Q9BSU3	1	3.9429	3
Hypothetical protein	S.FSDLYSSVIFY	Q9BTX1	3	2.7715	2
Hypothetical protein	F.MMMDDAVLCMCFSR.D	Q9BU59	1	2.5506	2

(continued)

Supplementary Table 1 (continued)

Protein	Peptide ^a	Swiss-Prot Accession ^b	Peptide Count ^c	Xcorr ^d	Charge State ^e
Hypothetical protein	I.YAGLANGSILVVDVR.N	Q9BU18	1	2.5755	2
Hypothetical protein	L.GLISPAYLFLWP	Q9BUN8	1	2.5815	2
Hypothetical protein	N.EGGAKPELASQATE.G	Q9BWC3	2	3.2948	2
Hypothetical protein	V.GGHTSLAGVFPASPSVSLKQ.V	Q9H0H3	1	3.0259	2
Hypothetical protein	I.LKADIAILRQEICTMKN.D	Q9H0H6	1	2.7003	2
Hypothetical protein	T.SGSAEGSLQKAEK.V	Q9H0K5	1	2.6018	2
Hypothetical protein	A.LCSTLIEGQKRSQV.S	Q9H0L3	1	2.2753	2
Hypothetical protein	W.LLKGLQTVGCMPPPVSSA.V	Q9H0M9	1	2.4845	2
Hypothetical protein	L.EVDILDSSLQALTSR.K	Q9HA85	1	2.7372	2
Hypothetical protein	E.VNDIITTFDSIV.G	Q9HAD3	1	2.4469	2
Hypothetical protein	V.LFSPCLVYGSVADMPI.F	Q9HAF5	1	2.5125	2
Hypothetical protein	K.MTLPLNLR.L	Q9NUJ7	1	2.4134	2
Hypothetical protein	I.ISLSFLSLGWNIFVCL.F	Q9NW96	1	2.5119	2
Hypothetical protein	E.GYIAVVLPKFEESK.S	Q9NX38	1	2.8054	2
Hypothetical protein	L.QNGHLRFPGIKTYIDP.D	Q9UF33	2	2.8565	2
Hypothetical protein	T.KNHNEIIQTKLKEIT.E	Q9UFE4	1	3.4016	2
Hypothetical protein	L.NYLFLQILIVE.S	Q9UFQ7	1	2.4772	2
Hypothetical protein	Q.AFCIEFSRIR.E	Q9UKZ1	1	2.4258	2

Hypothetical protein	L.QDNIMKIDIAEL.R	Q9UNU8	1	2.2277	2
Hypothetical protein	T.RRESEYPFIDGLQ.N	Q9Y3H6	1	3.1806	2
	Q.LLRIFELLADAG.V	Q9Y3N6	7	3.4086	2
Hypothetical protein (BA6J24.2)	F.EKVFEAVDPGA.V	Q9NWF6	1	2.8126	2
Hypothetical protein (Fragment)	R.AAAPRAGAAAASMAPSPR.T	O95902	1	3.2144	2
Hypothetical protein (Fragment)	N.QNGVLDFFQK.P	Q8N3C2	3	2.7652	2
Hypothetical protein (Fragment)	L.LAGSSAGGTGVLLNV.D	Q8N410	1	2.5011	2
Hypothetical protein (Fragment)	L.SFHVSVSGILVCOAGCVLE.E	Q8N465	1	2.557	2
Hypothetical protein (Fragment)	L.GSRASLADALPLHIAPR.W	Q8ND25	1	2.7087	2
Hypothetical protein (Fragment)	E.CLAPLGALEFLRLNG.N	Q8ND46	1	2.5802	1
Hypothetical protein (Fragment)	N.LQDLENTTPAQPK.N	Q8NDG1	1	2.5179	2
Hypothetical protein (Fragment)	K.QNVNILIDTEK.F	Q96BR4	1	2.0954	1
Hypothetical protein (Fragment)	C.ARLAAGPGAAEPLPV.E	Q96BV2	1	2.4451	2
Hypothetical protein (Fragment)	P.SEADCIAVQHVCTIVSFR	Q96EH2	1	3.0043	2
Hypothetical protein (Fragment)	S.SSPGGLPPVL.S	Q96HG1	1	2.412	2
Hypothetical protein (Fragment)	A.KVKLYMWPLSSLRRY.G	Q96HI2	1	3.1477	2
Hypothetical protein (Fragment)	A.LQVDIQTREGTLISLAKQ.A	Q96IF6	1	3.1485	2
Hypothetical protein (Fragment)	S.DLANILGA.E	Q9BSB5	1	2.2143	1
Hypothetical protein (Fragment)	A.ADSTEELAEVEEYG.V	Q9BTP1	1	2.4903	2
Hypothetical protein (Fragment)	K.EVERFLAQ.L	Q9BW53	1	2.5507	2

(continued)

Supplementary Table 1 (continued)

Protein	Peptide ^a	Swiss-Prot Accession ^b	Peptide Count ^c	Xcorr ^d	Charge State ^e
Hypothetical protein (Fragment)	L.LSRSPSVASMKAVPAA.S	Q9C074	1	2.3189	2
Hypothetical protein (Fragment)	S.GRIHRLALTGEKRADIQL.N	Q9NPR9	1	2.8377	2
Hypothetical protein (Fragment)	K.ILRELVHDRFHK.Q	Q9NSJ3	1	2.2765	2
Hypothetical protein (Fragment)	E.PLVEEAAQVLIV.T	Q9NT34	6	3.1535	2
Hypothetical protein (Fragment)	Q.TPKDDPAITLL.N	Q9NT45	1	2.519	2
Hypothetical protein (Fragment)	D.CPITAHMY.E	Q9UFV0	1	2.4132	2
Hypothetical protein (Fragment)	D.FPTENPNDNSVLGNL.R	Q9UG33	1	2.2081	1
Hypothetical protein (Fragment)	L.FRSPDSEHATSCPR.L	Q9Y3Y1	1	3.2626	2
Hypothetical protein (RNase P protein subunit p25)	K.VRSEEAPAGCGAE.G	Q9BUL9	1	2.5178	2
Hypothetical protein (Tumor ANGIOGENESIS marker)	M.FSQPPGPPQAPPGL.P	Q9H204	1	2.4134	2
Hypothetical protein BK223H9.2/MGC1346	K.IVNLGSSKTDLFYE.R	Q9UH06	1	2.5241	2
Hypothetical protein DJ1198H6.1 (Fragment)	M.EELPRVLYLPLFMEAF.S	O95521	1	2.5047	2
Hypothetical protein DJ845O24.2 (Fragment)	L.SQCPISQKLTLDLSGIRLTNYSL.V	O60810	1	2.3913	2
Hypothetical protein DKEZp451E012 (Fragment)	L.YMNSVSFLE.G	O60810	1	3.1095	2
Hypothetical protein DKEZp451F022 (Fragment)	F.NGQATKTPPESS.P	Q8N3L4	1	2.5309	2
Hypothetical protein FLJ10375	L.LMQNLNKLQTPPEKFD.F	Q8N3L3	1	2.7255	2
Hypothetical protein FLJ10470	K.VLVFNFLNCF.A.S	Q9NW15	1	2.8562	2
	L.QELDLKSNIRT.I	Q9NVW3	10	2.9369	2

Hypothetical protein FLJ10498	Q.EYGELDAK.D	Q9NVU7	1	2.2064	1
Hypothetical protein FLJ10540	K.QQEEQTRVALLEQQMQACTLDFENEK.L	Q9NVS7	4	3.6972	3
Hypothetical protein FLJ10900	E.PVTQLYVSDASTK.D	Q9NV66	1	2.598	2
Hypothetical protein FLJ11006	D.FHRLTLVELQF.K	Q9NV09	4	2.6564	2
Hypothetical protein FLJ11175	A.AATHLYF	Q9NUS2	1	2.2122	1
Hypothetical protein FLJ11274	L.VTVLGAGLL.C	Q9NUM3	3	2.3368	2
Hypothetical protein FLJ12562	V.AGRKRWGPGEQRALLPQG.G	Q9H9T4	1	2.5869	2
Hypothetical protein FLJ12647	F.EYQQVAFQPSILTE.P	Q9H9N0	1	2.6536	2
Hypothetical protein FLJ12889	V.ELKEMVSDVLSFNKLSFISLEL.C	Q9H9A6	1	3.6294	3
Hypothetical protein FLJ13215	N.EAIVPVGAWVEP.A	Q9H8U7	1	3.3425	2
Hypothetical protein FLJ13220	V.DANEGIQAQIVA.N	Q8N442	1	2.5887	2
Hypothetical protein FLJ13236	T.STSPASPGLHTGGTK.R	Q9H8T7	2	2.468	2
Hypothetical protein FLJ13405 (Zinc-finger protein ZBRK1)	E.RLQSESLVNR.R	Q9GZX5	1	2.5954	2
Hypothetical protein FLJ13491	P.LRERFLQPLMALLYDCGGRLDSHRA.F	Q9H8K6	1	2.9367	2
Hypothetical protein FLJ13693	A.PAFLLLLLLWPPQ.G	Q9H8E9	2	3.2813	2
Hypothetical protein FLJ13881	V.FRLEEGVASDEEAEEAQP.G	Q9H882	1	2.7824	2
Hypothetical protein FLJ13898 (Fragment)	L.CACEEYLSNLA.H	Q9H876	1	2.415	2
Hypothetical protein FLJ14235	N.MLATANKTEKTEFL.G	Q9H7U8	3	2.6133	2
Hypothetical protein FLJ14473	L.VTVSSASPTSPK.V	Q96K68	4	3.207	2
	G.QGTLVTVSSASPTSPK.V	Q96K68	2	3.3974	2

(continued)

Supplementary Table 1 (continued)

Protein	Peptide ^e	Swiss-Prot Accession ^b	Peptide Count ^f	Xcorr ^d	Charge State ^e
	G.TLVTVSSASPTSPK.V	Q96K68	8	2.2883	1
	Q.GTLVTVSSASPTSPK.V	Q96K68	14	3.1154	2
	T.TLVTVSSASPTSPK.V	Q96K68	1	2.6845	2
Hypothetical protein FLJ14500	Y.ADADEILQEEIKE.Y	Q96T18	1	2.4409	2
Hypothetical protein FLJ14568	F.ESPLELSAQ.G	Q96SY1	1	2.9682	2
Hypothetical protein FLJ14737	K.RQVAPGAPSAARRRGGHRGGRGFRGIR	Q96SN5	1	2.7384	2
Hypothetical protein FLJ14827	P.AADSQKLSMGGLHSSRPL	Q96K30	1	3.0482	2
Hypothetical protein FLJ14900 (Fragment)	S.LLSICPEAK.Q	Q96Y1	1	2.7845	2
Hypothetical protein FLJ14964	A.SWDEPQFSDNSGAE.L	Q96JU7	1	2.4041	2
	S.QPCKNGATCKDGANSFR	Q96JU7	1	2.3588	1
Hypothetical protein FLJ20174	P.FDAARGADFD	Q9NXL6	2	2.3403	1
Hypothetical protein FLJ20276	I.SRSDLEEILDTE	Q9NXG0	2	2.9279	2
Hypothetical protein FLJ20315	T.SSLFNILQKSSL.S	Q9NXD0	1	2.5566	2
Hypothetical protein FLJ20399	D.RRAYPAQITPKMCLE	Q9NX74	5	2.472	2
Hypothetical protein FLJ20539	V.FVAGKESRGARGV.R	Q9NWX0	1	2.7128	2
Hypothetical protein FLJ20772	L.WETVALALGVQ.R	Q9NWK6	1	2.4382	2
Hypothetical protein FLJ20958	G.VSRASPLLLLLVPSRPLAAAARRQLG.D	Q9H7F8	1	4.144	3
Hypothetical protein FLJ21101	N.KKENSETVVTGSL.D	Q9GZS3	5	3.0895	2
Hypothetical protein FLJ21497	G.SCLSSQHIFGR.P	Q9H721	1	2.6853	2

Hypothetical protein FLJ21511	Q.MSNKVILTLSAIAITLDR.I	1	3.0042	2	Q9H720
Hypothetical protein FLJ21845	S.RSVALFRGY.H	1	2.5199	2	Q9H6U8
Hypothetical protein FLJ21908	D.PDVFNQIVKIL.H	2	2.4173	2	Q9H6T3
Hypothetical protein FLJ22052	L.DPDVFNQIVKIL.H	1	2.2656	2	Q9H6T3
Hypothetical protein FLJ22449 (Mucopolipin)	E.LLEPVVDDVPKTTA.T	1	2.4451	2	Q9H6N4
Hypothetical protein FLJ22559	(Mucopolipin) (Mucopolipin) type R.KPCKLMLQVVK.I	1	2.2174	1	Q9GZU1
Hypothetical protein FLJ22774	L.DLPSLTSLSEKAKEFLMENR.V	1	2.4916	2	Q9H668
Hypothetical protein FLJ22944	A.CNCDLLQLKTW.L	1	2.9191	2	Q9H5Y7
Hypothetical protein FLJ23323	A.FNGLGLLKQLHINHNSLE.I	1	2.57	2	Q9H5Y7
Hypothetical protein FLJ23537	D.LIYGPVPLPSAIAIGLVGKEAETR.P	1	2.5535	2	Q9H5W3
Hypothetical protein FLJ23651	N.YENYIDI.V	3	2.3005	1	Q9H5L4
Hypothetical protein FLJ23865	S.QVEKLNFLSPDPVINYALTEA.T	1	3.9174	3	Q8NE42
Hypothetical protein FLJ25122	T.DWHTRSPALTF.T	1	2.431	2	Q8TEC6
Hypothetical protein FLJ25270	V.LPPPPQVPLLSPARG	1	2.5064	2	Q8TCH9
Hypothetical protein FLJ25506	R.EGPENMVRIALQLDD.G	1	2.6723	2	Q96LS5
Hypothetical protein FLJ30055	L.KSGTTPPPGA.A	1	2.3111	2	Q96DK4
Hypothetical protein FLJ30102	V.QGGGQFCPSGSAFLG.V	1	2.5004	2	Q8N7I6
Hypothetical protein FLJ30119	Q.AGGGIHFTVERTRQATE	1	3.2805	2	Q96NU7
	G.SQLEVLVHVQ.D	1	2.3859	1	Q969Y0
	L.VEKCTSVK.D	2	2.7278	2	Q96NT3

(continued)

Supplementary Table 1 (continued)

Protein	Peptide ^a	Swiss-Prot Accession ^b	Peptide Count ^c	Xcorr ^d	Charge State ^e
Hypothetical protein FLJ30131	S.EAQEGLQKFKVVRA.G	Q96NT0	1	2.2353	1
Hypothetical protein FLJ30136	R.PSQETTPDRSHHSGFGLFCGD.P	Q96NS8	1	2.4474	2
Hypothetical protein FLJ30277	T.RPDSSPFRPAARPR.M	Q96NR7	1	2.6359	2
Hypothetical protein FLJ30384	A.SSRGSIQMSAPDLSTALR.G	Q96NP8	1	2.3143	1
Hypothetical protein FLJ30469	D.PPTLSGAECYACIGV.H	Q96DR2	1	3.1211	2
Hypothetical protein FLJ30934	V.AMHEVFLQRLA.A	Q96NG4	1	3.1109	2
Hypothetical protein FLJ31359	M.KVFSKNVSK.C	Q96N64	1	2.5034	2
Hypothetical protein FLJ31400	S.QEKKEEAITLLKDSI.K	Q96N52	1	2.7493	2
Hypothetical protein FLJ31409 (Fragment)	A.KVELSPGPPKP.A	Q96IA7	1	2.736	2
Hypothetical protein FLJ31726 (Fragment)	L.QTLPLSTLESE.N	Q96MY0	1	2.4131	1
Hypothetical protein FLJ31890 (Zinc finger protein 25)	K.SALIVHQHTHSK.G	Q96MU2	1	2.2723	2
	N.KFQGPVTLKDVIV.E	Q96MU2	1	2.7191	2
Hypothetical protein FLJ31897	T.LPEEAPSNDER.T	Q96DN4	1	2.8396	2
Hypothetical protein FLJ32000	I.SLHPSGHFIVVGFADK.L	Q96MR6	1	2.4155	2
Hypothetical protein FLJ32658	G.GLELEEETAFQGALTSRQLPSGCP.E	Q96MC3	1	3.8413	3
Hypothetical protein FLJ32662	A.MACEIFNELR.L	Q96MC0	1	2.6101	2
Hypothetical protein FLJ32706 (Fragment)	A.DAIKTLHMAMSLPGMK.R	Q96MA4	1	2.4563	1
Hypothetical protein FLJ32786	E.VINADDLDVAYQKLSQLI.R	Q96M69	1	2.716	2

Hypothetical protein FLJ32867	M.ETKRTQEGE.A	Q96M31	1	3.1226	2
Hypothetical protein FLJ32933	K.AYKCSSTLSK.H	Q96M04	1	2.334	2
Hypothetical protein FLJ32978	I.IQVIYVEE.K	Q96LY9	2	2.275	1
Hypothetical protein FLJ33401	L.LFFYINGAGGR.E	Q8NBD7	1	2.553	2
Hypothetical protein FLJ33516	L.FVEANMNSEKKGIRVN.F	Q8N2C0	1	3.0213	2
Hypothetical protein FLJ33697	K.VVHGDVTPYDLV.R	Q8NBC6	1	2.7881	2
Hypothetical protein FLJ33868	F.YEFEGGVK.L	Q8N267	1	2.2153	1
Hypothetical protein FLJ34011	E.REEILKR.Y	Q8NBA2	1	2.5699	2
Hypothetical protein FLJ34087	L.KSRVKNIKTGSDFSMFEALRDITV.S	Q8NB85	1	4.0571	3
Hypothetical protein FLJ34146 (Fragment)	A.ISDGEEGGEGP.G.A	Q8NB73	1	2.4386	2
Hypothetical protein FLJ34889 (Fragment)	A.SNHTNQTL.S.D	Q8NAR9	1	2.2192	1
Hypothetical protein FLJ34907	N.PDLSWYHHANPI.L	Q8NAR6	1	2.767	2
Hypothetical protein FLJ34943	D.EIKNNSEVQNQE.C	Q8N157	4	3.0675	2
Hypothetical protein FLJ35382	L.LAFTSVAEELILGLE.K	Q8NAG7	1	2.2182	1
Hypothetical protein FLJ35502	Y.FVHREIYPGSKI.T	Q8NAD9	1	2.7928	2
Hypothetical protein FLJ35552	K.ENGQMAVSDGSVKGLLSVVRGWSR.G	Q8NAC9	1	3.8517	3
Hypothetical protein FLJ35727	S.LGIFLLFREDQPPGK.V	Q8NA94	2	2.4338	2
Hypothetical protein FLJ35936	L.KIKGKEDIDL.D	Q8NA19	1	2.4464	2
Hypothetical protein FLJ36029	E.DQIESDESELK.K	Q96HJ4	1	2.6729	2

(continued)

Supplementary Table 1 (continued)

Protein	Peptide ^a	Swiss-Prot Accession ^b	Peptide Count ^c	Xcorr ^d	Charge State ^e
Hypothetical protein FLJ36186	G.GRRVLSGGRTAFGGGRTAFGGGRTAFG	Q8N9U9	1	2.4533	2
Hypothetical protein FLJ36557	R.IQLQILE.A	Q8N9U0	1	2.2941	1
Hypothetical protein FLJ36558	A.SFLEWASAVLPTGPPEPL.S	Q8N9T9	1	2.201	2
Hypothetical protein FLJ36601	L.SRVVPYCSNNMPPICVQ.N	Q8N9S7	1	2.4527	2
Hypothetical protein FLJ37161	R.FRKVLGCCLPSPAPDL.L	Q8N9G9	2	2.4634	2
Hypothetical protein FLJ37393	D.FEENAYSYASV.D	Q8N1W2	1	2.6097	2
Hypothetical protein FLJ38020	K.ALDPVELVQH	Q8N1P7	3	2.6266	2
Hypothetical protein FLJ38072	A.LSLPSEGLSLKATPGAHH.K	Q8N1N9	1	2.4346	2
Hypothetical protein FLJ38144	P.SCPQLPPRDSR.C	Q8N1N9	1	2.5228	2
Hypothetical protein FLJ38183	I.QGIFMGE.H	Q8N9A1	1	2.4581	1
Hypothetical protein FLJ38508 (Fragment)	V.FIMAILVGV.K	Q8N994	2	2.6735	2
Hypothetical protein FLJ38763	L.NSSVPPGEPLEIK.G	Q8N922	1	2.4341	2
Hypothetical protein FLJ38940	L.QVFDEIR.S	Q8N8W3	1	2.4137	2
Hypothetical protein FLJ39325 (Fragment)	L.LLAHPACDSSLTDK.A	Q8N8S2	1	2.4902	2
Hypothetical protein FLJ39787	K.KLYMLKEMDKDLNSVVA.V	Q8N8K6	1	2.4401	2
Hypothetical protein FLJ40100	A.ISAGTGASGIVEVLTEV.P	Q8N897	3	2.9438	2
Hypothetical protein FLJ40115	K.HDLFTPEPHYV.P	Q8N830	1	2.4522	2
Hypothetical protein FLJ40115	R.IDCGEKPKYKCNCECGKTFGQ.N	Q8N823	1	2.609	2

