

Table S8

Genes that display a significant change in expression during larval stages (ANOVA, $P < 0.001$)

Gene ID mixed annotation (+ indicates sequence confirmation)

+ * 3e-25 predicted using Genefinder; cDNA EST comes from this * 4e-38 SPC1_HUMAN MICROSOMAL SIGNAL
CG1751 PEPTIDASE KD SUBUNIT (SPC25) * 3e-38 SPC1_CANFA MICR CG1751 10B17-10C1 dup:1/2 ID:101A12
CG12505+ unknown * CG12505 LD41905 50F6-50F6 ID:101A2
+ Ote motor_protein * 1e-174 OTE_DROME OTEFIN otefin - fruit fly (Drosophila melanogaster * 1e-176 DMOTEDA_2 Ote * *
CG5581 CG5581 LD41911 55C3-55C4 ID:101A4
CG17602+ unknown * CG17602 LD42024 20A1-20A1 ID:101B4
+ DNA_binding * 3e-59 CAC2_YEAST CHROMATIN ASSEMBLY FACTOR P60 SUBUNIT (CAF-1 KD SUBUNIT) * 8e-33
HIRA * 4e-11 YZLL_CAEEL HYPOTHETICAL 43.1 KD TRP-ASP REPEATS CONTA [GPROTEINB // WD40_REGION //
CG12892WD_REPEATS] CG12892 LD42270 47A9-47A9 ID:101D8
+ enzyme * 2e-30 5'-nucleotidase (EC 3.1.3.5) - mouse * 2e-31 5' nucleotidase (CD73) 5'-NUCLEOTIDASE PRECURSOR
(ECTO-NU * 1e-38 YfkN simila * 2', 3'-cudlic nuc [PHOSPHO_ESTER // 5_nucleotidase // SPAS] CG11883 LD42374 47B1-47B1
CG11883dup:2/2 ID:101E4
CG8121 + unknown * CG8121 LD42595 85D9-85D9 ID:101F3
+ grp protein_kinase * 5e-08 Ssp31 protein kinase * 2e-54 Ser/Thr kinase * 5e-13 serine/threonine kinase * 7e-27 Chk1;
CG17161 checkpoint kinase [PROTEIN_KINASE_DOM // pkinase] CG17161 LD42896 36A6-36A7 ID:101G7
+ unknown * putative transposase(aa) * 3e-05 ORF1 * 2e-07 putative transposase * Hermes transposase [AMP_BINDING]
CG11560CG11560 LD43225 68F3-68F3 ID:102B8
CG10165+ unknown * CG10165 LD43293 37F1-37F1 ID:102C2
+ structural_protein * 6E-55* 1e-06 R02F2.4 gene product * 2e-06 peritrophin * 7e-35 Gasp CG17052 LD43683 19C1-19C1
CG17052dup:1/2 ID:102F1
CG4702 + unknown * CG4702 LD43816 88A1-88A1 ID:102F9
CG4229 + unknown * CG4229 LD44179 77A1-77A1 ID:103A2
+ Cyp310a1cytochrome_P450 * cytochrome P450(aa) * DMLCPM Cyt-P450-rBF6-2 * 2e-29 cytochrome P450 monooxygenase *
CG10391 2e-17 similar to cytochrome P450 [EP450II // p450 // P450 // MITP450 // E] CG10391 LD44491 37A3-37A3 ID:103C12
+ pav motor_protein * 7e-35 YGW6_YEAST PUTATIVE KINESIN-LIKE PROTEIN YGL216W hypoth * PAV-KLP protein * 5e-91
Similar to kinesin-like protein; coded for by C. elegans cDN [kinesin // KINESIN_MOTOR_DOMAIN1 // KIN] CG1258 64B4-64B4
CG1258 dup:1/2 ID:103C2
+ chaperone * 5e-33 Similarity to Xenopus P58 protein cDNA EST * 3e-78 GP36b glycoprotein * 3e-83 coded for by C.
CG5510 elegans cDNA yk74e11.5; coded for by C. elegans CG5510 95E3-95E3 dup:2/2 ID:103C4
+ SPT4 enzyme * 3e-13 SPT4_YEAST TRANSCRIPTION INITIATION PROTEIN SPT4 SPT4 pro * 6e-30 contains similarity to
CG12372Saccharomyces cerevisiae Spt4 * 7e-39 unknown * 1e-39 CG12372 LD44495 49B5-49B5 ID:103D2
+ unknown * weak similarity to rat cytosolic acyl coenzyme A thioester hydrolase * acyl-CoA thioesterase(aa) * contains
CG1635 weak similarity to rat cytosolic acyl CG1635 LD44914 100D2-100D2 ID:103G3

+ transcription_factor * transcription factor IIC102(aa) * putative transcription factor subunit, TPR domains(aa) * Similarity
 CG8950 with yeast transcription factor TAU 131KDa [TPR_REGION // TPR_REPEAT // TPR] CG8950 LD44919 53F5-53F5 ID:103G4
 CG17469 + unknown * 1E-123 * CG17469 LD45277 102E2-102E3 dup:2/2 ID:104B4
 + EG:34F3.8 transporter * /match=(desc;; /match=(desc;; /match=(desc;; /match=(desc;; /motif=(desc;; the EST /match=(desc;;
 CG7359 /match=(desc;; /match=(desc;; /match=(desc;; /motif=(desc;; [SYNAPTOBREVIN // synaptobrevin] CG7359 LD45288 1C2-1C2 ID:104B6
 + 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
 CG4656 LD45535 94E-94E dup:2/2 ID:104D3
 + receptor * protein kinase C substrate 80K-H(aa) * similar to Human protein kinase C substrate, 80KD protein, heavy chain,
 CG6453 SWISS-PROT Accession Number * similar [LDLRA_2 // ER_TARGET // EF_HAND] CG6453 LD46533 36C4-36C4 ID:105D11
 + Gdi signal_transduction * 1e-135 GDI1_YEAST SECRETORY PATHWAY GDP DISSOCIATION INHIBITOR G * GDP
 dissociation inhibitor - fruit fly (Drosophila melanogaster) * Guanine nucleotide [RABGDI // RABGDI // GDI] CG4422 LD46767
 CG4422 30B8-30B9 ID:105F11
 + ribosomal_protein * ACIDIC RIBOSOMAL PROTEIN P0 HOMOLOG (L10E)(aa) * coded for by C. elegans cDNA
 CEESN26F; coded for by C. elegans cDNA CEESI89F; similar to 60S acidic [Ribosomal_L10] CG1381 LD47064 46E3-46E3
 CG1381 ID:106A5
 + endopeptidase * DMSTUBBLE_1 Sb * SERINE PROTEINASE STUBBLE (STUBBLE-STUBBLOID PROTEIN)(aa) * 2e-32
 similar to plasminogen and to trypsin-like serine proteases elegans [trypsin // CHYMOTRYPSIN // TRYPSIN_SER] CG4386
 CG4386 LD47230 58A2-58A2 ID:106B7
 + enzyme * 3e-55 probable membrane protein YPR066w - yeast (Saccharomyces cerevisiae) * 3e-21 ubiquitin activating
 enzyme * 1e-111 coded for by C. elegans cDNA [UBA_NAD // ThiF_family // NAD_BINDING] CG13343 LD47462 50C14-50C14
 CG13343 ID:106D10
 + stg protein_tyrosine_phosphatase * DMCD25_2 stg * 3e-21 MIPY_YEAST M-PHASE INDUCER PHOSPHATASE (MITOSIS
 INITIATION PROTEIN MIH1) (MITOT * cdc25 protein - fruit fly (Drosophila melanogaster) [RHODANASE // RHODANASE // MIPHPHTASE] CG1395
 CG1395 LD47579 99A5-99A6 dup:3/3 ID:106F9
 + protein_phosphatase * myotubularin related protein 1(aa) * 3e-14 YJ80_YEAST HYPOTHETICAL 80.2 KD PROTEIN IN
 CG5026 CPA2-NNF1 INTERGENIC REGION * 2e-19 SET domain binding factor CG5026 LD48015 66E5-66E5 ID:107C5
 + 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 // CARBOXYPTASEA // Zn]
 CG3108 CG3108 LP01044 5B6-5B8 ID:107D1
 + transcription_factor * DMRCPA_X kel * leucine-zipper-like transcriptional regulator, 1(aa) * 4e-12 YG52_YEAST
 HYPOTHETICAL 100.0 KD PROTEIN IN YHB1-PFK1 INTERGENIC REGION [BTB] CG3711 LP01394 1C5-1C5 dup:2/2
 CG3711 ID:107E9
 + peptidase * [pdb|1AYE| Human Procarboxypeptidase A2(aa) * 4e-45 YHT2_YEAST HYPOTHETICAL 49.8 KD PROTEIN IN
 ACT3-YCK1 INTERGENIC REGION PRECURSOR * 0.0000000006 * [CARBOXYPEPT_ZN_1 // CARBOXYPEPT_ZN_2 //]
 CG3097 CG3097 LP01667 5B6-5B6 ID:107G1
 CG5584 + enzyme * STERYL-SULFATASE PRECURSOR (STEROID SULFATASE) (STERYL-SULFATE SULFOHYDROLASE)

(ARYLSULFATASE C) (ASC)(aa) * 5e-14 weakly similar to arylsulfatase B [Sulfatase // SULFATASE_2] CG5584 LP01735 75A2-75A2 ID:107G6

+ Lcp65Ag1structural_protein * Lcp65Ag1 * 3e-44 cuticle protein LCP65Ag1 cuticle * 1e-30 cuticle homolog * CU15_MANSE

CG10530 CUTICLE PROTEIN CP14.6 PRECURSOR (MSCP14.6) cut [CUTICLE // insect_cuticle] CG10530 LP01749 65A-65A ID:107G7

+ transcription_factor * LIM-domain protein LMP-1(aa) * 6e-06 LRG1 * 7e-15 PINCH * 1e-18 UN97_CAEEL HOMEOBOX PROTEIN UNC-97 contains two LIM domain [LIM_DOMAIN_1 // LIM // LIM_DOMAIN_2] CG8242 LP02021 52C7-52C7 dup:3/3

CG8242 ID:107H6

CG13627 + unknown * CG13627 LP02282 96A20-96A20 ID:108A5

+ unknown * lbm * 1e-09 LBM_DROME LATE BLOOMER PROTEIN late bloomer me * 1e-11 lbm * [TM4_2] CG4471

CG4471 LP02988 42E2-42E2 ID:108C9

+ protein_kinase * SERINE/THREONINE-PROTEIN KINASE UNC-51(aa) * 5e-35 APG1_YEAST AUTOPHAGY SERINE/THREONINE-PROTEIN KINASE APG1 * 3e-24 p90 ribosomal S6 kinase * [PROTEIN_KINASE_ST // TYRKINASE //

CG10967 PROTE] CG10967 LP03175 69E1-69E2 dup:2/2 ID:108E3

+ Lsp1gamma larval_serum_protein * hexamerin A; arylphorin-like protein(aa) * Lsp1 bgr; * LARVAL SERUM PROTEIN BETA CHAIN PRECURSOR(aa) * 8e-06 AMYH_YEAST GLUCOAMYLASE S1/S2 PRECU[hemocyanin // HEMOCYANIN_2 //

CG6821 HAEMOCYAN] CG6821 LP03463 61A2-61A2 ID:108F5

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

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

+ translation_factor * kDa protein; Fun12p(aa) * 1e-120 YAD5_YEAST 112.3 KD PROTEIN IN PYK1-SNC1 INTERGENIC REGION * 1e-11 wacław * 3e-18 similar to initiation factor IF-[ELONGATNFC // NLS_BP // GTP_EFTU // AT] CG10840 LP03795

CG10840 63D2-63D2 ID:108G5

CG6981 + unknown * CG6981 LP03829 77A2-77A2 ID:108G7

+ enzyme Glycosyl transferase, similar to N-acetylgalactosaminyltransferase GLYC_TRANS, Glycos_transf_2,

CG8182 RICIN_B_LEC] CG8182 LP03835 ID:108G9

+ chaperone * DMTIDT4M_4 I(2)tid * 1e-22 MDJ1_YEAST MDJ1 PROTEIN PRECURSOR heat shock protein MDJ1 * 2e-42 Tid56 protein * 2e-42 YLW5_CAEEL HYPOTHETICAL 105.9 K[DnaJ_CXXCXGXXG // DNAJ_1 // DnaJ // DNAJ] CG7387 LP05202

CG7387 66B13-66B13 dup:1/2 ID:109C10

+ enzyme * beta-glucosidase(aa) * cardenolide 16-O-glucosylhydrolase(aa) * lactase phlorizinhydrolase(aa) * beta-galactosidase (EC 3.2.1.23) / glycosylceramidase [GLHYDRLASE1 // Glyco_hydro_1 // GLYCOSY] CG9701 LP05116 73B5-73B5

CG9701 ID:109C4

+ unknown * NG22(aa) * 3e-97 coded for by C. elegans cDNA CEESB82F; coded for by C. elegans cDNA CESE93F * 1e-79

CG11880 NG22 * CG11880 LP05177 99A1-99A1 dup:1/4 ID:109C9

+ endopeptidase * COAGULATION FACTOR X PRECURSOR (STUART FACTOR)(aa) * chymotrypsinogen B1(aa) * coagulation factor G beta chain precursor - horseshoe crab (Tachypleu [trypsin // CHYMOTRYPSIN // TRYPSIN_SER] CG10764

CG10764 LP05421 54C3-54C3 ID:109D4

+ unknown * 6e-35 C09B9.3 gene product * 5e-16 bestrophin homolog * 1e-106 vitelliform macular dystrophy (Best disease, CG6264 bestrophin) * 2e-48 RFP family member; t [Worm_family_8] CG6264 LP05915 85F13-85F14 dup:1/2 ID:109F6

