

SUPPORTING ONLINE MATERIAL (SOM)

MATERIALS AND METHODS

Isolation of midbodies

Midbody purification was adapted from techniques developed by Mullins and McIntosh (1982)(1), Sellitto and Kuriyama (1992)(2), and Kuriyama and Ensrud (1999)(3). CHO cells synchronized by successive thymidine and nocodazole treatments were isolated in a taxol and phalloidin-containing medium after furrow ingression to stabilize the midbody structure. Following lysis in a hypotonic buffer that included Triton X-100, insoluble midbodies were pelleted at 2000xg in 40% glycerol.

Characterization of midbody proteins using multidimensional protein identification

technology (MudPIT) Precipitated midbody protein preparations were dissolved in digestion buffer, digested by trypsin, and analyzed by LC/LC/MS/MS according to published protocols (4). Approximately 100 µg of protein was used for a 12-step LC/LC/MS/MS experiment and a total of four experiments were performed. MS/MS spectra obtained were analyzed by SEQUEST using a non-redundant mammalian database. The SEQUEST outputs were then analyzed by DTASelect (5). The DTASelect filter settings were: XCorr: +1 ions 1.8, +2 ions 2.5, +3 ions 3.8; delta CN: 0.08; only half or full tryptic peptides were considered; all subset proteins were removed (the “-o” option in DTASelect). Proteins with 4-5 peptides that passed the DTASelect filter were considered real hits. Proteins with one to four peptides that passed the DTASelect filter were further manually validated.

Bioinformatics & determination of homologues & paralogs

Systematic elimination of 417/577 proteins was performed manually using data from Proteome, Homogene and BLASTP analysis. Any protein that was predicted be nuclear, mitochondrial,

ribosomal, heat shock, transcription/translation-associated or contamination (i.e. keratin, BSA) was not further characterized in this study. The *C. elegans* homologues and paralogs of the 160 remaining proteins were determined from the peptides and subsequently accession/gi numbers retrieved after tandem mass spectrometric analysis. The mammalian accession numbers provided entire protein sequences, which were then used in a BLASTP search of WormPep to determine homology/orthology. Homologues were determined by taking the top scoring sequences (E-value $<10^{-10}$). They are listed in Table S1. In addition, we double-checked sequences on WormPD (Proteome); (<http://www.proteome.com>) and Homologene (NCBI); (<http://www.ncbi.nlm.nih.gov:80/entrez/query.fcgi?db=homologene>) for homology scores and protein function predictions across species. When two sequences were each other's best match (reciprocal best match), the genes corresponding to the sequences were considered putative orthologs. Paralogs to *C. elegans* genes were previously determined from Wormbase. An additional 11 *C. elegans* genes that had E-value scores between 10^{-9} and 10^{-3} were also included in our screen and are marked by an "*" in the Not Conserved column in Table S1. Two mammalian proteins, Annexin VI and noggin did not have *C. elegans* counterparts. Predicted gene products were systematically placed into functional classes by manual inspection using data from Proteome, Homologene and BLAST analysis. If a mammalian protein had already been shown to play a role in cytokinesis or to localize to the midbody or intercellular canal in *H. sapiens*, *C. griseus*, *D. melanogaster*, *D. discoïdium*, *S. cerevisiae*, *S. pombe*, *A. nidulans*, *A. thaliana*, *N. tabacum*, or *X. laevis*, an "X" was marked in the Published Cytokinesis Proteins column (33%, 52/160) and/or in the Previously Localized column (26%, 42/160) in Table S1.

Immunolocalization and Microscopy

HeLa cells were grown on 22 X 22 mm cover slips and fixed in 3.7% Formaldehyde, 0.1%

Glutaraldehyde and 0.3% Triton in 1X BRB80 (80mM PIPES pH 6.8, 1mM MgCl₂, 1mM EGTA). Immunofluorescence was performed using the following antibodies: DM1A: anti- α -tubulin (ICN Pharmaceuticals), Dynamin II: anti-Dyn2 and Kinesin Heavy Chain: anti-KHC (kind gifts of M. McNiven), RACK1: anti-RACK1 (BD Biosciences), IQGAP1: anti-IQGAP1 (Zymed), KEAP1: anti-Keap1 (kind gift of M. Velichkova and T. Hasson (6), Endoplasmic/GRP94: anti-GRP94 (StressGen), RAB-GDI: anti-RabGDI (Zymed), KIF4: anti-KIF4 (kind gift of A. Caceres (7)), Annexin II: anti-Annexin II (BD Biosciences)(Annexin II is the same as Calpactin I Light Chain), BiP: anti-BiP (BD Biosciences), Glut1: anti-Glut1 (H-43): sc-7903 (Santa Cruz Biotechnology, Inc.), V5: anti-V5 epitope (Invitrogen), GM130: anti-GM130 (BD Biosciences). Cells were immunostained with appropriate antibody (see above) and α -tubulin and then mounted in Vectashield with DAPI (Vector Labs). Alexa Fluor[®] 488 and Alexa Fluor[®] 568 secondary antibodies (Molecular Probes, Inc.) were used. Visualization was performed on an upright microscope equipped with a laser confocal imaging system (TCS NT; Leica).

Cell culture and Transfection

The full-length Novel/CGI-49 DNA sequence (BC026185) was obtained from Open Biosystems and cloned into the pcDNA/V5/GW/TOPO[®] vector (Invitrogen). The construct was transfected into HeLa cells using the GeneJammer[®] Transfection Reagent (Stratagene) via manufacture instructions. The cells were stained with anti-tubulin (DM1A) and anti-V5 epitope 3-4 days after transfection.

Generation of dsRNA

Primer pairs to specific *C. elegans* genes were obtained from Research Genetics online at (<http://www.wormbase.org>). If no primer pairs were available, primers to genes were

constructed in AcePrimer (<http://elegans.bcgsc.bc.ca/gko/aceprimer.shtml>). T7 sequences were added to each primer end to aid in RNA synthesis. It was not unusual that several genes from the Research Genetics primer sequences did not produce products; synthesizing new primers in AcePrimer circumvented this problem. PCR products were concentrated and precipitated using Qiagen MinElute™ PCR Purification Kit (#28006). We synthesized dsRNA using the Ambion T7 Megascript™ High Yield Transcription Kit (#1334). The RNA pellet was diluted in 10 µl of DEPC –treated ddH₂O, heated to 65°C and cooled on ice. We assessed the quality of the dsRNA by running 1% agarose gels. RNA concentrations varied from ~3-6 mg/ml.

RNAi screening

Injection of dsRNA against each gene into a TY3553 hermaphrodite strain (maintained at 25°C) expressing both β-tubulin::GFP and histone H2B::GFP was performed to assess spindle and chromosome defects. Injected hermaphrodites maintained for 24-36 hours at 25°C were cut open to release their progeny and germlines. We recorded 2-3 viable embryos and 4-5 dissected germlines of all viable injected animals using Improvision OpenLab™ software. Data were deposited into the *C. elegans* database, Wormbase (<http://www.wormbase.org>). Not all embryos observed after RNAi expressed tubulin::GFP brightly. EMB was defined as 10-100% dead embryos. STE/GON was defined as an animal that had a germline cytokinesis defect and was also sterile. STE animals were defined as those that had a brood size of less than 10 (Wild type is 50+) but had no apparent germline cytokinesis defect. See Table S1 legend for complete descriptions.

Supporting Online Tables

The following table is a PDF file:

Table S1

The following table is a PDF file:

Table S2

Table S1:

Mammalian midbody proteins identified, corresponding *C. elegans* genes and their RNAi

phenotypes. The mammalian proteins identified by tandem mass spectrometry are listed, followed to the right by the Genbank accession number, the functional group to which it was assigned, the corresponding *C. elegans* gene, and its chromosome location and reported locus. An “X” in columns to the left of the identified protein denotes those factors previously shown to play a role in cytokinesis “Published Cytokinesis Gene” and those previously localized to the midbody or intercellular canal in *H. sapiens*, *C. griseus*, *D. melanogaster*, *D. discoideum*, *S. cerevisiae*, *S. pombe*, *A. nidulans*, *A. thaliana*, *N. tabacum*, or *X. laevis* “Previously Localized”. Phenotypes upon RNAi depletion of each protein in *C. elegans* are noted as: CE: early cytokinesis defects, CL: late cytokinesis defects, STE/GON: sterile (no progeny) with germline cytokinesis defects (i.e. germline membrane organization defects), STE: sterile (no progeny), MITO: mitotic defects (including spindle assembly and cell cycle defects.), MEI: meiosis defects (embryos dead in meiosis and/or polar body extrusion defects), UNC: uncoordinated animals, WT: Wild type (No defects observed), EMB-embryonic lethal. An asterisk in the “Not Conserved” column denotes the mammalian proteins that did not have *C. elegans* homologues, and the 16 *C. elegans* genes showing similarity to the mammalian proteins, with E-value scores between 10^{-9} and 10^{-3} . Note: The underlined phenotypes are those not seen in our analysis but reported elsewhere (See Footnotes in Table S1).

Table S2:

Eliminated mammalian midbody proteins identified, corresponding accession numbers, and their Functional Group. The 417 eliminated mammalian proteins identified by tandem mass spectrometry are listed, followed to the right by the Genbank accession number and the functional group to which it was assigned.

Online Movies

Movies S1 and S2 correspond to Fig. 4 (see Fig. 4 legend)

Movie S1: Wild type Nomarski

Movie S2: K04D7.1-RACK1 RNAi

Movies S3 and S4 correspond to Fig. 5 (see Fig. 5 legend)

Movie S3: Wild type Histone H2B::GFP

Movie S4: T05E11.3-ENDOPLASMIN RNAi in a H2B::GFP background.

Supporting Online References

- S1. J. M. a. M. Mullins, J.R., *Journal of Cell Biology* **94**, 654, (1982).
- S2. C. Sellitto, M. Kimble, R. Kuriyama, *Cell Motil Cytoskeleton* **22**, 7, (1992).
- S3. R. Kuriyama, K. Ensrud, *Methods Cell Biol* **61**, 233, (1999).
- S4. A. J. Link et al., *Nat Biotechnol* **17**, 676, (1999).
- S5. D. L. Tabb, McDonald, WH, Yates JR 3rd, *Journal of Proteome* **1**, 21, (2002).
- S6. M. Velichkova et al., *Cell Motil Cytoskeleton* **51**, 147, (2002).
- S7. D. Peretti, L. Peris, S. Rosso, S. Quiroga, A. Caceres, *J Cell Biol* **149**, 141, (2000).