Hypothetical protein FLJ40137	R.EPQIVEFVFLLS	Q8N815	1	2.5132	1
Hypothetical protein FLJ40201	H.HNKKKHGVFSKLPARNPKTPTTERIYW.A	Q8N7Y9	1	2.5698	2
Hypothetical protein FLJ40441	D.WEQSAESLQPVQEDMA.L	Q8N7R5	1	2.6961	2
Hypothetical protein FLJ40584 (Fragment)	K.LHPNQAGLDSKVL	Q8N1K5	1	3.4389	2
Hypothetical protein FLJ90238	E.LFTIEDLQNSVTQLQL.Q	Q8NCI1	1	2.2697	1
	Q.FDASTPKNDISPPGR.F	Q8NCI1	1	2.4815	2
	S.INPNTSLFQFSSV.K	Q8NCI1	1	2.4921	2
Hypothetical protein FLJ90323	H.IYGYFDEEMAVK.Y	Q8NCD6	1	2.79	2
Hypothetical protein FLJ90492 (Fragment)	L.ALFNSAIVMQESGEVKLR	Q8NC50	1	2.73	2
Hypothetical protein FLJ90562	R.AGRHPQLLRPALH	Q8N2J0	1	2.9247	2
Hypothetical protein IMPACT (Imprinted and ancient)	E.SSVKALDFDISETRTEVE	Q9P2X3	1	2.5932	2
	R.IYCEDKQTFLO.D	Q9P2X3	7	2.8824	2
Hypothetical protein KIAA0056 (Fragment)	L.AAFTKLYESLL.P	P42695	1	2.3359	2
Hypothetical protein KIAA0077 (Fragment)	Q.WEQQLVNLFARLATDNIGYIDW.D	Q14997	1	2.5523	2
Hypothetical protein KIAA0100 (Fragment)	R.ILYSSTLR.W	Q14667	1	2.2669	2
Hypothetical protein KIAA0170	A.AESLTAIPEPASPQ.L	Q14676	1	2.4246	2
Hypothetical protein KIAA0182 (Fragment)	A.VFEAYQEHIIEEQNLERQVL	Q14687	1	3.2366	2
Hypothetical protein KIAA0209 (Fragment)	N.PLSMLLLNGIVDPVAVMGGFAKY.E	Q92608	1	2.4592	2
Hypothetical protein KIAA0225 (Fragment)	P.RTCLHAILNILEKG	Q92621	4	2.7687	2
Hypothetical protein KIAA0233	W.LDHATVIHSGDYFL	Q92508	4	2.7606	2
Hypothetical protein KIAA0261 (Fragment)	L.DFTEDLPGVPES.V	Q92549	1	2.5514	2

(continued)

Supplementary Table 1 (continued)

Protein	Peptide ^a	Swiss-Prot Accession ^b	Peptide Count ^c	Xcorr ^d	Charge State ^e
Hypothetical protein KIAA0263 (Fragment)	A.YPYVESETVEQ.D	Q92551	1	2.3222	1
Hypothetical protein KIAA0278 (HARG) (Activity-regulated)	R.HLLAEVSK.Q	Q9Y469	1	1.9753	1
Hypothetical protein KIAA0286 (HA6800) (Fragment)	P.WGSGVGGGTVRLLL.I	O14524	1	2.663	2
Hypothetical protein KIAA0308 (Fragment)	L.NPLLLSNILYP.G	O15025	1	2.8732	2
Hypothetical protein KIAA0339 (Fragment)	S.PKANGQNQ.A	O15047	1	2.5256	1
Hypothetical protein KIAA0364	R.PASPARSGSPAPETTNE.S	O15047	2	2.6665	2
Hypothetical protein KIAA0373	K.FSVNGDFIISNVDGK.G	O15070	1	2.3676	2
Hypothetical protein KIAA0380	T.LKDTKGAQKVINWHMK.I	O15078	1	2.5515	2
Hypothetical protein KIAA0398 (RNA (Guanine-7-))	L.FMEGLADSALED.V	O15085	1	2.7367	2
Hypothetical protein KIAA0445 (DJ37C10.5)	P.KDKSSTGDGTQNK.R	O43148	1	2.4942	2
Hypothetical protein KIAA0463 (Fragment)	Q.EAGELRRSLGEGAKEREAL.R	O75033	1	3.902	2
Hypothetical protein KIAA0522 (Fragment)	A.MLDYELHSDVSSL.I	O75051	1	2.4797	2
Hypothetical protein KIAA0528 (Fragment)	L.NCSSGSSSRDSLREPP.A	O60275	1	2.5865	2
Hypothetical protein KIAA0539 (Fragment)	L.HAFIAEVFAMVRAHV.A	O60280	2	2.3769	2
Hypothetical protein KIAA0556 (Fragment)	A.EGLAGPVQEVACLFNVTVMQLVA.A	O60287	1	2.2008	2
Hypothetical protein KIAA0560 (Fragment)	G.EGGETEARDK.G	O60303	1	2.3033	1
Hypothetical protein KIAA0620 (Fragment)	L.IGRPNKVTTVDRFQQQNDYIL.L	O60306	1	2.5749	2
Hypothetical protein KIAA0620 (Fragment)	V.RAMDTDTTLTQVKEKI.L	Q9Y4D7	1	2.5666	2

Hypothetical protein KIAA0623	G.ACGGVLAPPAGTAASSKA.V	O75119	1	3.048	2
Hypothetical protein KIAA0626	I.MEVVGLLEEQGNF.V	O75121	9	2.5827	2
Hypothetical protein KIAA0627 (Fragment)	A.GGPKVGGASKEGGAGAVDEDDFIKAF.T.D	O75122	1	2.5381	2
Hypothetical protein KIAA0634 (Fragment)	D.FEKKGGISFGRAKGT.S	O75129	2	3.1103	2
Hypothetical protein KIAA0710	E.DFDFKHYNKTLF.A	O75189	1	2.9994	2
	D.PEGVALEALPVQESVHIME.G	O75189	9	3.0571	2
Hypothetical protein KIAA0724 (RAN binding protein 13)	K.LPVPQGPNPVVVVVLQ.Q	O94829	1	2.5097	2
Hypothetical protein KIAA0775	K.DGSLLEVEKVSLQQRLNQ.F	O94873	2	2.5197	2
Hypothetical protein KIAA0780 (Fragment)	T.KLDEVVTSEK.T	O94877	1	2.8465	2
	V.KSKACEKVISVGGQTVITK.H	O94877	2	3.3772	2
Hypothetical protein KIAA0808	L.NMQQHQLTMQQP.L	O94900	2	3.4005	2
Hypothetical protein KIAA0842 (Fragment)	L.SSAEDSGVDEGQ.G	O94928	1	3.3494	2
Hypothetical protein KIAA0846	L.FDHLEPIELAEHLTFL.E	O94931	3	2.8713	2
Hypothetical protein KIAA0922	I.RNNLTVIDMIGVEGFGA.R	Q9H065	1	2.2343	2
Hypothetical protein KIAA0966	V.SLSATGPQFLSVEPAH.S	Q9Y2H2	5	2.6663	1
Hypothetical protein KIAA0969	V.DRCLFYKDEKEEESILGS.I	Q9Y2H5	1	2.8695	2
Hypothetical protein KIAA0999 (Fragment)	G.AAGAGTGGAGPAGRLLPPPA.P	Q9Y2K2	1	2.4821	2
Hypothetical protein KIAA1092 (Fragment)	R.SSIKDGTKQK.R	Q9UPR0	1	2.8611	2
Hypothetical protein KIAA1093 (Fragment)	A.KFPDYKSTWSPDPIGH.N	Q9UPQ9	1	2.9137	2
Hypothetical protein KIAA1138 (Fragment)	I.SHLSKQGEVEPPRRRGPVPPAR.P	Q9ULT2	1	4.0233	3

(continued)

Supplementary Table 1 (continued)

Protein	Peptide ^a	Swiss-Prot Accession ^b	Peptide Count ^c	Xcorr ^d	Charge State ^e
Hypothetical protein KIAA1147 (Fragment)	D.YNPCEEDLFLVLF	Q9ULS3	1	2.9733	2
Hypothetical protein KIAA1157 (Fragment)	L.FDGHAGSGAAVVASR.L	Q9ULR3	1	2.4185	2
Hypothetical protein KIAA1185	T.HELRVKGPLLYCAR.P	Q8N1G4	2	2.9629	2
Hypothetical protein KIAA1195 (Fragment)	S.EGRKNNHLLGHGK.S	Q9ULM5	1	2.4517	2
Hypothetical protein KIAA1202 (Fragment)	F.VGDLKVVNLLLSGLRARVENAL.N	Q9ULL8	1	2.4292	2
Hypothetical protein KIAA1206 (Fragment)	Y.AREIPRYKQMVVER.Y	Q9ULL4	1	2.3485	2
Hypothetical protein KIAA1259 (Fragment)	N.KDFLLGVNPLSPNLC	Q9ULG1	1	2.5547	2
Hypothetical protein KIAA1268 (Fragment)	N.LKLEDARR.E	Q9ULF2	1	2.5046	2
Hypothetical protein KIAA1272 (Fragment)	Y.LYELWYK.L	Q9ULE8	4	2.4782	2
Hypothetical protein KIAA1275 (Fragment)	K.LKSEMEEKVYNLT.R	Q9ULE5	1	2.3025	1
Hypothetical protein KIAA1276 (Fragment)	S.SFNPHPGYLTSPMK.K	Q9ULE4	1	2.7122	2
Hypothetical protein KIAA1294 (Fragment)	S.YLNALKKL.Q	Q9P2Q2	3	2.7195	2
Hypothetical protein KIAA1341 (Fragment)	F.GGMNRRGGGGGLEAMNSMGG.F	Q9P2K5	1	2.691	2
Hypothetical protein KIAA1363 (Fragment)	K.KSAWSSAQVK.V	Q9P2I4	1	2.314	2
Hypothetical protein KIAA1386 (Fragment)	G.EPYQHNTPLHYAAR.H	Q9P2G1	1	3.8319	3
Hypothetical protein KIAA1389 (Fragment)	K.DVPPFPPPIKGVTF.P	Q9P2F8	1	2.3461	1
Hypothetical protein KIAA1400 (Fragment)	L.LPFLLEMIVLL.L	Q9P2E7	1	2.254	2

Hypothetical protein KIAA1402 (Fragment) L.CPWGTHLAGPTT.M	1	2.4456	2	Q9P2E5
Hypothetical protein KIAA1403 (Fragment) G.LQLVPEPCLRQTLKLL.S	1	2.7764	2	Q9P2E4
Hypothetical protein KIAA1414 (Fragment) I.RMAFMMAATDHSNQ.L	2	2.4486	2	Q9P2D3
Hypothetical protein KIAA1443 (Fragment) M.PPNKEASGLSSSPAGL.I	1	2.4004	2	Q9P2A5
Hypothetical protein KIAA1461 (Fragment) Q.PPTTVLSLLRQSQMDSSA.V P.FKLMIGSSNAMGRL.Y	1	2.651	2	Q9P267
	1	2.8413	2	Q9P267
Hypothetical protein KIAA1514 (Fragment) A.FNAAGDGRSTPTQGQTQQ.A	1	2.5971	2	Q9P214
Hypothetical protein KIAA1552 (Fragment) A.QRSGPGPEFLKTP.L.G	1	2.5401	1	Q9HCM0
Hypothetical protein KIAA1573 (Fragment) A.FLRDLAEQNSGKY.G.V	1	3.1602	2	Q9HCJ9
Hypothetical protein KIAA1579 (Fragment) S.YVGGFAVVEYSTA.E	3	2.4614	2	Q9HCJ3
Hypothetical protein KIAA1614 (Fragment) I.VPTITQGSRDGHRSPA.R	1	2.2369	2	Q9HCF8
Hypothetical protein KIAA1632 (Fragment) A.VHPEIHSVLLDRVQE.T	1	2.7363	2	Q9HCE0
	1	2.7601	2	Q9HCE0
Hypothetical protein KIAA1633 (Fragment) I.KKITQELSDLQQ.E	2	2.6026	1	Q9HCD9
	1	2.9723	2	Q9HCD9
Hypothetical protein KIAA1693 (Fragment) N.DDDEDVQVEVAEKVQ.K	1	3.5023	2	Q9C0H0
Hypothetical protein KIAA1697 (Fragment) I.KLTDNFLRILENSIR.L	2	3.0952	2	Q9C0G6
Hypothetical protein KIAA1726 (Fragment) T.SDVKRGAPKRQSDPSIR.T	1	2.4465	2	Q9C0D7
Hypothetical protein KIAA1730 (Fragment) I.ISGLGSNKWIQQNLQ.C	1	2.5608	2	Q9C0D3
Hypothetical protein KIAA1733 (Fragment) S.REELIKR.G	4	2.6635	2	Q9C0D0
Hypothetical protein KIAA1734 (EC 6.3.2.19) (Ubiquitin- Y.LFDIQLPNIYPAVPPHFCYLSQC.S	1	3.7657	3	Q9C0C9

(continued)

Supplementary Table 1 (continued)

Protein	Peptide ^e	Swiss-Prot Accession ^b	Peptide Count ^f	Xcorr ^d	Charge State ^e
Hypothetical protein KIAA1770 (Fragment)	K.GKSPPMAEATPVIVTTEEIAEIKRKNEL	Q9C093	1	3.3549	2
Hypothetical protein KIAA1777 (Unc5h4)	F.ACHVLLDSFGTYALTGE.P	Q8WYP7	1	3.0272	2
Hypothetical protein KIAA1783 (Fragment)	P.TALLQPDAAGPGGGGVSAGVAVL.G	Q96JP2	1	2.704	1
Hypothetical protein KIAA1795 (Fragment)	Y.SSLVMGSQTESA.L	Q96JN0	2	2.4595	2
Hypothetical protein KIAA1797 (Fragment)	I.ARSAAATALSLVVPFILS	Q96JM8	1	2.3742	2
Hypothetical protein KIAA1798 (Fragment)	K.AWCWASYLEEEK.A	Q96JM7	3	2.4841	2
Hypothetical protein KIAA1801 (Fragment)	E.NVILQEKEIYKSKSE	Q96JM4	1	2.8299	2
Hypothetical protein KIAA1824 (Fragment)	M.KSCCFAGDRDQVILS.G	Q96JK2	1	2.3743	1
Hypothetical protein KIAA1829 (Fragment)	Y.RSHLNQHQ.R	Q96JJ8	1	2.4038	2
Hypothetical protein KIAA1890 (Fragment)	T.GSEGVVLSPNYPHNYTAGQ.I	Q96PZ7	1	2.9081	1
Hypothetical protein KIAA1934 (Fragment)	K.VFSGTASPSGEETFE	Q96PV4	1	2.4241	2
Hypothetical protein KIAA1981 (Fragment)	M.EATGSRATGMEATGVSATGVE	Q8TF21	1	2.7809	2
Hypothetical protein KIAA2001 (Fragment)	E.EEEEEEMK.Q	Q8NCM4	1	2.4536	2
Hypothetical protein KIAA2004 (Fragment)	V.RVPKPIPLPGV.R	Q8NCM4	2	2.3681	2
Hypothetical protein KIAA2018 (Fragment)	I.EALHKDEGNEAVE	Q8IVG6	4	2.7358	2
Hypothetical protein KIAA2018 (Fragment)	R.PSSLSASNSTQTFVSTM.S	Q8IVF3	1	2.5465	2
Hypothetical protein MGC27277	I.QQHMVSPEPASLKE.K	Q8IVP0	2	3.0187	2
Hypothetical protein MGC3103	A.FPNTGLEIGATGAG.D	Q8N644	1	2.9531	2
Hypothetical protein MGC45474 (Fragment)					

Hypothetical protein NT2RP2000279	T.GLVFIMGYVWVAGA.A	Q8N4M1	2	2.6515	2
Hypothetical protein NT2RP3002337	W.WPLPLLLLLLLLLLGP.A	Q8NBP7	1	2.7108	2
Hypothetical zinc finger protein KIAA0352	S.GSSNSSGDALVTRISILRLDPLTK.A	Q8NBH7	1	3.8008	3
Hypothetical zinc finger protein KIAA0637	E.ELALQGGQPGNSKYSCKV.C	O15060	1	2.306	1
Hypothetical zinc finger protein KIAA1956	E.DVAAFSSDDV.G	O75132	1	2.2714	1
ICB-1 γ	R.PYECNECGKSFQ.D	Q8TF45	1	2.425	2
ICOS ligand (B7 homolog 2) (B7-H2) (B7-like)	R.RHSSEGGVK.S	Q9BYB6	2	2.162	1
IDN3 protein	V.TLHVAAANFSVPVVSAPH.S	O75144	1	2.7797	2
Ig α -1 chain C region	R.DGRKLPWVDTIKE.S	Q9Y6Y4	1	2.6865	2
	K.GDTFCMVGHEALPLAFTQK.T	P01876	4	4.2155	2
	K.SGNTRRPEVH.L	P01876	14	2.601	2
	K.TPLTATLSK.S	P01876	61	2.3437	2
	E.PSQGTTTFAVTSILR.V	P01876	2	2.5593	2
	G.TTTFAVTSILR.V	P01876	1	2.4676	2
	K.KGDTFCMVGHEALPLAFTQK.T	P01876	1	3.6474	2
	K.SAVQPPER.D	P01876	9	2.7096	2
	K.TFTCTAAYPESK.T	P01876	12	2.8006	2
	K.YLTWASRQ	P01876	15	2.2961	2
	G.HEALPLAFTQK.T	P01876	5	3.2742	2
	L.SVTWSESGQVTAR.N	P01876	2	2.9064	2
	R.NFPPSQDASGDLYTSSQLTLPATQCLAGK.S	P01876	3	3.6236	2
	R.WLQGSQELPRE	P01876	63	3.6482	2
	T.FSCMVGHEALPLAFTQK.T	P01876	1	2.533	2
	R.DLCCGYSVSSVLPGCAEPWNHGK.T	P01876	2	3.8025	2
	R.DASGVFTFTWTPSSGK.S	P01876	80	3.8378	2
	R.VAAEDWK.K	P01876	3	2.205	2
	R.QEPSQGTTTFAVTSILR.V	P01876	16	3.5276	2
	R.LSLHRPALE.D	P01876	2	2.4597	2
	R.LSLHRPALED.L	P01876	1	2.5596	2

(continued)

Supplementary Table 1 (continued)

Protein	Peptide ^a	Swiss-Prot Accession ^b	Peptide Count ^c	Xcorr ^d	Charge State ^e
Ig α -2 chain C region	R.DLCGCYSVSSVLPGCAQPWNHGE.T	P01877	1	3.0137	2
	R.DASGATFTWTPSSGK.S	P01877	27	3.3717	2
Ig δ chain C region	K.VPTGGVEEGLLER.H	P01880	12	2.5157	2
	R.SLEVSVYVTDHGP.M.-	P01880	1	2.9273	2
Ig γ -1 chain C region	K.GFYPSDIAVEWESNGQPENNYK.T	P01857	18	3.1534	2
	K.THTCPPCPAPELGGPSVFLFPPKPK.D	P01857	29	4.293	3
	K.STSGGTAALGCLVK.D	P01857	45	2.7781	2
	K.THTCPPCPAPELGGPSVFLFPPK.P	P01857	7	4.2223	3
	K.THTCPPCPAPELGGPSVFL	P01857	2	3.379	2
	K.GPSVFLAPSSK.S	P01857	174	2.2058	1
	K.TTTPPVLDSDGSFFLYSK.L	P01857	220	2.5482	2
	G.GPSVFLFPPKPK.D	P01857	73	3.0976	2
	L.TVLHQDWLNGK.E	P01857	8	3.2111	2
	K.GFYPSDIAVE.W	P01857	1	2.7814	2
	K.NQVSLTCLVK.G	P01857	5	2.4965	2
	D.PEVKFNWYVDGVEVHNAK.T	P01857	4	4.2197	3
	E.LLGGPSVFLFPPKPK.D	P01857	8	2.4121	2
	K.TTTPPVLDSDGSFFL.Y	P01857	1	2.4787	1
	G.PSVFLFPPKPK.D	P01857	22	2.9777	2
	K.TTTPPVLDSDGSFFLYS.K	P01857	1	2.4591	1
	L.DSDGSFFLYSK.L	P01857	5	2.6834	2
	K.DYRPEPVTVSWN.S	P01857	1	2.6017	1
	K.FNWIYVDGVEVHNA.K	P01857	4	3.3127	2
	K.DYRPEPVTVSWNSG.A	P01857	1	2.649	1
K.DYRPEPVTVSWNSGALTSGVHTFPVAVLQSSGLYSLSSVVT	P01857	1	3.8436	3	
K.FNWIYVDGVEVHNAK.T	P01857	69	2.4171	2	
D.SDGSFFLYSK.L	P01857	3	2.76	2	
L.GGPSVFLFPPKPK.D	P01857	71	3.2669	2	
K.DTLMISR.T	P01857	23	2.5384	2	
F.NWIYVDGVEVHNAK.T	P01857	6	3.4653	2	
L.LGGPSVFLFPPKPK.D	P01857	7	2.4243	2	

