Quantitative proteome analysis of human neuroblastoma cells treated with *Clostridium botulinum* C3 exoenzyme

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Marika Victoria Mützelburg Hannover, den 01.09.2008

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Poster

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Muetzelburg, M.V., Muehlenstaedt, C., Just, I., Pich, A. (2008) Toxicoproteomics: C3 exoenzyme affects protein profile of a human neuroblastoma cell line. *Tagung der Deutschen Gesellschaft für experimentelle und klinische Pharmakologie und Toxikologie (DGPT)*

Vorträge

11-2007	Vortrag im Rahmen des Massenspektrometrie Forums Hannover „Heavy Isotopes for Quantitative Proteomics“
12-2006	Vortrag im Rahmen der Veranstaltung Basic Biological Questioner an der MHH „Quantitative Proteomics using ICPL™“
09-2005	eingeladener Vortrag auf dem Beckman Coulter User Meeting „Trennung isomerer Phosphopeptide mittels Kapillarzonenelektrophorese“
07-2004	Vortrag im Rahmen des Studierendenkollegs am Department of Chemistry and Biochemistry der Ohio University, Athens, Ohio, USA „Derivatization of amine-containing drugs using Cy5™-NHS monoreactive Dye for capillary electrophoresis and microfluidic devices”

Zusammenfassung

C3 Exoenzyme sind ADP-Ribosyltransferasen, die spezifisch die Rho-GTPasen RhoA, B und C modifizieren und damit inaktivieren. Rho-GTPasen sind molekulare „Schalter“, welche eine Vielzahl von Signalwegen in eukaryotischen Zellen kontrollieren. Die spezifische Inaktivierung der Rho-GTPasen führt zu einer Reorganisation des Aktinzytoskeletts und aller aktinabhängigen Zellfunktionen. In den letzten Jahren konnte eine Beteiligung der Rho-GTPasen an der neuronalen Entwicklung gezeigt werden. Die Zugabe von C3 aus Clostridium botulinum (C3*bot*) zu Hippocampuszellen resultiert in einem gesteigerten Auswachsen und einer verstärkten Verzweigung der Axone. Zur Aufklärung dieser C3*bot*-induzierten Wirkungen wurde mittels eines quantitativen Proteomic-Ansatzes das Proteinprofil von C3bot-behandelten mit unbehandelten humanen Neuroblastomzellen (SH-SY5Y) verglichen. Dazu wurden die zellulären Proteine mit „Isotope Coded Protein Label“ (ICPL™) bzw. die nach tryptischer Spaltung erhltenen Peptide mit „isobaric tags for relative and absolute quantification“ (iTRAQ™) markiert, mittels Gelelektrophorese- und Flüssigchromatographie-basierter Techniken getrennt und massenspektrometrisch analysiert.

In ersten Experimenten wurde ein Proteinprofil der SH-SY5Y Zellen mittels GeLC-MS/MS dargestellt und die Methodik optimiert. Mit der Reduzierung der Probenkomplexität auf Proteinebene konnten die Identifizierungsraten gesteigert und bis zu 3399 verschiedene Proteine identifiziert werden. Bislang existieren kaum Angaben über die Reproduzierbarkeit quantitativer Techniken für biologische Systeme. Daher wurde das ICPL™-Markierungsexperiment doppelt durchgeführt und eine durchschnittliche Variation von unter 30% bestimmt. Auf diese Weise konnten 1466 Proteine identifiziert werden, von denen 777 mit ICPL™ markiert waren. Zur ICPL™-Technik wurde alternativ die iTRAQ™-Methodik eingesetzt. In diesem Ansatz wurde das komplette Proteom zunächst tryptisch gespalten und dann modifiziert. Es wurden 355 Proteine identifiziert, von denen 235 mit iTRAQ™ markiert und quantifiziert werden konnten. Die extrem hohe Probenkomplexität des Peptidgemisches war verantwortlich für die im Vergleich zum ICPL™-Ansatz zu geringere Identifizierungsrate.

Insgesamt wurden 1774 verschiedene Proteine in beiden Experimenten identifiziert, von denen 417 Proteine, durch C3bot-Behandlung in ihrer Konzentration signifikant verändert wurden. Diese Proteine sind im Wesentlichen an zellulären Wachstumsprozessen, DNA-/RNA-Prozessierung sowie Zellzyklus und Organisation des Aktinzytoskeletts beteiligt. Die erhaltenen Resultate lieferten neue Ansatzpunkte für die weitere Erforschung der Wirkung des C3*bot* Exoenzyms auf neuronale Zellen.

Schlagworte: quantitative Proteomanalyse, Massenspektrometrie, C3*bot* Exoenzym

Abstract

The C3 exoenzymes are ADP-ribosyltransferases, which inactivate the GTPases RhoA, B, and C. Rho-GTPases are molecular switches that control a variety of signal transduction pathways in eukaryotic cells. The specific inactivation of Rho-GTPases results in reorganization of the actin cytoskeleton. Evidence that neuronal growth depends on inactivation of Rho-GTPases arises in the last years. Recently, it has been shown that C3 exoenzyme of Clostridium botulinum (C3*bot*) exhibits neurotrophic effects on neuronal cells. To further investigate this observation a large scale quantitative proteomic approach has been chosen to elucidate the protein expression profile of C3bot-treated versus untreated neuroblastoma SH-SY5Y cells. To reveal the altered protein abundance between C3*bot*-treated and untreated SH-SY5Y cells, isotope-coded protein label (ICPL™) as well as isobaric tags for relative and absolute quantitation (iTRAQ™) were applied for protein and peptide labeling, respectively, and the labeled mixtures were separated by gel-electrophoresis and liquid chromatography-based techniques, subsequently followed by MALDI mass analysis.

Starting experiments include profiling of the SH-SY5Y cells and the GeLC-MS/MS method was established. Previous results showed that a reduced complexity at protein level leads to an identification of up to 3399 different proteins. Since, only few reports exist that describe the reproducibility of stable isotope based quantitative proteomic methods for biological systems, the ICPL™ labeling was performed twice and an overall variation of below 30% was determined. Thus, with ICPL™ labeling up to 1466 proteins have been identified and out of them 777 where found labeled with the tagging reagent. Additionally to the ICPL™-approach the alternative iTRAQ™ technique was applied. With this method 355 proteins were identified and 235 out of them were found labeled with iTRAQ™ and could be quantified. Due to the labeling on peptide level after tryptic digestion of the proteins an extremely complex peptide mixture was produced, which resulted in a minor identification rate compared to the ICPL™ technique.

The analysis applying both the ICPL™, and the iTRAQ™ approach resulted in an overall amount of 1774 identified proteins of which a variety of about 417 different proteins was found regulated with distinct factors in C3bot-treated cells. Several proteins involved in growth factor signaling, DNA-/RNA-processing, cell cycle and actin cytoskeleton regulation were found with altered abundance. These results provide new starting-points for the investigation of C3*bot* effected neuronal cells.

Key words: quantitative proteomics, mass spectrometry, C3*bot* exoenzyme

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Abbreviations

2D	two-dimensional
2DE	two-dimensional gel-electrophoresis
ADP	Adenosine di-phosphate
BSA	bovine serum albumin
C.	*Clostridium*
C3*bot*	C3 exoenzyme derived from *Clostridium botulinum*
Cdk	cyclin-dependent kinases
CRMP-2	collapsing response mediator protein-2
DNA	deoxyribonucleic acid
Eel	electric power
Ekin	kinetic power
ER	endoplasmic reticulum
FA	formic acid
FCS	fetal calf serum
GAP	GTPase activating proteins
GAPDH	Glyceraldehyde-3-phosphate dehydrogenase
GDI	guanine nucleotide dissociation inhibitors
GDP	guanosine di-phosphate
GEF	guanine nucleotide exchange factors
GeLC	gel-electrophoresis coupled with liquid chromatography
GIST	global internal standard technology
GTP	guanosine tri-phosphate
GTPase	guanine nucleotide binding protein
HCCA	4-hydroxy-α-cyano cinnamic acid
H/L	heavy/light ratio
HPLC	high-performance liquid chromatography
ICAT	isotope-coded affinity tag
ICPL	isotope-coded protein label
iTRAQ	isobaric tags for relative and absolute quantitation
LC	liquid chromatography

LDH	lactate dehydrogenase
MALDI	matrix assisted laser desorption/ionization
MeCN	acetonitrile
MeOH	methanol
MS	mass spectrometry
MS/MS	tandem mass spectrometry
NAD	nicotinamide adenine dinucleotide
OVA	Ovalbumin
PAGE	polyacrylamide gel electrophoresis
RNA	ribonucleic acid
SC	sequence coverage
SD	standard deviation
SDS	sodium dodecyl sulfate
TFA	trifluoracetic acid
TOF	time-of-flight
UV	ultraviolet

1 Introduction

1.1 *Clostridium botulinum* and the C3 exoenzyme

The Gram-positive bacterium *Clostridium botulinum* produces the botulinum neurotoxin, which is the causative agent of botulism [1]. Serotype C coproduces also the C3 exoenzyme that exhibits ADP-ribosyltransferase activity. This exoenzyme has been discovered by Aktories et al. [2] and Rubin et al. [3] in the late 1980s. Just et al. identified the C3-like isoforms in *Clostridium limosum* [4, 5] and some years later also in *Bacillus cereus* [6], another Gram-positive microorganism. So far seven different C3 exoenzymes have been identified. Two isoforms are known from *C. botulinum*, three isoforms from *Staphylococus aureus* [7], one from *C. limosum,* and one from *B. cereus*.

C3-like exoenzymes are single-chain proteins with a molecular mass of about 25 kDa that transfer an ADP-ribose moiety from the co-substrate NAD^+ to asparagine-41 of RhoA, B or C [8] (Figure 1).

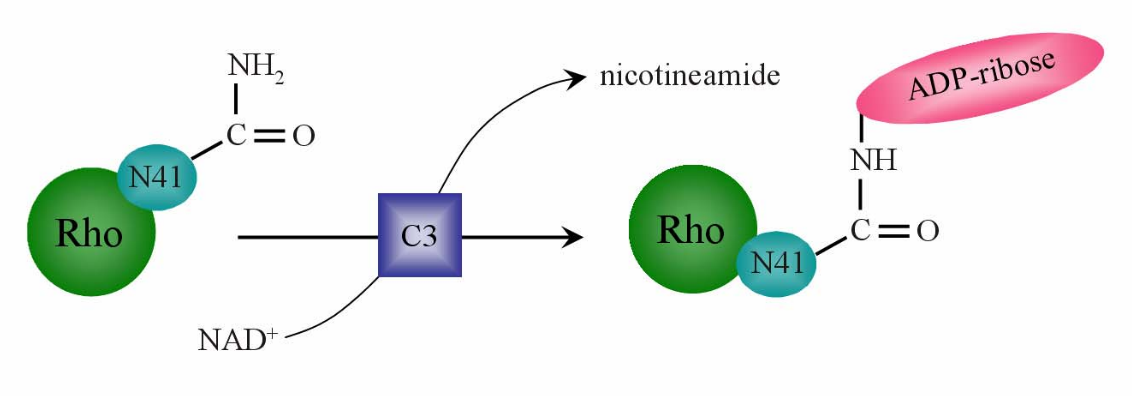


Figure 1. ADP-ribosylation of RhoA, B, or C. The transfer of the ADP-ribose moiety of NAD^+ to amino acid asparagin-41 will be catalyzed by C3 exoenzymes.

Important motives conserved in the exoenzyme are the ADP-ribosylation toxin-turn-turn (ARTT) loop, which is involved in the specific substrate recognition and is essential for the enzymatic activity and the phosphate-nicotineamide loop, which binds NAD [9].

Since C3 exoenzymes from *C. botulinum* selectively inactivate RhoA, B and C isoforms but not other members of Rho-family, they have frequently been used as tools for cell biological research [10]. Because of the absences of an apparent membrane binding and translocation domain, C3 has been classified as a mere exoenzyme and is therefore applied as cell permeable fusion toxin to enhance up-take in eukaryotic cells.

1.2 The small GTPases of the Rho-family

The Rho-family of low molecular weight guanine nucleotide (GTP)-binding proteins consists of the main subfamilies Rho (RhoA/B/C), Rac (Rac1/2/3 and RhoG), Cdc42 (Cdc42, Tc10, TCL, Wrch), Rnd (Rnd1/2/3 and RhoE), RhoD/Rif and RhoH/TTF. They belong to the Ras superfamily, which is composed of more than 150 members and has been divided into six families: Ras, Rho, Arf, Sar, Ran and Rab [11, 12].

The small GTP-binding proteins are nucleotide-driven signal transducers. In the GDP-bound form they are inactive and in the GTP-bound form they are active and competent for downstream signaling. Active GTPases interact with their specific downstream effector proteins to execute their cellular functions (Figure 2; p. 3). The GTP-GDP exchange reactions are regulated by guanine nucleotide exchange factors (GEFs) and guanine GTPase-activating proteins (GAPs); the inactive form is solubilized in the cytoplasm by guanine nucleotide dissociation inhibitors (GDIs).

Rho-GTPases are master regulators of the actin cytoskeleton and all cytoskeleton-associated functions [11] e.g. cell shape, morphogenesis, cell motility [13, 14], cytokinesis and trafficking [15, 16]. Small GTPases of the Rho-family are the major regulators of signaling pathways that link the extracellular growth factors or their receptors to the assembly of focal adhesions and associated structures [17-19]. Furthermore, Rho GTPases are also involved in the regulation of so-called stress-kinases such as p38-MAP-, c-Jun- and MAP-kinases. Specific inactivation of Rho-GTPases within the cell results in reorganization of the actin cytoskeleton and in some cases in cell death [20, 21].

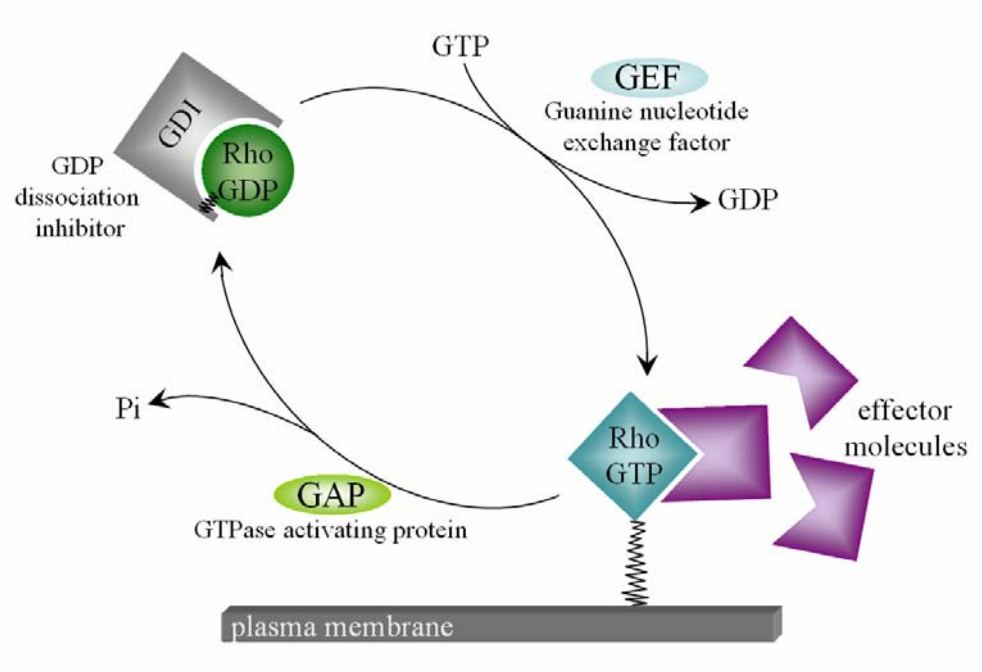


Figure 2. The GTPase molecular switch. GEFs release GDP from Rho-GTPases promoting the binding of GTP and thereby activation of Rho-GTPases. When bound to the cell membrane effector molecules can interact with the GTPase. GDI inhibits the dissociation of GDP from Rho-GTPases and thus prevents association of GDP-GTPase to cell membrane. GAPs stimulate the intrinsic GTPase activity of Rho-GTPases and convert GTP-bound form of Rho GTPases to inactive GDP-GTPases. In resting cells Rho-GTPases exist mostly in GDP-bound form and complexed with Rho-GDI in the cytoplasm.

Several lines of evidence have implicated that Rho-GTPases are involved in neuronal development [22-24]. The fact that neuronal growth depends on inactivation of Rho-GTPases was first described by Luo [25].

1.3 C3*bot* affects the small GTPases RhoA, B and C

The ADP-ribosylation of RhoA, B, or C at asparagine-41 renders the GTPases constitutively inactive (chapter 1.1, p.1) [26]. The functional consequences of the deactivation of Rho-GTPases are depicted in figure 3 (p. 4) and have been reviewed by Aktories and Just [21]. The major effect of ADP-ribosylation is the strong stabilization of the inactive form. Although, RhoA is ADP-ribosylated in the GDI-free state, this modification increases the affinity of the GTP-binding proteins to their GDIs [27] and inhibits the GEF mediated nucleotide exchange [28]. However, if GTP-bound RhoA is ADP-ribosylated it is still able to activate its effectors. Thus, the nucleotide binding is minor affected, the GAP-stimulated GTP hydrolase activity is still present. ADP-ribosylated Rho is entrapped by the GDIs in the cytoplasm to prevent signaling. Further reports describe the alteration of epithelial and endothelial barrier functions by Rho-inactivation [29, 30], the migration and signaling of immune cells including phagocytosis [31], the production of cytokines [32, 33], and adhesion [34] as well as de-adhesion [35].

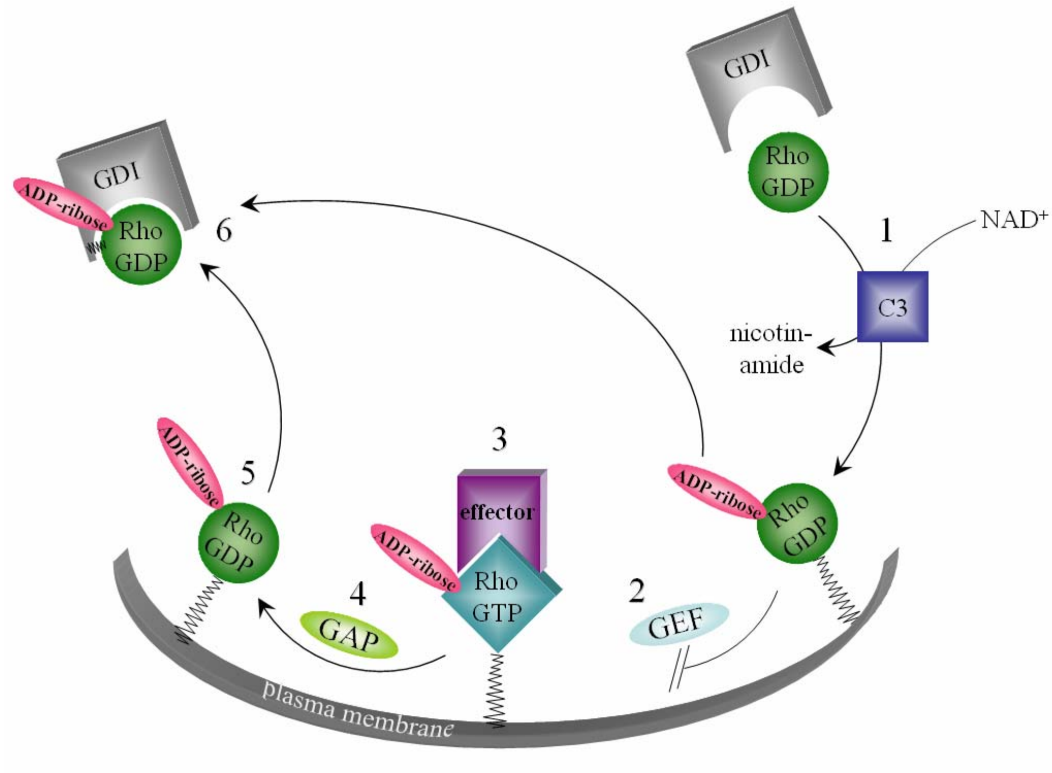


Figure 3. Consequences of the ADP-ribosylation of RhoA by C3*bot*. 1 RhoA is ADP-ribosylated by C3*bot* in the GDI-free form. **2** ADP-Ribosylation inhibits the activation of RhoA by GEF. **3** ADP-ribosylated Rho is still able to interact at least with some effectors such as kinases. **4** The GTP-hydrolysis is almost not affected by ADP-ribosylation. **5** ADP-ribosylation decreases membrane-binding of RhoA. **6** Binding of ADP-ribosylated RhoA to GDI is increased and RhoA resides in the inactive form in the cytoplasm.

Taken together, the inhibition of the activation of RhoA by GEFs and the binding of the ADP-ribosylated RhoA in the GDI-complex is most likely the basis of C3-induced blockade of Rho-dependent signaling, which leads to a dramatic redistribution of actin filaments and a depolymerization of stress fibers. Further studies showed that the C3 exoenzyme also binds with a high affinity to RalA, a small Ras GTPase; however, binding is not accompanied by Ral ADP-ribosylation [36, 37]. Cellular RalA functions are likely affected by C3-binding as Ral signaling to phospholipase D is inhibited.

Recently, another C3*bot* effect, which is independent of the ADP-ribosyltransferase activity, has been reported [38]. As previously described, Rho proteins regulate neurite outgrowth. The application of enzymatic active C3*bot* as well as the enzymatic inactive form promotes the axonal growth and branching in murine hippocampal neurons. Therefore, C3*bot* processes a novel neurotrophic function independent of its inherent transferase activity and has to be elucidated in further research.

1.4 Mass spectrometry and proteomics

Within the last 20 years, two main fields of research received central attraction in bioanalysis: genomics, the field of genome research and proteomics, which captures the examination of the totality of proteins in a cell, tissue or organism under defined conditions [39]. Whereas genes cover the construction plan of the cellular system, proteins are the effector molecules and liable for its realization and regulation. While the genome is rather constant, the proteome is highly dynamic and changes over time, differs from cell to cell and is constantly modified by its biochemical interactions. Genome analyses are already established and a lot of genomes have completely been sequenced and annotated. Today the challenge of research is proteome analysis because it gives a better understanding of a cell, tissue or an organism. Proteome analyses are not limited to the description of the protein composition of a given sample, but can be used to characterize and identify qualitative and quantitative changes in cellular protein patterns under certain conditions. Several protein identification techniques exist, but the most powerful to date is mass spectrometry (MS). MS started to become attractive for the analysis of large biological molecules with the establishment of the soft electrospray ionization (ESI) [40] and the matrix-assisted laser desorption/ionization (MALDI) [41, 42] developed by Fenn & Mann, Tanaka, and Karas & Hillenkamp in the late 1980s. These techniques eliminated the difficulties to transfer large molecules into the gas phase and subsequently ionize them.

1.4.1 MALDI - Matrix assisted laser desorption/ionization

One of the "soft ionization" techniques is MALDI. Sample molecules are co-crystalized with a matrix. To generate the gas phase and protonate the molecules the solids were irradiated by laser impulses (Figure 4, p. 7).

In this study a nitrogen laser operating at 337 nm with 50 Hz was used. Recently, Nd-YAG lasers with 1065 nm wavelength and repetition rates of up to 200 Hz were used. Commonly 4-hydroxy-α-cyano cinnamic acid (HCCA), dihydrobenzoic acid (DHB) or sinapinic acid were used to co-crystalize with the samples. Numerous variations of methods for MALDI sample preparation have been described [43, 44]. The best known is the dried-droplet method, where matrix and sample are mixed and subsequently spotted onto a MALDI target plate. More sensitivity is obtained by the thin-layer technique, where the sample is spotted on dried matrix to achieve a thin film which is sensitively ablated by the laser beam.

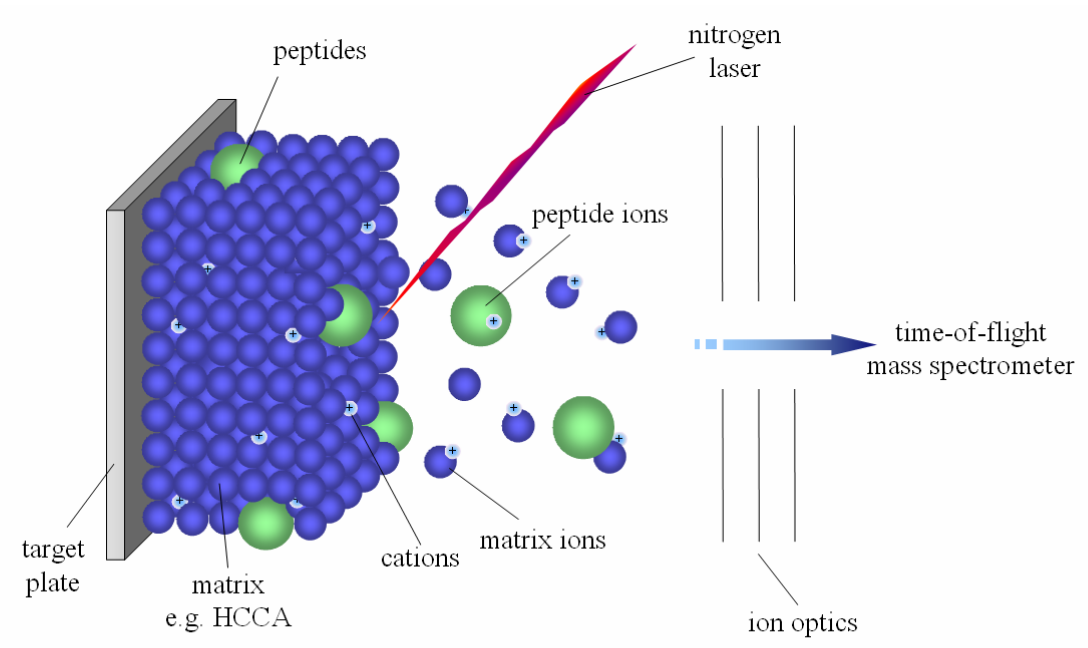


Figure 4. Matrix assisted laser desorption/ionization mechanism. Sample is prepared on a MALDI target. The sample molecules are surrounded by matrix molecules. Matrix could be e.g. 4-hydroxy-α-cyano cinnamic acid (HCCA). During laser irradiation the sample molecules evaporize and ionize. The ions are transferred by ion optics to a mass analyzer, accelerated and separated by e.g. time-of-flight mass spectrometry.

MALDI is often coupled to a time-of-flight (TOF) mass analyzer. The ionized molecules are transferred into the ion optics, accelerated to a fixed amount of energy by high voltage and separated according to their mass/charge (m/z) ratios in an evaporated flight tube: a MS spectrum is created.

The determination of the exact mass of a molecule is necessary for the identification of proteins. Proteins are degraded by action of proteases (e.g. trypsin) to peptides. The m/z values of these peptides can be determined according to the equations 1-3. Since each protein has its specific set of peptides, a so called peptide mass fingerprint is generated for a given protein.

$$(1)\qquad E_{el} = E_{kin} \qquad (2)\qquad z \cdot e \cdot U = \frac{1}{2}mv^2 \qquad (3)\qquad \frac{m}{z} = 2eU\frac{t^2}{s^2}$$

E_{el} electric energy, E_{kin} kinetic energy, z amount of charges, e elementary charge, U voltage, m molecular mass, v velocity, t time, s distance

For higher identification rates sequences of peptides can be obtained by tandem mass spectrometry (MS/MS). The application of higher energy during the acceleration process leads to a post source decay and a breakdown of the peptide backbone. The subsequent analysis of the obtained fragments leads to an adequate contingent of information to identify one specific peptide, and therefore identifies the protein of interest.

Several databases (MSDB, IPI human database, SwissProt) exist, which manage sequences of thousands of peptides and proteins. Search engines like Mascot use mass spectrometry data to identify proteins from primary sequence databases. The experimental mass values will be aligned with the calculated peptide mass or fragment ion mass values of the databases entries. By using a suitable scoring algorithm, the closest match or matches can be determined for the identification of the proteins.

1.4.2 Quantitative proteomics

The identification of intact proteins or their fragments on a proteome wide scale has widely been used to get specific insights into cell processes like signaling pathways or to compare samples taken under normal and diseased conditions to find biomarkers for specified diseases [39][45-47]. These studies require the ability to perform relative comparison of protein pattern from reference to control conditions. Although tools like cDNA microarrays are used to determine altered gene expression, the results often differ and do not correlate with protein abundance. That is affected by unequal concentrations of mRNA and proteins, degradation of proteins independent of mRNA levels or post-translational modifications of proteins like phosphorylation or glycosylation [48, 49]. Currently, there are several methods available to generate global quantitative protein profiles, including protein array-based quantitation [50], two-dimensional gel-electrophoresis (2DE) followed by MS analysis [51] or stable isotope labeling-based quantitations. Although, 2DE-MS is well established, quantitative determination is only possible if great affords are made due to the poor reproducibility of the 2D-gels. Additionally, certain protein groups like membrane proteins, very acidic or basic proteins and very small or excessively large proteins are difficult to analyze. To overcome some of the deficiencies of the 2D-gel based approaches non-gel-based quantitation techniques based on stable isotope labeling have been established.

Due to variability in ionization with MALDI and the influence of other ions in the sample the absolute signal intensity of a peptide ion measured in a MS run does not reflect the abundance of this peptide in the analyzed sample. Methods based on stable isotope labeling like isotope coded affinity tag (ICAT™) [52], the global internal standard technology (GIST) [53, 54], isobaric tags for relative and absolute quantitation (iTRAQ™) [55], isotope-coded protein labels (ICPL™) [56] and ExacTag™ (PerkinElmer, Waltham, MA, USA) allow quantification by MS analysis. In all methods labels that contain either light or heavy stable isotopes are bound to thiol or amine groups of the protein.

The overall principle of stable isotope labeling followed by MS analysis is identical for each tagging technique. Sample A is labeled with the light and sample B with the heavy reagent. Samples will be combined and the complexity is reduces applying methods like gel-electrophoresis (GE), free-flow-electrophoresis (FFE), capillary-electrophoresis (CE) or high performance liquid chromatography (HPLC) for separation on protein or peptide level. After separation the proteins are identified and relatively quantified in the mass spectrometer (Figure 5). Peptides labeled with agents containing different stable isotopes differ only in their specific mass that is given by the isotopes, but do not differ by other physicochemical parameters. Hence, the difference in intensity of the light and the heavy labeled peptide is directly proportional to the amount of the two corresponding peptides.

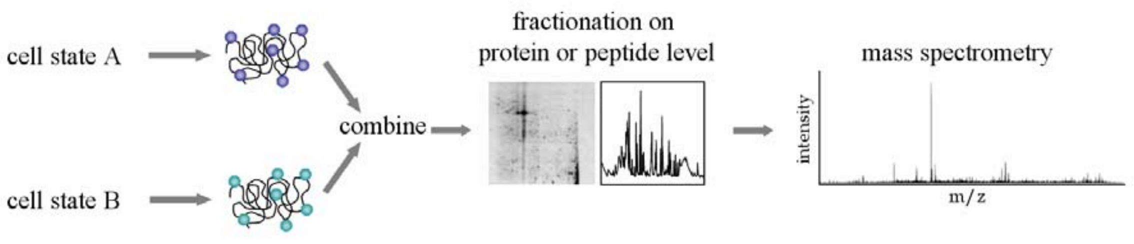


Figure 5. General workflow of a quantitative proteomic approach. After labeling the different cell states are combined and reduction of sample complexity is performed by several separation methods like GE, FFE or HPLC. For identification and quantitation mass spectrometric analysis is applied.

To achieve a global labeling on peptide level, retain the information of post-translational modification and facilitate multiplex sample analysis the iTRAQ™ reagent was developed by Ross et al. in 2004 [55]. The advanced approach labels up to eight different samples with independent reagents of the same mass displaying eight unique reporter ions in MS/MS upon fragmentation [57]. The most commonly used iTRAQ™ kit and the kit applied in this study is the original 4-plex tagging kit (Figure; p. 11). The reagents are designed as isobaric tags consisting of a charged reporter group that ranges in mass from m/z 114.1 to 171.1 Da, a balance group (28 to 31 Da) and a peptide reactive group. The overall mass of reporter and balance components of the molecule are kept constant using differential isotopic enrichment with ^{13}C, ^{15}N, and ^{18}O atoms to maintain an overall mass of 145.1 Da, thus avoiding problems with chromatographic separation seen with enrichment involving deuterium substitution [58].

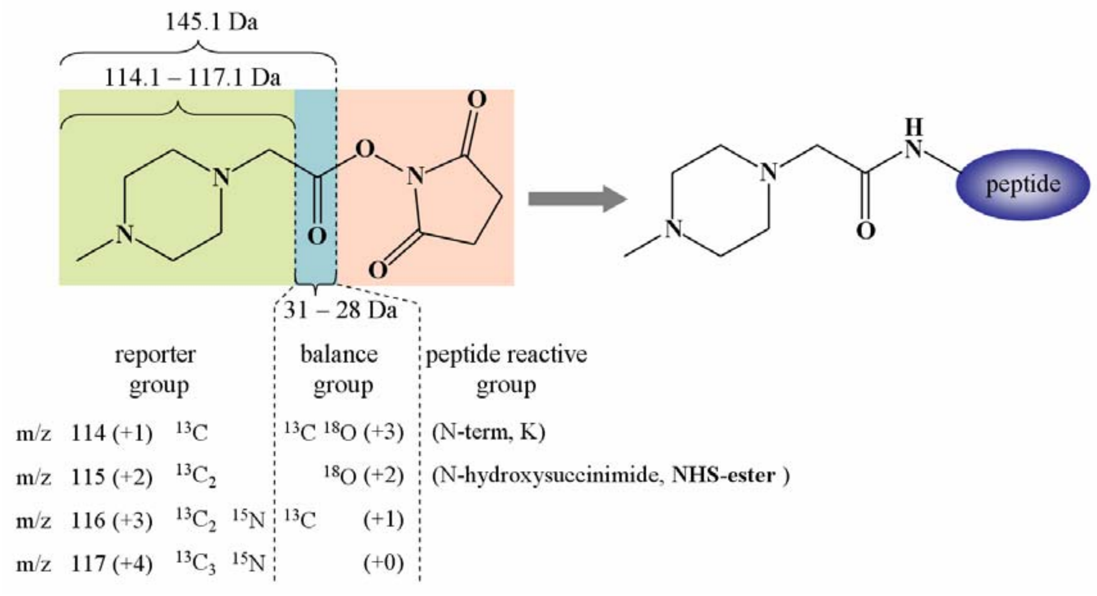


Figure 6. Composition of the iTRAQ™ tagging reagent. The complete molecule consists of a reporter group (based on N-methylpiperazine), a mass balance group (carbonyl), and a peptide-reactive group (NHS-ester). The peptide reactive group specifically reacts with the free N-terminus or lysine residues. All labeled peptides carry an isobaric tag of 145.1 Da. During PSD or CID, the reporter group ions are cleaved from the balance group that is bound to the peptide, displaying masses of 114.1, 115.1, 116.1 or 117.1 Da. The intensity of these fragments is used for quantitation.

The peptide reactive group, an N-hydroxysuccinimide-ester is generated to react with the N-terminus and the ε-amino group of the lysine side chain to label all peptides of a complex protein mixture. These amide linkages were broken in a similar fashion to backbone peptide bonds when subjected to post-source decay (PSD) or collision-induced-dissociation (CID) during MS/MS measurements. Following fragmentation the balance moiety is lost (neutral loss), while charge is retained by the reporter group fragment. All other peptide fragment ions remain isobaric and can be assigned by data base search. The relative abundance from the peptides of different samples is thus calculated from the relative intensities of the corresponding reporter ions.

The workflow of the used quantitative analysis applying the iTRAQ™ reagent is depicted in figure 7 (p. 12). After reduction of disulfides and alkylation of the free thiol group of cysteines, proteins are cleaved using trypsin. Subsequently peptides are tagged with the iTRAQ™ reagent. The labeled samples are combined and the next steps must be suitable to reduce the immense complexity.

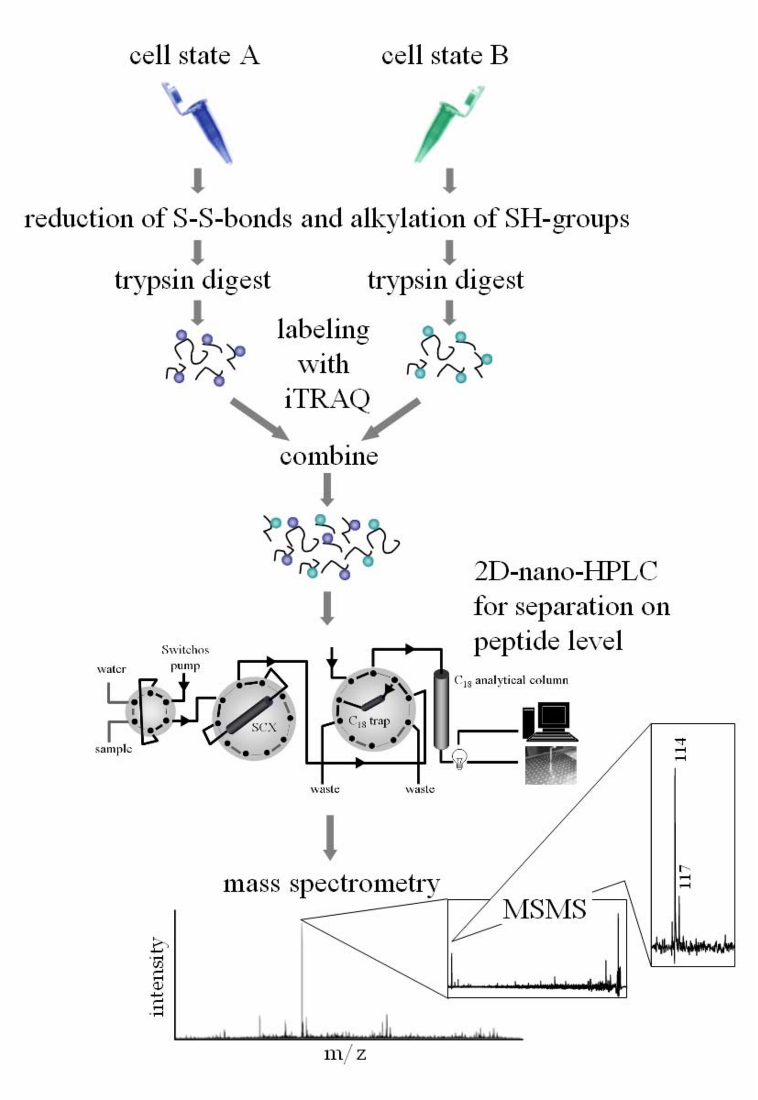


Figure 7. Overview of the workflow for comparative analysis using the iTRAQ™ labeling reagent. Samples of different stages were reduced, alkylated, digested and labeled in parallel. After combining the samples the complex peptide mixtures are separated by on-line 2D-nano-HPLC coupled to MALDI-MS/MS. Identification and quantification is performed by MS/MS measurements.

For this purpose, two commonly used protocols exist: off-line and on-line two dimensional HPLC separation, combining ion exchange with reversed-phase chromatography [59-61]. In this study an on-line 2D-LC approach was applied. Peptides bound to the cation exchange material are eluted by increasing salt concentrations and directly bound to the reversed-phase material. After desalting, peptides are eluted by an increasing hydrophobic solvent concentration. The strong cation exchange chromatography is also required to remove excess iTRAQ™ reagent, which can interfere in MS/MS measurements.

With the iTRAQ™ approach isotope labeling of peptides is performed after enzymatic cleavage of the proteins. Although most peptides are modified using this strategy, the highly effective separation dimension on protein level is lost.

In contrast ICPL™ is based on isotope tagging at free lysine residues and the N-terminus of proteins [56]. ICPL™ consists of nicotinic acid esterified with N-hydroxysuccinimide which acts as peptide reactive group (Figure 8). The nicotinic acid contains light and heavy carbon isotopes, and differs in mass by 6.02 Da.

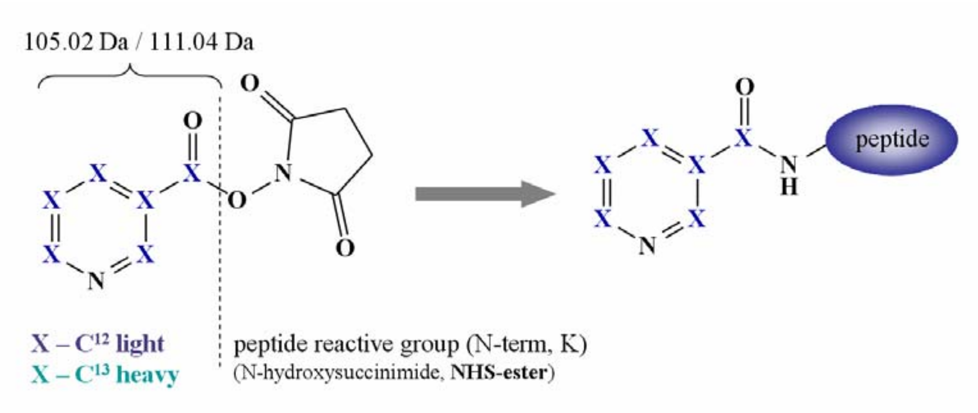


Figure 8. Chemical composition of the ICPL™ labeling reagent. The reagent contains the peptide reactive group and the nicotinamide moiety which will be transferred to free amino acids such as the free lysines and the N-terminal amino group. The mass of the labeled peptides increases about 105.02 and 111.04 Da and the difference between the light and the heavy type is 6.02 Da. The intensity of the peptide signals in a MS spectrum is used for relative quantitation.

Since the method is compatible with commonly used protein separation techniques such as SDS-PAGE, FFE or HPLC, several technical combinations with either a second protein separation method or peptide separation techniques are comfortable to reduce sample complexity [62]. A similar method called ICAT™ labels proteins at cysteine residues. The tag harbors a biotin group that facilitates further reduction of complexity by isolating cysteine containing peptides by biotin affinity chromatography. However, cysteines are relatively rare in proteins and thus some interesting proteins might get lost.

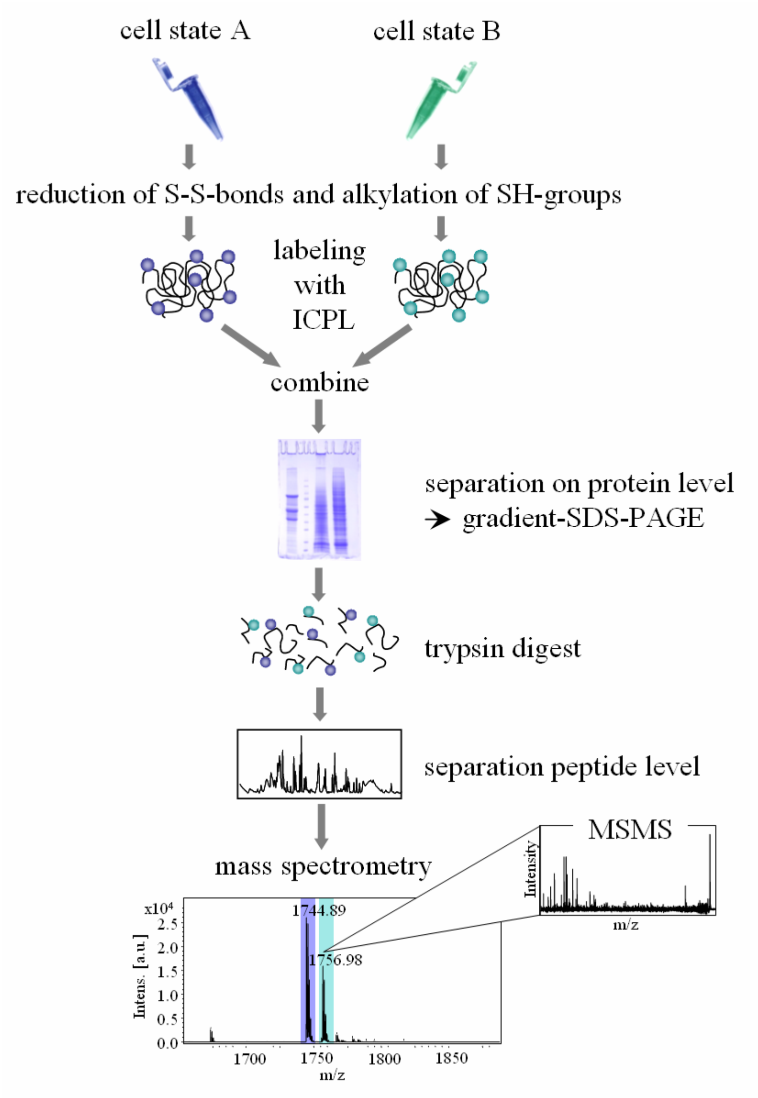


Figure 9. Overview of the ICPL™ workflow. Proteins from two different cell states are extracted and the cysteine-bonds are reduced and alkylated. The free amino groups are derivatized with the heavy or the light ICPL™ tags. After combining the two protein mixtures, any separation method e.g. SDS-PAGE can be employed to reduce the complexity on protein level. Tryptic digestion is applied and peptides can be separated with RP-chromatography. The heavy and light labeled peptides differ only in their masses and relative quantification is performed on MS level. Subsequently, the proteins are identified via peptide mass fingerprint (MS) and MS/MS measurement.

The workflow used in this study is depicted in figure 9. As described for the iTRAQ™ labeling, proteins are first reduced and alkylated and different cell states are individually labeled with the light or heavy ICPL™ tag. After combining the samples, protein separation via gradient-SDS-PAGE is applied. The proteins were cut out of the gel and cleaved with trypsin. Subsequently, the peptides were chromatographically separated followed by quantitation and identification of proteins by mass analysis and data base search.

1.5 High performance liquid chromatography

Over the past decades liquid chromatography (LC) has been routinely used for the separation and analysis of proteins and peptides. Because of its high resolving power, reproducibility and its compatibility with ESI and MALDI mass spectrometry, high-performance liquid chromatography (HPLC) represents an appealing alternative to gel electrophoresis for the separation of both proteins and peptides in proteomics.

In the HPLC technique, the sample is forced through a stationary phase by a liquid (mobile phase) at high pressure [63]. The column is packed either with irregularly or spherically shaped particles or with a monolithic layer [64]. An attractive feature of HPLC is the broad selection of stationary and mobile phases. A variety of modes have been used both alone and in combination: reversed-phase, ion-exchange, affinity and size-exclusion chromatography [65]. In comparison with gel-based separation methods, sample handling and preparation are minimal. Protein or peptide digests are separated by LC and can be introduced into the mass spectrometer either on-line using ESI or off-line via MALDI for identification and quantitative analysis. Increased resolution of proteins and peptides can be achieved by multidimensional chromatography (2D-LC) [66].

Currently, most LC separations in proteomics are done by reversed phase HPLC (RP-HPLC), because of its compatibility with MS [67]. In reversed phase chromatography the hydrophobic proteins or peptides bind to an immobilized hydrophobic molecule in a polar solvent. A buffer of increasing hydrophobicity is used to elute the bound molecules. The molecules will be released at the point the hydrophobic interaction towards the immobilized matrix is less favorable than the interaction to the solvent. Because the buffer system commonly contains only organic solvents such as acetonitrile (MeCN) or methanol (MeOH) and an ion pair reagent like acetic or trifluoracetic acid (FA, TFA), a coupling with tandem mass spectrometry (LC-MS/MS) is feasible. If RP-HPLC is coupled with ESI the TFA concentration is limited because of its ion suppressive effect [67]. Although, the RP-HPLC-MS/MS technique combines highly efficient separation of biological samples and sensitive identification of the individual components by mass analysis, this method is overloaded for the separation of a tryptic digest of a crude extract from e.g. a cell line. The chemistry within one given RP-column is insufficient to separate these analytes. Ion-suppression effects in MS are likely caused by overlapping signals from high and low abundance ions, resulting in a low identification yield of peptides. Thus, a two- or multidimensional chromatography should be used to increase separation efficiency. Commonly RP is combined with ion exchange chromatography (IEC) [59, 60, 68, 69] using a cation exchange material for the separation of peptides.

IEC utilizes ion exchange mechanism to separate analytes [70]. A charged stationary phase is used to separate charged compounds including peptides and proteins. In conventional methods the stationary phase is an ion exchange resin that carries charged functional groups which interact with oppositely charged groups of the compound to be retained (Figure 10). With increasing salt concentrations the retained molecules will elute and separate according to their charge.

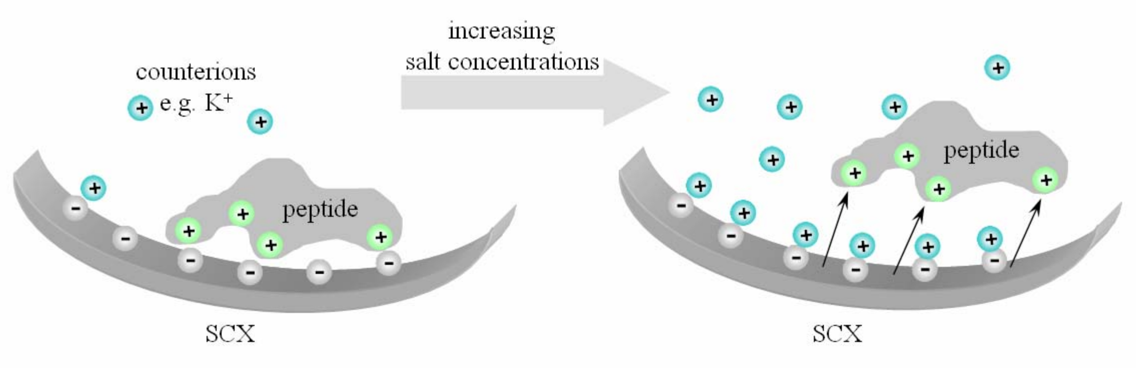


Figure 10. Mechanism of cation exchange chromatography. The positively charged groups of the peptide interact with the free e.g. sulfonyl-groups of the column material. Increasing concentrations of salt force the peptide to dissolve from the stationary phase and elute.

IEC is not directly combinable with MS because of the high salt concentrations used for elution. Potassium and sodium form salt cluster during ionization processes which interfere with the MS analysis [71, 72]. Therefore, ion exchange chromatography is combined with RP-chromatography. Salts used for elution of the ion exchange are removed through the RP-column. Thus, a powerful tool for cleaning and highly separating proteins and peptides is established by this separation method.

2 Materials and Methods

2.1 Reagents and Materials

Trifluoracetic acid (99% purity) was from J.T.Baker (Mallinckrodt Baker, Griesheim, Germany). The MS calibration standard and 4-hydroxy-α-cyano cinnamic acid (HCCA) were purchased from Bruker Daltonik GmbH (Bremen, Germany). The ICPL™ kit was from Serva Electrophoresis GmbH (Heidelberg, Germany) and Applied Biosystems (Framingham, MA, USA) offered the iTRAQ™ kit. Chemicals for cell culture were from Invitrogen GmbH (Karlsruhe, Germany). All aqueous solutions were prepared with deionized water having a resistance of at least 18 MΩ (Millipore, Schwalbach, Germany). Fluka (Sigma-Aldrich GmbH, Seelze, Germany) offered the sodium hydroxide, ammonium dihydrogenphosphate, Coomassie brilliant blue, the solvents ethanol and acetonitrile and all other chemicals in the highest purity available.

2.2 Cell culture and preparation of cell lysates

SH-SY5Y cells were cultivated in Dulbecco's minimum essential medium (DMEM) containing 14% fetal calf serum (FCS), 1% penicillin/streptomycin and 1% sodium pyruvate and maintained at 37°C in an atmosphere of 5% CO_2 in air. The medium was changed every 2 days and cells were splitted every 6 days. Cells were grown for one day before C3*bot*-treatment and then the exoenzyme was added to the medium in a concentration of 1µM. After 72 h the medium was removed and cells were washed three times with PBS. The cells were scratched from the culture flasks with a cell scraper and resolved in a small volume of lysis buffer (6 mol/L urea, 2 mmol/L DTT, 50 mmol/L NH_4HCO_3). Ultrasonic disruption was performed in a cycle of 10×5 sec, 5×10% sonic energy using a sonotrode (Bandelin Electronic, Berlin Germany). To remove the cell debris the lysates were centrifuged at 13.000 g at 4°C for 30 min. Protein concentration was determined using Coomassie brilliant blue [73] with BSA as a standard. Usually protein concentrations of 1.5 mg/mL were obtained with a yield of 0.75 mg protein per 1×10^7 cells.

2.3 ICPL-sample preparation

Before ICPL™-labeling protein samples were concentrated by a chloroform/methanol precipitation [74]. Therefor the sample was mixed with MeOH and chloroform in equal amounts. After addition of three volumes of water the suspension was centrifuged at 13.000 rpm for 2 min. The supernatant was discarded, mixed with three volumes of MeOH and the sample was centrifuged at 13.000 rpm for 2 min. The obtained pellets were dried and resuspended in the ICPL™-lysis buffer (6 mol/L guanidine-HCl, 0.1 mol/L HEPES, pH 8.5) and the protein concentration was adjusted to 5 mg/mL. The maximum protein amount suitable for the kit was 100 µg protein per sample. For test analysis a standard mixture of bovine serum albumin (BSA), ovalbumin (OVA) and lactate dehydrogenase (rabbit, LDH) was prepared. The two mixtures contain BSA in a ratio of 1:1, OVA in a ratio of 5:2 and LDH in a ratio of 1:2.

Prior to the labeling cysteine residues were reduced adding 0.5 µL of 200 mmol/L reduction solution (TCEP-HCl, tris(2-carboxy-ethyl)phosphine) and the samples were incubated at 60°C for 30 min. The cysteines were alkylated using 0.5 µL of 400 mmol/L iodoacetamide (IAA) at 25°C in the dark for 30 min. The reaction was stopped with 0.5 µL stop solution I (0.5 mol/L N-acetylcysteine) for 15 min at 25°C. To label the N-terminus and free amino groups at the lysine residues 3 µL of C^{12}- or C^{13}-nicotinoyl-oxysuccinimide (Nic-reagent) were added to each mixture, the sample vials were flushed with nitrogen, vortexed and incubated in an ultrasonic bath for 1 min. The reaction was performed at 25°C and 400 rpm for 2 h. To stop the labeling reaction and destroy excess of Nic-reagent 2 µL of stop solution II (1.5 mol/L hydroxylamine) were added and the reaction was allowed to proceed at 25°C for 20 min. The light and heavy labeled standard mixtures were combined and esters were hydrolyzed with 2 µL of 2 mol/L sodium hydroxide increasing the pH up to 12 for 20 min at 25°C. Samples were neutralized with 2 µL of 2 mol/L hydrochloric acid. Proteins were precipitated using acetone precipitation. Therefor one volume of water and five volumes of acetone (-20 °C) were added. The precipitation proceeded at -20°C over night. The protein pellets were washed with 80% (v/v) acetone and dried under vacuum in the SpeedVac. In all experiments, the untreated lysates were labeled with the light C^{12}-Nic-reagent and C3*bot*-treated lysates with the heavy C^{13}-Nic-reagent.

To validate the method and to determine the amount of artificial regulation, untreated cell lysate was labeled in a 1:1 ratio with C^{12}-Nic-reagent and C^{13}-Nic-reagent.

2.4 iTRAQ-sample preparation

Like the preparation in the ICPL™ procedure protein samples were concentrated by a chloroform/methanol precipitation, dried and dissolved in 30 µL iTRAQ™-dissolution buffer containing 0.5 mol/L triethylammonium bicarbonate at pH 8.5 and 1.5 µL 2% sodium-dodecyl-sulfate (SDS) with a protein concentration of 3 µg/µL. 100 µg protein per sample are appropriate for the iTRAQ™-tagging. The method was examined using a standard mixture of BSA, OVA, Toxin A from *Clostridium difficile* and recombinant C3 exoenzyme. The two mixtures include BSA and C3 in a ratio of 1:2, OVA in a ratio of 3:1 and Toxin A in a ratio of 1:1. The protein mixture and the cell lysates were reduced adding 2 µL of 50 mmol/L reduction solution (TCEP-HCl, tris(2-carboxy-ethyl)phosphine) and the samples were incubated at 60°C for 1 h. The cysteines were alkylated using 1 µL of 200 mmol/L methyl-methanthiosulfonate (MMTS) at 25°C for 10 min. 4 µL of 1 µg/µL modified trypsin (Promega, Madison, USA) in 50 mmol/L acetic acid were added to the samples and cleavage was performed at 37°C over night. Digests were dried under vacuum in the SpeedVac, resuspended in 30 µL 0.5 mol/L triethylammonium bicarbonate at pH 8.5, amino-labeled with one of the four iTRAQ™ tags at 25°C for at least 2 h and then combined in equal amounts. For further purification and separation of the labeled peptides using 2D-chromatography, samples were dried in the SpeedVac and diluted in 100 µL 2% MeCN, 0.1% FA (pH 3.5).

2.5 SDS-PAGE for GeLC-MS/MS analysis

200 µg protein extract from SH-SY5Y cells or the labeled protein pellets from the ICPL™-tagging were dissolved in 35 µL Laemmli [75] sample buffer and incubated at 95°C for 5 min. When using unlabeled samples, 2 µL acrylamide were added to alkylate the free cysteines and incubated at room temperature for 30 min. The proteins were separated on an 8.5% to 18% SDS-PAGE (8 cm x 12 cm) with 5% stacking gel according to the Laemmli procedure applying 60 V for 5 min, 100 V for 25 min and 200 V for approximately 2 h. The proteins were stained with Coomassie Brilliant Blue R-250 in 20% (v/v) MeOH, 10% (v/v) acetic acid.

2.6 Western Blot

Protein extracts from cell lysates were separated using SDS-PAGE (15% gel) and subsequently transferred onto nitrocellulose membranes by a semi-dry blot system (Trans-Blot® SD Semi Dry, BioRad Laboratories) over 72 min at 17 V using 25 mmol/L Tris-HCL, 192 mmol/L glycine in 20% (v/v) methanol. The membranes were blocked with 5% (w/v) nonfat dried milk in TBST (50 mmol/L Tris-HCL pH 7.2, 150 mmol/L NaCl, 0.05 % (v/v) Tween 20) for 60 min. Incubation with primary antibody was conducted over night at 4°C and treatment with the secondary antibody at room temperature for 60 min. For the chemoluminescence reaction Femto™ (Pierce, Thermo Fisher Scientific Inc., Rockford, IL, USA) or Immobilon™ (Millipore, Schwalbach, Germany) were used. The Signals were analyzed densitometrically using the KODAK 1D software and normalized to glyceraldehyde-3-phosphate dehydrogenase (GAPDH).

2.7 In-gel proteolytic cleavage

The Coomassie stained protein lanes were manually cut into several pieces. Pieces were washed and destained with 50 mmol/L NH_4HCO_3 in 50% (v/v) MeCN, shrunk with 100% MeCN and dried using vacuum evaporation. 100 µL of 4 ng/µL modified trypsin (Promega, Madison, USA) in 20 mmol/L NH_4HCO_3, 10% (v/v) MeCN were added to the gel pieces and rehydration was carried out for 1 h on ice. Surplus trypsin was removed and the gel pieces were covered with 20 mmol/L NH_4HCO_3 in 10% (v/v) MeCN. Cleavage was performed at 37°C over night. Reaction was stopped with 50 µL 50% (v/v) MeCN in 0.5% (v/v) TFA for 10 min and shaking at 400 rpm and gel pieces were washed with 200 µL 50% (v/v) MeCN in 0.2% (v/v) TFA for 30 min at 400 rpm and subsequently shrunk with 100 µL of 100% MeCN. All supernatants were collected, combined and dried in a SpeedVac centrifuge. The dried samples were dissolved in 30 µL 2% (v/v) MeCN in 0.1% (v/v) TFA for HPLC separation.

2.8 Peptide separation by reversed phase chromatography

Peptide separation was done by reversed phase chromatography using a nano-HPLC system (Dionex GmbH, Idstein, Germany) that consist of an autosampler (Famos), a loading pump (Switchos), a gradient pump (Ultimate) and a microfraction collector (Probot). An aliquot of 20 µL of each sample was injected onto a C18 trap column (PepMap™ 300 µm x 5 mm, 3 µm, 100 Å, Dionex) with 2% (v/v) MeCN in 0.1% (v/v) TFA and a flow rate of 30 µL/min. After loading the trap column was integrated into the nano flow of the gradient pump and the peptides were eluted onto a separation column (PepMap™, C18 reversed phase material, 75 µm x 150 mm, 3 µm, 100 Å, Dionex GmbH, Idstein, Germany) and separated using eluent A with 5% (v/v) MeCN in 0.1% (v/v) TFA and eluent B with 80% (v/v) MeCN in 0.1% (v/v) TFA with a gradient from 16% to 18% eluent B in 27 min, 18% to 24% eluent B in 40 min, 24% to 40% eluent B in 64 min and 40% to 100% eluent B in 10 min. 384 fractions of 90 nL were spotted directly onto a manually prespotted MALDI target plate with a collinear sheath flow of 2.5 µL/min 5% (v/v) MeCN 0.1% (v/v) TFA aqueous solution using a microfraction collector.

2.9 Peptide separation by on-line 2D-nano-HPLC

Peptide separation was done by strong cation exchange followed by reversed phase chromatography. In the first step of the separation, 10 µL of the standard protein mixtures or 19 µL of the peptide mixture of cell lysates were loaded with a flow of 15 µL/min 2 % MeCN in 0.1 % FA onto a ProSpere™ P-SCX-NP strong cation exchange column (2.5 µm, 50 mm, id 300 µm; Alltech Grom GmbH, Rottenburg-Hailfingen, Germany). 40 µL salt plugs containing increasing concentrations of KCl (30 mmol/L, 60 mmol/L, 100 mmol/L, 150 mmol/L, 300 mmol/L, 500 mmol/L, and 2 mol/L) were applied to elute the retained peptides from the SCX onto a C18 trap column (PepMap 300 µm x 5 mm, 3 µm, 100 Å, Dionex). Figure 11 (p. 22) presents the schematic workflow of the 2D-nano-LC-MALDI approach. Panel A shows the switching of the 10-port valves while injection or elution with the salt plugs. Peptides which flow through or which are eluted from the SCX are trapped on a short RP-trap-column. After 6 min the SCX column was closed out of the flow and the trap was washed with 2 % MeCN in 0.1 % FA to remove excess of any detergent.

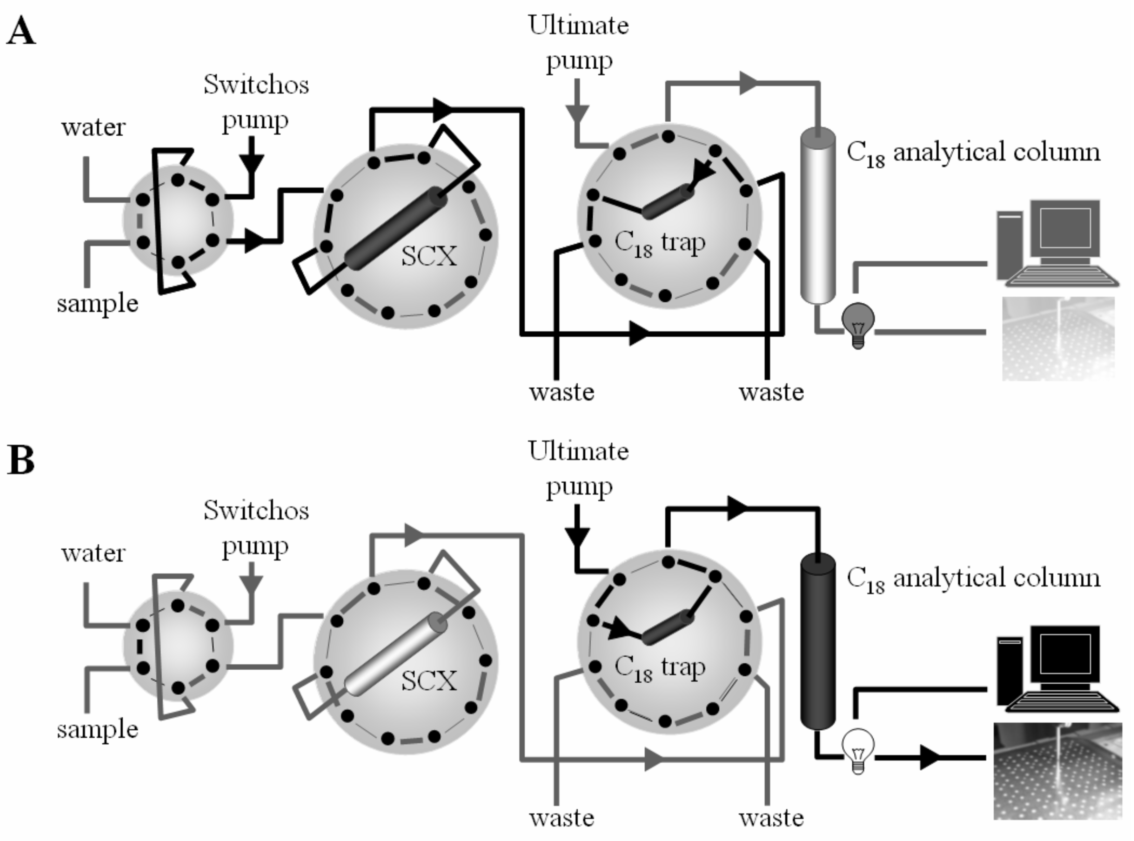


Figure 11. Schematic illustration of the 2D-HPLC system. A System operating in the SCX-mode. Peptides were bound onto a SCX-column with a flow of 15 µL/min from the Switchos pump. Peptides not retained at the SCX column were eluted onto a C18-trap column. **B** Separation mode in the second dimension. Peptides retained on the trap column were eluted using an acetonitrile gradient with a flow of 250 µL/min produced by the Ultimate pump, monitored and directly spotted onto a MALDI target.

After 3 min the trap column was integrated into the nano-flow of the gradient pump (250 nL/min, Figure 11 B). The peptides were eluted onto a separation column (PepMap, C18 reversed phase material, 75 µm x 150 mm, 3 µm, 100 Å, Dionex GmbH, Idstein, Germany) and separated using eluent A with 5 % MeCN in 0.1 % TFA and eluent B with 80 % MeCN in 0.1 % TFA with a gradient from 12 % to 40 % eluent B in 70 min, 40 % to 100 % eluent B in 3 min. 170 fractions of 104 nL were spotted directly onto a manually prespotted MALDI target plate with a continuously sheath flow of 3 µL/min 5 % MeCN in 0.1 % TFA.

2.10 MS-Analysis

2.10.1 MALDI target preparation

A matrix stock solution of 4 mg/mL HCCA in 50% (v/v) MeCN, 0.1% (v/v) TFA and 10 mmol/L $NH_4H_2PO_4$ was diluted 1:4 with ethanol. 0.6 µL of this matrix solution were spotted on each target of a MALDI Anchor Chip 600/384 or 600/1536 target plate (Bruker Daltonik GmbH). After sample spotting recrystallization was performed with 0.2 µL of 0.1% (v/v) TFA in ethanol. For MS calibration 0.3 µL of peptide calibration standard were spotted onto the target and recrystallized, too.

2.10.2 MALDI analysis

MALDI analysis was performed in an Ultraflex TOF/TOF I from Bruker Daltonik GmbH (Bremen, Germany) operating with FlexControl 2.4, FlexAnalysis 2.4, BioTools 3.0 and Warp-LC 1.1 software. To identify proteins searches against the MSDB database using Mascot version 2.1.04 software (Matrix Science, UK) were carried out. MS and MS/MS spectra were taken with a 50 Hz nitrogen laser operating at a wavelength of 337 nm. For MS spectra 300 shots were collected and compounds with a signal/noise ratio (S/N) above 30 were taken for MS/MS measurements for standard analysis as well as for ICPL™ labeled peptides and the S/N ratio for the iTRAQ™ labeled peptides was 10. 300 shots were applied for the parent ion counting only spectra with a half width < 1.3 and an intensity of 10 × laser energy. For the fragments 700 shots were summed up.

2.10.3 Identification and quantitation criteria

For protein identification a Mascot search was performed. Therefor MS/MS-spectra were matched with the MSDB database. Searches were accomplished only for human proteins looking for modifications like oxidation (M), hydroxylation (P) or phosphorylation (STY) beside the propionamide (C), ICPL™ or iTRAQ™ modifications. MSMS-spectra were utilized if the Mascot ion score was above 25. Decoy database searches performed with the MSDB random database yield in Mascot scores below 35. Therefore proteins were assessed as identified if the Mascot score was above 40 for standard proteome screening and ICPL™ analysis and above 30 for iTRAQ™ analysis. Proteins were found at least with two peptides.

Due to several repetitions of the ICPL™ and iTRAQ™ experiments the number of peptides belonging to one protein also contains multiple identified peptides. To calculate the Mascot score only the highest peptide scores of identical peptides were used.

iTRAQ™ quantification was done by calculating the ratio between the peak areas of the 114/115/116 or 117 reporter ions. For ICPL™-quantitation the heavy/light ratio (H/L) was calculated. To ascertain the regulation factor all found ratios were taken and the average ratio was determined.

3 Results

In the present work proteome changes in human neuroblastoma cells induced by the bacterial exoenzyme C3*bot* should be investigated. SH-SY5Y cells were chosen as model system, since hippocampus neurons that react with increased axonal growth and branching on C3*bot*-treatment, cannot be produced in adequate amounts. SH-SY5Y cells are also susceptible to C3*bot*-treatment and respond by reorganization of the actin cytoskeleton and the formation of neurites, called the cytopathic effect. The cytotoxic effect of C3*bot* involves the inactivation of Rho proteins that leads probably to cell cycle arrest and finally to cell death. Though the uptake of C3*bot* proceeds relatively quickly the cells were incubated for a long period of three days with high concentrations of the exoenzyme to facilitate the detection of considerable changes on the proteome level. The functional integrity of the SH-SY5Y maintains for the used incubation time. After the C3*bot*-treatment all cells appeared round and neurites have been formed (data not shown) To elucidate these effects on protein level crude extracts were prepared from C3*bot*-treated and untreated SH-SY5Y cells and proteins were labeled either with the ICPL™ or the iTRAQ™ tagging reagent followed by different separation techniques coupled with mass spectrometric analysis.

3.1 Isotope-coded protein labels and the GeLC-MS/MS approach

3.1.1 Examination of the GeLC-MS/MS method

For the examination of the GeLC-MS/MS approach unlabeled cell lysate was separated on a gradient SDS-PAGE, and a similar gel area was cut manually in 1, 3, or 10 pieces (Figure 12; p. 26). After in-gel tryptic digestion LC-MS/MS analysis of peptides was performed for each of the pieces.

The obtained results from this experiment are depicted in figure 13 (p. 27). As obvious from panel A, the number of identified pieces increases with the number of gel pieces. With the reduction of sample complexity the identification rate raises up (1 piece – 395 proteins, 3 pieces – 1130 proteins, 10 pieces – 2241 proteins), due to the decrease of overlapping signals and signal suppression in MS measurements. Also the feasibility of different peptides with the same mass eluting at the same time is decreased which results in assignment and identification of MS/MS spectra.

If the identification rates increase further, after cutting a similar gel area into more then 10 pieces was not elucidated. The LC-MS analysis of one gel pieces claimed two days of laboratory work. Thus, an analysis of about 30 gel pieces needs 60 days. If a gel area is cut into smaller pieces, more analyses have to be done resulting in an nearly unacceptable effort. When cutting smaller gel-pieces, one protein will be present in several pieces and some proteins might get below the detection limit. That leads to multiple identified proteins and the identification rate increases only apparently. To overcome these methodical restriction gel pieces were cut into different sizes. Gel areas with high protein content were cut into smaller pieces and gel areas with a lower protein concentration were cut into larger pieces. However, in figure 12 the different sizes of the gel pieces are not indicated. Using this distribution a highly comprehensive protein profile of SH-SY5Y cells was obtained.

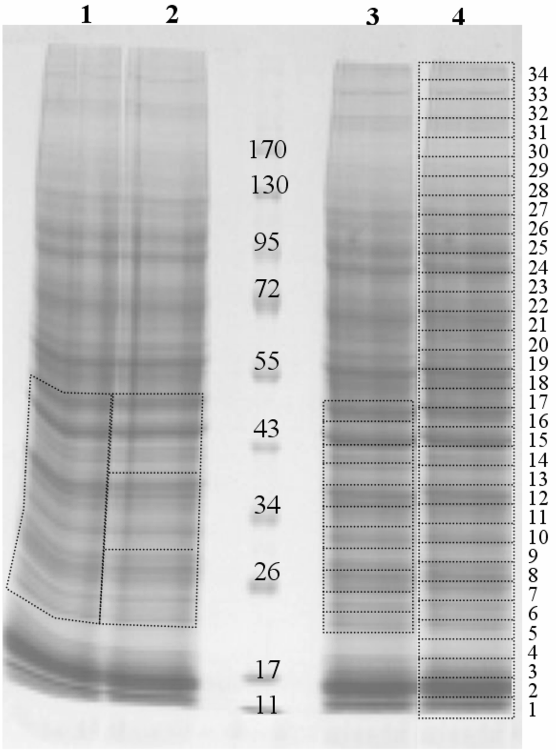


Figure 12. Gradient SDS-PAGE of SH-SY5Y cell extracts. Acrylamide/ bisacrylamide from 8.5% to 18% with a 5% stacking gel was used. Lanes 1-4 were loaded with 200 µg SH-SY5Y-cell extracts. Lane 1 was cut into one piece, lane 2 into 3 pieces and lane 3 was cut into 10 pieces as indicated. From lane 4 a whole SH-SY5Y screening was performed. The indicated size of the gel pieces does not correlate with the cut out size.

If sample complexity is reduced, identification of peptides and thus proteins is eased. This effect is also reflected in the abundance of identified proteins with Mascot scores higher than 2000 (Figure 13 B). An interesting fact is that the distribution of the Mascot scores in the three experiments is comparable and independent of the sample complexity (Figure 13 B/C). About 70% of all identified proteins were rated with a score below 100, whereas out of them 35% were found at the identification limit of score 40. Only a minority of 30% was found with scores above 100 with e.g. a top score of 2639 for alpha-enolase. Proteins found with scores between 40 and 50 were often identified by only one or two peptides and belong to the large group of less abundant proteins in cells. To exclude false positives, decoy database searches were performed. Using this procedure the software aligns the sequences from MS/MS measurements with non-sense-data bases, resulting in hits with a score below 35. That means proteins rated with scores below 35 show an increased risk to be a false positive finding. From this fact only that proteins with a score above 40 were rated as identified.

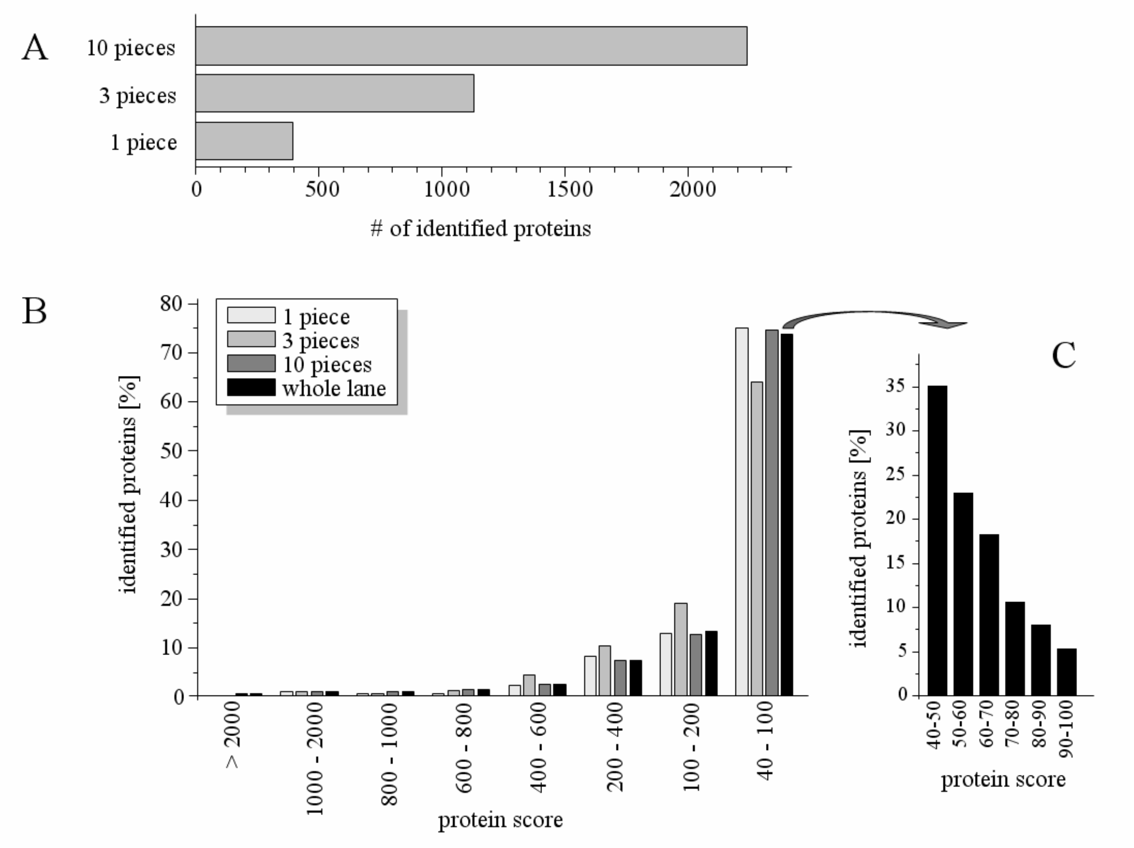


Figure 13. Number of identified proteins and the corresponding Mascot scores for identification. **A** Number of identified proteins in one gel piece, three or ten gel pieces. **B** Distribution of the Mascot scores used for the identification of the proteins. **C** Composition and distribution of the scores in the lower level between 40 and 100 corresponding to a whole lane.

Overall 3399 different proteins including fragments and isoforms were identified in SH-SY5Y cell analysis of all gel pieces from lane 4 (Figure 12 p. 26). A list of these proteins containing the SwissProt accession number, the Mascot score, the number of identified peptides and the molecular weight is given in supplementary table 1 (p. 70).

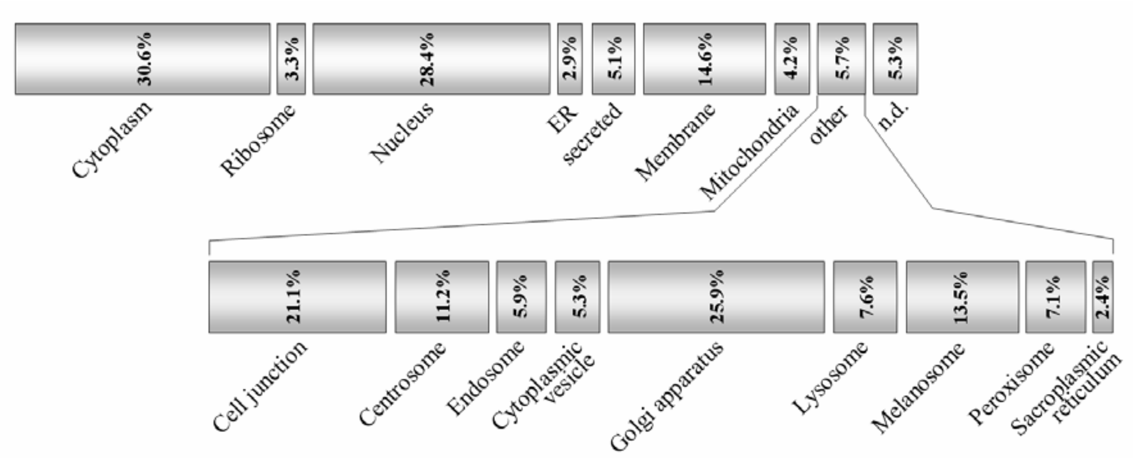


Figure 14. Allocation of the identified proteins of SH-SY5Y cells to different cellular compartments.

Proteins were found allocated in several compartments of the cells (Figure 14). The majority was localized in the cytoplasm (30.6%) and the nucleus (28.4%). 14.6% of the identified proteins are membrane proteins which approves the capability of this method, thus with classical 2D-gel-based proteome analysis membrane proteins are hardly detectable due to their hydrophobicity. Less abundant proteins coming from compartments like the mitochondria, the ribosome, and the lysosome, the ER or the Golgi apparatus have been identified with about 16% with this sensitive GeLC-MS/MS approach.

Based on this experiment C3*bot*-treated and untreated SH-SY5Y cells were labeled with ICPL™ and the proteins were separated on a gel which was cut into 34 pieces and analyzed by LC-MS/MS.

3.1.2 Technical adaptation of the ICPL™ method

Only few reports exist that show experimental data about proteomic approaches using the ICPL™ labeling technique [56, 62, 76]. Thus, several control experiments were performed at the beginning to validate the method and establish ICPL™ for the analysis of the proteome of C3*bot*-treated neuronal cells.

BSA, OVA and LDH were labeled respectively, in two repetitions with the heavy and light ICPL™ tags in the ratios 1:1, 5:2, and 1:2 (Figure 15). Proteins were combined, separated by SDS-PAGE, digested and the peptides were analyzed by LC-MS in eleven repetitions. BSA, OVA and LDH were identified by data base analysis with a high Mascot score of 730, 941 and 85.

