

Proteome Analysis of Brain Plasma Membranes Isolated by Affinity Two-Phase Partitioning

Running title: Plasma membrane proteomics of brain tissue

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ABBREVIATIONS

The abbreviations used are:

PEG, polyethylene glycol; PM, plasma membrane; RSA, relative specific activity; SV, synaptic vesicle; LC, liquid chromatography; MS, mass spectrometry; MS/MS, tandem mass spectrometry; SDS-PAGE, sodium dodecylsulfate polyacrylamide gel electrophoresis; WGA, wheat germ agglutinin; TMH, transmembrane helices; GPI, glycosylphosphatidyl-inositol; GABA, gamma-aminobutyric acid; LDS, lithium dodecylsulfate; MOPS, 4-morpholinepropanesulfonic acid; NADH, β -nicotinamide adenine dinucleotide; FT-ICR, Fourier-transform ion cyclotron resonance.

SUMMARY

A comprehensive analysis of plasma membrane proteins is essential to in-depth understanding of brain development, function, and diseases. Proteomics offers the potential to perform such a comprehensive analysis, yet it requires efficient protocols for the purification of the plasma membrane compartment. Here, we present a novel and efficient protocol for the separation and enrichment of brain plasma membrane proteins. It lasts only 4 hours and is easy to perform. It highly enriches plasma membrane proteins and can be applied to small amounts of brain tissue, such as the cerebellum of a single rat, which has been used in the present study. The protocol is based on affinity partitioning of microsomes in an aqueous two-phase system. Marker enzyme assays demonstrated a more than 12-fold enrichment of plasma membranes and a strong reduction of other compartments, such as mitochondria and the endoplasmic reticulum. 506 different proteins were identified when the enriched proteins underwent LC-MS/MS analysis subsequent to protein separation by SDS-PAGE. Using gene ontology, 146 proteins were assigned to a subcellular compartment. Ninety-three of those (64%) were membrane proteins and 49 (34%) were plasma membrane proteins. A combined literature and database search for all 506 identified proteins revealed subcellular information on 472 proteins, of which 197 (42%) were plasma membrane proteins. These comprised numerous transporters, channels, and neurotransmitter receptors, e.g. the inward rectifying potassium channel Kir7.1 and the cerebellum-specific GABA receptor GABRA6. Surface proteins involved in cell-cell contact and disease-related proteins were also identified. Six of the 146 assigned proteins were derived from mitochondrial membranes and 5 from membranes of the endoplasmic reticulum. Taken together, our protocol represents a simple, rapid, and reproducible tool for the proteomic characterization of brain plasma membranes. As it conserves membrane structure and protein interactions, it is also suitable to enrich multimeric protein complexes from the plasma membrane for subsequent analysis.

INTRODUCTION

Plasma membrane (PM) proteins play pivotal roles in various physiological processes of the brain, such as signal transduction, molecular transport, and cell-cell interactions. PM proteins include neurotransmitter receptors, G-proteins, carriers, and voltage-gated ion channels. Many of them display region- and time-specific expression patterns, therewith determining network specificity and information processing. The characterization of PM proteins is, therefore, essential for a better understanding of brain structure and function. Proteomics has the potential to effectively profile PM proteins and to provide unprecedented insight into the protein composition of a given sample. However, profiling PM proteins has proven to be particularly challenging due to their low abundance and the difficulties in resolving and identifying them. To overcome these limitations, new technologies are constantly under development. They include liquid chromatography coupled to mass spectrometry (LC-MS), thus obviating two-dimensional gels which are not suitable for separation of membrane proteins (1,2). They also involve novel strategies, such as protein tagging, which are aimed at a high enrichment of PM proteins (3,4). Ultimately, the new technologies should be capable of assessing the dynamic nature of expression, interactions, and posttranslational modifications of PM proteins (5). Furthermore, proteomic analyses should be applicable to very small tissue samples, e.g., to functionally or anatomically defined brain areas from model organisms such as rats and mice (6). Towards this goal, we here introduce a novel protocol for the isolation of PMs from microsomes. It is based on affinity purification in an aqueous two-phase system consisting of the polymers polyethylene glycol (PEG) and dextran. When solutions of these two structurally different polymers are mixed, aqueous two-phase systems can form, with the top phase being enriched in PEG, whereas the bottom phase is enriched in dextran (7). Membranes of different subcellular origin distribute in the aqueous two-phase system according to membrane surface properties such as charge and hydrophobicity. Consequently, they become enriched in either of the two phases. As PMs have a higher affinity to the PEG-enriched phase than all other membranes, they end up preferentially in the top phase (8). Further separation of PMs from contaminating membranes can be obtained by the subsequent use of the affinity ligand wheat germ agglutinin (WGA) coupled to dextran (9,10). As *N*-acetyl-D-glucosamine and sialic acid are surface molecules of PMs, but not of other microsomal membranes, and as both molecules bind strongly to WGA, the selective pulling of PMs into the WGA-dextran-enriched phase is enabled. Since glycosylated and non-glycosylated

PM proteins are co-distributed in the same membrane patches, both protein groups will co-partition in the WGA-dextran enriched bottom phase. In contrast, all other membranes remain in the PEG-enriched top phase. Furthermore, the aqueous two-phase system provides a mild environment preserving protein interactions. Hence, it can be combined with other procedures, such as blue native gel electrophoresis (11, 12), to characterize specific protein complexes. Our protocol omits time- and material-consuming density gradient centrifugation and yields PMs of high purity within 4 hours. The suitability of the protocol was assessed by a SDS-PAGE coupled to LC-MS/MS of the PM proteome of the cerebellum of a single young adult rat, resulting in the identification of 506 proteins, out of which 34%-42% were PM proteins.

EXPERIMENTAL PROCEDURES

Tissue preparation

Sprague-Dawley rats of both genders (8-9 weeks old) were deeply anesthetized by a peritoneal injection of 700 mg/kg chloral hydrate and sacrificed by decapitation. All protocols complied with the current German Animal Protection Law and were approved by the local animal care and use committee (Landesuntersuchungsamt Koblenz, Germany). The brains were rapidly removed and stored at -80 °C until further usage. The cerebellum was dissected from freshly prepared brains in a chilled (~4 °C) solution containing 25 mM NaHCO₃, 2.5 mM KCl, 1.25 mM NaH₂PO₄, 1 mM MgCl₂, 2 mM CaCl₂, 260 mM D-glucose, 2 mM sodium pyruvate, 3 mM myo-inositol and 1 mM kynurenic acid, pH 7.4. After dissection, the tissue was stored at -80 °C until further usage.

Chemicals

Dextran T500, Tris, Tween-20, glycine, and sucrose were purchased from Roth (Karlsruhe, Germany). Solvents and modifiers for liquid chromatography were obtained from Merck (Darmstadt, Germany). All other chemicals were from Sigma-Aldrich (Munich, Germany).

Preparation of microsomes

Microsomes were obtained by differential centrifugation as described previously (13). During the establishing phase of the protocol, 1.5 g brain tissue were homogenized in 4.5 mL 250 mM sucrose, 15 mM Tris, pH 7.4 by 20 strokes with rotation (250 rpm) in a glass teflon homogenizer at 4 °C. When the protocol was ultimately assessed in combination with LC-MS/MS analysis, the cerebellum of a single rat was used. Nuclei were pelleted by 10 min of centrifugation at 3,000 × g in a table top centrifuge, and the mitochondrial pellet was obtained by 12 min centrifugation at 10,000 × g in the same centrifuge. The supernatant was centrifuged for 1 h at 100,000 × g in a SW40 rotor to yield the microsomal pellet. The nuclear pellet and the mitochondrial pellet were re-extracted twice.

Preparation of WGA-dextran

All solvents used for activation of dextran were dried using molecular sieves; all glass material was dried in an oven. Freeze-dried dextran was activated with tresyl chloride, again freeze dried, and stored at $-20\text{ }^{\circ}\text{C}$; WGA was coupled to tresyl dextran as described previously (14).

Aqueous two-phase affinity partitioning

The two-phase affinity partitioning procedure is illustrated in figure 1. All steps were performed at $4\text{ }^{\circ}\text{C}$. Two-phase systems were prepared the day before use and stored in a refrigerator over night. The next day, $400\text{ }\mu\text{L}$ of resuspended microsomes were added to 3.6 g of a two-phase system, thus forming a 4 g two-phase system with microsomes (6.3% (w/w) PEG 3350, 6.3% (w/w) dextran T500 and 15 mM Tris/ H_2SO_4 , pH 7.8). The two-phase system was mixed by 20 invertations, vortexing, and another 20 invertations. Phase separation was accelerated by 5 min centrifugation at $150 \times g$. After phase separation, top phase 1 was removed and stored until further usage. The bottom phase was re-extracted with an equal volume of a fresh top phase (obtained from a two-phase system without microsomes). After mixing and phase separation, top phase 2 was removed and combined with the stored top phase 1. The combined top phases 1 and 2 were then layered on a fresh bottom phase of a 4 g two-phase system. After mixing and phase separation, the resulting top phase 3 was removed and extracted with a fresh bottom phase of a 4 g system prepared as above. The resulting top phase 4 was removed and mixed with a fresh affinity bottom phase of an 8 g system (6.3% (w/w) PEG 3350, 6.3% (w/w) dextran T500, $800\text{ }\mu\text{g}$ WGA in the form of WGA-dextran, 2 mM Li_2SO_4 , 15 mM Tris/borate, pH 7.8) to pull PMs into the dextran-enriched bottom phase. After mixing and phase separation, top phase 5 was discarded, and the bottom phase was washed with the same volume of a fresh top phase from a novel 8 g two-phase system (6.3% (w/w) PEG 3350, 6.3% (w/w) dextran T500, 2 mM Li_2SO_4 , 15 mM Tris/borate, pH 7.8). After mixing and phase separation, the resulting top phase 6 was discarded and the bottom phase was diluted 10-fold with 100 mM *N*-acetyl-D-glucosamine, 250 mM sucrose and 5 mM Tris, pH 7.8 in order to release the membranes from the WGA-dextran. The membranes were finally pelleted by centrifugation at $100,000 \times g$ for 1.5 h in a SW40 rotor.

High-salt washing and high-pH washing

To enrich integral PM proteins prior to LC-MS/MS analysis, the membranes obtained through two-phase affinity partitioning were resuspended in an ice-cold solution of 1 M KCl and 15 mM Tris, pH 7.4 (high-salt washing). After 15 minutes on ice, the solution was centrifuged at $233,000 \times g$ for one hour in a SW40 rotor. The pellet was re-extracted twice with the high-salt solution and subsequently washed three times with 0.1 M Na_2CO_3 , pH 11.5 (high-pH washing) as described (15). Both the high-salt solution and the high-pH solution reduce non-covalent protein-protein interactions, thus lowering the amount of peripheral proteins which were non-covalently bound to PM proteins (16). Moreover, the high-pH solution causes depolymerisation of actin bundles, thus resulting in their removal from the pellet (17).

Protein assays

Protein amounts were determined using the method of Bradford (18) with bovine serum albumin as standard. Marker enzymes for the various cellular compartments were as follows: alkaline phosphatase [EC 3.1.3.1] was used as a PM marker (19), succinate dehydrogenase [EC 1.3.5.1] as a marker for mitochondria (19), and NADH ferricyanide reductase [EC 1.6.2.2] as a marker for the endoplasmic reticulum (20).

1D-PAGE of purified plasma membrane proteins

The affinity-purified, high-salt and high-pH-treated proteins (30-50 μg) were resuspended via ultrasonication in 25 μL LDS-sample buffer (Invitrogen, Karlsruhe, Germany). After incubation at 75 °C for 15 min, the sample was applied to a 4-12% Bis-Tris gel with a MOPS buffer system (NUPAGE®-Novex, Invitrogen). Protein separation occurred for 15 min at 50 V and an additional 60 min at 200 V at 4 °C. Visualization of protein bands was performed by a modified colloidal Coomassie staining (21). Briefly, the gel was immersed for 16 h in a solution containing 34% (v/v) methanol, 2% (v/v) phosphoric acid (89%), 17% (w/v) ammonium sulphate, and 0.066% (w/v) Coomassie G250. Background gel staining was reduced by gentle washing in water. Subsequently, the gel lanes were cut in 1 mm slices and frozen at -80 °C until further usage.

Sample processing for mass spectrometry

Proteins were in-gel reduced and carbamidomethylated prior to tryptic digestion. Each gel slice was alternately washed three times with 50 mM ammonium hydrogen carbonate and 25 mM ammonium hydrogen carbonate, 50% acetonitrile, followed by incubation at 57 °C for 30 min with 10 mM dithiothreitol. Upon cooling to room temperature, the proteins were carbamidomethylated with 10 mM iodoacetamide for 30 min, followed by two alternate washing steps as stated before. The gel pieces were dried and proteins were subjected to trypsin proteolysis by adding 5 µL of a 25 µg/ml trypsin solution (sequencing grade, Promega, Madison, MA, USA) in 50 mM ammonium hydrogen carbonate and incubating at 37 °C for 16 h. Peptides were extracted by incubation in 15 µL 0.1% trifluoroacetic acid for 30 min at 37 °C.

Mass spectrometry

Separation of tryptic peptide mixtures was achieved by nano-scale reversed-phase liquid chromatography in combination with online ESI-MS. For the HPLC separation, a nano-LC system (Famos™, Switchos™, Ultimate™, Dionex, Idstein, Germany) was used, employing a linear gradient with a slope of 0.5 or 1% B/min (solvent A: 0.1% formic acid; solvent B: 0.1% formic acid, 84% acetonitrile) to a final concentration of 50% B. Followed by a 5 min washing period with 95% B, the columns were equilibrated in 5% B prior to the application of the next sample. The column system consisted of a precolumn (300 µm I.D. x 1 mm length, C18 PepMap™) and a separation column (75 µm I.D. x 150 mm length, C18 PepMap™), both purchased from Dionex, Idstein, Germany. Mass spectrometric analysis was performed on a Qtrap4000 linear ion trap system (Applied Biosystems, Darmstadt, Germany). For online coupling, a micro ion spray source (Applied Biosystems) was used, equipped with a New Objective ESI needle (10 µm tip diameter, MS Wil, Wil, Switzerland). Typical values for needle voltage were 2.1-2.4 kV in positive ion mode. The declustering potential was set to 60 V while the collision gas was set to high. A typical scan cycle consisted of an enhanced multiple charge survey scan (mass range 415 – 1,500 amu; 4,000 amu/s scan rate) followed by an enhanced resolution scan (250 amu/s scan rate) of the three most intense signals in the spectrum with an exclusion list for ion signals set to 30 seconds after one occurrence. Enhanced product ion spectra were recorded within the linear ion trap for doubly and triply charged precursor ions (mass range 100-1,500 amu; 4,000 amu/s scan rate), enabling the identification of major immonium ions as

well as sufficient ion series information for successful processing via database search algorithms. Data acquisition was accomplished using the Analyst 1.4 software (Applied Biosystems).

Mass spectrometric data interpretation

The derived mass spectrometric datasets were converted to Mascot Generic Format and searched against the Swiss-Prot database (release 46.0) with the species subset *Rattus* using the Mascot™ search algorithm (Matrix Science, London, UK). Generation of peak lists was accomplished using a Mascot script (mascot.dll, version 1.6b15, Matrix Science) as plug-in to the Analyst 1.4 software. All peaks below 0.1% of overall intensity were removed; spectra were centroided and doubly as well as triply charged precursors with more than 50 peaks were searched against the Swiss-Prot database.

As for the search parameters, the number of allowed miscleavages was set to one and carbamidomethylation was chosen as fixed as well as oxidation of methionine as variable modification. Ion tolerance for peptide and fragment ions was set to 0.4 amu while the search was confined to doubly and triply charged precursors. Only unique ion scores were monitored while discarding all scores below 29 for individual peptide hits. A protein hit was usually based on at least two identified peptides with subsequent manual validation. In case of assignments based on single spectra, the peptide sequence, Mascot™ score, and the observed mass and charge were included in the supplementary material.

Bioinformatics

Gene ontology searches were performed using the EASE program (<http://apps1.niaid.nih.gov/david/>) (22). Myristoylated proteins (23), glycosylphosphatidylinositol (GPI)-anchored proteins (24) as well as proteins containing hydrophobic α -helical domains (23) were predicted using the sequence analysis tools of the Institute of Molecular Pathology, Vienna, Austria (<http://mendel.imp.univie.ac.at/mendeljsp/index.jsp>). A manual search for subcellular location was based on literature and Genecards (<http://bioinformatics.weizmann.ac.il/cards/index.shtml>).

RESULTS

Establishment of affinity two-phase partitioning on brain tissue

As an alternative to density gradient centrifugation, PMs can be isolated by affinity partitioning of microsomes in aqueous two-phase systems (9,25). To establish an affinity partition system for brain PMs obtained from small amounts of tissue, we started with a protocol reported for the extraction of rat liver PMs (9). Microsomes were prepared by differential centrifugation and partitioned in a PEG/dextran two-phase system using WGA-dextran as affinity ligand. Unfortunately, subsequent enzyme marker assays revealed a strong contamination by mitochondria which we identified by succinate dehydrogenase activity (data not shown). Furthermore, it was unclear whether the protocol resulted in an optimal enrichment of brain PMs. We therefore modified the original protocol in several aspects. As the partitioning of subcellular compartments between the phases strongly depends on polymer and salt concentrations (7), several modifications of the concentrations of these components were performed to assess whether fractionation could be improved. In a first step, various concentrations of dextran T500 and PEG 3350 were explored, ranging from 5.4% to 6.9% (w/w), thus deviating from the value of 5.7% (w/w) used in the original protocol applied for rat liver PMs. At a concentration of 6.3% (w/w), PMs became most efficiently enriched in the top phase (Fig. 2). Furthermore, they became separated from the mitochondria, which comprised the main contamination. In a second step, the effect of different concentrations of Li_2SO_4 on the WGA-dextran affinity partitioning was analyzed. Li_2SO_4 influences membrane partitioning in the two-phase systems by generating a potential across the two phases (7). The bottom phase, which accumulates SO_4^{2-} , becomes more negative than the top phase, which contains most of the Li^+ . The resulting potential moves the negatively charged membranes into the top phase. Separation of PMs from other membranes in the bottom phase was improved compared to the original protocol (which used no Li_2SO_4) when 2 mM Li_2SO_4 was applied. Additionally, to further increase the yield and purity of the PMs, we adjusted the amount of WGA. Without WGA, only 23.5% of the PM marker alkaline phosphatase and 40.9% of the total protein amount were recovered in the bottom phase (Fig.2). Increasing amounts of WGA coupled to dextran led to increased recovery in the bottom phase. Highest recovery was obtained using 100 μg WGA/1 g system, which resulted in 84.9% of the PM marker activity and 59.4% of total protein amount in the bottom phase (data not shown).

Finally, we modified the washing procedure. Instead of applying the combined top phases 1 and 2 directly to the WGA-dextran bottom phase, as it was done in the original protocol, we inserted several re-extraction and washing steps in between (Fig. 1).

Enzyme marker assays

To evaluate the final protocol, enzyme assays were performed. In order to preserve enzyme activity, the PMs were not exposed to high-salt and high-pH washing. The marker enzyme alkaline phosphatase was used as a PM marker, whereas the mitochondrial succinate dehydrogenase and the NADH ferricyanide reductase of the endoplasmic reticulum were employed as markers of the two major contaminating compartments (Table 1). 10.4% of alkaline phosphatase activity was recovered in the microsomes compared to the activity obtained from the starting material. Determination of the relative specific activity (RSA) revealed a 2.4-fold enrichment. After affinity partitioning, 5.3% of the initial alkaline phosphatase activity was recovered in the final pellet, and the RSA value demonstrated a 12.3-fold enrichment compared to the starting material. Thus, the differential centrifugation for preparation of microsomes resulted in a loss of almost 90% of the PM marker and in an only 2.4-fold enrichment, whereas the affinity partitioning procedure (cf. Fig. 1) resulted in a recovery of 51% and an additional 5.1-fold enrichment (Table 1, compare yield and RSA between microsomes and pellet). This demonstrates the high efficiency of the affinity partitioning procedure. As demonstrated by succinate dehydrogenase activity, mitochondria were removed by 96.2% in the microsomes and by 99.8% after the affinity partitioning procedure. Thus, the contamination by mitochondria was further reduced 19-fold by applying the affinity partitioning procedure. The combination of differential centrifugation and affinity partitioning resulted in a final RSA of 0.5 compared to 0.8 obtained with microsomes, showing that mitochondria are further removed from PMs by the affinity partitioning procedure. NADH ferricyanide reductase activity revealed that the endoplasmic reticulum was removed by 94% in the microsomes and by 99.6% after the affinity partitioning procedure. Again, this shows the potential of our protocol to reduce contaminating compartments from the PMs. RSA values of 1.3 (microsomes) and 0.8 (final pellet) also show the benefits of the affinity partitioning procedure for the removal of the endoplasmic reticulum. Taken together, the enzyme and Bradford assays imply a high yield of PMs with our approach, because the PM marker activity in the final pellet amounted to 5.3% of the value obtained in the homogenate, whereas only 0.5% of the original protein amount was recovered. This conclusion is

further supported by the low values of mitochondrial and endoplasmic reticulum marker activity (0.2% and 0.4%, respectively). Furthermore, the enrichment of PMs (RSA=12.3) is paralleled by a reduction of contaminating compartments (mitochondrial RSA=0.5; endoplasmic reticulum RSA=0.8).

LC-MS/MS analysis of affinity-purified plasma membranes from cerebellum

To determine the extent of contamination by a method independent of marker enzymes and to demonstrate the suitability of the protocol for small amounts of tissue, affinity-purified PM proteins from the cerebellum (weight about 300 mg) of a single rat were analyzed by SDS-PAGE coupled to LC-MS/MS. As integral PM proteins are of primary interest for most neuroproteomic approaches, the affinity-purified PMs were washed with high-salt and high-pH buffers in order to remove peripheral and vesicle-enclosed membrane proteins (15). Proteins that were insoluble under high-salt and high-pH conditions were separated by 4-12% SDS-PAGE. To do so, two gels were loaded with 50 μ g or 30 μ g protein. Gel slices of equal size (about 1 mm) were excised and subjected to in-gel digestion using trypsin. The resulting peptides were extracted from each gel slice and analyzed by nano-LC-MS/MS for protein identification with either a short gradient (1% increase in solvent B per minute with the 50 μ g samples) or a long gradient (0.5% increase in solvent B per minute with the 30 μ g samples). The independent analysis of the sample by slightly different protocols was performed in order to demonstrate the reproducibility of the datasets obtained. This resulted in the identification of 351 proteins for the 50 μ g sample and 447 proteins for the 30 μ g sample. The higher number of identified proteins from the 30 μ g sample is due to the extended gradient providing improved peptide separation and also prolonged acquisition time during MS/MS analysis. Combining both gels, a total of 506 distinct proteins were identified (Tables 2 and supplementary Table 1) with 182 proteins (38.9%) identified by a single peptide. Using gene ontology, 146 proteins (29%) were assigned to their subcellular location. Ninety-three (64%) of them were annotated as membrane proteins, of which 74 (51%) were integral membrane proteins. Forty-nine (34%) of the 146 proteins were PM proteins, with 31 (21%) being integral PM proteins (Table 2). Six (4%) proteins were from mitochondrial membranes, and 5 (3%) were allocated to the membranes of the endoplasmic reticulum. Similar results were obtained when the datasets of the two gels were analyzed separately (Table 2). As only about 30% of the identified proteins could be allocated to their subcellular location when using gene ontology, we extended our analysis and performed a literature search to find further information

about the subcellular location. This search resulted in the subcellular allocation of 472 proteins, of which 197 (42%) were PM proteins (supplementary Table 1) with 55 proteins (27.9%) identified by a single peptide.

As transmembrane domains, GPI-anchor, and myristoylation consensus sequences are indicative of membrane proteins, the identified proteins were also analyzed for these motifs in order to provide an additional criterion for the evaluation (Table 2; supplementary Table 1). Among the 506 proteins identified, 249 (49.2%) proteins were predicted with at least one transmembrane domain and 168 (33.2%) with more than one transmembrane domain; 10 (2%) of the identified proteins were predicted to have a GPI-anchoring site, and 15 (2.9%) were predicted to have a myristoylation site that could anchor these proteins in the PM. Taken together, the results confirm the high enrichment of PM proteins obtained with our affinity partitioning protocol.