K.FNWYVDGVEVH.N	P01857	14	2.978	2
D.GSFFLYSK.L	P01857	7	2.4997	2
A.PELGGPSVFLFPPKPK.D	P01857	23	4.4611	3
K.VSNKALPAPIEK.T	P01857	2	3.2332	2
G.PSVFLFPPK.P	P01857	1	2.4892	2
K.ALPAPIEK.T	P01857	5	1.9172	1
C.PAPELGGPSVFLFPPKPK.D	P01857	1	4.3712	3
K.TTPPVLDSDGSFFLY.S	P01857	1	2.4916	1
C.VVVDVSHEDPEVK.F	P01857	4	2.8205	2
G.PSVFPLAPSSK.S	P01857	5	2.8708	2
T.PPVLDSDGSFFLYSK.L	P01857	12	2.4497	2
R.EPQVYTLPPSRDELTK.N	P01857	24	2.5186	2
R.EPQVYTLPPSR.D	P01857	51	2.3134	2
V.FPLAPSSK.S	P01857	1	2.367	1
V.SVLTVLHQDWLNGK.E	P01857	10	4.1905	2
N.WYVDGVEVHNAK.T	P01857	37	3.3426	2
V.PSSSLGTQYICNVNHKPSNTK.V	P01857	1	3.5693	2
T.KGPSVFLAPSSK.S	P01857	4	2.5896	2
Y.TLPPSRDELTK.N	P01857	7	2.6529	2
Y.VDGVVEVHNAK.T	P01857	2	3.2388	2
V.DGVVEVHNAK.T	P01857	5	2.354	1
P.APELLGGPSVFLFPPKPK.D	P01857	1	2.407	2
R.TPEVTCVVVDVSHEDPEVK.F	P01857	8	3.8225	3
T.CPPCAPELGGPSVFLFPPKPK.D	P01857	1	4.2484	3
V.VVTPSSSLGTQYICNVNHKPSNTK.V	P01857	1	3.155	2
W.YVDGVEVHNAK.T	P01857	12	3.1898	2
P.PVLDSDGSFFLYSK.L	P01857	2	2.4667	1
R.TPEVTCVVVDVSHED.P	P01857	14	2.9117	2
S.DGSFFLYSK.L	P01857	2	2.9834	2
V.VSVLTVLHQDWLNGK.E	P01857	1	3.7549	2
R.VVSVLTVLHQDWLNGK.E	P01857	54	4.6671	2
N.KALPAPIEK.T	P01857	1	2.4135	2
Ig γ -2 chain C region				
K.GPSVFLAPCSR.S	P01859	24	2.7903	2
K.CCCEPCPCAPPVAGPSVFLFPPKPK.D	P01859	1	2.9336	2
D.PEVQFNWYVDGVEVHNAK.T	P01859	1	4.6311	3
L.TVVHQDWLNGK.E	P01859	3	2.4332	2
K.TTPPMLDSDGSFFLY.S	P01859	1	2.4944	1

(continued)

Supplementary Table 1 (continued)

Protein	Peptide ^a	Swiss-Prot Accession ^b	Peptide Count ^c	Xcorr ^d	Charge State ^e	
Ig γ -3 chain C region (Heavy chain disease protein)	K-TTPPMLDSDGSFFLYSK.L	P01859	25	2.8899	1	
	P.VAGPSVFLFPPKPK.D	P01859	8	3.0164	2	
	P.PVAGPSVFLFPPKPK.D	P01859	1	3.0878	2	
	P.APPVAGPSVFLFPPKPK.D	P01859	1	3.2122	2	
	N.KGLPAPIEK.T	P01859	1	2.4636	2	
	T.PPMLDSDGSFFLYSK.L	P01859	9	5.4691	2	
	R.TPEVTCVVVDVSHEDPEVQ.F	P01859	6	4.2699	3	
	R.KCCVECPAPPPVAGPSVFLFPPKPK.D	P01859	1	3.7995	3	
	R.STSESTAALGCLVK.D	P01859	79	2.4073	2	
	Q.TYTCNVVDHKPSNTK.V	P01859	8	3.2012	2	
	V.SVLTVVHQDWLNGK.E	P01859	3	2.9983	2	
	R.VVSVLTVVHQDWLNGK.E	P01859	21	4.1463	2	
	Ig γ -4 chain C region	K-TPLGDTTHTCPR.C	P01860	5	3.4342	2
		K-SCDTPPPCPR.C	P01860	2	2.5104	2
		R.TPEVTCVVVDVSHEDPEVQFK.W	P01860	3	3.731	2
		K.YGPPCPCPAPEFLGGPSVFLRPPKPK.D	P01861	19	3.974	3
	G.PPCPCPAPEFLGGPSVFLRPPKPK.D	P01861	2	4.0916	3	
	K.YGPPCPCPAPEFLGGPSVFLRPPK.P	P01861	1	2.449	2	
	K-TTPPVLDSDGSFFLYSR.L	P01861	56	2.6959	2	
	R.WQEGNVFSCVMHEALHNHYTQK.S	P01861	2	3.5959	2	
	T.PPVLDSDGSFFLYSR.L	P01861	1	3.5294	2	
R.EPQVYTLPPSQEEMTK.N	P01861	2	2.4219	2		
Ig heavy chain V-I region EU	-QVQLVQSGAEVK.K	P01742	8	2.5261	2	
	Q.VQLVQSGAEVK.K	P01742	1	2.405	2	
Ig heavy chain V-I region ND (Fragments)	S.QTQLVQSGAEVR.K	P01744	1	2.7477	2	
	K.ALEWLAR.I	P01814	1	2.2803	2	
Ig heavy chain V-II region OU	-EVQLVESGGGLVQPGGSLR.L	P01766	26	4.1628	2	
	E.VQLVESGGGLVQPGGSLR.L	P01766	1	2.6194	2	
Ig heavy chain V-III region BRO						

Ig heavy chain V-III region CAM	-EVQLVESGGGLVQ.P	P01766	1	4.2614	2
	Q.LVESGGGLVQPGGSLR.L	P01766	3	3.5268	2
Ig heavy chain V-III region HIL	E.LVESGGGVVZPGR.S	P01768	3	2.6592	2
	Q.VELVESGGGVVZPGR.S	P01768	1	2.9024	2
Ig heavy chain V-III region JON	-QVKLVQAGGGVVQPGR.S	P01771	2	2.2302	1
	-DVQLVESGGGLVKPGGSLR.L	P01780	2	2.9562	2
Ig heavy chain V-III region TRO	Q.LVESGGGLVQPGGSLR.L	P01780	5	3.5131	2
	L.YYADSVK.G	P01762	1	2.433	1
Ig heavy chain V-III region VH26	-QVQLVQSGGGLVKPGGSLR.L	P01762	1	2.6661	1
	Q.SGGGLVKPGGSLR.L	P01762	1	2.5929	2
Ig heavy chain V-III region WEA	E.SGGGLVQPGGSLR.L	P01764	1	2.5381	2
	G.GGLVQPGGSLR.L	P01764	1	2.5369	2
Ig κ chain C region	C.EVQLLESGGGLVQPGGSLR.L	P01764	8	3.4551	2
	Q.LLESGGGLVQPGGSLR.L	P01764	5	2.5825	2
Ig κ chain C region	-QVQLVDSGGGLVEPVGSLR.L	P01763	2	2.9525	2
	G.LVEPVGSLR.L	P01763	1	2.4395	2
Ig κ chain C region	-TVAAPSVFIFPPSDEQLK.S	P01834	69	3.2727	1
	D.NALQSGNSQESVTEQDSK.D	P01834	1	4.436	2
Ig κ chain C region	C.LLNIFYPR.E	P01834	1	2.5045	2
	C.EVTHQGLSSPVT.K.S	P01834	7	3.0244	2
Ig κ chain C region	G.NSQESVTEQDSK.D	P01834	1	2.73	2
	A.SVVCLLNIFYPR.E	P01834	1	2.5007	1
Ig κ chain C region	D.STYLSSTLTLSK.A	P01834	1	2.5117	2
	A.PSVFIFPPSDEQLK.S	P01834	13	2.4003	1
Ig κ chain C region	F.PPSDEQLK.S	P01834	2	2.3414	1
	A.APSVFIFFPPSDEQLK.S	P01834	1	3.077	2
Ig κ chain C region	K.VYACEVTHQGLSSPVT.K	P01834	3	3.5838	2
	K.SGTASVVCLLNIFYPR.E	P01834	16	2.7916	1
Ig κ chain C region	K.VDNALQSGNSQESVTEQD.S	P01834	3	4.2554	2
	K.VYACEVTHQGLSSPVT.K.S	P01834	39	2.3083	2
Ig κ chain C region	K.DSTYLSSTLTLSK.A	P01834	436	2.37	2

(continued)

Supplementary Table 1 (continued)

Protein	Peptide ^a	Swiss-Prot Accession ^b	Peptide Count ^c	Xcorr ^d	Charge State ^e
Ig κ chain V-I region AG	K.VDNALQSGNSQESVTEQDSK.D	P01834	20	2.2791	2
	Q.SGNSQESVTEQDSK.D	P01834	9	2.2825	1
	N.SQESVTEQDSK.D	P01834	1	3.077	2
	W.KVDNALQSGNSQESVTEQDSK.D	P01834	1	3.8391	2
	Y.ACEVTHQGLSSPVTK.S	P01834	6	3.0483	2
	S.GNSQESVTEQDSK.D	P01834	1	2.3199	1
	N.ALQSGNSQESVTEQDSK.D	P01834	4	5.2592	2
	-.DIQMTQSPSSLSASVGDR.V	P01593	2	2.2449	1
	M.TQSPSSLSASVGDR.V	P01593	1	2.9558	2
	Q.SPSSLSASVGDR.V	P01593	7	3.3596	2
Ig κ chain V-I region BAN	-.DIQLTQSPSSLSASVGDR.V	P04430	4	5.6874	2
	-.DIQMTQSPSTLSASVGDR.V	P01596	4	5.0292	2
Ig κ chain V-I region CAR	Q.SPSTLSASVGDR.V	P01596	3	3.2201	2
	-.BIZMTQSPSSLSASVGDR.V	P01597	4	5.4398	2
Ig κ chain V-I region DEE	K.ASSLESGVPSR.F	P01598	2	2.6842	2
	T.EFTLTISS.L	P01598	1	2.2579	1
Ig κ chain V-I region EU	K.LLLYKASTLETIGVPSR.F	P01604	1	3.3818	2
	K.LLLYGASTR.E	P01605	6	3.1042	2
Ig κ chain V-I region Kue	K.LLLYDASNLETGVPSR.F	P01613	2	2.6146	2
	-.DIQMTQSPSSLSAIVGDR.V	P01613	2	4.0476	2
Ig κ chain V-I region OU	S.YLBWYZZKPKG.A	P01606	1	3.0164	2
	-.DIQMTQSPSSVVSASVGDR.V	P01611	4	4.9907	2
Ig κ chain V-I region Wes	R.FSGSGGTDFTLK.I	P01614	42	3.3221	2
	R.FSGSGGTDFTLKISR.V	P01614	1	3.2331	2
Ig κ chain V-II region Cum					

Ig κ chain V-II region MIL	R.FSGSGGTBFTLK.I	P01616	3	2.613	2
Ig κ chain V-III region B6	L.TZSPGTLSPGZR.A	P01619	1	2.6157	2
	G.NYLAWYQQK.P	P01619	1	2.5088	2
	Ig κ chain V-III region CLL (Rheumatoid factor)				
Ig κ chain V-III region IARC/BL41	G.EIVMTQSPATLSVSPGER.A	P04207	8	4.6199	2
	M.TQSPATLSVSPGER.A	P04207	2	2.6809	2
	Q.SPATLSVSPGER.A	P04207	2	3.4452	2
	G.EIVLTQSPGTLSPGES.A.T	P06311	8	3.4162	2
Ig κ chain V-III region SIE	-EIVLTQSPGTLSPGER.A	P01620	15	4.4352	2
	R.FSGSGGTDFLTISR.L	P01620	19	4.4635	2
	Q.SPGTLSPGER.A	P01620	7	3.2608	2
	R.LLIYGASSR.A	P01620	5	2.6433	2
Ig κ chain V-III region VG (Fragment)	L.TQSPATLSVSPGER.A	P04433	2	2.8327	2
	G.EIVLTQSPATLSVSPGER.A	P04433	2	4.1295	2
	Q.SPATLSVSPGER.A	P04433	2	2.6078	2
	R.LLIYDASNR.A	P04433	9	2.2025	2
Ig κ chain V-IV region (Fragment)	M.TQSPDSLAVSLGER.A	P06312	1	3.0771	2
	G.DIVMTQSPDSLAVSLGER.A	P06312	7	4.5946	2
	K.SSQSVLYSSNKK.N	P06312	1	2.3894	2
	D.SLAVSLGER.A	P06312	1	2.4892	2
Ig λ chain C regions	L.WISGAYGDIVMTQSPDSL.A.V	P06312	1	2.8694	2
	A.ASSYLSTPEQWK.S	P01842	2	3.3712	2
	K.ADSSPVKAGVETITPSK.Q	P01842	1	2.7622	2
	K.YAASSYLSTPEQWK.S	P01842	63	2.0906	1
	K.AGVETITPSK.Q	P01842	32	2.6242	2
	K.AAPSVTLFPPSSEELQANK.A	P01842	5	3.2199	1
	R.SYSCQVTHEGSTVEK.T	P01842	25	4.4168	2
	S.SYLSTPEQWK.S	P01842	1	2.402	2
	V.KAGVETITPSK.Q	P01842	2	2.4483	2
	Y.SCQVTHEGSTVEK.T	P01842	1	3.305	2
	R.FSGSLJGGK.A	P04211	1	2.238	2

(continued)

Supplementary Table 1 (continued)

Protein	Peptide ^a	Swiss-Prot Accession ^b	Peptide Count ^c	Xcorr ^d	Charge State ^e
Ig λ chain V-I region HA	K.RPSGVDPDR.F	P01700	3	2.7482	2
	K.SGTSASLAISGLR.S	P01700	2	3.4573	2
Ig λ chain V-I region NEW	K.RPSGIPDR.I	P01701	3	2.7973	2
	Q.SVLTQPPSVSAAPGQK.V	P01701	3	2.6266	2
Ig λ chain V-I region NEWM	Q.SVLTQPPSVSGAPGQR.V	P01703	4	2.6021	2
	K.LLLYDNNK.R	P01702	1	2.3171	2
Ig λ chain V-I region NIG-64	Q.SVLTQPPSVSAAPGQE.V	P01702	2	3.8645	2
	Y.YCSSYVDNNTNFVGGG.T	P01710	1	2.9867	2
Ig λ chain V-II region BO	H.FVSWYQQHPGK.A	P01706	1	2.4998	2
	K.YVSWYQQHPGK.A	P01708	2	3.211	2
Ig λ chain V-II region NEI	K.RPSGVSNR.F	P01705	1	3.1271	2
	K.LMIFDVTKRPSGVDPDR.L	P01707	1	2.2649	2
Ig λ chain V-II region TRO	N.RPSGVSDR.F	P01711	1	2.6662	2
	-YVLTQPPSVSVAPGETAR.L	P80748	9	4.4932	2
Ig λ chain V-II region VIL	D.RPSGIPER.F	P80748	2	2.5831	2
	-YVLTQPPSVSVAPGE.T	P80748	4	3.3739	2
Ig λ chain V-III region LOI	Q.PPSVSVAPGETAR.L	P80748	1	2.2112	1
	R.FSGNSGNTATLTISR.V	P80748	7	4.2559	2
Ig λ chain V-III region SH	-SELTQDPAVSVVALGQTVRI	P01714	3	3.5615	2
	K.RPSGIPZR.F	P06889	5	2.8532	2
Ig λ chain V-IV region MOL					

Ig λ chain V-VI region AR	D.FMLTQPHSVSESPGK.T	P01721	1	3.3123	2	
	-.DFMLTQPHSVSESPGK.T	P01721	1	3.1402	2	
Ig λ chain V-VI region EB4	A.NFMLTQPHSVSESPGK.T	P06319	1	4.8848	2	
	R.FSGSIDSSNSASLTISGLK.T	P06318	1	3.179	2	
Ig λ chain V-VI region WLT	K.QVSGSVTTDQVQAEAK.E	P01871	18	4.2165	2	
	K.NVPLPVIAELPPK.V	P01871	17	2.6365	2	
	K.DVMQGTDEHVVCK.V	P01871	4	4.0172	2	
	G.SGVTTDQVQAEAK.E	P01871	3	2.4402	2	
	K.YAATSQVLLPSK.D	P01871	31	3.5133	2	
	Q.VGSGVTTDQVQAEAK.E	P01871	1	2.8292	2	
	V.PLPVIAELPPK.V	P01871	6	2.253	1	
	I.PPSFASIFLTK.S	P04220	9	2.2694	1	
	K.VSVFVPPR.D	P04220	13	2.1894	1	
	K.QVSGSVTTDEVEAEAK.E	P04220	4	3.163	2	
	G.VTTDEVEAEAK.E	P04220	1	2.6993	2	
	K.GVALHRPDVYLLPPARE	P04220	56	4.8415	3	
Ig μ heavy chain disease protein (BOT)	G.SGVTTDEVEAEAK.E	P04220	8	4.2639	2	
	K.GVALHRPDVY.L	P04220	1	2.9459	2	
	K.YVTSAPMPEPQAPGR.Y	P04220	15	3.3754	2	
	R.EGKQVSGSVTTDEVEAEAK.E	P04220	1	3.0036	2	
	S.GVTTDEVEAEAK.E	P04220	1	2.5829	2	
	R.DGFFGNPR.K	P04220	4	2.3233	2	
	Q.VGSGVTTDEVEAEAK.E	P04220	15	4.4638	2	
	R.VFAIPPSFASIFLTK.S	P04220	4	2.8897	2	
	IκB kinase complex-associated protein	O95163	1	2.5016	2	
	Y.LLKQSLSFSTC.G					
	Immunoglobulin J chain	R.SSEDPNEDIVER.N	P01591	11	2.8919	2
		Immunoglobulin λ-like polypeptide 1				
Immunoglobulin λ-like polypeptide 1	F.PPSSEELQANK.A	P15814	21	2.2249	1	
	L.FPPSSEELQANK.A	P15814	1	2.4549	1	
	K.YAASSYLSTPEQWR.S	P15814	1	2.6749	2	
	Q.LTVLSQPK.A	P15814	1	2.4388	2	
	R.SYSCQVMHEGSTVEK.T	P15814	1	2.9023	2	

(continued)

Supplementary Table 1 (continued)

Protein	Peptide ^a	Swiss-Prot Accession ^b	Peptide Count ^c	Xcorr ^d	Charge State ^e
Import inner membrane translocase subunit TIM44	V.KESLHEVSKSDLGRKIKEGVEEA.A.K	O43615	1	2.3745	2
Importin 4	R.EVMPLLLAYLK.S	Q8TEX9	1	2.6054	2
Importin β -2 subunit (Karyopherin β -2 subunit)	L.NNIGDSSPLIRA.T	Q92973	1	2.3136	2
Immunoglobulin heavy chain (Fragment)	K.YYVDSVK.G	Q9ULB6	3	1.9731	1
	INGILP (P33) (Inhibitor of growth family, member 1-like)	O95698	1	2.9282	2
	L.KEIDDVYEK.Y	Q14571	1	2.8487	2
Inositol 1,4,5-trisphosphate receptor type 2	Q.VNTLFMKSHSNMVQRA.A	Q96PC2	1	2.3799	1
Inositol hexakisphosphate kinase 3	S.LVANPVK.E	O15357	1	2.2202	1
Inositol polyphosphate 5-phosphatase	E.DLEEAGV.Q	P14616	1	2.524	2
Insulin receptor-related protein (EC 2.7.1.112)	S.VMKAFKCHHVRLLG.V.V	P35858	1	2.9077	2
Insulin-like growth factor binding protein complex acid labile	R.AFWLDDVSHNR.L	P35858	2	2.337	2
	R.DFALQNPSAVPR.F	P35858	1	2.3599	2
	R.LEALPNSLLAPLGR.L	P56199	4	2.5754	2
Integrin α -1 (Laminin and collagen receptor) (VLA-1)	E.KDLLIVRSQNDK.F	P13612	2	2.9236	2
Integrin α -4 (Integrin α -IV) (VLA-4) (CD49d)	Y.LAVGSMKTLMLNVSLFN.A	Q13797	1	3.3476	2
Integrin α -9 (Integrin α -RLC)	L.ALGAVKNISLISISILGDDAYDAN.V	P08514	1	2.5607	2
Integrin α -IIb	A.EGGQCPSLLFDL.R	P08514	1	2.715	2
	P.WRAEGGQCPSLLFDL.R.D	P06756	1	2.4892	2
Integrin α -V (Vitronectin receptor α subunit)	D.VGPVVQHHIYEL.R	P18564	1	2.3196	2
Integrin β -6	A.KLIPGATVGLLQKDSGNIL.Q				