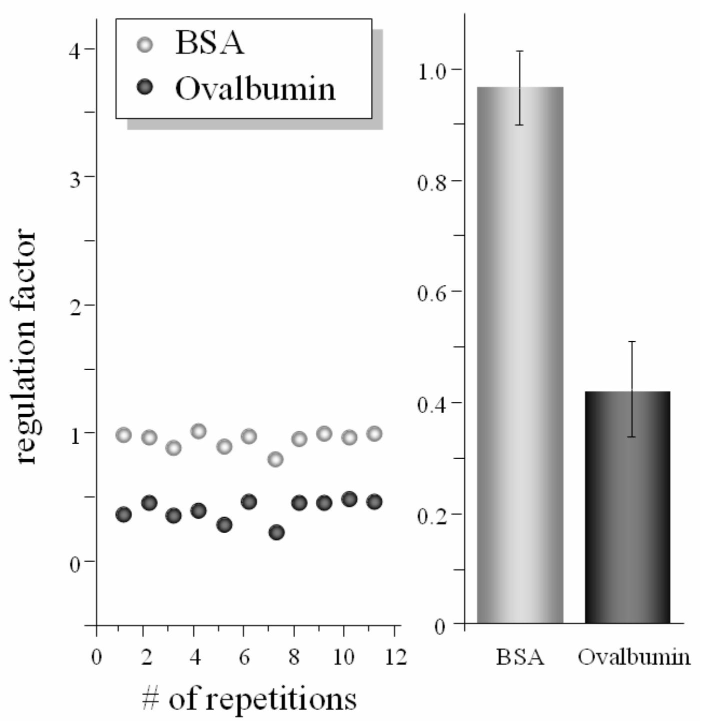


Figure 15. Quantification of BSA and OVA in eleven repetition experiments. BSA was labeled in an H/L ratio of 1:1 in the standard mixture and OVA with an H/L ratio of 2:5. The expected regulation factor for BSA is 1.0 and for ovalbumin 0.4.

For BSA and OVA almost all of the identified peptides harboring lysines were labeled and about 60% of these peptides were present with either the light or the heavy label. Only peptides with arginine residues at the end were identified in the ICPL™ labeled samples due to the property of trypsin to cleave like ArgC when proteins are labeled at the lysine residues. A slightly different peptide pattern was obvious for the LC-MS/MS analysis of unlabeled tryptic digested BSA or OVA, including peptides cleaved at the C-terminal side of lysine residues. However, the overall Mascot scores for unlabeled proteins were in the same range. This confirms the compatibility of the ICPL™ label with LC-MS. Although no labeled peptides were identified for the LDH, the protein was identified with two MS/MS spectra leading to the Mascot score of 85. However, none of these peptides contained a lysine residue and hence no labeling was detected. BSA and OVA were found in all expected ratios with a variation for all identified labeled peptides of 6% for BSA and 16% for OVA (Figure 15; p. 29).

To ascertain the variation between two labeling reactions the equal amount of the crude extract of SH-SY5Y cells was labeled with the heavy and the light ICPL™ label. Thus the expected regulation factor between these two samples should be 1.0. After labeling, combining, and separation by SDS-PAGE of the proteins six gel areas, with high protein content were cut out from the gel, digested, identified, and quantified by LC-MS/MS. About 250 proteins were identified containing the light as well as the heavy ICPL™ label (Figure 16).

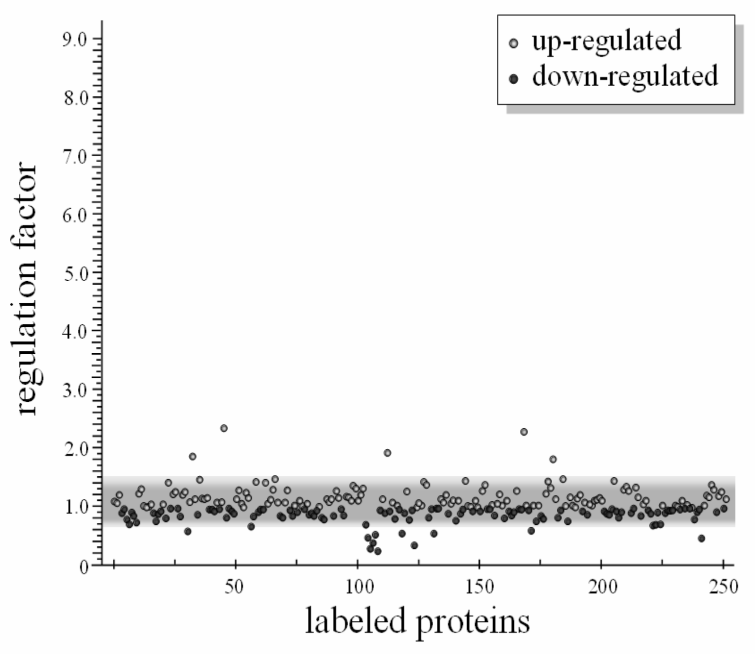


Figure 16. Regulation factor of complex 1:1 labeled SH-SY5Y cell lysate. The black dots show down-regulated and the gray dots up-regulated proteins. The gray area indicates the fluctuation margins. Proteins with higher or lower values are designated as changed.

The majority of these proteins (81%) showed an altered concentration below factor 1.3 whereas in a significant smaller part of 13% regulations of up to factor 1.5 were detected. A small amount of proteins (6%) exhibits higher regulation factors of up to 2.5. These proteins were identified by several MS/MS analysis of only the heavy or the light peptides and the corresponding labeled peptides were only identified with a small signal to noise ratio of 5-10 and, thus, not confirmed by MS/MS. Measurements become highly imprecise for peaks with such low signal to noise ratios. Therefore, it might be reasonable that a different peptide with by chance similar mass might interfere with the analysis.

To feel certain that a protein is actually regulated in response to C3*bot*, the regulation factor has to be at least 1.5 or higher and all peptides used for quantification have to be identified by MS/MS analysis. These settings were used for the classification of C3*bot* responsive proteins.

3.1.3 Analysis of C3bot altered proteome in SH-SY5Y cells

Proteins from C3*bot*-treated and untreated SH-SY5Y cells were labeled twice with the light and heavy ICPL™ tagging reagent, separated on protein level by gel-electrophoresis, digested and peptides were identified and quantified using LC-MS/MS by a MALDI mass spectrometer. In the first experiment a total of 689 different proteins were identified and 507 proteins were found labeled by both the heavy and light ICPL™ tag. In the second experiment sample preparation and analysis steps were further optimized. Most influence on a better analysis was exerted by an enhanced separation method in reversed phase chromatography (HPLC) with more specific gradients and an increased performance of the MALDI-MS due to better and automated sample preparation and fine-tuning of mass spectrometer calibration. That leads to an identification of about 1205 proteins where 586 out of them were tagged by both ICPL™ labels.

Based on the combination of the data sets from both experiments 1466 different proteins were identified and out of them 777 (53%) were labeled with the heavy and light ICPL™ reagent (Figure 17; p. 32). A complete list of all identified proteins including accession No, Mascot detection score, number of identified peptides, mass, isoelectric point, sequence coverage and found regulation is available as supplementary table 2 (p. 118).

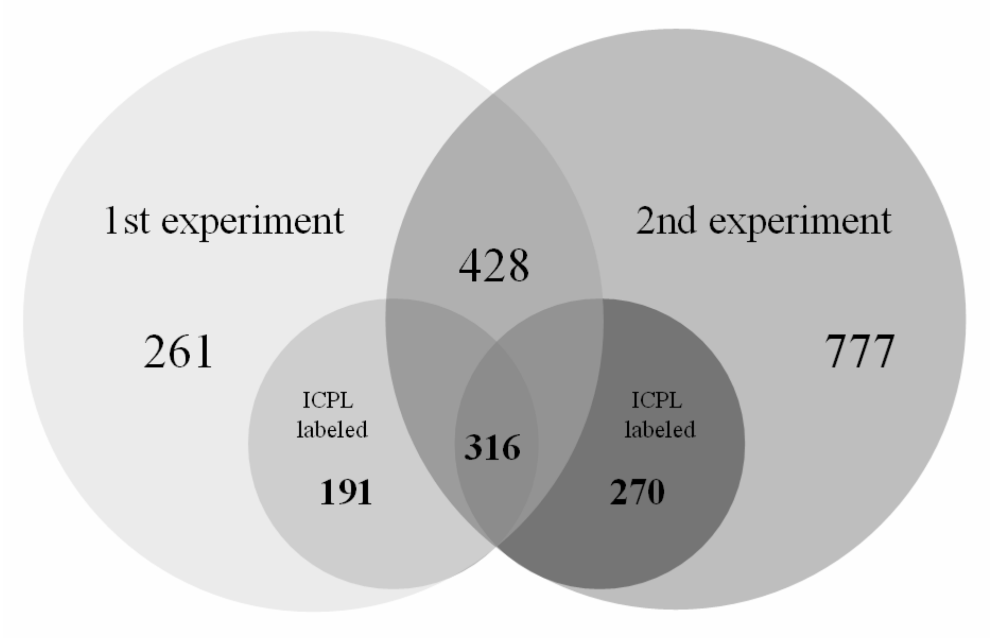


Figure 17. Comparison of two ICPL™ experiments. The amount of identified and quantified proteins in two independent experiments is displayed. The outer circles cover all identified proteins whereas the small inner circles include only the labeled ones. Proteins in the overlapping area are found in both experiments.

Two thirds of the proteins identified in the first experiment (428) were also identified in the second analysis. Almost similar values were obtained for the ICPL™ labeled proteins of which 316 were identified in each experiment. This difference is caused by the divergent number of identified proteins in both experiments. However, the reproducibility of the two experiments is in the range for high throughput proteomic analyses and comparable to other reports [77].

The cellular distribution of the identified 1466 different proteins into the particular compartments is shown in figure 18 (p. 33). The majority of the identified proteins localize to the cytoplasm (32.2%) and the nucleus (25.3%). About 10% of the identified proteins have been classified as membrane proteins. Since approximately 20% of all human proteins are known to be membrane proteins a considerable part of this group has been identified. Proteins exhibiting high pI values like histones were additionally detected. Both groups are known to be absent using two-dimensional gel-electrophoresis and are found herein due to the combination of one-dimensional gel-electrophoresis and reversed phase HPLC. In a minor abundance mitochondrial proteins and proteins from compartments like endoplasmic reticulum (ER), ribosomes, lysosomes or peroxisomes were retrieved.

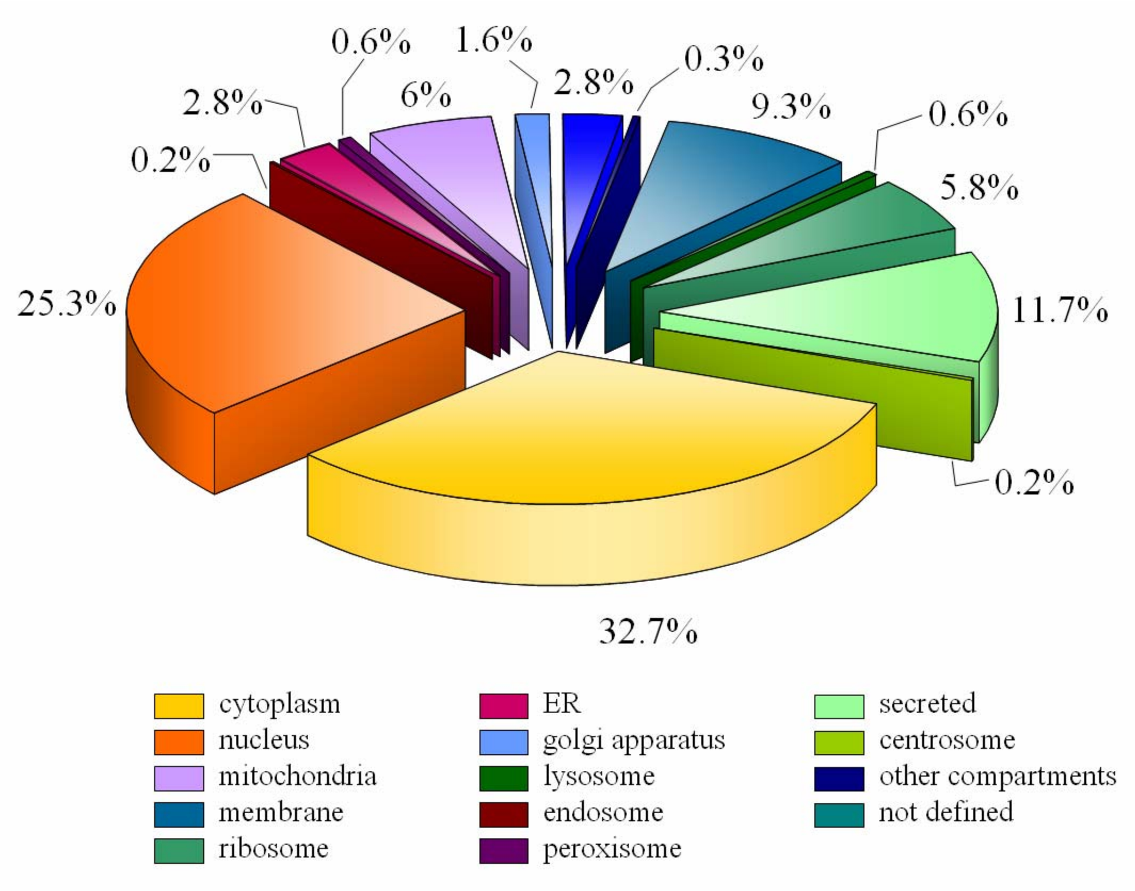


Figure 18. Allocation of the identified and quantified proteins in C3*bot*-treated SH-SY5Y cells.

A summary of all proteins found with an altered abundance by a factor of at least 1.5 due to C3*bot*-treatment is given in supplementary table 3 (p. 139). The table represents 254 proteins of which 140 were found down- and 114 up-regulated. Besides the regulation factor, the average H/L ratio with standard deviation and variation, accession number, MASCOT score, molecular mass, sequence coverage and number of identified and labeled peptide-pairs are also given. The proteins are sorted by functional categories. This classification is, however, to a large extent arbitrary, since many of these proteins are multitasking proteins playing different roles in diverse cellular processes and thus, they are multiply listed in the table.

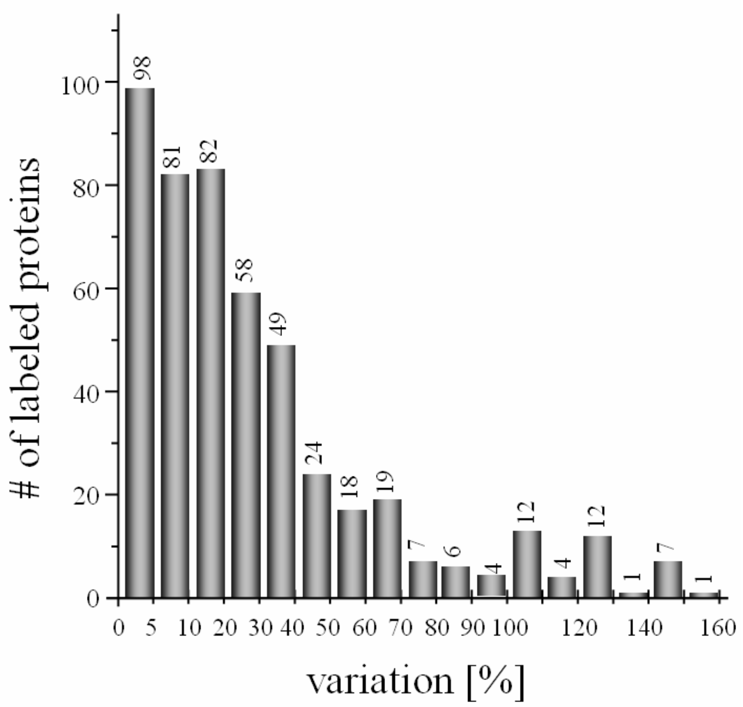
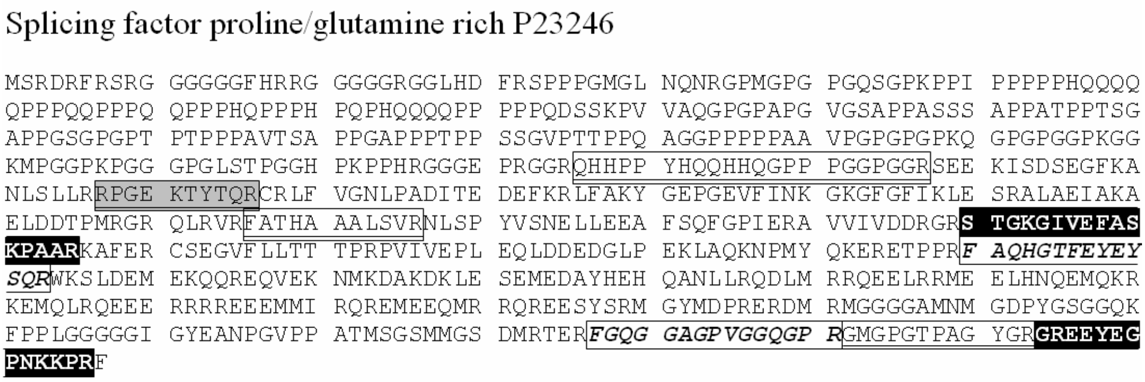


Figure 19. Variation in two different experiments of all ICPL™ labeled and identified proteins. The variation was calculated of all H/L ratios of the identified protein. The graph includes the variation of proteins found in both experiments.

The variation of the identified labeled peptides of one protein has found to be below 5% for all proteins showing the validity of the ICPL™ labeling reaction. Comparing the two conducted ICPL™ experiments the variation for identical proteins was found to be in the range 0 to 160% (Figure 19). Most proteins differ in their abundance by less than 50% but 15% showed variations of up to 160%. The average variation is at 30% which correlates well with the starting experiments where cell lysates were labeled in a 1:1 stoichiometry (Figure 16; p.30).

These data display the high level of reproducibility of the ICPL™ based experiments. Only a minor part of the identified proteins varies from experiment to experiment by a higher factor. A detailed view on those proteins exhibiting higher differences shows that most of them were quantified on the basis of few labeled peptides and for some of these peptides a modified form, e.g. oxidized peptide, was identified. Probably, the heavy-labeled peptide might be oxidized to a higher extend than the light-labeled one leading to an altered regulation level.

Another effect leading to variations could be a different regulation between full size proteins and their fragments. As example the splicing factor proline/glutamine rich and one of its fragments is shown (Figure 20). The full size protein is detected in the acrylamide gel at 53 kDa. Apparently a fragment of this protein has been identified in a gel area corresponding to about 34 kDa in both labeling experiments. The ICPL™ labeled peptide RPGEKTYTQR found in the smaller fragment was up-regulated whereas the peptides STGKGIVEFASKPAAR and GREEYEGPNKKPR found in the full size protein were down-regulated (black areas). This might be explained by partial degradation of the full length protein resulting in its decrease. The remaining fragment containing peptide RPGEKTYTQR should be stable and thus appears in a higher amount after ICPL™ labeling. If whole proteins and fragments are not clearly separated by SDS-PAGE, it is difficult to keep them apart by MS/MS analysis. This might lead to variations in the quantitative analysis. The same is also true if a protein contains post-translational modifications that influence labeling, separation by RP-chromatography or MS measurement.



