

Table S7

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

Gene ID mixed annotation (+ indicates sequence confirmation)

+ Trl transcription_factor * DMGAGATRA_4 Trl * GAGA-581 Adf-2 isoform * 1e-05 contains similarity to the kelch/MIPP family * 6e-05 leukemia/lymphoma related factor LRF [BTB // zf-C2H2 // ZINC_FINGER_C2H2] CG9343 LD41963 70F4-70F4 dup:1/2

CG9343 ID:101A10

+ * 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

+ 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

+ BcDNA:LD06837 DNA_replication_factor * Similarity to Human activator KD subunit (SW:AC13_HUMAN); cDNA EST CEESG65F comes from this gene; cDNA EST yk267e6.5 comes from this gene; cDNA EST [RFC] CG6258 LD41983 32D4-32D4 dup:2/2

CG6258 ID:101B1

CG1636 + unknown * CG1636 LD42063 7D21-7D21 dup:1/2 ID:101B10

+ Prat enzyme * AMIDOPHOSPHORIBOSYLTRANSFERASE PRECURSOR (GLUTAMINE PHOSPHORIBOSYLPYROPHOSPHATE AMIDOTRANSFERASE) (ATASE) (GPAT)(aa) * DMPRAT_2 Prat * 1e-55 PUR1_YE

CG2867 [Pribosyltran // PUR_PYR_PR_TRANSFER //] CG2867 LD42113 84E1-84E1 dup:1/3 ID:101B11

+ unknown * zinc finger protein(aa) * maf10(aa) * myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila))

CG1070 homolog); translocated to, 6(aa) * ALL1 fu [PHD] CG1070 LD42009 84C1-84C3 dup:1/3 ID:101B2

CG17602+ unknown * CG17602 LD42024 20A1-20A1 ID:101B4

+ Dap160 signal_transduction * Dap160 * 0.000000000000000004* dynamin associated protein isoform Dap160-1 * 5e-08 hum-1

CG1099 [EPS // EF_HAND // SH3DOMAIN // SH3 // N] CG1099 LD42142 39B1-39B1 ID:101C2

+ Gprk2 protein_kinase * 4e-45 protein kinase * GPRK2 * 1e-151 YQR1_CAEEL PROBABLE G PROTEIN-COUPLED RECEPTOR KINASE F19C6.1 * 1e-175 G protein-coupled receptor kinase 5; GR CG17998 LD42147 100C-100C dup:1/3

CG17998 ID:101C4

+ qua actin_binding * qua * QUA1_DROME VILLIN-LIKE PROTEIN QUAIL villin homolog qua * 9e-18 similar to gelsolin; cDNA

CG6433 EST comes from this gene * 3e-71 putative actin-bln [GELS // GELSOLIN] CG6433 LD42165 36C4-36C4 ID:101C8

CG15634+ unknown * CG15634 LD42284 25A4-25A4 ID:101D10

CG4036 + unknown * 5e-28 F09F7.7 gene product * [NLS BP] CG4036 LD42289 32F1-32F1 dup:1/2 ID:101D11

+ unknown * F35A5.8 gene product(aa) * CGI-61 protein(aa) * 2e-58 F35A5.8 gene product * 6e-06 antigen 6; AdamAS

CG9834 [NLS BP] CG9834 LD42223 56C10-56C11 ID:101D2

+ EG:39E1.1 unknown * 5e-33 YNJ2 YEAST HYPOTHETICAL 45.5 KD PROTEIN IN YPT53-RHO2 INTERGENIC REGION *

CG11596/match=(desc:: /ma * 6e-54 Similarity with yeast hypothetical prote [NLS BP] CG11596 LD42227 2B17-2B17 dup:2/2 ID:101D3

+ enzyme * DMPEROX_5 Pxd * 7e-87 PERO_DROME PEROXIDASE PRECURSOR myeloperoxidase (EC 1.11. * similar to peroxidase; cDNA EST comes from this gene; * 4e-93 PERM [MYB_2 // ANPEROXIDASE // peroxidase //] CG10211 LD42267

CG10211 37A1-37A1 ID:101D7

+ 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
 CG17129+ transcription_factor * [NLS_BP] CG17129 LD42420 61C9-61C9 dup:2/2 ID:101E10
 + osa DNA_binding * eyelid(aa) * eld * 3e-05 YM42_YEAST HYPOTHETICAL 162.7 KD PROTEIN IN SIP18-SPT21
 INTERGENIC REGION * 2e-37 coded for by C. elegans cDNA yk7c8.5; co [ARID // PRO_RICH // ANTIFREEZEI] CG7467 90C-
 CG7467 90C dup:4/4 ID:101E12
 + 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'-cuclic nuc [PHOSPHO_ESTER // 5_nucleotidase // SPAS] CG11883 LD42374 47B1-47B1
 CG11883 dup:2/2 ID:101E4
 + Grip91 cytoskeletal_structural_protein * gamma-tubulin interacting protein(aa) * gamma-tubulin ring protein Dgrip91(aa) * 1e-123
 spindle pole body protein spindle pole body protein spc98[DEHYDRATASE_SER_THR] CG10988 LD42379 12B7-12B7 dup:3/4
 CG10988 ID:101E5
 + Parg enzyme * poly(ADP-ribose) glycohydrolase * 6e-33 cDNA EST comes from this gene; cDNA EST co * 1e-100 poly(ADP-
 CG2864 ribose) glycohydrolase * 1e-102 poly (ADP-ribos [NLS_BP // ATP_GTP_A] CG2864 LD42380 3F2-3F2 dup:5/5 ID:101E6
 + BcDNA:LD29892 unknown * 4e-09 YKT7_CAEEL HYPOTHETICAL 53.2 KD PROTEIN C07A9.7 IN CHROMOSOME III * 1e-05
 CG8378 skm-BOP2 * 8e-52 inserted at base Both 5' and 3' ends of P element I [SET_DOMAIN] CG8378 48E10-48E10 dup:3/3 ID:101E8
 + Rep1 enzyme * Rep1 * 1e-121 DNA fragmentation factor DREP-1 * 1e-08 cell death activator CIDE-A * 4e-09 cell death-
 CG8357 inducing DFFA-like effector a c CG8357 48E2-48E2 dup:3/3 ID:101E9
 + 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
 + Aats-glupro enzyme * Aats-glupro * 1e-168 YHI0_YEAST PUTATIVE PROLYL-TRNA SYNTHETASE YHR020W (PROLINE--
 TRNA LIGASE) (PRORS * SYEP_DROME MULTIFUNCTIONAL AMINOACYL-TRNA S [WHEP-TRS // AA_TRNA_LIGASE_I //
 CG5394 tRNA-sy] CG5394 LD42739 95C13-95D1 ID:101F11
 + dock signal_transduction * dock * 6e-06 YG3D_YEAST HYPOTHETICAL 26.1 KD PROTEIN IN PAS5-CBF2 INTERGENIC
 REGION * 1e-157 SH2/SH3 adaptor protein * 4e-45 coded for by C. elegans[SH3DOMAIN // SH3 // NLS_BP // ATP_GTP_A]
 CG3727 CG3727 LD42588 21D2-21D2 ID:101F2
 CG8121 + unknown * CG8121 LD42595 85D9-85D9 ID:101F3
 + TH1 unknown * TH1(aa) * DMTH1X_3 TH1 * potential zinc-finger domains centered at aa and aa 364; kDa protein;
 CG9984 putative(aa) * DMTH1X_3 TH1 CG9984 LD42626 14C4-14C4 ID:101F4
 + Pabp2 RNA_binding * HYPOTHETICAL 29.0 KD PROTEIN IN BET1-PAN1 INTERGENIC REGION(aa) * DMROX2Y_3 Rox2 *
 CG2163 RNA binding protein(aa) * 3e-39 Similarity to Bovine Poly-A bind [RNP_1 // RBD // rrm] CG2163 LD42638 44A7-44A8 ID:101F6
 + DNA_binding * X-linked nuclear protein(aa) * 8e-36 RA54_YEAST DNA REPAIR AND RECOMBINATION PROTEIN RAD54
 RAD5 * 7e-41 RAD54 * 1e-145 strong similarity to the SNF2 [helicase_C // SNF2_N // NLS_BP] CG4548 LD42659 96E-96E2
 CG4548 dup:4/5 ID:101F7
 + unknown * NORBIN(aa) * neurochondrin-2(aa) * BLASTX 1.4E-23 Rattus mRNA for NORBIN, complete cds.(dna) * 2e-76
 CG2330 neurochondrin-1 (AB CG2330 LD42676 83F1-83F1 ID:101F8

+ enzyme * 3e-76 alpha esterase * 1e-40 strong similarity to the type-B carboxylesterase/lipase family e * 3e-47 pdb|1MAH|A
 CG9858 Chain A, Fasciculin2 - Mouse Acetyl [TONB_DEPENDENT_REC_1 // ESTERASE // COe] CG9858 LD42723 57F4-57F4 ID:101F9
 CG15312 + transmembrane_receptor * [ig] CG15312 LD42756 9B1-9B1 ID:101G1
 + enzyme * No definition line found(aa) * predicted secreted protein(aa) * 3e-06 predicted secreted protein * [NLS_BP]
 CG1745 CG1745 LD43003 10B15-10B15 dup:1/2 ID:101G12
 + enzyme * unknown(aa) * PROBABLE GMP SYNTHASE (GLUTAMINE-HYDROLYSING) (GLUTAMINE
 AMIDOTRANSFERASE) (GMP SYNTHETASE)(aa) * guanine-monophosphate synthetase; GM [CPSGATASE // GMP_synt_C //
 CG9242 ANTSNTHASEII] CG9242 LD42771 39B4-39B4 dup:2/2 ID:101G2
 + transcription_factor * zinc-finger-motif-protein * 1e-05 Bowel * 6e-05 predicted using Genefinder; similar to Zinc finger, C2H2
 CG6791 type (7 * 5e-14 zinc finger protein - mo[zf-C2H2 // ZINC_FINGER_C2H2 // ZINC_FIN] CG6791 87E1-87E1 dup:1/2 ID:101G3
 + Taf80 signal_transduction * 2e-17 TUP1_YEAST GLUCOSE REPRESSION REGULATORY PROTEIN TUP1 (FLOCCULATION
 SUPPRESSOR P * T2D4_DROME TRANSCRIPTION INITIATION FACTOR TFIID KD SUBUN[GPROTEINBRPT //
 CG7704 WD40_REGION // WD_REPEA] CG7704 LD42828 47C5-47C6 ID:101G5
 + 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
 CG5522 + GDP/GTP exchange factor for Ras GRF_CDC25, PH, PH_DOMAIN, RasGEF CG5522 dup:1/2 ID:101G8
 + BcDNA:GM10765 DNA_repair_protein * 5e-15 RA27_YEAST STRUCTURE SPECIFIC ENDONUCLEASE RAD27 hypothet * 2e-
 20 by match; 1-match_accession=SWISS-PROT:P397 * 5e-13 similar to the [53EXO_N_DOMAIN // 53EXO_I_DOMAIN // XPG]
 CG10670 CG10670 LD43032 64C12-64C12 ID:101H3
 CG6325 + unknown * [CYTOCHROME_C] CG6325 LD43055 86A5-86A6 ID:101H9
 + cell_cycle_regulator * pombe Cdc5-related protein(aa) * similar to MYB transforming protein; cDNA EST comes from this
 gene; cDNA EST comes from this gene; cDNA [MYB_1 // MYB_2 // myb_DNA-binding // MY] CG6905 LD43082 61C1-61C1 dup:2/2
 CG6905 ID:102A1
 CG5145 + unknown * CG5145 LD43096 77C2-77C2 ID:102A2
 + Chc transporter * DMCHC_2 Chc * CLH_YEAST CLATHRIN HEAVY CHAIN clathrin heavy chain - y * CLH_DROME
 CLATHRIN HEAVY CHAIN clathrin heavy chain - fr * CLH_CAEEL PRO[RCC1_2 // Clathrin_repeat // CLATHRIN_R] CG9012
 CG9012 LD43101 13F3-13F3 dup:1/3 ID:102A3
 + structural_protein * 7e-07 DR48_YEAST DDR48 STRESS PROTEIN (DNA DAMAGE-RESPONSIVE PROTEIN 48) (DDRP
 CG5787 48) (Y * 7e-07 M84D_DROME MALE SPECIFIC SPERM PROTEIN MST84DD testis- CG5787 LD43134 33F2-33F2 ID:102A8
 + unknown * ecdysone receptor isoform A - fruit fly (Drosophila melanogaster) (fragment)(aa) * EcR-A=ecdysone receptor
 CG8347 isoform melanogaster, Peptide Partial, * CG8347 LD43136 42A9-42A9 ID:102A9
 + 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
 CG11330 26F5-26F6 ID:102B11
 + storage_protein * s18 chorion protein(aa) * GCR protein - fruit fly (Drosophila melanogaster)(aa) * s19 chorion protein(aa) *
 CG5095 ATP-DEPENDENT RNA HELICASE A (NUCLEAR CG5095 LD43171 15E5-15E5 ID:102B2
 CG7660 + enzyme * 1e-98 PERO_DROME PEROXIDASE PRECURSOR myeloperoxidase (EC 1.11. * 6e-87 similar to eosinophil

peroxidase and myelo-peroxydase * 2e-65 PERT_MOUSE THY [ANPEROXIDASE // PEROXIDASE_3] CG7660 LD43174 90C-90C ID:102B3
 + unknown * putative transposase(aa) * 3e-05 ORF1 * 2e-07 putative transposase * Hermes transposase [AMP_BINDING]
 CG11560 CG11560 LD43225 68F3-68F3 ID:102B8
 + Orc4 DNA_replication_factor * 56-kDa subunit of recognition complex (ORC); Orc4p(aa) * recognition complex subunit 4-related
 CG2917 protein Orp4p(aa) * recognition complex, subunit (yea [ATP_GTP_A2 // ATP_GTP_A] CG2917 LD43280 60D16-60D16 ID:102C1
 + TRAP1 chaperone * heat shock protein 90(aa) * Hsp90-related protein TRAP1(aa) * 2e-55 HS82_YEAST HEAT SHOCK
 PROTEIN HSP82 heat shock protein * 1e-141 similar to heat [HEATSHOCK90 // HSP90] CG3152 LD43460 42B2-42B2 dup:2/2
 CG3152 ID:102C12
 + motor_protein * 7e-10 NUF1_YEAST NUF1 PROTEIN (SPINDLE POLY BODY SPACER PROTEIN SPC110) * 2e-14
 CG5740 nonmuscle myosin-II heavy chain * 1e-10 Similarity to Human endosoma CG5740 LD43488 94A-96C1 dup:2/2 ID:102D1
 + RplI215 enzyme * DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (VERSION 1)(aa) * DMRPRIIA_2 RplI215 *
 DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT(aa) * RNA poly [RNA_POL_II_REPEAT] CG1554 LD43558 10C4-
 CG1554 10C5 ID:102D12
 + Mtch transporter * transporter mitochondrial small-molecule carrier or transporter) * 4e-06 probable membrane protein
 CG6851 YPR011c - yeast (Saccharomyces cerevisiae) * 2e- [mito_carr] CG6851 LD43650 61A5-61A5 dup:2/2 ID:102E9
 + structural_protein * 6E-55* 1e-06 R02F2.4 gene product * 2e-06 peritrophin * 7e-35 Gasp CG17052 LD43683 19C1-19C1
 CG17052 dup:1/2 ID:102F1
 CG4497 + unknown * [GRAM_POS_ANCHORING] CG4497 LD43863 27E4-27E4 ID:102F12
 CG4702 + unknown * CG4702 LD43816 88A1-88A1 ID:102F9
 CG5694 + unknown * CG5694 LD44026 31B4-31B4 dup:1/2 ID:102G12
 + unc-119 unknown * 1e-124 UNC-119 * 3e-59 U119_CAEEL UNC-119 PROTEIN unc-119 protein - Caenorhabd * 2e-65 UNC-119
 CG1659 * 2e-65 unc119 (C.elegans) homolog RETIN CG1659 LD43876 7A3-7A4 ID:102G3
 + BG:BACR48E02.4 cell_adhesion * Ras suppressor protein 1(aa) * 3e-07 adenylate cyclase * 3e-06 CHAO_DROME CHAOPTIN
 PRECURSOR (PHOTORECEPTOR CELL-SPECIFIC MEMBRANE PROTEIN) * 3e-63 [LRR // LEURICHRPT] CG9031 LD43891
 CG9031 36E3-36E3 ID:102G5
 + enzyme * 1e-75 ALG8_YEAST GLUCOSYLTRANSFERASE ALG8 glucosyltransferase (* 3e-54 YXD3_CAEEL PUTATIVE
 CG4542 GLUCOSYLTRANSFERASE C08H9.3 (Z543 * 1e-104 glucosyltrans CG4542 LD44072 6D2-6D2 ID:102H5
 + BcDNA:GM13640 enzyme * DNA primase, p58 subunit(aa) * putative dna primase large subunit(aa) * primase, polypeptide 2A
 CG5553 (58kD)(aa) * PROBABLE DNA PRIMASE LARGE SUBUNIT(aa) CG5553 LD44074 77B4-77B4 ID:102H6
 + Tbp transcription_factor * Tbp * TRANSCRIPTION INITIATION FACTOR TFIID (TATA-BOX FACTOR) (TATA SEQUENCE-
 BINDING PROTEIN) (TBP) (TATA-BOX BINDING PROTEIN)(aa) * 4e-80 TF2D_YEAS [TFIID // TIFACTORIID // TBP] CG9874
 CG9874 LD44083 57F8-57F8 dup:1/2 ID:102H7
 + enzyme * 3alpha-hydroxysteroid dehydrogenase (B-specific) (EC 1.1.1.50) - Pseudomonas sp. (strain * DMGLUTAC_9 Glt *
 CG11005 DMADHA1_9 Adh * DMSCU scu [adh_short_C2 // GDHRDH // adh_short //] CG11005 LD44221 83B6-83B6 ID:103A10
 + Probeta2 endopeptidase * Pros bgr;2 * 3e-71 PRCF_YEAST PROTEASOME COMPONENT PUP1 PRECURSOR
 CG3329 (MACROPAIN SUBUNIT PUP1) (PROTEIN * 1e-146 20S proteasome beta2 subunit * 4e-49 pr [PROTEASOME_B //

PROTEASOME_PROTEASE //] CG3329 LD44234 71A3-71A3 ID:103A11
 + unknown * putative centromere protein(aa) * HYPOTHETICAL 75.7 KD PROTEIN T10F2.3 IN CHROMOSOME III(aa) * 6e-
 CG10107 12 SMT4_YEAST SMT4 PROTEIN SMT4 protein - yeast (CG10107 LD44235 65C3-65C3 dup:1/2 ID:103A12
 CG4229 + unknown * CG4229 LD44179 77A1-77A1 ID:103A2
 + signal_transduction * Taf80 * katanin p80 subunit(aa) * 5e-07 YCW2_YEAST HYPOTHETICAL 57.0 KD TRP-ASP
 REPEATS CONTAINING PROTEIN IN CPR4-SSK2 * 4e-09 transcription ini[GPROTEINBRPT // GPROTEINB // WD40_REGION]
 CG9910 CG9910 LD44201 14B11-14B11 ID:103A6
 + unknown * HYPOTHETICAL 58.0 KD PROTEIN C2C6.08 IN CHROMOSOME I(aa) * BLASTX 2.8E-35 YDL238C[Protein of
 CG18143 unknown function(dna) * 1e-72 YD3C_YEAST HYPOTHETICAL 5 CG18143 LD44207 82A-82A ID:103A8
 + signal_transduction * PACSIN(aa) * 3e-07 hypothetical protein YFR024c-a - yeast (Saccharomyces cerevisiae) * 7e-08
 Cortactin * 1e-52 weakly similar to surface[FCH // CDC15_NT // P67PHOX // SH3DOMAIN] CG15694 LD44220 92F13-92F13
 CG15694 dup:2/2 ID:103A9
 CG1503 + unknown * CG1503 LD44327 19E7-19E7 ID:103B10
 + unknown * 8e-74 GPI3_YEAST N-ACETYLGALACTOSAMINYL-PHOSPHATIDYLINOSITOL BIOSYNTHETIC PROTEIN
 CG6401 (GLCN * 6e-92 similar to phosphatidylinositol biosynthetic protein; [Glycos_transf_1] CG6401 LD44262 54E7-54E7 ID:103B2
 + enzyme * isopeptidase T(aa) * 3e-68 UBPE_YEAST UBIQUITIN CARBOXYL-TERMINAL HYDROLASE (UBIQUITIN
 THIOLESTERASE 14) * 1e-125 Similar to ubiquitin carboxyl-term [UBA // UCH_2_1 // UCH_2_2 // UCH_2_3 //] CG12082 LD44295
 CG12082 63B10-63B11 ID:103B7
 CG3995 + unknown * [NLS_BP] CG3995 89E12-89E12 dup:2/2 ID:103B9
 + CycA cell_cycle_regulator * cell cycle regulator cyclin) map_position:68E1-2 * DMCYCA_3 CycA * G2/MITOTIC-SPECIFIC
 CYCLIN A(aa) * 2e-27 CG23_YEAST G2/MITOTIC-SPECIFIC[cyclin // HELIX_LOOP_HELIX // CYCLINS] CG5940 LD44443 68D4-
 CG5940 68D4 dup:2/2 ID:103C10
 + 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
 CG9241 + function_unknown * Cdc23(aa) * * [NLS_BP] CG9241 LD44370 39B4-39B4 dup:1/2 ID:103C3
 + chaperone * 5e-33 Similarity to Xenopus P58 protein cDNA EST * 3e-78 GP36b glycoprotein * 3e-83 coded for by C. elegans
 CG5510 cDNA yk74e11.5; coded for by C. elegans CG5510 95E3-95E3 dup:2/2 ID:103C4
 + hdc signal_transduction * cell cytoplasm) map_position:99F6-11 * 4e-98 hdc protein - fruit fly (Drosophila melanogaster) (Z *
 CG15532 8e-11 similar to drosophila HCD protein * 1e-10 CG15532 LD44381 99F-99F3 dup:2/3 ID:103C5
 + unknown * tight junction protein (zona occludens 1)(aa) * TIGHT JUNCTION PROTEIN ZO-1 (TIGHT JUNCTION PROTEIN
 CG11782 1)(aa) * 1e-05 ZO-1 MDCK * [NLS_BP] CG11782 LD44404 85B4-85B4 ID:103C6
 + motor_protein * Nijmegen breakage syndrome (nibrin)(aa) * 2e-06 AMYH_YEAST GLUCOAMYLASE S1/S2 PRECURSOR
 (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPH * 1e-08 predicted u [FHA_DOMAIN // NLS_BP // FHA] CG6754 LD44438 67C-
 CG6754 67C dup:1/2 ID:103C9

+ Sb endopeptidase * trypsin-like serine protease(aa) * DMSTUBBLE_1 Sb * masquerade precursor - fruit fly (Drosophila melanogaster)(aa) * plasminogen activator, tiss[trypsin // CHYMOTRYPSIN // TRYPSIN_SER] CG4316 LD44584 89B9-89B9
 CG4316 dup:3/3 ID:103D10
 + Iswi DNA_binding * enzyme DNA dependent adenosinetriphosphatase) transcription factor binding transcription co-activator) map_position:72A3 * enzyme DNA dependent ad [helicase_C // SNF2_N // NLS_BP // ATP_G] CG8625 LD44594 49B6-49B7
 CG8625 ID:103D12
 + SPT4 enzyme * 3e-13 SPT4_YEAST TRANSCRIPTION INITIATION PROTEIN SPT4 SPT4 pro * 6e-30 contains similarity to
 CG12372 Saccharomyces cerevisiae Spt4 * 7e-39 unknown * 1e-39 CG12372 LD44495 49B5-49B5 ID:103D2
 + enzyme * DMANKY_5 Ank * calcium-independent phospholipase A2(aa) * Ca2+-independent phospholipase A2(aa) * 1e-08
 CG6718 ankyrin ankyrin m [ANK_REP // ank // ANK_REP_REGION] CG6718 LD44515 67C2-67C2 dup:2/2 ID:103D4
 + unknown * 1e-12 YKK4_CAEEL HYPOTHETICAL 30.2 KD PROTEIN C02F5.4 IN CHROMOSOME III * * [NLS_BP] CG9018
 CG9018 LD44521 62D3-62D3 dup:2/2 ID:103D5
 + motor_protein * CLIP-190 * 6e-05 microtubule binding protein D-CLIP-190 * 3e-05 myosin * 4e-06 ORF 73, contains large
 CG8621 complex repeat CR sarcoma-associated herpesv CG8621 LD44526 65E6-65E6 dup:2/2 ID:103D6
 + unknown * 4e-14 YZG1_CAEEL HYPOTHETICAL 28.7 KD PROTEIN F13E6.1 IN CHROMOSOME X * 1e-13 D52 * 7e-20
 CG5174 tumor protein D52-like hD54+ins2 isoform * 3e-14 CSPP28 CG5174 LD44733 55C11-55C11 dup:3/3 ID:103E10
 + unknown * F1N21.18(aa) * HYPOTHETICAL 51.8 KD PROTEIN ZK632.11 IN CHROMOSOME III(aa) * * [ZF_CCHC //
 CG4622 PRO_RICH // zf-CCHC // NLS_B] CG4622 LD44757 60D5-60D5 dup:3/3 ID:103E12
 + sut1 transporter * metabolite transport protein(aa) * membrane transporter like protein(aa) * ERD6 protein(aa) * solute carrier family (facilitated glucose transporte[SUGRTRNSPORT // SUGAR_TRANSPORT_2 // su] CG8714 LD44652 44A4-44A4 dup:4/4
 CG8714 ID:103E4
 CG5422 + RNA_binding CG5422 dup:2/2 ID:103E5
 + unknown * 7E-80* 4e-29 inserted at base Both 5' and 3' ends of P element Inverse PCR * [ATP_GTP_A] CG11104 LD44686
 CG11104 12B8-12B8 dup:2/2 ID:103E6
 CG7832 + unknown * [NLS_BP // ANTIFREEZEI] CG7832 LD44696 88C10-88C10 dup:3/3 ID:103E7
 + unknown * HYPOTHETICAL 37.2 KD PROTEIN C12C2.09C IN CHROMOSOME II(aa) * 1e-19 hypothetical protein
 CG7530 YDR492w - yeast (Saccharomyces cerevisiae) (U * 5e-26 C43G2 CG7530 LD44720 88D2-88D2 dup:3/3 ID:103E8
 + unknown * 5e-08 No definition line found * 5e-16 PSD-95/SAP90-associated protein-2 * 1e-16 PSD-95 binding protein * 1e-
 CG8390 171 inserted at base Unknown 5' end of [NLS_BP] CG8390 LD44824 41E5-41E5 ID:103F11
 + unknown * /match=(desc:; /match=(desc:(aa) * 8e-07 hypothetical protein YLR281c - yeast (Saccharomyces cerevisiae) (U *
 CG3767 7e-10 /match=(desc:; /ma * 7e-08 RF2_H [RF-1] CG3767 LD44791 53A2-53A2 ID:103F5
 CG17260 + nucleic_acid_binding * [ZF_RING] CG17260 LD44813 23C5-23C5 ID:103F8
 + unknown * BLASTX 4.0E-27 YER156C[Protein of unknown function(dna) * HYPOTHETICAL 38.2 KD PROTEIN IN BEM2-
 CG11980 NCB1 INTERGENIC REGION(aa) * 6e-60 similar to Yeast h CG11980 LD44814 85C3-85C3 dup:2/2 ID:103F9
 CG7347 + motor_protein * 8e-05 myosin heavy chain * * [PRO_RICH] CG7347 LD44887 75B10-75B10 ID:103G1
 + smid endopeptidase * DMSMMIN_2 smallminded * smallminded(aa) * 3e-68 AFG2_YEAST AFG2 PROTEIN valosin-containing
 CG8571 protein homolo * smallminded [ENDOLAPTASE // AAA // ATP_GTP_A] CG8571 65F5-65F6 dup:2/2 ID:103G2