Inter- α -trypsin inhibitor heavy chain H1					
	K.PLLVDVDLQYPQDAVLALTQNHKKQ	P19827	1	4.5499	2
	K.ELAAQTIK.K	P19827	1	1.9788	1
	K.AAISGENAGLVR.A	P19827	15	3.8034	2
	K.LDAQASFPLPKE	P19827	2	2.651	2
	R.GMADQDGLKPTIDKPSSED.S	P19827	1	2.8903	2
Inter- α -trypsin inhibitor heavy chain H2					
	K.HADPDFTR.K	P19823	1	2.3268	2
	K.FYNQVSTPLLR.N	P19823	8	2.629	2
	K.VQFELHYQEVK.W	P19823	2	3.6727	2
	K.IQPSGGTINIEALLR.A	P19823	19	2.6328	2
	K.AHVSFKPTVAQQR.I	P19823	3	3.1648	2
	R.SILQMSLDHHIVPLTSLVIEAGDER.M	P19823	1	3.0428	2
	R.SSALDMENFR.T	P19823	3	2.4109	2
	R.TEVNVLPGAK.V	P19823	4	2.472	2
	R.FLHVPDFTEGHFDGVPVISK.G	P19823	2	3.6127	3
	R.IYLQGR.L	P19823	1	2.2451	2
	R.IYGNQDTSSQLK.K	P19823	1	2.2484	2
	Y.FGGSEIVVAGK.F	P19823	1	2.4048	2
Inter- α -trypsin inhibitor heavy chain H4					
	K.GSEMVVAGK.L	Q14624	2	2.0274	1
	K.ETLFSVMPGLK.M	Q14624	1	2.2593	1
	K.SPEQQEIVLDGNLIIR.Y	Q14624	1	4.3896	2
	K.YIFHNFMERLWA.Y	Q14624	1	2.6452	2
	K.NVVFVIDK.S	Q14624	1	2.5834	1
	K.ILDDLSPR.D	Q14624	9	2.4285	2
	K.LALDNGGLAR.R	Q14624	8	2.2457	2
	G.RYSLFCLGFGFDVSYA.F	Q14624	1	2.621	2
	R.GPDVLTATVSGK.L	Q14624	20	3.4357	2
	R.FKPTLSQQQK.S	Q14624	1	2.4047	2
	R.LGVYELLK.V	Q14624	2	2.4013	2
	R.QGPVNLISDPEQGVETGQYER.E	Q14624	1	2.3516	2
	R.PSLVPASAENVNK.A	Q14624	1	2.4273	2
	R.VQGNDHSATRE	Q14624	1	2.4617	2
	R.AISGGSIQIENGYFVHYFAPEGLTTPK.N	Q14624	1	3.7068	2
Intercellular adhesion molecule-2 (ICAM-2)					
	T.FGKAAPAPQEATA.T	P13598	1	2.5933	2
Intercellular adhesion molecule-3 (ICAM-3)					
	N.CSTDCPSSEKIALETSL.S	P32942	1	2.4588	2

(continued)

Supplementary Table 1 (continued)

Protein	Peptide ^e	Swiss-Prot Accession ^b	Peptide Count ^c	Xcorr ^d	Charge State ^e
Interferon γ (IFN- γ) (Immune interferon)	N.LKKYFNAG.H	P01579	1	2.2278	1
Interferon- α / β receptor α chain (IFN- α)	L.VAVGPWVLSAAAAGGK.N	P17181	2	2.4844	2
Interferon-induced guanylate-binding protein 1	E.QEQLLKEGFK.E	P32455	1	2.434	1
Interferon-induced, double-stranded RNA-activated protein	S.LNSSLLMNGLRNNQ.R	P19525	1	3.9521	3
Interleukin 17 receptor-like protein long form	L.SLPLMEGLSTDQTETSS.L	Q8NFM7	3	3.3877	2
Interleukin-5 receptor α chain (IL-5R- α)	S.WASAEHLHAPPGSPG.T	Q01344	1	3.1002	2
Intrinsic factor-B12 receptor (Intrinsic factor-vitamin B12 receptor)	F.SYRIISCCGGVF.N	O60494	1	2.6294	2
ISCU2	V.KGKTVEEALTIKNTD.LA	Q9H1K1	1	2.5701	2
J domain containing protein 1	E.RKKEELASTAEK.T	Q9UKB3	2	2.9507	2
JM5 protein	A.CVSLNQPGTVVASASQ.K	Q9Y484	2	2.576	2
JNK-associated leucine-zipper protein	S.ELLGEDLPLEPSVTKAERSHLI.V	Q8IZX7	1	2.8982	2
Junctophilin 2 (Junctophilin type 2) (JP-2)	P.EPPPFEDQPEPE.V	Q9BR39	1	3.0921	2
Kallikrein 9 (EC 3.4.21.-) (Kallikrein-like protein 3)	V.VSGGAEPCSRPR.R	Q9UKQ9	1	2.4031	2
Kallistatin (Kallikrein inhibitor) (Protease inhibitor 4)	R.LGFTDLFSK.W	P29622	2	2.3991	2
κ B and V(D)J recombination signal sequences binding protein 1	R.VGSALFLSHNLK.F	P29622	2	2.8753	2
KCHIP2.5	S.PILGPPQPPDAPASGTEATR.G	Q9BZS0	2	2.8609	2
	V.IYRGFKNECPSGI.V	Q96T43	9	2.6627	2

Keratin, type I cytoskeletal 10 (Cytokeratin 10) (K10) (CK 10)					
K.GSLGGFSSGGFSGGFSR.G	P13645	1	3.5353	2	
R.ALEESNYELEGG.I	P13645	1	3.1253	2	
R.LASYLDKVR.A	P13645	1	3.1079	2	
Keratin, type I cytoskeletal 18 (Cytokeratin 18) (K18) (CK 18)					
L.QLETEIEALKE.E	P05783	1	2.7114	2	
Keratin, type I cytoskeletal 9 (Cytokeratin 9) (K9) (CK 9)					
R.GSGGSHGGGSGFGGE.S	P35527	1	2.4812	2	
R.FSSSSYGGGSSR.V	P35527	1	2.4463	2	
R.GSGGSGGGGGGGYGGGSGSR.G	P35527	3	4.8523	2	
T.SGGGGGGGLGSGGSIR.S	P35527	4	3.6493	2	
Keratin, type II cytoskeletal 1 (Cytokeratin 1) (K1) (CK 1) (67)					
K.SKAAEESLYQSK.Y	P04264	1	2.9608	2	
R.GGGGGYGGSSYGGGSGYSGGGGGGGR.G	P04264	1	3.0315	2	
R.SLVNLGSK.S	P04264	1	2.5239	2	
R.TNAENEFVTIKK.D	P04264	5	3.2352	2	
Keratin, type II cytoskeletal 2 epidermal (Cytokeratin 2e) (K2e)					
K.FASFIDKVR.F	P35908	1	2.8317	2	
Keratin, type II cytoskeletal 5 (Cytokeratin 5) (K5) (CK 5)					
G.LGVGFGGGGSSSVK.F	P13647	2	2.4956	2	
Keratin, type II cytoskeletal 6A (Cytokeratin 6A) (CK 6A)					
Q.DLVEDFKNKYEDEINKRTAAE.N	P02538	1	3.1645	2	
KIAA0147 protein (Fragment)	Q14160	9	2.6107	2	
KIAA0219 protein (Fragment)	Q92616	4	3.1104	2	
KIAA0399 protein (Fragment)	O43149	1	2.5174	2	
KIAA0423 protein (Fragment)	Q9Y4F4	6	2.6956	2	
KIAA0454 protein (Fragment)	O75042	3	2.4408	2	
KIAA0460 protein (Fragment)	O75048	1	2.4056	2	
KIAA0461 perrotein (Fragment)	O75049	2	2.4896	2	
KIAA0540 protein (Fragment)	O75049	1	2.8289	2	
	O60288	1	2.2059	1	

(continued)

Supplementary Table 1 (continued)

Protein	Peptide ^a	Swiss-Prot Accession ^b	Peptide Count ^c	Xcorr ^d	Charge State ^e
KIAA0546 protein (Fragment)	P.PQVSSLPLSQPY.V	O60293	1	2.7533	2
KIAA0594 protein (Fragment)	Q.NELKTTENCE.N	O60335	1	2.4296	1
KIAA0697 protein (Fragment)	I.KDPDKKEIDELI.P	O75179	2	2.2181	2
KIAA0701 protein (Fragment)	I.CIGILLRSAELA.L	O75183	1	2.2502	2
KIAA0756 protein (Fragment)	K.VGKQIVENFSPNQTK.F	O94856	1	2.5469	2
KIAA1000 protein (Fragment)	Q.HELNEVKERA.E	Q9Y2K3	1	2.6383	2
KIAA1078 protein (Fragment)	L.QIIHDTEKSPH.T	Q9UPS4	1	2.4905	2
KIAA1117 protein (Fragment)	S.VYSVHALTLSEVLAHL.L	Q9UPN5	6	2.6006	2
KIAA1224 protein (Fragment)	H.AGSSDQPHPSIQQ.G	Q9ULJ6	1	3.0545	2
KIAA1228 protein (Fragment)	L.EPLIGDMPLVGGALSIF	Q9ULJ2	1	2.8363	2
KIAA1255 protein (Fragment)	A.NNLEDIASTLVR.H	Q9ULG5	1	2.8331	2
KIAA1410 protein (Fragment)	Y.LEPIFSSDINQ.Q	Q9P2D7	1	2.4844	2
KIAA1412 protein (Fragment)	K.SYLPVQFQSPDKAETQ.R	Q9P2D5	1	2.7666	2
KIAA1417 protein (Fragment)	W.ALYGVIDGGSTSCN.E	Q9P2D5	1	2.9777	2
KIAA1438 protein (Fragment)	D.IIQSPSTGLLKSGK.T	Q9P2D0	1	2.4135	2
KIAA1500 protein (Fragment)	D.KDQMLQEKDKQ.I	Q9P2B0	1	3.1799	2
	L.KAVDADTEAESVTFIVQ.P	Q9P228	1	3.1696	2
	G.ASIGSALAAMLLLL.V	Q9P228	1	2.487	2
	V.WCATRPSDPASA.T	Q9P228	1	2.6831	2

KIAA1550 protein (Fragment)	F.NSSVQCQNTSYS.Y	Q9HCM2	1	2.6203	2
KIAA1686 protein (Fragment)	E.SSTIASYVTLRK.T	Q9C0H7	1	2.821	2
KIAA1689 protein (Fragment)	I.NPQDLTVNLVANVPQ.D	Q9C0H4	1	2.4158	2
KIAA1713 protein (Fragment)	S.TGQPLVTHSGSSKQKEY.L	Q9C0F0	1	2.9771	2
KIAA1803 protein (Fragment)	K.SLLENAEAK.K	Q96JM2	1	2.5222	1
KIAA1840 protein (Fragment)	P.LRRVHSTSLDSQKFTVPSSNEVVTNLE.VL	Q96J17	1	2.4395	2
Killer cell immunoglobulin-like receptor 2DL3	R.WCCNKKNNAVVMQDQ.E.P	P43628	1	2.7714	2
Killer inhibitory receptor 2-2-2 (Fragment)	L.HREGKFNDTLRLTGE.L	Q9Y5Q4	2	2.6951	2
Kinesin heavy chain isoform 5C	T.TQEQVYNACAKQIVKDVLEGYN.G	O60282	1	3.0149	2
Kinesin-like protein KIF14	N.AIQIVQQAVKYVQGLAVLKGSKL.H.F	Q15058	1	3.1006	2
Kinesin-like protein KIF3C	S.FLPGICKELIGSSLDFF.G	Q15058	1	2.4068	2
Kinetochore protein CENP-H	R.VNEDPKDTLLREFQEEIARLKAQLEK.R	O14782	2	3.9542	3
Kininogen (α -2-thiol proteinase inhibitor)	N.EIEEVKVAFEIK.K	Q9H3R5	5	3.5338	2
	K.AVDAALKK.Y	P01042	3	2.5254	2
	K.TVGSDFYFK.Y	P01042	2	2.6129	2
	K.AATGECTATVGK.R	P01042	2	3.2797	2
	K.YNSQNQSNNQFVLYR.I	P01042	6	2.4246	2
	R.DIPTNSPELEETLTHITK.L	P01042	5	2.6002	2
	R.VQVVAGK.K	P01042	3	2.0947	1
Kruppel-like zinc finger protein GLIS2	L.LPGTVLDSLSTGV.N	Q9BZE0	1	2.5489	2
Lamin B receptor	M.ASLIIVLKLCCGYIFRGA.N	Q14739	1	2.4691	2
Laminin α -2 chain (Laminin M chain)	A.VGGFKVGLDLLVE.F	P24043	1	3.1133	2
	R.NIPPFEGCIWNLV.I.N	P24043	1	2.4962	2

(continued)

Supplementary Table 1 (continued)

Protein	Peptide ^e	Swiss-Prot Accession ^b	Peptide Count ^f	Xcorr ^d	Charge State ^e
Laminin β -3 chain (Laminin 5 β 3)	G.CHRDCNILGSR.R	Q13751	1	2.5088	2
Latent transforming growth factor- β binding protein 4	C.ENHLACPGQECVNSPFSFQCRACP.S	O75441	12	3.4879	2
Lectomedin-3	Y.HDTSPYRWGGK.S	Q9HAR2	1	2.5366	2
Leucine-rich α -2-glycoprotein (LRG)	K.ALGHLDLDSGNI.L	P02750	4	2.3843	2
Leucine-rich repeat transmembrane protein FLRT1	I.YLYENDL.D	Q9NZU1	1	2.3803	2
Leucine-rich repeat-containing G protein-coupled receptor 5	M.AAVPLLGGSKYGASPLCLPL.P	O75473	1	2.4232	2
Leukocyte surface protein	I.RCSLESYGSSATL.Y	Q93033	1	2.9578	2
Leukocyte tyrosine kinase receptor (EC 2.7.1.112)	G.GFGGGGGACTAGGGGGGGY.R	P29376	2	2.6929	2
LIM domain only 7	E.INGIHDESNAFESK.A	Q8WWI1	1	2.6768	2
LIM protein	C.FKCVACECDLGGSSGA.E	Q8WWI1	1	2.4465	2
L-lactate dehydrogenase A-like (EC 1.1.1.27)	P.VPITSPAVSKVTSTNNMAYNKAPR.P	O60705	2	3.2345	2
Low-density lipoprotein receptor (LDL receptor)	A.FPKNRIIGSGCN.I.L	Q9BYZ2	1	2.4368	2
Low-density lipoprotein receptor-related protein 2	L.TQPRGVNWCERTTILSNGGCCQYL.C	P01130	1	2.4776	2
LSDR	D.ATQGGKTWSAFQNGTDRR.V	P98164	1	2.6886	2
LTRPC6 channel kinase 2	A.TTYTADLSSKSSITLIPSIL.S	Q8N705	1	2.4388	2
LTRPC7	H.RDCITIFDADSE.E	Q9BX84	1	3.0198	2
Lumican (Keratan sulfate proteoglycan lumican)	M.DRVAFVK.L	Q96QT4	1	2.2076	1
	K.ISNIPDEYFK.R	P51884	1	2.3599	2
	K.SLEDLQLTHNK.I	P51884	9	3.3003	2

Lung α/β hydrolase protein 1	R.FNALQYLR.L	P51884	1	2.2921	2
	R.LKEDAVSAAFK.G	P51884	8	3.0523	2
	R.NNQIDHIDEK.A	P51884	1	2.5147	2
	R.LPSGLPVSLTLTYLDNKK.I	P51884	2	3.6577	2
Lymphocyte antigen 6 complex locus G6C protein	D.SSQDPPDPTTQPIVLLLP.G.I	Q965E0	1	2.2638	1
	T.PALGLVFLTSLAGLGLWL.L	O95867	1	2.4238	2
Lymphocyte secreted C-type lectin	Q.ARCTARGGSLAQPADR.Q	Q9Y240	1	2.4084	2
Lymphotoxin- β (LT- β) (Tumor necrosis factor C) (TNF-C)	I.TVLAVLALVPDQ.Q.G	Q06643	1	2.5791	2
Lysosphingolipid receptor Edg5	I.VLGVFIVCWLPAFSILLLLDYAC.P	O95136	1	2.4452	2
LYSp100 protein (Lymphoid-restricted homolog of Sp100)	L.KTPQVTINEGEPKEL.S	Q13342	1	3.0131	2
Lysyl oxidase homolog 1 (EC 1.4.3.-) (Lysyl	G.GGVGAGAAAVASAGVIY.P	Q08397	1	2.2414	1
MAGE-like protein 2 (Necdin-like protein 1) (Protein nM15)	V.EAQPLSPLDER.A	Q9UJ55	1	2.2726	1
Maltase-glucoamylase, intestinal [Includes: Maltase	L.FWDDGQSIDITYGK.G	O43451	3	2.4646	2
Mannosyltransferase (Hypothetical protein FLJ90174)	P.MAVSSRRGNADSIVASLVLM.V	Q9H3S5	1	3.0963	2
Matrin 3	L.KKALWFQGRVCV.K	P43243	1	2.3797	2
Matrix metalloproteinase-15 (EC 3.4.24.-) (MMP-15)	G.PGLGGDTHFDADPEPW.T	P51511	1	2.5166	2
MDC-SIGNIA type II isoform	Q.LLSFTLLAGLLVQVSK.V	Q96QQ8	1	2.4284	2
MEGAP transcript variant a	R.PRPLSVYSHKLFN.G	Q8IZV8	2	2.7443	2
Melanocyte protein Pmel 17	T.PEATGMTPAEVSIVVL.S	P40967	1	2.7689	2
Melanoma-associated chondroitin sulfate proteoglycan	F.STLAPEAWPA.M	Q92675	2	2.5225	2
Melatonin receptor type 1A (Mel-1A-R)	N.AGNIFVVSLAVADLVVA.I	P48039	2	2.4727	2

(continued)

Supplementary Table 1 (continued)

Protein	Peptide ^e	Swiss-Prot Accession ^b	Peptide Count ^f	Xcorr ^d	Charge State ^e
Membrane-associated transporter protein (AIM-1 protein)	V.LFDFAADFID.G	Q9UMX9	1	2.3025	1
Metabotropic glutamate receptor 3 (mGluR3)	A.NASFTWVASDGGWGAQESIHKGSEH.V	Q14832	1	2.9402	2
Metabotropic glutamate receptor 4 (mGluR4)	T.EVRCGSGGPPITK.P	Q14833	1	2.5465	2
Metabotropic glutamate receptor 8 (mGluR8)	L.GGLFPVHAKGER.G	O00222	1	2.6596	2
Metalloproteinase inhibitor 4 (TIMP-4)	I.HLCNYIEPWE.D	Q99727	2	2.6213	2
Metaxin 1	Y.FPWDGAEVPPQR.Q	Q13505	1	2.5034	2
Methyl-CpG binding protein splice variant 2	T.VEPTSTSWNPRGW.P	Q9UNZ8	1	2.4027	2
Microtubule-actin crosslinking factor 1, isoform 4	V.LSAQLLDGGIFHEQTG.Q	Q96PK2	1	2.7991	2
Mitochondrial 28S ribosomal protein S28 (S28mt) (MRP-S28)	F.LRVFLFRPFR	Q9Y2Q9	5	2.5593	2
	I.FHIVENDL.Y	Q9Y2Q9	1	2.3048	1
Mitogen-activated protein kinase kinase 5 (EC 2.7.1.-)	F.RESILNDIR.K	Q99683	1	2.4098	2
Mitogen-activated protein kinase kinase kinase 3	S.TEDENQGTIKR.C	Q8IVH8	1	2.6721	2
Mitotic phosphoprotein 44	A.AFAVEPQGPALGSE.P	Q8TDJ1	2	2.4275	2
	Y.QSKLQARKALSKDGRIFGESIMI.G	Q8TDJ1	1	4.2342	3
Mitotic spindle coiled-coil related protein	L.HLEEDKTTVSQES	Q9BWE8	2	2.4147	2
Mixed lineage kinase 4 β	K.SSNILLLEEIEH.D	Q8WWN1	3	2.8236	2
Mix-like homeobox protein 1 (Homeodomain protein MIX)	A.SLGSPAPPKGAAPSA.S	Q9H2W2	1	2.2246	2
MO25 protein (CGI-66)	N.KTQPILDILK.N	Q9Y376	2	2.6734	1

MO25-like protein	H.KTQPIVEILLK.N	1	3.0324	1	Q9H9S4
Modulator recognition factor I (Fragment)	I.QNIPISLEDSPEAGGE.R	1	2.5282	1	Q03989
MOP-3	I.GDGAGVGGKRTIAGIYENYLLS.R	1	2.7968	2	Q9H3T8
MOP-4	S.NLNRQFLFRPHHIQK.P L.RMHLSNTLLDGEMLI	12	2.4761	2	Q9H3T7
mRNA capping enzyme (HCE) (HCAP1)	L.RMHLSNTLLDGEMLI	1	2.44	2	O60942
mRNA, complete cds, clone:RES4-22B	K.AKVVDLMSITEQKRE.E	1	2.7777	2	P78312
MSin3A associated polypeptide p30	A.AAVAAVVAA.A	1	2.4033	1	O75446
MSTP031	C.FFFILAIRAASF.H	1	2.4837	2	Q9H3F3
Multidrug resistance-associated protein 6	A.SMAAVLL.G	1	2.1341	1	O95255
Multiple membrane spanning receptor TRC8	L.QIFLRLFGVFASS.I	1	2.4437	2	O75485
Myelin P0 protein (Myelin protein zero)	A.VIGGVLGVLLLL.L	3	2.3345	2	P25189
Myelin transcription factor 1-like	C.REMPQNLSTKPDLC.A	1	3.0473	2	Q9UL68
Myeloblastin (EC 3.4.21.76)	A.LASVLLLAL.L	1	2.2013	2	P24158
Myosin heavy chain, cardiac muscle α isoform	D.RGKKDNANANK.G	1	2.4115	2	P13533
Myosin heavy chain, nonmuscle type A	E.EAIVELVE.N	1	2.2888	1	P35579
Myosin heavy chain, nonmuscle type B	R.ALEEALEAK.E	1	2.9337	2	P35580
Myosin heavy chain, skeletal muscle, perinatal	V.YKPEVVAAY.R	1	2.6702	2	P13535
Myosin light chain 1, slow-twitch muscle A isoform (MLC1sa)	G.PSISKPAAKPAAAGAPPK.T	1	2.5164	2	P14649
Myosin Vc (Myosin 5C)	K.AEVARLSKQVKTISEFE.K	6	2.562	2	Q9NQX4

(continued)

Supplementary Table 1 (continued)