Splicing factor proline/glutamine rich P23246

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MSRDRFRSRG GGGGGFHRRG GGGGRGGLHD FRSPPPGMGL NQNRGPMGPG PGQSGPKPPI PPPPPHQQQQ
QPPPQQPPPQ QPPPHQPPPH PQPHQQQQPP PPPQDSSKPV VAQGPGPAPG VGSAPPASSS APPATPPTSG
APPGSGPGPT PTPPPAVTSA PPGAPPPTPP SSGVPTTPPQ AGGPPPPPAA VPGPGPGPKQ GPGPGGPKGG
KMPGGPKPGG GPGLSTPGGH PKPPHRGGGE PRGGRQHHPP YHQQHHQGPP PGGPGGRSEE KISDSEGFKA
NLSLLRRPGE KTYTQRCRLF VGNLPADITE DEFKRLFAKY GEPGEVFINK GKGFGFIKLE SRALAEIAKA
ELDDTPMRGR QLRVRFATHA AALSVRNLSP YVSNELLEEA FSQFGPIERA VVIVDDRGRS TGKGIVEFAS
KPAARKAFER CSEGVFLLTT TPRPVIVEPL EQLDDEDGLP EKLAQKNPMY QKERETPPRF AQHGTFEYEY
SQRWKSLDEM EKQQREQVEK NMKDAKDKLE SEMEDAYHEH QANLLRQDLM RRQEELRRME ELHNQEMQKR
KEMQLRQEEE RRRREEEMMI RQREMEEQMR RQREESYSRM GYMDPRERDM RMGGGGAMNM GDPYGSGGQK
FPPLGGGGGI GYEANPGVPP ATMSGSMMGS DMRTERFGQG GAGPVGGQGP RGMGPGTPAG YGRGREEYEG
PNKKPRF
```

Figure 20. Protein sequence and MS/MS sequence coverage of the proline/glutamine rich splicing factor. All peptides identified by MS/MS analysis are boxed. Bold characters indicate those peptides found in the full size protein at 53 kDa as determined by SDS-PAGE; underlined peptides were identified in the fragment at 34 kDa. Peptides indicated by italic characters have been found in both. The peptide identified as down-regulated are underlayed in grey and the up-regulated peptide is underlayed in black.

In a deeper examination of table 3 (p. 139) about 254 proteins were found regulated by a factor higher than 1.5. Out of them 140 proteins were found down-regulated and 114 up-regulated. 124 of the regulated proteins have been found regulated more than two-fold. A minor abundance of about 24 proteins was altered more than five-fold in response to the C3*bot* treatment which are less than 4% of the identified proteins (Figure 21). Six Proteins were altered by more than factor ten and highest changes of factor 21.5 and 16.5 were measured for histones H1.1 and H1.4.

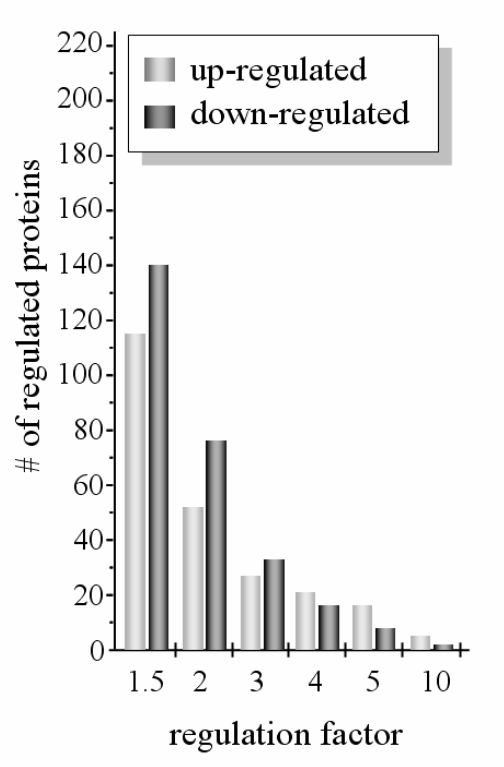

Figure 21. Number of the proteins regulated by factors ≥1.5.

All proteins with a changed abundance were grouped into functional categories (Figure 22; p. 37). The majority of proteins belonging to the categories “cell growth and proliferation”, “cell morphology”, “cell morphology and differentiation”, and “signal transduction” were in general down-regulated.

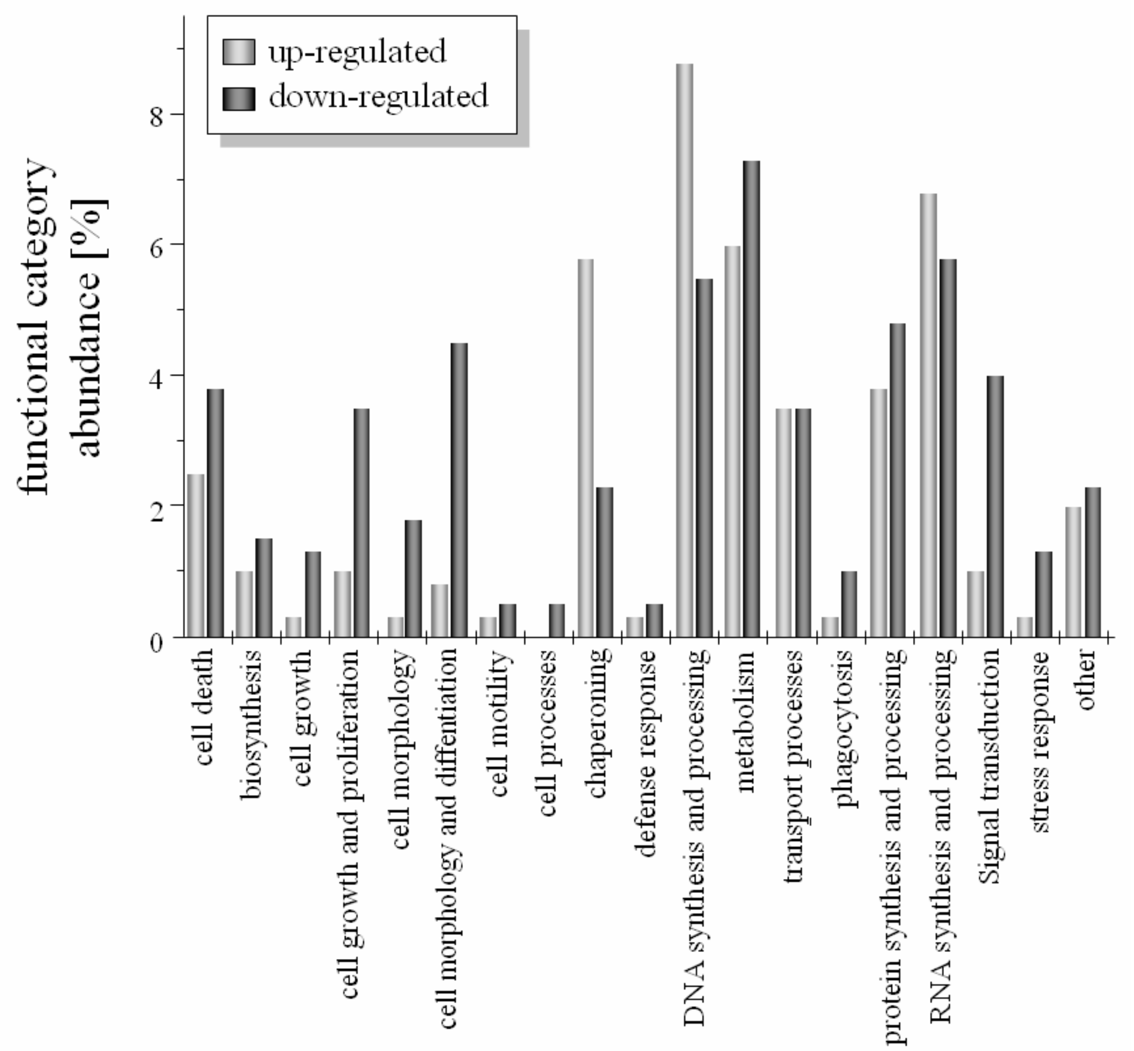

Figure 22. Abundance of proteins and their functional classes. Only proteins regulated by more than factor of 1.5 are included in this functional classification. The gray bars show up-regulated and the black bars indicate down-regulated proteins.

In contrast proteins belonging to the categories “chaperoning”, “DNA synthesis and Processing”, and “RNA synthesis and processing” were up-regulated. Interesting effects became more obvious after categorizing the regulated proteins in more detail (Figure 22).

The group “chaperoning” was divided into five subgroups (other chaperoning, protein folding, histone modification, stress response, and nucleosome assembly), and it became obvious that the general increase of the herein classified proteins is only due to proteins involved in the nucleosome assembly (Figure 23 B) because for the other functions the down-regulation prevails. A similar effect was identified analyzing proteins categorized as “protein synthesis and processing”: a deeper analysis revealed that only those proteins participating in protein polymerization processes like filament formation, are down-regulated to a high extend (Figure 23 D). This fits well to the cytopathic effects of the C3*bot* on SH-SY5Y cells. Also proteins involved in the microtubule network are generally down-regulated (Figure 23 F). Interestingly, nearly all identified glycolytic enzymes are down-regulated (Figure 23 E) whereas proteins of the fatty acid or lipid metabolism are up-regulated, and other metabolic proteins remain unchanged.

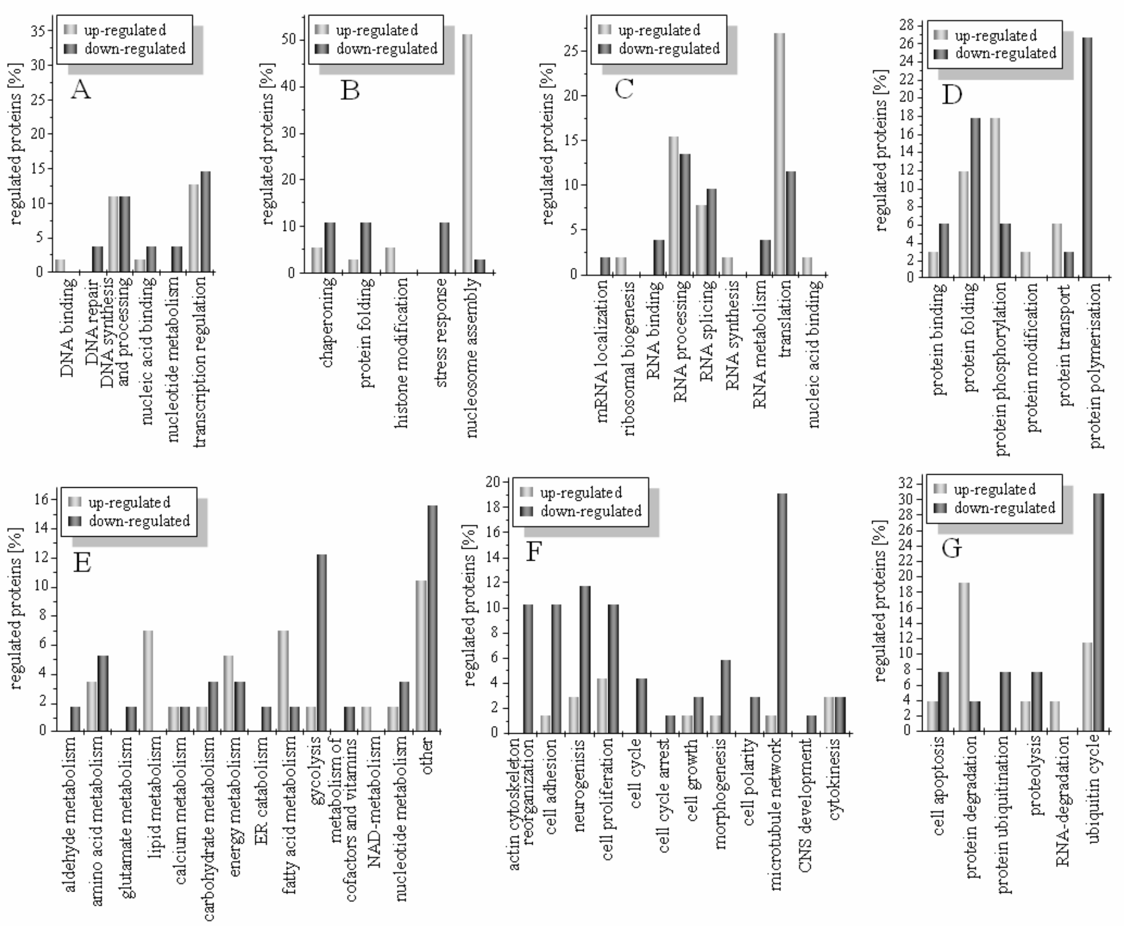

Figure 23. Regulation of the proteins in different functional classes. All proteins are regulated at least by a factor of 1.5. The functional classes are **A** DNA synthesis and processing, **B** chaperoning, **C** RNA synthesis and processing, **D** protein synthesis and processing, **E** metabolism, **F** cell morphology and growth and **G** cell death. Gray bars display up-regulation and black bars indicate down-regulation.

3.2 Quantitative proteomics using the iTRAQ™ and 2D-LC-MS/MS technology

3.2.1 Technical development of the iTRAQ™-approach using standard mixtures

The herein used 2D-LC-MS/MS approach is similar to the so called multidimensional identification technology (MudPit) that is based on the combination of cation exchange with RP-chromatography in a HPLC-system [68]. To establish the 2D-HPLC-MS/MS system C3 exoenzyme, BSA, Toxin A, and OVA were cleaved by trypsin, and the peptides were labeled by the iTRAQ™ reagent harboring the reporter ions 115 and 116 for C3, BSA, and Toxin A in the ratios 1:2, 1:2, 1:1 and the reporter ions 114 and 117 in a ratio of 1:3 for OVA. Analysis was done in four repetitions using the 2D-LC-MS/MS approach (Figure 24). All five proteins were identified after data base analysis with a high Mascot score (C3 83, BSA 868, Toxin A 202, OVA 69).

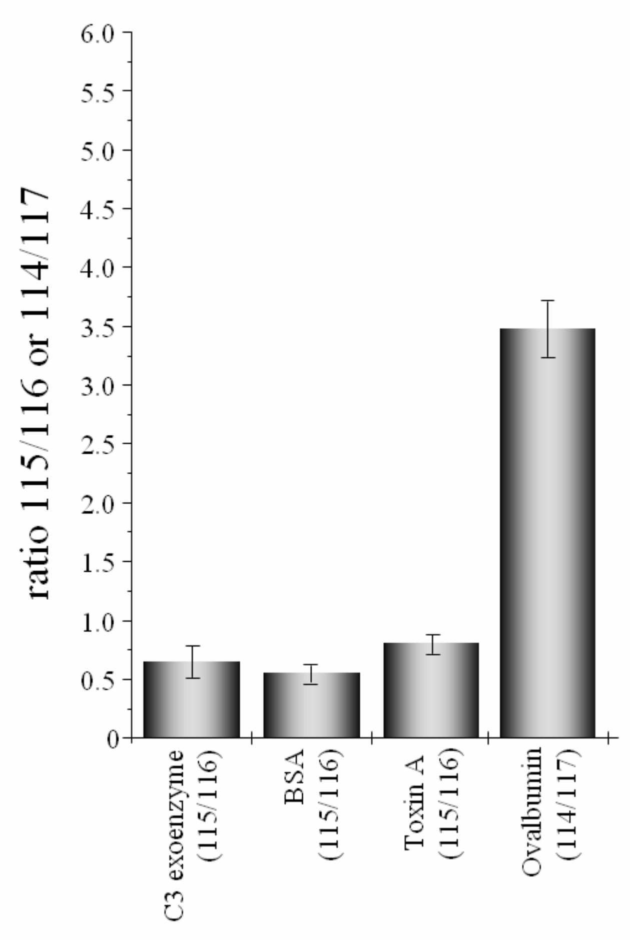

Figure 24. Quantitation of C3*bot* exoenzyme, BSA, Toxin A and *C. difficile* OVA in four repetition experiments. C3 exoenzyme as well as BSA was labeled in a L/H ratio of 1:2 in the standard mixture, Toxin A with a L/H ratio of 1:1 and ovalbumin with an L/H ratio of 1:3 for iTRAQ™ reporters 114 and 117. The expected regulation factors for C3 exoenzyme and BSA are 0.5, for Toxin A 1.0 and for ovalbumin 3.0.

For C3 exoenzyme (2 peptides), BSA (12 peptides) and OVA (4 peptides) all of the identified peptides were labeled whereas only 3 out of 4 peptides were found labeled for Toxin A. Sometimes, the iTRAQ™ kit containing labeling reagents were of bad quality and contaminated by each other, e.g. the reagent with the reporter group 114 might also contain some amount of the reporter group 115. Due to the presence of only the used reporter ions 114 and 117 in OVA and reporter ions 115 and 116 for C3, Toxin A and BSA, the examination of all relative ratios demonstrated that the reagent had the guaranteed quality and the reaction was nearly complete. If unlabeled C3 exoenzyme, BSA, Toxin A or OVA have been digested with trypsin and analyzed by 2D-LC-MS/MS a similar but unlabeled pattern was obvious for these proteins showing as well as the ICPL™ technique the compatibility of the iTRAQ™ label with 2D-LC-MS/MS. C3 exoenzyme, Toxin A, BSA and OVA were found in all expected ratios with a variation between 10% and 20% for all identified labeled peptides (20% for C3 exoenzyme, 12 % for BSA, 10% for Toxin A, 11% for ovalbumin). The standard deviation of the regulated peptides in a unique experiment is also between 10% and 20% which was previously shown by Ross et al. [55]. Concluding the results the regulation must be at least 10% to be sure that a protein is really regulated in response to C3*bot* and all peptides used for quantification must be identified by MS/MS analysis.

3.2.2 Analysis of C3bot induced changes of the SH-SY5Y proteome by iTRAQ™

Proteins from C3*bot*-treated and untreated SH-SY5Y cells were enzymatically cleaved and peptides were labeled with the iTRAQ™ reagent containing the reporter ions 114 and 117. Peptides were separated using the established on-line-2D-HPLC approach and the peptides were identified and quantified by a MALDI mass spectrometer.

The goals of first SCX-dimension in the performed quantitative 2D-LC-proteome analysis are the fractionation of a complex peptide mixture for subsequent peptide separation by RP-HPLC and the depletion of the excess iTRAQ™ reagent. Figure 25 (p. 41) represents a two-dimensional mass to charge plot for different SCX fractions eluted by the indicated KCl plugs.

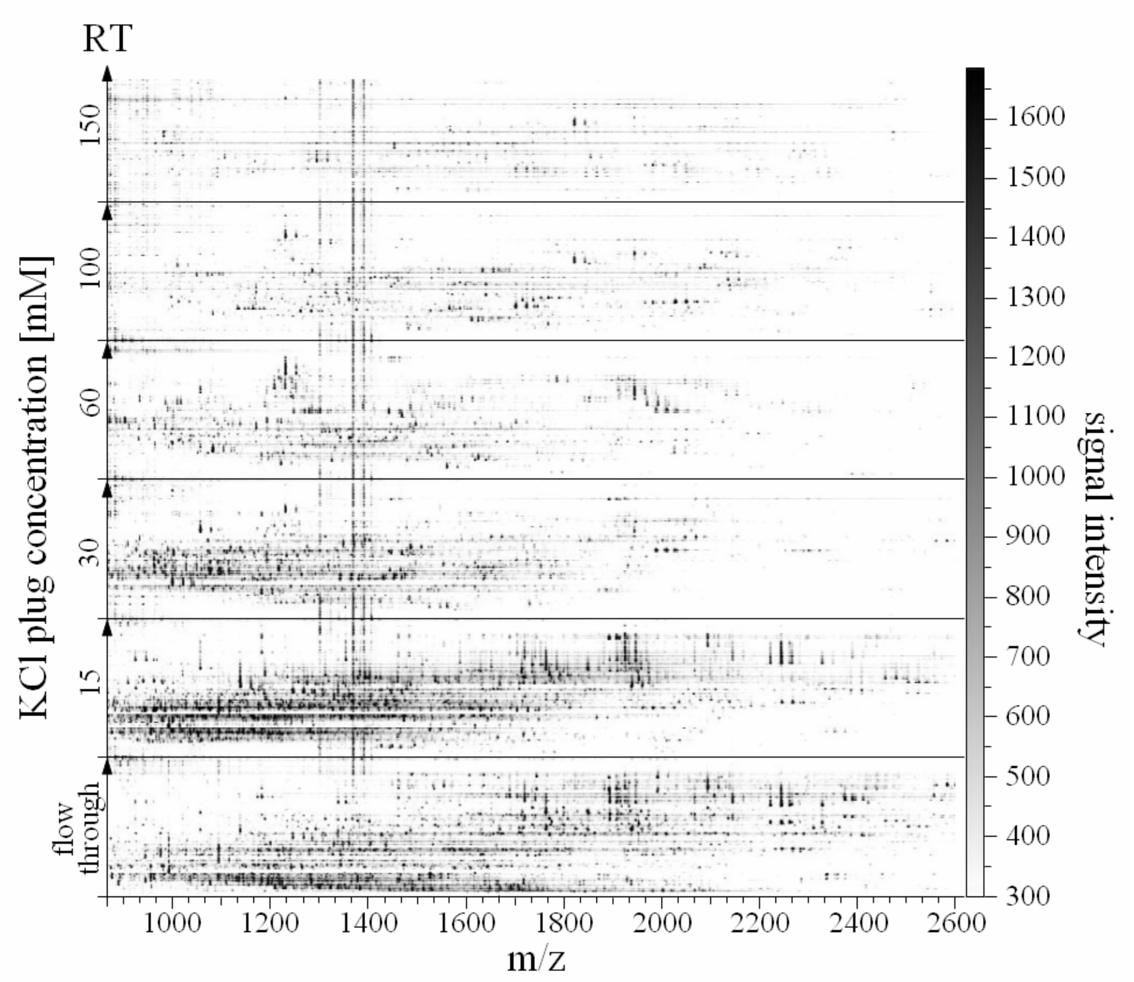

Figure 25. Two-dimensional mass to charge plot of the HPLC fractions. The intensity of the mass signals is coded by the gray scale on the right. Flow through and five salt plug elutions are represented by the different parts of the blot.

Peptides not retained at the SCX-column are depicted in the flow through. With increasing salt concentrations the number of eluted peptides decreases. Most peptides eluted with the flow through and the first two salt plugs. The salt strength was ranging in a narrow window from 0 to 30 mmol/L potassium chloride. This can be explained by the fact that the sample components were not individually separated but peptides with the same charge (1+, 2+, 3+, and 4+) elute from the column as poorly resolved clusters in the order of increasing charge [70, 78].

Cell lysates of human origin represent very complex protein mixtures of about 10.000 different proteins. The preserved peptide mixtures contain more than 200.000 peptides and, thus have a high complexity. A total of 355 proteins was identified with the established fast 2D-LC-MS/MS approach in five replicated measurements (Figure 26). Out of them 122 proteins were identified in more than one experiment, but 233 proteins were detected only once and assigned as “one-hit-wonders”.

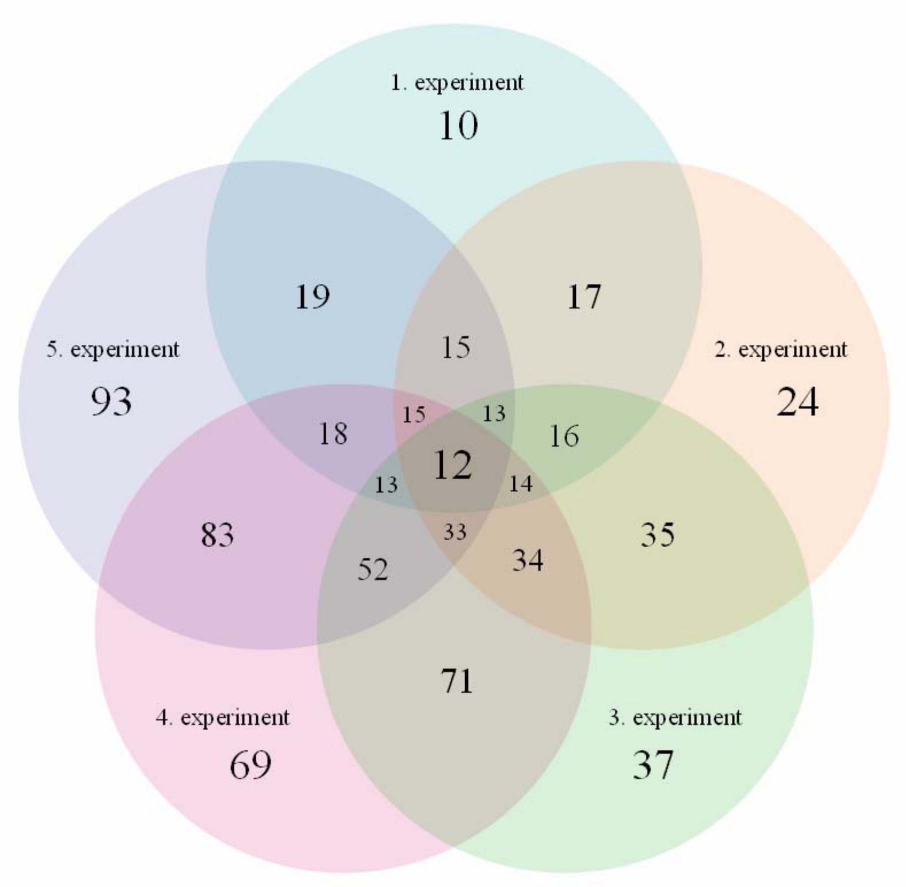

Figure 26. Number of identified proteins in five independent experiments. Proteins in the overlapping areas are found in two, three, four or all five experiments.

Only 12 proteins (3.4%) were identified in each of the five experimental setups. These 12 proteins belong to the high abundant proteins and are HSP 70 protein 1, heterogeneous nuclear ribonucleoprotein A3 and A2/B1, histone H3.1t and H4, nucleolin, nucleophosmin, pepdidyl-prolyl cis-trans isomerase A, profilin-1, stathmin, triosephosphat-isomerase, tubulin alpha-1A chain, and vimentin. Out of the identified proteins 120 were identified by unlabeled peptides with Mascot scores up to 60. At the first view the possibility of false positive findings might arise but the comparison with previous experiments confirms the identity of proteins identified with such low Mascot scores. Additionally all data were analyzed using decoy databases (p. 27) and scores below 35 were obtained indicating the specificity of the identified proteins. A probable explanation for the unlabeled peptides might be the incomplete labeling of the peptides probably by competition effects due to the high complexity of the peptide mixtures or different tagging reactions due to altered modifications in treated and untreated cells (previously described in the ICPL™ experiment, p. 35).

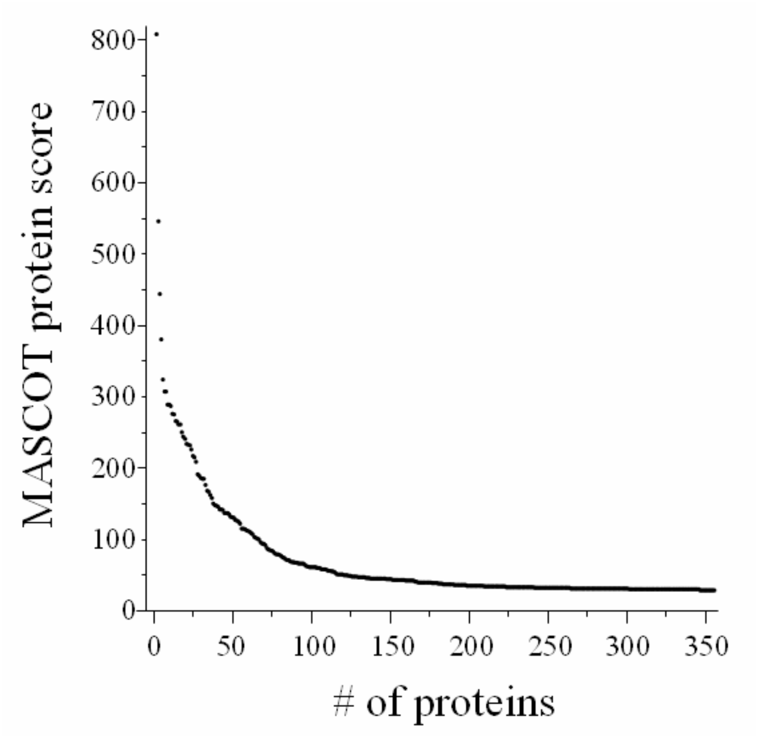

Figure 27. MASCOT protein score of the identified proteins.

Only one third of the identified proteins have been found with a score above 50, but up to 20% of all proteins were found with a score higher than 100 (Figure 27). This fits well to the results obtained in the GeLC-MS/MS experiments (Figure 13, p. 27). Better identification rates and Mascot scores might be possible if more fractions could be generated in the first dimension. The maximum fraction number in this study was limited by the size of the MALDI target plate, on which only 1536 single fractions could be spotted. The software did not allow combining more than one target plate for one analysis.

The allocation of the identified 355 different proteins into the particular compartments is similar to the distribution of the identified proteins in a standard SH-SY5Y screening (p. 28) or to the proteins identified in the ICPL™ (p. 33). Of the identified proteins 29.3% are located in the cytoplasm and 22.9 in the nucleus. About 9.7% of the identified proteins appear to be membrane proteins. With the iTRAQ™ approach as well as with the ICPL™ technique mitochondrial proteins and proteins from other compartments (ER, lysosome, peroxisome, Golgi apparatus) were retrieved in a minor abundance of up to 6%.

Proteins found regulated, using the iTRAQ™ method are shown in supplementary table 4 (p. 150). The proteins were categorized according to common functional features. For the ease of orientation, proteins were numbered according to the order of their appearance in the table. Besides the protein number, the average H/L ratio with standard deviation and variation, accession number, Mascot score, molecular mass, pI, sequence coverage and number of identified and labeled peptides are also displayed. With the applied technique 166 proteins were found regulated by at least 10% for the up-regulated proteins or 5% for the down-regulated proteins. The majority of 155 proteins was found up-regulated. Only 11 proteins were found down-regulated (7%), including α-2-HS-glycoprotein (3), macrophage migration inhibitory factor (12), stathmin (31), chromosomal protein 5 (56), poly-A-binding protein, pseudogene 2 (78), lamin A/C (86), the chromosomal region 20B protein (92), pygopus homolog 2 (113), the zinc finger protein ZFPM1 (122), HSP 27 (126) and one uncharacterized protein C8orf12 (166).

The variation of the identified labeled peptides of one protein was found to be below 10% for all proteins showing the validity of the iTRAQ™ labeling reaction. The comparison of all five executed experiments leads to a variation of abundance for identical proteins between 0% and 30%. The majority of proteins (53%) show a variation of less than 10% (35% were found regulated with only one peptide). The average variation of abundance of proteins identified in multiple iTRAQ™ experiments is 6% which fits well to the average variation of 10% obtained for the standard proteins.

The abundance of about 10 proteins was altered more than 50% in response to the C3*bot*-treatment which are less than 6% of the identified labeled proteins. Two proteins were altered by more than 70% and highest changes were measured for histone H4 (46) with 1.78, the transcription factor II-I (102) with 2.08 and the cell antigen II (156) with an altered concentration of factor 2.32 (Proteins displayed in table 4; p. 150).

The most potent down-regulation of factor 0.85 was recorded for stathmin (31) and with factor of 0.62 for the uncharacterized protein C8orf12 (166). This slight down-regulation correlates with the results obtained with the ICPL™ approach. Recently, Berenjeno et al., analyzed the influence of constitutively active RhoA on the gene expression pattern of NIH3T3 cells applying the DNA microarray technique [79]. In this study an up-regulation for stathmin was observed. In the present investigation RhoA was completely inactivated by the C3*bot* treatment and the opposite effect, a down-regulation of stathmin, was obtained.

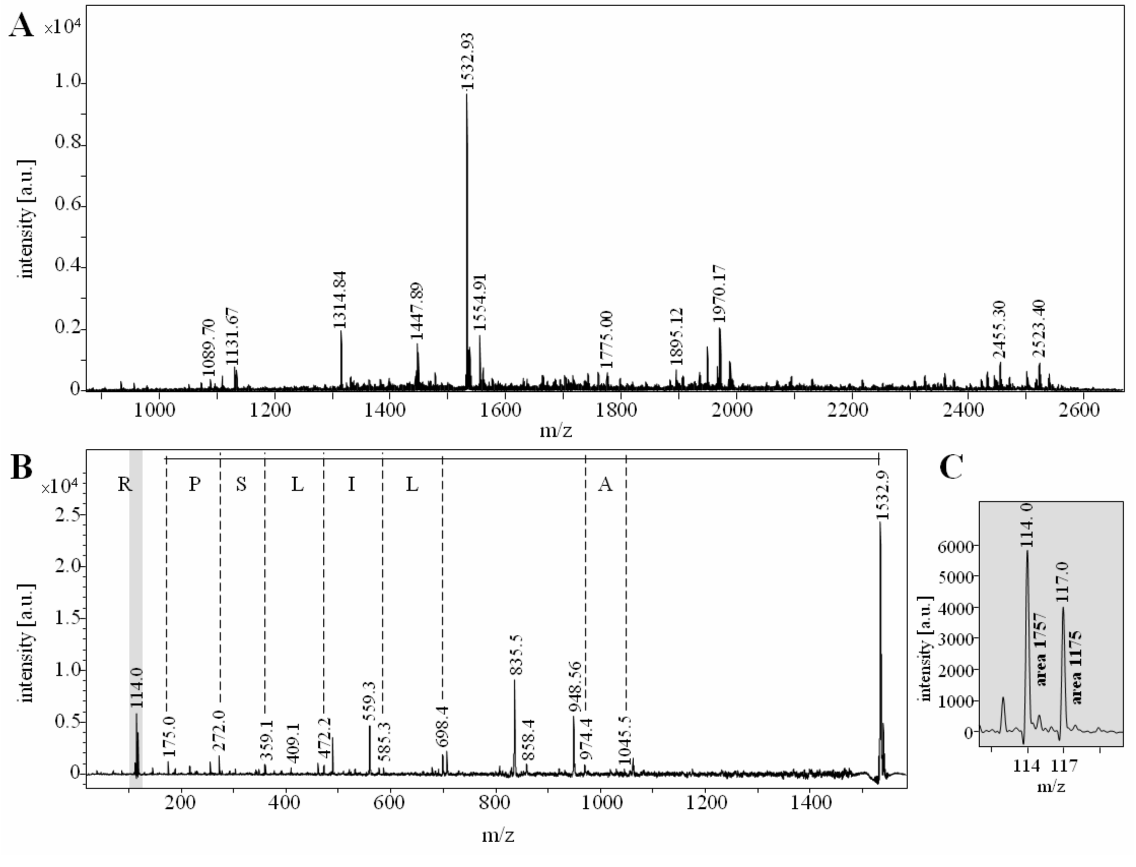

Figure 28. Mass spectra of the down-regulated stathmin. A MS spectrum of the fraction containing the labeled peptide belonging to stathmin is displayed. **B** MS/MS spectrum of the 1532.9 Da peptide with the calculated y-ion-series of the sequence ASGQAFELILSPR. **C** Signals belonging to the reporter ions 114 and 117 of the N-terminal labeled peptide. The m/z of 117 corresponds to the amount of stathmin in the C3 exoenzyme-treated extract.

Figure 28 (p. 45) shows the MS/MS analysis of one peptide derived from stathmin. The peptide containing the sequence ASGQAFELILSPR with a molecular weight of 1532.9 Da was found in the flow through with a Mascot ion score of 64. The regulation was calculated by correlating the peak areas of the 114 and 117 reporter ions. The calculated ratio was 0.67. Stathmin was characterized by 6 different peptides and quantified by 10 H/L ratios. The standard deviation was 14%.

In contrast the histone H4 was quantified with 43 H/L ratios and an up-regulation of factor 1.78 was found (Figure 29). The analyzed altered abundance is highly similar to the regulation found using the quantitative ICPL™ as previously described. The peptide ISGLIYEETR (m/z 1324.74) was identified by a Mascot ion score of 75 and the calculated ratio for this example is 1.72. The overall variation is only 7.5%. Thus, these data display a high level of reproducibility of the iTRAQ™ based experiment.

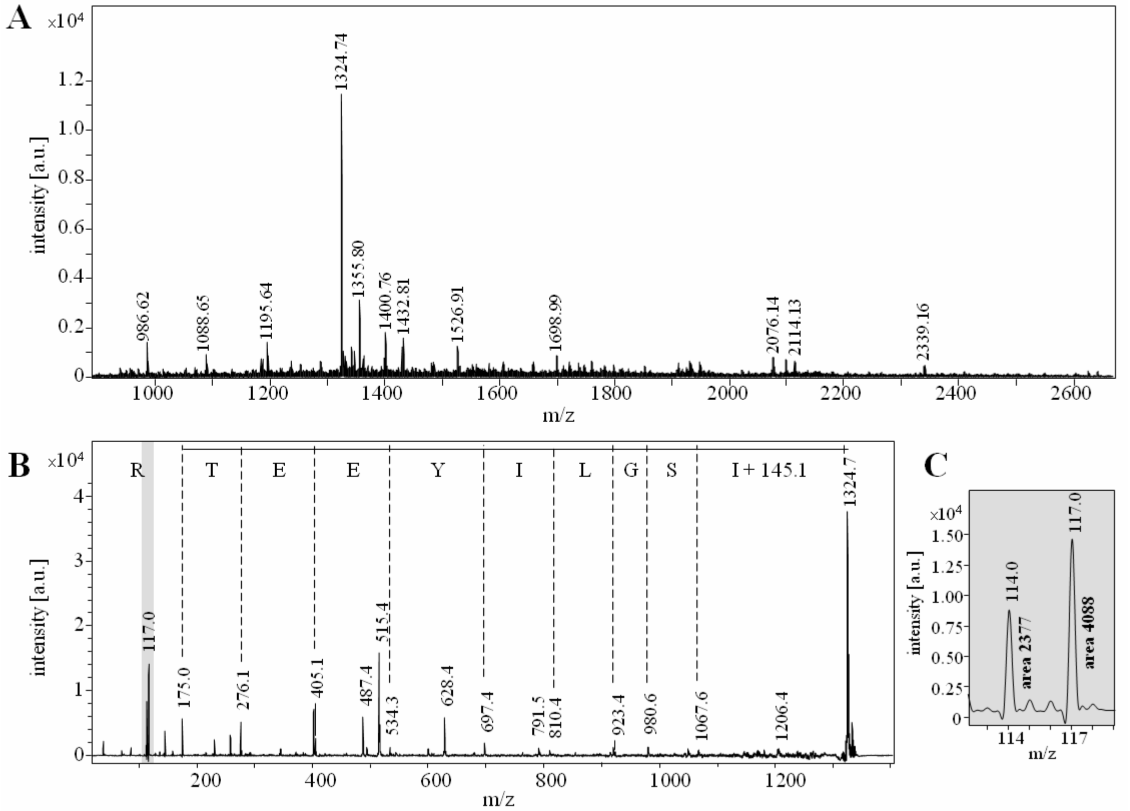

Figure 29. Mass spectra of the up-regulated histone H4. A MS spectrum of the fraction containing the labeled peptide belonging to histone H4 is displayed. **B** MS/MS spectrum of the chosen peptide with the calculated y-ion-series of the sequence ISGLIYEETR, MW 1324.7 Da. **C** Signals belonging to the reporter ions 114 and 117 of the N-terminal labeled peptide. The m/z of 117 corresponds to the amount of H4 in the C3 exoenzyme-treated extract.

However, with this method some contradictory results were produced, too. Using the iTRAQ™ approach alpha- and beta-tubulin were found up-regulated by a factor up to 1.3 whereas applying the ICPL™ method an up to 3-fold down-regulation was denoted. To examine these results western-blot analyses were applied.

3.3 Confirmation of data by western blot analysis

To validate the observations found by ICPL™ or iTRAQ™ labeling and MS analysis, western blot analysis were performed to quantify the amount of histone H1, H3, H4 as well as α-tubulin and β-tubulin. All three histones were found up-regulated in the ICPL™ approach (H1 20-fold, H3 and H4 two-fold). Using the iTRAQ™ method H3 and H4 were found slightly up-regulated (up to 1.78). Both tubulin subunits were identified as down-regulated in the ICPL™ (up to 3-fold) and up-regulated in the iTRAQ™ approach (1.3 fold), and the western blot was used to confirm either the ICPL™ or iTRAQ™ method. All western blot analyses were correlated to the amount of GAPDH that exhibited no observable regulation. The histone H1 up-regulation was approved by western blot. However, for H3 only a slight increase was determined and H4 was up-regulated to almost the same extend as H1 (Figure 30).

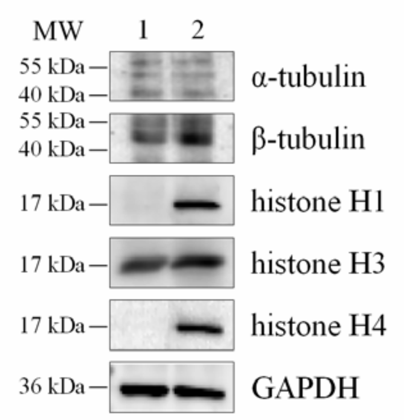

Figure 30. Western Blot analysis of α- and β-tubulin and the histones H1, H3 and H4. Lane 1 is the analysis of the untreated cell lysates and lane 2 displays the analysis of the C3*bot*-treated cell lysates. Extracts were separated by SDS-PAGE, blotted onto nitrocellulose membranes and detected with the appropriate primary and secondary antibodies.

It is obvious that α-tubulin as well as β-tubulin were not down-regulated as prognosticated by the ICPL™ method. In the performed western blot analyses α-tubulin remained stable whereas β-tubulin showed an increase in its abundance in C3*bot*-treated cells.

Although polyclonal antibodies were used, it might be possible that the western blot analysis was influenced by post-transcriptional modifications, for example acetylation. If the epitopes of the antigen are blocked by acetylation, they cannot be recognized by the antibody. The enormous up-regulation of the histones found by ICPL™ fits well to the western blot analysis. Since histones are highly modified at their lysine residues [88], this up-regulation might also indicate a change in modification of lysine residues. Particular this might be true for histone H4, which is only slightly changed as evident from the ICPL™ approach, but tremendously up-regulated as determined by western blot analysis.

4 Discussion

The exoenzyme C3 form *Clostridium botulinum* (C3*bot*) is the prototype of C3-like ADP-ribosyltransferases, which exclusively modify the Rho subfamily GTPases Rho A, -B, and -C by recruiting the ubiquitous co-substrate NAD^+ to transfer the ADP-ribose moiety onto asparagine-41 of Rho [8]. Rho-GTPases are molecular switches that control a variety of signal transduction pathways in eukaryotic cells [11][13][17-19]. They are master regulators of the actin cytoskeleton, cell polarity and they are involved in cell cycle progression, transcriptional activity, vesicular transport pathways, cell migration, and microtubule dynamics [15, 16]. The specific inactivation of Rho-GTPases results in reorganization of the actin cytoskeleton and cell death [20]. There are a lot of reports showing that Rho proteins are involved in neuronal development [22-24]. Recently, it has been shown that C3*bot* exhibits neurotrophic effects on murine hippocampal neurons to result in axonal growth. However, similar effects were observed with the enzymatic inactive C3*bot* suggesting an intrinsic new neurotrophic function of C3*bot* that is definitely not mediated by a direct inhibition of Rho A, B or C [38].

In this work SH-SY5Y cells were chosen as model system to characterize the effects of the C3-exoenzyme from *C. botulinum* on the protein profile of this human neuronal cell line. A large scale quantitative proteomics approach was initiated using isotope-coded protein label (ICPL™) [56, 62] and isobaric tags for relative and absolute quantitation (iTRAQ™). These methods were applied for a quantitative comparison of proteins in SH-SY5Y cells [59]. ICPL™ is based on isotope tagging at free lysine residues and the N-terminus of intact proteins whereas the iTRAQ™ reagent was developed to achieve a global labeling at the free amino groups on peptide level [55, 80]. Since the ICPL™ labeling is compatible with commonly used protein and peptide separation techniques; SDS-PAGE was used for protein separation and RP-HPLC for subsequent peptide separation followed by sequence analysis using MS/MS and database search. Because the iTRAQ™ technique is based on peptide labeling, a method, well suited for the separation of highly complex peptide mixtures, has been developed, which provides high peak capacity and identification with low detection limits. Thus, for the separation of the iTRAQ™ labeled peptides a technique combining multidimensional chromatography and mass spectrometry was established.

This approach, which is similar to MudPit [68], involves a strong cation exchange (SCX) column on-line coupled with a reversed phase (RP) column in the second dimension that is coupled with MS/MS analysis for sequence identification.

4.1 ICPL™ vs. iTRAQ™ – A comparison

An overall amount of 1774 different proteins was identified by using the ICPL™ and iTRAQ™ technologies. However, the proteome profiling of SH-SY5Y cells without labeling resulted in 3399 identified proteins, which is double the amount. When proteins are labeled with the ICPL™ reagent, the lysine cleavage side gets lost resulting in less produced peptides and decreased identification rates. Out of the 1774 proteins, 417 have been found altered by C3*bot*-treatment. For the ICPL™ approach high quality data sets were generated that enabled the identification of 1466 proteins and 53% out of them could be quantified. The ICPL™ labeling is based on modifying the proteins with different stable isotopes of nicotinic acid at the protein N-terminus and lysine residues. The tagging on protein level enables the highly demanded separation of the proteins using gradient gel-electrophoresis. Labeling efficiency of the detected lysine-containing peptides was nearly 100% indicating the high efficiency of the established protocol. The limiting fact, that only the N-terminal peptides and peptides including lysine residues ware tagged elucidates why only 53% of the identified proteins have been found labeled. Therefore another quantitative approach was examined. The iTRAQ™ method labels amino groups at peptide level. Thereby all peptides analyzed by MS/MS should be found at least N-terminal labeled which results in a high quantitative recovery [55]. However, the iTRAQ™ labeling coupled with multidimensional protein identification technology resulted in only 355 identified proteins which is only one fourth of the proteins identified by ICPL™ and GeLC-MS/MS. Only two thirds of the identified proteins were retrieved labeled with iTRAQ™ which might indicate an incomplete labeling. Comparison with the SH-SY5Y proteome screenings confirm the abundance of the unlabeled proteins in the cell extracts and underlines that an incomplete labeling had occurred. This probably happens due to the complexity of the system accompanied by competition reactions during the labeling procedure.

The identification rate in the iTRAQ™ experiment is low, compared to the GeLC-MS/MS approach. The multidimensional chromatography coupled with mass spectrometry used in this work, was limited by the maximum amount of only eight fractions from SCX and a reduced and short separation by RP-chromatography on one MALDI target plate. This technical limitation might have resulted in signal suppression and overlapping signals during MS/MS analysis, which leads to low identification scores below the limit of 30. To overcome the problems of high complexity of the biological systems and the wide dynamic rage of protein concentrations in the cells, a method with a higher resolution power, higher peak capacity and lower detection limits, that can employ more fractions (= more MALDI targets) should be used.

Nearly 100% of all identified proteins were found slightly up-regulated with the iTRAQ™ approach with a maximum of 2.3 fold for cell antigen 32. Even in five repetitions with different reporter ions, the same effect was obvious. The determined altered expression of histone H4, stathmin, ribosomal proteins, ubiquitin or prohibitin, a mediator of transcriptional activity [81] correlates well with the ICPL™ experiment.

Both methods the GeLC-MS/MS technique with ICPL™ labeling as well as the 2D-LC-MS/MS approach with iTRAQ™ tagging show similarities in the distribution of the Mascot scores and the allocation of the identified proteins in cells. It is obvious that the majority of proteins was identified with Mascot scores between 40 and 100 which is usual provoked by the complexity and the dynamic range of the measured samples.

Most of the identified proteins were localized in the cytoplasm (about 30%) or the nucleus (about 20%). Because of the lower abundance in the cell, proteins from smaller compartments like the lysosome or the Golgi apparatus were found in a minor quantity. Detected and quantified membrane (10%) or ribosomal proteins would have escaped detection by the classical 2-DE-MS/MS analysis due to their physicochemical properties and their translational regulation. That underlines the importance of examination, verification and application of both quantitative mass spectrometric methods.

Thus, repetitions of the experiments often end up in a low reproducibility rate. Two thirds of the identified proteins either with the GeLC-MS/MS technique as with the 2D-LC-MS/MS approach were only detected once (“one-hit-wonders”). Several factors are crucial for high reproducible analysis of complex mixtures including sample quality, sample preparation, the separation efficiency of the chromatographic system and the performance of the mass spectrometer [77, 82]. The average variation of the identified labeled proteins of the biological sample was 6% for the iTRAQ™ experiment and 30% for the ICPL™ approach. To minimize the rate of false positive regulated proteins only proteins with a minimum regulation 10% (factor 1.1) or of 50% (factor 1.5) were examined. The variation of single peptides in one protein was strikingly low and estimated to be under 5%, respectively 10% for both techniques. In recent studies similar variation coefficients below 10% were calculated for several peptides of one single protein [55, 56, 62]. However, in nearly all lately published studies the variation resulting from two or more different experiments was not shown. The average variation of factors determined herein for the two or multiple experiments should be the general divergence between more experiments.

Owing to the higher recovery of identified and regulated proteins, the ICPL™ technique in combination with GeLC-MS/MS analysis is a suitable high throughput screening method on protein level to detect differences in two samples. It is the method of choice to describe cellular effects, respectively. ICPL™ should also be favorable over the ICAT™ approach because the higher frequency of lysine residue compared to cysteine residues (amino acid that occurs at a frequency of 1.7% [83]) used in the well known ICAT™ approach results in high sequence coverage with less side reactions that is essential for the detection of post-translational modifications and protein isoforms. One advantage of the ICAT™ approach is the biotin based purification step of the labeled peptides. This leads to a reduced sample complexity which should increase the identification rate. However, some peptides might get lost using this approach. Silac [84] or ^{18}O-labeling [85] are also methods commonly used for quantitative MS. But as evident from the literature these methods comprise similar advantages and disadvantages.

4.2 Quantitative comparison of the SH-SY5Y protein profile using the ICPL™ approach

The most prominent group exhibiting alteration after C3*bot*-treatment are the histones which are up-regulated up to 21.5-fold. Histones are the main protein components of the chromatin. DNA winds around them and their synthesis is strongly synchronized with the replication of DNA during the S-phase (mitosis) of the cell cycle [86]. Whereas the core-histones H2A, H2B, H3 and H4 are assembled to form one octameric nucleosome core particle by wrapping the DNA, linker histone H1 binds the nucleosome allowing the formation of higher ordered structures. The first view of the data suggests an increase in DNA replication which is accompanied by an increased translation and protein synthesis (Figure 23 C, p. 38).

Nevertheless, histones are also subject to post-translational modifications which can be mapped to different nucleosomal structures and are involved in DNA synthesis and repair, cell proliferation and transcription [87]. One important modification is the acetylation of the N-terminally located lysine residues. A decreased histone acetylation in C3*bot* treated cells might lead to a higher labeling efficiency with ICPL™ due to a better accessibility of the labeling sites (as described on p. 47f). The hyperacetylation of the N-teminal histone tail is associated with transcriptionally active chromatin [88]; deacetylation indicates transcriptionally inactive chromatin which leads to a cell cycle arrest and finally to cell death. Histones belonging to the core histone family H2A are known to be major regulators of the cellular response to DNA damage and are associated with cell death [89]. As previously described from Berenjeno et al. constitutively active RhoA procures a down-regulation of the histone H3 family whereas in this work, RhoA was inactivated by C3*bot*-catalyzed ADP-ribosylation and – as expected - the opposite effect namely up-regulation of histone H3 was detected [79].

Another group of proteins affected by C3*bot* treatment are ribosomal proteins and proteins of the translational apparatus. Their synthesis is mainly regulated at the translational level and thus, differences between two cellular situations are unlikely detected by nucleic acid microarray techniques [90]. Most of the ribosomal proteins and splicing factors are up-regulated indicating an increased protein synthesis after C3*bot*-treatment (Figure 23 B, C, D, p. 38). Protein phosphorylation is one of the most abundant post-translational modifications in cellular systems and an important regulatory mechanism in prokaryotic and eukaryotic organisms [91]. Phosphatases and proteins involved in ubiquitinylation or SUMOylation are found to be up-regulated after C3*bot*-reatment which implicates an increased protein degradation [92-95]. Together with an enhanced proteins biosynthesis it can be concluded that C3*bot* might cause an overall increase in protein turnover. As one consequence, e.g. ADP-ribosylated inactive RhoA is subjected to proteolytic degradation [37].

Chaperones are specialized proteins that assist the folding/unfolding and the assembly/disassembly of other proteins and nucleosomes [96]. A large group of heat shock proteins are known to be stress markers, which are involved in signal transduction and can protect the cells from apoptosis [97, 98]. Heat shock proteins of the 70 kDa family like BIP or HSP 70 kDa protein 6 or protein 8 exhibit a lower abundance in C3*bot*-treated cells. It has been noted that increased expression of Hsp70 proteins results in decreased apoptosis [97]. Our findings of a decreased abundance of chaperones, the up-regulation of histones, followed by an increased translation as well as the degradation of proteins suggests the evidence of a potential cell cycle arrest which might result in cell death. However, lately published reports show that inactivation of Rho-GTPases, especially due to ADP-ribosylation by C3*bot*, leads to an increased cell survival and a reduced apoptosis in Purkinje and embryonic stem cell-derived neuronal precursors [99, 100]. It is known from the literature, that probable differentiation of neuronal cells is accompanied by altered cell proliferation and growth arrest [101-103]. Thus, C3*bot*-identified alteration on protein abundance might also reflect cellular changes that might result in cell differentiation.

Consequently, C3*bot* treatment changed the abundance of a large number of proteins involved in cell growth, cell proliferation and cell morphology (Figure 23 F, p. 38). The inactivation of Rho GTPases leads to the cytopathic effect which is reflected by the reorganization of the actin cytoskeleton, the microtubular network and the reduction of cell-adhesion accompanied by altered cell motility. Among the down-regulated proteins stathmin and tubulin which are involved in the regulation of the microtubule (MT) filament system were found. Tubulin is the major constituent of microtubules and the stabilization of formed mictrotubules is organized by stathmin. Berenjeno et al. showed that the transcription of tubulin and stathmin is up-regulated after transforming constitutively active RhoA into cells [79]. Vice versa an inactivation of RhoA due to ADP-ribosylation should decrease the transcription of tubulin and stathmin genes and therefore, their abundance in the cell. In the case of tubulin, the ICPL™ results fit to the transcriptional profiling. But it still has to be elucidated why western blot analysis and ICPL™ labeling show opposite results. The analysis using the iTRAQ™ technique revealed an increase in tubulin, as well as the western blot analyses, where an increase in the abundance of β-tubulin and an unchanged α-tubulin concentration was observed (p. 47). Since the identified down-regulation of the tubulin proteins found by the ICPL™-labeling is confirmed by the analyses of 165 peptides (60 peptides for β-tubulin; Table 3; p. 139) and high overall identified Mascot scores for the proteins. In contrast, the iTRAQ™ analysis is based on the identification of 108 peptides (only 35 peptides for β-tubulin; Table 4; p. 150) but confirmed by western blot analysis (p. 47). This discrepancy was found in all repetitions of the labeling and western blot analyses. All used experimental systems could lead to artificial results but at this step it is not possible to explain these differences. Probably further experiments with different antibodies should be helpful. However, the ICPL™ method is based on the most experimental data points and should display the biological situation at best, at least in the view of the author of this thesis.

Among the proteins participating in cell morphology and differentiation dihydropyrimidinase-related protein 2 also known as collapsing response mediator protein-2 (CRMP-2) was found with a lower abundance after C3*bot* treatment. It is well-known that CRMP-2 can regulate axonal growth through different mechanisms [104]. However, differential marker proteins like the microtubule-associated serine/threonine-protein kinase 2 (MAP-2) did not respond to C3*bot* in the chosen time window. It is known from MAP-2 to be prominent in differentiating neuronal cells after several days [101]. Because of the absence or the abundance below the detection limit no further differential markers could be identified with this method. The inactivation of Rho proteins by ADP-ribosylation probably leads to cell cycle arrest which is required for differentiation. The changed protein pattern of SH-SY5Y cells and the microscopically visible effects indicates this response to C3*bot*-treatment. In this context it is reasonable that one protein of cyclin dependent kinase family (cdk6) has been found down-regulated after C3*bot*-treatment. Recently, it has been shown that down-regulation of Cdk6 together with CCND1 induces cell cycle arrest [101]. Cdk proteins are involved in diverse cellular processes including neuronal migration, axonal growth, neurite extension, stress response and cellular senescence [103]. These results fit well to the findings of up-regulated histones, the decreased abundance of chaperones and an increased transcriptional activity which might step towards differentiation accompanied by a slow down of the cell cycle.

The finding of a decrease in the abundance of glycolytic enzymes like fructose-biphosphate aldolase A or glucose-6-phosphate isomerase and an up-regulation of enzymes involved in fatty acid and lipid metabolism like phospholipase D3 may implicate a protection against apoptosis [105]. Probably, the energy metabolism is changed towards fatty acid utilization. This might be either due to the treatment by C3*bot* but might also be explained by carbohydrate starvation. After 3 days of incubation the carbohydrate sources of medium might be exhausted and cells probably draw the energy from degrading lipids. This phenomenon has to be elucidated in further studies, e.g. by choosing earlier time points for the quantitative analysis.

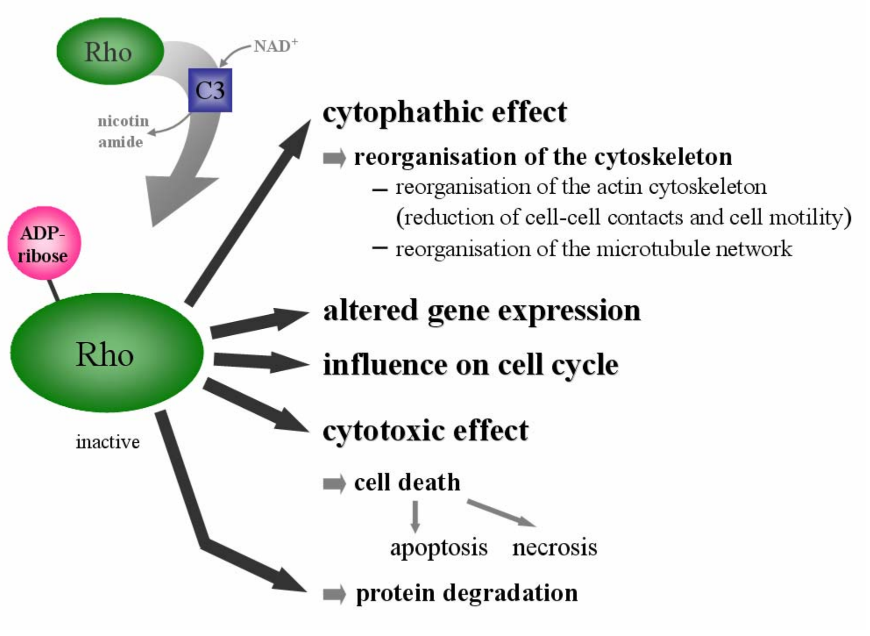

Figure 31. Effects of inactivation of Rho-GTPases on the cellular functions. Rho A, B and C are ADP-ribosylated by the C3 exoenzyme from *C. botulinum,* which result in cytopathic and cytotoxic effect.

Taken all findings together, the C3*bot*-induced effects in SH-SY5Y cells are shown in figure 31 (p. 56). The altered abundance of actin and microtubuli stabilizing proteins and proteins of the microtubular network is changed which is microscopically detectable as cell rounding and neurite outgrowth. The up-regulation of nucleosomal proteins like histones, the altered amount of chaperons and proteins involved in translational and transcriptional processes leads to the evidence of cell cycle arrest which on the one hand opens the possibility for differentiation and otherwise probably leads to cell death in form of apoptosis or necrosis.

Using ICPL-labeling for the comparison of the altered protein expression of C3*bot* treated SH-SY5Y cells combined with a GeLC-MALDI-MS/MS approach led us to discover several novel, differentially expressed proteins. The application of the iTRAQ™ label in combination with 2D-LC-MS/MS analysis seems to be a promising method for rapid quantitation and identification due to the shorter time needed for performing the experiments. However, for a better iTRAQ™ analysis work has to be done to enhance the separation.

Thus, with both approaches proteins could be discovered which are hardly identified by conventional 2D-gel-electrophoresis coupled to MS analysis like histones, ribosomal or membrane proteins. A combination of known aspects with the new found altered gene expression provides new starting points for further analysis and a better understanding of the cellular function of the C3 exoenzyme.

5 Outlook

In this study highly precise, sensitive and reproducible methods for relative quantitation of the altered proteome of C3*bot*-treated SH-SY5Y cells have been developed, verified and examined. The obtained results confirm currently known theories of processes followed inactivation of RhoA via ADP-ribosylation. Thus, many hints of neuronal growth were detected; the function of the probable cell cycle arrest in combination with cell death still remains to be elucidated. With quantitative proteome screening methods probable new interesting findings will be revealed which can further be examined applying biochemical methods such as western blot analysis. From this study prospective biochemical work is predicted on the area of the function of cell cycle arrest. Signal pathways leading to differentiation or cell death have to be analyzed. The analytical combination of mass spectrometric analysis with several protein or peptide separation techniques might also be further modified and improved. Future development focuses on further reduction of sample complexity; both for the application of ICPL™ and the use of iTRAQ™ tagging. Thus, a reduced sample complexity results in much better identification rates and therefore provides a larger overview of the biological processes. Reduction of biological complexity is obtained by dividing the cells in their different compartments like cytoplasm, nucleus, mitochondria or membranes [77]. Applying high-quality proteomics the identification rate of proteins localized in small, less abundant cell organelles (now between 0.5 and 10%) will highly increase. Attention has to be turned to the sample preparation for MALDI analysis using peptide separation techniques. It should be focused on the improvement of separation efficiency of SCX, especially applying 2D-HPLC analysis. Although, the developed method is a fast and highly reproducible technique, there is still a lack of peptide separation. Though, in cases of off-line SCX-RP-HPLC the number of SCX fractions can be increased (e.g. in ranges of low salt concentrations) and several HPLC-runs can be applied subsequently. The expenditure of analysis time would be highly similar to GeLC-MS/MS and thus the advantage of a fast method will be lost. To overcome this obvious challenge, on-line SCX-RP-HPLC should be performed by fractionating the separated peptides on several target plates with longer and more specific acetonitrile gradients. Therefor a perfectly equipped MS analysis system should be provided or at least software, which enables the combination of several LC-MS analyses.

6 References

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7 Supplementary material

Table 1. Identified proteins using the GeLC-MS/MS approach. The identified proteins of the proteome profiling of SH-SY5Y are sorted by the first letter. Accession number: SwissProt accession number; score: Mascot identification score; MW: molecular weight

Protein Name and Species	Accession	Score	MW [kDa]	# Pept.
100 kDa hexon-assembly associated protein	Q2KRW7	59	91,86	2
14-3-3 protein beta/alpha	P31946	373	27,93	11
14-3-3 protein epsilon	P62258	353	29,16	10
14-3-3 protein epsilon isoform transcript variant 1	Q4VJB6	209	26,49	4
14-3-3 protein eta	Q04917	314	28,17	8
14-3-3 protein gamma	P61981	617	28,15	14
14-3-3 protein theta	P27348	739	27,75	14
14-3-3 protein zeta/delta	P63104	967	35,31	18
2,4-dienoyl-CoA reductase [Precursor]	Q16698	99	35,81	2
250 kDa substrate of Akt	Q2PPJ7	79	210,77	5
26S protease regulatory subunit 6A	P17980	355	54,94	7
26S protease regulatory subunit 6B	P43686	361	47,34	5
26S protease regulatory subunit 8	P62195	456	45,61	7
26S protease regulatory subunit S10B	P62335	1063	44,15	22
26S proteasome non-ATPase regulatory subunit 1	Q99460	60	105,77	2
26S proteasome non-ATPase regulatory subunit 11	O00231	295	47,30	6
26S proteasome non-ATPase regulatory subunit 12	O00232	41	52,74	1
26S proteasome non-ATPase regulatory subunit 2	Q13200	407	100,12	13
26S proteasome non-ATPase regulatory subunit 3	O43242	80	59,54	5
26S proteasome non-ATPase regulatory subunit 5	Q16401	67	8,94	2
26S proteasome non-ATPase regulatory subunit 6	Q15008	340	45,50	7
26S proteasome non-ATPase regulatory subunit 7	P51665	432	37,26	6
26S proteasome non-ATPase regulatory subunit 9	O00233	220	24,64	5
28 kDa heat- and acid-stable phosphoprotein	Q13442	92	13,88	3
28S ribosomal protein S18a [Precursor]	Q9NVS2	63	22,18	3
2-acylglycerol O-acyltransferase 2	Q3SYC2	48	32,28	2
2B28 protein	Q9BV93	199	35,09	4
3'(2'),5'-bisphosphate nucleotidase 1	O95861	132	33,37	2
39S ribosomal protein L12 [Precursor]	P52815	139	10,54	4
39S ribosomal protein L13	Q9BYD1	61	19,90	2
39S ribosomal protein L34 [Precursor]	Q9BQ48	60	10,17	3
39S ribosomal protein L40 [Precursor]	Q9NQ50	96	24,48	2
39S ribosomal protein L44 [Precursor]	Q9H9J2	58	37,54	2
3-hydroxyacyl-CoA dehydrogenase type-2	Q99714	341	26,78	6
3-ketoacyl-CoA thiolase, mitochondrial	P42765	187	41,90	4
3-mercaptopyruvate sulfurtransferase variant [Fragment]	Q59HD5	149	34,73	5
40 kDa peptidyl-prolyl cis-trans isomerase	Q08752	246	40,61	5
40S ribosomal protein S10	P46783	348	18,89	7
40S ribosomal protein S11	P62280	119	18,29	4
40S ribosomal protein S12	P25398	92	14,52	2
40S ribosomal protein S13	P62277	202	17,21	5
40S ribosomal protein S14	P62263	186	16,26	4
40S ribosomal protein S15	P62841	91	17,03	2
40S ribosomal protein S15a	P62244	133	14,70	3
40S ribosomal protein S16	P62249	221	16,44	6
40S ribosomal protein S17	P08708	76	15,54	2
40S ribosomal protein S18	P62269	230	17,71	8
40S ribosomal protein S23	P62266	109	15,67	4
40S ribosomal protein S24	P62847	115	15,41	2
40S ribosomal protein S25	P62851	106	13,73	3
40S ribosomal protein S26	P62854	160	13,01	3
40S ribosomal protein S28	P62857	83	7,84	1
40S ribosomal protein S3	P23396	319	26,67	8
40S ribosomal protein S3a	P61247	203	29,79	6
40S ribosomal protein S4, X isoform	P62701	358	29,58	7
40S ribosomal protein S5	P46782	145	22,73	4
40S ribosomal protein S6	P62753	92	28,66	2
40S ribosomal protein S7	P62081	426	22,11	7
40S ribosomal protein S8	P62241	464	24,19	8
40S ribosomal protein S9	P46781	564	20,70	13
40S ribosomal protein SA	P08865	861	33,29	12
5'-3' exoribonuclease 2	Q9H0D6	45	103,74	1
59 kDa 2'-5'-oligoadenylate synthetase-like protein	Q15646	54	59,23	2

Table 1. continued

Protein Name and Species	Accession	Score	MW [kDa]	# Pept.
5'-AMP-activated protein kinase subunit gamma-2	Q9UGJ0	43	63,07	2
5-azacytidine-induced protein 1	Q9UPN4	78	122,06	4
5-oxoprolinase	O14841	46	137,46	2
60S acidic ribosomal protein P0	P05388	612	34,25	10
60S acidic ribosomal protein P2	P05387	47	11,66	1
60S ribosomal protein L10	P27635	222	24,43	5
60S ribosomal protein L10a	P62906	192	24,68	4
60S ribosomal protein L10-like	Q96L21	41	24,37	1
60S ribosomal protein L11	P62913	260	20,24	6
60S ribosomal protein L12	Q5VVV2	331	17,81	4
60S ribosomal protein L18	Q07020	404	21,49	10
60S ribosomal protein L18a	Q02543	216	20,75	5
60S ribosomal protein L19	P84098	113	23,45	3
60S ribosomal protein L21	P46778	173	18,42	5
60S ribosomal protein L22	P35268	98	14,79	3
60S ribosomal protein L23a	P62750	218	17,68	6
60S ribosomal protein L24	P83731	216	14,30	4
60S ribosomal protein L27	P61353	103	15,79	4
60S ribosomal protein L29	P47914	55	18,70	1
60S ribosomal protein L3	P39023	515	45,95	11
60S ribosomal protein L30	P62888	113	12,78	3
60S ribosomal protein L31	P62899	114	14,45	4
60S ribosomal protein L32	P62910	122	15,85	3
60S ribosomal protein L34	P49207	49	13,28	3
60S ribosomal protein L35	P42766	87	14,41	2
60S ribosomal protein L36	Q9Y3U8	59	12,11	3
60S ribosomal protein L38	P63173	78	8,21	1
60S ribosomal protein L3-like	Q92901	191	46,27	4
60S ribosomal protein L4	P36578	843	47,54	15
60S ribosomal protein L5	P46777	376	34,21	7
60S ribosomal protein L6	Q02878	776	32,58	12
60S ribosomal protein L7a	P62424	211	29,98	4
60S ribosomal protein L9	P32969	95	21,86	2
6-phosphofructo-2-kinase/fructose-2,6-biphosphata se 2	Q5VVQ3	64	54,37	3
6-phosphofructo-2-kinase/fructose-2,6-biphosphata se 3	Q5VX15	64	57,29	3
6-phosphofructokinase	P17858	111	84,92	5
6-phosphogluconate dehydrogenase, decarboxylating	Q4VXH6	503	53,11	11
6-phosphogluconolactonase	O95336	252	27,53	5
A kinase anchor protein 10 [Precursor]	O43572	42	73,82	3
A+U-rich element RNA binding factor	Q7KZ74	613	30,17	10
A1 chain of type XIX collagen [Fragment]	Q13709	44	15,29	2
ABI gene family member 3	Q9P2A4	48	38,92	2
Abl interactor 2	Q9NYB9	61	55,66	2
Absent in melanoma 1-like protein	Q8N1P7	76	50,95	5
Acetyl-CoA acetyltransferase [Precursor]	P24752	290	45,24	6
Acetyl-CoA acetyltransferase, cytosolic	Q9BWD1	219	41,23	5
Acetyl-CoA acetyltransferase, cytosolic variant [Fragment]	Q59GW6	463	42,11	6
Acetyl-CoA carboxylase 2	O00763	80	276,56	3
Achaete-scute complex homolog 2	Q6PEY9	71	28,92	3
Acidic (Leucine-rich) nuclear phosphoprotein 32 family, member B variant [Fragment]	Q53F35	221	28,66	4
Acidic (Leucine-rich) nuclear phosphoprotein 32 family, member E	Q5TB18	116	30,67	2
ACLY variant protein [Fragment]	Q4LE36	261	124,48	9
Aconitate hydratase [Precursor]	Q99798	282	85,41	7
ACTA2 protein [Fragment]	Q13707	125	36,78	2
Actin filament-associated protein 1	Q8N556	41	80,75	2
Actin gamma	P63261	1704	41,63	46
Actin related protein 2/3 complex subunit 1A variant [Fragment]	Q53GB6	85	40,95	3
Actin, alpha 1, skeletal muscle	Q5T8M7	190	37,80	4
Actin, alpha cardiac muscle 1	P68032	1034	41,99	32
Actin, aortic smooth muscle	P62736	129	42,08	4
Actin-bundling protein with BAIAP2 homology	Q765P7	53	79,88	4
Actinin-alpha-1	P12814	380	102,91	11
Actinin-alpha-2	P35609	105	103,79	4
Actinin-alpha-4	O43707	567	104,79	17
Actin-like protein [Fragment]	Q562X8	213	11,57	5
Actin-like protein 7B	Q9Y614	123	12,12	5
Actin-related protein 2	P61160	532	44,73	9
Actin-related protein 2/3 complex subunit 4	P59998	72	19,52	2
Actin-related protein 2/3 complex subunit 5	O15511	58	16,31	1
Actin-related protein 2/3 complex subunit 5-like protein	Q9BPX5	41	16,89	1
Activated CDC42 kinase 1	Q07912	51	119,29	3

Table 1. continued

Protein Name and Species	Accession	Score	MW [kDa]	# Pept.
Activated RNA polymerase II transcriptional coactivator p15	P53999	61	14,26	2
Activator of 90 kDa heat shock protein ATPase homolog 1	O95433	558	38,25	7
Acylamino-acid-releasing enzyme	P13798	120	81,17	4
Acyl-coenzyme A oxidase 1	Q15067	61	74,39	2
ADAM 22 [Precursor]	Q9P0K1	56	100,43	2
ADAM15 isoform 8	Q71S61	43	86,06	2
ADAM19 protein [Fragment]	Q8TBU7	53	52,69	4
ADAMTS-13 [Precursor]	Q76LX8	57	153,60	3
ADAMTS-14 [Precursor]	Q8WXS8	49	127,25	3
ADAMTS-2 [Precursor]	O95450	45	134,72	2
ADAMTS-20 [Precursor]	P59510	53	214,66	2
ADAMTS-4 [Precursor]	O75173	52	90,20	2
ADAMTS-5 [Precursor]	Q9UNA0	64	101,72	3
ADAMTS8 protein [Fragment]	Q5FWF1	74	98,74	3
ADAMTS8 protein [Fragment]	Q5FWF1	63	98,68	4
ADAMTS-like protein 2 [Precursor]	Q86TH1	47	104,62	2
ADAMTS-like protein 4 [Precursor]	Q6UY14	55	116,55	2
Adaptor-related protein complex 1, gamma 1 subunit	Q8IY97	80	91,70	4
Adaptor-related protein complex 2, alpha 2 subunit variant [Fragment]	Q53ET1	44	104,02	2
Adenine phosphoribosyltransferase	P07741	149	19,46	3
Adenomatous polyposis coli protein	P25054	91	311,65	4
Adenomatous polyposis coli protein 2	O95996	109	175,43	7
Adenosylhomocysteinase	P23526	317	47,55	7
Adenylate cyclase type 9	O60503	40	150,70	2
Adenylate kinase 5, isoform 2	Q5U622	60	60,45	2
Adenylate kinase isoenzyme 1	P00568	261	21,69	7
Adenylate kinase isoenzyme 2	P54819	214	26,46	5
Adenylosuccinate synthetase	Q5SVJ2	98	50,07	1
Adenylosuccinate synthetase isozyme 1	Q8N142	46	50,21	2
Adenylyl cyclase-associated protein 1	Q01518	127	51,51	2
Adherens junction-associated protein 1	Q9UKB5	77	44,54	3
Adipocyte plasma membrane-associated protein	Q9HDC9	234	47,72	6
ADP/ATP translocase 1	P12235	239	32,91	4
ADP/ATP translocase 2	P05141	384	28,04	6
ADP/ATP translocase 3	P12236	298	29,10	5
ADPRHL2 protein	Q6IAB8	160	38,92	5
ADP-ribosylation factor 1	P84077	206	20,55	4
ADP-ribosylation factor 4	P18085	159	20,37	3
ADP-ribosylation factor-like protein 2	P36404	46	20,84	2
ADP-ribosylation factor-like protein 6-interacting protein 4	Q66PJ3	46	38,40	2
ADP-sugar pyrophosphatase	Q9UKK9	199	24,24	3
Adrenocortical dysplasia protein homolog	Q96AP0	72	57,76	3
Adseverin	Q9Y6U3	46	69,96	3
AE binding protein 1	Q8IUX7	42	130,93	2
AF4/FMR2 family member 4	Q9UHB7	40	127,46	2
Afadin	P55196	91	205,61	4
AFG3 ATPase family gene 3-like 2	Q6P1L0	63	88,53	3
Aflatoxin B1 aldehyde reductase member 2	O43488	219	39,56	5
Aging-associated gene 7 protein	Q2TSD2	221	41,44	5
Aging-associated gene 9 protein	Q2TSD0	1630	36,03	28
Aging-associated protein 14b	Q1XBU6	81	28,35	2
Agrin [Precursor]	O00468	73	214,85	5
AKAP9-BRAF fusion protein	Q5IBP5	63	172,16	3
A-kinase anchor protein 2	Q9Y2D5	43	96,10	2
A-kinase anchor protein 4 [Precursor]	Q5JQC9	42	14,77	2
A-kinase anchor protein 6	Q13023	53	256,72	4
AKNA transcript C1 [Fragment]	Q64FY0	43	73,67	2
Alanyl-tRNA synthetase domain-containing protein 1	Q9BTE6	61	16,16	3
Alanyl-tRNA synthetase	P49588	139	106,76	6
ALB protein	Q8IUK7	54	45,13	1
Alcohol dehydrogenase [NADP+]	P14550	296	36,42	6
Alcohol dehydrogenase class-3	P11766	123	39,57	1
Aldehyde dehydrogenase 18 family, member A1	Q3KQU2	405	87,26	12
Aldehyde dehydrogenase family 16 member A1	Q8IZ83	64	23,19	1
ALDH1A3 protein	Q96GT2	48	10,76	3
Aldo-keto reductase family 1 member B10	O60218	59	41,88	2
Aldo-keto reductase family 1 member C1	Q04828	61	34,77	2
Aldose reductase	P15121	834	35,70	16
Alkylated DNA repair protein alkB homolog 1	Q13686	53	43,83	2
Alkylated DNA repair protein alkB homolog 5	Q6P6C2	55	51,38	3
Alpha 1 type VII collagen variant [Fragment]	Q59F16	96	96,81	4
Alpha subunit of GsGTP binding protein [Fragment]	Q14455	219	47,12	6

Table 1. continued

Protein Name and Species	Accession	Score	MW [kDa]	# Pept.
Alpha-1 type XIII collagen	Q14035	81	60,47	3
Alpha-1,3-mannosyl-glycoprotein 4-beta-N-acetylglucosaminyltransferase B	Q9UQ53	51	63,16	2
Alpha-1A adrenergic receptor	P35348	40	51,49	2
Alpha-1D adrenergic receptor	P25100	56	54,65	2
Alpha-1-syntrophin	Q13424	53	53,86	2
Alpha-2-HS-glycoprotein [Precursor]	P02765	123	39,30	2
Alpha-adducin	P35611	55	80,96	3
Alpha-internexin	Q16352	66	54,88	2
Alpha-protein kinase 3	Q96L96	95	201,30	4
Alpha-taxilin	P40222	154	61,85	6
Alstrom syndrome protein 1	Q8TCU4	99	460,65	6
Alveolar soft part sarcoma chromosome region, candidate 1	Q8WV59	81	60,16	3
Amiloride-sensitive cation channel 3	Q9UHC3	48	60,45	2
Amiloride-sensitive sodium channel subunit alpha	P37088	46	28,30	2
Aminoacylase-1	Q03154	65	45,86	2
Aminopeptidase B	Q7RU04	51	73,50	2
AMME syndrome candidate gene 1 protein	Q9Y4X0	50	35,44	2
Amphiphysin IIb-1	Q8WWH9	41	53,17	2
Amyloid beta A4 precursor protein-binding family A member 2	Q99767	54	82,51	2
Amyloid beta A4 precursor protein-binding family B member 2	Q92870	48	83,35	2
Amyotrophic lateral sclerosis 2 chromosomal region candidate gene 13 protein	Q6P1L5	44	61,97	2
AN1-type zinc finger protein 6	Q6FIF0	40	22,56	1
Anamorsin	Q6FI81	143	39,98	3
Androgen-induced proliferation inhibitor	Q9NTI5	52	164,67	2
Angiomotin-like protein 1	Q8IY63	61	106,57	3
Angiomotin-like protein 2	Q9Y2J4	57	85,75	3
Angiopoietin-related protein 6 [Precursor]	Q8NI99	49	38,40	2
Anion exchanger SLC4A3	Q6YIQ9	42	138,66	1
ANK repeat and LEM domain-containing protein KIAA0692	Q86XL3	48	104,12	2
ANKHD1 protein	Q8IWG5	44	91,41	2
Ankyrin 3, node of Ranvier	Q5VXD5	96	104,12	5
Ankyrin repeat and FYVE domain-containing protein 1	Q9P2R3	46	283,51	2
Ankyrin repeat and IBR domain-containing protein 1	Q9P2G1	55	122,02	2
Ankyrin repeat and SOCS box-containing protein 16 isoform	Q6Q622	40	29,48	2
Ankyrin repeat domain 15	Q5W0W1	57	106,71	2
Ankyrin repeat domain-containing protein 11	Q6UB99	72	298,02	3
Ankyrin repeat domain-containing protein 18A	Q8IVF6	56	115,60	2
Ankyrin repeat domain-containing protein 25	Q63ZY3	69	91,86	2
Ankyrin repeat domain-containing protein 26	Q9UPS8	46	196,32	2
Ankyrin repeat domain-containing protein 27	Q96NW4	49	116,98	2
Ankyrin repeat domain-containing protein 34A	Q69YU3	44	52,64	2
Ankyrin repeat domain-containing protein 43 [Precursor]	Q2M3V2	72	57,41	3
Ankyrin repeat domain-containing protein 44	Q8N8A2	44	102,49	1
Ankyrin repeat domain-containing protein 47	Q6NY19	60	88,43	3
Ankyrin repeat domain-containing protein 53	Q8N9V6	49	59,53	2
Ankyrin repeat domain-containing protein 57	Q53LP3	49	55,67	3
Ankyrin repeat domain-containing protein 9	Q96BM1	52	34,30	4
Ankyrin-1	P16157	46	206,27	2
Ankyrin-2	Q01484	85	430,34	4
Annexin A2	P07355	101	38,45	3
Annexin A4	P09525	86	35,73	2
Annexin A5	P08758	110	35,91	4
Annexin A6	P08133	123	75,69	7
Annexin A7 (ANXA7 protein)	Q5T0M6	50	50,28	1
ANP32A protein [Fragment]	Q6PKH8	131	24,05	4
Anti-colorectal carcinoma heavy chain	Q65ZQ1	140	50,57	3
Antigen identified by monoclonal antibody Ki-67	Q5VWH2	107	358,47	5
Antigen KI-67	P46013	114	358,69	7
Antigen MLAA-16 [Fragment]	Q6WG77	62	31,34	2
AP-1 complex subunit mu-1	Q9BXS5	103	48,43	4
AP2 associated kinase 1	Q2M2I8	57	93,52	2
AP-2 complex subunit alpha-1	O95782	40	107,56	2
APC2 protein [Fragment]	Q9UEM8	191	243,95	10
Apelin [Precursor]	Q9ULZ1	65	8,57	2
Apolipoprotein B-100 [Precursor]	P04114	50	515,56	2
Apoptosis inhibitor 5	Q9BZZ5	49	57,53	2
Apoptosis-inducing factor 1 [Precursor]	O95831	65	66,91	3
Apoptotic chromatin condensation inducer in the nucleus	Q9UKV3	72	151,89	4
Arginine vasopressin-induced protein 1	Q5T686	44	16,76	2
Arginine/serine-rich coiled-coil protein 1	Q96IZ7	58	38,65	2
Arginyl-tRNA synthetase, cytoplasmic	P54136	152	75,33	7
ARHGAP4 protein [Fragment]	Q6PJ34	53	38,21	4

Table 1. continued

Protein Name and Species	Accession	Score	MW [kDa]	# Pept.
ARHGEF18 protein	Q6DD92	65	116,24	4
ARID1A variant protein [Fragment]	Q4LE49	40	147,02	1
ARL3 protein [Fragment]	Q53X83	40	20,46	1
Armadillo repeat-containing protein 1	Q9NVT9	59	22,75	1
Armadillo repeat-containing protein 5	Q96C12	88	97,68	3
Armadillo repeat-containing X-linked protein 1	Q9P291	59	49,17	3
Aromatic-L-amino-acid decarboxylase	P20711	101	53,86	4
ARP3 actin-related protein 3 homolog variant [Fragment]	Q59FV6	538	42,23	12
ArsA arsenite transporter, ATP-binding, homolog 1 variant [Fragment]	Q53FC6	316	38,75	5
Arsenical pump-driving ATPase	O43681	318	38,81	5
Arsenic-transactivated protein 3 (Proliferation-inducing gene 14)	Q5XPB4	705	46,41	8
Aryl hydrocarbon receptor interacting protein	Q2M3Q2	94	37,64	2
Aryl hydrocarbon receptor nuclear translocator-like protein 1	O00327	52	68,76	3
Asp (Abnormal spindle) homolog, microcephaly associated	Q5VYL3	55	409,80	3
Aspartate aminotransferase [Precursor]	P00505	793	47,45	14
Aspartate aminotransferase, cytoplasmic	P17174	652	46,09	12
Aspartyl-tRNA synthetase [Precursor]	Q6PI48	69	73,52	2
Aspartyl-tRNA synthetase, cytoplasmic	P14868	207	57,16	7
Astrotactin-2 [Precursor]	O75129	54	142,45	2
ATAD2 protein	Q2KHQ7	65	155,68	3
Ataxin 1	Q17S02	57	86,92	2
Ataxin 2-binding protein 1 isoform 4 variant [Fragment]	Q59HD3	140	33,14	5
Ataxin-2	Q99700	68	140,14	4
Ataxin-7	O15265	83	95,45	4
Ataxin-7-like protein 2	Q5T6C5	73	77,18	3
ATF-A0 transcription factor protein [Fragment]	Q9UD83	40	33,68	3
Atherin	Q6SPF0	69	56,05	5
AT-hook-containing transcription factor	Q7Z591	46	155,14	2
AT-hook-containing transcription factor 1	Q8WYP5	96	253,46	4
ATP synthase mitochondrial F1 complex assembly factor 1 [Precursor]	Q5TC12	51	36,41	3
ATP synthase subunit alpha [Precursor]	P25705	948	60,75	17
ATP synthase subunit beta [Precursor]	P06576	1203	56,52	23
ATP synthase subunit e	P56385	75	7,80	2
ATP synthase subunit f	P56134	74	10,78	1
ATP synthase subunit g	O75964	102	11,42	2
ATP synthase subunit O [Precursor]	P48047	57	23,28	2
ATP synthase, H+ transporting F0 complex, subunit b isoform 1 variant [Fragment].- H	Q53GB3	68	28,82	2
ATPase family AAA domain-containing protein 2B	Q9ULI0	43	164,94	1
ATP-binding cassette sub-family A member 1	O95477	52	254,29	3
ATP-binding cassette sub-family B member 10 [Precursor]	Q9NRK6	49	79,15	2
ATP-binding cassette sub-family B member 8 [Precursor]	Q9NUT2	57	79,90	2
ATP-binding cassette sub-family E member 1	P61221	58	67,31	2
ATP-binding cassette, sub-family F (GCN20), member 1	Q2L6I2	127	91,62	6
ATP-dependent DNA helicase 2 subunit 1	P12956	219	69,83	6
ATP-dependent DNA helicase 2 subunit 2	P13010	527	82,52	16
ATP-dependent DNA helicase Q4	O94761	72	132,99	3
ATP-dependent RNA helicase 46	O43143	116	92,77	4
ATP-dependent RNA helicase A	Q08211	1131	140,79	23
ATP-dependent RNA helicase DDX1	Q92499	173	77,81	5
ATP-dependent RNA helicase DDX39	O00148	460	49,10	9
ATP-dependent RNA helicase DDX3X	O00571	528	73,07	16
ATP-dependent RNA helicase DDX3Y	O15523	454	73,11	14
Atrial natriuretic peptide receptor B [Precursor]	P20594	52	117,02	2
AT-rich interactive domain-containing protein 1A	O14497	87	242,05	5
AT-rich interactive domain-containing protein 2	Q68CP9	63	197,39	4
AT-rich interactive domain-containing protein 3B	Q8IVW6	53	60,64	2
AT-rich interactive domain-containing protein 5A	Q03989	58	64,07	2
AT-rich interactive domain-containing protein 5B	Q14865	63	132,32	2
Atrophin-1 interacting protein 1	A4D1C1	46	158,75	3
Autism susceptibility gene 2 protein	Q8WXX7	60	138,98	2
Autogenous vein graft remodeling associated protein 2	Q2HYQ4	68	36,29	3
Autophagy-related protein 2 homolog A	Q2TAZ0	40	212,92	2
Autophagy-related protein 7	O95352	44	74,95	2
AUTS2 protein	Q5D049	46	136,42	3
Axin 1 isoform a variant [Fragment]	Q59H83	59	56,97	2
BA395L14.12 (Novel protein similar to small nuclear ribonucleoprotein polypeptide A' (SNRPA1)).- Ho	Q9NU36	435	28,39	8
BAF53A protein	Q6FI97	166	47,35	4
BAI1-associated protein 3	O94812	75	131,90	3
Band 4.1-like protein 1	Q9H4G0	93	98,50	4
Barrier-to-autointegration factor	O75531	98	8,42	2

Table 1. continued

Protein Name and Species	Accession	Score	MW [kDa]	# Pept.
Basic salivary proline-rich protein 4 [Precursor]	P10163	45	31,41	1
Bax inhibitor 1	P55061	42	26,54	1
BAZ1B protein [Fragment]	Q6P1K4	51	93,06	3
Bcd orf2	O43839	63	23,35	3
B-cell CLL/lymphoma 9	Q1JQ81	49	149,21	2
B-cell linker protein [Fragment]	Q2MD49	41	44,45	3
B-cell lymphoma/leukemia 11B	Q9C0K0	81	88,42	3
B-cell receptor-associated protein 31	P51572	45	27,84	1
BCKDK protein [Fragment]	Q6FGL4	66	46,33	2
Bcl-2-related proline-rich protein	Q9HB09	85	36,82	4
BCL-6 corepressor	Q6W2J9	40	192,19	2
BCL9-2	Q67FY1	77	157,13	4
BCoR-like protein 1	Q5H9F3	51	182,53	3
Beige-like protein	Q8NFQ0	56	317,45	2
Bestrophin-2	Q8NFU1	50	57,14	2
Beta I spectrin form betaI sigma3 [Fragment]	Q8WX82	50	117,48	2
Beta-1,4-N-acetyl-galactosaminyl transferase 1	Q8N636	45	35,47	2
Beta-adducin	P35612	53	80,85	2
Beta-hexosaminidase beta chain [Precursor]	P07686	54	11,56	1
Beta-mannosidase [Precursor]	O00462	47	8,20	2
BH3-interacting domain death agonist	P55957	220	26,82	5
Bifunctional methylenetetrahydrofolate dehydrogenase/cyclohydrolase [Precursor]	P13995	173	37,30	2
Bifunctional purine biosynthesis protein PURH	P31939	118	64,58	4
Biliverdin reductase A [Precursor]	P53004	526	33,41	9
Bleomycin hydrolase	Q13867	54	52,24	1
BM-016	Q9NZE0	61	12,83	2
BolA-like protein 2	Q9H3K6	132	6,84	2
Bone marrow proteoglycan [Precursor]	P13727	46	11,28	2
Bone-type alkaline phosphatase [Fragment]	Q9Y447	47	3,30	1
BR serine/threonine-protein kinase 1	Q8TDC3	93	50,72	4
BR serine/threonine-protein kinase 2	Q8IWQ3	72	81,63	3
Brain acid soluble protein 1	P80723	40	22,69	2
Brain-rescue-factor-1	Q2TV78	44	76,75	2
Brain-specific angiogenesis inhibitor 1-associated protein 2-like protein 2	Q6UXY1	62	58,95	3
Brain-specific angiogenesis inhibitor 2 [Precursor]	O60241	101	171,14	4
Brain-specific angiogenesis inhibitor 3	Q5VY37	42	171,52	3
Branched chain aminotransferase 2 variant [Fragment]	Q53EW7	84	44,25	2
BRCA1 associated RING domain 1 variant [Fragment]	Q53F80	69	86,50	2
BRD1 protein	Q86X06	46	133,10	1
BRD4 protein	Q4G0X8	44	88,29	2