Functional categories of identified proteins

The identified proteins cover a broad range of different functions and belong to distinct families. Eighty-four of the classified proteins are listed in Table 3. We identified several proteins involved in neurotransmission, i.e., proteins acting as neurotransmitter release machinery, postsynaptic receptors, or neurotransmitter re-uptake systems. Twelve proteins were identified which mediate transmitter release through the fusion of synaptic vesicles (SVs) with the PM: 8 syntaxin proteins, namely STX1A, STX1B2, STX2, STX3, STX4, STX6, STX7, STX8; the syntaxin-associated protein unc18-homolog; and 3 synaptosomal associated proteins, namely SNAP23, SNAP25, and SNAP29. Among the neurotransmitter receptors, 14 distinct proteins were identified: the glutamate receptor subunits mGluR1, mGluR2, mGluR5, GluR1, GluR2, GluR3, GluR4 and GluRd2, the gamma-aminobutyric acid (GABA) receptors GABRA1, GABRA6, GABRB1, GABRB2 and GABRD, and the purinergic receptor P2Y12. Within the category of neurotransmitter re-uptake systems, several types of transporters were found: 3 excitatory amino acid transporters (EAAT1, EAAT2, and EAAT4); 3 GABA transporters (GAT1, GAT2 and GAT3), the glycine transporter GlyT1, and the orphan Na⁺/Cl⁻-dependent neurotransmitter transporter NTT4. Another important class of neuronal PM proteins contains primary transporters, secondary transporters, and non-receptor type channels, of which 33 were identified. The primary transporter proteins included 6 subunits of the Na⁺/K⁺-ATPase (ATP1A1, ATP1A2, ATP1A3, ATP1B1, ATP1B2, ATP1B3) and 4 Ca²⁺-ATPase subunits (ATP2B1, ATP2B2, ATP2B3, ATP2B4). The secondary transporter proteins comprised the Cl⁻/HCO₃⁻ exchanger

AE1, the anion exchange protein 2, the $\text{Na}^+/\text{Ca}^{2+}$ exchangers NCX1 and NCX2, the K^+/Cl^- -cotransporter KCC2, the $\text{Na}^+/\text{K}^+/\text{Cl}^-$ -cotransporter NKCC2, the facilitated glucose transporters Slc2a1, Slc2a3, Slc2a5, Slc2a8, and the monocarboxylate transporter MCT1. Twelve nonreceptor type channel proteins were identified: the water channels aquaporin 1 and aquaporin 4, the inward rectifying potassium channels Kir7.1 and Kir4.1, the gap junction protein Cx43, the sodium channel beta-2 subunit, the alpha subunit of sodium channel type II, potassium voltage gated channels Kv1.1, Kv3.3 and Kv4.3, the dihydropyridine-sensitive Ca^{2+} -channel alpha2/delta, and the voltage-dependent anion-selective channel protein 1. Another class represented surface proteins for cell-cell communication. Within this class, we identified 11 proteins: the BDNF/NT3 growth factor receptor, contactin 1 and 2, the contactin-associated protein 1, the kilon protein, N-CAM 140, Nr-CAM, neurofascin, neuroligin 1, neurexin 3, and neurotrimin. Finally, six disease-related PM proteins were identified: the amyloid beta A4 protein, the major prion protein, nicastrin, Nogo, and two apoptosis-related proteins, namely defender against cell death 1 and Fas apoptotic inhibitory molecule 2. Aside from PM proteins, our analysis also revealed contaminating proteins of various origin (supplementary Table 1). A great number of these could be categorized into 6 groups. The first group comprised mitochondrial proteins (37 of 472), e.g. cytochrome C oxidase subunit 2, phosphate carrier protein, ATP synthase protein 8, and monoamine oxidase. The second group was composed of proteins of the endoplasmic reticulum. Examples are the sarcoplasmic/endoplasmic reticulum calcium ATPases 1 and 2, calnexin, and the protein disulfide-isomerase A3. The third group consisted of SV membrane proteins, of we identified several Rab proteins, synaptotagmins, synaptobrevins, synaptophysin, the synaptic vesicle protein 2, the cysteine string protein, and the vesicular inhibitory amino acid transporter VIAAT. Proteins of the translation machinery composed the fourth group and consisted of 36 ribosomal proteins and the elongation factor EF1a1. The fifth and sixth group comprised cytoskeleton proteins (20 proteins) and chaperons (6 proteins), respectively. In summary, the protocol introduced in the present study is able to allocate as much as 34%-42% of the identified proteins to a PM origin. It is thus feasible to enrich PMs from minute brain samples and makes them available for proteomic analysis.

DISCUSSION

This study presents a novel fractionation protocol for neural PM proteins which is based on affinity two-phase partitioning. Fractionation by affinity partitioning is simple and requires no specific equipment. It is selective and much more rapid than conventional membrane preparation protocols. The highly specific enrichment of PMs by this approach is illustrated by marker enzyme analysis, which demonstrated a 12.3-fold enrichment compared to the initial homogenate. This enrichment is in good agreement with the 34%-42% PM proteins, identified by gene ontology or literature search, as they constitute between 0.4-2.5% of the homogenate (26). The use of a single enzyme activity as criterion for yield and enrichment might lead to erroneous estimations, due to the heterogeneity in the partitioned membrane patches. An alternative might therefore be the immunoblot analysis against multiple marker proteins. We used enzyme activity measurements, as these demonstrate a broader linear range compared to immunoblot analysis, and as enzyme tests were used in several previous analyses of two-phase systems (9,10,25). Furthermore, the subsequent identification of pre- and postsynaptic PM proteins by mass spectrometry argues against a preferential enrichment of different membrane components.

An important aspect in brain proteomics is the ability to analyze anatomically or functionally defined areas. Conventional protocols for the isolation of PMs from tissue combine two techniques, differential centrifugation and subsequent density gradient centrifugation. Most of these protocols are time- and material-consuming, and the yield of highly purified PMs is often low (14). Partitioning in an aqueous two-phase system, in contrast, requires only small amounts of material. The purification of PMs from fat cells by differential and density-gradient centrifugation required 16-24 rats, whereas partitioning in an aqueous two-phase system required only 1-2 rats (29). This efficacy is confirmed by our data which demonstrate that less than 300 mg of tissue are sufficient as starting material. Thus, small brain structures, such as the cerebellum of a single rat, can be analyzed. The protocol can probably further be downscaled by circumventing the initial preparation of microsomes. Being based on differential centrifugation, this step led to a loss of 90% of the initial PM protein amount and yielded only a 2.4-fold enrichment, whereas the affinity partitioning itself led to a 5-fold enrichment of PMs with a recovery of 50%. Other improvements may be the replacement of the SDS-PAGE coupled to LC-MS/MS analysis by multidimensional liquid chromatography coupled to mass spectrometry (1,30).

Our protocol therefore compares favorably with previously reported protocols of PM purification from brain tissue (27,28). The most important criteria for assessing the quality of protocols are the enrichment and yield of PM proteins. Whereas PM proteins constituted only 12-15% in the studies by Nielsen et al. (27) and 20% in the study by Olsen et al. (28), our protocol yielded 34-42% PM proteins. This represents a 2- to 3.5-fold higher enrichment of PM proteins as compared to the previously reported protocols. With respect to the starting material, all three studies applied similar amounts of tissue, i.e. between 150-300 mg. Only when using a more sensitive and accurate Fourier-transform ion cyclotron resonance (FT-ICR) mass spectrometry, Nielsen et al. (27) succeeded in the analysis of as little as 15-20 mg brain tissue and identified 1,685 different proteins. This high number of different proteins, as compared to our study, is likely due to the fact that they used - beside FT-ICR mass spectrometry - different criteria for data validation, and a different database for protein annotation. Furthermore, they used mouse tissue, for which more proteins are represented in the database than for rat tissue samples. In the well-annotated Swiss-Prot database, for instance, there are currently 9893 entries for mouse protein entries and only 4544 for rat proteins. Furthermore, the employed protein/peptide separation methods – two-dimensional LC (27) and 1D-PAGE coupled to one-dimensional LC in the present approach – are difficult to compare with advantages on both sides. Therefore, the number of identified PM proteins depends on several factors and is hardly comparable between the different approaches used in the three studies. However, another advantageous feature of affinity partitioning is that the aqueous polymer environment is gentle to membrane structure and function and preserves protein interactions (7). Aqueous polymer two-phase systems were used for binding studies and analysis of protein interactions (8,31,32). The protocol is therefore suitable to enrich multiprotein complexes of the PM, which are a major focus in proteome analysis (33-36). After affinity partitioning, these signaling complexes can be isolated further by complex-specific affinity techniques, such as immunoprecipitation or blue native gel techniques (11,12). In contrast, the high-salt, high-pH, and urea treatment in the stepwise depletion protocol used by Nielsen et al (27) likely destroys protein complexes. Taken together, our protocol provides the highest enrichment of PM proteins from small amount of brain tissue by simultaneously preserving protein complexes.

To validate our novel protocol, we analyzed the PM proteome of the rat cerebellum and identified many proteins known to be important for function of this brain region. These included proteins involved in neurotransmission, such as the neurotransmitter receptors and transporters. One of the

receptors, GABRA6 (Fig.3), is highly restricted to cerebellar granule cells (37). This demonstrates the potential to identify brain area-specific proteins by our approach. Another large group was comprised of proteins involved in cell-cell contact. Among the identified proteins were neurexin-3 and neuroligin-1, which play important roles in the formation and maintenance of the pre- and postsynaptic PMs (38). The postsynaptic protein neuroligin-1 was shown to induce presynaptic differentiation in axons (39). Neurexins are presynaptic interaction partners of neuroligins and induce postsynaptic specializations (40). Finally, we identified several proteins which play essential roles in neurological disorders, such as Alzheimer's disease (amyloid β A4 protein) or the BSE-Creutzfeld-Jacob syndrome (major prion protein). The protocol may therefore foster the proteome analysis of neurological disorders either by characterizing known mutant proteins or by identifying novel markers for pathological conditions. An unexpected finding comprised the numerous proteins of the translation machinery. Ribosomal proteins represent a large fraction of the total protein mass of a cell, and their sheer amount may explain their presence among the isolated proteins. An alternative explanation is provided by the existence of dendritic mRNA in cerebellar Purkinje cells, such as mRNA for calmodulin (41), inositol 1,4,5-trisphosphate receptor type 1 (42), and L7 (43). We conclude that the purified ribosomal proteins may be part of the dendritic translational machinery in the Purkinje cells, leading to their enclosure into the forming PM vesicles during tissue homogenization. In summary, we present here an easy to perform and rapid protocol that allows the preparation of highly enriched PMs from small brain areas. This will allow the proteome analysis of PMs of different brain regions, leading to improved understanding of the molecular repertoire underlying fundamental brain function and dysfunction.

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FIGURE LEGENDS

FIG. 1 **Affinity partitioning procedure for the enrichment of brain plasma membranes (PMs).** The complete procedure is described in Experimental Procedures. Microsomes obtained by differential centrifugation were separated in a two-phase system. Plasma membranes enriched in the top phase were collected and the bottom phase was re-extracted (first row). The combined top phases enriched in plasma membranes were washed twice by fresh bottom phases (second row). After washing, the top phase was applied to an affinity bottom phase coupled with WGA as affinity ligand for plasma membranes (third row). The affinity bottom phase (WGA-dextran), enriched in plasma membranes, was washed with fresh top phase and diluted with *N*-acetyl-D-glucosamine to release the PMs, which were finally concentrated by sedimentation.

FIG. 2 **Partitioning of total proteins, PMs, and mitochondria in two-phase systems with various polymer concentrations.** The effect of various polymer concentrations was assessed by marker enzyme assays. Alkaline phosphatase (AP) activity and succinate dehydrogenase (SDH) activity were used as PM marker and mitochondrial marker, respectively. Note that the percentage of PM marker activity in the top phase declined at polymer concentrations >6.0% (w/w), indicating that high polymer concentrations have negative effects on the recovery in the top phase. However, the relative specific activity (RSA) of the PM marker (i.e., the ratio between PM marker activity and protein amount) reached the highest value at a concentration of 6.3% (w/w) PEG/dextran, demonstrating that these polymer conditions lead to the highest enrichment of PMs in the top phase. Also note that the RSA of the mitochondrial marker SDH was substantially reduced in the top phase at a polymer concentration of 6.3% (w/w). Although an even lower value was obtained at a polymer concentration of 6.9% (w/w), we chose to use the 6.3% (w/w) condition for our subsequent analyses. Data represent mean values of three independent experiments.

FIG. 3 **MS/MS-spectrum of the GABRA6 peptide ILDNLLEGYDNR.** A Mascot search against the Swiss-Prot database with the species subset *Rattus* identified the peptide ILDNLLEGYDNR with an elution time of 32.45 min as unique to GABRA6. The peptide was derived from a doubly charged precursor ion ($m/z = 717.91$). For clarification only major ion series were annotated.

TABLE 1

Distribution of marker enzymes

| | Protein | Plasma membrane | | Mitochondria | | Endoplasmic reticulum | |
|---------------------|-----------|-----------------|------------|--------------|-----------|-----------------------|-----------|
| | Yield [%] | Yield [%] | RSA | Yield [%] | RSA | Yield [%] | RSA |
| Homogenate | 100 | 100 | 1 | 100 | 1 | 100 | 1 |
| Microsomes | 4.8 ± 1 | 10.4 ± 1.7 | 2.4 ± 0.9 | 3.8 ± 1.2 | 0.8 ± 0.3 | 6 ± 0.5 | 1.3 ± 0.2 |
| Final pellet | 0.5 ± 0.1 | 5.3 ± 1.2 | 12.3 ± 3.4 | 0.2 ± 0.1 | 0.5 ± 0.4 | 0.4 ± 0.1 | 0.8 ± 0.3 |

Yield and relative specific activity (RSA) of alkaline phosphatase [EC 3.1.3.1] (PM marker), succinate dehydrogenase [EC 1.3.5.1] (mitochondrial marker), and NADH ferricyanide reductase [EC 1.6.2.2] (marker for endoplasmic reticulum) were determined as the average of three independent experiments ± standard deviation in homogenate, the microsomal pellet, and the final pellet obtained through the affinity partitioning procedure. The RSA values obtained for the mitochondrial and the endoplasmic reticulum marker were reduced from the homogenate to the final pellet (mitochondria: from 0.8 to 0.5, which is equivalent to a 1.6-fold reduction; endoplasmic reticulum: from 1.3 to 0.8, equivalent to a 1.6-fold reduction). In contrast, the RSA of the PM marker increased in the procedure (from 2.4 to 12.3, which is equivalent to a 5.1-fold enrichment).

TABLE 2

Statistical analysis of identified proteins

| | 50 μ g gel | 30 μ g gel | both gels |
|--|-------------------|-------------------|--------------|
| number of identified proteins | 351 | 447 | 506 |
| with subcellular location (gene ontology) | 107 | 132 | 146 |
| membrane | 72 | 87 | 93 |
| integral to membrane | 56 | 68 | 74 |
| plasma membrane | 38 | 46 | 49 |
| integral to plasma membrane | 27 | 29 | 31 |
| integral to mitochondrial membrane | 6 | 5 | 6 |
| integral to endoplasmic reticulum membrane | 5 | 5 | 5 |
| with subcellular location (gene cards) | 317 | 416 | 472 |
| plasma membrane | 146 | 180 | 197 |
| mitochondria | 32 | 29 | 37 |
| endoplasmic reticulum | 17 | 23 | 24 |
| with 1 or more predicted transmembrane helices | 188 | 226 | 249 |
| with more than 1 predicted transmembrane helices | 126 | 154 | 168 |
| with predicted GPI-anchor | 10 | 8 | 10 |
| with predicted myristoylation | 12 | 14 | 15 |

Identified proteins from 50 μ g protein, separated by a short gradient (1% increase in solvent B per minute) and from 30 μ g protein, separated by a long gradient (0.5% increase in solvent B per minute) were investigated for their subcellular location using gene ontology and gene cards. Between 34% and 46% of all allocated proteins could be assigned to plasma membranes, depending on the sample and database used. Furthermore, at least one transmembrane helix was predicted for ~50% of the proteins.

TABLE 3

Selected plasma membrane proteins from cerebellum

| Neurotransmitter release | | | |
|---|--|-----|---------------------|
| Acc.no. | Protein name | TMH | Identified peptides |
| P32851 | Syntaxin-1A (STX1A) | 1 | 8 |
| P61265 | Syntaxin-1B2 (STX1B2) | 1 | 27 |
| P50279 | Epimorphin (STX2) | 1 | 1 |
| Q08849 | Syntaxin-3 (STX3) | 1 | 3 |
| Q08850 | Syntaxin-4 (STX4) | 1 | 7 |
| Q63635 | Syntaxin-6 (STX6) | 1 | 8 |
| O70257 | Syntaxin-7 (STX7) | 1 | 7 |
| Q9Z2Q7 | Syntaxin-8 (STX8) | 1 | 2 |
| P61765 | Syntaxin binding protein 1 (unc 18-homolog) | 0 | 13 |
| O70377 | Synaptosomal-associated protein SNAP23 | 0 | 3 |
| P60881 | Synaptosomal-associated protein SNAP25 | 0 | 24 |
| Q9Z2P6 | Synaptosomal-associated protein SNAP29 | 0 | 2 |
| Neurotransmitter receptors | | | |
| Acc.no. | Protein name | TMH | Identified peptides |
| P62813 | Gamma-aminobutyric-acid receptor alpha-1 (GABRA1) | 5 | 3 |
| P30191 | Gamma-aminobutyric-acid receptor alpha-6 (GABRA6) | 4 | 1 |
| P15431 | Gamma-aminobutyric-acid receptor beta-1 (GABRB1) | 5 | 1 |
| P63138 | Gamma-aminobutyric-acid receptor beta-2 (GABRB2) | 5 | 2 |
| P18506 | Gamma-aminobutyric-acid receptor delta (GABRD) | 5 | 1 |
| Q9EPX4 | P2Y purinoceptor 12 7 1 | 7 | 1 |
| P23385 | Metabotropic glutamate receptor 1 (mGluR1) | 8 | 2 |
| P31421 | Metabotropic glutamate receptor 2 (mGluR2) | 7 | 1 |
| P31424 | Metabotropic glutamate receptor 5 (mGluR5) | 6 | 2 |
| P19490 | Glutamate receptor 1 (GluR1) | 5 | 2 |
| P19491 | Glutamate receptor 2 (GluR2) | 4 | 2 |
| P19492 | Glutamate receptor 3 (GluR3) | 4 | 2 |
| P19493 | Glutamate receptor 4 (GluR4) | 5 | 1 |
| Q63226 | Glutamate receptor delta-2 subunit (GluRd2) | 4 | 8 |
| Neurotransmitter re-uptake systems | | | |
| Acc.no. | Protein name | TMH | Identified peptides |
| P24942 | Excitatory amino acid transporter 1 (EAAT1) | 10 | 18 |
| P31596 | Excitatory amino acid transporter 2 (EAAT2) | 12 | 15 |
| O35921 | Excitatory amino acid transporter 4 (EAAT4) | 8 | 10 |
| P23978 | Na ⁺ /Cl ⁻ -dependent GABA transporter 1 (GAT1) | 12 | 5 |
| P31647 | Na ⁺ /Cl ⁻ -dependent GABA transporter 3 (GAT3) | 12 | 9 |
| P31646 | Na ⁺ /Cl ⁻ -dependent GABA transporter 2 (GAT2) | 13 | 1 |
| P28572 | Na ⁺ /Cl ⁻ -dependent glycine transporter 1 (GlyT1) | 12 | 5 |
| P31662 | Orphan Na ⁺ /Cl ⁻ -dependent neurotransmitter transporter NTT4 | 11 | 5 |
| Primary and secondary transporters and non-receptor type channels | | | |
| Acc.no. | Protein name | TMH | Identified peptides |
| P06685 | Na ⁺ /K ⁺ -transporting ATPase alpha-1 chain (ATP1A1) | 8 | 50 |
| P06686 | Na ⁺ /K ⁺ -transporting ATPase alpha-2 chain (ATP1A2) | 9 | 65 |
| P06687 | Na ⁺ /K ⁺ -transporting ATPase alpha-3 chain (ATP1A3) | 8 | 56 |
| P07340 | Na ⁺ /K ⁺ -transporting ATPase beta-1 chain (ATP1B1) | 1 | 19 |
| P13638 | Na ⁺ /K ⁺ -transporting ATPase beta-2 chain (ATP1B2) | 1 | 11 |
| Q63377 | Na ⁺ /K ⁺ -transporting ATPase beta-3 chain (ATP1B3) | 1 | 5 |
| P11505 | Plasma membrane Ca ²⁺ -transporting ATPase 1 (ATP2B1) | 10 | 14 |
| P11506 | Plasma membrane Ca ²⁺ -transporting ATPase 2 (ATP2B2) | 9 | 38 |

| | | | |
|--------|---|----|----|
| Q64568 | Plasma membrane Ca ²⁺ -transporting ATPase 3 (ATP2B3) | 11 | 25 |
| Q64542 | Plasma membrane Ca ²⁺ -transporting ATPase 4 (ATP2B4) | 10 | 3 |
| P23562 | Band 3 anion transport protein (AE1) | 15 | 9 |
| P23347 | Anion exchange protein 2 | 10 | 1 |
| Q01728 | Na ⁺ /Ca ²⁺ exchange protein NCX1 | 11 | 3 |
| P48768 | Na ⁺ /Ca ²⁺ exchange protein NCX2 | 12 | 5 |
| Q63633 | K ⁺ /Cl ⁻ -cotransporter 2 (KCC2) | 14 | 18 |
| P55016 | Na ⁺ /K ⁺ /Cl ⁻ -cotransporter NKCC2 | 12 | 1 |
| P11167 | facilitated glucose transporter 1 (Slc2a1) | 11 | 3 |
| Q07647 | facilitated glucose transporter 3 (Slc2a3) | 11 | 2 |
| P43427 | facilitated glucose transporter 5 (Slc2a5) | 12 | 1 |
| Q9JJZ1 | facilitated glucose transporter 8 (Slc2a8) | 12 | 1 |
| P53987 | Monocarboxylate transporter 1 (MCT1) | 11 | 4 |
| P29975 | Aquaporin 1 | 7 | 4 |
| P47863 | Aquaporin 4 | 6 | 9 |
| O70617 | Inward rectifier potassium channel 13 (Kir7.1) | 2 | 4 |
| P49655 | Inward rectifier potassium channel 10 (Kir4.1) | 2 | 1 |
| P08050 | Gap junction alpha-1 protein (Cx43) | 4 | 12 |
| P54900 | Na ⁺ -channel beta-2 | 2 | 2 |
| P04775 | Na ⁺ -channel protein type II alpha | 24 | 1 |
| P10499 | Potassium voltage gated channel Kv1.1 | 6 | 3 |
| Q01956 | Potassium voltage gated channel Kv3.3 | 7 | 2 |
| Q63881 | Potassium voltage gated channel Kv4.2 | 7 | 1 |
| P54290 | Dihydropyridine-sensitive Ca ²⁺ channel alpha-2/delta | 3 | 1 |
| Q9Z2L0 | Voltage-dependent anion-selective channel 1 | 0 | 12 |

Cell-cell communication

| Acc.no. | Protein name | TMH | Identified peptides |
|---------|---|-----|---------------------|
| Q63604 | BDNF/NT-3 growth factor receptor | 2 | 2 |
| Q63198 | Contactin 1 | 2 | 51 |
| P22063 | Contactin 2 | 1 | 9 |
| P97846 | Contactin associated protein 1 | 3 | 4 |
| Q9Z0J8 | Neuronal growth regulator 1 (kilon protein) | 1 | 10 |
| P13596 | Neural cell adhesion molecule 1 (N-CAM140) | 2 | 28 |
| P97686 | Neuronal cell adhesion molecule (Nr-CAM) | 2 | 10 |
| P97685 | Neurofascin | 3 | 23 |
| Q62765 | Neuroigin | 3 | 1 |
| Q07310 | Neurexin 3-alpha | 2 | 1 |
| Q62718 | Neurotrimin | 2 | 7 |