| Published Cytokinesis Genes | Previously Localized To Midbody | Mammalian Protein | Accession Number | Functional Group | <i>C. elegans</i> Gene | <i>C. elegans</i> Chromosome | <i>C. elegans</i> Locus | RNAi Phenotypes | Mammalian E-value Score | Not Conserved in <i>C. elegans</i> |
|-----------------------------|---------------------------------|---------------------------------|-------------------------------------|-----------------------------|------------------------|------------------------------|-------------------------------------|--|-------------------------|------------------------------------|
| X | X | ACTIN | gi 113272 sp P04270 ACTC_HUMAN | Actin Associated | M03F4.2/T04C12.5 | X | <i>act-123, act-4, unc-92</i> | EMB STE/GON UNC | 2.70E-200 | |
| | | ACZONIN/PICCOLO HOMOLOG | gi 15139362 emb CAB60732.2 | Secretary & Membrane Assoc. | F45E4.3 | X | | UNC | 1.20E-26 | * |
| X | | ADP-RIBOSYLATION FACTOR-LIKE 1 | gi 4502227 ref NP_001168.1 | Secretary & Membrane Assoc. | B0336.2 | III | <i>arf-1</i> | EMB STE/GON CE UNC ^{1,2} | 1.30E-90 | |
| X | X | ALPHA ACTININ 4 | gi 4826639 ref NP_004915.1 | Actin Associated | W04D2.1 | V | <i>atn-1</i> | EMB MITO CL CE STE/GON | 2.50E-302 | |
| X | X | ALPHA II SPECTRIN | gi 1495198 emb CAA62350.1 | Actin Associated | K10B3.10 | X | <i>spc-1, imo-1</i> | EMB MITO UNC | 3.40E-193 | |
| X | X | ALPHA-TUBULIN | gi 3420929 gb AAC31959.1 | Microtubule | C47B2.3 | I | <i>tba-2</i> | MITO EMB | 2.20E-223 | |
| | | ANKYRIN B/ANK2 | gi 6634025 dbj BAA20833.2 | Actin Associated | B0350.2 | IV | <i>unc-44</i> | UNC STE/GON MEI CL | 5.30E-302 | |
| | | ANNEXIN V | gi 999937 pdb 1HVG | Secretary & Membrane Assoc. | ZC155.1/C28A5.3 | III | <i>nex-1, nex-3</i> | WT | 1.1E-63/2e-53 | |
| | | ANNEXIN VI | gi 113962 sp P08133 ANX6_HUMAN | Secretary & Membrane Assoc. | no homolog | | | N/A | N/A | * |
| | | ANNEXIN VII | gi 4502111 ref NP_001147.1 | Secretary & Membrane Assoc. | T07C4.9 | III | <i>nex-2</i> | STE/GON EMB | 4.70E-95 | |
| X | | ARP2 | gi 3121762 sp O15142 ARP2_HUMAN | Actin Associated | K07C5.1 | V | <i>arx-2</i> | EMB CE MEI | 3.00E-162 | |
| X | | ARP2/3 P21 SUBUNIT | gi 2209347 gb AAB61466.1 | Actin Associated | Y37D8A.1 | III | <i>arx-5</i> | WT | 7.10E-51 | |
| X | | ARP2/3 P34 SUBUNIT | gi 5031599 ref NP_005722.1 | Actin Associated | Y6D11A.2 | III | | EMB | 6.50E-112 | |
| X | | ARP2/3 P41 SUBUNIT | gi 3121763 sp O15143 AR41_HUMAN | Actin Associated | Y79H2A.6 | III | <i>arx-3</i> | EMB | 1.90E-112 | |
| X | | ARP3 | gi 416579 sp P32391 ARP3_HUMAN | Actin Associated | Y71F9AL.16 | I | <i>arx-1</i> | CHRSEG CL STE/GON ALIGN | 3.40E-177 | |
| | | ATAXIN 2 RELATED PROTEIN | gi 6005699 ref NP_009176.1 | Secretary & Membrane Assoc. | D2045.1 | III | <i>atx-2</i> | EMB STE/GON CE | 1.00E-17 | |
| X | X | AURORA KINASE B | gi 2979628 gb AAC12708.1 | Kinases | B0207.4 | I | <i>air-2, let-603, stu-7, cyk-6</i> | EMB STE/GON MITO CHRSEG CE ALIGN UNC MEI | 5.40E-92 | |
| | | BAF53A /ACTIN ASSOCIATED-LIKE 6 | gi 9789893 ref NP_062647.1 | Actin Associated | ZK616.4 | IV | | CE MITO STE | 9.79E-109 | |
| X | X | BAND 4.1 | gi 3064263 gb AAC40083.1 | Actin Associated | ZK270.2 | I | <i>frm-1</i> | WT | 9.00E-70 | |
| X | X | BETA SPECTRIN | gi 448251 prf 1916380A | Actin Associated | K11C4.3 | V | <i>unc-70, bgs-1</i> | UNC | 8.20E-242 | |
| X | X | BETA-TUBULIN | gi 2119275 pir I38370 | Microtubule | B0272.1/K01G5.7 | X, III | <i>tbb-4, tbb-1</i> | MITO EMB | 1E-232/5e-224 | |
| X | X | BIMC KINESIN/EG5 | gi 4160556 emb CAA11228.1 | Microtubule | F23B12.8 | V | <i>bmk-1, klp-14</i> | WT | 5.60E-122 | |
| | X | BIP | gi 6470150 gb AAF13605.1 AF188611_1 | Secretary & Membrane Assoc. | C15H9.6 | X | <i>hsp-3</i> | STE/GON | 2.00E-275 | |
| | | BUB3 | gi 7387554 sp O43684 BUB3_HUMAN | Other | Y54G9A.6 | II | | CHRSEG MITO ALIGN | 5.20E-71 | |
| | | CALCYCLIN | gi 116509 sp P06703 S106_HUMAN | Secretary & Membrane Assoc. | M03F4.7 | X | | CHRSEG CE UNC ¹ | 5.30E-78 | |

| | | | | | | | | | | |
|---|---|---|-------------------------------------|-----------------------------|-----------------|-------|-----------------------------|-------------------------------|-----------------|---|
| | | CALCYCLIN BINDING PROTEIN | gi 7656952 ref NP_055227.1 | Other | F53A2.4 | III | <i>nud-1</i> | EMB ALIGN UNC STE | 2.10E-83 | |
| | | CALM PROTEIN/CLATHRIN ASSEMBLY LYMPHOID-MYELOID LEUKEMIA GENE | gi 6005733 ref NP_009097.1 | Secretory & Membrane Assoc. | C32E8.10 | I | <i>unc-11</i> | EMB STE/GON UNC | 2.90E-111 | |
| X | X | CALMODULIN | gi 1710819 sp P50543 S111_MO USE | Other | C50C3.5 | III | | WT | 1.90E-11 | |
| | | CALNEXIN | gi 6671664 ref NP_031623.1 | Secretory & Membrane Assoc. | ZK632.6 | III | <i>cnx-1</i> | CE EMB | e-119 | |
| | | CALPACTIN I / ANNEXIN II ASSOCIATED LIGHT CHAIN | gi 6677833 ref NP_033138.1 | Secretory & Membrane Assoc. | F59D6.7/ZK856.8 | V, II | | WT | 2.1E-44/1.8e-52 | |
| X | | CALPONIN | gi 584956 sp P37397 CLP3_RAT | Actin Associated | F43G9.9 | I | <i>cpn-1</i> | CE MITO | 1.00E-25 | |
| | | CALRETICULIN | gi 253851 gb AAB22964.1 | Secretory & Membrane Assoc. | Y38A10A.5 | V | <i>crt-1</i> | STE/GON UNC ¹ | 3.00E-61 | |
| X | X | CAM KINASE II | gi 92035 pir A31908 | Kinases | K11E8.1 | IV | <i>unc-43, dec-8</i> | UNC MITO | 1.40E-178 | |
| | | CASEIN KINASE II | gi 89457 pir A25828 | Kinases | T01G9.6 | I | <i>kin-10</i> | EMB | 5.00E-88 | |
| X | | CDC16 | gi 1362769 pir A56519 | Other | F10B5.6 | II | <i>emb-27, apc-6, pod-6</i> | MITO MEI EMB | 8.00E-41 | |
| X | | CDC2 KINASE | gi 1082288 pir F54024 | Kinases | T05G5.3 | III | <i>cdk-1, ncc-1</i> | EMB MEI MITO STE ¹ | 1.30E-104 | |
| | | CDC20 | gi 4323528 gb AAD16405.1 | Other | ZK1307.6 | II | <i>fzr-1</i> | MITO STE MEI EMB | 2.00E-83 | |
| | | CDC28 PROTEIN KINASE 2 | gi 4502859 ref NP_001818.1 | Kinases | Y71G12B.27 | I | | MITO EMB MEI | 1.00E-24 | |
| X | X | CDC42 | gi 6531681 gb AAF15538.1 AF205635_1 | Actin Associated | R07G3.1 | II | <i>cdc-42</i> | EMB ALIGN | 4.00E-97 | |
| | | CDK INHIBITOR 1B | gi 4757962 ref NP_004055.1 | Other | T05A6.2 | II | <i>cki-2</i> | EMB MITO | 1.00E-07 | * |
| | | CDK4 | gi 2209290 gb AAC39521.1 | Kinases | F18H3.5 | X | <i>cdk-4</i> | MITO MEI ALIGN STE | 7.00E-58 | |
| X | X | CITRON-K KINASE | gi 3360514 gb AAC27933.1 | Kinases | F59A6.5/W02B8.2 | II | | EMB STE/GON | 2E-40/3E-33 | |
| | | CLATHRIN COAT ASSEMBLY PROTEIN AP50 | gi 113332 sp P20172 AP50_HUMAN | Secretory & Membrane Assoc. | R160.1 | X | <i>dpy-23, apm-2</i> | EMB STE/GON UNC | 7.00E-193 | |
| X | X | CLATHRIN HEAVY CHAIN | gi 1705915 sp P49951 CLH_BOVIN | Secretory & Membrane Assoc. | T20G5.1 | III | <i>Ce-chc</i> | STE/GON EMB CE | 1.70E-25 | |
| | | CLIP-170 | gi 88551 pir S22695 | Microtubule | C33D9.8 | IV | | EMB STE/GON ALIGN MITO | 6.50E-17 | |
| X | X | COFILIN | gi 105664 pir S12632 | Actin Associated | C38C3.5 | V | <i>unc-60</i> | UNC STE/GON EMB | 5.70E-10 | |
| | | CONTACTIN ASSOCIATED 1/SIDEKICK HOMOLOG | gi 6680954 ref NP_031753.1 | Secretory & Membrane Assoc. | Y42H9B.2 | X | <i>rig-4</i> | UNC EMB CE MITO | 9.20E-60 | |
| | | COPI COATOMER COMPLEX, ALPHA SUBUNIT | gi 2494888 sp Q27954 COPA_BOVIN | Secretory & Membrane Assoc. | Y71F9A1.17 | I | | STE/GON EMB UNC | 5.90E-26 | |

| | | | | | | | | | | |
|---|---|--|-------------------------------------|-----------------------------|------------------|-----|------------------------------|---------------------------------|-------------------|--|
| | | COPI COATOMER COMPLEX, BETA SUBUNIT | gi 8571380 gb AAF76856.1 AF231925_1 | Secretary & Membrane Assoc. | Y25C1A.5 | II | | STE/GON CE | 2.40E-302 | |
| X | X | COPINE I | gi 10719953 sp Q99829 CNE1_HUMAN | Secretary & Membrane Assoc. | T12A7.1 | IV | <i>gem-4</i> | ALIGN EMB MITO CL STE/GON | 3.60E-118 | |
| X | | CORONIN | gi 6753496 ref NP_035909.1 | Actin Associated | R01H10.3 | III | <i>cor-1</i> | STE/GON MEI | e-116 | |
| | | CULLIN 1 | gi 2493906 sp Q13616 CUL1_HUMAN | Other | D2045.6 | III | <i>cul-1, lin-19</i> | EMB STE MITO | e-128 | |
| X | X | DIAPHANOUS HOMOLOG 1 | gi 6225268 sp O60610 DIA1_HUMAN | Actin Associated | F11H8.4 | III | <i>cyk-1</i> | CL STE/GON | 2.00E-48 | |
| | | DREBRIN 1 | gi 2143704 pir S60588 | Actin Associated | K08E3.4 | III | | WT | 3.0E-19 | |
| | X | DYNACTIN ASSOCIATED/P150-GLUED | gi 6226857 sp Q14203 DYNA_HUMAN | Microtubule | ZK593.5 | IV | <i>dnc-1</i> | ALIGN MITO EMB | 2.00E-88 | |
| X | X | DYNAMIN 2 | gi 1706539 sp P50570 DYN2_HUMAN | Secretary & Membrane Assoc. | C02C6.1 | X | <i>dyn-1</i> | CL CE STE/GON EMB UNC | 2.70E-294 | |
| | | DYNAMIN-LIKE I | gi 16758468 ref NP_446107.1 | Secretary & Membrane Assoc. | D2013.5 | II | | ALIGN STE/GON | 9.71E-239 | |
| | X | DYNAMIN-LIKE PROTEIN DLP1 | gi 4868358 gb AAD31278.1 | Secretary & Membrane Assoc. | T12E12.4 | IV | <i>drp-1</i> | EMB STE/GON | 4.70E-226 | |
| | | DYNAMITIN/DYNACTIN ASSOCIATED COMPLEX 50KD SUBUNIT | gi 5453629 ref NP_006391.1 | Microtubule | C28H8.12 | III | <i>dnc-2</i> | ALIGN MITO EMB | 1.0E-12 | |
| | X | DYNEIN HC | gi 2224591 dbj BAA20783.1 | Microtubule | T21E12.4 | I | <i>dhc-1, let-354, spd-4</i> | MEI STE EMB | 8.39E-299 | |
| X | X | EB1 | gi 6912494 ref NP_036457.1 | Microtubule | Y59A8B.9 | V | | WT | 2.80E-17 | |
| | | ECM29P-LIKE | gi 2224677 dbj BAA20823.1 | Secretary & Membrane Assoc. | D2045.2 | III | | MITO STE/GON CE | 1.70E-133 | |
| X | X | ECT2 RHO GEF/PEBBLE HOMOLOG | gi 293332 gb AAA37536.1 | Actin Associated | T19E10.1 | II | | STE/GON <u>MEI</u> ³ | 4.90E-42 | |
| | | EH-DOMAIN CONTAINING 1/EHD-1 | gi 7106303 ref NP_034249.1 | Secretary & Membrane Assoc. | W06H8.1 | V | <i>rme-1</i> | STE/GON MEI CE CL EMB | 5.90E-205 | |
| | | ENDOPHILIN B1/SH3GLB2 | gi 9910352 ref NP_064530.1 | Secretary & Membrane Assoc. | F35A5.8 | X | <i>erp-1</i> | MEI CE EMB ALIGN STE/GON | 6.50E-80 | |
| | | ENDOPLASMIN PRECURSOR/GRP94 | gi 108003 pir A35954 | Secretary & Membrane Assoc. | T05E11.3 | IV | | CHRSEG STE/GON CE ALIGN | 3.30E-259 | |
| | | ENHANCER OF RUDIMENTARY | gi 4758302 ref NP_004441.1 | Other | T21C9.4 | V | | STE/GON EMB | 3.90E-27 | |
| | | ENIGMA | gi 8515740 gb AAF76152.1 | Actin Associated | T11B7.4 | IV | <i>eat-1</i> | WT | 4.80E-63 | |
| X | | EZRIN | gi 2119262 pir I45889 | Actin Associated | C01G8.5/F42A10.2 | I | <i>erm-1, nfm-1</i> | UNC EMB | 2.9E-164/6.3e-103 | |
| X | X | F-ACTIN ASSOCIATED CAPPING PROTEIN BETA SUBUNIT/CAPZ | gi 1345667 sp P47756 CAPB_HUMAN | Actin Associated | M106.5 | II | <i>cap-2</i> | ALIGN | 6.10E-100 | |

