

Supplemental Documents

Supplemental Materials and Methods

Characterization of aggregated SNCA

Lyophilized SNCA (purchased from R-Peptide) was dissolved in PBS at pH 7.4 prior to centrifugation at 85,000 rpm with a Beckman ultracentrifuge to remove any aggregated material. The protein solution (1 mg/ml; 70 μ M) was stirred at 37 °C with a mini-Teflon stir bar for 6 hrs. The aggregates prepared with this protocol (Liu et al., 2007) were identical to those generated by aging SNCA for 7 days *in vitro* without constant stirring (Zhang et al., 2005). The characteristics of aggregated SNCA include a size of 44-158 kDa and morphological structures of 3-5 nm diameters when determined by size exclusion chromatography and transmission electron microscopy (TEM), respectively. Additionally, these aggregates are congophilic that are demonstrable readily with thioflavin T fluorescence assays. More details on the methods of generating and charactering SNCA aggregates can be found in the two papers published from our lab previously (see Supplemental References below).

Sucrose density gradient

After treating with eSNCA and the pulse-chase experiment, MES cells were collected in 500 μ l of sucrose buffer [8% (w/v) sucrose in 20 mM Hepes, pH 7.3, and 1 mM EDTA], followed by a centrifugation at 1000 \times *g* for 10 min. Next, 360 μ l of the post-nuclear supernatant was loaded on the top of a tube containing 360 μ l aliquots of 40, 37, 34, 31, 28, 25, 22, 19, 16, 13, and 10% (w/v) sucrose in 20 mM Hepes, pH 7.3, 1 mM EDTA, sequentially overlaid. After centrifugation at 55,000 rpm in a SW60Ti rotor, 250 μ l were collected from the bottom of the tube, and resolved by SDS-PAGE.

Neurite outgrowth assay

MES cells were seeded onto a poly-D-lysine coated 4-well Lab-Tek II chambered coverglass (Nagle Nunc) at 0.01×10^6 /well. After 24 hrs incubation, cells were treated and fixed in 4% formaldehyde, followed by staining with a rabbit anti-MAP2 antibody

(1:1000) and a goat anti-rabbit IgG Alexa Fluor 568 secondary antibody (Invitrogen). Images of five randomly selected fields were then captured using a laser scanning confocal microscope. The length of neurites on MAP2+ cells and number of branching points were quantified using Neurolucida software (version 8.0, MicroBrightField, Williston, VT, USA) by an observer blind to the experimental settings.

SILAC MES proteome labeling

SILAC - stable isotope labeling for amino acids in culture - was carried with MES cells cultured using arginine and lysine depleted media. For cultures exposed to vehicle and eSNCA treatment, $^{12}\text{C}_6^{14}\text{N}_4$ L-arginine, $^{12}\text{C}_6^{14}\text{N}_2$ lysine (light) and $^{13}\text{C}_6^{15}\text{N}_4$ L-arginine, $^{13}\text{C}_6^{15}\text{N}_2$ lysine (heavy) were added, respectively. Cells were incubated at 37°C for at least five generations (Liu et al., 2007).

Protein analysis by $\mu\text{LC-MS/MS}$

The purified, labeled peptides were separated by a two dimensional microcapillary high performance liquid chromatography system, which integrates a strong cation-exchange (SCX) column (100 mm in length \times 0.32 mm inner diameter; particle size: 5 μm) with two alternating reverse phase (RP) μC18 columns (100 mm in length \times 0.18 mm inner diameter), followed by analysis of each peptide with tandem mass spectrometry (MS/MS) using an LCQ DECA XP PLUS ion trap (ThermoElectron, San Jose, CA, USA). Briefly, six fractions were eluted from SCX using a binary gradient of 2–90% solvent D (1.0 M ammonium chloride and 0.1% formic acid in 5% acetonitrile) versus solvent C (0.1% formic acid in 5% acetonitrile). Each fraction was injected into a RP μC18 column automatically with the peptides being resolved using a 120 min binary gradient of 5–80% solvent B (0.1% formic acid in acetonitrile) versus solvent A (0.1% formic acid in water). A flow rate of 160 $\mu\text{l}/\text{min}$ with a split ratio of 1/80 was used. Peptides were eluted directly into the electrospray ionization (ESI) ion trap MS capable of data-dependent acquisition.

The intensities of eluting peptide pairs (light *versus* heavy) were measured in the scanning mass spectrometer. Nonetheless, the entire peak area of each eluting peptide was reconstructed and used in the ratio calculation. To determine the amino acid sequence, the mass spectrometer operated in a data-dependent MS/MS mode (a full-scan mass spectrum followed by a tandem mass spectrum), where the precursor ion was selected "on the fly" from the previous scan. An m/z ratio for an ion that had been selected for fragmentation was placed in a list and dynamically excluded for 3 min from further fragmentation. Proteins from the mixture were later identified automatically using the computer program Sequest, which searched tandem mass spectra against the International Protein Index (IPI) database (ipi.rat-mouse.fasta, V3.24). Search parameters for Sequest used in this study were the following: tryptic; +10Da for ^{13}C ^{15}N isotopic-labeled arginine, +8Da for ^{13}C ^{15}N isotopic-labeled lysine and +16Da for oxidized methionine as differential options; +57 Da for carbamidomethyl cysteine as static option; mass tolerance \pm 3Da. Potential peptides and proteins were further analyzed with two software programs, PeptideProphetTM and ProteinProphetTM to enhance confidence of protein identification based on statistical models. PeptideProphetTM uses various SequestTM scores and a number of other parameters to calculate a probability score for each identified peptide. The peptides are then assigned a protein identification using ProteinProphetTM. ProteinProphetTM allows filtering of large-scale data sets with assessment of predictable sensitivity and false-positive identification error rates. In our study, only proteins with a high probability of accuracy ($p=1$, determined by ProteinProphetTM) were selected.

Relative protein abundance in experimental groups compared to controls was calculated using an algorithm termed the Automated Statistical Analysis of Protein abundance (ASAP) ratio. The algorithm utilized for calculation of ASAP Ratios of signals recorded for the different isotopic forms of peptides of identical sequence are based on numerical and statistical methods, such as Savitzky-Golay smoothing filters, statistics for weighted samples, and Dixon's test for outliers, to evaluate protein

abundance ratios and their associated errors. Information about these software tools and the software tools themselves can be found on line at www.systemsbio.org/Default.aspx?pagename_proteomicssoftware and downloaded freely (Liu et al., 2007).

Gene Ontology

All protein identifications were derived from the International Protein Index (IPI) database (version 3.24). The identified proteins were classified by cellular components and biological functions using Gene Ontology (GO) analysis as previously described (Shi et al., 2008).

Supplemental Results

Endosome-lysosome system plays a role in the traffic of eSNCA

Most internalized macromolecules are degraded by lysosomes via trafficking through a series of vesicular compartments. Usually the internalized products initially fuse with early endosomes, which in turn reach late endosomes either by budding off transport vesicles or by directly maturing to late endosomes and then into lysosomes for degradation. As a result, we investigated whether internalized eSNCA also followed this pathway, by analyzing the distribution of internalized eSNCA in the endosome-lysosome system of MES cells after sucrose gradient ultracentrifugation. The results, shown in **Fig S1**, demonstrated that internalized eSNCA was readily detectable at 0 hr of chase (after 3 hrs exposure), reached a plateau 3 hrs after chase, but started to decrease by 6 hrs after chasing (**Fig S1A**). **Fig S1B** indicated that the internalized eSNCA largely stayed in early endosomes (marker EEA1) at 0 hr of chase, but moved to the late endosomes (marker Lamp-1) by 3 and 6 hrs. The distribution of internalized eSNCA, as determined by sucrose gradient ultracentrifugation, was also confirmed by immunochemistry. More specifically, early endosomes and late endosomes were visualized with confocal microscopy at different time points after eSNCA treatment. As can be seen in **Fig S1C**, the merged images reveal that a majority of internalized eSNCA was co-localized with EEA1 and Lamp-1, 0, 3 or 6 hrs after chase, respectively.