+ endopeptidase * Ser12 * Ser6 * mas * DMSNAKE_2 snk [trypsin // CHYMOTRYPSIN // TRYPSIN_CATA] CG9675
 CG9675 LP05929 15A1-15A1 ID:109F7
 + structural_protein * peritrophin 1(aa) * 3e-08 Gasp precursor * 1e-07 R02F2.4 gene product * 2e-13 insect intestinal mucin
 CG10154 IIM22 CG10154 LP06444 70A8-70A8 ID:109G11
 CG4449 + unknown * CG4449 LP06117 97B1-94E9 ID:109G2
 CG6968 + unknown * [NLS_BP] CG6968 LP06178 78D-78D dup:1/3 ID:109G3
 CG14681 + unknown * 1e-08 H06A10.1 * 1E-168* CG14681 LP06211 86C2-86C2 ID:109G4
 + Ag5r unknown * antigen 5-related protein(aa) * Ag5r * 1e-156 antigen 5-related * 6e-33 antigen 5-related protein CG9538
 CG9538 LP06338 12F5-12F5 ID:109G8
 CG17836 + unknown * [NLS_BP] CG17836 SD01985 91D4-91D4 dup:2/2 ID:113D3
 + ligand_binding_or_carrier * ALPHA-TOCOPHEROL TRANSFER PROTEIN (ALPHA-TTP)(aa) * retinaldehyde-binding
 protein, CRALBP Peptide, * retinaldehyde-binding protein 1(aa) * tocophero [CRETINALDHBP // CRAL_TRIO] CG10026 SD02235
 CG10026 37E3-37E3 ID:113G7
 + enzyme * LCFACAS3; * LONG-CHAIN-FATTY-ACID--COA LIGASE (LONG-CHAIN ACYL-COA SYNTHETASE 4) (LACS
 4)(aa) * 1e-82 LCF4_YEAST LONG-CHAIN-FATTY-ACID--COA LIGASE ([AMP_BINDING // AMPBINDING // AMP-bindin]
 CG8732 CG8732 SD02373 44D4-44D ID:114A6
 + Hsf transcription_factor * DMHSPHEX_3 Hsf * 2e-23 HSF_YEAST HEAT SHOCK FACTOR PROTEIN (HSF) (HEAT SHOCK
 TRANSCRIPTION FACTOR) (HST * HSF_DROME HEAT SHOCK FACTOR PROTEIN (HSF) [HSFDOMAIN // HSF_ETS //
 CG5748 HSF_DNA-bind] CG5748 SD02833 55B5-55B5 ID:114G2
 + transporter * fatty acid transport protein 4; FATP4(aa) * 1e-64 very long-chain fatty acyl-CoA synthetase * 1e-129 coded for
 by C. elegans cDNA yk83h3.3; coded f [AMP_BINDING // AMP-binding // NLS_BP] CG7400 SD02910 31E5-31E6 dup:4/4
 CG7400 ID:114H2
 + electron_transfer * thioredoxin(aa) * 8e-20 TRX1_YEAST THIOREDOXIN I (TR-I) thioredoxin I - yeast (Sacc * 1e-17
 THIO_DROME THIOREDOXIN (DEADHEAD PROTEIN) thioredoxin-I [THIOREDOXIN // THIOREDOXIN_2 // thioered] CG3864
 CG3864 30C-30C2 ID:115A11
 + unknown * isopentenyl-diphosphate delta isomerase(aa) * 1e-44 IPPI_YEAST ISOPENTENYL-DIPHOSPHATE DELTA-
 CG5919 ISOMERASE (IPP ISOMERASE) * 3e-33 YMX3_CAEEL HYPOTHETIC CG5919 SD03046 93D4-93D4 ID:115A12
 CG13868 + unknown * 0.000000000000008* * CG13868 SD03066 56F17-57A dup:4/4 ID:115B4
 + I(2)not transmembrane_receptor * DMNOTB_2 I(2)not * Not22(aa) * putative Dol-P-Man dependent alpha(1-3)
 CG4084 mannosyltransferase involved in the biosynthesis of the lipid-linked oligosac CG4084 SD03142 59F5-59F5 ID:115C6
 + EG:63B12.12 unknown * 9e-50 /match=(desc: * 7e-40 inserted at base Both 5' and 3' ends of P element Inverse PCR *
 CG14818 CG14818 SD03316 2B14-2B14 dup:2/2 ID:115E7
 + enzyme * ripening-induced protein(aa) * 4e-20 putative protein * Strong similarity to auxin-induced protein from Vigna
 CG17221 radiata and a * ripening-induced pro [adh_zinc] CG17221 SD03451 23C5-23C5 ID:115G6
 + unknown * PBK1 protein(aa) * 5e-11 predicted using Genefinder; Weak similarity to Mouse CSA-19 protei * 2e-16 PBK1
 CG13096 protein * 7e-08 hypothetical protein [NLS_BP] CG13096 SD03546 29D1-29D1 ID:115H5

CG17436+ CG17436 ID:118A9
 CG1787 + enzyme CG1787 SD05059 ID:118C6
 + transporter * Ydr205wp(aa) * 5e-09 Zn/Cd resistance gene * 1e-06 cDNA EST yk447c2.5 comes from this gene; cDNA EST
 CG6672 co * 1e-06 zinc transporter ZnT-1 - mouse ZnT-1 [KININOGEN] CG6672 86D7-86D7 dup:1/2 ID:118G3
 CG6339 + motor_protein CG6339 SD05424 ID:118G5
 CG13384+ transporter putative amino acid transport protein AROMATIC_AA_PERMEASE_2 CG13384 SD05512 dup:2/4 ID:118H7
 + signal_transduction PLAP_MOUSE PHOSPHOLIPASE A-2-ACTIVATING PROTEIN GPROTEINBRPT, WD40,
 CG5105 WD40_REGION, WD_REPE] CG5105 SD05646 ID:119B6
 CG4822 + transporter * [ABC_TRANSPORTER // DA_BOX] CG4822 SD05880 21B-21B dup:6/6 ID:119E7
 + enzyme * PROBABLE SUCCINYL-COA:3-KETOACID-COENZYME A TRANSFERASE PRECURSOR (3-OXOACID COA-
 TRANSFERASE)(aa) * 3-oxoacid CoA transferase precursor; succinyl-Co [COA_TRANSF_1 // COA_TRANSF_2 // CoA_tra]
 CG1140 CG1140 GH01464 62B11-62B11 ID:30D6
 CG6210 + unknown * CG6210 GH01813 68A7-68A7 ID:30G1
 + enzyme * antennal-specific short-chain dehydrogenase/reductase(aa) * 4e-12 YM71_YEAST HYPOTHETICAL
 OXIDOREDUCTASE IN MRPL44-MTF1 INTERGENIC REGION * 8e-08 Si [GDHRDH // adh_short] CG3301 GH01837 93D4-93D4
 CG3301 ID:30G3
 + unknown * dipeptidyl peptidase III(aa) * 1e-109 hypothetical protein YOL057w - yeast (Saccharomyces cerevisiae) * 1e-105
 CG7415 similar to WD domain, G-beta repeat; CG7415 GH01916 84F14-84F15 dup:1/2 ID:30G7
 + unknown * 1e-25 kraken * 3e-13 dJ222E13.1 (N-terminal part of novel protein with some similarit * 7e-05 TPES_PSEPU
 TROPINESTERASE (ATROPINESTERASE) (ATROPINE [ESTERASE // abhydrolase] CG5707 GH02816 62D2-62D2 dup:2/2
 CG5707 ID:31E3
 + BcDNA:GH03502 unknown * unknown(aa) * 3e-55 YII3_YEAST HYPOTHETICAL 41.9 KD PROTEIN IN SDS3-TSH1
 CG5629 INTERGENIC REGION * 1e-75 inserted at base Both 5' and 3' ends of P element CG5629 GH03502 91F4-91F4 dup:1/2 ID:32A8
 CG7738 + CG7738 dup:2/2 ID:32C2
 + translation_factor * Eif4E * 1e-23 IF4E_YEAST EUKARYOTIC TRANSLATION INITIATION FACTOR 4E (EIF-4E) (EIF4E)
 CG8023 (MRNA CA * 2e-56 IF4E_DROME EUKARYOTIC TRANSLATION INITIATION [IF4E] CG8023 GH04024 66C-66C ID:32D6
 + 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
 + BcDNA:GH04245 motor_protein * contains TPR domain-like repeats(aa) * UDP-N-ACETYLGLUCOSAMINE--PEPTIDE N-
 ACETYLGLUCOSAMINYLTRANSFERASE KD SUBUNIT (O-GLCNAC TRANSFERASE [TPR_REGION // TPR_REPEAT // TPR //
 CG10392 NLS_] CG10392 GH04245 41A1-41A2 dup:3/4 ID:32E11
 + serpin * serine protease inhibitor(aa) * OVALBUMIN (PLAKALBUMIN) (ALLERGEN GAL D 2) (GAL D II)(aa) *
 CG9456 LEUKOCYTE ELASTASE INHIBITOR (LEI) (LEUCOCYTE NEUTRAL P [serpin] CG9456 GH04125 42C8-42C8 dup:2/2 ID:32E4
 + 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
 CG17259 GH04194 23C4-23C5 dup:2/2 ID:32E7

+ enzyme * aminomethyltransferase (glycine cleavage system protein T)(aa) * 2e-68 glycine cleavage T protein * 7e-91 partial
 CG6415 CDS, * 1e-97 GCST_HUMAN AMINOMETHY CG6415 GH04419 32A2-32A2 dup:1/2 ID:32G8
 + unknown * COP-COATED VESICLE MEMBRANE PROTEIN P24 PRECURSOR (P24A) (RNP21.4)(aa) * 3e-21
 EM24_YEAST ENDOSOMAL P24B PROTEIN PRECURSOR (24 KD ENOMEMBRANE PROTE [EMP24_GP25L] CG3564
 CG3564 GH04989 4C4-4C4 ID:33D2
 + endopeptidase * DMSER2_7 Ser99Db * 2e-45 serine proteinase (EC 3.4.21.-) precursor - fruit fly (Drosophila melanogaster) *
 9e-24 similar to peptidase family S1 (tr[trypsin // CHYMOTRYPSIN // TRYPSIN_SER] CG10472 GH05321 65A2-65A2 dup:2/2
 CG10472 ID:33E11
 + enzyme * HYPOTHETICAL ALDEHYDE-DEHYDROGENASE LIKE PROTEIN F01F1.6(aa) * antiquitin=26g turgor protein
 homolog {C-terminal} intestinal mucosa, Peptide Partial [aldedh // ALDEHYDE_DEHYDR_GLU] CG9629 GH05218 76A3-76A3
 CG9629 dup:2/2 ID:33E7
 CG5867 + BcDNA:GH05536 unknown * 0.0000002 * 3e-06 DMRNAPER_2 anon-3B1.2 * * CG5867 GH05588 34A10-34A11 ID:33G5
 + translation_factor * 2e-16 hypothetical protein YOR261c - yeast (Saccharomyces cerevisiae) * 1e-17 PRSC_DROME 26S
 PROTEASOME REGULATORY SUBUNIT S12 (PROTEASOME SUBUNIT P [Mov34 // MPN_DOMAIN] CG9769 GH05855 82D6-
 CG9769 82D6 ID:34A2
 + endopeptidase * human factor XII(aa) * 7e-31 masquerade precursor - fruit fly (Drosophila melanogaster) * 2e-05 similar to
 Trypsin * 5e-25 MCT6_MOUSE MAST CELL PRO [trypsin // CHYMOTRYPSIN // TRYPSIN_CATA] CG6639 GH06092 36C2-36C2
 CG6639 ID:34C3
 + enzyme * 3e-40 4-nitrophenylphosphatase (EC 3.1.3.41) - yeast (Saccharomyces cerevisiae) * 6e-26 by content; 1-meth *
 CG5567 4e-52 contains similarity to 4-nitrophenylphosphatase CG5567 GH06744 75A4-75A4 ID:34G7
 CG3752 + enzyme CG3752 dup:1/2 ID:34H5
 CG13480 + unknown * CG13480 GH07663 70E4-70E4 dup:2/2 ID:35E7
 CG8701 + unknown * CG8701 GH07855 44B9-44B9 ID:35G4
 CG3223 + unknown * [UBA // PHOSPHOPANTETHEINE] CG3223 GH08043 84E6-84E6 dup:1/2 ID:35H7
 + Cct5 chaperone * 1e-179 chaperonin TCP1 epsilon - yeast (Saccharomyces cerevisiae) * 7e-63 TCPA_DROME T-COMPLEX
 PROTEIN 1, ALPHA SUBUNIT (TCP-1-ALPHA) (CCT-ALPHA) * [TCP1_1 // TCP1_3 // TCOMPLEXTCP1 // CHA] CG8439
 CG8439 GH10122 48F1-48F1 ID:37F2
 + 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
 CG17309 86E18-86E19 dup:1/2 ID:37G1
 + norpA enzyme * contains similarity to phosphatidylinositol-specific phospholipase C, X domains (Pfam: PI-PLC-X.hmm, score:
 CG3620 200.23)(aa) * phospholipase C beta-4(aa) * CG3620 GH10316 4B6-4B6 dup:2/2 ID:37G8
 + ligand_binding_or_carrier * 1e-31 peptidyl-dipeptidase A (EC 3.4.15.1) 67k precursor - fruit fly (Drosophila me * 6e-09
 CG9047 coded for by C. elegans cDNA yk27b10.3; coded for by C. [PRO_RICH] CG9047 GH10774 60E3-60E3 dup:1/3 ID:38C11
 + endopeptidase * 5e-32 Similarity to human placental protein * 2e-42 glucocorticoid-sensitive T cell-specific protein - mouse *
 CG2145 5e-41 placental protein (serine protease) CG2145 GH10845 10A1-10A1 dup:2/2 ID:38D4

+ enzyme * DEOXYRIBONUCLEASE II PRECURSOR (DNASE II) (ACID DNASE) (LYSOSOMAL DNASE II)(aa) * 2e-48
 CG7780 YKU5_CAEEL HYPOTHETICAL 41.5 KD PROTEIN C07B5.5 IN CHROMOSOM CG7780 GH10876 90D-90D ID:38D8
 + receptor * glutaminyl cyclase(aa) * 3e-32 YFI8_YEAST HYPOTHETICAL 41.0 KD PROTEIN IN UGS1-FAB1 INTERGENIC
 CG10487 REGION * 3e-62 similar to guanylate cyclase; cDNA EST CG10487 GH11174 64F4-64F4 ID:38F11
 + transcription_factor * zinc finger protein(aa) * patched related protein translocated in renal cancer(aa) * protein(aa) *
 required to degrade misfolded ER luminal and i[zf-C3HC4 // PRO_RICH // ZF_RING] CG1937 GH11117 100E3-100E3 dup:1/2
 CG1937 ID:38F5
 + BcDNA:GH11322 cell_adhesion * Pxn * 6e-20 roundabout * 2e-15 hemicentin precursor * 1e-10 rig-1 protein [ig // fn3] CG16857
 CG16857 GH11322 24E4-24E4 dup:2/5 ID:38G12
 CG10599+ unknown * [NLS_BP] CG10599 GH11223 37B3-37B3 ID:38G3
 + flp signal_transduction * 2e-35 IRS1_MOUSE INSULIN RECEPTOR SUBSTRATE-1 insulin receptor sub * 9e-35
 IRS1_HUMAN INSULIN RECEPTOR SUBSTRATE-1 (IRS-1) insulin * 2e-35 IRS1_RAT [INSULINRSI // PH_DOMAIN] CG5686
 CG5686 GH11263 31C1-31C3 ID:38G6
 + unknown * unknown(aa) * 4e-12 putative Bop-like zinc finger protein * 1e-19 DMC103B4 [IPNS_1 // CYTOCHROME_C]
 CG8503 CG8503 GH11294 50E8-50E8 ID:38G9
 CG3624 + cell_adhesion * [ig] CG3624 GH11432 58D7-58D7 dup:2/2 ID:38H12
 + enzyme * HYPOTHETICAL 37.1 KD PROTEIN ZK892.4 IN CHROMOSOME III(aa) * 3e-53 similar to L-carnitine
 CG9319 dehydratase; cDNA EST yk206h7.5 comes from * 9e-87 alpha-m CG9319 GH11368 38E4-38E4 ID:38H4
 CG17567+ unknown * 1E-78* * CG17567 GH11551 37C-37C ID:39A10
 CG12907+ unknown * 1E-145* * [PRO_RICH // NLS_BP] CG12907 GH11521 47A-47A ID:39A8
 + enzyme * contains similarity to CDP-alcohol phosphotransferases(aa) * aminoalcoholphosphotransferase(aa) * 4e-24 sn-
 1,2-diacylglycerol cholinephosphotransf [CDP_ALCOHOL_P_TRANSF // CDP_ALCOHOL_P_T] CG7149 GH11618 28C8-28C9
 CG7149 ID:39B5
 + unknown * HSPC017(aa) * 5e-35 YOY9_CAEEL PUTATIVE UBIQUINONE BIOSYNTHESIS METHLYTRANSFERASE
 CG12162 ZK652.9 * 4e-17 apaG protein * APAG_ECOLI APAG PROTEIN apaG prote CG12162 GH11824 83A8-83A9 ID:39C7
 + transporter * 2e-50 Na(+)-dependent inorganic phosphate cotransporter mela * 7e-54 YLD2_CAEEL HYPOTHETICAL 52.7
 CG15095 KD PROTEIN C38C10.2 IN CHROMOSOME III * 2e-45 NPT1 [sugar_tr] CG15095 GH11849 55F1-55F1 ID:39C9
 CG9284 + unknown * CG9284 GH11908 58A2-58A2 ID:39D1
 + unknown * 4-HYDROXYPHENYLPYRUVATE DIOXYGENASE (4HPPD) (HPD)(aa) * 4-hydroxyphenylpyruvate-
 dioxygenase(aa) * 1e-139 HPPD_CAEEL 4-HYDROXYPHENYLPYRUVATE DIOXYGE CG11796 GH11957 77C1-77C1 dup:2/2
 CG11796 ID:39D6
 CG10841+ unknown * CG10841 GH12158 87F6-87F6 dup:2/2 ID:39E9
 CG17841+ BcDNA:GH12326 unknown * CG17841 GH12326 9B14-9B15 dup:2/2 ID:39F7
 + 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
 CG1435 GH12350 7A4-7A4 ID:39F9

