

Table S16

322 Maternal genes that are rapidly degraded

Gene ID mixed annotation (+ indicates sequence confirmation)

CG18543+ unknown * CG18543 LD47919 66C12-66C12 ID:107B1
 + unknown * 1e-07 ADPR_MOUSE ADIPOSE DIFFERENTIATION-RELATED PROTEIN (ADPR) * * [ATP_GTP_A] CG9057 13A11-
 CG9057 13A11 dup:2/2 ID:46D11
 + 26/29kD-proteinase * 26,29kDa proteinase(aa) * 8e-61 cysteine proteinase cysteine * 1e-56 predicted using Genefinder; similar to
 CG8947 cathepsin-like protease; cD * 2e-61 cath [THIOL_PROTEASE_CYS // PAPAIN // Peptida] CG8947 70C9-70C9 dup:1/2 ID:61C5
 + enzyme * 3-phosphoglycerate dehydrogenase(aa) * similar to D-3-Phosphoglycerate dehydrogenase; cDNA EST comes from this
 CG6287 gene; cDNA EST comes from this gene; [2-Hacid_DH // D_2_HYDROXYACID_DH_1 // A] CG6287 GH03305 32D5-32D5 ID:31H4
 CG8180 + unknown * 1E-178* * [ANTIFREEZEI] CG8180 LD38554 52A4-52A4 dup:1/2 ID:97G8
 + unknown * 5e-20 YNZ5_YEAST HYPOTHETICAL 17.1 KD PROTEIN IN SIP3-MRPL30 INTERGENIC REGION * 3e-12 RNA
 CG3800 helicase * 2e-25 cellular nucleic acid binding protein cl [ZF_CCHC // zf-CCHC] CG3800 LD48005 59B6-59B6 ID:107C1
 + electron_transfer * 3e-17 cytochrome b5 * 1e-18 Similarity to Human cytochrome b5 (SW:CYB5_HUMAN); cDNA EST EMBL:D * 5e-
 18 CYB5_MOUSE CYTOCHROME B5 * 7e-22 cytochrome b [CYTOCHROME_B5 // CYTOCHROME_B5_2 // NLS_] CG3566 GH05526
 CG3566 5E1-5E1 ID:33F10
 + enzyme * similar to aspartate aminotransferase(aa) * 1e-99 aspartate aminotransferase cerevisiae, Peptide Partial, * 1e-157 similar
 CG4233 to aspartate aminotransferase [aminotran_1 // AA_TRANSFER_CLASS_1 // T] CG4233 GH20337 22B8-22B8 dup:2/2 ID:72F2
 + yin transporter * opt1 long(aa) * 8e-17 PTR2_YEAST PEPTIDE TRANSPORTER PTR2 (PEPTIDE PERMEASE PTR2) * 8e-74 high-
 CG2913 affinity peptide transporter * 2e-06 cAMP inducible p [PTR2 // PTR2_1 // PTR2_2] CG2913 GH27264 4A1-4A1 dup:2/2 ID:81B12
 + BEAF-32 DNA_binding * boundary element-associated factor, 32k - fruit fly (Drosophila melanogaster)(aa) * 1e-146 DMBEAF32A_2
 CG10159 BEAF-32 * boundary element associated factor [NLS_BP] CG10159 GH10592 51C3-51C3 ID:38B2
 + motor_protein * receptor-associated protein(aa) * 9e-14 predicted using Genefinder; Similarity to Human alpha-2-macroglobulin * 2e-
 CG8507 16 heparin binding protein * 5e-18 CG8507 GH16343 86D1-86D1 dup:3/3 ID:68E5
 + enzyme * 3e-40 4-nitrophenylphosphatase (EC 3.1.3.41) - yeast (Saccharomyces cerevisiae) * 6e-26 by content; 1-meth * 4e-52
 CG5567 contains similarity to 4-nitrophenylphosphatase CG5567 GH06744 75A4-75A4 ID:34G7
 + enzyme * 1e-98 PERO_DROME PEROXIDASE PRECURSOR myeloperoxidase (EC 1.11. * 6e-87 similar to eosinophil peroxidase
 CG7660 and myeloperoxidase * 2e-65 PERT_MOUSE THY [ANPEROXIDASE // PEROXIDASE_3] CG7660 LD43174 90C-90C ID:102B3
 + exu RNA_binding * Exuperantia (exu) protein - fruit fly (Drosophila melanogaster)(aa) * exu * 1e-158 exuperantia protein - fruit fly
 CG8994 (Drosophila virilis) * exu [LECTIN_LEGUME_BETA] CG8994 LD26657 57B2-57B2 ID:85G4
 + unknown * 1E-178* 1e-105 inserted at base Both 5' and 3' ends of P element Inverse PCR * CG6770 GH05738 33B12-33B12
 CG6770 ID:33H4
 CG17469+ unknown * 1E-123* * CG17469 LD45277 102E2-102E3 dup:2/2 ID:104B4
 + electron_transfer * thioredoxin(aa) * 8e-20 TRX1_YEAST THIOREDOXIN I (TR-I) thioredoxin I - yeast (Sacc * 1e-17 THIO_DROME
 CG3864 THIOREDOXIN (DEADHEAD PROTEIN) thioredoxin-I [THIOREDOXIN // THIOREDOXIN_2 // thioired] CG3864 30C-30C2 ID:115A11
 CG6319 + aret RNA_binding * aret * 8e-06 polyadenylate-binding protein * 1e-148 testis-specific RNP-type RNA binding protein * 2e-29 elav-type

ribonucleoprotein coded [RBD // HUDSXL RNA // rrm] CG6319 33D-33D4 dup:3/3 ID:44D5
 + motor_protein * 7e-09 by content; 1-meth * 2e-07 homeotic most like HMPB_DROME: homeotic proboscipedia protein * 9e-07
 CG8677 Williams-Beuren syndrome deletion transcript [PHD // NLS_BP // ATP_GTP_A] CG8677 LD34730 39C1-39C1 dup:5/5 ID:49E10
 + BG:DS00180.8 cell_adhesion * DMTENA_3 Ten-a * DMC901PRT C901 * DMDelta_4 DI * 3e-20 C901 protein [EGF_2] CG16882
 CG16882 GH07717 34E1-34E1 dup:3/4 ID:59H10
 + ligand_binding_or_carrier * DMC30B8 * retinaldehyde-binding protein 1(aa) * tocopherol (alpha) transfer protein (ataxia (Friedreich-
 CG10237 like) with vitamin E deficiency)(aa) * 62D[CRETINALDHBP // CRAL_TRIO] CG10237 GH08711 37E3-37E3 dup:2/3 ID:60H5
 + receptor * protein kinase C substrate 80K-H(aa) * similar to Human protein kinase C substrate, 80KD protein, heavy chain, SWISS-
 CG6453 PROT Accession Number * similar [LDLRA_2 // ER_TARGET // EF_HAND] CG6453 LD46533 36C4-36C4 ID:105D11
 + fu12 enzyme * 1-ACYL-SN-GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE(aa) * PUTATIVE 1-ACYL-SN-GLYCEROL-3-
 PHOSPHATE ACYLTRANSFERASE T06E8.1 (1-AGP ACYLTRANSFERASE) (1-AG [GLYCEROL_ACYLTRANS] CG17608 GH26888
 CG17608 29C4-29C4 ID:80F12
 + Nacalphaunknown * 4e-13 EGD2_YEAST EGD2 PROTEIN EGD2 protein - yeast (Saccharomyc * 5e-73 alpha NAC * 1e-34 alpha
 CG8759 NAC/1.9.2. protein alpha-NAC, non-musc * 1e-34 Nasce CG8759 GH11940 49C2-49C2 dup:2/2 ID:63H12
 + Thiolaseenzyme * Thiolase * thiolase(aa) * 3e-37 THIL_YEAST ACETYL-COA ACETYLTRANSFERASE (ACETOACETYL-COA
 CG4581 THIOLASE) * 1e-140 YKA3_CAEEL HYPOTHETICAL 47.9 KD PROTEIN [thiolase] CG4581 GH13256 60A6-60A6 dup:2/2 ID:40E2
 + unknown * 5e-40 prediabetic NOD sera-reactive autoantigen muscul * 5e-10 IVR-like protein * IVR-like protein * [TPR_REGION //
 CG14444 TPR_REPEAT] CG14444 LD39177 6C1-6C1 dup:3/3 ID:98D4
 + Uch endopeptidase * DMUBICTHG_3 Uch * 3e-19 UBL1_YEAST UBIQUITIN CARBOXYL-TERMINAL HYDROLASE YUH1
 (UBIQUITIN THIOLESTERASE) * 1e-130 UBL_DROME UBIQUITIN CARBOXYL-TERMIN [UCH // UCH_1 // UBCTHYDLASE] CG4265
 CG4265 GH02396 23D1-23D1 dup:1/2 ID:31B8
 + Pglym78 enzyme * phosphoglyceromutase - fruit fly (Drosophila melanogaster)(aa) * DMPGLY_4 Pglym78 * 7e-48 pdb|4PGM|A Chain A,
 CG1721 Saccharomyces Cerevisiae Phosphoglycer [PGAM // PG_MUTASE] CG1721 GH13304 99A1-99A1 dup:2/2 ID:40E5
 + receptor * 5e-14 cDNA EST comes from this gene; cDNA EST co * 3e-35 peripheral-type benzodiazepine receptor isoquinoline-
 CG2789 binding protein - mouse * 1e-35 benzod CG2789 GH02075 21C6-21C6 dup:2/2 ID:30H12
 CG12024 + signal_transduction * 5e-25 BAW protein * * [NLS_BP] CG12024 GH08896 62E3-62E3 dup:1/2 ID:61B6
 + qua actin_binding * qua * QUAI_DROME VILLIN-LIKE PROTEIN QUAIL villin homolog qua * 9e-18 similar to gelsolin; cDNA EST
 CG6433 comes from this gene * 3e-71 putative actin-bin [GELS // GELSOLIN] CG6433 LD42165 36C4-36C4 ID:101C8
 CG5194 + unknown * CG5194 LD39537 66F1-66F1 ID:98F8
 CG5904 + islet mitochondrial antigen CG5904 LP03542 ID:108F8
 + enzyme * 3-KETOACYL-COA THIOLASE MITOCHONDRIAL (BETA-KETOTHIOLASE) (ACETYL-COA ACYLTRANSFERASE)
 (MITOCHONDRIAL 3-OXOACYL-COA THIOLASE)(aa) * 8e-54 pdb|1AFW|A [thiolase // THIOLASE_1 // THIOLASE_2 //] CG4600 LD40538
 CG4600 33A1-33A1 dup:1/2 ID:99F6
 + chaperone * FK506-binding protein FKBP51(aa) * 6e-20 FKBP_YEAST FK506-BINDING PROTEIN (FKBP) (PEPTIDYL-PROLYL
 CIS-TRANS ISOMERASE) (P * 6e-24 FKB2_DROME KD FK50 [TPR_REGION // FKBP // FKBP_PPIASE_1 //] CG4535 LD47530 30E1-
 CG4535 30E1 dup:2/2 ID:106E9
 CG4466 + Hsp27 chaperone * DMHSP27G_3 Hsp27 * 1e-118 HS27_DROME HEAT SHOCK PROTEIN heat shock protein - f * 3e-13 Contains

similarity to Pfam domain: (HSP20), Score=130.7, * 2 [TONB_DEPENDENT_REC_1 // HSP20 // ACRYST] CG4466 GM13686 67B2-67B2 ID:83A12

+ structural_protein * Similarity to Yeast YIP1 protein cDNA EST comes from this gene; cDNA EST comes from this gene; cDNA EST

CG3652 comes from this gene; cDNA EST comes from t CG3652 GH04132 24F1-24F1 dup:2/3 ID:56F4