Proteomic identification of proteins interacting with rab11a

245 proteins were identified after the results from three independent runs were combined [all identification with $p=1$, as determined by ProteinProphet (see detailed methods) and unique peptides ≥ 2]. The function of total identified proteins associated with rab11a was cataloged for their cellular location and molecular function based on GO analysis. Cellular location of these proteins included cytoplasm, lysosome/proteasome, endoplasmic reticulum (ER/Golgi), mitochondrion, and nucleus. With respect to molecular function, these proteins included transport, signal

transduction, protein modification, cell cycle, and metabolism. A graphic presentation of protein groups and a detailed list of proteins can be found in **Fig S4**, and **Appendix I**, respectively. Among identified proteins, 6 and 12 proteins in three separate experiments increased and decreased, respectively, between MES cells treated with and without eSNCA. It should be noted that proteins with changes in relative abundance are less likely to be contaminants or non-specific binding proteins during affinity purification. Additionally, these proteins are likely regulators of the processes involved in eSNCA endocytosis and/or subsequent effects of internalized eSNCA. Proteins that were altered in relative abundance after treatment with eSNCA and are potentially important to PD pathogenesis based on current knowledge are listed in **Supplemental Table 1**.

Figure S1. A) The amount of internalized SNCA at different chase periods. MES cells were pulsed with human eSNCA for 3 hrs and washed extensively. Next, fresh medium was added and cells were chased for different time points. Western blotting measurements elucidated the extent of internalization of eSNCA with β -actin as an internal control. Results were obtained from at least three independent experiments. **B)** Sucrose gradient fractionation procedure was developed to isolate the early-endosome/late-endosome systems. Cells were homogenized and adjusted to 10-40% discontinuous sucrose gradient centrifugation. Detection of EEA1 and Lamp-1, early endosome marker and late endosome marker respectively, was achieved by western blotting for each fraction. EEA1 was detected in fractions 4, 5, 6, 7, 8, 9, and 10. Lamp-1 was notable in fraction 2, 3, 4 and 5. **C)** MES cells were treated with pre-fluorescent labeled eSNCA at 250nM, chased for different times before being incubated with early endosome marker (EEA1), late-endosome marker (Lamp-1), respectively. The results were followed by fluorescent labeled secondary antibodies and examined with a confocal microscope. It was apparent that internalized eSNCA was co-localized both in early endosomes at chase 0 hr but largely moved to late-endosomes by 3-6 hrs chase (shown in merge column as yellow color).

Figure S2. Cells were pulsed with human eSNCA for 3 hrs and washed extensively with PBS. Fresh FBS-free medium was added, and cells were chased at different time points at 37°C and 18°C. At the end of the experiment, the media was collected, and eSNCA was detectable 3-6 hrs after the chase at 37°C. The eSNCA in the two time points of low temperature cannot be detected.

Figure S3. The amount of internalized eSNCA after silencing rab11a.

MES cells were pulsed with human pre-aggregated eSNCA for 3 hrs, and washed extensively with PBS after knocking down rab11a expression. The cells were collected and the uptake of eSNCA was measured. Western blotting measurements demonstrated that the internalization of eSNCA was not affected by rab11a siRNA in the MES cells (as compared to controls [CTL] and non-sense [NS] siRNA transfections), with β -actin as an internal control. Results were obtained from at least three independent experiments.

Figure S4. GO analysis and annotation of total proteins identified by 2 or more peptides (proteins identified with high confidence). **(A)** Proteins are classified according to their cellular components. **(B)** Proteins are classified based on their participation in specific biological functions.

Supplemental Table 1: Proteins Potentially Associated with PD Process

| IPI No. | Common Name/ Function | GO Annotation Cellular Component | Ratio |
|----------------|---|---|--------------|
| IPI00210945.7 | Tropomyosin alpha-1 chain/ Binds to actin filaments | Cytoplasm | 0.06±0.01 |
| IPI00230507.5 | ATP synthase subunit d mitochondrial/ Produces ATP from ADP in the presence of a proton gradient across the membrane generated by electron transport complexes of the respiratory chain | Mitochondrion | 0.57±0.04 |
| IPI00467338.4 | Ran GTPase-activating protein 1/ GTPase activator for the nuclear Ras-related regulatory protein | Cytoplasm | 0.57±0.14 |
| IPI00128491.1 | Adenine phosphoribosyltransferase/ Catalyzes a salvage reaction | Cytoplasm | 0.66±0.14 |
| IPI00133903.1 | Hspa9 stress-70 protein mitochondrial precursor/ Controls cell proliferation and cellular aging, also acts as a chaperone. | Mitochondrion | 1.53±0.21 |
| IPI00210566.3 | Heat shock protein 90-alpha/ Molecular chaperone and has ATPase activity | Cytoplasm | 1.65±0.26 |
| IPI00317794.5 | Nucleolin/ Plays a role in pre-rRNA transcription and ribosome assembly | Nucleus | 2.75±0.38 |
| IPI00227392.5 | 14-3-3 protein eta/ Adapter protein implicated in the regulation of a large spectrum of both general and specialized signaling pathway. | Cytoplasm | 2.30±0.31 |
| IPI00120984.5 | NADH dehydrogenase 1 alpha subcomplex subunit 8/ The immediate electron acceptor for the enzyme is believed to be ubiquinone | Mitochondrion | 3.79±0.36 |
| IPI00129516.1 | Cytochrome b-c1 complex subunit 6 mitochondrial precursor/ Mediates formation of the complex between cytochromes c and c1 | Mitochondrion | 6.13±0.41 |

Protein identifications are based on the IPI Rat-Mouse protein database (version 3.24). Protein functions are from the UniProtKB/Swiss-Prot database. Ratio: Relative protein

abundance in control groups compared to experimental groups (control/ $^{12}\text{C}_6^{14}\text{N}_4$ L-arginine, $^{12}\text{C}_6^{14}\text{N}_2$ lysine-labeled vs SNCA treatment/ $^{13}\text{C}_6^{15}\text{N}_4$ L-arginine, $^{13}\text{C}_6^{15}\text{N}_2$ lysine-labeled), calculated by an algorithm termed ASAP ratio. PD, Parkinson disease; IPI, International protein index; GO, Gene Ontology.

Supplemental Appendix I: Proteins/Protein Groups associated with rab11a

| Name(IPI) | Common Name | # of peptides |
|---|---|---------------|
| IPI00210945.7 IPI00227835.1 IPI00830884.1 | Tropomyosin 1 alpha isoform c Isoform 2 of tropomyosin alpha-1 chain 33 kDa protein | 6 |
| IPI00132963.1 | Zinc finger protein 706 | 3 |
| IPI00230507.5 IPI00623553.1 | ATP synthase subunit d mitochondrial LOC100039281 hypothetical protein | 3 |
| IPI00467338.4 IPI00471774.3 | Ran GTPase-activating protein 1 Ran GTPase activating protein 1 | 4 |
| IPI00471240.1 | Insulinoma-associated protein 1 | 2 |
| IPI00128491.1 IPI00625950.2 | Adenine phosphoribosyltransferase Aadenine phosphoribosyl transferase | 3 |
| IPI00719915.1 | Isoform 1 of ribonucleoprotein PTB-binding 1 | 2 |
| IPI00230830.5 IPI00474446.4 | Eukaryotic translation initiation factor 2 subunit 1 Eukaryotic translation initiation factor 2 subunit 1 | 7 |
| IPI00116279.3 | Cct5 T-complex protein 1 subunit epsilon | 15 |
| IPI00227299.6 IPI00230941.5 | Vimentin Vimentin | 6 |
| IPI00130353.5 | Valyl-tRNA synthetase | 4 |
| IPI00316740.4 IPI00324451.3 | DNA damage-binding protein 1 DNA damage-binding protein 1 | 3 |
| IPI00272238.5 | Methionine aminopeptidase | 10 |
| IPI00119581.2 IPI00208091.2 IPI00330634.1 IPI00848611.1 | LOC100044829 rRNA 2'-O-methyltransferase fibrillar rRNA 2'-O-methyltransferase fibrillar A1595406 rRNA/tRNA 2'-O-methyltransferase fibrillar-like LOC100044829 similar to fibrillar isoform 2 | 2 |
| IPI00196994.1 IPI00322312.3 | Rho GDP dissociation inhibitor (GDI) alpha Rho GDP-dissociation inhibitor 1 | 6 |
| IPI00231046.8 IPI00277001.4 | Proteasome subunit alpha type-4 Proteasome subunit alpha type-4 | 2 |
| IPI00117569.3 IPI00197713.9 IPI00625021.1 IPI00762542.2 IPI00782711.1 | Adult male cerebellum cDNA RIKEN full-length enriched library clone:1500004H08 product:ribosomal protein s11 full insert sequence 40S ribosomal protein S11 LOC100047777 hypothetical protein 40S ribosomal protein S11 20 kDa protein | 3 |
| IPI00130589.8 | Superoxide dismutase | 5 |
| IPI00130627.1 IPI00206298.3 IPI00515816.1 | Legumain precursor Legumain precursor Legumain | 2 |
| IPI00121319.1 IPI00200352.1 | Cysteine-rich protein 2 Cysteine-rich protein 2 | 4 |
| IPI00605037.1 IPI00648313.1 | Isoform 1 of Serine/arginine repetitive matrix protein 1 Serine/arginine repetitive matrix 1 | 3 |
| IPI00118384.1 IPI00325135.3 | 14-3-3 Protein epsilon 14-3-3 Protein epsilon | 8 |
| IPI00122696.5 IPI00366789.2 IPI00766382.1 IPI00828412.1 | Histone-binding protein RBBP4 Rbbp4 retinoblastoma binding protein 4 Similar to retinoblastoma binding protein 4 isoform 1 Rbbp4 retinoblastoma binding protein 4 | 3 |
| IPI00475138.1 IPI00551236.3 IPI00648723.1 IPI00649157.1 | LOC100039888 similar to Pr22 isoform 1 Stathmin 12 kDa protein 17 kDa protein | 7 |
| IPI00555187.2 | Adenylyl cyclase-associated protein 1 | 5 |
| IPI00116277.3 | T-complex protein 1 subunit delta | 18 |
| IPI00367441.3 | 50 kDa protein | 3 |
| IPI00779007.1 | 50 kDa protein | 4 |
| IPI00137787.3 IPI00215208.3 | 60S ribosomal protein L8 60S ribosomal protein L8 | 6 |
| IPI00314788.5 | Argininosuccinate lyase | 4 |