| | | | | | | | | | | |
|---|---|---|--|--------------------------------|------------------|---------|-----------------------|---------------------------------|------------------------|--|
| X | X | FILAMIN/ABP-278 | gi 3282771 gb AAC33845.1 | Actin Associated | Y66H1B.2 | IV | | STE/GON CHRSEG MEI EMB | 5.00E-204 | |
| | | FLOTILLIN 1 | gi 6679809 ref NP_032053.1 | Secretary & Membrane Assoc. | F12F3.3 | V | | CHRSEG EMB | 3.70E-100 | |
| | | G PROTEIN BETA 2 | gi 121009 sp P11017 GBB2_BO VIN | Other | F13D12.7 | II | <i>gpb-1</i> | EMB ALIGN STE ¹ | 5.11E-167 | |
| X | X | GAMMA TUBULIN COMPLEX PROTEIN 2 | gi 5729840 ref NP_006650.1 /gi 2 801701 gb AAC39728.1 | Microtubule | F58A4.8 | III | <i>tbg-1, sas-3</i> | MITO CHRSEG EMB STE | 6.79E-101 | |
| | | GAS-1/GROWTH ARREST SPECIFIC-1 | gi 6679941 ref NP_032112.1 | Other | F27E5.4 | II | <i>phg-1</i> | EMB MITO | 5.50E-67 | |
| | | GLUT1 TRANSPORTER C- TERMINAL BINDING PROTEIN | gi 3808216 gb AAC69268.1 | Secretary & Membrane Assoc. | R09B5.11 | V | | STE/GON CE | 4.00E-84 | |
| | | GLUT4 VESICLE PROTEIN | gi 4200444 gb AAD10190.1 | Secretary & Membrane Assoc. | T12A2.15 | III | | EMB STE/GON CE | 1.10E-39 | |
| | | GMX33/GOLPH3 | gi 8922589 ref NP_060648.1 | Secretary & Membrane Assoc. | Y47G6A.18 | I | | STE/GON EMB UNC ¹ | 1.50E-99 | |
| | | GOLGI STACKING PROTEIN HOMOLOG 55 | gi 5901572 gb AAD55350.1 AF1 10267_1 | Secretary & Membrane Assoc. | Y42H9AR.1 | IV | | WT | 2.10E-85 | |
| | | GTP-BINDING REGULATORY PROTEIN GI ALPHA- 2 CHAIN | gi 4218034 gb AAD12229.1 | Other | C26C6.2 | I | <i>goa-1</i> | EMB UNC STE MITO ALIGN | 6.19E-162 | |
| | | GUANINE NUCLEOTIDE BINDING PROTEIN, ALPHA 14/G ALPHA 14 | gi 6680035 ref NP_032163.1 | Secretary & Membrane Assoc. | M01D7.7 | I | <i>egl-30, gqa-1</i> | WT | 3.70E-157 | |
| | | HUNTINGTIN- ASSOCIATED PROTEIN INTERACTIN ASSOCIATEDG PROTEIN HIP1/DUO | gi 4504335 ref NP_003938.1 | Secretary & Membrane Assoc. | F55C7.7 | I | <i>unc-73</i> | UNC EMB ALIGN STE/GON | 1.00E-236 | |
| X | X | IQGAP1 | gi 1170586 sp P46940 IQGA_HU MAN | Actin Associated | F09C3.1 | I | <i>pes-7, tag-2</i> | CE STE/GON MEI | 3.60E-90 | |
| | | KEAP1 | gi 31543042 ref NM_016679.2 | Actin Associated | W02G9.2 | V | | MEI CE | 7.20E-75 | |
| | | KIF4 | gi 5802957 gb AAD51855.1 AF1 79308_1 | Microtubule | T01G1.1/Y43F4B.6 | IV, III | <i>klp-12, klp-19</i> | CL CE MITO STE/GON EMB | 2.8E-137/1.5e- 98 | |
| | | KIFC1/KAR3P HOMOLOG | gi 4050097 gb AAC97970.1 | Microtubule | T09A5.2 | II | <i>klp-3</i> | EMB MITO STE CHRSEG | 9.60E-79 | |
| | | KINESIN HEAVY CHAIN | gi 2119280 pir I84737 | Microtubule | R05D3.7 | III | <i>unc-116, khc-1</i> | UNC EMB STE | 8.30E-167 | |
| | | KINESIN LIGHT CHAIN | gi 8101107 gb AAF72543.1 | Microtubule | C18C4.10/M7.2 | V, IV | <i>klc-2, klc-1</i> | EMB ALIGN STE | 8.59E- 165/1.9e-121 | |
| | X | LAMIN A/C | gi 125962 sp P02545 LAMA_HU MAN | Other | F38B2.1 | X | <i>ifa-1</i> | STE CE MEI EMB | 1.00E-15 | |
| | X | LAMIN B1 | gi 125953 sp P20700 LAM1_HU MAN | Other | DY3.2 | I | <i>lmn-1</i> | EMB MITO | 1.20E-69 | |

| | | | | | | | | | | |
|---|---|--|--|-----------------------------|-----------------------|---------------|------------------------------|----------------------------------|-------------------|---|
| | | MAGO-NASHI PROTEIN | gi 6754616 ref NP_034890.1 | Other | R09B3.5 | I | <i>mag-1</i> | EMB STE | 1.20E-62 | |
| X | | MAP 1B | gi 5174525 ref NP_005900.1 | Microtubule | ZK593.6 | IV | <i>lgg-1</i> | EMB | 2.30E-36 | |
| X | X | MAP KINASE KINASE | gi 4200234 emb CAA22912.1 | Kinases | Y54E10BL.6 | I | <i>mek-2, let-537, glv-1</i> | STE EMB | 4.10E-103 | |
| | | MCAK/MITOTIC CENTROMERE ASSOCIATED KINESIN | gi 5803082 ref NP_006836.1 | Microtubule | K11D9.1 | III | <i>klp-7, CelMCAK</i> | CL EMB MITO | 3.30E-140 | |
| | | MEK BINDING PARTNER 1 | gi 9910452 ref NP_064304.1 | Other | C06H2.6 | V | | WT | 0.00045 | * |
| X | X | MKLP1 | gi 6754472 ref NP_004847.2 | Microtubule | M03D4.1 | IV | <i>zen-4, klp-9</i> | CL EMB | 4.80E-109 | |
| X | | MOESIN | gi 2218139 gb AAB61666.1 | Actin Associated | C01G8.5/F42A10.2 | I | <i>erm-1, nfm-1</i> | UNC EMB | 2.9E-164/6.3e-103 | |
| | | MYOFERLIN/FER-1 LIKE PROTEIN | gi 10834587 gb AAG23737.1 AF207990_1 | Secretary & Membrane Assoc. | F43G9.6 | I | <i>fer-1</i> | STE | 1.30E-154 | |
| X | X | MYOSIN I HC | gi 1083723 pir S52517 | Actin Associated | F29D10.4 | I | <i>hum-1</i> | WT | 1.50E-275 | |
| X | X | MYOSIN II NONMUSCLE | gi 10879497 gnl NCBIGenomeProt TR0001266 | Actin Associated | F20G4.3 | I | <i>nmy-2</i> | EMB CE STE ¹ | 1.20E-279 | |
| X | | MYOSIN LC | gi 127144 sp P16475 MLEN_HUMAN | Actin Associated | T12D8.6 | III | | WT EMB ¹ | 1.00E-34 | |
| X | | MYOSIN REGULATORY LIGHT CHAIN 2-B | gi 8393781 ref NP_059039.1 | Actin Associated | C56G7.1 | III | <i>mhc-4</i> | ALIGN MEI CE CL EMB ⁴ | 7.00E-67 | |
| | | MYOSIN VI | gi 6678992 ref NP_032688.1 | Secretary & Membrane Assoc. | Y66H1A.6 | IV | <i>hum-8</i> | STE/GON EMB | 6.79E-270 | |
| | | NADRIN/RICH1 RHOGAP | gi 9971185 dbj BAB12426.1 | Actin Associated | Y34B4A.8 | X | | EMB ALIGN CE STE/GON | 6.00E-34 | |
| | | NEDD4 UBIQUITIN LIGASE | gi 2144012 pir S70642 | Other | Y65B4BR.4 | I | <i>CeWwp1</i> | EMB | 4.10E-229 | |
| | | NIPSNAP1 | gi 7512727 pir T17302 | Secretary & Membrane Assoc. | K02D10.1 | III | | WT | 2.50E-48 | |
| | | NOGGIN | gi 7110675 ref NP_032737.1 | Other | no homolog | N/A | | N/A | N/A | * |
| | | NOVEL/AAC52863 | gi 1644455 gb AAC52863.1 | Other | H31G24.1 | I | | EMB CE STE/GON | 1.50E-09 | * |
| | | NOVEL/CGI-49 PROTEIN | gi 4929567 gb AAD34044.1 AF151807_1 | Other | F22F7.1/F22F7.2 | V | | STE | 2.6e-76/3.2e-62 | |
| | | NOVEL/CGI-94 PROTEIN | gi 18539291 gb AAL74316.1 | Other | C16C10.2 | III | | EMB | 1.30E-42 | |
| | | NOVEL/KIAA0102 | gi 7661908 ref NP_055567.1 | Other | Y37D8A.10 | III | | STE EMB UNC ¹ | 4.00E-16 | * |
| | | NOVEL/KIAA0377 | gi 7662084 ref NP_055474.1 | Other | F46F11.1 | I | | STE/GON | 9.71E-271 | |
| | | NSF | gi 6679140 ref NP_032766.1 | Secretary & Membrane Assoc. | H15N14.2 | I | <i>nsf-1</i> | EMB | 1.20E-78 | |
| | | N-TERMINAL KINASE LIKE PROTEIN 105-KDA | gi 10442581 gb AAG17393.1 AF276514_1 | Kinases | W07G4.3 | V | | STE/GON CE | 3.40E-124 | |
| | | NUCLEOPHOSMIN | gi 10835063 ref NP_002511.1 | Kinases | C33G8.2 | V | | MITO EMB | 8.00E-09 | * |
| | X | ORBIT/CLASP1 | gi 7513045 pir T00386 | Microtubule | R107.6/ZC84.3/C07H6.3 | III, III, III | <i>cls-2</i> | STE MITO EMB CHRSEG | 3e-29/8e-19/2e-26 | |

| | | | | | | | | | | |
|---|---|------------------------------------|-------------------------------------|-----------------------------|------------------|-----|-------------------------------|--|-------------|---|
| | | P120 CATENIN ISOFORM 4B | gi 3152867 gb AAC39829.1 | Other | Y105C5B.21 | IV | <i>jac-1</i> | STE/GON CE | 8.00E-76 | |
| | | PAR INTERACTIN ASSOCIATEDG PROTEIN | gi 7514041 pir T32731 | Other | K04C2.2 | III | | STE EMB | 5.90E-12 | * |
| X | X | PATCHED | gi:6679519 ref NP_032983 | Secretary & Membrane Assoc. | ZK675.1 | II | <i>ptc-1</i> | STE/GON EMB | 1.60E-195 | |
| | | PHOSPHOLIPASE C BETA 2 | gi 3688530 emb CAA09465.1 | Secretary & Membrane Assoc. | B0348.4 | V | <i>egl-8, pbo-1</i> | EMB | 1.00E-81 | |
| | | PINCH | gi 1346721 sp P48059 PINC_HUMAN | Actin Associated | F14D12.2 | X | <i>unc-97</i> | UNC EMB | e-119 | |
| | | PLECTIN | gi 1709655 sp P30427 PLEC_RA T | Actin Associated | ZK1151.1 | I | <i>vab-10</i> | EMB UNC | e-138 | |
| X | X | POLO-LIKE KINASE | gi 6755104 ref NP_035251.1 | Kinases | C14B9.4B | III | <i>plk-1, plc-1</i> | CL CE MEI CHRSEG MITO EMB STE ⁵ | e-163 | |
| | | PP1A | gi 7305405 ref NP_038664.1 | Kinases | F56C9.1 | III | <i>gsp-2, glc-7, CeGLC-7b</i> | EMB CE MEI MITO | e-177 | |
| X | | PP2A | gi 107304 pir B34541 | Kinases | F48E8.5 | III | <i>paa-1</i> | EMB ALIGN MITO STE ¹ | 1.80E-189 | |
| | | PP6C | gi 2499733 sp Q64620 PPP6_RA T | Kinases | C34C12.3 | III | | MITO CHRSEG | 1.90E-105 | |
| X | X | PROFILIN | gi 6755040 ref NP_035202.1 | Actin Associated | Y18D10A.20 | I | <i>pfn-1</i> | EMB CE STE UNC ² | 1.70E-21 | |
| | | RAB GDI ALPHA | gi 1707886 sp P31150 GDIA_HUMAN | Secretary & Membrane Assoc. | Y57G11C.10 | IV | <i>gdi-1</i> | CE CL STE/GON EMB | e-150 | |
| | | RAB22 | gi 9963781 gb AAG09690.1 AF183421_1 | Secretary & Membrane Assoc. | F26H9.6 | I | <i>rab-5</i> | EMB STE/GON | 3.40E-83 | |
| X | X | RAB6-KIFL | gi 6225915 sp O95235 RB6K_HUMAN | Secretary & Membrane Assoc. | MO3D4.1 | IV | <i>zen-4, klp-9</i> | CL EMB | 2.00E-37 | * |
| | | RAB7 | gi 4105819 gb AAD02565.1 | Secretary & Membrane Assoc. | W03C9.3 | II | <i>rab-7</i> | EMB CE | 2.00E-81 | |
| | | RACK 1 | gi 1083582 pir A36986 | Secretary & Membrane Assoc. | K04D7.1 | IV | | CL STE/GON EMB | 2.80E-127 | |
| X | X | RADIXIN | gi 6677699 ref NP_033067.1 | Actin Associated | C01G8.5/F42A10.2 | I | <i>erm-1, nfn-1</i> | UNC EMB | e-143/1E-80 | |
| | | RAS SUPPRESSOR PROTEIN/RSP1 | gi 6677825 ref NP_033131.1 | Kinases | C34C12.5 | III | | WT | 5.00E-82 | |
| X | | ROCK2 | gi 6677761 ref NP_033098.1 | Kinases | C10H11.9 | I | <i>let-502</i> | CL CE EMB ¹ | 1.20E-157 | |
| X | | SEC13 | gi 2498892 sp P55735 SC13_HUMAN | Secretary & Membrane Assoc. | Y77E11A.13 | IV | <i>npp-20</i> | STE/GON CE | 1.00E-72 | |
| | | SEC23 | gi 5454044 ref NP_006354.1 | Secretary & Membrane Assoc. | Y113G7A.3 | V | <i>sec-23</i> | STE/GON EMB | 6.00E-259 | |
| | | SEC31 | gi 7715039 gb AAF67836.1 | Secretary & Membrane Assoc. | T01G1.3 | IV | | CE EMB STE/GON | 3.00E-40 | |
| | | SEC3P-LIKE | gi 8922746 ref NP_060731.1 | Secretary & Membrane Assoc. | F52E4.7 | X | | EMB MEI STE/GON CE | e-114 | |
| X | X | SEPTIN 6 | gi 2500770 sp Q14141 SEP6_HUMAN | Actin Associated | Y50E8A.4 | V | <i>unc-61</i> | UNC EMB | 6.00E-99 | |
| X | X | SEPTIN/NEDD5 /CDCREL-1 | gi 6754816 ref NP_035021.1 | Actin Associated | W09C5.2 | I | <i>unc-59, unc-88</i> | MITO UNC | 3.00E-87 | |
| X | | SERINE THREONINE KINASE 24/STE20P | gi 2582413 gb AAB82560.1 | Kinases | T19A5.2 | V | <i>gck-1</i> | MITO MEI CL CHRSEG | e-103 | |