+ enzyme * 1e-19 FAT2_YEAST PEROXISOMAL-COENZYME A SYNTHETASE probable AMP * 3e-11 acetyl-CoA synthetase - fruit

CG5568 fly (*Drosophila melanogaster*) * 9e-40 similar [AMP-binding] CG5568 LD47944 64F3-64F3 ID:107B6

+ tumor_suppressor * 3e-09 /match=(desc;; /ma * 3e-16 predicted using Genefinder; Similarity to Human leukocyte surface * 4e-26

CG4999 CD82_MOUSE CD82 ANTIGEN (INDUCIBLE MEMBRA [transmembrane4 // TMFOUR // TM4_2] CG4999 GH11168 66E3-66E3 ID:38F10

+ ligand_binding_or_carrier * FGF intracellular binding protein(aa) * FGF-1 intracellular binding protein * CG8660 GH16593 76D3-76D3 ID:68G7

CG8660 76D3 ID:68G7

CG10254+ enzyme CG10254 SD05555 dup:4/4 ID:119A2.2

+ chaperone * KD HEAT SHOCK PROTEIN, MITOCHONDRIAL (HSP10) (10 KD CHAPERONIN)(aa) * 1e-17 CH10_YEAST KD HEAT SHOCK PROTEIN, MITOCHONDRIAL (HSP10) (10 KD CHAPERONI [LUM_BINDING // CHAPERONIN10 // cpn10] CG11267 GH05109

CG11267 69F2-69F2 ID:33D12

+ enzyme * ribulose-1,5-bisphosphate carboxylase/oxygenase N-methyltransferase(aa) * ribulose-1,5-bisphosphate

CG3042 carboxylase/oxygenase small subunit N-methyltra CG3042 LP01222 6E3-6E3 ID:107D9

CG12040+ unknown similar to GTPase-activating (rhoGAP) like protein CRAL_TRIO CG12040 GH28696 dup:2/2 ID:82F6

+ BcDNA:LD28120 transporter * similar to the monocarboxylate transporter family(aa) * Yol119cp(aa) * contains similarity to

CG8062 monocarboxylate transporters(aa) * MONOCARBOXYLATE TRA CG8062 LP01259 18C2-18C2 dup:3/5 ID:107D11

+ Pcd enzyme * Pcd * 5e-40 pterin-4a-carbinolamine dehydratase * 1e-24 similar to 4a-carbinolamine dehydratases * 4e-22 pterin-4-

CG1963 alpha-carbinolamine dehydratase (E [RIBOSOMAL_L23 // Pterin_4a] CG1963 GH23826 99C1-99C1 dup:1/2 ID:76H3

+ transporter * cationic amino acid transporter-1(aa) * solute carrier family (cationic amino acid transporter, y+ system), member 1(aa) *

CG11128 LOW-AFFINITY CATIONIC AMI [aa_permeases // AMINO_ACID_PERMEASE_2] CG11128 LD37241 79F5-79F6 dup:2/2 ID:96F8

+ unknown * 2e-16 YKJ2_CAEEL HYPOTHETICAL 36.9 KD PROTEIN C02D5.2 IN CHROMOSOME III * 1e-05 INIP_HUMAN

CG9796 GAMMA-INTERFERON-INDUCIBLE PROTEIN IP-30 PRECURSOR * 4e-1 CG9796 LD47508 87E10-87E10 dup:3/3 ID:106E4

+ motor_protein * dynein light chain-A(aa) * DYNEIN LIGHT INTERMEDIATE CHAIN 1, CYTOSOLIC (LIC57/59) (DYNEIN LIGHT

CG1938 CHAIN A) (DLC-A)(aa) * 1e-38 cDNA EST comes from th [ATP_GTP_A] CG1938 GH07739 10A10-10A10 dup:2/3 ID:60A3

+ enzyme * 1e-31 pdb|1SDY|A *Saccharomyces cerevisiae* *Saccharomyces cerevisiae* * 1e-34 SODC_DROME SUPEROXIDE

DISMUTASE (CU-ZN) superoxide dismuta * 5e-38 SODE_C [CUZNDISMUTASE // SOD_CU_ZN_1 // SOD_CU_Z] CG9027 47F6-47F7

CG9027 ID:76F8

CG12373+ CG12373 ID:109B8

+ defense/immunity_protein * cuticular molt protein precursor(aa) * 2e-29 peptidoglycan recognition protein precursor * 2e-31 TNF

CG8995 superfamily, member (LTB)-like (peptidoglycan r CG8995 GH01554 13F1-13F1 dup:2/2 ID:54E9

+ transporter * cystic fibrosis transmembrane conductance regulator(aa) * DMMDR49_2 Mdr49 * canalicular multispecific organic anion

CG7627 transporter (ABC superfamily)(a[ATP_GTP_A2 // ABC_TRANSPORTER // ABC_tr] CG7627 LD46040 29B2-29B2 dup:2/4 ID:104H4

+ CycJ cell_cycle_regulator * CycJ * 4e-11 CG22_YEAST G2/MITOTIC-SPECIFIC CYCLIN cyclin B2 - yeast * cyclin J * 3e-05 Similar to

CG10308 cyclin [cyclin // HELIX_LOOP_HELIX // NLS_BP] CG10308 GH04281 63D2-63D2 ID:56G5

CG4267

CG17822+ transcription_factor CG17822 GH20378 ID:72F5
+ transporter * sodium-dicarboxylate cotransporter SDCT1(aa) * 8e-08 YJT8_YEAST HYPOTHETICAL 97.7 KD MEMBRANE

CG4961 PROTEIN IN PRP21-UBP12 INTERGENIC REGIO * 4e-29 YKG6_C CG4961 GH25396 92C4-92C4 dup:2/2 ID:78F3

CG9537
+ enzyme * BLASTX 1.1E-34 Rattus sp. mRNA for hemC gene.(dna) * BLASTX 1.1E-34 Rattus sp. mRNA for hemC gene.(dna) * 7e-54 HEM3_YEAST PORPHOBILINOGEN DEAMINASE [PORPHBDMNASE // Porphobil_deam] CG9165 LD38107 61F7-61F7 dup:2/2

CG9165 ID:97D8
+ motor_protein * 6e-23 ARP5_YEAST ACTIN-LIKE PROTEIN ARP5 probable nuclear pro * 2e-12 ACTU_DROME ACTIN-LIKE

CG12321 PROTEIN 13E actin-related protein * 6e-11 similar to Act CG12321 LP02120 90E6-90E6 ID:107H11
+ swa RNA_binding * SWA_DROME SWALLOW PROTEIN gene swallow protein - fruit fl * DMSWAL_3 swa * * [NLS_BP] CG3429

CG3429 LD21771 5E6-5E7 dup:2/2 ID:83E6
+ unknown * 5e-08 No definition line found * 5e-16 PSD-95/SAP90-associated protein-2 * 1e-16 PSD-95 binding protein * 1e-171

CG8390 inserted at base Unknown 5' end of [NLS_BP] CG8390 LD44824 41E5-41E5 ID:103F11
+ fs(1)Ya cell_cycle_regulator * mitosis initiation protein fs(1)Ya - fruit fly (Drosophila melanogaster)(aa) * FSYA_DROME MITOSIS

CG2707 INITIATION PROTEIN FS(1)YA fs(1)Ya prote * DMFS1Y [ZINC_FINGER_C2H2] CG2707 LD40381 3B6-3B6 dup:2/2 ID:99E2

CG14764+ unknown * CG14764 LD39211 43F6-43F6 ID:98D5
+ glutathione_transferase * predicted using Genefinder; similar to Glutathione S-transferases.(aa) * 2e-11 YKJ3_CAEEL

CG6662 HYPOTHETICAL 42.8 KD PROTEIN C02D5.3 IN CHROMOSOME III * 7 [GST] CG6662 66D5-66D5 dup:2/2 ID:40H2

CG11844+ unknown CG11844 SD06613 dup:1/2 ID:120A6.2
+ transporter * Phosphate Permease(aa) * leukemia virus receptor - human(aa) * 3e-27 YB8I_YEAST PUTATIVE PHOSPHATE-

CG7628 REPRESSIBLE PHOSPHATE PERMEASE YBR29C * 9e-52 Sim [PHO4] CG7628 GH23727 70E3-68A5 ID:76F9

CG13850+ unknown * CG13850 GH07286 96E1-96E1 ID:35C4
+ unknown * CGI-101 protein(aa) * 2e-10 hypothetical protein YDR411c - yeast (Saccharomyces cerevisiae) (U * 5e-79 putative NADH

CG14899 oxidoreductase complex I subuni CG14899 GH09689 89C6-89C6 ID:37C3
+ DNA_binding * DNA helicase(aa) * HYPOTHETICAL 175.7 KD PROTEIN C05C10.2 IN CHROMOSOME II(aa) * DNA helicase A;

CG6967 Hcs1p(aa) * hypothetical helicase(aa) [ATP_GTP_A] CG6967 LD34829 53F5-53F6 ID:49F6
+ DNAPol-alpha50 DNA_replication_factor * DMDPRI_2 DNAPol- agr;50 * 8e-62 p48 DNA primase (AA 1-409) * PRI1_DROME DNA

CG7108 PRIMASE SMALL SUBUNIT (DNA PRIMASE KD SUBUNIT) (DNA POLYMERAS * 3e-64 N CG7108 LD46032 66C8-66C8 ID:104H2

CG9578 + CG9578 ID:83D8
+ * similar to Gila monster phospholipase A2; similar to * 2e-22 phospholipase A2 (EC 3.1.1.4) Pa5 - Gila monster phosp * 8e-89

CG1583 inserted at base Both 5' [PA2_HIS] CG1583 7D14-7D15 dup:2/2 ID:83B8
+ unknown * 2e-20 coded for by C. elegans cDNA yk173c12.5 * 3e-11 unknown protein * contains similarity to Physcomitrella patens

CG10509 glyceraldehyde 3-phosphate dehy CG10509 GH03649 57D3-57D4 dup:1/2 ID:56B3
+ enzyme * 2e-32 YPT6_YEAST GTP-BINDING PROTEIN YPT6 YPT6 protein - yeas * 2e-34 rab6 * 3e-53 similar to ras-related

CG17515 protein * 9e-34 RB17_MOUSE RAS-RELATED PRO [ALDEHYDE_DEHYDR_CYS // ras // ATP_GTP_A] CG17515 GH27649

cyto_unknown ID:81F2

+ chaperone * FK506-binding protein 6(aa) * FK506-binding protein - Arabidopsis thaliana(aa) * FKBP (FK506 binding protein) 13;

CG4735 peptidylprolyl cis-trans isomerase [FKBP // FKBP_PPIASE_3 // TPR_REPEAT] CG4735 LD24746 60A4-60A4 ID:43G6

+ Tpi enzyme * Chain A, Does The His12-Lys13 Pair Play A Role In The Adaptation Of Thermophilic Tims To High Temperatures ?(aa) *

CG2171 DMTPIG_2 Tpi * TRIOSEPHOSPHATE IS [TIM] CG2171 GH02005 99E-99E dup:1/3 ID:30H5

CG4790 + unknown * CG4790 LD27288 5C8-5C9 ID:86D8

+ enzyme * 7e-52 acyl-coenzyme A oxidase * 1e-120 similar to ACYL-COENZYME A OXIDASE, PEROXISOMAL (EC 1.3.3.6) (PALM

CG9707 * 1e-125 peroxisomal acyl-CoA oxidase * 1e CG9707 GH01226 57D11-57D11 dup:1/3 ID:54C1

CG8159 + transcription_factor CG8159 SD05592 ID:119A8

+ unknown * 5e-69 YG4W_YEAST HYPOTHETICAL 34.9 KD PROTEIN IN SMI1-PHO81 INTERGENIC REGION * 2e-29

CG15081 L2CC_DROME L(2)37CC PROTEIN Cc protein - fruit fly (Drosop * 3 [PROHIBITIN // Band_7] CG15081 LD46344 55F2-55F2 ID:105C4