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|---|---|----|
| IPI00204375.2 IPI00313962.3 IPI00653686.1 IPI00777816.1 | Ubiquitin carboxyl-terminal hydrolase isozyme L1 Ubiquitin carboxyl-terminal hydrolase isozyme L1 NOD-derived CD11c +ve dendritic cells cDNA RIKEN full-length enriched library clone:F630116G18 product:ubiquitin carboxy-terminal hydrolase L1 full insert sequence (Fragment) 25 kDa protein | 11 |
| IPI00191444.3 IPI00269481.7 IPI00365283.1 IPI00406800.4 IPI00474883.2 IPI00649604.1 IPI00776140.1 IPI00776265.1 IPI00776374.1 | 31 kDa protein Isoform 2 of f-actin-capping protein subunit beta F-actin-capping protein subunit beta Isoform 1 of f-actin-capping protein subunit beta Capping protein (actin filament) muscle z-line beta Capping protein (actin filament) muscle z-line beta Capping protein (actin filament) muscle z-line beta Capping protein (actin filament) muscle z-line beta Capping protein (actin filament) muscle z-line beta | 6 |
| IPI00130280.1 IPI00857439.1 | ATP synthase subunit alpha mitochondrial precursor 55 kDa protein | 8 |
| IPI00114209.1 IPI00324633.2 | Glutamate dehydrogenase 1 mitochondrial precursor Glutamate dehydrogenase 1 mitochondrial precursor | 3 |
| IPI00113845.1 | Proteasome subunit beta type-1 precursor | 4 |
| IPI00137730.7 | Phosphatidylethanolamine-binding protein 1 | 20 |
| IPI00109813.1 | 12 days embryo head cDNA, RIKEN full-length enriched library, clone:3010025E17 product:Heterogeneous nuclear ribonucleoprotein A0 (hnRNP A0) homolog | 5 |
| IPI00126248.3 IPI00214665.2 IPI00214801.3 IPI00762047.1 | Adult male testis cDNA RIKEN full-length enriched library clone:4922505F07 product:ATP citrate lyase full insert sequence ATP citrate lyase isoform 1 Isoform 2 of ATP-citrate synthase ATP-citrate synthase | 6 |
| IPI00373591.3 | Far upstream element (FUSE) binding protein 1 | 11 |
| IPI00117264.1 | Protein DJ-1 | 3 |
| IPI00318841.4 IPI00408350.1 IPI00470317.5 IPI00664589.1 | Elongation factor 1-gamma Hypothetical protein isoform 1 Elongation factor 1-gamma LOC633223 hypothetical protein isoform 1 | 4 |
| IPI00555113.2 IPI00557647.1 | 60S ribosomal protein L18 21 kDa protein | 2 |
| IPI00275539.6 IPI00469392.2 IPI00470167.3 | RTN4 Isoform 1 of reticulon-4 Nogo-B | 2 |
| IPI00122565.1 IPI00197568.2 IPI00416577.1 IPI00566673.1 | Isoform 1 of rab GDP dissociation inhibitor beta Rab GDP dissociation inhibitor beta Isoform 2 of Rab GDP dissociation inhibitor beta 47 kDa protein | 5 |
| IPI00363565.3 IPI00469103.1 IPI00560366.2 IPI00620145.1 IPI00666196.1 | 68 kDa protein Lysyl-tRNA synthetase Lysyl-tRNA synthetase Lysyl-tRNA synthetase LOC631033 similar to lysyl-tRNA synthetase isoform 1 | 5 |
| IPI00205912.3 IPI00320016.7 | Non-POU domain-containing octamer-binding protein Isoform 1 of Non-POU domain-containing octamer-binding protein | 4 |
| IPI00230440.6 IPI00476295.7 | ENSMUSG00000048538;Ahcy Adenosylhomocysteinase Ahcy Adenosylhomocysteinase | 5 |
| IPI00221581.1 IPI00373045.1 | Eukaryotic translation initiation factor 4B Eukaryotic translation initiation factor 4B | 8 |
| IPI00353563.4 IPI00763106.1 IPI00767873.1 | Fascin LOC683788 similar to fascin (singed-like protein) isoform 1 LOC683788 similar to fascin (singed-like protein) isoform 2 | 10 |
| IPI00120045.1 IPI00263863.8 | EG628438;Hspe1-rs1 CPN10-like protein 10 kDa heat shock protein mitochondrial | 11 |
| IPI00129526.1 IPI00365985.4 IPI00734561.1 | Hsp90b1 Endoplasmin precursor Tra1_predicted 93 kDa protein Tra1_predicted tumor rejection antigen gp96 | 4 |
| IPI00137409.3 | Transketolase | 18 |
| IPI00229080.7 IPI00471584.7 | Heat shock protein 84b Heat shock protein HSP 90-beta | 36 |
| IPI00230139.5 | FK506-binding protein 4 | 3 |
| IPI00198590.2 IPI00460253.2 IPI00560357.1 IPI00849741.1 IPI00856171.1 | Protein BUD31 homolog Protein BUD31 homolog 12 kDa protein LOC100045848 similar to BUD31 homolog (S. cerevisiae) isoform 1 17 kDa protein | 3 |