Disease-related PM proteins

| Acc.no. | Protein name | TMH | Identified peptides |
|---------|-------------------------------------|-----|---------------------|
| P08592 | Amyloid beta A4 protein | 2 | 4 |
| P13852 | Major prion protein | 3 | 3 |
| Q8CGU6 | Nicastrin | 2 | 4 |
| Q9JK11 | Nogo (Reticulon 4) | 3 | 9 |
| P61805 | Defender against cell death 1 | 3 | 3 |
| O88407 | Fas apoptotic inhibitory molecule 2 | 7 | 2 |

Selected proteins that were identified by LC-MS/MS were categorized in neurotransmitter release machinery, neurotransmitter receptors, neurotransmitter re-uptake system, primary and secondary transporters and non-receptor type channels, cell-cell communication, and disease-related PM

proteins. For each protein, the Swiss prot accession number, the protein name, the number of predicted transmembrane helices (TMH) (23) and the number of different identified peptides are indicated.

| Entrz Name | Acc.no. | protein name | # pept. in 50 µg gel | # pept. in 30 µg gel | # pept. in both gels | Score | Expect | m/z | charge | sequence | subcell location | TMH | GPI-anchor | myristoylation |
|------------|---------|--|----------------------|----------------------|----------------------|-------|----------|--------|--------|---------------------|-----------------------|-----|------------|----------------|
| 1433B_RAT | P35213 | 14-3-3 protein beta/alpha | 2 | 2 | 2 | | | | | | n.d. | 0 | | |
| 1433E_RAT | P62260 | 14-3-3 protein epsilon | 3 | 8 | 9 | | | | | | n.d. | 0 | | |
| 1433G_RAT | P61983 | 14-3-3 protein gamma | 0 | 1 | 1 | 51 | 7.5e-005 | 540.79 | 2+ | YLAEVATGKEK | n.d. | 0 | | |
| 1433T_RAT | P68255 | 14-3-3 protein tau | 1 | 1 | 1 | 67 | 8.9e-007 | 715.76 | 3+ | TAFDEAIAELDTLNEDSYK | n.d. | 0 | | |
| 1433Z_RAT | P63102 | 14-3-3 protein zeta/delta | 3 | 5 | 6 | | | | | | n.d. | 0 | | |
| 5NTD_RAT | P21588 | 5'-nucleotidase | 4 | 8 | 9 | | | | | | plasma membrane | 2 | x | |
| A4_RAT | P08592 | Amyloid beta A4 protein | 2 | 2 | 4 | | | | | | plasma membrane | 2 | | |
| AAA1_RAT | P63116 | Asc-type amino acid transporter 1 | 0 | 1 | 1 | 36 | 0.0024 | 436.22 | 2+ | FTESMTR | plasma membrane | 12 | | |
| AA1C_RAT | P13221 | Aspartate aminotransferase, cytoplasmic | 0 | 1 | 1 | 65 | 3.1e-006 | 443.78 | 3+ | VGNLTVVGK | cytoplasm | 0 | | |
| AA1M_RAT | P00507 | Aspartate aminotransferase, mitochondrial | 0 | 2 | 2 | | | | | | mitochondria | 0 | | |
| ACE_RAT | P47820 | Angiotensin-converting enzyme, somatic isoform | 20 | 24 | 26 | | | | | | plasma membrane | 2 | | |
| ACON_RAT | Q9ER34 | Aconitate hydratase, mitochondrial | 0 | 1 | 1 | 34 | 0.0034 | 493.20 | 2+ | EGWPLDIR | mitochondria | 0 | | |
| ACSL1_RAT | P18163 | Long-chain-fatty-acid-CoA ligase 1 | 0 | 2 | 2 | | | | | | mitochondria | 0 | | |
| ACTA_RAT | P62738 | Actin, aortic smooth muscle | 6 | 18 | 13 | | | | | | cytoskeleton | 0 | | |
| ACTB_RAT | P60711 | Actin, cytoplasmic 1 | 13 | 18 | 20 | | | | | | cytoskeleton | 0 | | |
| ACTC_RAT | P63035 | Actin, alpha cardiac | 6 | 6 | 8 | | | | | | cytoskeleton | 0 | | |
| ADT1_RAT | Q03962 | ADP-ATP carrier protein 1 | 10 | 13 | 14 | | | | | | mitochondria | 0 | | |
| ADT2_RAT | Q09073 | ADP-ATP carrier protein 2 | 5 | 13 | 13 | | | | | | mitochondria | 0 | | |
| AL3A2_RAT | P30839 | Fatty aldehyde dehydrogenase | 5 | 4 | 5 | | | | | | microsome | 1 | | |
| ALBU_RAT | P02770 | Serum albumin | 5 | 6 | 7 | | | | | | blood | 1 | | |
| ALDOA_RAT | P05065 | Fructose-bisphosphate aldolase A | 5 | 6 | 8 | | | | | | cytoplasm | 0 | | |
| ALDOC_RAT | P09117 | Fructose-bisphosphate aldolase C | 8 | 10 | 13 | | | | | | cytoplasm | 0 | | |
| AMPN_RAT | P15684 | Aminopeptidase N | 3 | 11 | 13 | | | | | | plasma membrane | 1 | | |
| ANXA3_RAT | P14669 | Annexin A3 | 2 | 5 | 5 | | | | | | n.d. | 0 | | |
| ANXA5_RAT | P14668 | Annexin A5 | 1 | 2 | 3 | | | | | | n.d. | 0 | | |
| ANXA6_RAT | P48037 | Annexin A6 | 1 | 1 | 2 | | | | | | n.d. | 0 | | |
| AOFA_RAT | P21396 | Amine oxidase [flavin-containing] A | 1 | 0 | 1 | 30 | 0.0067 | 604.28 | 2+ | IFSVTNGGQER | mitochondria | 1 | | |
| AP180_RAT | Q05140 | Clathrin coat assembly protein AP180 | 0 | 1 | 1 | 51 | 6.8e-005 | 713.45 | 2+ | NTLFLNSFLDK | plasma membrane | 1 | | |
| AP2A2_RAT | P18484 | Adapter-related protein complex 2 alpha 2 subunit | 0 | 3 | 3 | | | | | | plasma membrane | 1 | | |
| AP2M1_RAT | P84092 | Clathrin coat assembly protein AP50 | 0 | 1 | 1 | 36 | 0.0027 | 429.23 | 2+ | SPVTNIAR | plasma membrane | 1 | | |
| AP2S1_RAT | P62744 | Clathrin coat assembly protein AP17 | 0 | 1 | 1 | 40 | 0.0012 | 452.29 | 2+ | FILIQNR | plasma membrane | 0 | | |
| APLP2_RAT | P15943 | Amyloid-like protein 2 | 2 | 4 | 5 | | | | | | plasma membrane | 3 | | |
| APOE_RAT | P02650 | Apolipoprotein E | 7 | 11 | 12 | | | | | | secretory | 0 | | |
| AQP1_RAT | P29975 | Aquaporin-CHIP | 3 | 4 | 4 | | | | | | plasma membrane | 7 | | |
| AQP4_RAT | P47863 | Aquaporin 4 | 7 | 6 | 9 | | | | | | plasma membrane | 6 | | |
| ARF1_RAT | P84079 | ADP-ribosylation factor 1 | 4 | 6 | 7 | | | | | | Golgi complex | 0 | | |
| ARF4_RAT | P61751 | ADP-ribosylation factor 4 | 0 | 2 | 2 | | | | | | Golgi complex | 0 | | x |
| ARF6_RAT | P62332 | ADP-ribosylation factor 6 | 0 | 3 | 3 | | | | | | Golgi complex | 0 | | x |
| ARG1_RAT | P07824 | Arginase 1 | 1 | 0 | 1 | 44 | 0.00042 | 429.35 | 2+ | AGLVEKLK | cytoplasm | 0 | | |
| ASSY_RAT | P09034 | Argininosuccinate synthase | 0 | 1 | 1 | 36 | 0.0036 | 429.79 | 2+ | IDIVENR | cytoplasm | 0 | | |
| AT1A1_RAT | P06685 | Sodium/potassium-transporting ATPase alpha-1 chain | 38 | 41 | 50 | | | | | | plasma membrane | 8 | | |
| AT1A2_RAT | P06686 | Sodium/potassium-transporting ATPase alpha-2 chain | 55 | 56 | 65 | | | | | | plasma membrane | 9 | | |
| AT1A3_RAT | P06687 | Sodium/potassium-transporting ATPase alpha-3 chain | 45 | 48 | 56 | | | | | | plasma membrane | 8 | | |
| AT1B1_RAT | P07340 | Sodium/potassium-transporting ATPase beta-1 chain | 11 | 16 | 19 | | | | | | plasma membrane | 1 | | |
| AT1B2_RAT | P13638 | Sodium/potassium-transporting ATPase beta-2 chain | 5 | 9 | 11 | | | | | | plasma membrane | 1 | | |
| AT1B3_RAT | Q63377 | Sodium/potassium-transporting ATPase beta-3 chain | 3 | 5 | 5 | | | | | | plasma membrane | 1 | | |
| AT2A1_RAT | Q64578 | Sarcoplasmic/endoplasmic reticulum calcium ATPase 1 | 3 | 5 | 7 | | | | | | endoplasmic reticulum | 8 | | |
| AT2A2_RAT | P11507 | Sarcoplasmic/endoplasmic reticulum calcium ATPase 2 | 9 | 18 | 23 | | | | | | endoplasmic reticulum | 11 | | |
| AT2B1_RAT | P11505 | Plasma membrane calcium-transporting ATPase 1 | 10 | 9 | 14 | | | | | | plasma membrane | 10 | | |
| AT2B2_RAT | P11506 | Plasma membrane calcium-transporting ATPase 2 | 22 | 30 | 38 | | | | | | plasma membrane | 9 | | |
| AT2B3_RAT | Q64568 | Plasma membrane calcium-transporting ATPase 3 | 15 | 20 | 25 | | | | | | plasma membrane | 11 | | |
| AT2B4_RAT | Q64542 | Plasma membrane calcium-transporting ATPase 4 | 0 | 3 | 3 | | | | | | plasma membrane | 10 | | |
| AT5F1_RAT | P19511 | ATP synthase B chain, mitochondrial | 5 | 8 | 8 | | | | | | mitochondria | 1 | | |
| ATP5H_RAT | P31399 | ATP synthase D chain, mitochondrial | 5 | 5 | 7 | | | | | | mitochondria | 0 | | |
| ATP5I_RAT | P29419 | ATP synthase e chain, mitochondrial | 3 | 4 | 4 | | | | | | mitochondria | 0 | | |
| ATP8_RAT | P11608 | ATP synthase protein 8 | 2 | 0 | 2 | | | | | | mitochondria | 1 | | |
| ATPA_RAT | P15999 | ATP synthase alpha chain, mitochondrial | 7 | 12 | 13 | | | | | | mitochondria | 0 | | |
| ATPB_RAT | P10719 | ATP synthase beta chain, mitochondrial | 4 | 10 | 11 | | | | | | mitochondria | 0 | | |
| ATPG_RAT | P35435 | ATP synthase gamma chain, mitochondrial | 1 | 2 | 3 | | | | | | mitochondria | 0 | | |
| ATPO_RAT | Q06647 | ATP synthase oligomycin sensitivity conferral protein, mitochondrial | 1 | 4 | 4 | | | | | | mitochondria | 0 | | |
| ATRN_RAT | Q99J96 | Attractin | 0 | 1 | 1 | 31 | 0.0066 | 534.67 | 3+ | MVAAAAAAATEARLR | plasma membrane | 6 | | |
| B3A2_RAT | P23347 | Anion exchange protein 2 | 0 | 1 | 1 | 33 | 0.0048 | 639.81 | 2+ | FEELQEAGSR | plasma membrane | 15 | | |
| B3A1T_RAT | P23362 | Band 3 anion transport protein | 7 | 9 | 9 | | | | | | plasma membrane | 15 | | |
| BAC1_RAT | P28463 | Basigin | 7 | 6 | 11 | | | | | | plasma membrane | 2 | | |
| BASP_RAT | Q05175 | Brain acid soluble protein 1 | 2 | 3 | 3 | | | | | | plasma membrane | 5 | | |
| BR44_RAT | P38718 | Brain protein 44 | 0 | 3 | 3 | | | | | | n.d. | 0 | | x |
| C11C_RAT | P27653 | C-1-tetrahydrofolate synthase, cytoplasmic | 1 | 0 | 1 | 42 | 0.00053 | 595.31 | 2+ | DVDGLTSINAGK | cytoplasm | 0 | | |
| CAC2D_RAT | P54290 | Dihydropyridine-sensitive L-type, calcium channel alpha-2/delta subunits | 0 | 1 | 1 | 34 | 0.0032 | 690.88 | 2+ | IIMLFDTGGEER | plasma membrane | 3 | | |
| CADH2_RAT | Q921Y3 | Neural-cadherin | 0 | 2 | 2 | | | | | | plasma membrane | 2 | | |
| CAH4_RAT | P48284 | Carbonic anhydrase IV | 5 | 8 | 10 | | | | | | plasma membrane | 1 | x | |
| CALM_RAT | P62161 | Calmodulin | 5 | 3 | 5 | | | | | | cytoplasm | 0 | | |
| CALX_RAT | P35565 | Calnexin | 11 | 14 | 17 | | | | | | endoplasmic reticulum | 2 | | |
| CAP1_RAT | Q08163 | Adenylyl cyclase-associated protein 1 | 0 | 2 | 2 | | | | | | plasma membrane | 0 | | |
| CAV1_RAT | P41350 | Caveolin-1 | 2 | 0 | 2 | | | | | | plasma membrane | 1 | | |
| CD14_RAT | Q63691 | Monocyte differentiation antigen CD14 | 0 | 1 | 1 | 75 | 2.9e-007 | 521.62 | 3+ | VPLQALDLSHNSLR | plasma membrane | 0 | | |
| CD166_RAT | Q35112 | CD166 antigen | 9 | 17 | 19 | | | | | | plasma membrane | 2 | | |

| | | | | | | | | | | | | | |
|------------|--------|--|----|----|----|----|----------|---------|----|-------------------------|-----------------------|----|---|
| GBB5_RAT | P62882 | Guanine nucleotide-binding protein beta subunit 5 | 1 | 0 | 1 | 31 | 0.0074 | 615.32 | 2+ | CSVYPLTFDK | plasma membrane | 0 | |
| GBRA1_RAT | P62813 | Gamma-aminobutyric-acid receptor alpha-1 subunit | 2 | 2 | 3 | | | | | | plasma membrane | 5 | |
| GBRA6_RAT | P30191 | Gamma-aminobutyric-acid receptor alpha-6 subunit | 1 | 0 | 1 | 86 | 2.2e-008 | 717.91 | 2+ | ILDNLLEGYDNR | plasma membrane | 4 | |
| GBRB1_RAT | P15431 | Gamma-aminobutyric-acid receptor beta-1 subunit | 0 | 1 | 1 | 38 | 0.00086 | 684.69 | 3+ | VADQLWVPDITYFLNDKK | plasma membrane | 5 | |
| GBRB2_RAT | P63138 | Gamma-aminobutyric-acid receptor beta-2 subunit | 0 | 2 | 2 | | | | | | plasma membrane | 5 | |
| GBRD_RAT | P18506 | Gamma-aminobutyric-acid receptor delta subunit | 0 | 1 | 1 | 31 | 0.0062 | 535.26 | 3+ | LKPIDADTIDIYAR | plasma membrane | 5 | |
| GCS1_RAT | Q88941 | Mannosyl-oligosaccharide glucosidase | 1 | 2 | 2 | | | | | | endoplasmic reticulum | 1 | |
| GDPIC_RAT | P50399 | Rab GDP dissociation inhibitor beta-2 | 0 | 1 | 1 | 33 | 0.004 | 676.32 | 2+ | DLGTDSDQIFISR | plasma membrane | 0 | |
| GEPH_RAT | Q03555 | Gephyrin | 0 | 1 | 1 | 33 | 0.0052 | 503.80 | 2+ | VLAQDVYAK | cytoskeleton | 0 | |
| GFAP_RAT | P47819 | Glial fibrillary acidic protein, astrocyte | 3 | 5 | 8 | | | | | | cytoskeleton | 0 | |
| GLNA_RAT | P09606 | Glutamine synthetase | 1 | 8 | 9 | | | | | | cytoplasm | 0 | |
| GNA11_RAT | Q9JID2 | Guanine nucleotide-binding protein, alpha-11 subunit | 0 | 1 | 1 | 36 | 0.0015 | 1118.96 | 2+ | VPPTGIEYFPDLENIIFR | plasma membrane | 0 | |
| GNA12_RAT | Q63210 | Guanine nucleotide-binding protein, alpha-12 subunit | 1 | 1 | 1 | 57 | 1.9e-005 | 529.35 | 2+ | ILLLGAGESGK | plasma membrane | 0 | |
| GNA1_RAT | P10824 | Guanine nucleotide-binding protein G(i), alpha-1 subunit | 5 | 5 | 5 | | | | | | plasma membrane | 0 | x |
| GNA2_RAT | P04897 | Guanine nucleotide-binding protein G(i), alpha-2 subunit | 7 | 10 | 11 | | | | | | plasma membrane | 1 | x |
| GNAO1_RAT | P59215 | Guanine nucleotide-binding protein G(o), alpha subunit 1 | 14 | 18 | 23 | | | | | | plasma membrane | 0 | x |
| GNAO2_RAT | P30033 | Guanine nucleotide-binding protein G(o), alpha subunit 2 | 14 | 22 | 23 | | | | | | plasma membrane | 0 | x |
| GNAQ_RAT | P82471 | Guanine nucleotide-binding protein G(q), alpha subunit | 6 | 8 | 9 | | | | | | plasma membrane | 0 | x |
| GNMT_RAT | P13255 | Glycine N-methyltransferase | 1 | 0 | 1 | 32 | 0.0054 | 441.78 | 2+ | MLKYALK + Oxidation (M) | cytoplasm | 0 | |
| GOSR1_RAT | Q62931 | 28 kDa Golgi SNARE protein | 0 | 1 | 1 | 30 | 0.0094 | 551.26 | 2+ | QLENELDLK | Golgi complex | 0 | |
| GPX41_RAT | P36970 | Phospholipid hydroperoxide glutathione peroxidase, mitochondrial | 0 | 1 | 1 | 59 | 1.2e-005 | 661.86 | 2+ | ILAFFPCNQFGR | mitochondria | 1 | |
| GRIA1_RAT | P19490 | Glutamate receptor 1 | 0 | 2 | 2 | | | | | | plasma membrane | 5 | |
| GRIA2_RAT | P19491 | Glutamate receptor 2 | 0 | 2 | 2 | | | | | | plasma membrane | 4 | |
| GRIA3_RAT | P19492 | Glutamate receptor 3 | 0 | 2 | 2 | | | | | | plasma membrane | 4 | |
| GRIA4_RAT | P19493 | Glutamate receptor 4 | 0 | 1 | 1 | 37 | 0.0016 | 590.78 | 2+ | FVIDCEIER | plasma membrane | 5 | |
| GRID2_RAT | Q63226 | Glutamate receptor delta-2 subunit | 5 | 4 | 8 | | | | | | plasma membrane | 4 | |
| GRP78_RAT | P06761 | 78 kDa glucose-regulated protein | 12 | 21 | 24 | | | | | | n.d. | 1 | |
| GSLG1_RAT | Q62638 | Golgi apparatus protein 1 | 5 | 13 | 13 | | | | | | Golgi complex | 2 | |
| GSTM1_RAT | P04905 | Glutathione S-transferase Mu 1 | 0 | 2 | 2 | | | | | | cytoplasm | 0 | |
| GSTM4_RAT | P08009 | Glutathione S-transferase Yb-3 | 0 | 2 | 2 | | | | | | cytoplasm | 0 | |
| GTR1_RAT | P11167 | Solute carrier family 2, facilitated glucose transporter, member 1 | 3 | 3 | 3 | | | | | | plasma membrane | 11 | |
| GTR3_RAT | Q07647 | Solute carrier family 2, facilitated glucose transporter, member 3 | 2 | 2 | 2 | | | | | | plasma membrane | 11 | |
| GTR5_RAT | P43427 | Solute carrier family 2, facilitated glucose transporter, member 5 | 1 | 1 | 1 | 63 | 4.3e-006 | 655.36 | 2+ | TFVEINQIFAK | plasma membrane | 12 | |
| GTR8_RAT | Q9JJZ1 | Solute carrier family 2, facilitated glucose transporter, member 8 | 0 | 1 | 1 | 43 | 0.0004 | 467.92 | 3+ | TLEQITAHFEGR | plasma membrane | 12 | |
| H2A1_RAT | P02262 | Histone H2A.1 | 1 | 1 | 1 | 67 | 2e-006 | 472.83 | 2+ | AGLOFPVGR | nucleus | 1 | |
| H2B_RAT | Q00715 | Histone H2B | 0 | 2 | 2 | | | | | | nucleus | 0 | |
| H2BT_RAT | Q00729 | Histone H2B, testis | 1 | 1 | 1 | 51 | 7.5e-005 | 477.32 | 2+ | LLLPGELAK | nucleus | 0 | |
| H4_RAT | P62804 | Histone H4 | 4 | 5 | 6 | | | | | | nucleus | 0 | |
| HBA_RAT | P01946 | Hemoglobin alpha-1 and alpha-2 chains | 3 | 6 | 6 | | | | | | blood | 0 | |
| HBB1_RAT | P02091 | Hemoglobin beta chain, major-form | 10 | 11 | 12 | | | | | | blood | 0 | |
| HBB2_RAT | P11517 | Hemoglobin beta chain, minor-form | 10 | 10 | 11 | | | | | | blood | 0 | |
| HCK_RAT | P50545 | Tyrosine-protein kinase HCK | 1 | 0 | 1 | 36 | 0.0025 | 446.69 | 2+ | GSLDLFLK | plasma membrane | 0 | x |
| HOMER3_RAT | Q9Z2X5 | Homer protein homolog 3 | 6 | 7 | 10 | | | | | | plasma membrane | 0 | |
| HPCA_RAT | P84076 | Neuron specific calcium-binding protein hippocalcin | 2 | 0 | 2 | | | | | | cytoplasm | 0 | x |
| HPCL1_RAT | P62749 | Hippocalcin-like protein 1 | 2 | 3 | 3 | | | | | | cytoplasm | 0 | x |
| HPLN1_RAT | P03994 | Hyaluronan and proteoglycan link protein 1 | 0 | 1 | 1 | 59 | 1.2e-005 | 500.82 | 2+ | LLVEAEQAK | n.d. | 0 | |
| HS90B_RAT | P34058 | Heat shock protein HSP 90-beta | 2 | 11 | 11 | | | | | | cytoplasm | 0 | |
| HSP47_RAT | P29457 | 47 kDa heat shock protein | 1 | 1 | 2 | | | | | | cytoplasm | 2 | |
| HSP7C_RAT | P63018 | Heat shock cognate 71 kDa protein | 12 | 26 | 27 | | | | | | cytoplasm | 0 | |
| HSPB1_RAT | P42930 | Heat-shock protein beta-1 | 0 | 1 | 1 | 49 | 0.00013 | 538.23 | 2+ | QLSSGVSEIR | cytoskeleton | 0 | |
| HXK1_RAT | P05708 | Hexokinase, type I | 0 | 2 | 2 | | | | | | cytoplasm | 0 | |
| HYEP_RAT | P07687 | Epoxide hydrolase 1 | 0 | 1 | 1 | 37 | 0.0018 | 505.25 | 2+ | IIPLLTDPK | microsome | 1 | |
| I2C2_RAT | Q9QZ81 | Eukaryotic translation initiation factor 2C 2 | 0 | 1 | 1 | 35 | 0.003 | 507.72 | 2+ | QCTEVHLK | plasma membrane | 0 | |
| ICAM1_RAT | Q00238 | Intercellular adhesion molecule-1 | 1 | 2 | 2 | | | | | | plasma membrane | 2 | |
| ICMT_RAT | Q9VVM4 | Protein-S-isoprenylcysteine O-methyltransferase | 0 | 1 | 1 | 36 | 0.0022 | 486.21 | 2+ | VPTGLPFIK | endoplasmic reticulum | 2 | |
| INIB_RAT | P26376 | Interferon-inducible protein | 0 | 2 | 2 | | | | | | n.d. | 2 | |
| IRK10_RAT | P49655 | ATP-sensitive inward rectifier potassium channel 10 | 0 | 1 | 1 | 87 | 1.8e-008 | 765.91 | 2+ | YVADFSLFDQVVK | plasma membrane | 3 | |
| IRK13_RAT | Q70617 | Inward rectifier potassium channel 13 | 3 | 3 | 4 | | | | | | plasma membrane | 2 | |
| ITB1_RAT | P49134 | Integrin beta-1 | 4 | 9 | 10 | | | | | | plasma membrane | 2 | |
| ITPR1_RAT | P29994 | Inositol 1,4,5-trisphosphate receptor type 1 | 6 | 15 | 18 | | | | | | endoplasmic reticulum | 1 | |
| ITPR2_RAT | P29995 | Inositol 1,4,5-trisphosphate receptor type 2 | 1 | 1 | 1 | 47 | 0.00016 | 628.73 | 2+ | TTCFCGLER | endoplasmic reticulum | 10 | |
| K6PF_RAT | P47858 | 6-phosphofructokinase, muscle type | 1 | 8 | 9 | | | | | | cytoplasm | 0 | |
| K6FP_RAT | P47860 | 6-phosphofructokinase, type C | 2 | 1 | 3 | | | | | | cytoplasm | 1 | |
| KAP0_RAT | P03456 | cAMP-dependent protein kinase type I-alpha regulatory subunit | 0 | 1 | 1 | 51 | 4.7e-005 | 492.36 | 3+ | VSILESCLKWER | cytoplasm | 0 | |
| KAP2_RAT | P12368 | cAMP-dependent protein kinase type II-alpha regulatory subunit | 0 | 1 | 1 | 58 | 1.4e-005 | 505.21 | 2+ | GTVDILVTK | cytoplasm | 0 | |
| KAPCB_RAT | P68182 | cAMP-dependent protein kinase, beta-catalytic subunit | 0 | 1 | 1 | 31 | 0.0042 | 662.71 | 3+ | KWENPPPSNAGLEDFER | cytoplasm | 0 | x |
| KCC2A_RAT | P11275 | Calcium/calmodulin-dependent protein kinase type II alpha chain | 4 | 5 | 8 | | | | | | cytoplasm | 1 | |
| KCC2B_RAT | P08413 | Calcium/calmodulin-dependent protein kinase type II beta chain | 0 | 8 | 8 | | | | | | cytoplasm | 1 | |
| KCC2D_RAT | P15791 | Calcium/calmodulin-dependent protein kinase type II delta chain | 0 | 2 | 2 | | | | | | cytoplasm | 1 | |
| KCNA1_RAT | P10499 | Potassium voltage-gated channel subfamily A member 1 | 0 | 3 | 3 | | | | | | plasma membrane | 6 | |
| KCNC3_RAT | Q01956 | Potassium voltage-gated channel subfamily C member 3 | 0 | 2 | 2 | | | | | | plasma membrane | 7 | |
| KCND2_RAT | Q63881 | Potassium voltage-gated channel subfamily D member 2 | 0 | 1 | 1 | 31 | 0.006 | 662.30 | 2+ | FQTWQDTLER | plasma membrane | 7 | |
| KCRB_RAT | P07335 | Creatine kinase, B chain | 11 | 10 | 13 | | | | | | cytoplasm | 0 | |
| KCRU_RAT | P25809 | Creatine kinase, ubiquitous mitochondrial | 0 | 1 | 1 | 29 | 0.014 | 500.79 | 2+ | VVVDALSGLK | cytoplasm | 0 | |
| KIF5C_RAT | P56536 | Kinesin heavy chain isoform 5C | 0 | 1 | 1 | 36 | 0.0021 | 638.85 | 2+ | VSYFEIYLDK | cytoskeleton | 0 | |
| KPCA_RAT | P05696 | Protein kinase C, alpha type | 1 | 0 | 1 | 52 | 6.2e-005 | 487.73 | 2+ | LGGCPGEGR | cytoplasm | 0 | |
| KPCB_RAT | P68403 | Protein kinase C, beta type | 0 | 1 | 1 | 30 | 0.011 | 440.25 | 2+ | AGVDGWFK | cytoplasm | 0 | |