Breakpoint cluster region protein [Fragment]	Q12844	41	100,54	2
Breast carcinoma-amplified sequence 3	Q9H6U6	51	101,12	2
Brevican	Q5SZ10	41	99,12	2
Brevican core protein [Precursor]	Q96GW7	43	67,87	3
BRICHOS domain-containing protein C16orf79	Q6PL45	63	28,47	2
BRIX	Q3ZTT4	101	41,37	2
Bromo adjacent homology domain-containing 1 protein	Q8TBE0	47	84,65	3
Bromodomain adjacent to zinc finger domain protein 1B	Q9UIG0	42	170,90	2
Bromodomain adjacent to zinc finger domain protein 2A	Q9UIF9	77	208,36	4
Bromodomain adjacent to zinc finger domain, 1A isoform b variant [Fragment]	Q59G54	49	136,54	2
Bromodomain PHD finger transcription factor	Q7Z7D6	91	307,90	4
Bromodomain-containing protein 2	P25440	71	88,06	3
Brorin [Precursor]	Q2TAL6	43	35,28	2
BTB/POZ domain-containing protein 7	Q9P203	42	126,29	2
BTB/POZ domain-containing protein KCTD12	Q96CX2	245	35,68	8
BTB/POZ domain-containing protein KCTD9	Q7L273	49	42,57	2
BUB1 budding uninhibited by benzimidazoles 1 homolog beta	Q8WV50	67	119,43	3
Bullous pemphigoid antigen 1, isoforms 6/9/10	O94833	70	590,99	5
Butyrate response factor 1	Q07352	61	36,31	2
Butyrate response factor 2	P47974	43	51,06	2
Butyrophilin subfamily 2 member A1 [Precursor]	Q7KYR7	40	60,13	2
BV02S1J1.4 protein [Fragment]	Q5ZGK0	51	8,20	2
C/EBP-induced protein	Q9C073	89	48,29	4
C1 protein	Q9UGE8	63	104,99	4
C11orf56 protein	Q8N612	54	105,50	2
C11orf9	Q9P1Q6	70	120,23	2
C15orf39 protein [Fragment]	Q2VPA3	43	53,08	2
C1q receptor protein [Precursor]	Q8IXK1	67	68,52	3
C-1-tetrahydrofolate synthase, cytoplasmic	P11586	142	101,36	6
C8orfK32 protein	Q2WGJ7	48	125,56	2
CA6 protein	Q8N4G4	45	19,66	2

Table 1. continued

Protein Name and Species	Accession	Score	MW [kDa]	# Pept.
CAD protein	P27708	145	235,03	4
Cadherin EGF LAG seven-pass G-type receptor 1 [Precursor]	Q9NYQ6	45	329,49	2
Cadherin EGF LAG seven-pass G-type receptor 3 [Precursor]	Q9NYQ7	65	358,26	3
Cadherin related 23	Q5SQD0	48	369,59	2
Cadherin, EGF LAG seven-pass G-type receptor 2	Q5T2Y7	44	317,45	2
Cadherin-15 [Precursor]	P55291	40	88,92	2
Calcium binding protein 1	Q8N6H5	41	39,87	2
Calcium binding protein Cab45 (Cab45)	Q5T7L8	60	39,58	2
Calcium channel, voltage-dependent, beta 1 subunit	Q8N3X9	44	65,70	2
Calcium channel, voltage-dependent, N type, alpha 1B subunit	Q00975	51	262,50	2
Calcium channel, voltage-dependent, T type, alpha 1G subunit	Q2TAC4	44	250,22	2
Calcium/calmodulin-dependent protein kinase kinase 2	Q96RR4	62	64,73	2
Calcium/calmodulin-dependent protein kinase type IV	Q16566	41	54,55	2
Calcium-regulated heat stable protein 1	Q9Y2V2	65	15,89	3
Calcium-response factor	Q8N187	47	23,20	2
Caldesmon	Q05682	436	64,22	12
Calmodulin-binding transcription activator 1	Q9Y6Y1	100	183,67	4
Calnexin [Precursor]	P27824	377	67,53	7
Calpain small subunit 1	P04632	128	28,30	2
Calpain-1 catalytic subunit	P07384	156	81,84	6
Calponin 2 isoform a variant [Fragment]	Q53GK7	64	33,62	3
Calponin-3	Q15417	319	36,39	9
Calreticulin variant [Fragment]	Q53G71	167	46,89	3
Calsyntenin-1 [Precursor]	O94985	62	109,79	3
Calsyntenin-3 [Precursor]	Q9BQT9	46	106,03	4
Calumenin	Q6IAW5	182	37,08	4
CaM kinase II isoform	O15302	52	26,74	2
cAMP-dependent protein kinase, alpha-catalytic subunit	P17612	240	40,43	4
cAMP-dependent protein kinase, beta-catalytic subunit	P22694	212	40,47	4
cAMP-specific 3',5'-cyclic phosphodiesterase 4C	Q08493	50	48,25	2
Cancer antigen 1	Q5TAM0	48	98,50	2
Cancer/testis antigen 2	O75638	47	18,23	2
CAP-GLY domain containing linker protein 1	Q29RG0	72	156,77	3
CAP-Gly domain-containing linker protein 3	Q96DZ5	64	59,56	2
Carbamoylphosphate synthetase I	Q5R207	42	102,15	2
Carbohydrate sulfotransferase 8	Q9H2A9	40	48,83	2
Carbonic anhydrase 1	P00915	43	28,87	2
Carbonyl reductase [NADPH] 1	P16152	128	30,22	4
Carboxyl-terminal PDZ ligand of neuronal nitric oxide synthase protein	O75052	50	64,32	2
Carboxypeptidase N subunit 2 [Precursor]	P22792	42	60,62	2
Cardiac sodium channel alpha subunit Nav1.5	Q8IZC9	94	226,81	5
Cardiomyopathy-associated protein 3	Q5MJ67	97	379,23	4
CArG binding factor	Q6SPF2	199	33,19	3
Carnitine O-acetyltransferase	P43155	58	70,50	3
Cartilage intermediate layer protein 1 [Precursor]	O75339	55	132,55	3
Cartilage intermediate layer protein 2 [Precursor]	Q8IUL8	97	126,29	5
Cartilage oligomeric matrix protein [Precursor]	P49747	52	82,83	2
Casein kinase 2, beta polypeptide [Fragment]	Q5SQ52	116	21,60	3
Casein kinase I isoform gamma-2	P78368	41	47,46	1
Casein kinase II subunit alpha'	P19784	181	41,19	3
Caskin-2	Q8WXE0	60	126,63	3
Cat eye syndrome critical region protein 2	Q9BXF3	55	164,21	2
Cat eye syndrome critical region protein 5 [Precursor]	Q9BXW7	374	43,56	6
Catenin, alpha 1	P35221	74	100,01	3
Catenin, alpha 2	Q7Z3Y0	73	100,38	3
Cathepsin D [Precursor]	P07339	78	44,52	2
Cathepsin H [Precursor]	P09668	43	37,38	2
Cation-independent mannose-6-phosphate receptor [Precursor]	P11717	52	274,28	3
Cation-transporting ATPase [Fragment]	Q7Z6E5	44	115,64	2
Cbp/p300-interacting transactivator 4	Q96RK1	40	18,56	1
CCDC41 protein [Fragment]	Q3B787	42	25,93	2
CD177 antigen [Precursor]	Q8N6Q3	44	64,36	2
CDC2 protein	Q3B785	107	25,92	3
CDC37 protein	Q6FG59	232	44,43	5
CDC42 binding protein kinase alpha (DMPK-like) [Fragment]	Q5T7A0	47	81,52	2
Cdc42 GTPase-activating protein	Q2M1Z3	97	157,02	5
CDC42-binding protein kinase beta	Q8IWQ7	85	186,04	6
CDK4 protein	Q6FG61	51	33,73	2
CDK5 regulatory subunit associated protein 2 [Fragment]	Q5JSG4	54	145,59	3
CDK-activating kinase assembly factor MAT1	P51948	58	35,82	4
CDKN1A interacting zinc finger protein 1	Q5SYW2	45	96,78	3
CDRT15 protein	Q96T59	53	20,64	2

Table 1. continued

Protein Name and Species	Accession	Score	MW [kDa]	# Pept.
Cell division cycle 2-like protein kinase 5	Q14004	81	164,92	3
Cell division cycle 2-related protein kinase 7	Q9NYV4	114	9,77	3
Cell division cycle 5-like protein	Q99459	85	92,19	3
Cell division cycle 7-related protein kinase	O00311	56	63,89	3
Cell division cycle protein 20 homolog	Q12834	127	10,89	8
Cell division cycle-associated protein 3	Q99618	44	29,00	2
Cell division protein kinase 6	Q00534	107	34,61	4
Cell growth-regulating nucleolar protein	Q9NX58	75	43,59	1
Cell-cycle related and expression-elevated protein in tumor	Q1WDE7	201	36,88	4
Cellular retinoic acid-binding protein 1	P29762	316	15,42	6
Cellular retinoic acid-binding protein 2	P29373	107	15,53	2
Cementoblastoma-derived protein 1	Q6PRD7	44	25,96	1
Centaurin-delta-1	Q8WZ64	42	193,42	2
Centaurin-gamma-1	Q99490	41	124,67	2
CENTG3 protein	Q86ST5	73	61,82	3
Centlein	Q9NXG0	51	161,62	2
Centriolin	Q7Z7A1	46	268,73	3
Centromere/kinetochore protein zw10 homolog	O43264	61	88,83	3
Centrosomal protein of 170 kDa	Q5SW79	47	175,29	2
Centrosome and spindle pole-associated protein 1	Q1MSJ5	42	141,75	2
Centrosome-associated protein 350	Q5VT06	95	350,72	6
Centrosome-associated protein CEP250	Q9BV73	47	281,14	2
Cerebellar degeneration-related protein 2-like	Q86X02	61	53,01	3
CERK protein	Q6I9Z0	56	21,67	2
CGI-111 protein	Q9Y3B5	175	22,07	4
CGI-150 protein	Q9Y3E8	70	54,98	3
Chaperonin 10-related protein [Fragment]	Q9UNM1	303	10,29	8
Chaperonin containing TCP1, subunit 6A isoform a variant [Fragment]	Q59ET3	166	57,73	7
Charged multivesicular body protein 4b	Q9H444	112	24,93	3
Chimeric MOZ-ASXH2 fusion protein	Q76L81	100	244,50	4
Chloride anion exchanger	P40879	47	84,51	2
Chloride channel Kb	Q5T5Q7	41	57,00	2
Chloride intracellular channel 1	Q5SRT5	158	17,76	3
Chloride intracellular channel protein 4	Q9Y696	324	28,62	5
Chondroadherin-like protein [Precursor]	Q6NUI6	51	85,17	3
Chondroitin sulfate proteoglycan 4 [Precursor]	Q6UVK1	50	250,50	2
Chondroitin sulfate proteoglycan 5 [Precursor]	O95196	88	60,06	4
Chondroitin sulfate proteoglycan 6	Q9UQE7	84	141,45	2
Chondroitin sulfate synthase 1	Q86X52	43	91,78	2
Chondroitin sulfate synthase 2	Q8IZ52	54	62,95	2
CHRNA4 protein	Q4VAQ5	86	60,95	4
Chromobox protein homolog 2	Q14781	62	56,08	2
Chromobox protein homolog 3	Q13185	197	20,80	4
Chromobox protein homolog 8	Q9HC52	56	43,40	2
Chromodomain-helicase-DNA-binding protein 4	Q14839	57	217,99	3
Chromodomain-helicase-DNA-binding protein 5	Q8TDI0	53	222,91	3
Chromosome 1 open reading frame 167	Q5SNV8	48	56,58	2
Chromosome 6 open reading frame 134 [Fragment]	Q5JP39	40	47,24	3
Chromosome 6 open reading frame 31	Q5SSW4	101	39,72	3
Chromosome 6 open reading frame 55	Q5TGM0	69	27,31	2
Chromosome 9 open reading frame 151	Q5SXM7	57	12,56	2
Chromosome-associated kinesin KIF4A	O95239	62	139,88	3
Ciliary dynein heavy chain 8	Q96JB1	45	514,66	2
Ciliary dynein heavy chain 9	Q9NYC9	65	511,93	4
CIP29 protein	Q567R9	47	16,82	1
Citrate synthase [Precursor]	O75390	171	45,59	5
CKAP4 protein [Fragment]	Q6NWZ1	57	67,78	2
Class IVb beta tubulin	Q8IWP6	1097	49,72	35
Clathrin coat assembly protein AP180	O60641	51	92,50	3
Clathrin heavy chain 1	Q00610	1597	191,36	41
Clathrin interactor 1	Q14677	60	71,40	3
Claudin-3	O15551	54	23,32	2
CLE	Q5RLJ0	168	27,95	3
Cleavage and polyadenylation specific factor 3, 73kDa variant [Fragment]	Q53F02	67	77,42	2
Cleavage and polyadenylation specificity factor subunit 5	O43809	134	26,15	4
Cleavage and polyadenylation specificity factor subunit 7	Q8N684	55	52,05	3
Cleavage stimulation factor 64 kDa subunit, tau variant	Q9H0L4	50	64,42	2
Cleavage stimulation factor 77 kDa subunit	Q12996	51	81,99	2
CLIP1 protein [Fragment]	Q6P5Z9	50	71,73	2
CLK2P protein [Fragment]	Q4G1B5	56	56,58	2
CMRF35-like molecule 9 [Precursor]	Q6UXG3	76	1,03	5
C-myc intron-binding protein 1	Q38G99	88	268,80	4

Table 1. continued

Protein Name and Species	Accession	Score	MW [kDa]	# Pept.
c-Myc-responsive protein Rcl	O43598	107	19,10	2
CNN2 protein [Fragment]	Q6FHC3	82	33,73	3
Coagulation factor VIII-associated (Intronic transcript) 1 (Coagulation factor VIII-associated (Int	Q5HY66	69	39,08	1
Coatomer subunit alpha	P53621	44	138,24	2
Coatomer subunit beta	P35606	75	102,29	3
Coatomer subunit delta	P48444	44	61,56	2
Coatomer subunit gamma-2	Q9UBF2	63	81,43	3
Cofilin isoform	Q549N0	130	18,72	3
Cofilin-1	P23528	701	18,36	9
COG1 protein	Q4G0L8	119	104,71	5
COG4 protein [Fragment]	Q6PIW8	42	86,65	2
Cohesin subunit SA-2	Q8N3U4	67	141,33	3
Coiled-coil and C2 domain-containing protein 1A	Q6P1N0	68	103,86	4
Coiled-coil and C2 domain-containing protein 1B	Q5T0F9	49	94,22	2
Coiled-coil domain containing 6	Q6GSG7	41	53,30	1
Coiled-coil domain-containing protein 108	Q6ZU64	48	217,25	2
Coiled-coil domain-containing protein 131	O60293	46	226,36	2
Coiled-coil domain-containing protein 78	A2IDD5	40	48,52	2
Coiled-coil domain-containing protein 8	Q9H0W5	44	59,37	2
Coiled-coil domain-containing protein 80 [Precursor]	Q76M96	57	108,17	2
Coiled-coil domain-containing protein 85A	Q96PX6	45	59,97	2
Coiled-coil domain-containing protein 86	Q9H6F5	66	40,24	2
Coiled-coil domain-containing protein KIAA1656	Q569K6	52	83,91	2
Coiled-coil-helix-coiled-coil-helix domain containing 3	A4D1N4	93	26,14	2
Coiled-coil-helix-coiled-coil-helix domain-containing protein 9 [Precursor]	Q5T1J5	47	15,48	1
COL20A1 protein	Q8IVX1	52	68,12	2
COL22A1 protein [Fragment]	Q8IVT9	45	161,12	2
Cold shock domain-containing protein E1	O75534	134	85,68	6
Collagen alpha-1(I) chain [Precursor]	P02452	135	138,91	7
Collagen alpha-1(II) chain [Precursor]	P02458	196	141,79	8
Collagen alpha-1(IV) chain [Precursor]	P02462	107	160,51	5
Collagen alpha-1(V) chain [Precursor]	P20908	87	183,51	5
Collagen alpha-1(VII) chain [Precursor]	Q02388	152	295,22	9
Collagen alpha-1(XI) chain [Precursor]	P12107	81	181,03	5
Collagen alpha-1(XIII) chain	Q5TAT6	41	69,95	2
Collagen alpha-1(XIX) chain [Precursor]	Q14993	71	115,02	3
Collagen alpha-1(XVI) chain [Precursor]	Q07092	68	157,75	3
Collagen alpha-1(XVII) chain	Q9UMD9	42	150,42	2
Collagen alpha-1(XVIII) chain [Precursor]	P39060	46	178,16	2
Collagen alpha-1(XXII) chain [Precursor]	Q8NFW1	47	161,12	3
Collagen alpha-1(XXIV) chain [Precursor]	Q17RW2	49	175,39	3
Collagen alpha-1(XXVII) chain [Precursor]	Q8IZC6	109	186,89	5
Collagen alpha-2(I) chain [Precursor]	P08123	90	129,29	5
Collagen alpha-2(IV) chain [Precursor]	P08572	115	167,55	5
Collagen alpha-2(V) chain [Precursor]	P05997	71	144,91	3
Collagen alpha-2(VI) chain [Precursor]	P12110	61	108,58	3
Collagen alpha-2(XI) chain [Precursor]	P13942	66	171,68	3
Collagen alpha-3(VI) chain [Precursor]	P12111	47	343,55	1
Collagen alpha-4(IV) chain [Precursor]	P53420	123	164,00	7
Collagen alpha-6(IV) chain [Precursor]	Q14031	76	163,81	3
Collagen and calcium-binding EGF domain-containing protein 1 [Precursor]	Q6UXH8	45	44,10	2
Collagen, type V, alpha 3 preproprotein variant [Fragment]	Q59GD4	77	162,67	3
Collagen, type XI, alpha 2	Q5JP94	47	162,19	2
Complement C1q subcomponent subunit B [Precursor]	P02746	46	26,46	2
Complement C4-B [Precursor]	P0C0L5	67	192,79	4
Complement component 1 Q subcomponent-binding protein [Precursor]	Q07021	172	31,34	2
Complement component C6 [Precursor]	P13671	56	25,28	2
COMT protein	Q6ICE6	47	30,05	1
Connector enhancer of kinase suppressor of Ras 1	Q969H4	54	79,71	3
Contactin associated protein-like 3B	B1B0V8	80	42,40	4
Contactin-1 [Precursor]	Q12860	101	113,25	4
Contactin-5 [Precursor]	O94779	65	120,69	2
COP9 signalosome complex subunit 5	Q92905	78	37,55	3
COP9 signalosome complex subunit 6	Q7L5N1	126	33,55	3
COP9 signalosome complex subunit 8	Q99627	133	23,21	2
COP9 signalosome subunit 4 variant [Fragment]	Q53FV3	263	46,24	6
Copine-1	Q99829	105	58,60	3
Copine-3	O75131	72	60,44	2
Copine-6	O95741	77	61,97	3
Copine-7	Q9UBL6	48	70,29	2
Coproporphyrinogen oxidase variant [Fragment]	Q53F08	252	50,13	6

Table 1. continued

Protein Name and Species	Accession	Score	MW [kDa]	# Pept.
Cordon-bleu protein-like 1	Q53SF7	74	131,79	3
Coronin, actin binding protein, 1C variant [Fragment]	Q53G58	87	53,25	2
Coronin-1A	P31146	54	51,03	2
Cortactin isoform a variant [Fragment]	Q53HG7	153	61,52	4
Corticotropin-lipotropin [Precursor]	P01189	110	4,54	7
Cortistatin	Q5T6G0	42	17,19	1
CRADD protein	Q8IY43	48	22,73	2
Creatine kinase B-type	P12277	425	42,62	7
Creatine kinase M-type	P06732	77	43,04	2
Crk-like protein	P46109	661	33,76	10
CRMP1 protein [Fragment]	Q96I11	49	43,72	3
CS0DF038YO05 variant [Fragment]	Q59EK7	90	37,23	2
CSMD2 protein	Q53TY4	50	394,99	2
CSNK2A1 protein	Q5U5J2	829	45,88	12
C-terminal binding protein 1, isoform 1	Q4KMQ8	155	47,47	3
C-terminal binding protein 2	Q5SQP7	163	106,12	4
CTP synthase 1	P17812	252	66,66	8
CTP synthase 2	Q9NRF8	44	65,68	1
C-type lectin domain family 14 member A [Precursor]	Q86T13	47	12,55	3
CUB and sushi domain-containing protein 2	Q7Z408	48	379,80	3
CUB and sushi domain-containing protein 3 [Precursor]	Q7Z407	66	401,70	4
CUG-BP- and ETR-3-like factor 6	Q96J87	44	50,48	2
Cullin-1	Q13616	75	87,33	3
Cullin-associated NEDD8-dissociated protein 1	Q86VP6	57	141,47	3
Cutaneous T-cell lymphoma-associated antigen 5	O15320	43	90,95	2
CWF19-like protein 1	Q69YN2	50	60,62	2
CXorf2 protein [Fragment]	Q96KU0	53	13,23	2
Cyclic AMP-dependent transcription factor ATF-6 alpha	P18850	53	74,52	2
Cyclin M4	Q6P4Q7	45	86,65	2
Cyclin-J-like protein	Q8IV13	43	48,41	2
Cystathionine beta-synthase	P35520	80	60,42	3
Cystatin-B	P04080	200	11,17	3
Cysteine and glycine-rich protein 2	Q16527	156	20,81	3
Cysteine and histidine-rich domain (CHORD)-containing, zinc binding protein 1.- Homo sapiens (Human	Q6IN49	140	37,47	4
Cysteine-rich protein 2 variant [Fragment]	Q53FN1	58	22,48	1
Cytochrome b5	P00167	53	15,32	1
Cytochrome b-c1 complex subunit 1 [Precursor]	P31930	273	52,61	4
Cytochrome b-c1 complex subunit 2 [Precursor]	P22695	439	48,41	5
Cytochrome b-c1 complex subunit 7	P14927	65	9,77	1
Cytochrome c	P99998	137	11,61	2
Cytochrome c oxidase subunit Va	Q8TB65	77	16,75	2
Cytochrome P450 4A11 [Precursor]	Q02928	51	59,35	2
Cytoplasmic dynein 1 light intermediate chain 2	O43237	44	54,10	3
Cytoskeleton-associated protein 5	Q14008	50	225,51	3
Cytosol aminopeptidase	P28838	63	52,61	3
Cytosolic acyl coenzyme A thioester hydrolase	O00154	432	41,77	10
Cytosolic carboxypeptidase 1	Q9UPW5	43	138,45	2
Cytosolic carboxypeptidase 3	Q8NEM8	74	116,01	5
Cytospin-A	Q69YQ0	43	124,59	3
D site-binding protein	Q10586	50	34,34	2
D(1B) dopamine receptor	P21918	50	52,95	2
D-3-phosphoglycerate dehydrogenase	O43175	142	56,48	3
Dapper homolog 2	Q5SW24	56	82,70	2
DAZ-associated protein 1	Q96EP5	92	43,36	2
DBH-like monooxygenase protein 1 [Precursor]	Q6UVY6	56	69,65	3
DCN1-like protein 4	Q92564	49	34,05	2
D-dopachrome decarboxylase	P30046	82	12,57	3
DDX19B protein [Fragment]	Q2NL95	63	50,64	2
DDX48 protein	Q6IBQ2	630	46,84	11
DEAD (Asp-Glu-Ala-Asp) box polypeptide 50	Q5VX37	64	82,51	3
DEAD box polypeptide 17 isoform p82 variant [Fragment]	Q59F66	408	81,02	13
DEAD box protein	Q9H4E3	60	50,60	2
DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 16	Q5JP45	41	119,21	3
Death domain-associated protein 6	Q9UER7	57	81,36	2
Dedicator of cytokinesis protein 11	Q5JSL3	53	237,95	3
Dedicator of cytokinesis protein 6	Q96HP0	55	94,30	2
Dedicator of cytokinesis protein 9	Q9BZ29	53	236,45	3
Deleted in liver cancer 1	Q7Z5R8	47	170,49	2
Deleted in malignant brain tumors 1 protein [Precursor]	Q9UGM3	44	59,08	2
Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase [Precursor]	Q13011	74	35,79	1
Dematin	Q08495	45	45,51	2

Table 1. continued

Protein Name and Species	Accession	Score	MW [kDa]	# Pept.
Dendrin	O94850	45	69,91	1
DENN domain-containing protein 2D	Q9H6A0	41	53,67	2
Density-regulated protein	O43583	42	26,49	1
Denticleless protein homolog	Q9NZJ0	67	79,44	3
Deoxycytidine kinase	P27707	59	30,50	1
Deoxyuridine 5'-triphosphate nucleotidohydrolase [Precursor]	P33316	43	24,31	1
Desmin	P17661	108	24,16	4
Desmoplakin	P15924	179	331,77	10
Desmoyokin	Q09666	52	312,29	4
Desmuslin	O15061	55	172,77	2
Developmentally-regulated GTP-binding protein 1	Q9Y295	152	40,52	4
Diablo homolog	Q502X2	256	21,22	6
Diacylglycerol kinase theta	P52824	52	101,40	3
Diacylglycerol kinase zeta	Q13574	60	124,12	3
Diacylglycerol kinase, theta 110kDa	Q6P3W4	49	101,11	2
Diacylglycerol kinase, theta variant [Fragment]	Q59FF7	63	95,69	2
Diencephalon/mesencephalon homeobox protein 1	Q8NFW5	63	41,20	2
Differential display and activated by p53 [Fragment]	Q5T2Z2	41	31,73	2
Dihydrolipoyl dehydrogenase [Precursor]	P09622	44	54,12	2
Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex [Precursor]	P36957	249	48,61	5
Dihydropyrimidinase-like 2 variant [Fragment]	Q59GB4	429	68,14	12
Dimethylarginine dimethylaminohydrolase 2 [Fragment]	Q5SRR9	150	19,95	4
Dipeptidase 3 [Precursor]	Q9H4B8	45	53,69	2
Dipeptidyl aminopeptidase-like protein 6	P42658	48	97,53	1
Dipeptidyl-peptidase 1 [Precursor]	P53634	45	13,41	1
Dipeptidyl-peptidase 3	Q9NY33	201	82,54	6
Diphosphoinositol polyphosphate phosphohydrolase 1	O95989	122	19,46	3
Discs, large (Drosophila) homolog-associated protein 4	Q5T2Y6	85	49,48	3
Disheveled-associated activator of morphogenesis 2	Q86T65	62	143,84	3
Disks large homolog 3	Q92796	46	90,34	2
Disks large homolog 5	Q8TDM6	93	140,20	4
Disks large-associated protein 1	O14490	65	108,87	3
Disks large-associated protein 2	Q9P1A6	44	117,62	2
Disks large-associated protein 4	Q9Y2H0	73	107,57	4
Disrupted in schizophrenia 1 protein	Q9NRI5	48	93,61	2
DJ1175B15.2 [Fragment]	Q8WX29	43	115,76	1
DJ-1-binding protein	Q5THR3	66	172,93	2
DJ34F7.1.1	Q9NPK9	92	463,94	6
DNA cytosine methyltransferase 3 alpha isoform a variant [Fragment]	Q59HC6	65	89,71	2
DNA excision repair protein ERCC-6	Q03468	76	168,31	3
DNA mismatch repair protein Msh3	P20585	43	127,46	3
DNA mismatch repair protein MSH6	P52701	67	152,69	4
DNA polymerase epsilon catalytic subunit protein isoform b	Q9Y5S4	61	261,38	4
DNA polymerase iota	Q9UNA4	45	80,35	2
DNA polymerase theta	O75417	50	197,60	2
DNA replication licensing factor MCM4	P33991	136	102,98	6
DNA replication licensing factor MCM6	Q14566	188	88,89	7
DNA replication licensing factor MCM9	Q9NXL9	64	127,34	2
DNA topoisomerase 2-alpha	P11388	47	174,39	2
DNA topoisomerase 2-binding protein 1	Q92547	79	160,45	3
DNA topoisomerase 3-beta-1	O95985	46	96,66	2
DNA-(apurinic or apyrimidinic site) lyase	P27695	597	35,55	9
DNAation factor, 45kDa, alpha polypeptide	Q5T6G5	184	29,39	3
DNA-binding protein	Q9Y474	62	179,97	4
DNA-binding protein RFX5	P48382	51	65,32	2
DNA-dependent protein kinase catalytic subunit	P78527	230	465,27	9
DNA-directed RNA polymerase	Q8IW34	40	155,54	1
DNA-directed RNA polymerase III subunit RPC4	P05423	51	44,40	2
DNA-directed RNA polymerases I, II, and III subunit RPABC3	P52434	49	17,00	1
DnaJ (Hsp40) homolog, subfamily A, member 3 variant [Fragment]	Q53G26	172	52,46	6
DnaJ (Hsp40) homolog, subfamily B, member 4 variant [Fragment]	Q59E89	79	38,61	2
DnaJ homolog subfamily A member 2	O60884	230	45,72	4
DnaJ homolog subfamily B member 1	P25685	292	37,89	6
DnaJ homolog subfamily C member 14	Q6Y2X3	42	78,57	2
DnaJ homolog subfamily C member 8	O75937	61	29,82	2
DNAJB11 protein	Q6IAQ8	187	40,52	3
DNAJC7 protein	Q7Z784	42	50,06	2
Docking protein 1	Q99704	54	55,33	2
Dolichol-phosphate mannosyltransferase	O60762	69	28,80	2
Dolichyl-diphosphooligosaccharide-protein glycosyltransferase	Q5VWA5	437	50,77	7

Table 1. continued

Protein Name and Species	Accession	Score	MW [kDa]	# Pept.
Dolichyl-diphosphooligosaccharide-protein glycosyltransferase 63 kDa subunit [Precursor]	P04844	57	67,68	3
Dopamine beta-hydroxylase	P09172	162	67,58	4
Dopamine receptor interacting protein 4	Q4W4Y1	288	96,02	7
Double homeobox protein 5	Q96PT3	47	22,16	2
Double-stranded RNA-binding protein Staufen homolog 1	O95793	45	63,18	1
Double-stranded RNA-specific adenosine deaminase	P55265	149	103,60	6
Down syndrome cell adhesion molecule splice variant [Fragment]	Q8WY19	66	192,50	3
Down syndrome cell adhesion molecule-like protein 1 [Precursor]	Q8TD84	117	224,46	5
Down-regulator of transcription 1 variant [Fragment]	Q53F47	68	19,46	1
DPYSL3 protein	Q6DEN2	173	73,86	7
Drebrin	Q16643	327	71,25	6
Drebrin-like protein	Q9UJU6	153	48,16	4
DSP variant protein [Fragment]	Q4LE79	64	265,03	3
Dual oxidase 1 [Precursor]	Q9NRD9	57	177,16	2
Dual specificity mitogen-activated protein kinase kinase 1	Q02750	83	43,28	2
Dual specificity phosphatase 8	Q86SS8	47	65,83	2
Dual specificity protein phosphatase 12	Q9UNI6	66	20,42	4
Dual specificity tyrosine-phosphorylation-regulated kinase 1A	Q13627	56	85,55	2
Dual specificity tyrosine-phosphorylation-regulated kinase 2	Q92630	70	66,65	3
Dual specificity tyrosine-phosphorylation-regulated kinase 4	Q9NR20	47	59,61	2
DUTP pyrophosphatase	Q6NSA3	368	26,55	7
Dynactin subunit 1	Q14203	82	141,70	4
Dynactin subunit 2	Q13561	209	44,07	4
Dynamin-1	Q05193	96	97,35	3
Dynamin-1-like protein	O00429	85	78,99	3
Dynamin-2	P50570	113	97,53	4
Dynamin-3	Q9UQ16	79	97,68	4
DYNC1I2 protein	Q5BJF8	120	68,38	3
Dynein heavy chain 1, axonemal	Q9P2D7	69	493,97	4
Dynein heavy chain 3, axonemal	Q8TD57	55	470,77	3
Dynein heavy chain 5, axonemal	Q8TE73	50	43,08	2
Dynein heavy chain 6, axonemal	Q9C0G6	67	193,65	4
Dynein heavy chain 7	Q9UMS3	48	461,14	1
Dynein heavy chain 7, axonemal	Q8WXX0	45	460,85	3
Dynein heavy chain, cytosolic	Q14204	604	533,40	16
Dynein light chain roadblock-type 1	Q9NP97	48	10,78	1
Dysbindin domain-containing protein 2	Q9BQY9	62	8,93	3
Dystonin	Q5TBT1	65	624,61	3
Dystroglycan [Precursor]	Q14118	43	97,58	2
E1A-binding protein p400	Q96L91	51	343,65	2
E3 SUMO-protein ligase PIAS3	Q9Y6X2	53	68,02	3
E3 SUMO-protein ligase RanBP2	P49792	70	8,51	2
E3 ubiquitin-protein ligase BRE1A	Q5VTR2	79	113,66	3
E3 ubiquitin-protein ligase CBL	P22681	51	99,65	2
E3 ubiquitin-protein ligase CBL-B	Q13191	59	109,45	2
E3 ubiquitin-protein ligase HECTD1	Q9ULT8	89	289,41	6
E3 ubiquitin-protein ligase HECW1	Q76N89	47	179,65	2
E3 ubiquitin-protein ligase HECW2	Q9P2P5	50	175,77	2
E3 ubiquitin-protein ligase HUWE1	Q7Z6Z7	57	220,49	2
E3 ubiquitin-protein ligase HUWE1	Q7Z6Z7	67	481,59	5
E3 ubiquitin-protein ligase NEDD4	P46934	58	114,94	2
E3 ubiquitin-protein ligase SMURF1	Q9HCE7	49	86,11	3
E3 ubiquitin-protein ligase UBR2	Q8IWV8	50	200,54	3
E3 ubiquitin-protein ligase UBR4	Q5T4S7	67	573,48	5
E3 ubiquitin-protein ligase UBR5	O95071	57	309,35	3
E3 ubiquitin-protein ligase UHRF2	Q96PU4	55	56,04	2
Early growth response protein 4	Q05215	58	50,80	4
EBNA1BP2 protein (EBNA1 binding protein 2 variant) (EBNA1 binding protein 2).- Homo sapiens (Human)	Q6IB29	222	34,83	4
EBNA-2 co-activator variant [Fragment]	Q59FF0	511	107,37	14
Echinoderm microtubule-associated protein-like 1	O00423	48	89,82	2
Echinoderm microtubule-associated protein-like 4	Q9HC35	80	101,47	3
Echinoderm microtubule-associated protein-like 5	Q05BV3	63	219,37	4
EF-hand calcium-binding domain-containing protein 4A	Q8N4Y2	44	32,75	3
EF-hand calcium-binding domain-containing protein 5	A4FU69	68	173,42	3
EF-hand calcium-binding domain-containing protein 6	Q5THR3	71	172,82	3
EF-hand domain-containing protein 1	Q5JVL4	47	73,99	2
EGF-containing fibulin-like extracellular matrix protein 2 [Precursor]	O95967	66	49,41	4
Egl nine homolog 1	Q9GZT9	67	46,02	3
EH domain-binding protein 1-like protein 1	Q8N3D4	67	161,85	3
EIF2S2 protein	Q6IBR8	42	38,36	1

Table 1. continued

Protein Name and Species	Accession	Score	MW [kDa]	# Pept.
EIF3A protein [Fragment]	Q96C72	45	48,62	2
EIF3H protein	Q5BKY2	134	39,58	4
EIF3S4 protein	Q6IAM0	81	35,58	3
EIF3S5 protein	Q6IB45	438	37,54	5
EIF3S6 protein [Fragment]	Q6FG33	356	52,19	7
EIF4B protein [Fragment]	Q7Z5Y0	117	39,19	4
EIF4G1 variant protein [Fragment]	Q4LE58	64	178,04	2
ELAV (Embryonic lethal, abnormal vision, Drosophila)-like 1 (Hu antigen R)	Q53XN6	260	36,07	6
ELAV (Embryonic lethal, abnormal vision, Drosophila)-like 4 (Hu antigen D)	Q5SXT5	44	42,37	2
ELAV-like protein 4	P26378	121	41,73	5
Electron transfer flavoprotein subunit alpha [Precursor]	P13804	63	32,69	1
Electron transfer flavoprotein subunit beta	P38117	65	27,70	1
ELK1, member of ETS oncogene family variant [Fragment]	Q59GR2	45	53,33	2
ELKS/RAB6-interacting/CAST family member 1	Q8IUD2	42	113,85	2
ELL-associated factor 2	Q96CJ1	49	28,77	2
Ells2 [Fragment]	Q8NEX1	51	18,82	2
Elongation factor 1-alpha 1	P68104	1072	50,11	26
Elongation factor 1-alpha 2	Q05639	354	50,44	7
Elongation factor 1-delta	P29692	604	30,97	11
Elongation factor 1-gamma	P26641	854	49,96	14
Elongation factor 2	P13639	1425	95,15	37
Elongation factor G 1 [Precursor]	Q96RP9	112	83,42	5
Elongation factor RNA polymerase II variant [Fragment]	Q59HG4	65	62,12	4
Elongation factor Tu [Precursor]	P49411	566	49,84	9
Em:AC004832.5 protein	Q6ICM2	46	40,24	2
Emerin	P50402	67	28,98	2
EMILIN-1 [Precursor]	Q9Y6C2	208	106,60	5
Enamelin	Q8IWP4	49	128,73	2
Endonuclease III-like protein 1	P78549	64	34,39	3
Endonuclease VIII-like 1	Q96FI4	46	43,68	2
Endoribonuclease Dicer	Q9UPY3	47	217,63	2
Endothelial differentiation inhibitory protein D18	Q4G5Y3	63	79,54	1
Endothelial zinc finger protein induced by tumor necrosis factor alpha	Q9NQZ8	47	54,50	2
Enhanced at puberty protein 1	Q9H1B7	55	82,66	3
Enhancer of polycomb homolog 2	Q52LR7	50	91,10	3
ENO1P protein	Q86TP5	189	42,31	4
Enolase gamma	P09104	878	47,11	10
Enolase, alpha	P06733	2639	47,01	44
Enolase, beta	P13929	900	46,83	9
Enoyl-CoA hydratase [Precursor]	P30084	83	31,26	1
Ensconsin	Q14244	42	84,05	2
EP300-interacting inhibitor of differentiation 1	Q9Y6B2	58	15,04	3
EPH receptor B6	Q2TB23	76	110,63	2
Ephrin receptor	Q7Z635	53	108,30	2
Ephrin receptor EphA5 isoform a variant [Fragment]	Q59FT4	54	112,12	3
Ephrin type-A receptor 6 [Precursor]	Q9UF33	41	116,12	2
Epidermal growth factor receptor kinase substrate 8-like protein 1	Q8TE68	83	80,26	4
Epidermal growth factor receptor substrate 15	P42566	49	98,66	1
Epidermal growth factor receptor substrate 15-like 1	Q9UBC2	51	38,69	4
Epithelial protein lost in neoplasm beta variant [Fragment]	Q53GG0	99	85,20	3
EPM2A-interacting protein 1	Q7L775	41	70,37	1
Epsilon-COP	Q7Z4Z1	93	34,38	3
ER mannosyl-oligosaccharide 1,2-alpha-mannosidase	Q9UKM7	54	79,58	2
ER protein ERp29 [Precursor]	P30040	149	28,98	4
Erlin-2 [Precursor]	O94905	138	37,82	3
ERO1-like protein alpha [Precursor]	Q96HE7	57	54,36	3
Erythrocyte membrane protein band 4.1-like 2 [Fragment]	Q5JRN3	40	22,95	1
ES1 protein homolog [Precursor]	P30042	66	28,12	2
ESFI5812	Q6UXV9	66	14,76	3
Ester hydrolase C11orf54	Q9H0W9	76	34,83	2
Estrogen receptor beta	Q92731	65	59,22	3
ETS translocation variant 3	P41162	57	56,97	3
Eukaryotic initiation factor 4A-I	P60842	1154	46,12	29
Eukaryotic initiation factor 4A-II	Q14240	731	46,37	20
Eukaryotic translation elongation factor 1 alpha 1 variant [Fragment]	Q53G89	659	46,86	20
Eukaryotic translation initiation factor 2 subunit 1	P05198	379	35,96	10
Eukaryotic translation initiation factor 2 subunit 3	P41091	92	50,95	2
Eukaryotic translation initiation factor 2B, subunit 2 beta, 39kDa	Q9BPX4	132	38,98	3
Eukaryotic translation initiation factor 2C 2	Q9UKV8	59	97,15	3
Eukaryotic translation initiation factor 3 subunit 1	O75822	113	29,04	3
Eukaryotic translation initiation factor 3 subunit 2	Q13347	349	36,48	7
Eukaryotic translation initiation factor 3 subunit 5	O00303	234	13,94	3

Table 1. continued

Protein Name and Species	Accession	Score	MW [kDa]	# Pept.
Eukaryotic translation initiation factor 3 subunit B	P55884	207	92,43	7
Eukaryotic translation initiation factor 3 subunit C	Q99613	230	105,28	10
Eukaryotic translation initiation factor 3 subunit D	O15371	49	63,93	2
Eukaryotic translation initiation factor 3 subunit E-interacting protein	Q9Y262	103	66,70	8
Eukaryotic translation initiation factor 3 subunit J	O75822	46	29,06	2
Eukaryotic translation initiation factor 3 subunit K	Q9UBQ5	95	21,62	2
Eukaryotic translation initiation factor 4 gamma, 3	Q5SWC3	59	176,65	3
Eukaryotic translation initiation factor 4B	Q6GPH5	210	69,13	6
Eukaryotic translation initiation factor 4H	Q15056	118	25,47	4
Eukaryotic translation initiation factor 5A-1	P63241	186	16,82	5
EVH1 domain binding protein	Q9NZI9	50	90,65	2
Ewing sarcoma breakpoint region 1	Q96FE8	68	68,35	2
Excision repair cross-complementing rodent repair deficiency, complementation group 3 variant [Fragment]	Q53HW5	48	89,15	2
Exocyst complex component 2	Q96KP1	43	104,00	2
Exocyst complex component 7	Q9UPT5	60	83,38	3
Exosome complex exonuclease RRP41	Q9NPD3	63	26,24	1
Exosome complex exonuclease RRP42	Q15024	69	31,68	1
Exportin-1	O14980	122	123,26	3
Exportin-2	P55060	292	110,26	10
Exportin-7	Q9UIA9	82	123,70	4
Exportin-T	O43592	106	109,92	4
Extended-synaptotagmin-1	Q9BSJ8	90	122,78	3
Extracellular matrix protein FRAS1 [Precursor]	Q86XX4	75	442,93	4
Eyes absent homolog 2	O00167	60	63,58	3
Eyes absent homolog 3	Q99504	49	62,56	2
Ezrin	P15311	347	69,37	13
Ezrin-radixin-moesin-binding phosphoprotein 50	O14745	84	38,71	1
Facioscapulohumeral muscular dystrophy	Q14333	112	89,03	5
FACT complex subunit SPT16	Q9Y5B9	234	119,84	5
FACT complex subunit SSRP1	Q08945	394	72,78	11
F-actin-capping protein subunit alpha-1	P52907	232	32,89	4
F-actin-capping protein subunit alpha-2	P47755	125	32,80	2
F-actin-capping protein subunit beta	P47756	80	31,20	2
FAM129B protein [Fragment]	Q2YD88	42	35,21	3
FAM129C protein [Fragment]	Q7Z6H6	56	77,40	3
FAM13A1_v2 protein	Q24JP0	51	116,93	2
FAM54B protein (Hypothetical protein HYST1888)	Q9NUI7	162	31,94	3
Familial Alzheimer's disease protein 1	Q7M4L1	53	47,04	3
Fanconi anemia group A protein	O15360	50	162,70	3
Fanconi anemia group C protein	Q00597	41	63,43	2
Fanconi anemia-associated protein of 100 kDa	Q0VG06	60	93,42	2
Far upstream element-binding protein 1	Q96AE4	116	67,43	4
Far upstream element-binding protein 2	Q92945	979	72,85	18
Farnesyl pyrophosphate synthetase	P14324	222	40,51	5
Farnesyl pyrophosphate synthetase like-4 protein [Fragment]	Q14329	219	39,64	5
FAS-associated factor 1	Q9UNN5	44	53,62	1
Fas-binding factor 1	Q8TES7	70	125,45	3
Fascin	Q16658	642	54,37	13
FASN variant protein [Fragment]	Q4LE83	897	277,20	23
FAT tumor suppressor homolog 4	Q6V0I7	60	542,69	3
Fatty acid synthase	P49327	849	273,28	22
Fatty acid-binding protein, epidermal	Q01469	47	15,02	1
FBL protein (Hypothetical protein) [Fragment]	Q96BS4	443	28,43	8
F-box only protein 22	Q8NEZ5	53	44,51	2
F-box only protein 31	Q5K680	49	60,66	2
F-box only protein 38	Q6PIJ6	42	133,97	2
F-box/LRR-repeat protein 19	Q6PCT2	66	57,61	3
F-box/WD repeat-containing protein 2	Q9UKT8	52	51,41	2
FCH domain only protein 2	Q0JRZ9	41	88,92	2
FCRLB protein	Q6NXH0	41	32,67	2
FERM and PDZ domain-containing protein 3	Q5JV73	79	199,21	4
FERM domain-containing protein 3	A2A2Y4	45	66,82	2
FERM domain-containing protein 4A	Q9P2Q2	78	113,97	3
FERM domain-containing protein 6	Q96NE9	52	72,04	2
FERM, RhoGEF (ARHGEF) and pleckstrin domain protein 1 [Fragment]	Q5JV91	40	17,15	2
FERM, RhoGEF and pleckstrin domain-containing protein 2	O94887	64	19,22	3
Fermitin family homolog 2	Q96AC1	40	77,84	1
Ferredoxin reductase, isoform 1 (Ferredoxin reductase isoform 1 variant) (Ferredoxin reductase).- H	Q6GSK2	159	53,80	5
Ferritin heavy chain	P02794	167	20,01	3
Fez family zinc finger protein 2	Q8TBJ5	41	48,81	2

Table 1. continued

Protein Name and Species	Accession	Score	MW [kDa]	# Pept.
FH2 domain-containing protein 1	Q9C0D6	44	124,76	3
Fibrillin 2 (Congenital contractural arachnodactyly) variant [Fragment]	Q59ES6	54	215,63	2
Fibroblast growth factor 11 variant [Fragment]	Q59FR9	47	36,41	2
Fibroblast growth factor receptor subtype 1 [Fragment]	Q9UD50	53	31,08	2
Fibroblast growth factor-2 repression protein-1	Q4L233	42	23,69	3
Fibroblast growth factor-binding protein 3 [Precursor]	Q8TAT2	44	27,59	2
Fibronectin [Precursor]	P02751	67	262,61	3
Fibronectin type 3 and ankyrin repeat domains 1 protein	Q9DAM9	83	34,18	4
Fibronectin type 3 and ankyrin repeat domains protein 1	Q8TC84	941	34,18	17
Fibronectin type III domain-containing protein 1	Q4ZHG4	81	199,42	4
Ficolin-2 [Precursor]	Q15485	82	8,25	4
Filaggrin	P20930	62	435,17	4
Filamin-A	P21333	203	280,45	6
Filamin-A-interacting protein 1	Q7Z7B0	71	138,11	2
Filamin-B	O75369	59	278,20	3
Filamin-C	Q14315	82	290,78	2
Fizzy-related protein homolog	Q9UM11	127	55,18	6
FK506-binding protein 2 [Precursor]	P26885	49	15,64	1
FK506-binding protein 3 variant [Fragment]	Q53GD8	91	25,19	1
FK506-binding protein 4	Q02790	216	51,64	5
Flagellar M-ring protein FliF	Q5HWF3	56	62,59	3
Flap endonuclease 1	P39748	153	42,57	2
Flotillin 1	Q5JP64	104	33,43	2
Flt3-interacting zinc finger protein 1	Q96SL8	50	51,96	2
FMI protein	Q92735	67	161,60	3
FNIP1-like protein	Q9P278	52	122,12	2
Folylpolyglutamate synthetase mitochondrial isoform [Fragment]	Q96DJ7	51	4,10	1
Forkhead box D2	Q5SVZ3	84	48,75	3
Forkhead box protein E2	Q99526	43	52,36	1
Forkhead-associated (FHA) phosphopeptide binding domain 1 [Fragment]	Q5JYW6	65	75,30	2
Formin-binding protein 4	Q8N3X1	51	110,00	2
Formin-like protein 2	Q96PY5	65	123,40	2
Fos-related antigen 2	P15408	57	35,19	3
Four and a half LIM domains protein 1	Q13642	50	36,26	2
FOXD4-like 2	Q3SYB3	53	45,82	3
Fragile X mental retardation syndrome related protein 2	Q86V09	40	74,19	2
FRAS1-related extracellular matrix protein 2 [Precursor]	Q5SZK8	59	351,16	3
Frequently rearranged in advanced T-cell lymphomas	Q5JTI1	63	29,08	3
Fructose-bisphosphate aldolase A	P04075	1897	39,40	26
Fructose-bisphosphate aldolase C	P09972	912	39,43	14
Full-length cDNA 5-PRIME end of clone CS0DF013YM24 of Fetal brain of Homo sapiens (Human) variant [Fragment]	Q53GF9	116	25,62	3
Full-length cDNA 5-PRIME end of clone CS0DI001YE04 of Placenta of Homo sapiens [Fragment]	Q86TR4	56	63,46	2
Full-length cDNA clone CS0DI085YI08 of Placenta of Homo sapiens [Fragment]	Q86TV4	72	60,02	3
Fumarate hydratase	Q5SY06	79	54,60	1
FUS interacting protein (Serine-arginine rich) 1	Q5JRH9	290	31,28	6
Fused predicted acetyl-CoA:acetoacetyl-CoA transferase	A1ABN1	457	24,08	10
FWP004	Q5QTS3	91	23,65	3
G patch domain and KOW motifs-containing protein	Q92917	46	52,23	2
G protein-coupled receptor 156 variant [Fragment]	Q59FU7	80	59,03	4
G protein-coupled receptor 37	A4D0Y6	53	67,11	2
G protein-regulated inducer of neurite outgrowth 1	Q7Z2K8	84	102,37	4
G protein-regulated inducer of neurite outgrowth 3	Q6ZVF9	75	82,44	3
G1 to S phase transition protein 2 homolog	Q8IYD1	81	68,91	4
G2 and S phase-expressed protein 1	Q9NYZ3	46	76,62	3
G2/M phase-specific E3 ubiquitin-protein ligase	Q7L622	58	80,45	1
G2/mitotic-specific cyclin-B3	Q8WWL7	50	157,82	2
GABA/noradrenaline transporter	Q13032	45	80,08	2
Gag polyprotein	P03345	64	47,50	2
Gag polyprotein	P63145	49	130,16	2
Galectin-1	P09382	196	14,71	4
Galectin-related protein	Q3ZCW2	50	18,97	2
Gametogenetin	Q86UU5	55	66,70	2
Gamma1-COP	Q54AC4	58	97,66	2
Gamma-aminobutyric acid receptor subunit alpha-3 [Precursor]	P34903	60	55,17	5
Gamma-glutamyl carboxylase variant [Fragment]	Q53GV4	50	87,53	2
Gamma-glutamyl hydrolase [Precursor]	Q92820	159	35,94	3
Ganglioside-induced differentiation-associated protein 1	Q8TB36	83	41,23	2
Gap junction protein	Q8N2R7	50	40,14	2
GARS protein	Q7Z5H0	51	84,59	2
GAS2-like protein 1	Q99501	75	72,67	3

Table 1. continued

Protein Name and Species	Accession	Score	MW [kDa]	# Pept.
GAS2-like protein 2	Q8NHY3	63	96,46	3
GAS2-like protein 3	Q86XJ1	50	75,21	2
GATA binding protein 6 variant [Fragment]	Q53EU2	67	60,06	3
GCN1-like protein 1	Q92616	164	292,43	5
GDI2 protein (GDP dissociation inhibitor 2)	Q6IAT1	1501	50,63	25
GDP dissociation inhibitor 2 [Fragment]	Q5SX87	44	29,84	2
GDP-fucose protein O-fucosyltransferase 1 [Precursor]	Q9H488	99	43,93	4
GDP-L-fucose synthetase	Q13630	58	35,89	2
Gem (Nuclear organelle) associated protein 4	Q8WUM5	64	120,04	2
GEM-interacting protein	Q9P107	84	106,67	3
General transcription factor 3C polypeptide 1	Q12789	59	238,65	3
General transcription factor 3C polypeptide 2	Q8WUA4	46	100,68	2
General transcription factor II, i	Q499G6	166	110,01	5
General transcription factor II-I	P78347	56	112,42	4
General vesicular transport factor p115	O60763	52	77,46	2
Glia maturation factor beta	P60983	87	16,57	1
Gliomedin	Q6ZMI3	40	58,96	1
Glucagon-like peptide 1 receptor [Precursor]	P43220	124	53,06	7
Glucocorticoid receptor AF-1 specific elongation factor [Fragment]	Q9NZS6	162	46,24	4
Glucocorticoid receptor DNA-binding factor 1	Q9NRY4	64	8,68	4
Glucosamine-6-phosphate isomerase	P46926	98	35,99	4
Glucose-6-phosphate 1-dehydrogenase [Fragment]	Q2Q9H2	130	54,79	5
Glucose-6-phosphate isomerase	P06744	188	62,98	5
Glucosidase 2 subunit beta [Precursor]	P14314	408	59,26	12
Glucosylceramidase [Precursor]	P04062	49	59,72	2
Glucuronosyltransferase-S	Q9NPZ5	58	54,24	3
Glutamate [NMDA] receptor subunit epsilon-4 [Precursor]	O15399	42	143,56	2
Glutamate dehydrogenase 1 [Precursor]	P00367	157	61,36	4
Glutamate receptor delta-1 subunit [Precursor]	Q9ULK0	41	112,13	2
Glutamate receptor-interacting protein 1	Q9Y3R0	40	122,42	2
Glutamate receptor-interacting protein 2	Q9C0E4	50	112,43	3
Glutamate-rich WD repeat-containing protein 1	Q9BQ67	59	49,42	3
Glutaminase kidney isoform [Precursor]	O94925	88	102,18	4
Glutamine-rich protein 2	Q9H0J4	65	180,83	3
Glutaminyl-tRNA synthetase variant [Fragment]	Q53HS0	311	87,65	10
Glutaredoxin-3	O76003	207	32,59	4
Glutaredoxin-related protein 5	Q86SX6	81	16,65	2
Glutathione peroxidase 7 [Precursor]	Q96SL4	75	21,00	4
Glutathione reductase [Precursor]	P00390	48	56,26	2
Glutathione S-transferase Mu 3	P21266	46	26,41	1
Glutathione S-transferase P	P09211	501	23,36	10
Glutathione transferase omega-1	P78417	151	15,81	3
Glyceraldehyde-3-phosphate dehydrogenase	P04406	2081	36,03	40
Glycerophosphodiester phosphodiesterase 1	Q9NZC3	68	37,72	4
Glycine dehydrogenase (Decarboxylating)	Q2M2F8	71	112,66	3
Glycine/arginine-rich protein 1	Q8TAY7	47	28,71	2
Glycine/arginine-rich protein 1	Q9H7Z4	80	28,71	4
Glycogen phosphorylase, brain form	P11216	92	96,50	4
Glycoprotein Ib beta	Q14422	64	21,72	3
Glycosyltransferase 25 family member 3 [Precursor]	Q5T4B2	57	67,53	2
Glycyl-tRNA synthetase	P41250	529	77,48	12
Glyoxylate reductase/hydroxypyruvate reductase [Fragment]	Q5T945	151	35,65	3
GMPR2 protein	Q6PKC0	107	44,98	2
GNAS complex locus	Q5JWF1	255	78,77	7
Golgin subfamily A member 3	Q08378	50	167,36	2
GPR61 protein [Fragment]	Q4VBN0	45	45,60	2
G-protein-signaling modulator 1	Q86YR5	54	72,14	2
Grainyhead-like protein 1 homolog	Q9NZI5	48	70,11	1
GRAM domain-containing protein 1A	Q96CP6	81	9,02	6
Granulocyte colony-stimulating factor receptor [Precursor]	Q99062	40	92,16	1
GRB2-related adapter protein 2	O75791	76	11,42	2
G-rich sequence factor 1	Q12849	74	47,01	2
GRIP and coiled-coil domain-containing protein 2	Q8IWJ2	59	184,66	2
Growth arrest-specific protein 6 [Precursor]	Q14393	61	79,68	3
Growth factor receptor-bound protein 10	Q13322	46	60,91	2
Growth/differentiation factor 7 [Precursor]	Q7Z4P5	44	46,97	2
GSPT1 protein	Q96GF2	228	68,40	7
GTBP-ALT	Q1L838	45	121,09	2
GTPase NRas [Precursor]	P01111	62	21,22	2
GTP-binding nuclear protein Ran	P62826	367	24,28	8
GTP-binding protein GUF1 homolog	Q8N442	84	74,33	3
GTSE1 protein	Q20WK2	70	76,57	3

Table 1. continued

Protein Name and Species	Accession	Score	MW [kDa]	# Pept.
Guanine nucleotide exchange factor DBS	O15068	44	128,11	2
Guanine nucleotide-binding protein alpha-13 subunit	Q14344	330	44,02	6
Guanine nucleotide-binding protein G(i), alpha-1 subunit	P63096	197	40,20	4
Guanine nucleotide-binding protein G(i), alpha-2 subunit	P04899	172	40,29	4
Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1	P62873	425	37,22	5
Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2	P62879	360	37,18	6
Guanine nucleotide-binding protein G(k) subunit alpha	P08754	226	40,38	5
Guanine nucleotide-binding protein G(o) subunit alpha 1	P09471	76	40,05	2
Guanine nucleotide-binding protein G(s) subunit alpha isoforms short	P63092	283	45,72	7
Guanine nucleotide-binding protein G(s) subunit alpha isoforms XLas	Q5JWF2	40	111,03	2
Guanine nucleotide-binding protein subunit beta-2-like 1	P63244	234	34,92	4
Guanine nucleotide-releasing protein	Q13972	58	145,29	2
Guanylate binding protein 2, interferon-inducible	Q6GPH0	43	67,23	2
Guanylate cyclase soluble subunit beta-1	Q02153	50	70,47	1
H/ACA ribonucleoprotein complex subunit 2	Q9NX24	117	17,19	2
H1 histone family member O, oocyte-specific	Q8IZA3	58	35,81	2
Haloacid dehalogenase-like hydrolase domain-containing protein 2	Q9H0R4	48	28,54	2
HBS1-like protein	Q9Y450	43	75,47	2
HBxAg transactivated protein 2 (XTP2)	Q5TI99	77	295,82	3
HDDM36	Q8TDY8	81	134,13	3
HEAT repeat-containing protein 1	Q9H583	47	242,37	2
HEAT repeat-containing protein 2	Q86Y56	63	93,53	2
Heat shock 105 kDa/110 kDa protein 1	Q5TBM7	399	92,20	11
Heat shock 70 kDa protein 1	P08107	938	69,98	20
Heat shock 70 kDa protein 12A	O43301	75	74,98	3
Heat shock 70 kDa protein 12B	Q96MM6	48	75,69	3
Heat shock 70 kDa protein 1-like variant [Fragment]	Q53FA3	555	70,36	10
Heat shock 70 kDa protein 4 isoform a variant [Fragment]	Q59GF8	434	87,95	10
Heat shock 70 kDa protein 5	P11021	1798	72,29	34
Heat shock 70 kDa protein 6	P17066	378	70,98	7
Heat shock 70 kDa protein 6 (HSP70B') variant [Fragment]	Q53FC7	224	70,96	6
Heat shock 70 kDa protein 8 isoform 1 variant [Fragment]	Q53GZ6	187	70,86	6
Heat shock 70 kDa protein 8 isoform 2 variant [Fragment]	Q53HF2	182	53,47	5
Heat shock 70 kDa protein 9B variant [Fragment]	Q53H23	67	73,63	2
Heat shock protein 40 kDa protein 4	P31689	850	44,85	11
Heat shock protein 60 kDa	P10809	1216	61,17	18
Heat shock protein 70 kDa protein 8	P11142	791	70,85	20
Heat shock protein 75 kDa [Precursor]	Q12931	115	66,01	3
Heat shock protein 90 kDa AA1 protein [Fragment]	Q2VPJ6	176	68,33	4
Heat shock protein 90 kDa alpha	P08238	2302	83,08	42
Heat shock protein 90 kDa beta	P07900	2146	98,08	41
Heat shock protein 90Bb	Q58FF8	605	49,09	12
Heat shock protein A12B [Fragment]	Q5BKZ8	43	75,91	2
Heat shock protein beta-1	P04792	408	22,77	10
HECT domain and RCC1-like domain-containing protein 1	Q15751	128	531,85	5
Helicase	Q8NHC9	135	261,21	7
Helicase SRCAP	Q6ZRS2	78	343,53	3
Hematological and neurological expressed 1-like protein	Q9H910	54	14,64	3
Heme oxygenase (Decycling) 1	Q96DI8	43	32,80	2
Hemicentin-1 [Precursor]	Q96RW7	82	613,00	4
Hemicentin-2 [Fragment]	Q8NDA2	40	143,89	2
Hemoglobin subunit alpha	P69905	66	15,25	1
Hemojuvelin [Precursor]	Q6ZVN8	42	45,05	2
Heparan-sulfate 6-O-sulfotransferase 3	Q8IZP7	66	54,81	2
Heparin-binding protein HBp15	Q7Z4W8	115	14,81	2
Hepatocellular carcinoma-associated antigen 59 [Fragment]	Q6GVN4	94	22,54	2
Hepatocyte cell adhesion molecule [Precursor]	Q14CZ8	40	16,57	2
Hepatocyte growth factor-regulated tyrosine kinase substrate	O14964	61	86,14	2
Hepatocyte nuclear factor 3-alpha	P55317	43	49,32	2
Hepatoma-derived growth factor	P51858	944	26,77	15
Hepatoma-derived growth factor 2 (HGDF-related pro 2)	Q7Z4V5	105	74,27	4
Hepatoma-derived growth factor-related protein 3	Q9Y3E1	65	74,78	3
Hepatopoietin PCn127	Q1AHP8	229	28,00	4
Hephaestin	Q5JUU0	61	130,45	2
HERV-K_11q22.1 provirus ancestral Pol protein	P63136	64	93,56	3
HERV-K_1q22 provirus ancestral Pol protein	P63135	49	165,18	1
HERV-K_3q12.3 provirus ancestral Gag polyprotein	Q9HDB9	47	73,59	2
HERV-K_5q33.3 provirus ancestral Gag polyprotein	P87889	57	74,14	2
HERV-W_3q26.32 provirus ancestral Gag polyprotein	Q9NRZ4	72	41,06	3
Heterochromatin protein 1, binding protein 3 [Fragment]	Q5SWC6	115	36,49	4
Heterogeneous nuclear ribonucleoprotein A/B	Q99729	522	31,21	10
Heterogeneous nuclear ribonucleoprotein A1	P09651	1202	38,69	22

Table 1. continued

Protein Name and Species	Accession	Score	MW [kDa]	# Pept.
Heterogeneous nuclear ribonucleoprotein A3	P51991	781	15,97	14
Heterogeneous nuclear ribonucleoprotein AB isoform a variant [Fragment]	Q53F64	659	35,97	11
Heterogeneous nuclear ribonucleoprotein C-like 1	O60812	44	14,99	1
Heterogeneous nuclear ribonucleoprotein D-like	O14979	98	33,19	2
Heterogeneous nuclear ribonucleoprotein F	P52597	677	45,51	9
Heterogeneous nuclear ribonucleoprotein G	P38159	709	47,42	13
Heterogeneous nuclear ribonucleoprotein H	P31943	713	49,07	12
Heterogeneous nuclear ribonucleoprotein H3 isoform a variant [Fragment]	Q53F48	619	36,90	9
Heterogeneous nuclear ribonucleoprotein K	Q5T6W5	326	47,53	9
Heterogeneous nuclear ribonucleoprotein K transcript variant	Q5EC54	653	51,03	14
Heterogeneous nuclear ribonucleoprotein M	P52272	70	77,33	4
Heterogeneous nuclear ribonucleoprotein Q	O60506	214	62,62	7
Heterogeneous nuclear ribonucleoprotein R	O43390	68	68,32	4
Heterogeneous nuclear ribonucleoprotein U	Q00839	277	90,29	5
Heterogeneous nuclear ribonucleoprotein U [Fragment]	Q5RI17	620	79,79	11
Heterogeneous nuclear ribonucleoprotein U-like protein 2	Q1KMD3	84	85,05	2
Heterogeneous nuclear ribonucleoproteins A2/B1	P22626	2047	37,41	41
Heterogeneous nuclear ribonucleoproteins C1/C2	P07910	805	32,37	15
Hexosaminidase domain-containing protein	Q8WVB3	52	53,79	2
HF protein [Fragment]	Q14006	43	74,25	2
HIBCH protein [Fragment]	Q9BS94	79	40,39	2
High affinity cAMP-specific and IBMX-insensitive 3',5'-cyclic phosphodiesterase 8B	O95263	68	98,92	2
High mobility group protein B1	P09429	388	12,89	8
High mobility group protein B2	P26583	305	23,89	6
High mobility group protein B3	O15347	41	22,83	2
High mobility group protein B3	O15347	86	22,98	2
Histidine triad nucleotide-binding protein 1	P49773	233	13,66	4
Histidyl-tRNA synthetase, cytoplasmic	P12081	56	57,37	2
Histone acetyltransferase MYST4	Q8WYB5	94	231,38	6
Histone cluster 2, H3, pseudogene 2	Q5TEC6	67	15,42	4
Histone deacetylase 1 [Fragment]	Q5TEE2	88	24,53	2
Histone deacetylase 5	Q9UQL6	47	116,64	2
Histone deacetylase complex subunit SAP18	O00422	41	17,55	1
Histone H1 [Fragment]	Q14463	51	5,85	1
Histone H1x	Q92522	128	22,47	3
Histone H2A type 1	P0C0S8	248	14,08	5
Histone H2A type 1-A	Q96QV6	150	14,09	2
Histone H2A type 1-B	P04908	260	14,03	4
Histone H2A.1	O75367	489	39,46	7
Histone H2AV	Q71UI9	242	13,37	4
Histone H2B	Q3KP43	128	7,64	2
Histone H2B type 1-A	Q96A08	172	14,03	3
Histone H2B type 1-C/E/F/G/I	P62807	47	13,82	2
Histone H2B type 1-D	P58876	103	13,80	4
Histone H2B type 1-H	Q93079	357	13,75	13
Histone H2B type 1-J	P06899	41	13,61	1
Histone H2B type 1-L	Q99880	47	13,95	2
Histone H2B type 1-O	P23527	288	13,77	12
Histone H2B type 2-C	Q6DN03	74	21,33	3
Histone H2B type 2-D	Q6DRA6	106	18,02	7
Histone H2B type 3-B	Q8N257	296	13,77	12
Histone H3.1	P68431	117	12,32	7
Histone H3.1t	Q16695	45	15,37	2
Histone H3-like	Q6NXT2	45	15,23	2
Histone H3-like centromeric protein A	P49450	42	15,99	2
Histone H4	P62805	486	11,36	9
Histone-lysine N-methyltransferase SUV420H1	Q4FZB7	49	99,19	2
Histone-lysine N-methyltransferase, H3 lysine-4 specific SET1	O15047	78	185,92	4
Histone-lysine N-methyltransferase, H3 lysine-79 specific	Q8TEK3	66	133,25	3
HLA class I histocompatibility antigen, A-3 alpha chain [Precursor]	P04439	95	41,34	3
HLA class I histocompatibility antigen, A-36 alpha chain [Precursor]	P30455	49	40,93	2
HLA-A26 protein	O19633	40	24,29	2
HMG-1	Q14321	601	24,98	10
HNRPA0 protein	Q6IB18	437	30,82	7
HNRPCL1 protein [Fragment]	Q6PKD2	398	22,64	6
HNRPL protein	Q6NTA2	316	60,20	9
HNRPR protein	Q9BV64	420	71,17	10
Homeobox protein ARX	Q96QS3	73	58,16	3
Homeobox protein cut-like 2	O14529	68	154,20	3
Homeobox protein Hox-A4	Q00056	59	34,50	3
Homeobox protein Hox-B6	P17509	41	25,43	1

Table 1. continued

Protein Name and Species	Accession	Score	MW [kDa]	# Pept.
Homeobox protein MIXL1	Q9H2W2	42	24,66	1
Homeobox protein MSX-1	P28360	92	38,15	5
Homeobox protein NOBOX	O60393	68	73,71	3
Homeodomain-interacting protein kinase 3	Q9H422	76	7,60	3
Homo sapiens (clone S25) gene from CpG-enriched DNA, partial cds. [Fragment]	Q14075	44	9,39	2
Hook homolog 1	Q9UJC3	62	84,65	2
Hormone-sensitive lipase	Q05469	83	85,43	3
Hornerin	Q5U1F4	60	282,37	3
Host cell factor	P51610	75	208,73	3
Host cell factor C2 variant [Fragment]	Q53FE7	43	86,79	2
HPHase	Q9BY47	152	40,05	5
HPMSR6	Q13670	43	28,54	2
HSAL1 transcription factor [Fragment]	O43459	62	8,55	3
HSD21	Q6X960	47	45,57	2
Hsp70-binding protein 1	Q9NZL4	178	39,28	4
HSPC109	Q9P041	44	43,99	2
HSPC190	Q9P0T3	42	20,69	1
HSPC255 [Fragment]	Q9P0C6	61	31,80	1
Hu antigen C long	Q96J71	90	34,65	2
Human immunodeficiency virus type I enhancer-binding protein 3 [Fragment]	Q9HCL7	98	259,47	5
HUMEEP	Q7Z524	135	50,48	4
Hydroxyacyl-coenzyme A dehydrogenase [Precursor]	Q16836	71	42,10	5
HYOU1 protein	Q6IN67	93	75,30	2
Hypermethylated in cancer 1 protein	Q14526	52	76,42	3
Hyperthetical protein KIAA0521 [Fragment]	O60274	49	117,78	2
Hypothetical class II basic helix-loop-helix protein [Fragment]	Q7RTU4	76	42,42	3
Hypothetical gene supported by BC025338	A4D189	89	27,02	3
Hypothetical gene supported by BC031673	Q8N5S0	65	27,58	2
Hypothetical protein	Q8WZ03	47	11,02	2
Hypothetical protein	Q12984	82	41,02	5
Hypothetical protein	Q9HBN7	46	16,17	2
Hypothetical protein	Q6IPB4	109	22,43	2
Hypothetical protein	Q7Z4U9	61	33,04	2
Hypothetical protein	Q2YDA4	618	33,28	11
Hypothetical protein	Q3KQU0	439	37,00	9
Hypothetical protein	Q9HBQ9	78	37,24	3
Hypothetical protein	Q86Z24	52	44,17	2
Hypothetical protein	Q6IEE7	46	107,03	3
Hypothetical protein	O95428	70	133,39	3
Hypothetical protein FLJ39639 [Fragment]	Q2M3D8	77	30,67	3
Hypothetical protein [Fragment]	Q9BUV6	89	7,81	3
Hypothetical protein [Fragment]	Q8TCC4	79	21,66	3
Hypothetical protein [Fragment]	Q66K43	87	47,68	3
Hypothetical protein [Fragment]	O14738	54	9,98	2
Hypothetical protein [Fragment]	Q3B7W7	50	15,19	1
Hypothetical protein [Fragment]	Q8TAS0	121	32,23	4
Hypothetical protein [Fragment]	Q99785	40	32,35	2
Hypothetical protein [Fragment]	Q8TB56	84	34,23	3
Hypothetical protein ACTR1B	Q53SK5	40	42,27	1
Hypothetical protein ALS2CR19 [Fragment]	Q53T65	64	37,21	2
Hypothetical protein ARPC2	Q53R19	189	34,31	6
Hypothetical protein BC002926	Q66K64	64	66,46	3
Hypothetical protein CUL3 [Fragment]	Q53S54	42	86,41	1
Hypothetical protein DKFZp434C0631	Q8NDQ9	80	14,63	3
Hypothetical protein DKFZp434F1016 [Fragment]	Q9NTG2	63	157,89	3
Hypothetical protein DKFZp434I0113 [Fragment]	Q8NDA8	51	185,78	3
Hypothetical protein DKFZp434M102 [Fragment]	Q9NTB5	56	14,51	4
Hypothetical protein DKFZp434M131 [Fragment]	Q9Y4N5	61	34,67	2
Hypothetical protein DKFZp434N1235 (Sperm flagellar energy carrier protein) (ADP/ATP carrier isofor	Q9H0C2	189	35,00	3
Hypothetical protein DKFZp451B223 [Fragment]	Q86TB6	44	110,73	2
Hypothetical protein DKFZp451D042 [Fragment]	Q8TCG7	78	112,08	4
Hypothetical protein DKFZp564E242	Q659F9	267	31,40	4
Hypothetical protein DKFZp586B0320	Q8NDN8	67	49,43	3
Hypothetical protein DKFZp586H1322	Q9H065	97	138,69	3
Hypothetical protein DKFZp667G1915 [Fragment]	Q8TCK7	52	13,34	3
Hypothetical protein DKFZp686C1968	Q5H9U4	92	153,72	4
Hypothetical protein DKFZp686E1899	Q5HYL6	199	39,53	4
Hypothetical protein DKFZp686G12159 (Death-associated protein 3)	Q68CT7	112	45,54	3
Hypothetical protein DKFZp686H1668	Q68DG7	55	121,61	2
Hypothetical protein DKFZp686J072	Q5JPJ6	107	168,17	6
Hypothetical protein DKFZp686J1372	Q5HYB6	325	27,16	8

Table 1. continued

Protein Name and Species	Accession	Score	MW [kDa]	# Pept.
Hypothetical protein DKFZp686M0519	Q63HP1	102	22,76	3
Hypothetical protein DKFZp686M0619 [Fragment]	Q5HYD9	101	11,87	1
Hypothetical protein DKFZp686M0843	Q5H9T4	79	249,87	3
Hypothetical protein DKFZp686O1168 [Fragment]	Q6AW90	44	245,40	2
Hypothetical protein DKFZp686P03159	Q6N0B3	1632	40,33	23
Hypothetical protein DKFZp727C231 [Fragment]	Q8TCQ0	73	33,27	6
Hypothetical protein DKFZp762A083 [Fragment]	Q69YP8	85	196,39	3
Hypothetical protein DKFZp781A0295 [Fragment]	Q6AI58	54	120,24	2
Hypothetical protein DKFZp781F05101 [Fragment]	Q5H9R5	59	88,28	2
Hypothetical protein DKFZp781J2344 [Fragment]	Q68DE1	85	229,12	3
Hypothetical protein DKFZp781L0540 [Fragment]	Q7Z3K9	49	89,97	2
Hypothetical protein DKFZp781L0846	Q68CS5	61	60,93	2
Hypothetical protein EVI5L	Q96CN4	103	91,32	4
Hypothetical protein FLJ00006 [Fragment]	Q9NXX9	52	44,64	2
Hypothetical protein FLJ00011 [Fragment]	Q9H7Q6	40	41,92	1
Hypothetical protein FLJ00089 [Fragment]	Q9H7J1	45	37,64	2
Hypothetical protein FLJ00096 [Fragment]	Q9H7I8	54	22,28	2
Hypothetical protein FLJ00338 [Fragment]	Q8NF54	85	12,42	1
Hypothetical protein FLJ00369 [Fragment]	Q8NF33	68	76,10	2
Hypothetical protein FLJ00399 [Fragment]	Q8NF05	69	18,03	3
Hypothetical protein FLJ00407 [Fragment]	Q6ZMJ8	42	65,23	1
Hypothetical protein FLJ10404 [Fragment]	Q6IPW0	61	53,84	2
Hypothetical protein FLJ13841	Q96AX3	95	59,35	3
Hypothetical protein FLJ20465	Q9NX34	244	19,36	6
Hypothetical protein FLJ20534 (Hypothetical protein C4orf27) (Hypothetical protein DKFZp564H1372).-	Q9NWY4	180	39,38	4
Hypothetical protein FLJ21497	Q9H721	41	14,52	1
Hypothetical protein FLJ21610	Q9H706	67	97,04	3
Hypothetical protein FLJ21777	Q9H6X1	73	21,92	3
Hypothetical protein FLJ23617	Q8TED6	57	28,03	1
Hypothetical protein FLJ25678	Q8N7G1	157	32,53	5
Hypothetical protein FLJ25778	Q6ZU65	46	136,52	2
Hypothetical protein FLJ26554	Q6ZP37	218	42,93	6
Hypothetical protein FLJ26728	Q6ZP14	71	44,30	3
Hypothetical protein FLJ26816	Q6ZNZ8	57	54,46	3
Hypothetical protein FLJ30934	Q8IW53	80	46,45	2
Hypothetical protein FLJ35848	Q4G0Y1	42	70,80	2
Hypothetical protein FLJ36157	Q8N9V7	45	77,57	3
Hypothetical protein FLJ37310	Q8N1X5	52	16,49	2
Hypothetical protein FLJ42946	Q6ZV65	40	34,56	1
Hypothetical protein FLJ46347	Q6ZRH9	46	53,62	2
Hypothetical protein gs52	Q96S13	40	47,96	2
Hypothetical protein gs64	Q96S07	119	40,97	4
Hypothetical protein gs93	Q96RZ4	48	38,34	2
Hypothetical protein HISPPD1	Q8TB50	40	138,02	2
Hypothetical protein HNRPA3 (Heterogeneous nuclear ribonucleoprotein A3)	Q53RW7	1305	39,57	20
Hypothetical protein HNRPD	Q4W5A1	1121	38,41	15
Hypothetical protein HSU53209 (Putative MAPK activating protein)	Q549U1	211	32,67	5
Hypothetical protein JTV1	Q75MR1	176	35,33	2
Hypothetical protein KIAA0013 [Fragment]	Q9Y3S6	53	120,88	2
Hypothetical protein KIAA0309 [Fragment]	O15026	100	343,53	5
Hypothetical protein KIAA0324 [Fragment]	O60382	138	191,19	6
Hypothetical protein KIAA0415	A4D1Z4	57	164,57	3
Hypothetical protein KIAA0430 [Fragment]	Q9Y4F3	51	167,63	2
Hypothetical protein KIAA0491 [Fragment]	Q5H8U5	159	43,50	4
Hypothetical protein KIAA0586	Q6NYC6	42	160,14	2
Hypothetical protein KIAA0819 (MICAL3) [Fragment]	O94909	59	109,82	3
Hypothetical protein KIAA0921 splice variant 1 [Fragment]	Q5W9F7	42	155,33	2
Hypothetical protein KIAA1084 [Fragment]	Q9UPR8	45	86,36	1
Hypothetical protein KIAA1109 [Fragment]	Q9UPP3	64	555,30	3
Hypothetical protein KIAA1217 [Fragment]	Q9ULK3	53	146,09	2
Hypothetical protein KIAA1420 [Fragment]	Q9P2C7	62	147,29	3
Hypothetical protein KIAA1447 [Fragment]	Q9P281	66	182,43	2
Hypothetical protein KIAA1481 [Fragment]	Q9P247	44	149,66	2
Hypothetical protein KIAA1529 [Fragment]	Q86Y65	53	104,49	3
Hypothetical protein KIAA1539	Q5VYM4	72	45,58	3
Hypothetical protein KIAA1678 [Fragment]	Q9C0I5	63	186,46	3
Hypothetical protein KIAA1680 [Fragment]	Q9C0I3	52	99,76	2
Hypothetical protein KIAA1736 [Fragment]	Q9C0C7	49	142,51	2
Hypothetical protein LOC100049716 [Fragment]	Q8N503	47	30,63	2
Hypothetical protein LOC115098	Q96CT7	47	25,82	3
Hypothetical protein LOC130589	Q53RY1	89	37,74	3

Table 1. continued

Protein Name and Species	Accession	Score	MW [kDa]	# Pept.
Hypothetical protein LOC138046	Q8N1C2	87	32,31	2
Hypothetical protein LOC146909 [Fragment]	Q6NWY8	58	28,33	3
Hypothetical protein LOC400566 [Fragment]	Q6NSI2	49	44,26	2
Hypothetical protein LOC541467 [Fragment]	Q8N460	62	27,07	2
Hypothetical protein LOC649159	Q6PQ33	48	49,32	2
Hypothetical protein MARCO	Q4ZG40	51	52,63	2
Hypothetical protein MDH2 [Fragment]	Q75MT9	1582	33,21	22
Hypothetical protein MGC14289	Q96H79	89	32,92	1
Hypothetical protein MGC24975	Q8IZ63	59	43,77	2
Hypothetical protein MGC33584	Q8IY24	50	40,94	2
Hypothetical protein Nbla10058	Q3LIA5	461	48,59	11
Hypothetical protein NEDD5 [Fragment]	Q53QU3	54	36,60	1
Hypothetical protein NIF3L1	Q53TX4	129	41,94	5
Hypothetical protein NOP17	Q9BVL0	102	32,43	2
Hypothetical protein PER2	Q4ZG49	67	136,49	3
Hypothetical protein PTD004 [Fragment]	Q53SW9	58	19,95	2
Hypothetical protein RFC2 (Replication factor C (Activator 1) 2, 40kDa)	Q75MT5	146	35,22	4
Hypothetical protein RPRC1	Q3KQU3	45	92,76	2
Hypothetical protein TNS	Q4ZG71	96	185,59	4
Hypothetical protein TP53I13	Q7L5U3	54	39,68	4
Hypothetical protein UCHL1	Q4W5K6	445	24,81	8
Hypothetical protein WBSCR1 [Fragment]	Q75MT8	142	10,19	4
Hypothetical rhabdomyosarcoma antigen MU-RMS-40.5 [Fragment]	Q5GJ64	43	84,47	2
Hypothetikal protein FLJ00128 [Fragment]	Q8TER5	75	164,65	3
Hypothetikal protein FLJ00203 [Fragment]	Q8TEJ4	61	493,97	2
Hypothetikal protein FLJ00250 [Fragment]	Q8TEE7	50	36,45	2
Hypothetikal protein FLJ30092 [Fragment]	Q8WU73	63	83,39	3
Hypothetikal protein KIAA0515	Q9BU62	83	36,38	4
Hypothetikal protein KIAA1853 [Fragment]	Q96JH4	50	68,59	2
Hypothetikal protein KIAA1856 [Fragment]	Q96JH1	63	14,45	3
Hypothetikal protein KIAA1931 [Fragment]	Q96PV7	64	56,01	3
Hypothetikal protein KIAA1987 [Fragment]	Q8TF15	57	38,67	2
Hypothetikal protein LOC644538 [Fragment]	Q96HG1	49	14,45	2
Hypoxanthine-guanine phosphoribosyltransferase	P00492	47	24,43	2
Ibd1 protein [Fragment]	Q12915	84	22,08	3
ICAM2 protein	Q6FHE2	56	30,65	2
ICAM5 protein [Fragment]	Q8N6I2	48	84,56	2
Ig alpha-2 chain C region	P01877	42	36,51	1
Ig delta chain C region	P01880	45	42,13	2
Ig gamma-1 chain C region	P01857	47	36,11	2
Ig gamma-2 chain C region	P01859	68	35,89	3
Ig heavy chain V-I region EU	P01742	71	12,47	3
Ig heavy chain V-I region HG3 [Precursor]	P01743	124	17,24	6
Ig heavy chain V-I region ND [Precursor] [Fragments]	P01744	44	17,07	2
Ig heavy chain V-I region V35 [Precursor]	P23083	47	13,01	3
Ig heavy chain V-II region ARH-77 [Precursor]	P06331	57	13,33	2
Ig heavy chain V-II region SESS [Precursor]	P04438	43	15,47	2
Ig heavy chain V-III region CAM	P01768	73	13,74	2
Ig heavy chain V-III region GAL	P01781	57	12,73	2
Ig heavy chain V-III region HIL	P01771	41	13,43	1
Ig heavy chain V-III region VH26 [Precursor]	P01764	47	9,07	3
Ig kappa chain V-I region AU	P01594	82	13,92	3
Ig kappa chain V-I region EU	P01598	40	11,79	1
Ig kappa chain V-I region Gal	P01599	79	11,81	3
Ig kappa chain V-I region Hau	P01600	58	10,09	1
Ig kappa chain V-I region HK102 [Precursor] [Fragment]	P01602	40	12,05	1
Ig kappa chain V-I region Roy	P01608	40	12,07	1
Ig kappa chain V-I region Walker [Precursor]	P04431	60	14,07	2
Ig kappa chain V-III region HAH [Precursor]	P18135	40	9,58	2
Ig kappa chain V-III region SIE	P01620	41	11,78	1
Ig kappa chain V-III region VG [Precursor] [Fragment]	P04433	48	12,58	2
Ig kappa chain V-IV region B17 [Precursor]	P06314	63	14,97	2
Ig kappa chain V-IV region Len	P01625	41	12,64	3
Ig lambda chain C regions	P01842	49	28,85	1
Ig lambda chain V-I region BL2 [Precursor]	P06316	87	13,56	4
Ig lambda chain V-I region NIG-64	P01702	45	11,45	2
Ig lambda chain V-I region VOR	P01699	64	11,52	3
Ig lambda chain V-I region WAH	P04208	46	11,73	2
Ig lambda chain V-II region BOH	P01706	40	10,48	1
Ig lambda chain V-II region MGC	P01709	48	8,19	2
Ig lambda chain V-V region DEL	P01719	53	11,00	2
Ig lambda chain V-VI region SUT	P06317	66	13,61	2

Table 1. continued

Protein Name and Species	Accession	Score	MW [kDa]	# Pept.
Ig mu chain C region	P01871	52	49,56	2
IgGFc-binding protein [Precursor]	Q9Y6R7	63	571,72	4
IGHG4 protein	Q8TC63	51	51,99	2
Imidazoline receptor antisera-selected protein [Fragment]	Q9UEU4	47	65,31	1
Immediate early response gene 5 protein	Q5VY09	58	33,70	2
Immunodeficiency virus type I enhancer binding protein 3	Q5T1R5	70	259,47	4
Immunoglobulin iota chain [Precursor]	P12018	91	16,61	4
Immunoglobulin lambda-like polypeptide 1 [Precursor]	P15814	40	28,82	3
Immunoglobulin superfamily member 1 [Fragment]	O15070	45	147,81	2
Immunoglobulin superfamily member 10 [Precursor]	Q6WRI0	75	290,84	3
Immunoglobulin superfamily member 22	Q8N9C0	52	100,26	2
Import inner membrane translocase subunit TIM50 [Precursor]	Q3ZCQ8	208	39,62	6
Importin subunit beta-3	O00410	170	123,42	5
Importin-7	O95373	157	116,30	4
Importin-9	Q96P70	112	115,89	3
InaD-like protein	Q8NI35	52	196,37	3
Inhibin beta C chain [Precursor]	P55103	54	38,24	3
Inhibitor of Bruton tyrosine kinase	Q9P2D0	81	150,53	3
Inner centromere protein	Q9NQS7	45	106,11	2
Inorganic pyrophosphatase	Q8IYX2	58	35,45	2
Inorganic pyrophosphatase 2 [Precursor]	Q9H2U2	103	36,52	4
Inositol 1,4,5-trisphosphate receptor type 1	Q14643	66	313,95	4
Inositol 1,4,5-trisphosphate receptor type 2	Q14571	58	308,08	2
Inositol 1,4,5-trisphosphate receptor type 3 variant [Fragment]	Q59ES2	46	267,02	2
Inositol monophosphatase	P29218	87	29,64	3
Inositol-3-phosphate synthase	Q9NPH2	58	57,74	1
Insulin receptor [Fragment]	Q4JME2	48	5,56	2
Insulin receptor substrate 2	Q9Y4H2	54	136,40	3
Insulin receptor substrate 2 insertion mutant [Fragment]	Q96RG4	72	137,32	2
Insulin-like growth factor 1 receptor [Precursor]	P08069	42	154,69	2
Insulin-like growth factor 2 mRNA-binding protein 1	Q9NZI8	67	63,44	2
Insulin-like growth factor 2 mRNA-binding protein 3	O00425	136	63,68	5
INT1 protein [Fragment]	Q9BT91	57	75,06	3
Integrase catalytic domain-containing protein KIAA1305	Q9P2P1	88	208,37	4
Integrator complex subunit 1	Q8N201	71	244,30	3
Integrator complex subunit 11	Q5TA45	47	67,66	2
Integrator complex subunit 6	Q9UL03	46	100,39	2
Integrin alpha-9 [Precursor]	Q13797	74	114,56	4
Integrin alpha-D [Precursor]	Q13349	50	126,89	2
Integrin alpha-M [Precursor]	P11215	45	127,23	2
Integrin beta-3 [Precursor]	P05106	1154	37,47	15
Interferon alpha-4 [Precursor]	P05014	46	21,76	2
Interferon-stimulated gene factor 3 alpha 91/84 kDa protein [Fragments]	Q9UDL5	45	17,99	1
Interleukin enhancer binding factor 2 variant [Fragment]	Q53FG3	226	43,02	6
Interleukin enhancer-binding factor 2	Q12905	280	44,67	6
Interleukin enhancer-binding factor 3	Q12906	507	75,98	13
Interleukin-1 receptor-like 1 [Precursor]	Q01638	45	63,36	2
Interleukin-16 [Precursor]	Q14005	68	66,65	2
Interleukin-2 [Precursor]	P60568	46	17,63	2
Iporin	Q8N2Y8	60	161,20	3
IQ motif and Sec7 domain-containing protein 1	Q6DN90	72	8,22	7
Iron-sulfur cluster assembly 1 homolog [Precursor]	Q9BUE6	52	16,42	2
Islet cell autoantigen ICAp69	Q6LCR0	50	30,17	2