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|---|--|----|
| IPI00131186.2 IPI00372004.2 IPI00515257.1 | LOC100041823 isoform 2 of transcription factor BTF3 Basic transcription factor 3 Isoform 1 of transcription factor BTF3 | 9 |
| IPI00116281.3 IPI00188111.1 IPI00780515.1 | T-complex protein 1 subunit zeta Chaperonin subunit 6a Cct6a protein | 14 |
| IPI00323592.2 | Malate dehydrogenase, mitochondrial precursor | 27 |
| IPI00133185.3 IPI00473728.1 | 60S ribosomal protein L14 ES cells cDNA RIKEN full-length enriched library clone:2410026P17 product:ribosomal protein L14 cytosolic homolog | 3 |
| IPI00370815.3 IPI00469268.5 | Predicted chaperonin subunit 8 Complex protein 1 subunit theta | 11 |
| IPI00464735.1 | Cell growth-regulating nucleolar protein | 3 |
| IPI00554989.3 | Peptidyl-prolyl cis-trans isomerase | 5 |
| IPI00133801.3 IPI00365946.3 | EG625193 nuclear protein hcc-1 RGD1305692 nuclear protein hcc-1 | 11 |
| IPI00222419.5 IPI00231864.5 IPI00265239.1 IPI00362298.1 | Cytochrome c somatic Cytochrome c somatic LOC100045925 similar to cytochrome c LOC684936 similar to cytochrome c somatic | 15 |
| IPI00468481.2 | ATP synthase subunit beta, mitochondrial precursor | 17 |
| IPI00265471.2 IPI00308217.1 | Lung RCB-0558 LLC cDNA RIKEN full-length enriched library clone:G730029K06 product:adenylosuccinate lyase full insert sequence Adenylosuccinate lyase | 4 |
| IPI00113223.2 | Fatty acid synthase | 6 |
| IPI00327830.3 | Fatty acid-binding protein, epidermal | 9 |
| IPI00126338.5 | Isoform alpha of lamina-associated polypeptide 2 isoforms alpha/zeta | 11 |
| IPI00221402.7 IPI00856379.1 | Fructose-bisphosphate aldolase A Fructose-bisphosphate aldolase | 23 |
| IPI00122350.4 | Small nuclear ribonucleoprotein A | 5 |
| IPI00127707.1 IPI00221796.1 IPI00608171.1 | Isoform 1 of poly(rc)-binding protein 2 Isoform 2 of poly(rc)-binding protein 2 Pcbp2 protein | 6 |
| IPI00201500.8 IPI00322562.5 | 40S ribosomal protein s14 40S ribosomal protein s14 | 6 |
| IPI00119478.1 IPI00373505.2 | Tropomodulin-3 Tropomodulin 3 | 3 |
| IPI00111831.1 IPI00121297.1 IPI00371266.1 IPI00766113.2 | Nascent polypeptide-associated complex subunit alpha muscle-specific form Nascent polypeptide-associated complex subunit alpha Predicted nascent-polypeptide-associated complex alpha polypeptide Predicted 214 kDa protein | 10 |
| IPI00134621.3 IPI00212796.3 | LOC100045999 GTP-binding nuclear protein Ran Ran GTP-binding nuclear protein Ran | 16 |
| IPI00123313.1 | Ubiquitin-like modifier-activating enzyme 1 X | 6 |
| IPI00123333.5 IPI00364589.1 | WW domain-binding protein 11 WW domain-binding protein 11 | 5 |
| IPI00134599.1 IPI00212776.1 | 40S ribosomal protein s3 40S ribosomal protein s3 | 24 |
| IPI00231134.4 IPI00317740.5 | Guanine nucleotide-binding protein subunit beta-2-like 1 Guanine nucleotide-binding protein subunit beta-2-like 1 | 12 |
| IPI00116074.1 | Aconitate hydratase, mitochondrial precursor | 15 |
| IPI00127415.1 IPI00197553.1 IPI00515155.1 IPI00778173.1 IPI00849626.1 | Nucleophosmin Isoform B23.1 of nucleophosmin Nucleophosmin 1 30 kDa protein LOC100046628 similar to nucleophosmin | 22 |
| IPI00393643.4 IPI00421451.4 IPI00469918.4 IPI00566464.2 IPI00767883.1 IPI00850220.1 IPI00881758.1 | RGD1559743_predicted similar to 40s ribosomal protein s16 Similar to 40s ribosomal protein s16 ENSMUSG00000060419 Rps16 protein 19 kDa protein LOC691983 similar to 40S ribosomal protein S16 LOC100047501 similar to rps16 protein ENSMUSG00000060419 | 2 |
| IPI00116254.1 IPI00208209.1 | Peroxisredoxin-4 PRx IV | 3 |

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|---|---|----|
| IPI00124979.2 IPI00370207.3 IPI00474144.1 IPI00559910.1 IPI00663587.1 IPI00763272.1 IPI00766882.1 IPI00775821.1 IPI00775899.1 | Heterogeneous nuclear ribonucleoprotein G LOC302855 Similar to heterogeneous nuclear ribonucleoprotein G-human 42 kDa protein Predicted heterogeneous nuclear ribonucleoprotein G RNA binding motif protein X chromosome retrogene Similar to Heterogeneous nuclear ribonucleoprotein G (hnRNP G) (RNA-binding motif protein X chromosome) isoform 1 Similar to Heterogeneous nuclear ribonucleoprotein G (hnRNP G) (RNA-binding motif protein X chromosome) isoform 1 RNA binding motif protein X chromosome RNA binding motif protein X chromosome | 4 |
| IPI00421392.1 IPI00467833.5 IPI00765670.1 | LOC500959 triosephosphate isomerase Triosephosphate isomerase LOC500959 similar to triosephosphate isomerase | 10 |
| IPI00459493.5 | Isoform 1 of T-complex protein 1 subunit alpha B | 12 |
| IPI00123862.1 IPI00130185.1 IPI00203358.1 IPI00203390.3 IPI00208265.1 IPI00227773.1 IPI00231715.1 IPI00311873.5 IPI00875406.1 | Isoform gamma-1 of serine/threonine-protein phosphatase PP1-gamma catalytic subunit Serine/threonine-protein phosphatase PP1-alpha catalytic subunit Isoform gamma-1 of serine/threonine-protein phosphatase PP1-gamma catalytic subunit Serine/threonine-protein phosphatase PP1-beta catalytic subunit Serine/threonine-protein phosphatase PP1-alpha catalytic subunit Isoform gamma-2 of serine/threonine-protein phosphatase PP1-gamma catalytic subunit Isoform gamma-2 of Serine/threonine-protein phosphatase PP1-gamma catalytic subunit Serine/threonine-protein phosphatase PP1-beta catalytic subunit Serine/threonine protein phosphatase (fragment) | 6 |
| IPI00373651.3 IPI00399961.2 IPI00754418.1 | Predicted similar to apoptosis inhibitor 5 11 days embryo head cDNA RIKEN full-length enriched library clone:6230411L24 product:apoptosis inhibitor 5 full insert sequence Apoptosis inhibitor 5 | 6 |
| IPI00331361.2 | Myb-binding protein 1a | 7 |
| IPI00411074.2 IPI00411075.1 IPI00558998.2 | Poly(rC) binding protein 3 Isoform 2 of poly(rC)-binding protein 3 36 kDa protein | 9 |
| IPI00207355.4 IPI00387494.1 | Heat shock-related 70 kDa protein 2 Heat shock protein 2 | 9 |
| IPI00117910.3 | Peroxiredoxin-2 | 13 |
| IPI00203214.6 IPI00466069.3 | Elongation factor 2 Elongation factor 2 | 54 |
| IPI00115987.1 IPI00130959.5 IPI00209377.2 IPI00365215.1 IPI00830976.1 | Nuclear autoantigenic sperm protein isoform 1 LOC100043974; Isoform 1 of Nuclear autoantigenic sperm protein 49 kDa protein Nuclear autoantigenic sperm protein nuclear autoantigenic sperm protein isoform 2 | 2 |
| IPI00857345.1 IPI00886474.1 | 20 kDa protein Putative uncharacterized protein | 7 |
| IPI00208123.4 IPI00225633.3 | Activated RNA polymerase II transcriptional coactivator p15 Activated RNA polymerase II transcriptional coactivator p15 | 8 |
| IPI00322492.3 IPI00364603.2 IPI00515199.1 IPI00742310.4 IPI00764664.2 IPI00765468.1 IPI00765782.1 IPI00766592.1 IPI00767290.2 IPI00768647.1 IPI00875852.1 | Ewing sarcoma homolog Similar to Ewing sarcoma breakpoint region 1 isoform EWS Ewing sarcoma homolog RNA-binding protein EWS Similar to Ewing sarcoma breakpoint region 1 isoform EWS isoform 5 Similar to Ewing sarcoma breakpoint region 1 isoform EWS isoform 3 Similar to RNA-binding protein EWS isoform 2 Ewing sarcoma breakpoint region 1 Similar to RNA-binding protein EWS isoform 4 Similar to RNA-binding protein EWS isoform 1 Ewing sarcoma breakpoint region 1 | 5 |
| IPI00212186.1 IPI00323819.3 IPI00475776.1 IPI00777367.1 | Predicted similar to 40S ribosomal protein S20 40S ribosomal protein S20 40S ribosomal protein S20 13 kDa protein | 11 |
| IPI00136883.3 IPI00231555.1 IPI00390239.1 IPI00390801.2 IPI00475378.4 IPI00562850.1 IPI00749991.5 | Activated spleen cDNA RIKEN full-length enriched library clone:F830304D19 product:polypyrimidine tract binding protein 1 full insert sequence Isoform PYBP1 of polypyrimidine tract-binding protein 1 Ptbp1 protein 56 kDa protein Polypyrimidine tract binding protein 1 isoform 1 Ptbp1 59 kDa protein Polypyrimidine tract-binding protein 1 | 16 |
| IPI00123129.1 | Staphylococcal nuclease domain-containing protein 1 | 27 |
| IPI00308885.6 IPI00339148.2 | Isoform 1 of 60 kDa heat shock protein mitochondrial precursor 60 kDa heat shock protein mitochondrial precursor | 32 |
| IPI00122426.1 | LOC100046041;Rp119 60S ribosomal protein L19 | 2 |