| | | | | | | | | | | | | | | | | | | | | | | | | | | |
|-----------|--------|---|---|----|----|--|--|----|----------|--------|----|-------------------------------|--|--|--|--|--|--|--|--|-----------------|-----------------------|----|--|---|--|
| PGRC1_RAT | P70580 | Membrane associated progesterone receptor component 1 | 0 | 2 | 2 | | | | | | | | | | | | | | | | microsome | 1 | | | | |
| PHB_RAT | P67779 | Prohibitin | 6 | 9 | 10 | | | | | | | | | | | | | | | | | cytoplasm | 0 | | | |
| PHOS_RAT | P20942 | Phosducin | 1 | 0 | 1 | | | 87 | 1.8e-008 | 741.42 | 2+ | FSSDVLPTLLVYK | | | | | | | | | plasma membrane | 0 | | | | |
| PHS1_RAT | P09811 | Glycogen phosphorylase, liver form | 2 | 2 | 3 | | | | | | | | | | | | | | | | | cytoplasm | 0 | | | |
| PHS2_RAT | P09812 | Glycogen phosphorylase, muscle form | 0 | 1 | 1 | | | 42 | 0.00033 | 822.05 | 3+ | VIPAADLSEQISTAGTEASGTGNMK | | | | | | | | | | cytoplasm | 0 | | | |
| PHS3_RAT | P53534 | Glycogen phosphorylase, brain form | 3 | 10 | 11 | | | | | | | | | | | | | | | | | cytoplasm | 0 | | | |
| PIGS_RAT | Q5X131 | GPI transamidase component PIG-S | 0 | 2 | 2 | | | | | | | | | | | | | | | | | endoplasmic reticulum | 3 | | | |
| PLLP_RAT | P47987 | Plasmolipin | 0 | 2 | 2 | | | | | | | | | | | | | | | | | plasma membrane | 4 | | | |
| PLM_RAT | Q08589 | Phospholemman | 1 | 1 | 1 | | | 87 | 1.4e-008 | 683.84 | 2+ | TGEPDEEEGTFR | | | | | | | | | | plasma membrane | 2 | | | |
| PPBT_RAT | P08289 | Alkaline phosphatase, tissue-nonspecific isozyme | 2 | 5 | 6 | | | | | | | | | | | | | | | | | plasma membrane | 1 | | x | |
| PPIA_RAT | P10111 | Peptidyl-prolyl cis-trans isomerase A | 4 | 4 | 5 | | | | | | | | | | | | | | | | | n.d. | 0 | | | |
| PRA1_RAT | Q35394 | Prenylated Rab acceptor protein 1 | 1 | 0 | 1 | | | 71 | 6.2e-007 | 772.52 | 2+ | DAEVEGLSATTLLPK | | | | | | | | | | Golgi complex | 2 | | | |
| PRAF3_RAT | Q9ES40 | PRA1 family protein 3 | 3 | 1 | 3 | | | | | | | | | | | | | | | | | n.d. | 4 | | | |
| PRDX1_RAT | Q63716 | Peroxiredoxin 1 | 2 | 3 | 3 | | | | | | | | | | | | | | | | | cytoplasm | 0 | | | |
| PRDX2_RAT | P35704 | Peroxiredoxin 2 | 0 | 3 | 3 | | | | | | | | | | | | | | | | | cytoplasm | 0 | | | |
| PRDX5_RAT | Q9R063 | Peroxiredoxin 5, mitochondrial | 2 | 0 | 2 | | | | | | | | | | | | | | | | | cytoplasm | 0 | | | |
| PRIO_RAT | P13852 | Major onion protein | 1 | 3 | 3 | | | | | | | | | | | | | | | | | plasma membrane | 3 | | x | |
| PROF1_RAT | P62963 | Prolin-1 | 1 | 1 | 1 | | | 57 | 2e-005 | 607.33 | 2+ | DSPSVWAAVPGK | | | | | | | | | | n.d. | 0 | | | |
| PROF2_RAT | Q9EPC6 | Prolin-2 | 1 | 1 | 1 | | | 31 | 0.0079 | 454.79 | 2+ | VLVFMGK + Oxidation (M) | | | | | | | | | | n.d. | 0 | | | |
| FRS6B_RAT | Q63570 | 26S protease regulatory subunit 6B | 0 | 1 | 1 | | | 31 | 0.0084 | 626.26 | 2+ | GVLMYGPPGCGK | | | | | | | | | | cytoplasm | 0 | | | |
| FRS7_RAT | Q63347 | 26S protease regulatory subunit 7 | 1 | 0 | 1 | | | 31 | 0.0086 | 569.29 | 2+ | YVGEGARIVR | | | | | | | | | | cytoplasm | 0 | | | |
| FRS8_RAT | P62198 | 26S protease regulatory subunit 8 | 1 | 0 | 1 | | | 33 | 0.004 | 645.81 | 2+ | LEGSGGDSEVQR | | | | | | | | | | cytoplasm | 0 | | | |
| PSA1_RAT | P18420 | Proteasome subunit alpha type 1 | 0 | 1 | 1 | | | 32 | 0.0059 | 673.36 | 2+ | ETLPAEQDLTKK | | | | | | | | | | cytoplasm | 0 | | | |
| PSD1_RAT | Q98761 | 26S proteasome non-ATPase regulatory subunit 1 | 1 | 0 | 1 | | | 30 | 0.0091 | 588.40 | 2+ | NNNTDLMLK | | | | | | | | | | cytoplasm | 1 | | | |
| PSN1_RAT | P97887 | Presenilin 1 | 0 | 1 | 1 | | | 51 | 3.9e-005 | 677.71 | 3+ | AAVQELSGSILTSDEPEER | | | | | | | | | | Golgi complex | 10 | | | |
| PTN5_RAT | P35234 | Tyrosine-protein phosphatase, non-receptor type 5 | 1 | 1 | 1 | | | 39 | 0.0014 | 436.78 | 2+ | EGVVDILK | | | | | | | | | | cytoplasm | 0 | | | |
| PTPRA_RAT | Q03348 | Receptor-type tyrosine-protein phosphatase alpha | 1 | 0 | 1 | | | 35 | 0.0027 | 598.36 | 2+ | EETVNDFWR | | | | | | | | | | plasma membrane | 2 | | | |
| RAB10_RAT | P35281 | Ras-related protein Rab-10 | 4 | 4 | 4 | | | | | | | | | | | | | | | | | vesicle | 0 | | | |
| RAB14_RAT | P61107 | Ras-related protein Rab-14 | 9 | 12 | 15 | | | | | | | | | | | | | | | | | vesicle | 0 | | | |
| RAB1A_RAT | Q6NBY7 | Ras-related protein Rab-1A | 9 | 8 | 11 | | | | | | | | | | | | | | | | | vesicle | 0 | | | |
| RAB1B_RAT | P10536 | Ras-related protein Rab-1B | 5 | 4 | 5 | | | | | | | | | | | | | | | | | vesicle | 0 | | | |
| RAB2A_RAT | P05712 | Ras-related protein Rab-2A | 9 | 6 | 9 | | | | | | | | | | | | | | | | | vesicle | 0 | | | |
| RAB3A_RAT | P63012 | Ras-related protein Rab-3A | 6 | 10 | 11 | | | | | | | | | | | | | | | | | synaptic vesicle | 0 | | | |
| RAB3B_RAT | Q63941 | Ras-related protein Rab-3B | 0 | 1 | 1 | | | 71 | 4.6e-007 | 854.46 | 2+ | TYSWDNAQVILVGNK | | | | | | | | | | synaptic vesicle | 0 | | | |
| RAB3C_RAT | P62824 | Ras-related protein Rab-3C | 0 | 1 | 1 | | | 39 | 0.0011 | 790.31 | 2+ | MSESLTDPAITAAK | | | | | | | | | | vesicle | 0 | | | |
| RAB3D_RAT | Q63942 | GTP-binding protein Rab-3D | 0 | 2 | 2 | | | | | | | | | | | | | | | | | vesicle | 0 | | | |
| RAB6A_RAT | Q9WVB1 | Ras-related protein Rab-6A | 5 | 9 | 11 | | | | | | | | | | | | | | | | | vesicle | 0 | | | |
| RAB7_RAT | P09527 | Ras-related protein Rab-7 | 9 | 11 | 13 | | | | | | | | | | | | | | | | | vesicle | 0 | | | |
| RAB8B_RAT | P70550 | Ras-related protein Rab-8B | 2 | 5 | 5 | | | | | | | | | | | | | | | | | vesicle | 0 | | | |
| RABE1_RAT | Q35550 | Rab GTPase binding effector protein 1 | 1 | 2 | 2 | | | | | | | | | | | | | | | | | vesicle | 0 | | | |
| RAC1_RAT | Q6RUV5 | Ras-related C3 botulinum toxin substrate 1 | 6 | 8 | 8 | | | | | | | | | | | | | | | | | plasma membrane | 0 | | | |
| RALA_RAT | P63322 | Ras-related protein Ral-A | 5 | 7 | 9 | | | | | | | | | | | | | | | | | vesicle | 0 | | | |
| RALB_RAT | P36860 | Ras-related protein Ral-B | 0 | 4 | 4 | | | | | | | | | | | | | | | | | n.d. | 0 | | | |
| RAP1A_RAT | P62836 | Ras-related protein Rap-1A | 4 | 4 | 5 | | | | | | | | | | | | | | | | | plasma membrane | 0 | | | |
| RAP1B_RAT | Q62636 | Ras-related protein Rap-1b | 3 | 0 | 3 | | | | | | | | | | | | | | | | | vesicle | 0 | | | |
| RAP2B_RAT | P61227 | Ras-related protein Rap-2b | 2 | 3 | 3 | | | | | | | | | | | | | | | | | vesicle | 0 | | | |
| RASH_RAT | P20171 | Transforming protein p21/H-Ras-1 | 0 | 2 | 2 | | | | | | | | | | | | | | | | | n.d. | 0 | | | |
| RASK_RAT | P08644 | Transforming protein p21 | 0 | 2 | 2 | | | | | | | | | | | | | | | | | n.d. | 0 | | | |
| RASM_RAT | P97538 | Ras-related protein M-Ras | 0 | 1 | 1 | | | 75 | 1.8e-007 | 957.97 | 2+ | IFVDPDYDPTIEDSYLK | | | | | | | | | | n.d. | 0 | | | |
| RB11A_RAT | P62494 | Ras-related protein Rab-11A | 0 | 8 | 8 | | | | | | | | | | | | | | | | | plasma membrane | 0 | | | |
| RB11B_RAT | Q35509 | Ras-related protein Rab-11B | 9 | 0 | 9 | | | | | | | | | | | | | | | | | vesicle | 0 | | | |
| RED2_RAT | P97616 | Double-stranded RNA-specific endonuclease B2 | 0 | 1 | 1 | | | 30 | 0.012 | 467.17 | 2+ | TLAGIVMTK | | | | | | | | | | nucleus | 0 | | | |
| RENBP_RAT | P51607 | N-acetylglucosamine 2-epimerase | 0 | 1 | 1 | | | 29 | 0.018 | 429.79 | 2+ | VELLDAK | | | | | | | | | | n.d. | 0 | | | |
| RGS7_RAT | P49803 | Regulator of G-protein signaling 7 | 0 | 1 | 1 | | | 65 | 2.7e-006 | 729.38 | 2+ | FLESEFSSENLR | | | | | | | | | | synaptic vesicle | 0 | | | |
| RHEB_RAT | Q62639 | GTP-binding protein Rheb | 0 | 1 | 1 | | | 43 | 0.00047 | 589.78 | 2+ | ENQTAVDVFR | | | | | | | | | | n.d. | 0 | | | |
| RHOA_RAT | P61589 | Transforming protein RhoA | 3 | 8 | 9 | | | | | | | | | | | | | | | | | plasma membrane | 0 | | | |
| RHOB_RAT | P62747 | Rho-related GTP-binding protein RhoB | 0 | 2 | 2 | | | | | | | | | | | | | | | | | plasma membrane | 0 | | | |
| RIB1_RAT | P07153 | Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 67 kDa subunit | 4 | 12 | 13 | | | | | | | | | | | | | | | | | endoplasmic reticulum | 2 | | | |
| RIB2_RAT | P25235 | Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 63 kDa subunit | 3 | 8 | 8 | | | | | | | | | | | | | | | | | endoplasmic reticulum | 3 | | | |
| RL11_RAT | P62914 | 60S ribosomal protein L11 | 0 | 1 | 1 | | | 52 | 6.8e-005 | 488.25 | 2+ | YDGIILPGK | | | | | | | | | | cytoplasm | 0 | | | |
| RL12_RAT | P23358 | 60S ribosomal protein L12 | 1 | 0 | 1 | | | 46 | 0.00021 | 441.40 | 2+ | IGPLGLSPK | | | | | | | | | | cytoplasm | 0 | | | |
| RL13_RAT | P41123 | 60S ribosomal protein L13 | 0 | 3 | 3 | | | | | | | | | | | | | | | | | cytoplasm | 0 | | | |
| RL13A_RAT | P35427 | 60S ribosomal protein L13a | 0 | 1 | 1 | | | 59 | 1.2e-005 | 626.81 | 2+ | YQAVTATLEEK | | | | | | | | | | cytoplasm | 0 | | | |
| RL14_RAT | Q63507 | 60S ribosomal protein L14 | 0 | 1 | 1 | | | 86 | 1.9e-008 | 677.86 | 2+ | LVAIVDIVQNR | | | | | | | | | | cytoplasm | 0 | | | |
| RL18_RAT | P12001 | 60S ribosomal protein L18 | 1 | 0 | 3 | | | | | | | | | | | | | | | | | cytoplasm | 0 | | | |
| RL18A_RAT | P62718 | 60S ribosomal protein L18a | 0 | 3 | 3 | | | | | | | | | | | | | | | | | cytoplasm | 0 | | | |
| RL19_RAT | P84100 | 60S ribosomal protein L19 | 0 | 1 | 1 | | | 30 | 0.013 | 453.22 | 2+ | NFGIWLK | | | | | | | | | | cytoplasm | 0 | | | |
| RL21_RAT | P20280 | 60S ribosomal protein L21 | 0 | 1 | 1 | | | 75 | 3.5e-007 | 493.80 | 2+ | LLADQAEAR | | | | | | | | | | cytoplasm | 0 | | | |
| RL23_RAT | P62832 | 60S ribosomal protein L23 | 0 | 1 | 1 | | | 49 | 8e-005 | 552.26 | 3+ | YVNVTOHAVGIIVNK | | | | | | | | | | cytoplasm | 0 | | | |
| RL23A_RAT | P62752 | 60S ribosomal protein L23a | 1 | 0 | 3 | | | 33 | 0.0053 | 450.83 | 2+ | GSAITGPVAK | | | | | | | | | | cytoplasm | 0 | | | |
| RL24_RAT | P83732 | 60S ribosomal protein L24 | 0 | 1 | 1 | | | | | | | | | | | | | | | | | cytoplasm | 0 | | | |
| RL26_RAT | P12749 | 60S ribosomal protein L26 | 0 | 1 | 1 | | | 79 | 1.1e-007 | 639.32 | 2+ | AITGASLADIMAK + Oxidation (M) | | | | | | | | | | cytoplasm | 0 | | | |
| RL27_RAT | P61354 | 60S ribosomal protein L27 | 1 | 1 | 1 | | | 36 | 0.0021 | 478.19 | 2+ | YVYIER | | | | | | | | | | cytoplasm | 0 | | | |
| RL31_RAT | P62902 | 60S ribosomal protein L31 | 1 | 1 | 1 | | | 56 | 2.4e-005 | 525.25 | 2+ | YSVDIPLDK | | | | | | | | | | cytoplasm | 0 | | | |
| RL32_RAT | P62912 | 60S ribosomal protein L32 | 1 | 1 | 1 | | | 61 | 9.3e-006 | 494.75 | 2+ | SAINVVVTR | | | | | | | | | | cytoplasm | 0 | | | |
| RL34_RAT | P11250 | 60S ribosomal protein L34 | 1 | 0 | 2 | | | 44 | 0.0004 | 489.28 | 3+ | SYCAEIAHVSSK | | | | | | | | | | cytoplasm | 0 | | | |
| RL35_RAT | P17078 | 60S ribosomal protein L35 | 1 | 1 | 1 | | | 51 | 7.2e-005 | 572.31 | 2+ | VLTVINQTK | | | | | | | | | | cytoplasm | 0 | | | |

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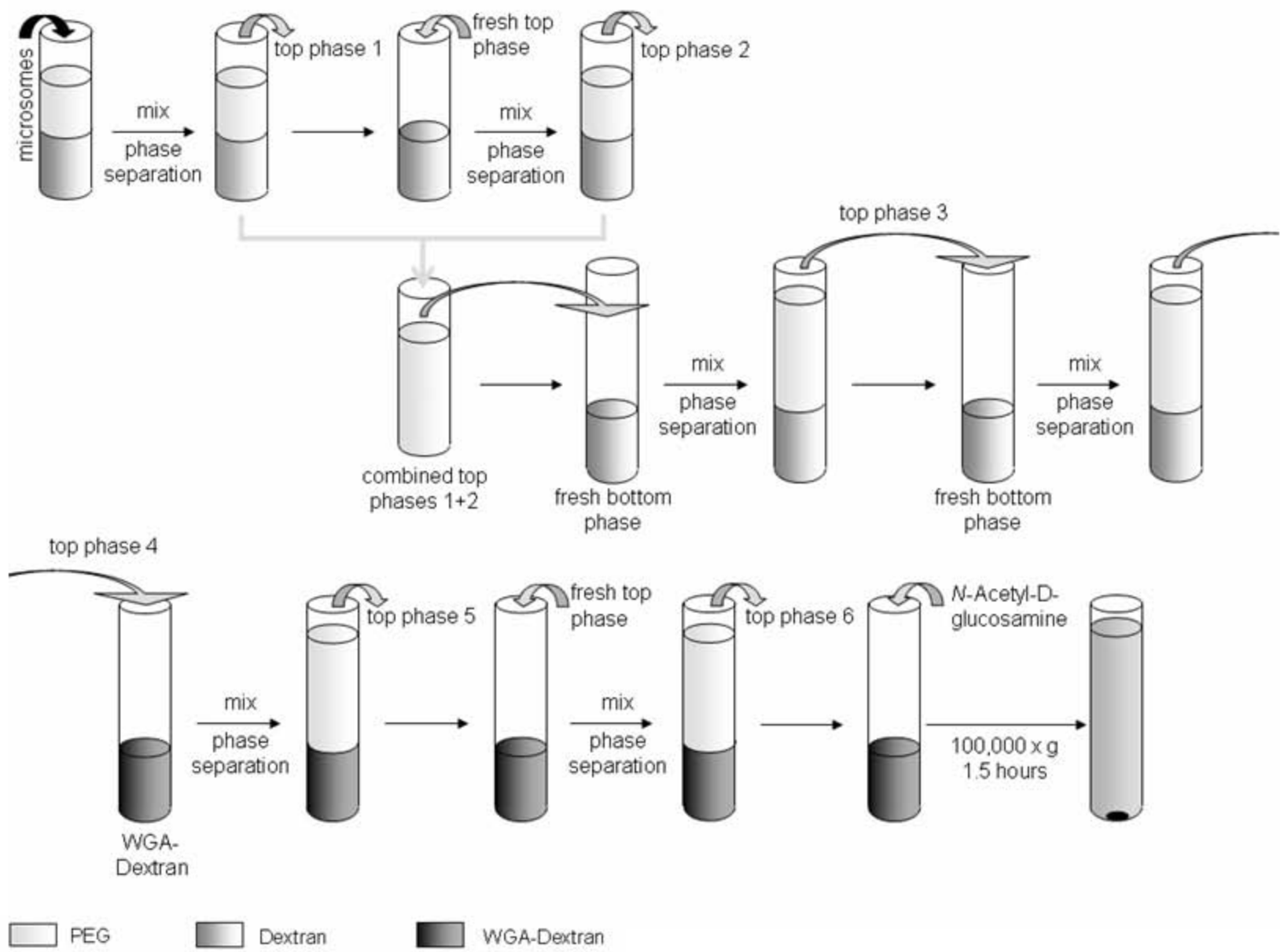


Fig.1 Schindler et al.