Isocitrate dehydrogenase [NAD] subunit beta [Precursor]	O43837	102	41,86	2
Isocitrate dehydrogenase 2 (NADP+) variant [Fragment]	Q53GL5	264	50,88	6
Isocitrate dehydrogenase 3 (NAD+) alpha variant [Fragment]	Q53GF8	163	39,59	5
Isoleucyl-tRNA synthetase, cytoplasmic	P41252	138	144,38	6
ITGB4 protein [Fragment]	Q2VP98	49	72,00	2
ITGB4BP protein	Q6IBN8	132	26,58	3
JARID2 protein [Fragment]	Q86X63	41	41,21	1
Jerky protein homolog-like	Q9Y4A0	73	8,41	2
JmjC domain-containing histone demethylation protein 1B	Q8NHM5	56	152,52	4
JmjC domain-containing histone demethylation protein 2A	Q9Y4C1	57	147,33	3
JmjC domain-containing histone demethylation protein 2B	Q7LBC6	51	191,61	3
Junctophilin-4	Q96JJ6	53	65,86	2
Kappa B and V(D)J recombination signal sequences binding protein	Q9BZS0	46	259,47	2
Kappa-actin	Q9BYX7	149	41,99	3
Katanin p60 subunit A-like protein 2	Q8IYT4	68	52,81	3
Kazrin	Q674X7	49	86,35	2
Kelch domain-containing protein 7B	Q96G42	53	128,92	3
Kelch repeat and BTB domain-containing protein 2	Q8IY47	48	71,28	3
Kelch repeat and BTB domain-containing protein 3	Q8NAB2	41	69,35	2

Table 1. continued

Protein Name and Species	Accession	Score	MW [kDa]	# Pept.
Kelch-like protein 28	Q9NXS3	74	128,92	3
Keratin 2A (Epidermal ichthyosis bullosa of Siemens)	Q4VAQ2	169	65,39	3
Keratin, type I cuticular Ha5	Q92764	91	47,56	2
Keratin, type I cytoskeletal 10	P13645	242	57,21	7
Keratin, type I cytoskeletal 13	P13646	88	49,59	4
Keratin, type I cytoskeletal 17	Q04695	100	48,11	4
Keratin, type I cytoskeletal 40	Q6A162	40	24,30	2
Keratin, type I cytoskeletal 9	P35527	105	61,95	1
Keratin, type II cytoskeletal 1	P04264	266	65,85	1
Keratin, type II cytoskeletal 2 epidermal	P35908	89	65,39	3
Keratin, type II cytoskeletal 6A	P02538	47	60,05	2
Keratin, type II cytoskeletal 6B	P04259	93	60,03	3
Keratin, type II cytoskeletal 79	Q5XKE5	98	57,81	3
Keratin, type II cytoskeletal 8	P05787	96	53,54	3
KH domain-containing, RNA-binding, signal transduction-associated protein 2	Q5VWX1	61	38,93	3
KHK protein	Q6IBK2	56	32,73	2
KIF27C	Q86VH0	86	148,89	3
KIF6 protein	Q4KMP8	47	33,11	1
Killer cell lectin-like receptor subfamily G member 2	A4D1S0	54	42,82	2
Kinase insert domain receptor (A type III receptor tyrosine kinase) variant [Fragment].- Homo sapie	Q59EB0	71	161,50	3
Kinesin family member 26B	Q2KJY2	76	223,74	3
Kinesin light chain 2	Q9H0B6	66	68,94	3
Kinesin light chain 4	Q9NSK0	74	61,53	3
Kinesin-like protein KIF13A	Q9H1H9	51	202,31	2
Kinesin-like protein KIF13B	Q9NQT8	77	202,67	4
Kinesin-like protein KIF21A variant	Q2UVF1	63	180,48	3
Kinesin-like protein KIF26A	Q9ULI4	154	190,20	4
Kinesin-like protein KIF26B	Q2KJY2	104	223,88	5
Kinesin-like protein KIF27	Q86VH2	59	160,28	2
Kinesin-like protein KIFC1	Q9BW19	74	78,67	3
Kinesin-like protein KIFC3	Q9BVG8	51	77,82	2
Krueppel-like factor 4	O43474	45	50,08	2
Krueppel-related zinc finger protein SBZF5	Q9HD72	48	45,26	2
L1 protein	Q9Y4Y5	49	60,04	2
La 4.1 protein [Fragment]	Q14730	283	33,74	4
Lactacte dehydrogenase (EC 1.1.1.27)	Q6DUY4	74	41,92	1
Lactate dehydrogenase C	Q7Z7J4	66	36,23	2
Lactotransferrin [Precursor]	P02788	85	78,29	3
Lactoylglutathione lyase	Q04760	68	20,58	3
Ladybird homeobox corepressor 1	P84550	48	99,83	3
LAG3 protein	Q7Z643	51	39,10	2
Lambda-crystallin homolog	Q9Y2S2	51	35,42	2
Lamin-A/C	P02545	529	65,10	16
Lamina-associated polypeptide 2 isoform alpha	P42166	169	75,31	4
Lamina-associated polypeptide 2, isoforms beta/gamma	P42167	181	50,51	4
Lamin-B receptor	Q14739	102	10,00	6
Lamin-B1	P20700	157	66,37	6
Lamin-B2	Q03252	338	67,65	14
Laminin alpha 3 splice variant b2	Q6VU67	73	360,21	4
Laminin subunit alpha-5 [Precursor]	O15230	70	399,76	4
Laminin subunit beta-2 [Precursor]	P55268	106	195,98	5
Laminin subunit beta-4 [Precursor]	A4D0S4	68	193,32	2
LANCL1 protein [Fragment]	Q6FHH6	472	45,24	10
La-related protein 1	Q6PKG0	108	123,43	4
Large proline-rich protein BAT2	P48634	247	228,69	14
Large proline-rich protein BAT3	P46379	96	118,65	5
Lariat debranching enzyme	Q9UK59	84	61,64	3
Late cornified envelope protein 1A	Q5T7P2	64	10,98	3
Latent TGF-beta binding protein-4	O00508	67	173,44	3
Latent transforming growth factor-beta binding protein 4 [Fragment]	O75441	61	71,70	3
Latent transforming growth factor-beta binding protein 4S	O75412	65	173,44	3
Latent-transforming growth factor beta-binding protein 2 [Precursor]	Q14767	74	195,07	3
Latent-transforming growth factor beta-binding protein 4 [Precursor]	Q8N2S1	117	173,44	8
Latent-transforming growth factor beta-binding protein, isoform 1L [Precursor]	Q14766	47	173,23	1
Lebercilin	Q86VQ0	44	80,55	1
Leiomodin-2	Q6P5Q4	66	61,68	1
Leucine carboxyl methyltransferase 2	O60294	76	75,60	2
Leucine rich repeat neuronal 3	A4D0T1	42	79,37	2
Leucine zipper protein 1	Q86V48	44	120,28	2
Leucine zipper protein 2 [Precursor]	Q86TE4	41	45,75	2
Leucine-rich alpha-2-glycoprotein [Precursor]	P02750	41	34,33	2

Table 1. continued

Protein Name and Species	Accession	Score	MW [kDa]	# Pept.
Leucine-rich PPR motif-containing protein [Precursor]	P42704	245	157,86	7
Leucine-rich repeat and fibronectin type-III domain-containing protein 2 [Precursor]	Q9ULH4	49	84,68	2
Leucine-rich repeat and fibronectin type-III domain-containing protein 6 [Precursor]	Q5R3F8	57	89,69	3
Leucine-rich repeat flightless-interacting protein 1	Q32MZ4	81	89,25	3
Leucine-rich repeat protein LRIG1	Q5XWD3	51	119,14	2
Leucine-rich repeat serine/threonine-protein kinase 1	Q38SD2	46	227,84	2
Leucine-rich repeat-containing protein 27	Q9C0I9	44	60,09	2
Leucine-rich repeat-containing protein 33 [Precursor]	Q86YC3	67	76,32	2
Leucine-rich repeat-containing protein 47	Q8N1G4	161	63,43	7
Leucine-rich repeat-containing protein 56	Q8IYG6	48	58,73	1
Leucine-rich repeat-containing protein 59	Q96AG4	90	34,91	2
Leucine-rich repeat-containing protein 7	Q96NW7	41	171,60	2
Leucine-zipper-like transcriptional regulator 1	Q8N653	44	94,72	2
Leucocyte antigen B	Q9UIM5	40	6,90	1
Leucocyte antigen Cw [Fragment]	Q9GJF2	41	41,19	1
Leucyl-tRNA synthetase, cytoplasmic	Q9P2J5	198	27,53	3
Leukocyte immunoglobulin-like receptor subfamily A member 2 [Precursor]	Q8N149	63	52,99	3
Leukocyte receptor cluster member 1	Q96BZ8	48	64,62	2
LGMN protein	Q6I9U9	157	49,32	2
Likely orthologue of Mus musculus enhancer trap locus 4	Q5T5P3	57	214,12	3
LIM and SH3 domain protein 1	Q14847	75	35,99	2
LIM domain protein	Q53Y39	47	25,85	1
Lin-28 homolog B	Q6ZN17	59	27,05	2
Lin-9 homolog	Q5TKA1	58	76,80	3
Lipid phosphate phosphatase-related protein type 3	Q6T4P5	66	76,04	3
Lipolysis-stimulated lipoprotein receptor	Q86X29	47	71,44	3
Liprin-alpha-1	Q13136	54	135,78	3
Liprin-alpha-3	O75145	42	133,50	3
Liprin-beta-1	Q86W92	52	114,02	2
L-lactate dehydrogenase A chain	P00338	800	36,67	13
L-lactate dehydrogenase B chain	P07195	921	36,62	15
LMO6 protein	Q6IAE4	48	68,64	2
Lon protease homolog	Q8N8K8	276	100,33	8
Lon protease homolog [Precursor]	P36776	281	95,13	8
Long palate, lung and nasal epithelium carcinoma-associated protein 4	P59827	42	60,95	2
Long-chain fatty acid transport protein 3	Q5K4L6	47	68,23	3
Low density lipoprotein receptor-related protein associated protein 1 variant [Fragment].- Homo sap	Q53HQ3	240	41,50	4
Low molecular weight phosphotyrosine protein phosphatase	P24666	121	17,90	2
Low-density lipoprotein receptor-related protein 1B [Precursor]	Q9NZR2	60	515,50	2
Low-density lipoprotein receptor-related protein 4 [Precursor]	O75096	41	215,97	2
Low-density lipoprotein receptor-related protein 5 [Precursor]	O75197	42	179,15	2
Low-density lipoprotein receptor-related protein 8 [Precursor]	Q14114	49	99,03	2
LSM14 protein homolog A	Q8ND56	40	50,53	2
LSM2 protein	Q6FGG1	138	10,83	2
LTK protein	Q4G0N3	59	48,19	2
Lupus La protein	P05455	464	46,81	6
Lutropin-choriogonadotropic hormone receptor [Precursor]	P22888	50	78,62	2
Lymphokine-activated killer T-cell-originated protein kinase	Q96KB5	66	9,63	2
Lymphotoxin-beta	Q06643	59	7,78	2
LYN protein [Fragment]	Q6NUK7	84	65,81	3
Lysophospholipase II [Fragment]	Q5QPN5	40	9,73	1
Lysosomal alpha-glucosidase [Precursor]	P10253	113	97,96	5
Lysosomal-trafficking regulator	Q99698	40	429,14	2
Lysosome membrane protein 2	Q14108	84	54,12	2
MAB21L1 protein	Q6I9T5	124	40,90	4
Macrophage metalloelastase [Precursor]	P39900	48	54,00	2
Macrophage migration inhibitory factor	P14174	113	12,34	5
MAD1 mitotic arrest deficient-like 1	A4D218	91	91,66	5
MAGUK p55 subfamily member 2	Q14168	43	64,59	1
MAK16-like protein RBM13	Q9BXY0	117	35,35	3
Makorin-3	Q13064	46	55,65	2
Makorin-4	Q13434	42	52,88	2
Malate dehydrogenase, cytoplasmic	P40925	305	36,27	4
Malignant T cell amplified sequence 1	Q9ULC4	98	20,54	2
Mannose-6-phosphate receptor-binding protein 1	O60664	156	47,02	3
Mannosyl-oligosaccharide glucosidase	Q13724	185	91,85	7
MAP kinase interacting kinase [Fragment]	A4CYL7	41	52,53	1
MAP kinase interacting serine/threonine kinase 1	Q5TC08	49	29,82	1
MAP kinase-activating death domain protein	Q8WXG6	49	183,30	2

Table 1. continued

Protein Name and Species	Accession	Score	MW [kDa]	# Pept.
MAP/microtubule affinity-regulating kinase 3	P27448	40	9,26	2
MAP/microtubule affinity-regulating kinase 4	Q3LID9	69	40,71	4
MAP/microtubule affinity-regulating kinase 4	Q96L34	42	40,68	3
MAP6 protein [Fragment]	Q6P3T0	84	77,02	4
MAP7 domain-containing protein 2	Q96T17	66	81,96	3
MAP7 protein	Q8TAU5	93	84,03	4
MAPKBP1 protein	Q49AJ8	61	109,02	4
Matrilin 3	Q15232	40	52,82	1
Matrin-3	P43243	807	94,56	18
Matrix metalloproteinase-23 [Precursor]	O75900	57	43,94	3
Matrix-remodeling-associated protein 5 [Precursor]	Q9NR99	50	312,28	2
May bind to RNA via its Arg/Ser-rich domain.	Q9Y383	90	47,59	2
MBT domain-containing protein 1	Q05BQ5	42	70,55	2
MCF2L2 protein	Q6P2B8	45	81,75	2
MCM7 minichromosome maintenance deficient 7	A4D2A1	398	81,26	12
Mediator of DNA damage checkpoint protein 1	Q14676	66	226,67	2
Mediator of RNA polymerase II transcription subunit 12-like protein	Q86YW9	75	240,12	3
Mediator of RNA polymerase II transcription subunit 15	Q96RN5	40	86,75	2
Mediterranean fever	Q3MJ84	42	86,42	2
Medium-chain specific acyl-CoA dehydrogenase [Precursor]	P11310	203	46,56	6
Melanoma antigen family D, 2	Q5H907	112	55,76	5
Melanoma-associated antigen B3	O15480	40	39,18	3
Membrane progestin receptor alpha	Q86WK9	65	56,57	3
Membrane-associated DHHC8 zinc finger protein	Q2TGE9	58	81,44	2
Membrane-associated guanylate kinase, WW and PDZ domain-containing protein 1	Q96QZ7	51	164,64	2
Membrane-associated guanylate kinase, WW and PDZ domain-containing protein 2	Q86UL8	73	158,75	4
Membrane-associated phosphatidylinositol transfer protein 1	O00562	51	134,85	2
Membrane-associated phosphatidylinositol transfer protein 2	Q9BZ72	48	148,93	2
Membrane-associated progesterone receptor component 1	O00264	161	21,53	3
Membrane-associated progesterone receptor component 2	O15173	102	23,80	3
Membrane-bound O-acyltransferase domain-containing protein 5	Q6P1A2	46	56,04	2
MEN1 protein [Fragment]	Q9BUF0	42	31,06	2
Meningioma (Disrupted in balanced translocation) 1	Q5T313	42	136,00	2
Metabotropic glutamate receptor 1 [Precursor]	Q13255	50	132,37	2
Metabotropic glutamate receptor 4 [Precursor]	Q14833	52	101,87	2
Metabotropic glutamate receptor 5 [Precursor]	P41594	65	132,47	3
Metal transporter CNNM1	Q9NRU3	85	97,37	3
Metastasis associated protein variant [Fragment]	Q59FW1	71	57,26	3
Metastasis suppressor protein 1	O43312	44	82,20	2
Metastasis-associated protein MTA2	O94776	40	75,02	2
Metaxin-1	Q13505	55	47,98	3
Methenyltetrahydrofolate synthetase domain-containing protein	Q2M296	48	42,25	2
Methionine adenosyltransferase II beta variant 2	Q1WAI7	88	34,56	2
Methionine adenosyltransferase regulatory beta subunit	Q9NZL9	249	37,53	5
Methionyl-tRNA synthetase, cytoplasmic	P56192	133	101,04	4
Methyl-CpG-binding domain protein 2	Q9UBB5	53	43,26	3
Methyl-CpG-binding protein 2	P51608	72	23,30	3
Methylosome subunit pICln	P54105	176	26,20	5
MGC21881 protein	Q96BV1	84	10,63	4
MICAL-like protein 1	Q8N3F8	101	93,44	4
MICAL-like protein 2	Q8IY33	81	97,44	4
Microtubule-actin cross-linking factor 1, isoform 4	Q96PK2	77	599,49	5
Microtubule-actin cross-linking factor 1, isoforms 1/2/3/5	Q9UPN3	80	613,65	4
Microtubule-associated protein [Fragment]	Q68D74	123	50,82	6
Microtubule-associated protein 1A	P78559	185	306,29	10
Microtubule-associated protein 1B	P46821	59	270,45	3
Microtubule-associated protein 1S	Q66K74	42	112,21	2
Microtubule-associated protein 2	P11137	76	199,54	3
Microtubule-associated protein 4	P27816	52	121,02	3
Microtubule-associated protein 9	Q49MG5	65	74,19	3
Microtubule-associated protein RP/EB family member 1	Q15691	104	29,85	2
Microtubule-associated protein tau	P10636	93	80,84	4
Microtubule-associated serine/threonine-protein kinase 1	Q9Y2H9	61	170,68	3
Microtubule-associated serine/threonine-protein kinase 3	O60307	61	143,05	3
Microtubule-associated serine/threonine-protein kinase 4	O15021	80	266,11	4
Migration-inducing gene 13	Q5J8M5	139	30,98	2
Minichromosome maintenance deficient protein 5 variant [Fragment]	Q53FG5	102	82,18	3
Minichromosome maintenance protein 3 variant [Fragment]	Q53HJ4	261	90,92	8
Misshapen/NIK-related kinase isoform 2 variant [Fragment]	Q59FL0	47	93,22	2
Mitochondrial 28S ribosomal protein S22	P82650	98	41,25	3

Table 1. continued

Protein Name and Species	Accession	Score	MW [kDa]	# Pept.
Mitochondrial 2-oxoglutarate/malate carrier protein	Q02978	128	33,91	5
Mitochondrial 39S ribosomal protein L4	Q9BYD3	150	29,48	2
Mitochondrial ATP synthase, O subunit variant [Fragment]	Q53HH2	237	23,25	4
Mitochondrial carrier family protein (Hypothetical protein MCFP)	Q8TBP6	88	38,10	1
Mitochondrial carrier homolog 2 variant [Fragment]	Q53G34	65	33,29	2
Mitochondrial citrate transport protein [Fragment]	Q6LAP8	41	34,77	1
Mitochondrial fission 1 protein	Q9Y3D6	73	16,93	2
Mitochondrial import inner membrane translocase subunit Tim13	Q9Y5L4	82	10,49	1
Mitochondrial import inner membrane translocase subunit Tim8 A	O60220	58	10,99	1
Mitochondrial import receptor subunit TOM22 homolog	Q9NS69	52	15,51	1
Mitochondrial inner membrane protein	Q16891	366	68,15	8
Mitochondrial Rho GTPase 1	Q8IXI2	68	21,21	3
Mitochondrial ribosomal protein 63	Q9BQC6	48	12,27	2
Mitochondrial ribosomal protein L38	Q96DV4	117	40,73	3
Mitochondrial ribosomal protein S18A [Fragment]	Q5QPA5	49	29,70	2
Mitochondrial ribosomal protein S23	Q9Y3D9	68	21,77	2
Mitochondrial tumor suppressor 1	Q9ULD2	82	141,40	5
Mitoferrin-2	Q96A46	59	39,27	2
Mitogen activated protein kinase-binding protein 1 [Fragment]	O60336	75	131,02	3
Mitogen-activated protein kinase 1	P28482	295	38,66	7
Mitogen-activated protein kinase 15	Q8TD08	77	59,81	2
Mitogen-activated protein kinase kinase 1 interacting protein 1 variant [Fragment]	Q53FH6	45	13,55	1
Mitogen-activated protein kinase kinase kinase	Q5TCX8	58	113,96	2
Mitogen-activated protein kinase kinase kinase 10	Q02779	65	103,69	3
Mitogen-activated protein kinase kinase kinase 12	Q12852	66	93,22	3
Mitogen-activated protein kinase kinase kinase 12 variant [Fragment]	Q59FK7	62	27,01	4
Mitotic checkpoint protein BUB3	O43684	414	36,93	8
Mitotic spindle assembly checkpoint protein MAD2A	Q13257	43	21,40	1
MKI67 FHA domain-interacting nucleolar phosphoprotein	Q9BYG3	144	34,23	3
MKL/myocardin-like protein 1	Q969V6	46	77,38	2
MLLT6 protein	Q6P2C6	62	35,10	2
Monocarboxylate transporter 8	P36021	76	64,75	3
MORC family CW-type zinc finger protein 3	Q14149	44	107,11	2
MORN repeat-containing protein 1	Q5T089	55	53,82	3
Motor neuron and pancreas homeobox protein 1	P50219	43	40,91	2
MRPS9 protein [Fragment]	Q86WV4	140	35,13	4
MST148 protein	Q7Z2R3	58	16,04	2
MSTP024 (C12orf10 protein)	Q8WYI2	324	24,98	7
Msx2-interacting protein	Q96T58	132	75,02	6
MTAP protein	Q8WV80	63	16,96	2
Mucin	Q5BLQ2	75	289,66	5
Mucin [Precursor] [Fragment]	O76037	60	106,74	2
Mucin-16	Q8WXI7	179	2351,81	14
Mucin-20 [Precursor]	Q8N307	47	71,99	2
Mucin-4 [Precursor]	Q99102	70	231,58	4
Mucin-5AC [Precursor] [Fragments]	P98088	41	112,97	2
Mucin-5B [Precursor]	Q9HC84	119	590,12	5
Mucosal vascular addressin cell adhesion molecule 1 transcript variant 1	Q4PKD0	43	238,70	2
Muellerian-inhibiting factor [Precursor]	P03971	71	59,22	3
Multifunctional protein ADE2	P22234	312	46,92	5
Multiple ankyrin repeats single KH domain protein isoform 2	Q8IWZ2	76	277,18	3
Multiple C2 and transmembrane domain-containing protein 1	Q6DN14	41	111,62	2
Multiple epidermal growth factor-like domains 10 [Precursor]	Q96KG7	44	122,21	2
Multiple epidermal growth factor-like domains 8	Q7Z7M0	68	254,57	3
Multiple epidermal growth factor-like domains 9 [Precursor]	Q9H1U4	59	62,98	3
Multiple inositol polyphosphate phosphatase 1 [Precursor]	Q9UNW1	69	55,12	2
Multiple myeloma tumor-associated protein 2	Q9BU76	48	29,41	2
Multisynthetase complex auxiliary component p43	Q12904	224	34,33	3
Muscle alpha-kinase	Q96L96	82	201,18	4
MutS homolog 2 variant [Fragment]	Q53FK0	86	98,16	4
MutS protein homolog 4	O15457	50	104,76	2
My027 protein (Chromosome 17 open reading frame 25)	Q9H3J8	59	33,21	2
Myeloid/lymphoid or mixed-lineage leukemia (Trithorax homolog, Drosophila); translocated to, 4	Q5TIG5	53	189,15	2
Myeloid/lymphoid or mixed-lineage leukemia protein 2	O14686	64	564,19	3
Myeloid/lymphoid or mixed-lineage leukemia protein 3 homolog	Q8NEZ4	67	541,31	3
Myeloid/lymphoid or mixed-lineage leukemia/clathrin assembly protein fusion protein [Fragment]	Q8N6B4	51	63,35	3
MYH10 variant protein [Fragment]	Q4LE45	226	233,71	6
MYO9B variant protein [Fragment]	Q4LE74	51	229,57	2
Myocyte enhancer factor 2D/deleted in azoospermia associated protein 1 fusion protein	Q5IRN4	41	50,41	2

Table 1. continued

Protein Name and Species	Accession	Score	MW [kDa]	# Pept.
Myocyte-specific enhancer factor 2B	Q02080	66	38,64	4
Myoferlin	Q9NZM1	60	234,71	4
Myomesin 1	Q6H969	77	187,51	2
Myomesin-3	Q5VTT5	48	162,09	2
Myopalladin	Q86TC9	46	153,00	2
Myosin [Fragment]	Q14788	44	228,48	2
Myosin light chain kinase, smooth muscle	Q15746	49	210,77	2
Myosin light polypeptide 6	P60660	242	16,92	8
Myosin regulatory light chain 2, nonsarcomeric	P19105	242	19,65	5
Myosin VIIA variant [Fragment]	Q59F32	48	96,13	1
Myosin XV variant [Fragment]	Q59FN7	51	121,93	2
Myosin-11	P35749	120	214,22	3
Myosin-15	Q9Y2K3	68	224,61	2
Myosin-4	Q9Y623	40	223,01	2
Myosin-9	P35579	189	226,60	5
Myosin-binding protein C, cardiac-type	Q14896	69	140,52	3
Myosin-binding protein C, fast-type	Q14324	68	128,14	2
Myosin-Ib	O43795	55	131,90	2
Myosin-IXb	Q13459	75	243,56	4
Myosin-Vc	Q9NQX4	42	202,79	2
Myosin-XV	Q9UKN7	94	395,17	4
Myosin-XVIIIa	Q92614	62	231,06	2
Myosin-XVIIIb	Q8IUG5	55	73,77	2
Myotrophin	P58546	85	12,76	1
Myotubularin-related protein 12	Q9C0I1	40	86,15	1
Myotubularin-related protein 5	O95248	62	208,32	3
Myristoylated alanine-rich C-kinase substrate	P29966	109	31,40	2
N(6)-adenine-specific DNA methyltransferase 1	Q9Y5N5	41	38,64	2
N(G),N(G)-dimethylarginine dimethylaminohydrolase 1	O94760	254	30,97	4
NAB2 protein	Q96I83	53	25,93	2
NACA2 [Fragment]	Q2VIR9	64	22,64	1
N-acetylglucosamine kinase	Q9UJ70	46	37,35	3
N-acetylglucosamine-6-sulfatase [Precursor]	P15586	64	62,04	3
N-acetylneuraminic acid synthase (Sialic acid synthase) [Fragment]	Q5TBR1	65	15,41	1
N-acetylserotonin O-methyltransferase-like protein	O95671	56	67,15	2
N-acetyltransferase 6	Q93015	63	31,45	2
NACHT, LRR and PYD domains-containing protein 6	P59044	72	98,73	3
NAD kinase	Q5QPS4	94	63,46	4
NAD(P) transhydrogenase [Precursor]	Q13423	44	113,90	2
NAD-dependent deacetylase sirtuin-1	Q96EB6	62	81,63	2
NAD-dependent deacetylase sirtuin-2	Q8IXJ6	73	43,18	3
NAD-dependent deacetylase sirtuin-7	Q9NRC8	52	44,90	2
NAD-dependent malic enzyme [Precursor]	P23368	53	62,03	2
NADH dehydrogenase	Q549M5	48	14,19	2
NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 9	Q9Y6M9	59	21,69	1
NADH-cytochrome b5 reductase 3	P00387	44	26,46	1
NADH-ubiquinone oxidoreductase 75 kDa subunit [Precursor]	P28331	49	79,47	2
Nanos homolog 3	P60323	41	18,84	1
NARG1 protein [Fragment]	Q58F05	62	72,34	3
Nasal embryonic luteinizing hormone-releasing hormone factor	Q6X4W1	84	24,66	5
Nascent polypeptide-associated complex subunit alpha	Q13765	269	23,37	4
NAV3 protein [Fragment]	Q6PJB7	45	72,47	2
NDST2 protein [Fragment]	Q8WV68	61	11,02	2
NDUFA10 protein	Q8N1B9	83	22,36	1
Nebulin	P20929	52	773,21	4
Nebulin-related anchoring protein	Q5VWI3	65	193,78	3
Necdin	Q99608	40	36,09	1
NEDD8 [Precursor]	Q15843	178	8,56	3
NEDD8-conjugating enzyme Ubc12	P61081	238	20,89	6
NEDD9-interacting protein with calponin homology and LIM domains	Q8TDZ2	74	117,88	3
Negative elongation factor E	P18615	49	36,96	2
Nephrin [Precursor]	O60500	41	134,66	2
Nephrocystin-3	Q7Z494	40	150,86	2
Nephrocystin-4	O75161	82	157,60	5
Nestin	P48681	154	177,33	4
Netrin-2-like protein [Precursor]	O00634	41	61,43	2
Neural interleukin 16 protein	Q6VVE6	41	141,68	2
Neurexin-1-alpha [Precursor]	Q9ULB1	61	161,88	3
Neurexin-2-alpha [Precursor]	Q9P2S2	43	155,33	2
Neurobeachin	Q5W0E7	72	327,55	4
Neuroendocrine secretory protein 55	O95467	55	28,03	2
Neurofibromin	P21359	50	319,37	3

Table 1. continued

Protein Name and Species	Accession	Score	MW [kDa]	# Pept.
Neurofilament heavy polypeptide	P12036	55	111,71	2
Neurogenic locus notch homolog protein 3 [Precursor]	Q9UM47	56	243,66	3
Neurogenic locus notch homolog protein 4 [Precursor]	Q99466	52	114,73	3
Neurogranin	Q92686	100	7,62	3
Neuroligin-1 [Precursor]	Q8N2Q7	50	93,84	3
Neuroligin-2 [Precursor]	Q8NFZ4	95	90,76	2
Neuron navigator 1	Q8NEY1	57	202,47	2
Neuron navigator 2	Q8IVL1	92	268,13	4
Neuron navigator 3	Q8IVL0	89	244,26	3
Neuronal calcium sensor 1	P62166	51	21,73	2
Neuronal pentraxin-1 [Precursor]	Q15818	44	47,12	2
Neuronal thread protein AD7c-NTP	O60448	50	41,72	2
Neuropilin-2a(17) (Neuropilin 2)	Q7LBX6	62	104,19	3
Neutral alpha-glucosidase AB [Precursor]	Q14697	813	106,70	24
Neutrophil defensin 3 [Precursor]	P59666	65	12,08	2
NF-kappa-B inhibitor epsilon	O00221	46	38,45	2
NFX1-type zinc finger-containing protein 1	Q9P2E3	88	220,23	5
N-glycosylase/DNA lyase	O15527	54	38,78	2
NHP2-like protein 1	P55769	124	14,03	3
NHR domain-containing protein KIAA1787	Q96JN8	50	166,91	2
Nicotinate-nucleotide pyrophosphorylase [carboxylating]	Q15274	205	30,81	4
Nipped-B-like protein	Q6KC79	65	257,09	4
Nipsnap homolog 3A (C. elegans)	Q5VX32	73	28,45	2
Nitric oxide synthase, brain	P29475	47	160,97	3
Nitric oxide synthase, inducible	P35228	47	131,12	2
Nitric oxide synthase-interacting protein	Q9Y314	53	33,17	2
NMDA receptor 1 isoform NR1-2 variant [Fragment]	Q59GW0	58	73,98	2
NMDA receptor 1 isoform NR1-2 variant [Fragment]	Q59H41	61	104,18	3
NMDA receptor subunit 3B	Q5F0I5	72	112,89	3
N-methyl-D-aspartate receptor 2C subunit [Precursor]	O15398	48	134,46	5
Nodal modulator 1 [Precursor]	Q15155	51	134,35	2
NOL1 protein	Q3KQS4	74	92,80	3
Non-POU domain-containing octamer-binding protein	Q15233	579	54,22	13
Non-receptor tyrosine-protein kinase TNK1	Q13470	68	72,47	5
Non-receptor tyrosine-protein kinase TYK2	P29597	66	133,65	2
Notch homolog 4	Q5SPL1	64	209,66	3
NOTCH2 protein	Q6IQ50	42	132,11	2
Novel protein	Q5TGS3	60	23,13	4
Novel protein	Q5T232	83	84,24	4
Novel protein [Fragment]	Q5TAA1	72	19,00	2
Novel protein similar to beta-tubulin 4Q (TUBB4Q) (LOC253936)	Q5SQY0	171	45,46	6
Novel protein similar to multidomain presynaptic cytomatrix protein Piccolo; piccolo	Q5HYW2	58	76,30	3
NPD011	Q9H2R7	161	24,34	2
NR1H4 protein [Fragment]	Q6IPQ7	47	54,61	3
NUAK family SNF1-like kinase 1	O60285	42	74,31	1
Nuclear autoantigen Sp-100	P23497	64	100,42	3
Nuclear autoantigenic sperm protein	P49321	234	85,19	8
Nuclear autoantigenic sperm protein	Q5T624	82	45,77	3
Nuclear cap-binding protein subunit 1	Q09161	76	91,78	4
Nuclear factor NF-kappa-B p100 subunit	Q00653	41	96,75	1
Nuclear factor of activated T-cells, cytoplasmic 1	O95644	90	101,18	3
Nuclear migration protein nudC	Q9Y266	161	38,19	2
Nuclear mitotic apparatus protein 1	Q14980	96	107,23	5
Nuclear mitotic apparatus protein 1 [Fragment]	Q9UNL7	49	31,72	2
Nuclear mitotic apparatus protein 1 variant [Fragment]	Q59HB8	58	178,08	3
Nuclear phosphoprotein similar to S. cerevisiae PWP1 variant [Fragment]	Q53FW9	65	55,73	3
Nuclear pore complex protein Nup133	Q8WUM0	47	128,82	2
Nuclear pore complex protein Nup88	Q99567	79	83,49	3
Nuclear pore complex protein Nup93	Q8N1F7	172	94,57	7
Nuclear receptor coactivator 1	Q15788	51	156,76	2
Nuclear receptor coactivator 3 isoform a variant [Fragment]	Q59EE8	48	155,66	2
Nuclear receptor coactivator 5	Q9HCD5	82	65,54	5
Nuclear receptor corepressor 1	O75376	87	270,21	5
Nuclear receptor corepressor 2	Q9Y618	62	159,45	5
Nuclear receptor subfamily 1 group D member 1	P20393	44	66,76	2
Nuclear transcription factor NFX2	Q9BXI1	44	113,55	2
Nuclear transport factor 2	P61970	41	14,47	1
Nuclear-localized factor 1	Q8NCU7	68	65,54	3
Nuclear-localized factor 3	Q8TF44	75	39,73	3
Nuclease sensitive element-binding protein 1	P67809	788	35,77	13
Nucleobindin 1 variant [Fragment]	Q53GX6	125	53,87	4

Table 1. continued

Protein Name and Species	Accession	Score	MW [kDa]	# Pept.
Nucleobindin-2 [Precursor]	P80303	49	50,22	1
Nucleolar and coiled-body phosphoprotein 1	Q5VV70	92	73,56	4
Nucleolar complex protein 2 homolog	Q9Y3T9	56	84,91	3
Nucleolar phosphoprotein p130	Q14978	72	73,60	3
Nucleolar pre-ribosomal-associated protein 1	O60287	40	254,40	1
Nucleolar protein 3 (Apoptosis repressor with CARD domain)	Q5TZN6	62	22,62	1
Nucleolar RNA helicase 2	Q9NR30	400	89,20	12
Nucleolar transcription factor 1	P17480	52	89,35	2
Nucleolin	P19338	165	76,44	3
Nucleolysin TIA-1 isoform p40	P31483	64	42,93	2
Nucleophosmin	P06748	534	75,31	9
Nucleophosmin	Q5EU94	693	32,44	12
Nucleoporin 153kDa	Q5T9I7	65	153,94	2
Nucleoporin NUP188 homolog	Q5SRE5	76	196,04	3
Nucleoporin Nup43	Q8NFH3	101	42,12	1
Nucleoporin NUP53	Q8NFH5	60	13,37	1
Nucleoporin SEH1-like	Q96EE3	72	46,58	3
Nucleoside diphosphate kinase	Q86XQ2	458	19,64	10
Nucleoside diphosphate kinase	Q1WM23	379	30,12	8
Nucleosome assembly protein 1-like 1	P55209	137	45,35	3
Nucleosome assembly protein 1-like 4	Q99733	89	42,80	2
Nucleosome-remodeling factor subunit BPTF	Q12830	80	324,22	3
NudC domain-containing protein 3	Q8IVD9	41	40,82	2
Nudix (Nucleoside diphosphate linked moiety X)-type motif 1	Q7Z7N6	63	19,00	2
NUMA1 protein	Q9BTE9	146	109,21	6
NUMA1 protein [Fragment]	Q3SYK8	47	78,27	2
NUMA1 variant protein [Fragment]	Q4LE64	82	238,71	4
Numb-like protein	Q9Y6R0	41	64,89	2
NUP153 variant protein [Fragment]	Q4LE47	41	151,46	2
NY-REN-50 antigen [Fragment]	Q9Y595	50	48,67	2
Obscurin	Q5VST9	99	868,49	5
Obscurin-like protein 1 [Precursor]	O75147	63	152,88	3
OCIA domain-containing protein 1	Q9NX40	100	27,61	3
OK/SW-CL.16	Q8NI70	48	15,49	2
Olfactory receptor 10K2	Q6IF99	40	35,01	2
Olfactory receptor 2B11	Q5JQS5	56	49,70	3
Olfactory receptor 7E24	Q6IFN5	120	68,16	7
Oligodendrocyte transcription factor 2	Q13516	75	32,39	3
Opioid growth factor receptor	Q9NZT2	85	73,33	3
Ornithine aminotransferase [Precursor]	P04181	286	48,50	5
Ornithine decarboxylase antizyme	P54368	56	25,41	3
Otopetrin-1	Q7RTM1	91	67,35	3
OTU domain-containing protein 5	Q96G74	41	57,97	2
OTU domain-containing protein 6B	Q8N6M0	136	33,79	3
OTU domain-containing protein 7A	Q8TE49	56	100,61	2
OTU domain-containing protein 7B	Q6GQQ9	56	92,53	3
Outer dense fiber protein 2	Q5BJF6	60	95,40	2
Ovochymase-1 [Precursor]	Q7RTY7	42	125,07	2
OXCT protein	Q6IAV5	109	56,16	3
Oxysterol-binding protein [Fragment]	Q641R2	42	82,55	2
Oxysterol-binding protein-like protein 5, isoform b	Q8N596	49	90,74	3
Oxysterol-binding protein-related protein 10	Q9BXB5	160	83,97	7
P protein	Q04671	40	92,85	2
p53-associated parkin-like cytoplasmic protein	Q8IWT3	63	196,46	4
PAB-dependent poly(A)-specific ribonuclease subunit 3	Q58A45	46	82,18	2
PABP3 [Fragment]	Q2VIP3	109	69,89	5
PABPCP2 protein	Q6NV95	59	29,86	2
Paired box protein Pax-1	P15863	59	46,30	2
Paired mesoderm homeobox protein 2A	O14813	179	29,63	4
Paired mesoderm homeobox protein 2B	Q99453	209	31,59	5
Palladin	Q8WX93	44	150,54	2
Palmitoyltransferase ZDHHC18	Q9NUE0	56	42,00	2
PAPLN protein	Q8IVU0	46	137,80	1
Pappalysin-1 [Precursor]	Q13219	46	181,14	1
Pappalysin-2 [Precursor]	Q9BXP8	71	198,54	4
Par-3 partitioning defective 3 homolog	Q5T2U1	72	108,55	3
Parafibromin	Q6P1J9	52	33,45	2
Paraspeckle component 1	Q8WXF1	97	45,54	3
Parathymosin	P20962	118	11,39	2
Patatin-like phospholipase domain-containing protein 1	Q8N8W4	44	57,92	2
Patched domain-containing protein 2	Q9P2K9	40	153,05	1
Paternally-expressed gene 3 protein	Q9GZU2	42	172,92	2

Table 1. continued

Protein Name and Species	Accession	Score	MW [kDa]	# Pept.
Paxillin variant [Fragment]	Q59GS5	46	75,59	2
PC4 and SFRS1-interacting protein	O75475	52	40,11	2
PDZ and LIM domain protein 2	Q96JY6	85	37,46	4
PDZ and LIM domain protein 3	Q53GG5	159	34,25	3
PDZ and LIM domain protein 4	P50479	141	35,28	5
PDZ domain-containing protein 2	O15018	84	280,04	4
PDZ domain-containing protein 7	Q9H5P4	41	55,64	6
PDZ domain-containing protein 8	Q8NEN9	50	128,56	2
PDZ domain-containing protein MAGIX	Q9H6Y5	68	35,22	4
PDZD4 protein	Q17RL8	53	86,88	3
Peptidase M20 domain-containing protein 1	Q6GTS8	48	55,73	3
Peptidoglycan recognition protein I-alpha [Precursor]	Q96LB9	45	37,61	1
Peptidyl-prolyl cis-trans isomerase A	P62937	668	18,00	21
Peptidyl-prolyl cis-trans isomerase B [Precursor]	P23284	290	22,73	10
Peptidyl-prolyl cis-trans isomerase-like 2	Q13356	60	58,82	3
Periaxin	Q9BXM0	74	148,33	3
Period circadian protein homolog 1	O15534	103	136,24	4
Period circadian protein homolog 3	P56645	68	131,87	4
Peripheral-type benzodiazepine receptor-associated protein 1	O95153	190	186,93	3
Peripherin	P41219	67	53,62	2
Periphilin-1	Q8NEY8	41	52,74	2
Peroxidasin homolog [Fragment]	Q92626	68	165,28	2
Peroxiredoxin 3 isoform a variant [Fragment]	Q53HC2	166	27,61	2
Peroxiredoxin-1	Q06830	587	18,96	14
Peroxiredoxin-2	P32119	637	21,75	12
Peroxiredoxin-4	Q13162	262	30,52	5
Peroxiredoxin-5 [Precursor]	P30044	255	22,01	6
Peroxiredoxin-6	P30041	459	24,32	9
Peroxisomal bifunctional enzyme	Q08426	59	79,34	3
Peroxisomal leader peptide-processing protease	Q2T9J0	50	59,31	2
Peroxisomal multifunctional enzyme type 2	P51659	251	79,51	7
Peroxisomal N(1)-acetyl-spermine/spermidine oxidase	Q6QHF9	42	8,69	2
Peroxisome assembly factor 1	P28328	49	55,47	2
Peroxisome proliferator-activated receptor gamma coactivator-related protein 1	Q5VV67	52	177,54	2
PERQ amino acid-rich with GYF domain-containing protein 1	O75420	44	114,60	2
PERQ amino acid-rich with GYF domain-containing protein 2	Q6Y7W6	49	149,98	2
PEST proteolytic signal-containing nuclear protein	Q8WW12	62	13,26	3
PH and SEC7 domain-containing protein 1	A5PKW4	44	116,49	2
PH domain leucine-rich repeat-containing protein phosphatase	O60346	91	184,67	4
PHD finger protein 3	Q92576	46	229,48	2
PH-interacting protein	Q8WWQ0	40	206,56	2
Phosphatase and actin regulator 1	Q9C0D0	92	66,31	5
Phosphatase and actin regulator 2	O75167	51	69,65	2
Phosphatase and actin regulator 4	Q8IZ21	43	78,21	1
Phosphatidylcholine-sterol acyltransferase [Precursor]	P04180	56	49,55	2
Phosphatidylethanolamine-binding protein 1	P30086	73	20,33	2
Phosphatidylinositol 4,5-bisphosphate 5-phosphatase A	Q15735	70	107,20	3
Phosphatidylinositol transfer protein beta isoform	P48739	117	31,39	5
Phosphatidylinositol-3,4,5-trisphosphate 5-phosphatase 2	O15357	54	138,50	3
Phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic subunit beta isoform	P42338	43	122,68	1
Phosphatidylinositol-4-phosphate 3-kinase C2 domain-containing alpha polypeptide	O00443	54	190,68	2
Phosphodiesterase 4B, cAMP-specific	Q5TEK7	48	11,25	2
Phosphodiesterase 4C [Fragment]	P78505	47	77,60	2
Phosphofructo-1-kinase isozyme A	P08237	224	85,13	8
Phosphofructo-1-kinase isozyme B	P17858	174	84,86	5
Phosphofructo-1-kinase isozyme C	Q01813	298	85,54	11
Phosphoglycerate kinase 1	P00558	2217	44,59	36
Phosphoglycerate mutase 1	P18669	930	28,79	11
Phosphoinositide 3-kinase regulatory subunit 5	Q8WYR1	106	54,84	6
Phosphoinositide phospholipase C	P19174	65	148,53	3
Phospholipase C eta 1	Q4KWH8	40	189,10	2
Phospholipase C, epsilon 1	Q5VWL4	54	223,73	2
Phospholipase C-beta-1	Q9NQ66	41	138,57	1
Phospholipase C-eta-2	O75038	69	154,67	4
Phospholipase D3	Q8IV08	97	54,67	3
Phospholipid scramblase 1	O15162	109	34,21	5
Phosphoribosyl pyrophosphate synthetase-associated protein 1	Q14558	213	39,45	4
Phosphoribosylformylglycinamidine synthase	O15067	94	144,57	3
Phosphorylase b kinase regulatory subunit beta	Q93100	41	124,88	2
Phosphoserine aminotransferase 1	Q5T7G6	954	40,40	20
Phosphoserine phosphatase variant [Fragment]	Q53EY1	84	24,93	3

Table 1. continued

Protein Name and Species	Accession	Score	MW [kDa]	# Pept.
PIK4CA variant protein [Fragment]	Q4LE69	42	238,70	3
PITSLRE serine/threonine-protein kinase CDC2L2	Q9UQ88	73	90,97	3
PKD1L2 protein [Fragment]	Q96CM9	41	24,19	1
PKM2 protein	Q4V9L8	103	30,26	2
Plakophilin-2	Q99959	41	97,40	3
Plasma alpha-L-fucosidase [Precursor]	Q9BTY2	46	14,96	3
Plasminogen [Precursor]	P00747	62	90,57	3
Plasminogen activator inhibitor 1 RNA-binding protein	Q8NC51	147	43,17	4
Plastin-2	P13796	41	70,29	2
Plastin-3	P13797	70	70,39	2
Platelet-activating factor acetylhydrolase IB subunit alpha	P43034	67	20,09	2
Platelet-activating factor acetylhydrolase IB subunit beta	P68402	200	25,55	3
Platelet-activating factor acetylhydrolase IB subunit gamma	Q15102	163	25,72	3
Platelet-derived growth factor A chain [Precursor]	P04085	40	12,33	2
PLCH2 protein [Fragment]	Q86XJ2	65	134,13	3
Pleckstrin and Sec7 domain-containing protein [Fragment]	Q8IVG0	63	109,57	3
Pleckstrin homology domain containing, family A member 6	Q5VTI5	63	119,29	3
Pleckstrin homology domain containing, family O member 1 [Fragment]	Q5T4P8	40	24,57	2
Pleckstrin homology domain-containing family A member 4	Q9H4M7	59	85,34	2
Pleckstrin homology domain-containing family A member 7	Q6IQ23	56	127,04	1
Pleckstrin homology domain-containing family G member 4B	Q96PX9	53	141,33	3
Pleckstrin homology-like domain family B member 1	Q86UU1	74	151,16	5
Plectin 10	Q6S377	49	516,16	4
Plectin 6	Q6S380	98	531,47	5
Plectin-1	Q15149	93	518,17	5
PLEKHG1 protein [Fragment]	Q5EBL9	44	134,08	2
Plexin-A2 [Precursor]	O75051	43	212,66	1
Plexin-A3 [Precursor]	P51805	79	207,70	4
Plexin-C1 [Precursor]	O60486	43	175,74	2
Plexin-D1 [Precursor]	Q9Y4D7	43	212,10	2
PMAIP1 protein	Q8N589	55	14,95	2
PML-RARA-regulated adapter molecule 1	Q96QH2	40	79,22	2
PNMA-like protein 2	Q9ULN7	44	68,84	2
Pol protein	Q86UH8	48	131,39	2
POLR2C protein	Q6FGR6	85	31,42	2
Poly (ADP-ribose) polymerase family, member 4	Q5QNZ9	47	192,60	2
Poly [ADP-ribose] polymerase 1	P09874	102	112,88	3
Poly [ADP-ribose] polymerase 14	Q460N5	54	789,74	2
Poly [ADP-ribose] polymerase 15	Q460N3	43	72,54	3
Poly [ADP-ribose] polymerase 4	Q9UKK3	52	192,59	3
Poly(A) binding protein, cytoplasmic 4	Q5SPS4	51	70,78	2
Poly(ADP-ribose) glycohydrolase	Q86W56	49	111,11	2
Poly(RC) binding protein 3	Q5MJP6	273	38,13	7
Poly(rC)-binding protein 1	Q15365	192	37,50	8
Poly(rC)-binding protein 2	Q15366	430	36,78	9
Polyadenylate-binding protein 1	P11940	223	70,28	7
Polyadenylate-binding protein 1-like	Q4VXU2	85	68,35	3
Polyadenylate-binding protein 4	Q13310	957	65,92	17
Polycomb group RING finger protein 1	Q9BSM1	51	22,75	2
Polycystic kidney and hepatic disease 1	Q5VUA2	43	371,65	2
Polycystic kidney disease 1-like 1 protein	Q8TDX9	158	315,44	8
Polycystic kidney disease-associated protein	Q15142	52	392,19	2
Polycystin 1 isoform 2 variant [Fragment]	Q59EY6	49	104,33	2
Polycystin-1 [Precursor]	P98161	84	462,28	4
Polycystin-2	Q13563	50	109,62	3
Polyhomeotic-like protein 3	Q8NDX5	42	106,16	2
Polypyrimidine tract-binding protein 1	P26599	321	57,19	5
Polypyrimidine tract-binding protein 1 isoform c variant [Fragment]	Q59H49	80	35,53	1
Polyribonucleotide nucleotidyltransferase 1 [Precursor]	Q8TCS8	62	85,95	2
POM121 membrane glycoprotein	Q96HA1	55	99,04	2
Postmeiotic segregation increased 2-like protein 2	O95744	98	6,15	3
Potassium channel subfamily K member 12	Q9HB15	46	46,89	2
Potassium channel subfamily T member 1	Q5JUK3	47	138,34	2
Potassium voltage-gated channel subfamily A member 5	P22460	45	67,23	2
Potassium voltage-gated channel subfamily KQT member 5	Q9NR82	40	102,18	2
Potassium voltage-gated channel subfamily S member 2	Q9ULS6	47	54,24	2
Potassium/sodium hyperpolarization-activated cyclic nucleotide-gated channel 2	Q9UL51	40	96,95	2
Potassium/sodium hyperpolarization-activated cyclic nucleotide-gated channel 3	Q9P1Z3	45	63,36	3
Potassium/sodium hyperpolarization-activated cyclic nucleotide-gated channel 4	Q9Y3Q4	83	128,96	4
Potential tRNA (adenine-N(1)-)-methyltransferase	Q9BVS5	80	52,97	3
POZ-, AT hook-, and zinc finger-containing protein 1	Q9HBE1	71	76,73	3
PP10752	Q71RE0	55	11,98	2

Table 1. continued

Protein Name and Species	Accession	Score	MW [kDa]	# Pept.
PP13187	Q71RC4	50	16,74	2
PPM1G protein	Q6IAU5	232	59,23	7
PR domain containing 16	Q5VU52	48	138,18	2
PR domain containing 2, with ZNF domain	Q5THJ1	84	162,11	4
PR domain containing 2, with ZNF domain [Fragment]	Q5THJ0	63	168,56	4
PR domain zinc finger protein 12	Q9H4Q4	49	40,40	2
PR domain zinc finger protein 6 [Fragment]	Q9NQX0	71	66,56	3
PRA1 family protein 2	O60831	54	19,25	1
PRAME family member 2	O60811	40	54,87	1
Predicted protein product of Nbla02942	Q3LIE9	971	48,74	15
Prefoldin subunit 2	Q9UHV9	70	16,64	2
Prefoldin subunit 6	Q5STK2	77	14,57	1
Pregnancy-specific beta-1-glycoprotein 2 [Precursor]	P11465	42	37,22	2
Pre-mRNA branch site protein p14	Q9Y3B4	42	14,58	2
Pre-mRNA-processing factor 40 homolog A	O75400	53	24,28	1
Pre-mRNA-processing factor 6	O94906	116	107,05	5
Pre-mRNA-processing-splicing factor 8	Q6P2Q9	148	273,61	4
Pre-mRNA-splicing factor ISY1 homolog	Q9ULR0	144	37,54	5
Pre-rRNA-processing protein TSR1 homolog	Q2NL82	76	91,75	2
Prickle-like protein 4	Q2TBC4	62	37,55	2
PRMT1 protein [Fragment]	Q2VP93	262	40,05	4
PRO2605	Q9P1C7	59	17,37	2
PRO2832	Q9P145	43	8,62	1
Probable aminopeptidase NPEPL1	Q8NDH3	47	55,86	2
Probable ATP-dependent RNA helicase DDX31	Q9H8H2	45	94,09	2
Probable ATP-dependent RNA helicase DDX5	P17844	395	69,10	12
Probable ATP-dependent RNA helicase DDX52	Q9Y2R4	90	11,94	5
Probable ATP-dependent RNA helicase DDX59	Q5T1V6	51	68,81	3
Probable ATP-dependent RNA helicase DHX37	Q8IY37	81	129,55	3
Probable cation-transporting ATPase 13A4	Q4VNC1	68	133,87	3
Probable E3 ubiquitin-protein ligase HERC2	O95714	73	527,14	4
Probable E3 ubiquitin-protein ligase MYCBP2	O75592	100	509,84	9
Probable E3 ubiquitin-protein ligase HECTD1	Q9ULT8	59	289,60	3
Probable G-protein coupled receptor 112	Q8IZF6	44	134,50	3
Probable G-protein coupled receptor 123	Q86SQ6	62	137,20	4
Probable G-protein coupled receptor 124 [Precursor]	Q96PE1	81	128,15	4
Probable G-protein coupled receptor 144	Q7Z7M1	44	104,37	2
Probable G-protein coupled receptor 156	Q8NFN8	48	89,08	2
Probable G-protein coupled receptor 157	Q5UAW9	50	36,62	2
Probable G-protein coupled receptor 179 [Precursor]	Q6PRD1	97	257,20	4
Probable G-protein coupled receptor 37 [Precursor]	O15354	71	67,11	4
Probable G-protein coupled receptor 78	Q96P69	43	36,91	2
Probable helicase senataxin	Q7Z333	77	183,55	4
Probable histidyl-tRNA synthetase [Precursor]	P49590	62	56,85	2
Probable histone-lysine N-methyltransferase ASH1L	Q9NR48	131	332,79	6
Probable histone-lysine N-methyltransferase NSD2	O96028	57	152,26	3
Probable methyltransferase C20orf7 [Precursor]	Q5TEU4	61	32,35	3
Probable mitochondrial import receptor subunit TOM40 homolog	O96008	56	37,89	2
Probable phospholipid-transporting ATPase IIB	O43861	43	123,64	2
Probable phospholipid-transporting ATPase IK	O60423	49	148,03	2
Probable serine protease HTRA3 [Precursor]	P83110	61	37,92	3
Probable transcription factor PML	P29590	47	97,52	2
Procollagen-lysine,2-oxoglutarate 5-dioxygenase 1 [Precursor]	Q02809	91	83,50	4
Procollagen-lysine,2-oxoglutarate 5-dioxygenase 3 [Precursor]	O60568	233	84,73	10
Profilaggrin [Fragment]	Q15206	45	106,45	3
Programmed cell death 6-interacting protein	Q8WUM4	46	96,02	2
Programmed cell death protein 10	Q9BUL8	65	24,69	2
Programmed cell death protein 4	Q53EL6	67	51,70	2
Programmed cell death protein 5	O14737	50	14,15	2
Programmed cell death protein 6	O75340	120	21,85	2
Prohibitin	Q6PUJ7	646	29,80	10
Proliferating cell nuclear antigen	P12004	111	28,75	5
Proliferation-associated protein 2G4	Q9UQ80	392	38,04	10
Proline dehydrogenase 2 [Fragment]	O00420	41	90,81	2
Proline-, glutamic acid-, leucine-rich protein 1	Q6NTE6	85	119,62	3
Proline/serine-rich coiled-coil protein 1	Q6PGN9	54	38,80	3
Proline-rich protein 12	Q9ULL5	47	129,99	4
Proline-rich protein 18	Q8N4B5	49	30,91	3
Proline-rich protein 6	Q7Z7K6	136	29,93	3
Proline-rich transmembrane protein 1	Q5SSX7	71	31,43	3

Table 1. continued

Protein Name and Species	Accession	Score	MW [kDa]	# Pept.
Proline-rich transmembrane protein 3 [Precursor]	Q5FWE3	54	71,39	2
Prolow-density lipoprotein receptor-related protein 1 [Precursor]	Q07954	67	504,58	3
Prolyl endopeptidase	Q8N6D4	124	80,65	5
Promyelocytic leukemia	Q9BWP7	49	85,68	2
Promyelocytic leukemia protein isoform 1 variant [Fragment]	Q59FP9	40	95,66	2
Pro-neuregulin-1, membrane-bound isoform [Precursor]	Q02297	49	70,39	2
Properdin [Precursor]	P27918	41	51,28	2
Proprotein convertase subtilisin/kexin type 4 [Precursor]	Q6UW60	55	26,10	2
Proprotein convertase subtilisin/kexin type 5 [Precursor]	Q92824	68	101,78	3
ProSAAS [Precursor]	Q9UHG2	69	27,37	2
Prostacyclin synthase	Q16647	42	57,10	2
Prostaglandin E synthase 3	Q15185	160	18,69	3
Prostaglandin E2 receptor EP1 subtype	P34995	70	44,21	5
Proteasome (Prosome, macropain) 26S subunit, ATPase, 1	Q6NW36	149	49,10	5
Proteasome (Prosome, macropain) 26S subunit, non-ATPase, 13	Q53XU2	761	42,89	16
Proteasome (Prosome, macropain) 26S subunit, non-ATPase, 5	Q4VXG8	103	56,16	4
Proteasome (Prosome, macropain) 26S subunit, non-ATPase, 8	Q5U0B3	86	29,90	2
Proteasome (Prosome, macropain) subunit, alpha type, 1	Q53YE8	114	29,58	4
Proteasome (Prosome, macropain) subunit, beta type, 4	Q5SZS5	91	29,19	2
Proteasome (Prosome, macropain) subunit, beta type, 7	Q5TBG6	62	29,95	2
Proteasome activator complex subunit 1	Q06323	74	16,28	2
Proteasome activator complex subunit 2	Q9UL46	179	27,21	4
Proteasome alpha 5 subunit	Q3T1C1	214	26,39	3
Proteasome subunit alpha type-2	P25787	170	25,75	2
Proteasome subunit alpha type-3	P25788	185	28,28	5
Proteasome subunit alpha type-4	P25789	171	29,47	4
Proteasome subunit alpha type-6	P60900	217	27,38	4
Proteasome subunit alpha type-7	O14818	201	27,87	4
Proteasome subunit beta type-1 [Precursor]	P20618	68	26,47	3
Proteasome subunit beta type-2	P49721	118	22,82	2
Proteasome subunit beta type-5 [Precursor]	P28074	355	28,46	7
Proteasome subunit beta type-6 [Precursor]	P28072	150	25,38	4
Proteasome subunit p58	O95325	55	13,35	2
Protein AHNAK2	Q8IVF2	53	616,63	3
Protein ajuba	Q96IF1	45	56,93	2
Protein arginine N-methyltransferase 6	Q96LA8	65	41,94	2
Protein ARMET [Precursor]	P55145	56	20,24	1
Protein bassoon	Q9UPA5	97	416,11	5
Protein C10	Q99622	69	13,17	1
Protein C15orf2	Q9NZP6	49	120,98	2
Protein C9orf140	Q86UD0	46	42,64	2
Protein canopy homolog 2 [Precursor]	Q9QXT0	80	20,75	1
Protein CASC3	O15234	43	76,28	2
Protein COQ10 A [Precursor]	Q96MF6	46	27,69	4
Protein cordon-bleu	O75128	75	141,15	5
Protein CutA [Precursor]	O60888	126	16,82	3
Protein Daple	Q9P219	90	228,21	4
Protein DBF4 homolog A	Q9UBU7	43	76,86	1
Protein DEK	P35659	113	42,33	3
Protein DGCR13	Q49AH7	44	40,56	2
Protein disulfide-isomerase [Precursor]	P07237	335	57,07	10
Protein disulfide-isomerase A3 [Precursor]	P30101	586	56,76	12
Protein disulfide-isomerase A4 [Precursor]	P13667	1087	72,89	29
Protein disulfide-isomerase A6 [Precursor]	Q15084	819	46,17	10
Protein DJ-1	Q99497	244	19,83	6
Protein Dos	Q8N350	46	75,78	2
Protein downstream neighbor of Son	Q9NYP3	52	62,72	3
Protein enabled homolog	Q8N8S7	222	66,48	6
Protein ENL	Q03111	42	62,06	1
Protein FAM104A	Q969W3	53	13,19	2
Protein FAM117A	Q9C073	50	48,32	2
Protein FAM122B	Q7Z309	49	26,93	2
Protein FAM124A	Q86V42	47	60,10	2
Protein FAM149A	A5PLN7	49	69,85	1
Protein FAM149B1	Q96BN6	42	64,62	2
Protein FAM21A	Q641Q2	44	44,46	2
Protein FAM38A	Q92508	101	157,72	6
Protein FAM38A	Q92508	61	239,62	3
Protein FAM43B	Q6ZT52	56	36,78	3
Protein FAM50A	Q14320	103	40,22	3
Protein FAM53A	Q6NSI3	51	42,59	2
Protein FAM55A [Precursor]	Q8N323	77	63,18	3

Table 1. continued

Protein Name and Species	Accession	Score	MW [kDa]	# Pept.
Protein FAM55B	Q96DL1	75	41,60	4
Protein FAM59B [Fragment]	Q75VX8	68	96,85	3
Protein FAM73B	Q7L4E1	44	65,49	2
Protein FAM82A	Q96LZ7	45	47,40	1
Protein FAM82B	Q96DB5	156	5,74	9
Protein FAM83H	Q6ZRV2	64	127,10	2
Protein FAM84A	Q96KN4	71	37,73	4
Protein GATS	Q8NAP1	42	17,85	1
Protein hairless	O43593	42	127,50	3
Protein Jade-2	Q9NQC1	70	87,47	3
Protein Jade-3	Q92613	47	93,81	2
Protein jagged-2 [Precursor]	Q9Y219	61	133,37	3
Protein Jumonji	Q92833	73	138,73	3
Protein KIAA0284	Q9Y4F5	67	171,69	3
Protein KIAA0649	Q5T8A7	53	127,35	2
Protein KIAA0649 [Fragment]	Q9Y4D3	68	127,35	3
Protein KIAA1324 [Precursor]	Q6UXG2	53	111,38	3
Protein KIAA1409 [Fragment]	Q9P2D8	88	275,31	4
Protein KIAA1967	Q8N163	51	39,82	1
Protein kinase [Fragment]	Q5SZH1	68	28,88	3
Protein kinase C iota type	P41743	40	67,26	2
Protein kinase, lysine deficient 2	Q5VWF1	54	104,94	3
Protein LAP2	Q96RT1	71	14,62	4
Protein LAP4	Q14160	72	68,22	3
Protein mago nashi homolog	P61326	66	17,15	2
Protein MICAL-2	O94851	79	126,69	3
Protein MTO1 homolog [Precursor]	Q9Y2Z2	92	79,96	4
Protein NipSnap1	Q9BPW8	68	33,29	2
Protein NLRC3	Q7RTR2	56	114,66	2
Protein p65	O43245	53	68,62	2
Protein phosphatase 1 regulatory subunit 12B	O60237	80	110,40	3
Protein phosphatase 1 regulatory subunit 12C	Q9BZL4	47	84,88	2
Protein phosphatase 1 regulatory subunit 14B	Q96C90	143	15,90	2
Protein phosphatase 1 regulatory subunit 14C	Q8TAE6	71	17,80	2
Protein phosphatase 1 regulatory subunit 7	Q15435	43	36,81	1
Protein phosphatase 1, regulatory (Inhibitor) subunit 8	Q5TIF3	206	38,45	3
Protein phosphatase 1, regulatory subunit 3D	Q86X09	77	32,54	4
Protein phosphatase 1E	Q8WY54	46	85,24	2
Protein phosphatase 2A, regulatory subunit B' (PR 53)	Q5TZQ2	151	36,75	4
Protein phosphatase methylesterase 1	Q9Y570	40	42,16	1
Protein piccolo	Q9Y6V0	135	566,31	8
Protein quaking	Q96PU8	109	37,65	3
Protein RCC2	Q9P258	128	56,05	5
Protein regulator of cytokinesis 1	O43663	50	71,62	2
Protein SET	Q01105	88	33,47	3
Protein Shroom2	Q13796	43	170,47	2
Protein sidekick-1 [Precursor]	Q7Z5N4	86	241,93	4
Protein sidekick-2 [Precursor]	Q58EX2	53	239,12	3
Protein SMF	Q12766	58	168,33	2
Protein SMG7	Q92540	43	89,67	2
Protein TBRG4	Q969Z0	105	70,73	4
Protein timeless homolog	Q9UNS1	44	54,48	2
Protein transport protein Sec23A	Q15436	175	86,09	5
Protein transport protein Sec24C	P53992	50	121,89	2
Protein TRS85 homolog	Q9Y2L5	41	75,14	2
Protein tyrosine phosphatase receptor pi	Q9Y4I6	62	109,72	3
Protein tyrosine phosphatase, non-receptor type 14	Q5VTH8	65	135,26	3
Protein tyrosine phosphatase, receptor type, D	Q5VVL9	68	213,90	2
Protein unc-13 homolog A	Q9UPW8	69	39,56	3
Protein VPRBP	Q9Y4B6	50	169,01	3
Protein Wiz	O95785	72	178,67	4
Protein WWC1	Q8IX03	69	125,30	3
Protein-cysteine N-palmitoyltransferase HHAT-like protein	Q9HCP6	43	56,67	1
Protein-glutamine gamma-glutamyltransferase K	P22735	64	89,79	2
Protein-tyrosine phosphatase-like member A	Q9HB93	52	32,73	2
Proteoglycan-4 [Precursor]	Q92954	83	151,00	5
Protocadherin alpha 4 isoform 1 variant [Fragment]	Q59H34	57	99,71	2
Protocadherin beta-15 [Precursor]	Q9Y5E8	43	86,33	2
Protocadherin Fat 2 [Precursor]	Q9NYQ8	57	479,07	3
Protocadherin Fat 3 [Precursor]	Q8TDW7	40	120,55	2
Protocadherin gamma C3 [Precursor]	Q9UN70	66	97,89	4
Protocadherin gamma-C4 [Precursor]	Q9Y5F7	50	37,40	4

Table 1. continued

Protein Name and Species	Accession	Score	MW [kDa]	# Pept.
Protocadherin-1 [Precursor]	Q08174	49	111,20	2
Protocadherin-16 [Precursor]	Q96JQ0	64	345,97	4
Protocadherin-18 [Precursor]	Q9HCL0	55	125,23	3
Proton/amino acid transporter 4	Q6YBV0	44	56,12	2
Proto-oncogene DBL	P10911	42	65,60	2
PROX2 protein [Fragment]	Q3B8N5	43	65,44	2
PRP4 pre-mRNA processing factor 4 homolog [Fragment]	Q5T1M8	64	58,41	3
PRP4 pre-mRNA processing factor 4 homolog B	Q8IVC3	47	116,99	2
PRPSAP2 protein (Phosphoribosyl pyrophosphate synthetase-associated protein 2).- Homo sapiens (Huma	Q6IAS2	181	40,90	3
PSMD3 protein	Q6IBN0	46	60,91	2
Pterin-4-alpha-carbinolamine dehydratase	P61457	80	11,86	2
PTK2B protein tyrosine kinase 2 beta	Q6PID4	48	115,91	2
PTK7 protein tyrosine kinase 7 isoform a variant [Fragment]	Q59FV9	52	84,31	2
PTPRM protein	Q86V60	56	156,94	2
PURA protein [Fragment]	Q2NLC9	166	34,15	3
Pur-gamma B-form	Q8TE64	81	36,55	3
Puromycin-sensitive aminopeptidase	P55786	316	98,44	12
Putative ATP-dependent RNA helicase DHX29	Q7Z478	53	155,24	2
Putative ATP-dependent RNA helicase DHX30	Q7L2E3	43	133,94	2
Putative ATP-dependent RNA helicase DHX33	Q9H6R0	49	78,74	2
Putative ATP-dependent RNA helicase DHX57	Q6P158	53	155,60	3
Putative DNA helicase INO80 complex homolog 1	Q9ULG1	71	176,75	3
Putative heat shock 70 kDa protein 7	P48741	103	26,89	3
Putative helicase MOV-10	Q9HCE1	49	113,67	3
Putative homeodomain transcription factor 1	Q5VWP6	52	82,32	2
Putative lipid kinase (Multiple substrate lipid kinase) (CDNA FLJ10842 fis, clone NT2RP4001343).- H	Q9NP48	75	47,11	3
Putative Polycomb group protein ASXL1	Q8IXJ9	76	165,43	5
Putative protein ORAI2-2	Q9H9Y3	43	19,84	2
Putative RNA-binding protein 15	Q96T37	72	107,19	4
Putative RNA-binding protein Luc7-like 2	Q9Y383	136	45,67	3
Putative S100 calcium-binding protein H_NH0456N16.1	Q9UDP3	45	11,51	2
Putative splicing factor, arginine/serine-rich 14	Q8IX01	58	120,24	4
Putative Taste receptor type 2 member 12	P59531	42	30,81	2
Putative testis protein CYorf15A	Q9BZA5	82	21,48	4
Putative thiosulfate sulfurtransferase KAT	Q8NFU3	166	32,95	3
Putative uncharacterized protein C10orf114	Q5T4H9	47	14,84	1
Putative uncharacterized protein C14orf165	Q86U02	69	21,73	3
Putative uncharacterized protein C8orf49	Q96NF6	46	13,67	1
Putative uncharacterized protein CXorf62	Q8N2A0	49	20,06	2
Putative uncharacterized protein DKFZp434C196 [Fragment]	Q9UF83	113	61,05	9
Putative uncharacterized protein gs85	Q96S00	70	68,75	3
Putative uncharacterized protein LRP2 [Fragment]	Q4ZG84	42	435,76	2
Putative uncharacterized protein MGC24975	Q8IZ63	82	43,80	4
Putative uncharacterized protein UNQ6490/PRO21339 [Precursor]	Q6UXU1	58	18,16	2
Putative uncharacterized protein UNQ6494/PRO21346 [Precursor]	Q6UXR6	48	19,53	2
Putative uncharacterized protein ZFHX1B [Fragment]	Q53TD9	61	121,41	2
Pygopus homolog 1	Q9Y3Y4	58	45,09	3
Pyridoxal kinase	O00764	331	35,08	5
Pyridoxal-dependent decarboxylase domain-containing protein 1	Q6P996	44	86,71	1
Pyrin and HIN domain family, member 1 [Fragment]	Q5T3W6	45	16,87	2
Pyrophosphatase 1	Q2M348	449	32,64	8
Pyrroline 5-carboxylate reductase isoform	Q4W8W1	108	33,71	2
Pyruvate dehydrogenase complex component E2 [Fragment]	Q9HAN0	62	11,23	2
Pyruvate dehydrogenase E1 component subunit alpha, somatic form [Precursor]	P08559	92	43,27	2
Pyruvate dehydrogenase E1 component subunit beta [Precursor]	P11177	123	39,21	2
Pyruvate dehydrogenase; kinase isozyme 3 [Precursor]	Q15120	44	67,23	1
Pyruvate dehydrogenase; phosphatase 2 [Precursor]	Q9P2J9	49	59,98	2
Pyruvate kinase isozymes M1/M2	P14618	1035	57,77	25
Pyruvate kinase isozymes R/L	P30613	82	58,43	2
Q86VS1	Q86VS1	41	65,51	1
Queuine tRNA-ribosyltransferase	Q9BXR0	66	14,46	3
Quinone oxidoreductase	Q08257	503	35,18	7
R30783_1	O75243	54	15,98	2
Rab GDP dissociation inhibitor alpha	P31150	366	50,39	8
Rab GDP dissociation inhibitor beta	P50395	288	10,26	7
Rab11 family-interacting protein 5	Q9BXF6	55	70,42	3
RAB11B, member RAS oncogene family	Q2YDT2	94	24,47	3
RAB11-FIP2 long isoform	Q3I768	48	60,61	2
RAB40B, member RAS oncogene family variant [Fragment]	Q59EV0	40	42,05	2
Rab5-activating protein 6	Q2Q1W1	61	164,98	2

Table 1. continued

Protein Name and Species	Accession	Score	MW [kDa]	# Pept.
RAB5C protein (RAB5C, member RAS oncogene family, isoform b)	Q6FH55	160	23,47	4
RAB6B protein	Q6AZ91	49	23,42	1
Rab9 effector protein with Kelch motifs	Q7Z6M1	56	8,99	2
Rac GTPase-activating protein 1	Q9H0H5	42	71,03	3
RAD23 homolog A	Q5M7Z1	60	39,48	3
RAD54-like 2	Q8TB57	65	162,80	3
Radixin	P35241	287	68,52	11
RAE1 (RNA export 1, S.pombe) homolog	Q3SYL7	254	40,94	6
Rai-like protein RaLP	Q6S5L8	93	68,74	3
Ral GEF with PH domain and SH3 binding motif 1	Q5VXM4	63	62,13	2
Ral guanine nucleotide dissociation stimulator	Q12967	43	100,61	1
Ral guanine nucleotide dissociation stimulator-like 3	Q3MIN7	68	54,28	3
RALGPS1 protein	Q8N5H4	72	34,74	3
Rap GTPase interactor	Q0VFZ9	48	117,43	3
Rap guanine nucleotide exchange factor 1	Q13905	58	120,53	3
Rap guanine nucleotide exchange factor 6	Q8TEU7	40	179,29	2
Ras and Rab interactor 2	Q8WYP3	46	100,16	2
Ras association (RalGDS/AF-6) domain family 5 isoform B variant [Fragment]	Q59GG4	62	39,23	2
Ras association domain-containing protein 7	Q02833	48	39,95	4
Ras GTPase-activating protein SynGAP	Q96PV0	89	148,28	4
Ras guanine nucleotide exchange factor 2 [Fragment]	Q9UK56	103	140,76	4
Ras suppressor protein 1	Q15404	62	31,39	1
Ras-associated and pleckstrin homology domains-containing protein 1	Q70E73	64	141,17	3
Ras-GTPase-activating protein SH3-domain-binding protein	Q5U0Q1	179	52,13	4
Ras-interacting protein 1	Q5U651	80	103,53	4
RASIP1 protein [Fragment]	Q8IUR2	63	54,60	3
Ras-related C3 botulinum toxin substrate 1 [Precursor]	P63000	43	20,12	1
Ras-related C3 botulinum toxin substrate 2 [Precursor]	P15153	169	21,42	4
Ras-related C3 botulinum toxin substrate 3 [Precursor]	P60763	176	20,12	4
Ras-related protein Rab-10	P61026	144	22,53	3
Ras-related protein Rab-1B	Q9H0U4	133	22,16	5
Ras-related protein Rab-7a	P51149	290	23,47	5
Ras-related protein Rab-8A	P61006	68	23,58	3
Ras-related protein Rap-2a [Precursor]	P10114	98	84,96	3
RBBP8 protein	Q8NHQ3	46	102,66	2
RcTPM3 [Fragment]	Q2QD06	57	28,81	2
Receptor expression-enhancing protein 1	Q9H902	40	22,26	1
Receptor for advanced glycosylation end-products deletion exon2-6 variant	Q3L1R3	45	3,56	2
Receptor-type tyrosine-protein phosphatase delta [Precursor]	P23468	43	214,76	2
Receptor-type tyrosine-protein phosphatase gamma [Precursor]	P23470	60	9,06	4
Receptor-type tyrosine-protein phosphatase kappa [Precursor]	Q15262	72	162,10	3
Receptor-type tyrosine-protein phosphatase U [Precursor]	Q92729	50	160,23	2
Recombining binding protein suppressor of hairless	Q06330	54	55,66	2
RecQ protein-like 5	Q6P4G0	40	106,05	1
Regulating synaptic membrane exocytosis protein 1	Q86UR5	113	189,07	7
Regulator of chromosome condensation	P18754	183	42,75	4
Regulator of G-protein signaling 12	O14924	61	156,36	4
Regulator of G-protein signaling 14	O43566	74	64,92	3
Regulator of G-protein signaling 20	O76081	44	43,69	1
Regulator of G-protein signaling 3	P49796	51	120,89	2
Regulator of G-protein signaling 3	Q5VXB8	49	67,24	2
Regulator of G-protein signaling 6	P49758	49	64,47	2
Regulator of G-protein signaling 9	O75916	73	76,78	4
Regulatory factor X domain-containing protein 2	Q2KHR2	85	146,90	3
Regulatory factor X, 5 variant [Fragment]	Q53EW3	51	65,27	3
Regulatory-associated protein of mTOR	Q8N122	50	148,94	3
Replication factor C subunit 1	P35251	64	128,26	2
Replication factor C subunit 4	P35249	99	39,64	3
Replication protein A 14 kDa subunit	P35244	60	13,56	1
Ret proto-oncogene	Q9BTB0	64	119,82	3
Reticulocalbin-1 [Precursor]	Q15293	127	38,87	4
Reticulon 2	Q6GMT0	51	59,32	2
Reticulon-3	O95197	46	112,61	2
Retinitis pigmentosa 1-like 1 protein	Q8IWN7	85	261,11	4
Retinoblastoma-binding protein 6	Q7Z6E9	52	102,16	2
Retinoic acid inducible in neuroblastoma cells RAINB1d	Q8TDE9	60	261,56	3
Retinoic acid-induced protein 1	Q7Z5J4	61	203,35	3
Retinol-binding protein I, cellular	P09455	165	15,84	7
Retrotransposon gag domain-containing protein 1	Q8NET4	111	144,28	5
RFC5 protein [Fragment]	Q6LES9	185	38,37	4
RFVG5814	Q6UXX8	46	21,16	2

Table 1. continued

Protein Name and Species	Accession	Score	MW [kDa]	# Pept.
RGD, leucine-rich repeat, tropomodulin and proline-rich containing protein [Fragment]	Q6F5E8	62	154,69	2
Rgr protein [Fragment]	Q3ZCN2	47	59,53	2
RGS12 protein [Fragment]	Q56A82	41	25,85	2
Rho GDP-dissociation inhibitor 1	P52565	432	23,06	9
Rho GTPase-activating protein 1	Q07960	154	50,40	3
Rho GTPase-activating protein 22	Q7Z5H3	46	76,78	2
Rho GTPase-activating protein 23	Q9P227	40	81,09	2
Rho GTPase-activating protein 24	Q8N264	46	84,26	2
Rho GTPase-activating protein 6	O43182	127	105,95	5
Rho GTPase-activating protein SYDE1	Q6ZW31	51	79,74	3
Rho guanine nucleotide exchange factor 1	Q92888	75	102,44	3
Rho guanine nucleotide exchange factor 12	Q9NZN5	68	173,23	3
Rho guanine nucleotide exchange factor 15	O94989	75	91,95	3
Rho guanine nucleotide exchange factor 17	Q96PE2	129	221,67	7
Rho-interacting, serine/threonine-protein kinase 21	O14578	49	178,53	3
Rhotekin	Q9BST9	80	62,67	4
Ribonuclease inhibitor	P13489	306	49,81	6
Ribonucleoprotein PTB-binding 1	Q8IY67	75	57,62	2
Ribonucleoside-diphosphate reductase [Fragment]	Q53GZ5	157	89,91	5
Ribose-phosphate pyrophosphokinase 2	P11908	87	34,75	3
Ribosomal L1 domain-containing protein 1	O76021	1217	34,18	16
Ribosomal protein L13	Q6NZ55	271	24,25	7
Ribosomal protein L14 variant [Fragment]	Q53G20	300	23,63	7
Ribosomal protein L22-like 1	Q6P5R6	49	14,60	1
Ribosomal protein L27a	Q6NZ52	83	16,47	2
Ribosomal protein L39 variant [Fragment]	Q59GN2	40	8,43	2
Ribosomal protein L7a [Fragment]	Q5T8U3	156	21,53	5
Ribosomal protein S10	Q5TZB9	42	19,86	2
Ribosomal protein S19 [Fragment]	Q8WVX7	242	17,27	5
Ribosomal protein S2	Q3KQT6	283	31,36	7
Ribosomal protein S27a	Q5RKT7	413	17,89	6
Ribosomal protein S6 kinase, 90kDa, polypeptide 2	Q5TI62	41	18,87	1
Ribosomal protein S6 kinase-like 1	Q9Y6S9	44	60,04	2
Ribosomal protein S6 modification-like protein A	Q8IXN7	48	42,86	2
Ribosome biogenesis regulatory protein homolog	Q15050	63	41,17	3
Ribosome-binding protein 1	Q9P2E9	53	152,47	2
Ribulose-phosphate 3-epimerase family protein	Q723F1	44	24,79	1
RING and PHD-finger domain-containing protein KIAA1542	Q9P1Y6	54	178,61	2
RING finger and WD repeat domain-containing protein 3	Q6PCD5	45	66,35	2
RING finger protein 208	Q9H0X6	40	19,40	2
RING finger protein C13orf7	Q5W0B1	75	81,12	5
RING finger protein C1orf164	Q5VTB9	43	62,73	2
RING finger protein unkempt homolog	Q9C0B0	67	88,08	3
RNA binding motif [Fragment]	Q13382	108	4,44	6
RNA binding motif protein 4	Q4VC48	617	40,29	10
RNA binding protein	Q9UQ35	157	299,50	8
RNA binding protein (Autoantigenic, hnRNP-associated with lethal yellow), long isoform	Q2M365	498	32,44	10
RNA binding protein [Fragment]	Q9UQ39	99	106,46	6
RNA exonuclease 1 homolog	Q8N1G1	92	131,53	4
RNA exonuclease 4	Q9GZR2	41	46,67	1
RNA polymerase II subunit A C-terminal domain phosphatase	Q9Y5B0	86	104,30	4
RNA polymerase II-associated protein 1	Q9BWH6	72	152,76	4
RNA-binding motif protein, Y chromosome, family 1 member A1	Q15414	48	55,78	2
RNA-binding protein 12	Q9NTZ6	124	100,10	5
RNA-binding protein 14	Q96PK6	469	69,48	10
RNA-binding protein 4B	Q9BQ04	352	40,12	7
RNA-binding protein 8A	Q9Y5S9	138	19,88	4
RNA-binding protein Musashi homolog 1	O43347	136	39,10	2
RNA-binding protein NOB1	Q9ULX3	75	46,65	2
RNA-binding Raly-like protein	Q86SE5	47	14,48	2
Rootletin	Q5TZA2	74	228,52	5
Rotatin	Q86VV8	51	248,57	2
Roundabout homolog 3 [Precursor]	Q96MS0	75	148,21	3
RPL26 protein	Q6IBH6	232	17,23	4
RPL29 protein	Q6IPI1	44	17,94	2
RPN1 protein	Q6IBR0	134	68,56	5
RPS21 protein	Q8WVC2	173	8,84	4
RTN4	Q7L7Q8	91	129,85	3
Runt-related transcription factor 1	Q01196	65	50,81	3
RuvB-like 1	Q9Y265	147	50,20	3

Table 1. continued

Protein Name and Species	Accession	Score	MW [kDa]	# Pept.
RuvB-like 2	Q9Y230	427	50,99	10
RWD domain-containing protein 4A	Q6NW29	42	21,24	1
Ryanodine receptor 1	P21817	51	564,81	4
Ryanodine receptor 2	Q92736	61	564,38	5
Ryanodine receptor 3	Q15413	88	551,93	4
Sacsin	Q9NZJ4	77	521,13	4
S-adenosylmethionine synthetase isoform type-2	P31153	98	43,63	2
SAFB-like transcription modulator	Q9NWH9	67	117,15	3
Sal-like protein 3	Q9BXA9	76	135,37	3
SAPS domain family, member 2	Q5U5P3	69	101,40	3
SAR1a gene homolog 1 (S. cerevisiae) (Small GTP-binding protein)	Q5SQT9	94	22,35	3
SASS6 protein	Q495U0	55	55,25	2
Scaffold attachment factor B1	Q15424	181	102,57	7
SCAN domain-containing protein 2	Q9GZW5	45	34,22	2
SCAP protein	Q6PIX8	60	38,19	2
Scavenger receptor class F member 2 [Precursor]	Q96GP6	53	91,72	3
Scavenger receptor cysteine-rich domain-containing group B protein [Precursor]	Q8WTU2	44	60,78	2
SCL protein	Q9NY94	69	34,53	3
Scm-like with four MBT domains protein 2	Q5VUG0	95	100,56	4
SCO-spondin homolog [Fragment]	Q76B61	44	139,62	2
SEC13-like 1, isoform b	Q5BJF0	206	35,52	4
SEC16 homolog A	O15027	51	233,37	4
Sec23 homolog B	Q503A9	175	86,44	5
SEC6-like protein C14orf73	Q17RC7	42	79,88	1
SECIS-binding protein 2	Q96T21	53	95,46	2
Secreted frizzled-related protein 4 [Precursor]	Q6FHJ7	77	49,53	3
Securin	O95997	47	22,02	2
Segment polarity protein dishevelled homolog DVL-1-like	P54792	42	73,25	2
Selenophosphate synthetase 1	Q5T5U8	280	42,88	4
Selenoprotein O	Q2TAL2	73	73,49	3
SEMA4C protein [Fragment]	Q6P5A5	64	59,99	3
Semaphorin-5B	Q9P283	64	131,07	3
Semaphorin-6C [Precursor]	Q9H3T2	49	99,68	3
Sentrin-specific protease 6	Q9GZR1	46	126,15	2
Septin-11	Q9NVA2	134	49,24	4
Septin-2	Q15019	1609	42,12	18
Septin-9	Q9UHD8	484	65,36	15
Serine hydroxymethyltransferase [Fragment]	Q5BJF5	126	52,88	4
Serine protease HTRA2 [Precursor]	O43464	338	48,81	8
Serine/arginine repetitive matrix protein 1	Q8IYB3	126	103,33	9
Serine/arginine repetitive matrix protein 2	Q9UQ35	122	299,50	8
Serine/threonine kinase 23	Q4F970	53	61,89	2
Serine/threonine phosphatase 1 gamma [Fragment]	Q9UPN1	769	33,75	13
Serine/threonine protein phosphatase (EC 3.1.3.16)	Q5U0A2	61	35,12	2
Serine/threonine protein phosphatase (EC 3.1.3.16)	Q6I9T8	547	35,53	10
Serine/threonine protein phosphatase [Fragment]	Q9BPW0	44	55,06	2
Serine/threonine-protein kinase LMTK3 [Precursor]	Q96Q04	44	155,86	3
Serine/threonine-protein kinase MRCK alpha	Q5VT25	41	194,12	2
Serine/threonine-protein kinase MRCK beta	Q9Y5S2	53	194,32	2
Serine/threonine-protein kinase N3	Q6P5Z2	83	99,42	3
Serine/threonine-protein kinase Nek1	Q96PY6	51	142,83	3
Serine/threonine-protein kinase Nek5	Q6P3R8	50	81,45	2
Serine/threonine-protein kinase OSR1	O95747	52	32,46	2
Serine/threonine-protein kinase PAK 4	O96013	82	64,07	4
Serine/threonine-protein kinase PLK1	P53350	52	68,25	2
Serine/threonine-protein kinase PLK4	O00444	65	108,97	3
Serine/threonine-protein kinase SMG1	Q96Q15	58	340,46	4
Serine/threonine-protein kinase ULK1	O75385	69	112,60	4
Serine/threonine-protein kinase ULK2	Q8IYT8	67	112,73	3
Serine/threonine-protein phosphatase 2B catalytic subunit alpha isoform	Q08209	79	57,62	3
Serine/threonine-protein phosphatase 4 catalytic subunit	P60510	225	35,06	4
Serine/threonine-protein phosphatase PP1-alpha catalytic subunit	P62136	863	37,49	14
Serine/threonine-protein phosphatase PP1-beta catalytic subunit	P62140	824	37,15	16
Serine\/arginine repetitive matrix 1	Q5VVN3	78	103,33	6
Serpin H1 [Precursor]	P50454	98	46,41	1
Serum albumin [Precursor]	P02768	173	69,32	4
Seryl-tRNA synthetase, cytoplasmic	P49591	73	58,61	2
SET and MYND domain-containing protein 5	Q6GMV2	51	47,34	3
SET domain-containing protein 5	Q9C0A6	117	157,52	6
SET translocation (Myeloid leukemia-associated) (SET translocation (Myeloid leukemia-associated) va	Q5VXV1	617	32,08	8
SET-binding protein	Q9Y6X0	68	169,63	3

Table 1. continued

Protein Name and Species	Accession	Score	MW [kDa]	# Pept.
Seven transmembrane helix receptor	Q8NGB0	40	156,51	2
Sex comb on midleg-like protein 4	Q8N228	41	38,56	2
SF3B2 protein [Fragment]	Q9BWD2	263	100,03	7
SFN protein	Q6FH51	144	27,76	4
S-formylglutathione hydrolase	P10768	71	10,96	1
SGTA protein (Small glutamine rich protein with tetratricopeptide repeats 1)	Q6FIA9	345	34,04	4
SH2 domain-containing adapter protein B	Q15464	60	55,04	3