+ Tim10 unknown * small zinc finger-like protein(aa) * small zinc finger-like protein(aa) * small zinc finger-like protein(aa) * 5e-10

CG9878 hypothetical protein YHR004c-a CG9878 LD46744 57F8-57F8 dup:2/2 ID:105F7

+ unknown * 5e-09 SHP1_YEAST SHP1 PROTEIN hypothetical protein YBL058w - ye * 1e-34 p47 * 2e-33 p47 XY40 * undulin -

CG11139 human (fragment) undulin CG11139 GH01724 43C4-43C5 dup:3/3 ID:30F6

+ CDC45L DNA_replication_factor * CDC45L * 2e-31 Cdc45p: assembles into a complex with Cdc46p/Mcm5p * CDC45L * 1e-30 predicted

CG3658 using Genefinder; cDNA EST yk307h3.3 comes from this ge CG3658 LD35753 1E1-1E1 ID:95D1

+ unknown * 4e-21 YS48_CAEEL HYPOTHETICAL 66.5 KD PROTEIN ZK177.8 IN CHROMOSOME II (U * 2e-20 MG11_MOUSE

CG9670 INTERFERON-GAMMA INDUCIBLE PROTEIN MG11 unkn * 4e-20 hy CG9670 LD25913 76A5-76A6 dup:3/3 ID:44B11

CG7143 + DNA_repair_protein CG7143 SD05329 dup:2/2 ID:118F3

+ RfC40 DNA_replication_factor * 3e-99 RFC4_YEAST ACTIVATOR KD SUBUNIT (REPLICATION FACTOR C KD SUBUNIT) *

AC14_DROME ACTIVATOR KD SUBUNIT (REPLICATION FACTOR C KD SUBUNIT) (A1 * 1 [ATP_GTP_A] CG14999 LD40483 64A10-

CG14999 64A10 dup:2/2 ID:99E11

CG1691 + RNA_binding CG1691 SD07045 dup:1/3 ID:120E7.2

+ enzyme * contains similarity to enoyl-CoA hydratases/isomerases Score=59.1, E=3.3e-16, N=1)(aa) * 3e-51 Similar to enoyl-coA

CG5844 hydratase * 2e-15 ECH1_MOUSE PRO [ECH] CG5844 LP03547 87B15-87B15 ID:108F9

CG8592 + stil unknown * 1e-171 STAND STILL (Y * 1e-173 stil * * [NLS_BP] CG8592 GH06596 49B2-49B2 ID:59A10

+ Sptr enzyme * sepiapterin reductase (7,8-dihydrobiopterin:NADP+ oxidoreductase)(aa) * ORF 7(aa) * similar to glucose 1-

CG12117 dehydrogenase(aa) * sepiapterin reductase; [GDHRDH // adh_short] CG12117 GH04031 7E7-7E7 ID:32D8

+ ribosomal_protein * ribosome recycling factor(aa) * RRF_HAEIN RIBOSOME RECYCLING FACTOR (RIBOSOME RELEASING

CG4447 FACTOR) (RRF) * RRF_CLOPE RIBOSOME RECYCLING FACTOR (RIBOS CG4447 GH21184 67B1-67B1 dup:2/2 ID:73E11

+ transcription_factor * crol * 1e-32 CROL ALPHA * 1e-17 final three exons similar to C2H2-type zinc finger * 1e-31 kruppel-type zinc

CG12397 finger protein [zf-C2H2 // ZINC_FINGER_C2H2 // ZINC_FIN] CG12397 GH01265 42B3-42B3 ID:30B9

+ unknown * cDNA EST comes from this gene; cDNA EST comes from this gene(aa) * huntingtin interacting protein HYPE(aa) * 9e-84

CG9523 cDNA EST comes from this gene; c [TPR_REGION // TPR_REPEAT] CG9523 LD47713 26D3-26D3 ID:106H2

CG6233 + enzyme * ubiquitin fusion degradation protein; Ufd1p(aa) * UBIQUITIN FUSION DEGRADATION PROTEIN HOMOLOG (UB

FUSION PROTEIN 1)(aa) * 2e-47 UFD1_YEAST UBIQUITIN CG6233 GH18603 70E3-70E3 ID:70G10

CG8861 + unknown * CG8861 GH27383 85D7-85D7 ID:81C12
+ * cDNA EST yk335d8.5 comes from this gene; cDNA EST yk335d8.3 comes from this gene(aa) * 2e-23 cDNA EST yk335d8.5

CG4972 comes from this gene; cDNA EST yk335 CG4972 31D7-31D8 dup:2/2 ID:67A10

CG9828 + chaperone DnaJ homolog 2 DNAJPROTEIN CG9828 LD27049 dup:2/2 ID:86B6
+ Cyp6u1 cytochrome_P450 * PUTATIVE CYTOCHROME P450 T10B9.7 IN CHROMOSOME II(aa) * similar to cytochrome P450(aa) *
DMCYP6A2A_5 Cyp6a2 * 3e-16 CP51_YEAST CYTOCHROME P450 (CYP [EP450II // p450 // P450 // MITP450 // C] CG3567 GH27663

CG3567 42D4-42D4 ID:81F6
+ Gdi signal_transduction * 1e-135 GDI1_YEAST SECRETORY PATHWAY GDP DISSOCIATION INHIBITOR G * GDP dissociation

CG4422 inhibitor - fruit fly (Drosophila melanogaster) * Guanine nucleo [RABGDIREP // RABGDI // GDI] CG4422 LD46767 30B8-30B9 ID:105F11

CG15893+ unknown * 1e-142 inserted at base Both 5' and 3' ends of P element Inverse PCR * * CG15893 LD32923 5E4-5E4 dup:2/2 ID:48E5
+ chaperone * similar to chaperonins cpn60 and TCP-1 (Pfam: cpn60_TCP1.hmm, score: 416.20 and 102.94)(aa) * Cytoplasmic
chaperonin subunit gamma; Cct3p(aa) * chap [TCP1_1 // TCP1_2 // TCP1_3 // TCOMPLEXT] CG7033 GH15038 8C13-8C13 dup:2/2

CG7033 ID:67B3
+ unknown * 7e-07 probable membrane protein YOL031c - yeast (Saccharomyces cerevisiae) * 1e-11 SLS1_YARLI SLS1 PROTEIN

CG10420 PRECURSOR Sls1 protein precursor * 7e-83 i CG10420 GH27496 96C3-96C3 dup:3/4 ID:81E3
+ cell_adhesion * 2e-09 SLIT_DROME SLIT PROTEIN PRECURSOR slit protein precursor * 2e-06 coded for by C. elegans cDNA

CG17667 yk133e1.5; coded for by C. elegans cDNA yk133d4.5 [LRR] CG17667 LD45603 69E1-69E2 dup:2/2 ID:104E3

CG18525+ unknown * CG18525 GH14439 88E7-88E7 dup:2/2 ID:41E4
+ protein_kinase * DMDFR2_2 btl * 3e-43 ABL_DROME TYROSINE-PROTEIN KINASE DASH/ABL protein-tyrosine * 7e-41 Tyrosine-
protein kinase ABL-1; cDNA EST comes from th[PROTEIN_KINASE_TYR // TYRKINASE // PROT] CG17309 GH10267 86E18-86E19

CG17309 dup:1/2 ID:37G1

CG9924 + actin_binding CG9924 LD28030 dup:2/2 ID:87B2
+ BG:DS01219.1 unknown * 1e-20 YKQ3_CAEEL HYPOTHETICAL 42.1 KD PROTEIN C06E1.3 IN CHROMOSOME III (L1 * * CG4482

CG4482 LD27791 35B9-35B9 ID:86H4
+ unknown * hormone-sensitive lipase testicular isoform(aa) * 1e-07 similar to the 'GDYG' family of lipolytic enzymes * 4e-83 hormone-
sensitive lipase * 2e-85 I [ESTERASE] CG11055 LD36294 56F15-56F15 ID:95H7

CG11055 + RNAS_binding homology with Drosophila dip1 (disco interacting protein) gene, a new member of the Staufen family of RNA binding
proteins CG17452 SD05690 ID:119C6

CG17452 + transmembrane_receptor * HYPOTHETICAL PROTEIN * cysteine-rich protein (intestinal)(aa) * 4e-09 MLP2_DROME MUSCLE LIM
PROTEIN MLP84B muscle L * 4e-18 gene product [LIM_DOMAIN_1 // LIM // LIM_DOMAIN_2 //] CG4656 LD45535 94E-94E dup:2/2

CG4656 ID:104D3
+ I(2)37Cc unknown * HYPOTHETICAL 31.8 KD PROTEIN IN CHROMOSOME II(aa) * DMCCR_5 I(2)37Cc * mitochondrial protein,

CG10691 prohibitin homolog; similar to S. cerevisiae Phb2p; Ph [PROHIBITIN // Band_7] CG10691 GH12454 37C1-37C1 ID:39G6
+ transporter * 2e-14 aquaporin * 5e-22 BIB_DROME NEUROGENIC PROTEIN BIG BRAIN bib protein - frui * 6e-22 similar to MIP

CG7777 transmembrane protein; cDNA EST yk459g7.3 c [MINTRINSICP // MIP] CG7777 LD27313 47F13-47F13 ID:86D9

+ glycerol_kinase * 1e-83 GLPK_YEAST GLYCEROL KINASE (ATP:GLYCEROL 3-PHOSPHOTRANSFERASE) (GLYCEROKINASE)
 (* 1e-116 similar to glycerol kinase * 1e-147 GLPK_MOUSE G[FGGY_KINASES_1 // FGGY_KINASES_2 // FGG] CG7995 GH18690 62B1-
 CG7995 62B1 dup:2/3 ID:70H9
 + peptidase * 1e-112 APE2_YEAST AMINOPEPTIDASE II (YSCII) aminopeptidase yscII * 1e-110 Similarity to Human aminopeptidase
 N (SW:AMPN_HUMAN); cDNA EST EMB * 1e-16 [ALADIPTASE // Peptidase_M1 // ZINC_PROT] CG8775 GH12821 87E6-87E6 dup:2/2
 CG8775 ID:40B8
 CG4449 + unknown * CG4449 LP06117 97B1-94E9 ID:109G2
 + unknown * 1e-25 kraken * 3e-13 dJ222E13.1 (N-terminal part of novel protein with some similarit * 7e-05 TPES_PSEPU
 CG5707 TROPINESTERASE (ATROPINESTERASE) (ATROPINE [ESTERASE // abhydrolase] CG5707 GH02816 62D2-62D2 dup:2/2 ID:31E3
 + Pi3K21B signal_transduction * p60(aa) * DMPK57 Pi3K21B * p60 p * 2e-08 similar to vav proto-oncogene [PI3KINASEP85 //
 CG2699 SH2DOMAIN // SH2] CG2699 LD42724 21B7-21B7 dup:2/2 ID:101F10
 + Eno enzyme * DMENOLAS_2 Eno * 1e-154 phosphopyruvate hydratase (EC 4.2.1.11) - yeast (Saccharomyces cerevisiae) >g *
 CG17654 ENO_DROME ENOLASE (2-PHOSPHOGLYCERATE DEHYD [ENOLASE // enolase] CG17654 GH01942 22F3-22F3 ID:55A2
 + transporter * MITOCHONDRIAL FAD CARRIER PROTEIN FLX1(aa) * UCP2(aa) * 5e-26 YIA6_YEAST PUTATIVE
 MITOCHONDRIAL CARRIER YIL006W probabl * 4e-09 ADT_DROME ADP,ATP CA [mito_carr] CG8026 GH22139 45B4-45B5 dup:2/2
 CG8026 ID:74E9

