

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. discoideum*, *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 Improvion 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 <u>STE</u> 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 6677699 ref NP_033067.1	Actin Associated	C01G8.5/F42A10.2	I	<i>erm-1, nfm-1</i>	UNC	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	
		FLOTILIN 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 6677699 ref NP_033067.1	Actin Associated	C01G8.5/F42A10.2	I	<i>erm-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_RAT	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 <u>STE⁵</u>	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 <u>STE¹</u>	1.80E-189	
		PP6C	gi 2499733 sp Q64620 PPP6_RAT	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 <u>UNC²</u>	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</i>	UNC	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 <u>EMB¹</u>	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 ACETYLDHYDROLASE IB ALPHA SUBUNIT (PAFACETYLDHYDROLASE45KDASUBUNIT)(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 HMGB-BOX DOMAIN B OF RAT HMGI) (NMR, 30 STRUCTURES)	1HME	Nuclear
HIGH MOBILITY GROUP PROTEIN HMGI (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 HOMOLOG 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