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|---------------|---|----|
| IPI00202214.1 | 60S ribosomal protein L19 | |
| IPI00264398.3 | LOC100041511 similar to Mus musculus ribosomal protein L19 | |
| IPI00648315.1 | Ribosomal protein L19 | |
| IPI00850221.1 | Ribosomal protein L19 | |
| IPI00115620.1 | Phosphoserine aminotransferase | 3 |
| IPI00848485.1 | LOC100047252 similar to Phosphoserine aminotransferase 1 isoform 2 | |
| IPI00849478.1 | LOC100047252 similar to Phosphoserine aminotransferase 1 isoform 1 | |
| IPI00885829.1 | Psat1 Bone marrow macrophage cDNA RIKEN full-length enriched library clone:I830122I01 product:phosphoserine aminotransferase 1 full insert sequence | |
| IPI00407130.4 | Isoform M2 of Pyruvate kinase isozymes M1/M2 | 26 |
| IPI00231426.6 | Phosphoglycerate kinase 1 | 9 |
| IPI00320217.9 | Cct2 T-complex protein 1 subunit beta | 16 |
| IPI00331174.5 | Cct7 T-complex protein 1 subunit eta | 9 |
| IPI00364286.3 | Cct7_predicted chaperonin subunit 7 | |
| IPI00114945.1 | Septin-2 | 3 |
| IPI00208304.1 | Septin-2 | |
| IPI00321308.4 | Alanyl-tRNA synthetase cytoplasmic | 5 |
| IPI00363563.3 | Aars similar to alanyl-tRNA synthetase | |
| IPI00198717.8 | Malate dehydrogenase cytoplasmic | 8 |
| IPI00336324.1 | Malate dehydrogenase cytoplasmic | |
| IPI00231693.5 | 40S ribosomal protein S3a | 10 |
| IPI00331345.5 | 40S ribosomal protein S3a | |
| IPI00473521.1 | LOC100043780 similar to ribosomal protein S3a | |
| IPI00132460.1 | 60S ribosomal protein L26 | 4 |
| IPI00200552.3 | 60S ribosomal protein L26 | |
| IPI00358844.3 | RGD1565215_predicted similar to 60S ribosomal protein L26 | |
| IPI00474008.2 | EG433050 similar to ribosomal protein L26 | |
| IPI00649136.1 | Ribosomal protein L26 | |
| IPI00874521.1 | 17 kDa protein | |
| IPI00880492.1 | Ribosomal protein L26 | |
| IPI00108454.2 | 29 kDa protein | 3 |
| IPI00113655.1 | LOC667739 40S ribosomal protein S6 | |
| IPI00192486.1 | 40S ribosomal protein S6 | |
| IPI00474622.1 | LOC100043734 hypothetical protein isoform 1 | |
| IPI00671512.3 | LOC675985 similar to ribosomal protein S6 | |
| IPI00112555.3 | Glycyl-tRNA synthetase | 5 |
| IPI00364262.3 | Gars similar to glycyl-tRNA synthetase | |
| IPI00766072.1 | Gars similar to glycyl-tRNA synthetase | |
| IPI00196661.1 | 14-3-3 protein theta | 7 |
| IPI00408378.4 | Isoform 1 of 14-3-3 protein theta | |
| IPI00656269.1 | Isoform 2 of 14-3-3 protein theta | |
| IPI00853924.1 | 34 kDa protein | |
| IPI00127172.3 | ATP-dependent RNA helicase DDX1 | 3 |
| IPI00555314.1 | ATP-dependent RNA helicase DDX1 | |
| IPI00119220.1 | Small nuclear ribonucleoprotein Sm D2 | 6 |
| IPI00364045.1 | LOC680309;LOC686737 hypothetical protein LOC680309 | |
| IPI00128904.1 | Poly(rC)-binding protein 1 | 6 |
| IPI00882480.1 | RGD1561319_predicted similar to Poly(rC)-binding protein 1 | |
| IPI00331092.7 | 40S ribosomal protein S4 X isoform | 11 |
| IPI00475474.3 | 40S ribosomal protein S4 X isoform | |
| IPI00752798.2 | EG668668 predicted gene | |
| IPI00829470.1 | EG668668- 29 kDa protein | |
| IPI00222546.5 | mCG_130059 60S ribosomal protein L22 | 11 |
| IPI00551563.3 | 15 kDa protein | |
| IPI00121443.1 | Cytochrome c oxidase polypeptide vIa | 4 |
| IPI00849793.1 | 60S ribosomal protein L12 | 16 |
| IPI00119305.3 | Proliferation-associated protein 2G4 | 50 |
| IPI00130095.1 | Ras GTPase-activating protein-binding protein 1 | 14 |
| IPI00154054.1 | Acetyl-CoA acetyltransferase, mitochondrial precursor | 3 |
| IPI00132578.1 | mRNA turnover protein 4 homolog | 4 |
| IPI00365290.3 | RGD1311709_predicted hypothetical protein LOC298586 | |
| IPI00461025.1 | Muscle protein 684 (Fragment) | |
| IPI00649024.1 | MRT4 mRNA turnover 4 homolog | |
| IPI00848436.1 | LOC434693 hypothetical protein isoform 1 | |
| IPI00890117.1 | Cofilin-1 | 10 |
| IPI00118899.1 | Alpha-actinin-4 | 4 |
| IPI00209082.1 | Alpha-actinin-1 | |
| IPI00213463.2 | Alpha-actinin-4 | |
| IPI00331664.3 | Alpha-actinin-2 | |
| IPI00363022.3 | Predicted similar to actinin alpha 2 | |
| IPI00380436.1 | Alpha-actinin-1 | |
| IPI00387557.3 | Actn2 actinin alpha 2 | |
| IPI00454431.1 | Brain-specific alpha actinin 1 isoform | |
| IPI00775849.2 | Alpha-actinin | |