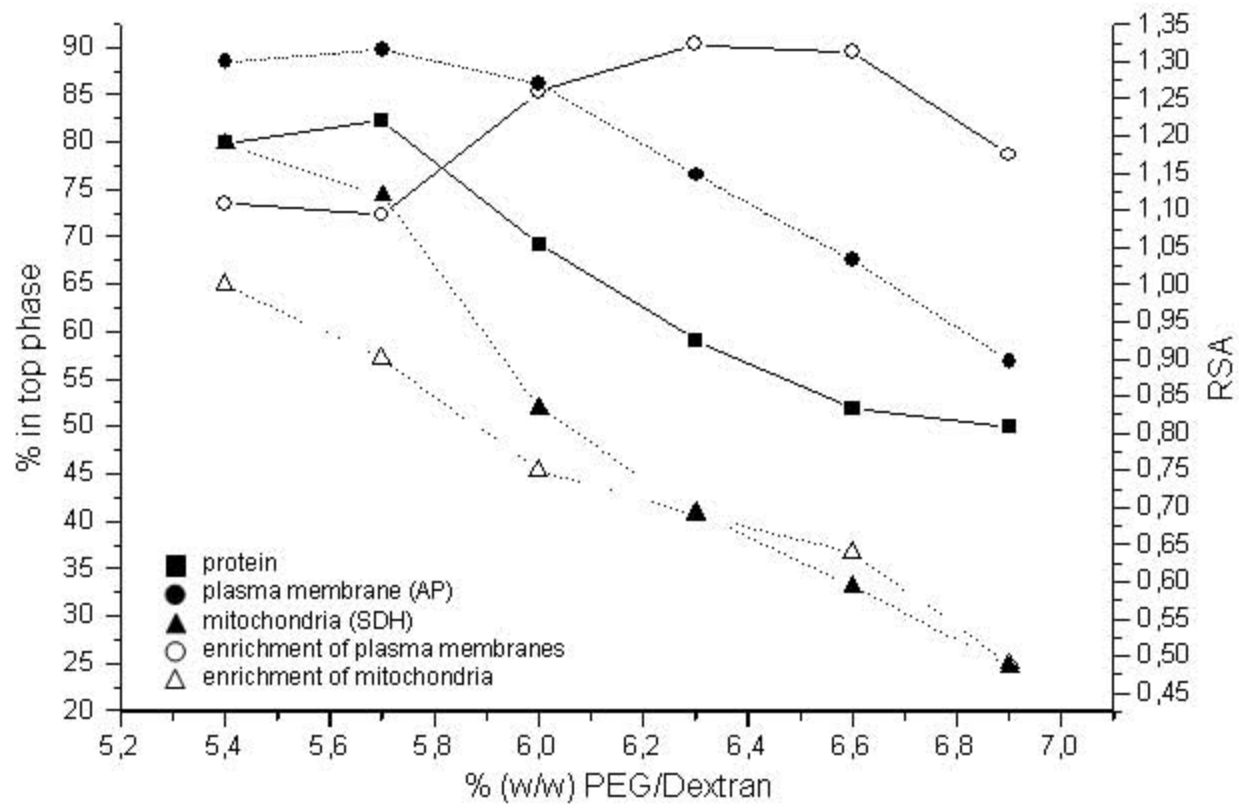


Fig.2 Schindler et al.

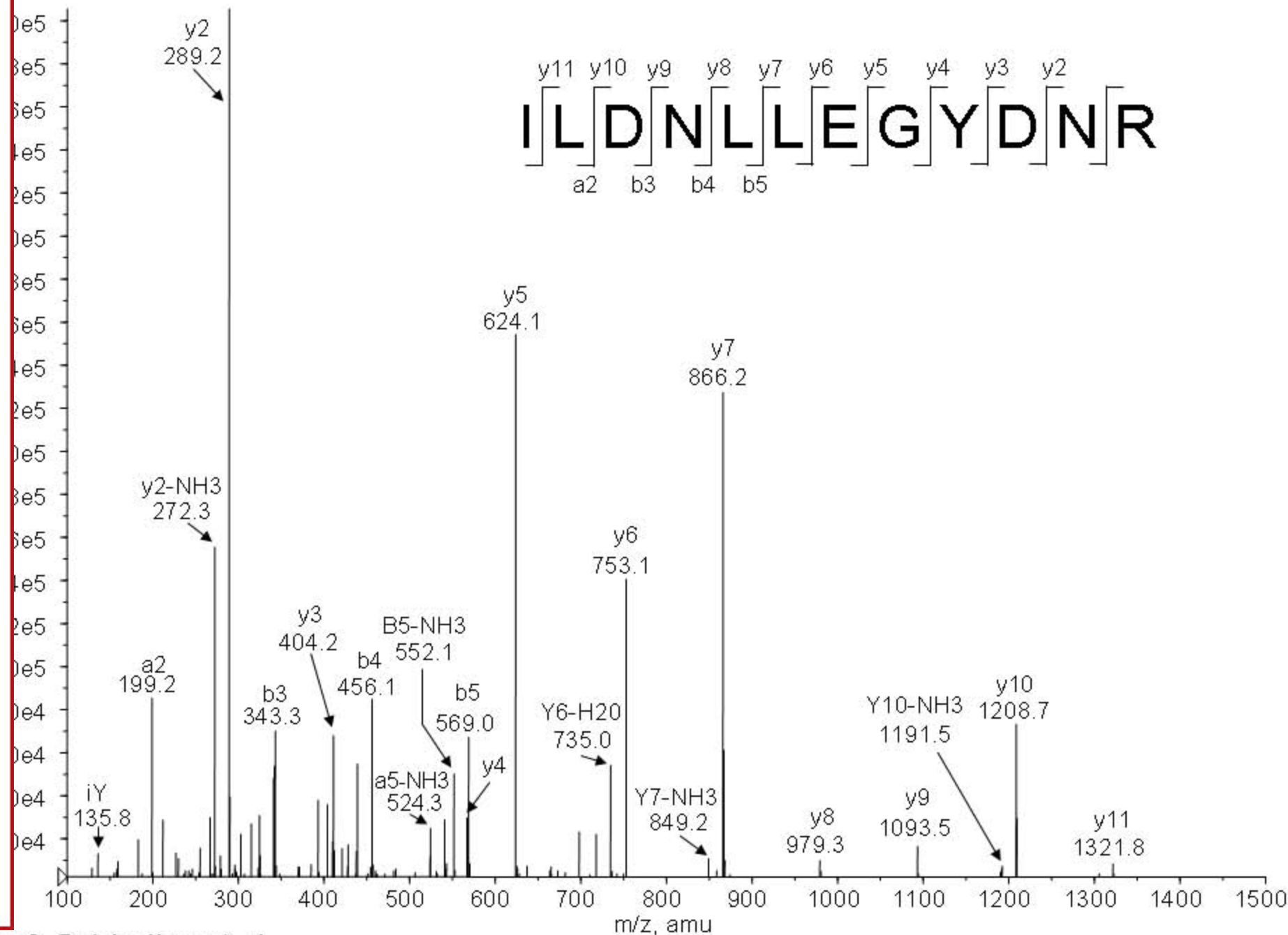


Fig.3 Schindler et al.

| Entrz Name | Acc.no. | protein name | # pept. in 50 µg gel | # pept. in 30 µg gel | # pept. in both gels | Score | Expect | m/z | charge | sequence | subcell location | TMH | GPI-anchor | myristoylation |
|------------|---------|--|----------------------|----------------------|----------------------|-------|----------|--------|--------|---------------------|-----------------------|-----|------------|----------------|
| 1433B_RAT | P35213 | 14-3-3 protein beta/alpha | 2 | 2 | 2 | | | | | | n.d. | 0 | | |
| 1433E_RAT | P62260 | 14-3-3 protein epsilon | 3 | 8 | 9 | | | | | | n.d. | 0 | | |
| 1433G_RAT | P61983 | 14-3-3 protein gamma | 0 | 1 | 1 | 51 | 7.5e-005 | 540.79 | 2+ | YLAEVATGKEK | n.d. | 0 | | |
| 1433T_RAT | P68255 | 14-3-3 protein tau | 1 | 1 | 1 | 67 | 8.9e-007 | 715.76 | 3+ | TAFDEAIAELDTLNEDSYK | n.d. | 0 | | |
| 1433Z_RAT | P63102 | 14-3-3 protein zeta/delta | 3 | 5 | 6 | | | | | | n.d. | 0 | | |
| 5NTD_RAT | P21588 | 5'-nucleotidase | 4 | 8 | 9 | | | | | | plasma membrane | 2 | x | |
| A4_RAT | P08592 | Amyloid beta A4 protein | 2 | 2 | 4 | | | | | | plasma membrane | 2 | | |
| AAA1_RAT | P63116 | Asc-type amino acid transporter 1 | 0 | 1 | 1 | 36 | 0.0024 | 436.22 | 2+ | FTESMTR | plasma membrane | 12 | | |
| AA1C_RAT | P13221 | Aspartate aminotransferase, cytoplasmic | 0 | 1 | 1 | 65 | 3.1e-006 | 443.78 | 3+ | VGNLTVVGK | cytoplasm | 0 | | |
| AA1M_RAT | P00507 | Aspartate aminotransferase, mitochondrial | 0 | 2 | 2 | | | | | | mitochondria | 0 | | |
| ACE_RAT | P47820 | Angiotensin-converting enzyme, somatic isoform | 20 | 24 | 26 | | | | | | plasma membrane | 2 | | |
| ACON_RAT | Q9ER34 | Aconitate hydratase, mitochondrial | 0 | 1 | 1 | 34 | 0.0034 | 493.20 | 2+ | EGWPLDIR | mitochondria | 0 | | |
| ACSL1_RAT | P18163 | Long-chain-fatty-acid-CoA ligase 1 | 0 | 2 | 2 | | | | | | mitochondria | 0 | | |
| ACTA_RAT | P62738 | Actin, aortic smooth muscle | 6 | 18 | 13 | | | | | | cytoskeleton | 0 | | |
| ACTB_RAT | P60711 | Actin, cytoplasmic 1 | 13 | 18 | 20 | | | | | | cytoskeleton | 0 | | |
| ACTC_RAT | P63035 | Actin, alpha cardiac | 6 | 6 | 8 | | | | | | cytoskeleton | 0 | | |
| ADT1_RAT | Q03962 | ADP-ATP carrier protein 1 | 10 | 13 | 14 | | | | | | mitochondria | 0 | | |
| ADT2_RAT | Q09073 | ADP-ATP carrier protein 2 | 5 | 13 | 13 | | | | | | mitochondria | 0 | | |
| AL3A2_RAT | P30839 | Fatty aldehyde dehydrogenase | 5 | 4 | 5 | | | | | | microsome | 1 | | |
| ALBU_RAT | P02770 | Serum albumin | 5 | 6 | 7 | | | | | | blood | 1 | | |
| ALDOA_RAT | P05065 | Fructose-bisphosphate aldolase A | 5 | 6 | 8 | | | | | | cytoplasm | 0 | | |
| ALDOC_RAT | P09117 | Fructose-bisphosphate aldolase C | 8 | 10 | 13 | | | | | | cytoplasm | 0 | | |
| AMPN_RAT | P15684 | Aminopeptidase N | 3 | 11 | 13 | | | | | | plasma membrane | 1 | | |
| ANXA3_RAT | P14669 | Annexin A3 | 2 | 5 | 5 | | | | | | n.d. | 0 | | |
| ANXA5_RAT | P14668 | Annexin A5 | 1 | 2 | 3 | | | | | | n.d. | 0 | | |
| ANXA6_RAT | P48037 | Annexin A6 | 1 | 1 | 2 | | | | | | n.d. | 0 | | |
| AOFA_RAT | P21396 | Amine oxidase [flavin-containing] A | 1 | 0 | 1 | 30 | 0.0067 | 604.28 | 2+ | IFSVTNGGQER | mitochondria | 1 | | |
| AP180_RAT | Q05140 | Clathrin coat assembly protein AP180 | 0 | 1 | 1 | 51 | 6.8e-005 | 713.45 | 2+ | NTLFNLSNFLDK | plasma membrane | 1 | | |
| AP2A2_RAT | P18484 | Adapter-related protein complex 2 alpha 2 subunit | 0 | 3 | 3 | | | | | | plasma membrane | 1 | | |
| AP2M1_RAT | P84092 | Clathrin coat assembly protein AP50 | 0 | 1 | 1 | 36 | 0.0027 | 429.23 | 2+ | SPVTNIAR | plasma membrane | 1 | | |
| AP2S1_RAT | P62744 | Clathrin coat assembly protein AP17 | 0 | 1 | 1 | 40 | 0.0012 | 452.29 | 2+ | FILIQNR | plasma membrane | 0 | | |
| APLP2_RAT | P15943 | Amyloid-like protein 2 | 2 | 4 | 5 | | | | | | plasma membrane | 3 | | |
| APOE_RAT | P02650 | Apolipoprotein E | 7 | 11 | 12 | | | | | | secretory | 0 | | |
| AQP1_RAT | P29975 | Aquaporin-CHIP | 3 | 4 | 4 | | | | | | plasma membrane | 7 | | |
| AQP4_RAT | P47863 | Aquaporin 4 | 7 | 6 | 9 | | | | | | plasma membrane | 6 | | |
| ARF1_RAT | P84079 | ADP-ribosylation factor 1 | 4 | 6 | 7 | | | | | | Golgi complex | 0 | | |
| ARF4_RAT | P61751 | ADP-ribosylation factor 4 | 0 | 2 | 2 | | | | | | Golgi complex | 0 | | x |
| ARF6_RAT | P62332 | ADP-ribosylation factor 6 | 0 | 3 | 3 | | | | | | Golgi complex | 0 | | x |
| ARG1_RAT | P07824 | Arginase 1 | 1 | 0 | 1 | 44 | 0.00042 | 429.35 | 2+ | AGLVEKLK | cytoplasm | 0 | | |
| ASSY_RAT | P09034 | Argininosuccinate synthase | 0 | 1 | 1 | 36 | 0.0036 | 429.79 | 2+ | IDIVENR | cytoplasm | 0 | | |
| AT1A1_RAT | P06685 | Sodium/potassium-transporting ATPase alpha-1 chain | 38 | 41 | 50 | | | | | | plasma membrane | 8 | | |
| AT1A2_RAT | P06686 | Sodium/potassium-transporting ATPase alpha-2 chain | 55 | 56 | 65 | | | | | | plasma membrane | 9 | | |
| AT1A3_RAT | P06687 | Sodium/potassium-transporting ATPase alpha-3 chain | 45 | 48 | 56 | | | | | | plasma membrane | 8 | | |
| AT1B1_RAT | P07340 | Sodium/potassium-transporting ATPase beta-1 chain | 11 | 16 | 19 | | | | | | plasma membrane | 1 | | |
| AT1B2_RAT | P13638 | Sodium/potassium-transporting ATPase beta-2 chain | 5 | 9 | 11 | | | | | | plasma membrane | 1 | | |
| AT1B3_RAT | Q63377 | Sodium/potassium-transporting ATPase beta-3 chain | 3 | 5 | 5 | | | | | | plasma membrane | 1 | | |
| AT2A1_RAT | Q64578 | Sarcoplasmic/endoplasmic reticulum calcium ATPase 1 | 3 | 5 | 7 | | | | | | endoplasmic reticulum | 8 | | |
| AT2A2_RAT | P11507 | Sarcoplasmic/endoplasmic reticulum calcium ATPase 2 | 9 | 18 | 23 | | | | | | endoplasmic reticulum | 11 | | |
| AT2B1_RAT | P11505 | Plasma membrane calcium-transporting ATPase 1 | 10 | 9 | 14 | | | | | | plasma membrane | 10 | | |
| AT2B2_RAT | P11506 | Plasma membrane calcium-transporting ATPase 2 | 22 | 30 | 38 | | | | | | plasma membrane | 9 | | |
| AT2B3_RAT | Q64568 | Plasma membrane calcium-transporting ATPase 3 | 15 | 20 | 25 | | | | | | plasma membrane | 11 | | |
| AT2B4_RAT | Q64542 | Plasma membrane calcium-transporting ATPase 4 | 0 | 3 | 3 | | | | | | plasma membrane | 10 | | |
| AT5F1_RAT | P19511 | ATP synthase B chain, mitochondrial | 5 | 8 | 8 | | | | | | mitochondria | 1 | | |
| ATP5H_RAT | P31399 | ATP synthase D chain, mitochondrial | 5 | 5 | 7 | | | | | | mitochondria | 0 | | |
| ATP5I_RAT | P29419 | ATP synthase e chain, mitochondrial | 3 | 4 | 4 | | | | | | mitochondria | 0 | | |
| ATP8_RAT | P11608 | ATP synthase protein 8 | 2 | 0 | 2 | | | | | | mitochondria | 1 | | |
| ATPA_RAT | P15999 | ATP synthase alpha chain, mitochondrial | 7 | 12 | 13 | | | | | | mitochondria | 0 | | |
| ATPB_RAT | P10719 | ATP synthase beta chain, mitochondrial | 4 | 10 | 11 | | | | | | mitochondria | 0 | | |
| ATPG_RAT | P35435 | ATP synthase gamma chain, mitochondrial | 1 | 2 | 3 | | | | | | mitochondria | 0 | | |
| ATPO_RAT | Q06647 | ATP synthase oligomycin sensitivity conferral protein, mitochondrial | 1 | 4 | 4 | | | | | | mitochondria | 0 | | |
| ATRN_RAT | Q99J96 | Attractin | 0 | 1 | 1 | 31 | 0.0066 | 534.67 | 3+ | MVAAAAAAATEARLR | plasma membrane | 6 | | |
| B3A2_RAT | P23347 | Anion exchange protein 2 | 0 | 1 | 1 | 33 | 0.0048 | 639.81 | 2+ | FEELQEAGSR | plasma membrane | 15 | | |
| B3A1T_RAT | P23362 | Band 3 anion transport protein | 7 | 9 | 9 | | | | | | plasma membrane | 15 | | |
| BAG1_RAT | P28463 | Basigin | 7 | 6 | 11 | | | | | | plasma membrane | 2 | | |
| BASP_RAT | Q05175 | Brain acid soluble protein 1 | 2 | 3 | 3 | | | | | | plasma membrane | 5 | | x |
| BR44_RAT | P38718 | Brain protein 44 | 0 | 3 | 3 | | | | | | n.d. | 0 | | |
| C11C_RAT | P27653 | C-1-tetrahydrofolate synthase, cytoplasmic | 1 | 0 | 1 | 42 | 0.00053 | 595.31 | 2+ | DVDGLTSLNAGK | cytoplasm | 0 | | |
| CAC2D_RAT | P54290 | Dihydropyridine-sensitive L-type, calcium channel alpha-2/delta subunits | 0 | 1 | 1 | 34 | 0.0032 | 690.88 | 2+ | IIMLFDTGGEER | plasma membrane | 3 | | |
| CADH2_RAT | Q921Y3 | Neural-cadherin | 0 | 2 | 2 | | | | | | plasma membrane | 2 | | |
| CAH4_RAT | P48284 | Carbonic anhydrase IV | 5 | 8 | 10 | | | | | | plasma membrane | 1 | x | |
| CALM_RAT | P62161 | Calmodulin | 5 | 3 | 5 | | | | | | cytoplasm | 0 | | |
| CALX_RAT | P35565 | Calnexin | 11 | 14 | 17 | | | | | | endoplasmic reticulum | 2 | | |
| CAP1_RAT | Q08163 | Adenylyl cyclase-associated protein 1 | 0 | 2 | 2 | | | | | | plasma membrane | 0 | | |
| CAV1_RAT | P41350 | Caveolin-1 | 2 | 0 | 2 | | | | | | plasma membrane | 1 | | |
| CD14_RAT | Q63691 | Monocyte differentiation antigen CD14 | 0 | 1 | 1 | 75 | 2.9e-007 | 521.62 | 3+ | VPLQALDLSHNSLR | plasma membrane | 0 | | |
| CD166_RAT | Q35112 | CD166 antigen | 9 | 17 | 19 | | | | | | plasma membrane | 2 | | |