 CG13458+ unknown * 1E-160* * [COPPER_BLUE] CG13458 GH20023 71B2-71B2 ID:72B12
 CG18282+ unknown * CG18282 LD22270 5E1-5E1 ID:83F11
 + motor_protein * 8e-08 /motif=(desc: * 7e-11 contains similarity to a C3HC4-class zinc finger * 1e-20 mTRIP * 3e-20 hTRIP [zf-
 CG5140 C3HC4 // NLS_BP // ZF_RING] CG5140 GH03577 55B9-55B9 ID:56A7
 + enzyme * protein(aa) * 3e-07 FMS1_YEAST FMS1 PROTEIN FMS1 protein - yeast (Saccharom * 6e-12 Cs protein [ADXRDTASE //
 CG17149 NAD_BINDING] CG17149 LD45081 77A4-77A4 ID:103H4
 + Orc4 DNA_replication_factor * 56-kDa subunit of recognition complex (ORC); Orc4p(aa) * recognition complex subunit 4-related protein
 CG2917 Orp4p(aa) * recognition complex, subunit (yea [ATP_GTP_A2 // ATP_GTP_A] CG2917 LD43280 60D16-60D16 ID:102C1
 + chaperone * similar to chaperonins cpn60 and TCP-1 (Pfam: cpn60_TCP1.hmm, score: 416.20 and 102.94)(aa) * Component of
 CG8351 Chaperonin Containing T-complex subunit s [TCP1_2 // TCP1_3 // TCOMPLEXTCP1 // CHA] CG8351 LD47396 85E9-85E9 ID:106C10
 + enzyme * 5e-19 VIT1_DROME VITELLOGENIN I PRECURSOR (YOLK PROTEIN 1) vitell * 6e-23 pancreatic lipase related protein *
 CG17292 3e-25 pancreatic lipase-related protei [TAGLIPASE // ESTERASE // lipase] CG17292 GH01208 29B3-29B3 ID:54B11
 CG10373+ unknown * gene product(aa) * 6e-19 gene product * 2e-23 JWA protein * JM4 CG10373 GH05842 37A4-37A4 ID:58D2
 + La RNA_binding * LA PROTEIN HOMOLOG (LA RIBONUCLEOPROTEIN) (LA AUTOANTIGEN HOMOLOG)(aa) * La * LUPUS LA
 PROTEIN (SJOGREN SYNDROME TYPE B ANTIGEN (SS-B)) (LA RIBONUCL [RNP_1 // RBD // rrm // NLS_BP // LUPUSL] CG10922
 CG10922 LD24519 38C7-38C7 ID:84C12
 CG11169+ unknown * CG11169 LP04006 60A1-60A2 ID:108H6
 + chaperone * 1e-13 gene product * 1e-09 disulfide-like protein prote * [THIOREDOXIN_2] CG11790 GH08893 96B15-96B15 dup:1/2
 CG11790 ID:61B4

CG14971+ unknown Homo sapiens CGI-15 protein CG14971 SD04505 ID:117D9

CG13853+ unknown * CG13853 GH02671 96E1-96E1 ID:31D6

+ receptor * glutaminyl cyclase(aa) * 3e-32 YFI8_YEAST HYPOTHETICAL 41.0 KD PROTEIN IN UGS1-FAB1 INTERGENIC REGION

CG10487* 3e-62 similar to guanylate cyclase; cDNA EST CG10487 GH11174 64F4-64F4 ID:38F11

+ transporter * 8e-72 contains similarity to xanthine/uracil permeases family elegans * 1e-136 yolk sac permease-like molecule * 1e-136

CG6293 sodium-dependent vitamin C tr [xan_ur_permease // XANTH_URACIL_PERMASE] CG6293 LD30822 86A2-86A2 ID:47C11

+ transcription_factor_binding * WD-repeat protein(aa) * 3e-05 YGA3_YEAST HYPOTHETICAL 62.8 KD TRP-ASP REPEATS

CONTAINING PROTEIN IN PMC1-TFG2 * 1e-07 Method: conceptual translation [WD40_REGION // WD40] CG11330 LD43270 26F5-26F6

CG11330 ID:102B11

+ chaperone * t-complex polypeptide 20(aa) * 1e-142 TCPZ_YEAST T-COMPLEX PROTEIN 1, ZETA SUBUNIT (TCP-1-ZETA) (CCT-ZETA) * 7e-46 CCT-gamma protein * 1e-178 TCPZ_ [TCP1_1 // TCP1_2 // TCP1_3 // TCOMPLEXT] CG8231 GH13725 13E17-13E17

CG8231 ID:40G12

CG5721 + pioneer protein CG5721 SD05591 ID:119A7

+ enzyme * carnitine racemase - Escherichia coli(aa) * ENOYL-COA HYDRATASE, MITOCHONDRIAL PRECURSOR (SHORT CHAIN ENOYL-COA HYDRATASE) (SCEH) (ENOYL-COA HYDRATA [GRAM_POS_ANCHORING // ECH] CG6984 GH22096 53F10-53F10

CG6984 dup:2/2 ID:74E5

+ unknown * GLUTAMATE--CYSTEINE LIGASE REGULATORY SUBUNIT (GAMMA-GLUTAMYL-CYSTEINE SYNTHETASE)

CG4919 (GAMMA-ECS) (GCS LIGHT CHAIN)(aa) * glutamate-cysteine ligase regu CG4919 GH03051 94C3-94C3 ID:31G2

+ Khc motor_protein * DMKINHCA_2 Khc * cos * KINESIN HEAVY CHAIN(aa) * recombinant kinesin heavy chain(aa) [kinesin //

CG7765 KINESIN_MOTOR_DOMAIN1 // KIN] CG7765 SD02406 53A-53A dup:1/2 ID:114A9

+ cytoskeletal_structural_protein * 8e-19 protein * sorting nexin * Y254_HUMAN HYPOTHETICAL PROTEIN KIA * [BEM_DOMAIN //

CG1514 GRK] CG1514 GH16154 7C8-7C8 ID:68C11

+ enzyme * G4 nucleic acid binding protein, involved in tRNA aminoacylation; Arc1p(aa) * PROBABLE METHIONYL-TRNA

CG8235 SYNTHETASE (METHIONINE--TRNA LIGASE) (METRS)(a CG8235 GH27932 44F9-44F9 ID:82A6

+ signal_transduction * (putative) small GTPase, similar to Gtr1; Gtr2p(aa) * yeast gtr2 homolog, novel small GTPase subfamily

CG8707 protein(aa) * homologous to the yeast YGR163 [CRYSTALLIN_BETAGAMMA // ATP_GTP_A] CG8707 GH16429 44B-44B ID:68F3

+ Rpt5 endopeptidase * contains similarity to the AAA family of ATPases (Pfam; AAA, score; 259.07); most similar to human probable

CG10370 26S protease subunit TBP-1 * putative [AAA // MITOCH_CARRIER // ATP_GTP_A] CG10370 GH12068 95B7-95B7 ID:39D12

CG17018+ unknown CG17018 LD26456 dup:1/2 ID:85F2

+ T-cp1 chaperone * DMTCP1_2 T-cp1 * T-COMPLEX PROTEIN 1, ALPHA SUBUNIT (TCP-1-ALPHA) (CCT-ALPHA)(aa) * 1e-178 T

complex protein (put.); putative * similar to T-complex [TCP1_1 // TCP1_2 // TCP1_3 // TCOMPLEXT] CG5374 GH10347 94B4-94B4

CG5374 ID:37H1

CG6407 + signal_transduction CG6407 dup:3/3 ID:87H5

+ enzyme * NADH:ubiquinone dehydrogenase kDa subunit(aa) * similar to NADH-ubiquinone oxidoreductase; cDNA EST comes from

CG9140 this gene; cDNA EST comes from this [COMPLEX1_51K_1 // COMPLEX1_51K_2] CG9140 GM14163 26B3-26B3 ID:83B12

+ unknown * 8e-15 YKK3_CAEEL HYPOTHETICAL 64.3 KD GTP-BINDING PROTEIN C02F5.3 IN CHROMOSOME III >g *

CG10795 YJ05_CAEEL HYPOTHETICAL 85.1 KD NUCLEASE C41D11.5 simila * CG10795 LD27358 57D11-57D11 dup:2/2 ID:86E3

+ Prosalpha1 unknown * endopeptidase multicatalytic endopeptidase) cell 26S proteasome) map_position:54B3-5 * 20S proteasome
 CG18495 subunit alpha1(aa) * endopeptidase multicatalytic CG18495 SD02332 43F-43F dup:2/2 ID:114A1
 CG17678+ CG17678 dup:2/2 ID:89B3
 + UbcD4 enzyme * 3e-33 UBC1_YEAST UBIQUITIN-CONJUGATING ENZYME E2-24 KD (UBIQUITIN-PROTEIN LIGASE) (UBI * 1e-107
 ubiquitin conjugating enzyme * 7e-54 contains simila [UBA // UBIQUITIN_CONJUGAT // UQ_con //] CG8284 LD27480 67B12-67B12
 CG8284 dup:2/2 ID:86E11
 CG17260+ nucleic_acid_binding * [ZF_RING] CG17260 LD44813 23C5-23C5 ID:103F8
 CG6311 + unknown * CG6311 LD37618 74D2-74D2 dup:1/2 ID:96H12
 + peptidase * insulin-regulated membrane aminopeptidase IRAP(aa) * LEUKOTRIENE A-4 HYDROLASE (LTA-4 HYDROLASE)
 (LEUKOTRIENE A(4) HYDROLASE)(aa) * LEUKOTRIENE A-4 [ALADIPTASE // Peptidase_M1 // ZINC_PROT] CG10602 LD27070 37B4-
 CG10602 37B5 ID:86B9

+ RNA_binding * 3e-18 predicted using Genefinder; similar to KH domain family of RNA b * 3e-12 predicted using Genefinder; similar
 CG2950 to KH domain family of RNA b * [KH-domain // KH_DOMAIN] CG2950 GH11071 25B3-25B3 dup:1/2 ID:38F1
 + signal_transduction * Plenty of SH3s; POSH(aa) * 5e-09 hypothetical protein YHR016c - yeast (Saccharomyces cerevisiae) (U1 *
 4e-05 DRK_DROME PROTEIN E(SEV)2B (SH2-SH3 A[zf-C3HC4 // ZINC_FINGER_C3HC4 // P67PHO] CG4909 LD45365 54D1-54D1
 CG4909 ID:104C3
 + protein_phosphatase * myotubularin related protein 1(aa) * 3e-14 YJ80_YEAST HYPOTHETICAL 80.2 KD PROTEIN IN CPA2-
 CG5026 NNF1 INTERGENIC REGION * 2e-19 SET domain binding factor CG5026 LD48015 66E5-66E5 ID:107C5
 + unknown * conserved protein(aa) * 1e-133 YP65_CAEEL HYPOTHETICAL 81.5 KD PROTEIN IN CHROMOSOME II (U2 * 1e-125
 CG8613 YYAL_BACSU HYPOTHETICAL 78.8 KD PROTEIN IN TET [CARBOXYPEPT_ZN_2] CG8613 GH13403 50F6-50F6 ID:65D5
 + eIF-4E translation_factor * Eif4E * 2e-28 IF4E_YEAST EUKARYOTIC TRANSLATION INITIATION FACTOR 4E (EIF-4E) (EIF4E) (MRNA
 CG4035 CA * 1e-121 IF4E_DROME EUKARYOTIC TRANSLATION INITIATION CG4035 SD05406 67B2-67B2 dup:3/4 ID:118G2.2
 + enzyme * phosphatidylserine-specific phospholipase A1 deltaC(aa) * PS-PLA1(aa) * DMYOLK_4 Yp1 * VITELLOGENIN I
 CG4979 PRECURSOR (YOLK PROTEIN 1)(aa) [TAGLIPASE // ESTERASE // lipase] CG4979 GH05003 89B7-89B7 dup:2/2 ID:33D4
 + unknown * 4e-14 weak similarity to Bos taurus mitochondrial ATP synthase coupling factor B (SP * 1e-11 unknown * 8e-06
 CG10731 ATPW_BOVIN ATP SYNTHASE COUPLING FACTOR CG10731 GH24822 52F3-52F3 ID:77H11
 + Rpn7 endopeptidase * Subunit of the regulatory particle of the proteasome; Rpn7p(aa) * HYPOTHETICAL PROTEIN * 1e-66
 CG5378 hypothetical protein YPR108w - yeast (Saccharomyces c [PCI_DOMAIN // PCI] CG5378 LD47143 94B3-94B3 ID:106A8
 + nod motor_protein * DMKINLA_3 nod * KINESIN-LIKE PROTEIN NOD(aa) * 4e-19 Cin8p kinesin-related * 9e-46 similar to Kinesin
 motor domain; cDNA EST yk256h1.3 comes from t [kinesin // KINESIN_MOTOR_DOMAIN1 // KIN] CG1763 SD02282 10C5-10C6
 CG1763 ID:113H6
 + enzyme * 9e-41 /match=(desc;; /ma * 5e-35 cDNA EST comes from this gene; cDNA EST co * 9e-06 Ubc84D * contains similarity to
 CG4502 ubiquitin-conjugatin enzymes (Pf [UQ_con // UBIQUITIN_CONJUGAT_2] CG4502 LD39243 27E4-27E4 ID:98D9
 + peptidase * [pdb]1AYE Human Procarboxypeptidase A2(aa) * CARBOXYPEPTIDASE B(aa) * 3e-37 YHT2_YEAST
 HYPOTHETICAL 49.8 KD PROTEIN IN ACT3-YCK1 INTERGENIC REGION [CARBOXYPEPT_ZN_1 // CRBOXYPTASEA // Zn_] CG3108
 CG3108 LP01044 5B6-5B8 ID:107D1