+ 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
 + Msr-110 unknown * Msr-110 = EN protein binding gene/engrailed nuclear homeoprotein-regulator * * CG10596 LD44960
 CG10596 64E-64E dup:1/3 ID:103G6
 + enzyme * hypothetical protein(aa) * 3e-93 SUCB_YEAST PROBABLE SUCCINYL-COA LIGASE (GDP-FORMING), BETA-
 CHAIN PRECURSOR (SU * 1e-134 SCB2_CAEEL PROBABLE SUCCI [SUCCINYL_COA_LIG_3 // ligase-CoA] CG10622 LD44970
 CG10622 64E-64E ID:103G7
 + unknown * NY-REN-2 antigen(aa) * 1e-27 hypothetical protein YDR374c - yeast (Saccharomyces cerevisiae) (U * 9E-49*
 CG6422 Similarity to A. thaliana gene product F21M [PRO_RICH] CG6422 LD44979 96B14-96B15 ID:103G8
 + rdgBbetatransporter * PHOSPHATIDYLINOSITOL TRANSFER PROTEIN BETA ISOFORM (PTDINS TRANSFER PROTEIN
 BETA) (PTDINSTP) (PI-TP-BETA)(aa) * BLASTX 3.1E-49 M.musculus mRNA for D [PITRANSFER] CG17818 LD44980 54E3-54E3
 CG17818 ID:103G9
 + unknown * 7e-07 hypothetical protein YOR295w - yeast (Saccharomyces cerevisiae) * 9e-09 weak similarity to D.
 CG1240 melanogaster salivary gland-specific protein (PI [TUBULIN // NLS_BP] CG1240 LD45195 63A1-63A1 dup:2/2 ID:103H12
 + enzyme * protein(aa) * 3e-07 FMS1_YEAST FMS1 PROTEIN FMS1 protein - yeast (Saccharom * 6e-12 Cs protein
 CG17149 [ADXRDTASE // NAD_BINDING] CG17149 LD45081 77A4-77A4 ID:103H4
 + RNA_binding * spliceosome associated protein 145, SF3b subunit(aa) * spliceosome associated protein-like(aa) * BLASTX
 CG3605 7.8E-75 Human spliceosome associated protein [NLS_BP] CG3605 LD45152 23C4-23C4 ID:103H9
 CG17686 + DIP1 RNA_binding * [NLS_BP // DSRBD] CG17686 LD45242 cyto_unknown dup:1/2 ID:104A6
 + unknown * short of similarity to human transforming protein (tre) * similar to human (TRE) transforming protein *
 CG5916 Ypl249cp(aa) * pollux(aa) [TBC // RAB_GAP] CG5916 LD45246 89B9-89B9 ID:104A9
 CG17469 + unknown * 1E-123** CG17469 LD45277 102E2-102E3 dup:2/2 ID:104B4
 + endopeptidase * energy-dependent regulator of proteolysis(aa) * 9e-61 YB77_YEAST HYPOTHETICAL 57.9 KD PROTEIN
 IN PDB1-ABD1 INTERGENIC REGION * 1e-104 Similarity to [AAA // ATP_GTP_A] CG4538 LD45279 92B9-92B9 dup:3/3
 CG4538 ID:104B5
 + snf RNA_binding * DMD25SNRN_2 snf * U1 SMALL NUCLEAR RIBONUCLEOPROTEIN A (U1 SNRNP A PROTEIN) (SEX
 DETERMINATION PROTEIN SNF)(aa) * 3e-05 YIS9_YEAST HYPOTHETICAL 12.8 [RNP_1 // RBD // rrm] CG4528 LD45302 4F1-
 CG4528 4F2 dup:3/3 ID:104B7
 CG10825 + unknown * [NLS_BP] CG10825 LD45317 95F1-95F1 ID:104B8
 + unknown * fruit fly STS clone T7(dna) * PUTATIVE PEROXISOMAL ANTIOXIDANT ENZYME (LIVER TISSUE 2D-PAGE
 CG7217 SPOT 71B)(aa) * PEROXISOMAL MEMBRANE PROTEIN PMP20(aa) * [AhpC-TSA] CG7217 LD45324 90E-90E dup:2/2 ID:104B9
 + transcription_factor_binding * CHROMATIN ASSEMBLY FACTOR P55 SUBUNIT (CAF-1 P55 SUBUNIT) (DCAF-1)(aa) *
 SULFUR CONTROLLER-2 (SCON2)(aa) * putative WD-repeat containing protein [WD40_REGION // WD_REPEATS // WD40]
 CG1523 CG1523 LD45447 98E4-98E4 ID:104C10
 + ion_channel * HISTIDINE-RICH GLYCOPROTEIN PRECURSOR(aa) * histidine-rich protein - Plasmodium lophurae
 CG9411 (fragment) hi * [PRO_RICH] CG9411 LD45449 12E8-12E8 ID:104C11
 CG11988 + neur DNA_binding * finger protein neuralized - fruit fly (Drosophila melanogaster)(aa) * DMC3HC4ZF_2 neur * 3e-89 coded for

by C. elegans cDNA yk27g3.5; coded for by C [zf-C3HC4 // ZF_RING] CG11988 LD45505 85C4-85C5 dup:1/2 ID:104C12

CG8833 + unknown * R07E5.1 protein (clone R07E5) - Caenorhabditis elegans(aa) * 7e-49 inserted at base Both 5' and 3' ends of P element Inverse PCR * cDNA EST comes fr [PRO_RICH // D111_DOMAIN // NLS_BP] CG8833 LD45361 74B1-74B1 ID:104C2

+ 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

CG4909 54D1-54D1 ID:104C3

+ unknown * BLASTX 6.9E-07 YJL064W|Protein of unknown function(dna) * BLASTX 8.2E-11 G.gallus PR264 mRNA.(dna) * CG10084 2e-17 No definition line found * [ZF_CCCH // NLS_BP] CG10084 LD45403 37E5-37E5 dup:2/3 ID:104C7

CG1780 + Idgf4 signal_transduction imaginal disc growth factor 4 Glyco_hydro_18 CG1780 ID:104D10

+ 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

CG4656 94E-94E dup:2/2 ID:104D3

+ bl RNA_binding * hnRNP-K protein(aa) * 1e-05 YB83_YEAST HYPOTHETICAL 45.8 KD PROTEIN IN PCS60-ABD1

CG13425 INTERGENIC REGION * 4e-05 unknown * 9e-32 coded for by C. elegans CG13425 LD45549 57B1-57B1 dup:2/2 ID:104D5

CG18638+ CG18638 36A7-36A7 ID:104D7

+ unknown * nucleic acid binding protein(aa) * cDNA EST comes from this gene; cDNA EST comes from this gene; cDNA EST CG18426 yk414e4.3 comes from this gene; cDNA EST CG18426 LD45577 60A4-60A5 ID:104D9

+ cell_adhesion * 2e-09 SLIT_DROME SLIT PROTEIN PRECURSOR slit protein precurs * 2e-06 coded for by C. elegans

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

+ up ligand_binding_or_carrier * DMTROPT_2 up * clot.789(dna)* 1e-112 troponin T - fruit fly (Drosophila melanogaster) * 4e-28 TRT_CAEEL TROPONIN T coded for by C. elegans cDNA yk7 [Troponin // NLS_BP] CG7107 LD45641 12A2-12A4 dup:2/2

CG7107 ID:104E5

CG11456+ CG11456 dup:2/2 ID:104E6

+ motor_protein * 9e-09 NUF1_YEAST NUF1 PROTEIN (SPINDLE POLY BODY SPACER PROTEIN SPC110) * 6e-12

CG4925 microtubule binding protein D-CLIP-190 * 2e-29 predicted using Genef CG4925 LD45682 72E5-72E5 dup:3/3 ID:104E9

+ endopeptidase * autoantigen(aa) * 1e-67 Ki antigen PA2 * 3e-65 Ki nuclear autoantigen - human Ki nuclear autoantigen *

CG1591 IGUP_HUMAN INTERFERON GAMMA UP-REGULATED PR CG1591 LD45860 11D10-11D10 dup:2/2 ID:104F11

+ unknown * partner of Ral-binding protein 1(aa) * 3e-09 PAN1_YEAST PAN1 PROTEIN poly(A)-specific ribonuclease (EC *

CG6192 6e-06 PAST-1 * 3e-05 contain EF-hand-like c [EPS // PRO_RICH // EF_HAND_2] CG6192 LD45769 32D3-32D4 ID:104F7

+ motor_protein * protein(aa) * stromal interaction molecule 1(aa) * 2e-53 cDNA EST comes from this gene; cDNA EST co *

CG9126 1e-90 stromal cell protein [SAM_DOMAIN] CG9126 LD45776 13F14-13F14 ID:104F8

+ 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

+ * Protein kinase C-related kinase (PRKSD)(aa) * DMPKCR_2 Pkc53E * 2e-97 KPC1_YEAST PROTEIN KINASE C-LIKE (PKC 1) serine/threoni * 9e-57 p90 ribosomal [PROTEIN_KINASE_ST // PROTEIN_KINASE_DOM] CG2055 45C-45C3 dup:2/3

CG2055 ID:104G7

CG7108 + DNAPol-alpha50 DNA_replication_factor * DMDPRI_2 DNAPol- agr;50 * 8e-62 p48 DNA primase (AA 1-409) * PRI1_DROME

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

+ transporter * cystic fibrosis transmembrane conductance regulator(aa) * DMMDR49_2 Mdr49 * canalicular multispecific organic anion transporter (ABC superfamily)(a[ATP_GTP_A2 // ABC_TRANSPORTER // ABC_tr] CG7627 LD46040 29B2-29B2 dup:2/4 ID:104H4

CG7627 + ash2 transcription_factor * ash2 * trithorax protein ASH2 * 6e-83 Y17G7B.2a * 1e-134 similar to Drosophila ash2

CG6677 [SPRY_DOMAIN // NLS_BP] CG6677 LD46053 96A17-96A17 ID:104H8

+ BG:DS00004.12 unknown * hypothetical 23.1kd-like protein(aa) * 2e-17 YBF7_YEAST HYPOTHETICAL 23.1 KD PROTEIN IN

CG1307 SHP1-PTC3 INTERGENIC REGION * 9e-15 No definition line found CG1307 LD46144 84C4-84C4 ID:105A4

+ unknown * farnesoic acid o-methyltransferase(aa) * 2e-21 farnesoic acid o-methyltransferase farne * CG10527 LD46156

CG10527 57B20-57B20 ID:105A6

+ pit RNA_binding * helicase pitchoune(aa) * pit * 1e-156 HAS1_YEAST PROBABLE ATP-DEPENDENT RNA HELICASE HAS1 hypo * 1e-162 similar to DEAD-box helicases (Pfam: DEAD.[helicase_C // HELICASE // DEAD // NLS_B] CG6375 LD46167 94A1-94A1 dup:2/2 ID:105A7

CG6375 + DNA_binding * 2e-19 blastopia polypeptide - fruit fly (Drosophila melanogaster) * 4e-53 neural plakophilin related arm-repeat protein * 1e-56 neural plakophilin-r [ARM_REPEAT // Armadillo_seg] CG17484 41A1-41A1 dup:1/2 ID:105A8

CG17484 + alien endopeptidase * COP9 complex homolog subunit DCH2(aa) * alien * COP9 complex subunit 2(aa) * thyroid receptor interacting protein 15(aa) CG9556 LD46201 29F8-29F8 ID:105A9

CG9556 CG4949 + unknown * [ATP_GTP_A] CG4949 LD46305 15D1-15D1 ID:105B10

+ nucleic_acid_binding * 3e-05 YNN6_YEAST HYPOTHETICAL 49.4 KD PROTEIN IN NAM9-FPR1 INTERGENIC REGION * 2e-06 RU17_DROME U1 SMALL NUCLEAR RIBONUCLEOPROTEIN KD (U1 SNRNP KD) [PRO_RICH // NLS_BP] CG5146

CG5146 LD46256 64E-64E ID:105B4

+ actin_binding * talin(aa) * 7e-11 cytoskeleton assembly control protein SLA2 - yeast (Saccharomyces cerevisiae) * 8e-08

CG6831 merlin * talin [BAND_41_1 // Band_41 // BAND_41_3 // PR] CG6831 LD46304 66D6-66D6 dup:1/2 ID:105B9

CG6831 CG5726 + unknown * CG5726 LD46389 55B9-55B9 ID:105C10

CG5726 CG16753 + unknown * [NLS_BP] CG16753 LD46404 63B5-63B5 dup:1/2 ID:105C12

CG16753 + enzyme * similar to tumor suppressor p33ING1; similar to * Unknown protein(aa) * 5e-17 YNJ7_YEAST HYPOTHETICAL

CG9293 37.0 KD PROTEIN IN RAS2-YPT53 INTERGENIC REGI [PHD // NLS_BP] CG9293 LD46333 34B6-34B6 ID:105C2

+ Sry-delta transcription_factor * DMSRYG1_25 Sry- dgr; * serendipity beta protein(aa) * 2e-13 contains similarity to multiple C2H2-type zinc fingers (Pfam: zf-C2H2.hmm, sc * 2e-22 O [zf-C2H2 // ZINC_FINGER_C2H2_2] CG17958 LD46336 99D5-99D5

CG17958 ID:105C3

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

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

CG15081 ID:105C4

+ xl6 RNA_binding * similar to pre-mRNA splicing factor like protein; cDNA EST comes from this gene; cDNA EST comes from this gene; cDNA EST comes from this gene; cDNA [RBD // ZF_CCHC // rrm // zf-CCHC // NLS] CG10203 LD46359 27C-27C

CG10203 ID:105C6

+ unknown * 4e-41 protein * 1e-09 putative protein * coded for by C. elegans cDNA yk93e11.5; coded for by C. elegans cDNA
 CG10473 yk103a11.5; * [NLS_BP] CG10473 LD46360 37B11-37B12 ID:105C7
 + transcription_factor * zinc finger homeodomain enhancer-binding protein-1(aa) * BLASTX 1.9E-18 H.sapiens OZF
 mRNA.(dna) * transcription factor RREB-1(aa) * similar to Z[zf-C2H2 // ZINC_FINGER_C2H2 // ZINC_FIN] CG3941 LD46363
 CG3941 59E3-59E3 ID:105C9
 + SelD enzyme * SelD protein * 2e-93 similar to AIR synthase related proteins elegans * 1e-143 selenophosphate synthetase *
 CG8553 1e-159 SELD_HUMAN SELENIDE, WATER DIKINAS [AIRS] CG8553 LD46437 50F-50F dup:1/2 ID:105D2
 + unknown * 2e-42 similar to Zinc finger, C2H2 type; cDNA EST comes from * 5e-53 inserted at base 5' end of P element
 CG9890 Inverse PCR * [zf-C2H2 // ZINC_FINGER_C2H2_2] CG9890 LD46465 59C3-59C3 ID:105D4
 + DNA_binding * Smarce1-related protein(aa) * 4e-05 ORF YBR089c-a * 0.00000000002 * 5e-09 ribosomal transcription factor
 CG9418 UBF2 - Chinese hamster [HMG // HMG_box // PRO_RICH // NLS_BP] CG9418 LD46483 57C3-57C3 ID:105D6
 + transporter * nucleoporin Nup153 homolog(aa) * Ran/TC4-binding nucleopore protein(aa) * NUCLEAR PORE COMPLEX
 PROTEIN NUP153 (NUCLEOPORIN NUP153) (153 KD NUCLEOPOR [zf-RanBP // ZF_RANBP] CG4453 LD46585 14F2-14F2
 CG4453 dup:5/6 ID:105E3
 + Cpr enzyme * NADPH-CYTOCHROME P450 REDUCTASE (CPR)(aa) * DMNCP450R_2 Cpr * NADPH--ferrihemoprotein
 reductase(aa) * 3e-92 NADPH-cytochrome P450 reductase precursor [oxidored_fad // FPNCR // FLAVODOXIN //] CG11567
 CG11567 LD46590 28C7-26C4 dup:4/4 ID:105E4
 + cytoskeletal_structural_protein * protein(aa) * similar to ankyrin motifs; cDNA EST CEMSH89F comes from this gene; cDNA
 EST CEMSH89R comes from this gene; cDNA E[ANK_REP // ank // ANK_REP_REGION // PRE] CG6896 LD46604 75D2-75D2
 CG6896 dup:2/2 ID:105E5
 CG5877 + unknown * CG5877 13B9-13B9 ID:105F1
 + structural_protein * 6e-14 CUP7_DROME PUPAL CUTICLE PROTEIN EDG-78 PRECURSOR ecdyson * 2e-28
 CUD4_LOCM1 ENDOCUTICLE STRUCTURAL GLYCOPROTEIN (ABD-4A) g * 7e-16 DMEDG78B_2 [CUTICLE // insect_cuticle]
 CG8505 CG8505 49A3-49A3 ID:105F10
 + Gdi signal_transduction * 1e-135 GDI1_YEAST SECRETORY PATHWAY GDP DISSOCIATION INHIBITOR G * GDP
 dissociation inhibitor - fruit fly (Drosophila melanogaster) * Guanine nucleo [RABGDI REP // RABGDI // GDI] CG4422 LD46767
 CG4422 30B8-30B9 ID:105F11
 + transcription_factor * 7e-06 MLP2_DROME MUSCLE LIM PROTEIN MLP84B muscle L * 2e-41 similar to LIM domain
 containing proteins (5 domains); cDNA EST yk * 1e-25 TES2_M[LIM_DOMAIN_1 // LIM // LIM_DOMAIN_2] CG11914 LD46723
 CG11914 73D1-73D3 dup:2/2 ID:105F4
 + motor_protein * DMBNBR_2 bnb * mu2 * 1e-07 RRP1_DROME RECOMBINATION REPAIR PROTEIN (DNA-(APURINIC
 CG14896 OR APYRIMIDINIC SITE) L * 2e-21 C. elegans UNC-89 CG14896 LD46725 89C4-89C4 dup:1/3 ID:105F5
 + msl-1 transcription_factor * MALE-SPECIFIC LETHAL-1 PROTEIN(aa) * DMMSL1A_2 msl-1 * DMMSL1A_2 msl-1 * male-
 CG10385 specific lethal-1 protein - fruit fly (Drosophila melanogaster) CG10385 LD46729 37A4-37A4 dup:4/4 ID:105F6
 + nucleic_acid_binding * 2e-08 SFP1 * 3e-06 zinc-finger protein Pur-1 - mouse * 3e-06 MAZ * 3e-06 serum amyloid A-
 CG12054 activating factor SAF-8 [zf-C2H2 // ZINC_FINGER_C2H2 // ZINC_FIN] CG12054 LD46863 100B9-100B9 dup:1/2 ID:105G10
 CG8253 + unknown * unknown protein(aa) * 2e-21 R06C7.6 * 1e-32 unknown protein * CG8253 LD46868 52D2-52D2 ID:105G11

+ unknown * HYPOTHETICAL 32.6 KD PROTEIN C1F3.04C IN CHROMOSOME I(aa) * No definition line found(aa) *
 CG4338 Yor006cp(aa) * 7e-49 YO06_YEAST HYPOTHETICAL 35.7 KD PROT CG4338 LD46811 88E9-88E9 ID:105G2
 CG12096+ unknown * [NLS_BP] CG12096 LD46817 11D8-11D8 ID:105G4
 CG7663 + structural_protein CUTICLE PROTEIN AMP1B CUTICLE, insect_cuticle CG7663 LD46979 ID:105H11
 CG4813 + unknown * [ZF_RING] CG4813 LD46938 96F3-96F3 ID:105H5
 + unknown * protein(aa) * 3e-25 probable membrane protein YPL012w - yeast (*Saccharomyces cerevisiae*) * 7e-18 putative
 CG2691 protein (fragment) * unknown [NLS_BP] CG2691 LD46946 12A5-12A6 dup:4/4 ID:105H6
 + l(3)mbt transcription_factor * tumor-suppressor(aa) * DMMBT163 l(3)mbt * tumor-suppressor * 2e-18 predicted using Genefinder;
 CG5954 cDNA EST yk292d9.5 comes from this gen [NLS_BP] CG5954 LD46950 97F4-97F4 ID:105H7
 CG8320 + CG8320 ID:105H9
 + * 4e-10 similar to thyroglobulin and EF hand domains elega * 8e-05 testican * 6e-09 testican-3 * 8e-05 EQST_ACTEQ
 CG2264 EQUISTATIN [thyroglobulin_1 // THYROGLOBULIN_1 // k] CG2264 46D8-46D9 dup:2/2 ID:106A12
 + signal_transduction * 5e-48 pdb|1GKY| Guanylate Kinase (E.C.2.7.4.8) Complex With Guanosine Monophosphate * 2e-19
 DLG1_DROME LETHAL(1)DISCS LARGE-1 TUMOR SUPPRESSOR PROTE [PRO_RICH] CG7983 LD47023 67E5-67E5
 CG7983 ID:106A2
 + cytoskeletal_structural_protein * 1e-62 cell division cycle protein * 1e-178 SEP2_DROME SEPTIN septin * 3e-82 CDC10 *
 1e-148 SEP2_HUMAN SEPTIN HOMOLOG The gen [COPPER_BLUE // GTP_CDC // NLS_BP // ATP] CG2916 LD47044 43F7-
 CG2916 43F7 dup:1/2 ID:106A3
 + Actr13E cytoskeletal_structural_protein * DMARP_2 Actr13E * 2e-45 ACT_YEAST ACTIN actin - yeast (*Saccharomyces*
cerevisiae) * ACTU_DROME ACTIN-LIKE PROTEIN 13E actin-related protein * 1e-70 [actin] CG11678 LD47054 13E15-13E16
 CG11678 ID:106A4
 + 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 acidi [Ribosomal_L10] CG1381 LD47064 46E3-46E3
 CG1381 ID:106A5
 + unknown * CGI-67 protein(aa) * Similarity to *S. Pombe* BEM1/BUD5 suppressor; cDNA EST comes from this gene; cDNA
 CG11935 EST yk482d4.3 comes from this gene; cDNA EST y [ESTERASE] CG11935 LD47093 96B19-96B19 ID:106A6
 + unknown * clot.672(dna)* 7e-07 YEQ8_YEAST HYPOTHETICAL 58.0 KD PEPTIDASE IN PTP3-ILV1 INTERGENIC
 CG11367 REGION * 5e-08 similar to the peptidase family M24B * 3e-12 CG11367 LD47277 79F2-79F2 dup:2/2 ID:106B10
 + chaperone * 2e-11 SCJ1_YEAST SCJ1 PROTEIN SCJ1 protein - yeast (*Saccharomyce* * 6e-11 Tid(56) protein - fruit fly
 CG8448 (*Drosophila melanogaster*) * 2e-07 similar to DN [DNAJ_1 // DnaJ // DNAJ_2] CG8448 LD47190 52F8-52F9 dup:1/2 ID:106B3
 + enzyme * 3-hydroxyisobutyryl-coenzyme A hydrolase(aa) * 4e-37 YDAK_YEAST HYPOTHETICAL 56.3 KD PROTEIN IN
 CG5044 ARO3-KRS1 INTERGENIC REGION * 5e-89 similar to enoy [ECH] CG5044 LD47223 88F1-88F1 ID:106B5
 + endopeptidase * DMSTUBBLE_1 Sb * SERINE PROTEINASE STUBBLE (STUBBLE-STUBBLOID PROTEIN)(aa) * 2e-32
 similar to plasminogen and to trypsin-like serine proteases elega [trypsin // CHYMOTRYPSIN // TRYPSIN_SER] CG4386 LD47230
 CG4386 58A2-58A2 ID:106B7
 + chaperone * similar to chaperonins cpn60 and TCP-1 (Pfam: cpn60_TCP1.hmm, score: 416.20 and 102.94)(aa) *
 CG8351 Component of Chaperonin Containing T-complex subunit s [TCP1_2 // TCP1_3 // TCOMPLEXTCP1 // CHA] CG8351 LD47396

85E9-85E9 ID:106C10

+ unknown * calcium-regulated heat stable protein CRHSP-24(aa) * calcium-regulated heat stable protein CRHSP-24(aa) *

CG9705 RNA-binding protein PIPPin - rat PIPPin pr [CSD] CG9705 LD47312 73C-73C ID:106C2

+ ligand_binding_or_carrier * Rab2 * BACR37P7.a(aa) * 5e-33 YP51_YEAST GTP-BINDING PROTEIN YPT51/VPS21 GTP-

CG3870 binding pr * 7e-28 rab1 [ras // ATP_GTP_A // RASTRNSFRMNG] CG3870 LD47384 59E-59E ID:106C7

CG1103 + unknown * CG1103 LD47387 82A6-82A6 ID:106C8

+ Gbp signal_transduction * striatin, calmodulin-binding protein(aa) * WD-40-family-member * 3e-16 SFL2 gene product (AA 1-669) * 2e-19 transcription initiation factor IID-as[GPROTEINBRPT // WD40_REGION // WD_REPEA] CG5519 LD47390 55C13-55C13 ID:106C9

+ 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 ID:106D10

+ dah unknown * dystrobrevin(aa) * similar to the kDA Torpedo acetylcholine receptor-associated protein; similar to rat

CG6157 apodystrophin-3, PIR Accession Number * dah [ZF_ZZ // ZZ] CG6157 LD47411 13C1-13C1 ID:106D2

+ unknown * hypothetical protein(aa) * HSPC039 protein(aa) * 2e-11 LAS1_YEAST LAS1 PROTEIN LAS1 protein - yeast

CG6316 (Saccharomyc * CG6316 LD47413 70E1-70E1 ID:106D3

+ unknown * C26E6.5 gene product(aa) * 1e-36 C9 * 2e-38 C9 * [SPRY_DOMAIN // WD_REPEATS // GAMMA_CARB]

CG4643 CG4643 LD47425 49F13-49F13 ID:106D4

CG4037 + DNA_binding * [NLS_BP] CG4037 LD47433 49F8-49F9 ID:106D5

+ RNA_binding * SP62_HUMAN; SAP 62; SF3A66(aa) * 1e-13 PR11_YEAST PRE-MRNA SPLICING FACTOR PRP11 PRP11 protein * 4e-94 Similarity to Human splicosome-associated pro [ZF_MATRIN // PRO_RICH] CG10754 LD47455 69E2-69E2 dup:2/2 CG10754 ID:106D8

+ Gs1 enzyme * glutamate-ammonia ligase (glutamine synthase)(aa) * GLUTAMINE SYNTHETASE 2, CYTOPLASMIC (GLUTAMATE--AMMONIA LIGASE 2)(aa) * predicted using Genefind [GLNA_1 // gln-synt // GLNA_ATP] CG2718 LD47536 21B-21B dup:4/4 ID:106E11