Protein	Peptide ^a	Swiss-Prot Accession ^b	Peptide Count ^c	Xcorr ^d	Charge State ^e
Myosin-binding protein C, cardiac-type (Cardiac MyBP-C)	V.SAFSKKPRSVVEVAAGS.P	Q14896	1	2.4212	2
	K.IIWMKMKMEIQGN.P	Q13203	1	2.6362	2
Myosin-binding protein H (MyBP-H) (H-protein)	K.IIWMKMKMEIQGN.P	Q9UL88	1	2.3207	2
	-EVQLVESGGGLVKPGGSLR.L	Q9UL88	11	3.5112	2
Myosin-reactive immunoglobulin heavy chain variable region	K.GLEWVGR.I	Q9UL88	5	3.0079	2
	K.TDGGTTDYAAPVK.G	Q9UL88	2	4.2997	2
	-EVQLVESGGGLVK.P	Q9UL92	31	2.8077	2
	-EVQLVESGAEVK.K	Q9UL92	7	2.6125	2
	E.VQLVESGAEVK.K	Q9UL82	4	2.2157	2
	K.DTERPSGIPER.F	Q9UL82	4	2.2157	2
N2B-titin isoform	I.VVEKPGRIVPGVIGLMR.A	Q8WZB3	1	2.6007	2
	K.KSDQKTTTESTVTR.K	Q8WZB3	1	2.4025	2
N-acetylglucosamine 6-O-sulfotransferase GST-4 β	G.SMITGYIVEKR.D	Q8WZB3	1	2.859	2
	E.KEQALIRKKMAK.D	Q8WZB3	1	2.4414	2
	W.TTLSQGSAAATLHMAVRDLVRS	Q9GZX3	1	2.9387	2
	C.QSTTSVYSSFVFNLF	Q96MN2	1	2.7715	2
NAD(P) transhydrogenase, mitochondrial	P.PAKILIVGGVA	Q13423	1	2.9169	2
	T.ASVAVAGILAA.L	Q16798	1	2.5236	2
NADPH thyroid oxidase 1	R.SNDTVLEATAALYN.Q	Q9NRD9	1	2.4706	2
	N.ERKYRQHPDITVKFTSVPDSM.I.G	P20929	1	4.0472	3
Nectin-like protein 3	Q.PPDKCLKFTSVDTSLEQV.L	P20929	1	2.4422	2
	K.DVKYLLKKEDANRKTFT.T	Q8IZP8	1	2.6379	2
Neighbor of A-kinase anchoring protein 95	S.RLPSLFSQNIHPE.Y	Q9ULX6	1	3.0061	2

Nestin						
Neurexophilin 2 (Fragment)	L..DQEIARPLENENQEFLLK.S	P48681	2	2.4831	2	
Neuroblast differentiation associated protein AHNAK	L..RPLARVLVTGLLQ.L	O95156	1	2.4959	2	
Neurogenic locus notch homolog protein 2	G.PDPKLVKPKVKMPEINIK.A	Q09666	4	2.9037	2	
Neurogenic locus notch homolog protein 3	P.KVSMPPDVLNLKGPKL.K	Q09666	1	2.4233	1	
Neurogenic locus notch homolog protein 3	L..FLAAAREGSYEAAK.I	Q04721	1	2.5615	2	
Neuronal double zinc finger protein	P.PEELLRSSADFLQRLSAILRISLRF.R	Q9UM47	9	2.7004	2	
Neuronal pentraxin receptor	L..VRKVKRITLPSPP	Q9UPA5	1	2.4179	2	
Neuropeptide Y receptor type 1 (NPY1-R)	A.NEIVLLEAGHE.P	O95502	1	2.4725	2	
NF-κB essential modulator (NEMO)	V.SITVSIFSILVLAVERHQIIL.N	P25929	1	3.502	3	
Niban protein	K.KELLQEQ.L	Q9Y6K9	2	2.651	2	
NIF3-like protein 1	H.ECQWVVEDA.P	Q9BZQ8	1	2.523	2	
Ninein	D.SHLENKINIILSETDR.D	Q9GZT8	1	2.4268	2	
NIR1	R.LELEDKVR.H	Q9UH61	1	2.537	2	
Nonhistone chromosomal protein HMG-14	S.CKTHVLLLVHGGNILDITGAGDPSCKA.A	Q9BZ71	1	2.5153	2	
Novel member of serine-arginine domain protein, SR129	G.ETKTEESPASDEAGEKEA.K	P05114	1	3.2398	2	
NT-3 growth factor receptor (EC 2.7.1.112)	M.PSSDLADEKV	Q99590	1	2.812	2	
Nuclear factor RIP140 (Nuclear receptor interacting protein 1)	C.IVGANLLVK.I	Q16288	1	2.6534	2	
Nuclear LIM interactor-interacting factor 1	I.TDAEKNEYEKDSPRLTKT.N	P48552	1	2.7777	2	
	P.SPSVLPPLVEENGGGLQK.P	O15194	1	3.0037	2	
	P.PLVEENGGGLQK.P	O15194	1	3.2103	2	

(continued)

Supplementary Table 1 (continued)

Protein	Peptide ^a	Swiss-Prot Accession ^b	Peptide Count ^c	Xcorr ^d	Charge State ^e
Nuclear pore complex protein Nup155 (Nucleoporin Nup155)	F.LHELEEK.M	O75694	3	2.2444	1
Nuclear receptor coactivator 3 (EC 2.3.1.48) (NCoA-3)	A.TGLEEIDRA.L	Q9Y6Q9	3	2.5105	2
Nuclear RNA export factor 2 (TAP-like protein 2) (TAPL-2)	V.EGQSQGSVLAFTRFIA.T	Q9GZY0	1	2.3934	2
Nucleobindin 1 (CALNUC)	R.FNPKTFFILHDINS.D	Q02818	1	2.7697	2
Nucleolar protein Nop56 (Nucleolar protein 5A)	K.KKVLVGVGDPKIGAAIQE	O00567	1	2.9175	2
Nucleolar RNA-associated protein α	L.LGEGFADESL.D	Q8TEZ1	1	2.3393	2
Nucleolin (Protein C23)	D.RETGSSKGFVDF.N	P19338	1	2.5402	2
Nucleosome assembly protein 1-like 1 (NAP-1 related protein)	L.RERIIPRSVLY.F	P55209	1	2.5208	2
Nucleosome assembly protein 1-like 3	A.EADFKMSEPVAHGVAEEEMASSTSD.S	Q99457	1	2.5528	2
Nucleotide binding protein (NBP) (POV-2)	R.PPYERPELPTCLYVIGLTGSGKSSI.A	Q13057	1	2.5609	2
NUP196 nucleoporin	D.CSGNDLEQ.L	Q8WYB0	1	2.204	1
O-acetyltransferase	A.HEISQITNDL.A	Q8WZ77	1	2.2852	2
Obscurin	W.ASFSCELSHEDDEEVE.W	Q96AA2	1	2.8326	2
Ocular albinism type 1 protein	P.VRTAAKTTWFIMGILNPAQGFLLSLAF.Y	P51810	1	2.8424	2
Olfactory receptor (Fragment)	N.IINHFTCEILAVQKLACAD.I	Q96R43	1	3.7938	3
Olfactory receptor 11A1 (Hs6M1-18)	F.YVAPSAVHSQLLSKVFS	Q9GZK7	2	2.2275	2
Olfactory receptor 5B16	L.NPLVYSLRNKEVKSAF.K	Q96R08	1	2.7789	2

Olfactory receptor 8D2 (Olfactory receptor-like protein JCG2) T.QRPELQLPLFLL.F	1	2.7681	2	Q9GZM6
Oligodendrocyte transcription factor 2 (Basic helix-loop-helix H.SAPLPAATAHPAAAAHAA.A	2	2.9077	2	Q13516
Oligodendrocyte-myelin glycoprotein Q.DGMVINTSLTSSTK.S	1	2.4244	1	P23515
Oligophrenin-1 like protein E.SLMKMKKENPLEHK.T	1	2.7902	2	Q9UNA1
One cut domain family member 2 A.HQELGTAAAAAAAASRSA.M	1	2.6498	2	O95948
Oocyte-specific histone H1 K.PDKAMRAPSSAG.G	1	2.2817	1	Q8IZA3
Organic cation transporter M.SNLLAGAACLVMIIFISPD.LH	4	2.5134	2	O15245
Ornithine decarboxylase antizyme 2 (ODC-Az 2) (AZ2) K.GREDRAPLLK.T	1	2.3462	2	O95190
Orphan nuclear receptor TR4 (Orphan nuclear receptor TAK1) V.QKTYSEDTYRLARIL.V	2	2.1216	1	P49116
Ovarian cancer related tumor marker CA125 F.VTGSTEMAITNQ.T	1	2.9486	2	Q8WXI7
A.IVSMSTTTWPESTRARTE	1	2.5337	2	Q8WXI7
S.QSLGRVSSVLSSESTTEGVTD.S	1	3.0726	2	Q8WXI7
Oxygen-regulated protein 1 (Retinitis pigmentosa RP1) I.MEEKRMNGIYELI	1	2.7163	2	P56715
Oxysterol binding protein-related protein 9 S.MVESIKHCIVLLQJAK.D	1	2.4683	2	Q96SU4
Oxysterols receptor LXR-β (Liver X receptor β) T.DEASSACSTDWV.IP	1	2.4166	2	P55055
P120E4F transcription factor V.EAASLAADI.S	1	2.2877	2	O00146
P53 induced protein (Fragment) L.MKGTHSGAALAV.A	1	2.3308	2	O14680
Pancreatic hormone (Pancreatic polypeptide) (PP) S.LLLSTCVALLL.Q	2	2.602	2	P01298
Pantothenate kinase 4 (EC 2.7.1.33) A.ALVRERGADLVVIE.G	1	2.88	2	Q9NVE7
Parathyroid hormone/parathyroid hormone-related peptide F.LSFMLRAVSIF.V	1	2.9378	2	Q03431

(continued)

Supplementary Table 1 (continued)

Protein	Peptide ^e	Swiss-Prot Accession ^b	Peptide Count ^f	Xcorr ^d	Charge State ^e
Patched protein homolog 2 (PTC2)	F.SLYEVALVTQ.G	Q9Y6C5	1	2.4288	2
Paternally expressed gene 3 isoform 1	R.TKKEIIIELLVLEQYLTI.I	Q9GZU2	3	2.6722	2
Pecanex-like protein 1	F.FRDIWVVFQ.FC	Q96RV3	1	2.7288	2
Peptide transporter 3	R.RAAGA AAVLLVEML.E	Q9P2X9	1	2.5192	2
Peptidoglycan recognition protein L	K.EYGVVLAPDGGSTVAVEPLLAGEAGLQGR.R	Q96PD5	2	6.0437	3
	R.PSLSHLLSQYYGAGVAR.D	Q96PD5	1	4.3083	3
	R.DGSPDVTTADIGANTPDATK.G	Q96PD5	1	2.9672	2
	R.AGLLRPDYALLGHR.Q	Q96PD5	2	3.5976	3
Peptidyl-prolyl cis-trans isomerase like 2 (EC 5.2.1.8)	A.QERKTQLKV.A	Q13356	1	2.7412	2
Pericentrin 2 (Kendrin)	K.ELAEQRAELEKIFQDKNQAEALRNL.E	O95613	1	4.1235	3
Phosphate regulating neutral endopeptidase (EC 3.4.24.-)	S.EAMYNKMNISELSAMI.P	P78562	1	2.5371	2
Phosphatidyl inositol glycan class T (DJ453C12.7)	T.RWDELQREGVSHYR.L	Q969N2	1	2.4526	2
Phosphatidylinositol 3,4,5-trisphosphate-dependent Rac	G.YLLSPIQ.R	Q8TCU6	1	2.2952	1
Phosphatidylinositol 3-kinase regulatory β subunit	P.RPLPARPR.D	O00459	1	2.401	2
Phosphatidylinositol-4-phosphate 3-kinase C2	G.GEVKLSISYKNNKLF.I.M	O00750	1	2.5008	2
Phosphatidylinositol-glycan biosynthesis, class O protein	V.SLVPTLALLLGLPI.P	Q8TEQ8	1	2.2148	2
Phosphatidylinositol-glycan-specific phospholipase D 1	R.IADVTSGLIGGEDGR.V	P80108	1	2.9622	2
Phosphoacetylglucosamine mutase (EC 5.4.2.3) (PAGM)	R.VYAEADSQ.E	O95394	1	2.3207	1
Phosphoglycerate kinase 1 (EC 2.7.2.3)	K.ALESPERPFLAILGGAK.V	P00558	5	3.7099	3
	P.FLAILGGAKVADK.I	P00558	3	2.9481	1

Phosphoinositide-binding proteins					
A.QDKAPDSSQISAPTP.A	Q8WWN8	1	2.7141	2	
Phosphoinositide-specific phospholipase C PLC-epsilon					
K.APRVSTAQDVIQQTL	Q9HBX6	2	2.8144	2	
Phosphorylase kinase catalytic subunit PHKG2 homolog					
F.LDPVSRRPPTSCW.P	Q16221	5	2.332	2	
Phytanoyl-CoA dioxygenase, peroxisomal					
K.PLGLTVMRDVTISK.S	O14832	2	2.3167	2	
Piccolo protein (Aczonin) (Fragments)					
L.KHQIKQEFR.R	Q9Y6V0	1	2.8833	2	
Pigment epithelium-derived factor (PEDF) (EPC-1)					
K.TSLEDFYLDEER.T	P36955	1	2.728	2	
K.IQSLFDSPDFSKI	P36955	4	2.3572	2	
R.ALYYDLISSPDHGTGTYK.E	P36955	2	3.3162	2	
PKY protein kinase					
K.YIFNSLDDVAHVNTV.M	O14632	1	2.2935	1	
Plasma kallikrein (EC 3.4.21.34) (Plasma					
K.DSVTGTLPK.V	P03952	2	2.348	2	
K.VSEGNHDIALIK.L	P03952	7	2.3523	2	
K.EIIHQNYK.V	P03952	1	2.5645	2	
Plasma membrane calcium-transporting ATPase 3					
A.LTPKILDLLVHAISNSA.Y	Q16720	1	2.3597	2	
Plasma membrane calcium-transporting ATPase 4					
L.DEEEEENPDKAS.K	P23634	1	2.5576	2	
D.SSLQSLETSV.-	P23634	1	2.4529	2	
Plasminogen (EC 3.4.21.7) [Contains: Angiostatin]					
K.LSSPAVITDK.V	P00747	2	2.467	2	
R.YEFLNGR.V	P00747	1	2.3082	2	
R.NPDGDVGGPWCYTTNPR.K	P00747	3	5.1004	2	
R.HSIFTPETNPR.A	P00747	17	2.6175	2	
Platelet factor 4 variant (PF4var1) (PF4alt)					
R.HITSLEVIK.A	P10720	1	2.8528	2	
Platelet glycoprotein Ib alpha chain					
P.TTPEPTPIPTIATSPITLV.S	P07359	1	2.7724	2	
Platelet receptor for type III collagen (Fragment)					
F.SRVANVKNFVSLKLCIA.C	Q8NFD8	1	2.508	2	
L.TILRKMSHVGL.T	Q8NFD8	1	2.2125	2	

(continued)

Supplementary Table 1 (continued)

Protein	Peptide ^e	Swiss-Prot Accession ^b	Peptide Count ^f	Xcorr ^d	Charge State ^c
Poly(A) polymerase β (EC 2.7.7.19) (PAP β)	K.EWIREISESKSLPQSV.I	Q9NRJ5	1	2.4495	2
Polyadenylate-binding protein 4 (Poly(A)-binding protein 4)	T.DSCQSGGVPIA.V	Q13310	1	2.5145	2
Polycystic kidney and hepatic disease 1	H.GSLPEVIVT.C	Q8TCZ9	1	2.3634	1
	S.VEFNSVSAG.S	Q8TCZ9	4	2.6867	1
Polycystic kidney disease and receptor for egg jelly related	Q.AIDESTNGFTY.K	Q9NTG1	1	2.9572	2
Polymeric-immunoglobulin receptor	Q.YLCQAGDDSDNSNK.K	P01833	8	2.8531	2
Potassium channel subfamily K member 7	G.LPASLALVATLR.H	Q9Y2U2	2	2.5818	2
Potassium voltage-gated channel subfamily G member 2	S.YSELKEQ.Q	Q9UJ96	4	2.689	1
Potassium voltage-gated channel subfamily V member 2	R.SALNILDIV.A	Q8TDN2	1	2.7792	2
Potassium-transporting ATPase α chain 1 (EC 3.6.3.10)	L.AILFGATFE.I	P20648	1	2.2942	1
Potentail helicase MOV-10	L.LIIVGNPLLLGH.D	Q9HCE1	1	2.9244	2
Potential phospholipid-transporting ATPase IH (EC 3.6.3.1)	T.AYLTLYNISFTSL.P	P98196	2	2.528	2
Pre-B-cell leukemia transcription factor-1	R.LDNMMLLAEGVAGPEKGGSA.A	P40424	1	2.4949	2
Presynaptic protein SAP102	L.NDMYAPPDYASTFTALA.D	Q92796	1	2.2022	2
PRO1635 (Hypothetical protein)	T.LPSQAGATPTPRTKAKLIPTGRDVGVPVPLKPVPGKSTPKL.N	Q92796	1	3.8574	3
PRO1855	S.SFERAPAMVVNSLC	Q9P1I8	1	2.8836	2
PRO2523	L.QQQPLCTSVNTIYDNA.V	Q9P189	1	2.4082	2
	E.ISAPVQVITFK	Q9H3A0	3	2.5596	2

Probable aminopeptidase NPEPL1 (EC 3.4.11.-) T.VEINNTDAEGRILVLA.D	Q8NDH3	1	2.919	2
Probable G protein-coupled receptor GPR31 C.SAPSTVVATAVGV.L	O00270	1	2.5785	2
Probable G protein-coupled receptor GPR62 (hGPCR8) A.GGLGPRPLWALLAFALPALLLLGA.Y	Q9BZJ7	1	2.4797	2
Probable G protein-coupled receptor GPR85 (Super N.I.SPLTAFCLKLTSILGFIIGVSVVGNLL.I	Q9NPD1	1	2.5816	2
Probable serine/threonine protein kinase SNFILK (EC 2.7.1.-) L.EVYPQEGLSTDPFRPA.L	P57059	1	2.4149	2
Proliferation potential-related protein Y.NNDNTAPAEDVIIMIIVPQ.S	Q96PH3	1	3.4172	2
Proliferation-associated protein 2G4 - L.KEGDIVKIDL.G	Q9UQ80	1	2.3656	2
Proline-rich protein BCA3 IGNGQRKDRKKTSLGPG.G	Q9NQ31	1	2.6369	2
Prolyl 4-hydroxylase α -2 subunit (EC 1.14.11.2) A.EFFTSIGHMTDLI.A	O15460	1	3.0333	2
Prostaglandin E2 receptor, EP3 subtype G.EDCGSVSVAFPITML.L	P43115	1	2.6994	2
Protein BAP28 V.DTLGAEKFLWILLJLLF	Q9H583	1	2.3212	2
Protein C20orf102 V.EMACSRGSGSPSYSL.E	Q96N03	1	2.4767	2
Protein C20orf13 E.DGVLGGVIVL.R	Q9H6P5	6	2.3734	1
Protein C20orf77 L.EKKLSELSNSQQ.S	Q9NQG5	1	3.5134	2
Protein CGI-147 D.TESEASILGDSGEYK.M	Q9Y3E5	1	2.5078	2
Protein inhibitor of activated STAT protein 3 K.KPTWTCPVCDK.K	Q9Y6X2	1	2.7316	2
Protein KIAA0020 A.NKVKAALKSLIPTLEK.T	Q15397	1	2.8794	2
Protein KIAA1404 A.SGVDIEEETEKNLE.K	Q9P2E3	1	3.1212	2
Protein KIAA1510 S.TKEQVLA AVRRLR.Y	Q9P2I8	1	2.7169	2

(continued)

Supplementary Table 1 (continued)

Protein	Peptide ^e	Swiss-Prot Accession ^b	Peptide Count ^f	Xcorr ^d	Charge State ^c
Protein kinase BRPK (PTEN induced putative kinase 1)	L.RFFRQSVAGLAARLQR.Q	Q9BXM7	1	3.1386	2
Protein kinase C, iota type (EC 2.7.1.37) (nPKC-iota) (Atypical)	V.QTEKHVFE.Q	P41743	2	2.4365	2
Protein kinase C, μ type (EC 2.7.1.-) (nPKC-μ) (Protein)	R.SATFEDFQIR.P	Q15139	26	2.4224	2
Protein kinase C-binding protein NELL1 (NEL-like)	G.PKCGENSECKNWNTKA.T	Q92832	1	2.6256	2
Protein phosphatase 1 regulatory inhibitor subunit 16B (TGF- β 1RI)	A.ATCGHINLVKIL.V	Q96T49	1	2.2873	2
Protein PM1	T.IALAALVYCVK.K	P17152	1	2.4911	2
Protein pM5	Y.KSENLDNPIQ.T	Q15155	4	2.6561	2
Protein PTD011 (Protein TS58)	G.VREKRSKKIMPAGLVAGLSL.M	Q9Y6G1	1	2.4138	2
Protein transport protein Sec24C (SEC24-related protein C)	A.YRGVLNSPVKAVRDTLI.T	P53992	1	2.5364	2
Protein tyrosine phosphatase receptor-type O truncated	I.RVGFVITYNKVLHF.Y	P53992	1	2.5524	2
Protein-tyrosine phosphatase, receptor-type, O	K.LITNPVQLDDF.D	Q9UBF0	2	2.5121	2
Prothrombin (EC 3.4.21.5) (Coagulation factor II)	G.DPELSCCDSSTISF.I	Q16827	1	2.5215	1
	K.LAACLEGNCAEGLGTNYR.G	P00734	2	3.1127	2
	R.TATSEYQTFNPR.T	P00734	10	2.9578	2
	R.ELLESYIDGR.I	P00734	2	2.4292	2
	R.ETAASLLQAGYK.G	P00734	3	2.5217	2
Protocadherin α 1 (PCDH- α 1)	E.VNLQNGILFVNSR.I	Q9Y5I3	1	3.0855	2
Protocadherin β 16 (PCDH- β 16)	V.LVFFVLLSLSGA.G	Q9NRJ7	3	2.4812	2
Protocadherin β 5 (PCDH- β 5)	Y.EVCLTGDGSGAGE.F	Q9Y5E4	2	2.4851	2