+ RpA-70 DNA_replication_factor * DMRPA1_3 RpA-70 * REPLICATION PROTEIN A KD DNA-BINDING SUBUNIT (RP-A) (RF-A)
 CG9633 (REPLICATION FACTOR-A PROTEIN 1) (SINGLE-STRANDED DNA-BINDING PROTEIN) CG9633 LD40420 84F-84F dup:4/4 ID:99E5
 + unknown * R01H10.7(aa) * inositol polyphosphate 4-phosphatase, type II(aa) * inositol polyphosphate 4-phosphatase type II-
 CG1846 alpha(aa) * 4e-58 inositol polypho [PH_DOMAIN] CG1846 GH24251 12E1-12E1 dup:2/2 ID:77D3
 + enzyme * UTP--GLUCOSE-1-PHOSPHATE URIDYLYLTRANSFERASE (UDP-GLUCOSE PYROPHOSPHORYLASE) (UDPGP)
 CG4347 (UGPASE)(aa) * similar to UTP--GLUCOSE-1-PHOSPHATE URIDYLYLTRA CG4347 GH06691 67A9-67B1 dup:1/3 ID:59B7
 + Fragile-X-related RNA_binding * FRAGILE X MENTAL RETARDATION SYNDROME RELATED PROTEIN 1(aa) * Fxr2h(aa) * protein
 isoform d(aa) * 6e-81 FMR1_MOUSE FRAGILE X MENTAL RETARDATION [KH-domain // TONB_DEPENDENT_REC_1 // KH] CG6203
 CG6203 GH22839 85F10-85F11 ID:75D2
 + bgcn unknown * EUKARYOTIC TRANSLATION INITIATION FACTOR (EIF-6)(aa) * map_position:60A2+ * EUKARYOTIC
 CG17611 TRANSLATION INITIATION FACTOR (EIF-6)(aa) * integrin beta bin CG17611 GH08760 60A4-60A4 dup:1/2 ID:60H9
 + unknown * 5e-70 weak similarity to HSP90 * 1e-05 YXAQ_BACSU HYPOTHETICAL 37.5 KD PROTEIN IN GNTR-HTPG
 CG2982 INTERGENIC REGION * CG2982 LD40453 4B5-4B5 dup:2/2 ID:99E8
 + Gr enzyme * 4e-59 glutathine reductase * GSHR_DROME GLUTATHIONE REDUCTASE (GR) (GRASE) glutathione * 1e-125
 TRXB_CAEEL PROBABLE THIOREDOXIN REDUCTASE Similar t [HGRDTASE // FADPNR // pyr_redox // PYRI] CG2151 GM14215
 CG2151 7D18-7D18 ID:83C1
 + unknown * 9e-36 by content; 1-meth * 1e-43 YS15_CAEEL HYPOTHETICAL 41.1 KD PROTEIN IN CHROMOSOME II * 1e-42 Sqv-
 CG3881 8-like protein * 7e-47 UDP-glucuronyltransfera CG3881 GH16433 30C2-30C2 ID:68F5
 + unknown * queuine trna-ribosyltransferase(aa) * 7e-98 TGT_CAEEL PUTATIVE QUEUINE TRNA-RIBOSYLTRANSFERASE
 CG4947 (TRNA-GUANINE TRANSGLYCOSYLA * TGT_BACSU QUEUINE TR CG4947 LP01967 21F1-21F1 ID:107H4
 + chaperone * HYPOTHETICAL 39.9 KD PROTEIN T15H9.1 IN CHROMOSOME II PRECURSOR(aa) * DNAJ PROTEIN HOMOLOG
 CG9089 (DROJ1)(aa) * 1e-06 SCJ1_YEAST SCJ1 PROTEIN SCJ1 protein [DnaJ // DNAJ_2] CG9089 LD21896 15B4-15B4 dup:2/2 ID:83E11
 + chaperone * 1e-07 STI1_YEAST HEAT SHOCK PROTEIN STI1 stress-induced protein * 1e-08 Hsp70/Hsp90 organizing protein
 CG2947 homolog * 1e-54 similar to TPR Domain (2 doma [RNP_1 // TPR_REGION // TPR_REPEAT // TP] CG2947 3F6-3F6 dup:3/4 ID:45F9
 CG2604 + unknown CG2604 SD10384 dup:1/2 ID:125B2.2
 + transcription_factor * DMSUHW_6 su(Hw) * crol * zf43C * 7e-08 zinc finger 30C [zf-C2H2 // ZINC_FINGER_C2H2 // ZINC_FIN]
 CG7101 CG7101 GH24178 17E1-17E1 ID:77C7
 + Klp68D motor_protein * Klp68D * KINESIN-LIKE PROTEIN KLP68D(aa) * 1e-38 Cin8p kinesin-related * 1e-115 Similarity to urchin
 CG7293 kinensin-2 (PIR Acc. No. cDNA EST EM [kinesin // KINESINHEAVY] CG7293 GH23075 68D2-68D2 ID:75G8
 + CRAG ligand_binding_or_carrier * CRAG protein * 1e-145 contains similarity to human MAP kinase-activating death domain * 1e-120
 CG12737 protein * 3e-16 Rab3 GDP/GTP exchange protein [DENN_DOMAIN // CYTOCHROME_C] CG12737 LD26363 7F4-7F4 dup:6/6 ID:85E3
 + unknown * HYPOTHETICAL 37.2 KD PROTEIN C12C2.09C IN CHROMOSOME II(aa) * 1e-19 hypothetical protein YDR492w -
 CG7530 yeast (Saccharomyces cerevisiae) (U * 5e-26 C43G2 CG7530 LD44720 88D2-88D2 dup:3/3 ID:103E8
 + Mgstl enzyme (Microsomal glutathione S-transferase-like) microsomal glutathione S-transferase-like protein [Drosophila melanogaster]
 CG1742 >g MAPEG CG1742 GH08455 dup:1/2 ID:60F10
 CG3508 + unknown * HMBA-inducible(aa) * 3e-11 HIS1 protein * [NLS_BP] CG3508 LD30520 88C11-88C11 ID:47B4
 CG1114 + unknown * growth factor-responsive protein, vascular smooth muscle - rat(aa) * 3e-47 Weak similarity with apoptosis protein RP-8;

cDNA EST * SM-20 * CG1114 GH23732 83A1-83A1 ID:76F11

CG6339 + motor_protein CG6339 SD05424 ID:118G5

+ unknown * Ypr147cp(aa) * 1e-11 probable membrane protein YPR147c - yeast (*Saccharomyces cerevisiae*) * 1e-20 predicted using

CG9186 Genefinder; Similarity to *C.elegans* [ESTERASE // LIPASE_SER] CG9186 LP01162 62B4-62B4 dup:2/2 ID:107D5

+ enzyme * dihydrosphingosine phosphate lyase (also known as sphingosine phosphate lyase); Dpl1p(aa) * Similar to glutamate

CG8946 decarboxylase(aa) * sphingosine-1-p CG8946 SD02978 53F10-53F10 dup:3/3 ID:114H12

+ unknown * 9e-56 cDNA EST comes from this gene; cDNA EST co ** [AROMATIC_AA_PERMEASE_2] CG5262 LD43196 77C1-
CG5262 77C1 ID:102B5

CG13773+ enzyme * 4e-10 match to * 3e-06 hypothetical protein * [NLS_BP] CG13773 GH23590 27C3-27C3 ID:76D12

CG3416 + translation_factor CG3416 LD22193 dup:2/2 ID:83F10

+ Sin3A transcription_factor * 3e-58 SIN3_YEAST PAIRED AMPHIPATHIC HELIX PROTEIN regulatory * transcription factor * 2e-31

cDNA EST comes from this gene; cDNA EST co * 1e-135 co-r [ATPASE_ALPHA_BETA // NLS_BP] CG8815 GH11769 49B2-49B3 dup:1/2

CG8815 ID:63G12

+ enzyme * ATP SYNTHASE LIPID-BINDING PROTEIN P2 PRECURSOR (PROTEIN 9) (SUBUNIT C)(aa) * 5e-12 ATP synthase (EC

CG1746 3.6.1.-) c chain - *Caenorhabditis elegans* * 3e- [ATPASE_C // ATPASEC // ATP-synt_C] CG1746 GH04827 100B9-100B9 ID:57C6

+ EG:132E8.4 motor_protein * DMC132E8 * 4e-06 USO1_YEAST INTRACELLULAR PROTEIN TRANSPORT PROTEIN USO1 (* melanog

CG11448 * 2e-31 similar to coiled coil domains; cDNA EST yk302g12.5 com CG11448 GH23825 2A3-2A3 ID:76H2

+ endopeptidase * Ypl125wp(aa) * possible RanBP7-importin-beta-Cse1p superfamily(aa) * 1e-36 hypothetical protein YPL125w -

CG8212 yeast (*Saccharomyces cerevisiae*) (* 1e-[trypsin // CHYMOTRYPSIN // IBN_NT // TR] CG8212 GH15020 52C-52C dup:1/2 ID:67A11

+ protein_kinase * 1e-07 probable membrane protein YDL146w - yeast (*Saccharomyces cerevisiae*) * 3e-09 hypothetical protein *

CG2258 [SH3] CG2258 LD26707 7D9-7D9 dup:1/3 ID:85G7

CG14303+ unknown * 7E-86* * CG14303 GM13930 91B6-91B6 ID:83B9

+ enzyme * 1e-152 Naglu * 1e-153 N-acetylglucosaminidase, alpha- (Sanfilippo disease IIIB) * 1e-113 alpha-N-acetylglucosaminidase

CG13397* alpha-N-acetylglucosaminida CG13397 LP03571 29C1-29C1 ID:108F10

+ unknown * UNKNOWN; PRC1(aa) * protein regulating cytokinesis 1; PRC1 * [G_PROTEIN_GAMMA] CG1655 SD02150 9F5-9F5