SH2 domain-containing adapter protein E	Q5VZ18	55	53,95	2
SH3 and multiple ankyrin repeat domains protein 1	Q9Y566	109	225,02	6
SH3 and multiple ankyrin repeat domains protein 3	Q9BYB0	43	186,30	2
SH3 and PX domain-containing protein 2A	Q5TCZ1	68	125,29	3
SH3 domain and tetratricopeptide repeats-containing protein 1	Q8TE82	64	146,93	3
SH3 domain-binding glutamic acid-rich-like protein	O75368	95	12,77	2
SH3 multiple domains protein 4 [Precursor]	Q8TEJ3	49	92,78	2
SH3-domain kinase binding protein 1	Q5VSN0	51	61,43	2
SH3KBP1-binding protein 1	Q8TBC3	45	76,34	2
SHC (Src homology 2 domain containing) transforming protein 3	Q5T7I7	54	64,02	2
Short coiled-coil protein	Q6P5T9	46	13,85	1
Short stature homeobox protein 2	O60902	58	34,95	2
Short-chain specific acyl-CoA dehydrogenase [Precursor]	P16219	47	44,30	3
SIAH1 protein	Q49A58	58	31,10	2
Siah-interacting protein (SIP)	Q5R370	412	21,21	6
Sialic acid synthase	Q9NR45	91	40,28	2
Sialic acid-binding Ig-like lectin 10 [Precursor]	Q96LC7	79	76,59	3
Sialidase-4	Q8WWR8	104	8,79	5
Sialoadhesin [Precursor]	Q9BZZ2	57	182,62	2
Sickle tail protein homolog	Q5T5P2	93	95,09	5
SID1 transmembrane family member 2 [Precursor]	Q8NBJ9	46	94,45	2
Sideroflexin-1	Q9H9B4	126	35,47	4
Sideroflexin-3	Q9BWM7	71	35,48	2
Signal recognition particle 14kD	Q96Q14	107	14,50	2
Signal recognition particle 68 kDa protein	Q9UHB9	40	70,20	2
Signal recognition particle 9 kDa protein	P49458	77	9,97	3
Signal recognition particle receptor, beta subunit	Q6P595	52	29,70	1
Signal-induced proliferation-associated 1-like protein 2	Q9P2F8	41	190,44	2
Signal-induced proliferation-associated 1-like protein 3	O60292	55	194,49	2
Signal-induced proliferation-associated protein 1	Q96FS4	53	112,15	2
Similar to LOC149651	Q8TB00	57	8,44	3
Similar to phospholipase C, beta 3 (Phosphatidylinositol-specific) [Fragment].- Homo sapiens (Human	Q8N1A4	79	133,42	5
Similar to polycystic kidney disease 1-like 3	A4D236	41	74,44	2
Similar to portion of neuronal pentraxin i NPX1 or NP1	Q96A99	59	52,34	3
Single-stranded DNA binding protein 1	Q567R6	125	17,35	3
Ski oncogene	P12755	40	80,01	1
SLAIN motif-containing protein 2	Q9P270	59	62,54	3
SLC12A1 protein	Q8IUN5	41	46,48	1
SLC4A2 protein	Q6PJY3	66	119,96	2
Slit homolog 1	Q5VW18	46	159,66	2
SLIT-ROBO Rho GTPase-activating protein 1	Q7Z6B7	47	72,88	2
Slp homolog lacking C2 domains b	Q8NEV8	61	222,41	4
Small G protein signaling modulator 2	O43147	57	113,29	2
Small glutamine-rich tetratricopeptide repeat-containing protein A	O43765	160	37,50	4
Small nuclear ribonucleoprotein F	P62306	46	9,70	1
Small nuclear ribonucleoprotein Sm D1	Q7Z5A3	150	13,28	2
Small nuclear ribonucleoprotein Sm D2	P62316	158	13,52	5
Small nuclear ribonucleoprotein Sm D3	P62318	181	13,91	3
Small nuclear ribonucleoprotein-associated proteins B and B'	P14678	99	9,44	2
Small subunit processome component 20 homolog	O75691	62	318,22	3
SMARCA4 isoform 2	Q9HBD4	75	188,03	2
Smoothelin	P53814	72	98,89	3
Smoothened homolog	A4D1K5	55	86,34	2
SMRTE-tau	Q56D06	75	268,46	3
Sn1-specific diacylglycerol lipase alpha	Q9Y4D2	51	114,88	3
SNAP-25-interacting protein	Q75T46	55	127,01	4
SNAP-25-interacting protein	Q75T46	87	127,09	4
SNF-related serine/threonine-protein kinase	Q9NRH2	45	84,22	2
snRNA-activating protein complex subunit 4	Q5SXM2	73	159,32	4
SNW domain-containing protein 1	Q13573	64	61,46	4
SNX6 protein	Q9BUY3	86	33,57	2
Sodium- and chloride-dependent GABA transporter 2	Q9NSD5	69	63,75	3
Sodium channel protein type 1 subunit alpha	P35498	69	228,97	3
Sodium channel protein type 4 subunit alpha	P35499	58	208,03	2

Table 1. continued

Protein Name and Species	Accession	Score	MW [kDa]	# Pept.
Sodium/bile acid cotransporter 5 [Precursor]	Q5PT55	49	48,87	2
Sodium/hydrogen exchanger 3	P48764	50	92,91	2
Sodium/iodide cotransporter	Q92911	42	68,67	2
Sodium/potassium/calcium exchanger 4 [Precursor]	Q8NFF2	41	18,42	1
Sodium/potassium-transporting ATPase gamma chain	P54710	60	10,26	5
Sodium/potassium-transporting ATPase subunit beta-1-interacting protein 1	Q4KMZ8	45	23,29	2
Solute carrier family 12 member 5	Q9H2X9	43	126,18	2
Solute carrier family 12 member 9	Q9BXP2	41	96,11	2
Solute carrier family 25, member 13 (Citrin) variant [Fragment]	Q53GR7	92	74,07	3
Solute carrier family 34 (Sodium phosphate), member 1	Q7Z725	45	68,83	2
Solute carrier family 37 (glycerol-3-phosphate transporter), member 2	Q8TED4	65	54,44	2
Somatostatin receptor type 3	P32745	57	45,85	2
Son of sevenless homolog 2	Q17RN1	61	152,98	3
SON protein	P18583	66	263,85	3
Sorbin and SH3 domain containing 1	Q5T924	63	142,51	3
Sorbitol dehydrogenase	Q00796	542	38,14	10
SORBS2 protein	Q96EX0	43	71,86	2
Sorcin	P30626	190	21,66	4
Sorting nexin-3	O60493	43	18,62	2
Special AT-rich sequence binding protein 1 variant [Fragment]	Q59EQ0	43	89,33	3
Specifically androgen-regulated gene protein	Q9BW04	40	63,97	2
Spectrin alpha chain, brain	Q13813	143	284,11	4
Spectrin beta chain, brain 1	Q01082	176	251,26	5
Spectrin beta chain, brain 2	O15020	49	54,68	2
Spectrin beta chain, brain 3	Q9H254	69	288,81	3
Spectrin beta chain, brain 4	Q9NRC6	55	416,84	2
Sperm antigen with calponin homology and coiled-coil domains 1	Q5M775	54	118,59	2
Sperm-associated antigen 17	Q6Q759	43	251,74	2
Sperm-associated antigen 4-like protein	Q8TC36	53	43,08	2
Spermatogenesis and oogenesis specific basic helix-loop-helix 1 [Fragment]	Q5JUK2	62	34,49	2
Spermatogenesis-associated protein 16	Q9BXB7	42	65,23	2
Spermatogenesis-associated protein 20 [Precursor]	Q8TB22	43	87,93	3
Spermatogenesis-associated protein 2-like protein	Q8IUW3	55	17,05	2
Spermatogenesis-associated protein 3	Q8NHX4	65	19,95	4
Spermatogenesis-associated protein 5	Q8NB90	45	97,89	2
Spermidine synthase	P19623	134	33,80	5
Spermine synthase	P52788	160	39,47	3
S-phase kinase-associated protein 1	P63208	119	18,52	2
S-phase kinase-associated protein 2	Q13309	43	47,76	2
Sphingomyelin phosphodiesterase 4	Q9NXE4	40	93,35	2
Sphingosine 1-phosphate receptor Edg-8	Q9H228	52	41,78	2
Sphingosine kinase 1	Q8N632	67	51,08	3
Spindle assembly abnormal protein 6 homolog	Q6UVJ0	53	74,40	2
SPINT2 protein [Fragment]	Q6LEU8	46	28,24	2
Spliceosome RNA helicase BAT1	Q13838	494	48,99	10
Splicing factor 1	Q15637	135	68,15	5
Splicing factor 3 subunit 1	Q15459	90	88,83	3
Splicing factor 3a, subunit 3 variant [Fragment]	Q53HM6	113	58,84	3
Splicing factor 3B subunit 3	Q15393	270	139,41	6
Splicing factor prolin/glutamin rich [Fragment]	Q9BSV4	120	68,59	3
Splicing factor proline/glutamine-rich	Q86VG2	725	76,14	12
Splicing factor U2AF 35 kDa subunit	Q01081	190	27,72	4
Splicing factor, arginine/serine-rich 1	Q07955	498	27,60	15
Splicing factor, arginine/serine-rich 16	Q8N2M8	42	75,21	2
Splicing factor, arginine/serine-rich 19	Q9H7N4	82	139,27	5
Splicing factor, arginine/serine-rich 2	Q01130	142	25,33	3
Splicing factor, arginine/serine-rich 2B	Q9BRL6	52	31,38	2
Splicing factor, arginine/serine-rich 5	Q13243	46	31,26	1
Splicing factor, arginine/serine-rich 6	Q13247	51	39,56	1
Splicing factor, arginine/serine-rich 7	Q16629	389	13,24	9
Splicing factor, arginine/serine-rich 9	Q13242	210	25,53	6
Splicing factor, proline- and glutamine-rich	P23246	846	76,10	16
SRA stem-loop-interacting RNA-binding protein [Precursor]	Q9GZT3	71	10,93	2
Stabilin-1 [Precursor]	Q9NY15	54	275,48	2
Stathmin	P16949	463	17,16	9
Stathmin-2	Q93045	66	20,83	2
STE20-like serine/threonine-protein kinase	Q9H2G2	48	138,91	3
Sterile alpha motif domain-containing protein 4A	Q9UPU9	48	58,61	2
Steroidogenic acute regulatory protein [Precursor]	P49675	94	31,91	6
Steroidogenic factor 1	Q13285	54	51,64	1
Sterol regulatory element binding transcription factor 1	Q6P4R7	52	121,68	3
Sterol regulatory element-binding protein 1	P36956	44	12,68	2

Table 1. continued

Protein Name and Species	Accession	Score	MW [kDa]	# Pept.
Sterol-4-alpha-carboxylate 3-dehydrogenase, decarboxylating	Q15738	133	41,87	3
STIP1 homology and U box-containing protein 1	Q9UNE7	114	34,77	2
Stomatin (EPB72)-like 2 variant [Fragment]	Q53G29	524	38,52	8
Stomatin-like protein 2	Q9UJZ1	522	38,49	8
Storkhead-box protein 1	Q6ZVD7	67	110,96	2
Stress-70 protein [Precursor]	P38646	431	73,68	9
Stress-induced-phosphoprotein 1	P31948	471	62,60	15
Striated muscle preferentially expressed protein kinase	Q15772	146	348,69	9
Stromal RNA regulating factor	Q5JB52	55	56,47	2
Structural maintenance of chromosomes flexible hinge domain-containing protein 1	Q6AHX6	52	226,37	2
Structural maintenance of chromosomes protein 1A	Q14683	55	143,23	2
Structural maintenance of chromosomes protein 5	Q8IY18	47	128,81	1
Structural maintenance of chromosomes protein 6	Q96SB8	71	126,33	3
Structure protein NSP5b3b	Q5IBP1	76	118,32	4
Succinate dehydrogenase [ubiquinone] flavoprotein subunit [Precursor]	P31040	107	72,65	4
Succinate-CoA ligase, ADP-forming, beta subunit	Q5T9Q4	50	50,29	1
Succinyl-CoA ligase [GDP-forming] beta-chain [Precursor]	Q96I99	52	21,29	1
SUMO-activating enzyme subunit 1	Q9UBE0	239	38,43	5
SUMO-activating enzyme subunit 2	Q9UBT2	163	71,18	5
Superoxide dismutase [Cu-Zn]	P00441	84	15,93	1
Supervillin	O95425	55	200,72	3
Suppression of tumorigenicity 7 like	Q5SP56	51	60,82	2
Suppression of tumorigenicity protein 18	O60284	41	115,16	2
Suppressor of G2 allele of SKP1 homolog	Q9Y2Z0	65	40,87	1
Surfactant protein A-binding protein	Q15509	78	31,82	3
Surfeit locus protein 1	Q15526	41	33,31	1
Sushi, nidogen and EGF-like domain-containing protein 1 [Precursor]	Q8TER0	43	152,20	2
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin c2 isoform b variant [Fragment]	Q59G16	149	127,30	7
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily C member 1	Q92922	142	122,68	9
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily C member 2	Q8TAQ2	75	53,93	4
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily E member 1	Q969G3	60	46,65	5
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily E member 1-related	Q9P0W2	52	35,81	2
Synapsin-3	O14994	47	63,30	4
Synaptic vesicle membrane protein VAT-1 homolog	Q99536	40	33,72	1
Synaptojanin-1	O43426	45	173,35	2
Synaptopodin	Q8N3V7	41	99,46	2
Synaptopodin-2	Q9UMS6	55	117,44	2
Synaptotagmin-3	Q9BQG1	61	63,30	2
Synaptotagmin-like protein 4	Q96C24	55	76,01	3
Synaptotagmin-like protein 5	Q8TDW5	75	81,52	5
Synemin	Q8TE61	45	172,38	2
SYNJ1 protein	Q4KMR1	43	58,07	2
Syntaxin-binding protein 5	Q5T5C0	47	127,57	3
T calcium channel alpha 1G subunit variant 184	Q19R04	86	244,25	4
TAF15 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 68kDa	Q86X94	66	52,03	2
TAF5 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 100kDa	Q5SYD5	50	86,78	2
TAF6 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 80kDa	A4D2B2	105	72,62	7
TAFII105-E9	Q29YA4	54	63,32	2
TALDO1 protein [Fragment]	Q8WV32	357	37,39	9
Talin-1	Q9Y490	69	269,60	4
Talin-2	Q9Y4G6	49	202,86	2
TAR DNA binding protein variant [Fragment]	Q53H27	209	44,64	2
TATA box-binding protein-like protein 1	P62380	41	20,87	1
Tau-tubulin kinase	Q8IWY7	53	182,47	2
TBC1 domain family member 12	O60347	66	84,87	3
TBC1 domain family member 22A	Q8WUA7	50	59,12	2
TBC1 domain family member 5	Q92609	67	88,95	3
TC10/CDC42 GTPase-activating protein	O14559	46	31,23	2
T-cell receptor alpha chain V region HPB-MLT [Precursor] [Fragment]	P04436	53	14,77	2
T-cell receptor alpha chain V region PY14 [Precursor]	P01737	41	14,71	1
T-cell receptor beta chain V region CTL-L17 [Precursor]	P04435	56	8,50	3
TCOF1 protein [Fragment]	Q7Z5W9	55	113,52	2
T-complex protein 1 subunit alpha	P17987	738	60,31	15

Table 1. continued

Protein Name and Species	Accession	Score	MW [kDa]	# Pept.
T-complex protein 1 subunit beta	P78371	316	57,32	6
T-complex protein 1 subunit delta	P50991	253	57,76	7
T-complex protein 1 subunit epsilon	P48643	248	59,63	8
T-complex protein 1 subunit eta	Q99832	248	59,33	7
T-complex protein 1 subunit gamma	P49368	229	60,29	6
T-complex protein 1 subunit theta	P50990	719	59,45	16
T-complex protein 1 subunit zeta	P40227	185	57,86	7
T-complex protein 1 subunit zeta-2	Q92526	53	57,60	2
T-complex protein 10A homolog	Q12799	60	45,47	2
TDRD1 protein [Fragment]	Q4G0Y8	68	131,97	3
Telomerase reverse transcriptase	O14746	50	127,00	2
Telomere-associated protein RIF1	Q5UIP0	58	274,47	3
Tenascin XB [Fragment]	Q5JNX3	43	358,55	2
Tenascin-N [Precursor]	Q9UQP3	46	144,03	2
Tenascin-X [Precursor]	P22105	74	464,46	5
TENC1 protein [Fragment]	Q2NL80	89	139,41	4
Teneurin-1	Q9UKZ4	51	305,01	2
Teneurin-4	Q6N022	116	44,50	8
Tensin 3	Q8IZW7	57	155,18	2
Tensin 3 variant [Fragment]	Q59GW4	65	136,24	3
Tensin-1	Q9HBL0	50	185,59	2
Tensin-4 [Precursor]	Q8IZW8	62	76,90	2
TESK1 protein	Q8IXZ8	46	67,68	3
Testin	Q9UGI8	87	47,96	2
Testis specific basic protein	Q13647	60	63,32	2
Testis-expressed sequence 13A protein	Q9BXU3	43	45,58	2
Testis-expressed sequence 2 protein	Q8IWB9	57	125,30	4
Testis-expressed sequence 264 protein [Precursor]	Q9Y6I9	49	12,94	2
Tether containing UBX domain for GLUT4	Q9BZE9	56	60,18	2
Tetraspanin-10	Q9H1Z9	62	36,49	3
Tetratricopeptide repeat protein 15	Q8WVT3	61	22,81	4
Tetratricopeptide repeat protein 21A	Q8NDW8	48	150,92	2
Tetratricopeptide repeat protein 22	Q5TAA0	67	63,36	2
Tetratricopeptide repeat protein 28	Q96AY4	46	270,71	2
Tetratricopeptide repeat, ankyrin repeat and coiled-coil-containing protein 1 [Fragment]	Q9C0D5	61	179,31	7
TGS2	Q8IWQ1	80	60,07	4
Thimet oligopeptidase	P52888	110	78,79	6
Thioredoxin	P10599	103	11,60	6
Thioredoxin domain containing 4	Q4VXC1	85	46,94	1
Thioredoxin domain containing 5	Q5TCQ0	167	47,60	3
Thioredoxin domain-containing protein 17	Q9BRA2	100	13,93	2
Thioredoxin domain-containing protein 2	Q86VQ3	46	60,46	2
Thioredoxin domain-containing protein 5 [Precursor]	Q8NBS9	139	47,60	3
Thioredoxin reductase 1, cytoplasmic	Q16881	78	63,92	3
Thioredoxin-like 3	Q5JV01	159	37,41	4
Thioredoxin-like protein 1	O43396	169	32,10	3
Thiosulfate sulfurtransferase	Q16762	168	32,95	5
THO complex subunit 4	Q86V81	192	26,74	4
THO complex subunit 6 homolog	Q86W42	99	32,90	3
Threonine aspartase 1	Q9H6P5	72	44,46	3
Threonyl-tRNA synthetase variant [Fragment]	Q53GX7	253	83,39	8
Thrombospondin type-1 domain-containing protein 4 [Fragment]	Q6ZMP0	80	112,45	3
Thromboxane A2 receptor	P21731	177	40,09	8
Thymidine kinase, cytosolic	P04183	66	25,48	2
Thymidylate kinase	P23919	42	23,82	2
Thymus expressed gene 3-like	Q96B18	50	41,43	2
Thyroglobulin [Precursor]	P01266	41	304,79	2
Thyroglobulin variant [Fragment]	Q59GF0	46	173,07	2
Thyroid hormone receptor interactor 12	Q14669	45	59,27	3
Thyroid hormone receptor-associated protein 3	Q9Y2W1	111	108,63	5
Thyroid receptor-interacting protein 11	Q15643	62	227,64	3
Thyroid receptor-interacting protein 13	Q15645	202	48,52	5
Titin	Q8WZ42	276	3813,84	25
Titin	Q0Y6L9	87	631,57	4
T-lymphoma invasion and metastasis-inducing protein 1	Q13009	97	177,53	5
TMEM181 protein [Fragment]	Q8N4V6	94	59,38	5
TMEM43 protein [Fragment]	Q7L4N5	169	35,64	3
TMOD2 protein	Q4G0W6	72	34,50	1
TNRC11 protein	Q7Z3Z5	60	226,32	3
Toll-like receptor 5 [Precursor]	O60602	54	97,80	2
TRAF2 and NCK-interacting protein kinase	Q9UKE5	62	154,94	2

Table 1. continued

Protein Name and Species	Accession	Score	MW [kDa]	# Pept.
Trafficking kinesin-binding protein 1	Q9UPV9	44	106,04	2
Transaldolase	P37837	124	9,37	3
Transcription elongation factor A protein 1	P23193	209	33,95	8
Transcription elongation factor B polypeptide 1	Q15369	76	12,47	1
Transcription elongation regulator 1	O14776	161	121,61	8
Transcription elongation regulator 1, isoform 2	Q2NKN2	41	121,61	1
Transcription factor 12	Q99081	41	57,07	1
Transcription factor COE4	Q9BQW3	50	64,47	2
Transcription factor EB	P19484	40	56,65	1
Transcription factor IIIA	Q92664	42	41,52	2
Transcription factor IIIB 90 kDa subunit	Q92994	62	74,34	2
Transcription factor p65	Q04206	48	60,22	3
Transcription factor PAX4	Q1W386	58	28,37	2
Transcription factor RelB	Q01201	82	62,13	4
Transcription factor SOX-11	P35716	78	46,65	2
Transcription factor SOX-30	O94993	65	81,80	2
Transcription factor Sp1	P08047	53	80,69	2
Transcription initiation factor IIF subunit beta	P13984	88	26,29	1
Transcription initiation factor TFIID 210 kDa subunit	Q8IZX4	43	207,30	2
Transcription initiation factor TFIID subunit 1	P21675	47	212,68	2
Transcription initiation factor TFIID subunit 3	Q5VWG9	65	103,58	3
Transcription initiation factor TFIID subunit 4	O00268	68	110,11	3
Transcription intermediary factor 1-beta	Q13263	484	88,36	12
Transcription regulator protein BACH2	Q9BYV9	41	94,11	1
Transcription termination factor 2	Q9UNY4	42	129,59	2
Transcriptional activator protein Pur-beta	Q96QR8	315	33,09	5
Transcriptional adapter 2-like	O75478	82	51,50	3
Transcriptional regulator ATRX	P46100	65	282,57	4
Transducin (Beta)-like 3	Q8IVB7	69	88,94	3
Transducin-like enhancer of split 3 splice variant 1	Q6PRX3	41	82,61	3
Transducin-like enhancer protein 3	Q04726	63	83,30	2
Transferrin receptor protein 1	P02786	74	84,85	3
Transformation-related protein 4	Q56VW5	53	14,17	2
Transforming acidic coiled-coil-containing protein 2	O95359	46	309,43	2
Transforming growth factor beta-1-induced transcript 1 protein	O43294	74	49,81	3
Transgelin-2	P37802	235	22,25	9
Transglutaminase 2	Q6B838	84	77,28	3
Transient receptor potential cation channel subfamily M member 4	Q8TD43	82	134,30	3
Transient receptor potential cation channel subfamily M member 7	Q96QT4	51	212,70	3
Transient receptor potential cation channel subfamily V member 3	Q8NET8	40	90,64	1
Transitional ER ATPase	P55072	874	89,13	25
Transketolase	P29401	347	49,88	10
Translin variant [Fragment]	Q53GR3	86	26,25	2
Translocon-associated protein subunit alpha [Precursor]	P43307	140	29,26	2
Translocon-associated protein subunit delta [Precursor]	P51571	52	16,24	1
Transmembrane and coiled-coil domains protein 2	O75069	59	77,45	3
Transmembrane channel-like protein 2	Q8TDI7	52	100,97	2
Transmembrane channel-like protein 5	Q6UXY8	91	114,77	4
Transmembrane protease, serine 13	Q9BYE2	64	62,68	4
Transmembrane protease, serine 9	Q7Z410	54	114,02	2
Transmembrane protein 108 [Precursor]	Q6UXF1	45	49,18	1
Transmembrane protein 109 [Precursor]	Q9BVC6	75	21,84	1
Transmembrane protein 128	Q5BJH2	73	15,74	3
Transmembrane protein 132E [Precursor]	Q6IEE7	46	107,09	2
Transmembrane protein 2	Q9UHN6	46	154,37	2
Transmembrane protein 33	P57088	72	27,93	2
Transmembrane protein 8 [Precursor]	Q9HCN3	43	76,23	2
Treacle protein	Q13428	161	144,23	7
Tribbles homolog 3	Q96RU7	53	39,54	2
Trichohyalin	Q07283	46	247,08	2
Trifunctional enzyme subunit beta [Precursor]	P55084	543	51,26	16
Trifunctional purine biosynthetic protein adenosine-3	P22102	229	107,70	7
Trinucleotide repeat-containing gene 18 protein	O15417	66	314,52	2
TRIO and F-actin-binding protein	Q9H2D6	86	261,38	5
Triosephosphate isomerase	P60174	1022	26,52	15
Tripartite motif family-like protein 2	Q8N7C3	47	43,98	2
Tripartite motif-containing 3	Q4V9L4	48	80,83	2
Tripartite motif-containing protein 14	Q14142	77	49,77	4
Tripartite motif-containing protein 22	Q8IYM9	54	56,95	2
Tripartite motif-containing protein 35	Q9UPQ4	44	57,70	2
Tripartite motif-containing protein 41	Q8WV44	59	71,62	3
Tripartite motif-containing protein 47	Q96LD4	57	69,53	3

Table 1. continued

Protein Name and Species	Accession	Score	MW [kDa]	# Pept.
Tripartite motif-containing protein 9	Q9C026	46	79,13	2
Tripeptidyl-peptidase 2	P29144	64	138,13	2
Tripeptidyl-peptidase I variant [Fragment]	Q53HP2	247	61,17	3
Triple functional domain protein	O75962	53	341,62	3
TRM112-like protein	Q9UI30	131	14,19	3
tRNA (cytosine-5-)-methyltransferase NSUN2	Q08J23	106	76,37	4
tRNA-dihydrouridine synthase 3-like	Q96G46	58	72,59	3
Tropomodulin 4 (Muscle)	Q5JR83	84	39,31	1
Tropomyosin 1 alpha variant 6	Q1ZYL5	233	28,49	6
Tropomyosin 3	Q5VU71	385	28,85	10
Tropomyosin alpha-1 chain	P09493	152	32,60	4
Tropomyosin alpha-4 chain	P67936	411	28,37	10
Tryptase gamma [Precursor]	Q9NRR2	44	33,81	1
TSHR [Fragment]	Q9ULA3	45	6,33	1
TSNARE1 protein [Fragment]	Q6P186	40	33,42	2
Tubby-related protein 1	O00294	66	60,67	3
TUBG1 protein [Fragment]	Q53X79	139	51,14	3
Tubulin alpha 6 variant [Fragment]	Q53GA7	518	49,79	10
Tubulin alpha-1A chain	Q71U36	1136	50,13	19
Tubulin alpha-1B chain	P68363	1139	50,12	18
Tubulin alpha-3E chain	Q6PEY2	751	49,88	11
Tubulin alpha-4 chain	Q9H853	43	105,55	1
Tubulin alpha-4A chain	P68366	832	49,76	15
Tubulin alpha-8 chain	Q9NY65	607	50,06	11
Tubulin beta polypeptide	Q5JP53	377	47,74	10
Tubulin beta-2A chain	Q13885	251	49,88	7
Tubulin beta-2B chain	Q9BVA1	1124	49,92	33
Tubulin beta-2C chain	P68371	204	9,30	6
Tubulin beta-4 chain	P04350	866	49,60	26
Tubulin beta-6 chain	Q9BUF5	374	49,83	16
Tubulin-specific chaperone A	O75347	168	12,72	5
Tubulin-specific chaperone D	Q9BTW9	59	138,56	3
Tubulin--tyrosine ligase-like protein 12	Q14166	73	74,36	3
Tudor domain-containing protein 5	Q8NAT2	53	109,74	2
Tudor domain-containing protein 6	O60522	43	236,52	2
Tumor necrosis factor receptor superfamily member 10A [Precursor]	O00220	43	50,06	2
Tumor protein D52-like 2 isoform e variant [Fragment]	Q53GA0	130	22,25	4
Tumor protein p53-inducible protein 13	Q8NBR0	72	42,24	3
Tumor protein, translationally-controlled 1	Q5W0H4	54	21,51	2
Tumor rejection antigen (Gp96) 1	Q5CAQ5	1140	92,28	26
Tumor suppressor p53-binding protein 1	Q12888	66	213,57	4
Twinfilin-1	Q12792	104	42,18	5
Twinfilin-2	Q6IBS0	693	39,55	9
Type II hair keratin 2	Q701L7	58	56,61	2
TYRO protein tyrosine kinase-binding protein [Precursor]	O43914	60	12,18	3
Tyrosine-protein kinase BTK	Q06187	46	76,28	2
Tyrosine-protein kinase JAK3	P52333	66	125,10	3
Tyrosine-protein kinase receptor TYRO3 [Precursor]	Q06418	47	30,80	1
Tyrosine-protein kinase ZAP-70	P43403	41	69,87	2
Tyrosine-protein phosphatase non-receptor type 23	Q9H3S7	42	27,76	2
Tyrosyl-tRNA synthetase, cytoplasmic	P54577	150	58,98	4
U1 small nuclear ribonucleoprotein 70 kDa	P08621	211	51,53	8
U1 small nuclear ribonucleoprotein A	P09012	125	31,13	2
U2 small nuclear RNA auxiliary factor 2	Q96HC5	70	53,09	2
U2-associated protein SR140	O15042	55	118,29	3
U3 small nucleolar RNA-associated protein 14 homolog C	Q5TAP6	51	87,19	2
U3 small nucleolar RNA-interacting protein 2	O43818	42	51,81	2
U4/U6 small nuclear ribonucleoprotein Prp3	O43395	66	77,36	3
U4/U6.U5 tri-snRNP-associated protein 1	O43290	108	90,20	5
U5 small nuclear ribonucleoprotein 200 kDa helicase	O75643	83	244,35	3
U6 snRNA-associated Sm-like protein LSm3	P62310	75	11,71	2
U6 snRNA-associated Sm-like protein LSm8	O95777	157	10,27	3
U7 snRNA-associated Sm-like protein LSm11	P83369	85	39,50	3
UBE2Z protein [Fragment]	Q7L354	240	27,43	7
Ubiquilin 1	Q5T6J5	74	59,18	1
Ubiquilin-3	Q9H347	48	72,68	2
Ubiquinone biosynthesis protein COQ9 [Precursor]	O75208	94	35,84	1
Ubiquitin	P62988	317	68,45	5
Ubiquitin carboxyl-terminal hydrolase	Q5BKT5	90	62,64	4
Ubiquitin carboxyl-terminal hydrolase 14	P54578	67	55,90	1
Ubiquitin carboxyl-terminal hydrolase 19	O94966	57	145,65	3
Ubiquitin carboxyl-terminal hydrolase 2	O75604	40	68,07	2

Table 1. continued

Protein Name and Species	Accession	Score	MW [kDa]	# Pept.
Ubiquitin carboxyl-terminal hydrolase 24	Q9UPU5	64	211,07	3
Ubiquitin carboxyl-terminal hydrolase 25	Q9UHP3	58	125,75	2
Ubiquitin carboxyl-terminal hydrolase 31	Q70CQ4	107	146,54	6
Ubiquitin carboxyl-terminal hydrolase 34	Q70CQ2	45	387,12	2
Ubiquitin carboxyl-terminal hydrolase 35	Q9P2H5	55	113,35	2
Ubiquitin carboxyl-terminal hydrolase 36	Q9P275	57	122,65	3
Ubiquitin carboxyl-terminal hydrolase 5	P45974	205	93,25	5
Ubiquitin carboxyl-terminal hydrolase L5 [Fragment]	Q5LJB1	45	18,26	2
Ubiquitin carboxyl-terminal hydrolase L5 [Fragment]	Q5LJA3	69	25,32	1
Ubiquitin conjugation factor E4 B	O95155	74	146,19	4
Ubiquitin domain-containing protein 1	Q9HAC8	88	8,56	2
Ubiquitin domain-containing protein UBFD1	O14562	41	5,79	2
Ubiquitin fusion degradation protein 1 homolog	Q92890	219	38,70	3
Ubiquitin thioesterase OTUB1	Q96FW1	267	31,26	4
Ubiquitin-activating enzyme E1	P22314	968	117,77	19
Ubiquitin-activating enzyme E1-like protein 2	A0AVT1	40	117,97	2
Ubiquitin-associated protein 2	Q5T6F2	42	117,12	2
Ubiquitin-conjugating enzyme E2 N	P61088	244	17,13	4
Ubiquitin-conjugating enzyme E2 variant 1	Q13404	84	25,80	4
Ubiquitin-conjugating enzyme E2 variant 2	Q15819	70	14,03	3
Ubiquitin-conjugating enzyme E2C (UBE2C protein)	Q5TZN3	46	19,64	1
Ubiquitin-conjugating enzyme E2N-like	Q5JXB2	97	17,37	2
Ubiquitin-like domain-containing CTD phosphatase 1	Q8WVY7	67	36,78	3
Ubiquitous mitochondrial creatine kinase variant [Fragment]	Q53FC4	85	46,94	1
Ubiquitously transcribed Y chromosome tetratricopeptide repeat protein	O14607	85	8,68	4
UBX domain-containing protein 1	Q9BZV1	51	49,72	2
UBX domain-containing protein 5	Q5T124	43	57,37	2
UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 3	Q9Y2A9	58	42,53	3
UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 4	Q9C0J1	53	42,31	3
UK114 protein	Q6IBG0	64	14,48	1
UMP-CMP kinase (UMP-CMPK)	Q5SVZ1	107	18,97	2
UNC13B variant protein [Fragment]	Q4LE73	57	183,98	2
UNC45 homolog A	Q9H3U1	47	103,08	2
Uncharacterized protein C10orf64	Q6ZS81	56	114,92	2
Uncharacterized protein C10orf90	Q96M02	57	77,91	3
Uncharacterized protein C10orf95	Q9H7T3	66	26,27	3
Uncharacterized protein C11orf16	Q9NQ32	53	44,37	2
Uncharacterized protein C11orf2	Q9UID3	45	78,62	2
Uncharacterized protein C11orf48	Q9BQE6	49	31,57	2
Uncharacterized protein C11orf81	Q6ZV59	78	38,01	3
Uncharacterized protein C12orf26	Q8N6Q8	47	68,21	2
Uncharacterized protein C12orf28 [Precursor]	Q96LU7	47	127,56	2
Uncharacterized protein C12orf45	Q8N5I9	58	20,47	2
Uncharacterized protein C13orf3	Q8IX90	56	43,95	3
Uncharacterized protein C14orf33	Q86SY8	43	16,74	2
Uncharacterized protein C14orf44	Q96MY7	48	73,60	2
Uncharacterized protein C15orf37 [Fragment]	Q96AL6	68	20,75	2
Uncharacterized protein C15orf39	Q6ZRI6	56	110,79	3
Uncharacterized protein C15orf42	Q7Z2Z1	93	210,86	4
Uncharacterized protein C17orf56	Q96N21	89	55,14	4
Uncharacterized protein C18orf58	Q8NAR6	75	44,64	3
Uncharacterized protein C19orf19	Q3SX64	41	30,78	1
Uncharacterized protein C19orf21	Q8IVT2	91	75,36	4
Uncharacterized protein C19orf43	Q9BQ61	65	18,42	3
Uncharacterized protein C19orf64	Q8N7K9	61	59,86	3
Uncharacterized protein C1orf106	Q3KP66	74	72,86	3
Uncharacterized protein C1orf159 [Precursor]	Q96HA4	62	40,28	3
Uncharacterized protein C1orf172	Q8NAX2	48	43,64	2
Uncharacterized protein C1orf175	Q68CQ1	65	141,51	3
Uncharacterized protein C1orf185	Q5T7R7	69	22,41	5
Uncharacterized protein C1orf210	Q8IVY1	63	12,02	3
Uncharacterized protein C1orf26	Q5T5J6	69	103,22	3
Uncharacterized protein C1orf43	Q9BWL3	80	28,78	5
Uncharacterized protein C20orf160	Q9NUG4	48	62,18	2
Uncharacterized protein C20orf174	Q5JPB2	61	177,95	3
Uncharacterized protein C20orf177	Q9NTX9	75	42,05	3
Uncharacterized protein C20orf43	Q9BY42	88	33,87	4
Uncharacterized protein C21orf124	Q96HW9	43	17,32	1
Uncharacterized protein C21orf56	Q9H0A9	76	9,95	4
Uncharacterized protein C21orf63 [Precursor]	P58658	43	49,48	1
Uncharacterized protein C21orf84	P59037	44	8,51	1
Uncharacterized protein C22orf30	Q5THK1	77	237,30	5

Table 1. continued

Protein Name and Species	Accession	Score	MW [kDa]	# Pept.
Uncharacterized protein C2orf29	Q9UKZ1	74	55,22	3
Uncharacterized protein C2orf43	Q9H6V9	83	6,73	3
Uncharacterized protein C2orf57	Q53QW1	45	41,59	2
Uncharacterized protein C5orf25	Q8NDZ2	61	96,95	2
Uncharacterized protein C5orf34	Q96MH7	48	72,88	3
Uncharacterized protein C6orf12	Q2KJ03	45	22,36	1
Uncharacterized protein C6orf120 [Precursor]	Q7Z4R8	58	20,77	4
Uncharacterized protein C6orf174 [Precursor]	Q5TF21	50	103,20	2
Uncharacterized protein C6orf64	Q9NPB0	51	20,16	1
Uncharacterized protein C7orf46	A4D161	47	33,08	1
Uncharacterized protein C7orf51	Q6ZVC0	83	87,93	4
Uncharacterized protein C8orf77	Q0IIN9	63	22,48	3
Uncharacterized protein C9orf102 [Fragment]	Q8N663	42	52,56	2
Uncharacterized protein C9orf4	Q9P0K9	53	37,25	2
Uncharacterized protein C9orf50	Q5SZB4	48	47,64	2
Uncharacterized protein C9orf79	Q6ZUB1	51	157,14	2
Uncharacterized protein C9orf85	Q96MD7	90	20,17	4
Uncharacterized protein CXorf20	Q8NDZ0	87	87,92	5
Uncharacterized protein CXorf36 [Precursor]	Q9H7Y0	54	20,67	2
Uncharacterized protein CXorf42	Q8N9T2	46	13,72	2
Uncharacterized protein DKFZP586J0619	A4D212	52	265,77	3
Uncharacterized protein FKSG24	Q567V2	52	23,18	2
Uncharacterized protein KIAA0240	Q6AI39	65	115,08	3
Uncharacterized protein KIAA0423	Q9Y4F4	64	189,71	3
Uncharacterized protein KIAA0467	Q5T011	99	231,12	5
Uncharacterized protein KIAA0515	Q5JSZ5	49	165,53	3
Uncharacterized protein KIAA0802	Q9Y4B5	90	176,80	4
Uncharacterized protein KIAA0831	Q6ZNE5	49	55,31	2
Uncharacterized protein KIAA0947	Q9Y2F5	86	254,17	4
Uncharacterized protein KIAA1109	Q2LD37	107	180,39	2
Uncharacterized protein KIAA1143	Q96AT1	64	17,47	1
Uncharacterized protein KIAA1267	Q7Z3B3	114	120,97	4
Uncharacterized protein KIAA1462	Q9P266	81	148,61	3
Uncharacterized protein KIAA1522	Q9P206	54	107,93	2
Uncharacterized protein KIAA1543	Q9P1Y5	81	134,75	4
Uncharacterized protein KIAA1602	Q9HCH0	65	104,75	3
Uncharacterized protein KIAA1671	Q9BY89	115	40,84	6
Uncharacterized protein KIAA1688	Q9C0H5	66	121,29	2
Uncharacterized protein KIAA1755	Q5JYT7	56	130,85	3
Uncharacterized protein KIAA2026	Q5HYC2	49	133,73	2
Uncharacterized protein LOC340602	Q86X51	76	51,86	4
Uncharacterized protein LOC391356	Q6GMV3	69	15,80	1
Uncharcterized protein C10orf40	A4QN01	86	15,29	5
Uncharcterized protein C11orf37	Q96N53	43	15,42	2
Uncharcterized protein C14orf25	Q8IY25	42	53,63	2
Uncharcterized protein C15orf56	Q8N910	57	17,04	2
Uncharcterized protein C8orf44	Q96CB5	86	18,32	4
Uncharcterized protein CXorf18	Q8N9U9	96	13,25	6
Uncoupling protein 2 variant [Fragment]	Q53HM3	46	33,24	2
Undifferentiated embryonic cell transcription factor 1	Q5T230	60	36,44	3
Unr-interacting protein	Q5TZT4	424	38,36	7
UPF0027 protein C22orf28	Q9Y3I0	60	55,21	2
UPF0318 protein FAM120A	Q9NZB2	47	121,89	3
UPF0318 protein FAM120C	Q9NX05	46	17,02	2
UPF0378 family protein KIAA0100 [Precursor]	Q14667	51	253,70	2
UPF0414 transmembrane protein C20orf30	Q96A57	41	13,19	2
UPF0432 protein	Q2VPK5	72	56,11	4
UPF0449 protein C19orf25	Q9UFG5	73	12,88	4
UPF0492 protein C20orf94	Q5VYV7	61	45,55	3
UPF0510 protein C19orf63 [Precursor]	Q5UCC4	43	27,35	3
Urokinase-type plasminogen activator [Precursor]	P00749	40	48,53	2
Uroporphyrinogen decarboxylase	P06132	308	39,75	7
Urotensin 2	Q5H8X8	50	16,28	1
Usherin [Precursor]	O75445	82	575,23	4
Utrophin	Q5SZ57	41	394,22	2
UV excision repair protein RAD23 homolog B	P54727	201	43,17	6
Vacuolar ATP synthase catalytic subunit A	P38606	60	68,26	3
Vacuolar ATP synthase subunit B, brain isoform	P21281	99	56,46	2
Vacuolar ATP synthase subunit C 1	P21283	111	43,78	2
Vacuolar ATP synthase subunit D	Q9Y5K8	90	28,25	2
Vacuolar ATP synthase subunit e 1	O15342	51	9,37	2
Vacuolar protein sorting 11 (Yeast homolog) variant [Fragment]	Q53FX3	79	107,77	3

Table 1. continued

Protein Name and Species	Accession	Score	MW [kDa]	# Pept.
Vacuolar protein sorting-associated protein 13B	Q7Z7G8	63	448,73	3
Vacuolar protein sorting-associated protein 13D	Q5THJ4	44	491,85	1
Vacuolar protein sorting-associated protein 18 homolog	Q9P253	62	110,19	2
Vacuolar protein sorting-associated protein 26A	O75436	165	38,00	3
Vacuolar protein sorting-associated protein 35	Q96QK1	145	91,55	6
Vacuolar protein sorting-associated protein 8 homolog	Q8N3P4	44	161,74	2
Vacuolar protein sorting-associating protein 4B	O75351	40	56,12	2
Valyl-tRNA synthetase	P26640	366	140,38	10
Vascular non-inflammatory molecule 3 [Precursor]	Q9NY84	63	49,30	2
Vasodilator-stimulated phosphoprotein	P50552	66	39,67	2
V-crk sarcoma virus CT10 oncogene homolog	Q96GA9	62	22,89	2
V-crk sarcoma virus CT10 oncogene homolog, isoform a (V-crk sarcoma virus CT10 oncogene homolog) (A	Q96HJ0	394	33,81	7
Vesicle amine transport protein 1	Q5BKZ7	125	41,89	2
Vesicle transport protein USE1	Q9NZ43	48	29,35	2
Vesicle-fusing ATPase	P46459	49	82,54	2
Vesicular integral-membrane protein VIP36 [Precursor]	Q12907	51	40,20	1
Vigilin (high density lipoprotein binding protein)	Q00341	97	141,44	4
Vimentin	P08670	2191	53,49	46
Vimentin variant [Fragment]	Q53HU8	2195	53,65	47
Vinculin	P18206	69	123,59	1
Vinexin	O60504	50	75,33	3
Voltage-dependent anion channel 2 [Fragment]	Q5VWK3	131	30,33	2
Voltage-dependent anion-selective channel protein 1	P21796	91	30,62	2
Voltage-dependent anion-selective channel protein 3	Q9Y277	79	30,64	1
Voltage-dependent calcium channel gamma-8 subunit	Q8WXS5	82	43,48	3
Voltage-dependent calcium channel subunit alpha-2/delta-2 [Precursor]	Q9NY47	51	110,12	2
Voltage-dependent L-type calcium channel subunit alpha-1C	Q13936	43	13,76	2
Voltage-dependent L-type calcium channel subunit alpha-1F	O60840	56	219,50	3
Voltage-dependent P/Q-type calcium channel subunit alpha-1A	O00555	67	28,33	3
Voltage-dependent R-type calcium channel subunit alpha-1E	Q15878	55	261,72	3
Voltage-dependent T-type calcium channel subunit alpha-1H	O95180	88	259,16	5
Voltage-dependent T-type calcium channel subunit alpha-1I	Q9P0X4	51	244,95	3
Voltage-gated calcium channel alpha 1 subunit [Fragment]	Q71UT1	85	13,88	3
Voltage-gated potassium channel KV11.1 transcript variant 1	Q15BH2	64	126,60	5
Voltage-gated sodium channel alpha subunit splice variant SCN3A-s	Q9C007	48	221,38	2
von Willebrand factor C and EGF domain-containing protein [Precursor]	Q96DN2	42	99,89	2
VPS10 domain-containing receptor SorCS2 [Precursor]	Q96PQ0	104	128,08	6
VPS9 domain-containing protein FLJ45909	Q6ZS11	46	50,02	2
WAP four-disulfide core domain protein 10A [Precursor]	Q9H1F0	50	8,94	2
WAS/WASL-interacting protein family member 1	O43516	57	51,24	3
WAS/WASL-interacting protein family member 2	Q8TF74	52	46,29	4
WD repeat and FYVE domain-containing protein 3	Q8IZQ1	55	395,26	4
WD repeat protein 86 [Fragment]	Q86TI4	75	53,04	3
WD repeat-containing protein 19	Q8NEZ3	53	151,58	2
WD repeat-containing protein 22	Q96JK2	40	103,96	2
WD repeat-containing protein 23	Q8TEB1	51	61,67	2
WD repeat-containing protein 57	Q96DI7	315	39,27	6
WD repeat-containing protein 68	P61962	297	38,90	5
WD repeat-containing protein 7	Q9Y4E6	45	163,81	2
WD repeat-containing protein 8	Q9P2S5	63	51,59	3
WD repeat-containing protein 87	Q6ZQQ6	60	333,17	4
WDR33 protein [Fragment]	Q05DP8	53	39,52	4
Wee1-like protein kinase 2	P0C1S8	45	85,30	2
Wilms tumor protein	P19544	50	62,38	2
Wings apart-like protein homolog	Q7Z5K2	95	143,53	4
WSC domain-containing protein 1	Q658N2	44	65,69	2
WUGSC:H_2G3A.1 protein	Q99993	45	60,09	2
WUGSC:H_RG054D04.1 protein	O95036	277	29,02	6
WW domain-binding protein 11	Q9Y2W2	67	69,95	2
WW domain-binding protein 7	Q9UMN6	76	293,33	4
WW-domain binding protein 2	Q7Z511	70	28,05	3
Xaa-Pro dipeptidase	P12955	73	54,38	4
Xaa-Pro dipeptidase	P12955	119	54,38	3
XK-related protein 7	Q5GH72	87	63,83	3
X-ray radiation resistance-associated protein 1	Q6P2D8	54	89,86	3
XRCC1 protein	Q6IBS4	41	69,45	2
XTP3-transactivated gene A protein	Q9H773	151	18,67	5
Xylan 1,4-beta-xylosidase 1 [Fragment]	O76044	40	14,42	1
Xylosyltransferase 1	Q86Y38	66	107,57	4
Xylosyltransferase 2	Q9H1B5	70	96,77	3
Xylulose kinase	O75191	44	57,37	1

Table 1. continued

Protein Name and Species	Accession	Score	MW [kDa]	# Pept.
Y-box-binding protein 2	Q9Y2T7	223	38,54	5
YKT6 protein [Fragment]	Q6FGU9	45	22,40	1
YTH domain-containing protein 2	Q9H6S0	47	150,88	2
Zinc finger and BTB domain containing 22	Q5HYV4	79	70,44	3
Zinc finger and BTB domain-containing protein 37	Q5TC79	44	56,06	1
Zinc finger and BTB domain-containing protein 45	Q96K62	45	53,97	1
Zinc finger and BTB domain-containing protein 6	Q15916	48	48,24	2
Zinc finger and BTB domain-containing protein 9	Q96C00	51	50,60	2
Zinc finger and SCAN domain-containing protein 10	Q96SZ4	57	80,34	2
Zinc finger CCCH domain-containing protein 11A	O75152	56	89,13	3
Zinc finger CCCH domain-containing protein 13	Q5T200	55	184,75	3
Zinc finger CCCH domain-containing protein 18	Q86VM9	71	80,41	4
Zinc finger CCCH domain-containing protein 3	Q8IXZ2	128	101,93	7
Zinc finger CCCH domain-containing protein 7B	Q9UGR2	42	111,51	2
Zinc finger CCCH domain-containing protein C19orf7	Q9UPT8	102	140,26	4
Zinc finger CCCH-type-containing protein 12C [Fragment]	Q9C0D7	52	70,73	2
Zinc finger CCCH-type-containing protein 12D [Fragment]	Q8NF40	49	38,91	2
Zinc finger CCHC domain-containing protein 6	Q5VYS8	48	171,23	2
Zinc finger CW-type PWWP domain protein 1	Q9H0M4	59	53,19	2
Zinc finger FYVE domain-containing protein 1	Q9HBF4	42	6,37	3
Zinc finger FYVE domain-containing protein 19	Q96K21	85	51,53	4
Zinc finger FYVE domain-containing protein 26	Q68DK2	71	284,64	4
Zinc finger FYVE domain-containing protein 28	Q9HCC9	46	96,50	2
Zinc finger homeobox protein 2	Q9C0A1	63	152,10	3
Zinc finger homeobox protein 3	Q15911	52	404,42	4
Zinc finger homeobox protein 4	Q86UP3	69	393,73	3
Zinc finger protein 107	Q9UII5	42	98,89	2
Zinc finger protein 212	Q9UDV6	44	55,45	2
Zinc finger protein 217	O75362	42	115,27	2
Zinc finger protein 318	Q5VUA4	71	251,11	4
Zinc finger protein 324B	Q6AW86	54	60,60	2
Zinc finger protein 326	Q5BKZ1	77	65,61	3
Zinc finger protein 38 homolog	Q9Y5A6	46	53,66	2
Zinc finger protein 423	Q2M1K9	51	144,61	2
Zinc finger protein 469	Q96JG9	81	258,55	3
Zinc finger protein 503	Q96F45	63	62,56	2
Zinc finger protein 513	Q8N8E2	48	11,25	2
Zinc finger protein 554	Q86TJ5	64	60,58	3
Zinc finger protein 574	Q6ZN55	46	98,90	2
Zinc finger protein 580	Q9UK33	73	18,76	5
Zinc finger protein 592	Q2M1T2	75	137,53	4
Zinc finger protein 614	Q8N883	68	67,17	3
Zinc finger protein 629	Q9UEG4	58	96,62	3
Zinc finger protein 638	Q14966	59	220,63	2
Zinc finger protein 703	Q9H7S9	41	58,22	2
Zinc finger protein 778	Q96MU6	50	48,61	2
Zinc finger protein 99	Q8WTZ3	175	27,16	9
Zinc finger protein castor homolog 1	Q86V15	58	190,15	4
Zinc finger protein Gfi-1 variant [Fragment]	Q59F55	54	46,63	2
Zinc finger protein GLI1	P08151	45	117,90	2
Zinc finger protein GLI3	P10071	57	115,29	4
Zinc finger protein HRX	Q03164	91	431,76	5
Zinc finger protein with KRAB and SCAN domains 2	Q63HK3	41	110,91	2
Zinc finger protein ZFPM1	Q8IX07	51	104,55	2
Zinc finger protein, multitype 2	Q32MA5	43	128,15	2
Zinc finger Ran-binding domain-containing protein 3	Q5FWF4	42	123,17	2
Zinc finger, CCHC domain containing 14	Q3MJD8	62	100,07	4
Zinc finger, FYVE domain containing 9	Q5T0F7	45	156,30	2
Zinc fingers and homeoboxes protein 2	Q9Y6X8	68	92,31	3
Zinc phosphodiesterase ELAC protein 2	Q9BQ52	46	92,22	3
Zinc/RING finger protein 4 [Precursor]	Q8WWF5	42	46,96	2
ZNF257 protein	Q8NE34	45	61,92	2
ZNF276 protein	Q3KR18	47	44,71	2
ZNF483 protein	Q6P088	40	28,10	2
ZNF516 protein [Fragment]	Q2YDX2	93	54,49	4
ZNF557 protein [Fragment]	Q4G137	45	46,18	2
Zona pellucida sperm-binding protein 4 [Precursor]	Q12836	42	59,40	1
Zonadhesin [Precursor]	Q9Y493	74	305,57	3
ZSCAN10 protein [Fragment]	Q1WWM2	44	71,17	2
Zygote arrest protein 1	Q86SH2	67	45,87	3
ZYX protein [Fragment]	Q9BUS0	47	62,41	2
Zyxin	Q15942	177	61,24	6

Table 2. Proteins identified in the ICPL™ experiments including the labeled and unlabeled ones. The regulation is given: n.d. = no labeled peptides found; 0 = found regulation is below factor 1.3; -/+ = slight down- or up-regulation up to factor 1.5; --/++ = regulated proteins factor > 1.5

Protein Name and Species	Accession	Score	MW [kDa]	pI	SC [%]	# Pept.	regulated
1,2-dihydroxy-3-keto-5-methylthiopentene dioxygenase	Q9BV57	58	20,32	5,86	16,18	2	n.d.
13 kDa differentiation-associated protein variant [Fragment]	Q53HG1	54	17,20	9,97	8,22	1	n.d.
14-3-3 protein beta/alpha	P31946	94	27,93	4,61	13,47	5	0
14-3-3 protein epsilon isoform transcript variant 1	Q4VJB6	129	26,49	4,61	10,73	36	0
14-3-3 protein gamma	P61981	173	28,36	4,65	14,98	24	0
14-3-3 protein theta	P27348	231	27,75	4,53	13,47	14	0
14-3-3 protein zeta/delta	P63104	101	27,73	4,57	5,71	14	0
2',3'-cyclic-nucleotide 3'-phosphodiesterase	P09543	63	47,55	9,80	4,99	2	0
250 kDa substrate of Akt	Q2PPJ7	53	0,00	11,57	5,75	2	n.d.
26S protease regulatory subunit 6A	P17980	85	54,97	5,26	4,48	3	0
26S protease regulatory subunit 6B	P43686	62	47,34	4,95	6,94	3	0
26S protease regulatory subunit 7	P35998	249	48,47	5,62	17,36	8	-
26S protease regulatory subunit 8	P62195	288	45,61	8,71	20,69	15	0
26S protease regulatory subunit S10B	P62335	192	44,15	7,79	15,42	6	+
26S proteasome non-ATPase regulatory subunit 11	O00231	164	47,30	6,06	11,16	5	0
26S proteasome non-ATPase regulatory subunit 7	P51665	61	37,26	9,26	3,99	4	+
26S proteasome non-ATPase regulatory subunit 9	O00233	52	24,64	6,52	5,38	2	0
28 kDa heat- and acid-stable phosphoprotein	Q13442	226	20,62	9,38	33,15	22	0
39S ribosomal protein L11	Q9Y3B7	99	20,67	10,46	23,96	5	++
39S ribosomal protein L15	Q9P015	69	33,40	10,52	9,12	3	++
39S ribosomal protein L19 [Precursor]	P49406	52	0,00	10,24	6,43	2	n.d.
39S ribosomal protein L4	Q9BYD3	139	35,00	9,79	14,47	3	++
39S ribosomal protein L49	Q13405	41	19,19	9,93	7,83	1	n.d.
39S ribosomal protein L53 [Precursor]	Q96EL3	60	12,10	10,48	19,64	3	0
39S ribosomal protein L55 [Precursor]	Q7Z7F7	78	14,69	11,29	12,00	1	++
3-hydroxyacyl-CoA dehydrogenase type-2	Q99714	39	26,78	9,19	3,08	1	n.d.
3-ketoacyl-CoA thiolase	P42765	242	41,90	9,28	11,84	11	+
3-mercaptopyruvate sulfurtransferase	P25325	102	32,95	6,00	12,50	3	0
40 kDa peptidyl-prolyl cis-trans isomerase	Q08752	53	40,61	6,93	6,78	2	0
40S ribosomal protein S10 variant	Q59GE4	147	19,85	10,44	13,79	2	0
40S ribosomal protein S11	P62280	132	18,42	10,95	17,09	5	0
40S ribosomal protein S12	P25398	76	14,52	6,38	31,82	7	0
40S ribosomal protein S13	P62277	387	17,21	10,96	49,67	26	0
40S ribosomal protein S14	P62263	284	16,26	10,93	27,15	11	0
40S ribosomal protein S15	P62841	90	17,03	10,81	20,69	5	0
40S ribosomal protein S15a	P62244	241	14,71	11,03	41,09	22	0
40S ribosomal protein S16	P62249	435	16,44	10,75	60,96	27	0
40S ribosomal protein S17	P08708	333	15,54	10,35	50,37	34	0
40S ribosomal protein S18	P62269	481	17,71	11,47	57,24	21	0
40S ribosomal protein S19	P39019	405	16,05	10,75	51,72	18	0
40S ribosomal protein S20	P60866	232	13,36	10,69	45,38	15	0
40S ribosomal protein S21	P63220	235	9,11	9,66	72,29	18	0
40S ribosomal protein S23	P62266	71	15,67	11,32	8,45	4	0
40S ribosomal protein S24	P62847	270	15,06	11,36	71,54	17	-
40S ribosomal protein S25	P62851	88	13,73	10,64	15,20	3	0
40S ribosomal protein S26	P62854	187	13,01	12,19	44,35	21	0
40S ribosomal protein S27	P42677	121	9,32	10,79	28,92	6	0
40S ribosomal protein S27a	P62979	259	17,95	10,40	28,85	5	--
40S ribosomal protein S27-like protein	Q71UM5	114	9,47	10,74	30,95	3	0
40S ribosomal protein S28	P62857	240	7,84	11,60	49,28	12	0
40S ribosomal protein S3	P23396	323	26,67	10,27	37,04	15	0
40S ribosomal protein S30	P62861	161	6,64	12,65	76,27	7	-
40S ribosomal protein S3a	P61247	335	29,79	10,36	26,36	25	0
40S ribosomal protein S4, X isoform	P62701	323	29,58	10,83	28,14	18	0
40S ribosomal protein S5	P46782	211	22,73	10,36	15,76	9	0
40S ribosomal protein S6	P62753	293	28,66	11,54	27,71	19	0
40S ribosomal protein S7	P62081	325	22,11	10,58	37,11	21	0
40S ribosomal protein S8	P62241	448	24,19	10,99	54,81	29	0
40S ribosomal protein S9	P46781	741	22,45	11,24	61,66	46	0
40S ribosomal protein SA	P08865	361	32,70	4,64	34,88	33	0
48 kDa TATA box-binding protein-interacting protein	Q9Y230	409	50,99	5,37	23,16	17	0
5'(3')-deoxyribonucleotidase	Q8TCD5	55	13,29	6,37	15,38	1	n.d.
5,6-dihydroxyindole-2-carboxylic acid oxidase [Precursor]	P17643	58	60,69	5,58	5,96	2	n.d.
52 kDa Ro protein	P19474	42	54,17	10,70	16,07	2	n.d.
5'-3' exoribonuclease 2	Q9H0D6	38	103,74	8,96	0,88	1	++
54 kDa nuclear RNA- and DNA-binding protein	Q15233	539	54,22	9,33	25,42	41	0
5-methyltetrahydrofolate-homocysteine methyltransferase	Q5VXE1	41	0,00	5,28	0,95	1	n.d.
6.8 kDa mitochondrial proteolipid	P56378	56	8,61	10,42	18,67	2	0
60S acidic ribosomal protein P0	Q3B7A4	80	27,42	9,25	6,67	10	0
60S ribosomal protein L10	P27635	392	24,48	10,04	46,48	20	0

Table 2. continued

Protein Name and Species	**Accession**	**Score**	**MW [kDa]**	**pI**	**SC [%]**	**# Pept.**	**regulated**
60S ribosomal protein L10a	P62906	116	24,68	10,51	7,41	3	n.d.
60S ribosomal protein L10-like	Q96L21	68	24,37	10,95	9,39	2	++
60S ribosomal protein L11	P62913	319	20,24	10,31	40,23	25	0
60S Ribosomal protein L12	P30050	305	17,81	10,26	36,43	6	0
60S ribosomal protein L13	Q6NZ55	369	24,25	12,21	42,18	26	0
60S ribosomal protein L17	P18621	88	21,38	10,86	11,96	6	+
60S ribosomal protein L18	Q07020	667	21,49	12,34	62,57	27	0
60S ribosomal protein L18a	Q02543	305	20,75	11,74	42,61	16	0
60S ribosomal protein L21	P46778	84	18,42	11,00	20,13	2	0
60S ribosomal protein L23	P62829	181	15,03	11,55	46,43	12	0
60S ribosomal protein L24	P83731	243	17,77	11,85	42,04	20	+
60S ribosomal protein L27	P61353	130	15,79	10,99	25,00	4	0
60S ribosomal protein L27a	P46776	288	16,42	11,78	56,46	11	0
60S ribosomal protein L28	P46779	277	15,87	12,14	47,55	16	0
60S ribosomal protein L3	P39023	127	45,95	10,77	8,21	9	0
60S ribosomal protein L30	P62888	108	12,78	10,24	27,83	3	-
60S ribosomal protein L31	P62899	235	14,45	10,99	36,80	15	0
60S ribosomal protein L32	P62910	134	15,85	12,06	23,70	6	0
60S ribosomal protein L34	P49207	209	13,28	12,41	38,46	16	-
60S ribosomal protein L35	P42766	346	14,41	11,52	55,74	16	0
60S ribosomal protein L35a	P18077	208	12,49	11,53	51,82	15	0
60S ribosomal protein L36	Q9Y3U8	294	12,11	12,20	72,12	20	0
60S ribosomal protein L36a	P83881	124	12,30	11,68	40,00	5	0
60S ribosomal protein L36a-like	Q969Q0	61	12,46	11,81	17,92	2	0
60S ribosomal protein L37	P61927	126	11,07	12,69	43,30	13	0
60S ribosomal protein L37a	P61513	60	10,27	11,48	14,13	2	0
60S ribosomal protein L38	P63173	101	8,21	10,65	47,14	9	0
60S ribosomal protein L4	P36578	286	47,54	11,80	15,26	13	-
60S ribosomal protein L40	P62987	253	16,16	10,80	46,15	9	-
60S ribosomal protein L5	P46777	352	34,21	10,19	26,69	16	0
60S ribosomal protein L5 variant	Q59GX9	310	35,18	10,31	35,97	13	0
60S ribosomal protein L6	Q02878	197	32,58	11,08	48,00	20	0
60S ribosomal protein L7	P18124	147	29,02	11,21	18,62	5	0
60S ribosomal protein L7a	P62424	188	29,98	11,25	19,92	9	0
60S ribosomal protein L8	P62917	412	28,01	11,86	42,80	51	++
60S Ribosomal protein P0 variant	Q53HW2	102	34,28	5,63	15,36	5	0
6-phosphogluconolactonase	O95336	216	27,53	5,66	23,26	8	0
Abhydrolase domain-containing protein 14B	Q96IU4	97	14,81	6,35	16,90	2	n.d.
Absent in melanoma 1 protein	Q9Y4K1	41	0,00	9,35	26,74	1	n.d.
ACAT1 (Acetyl-Coenzyme A acetyltransferase 1 oder acetoacetyl Coenzyme A thiolase)	Q6P3T4	73	30,97	10,06	5,85	4	n.d.
Acetyl-CoA acetyltransferase	Q59GW6	178	42,11	7,95	9,90	3	0
Acetyl-CoA acyltransferase	P42765	69	41,90	9,28	6,80	2	++
Achaete-scute complex homolog 2	Q6PEY9	56	0,00	12,11	10,43	2	n.d.
Acidic (Leucine-rich) nuclear phosphoprotein 32 family	Q5TB18	192	28,54	3,83	14,06	10	0
Aconitate hydratase, mitochondrial [Precursor]	Q99798	60	85,41	7,39	1,92	1	n.d.
ACTA2	Q13707	161	36,78	5,07	16,06	13	0
Actin alpha	P62736	90	37,80	5,28	9,65	2	n.d.
Actin beta	P60709	515	41,17	5,18	42,93	66	-
Actin gamma	P63261	848	41,77	5,20	50,93	258	0
Actin related protein 2/3 complex	Q2LE71	73	20,55	9,49	8,99	7	0
Actin, alpha 1, skeletal muscle	Q5T8M7	373	37,80	5,28	9,65	44	0
Actin-binding Rho-activating protein	Q8N0Z2	49	0,00	9,40	5,51	2	n.d.
Actinin-associated LIM protein	Q53GG5	50	34,25	9,40	4,75	2	0
Actin-like protein	Q562Z4	160	11,55	7,72	49,51	10	0
Actin-like protein [Fragment]	Q562M3	154	11,53	6,21	49,51	15	0
Actin-like protein 6A	O96019	63	47,35	5,40	4,90	4	0
Actin-related protein 2/3 complex subunit 2	O15144	91	34,31	7,02	11,67	3	0
Actin-related protein 2/3 complex subunit 4	P59998	146	19,52	9,36	22,75	5	0
Actin-related protein 3	P61158	144	47,21	5,54	10,31	6	0
Activated RNA polymerase II transcriptional coactivator p15	P53999	113	14,26	10,13	24,60	6	-
Activator of 90 kDa heat shock protein ATPase homolog 1	O95433	200	29,56	5,45	18,32	6	--
Activin receptor interacting protein 5	Q49SH3	176	15,92	5,86	25,52	4	+
Acyl-CoA dehydrogenase precursor, medium-chain-specific	P11310	71	46,56	9,38	8,08	3	++
Acylphosphatase-1	P07311	83	11,25	9,78	15,15	2	0
Acyl-protein thioesterase 2	O95372	102	24,72	6,92	9,96	6	0
Adaptin ear-binding coat-associated protein 1	Q8NC96	51	14,34	9,36	12,40	2	n.d.
Adenine phosphoribosyltransferase	P07741	238	19,46	5,69	32,96	9	0
Adenomatous polyposis coli protein	P25054	52	311,65	8,34	1,24	2	n.d.
Adenomatous polyposis coli protein 2	O95996	43	175,43	10,81	1,60	2	n.d.
Adenosylhomocysteinase	P23526	81	47,55	5,91	4,64	3	--
Adenylate cyclase-stimulating G alpha protein	P63092	62	44,24	5,89	9,21	2	n.d.

Table 2. continued

Protein Name and Species	**Accession**	**Score**	**MW [kDa]**	**pI**	**SC [%]**	**# Pept.**	**regulated**
Adenylate kinase 1	Q5T9B7	128	23,40	9,53	23,33	5	0
Adenylate kinase isoenzyme 1	P00568	73	21,69	9,38	14,43	3	0
Adenylate kinase isoenzyme 2	P54819	265	26,33	8,97	33,19	19	0
Adenylate kinase isoenzyme 4 (ATP-AMP transphosphorylase)	P27144	40	25,25	9,23	7,62	1	n.d.
Adenylyl cyclase-associated protein 1	Q01518	50	51,51	8,94	4,01	1	--
ADP/ATP translocase 2	P05141	71	32,74	10,27	6,73	5	0
ADP-ribosylation factor 1	P84077	116	12,86	5,49	18,18	2	n.d.
ADP-sugar pyrophosphatase	Q9UKK9	134	24,24	4,59		8	-
Adrenocortical dysplasia protein homolog	Q96AP0	52	48,94	5,04	8,30	2	n.d.
AF4/FMR2 family member 1	P51825	51	131,42	9,99	2,90	2	n.d.
Aflatoxin B1 aldehyde reductase member 2 (Aldoketoreductase 7)	O43488	65	39,56	6,80	5,57	3	0
Aflatoxin B1 aldehyde reductase member 3	O95154	52	38,47	6,76	8,12	2	n.d.
Aging-associated gene 9 protein	Q2TSD0	201	36,03	9,26	11,34	12	0
Aging-associated protein 14b	Q1XBU6	40	28,35	9,54	3,14	1	-
A-kinase anchor protein 9	Q99996	40	0,00	4,80	1,46	2	n.d.
Albumin D box-binding protein	Q10586	59	34,35	9,92	24,35	5	n.d.
Alcohol dehydrogenase	P14550	71	36,42	6,36	6,48	3	0
Aldehyde dehydrogenase [Precursor]	P05091	40	53,88	5,62	2,63	2	0
Aldose reductase	P15121	99	35,70	6,58	10,16	5	+
Alpha-1,3-mannosyl-glycoprotein 4-beta-N-acetylglucosaminyltransferase B	Q9UQ53	59	63,11	9,89	6,67	2	n.d.
Alpha-1,4-galactosyltransferase	Q7Z7C5	68	38,78	11,87	8,62	2	n.d.
Alpha-1A adrenergic receptor	P35348	53	51,49	10,42	5,01	3	n.d.
Alpha-centractin	P61163	47	42,59	6,19	4,26	2	--
Alpha-parvin	Q9NVD7	56	42,19	5,60	6,18	2	n.d.
Alpha-protein kinase 2	Q86TB3	49	122,28	4,68	3,54	2	n.d.
Angiomotin-like protein 1	Q8IY63	62	106,57	6,69	5,82	2	n.d.
Angiopoietin-related protein 4 [Precursor]	Q9BY76	63	45,18	10,10	6,16	2	n.d.
Angiotensin-converting enzyme, somatic isoform [Precursor]	P12821	58	0,00	6,25	7,71	2	n.d.
ANKDD1A protein [Fragment] (Ankyrin repeat and death domain-containing protein 1A precursor)	Q6PI29	43	22,71	9,40	5,03	1	n.d.
Ankyrin repeat and zinc finger domain-containing protein 1	Q9H8Y5	54	80,88	9,57	3,03	2	n.d.
Ankyrin-2	Q01484	42	75,74	11,86	6,38	2	n.d.
Annexin A2	P07355	318	38,45	8,53	22,19	15	--
Annexin IV	P09525	138	35,73	5,76	9,43	3	++
Annexin V	P08758	262	35,07	4,99	24,36	6	0
Antigen KI-67	P46013	40	358,69	10,13	0,64	2	n.d.
Antigen MLAA-42 (Fragment)	Q6W6M8	41	16,86	5,35	13,91	1	n.d.
Apolipoprotein O [Precursor]	Q9BUR5	46	22,27	9,64	5,56	2	n.d.
Arginine vasopressin-induced protein 1	Q5T686	58	16,76	12,28	24,26	2	n.d.
Arginine/serine-rich splicing factor 6 variant [Fragment]	Q59GY3	51	31,85	11,68	5,02	1	--
ARHGAP4 protein [Fragment]	Q6PJ34	56	38,21	5,45	13,48	3	n.d.
ARL3 protein [Fragment]	Q53X83	66	20,46	7,64	9,89	2	0
Armadillo repeat protein deleted in velo-cardio-facial syndrome	O00192	56	49,09	9,08	10,86	2	n.d.
Arsenic-transactivated protein 3 / Collagen binding protein	P50454	242	46,41	9,31	10,29	4	0
Aspartate aminotransferase	P17174	85	46,09	6,59	5,83	3	0
Aspartate aminotransferase [Precursor]	P00505	70	47,45	9,82	6,05	2	n.d.
Aspartyl-tRNA synthetase	P14868	52	57,16	6,21	3,00	1	n.d.
Ataxin-2	Q99700	53	140,14	10,16	2,97	2	n.d.
Atherin	Q6SPF0	53	56,02	7,90	5,93	3	n.d.
AT-hook-containing transcription factor	Q7Z591	59	155,14	10,17	6,41	3	n.d.
ATP synthase B chain, mitochondrial [Precursor]	P24539	115	34,03	4,76	10,58	2	n.d.
ATP synthase delta chain [Fragment]	Q53HH2	330	23,25	10,53	36,15	11	++
ATP synthase epsilon chain	P56381	40	5,65	10,49	20,00	2	+
ATP synthase gamma chain [Fragment]	Q8TAS0	54	32,23	9,61	5,15	2	+
ATP synthase subunit alpha [Precursor]	P25705	103	59,71	9,61	8,50	21	--
ATP synthase subunit alpha [Precursor]	P25705	620	59,71	9,61	24,23	44	++
ATP synthase subunit beta [Precursor]	P06576	105	57,92	5,75	15,68	18	--
ATP synthase subunit beta [Precursor]	P06576	724	57,92	5,75	39,29	31	++
ATP synthase subunit e	P56385	259	7,93	9,43	72,46	8	+
ATP synthase subunit g	O75964	82	11,42	10,00	19,42	4	0
ATPase inhibitor [Precursor]	Q9UII2	63	8,85	9,59	25,33	5	0
ATP-dependent DNA helicase Q1	P46063	45	73,41	9,22	1,69	1	n.d.
ATP-dependent DNA helicase Q4	O94761	42	133,08	9,63	1,24	2	n.d.
ATP-dependent RNA helicase A	Q08211	131	140,79	6,35	3,86	4	n.d.
AT-rich interactive domain-containing protein 2	Q68CP9	40	0,00	10,37	13,68	2	0
Autophagy-related protein 3	Q9NT62	60	36,17	4,54	6,94	1	--
BAG family molecular chaperone regulator 2	O95816	65	7,54	5,19	37,31	2	n.d.
Bcd orf2	O43839	55	0,00	11,55	11,16	2	n.d.
B-cell lymphoma/leukemia 11A	Q9H165	44	91,20	5,87	4,38	2	n.d.

Table 2. continued

Protein Name and Species	Accession	Score	MW [kDa]	pI	SC [%]	# Pept.	regulated
BH3-interacting domain death agonist	P55957	306	21,98	5,14	29,74	5	n.d.
Biliverdin reductase A [Precursor]	P53004	107	33,44	6,04	9,46	3	--
BiP (HSP70 protein 5)	P11021	98	70,89	5,09	8,45	7	--
Bloom syndrome protein	P54132	41	159,00	7,86	1,20	1	n.d.
BolA-like protein 2	Q9H3K6	143	10,11	6,09	37,21	2	--
BR serine/threonine-protein kinase 1	Q8TDC3	50	81,51	10,10	7,61	4	n.d.
Brain-rescue-factor-1	Q2TV78	50	0,00	9,53	3,63	1	n.d.
Bromodomain adjacent to zinc finger domain protein 2A	Q9UIF9	50	94,51	9,52	3,94	3	n.d.
Bromodomain and PHD finger containing, 1	Q7Z6E0	59	138,10	8,74	3,52	2	n.d.
BTB/POZ domain-containing protein 11	Q6ZV99	52	68,09	6,01	4,14	2	n.d.
BTB/POZ domain-containing protein KCTD12	Q96CX2	122	35,68	5,36	9,85	6	n.d.
Butyrophilin-like protein 3 [Precursor]	Q6UXE8	57	52,28	5,81	5,36	2	--
C1 protein	Q9UGE8	52	104,99	6,03	4,65	2	n.d.
C20orf77 protein (Fragment)	Q6PKF4	82	25,03	9,19	12,27	2	+
Calcium binding protein 1	Q8N6H5	51	39,87	6,47	6,07	2	n.d.
Calcium-activated non-selective cation channel 1	Q7Z5D9	46	118,55	9,10	0,75	1	n.d.
Calcium-binding protein p22	Q99653	77	22,31	4,84	14,43	2	n.d.
Calcium-regulated heat stable protein 1	Q9Y2V2	40	0,00	9,16	14,71	2	n.d.
Calcyclin binding protein	Q5R371	57	26,19	9,03	9,65	2	n.d.
Caldesmon (Fragment)	Q9UD91	42	33,65	10,01	6,40	2	++
Caldesmon 1 (actin- and calmodulin-binding protein)	Q6PJM5	108	36,67	5,22	9,87	2	--
Calmodulin	P62158	199	16,70	3,93	21,62	24	-
Calnexin [Precursor]	P27824	61	40,81	4,06	4,21	2	0
Calpain small subunit 1	P04632	106	28,30	4,91	11,19	2	0
Calumenin	Q6IAW5	44	37,08	4,32	2,22	1	n.d.
Calumenin [Precursor]	O43852	64	34,97	4,24	5,07	2	n.d.
cAMP-specific 3',5'-cyclic phosphodiesterase 4C	Q08493	48	75,60	4,72	2,94	2	n.d.
Capping protein (Actin filament) muscle Z-line, beta	Q5VVZ5	262	33,76	6,00	27,91	12	0
Carbonyl reductase [NADPH] 1	P16152	264	30,22	9,52	25,00	19	0
Carboxy terminus of Hsp70-interacting protein	Q9UNE7	135	34,77	5,44	18,81	10	0
Casein kinase 2	Q5SQ52	48	21,60	4,69	10,22	1	0
Cat eye syndrome critical region protein 1 isoform a variant [Fragment]	Q59F13	40	33,86	10,05	2,97	1	n.d.
Cat eye syndrome critical region protein 5 [Precursor]	Q9BXW7	56	43,56	6,47	5,09	1	n.d.
Catalase	P04040	52	59,59	7,01	4,37	2	n.d.
Cathepsin B [Precursor]	P07858	74	37,78	5,87	5,01	4	n.d.
Cathepsin C	Q8WY99	82	51,87	6,59	2,59	2	n.d.
Cathepsin D [Precursor]	P07339	40	44,52	6,11	1,94	1	n.d.
CBX5 protein	Q6I9T7	72	22,15	5,87	8,90	1	n.d.
CCR4-NOT transcription complex subunit 6	Q9ULM6	43	0,00	6,92	2,15	2	n.d.
CDA11	Q9BY40	64	33,58	6,58	9,09	3	++
CDC2 protein	Q3B785	44	25,92	9,11	4,44	1	n.d.
CDC37 protein	Q6FG59	75	44,43	5,03	6,88	3	--
CDC42 binding protein kinase alpha [Fragment]	Q5T799	46	109,87	9,11	3,36	2	n.d.
CDC42 GTPase-activating protein	Q07960	93	50,40	5,83	7,74	3	0
CDGSH iron sulfur domain 2	Q8N5K1	101	15,27	10,44	17,78	2	0
CDNA FLJ11798 fis, clone HEMBA1006198, weakly similar to PROLINE-RICH PROTEIN MP-2	Q9HAD2	62	26,61	12,40	15,14	2	n.d.
CDNA FLJ23801 fis, clone HEP22544	Q8TE87	55	19,48	12,60	17,20	2	n.d.
CDNA FLJ23893 fis, clone LNG14589	Q8TCH5	45	18,79	13,26	11,24	2	n.d.
CDNA FLJ29006 fis, clone STM02533	Q6ZNM3	46	35,38	0,00	5,79	2	n.d.
CDNA FLJ30534 fis, clone BRAWH2001141	Q96NM8	39	15,92	0,00	7,74	1	--
CDNA FLJ32205 fis, clone PLACE6003094	Q96ML1	52	22,57	12,37	8,22	2	n.d.
CDNA FLJ33592 fis, clone BRAMY2012691	Q8N2A4	46	14,88	13,22	13,43	1	n.d.
CDNA FLJ35074 fis, clone PLACE6001118	Q8NAN4	40	13,30	12,58	12,30	1	n.d.
CDNA FLJ35113 fis, clone PLACE6007242	Q8NAM3	60	13,70	7,80	19,08	3	n.d.
CDNA FLJ36157 fis, clone TESTI2025656. [Fragment]	Q8N9V7	59	77,57	9,65	2,73	2	n.d.
CDNA FLJ37258 fis, clone BRAMY2010208	Q8N1Y5	42	22,02	12,40	10,63	2	n.d.
CDNA FLJ37941 fis, clone CTONG2008269	Q8N1R6	55	27,77	12,66	13,19	4	n.d.
CDNA FLJ40951 fis, clone UTERU2010124	Q8N7K5	51	13,82	12,08	27,69	2	n.d.
CDNA FLJ41409 fis, clone BRHIP2000920	Q6ZW97	43	25,67	12,21	6,17	1	n.d.
CDNA FLJ41761 fis, clone IMR322003675	Q6ZW19	47	27,22	12,88	13,95	2	n.d.
CDNA FLJ41781 fis, clone IMR322018117	Q6ZW18	52	17,48	9,43	22,09	2	n.d.
CDNA FLJ41879 fis, clone OCBBF2020741	Q6ZVZ6	57	20,68	12,80	21,32	2	n.d.
CDNA FLJ43329 fis, clone NT2RI3005202	Q6ZUU3	40	0,00	12,51	10,29	1	0
CDNA FLJ43706 fis, clone TESOP2001849	Q6ZUH7	48	30,69	5,56	17,63	2	n.d.
CDNA FLJ43752 fis, clone TESTI2037643	Q6ZUF6	54	20,93	12,46	15,15	3	n.d.
CDNA FLJ44007 fis, clone TESTI4023762	Q6ZU43	41	94,36	4,92	2,26	1	n.d.
CDNA FLJ46097 fis, clone TESTI2021112	Q6ZRU3	56	15,20	12,22	9,29	2	n.d.
CDNA FLJ46214 fis, clone TESTI4012623	Q6ZRN7	47	21,15	12,72	12,02	2	n.d.
CDNA FLJ46363 fis, clone TESTI4050954	Q6ZRH0	40	12,35	12,24	18,33	1	n.d.
Cell division cycle 2-like protein kinase 5	Q14004	52	0,00	10,23	2,45	2	0
Cell division cycle protein 20 homolog	Q12834	42	10,89	11,44	14,00	2	n.d.
Cell division protein kinase 5	Q00535	165	33,28	8,73	17,81	7	0

Table 2. continued

Protein Name and Species	**Accession**	**Score**	**MW [kDa]**	**pI**	**SC [%]**	**# Pept.**	**regulated**
Cell growth-inhibiting protein 38	O00422	117	17,55	9,88	16,34	4	0
Cellular nucleic acid binding protein beta variant 2	Q4JGY0	41	18,96	9,31	8,72	1	--
Cellular retinoic acid-binding protein 1	P29762	268	15,42	5,13	65,44	14	--
Cellular retinoic acid-binding protein 2	P29373	186	15,55	5,23	50,36	7	0
Cementum attachment protein	Q6JIC5	61	14,92	9,22	10,00	2	0
Centaurin-beta-1	Q15027	54	81,54	9,22	4,52	2	n.d.
CENTG3 protein	Q86ST5	50	61,82	11,79	6,60	2	n.d.
Centrosomal protein of 41 kDa	Q9BYV8	54	41,28	9,29	11,26	2	n.d.
Chaperonin 10-related protein	Q9UNM1	41	10,29	9,27	8,25	2	+
Chaperonin containing TCP1, subunit 3 (Gamma)	Q59H77	72	63,54	6,02	5,20	2	--
Chloride intracellular channel protein 1	O00299	88	26,77	4,94	7,08	2	n.d.
Chloride intracellular channel protein 4	Q9Y696	156	28,62	5,33	12,30	3	--
Choriogonadotropin subunit beta	P01233	53	0,00	10,48	24,53	2	n.d.
Chromatin-modifying protein 4b	Q9H444	106	24,93	4,61	12,05	3	-
Chromobox protein homolog 3	Q13185	44	20,81	5,08	9,29	2	--
Chromobox protein homolog 8	Q9HC52	53	43,37	10,43	6,17	2	n.d.
Chromodomain helicase DNA binding protein 5	Q5TG85	41	91,97	5,42	1,73	1	n.d.
Chromosome 1 open reading frame 26 [Fragment]	Q5TC96	51	17,82	10,64	12,50	2	n.d.
Chromosome 10 open reading frame 8	Q5T8Y8	40	20,18	9,09	6,82	1	n.d.
Chromosome 7 open reading frame 11	A4D1W6	129	19,14	10,60	13,97	1	n.d.
Chromosome 9 open reading frame 32	Q5SZB9	51	15,89	9,99	13,79	2	--
Chromosome 9 open reading frame 49 (Coiled-coil-helix-coiled-coil-helix domain-containing protein 9)	Q5T1J5	117	15,48	11,37	18,54	1	n.d.
Cingulin-like protein 1	Q0VF96	51	0,00	5,56	1,31	2	n.d.
Citrate synthase [Precursor]	O75390	51	45,59	6,55	2,69	4	n.d.
CKAP1 protein	Q6FGY5	148	21,79	4,69	21,76	10	0
Clathrin	Q53Y37	41	23,17	4,48	6,16	1	--
Clathrin heavy chain 1	Q00610	176	191,40	5,39	3,52	11	--
Clathrin light chain A	P09496	218	25,69	4,26	18,22	4	--
c-Myc-responsive protein Rcl (reactive center loop)	O43598	243	19,10	4,82	22,99	7	0
Cofilin-1	P23528	132	18,36	9,19	18,79	9	0
Coiled-coil domain-containing protein 124	Q96CT7	81	25,82	10,03	13,00	5	0
Coiled-coil domain-containing protein 16	Q96NB3	50	41,99	11,79	26,79	2	n.d.
Coiled-coil domain-containing protein 47 [Precursor]	Q96A33	41	41,57	9,71	2,79	2	0
Coiled-coil domain-containing protein 56	Q9Y2R0	54	11,72	9,96	12,26	2	++
Coiled-coil domain-containing protein 58	Q4VC31	63	16,27	9,23	9,93	2	0
Coiled-coil domain-containing protein 74B	Q96LY2	48	41,83	10,99	7,01	3	n.d.
Coiled-coil-helix-coiled-coil-helix domain containing 3	A4D1N4	209	26,14	9,32	29,96	8	++
Cold inducible RNA binding protein	Q53XX5	41	18,64	9,78	8,14	2	+
Collagen alpha-1(VII) chain [Precursor]	Q02388	76	295,08	5,82	2,34	3	n.d.
Collagen alpha-1(XI) chain [Precursor]	P12107	54	181,12	4,94	2,55	4	0
Collagen alpha-1(XX) chain [Precursor]	Q9P218	53	140,20	8,48	2,33	2	n.d.
Collagen alpha-1(XXV) chain	Q9BXS0	51	0,00	9,60	6,23	2	n.d.
Collagen alpha-2(I) chain [Precursor]	P08123	51	72,21	8,95	7,97	2	++
Collagen alpha-2(V) chain [Precursor]	P05997	54	145,21	5,97	1,80	2	n.d.
Collagen alpha-2(XI) chain [Precursor]	P13942	89	171,78	9,21	4,40	3	n.d.
Collagen alpha-3(IV) chain [Precursor]	Q01955	46	161,81	10,13	3,87	2	n.d.
Collagen alpha-3(VI) chain [Precursor]	P12111	56	343,58	6,39	1,26	7	0
Collagen alpha-4(IV) chain [Precursor]	P53420	44	164,00	6,87	6,57	2	n.d.
COMM domain containing 3 [Fragment]	Q5T8Y8	52	20,18	9,09	6,82	1	n.d.
Core binding factor beta	Q13951	127	21,49	6,26	28,02	4	0
Core binding factor beta isoform PEBP2B	Q9HCT2	144	21,98	5,34	29,95	6	--
Core histone macro-H2A.2	Q9P0M6	97	39,90	10,28	7,28	4	++
Coronin, actin binding protein, 1C variant [Fragment]	Q53G58	147	53,25	6,74	10,76	6	--
Corticotropin-lipotropin [Precursor]	P01189	193	4,54	9,26	100,00	18	n.d.
Creatine kinase B-type	P12277	440	42,62	5,25	22,31	15	-
Creatine kinase, ubiquitous [Precursor]	P12532	165	46,94	9,57	11,75	3	+
Crk-like protein	P46109	111	33,76	6,28	21,45	3	++
Crumbs homolog 2 [Precursor]	Q5IJ48	55	99,76	5,75	4,20	2	n.d.
C-terminal binding protein 1	Q4KMQ8	107	47,47	6,30	6,82	3	--
C-terminal binding protein 2	Q5SQP8	102	56,07	6,54	7,80	4	--
C-type lectin domain family 14 member A [Precursor]	Q86T13	41	12,55	11,74	14,52	2	-
Cyclin-dependent kinase 4 inhibitor C	P42773	90	16,98	6,34	15,38	1	n.d.
Cyclin-dependent kinase 6, chain A	Q00534	223	34,61	6,53	20,00	5	++
Cyclin-dependent kinase 9	P50750	48	42,73	9,65	3,76	1	0
Cyclin-dependent kinases regulatory subunit 1	P61024	84	9,65	9,39	36,71	2	n.d.
Cystathionine beta-synthase	P35520	62	60,42	6,21	3,09	1	--
Cysteine-rich protein 2 variant [Fragment]	Q53FN1	99	22,48	9,94	12,98	8	0
Cytochrome b5 type B [Precursor]	O43169	157	16,33	4,57	43,93	30	-
Cytochrome b-c1 complex subunit 1[Precursor]	P31930	107	52,61	5,92	5,21	3	+
Cytochrome b-c1 complex subunit 2 [Precursor]	P22695	74	48,41	9,32	5,74	5	++
Cytochrome b-c1 complex subunit 8	O14949	187	8,36	11,98	56,00	7	++
Cytochrome c oxidase subunit 2	P00403	60	25,57	4,53	4,41	1	n.d.
Cytochrome c oxidase subunit 2	Q85KX8	56	25,55	4,53	4,41	1	n.d.

Table 2. continued

Protein Name and Species	Accession	Score	MW [kDa]	pI	SC [%]	# Pept.	regulated
Cytochrome c-1	P08574	85	35,40	9,82	12,31	2	n.d.
Cytoglobin	Q8WWM9	45	21,39	6,36	7,89	2	n.d.
Cytosol aminopeptidase	P28838	95	52,61	6,32	6,78	3	0
Cytosolic 5'-nucleotidase 1B	Q96P26	57	68,80	9,82	4,59	2	n.d.
Cytosolic carboxypeptidase 3	Q8NEM8	55	7,47	11,83	30,43	2	n.d.
Cytosolic carboxypeptidase-like protein 5	Q8NDL9	54	97,53	10,25	4,18	2	n.d.
D(1B) dopamine receptor	P21918	56	52,93	5,12	2,52	2	n.d.
D-3-phosphoglycerate dehydrogenase	O43175	187	56,48	6,31	10,34	10	--
Dapper homolog 3	Q96B18	54	0,00	12,29	7,92	2	n.d.