Protocadherin γ A1 short form protein	E.KKGFLSAPQSLLE	Q9Y5D6	1	2.5771	2
Protocadherin γ A8	S.NMSLSLFLVDQNDNAPEI	Q9Y5G5	1	3.1752	2
Protocadherin-9	D.PDTGFNGVQHYELLNGQS K.LCAGASYAEENE.C	Q9HC56 Q9HC56	1 1	3.062 2.4405	2 2
PTB-like protein L (Polypyrimidine tract binding protein 2)	R.EGLDDQGL.T	Q969N9	1	2.5178	2
PTPsigma (Fragment)	N.GLTLDVDGR.T	O75870	1	2.5754	2
Put. B7,3 molecule of CD80-CD86 family	P.QIQWSNNKGENI.P	Q99420	1	2.601	2
Putative adenosylhomocysteinase 3 (EC 3.3.1.1)	A.KVPEVELKDLSPSEA.E	Q96HN2	1	2.4557	2
Putative ATP-dependent mitochondrial RNA helicase	L.DKNEVKKVLDKFKYKR.K	O43630	1	2.823	2
Putative DMO orthologue (Fragment)	Q.STGGPAAGAALGL.G	Q9H4B9	2	2.8871	2
Putative fork head domain transcription factor AFX1	R.SGLSGFSLQHPGVGTG.P	P98177	1	2.6171	2
Putative G-protein coupled receptor	R.SASLCVWGSVSETLCLSLG.L	Q8TDV3	1	2.5648	2
Putative integral membrane transport protein	F.AHGNEVIPTIIRARA.M	Q8IVM8	2	2.475	2
Putative ribosomal RNA methyltransferase 1 (EC 2.1.1.-)	I.IVPPVTCGDLS.S	Q9UET6	1	2.519	2
Putative seven pass transmembrane protein (Similar to L.FISLVFLLVNL.T	L.FISLVFLLVNL.T	O60478	2	2.616	2
Putative transcription factor CA150	M.QAKEDFKKMEEA.K	O14776	1	2.4429	1
Putative transmembrane protein NMA	L.RSENKRLQDQR.Q	Q13145	1	2.6512	2
PYRIN-containing APAFI-like protein 6	L.MEVTVYLQSDKD.M	P59045	1	2.5442	2
PYRIN-containing APAFI-like protein 7 (Monarch-1)	R.LLLVKEHSNPMQ.V	P59046	1	3.2529	2
Pyrroline-5-carboxylate reductase (EC 1.5.1.2) (P5CR)	A.GVTISSIEKKLS.A	P32322	1	2.4898	2

(continued)

Supplementary Table 1 (continued)

Protein	Peptide ^a	Swiss-Prot Accession ^b	Peptide Count ^c	Xcorr ^d	Charge State ^e
Quinone oxidoreductase-like 1 (QOH-1)	Q.PDDEVVGGILPLD	O95825	1	2.6793	2
	R30923_1 (Fragment)	O94999	1	2.5581	2
R31167_1, partial protein (Fragment)	I.AQETFDAAVR.E	O9Y2P2	1	3.0607	2
	C.GWASVKYKQKLDK.Y	O9Y2P2	1	2.2495	1
Rabconnectin	G.SSVSGGGGGGAG.A	O8TDJ6	1	2.2485	2
	L.QSPPLPPTTLPLLS	O8TDJ6	1	2.4273	2
Rabphilin-3A	I.GPLSYTGGVSELARI	O9Y2J0	1	2.6021	2
	A.EKMEEMEQE.R	P04049	1	3.0119	2
RAF proto-oncogene serine/threonine-protein kinase	S.NGEGFKDAVFDGSS	O15211	1	2.5585	2
Ral guanine nucleotide dissociation stimulator-like 2	R.LQNECRGYNLQPD	P47736	1	2.5617	2
Rap1 GTPase-activating protein 1 (Rap1GAP)	Q.KVKLQDFK.G	P52306	1	2.4927	2
Rap1 GTPase-GDP dissociation stimulator 1	F.LKSEMPVQFK	O43374	1	2.7946	2
RasGAP-activating-like protein 2	L.RAHLGALISALSRVRAC.P	Q15303	1	2.5501	2
Receptor protein-tyrosine kinase erbB-4	V.TIGGRVLYSGLLLI	Q13546	1	3.1589	2
Receptor-interacting serine/threonine protein kinase 2	D.NTTSLTDKHLDPIR.E	Q13127	2	2.5042	2
REST protein	Q.VLIEVGLVPVK.D	Q9NQC3	2	2.2658	1
Reticulon 4 (Neurite outgrowth inhibitor) (Nogo protein)	P.TALTCLKV.E	O8TDV9	1	2.5251	2
Retinal short chain dehydrogenase reductase	V.EKIVEAILQE.K	Q8NHQ3	1	3.0942	2
Retinoblastoma binding protein 8	E.KSSMLFYIDEER.K				

Retinoblastoma-associated factor 600	R.GREWESAALQNANTK.C	Q8TDN5	1	2.243	2
Retinoblastoma-associated protein (P110) (P105-RB) (RB)	D.FYKVIIESFIKAE.G	P06400	1	3.2513	2
Retinoblastoma-associated protein HEC	Q.QIINKLTK.D	O14777	1	2.437	2
Retinol dehydrogenase similar protein	S.IKAAAQWVR.D	Q8NEX9	1	2.6492	2
Rho-GTPase-activating protein 7	K.DLNENLAATQGLA.H	Q96QB1	2	2.7136	2
Rho-related BTB domain-containing protein 1	L.QFLYTGQ.L	O94844	1	2.3455	1
Ribokinase (EC 2.7.1.15)	D.IRAAANVISR.A	Q9H477	3	2.5389	2
Ribonucleases P/ MRP protein subunit POP1 (EC 3.1.26.5)	R.LGWGSGWDVLLPK.G	Q99575	1	2.3405	2
Ribonucleoside-diphosphate reductase M2 chain (EC	L.TFSNELISRDEGLHCD.F	P31350	1	2.4983	2
Ribosomal protein S6 kinase α 6 (EC 2.7.1.37)	D.PEFTAKTPKDSPLPASANAHLQ.L.F	Q9UK32	1	2.6972	2
Ris		Q9NYNI	1	2.471	2
RNA-binding protein regulatory subunit	P.LEVNLAILGRRRGAGK.S	O14805	1	3.0995	2
Rod cGMP-specific 3',5'-cyclic phosphodiesterase	V.KEILKEQ.E	P16499	1	2.7598	2
RRP5 protein homolog (Fragment)	Q.EIVFPLDMGIV.G	Q14690	1	3.6169	2
RW1 protein (Fragment)	D.LAITSLLLNQCLEELQ.G	Q92545	1	2.4146	2
Ryanodine receptor 1 (Skeletal muscle-type ryanodine	L.LVIGTAYLEAQ.G	P21817	1	2.4891	2
	F.FPVVFSFAGVKVRF.L	P21817	1	2.9356	2
	P.EPEPEPELEPEK.A	Q15413	1	2.4907	2
Ryanodine receptor 3 (Brain-type ryanodine receptor) (RyR3)	E.DLVGIIISIPLK.L	P29034	1	2.6263	2
S100 calcium-binding protein A2 (S-100L protein) (CAN19)	E.KVDEEGLK.L	Q9NZJ4	1	2.1683	1
Sacsin	Y.TLLMDPMNVF.Y				

(continued)

Supplementary Table 1 (continued)

Protein	Peptide ^a	Swiss-Prot Accession ^b	Peptide Count ^c	Xcorr ^d	Charge State ^e
Salivary proline-rich protein 1 (Fragment)	R-SPRKPOGPPPOGGNQPGPPPPGKPKQ.G	Q15214	1	5.1993	3
	Q-APPAGKPOGPPPPPPQ.G	P10162	1	4.0888	2
Salivary proline-rich protein PO (Allele K)	R-SPPGKPOGPPQEG.N	P10163	1	3.4706	2
	R-SPPGKPOGPPQ.Q	P10163	1	3.1865	2
	R-SPPGKPOGPPQ.E	P10163	1	3.3821	2
	R-SPPGKPOGPPQ.E.G	P10163	1	2.8876	2
	R-SPPGKPOGPPQEGNKPKQ.G	P10163	1	3.8327	2
	R-SPPGKPOGPPQ.G	P04280	3	3.1891	2
Salivary proline-rich protein (Clones CP3, CP4 and CP5)	R-APPGKPOGPPQEGNPPQ.G	P04280	1	4.2882	2
	R-APPGKPOGPPQ.E.G	P04280	1	2.7704	2
	F.G.L.L.L.P.V.L.F.I.L	Q9NR16	1	2.2491	1
Scavenger receptor cysteine-rich type 1 protein M160	V.SVGAVPVLSKECASSGERRRMSQ.M	Q96T21	1	2.4606	2
SECIS-binding protein 2	K.LPTDSELAPR.S	P49908	1	2.4386	2
Selenoprotein P (SeP)	R.CQAYGAACADCCLARDPY.C	Q13275	1	2.4417	2
Semaphorin 3F (Semaphorin IV) (Sema IV)	K.HTQLVEQLDES.S	Q9NTN9	1	2.4081	2
Semaphorin 4G	S.RDLPDDVL.T	Q9H3T2	1	2.4384	2
Semaphorin 6C (Semaphorin Y) (Sema Y)	D.EKADIALIKIDHQGK.L	Q92743	1	2.2121	1
Serine protease HTRA1 (EC 3.4.21.-) (L56)	K-SRAEGRAPNPARK.A	Q15831	1	2.3568	2
Serine/threonine protein kinase 11 (EC 2.7.1.37)	I.QQEITVLSQCDSPYIT.R	O00506	1	2.4364	2
Serine/threonine protein kinase 25 (EC 2.7.1.37)	N.GFALPLKBEHKIF.L	Q13362	1	2.7473	2

Supplementary Table 1 (continued)

Protein	Peptide ^a	Swiss-Prot Accession ^b	Peptide Count ^c	Xcorr ^d	Charge State ^e
	G.YFAVAVVK.K	P02787	1	2.4601	2
	K.DSAHGFLK.V	P02787	48	2.3397	2
	D.SGFQMNQLR.G	P02787	1	2.5966	2
	K.SKEQLFSSPHG.K	P02787	1	2.4908	2
	L.DGGFVYIAGK.C	P02787	1	2.4901	2
	K.NPDPWAK.N	P02787	1	2.3352	2
	K.NLNEKDYELLCLDGTR.K	P02787	1	4.2783	2
	K.SASDLTWDNLK.G	P02787	56	3.0296	2
	K.SCHTAVGR.T	P02787	1	2.0609	1
	K.MYLGYYVTAIR.N	P02787	218	4.4578	2
	K.SKEQLFSSPH.G	P02787	5	2.6662	2
	K.IECVSAETTEDCIAK.I	P02787	4	4.373	2
	K.SKEQLFSSPHGK.D	P02787	6	3.6338	3
	E.KYLGEEYVK.A	P02787	3	2.4243	2
	L.GYEVYTAIR.N	P02787	1	3.2149	2
	L.KPVVAEFYGSK.E	P02787	2	2.783	2
	K.LCMGSLNICEPNNK.E	P02787	4	4.0563	2
	G.GFVYIAGK.C	P02787	1	2.4729	1
	E.GYYGTGAFR.C	P02787	2	2.5645	2
	G.AGDVAFVK.H	P02787	5	3.0831	2
	K.YLGEEYVK.A	P02787	18	1.9693	1
	K.IMNGEADAMSLDGGFVYIAGK.C	P02787	2	4.8013	3
	K.KDSGFQMNQLR.G	P02787	3	3.6875	3
	R.KPVDEYK.D	P02787	1	2.0546	1
	Y.LAPNNLKPVVAEFY	P02787	1	2.3204	2
	R.AIAANEADAVTLDAGLVYDAYLAPNNLKPVVAEFYGSK.E	P02787	4	4.6121	3
	Y.LAPNNLKPVVAEFY.G	P02787	1	2.3829	2
	R.FDEFFSEGCAPGSK.K	P02787	13	4.2736	2
	R.DDTVCLAK.L	P02787	12	2.0125	1
	N.NLKPVVAEFYGSK.E	P02787	7	3.9039	3
	R.LKCDSEWSVNSVGK.I	P02787	6	3.2895	2
	Y.YGYTGAFR.C	P02787	1	2.5168	2
	R.WCAVSEHEATK.C	P02787	12	3.1044	2
	R.KPVVEYANCHLA.R	P02787	1	3.2487	2
	R.APNHAVVTR.K	P02787	22	2.2269	2

Y.LAPNNLKPVVAEFYGSK.E	P02787	5	2.7084	2
R.SMGKEDLIWELLNQAQEHFGK.D	P02787	2	5.0312	2
R.TAGWNIPMGLLYNK.I	P02787	34	3.7701	2
R.KPVEEYANCHLAR.A	P02787	3	4.223	2
R.DQYELLCLDNTR.K	P02787	5	2.342	1
Serum albumin				
C.VADESAENCDK.S	P02768	1	2.2135	1
C.PFEDHVK.L	P02768	6	2.4761	2
D.LPSLAADFVESK.D	P02768	79	2.7488	2
M.DDFAAFVEK.C	P02768	4	2.9142	2
M.PADLPSLAADFVESK.D	P02768	39	3.6317	2
D.LGEENFK.A	P02768	1	2.5048	2
C.FSALEVDETYVPK.E	P02768	15	3.1639	2
L.VNEVTEFAK.T	P02768	11	2.2693	1
C.TAFHDNEETFLK.K	P02768	27	2.9649	2
C.IAEVENDEMPADLPSLAADFVESK.D	P02768	2	4.6841	2
K.YICENQDSISSK.L	P02768	211	3.5211	2
K.VPQVSTPTLVEVSR.N	P02768	293	2.1218	1
L.AADFVESK.D	P02768	5	2.2232	1
L.DELRDEGK.A	P02768	15	2.4699	2
C.ELFEQLGEYK.F	P02768	1	2.5176	2
D.FAAAFVEK.C	P02768	1	2.5063	2
L.KAVMDDFAAFVEK.C	P02768	3	2.6057	2
L.HTLFGDK.L	P02768	1	2.7119	2
A.FHDNEETFLK.Y	P02768	1	3.1543	2
A.FHDNEETFLK.K	P02768	4	2.7915	2
D.DFAAFVEK.C	P02768	8	2.4105	1
A.LEVDETYVPK.E	P02768	12	3.2249	2
A.DESAENCDK.S	P02768	1	2.2606	1
L.PSLAADFVESK.D	P02768	89	2.4573	1
L.VAASQAALGL.-	P02768	4	2.8057	2
A.KTYETTLEK.C	P02768	1	2.7902	2
L.GEYKFNALIVR.Y	P02768	1	2.7272	2
L.FEQLGEYK.F	P02768	2	3.0426	2
D.KLCTVATLR.E	P02768	4	2.7819	2
K.YLYEIAR.R	P02768	237	2.4334	2
A.PELLFFAK.R	P02768	25	2.9489	2
A.DLPSLAADFVESK.D	P02768	16	3.4824	2

(continued)

Supplementary Table 1 (continued)

Protein	Peptide ^a	Swiss-Prot Accession ^b	Peptide Count ^c	Xcorr ^d	Charge State ^e
	D.KAACLLPK.L	P02768	1	2.5052	2
	K.SHCIAEVENDEMPADLPISLAADFVES.K	P02768	1	3.5931	2
	K.QNCELFEQLGEYK.F	P02768	16	4.7689	2
	K.QNCELFEQLGEYKFNALLVR.Y	P02768	3	2.2681	2
	K.KVPQVSTPTLVEVS.R	P02768	27	2.6297	2
	K.KVPQVSTPTLVEV.S	P02768	1	2.9706	2
	K.QTALVELVK.H	P02768	7	2.2255	2
	K.AEFAEVSKLVTDLTK.V	P02768	28	3.1275	2
	K.KVPQVSTPTLVE.V	P02768	6	3.1839	2
	K.AEFAEVSK.L	P02768	78	2.949	2
	G.DLLECADDR.A	P02768	1	2.8032	2
	E.MPADLPISLAADFVESK.D	P02768	1	4.7383	2
	E.VDETYVPK.E	P02768	1	3.0762	2
	K.KVPQVSTPTL.V	P02768	3	2.7253	2
	F.KPLVEEPQNLJK.Q	P02768	18	4.1808	2
	H.TLFGDKLCTVATLR.E	P02768	1	3.7417	2
	K.LVAASQAALG.L	P02768	6	2.4727	2
	K.LVAASQAALG.L-	P02768	105	2.4283	2
	K.SLHTLFGD.K	P02768	2	2.6868	2
	E.FKPLVEEPQNLJK.Q	P02768	5	3.2151	2
	K.AVMDDFAAFVEKCK.A	P02768	1	4.4214	2
	F.GDKLCTVATLR.E	P02768	1	2.5301	2
	K.RMPCAEEDYLSVVLNQLCVLHEK.T	P02768	1	4.7732	2
	F.YAPELFFAK.R	P02768	1	2.2134	1
	K.LKBCCEKPLEK.S	P02768	15	3.0054	2
	K.LDELRLDEGKASSAK.Q	P02768	7	2.8938	2
	K.LDELRLDEGK.A	P02768	211	2.6603	2
	I.CENQDSISSK.L	P02768	3	2.3516	1
	K.LDELRLDEG.K	P02768	1	2.5294	2
	K.AVMDDFAAFVEK.C	P02768	164	2.2103	2
	F.DEFKPLVEEPQNLJK.Q	P02768	19	3.74	2
	F.SALEVDETYVPK.E	P02768	17	2.7027	2
	K.NYAEAK.D	P02768	8	1.9491	1
	K.LVAASQAAL.G	P02768	2	2.7578	2
	K.NYAEAKDVFLGMFLYEYAR.R	P02768	4	3.509	3

K.KVPQVSTPTLVEVSR.N	P02768	140	3.8393	3
F.HADICTLSEKE	P02768	1	3.2448	2
F.HDNEETFLK.K	P02768	20	3.0986	2
K.LCTVATLR.E	P02768	2	2.2198	2
K.VHTECCGDLLECADDR.A	P02768	24	3.8658	2
K.SHCIAEVENDEMPADLPSLAADFVESK.D	P02768	28	3.9947	2
K.PLVEEPQNLIK.Q	P02768	62	3.3402	2
K.KYLYEIAR.R	P02768	14	2.9725	2
E.VENDEMPADLPSLAADFVESK.D	P02768	1	2.6557	2
K.SLHTLFGDK.L	P02768	321	2.0783	1
K.LDELRLDE.G	P02768	11	2.4045	2
K.DLGEENFKALVLIJAFAYLQQCFEDHVK.L	P02768	1	4.089	3
K.AAFTECCQAADK.A	P02768	122	2.7853	2
K.AAFTECCQA.A	P02768	1	2.2315	1
K.DLGEENFK.A	P02768	95	2.7377	2
K.VFDEFKPL.V	P02768	3	2.5767	2
K.LVNEVTEFA.K	P02768	1	2.8405	2
K.VFDEFKPLV.E	P02768	1	3.2405	2
K.VFDEFKPLVE.E	P02768	10	2.479	2
K.VFDEFKPLVEE.P	P02768	29	2.8304	2
G.DKLCIVATLR.E	P02768	1	2.4117	2
K.VFDEFKPLVEEPQN.L	P02768	2	2.4758	2
K.TYETTLEK.C	P02768	2	2.3174	2
K.VFDEFKPLVEEPQNL.I	P02768	1	3.4544	2
K.EFNAETTFHADICTLSEKE	P02768	10	2.4651	2
K.VFDEFKPLVEEPQNL.I.K	P02768	14	3.6136	1
K.VFDEFKPLVEEPQNL.I.Q	P02768	307	4.0127	3
K.ECCCKPILLEK.S	P02768	8	2.8553	2
K.LVTDLTK.V	P02768	3	1.9185	1
K.VFDEFKPLVEEPQNL.IK.Q.N	P02768	3	4.2323	3
K.LVNEVTEFAK.T	P02768	1689	2.5788	2
K.DVFLGMFLYEYAR.R	P02768	17	2.3683	1
K.VFDEFKPLVEEPQ.N	P02768	39	2.985	2
K.ADDKETCFAEEGK.K	P02768	7	3.5972	2
K.KQTALVELVK.H	P02768	214	2.444	2
K.SLHTLFGDKL.C	P02768	52	2.4257	2
K.SLHTLFGDKLCTVAT.L	P02768	1	2.9609	2
H.KDDNP.NLPR.L	P02768	2	2.7154	2

(continued)

Supplementary Table 1 (continued)