| | | | | | | | | | | | | | | | | |
|-----------|--------|--|----|----|----|--|----|----------|--------|----|-------------------------------|-----------------------|----|--|---|---|
| CD36_RAT | Q07969 | Platelet glycoprotein IV | 0 | 1 | 1 | | 55 | 2.5e-005 | 461.79 | 2+ | VAIDITYK | plasma membrane | 2 | | | |
| CD38_RAT | Q64244 | ADP-ribosyl cyclase 1 | 2 | 2 | 3 | | | | | | | plasma membrane | 1 | | | |
| CD44_RAT | P26051 | CD44 antigen | 0 | 1 | 1 | | 71 | 7.2e-007 | 462.90 | 3+ | YGFIEGHVVIPR | plasma membrane | 3 | | | |
| CD59_RAT | P27274 | CD59 glycoprotein | 5 | 4 | 5 | | | | | | | plasma membrane | 2 | | x | |
| CD81_RAT | Q62745 | CD81 antigen | 4 | 4 | 4 | | | | | | | plasma membrane | 4 | | | |
| CD82_RAT | O70352 | CD82 antigen | 1 | 3 | 3 | | | | | | | plasma membrane | 4 | | | |
| CD9_RAT | P40241 | CD9 antigen | 3 | 3 | 4 | | | | | | | plasma membrane | 4 | | | |
| CDIPT_RAT | P70500 | CDP-diacylglycerol-inositol 3-phosphatidyltransferase | 4 | 5 | 6 | | | | | | | plasma membrane | 5 | | | |
| CERU_RAT | P13635 | Ceruloplasmin | 5 | 7 | 11 | | | | | | | cytoplasm | 1 | | | |
| CGT_RAT | Q09426 | 2-hydroxyacyl sphingosine 1-beta-galactosyltransferase | 1 | 0 | 1 | | 30 | 0.01 | 481.65 | 2+ | VINNPSYR | n.d. | 3 | | | |
| CH10_RAT | P26772 | 10 kDa heat shock protein, mitochondrial | 1 | 0 | 1 | | 42 | 0.0006 | 538.85 | 2+ | VLLPEYGGTK | mitochondria | 0 | | | |
| CH60_RAT | P63039 | 60 kDa heat shock protein, mitochondrial | 1 | 1 | 2 | | | | | | | mitochondria | 0 | | | |
| CHP1_RAT | P61023 | Calcium-binding protein p22 | 2 | 4 | 5 | | | | | | | cytoplasm | 0 | | | x |
| CHST3_RAT | Q902L2 | Carbohydrate sulfotransferase 3 | 1 | 1 | 1 | | 34 | 0.0053 | 430.28 | 2+ | ENKIISR | Golgi complex | 1 | | | |
| CLD11_RAT | Q99P82 | Claudin-11 | 1 | 1 | 1 | | 72 | 4.6e-007 | 506.94 | 3+ | FYSSGSSSPTHAK | plasma membrane | 5 | | | |
| CLH_RAT | P11442 | Claudin heavy chain | 4 | 19 | 20 | | | | | | | vesicle | 0 | | | |
| CLIC6_RAT | Q811Q2 | Chloride intracellular channel 6 | 1 | 1 | 1 | | | | | | | plasma membrane | 0 | | | |
| CN37_RAT | P13233 | 2',3'-cyclic-nucleotide 3'-phosphodiesterase | 19 | 20 | 24 | | 29 | 0.013 | 594.78 | 2+ | APDGLDGEAAK | plasma membrane | 0 | | | |
| CNTN1_RAT | Q63198 | Contactin 1 | 40 | 36 | 51 | | | | | | | plasma membrane | 2 | | x | |
| CNTN2_RAT | P22063 | Contactin 2 | 5 | 6 | 9 | | | | | | | plasma membrane | 1 | | | |
| CNTP1_RAT | P97846 | Contactin associated protein 1 | 1 | 4 | 4 | | | | | | | plasma membrane | 3 | | | |
| COF1_RAT | P45592 | Cofilin, non-muscle isoform | 3 | 2 | 4 | | | | | | | cytoplasm | 0 | | | |
| COX2_RAT | P00406 | Cytochrome c oxidase subunit 2 | 3 | 5 | 6 | | | | | | | mitochondria | 2 | | | |
| COX41_RAT | P10888 | Cytochrome c oxidase subunit IV isoform 1, mitochondrial | 6 | 7 | 9 | | | | | | | mitochondria | 1 | | | |
| COX5A_RAT | P11240 | Cytochrome c oxidase polypeptide Va, mitochondrial | 2 | 2 | 2 | | | | | | | mitochondria | 0 | | | |
| COX5B_RAT | P12075 | Cytochrome c oxidase polypeptide Vb, mitochondrial | 1 | 1 | 1 | | 36 | 0.0029 | 501.79 | 2+ | LVPYQMVH + Oxidation (M) | mitochondria | 0 | | | |
| CP4F4_RAT | P51869 | Cytochrome P450 4F4 | 0 | 1 | 1 | | 39 | 0.00063 | 666.35 | 3+ | LDMFKNLSMLTLDLQK | endoplasmic reticulum | 2 | | | |
| CRTC_RAT | P18418 | Calreticulin | 1 | 1 | 2 | | | | | | | plasma membrane | 1 | | | |
| CRYAB_RAT | P23928 | Alpha crystallin B chain | 1 | 3 | 3 | | | | | | | n.d. | 0 | | | |
| CX6C2_RAT | P11951 | Cytochrome c oxidase polypeptide VIc-2 | 5 | 4 | 5 | | | | | | | mitochondria | 1 | | | |
| CX7A2_RAT | P35171 | Cytochrome c oxidase polypeptide VIIa-liver/heart, mitochondrial | 1 | 0 | 1 | | 36 | 0.002 | 515.30 | 3+ | LFOEDNGMPVHLK + Oxidation (M) | mitochondria | 1 | | | |
| CXA1_RAT | P08050 | Gap junction alpha-1 protein | 9 | 10 | 12 | | | | | | | plasma membrane | 4 | | | |
| CYB5_RAT | P00173 | Cytochrome b5 | 3 | 3 | 4 | | | | | | | endoplasmic reticulum | 1 | | | |
| D3D2_RAT | P23965 | 3,2-trans-enoyl-CoA isomerase, mitochondrial | 1 | 0 | 1 | | 41 | 0.00052 | 583.99 | 3+ | VGLVDEVVPEDQVHSK | mitochondria | 0 | | | |
| DAD1_RAT | P61805 | Defender against cell death 1 | 1 | 2 | 3 | | | | | | | n.d. | 3 | | | |
| DHB4_RAT | P97852 | Peroxisomal multifunctional enzyme type 2 | 0 | 1 | 1 | | 31 | 0.0072 | 676.80 | 2+ | AVANYDSVEAGEK | peroxisomes | 0 | | | |
| DHE3_RAT | P10860 | Glutamate dehydrogenase 1, mitochondrial | 1 | 1 | 2 | | | | | | | mitochondria | 0 | | | |
| DLP1_RAT | P97836 | Disks large-associated protein 1 | 0 | 1 | 1 | | 30 | 0.011 | 474.29 | 2+ | HLVHSVQK | plasma membrane | 0 | | | |
| DNJA2_RAT | Q35824 | DnaJ homolog subfamily A member 2 | 1 | 0 | 1 | | 44 | 0.0004 | 411.72 | 2+ | YGEQGLR | n.d. | 0 | | | |
| DNJCS_RAT | P60905 | DnaJ homolog subfamily C member 5 | 3 | 4 | 4 | | | | | | | synaptic vesicle | 1 | | | |
| DPP6_RAT | P46101 | Dipeptidyl aminopeptidase-like protein 6 | 4 | 10 | 10 | | | | | | | plasma membrane | 1 | | | |
| DPYL1_RAT | Q62950 | Dihydropyrimidinase related protein-1 | 1 | 1 | 1 | | 49 | 8.1e-005 | 662.36 | 2+ | QIGENLIVPGGVK | cytoplasm | 0 | | | |
| DPYL2_RAT | P47942 | Dihydropyrimidinase related protein-2 | 5 | 6 | 8 | | | | | | | cytoplasm | 0 | | | |
| DYHC_RAT | P38650 | Dynein heavy chain, cytosolic | 4 | 8 | 12 | | | | | | | cytoplasm | 0 | | | |
| DYN1_RAT | P21575 | Dynamin-1 | 4 | 7 | 10 | | | | | | | cytoskeleton | 0 | | | |
| DYN3_RAT | Q08877 | Dynamin 3 | 0 | 3 | 3 | | | | | | | cytoskeleton | 0 | | | |
| DYNA_RAT | P28023 | Dynactin-1 | 0 | 1 | 1 | | 38 | 0.0021 | 445.25 | 2+ | ETELELR | cytoplasm | 0 | | | |
| EAA1_RAT | P24942 | Excitatory amino acid transporter 1 | 13 | 16 | 18 | | | | | | | plasma membrane | 10 | | | |
| EAA2_RAT | P31596 | Excitatory amino acid transporter 2 | 14 | 11 | 15 | | | | | | | plasma membrane | 12 | | | |
| EAA4_RAT | Q35921 | Excitatory amino acid transporter 4 | 7 | 10 | 10 | | | | | | | plasma membrane | 8 | | | |
| EBP_RAT | Q9JJ46 | 3-beta-hydroxysteroid-delta(8),delta(7)-isomerase | 0 | 1 | 1 | | 37 | 0.0019 | 492.78 | 2+ | VSVVPLGTGR | endoplasmic reticulum | 5 | | | |
| ECHA_RAT | Q64428 | Trifunctional enzyme alpha subunit, mitochondrial | 1 | 0 | 1 | | 38 | 0.0011 | 616.36 | 3+ | LPAPKEVSSDEDIQYR | mitochondria | 0 | | | |
| EDG1_RAT | P48303 | Sphingosine 1-phosphate receptor Edg-1 | 2 | 3 | 3 | | | | | | | plasma membrane | 7 | | | |
| EDG2_RAT | P61794 | Lysophosphatidic acid receptor Edg-2 | 1 | 0 | 1 | | 31 | 0.0092 | 489.19 | 2+ | QILCCQR | plasma membrane | 7 | | | |
| EDNRB_RAT | P21451 | Endothelin B receptor | 0 | 1 | 1 | | 58 | 1.3e-005 | 667.84 | 2+ | LTLYDQSNPQR | plasma membrane | 8 | | | |
| EF1A1_RAT | P62630 | Elongation factor 1-alpha 1 | 4 | 5 | 7 | | | | | | | cytoplasm | 0 | | | |
| EF2_RAT | P05197 | Elongation factor 2 | 0 | 1 | 1 | | 51 | 7e-005 | 689.82 | 2+ | CLYASVLTQAQR | cytoplasm | 0 | | | |
| EMB_RAT | Q88775 | Embigin | 1 | 3 | 4 | | | | | | | n.d. | 2 | | | |
| ENOA_RAT | P04764 | Alpha enolase | 7 | 6 | 11 | | | | | | | plasma membrane | 0 | | | |
| ENP1_RAT | P97687 | Ectonucleoside triphosphate diphosphohydrolase 1 | 0 | 2 | 2 | | | | | | | plasma membrane | 3 | | | |
| ENP2_RAT | Q35795 | Ectonucleoside triphosphate diphosphohydrolase 2 | 1 | 1 | 2 | | | | | | | plasma membrane | 3 | | | |
| FAHPE_RAT | P55053 | Fatty acid-binding protein, epidermal | 0 | 1 | 1 | | 60 | 7.9e-006 | 464.32 | 2+ | ELGVGLALR | cytoplasm | 0 | | | |
| FAH2_RAT | Q98407 | Fas apoptotic inhibitor molecule 2 | 1 | 2 | 2 | | | | | | | plasma membrane | 7 | | | |
| FAS_RAT | P13785 | Fatty acid synthase | 0 | 1 | 1 | | 36 | 0.0015 | 944.92 | 2+ | EQGVTFPSGAEQELIR | cytoplasm | 0 | | | |
| FCER2_RAT | P20411 | High affinity immunoglobulin epsilon receptor gamma-subunit | 1 | 2 | 2 | | | | | | | plasma membrane | 2 | | | |
| FLOT1_RAT | Q621E1 | Flotillin-1 | 2 | 3 | 4 | | | | | | | plasma membrane | 0 | | | |
| FLOT2_RAT | Q622S9 | Flotillin-2 | 2 | 2 | 3 | | | | | | | plasma membrane | 0 | | | |
| FOLH1_RAT | P70627 | Glutamate carboxypeptidase II | 4 | 6 | 9 | | | | | | | plasma membrane | 1 | | | |
| FRH_RAT | P19132 | Ferritin heavy chain | 2 | 1 | 2 | | | | | | | cytoplasm | 0 | | | |
| FRIL1_RAT | P02793 | Ferritin light chain 1 | 3 | 4 | 5 | | | | | | | cytoplasm | 0 | | | |
| FXVD6_RAT | Q91XV6 | FXVD domain-containing ion transport regulator 6 | 2 | 3 | 3 | | | | | | | plasma membrane | 2 | | | |
| FXVD7_RAT | P59649 | FXVD domain-containing ion transport regulator 7 | 1 | 1 | 1 | | 40 | 0.0011 | 557.82 | 2+ | SELPSSAPGGGGV | plasma membrane | 1 | | | |
| FZD2_RAT | Q08464 | Frizzled 2 | 1 | 0 | 1 | | 34 | 0.0051 | 494.77 | 2+ | VQCSPELR | plasma membrane | 8 | | | |
| G3P_RAT | P04797 | Glyceroldehyde-3-phosphate dehydrogenase | 7 | 13 | 15 | | | | | | | cytoplasm | 0 | | | |
| GABT_RAT | P50554 | 4-aminobutyrate aminotransferase, mitochondrial | 1 | 0 | 1 | | | | | | | mitochondria | 0 | | | |
| GBB1_RAT | P54311 | Guanine nucleotide-binding protein G(I)/G(S)/G(T) beta subunit 1 | 8 | 5 | 10 | | 31 | 0.01 | 489.39 | 2+ | AFLLTTRR | plasma membrane | 0 | | | |
| GBB2_RAT | P54313 | Guanine nucleotide-binding protein G(I)/G(S)/G(T) beta subunit 2 | 2 | 5 | 5 | | | | | | | plasma membrane | 0 | | | |

| | | | | | | | | | | | | | |
|------------|--------|--|----|----|----|----|----------|---------|----|-------------------------|-----------------------|----|---|
| GBB5_RAT | P62882 | Guanine nucleotide-binding protein beta subunit 5 | 1 | 0 | 1 | 31 | 0.0074 | 615.32 | 2+ | CSVYPLTFDK | plasma membrane | 0 | |
| GBRA1_RAT | P62813 | Gamma-aminobutyric-acid receptor alpha-1 subunit | 2 | 2 | 3 | | | | | | plasma membrane | 5 | |
| GBRA6_RAT | P30191 | Gamma-aminobutyric-acid receptor alpha-6 subunit | 1 | 0 | 1 | 86 | 2.2e-008 | 717.91 | 2+ | ILDNLLEGYDNR | plasma membrane | 4 | |
| GBRB1_RAT | P15431 | Gamma-aminobutyric-acid receptor beta-1 subunit | 0 | 1 | 1 | 38 | 0.00086 | 684.69 | 3+ | VADQLWVPDITYFLNDKK | plasma membrane | 5 | |
| GBRB2_RAT | P63138 | Gamma-aminobutyric-acid receptor beta-2 subunit | 0 | 2 | 2 | | | | | | plasma membrane | 5 | |
| GBRD_RAT | P18506 | Gamma-aminobutyric-acid receptor delta subunit | 0 | 1 | 1 | 31 | 0.0062 | 535.26 | 3+ | LKPIDADTIDIYAR | plasma membrane | 5 | |
| GCS1_RAT | Q88941 | Mannosyl-oligosaccharide glucosidase | 1 | 2 | 2 | | | | | | endoplasmic reticulum | 1 | |
| GDC1_RAT | P50399 | Rab GDP dissociation inhibitor beta-2 | 0 | 1 | 1 | 33 | 0.004 | 676.32 | 2+ | DLGTDSDQIFISR | plasma membrane | 0 | |
| GEPH_RAT | Q03555 | Gephyrin | 0 | 1 | 1 | 33 | 0.0052 | 503.80 | 2+ | VLAQDVYAK | cytoskeleton | 0 | |
| GFAP_RAT | P47819 | Glial fibrillary acidic protein, astrocyte | 3 | 5 | 8 | | | | | | cytoskeleton | 0 | |
| GLNA_RAT | P09606 | Glutamine synthetase | 1 | 8 | 9 | | | | | | cytoplasm | 0 | |
| GNA11_RAT | Q9JID2 | Guanine nucleotide-binding protein, alpha-11 subunit | 0 | 1 | 1 | 36 | 0.0015 | 1118.96 | 2+ | VPPTGIEYFPDLENIIFR | plasma membrane | 0 | |
| GNA12_RAT | Q63210 | Guanine nucleotide-binding protein, alpha-12 subunit | 1 | 1 | 1 | 57 | 1.9e-005 | 529.35 | 2+ | ILLLGAGESGK | plasma membrane | 0 | |
| GNA1_RAT | P10824 | Guanine nucleotide-binding protein G(i), alpha-1 subunit | 5 | 5 | 5 | | | | | | plasma membrane | 0 | x |
| GNA2_RAT | P04897 | Guanine nucleotide-binding protein G(i), alpha-2 subunit | 7 | 10 | 11 | | | | | | plasma membrane | 1 | x |
| GNAO1_RAT | P59215 | Guanine nucleotide-binding protein G(o), alpha subunit 1 | 14 | 18 | 23 | | | | | | plasma membrane | 0 | x |
| GNAO2_RAT | P30033 | Guanine nucleotide-binding protein G(o), alpha subunit 2 | 14 | 22 | 23 | | | | | | plasma membrane | 0 | x |
| GNAQ_RAT | P82471 | Guanine nucleotide-binding protein G(q), alpha subunit | 6 | 8 | 9 | | | | | | plasma membrane | 0 | x |
| GNMT_RAT | P13255 | Glycine N-methyltransferase | 1 | 0 | 1 | 32 | 0.0054 | 441.78 | 2+ | MLKYALK + Oxidation (M) | cytoplasm | 0 | |
| GOSR1_RAT | Q62931 | 28 kDa Golgi SNARE protein | 0 | 1 | 1 | 30 | 0.0094 | 551.26 | 2+ | QLENELDKR | Golgi complex | 0 | |
| GPX41_RAT | P36970 | Phospholipid hydroperoxide glutathione peroxidase, mitochondrial | 1 | 0 | 1 | 59 | 1.2e-005 | 661.86 | 2+ | ILAFPCNQFGR | mitochondria | 1 | |
| GRIA1_RAT | P19490 | Glutamate receptor 1 | 0 | 2 | 2 | | | | | | plasma membrane | 5 | |
| GRIA2_RAT | P19491 | Glutamate receptor 2 | 0 | 2 | 2 | | | | | | plasma membrane | 4 | |
| GRIA3_RAT | P19492 | Glutamate receptor 3 | 0 | 2 | 2 | | | | | | plasma membrane | 4 | |
| GRIA4_RAT | P19493 | Glutamate receptor 4 | 0 | 1 | 1 | 37 | 0.0016 | 590.78 | 2+ | FVIDCEIER | plasma membrane | 5 | |
| GRID2_RAT | Q63226 | Glutamate receptor delta-2 subunit | 5 | 4 | 8 | | | | | | plasma membrane | 4 | |
| GRP78_RAT | P06761 | 78 kDa glucose-regulated protein | 12 | 21 | 24 | | | | | | n.d. | 1 | |
| GSLG1_RAT | Q62638 | Golgi apparatus protein 1 | 5 | 13 | 13 | | | | | | Golgi complex | 2 | |
| GSTM1_RAT | P04905 | Glutathione S-transferase Mu 1 | 0 | 2 | 2 | | | | | | cytoplasm | 0 | |
| GSTM4_RAT | P08009 | Glutathione S-transferase Yb-3 | 0 | 2 | 2 | | | | | | cytoplasm | 0 | |
| GTR1_RAT | P11167 | Solute carrier family 2, facilitated glucose transporter, member 1 | 3 | 3 | 3 | | | | | | plasma membrane | 11 | |
| GTR3_RAT | Q07647 | Solute carrier family 2, facilitated glucose transporter, member 3 | 2 | 2 | 2 | | | | | | plasma membrane | 11 | |
| GTR5_RAT | P43427 | Solute carrier family 2, facilitated glucose transporter, member 5 | 1 | 1 | 1 | 63 | 4.3e-006 | 655.36 | 2+ | TFVEINQIFAK | plasma membrane | 12 | |
| GTR8_RAT | Q9JJZ1 | Solute carrier family 2, facilitated glucose transporter, member 8 | 0 | 1 | 1 | 43 | 0.0004 | 467.92 | 3+ | TLEQITAHFEGR | plasma membrane | 12 | |
| H2A1_RAT | P02262 | Histone H2A.1 | 1 | 1 | 1 | 67 | 2e-006 | 472.83 | 2+ | AGLOFPVGR | nucleus | 1 | |
| H2B_RAT | Q00715 | Histone H2B | 0 | 2 | 2 | | | | | | nucleus | 0 | |
| H2BT_RAT | Q00729 | Histone H2B, testis | 1 | 1 | 1 | 51 | 7.5e-005 | 477.32 | 2+ | LLLPGELAK | nucleus | 0 | |
| H4_RAT | P62804 | Histone H4 | 4 | 5 | 6 | | | | | | nucleus | 0 | |
| HBA_RAT | P01946 | Hemoglobin alpha-1 and alpha-2 chains | 3 | 6 | 6 | | | | | | blood | 0 | |
| HBB1_RAT | P02091 | Hemoglobin beta chain, major-form | 10 | 11 | 12 | | | | | | blood | 0 | |
| HBB2_RAT | P11517 | Hemoglobin beta chain, minor-form | 10 | 10 | 11 | | | | | | blood | 0 | |
| HCK_RAT | P50545 | Tyrosine-protein kinase HCK | 1 | 0 | 1 | 36 | 0.0025 | 446.69 | 2+ | GSLLDFLK | plasma membrane | 0 | x |
| HOMER3_RAT | Q9Z2X5 | Homer protein homolog 3 | 6 | 7 | 10 | | | | | | plasma membrane | 0 | |
| HPCA_RAT | P84076 | Neuron specific calcium-binding protein hippocalcin | 2 | 0 | 2 | | | | | | cytoplasm | 0 | x |
| HPCL1_RAT | P62749 | Hippocalcin-like protein 1 | 2 | 3 | 3 | | | | | | cytoplasm | 0 | x |
| HPLN1_RAT | P03994 | Hyaluronan and proteoglycan link protein 1 | 0 | 1 | 1 | 59 | 1.2e-005 | 500.82 | 2+ | LLVEAEQAK | n.d. | 0 | |
| HS90B_RAT | P34058 | Heat shock protein HSP 90-beta | 2 | 11 | 11 | | | | | | cytoplasm | 0 | |
| HSP47_RAT | P29457 | 47 kDa heat shock protein | 1 | 1 | 2 | | | | | | cytoplasm | 2 | |
| HSP7C_RAT | P63018 | Heat shock cognate 71 kDa protein | 12 | 26 | 27 | | | | | | cytoplasm | 0 | |
| HSPB1_RAT | P42930 | Heat-shock protein beta-1 | 0 | 1 | 1 | 49 | 0.00013 | 538.23 | 2+ | QLSSGVSEIR | cytoskeleton | 0 | |
| HXK1_RAT | P05708 | Hexokinase, type I | 0 | 2 | 2 | | | | | | cytoplasm | 0 | |
| HYEP_RAT | P07687 | Epoxide hydrolase 1 | 0 | 1 | 1 | 37 | 0.0018 | 505.25 | 2+ | IIPLLTDPK | microsome | 1 | |
| I2C2_RAT | Q9QZ81 | Eukaryotic translation initiation factor 2C 2 | 0 | 1 | 1 | 35 | 0.003 | 507.72 | 2+ | QCTEVHLK | plasma membrane | 0 | |
| ICAM1_RAT | Q00238 | Intercellular adhesion molecule-1 | 1 | 2 | 2 | | | | | | plasma membrane | 2 | |
| ICMT_RAT | Q9VVM4 | Protein-S-isoprenylcysteine O-methyltransferase | 0 | 1 | 1 | 36 | 0.0022 | 486.21 | 2+ | VPTGLPFK | endoplasmic reticulum | 2 | |
| INIB_RAT | P26376 | Interferon-inducible protein | 0 | 2 | 2 | | | | | | n.d. | 2 | |
| IRK10_RAT | P49655 | ATP-sensitive inward rectifier potassium channel 10 | 0 | 1 | 1 | 87 | 1.8e-008 | 765.91 | 2+ | YVADFSLFDQVVK | plasma membrane | 3 | |
| IRK13_RAT | Q70617 | Inward rectifier potassium channel 13 | 3 | 3 | 4 | | | | | | plasma membrane | 2 | |
| ITB1_RAT | P49134 | Integrin beta-1 | 4 | 9 | 10 | | | | | | plasma membrane | 2 | |
| ITPR1_RAT | P29994 | Inositol 1,4,5-trisphosphate receptor type 1 | 6 | 15 | 18 | | | | | | endoplasmic reticulum | 1 | |
| ITPR2_RAT | P29995 | Inositol 1,4,5-trisphosphate receptor type 2 | 1 | 1 | 1 | 47 | 0.00016 | 628.73 | 2+ | TTCFCGLER | endoplasmic reticulum | 10 | |
| K6PF_RAT | P47858 | 6-phosphofructokinase, muscle type | 1 | 8 | 9 | | | | | | cytoplasm | 0 | |
| K6FP_RAT | P47860 | 6-phosphofructokinase, type C | 2 | 1 | 3 | | | | | | cytoplasm | 1 | |
| KAP0_RAT | P03456 | cAMP-dependent protein kinase type I-alpha regulatory subunit | 0 | 1 | 1 | 51 | 4.7e-005 | 492.36 | 3+ | VSILESCLKWER | cytoplasm | 0 | |
| KAP2_RAT | P12368 | cAMP-dependent protein kinase type II-alpha regulatory subunit | 0 | 1 | 1 | 58 | 1.4e-005 | 505.21 | 2+ | GTVDILVTK | cytoplasm | 0 | |
| KAPCB_RAT | P68182 | cAMP-dependent protein kinase, beta-catalytic subunit | 0 | 1 | 1 | 31 | 0.0042 | 662.71 | 3+ | KWENPPPSNAGLEDFER | cytoplasm | 0 | x |
| KCC2A_RAT | P11275 | Calcium/calmodulin-dependent protein kinase type II alpha chain | 4 | 5 | 8 | | | | | | cytoplasm | 1 | |
| KCC2B_RAT | P08413 | Calcium/calmodulin-dependent protein kinase type II beta chain | 0 | 8 | 8 | | | | | | cytoplasm | 1 | |
| KCC2D_RAT | P15791 | Calcium/calmodulin-dependent protein kinase type II delta chain | 0 | 2 | 2 | | | | | | cytoplasm | 1 | |
| KCNA1_RAT | P10499 | Potassium voltage-gated channel subfamily A member 1 | 0 | 3 | 3 | | | | | | plasma membrane | 6 | |
| KCNB3_RAT | Q01956 | Potassium voltage-gated channel subfamily C member 3 | 0 | 2 | 2 | | | | | | plasma membrane | 7 | |
| KCND2_RAT | Q63881 | Potassium voltage-gated channel subfamily D member 2 | 0 | 1 | 1 | 31 | 0.006 | 662.30 | 2+ | FQTWQDTLER | plasma membrane | 7 | |
| KCRB_RAT | P07335 | Creatine kinase, B chain | 11 | 10 | 13 | | | | | | cytoplasm | 0 | |
| KCRU_RAT | P25809 | Creatine kinase, ubiquitous mitochondrial | 0 | 1 | 1 | 29 | 0.014 | 500.79 | 2+ | VVVDALSGLK | cytoplasm | 0 | |
| KIF5C_RAT | P56536 | Kinesin heavy chain isoform 5C | 0 | 1 | 1 | 36 | 0.0021 | 638.85 | 2+ | VSYFEIYLDK | cytoskeleton | 0 | |
| KPCA_RAT | P05696 | Protein kinase C, alpha type | 1 | 0 | 1 | 52 | 6.2e-005 | 487.73 | 2+ | LGGCPEGER | cytoplasm | 0 | |
| KPCB_RAT | P68403 | Protein kinase C, beta type | 0 | 1 | 1 | 30 | 0.011 | 440.25 | 2+ | AGVDGWFK | cytoplasm | 0 | |