| | | | | | | | | | | |
|---|---|---|-------------------------------------|-----------------------------|----------------------|-----|----------------------|---------------------------------|-----------------|---|
| | | HOMOLOG | | | | | | STE/GON | | |
| | | SMOOTHELIN B | gi 7547259 gb AAF25580.2 | Actin Associated | T15B12.1 | III | | WT | 1.00E-31 | |
| | | SORTING NEXIN 4 | gi 10720282 sp O95219 SNX4_HUMAN | Secretary & Membrane Assoc. | C05D9.1 | X | <i>snx-1</i> | STE/GON CE MEI EMB | 9.00E-67 | |
| | | STAUFEN | gi 6755674 ref NP_035620.1 | Secretary & Membrane Assoc. | F55A4.5 | X | | EMB MEI | 5.00E-25 | |
| | | STE20-RELATED KINASE SMAK | gi 4741823 gb AAD28717.1 AF112855_1 | Kinases | C04A11.3 | X | | STE/GON <u>UNC</u> ¹ | 9.20E-148 | |
| X | X | TALIN | gi 227256 prf I617167A | Actin Associated | Y71G12B.11 | IV | | EMB | 1.20E-274 | |
| | | TMP21 PRECURSOR/ERV25P | gi 7513284 pir G01159 | Secretary & Membrane Assoc. | F47G9.1 | V | | EMB | 1.00E-58 | |
| | | TOG /XMAP215 HOMOLOG | gi 2136282 pir S68176 | Microtubule | F22B5.7 | II | <i>zyg-9</i> | EMB ALIGN CL | 6.40E-12 | |
| | X | TORSIN A | gi 10798614 emb CAC12785.1 | Other | C18E9.11 | II | <i>ooc-5</i> | ALIGN EMB MEI | 3.80E-59 | |
| | | TORSIN B | gi 10798612 emb CAC12814.1 | Secretary & Membrane Assoc. | Y37A1B.13 | IV | <i>tor-2, dyt-1</i> | STE/GON MITO CL EMB | 1.90E-64 | |
| | | T-PLASTIN/FIMBRIN | gi 2780868 pdb 1AOA | Actin Associated | Y104H12BR.1/Y73B3B.1 | IV | | EMB STE/GON CE | 1.6E-53/8.1e-41 | |
| X | | TROPOMYOSIN | gi 7513846 pir JC5710 | Actin Associated | Y105E8B.1 | I | <i>lev-11, tmy-1</i> | EMB UNC | 0.017 | * |
| | | TUFTELIN-INTERACTIN ASSOCIATEDG PROTEIN 33/SHORT STOP HOMOLOG | gi 10190660 ref NP_061253.2 | Actin Associated | ZK1151.2 | I | <i>vab-10</i> | STE/GON EMB UNC | 7.91E-245 | |
| | | VACULAR SORTING VPS35P | gi 10435637 dbj BAB14626.1 | Secretary & Membrane Assoc. | F59G1.3 | V | <i>vps-35</i> | WT | 5.20E-158 | |
| | | VAMP-ASSOCIATED PROTEIN A | gi 4240462 gb AAD13579.1 | Secretary & Membrane Assoc. | F33D11.11 | I | | EMB | 8.10E-34 | |
| X | X | VIMENTIN | gi 138536 sp P20152 VIME_MOUSE | Actin Associated | F38B2.1 | IV | <i>aly-2</i> | WT | 8.80E-39 | |
| | | VINCULIN | gi 6724323 ref NP_033528.1 | Actin Associated | ZC477.9 | IV | <i>deb-1, pat-8</i> | EMB | 7.00E-84 | |
| | | ZO-1/PLAKOGLOBIN | gi 1709649 sp Q02257 PLAK_MOUSE | Actin Associated | K05C4.6 | I | <i>hmp-2</i> | EMB UNC | 1.00E-84 | |
| | | ZO-2 | gi 7549795 ref NP_035727.1 | Actin Associated | C25F6.2 | X | <i>dlg-1</i> | EMB | e-143 | |

Note: The underlined phenotypes represent phenotypes not seen in our analysis but were reported elsewhere.

¹ (Kamath et al, 2003)

² (Simmer et al, 2003)

³ (Kaitna et al, 2002)

⁴ (Piekny et al, 2002)

⁵ (Piano et al, 2002)

| Mammalian Protein | Accession Number | Functional Group |
|---|-------------------------|-------------------------|
| 170kDa GLUCOSE REGULATED PROTEIN GRP170 PRECURSOR [MUS MUSCULUS] | Q60432 | Mitochondrial |
| 6-PHOSPHO FRUCTO KINASE (EC2.7.1.11)-RAT | NP_037322.1 | Mitochondrial |
| 78kDa GLUCOSE-REGULATED PROTEIN [MUS MUSCULUS] | BAD15288 | Mitochondrial |
| ACONITATE HYDRATASE (EC4.2.1.3) PRECURSOR, BOVINE | NP_002188 | Mitochondrial |
| ACYLCARRIERPROTEIN, MITOCHONDRIAL (ACP)(NADH-UBIQUINONEOXIDOREDUCTASE9.6kDaSUBUNIT)(CI-SDAP) | NP_004994 | Mitochondrial |
| ACYL-COENZYME A OXIDASEISOFORMB; ACYL-COENZYMEAOXIDASE 1 [HOMO SAPIENS] | AAA19114.1 | Mitochondrial |
| ADENINE PHOSPHORIBOSYL TRANSFERASE (APRT) | NP_000476.1 | Mitochondrial |
| ADENOSINE KINASE (EC2.7.1.20)-RAT | NP_037027.1 | Mitochondrial |
| ADP, ATP CARRIER PROTEIN, FIBROBLAST ISOFORM (ADP/ATPTRANSLOCASE2) (ADENINE NUCLEOTIDE TRANSLOCATOR 2) | NP_001143.1 | Mitochondrial |
| ALCOHOL DEHYDROGENASE [NADP+](ALDEHYDEREDUCTASE)(3-DG-REDUCINGENZYME) | BAA01627.1 | Mitochondrial |
| ALDEHYDE DEHYDROGENASE2, MITOCHONDRIAL [MUS MUSCULUS] | P47738 | Mitochondrial |
| ALDOLASE A [HOMO SAPIENS] | P04075 | Mitochondrial |
| ALKYL DIHYDROXY ACETONEPHOSPHATE SYNTHASE PRECURSOR (ALKYL-DHAPSYNTHASE) | NP_003650.1 | Mitochondrial |
| ANTI-OXIDANTPROTEIN1; MITOCHONDRIAL TRX DEPENDENT PEROXIDE REDUCTASE PRECURSOR | P20108 | Mitochondrial |
| ASPARTATE TRANSAMINASE (EC2.6.1.1) PRECURSOR, MITOCHONDRIAL-HUMAN | NP_002071.1 | Mitochondrial |
| ATP-BINDING CASSETTE, SUB-FAMILY A, MEMBER 2 [HOMO SAPIENS] | NP_001597.1 | Mitochondrial |
| ATP CITRATATELYASE [RATTUS NORVEGICUS] | P16638 | Mitochondrial |
| ATP SYNTHASE, H+TRANSPORTING, MITOCHONDRIAL F1 COMPLEX, ALPHA SUBUNIT,ISOFORM 1 [MUS MUSCULUS] | Q03265 | Mitochondrial |
| ATP SYNTHASE BETA CHAIN, MITOCHONDRIAL PRECURSOR | AAA51809.1 | Mitochondrial |
| ATP SYNTHASE GAMMA CHAIN, MITOCHONDRIAL PRECURSOR | BAA03995.1 | Mitochondrial |
| BETA ENOLASE (2-PHOSPHO-D-GLYCERATEHYDRO-LYASE)(SKELETALMUSCLEENOLASE)(MSE) | CAA40163.1 | Mitochondrial |
| BETA-GALACTOSIDE-BINDING LECTIN [RATTUS NORVEGICUS] | P11762 | Mitochondrial |
| CAD PROTEIN [INCLUDES: GLUTAMINE-DEPENDENT CARBAMOYL-PHOSPHATE SYNTHASE; ASPARTATE CARBAMOYL TRANSFERASE; DIHYDROOROTASE] | NP_004332.1 | Mitochondrial |
| CATALASE | NP_036652.1 | Mitochondrial |
| CGI-51 PROTEIN [HOMO SAPIENS]/PREDICTED CELL SURFACE PROTEIN HOMOLOGOUS TO BACTERIAL OUTER MEMBRANE PROTEIN S | NP_056195 | Mitochondrial |
| CHAINA, HUMAN DIHYDROOROTATE DEHYDROGENASE COMPLEXED WITH ANTIPROLIFERATIVE AGENT A771726 | 1D3G | Mitochondrial |
| CHAIN C, BOVINE MITOCHONDRIALF1-ATPASE COMPLEXED WITH THE PEPTIDE ANTIBIOTIC EFRAPEPTIN | 1EFR | Mitochondrial |
| CHAIN J, THIOREDOXIN PEROXIDASEBFROMREDBLOODCELLS | 1QMV | Mitochondrial |
| CREATINE KINASE, MITOCHONDRIAL 1 (UBIQUITOUS); CREATINE KINASE, MITOCHONDRIAL [HOMO SAPIENS] | P12532 | Mitochondrial |
| CYTOCHROME C OXIDASE, SUBUNIT VIII B; COX VIII-H [MUS MUSCULUS] | NP_031777 | Mitochondrial |
| CYTOCHROME C, SOMATIC [MUS MUSCULUS] | P00009 | Mitochondrial |
| CYTOCHROME C [HOMO SAPIENS] | NP_218190 | Mitochondrial |
| CYTOCHROME C1, HEMEPROTEIN | 1BE3 | Mitochondrial |
| CYTOCHROME C OXIDASE, SUBUNIT VA [MUS MUSCULUS] | P12787 | Mitochondrial |
| CYTOCHROME C OXIDASEPOLYPEPTIDE VIB (AED) | P80430 | Mitochondrial |
| CYTOCHROME C OXIDASEPOLYPEPTIDE VIII-LIVER | Q64445 | Mitochondrial |
| CYTOCHROME P450, 24 [MUS MUSCULUS] | BAA08416.1 | Mitochondrial |
| CYTOSOLIC ACYL COENZYME A THIOESTER HYDROLASE [RATTUS NORVEGICUS] | O00154 | Mitochondrial |
| D-3-PHOSPHOGLYCERATE DEHYDROGENASE (PGDH)(A10) | AAB67986.1 | Mitochondrial |
| DEATH ASSOCIATED PROTEIN 3[HOMO SAPIENS] | P51398 | Mitochondrial |