+ peptidase * PUTATIVE AMINOPEPTIDASE ZK353.6 IN CHROMOSOME III(aa) * Chain A, Bovine Lens Leucine
 CG4750 Aminopeptidase Complexed With L-Leucine Phosphonic Acid(aa) * [Peptidase_M17] CG4750 GH12543 53C-53C ID:39G10
 + enzyme * D-ASPARTATE OXIDASE (DASOX) (DDO)(aa) * D-AMINO ACID OXIDASE (DAMOX) (DAO) (DAAO)(aa) *
 similar to D-amino acid oxidase(aa) * D-aspartate oxidase i [DAO // FMOXYGENASE // PROTEIN_KINASE_AT] CG11236
 CG11236 GH12548 28E7-28E7 ID:39G11
 + Dat ligand_binding_or_carrier * DMNAT1_2 Aanat1 * N-acetyltransferase(aa) * aralkylamine N-acetyltransferase (EC
 CG3318 2.3.1.87) - fruit fly (Drosophila melano * CG3318 GH12636 60B9-60B9 ID:39H12
 + transporter * 5e-75 Na(+)-dependent inorganic phosphate cotransporter mela * 7e-67 YLD2_CAEEL HYPOTHETICAL 52.7
 CG3036 KD PROTEIN C38C10.2 IN CHROMOSOME III * 4e-46 NPT1 [NLS_BP] CG3036 GH13494 26D1-26D1 dup:3/4 ID:40F10
 + OstStt3 enzyme * STT3_YEAST OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT STT3 * STT3_CAEEL
 OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT HOMOLOG * STT3_MOUSE OLIGOSACCHARYL
 CG7748 [ATPASE_ALPHA_BETA] CG7748 GH13452 98F6-98F6 ID:40F6
 + Pgd enzyme * 6-phosphogluconate dehydrogenase(aa) * DMPGD_1 Pgd * 1e-177 6PG1_YEAST 6-PHOSPHOGLUCONATE
 DEHYDROGENASE, DECARBOXYLATING * 6PGD_DROME 6-PHOSPHOGLU [6PGD // 6PGDHDRGNASE] CG3724 GH13486
 CG3724 2D6-2D6 ID:40F9
 + peptidase * 9e-99 AMP1_YEAST METHIONINE AMINOPEPTIDASE PRECURSOR (METAP 1) (PEPTIDASE M 1) (MAP *
 1e-141 AMP1_HUMAN PUTATIVE METHIONINE AMINOPEPTIDASE (METAP 1) [Peptidase_M24 // MAPEPTIDASE // MAP_1]
 CG13630 CG13630 GH13823 96A20-96A20 ID:40H10
 + 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
 + Odc1 enzyme * ornithine decarboxylase(aa) * ornithine decarboxylase(aa) * Ornithine decarboxylase; Spe1p(aa) * ornithine
 CG8721 decarboxylase(aa) [ODR_DC_2_1 // ODR_DC_2_2 // Orn_DAP_Arg] CG8721 GH13851 43F9-44A1 dup:2/2 ID:41A4
 + unknown * BLASTX 9.9E-08 Human mRNA for hU1-70K snRNP protein (RNP8).(dna) * * [NLS_BP] CG12239 GH14380
 CG12239 5B8-5B8 ID:41D11
 CG7567 + unknown * CG7567 GH14364 99B5-99B5 ID:41D8
 + electron_transfer * 9e-06 PDI_YEAST PROTEIN DISULFIDE ISOMERASE PRECURSOR (PDI) / DOLICHYL-
 DIPHOSPHOOLIGOS * 2e-08 PDI_DROME PROTEIN DISULFIDE ISOMERASE PRECURSOR (PDI) [THIOREDOXIN //
 CG3315 THIOREDOXIN_2 // thioered] CG3315 GH14562 4F2-4F2 ID:41F1
 + enzyme * DMGST_3 Gsd1 * 2e-10 probable membrane protein YLL060c - yeast (Saccharomyces cerevisiae) * 3e-37
 CG5164 GTT1_DROME GLUTATHIONE S-TRANSFERASE 1-1 (CLASS-T [GST] CG5164 GH14654 55C9-55C9 ID:41F10
 + structural_protein * 3e-05 MAGE tumor antigen D1 * 5e-13 FMRA_ATEL ANTHO-RFAMIDE NEUROPEPTIDE
 PRECURSOR Antho-RFa * LWamide neuropeptide precursor protein * 33K hydroxy CG11395 GH14572 54A2-54A2 dup:2/2
 CG11395 ID:41F2
 + EG:86E4.2 enzyme * 6e-67 YH04_YEAST HYPOTHETICAL 91.2 KD PROTEIN IN RPS7A-SCH9 INTERGENIC REGION *
 /match=(desc;; /ma * 1e-157 similar to mannosyl-oligosaccharide alph [GLYHDLASE47] CG3810 GH14693 2B15-2B16 dup:1/2
 CG3810 ID:41G2
 CG8453 + Cyp6g1 cytochrome_P450 * CYP6-like microsomal cytochrome P450 * 1e-33 YRV5_CAEEL PUTATIVE CYTOCHROME P450

T10B9.5 IN CHROMOSOME II * 1e-59 cytochrome P450 3A11 - mouse c[EP450II // p450 // P450 // MITP450 // C] CG8453
GH14851 48F1-48F1 dup:2/4 ID:41H5
+ * ribosomal protein L24(aa) * Ribosomal protein L24B (rp29) (YL21) (L30B); Rpl24bp(aa) * 60S RIBOSOMAL PROTEIN
CG9282 L24 (L30)(aa) * Similar to 60S ribosoma [Ribosomal_L24e // NLS_BP] CG9282 34B6-34B6 dup:1/5 ID:42A12
+ enzyme * Adh-Finnegan(aa) * fat body protein 2(aa) * development-specific 25K protein - flesh fly (Sarcophaga
peregrina)(aa) * 7e-09 YM71_YEAST HYPOTHETICAL [adh_short // ADH_SHORT // adh_short_C] CG4842 GH15220 72F1-72F1
CG4842 ID:42B10
+ cell_cycle_regulator * 6e-16 YG13_YEAST CULLIN B hypothetical protein YGR003w - yeas * 2e-71 LI19_DROME LIN-19
HOMOLOG PROTEIN lin19 protein * 1e-173 CUL5_CAEEL CUL-5 P[CULLIN_2 // NLS_BP // ANTIFREEZEI // Cu] CG1401
CG1401 GH15159 98F10-98F10 ID:42B5
+ transcription_factor * HYPOTHETICAL 46.7 KD PROTEIN C50C3.8 IN CHROMOSOME III(aa) * hypothetical protein(aa) *
CG11275 intracisternal A particle-promoted polypeptide(aa) * 2e-08 [BTB] CG11275 GH15267 58C5-58C5 ID:42C2
CG3510 + CycB cell_cycle_regulator G2/MITOTIC-SPECIFIC CYCLIN B CYCLINS, cyclin CG3510 dup:2/4 ID:43B3
+ enzyme * 1e-34 GLO2_YEAST HYDROXYACYLGLUTATHIONE HYDROLASE ISOZYME (GLYOXALASE II) (GLX II) * 8e-
CG4365 60 similar to Metallo-beta-lactamase superfamily el * 3e-85 [lactamase_B] CG4365 77E-77E dup:1/3 ID:43C6
+ Mpcp transporter * 2e-71 YEO3_YEAST PUTATIVE MITOCHONDRIAL CARRIER YER053C hypoth * phosphate transporter
precursor melanogas * 1e-132 MPCP_CAEEL MITOCHONDRIAL PHOSPHA [mito_carr // RCC1_2 // MITOCH_CARRIER]
CG4994 CG4994 LD23031 70E-70E dup:3/4 ID:43D12
+ unknown * myelodysplasia/myeloid leukemia factor 1(aa) * Y17G7B.17(aa) * 6e-27 myeloid leukemia factor
CG8295 myelodysplasia/myel * t(3;5)(q25.1;p34) fusion gene CG8295 LD22883 52D11-52D11 dup:2/2 ID:43D3
+ Cyt-c2 electron_transfer * DMCYCDC4_4 Cyt-c2 * 9e-36 pdb|2YCC| Cytochrome c (Isozyme 1) (Oxidized) (Mutant With Cys
Replaced By Thr) (C102T * 1e-59 CYC2_DROME CYTOCHROME C-2 c [CYTCHRMEDIA // cytochrome_c] CG17903 LD23501
CG17903 36A7-36A7 ID:43F5
+ mus210 DNA_repair_protein * DNA-REPAIR PROTEIN COMPLEMENTING XP-C CELLS HOMOLOG (XERODERMA
PIGMENTOSUM GROUP C COMPLEMENTING PROTEIN HOMOLOG) (XPCDM)(aa) * DMXPCCF_2 Xpcc * 4e- [MYB_1 //
CG8153 NLS_BP] CG8153 51F4-51F5 dup:1/3 ID:43G11
+ dbp unknown * DMDRIBBLE dbp * dribble(aa) * 9e-98 YCF9_YEAST HYPOTHETICAL 37.2 KD PROTEIN IN CHA1-PRD1
CG4258 INTERGENIC REGION * 5e-88 similar to human REV interacting CG4258 LD24634 21E3-21E3 ID:43G5
CG3167 + unknown * CG3167 LD24895 60B1-60B1 ID:43G9
CG13322 + unknown CG13322 LD26432 dup:2/3 ID:44D11
CG2994 + CG2994 LD26546 dup:4/4 ID:44E6
+ signal_transduction homology to actin interacting protein 1 and WD repeat-containing protein 1 GPROTEINBRPT, WD40,
CG10724 WD40_REGION CG10724 LD27045 dup:2/3 ID:44G2
+ Ac3 enzyme adenylyl cyclase isoform DAC3 [Drosophila melanogaster] GUANYLATE_CYCLASES,
CG1506 GUANYLATE_CYCLASES_] CG1506 LD27878 dup:2/2 ID:45B12
+ unknown * 5e-24 hypothetical protein YDL087c - yeast (Saccharomyces cerevisiae) * 4e-34 YP68_CAEEL
CG7564 HYPOTHETICAL 37.0 KD PROTEIN IN CHROMOSOME II (U2 * 2e-23 p [NLS_BP] CG7564 LD28402 74D1-74D1 dup:4/4

ID:45E12
+ Gdh enzyme * 7e-28 glutamate dehydrogenase dehyd * glutamate dehydrogenase (NAD(P)+) * 1e-180 Similarity to Drosophila Glutamate dehydrogenase cDNA * DHE3_MOUSE [GLFV_DEHYDROGENASE // GLFDHDRGNASE // G] CG5320 95C-95C13

CG5320 dup:2/2 ID:45F11

CG4300 + unknown spermine synthase SAM_BIND CG4300 LD28457 ID:45F5
+ chaperone * 1e-07 STI1_YEAST HEAT SHOCK PROTEIN STI1 stress-induced protein * 1e-08 Hsp70/Hsp90 organizing protein homolog * 1e-54 similar to TPR Domain (2 doma [RNP_1 // TPR_REGION // TPR_REPEAT // TP] CG2947 3F6-3F6

CG2947 dup:3/4 ID:45F9

CG16944+ sesB transporter ADP/ATP translocase ADPTRNSLCASE, MITOCARRIER CG16944 ID:46A4

CG7563 + calpain CG7563 dup:1/4 ID:46C8

CG10928+ CG10928 LD29844 dup:3/3 ID:46E11
+ transporter * ATP-DEPENDENT RNA HELICASE GLH-1(aa) * 1e-08 EAST_DROME SERINE PROTEASE EASTER

CG3820 PRECURSOR serine protein * 6e-22 similar to nucleoporin; cDNA EST com CG3820 LD29808 59B4-59B4 dup:3/4 ID:46E7

CG9107 + CG9107 LD29822 dup:3/3 ID:46E8
+ Dp1 DNA_binding * 2e-44 SCP160 * 4e-09 KH-domain putative RNA binding protein * 951003: Homology with human lipoprotein-binding protein (PIR Acc. * high density lipop [KH-domain // KH_DOMAIN // NLS_BP] CG5170 LD29992 55C10-55C11

CG5170 dup:1/5 ID:46G2
+ transcription_factor_binding * 4e-71 YER2_YEAST HYPOTHETICAL 62.3 KD PROTEIN IN PTP3-ILV1 INTERGENIC REGION * 9e-94 Similarity to Yeast hypothetical protein YER2 (SW:YER2_YEAS[WD40_REGION // WD_REPEATS // WD40]

CG2260 LD30339 7D11-7D11 ID:46H10
+ chaperone It encodes a chaperone involved in proteolysis and peptidolysis which is a component of the mitochondrion

CG4164 DNAJPROTEIN, DNAJ_1, DNAJ_2, DnaJ CG4164 LD30318 ID:46H8
+ SNF4Agamma protein_kinase * SNF4A ggr; * protein kinase protein serine/threonine kinase) map_position:93C * 8e-29 SNF4_YEAST NUCLEAR PROTEIN SNF4 (REGULATORY PROTEIN CAT3) * 1 [CBS // SNF4_REP // NLS_BP] CG17299