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|---------------|---|----|
| IPI00122815.3 | 17 Days embryo kidney cDNA RIKEN full-length enriched library clone:I920160L24 product:prolyl 4-hydroxylase beta polypeptide full insert sequence | 7 |
| IPI00133522.1 | Protein disulfide-isomerase precursor | 7 |
| IPI00230707.6 | 14-3-3 protein gamma | 7 |
| IPI00230835.5 | 14-3-3 protein gamma | 7 |
| IPI00123342.4 | Hypoxia up-regulated protein 1 precursor | 6 |
| IPI00230914.5 | 60S ribosomal protein L5 | 3 |
| IPI00308706.4 | LOC100043295 60S ribosomal protein L5 | |
| IPI00361473.2 | RGD1564051_predicted similar to 60S ribosomal protein L5 | |
| IPI00881253.1 | Rpl5 Blastocyst blastocyst cDNA RIKEN full-length enriched library clone:I1C0019E04 product:ribosomal protein L5 full insert sequence | |
| IPI00210090.3 | Hnrpu SP120 | 12 |
| IPI00458583.3 | Hnrnpu Osteoclast-like cell cDNA RIKEN full-length enriched library clone:I420039N16 product:heterogeneous nuclear ribonucleoprotein U full insert sequence | |
| IPI00566967.1 | Hnrpu 90 kDa protein | |
| IPI00116284.4 | Isoform CW17 of splicing factor 1 | 4 |
| IPI00387376.3 | Isoform 3 of splicing factor 1 | |
| IPI00471888.1 | Splicing factor 1 | |
| IPI00558327.2 | Splicing factor 1 isoform 2 | |
| IPI00561804.2 | Splicing factor 1 isoform 1 | |
| IPI00830797.1 | Splicing factor 1 isoform 2 | |
| IPI00830819.1 | Splicing factor 1 isoform 1 | |
| IPI00856488.1 | Sf1 62 kDa protein | |
| IPI00779903.1 | 14 kDa protein | 4 |
| IPI00139168.2 | Parp1 17 days pregnant adult female amnion cDNA, RIKEN full-length enriched library, clone:I920184D05 product:ADP-ribosyltransferase (NAD+; poly (ADP-ribose) polymerase) 1, full insert sequence | 10 |
| IPI00108125.4 | Eukaryotic translation initiation factor 5a-1 | 30 |
| IPI00211216.4 | Eukaryotic translation initiation factor 5a-1 | |
| IPI00132473.3 | Cleavage and polyadenylation specificity factor subunit 5 | 4 |
| IPI00363489.1 | Cleavage and polyadenylation specificity factor subunit 5 | |
| IPI00132942.1 | Nuclear migration protein nudc | 6 |
| IPI00196440.1 | Neural Wiskott-Aldrich syndrome protein | 2 |
| IPI00468996.2 | Neural Wiskott-Aldrich syndrome protein | |
| IPI00225390.5 | Cytochrome c oxidase subunit VIb isoform 1 | 3 |
| IPI00389152.4 | RGD1565270_predicted similar to cytochrome c oxidase subunit VIb polypeptide 1 | |
| IPI00391366.3 | LOC681754 similar to cytochrome c oxidase subunit VIb polypeptide 1 | |
| IPI00768953.1 | LOC687571 similar to cytochrome c oxidase subunit VIb polypeptide 1 | |
| IPI00195372.1 | Elongation factor 1-alpha 1 | 39 |
| IPI00307837.6 | Elongation factor 1-alpha 1 | |
| IPI00551729.1 | 50 kDa protein | |
| IPI00874456.1 | Dihydrolipoyl dehydrogenase, mitochondrial precursor | 6 |
| IPI00200409.3 | Glycylpeptide n-tetradecanoyltransferase 1 | 13 |
| IPI00224128.7 | Glycylpeptide n-tetradecanoyltransferase 1 | |
| IPI00194974.2 | Hnrpk protein | 15 |
| IPI00223253.1 | Isoform 1 of heterogeneous nuclear ribonucleoprotein k | |
| IPI00224575.1 | Isoform 2 of heterogeneous nuclear ribonucleoprotein k | |
| IPI00465574.2 | Bone marrow macrophage cDNA RIKEN full-length enriched library clone:I830091E20 product:heterogeneous nuclear ribonucleoprotein k full insert sequence | |
| IPI00780608.1 | Hnrpk 48 kDa protein | |
| IPI00890005.1 | Isoform 3 of heterogeneous nuclear ribonucleoprotein k | |
| IPI00331321.1 | 10 days embryo whole body cDNA RIKEN full-length enriched library clone:2610201K07 product:Ras suppressor protein 1 full insert sequence | 4 |
| IPI00364932.2 | LOC684929 hypothetical protein LOC680419 | |
| IPI00652828.1 | 16 days embryo heart cDNA RIKEN full-length enriched library clone:I920078P22 product:Ras suppressor protein 1 full insert sequence | |
| IPI00755220.1 | Ras suppressor protein 1 | |
| IPI00782386.1 | 27 kDa protein | |
| IPI00421428.9 | Phosphoglycerate mutase 1 | 4 |
| IPI00457898.3 | Phosphoglycerate mutase 1 | |
| IPI00330862.5 | LOC100044177;Ezr Ezrin | 6 |
| IPI00466032.3 | Embryonic lethal abnormal vision Drosophila like 1 | 3 |
| IPI00869767.1 | Embryonic lethal abnormal vision Drosophila like 1 | |
| IPI00778270.1 | 68 kDa protein | 10 |
| IPI00116498.1 | 14-3-3 protein zeta/delta | 16 |
| IPI00324893.4 | 14-3-3 protein zeta/delta | |
| IPI00137229.1 | Isoform 2 of cellular nucleic acid-binding protein | 8 |
| IPI00454151.1 | Isoform 3 of cellular nucleic acid-binding protein | |
| IPI00206624.1 | 78 kDa glucose-regulated protein precursor | 22 |
| IPI00319992.1 | 78 kDa glucose-regulated protein precursor | |
| IPI00113394.5 | EG639162 similar to rps15a protein | 4 |
| IPI00203481.1 | LOC687680 similar to ribosomal protein s15a | |
| IPI00230660.5 | 40S ribosomal protein s15a | |
| IPI00231474.5 | 40S ribosomal protein s15a | |

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|---------------|---|----|
| IPI00475811.1 | 15 kDa protein | |
| IPI00569434.1 | LOC680996 similar to ribosomal protein s15a | |
| IPI00749889.1 | LOC664903 similar to hCG1994130 | |
| IPI00766688.1 | LOC691065 similar to ribosomal protein s15a | |
| IPI00849692.1 | LOC100044556 similar to hCG1994130 | |
| IPI00857288.1 | Rps15a 8 kDa protein | |
| IPI00857457.1 | Rps15a 12 kDa protein | |
| IPI00857931.1 | Rps15a 8 kDa protein | |
| IPI00124820.2 | Coronin-1c | 8 |
| IPI00388015.3 | RGD1564490_predicted hypothetical protein LOC501841 | |
| IPI00319994.6 | L-lactate dehydrogenase a chain | 14 |
| IPI00751369.1 | L-lactate dehydrogenase | |
| IPI00117352.1 | Tubulin beta-5 chain | 16 |
| IPI00197579.2 | Isoform 1 of tubulin beta-5 chain | |
| IPI00127841.3 | ADP/ATP translocase 2 | 4 |
| IPI00200466.3 | ADP/ATP translocase 2 | |
| IPI00366141.3 | 35 kDa protein | |
| IPI00462250.2 | EG433326 similar to adenine nucleotide translocase | |
| IPI00558425.2 | Slc25a5 27 kDa protein | |
| IPI00561209.2 | Slc25a5 22 kDa protein | |
| IPI00564294.2 | 34 kDa protein | |
| IPI00565507.2 | 32 kDa protein | |
| IPI00568360.2 | RGD1564131_predicted similar to solute carrier family 25 member 5 | |
| IPI00569825.1 | 35 kDa protein | |
| IPI00569831.2 | 35 kDa protein | |
| IPI00658303.1 | Slc25a5 27 kDa protein | |
| IPI00776957.1 | LOC630624 similar to adenine nucleotide translocase isoform 1 - 33 kDa protein | |
| IPI00122421.5 | EG621100 60S ribosomal protein L27 | 3 |
| IPI00231360.9 | 60S ribosomal protein L27 | |
| IPI00132653.1 | Succinyl-coA:3-ketoacid-coenzyme a transferase 1 mitochondrial precursor | 4 |
| IPI00367445.3 | LOC678860 similar to 3-oxoacid coA transferase 1 isoform 1 | |
| IPI00766788.1 | LOC678860 similar to 3-oxoacid coA transferase 1 isoform 2 | |
| IPI00768711.1 | Oxct1 similar to 3-oxoacid coA transferase 1 | |
| IPI00858156.1 | Oxct1 CRL-1722 L5178Y-R cDNA RIKEN full-length enriched library clone:I730058H05 product:3-oxoacid coA transferase full insert sequence | |
| IPI00117168.3 | Protein dpy-30 homolog | 8 |
| IPI00462291.5 | High mobility group protein B2 | 30 |
| IPI00196353.1 | RGD1310931_predicted hypothetical protein LOC290642 | 2 |
| IPI00458723.2 | Coiled-coil domain-containing protein 124 | |
| IPI00119227.1 | Ube2i;LOC100044900 SUMO-conjugating enzyme UBC9 | 5 |
| IPI00199424.1 | SUMO-conjugating enzyme UBC9 | |
| IPI00475301.2 | LOC100045388 similar to chain A crystal structure of human Rangap1-Ubc9 | |
| IPI00850259.1 | LOC100043681 similar to chain A crystal structure of human Rangap1-Ubc9 | |
| IPI00118676.3 | Eukaryotic initiation factor 4a-1 | 16 |
| IPI00369618.1 | Eukaryotic translation initiation factor 4a1 | |
| IPI00561527.2 | 35 kDa protein | 5 |
| IPI00781417.1 | 35 kDa protein | |
| IPI00136929.1 | Gamma actin-like protein | 22 |
| IPI00354819.5 | Isoform smooth muscle of myosin light polypeptide 6 | 5 |
| IPI00365944.5 | Myl6_predicted myosin light polypeptide 6 | |
| IPI00392935.2 | 17 kDa protein | |
| IPI00409817.2 | Isoform non-muscle of myosin light polypeptide 6 | |
| IPI00462232.3 | EG433297 similar to MYL6 protein | |
| IPI00474757.4 | EG546101 similar to 17kD myosin light chain | |
| IPI00817070.1 | LOC684520;LOC685867 hypothetical protein LOC685867 | |
| IPI00870820.1 | LOC685883 hypothetical protein LOC685883 | |
| IPI00114407.2 | Isoform 1 of THO complex subunit 4 | 20 |
| IPI00763263.2 | LOC688305 similar to THO complex subunit 4 isoform 2 | |
| IPI00768839.2 | LOC688305 similar to THO complex subunit 4 isoform 1 | |
| IPI00366785.4 | Tyrosyl-tRNA synthetase, cytoplasmic | 4 |
| IPI00382191.1 | 6-Phosphogluconate dehydrogenase decarboxylating | 4 |
| IPI00466919.7 | 6-Phosphogluconate dehydrogenase decarboxylating | |
| IPI00569969.2 | Cort 53 kDa protein | |
| IPI00882447.1 | Cort 117 kDa protein | |
| IPI00321978.3 | Ran-specific GTPase-activating protein (Fragment) | 6 |
| IPI00119224.1 | Small nuclear ribonucleoprotein Sm D3 | 7 |
| IPI00766278.1 | LOC687711 similar to small nuclear ribonucleoprotein D3 | |
| IPI00212783.6 | 60S ribosomal protein L35 | 9 |
| IPI00263879.4 | LOC100038991 60S ribosomal protein L35 | |
| IPI00322749.3 | Small nuclear ribonucleoprotein Sm D1 | 4 |
| IPI00363471.1 | Snrpd1_predicted small nuclear ribonucleoprotein D1 | |
| IPI00569308.2 | LOC684715 similar to Small nuclear ribonucleoprotein Sm D1 | |
| IPI00108206.1 | Gag-Pol polyprotein | 2 |
| IPI00112448.1 | 40S ribosomal protein S10 | 11 |