| | | |
|---|-------------|---------------|
| DIHYDROLIPOAMIDE ACETYL TRANSFERASE [HOMO SAPIENS] | AAA52202 | Mitochondrial |
| DIHYDROLIPOAMIDE SUCCINYLTRANSFERASE [HOMO SAPIENS] | AAA61786 | Mitochondrial |
| DIHYDRO OROTATE DEHYDROGENASE [MUS MUSCULUS] | AAB82948.2 | Mitochondrial |
| DIHYDRO OROTATEOXIDASE (EC1.3.3.1)-RAT | NP_110497 | Mitochondrial |
| DJ570L12.1 (PHOSPHOGLYCERATEKINASE1)[HOMO SAPIENS] | NP_920013 | Mitochondrial |
| DJ633O20.1 (SIMILARTOBOSTAURUSP14)[HOMO SAPIENS] | CAB44372 | Mitochondrial |
| DJ796I17.2 [HOMO SAPIENS] | CAB51401 | Mitochondrial |
| DNA K-TYPE MOLECULAR CHAPERONE PRECURSOR, MITOCHONDRIAL-HUMAN | B48127 | Mitochondrial |
| DOLICHYL-DIPHOSPHOOLIGOSACCHARIDE—PROTEIN GLYCOSYLTRANSFERASE 67kDa SUBUNIT PRECURSOR (RIBOPHORINI) (RPN-I) | NP_002941.1 | Mitochondrial |
| ENDOPEPTIDASE LA HOMOLOG (EC3.4.21) PRECURSOR, MITOCHONDRIAL (VERSION2)-HUMAN | NP_004784.1 | Mitochondrial |
| ESTRADIOL 17 BETA-DEHYDROGENASE (EC1.1.1.62) TYPE4-HUMAN | NP_000405.1 | Mitochondrial |
| F1 BETA SUBUNIT [HOMO SAPIENS] | NP_001677.1 | Mitochondrial |
| FATTY ACID SYNTHASE [HOMO SAPIENS] | AAH63242 | Mitochondrial |
| FIBRILLIN 1 [HOMO SAPIENS] | P35555 | Mitochondrial |
| FLJ00023 PROTEIN [HOMO SAPIENS]/MITOCHONDRIAL RIBOSOMAL PROTEIN S25 | BAB15723 | Mitochondrial |
| FUMARATE HYDRATASE [RATTUS NORVEGICUS] | P14408 | Mitochondrial |
| GAPDH-2 LIKE [HOMO SAPIENS] | AAB64181 | Mitochondrial |
| GLUTAMATE-CYSTEINE LIGASE REGULATORY PROTEIN; GAMMA-GLUTAMYL CYSTEINE SYNTHETASE; GSC LIGHT CHAIN[HOMO SAPIENS] | P4850 | Mitochondrial |
| GLUTAMATE DEHYDROGENASE 1 PRECURSOR (GDH) | NP_005262.1 | Mitochondrial |
| GLUTATHIONE-S-TRANSFERASE, MU1 [MUS MUSCULUS] | P10649 | Mitochondrial |
| GLUTATHIONES-TRANSFERASE M5 [RATTUS NORVEGICUS] | AAD00603 | Mitochondrial |
| GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE [MUS MUSCULUS] | P16858 | Mitochondrial |
| GLYCEROL-3-PHOSPHATEDEHYDROGENASE, MITOCHONDRIAL PRECURSOR (GPD-M)(GPDH-M) | NP_036868.1 | Mitochondrial |
| HEMEOXYGENASE1 (HO-1)(HSP32) | NP_036712.1 | Mitochondrial |
| HEPARANSULFATE PROTEOGLYCAN 2 (PERLECAN)[HOMO SAPIENS] | P98160 | Mitochondrial |
| HEXOKINASE 1 ISOFORM TD [HOMO SAPIENS] | AAF82320 | Mitochondrial |
| HEXOKINASE2 [MUS MUSCULUS] | O08528 | Mitochondrial |
| HYDROXYSTEROID 17-BETA DEHYDROGENASE 4 [MUS MUSCULUS] | P51660 | Mitochondrial |
| HYPOTHETICAL PROTEIN DKFZ P586G1517.1-HUMAN (FRAGMENT) | CAB55934.1 | Mitochondrial |
| IMP (INOSINEMONOPHOSPHATE) DEHYDROGENASE 2 [HOMO SAPIENS] | AAA36112.1 | Mitochondrial |
| ISOCITRATE DEHYDROGENASE 3(NAD+), GAMMA [MUS MUSCULUS] | P70404 | Mitochondrial |
| KIAA0418 GENE PRODUCT [HOMO SAPIENS], NADPH OXIDASE DOMAIN, MITOCHONDRIAL | BAA24848 | Mitochondrial |
| LACTATE DEHYDROGENASE 1, A CHAIN [MUS MUSCULUS] | P06151 | Mitochondrial |
| LACTATE DEHYDROGENASE A [RATTUS NORVEGICUS] | P04642 | Mitochondrial |
| LEUCINE AMINO PEPTIDASE (UNLIGATED) | 1LAN | Mitochondrial |
| LONG-CHAIN-FATTY-ACIDBETA-OXIDATION MULTI ENZYME COMPLEX BETA CHAIN PRECURSOR, MITOCHONDRIAL-RAT | BAA03940.1 | Mitochondrial |
| MALATE DEHYDROGENASE, MITOCHONDRIALPRECURSOR | CAA30274.1 | Mitochondrial |
| METAXIN 2[MUS MUSCULUS] | BAA95046.1 | Mitochondrial |
| METHYLENE TETRAHYDROFOLATE DEHYDROGENASE (NAD+DEPENDENT), METHENYL TETRAHYDROFOLATE CYCLOHYDROLASE [MUS MUSCULUS] | P18155 | Mitochondrial |
| MITOCHONDRIAL HYDROXYACYL DEHYDROGENASE, SUBUNIT B; 3-KETOACYL-COENZYME A THIOLASE; TRIFUNCTIONAL | NP_000174.1 | Mitochondrial |

| | | |
|--|-------------|---------------|
| PROTEIN, BETA SUBUNIT [HOMO SAPIENS] | | |
| MITOCHONDRIAL ACONITASE [RATTUS NORVEGICUS] | AAC18425.1 | Mitochondrial |
| MITOCHONDRIAL IMPORT STIMULATION FACTOR (MSF) L SUBUNIT | BAA06401 | Mitochondrial |
| MITOCHONDRIAL NADH DEHYDROGENASE (UBIQUINONE) 51kDa SUBUNIT | AAA21466.1 | Mitochondrial |
| MITOCHONDRIAL TRIFUNCTIONAL ENZYME ALPHA SUBUNIT PRECURSOR (TP-ALPHA) | Q64428 | Mitochondrial |
| MITOCHONDRIAL VOLTAGE DEPENDENT ANION CHANNEL [RATTUS NORVEGICUS] | AAF80115.1 | Mitochondrial |
| MITOFILIN [HOMO SAPIENS] | AAF73126 | Mitochondrial |
| NADH-CYTOCHROME B5 REDUCTASE | P00387 | Mitochondrial |
| NADH DEHYDROGENASE (UBIQUINONE)(EC1.6.5.3) 75KCHAINPRECURSOR-HUMAN | NP_004997.1 | Mitochondrial |
| NADH DEHYDROGENASE (UBIQUINONE)(EC1.6.5.3) CHAINCI-PDSW-BOVINE | Q02373 | Mitochondrial |
| NADH DEHYDROGENASE (UBIQUINONE)(EC1.6.5.3) FLAVOPROTEIN1PRECURSOR-HUMAN | AAD40373.1 | Mitochondrial |
| NADH DEHYDROGENASE (UBIQUINONE) FE-S PROTEIN 4(18kD)(NADH-COENZYMEQREDUCTASE)[HOMO SAPIENS] | O43181 | Mitochondrial |
| NADH DEHYDROGENASE (UBIQUINONE) FLAVOPROTEIN 2(24kD)[HOMO SAPIENS] | P19404 | Mitochondrial |
| NADH DEHYDROGENASE-UBIQUINONE 30kDa SUBUNIT [HOMO SAPIENS] | NP_004542.1 | Mitochondrial |
| NADPH-DEPENDENT THIOREDOXIN REDUCTASE [RATTUS NORVEGICUS] | AAD43039 | Mitochondrial |
| NICOTINAMIDE NUCLEOTIDE TRANSHYDROGENASE [MUS MUSCULUS] | AAH08518 | Mitochondrial |
| P100 CO-ACTIVATOR [MUS MUSCULUS] | BAA84944.1 | Mitochondrial |
| P105 CO-ACTIVATOR [RATTUS NORVEGICUS] | NP_073185 | Mitochondrial |
| PEPTIDYL PROLYLISOMERASE A (CYCLOPHILINA)[RATTUS NORVEGICUS] | P10111 | Mitochondrial |
| PEROXIREDOXIN 3; ANTI-OXIDANT PROTEIN 1; MITOCHONDRIAL TRX DEPENDENT PEROXIDE REDUCTASE PRECURSOR; MITOCHONDRIAL THIOREDOXIN DEPENDENT PEROXIDE REDUCTASE PRECURSOR; PRX III; ANTIOXIDANT PROTEIN 1 [MUS MUSCULUS] | NP_031478 | Mitochondrial |
| PEROXIREDOXIN 1[HOMO SAPIENS] | Q06830 | Mitochondrial |
| PEROXIREDOXIN 4;ANTIOXIDANTENZYME AOE372 [MUS MUSCULUS] | AAB57846.1 | Mitochondrial |
| PHOSPHATE CARRIER PROTEIN, FORMB-HUMAN | NP_002626.1 | Mitochondrial |
| PHOSPHOGLYCERATE KINASE 1 [MUS MUSCULUS] | P09411 | Mitochondrial |
| PHOSPHOGLYCERATEMUTASE, BRAINFORM (PGAM-B)(BPG-DEPENDENTPGAM) | AAA41834.1 | Mitochondrial |
| PHOSPHOPYRUVATE HYDRATASE (EC4.2.1.11) ALPHA-RAT | NP_036686.1 | Mitochondrial |
| PHOSPHO RIBOSYL GLYCINAMIDE FORMYL TRANSFERASE [MUS MUSCULUS] | Q64737 | Mitochondrial |
| PHOSPHO RIBOSYL PYROPHOSPHATE SYNTHETASE 2[HOMO SAPIENS] | P11908 | Mitochondrial |
| PLATELET-ACTIVATING FACTOR ACETYLHYDROLASE IB ALPHA SUBUNIT (PAFACETYLHYDROLASE45KDASUBUNIT)(PAF-AH45kDaSUBUNIT)(PAF-AHALPHA)(PAFAHALPHA)(LISSENCEPHALY-1PROTEIN)(LIS-1) | AAC27975.1 | Mitochondrial |
| PLC ALPHA [BOSTAURUS] | P38657 | Mitochondrial |
| POLYPEPTIDE N-ACETYLGALACTOSAMINYLTRANSFERASE2; UDP-N-ACETYL-ALPHA-D-GALACTOSAMINE; PROTEIN-UDPACETYLGALACTOSAMINYLTRANSFERASE; UDP-GALNACTRANSFERASE 2 [HOMO SAPIENS] | P34678 | Mitochondrial |
| PRO2455 | AB02036.1 | Mitochondrial |
| PROCOLLAGEN-LYSINE, 2-OXOGLUTARATE5-DIOXYGENASE 3; LYSYL HYDROXYLASE2 [MUS MUSCULUS] | AAD54618.1 | Mitochondrial |
| PROHIBITIN-HUMAN | NP_002625.1 | Mitochondrial |
| PROTEINDISULFIDE-ISOMERASE (EC5.3.4.1) ER60 PRECURSOR-HUMAN | CAA89996.1 | Mitochondrial |
| PR XIV [RATTUS NORVEGICUS] | A26456.1 | Mitochondrial |
| PYRUVATE DEHYDROGENASE (LIPOAMIDE)(EC1.2.4.1) BETA CHAIN-RAT | P49432 | Mitochondrial |
| PYRUVATE KINASE (EC2.7.1.40) ISOZYME M1-RAT | P11980 | Mitochondrial |
| PYRUVATE KINASE (EC2.7.1.40) ISOZYME M2-HUMAN | AAA36672.1 | Mitochondrial |