CG17299LD30628 93C4-95F5 dup:1/11 ID:47C1
+ BcDNA:GH04637 protein_phosphatase * Sbf * Yjr110wp(aa) * myotubularin related protein 7(aa) * similar to FYVE zinc finger; cDNA EST yk416b6.5 comes from this gene; cDNA E[TYR_PHOSPHATASE_1 // TYR_PHOSPHATASE_2] CG3530 LD31402

CG3530 59D9-59D10 dup:1/3 ID:47G5
+ enzyme * cystathionine beta-synthetase; CBS(aa) * BLASTX 8.7E-06 CYS4|Cystathionine beta-synthase (beta-CTSase),

CG1753 converts serine and homocysteine to cystathi [CBS // SNF4_REP // S_T_dehydratase // C] CG1753 LD32051 19E6-19E6 ID:48A9
+ unknown * 1e-142 inserted at base Both 5' and 3' ends of P element Inverse PCR * * CG15893 LD32923 5E4-5E4 dup:2/2

CG15893ID:48E5
+ unknown * protein(aa) * 3e-09 PC11_YEAST PCF11 PROTEIN hypothetical protein YDR228c - * 3e-21 YRR2_CAEEEL HYPOTHETICAL 91.1 KD PROTEIN R144.2 IN CHROMOSOME III [PRENYLATION // PRO_RICH // NLS_BP // CY] CG10228

CG10228LD33132 51D2-51D2 ID:48G2

CG5793 + unknown * 5-oxo-1,2,5-tricarboxylic-3-penten acid decarboxilase/isomer(aa) * 3e-26 YNQ8_YEAST HYPOTHETICAL 28.8

KD PROTEIN IN PSD1-SKO1 INTERGENIC REGION * 9e CG5793 LD33646 95F1-95F1 ID:49A1
 + enzyme * 2e-60 COXX_YEAST CYTOCHROME C OXIDASE ASSEMBLY PROTEIN COX10 PRECURSOR * 5e-94 heme
 A: farnesyltransferase * 4e-46 putative heme A:farnesyltransferase [COX10_ctaB_cyoE // COX10_CTAB_CYOE] CG5037 LD33876
 CG5037 31D9-31D9 dup:3/3 ID:49B6
 + transporter * MITOCHONDRIAL IMPORT RECEPTOR SUBUNIT TOM20 HOMOLOG (MITOCHONDRIAL KD OUTER
 MEMBRANE PROTEIN) (OUTER MITOCHONDRIAL MEMBRANE RECEPTOR TOM20)(aa) * 2e [NLS_BP] CG7654 LD34461
 CG7654 76E2-76E2 ID:49D10
 + peptidase * PROBABLE CYTOSOL AMINOPEPTIDASE (LEUCINE AMINOPEPTIDASE) (LAP)(aa) * leucine
 aminopeptidase(aa) * PUTATIVE AMINOPEPTIDASE ZK353.6 IN CHROMOSOME III([LAMNOPPTDASE // RCC1_2 //
 CG7340 Peptidase_M17] CG7340 LD34492 87D7-88E1 ID:49D12
 + Keren signal_transduction * DMSH2P_2 spi * 6e-39 SPIT_DROME PROTEIN SPITZ PRECURSOR probable EGF-like gro *
 8e-07 heregulin precursor, splice form alpha - human * 5e-08 neu d[EGF_1 // EGF // EGF_2 // PRO_RICH] CG8056 LD34429
 CG8056 74E3-74E4 dup:2/3 ID:49D9
 + motor_protein * 7e-09 by content; 1-meth * 2e-07 homeotic most like HMPB_DROME: homeotic proboscipedia protein * 9e-
 07 Williams-Beuren syndrome deletion transcript [PHD // NLS_BP // ATP_GTP_A] CG8677 LD34730 39C1-39C1 dup:5/5
 CG8677 ID:49E10
 + enzyme * nuclear protein methyltransferase (mono- and asymmetrically dimethylating enzyme); Hmt1p(aa) * protein N-
 CG6563 methyltransferase 3(aa) * protein N-methy [SAM_BIND] CG6563 LD34544 88E8-88E8 dup:2/2 ID:49E3
 + ligand_binding_or_carrier * 2e-05 odorant-binding protein Rpal2' palmaru * * [PBP_GOBP] CG13421 GH01026 57A6-57A6
 CG13421 ID:54A2
 + enzyme_inhibitor * 7B2(aa) * cDNA EST comes from this gene(aa) * 2e-22 cDNA EST comes from this gene * CG1168
 CG1168 GH01053 83A5-83A5 ID:54A6
 CG7066 + unknown * 5e-14 Y256_HUMAN HYPOTHETICAL PROTEIN KIA * * CG7066 GH01354 66C5-66C6 ID:54C12
 + syt transporter * similar to synaptotagmin(aa) * SYNAPTOTAGMIN (P65)(aa) * 2e-09 probable membrane protein YOR086c -
 yeast (Saccharomyces cerevisiae) * 3e-49 SYT1_CAE [C2_DOMAIN_1 // SYNAPTOTAGMIN // C2 // C2] CG3139 GH01240 23B1-
 CG3139 23B2 dup:1/4 ID:54C2
 + structural_protein * Peritrophin-A * cDNA EST comes from this gene; cDNA EST yk369a9.5 comes from this gene; cDNA
 CG11142 EST yk438c12.3 comes from this gene; cDNA EST yk438c12 CG11142 GH01453 26A-26A ID:54D11
 + RecQ5 DNA_repair_protein * Recq helicase 5(aa) * Recq helicase 5(aa) * 3e-73 SGS1_YEAST HELICASE SGS1 (HELICASE
 TPS1) DNA helicase TP * 1e-06 RM62_DROME PUTATIVE ATP-DEPENDENT [helicase_C // HELICASE // DEAD] CG4879
 CG4879 GH01404 70E6-70E7 ID:54D5
 CG1545 + unknown * CG1545 GH01560 10A-10A dup:2/2 ID:54E10
 CG10680+ * CG10680 38B1-38B1 dup:2/3 ID:54F11
 CG11446+ unknown * CG11446 GH01717 2A3-2A3 ID:54G6
 + enzyme * alkaline phosphatase(aa) * MEMBRANE-BOUND ALKALINE PHOSPHATASE PRECURSOR (M-ALP)(aa) *
 DMALKPHOS_2 Aph-4 * intestinal alkaline phosphatase VII; IAP [ALKALINE_PHOSPHATASE // ALKPHPTASE //] CG3290
 CG3290 GH01891 58C7-58C7 ID:54H10

CG3955 + unknown * CG3955 GH01933 49F5-49F5 ID:54H12

CG5588 + Mtl enzyme CG5588 GH01976 ID:55A4
+ * MYO-INOSITOL-1(OR 4)-MONOPHOSPHATASE (IMP) (INOSITOL MONOPHOSPHATASE) (LITHIUM-SENSITIVE MYO-INOSITOL MONOPHOSPHATASE A1)(aa) * 2e-41 hypothetical p [inositol_P // INOSHPHTASE // IMP_1 //] CG9391

CG9391 78C7-78C7 dup:2/2 ID:55B1
+ enzyme * DMPGMII_3 agr;-Man-II * alpha-mannosidase(aa) * alpha-mannosidase (EC 3.2.1.24) precursor - human(aa) *

CG9466 LYSOSOMAL ALPHA-MANNOSIDASE PRECURSOR (MANN [Glyco_hydro_38] CG9466 GH02475 29F1-29F1 ID:55C11
+ enzyme * 1e-47 CACP_YEAST CARNITINE O-ACETYLTRANSFERASE PRECURSOR (CARNITINE ACETYLASE) * 4e-

CG12428 37 choline acetyltransferase * 3e-66 similar to Carnitine acyltr [Carn_acyltransf] CG12428 GH02484 98A8-98A9 dup:1/4 ID:55C12
+ unknown * 9E-36* 7e-34 cDNA EST comes from this gene; cDNA EST co * 3e-59 cytoplasmic protein Ndr1 * 2e-60 RTP

CG15668 nickel-specific inductio CG15668 GH02495 57E8-57E dup:2/4 ID:55D1
+ enzyme * Sar oxidase(aa) * * 7e-63 cDNA EST comes from this gene; cDNA EST co * 2e-41 unknown protein CG3270

CG3270 GH02863 42C6-42C6 dup:2/2 ID:55E5
+ EG:100G10.2 unknown * by motif; 1-match_description=ATP/GTP-binding site motif A (P-loop).; by match; 2-

CG2681 match_accession=SPTRE...(aa) * by motif; * 2e-10 seven-in-absentia CG2681 GH02982 3B5-3B5 ID:55F2

CG18249+ unknown * CG18249 GH03003 84F5-84F5 ID:55F4

CG16772+ unknown * CG16772 GH03035 38B1-38B1 ID:55F6

CG9005 + cell_adhesion * 0.0000000000000000003* * CG9005 GH03037 48B1-48B2 dup:2/5 ID:55F7
+ serpin * THYROXINE-BINDING GLOBULIN PRECURSOR (T4-BINDING GLOBULIN)(aa) * alpha-1-antichymotrypsin

CG9334 precursor(aa) * 8e-42 Similar to serine protease inhibito [serpin] CG9334 GH03095 38E9-38E9 ID:55G1

CG8620 + unknown * CG8620 GH03505 65E6-65E6 ID:55H11

CG12106+ unknown * 1e-05 bup=5'of bmi-1 proviral insertion locus Peptide, s * * CG12106 GH03263 8D2-8D2 ID:55H2
+ DNA_repair_protein * putative antisense basic fibroblast growth factor(aa) * antisense basic fibroblast growth factor B(aa) *

CG8128 4e-30 GFG_RAT PROTEIN GFG antisense basic f [MUTT // mutT // MUTTDOMAIN] CG8128 GH03273 13E13-13E14 ID:55H3

CG2767 + enzyme aldose reductase ALDOKETO_REDUCTASE_1, ALDOKETO_REDUCTASE] CG2767 ID:56C2
+ Bc larval_serum_protein * pro-phenol oxidase A1 * pro-phenol oxidase subunit 1; proPO-p1 * DMORA_2 Bc *

CG5779 prophenoloxidase [TYROSINASE_2 // hemocyanin // HEMOCYANI] CG5779 GH04080 55A1-55A1 dup:2/2 ID:56E11
+ unknown * 1e-35 hypothetical protein YDR531w - yeast (Saccharomyces cerevisiae) (U * 3e-27 No definition line found *

CG5725 5e-42 putative protein * coded for by C. CG5725 GH04001 77B6-77B6 dup:3/3 ID:56E4
+ enzyme * alkaline phosphatase(aa) * soluble alkaline phosphatase(aa) * 1e-27 repressible alkaline phosphatase (EC 3.1.3.1) * 2e-96 alkaline phosphatase (EC [ALKALINE_PHOSPHATASE // ALKPHPTASE //] CG1809 GH04113 45F3-45F3

CG1809 ID:56F2
+ ligand_binding_or_carrier * 3e-07 similar to agrin and follistatin; egf-like repeats * 2e-08 FSA_MOUSE FOLLISTATIN

CG12955 PRECURSOR (FS) (ACTIVIN-BINDING PROTEIN) * 9e-08 follistatin [kazal] CG12955 GH04473 51E9-51E9 ID:57A2
+ transporter * 3e-23 YNK1_YEAST HYPOTHETICAL 80.0 KD PROTEIN IN POL1-RAS2 INTERGENIC REGION * 4e-58

CG8785 cDNA EST comes from this gene; cDNA EST * 7e-21 putative amino [AROMATIC_AA_PERMEASE_2] CG8785 GH04538 49B7-

49B7 ID:57A5
+ RNA_binding * Putative RNA helicase(aa) * BRR2_YEAST PRE-MRNA SPLICING HELICASE BRR2 hypothetical * 1e-23
mus308 * similar to Helicases conserved C-terminal doma [EF_HAND // HELICASE // DEAD // ATP_GTP_] CG5931 GH04577

CG5931 72C1-72C1 dup:1/2 ID:57B1
+ enzyme * DMALKPHOS_2 Aph-4 * 7e-27 PPB_YEAST REPRESSIBLE ALKALINE PHOSPHATASE PRECURSOR al * 2e-
86 alkaline phosphatase * 1e-100 PPBT_MOUSE ALKALINE PHOSPHAT [ALKPHPTASE // alk_phosphatase] CG5150

CG5150 GH04680 64E-64E ID:57B10
+ cell_adhesion * Kallmann syndrome KAL product - quail(aa) * 3e-18 similar to WAP-type (Whey Acidic Protein) 'four-
disulfide core', F * 4e-29 Kallmann syndrome prote [wap // 4_DISULFIDE_CORE // 4DISULPHCORE] CG6173 GH04611 95E1-
CG6173 95E1 ID:57B4

CG4294 + motor_protein * [PPASE // PRO_RICH // NLS_BP] CG4294 GH04951 58F1-58F1 dup:3/4 ID:57D11
+ unknown * hypothetical protein - Chinese hamster (fragment)(aa) * DHFR-coamplified protein * hypothetical protein -
CG7231 Chinese hamster (fragment)(aa) * 4e-44 ins [ACTININ_1] CG7231 GH04938 30C1-30C1 dup:2/3 ID:57D8

CG9686 + unknown * CG9686 GH05060 9A2-9A2 dup:2/2 ID:57E11
+ transporter * WHITE PROTEIN HOMOLOG(aa) * 4e-43 ORF YOL075c * 7e-39 SCRT_DROME SCARLET PROTEIN
scarlet protein mel * 4e-37 Similarity to Drosophila white protein[ATP_GTP_A2 // ABC_TRANSPORTER // ABC_tr] CG17646

CG17646 GH05015 22F3-22F3 dup:3/3 ID:57E6
+ Cyp6a8 cytochrome_P450 * DMCYP6A2A_5 Cyp6a2 * cytochrome p450 monooxygenase * 3e-37 predicted using Genefinder;
similar to cytochrome P450 * 5e-49 cytochrome P450 3A11 - mou [EP450II // p450 // P450 // MITP450 // C] CG10248 GH05558

CG10248 51D2-51D2 ID:58A6

CG12612+ CG12612 GH06062 dup:2/2 ID:58E6
+ EG:BACN32G11.3 unknown * BACN32G11.f * 1e-29 L130_HUMAN KD LEUCINE-RICH PROTEIN (LRP 130) (GP130) le *
CG14786 leucine-rich protein - human leucine-rich protein sa * BACN32G11.l CG14786 GH06301 2B1-2B1 ID:58G4

+ Rm62 RNA_binding * DMRM62RH_2 Rm62 * p68 RNA helicase(aa) * PUTATIVE ATP-DEPENDENT RNA HELICASE P62(aa)
* 1e-147 DBP2_YEAST P68-LIKE PROTEIN RNA helicase DBP2 - yeast [helicase_C // RNP_1 // HELICASE // DEAD] CG10279