+ transcription_factor * 8e-33 cDNA EST yk416a1.3 comes from this gene; cDNA EST yk466h2.3 comes * 1e-13 hypothetical

CG7845 protein * [NLS_BP // WD40] CG7845 LD47540 42A5-42A6 dup:2/2 ID:106E12

CG7269 + RNA_binding CG7269 dup:2/2 ID:106E3

+ 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

+ Dbp45A RNA_binding * DMDBP45A_18 Dbp45A * probable ATP-dependent RNA helicase Dbp45A - fruit fly (Drosophila melanogaster)(aa) * 1e-77 DBP8_YEAST PROBABLE ATP-DEPEND[helicase_C // ALDEHYDE_DEHYDR_CYS // HE] CG12759 CG12759 LD47509 45A11-45A11 dup:3/3 ID:106E5

+ signal_transduction * 1e-71 YG4C_YEAST HYPOTHETICAL 89.4 KD TRP-ASP REPEATS CONTAINING PROTEIN IN PMT6-PCT1 * 7e-09 Lis1 homolog * 8e-08 YKY4_CAEEL HYPOTHETICAL[GPROTEINBRPT // WD40_REGION // WD_REPEA] CG11887 CG11887 LD47515 47B1-47B1 dup:3/3 ID:106E6

CG2182 + unknown * [NLS_BP] CG2182 LD47517 83B7-83B7 dup:3/3 ID:106E7

+ 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
 CG4535 LD47530 30E1-30E1 dup:2/2 ID:106E9
 + peptidase * VITELLOGENIC CARBOXYPEPTIDASE PRECURSOR(aa) * Probable serine-type carboxypeptidase (EC 3.4.16.1); Ybr139wp(aa) * Similarity to Human lysosomal pro [CARBOXYPEPT_SER_SER // CARBOXYPEPT_SER_] CG4572
 CG4572 LD47549 92B6-92B6 ID:106F2
 + signal_transduction * Ylr222cp(aa) * WD repeat protein(aa) * coatomer alpha subunit(aa) * BLASTX 2.6E-32 YLR222C|Protein of unknown function, has beta-transducin (WD-[GPROTEINBRPT // WD40_REGION // WD_REPEA] CG1671
 CG1671 LD47550 46B13-46B14 ID:106F3
 CG13852+ unknown * CG13852 LD47553 96E1-96E1 ID:106F5
 + mbt protein_kinase * protein kinase protein serine/threonine kinase) * 3e-36 serine/threonine protein kinase * 1e-146 Ste20 serine/threonine protein kinase homolog[TYRKINASE // PROTEIN_KINASE_DOM // pkin] CG18582 LD47563 14F2-14F2 dup:2/2
 CG18582 ID:106F7
 + transcription_factor_binding * hypothetical protein(aa) * 2e-05 serine-threonine kinase receptor-associated protein * 2e-05
 CG5632 WD-40 repeat protein * 3e-05 DMEST6P_15 Est-P [WD40_REGION // WD40] CG5632 LD47568 68F8-68F8 dup:1/2 ID:106F8
 + stg protein_tyrosine_phosphatase * DMCDC25_2 stg * 3e-21 MPIP_YEAST M-PHASE INDUCER PHOSPHATASE (MITOSIS INITIATION PROTEIN MIH1) (MITOT * cdc25 protein - fruit fly (D[Rhodanese // RHODANESE // MPIPHPHTASE] CG1395
 CG1395 LD47579 99A5-99A6 dup:3/3 ID:106F9
 + ea endopeptidase * DMEAST_4 ea * SERINE PROTEASE EASTER PRECURSOR(aa) * 5e-20 kallikrein * 8e-29 airway
 CG4920 trypsin-like protease a [ANTENNAPEDIA // trypsin // CHYMOTRYPSIN] CG4920 LD47701 90E1-90E1 ID:106G12
 CG14965+ motor_protein * CG14965 LD47616 63B13-63B13 ID:106G2
 CG14954+ unknown * CG14954 LD47625 63F4-63F4 ID:106G4
 + unknown * cDNA EST comes from this gene; cDNA EST comes from this gene; cDNA EST comes from this gene; cDNA
 CG8399 EST comes from this gene; cDNA EST yk226e12.3 com CG8399 LD47639 52E1-52E3 dup:2/2 ID:106G6
 + unknown * 5e-14 /match=(desc: * 6e-43 weak similarity to drosophila tyrosine kinase ele * 5e-23 The gene is expressed ubiquitously.; The protein * 1e-20 caffe [PAP_ASSOCIATED // PAP_CORE // PAP // PR] CG15737 LD47659 10F5-10F6 dup:1/2
 CG15737 ID:106G9
 + transcription_factor * ovo * DMSPALTR_3 salr * 6e-29 GLAS_DROME GLASS PROTEIN finger protein glass - fruit fly [zf-
 CG3281 C2H2 // ZINC_FINGER_C2H2 // HISTONE_] CG3281 LD47774 87A7-87A7 ID:106H11
 + unknown * cDNA EST comes from this gene; cDNA EST comes from this gene(aa) * huntingtin interacting protein HYPE(aa)
 CG9523 * 9e-84 cDNA EST comes from this gene; c [TPR_REGION // TPR_REPEAT] CG9523 LD47713 26D3-26D3 ID:106H2
 + unknown * 2e-09 YNY5_YEAST HYPOTHETICAL 20.4 KD PROTEIN IN RPA49-SUI1 INTERGENIC REGION * 2e-08 coded
 CG2843 for by C. elegans cDNA yk127b8.5; coded for by C. elegans [NLS_BP] CG2843 LD47748 23A7-23A7 ID:106H9
 CG18543+ unknown * CG18543 LD47919 66C12-66C12 ID:107B1
 + enzyme * 1e-19 FAT2_YEAST PEROXISOMAL-COENZYME A SYNTHETASE probable AMP * 3e-11 acetyl-CoA
 CG5568 synthetase - fruit fly (Drosophila melanogaster) * 9e-40 similar [AMP-binding] CG5568 LD47944 64F3-64F3 ID:107B6
 CG4069 + unknown * Kelch-repeat protein, similar to Kel1 and Kel2; Kel3p(aa) * 2e-32 hypothetical protein YPL263c - yeast

(Saccharomyces cerevisiae) * 9e-06 host cell [NLS_BP] CG4069 LD47970 69C4-69C4 ID:107B8
 + unknown * 5e-17 probable membrane protein YLR418c - yeast (Saccharomyces cerevisiae) * 1e-10 unknown conserved
 CG11990 hypothetical protein * [DDC_GAD_HDC_YDC] CG11990 LD47989 85C5-85C5 dup:3/3 ID:107B9
 + 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
 + enzyme * MALEYLACETOACETATE ISOMERASE (MAAI)(aa) * glutathione transferase zeta 1(aa) * similar to glutathione S-
 CG9362 transferase(aa) * 9e-06 glutathione transfer [GST] CG9362 LD48010 85D18-85D18 ID:107C4
 + 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 // CRBOXYPTASEA // Zn_]
 CG3108 CG3108 LP01044 5B6-5B8 ID:107D1
 + 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
 CG12237 + unknown * 8e-24 putative phosphatase * * CG12237 LP01149 18D10-18D10 ID:107D4
 + transporter * 9e-23 probable membrane protein YPR011c - yeast (Saccharomyces cerevisiae) * 2e-07 colt * 2e-39 Similar to
 CG6608 mitochondrial carrier protein * 6e-15 bra [mito_carr // MITOCARRIER // MITOCH_CARR] CG6608 LP01207 86C7-86C7 ID:107D8
 + 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
 + Cht3 enzyme * chitinase(aa) * 2e-22 probable membrane protein YDR371w - yeast (Saccharomyces cerevisiae) * 2e-63
 CG18140 chitinase * 1e-44 CHIT_CAEEL PUTATIVE ENDOCHITIN CG18140 LP01426 40D5-40D5 dup:4/4 ID:107E10
 CG1252 + Ccp84Ab structural_protein cuticle cluster 7 CUTICLE, insect_cuticle CG1252 LP01435 dup:2/2 ID:107E11
 CG4664 + CG4664 dup:2/2 ID:107E12
 + LanA cell_adhesion * 7e-05 RA50_YEAST DNA REPAIR PROTEIN RAD50 (153 KD PROTEIN) RAD50 * LMA_DROME
 LAMININ ALPHA CHAIN PRECURSOR laminin chain A * 1e-114 similar to [RNP_1 // EGF_1 // EGFLAMININ // LAMININ] CG10236
 CG10236 LP01316 65A6-65A6 dup:5/5 ID:107E3
 + tok endopeptidase * tok * development protein tolkin - fruit fly (Drosophila melanogaster) * 1e-145 similar to developmentally
 CG6863 important proteins like human BMP-1 [EGF // CUB // ASTACIN // Astacin // EGF] CG6863 LP01328 96A20-96A22 dup:3/3 ID:107E4
 CG1153 + unknown * CG1153 LP01348 83E2-83E2 dup:2/2 ID:107E8
 + transcription_factor * DMRCPA_X kel * leucine-zipper-like transcriptional regulator, 1(aa) * 4e-12 YG52_YEAST
 CG3711 HYPOTHETICAL 100.0 KD PROTEIN IN YHB1-PFK1 INTERGENIC REGION [BTB] CG3711 LP01394 1C5-1C5 dup:2/2 ID:107E9
 + signal_transduction * similar to epidermal growth factor receptor kinase substrate; cDNA EST comes from this gene; cDNA
 CG8907 EST comes from this gene; cDNA EST yk246h9.3 come [SH3 // PRO_RICH] CG8907 LP01469 92C1-92C1 ID:107F1
 + receptor * 4e-06 LDL receptor-like repeat; orfla * 2e-47 coded for by C. elegans cDNA yk9e10.5; coded for by C. elegans
 CG8756 cDNA yk9e10.3; mu * 3e-07 very low dens [LDLRA_2 // ldl_recept_a // LDLRA_1] CG8756 LP01646 76C-76C ID:107F11
 + enzyme * steroid sulfotransferase 3(aa) * 7e-25 tyrosine-ester sulfotransferase * 2e-24 SUPM_HUMAN MONOAMINE-
 CG5431 SULFATING PHENOL SULFOTRANSFERASE (SULFOTRANSFER [Sulfotransfer] CG5431 LP01553 59F4-59F4 ID:107F4

+ enzyme * 1e-107 ecto-5'-nucleotidase * 1e-105 5' nucleotidase (CD73) 5'-NUCLEOTID * 1e-132 putative 5'-nucleotidase *
 CG4827 3e-08 inserted at base 5' end of P elem [PHOSPHO_ESTER // 5_nucleotidase // 5_NU] CG4827 LP01562 54C6-54C6 ID:107F5
 + 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
 + transmembrane_receptor * 2e-08 /match=(desc: * 6e-55 predicted using Genefinder * No definition line found * predicted
 CG14205 using Genefinder CG14205 LP01839 18D7-18D7 ID:107G10
 + Lnk signal_transduction * 3e-08 corkscrew protein 4A * 5e-61 Pro-rich, PH, SH2 domain-containing signaling mediator * 9e-63
 CG17367 hypothetical protein [SH2DOMAIN // SH2 // PH_DOMAIN] CG17367 LP01675 96F7-96F ID:107G3
 + EG:34F3.7 enzyme * DOLICHYL-PHOSPHATE-MANNOSE--PROTEIN MANNOSYLTRANSFERASE 1(aa) * BLASTX 2.9E-25
 CG12311 PMT4|Mannosyltransferase (dolichyl phosphate-D-mannose:protein O-D-ma CG12311 LP01681 1C2-1C2 ID:107G4
 + 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-
 CG5584 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
 CG16926+ unknown * CG16926 LP01766 56D10-56D10 ID:107G8
 + motor_protein * 6e-23 ARP5_YEAST ACTIN-LIKE PROTEIN ARP5 probable nuclear pro * 2e-12 ACTU_DROME ACTIN-
 CG12321 LIKE PROTEIN 13E actin-related protein * 6e-11 similar to Act CG12321 LP02120 90E6-90E6 ID:107H11
 + transcription_factor * LIM-domain protein LMP-1(aa) * 6e-06 LRG1 * 7e-15 PINCH * 1e-18 UN97_CAEEL HOMEBOX
 PROTEIN UNC-97 contains two LIM domain [LIM_DOMAIN_1 // LIM // LIM_DOMAIN_2] CG8242 LP02021 52C7-52C7 dup:3/3
 CG8242 ID:107H6
 + crol transcription_factor * crol * BLASTX 2.3E-25 Human kruppel-related zinc finger protein (ZNF184) mRNA, partial cds.(dna) *
 CROL GAMMA * 4e-14 HSN motor neurons m[zf-C2H2 // ZINC_FINGER_C2H2 // ZINC_FIN] CG14938 LP02106 33B1-33B1
 CG14938 dup:2/2 ID:107H9
 + receptor * putative mitochondrial inner membrane protein import receptor(aa) * MITOCHONDRIAL IMPORT INNER
 CG11779 MEMBRANE TRANSLOCASE SUBUNIT TIM44 PRECURSOR(aa) * P CG11779 91F4-91F4 dup:1/2 ID:108A11
 + ligand_binding_or_carrier * 2e-08 galactose specific C-type lectin * 3e-10 lectin lambda * 7e-13 mannose receptor, C type
 CG9134 MACROPH * 3e-08 C-type lectin-like protein [lectin_c // C_TYPE_LECTIN_1 // C_TYPE_L] CG9134 LP02252 61F4-61F4 ID:108A3
 CG18179+ unknown * CG18179 LP02275 67B-67B ID:108A4
 CG13627+ unknown * CG13627 LP02282 96A20-96A20 ID:108A5
 + ligand_binding_or_carrier * retinaldehyde-binding protein 1(aa) * ALPHA-TOCOPHEROL TRANSFER PROTEIN (ALPHA-
 TTP)(aa) * 8e-07 SC14_YEAST SEC14 CYTOSOLIC FACTOR (PHOSPHATIDYLINOSI [CRETINALDHBP // CRAL_TRIO] CG5958
 CG5958 LP02316 27F7-27F7 ID:108A6
 + P5cr enzyme * 6e-29 PROC_YEAST PYRROLINE-5-CARBOXYLATE REDUCTASE (P5CR) (P5C REDUCTASE) * 1e-157
 CG6009 pyrroline 5-carboxylate reductase * 3e-52 similar to pyrroline-5- [P5CR] CG6009 LP02537 91E4-91E4 ID:108B2
 CG10200+ unknown * CG10200 LP02570 51C5-51C5 ID:108B4

+ ligand_binding_or_carrier * 9e-14 accessory gland protein Acp29AB * 1e-07 coded for by C. elegans cDNA CEESH64R;
 coded for by C. elegans cDNA CEMSH13F; co * 8e-06 MABA_MOUSE MA [lectin_c // C_TYPE_LECTIN_2] CG15818 LP02603
 CG15818 27F6-27F6 ID:108B6
 + actin_binding * kelch protein; ring canal component involved in cytoplasmic bridges; 77% Similarity to * 2e-93 kelch protein,
 CG17754 long form - fruit fly (Drosophila mela [BTB // Kelch] CG17754 LP02641 8D6-8D6 dup:2/2 ID:108B7
 + endopeptidase serine proteinase (EC 3.4.21.-) 2 precursor - fruit fly CHYMOTRYPSIN, TRYPSIN_CATAL, TRYPSIN_SER,]
 CG10475 CG10475 ID:108C1
 + peptidase * 1e-109 AAP1_YEAST ALANINE/ARGININE AMINOPEPTIDASE aminopeptidase * 1e-121 F49E8.3 gene
 product * 1e-175 AMPE_MOUSE GLUTAMYL AMINOPEPTIDASE (EAP) (AM [ALADIPTASE // Peptidase_M1 // ZINC_PROT]
 CG8773 CG8773 LP02833 87E5-87E5 ID:108C3
 CG18546 + unknown * CG18546 LP02835 87A6-87A6 ID:108C4
 + 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
 CG4799 LP03126 31A1-31A1 ID:108D10
 CG13330 + unknown * [NLS_BP] CG13330 50B2-50B2 dup:1/2 ID:108D11
 + Ald enzyme * plastidic aldolase(aa) * ALDOLASE-RELATED PROTEIN(aa) * DMALD_10 Ald * 1e-118 similar to Fructose-
 biphosphate aldolase class-I; cDNA EST yk252e [glycolytic_enzy // ALDOLASE_CLASS_I //] CG6058 LP03138 97A6-97A6
 CG6058 dup:4/4 ID:108D12
 + protein_kinase * DMCDK46_3 Cdk4/6 * DMCDK5_3 Cdk5 * SNF1A * DMMAPKIN_4 rl [LDLRA_2 //
 CG8250 RECEPTOR_TYR_KIN_II // PROTE] CG8250 LP03070 53C10-53C11 ID:108D5
 + serpin * ZG-21p protein - rat(aa) * protease inhibitor (ovalbumin type)(aa) * 9e-10 Similar to serine protease inhibitor * 2e-17
 CG1342 PAI2_MOUSE PLASMINOGEN ACTIV [serpin] CG1342 LP03106 100A3-100A3 ID:108D8
 + sktl enzyme * phosphatidylinositol 4-phosphate 5-kinase(aa) * skittles * 7e-28 'multicopy suppressor of stt4 mutation (MSS4)'
 CG9985 cerev * phosphatidylinositol 4-phosp [NLS_BP] CG9985 LP03320 57B6-57B6 dup:2/2 ID:108E11
 + transporter * 4e-15 hypothetical protein YDR387c - yeast (Saccharomyces cerevisiae) (U * 2e-35 GTRL_DROME GLUCOSE
 TRANSPORTER-LIKE PROTEIN glucose transpo * 3e-[SUGRTRNSPORT // SUGAR_TRANSPORT_1 // SU] CG7801 LP03341
 CG7801 48B5-48B5 dup:2/2 ID:108E12
 + 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
 + unknown * predicted using Genefinder; similar to GNS1/SUR4 family; cDNA EST comes from this gene(aa) * CGI-88
 CG5326 protein(aa) * 9e-15 SUR4_YEAST SUR4 PROTEIN (SRE CG5326 LP03255 94B5-94B5 dup:2/2 ID:108E4
 + caup transcription_factor * DMCAUP_2 caup * 2e-07 CUP9_YEAST HOMEBOX PROTEIN CUP9 copper homeostasis pro *
 CAUP_DROME HOMEBOX PROTEIN CAUPOLICAN caupo * 2e-24 IRXH_[HOMEBOX_1 // homeobox // HOMEBOX_2]
 CG10605 CG10605 LP03275 69C9-69C11 dup:2/2 ID:108E8
 + Lsp1gamma larval_serum_protein * hexamerin A; arylphorin-like protein(aa) * Lsp1 bgr; * LARVAL SERUM PROTEIN BETA
 CG6821 CHAIN PRECURSOR(aa) * 8e-06 AMYH_YEAST GLUCOAMYLASE S1/S2 PRECU[hemocyanin // HEMOCYANIN_2 //

HAEMOCYAN] CG6821 LP03463 61A2-61A2 ID:108F5
+ enzyme * hydroxysteroid (17-beta) dehydrogenase 4(aa) * peroxisomal multifunctional beta-oxidation protein; Fox2p(aa) *
ESTRADIOL BETA-DEHYDROGENASE (17-BETA [GDHRDH // adh_short // ADH_SHORT // THI] CG3415 LP03478 14B11-14B11
CG3415 dup:2/2 ID:108F6
+ BcDNA:GH09358 unknown * cDNA EST comes from this gene; cDNA EST comes from this gene; cDNA EST comes from this
CG2967 gene; cDNA EST comes from this gene; cDNA EST comes from thi CG2967 LP03505 9B6-9B7 dup:4/4 ID:108F7
CG5904 + islet mitochondrial antigen CG5904 LP03542 ID:108F8
+ enzyme * contains similarity to enoyl-CoA hydratases/isomerases Score=59.1, E=3.3e-16, N=1)(aa) * 3e-51 Similar to enoyl-
CG5844 coA hydratase * 2e-15 ECH1_MOUSE PRO [ECH] CG5844 LP03547 87B15-87B15 ID:108F9
+ brat transcription_factor * transcription factor(aa) * 1e-142 YOG2_CAEEL HYPOTHETICAL ZINC FINGER PROTEIN ZK112.2
IN CHROMOSOME III * 2e-38 protein * 9e-38 RING finger[ZF_BBOX // NHL // ZINC_FINGER_C2H2 // Z] CG10719 LP03649 37C4-
CG1071937C dup:3/5 ID:108G1
CG1806 + unknown * CG1806 LP03706 11A3-11A3 ID:108G2
+ translation_factor * kDa protein; Fun12p(aa) * 1e-120 YAD5_YEAST 112.3 KD PROTEIN IN PYK1-SNC1 INTERGENIC
REGION * 1e-11 waclaw * 3e-18 similar to initiation factor IF-[ELONGATNFCT // NLS_BP // GTP_EFTU // AT] CG10840 LP03795
CG1084063D2-63D2 ID:108G5
CG6981 + unknown * CG6981 LP03829 77A2-77A2 ID:108G7
+ enzyme * HemE homolog(aa) * uroporphyrinogen decarboxylase; Hem12p(aa) * UROPORPHYRINOGEN
DECARBOXYLASE (UPD)(aa) * UROPORPHYRINOGEN DECARBOXYLASE (URO-D)(a [UROD_1 // UROD_2 // URO-D] CG1818
CG1818 LP03960 45F4-45F4 ID:108H1
+ transporter * renal organic cation transporter(aa) * solute carrier family (organic cation transporter), member 5(aa) * sodium-
CG17752 dependent carnitine transporter(aa) [sugar_tr] CG17752 LP04053 94D3-94D3 ID:108H10
CG6234 + motor_protein * 1e-06 TRFA * * CG6234 LP04345 87C6-87C6 dup:1/2 ID:108H11
+ serpin * SQUAMOUS CELL CARCINOMA ANTIGEN (SCCA-2) (LEUPIN)(aa) * ALPHA-1-ANTIPROTEINASE PRECURSOR
CG6687 (ALPHA-1-ANTITRYPSIN) (ALPHA-1-PROTEINASE INHIBITOR)(aa) * [serpin] CG6687 LP04383 88E7-88E7 ID:108H12
CG11169+ unknown * CG11169 LP04006 60A1-60A2 ID:108H6
+ 6-phosphofructo-2-kinase enzyme * 6-phosphofructo 2-kinase/fructose 2,6-bisphosphatase long form(aa) * 1e-105 F26_YEAST
FRUCTOSE-2,6-BISPHOSPHATASE fructose-2,6-bisp * 1[6PFRUCTKNASE // PGAM // PG_MUTASE // IG] CG3400 LP04008
CG3400 18D1-18D1 dup:4/4 ID:108H7
+ kst actin_binding * DMBHSPEC kst * beta-heavy-spectrin(aa) * SPCA_DROME SPECTRIN ALPHA CHAIN spectrin alpha
chain - fr * Similar to spectrin beta chain; coded for [SPECTRINPH // spectrin // CH_DOMAIN //] CG12008 LP04011 63C5-63D
CG12008dup:4/5 ID:108H8
CG14766+ unknown CG14766 LP04033 ID:108H9
+ unknown * No definition line found(aa) * 1e-07 YJU7_YEAST HYPOTHETICAL 229.9 KD PROTEIN IN NUC1-NCE1
CG2747 INTERGENIC REGION * 6e-20 Unknown protein * HYPOTHETICAL CG2747 84E6-84E6 dup:1/7 ID:109A1
CG3628 + unknown * 1e-118 inserted at base Both 5' and 3' ends of P element Inverse PCR * 1e-118 inserted at base Both 5' and 3'

ends of P element Inverse PCR * CG3628 67B4-67B4 dup:1/3 ID:109A10

+ DnaJ-60 chaperone * dnaJ-like protein(aa) * DMDNALP_2 DnaJ-60 * 3e-08 SCJ1_YEAST SCJ1 PROTEIN SCJ1 protein - yeast
CG12240 (Saccharomyce * 1e-114 dnaJ-like protein [DnaJ // DNAJ_2] CG12240 LP04971 60B9-60B9 dup:3/3 ID:109B12

CG12373+ CG12373 ID:109B8

+ enzyme * lipoamide dehydrogenase(aa) * 1e-157 DLDH_YEAST DIHYDROLIPOAMIDE DEHYDROGENASE PRECURSOR
dihydr * 7e-19 GSHR_DROME GLUTATHIONE REDUCTASE (GR) (GRAS [HGRDTASE // FADPNR // pyr_redox // PYRI] CG7430

CG7430 LP04889 75A4-75A4 ID:109B9

+ chaperone * DMTIDT4M_4 l(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

+ endopeptidase * zgr;Try * chimeric AFGP/trypsinogen-like serine protease precursor(aa) * 1e-40 TRYA_DROME TRYPSIN
ALPHA PRECURSOR trypsin-like proteinase (* 4e-27 [trypsin // CHYMOTRYPSIN // G_PROTEIN_RE] CG10882 LP05220 23D1-
CG10882 22D4 ID:109C11

+ unknown * 3e-97 transmembrane protein * 3e-07 similar to cuticulin 1; cDNA EST comes from this gene; * 4e-99

CG15013 DMDUSKY_1 dy * 5E-84 CG15013 LP05062 64B6-64B6 ID:109C3

+ m1 unknown * M1 protein(aa) * 4e-82 M1 protein * 3e-05 Similarity to Crayfish proteinase inhibitor cDNA ES * 5e-05

CG8342 IOV7_CHICK OVOINHIBITOR PRECURSOR ovoinhibito CG8342 LP05127 96F10-96F10 ID:109C5

+ 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

+ Neurotactin cell adhesion axon, ocellar nerve, ventral nerve cord CARBOXYLESTERASE_B_2, COesterase, ESTERA] CG9704

CG9704 LP05519 ID:109D11

+ Oscp enzyme * DMOSCPPRE_2 Oscp * ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit (oligomycin
sensitivity conferring protein)(aa) * coded for b [ATPASEDELTA // OSCP] CG4307 90D1-90D1 dup:2/2 ID:109D2

CG4307 + Rrp1 DNA_repair_protein * DMRRP1_2 Rrp1 * RECOMBINATION REPAIR PROTEIN (DNA-(APURINIC OR APYRIMIDINIC
SITE) LYASE)(aa) * 7e-63 similar to AP endonucleases family 1; cDNA EST [AP_NUCLEASE_F1_3 // AP_endonucleas1 //]

CG3178 CG3178 LP05366 23C2-23C2 ID:109D3

+ transcription_factor * DMBTDGN_2 btd * 3e-18 ODD_DROME ODD-SKIPPED PROTEIN odd * 5e-19 Similarity to
Drosophila scratch neuronal zinc-finger transcriptio * 2e-35 Z13 prote [zf-C2H2 // ZINC_FINGER_C2H2 // ZINC_FIN] CG6911

CG6911 LP05442 4D1-4D1 ID:109D5

+ RNA_binding * ventral antigen 1(aa) * astrocytic NOVA-like RNA-binding protein(aa) * 0.00000003 * 2e-13 similar to RNA
binding protein; cDNA EST comes from th [KH-domain // KH_DOMAIN // ANTIFREEZEI] CG8144 LP05458 85D-85D ID:109D7