D-dopachrome decarboxylase	P30046	212	12,57	8,07	36,75	10	-
DDX19B protein [Fragment]	Q2NL95	82	50,61	7,68	5,79	2	--
DDX48 protein	Q6IBQ2	151	46,84	6,32	7,54	4	++
DEAD box polypeptide 17 isoform p82 variant (Fragment)	Q59F66	59	81,02	9,02	3,80	2	--
Dedicator of cytokinesis 1	Q5VXF6	52	220,59	6,90	1,62	2	n.d.
Dedicator of cytokinesis protein 6	Q96HP0	55	229,66	6,31	1,86	2	n.d.
Dehydrogenase/reductase SDR family member 4-like protein 2	Q6PKH6	40	0,00	11,10	10,00	1	n.d.
Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase [Precursor]	Q13011	114	35,79	9,19	8,84	7	++
Deoxycytidine kinase	Q5TZY7	42	30,51	5,00	7,69	1	n.d.
Desmin	P17661	94	53,49	5,07	12,16	5	0
Destrin	P60981	104	18,36	9,30	15,24	4	0
DHX9 protein [Fragment]	Q6PJK6	61	67,40	5,77	3,67	6	n.d.
Diacylglycerol kinase zeta	Q13574	47	124,04	10,18	3,85	2	n.d.
Dihydropyridine receptor alpha 2 subunit	Q9UIU0	66	125,23	5,07	2,52	3	++
Dihydropyrimidinase-related protein 2	Q16555	95	21,40	10,40	15,15	5	--
Dimethylargininase-1	O94760	40	30,97	5,45	3,87	2	0
Dimethylargininase-2	O95865	291	29,63	5,61	37,54	9	+
Dimethylarginine dimethylaminohydrolase 1	O94760	82	30,97	5,45	7,39	3	+
Disks large homolog 5	Q8TDM6	58	201,96	8,64	1,27	2	n.d.
Disks large-associated protein 3	O95886	50	106,04	9,82	2,96	4	n.d.
DNA (cytosine-5)-methyltransferase 1	P26358	50	183,17	8,86	2,72	4	n.d.
DNA damage-binding protein 1	Q16531	49	126,83	5,01	1,40	2	--
DNA polymerase epsilon subunit 3	Q9NRF9	45	16,85	4,53	11,56	1	--
DNA polymerase subunit delta-3	Q15054	42	54,05	10,09	2,65	1	n.d.
DNA replication licensing factor MCM4	P33991	67	102,98	9,22	3,68	4	n.d.
DNA-(apurinic or apyrimidinic site) lyase	P27695	166	31,06	8,77	36,00	6	0
DNAation factor, 45kDa, alpha polypeptide	Q5T6G5	89	29,39	4,33	11,57	5	n.d.
DNA-binding protein amplifying expression of surfactant protein B	Q13862	40	11,06	12,23	16,04	1	n.d.
DNA-dependent protein kinase catalytic subunit	P78527	61	465,27	6,89	0,59	4	n.d.
DnaJ homolog subfamily B member 1	P25685	60	37,89	9,42	6,49	3	--
DnaJ homolog subfamily C member 17	Q9NVM6	42	34,67	9,27	5,26	1	n.d.
DnaJ homolog subfamily C member 9	Q8WXX5	109	29,89	5,46	13,85	4	+
DnaJA2	Q86TL9	172	37,02	9,78	24,47	7	++
DNAJB11 protein	Q6IAQ8	122	40,52	5,76	12,29	8	0
Down syndrome cell adhesion molecule splice variant [Fragment]	Q8WY19	50	0,00	8,74	2,29	2	n.d.
Down-regulator of transcription 1 variant	Q53F47	46	19,46	4,53	5,68	2	0
Drebrin	Q16643	72	71,25	4,25	4,01	2	--
Drebrin-like protein variant	Q59FH4	39	0,00	4,91	5,87	1	n.d.
DTYMK protein [Fragment]	Q6FGU2	43	23,80	9,34	5,66	2	0
Dual oxidase 1 [Precursor]	Q9NRD9	59	177,16	9,00	1,55	2	n.d.
Dual specificity mitogen-activated protein kinase kinase 1	Q02750	86	43,28	6,19	6,12	3	--
Dual specificity protein phosphatase 23	Q9BVJ7	80	16,58	9,61	16,67	2	n.d.
Dual specificity tyrosine-phosphorylation-regulated kinase 2	Q92630	61	66,61	10,31	6,49	2	n.d.
dUTP pyrophosphatase	P33316	160	26,55	10,19	18,90	7	--
Dynactin 2 variant [Fragment]	Q53H88	145	44,79	4,89	10,10	4	-
Dynein light chain 2A	Q9NP97	85	10,78	7,68	12,63	2	n.d.
E2-induced gene 5 protein	Q96A26	73	17,33	10,59	9,09	2	-
E3 ubiquitin-protein ligase BRE1B	O75150	48	0,00	5,92	3,79	2	n.d.
E3 ubiquitin-protein ligase CBL	P22681	45	99,58	6,09	1,88	1	n.d.
E3 ubiquitin-protein ligase EDD1	O95071	54	309,16	5,51	1,04	2	n.d.
E3 ubiquitin-protein ligase RNF123	Q5XPI4	48	148,15	6,31	2,51	2	n.d.
E3 ubiquitin-protein ligase SIAH1	Q8IUQ4	62	31,12	6,40	7,45	4	n.d.
EBNA1BP2 protein	Q6IB29	123	34,83	10,59	11,11	7	0
Ecto-ADP-ribosyltransferase 5 [Precursor]	Q96L15	41	0,00	9,68	6,85	1	n.d.
EF-hand calcium-binding domain-containing protein 4A	Q8N4Y2	59	49,04	11,71	8,33	3	n.d.
EH domain-binding protein 1-like protein 1	Q8N3D4	59	160,21	4,62	1,39	2	n.d.
EIF3H protein	Q5BKY2	42	39,58	5,95	4,30	1	0
EIF3S4 protein	Q6IAM0	51	35,58	5,80	7,50	3	+
EIF3S5 protein	Q6IB45	90	37,54	5,13	8,96	2	n.d.

Table 2. continued

Protein Name and Species	Accession	Score	MW [kDa]	pI	SC [%]	# Pept.	regulated
Elastase-3B [Precursor]	P08861	41	17,36	7,71	9,76	1	n.d.
Elastin microfibril interfacer 1	Q9Y6C2	61	59,86	4,46	5,00	2	n.d.
ELAV (Embryonic lethal, abnormal vision, Drosophila)-like 1 oder Heterogeneous nuclear ribonucleoprotein A3, geringer Blast Score	Q53XN6	300	36,07	9,79	21,78	18	0
Electron transfer flavoprotein subunit beta	P38117	87	27,70	9,31	12,99	7	+
ELK1, member of ETS oncogene family variant [Fragment]	Q59GR2	59	53,33	8,81	4,73	2	n.d.
Elongation factor 1-alpha 1	P68104	487	49,51	7,92	23,89	49	0
Elongation factor 1-delta	P29692	413	30,97	4,75	30,36	31	0
Elongation factor 1-gamma	P26641	332	49,96	6,26	16,74	13	--
Elongation factor 2	P13639	191	95,15	6,42	7,00	23	--
Elongation factor RNA polymerase II variant [Fragment]	Q59HG4	52	62,09	10,06	6,37	2	n.d.
Elongation factor Tu [Precursor]	P49411	319	49,51	7,92	16,81	11	++
Emerin	Q5HY57	55	24,92	4,70	7,76	1	n.d.
Endoplasmic reticulum protein ERp29 [Precursor]	P30040	63	28,98	7,52	8,05	4	0
Endoplasmic reticulum-associated amyloid beta-peptide-binding protein	Q99714	92	26,78	9,19	11,92	3	++
Endoplasmin [Precursor]	Q95M18	93	92,28	4,62	3,12	4	0
Endothelial differentiation-related factor 1	O60869	180	16,36	10,44	35,81	8	++
Endothelial monocyte-activating polypeptide 2	Q12904	116	34,33	9,43	6,73	2	-
Enhancer of yellow 2 transcription factor homolog	Q9NPA8	128	11,52	10,16	28,71	5	0
Enolase alpha	P06733	593	47,01	7,70	26,79	256	--
Enolase gamma	P09104	320	47,11	4,76	17,78	67	0
Ester hydrolase C11orf54	Q9H0W9	52	35,03	6,25	6,98	2	n.d.
Eukaryotic initiation factor 4A-II	Q14240	401	46,12	5,19	25,37	19	0
Eukaryotic initiation factor 4A-III	P38919	262	46,71	6,32	15,85	17	0
Eukaryotic translation initiation factor 2 subunit 1	P05198	79	35,96	4,86	6,69	2	0
Eukaryotic translation initiation factor 2, subunit 2 beta, 38kDa	Q6IBR8	68	38,36	5,49	6,61	4	--
Eukaryotic translation initiation factor 3 subunit 3	O15372	55	39,58	5,95	4,30	2	0
Eukaryotic translation initiation factor 3 subunit 5	O00303	212	37,54	5,13	14,01	3	n.d.
Eukaryotic translation initiation factor 3 subunit 8	Q99613	52	105,28	5,41	1,64	1	n.d.
Eukaryotic translation initiation factor 3, subunit 1	O75822	108	29,04	4,56	8,14	1	--
Eukaryotic translation initiation factor 4A-I	P60842	295	46,12	5,19	19,95	31	0
Eukaryotic translation initiation factor 4B	Q4G0E3	68	69,06	5,34	2,62	2	--
Eukaryotic translation initiation factor 4H	Q15056	200	25,47	9,25	18,70	10	0
Eukaryotic translation initiation factor 5A-1	P63241	192	16,82	4,94	14,94	5	n.d.
Eukaryotic translation initiation factor 6	P56537	126	11,82	5,85	25,93	2	n.d.
Ewing sarcoma breakpoint region 1	Q96FE8	46	68,35	9,73	2,90	1	n.d.
Exosome complex exonuclease MTR3	Q5RKV6	40	28,22	6,02	5,88	1	n.d.
Exportin-2	P55060	61	110,26	5,52	2,68	2	n.d.
Ezrin (Cytovillin)	P15311	124	69,22	5,89	6,32	4	-
Facilitates chromatin transcription complex subunit SPT16	Q9Y5B9	66	71,95	9,07	6,00	2	0
FACT complex subunit SSRP1	Q08945	72	81,02	6,46	3,39	2	-
F-actin capping protein subunit alpha-1	P52907	124	32,90	5,36	17,83	3	0
F-actin-capping protein subunit beta	P47756	151	31,20	5,24	17,39	5	-
Far upstream element-binding protein 1 / DNA helicase V	Q96AE4	117	67,43	7,78	6,84	8	--
Farnesyl pyrophosphate synthetase	P14324	190	40,51	4,91	16,15	4	0
Fascin	Q16658	355	54,37	7,02	14,02	57	0
Fatty acid-binding protein	Q01469	60	15,02	7,62	15,67	2	-
FBL protein	Q96BS4	230	28,43	9,99	28,85	7	++
FERM domain-containing protein 4A	Q9P2Q2	50	113,97	9,57	3,71	3	n.d.
Ferritin heavy chain	P02794	62	21,23	6,13	4,85	2	++
Ferritin light chain	P02792	101	26,81	5,44	13,28	2	n.d.
Fibronectin type 3 and ankyrin repeat domains protein 1	Q8TC84	173	34,18	9,73	14,69	4	--
Ficolin-2 [Precursor]	Q15485	44	7,70	10,61	14,06	2	+
Filamin-A	P21333	62	280,45	5,69	11,29	4	--
FK506-binding protein 1A (Peptidyl-prolyl cis-trans isomerase)	P62942	168	11,81	9,24	46,73	6	0
FK506-binding protein 2	P26885	103	15,64	10,05	15,49	3	0
FK506-binding protein 2 [Precursor] (Peptidyl-prolyl cis-trans isomerase)	P26885	111	15,64	10,05	15,49	5	0
FK506-binding protein 4 (Peptidyl-prolyl cis-trans isomerase)	Q02790	132	51,64	5,22	6,99	2	n.d.
Flap endonuclease 1	P39748	299	42,57	9,53	26,32	17	-
FLJ00279 protein	Q6ZNL4	55	65,73	9,69	4,44	2	--
FLYWCH-type zinc finger 1	Q4VC44	59	80,04	9,77	5,59	4	n.d.
FMI protein	Q92735	62	0,00	5,97	2,08	3	n.d.
Forkhead box D2	Q5SVZ3	60	0,00	6,86	6,87	3	n.d.
Forkhead box protein L1	Q12952	49	36,49	10,10	6,09	1	n.d.
Four and a half LIM domains 1 [Fragment]	Q5JXH7	65	23,31	9,95	12,68	2	0
FRAS1-related extracellular matrix protein 2 [Precursor]	Q5SZK8	44	350,94	4,75	0,92	2	n.d.
Fructosamine-3-kinase	Q9H479	64	35,15	7,87	8,41	2	0
Fructose-bisphosphate aldolase A	P04075	435	39,26	9,24	34,71	37	--

Table 2. continued

Protein Name and Species	Accession	Score	MW [kDa]	pI	SC [%]	# Pept.	regulated
Fructose-bisphosphate aldolase C	P09972	259	39,43	6,46	14,01	7	0
FUN14 domain containing 2 [Fragment]	Q5HYP8	46	23,32	11,07	4,59	1	+
FUS interacting protein (Serine/arginine-rich) 1	Q5JRI1	268	20,90	10,89	35,47	11	n.d.
FWP004	Q5QTS3	57	23,65	11,57	8,87	2	0
G protein-regulated inducer of neurite outgrowth 1	Q7Z2K8	52	102,31	9,25	5,38	4	n.d.
G protein-regulated inducer of neurite outgrowth 2	O60269	39	47,42	6,30	3,49	1	n.d.
GABA(A) receptor-associated protein	Q6IAW1	43	13,91	9,22	15,38	1	n.d.
Galactosidase, beta 1 variant (Fragment)	Q53G40	44	76,02	6,11	1,48	1	n.d.
Galactosylgalactosylxylosylprotein 3-beta-glucuronosyltransferase 2	Q9NPZ5	53	36,92	12,18	8,61	2	n.d.
Galectin 1	P09382	104	14,71	5,18	35,56	4	--
Gametogenetin	Q86UU5	54	66,83	11,39	8,13	4	n.d.
Gamma-aminobutyraldehyde dehydrogenase	P49189	77	50,92	5,59	5,79	2	--
Gamma-glutamyltranspeptidase 1 [Precursor]	P19440	42	0,00	9,49	3,01	1	n.d.
GAPDH Glyceraldehyde-3-phosphate dehydrogenase	P04406	230	35,85	6,63	11,34	96	0
GATA-4 protein [Fragment]	Q13222	51	20,10	12,09	13,79	2	n.d.
GATS protein [Fragment]	Q6PII7	52	26,08	12,26	18,93	4	--
GATS protein [Fragment]	Q6P198	50	23,59	12,09	8,26	2	n.d.
GDP dissociation inhibitor 2 [Fragment]	Q5SX87	71	29,84	6,25	8,37	3	0
General transcription factor 3C polypeptide 1	Q12789	52	238,27	7,16	1,42	2	n.d.
Glia maturation factor beta	P60983	110	13,41	5,10	35,34	5	0
Glioblastoma amplified sequence (Fragment)	Q53X96	70	33,72	9,96	6,29	3	0
Glucose phosphate isomerase variant [Fragment]	Q59F85	52	0,00	10,85	4,23	1	n.d.
Glucose-6-phosphate 1-dehydrogenase	Q2Q9B8	282	54,79	6,70	17,05	7	0
Glucose-6-phosphate isomerase	P06744	161	62,98	9,14	7,18	21	--
Glutamate dehydrogenase 1	P00367	64	61,36	8,53	3,58	2	++
Glutaredoxin-related protein 5	Q86SX6	61	16,65	6,36	8,92	1	n.d.
Glutathione S-transferase Mu 3	P21266	48	26,41	5,25	4,91	1	n.d.
Glutathione S-transferase P	P09211	196	23,34	5,32	30,95	21	0
Glutathione transferase omega-1	P78417	78	27,55	6,26	17,86	15	0
Glycine/arginine-rich protein 1	Q9H7Z4	65	32,13	12,79	12,46	4	n.d.
Glycosyltransferase-like protein LARGE1	O95461	63	88,07	9,55	4,04	2	n.d.
Golgi-associated PDZ and coiled-coil motif-containing protein	Q9HD26	40	50,49	5,54	6,93	2	n.d.
Golgin subfamily B member 1	Q14789	44	376,02	4,82	1,24	2	n.d.
G-protein coupled receptor 143	P51810	52	0,00	8,83	4,95	1	n.d.
Growth factor receptor-bound protein 2	P62993	59	11,42	9,86	15,31	2	n.d.
GTP cyclohydrolase I	P30793	44	23,12	7,78	13,88	1	n.d.
GTPase NRas [Precursor]	P01111	48	4,41	7,11	28,21	2	n.d.
GTP-binding and GTPase-activating protein 2	Q99490	45	124,67	10,63	4,11	2	--
GTP-binding protein ARD-1	P36406	41	64,07	6,43	10,37	1	n.d.
Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta 1	P62873	186	37,22	5,56	19,17	16	0
Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta 2	P62879	84	56,52	5,14	9,64	3	0
Guanine nucleotide-binding protein subunit beta-2-like 1 (RACK 1)	P63244	62	34,92	8,83	3,16	3	n.d.
H/ACA ribonucleoprotein complex subunit 2	Q9NX24	147	17,19	9,43	26,14	5	++
H/ACA ribonucleoprotein complex subunit 3	Q9NPE3	52	8,25	5,09	35,06	2	n.d.
H1 histone family member O, oocyte-specific	Q8IZA3	49	35,81	11,76	12,14	2	0
Haloacid dehalogenase-like hydrolase domain-containing protein 2	Q9H0R4	41	28,52	5,81	7,34	1	+
Heat shock protein 10 kDa	P61604	75	10,79	9,19	17,82	3	+
Heat shock protein 27 kDa	P04792	222	22,77	5,97	21,95	14	--
Heat shock protein 40 kDa protein 1	P25685	78	37,89	9,42	8,26	4	0
Heat shock protein 40 kDa protein 4	P31689	135	44,85	6,78	7,30	2	-
Heat shock protein 60 kDa	Q38L19	102	61,17	5,59	6,96	4	-
Heat shock protein 60 kDa [Fragment]	Q9UCR6	50	2,99	4,38	37,93	3	0
Heat shock protein 60 kDa [Precursor]	P10809	268	61,17	5,59	15,48	37	0
Heat shock protein 70 kDa 1-like variant	Q53FA3	107	70,36	5,90	5,62	2	n.d.
Heat shock protein 70 kDa protein 1	P08107	342	70,05	6,75	19,47	56	0
Heat shock protein 70 kDa protein 1L	P34931	133	70,36	5,67	6,86	4	n.d.
Heat shock protein 70 kDa protein 6	P17066	138	70,81	5,59	9,80	10	--
Heat shock protein 70 kDa protein 8	P11142	560	70,85	5,24	22,76	29	--
Heat shock protein 70 kDa protein 8 isoform 1 variant [Fragment]	Q53GZ6	325	70,86	5,14	15,48	91	0
Heat shock protein 70 kDa protein 8 isoform 2 variant [Fragment]	Q53HF2	376	53,47	5,52	23,73	50	0
Heat shock protein 70 kDa protein 9	P38646	160	73,68	5,98	8,10	12	-
Heat shock protein 70kDa A5	Q2KHP4	444	72,38	4,92	21,22	30	--
Heat shock protein 75 kDa [Precursor]	Q12931	103	66,01	7,07	2,42	41	0
Heat shock protein 90 kDa AA1	Q96HX7	105	49,16	5,32	5,69	2	n.d.
Heat shock protein 90 kDa AA1 protein [Fragment]	Q2VPJ6	485	68,33	4,97	15,38		n.d.
Heat shock protein 90 kDa AB1	Q5T9W4	129	19,66	9,75	19,41	4	n.d.

Table 2. continued

Protein Name and Species	Accession	Score	MW [kDa]	pI	SC [%]	# Pept.	regulated
Heat shock protein 90 kDa alpha	P07900	320	98,08	4,93	8,67	61	0
Heat shock protein 90 kDa beta	P08238	381	83,08	4,82	11,07	83	0
Heat shock protein 90 kDa beta member 1 (Endoplasmin)	P14625	328	92,28	4,62	11,47	50	-
Heat shock protein apg-1 (HSP 70 family)	Q53ZP9	52	94,45	5,56	4,29	2	--
Heat shock-related 70 kDa protein 2	P54652	167	69,95	5,44	6,42	4	n.d.
Heat-responsive protein 12	Q6IBG0	135	14,48	9,41	25,55	7	0
Hematological and neurological expressed 1 protein	Q9UK76	40	15,87	5,35	7,84	1	n.d.
Heparin-binding protein HBp15	Q7Z4W8	150	14,81	9,84	36,72	15	+
Hepatopoietin PCn127	Q1AHP8	65	28,00	3,88	5,71	6	0
HERV-K_5q33.3 provirus ancestral Gag polyprotein	P87889	42	0,00	9,72	1,50	1	n.d.
Heterogeneous nuclear ribonucleoprotein A0	Q6IB18	135	30,82	9,81	14,43	15	0
Heterogeneous nuclear ribonucleoprotein A1 (Helix-destabilizing protein)	P09651	498	38,69	9,65	26,42	93	0
Heterogeneous nuclear ribonucleoprotein A3 (oder A1, A2/B1)	P51991	257	39,57	9,58	10,14	22	+
Heterogeneous nuclear ribonucleoprotein AB isoform a variant [Fragment]	Q53F64	77	35,97	7,59	6,93	1	--
Heterogeneous nuclear ribonucleoprotein C-like 1 [Fragment]	Q6PKD2	143	22,64	10,41	6,28	6	0
Heterogeneous nuclear ribonucleoprotein D-like	Q6SPF2	240	33,19	8,83	19,80	12	0
Heterogeneous nuclear ribonucleoprotein F	P52597	466	45,64	5,27	29,40	25	0
Heterogeneous nuclear ribonucleoprotein G	P38159	501	47,42	9,86	35,93	23	++
Heterogeneous nuclear ribonucleoprotein H (hnRNP H)	P31943	480	49,07	5,87	21,43	48	0
Heterogeneous nuclear ribonucleoprotein H3	P31942	432	36,90	6,41	36,99	21	0
Heterogeneous nuclear ribonucleoprotein H3 isoform a variant [Fragment]	Q53F48	337	36,90	6,97	22,54	20	0
Heterogeneous nuclear ribonucleoprotein I	P26599	255	57,19	9,76	10,36	41	0
Heterogeneous nuclear ribonucleoprotein K	P61978	68	9,68	9,30	21,35	2	0
Heterogeneous nuclear ribonucleoprotein K transcript variant	Q5EC54	361	51,03	5,05	22,20	48	0
Heterogeneous nuclear ribonucleoprotein L	P14866	83	64,05	9,20	5,43	7	--
Heterogeneous nuclear ribonucleoprotein M (hnRNP M)	P52272	168	77,33	9,59	9,05	42	--
Heterogeneous nuclear ribonucleoprotein Q	O60506	87	68,32	9,50	4,24	2	n.d.
Heterogeneous nuclear ribonucleoprotein R	O43390	87	68,32	9,50	4,24	2	n.d.
Heterogeneous nuclear ribonucleoprotein U	Q00839	358	88,92	5,50	14,64	64	0
Heterogeneous nuclear ribonucleoprotein U (Scaffold attachment factor A) (Fragment)	Q5RI17	154	79,79	8,83	9,54	15	0
Heterogeneous nuclear ribonucleoprotein-R2	Q2L7G6	82	66,94	8,96	4,54	6	0
Heterogeneous nuclear ribonucleoproteins A2/B1	P22626	893	35,98	9,10	49,85	123	+
Heterogeneous nuclear ribonucleoproteins C1/C2	P07910	449	32,32	4,79	29,01	54	0
High mobility group AT-hook 1	Q5T6U8	59	10,67	10,82	40,63	2	n.d.
High mobility group protein B1	P09429	92	24,75	5,49	17,28	13	0
High mobility group protein B2	P26583	170	23,89	8,74	15,87	13	++
High mobility group-like nuclear protein 2 homolog 1	P55769	95	14,03	9,69	14,96	7	++
Histidine triad nucleotide binding protein 2	Q5TCW3	121	17,15	9,81	25,15	4	0
Histidine triad nucleotide-binding protein 1	P49773	183	13,79	6,49	48,41	10	-
Histone cluster 1, H1e	Q4VB24	158	21,88	11,53	21,00	7	++
Histone cluster 2, H3, pseudogene 2	Q5TEC6	438	15,42	11,89	50,74	43	++
Histone deacetylase 5	Q9UQL6	41	0,00	5,75	1,85	1	n.d.
Histone H1.0	P07305	138	20,87	11,40	17,53	7	++
Histone H1.2	P16403	242	21,22	11,43	36,79	6	++
Histone H1.4	P10412	279	21,85	11,53	35,78	26	++
Histone H1.5	P16401	180	22,44	11,41	20,44	16	++
Histone H1x	Q92522	108	22,47	11,23	13,15	4	--
Histone H2A type 1	P0C0S8	399	13,95	11,37	53,49	17	++
Histone H2A type 1-B	P04908	169	14,03	11,52	20,93	16	++
Histone H2A type 1-C	Q93077	571	13,97	11,52	85,27	40	+
Histone H2A type 2-A	Q6FI13	356	13,96	11,37	53,49	10	++
Histone H2A type 2-B	Q8IUE6	200	13,86	11,35	24,03	11	0
Histone H2A.x	P16104	88	15,00	11,18	11,97	2	+
Histone H2A.Z	P0C0S5	293	13,54	11,05	28,13	36	0
Histone H2AV	Q71UI9	231	13,50	11,05	28,13	18	++
Histone H2B	Q6GMR5	247	7,39	10,28	88,06	17	+
Histone H2B type 1-A	Q96A08	72	14,03	10,78	20,63	1	n.d.
Histone H2B type 1-B	P33778	205	13,81	10,78	60,00	20	++
Histone H2B type 1-C/E/F/G/I	P62807	226	13,68	10,78	59,68	9	+
Histone H2B type 1-J	P06899	45	13,61	10,53	5,60	7	++
Histone H2B type 1-N	Q99877	209	13,78	10,78	60,00	9	+
Histone H2B type 2-C	Q6DN03	65	21,33	12,18	13,02	3	++
Histone H2B type 2-E	Q16778	223	13,78	10,78	60,00	9	+
Histone H3.1	P68431	420	15,43	11,89	59,12	156	++
Histone H3.3	P84243	455	15,19	11,89	60,00	67	++
Histone H3-like	Q6NXT2	51	15,23	11,88	23,70	2	++

Table 2. continued

Protein Name and Species	Accession	Score	MW [kDa]	pI	SC [%]	# Pept.	regulated
Histone H3L-like	Q6TXQ4	201	12,10	11,24	63,55	7	++
Histone H4	P62805	444	11,36	11,85	75,73	74	++
Histone-binding protein RBBP4	Q09028	56	6,52	4,37	27,27	1	n.d.
HLA-B associated transcript 1 [Fragment]	Q5STU9	45	18,51	5,67	6,21	2	n.d.
HMG-1	Q14321	108	24,98	5,65	15,35	4	0
HMGA1 protein	Q6IPL9	155	11,56	11,82	52,34	3	n.d.
HMOX2 protein (Fragment)	Q6FHB5	44	36,03	5,19	6,01	1	n.d.
HNRPCL1 protein (Fragment)	Q6PKD2	166	22,64	10,41	15,46	16	0
Homeobox protein cut-like 1	P39880	53	0,00	5,66	2,59	2	n.d.
Homeobox protein Hox-A10	P31260	50	40,54	12,21	4,03	2	n.d.
Homo sapiens (clone S25) gene from CpG-enriched DNA, partial cds. [Fragment]	Q14075	40	0,00	10,75	23,08	1	n.d.
Hook homolog 1	Q9UJC3	40	84,65	4,95	3,43	1	n.d.
Hornerin	Q5U1F4	52	282,20	10,42	1,40	5	n.d.
H-Ras-1 (GTPase HRas [Precursor])	P01112	48	21,28	5,02	6,35	1	n.d.
HSALDA2 NID: - Homo sapiens	CAA29654	98	11,93	9,46	39,81	3	0
HSATPFIB NID: - Homo sapiens	CAA27246	95	57,92	5,75	5,38	2	n.d.
HSTUBAG NID: - Homo sapiens	CAA25855	541	50,13	4,89	26,61	9	--
Hypothetical protein	Q6IPB4	135	22,43	5,24	25,00	6	--
Hypothetical protein	Q8WZ41	41	9,97	5,72	7,61	1	n.d.
Hypothetical protein (Ferritin P02794)	Q6GMW9	49	11,71	9,04	30,10	2	n.d.
Hypothetical protein (Fragment)	Q3B830	62	20,62	3,86	5,75	2	0
Hypothetical protein DKFZp686J01190 (Fragment)	Q7Z2V5	42	45,97	9,52	4,19	1	--
Hypothetical protein DKFZp686K23100	Q68D11	51	94,41	5,78	2,24	3	n.d.
Hypothetical protein DKFZp686L04275	Q7Z3M3	200	53,93	9,89	14,82	5	--
Hypothetical protein DKFZp686P07163	Q5HYB7	45	33,75	4,92	4,78	1	n.d.
Hypothetical protein FLJ23801	Q8TE87	59	19,48	12,60	17,74	2	n.d.
hypothetical protein KIAA0543	O60290	44	125,03	7,43	1,44	2	n.d.
Hypothetical protein LOC374920	Q86XI8	43	64,14	10,18	2,77	1	n.d.
Hypoxanthine-guanine phosphoribosyltransferase	P00492	91	24,43	6,25	13,82	1	n.d.
Hypoxia-inducible factor 3 alpha	Q9Y2N7	66	0,00	5,94	5,11	3	n.d.
IFIT5 protein	Q6IAX3	40	55,84	7,21	2,70	1	n.d.
Ig alpha-1 chain C region	P01876	119	50,99	8,97	5,68	2	n.d.
Ig heavy chain V-I region EU	P01742	58	12,47	9,37	28,57	2	n.d.
Ig heavy chain V-II region WAH	P01824	44	15,08	9,44	20,35	2	n.d.
Ig heavy chain V-III region BRO	P01766	68	13,23	6,71	20,28	2	n.d.
Ig heavy chain V-III region CAM	P01768	67	13,96	9,54	14,84	1	n.d.
Ig heavy chain V-III region GA	P01769	54	12,72	5,67	15,83	2	n.d.
Ig heavy chain V-III region HIL	P01771	57	8,06	k.A.	37,50	4	n.d.
Ig heavy chain V-III region TRO	P01762	39	14,19	9,46	14,96	1	n.d.
Ig heavy chain V-III region VH26 [Precursor]	P01764	41	12,58	4,68	44,23	2	n.d.
Ig heavy chain V-III region WEA	P01763	42	0,00	9,05	15,79	1	n.d.
Ig kappa chain V-I region CAR	P01596	39	11,70	9,39	15,09	1	n.d.
Ig kappa chain V-II region GM607	P06309	48	0,00	5,47	29,49	2	n.d.
Ig kappa chain V-III region CLL [Precursor]	P04207	72	11,87	10,13	17,86	2	n.d.
Ig lambda chain V-I region BL2 [Precursor]	P06316	40	11,61	4,87	15,45	2	n.d.
Ig lambda chain V-I region WAH	P04208	49	11,73	9,01	32,11	3	0
I-kappa-B-related protein variant [Fragment]	Q59GI3	51	97,07	5,76	4,91	2	n.d.
Immunglobulin lambda chain V-I region WAH	P04208	42	7,15	10,37	23,61	1	n.d.
Immunoglobulin J chain	P01591	53	18,09	4,95	9,30	2	n.d.
Importin beta-1 subunit (Fragment)	Q14974	102	50,99	4,44	5,90	14	n.d.
Inosine-5'-monophosphate dehydrogenase 2	P12268	158	55,77	6,48	9,14	5	0
Inositol (1,3,4,5)-tetrakisphosphate 3-phosphatase	Q9UNW1	62	55,02	8,88	4,11	3	n.d.
Inositol-trisphosphate 3-kinase B	P27987	47	102,34	9,59	4,65	2	++
Insulin receptor substrate 2	Q9Y4H2	57	137,33	9,75	2,87	2	n.d.
Integrin alpha 3 isoform b, variant [Fragment]	Q59F03	57	82,00	9,23	3,87	3	n.d.
Integrin beta 4 binding protein	Q5JWN4	89	11,82	5,85	25,93	3	n.d.
Interferon-inducible double stranded RNA-dependent protein kinase activator A	O75569	79	31,62	9,59	10,07	3	0
Interleukin enhancer binding factor 2 variant [Fragment]	Q53FG3	170	43,02	5,05	7,18	6	0
Interleukin enhancer-binding factor 2	Q12905	108	43,04	5,05	6,41	6	0
Interleukin enhancer-binding factor 3	Q12906	124	95,28	9,35	4,47	6	0
Inversin	Q9Y283	49	117,83	10,14	3,00	2	n.d.
IQ motif and Sec7 domain-containing protein 2	Q5JU85	47	161,74	9,62	3,65	2	n.d.
Isochorismatase domain-containing protein 2 [Precursor]	Q96AB3	100	24,08	9,11	6,79	1	n.d.
Isocitrate dehydrogenase 1 (NADP+), soluble, isoform CRA_a	Q6FHQ6	84	46,63	6,60	4,59	4	0
Isocitrate dehydrogenase 2 (NADP+) [Fragment]	Q53GL5	212	50,88	9,45	13,05	13	0
Jerky homolog-like	Q32MC2	40	59,87	9,06	2,67	1	--
Kallikrein-like protein 5-related protein 2	Q9UKR2	36	11,98	12,20	8,11	1	n.d.
Keratin, type I cytoskeletal 10	P13645	225	59,49	5,04	8,26	18	n.d.
Keratin, type I cytoskeletal 14	P02533	42	51,46	4,94	3,18	1	n.d.
Keratin, type I cytoskeletal 17	Q04695	105	7,68	11,37	38,27	11	n.d.
Keratin, type I cytoskeletal 9	P35527	169	62,09	5,06	6,90	3	n.d.

Table 2. continued

Protein Name and Species	Accession	Score	MW [kDa]	pI	SC [%]	# Pept.	regulated
Keratin, type II cytoskeletal 1, (Hair alpha protein)	P04264	708	65,85	8,82	16,02	48	n.d.
Keratin, type II cytoskeletal 2 epidermal	P35908	317	65,39	8,85	14,24	20	n.d.
Keratin, type II cytoskeletal 4	P19013	47	35,64	4,96	2,78	1	n.d.
Keratin, type II cytoskeletal 5	P13647	68	62,34	8,61	4,41	2	n.d.
Keratin, type II cytoskeletal 6B	P04259	89	0,00	12,80	31,40	7	n.d.
Keratin, type II cytoskeletal 8	P05787	66	55,87	5,49	5,54	2	0
Ketosamine-3-kinase	Q9HA64	61	34,39	7,02	6,80	2	--
KH domain-containing, RNA-binding, signal transduction-associated protein 2	Q5VWX1	54	38,90	5,90	2,58	2	+
KHSRP protein	Q5U4P6	154	72,85	8,90	8,17	12	--
KIAA1856 protein [Fragment]	Q96JH1	48	0,00	10,06	3,44	4	n.d.
Kinesin heavy chain isoform 5A	Q12840	43	117,38	9,29	15,28	1	n.d.
Kinesin-like protein KIF26A	Q9ULI4	82	190,20	10,30	3,97	6	n.d.
L antigen family member 3	Q14657	54	14,79	10,44	16,08	1	n.d.
Lactosylceramide 4-alpha-galactosyltransferase	Q9NPC4	69	40,50	11,35	18,48	2	n.d.
Lactotransferrin [Precursor]	P02788	69	78,29	9,65	2,67	4	n.d.
Lamin-A/C	P02545	139	74,09	6,60	7,08	8	0
Lamin-B receptor	Q14739	69	0,00	10,70	14,77	4	n.d.
Lamin-B1	P20700	61	66,37	4,96	4,44	7	+
Laminin receptor-like protein LAMRL5	Q96RS2	87	33,04	5,52	11,86	3	0
Laminin subunit beta-3 [Precursor]	Q13751	43	0,00	7,89	1,47	1	n.d.
Laminin, alpha 2	Q5VUM2	41	343,68	5,99	0,38	1	n.d.
LANCL1 protein (Fragment)	Q6FHH6	98	45,24	8,75	7,77	2	++
Large proline-rich protein BAT2	P48634	78	228,86	9,96	1,76	10	n.d.
Latent-transforming growth factor beta-binding protein 4 [Precursor]	Q8N2S1	66	173,34	5,15	3,76	5	n.d.
Lectin, mannose-binding, 1 variant [Fragment]	Q53FS4	42	57,52	6,35	1,96	1	--
Lethal(3)malignant brain tumor-like protein	Q9Y468	45	0,00	9,55	4,36	2	0
Leucine-rich repeat flightless-interacting protein 1	Q32MZ4	50	0,00	4,63	3,80	1	n.d.
Leukocyte antigen CD37	P11049	45	0,00	10,27	13,68	2	--
Leukocyte specific transcript 1 [Fragment]	Q5STB1	47	2,83	7,06	39,29	1	n.d.
L-iditol 2-dehydrogenase	Q00796	193	38,29	9,30	16,53	3	n.d.
LIM and SH3 domain protein 1	Q14847	100	35,99	9,88	10,22	10	0
LIM domain kinase 2	Q7L3H5	46	77,84	6,71	3,79	2	n.d.
Lin-7 homolog C variant [Fragment]	Q53FX5	181	21,81	9,00	23,35	4	0
L-lactate dehydrogenase B chain	P07195	121	36,62	5,66	7,49	2	n.d.
L-lactate dehydrogenase C chain	P07864	107	36,27	7,83	3,61	7	n.d.
LOC389203 protein [Fragment]	Q9BRT5	74	9,69	0,00	41,57	3	0
LOC389533	A4D1I6	41	10,98	10,62	18,10	1	n.d.
LOC399818 protein	Q8TC28	40	0,00	5,33	7,81	1	-
LOC401385	A4D1C8	55	27,32	12,42	14,89	4	n.d.
Low molecular weight phosphotyrosine protein phosphatase	P24666	157	17,90	6,38	21,66	3	0
Low-density lipoprotein receptor-related protein 4 [Precursor]	O75096	43	0,00	4,99	1,54	2	n.d.
Low-density lipoprotein receptor-related protein 5 [Precursor]	O75197	51	179,15	5,98	0,47	1	n.d.
LSM2 protein	Q6FGG1	125	10,83	6,10	20,00	2	n.d.
Lysophospholipase I, isoform CRA_a	Q6IAQ1	40	24,65	6,34	5,65	1	n.d.
Lysosomal alpha-glucosidase [Precursor]	P10253	65	105,26	5,58	1,89	3	n.d.
Lysozyme C [Precursor]	P61626	122	16,53	10,60	14,19	8	n.d.
Macropain iota chain	P60900	107	27,38	6,42	11,38	2	n.d.
Macrophage migration inhibitory factor (Glycosylation-inhibiting factor)	P14174	122	12,34	9,35	21,05	31	n.d.
Malate dehydrogenase	Q6FHZ0	168	35,54	9,82	12,72	10	n.d.
Malate dehydrogenase [Fragment]	Q75MT9	99	33,21	9,47	4,75	5	n.d.
Malignant T cell amplified sequence 1	Q9ULC4	42	20,54	9,73	4,97	1	n.d.
Mannosyl-oligosaccharide glucosidase	Q13724	40	91,85	9,44	1,08	1	n.d.
Matrin-3	P43243	157	94,56	5,83	6,38	13	n.d.
MCM7 minichromosome maintenance deficient 7	A4D2A1	60	81,26	6,05	3,34	3	--
Mediator of RNA polymerase II transcription subunit 11	Q9P086	41	13,12	5,64	16,24	1	n.d.
Medium-chain specific acyl-CoA dehydrogenase [Precursor]	P11310	87	42,58	6,07	7,24	3	++
Melastatin-4	Q8TD43	53	134,22	9,46	2,72	4	n.d.
Membrane-associated progesterone receptor component 1	O00264	154	21,53	4,39	22,68	7	n.d.
Membrane-associated progesterone receptor component 2	O15173	55	23,80	4,59	8,97	2	n.d.
Membrane-associated RING finger protein 7	Q9H992	44	78,00	6,33	2,56	1	n.d.
Metastasis suppressor protein 1	O43312	55	82,25	5,93	7,67	2	n.d.
Methenyltetrahydrofolate cyclohydrolase	P13995	74	37,30	9,59	10,47	2	--
Methionine adenosyltransferase 2	P31153	176	43,63	6,02	11,39	5	0
Methionine adenosyltransferase II beta	Q9NZL9	187	37,53	7,09	16,47	8	0
Methionine sulfoxide reductase B2	Q5QP77	42	13,21	10,26	9,24	1	n.d.
Methyl-CpG-binding protein 2	P51608	51	0,00	10,15	17,35	6	+
MGC70857 protein	Q6GMR2	82	22,79	11,98	16,35	2	n.d.

Table 2. continued

Protein Name and Species	Accession	Score	MW [kDa]	pI	SC [%]	# Pept.	regulated
Microcephalin [Fragment]	Q6RAS8	53	42,00	7,90	4,69	2	n.d.
Microtubule-associated protein 1A	P78559	46	306,29	4,71	1,18	4	n.d.
Microtubule-associated protein RP/EB family member 1	Q15691	63	29,85	4,87	4,87	4	0
Microtubule-associated proteins 1A/1B light chain 3B [Precursor]	Q9GZQ8	85	14,55	9,56	17,74	5	--
Microtubule-associated serine/threonine-protein kinase 2	Q6P0Q8	46	196,44	9,95	9,43	2	0
Mid-1-related chloride channel 4	Q8WYP8	39	39,81	5,42	3,28	1	n.d.
Mitochondrial 39S ribosomal protein L23	Q16540	145	17,77	9,97	29,41	4	n.d.
Mitochondrial 39S ribosomal protein L50	Q8N5N7	57	18,35	9,07	6,96	1	n.d.
Mitochondrial A kinase PPKA anchor protein 10	Q2XPN4	54	67,66	6,17	2,15	2	n.d.
Mitochondrial carrier homolog 2 variant	Q53G34	53	33,29	9,31	2,97	1	n.d.
Mitochondrial fission 1 protein	Q9Y3D6	87	16,93	9,39	16,45	5	0
Mitochondrial import inner membrane translocase subunit TIM14	Q96DA6	49	12,36	10,53	15,65	2	++
Mitochondrial import inner membrane translocase subunit Tim9	Q9Y5J7	108	10,37	7,67	25,84	1	0
Mitochondrial inner membrane protein	Q16891	57	83,63	6,06	3,03	3	+
Mitochondrial ribosomal protein L11	Q32P46	109	18,19	10,28	22,29	3	+
Mitochondrial ribosomal protein L39, isoform a	Q32Q74	53	38,70	8,73	4,44	1	n.d.
Mitochondrial ribosomal protein S18A	Q5QPA5	46	29,70	11,88	5,68	2	+
Mitochondrial-processing peptidase subunit beta [Precursor]	O75439	68	54,33	6,41	4,09	2	n.d.
Mitoferrin-1	Q9NYZ2	45	6,47	7,54	37,70	4	n.d.
Mitogen-activated protein kinase kinase kinase 1	Q13233	63	163,55	9,56	2,21	2	n.d.
Mitogen-activated protein kinase kinase kinase 5 variant [Fragment]	Q59GL6	58	162,86	5,58	1,03	2	n.d.
Mitotic checkpoint protein BUB3	O43684	66	36,93	6,41	4,91	4	0
Mitotic spindle assembly checkpoint protein MAD2A	Q13257	80	21,40	4,82	11,76	2	--
Molecule interacting with Rab13	Q8N3F8	53	91,20	8,80	2,86	2	n.d.
MRNA decapping enzyme variant (Fragment)	Q53G42	75	38,59	5,92	8,61	2	n.d.
mRNA export factor	P78406	58	40,94	9,05	6,52	2	0
mRNA turnover protein 4	Q9UKD2	45	27,54	9,08	6,69	1	0
Mucin-16	Q8WXI7	55	2351,81	5,60	0,13	2	n.d.
Mucin-5B [Precursor]	Q9HC84	81	590,12	6,25	0,37	2	n.d.
Multisynthetase complex auxiliary component p38	Q13155	71	17,55	6,16	15,53	1	n.d.
Mutant truncated midkine A	Q2LEK4	65	9,51	11,03	11,49	1	n.d.
Myc target protein 1	Q8N699	53	22,81	11,16	16,18	2	n.d.
Myeloid/lymphoid or mixed-lineage leukemia protein 3 homolog	Q8NEZ4	43	541,31	6,05	0,73	2	n.d.
MYH10 variant protein [Fragment]	Q4LE45	68	233,71	5,34	1,24	5	--
Myocyte enhancer factor 2D/deleted in azoospermia associated protein 1 fusion protein	Q5IRN4	77	50,38	7,72	3,80	2	++
Myosin heavy chain 9	P35579	63	226,26	5,38	1,02	4	0
Myosin light polypeptide 6	P60660	103	16,92	4,41	13,25	4	n.d.
Myosin regulatory light chain 2, nonsarcomeric	P19105	369	19,65	4,50	40,00	18	0
N(G),N(G)-dimethylarginine dimethylaminohydrolase 2	O95865	56	29,63	5,61	8,42	2	0
N-acetyltransferase 13	Q9GZZ1	107	19,39	9,65	18,93	5	-
NAD+-specific isocitrate dehydrogenase b subunit (Fragment)	Q9UIC5	45	16,99	6,51	5,77	1	n.d.
NAD-dependent deacetylase sirtuin-2	Q8IXJ6	51	0,00	9,58	29,82	2	n.d.
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 2	O43678	199	10,78	10,44	46,94	8	++
NADH-ubiquinone oxidoreductase 30 kDa subunit	O75489	182	22,20	5,19	27,89	5	++
NDST2 protein [Fragment]	Q8WV68	58	11,02	12,45	41,96	2	n.d.
NEDD8-conjugating enzyme Ubc12	P61081	49	20,89	8,84	4,37	1	n.d.
Neogenin homolog 1 variant	Q59FP8	49	123,88	6,58	2,48	2	n.d.
Nephrocystin-4	O75161	59	133,26	8,53	2,88	2	n.d.
Neurexin-2-beta [Precursor]	P58401	54	70,88	5,94	3,30	2	n.d.
Neurobeachin-like protein 2 [Fragment]	Q6ZNJ1	61	302,93	5,93	0,87	3	n.d.
Neurogenic locus notch homolog protein 2 [Precursor]	Q04721	52	265,41	5,87	6,21	2	n.d.
Neurogenic locus notch homolog protein 3 [Precursor]	Q9UM47	64	243,47	5,07	1,12	2	n.d.
Neurogranin	Q92686	74	7,62	10,13	28,05	3	n.d.
Neuron navigator 3	Q8IVL0	48	244,26	9,44	0,66	2	n.d.
Neurturin [Precursor]	Q99748	42	0,00	11,00	11,65	1	n.d.
Neurturin neurotrophic factor analog [Precursor]	Q99748	53	11,82	11,00	11,65	1	n.d.
Neutral alpha-glucosidase AB [Precursor]	Q14697	85	106,81	5,70	3,07	7	++
NGFI-A-binding protein 2	Q15742	58	0,00	5,17	9,58	2	n.d.
Nicotinate-nucleotide pyrophosphorylase [carboxylating]	Q15274	140	30,81	5,79	14,48	8	--
Ninein-like protein	Q5JYP0	49	156,25	4,87	1,45	2	n.d.
Nitrilase 1	Q5SY59	74	35,87	9,25	6,42	2	n.d.
NK-tumor recognition protein	P30414	44	165,58	10,58	2,19	2	n.d.
N-MYC	Q9H224	64	11,77	11,91	22,32	2	n.d.

Table 2. continued

Protein Name and Species	Accession	Score	MW [kDa]	pI	SC [%]	# Pept.	regulated
Nonhistone chromosomal protein HMG-17	P05204	78	9,26	10,54	22,47	2	n.d.
NPD007	Q9HBK7	57	46,62	9,80	6,22	2	n.d.
NUCKS protein (Nuclear ubiquitous casein and cyclin-dependent kinases substrate)	Q6IA16	53	18,74	4,58	6,75	4	++
Nuclear autoantigenic sperm protein	Q5T624	55	45,77	4,16	2,61	1	--
Nuclear factor of activated T-cells, cytoplasmic 2-interacting protein	Q8NCF5	53	45,79	6,18	9,31	2	n.d.
Nuclear migration protein nudC	Q9Y266	244	38,19	5,20	22,66	6	--
Nuclear mitotic apparatus protein 1 [Fragment]	Q9UNL7	76	0,00	11,41	19,05	3	n.d.
Nuclear pore complex protein Nup133	Q8WUM0	55	128,82	4,82	2,68	2	n.d.
Nuclear protein Hcc-1	P82979	254	23,53	6,07	33,49	9	0
Nuclear protein NHN1	Q86VM9	54	0,00	8,88	3,25	2	n.d.
Nuclear receptor-binding protein 2	Q9NSY0	64	36,02	10,70	12,97	10	n.d.
Nuclear structure protein 5	Q5M775	51	118,59	6,28	4,12	2	++
Nuclease sensitive element-binding protein 1	P67808	271	35,77	0,00	24,46	19	++
Nucleolar and coiled-body phosphoprotein 1	Q5VV70	75	73,56	9,95	2,15	1	n.d.
Nucleolar MIF4G domain-containing protein 1	Q5C9Z4	55	96,26	9,09	4,07	2	n.d.
Nucleolar protein 6	Q9H6R4	52	127,59	7,46	2,05	2	n.d.
Nucleolin	P19338	135	76,44	4,45	5,64	13	0
Nucleophosmin	P06748	124	32,44	4,52	8,19	8	n.d.
Nucleoporin NUP53	Q8NFH5	69	34,68	9,71	14,11	2	+
Nucleoside diphosphate kinase	Q4TT34	112	21,51	11,19	14,87	5	+
Nucleoside diphosphate kinase B	P22392	273	17,16	9,58	35,76	34	0
Nucleoside diphosphate-linked moiety X motif 16	Q96DE0	40	21,26	6,44	6,67	1	0
Nucleosome assembly protein 1-like 1	P55209	109	45,35	4,21	7,67	6	0
Nucleosome assembly protein 1-like 4	Q99733	60	42,80	4,45	2,93	2	--
Nucleotide-binding oligomerization domain protein 3	Q7RTR2	58	114,66	9,41	4,85	2	n.d.
Nudix (nucleoside diphosphate linked moiety X)-type motif 21	Q5HYH5	45	12,36	10,30	19,05	2	--
Obscurin	Q5VST9	63	868,48	5,62	0,18	2	+
ORF protein	Q7KYM9	178	59,93	9,51	9,12	8	0
ORM1-like protein 2	Q53FV1	45	16,96	9,88	13,33	2	n.d.
Ornithine decarboxylase antizyme	P54368	59	24,35	8,97	14,16	4	n.d.
OTTHUMP00000017000 [Fragment]	Q5T253	48	41,30	10,41	6,56	2	n.d.
OTTHUMP00000018488 [Fragment]	Q5T6S7	196	28,08	9,62	10,14	2	++
OTTHUMP00000028514 [Fragment]	Q5JZ84	75	83,86	9,22	5,09	3	n.d.
OTTHUMP00000029973	Q5JXA3	163	30,20	4,86	22,63	5	0
OTU domain-containing protein 7A	Q8TE49	53	0,00	9,54	3,67	3	n.d.
Ovarian carcinoma antigen CA125	Q8WXI7	52	2351,81	5,60	0,13	2	n.d.
Ovarian carcinoma immunoreactive antigen	Q9NX40	43	27,61	7,76	3,67	2	+
Oxysterol-binding protein	Q9NX98	51	65,97	7,08	3,55	2	n.d.
P15RS protein	Q96FY9	277	32,90	6,23	39,45	7	0
P37 AUF1	Q12771	39	31,46	7,71	6,99	1	n.d.
p53 and DNA damage-regulated protein 1	Q9NUG6	51	15,51	5,13	17,00	2	0
PAI-1 mRNA-binding protein	Q5VU19	130	44,94	9,28	11,03	6	--
PAI-1 mRNA-binding protein	Q5VU22	96	44,23	9,30	5,97	2	--
Paired mesoderm homeobox protein 2A	O14813	88	29,63	9,77	11,27	4	0
Palmitoyl-protein thioesterase 1 [Fragment]	Q5T0S4	53	19,98	5,83	8,47	2	0
Palmitoyl-protein thioesterase 1 [Precursor]	P50897	75	34,16	6,08	11,44	4	++
Parathymosin	P20962	119	11,52	3,98	41,18	2	+
PAS domain-containing serine/threonine-protein kinase	Q96RG2	55	142,93	4,61	3,78	2	n.d.
Peptidyl-prolyl cis-trans isomerase A	P62937	431	18,00	9,05	41,21	63	0
Peptidylprolyl cis-trans isomerase A-like 4	Q9Y536	123	18,17	10,11	19,51	12	n.d.
Peptidyl-prolyl cis-trans isomerase B [Precursor]	P23284	194	22,73	9,85	17,79	14	0
Peptidyl-prolyl cis-trans isomerase D	Q6FGM6	102	40,75	6,98	11,08	5	++
Peptidyl-prolyl cis-trans isomerase F	Q2YDB7	97	16,53	10,69	23,23	5	+
Peptidyl-prolyl cis-trans isomerase H [Fragment]	Q6FH36	143	19,20	9,47	14,69	8	0
Peptidyl-prolyl cis-trans isomerase NIMA-interacting 1	Q13526	97	17,22	10,20	22,22	7	0
Pericentriolar material 1 protein	Q15154	49	0,00	4,85	2,08	2	n.d.
Peripheral-type benzodiazepine receptor-associated protein 1	O95153	69	200,05	4,88	2,88	7	n.d.
Peroxiredoxin 3 isoform a variant [Fragment]	Q53HC2	94	27,61	8,92	5,47	2	n.d.
Peroxiredoxin-1	Q06830	258	18,96	6,52	23,98	47	0
Peroxiredoxin-2	P32119	442	21,75	5,59	29,95	47	+
Peroxiredoxin-3	P30048	86	27,61	8,92	5,47	1	n.d.
Peroxiredoxin-4	Q13162	146	30,52	5,85	16,24	6	n.d.
Peroxiredoxin-5 [Precursor]	P30041	251	24,32	5,97	23,39	30	+
Peroxisomal biogenesis factor 6	Q5T8W1	60	104,00	5,93	1,84	4	-
Peroxisomal multifunctional enzyme type 2	P51659	100	79,64	9,58	3,40	5	0
PEST-containing nuclear protein variant	Q53GF3	101	18,91	5,99	16,85	2	0
PH domain leucine-rich repeat-containing protein phosphatase	O60346	85	0,00	5,86	3,20	7	n.d.
PHD finger-like domain-containing protein 5A	Q7RTV0	71	12,40	10,02	19,09	3	+

Table 2. continued

Protein Name and Species	**Accession**	**Score**	**MW [kDa]**	**pI**	**SC [%]**	**# Pept.**	**regulated**
PHGDH protein [Fragment]	Q8N5M8	95	33,83	6,44	14,60	7	-
PHLDB2 protein	Q8IXY4	58	56,86	9,41	8,09	2	n.d.
Phosphatase 2A inhibitor I2PP2A	Q01105	96	32,08	3,96	7,58	18	++
Phosphatidylinositol transfer protein beta isoform	P48739	76	31,39	6,46	11,48	3	+
Phosphatidylinositol-4-phosphate 5-kinase type-1 alpha	Q99755	45	0,00	5,33	4,52	2	n.d.
Phosphoglucomutase-1	P36871	50	65,93	9,31	4,30	2	n.d.
Phosphoglycerate kinase 1	P00558	371	44,59	9,22	23,50	62	0
Phosphoglycerate kinase 2	P07205	143	44,64	9,54	11,54	10	0
Phosphoglycerate mutase 1	P18669	397	28,65	6,82	35,18	32	--
Phosphoglycerate mutase 2	P15259	117	28,75	9,65	12,65	7	n.d.
Phosphohistidine phosphatase 1	Q5T5S3	47	13,82	5,63	10,40	6	0
Phosphoinositide phospholipase C	Q01970	55	138,71	5,59	2,51	2	n.d.
Phosphoinositol 3-phosphate-binding protein 1	Q9H4M7	52	85,40	9,70	11,43	2	n.d.
Phospholipase D3	Q8IV08	140	54,67	6,02	7,55	5	++
Phosphomevalonate kinase	Q15126	350	21,85	5,45	39,27	20	-
Phosphoribosylaminoimidazole carboxylase	P22234	261	46,92	7,75	12,26	33	--
Phosphoserine aminotransferase	Q5T7G6	101	40,40	8,65	10,00	4	--
PIG48	Q2TU64	116	60,54	5,95	8,44	11	0
PIK4CA variant protein	Q4LE69	40	238,54	6,80	0,99	1	n.d.
PIN4 protein	Q3MHV0	48	14,88	10,47	9,93	1	0
Pinin	Q9H307	39	81,43	6,77	1,54	1	--
Platelet-activating factor acetylhydrolase IB subunit beta	P68402	120	25,55	5,52	11,79	3	++
Platelet-activating factor acetylhydrolase IB subunit gamma	Q15102	144	25,72	6,36	20,35	6	n.d.
Plexin-A1 [Precursor]	Q9UIW2	41	211,09	6,56	0,47	1	n.d.
Podoplanin [Precursor]	Q86YL7	52	16,68	5,12	15,97	2	n.d.
Poly(rC)-binding protein 1	Q15365	285	37,50	6,81	20,51	13	0
Poly(rC)-binding protein 2	Q15366	100	36,78	6,74	14,90	13	0
Polyadenylate-binding protein 1	P11940	50	18,99	9,72	10,12	3	n.d.
Polycystic kidney disease 2-like 1	Q5W039	42	91,92	5,23	3,85	2	n.d.
Polycystin-1 [Precursor]	P98161	60	462,57	9,73	1,86	2	n.d.
Polyhomeotic-like protein 1 variant [Fragment]	Q59GP6	55	115,44	10,15	4,19	3	n.d.
Polymerase (RNA) II (DNA directed) polypeptide C	Q6FGR6	60	31,42	4,64	16,00	3	++
Potassium voltage-gated channel subfamily C member 4	Q03721	56	64,51	6,78	4,30	2	n.d.
Potassium voltage-gated channel subfamily KQT member 2	O43526	57	0,00	10,11	4,47	6	n.d.
Potassium/sodium hyperpolarization-activated cyclic nucleotide-gated channel 4	Q9Y3Q4	55	0,00	9,74	1,83	4	n.d.
PPP1R15A protein	Q6IA96	53	73,48	4,40	1,78	2	n.d.
PPT1 protein	Q6FGQ4	225	34,17	6,08	15,69	6	+
Prefoldin subunit 2	Q5SY55	120	16,64	6,23	16,23	5	++
Prefoldin subunit 6	Q5STK2	255	14,57	9,39	31,01	9	0
Pre-mRNA-processing factor 19	Q9UMS4	92	55,15	6,15	4,76	2	0
Pre-mRNA-processing factor 6	O94906	42	106,93	9,33	0,74	1	n.d.
PRKR-interacting protein 1	Q7LCM6	55	22,30	13,08	9,81	2	0
PRO1386	Q9UHV1	45	8,55	10,67	24,00	2	n.d.
PRO2242	Q9P1D9	150	8,43	5,07	46,58	5	-
Probable E3 ubiquitin-protein ligase HERC2	O95714	52	527,47	5,83	0,81	2	n.d.
Probable G-protein coupled receptor 101	Q96P66	43	0,00	6,02	3,22	1	n.d.
Probable histone-lysine N-methyltransferase ASH1L	Q9NR48	51	0,00	10,12	1,27	2	n.d.
Probable protein BRICK1	Q8WUW1	67	8,74	5,22	28,00	2	--
Probable transcription factor PML L	Q15959	55	70,32	5,82	7,64	2	n.d.
Processing of 7, ribonuclease P subunit	A4D2E0	84	15,64	9,90	24,29	2	n.d.
Profilin-1	P07737	174	14,84	9,44	23,91	13	0
Profilin-2	P35080	138	14,85	5,74	25,36	14	-
Progestin and adipoQ receptor family member 9	Q6ZVX9	55	42,69	9,90	8,22	2	n.d.
Programmed cell death 6	Q2YDC2	69	21,65	5,01	5,82	3	n.d.
Programmed cell death protein 5	O14737	169	14,15	5,70	32,26	7	--
Prohibitin [Fragment]	P35232	473	29,81	5,47	37,50	33	++
Prohibitin-2	Q99623	529	33,28	10,21	52,17	33	++
Proliferation associated cytokine-inducible protein CIP29	A4D286	128	20,68	9,99	22,70	5	0
Proliferation-associated protein 2G4	Q9UQ80	108	43,63	6,12	6,36	2	--
Proliferation-inducing protein 45	Q2TU78	71	20,63	6,07	6,53	2	n.d.
Proline-rich protein 6	Q7Z7K6	171	29,93	10,73	26,18	5	0
Proopiomelanocortin (corticotropin)	Q5TZZ7	48	4,54	9,26	56,41	1	n.d.
Prostaglandin E synthase 3	Q15185	45	18,69	4,16	6,25	3	0
Proteasome (Prosome, macropain) 26S subunit, non-ATPase, 4 [Fragment]	Q5VWC4	79	41,05	4,55	6,84	3	-
Proteasome (Prosome, macropain) 26S subunit, non-ATPase, 8	Q5U0B3	66	29,90	7,58	7,00	3	0
Proteasome (Prosome, macropain) subunit, alpha type, 7 [Fragment]	Q5JXJ1	111	29,58	6,16	9,89	6	0
Proteasome (Prosome, macropain) subunit, beta type, 4 [Fragment]	Q5SZS5	85	29,19	5,63	5,68	6	0
Proteasome activator complex subunit 1	Q06323	75	16,28	7,84	20,71	3	-
Proteasome activator complex subunit 2	Q9UL46	87	27,21	5,33	11,76	4	n.d.

Table 2. continued

Protein Name and Species	Accession	Score	MW [kDa]	pI	SC [%]	# Pept.	regulated
Proteasome activator complex subunit 3	P61289	111	29,49	5,61	18,90	4	--
Proteasome subunit alpha type	Q53YE8	72	29,58	6,16	9,89	3	0
Proteasome subunit alpha type 3	P25788	52	28,28	5,06	5,51	1	n.d.
Proteasome subunit alpha type-4	P25789	47	29,47	8,67	3,45	2	n.d.
Proteasome subunit alpha type-5	P28066	45	26,39	4,59	4,15	1	n.d.
Proteasome subunit alpha type-6	P60900	134	27,38	6,42	11,38	2	n.d.
Proteasome subunit beta type	Q6IAT9	138	25,34	4,65	9,21	7	0
Proteasome subunit beta type 2 (Macropain subunit C7-I)	P49721	303	22,82	6,64	30,85	11	0
Proteasome subunit beta type-1 [Precursor]	P20618	140	26,47	9,13	17,01	5	0
Proteasome subunit beta type-3	P49720	126	16,61	9,49	18,79	5	0
Proteasome subunit beta type-5 [Precursor]	P28074	303	28,46	6,54	19,77	8	0
Protein ADRM1	Q16186	40	32,56	6,39	3,49	2	0
Protein arginine N-methyltransferase 6	Q96LA8	47	9,44	9,15	17,65	2	n.d.
Protein ARMET (arginine rich protein)	P55145	50	20,24	9,62	9,50	1	++
Protein atonal homolog 7	Q8N100	40	16,87	10,68	9,21	2	n.d.
Protein BUD31 homolog	P41223	42	16,99	10,15	6,25	1	0
Protein canopy homolog 2 [Precursor]	Q9Y2B0	300	20,64	4,66	39,01	11	0
Protein CDV3 homolog	Q9UKY7	74	27,32	6,03	14,34	3	0
Protein CTF18 homolog	Q96S08	75	129,27	10,32	1,44	2	n.d.
Protein CWC15 homolog	Q9P013	129	26,59	5,43	17,90	8	-
Protein DEK	P35659	60	42,33	9,37	4,57	2	--
Protein DGCR14	Q96DF8	52	0,00	7,77	4,63	2	n.d.
Protein disulfide-isomerase [Precursor]	P07237	123	13,25	5,91	38,33	9	--
Protein disulfide-isomerase A3 [Precursor]	P30101	314	56,76	5,95	16,24	13	--
Protein disulfide-isomerase A4 [Precursor]	P13667	193	72,89	4,81	9,61	20	--
Protein disulfide-isomerase A6 [Precursor]	Q15084	152	53,90	5,04	32,30	26	--
Protein DJ-1	Q99497	85	19,83	6,40	16,40	7	-
Protein Dos	Q8N350	52	75,82	9,41	8,05	2	n.d.
Protein FAM123A	Q8N7J2	48	57,55	9,51	5,98	4	n.d.
Protein FAM71B	Q8TC56	49	0,00	10,14	5,79	2	n.d.
Protein FAM82B	Q96DB5	61	5,74	13,04	43,40	7	0
Protein FAM84A	Q96KN4	73	37,73	11,75	14,69	3	n.d.
Protein jagged-2 [Precursor]	Q9Y219	51	133,37	5,46	1,62	4	n.d.
Protein Jub	Q96IF1	43	0,00	7,10	3,72	2	--
Protein KIAA0284	Q9Y4F5	59	163,53	6,53	1,84	5	++
Protein kinase NYD-SP15	Q9BWV3	46	61,12	9,82	5,95	3	n.d.
Protein KRBA1	A5PL33	47	0,00	9,44	4,02	2	n.d.
Protein LAP4	Q14160	39	0,00	6,36	0,96	1	n.d.
Protein LRP16	Q9BQ69	94	27,12	9,56	15,23	4	0
Protein MGR2 homolog	P60602	60	8,18	11,94	21,52	1	-
Protein NipSnap1	Q9BPW8	59	33,29	9,83	6,69	2	+
Protein NipSnap3A	Q9UFN0	42	28,47	8,96	15,15	2	n.d.
Protein phosphatase 1 regulatory subunit 14B	Q96C90	82	15,90	4,60	23,81	2	--
Protein phosphatase 1 regulatory subunit 3E [Fragment]	Q9H7J1	55	37,64	11,57	8,31	2	n.d.
Protein phosphatase 1G (Formerly 2C), magnesium-dependent, gamma isoform	Q6IAU5	172	59,23	4,12	8,79	4	--
Protein phosphatase 2 (Formerly 2A), regulatory subunit B'', beta [Fragment]	Q5JNV4	52	0,00	12,08	8,33	2	n.d.
Protein RCC2	Q9P258	179	60,44	9,84	9,40	4	0
Protein spinster homolog 3	Q6ZMD2	58	54,81	7,69	7,62	2	n.d.
Protein syndesmos	Q9BRJ7	118	25,96	10,44	12,55	2	n.d.
Protein translocation complex beta variant [Fragment]	Q53FA5	57	10,04	12,41	15,63	4	-
Protein VI	Q2KRX1	51	25,18	10,37	12,93	2	n.d.
Protein Wnt-9b [Precursor]	O14905	56	0,00	10,84	9,97	2	n.d.
Protein ZNF767	Q75MW2	60	17,19	10,29	14,84	4	n.d.
Pterin-4-alpha-carbinolamine dehydratase	P61457	165	11,86	6,33	27,18	6	0
Pumilio homolog 1	Q5VXY5	63	130,03	6,44	2,61	2	0
Purine nucleoside phosphorylase	P00491	90	32,13	6,52	8,30	2	n.d.
Purine-rich element binding protein B	A4D2L7	80	33,22	5,20	10,90	4	++
Putative eukaryotic translation initiation factor 1A	O75642	72	16,32	4,81	13,29	2	++
Putative MAPK activating protein	Q549U1	91	32,67	11,79	15,60	3	n.d.
Putative RNA-binding protein 3	P98179	59	17,16	9,22	9,55	1	n.d.
Putative RNA-binding protein Luc7-like 2	Q9Y383	82	45,67	10,83	6,27	5	++
Putative ubiquitin-conjugating enzyme E2 N-like	Q5JXB2	68	17,37	5,59	12,42	2	0
Putative uncharacterized protein	Q1T7F1	46	8,81	6,09	22,22	1	n.d.
Putative uncharacterized protein	Q7Z4R7	48	18,94	6,33	13,26	2	n.d.
Putative uncharacterized protein	Q8N647	54	5,71	12,38	42,59	2	n.d.
Putative uncharacterized protein	Q8NCU7	58	0,00	12,21	9,49	2	n.d.
Putative uncharacterized protein	Q96I54	49	5,84	4,27	30,36	2	n.d.
Putative uncharacterized protein C14orf25	Q8IY25	46	48,81	10,38	7,05	2	n.d.
Putative uncharacterized protein C21orf32	P57056	52	0,00	12,09	17,96	4	n.d.
Putative uncharacterized protein COP9	Q53QS9	80	23,21	5,12	16,27	1	-

Table 2. continued

Protein Name and Species	**Accession**	**Score**	**MW [kDa]**	**pI**	**SC [%]**	**# Pept.**	**regulated**
Putative uncharacterized protein DKFZp313I142	Q9NW00	57	48,78	10,16	6,70	2	n.d.
Putative uncharacterized protein DKFZp434B061 [Fragment]	Q9UFS5	45	32,83	13,59	9,40	2	n.d.
Putative uncharacterized protein DKFZp434E2321 [Fragment]	Q9UF43	54	35,87	10,71	6,59	2	n.d.
Putative uncharacterized protein DKFZp564G0422	Q5JXL8	123	12,40	10,05	29,91	4	0
Putative uncharacterized protein DKFZp586A0617	Q5GMH6	45	12,23	11,30	22,32	1	n.d.
Putative uncharacterized protein DKFZp586E1422 [Fragment]	Q9Y3Y1	64	5,82	12,85	34,59	2	n.d.
Putative uncharacterized protein DKFZp686F1032 [Fragment]	Q6AWA5	44	0,00	10,18	1,79	1	n.d.
Putative uncharacterized protein DKFZp686I1750	Q7Z3N8	55	71,38	6,16	5,48	2	n.d.
Putative uncharacterized protein DKFZp686J11229 [Fragment]	Q6MZF9	41	5,52	11,90	21,15	1	n.d.
Putative uncharacterized protein EIF2B4	Q53RY7	51	57,46	10,13	9,77	2	n.d.
Putative uncharacterized protein EMILIN1	Q53SY9	61	106,60	4,94	2,85	3	n.d.
Putative uncharacterized protein FLJ38377	Q8N944	47	90,46	5,39	4,76	3	n.d.
Putative uncharacterized protein gs114	Q96RY6	49	31,18	12,59	15,75	2	n.d.
Putative uncharacterized protein gs52	Q96S13	58	0,00	10,17	6,37	2	n.d.
Putative uncharacterized protein LSM6	Q4W5J5	58	9,12	0,00	15,00	2	0
Putative uncharacterized protein MMRN	Q4W5L1	40	138,02	8,97	1,22	1	n.d.
Putative uncharacterized protein SOS1 [Fragment]	Q53SF8	52	0,00	6,34	2,53	2	n.d.
Putative uncharacterized protein UCHL1	Q4W5K6	100	24,81	5,22	10,76	5	+
Putative uncharacterized protein YWHAQ [Fragment]	Q53RR5	52	11,19	7,21	14,29	4	n.d.
Pyrophosphate phospho-hydrolase	Q15181	52	32,64	5,47	3,11	2	n.d.
Pyruvate dehydrogenase E1 component subunit alpha, somatic form [Precursor]	P08559	108	43,27	9,26	8,21	6	++
Pyruvate dehydrogenase E1 component subunit beta	P11177	76	39,21	6,22	4,46	1	n.d.
Pyruvate kinase isozymes M1/M2	P14618	275	57,77	8,96	16,57	123	--
Quinone oxidoreductase	PN0448	48	35,18	9,20	3,95	2	++
Rab GDP dissociation inhibitor beta	P50395	103	41,01	8,86	6,96	3	0
RAB5C protein (member RAS oncogene family)	Q6FH55	93	23,47	9,50	18,52	4	--
Rab6-interacting protein 1	Q6IQ26	43	147,10	6,88	3,75	2	n.d.
Rab-like protein 4 (Putative GTP-binding protein RAY-like) Ras family	Q9BW83	40	20,47	5,15	11,83	2	-
Rac3 (Ras-related C3 botulinum toxin substrate 3)	P60763	105	21,37	9,41	14,06	3	-
RAD23-like protein B	Q7Z5K8	64	35,01	4,49	5,64	1	n.d.
Ral GEF with PH domain and SH3 binding motif 1	Q5VXM4	52	0,00	9,82	7,00	2	n.d.
Ral guanine nucleotide dissociation stimulator-like 2	O15211	40	12,96	10,08	24,59	1	n.d.
RAP1B, member of RAS oncogene family	Q502X3	42	20,86	5,51	4,89	2	-
Ras suppressor protein 1	Q15404	82	31,52	9,13	7,58	2	-
Ras-like protein TC4 (GTP-binding nuclear protein Ran)	P62826	90	14,72	5,88	23,44	7	0
Ras-related C3 botulinum toxin substrate 1 [Precursor] (p21-Rac1)	P63000	101	21,44	9,66	11,46	9	-
Ras-related protein Rab-10	P61026	69	22,53	9,44	6,00	1	n.d.
Ras-related protein Rab-2A	P61019	70	23,55	6,09	11,79	3	0
Ras-related protein Rab-7a	P51149	125	23,52	5,59	14,01	4	--
RBM 1 (RNA-binding motif)	Q2VIN3	77	41,44	10,06	7,81	5	--
RcNSEP1 [Fragment]	Q2VIK8	191	35,44	10,33	13,79	7	-
RcTPM3 (Fragment)	Q2QD06	229	28,81	4,61	19,03	7	-
Regulating synaptic membrane exocytosis 1 [Fragment]	Q5JS64	49	0,00	10,04	3,13	2	n.d.
RelA-associated inhibitor	Q8WUF5	56	89,09	6,39	5,56	2	n.d.
Replication factor C subunit 3	P40938	54	12,02	10,18	11,32	2	--
Replication factor C subunit 4	Q6FHX7	61	39,66	9,29	6,61	2	0
Retinitis pigmentosa 1-like 1 protein	Q8IWN7	41	260,95	4,23	0,65	1	n.d.
Retinoic acid receptor alpha	P10276	41	0,00	9,80	3,46	1	n.d.
Retinoic acid-induced protein 16	Q86V87	59	82,34	5,22	2,64	2	n.d.
Retinol-binding protein I, cellular	P09455	151	15,84	4,84	39,26	5	0
Retrotransposon gag domain-containing protein 1	Q8NET4	85	144,28	5,76	7,13	4	n.d.
Rho GDP-dissociation inhibitor 1 (Rho GDI 1)	P52565	134	23,06	4,86	20,56	11	0
Rho guanine nucleotide exchange factor 17	Q96PE2	39	0,00	10,42	3,99	1	n.d.
RhoG	P84095	45	21,32	9,51	10,99	2	0
Rhotekin	Q9BST9	49	62,67	6,45	6,53	2	n.d.
Ribonuclease H2 subunit C	Q8TDP1	70	17,83	4,78	10,37	2	n.d.
Ribonuclease inhibitor	P13489	49	49,81	4,56	4,57	2	++
Ribonuclease/angiogenin inhibitor 1	Q9BQ80	114	49,92	4,56	6,94	2	--
Ribonucleoprotein [Fragment]	Q15367	130	40,57	9,15	8,45	3	--
Ribonucleoprotein RNA-binding protein 8A	Q9Y5S9	49	19,75	5,57	4,05	3	++
Ribose-phosphate pyrophosphokinase 1	P60891	89	34,81	6,58	9,75	5	--
Ribose-phosphate pyrophosphokinase II	P11908	76	34,75	6,16	5,35	2	0
Ribosomal L1 domain-containing protein 1	O76021	143	34,18	9,73	10,31	8	-
Ribosomal protein L10 [Fragment]	Q5HY50	119	26,58	11,06	14,78	8	0
Ribosomal protein L11 [Fragment]	Q5VVC8	81	19,94	10,43	19,54	5	++
Ribosomal protein L13A [Fragment]	Q9BSQ6	224	23,36	11,49	30,35	17	0

Table 2. continued

Protein Name and Species	Accession	Score	MW [kDa]	pI	SC [%]	# Pept.	regulated
ribosomal protein L14 variant	Q6IPH7	94	23,77	11,64	8,18	3	n.d.
Ribosomal protein L15 pseudogene 3	Q5T6E0	228	24,16	12,22	38,24	14	0
Ribosomal protein L19 [Fragment]	Q8IWR8	271	20,81	12,01	30,06	20	0
ribosomal protein L26	Q6IBH6	205	17,23	11,00	40,69	15	++
Ribosomal protein L27a	Q6NZ52	119	16,47	11,78	12,16	9	0
Ribosomal protein L28 variant [Fragment]	Q59F34	48	10,69	11,42	15,79	2	++
Ribosomal protein L29	Q6IPI1	341	17,94	12,27	44,72	22	0
ribosomal protein L7	Q3KQU0	207	37,00	11,17	22,01	14	0
ribosomal protein L7a [Fragment]	Q5T8U3	89	21,53	11,85	18,85	10	0
Ribosomal protein L9 isoform	Q53Z07	87	21,85	10,54	8,85	4	0
Ribosomal protein S10	Q5TZB9	52	19,86	10,37	8,72	3	n.d.
Ribosomal protein S19 [Fragment]	Q8WVX7	46	17,27	10,96	7,64	1	-
Ribosomal RNA upstream binding transcription factor [Fragment]	O00164	39	0,00	9,32	1,83	1	n.d.
Ribosome biogenesis regulatory protein homolog	Q15050	76	41,17	11,25	8,22	5	+
RNA binding motif protein 4	Q4VC48	190	40,29	6,69	15,11	3	0
RNA binding motif protein, X-linked-like 1 [Fragment]	Q5T9T9	52	16,84	10,76	11,32	4	0
RNA polymerase II subunit A C-terminal domain phosphatase	Q9Y5B0	55	60,51	5,16	4,60	2	n.d.
RNA-binding protein Raly	Q9UKM9	135	32,44	9,64	20,59	9	0
RPS3 protein	Q6IPX9	280	13,06	10,47	60,68	10	0
RTN4 protein	Q6IPN0	42	36,90	4,57	3,79	3	n.d.
SAR1 gene homolog A (Small GTP-binding protein)	Q5SQT9	78	22,35	6,25	9,09	2	0
Scavenger mRNA-decapping enzyme DcpS	Q96C86	75	38,66	5,83	8,61	2	n.d.
Scavenger receptor class F member 2 [Precursor]	Q96GP6	85	24,94	11,68	18,52	7	--
Sentrin-specific protease 7	Q9BQF6	43	112,19	6,06	1,12	1	n.d.
Septin-2	Q15019	265	46,56	7,16	16,50	4	0
Septin-6	Q14141	40	0,00	6,24	5,07	1	n.d.
Septin-9	Q9UHD8	45	65,36	9,69	4,95	3	--
Serine hydroxymethyltransferase	Q8N1A5	403	54,83	9,54	24,49	13	0
Serine protease HTRA2 [Precursor]	O43464	73	38,47	11,27	8,98	5	++
Serine/arginine repetitive matrix 1	Q5VVN3	66	103,33	12,36	3,07	5	n.d.
Serine/arginine repetitive matrix protein 2	Q9UQ35	48	136,79	12,92	2,98	2	n.d.
Serine/threonine protein phosphatase [Fragment]	Q9UPN1	166	33,75	4,95	15,99	11	0
Serine/threonine-protein kinase Nek3	P51956	49	62,64	10,24	5,49	2	n.d.
Serine/threonine-protein kinase Nek5	Q6P3R8	51	67,86	9,72	1,84	2	n.d.
Serine/threonine-protein kinase TAO2	Q9UL54	72	138,25	7,21	4,32	7	n.d.
Serine/threonine-protein kinase VRK3	Q8IV63	54	0,00	9,93	8,65	2	n.d.
Serine/threonine-protein kinase WNK3	Q9BYP7	53	191,79	5,28	2,89	2	n.d.
Serine/threonine-protein phosphatase 2A catalytic subunit beta isoform	P62714	225	35,55	5,10	23,62	9	0
Serine/threonine-protein phosphatase PP1-alpha catalytic subunit	P62136	161	37,49	5,92	18,48	8	0
Serine/threonine-protein phosphatase PP1-beta catalytic subunit	P62140	192	37,03	5,80	17,18	6	0
Serine/threonine-protein phosphatase PP1-gamma catalytic subunit	P36873	123	37,03	5,80	10,12	4	0
Serpin H1 [Precursor]	P50454	358	46,41	9,31	17,22	9	0
Serum albumin [Precursor]	P02768	58	69,32	5,88	1,97	1	n.d.
S-formylglutathione hydrolase (Esterase D)	P10768	104	31,44	6,62	10,28	3	-
SGTA protein	Q6FIA9	172	34,04	4,64	10,54	5	++
SH3 and multiple ankyrin repeat domains protein 1	Q9Y566	52	225,02	7,06	1,55	2	n.d.
SH3 and multiple ankyrin repeat domains protein 2	Q9UPX8	51	0,00	5,33	3,43	2	n.d.
SH3 domain binding glutamic acid-rich protein like 3	Q5T123	112	9,37	10,03	34,09	7	0
SH3 domain-binding glutamic acid-rich-like protein	O75368	63	12,77	5,07	8,77	3	n.d.
SH3 domain-binding protein 1	Q9Y3L3	52	68,44	5,86	5,34	2	n.d.
Short transient receptor potential channel 6	Q9Y210	44	106,33	6,24	0,97	1	++
Sideroflexin-1 (Tricarboxylate carrier protein) (TCC)	Q9H9B4	134	35,47	9,99	10,28	7	0
Signal recognition particle 14 kDa	Q96Q14	236	14,50	10,64	63,97	24	++
Signal recognition particle 9 kDa isoform	Q6NVX0	52	9,12	9,22	30,49	2	++
Signal recognition particle 9 kDa protein	P49458	105	9,97	9,24	36,47	6	0
Signal-induced proliferation-associated 1-like protein 3	O60292	77	194,61	9,31	3,03	3	n.d.
Similar to CG32656-PA	Q86X51	51	0,00	11,51	3,58	2	n.d.
Similar to poly(RC) binding protein 2	Q15366	64	36,78	6,74	5,73	2	0
Similar to Unc4.1 homeobox	A4D221	41	0,00	10,92	5,81	1	n.d.
SIN3B protein	Q2NL91	62	39,48	9,27	5,38	2	--
Single-stranded DNA binding protein 1	Q567R6	63	17,35	10,07	14,19	2	n.d.
Single-stranded DNA-binding protein [Precursor]	Q04837	144	17,25	9,93	19,59	8	++
SLAIN motif family member 2 [Fragment]	Q9P270	43	65,55	10,22	8,66	2	n.d.
SMAC3	Q6W3F3	143	22,27	5,61	16,92	7	+
Small nuclear ribonucleoprotein F	P62306	106	12,88	4,84	17,95	3	n.d.
Small nuclear ribonucleoprotein polypeptide C	Q53G33	54	17,44	10,34	12,58	2	0
Small nuclear ribonucleoprotein polypeptide G	Q49AN9	75	7,10	7,63	31,25	4	n.d.
Small nuclear ribonucleoprotein Sm D1	P62314	97	9,04	10,06	13,75	2	n.d.

Table 2. continued

Protein Name and Species	Accession	Score	MW [kDa]	pI	SC [%]	# Pept.	regulated
Small nuclear ribonucleoprotein Sm D2	P62316	138	13,52	10,57	29,66	5	0
Small nuclear ribonucleoprotein Sm D3	P62318	177	13,91	11,07	30,95	2	n.d.
Small nuclear ribonucleoprotein-associated proteins B and B'	P14678	63	10,24	10,22	18,75	4	n.d.
Small ubiquitin-related modifier 3	P55854	45	11,63	5,21	13,59	2	0
SmB /B' autoimmune antigene [Fragment]	Q6LBS1	62	21,98	12,11	10,09	2	n.d.
Smooth muscle cell-associated protein 3 (SMAP-3)	O43583	81	26,49	5,75	11,52	4	0
Smu-1 suppressor of mec-8 and unc-52 protein homolog	Q2TAY7	59	57,54	6,84	3,90	2	n.d.
SNAP-25-interacting protein	Q9C0H9	44	81,43	9,83	3,67	1	n.d.
SNX14 protein	Q6PI37	40	104,62	6,00	1,22	1	n.d.
Solute carrier family 13 member 5	Q86YT5	57	36,81	9,27	7,78	2	n.d.
Solute carrier family 25 (Mitochondrial carrier; adenine nucleotide translocator), member 6 [Fragment]	Q5JQ50	68	17,30	10,33	12,66	3	0
Solute carrier family 25 (Mitochondrial carrier; phosphate carrier)	Q7Z7N7	111	41,90	10,09	6,91	4	0
Solute carrier family 25 member 4 variant [Fragment]	Q59EP7	56	29,33	10,51	7,66	2	+
Solute carrier organic anion transporter family, member 2A1	Q8IUN2	41	70,00	10,20	1,40	1	n.d.
Sorbin and SH3 domain containing 2, isoform CRA_b	Q96EX0	70	71,86	9,71	8,22	3	n.d.
Sorbin and SH3 domain containing 3	Q6NX54	54	0,00	10,00	1,68	2	n.d.
Sorcin	P30626	201	21,66	5,20	24,24	11	0
Sorting nexin-12	Q9UMY4	79	18,62	9,50	13,04	2	-
Spectrin beta chain	Q9H254	54	288,81	5,66	1,21	2	n.d.
Spermatogenesis-associated protein 2-like protein	Q8IUW3	55	46,18	5,24	6,60	2	n.d.
Spermidine synthase	P19623	79	33,80	5,19	7,95	8	++
Spermidine/spermine N(1)-acetyltransferase-like protein 1	Q86VE3	40	55,83	5,29	1,80	1	n.d.
S-phase kinase-associated protein 1A	P63208	72	18,52	4,24	11,11	2	--
Sphingosine 1-phosphate receptor Edg-6	O95977	41	43,10	11,93	3,00	1	n.d.
Spliceosome RNA helicase BAT1	Q13838	152	48,99	5,43	9,58	9	0
Splicing factor 1 (Zinc finger protein 162)	Q15637	43	68,40	9,78	2,03	1	n.d.
Splicing factor proline/glutamine-rich [Fragment]	Q6PIX2	173	55,44	10,40	10,86	14	0
Splicing factor proline/glutamine-rich [Fragment]	Q9BSV4	169	68,59	9,42	9,62	12	++
Splicing factor U2AF 35 kDa subunit	Q01081	88	27,72	10,14	12,13	8	0
Splicing factor, arginine/serine-rich 1	Q07955	632	27,60	10,83	52,63	45	+
Splicing factor, arginine/serine-rich 10	P62995	140	21,92	10,51	26,60	3	+
Splicing factor, arginine/serine-rich 19	Q9H7N4	63	139,27	9,94	2,82	4	n.d.
Splicing factor, arginine/serine-rich 2	Q01130	78	25,33	12,36	7,27	4	++
Splicing factor, arginine/serine-rich 3	P84103	375	13,24	11,40	66,09	26	++
Splicing factor, arginine/serine-rich 7	Q16629	255	15,75	10,56	46,72	48	0
Splicing factor, arginine/serine-rich 9	Q13242	218	25,53	9,25	27,60	12	0
Splicing factor, proline- and glutamine-rich	P23246	181	45,22	6,37	11,36	13	--
Splicing protein spf31	O75937	102	29,82	9,52	12,25	4	0
SPRY domain-containing SOCS box protein 3	Q6PJ21	40	39,37	9,94	5,35	2	n.d.
SRA stem-loop-interacting RNA-binding protein [Precursor]	Q9GZT3	217	12,34	11,04	53,21	12	0
Stabilin-1	Q9NY15	53	275,17	6,04	1,28	2	n.d.
Staphylococcal nuclease domain-containing protein 1	Q7KZF4	54	99,61	6,54	3,28	2	n.d.
Stathmin	P16949	443	17,16	5,68	43,92	27	--
Stathmin-2	Q92945	376	72,85	8,90	13,38	11	0
Steerin-2	Q8IVL1	52	267,95	9,77	1,41	2	n.d.
Sterile alpha motif domain-containing protein 14	Q8IZD0	48	45,06	9,99	8,09	2	n.d.
Sterile alpha motif domain-containing protein 4B	Q5PRF9	57	75,44	6,39	3,03	2	n.d.
Sterile alpha motif domain-containing protein 9	Q5K651	41	184,28	8,78	1,00	1	0
STIP1 protein	Q3ZCU9	118	68,00	8,63	3,39	3	0
Stomatin-like protein 2	Q9UJZ1	83	38,73	6,46	7,28	2	++
Stress Activated Protein Kinase (SAPK) substrate protein 1	Q04323	67	35,09	5,18	6,73	3	n.d.
Stress-induced-phosphoprotein 1	P31948	44	62,60	6,42	4,97	3	--
Stromal cell-derived factor 2-like protein 1 [Precursor]	Q9HCN8	55	23,60	6,42	9,05	2	n.d.
SUMO-activating enzyme subunit 1	Q9UBE0	55	38,43	5,04	5,78	1	++
Superoxide dismutase [Cu-Zn]	P00441	108	17,91	6,27	21,64	5	+
Surfeit 6	Q5T8U1	73	41,43	11,22	12,19	5	++
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily E member 1	Q969G3	42	46,69	4,69	2,43	1	n.d.
Synapse defective 1 Rho GTPase homolog 1	Q6ZW31	45	79,74	9,60	1,36	1	n.d.
Synapsin I	Q5H9B0	77	70,03	10,37	7,47	7	0
Synaptopodin	Q8N3V7	59	99,46	10,38	3,10	3	n.d.
T calcium channel alpha 1G subunit variant 216	Q19R00	53	243,36	6,60	1,64	2	n.d.
TAR DNA binding protein variant [Fragment]	Q53H27	78	44,64	6,02	4,35	4	n.d.
TAR DNA-binding protein 43	Q13148	219	44,71	5,80	13,04	2	n.d.
Tau-tubulin kinase 1	Q5TCY1	50	142,74	6,53	6,76	5	n.d.
TBK1-binding protein 1 [Fragment]	O94873	43	70,16	5,82	4,69	2	n.d.
T-box transcription factor TBX2	Q13207	64	68,85	9,79	4,92	2	n.d.
T-cell receptor alpha chain V region CTL-L17 [Precursor]	P04437	45	15,44	9,26	28,93	2	++
T-cell receptor beta chain C region	P01850	42	19,90	4,91	26,80	1	n.d.

Table 2. continued

Protein Name and Species	**Accession**	**Score**	**MW [kDa]**	**pI**	**SC [%]**	**# Pept.**	**regulated**
T-complex protein 1 subunit alpha	P17987	71	60,31	5,74	4,68	15	--
T-complex protein 1 subunit beta	P78371	421	57,42	6,00	19,81	26	0
T-complex protein 1 subunit delta	P50991	336	57,76	9,08	14,87	21	0
T-complex protein 1 subunit epsilon	P48643	51	0,00	5,34	1,85	1	n.d.
T-complex protein 1 subunit eta	Q99832	81	59,33	8,60	4,24	2	0
T-complex protein 1 subunit theta	P50990	77	59,45	5,31	4,57	7	0
T-complex protein 1 subunit zeta	P40227	56	57,86	6,24	3,77	2	n.d.
TCP-1-gamma	P49368	51	21,77	5,38	11,44	2	0
Telomerase-binding protein EST1A	Q86US8	47	0,00	9,84	5,58	2	--
Teneurin-2	Q9NT68	60	238,46	5,89	1,21	2	n.d.
Tensin-like C1 domain-containing phosphatase	Q63HR2	48	162,77	9,62	2,13	2	n.d.
Tetratricopeptide repeat protein 35	Q15006	64	17,36	5,10	15,75	3	0
Tetratricopeptide repeat protein 9C	Q8N5M4	132	20,00	9,51	25,15	6	0
TFAM protein (transcription factor A, mitochondrial)	Q6LES8	89	29,06	10,29	13,41	3	++
Thioredoxin domain containing 4	Q4VXC1	138	46,94	4,96	11,82	5	+
Thioredoxin domain-containing protein 17	Q9BRA2	106	13,93	5,27	11,38	2	n.d.
Thioredoxin domain-containing protein 5 [Precursor]	Q8NBS9	188	47,60	5,58	11,81	6	-
Thioredoxin-like protein 1	O43396	79	32,10	4,69	10,76	3	0
Thyroid hormone receptor-associated protein 3	Q9Y2W1	60	75,81	10,83	3,87	4	++
TIP41, TOR signalling pathway regulator-like	Q8IZ86	78	20,20	5,48	10,11	1	n.d.
TJP3 protein [Fragment]	Q2VPE5	60	103,13	6,17	3,31	2	n.d.
Toll interacting protein	Q6FIE9	49	30,26	5,61	5,11	1	n.d.
TPM1 protein variant [Fragment]	Q59GR8	57	34,38	5,21	10,23	2	n.d.
Transaldolase	P37837	57	37,39	6,39	3,27	6	0
Transcription elongation factor A protein 1	P23193	389	33,95	9,55	27,57	7	-
Transcription elongation factor B polypeptide 2	Q15370	160	11,04	4,78	34,69	4	--
Transcription elongation factor B polypeptide 3B	Q3SY90	48	83,82	10,40	6,11	2	n.d.
Transcription elongation factor SPT4	P63272	49	15,25	6,22	11,85	2	0
Transcription factor 20	Q9UGU0	51	78,12	10,37	5,87	4	n.d.
Transcription intermediary factor 1-beta	Q13263	123	88,36	5,44	4,91	11	0
Transcriptional activator protein Pur-beta	Q96QR8	52	33,09	5,20	4,50	2	+
Transcriptional coactivator Aly/REF	Q86V81	265	26,87	11,64	19,07	18	0
Transcriptional coactivator p75/p51	O75475	67	37,25	9,76	9,12	3	--
Transcriptional enhancer factor TEF-5	Q99594	39	54,19	9,84	2,05	1	n.d.
Transforming, acidic coiled-coil containing protein 3	Q2NKK4	48	0,00	4,81	2,39	2	n.d.
Transgelin-2	P37802	227	22,25	9,41	36,87	20	--
Transient receptor potential cation channel subfamily M member 3	Q9HCF6	46	197,53	6,49	2,23	2	n.d.
Transient receptor potential cation channel subfamily M member 8	Q7Z2W7	45	127,69	7,35	2,76	3	0
Transient receptor potential cation channel, subfamily M, member 2, striatum short form	Q5KTC1	57	147,15	6,69	1,94	2	n.d.
Transitional endoplasmic reticulum ATPase	P55072	67	89,13	5,00	4,60	4	--
Transketolase variant [Fragment]	Q53EM5	46	67,86	8,83	2,57	5	0