CG10279 GH06343 83D-83D dup:2/2 ID:58G7

CG4377 + unknown * CG4377 GH06474 58A3-58A3 ID:58H6
+ Scp2 ligand_binding_or_carrier * 6e-95 calcium-binding protein Cex C * 1e-15 YSO6_CAEEL HYPOTHETICAL CALCIUM-
BINDING PROTEIN F56D1.6 IN CHROMOSOME II * 2e-33 calexcitin * 7[EF_HAND // EF_HAND_2 // ATP_GTP_A] CG14904

CG14904 GH06666 92A1-89D4 dup:2/4 ID:59B6
+ * TRIACYLGLYCEROL LIPASE (LIPASE, PANCREATIC)(aa) * 2e-16 VIT1_DROME VITELLOGENIN I PRECURSOR
CG10116 (YOLK PROTEIN 1) vitell * 2e-19 LIPL_MOUSE LIPOPROTEIN L [lipase] CG10116 73D5-73D5 dup:2/2 ID:59D6

CG3588 + EG:100G7.6 structural_protein * map_position:3C5 * * [PRO_RICH] CG3588 GH07242 3C4-3C4 dup:2/2 ID:59E3
+ TM4SF unknown * TM4SF * 1e-156 belong to the membrane protein group of Transmembrane Super * 9e-07 CD53_MOUSE
LEUKOCYTE SURFACE ANTIGEN CD53 (CELL SURFACE GLYCOPROT [TMFOUR // TM4_2] CG11303 GH07902 60A7-60A7

CG11303 dup:2/3 ID:60B10

CG16887+ BG:DS00941.11 unknown * AAs(aa) * AAs(aa) * CG16887 GH07914 34D4-34D4 dup:2/3 ID:60B12
 + Rbp9 RNA_binding * 3e-14 PUB1_YEAST NUCLEAR AND CYTOPLASMIC POLYADENYLATED RNA-BINDING PROTEIN
 PUB1 (ARS * 1e-175 RNA-binding protein * 5e-70 Similar to the human para [RNP_1 // RBD // HUDSXL RNA // rrm] CG3151
 CG3151 GH07919 23C1-23C2 dup:1/2 ID:60C1
 + unknown * 7e-30 weak similarity to rat cytosolic acyl coenzyme A thioester hydrolase * 1e-58 CGI-16 protein * 6e-27
 CG1774 hypothetical protein * contains weak simil CG1774 GH08048 100D2-100D2 dup:2/3 ID:60D2
 + enzyme * spermidine synthase(aa) * SPERMIDINE SYNTHASE (PUTRESCINE AMINOPROPYLTRANSFERASE)
 (SPDSY)(aa) * 1e-77 SPEE_YEAST SPERMIDINE SYNTHASE (PUTRESCINE AMI [SAM_BIND // ATP_GTP_A] CG8327
 CG8327 GH08387 85E2-85E2 dup:2/3 ID:60F4
 + ion_channel * 1e-35 VM106R.1 * 2e-06 (novel protein similar to and mouse, worm an * similar to TNF-alpha induced Protein
 CG10830B12 * similar to human tumor necrosis fac CG10830 GH08630 93A2-93A2 dup:1/2 ID:60G10
 + ligand_binding_or_carrier * DMC30B8 * retinaldehyde-binding protein 1(aa) * tocopherol (alpha) transfer protein (ataxia
 (Friedreich-like) with vitamin E deficiency)(aa) * 62D[CRETINALDHP // CRAL_TRIO] CG10237 GH08711 37E3-37E3 dup:2/3
 CG10237 ID:60H5
 CG13432+ unknown CG13432 GH08941 dup:1/2 ID:61B12
 + transporter * Ser89E * Glut1; * 5e-38 YB91_YEAST PROBABLE METABOLITE TRANSPORT PROTEIN YBR241C * 4e-31
 GTRL_DROME GLUCOSE TRANSPORTER-LIKE PROTEIN glucose transp[HELIX_LOOP_HELIX // SUGRTRNSPORT // SUG]
 CG1208 CG1208 GH09052 83C4-83C4 dup:1/2 ID:61C10
 CG6304 + unknown * [NLS_BP] CG6304 GH09088 36A14-36A14 dup:2/3 ID:61D2
 CG4302 + CG4302 CG11051 GH09393 ID:61F9
 + DNA_binding * pNORF1(aa) * NAM7_YEAST NAM7 PROTEIN (NONSENSE-MEDIATED MRNA DECAY PROTEIN 1)
 (UP-FRAMESHIFT * nonsense-mediated mRNA decay trans-acting factor * 3 [ATP_GTP_A] CG1559 GH09524 10F6-10F7
 CG1559 dup:1/2 ID:61G7
 + G-alpha47A signal_transduction GUANINE NUCLEOTIDE-BINDING PROTEIN G(O), ALPHA SUBUNIT (CLASS-I) >gil
 CG2204 ATP_GTP_A, G-alpha, GPROTEINA, GPROTEINA] CG2204 GH09771 dup:3/4 ID:61H10
 + transmembrane_receptor * 2e-09 /match=(desc: * 2e-52 YP84_CAEEL HYPOTHETICAL 90.9 KD PROTEIN C08B11.4 IN
 CG3106 CHROMOSOME II * predicted using Genefinder * cDNA EST comes from thi CG3106 GH10201 8F2-8F2 ID:62C6
 CG18069+ CaMKII protein_kinase proline rich calmodulin-dependent protein kinase PROTEIN_KINASE_DOM, pkinase CG18069 ID:62D9
 + unknown * 2e-05 No definition line found * 4e-16 type II membrane protein * 1E-175* [SAP_B // ER_TARGET] CG12918
 CG12918 GH10427 46D7-46D7 dup:2/2 ID:62E2
 CG16979+ unknown * 3e-61 F38A5.1 gene product * 1e-40 putative protein * CG16979 GH10640 71D3-71D3 ID:62F11
 + enzyme * similar to chitin synthases(aa) * 9e-13 CHS3_YEAST CHITIN SYNTHASE (CHITIN-UDP ACETYL-
 CG2666 GLUCOSAMINYL TRANSFERASE 3) * 8e-06 hyaluronan synthase * 8e- CG2666 GH10726 83A5-83A5 ID:62G3
 none + none GH10751 ID:62G7
 + enzyme * similar to plant chloroplast and prokaryotic carbonic anhydrases(aa) * 2e-63 similar to plant chloroplast and
 CG11967 prokaryotic carbonic anhydrases * 2e-1 [Pro_CA] CG11967 GH10821 85C3-85C3 ID:62H4

+ enzyme * similarity to enoyl CoA hydratase. Amino terminus shows similarity to acyl-CoA binding domains; cDNA EST
 CG13890 comes from this gene; cDNA EST comes from [ECH // NLS_BP] CG13890 GH11143 61D4-61D4 ID:63B12
 + enzyme * gamma-aminobutyric acid transaminase(aa) * PROBABLE 4-AMINOBTYRATE AMINOTRANSFERASE,
 MITOCHONDRIAL PRECURSOR (GAMMA-AMINO-N-BUTYRATE TRANSAMINASE) CG7433 GH11161 76E2-76E2 dup:1/4
 CG7433 ID:63C3
 + EG:100G10.4 enzyme * by content; by match; 2-match_description=4-NITROPHENYLPHOSPHATASE.; 2-match...(aa) *
 CG2680 BLASTX 8.9E-14 PHO13|4-Nitrophenylphosphatase(dna) * 1e-20 4- CG2680 GH11163 3B5-3B5 ID:63C4
 + unknown * 1e-37 Contains similarity to Pfam domain: (zf-C3HC4), Score=13.0 * 9e-33 nicotinic acetylcholine receptor-
 CG1909 associated 46K protein - mouse (J03 * 5e-3 [TPR_REPEAT // ZF_RING] CG1909 GH11191 102C5-102C5 dup:1/3 ID:63C6
 + porin ion_channel * DMMITPORN_2 porin * 1e-24 porin - yeast (Saccharomyces cerevisiae) outer mitochondri * 1e-162 voltage
 dependent anion-selective channel * 2e-55 code [Euk_porin // EUKARYTPORIN // EUKARYOTIC] CG6647 GH11331 32B3-32B4
 CG6647 dup:2/3 ID:63D2
 + Cbp53E calcium_binding * DMCALB32A_2 Cbp53E * calbindin 2, (29kD, calretinin)(aa) * CALRETININ (CR)(aa) * CALBINDIN-
 CG6702 32(aa) [EF_HAND // efhand // EF_HAND_2] CG6702 GH11671 53E7-53E10 ID:63F12
 CG1324 + unknown * [ATP_GTP_A] CG1324 GH11587 19E3-19E3 ID:63F6
 + grh transcription_factor * DMELF1_2 grh * transcription factor NTF1 - fruit fly (Drosophila melanogaster) (fragment) * 1e-22
 CG5058 alpha-globin transcription factor CP2 - mouse * 9e [NLS_BP] CG5058 GH11672 54F1-54F4 ID:63G1
 + unknown * 1e-06 ectodermal (ect) - fruit fly (Drosophila melanogaster) (strain Oregon-R) ** [NLS_BP] CG6611 GH11838
 CG6611 67D2-67D2 ID:63H3
 + zfh2 transcription_factor * ZINC-FINGER PROTEIN (ZINC-FINGER HOMEODOMAIN PROTEIN 2)(aa) * DMZFH2_2 zfh2 * 7e-
 40 Contains similarity to Pfam domain: (zf-C2H2), Score=[HOMEBOX_1 // homeobox // ZF_MATRIN //] CG1449 GH11902
 CG1449 102C1-102C3 dup:2/2 ID:63H9
 + unknown * 1e-10 cDNA EST yk471b2.5 comes from this gene; cDNA EST yk471b2.3 come ** CG4742 GH12140 15A5-
 CG4742 15A5 ID:64C2
 + unknown * 6e-05 transmembrane protein * 2e-12 Similarity to C.elegans cuticulin (SW:CUT1_CAEEL) * 7e-07
 CG3541 DMDUSKY_1 dy * similar to cuticlin CG3541 GH12163 60D7-60D8 dup:1/2 ID:64C4
 + unknown * 8e-42 YMS5_CAEEL HYPOTHETICAL 159.2 KD PROTEIN K03H1.5 IN CHROMOSOME III * 8e-17 alpha
 CG15560 tectorin * 2e-16 tectorin alpha alpha-tectorin * 1e-15 alpha CG15560 GH12365 100B8-100B8 ID:64D8
 + nucleic_acid_binding * 2e-11 coded for by C. elegans cDNA yk98h8.3; coded for by C. elegans cDNA yk98h8.5 * *
 CG14682 CG14682 GH12580 86C2-86C2 ID:64F6
 + Snap transporter * Snap * soluble NSF attachment protein(aa) * 3e-40 transport vesicle fusion protein SEC17 - yeast
 CG6625 (Saccharomyces cerevisiae) * 1e-73 coded for by C. [NSFATTACHMNT] CG6625 GH12751 77B3-77B3 dup:1/2 ID:64G9
 + enzyme * NADH-UBIQUINONE OXIDOREDUCTASE KD SUBUNIT PRECURSOR (COMPLEX I-49KD) (CI-49KD)(aa) *
 BLASTX 2.1E-17 Bovine mRNA fragment for kDa subunit of mitochon [COMPLEX1_49K // complex1_49Kd] CG1970 GH13128
 CG1970 102C5-102C5 dup:2/3 ID:65B10
 + protein_kinase * serine/threonine kinase(aa) * predicted using Genefinder; Similarity to Arabidopsis serine/threonine
 CG6114 protein kinase (PIR Acc. No. cDNA EST comes f [PROTEIN_KINASE_ST // TYRKINASE // PROTE] CG6114 GH13047 72A5-

72B1 ID:65B6

CG6123 + unknown * [NLS_BP] CG6123 GH13094 17A7-17A7 ID:65B9
+ sax transmembrane_receptor * DMTVP_2 tkv * DMBKR4A_2 sax * 9e-13 NRK1_YEAST SERINE/THREONINE-PROTEIN KINASE NRK1 (N-RICH KINASE 1) * receptor protein serine/threoni[PROTEIN_KINASE_ST // PROTEIN_KINASE_DOM] CG1891

CG1891 GH13369 43E18-43E18 dup:2/2 ID:65D2
+ cytoskeletal_structural_protein * 2e-47 dystrophin * 1e-117 unnamed protein product * 1e-143 dystrobrevin dystrobrevin *

CG8529 1e-143 dystrobrevin B [ZF_ZZ // ZZ // CYTOCHROME_C] CG8529 GH13689 49A6-49A7 dup:2/2 ID:65E12
+ transporter * HYPOTHETICAL 48.6 KD PROTEIN IN CHROMOSOME II(aa) * DMORCT2_2 Orct * solute carrier family

CG7342 (organic cation transporter), member 1(aa) * 1e-42 putati [sugar_tr] CG7342 GH13557 92A11-94D3 dup:2/2 ID:65E3

CG1314 + unknown * CG1314 GH13802 19E4-19E4 ID:65F10
+ unknown * similar to Arabidopsis thaliana male sterility protein * 3e-52 /match=(desc;; /ma * 3e-32 male sterility 2-like

CG1441 protein * 3e-54 DMC103B4 CG1441 GH13752 46C5-46C5 ID:65F4
+ endopeptidase * INSULIN-DEGRADING ENZYME (INSULYSIN) (INSULINASE) (INSULIN PROTEASE)(aa) * DMD1DE_2

CG2025 10F2 ID:65G10
+ endopeptidase * mas * Ser5 * Tequila * zgr;Try [trypsin // CHYMOTRYPSIN // TRYPSIN_SER] CG11912 GH13929 21B7-

CG11912 21B8 ID:65G7
+ Cyp6a2 cytochrome_P450 * PUTATIVE CYTOCHROME P450 T10B9.7 IN CHROMOSOME II(aa) * DMCYP6A2A_5 Cyp6a2 *

CG9438 ID:65G9
+ CYP6A2 * 3e-43 similar to cytochrome P450 [EP450II // MITP450 // CYTOCHROME_P450 /] CG9438 GH13965 42C5-42C5

CG15390 + unknown * CG15390 GH14074 22E-22E ID:65H11
+ jar motor_protein * DMMHC95F Mhc95F * 1e-116 MYS4_YEAST MYOSIN-4 ISOFORM myosin MYO4 - yeast (Saccharo * MYS9_DROME MYOSIN HEAVY CHAIN 95F (95F MHC) myosin heavy * sim [myosin_head // IQ // MYOSINHEAVY // NLS]

CG5695 CG5695 GH14351 95F-95F ID:66C4
+ actin_binding * DMRCPA_X kel * protein(aa) * [BTB // KELCHREPEAT // Kelch] CG3571 GH14381 87A-87A dup:2/2

CG3571 ID:66C6

CG9813 + unknown * [ATPASE_ALPHA_BETA] CG9813 GH14502 87E8-87E9 dup:1/2 ID:66D11

none + none GH14469 ID:66D6

CG8332 + CG8332 dup:3/5 ID:66D9

CG1394 + unknown * CG1394 GH14622 10A11-10A11 ID:66F4
+ cell_adhesion * 4e-06 UNC-89 * 6e-05 VGR2_MOUSE VASCULAR ENDOTHELIAL GROWTH FACTOR RECEPTOR