CG1655 ID:113F5

+ translation_factor * hypothetical translation initiation factor(aa) * HYPOTHETICAL 40.9 KD PROTEIN C01G10.9 IN CHROMOSOME

CG11334V(aa) * 3e-66 YP18_YEAST HYPOTHETICAL 45.0 KD P [IF-2B] CG11334 GH08894 100C-100C dup:1/2 ID:61B5

+ enzyme * PUTATIVE UBIQUINONE BIOSYNTHESIS MONOOXYGENASE COQ6(aa) * CGI-10 protein(aa) * UbiH-like protein(aa) *

CG7277 COQ6 monooxygenase; Coq6p(aa) [UBIH // Monooxygenase // RINGMONOXGNASE] CG7277 GH22740 25E6-25E6 ID:75C2

CG4300 + unknown spermine synthase SAM_BIND CG4300 LD28457 ID:45F5

+ enzyme * 1e-43 CCR4_YEAST GLUCOSE-REPRESSIBLE ALCOHOL DEHYDROGENASE TRANSCRIPTIONAL EFFECTOR (C *

CG5534 2e-07 ANGEL * 3e-86 predicted using Genefinder; Similarity CG5534 GH27503 95E6-95E6 dup:2/2 ID:81E4

+ Grip91 cytoskeletal_structural_protein * gamma-tubulin interacting protein(aa) * gamma-tubulin ring protein Dgrip91(aa) * 1e-123 spindle

CG10988 pole body protein spindle pole body protein spc98[DEHYDRATASE_SER_THR] CG10988 LD42379 12B7-12B7 dup:3/4 ID:101E5

CG12104+ unknown * 4e-11 protein * protein * CAGF9 * [HMG // HMG_box] CG12104 LP01188 62A-62A ID:107D7

CG11329+ unknown * 1e-16 inserted at base 5' end of P element Inverse PCR * * CG11329 LD26217 26F6-26F6 ID:44C11
+ unknown * 6e-43 COX11 (AA 1-277) * 2e-44 cDNA EST comes from this gene; cDNA EST co * 1e-124 protein * 3e-51 component

CG6922 involved in Haem biosynthesis americana CG6922 GH24534 25E6-25E6 ID:77F11
+ enzyme * similarity to enoyl CoA hydratase. Amino terminus shows similarity to acyl-CoA binding domains; cDNA EST comes from

CG13890 this gene; cDNA EST comes from [ECH // NLS_BP] CG13890 GH11143 61D4-61D4 ID:63B12
+ Ckl1alpha protein_kinase * 1e-103 KC21_YEAST CASEIN KINASE II, ALPHA CHAIN (CK II) casein ki * KC2A_DROME CASEIN KINASE II, ALPHA CHAIN (CK II) casein kina * 1e-151 KC2A_CAE[PROTEIN_KINASE_ST // PROTEIN_KINASE_DOM] CG17520 LD27706

CG17520 cyto_unknown ID:86G9
+ lic protein_kinase (licorn) stress activated MAP kinase kinase 3 [Drosophila melanogaster] PROTEIN_KINASE_DOM,

CG12244 PROTEIN_KINASE_ST, p] CG12244 SD04985 ID:118B12
+ az2 transcription_factor * zf43C * 2e-09 AZF1_YEAST ASPARAGINE-RICH ZINC FINGER PROTEIN AZF1 fin * putative zinc finger

CG1605 protein * 3e-09 similar to Zinc finger, C2H2 type (3 do [SERPIN // zf-C2H2 // ZINC_FINGER_C2H2] CG1605 43D3-43D3 dup:3/3 ID:77E5
+ Lrr47 actin_binding * LRR47 protein - fruit fly (Drosophila melanogaster)(aa) * DMLRR47_3 Lrr47 * 2e-05 predicted using Genefinder;

CG6098 Similarity to Glucose-repressible alco [LRR // LEURICHRPT] CG6098 GH06740 31E6-31E6 ID:59B11
+ enzyme * type II membrane protein(aa) * Similarity with yeast hypothetical protein (PIR accession number * brn * beta-1,3-N-

CG8668 acetylglucosaminyltransferase(a [ALDOKETO_REDUCTASE_3] CG8668 SD02482 28E-28E ID:114B11

CG5541 + unknown * [C_TYPE_LLECTIN_1] CG5541 LD37145 13A8-13A8 dup:3/3 ID:96E6

CG1927 + BcDNA:GH11112 unknown * CG1927 GH11112 62B11-62B11 ID:38F4
+ Tsc1 cell_cycle Tuberous Sclerosis Complex 1 tumor-suppressor gene. also gigas, rocky. regulates cell size and cell cycle

CG6147 ATPASE_ALPHA_BETA, NLS_BP CG6147 LD25933 dup:2/2 ID:85B5
+ enzyme * coded for by C. elegans cDNA yk4d2.3; coded for by C. elegans cDNA yk4d2.5; coded for by C. elegans cDNA yk109a1.5;

CG16757 similar to protein tyrosine phos [PHOSPHOPANTETHEINE // PDZ // PRO_RICH] CG16757 62E7-62E7 dup:5/6 ID:89B7
+ unknown * BLASTX 7.0E-38 YLR386W|Protein of unknown function(dna) * BLASTX 7.0E-38 YLR386W|Protein of unknown

CG5608 function(dna) * BLASTX 7.0E-38 YLR386W|Protein o CG5608 SD04925 87C-87C dup:2/2 ID:118A11

CG12375+ unknown * 1e-05 hypothetical protein * * [lactamase_B] CG12375 GH20064 28E-28E ID:72C5
+ Atpalphatransporter * 3e-78 ATC1_YEAST CALCIUM-TRANSPORTING ATPASE (GOLGI CA2+-ATPASE) * ATNA_DROME SODIUM/POTASSIUM-TRANSPORTING ATPASE ALPHA CHAIN (SODIUM PUMP) (NA+/ [NAKATPASE // Na_K_ATPase_C //

CG5670 ATPASE_E1] CG5670 GH23483 93B-93B dup:2/3 ID:76C12

CG16928+ CG16928 dup:3/3 ID:44E9
+ unknown * Yor243cp(aa) * 2e-79 YO43_YEAST HYPOTHETICAL 77.0 KD PROTEIN IN HES1-SEC63 INTERGENIC REGION * 3e-

CG6745 35 YQ4B_CAEEL HYPOTHETICAL 64.6 KD PROTEIN IN CHRO [UPF0024 // NLS_BP] CG6745 GH24787 66D4-66D4 ID:77H10
+ unknown * coded for by C. elegans cDNA cm04e9; coded for by C. elegans cDNA CESAC59F(aa) * unknown(aa) * * CG18112

CG18112 SD03121 99C5-99C5 ID:115C3
+ unknown * coded for by C. elegans cDNA yk61f1.3; coded for by C. elegans cDNA yk109h8.3; coded for by C. elegans cDNA

CG8576 CEESX42F; coded for by C. elegans cDNA CG8576 SD02002 65F5-65F5 ID:113D5
+ electron_transfer * 1e-11 C05E11.1 gene product * 2e-07 hypothetical protein * 3e-45 inserted at base Both 5' and 3' ends of P

CG8735 element Inverse PCR * [CYTOCHROME_C] CG8735 LD34731 44D-44D2 dup:3/3 ID:49E11

+ unknown * 5e-14 /match=(desc: * 6e-43 weak similarity to drosophila tyrosine kinase ele * 5e-23 The gene is expressed
 CG15737 ubiquitously.; The protein * 1e-20 caffe [PAP_ASSOCIATED // PAP_CORE // PAP // PR] CG15737 LD47659 10F5-10F6 dup:1/2 ID:106G9
 + motor_protein * HYPOTHETICAL 25.4 KD PROTEIN F53F4.3 IN CHROMOSOME V(aa) * 3e-12 YNO8_YEAST HYPOTHETICAL
 28.4 KD PROTEIN IN RPC8-MFA2 INTERGENIC REGION * 9e-07 kine [CAP_GLY_2 // CAP_GLY] CG11242 LD35048 56D9-56D9
 CG11242 dup:2/2 ID:49G2
 + mub RNA_binding * DMMUB_6 mub * PUTATIVE HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN X (HNRNP X) (CBP)(aa) *
 CG7437 nucleic acid binding protein(aa) * 4e-13 YB83_YEAST HYPOTHETI [KH-domain // KH_DOMAIN] CG7437 LD32520 79B1-79B1 ID:48C7
 + motor_protein * kda paraneoplastic cerebellar degeneration-associated antigen Peptide, * MYOSIN HEAVY CHAIN D (MHC D)(aa) *
 CG1962 CLIP-190 * 7e-05 microtubule binding pro [NLS_BP] CG1962 38E-38E dup:3/5 ID:48G3
 + BcDNA:GH02220 enzyme * OXA1 homolog - human(aa) * 3e-25 OXA1_YEAST CYTOCHROME OXIDASE BIOGENESIS PROTEIN
 CG6404 OXA1 PRECURSOR * 2e-29 Similarity to Human OXA1HS protein (cytochr CG6404 LD40470 67F4-67F4 dup:3/3 ID:99E10
 + DNA_repair_protein * REV1 protein(aa) * 2e-56 REV1_YEAST DNA REPAIR PROTEIN REV1 REV1 protein - yeast * 2e-78 similar
 to DNA repair protein (REV1); cDNA EST co[UMUC_DOMAIN // IMS // BRCT_DOMAIN // BR] CG12189 GH05320 61C8-61C8 dup:2/2
 CG12189 ID:33E10
 CG9896 + unknown * [NLS_BP] CG9896 GH05301 59C1-59C1 ID:57G12
 + * EPIDIDYMAL SECRETORY PROTEIN E1 PRECURSOR (CE1)(aa) * 4e-22 epididymal secretory protein * 9e-23 EP1_HUMAN
 CG7291 EPIDIDYMAL SECRETORY PROTEIN E1 PRECURSOR CG7291 22B8-22B8 dup:2/3 ID:88D3
 + enzyme * similar to pig tubulin-tyrosine ligase.(aa) * 4e-06 YBU4_YEAST HYPOTHETICAL 86.4 KD PROTEIN IN PHO5-VPS15
 CG16833 INTERGENIC REGION * 1e-76 similar to tubul CG16833 GH09663 32C5-34A5 dup:1/3 ID:61H3
 CG7962 + CG7962 GH23282 ID:76A8
 CG6903 + unknown * CG6903 GH13389 4D1-4D1 ID:65D4
 + CHIP chaperone * defined colon cancer antigen 7(aa) * carboxy terminus of Hsp70-interacting protein(aa) * 3e-09 hypothetical protein
 CG5203 YOR007c - yeast (Saccharomyces c [TPR_REGION // TPR_REPEAT // TPR] CG5203 LD32251 33D1-33D1 ID:48B6
 + unknown * 4e-11 YMH6_CAEEL HYPOTHETICAL 19.1 KD PROTEIN F58A4.6 IN CHROMOSOME III ** CG12123 GH02722 7E6-
 CG12123 7E6 ID:55D12
 CG9216 + unknown * [NLS_BP] CG9216 14A6-14A8 ID:88B5
 + enzyme * PROBABLE SERYL-TRNA SYNTHETASE (SERINE--TRNA LIGASE) (SERRS)(aa) * SERYL-TRNA SYNTHETASE
 (SERINE--TRNA LIGASE) (SERRS)(aa) * seryl-tRNA synthetase(a [tRNA-synt_2b // TRNASYNTHSER] CG17259 GH04194 23C4-23C5
 CG17259 dup:2/2 ID:32E7
 + tos DNA_repair_protein * DMTOSCAP1_2 tos * Tosca(aa) * 7e-47 EXO1_YEAST EXONUCLEASE I (EXO I) (DHS1 PROTEIN) DHS1
 CG10387 pr * Tosca [53EXO_N_DOMAIN // 53EXO_I_DOMAIN // XPG] CG10387 LD31018 37A4-37A4 dup:2/2 ID:47E5
 + transporter * similar to Mitochondrial carrier proteins (2 domains); cDNA EST yk309c6.5 comes from this gene; cDNA EST
 yk309c6.3 comes from this gene; cDNA EST [mito_carr // MITOCARRIER // MITOCH_CARR] CG5805 GH22160 98E1-98E1 dup:2/2
 CG5805 ID:74E10
 + enzyme_inhibitor * nuclear inhibitor of phosphatase-1(aa) * similar to forkhead-associated (FHA) domains (Pfam: FHA.hmm, score:
 CG8980 28.36)(aa) * NIPP-1, nuclear inhibitor [FHA_DOMAIN // FHA] CG8980 SD02428 53E10-53E11 ID:114B3
 CG4877 + unknown * [NLS_BP] CG4877 LD36996 72F1-72F1 dup:2/2 ID:96D5