| | | |
|--|-------------|---------------|
| RAT OUTER MITOCHONDRIAL MEMBRANE CYTOCHROME B5 | IICC_A | Mitochondrial |
| RIBOSE-PHOSPHATE PYROPHOSPHOKINASE (EC2.7.6.1) CATALYTIC CHAIN III-HUMAN | AAB59463.1 | Mitochondrial |
| RIBOSE-PHOSPHATE PYROPHOSPHO KINASE I (PHOSPHO RIBOSYL PYRO PHOSPHATE SYNTHETASEI)(PPRIBP)(PRS-I) | NP_002755.1 | Mitochondrial |
| RIBOSOMAL PROTEIN, MITOCHONDRIAL, L12 [HOMO SAPIENS] | CAA56249.1 | Mitochondrial |
| SERINE HYDROXY METHYL TRANSFERASE (EC2.1.2) 2-MOUSE | CAA64226.1 | Mitochondrial |
| SEROTRANSFERRIN PRECURSOR (SIDEROPHILIN)(BETA-1-METAL BINDING GLOBULIN) | AAA96735.1 | Mitochondrial |
| SIMILAR TO DIHYDROLIPOAMIDE S-SUCCINYL TRANSFERASE (E2 COMPONENT OF 2-OXO-GLUTARATE COMPLEX) [RATTUS NORVEGICUS] | XP_216753 | Mitochondrial |
| SUCCINATE DEHYDROGENASE COMPLEX, SUBUNIT D PRECURSOR [HOMO SAPIENS] | AAH09574 | Mitochondrial |
| SUCCINATE—CO A LIGASE (GDP-FORMING)(EC6.2.1.4) ALPHA CHAIN PRECURSOR-RAT | P13086 | Mitochondrial |
| SUCCINATE DEHYDROGENASE FP SUBUNIT [MUS MUSCULUS] | XP_127445 | Mitochondrial |
| SUPEROXIDE DIMUTASE 2, MITOCHONDRIAL [RATTUS NORVEGICUS] | P07895 | Mitochondrial |
| THIOREDOXIN [MUS MUSCULUS] | BAA04881.1 | Mitochondrial |
| THIOREDOXIN REDUCTASE 1[MUS MUSCULUS] | BAA86985.1 | Mitochondrial |
| THYMIDYLATE SYNTHASE (EC2.1.1.45)-MOUSE | P07607 | Mitochondrial |
| TRANSAMINASE, GLUTAMATE OXALOACETATE [RATTUS NORVEGICUS] | AAH61877 | Mitochondrial |
| TRANSKETOLASE [MUS MUSCULUS] | NP_033414.1 | Mitochondrial |
| TRANSLATION ELONGATION FACTOR TU-LIKE PROTEIN P43 PRECURSOR, MITOCHONDRIAL-HUMAN | AAC60647.1 | Mitochondrial |
| TRANSLOCASE OF INNER MITOCHONDRIAL MEMBRANE 10 HOMOLOG (YEAST) [MUS MUSCULUS] | AAD40007.1 | Mitochondrial |
| TRANSLOCASE OF OUTER MITOCHONDRIAL MEMBRANE 70 (YEAST) HOMOLOG A [HOMO SAPIENS] | BAA34439.1 | Mitochondrial |
| UBIQUINOL--CYTOCHROME-C REDUCTASE (EC1.10.2.2) CORE PROTEIN I-HUMAN | NP_003356.1 | Mitochondrial |
| UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX CORE PROTEIN I PRECURSOR | CAA42213.1 | Mitochondrial |
| UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 11(UBIQUITIN THIOLESTERASE 11)(UBIQUITIN-SPECIFIC PROCESSING PROTEASE11) | NP_004642.1 | Mitochondrial |
| UDP GLUCOSE 6-DEHYDROGENASE (EC1.1.1.22)-BOVINE | AAB32227.1 | Mitochondrial |
| VOLTAGE-DEPENDENT ANION CHANNEL 1 [MUS MUSCULUS] | NP_035824.1 | Mitochondrial |
| VOLTAGE-DEPENDENT ANIONCHANNEL 2 [MUS MUSCULUS] | Q60930 | Mitochondrial |
| VOLTAGE-DEPENDENT ANIONCHANNEL 3 [MUS MUSCULUS] | Q60931 | Mitochondrial |
| VOLTAGE-DEPENDENT ANION-SELECTIVE CHANNEL PROTEIN 2 (HVDAC2) (OUTER MITOCHONDRIAL MEMBRANE PROTEINPORIN 2) | AAA60144.1 | Mitochondrial |
| 40S RIBOSOMAL PROTEIN S10 | NP_001005.1 | Ribosomal |
| 40S RIBOSOMAL PROTEIN S11 | AAA42076.1 | Ribosomal |
| 40S RIBOSOMAL PROTEIN S12 | NP_001007.1 | Ribosomal |
| 40S RIBOSOMAL PROTEIN S15 (RIG PROTEIN) | NP_001009.1 | Ribosomal |
| 40S RIBOSOMAL PROTEIN S2 (S4) (LLREP3 PROTEIN) | P25444 | Ribosomal |
| 40S RIBOSOMAL PROTEIN S23 | CAA54584.1 | Ribosomal |
| 40S RIBOSOMAL PROTEIN S27A | AAH02108 | Ribosomal |
| 40S RIBOSOMAL PROTEIN S3A | NP_000997.1 | Ribosomal |
| 40S RIBOSOMAL PROTEIN S4 | BAA21078.1 | Ribosomal |
| 40S RIBOSOMAL PROTEIN S5 | NP_001000.1 | Ribosomal |
| 40S RIBOSOMAL PROTEIN S7 (S8) | NP_001002.1 | Ribosomal |
| 40S RIBOSOMAL PROTEIN S9 | NP_001004.1 | Ribosomal |
| 40S RIBOSOMAL PROTEIN SA (P40) (34/67 kD LAMININ RECEPTOR) | BAA04953.1 | Ribosomal |

| | | |
|---|-------------|-----------|
| 60S ACIDIC RIBOSOMAL PROTEIN P0 (L10E) | NP_000993.1 | Ribosomal |
| 60S ACIDIC RIBOSOMAL PROTEIN P2 | AAC48755.1 | Ribosomal |
| 60S RIBOSOMAL PROTEIN L10 (QM PROTEIN) (TUMOR SUPPRESSOR QM) (LAMININ RECEPTOR HOMOLOG) | NP_006004.1 | Ribosomal |
| 60S RIBOSOMAL PROTEIN L13 | P41123 | Ribosomal |
| 60S RIBOSOMAL PROTEIN L14 (CAG-ISL 7) | AAC16021.1 | Ribosomal |
| 60S RIBOSOMAL PROTEIN L24 (L30) | CAA55203.1 | Ribosomal |
| 60S RIBOSOMAL PROTEIN L38 | NP_000990.1 | Ribosomal |
| 60S RIBOSOMAL PROTEIN L8 | NP_000964.1 | Ribosomal |
| 60S RIBOSOMAL PROTEIN L9 [MUS MUSCULUS] | P51410 | Ribosomal |
| ACIDIC RIBOSOMAL PROTEIN P1 - HUMAN | NP_000994.1 | Ribosomal |
| CB1E7.2 (RIBOSOMAL PROTEIN S17-LIKE 4) [HOMO SAPIENS] | BAB03097 | Ribosomal |
| CGI-117/HSPC111 | NP_057475.1 | Ribosomal |
| CGI-147 | Q8R2Y8 | Ribosomal |
| CGI-37 PROTEIN [HOMO SAPIENS] / HSPC031/NIP7 HOMOLOG | NP_057185.1 | Ribosomal |
| PROTEIN (16kDa) SIMILAR TO HUMAN SYK INTERACTING PROTEIN [MUS MUSCULUS] | CAA36322.1 | Ribosomal |
| RIBOPHORIN [MUS MUSCULUS] | BAA06525.1 | Ribosomal |
| RIBOPHORIN II PRECURSOR - HUMAN | B26168 | Ribosomal |
| RIBOSOMAL PROTEIN L10, CYTOSOLIC - HUMAN (FRAGMENT) | AAB22173.1 | Ribosomal |
| RIBOSOMAL PROTEIN L10A [HOMO SAPIENS] | P53025 | Ribosomal |
| RIBOSOMAL PROTEIN L11 [RATTUS RATTUS] | CAA44072 | Ribosomal |
| RIBOSOMAL PROTEIN L15 - RAT | P41051 | Ribosomal |
| RIBOSOMAL PROTEIN L17 [HOMO SAPIENS] | AAH66323 | Ribosomal |
| RIBOSOMAL PROTEIN L18 [MUS MUSCULUS] | AAA40067.1 | Ribosomal |
| RIBOSOMAL PROTEIN L19 - HUMAN | NP_000972.1 | Ribosomal |
| RIBOSOMAL PROTEIN L21 [MUS MUSCULUS] | O09167 | Ribosomal |
| RIBOSOMAL PROTEIN L22 [HOMO SAPIENS] | P35268 | Ribosomal |
| RIBOSOMAL PROTEIN L23 - HUMAN | AAH10114 | Ribosomal |
| RIBOSOMAL PROTEIN L23A [HOMO SAPIENS] | AAH58041 | Ribosomal |
| RIBOSOMAL PROTEIN L26; 60S RIBOSOMAL PROTEIN L26 [HOMO SAPIENS] | NP_000978 | Ribosomal |
| RIBOSOMAL PROTEIN L3 [HOMO SAPIENS] | AAH15767 | Ribosomal |
| RIBOSOMAL PROTEIN L3 PRECURSOR, MITOCHONDRIAL - RAT | P18665 | Ribosomal |
| RIBOSOMAL PROTEIN L30, CYTOSOLIC - HUMAN | NP_000980.1 | Ribosomal |
| RIBOSOMAL PROTEIN L32 - RAT | NP_037358.1 | Ribosomal |
| RIBOSOMAL PROTEIN L37A - HUMAN | NP_000989.1 | Ribosomal |
| RIBOSOMAL PROTEIN L4 - RAT | AAH63811 | Ribosomal |
| RIBOSOMAL PROTEIN L5 | AAH60561 | Ribosomal |
| RIBOSOMAL PROTEIN L7 | AAH51261 | Ribosomal |
| RIBOSOMAL PROTEIN L7A (AA 1-266) [RATTUS RATTUS] | AAH65176 | Ribosomal |
| RIBOSOMAL PROTEIN L9, MUTANT | AAA85685 | Ribosomal |
| RIBOSOMAL PROTEIN P1 [RATTUS RATTUS] | CAA33200.1 | Ribosomal |
| RIBOSOMAL PROTEIN P2=IRON-BINDING PROTEIN [RATS, LIVER, PEPTIDE PARTIAL, 12 AA, SEGMENT 3 OF 4] | AAB23472 | Ribosomal |
| RIBOSOMAL PROTEIN S10 [MUS MUSCULUS] | AAH19725 | Ribosomal |
| RIBOSOMAL PROTEIN S11 [RATTUS NORVEGICUS] | AAH58465 | Ribosomal |

| | | |
|---|-------------|-----------|
| RIBOSOMAL PROTEIN S13 [HOMO SAPIENS] | AAH66322 | Ribosomal |
| RIBOSOMAL PROTEIN S14 - MOUSE | AAH42940 | Ribosomal |
| RIBOSOMAL PROTEIN S16 [MUS MUSCULUS] | P14131 | Ribosomal |
| RIBOSOMAL PROTEIN S17 [RATTUS NORVEGICUS] | AAH58484 | Ribosomal |
| RIBOSOMAL PROTEIN S19 [MUS MUSCULUS] | AAH34506 | Ribosomal |
| RIBOSOMAL PROTEIN S2 [HOMO SAPIENS] | AAH66321 | Ribosomal |
| RIBOSOMAL PROTEIN S21 - RAT | P05765 | Ribosomal |
| RIBOSOMAL PROTEIN S26 - RAT | NP_037356.1 | Ribosomal |
| RIBOSOMAL PROTEIN S3 [HOMO SAPIENS] | CAA39248.1 | Ribosomal |
| RIBOSOMAL PROTEIN S6 [MUS MUSCULUS] | CAA90936.1 | Ribosomal |
| RIBOSOMAL PROTEIN S8 [HOMO SAPIENS] | CAA47670.1 | Ribosomal |
| RIBOSOME-BINDING PROTEIN P34 - RAT | S36779 | Ribosomal |
| RIBOSOMAL PROTEIN L10A [MUS MUSCULUS] | P53026 | Ribosomal |
| SIK SIMILAR PROTEIN [MUS MUSCULUS] | AAC08435.1 | Ribosomal |
| SIMILAR TO RIBOSOMAL PROTEIN L3 (H. SAPIENS) [HOMO SAPIENS] | P39023 | Ribosomal |
| SYT INTERACTING PROTEIN [HOMO SAPIENS] | AAC64058.1 | Ribosomal |
| APOPTOTIC CHROMATIN CONDENSATION INDUCER IN THE NUCLEUS; ACINUSS [MUS MUSCULUS] | AAD56723.1 | Nuclear |
| BROMODOMAIN PROTEIN [HOMO SAPIENS] | AAF19526.1 | Nuclear |
| CELLULAR APOPTOSIS SUSCEPTIBILITY PROTEIN CAS - HUMAN | NP_001307.1 | Nuclear |
| CGI-55 PROTEIN [HOMO SAPIENS]-CHROMATIN BINDING | AAK51130 | Nuclear |
| CHAIN B, SOLUTION STRUCTURE OF HUMAN BARRIER-TO-AUTOINTEGRATION FACTOR BAF, NMR, REGULARIZED MEAN STRUCTURE PLUS 20 INDIVIDUAL SIMULATED ANNEALING STRUCTURES | 1QCK | Nuclear |
| CHROMATIN STRUCTURAL PROTEIN HOMOLOG SUPT5HP - MOUSE | AAC40052.1 | Nuclear |
| DEK PROTEIN | NP_003463.1 | Nuclear |
| DJ686C3.2 (NUCLEOLAR PROTEIN HNOP56) [HOMO SAPIENS] | CAC01444 | Nuclear |
| DNA (CYTOSINE-5-)-METHYLTRANSFERASE (EC 2.1.1.37) - RAT | S01845 | Nuclear |
| ERBB3 BINDING PROTEIN EBP1 [HOMO SAPIENS] | AAD00646 | Nuclear |
| FRALE X MENTAL RETARDATION SYNDROME RELATED PROTEIN FXR1 - HUMAN | NP_005078.1 | Nuclear |
| FUSE BINDING PROTEIN 3 [HOMO SAPIENS]-APOPTOSIS ASSOCIATED | AAC50893 | Nuclear |
| G1/S TRANSITION CONTROL PROTEIN-BINDING PROTEIN RBAP46 - HUMAN | NP_002884.1 | Nuclear |
| GTP-BINDING NUCLEAR PROTEIN RAN (TC4) | NP_006316 | Nuclear |
| GUANOSINE DIPHOSPHATE (GDP) DISSOCIATION INHIBITOR 3; GDI BETA [MUS MUSCULUS] | AAA78786.1 | Nuclear |
| HIGH MOBILITY GROUP PROTEIN FRAGMENT-B (HMGB) (DNA-BINDING HMG-BOX DOMAIN B OF RAT HMG1) (NMR, 30 STRUCTURES) | 1HME | Nuclear |
| HIGH MOBILITY GROUP PROTEIN HMG1 (HMG-1) | NP_002119.1 | Nuclear |
| HISTONE H1.1 - HUMAN | NP_005316.1 | Nuclear |
| HISTONE H2A - MOUSE | CAA83210.1 | Nuclear |
| HISTONE H2A.X - HUMAN | NP_002096.1 | Nuclear |
| HISTONE H2A.Z - HUMAN | NP_002097.1 | Nuclear |
| HISTONE H2B [RATTUS NORVEGICUS] | AAH66243 | Nuclear |
| HISTONE H3 - MOUSE | CAA83209.1 | Nuclear |
| HISTONE H3.4 - MOUSE | HSMS34 | Nuclear |
| HISTONE H4 [HOMO SAPIENS] | AAH16336 | Nuclear |