CG7607 PRECURSOR (VEGFR-2) (PR * 1e-05 protein tyrosine phosphatase, receptor t [ig] CG7607 GH14648 68A8-68A8 ID:66F6

CG12699 + unknown * CG12699 GH14656 54B7-54B7 ID:66F9
+ alpha-Est2 enzyme * alpha esterase(aa) * agr;-Est2 * carboxylesterase MdaE7(aa) * alpha esterase [CHOLNESTRASE //

CG2505 ESTERASE // COesterase] CG2505 GH15053 84D6-85A3 ID:67B5

CG2140 + electron_transfer * CYTOCHROME B5 (CYTB5)(aa) * 3e-17 cytochrome b5 * 1e-25 Similarity to Human cytochrome b5

(SW:CYB5_HUMAN); cDNA EST EMBL:D * 2e-30 CYB5_MOUSE CY[CYTOCHROME_B5 // CYTOCHROME B5 // CYTOCH]

CG2140 GH15091 43D-43D dup:3/3 ID:67B9

+ endopeptidase * PROCLOTTING ENZYME PRECURSOR(aa) * DMEAST_4 ea * 6e-67 EAST_DROME SERINE
PROTEASE EASTER PRECURSOR serine protein * 3e-29 anticoagulant protein C [trypsin // CHYMOTRYPSIN // TRYPSIN_SER

CG3066] CG3066 GH15156 85B1-85B1 dup:2/5 ID:67C3

+ endopeptidase * cathepsin L-like protease precursor(aa) * cysteine proteinase 1(aa) * cathepsin H(aa) * Cp1 [PAPAIN //

CG11459 Peptidase_C1 // THIOL_PROTEAS] CG11459 GH15170 83E1-83E1 ID:67C4

CG1999 + unknown * CG1999 GH15272 7A4-7A4 ID:67D3

CG2225 + unknown * CG2225 GH15653 39E5-39E ID:67H2

CG7105 + unknown * [FLAGELLA_BB_ROD] CG7105 GH15664 28D3-28D3 ID:67H3

CG7742 + unknown * [TBC // RAB_GAP] CG7742 GH15768 25C9-25C9 ID:68A4

+ cell_adhesion * 7e-56 strong similarity to rat integral membrane glycoprotein GP120 precursor (SP:P116 * 4e-18 protein *

CG7897 1e-95 GP21_RAT INTEGRAL MEMBRANE GLYCOPROTE CG7897 GH16206 41F-41F dup:4/6 ID:68D5

CG12191 + cell_adhesion * 8e-05 adhesion molecule L1.1 * * [ig] CG12191 GH16485 61D4-61D4 ID:68F12

+ * DMWHEELER_2 18w * DMCOP10_2 chp * 1e-20 leucine-rich motif (LRR) protein homology to interleukin receptor cy *

CG11910 2e-16 coded for by C. elegans cDNA yk [LRR] CG11910 96D2-96D2 dup:2/2 ID:68G8

none + none GH16763 ID:68H11

+ unknown * conserved hypothetical protein(aa) * CGI-111 protein(aa) * predicted using Genefinder; Similarity to E.coli

CG3663 hypothetical protein YCAC (SW:YCAC_ECOL [Isochorismatase // ATP_GTP_A] CG3663 GH17932 60D10-60D10 dup:1/3 ID:70A3

+ tko ribosomal_protein * 2e-21 YN8K_YEAST PUTATIVE 40S MITOCHONDRIAL RIBOSOMAL PROTEIN YNR036C * 2e-76
RT12_DROME MITOCHONDRIAL 40S RIBOSOMAL PROTEIN S12 PRECURSOR (TECHNICA [RIBOSOMAL_S12 //

CG7925 Ribosomal_S12 // RIBOS] CG7925 GH17961 3A2-3A2 ID:70A6

+ unknown * hypothetical protein(aa) * 3e-09 hypothetical protein * 3e-91 inserted at base Both 5' and 3' ends of P element

CG17223 Inverse PCR * CG17223 GH17972 23C4-23C4 ID:70A7

+ Gad1 enzyme * DCE_DROME GLUTAMATE DECARBOXYLASE (GAD) glutamate decarbo * 1e-163 predicted using
Genefinder; similar to Pyridoxal-dependent decar * 1e-169 67kD g [DDC_GAD_HDC_YDC // pyridoxal_deC] CG14994 GH18029

CG14994 64A5-64A7 ID:70B5

+ * 2e-09 SUR4_YEAST SUR4 PROTEIN (SRE1 PROTEIN) SUR4 protein - yea * 2e-13 predicted using Genefinder; similar

CG12138 to GNS1/SUR4 family; cDNA EST * 3e-12 MU [NLS_BP] CG12138 46C-46C dup:3/4 ID:70C10

+ ine neurotransmitter_transporter * ine * DMROSA_2 rosa * neurotransmitter transporter * 1e-119 Similarity to Human

CG15444 Na(+)/Cl(-)-dependent GABA transporter (SW:NTG [NANEUSMPORT // SNF] CG15444 GH18083 24F6-24F6 ID:70C4

+ deltaCOPligand_binding_or_carrier * 7e-29 COPD_YEAST COATOMER DELTA SUBUNIT (DELTA-COAT PROTEIN) (DELTA-
COP) * /motif=(desc;; /ma * 1e-103 COPD_CAEEL PROBABLE COATOMER DELTA SUBUNIT (D [ATP_GTP_A] CG14813

CG14813 GH18123 2B12-2B13 ID:70C8

CG18568 + unknown * CG18568 GH18325 50C21-50C21 dup:2/2 ID:70E3

CG4975 + unknown * 4e-05 BE46_MOUSE BRAIN PROTEIN E46 gene E46 protein - mouse * * CG4975 GH18454 54E5-54E5

ID:70F8

+ enzyme * ubiquitin fusion degradation protein; Ufd1p(aa) * UBIQUITIN FUSION DEGRADATION PROTEIN HOMOLOG
CG6233 (UB FUSION PROTEIN 1)(aa) * 2e-47 UFD1_YEAST UBIQUITI CG6233 GH18603 70E3-70E3 ID:70G10
CG8838 + unknown * [NLS_BP // ATP_GTP_A] CG8838 GH18521 25A1-25A1 ID:70G2
+ enzyme * F08F3.4 gene product(aa) * 2e-06 GALX_YEAST UDP-GLUCOSE 4-EPIMERASE (GALACTOWALDENASE) /
CG5955 ALDOSE 1-EPIMERASE (MUTA * 4e-84 F08F3.4 gene product * 2e- CG5955 GH18546 77C2-77C2 ID:70G5
+ unknown * T03G11.3 gene product(aa) * CGI-62 protein(aa) * 1e-16 T03G11.3 gene product * CG10999 GH18838 83C3-
CG10999 83C3 dup:1/2 ID:71A3
+ enzyme * 1e-05 GCST_YEAST AMINOMETHYLTRANSFERASE PRECURSOR (GLYCINE CLEAVAGE SYSTEM T
PROTEIN) * 1e-10 partial CDS, * 4e-08 sarcosine oxidase * sarcosine deh [FAD_Gly3P_dh // NAD_BINDING] CG6385 GH19226
CG6385 54E7-54E8 ID:71D6
+ protein_phosphatase * enolase-phosphatase E-1(aa) * Similarity to klebsiella oxytoca E-1 enzyme (TREMBL ID * 1e-24
UTR4_YEAST UTR4 PROTEIN (UNKNOWN TRANSCRIPT PROTEIN) U [Hydrolase // HADHALOGNASE] CG12173 GH19505
CG12173 83A1-83A1 ID:71F4
CG4679 + unknown * CG4679 GH19550 49F14-49F15 ID:71F9
+ peptidase * 3e-78 aminopeptidase yscII * 9e-93 Similarity to Human aminopeptidase N (SW:AMPN_HUMAN); cDNA EST
EMB * 1e-102 AMPN_MOUSE AMINOPEPTIDASE N (MICROSOM [ALADIPTASE // Peptidase_M1 // ZINC_PROT] CG5839
CG5839 GH19677 93F4-93F6 dup:3/7 ID:71G10
+ transcription_factor * 3e-30 zinc finger motif protein * 6e-09 contains multiple of strong similarity to C2H2-type zinc fingers
CG3282 (PS:PS00 * 4e-25 zinc finger pro[zf-C2H2 // ZINC_FINGER_C2H2 // ZINC_FIN] CG3282 GH19637 57B16-57B16 dup:1/2 ID:71G6
+ unknown * 1e-24 YLS5_CAEEL HYPOTHETICAL 55.1 KD PROTEIN F09G8.5 IN CHROMOSOME III * 2e-25 c21ORF-
CG15208 HumF09G8.5 * 5e-08 outer arm dynein light chain reinhar * 2e- CG15208 GH19655 9F12-9F12 ID:71G8
+ peptidase * 1e-100 aminopeptidase yscII * 1e-112 Similarity to Human aminopeptidase N (SW:AMPN_HUMAN); cDNA EST
EMB * 1e-165 AMPE_MOUSE GLUTAMYL AMINOPEPTIDASE [ALADIPTASE // NUCLEASE_NON_SPEC // Pept] CG8774
CG8774 GH19688 87E5-87E5 ID:71H1
+ transporter * Similarity to sugar transporters(aa) * DMORCT2_2 Orct * 2e-08 HXT5_YEAST PROBABLE GLUCOSE
TRANSPORTER HXT5 hexose trans * 3e-90 putative organic ca [SUGAR_TRANSPORT_1 // sugar_tr] CG6126 89B13-89B13
CG6126 dup:1/4 ID:72A7
CG13458 + unknown * 1E-160 * [COPPER_BLUE] CG13458 GH20023 71B2-71B2 ID:72B12
+ serpin * 3e-34 Similar to serine protease inhibitor * 6e-38 proteinase inhibitor Spi3 - mouse serine proteinase inhib * 1e-35
CG1865 cytoplasmic antiproteinase, CAP [serpin // SERPIN] CG1865 GH20213 42F1-42F1 ID:72D9
+ unknown * 1e-39 /match=(desc:; /ma * 3e-06 F20D6.5 gene product * predicted using Genefinder * cDNA EST yk381e5.3
CG10514 comes from this gene [NLS_BP] CG10514 GH20308 96C7-96C7 dup:2/2 ID:72E7
+ enzyme * similar to aspartate aminotransferase(aa) * 1e-99 aspartate aminotransferase cerevisiae, Peptide Partial, * 1e-157
CG4233 similar to aspartate aminotransfe [aminotran_1 // AA_TRANSFER_CLASS_1 // T] CG4233 GH20337 22B8-22B8 dup:2/2 ID:72F2
CG17822 + transcription_factor CG17822 GH20378 ID:72F5

CG18020+ projectin [Drosophila melanogaster] CG18020 ID:72G5
+ transporter * pot. w(+) polypeptide(aa) * WHITE PROTEIN HOMOLOG(aa) * Active transport ATPase; Adp1p(aa) * BROWN

CG3327 PROTEIN(aa) [ATP_GTP_A2 // ABC_TRANSPORTER // ABC_tr] CG3327 GH20863 25A1-25A1 ID:73B9
+ Vha68 enzyme * VACUOLAR ATP SYNTHASE CATALYTIC SUBUNIT A (V-ATPASE KD SUBUNIT) (VAA3-1)(aa) * encodes a protein with three (ABC) that is spliced to yield the extei [ATP-synt_ab // ATP-synt_ab_C // ATPASE_] CG12403 GH21132 34A-
CG12403 34A ID:73D11
+ Cyp4p2 cytochrome_P450 * DMC152A3 * DMCYP4D2_12 Cyp4d2 * 6e-09 CP56_YEAST CYTOCHROME P450-DIT2 (CYTOCHROME P450 56) cyt * 3e-53 cytochrome P450 cytochrome P4 [EP450II // p450 // P450 // MITP450 // C] CG1944

CG1944 GH21174 45C-45C dup:2/2 ID:73E8
+ DNA_binding * DMHMGDA_2 HmgD * HIGH MOBILITY GROUP PROTEIN Z (HMG-Z)(aa) * 2e-11 HMGD_DROME HIGH MOBILITY GROUP PROTEIN D (HMG-D) high mob * 2e-05 SSRP_CAEEL PROB [HIGHMOBLTY12 // HMG_box] CG7045

CG7045 GH21448 94B4-94B4 ID:73G1
+ transporter * 5e-27 HXT0_YEAST HEXOSE TRANSPORTER HXT10 hexose transport pro * 9e-42 GTRL_DROME GLUCOSE TRANSPORTER-LIKE PROTEIN glucose transpo * 4e-22 predicted [SUGRTRNSPORT // SUGAR_TRANSPORT_1 //

CG6484 SU] CG6484 GH21490 54D2-54D2 ID:73G7
+ unknown * 2e-07 /match=(desc: * 3e-08 MPV1_MOUSE MPV17 PROTEIN mpv17 protein - mouse * 1e-07 MpV17

CG12355 transgene, murine homolog, glomerulosclerosis * 1e-06 PMP2_ CG12355 GH21685 75F9-75F9 ID:74A4
+ EG:4F1.1cell_adhesion * /match=(desc:; /match=(desc:(aa) * sarcoglycan, delta (35kD dystrophin-associated glycoprotein)(aa) *

CG14808 4e-06 delta sarcoglycan * 9e-05 delta-sarcogl CG14808 GH21860 2B8-2B9 ID:74B10
+ metabolism * 3601, 14-kDa protein subunit of reductase complex(aa) * ubiquinol-cytochrome c reductase binding

CG3560 protein(aa) * UBIQUINOL-CYTOCHROME C REDUCTASE COMP CG3560 GH21854 14B12-14B12 ID:74B9
+ transcription_factor * TRANSCRIPTION FACTOR ADF-1 (ADH DISTAL FACTOR 1)(aa) * DMADF1A_2 Adf1 * 3e-07 cDNA

CG10949 EST comes from this gene; cDNA EST yk319a3.5 come [NLS_BP // ATP_GTP_A] CG10949 GH22016 38C9-38C9 ID:74D3
+ enzyme * 3-hydroxy-3-methylglutaryl-CoA-synthase(aa) * Similar to hydroxymethylglutaryl-CoA synthase; coded for by C. elegans cDNA cm01e7(aa) * 3-hydroxy-3- [HMG_CoA_synt // HMG_COA_SYNTHASE] CG4311 GH22436 53A5-53B1 dup:2/4

CG4311 ID:74G8
+ transcription_factor * putative zinc finger protein; Mot2p(aa) * coded for by C. elegans cDNA yk134f9.5; coded for by C.