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| IPI00191142.1 IPI00361431.1 | 40S ribosomal protein S10 RGD1564698_predicted similar to ribosomal protein S10 | |
| IPI00229517.5 | Galectin-1 | 11 |
| IPI00116668.2 IPI00194728.1 IPI00857352.1 | Integrin-linked protein kinase Integrin-linked protein kinase Ilk 20 kDa protein | 2 |
| IPI00127358.1 | SH3 domain-binding glutamic acid-rich-like protein 3 | 3 |
| IPI00132456.1 IPI00421395.1 IPI00766649.1 | 2700060E02Rik UPF0568 protein C14orf166 homolog RGD1304704 LRRGT00192 RGD1304704 28 kDa protein | 6 |
| IPI00420363.2 IPI00464718.1 | Probable ATP-dependent RNA helicase DDX5 Ddx5 gene | 5 |
| IPI00207050.5 IPI00221798.1 IPI00782427.1 | Rcn3_predicted reticulocalbin 3 EF-hand calcium binding domain Reticulocalbin-3 precursor LOC361571 38 kDa protein | 2 |
| IPI00131406.1 IPI00231539.1 | Proteasome subunit alpha type-7 Isoform RC6-IS of proteasome subunit alpha type-7 | 4 |
| IPI00198481.1 IPI00227850.5 IPI00752633.1 IPI00758445.2 | Isoform ARPP-19 of cAMP-regulated phosphoprotein 19 Isoform ARPP-19 of cAMP-regulated phosphoprotein 19 Isoform ARPP-16 of cAMP-regulated phosphoprotein 19 Isoform ARPP-16 of cAMP-regulated phosphoprotein 19 | 5 |
| IPI00123639.1 | Calreticulin precursor | 17 |
| IPI00191895.4 IPI00621272.3 IPI00829481.1 | MGC72932 NHP2-like protein 1 Nhp211;EG434401 NHP2-like protein 1 14 kDa protein | 12 |
| IPI00110827.1 IPI00114593.1 IPI00189813.1 IPI00194087.3 IPI00480406.1 IPI00653007.1 IPI00654242.1 | Actin alpha skeletal muscle Actin alpha cardiac muscle 1 Actin alpha skeletal muscle Actin alpha cardiac muscle 1 17 days embryo head cDNA RIKEN full-length enriched library clone:3200002L22 product:actin alpha cardiac full insert sequence 17 days embryo heart cDNA RIKEN full-length enriched library clone:1920058J24 product:actin alpha cardiac full insert sequence 17 days embryo heart cDNA RIKEN full-length enriched library clone:1920072D16 product:actin alpha cardiac full insert sequence | 14 |
| IPI00139795.2 | 60S acidic ribosomal protein P2 | 17 |
| IPI00125901.5 IPI00366014.3 IPI00751092.1 IPI00765221.1 | Rps13 LOC684988 40S ribosomal protein S13 LOC668239 similar to Rps13 protein LOC683961 similar to ribosomal protein S13 | 7 |
| IPI00364061.4 IPI00620362.4 IPI00653643.3 IPI00765134.1 | Hnrpl protein Hnrpl protein Lung RCB-0558 LLC cDNA RIKEN full-length enriched library clone:G730022P12 product:heterogeneous nuclear ribonucleoprotein L full insert sequence Similar to heterogeneous nuclear ribonucleoprotein L | 15 |
| IPI00116302.3 | Eukaryotic translation initiation factor 2 subunit 2 | 9 |
| IPI00117063.1 IPI00362587.3 IPI00830623.1 | RNA-binding protein FUS Fusion derived from t(12;16) malignant liposarcoma Fusion derived from t(12;16) malignant liposarcoma | 11 |
| IPI00230264.5 IPI00369397.5 | Histone H2A.x RGD1566119_predicted hypothetical protein LOC500987 | 5 |
| IPI00229685.2 IPI00403914.2 | Isoform 1 of protein wibg homolog Isoform 2 of protein wibg homolog | 6 |
| IPI00113141.1 | Citrate synthase, mitochondrial precursor | 31 |
| IPI00129430.1 IPI00627068.1 IPI00767277.1 IPI00849080.1 | Splicing factor proline- and glutamine-rich Splicing factor proline/glutamine rich Similar to NonO/p54nrb homolog LOC100045887 similar to PTB-associated splicing factor | 10 |
| IPI00317794.5 | Nucleolin | 17 |
| IPI00215291.3 IPI00409462.2 | Spliceosome RNA helicase Bat1 Spliceosome RNA helicase Bat1 | 3 |
| IPI00120790.2 | P21-activated protein kinase-interacting protein 1 | 7 |
| IPI00756424.3 | Eukaryotic translation initiation factor 5B | 18 |
| IPI00222496.3 | Pdia6 CRL-1722 L5178Y-R cDNA, RIKEN full-length enriched library, clone:I730077L17 product:thioredoxin domain containing 7, full insert sequence | 6 |
| IPI00135700.1 IPI00205496.1 | 2410015N17Rik XTP3-transactivated gene a protein homolog Rs21c6 XTP3-transactivated gene a protein homolog | 2 |
| IPI00124742.3 IPI00222560.7 IPI00370315.1 IPI00779902.1 | Isoform Long of Eukaryotic translation initiation factor 4H Isoform Short of Eukaryotic translation initiation factor 4H Eukaryotic translation initiation factor 4H 25 kDa protein | 9 |
| IPI00231340.8 IPI00329998.3 IPI00364897.3 | 11 kDa protein 11 kDa protein 11 kDa protein | 11 |