| | | |
|---|-------------|---------|
| HSPC120 [HOMO SAPIENS] | AAF29084 | Nuclear |
| HYPOTHETICAL PROTEIN FLJ10604 [HOMO SAPIENS] | BAA91708.1 | Nuclear |
| HYPOTHETICAL PROTEIN FLJ10814 [HOMO SAPIENS] | BAA91829.1 | Nuclear |
| IMPORTIN BETA [RATTUS NORVEGICUS] | AAC42047.1 | Nuclear |
| IMPORTIN BETA-1 SUBUNIT (KARYOPHERIN BETA-1 SUBUNIT) (NUCLEAR FACTOR P97) (IMPORTIN 90) RT FACTOR - HUMAN | Q14974 | Nuclear |
| KIAA0095 GENE PRODUCT [HOMO SAPIENS] /NUCLEOPORIN INTERACTING COMPONENT | BAA07680.1 | Nuclear |
| KIAA1470 PROTEIN [HOMO SAPIENS]/RCC1-LIKE | BAA95994 | Nuclear |
| LAMININ RECEPTOR, 67K - HUMAN | AAB22299.1 | Nuclear |
| MATERNAL EMBRYONIC MESSAGE 3 [MUS MUSCULUS] | AAB18153.1 | Nuclear |
| MATRIN 3 [RATTUS NORVEGICUS] | AAB63955.1 | Nuclear |
| MINI CHROMOSOME MAINTENANCE DEFICIENT 5 (S. CEREVISIAE) [MUS MUSCULUS] | BAA05083.1 | Nuclear |
| MINI CHROMOSOME MAINTENANCE DEFICIENT 6 (S. CEREVISIAE) [MUS MUSCULUS] | P97311 | Nuclear |
| MINI CHROMOSOME MAINTENANCE DEFICIENT 7 (S. CEREVISIAE) [MUS MUSCULUS] | BAA05084.1 | Nuclear |
| M-PHASE PHOSPHOPROTEIN 11 [HOMO SAPIENS] | CAA66913 | Nuclear |
| NONHISTONE CHROMOSOMAL PROTEIN HMG-2 - HUMAN | P26583 | Nuclear |
| NONHISTONE CHROMOSOMAL PROTEIN HMG-2B - HUMAN (FRAGMENT) | CAA78938.1 | Nuclear |
| NON-POU DOMAIN-CONTAINING OCTAMER (ATGCAAAT) BINDING PROTEIN [HOMO SAPIENS] | AAA03427.1 | Nuclear |
| NOPP140 | AAA41718 | Nuclear |
| NUCLEAR CORE GLYCOPROTEIN | AAA60741 | Nuclear |
| NUCLEAR COREPRESSOR KAP-1 [HOMO SAPIENS] | AAB37341 | Nuclear |
| NUCLEAR DISTRIBUTION GENE C HOMOLOG (ASPERLLUS) [MUS MUSCULUS] | CAA75677.1 | Nuclear |
| NUCLEAR FACTOR OF KAPPA LIGHT POLYPEPTIDE GENE ENHANCER IN B-CELLS 2, P49/P100 [MUS MUSCULUS] | AAD39462.1 | Nuclear |
| NUCLEAR INHIBITOR OF PROTEIN PHOSPHATASE-1 (NIPP-1) (PROTEIN PHOSPHATASE 1, REGULATORY INHIBITOR SUBUNIT 8) | CAA90625.1 | Nuclear |
| NUCLEAR MATRIX PROTEIN NMP200 [HOMO SAPIENS] | NP_055317.1 | Nuclear |
| NUCLEAR MYOSIN I BETA [MUS MUSCULUS] | AAG02570 | Nuclear |
| NUCLEAR PORE COMPLEX GLYCOPROTEIN P62 - MOUSE | A56573 | Nuclear |
| NUCLEAR PORE COMPLEX PROTEIN NUP153 - HUMAN | NP_005115.1 | Nuclear |
| NUCLEAR PROTEIN SDK3 [HOMO SAPIENS] | AAF17209 | Nuclear |
| NUCLEAR PROTEIN, 25K - MOUSE | NP_663449 | Nuclear |
| NUCLEAR RNA HELICASE [RATTUS NORVEGICUS] | AAC16391 | Nuclear |
| NUCLEOLAR PROTEIN P120 - MOUSE (FRAGMENT) | A48998 | Nuclear |
| NUCLEOLIN [RATTUS NORVEGICUS] | P13383 | Nuclear |
| NUCLEOPORIN 98kD [HOMO SAPIENS] | P52948 | Nuclear |
| NUCLEOPORIN P54 [RATTUS NORVEGICUS] | AAC52790.1 | Nuclear |
| NUCLEOPORIN P58 [RATTUS NORVEGICUS] | AAC52789 | Nuclear |
| NUCLEOPROTEIN TPR | NP_003283.1 | Nuclear |
| NUCLEOSIDE DIPHOSPHATE KINASE A (NDK A) (NDP KINASE A) (TUMOR METASTATIC PROCESS-ASSOCIATED PROTEIN) (METASTASIS INHIBITION FACTOR NM23) (NDPK-A) | AAB87689.1 | Nuclear |
| NUCLEOSOME ASSEMBLY PROTEIN-1 [MUS MUSCULUS] | BAA02142.1 | Nuclear |
| NUP98-NUP96 PRECURSOR SPLICE VARIANT 1 [HOMO SAPIENS] | AAD22396 | Nuclear |
| OCTAMER-BINDING PROTEIN NONO - MOUSE | A54691 | Nuclear |
| P38-2G4 PROTEIN - MOUSE | CAA59260.1 | Nuclear |
| PROLIFERATING CELL NUCLEAR ANTIGEN [MUS MUSCULUS] | CAA40938.1 | Nuclear |

| | | |
|--|-------------|---------------------------|
| PROLIFERATING CELL NUCLEAR PROTEIN P120 | P46087 | Nuclear |
| PUTATIVE HISTONE DEACETYLASE [MUS MUSCULUS] | AAB68398 | Nuclear |
| RAN-BINDING PROTEIN 2 [MUS MUSCULUS] | NP_035370 | Nuclear |
| RAN-BP1(RAN-BINDING PROTEIN 1) [HOMO SAPIENS] | NP_002873 | Nuclear |
| RAP1A, MEMBER OF RAS ONCOGENE FAMILY [HOMO SAPIENS] | CAB55685.1 | Nuclear |
| RAS-GTPASE ACTIVATING PROTEIN SH3 DOMAIN-BINDING PROTEIN 2 [HOMO SAPIENS] | AAC95292.1 | Nuclear |
| RETINOBLASTOMA BINDING PROTEIN 2 HOMOLOG 1 [HOMO SAPIENS] | AAD16061 | Nuclear |
| RETINOBLASTOMA BINDING PROTEIN 4 [MUS MUSCULUS] | AAC52275.1 | Nuclear |
| SIMILAR TO NON-HISTONE CHROMOSOME PROTEIN 2 (S. CEREVISIAE)-LIKE 1 (H. SAPIENS) [HOMO SAPIENS] | P55769 | Nuclear |
| SMC1 (STRUCTURAL MAINTENANCE OF CHROMOSOMES 1, YEAST)-LIKE 1 [HOMO SAPIENS] | AAB34405.1 | Nuclear |
| SNF2 PROTEIN HOMOLOG - HUMAN | NP_003060.1 | Nuclear |
| STRUCTURE-SPECIFIC RECOGNITION PROTEIN 1 (SSRP1) (RECOMBINATION SIGNAL SEQUENCE RECOGNITION PROTEIN) (T160) | Q08943 | Nuclear |
| SWI/SNF RELATED, MATRIX ASSOCIATED, ACTIN DEPENDENT REGULATOR OF CHROMATIN, SUBFAMILY E, MEMBER 1 [HOMO SAPIENS] | AAC04509.1 | Nuclear |
| TELOMERASE BINDING PROTEIN P23 [MUS MUSCULUS] | NP_062740 | Nuclear |
| TOPOISOMERASE (DNA) II ALPHA [MUS MUSCULUS] | Q01320 | Nuclear |
| TOPOISOMERASE (DNA) II BETA [MUS MUSCULUS] | Q64511 | Nuclear |
| TUMOR NECROSIS FACTOR TYPE 1 RECEPTOR ASSOCIATED PROTEIN [HOMO SAPIENS] | AAF15314.1 | Nuclear |
| UBIQUITOUS NUCLEAR PROTEIN [MUS MUSCULUS] | P35123 | Nuclear |
| ZINC FINGER PROTEIN 162 [MUS MUSCULUS] | CAA73359.1 | Nuclear |
| CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR 100k CHAIN - BOVINE | Q10568 | Transcription/Translation |
| DEAD (ASPARTATE-GLUTAMATE-ALANINE-ASPARTATE) BOX POLYPEPTIDE 6; D-E-A-D (ASPARTATE-GLUTAMATE-ALANINE-ASPARTATE) BOX POLYPEPTIDE 6 [MUS MUSCULUS] | P54823 | Transcription/Translation |
| DEAD/H (ASP-GLU-ALA-ASP/HIS) BOX POLYPEPTIDE 15 [HOMO SAPIENS] | BAA23987.1 | Transcription/Translation |
| DEAD/H (ASP-GLU-ALA-ASP/HIS) BOX POLYPEPTIDE 17 (72kD) [HOMO SAPIENS] | Q92841 | Transcription/Translation |
| EUKARYOTIC TRANSLATION INITIATION FACTOR 3 SUBUNIT 10 (EIF-3 THETA) (EIF3 P167) (EIF3 P180) (EIF3 P185) (P162 PROTEIN) (CENTROSOMIN) | AAA90910.1 | Transcription/Translation |
| EUKARYOTIC TRANSLATION INITIATION FACTOR 3 SUBUNIT 5 (EIF-3 EPSILON) (EIF3 P47) | NP_003745.1 | Transcription/Translation |
| EUKARYOTIC TRANSLATION INITIATION FACTOR 3 SUBUNIT 6 (EIF-3 P48) (MAMMARY TUMOR-ASSOCIATED PROTEIN INT-6) (VIRAL INTEGRATION SITE PROTEIN INT-6) | NP_001559.1 | Transcription/Translation |
| FIVE SH3 DOMAINS [MUS MUSCULUS] | CAA07416.1 | Transcription/Translation |
| HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN L (HNRNP L) | NP_001524.1 | Transcription/Translation |
| HETEROGENEOUS RIBONUCLEAR PARTICLE PROTEIN A1 - HUMAN | NP_002127.1 | Transcription/Translation |
| INITIATION FACTOR 5A (EIF-5A) (EIF-4D) (REV BINDING FACTOR) | NP_001961.1 | Transcription/Translation |
| METHIONINE AMINOPEPTIDASE 2; INITIATION FACTOR 2-ASSOCIATED PROTEIN (P67) [MUS MUSCULUS] | O08663 | Transcription/Translation |
| MSL3-2 PROTEIN [HOMO SAPIENS] | Q15014 | Transcription/Translation |
| P68 RNA HELICASE [MUS MUSCULUS] | CAA63974 | Transcription/Translation |
| POLYADENYLATE BINDING PROTEIN II - HUMAN | CAA88401.1 | Transcription/Translation |
| POLYPYRIMIDINE TRACT-BINDING PROTEIN 1 - RAT | CAA43202.1 | Transcription/Translation |
| POLYPYRIMIDINE TRACT-BINDING PROTEIN 2 - RAT | CAA43203.1 | Transcription/Translation |
| REGULATOR OF NONSENSE TRANSCRIPTS 1 [HOMO SAPIENS] | AAC50771.1 | Transcription/Translation |
| REPTIN52 [HOMO SAPIENS] | CAB66677.1 | Transcription/Translation |