CG8144 + ppl enzyme * predicted using Genefinder(aa) * 5e-19 GCSH_YEAST GLYCINE CLEAVAGE SYSTEM H PROTEIN

CG7758 PRECURSOR F * 3e-28 predicted using Genefinder * 7e-32 glycine c [LIPOYL] CG7758 LP05579 78C8-78C8 dup:2/2 ID:109E4

+ Cyt-c1 electron_transfer * CYTOCHROME C(aa) * 1e-32 pdb|1YCC| Cytochrome C (Isozyme 1) (Reduced) Saccharomyces
cerevisia * 2e-58 CYC1_DROME CYTOCHROME C-1 cytochrome c[CYTCHRMEDIAB // cytochrome_c // CYTOCHR] CG13263

CG13263 LP05614 36A7-36A7 dup:2/2 ID:109E5

CG6933 + structural_protein * peritrophin-48a precursor(aa) * peritrophin-44(aa) * SW-peritrophin-48 precursor(aa) * CG6933

LP05638 77A-77A dup:3/3 ID:109E6
 + actin_binding * 5e-06 alternatively spliced form * 9e-06 alpha-actinin * protein * 9e-06 alpha-actinin - rabbit (fragment) muscle
 CG11685 alp [CH_DOMAIN] CG11685 LP05986 85F7-85F7 ID:109F10
 CG9568 + unknown * CG9568 LP05845 29F8-29F8 ID:109F2
 + Rab3 signal_transduction * enzyme RHO small GTPase) map_position:47B * 2e-47 SEC4_YEAST RAS-RELATED PROTEIN
 SEC4 GTP-binding protein SE * 1e-127 RAB3_DROME RAS-RELATED PROTEIN [ras // ATP_GTP_A // RASTRNSFRMNG]
 CG7576 CG7576 LP05860 47B7-47B7 ID:109F3
 + enzyme * MEMBRANE-BOUND ALKALINE PHOSPHATASE PRECURSOR (M-ALP)(aa) * DMALKPHOS_2 Aph-4 * 8e-26
 repressible alkaline phosphatase (EC 3.1.3.1) * 9e-78 alkaline [ALKPHPTASE // alk_phosphatase] CG5656 LP05865 78D5-78D5
 CG5656 dup:2/2 ID:109F4
 CG9795 + unknown * CG9795 LP05867 82A5-82A5 dup:2/2 ID:109F5
 + 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
 CG5770 + unknown * CG5770 LP06072 55B-55B ID:109G1
 CG4449 + unknown * CG4449 LP06117 97B1-94E9 ID:109G2
 CG14681 + unknown * 1e-08 H06A10.1 * 1E-168* CG14681 LP06211 86C2-86C2 ID:109G4
 CG14455 + CG14455 LP06288 ID:109G6
 CG18324 + unknown * CG18324 SD01736 50E4-50E4 ID:113A12
 + puckeredprotein_phosphatase YEAST PROTEIN-TYROSINE PHOSPHATASE MSG5 DSPc, TYR_PHOSPHATASE_1,
 CG7850 TYR_PHOSPHATASE] CG7850 SD01814 ID:113B11
 + serpin * 2e-44 Similar to serine protease inhibitor * 6e-55 NEUS_MOUSE NEUROSERPIN PRECURSOR (PROTEASE
 CG9453 INHIBITOR 17) * 1e-54 protease inhibitor (neuroserpin) [serpin // ER_TARGET] CG9453 SD01756 42C8-42C8 dup:2/2 ID:113B2
 + pbl signal_transduction * ect2 oncogene(aa) * 4e-05 regulatory protein CLS4 - yeast (Saccharomyces cerevisiae) * 3e-08
 /match=(desc;; /ma * 1e-30 similar to transf[GRF_DBL // BRCT_DOMAIN // G_PROTEIN_REC] CG8114 SD01796 66A18-66A20
 CG8114 dup:2/4 ID:113B7
 + signal_transduction * phosphatidylinositol-4-phosphate 5-kinase isolog(aa) * HYPOTHETICAL PROTEIN * 1e-06 weak
 similarity with BRKA gene from Bordetella Pertussis; cDNA[RCC1 // RCC1_2 // GRF_RCC // RCCNDNSATI] CG7158 SD01835
 CG7158 78F2-78F2 ID:113C1
 + LanB2 cell_adhesion * DMLAMB01_2 LanB2 * LAMININ-LIKE PROTEIN C54D1.5 PRECURSOR(aa) * LAMININ GAMMA-1
 CHAIN PRECURSOR (LAMININ B2 CHAIN)(aa) * 2e-06 putative [ADH_ZINC // laminin_B // laminin_EGF //] CG3322 SD01934
 CG3322 67B-67B ID:113C10
 + unknown * 8e-21 ERP6_YEAST ERP6 PROTEIN PRECURSOR probable membrane pro * 9e-39 similar to
 emp24/gp25L/p24 family * 8e-72 associated to apparatus * 2e-51 G25L [EMP24_GP25L] CG9443 SD01878 85E4-85E5 dup:1/2
 CG9443 ID:113C5
 + unknown * * 5e-87 lclprt_seq No definition line found * YB3C_SCHPO HYPOTHETICAL 60.9 KD PROTEIN C2F12.12C IN
 CG1676 CHROMOSOME II * [NLS_BP] CG1676 SD01916 19D2-19D2 ID:113C9

+ actin_binding * TENSIN(aa) * 3e-63 coded for by C. elegans cDNA yk126c6.3; coded for by C. elegans cDNA yk125d8.5; *
 CG9379 2e-74 tensin - chicken tensin * coded for by C. [SH2] CG9379 SD01953 85D23-85D23 ID:113D1
 CG17836+ unknown * [NLS_BP] CG17836 SD01985 91D4-91D4 dup:2/2 ID:113D3
 CG13323+ unknown CG13323 ID:113D4
 + unknown * coded for by C. elegans cDNA yk61f1.3; coded for by C. elegans cDNA yk109h8.3; coded for by C. elegans
 CG8576 cDNA CEESX42F; coded for by C. elegans cDNA CG8576 SD02002 65F5-65F5 ID:113D5
 + enzyme * 5e-16 YM71_YEAST HYPOTHETICAL OXIDOREDUCTASE IN MRPL44-MTF1 INTERGENIC REGION * 2e-12
 antennal-specific short-chain dehydrogenase/reductase * 2e-64 [adh_short_C2 // GDHRDH // adh_short //] CG10672 SD02021
 CG10672 64C12-64C12 dup:2/2 ID:113D8
 + unknown * similar to S. cerevisiae hypothetical 240.3 kd protein in MSH3 3' * GENERAL NEGATIVE REGULATOR OF
 TRANSCRIPTION SUBUNIT 1(aa) * t7i23.15 protein.(a [LECTIN_LEGUME_BETA // FGGY_KINASES_2 //] CG1884 SD02024
 CG1884 45F3-45F4 dup:5/7 ID:113D9
 + motor_protein * contains similarity to ATP synthase subunit B(aa) * Segregation of mitotic chromosomes (SMC1, yeast
 human homolog of(aa) * 1e-124 SMC1_YEAST CHROMOS [DA_BOX // NLS_BP // ATP_GTP_A] CG6057 SD02122 95D5-95D5
 CG6057 dup:2/2 ID:113E11
 + Rpl135 enzyme * DMRP135_2 Rpl135 * DNA-DIRECTED RNA POLYMERASE I KD POLYPEPTIDE (RNA POLYMERASE I
 SUBUNIT 2)(aa) * RPA2_YEAST DNA-DIRECTED RNA POLYMERASE I KD POLY [RNA_pol_B // RNA_POL_BETA] CG4033
 CG4033 SD02110 21C2-21C2 dup:4/4 ID:113E8
 + aft unknown * 2e-05 YBR1_YEAST HYPOTHETICAL 34.7 KD PROTEIN IN ORC2-TIP1 INTERGENIC REGION * Adrift * 2e-22
 CG5032 contains similarity to Methanococcus jannaschii cell d CG5032 SD02116 54E10-54E10 dup:3/3 ID:113E9
 none + none SD02145 ID:113F3
 + enzyme_inhibitor * protein(aa) * protein(aa) * protein(aa) * [ANK_REP // ank // ANK_REP_REGION] CG8465 SD02148
 CG8465 16B5-16B6 dup:2/4 ID:113F4
 + unknown * UNKNOWN; PRC1(aa) * protein regulating cytokinesis 1; PRC1 * [G_PROTEIN_GAMMA] CG1655 SD02150
 CG1655 9F5-9F5 ID:113F5
 CG9042 + enzyme CG9042 ID:113F9
 + enzyme * similar to aspartyl-tRNA synthetase; cDNA EST yk250e3.3 comes from this gene(aa) * 2e-40 SYDM_YEAST
 ASPARTYL-TRNA SYNTHETASE, MITOCHONDRIAL (ASPARTA [tRNA-synt_2 // TRNASYNTHLYS // TRNASYNT] CG17938
 CG17938 SD02215 36A10-36A10 ID:113G1
 + 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
 + 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
 CG1763 10C5-10C6 ID:113H6
 + signal_transduction * beta2-chimerin, cerebellar - human(aa) * beta2-chimerin, cerebellar - rat (fragment)(aa) * 2e-07
 CG3208 BEM2_YEAST GTPASE ACTIVATING PROTEIN BEM2/IP[RHO_GAP // RhoGAP // DAG_PE_BINDING_DOM] CG3208 SD02309

5A8-5A8 dup:1/3 ID:113H7

+ Prosalpha1 unknown * endopeptidase multicatalytic endopeptidase) cell 26S proteasome) map_position:54B3-5 * 20S

CG18495 proteasome subunit alpha1(aa) * endopeptidase multicatalytic endopeptidase) cell 26S proteasome) map_position:54B3-5 * 20S

+ 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-binding] CG8732

CG8732 SD02373 44D4-44D ID:114A6

+ transcription_factor * CCAAT-box-binding transcription factor(aa) * 6e-35 probable membrane protein YDR060w - yeast

CG7839 (Saccharomyces cerevisiae) * 1e-76 predicted using Gene [NLS_BP] CG7839 SD02424 70E1-68A3 ID:114B2

+ hts actin_binding * adducin homolog - fruit fly (Drosophila melanogaster)(aa) * similar to alpha-adducins(aa) * DMADDLIKE_3

CG9325 hts * adducin-like(aa) [Aldolase_II] CG9325 SD02552 56D5-56D6 ID:114C12

+ motor_protein * 1e-05 microtubule binding protein D-CLIP-190 * 6e-08 Similarity with drosophila MSP-300 protein (PIR acc.

CG15165 no. * 5e-08 CENP-E protein * 1e-09 myosin I CG15165 SD02507 37A3-37A4 ID:114C2

CG7434 + RpL22 ribosomal_protein Ribosomal protein L22 60S subunit ANTIFREEZE1 CG7434 SD02522 ID:114C6

+ ligand_binding_or_carrier * chromatin assembly factor I (150 kDa)(aa) * chromatin assembly factor I p150 chain - human *

CG12109[NLS_BP] CG12109 SD02526 7F4-7F5 dup:1/2 ID:114C7

+ unknown * 4e-15 MTRP_MOUSE GOLGI 4-TRANSMEMBRANE SPANNING TRANSPORTER MTP * 6e-15 MTRP_HUMAN

CG8575 GOLGI 4-TRANSMEMBRANE SPANNING TRANSPORTER MTP * * CG8575 SD02746 44D8-44D8 dup:1/2 ID:114F2

+ Vha16 enzyme * DMCSUC_5 Vha16 * VACUOLAR ATP SYNTHASE KD PROTEOLIPID SUBUNIT (DUCTIN)(aa) * 5e-56

VATL_YEAST VACUOLAR ATP SYNTHASE KD PROTEOLIPID SUBUNIT * 1e-53 [VACATPASE // ATP-synt_C] CG3161

CG3161 SD02875 42B2-42B2 dup:2/4 ID:114G8

+ enzyme * LONG-CHAIN-FATTY-ACID--COA LIGASE (LONG-CHAIN ACYL-COA SYNTHETASE 2) (LACS 2)(aa) * 1e-83

LCF2_YEAST LONG-CHAIN-FATTY-ACID--COA LIGASE (LONG-CHAIN A [AMP_BINDING // AMPBINDING // AMP-binding]

CG3961 CG3961 SD02971 75E2-75E2 ID:114H10

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

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

+ 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

+ * predicted using Genefinder; similar to thrombospondin like; cDNA EST comes from this gene; cDNA EST comes from this

CG2131 gene; cDNA EST yk195c9.3 comes [TSP1 // ig // NLS_BP // tsp_1 // ATP_GT] CG2131 39E7-39F1 dup:1/2 ID:115A3

CG13868+ unknown * 0.0000000000000008* * CG13868 SD03066 56F17-57A dup:4/4 ID:115B4

CG10439+ unknown * contains a single LIM domain at the N-terminus.; cDNA EST comes from this gene; cDNA EST comes from this

gene; cDNA EST yk357g9.5 comes from this ge [LIM_DOMAIN_1 // LIM_DOMAIN_2] CG10439 SD03168 57B1-57B1 ID:115C12
 + 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
 CG15319+ CG15319 SD03263 ID:115D11
 + Cyp12a4 cytochrome_P450 * CYTOCHROME P450 CYP12A2(aa) * 3e-17 lanosterol 14-demethylase cytochrome P450 * 5e-24
 cytochrome P450 cytochrome P4 * 4e-20 YS45_CAEEL PUTATIVE CYTO [EP450II // p450 // P450 // MITP450 // C] CG6042
 CG6042 SD03227 91F3-91F4 ID:115D8
 + cell_adhesion * DMDACHSOU_2 ds * contains similarity to multiple cadherin-type repeats(aa) * cadherin 18(aa) *
 CG6977 DMDEC_1 shg [CADHERIN // cadherin] CG6977 SD03311 87A-87A dup:5/5 ID:115E6
 + 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
 + Aac11 apoptosis_inhibitor * apoptosis inhibitor 5(aa) * Aac11(aa) * 1e-110 unknown * 1e-35 unknown protein CG6582
 CG6582 SD03364 36C3-36C3 ID:115F2
 CG18278+ unknown * CG18278 SD03412 50A9-50A9 ID:115F5
 + Es2 enzyme * HYPOTHETICAL 58.3 KD PROTEIN F42H10.7 IN CHROMOSOME III(aa) * ES2 protein(aa) * ES2 protein(aa) *
 CG1474 Es2 CG1474 SD03464 7E7-7E7 ID:115G8
 + gammaCoptransporter * coat protein gamma-cop(aa) * COATOMER GAMMA SUBUNIT (GAMMA-COAT PROTEIN) (GAMMA-
 COP)(aa) * 1e-123 COPG_YEAST COATOMER GAMMA SUBUNIT (GAMMA-COAT PROT CG1528 SD03531 100D-100D
 CG1528 ID:115H4
 + 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
 + esc transcription_factor * DMESCOMBS_4 esc * 3e-08 YCW2_YEAST HYPOTHETICAL 57.0 KD TRP-ASP REPEATS
 CONTAINING PROTEIN IN CPR4-SSK2 * extra sex combs protein - fruit fly (Dr[GPROTEINBRPT // RCC1_2 // WD40_REGION /]
 CG14941 CG14941 SD03549 33B1-33B2 ID:115H6
 CG12004+ unknown CG12004 SD03655 ID:116A6
 + ppan unknown * Peter Pan(aa) * 4e-35 SSF1_YEAST SSF1 PROTEIN SSF1 protein - yeast (Saccharomyc * 1e-53 contains
 CG5786 similarity to human RNA-binding protein FUS/TLS * 1 [NLS_BP] CG5786 SD03871 95F1-95F1 dup:1/3 ID:116C10
 + EG:100G10.8 unknown * DMC95B7 * * by content; by match; LD Drosophila melanogaster...(aa) * by content; 1-meth CG2694
 CG2694 SD03887 3B5-3B5 dup:1/2 ID:116C11
 CG10192+ translation_factor CG10192 SD03848 ID:116C4
 + signal_transduction * HYPOTHETICAL 94.2 KD PROTEIN C38D4.5 IN CHROMOSOME III(aa) * 2e-05 /match=(desc:; /ma *
 2e-05 RIP1 * 3e-12 98K GTPase-activating protein ABR, brain [RHO_GAP // RhoGAP] CG7122 SD04011 16F7-16F7 dup:4/5
 CG7122 ID:116E6
 CG1902 + CRAL_TRIO ligand_binding_or_carrier CG1902 SD04017 dup:2/2 ID:116E8
 CG10712+ translation_factor * 3e-06 Pdd1p Pdd1p thermoph * * [chromo // CHROMO_2] CG10712 79F5-79F5 dup:3/4 ID:116F1
 none + none SD04091 ID:116F10

+ alpha-Adaptin transporter * highly similar to alpha-adaptin (rat and mouse)(aa) * DMALPADPT_2 agr;-Adaptin * adaptor-related
 CG4260 protein complex AP-2, alpha subunit(aa) * ALPHA-AD CG4260 SD04083 21C2-21C2 dup:2/3 ID:116F9
 + alpha-Spec actin_binding * DMLETHAL_2 Actn * DMSPCA_2 agr;-Spec * SPECTRIN ALPHA CHAIN(aa) * 3e-15 USO1_YEAST
 INTRACELLULAR PROTEIN TRANSPORT PROTEIN USO1 ([spectrin // SPEC_REPEAT // EF_HAND // S] CG1977 SD04436
 CG1977 62B-62B dup:2/7 ID:117C8
 CG14971+ unknown Homo sapiens CGI-15 protein CG14971 SD04505 ID:117D9
 CG9531 + CG9531 SD04586 dup:3/3 ID:117E5
 + G_protein_linked_receptor * CL3BC(aa) * protein(aa) * 4e-20 similar to G-protein coupled receptor protein; cDNA EST * 2e-
 14 EMR1_MOUSE CELL SURFACE GLYCOPROTEIN[7tm_2 // RECEPTOR_PKD // GAL_LLECTIN //] CG8639 SD04590 44D2-
 CG8639 44D2 dup:5/5 ID:117E6
 + cell_adhesion * robo * similar to IG (immunoglobulin) superfamily (17 domains), Low-density lipoprotein receptor domain
 class A (3 domains), Laminin EGF-like (Doma[LDLRA_2 // ig // RNP_1 // EGF_1 // EGF] CG7981 SD04592 3A2-3A3 dup:4/4
 CG7981 ID:117E7
 CG17156+ transcription_factor CG17156 SD04616 dup:2/2 ID:117E9
 + defense/immunity_protein * tag7(aa) * 2e-20 peptidoglycan recognition protein precursor * 4e-20 TNF superfamily, member
 CG4432 (LTB)-like (peptidoglycan recognition * 2e-19 peptidogl [HTH_ARAC_FAMILY_1] CG4432 SD04722 67A8-67A9 dup:2/2 ID:117F12
 CG8151 + CG8151 SD04652 ID:117F3
 + protein_kinase * protein(aa) * cdc2-like protein kinase(aa) * 3e-65 CTK1_YEAST CTD KINASE ALPHA SUBUNIT (CTD
 KINASE KD SUBUNIT) (CTDK-I ALPHA SUB * 6e-69 posi[PROTEIN_KINASE_ST // PROTEIN_KINASE_DOM] CG7597 SD04681
 CG7597 78E1-78E1 dup:2/3 ID:117F7.2
 CG8190 + CG8190 SD04737 dup:1/2 ID:117G5
 CG6006 + Orct transporter Orct Organic cation transporter 2 CG6006 SD04753 ID:117G9
 CG18061+ CG18061 SD04793 ID:117H2
 + 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
 + unknown * 1e-28 weak similarity to chromosomal replicator initiator protein DNAA (* similar to a C.elegans protein encoded
 CG11943in cosmid * CG11943 SD04935 19A3-19A3 dup:3/7 ID:118A12
 CG3353 + CG3353 dup:1/6 ID:118A7
 + lic protein_kinase (licorn) stress activated MAP kinase kinase 3 [Drosophila melanogaster] PROTEIN_KINASE_DOM,
 CG12244PROTEIN_KINASE_ST, p] CG12244 SD04985 ID:118B12
 + GTP_binding 108000000 SD05004 ID:118C1
 CG1787 + enzyme CG1787 SD05059 ID:118C6
 CG9366 + enzyme CG9366 SD05212 ID:118D6
 none + none SD05284 ID:118E10
 CG17148+ enzyme CG17148 SD05284 ID:118E10.2
 CG5841 + cytoskeletal_structural_protein homolog of human KIAA1323 protein, similar to ankyrin proteins ANK_REP,

ANK_REP_REGION, ZF_RING, ZF_ZZ,] CG5841 SD05267 dup:3/3 ID:118E5

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

+ BcDNA:GH13356 enzyme beta galactosyltransferase MITOCH_CARRIER, XYLOSE_ISOMERASE_2 CG8536 SD05469 dup:1/2

CG8536 ID:118G11

+ Rpn4 endopeptidase * proteasome (prosome, macropain) 26S subunit, non-ATPase, 13(aa) * 26S proteasome subunit

CG10230 p40.5(aa) * 3e-43 hypothetical protein YDR427w - yeast (Sac [PCI_DOMAIN] CG10230 SD05423 95B5-95B5 dup:1/2 ID:118G4

CG6339 + motor_protein CG6339 SD05424 ID:118G5

+ transporter * 1e-14 YNM5_YEAST HYPOTHETICAL 73.8 KD PROTEIN IN SPC98-TOM70 INTERGENIC REGION * 1e-61

CG13907 /match=(desc;; /ma * 6e-43 K05B2.5 gene product * 3e-26 MOT1_ CG13907 SD05443 61E1-61E1 dup:1/3 ID:118G6

CG7110 + unknown * [NLS_BP] CG7110 SD05480 34B7-34B7 dup:2/3 ID:118H1

CG8902 + CG8902 dup:2/4 ID:118H6

CG13384 + transporter putative amino acid transport protein AROMATIC_AA_PERMEASE_2 CG13384 SD05512 dup:2/4 ID:118H7

+ enzyme * 3e-31 prolyl 4-hydroxylase alpha subunit * 2e-40 Similarity to Human Prolyl 4-hydroxylase alpha subunit

CG12088 (SW:P4HA_HU * 3e-42 P4H1_MOUSE PROLYL 4-HYDR CG12088 SD05564 99F7-99F7 dup:2/3 ID:119A3.2

CG5721 + pioneer protein CG5721 SD05591 ID:119A7

+ stnB stoned B, mutations affect multivesicular body, nerve terminal, synaptic vesicle Adap_comp_sub, CLATHRINADPT,

CG12473 PRO_RICH CG12473 SD05593 ID:119A9

+ signal_transduction PLAP_MOUSE PHOSPHOLIPASE A-2-ACTIVATING PROTEIN GPROTEINBRPT, WD40,

CG5105 WD40_REGION, WD_REPE] CG5105 SD05646 ID:119B6

+ kis motor_protein * BLASTX 1.2E-06 Plasmodium falciparum GGM tandem repeat protein mRNA, partial cds.(dna) * kismet(aa)

CG3696 * 1e-07 contains similarity to chromo (chromatin [NLS_BP // ATP_GTP_A] CG3696 SD05649 21B4-21B4 dup:4/8 ID:119B7

+ RpS3A ribosomal_protein * DMRPS3A_2 RpS3A * ribosomal protein S3a(aa) * 3e-63 RS3A_YEAST 40S RIBOSOMAL

PROTEIN RP10A ribosomal protein * 4e-78 RS3A_CAEEL PROBABLE 40S RIBOS[RIBOSOMAL_S3AE // Ribosomal_S3Ae //

CG2168 NLS] CG2168 SD05650 101F1-101F1 ID:119B8

CG7821 + CG7821 SD05678 ID:119C2

CG11168 + cytoskeletal_structural_protein CG11168 SD05685 ID:119C4

+ protein_kinase * CaMKI * similar to serine/threonine kinase (KIN1/SNF1/Nim1 subfamily); cDNA EST comes from this gene;

cDNA EST comes from this gene; cDNA EST [UBA // PROTEIN_KINASE_ST // TYRKINASE /] CG8201 SD05712 56D7-56D9

CG8201 dup:3/4 ID:119C9.2

+ enzyme * lysine ketoglutarate reductase/saccharopine dehydrogenase(aa) * similar to saccharopine dehydrogenases(aa) *

CG7144 lysine-ketoglutarate reductase /sacch CG7144 SD05742 28C9-28D dup:2/2 ID:119D4

CG7958 + unknown CG7958 SD05917 dup:2/2 ID:119E12

+ protein_kinase similar to serine/threonine kinases PROTEIN_KINASE_ATP, PROTEIN_KINASE_DOM,] CG17090 SD05876

CG17090 dup:4/5 ID:119E6

CG4822 + transporter * [ABC_TRANSPORTER // DA_BOX] CG4822 SD05880 21B-21B dup:6/6 ID:119E7

CG11526 + pioneer protein with human homolog (KIAA1170) CG11526 SD05886 dup:2/2 ID:119E8