+ pelo unknown * pelo * 9e-61 DOM34 protein - yeast (*Saccharomyces cerevisiae*) (X77 * PELO_DROME PELOTA PROTEIN pelota *
 CG3959 1e-120 YNU6_CAEEL HYPOTHETICAL 42.9 KD PROT CG3959 LD34262 30C6-30C7 ID:49D2
 CG9646 + unknown * No definition line found(aa) * protein(aa) * No definition line found * [NLS_BP] CG9646 LD47968 53F4-53F5 ID:107B7
 + Hs2st enzyme * DMSD_2 Sd * SEGREGATION DISTORTER PROTEIN(aa) * 2e-74 cDNA EST yk273d10.3 comes from this gene;
 CG10234 cDNA EST yk273d10.5 come * 1e-101 heparan sulfate 2- CG10234 GH20044 37E3-37E3 ID:72C3
 + protein_phosphatase * Hop * DMPPY_2 PpY-55A * serine/threonine protein phosphatase PPT1(aa) * 7e-88 PPT1_YEAST
 SERINE/THREONINE PROTEIN PHOSPHATASE T (PPT) [TPR_REGION // PHOSPHO_ESTER // STPHPHTA] CG8402 GH12714 85E6-
 CG8402 85E6 ID:40B1
 CG13316+ * 0.000000002* * CG13316 3F2-3F2 ID:82G7
 CG11403+ DNA_repair_protein CG11403 LD24267 dup:2/2 ID:84C8
 + Ndr protein_kinase * DMPROKINX_2 Ndr * Ndr protein kinase(aa) * 1e-128 KNQ1_YEAST PROBABLE SERINE/THREONINE-
 PROTEIN KINASE YNL161W * 1e-175 coded for by *C. elegans* [PROTEIN_KINASE_ST // PROTEIN_KINASE_DOM] CG8637 LD37189
 CG8637 76D3-76D3 dup:2/2 ID:96E10
 + protein_kinase * 9e-52 SSK2_YEAST SERINE/THREONINE PROTEIN KINASE SSK2 (SUPPRESSOR OF SENSOR KINASE 2) *
 5e-34 protein kinase (EC 2.7.1.37) 2B - fruit fly (*Drosop*[PROTEIN_KINASE_ST // PROTEIN_KINASE_DOM] CG7717 LD39970 93F9-93F9
 CG7717 dup:3/5 ID:99B2
 + transcription_factor * C43H6.7 gene product(aa) * HYPOTHETICAL 38.1 KD PROTEIN C2F12.15C IN CHROMOSOME II(aa) *
 CG5880 hypothetical protein(aa) * 5e-15 probable membrane protei [ZF_DHHC] CG5880 LD25420 97E8-97E8 ID:84F9
 + Rpn5 endopeptidase * proteasome (prosome, macropain) 26S subunit, non-ATPase, 12(aa) * 5e-42 hypothetical protein YDL147w -
 CG1100 yeast (*Saccharomyces cerevisiae*) * 2e-81 No d [PCI_DOMAIN // PCI // NLS_BP] CG1100 GH11341 83C-83C ID:38H3
 CG10346+ chaperone * CG10346 37A4-37A4 dup:1/3 ID:87G7
 + Rep1 enzyme * Rep1 * 1e-121 DNA fragmentation factor DREP-1 * 1e-08 cell death activator CIDE-A * 4e-09 cell death-inducing DFFA-
 CG8357 like effector a c CG8357 48E2-48E2 dup:3/3 ID:101E9
 + TfiIS transcription_factor * 2e-20 DST1 DNA strand transferase alpha * 1e-124 TFS2_DROME TRANSCRIPTION ELONGATION
 CG3710 FACTOR S-II (RNA POLYMERASE II ELONGATION FA * 3e-42 TFS2_CAEEL [TFIIS] CG3710 LD34766 35C1-35C1 ID:49F1
 + unknown * BLASTX 4.0E-27 YER156C|Protein of unknown function(dna) * HYPOTHETICAL 38.2 KD PROTEIN IN BEM2-NCB1
 CG11980 INTERGENIC REGION(aa) * 6e-60 similar to Yeast h CG11980 LD44814 85C3-85C3 dup:2/2 ID:103F9
 + cell_adhesion THYROGLOBULIN PRECURSOR 4_DISULFIDE_CORE, ATP_GTP_A, EGF_1, THYR] CG5639 LD31017 dup:2/2
 CG5639 ID:47E4
 CG10018+ DNA_repair_protein homology to mouse and human SNM1 protein NLS_BP CG10018 LD28027 dup:1/2 ID:45C8
 + Rbf cell_cycle_regulator * DMRBFPRTN_2 Rbf * EST comes from the 3' UTR m * 3e-24 similar to retinoblastoma proteins * 1e-84
 CG7413 RBL1_MOUSE RETINOBLASTOMA-LIKE PROTEIN (107 KD RETI CG7413 GH05946 1C2-1C2 ID:58D10
 CG3273 + unknown * CG3273 GH05256 42B3-42B3 dup:2/2 ID:33E8
 + peptidase * PROBABLE CYTOSOL AMINOPEPTIDASE (LEUCINE AMINOPEPTIDASE) (LAP)(aa) * leucine aminopeptidase(aa) *
 PUTATIVE AMINOPEPTIDASE ZK353.6 IN CHROMOSOME III([LAMNOPPTDASE // RCC1_2 // Peptidase_M17] CG7340 LD34492
 CG7340 87D7-88E1 ID:49D12

+ transporter * 8e-11 syntaxin * 3e-17 hypothetical protein * 2e-17 syntaxin * 1e-19 inserted at base 5' end of P element Inverse PCR
 CG11278[T_SNARE // Syntaxin] CG11278 LD27581 69F2-69F2 ID:86F9
 + ligand_binding_or_carrier * Pen * 1e-107 IMA1_YEAST IMPORTIN ALPHA SUBUNIT (KARYOPHERIN ALPHA SUBUNIT)
 (SERINE-RICH RNA P * overgrown hematopoietic organs-31 tumor suppressor O [ARM_REPEAT // Armadillo_seg] CG4799 LP03126
 CG4799 31A1-31A1 ID:108D10
 + translation_factor * UNKNOWN(aa) * 7e-86 inserted at base Both 5' and 3' ends of P element Inverse PCR * eukaryotic translation
 CG12131 initiation factor eIF3, p35 subunit * CG12131 GH12681 46C10-46C11 ID:40A7
 + bcd transcription_factor * DNA-binding-protein,transcription-factor(aa) * DMBCDG_3 bcd * 1e-125 bcd protein * 8e-52 homeotic protein
 CG1034 bicoid - fruit fly (Drosophila ps[RNP_1 // HOMEBOX_1 // homeobox // HOME] CG1034 LD27003 84D1-84D1 dup:1/2 ID:86A8
 + Psi RNA_binding * Psi * PSI=P element somatic inhibitor Peptide, * 1E-176* 3e-37 similar to RNA binding protein [KH-domain //
 CG8912 PFKB_KINASES_1 // KH_DOMAI] CG8912 LD38872 53D14-53D14 dup:1/2 ID:98B5
 CG4916 + RNA_binding CG4916 dup:2/2 ID:46C4
 + RnrS enzyme * 1e-113 RIR2_YEAST RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE SMALL CHAIN (RIBONUCLEOTIDE R * 1e-
 107 RIR2_DROME PROBABLE RIBONUCLEOSIDE-DIPHOSPHATE REDUCTA [RIBORED_SMALL] CG8975 LD32770 48D8-48D8
 CG8975 ID:48D10
 + transcription_factor * 5e-87 inserted at base 5' end of P element Inverse PCR * * [zf-C2H2 // ZINC_FINGER_C2H2 // ZINC_FIN]
 CG8961 CG8961 LD32631 53F5-53F5 ID:48D3
 CG15217+ transmembrane_receptor * CG15217 GH01875 40C2-40C2 ID:54H7
 + dah unknown * dystrobrevin(aa) * similar to the kDA Torpedo acetylcholine receptor-associated protein; similar to rat apodystrophin-3,
 CG6157 PIR Accession Number * dah [ZF_ZZ // ZZ] CG6157 LD47411 13C1-13C1 ID:106D2
 CG18218+ CG18218 SD07272 dup:1/4 ID:120H6.2
 + unknown * predicted using Genefinder; Similarity in 3' end to Human protein cDNA EST comes from this gene; cDNA EST comes
 CG9986 from this gene; cDNA EST comes from CG9986 LD27564 98D4-98D4 ID:86F8
 + EG:114E2.2 * MAX BINDING PROTEIN MNT (ROX PROTEIN) (MYC ANTAGONIST MNT)(aa) * MAX BINDING PROTEIN MNT (ROX
 PROTEIN) (MYC ANTAGONIST MNT)(aa) * by content; by mat [THIOLASE_3 // HLH // HELIX_LOOP_HELIX_2] CG2856 3F2-3F2 dup:2/2
 CG2856 ID:95D2
 + EG:52C10.5 enzyme * 3e-54 FAB1_YEAST PROBABLE PHOSPHATIDYLINOSITOL-4-PHOSPHATE 5-KINASE FAB1 (1-PHOSPHATID
 * by content; 1-meth * 8e-60 similar to FYVE zinc finger; cDN [DEP_DOMAIN // FYVE_DOMAIN // FYVE // ZI] CG6355 LD46512 54E9-
 CG6355 54E9 dup:2/3 ID:105D9
 + transcription_factor * 7e-10 AZF1_YEAST ASPARAGINE-RICH ZINC FINGER PROTEIN AZF1 fin * 2e-37 transcription factor YY1
 CG3445 homolog * 1e-14 contains similarity to C2H2-type z[zf-C2H2 // ZINC_FINGER_C2H2 // ZINC_FIN] CG3445 67B4-67B4 dup:3/4 ID:56G10
 + pav motor_protein * 7e-35 YGW6_YEAST PUTATIVE KINESIN-LIKE PROTEIN YGL216W hypoth * PAV-KLP protein * 5e-91 Similar to
 CG1258 kinesin-like protein; coded for by C. elegans cDN [kinesin // KINESIN_MOTOR_DOMAIN1 // KIN] CG1258 64B4-64B4 dup:1/2 ID:103C2
 CG3021 + CG3021 LD29918 dup:1/2 ID:46F9
 + dco protein_kinase * serin/threonin-kinase(aa) * dbt * Ckl agr; * DMDG2CD5_3 for [PROTEIN_KINASE_ST //
 CG2048 PROTEIN_KINASE_DOM] CG2048 LD27173 100B-100B ID:86C9
 CG3918 + NLS_BP, ZF_CCHC CG3918 ID:56H5

CG6605 + motor_protein CG6605 ID:46B12
+ unknown * androgen-induced prostate proliferative shutoff associated protein(aa) * protein(aa) * 1e-28 unknown * 6e-40 cDNA EST