| | | | | | | | | | | | | | | | | | | | | | | | | | |
|-----------|--------|--|----|----|----|-----|----------|--------|----|--|--|--|--|--|--|--|--|--|--|-----------|-----------------------|----|---|---|--|
| KPCG_RAT | P63319 | Protein kinase C, gamma type | 5 | 11 | 12 | | | | | | | | | | | | | | | cytoplasm | 0 | | | | |
| KPYM_RAT | P11980 | Pyruvate kinase, isozymes M1/M2 | 12 | 12 | 15 | | | | | | | | | | | | | | | | cytoplasm | 0 | | | |
| L1CAM_RAT | Q05695 | Neural cell adhesion molecule L1 | 0 | 1 | 1 | 54 | 3.6e-005 | 673.85 | 2+ | | | | | | | | | | | | plasma membrane | 2 | | | |
| LAMP1_RAT | P14562 | Lysosome-associated membrane glycoprotein 1 | 5 | 7 | 7 | | | | | | | | | | | | | | | | plasma membrane | 2 | | | |
| LAMP2_RAT | P17046 | Lysosome-associated membrane glycoprotein 2 | 2 | 3 | 3 | | | | | | | | | | | | | | | | plasma membrane | 3 | | | |
| LAT1_RAT | Q63016 | Large neutral amino acids transporter small subunit 1 | 2 | 2 | 3 | | | | | | | | | | | | | | | | plasma membrane | 14 | | | |
| LCAP_RAT | P97629 | Leucyl-cystinyl aminopeptidase | 0 | 2 | 2 | | | | | | | | | | | | | | | | plasma membrane | 1 | | | |
| LDHA_RAT | P04642 | L-lactate dehydrogenase A chain | 1 | 2 | 2 | | | | | | | | | | | | | | | | cytoplasm | 0 | | | |
| LDHB_RAT | P42123 | L-lactate dehydrogenase B chain | 3 | 7 | 8 | | | | | | | | | | | | | | | | cytoplasm | 0 | | | |
| LIPH_RAT | P07867 | Hepatic triacylglycerol lipase | 0 | 2 | 2 | | | | | | | | | | | | | | | | secretory | 1 | | | |
| LMO3_RAT | Q99MB5 | LIM-only protein 3 | 0 | 1 | 1 | 32 | 0.007 | 482.23 | 2+ | | | | | | | | | | | | n.d. | 0 | | | |
| LPP1_RAT | O08564 | Lipid phosphate phosphohydrolase 1 | 1 | 1 | 1 | 41 | 0.00066 | 578.24 | 2+ | | | | | | | | | | | | plasma membrane | 6 | | | |
| LPP3_RAT | P97544 | Lipid phosphate phosphohydrolase 3 | 6 | 5 | 7 | | | | | | | | | | | | | | | | plasma membrane | 6 | | | |
| LSAMP_RAT | Q62813 | Limbic system-associated membrane protein | 8 | 8 | 10 | | | | | | | | | | | | | | | | plasma membrane | 2 | x | | |
| M2OM_RAT | P97700 | Mitochondrial 2-oxoglutarate/malate carrier protein | 3 | 8 | 8 | | | | | | | | | | | | | | | | mitochondria | 1 | | | |
| MACS_RAT | P30009 | Myristoylated alanine-rich C-kinase substrate | 6 | 7 | 7 | | | | | | | | | | | | | | | | cytoplasm | 1 | | x | |
| MACS_RAT | P07722 | Myelin-associated glycoprotein | 0 | 3 | 3 | | | | | | | | | | | | | | | | plasma membrane | 1 | | | |
| MBP_RAT | P02688 | Myelin basic protein S | 8 | 7 | 9 | | | | | | | | | | | | | | | | plasma membrane | 0 | | | |
| MDR1_RAT | P43245 | Multidrug resistance protein 1 | 2 | 1 | 2 | | | | | | | | | | | | | | | | plasma membrane | 9 | | | |
| MECP2_RAT | Q00566 | Methyl-CpG-binding protein 2 | 1 | 1 | 1 | 33 | 0.0046 | 699.37 | 2+ | | | | | | | | | | | | nucleus | 0 | | | |
| MGAT2_RAT | Q09326 | Alpha-1,6-mannosyl-glycoprotein 2-beta-N-acetylglucosaminyltransferase | 0 | 1 | 1 | 48 | 0.00019 | 479.21 | 2+ | | | | | | | | | | | | Golgi complex | 1 | | | |
| MGR1_RAT | P23385 | Metabotropic glutamate receptor 1 | 0 | 1 | 2 | | | | | | | | | | | | | | | | plasma membrane | 8 | | | |
| MGR2_RAT | P31421 | Metabotropic glutamate receptor 2 | 1 | 0 | 1 | 43 | 0.0004 | 757.97 | 2+ | | | | | | | | | | | | plasma membrane | 7 | | | |
| MGR5_RAT | P31424 | Metabotropic glutamate receptor 5 | 1 | 1 | 2 | | | | | | | | | | | | | | | | plasma membrane | 6 | | | |
| MIF_RAT | P30904 | Macrophage migration inhibitory factor | 0 | 1 | 1 | 68 | 1.3e-006 | 644.35 | 2+ | | | | | | | | | | | | n.d. | 0 | | | |
| MOG_RAT | Q63345 | Myelin-oligodendrocyte glycoprotein | 8 | 6 | 10 | | | | | | | | | | | | | | | | plasma membrane | 3 | | | |
| MOT1_RAT | P53987 | Monocarboxylate transporter 1 | 4 | 3 | 4 | | | | | | | | | | | | | | | | plasma membrane | 11 | | | |
| MPCP_RAT | P16036 | Phosphate carrier protein, mitochondrial | 5 | 6 | 6 | | | | | | | | | | | | | | | | mitochondria | 2 | | | |
| MTA1_RAT | Q62599 | Metastasis-associated protein | 1 | 0 | 1 | 33 | 0.0054 | 694.91 | 2+ | | | | | | | | | | | | cytoplasm | 0 | | | |
| MYCD_RAT | Q8R517 | Mycardin | 1 | 0 | 1 | 29 | 0.0056 | 657.65 | 2+ | | | | | | | | | | | | nucleus | 0 | | | |
| MYH10_RAT | Q9JL70 | Myosin heavy chain, nonmuscle type B | 1 | 0 | 1 | 29 | 0.014 | 487.23 | 2+ | | | | | | | | | | | | cytoskeleton | 0 | | | |
| MYH11_RAT | Q63862 | Myosin heavy chain, smooth muscle isoform | 1 | 1 | 2 | | | | | | | | | | | | | | | | cytoskeleton | 0 | | | |
| MYO5B_RAT | P70569 | Myosin Vb | 1 | 0 | 1 | 31 | 0.0011 | 475.42 | 3+ | | | | | | | | | | | | cytoskeleton | 0 | | | |
| MYP0_RAT | P06907 | Myelin P0 protein | 5 | 6 | 6 | | | | | | | | | | | | | | | | plasma membrane | 2 | | | |
| MYPR_RAT | P60203 | Myelin proteolipid protein | 8 | 9 | 9 | | | | | | | | | | | | | | | | plasma membrane | 4 | | | |
| N5BM_RAT | Q80W89 | NADH-ubiquinone oxidoreductase subunit B14.7 | 2 | 1 | 2 | | | | | | | | | | | | | | | | mitochondria | 3 | | | |
| NAC1_RAT | Q01728 | Sodium/calcium exchanger 1 | 1 | 2 | 3 | | | | | | | | | | | | | | | | plasma membrane | 11 | | | |
| NAC2_RAT | P48768 | Sodium/calcium exchanger 2 | 2 | 4 | 5 | | | | | | | | | | | | | | | | plasma membrane | 12 | | | |
| NCAM1_RAT | P13596 | Neural cell adhesion molecule 1, 140 kDa isoform | 16 | 24 | 28 | | | | | | | | | | | | | | | | plasma membrane | 2 | | | |
| NCB5R_RAT | P20070 | NADH-cytochrome b5 reductase | 1 | 4 | 4 | | | | | | | | | | | | | | | | endoplasmic reticulum | 11 | | x | |
| NCKX2_RAT | O54701 | Sodium/potassium/calcium exchanger 2 | 0 | 1 | 1 | 38 | 0.001 | 604.38 | 3+ | | | | | | | | | | | | plasma membrane | 12 | | | |
| NCPR_RAT | P00388 | NADPH--cytochrome P450 reductase | 1 | 0 | 1 | 41 | 0.00073 | 476.85 | 2+ | | | | | | | | | | | | endoplasmic reticulum | 1 | | | |
| NDKA_RAT | Q05982 | Nucleoside diphosphate kinase A | 1 | 0 | 1 | 35 | 0.002 | 601.38 | 3+ | | | | | | | | | | | | cytoplasm | 0 | | | |
| NEGR1_RAT | Q9Z0J8 | Neuronal growth regulator 1 | 5 | 10 | 10 | | | | | | | | | | | | | | | | plasma membrane | 1 | | | |
| NEP_RAT | P07861 | Nephrilysin | 0 | 2 | 2 | | | | | | | | | | | | | | | | n.d. | 1 | | | |
| NEUM_RAT | P07936 | Neuromodulin | 3 | 3 | 4 | | | | | | | | | | | | | | | | plasma membrane | 4 | | | |
| NFASC_RAT | P97685 | Neurofascin | 11 | 22 | 23 | | | | | | | | | | | | | | | | plasma membrane | 3 | | | |
| NFH_RAT | P16884 | Neurofilament triplet H protein | 0 | 1 | 1 | 54 | 0.01 | 503.23 | 2+ | | | | | | | | | | | | cytoskeleton | 0 | | | |
| NFL_RAT | P19527 | Neurofilament triplet L protein | 0 | 3 | 3 | | | | | | | | | | | | | | | | cytoskeleton | 0 | | | |
| NICA_RAT | Q8CGU6 | Nicastrin | 2 | 2 | 4 | | | | | | | | | | | | | | | | plasma membrane | 2 | | | |
| NLGN1_RAT | Q62765 | Neurologin 1 | 1 | 0 | 1 | 64 | 3.6e-006 | 635.33 | 2+ | | | | | | | | | | | | plasma membrane | 3 | | | |
| NLTP_RAT | P11915 | Nonspecific lipid-transfer protein, mitochondrial | 0 | 2 | 2 | | | | | | | | | | | | | | | | cytoplasm | 0 | | | |
| NOP5_RAT | Q9OZ86 | Nucleolar protein NOP5 | 1 | 0 | 1 | 29 | 0.012 | 496.28 | 2+ | | | | | | | | | | | | nucleus | 0 | | | |
| NPT1_RAT | Q62795 | Renal sodium-dependent phosphate transport protein 1 | 0 | 1 | 1 | 35 | 0.0026 | 434.74 | 2+ | | | | | | | | | | | | plasma membrane | 12 | | | |
| NRCAM_RAT | P97686 | Neuronal cell adhesion molecule | 5 | 9 | 10 | | | | | | | | | | | | | | | | plasma membrane | 2 | | | |
| NRX3A_RAT | Q07310 | Neurexin 3-alpha | 1 | 0 | 1 | 30 | 0.011 | 460.78 | 2+ | | | | | | | | | | | | plasma membrane | 2 | | | |
| NSG1_RAT | P02683 | Neuron specific protein family member 1 | 3 | 2 | 4 | | | | | | | | | | | | | | | | Golgi complex | 0 | | | |
| NTRI_RAT | Q62718 | Neurotrinin | 3 | 6 | 7 | | | | | | | | | | | | | | | | plasma membrane | 2 | | x | |
| NTRK2_RAT | Q63604 | BDNF/NT-3 growth factors receptor | 0 | 2 | 2 | | | | | | | | | | | | | | | | plasma membrane | 2 | | | |
| NU5M_RAT | P11661 | NADH-ubiquinone oxidoreductase chain 5 | 0 | 1 | 1 | 41 | 0.00079 | 597.28 | 2+ | | | | | | | | | | | | cytoplasm | 14 | | | |
| NUDC_RAT | Q63525 | Nuclear migration protein nudc | 1 | 1 | 1 | 36 | 0.0024 | 546.26 | 2+ | | | | | | | | | | | | nucleus | 0 | | | |
| ODD2_RAT | Q01205 | Dihydrodipolyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase | 2 | 2 | 2 | | | | | | | | | | | | | | | | mitochondria | 0 | | | |
| ODP2_RAT | P08461 | Dihydrodipolyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex | 0 | 2 | 2 | | | | | | | | | | | | | | | | mitochondria | 0 | | | |
| OPGM_RAT | P32736 | Opicid binding protein/cell adhesion molecule | 3 | 5 | 5 | | | | | | | | | | | | | | | | plasma membrane | 1 | | | |
| OX2G_RAT | P04218 | OX-2 membrane glycoprotein | 1 | 0 | 1 | | | | | | | | | | | | | | | | plasma membrane | 3 | | | |
| P24_RAT | Q63524 | Cox-coated vesicle membrane protein p24 | 0 | 1 | 1 | 53 | 3.2e-005 | 722.33 | 2+ | | | | | | | | | | | | Golgi complex | 3 | | | |
| P2Y12_RAT | Q9EPX4 | P2Y purinoceptor 12 | 1 | 0 | 1 | 37 | 0.0016 | 491.32 | 2+ | | | | | | | | | | | | plasma membrane | 7 | | | |
| PARK7_RAT | Q88767 | DJ-1 protein | 1 | 1 | 1 | 55 | 2.3e-005 | 788.34 | 2+ | | | | | | | | | | | | nucleus | 0 | | | |
| PCYOX_RAT | Q99ML5 | Prenylcysteine oxidase | 1 | 6 | 6 | | | | | | | | | | | | | | | | lysosomes | 1 | | | |
| PDI1A_RAT | P04785 | Protein disulfide-isomerase | 0 | 2 | 2 | | | | | | | | | | | | | | | | endoplasmic reticulum | 0 | | | |
| PDI1B_RAT | P11598 | Protein disulfide-isomerase A3 | 3 | 7 | 10 | | | | | | | | | | | | | | | | endoplasmic reticulum | 1 | | | |
| PDI1C_RAT | Q63081 | Protein disulfide-isomerase A6 | 0 | 1 | 1 | 75 | 2.5e-007 | 742.36 | 2+ | | | | | | | | | | | | endoplasmic reticulum | 1 | | | |
| PDZK3_RAT | Q9CZ88 | PDZ domain containing protein 3 | 0 | 1 | 1 | 33 | 0.0042 | 478.01 | 3+ | | | | | | | | | | | | nucleus | 0 | | | |
| PEBP_RAT | P31044 | Phosphatidylethanolamine-binding protein | 1 | 1 | 1 | 100 | 8.1e-010 | 676.36 | 2+ | | | | | | | | | | | | cytoplasm | 0 | | | |
| PET2_RAT | Q63424 | Oligopeptide transporter, kidney isoform | 2 | 1 | 2 | | | | | | | | | | | | | | | | plasma membrane | 14 | | | |
| PGAM1_RAT | P25113 | Phosphoglycerate mutase 1 | 1 | 1 | 1 | 36 | 0.001 | 811.75 | 3+ | | | | | | | | | | | | cytoplasm | 0 | | | |
| PGK1_RAT | P16617 | Phosphoglycerate kinase 1 | 3 | 5 | 7 | | | | | | | | | | | | | | | | cytoplasm | 0 | | | |