+ coiled-coil protein, homology to golgi autoantigen, golgin subfamily and nonmuscle myosin heavy GRIP CG3493 SD05887
 CG3493 dup:4/4 ID:119E9
 + DNA_binding * selected as a weak suppressor of a mutant of the subunit AC40 of DNA dependant RNA polymerase I and
 CG7421 III(aa) * nucleolar phosphoprotein - African cla [NLS_BP // HISTONEH5] CG7421 SD05988 79A5-79A5 ID:119F11
 CG4427 + transcription_factor CG4427 SD06353 dup:2/2 ID:119G5.2
 + transcription_factor * ATFx(aa) * leucine-zipper protein(aa) * 7e-05 Similarity to Human transcription factor ATF-4
 (SW:ATF4_HUMAN); cD * 3e-09 ATF4_MOUSE CYCLIC-AMP-DEPE[B_ZIP // bZIP // BZIP_BASIC // NLS_BP] CG8669 39D2-
 CG8669 39D2 dup:3/3 ID:119H1
 CG11860+ BG:DS07851.11 unknown * CG11860 35C4-35C4 dup:2/2 ID:119H7
 + unknown * 2e-83 inserted at base 5' end of P element Inverse PCR * 1e-124 inserted at base Both 5' and 3' ends of P
 CG2765 element Inverse PCR * CG2765 SD07219 60E5-60E5 dup:3/5 ID:120G10.2
 CG3879 + transporter CG3879 SD10012 dup:1/3 ID:124E12.2
 CG15009+ CG15009 SD10052 dup:1/2 ID:124F9.2
 CG5370 + endopeptidase CG5370 SD10530 dup:1/2 ID:125C11.2
 + TER94 endopeptidase * 8e-87 CC48_YEAST CELL DIVISION CONTROL PROTEIN cell divisi * 1E-145* 1e-118 TER1_CAEEL
 TRANSITIONAL ENDOPLASMIC RETICULUM ATPASE HOMOLOG (P97/CDC48 [ENDOLAPTASE // AAA // ATP_GTP_A]
 CG2331 CG2331 GH01132 46D1-46D1 dup:1/3 ID:30A11
 + emb transporter * CRM1_YEAST CHROMOSOME REGION MAINTENANCE PROTEIN CRM1 * strong similarity to CRM1
 chromosome maintenance protein from y * exportin (CRM1, yeast, ho [LIPOYL // IBN_NT] CG13387 GH01059 29C1-29C1 dup:1/2
 CG13387 ID:30A3
 + Nmdmc NAD-DEPENDENT METHYLENETETRAHYDROFOLATE DEHYDROGENASE CG18466 GH01066 85C5-85C5
 CG18466 ID:30A5
 + BcDNA:GH01073 RNA_binding * unknown(aa) * 7e-08 CYP6_YEAST PEPTIDYL-PROLYL CIS-TRANS ISOMERASE CYP6
 (PPIASE) (ROTAMASE) * 7e-06 RNA-binding protein * 1e-103 Similarity to pepti [RBD // pro_isomerase // rrm // CSA_PPIA]
 CG5808 CG5808 GH01073 96B1-96B1 ID:30A6
 + structural_protein * unknown(aa) * Allele: hi4(aa) * gene is related to S.cerevisiae NIC96 gene.(aa) * 7e-24 NI96_YEAST KD
 CG7262 NUCLEOPORIN-INTERACTING COMPONENT nucle CG7262 GH01087 88D8-88D8 ID:30A8
 + Traf2 signal_transduction * TNF-receptor-associated factor melanoga * 8e-06 YQ57_CAEEL HYPOTHETICAL 24.9 KD
 PROTEIN C16C10.7 IN CHROMOSOME III * 4e-38 TRAF6 * 1e-36 TNF recept[RNP_1 // zf-C3HC4 // ZINC_FINGER_C3HC4]
 CG10961 CG10961 GH01161 7D14-7D14 ID:30B3
 + unknown * Ykr081cp(aa) * 5e-49 YK61_YEAST HYPOTHETICAL 39.6 KD PROTEIN IN MTD1-NUP133 INTERGENIC
 CG7993 REGION * ORF YKR401 * CG7993 GH01229 90F1-90F1 ID:30B8
 + transcription_factor * crol * 1e-32 CROL ALPHA * 1e-17 final three exons similar to C2H2-type zinc finger * 1e-31 kruppel-
 CG12397 type zinc finger protein [zf-C2H2 // ZINC_FINGER_C2H2 // ZINC_FIN] CG12397 GH01265 42B3-42B3 ID:30B9
 + DNA_binding * ISWI PROTEIN (IMITATION SWI PROTEIN) (NUCLEOSOME REMODELING FACTOR KD SUBUNIT)
 (NURF-140) (CHRAK KD SUBUNIT)(aa) * DMISWI_6 lswi * 8e-94 YAB9_YEAST [helicase_C // SNF2_N] CG5899 GH01406
 CG5899 33A1-33A1 ID:30C10

+ Mer actin_binding * merlin * 1e-105 coded for by C. elegans cDNA yk167f5.5; coded for by C. elegans cDNA yk130f8.5; * 1e-135 MERL_MOUSE MERLIN (SCHWANNOMIN) merlin - mo [Band_41 // BAND41 // ERM // ERMFAMILY] CG14228 GH01330

CG14228 18E1-18E1 ID:30C2

+ enzyme * protein kinase C-binding protein RACK7(aa) * deformed epidermal autoregulatory factor 1(aa) * No definition line

CG1815 found(aa) * adenovirus E1A binding [PHD] CG1815 GH01331 100D4-100D4 dup:1/2 ID:30C3

+ protein_phosphatase * 3e-41 LAR_DROME PROTEIN-TYROSINE PHOSPHATASE DLAR PRECURSOR (PROTEIN-TYROSINE-PHOSPHAT * 5e-40 similar to protein-tyrosine phosphatase with [Y_phosphatase // TYR_PHOSPHATASE_PTP //]

CG4355 CG4355 GH01353 22A1-22A1 dup:1/3 ID:30C7

+ Hn enzyme * DMPAH Hn * phenylalanine 4-monooxygenase (EC 1.14.16.1) - fruit fly (Drosophila melanogaster)(aa) *

CG7399 phenylalanine 4-monooxygenase (EC 1.14.16.1) - f CG7399 GH01426 66A11-66A12 dup:2/2 ID:30D2

+ enzyme * inhibitor of growth 1-like(aa) * 3e-12 YHP0_YEAST HYPOTHETICAL 32.1 KD PROTEIN IN GAR1-MSR1

CG7379 INTERGENIC REGION * 5e-11 predicted using Genefinder; si [PHD] CG7379 GH01429 93B1-93B1 dup:1/2 ID:30D4

+ 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

+ function_unknown * similar to NifU protein homolog(aa) * Iron-sulfur cluster nifU-like protein; Isu1p(aa) * NifU-like protein(aa)

CG9836 * Y45F10D.4(aa) CG9836 GH01635 85B4-85B4 dup:2/2 ID:30E10

+ endopeptidase * 3e-64 cysteine proteinase cysteine * 2e-56 predicted using Genefinder; similar to cathepsin-like protease; cD * 1e-59 cathepsin K * 1e-59 cathepsin[THIOL_PROTEASE_CYS // PAPAIN // Peptida] CG4847 GH01592 54C9-54C9 dup:3/4

CG4847 ID:30E3

+ enzyme * coded for by C. elegans cDNA yk108f3.3; coded for by C. elegans cDNA yk104h5.3; coded for by C. elegans

CG5590 cDNA yk117a1.3; coded for by C. elegans cDN [GDHRDH // adh_short] CG5590 GH01709 98A6-98A6 ID:30F4

+ 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

CG6210 + unknown * CG6210 GH01813 68A7-68A7 ID:30G1

+ endopeptidase * endothelin converting enzyme-2 - bovine (fragment)(aa) * endothelin converting enzyme-like 1(aa) * 7e-30 similar to Zinc-binding metalloprotease; cD [NEPRILYSIN // PRENYLATION // ZINC_PROTE] CG14528 GH01940 98F-98F

CG14528 ID:30G10

+ endopeptidase * HYPOTHETICAL 37.7 KD PROTEIN C08B11.7 IN CHROMOSOME II(aa) * DMUBICTHG_3 Uch * BRCA1 associated protein-1 (ubiquitin carboxy-terminal hydrolase)(aa) [UCH // UBCTHYDRLASE // ATP_GTP_A] CG8445 GH01941 52F7-

CG8445 52F7 ID:30G11

+ I(2)efl chaperone * similar to the small heat shock protein (HSP20) family(aa) * DMHS09_2 Hsp23 * DMHSP27G_3 Hsp27 * HYPOTHETICAL 12.3 KD PROTEIN C14B9.1 IN CHROMOSOME [HSP20 // ACRYSTALLIN] CG4533 GH01960 59F4-59F4

CG4533 ID:30G12

+ 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

+ receptor * 5e-14 cDNA EST comes from this gene; cDNA EST co * 3e-35 peripheral-type benzodiazepine receptor

CG2789 isoquinoline-binding protein - mouse * 1e-35 benzod CG2789 GH02075 21C6-21C6 dup:2/2 ID:30H12

+ Tpi enzyme * Chain A, Does The His12-Lys13 Pair Play A Role In The Adaptation Of Thermophilic Tims To High Temperatures
CG2171 ?(aa) * DMTPIG_2 Tpi * TRIOSEPHOSPHATE IS [TIM] CG2171 GH02005 99E-99E dup:1/3 ID:30H5
+ Ca-alpha1D ion_channel * DMCA1_2 Ca- agr;1D * calcium channel alpha-1 subunit * putative L-type calcium channel alpha subunit * voltage-dependent calcium channel complex alp [NACHANNEL // CACHANNEL // THIOL_PROTEAS] CG4894 GH02029
CG4894 35F1-35F3 ID:30H9
CG12182+ BcDNA:GH02340 unknown * CG12182 GH02340 62F1-62F1 ID:31B5
+ 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
+ BcDNA:GH02419 enzyme * alpha-mannosidase II(aa) * lysosomal alpha-mannosidase(aa) * 1e-70 alpha-mannosidase II * 1e-153 similar to alpha-mannosidase (a glycosyl hydrolase [Glyco_hydro_38] CG6206 GH02419 33D1-33D1 dup:2/2 ID:31B9
+ arginaseenzyme * putative * 1e-11 ARG1_YEAST ARGINASE (EC 3.5.3.1) - yeast (Saccharo * 1e-107 /motif=(desc;; /ma * 1e-08
CG18104 similar to CG18104 GH02581 1B5-1B5 ID:31C12
+ Argk * Argk * ARGININE KINASE (AK)(aa) * 1e-131 KAG1_CAEEL PROBABLE ARGININE KINASE F46H5.3 (AK) similar t * 7e-76 KCRM_MOUSE CREATINE KINASE, M CHAIN (M-C [GUANIDO_KINASE // ATP-gua_Ptrans] CG5173 68E1-68E1 dup:1/3
CG5173 ID:31C7
+ BcDNA:GH02536 unknown * Contains similarity to from C. elegans.(aa) * unknown(aa) * 2e-88 predicted using Genefinder; cDNA
CG8230 EST comes from this g * 2e-49 Contains similarity CG8230 GH02536 44F12-44F12 ID:31C8
+ 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
+ BG:DS00797.1 unknown * unknown protein(aa) * 1e-113 EMP70 protein precursor - yeast (Saccharomyces cerevisiae) *
CG7364 Similarity to Yeast endosomal P24A protein (SW:EM70_YEAST CG7364 GH02822 34D1-34D1 dup:2/2 ID:31E4
+ BcDNA:GH02833 RNA_binding * DMDBP45A_18 Dbp45A * pit * 3e-64 DBP7_YEAST ATP-DEPENDENT RNA HELICASE DBP7 probable purin * 1e-58 helicase pitchoune [helicase_C // HELICASE // DEAD // NLS_B] CG8611 GH02833 16A1-16A2 dup:3/3
CG8611 ID:31E5
+ unknown * actin-fragmin kinase(aa) * putative protein kinase(aa) * HYPOTHETICAL 143.1 KD PROTEIN F33C8.1 IN CHROMOSOME X PRECURSOR(aa) * 4e-10 YG52_YEAST HYP [FBOX_DOMAIN] CG6758 GH02866 58C5-58C5 dup:2/2
CG6758 ID:31E7
+ DNA_binding * DNA TOPOISOMERASE III(aa) * topoisomerase alpha(aa) * DNA topoisomerase III(aa) * 1e-97 TOP3_YEAST DNA TOPOISOMERASE III DNA topoisomerase (EC 5.9 [PRTPISMRASEI // TOPOISOMERASE_I_PROK //]
CG10123 CG10123 GH02886 37E5-37E5 dup:3/3 ID:31E9
+ BEST:GH02921 endopeptidase * easter(aa) * DMEAST_4 ea * 1e-106 EAST_DROME SERINE PROTEASE EASTER PRECURSOR serine protein * 5e-33 KAL_MOUSE PLASMA KALLIKREIN PRECURSOR (PLASMA P [ANTENNAPEDIA // trypsin
CG1102 // CHYMOTRYPSIN] CG1102 GH02921 82A5-82A5 ID:31F2
CG1408 + BcDNA:GH03163 unknown * * CG1408 GH03163 100B-100B dup:1/2 ID:31G10
CG4919 + unknown * GLUTAMATE--CYSTEINE LIGASE REGULATORY SUBUNIT (GAMMA-GLUTAMYL-CYSTEINE SYNTHETASE)

(GAMMA-ECS) (GCS LIGHT CHAIN)(aa) * glutamate-cysteine ligase regu CG4919 GH03051 94C3-94C3 ID:31G2
+ karyopherin-alpha1 ligand_binding_or_carrier * karyopherin- agr;1 * karyopherin alpha 1(aa) * 1e-129 IMA1_YEAST IMPORTIN ALPHA SUBUNIT (KARYOPHERIN ALPHA SUBUNIT) (SERINE-RICH RNA[ARM_REPEAT // Armadillo_seg // NLS_BP] CG8548
CG8548 GH03057 76D2-76D3 ID:31G3
+ BcDNA:GH03108 chaperone * similar to DnaJ, prokaryotic heat shock protein, Zinc finger, C2H2 type; cDNA EST yk290e12.5 comes from this gene; cDNA EST yk290e12.3 comes from th [ZF_MATRIN // ZINC_FINGER_C2H2 // DNAJ_1] CG2790 GH03108
CG2790 60E5-60E5 ID:31G7
+ enzyme * 3-phosphoglycerate dehydrogenase(aa) * similar to D-3-Phosphoglycerate dehydrogenase; cDNA EST comes from this gene; cDNA EST comes from this gene; [2-Hacid_DH // D_2_HYDROXYACID_DH_1 // A] CG6287 GH03305 32D5-32D5
CG6287 ID:31H4
+ enzyme * DMCSUDUC_5 Vha16 * VACUOLAR ATP SYNTHASE KD PROTEOLIPID SUBUNIT (DUCTIN)(aa) * ATP synthase
CG7007 subunit(aa) * proteolipid protein of the proton ATPase; P [VACATPASE // ATP-synt_C] CG7007 GH03514 90B1-90B1 ID:32A10
+ BcDNA:GH03502 unknown * unknown(aa) * 3e-55 YII3_YEAST HYPOTHETICAL 41.9 KD PROTEIN IN SDS3-THS1
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
+ structural_protein * 2e-05 CUP7_DROME PUPAL CUTICLE PROTEIN EDG-78 PRECURSOR ecdyson * 8e-06
CU26_ARADI ADULT-SPECIFIC RIGID CUTICULAR PROTEIN 12.6 (ACP 12.6) * 2e-07 DM [CUTICLE // insect_cuticle] CG12045
CG12045 GH03728 100B-100B ID:32B12
+ Vha26 enzyme * Vha26 * ATPase, H+ transporting, lysosomal (vacuolar proton pump) 31kD(aa) * VACUOLAR ATP SYNTHASE
CG1088 SUBUNIT E (V-ATPASE E SUBUNIT) (V-ATPASE KD SUBUN CG1088 GH03683 83B4-83B4 ID:32B5
+ Rab7 enzyme * Rab7 * 6e-61 YPT7_YEAST GTP-BINDING PROTEIN YPT7 GTP-binding protein Y * 1e-111 small ras-like
GTPase * 6e-77 similar to ras related protein; cDNA E [ras // ATP_GTP_A // RASTRNSFRMNG] CG5915 GH03685 97F1-97F1
CG5915 ID:32B6
+ BcDNA:GH03693 signal_transduction * contains similarity to Src homology domain (SH3) (Pfam: SH3.hmm, score: 50.59)(aa) *
6e-90 contains similarity to Src homology domain [GRF_DBL // RhoGEF // SH3 // PRO_RICH //] CG3799 GH03693 73E1-73E1
CG3799 dup:2/2 ID:32B7
+ transcription_factor * pleiomorphic adenoma gene-like 2; PLAG-like 2(aa) * DMZFH1_2 zfh1 * 1e-06 ZFH1_DROME ZINC-
FINGER PROTEIN (ZINC-FINGER HOMEODOMAIN PROTEIN [zf-C2H2 // ZINC_FINGER_C2H2 // ZINC_FIN] CG12744 GH03826
CG12744 46C1-46C1 dup:1/2 ID:32C5
CG4184 + BcDNA:GH03922 unknown * CG4184 GH03922 21C3-21C dup:1/3 ID:32C9
CG3556 + unknown * CG3556 GH04077 4C4-4C4 ID:32D12
CG10658 + Os9 unknown * Os9 * * CG10658 GH03980 38B1-38B1 ID:32D2
+ 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
+ unknown * 7e-06 pdb|1BIH|A Chain A, Crystal Structure Of The Insect Immune Protein Hemolin: A New Domain *
CG5597 HEMO_HYACE HEMOLIN PRECURSOR (P4 PROTEIN) (HEMOCYT [ig] CG5597 GH04238 60A8-60A8 dup:2/2 ID:32E10
+ Trip1 translation_factor * 3e-80 IF34_YEAST EUKARYOTIC TRANSLATION INITIATION FACTOR DELTA SUBUNIT (EIF-3
CG8882 DELTA * IF34_DROME EUKARYOTIC TRANSLATION INITIATION FACTOR DEL[GPROTEINBRPT // WD40_REGION //

WD_REPEA] CG8882 GH04085 25B-25B dup:2/2 ID:32E2

+ serpin * serine protease inhibitor(aa) * OVALBUMIN (PLAKALBUMIN) (ALLERGEN GAL D 2) (GAL D II)(aa) * LEUKOCYTE
CG9456 ELASTASE INHIBITOR (LEI) (LEUCOCYTE NEUTRAL P [serpin] CG9456 GH04125 42C8-42C8 dup:2/2 ID:32E4

+ metabolism * 1e-47 PNPY_YEAST PROBABLE PURINE NUCLEOSIDE PHOSPHORYLASE (INOSINE
PHOSPHORYLASE) (PN * 3e-51 similar to purine nucleoside phosphorylases * 4e-73 pu [Mtap_PNP] CG16758 GH04159 62E6-
CG16758 62E6 dup:5/5 ID:32E5

+ ion_channel * 6e-15 similar to PDZ domain (Also known as DHR or GLGF).; cDNA EST EMBL: * 3e-17 protein co-factor * 1e-
CG10939 18 E3KARP Na+/H+ exchanger regulatory facto [PDZ // NLS_BP] CG10939 GH04176 54B18-54C1 dup:2/2 ID:32E6

+ 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

CG5080 + CG5080 ID:32F10

CG6186 + CG6186 dup:2/2 ID:32G1

+ actin_binding * dystrophin(aa) * DMDYDTRO dystrophin * 1e-126 DYS-1 protein * cytoskeletal protein CG7240 92A7-
CG7240 92A11 dup:1/2 ID:32G3

+ Appl unknown * DMS1C4_1 Appl * 2e-25 beta-amyloid homolog apl-1 - Caenorhabditis elegans beta- * 4e-21 Alzheimer's
disease amyloid beta/A4 protein homolog precursor [A4_EXTRA // A4_INTRA // AMYLOIDA4 // NL] CG7727 GH04413 1B7-1B8
CG7727 dup:1/2 ID:32G7

+ 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

+ n-syb transporter * 2e-21 synaptobrevin isoform B - fruit fly (Drosophila melanogaster) (L142 * 2e-21 SNB-1; synaptobrevin SNB-
1; sy * 6e-24 SYB2_MOUSE SYNAPTOBREVII[SYNAPTOBREVN // SYNAPTOBREVIN // synapt] CG17248 GH04664 62A10-
CG17248 62A10 dup:2/2 ID:32H12

+ BcDNA:GH04753 enzyme * glutathione transferase (EC 2.5.1.18) D26 - fruit fly (Drosophila melanogaster)(aa) * glutathione
CG16936 transferase (EC 2.5.1.18) D21 - fruit fly (Drosoph [GST] CG16936 GH04753 60D14-60D14 dup:2/2 ID:33A11

+ transporter * 4e-41 similar to matrin F/G containing C4-type zinc-fingers * 4e-79 PGT_HUMAN PROSTAGLANDIN
CG3811 TRANSPORTER (PGT) prostaglandin tr * 2e-76 PGT_RAT PROST CG3811 GH04717 30B10-30B10 ID:33A7

+ enzyme * weakly similar to furin-like proteases; 35% Similarity to * weakly similar to furin-like proteases in 3' exon(aa) * 2e-
CG8481 17 weakly similar to furin-I [Acetyltransf // NLS_BP] CG8481 GH04732 85E8-85E8 ID:33A9

+ unknown * 1e-87 cDNA EST yk500f6.3 comes from this gene; cDNA EST come * 1e-119 unknown * 1e-88 hypothetical
CG14997 protein * CGI-44 protein [FADPNR] CG14997 GH04863 64E2-64B4 ID:33B10

+ alphaCopsignal_transduction * agr;Cop * coatomer alpha subunit(aa) * alpha-COP (Z466 * 5e-67 Similarity to Human Coatomer
beta' subunit (SW:COPP_HUMAN); cDNA E [GPROTEINBRPT // WD40_REGION // WD_REPEA] CG7961 GH04856 62A10-
CG7961 62A10 dup:2/3 ID:33B8

+ unknown * HSPC015(aa) * 8e-45 hypothetical protein YOR173w - yeast (Saccharomyces cerevisiae) (* hypothetical protein
CG2091 YLR270w - yeast (Saccharomyces cerevisi CG2091 GH04919 83C-83C ID:33C2

CG4123 + Mipp1 protein_phosphatase * multiple inositol polyphosphate phosphatase 1; MIPP1(aa) * Mipp1 * 1e-22 multiple inositol

polyphosphate phosphatase * 2e-23 multiple inositol polyp [acid_phosphat] CG4123 GH04949 77A1-77A1 dup:4/7 ID:33C7
 + BcDNA:GH04978 protein_kinase * 2e-39 YAK1_YEAST PROTEIN KINASE YAK1 protein kinase YAK1 (EC 2. * 3e-43
 serin/threonin-kinase * 1e-126 similar to serine/threonine kinase; cDNA EST[PROTEIN_KINASE_ST // PROTEIN_KINASE_DOM]
 CG7028 CG7028 GH04978 61A6-61A6 ID:33D1
 CG4250 + unknown * [EGF_2] CG4250 GH05106 58F3-58F3 dup:2/2 ID:33D11
 + unknown * protein(aa) * 1e-26 protein * [C2 // RECEPTOR_CYTOKINES_2 // ATPASE_AL] CG6606 GH05001 17C4-17C5
 CG6606 ID:33D3
 + 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
 CG18251 + Msp-300 unknown * CG18251 GH05169 25C8-25C8 dup:2/2 ID:33E5
 + enzyme * HYPOTHETICAL ALDEHYDE-DEHYDROGENASE LIKE PROTEIN F01F1.6(aa) * antiquitin=26g turgor protein
 homolog {C-terminal} intestinal mucosa, Peptide Partial [aldehyd // ALDEHYDE_DEHYDR_GLU] CG9629 GH05218 76A3-76A3
 CG9629 dup:2/2 ID:33E7
 CG3273 + unknown * CG3273 GH05256 42B3-42B3 dup:2/2 ID:33E8
 + 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
 CG3566 GH05526 5E1-5E1 ID:33F10
 + Scs-fp enzyme * succinate dehydrogenase (ubiquinone) (EC 1.3.5.1) flavoprotein precursor, mitochondrial - bovine(aa) *
 DMSUCDEHF Scs-fp * DHSA_YEAST SUCCINATE DEHY [FADPNR // PNDRTASEI // FAD_binding_2 /] CG17246 GH05404
 CG17246 56D4-56D4 dup:3/3 ID:33F2
 + Mlc1 * DMMYLALK_2 Mlc1 * indirect flight muscle isoform; putative(aa) * 1e-07 YGK6_YEAST HYPOTHETICAL CALCIUM-
 BINDING PROTEIN IN TAF60-G4P1 INTERGENIC REGI [THIOL_PROTEASE_HIS // EF_HAND_2] CG5596 98A6-98A6 dup:2/4
 CG5596 ID:33F5
 CG10151 + unknown * [GRAM_POS_ANCHORING // ATP_GTP_A] CG10151 GH05433 51C2-51C2 ID:33F6
 CG8740 + BcDNA:GH05582 motor_protein * [NLS_BP] CG8740 GH05582 44E1-44E1 dup:5/6 ID:33G4
 CG3364 + unknown * CG3364 GH05668 42D5-42D6 ID:33G9
 + unknown * 1E-178* 1e-105 inserted at base Both 5' and 3' ends of P element Inverse PCR * CG6770 GH05738 33B12-
 CG6770 33B12 ID:33H4
 + peptidase * ANGIOTENSIN-CONVERTING ENZYME PRECURSOR, TESTIS-SPECIFIC (ACE-T) (DIPEPTIDYL
 CARBOXYPEPTIDASE I) (KININASE II)(aa) * metallopeptidase(aa) * ANGIOTEN [PEPDIPTASEA // Peptidase_M2 // T2SP_F]
 CG10142 CG10142 GH05754 60E3-60E4 ID:33H9
 + cell_adhesion * neurexin III beta precursor (clone pB794-5) - bovine(aa) * DMFAT_2 ft * CadN * similar to IG
 (immunoglobulin) superfamily (17 domains), Low-dens[EGF // PRO_RICH // laminin_G // LAM_G_D] CG7050 GH05937 94B4-94B4
 CG7050 dup:1/4 ID:34A10
 + signal_transduction * TOM1(aa) * 2e-17 YHQ8_YEAST HYPOTHETICAL 64.3 KD PROTEIN IN CDC12-ERP5
 CG3529 INTERGENIC REGION * 2e-62 weak similarity to yeast hypothetical protein in C [VHS // HRS_DOMAIN] CG3529 GH05942 67B4-

67B4 ID:34A11

CG15900+ unknown * CG15900 GH05918 41E4-41E4 ID:34A6
+ unknown * SEC14 (S. cerevisiae)-like(aa) * HYPOTHETICAL 84.0 KD PROTEIN T23G5.2 IN CHROMOSOME III(aa) * 4e-21
CG9528 pdb|1AUA| Phosphatidylinositol Transfer Protein [CRAL_TRIO] CG9528 GH05975 26D3-26D4 ID:34B2
+ cytoskeletal_structural_protein * 7e-12 YIL2_YEAST HYPOTHETICAL 123.6 KD PROTEIN IN POR2-COX5B INTERGENIC
REGION * 3e-11 ankyrin ankyrin m * 1e-10 contains similarity to[ANK_REP // ank // ANK_REP_REGION] CG5822 GH05978 25C1-
CG5822 25C1 dup:3/4 ID:34B3
+ VhaSFD transporter * kDa vacuolar H(+)-ATPase subunit(aa) * coded for by C. elegans cDNA yk89e9.5; coded for by C. elegans
CG17332 cDNA cm7g5; coded for by C. elegans cDNA cm14 CG17332 GH05981 36A7-36A7 ID:34B4
+ acyl-CoA_dehydrogenase * fadE19(aa) * PROBABLE GLUTARYL-COA DEHYDROGENASE PRECURSOR (GCD)(aa) *
acyl-Coenzyme A dehydrogenase, short/branched chain precursor(aa) * acyl-CoA [Acyl-CoA_dh] CG9547 GH06693 26D7-26D7
CG9547 ID:34G1
+ enzyme * 2e-69 similar to 3-HYDROXYISOBUTYRATE DEHYDROGENASE PRECURSOR (EC 1.1.1. * 2e-77 D3HI_RAT 3-
HYDROXYISOBUTYRATE DEHYDROGENASE PRECURSOR (HIBADH) * mm [6PGDHDRGNASE] CG15093 GH06781 55F1-
CG15093 55F1 ID:34G10
+ 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-nitrophe CG5567 GH06744 75A4-75A4 ID:34G7
+ unknown * 6e-10 microfilarial chitinase * microfilarial chitinase * CHIT_BRUMA ENDOCHITINASE PRECURSOR (MF1
CG14125 ANTIGEN) chitinas * CG14125 68E3-68E3 dup:2/2 ID:34H10
CG3752 + enzyme CG3752 dup:1/2 ID:34H5
CG12279+ chaperone HEAT SHOCK PROTEIN 67B2 RHODANESE, RHODANESE_2 CG12279 dup:2/2 ID:34H6
+ enzyme * transcriptional adaptor (ADA2, yeast homolog)-3 like (PCAF histone acetylase complex)(aa) * 4e-32 ADA3-like
CG7098 protein * CG7098 16F7-16F7 dup:3/3 ID:34H7
+ mfas signal_transduction * midline fasciclin precursor * 3e-31 p68(beta ig-h3) beta-ig-h3 gene musc * 1e-29 transforming growth
CG3359 factor, beta-induced, 68kD TRANSFORM * 3e-29 RG [BIGH3_DOMAIN] CG3359 87A8-87A dup:3/3 ID:34H9
+ unknown * 2e-22 YJJ7_YEAST HYPOTHETICAL 24.5 KD PROTEIN IN SAP185-BCK1 INTERGENIC REGION * 4e-40 No
CG6746 definition line found * 2e-68 inserted at base Both 5' and CG6746 GH07085 33B9-33B9 ID:35A11
CG8547 + DNA_binding * [PRENYLATION] CG8547 50F-50F dup:1/3 ID:35A2
CG5059 + unknown * CG5059 GH07036 77C4-77C4 ID:35A4
+ I(2)35DfRNA_binding * MTR4_YEAST ATP-DEPENDENT RNA HELICASE DOB1 (MRNA TRANSPORT REGULATOR MTR4) *
YH27_CAEEL PUTATIVE HELICASE W08D2.7 IN CHROMOSOME IV * 1e-153 hypoth [HELICASE // DEAD // ATP_GTP_A]
CG4152 CG4152 GH07290 35D6-35D6 ID:35C5
+ Rab-RP1 enzyme * rab-related protein 3(aa) * Rab-RP3 * 4e-28 YPT7_YEAST GTP-BINDING PROTEIN YPT7 GTP-binding
protein Y * 2e-25 strong similarity to the YPT1 sub-fami [ras // NLS_BP // PROTEIN_KINASE_ATP //] CG8024 GH07310 45B3-
CG8024 45B4 ID:35C8
CG9761 + BcDNA:GH07643 endopeptidase * unknown(aa) * 1e-59 similar to Zinc-binding metalloprotease; cDNA EST come * 1e-132