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| IPI00368659.3 | 11 kDa protein | |
| IPI00407339.7 | Hist1h4b | |
| IPI00559188.1 | 11 kDa protein | |
| IPI00561052.3 | Hist1h4m_predicted | |
| IPI00561706.1 | 11 kDa protein | |
| IPI00621374.1 | 11 kDa protein | |
| IPI00621789.1 | 11 kDa protein | |
| IPI00623776.3 | LOC674678 similar to histone H4 | |
| IPI00624840.2 | 12 kDa protein | |
| IPI00624933.1 | 12 kDa protein | |
| IPI00764726.1 | LOC679840 similar to germinal histone H4 gene | |
| IPI00778180.1 | 11 kDa protein | |
| IPI00844736.1 | 12 kDa protein | |
| IPI00874920.1 | 11 kDa protein | |
| IPI00876005.1 | 11 kDa protein | |
| IPI00130883.1 | Putative RNA-binding protein 3 | 8 |
| IPI00367437.4 | Similar to RNA binding motif protein 3 | |
| IPI00378187.2 | 7 days embryo whole body cDNA RIKEN full-length enriched library clone:C430044A22 product:RNA binding motif protein 3 full insert sequence | |
| IPI00231955.6 | Calmodulin | 16 |
| IPI00467841.6 | Calm2 12 days pregnant adult female placenta cDNA RIKEN full-length enriched library clone:I530005B05 product:calmodulin 1 full insert sequence | |
| IPI00761696.2 | Calmodulin | |
| IPI00123007.1 | Rpl31;EG667682;LOC100042740;LOC100047426 60S ribosomal protein L31 | 6 |
| IPI00207486.1 | 14 kDa protein | |
| IPI00231042.6 | 60S ribosomal protein L31 | |
| IPI00361677.1 | RGD1564839_predicted similar to ribosomal protein L31 | |
| IPI00563665.2 | Similar to ribosomal protein L31 | |
| IPI00677102.1 | LOC638399 hypothetical protein isoform 1 | |
| IPI00768353.1 | LOC688416 similar to ribosomal protein L31 | |
| IPI00454008.1 | Serine hydroxymethyltransferase | 16 |
| IPI00212969.3 | Predicted heterogeneous nuclear ribonucleoprotein B0b | 12 |
| IPI00405058.6 | Isoform 3 of heterogeneous nuclear ribonucleoproteins A2/B1 | |
| IPI00622847.2 | Isoform 2 of heterogeneous nuclear ribonucleoproteins A2/B1 | |
| IPI00828488.1 | Isoform 1 of heterogeneous nuclear ribonucleoproteins A2/B1 | |
| IPI00853914.1 | LOC100045191 similar to heterogeneous nuclear ribonucleoprotein A2/B1 | |
| IPI00867934.1 | Hnrpa2b1_predicted heterogeneous nuclear ribonucleoprotein B1 | |
| IPI00890022.1 | Hnrnpa2b1 43 kDa protein | |
| IPI00117288.3 | Heterogeneous nuclear ribonucleoprotein A/B | 20 |
| IPI00208193.1 | Nucleic acid binding factor pRM10 | |
| IPI00212723.2 | Hnrpab heterogeneous nuclear ribonucleoprotein A/B | |
| IPI00212724.1 | Type A/B hnRNP p40 | |
| IPI00277066.4 | Hnrpab heterogeneous nuclear ribonucleoprotein A/B isoform 1 | |
| IPI00648228.3 | Hnrpab protein | |
| IPI00463344.5 | 34 kDa protein | 7 |
| IPI00471678.1 | DnaJ homolog subfamily c member 8 | |
| IPI00648539.2 | DnaJ (Hsp40) homolog subfamily c member 8 | |
| IPI00757611.1 | DnaJ homolog subfamily c member 8 | |
| IPI00369635.3 | Radixin | 11 |
| IPI00653921.2 | Radixin isoform a | |
| IPI00214889.1 | Proteasome subunit beta type-3 | 3 |
| IPI00314467.3 | Proteasome subunit beta type-3 | |
| IPI00131695.3 | Serum albumin precursor | 5 |
| IPI00204316.1 | ATP synthase-coupling factor 6, mitochondrial precursor | 2 |
| IPI00475835.3 | D-3-phosphoglycerate dehydrogenase | 3 |
| IPI00274739.1 | Isoform 2 of DNA-binding protein A | 4 |
| IPI00330591.1 | Isoform 1 of DNA-binding protein A | |
| IPI00208277.1 | 28 kDa heat- and acid-stable phosphoprotein | 15 |
| IPI00352475.3 | 28 kDa heat- and acid-stable phosphoprotein | |
| IPI00109696.1 | EG628161 peptidyl-prolyl cis-trans isomerase NIMA-interacting 4 | 6 |
| IPI00765109.1 | LOC684441 similar to peptidyl-prolyl cis-trans isomerase NIMA-interacting 4 | |
| IPI00224152.5 | DNA-(apurinic or apyrimidinic site) lyase | 23 |
| IPI00135686.2 | Peptidylprolyl isomerase B | 32 |
| IPI00471325.2 | Endothelial differentiation-related factor 1 | 4 |
| IPI00870805.1 | Edf1_predicted endothelial differentiation-related factor 1 | |
| IPI00222509.1 | Protein RCC2 | 24 |
| IPI00132799.4 | Complement component 1, q subcomponent binding protein | 15 |
| IPI00371043.2 | Predicted Protein ARMET precursor | 8 |
| IPI00404019.1 | Armet protein | |
| IPI00775791.1 | Armet RCB-0035 WEHI-3 cDNA RIKEN full-length enriched library clone:G430091B19 product:arginine-rich mutated in early stage tumors full insert sequence | |
| IPI00227808.3 | Isoform 1 of protein CDV3 | 7 |
| IPI00314153.4 | Tyrosyl-tRNA synthetase | 30 |
| IPI00110588.4 | Moesin | 7 |

| | | |
|---|--|----|
| IPI00212314.5 IPI00778167.1 | Moesin 68 kDa protein | |
| IPI00360269.4 IPI00780039.1 | 25 kDa protein 25 kDa protein | 7 |
| IPI00230108.6 | Protein disulfide-isomerase A3 precursor | 16 |
| IPI00133903.1 IPI00880839.1 | Hspa9 Stress-70 protein mitochondrial precursor Hspa9 heat shock protein 9 | 18 |
| IPI00210566.3 IPI00330804.4 | Heat shock protein HSP 90-alpha Heat shock protein HSP 90-alpha | 9 |
| IPI00112223.1 IPI00200410.3 IPI00226872.1 | EF-hand domain-containing protein D2 EF-hand domain-containing protein D2 Efhd2 16 days embryo head cDNA RIKEN full-length enriched library clone:C130064C02 product:SWIPROSIN 1 full insert sequence | 2 |
| IPI00135512.1 IPI00205163.3 IPI00808645.1 | Protein canopy homolog 2 precursor Similar to MIR-interacting saposin-like protein LOC684485 similar to MIR-interacting saposin-like protein precursor | 2 |
| IPI00776522.1 | 31 kDa protein | 4 |
| IPI00222430.5 IPI00667117.2 IPI00831604.1 | Diazepam binding inhibitor isoform 1 Dbi acyl-CoA-binding protein Dbi protein | 5 |
| IPI00227392.5 IPI00231677.5 | 14-3-3 protein eta 14-3-3 protein eta | 3 |
| IPI00788324.1 | Myh9 15 days pregnant adult female amnion cDNA, RIKEN full-length enriched library, clone:M421002E03 product:myosin heavy chain IX, full insert sequence | 3 |
| IPI00231827.6 IPI00882501.1 | Nucleolin Nucleolin | 6 |
| IPI00227657.6 | Stromal cell-derived factor 2-like protein 1 precursor | 3 |
| IPI00120984.5 | NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 8 | 2 |
| IPI00129516.1 IPI00369093.1 | Cytochrome b-c1 complex subunit 6 mitochondrial precursor Cytochrome b-c1 complex subunit 6 mitochondrial precursor | 2 |

IPI: International Protein Index. Protein names are derived from the IPI database (Rat-Mouse; version 3.24). All proteins listed are with probability (p) =1 and identified by \geq two peptides. Proteins listed in the same cell are either the same proteins with different IPI or proteins cannot be differentiated in the current database with the identified peptides.

Supplemental References

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