CG5251 elegans cDNA yk15g6.5; coded for by C. elegans cDN [RBD // rrm // ZF_RING] CG5251 31E1-31E1 ID:75A7
+ unknown * C25E10.5 gene product(aa) * 7e-38 weak similarity to two short of multi-drug resistance proteins * No definition

CG8596 line found * Similarity to multidr CG8596 GH22722 65F3-65F3 ID:75B11
+ enzyme * PUTATIVE UBIQUINONE BIOSYNTHESIS MONOOXYGENASE COQ6(aa) * CGI-10 protein(aa) * UbiH-like protein(aa) * COQ6 monooxygenase; Coq6p(aa) [UBIH // Monooxygenase // RNGMNOXGNASE] CG7277 GH22740 25E6-25E6

CG7277 ID:75C2
+ enzyme * 1e-151 GLS1_CAEEL PUTATIVE GLUTAMINASE DH11.1 (GLS) (L-GLUTAMINE AMIDOHYDROLASE) * 1e-170 protein * 1e-171 GLSK_RAT GLUTAMINASE, KIDNEY ISOFORM PREC [ANK_REP // ank // ANK_REP_REGION] CG8772

CG8772 GH22838 49B8-49B8 dup:2/2 ID:75D1

CG15658+ cell_adhesion * 2e-11 CHAO_DROME CHAOPTIN PRECURSOR (PHOTORECEPTOR CELL-SPECIFIC MEMBRANE

PROTEIN) * 3e-06 Similarity to Rat insulin-like growth factor binding prote [LRR // LEURICHRPT // NLS_BP] CG15658 GH22922
 57C7-57C7 dup:2/2 ID:75E6
 + enzyme * PHOSPHOMANNOMUTASE (PMM)(aa) * 2e-91 YM8L_YEAST HYPOTHETICAL 71.1 KD PROTEIN IN DSK2-
 CAT8 INTERGENIC REGION * 1e-114 similar to Phosphoglucosmutase a [PGM_PMM // PGMPMM] CG10202 GH22984 51C5-
 CG10202 51C5 ID:75F1
 + dei transcription_factor * DMDELILAH_2 dei * HELIX-LOOP-HELIX PROTEIN DELILAH(aa) * 2e-08 ATH2_MOUSE ATONAL
 PROTEIN HOMOLOG (HELIX-LOOP-HELIX PROTEIN MATH-2) (MATH2) (* 6e[HLH // HELIX_LOOP_HELIX // HELIX_LOOP_H]
 CG5441 CG5441 GH22991 100A5-100A5 ID:75F3
 + structural_protein * Ran/TC4-binding nucleopore protein(aa) * RanBP2 protein - mouse (fragment)(aa) * RAN binding
 protein 2; nucleoporin 358(aa) * HTF9-A protein[GRAM_POS_ANCHORING // zf-RanBP // ZF_RA] CG11856 GH23370 96C4-
 CG11856 96C5 dup:2/4 ID:76B5
 + unknown * cDNA EST comes from this gene; cDNA EST comes from this gene; cDNA EST comes from this gene; cDNA
 CG10383 EST comes from this gene; cDNA EST yk270e3.3 come CG10383 GH23377 37A4-37A4 ID:76B6
 CG3348 + unknown * CG3348 GH23384 97F6-97F6 ID:76B8
 + Ark unknown * 1e-05 apoptotic protease activating factor * 3e-06 apoptotic protease activating factor * 2e-34 inserted at base
 CG6829 Both 5' and 3' ends of P element In [ATP_GTP_A] CG6829 GH23583 53F1-53F1 ID:76D11
 + unknown * 0-44 PROTEIN(aa) * HYPOTHETICAL 14.6 KD PROTEIN IN REC104-SOL3 INTERGENIC REGION(aa) *
 CG9396 HYPOTHETICAL 16.3 KD PROTEIN F53F10.3 IN CHROMOSOME I(aa) * h CG9396 GH23618 86C3-86C3 dup:2/2 ID:76E7
 + unknown * growth factor-responsive protein, vascular smooth muscle - rat(aa) * 3e-47 Weak similarity with apoptosis protein
 CG1114 RP-8; cDNA EST * SM-20 * CG1114 GH23732 83A1-83A1 ID:76F11
 + enzyme * hexaprenyl pyrophosphate synthetase; Coq1p(aa) * 9e-26 COQ1_YEAST HEXAPRENYL PYROPHOSPHATE
 CG10585 SYNTHETASE PRECURSOR (HPS) * 9e-13 trans-prenyltransferas [ATP_GTP_A] CG10585 GH23839 78A6-78A6 ID:76H7
 CG3192 + CG3192 ID:76H8
 + motor_protein * LL5 protein - rat(aa) * protein(aa) * 4e-06 kinesin-73 * 5e-08 Khc-73 [PH // NLS_BP // PH_DOMAIN]
 CG5004 CG5004 GH23978 15D4-15D6 dup:1/2 ID:77A10
 CG10570 + unknown * 1E-125* * CG10570 GH23934 37B1-37B1 ID:77A3
 + protein_kinase * DMSTPK Pk61C * DMFUSED_2 fu * similar to the CDF-1/PDGF receptor family of tyrosine protein
 CG8866 kinases(aa) * DMRSK_2 S6kII [PROTEIN_KINASE_ST // TYRKINASE // PROTE] CG8866 GH23955 85D8-85D9 ID:77A4
 + enzyme * DMGST_3 GsdD1 * 2e-44 unknown * 1e-13 GTT1_MOUSE GLUTATHIONE S-TRANSFERASE THETA (CLASS-
 CG17534 THETA) * 6e-16 glutathione S-transferase theta GLUTATHIONE S [GST] CG17534 55C9-55C9 dup:4/4 ID:77B3
 + Cyp4ac1 cytochrome_P450 * 2e-75 /motif=(desc; /ma * 3e-80 similar to Cytochrome P450 * 1e-54 cytochrome P450 Cyp4a -
 CG14032 mouse * 2E-56 [EP450II // p450 // P450 // MITP450 // C] CG14032 GH24257 25D2-25D2 ID:77D4
 + az2 transcription_factor * zf43C * 2e-09 AZF1_YEAST ASPARAGINE-RICH ZINC FINGER PROTEIN AZF1 fin * putative zinc
 finger protein * 3e-09 similar to Zinc finger, C2H2 type (3 do [SERPIN // zf-C2H2 // ZINC_FINGER_C2H2] CG1605 43D3-43D3
 CG1605 dup:3/3 ID:77E5
 + enzyme * DMC103B4 * 1e-05 LYS2_YEAST AMINOADIPATE-SEMIALDEHYDE DEHYDROGENASE LARGE SUBUNIT
 CG12268 (ALPHA-AMINOADI * 2e-53 /match=(desc; /ma * 4e-75 similar to Arab [HELIX_LOOP_HELIX] CG12268 GH24480 95C13-95C13

ID:77F5
+ Uba1 enzyme * ubiquitin-activating enzyme * ubiquitin activating enzyme * predicted using Genefinder; Similarity to Mouse ubiquitin-activati * UBA1_MOUSE UBIQUIT [UBA_NAD // ThiF_family // UBIQUITIN_ACT] CG1782 GH24511 46A1-46A1 dup:3/3

CG1782 ID:77F8

CG14989+ unknown * 1E-128* * CG14989 64A7-64A7 dup:2/2 ID:77F9

CG11148+ unknown * CG11148 GH25014 102F8-102F8 dup:2/2 ID:78B9
+ chif cell_cycle_regulator * activator of S phase kinase(aa) * map_position:35F11-36A2 * BLASTX 8.0E-09 Lytechinus variegatus Endo16 homolog (LvEndo16) mRNA, partial cds.(dna) * [GRAM_POS_ANCHORING // NLS_BP] CG5813 GH25089 35F9-35F10

CG5813 dup:1/2 ID:78C4
+ 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
+ EG:100G10.3 translation_factor * by match; 1-match_description=TRANSLATION INITIATION FACTOR EIF-2B BETA SUBUNIT (EIF-2B GDP-GTP EXCHANGE FACTOR).; 1-match_species=RATTUS NORVEGICUS [IF-2B] CG2677 GH25592 3B5-3B5

CG2677 ID:78H7
+ ligand_binding_or_carrier * GTP binding protein, almost identical to Gsp1p; Gsp2p(aa) * 3e-70 GSP2_YEAST GTP-BINDING NUCLEAR PROTEIN GSP2/CNR2 GTP-bind * 3e-23 rab11 * 6e[ras // GTPRANTC4 // ATP_GTP_A // RASTRN]

CG7815 CG7815 GH25818 75F9-75F9 ID:79B9
+ unknown * hypothetical 43.2 kDa protein(aa) * predicted using Genefinder; Similarity to Yeast hypothetical protein YAE2

CG7011 (SW:YAE2_YEAST); cDNA EST comes from t CG7011 GH25868 71B3-71B3 dup:2/2 ID:79C6

CG3682 + enzyme phosphatidylinositol 4-phosphate 5-kinase CG3682 ID:79D9

CG17470+ unknown * CG17470 GH26094 38E-38E dup:2/2 ID:79E10
+ transcription_factor * determined by GENSCAN prediction and spliced EST; match to EST * 5e-09 YK09_YEAST HYPOTHETICAL 85.5 KD PROTEIN IN SAP190-SPO14 INTERGENIC REGIO[SET_DOMAIN // SET // PHD // NLS_BP] CG9007

CG9007 GH26152 70C9-70C10 dup:2/2 ID:79F7

CG6836 + unknown * CG6836 GH26215 75E6-75E6 ID:79G4
+ unknown * 5e-07 hypothetical protein YOL114c - yeast (Saccharomyces cerevisiae) * 2e-17 R02F2.2 gene product * 3e-23

CG6094 immature colon carcinoma transcript prote [NLS_BP] CG6094 GH26345 31E5-31E5 ID:79H6

CG17348
+ motor_protein * BACR37P7.j(aa) * MICRONUCLEAR LINKER HISTONE POLYPROTEIN (MIC LH) LINKER HISTONE

CG9392 PROTEINS ALPHA, BETA, DELTA AND * * CG9392 GH26462 76C1-76C1 ID:80B3

CG5755 + transporter * TB1(aa) * * [mito_carr] CG5755 GH26696 36E-36E ID:80D7
+ 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

CG17608 GH26888 29C4-29C4 ID:80F12

CG8012 + unknown * CG8012 GH26995 67E7-67E7 ID:80H3

CG18138+ unknown * CG18138 GH27024 65E5-65E5 ID:80H4

+ enzyme * threonyl-tRNA synthetase(aa) * threonyl-tRNA synthetase (aa 1-734) * SYTC_CAEEL PROBABLE THREONYL-TRNA SYNTHETASE, CYTOPLASMIC (THREONINE--TRNA LIG [TRNASYNTHTHR // tRNA-synt_2b // AA_TRNA] CG5353
 CG5353 GH27773 33C1-33C1 ID:81G11
 CG5048 + unknown * CG5048 GH27783 70F1-70F1 ID:81H2
 + RNA_binding * protein(aa) * 2e-49 ovarian protein - fruit fly (Drosophila melanogaster) s * 8e-75 YLF1_CAEEL
 HYPOTHETICAL 42.4 KD PROTEIN C40H1.1 IN CHROMOSOME II [RNP_1 // RBD // PFKB_KINASES_1 // rrm] CG5735
 CG5735 GH28038 66E4-66E4 dup:2/3 ID:82B7
 + transporter * chromaffin granule ATPase II homolog(aa) * ATC3_YEAST PROBABLE CALCIUM-TRANSPORTING
 ATPASE (ENDOPLASMIC RETICULUM CA2+-AT * 9e-12 OBA5_DROME PUTAT [ATPASE_E1_E2 // CATATPASE // NLS_BP //
 CG17034] CG17034 GH28327 50A9-50A9 ID:82C4
 + RNA_binding * hypothetical protein(aa) * heterogeneous nuclear ribonucleoprotein R(aa) * 1e-08 RN15_YEAST MRNA 3'-
 END PROCESSING PROTEIN RNA15 RNA15 pro * 6e-16 p [RBD // rrm // NLS_BP] CG17838 GH28335 92F10-92F10 dup:2/5
 CG17838 ID:82C6
 + endopeptidase * DMSTUBBLE_1 Sb * 7e-07 T2D4_YEAST TRANSCRIPTION INITIATION FACTOR TFIIID KD SUBUNIT
 (TAFII-90) * 2e-26 EAST_DROME SERINE PROTEASE EASTER PRECURSOR se [trypsin // CHYMOTRYPSIN //
 CG1773 TRYPSIN_SER] CG1773 GH28342 46A3-46A3 ID:82C7
 CG7206 + unknown * CG7206 GH28353 16F7-16F7 dup:2/2 ID:82D1
 + AcCoAS enzyme * DMACOASYN_2 AcCoAS * 1e-154 ACS2_YEAST ACETYL-COENZYME A SYNTHETASE (ACETATE--
 COA LIGASE 2) (ACYL-ACTIVAT * acetyl-CoA synthetase - fruit fly (Droso [AMP_BINDING // AMPBINDING // AMP-bindin]
 CG9390 CG9390 78C7-78C7 ID:82D4
 CG6908 + unknown * 6e-20 /match=(desc;; /ma ** CG6908 GH28576 86F1-86F1 dup:2/2 ID:82E7
 + igl ligand_binding_or_carrier * ligand binding or carrier calmodulin binding) map_position:51E * 6e-51 growth-associated
 CG18285 protein GAP-43 homolog=igloo-L melanogas * 6e-53 igl * gro [IQ] CG18285 GH28577 51A4-51E7 dup:2/2 ID:82E8
 + unknown * clot.599(dna)* 1e-104 l(3)j1D5 l(3)j1D5 inserted at base Both 5' and 3' ends of P element Inverse PCR *
 CG8588 CG8588 GH28656 65F4-65F4 dup:3/4 ID:82F1
 + peptidase * leucyl aminopeptidase - like protein (partial)(aa) * 1e-103 leucine aminopeptidase * 1e-105 AMPL_BOVIN
 CYTOSOL AMINOPEPTIDASE (LEUCINE AMINOPEPTIDAS [LAMNOPPTDASE // CRYSTALLIN_BETAGAMMA //] CG8040
 CG8040 GH28719 67D12-67D13 dup:3/3 ID:82F9
 + CREG unknown * CREG * 1e-112 cellular repressor of E1A-stimulated genes CREG * 8e-25 cellular repressor of E1A-
 CG5413 stimulated genes CREG * 2e-22 UNKNOWN cellular repre CG5413 GH28782 90A6-90A6 ID:82G3
 + lat DNA_replication_factor * recognition complex subunit mela * 8e-92 recognition complex subunit * 9e-95 recognition
 complex associated protein p81 * 2e-92 inserted at base Bot [NLS_BP // ATP_GTP_A] CG4088 GH28787 49F10-49F10 dup:1/2
 CG4088 ID:82G4
 CG2640 + unknown * CG2640 GH28833 84C-84C ID:82H2
 + 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
 CG4466 GM13686 67B2-67B2 ID:83A12