| | | |
|---|-------------|---------------------------|
| RNA BINDING MOTIF PROTEIN 5 [HOMO SAPIENS] | AAD04159.1 | Transcription/Translation |
| RNA HELICASE II/GU PROTEIN [HOMO SAPIENS] | AAF78930 | Transcription/Translation |
| RNASE L INHIBITOR - HUMAN | NP_002931.1 | Transcription/Translation |
| S1-1 PROTEIN [RATTUS NORVEGICUS] | BAA12144 | Transcription/Translation |
| SIMILAR TO HUMAN HSGCN1 U77700 (PID: G2282576); SIMILAR TO YEAST TRANSLATION ACTIVATOR GCN1 | AAC83183 | Transcription/Translation |
| TFII-I PROTEIN LONG FORM; P128 [MUS MUSCULUS] | AAC02990 | Transcription/Translation |
| TRANSCRIPTION FACTOR ARF6 CHAIN B - MOUSE | NP_032310 | Transcription/Translation |
| TRANSCRIPTIONAL INTERMEDIARY FACTOR 1, BETA [MUS MUSCULUS] | AAB17272.1 | Transcription/Translation |
| TRANSLATION ELONGATION FACTOR EEF-1 ALPHA CHAIN - RAT | P20001 | Transcription/Translation |
| TRANSLATION ELONGATION FACTOR EEF-2 - HUMAN | NP_001952.1 | Transcription/Translation |
| TRANSLATION ELONGATION FACTOR EF-G, MITOCHONDRIAL - RAT | Q07803 | Transcription/Translation |
| TRANSLATION INITIATION FACTOR EIF-4A2 HOMOLOG - HUMAN | P38919 | Transcription/Translation |
| TRANSLATION REPRESSOR NAT1 [HOMO SAPIENS] | AAC51166 | Transcription/Translation |
| 38KDA SPLICING FACTOR; SPF 38 [HOMO SAPIENS] | AAC64084 | Splicing |
| AB044414 [MUS MUSCULUS]/INVOLVED IN SPLICE SITE SELECTION IN ALTERNATIVE MRNA SPLICING | BAA96656.1 | Splicing |
| ALTERNATIVE SPLICING FACTOR ASF-1 - HUMAN | NP_008855.1 | Splicing |
| APURINIC/APYRIMIDINIC ENDONUCLEASE [MUS MUSCULUS] | BAA07270.1 | Splicing |
| BA353C18.3.1 (NOVEL PROTEIN SIMILAR TO A SPLICING FACTOR (CC1.4) [HOMO SAPIENS]/SR FAMILY OF ALTERNATIVE SPLICING FACTORS | AAA16347.1 | Splicing |
| CLEAVAGE STIMULATION FACTOR SUBUNIT 1 [HOMO SAPIENS] | Q05048 | Splicing |
| DKFZP566J153 PROTEIN [HOMO SAPIENS]/PRE-MRNA PROCESSING FACTOR 31 | CAB43677.1 | Splicing |
| DUF52/CGI-27 | AAD27736.1 | Splicing |
| HYPOTHETICAL PROTEIN DKFZP564H2171.1 - HUMAN (FRAGMENT)/RNA PROCESSING | CAB55989.1 | Splicing |
| NASCENT POLYPEPTIDE-ASSOCIATED COMPLEX ALPHA CHAIN - HUMAN | NP_005585.1 | Splicing |
| NEURONAL DIFFERENTIATION-RELATED GENE [RATTUS NORVEGICUS] | NP_647549 | Splicing |
| POLY (RC)-BINDING PROTEIN 1 [MUS MUSCULUS] | AAD51921.1 | Splicing |
| POLYADENYLATE-BINDING PROTEIN 1 [BOS TAURUS] | CAB96752 | Splicing |
| POLYPYRIMIDINE TRACT-BINDING PROTEIN - MOUSE | AAH10255 | Splicing |
| PTB-ASSOCIATED SPLICING FACTOR [MUS MUSCULUS] | AAK60397 | Splicing |
| SM-D RIBONUCLEOPROTEIN AUTOANTIGEN - HUMAN | NP_008869.1 | Splicing |
| SPLICEOSOMAL PROTEIN SAP 130 [HOMO SAPIENS] | CAB56791 | Splicing |
| SPLICEOSOMAL PROTEIN SAP155 [RATTUS NORVEGICUS] | AAG01404 | Splicing |
| SPLICING FACTOR 3A, SUBUNIT 1, 120kD [HOMO SAPIENS] | NP_005868.1 | Splicing |
| SPLICING FACTOR PRP8 [HOMO SAPIENS] | AAC61776 | Splicing |
| SPLICING FACTOR, ARGININE/SERINE-RICH 7 (SPLICING FACTOR 9G8) | AAA88098.1 | Splicing |
| SPLICING FACTOR, ARNINE/SERINE-RICH 3 (SRP20) [MUS MUSCULUS] | CAA62844.1 | Splicing |
| TRANSCRIPTION FACTOR BTF3A - HUMAN | JC1235 | Splicing |
| U1 SMALL RIBONUCLEOPROTEIN 1SNRP HOMOLOG; MATCH TO PID: G4050087 [HOMO SAPIENS] | AAF19255 | Splicing |
| U2 SMALL NUCLEAR RIBONUCLEOPROTEIN AUXILIARY FACTOR (65KD) [HOMO SAPIENS] | CAA45409.1 | Splicing |
| U2 SNRNP PROTEIN A' - HUMAN | CAA31838.1 | Splicing |
| U5 SNRNP-SPECIFIC 200KD PROTEIN [HOMO SAPIENS] | CAA94089 | Splicing |
| U5 SNRNP-SPECIFIC 40 kDa PROTEIN (HPRP8-BINDING) [HOMO SAPIENS] | AAC69625.1 | Splicing |
| U5 SNRNP-SPECIFIC PROTEIN (220 kD), ORTHOLOG OF S. CEREVISIAE PRP8P [HOMO SAPIENS] | BAA22563.1 | Splicing |

| | | |
|---|-------------|---------------|
| U5 SNRNP-SPECIFIC PROTEIN, 116 KD [HOMO SAPIENS] | BAA04699.1 | Splicing |
| 47-KDA HEAT SHOCK PROTEIN [MUS MUSCULUS] | CAB7542 | Heat Shock |
| CHAIN A, E175S MUTANT OF BOVINE 70 KILODALTON HEAT SHOCK PROTEIN | 1QOQ_A | Heat Shock |
| CHAPERONE PROTEIN HSP90 BETA [HOMO SAPIENS] | AF275719_1 | Heat Shock |
| CHAPERONIN CONTAINING TCP1, SUBUNIT 4 (DELTA) [HOMO SAPIENS] | AAC50384.1 | Heat Shock |
| CHAPERONIN GROEL PRECURSOR - MOUSE | CAA38762.1 | Heat Shock |
| CHAPERONIN SUBUNIT 2 (BETA) [MUS MUSCULUS] | CAA83428.1 | Heat Shock |
| CHAPERONIN SUBUNIT 4 (DELTA) [MUS MUSCULUS] | BAA81875.1 | Heat Shock |
| CHAPERONIN SUBUNIT 5 (EPSILON) [MUS MUSCULUS] | BAA81876.1 | Heat Shock |
| CHAPERONIN SUBUNIT 6A (ZETA) [MUS MUSCULUS] | BAA81876.1 | Heat Shock |
| CHAPERONIN SUBUNIT 6B (ZETA) [MUS MUSCULUS] | CAA90574.1 | Heat Shock |
| CHAPERONIN SUBUNIT 8 (THETA) [MUS MUSCULUS] | CAA85521.1 | Heat Shock |
| DNAJ HOMOLOG 2 [RATTUS NORVEGICUS] | AAB64094.1 | Heat Shock |
| DNAK-TYPE MOLECULAR CHAPERONE HSPA5 PRECURSOR - HUMAN | AAA52614.1 | Heat Shock |
| DNAK-TYPE MOLECULAR CHAPERONE HSPA6 - HUMAN | CAA36061.1 | Heat Shock |
| FK506 BINDING PROTEIN 4 (59 kDa) [MUS MUSCULUS] | CAA50231.1 | Heat Shock |
| HEAT SHOCK COGNATE 71 kDa PROTEIN | AAA41354.1 | Heat Shock |
| HEAT SHOCK PROTEIN 20-LIKE PROTEIN [MUS MUSCULUS] | AAF65563.1 | Heat Shock |
| HEAT SHOCK PROTEIN 47 PRECURSOR - RAT | AAA41270.1 | Heat Shock |
| HEAT SHOCK PROTEIN HSP 90-ALPHA (HSP 86) | CAA33259.1 | Heat Shock |
| HEAT SHOCK PROTEIN HSP 90-BETA (HSP 84) (HSP 90) | NP_031381.1 | Heat Shock |
| HEAT SHOCK PROTEIN HSP27 | AAA41353.1 | Heat Shock |
| HEAT SHOCK PROTEIN, 105 kDa; HSP105 42 C-HSP [MUS MUSCULUS] | AAA99485.1 | Heat Shock |
| HEAT SHOCK PROTEIN, 84 kDa 1 [MUS MUSCULUS] | AAA37865.1 | Heat Shock |
| HEAT SHOCK PROTEIN, 86 kDa 1 [MUS MUSCULUS] | AAA53068.1 | Heat Shock |
| HEAT-SHOCK COGNATE 70kD PROTEIN (44KD ATPASE N-TERMINAL FRAGMENT) (E.C.3.6.1.3) | 1NGJ | Heat Shock |
| HEPATOCELLULAR CARCINOMA-ASSOCIATED ANTIGEN 57 [HOMO SAPIENS] | AF244136_1 | Heat Shock |
| HIRA INTERACTING PROTEIN 4 (DNAJ-LIKE) [HOMO SAPIENS] | CAA04669.1 | Heat Shock |
| HSC70-INTERACTING PROTEIN (PROGESTERONE RECEPTOR-ASSOCIATED P48 PROTEIN) (PUTATIVE TUMOR SUPPRESSOR ST13) | CAB10844.1 | Heat Shock |
| HSP60 PROTEIN (AA 1-547) [RATTUS NORVEGICUS] | A32800 | Heat Shock |
| HYPOTHETICAL PROTEIN FLJ10737 [HOMO SAPIENS] | BAA91780.1 | Heat Shock |
| ISCHEMIA RESPONSIVE 94 kDa PROTEIN [RATTUS NORVEGICUS] | AAC27937.1 | Heat Shock |
| P59 PROTEIN (HSP BINDING IMMUNOPHILIN) (HBI) (POSSIBLE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE) (PPIASE) (ROTAMASE) | NP_002005.1 | Heat Shock |
| PRE-MTHSP70 [RATTUS SP.] | AAB33049.1 | Heat Shock |
| STIP1 HOMOLOGY AND U-BOX CONTAINING PROTEIN 1; CARBOXY TERMINUS OF HSP70-INTERACTING PROTEIN [MUS MUSCULUS] | AAD33401.1 | Heat Shock |
| T-COMPLEX PROTEIN 1, ALPHA SUBUNIT (TCP-1-ALPHA) (CCT-ALPHA) | P17987 | Heat Shock |
| TCP1 RING COMPLEX PROTEIN TRIC5 - HUMAN | NP_005989.1 | Heat Shock |
| ALPHA-1-ANTITRYPSIN PRECURSOR - BOVINE | CAA44840.1 | Contamination |
| ALPHA-2-HS-GLYCOPROTEIN PRECURSOR (FETUIN) | CAA34596.1 | Contamination |
| CHAIN A, BOVINE TRYPSIN COMPLEXED WITH RPR128515 | BAA07516.1 | Contamination |

| | | |
|---|-------------|---------------|
| CHAIN D, PLATELET FACTOR 4 | 1PLF | Contamination |
| CHAIN E, BOVINE TRYPSIN (E.C.3.4.21.4) COMPLEX WITH A MODIFIED SSI (STREPTOMYCES SUBTILISIN INHIBITOR) WITH MET 70 REPLACED BY GLY AND MET 73 REPLACED BY LYS (SSI (M70G, M73K))" | 3BTW_E | Contamination |
| CHAIN P, CRYSTAL STRUCTURE OF THE THROMBIN-THROMBOMODULIN COMPLEX | 1DX5 | Contamination |
| CHAIN S, THE CRYSTAL STRUCTURE OF MODIFIED BOVINE FIBRINOGEN (AT ~4 ANGSTROM RESOLUTION) | NP_476787 | Contamination |
| COAGULATION FACTOR V PRECURSOR - BOVINE | AAA30512.1 | Contamination |
| HEMOGLOBIN ALPHA CHAIN | 1HDA | Contamination |
| HEMOGLOBIN ALPHA CHAIN [BOS TAURUS] | P01966 | Contamination |
| HEMOGLOBIN BETA CHAIN - BOVINE | P02070 | Contamination |
| KERATIN, TYPE II CYTOSKELETAL 1 (CYTOKERATIN 1) (K1) (CK 1) (67 kDa CYTOKERATIN) (HAIR ALPHA PROTEIN) | NP_006112.1 | Contamination |
| MODIFIED BETA TRYPSIN (MONOISOPROPYLPHOSPHORYL INHIBITED) (E.C.3.4.21.4) (NEUTRON DATA) | 1NTP | Contamination |
| PLASMIN (EC 3.4.21.7) PRECURSOR - BOVINE | CAA55939.1 | Contamination |
| SERUM ALBUMIN PRECURSOR - BOVINE | P02769 | Contamination |
| THYMOPOIETINS BETA AND GAMMA (TP BETA AND TP GAMMA) | AAB60330.1 | Contamination |