Protein	Peptide ^a	Swiss-Prot Accession ^b	Peptide Count ^c	Xcorr ^d	Charge State ^e
	K.ADDKETCFAEEGKK.L	P02768	10	3.4938	2
	K.KLVAAASQAALGL.-	P02768	11	2.6686	2
	K.KLVAAASQAALG.L	P02768	1	2.5443	2
	K.CCAAADPHECYAK.V	P02768	8	2.9973	2
	K.SLHTLFGDKLCTVATLR.E	P02768	33	3.508	3
	K.TYETTLEKCCAAADPHECYAK.V	P02768	5	3.0864	2
	K.DVCKNYAEAK.D	P02768	3	2.5606	2
	K.TYETTLEKCCAAAD.P	P02768	3	2.5775	2
	K.CCTESLVNR.R	P02768	12	2.3707	2
	K.DDNPMLPR.L	P02768	70	2.3939	2
	K.FQNALLVR.Y	P02768	149	2.8479	2
	H.DNEETFLKK.Y	P02768	2	2.727	2
	K.TCVADESAENCDK.S	P02768	32	3.6576	2
	K.AAFTECCQAADKAAACLLPK.L	P02768	1	3.1123	2
	K.TPVSDRVTK.C	P02768	4	2.4127	2
	F.KDLGEENFK.A	P02768	1	2.7087	2
	K.KVPQVSTPT.L	P02768	2	2.4089	2
	K.ALVLIAFAQYLQQCFEDHVK.L	P02768	2	4.6559	2
	N.DEMPADLPSLAADFVESK.D	P02768	2	2.9968	2
	P.KAEFAEVSK.L	P02768	1	3.1145	2
	P.ADLPSLAADFVESK.D	P02768	2	2.5425	2
	P.SLAADFVESK.D	P02768	3	3.029	2
	P.KLDELIRDEGK.A	P02768	3	3.2511	2
	P.YFYAPELLEFFAK.R	P02768	25	2.5656	2
	R.LSQRFPKAEFAEVSK.L	P02768	1	3.0029	2
	R.HPYFYAPELLEFF.A	P02768	1	2.7031	2
	V.ADESAENCDK.S	P02768	2	2.4039	1
	R.NECFLQHKDDNPMLPR.L	P02768	4	4.5359	2
	R.NECFLQHK.D	P02768	8	2.7011	2
	R.MPCAEDYLSVVLNQLCVLHEK.T	P02768	9	2.4544	2
	R.RHPDYSVVLILR.L	P02768	29	3.5491	3
	R.LVRPEVDVM.C	P02768	3	2.7478	2
	R.RHPYFYAPELLEFF.A	P02768	1	2.5794	2
	R.LSQRFPK.A	P02768	1	2.5011	2
	S.ALEVDETYVPK.E	P02768	7	2.9068	2

R.LAKTYETTLEK.C	P02768	4	3.3129	2
V.KLVNEVTEFAK.T	P02768	26	3.5777	2
R.HPYFYAPELFFFAK.R	P02768	62	2.8061	2
R.HPYFYAPELFFFA.K	P02768	2	2.5292	2
R.LVRPEVDVMCTAFHDNEETFLK.K	P02768	27	3.9553	2
S.TPTLVEVSR.N	P02768	13	2.7069	2
R.YTKKVPQVSTPTLVEVSR.N	P02768	3	3.6723	3
R.VTKCCTESLVNR.R	P02768	1	3.2955	2
Y.FYAPELFFFAK.R	P02768	80	2.9079	2
Y.GEMADCCCAK.Q	P02768	1	2.2502	1
R.RPCFSALEVDETY.V	P02768	1	2.6754	2
T.YGEMADCCCAK.Q	P02768	1	2.3849	1
S.LAADFVESK.D	P02768	4	2.7609	2
V.FDEFKPLVEEPQNLJK.Q	P02768	11	2.5653	2
T.AFHDNEETFLK.K	P02768	12	2.5615	1
Y.KAAFFECCQAADK.A	P02768	6	2.8013	2
T.PTLVEVSR.N	P02768	25	2.5143	2
R.RPCFSALEVDETYVVK.E	P02768	30	2.7881	2
R.RHPYFYAPELFFFAK.R	P02768	15	4.0128	3
R.RHPYFYAPELFFFA.K	P02768	1	2.9058	2
S.KLVTDLTK.V	P02768	10	2.85	2
R.FPKAEFAEVSK.L	P02768	3	3.3056	2
R.HPYFYAPELL.F	P02768	4	2.3487	1
R.AFKAWAVAR.L	P02768	1	2.5953	2
Q.TALVELVK.H	P02768	37	2.9732	2
V.PQVSTPTLVEVSR.N	P02768	43	3.1281	2
R.FKDLGGEN.F	P02768	2	2.7486	2
R.FKDLGGEN.F.K	P02768	16	2.4418	2
R.FKDLGGENFK.A	P02768	204	2.8391	2
R.DAHKSEVAHR.F	P02768	1	2.7348	2
R.FKDLGGENFKAL.V	P02768	1	3.547	2
R.ETYGEMADCCCAK.Q	P02768	36	2.1802	1
R.HPDYSVLLLR.L	P02768	43	2.2205	2
V.NEVTEFAK.T	P02768	2	2.3415	1
V.MDDFAAFVEK.C	P02768	3	2.241	1
Y.APELLFFFAK.R	P02768	7	2.2681	1
R.FRPDGLPK.K	P35542	1	2.4699	2
R.GPGGVWAAK.L	P35542	3	2.948	2

Serum amyloid A-4 protein

(continued)

Supplementary Table 1 (continued)

Protein	Peptide ^a	Swiss-Prot Accession ^b	Peptide Count ^c	Xcorr ^d	Charge State ^e
Serum paraoxonase/arylesterase 1 (EC 3.1.1.2)	K.YVYIAELLAHK.I	P27169	1	2.4299	2
	R.IQNILTEEPK.V	P27169	5	3.4774	2
	P.SFPITNYLAPVSASVPSA.V	P11831	1	2.4813	2
Sestrin 1 (p53-regulated protein PA26)	E.DHGYSLVNR.L	Q9Y6P5	1	2.4525	2
Seven transmembrane helix receptor	S.TCGAHVTVTVYYVPC.A	Q8NGC4	2	3.6623	2
	G.VALLITSVAPL.L	Q8NGE2	1	2.6255	2
Seven transmembrane helix receptor	T.MFILLGFTDHPQLQ.A	Q8NGJ0	1	2.2971	1
Seven transmembrane helix receptor	N.KVSVIGLGVFVRA.L	Q8NGJ4	1	2.4457	2
Seven transmembrane helix receptor	L.STTTVPKALAIFWLQAH.N	Q8NGM7	1	2.45	2
Seven transmembrane helix receptor	G.PNVIDHFSCDASPLLA	Q8NGQ2	1	2.6759	2
Seven transmembrane helix receptor	L.LLVSYVILVSPK	Q8NH43	2	2.4447	2
Seven transmembrane helix receptor	F.CDVPPILALSCSNVDIN.I	Q8NH90	1	2.5365	1
SH2 domain-containing phosphatase anchor protein 2b	E.VTSKPLNIQVQGV.P	Q96P30	1	2.6009	2
SH3 and multiple ankyrin repeat domains protein 2 (Shank2)	E.GGENVDCTVYADGQAFMVDKPPV.P	Q9UPX8	1	2.6305	2
SH3-domain binding protein 1 (3BP-1)	A.QLDAASVSIQVVGVVEAL.I	Q9Y3L3	1	2.3908	2
Sialic acid binding Ig-like lectin 5 (Siglec-5)	T.PISNTGILELR.R	O15389	1	2.3276	1
Sialoadhesin (Sialic acid binding Ig-like lectin-1)	L.LRVEIHNPILLEE.E	Q9BZZ2	1	3.127	2
Signal recognition particle 14 kDa protein (SRP14)	-I.MVLESEQFLTELTR.L	P37108	1	2.8671	2

Similar to chromosome 6 open reading frame 32 A.TSPASKAARE.S	Q9BQ28	1	2.4803	2
Similar to cyclin-dependent kinase-like 3 D.LDLLHKIVLKV.G	Q8IVW4	1	4.1075	2
Similar to differential display and activated by p53 F.IVDETLDFGGL.S	Q9BV77	1	2.4964	2
Similar to early development regulator 2 F.YVASFPVALPLQ.PP	Q8N195	1	2.5895	2
Similar to endothelial and smooth muscle cell-derived P.DIRNTTVPNVTKDVALAAVLPVLMVLTLL.L	Q8N6M4	1	2.4262	2
Similar to Fgd1 family, member 2 Q.DLWEVYQ.R	Q8IZ32	1	2.4001	1
Similar to fring L.VLLVLGQQPVI.S	Q8TBY7	1	2.2758	2
Similar to GA binding protein transcription factor, β subunit Q.YGHYSTAEVLLRAGVSRDARTKVDRT.P	Q8TAK5	1	3.7882	3
Similar to gene near HD on 4p16.3 K.QLCRPLTCEKSKPVPLK.L	Q8TBR6	1	2.2541	2
Similar to hypothetical protein Y.FVVGDVPEESKELLQRA.L	Q8TC38	2	2.8499	2
Similar to hypothetical protein 384D8_6 W.EDTVQPLLQE.Q	Q9BUT3	1	2.4046	2
Similar to hypothetical protein dJ462O23.2 K.DFLRRYVLSFVGCGLAVVGTYLL.V	Q9BVE6	1	3.0387	2
Similar to hypothetical protein DKFZp434G0522 I.LFGGEYFNGQKT.F	Q96F29	1	2.4756	2
Similar to hypothetical protein DKFZp564D172 I.NEDLDSGTQIPFIK.R	Q8WUF8	1	2.4551	2
Similar to hypothetical protein FLJ10101 (Fragment) R.PFVEEYIPTQEIQV.T	Q8IWK1	2	2.9171	2
Similar to hypothetical protein FLJ11807 W.FFSGRPLTDKMKFEELK.I	Q8WUN7	1	2.8603	2
Similar to hypothetical protein FLJ12618 S.PRSRSDGMQYPIVKNKTK.G	Q9BRR1	1	3.8619	3
Similar to hypothetical protein FLJ14840 V.AIDESWKGGGPV.T	Q8WU96	1	2.3186	2
Similar to hypothetical protein FLJ14886 (Fragment) M.NRITTKKATSSCPPK	Q96AS3	1	2.2543	1

(continued)

Supplementary Table 1 (continued)

Protein	Peptide ^a	Swiss-Prot Accession ^b	Peptide Count ^c	Xcorr ^d	Charge State ^e
Similar to hypothetical protein FLJ22582	K.NTKLDMQFIKDSR.Q	Q96BG7	1	3.4999	2
Similar to hypothetical protein MGC26988	K.EAAAAGAAAGAATGTVAG.A	Q8IYT1	1	2.525	2
Similar to leucine zipper protein FKSG14 (P33)	P.YVELLLR.N	Q9BS16	4	2.4892	2
Similar to leucine-rich neuronal protein	N.LPGVHCGPSSGAGPGFGPGSW.S	Q96I18	1	2.7274	2
Similar to opioid growth factor receptor	N.DNQDNENPGNTNCHDVV.L	Q8NEQ4	1	2.6838	2
Similar to protease, serine, 8 (Prostasin) (Fragment)	R.PVPLSARVQPVCLPVP.G	Q8N171	1	2.8921	2
Similar to protein phosphatase 1, regulatory (inhibitor) subunit	L.VEHLLELLQK.K	Q8N179	1	2.4289	2
Similar to putative	G.HTVTLTLTYLFIKEY.S	Q8NHU3	1	2.5384	2
Similar to regulatory factor X, 4	Q.CMYGTSNQYPAQETL.D	Q8HWS3	1	3.2101	2
Similar to RIKEN cDNA 0610037N03 gene	L.GKENSWKPR.L.P	Q9BSE9	1	2.1571	1
Similar to RIKEN cDNA 1110014F24 gene (Fragment)	Y.FSRLWEDF.K	Q9BSY6	2	2.4966	2
Similar to RIKEN cDNA 2210017A09 gene	K.GLAEEVKSRWEK.E	Q8WVVF5	3	2.9673	2
Similar to RIKEN cDNA 2310014B08 gene (Fragment)	G.SCLLLGGFSLALSFAFW.C	Q96B33	1	2.4652	2
Similar to RIKEN cDNA 2410127L17 gene	Y.QPIKEILKNFPK.E	Q8N4J0	1	2.4011	2
Similar to RIKEN cDNA 2610017G09 gene	A.AWDALIVR.P	Q9BRR6	1	2.5324	2
Similar to RIKEN cDNA 2810049G06 gene	I.TWIVTQVAISY.T	Q96KY4	1	2.4325	2
Similar to RIKEN cDNA 2810405F18 gene	I.ELLANQYSIQVQVEDL.T	Q96CB9	2	2.5181	2

Supplementary Table 1 (continued)

Protein	Peptide ^a	Swiss-Prot Accession ^b	Peptide Count ^c	Xcorr ^d	Charge State ^e
SMF protein (Fragment)	E.EVGALITQSGAVQE.I	Q12766	2	3.0359	2
Sodium- and chloride-dependent taurine transporter	D.GIEDMIGYR.P	P31641	6	2.4274	2
Sodium bicarbonate cotransporter	M.QGVLESFLGTAVS.G V.LSITHVNSLK.L	O15153 O95233	1 1	3.1812 2.6351	2 2
Sodium/nucleoside cotransporter 1 (Na(+)/nucleoside)	Y.LADMTLSEVHVVMGTGGY.A	O00337	1	2.5407	2
Sodium/potassium/calcium exchanger 3	L.YGVFLCFSLM	Q9HC58	1	2.3913	2
Sodium/potassium-transporting ATPase α -1 chain	F.FVSIVVVQW.A	P05023	1	2.7097	2
Sodium/potassium-transporting ATPase α -4 chain	K.GAPERILEFCSTFLLNGQEY.S	Q13733	1	2.533	2
Sodium-dependent serotonin transporter (5HT transporter)	Y.SAVPSPGAGDDTR.H	P31645	1	2.4466	2
Solute carrier family 12 member 5	Q.SAPSCPSSSPGEEPEGEGETDPEK.V	Q9H2X9	1	2.4138	2
Solute carrier family 12 member 7	R.TLSRRSFDACVK.A	Q9Y666	2	2.9436	2
Solute carrier family 21 member 3	Y.IGLVETGAIIG.P	P46721	1	2.4178	2
Solute carrier family 21 member 9	R.RAVCRYNNNDL.L	O94956	1	2.5026	2
Solute carrier family 23, member 2	S.PTFVGYTWKGLRKSDN.S	Q9UGH3	3	3.0681	2
Solute carrier family 26 member 6 (Pendrin-like protein 1)	V.GNIPAGLVPPVA.P	Q9BXS9	1	3.0686	2
Sortilin 1	A.CVLGKIMYIFGGYEQ.Q	Q96GH7	1	2.4475	2
Sorting nexin 4	R.RYSEFELLR.S	O95219	1	2.3472	2
Source of immunodominant MHC-associated peptides	S.GGLSQPAGWQSL.L	Q8TCJ2	1	2.7635	2

SOX-13 protein (Type 1 diabetes autoantigen ICA12) S.QLALPIQPIPCPK.V	Q9UN79	1	2.4151	1
SOX-15 protein (SOX-20 protein) S.SSSGPQEREGA.G	O60248	1	2.4355	2
Sp110 nuclear body protein (Speckled 110 kDa) A.EEDSEEMPSLLTSTV.Q	Q9HB58	1	2.8075	2
Spectrin α chain, brain L.EAQSHFRKVEDLFLTFAKKASAF.N	Q13813	1	2.9413	2
Spectrin β chain, brain 1 V.QTKFMELLEPLNE.R	Q01082	1	3.14	2
Sperm membrane protein BS-63 S.FYQGLEYIGRSVHYWK.K	Q99666	1	2.4871	2
Splicing factor, arginine/serine-rich 5 R.SRSRSRSKRSRSVSRSP.V	Q13243	1	2.7201	2
Statherin A.DSSEKFL.R	P02808	1	2.2224	2
Steroid hormone receptor ERRI N.ALVSHLLVVEPEK.L	P11474	1	2.8693	2
Sterol regulatory element binding protein cleavage-activating P.VLSQAPEDEGGSEPK.G	Q12770	1	2.6603	2
Sterol regulatory element binding protein-2 (SREBP-2) S.LRRLAHSFRPAYR.K	Q12772	1	2.4275	2
Stress-70 protein, mitochondrial K.VQQTVQDLFGR.A	P38646	1	2.2248	2
Striatin 3 (Cell-cycle autoantigen SG2NA) (S/G2 antigen) D.EENDMIEGPEGKDKHRMNMKHKIG.N	Q13033	1	3.7522	3
Stromal interaction molecule 1 N.GSIGEETDSS.P	Q13586	1	2.6759	1
Succinate dehydrogenase [ubiquinone] flavoprotein subunit, A.KAWPTVLQ.T	P31040	1	2.4621	2
Sulfonylurea receptor 1 T.RVETTRRK.E	Q09428	1	2.5774	2
Synaptonemal complex protein 1 (SCP-1 protein) D.KVNQLEEK.T	Q15431	1	2.7568	2
Synaptosomal-associated protein 29 (SNAP-29) Q.YLQRQEVLRRAEATAA.S	O95721	1	2.5487	2
Syndecan-1 (SYND1) (CD138 antigen) V.AVEPDRRNQSPVDQ.G	P18827	1	2.77	2

(continued)

Supplementary Table 1 (continued)

Protein	Peptide ^a	Swiss-Prot Accession ^b	Peptide Count ^c	Xcorr ^d	Charge State ^e
Syndecan-2 (Fibroglycan)	P.KVETTTLNI.Q	P34741	1	2.7336	2
Syntaxin 8	E.KIQQRNQYERKGEKAP.K	Q9UNK0	1	2.389	1
TAFII40 protein (Fragment)	K.IKEFEDVDPKVKLKDGLVRKEKE	Q9BQS9	1	2.7377	2
Talin 1	A.ASLGAEDPETQVVL.I	Q9Y490	1	2.2588	2
Taste receptor type 2 member 10 (T2R10)	K.ILNDYKTK.N	Q9NYW0	1	2.5404	1
Taste receptor type 2 member 14 (T2R14)	G.SWCVSVFFPALF.A	Q9NYV8	1	2.9541	2
Taste receptor type 2 member 3 (T2R3)	H.KRAIRIILSFFFLF.L	Q9NYW6	2	2.224	1
TATA element modulatory factor (TMF)	K.ALLEEAFDNLKDE.M	P82094	1	2.6797	2
TBC1 domain family member 4	K.MKSLIRTLEQ.E	O60343	1	2.5496	2
T-brain-1 protein (T-box brain protein 1) (TBR-1) (TES-56)	R.RISPADTPVSESSPL.K	Q16650	1	2.7184	1
T-cell surface glycoprotein CD3 epsilon chain	W.QHNDKNIIGDE.D	P07766	2	2.6309	2
T-complex protein 1, δ subunit (TCP-1- δ) (CCT- δ)	K.MIQDGGKGDVTTNDGA.T	P50991	1	2.4246	2
Telomerase-associated protein TP-1	R.VNNSNCLLSEPP.S	Q99973	1	2.9339	2
Tensin 3	E.RLAPGTRRGLSAQ.E	Q8IZW7	1	2.2837	1
Tesmin (Metallothionein-like 5, testis-specific)	Q.MLCIDNSRTRELKALHLV.P	Q9Y4I5	2	4.2081	2
Testis-specific adriamycin sensitivity protein	G.YSFLSLY.R	Q9NS86	1	2.3742	1
Tetranectin (TN)	R.LDTLAQEVALIK.E	P05452	1	2.6208	2

Tetrodotoxin-resistant voltage-gated sodium channel					
	K.QIAAKQGTKKAR.E				
TGF- β receptor type I (EC 2.7.1.37) (TGFR-1)					
	A.AAAAAALLPGA.T	1	2.4867	2	
THAP domain protein 1					
	L.EKLKEVVHFQKEKDDVSEYGY.V	1	2.5077	2	
THEG protein (Testicular haploid expressed gene)					
	G.PEDPEEELPPEE.V	1	3.0214	2	
Thioredoxin-dependent peroxide reductase, mitochondrial					
	F.KDLSLDDDFK.G	1	2.528	2	
	E.FKDLSLDDDFK.G	36	2.6402	2	
Thioredoxin-like protein					
	P.TFLFFK.N	1	2.5753	2	
Thymopoietin, isoform α (TP α)					
	V.SSREATQILSVPKVDDE.I	1	2.8232	2	
Thymus-specific serine protease (EC 3.4.-.-)					
	V.WLAQWLGPLLLVSLW.G	1	2.8826	2	
Thyroglobulin					
	V.DPSIRHFDVAHVSTAA.T	2	2.6669	2	
Thyroid hormone receptor α (C-erbA- α) (c-erbA-1)					
	K.PSKVECGSDPEENSARS.P	1	3.0209	2	
Thyroid hormone receptor-associated protein complex 100					
	D.CTNFLLQECGK.Q	1	2.4542	2	
Thyroid hormone receptor-associated protein complex 240					
	F.I LAPVKDKQTEL.G.E	1	2.6392	2	
Thyroliberin (Thyrotropin releasing hormone) (TRH)					
	V.EEEEEEGGAVGPHKRQ.H	1	2.5278	2	
Thyroxine-binding globulin (T4-binding globulin)					
	K.NALALFVLPK.E	1	2.5162	2	
Tight junction protein ZO-1 (Zonula occludens 1 protein)					
	G.GVLSSEITGVSHI.P	1	2.6547	2	
Tight junction protein ZO-2 (Zonula occludens 2 protein)					
	R.DNAGDRADFW.R	1	2.4206	2	
Titin					
	E.EKVLVAVTKKEAPPKA.R	1	2.5971	2	
	E.EIVPEEEVLPPEE.E	1	3.8064	2	
	V.LEEKVSVAFRQEV.V	1	2.3421	2	
	Q.QAIPDSTVEFKA.I	2	2.5622	2	