NEP_MOUSE NEPRILYSIN (NEUTRAL ENDOPEPTIDASE) (NEP) (ENKE[NEPRILYSIN // ZINC_PROTEASE // Peptidas] CG9761
GH07643 82D6-82D7 dup:2/2 ID:35E5

CG13480+ unknown * CG13480 GH07663 70E4-70E4 dup:2/2 ID:35E7
+ cell_adhesion * DMSLIT_2 sli * DMNOTCH3_2 N * 2e-05 NOTC_DROME NEUROGENIC LOCUS NOTCH PROTEIN
PRECURSOR growth * 7e-07 GLP1_CAEEL GLP-1 PROTEIN PRECURSOR glp1 prote [EGF_2] CG9572 GH07746 19C1-19C1
CG9572 ID:35F1
+ BG:DS00180.12 cell_adhesion * 7e-18 C901 protein * 2e-23 similar to EGF-like domain; cDNA EST yk299a12.3 comes from this *
CG8855 7e-18 Ten-m2 * 1e-14 acetyl LDL receptor; SREC=scavenge [EGF_1 // EGF_2] CG8855 GH07762 34E1-34E1 ID:35F2
+ BcDNA:GH07921 RNA_binding * homeobox-containing protein Wariai(aa) * 3e-05 PEP_DROME ZINC FINGER PROTEIN ON
ECDYSONE PUFFS PEP prote * 3e-05 Pep protein - fruit fly (Dr[ZINC_FINGER_C2H2 // NLS_BP // CYTOCHROM] CG8108
CG8108 GH07921 67C3-67C3 dup:1/4 ID:35G10
+ transcription_factor * skeletal muscle LIM protein(aa) * DRAL gene product(aa) * skeletal muscle LIM-protein 1(aa) *
CG11916testin(aa) [LIM] CG11916 GH07858 73D4-73D4 ID:35G5
+ Hr78 transcription_factor * DMSVP1_2 svp * Hr78 * nuclear receptor XR78E/F(aa) * HR78_DROME NUCLEAR HORMONE
RECEPTOR HR78 (DHR78) (NUCLEAR RECEPTOR XR78E/F) [STROIDFINGER // hormone_rec // zf-C4 //] CG7199 GH08073
CG7199 78D7-78D7 ID:35H10
+ unknown * similar to Protein phosphatase 2C (2 domains); cDNA EST yk279g8.5 comes from this gene(aa) *
CG12091 HYPOTHETICAL 41.2 KD PROTEIN IN ERG7-NMD2 INTERGENIC R CG12091 GH07996 62A6-62A6 ID:35H5
CG3223 + unknown * [UBA // PHOSPHOPANTETHEINE] CG3223 GH08043 84E6-84E6 dup:1/2 ID:35H7
+ unknown * No definition line found(aa) * 8e-31 IPPI_YEAST ISOPENTENYL-DIPHOSPHATE DELTA-ISOMERASE (IPP
CG3308 ISOMERASE) * 4e-44 isopentenyl-diphosphate delta isome [UPF0006] CG3308 GH08045 93D4-93D4 ID:35H8
+ protein_kinase * similar to Saccharomyces cerevisiae ORF YGL208W, EMBL Accession Number * 4e-15 SIP2_YEAST SIP2
CG8057 PROTEIN (SPM2 PROTEIN) SIP2 protein - ye * 9e-51 cDNA CG8057 GH09374 45B1-45B1 ID:37A1
+ CH4 * COP9 complex subunit 4(aa) * COP9 complex homolog subunit DCH4(aa) * 5e-12 hypothetical protein YDL147w -
CG8725 yeast (Saccharomyces cerevisiae) * 7e-13 [PCI_DOMAIN // PCI] CG8725 43F8-43F8 dup:1/2 ID:37A9
+ peptidase * 1e-34 membrane dipeptidase (EC 3.4.13.19) precursor - mouse * 4e-35 MDP1_HUMAN MICROSOMAL
DIPEPTIDASE PRECURSOR (MDP) (DEHYDROPEPTIDASE-I) (RENAL DI [Renal_dipeptase] CG5282 GH09573 77B9-77C1
CG5282 ID:37B3
+ unknown * 4e-24 MANB_CAEEL PROBABLE BETA-MANNOSIDASE PRECURSOR (MANNANASE) (MANNASE) * 2e-39
CG12582mannosidase, beta A, lysosomal BETA-MANNOSIDASE PRECURSO * 1e-40 CG12582 GH09594 82A-82A ID:37B4
+ transporter * Similarity to B.subtilis tetracycline resistance protein (SW:TCR2_BACSU); cDNA EST comes from this gene;
CG8428 cDNA EST comes from this gene(aa) * 1e-06 [TCRTETB // sugar_tr] CG8428 GH09820 52F2-52F2 dup:2/2 ID:37D2
+ 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
CG1730986E18-86E19 dup:1/2 ID:37G1
+ BcDNA:GH10333 unknown * 2e-91 hypothetical protein * * [ALDOKETO_REDUCTASE_3] CG12152 GH10333 7B8-7B8
CG12152ID:37G11

+ enzyme * NADH-UBIQUINONE DEHYDROGENASE KD SUBUNIT PRECURSOR(aa) * NADH-UBIQUINONE
 OXIDOREDUCTASE KD SUBUNIT PRECURSOR(aa) * NADH-UBIQUINONE OXIDOREDUCTASE KD [COMPLEX1_24K //
 CG5703 complex1_24kD // NLS_BP] CG5703 16B10-16B10 dup:1/3 ID:37G5
 + BcDNA:GH08860 * 9e-86 cif1 * 1e-37 predicted using Genefinder; similar to trehalose phosphate synthas * 4e-86 TPS1_KLULA
 CG4104 ALPHA,ALPHA-TREHALOSE-PHOSPHATE SYNTHASE (U [TrehaloseP_syn] CG4104 24F1-24F1 dup:1/3 ID:37G7
 CG1469 + Fer2LCH ligand_binding_or_carrier FERRITIN PRECURSOR CG1469 ID:37H10
 + ubiquitin-protein_ligase ubiquitin-conjugating enzyme E2B (RAD6 homolog) UBIQUITIN_CONJUGAT_2 CG10536 GH10432
 CG10536 ID:37H11
 + protein_kinase * Pak * DMAURG_2 aur * MST1(aa) * SERINE/THREONINE-PROTEIN KINASE PLO1(aa) [TYRKINASE //
 CG11228 PROTEIN_KINASE_DOM // pkin] CG11228 GH10354 56D10-56D10 ID:37H3
 + transporter * No definition line found(aa) * sodium-dependent multi-vitamin transporter(aa) * unknown(aa) * sodium-
 CG5687 dependent multivitamin transporter(aa) [NA_SOLUTE_SYMP_3] CG5687 GH10366 62B10-62B10 ID:37H5
 + nAcRbeta-64B ion_channel * ACH3_DROME ACETYLCHOLINE RECEPTOR PROTEIN, BETA-LIKE CHAIN PRECURSOR *
 1e-97 similar to neuronal acetylcholine receptor * 1e-78 neuronal n[NICOTINICR // neur_chan // NEUROTR_ION_] CG12606
 CG12606 GH10531 64B11-64B11 dup:1/2 ID:38A12
 + unknown * /match=(desc:; /match=(desc:(aa) * 5e-21 /match=(desc:; /ma * 1e-05 predicted using Genefinder * No definition
 CG10562 line found CG10562 GH10454 96C8-96C8 ID:38A2
 + structural_protein * U4/U6-associated RNA splicing factor(aa) * 9e-24 hypothetical protein YDR473c - yeast (Saccharomyces
 CG7757 cerevisiae) (U * 1e-101 cDNA EST comes from thi [NLS_BP] CG7757 GH10477 76D7-76D7 ID:38A4
 + enzyme * 405aa long hypothetical succinyl-CoA synthetase beta chain(aa) * PROBABLE SUCCINYL-COA LIGASE (GDP-
 CG11963 FORMING), BETA-CHAIN PRECURSOR (SUCCINYL-COA SYNT [ligase-CoA] CG11963 GH10480 85C1-85C2 ID:38A5
 + Su(fu) unknown * DMSF_2 Su(fu) * Su(fu) protein(aa) * gene suppressor of fused protein - fruit fly (Drosophila melanogaster) *
 CG6054 6e-80 Su(fu) protein CG6054 GH10488 87C8-87C8 ID:38A6
 + BEAF-32 DNA_binding * boundary element-associated factor, 32k - fruit fly (Drosophila melanogaster)(aa) * 1e-146
 CG10159 DMBEAF32A_2 BEAF-32 * boundary element associated factor [NLS_BP] CG10159 GH10592 51C3-51C3 ID:38B2
 + unknown * 1e-45 YABC_ECOLI HYPOTHETICAL 34.9 KD PROTEIN IN FRUR-FTSL INTERGENIC REGION (ORFB) >g *
 CG14683 1E-170* hypothetical protein * hypothetical protein CG14683 GH10770 86C2-86C2 ID:38C10
 + ligand_binding_or_carrier * 1e-31 peptidyl-dipeptidase A (EC 3.4.15.1) 67k precursor - fruit fly (Drosophila me * 6e-09 coded
 CG9047 for by C. elegans cDNA yk27b10.3; coded for by C. [PRO_RICH] CG9047 GH10774 60E3-60E3 dup:1/3 ID:38C11
 + electron_transfer * 7e-17 TRX1_YEAST THIOREDOXIN I (TR-I) thioredoxin I - yeast (Sacc * 1e-12 THIO_DROME
 THIOREDOXIN (DEADHEAD PROTEIN) thioredoxin-I * 5e-18 similar to [FUMARATE_LYASES // THIOREDOXIN // THIOR]
 CG5495 CG5495 GH10696 66A5-66A5 ID:38C2
 + unknown * protein(aa) * cDNA EST yk269g12.5 comes from this gene; cDNA EST comes from this gene; cDNA EST comes
 CG7146 from this gene; cDNA EST comes from this gene CG7146 GH10703 90F6-90F6 ID:38C3
 + Su(H) DNA_binding * DMSUHA_2 Su(H) * RBJK_DROME J KAPPA-RECOMBINATION SIGNAL BINDING PROTEIN (RBP-J
 KAPPA) (SUPPRESSO * 1e-134 DNA-binding protein LAG-1 lag-1 ge * RB [LIPOCALIN] CG3497 GH10914 35C1-35C1 dup:2/2
 CG3497 ID:38D10

+ signal_transduction * glucosyltransferase; Die2p(aa) * 1e-16 DIE2_YEAST DIE2 PROTEIN DIE2 protein - yeast (Saccharom
 CG7624 * 6e-23 Similarity to Yeast DIE2 protein elega * 4e-4 [SH3] CG7624 GH10931 68A6-68A7 ID:38D12
 + endopeptidase * PROBABLE CLPP-LIKE PROTEASE (ENDOPEPTIDASE CLP)(aa) * PUTATIVE ATP-DEPENDENT CLP
 PROTEASE PROTEOLYTIC SUBUNIT, MITOCHONDRIAL PRECURSOR (ENDOPEPTIDAS [CLP_protease //
 CG5045 CLP_PROTEASE_SER // CLP] CG5045 GH10833 31D10-31D10 ID:38D2
 + 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
 + enzyme * 2e-12 probable membrane protein YLR118c - yeast (Saccharomyces cerevisiae) * 2e-21 Similarity to some
 CG6567 prokaryotic esterases; cDNA EST com * 3e-26 ly [ESTERASE] CG6567 GH11067 86C7-86C7 dup:2/2 ID:38E12
 + Dredd endopeptidase * DREDD isoform delta * 2e-16 interleukin-1 beta-converting enzyme homolog CED-3 - Caenorhabditis
 elegans * 1e-18 caspase-8 caspase-8 * 5e-18 caspas[CASPASE_P10 // ICE_p10 // CASPASE_P20 //] CG7486 GH10971 1B10-
 CG7486 1B10 dup:2/2 ID:38E5
 CG6456 + unknown * 9e-07 prepro-APGWamide * APGWamide * [NLS_BP] CG6456 GH11008 74B-74B dup:2/2 ID:38E7
 + RNA_binding * 3e-18 predicted using Genefinder; similar to KH domain family of RNA b * 3e-12 predicted using Genefinder;
 CG2950 similar to KH domain family of RNA b * [KH-domain // KH_DOMAIN] CG2950 GH11071 25B3-25B3 dup:1/2 ID:38F1
 + tumor_suppressor * 3e-09 /match=(desc;; /ma * 3e-16 predicted using Genefinder; Similarity to Human leukocyte surface *
 4e-26 CD82_MOUSE CD82 ANTIGEN (INDUCIBLE MEMBRA [transmembrane4 // TMFOUR // TM4_2] CG4999 GH11168 66E3-
 CG4999 66E3 ID:38F10
 + receptor * glutamyl 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
 + BcDNA:GH11110 RNA_binding * 6e-06 heterogeneous nuclear RNP protein clone pHRP40.2 - fruit fly (Drosophila melan * 2e-25
 CG2910 contains similarity to RNA recognition motifs (Pfam; rr [RBD // rm] CG2910 GH11110 43F7-43F8 dup:1/3 ID:38F3
 CG1927 + BcDNA:GH11112 unknown * CG1927 GH11112 62B11-62B11 ID:38F4
 + TFIIEalpha transcription_factor * 6e-23 T2EA_YEAST TRANSCRIPTION INITIATION FACTOR IIE, ALPHA SUBUNIT (TFIIE-
 CG10415 ALPHA) (TRA * TFIIE large subunit * 7e-35 cDNA EST yk210d12.5 comes from CG10415 GH11150 68C13-68C13 ID:38F9
 + Rab-RP4 enzyme * Rab4 * rab-related protein 4(aa) * 2e-29 SEC4_YEAST RAS-RELATED PROTEIN SEC4 GTP-binding protein
 SE * 1e-32 strong similarity to the YPT1 sub-family [SIGMA54_INTERACT_1 // SAR1GTPBP // ras] CG3129 GH11193 5A12-5A12
 CG3129 ID:38G1
 + receptor * 7e-29 Contains similarity to Pfam domain: (thyroglobulin_1), * 9e-29 testican * 9e-29 testican - human * 6e-09
 HG2A_RAT H-2 CLASS II HISTOCOMPATIBIL [thyroglobulin_1 // THYROGLOBULIN_1 // k] CG13830 GH11316 94D13-94E
 CG13830 dup:1/2 ID:38G11
 + BcDNA:GH11322 cell_adhesion * Pxn * 6e-20 roundabout * 2e-15 hemocytin precursor * 1e-10 rig-1 protein [ig // fn3] CG16857
 CG16857 GH11322 24E4-24E4 dup:2/5 ID:38G12
 + unknown * 5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase/IMP cyclohydrolase(aa) * 5-aminoimidazole-4-
 CG11089 carboxamide ribonucleotide (AICAR) trans [ATP_GTP_A] CG11089 GH11240 96B4-96B5 ID:38G4

+ Nmd3 unknown * 1e-115 NMD3_YEAST NONSENSE-MEDIATED MRNA DECAY PROTEIN Nmd3p * 1e-125 Similarity to
 Yeast nonsense-mediated mRNA decay protein (SW:NMD3_Y * 1e-143 CG [CYTOCHROME_C] CG3460 GH11261 2E1-2E1
 CG3460 ID:38G5
 + 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
 + BcDNA:GH11415 unknown * 1e-104 mab-21 * 1e-139 CAGR1 cell fate specificati * 1e-140 XMAB21 * cDNA EST yk376f11.5
 CG4766 comes from this gene; cDNA EST yk282h5.5 comes CG4766 GH11415 5D1-5D1 ID:38H10
 CG3624 + cell_adhesion * [ig] CG3624 GH11432 58D7-58D7 dup:2/2 ID:38H12
 + Rpn5 endopeptidase * proteasome (prosome, macropain) 26S subunit, non-ATPase, 12(aa) * 5e-42 hypothetical protein
 CG1100 YDL147w - yeast (Saccharomyces cerevisiae) * 2e-81 No d [PCI_DOMAIN // PCI // NLS_BP] CG1100 GH11341 83C-83C ID:38H3
 + enzyme * peroxinectin - signal crayfish(aa) * ovoperoxidase(aa) * peroxidase(aa) * coded for by C. elegans cDNA yk30f1.3;
 CG8913 coded for by C. elegans cDNA yk40 [ANPEROXIDASE // PEROXIDASE_3] CG8913 GH11385 92C1-92C1 ID:38H5
 + RNA_binding * pre-mRNA splicing factor(aa) * contains similarity to G-beta repeats(aa) * 1e-76 Cdc40p * 3e-15
 T2D4_DROME TRANSCRIPTION INITIATION FACTOR TFIID KD [GPROTEINBRPT // WD40_REGION // WD_REPEA] CG6015
 CG6015 GH11406 94A1-94A1 ID:38H8
 + RNA_binding * polyadenylate binding protein II - human(aa) * myelin gene expression factor 2(aa) * DMB52_2 B52 * Gbp1p
 CG9373 protein - Chlamydomonas reinhardtii(aa) [RBD // rrm] CG9373 GH11495 86C1-86C1 dup:1/2 ID:39A4
 + vkg cell_adhesion * DMINTGRNB_2 Cg25C * vkg * collagen type IV alpha * 7e-25 Similar to cuticular collagen; F58F6.2
 CG16858[COLLAGEN_REP // Collagen // C4] CG16858 GH11516 25C1-25C1 ID:39A7
 CG12907 + unknown * 1E-145** [PRO_RICH // NLS_BP] CG12907 GH11521 47A-47A ID:39A8
 + * 1e-29 cDNA EST yk428d5.3 comes from this gene; cDNA EST yk428d5.5 comes * 3e-12 conserved hypothetical secreted
 CG13865 protein pylori * putative pylori * c CG13865 cyto_unknown dup:3/3 ID:39B1
 + BcDNA:GH11690 unknown * 2e-08 hypothetical protein YLR424w - yeast (Saccharomyces cerevisiae) (U * 1e-102 weak similarity
 with viral DNA polymerase (Swiss Prot accession nu [PRO_RICH // D111_DOMAIN // NLS_BP // AT] CG7238 GH11690 27E1-27E1
 CG7238 ID:39B11
 + Pcaf enzyme * Pcaf SPTR(aa) * BLASTX 2.0E-35 GCN5|Component of the nucleosomal histone acetyltransferase (Spt-Ada-
 CG4107 Gcn5-Acetyltransferase or SAGA) complex(dna) * B [NLS_BP] CG4107 GH11602 69C3-69C3 dup:2/2 ID:39B3
 + 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
 + signal_transduction * 3e-48 cdc4, incomplete, len: 579, CAI, 0.15, CC4_YEAST CELL DIVISI * 2e-61 Slimb * 5e-32
 YKY4_CAEEL HYPOTHETICAL 40.4 KD TRP-ASP REPEATS CO[GPROTEINBRPT // F-box // WD_REPEATS //] CG15010
 CG15010 GH11648 64B4-64B4 dup:2/3 ID:39B6
 + unknown * MYO-INOSITOL-1(OR 4)-MONOPHOSPHATASE (IMP 2) (INOSITOL MONOPHOSPHATASE 2)(aa) * MYO-
 INOSITOL-1(OR 4)-MONOPHOSPHATASE (IMP) (INOSITOL MONOPHOSPHATASE [inositol_P // INFBPHPTASE //
 CG17027 INOSPHT] CG17027 GH11740 72C1-72C1 ID:39C2
 CG2934 + transporter * 40-kDa V-ATPase subunit(aa) * 3e-85 VATX_YEAST VACUOLAR ATP SYNTHASE SUBUNIT AC39 (V-

ATPASE AC39 SUBUNIT) (V-ATPASE * 1e-172 Ac39/physophilin * 1e- CG2934 GH11776 4A1-4A1 ID:39C4
+ enzyme * FLAVONOL 3-SULFOTRANSFERASE (F3-ST)(aa) * steroid sulfotransferase 3(aa) * sulfotransferase family 2B,
CG5428 member 1(aa) * sulfotransferase, estrogen-pre [Sulfotransfer] CG5428 GH11818 59F4-59F4 ID:39C6
CG13928+ unknown * inserted at base Both 5' and 3' ends of P element Inverse PCR * * CG13928 GH11843 62A-62A ID:39C8
+ transporter * 2e-50 Na(+)-dependent inorganic phosphate cotransporter mela * 7e-54 YLD2_CAEEL HYPOTHETICAL 52.7
CG15095KD 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
+ transporter * Contains similarity to equilibrative nucleoside transporter from Homo sapiens. ESTs and come from this
CG11045 gene.(aa) * NBMPR-insensitive nucleoside tr [DERENTRNSPRT] CG11045 GH12067 26E2-26E2 ID:39D11
+ Rpt5 endopeptidase * contains similarity to the AAA family of ATPases (Pfam; AAA, score; 259.07); most similar to human
probable 26S protease subunit TBP-1 * putative [AAA // MITOCH_CARRIER // ATP_GTP_A] CG10370 GH12068 95B7-95B7
CG10370 ID:39D12
+ BcDNA:GH11973 unknown * 2e-05 CD94 C-type lectin receptor musculus * 4e-05 regenerating islet-derived alpha (pancreatic
stone protein, pancreatic thread protein) * 7e-05 PA2 [lectin_c // C_TYPE_LLECTIN_2 // NLS_BP] CG6014 GH11973 78D4-78D4
CG6014 dup:3/3 ID:39D7
+ unknown * 2e-12 HNK-1 sulfotransferase HNK-1 sulfotransferase * 2e-12 HNK-1 sulfotransferase * [PRO_RICH] CG14024
CG14024 GH11985 25D4-25D5 ID:39D8
CG1146 + unknown * CG1146 GH12037 62E6-62E6 ID:39D9
+ BcDNA:GH12174 DNA_binding * 1e-05 eyelid * 6e-45 YP83_CAEEL HYPOTHETICAL 139.1 KD PROTEIN C08B11.3 IN
CHROMOSOME II * 5e-06 FMO5_MOUSE DIMETHYLANILINE MONOOXYGENASE (N-OXIDE FO [ARID] CG3274 GH12174
CG3274 42B2-42B3 dup:4/4 ID:39E10
+ Pfk enzyme * DMPFK_5 Pfk * DMPFK_5 Pfk * 1e-151 phosphofructokinase, beta subunit * K6PF_DROME 6-
PHOSPHOFRUCTOKINASE (PHOSPHOFRUCTOKINASE) (PHOSPHOHEXOKINASE) [PFK // PHFRCTKINASE] CG4001
CG4001 GH12192 46E4-46E4 dup:4/5 ID:39E11
+ enzyme * 1e-30 YHX6_YEAST HYPOTHETICAL 42.4 KD PROTEIN IN ENO2-STB5 INTERGENIC REGION * 9e-53 similar
to flavin-containing monooxygenases * 2e-29 FMO3_MOUSE [ADXRDTASE // FADPNR // FMO-like // PNDR] CG3174 GH12207
CG3174 42B3-42B3 dup:2/2 ID:39E12
+ bw transporter * BROWN PROTEIN(aa) * DMBROWN_1 bw * brown protein(aa) * BROWN PROTEIN(aa) [ATP_GTP_A2 //
CG17632ABC_tran // DA_BOX] CG17632 GH12107 59E-59E3 dup:2/2 ID:39E3
CG9119 + unknown * 2e-25 No definition line found * * CG9119 61F3-61F3 dup:5/5 ID:39E5
+ BcDNA:GH12144 unknown * Contains similarity to Pfam domain: (TPR), Score=38.0, E-value=6.9e-08, N=6(aa) * weakly similar
CG4341 to E. nidulans bimA gene product * * [TPR_REGION // TPR_REPEAT] CG4341 GH12144 21D4-21E dup:3/3 ID:39E7
CG4929 + CG4929 dup:2/2 ID:39E8
+ cher actin_binding * contains similarity to the x aa approximate repeats found in human filamin * filamin, Mueller cell -
chicken(aa) * filamin (actin-binding protein[Filamin // FILAMIN_REPEAT // GRAM_POS_A] CG3937 GH12209 92D1-92D1 dup:2/5
CG3937 ID:39F1