CG17509 comes from this gene elegans CG17509 GH12788 48E2-48E2 dup:3/3 ID:64H3
+ Orc2 DNA_replication_factor * recognition complex, subunit (yeast homolog)-like(aa) * ORIGIN RECOGNITION COMPLEX PROTEIN, SUBUNIT (XORC2)(aa) * Orc2 * ORIGIN RECOGNITION COMPLE[ALDOKETO_REDUCTASE_3 // SUBTILASE_ASP] CG3041 GH13824

CG3041 88A4-88A4 ID:40H11
+ chaperone * 2e-09 Similarity to Rat peroxisome assembly factor-1 (SW:PAF1_RAT) * 1e-33 peroxisome membrane protein PEX2 *

CG7081 4e-32 peroxisomal membrane protein (35 [zf-C3HC4 // ZINC_FINGER_C3HC4 // ZF_RIN] CG7081 LD46714 66C8-66C8 dup:2/2 ID:105F3
+ motor_protein * KINESIN CENTRAL MOTOR (XKCM1)(aa) * kinesin heavy chain member 2(aa) * kinesin-like (mitotic centromere-associated kinesin)(aa) * kinesin heavy c[kinesin // KINESIN_MOTOR_DOMAIN1 // KIN] CG1453 LD47558 10A6-10A8 dup:2/2 ID:106F6

CG1453 associated kinesin(aa) * kinesin heavy c[kinesin // KINESIN_MOTOR_DOMAIN1 // KIN] CG1453 LD47558 10A6-10A8 dup:2/2 ID:106F6
+ alpha-Man-II enzyme * LYSOSOMAL ALPHA-MANNOSIDASE PRECURSOR (MANNOSIDASE, ALPHA B) (LYSOSOMAL ACID ALPHA-MANNOSIDASE)(aa) * truncated lysosomal acid alpha-mannosidase(aa) [Glyco_hydro_38 // NLS_BP] CG8139 GH03876 85D16-85D16

CG8139 ID:32C7
+ Mipp2 protein_phosphatase * Mipp2 * multiple inositol polyphosphate phosphatase 2; MIPP2 * 1e-27 multiple inositol polyphosphate phosphatase * 1e-25 multiple inositol polyphosp [CYTOCHROME_B_QO] CG4317 GH13296 5D2-5D2 dup:4/4 ID:40E4

CG4317 phosphatase * 1e-25 multiple inositol polyphosp [CYTOCHROME_B_QO] CG4317 GH13296 5D2-5D2 dup:4/4 ID:40E4
+ CBP calcium_binding * CBP * sarcoplasmic calcium-binding protein(aa) * 1e-161 sarcoplasmic calcium-binding protein * 4e-23 SCP_PERVT SARCOPLASMIC CALCIUM-BINDING PROTEIN [EF_HAND // NLS_BP // efhand // EF_HAND_] CG1435 GH12350 7A4-7A4 ID:39F9

CG1435 7A4 ID:39F9
+ lace enzyme * 1e-107 LCB2_YEAST SERINE PALMITOYLTRANSFERASE (LONG CHAIN BASE BIOSYNTHESIS PROTEIN * 2e-24 delta-aminolevulinate synthase * 1e-128 Similar to serin [aminotran_2 // AA_TRANSFER_CLASS_2 // N] CG4162 LD36009 35D3-35D3

CG4162 dup:2/2 ID:95E11
+ unknown * 1e-52 NUC1_YEAST MITOCHONDRIAL NUCLEASE nuclease NUC1 (EC 3.1.30 * 5e-77 YJ05_CAEEL HYPOTHETICAL 85.1 KD NUCLEASE C41D11.5 simila * 2e-68 NUCG_MOUSE [NUCLEASE_NON_SPEC // Endonuclease] CG8862 LD35517 48F1-48F1

CG8862 ID:95B2
+ TfiIealpa transcription_factor * 6e-23 T2EA_YEAST TRANSCRIPTION INITIATION FACTOR IIE, ALPHA SUBUNIT (TFIIE-ALPHA)

CG10415 (TRA * TFIIE large subunit * 7e-35 cDNA EST yk210d12.5 comes from CG10415 GH11150 68C13-68C13 ID:38F9
+ sut1 transporter * metabolite transport protein(aa) * membrane transporter like protein(aa) * ERD6 protein(aa) * solute carrier family

CG8714 (facilitated glucose transporte[SUGRTRANSPORT // SUGAR_TRANSPORT_2 // su] CG8714 LD44652 44A4-44A4 dup:4/4 ID:103E4
CG11484 + transcription_factor_binding * [UBA] CG11484 LD47780 102D1-102D3 ID:106H12

CG11484 + receptor * 4e-16 VT11_YEAST VESICLE TRANSPORT V-SNARE PROTEIN VT11 proba * 3e-27 cDNA EST yk433f11.3 comes from
CG3279 this gene; cDNA EST yk433f11.5 come * 3e-32 put CG3279 LD27967 61C9-61C9 dup:1/3 ID:87A9

CG3279 put * 3e-32 put CG3279 LD27967 61C9-61C9 dup:1/3 ID:87A9
CG7825 + Rad17 DNA_repair_protein DNA repair protein ATP_GTP_A, ATP_GTP_A2, RFC CG7825 LD27993 ID:45C7

CG7825 + enzyme * cDNA EST comes from this gene; cDNA EST yk282d3.5 comes from this gene(aa) * 1e-06 CCA1_YEAST TRNA NUCLEOTIDYLTRANSFERASE PRECURSOR (TRNA ADENYLYLT [MET_TRANS // SAM_BIND] CG1239 LP01332 83C1-83C1 dup:2/2

CG1239 ID:107E5
+ Rack1 signal_transduction * Rack1 * GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN (RECEPTOR OF

CG7111 ACTIVATED PROTEIN KINASE C HOMOLOG)(aa) * 3e-89 GBLP_YEAS[GPROTEINBRPT // WD40_REGION // WD_REPEA] CG7111

GH11320 28D2-28D2 dup:2/3 ID:63C12
 + unknown * 5e-07 hypothetical protein YOL114c - yeast (*Saccharomyces cerevisiae*) * 2e-17 R02F2.2 gene product * 3e-23 immature
 CG6094 colon carcinoma transcript prote [NLS_BP] CG6094 GH26345 31E5-31E5 ID:79H6
 + ial protein_kinase * Ipl1/aur serine/threonine kinase(aa) * 2e-68 IPL1_YEAST SERINE/THREONINE-PROTEIN KINASE IPL1 probable
 CG6620 * 1e-75 protein kinase (EC 2.7.1.37) aurora - [PROTEIN_KINASE_ST // TYRKINASE // PROTE] CG6620 32B4-32B4 dup:4/5 ID:98E9
 + DNA_binding * protein(aa) * 3e-65 YEZ9_YEAST PUTATIVE 90.2 KD ZINC FINGER PROTEIN IN CCA1-ADK2 INTERGENIC
 CG15835 REGION > * 2e-26 Similarity to Human XE169 protein (SW:X CG15835 LD33386 43F5-43F5 ID:48H3
 + cell_cycle_regulator * sorting nexin 9(aa) * 2e-11 YJD6_YEAST HYPOTHETICAL 49.0 KD PROTEIN IN NSP1-KAR2 INTERGENIC
 REGION * 5e-74 similar to PhoX homologous domain, pres[PX // BEM_DOMAIN // SH3DOMAIN // SH3] CG6757 LD47602 67B13-67B13
 CG6757 ID:106F10
 CG3876 + unknown CG3876 ID:88A4
 + unknown * short of similarity to human transforming protein (tre) * similar to human (TRE) transforming protein * Ypl249cp(aa) *
 CG5916 pollux(aa) [TBC // RAB_GAP] CG5916 LD45246 89B9-89B9 ID:104A9
 + motor_protein * Mklp1 * kinesin motor protein KIFC3(aa) * 2e-20 NUF1_YEAST NUF1 PROTEIN (SPINDLE POLY BODY SPACER
 PROTEIN SPC110) * 4e-30 microtubule binding prote [kinesin // KINESIN_MOTOR_DOMAIN1 // KIN] CG4831 LD36932 32E4-32E4
 CG4831 ID:96D1
 + signal_transduction * beta2-chimerin, cerebellar - human(aa) * beta2-chimerin, cerebellar - rat (fragment)(aa) * 2e-07 BEM2_YEAST
 GTPASE ACTIVATING PROTEIN BEM2/IP[RHO_GAP // RhoGAP // DAG_PE_BINDING_DOM] CG3208 SD02309 5A8-5A8 dup:1/3
 CG3208 ID:113H7
 + Es2 enzyme * HYPOTHETICAL 58.3 KD PROTEIN F42H10.7 IN CHROMOSOME III(aa) * ES2 protein(aa) * ES2 protein(aa) * Es2
 CG1474 CG1474 SD03464 7E7-7E7 ID:115G8
 + enzyme * 1e-45 ESTs and come from this gene. th * unknown * BIOC_SERMA BIOTIN SYNTHESIS PROTEIN BIOC the p *
 CG8067 CG8067 LD45826 50C22-50C23 ID:104F9
 + E2f2 transcription_factor * E2f2 * 1e-174 E2F-like transcription factor (E2F2) * 7e-14 predicted using Genefinder; cDNA EST comes
 CG1071 from this * 3e-18 E2F5_MOUSE TRANSCRIPTION FAC CG1071 GH13089 39B3-39B3 ID:40D1
 + dim-7 unknown * RanBP7(aa) * 1e-73 NMD5_YEAST NONSENSE-MEDIATED MRNA DECAY PROTEIN NMD5 * 8E-26*
 CG7935 RanBP7/importin [IBN_NT] CG7935 GH01576 66B9-67E3 dup:3/3 ID:30E1
 CG10428+ RCC1_2, SAM_BIND CG10428 dup:3/5 ID:89B11
 + enzyme * Depressed growth-rate protein; Deg1p(aa) * PROBABLE PSEUDOURIDYLATE SYNTHASE E02H1.3 (PSEUDOURIDINE
 CG3045 SYNTHASE)(aa) * 6e-54 PUS3_YEAST PSEUDOURIDYLATE [PseudoU_synth_1] CG3045 GH14326 58C5-58C5 dup:2/2 ID:41D5
 + ribosomal_protein * predicted using Genefinder; Similarity to Prototheca mitochondiral ribosomjal protein S11 (SW:RT11_PROWI);
 CG5184 cDNA EST yk372e6.3 comes from this gene; [Ribosomal_S11] CG5184 GM13519 89E13-89E13 ID:83A11
 CG3510 + CycB cell_cycle_regulator G2/MITOTIC-SPECIFIC CYCLIN B CYCLINS, cyclin CG3510 dup:2/4 ID:43B3
 + ligand_binding_or_carrier * 3e-51 ARF1_YEAST ADP-RIBOSYLATION FACTOR ADP-ribosylation fac * 3e-49 ARF1_DROME ADP-
 RIBOSYLATION FACTOR ADP-ribosylation fac * 1e-52 ARFL_CA[arf // SAR1GTPBP // RASTRNSFRMNG] CG7197 LD31204 66C5-66C5
 CG7197 dup:2/5 ID:47F5
 CG3920 + unknown * CG3920 GH05923 24C-24C dup:1/2 ID:58D7

CG7730 + unknown * CG7730 LD31138 73E4-73E4 dup:2/2 ID:47E12
+ enzyme * 3e-55 probable membrane protein YPR066w - yeast (*Saccharomyces cerevisiae*) * 3e-21 ubiquitin activating enzyme * 1e-
CG13343111 coded for by *C. elegans* cDNA [UBA_NAD // ThiF_family // NAD_BINDING /] CG13343 LD47462 50C14-50C14 ID:106D10