(continued)

Supplementary Table 1 (continued)

Protein	Peptide ^e	Swiss-Prot Accession ^b	Peptide Count ^f	Xcorr ^d	Charge State ^e
Titin fetal isoform (Fragment)	V.VPEKKKVPVPPPKKPEVPPPTKVPKVPKVA.V.P	Q8WZ42	2	3.9008	3
	V.HKLTITADV.R.A	Q8WZ42	1	2.6629	2
Titin Z-disc (Fragment)	A.SKEVIREEKVPLAPPKEPE	Q8WZ50	2	2.5663	2
	K.VPEALQEIIVPEKKTL.V	Q8WZ50	1	2.7658	2
	T.TRGIFPEVEPPEA.IPE.I	Q8WZ50	1	3.1555	2
T-lymphocyte surface antigen Ly-9 (Lymphocyte)	K.EAEKTA.VTKVVVAADK.A	Q92762	1	2.6574	2
	Y.EVFDQV.TQEGAG.H	Q9HBG7	1	2.5509	2
T-lymphoma invasion and metastasis inducing protein 1	F.LIENKMQLYVPQPEEDIVYELLYKELE	Q13009	1	3.8712	3
	Y.RQMDLQ.TPDSHL.R.Q	Q9NRV3	1	2.6315	2
TNF receptor associated factor 1	M.KEKLLAELEGG.K.L	Q13077	1	2.6457	2
Toll-like receptor 5	R.IANIQDAI.WNSRK.I	O60602	1	2.6799	2
Transcription elongation factor Elongin A3	G.DGGSVSGGGSSNR.H	Q8NG57	1	2.4436	2
	Q.DKD.VNEGETSDG.VRK.S	Q9Y5Q9	1	3.2655	2
Transcription factor III C90	D.GKVRQ.VIPIFTDVA.L	Q9UKN8	1	2.9354	2
Transcription factor RelB (I-Rel)	D.FFSGTV.SLP.G	Q01201	1	2.2607	1
Transcription factor-like protein MIRGX	R.GQQSA.EEENFKKPT.R	Q15014	1	2.7287	2
	- .MAAPLLH.TRLP.GDAAA.S	Q9H4F0	1	2.5418	2
Transcription initiation factor TFIID 100 kDa subunit	T.NNGPN.GGGGNV.A	Q15542	1	2.2735	1
Transcription initiation factor TFIID 55 kDa subunit (TAFII-55)	Q.KQIDNM.KGKIQE.T	Q15545	1	2.9982	1

Transcription initiation factor TFIID 70 kDa subunit (TAFII-70) E.EKEVDLSDIINTPLPR.V	P49848	1	2.974	2
Transcription intermediary factor 1- α (TIF1- α) A.SAAAASGGPSAAPS	O15164	3	2.9144	2
Transcriptional repressor CTCFL (CCCTC-binding factor) L.ELMPEKGLKEEK.K	Q8NI51	1	2.4118	1
Transforming acidic coiled-coil-containing protein 1 K.ICDELIAKLGKTD.-	O75410	1	2.6635	2
Transforming acidic coiled-coil-containing protein 2 K.AGNSCEPELVPSRRSK.L	O75410	1	1.9926	1
Transforming acidic coiled-coil-containing protein 2 P.PPPPEVIPEPEVSTQPPPEEPGCGSETVVPVDPGPR.S	O95359	1	2.4276	2
Transgelin 2 (SM22- α homolog) V.ARDDGLFSGDPNWFPPKK.S	P37802	1	3.0173	2
Transitional EPITHELIA response protein L.LVGC AVAVLAV.H	Q9Y5Z9	2	3.0804	2
Transmembrane cochlear-expressed protein 2 K.KIQVLRVEVE.K	Q8TDI7	1	2.5057	2
Transmembrane protease, serine 4 (EC 3.4.21.-) T.FRKVGPIII.A	Q9NRS4	1	2.4867	2
Transthyretin (Prealbumin) (TBPA) (TTR) (ATTR) K.AAADDTWEPFASGK.T	P02766	6	4.1857	2
Transthyretin (Prealbumin) (TBPA) (TTR) (ATTR) K.TSESGELHGLTTEEEFVEGIYKVEIDTK.S	P02766	1	4.2219	2
Transthyretin (Prealbumin) (TBPA) (TTR) (ATTR) R.KAADDTWEPFASGK.T	P02766	4	4.5456	2
Transthyretin (Prealbumin) (TBPA) (TTR) (ATTR) R.RYTIAALLSPYSYSTTAVVTNPK.E	P02766	1	5.0544	2
Triadin K.GTSEVTESGKKK.T	Q13061	1	2.3366	2
Tripartite motif protein 15 (Zinc finger protein B7) V.ETAFERLQQELEQQ.R	Q9C019	1	2.4086	2
Tripeptidyl-peptidase II (EC 3.4.14.10) (TPP-II) K.PLGSRDVLPNNRQL.Y	P29144	2	2.9988	2
Tripin K.ENNLENEKMKVKNK.P	Q8IZK1	1	2.2188	2
Triple homeobox 1 protein T.VTSVPKQPGVAPLN	Q9H4I2	1	2.5015	2
Trophinin S.AGFGGALNTNASFGCAVST.S	Q12816	1	3.0144	2
Tuberin (Tuberous sclerosis 2 protein) A.LFFKVIK.D	P49815	1	2.4878	2

(continued)

Supplementary Table 1 (continued)

Protein	Peptide ^a	Swiss-Prot Accession ^b	Peptide Count ^c	Xcorr ^d	Charge State ^e
Tubulin α -1 chain (α -tubulin 1)	T.VIDEVRTIGTY.R	P05209	2	2.4574	2
Tubulin-specific chaperone C (Tubulin-folding cofactor C)	L.LERAESEVERLEE.A	Q15814	13	2.6337	2
TUBULOINTERSTITIAL NEPHRITIS antigen-related protein	Y.LGAICYCDLFCNRIVSD.C	Q9GZM7	1	2.5505	2
Tumor necrosis factor receptor superfamily member Fn14	A.LSLTFVLGLSGFLVWR.R	Q9NP84	1	3.5492	2
Tumor necrosis factor receptor superfamily member XEDAR	F.TMACTSESHSH.W	Q9HAV5	1	2.5449	2
Tumor necrosis factor receptor type 1 associated DEATH	E.ELAELEDALR.N	Q15628	1	2.5394	2
Tumor suppressor p53-binding protein 1	I.FIPSPSLEEQSNDG.K	Q12888	1	2.4352	2
Type I transmembrane receptor	I.QVQTLNLSQEE.E	Q9UJ47	4	2.4625	1
Type IIc Na ⁺ /Pi cotransporter (Hypothetical protein FLJ38680)	T.DPWTLPLQKDKTSQPW.K	Q8N130	1	2.9532	2
Tyrosine-protein kinase receptor Tie-1	L.KMNAAIKML.K	P35590	1	2.1605	1
Tyrosine-protein kinase receptor UFO (EC	P.QDRPSFTELREDLE	P30530	1	2.5225	2
U5 snRNP 100 kDa protein	G.ELADKDRDA.S	O43188	3	2.5245	2
Ubiquitin carboxyl-terminal hydrolase 10 (EC 3.1.2.15)	I.SSTLNPQAPEFI	Q14694	1	2.4219	2
Ubiquitin carboxyl-terminal hydrolase 24 (EC 3.1.2.15)	P.PISIAPSSPLLPL.H	Q9UPU5	2	2.5867	2
Ubiquitin carboxyl-terminal hydrolase 25 (EC 3.1.2.15)	A.RLVKLAQEDTPPETDY.R	Q9UHP3	1	2.4768	2
Ubiquitin conjugation factor E4 A	L.LKTPGVVENHG.Y	Q14139	24	2.4569	2
Ubiquitin-activating enzyme E1 (A1S9 protein)	K.ISFKSLVASL.A	P22314	1	2.5135	2

Ubiquitin-protein ligase E3A (EC 6.3.2.-) V.SKEFFQLVVEE.I	Q05086	1	2.4546	2
Ubiquitin—protein ligase EDD (EC 6.3.2.-) T.VGTQVCLRNPNLYHAGAVAFSISAGIPK.V	O95071	1	2.7194	2
UDP-GaINAc:polypeptide <i>N</i> -acetyl galactosaminyltransferase R.SRGISSECLDYNSPDNNPTG.A	O00208	1	2.5949	2
UDP-GaINAc:polypeptide <i>N</i> -acetyl galactosaminyltransferase W.YLNNIYPEVYVPDLN.P	Q14435	3	2.9917	2
UDP-glucose:glycoprotein glucosyltransferase 1 S.MNYLTKKGMSSK.E	Q9NYU2	1	2.9609	2
UDP-glucose:glycoprotein glucosyltransferase 2 K.VWELQDLSFQAASQIMSTPVYD.A	Q9NYU1	1	2.418	2
UDP-glucuronosyltransferase 1-7, microsomal L.LLGFSDAMTFKERV.W	Q9HAW7	1	2.4397	2
UDP- <i>N</i> -acetylglucosamine-2-epimerase S.QDIDHILETLA.L	Q9Y223	1	2.4435	2
ULBP1 protein (ALCAN-β) (Retinoic acid early transcript 1) E.VQGLVDERPFLHYDCV.N	Q9BZM6	1	2.5731	2
Unc-119 protein homolog (Retinal protein 4) (HRG4) Y.DPPPLSEELISE.M	Q13432	1	2.4414	2
Unc-93 related protein M.LLVLGLCGAAYRPTEEIDL.R	Q9H1C4	1	4.7339	3
Urea transporter UT-A1 R.KDDGVAHR.D	Q96PH5	1	1.9622	1
Uromodulin (Tamm-Horsfall urinary glycoprotein) F.ALLMTNCYATPSSNA.T	P07911	1	2.4672	2
Uroporphyrinogen-III synthase (EC 4.2.1.75) (UROS) K.SVYVVG NATASLYSKIGLD.T	P10746	1	2.4584	2
UTP—glucose-1-phosphate uridylyltransferase 1 (EC 2.7.7.9) L.LDTFLEEGKEYIF.V	Q07131	1	2.4088	1
Uveal autoantigen Q.TLQKEIEKVYLDNKLLK.E	Q9BZF9	14	2.6899	2
V(D)J recombination activating protein 1 (RAG-1) S.CDICNTARRGLKRKSLQPNLQLSKLKLK.T	P15918	1	3.8467	3
Vacuolar ATP synthase subunit H (EC 3.6.3.14) (V-ATPase H) I.LTKLLEVSDDPQVLA.V	Q9UII2	1	2.6539	2
Vacuolar proton pump 116 kDa accessory subunit A.LKQSFLELTELK.Y	Q9HBG4	1	2.4288	2

(continued)

Supplementary Table 1 (continued)

Protein	Peptide ^e	Swiss-Prot Accession ^b	Peptide Count ^f	Xcorr ^d	Charge State ^e	
Very long-chain acyl-CoA synthetase homolog 1	G.RIGAIGRTNLFYKLLSTFDLI	Q9Y2P4	3	4.5431	3	
	F.EKAENSSLNLJGK.A	P46459	1	2.7272	2	
Vesicle-fusing ATPase (EC 3.6.4.6)	K.KSNDSPYDIDK.M	P46459	1	1.9378	1	
	G.TLVTVSSASTK.G	Q9Y509	9	2.883	2	
VH3 protein (Fragment)	Q.GTLVTVSSASTK.G	Q9Y509	15	2.6799	2	
	W.GQGTLVTVSSASTK.G	Q9Y509	6	2.7864	2	
	R.VTISVDTSK.N	O95973	1	1.9445	1	
Vinculin (Metavinculin)	D.TEAMKRALASIDSK.L	P18206	1	2.4261	2	
Vitamin D-binding protein (DBP)	K.ELSSFIDK.G	P02774	4	2.165	1	
	K.VPTADLEDVLP LAEDITNILSK.C	P02774	5	2.2519	2	
	K.FPSGTFEQVSQLVK.E	P02774	3	2.483	2	
	K.HLSLLTTLNLR.V	P02774	12	2.938	2	
	K.KELSSFIDK.G	P02774	2	2.7126	2	
	K.LCDNLSTK.N	P02774	1	1.9832	1	
	L.PLAEDITNILSK.C	P02774	1	2.6748	1	
	K.YTFELSR.R	P02774	1	1.9585	1	
	R.VCSQYAAAYGEK.K	P02774	1	2.8862	2	
	R.THLPEVFLSK.V	P02774	30	2.5169	2	
	Vitamin K-dependent protein S	K.IETISHEDLQR.Q	P07225	1	3.2217	2
		K.VYFAGRPR.K	P07225	1	2.2473	2
		R.NNLELSTPLK.I	P07225	1	2.2884	2
	Vitronectin (Serum spreading factor) (S-protein)	G.PIDAAFTIR.I	P04004	1	2.5102	2
		E.GPIDAAFTIR.I	P04004	2	2.5678	2
		E.DGVLDPDYPR.N	P04004	1	2.7643	2
K.AVRPGYPK.L		P04004	3	2.2912	2	
R.VDTVDPYPR.S		P04004	2	2.8167	2	
R.DVWVGIEGPIDAAFTIR.I		P04004	1	3.7382	2	

	R.SIAQYWLGCPAPGHL.-	P04004	1	3.2347	2
	R.FEDGVLDPDYPR.N	P04004	11	2.9316	2
	R.DWHGVPQGQVDAAMAGR.I	P04004	1	3.2158	2
Voltage-dependent calcium channel γ -8 subunit	V.RASSIFPILSAILL	Q8WXS5	1	2.5263	2
Voltage-dependent L-type calcium channel α -1F subunit	K.HKTVAVASAQRS.S	O60840	1	2.2868	2
Voltage-gated calcium channel $\alpha(2)\delta$ -4 subunit	D.GAVEDYEPVFEK.Y	Q8IZS9	1	2.4891	2
Von Willebrand factor (vWF)	K.VIVIPVGIGPHANLK.Q	P04275	1	2.4553	2
VPS10 domain-containing receptor SorCS1	E.RARGTGASMAVAAR.S	Q8WY21	1	2.4231	2
VPS10 domain-containing receptor SorCS3	A.VFPGLP TSAELFILPPK.N	Q9UPU3	1	2.4664	2
VRK1	V.VKVEPSDNGP.L	Q99986	1	2.4935	2
WD repeat domain 11 protein (Fragment)	R.KNKIYSINPK.K	Q8WWQ0	1	2.2513	2
WD-repeat protein 21	I.DRPGMLCSFRIPGA.W	Q8WV16	1	2.2799	2
Wee1-like protein kinase (EC 2.7.1.112) (WEE1hu)	M.KSRYTTEFHELEKIGSERG	P30291	1	3.3044	2
Wnt-1 proto-oncogene protein	I.FAITSAGVTHSVARSCSEGS.IE	P04628	1	2.3768	2
WUGSC:H_DJ0751H13.1 protein (Fragment)	C.HCALPGENQTVQPMATPA.A	O75851	1	2.5051	2
WUGSC:H_RG015P03.1 protein (Fragment)	E.RLKQIKIPDIQILNEKV.C	Q9Y6U6	1	2.6856	2
XG glycoprotein (Protein PBDX)	I.YPKPKPPYYPQENPDSG.G	P55808	1	2.4266	2
X-kinase	L.IEEAAKMKKI.K	Q8NFD2	1	2.2001	2
X-like 1 protein	A.IASSHDVQELDVSGILATQVYT.W	Q9Y485	2	2.4652	2
Xylosyltransferase I (EC 2.4.2.26) (Fragment)	W.TAMDICATGPTAC.P	Q9H1B6	3	2.5892	2
Zinc finger and BTB domain containing protein 1	K.QNSKMI FGV RMYE.D	Q9Y2K1	2	3.1442	2

(continued)

Supplementary Table 1 (continued)

Protein	Peptide ^a	Swiss-Prot Accession ^b	Peptide Count ^c	Xcorr ^d	Charge State ^e
Zinc finger DHHC domain containing protein 8	V.YDAPSSYSLQQ.A	Q9ULC8	1	2.5384	2
Zinc finger protein	S.ILTAGMQEQESSGPQLE.T.V	O95625	1	3.9003	3
Zinc finger protein 117 (Zinc finger protein HFP9) (Fragment)	K.LYKCEECGKAFNSSNL.T	Q03924	1	2.506	2
Zinc finger protein 208	F.NRSAILIKHK.R	O43345	1	2.4712	2
Zinc finger protein 228	E.DIMKVS.L.L	Q9UJU3	1	2.2496	1
Zinc finger protein 234 (Zinc finger protein HZF4) (Fragment)	Y.QDVMLENFRNLLSVGHHPFKHDV.F	Q14588	1	3.9568	3
Zinc finger protein 271 (Zinc finger protein HZF7)	S.DGENKTKIGKPASEE.G	Q14591	1	2.2314	1
Zinc finger protein 272 (Zinc finger protein HZF8) (Fragment)	R.RSPLTRHQR.I	Q14592	1	2.2283	2
Zinc finger protein 294	N.DQLIPFIDAVLK.D	O94822	1	2.4703	2
Zinc finger protein 42 (Myeloid zinc finger 1) (MZF-1)	A.LVDGLRRPPGG.P	P28698	1	2.5421	2
Zinc finger protein 6	M.VYMAVKDSSQEEDDI.S	Q9Y462	1	2.5665	2
Zinc finger protein GLL3	V.QDCVSGVDSPTMVSEEV.L.V	Q9Y462	1	3.4986	2
Zinc finger protein HIRX (ALL-1) (Trithorax-like protein)	K.VPHGPGDFDAP.G	P10071	1	2.486	2
Zinc- α -2-glycoprotein (Zn- α -2-glycoprotein)	A.GQVAVLPEVQVT.Q	Q03164	1	2.7056	2
Zinc-finger helicase	D.PPSVVVTSHQAPGEK.K	P25311	7	3.8944	3
	K.AREDIFMETLK.D	P25311	1	3.8465	2
	E.RPEGETGDLGKRE	Q9Y410	1	2.4184	1

ZYG homologue						
14-3-3 protein eta (Protein AS1)	I.EHCSNFKEENMDT.S	O00156	1	2.5284	1	
150 kDa oxygen-regulated protein (Orp150)	D.REQLLQR.A	Q04917	1	2.4934	2	
180 kDa transmembrane PLA2 receptor	G.EQVELKEEAEPVEDGSGQPPPEPKGDA.T M.DQIFTEVEMTTLEKVL.N	Q9Y4L1 Q9Y4L1	1 1	2.4267 2.7068	2 2	
1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase	K.QPVENQE.K	Q13018	4	2.4235	1	
1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase	E.EPFVFEKILMPEL.A	Q00722	2	3.3143	2	
265 proteasome non-ATPase regulatory subunit 11	N.FQTLDVAMQLNAGVFE	Q01970	1	2.4052	2	
265 proteasome non-ATPase regulatory subunit 2	D.IQENDEEAVQVKE.Q	O00231	1	4.1121	2	
3'-5' exonuclease TREX2-like protein	F.AMGMVGSGTNNAR.L	Q13200	1	2.4579	2	
40 kDa peptidyl-prolyl cis-trans isomerase (EC 5.2.1.8)	C.DLLMEIEQVDMLEKIDIDE	Q13200	3	3.9041	3	
43 kDa receptor-associated protein of the synapse (RAPSYN)	L.SSEGLARCRKAGFDGA.V	Q9BQ50	1	2.6104	2	
52 kDa repressor of the inhibitor of the protein kinase	K.YAEVLRVVDSSKAVIE.T	Q08752	1	2.5893	2	
55 kDa erythrocyte membrane protein (p55)	K.GLQLYQSNQTEKALQV.W	Q13702	1	2.7615	2	
5-hydroxytryptamine 2B receptor (5-HT-2B)	G.LNMEYCR.G	O43422	1	2.6228	2	
5-hydroxytryptamine 4 receptor (5-HT-4) (Serotonin receptor)	K.KDNLIPCKEAGLK.F	Q00013	1	2.7915	2	
5'-nucleotidase (EC 3.1.3.5) (Ecto-5'-nucleotidase)	R.TSTIGKKSQVQTISNEQ.R	P41595	1	2.6535	2	
60S ribosomal protein L5	L.GGCWVVIPTFISF.L K.VRGVDVVVGGHSNTFLY.T D.PLKMDEVYKVLPNFL.A E.FNAEVHRKHMGMQN.V	Q13639 P21589 P21589 P46777	1 1 1 1	2.5467 2.4808 2.4639 3.3221	2 2 2 2	

(continued)

Supplementary Table 1 (continued)

Protein	Peptide ^a	Swiss-Prot Accession ^b	Peptide Count ^c	Xcorr ^d	Charge State ^e
60S ribosomal protein L7a (Surfeit locus protein 3)	R.QTATQLLK.L	P11518	1	2.2646	2
7-dehydrocholesterol reductase (EC 1.3.1.21)	P.VVDIVTGHARLS	Q9UBM7	4	2.9046	2

^aSequences of the peptides identified by tandem MS are bracketed by periods, outside of which are the residues immediately N and C terminal to the identified peptide.

^bSwiss-Prot protein accession references.

^cNumber of times a peptide was identified in the 140 [__LC-MS/MS analyses.

^dSEQUEST cross correlation score.

^eCharge state of the peptide molecular ion chosen for tandem MS.

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