+ protein_phosphatase * 4e-11 PVH1_YEAST PROTEIN-TYROSINE PHOSPHATASE YVH1 (PTPASE YVH1) * 5e-22
 CG14080 puckered protein * 3e-32 Similar to protein-tyrosine phosphatase * 1e-26 DU [DSPc] CG14080 GM13896 75F5-75F5 ID:83B6
 + ribosomal_protein * 60S RIBOSOMAL PROTEIN L21(aa) * 7e-46 R21A_YEAST 60S RIBOSOMAL PROTEIN L21E A
 ribosomal protein * 5e-50 RL21_CAEEL PROBABLE 60S RIBOSOMAL PROTEIN L2 [RIBOSOMAL_L21E // Ribosomal_L21e]
 CG12775 CG12775 GM14242 40D2-40D2 ID:83C2
 CG6050 + translation_factor CG6050 GM14682 ID:83C4
 + motor_protein * DNA segment, single copy, probe pH4 (transforming sequence, thyroid-1,(aa) * 1e-07 microtubule binding
 CG6664 protein D-CLIP-190 * 1e-20 YRU4_CAEEL HYPOTHE CG6664 LD23434 73E2-73E3 dup:2/2 ID:84B11
 + 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 //
 CG10922 LUPUSL] CG10922 LD24519 38C7-38C7 ID:84C12
 CG13345 + unknown CG13345 dup:2/3 ID:84H11
 + enzyme * 7e-52 DEOC_CAEEL PUTATIVE DEOXYRIBOSE-PHOSPHATE ALDOLASE
 (PHOSPHODEOXYRIBOALDOLASE) (* 9e-69 CGI-26 protein * 1e-26 2-deoxyribose 5-phosphate aldol CG8525 LD25963 49A4-
 CG8525 49A5 ID:85B10
 + enzyme * unknown(aa) * putative FAD synthetase(aa) * similar to FAD-1 like protein; cDNA EST yk313h1.5 comes from
 CG4407 this gene; cDNA EST yk457a9.3 comes from CG4407 LD26737 11C4-11D1 ID:85G10
 + enzyme * Similar to carbonic anhydrase; coded for by C. elegans cDNA yk72d10.3; coded for by C. elegans cDNA
 CG6906 yk119b1.3; coded for by C. elegans cDNA cm18b8; [carb_anhydrase] CG6906 LD26647 68F7-68F7 dup:2/2 ID:85G2
 CG2006 + unknown * cDNA EST CEMSA26F comes from this gene(aa) * * CG2006 LD27084 99B3-99B3 ID:86B11
 + Mcr enzyme_inhibitor * ovomacroglobulin, ovostatin(aa) * complement C3-Q2(aa) * COMPLEMENT C3-1 (CONTAINS: C3A
 ANAPHYLATOXIN)(aa) * 3e-83 similar to Alpha-2-macroglobulin [LDLRA_2 // RNP_1 // A2M // ldl_recept_a] CG7586 LD27113
 CG7586 28E3-28E3 ID:86C4
 + enzyme * Drosophila melanogaster P lethal line Drosophila melanogaster genomic Sequence recovered from 5' end of P
 element, genomic survey sequence(dna) * IS [tRNA-synt_1 // AA_TRNA_LIGASE_I // TRNA] CG11471 LD27166 79E2-79E2
 CG11471 dup:1/2 ID:86C7
 + enzyme PUTATIVE STEROID DEHYDROGENASE ADH_SHORT, GDHRDH, adh_short CG1444 LD27387 dup:3/3
 CG1444 ID:86E5
 + chaperone * 9e-13 XDJ1 protein - yeast (Saccharomyces cerevisiae) Xdj1p: H * 4e-09 DNJ1_DROME DNAJ PROTEIN
 CG8531 HOMOLOG (DROJ1) droj1 * 1e-46 contains strong similar [DnaJ // DNAJ_2] CG8531 LD27406 50E9-50E9 dup:2/2 ID:86E7
 + metabolism * MALATE OXIDOREDUCTASE, CHLOROPLAST (MALIC ENZYME) (ME) (NADP-DEPENDENT MALIC
 ENZYME) (NADP-ME)(aa) * malic enzyme 1, soluble(aa) * MALATE OXIDOREDUCT [MALIC_ENZYMES // MALOXRDTASE //
 CG10120 malic] CG10120 LD27718 87C9-87D dup:1/3 ID:86G10
 + signal_transduction * 3e-05 GRR1_YEAST GRR1 PROTEIN GRR1 protein - yeast (Saccharomyce * 1e-11 YKK7_CAEEL
 HYPOTHETICAL 54.9 KD PROTEIN C02F5.7 IN CHROMOSOME III * 2e-11 p [LRR // FBOX_DOMAIN] CG8272 LD27656 44F7-
 CG8272 44F7 ID:86G2
 CG4710 + unknown * CG4710 21E-21E dup:2/2 ID:86H5

+ protein_kinase * CASEIN KINASE I, GAMMA ISOFORM (CKI-GAMMA 1)(aa) * CASEIN KINASE I, ALPHA ISOFORM (CKI-
 CG6963 ALPHA)(aa) * 1e-89 CK12_YEAST CASEIN KINASE I HOMOLOG casein [pkinase] CG6963 LD28216 89B17-89B19 ID:87C12
 CG7275 + signal_transduction transducin (beta) like 1 protein GPROTEINBRPT, WD40 CG7275 LD28275 dup:2/3 ID:87D5
 CG13777+ unknown * 2e-20 protein * * CG13777 LD28289 27D3-27D4 dup:3/5 ID:87D7
 + Acer peptidase * DMACERMET_2 Acer * dipeptidyl carboxypeptidase I converting enzyme)(aa) * metallopeptidase(aa) *
 CG10593 enzyme-like protein(aa) [PEPDIPTASEA // Peptidase_M2 // ZINC_PRO] CG10593 LD28328 31B1-31B1 ID:87D9
 CG6988 + CG6988 dup:1/3 ID:87F2
 + trio cytoskeletal_structural_protein huntingtin-associated protein interacting protein CRAL_TRIO, GRF_DBL, PH_DOMAIN,
 CG9208 RhoGEF, S] CG9208 LD28463 dup:2/3 ID:87F3
 CG10627+ CG10627 ID:87F7
 CG6407 + signal_transduction CG6407 dup:3/3 ID:87H5
 CG17927+ Mhc motor_protein Myosin heavy chain CG17927 ID:88B3
 + unknown * contains similarity to a BR-C/TTK domain(aa) * 5e-10 kelch protein, long form - fruit fly (Drosophila
 CG1826 melanogaster) * 7e-12 Kelch motif containing [BTB // PROTEIN_SPLICING // NLS_BP] CG1826 9E2-9E2 dup:2/2 ID:88B4
 CG3661
 + apoptosis_inhibitor * DIHA(aa) * lap2 * 3e-07 inhibitor of apoptosis protein * 8e-06 coded for by C. elegans cDNA yk27g3.5;
 CG17019 coded for by C. elegans cDNA yk27g3.3; Si [NLS_BP // ZF_RING] CG17019 49E1-49E1 dup:6/6 ID:88E10
 + ion_channel * NY-REN-45 antigen(aa) * contains similarity to the A-type potassium current class of channel proteins(aa) *
 CG9467 /match=(desc;; /match=(desc;; /match=(d [BTB // GAPDH // WD_REPEATS] CG9467 85E10-85E10 dup:3/5 ID:88F9
 CG17138+ CG17138 dup:2/2 ID:88G10
 CG9277 + betaTub56D cytoskeletal_structural_protein beta-1 tubulin TUBULIN, TUBULIN_B_AUTOREG, tubulin CG9277 ID:89A3
 + Nop60B enzyme * CENTROMERE/MICROTUBULE BINDING PROTEIN CBF5 (CENTROMERE-BINDING FACTOR 5)
 (NUCLEOLAR PROTEIN CBF5)(aa) * major low affinity kDa Centromere/microtubu CG3333 LD30073 60B10-60B10 dup:4/4
 CG3333 ID:89E9
 + RpP0 * DMAP3A_2 RpP0 * ACIDIC RIBOSOMAL PROTEIN P0 HOMOLOG (L10E) (RIBOSOMAL PROTEIN L10)(aa) * 60S
 ACIDIC RIBOSOMAL PROTEIN P0 (DEOXYRIBONUCLEASE (APURINI [60s_ribosomal // Ribosomal_L10] CG7490 79C3-79C3
 CG7490 dup:3/3 ID:89F5
 + transcription_factor * fruitless protein(aa) * fruitless class I male isoform(aa) * 3e-21 LOLS_DROME LOLA PROTEIN,
 SHORT ISOFORM (LONGITUDINALS LACKING PROTEIN) * 2e-06 co [BTB // HTH_FIS_FAMILY // NLS_BP] CG7230 56C-56C
 CG7230 dup:6/10 ID:89H5
 CG5456 + unknown * CG5456 LD35728 94A3-94A3 ID:95C10
 + motor_protein * 1e-34 cDNA EST comes from this gene; cDNA EST co * 3e-61 protein * 4e-19 SAD1_SCHPO SPINDLE
 CG3287 POLE BODY ASSOCIATED PROTEIN SAD1 sp * 4e-29 inserted at CG3287 LD35815 42D1-42D1 dup:2/2 ID:95D6
 + 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
 CG4162 LD36009 35D3-35D3 dup:2/2 ID:95E11

+ unknown * dimethylase(aa) * 2e-97 DIM1_YEAST DIMETHYLADENOSINE TRANSFERASE (S-ADENOSYLMETHIONINE-6-N', N'-ADENOSY * 4e-99 YQN1_CAEEL HYPOTHETICAL 34.1 KD PROT [RnaAD // RNA_A_DIMETH // SAM_BIND]
 CG11837 CG11837 LD35950 98F9-98F9 dup:2/2 ID:95E6
 + Hsp67Bb chaperone * DMHSG2_7 Hsp67Bb * 1e-14 hypothetical protein YOR285w - yeast (Saccharomyces cerevisiae) * 5e-60 HS6B_DROME HEAT SHOCK PROTEIN 67B2 heat shock prot [Rhodanese // RHODANESE] CG4456 LD36162 67B1-67B1
 CG4456 ID:95G6
 + unknown * HYPOTHETICAL 32.0 KD PROTEIN C16C10.10 IN CHROMOSOME III(aa) * CGI-150 protein(aa) * 3e-21
 CG1532 Similar to protein from Brassica oleracea which is simila [Glyoxalase] CG1532 LD36566 19E6-19E6 ID:96B4
 + enzyme * GLY7(aa) * 1e-165 GLY7 * 1e-104 polypeptide GalNAc transferase-T1 * 1e-103 PAGT_HUMAN POLYPEPTIDE N-ACETYLGALACTOSAMINYLTRANSFERASE (PROTEIN-UDP ACE [RICIN_B_LLECTIN // GLYC_TRANS // Glycos_] CG6394
 CG6394 LD36616 17B4-17B4 dup:1/2 ID:96B8
 + unknown TRAM PROTEIN (TRANSLOCATING CHAIN-ASSOCIATING MEMBRANE PROTEIN)(aa) NLS_BP CG11642
 CG11642 LD36954 dup:2/2 ID:96D3
 + EG:100G10.5 transporter * by content; by match; 2-match_description=UDP-GALACTOSE TRANSLOCATOR (UDP-...(aa) * No
 CG2675 definition line found(aa) * 8e-71 Similarity to Mouse CMP-s CG2675 LD37122 3B5-3B5 dup:2/2 ID:96E3
 CG4865 + EG:EG0007.10 unknown * by content; * 1e-92 by content; 1-meth * 1E-94* CG4865 LD37360 4B1-4B1 ID:96G8
 + enzyme * coded for by C. elegans cDNA yk16b2.3; coded for by C. elegans cDNA yk16b2.5; Similar to amidase.(aa) * 1e-
 CG5112 23 putative yeast amidase * 3e-21 coded f [Amidase // AMIDASES] CG5112 LD38433 99B4-99B4 ID:97F10
 CG3221 + motor_protein * 3e-05 unknown protein IT1 * * CG3221 LD38682 57B15-57B15 ID:97H5
 + transcription_factor * hypothetical protein(aa) * 1e-19 YFJ1_YEAST HYPOTHETICAL 55.1 KD PROTEIN IN FAB1-PES4
 CG7986 INTERGENIC REGION * 3e-69 No definition line found * 3e-24 un [ATP_GTP_A] CG7986 LD38705 66B13-66B13 ID:97H7
 CG4501 + enzyme CG4501 ID:98H6
 + Ama cell_adhesion * DMAMA_5 Ama * Immunoglobulin-C2-type-domain protein * 1e-15 hemicentin precursor * 3e-19 cell
 CG2198 adhesion molecule (AA - 681) is 1st base in codon [ig] CG2198 LD39923 84D1-84D1 ID:99A4
 + BcDNA:LD23181 protein_phosphatase * 1e-41 inserted at base Both 5' and 3' ends of P element Inverse PCR * *
 CG6542 [TYR_PHOSPHATASE_1] CG6542 LD39930 54C1-54C3 ID:99A6
 + Rab10 cell_cycle_regulator * Rab1 * 4e-56 SEC4_YEAST RAS-RELATED PROTEIN SEC4 GTP-binding protein SE * 1e-111
 Rab10 * 9e-80 strong similarity to the YPT1 sub-family of RAS pro[SIGMA54_INTERACT_1 // ras // ATP_GTP_A] CG17060
 CG17060 LD39986 19C1-19C2 ID:99B3
 CG9866 + unknown * CG9866 LD40170 22E-22E ID:99C4
 + unknown * ilvB (bacterial acetolactate synthase)-like(aa) * BLASTX 4.8E-22 YEL020C|Protein with similarity to oxalyl-CoA
 CG11208 decarboxylase from Oxalobacter formig [TPP_enzymes // TPP_ENZYMES] CG11208 LD40177 56F14-56F14 ID:99C5
 + BcDNA:GH02220 enzyme * OXA1 homolog - human(aa) * 3e-25 OXA1_YEAST CYTOCHROME OXIDASE BIOGENESIS
 PROTEIN OXA1 PRECURSOR * 2e-29 Similarity to Human OXA1HS protein (cytochr CG6404 LD40470 67F4-67F4 dup:3/3
 CG6404 ID:99E10
 + unknown * Loc7p(aa) * 13S condensin XCAP-D2 subunit(aa) * gene product is related to yeast protein * 8e-38 hypothetical
 CG1911 protein YLR272c - yeast (Saccharomyce [NLS_BP] CG1911 LD40412 99B-99B dup:2/2 ID:99E3

+ 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
 + M(2)21ABenzyme * 1e-88 METK_YEAST S-ADENOSYLMETHIONINE SYNTHETASE (METHIONINE
 ADENOSYLTRANSFERASE 1) * 1e-142 METK_DROME S-ADENOSYLMETHIONINE SYNTHETASE (METHIONINE
 CG2674 [ADOMET_SYNTHETASE_1 // ADOMET_SYNTHETAS] CG2674 LD40460 21B-21B dup:2/2 ID:99E9
 + signal_transduction * Caf1 * Nle * Taf80 * 5e-13 T2D4_YEAST TRANSCRIPTION INITIATION FACTOR TFIID KD
 CG6724 SUBUNIT (TAFII-90) [GPROTEINBRPT // WD40_REGION // WD_REPEA] CG6724 LD40657 32A5-32A5 ID:99G1
 CG7873 + protein_kinase CG7873 Src42 dup:2/3 ID:Farhad's BB12
 CG4376 + Actn alpha-actinin (Flightless A) CG4376 GH06025 ID:Farhad's BB6