+ ligand_binding_or_carrier * ALPHA-TOCOPHEROL TRANSFER PROTEIN (ALPHA-TTP)(aa) * 4e-08 YKJ1_YEAST 36.1 KD
 PROTEIN IN BUD2-MIF2 INTERGENIC REGION * 5e-10 62D9.a * 2e-25 cellular [CRETINALDHBP // CRAL_TRIO] CG5973
 CG5973 GH12376 27F7-28A1 ID:39F12
 + enzyme * Ynr027wp(aa) * 8e-44 YEC9_YEAST HYPOTHETICAL 35.6 KD PROTEIN IN MCM3-VMA3 INTERGENIC
 CG4446 REGION * 2e-57 PDXK_CAEEL PUTATIVE PYRIDOXINE KINASE (PYRIDOXAL [pfkB] CG4446 GH12231 67B1-67B1 ID:39F3
 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 GH12350
 CG1435 7A4-7A4 ID:39F9
 + 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
 + BcDNA:GH12558 enzyme * MITOCHONDRIAL TRIFUNCTIONAL ENZYME ALPHA SUBUNIT PRECURSOR (TP-ALPHA) LONG-
 CHAIN ENOYL-COA HYDRATASE ; LONG CHAIN 3-HYDROXYACYL-COA DEHYDROGENASE * s [ECH // 3HCDH //
 CG4389 ENOYL_COA_HYDRATASE] CG4389 GH12558 30B12-30B12 ID:39G12
 + enzyme * DMC23E12 * gamma-glutamyltransferase (EC 2.3.2.2) precursor - rat(aa) * gamma-glutamyl transpeptidase (EC
 CG4829 2.3.2.2)(aa) * gamma-glutamyl transpeptida [G_glu_transpept] CG4829 GH12430 15A8-15A8 dup:1/2 ID:39G5
 + I(2)37Ccunknown * 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
 + ken transcription_factor * ken * ken(aa) * 8e-09 AZF1_YEAST ASPARAGINE-RICH ZINC FINGER PROTEIN AZF1 fin * 9e-10
 CG5575 zinc finger protein PAG-3 [BTB // zf-C2H2 // ZINC_FINGER_C2H2 // Z] CG5575 GH12495 60A6-60A7 ID:39G8
 + Dat ligand_binding_or_carrier * DMNAT1_2 Aanat1 * N-acetyltransferase(aa) * aralkylamine N-acetyltransferase (EC 2.3.1.87)
 CG3318 - fruit fly (Drosophila melano * CG3318 GH12636 60B9-60B9 ID:39H12
 + Idgf2 enzyme * IDGF2 * 5e-09 probable membrane protein YDR371w - yeast (Saccharomyces cerevisiae) * disc growth factor *
 CG4475 3e-24 CHIT_CAEEL PUTATIVE ENDOCHITINASE co [2SGLOBULIN // Glyco_hydro_18] CG4475 GH12581 36A1-36A1 ID:39H4
 + chaperone * embryonal lethal (2)13-1 (el(2)13-1) - fruit fly (Drosophila melanogaster)(aa) * 4e-16 HS27_DROME HEAT
 CG4461 SHOCK PROTEIN heat shock protein - f * 9e-10 [HSP20] CG4461 GH12586 67B1-67B1 ID:39H6
 + SNF1A protein_kinase * SNF1A * SNF1A/AMP-activated protein kinase(aa) * 1e-108 SNF1_YEAST CARBON CATABOLITE
 DEREPRESSING PROTEIN KINASE p * SNF1A/AMP-activated protein kin [PROTEIN_KINASE_ST // TYRKINASE // PROTE]
 CG3051 CG3051 GH12596 2A2-2A2 ID:39H8
 + BcDNA:GH12663 unknown * unknown(aa) * 1e-29 YNC2_CAEEL HYPOTHETICAL 83.6 KD PROTEIN R05D3.2 IN
 CG5807 CHROMOSOME III * 1e-86 unknown * 7e-49 inserted at base Both 5' and 3' ends o CG5807 GH12663 98E1-96B1 ID:40A4
 + Rh4 G_protein_linked_receptor * opsin(aa) * Rh4 * OPS4_DROME OPSIN RH4 (INNER R7 PHOTORECEPTOR CELLS
 OPSIN) * 2e-15 YXX5_CAEEL PUTATIVE NEUROPEPTIDE Y RECEPTOR (NPY-R) simila [GPCRRHODOPSN // OPSIN //
 CG9668 OPSINRH3RH4] CG9668 GH12673 73C5-73D1 ID:40A5
 + translation_factor * UNKNOWN(aa) * 7e-86 inserted at base Both 5' and 3' ends of P element Inverse PCR * eukaryotic
 CG12131 translation initiation factor eIF3, p35 subunit * CG12131 GH12681 46C10-46C11 ID:40A7

+ 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
 CG8402 GH12714 85E6-85E6 ID:40B1
 + enzyme * GFA1_YEAST GLUCOSAMINE--FRUCTOSE-6-PHOSPHATE AMINOTRANSFERASE (ISOMERIZING) (HEX *
 similar to glucosamine-fructose-6-phosphate aminotransferase; cD [CRYSTALLIN_BETAGAMMA // GATase_2 // GAT] CG1345
 CG1345 GH12731 98C3-98C3 ID:40B3
 + unknown * ABC transporter, ATP-binding protein, putative(aa) * 2e-18 conserved protein * daunorubicin resistance
 CG6166 membrane protein (drrB) * CG6166 GH12746 97A9-97A9 dup:1/2 ID:40B5
 + Zn72D peptidase * zinc finger RNA binding protein(aa) * Zn72D * zinc-finger protein Zn72D * 3e-47 M-phase phosphoprotein
 CG5215 [ZF_MATRIN // zf-C2H2 // ZINC_FINGER_C2H] CG5215 GH12756 72D5-72D6 ID:40B6
 + 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
 CG8775 GH12821 87E6-87E6 dup:2/2 ID:40B8
 + structural_protein * nuclear pore protein; Nsp1p(aa) * nucleoporin p62(aa) * similar to nucleoporins(aa) * NUCLEAR PORE
 CG6251 GLYCOPROTEIN P62 (NUCLEOPORIN P62)(aa) CG6251 GH12838 53B1-53B1 ID:40B9
 + signal_transduction * centaurin beta 1A(aa) * BLASTX 1.6E-48 Human mRNA for gene, partial cds.(dna) * HYPOTHETICAL
 CG6742 PROTEIN * centaurin beta2(aa) [ANK_REP // ArfGap // GLYCOSYL_HYDROL_F5] CG6742 GH12888 94E-94E dup:1/2 ID:40C1
 + unknown * 9e-07 PAC2_YEAST PAC2 PROTEIN PAC2 protein - yeast (Saccharomy * 3e-46 No definition line found * 1e-23
 CG12214 tubulin-specific chaperone e cofactor E * CG12214 GH13040 46F1-46F1 dup:1/2 ID:40C10
 CG5506 + unknown * CG5506 GH13083 75A6-75A6 ID:40C12
 + unknown * Similar to Plasmodium falciparum glutamic acid-rich protein precursor * cDNA EST comes from this gene; cDNA
 CG10955 EST comes from this gene; cDNA EST come [PRO_RICH] CG10955 GH12904 58D6-58D6 dup:1/3 ID:40C2
 CG6306 + unknown * CG6306 GH12946 17B1-17B1 ID:40C7
 + transporter * VACUOLAR ATP SYNTHASE SUBUNIT D (V-ATPASE D SUBUNIT) (V-ATPASE KD ACCESSORY
 PROTEIN)(aa) * 1e-58 VATD_YEAST VACUOLAR ATP SYNTHASE SUBUNIT D (V-ATPAS CG8186 GH12958 52A10-52A10
 CG8186 ID:40C8
 + E2f2 transcription_factor * E2f2 * 1e-174 E2F-like transcription factor (E2F2) * 7e-14 predicted using Genefinder; cDNA EST
 CG1071 comes from this * 3e-18 E2F5_MOUSE TRANSCRIPTION FAC CG1071 GH13089 39B3-39B3 ID:40D1
 + ligand_binding_or_carrier * mannose receptor, C type 1(aa) * 1e-05 similar to Lectin C-type domain short and long forms (2
 domains) * 9e-06 lectin lambda * 6e-0 [lectin_c // C_TYPE_LLECTIN_1 // C_TYPE_L] CG8343 GH13116 42A10-42A10 dup:2/2
 CG8343 ID:40D2
 + translation_factor * translation initiation factor eIF3 subunit; Tif35p(aa) * 7e-28 IF35_YEAST EUKARYOTIC TRANSLATION
 CG10881 INITIATION FACTOR RNA-BINDING SUBUNIT (EIF- * 6e-34 [RNP_1 // RBD // rrm] CG10881 GH13208 92E3-92E3 ID:40D8
 + translation_factor * BLASTX 4.7E-83 Human translation initiation factor eIF3 p66 subunit mRNA, complete cds.(dna) *
 CG10161 HYPOTHETICAL 64.2 KD PROTEIN R08D7.3 IN CHROMOSOME II CG10161 GH13209 97D8-97D8 dup:3/4 ID:40D9
 + transcription_factor * HYPOTHETICAL 43.4 KD PROTEIN C6F12.11C IN CHROMOSOME I(aa) * transcription factor
 CG10563 IIC63(aa) * 1e-05 TFC1_YEAST TRANSCRIPTION FACTOR TAU KD SUBUNIT CG10563 GH13253 37C1-37C1 dup:2/2

ID:40E1
+ transcription_factor * zf30C * DMSPALTR_3 salr * 5e-05 YEW0_YEAST PUTATIVE 50.3 KD ZINC FINGER PROTEIN IN
PAK1-RPS26B INTERGENIC REGIO * 9e-06 spalt-related [zf-C2H2 // ZINC_FINGER_C2H2 // ZINC_FIN] CG2199 GH13336

CG2199 61F7-61F7 dup:2/2 ID:40E10
+ unknown * insect intestinal mucin IIM22(aa) * putative cell surface glycoprotein; Sed1p(aa) * 71(aa) * GLYCOPROTEIN X

CG7874 PRECURSOR(aa) CG7874 GH13361 18B6-18B6 dup:2/2 ID:40E12
+ Thiolaseenzyme * Thiolase * thiolase(aa) * 3e-37 THIL_YEAST ACETYL-COA ACETYLTRANSFERASE (ACETOACETYL-COA
THIOLASE) * 1e-140 YKA3_CAEEL HYPOTHETICAL 47.9 KD PROTEIN [thiolase] CG4581 GH13256 60A6-60A6 dup:2/2

CG4581 ID:40E2
+ 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

CG4317 ID:40E4
+ Pglym78 enzyme * phosphoglyceromutase - fruit fly (Drosophila melanogaster)(aa) * DMPGLY_4 Pglym78 * 7e-48 pdb|4PGM|A

CG1721 Chain A, Saccharomyces Cerevisiae Phosphoglycer [PGAM // PG_MUTASE] CG1721 GH13304 99A1-99A1 dup:2/2 ID:40E5
+ enzyme * phosphoglucomutase(aa) * 1e-152 PGM2_YEAST PHOSPHOGLUCOMUTASE (GLUCOSE PHOSPHOMUTASE
2) (PGM 2) * coded for by C. elegans cDNA cm17h1; coded for by [PGM_PMM // PGMPMM // ATP_GTP_A] CG5165 GH13311

CG5165 72D7-72D7 dup:2/2 ID:40E6
+ actin_binding * 2e-12 putative actin-binding protein UNC-115 * 2e-11 protein * 2e-05 talin homologue * 5e-05 qua CG9489

CG9489 GH13330 85E5-85E5 dup:3/3 ID:40E9
+ 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
+ RNA_binding * LET 858(aa) * conserved hypothetical protein(aa) * BLASTX 7.4E-44 Caenorhabditis elegans Nucampholin

CG12750 (let-858) mRNA, complete cds.(dna) * BLASTX 3 [NLS_BP] CG12750 GH13383 36F7-36F7 dup:3/3 ID:40F2

CG5903 + unknown * 6e-06 K02F3.10 gene product ** CG5903 GH13386 89B9-89B9 ID:40F3
+ enzyme * MALATE OXIDOREDUCTASE, CHLOROPLAST PRECURSOR (MALIC ENZYME) (ME) (NADP-DEPENDENT
MALIC ENZYME) (NADP-ME)(aa) * malic enzyme(aa) * 4e-86 MAOX_YEAST [MALOXRDTASE // malic // ATP_GTP_A] CG5889

CG5889 GH13437 97E11-97F ID:40F4
+ Fpps enzyme * 8e-80 FPPS_YEAST FARNESYL PYROPHOSPHATE SYNTHETASE (FPP SYNTHETASE) (FPS) (FARNESYL
DI * farnesyl pyrophosphate synthase melanogas * 2e-37 predicted [polyprenyl_synt // POLYPRENYL_SYNTHET_1] CG12389

CG12389 GH13450 47E5-47E6 dup:2/2 ID:40F5

CG7021 + Ela unknown * [COLLAGEN_REP] CG7021 GH13458 96B4-96B4 ID:40F7
+ 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
+ transcription_factor * DNZDHHHC/NEW1 zinc finger protein 11(aa) * 3e-15 probable membrane protein YLR246w - yeast

CG8314 (Saccharomyces cerevisiae) * 1e-67 No definition line foun [ZF_DHHC] CG8314 GH13672 52E1-52E1 dup:1/2 ID:40G10

CG8251 + Pgi enzyme * glucosephosphate isomerase(aa) * DMPGIAAAA_11 * glucose-6-phosphate isomerase(aa) * G6PI_YEAST

GLUCOSE-6-PHOSPHATE ISOMERASE (GPI) (PHOSPHOGLUCOSE [PGI // P_GLUCOSE_ISOMERASE_1 // P_GLUCO]
 CG8251 GH13575 44F9-44F9 ID:40G4
 + RNA_binding * 3e-16 RNA-binding protein cabeza - fruit fly (Drosophila melanogaster) (* 4e-14 EWS_MOUSE RNA-
 BINDING PROTEIN EWS RNA-binding protein E * 2e-15 TLS [RBD // zf-RanBP // rrm // ZF_RANBP] CG14718 GH13594 86F1-
 CG14718 86F1 ID:40G5
 + 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 CG3041 GH13824 88A4-88A4 ID:40H11
 + 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
 + bun transcription_factor * shortsighted class 2(aa) * DMSHA_5 bun * shortsighted class * 2e-07 protein [TSC22] CG5461
 CG5461 GH13775 33E-33E6 ID:40H5
 + enzyme * METHIONYL-TRNA SYNTHETASE (METHIONINE--TRNA LIGASE) (METRS)(aa) * 2e-67 SYMM_YEAST
 METHIONYL-TRNA SYNTHETASE, MITOCHONDRIAL (METHIONINE--TRNA LIGASE [tRNA-synt_1 // TRNASYNTHMET]
 CG8684 CG8684 GH13807 88B5-88B5 ID:40H7
 CG2046 + unknown * CG2046 GH13924 83C-83C ID:41A10
 + unknown * 3e-66 EMP70 protein precursor - yeast (Saccharomyces cerevisiae) * 2e-88 Similarity to Yeast endosomal P24A
 CG10590 protein (SW:EM70_YEAST); cDNA E * 4e-93 [CRYSTALLIN_BETAGAMMA] CG10590 GH13842 64E3-64E3 ID:41A2
 + protein_kinase * serine/threonine protein kinase; Cdc7p(aa) * protein kinase Cdc7(aa) * DMSTPK Pk61C * HsCdc7(aa)
 CG5790 [PROTEIN_KINASE_ST // PROTEIN_KINASE_DOM] CG5790 GH13884 36F-36F ID:41A7
 + peptidase * lysosomal Pro-X carboxypeptidase - like protein(aa) * similar to alpha/beta hydrolase fold(aa) * 1e-77 similar to
 CG9953 lysosomal carboxypeptidase; cDNA [ESTERASE // abhydrolase] CG9953 GH14014 65D5-65D5 ID:41B7
 + RhoBTB ligand_binding_or_carrier * protein(aa) * protein(aa) * 6e-24 RHO1_YEAST RHO1 PROTEIN transforming protein RHO1
 - yeast * 9e-27 RHO1_DROME RAS-LIKE GTP-BINDING PR[BTB // PRO_RICH // ras // ATP_GTP_A //] CG5701 GH14096 77B6-
 CG5701 77B6 dup:1/2 ID:41C1
 CG2176 + unknown * CG2176 GH14263 99E2-99E2 ID:41C11
 + v enzyme * DMVERM_2 v * VERM_DROME TRYPTOPHAN 2,3-DIOXYGENASE (TRYPTOPHAN PYRROLASE)
 (VERMILION PROTEIN) * 1e-102 T230_CAEEL PUTATIVE TRYPTOPHAN 2,3-DIOXYGENA CG2155 GH14143 9F13-10A1
 CG2155 ID:41C4
 none + none GH14214 ID:41C7
 + enzyme * Depressed growth-rate protein; Deg1p(aa) * PROBABLE PSEUDOURIDYLATE SYNTHASE E02H1.3
 (PSEUDOURIDINE SYNTHASE)(aa) * 6e-54 PUS3_YEAST PSEUDOURIDYLATE [PseudoU_synth_1] CG3045 GH14326 58C5-
 CG3045 58C5 dup:2/2 ID:41D5
 + unknown * TEGT(aa) * 3e-31 testis enhanced gene transcript protein * 3e-29 TEGT * testis enhanced gene transcript T
 CG7188 [UPF0005] CG7188 GH14327 66C6-66C6 ID:41D6
 + gek protein_kinase * gek * myotonic dystrophy kinase-related Cdc42-binding kinase(aa) * CDC42-binding protein kinase beta
 CG4012 (DMPK-like)(aa) * myotonic dystrophy kinase-re [DAG_PE_BINDING_DOMAIN // PROTEIN_KINASE] CG4012 GH14340 60B5-

60B5 ID:41D7

CG7567 + unknown * CG7567 GH14364 99B5-99B5 ID:41D8
+ defense/immunity_protein * UNKNOWN(aa) * 3e-07 peptidoglycan recognition protein precursor * TNF superfamily, member
CG5523 (LTB)-like (peptidoglycan recognition * hypothetical prote CG5523 GH14535 66A5-66A5 dup:2/2 ID:41E10
+ enzyme * cytochrome c oxidase subunit IV(aa) * CYTOCHROME C OXIDASE POLYPEPTIDE IV PRECURSOR(aa) * 2e-22
CG10664 COX4_MOUSE CYTOCHROME C OXIDASE POLYPEPTIDE IV PRECU CG10664 GH14536 38A8-38A8 dup:2/2 ID:41E11
+ unknown * CGI-149 protein(aa) * 3e-22 YKE1_YEAST HYPOTHETICAL 26.2 KD PROTEIN IN SPC42-PTM1 INTERGENIC
CG9779 REGION * 2e-42 T27F7.1 gene product * 2e-25 putative en CG9779 GH14561 82A5-82A5 dup:2/2 ID:41E12
+ signal_transduction * 2e-17 activin beta precursor * 3e-14 CET-1 * 2e-22 IHBA_MOUSE INHIBIN BETA A CHAIN
PRECURSOR (ACTIVIN BETA-A CHAIN) * 5e-23 inhibin, beta A[TGF-beta // TGF_BETA // TGF_BETA_2 // Z] CG16987 GH14433
CG16987 23B2-23B2 dup:2/2 ID:41E2
+ Hr96 steroid_hormone_receptor * Hr96 * NUCLEAR HORMONE RECEPTOR HR96 (DHR96)(aa) * 1e-28 similar to nuclear
hormone receptor * 9e-24 VDR_MOUSE VITAMIN D3 RECEPTOR ([STROIDFINGER // hormone_rec // zf-C4 //] CG11783
CG11783 GH14435 96B14-96B14 dup:2/2 ID:41E3
CG18525+ unknown * CG18525 GH14439 88E7-88E7 dup:2/2 ID:41E4
+ electron_transfer * 3e-39 ETFB_YEAST PROBABLE ELECTRON TRANSFER FLAVOPROTEIN BETA-SUBUNIT (BETA-
CG7834 ETF) * 7e-61 contains similarity to electron transfer flavoprotein beta [ETF_beta] CG7834 GH14462 99C4-99C4 dup:2/2 ID:41E7
+ unknown * HNK-1 sulfotransferase(aa) * 1e-20 HNK-1 sulfotransferase HN * [NLS_BP] CG4826 GH14503 36A11-36A11
CG4826 dup:3/3 ID:41E9
+ enzyme * DMGST_3 GstD1 * 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
CG10675+ motor_protein * 2e-17 /match=(desc;; /ma * * CG10675 GH14673 96C9-96C9 ID:41F11
+ structural_protein * 3e-05 MAGE tumor antigen D1 * 5e-13 FMRA_ANTEL ANTHO-RFAMIDE NEUROPEPTIDE
PRECURSOR Antho-RFa * LWamide neuropeptide precursor protein * 33K hydroxy CG11395 GH14572 54A2-54A2 dup:2/2
CG11395 ID:41F2
+ signal_transduction * 6e-05 particle 102K chain - human * 4e-05 katanin p80 subunit * 7e-05 Lis1 * coatomer protein
CG9144 complex, subunit beta (beta prime) [WD40_REGION // F-box // FBOX_DOMAIN //] CG9144 GH14636 26B3-26B3 ID:41F7
+ motor_protein * protein(aa) * 3e-36 IF31_YEAST EUKARYOTIC TRANSLATION INITIATION FACTOR ALPHA SUBUNIT
CG8443 (EIF-3 ALPH * 7e-05 KNLC_DROME KINESIN LIGHT CHAIN (KLC) kines [ATP_GTP_A] CG8443 GH14653 52F7-52F7 ID:41F9
+ ribosomal_protein * similar to Ribosomal protein L7Ae; cDNA EST comes from this gene(aa) * 2e-18 NHP2_YEAST HIGH
MOBILITY GROUP-LIKE NUCLEAR PROTEIN hi * 2e-27 similar [Ribosomal_L7Ae // L7ARS6FAMILY // NUCLE] CG5258
CG5258 GH14757 70F6-70F6 ID:41G10
+ motor_protein * Cdic * cytoplasmic dynein intermediate chain isoform DIC2c(aa) * DYNEIN INTERMEDIATE CHAIN 3,
CG10859 CILIARY(aa) * 3e-07 cytoplasmic dynein intermediate ch [NLS_BP] CG10859 GH14707 34B7-34B7 ID:41G3
+ unknown * TRANSMEMBRANE PROTEIN PFT27(aa) * probable membrane protein; Ybr187wp(aa) * 5e-34 YB37_YEAST
CG4196 HYPOTHETICAL 30.3 KD PROTEIN IN MBA1-RPS13 INTERGENIC R [UPF0016] CG4196 GH14710 88E7-88E7 ID:41G4
CG17921+ HmgZ DNA_binding * 2e-07 cerevisiae mitochondrial protein gene, complete gene produc * 5e-42 HMGZ_DROME HIGH

MOBILITY GROUP PROTEIN Z (HMG-Z) high mob * 2e-11 SSRP_CAE [HMG // HMG_box // NLS_BP] CG17921 GH14749 57F8-57F9 ID:41G9
 + unknown * 3e-06 LBM_DROME LATE BLOOMER PROTEIN late bloomer me * 4e-08 lbm * * [transmembrane4 // TMFOUR
 CG12840// TM4_2] CG12840 GH14950 42E2-42E2 ID:41H10
 + 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
 CG8453 GH14851 48F1-48F1 dup:2/4 ID:41H5
 + metabolism * similar to glutamate synthase; cDNA EST comes from this gene; cDNA EST comes from this gene; cDNA EST
 comes from this gene; cDNA EST comes from thi [ADXRDTASE // FADPNR // PNDRDTASEII] CG9674 GH14941 73C-73C2
 CG9674 dup:4/5 ID:41H9
 + enzyme * stromal cell-derived factor 2(aa) * 2e-09 PMT6_YEAST DOLICHYL-PHOSPHATE-MANNOSE--PROTEIN
 CG11999MANNOSYLTRANSFERASE * 7e-07 /match=(desc;; /ma * 3e-47 cont CG11999 GH15022 83A4-83A4 ID:42A4
 + EG:63B12.8 unknown * 1e-50 PEP8_YEAST VACUOLAR PROTEIN SORTING/TARGETING PROTEIN PEP8 * /match=(desc;;
 /ma * 1e-111 YLNO_CAEEL HYPOTHETICAL 37.4 KD PROTEIN T20D3.7 IN CH [NLS_BP] CG14804 GH15034 2B13-2B13
 CG14804 ID:42A6
 + unknown * 2e-81 YN28_YEAST HYPOTHETICAL 41.2 KD PROTEIN IN PLC1-SEC21 INTERGENIC REGION * 4e-94
 CG14213C26E6.3 gene product * 1e-124 protein involved in sexual devel CG14213 GH15157 18D10-18D10 ID:42B4
 + 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
 + enzyme * coded for by C. elegans cDNA yk16b2.3; coded for by C. elegans cDNA yk16b2.5; Similar to amidase.(aa) *
 PUTATIVE AMIDASE AMIA2(aa) * 3364, putative [CRYSTALLIN_BETAGAMMA // Amidase] CG7910 GH15201 84E10-84E10
 CG7910 ID:42B9
 CG18522+ unknown * CG18522 GH15266 88F-88F8 dup:1/2 ID:42C1
 + scf ligand_binding_or_carrier * scf * 1e-110 supercoiling factor * 1e-72 coded for by C. elegans cDNA yk67a3.5; coded for by C.
 CG9148 elegans cDNA yk90a3.5; co * 7e-90 calumenin [EF_HAND // EF_HAND_2] CG9148 GH15277 62B4-62B4 ID:42C4
 + signal_transduction * predicted using Genefinder; similar to RNA recognition motif. (aka RRM, RBD, or RNP domain); cDNA
 EST comes from this gene; cDNA EST comes from thi [ArfGap // ZF_GCS // REVINTRACTNG] CG8243 GH15285 44F9-44F9
 CG8243 ID:42C5
 + ligand_binding_or_carrier * DMC30B8 * ALPHA-TOCOPHEROL TRANSFER PROTEIN (ALPHA-TTP)(aa) * alpha
 CG2663 tocopherol transfer protein(aa) * 62D9.a(aa) [CRETINALDHBP // CRAL_TRIO] CG2663 GH15295 83A6-83A6 ID:42C7
 + signal_transduction * serine/threonine kinase with Dbl- and pleckstrin homology domains(aa) * actin-filament binding protein
 Frabin(aa) * 5e-12 ROM1_YEAST RHO1 GDP-GTP E [GRF_DBL // RhoGEF // PRO_RICH // NLS_BP] CG8606 LD21492 65F2-
 CG8606 65F2 ID:43A5
 CG11993+ Mst85C unknown * CG11993 LD21554 85C6-85C6 ID:43A6
 + transcription_factor_binding * 6e-06 DIP2_YEAST DOM34 INTERACTING PROTEIN DIP2 protein - y * 2e-06 similar to beta
 CG14722transducin proteins containing TRP-ASP domains el * 6e-11 ap[WD40_REGION // WD_REPEATS // WD40] CG14722 LD21659

86F6-86F6 ID:43A8

+ RNA_binding * RNA helicase isolog(aa) * RNA helicase HEL117 - rat(aa) * protein(aa) * putative ATP-dependent RNA
CG6227 helicase(aa) [helicase_C // ANTIFREEZEI // AA_TRANSFE] CG6227 LD21880 13C1-13C1 dup:1/4 ID:43A9

+ motor_protein * 1e-34 3-hydroxyisobutyrate dehydrogenase * 1e-10 inserted at base Both 5' and 3' ends of P element
CG4747 Inverse PCR * YKWC_BACSU HYPOTHETICAL 30.7 KD PR CG4747 LD22344 30F5-30F5 ID:43B10

+ CycB cell_cycle_regulator G2/MITOTIC-SPECIFIC CYCLIN B CYCLINS, cyclin CG3510 dup:2/4 ID:43B3
+ DNA_binding * SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily e, member 1(aa) *
CG7055 BAF57(aa) * 1e-08 HMG1-related DNA-binding [HMG // HMG_box // PRO_RICH] CG7055 LD22182 8C17-8D1 ID:43B5

CG17252+ BCL7-like CG17252 LD22180 dup:2/2 ID:43B6

CG8954 + unknown * [NLS_BP] CG8954 LD22235 34D6-34D6 dup:2/2 ID:43B8
+ BcDNA:LD21293 enzyme * unknown(aa) * 1e-27 unknown * [ATP_GTP_A2 // ATP_GTP_A] CG7139 LD22250 79C2-79C3