| | | | | | | | | | | | | | | | | | | | | | | | | | |
|-----------|--------|--|---|----|----|--|--|----|----------|--------|----|-------------------------------|--|--|--|--|--|--|--|--|-----------|-----------------------|----|---|--|
| PGRCT_RAT | P70580 | Membrane associated progesterone receptor component 1 | 0 | 2 | 2 | | | | | | | | | | | | | | | | microsome | 1 | | | |
| PHB_RAT | P67779 | Prohibitin | 6 | 9 | 10 | | | | | | | | | | | | | | | | | cytoplasm | 0 | | |
| PHOS_RAT | P20942 | Phosducin | 1 | 0 | 1 | | | 87 | 1.8e-008 | 741.42 | 2+ | FSSDVLPTLLVYK | | | | | | | | | | plasma membrane | 0 | | |
| PHS1_RAT | P09811 | Glycogen phosphorylase, liver form | 2 | 2 | 3 | | | | | | | | | | | | | | | | | cytoplasm | 0 | | |
| PHS2_RAT | P09812 | Glycogen phosphorylase, muscle form | 0 | 1 | 1 | | | 42 | 0.00033 | 822.05 | 3+ | VIPAADLSEQISTAGTEASGTGNMK | | | | | | | | | | cytoplasm | 0 | | |
| PHS3_RAT | P53534 | Glycogen phosphorylase, brain form | 3 | 10 | 11 | | | | | | | | | | | | | | | | | cytoplasm | 0 | | |
| PIGS_RAT | Q5X131 | GPI transamidase component PIG-S | 0 | 2 | 2 | | | | | | | | | | | | | | | | | endoplasmic reticulum | 3 | | |
| PLLIP_RAT | P47987 | Plasmolipin | 0 | 2 | 2 | | | | | | | | | | | | | | | | | plasma membrane | 4 | | |
| PLM_RAT | Q08589 | Phospholemman | 1 | 1 | 1 | | | 87 | 1.4e-008 | 683.84 | 2+ | TGEPDEEEGTFR | | | | | | | | | | plasma membrane | 2 | | |
| PPBT_RAT | P08289 | Alkaline phosphatase, tissue-nonspecific isozyme | 2 | 5 | 6 | | | | | | | | | | | | | | | | | plasma membrane | 1 | x | |
| PPIA_RAT | P10111 | Peptidyl-prolyl cis-trans isomerase A | 4 | 4 | 5 | | | | | | | | | | | | | | | | | n.d. | 0 | | |
| PRA1_RAT | Q35394 | Prenylated Rab acceptor protein 1 | 1 | 0 | 1 | | | 71 | 6.2e-007 | 772.52 | 2+ | DAEVEGLSATTLLPK | | | | | | | | | | Golgi complex | 2 | | |
| PRAF3_RAT | Q9ES40 | PRA1 family protein 3 | 3 | 1 | 3 | | | | | | | | | | | | | | | | | n.d. | 4 | | |
| PRDX1_RAT | Q63716 | Peroxiredoxin 1 | 2 | 3 | 3 | | | | | | | | | | | | | | | | | cytoplasm | 0 | | |
| PRDX2_RAT | P37074 | Peroxiredoxin 2 | 0 | 3 | 3 | | | | | | | | | | | | | | | | | cytoplasm | 0 | | |
| PRDX5_RAT | Q9R063 | Peroxiredoxin 5, mitochondrial | 2 | 0 | 2 | | | | | | | | | | | | | | | | | cytoplasm | 0 | | |
| PRIO_RAT | P13852 | Major onion protein | 1 | 3 | 3 | | | | | | | | | | | | | | | | | plasma membrane | 3 | x | |
| PROF1_RAT | P62963 | Prollin-1 | 1 | 1 | 1 | | | 57 | 2e-005 | 607.33 | 2+ | DSPSVWAAVPGK | | | | | | | | | | n.d. | 0 | | |
| PROF2_RAT | Q9EPC6 | Prollin-2 | 0 | 1 | 1 | | | 31 | 0.0079 | 454.79 | 2+ | VLVFMGK + Oxidation (M) | | | | | | | | | | n.d. | 0 | | |
| FRS6B_RAT | Q63570 | 26S protease regulatory subunit 6B | 0 | 1 | 1 | | | 31 | 0.0084 | 626.26 | 2+ | GVLMYGPPGCGK | | | | | | | | | | cytoplasm | 0 | | |
| FRS7_RAT | Q63347 | 26S protease regulatory subunit 7 | 1 | 0 | 1 | | | 31 | 0.0086 | 569.29 | 2+ | YVGEGARIVR | | | | | | | | | | cytoplasm | 0 | | |
| FRS8_RAT | P62198 | 26S protease regulatory subunit 8 | 1 | 0 | 1 | | | 33 | 0.004 | 645.81 | 2+ | LEGGSGDSEVQR | | | | | | | | | | cytoplasm | 0 | | |
| PSA1_RAT | P18420 | Proteasome subunit alpha type 1 | 0 | 1 | 1 | | | 32 | 0.0059 | 673.36 | 2+ | ETLPAEQDLTKK | | | | | | | | | | cytoplasm | 0 | | |
| PSD1_RAT | Q88761 | 26S proteasome non-ATPase regulatory subunit 1 | 1 | 0 | 1 | | | 30 | 0.0091 | 588.40 | 2+ | NNNTDLMILK | | | | | | | | | | cytoplasm | 1 | | |
| PSN1_RAT | P97887 | Presenilin 1 | 0 | 1 | 1 | | | 51 | 3.9e-005 | 677.71 | 3+ | AAVQELSGSILTSEDEPER | | | | | | | | | | Golgi complex | 10 | | |
| PTN5_RAT | P35234 | Tyrosine-protein phosphatase, non-receptor type 5 | 1 | 1 | 1 | | | 39 | 0.0014 | 436.78 | 2+ | EGVVDILK | | | | | | | | | | cytoplasm | 0 | | |
| PTPRA_RAT | Q03348 | Receptor-type tyrosine-protein phosphatase alpha | 1 | 0 | 1 | | | 35 | 0.0027 | 598.36 | 2+ | EETVNDFWR | | | | | | | | | | plasma membrane | 2 | | |
| RAB10_RAT | P35281 | Ras-related protein Rab-10 | 4 | 4 | 4 | | | | | | | | | | | | | | | | | vesicle | 0 | | |
| RAB14_RAT | P61107 | Ras-related protein Rab-14 | 9 | 12 | 15 | | | | | | | | | | | | | | | | | vesicle | 0 | | |
| RAB1A_RAT | Q6NYB7 | Ras-related protein Rab-1A | 9 | 8 | 11 | | | | | | | | | | | | | | | | | vesicle | 0 | | |
| RAB1B_RAT | P10536 | Ras-related protein Rab-1B | 5 | 4 | 5 | | | | | | | | | | | | | | | | | vesicle | 0 | | |
| RAB2A_RAT | P05712 | Ras-related protein Rab-2A | 9 | 6 | 9 | | | | | | | | | | | | | | | | | vesicle | 0 | | |
| RAB3A_RAT | P63012 | Ras-related protein Rab-3A | 6 | 10 | 11 | | | | | | | | | | | | | | | | | synaptic vesicle | 0 | | |
| RAB3B_RAT | Q63941 | Ras-related protein Rab-3B | 0 | 1 | 1 | | | 71 | 4.6e-007 | 854.46 | 2+ | TYSWDNAQVILVGNK | | | | | | | | | | synaptic vesicle | 0 | | |
| RAB3C_RAT | P62824 | Ras-related protein Rab-3C | 0 | 1 | 1 | | | 39 | 0.0011 | 790.31 | 2+ | MSESLTDPAITAAK | | | | | | | | | | vesicle | 0 | | |
| RAB3D_RAT | Q63942 | GTP-binding protein Rab-3D | 0 | 2 | 2 | | | | | | | | | | | | | | | | | vesicle | 0 | | |
| RAB6A_RAT | Q9WVB1 | Ras-related protein Rab-6A | 5 | 9 | 11 | | | | | | | | | | | | | | | | | vesicle | 0 | | |
| RAB7_RAT | P09527 | Ras-related protein Rab-7 | 9 | 11 | 13 | | | | | | | | | | | | | | | | | vesicle | 0 | | |
| RAB8B_RAT | P70550 | Ras-related protein Rab-8B | 2 | 5 | 5 | | | | | | | | | | | | | | | | | vesicle | 0 | | |
| RABE1_RAT | Q35550 | Rab GTPase binding effector protein 1 | 1 | 2 | 2 | | | | | | | | | | | | | | | | | vesicle | 0 | | |
| RAC1_RAT | Q6RUV5 | Ras-related C3 botulinum toxin substrate 1 | 6 | 8 | 8 | | | | | | | | | | | | | | | | | plasma membrane | 0 | | |
| RALA_RAT | P63322 | Ras-related protein Ral-A | 5 | 7 | 9 | | | | | | | | | | | | | | | | | vesicle | 0 | | |
| RALB_RAT | P36860 | Ras-related protein Ral-B | 0 | 4 | 4 | | | | | | | | | | | | | | | | | n.d. | 0 | | |
| RAP1A_RAT | P62836 | Ras-related protein Rap-1A | 4 | 4 | 5 | | | | | | | | | | | | | | | | | plasma membrane | 0 | | |
| RAP1B_RAT | Q62636 | Ras-related protein Rap-1b | 3 | 0 | 3 | | | | | | | | | | | | | | | | | vesicle | 0 | | |
| RAP2B_RAT | P61227 | Ras-related protein Rap-2b | 2 | 3 | 3 | | | | | | | | | | | | | | | | | vesicle | 0 | | |
| RASH_RAT | P20171 | Transforming protein p21/H-Ras-1 | 0 | 2 | 2 | | | | | | | | | | | | | | | | | n.d. | 0 | | |
| RASK_RAT | P08644 | Transforming protein p21 | 0 | 2 | 2 | | | | | | | | | | | | | | | | | n.d. | 0 | | |
| RASM_RAT | P97538 | Ras-related protein M-Ras | 0 | 1 | 1 | | | 75 | 1.8e-007 | 957.97 | 2+ | IFVPDYDPTIEDSYLK | | | | | | | | | | n.d. | 0 | | |
| RB11A_RAT | P62494 | Ras-related protein Rab-11A | 0 | 8 | 8 | | | | | | | | | | | | | | | | | plasma membrane | 0 | | |
| RB11B_RAT | Q35509 | Ras-related protein Rab-11B | 9 | 0 | 9 | | | | | | | | | | | | | | | | | vesicle | 0 | | |
| RED2_RAT | P97616 | Double-stranded RNA-specific endonuclease B2 | 0 | 1 | 1 | | | 30 | 0.012 | 467.17 | 2+ | TLAGIVMTK | | | | | | | | | | nucleus | 0 | | |
| RENB_P | P51607 | N-acetylglucosamine 2-epimerase | 0 | 1 | 1 | | | 29 | 0.018 | 429.79 | 2+ | VELLDAAK | | | | | | | | | | n.d. | 0 | | |
| RGS7_RAT | P49803 | Regulator of G-protein signaling 7 | 0 | 1 | 1 | | | 65 | 2.7e-006 | 729.38 | 2+ | FLSEFSSENLR | | | | | | | | | | synaptic vesicle | 0 | | |
| RHEB_RAT | Q62639 | GTP-binding protein Rheb | 0 | 1 | 1 | | | 43 | 0.00047 | 589.78 | 2+ | ENQTAVDVFR | | | | | | | | | | n.d. | 0 | | |
| RHOA_RAT | P61589 | Transforming protein RhoA | 3 | 8 | 9 | | | | | | | | | | | | | | | | | plasma membrane | 0 | | |
| RHOB_RAT | P62747 | Rho-related GTP-binding protein RhoB | 0 | 2 | 2 | | | | | | | | | | | | | | | | | plasma membrane | 0 | | |
| RIB1_RAT | P07153 | Dolichyl-diphosphooligosaccharide-protein glycosyltransferase 67 kDa subunit | 4 | 12 | 13 | | | | | | | | | | | | | | | | | endoplasmic reticulum | 2 | | |
| RIB2_RAT | P25235 | Dolichyl-diphosphooligosaccharide-protein glycosyltransferase 63 kDa subunit | 3 | 8 | 8 | | | | | | | | | | | | | | | | | endoplasmic reticulum | 3 | | |
| RL11_RAT | P62914 | 60S ribosomal protein L11 | 0 | 1 | 1 | | | 52 | 6.8e-005 | 488.25 | 2+ | YDGILLPGK | | | | | | | | | | cytoplasm | 0 | | |
| RL12_RAT | P23358 | 60S ribosomal protein L12 | 1 | 0 | 1 | | | 46 | 0.00021 | 441.40 | 2+ | IGPLGLSPK | | | | | | | | | | cytoplasm | 0 | | |
| RL13_RAT | P41123 | 60S ribosomal protein L13 | 0 | 3 | 3 | | | | | | | | | | | | | | | | | cytoplasm | 0 | | |
| RL13A_RAT | P36427 | 60S ribosomal protein L13a | 0 | 1 | 1 | | | 59 | 1.2e-005 | 626.81 | 2+ | YQAVTATLEEK | | | | | | | | | | cytoplasm | 0 | | |
| RL14_RAT | Q63507 | 60S ribosomal protein L14 | 0 | 1 | 1 | | | 86 | 1.9e-008 | 677.86 | 2+ | LVAIVDIDQNR | | | | | | | | | | cytoplasm | 0 | | |
| RL18_RAT | P12001 | 60S ribosomal protein L18 | 1 | 0 | 3 | | | | | | | | | | | | | | | | | cytoplasm | 0 | | |
| RL18A_RAT | P62718 | 60S ribosomal protein L18a | 0 | 1 | 1 | | | 30 | 0.013 | 453.22 | 2+ | NFGIWLK | | | | | | | | | | cytoplasm | 0 | | |
| RL19_RAT | P84100 | 60S ribosomal protein L19 | 0 | 1 | 1 | | | 75 | 3.5e-007 | 493.80 | 2+ | LLADQAEAR | | | | | | | | | | cytoplasm | 0 | | |
| RL21_RAT | P20280 | 60S ribosomal protein L21 | 0 | 1 | 1 | | | 49 | 8e-005 | 552.26 | 3+ | YYNVTOHAVGIIVNK | | | | | | | | | | cytoplasm | 0 | | |
| RL23_RAT | P62832 | 60S ribosomal protein L23 | 1 | 0 | 1 | | | 33 | 0.0053 | 450.83 | 2+ | GSAITGPVAK | | | | | | | | | | cytoplasm | 0 | | |
| RL23A_RAT | P62752 | 60S ribosomal protein L23a | 1 | 2 | 2 | | | | | | | | | | | | | | | | | cytoplasm | 0 | | |
| RL24_RAT | P83732 | 60S ribosomal protein L24 | 0 | 1 | 1 | | | 79 | 1.1e-007 | 639.32 | 2+ | AITGASLADIMAK + Oxidation (M) | | | | | | | | | | cytoplasm | 0 | | |
| RL26_RAT | P12749 | 60S ribosomal protein L26 | 0 | 1 | 1 | | | 36 | 0.0021 | 478.19 | 2+ | YVYIER | | | | | | | | | | cytoplasm | 0 | | |
| RL27_RAT | P61354 | 60S ribosomal protein L27 | 1 | 1 | 1 | | | 56 | 2.4e-005 | 525.25 | 2+ | YSVDIPLDK | | | | | | | | | | cytoplasm | 0 | | |
| RL31_RAT | P62902 | 60S ribosomal protein L31 | 1 | 1 | 1 | | | 61 | 9.3e-006 | 494.75 | 2+ | SAINVVVTR | | | | | | | | | | cytoplasm | 0 | | |
| RL32_RAT | P62912 | 60S ribosomal protein L32 | 1 | 0 | 1 | | | 44 | 0.0004 | 489.28 | 3+ | SYCAEIAHNVSSK | | | | | | | | | | cytoplasm | 0 | | |
| RL34_RAT | P11250 | 60S ribosomal protein L34 | 1 | 1 | 2 | | | | | | | | | | | | | | | | | cytoplasm | 0 | | |
| RL36_RAT | P17078 | 60S ribosomal protein L35 | 1 | 1 | 1 | | | 51 | 7.2e-005 | 572.31 | 2+ | VLTVINQTK | | | | | | | | | | cytoplasm | 0 | | |

| | | | | | | | | | | | | | | | | | | | | | | | |
|-----------|--------|---|----|----|----|--|-----|----------|--------|----|---------------------------|--|--|--|--|--|--|--|--|-----------------------|----|--|---|
| RL35A_RAT | P04646 | 60S ribosomal protein L35a | 2 | 1 | 2 | | | | | | | | | | | | | | | cytoplasm | 0 | | |
| RL38_RAT | P63174 | 60S ribosomal protein L38 | 1 | 0 | 1 | | 35 | 0.003 | 505.29 | 2+ | QSLPPGLAVK | | | | | | | | | cytoplasm | 0 | | |
| RL7_RAT | P05426 | 60S ribosomal protein L7 | 0 | 1 | 1 | | 106 | 2.3e-010 | 586.79 | 2+ | IALTDNSLVAR | | | | | | | | | cytoplasm | 0 | | |
| RL7A_RAT | P62425 | 60S ribosomal protein L7a | 1 | 1 | 2 | | | | | | | | | | | | | | | cytoplasm | 0 | | |
| RS13_RAT | P62278 | 40S ribosomal protein S13 | 0 | 1 | 1 | | 46 | 0.00025 | 546.28 | 2+ | GLSQSALPYR | | | | | | | | | cytoplasm | 0 | | |
| RS14_RAT | P13471 | 40S ribosomal protein S14 | 0 | 1 | 1 | | 39 | 0.00097 | 715.37 | 2+ | IIEVTPPIPSDSTR | | | | | | | | | cytoplasm | 0 | | |
| RS15A_RAT | P62246 | 40S ribosomal protein S15a | 0 | 1 | 1 | | 54 | 5.4e-005 | 495.76 | 2+ | MNVLADALK + Oxidation (M) | | | | | | | | | cytoplasm | 0 | | |
| RS16_RAT | P62250 | 40S ribosomal protein S16 | 0 | 1 | 1 | | 64 | 3.7e-006 | 547.84 | 2+ | LLEPVLLLGK | | | | | | | | | cytoplasm | 0 | | |
| RS18_RAT | P62271 | 40S ribosomal protein S18 | 3 | 7 | 7 | | | | | | | | | | | | | | | cytoplasm | 0 | | |
| RS19_RAT | P17074 | 40S ribosomal protein S19 | 0 | 1 | 1 | | 47 | 0.00016 | 485.74 | 2+ | VLQALEGLK | | | | | | | | | cytoplasm | 0 | | |
| RS20_RAT | P60868 | 40S ribosomal protein S20 | 1 | 1 | 1 | | 46 | 0.00022 | 450.94 | 3+ | LIDLHSPSEIVK | | | | | | | | | cytoplasm | 0 | | |
| RS25_RAT | P62853 | 40S ribosomal protein S25 | 1 | 1 | 2 | | | | | | | | | | | | | | | cytoplasm | 0 | | |
| RS26_RAT | P62856 | 40S ribosomal protein S26 | 2 | 1 | 2 | | | | | | | | | | | | | | | cytoplasm | 1 | | |
| RS3_RAT | P62909 | 40S ribosomal protein S3 | 0 | 1 | 1 | | 59 | 9e-006 | 735.92 | 2+ | DEILPTTPISEK | | | | | | | | | cytoplasm | 0 | | |
| RS6_RAT | P62755 | 40S ribosomal protein S6 | 0 | 1 | 1 | | 32 | 0.0077 | 494.76 | 2+ | LIEVDDER | | | | | | | | | cytoplasm | 0 | | |
| RS7_RAT | P62083 | 40S ribosomal protein S7 | 1 | 0 | 1 | | 31 | 0.0065 | 692.86 | 2+ | DVNFEPPEFQL | | | | | | | | | cytoplasm | 0 | | |
| RS8_RAT | P62343 | 40S ribosomal protein S8 | 0 | 1 | 1 | | 48 | 0.00012 | 657.93 | 2+ | LTPFEEELINK | | | | | | | | | cytoplasm | 0 | | |
| RS9_RAT | P23314 | 40S ribosomal protein S9 | 0 | 2 | 2 | | | | | | | | | | | | | | | cytoplasm | 0 | | |
| RTN1_RAT | Q64548 | Reticulon 1 | 7 | 3 | 7 | | | | | | | | | | | | | | | endoplasmic reticulum | 2 | | |
| RTN4_RAT | Q9JK11 | Reticulon 4 | 3 | 5 | 9 | | | | | | | | | | | | | | | plasma membrane | 3 | | |
| SI2A1_RAT | P56016 | Solute carrier family 12, member 1 | 0 | 1 | 1 | | 63 | 4.4e-006 | 528.71 | 2+ | GGGAYYLISR | | | | | | | | | plasma membrane | 12 | | |
| SI2A5_RAT | Q63633 | Solute carrier family 12, member 5 | 7 | 15 | 18 | | | | | | | | | | | | | | | plasma membrane | 13 | | |
| S38A3_RAT | Q9JH29 | System N amino acid transporter 1 | 4 | 6 | 7 | | | | | | | | | | | | | | | plasma membrane | 10 | | |
| S61A1_RAT | P61621 | Protein transport protein Sec61 alpha subunit isoform 1 | 0 | 1 | 1 | | 67 | 1.9e-006 | 486.23 | 2+ | IIEVGDTPK | | | | | | | | | endoplasmic reticulum | 10 | | |
| S6A11_RAT | P31647 | Sodium- and chloride-dependent GABA transporter 3 | 7 | 8 | 9 | | | | | | | | | | | | | | | plasma membrane | 12 | | |
| S6A13_RAT | P31646 | Sodium- and chloride-dependent GABA transporter 2 | 1 | 0 | 1 | | 46 | 0.00028 | 524.31 | 2+ | VEEDGTLER | | | | | | | | | plasma membrane | 13 | | |
| S6A17_RAT | P31662 | Orphan sodium- and chloride-dependent neurotransmitter transporter NTT4 | 1 | 4 | 5 | | | | | | | | | | | | | | | plasma membrane | 11 | | |
| SAP_RAT | P10960 | Sulfated glycoprotein 1 | 0 | 1 | 1 | | 48 | 0.00014 | 558.25 | 2+ | LVTDIQTAVR | | | | | | | | | extracellular | 0 | | |
| SC5A5_RAT | Q63008 | Sodium/iodide cotransporter | 2 | 3 | 3 | | | | | | | | | | | | | | | plasma membrane | 13 | | |
| SC6A1_RAT | P23978 | Sodium- and chloride-dependent GABA transporter 1 | 3 | 5 | 5 | | | | | | | | | | | | | | | plasma membrane | 12 | | |
| SC6A9_RAT | P28572 | Sodium- and chloride-dependent glycine transporter 1 | 2 | 5 | 5 | | | | | | | | | | | | | | | plasma membrane | 12 | | |
| SCAM1_RAT | P56603 | Secretory carrier-associated membrane protein 1 | 4 | 5 | 5 | | | | | | | | | | | | | | | plasma membrane | 4 | | |
| SCAM5_RAT | Q9JKE3 | Secretory carrier-associated membrane protein 5 | 2 | 2 | 2 | | | | | | | | | | | | | | | plasma membrane | 5 | | |
| SCN2A_RAT | P04775 | Sodium channel protein type II alpha subunit | 0 | 1 | 1 | | 51 | 8.6e-005 | 552.29 | 2+ | ISNDCELPR | | | | | | | | | plasma membrane | 24 | | |
| SCN2B_RAT | P54900 | Sodium channel beta-2 subunit | 2 | 1 | 2 | | | | | | | | | | | | | | | plasma membrane | 2 | | |
| SCRB1_RAT | P97943 | Scavenger receptor class B member 1 | 1 | 0 | 1 | | 40 | 0.0008 | 448.77 | 2+ | LTYQESR | | | | | | | | | plasma membrane | 4 | | |
| SCRB2_RAT | P27615 | Lysosome membrane protein II | 1 | 5 | 5 | | | | | | | | | | | | | | | lysosomes | 2 | | |
| SDC4_RAT | P34901 | Syndecan-4 | 1 | 1 | 2 | | | | | | | | | | | | | | | plasma membrane | 2 | | |
| SEPT7_RAT | Q9WVC0 | Septin 7 | 2 | 1 | 2 | | | | | | | | | | | | | | | cytoskeleton | 0 | | |
| SERA_RAT | Q08651 | D-3-phosphoglycerate dehydrogenase | 0 | 2 | 2 | | | | | | | | | | | | | | | cytoplasm | 0 | | |
| SFXN1_RAT | Q63965 | Sideroflexin 1 | 1 | 1 | 1 | | 47 | 0.00015 | 534.28 | 3+ | YAYDSAFHPDTGEK | | | | | | | | | mitochondria | 3 | | |
| SFXN3_RAT | Q9JHY2 | Sideroflexin 3 | 1 | 3 | 3 | | | | | | | | | | | | | | | mitochondria | 1 | | |
| SH3G1_RAT | Q35964 | SH3-containing GRB2-like protein 1 | 0 | 2 | 2 | | | | | | | | | | | | | | | cytoplasm | 0 | | |
| SH3G2_RAT | Q35179 | SH3-containing GRB2-like protein 2 | 1 | 0 | 1 | | 44 | 0.00025 | 929.47 | 2+ | ALYDFEPENEGELGFK | | | | | | | | | plasma membrane | 0 | | |
| SHPS1_RAT | P97710 | Tyrosine-protein phosphatase non-receptor type substrate 1 | 3 | 7 | 7 | | | | | | | | | | | | | | | plasma membrane | 2 | | |
| SNAA_RAT | P54921 | Alpha-soluble NSF attachment protein | 0 | 1 | 1 | | 65 | 3.1e-006 | 695.38 | 2+ | LDOWLTTMLLR | | | | | | | | | cytoplasm | 0 | | |
| SNG1_RAT | Q62876 | Synaptogyrin-1 | 2 | 2 | 2 | | | | | | | | | | | | | | | plasma membrane | 4 | | |
| SNG2_RAT | Q54980 | Synaptogyrin-2 | 0 | 1 | 1 | | 64 | 4.6e-006 | 588.85 | 2+ | YVSQPQVVTR | | | | | | | | | plasma membrane | 4 | | |
| SNP23_RAT | Q70377 | Synaptosomal-associated protein 23 | 1 | 3 | 3 | | | | | | | | | | | | | | | plasma membrane | 0 | | |
| SNP25_RAT | P60881 | Synaptosomal-associated protein 25 | 14 | 21 | 24 | | | | | | | | | | | | | | | plasma membrane | 0 | | |
| SNP29_RAT | Q9Z2P6 | Synaptosomal-associated protein 29 | 1 | 1 | 2 | | | | | | | | | | | | | | | plasma membrane | 0 | | |
| SO1A5_RAT | Q88397 | Solute carrier organic anion transporter family, member 1A5 | 3 | 5 | 5 | | | | | | | | | | | | | | | plasma membrane | 12 | | |
| SO2B1_RAT | Q9JH13 | Solute carrier organic anion transporter family, member 2B1 | 2 | 1 | 2 | | | | | | | | | | | | | | | plasma membrane | 12 | | |
| SORT_RAT | Q54861 | Sortilin | 0 | 1 | 1 | | 46 | 0.00021 | 485.26 | 2+ | IYSFGLGGR | | | | | | | | | plasma membrane | 1 | | |
| SPC18_RAT | P42667 | Microsomal signal peptidase 18 kDa subunit | 1 | 2 | 2 | | | | | | | | | | | | | | | endoplasmic reticulum | 2 | | |
| SPC21_RAT | Q9WTR7 | Microsomal signal peptidase 21 kDa subunit | 1 | 2 | 2 | | | | | | | | | | | | | | | endoplasmic reticulum | 2 | | |
| SP7A2_RAT | P16086 | Spectrin alpha chain, brain | 2 | 4 | 5 | | | | | | | | | | | | | | | plasma membrane | 0 | | |
| SRC_RAT | Q9WUD9 | Proto-oncogene tyrosine-protein kinase SRC | 0 | 1 | 1 | | 33 | 0.0044 | 520.30 | 2+ | LLLNAENPR | | | | | | | | | n.d. | 0 | | |
| SSRD_RAT | Q07984 | Translocon-associated protein, delta subunit | 4 | 4 | 5 | | | | | | | | | | | | | | | endoplasmic reticulum | 2 | | |
| SSRG_RAT | Q08013 | Translocon-associated protein, gamma subunit | 1 | 1 | 1 | | 57 | 1.3e-005 | 569.98 | 3+ | QQSEEDLLQDFSR | | | | | | | | | endoplasmic reticulum | 14 | | |
| STMN2_RAT | P21818 | Stathmin 2 | 1 | 0 | 1 | | 45 | 0.00029 | 550.33 | 2+ | EANLAAIER | | | | | | | | | plasma membrane | 0 | | |
| STMN3_RAT | Q9JHU6 | Stathmin 3 | 0 | 1 | 1 | | 62 | 5.8e-006 | 589.77 | 2+ | ASGQSFEVILK | | | | | | | | | plasma membrane | 0 | | |
| STX1A_RAT | P32851 | Syntaxin-1A | 21 | 18 | 27 | | | | | | | | | | | | | | | plasma membrane | 1 | | |
| STX1C_RAT | P61265 | Syntaxin-1B2 | 0 | 1 | 1 | | | | | | | | | | | | | | | plasma membrane | 1 | | |
| STX2_RAT | P50279 | Epimorphin | 2 | 1 | 1 | | 42 | 0.0005 | 491.91 | 3+ | NVNSVDYVEHAK | | | | | | | | | plasma membrane | 1 | | |
| STX3_RAT | Q08849 | Syntaxin-3 | 1 | 3 | 3 | | | | | | | | | | | | | | | plasma membrane | 1 | | |
| STX4_RAT | Q08860 | Syntaxin-4 | 3 | 5 | 7 | | | | | | | | | | | | | | | plasma membrane | 1 | | |
| STX6_RAT | Q63635 | Syntaxin-6 | 6 | 6 | 8 | | | | | | | | | | | | | | | plasma membrane | 1 | | |
| STX7_RAT | Q70257 | Syntaxin-7 | 4 | 5 | 7 | | | | | | | | | | | | | | | plasma membrane | 1 | | |
| STX8_RAT | Q9Z2Q7 | Syntaxin-8 | 1 | 2 | 2 | | | | | | | | | | | | | | | plasma membrane | 1 | | |
| STXB1_RAT | P61765 | Syntaxin binding protein 1 | 6 | 12 | 13 | | | | | | | | | | | | | | | plasma membrane | 0 | | x |
| SV2_RAT | Q02563 | Synaptic vesicle protein 2 | 5 | 6 | 8 | | | | | | | | | | | | | | | synaptic vesicle | 12 | | |
| SYCP1_RAT | Q03410 | Synaptonemal complex protein 1 | 1 | 1 | 1 | | 32 | 0.0077 | 488.20 | 2+ | DELESVRK | | | | | | | | | nucleus | 0 | | |
| SYJ2B_RAT | Q9WVJ4 | Synaptotagmin 2 binding protein | 1 | 0 | 1 | | 50 | 0.0001 | 543.87 | 2+ | IILSVNGDLK | | | | | | | | | mitochondria | 1 | | |
| SYN1_RAT | P09951 | Synapsin-1 | 0 | 1 | 1 | | 31 | 0.0059 | 663.87 | 2+ | TYATAEPFIDAK | | | | | | | | | synaptic vesicle | 0 | | |
| SYN2_RAT | Q63537 | Synapsin-2 | 0 | 1 | 1 | | 33 | 0.0033 | 541.39 | 3+ | VLLVDEPHTDWAK | | | | | | | | | synaptic vesicle | 0 | | |
| SYNPR_RAT | P22831 | Synaptoporphin | 1 | 1 | 1 | | 63 | 4.1e-006 | 590.36 | 2+ | EVLLLSACK + Oxidation (M) | | | | | | | | | synaptic vesicle | 4 | | |