Translation initiation factor eIF-2B subunit delta	Q9UI10	47	57,56	10,20	8,84	2	n.d.
translation initiation factor eIF-4A I - mouse	P60842	44	46,12	5,19	2,46	1	n.d.
translation initiation factor eIF-5A [validated] - human	P63241	126	16,82	4,94	14,94	1	n.d.
Translocase of outer mitochondrial membrane 33	Q6IBN7	56	34,54	9,79	11,65	3	0
Translocon-associated protein subunit delta	P51571	41	16,24	5,40	7,43	1	n.d.
Transmembrane protease, serine 13	Q9BYE2	50	62,68	9,98	1,72	1	n.d.
Transmembrane protein 108 [Precursor]	Q6UXF1	42	59,95	10,56	10,15	4	n.d.
Transmembrane protein 109 [Precursor]	Q9BVC6	143	26,19	10,90	13,99	7	0
Transmembrane protein 181	Q9P2C4	48	69,33	9,75	3,92	6	n.d.
Transmembrane protein 32 [Precursor]	Q8N4V1	54	13,79	9,17	8,87	1	n.d.
Transmembrane protein 33	P57088	116	27,93	10,59	10,93	3	n.d.
Transmembrane protein 46	Q5W0G8	53	31,35	9,32	10,85	2	n.d.
Transmembrane protein 74	Q96NL1	42	33,32	4,98	4,26	1	n.d.
Transmembrane protein 97	Q5BJF2	57	20,83	9,96	10,23	2	0
Treacle protein	Q13428	85	96,70	5,42	6,37	7	0
Tripartite motif-containing 11	Q5VSU1	39	0,00	5,40	2,78	1	n.d.
Tripartite motif-containing protein 67	Q6ZTA4	40	80,98	8,84	3,74	2	n.d.
Tripeptidyl-peptidase I variant [Fragment]	Q53HP2	182	61,17	6,01	7,46	7	n.d.
TRM112-like protein	Q9UI30	158	14,19	5,09	26,40	8	0
tRNA (adenine-N(1)-)-methyltransferase catalytic subunit TRM61	Q96FX7	44	34,69	8,06	5,63	1	n.d.
Tropomodulin-1	P28289	76	40,54	4,98	7,80	2	-
Tropomyosin alpha-4 chain	P67936	587	28,37	4,52	39,68	31	0
Tropomyosin gamma	P06753	549	28,74	4,55	37,50	44	0
TSC22D4 protein	Q8IV54	79	0,00	9,80	18,71	3	n.d.
TUBB protein	Q9BUU9	165	38,29	4,60	17,94	6	0
Tubby-related protein 4	Q9NRJ4	52	75,80	6,00	3,10	2	n.d.
Tubulin alpha 6 variant [Fragment]	Q53GA7	144	49,79	4,87	10,47	4	-
Tubulin alpha chain-like 3	A6NHL2	56	49,91	5,88	8,13	2	0
Tubulin alpha-1A chain	Q71U36	572	50,13	4,89	29,27	147	--

Table 2. continued

Protein Name and Species	Accession	Score	MW [kDa]	pI	SC [%]	# Pept.	regulated
Tubulin alpha-1B chain	P68363	703	50,12	4,81	31,26	44	-
Tubulin alpha-1C chain	Q9BQE3	132	50,10	4,81	10,64	9	--
Tubulin alpha-3C/D chain	Q13749	459	46,08	4,41	24,50	66	--
Tubulin alpha-3E chain	Q6PEY2	195	49,88	4,84	18,52	21	--
Tubulin alpha-4A chain	P68366	386	49,76	4,79	19,24	63	-
Tubulin alpha-8 chain	Q9NY65	404	50,06	4,80	23,61	60	-
Tubulin B6 protein	Q2NKY5	127	50,06	4,64	7,38	9	n.d.
Tubulin beta 4	Q7KZS6	302	88,32	5,49	8,91	62	--
Tubulin beta 5	P04350	130	9,30	4,72	19,05	11	--
Tubulin beta polypeptide	Q5JP53	413	47,74	4,55	19,95	215	--
Tubulin beta-1 chain	Q9H4B7	225	49,83	4,62	13,45	7	--
Tubulin beta-2A chain	Q13885	256	49,88	4,67	15,73	26	+
Tubulin beta-2B chain	Q9BVA1	369	49,92	4,64	19,10	37	0
Tubulin beta-2C chain	P68371	192	9,30	4,72	19,05	36	0
Tubulin beta-3 chain	Q13509	167	50,40	4,68	11,56	16	--
Tubulin beta-6 chain	Q9BUF5	210	49,83	4,62	9,87	28	0
Tubulin Class IVb beta tubulin	Q8IWP6	323	49,72	4,67	15,73	50	-
Tubulin TUBAL3 protein	Q4QQJ5	66	45,49	5,88	8,13	8	0
Tubulin-specific chaperone A	O75347	272	12,72	5,10	56,07	21	-
Tubulin-specific chaperone D	Q9BTW9	56	138,56	5,96	1,12	2	n.d.
Tubulin--tyrosine ligase-like protein 7	Q6ZT98	39	92,04	9,92	1,14	1	n.d.
Tumor necrosis factor receptor superfamily, member 18	Q5T7K5	51	26,83	11,55	5,10	2	n.d.
Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, beta polypeptide [Fragment]	Q4VY19	94	11,54	5,39	33,00	7	0
Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, beta polypeptide variant [Fragment]	Q59EQ2	72	22,16	9,56	13,23	2	+
U1 small nuclear ribonucleoprotein A	P09012	138	31,13	10,28	15,66	6	++
U2 small nuclear ribonucleoprotein A'	P09661	55	18,69	9,33	12,96	2	0
U2 small nuclear ribonucleoprotein B''	P08579	77	10,88	10,53	19,15	5	++
U3 small nucleolar ribonucleoprotein protein IMP3	Q9NV31	67	21,84	10,14	8,15	1	n.d.
U6 snRNA-associated Sm-like protein LSm1	O15116	142	15,17	4,97	26,32	3	0
U6 snRNA-associated Sm-like protein LSm3	P62310	60	11,71	4,42	11,88	1	n.d.
U6 snRNA-associated Sm-like protein LSm8	O95777	153	10,27	4,17	35,79	2	n.d.
Ubiquinol-cytochrome c reductase complex 14 kDa protein	P14927	110	13,39	9,32	22,73	3	++
Ubiquinol-cytochrome-c reductase complex core protein 1	P31930	153	52,61	5,92	9,17	4	++
Ubiquinone biosynthesis protein COQ9	O75208	57	22,92	5,70	11,82	3	++
Ubiquitin	P62988	207	8,56	7,58	39,47	46	++
Ubiquitin C splice variant	Q5UGI3	251	17,14	9,05	31,37	5	--
Ubiquitin C variant [Fragment]	Q59EM9	210	147,25	8,29	3,21	5	--
Ubiquitin carboxyl-terminal hydrolase 2	O75604	50	68,07	9,86	5,29	2	n.d.
Ubiquitin carboxyl-terminal hydrolase 31	Q70CQ4	60	146,54	10,20	3,92	12	n.d.
Ubiquitin carboxyl-terminal hydrolase 5	P45974	53	0,00	4,82	4,07	2	n.d.
Ubiquitin carboxyl-terminal hydrolase 6	P35125	67	158,66	7,90	4,32	3	n.d.
Ubiquitin carboxyl-terminal hydrolase isozyme L1	P09936	159	23,01	5,19	28,85	4	0
Ubiquitin carrier protein	Q8N924	128	16,77	7,70	26,35	4	0
Ubiquitin fusion degradation protein 1 homolog	Q92890	119	38,70	5,93	15,45	3	--
Ubiquitin thioesterase L1	P09936	199	24,81	5,22	26,01	8	0
Ubiquitin thioesterase OTUB1	Q96FW1	191	31,26	4,76	20,59	10	0
Ubiquitin-activating enzyme E1	P22314	159	90,33	5,72	6,10	15	n.d.
Ubiquitin-conjugating enzyme E2 N	P61088	181	17,13	6,17	27,63	20	0
Ubiquitin-conjugating enzyme E2 variant 1	Q13404	120	16,48	9,01	20,41	6	0
Ubiquitin-conjugating enzyme E2 variant 2	Q15819	125	16,22	9,13	20,83	7	0
Ubiquitin-conjugating enzyme E2-25 kDa	P61086	52	22,26	5,20	7,54	1	n.d.
Ubiquitin-fold modifier conjugating enzyme 1	Q5VTX1	132	19,45	7,74	15,57	9	0
Ubiquitin-like protein 5	Q9BZL1	86	8,54	9,43	31,51	1	++
Ubiquitin-like protein Nedd8	Q15843	147	8,44	7,55	22,97	6	--
UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 8	Q7Z7M8	37	43,37	9,67	2,27	1	n.d.
UDP-N-acetylglucosamine: alpha-1,3-D-mannoside beta-1,4-N-acetylglucosaminyltransferase IVb	Q9UQ53	66	41,83	9,89	5,00	2	n.d.
Uncharacterized protein C10orf38 [Precursor]	Q5VUB5	48	0,00	4,89	7,16	2	n.d.
Uncharacterized protein C11orf2	Q9UID3	44	86,04	6,04	3,58	1	n.d.
Uncharacterized protein C14orf131 [Fragment]	Q86TU1	48	0,00	10,01	10,20	2	n.d.
Uncharacterized protein C14orf93 [Precursor]	Q9H972	41	58,70	5,10	3,21	1	n.d.
Uncharacterized protein C17orf47	Q8NEP4	41	63,05	9,91	1,93	1	n.d.
Uncharacterized protein C17orf84 [Fragment]	Q9H656	46	0,00	12,11	9,72	1	n.d.
Uncharacterized protein C18orf16	Q96NN2	49	0,00	11,24	7,86	2	n.d.
Uncharacterized protein C19orf10 [Precursor]	Q969H8	49	18,33	6,24	10,12	3	0
Uncharacterized protein C19orf43	Q9BQ61	84	18,41	10,02	7,95	4	-
Uncharacterized protein C1orf172	Q8NAX2	57	0,00	6,10	9,30	2	n.d.
Uncharacterized protein C20orf116 [Precursor]	Q96HY6	54	35,59	4,98	10,19	3	n.d.
Uncharacterized protein C2orf32	Q96F85	40	18,64	8,90	9,76	2	0
Uncharacterized protein C4orf28	Q8N7B6	51	27,15	10,50	16,13	2	--
Uncharacterized protein C7orf23	Q9BS37	56	12,93	9,59	9,65	1	n.d.

Table 2. continued

Protein Name and Species	Accession	Score	MW [kDa]	pI	SC [%]	# Pept.	regulated
Uncharacterized protein C8orf55 [Precursor]	Q8WUY1	59	23,79	11,45	7,21	2	n.d.
Uncharacterized protein C8orf79	Q8N9K7	60	13,66	12,33	16,53	2	n.d.
Uncharacterized protein C9orf64	Q5T6V5	93	39,00	5,54	14,37	4	0
Uncharacterized protein C9orf85	Q96MD7	55	11,57	12,41	19,63	8	n.d.
Uncharacterized protein F0470 protein C19orf51	Q8N9W5	50	66,53	5,92	5,59	2	n.d.
Uncharacterized protein KIAA0226	Q92622	40	108,49	5,83	1,65	1	n.d.
Uncharacterized protein KIAA0802	Q9Y4B5	64	108,64	6,05	4,41	2	n.d.
Uncharacterized protein KIAA1622	Q6NUP7	55	101,27	9,29	3,48	2	n.d.
Uncharacterized protein KIAA1849	Q96JH8	50	116,70	7,16	2,42	2	n.d.
Uncoupling protein 2 variant [Fragment]	Q53HM3	55	33,24	10,43	11,97	2	n.d.
unnamed protein product	CAE93995	107	14,23	12,03	26,83	4	0
unnamed protein product	CAF17826	58	7,79	7,78	26,47	6	+
unnamed protein product	CAF16949	42	7,76	7,92	21,43	2	++
unnamed protein product	CAF01646	49	5,51	12,50	38,89	2	++
unnamed protein product	CAC34691	42	0,00	7,61	11,17	2	n.d.
unnamed protein product	CAD61578	74	11,08	12,22	40,37	8	n.d.
unnamed protein product	CAD61591	44	5,89	10,53	51,67	5	n.d.
unnamed protein product	CAD69584	47	0,00	11,86	6,38	2	n.d.
unnamed protein Product	CAD69629	72	16,91	12,39	20,38	2	n.d.
unnamed protein product	CAD69656	47	0,00	11,12	2,24	2	n.d.
unnamed protein product	CAD69727	51	0,00	12,80	12,27	2	n.d.
unnamed protein product	CAD69997	47	29,51	13,40	8,66	2	n.d.
unnamed protein product	CAD70044	59	34,21	13,66	11,11	2	n.d.
unnamed protein product	CAD70089	55	0,00	12,38	3,96	2	n.d.
unnamed protein product	CAE45995	80	78,77	5,94	1,99	1	n.d.
unnamed protein product	CAE89494	45	0,00	12,50	16,31	1	n.d.
unnamed protein product	CAE90964	54	12,60	12,50	26,72	2	n.d.
unnamed protein product	CAE91331	61	0,00	9,76	13,08	4	n.d.
unnamed protein product	CAE94090	45	15,72	11,85	12,98	2	n.d.
unnamed protein product	CAE98601	53	0,00	12,80	32,73	2	n.d.
unnamed protein product	CAE98864	46	7,00	11,02	43,94	6	n.d.
unnamed protein product	CAE99173	50	8,05	11,63	11,84	2	n.d.
unnamed protein product	CAF00484	51	0,00	10,97	22,45	2	n.d.
unnamed protein product	CAF00626	74	7,74	12,74	36,49	8	n.d.
unnamed protein product	CAF00635	41	0,00	4,64	36,00	2	n.d.
unnamed protein product	CAF00780	79	8,58	11,04	28,00	5	n.d.
unnamed protein product	CAF00806	44	6,37	10,01	49,15	4	n.d.
unnamed protein product	CAF01289	53	7,29	13,28	35,29	7	n.d.
unnamed protein product	CAF01537	57	7,47	11,83	18,84	2	n.d.
unnamed protein product	CAF14464	45	17,63	11,52	16,35	2	n.d.
unnamed protein product	CAF14683	40	6,71	7,81	36,51	2	n.d.
unnamed protein product	CAF15702	52	0,00	11,80	46,97	2	n.d.
unnamed protein product	CAF16040	50	0,00	12,41	19,63	4	n.d.
unnamed protein product	CAF16713	41	0,00	13,11	20,00	1	n.d.
unnamed protein product	CAF16721	42	0,00	12,30	19,61	4	n.d.
unnamed protein product	CAF17189	54	0,00	11,70	25,71	2	n.d.
unnamed protein product	CAF17251	50	10,12	12,41	34,41	2	n.d.
unnamed protein product	CAF17318	51	0,00	9,58	32,08	2	n.d.
unnamed protein product	CAF17489	44	6,64	11,41	32,26	3	n.d.
unnamed protein product	CAF17758	54	0,00	10,92	44,64	3	n.d.
unnamed protein product	CAF17768	40	5,86	10,13	24,07	1	n.d.
unnamed protein product	CAF18012	89	6,11	6,31	36,21	4	n.d.
unnamed protein product	CAF18044	62	0,00	12,13	18,75	3	n.d.
unnamed protein product	CAF18087	75	0,00	12,05	27,36	2	n.d.
unnamed protein product	CAF86678	57	0,00	12,98	11,95	2	n.d.
Unr-interacting protein	Q5TZT4	77	38,36	4,89	5,14	2	n.d.
UPF0287 protein C16orf61	Q9NRP2	59	9,45	9,15	13,92	2	--
UPF0366 protein C11orf67	Q9H7C9	49	13,32	9,46	16,39	1	0
UPF0404 protein C11orf59	Q6IAA8	45	17,71	5,01	8,07	2	n.d.
Up-regulated during skeletal muscle growth protein 5	Q96IX5	87	6,45	10,25	44,83	1	+
Urotensin 2	Q5H8X8	53	0,00	10,47	5,76	1	n.d.
Usherin [Precursor]	O75445	44	575,60	6,41	0,73	2	n.d.
Vacuolar ATP synthase subunit B, brain isoform	P21281	83	56,46	5,48	7,24	5	n.d.
Vacuolar ATP synthase subunit E 1	P36543	57	26,21	9,12	9,29	5	-
Vacuolar ATP synthase subunit G 1	O75348	98	13,62	9,75	13,68	2	0
Vacuolar protein-sorting-associated protein 25	Q9BRG1	202	20,73	5,95	27,84	13	-
Valosin-containing protein	Q9HAP1	51	34,37	6,04	8,47	2	--
Vasohibin-1	Q7L8A9	47	0,00	5,01	14,71	2	n.d.
Vesicle-associated membrane protein-associated protein A	Q9P0L0	75	19,42	6,12	14,62	6	--
Vesicle-associated membrane protein-associated protein B/C	O95292	100	27,21	7,70	13,99	3	0
VHL protein [Fragment]	Q9UMS8	56	3,41	12,33	45,45	2	n.d.
Vimentin	P08670	1244	53,49	4,91	57,20	416	-

Table 2. continued

Protein Name and Species	Accession	Score	MW [kDa]	pI	SC [%]	# Pept.	regulated
Vinexin	O60504	83	75,33	9,95	6,11	3	n.d.
Voltage-dependent anion-selective channel protein 1	P21796	54	30,62	9,27	6,74	2	n.d.
Voltage-dependent T-type calcium channel subunit alpha-1H	O95180	52	259,16	7,29	1,15	4	n.d.
VPS29 protein	Q6FIF8	59	20,43	6,33	7,14	1	n.d.
WD repeat protein 74	Q6RFH5	45	40,18	9,78	4,10	1	++
WDR22 protein	Q8TBB7	54	36,57	9,71	5,21	2	n.d.
Werner syndrome ATP-dependent helicase	Q14191	50	0,00	9,98	3,80	2	0
Wings apart-like protein homolog	Q7Z5K2	48	132,95	5,68	2,90	2	n.d.
WUGSC:H_RG054D04.1 protein	O95036	76	29,02	11,21	10,12	2	0
XTP3TPA-transactivated protein 1	Q1KSF8	111	23,61	6,53	15,87	3	n.d.
XTP3-transactivated gene A protein	Q9H773	71	18,67	4,78	13,53	2	n.d.
Y-box-binding protein 2	Q9Y2T7	50	38,54	11,36	7,14	2	n.d.
Zinc finger CCCH domain-containing protein 3	Q8IXZ2	51	101,93	12,12	4,34	2	n.d.
Zinc finger protein 231	Q9UPA5	55	409,95	7,58	1,04	2	n.d.
Zinc finger protein 516	Q92618	49	124,29	10,08	1,98	2	n.d.
Zinc finger protein 592	Q2M1T2	48	137,44	9,25	3,39	2	n.d.
Zinc finger protein 786	Q8N393	54	0,00	11,14	10,51	2	n.d.
Zinc finger protein 8	P17098	39	64,93	7,20	2,61	1	n.d.
Zinc finger protein 99	Q8WTZ3	50	8,58	11,04	28,00	6	n.d.
Zinc finger protein HRX	Q03164	45	431,76	10,73	1,21	2	n.d.
Zinc finger protein ZNF276 protein	Q3KR18	51	0,00	10,83	5,78	2	n.d.
Zinc transporter SLC39A7	Q92504	50	0,00	9,77	10,15	2	n.d.
Zink finger protein ZNFX1 protein [Fragment]	Q6P6B6	42	51,07	6,61	2,47	1	n.d.

Table 3. **Regulated proteins in C3*bot* treated SH-SY5Y cells analyzed with ICPL™.** The regulation factor is greater than 1.5.

Protein Name and Species	Accession[1]	Sc.[2]	MW [kDa]	SC [%][3]	# Pep.[4]	# H/L[5]	Avg H/L[6]	AvgSD H/L[7]	CV [%] H/L[8]	reg. fact.[9]
cell growth and proliferation										
Adenylyl cyclase-associated protein 1	Q01518	50	51.51	4.01	1	1	0.53			***1.89***
Annexin A2	P07355	318	38.45	22.19	15	6	0.53	0,06	11,32	***1.89***
Annexin IV	P09525	138	35.73	9.43	3	1	2.05			2.05
Collagen alpha-2(I) chain [Precursor]	P08123	51	72.21	7.97	2	1	2.26			2.26
Cyclin-dependent kinase 6, chain A	Q00534	223	34.61	20.00	5	1	3.14			3.14
DEAD (Asp-Glu-Ala-Asp) box polypeptide 5	Q7Z2V5	42	45.97	4.19	1	1	0.40			***2.50***
Fibronectin type 3 and ankyrin repeat domains protein 1	Q8TC84	173	34.18	14.69	4	2	0.37	0,09	25,00	***2.71***
Galectin 1	P09382	104	14.71	35.56	4	1	0.43			***2.35***
Jerky homolog-like	Q32MC2	40	59.87	2.67	1	1	0.31			***3.23***
MCM7 minichromosome maintenance deficient 7	A4D2A1	60	81.26	3.34	3	1	0.50			***1.99***
Mitotic spindle assembly checkpoint protein MAD2A	Q13257	80	21.40	11.76	2	1	0.40			***2.50***

[1] SwissProt or NCBI accession number.

[2] Mascot search protein score. A protein is identified if the Mascot score is greater than 40.

[3] Sequence coverage of the protein.

[4] Number of all peptides used for identification of the protein.

[5] Number of heavy/light labeled peptide pairs used for quantification.

[6] Average regulation ratio of the heavy/light labeled peptides.

[7] Standard deviation of the regulation ratio.

[8] Variation of the heavy/light ratios.

[9] Regulation factor for the identified proteins. Bold and italic written regulation factors belong to down-regulated proteins.

Table 3. continued

Protein Name and Species	Accession[1]	Sc.[2]	MW [kDa]	SC [%][3]	# Pep.[4]	# H/L[5]	Avg H/L[6]	AvgSD H/L[7]	CV [%] H/L[8]	reg. fact.[9]
Myosin, heavy polypeptide 10	Q4LE45	68	233.71	1.24	5	4	0.54	0,44	81,48	***1.85***
Nuclear migration protein nudC	Q9Y266	244	38.19	22.66	6	3	0.60	0,77	128,21	***1.67***
Pinin	Q9H307	39	81.43	1.54	1	1	0.43			***2.32***
Prohibitin [Fragment]	P35232	473	29.81	37.50	33	10	1.77	0,42	23,73	1.77
Proliferation-associated protein 2G4	Q9UQ80	108	43.63	6.36	2	1	0.30			***3.37***
Protein DEK	P35659	60	42.33	4.57	2	2	0.30	0,01	3,48	***3.37***
Protein Jub	Q96IF1	43	0.00	3.72	2	2	0.27	0,40	147,06	***3.69***
Protein phosphatase 1G (Formerly 2C), magnesium-dependent, gamma isoform	Q6IAU5	172	59.23	8.79	4	3	0.49	0,28	57,89	***2.04***
Scavenger receptor class F member 2 [Precursor]	Q96GP6	85	24.94	18.52	7	2	0.45	0,54	120,00	***2.22***
Septin-9	Q9UHD8	45	65.36	4.95	3	2	0.55	0,14	25,79	***1.83***
Ubiquitin-like protein Nedd8	Q15843	147	8.44	22.97	6	3	0.54	0,05	9,26	***1.85***
cell morphology and diffentiation										
Adenylyl cyclase-associated protein 1	Q01518	50	51.51	4.01	1	1	0.53			***1.89***
Alpha-centractin	P61163	47	42.59	4.26	2	1	0.49			***2.04***
BolA-like protein 2	Q9H3K6	143	10.11	37.21	2	1	0.61			***1.65***
Chloride intracellular channel protein 4	Q9Y696	156	28.62	12.30	3	2	0.63	0,06	9,76	***1.59***
Coronin, actin binding protein, 1C variant [Fragment]	Q53G58	147	53.25	10.76	6	3	0.55	0,04	6,98	***1.80***
Dihydropyrimidinase-related protein 2	Q16555	95	21.40	15.15	5	1	0.57			***1.75***
Drebrin	Q16643	72	71.25	4.01	2	1	0.41			***2.42***
dUTP pyrophosphatase	P33316	160	26.55	18.90	7	1	0.15			***6.67***
Galectin 1	P09382	104	14.71	35.56	4	1	0.43			***2.35***
Glucose-6-phosphate isomerase	P06744	161	62.98	7.18	21	14	0.59	0,20	33,90	***1.69***
Myosin heavy chain 9	Q6ZNL4	55	65.73	4.44	2	1	0.31			***3.25***
Myosin, heavy polypeptide 10	Q4LE45	68	233.71	1.24	5	4	0.54	0,44	81,48	***1.85***
Nuclear structure protein 5	Q5M775	51	118.59	4.12	2	1	3.08			3.08
Palmitoyl-protein thioesterase 1 [Precursor]	P50897	75	34.16	11.44	4	2	2.41	0,05	1,91	2.41
Probable protein BRICK1	Q8WUW1	67	8.74	28.00	2	1	0.63			***1.58***
Protein KIAA0284	Q9Y4F5	59	163.53	1.84	5	1	1.61			1.61
Purine-rich element binding protein B	A4D2L7	80	33.22	10.90	4	3	1.89	2,08	109,89	1.89
Stathmin	P16949	443	17.16	43.92	27	13	0.40	0,15	37,50	***2.50***
Tubulin alpha-1A chain	Q71U36	572	50.13	29.27	147	54	0.66	0,28	42,42	***1.52***
Tubulin alpha-1C chain	Q9BQE3	132	50.10	10.64	9	1	0.53			***1.89***
Tubulin alpha-3C/D chain	Q13749	459	46.08	24.50	66	24	0.34	0,23	67,65	***2.94***
Tubulin alpha-3E chain	Q6PEY2	195	49.88	18.52	21	2	0.53	0,20	37,74	***1.89***
Tubulin beta 4	Q7KZS6	302	88.32	8.91	62	11	0.56	0,34	60,71	***1.79***
Tubulin beta 5	P04350	130	9.30	19.05	11	4	0.32	0,22	68,75	***3.13***
Tubulin beta polypeptide	Q5JP53	413	47.74	19.95	215	60	0.63	0,29	46,03	***1.59***
Tubulin beta-1 chain	Q9H4B7	225	49.83	13.45	7	2	0.52	0,04	7,50	***1.94***
Tubulin beta-3 chain	Q13509	167	50.40	11.56	16	7	0.49	0,11	22,45	***2.04***
metabolism										
Acetyl-CoA acyltransferase	P42765	69	41.90	6.80	2	2	1.52	1,95	128,21	1.52
Acyl-CoA dehydrogenase precursor, medium-chain-specific	P11310	71	46.56	8.08	3	2	2.00	2,56	128,21	2.00

Table 3. continued

Protein Name and Species	Accession[1]	Sc.[2]	MW [kDa]	SC [%][3]	# Pep.[4]	# H/L[5]	Avg H/L[6]	AvgSD H/L[7]	CV [%] H/L[8]	reg. fact.[9]
Adenosylhomocysteinase	P23526	81	47.55	4.64	3	2	0.63	0,04	6,12	***1.58***
ATP synthase delta chain [Fragment]	Q53HH2	330	23.25	36.15	11	5	1.53	0,31	20,26	1.53
ATP synthasesubunit alpha [Precursor]	P25705	103	59.71	8.50	21	11	0.39	0,13	33,33	***2.56***
ATP synthase subunit alpha [Precursor]	P25705	620	59.71	24.23	44	13	1.82	0,76	41,76	1.82
ATP synthase subunit beta [Precursor]	P06576	105	57.92	15.68	18	4	0.47	0,09	19,15	***2.13***
ATP synthase subunit beta [Precursor]	P06576	724	57.92	39.29	31	7	2.18	1,14	52,29	2.18
Biliverdin reductase A [Precursor]	P53004	107	33.44	9.46	3	1	0.67			***1.49***
Caldesmon (Fragment)	Q9UD91	42	33.65	6.40	2	1	2.40			2.40
Caldesmon 1 (actin- and calmodulin-binding protein)	Q6PJM5	108	36.67	9.87	2	1	0.15			***6.46***
Cellular retinoic acid-binding protein 1	P29762	268	15.42	65.44	14	8	0.38	0,13	34,21	***2.63***
Cystathionine beta-synthase	P35520	62	60.42	3.09	1	1	0.40			***2.50***
D-3-phosphoglycerate dehydrogenase	O43175	187	56.48	10.34	10	2	0.23	0,15	65,22	***4.35***
Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase [Precursor]	Q13011	114	35.79	8.84	7	3	2.16	0,42	19,44	2.16
dUTP pyrophosphatase	P33316	160	26.55	18.90	7	1	0.15			***6.67***
Endoplasmic reticulum-associated amyloid beta-peptide-binding protein	Q99714	92	26.78	11.92	3	1	1.77			1.77
Enolase alpha	P06733	593	47.01	26.79	256	138	0.53	0,27	50,10	***1.89***
Ferritin heavy chain	P02794	62	21.23	4.85	2	1	1.51			1.51
Fibronectin type 3 and ankyrin repeat domains protein 1	Q8TC84	173	34.18	14.69	4	2	0.37	0,09	25,00	***2.71***
Fructose-bisphosphate aldolase A	P04075	435	39.26	34.71	37	24	0.56	0,29	51,79	***1.79***
Gamma-aminobutyraldehyde dehydrogenase	P49189	77	50.92	5.79	2	1	0.40			***2.50***
Glucose-6-phosphate isomerase	P06744	161	62.98	7.18	21	14	0.59	0,20	33,90	***1.69***
Glutamate dehydrogenase 1	P00367	64	61.36	3.58	2	1	1.64			1.64
Inositol-trisphosphate 3-kinase B	P27987	47	102.34	4.65	2	1	8.08			8.08
Ketosamine-3-kinase	Q9HA64	61	34.39	6.80	2	1	0.58			***1.72***
Leukocyte antigen CD37	P11049	45	0.00	13.68	2	1	0.41			***2.42***
Medium-chain specific acyl-CoA dehydrogenase [Precursor]	P11310	87	42.58	7.24	3	2	1.61	0,01	0,80	1.61
Methenyltetrahydrofolate cyclohydrolase	P13995	74	37.30	10.47	2	2	0.42	0,02	3,70	***2.41***
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 2	O43678	199	10.78	46.94	8	4	2.01	0,18	8,96	2.01
Neutral alpha-glucosidase AB [Precursor]	Q14697	85	106.81	3.07	7	1	6.89			6.89
Nicotinate-nucleotide pyrophosphorylase [carboxylating]	Q15274	140	30.81	14.48	8	1	0.59			***1.69***
NUCKS protein (Nuclear ubiquitous casein and cyclin-dependent kinases substrate)	Q6IA16	53	18.74	6.75	4	2	2.81	1,91	67,97	2.81
Phosphoglycerate mutase 1	P18669	397	28.65	35.18	32	14	0.64	0,37	57,81	***1.56***
Phospholipase D3	Q8IV08	140	54.67	7.55	5	2	1.94	0,30	15,46	1.94
Phosphoribosylaminoimidazole carboxylase	P22234	261	46.92	12.26	33	20	0.46	0,30	65,22	***2.17***
Phosphoserine aminotransferase	Q5T7G6	101	40.40	10.00	4	3	0.66	0,97	147,06	***1.51***
Platelet-activating factor acetylhydrolase IB subunit beta	P68402	120	25.55	11.79	3	1	1.51			1.51
Protein disulfide-isomerase [Precursor]	P07237	123	13.25	38.33	9	7	0.60	0,25	41,67	***1.67***

Table 3. continued

Protein Name and Species	Accession[1]	Sc.[2]	MW [kDa]	SC [%][3]	# Pep.[4]	# H/L[5]	Avg H/L[6]	AvgSD H/L[7]	CV [%] H/L[8]	reg. fact.[9]
Protein disulfide-isomerase A3 [Precursor]	P30101	314	56.76	16.24	13	4	0.59	0,38	64,41	***1.69***
Protein disulfide-isomerase A4 [Precursor]	P13667	193	72.89	9.61	20	15	0.47	0,26	55,33	***2.13***
Protein disulfide-isomerase A6 [Precursor]	Q15084	152	53.90	32.30	26	10	0.51	0,13	25,49	***1.96***
Putative RNA-binding protein Luc7-like 2	Q9Y383	82	45.67	6.27	5	4	1.60	1,76	110,00	1.60
Pyruvate dehydrogenase E1 component subunit alpha, somatic form [Precursor]	P08559	108	43.27	8.21	6	2	1.50	0,34	22,67	1.50
Pyruvate kinase isozymes M1/M2	P14618	275	57.77	16.57	123	35	0.58	0,27	46,55	***1.72***
Quinone oxidoreductase	PN0448	48	35.18	3.95	2	1	1.72			1.72
Ribose-phosphate pyrophosphokinase 1	P60891	89	34.81	9.75	5	1	0.40			***2.50***
Septin-9	Q9UHD8	45	65.36	4.95	3	2	0.55	0,14	25,79	***1.83***
Stomatin-like protein 2	Q9UJZ1	83	38.73	7.28	2	1	2.34			2.34
SUMO-activating enzyme subunit 1	Q9UBE0	55	38.43	5.78	1	1	1.74			1.74
Transitional endoplasmic reticulum ATPase	P55072	67	89.13	4.60	4	1	0.37			***2.71***
WD repeat protein 74	Q6RFH5	45	40.18	4.10	1	1	4.41			4.41
DNA synthesis and processing										
Cellular nucleic acid binding protein beta variant 2	Q4JGY0	41	18.96	8.72	1	1	0.28			***3.61***
Core binding factor beta isoform PEBP2B	Q9HCT2	144	21.98	29.95	6	4	0.55			***1.82***
Core histone macro-H2A.2	Q9P0M6	97	39.90	7.28	4	2	2.41	3,55	147,06	2.41
C-terminal binding protein 1	Q4KMQ8	107	47.47	6.82	3	1	0.62			***1.61***
C-terminal binding protein 2	Q5SQP8	102	56.07	7.80	4	1	0.62			***1.61***
DEAD box polypeptide 17 isoform p82 variant (Fragment)	Q59F66	59	81.02	3.80	2	1	0.42			***2.41***
DNA damage-binding protein 1	Q16531	49	126.83	1.40	2	1	0.26			***3.82***
DNA polymerase epsilon subunit 3	Q9NRF9	45	16.85	11.56	1	1	0.58			***1.71***
dUTP pyrophosphatase	P33316	160	26.55	18.90	7	1	0.15			***6.67***
Endothelial differentiation-related factor 1	O60869	180	16.36	35.81	8	6	1.62	1,28	79,01	1.62
Enolase alpha	P06733	593	47.01	26.79	256	138	0.53	0,27	50,10	***1.89***
Far upstream element-binding protein 1 / DNA helicase V	Q96AE4	117	67.43	6.84	8	4	0.66	0,32	48,48	***1.52***
High mobility group protein B2	P26583	170	23.89	15.87	13	7	1.71	0,90	52,63	1.71
Jerky homolog-like	Q32MC2	40	59.87	2.67	1	1	0.31			***3.23***
KHSRP protein	Q5U4P6	154	72.85	8.17	12	2	0.32	0,12	37,50	***3.13***
MCM7 minichromosome maintenance deficient 7	A4D2A1	60	81.26	3.34	3	1	0.50			***1.99***
Myocyte enhancer factor 2D/deleted in azoospermia associated protein 1 fusion protein	Q5IRN4	77	50.38	3.80	2	1	1.65			1.65
Nuclear autoantigenic sperm protein	Q5T624	55	45.77	2.61	1	1	0.14			***7.05***
OTTHUMP00000018488 [Fragment]	Q5T6S7	196	28.08	10.14	2	1	4.40			4.40
PAI-1 mRNA-binding protein Isoform	Q5VU22	96	44.23	5.97	2	2	0.31	0,08	25,00	***3.23***
Phosphatase 2A inhibitor I2PP2A	Q01105	96	32.08	7.58	18	11	1.83	1,22	66,66	1.83
Polymerase (RNA) II (DNA directed) polypeptide C	Q6FGR6	60	31.42	16.00	3	1	1.75			1.75

Table 3. continued

Protein Name and Species	Accession[1]	Sc.[2]	MW [kDa]	SC [%][3]	# Pep.[4]	# H/L[5]	Avg H/L[6]	AvgSD H/L[7]	CV [%] H/L[8]	reg. fact.[9]
Prohibitin [Fragment]	P35232	473	29.81	37.50	33	10	1.77	0,42	23,73	1.77
Prohibitin-2	Q99623	529	33.28	52.17	33	10	1.72	0,43	25,00	1.72
Purine-rich element binding protein B	A4D2L7	80	33.22	10.90	4	3	1.89	2,08	109,89	1.89
Replication factor C subunit 3	P40938	54	12.02	11.32	2	1	0.58			***1.71***
Ribose-phosphate pyrophosphokinase 1	P60891	89	34.81	9.75	5	1	0.40			***2.50***
SIN3B protein	Q2NL91	62	39.48	5.38	2	1	0.44			***2.28***
Single-stranded DNA-binding protein [Precursor]	Q04837	144	17.25	19.59	8	3	1.86	0,30	16,13	1.86
Splicing factor proline/glutamine-rich [Fragment]	Q9BSV4	169	68.59	9.62	12	2	3.05	2,60	85,25	3.05
Surfeit 6	Q5T8U1	73	41.43	12.19	5	3	2.36	0,56	23,73	2.36
Thyroid hormone receptor-associated protein 3	Q9Y2W1	60	75.81	3.87	4	2	4.02	4,58	113,93	4.02
Transcription factor A	Q6LES8	89	29.06	13.41	3	1	2.15			2.15
Transcriptional coactivator p75/p51	O75475	67	37.25	9.12	3	1	0.06			***16.67***
chaperoning										
Activator of 90 kDa heat shock protein ATPase homolog 1	O95433	200	29.56	18.32	6	1	0.63			***1.59***
BiP (HSP70 protein 5)	P11021	98	70.89	8.45	7	3	0.31	0,06	19,35	***3.23***
Chaperonin containing TCP1, subunit 3 (Gamma)	Q59H77	72	63.54	5.20	2	2	0.45	0,06	13,79	***2.24***
Heat shock protein 70 kDa protein 6	P17066	138	70.81	9.80	10	1	0.57			***1.75***
Heat shock protein 70 kDa protein 8	P11142	560	70.85	22.76	29	11	0.56	0,34	60,71	***1.79***
Heat shock protein 70kDa A5	Q2KHP4	444	72.38	21.22	30	9	0.59	0,21	35,59	***1.69***
Heat shock protein apg-1 (HSP 70 family)	Q53ZP9	52	94.45	4.29	2	1	0.45			***2.24***
Histone cluster 1, H1e	Q4VB24	158	21.88	21.00	7	2	8.85	3,90	44,07	8.85
Histone cluster 2, H3, pseudogene 2	Q5TEC6	438	15.42	50.74	43	21	1.53	0,19	12,42	1.53
Histone H1.0	P07305	138	20.87	17.53	7	1	21.50			21.50
Histone H1.2	P16403	242	21.22	36.79	6	4	11.10	0,81	7,30	11.10
Histone H1.4	P10412	279	21.85	35.78	26	16	16.50	5,48	33,21	16.50
Histone H1.5	P16401	180	22.44	20.44	16	9	9.89	2,49	25,18	9.89
Histone H1x	Q92522	108	22.47	13.15	4	1	0.11			***9.09***
Histone H2A type 1	P0C0S8	399	13.95	53.49	17	3	1.57	0,03	1,97	1.57
Histone H2A type 1-B	P04908	169	14.03	20.93	16	2	5.33	0,29	5,44	5.33
Histone H2A type 2-A	Q6FI13	356	13.96	53.49	10	3	1.57	0,03	1,96	1.57
Histone H2AV	Q71UI9	231	13.50	28.13	18	3	1.53	0,63	41,18	1.53
Histone H2B type 1-B	P33778	205	13.81	60.00	20	6	2.01	0,63	31,34	2.01
Histone H2B type 1-J	P06899	45	13.61	5.60	7	4	2.13	0,77	36,15	2.13
Histone H2B type 2-C	Q6DN03	65	21.33	13.02	3	1	1.51			1.51
Histone H3.1	P68431	420	15.43	59.12	156	76	2.02	0,72	35,64	2.02
Histone H3.3	P84243	455	15.19	60.00	67	33	2.18	0,68	31,19	2.18
Histone H3-like	Q6NXT2	51	15.23	23.70	2	1	7.07			7.07
Histone H3L-like	Q6TXQ4	201	12.10	63.55	7	4	1.95	0,17	8,66	1.95
Histone H4	P62805	444	11.36	75.73	74	36	1.78	0,22	12,36	1.78
Mitochondrial import inner membrane translocase subunit TIM14	Q96DA6	49	12.36	15.65	2	1	1.63			1.63
Phosphatase 2A inhibitor I2PP2A	Q01105	96	32.08	7.58	18	11	1.83	1,22	66,66	1.83
Prohibitin [Fragment]	P35232	473	29.81	37.50	33	10	1.77	0,42	23,73	1.77

Table 3. continued

Protein Name and Species	**Accession[1]**	**Sc.[2]**	**MW [kDa]**	**SC [%][3]**	**# Pep.[4]**	**# H/L[5]**	**Avg H/L[6]**	**AvgSD H/L[7]**	**CV [%] H/L[8]**	**reg. fact.[9]**
SGTA protein	Q6FIA9	172	34.04	10.54	5	3	2.52	2,51	99,60	2.52
T-complex protein 1 subunit alpha	P17987	71	60.31	4.68	15	2	0.40	0,45	112,50	***2.50***
RNA synthesis and processing										
39S ribosomal protein L11	Q9Y3B7	99	20.67	23.96	5	3	2.15	0,15	7,14	2.15
39S ribosomal protein L15	Q9P015	69	33.40	9.12	3	1	2.03			2.03
39S ribosomal protein L4	Q9BYD3	139	35.00	14.47	3	1	1.83			1.83
39S ribosomal protein L55 [Precursor]	Q7Z7F7	78	14.69	12.00	1	1	1.69			1.69
40S ribosomal protein S27a	P62979	259	17.95	28.85	5	2	0.32	0,00	1,21	***3.13***
60S ribosomal protein L10-like	Q96L21	68	24.37	9.39	2	1	1.61			1.61
60S ribosomal protein L31	P62899	62	14.45	14.40	2	1	1.61			1.61
60S ribosomal protein L8	P62917	412	28.01	42.80	51	29	3.96	4,47	112,88	3.96
Adenylyl cyclase-associated protein 1	Q01518	50	51.51	4.01	1	1	0.53			***1.89***
Arginine/serine-rich splicing factor 6 variant [Fragment]	Q59GY3	51	31.85	5.02	1	1	0.54			***1.85***
BolA-like protein 2	Q9H3K6	143	10.11	37.21	2	1	0.61			***1.65***
DDX19B protein [Fragment]	Q2NL95	82	50.61	5.79	2	1	0.50			***1.99***
DDX48 protein	Q6IBQ2	151	46.84	7.54	4	2	1.54	1,97	128,21	1.54
Elongation factor 1-gamma	P26641	332	49.96	16.74	13	6	0.58	0,20	34,48	***1.72***
Elongation factor 2	P13639	191	95.15	7.00	23	12	0.57	0,29	50,88	***1.75***
Elongation factor Tu [Precursor]	P49411	319	49.51	16.81	11	2	1.65	0,00	0,00	1.65
Eukaryotic translation initiation factor 2, subunit 2 beta, 38kDa	Q6IBR8	68	38.36	6.61	4	3	0.54	0,41	75,93	***1.85***
Eukaryotic translation initiation factor 3, subunit 1	O75822	108	29.04	8.14	1	1	0.25			***4.06***
Eukaryotic translation initiation factor 4B	Q4G0E3	68	69.06	2.62	2	1	0.22			***4.56***
FBL protein (Fibrillarin)	Q96BS4	230	28.43	28.85	7	4	1.63	1,79	109,89	1.63
H/ACA ribonucleoprotein complex subunit 2	Q9NX24	147	17.19	26.14	5	2	1.51	0,22	14,57	1.51
Heterogeneous nuclear ribonucleoprotein AB isoform a variant [Fragment]	Q53F64	77	35.97	6.93	1	1	0.22			***4.64***
Heterogeneous nuclear ribonucleoprotein G	P38159	501	47.42	35.93	23	6	1.93	1,36	70,47	1.93
Heterogeneous nuclear ribonucleoprotein L	P14866	83	64.05	5.43	7	6	0.45	0,25	55,56	***2.22***
Heterogeneous nuclear ribonucleoprotein M (hnRNP M)	P52272	168	77.33	9.05	42	20	0.53	0,22	41,51	***1.89***
High mobility group protein B2	P26583	170	23.89	15.87	13	7	1.71	0,90	52,63	1.71
High mobility group-like nuclear protein 2 homolog 1	P55769	95	14.03	14.96	7	4	1.78	0,58	32,58	1.78
Nuclease sensitive element-binding protein 1	P67808	271	35.77	24.46	19	9	3.65	5,70	156,16	3.65
Nudix (nucleoside diphosphate linked moiety X)-type motif 21	Q5HYH5	45	12.36	19.05	2	1	0.54			***1.85***
OTTHUMP00000018488 [Fragment]	Q5T6S7	196	28.08	10.14	2	1	4.40			4.40
PAI-1 mRNA-binding protein Isoform	Q5VU19	130	44.94	11.03	6	5	0.23	0,02	8,70	***4.35***
PAI-1 mRNA-binding protein Isoform	Q5VU22	96	44.23	5.97	2	2	0.31	0,08	25,00	***3.23***
Proliferation-associated protein 2G4	Q9UQ80	108	43.63	6.36	2	1	0.30			***3.37***
Putative eukaryotic translation initiation factor 1A	O75642	72	16.32	13.29	2	1	4.68			4.68
RBM 1 (RNA-binding motif)	Q2VIN3	77	41.44	7.81	5	2	0.53	0,57	107,55	***1.89***

Table 3. continued

Protein Name and Species	**Accession[1]**	**Sc.[2]**	**MW [kDa]**	**SC [%][3]**	**# Pep.[4]**	**# H/L[5]**	**Avg H/L[6]**	**AvgSD H/L[7]**	**CV [%] H/L[8]**	**reg. fact.[9]**
Ribonuclease/angiogenin inhibitor 1	P13489	114	49.92	6.94	2	1	0.43			***2.35***
Ribonucleoprotein [Fragment]	Q15367	130	40.57	8.45	3	2	0.49	0,05	10,53	***2.04***
Ribonucleoprotein RNA-binding protein 8A	Q9Y5S9	49	19.75	4.05	3	1	1.54			1.54
Ribosomal protein L11 [Fragment]	Q5VVC8	81	19.94	19.54	5	3	1.63	0,05	3,07	1.63
ribosomal protein L26	Q6IBH6	205	17.23	40.69	15	9	1.81	1,15	63,54	1.81
Ribosomal protein L28 variant [Fragment]	Q59F34	48	10.69	15.79	2	1	1.90			1.90
Splicing factor proline/glutamine-rich	P23246	181	45.22	11.36	13	4	0.54	0,10	18,52	***1.85***
Splicing factor proline/glutamine-rich [Fragment]	Q9BSV4	169	68.59	9.62	12	2	3.05	2,60	85,25	3.05
Splicing factor, arginine/serine-rich 2	Q01130	78	25.33	7.27	4	1	1.77			1.77
Splicing factor, arginine/serine-rich 3	P84103	375	13.24	66.09	26	6	1.65	0,43	26,06	1.65
Surfeit 6	Q5T8U1	73	41.43	12.19	5	3	2.36	0,56	23,73	2.36
Telomerase-binding protein EST1A	Q86US8	47	0.00	5.58	2	1	0.55			***1.80***
Transcription elongation factor B polypeptide 2	Q15370	160	11.04	34.69	4	2	0.60	0,01	1,08	***1.67***
U1 small nuclear ribonucleoprotein A	P09012	138	31.13	15.66	6	3	5.27	7,05	133,78	5.27
U2 small nuclear ribonucleoprotein B''	P08579	77	10.88	19.15	5	2	7.11	8,90	125,18	7.11
biosynthesis										
Annexin A2	P07355	318	38.45	22.19	15	6	0.53	0,06	11,32	***1.89***
Annexin IV	P09525	138	35.73	9.43	3	1	2.05			2.05
Core histone macro-H2A.2	Q9P0M6	97	39.90	7.28	4	2	2.41	3,55	147,06	2.41
Cystathionine beta-synthase	P35520	62	60.42	3.09	1	1	0.40			***2.50***
D-3-phosphoglycerate dehydrogenase	O43175	187	56.48	10.34	10	2	0.23	0,15	65,22	***4.35***
Inositol-trisphosphate 3-kinase B	P27987	47	102.34	4.65	2	1	8.08			8.08
Nicotinate-nucleotide pyrophosphorylase [carboxylating]	Q15274	140	30.81	14.48	8	1	0.59			***1.69***
Phosphoribosylaminoimidazole carboxylase	P22234	261	46.92	12.26	33	20	0.46	0,30	65,22	***2.17***
RBM 1 (RNA-binding motif)	Q2VIN3	77	41.44	7.81	5	2	0.53	0,57	107,55	***1.89***
Spermidine synthase	P19623	79	33.80	7.95	8	2	1.55	0,07	4,52	1.55
protein synthesis and processing										
Chaperonin containing TCP1, subunit 3 (Gamma)	Q59H77	72	63.54	5.20	2	2	0.45	0,06	13,79	***2.24***
Crk-like protein	P46109	111	33.76	21.45	3	1	1.55			1.55
Cyclin-dependent kinase 6, chain A	1BLXA	223	34.61	20.00	5	1	3.14			3.14
Cytochrome b-c1 complex subunit 2 [Precursor]	P22695	74	48.41	5.74	5	1	1.65			1.65
Cytochrome b-c1 complex subunit 8	O14949	187	8.36	56.00	7	2	1.52	0,03	1,97	1.52
DnaJ homolog subfamily B member 1	P25685	60	37.89	6.49	3	1	0.44			***2.28***
DnaJA2	Q86TL9	172	37.02	24.47	7	3	1.77	2,27	128,21	1.77
Heat shock protein 70 kDa protein 6	P17066	138	70.81	9.80	10	1	0.57			***1.75***
Heat shock protein 70 kDa protein 8	P11142	560	70.85	22.76	29	11	0.56	0,34	60,71	***1.79***
Heat shock protein apg-1 (HSP 70 family)	Q53ZP9	52	94.45	4.29	2	1	0.45			***2.24***
High mobility group-like nuclear protein 2 homolog 1	P55769	95	14.03	14.96	7	4	1.78	0,58	32,58	1.78

Table 3. continued

Protein Name and Species	Accession[1]	Sc.[2]	MW [kDa]	SC [%][3]	# Pep.[4]	# H/L[5]	Avg H/L[6]	AvgSD H/L[7]	CV [%] H/L[8]	reg. fact.[9]
Lectin, mannose-binding, 1 variant [Fragment]	Q53FS4	42	57.52	1.96	1	1	0.45			***2.21***
Nucleosome assembly protein 1-like 4	Q99733	60	42.80	2.93	2	2	0.38	< 0.01	0,10	***2.62***
Peptidyl-prolyl cis-trans isomerase D	Q6FGM6	102	40.75	11.08	5	2	2.01	2,50	124,12	2.01
Prefoldin subunit 2	Q5SY55	120	16.64	16.23	5	3	9.93	3,36	33,84	9.93
Protein phosphatase 1 regulatory subunit 14B	Q96C90	82	15.90	23.81	2	1	0.23			***4.33***
Protein phosphatase 1G (Formerly 2C), magnesium-dependent, gamma isoform	Q6IAU5	172	59.23	8.79	4	3	0.49	0,28	57,89	***2.04***
Putative eukaryotic translation initiation factor 1A	O75642	72	16.32	13.29	2	1	4.68			4.68
Putative RNA-binding protein Luc7-like 2	Q9Y383	82	45.67	6.27	5	4	1.60	1,76	110,00	1.60
SGTA protein	Q6FIA9	172	34.04	10.54	5	3	2.52	2,51	99,60	2.52
Signal recognition particle 14 kDa	Q96Q14	236	14.50	63.97	24	13	2.08	2,23	107,21	2.08
Signal recognition particle 9 kDa isoform	Q6NVX0	52	9.12	30.49	2	2	2.12	0,82	38,41	2.12
Transgelin-2	P37802	227	22.25	36.87	20	9	0.56	0,19	33,93	***1.79***
Tubulin alpha-1A chain	Q71U36	572	50.13	29.27	147	54	0.66	0,28	42,42	***1.52***
Tubulin alpha-1C chain	Q9BQE3	132	50.10	10.64	9	1	0.53			***1.89***
Tubulin alpha-3C/D chain	Q13749	459	46.08	24.50	66	24	0.34	0,23	67,65	***2.94***
Tubulin alpha-3E chain	Q6PEY2	195	49.88	18.52	21	2	0.53	0,20	37,74	***1.89***
Tubulin beta 4	Q7KZS6	302	88.32	8.91	62	11	0.56	0,34	60,71	***1.79***
Tubulin beta 5	P04350	130	9.30	19.05	11	4	0.32	0,22	68,75	***3.13***
Tubulin beta-1 chain	Q9H4B7	225	49.83	13.45	7	2	0.52	0,04	7,50	***1.94***
Tubulin beta-3 chain	Q13509	167	50.40	11.56	16	7	0.49	0,11	22,45	***2.04***
Tubulin beta polypeptide	Q5JP53	413	47.74	19.95	215	60	0.63	0,29	46,03	***1.59***
Ubiquinol-cytochrome c reductase complex 14 kDa protein	P14927	110	13.39	22.73	3	1	4.79			4.79
Ubiquinol-cytochrome-c reductase complex core protein 1	P31930	153	52.61	9.17	4	1	2.35			2.35
defense response										
Butyrophilin-like protein 3 [Precursor]	Q6UXE8	57	52.28	5.36	2	1	0.26			***3.88***
Chromosome 9 open reading frame 32	Q5SZB9	51	15.89	13.79	2	1	0.62			***1.63***
T-cell receptor alpha chain V region CTL-L17 [Precursor]	P04437	45	15.44	28.93	2	1	1.69			1.69
cell death										
5'-3' exoribonuclease 2	Q9H0D6	38	103.74	0.88	1	1	10.84			10.84
Autophagy-related protein 3	Q9NT62	60	36.17	6.94	1	1	0.45			***2.24***
Cytochrome b-c1 complex subunit 2 [Precursor]	P22695	74	48.41	5.74	5	1	1.65			1.65
Cytochrome b-c1 complex subunit 8	O14949	187	8.36	56.00	7	2	1.52	0,03	1,97	1.52
DNA damage-binding protein 1	Q16531	49	126.83	1.40	2	1	0.26			***3.82***
Galectin 1	P09382	104	14.71	35.56	4	1	0.43			***2.35***
Microtubule-associated proteins 1A/1B light chain 3B [Precursor]	Q9GZQ8	85	14.55	17.74	5	4	0.57	0,11	19,30	1.75
Palmitoyl-protein thioesterase 1 [Precursor]	P50897	75	34.16	11.44	4	2	2.41	0,05	1,91	2.41
Phosphatase 2A inhibitor I2PP2A	Q01105	96	32.08	7.58	18	11	1.83	1,22	66,66	1.83

Table 3. continued

Protein Name and Species	Accession[1]	Sc.[2]	MW [kDa]	SC [%][3]	# Pep.[4]	# H/L[5]	Avg H/L[6]	AvgSD H/L[7]	CV [%] H/L[8]	reg. fact.[9]
Programmed cell death protein 5	O14737	169	14.15	32.26	7	1	0.57			***1.75***
Proliferation-associated protein 2G4	Q9UQ80	108	43.63	6.36	2	1	0.30			***3.37***
Proteasome activator complex subunit 3	P61289	111	29.49	18.90	4	1	0.63			***1.59***
Serine protease HTRA2 [Precursor]	O43464	73	38.47	8.98	5	2	1.75	0,57	32,57	1.75
S-phase kinase-associated protein 1A	P63208	72	18.52	11.11	2	1	0.26			***3.88***
SUMO-activating enzyme subunit 1	Q9UBE0	55	38.43	5.78	1	1	1.74			1.74
Transcription elongation factor B polypeptide 2	Q15370	160	11.04	34.69	4	2	0.60	0,01	1,08	***1.67***
Transitional endoplasmic reticulum ATPase	P55072	67	89.13	4.60	4	1	0.37			***2.71***
Ubiquinone biosynthesis protein COQ9	O75208	57	22.92	11.82	3	2	1.72	0,02	0,89	1.72
Ubiquitin	P62988	207	8.56	39.47	46	21	2.24	0,82	36,61	2.24
Ubiquitin C splice variant	Q5UGI3	251	17.14	31.37	5	3	0.37	0,04	10,34	***2.67***
Ubiquitin C variant [Fragment]	Q59EM9	210	147.25	3.21	5	3	0.30	0,03	8,70	***3.37***
Ubiquitin fusion degradation protein 1 homolog	Q92890	119	38.70	15.45	3	1	0.66			***1.51***
Ubiquitin-like protein 5	Q9BZL1	86	8.54	31.51	1	1	1.75			1.75
Ubiquitin-like protein Nedd8	Q15843	147	8.44	22.97	6	3	0.54	0,05	9,26	***1.85***
Valosin-containing protein	Q9HAP1	51	34.37	8.47	2	1	0.15			***6.50***
Signal transduction										
Annexin A2	P07355	318	38.45	22.19	15	6	0.53	0,06	11,32	***1.89***
Annexin IV	P09525	138	35.73	9.43	3	1	2.05			2.05
Centaurin gamma 1	Q99490	45	124.67	4.11	2	1	0.08			***12.92***
Coronin, actin binding protein, 1C variant [Fragment]	Q53G58	147	53.25	10.76	6	3	0.55	0,04	6,98	***1.80***
Crk-like protein	P46109	111	33.76	21.45	3	1	1.55			1.55
Inositol-trisphosphate 3-kinase B	P27987	47	102.34	4.65	2	1	8.08			8.08
LANCL1 protein (Fragment)	Q6FHH6	98	45.24	7.77	2	1	1.52			1.52
RAB5C protein (member RAS oncogene family)	Q6FH55	93	23.47	18.52	4	1	0.66			***1.52***
Ras-related protein Rab-7a	P51149	125	23.52	14.01	4	1	0.32			***3.13***
Stathmin	P16949	443	17.16	43.92	27	13	0.40	0,15	37,50	***2.50***
Tubulin alpha-1A chain	Q71U36	572	50.13	29.27	147	54	0.66	0,28	42,42	***1.52***
Tubulin alpha-1C chain	Q9BQE3	132	50.10	10.64	9	1	0.53	0,00	0,00	***1.89***
Tubulin alpha-3C/D chain	Q13749	459	46.08	24.50	66	24	0.34	0,23	67,65	***2.94***
Tubulin alpha-3E chain	Q6PEY2	195	49.88	18.52	21	2	0.53	0,20	37,74	***1.89***
Tubulin beta 4	Q7KZS6	302	88.32	8.91	62	11	0.56	0,34	60,71	***1.79***
Tubulin beta 5	P04350	130	9.30	19.05	11	4	0.32	0,22	68,75	***3.13***
Tubulin beta-1 chain	Q9H4B7	225	49.83	13.45	7	2	0.52	0,04	7,50	***1.94***
Tubulin beta-3 chain	Q13509	167	50.40	11.56	16	7	0.49	0,11	22,45	***2.04***
Tubulin beta polypeptide	Q5JP53	413	47.74	19.95	215	60	0.63	0,29	46,03	***1.59***
Vesicle-associated membrane protein-associated protein A	Q9P0L0	75	19.42	14.62	6	4	0.51	0,09	17,65	***1.96***
stress response										
Heat shock protein 70 kDa A5	Q2KHP4	444	72.38	21.22	30	9	0.59	0,21	35,59	***1.69***
Heat shock protein 70 kDa protein 6	P17066	138	70.81	9.80	10	1	0.57			***1.75***

Table 3. continued

Protein Name and Species	Accession[1]	Sc.[2]	MW [kDa]	SC [%][3]	# Pep.[4]	# H/L[5]	Avg H/L[6]	AvgSD H/L[7]	CV [%] H/L[8]	reg. fact.[9]
Heat shock protein 70 kDa protein 8	P11142	560	70.85	22.76	29	11	0.56	0,34	60,71	***1.79***
Heat shock protein apg-1 (HSP 70 family)	Q53ZP9	52	94.45	4.29	2	1	0.45	0,00	0,00	***2.24***
Serine protease HTRA2 [Precursor]	O43464	73	38.47	8.98	5	2	1.75	0,57	32,57	1.75
Stress-induced-phosphoprotein 1	P31948	44	62.60	4.97	3	2	0.43	0,55	128,21	***2.32***
transport processes										
Alpha-centractin	P61163	47	42.59	4.26	2	1	0.49			***2.04***
Chloride intracellular channel protein 4	Q9Y696	156	28.62	12.30	3	2	0.63	0,06	9,76	***1.59***
Collagen alpha-2(I) chain [Precursor]	P08123	51	72.21	7.97	2	1	2.26			2.26
Cytochrome b-c1 complex subunit 2 [Precursor]	P22695	74	48.41	5.74	5	1	1.65			1.65
Cytochrome b-c1 complex subunit 8	O14949	187	8.36	56.00	7	2	1.52	0,03	1,97	1.52
Dihydropyridine receptor alpha 2 subunit	Q9UIU0	66	125.23	2.52	3	1	3.93			3.93
Dual specificity mitogen-activated protein kinase kinase 1	Q02750	86	43.28	6.12	3	2	0.36	0,04	10,71	***2.77***
Far upstream element-binding protein 1 / DNA helicase V	Q96AE4	117	67.43	6.84	8	4	0.66	0,32	48,48	***1.52***
Lectin, mannose-binding, 1 variant [Fragment]	Q53FS4	42	57.52	1.96	1	1	0.45			***2.21***
Medium-chain specific acyl-CoA dehydrogenase [Precursor]	P11310	87	42.58	7.24	3	2	1.61	0,01	0,80	1.61
Mitochondrial import inner membrane translocase subunit TIM14	Q96DA6	49	12.36	15.65	2	1	1.63			1.63
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 2	O43678	199	10.78	46.94	8	4	2.01	0,18	8,96	2.01
NADH-ubiquinone oxidoreductase 30 kDa subunit	O75489	182	22.20	27.89	5	2	2.45	0,14	5,66	2.45
Protein disulfide-isomerase [Precursor]	P07237	123	13.25	38.33	9	7	0.60	0,25	41,67	***1.67***
Protein disulfide-isomerase A3 [Precursor]	P30101	314	56.76	16.24	13	4	0.59	0,38	64,41	***1.69***
Protein disulfide-isomerase A4 [Precursor]	P13667	193	72.89	9.61	20	15	0.47	0,26	55,33	***2.13***
Protein disulfide-isomerase A6 [Precursor]	Q15084	152	53.90	32.30	26	10	0.51	0,13	25,49	***1.96***
RAB5C protein (member RAS oncogene family)	Q6FH55	93	23.47	18.52	4	1	0.66			***1.52***
Ras-related protein Rab-7a	P51149	125	23.52	14.01	4	1	0.32			***3.13***
Ribonucleoprotein RNA-binding protein 8A	Q9Y5S9	49	19.75	4.05	3	1	1.54			1.54
Short transient receptor potential channel 6	Q9Y210	44	106.33	0.97	1	1	9.84			9.84
Signal recognition particle 14 kDa	Q96Q14	236	14.50	63.97	24	13	2.08	2,23	107,21	2.08
Signal recognition particle 9 kDa isoform	Q6NVX0	52	9.12	30.49	2	2	2.12	0,82	38,41	2.12
Transitional endoplasmic reticulum ATPase	P55072	67	89.13	4.60	4	1	0.37			***2.71***
Ubiquinol-cytochrome c reductase complex 14 kDa protein	P14927	110	13.39	22.73	3	1	4.79			4.79
Ubiquinol-cytochrome-c reductase complex core protein 1	P31930	153	52.61	9.17	4	1	2.35			2.35
Valosin-containing protein	Q9HAP1	51	34.37	8.47	2	1	0.15			***6.50***

Table 3. continued

Protein Name and Species	**Accession[1]**	**Sc.[2]**	**MW [kDa]**	**SC [%][3]**	**# Pep.[4]**	**# H/L[5]**	**Avg H/L[6]**	**AvgSD H/L[7]**	**CV [%] H/L[8]**	**reg. fact.[9]**
cell motility										
Chloride intracellular channel protein 4	Q9Y696	156	28.62	12.30	3	2	0.63	0,06	9,76	***1.59***
Crk-like protein	P46109	111	33.76	21.45	3	1	1.55			1.55
Filamin-A	P21333	62	280.45	11.29	4	1	0.61			***1.65***
cell processes										
Centaurin gamma 1	Q99490	45	124.67	4.11	2	1	0.08			***12.92***
Dual specificity mitogen-activated protein kinase kinase 1	Q02750	86	43.28	6.12	3	2	0.36	0,04	10,71	***2.77***
phagocytosis										
Clathrin	Q53Y37	41	23.17	6.16	1	1	0.38			***2.60***
Clathrin heavy chain 1	Q00610	176	191.40	3.52	11	4	0.53	0,30	56,60	***1.89***
Clathrin light chain A	P09496	218	25.69	18.22	4	3	0.57	0,11	18,92	***1.76***
Core histone macro-H2A.2	Q9P0M6	97	39.90	7.28	4	2	2.41	3,55	147,06	2.41
Ras-related protein Rab-7a	P51149	125	23.52	14.01	4	1	0.32			***3.13***
other										
CDA11	Q9BY40	64	33.58	9.09	3	2	1.66	0,18	11,11	1.66
CDC37 protein	Q6FG59	75	44.43	6.88	3	1	0.57			***1.76***
CDNA FLJ30534 fis, clone BRAWH2001141	Q96NM8	39	15.92	7.74	1	1	0.10			***9.69***
Chromobox protein homolog 3	Q13185	44	20.81	9.29	2	1	0.41			***2.42***
Coiled-coil domain-containing protein 56	Q9Y2R0	54	11.72	12.26	2	1	1.64			1.64
Coiled-coil-helix-coiled-coil-helix domain containing 3	A4D1N4	209	26.14	29.96	8	5	1.55	0,05	2,97	1.55
GATS protein [Fragment]	Q6PII7	52	26.08	18.93	4	1	0.21			***4.76***
Hypothetical protein	Q6IPB4	135	22.43	25.00	6	4	0.29	0,20	68,97	***3.45***
Hypothetical protein DKFZp686L04275	Q7Z3M3	200	53.93	14.82	5	1	0.15			***6.50***
Nuclear structure protein 5	Q5M775	51	118.59	4.12	2	1	3.08			3.08
Platelet-activating factor acetylhydrolase IB subunit beta	P68402	120	25.55	11.79	3	1	1.51			1.51
Protein ARMET (arginine rich protein)	P55145	50	20.24	9.50	1	1	1.65			1.65
Uncharacterized protein C4orf28	Q8N7B6	51	27.15	16.13	2	2	0.52	0,32	62,50	***1.94***
unnamed protein product	CAF16949	42	7.76	21.43	2	1	1.51			1.51
unnamed protein product	CAF01646	49	5.51	38.89	2	1	9.78			9.78
UPF0287 protein C16orf61	Q9NRP2	59	9.45	13.92	2	1	0.57			***1.76***
Vesicle-associated membrane protein-associated protein A	Q9P0L0	75	19.42	14.62	6	4	0.51	0,09	17,65	***1.96***

Table 4. Regulated proteins in C3*bot* treated SH-SY5Y cells analyzed with iTRAQ™.

#	Protein Name and Species	Accession[1]	Score[2]	MW [kDa]	pI[3]	SC [%][4]	# of (H/L)[5]	(H/L)[6]	CV [%][7]
	cell death								
1	Caspase 8 [Precursor]	Q6NVI2	38	32.4	5.5	2.5	1	1.28	-
2	Exportin-2	P55060	33	110.4	6.2	2.0	8	1.33	2,97
	biological processes								
3	Alpha-2-HS-glycoprotein [Precursor]	P02765	33	39.3	5.4	3.3	1	**0.90**	-
4	Aquaporin-6	Q13520	53	29.5	10.0	3.2	2	1.15	0,76
5	Endonuclease G-like 1	Q9Y2C4	35	41.1	9.4	1.6	5	1.13	0,81
6	Heat shock protein 10 kDa	P61604	44	6.4	9.6	37.9	1	1.30	-
	cell cycle								
7	Acidic (Leucine-rich) nuclear phosphoprotein 32 family, member B [Fragment]	Q5T6W8	79	19.2	3.3	10.3	2	1.17	5,47
8	Nucleosome assembly protein 1-like 1	P55209	62	45.3	4.2	6.9	2	1.16	1,37
9	Nucleosome assembly protein 1-like 4	Q99733	46	42.8	4.4	2.7	3	1.14	6,08
10	Peroxiredoxin-2	P32119	64	21.7	5.6	8.6	1	1.36	-
	cell growth								
11	28 kDa heat- and acid-stable phosphoprotein	Q13442	43	20.6	9.4	7.2	3	1.15	4,38
12	Macrophage migration inhibitory factor	P14174	143	12.3	9.3	17.5	15	**0.91**	1,08
13	Nucleolin	P19338	251	74.3	4.4	11.4	24	1.17	5,15
14	Protein DJ-1	Q99497	41	19.8	6.4	7.9	3	1.20	15,40
15	Striated muscle preferentially expressed protein kinase	Q15772	36	348.9	8.3	0.5	9	1.35	1,72
	cell morphology								
16	14-3-3 protein beta/alpha	P31946	62	27.9	4.6	7.3	2	1.31	2,56
17	14-3-3 protein epsilon isoform transcript variant 1	Q4VJB6	85	26.5	4.6	9.0	3	1.28	2,33
18	14-3-3 protein gamma	P61981	116	28.4	4.5	13.0	6	1.31	3,75
19	14-3-3 protein theta	P27348	69	27.7	4.5	9.8	3	1.28	2,62
20	14-3-3 protein zeta/delta	P63104	116	27.7	4.6	13.1	8	1.27	0,85
21	ACTA2	Q13707	159	36.8	5.1	12.4	8	1.56	4,16
22	Actin alpha 2	P62736	190	42.1	5.1	13.3	4	1.52	16,10
23	Actin beta variant [Fragment]	Q53G99	445	41.7	5.3	32.3	23	1.48	-
24	Actin gamma	P63261	267	41.6	5.2	18.4	20	1.41	18,31
25	Actin kappa	Q562R1	37	42.0	5.7	17.5	3	1.57	11,52
26	Actin, alpha cardiac muscle 1	P68032	276	42.0	5.1	19.1	9	1.52	6,44
27	Cell adhesion molecule 2 [Precursor]	Q8N3J6	31	44.4	5.3	2.5	1	1.21	-
28	Cofilin-1	P23528	102	18.4	9.2	18.8	9	1.16	4,13
29	Collagen alpha-4(IV) chain [Precursor]	P53420	43	125.7	10.0	2.4	2	1.11	15,40
30	Profilin-1	P07737	177	14.8	9.4	21.7	14	1.12	2,88
31	Stathmin	P16949	101	20.6	5.7	15.5	10	**0.85**	14,93
32	Synapse-associated protein 102 variant [Fragment]	Q59FY1	31	99.8	6.4	1.9	1	1.14	-
33	Tubulin alpha-1A chain	Q71U36	288	50.1	4.8	22.4	44	1.25	14,66
34	Tubulin alpha-3C/D chain	Q13748	72	50.0	4.4	18.5	9	1.21	17,32

[1] SwissProt or NCBI accession number.

[2] Mascot search protein score. A protein is identified if the Mascot score is greater than 30.

[3] Sequence coverage of the protein.

[4] Number of heavy/light labeled peptides used for quantification.

[5] Average regulation ratio of the heavy/light labeled peptides. Bold: regulation factors belonging to down-regulated proteins.

[6] Standard deviation of the regulation ratio.

[7] Variation of the heavy/light ratios.

Table 4. continued

#	Protein Name and Species	Accession[1]	Score[2]	MW [kDa]	pI[3]	SC [%][4]	# of (H/L)[5]	(H/L)[6]	CV [%][7]
35	Tubulin alpha-4 chain	Q9H853	138	27.5	9.4	16.6	5	1.37	13,69
36	Tubulin alpha-4A chain	P68366	227	49.8	4.8	19.2	15	1.33	8,54
37	Tubulin beta polypeptide	Q5JP53	262	47.7	4.6	18.1	35	1.25	2,35
	chaperoning								
38	Histone H2A type 1	P0C0S8	242	14.1	11.4	27.7	26	1.57	0,86
39	Histone H2A type 1-A	Q96QV6	187	14.1	11.3	30.8	6	1.56	6,45
40	Histone H2AV	Q71UI9	138	13.4	11.1	23.6	6	1.46	18,42
41	Histone H2B type 1-B	P33778	266	13.8	10.8	40.8	12	1.33	4,52
42	Histone H2B type 1-C/E/F/G/I	P62807	148	13.7	10.8	28.2	5	1.36	9,07
43	Histone H2B type 1-D	P58876	308	13.8	10.8	41.6	34	1.35	3,88
44	Histone H2B type 1-J	P06899	210	13.6	10.5	27.2	17	1.40	7,44
45	Histone H3.1t	Q16695	110	15.4	11.9	17.0	16	1.32	12,69
46	Histone H4	P62805	325	11.4	11.8	57.3	43	1.78	7,65
	DNA synthesis and processing								
47	40S ribosomal protein S28	P62857	61	7.8	11.6	17.4	4	1.14	4,94
48	40S ribosomal protein S7	P62081	47	22.1	10.6	5.7	2	1.19	7,95
49	54 kDa nuclear RNA- and DNA-binding protein	Q15233	123	54.2	9.3	10.0	7	1.26	4,72
50	60S ribosomal protein L6	Q02878	67	32.6	11.1	9.4	5	1.13	1,62
51	DNA-binding protein inhibitor ID-1	P41134	47	16.1	7.6	12.3	2	1.10	0,67
52	Heparin-binding protein HBp15	Q7Z4W8	33	14.8	9.8	10.2	1	1.17	-
53	Prohibitin [Fragment]	Q6FHP5	35	29.8	5.5	3.7	2	1.24	2,48
54	Protein SET	Q01105	143	32.1	4.0	11.6	7	1.15	7,03
55	Ribosomal protein S10	Q5TZB9	35	19.9	10.4	8.7	1	1.14	-
56	Structural maintenance of chromosomes protein 5	Q8IY18	35	144.1	9.4	0.6	1	**0.95**	-
57	translation initiation factor eIF-5A [validated] - human	P63241	78	16.8	4.9	7.8	6	1.11	7,30
	metabolism								
58	5-oxoprolinase	O14841	37	137.5	11.7	2.8	6	1.15	5,43
59	ARF GTPase-activating protein GIT1	Q9Y2X7	33	84.3	12.4	3.9	2	1.21	4,71
60	ATP synthase subunit alpha, mitochondrial [Precursor]	P25705	87	59.7	9.6	7.1	8	1.26	4,52
61	ATP synthase subunit beta, mitochondrial [Precursor]	P06576	277	56.5	5.1	19.3	27	1.27	3,95
62	ATP synthase subunit delta, mitochondrial [Precursor]	P30049	38	17.5	5.2	8.3	1	1.14	-
63	ATPase type 13A1	Q9EPE9	60	108.5	9.4	1.4	1	1.35	-
64	Bifunctional protein NCOAT	O60502	37	67.8	4.6	1.2	4	1.39	2,00
65	Diacylglycerol kinase alpha	P23743	35	82.7	8.8	1.8	3	1.12	2,24
66	Fructose-bisphosphate aldolase A	P04075	68	39.4	9.2	6.9	4	1.11	2,22
67	Glutathione S-transferase P	P09211	48	23.2	5.3	5.3	9	1.70	3,32
68	L-lactate dehydrogenase chain B	P07195	41	36.6	5.7	3.6	1	1.18	-
69	Malate dehydrogenase	Q6FHZ0	216	35.5	9.8	20.4	16	1.23	5,54
70	Phosphoglycerate kinase 1	P00558	126	44.6	9.2	10.1	9	1.27	2,54
71	Phosphoglycerate kinase 2	P07205	67	44.6	9.5	3.4	2	1.28	4,99
72	Putative Xaa-Pro aminopeptidase 3	Q9NQH7	32	57.0	6.4	1.4	3	1.35	3,58
73	Pyruvate kinase isozymes M1/M2	P14618	128	57.8	9.0	7.7	6	1.36	1,95
	nucleotide metabolism								
74	Neuron navigator 2	Q8IVL1	46	115.1	10.0	2.4	1	1.28	-
75	Nucleophosmin	P06748	218	29.4	4.3	20.8	23	1.17	2,85
76	Nucleoside diphosphate kinase	Q1WM23	245	30.1	9.8	27.3	16	1.12	4,00
77	Nucleoside diphosphate kinase B	P22392	33	17.2	9.6	6.0	1	1.25	-
78	Poly(A) binding protein, cytoplasmic, pseudogene 2	Q6NV95	44	29.9	9.7	3.3	1	**0.91**	-
79	Zinc finger protein 803	O95785	35	178.7	6.6	1.9	1	1.30	-
	protein synthesis and processing								
80	Calreticulin	Q9UDG2	46	24.3	4.3	5.6	1	1.18	-
81	Enolase gamma	P09104	133	47.1	4.8	7.2	5	1.20	0,80

Table 4. continued

#	Protein Name and Species	Accession[1]	Score[2]	MW [kDa]	pI[3]	SC [%][4]	# of (H/L)[5]	(H/L)[6]	CV [%][7]
82	Fusion	Q8TBR3	48	53.4	9.8	1.7	1	1.25	-
83	Heat shock protein 60 kDa [Precursor]	P10809	44	6.0	4.6	32.7	3	1.41	4,68
84	Heat shock protein 75 kDa	Q12931	67	66.0	7.1	2.4	5	1.26	10,76
85	Kelch repeat and BTB domain-containing protein 3	Q8NAB2	35	69.3	5.1	1.2	5	1.13	0,81
86	Lamin-A/C	P02545	68	80.0	6.6	4.1	2	**0.95**	6,73
87	Peptidyl-prolyl cis-trans isomerase A	P62937	381	18.0	9.0	47.3	51	1.12	4,68
88	Peptidyl-prolyl cis-trans isomerase B [Precursor]	P23284	70	22.7	9.9	6.7	6	1.19	4,22
89	Peroxiredoxin-4	Q13162	31	30.5	5.8	3.0	1	1.30	-
90	Protein disulfide-isomerase A3 [Precursor]	P30101	75	63.7	6.2	4.0	6	1.12	12,91
91	Sat-2 short	Q6PZN5	31	15.5	10.7	5.2	1	1.28	-
92	Williams-Beuren syndrome chromosomal region 20B protein	Q3KNT7	33	16.5	11.3	11.0	3	**0.89**	4,33
93	Zinc finger CCCH domain-containing protein 4	Q9UPT8	43	31.0	9.9	13.5	3	1.35	8,42
94	Zinc finger CCHC domain-containing protein 14	Q8WYQ9	51	89.2	9.8	3.4	1	1.13	-
	RNA synthesis and processing								
95	60S ribosomal protein L36	Q9Y3U8	48	12.1	12.2	20.2	3	1.16	3,07
96	chromosome 14 open reading frame 43	Q6PJG2	31	115.0	10.0	8.3	1	1.28	-
97	Doublesex and mab-3 related transcription factor 1 c	Q6T1H8	49	18.3	12.3	23.4	1	1.31	-
98	Elongation factor 1-alpha 1	P68104	149	50.1	9.7	6.7	14	1.37	5,72
99	Enolase alpha	P06733	290	47.0	7.7	17.3	24	1.17	4,49
100	Far upstream element-binding protein 1	Q96AE4	66	67.4	7.8	4.0	2	1.17	3,06
101	Far upstream element-binding protein variant [Fragment]	Q59FU3	46	52.0	9.1	4.1	2	1.16	11,25
102	General transcription factor II-I repeat domain-containing protein 2A	Q86UP8	41	107.2	8.5	1.6	10	2.08	10,92
103	Heterogeneous nuclear ribonucleoprotein A0	Q6IB18	69	30.8	9.8	7.5	9	1.11	3,98
104	Heterogeneous nuclear ribonucleoprotein H (hnRNP H)	P31943	136	49.1	5.9	7.4	10	1.18	7,78
105	Heterogeneous nuclear ribonucleoprotein M (hnRNP M)	P52272	33	77.3	9.6	3.2	1	1.12	-
106	Heterogeneous nuclear ribonucleoprotein U	Q00839	103	90.3	5.7	4.0	4	1.21	9,64
107	Homeobox protein EMX2	Q04743	47	28.3	10.3	7.5	2	1.35	29,86
108	Mediator complex subunit 15	Q6PKB8	46	84.3	10.6	3.0	2	1.12	8,59
109	Mediator of RNA polymerase II transcription subunit 15	Q96RN5	43	86.7	10.2	3.2	1	1.24	-
110	Polypyrimidine tract-binding protein 1	P26599	35	57.2	9.8	4.3	1	1.27	-
111	Prohibitin-2	Q99623	51	33.3	10.2	12.0	2	1.22	1,51
112	PSIP1 protein	Q8N4N4	40	5.7	9.3	16.0	1	1.17	-
113	Pygopus homolog 2	Q5T170	55	41.2	7.7	8.1	1	**0.92**	-
114	Ribosomal protein L7	Q3KQU0	30	37.0	11.2	3.5	1	1.21	-
115	Sex determining region Y [Fragment]	Q8WZ47	31	23.0	10.1	4.0	1	1.28	-
116	Splicing factor proline/glutamine-rich [Fragment]	Q6PIX2	37	55.4	10.4	3.0	1	1.22	-
117	Splicing factor, arginine/serine-rich 1	Q07955	63	27.6	10.8	10.1	6	1.15	5,26
118	Splicing factor, arginine/serine-rich 3	P84103	84	19.3	12.3	14.0	11	1.16	0,77
119	Splicing factor, arginine/serine-rich 7	Q16629	62	15.8	10.6	16.8	2	1.21	1,79
120	SRA stem-loop-interacting RNA-binding protein, mitochondrial [Precursor]	Q9GZT3	48	10.9	11.7	10.2	2	1.16	2,32
121	Transcription intermediary factor 1-beta	Q13263	31	88.6	5.4	2.0	1	1.25	-
122	Zinc finger protein ZFPM1	Q8IX07	41	104.5	9.2	3.6	1	**0.92**	-
	stress response								
123	Heat shock 70 kDa protein 1	P08107	127	41.8	6.8	14.5	14	1.12	11,49
124	Heat shock 70 kDa protein 5	P11021	186	72.1	4.9	12.3	18	1.11	3,68
125	Heat shock 70 kDa protein 9	P38646	147	73.7	6.0	7.4	12	1.17	2,54
126	Heat shock protein 27 kDa	P04792	163	22.8	6.0	18.0	12	**0.88**	8,20

Table 4. continued

#	Protein Name and Species	Accession[1]	Score[2]	MW [kDa]	pI[3]	SC [%][4]	# of (H/L)[5]	(H/L)[6]	CV [%][7]
127	Heat shock protein 70 kDa protein 6	P17066	104	71.0	5.8	6.2	8	1.13	11,53
128	Heat shock protein 70 kDa protein 8 isoform 1 variant [Fragment]	Q53GZ6	290	70.9	5.1	14.6	30	1.12	11,86
129	Heat shock protein 70 kDa protein 8 isoform 2 variant [Fragment]	Q53HF2	262	53.5	5.5	16.8	7	1.11	8,41
130	Heat shock protein 90 kDA AA1 protein [Fragment] class A member 1	Q2VPJ6	131	68.3	5.0	6.3	13	1.20	19,89
131	Heat shock protein 90 kDa alpha	P07900	73	84.7	4.9	4.0	6	1.26	7,03
132	Heat shock protein 90 kDa Bb	Q58FF8	32	49.1	4.9	3.6	1	1.35	-
133	Heat shock protein 90 kDa beta	P08238	168	83.2	4.8	7.2	23	1.28	4,96
134	Prothymosin alpha	P06454	113	13.4	3.5	12.7	2	1.27	0,73
135	Scavenger receptor cysteine-rich type 1 protein M130 [Precursor]	Q86VB7	32	124.7	5.5	0.8	1	1.22	-
136	STIP1 protein	Q3ZCU9	32	68.0	8.6	1.7	1	1.31	-
137	TANK-binding kinase 1-binding protein	A7MCY6	31	67.7	5.8	2.0	1	1.11	-
138	Amiloride-sensitive sodium channel subunit alpha	P37088	31	75.7	8.5	1.3	1	1.11	-
139	Collagen alpha-3(IX) chain [Precursor]	Q14050	59	63.6	8.8	5.6	1	1.17	-
140	Cytochrome c	P99999	36	11.6	10.2	10.6	3	1.45	9,08
141	Mucolipin-2	Q8IZK6	38	62.7	4.8	4.0	1	1.28	-
142	Neuronal nitric-oxide synthase isoform mu [Fragment]	O75713	31	7.5	9.6	9.0	1	1.22	-
	ubiquitin cycle								
143	Ubiquitin	P62988	186	8.6	7.6	52.6	57	1.26	3,28
144	Ubiquitin carboxyl-terminal esterase L1 (Ubiquitin thiolesterase), isoform CRA_e	P09936	72	24.8	5.2	8.1	4	1.29	3,71
145	Ubiquitin carboxyl-terminal hydrolase 48	Q86UV5	33	119.0	4.6	1.9	3	1.12	2,24
	other								
146	Abhydrolase domain-containing protein 13	Q7L211	32	38.5	8.9	3.0	4	1.12	0,53
147	CD40 antigen isoform 2 variant [Fragment]	Q59F01	42	28.1	12.3	10.0	1	1.14	-
148	cDNA FLJ37045 fis, clone BRACE2012185	Q8N9J4	31	13.5	5.7	9.4	1	1.19	-
149	cDNA FLJ45820 fis, clone NT2RP8001407	Q6ZS55	33	24.8	11.8	3.5	1	1.17	-
150	Chaperonin 10-related protein [Fragment]	Q9UNM1	114	10.3	9.3	19.6	16	1.28	9,01
151	Chromosome 12 open reading frame 47	Q8N8E1	32	13.2	12.3	9.4	1	1.24	-
152	Complement component 1 Q subcomponent-binding protein, mitochondrial [Precursor]	Q07021	42	20.8	4.4	6.0	1	1.27	-
153	HBxAg transactivated protein 2	Q9Y520	30	186.1	10.2	0.4	1	1.36	-
154	MAP7 domain-containing protein 1	Q3KQU3	46	92.8	10.8	3.8	1	1.31	-
155	Myosin regulatory light chain 2, nonsarcomeric	P19105	57	19.7	4.5	6.5	1	1.18	-
156	Probable mast cell antigen 32 homolog [Precursor]	Q7Z6M3	30	38.7	8.7	2.5	2	2.32	1,81
157	ProSAPiP1 protein	Q8IXX8	31	66.5	6.4	1.3	1	1.44	-
158	Putative uncharacterized protein	Q86Z22	32	23.8	10.2	6.6	1	1.14	-
159	Putative uncharacterized protein	Q86YZ7	40	137.5	6.2	0.6	1	1.24	-
160	Putative uncharacterized protein	Q8IYK6	32	14.3	12.0	11.7	1	1.31	-
161	Putative uncharacterized protein DKFZp686A2214 [Fragment]	Q69YR4	46	44.0	10.0	5.7	3	1.17	7,03
162	Putative uncharacterized protein FLJ10324	Q75LH2	32	40.0	6.2	5.7	1	1.14	-
163	Putative uncharacterized protein FLJ23865	Q8TCH9	36	14.3	8.2	9.4	2	1.11	4,77
164	Retrotransposon gag domain-containing protein 1	Q8NET4	33	144.2	5.8	2.0	1	1.24	-
165	SH3 domain-binding glutamic acid-rich-like protein	O75368	34	12.8	5.1	8.8	1	1.36	-
166	Uncharacterized protein C8orf12	Q96KT0	37	11.6	10.5	24.0	1	**0.62**	-

Curriculum Vitae

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Berufstätigkeit, Praktika, Auslandsaufenthalte

07-2005 bis 05-2008	**Promotionsarbeit** zum Dr. rer. nat. an der Medizinischen Hochschule Hannover Institut für Toxikologie bei Prof. Dr. med. Ingo Just und am Institut für Technische Chemie der Gottfried Wilhelm Leibniz Universität Hannover bei Prof. Dr. Thomas Scheper; Thema „Quantitative proteome analysis of human neuroblastoma cells treated with *Clostridium botulinum* C3 exoenzyme“
11-2004 bis 06-2005	**Diplomarbeit** an der Universität Leipzig Arbeitsgruppe Bioanalytik bei Prof. Dr. rer. nat. Ralf Hoffmann, BBZ Leipzig; Thema „Trennung isomerer Phosphopeptide mittels Kapillarelekrophorese und Chromatographie“
08-2004 bis 10-2004	**Vertiefungspraktikum** und **Studentische Hilfskraft** an der Universität Leipzig, Arbeitsgruppe Bioanalytik Prof. Hoffmann, BBZ Leipzig
03-2004 bis 07-2004	**Auslandssemester** an der OHIO University Athens, OH, USA
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07-2001 bis 06-2005	**Studentische Hilfskraft** im Institut für Troposphärenforschung, Abteilung Chemie/ Analytik, Leipzig

Ausbildung

09-2000 bis 06-2005	Studium – Diplom-Chemikerin, Universität Leipzig

Schulausbildung

1992 – 2000	Friedrich-Schiller-Schule - Gymnasium - , Leipzig
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Publikationen / Poster / Vorträge

Wissenschaftliche Publikationen

Alnajjar, A., Idris, A.M., **Multzenberg, M.**, McCord, B. (2007) Development of a capillary electrophoresis method for the screening of human urine for multiple drugs of abuse. *J Chromatogr B Analyt Technol Biomed Life Sci.* 856, 62-67. (Schreibfehler)

Muetzelburg, M.V., Hoffmann, R. (2008) Separation of multiphosphorylated peptide isomers by capillary zone electrophoresis. Submitted to Electrophoresis (review process)

Muetzelburg, M.V., Hofmann, F., Hahner, S., Just, I., Pich, A. (2008) Quantitative proteome analysis of human neuroblastoma cells treated with *Clostridium botulinum* C3 exoenzyme – application of isotope-coded protein labels and LC-MALDI techniques. Manuscript submitted for publication in *Mol Cell Proteomics*

Muetzelburg, M.V., Hofmann, F., Just, I., Pich, A. (2008) Isobaric tags for relative and absolute quantitation coupled with 2D-LC-MALDI-MS/MS techniques enable the identification of biomarkers of C3 exoenzyme treated human neuroblastoma cell lines. Manuscript submitted for publication in *J Chromtogr B.*

Muetzelburg, M.V., Czentnár, Z., Luecke, N., Just, I., Pich, A. (2008) Protein profiling of complex protein mixtures – A comparison between LC-MALDI-MS/MS and CE-ESI-MS/MS techniques. Manuscript in preparation

Luecke, N., Templin, C., Kotlarz, D., **Muetzelburg, M.V.**, Just, I., Pich, A. (2008) Secretom analysis of the hematopoethic progenitor cell line DKmix using LC-MALDI techniques. Manuscript in preparation

Poster

Alnajjar, A., **Muetzelburg, M.**, Butcher, J., McCord, B. (2004) Determination of multiple drugs of abuse in human urine using capillary electrophoresis with fluorescence detection. *Studiertenkolleg, Department of Chemistry and Biochemistry, Ohio University, Athens, Ohio, USA*

Muetzelburg, M.V., Hoffmann, P., Singer, D., Hoffmann, R. (2005) Separation of phosphopeptide isomers using capillary-zone-electrophoresis. *Biotechnology Symposium BBZ in Leipzig, Anakon* und *Beckman Coulter User Meeting* (zweimal Posterpreis)

Muetzelburg, M.V., Muehlenstaedt, C., Just, I., Pich, A. (2008) Isotope-coded protein labels and LC-MALDI techniques used for quantitative proteome analysis of intoxicated human neuroblastoma cells. *Tagung der Deutschen Gesellschaft für Massenspektrometrie (DGMS)*

Muetzelburg, M.V., Muehlenstaedt, C., Just, I., Pich, A. (2008) Toxicoproteomics: C3 exoenzyme affects protein profile of a human neuroblastoma cell line. *Tagung der Deutschen Gesellschaft für experimentelle und klinische Pharmakologie und Toxikologie (DGPT)*

Vorträge

11-2007	Vortrag im Rahmen des Massenspektrometrie Forums Hannover „Heavy Isotopes for Quantitative Proteomics“
12-2006	Vortrag im Rahmen der Veranstaltung Basic Biological Questioner an der MHH „Quantitative Proteomics using ICPL™“
09-2005	eingeladener Vortrag auf dem Beckman Coulter User Meeting „Trennung isomerer Phosphopeptide mittels Kapillarzonenelektrophorese“
07-2004	Vortrag im Rahmen des Studierendenkollegs am Department of Chemistry and Biochemistry der Ohio University, Athens, Ohio, USA „Derivatization of amine-containing drugs using Cy5™-NHS monoreactive Dye for capillary electrophoresis and microfluidic devices”