CG7139 ID:43B9
+ not endopeptidase * PUTATIVE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE C13A11.04C (UBIQUITIN
THIOLESTERASE) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE) (DEUBIQUITINATING EN[UCH_2_1 // UCH_2_3 // UCH-1
CG4166 // NLS_BP /] CG4166 LD22730 75D1-75D1 dup:1/2 ID:43C10

+ noi RNA_binding * noi * noisette(aa) * 1e-30 PR09_YEAST PRE-MRNA SPLICING FACTOR PRP9 PRP9 protein - ye *
CG2925 noisette [ZF_MATRIN] CG2925 LD22754 83B4-83B4 ID:43C11

+ Mcm2 DNA_replication_factor * BLASTX 4.1E-84 Homo sapiens mRNA for DNA replication licensing factor (huMCM2),
complete cds.(dna) * BLASTX 4.1E-84 Homo sapiens mRNA for DNA replic [MCM // MCM_1 // MCM_2] CG7538 LD22409 84F-84F
CG7538 dup:1/2 ID:43C3

+ 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

CG7752 + transcription_factor CG7752 ID:43C7
+ 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
+ transcription_factor * 6e-09 predicted using Genefinder; cDNA EST comes from this g * 4e-05 hepatoma-derived growth
CG8569 factor * 2e-20 BS69 protein - human binds directly to a [PWWP // NLS_BP] CG8569 LD22977 49A10-49A10 dup:2/2 ID:43D7

+ car transporter * 9e-22 SLP1 protein homolog - Caenorhabditis elegans SLP-1 protei * 1e-116 vacuolar protein sorting homolog
CG12230 r-vps33a * SLP1_CAEEL SLP-1 PROTEIN * C5 [Sec1 // CYTOCHROME_C] CG12230 LD23088 18D5-18D5 dup:3/3 ID:43E5

CG5926 + CG5926 dup:2/2 ID:43E9
+ TfiIFbeta transcription_factor * TfiIF bgr; * TRANSCRIPTION INITIATION FACTOR IIF, BETA SUBUNIT (TFIIF-BETA)(aa) * 6e-
CG6538 05 T2FB_YEAST TRANSCRIPTION INITIATION FACTOR IIF, BETA SUBUNIT CG6538 LD23340 86C4-86C4 dup:1/2 ID:43F2

+ Mat1 transcription_factor CDK7/cyclin H assembly factor NLS_BP, ZF_RING, ZINC_FINGER_C3HC4, zf-C] CG7614 LD23429
CG7614 ID:43F4

+ Cyt-c2 electron_transfer * DMCYC4_4 Cyt-c2 * 9e-36 pdb|2YCC| Cytochrome c (Isozyme 1) (Oxidized) (Mutant With Cys
CG17903 Replaced By Thr) (C102T * 1e-59 CYC2_DROME CYTOCHROME C-2 c [CYTCHRMEDIA // cytochrome_c] CG17903 LD23501

36A7-36A7 ID:43F5
+ Bub3 signal_transduction * WD-40 repeat protein(aa) * 7e-49 YET7_YEAST HYPOTHETICAL 40.5 KD TRP-ASP REPEATS CONTAINING PROTEIN IN NUP157-PDH * 7e-72 predicted using Genefinder [GPROTEINBRPT // WD40_REGION // WD_REPEA]

CG7581 CG7581 LD23540 99B-99B ID:43F6
+ transcription_factor * zinc-finger protein - African clawed frog(aa) * 1e-15 YJF6_YEAST HYPOTHETICAL 98.9 KD ZINC FINGER PROTEIN IN BTN1-PEP8 INTERGENIC REG * 6[zf-C2H2 // ZINC_FINGER_C2H2 // ZINC_FIN] CG6254 LD23879 85F13-

CG6254 85F13 dup:1/2 ID:43F9
+ 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
+ chaperone * FK506-binding protein 6(aa) * FK506-binding protein - Arabidopsis thaliana(aa) * FKBP (FK506 binding protein)

CG4735 13; peptidylprolyl cis-trans isomerase [FKBP // FKBP_PPIASE_3 // TPR_REPEAT] CG4735 LD24746 60A4-60A4 ID:43G6
+ Dom transcription_factor * DOMINA protein (WHN-homologue)(aa) * 1e-12 FKH2_YEAST FORK HEAD PROTEIN HOMOLOG FKH2 protein - y * 4e-16 SLP1_DROME FORK HEAD DOMAIN TRANSCRIPTION F [Fork_head // FORKHEAD] CG4029 LD24749

CG4029 86A2-86A3 ID:43G7

CG3167 + unknown * CG3167 LD24895 60B1-60B1 ID:43G9

CG7600 + NLS_BP, PLANT_GLOBIN CG7600 LD25031 dup:1/2 ID:43H1
+ Srp54k ligand_binding_or_carrier * 1e-119 SR54_YEAST SIGNAL RECOGNITION PARTICLE KD PROTEIN HOMOLOG (SRP54) * similar to signal recognition particle protein (SRP54); cDNA EST E * SR5 [SRP54 // ATP_GTP_A] CG4659 LD25385

CG4659 64C12-64C12 dup:1/3 ID:43H11
+ protein_phosphatase * DPP2C1(aa) * protein phosphatase 1B (formerly 2C), magnesium-dependent, beta isoform(aa) * 3e-44 P2C2_YEAST PROTEIN PHOSPHATASE 2C HOMOLOG (PP2C-2) [PP2C_1 // PP2C // PP2C_2] CG1906 LD25115 99B6-

CG1906 99B6 ID:43H5

CG9967 + CG9967 LD25280 dup:1/2 ID:43H7
+ ATPsyn-beta * DMATPSYNB ATPsyn- bgr; * 1e-173 H+-transporting ATP synthase (EC 3.6.1.34) beta chain precursor - yeast (Sacch * ATPB_DROME ATP SYNTHASE BETA CHAIN [ATP-synt_ab // ATP-synt_ab_C // ATPASE_] CG11154 102F6-102F6

CG11154 dup:3/4 ID:43H8
+ motor_protein * 1e-155 inserted at base 5' end of P element Inverse PCR * [bZIP] CG3183 LD25484 42B3-42B3 dup:1/2

CG3183 ID:44A3
+ enzyme homology to NADPH--ferrihemoprotein reductase and NADPH-cytochrome P450 reductase FAD_binding,

CG13667 FLAVODOXIN, FPNCR, PHEHYDRX] CG13667 LD25514 dup:2/2 ID:44A6
+ unknown * 4e-21 YS48_CAEEL HYPOTHETICAL 66.5 KD PROTEIN ZK177.8 IN CHROMOSOME II (U * 2e-20

MG11_MOUSE INTERFERON-GAMMA INDUCIBLE PROTEIN MG11 unkn * 4e-20 hy CG9670 LD25913 76A5-76A6 dup:3/3

CG9670 ID:44B11

CG7531 + CG7531 LD25711 dup:2/2 ID:44B2

+ huckebein transcription_factor specific RNA polymerase II transcription factor ZINC_FINGER_C2H2, ZINC_FINGER_C2H2_2, zf]
 CG9768 CG9768 LD25709 dup:2/3 ID:44B3
 + unknown * Putative homolog of subunit of bovine prefoldin, a chaperone comprised of six subunits; Gim5p(aa) * c-myc
 CG7048 binding protein MM-1(aa) * 4e-21 YMJ4_YEAS CG7048 LD25740 94B4-94B4 ID:44B4
 + Similar sequences have been identified in Caenorhabditis elegans , Homo sapiens and Schizosaccharomyces pombe
 CG5383 CG5383 LD25827 dup:2/2 ID:44B7
 + endopeptidase serine proteinase [Anopheles gambiae] CHYMOTRYPSIN, TRYPSIN_CATAL, TRYPSIN_HIS] CG11836
 CG11836 LD25830 dup:2/2 ID:44B8
 + peroxidase MITOCHONDRIAL THIOREDOXIN-DEPENDENT PEROXIDE REDUCTASE AhpC-TSA CG5826 LD25877
 CG5826 dup:2/3 ID:44B9
 CG11329+ unknown * 1e-16 inserted at base 5' end of P element Inverse PCR * * CG11329 LD26217 26F6-26F6 ID:44C11
 + PEK protein_kinase * 8e-30 protein kinase GCN2 (EC 2.7.1.-) - yeast (Saccharomyces cerevisiae) * 2e-24 eIF-2alpha kinase *
 2e-55 similar to serine/threonine kinase (2 do [Bacterial_PQQ // PROTEIN_KINASE_ST // P] CG2087 LD25978 83A8-83A8
 CG2087 ID:44C5
 + unknown * 9e-61 inserted at base Both 5' and 3' ends of P element Inverse PCR * * [SAM_DOMAIN] CG8572 LD26045
 CG8572 65F5-65F5 dup:2/2 ID:44C6
 CG13322+ unknown CG13322 LD26432 dup:2/3 ID:44D11
 + aret RNA_binding * aret * 8e-06 polyadenylate-binding protein * 1e-148 testis-specific RNP-type RNA binding protein * 2e-29
 CG6319 elav-type ribonucleoprotein coded [RBD // HUDSXL RNA // rrm] CG6319 33D-33D4 dup:3/3 ID:44D5
 + signal_transduction * Polyadenylation Factor I subunit; Pfs2p(aa) * 3e-17 alpha-COP (Z466 * 3e-18 lissencephaly-1 * 3e-15
 CG1109 SEL-10 [GPROTEINBRPT // WD40_REGION // WD40] CG1109 LD26389 83B7-83B7 dup:2/3 ID:44D6
 CG18622+ CHROMO_2, chromo CG18622 LD26416 dup:2/3 ID:44D9
 + Sr-CII cell_adhesion Scavenger receptor class C, type II MAM, MAM_2, SOMATOMEDIN_B, Somatomedin_B] CG8856
 CG8856 LD26673 dup:3/3 ID:44E10
 + cdc2 protein_kinase * CDK5 kinase(aa) * DMCD2_2 cdc2 * 1e-101 CC28_YEAST CELL DIVISION CONTROL PROTEIN
 protein kinase * 1e-174 CC2_DROME CELL DIVISION CONTROL PROT[PROTEIN_KINASE_ST // PROTEIN_KINASE_DOM]
 CG5363 CG5363 LD26702 31D11-31D11 dup:3/3 ID:44E11
 CG2994 + CG2994 LD26546 dup:4/4 ID:44E6
 CG16928+ CG16928 dup:3/3 ID:44E9
 + endopeptidase * Saccharolysin (oligopeptidase yscD); Prd1p(aa) * NEUROLYSIN PRECURSOR (NEUROTENSIN
 ENDOPEPTIDASE) (MITOCHONDRIAL OLIGOPEPTIDASE M) (MICROSOMAL ENDOP [Peptidase_M3] CG11771 LD26931
 CG11771 98F1-98F1 dup:4/5 ID:44F10
 CG4785 + CG4785 LD26982 dup:2/2 ID:44F11
 + protein_phosphatase * 4e-56 P2C2_YEAST PROTEIN PHOSPHATASE 2C HOMOLOG (PP2C-2) hyp * 9e-20 unknown *
 1e-108 P2C2_CAEEL PROBABLE PROTEIN PHOSPHATASE 2C T23F11.1 (PP2C) * 4 [PP2C // PP2C_1 // PP2C_2] CG17746
 CG17746 64A3-64A3 dup:4/4 ID:44F12

+ ligand_binding_or_carrier * 4e-05 fizzy-related protein * 1e-05 transducin (beta)-like transducin (beta) like pr * 1e-05
 CG16892 hypothetical protein * 5e-07 DMRNAFRP fzf CG16892 LD26813 8D7-8D8 dup:2/2 ID:44F4
 + 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
 CG4303 + Bap60 Brahma associated protein 60kD NLS_BP, PRO_RICH CG4303 LD27052 dup:1/2 ID:44G4
 + transcription_factor * 9e-06 Z33A_HUMAN ZINC FINGER PROTEIN 33A (ZINC FINGER PROTEIN KOX31) (HA09 * 8e-05
 zinc finger protein XFDL * 3e-05 DMDROSOPH_4 wdn * zinc finger;[zf-C2H2 // ZINC_FINGER_C2H2 // ZINC_FIN] CG11906
 CG11906 LD27134 56C7-56C8 ID:44G9
 + Klp67A motor_protein kinesin family protein 3B ATP_GTP_A, KINESINHEAVY, KINESIN_MOTOR_D] CG10923 LD27326
 CG10923 dup:2/2 ID:44H12
 CG6564 + unknown CG6564 LD27203 ID:44H2
 + transcription_factor * 2e-10 CROL GAMMA * 5e-16 predicted using Genefinder; similar to Zinc finger, C2H2 type (5 d * 1e-11
 CG3847 zinc finger protein - mouse zinc finger protein [zf-C2H2 // ZINC_FINGER_C2H2 // ZINC_FIN] CG3847 LD27244 5E5-5E5 ID:44H4
 + chaperone * DMNINAA_7 ninaA * DMCYP1_2 Cyp1 * 5e-23 CYPC_YEAST PEPTIDYL-PROLYL CIS-TRANS ISOMERASE
 C PRECURSOR (PPIASE) (ROTAMASE) (* 1e-20 CYPH_DROME PEPTIDYL [pro_isomerase // CSA_PPIASE_2 // WD40_R]
 CG3511 CG3511 LD27277 60D5-60D5 dup:1/2 ID:44H8
 + enb signal_transduction * map_position:56B5 * clot.396(dna)* 1e-124 Abl substrate ena (enabled) - fruit fly (Drosophila
 melanogaster) * 6e-39 neural variant mena+ protein [WH1 // PRO_RICH // RANBP1_WASP] CG15112 LD27343 56B5-56B5
 CG15112 dup:3/5 ID:45A1
 + transcription_factor similar to crol protein ZINC_FINGER_C2H2, ZINC_FINGER_C2H2_2, z] CG2678 LD27553 dup:1/2
 CG2678 ID:45A10
 CG18608 + unknown * CG18608 LD27570 56A-56A dup:1/2 ID:45A11
 + BcDNA:LD22910 endopeptidase * reserved(aa) * 1e-12 UBP9_YEAST UBIQUITIN CARBOXYL-TERMINAL HYDROLASE
 (UBIQUITIN THIOLESTERASE 9) (* 1e-08 UBPX_CAEEL PROBABLE UBIQUITIN CARBOXYL[UCH_2_2 // UCH_2_3 //
 CG15817 PRO_RICH // UCH-2] CG15817 99A5-99A5 dup:2/2 ID:45A6
 + unknown * Ygr090wp(aa) * hypothetical protein(aa) * 4e-17 YG2L_YEAST HYPOTHETICAL 140.5 KD PROTEIN IN CTT1-
 CG12785 PRP31 INTERGENIC REGION CG12785 LD27528 89B17-89B17 dup:2/2 ID:45A9
 + actin_binding * has homology to the Dictyostelium and human actin-binding protein coronin; Crn1p(aa) * coronin-1(aa) * 3e-
 76 CORO_YEAST CORONIN-LIKE PROTEIN hypothe [WD40_REGION // ARGINASE_2 // WD_REPEATS] CG9446 42C8-42C8
 CG9446 dup:3/3 ID:45B2
 CG8632 + embryonic lung protein [Homo sapiens] CG8632 LD27783 dup:1/2 ID:45B7
 CG11970 + BcDNA:LD23876 similar to nuclear factor related to kappa B binding protein CG11970 LD28082 dup:2/4 ID:45C12
 + RNA_binding * similar to RNA recognition motif. (aka RRM, RBD, or RNP domain) (2 domains); cDNA EST yk211a9.5 comes
 CG4806 from this gene; cDNA EST yk266e11.5 comes from [RNP_1 // RBD // rrm // NLS_BP] CG4806 LD27920 60D10-60D10 ID:45C2
 CG5126 + unknown * CG5126 LD27921 21F1-21F1 dup:1/2 ID:45C3
 CG9506 + protein_phosphatase * CG9506 LD27991 28D1-28D1 dup:1/2 ID:45C6

CG7825 + Rad17 DNA_repair_protein DNA repair protein ATP_GTP_A, ATP_GTP_A2, RFC CG7825 LD27993 ID:45C7
 CG10018+ DNA_repair_protein homology to mouse and human SNM1 protein NLS_BP CG10018 LD28027 dup:1/2 ID:45C8
 CG4609 + fax failed axon connections protein CG4609 LD28084 dup:2/2 ID:45D1
 + unknown * 1e-106 probable membrane protein YPL217c - yeast (*Saccharomyces cerevisiae*) * 2e-11 No definition line found
 CG7728 * 1E-152* 1e-100 conserved hypothetical [NLS_BP // ATP_GTP_A] CG7728 LD28182 73E3-73E4 dup:3/3 ID:45D11
 CG5003 + unknown * [FBOX_DOMAIN] CG5003 LD28210 98B2-98B2 ID:45D12
 CG6994 + cytoskeletal_structural_protein CG6994 LD28101 dup:2/2 ID:45D5
 CG9213 + enzyme CG9213 LD28117 dup:2/2 ID:45D7
 + unknown * 5e-24 hypothetical protein YDL087c - yeast (*Saccharomyces cerevisiae*) * 4e-34 YP68_CAEEL HYPOTHETICAL
 CG7564 37.0 KD PROTEIN IN CHROMOSOME II (U2 * 2e-23 p [NLS_BP] CG7564 LD28402 74D1-74D1 dup:4/4 ID:45E12
 + enzyme * nudix (nucleoside diphosphate linked moiety X)-type motif 3(aa) * 7e-40 diphosphoinositol polyphosphate
 CG6391 phosphohydrolase (A * [MUTT // mutT] CG6391 LD28241 67F4-67F4 dup:3/4 ID:45E3
 + Weak homology to SNF2 family (CHD1 subfamily) chromodomain protein [*Arabidopsis thaliana*] CHROMO_2 CG9933
 CG9933 LD28372 dup:5/5 ID:45E9
 + 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
 + Doa protein_kinase * PROTEIN KINASE DOA (PROTEIN DARKENER OF APRICOT)(aa) * DMDOA_2 Doa * 2e-60 ORF
 YLL019c * 1e-127 Similarity to *Drosophila* Doa kinase (PIR Acc. No. cD [PROTEIN_KINASE_ST // PROTEIN_KINASE_DOM]
 CG1658 CG1658 98F-98F2 dup:3/3 ID:45F12
 + EG:66A1.2 transcription_factor_binding * map_position:4C6 * map_position:4C6 * map_position:4C6 * by match; 1-mat
 CG12179CG12179 LD28429 4C6-4C7 ID:45F3
 CG14657+ unknown CG14657 LD28447 ID:45F4
 CG4300 + unknown spermine synthase SAM_BIND CG4300 LD28457 ID:45F5
 + unknown * 7e-10 /match=(desc: * 9e-10 K10D2.3 gene product * 1e-10 The gene is expressed ubiquitously.; The protein *
 CG1091 1e-09 caffeine-induced death protein >g [PAP_ASSOCIATED // PAP_CORE // PAP // AA] CG1091 84C1-84C1 dup:3/3 ID:45F7
 + 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
 + ribosomal_protein * 1e-48 RL7A_YEAST 60S RIBOSOMAL PROTEIN YL17-A ribosomal protein * 4e-66 ribosomal protein
 L17 60S RIBOSOM * 1e-65 RL17_RAT 60S RIBOSOMAL PROTEIN L17 [Ribosomal_L22 // RIBOSOMAL_L22] CG3203 6C10-
 CG3203 6C10 dup:1/5 ID:45G12
 + unknown * Cys-rich protein(aa) * FIM protein(aa) * zinc finger protein 261(aa) * BLASTX 3.6E-13 *Dictyostelium discoideum*
 CG5965 sp96 gene for spore coat protein SP9 CG5965 97F4-97F4 dup:2/3 ID:45G2
 + sgg protein_kinase * DMSGG46_2 sgg * 5e-98 MDS1_YEAST SERINE/THREONINE-PROTEIN KINASE MDS1/RIM11 pr *
 CG2621 zeste-white 3-A - fruit fly (*Drosophila melanogaster*) * 1e-141 pred [PROTEIN_KINASE_ST // PROTEIN_KINASE_DOM] CG2621

3B2-3B3 dup:1/2 ID:45G9
 + unknown * phosphatidylinositol glycan, class B(aa) * 2e-29 YGO2_YEAST HYPOTHETICAL 72.6 KD PROTEIN IN MRF1-
 CG12006 SEC27 INTERGENIC REGION * 5e-08 coded for by C. ele CG12006 64C4-64C4 dup:2/2 ID:45H10
 CG11207 + unknown CG11207 dup:2/2 ID:45H2
 CG2890 + CG2890 dup:2/3 ID:45H3
 CG10640 + CG10640 dup:4/4 ID:45H8
 + smg * cloned by ability to arrest the cell cycle when expressed in the fission yeast Schizosaccharomyces pombe(aa) * 1e-124
 CG5263 cloned by ability to arrest th CG5263 66F1-66F1 dup:1/5 ID:46A10
 CG8309 + CG8309 dup:2/3 ID:46A12
 CG8379 + * CG8379 85B4-85B4 dup:1/3 ID:46A2
 CG16944 + sesB transporter ADP/ATP translocase ADPTRNSLCASE, MITOCARRIER CG16944 ID:46A4
 + ncd motor_protein * DMCLARET_4 ncd * 3e-75 KAR3_YEAST KINESIN-LIKE PROTEIN KAR3 (NUCLEAR FUSION
 PROTEIN) * NCD_DROME CLARET SEGREGATIONAL PROTEIN * 4e-61 YNZ2_CAEEL PU [kinesin //
 CG7831 KINESIN_MOTOR_DOMAIN1 // KIN] CG7831 99C5-99C5 ID:46A9
 CG6605 + motor_protein CG6605 ID:46B12
 CG9805 + translation_factor eukaryotic translation initiation factor 3 subunit NLS_BP, PCI_DOMAIN CG9805 ID:46B4
 CG7414 + CG7414 79A4-79A4 dup:2/2 ID:46B6
 + unknown * MA3(aa) * 3e-70 apoptosis protein MA-3 - mouse apoptosis-i * 1e-69 nuclear protein H731 - human nuclear
 CG10990 antigen H731 * nuclear antigen H731-like pr [RCC1_2 // NLS_BP] CG10990 12B8-12B8 ID:46B7
 CG4916 + RNA_binding CG4916 dup:2/2 ID:46C4
 CG7563 + calpain CG7563 dup:1/4 ID:46C8
 + unknown * 1e-07 ADRP_MOUSE ADIPOSE DIFFERENTIATION-RELATED PROTEIN (ADRP) * * [ATP_GTP_A] CG9057
 CG9057 13A11-13A11 dup:2/2 ID:46D11
 CG5991 + enzyme PHOSPHATIDYLSERINE DECARBOXYLASE PROENZYME CG5991 ID:46D2
 CG8073 + enzyme CG8073 ID:46D3
 CG2034 + CG2034 ID:46D4
 CG1101 + CG1101 dup:4/5 ID:46D7
 CG10928 + CG10928 LD29844 dup:3/3 ID:46E11
 + transcription_factor * host cell factor C1 (VP16-accessory protein)(aa) * HOST CELL FACTOR C1 (HCF) (VP16
 CG1710 ACCESSORY PROTEIN) (HFC1) (VCAF) (CFF)(aa) * host cell factor 2(a CG1710 LD29768 102B3-102B3 dup:3/3 ID:46E3
 + 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
 + enzyme * (novel PUTATIVE protein similar to hypothetical proteins S. pombe C22F3.14C and C. elegans C16A3.8)(aa) * 1e-
 CG4263 32 RLR1_YEAST RLR1 PROTEIN RLR1 protei [NLS_BP] CG4263 LD29940 22C3-22C3 dup:3/3 ID:46F10

CG8730 + drosha RNA binding ribonuclease III DSRBD, PRO_RICH, RIBONUCLEASE_III, RNASE] CG8730 LD29995 dup:2/3 ID:46F12
 + unknown * PiUS(aa) * 6e-18 KCS1 protein - yeast (Saccharomyces cerevisiae) (Z49 * 7e-27 cDNA EST comes from this
 CG10082 gene * 2e-43 Similar to S.cerevisiae protein CG10082 LD29913 57F6-57F6 dup:2/2 ID:46F6
 + RhoGEF3 signal_transduction RHO guanyl-nucleotide exchange factor ATP_GTP_A, GRF_DBL, RhoGEF, SH3 CG1225
 CG1225 LD29915 dup:1/2 ID:46F8
 CG3021 + CG3021 LD29918 dup:1/2 ID:46F9
 + endopeptidase * hypothetical protein unp - mouse(aa) * Sad1p(aa) * putative protein(aa) * Contains similarity to Pfam
 CG7288 domain: (UCH-1), Score=13.8, E-value=0.14, N= [UCH_2_3 // UCH-2] CG7288 LD30129 17E4-17E4 dup:1/3 ID:46G10
 + 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
 CG3309 + unknown * 3e-62 No definition line found * No definition line found * CG3309 LD30005 4F2-4F2 dup:1/2 ID:46G3
 CG17681 + unknown * CG17681 LD30009 36E-36E ID:46G4
 + transmembrane_receptor * nucleoporin Nup84(aa) * 6e-46 nucleoporin 88kD 88kDa nuclear * 3e-47 nucleoporin Nup84 *
 CG6819 CG6819 LD30108 87C7-87C7 ID:46G7
 + 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 CG2260 LD30339 7D11-7D11 ID:46H10
 + Transcription factor IIA L transcription_factor general RNA polymerase II transcription factor, PHOSPHOPANTETHEINE CG5930
 CG5930 LD30231 dup:2/2 ID:46H2
 CG9949 + SEVEN IN ABSENTIA DNA binding ubiquitin-dependent protein degradation ZF_RING CG9949 LD30265 ID:46H3
 CG1647 + glass transcription_factor photoreceptor determination ZINC_FINGER_C2H2 CG1647 LD30287 dup:2/2 ID:46H5
 CG14005 + unknown * CG14005 LD30293 26A2-26A2 dup:2/3 ID:46H6
 + motor_protein * 4e-28 KIP1_YEAST KINESIN-LIKE PROTEIN KIP1 kinesin-related prot * 6e-33 PAV-KLP protein * 4e-33
 Similar to kinesin-like protein; coded for by C. ele [kinesin // KINESIN_MOTOR_DOMAIN2 // KIN] CG12298 LD30305 54E7-54E7
 CG12298 ID:46H7
 + 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
 CG1677 + CG1677 LD30482 ID:47A10
 CG2682 + transcription_factor CG2682 ID:47A11
 CG12306 + protein_kinase CG12306 ID:47A2
 CG8617 + CG8617 LD30408 dup:1/2 ID:47A4
 + snRNP70KRNA_binding * U1 SMALL NUCLEAR RIBONUCLEOPROTEIN KD (U1 SNRNP KD) (SNRNP70)(aa) * DMRNP70K_6
 snRNP27D * ribonucleoprotein antigen(aa) * small nuclear ribonucleopr [RNP_1 // RBD // rrm // NLS_BP] CG8749 LD30455 27C7-
 CG8749 27C7 dup:1/2 ID:47A8
 CG9797 + transcription_factor * b34I8.1 (Kruppel related Zinc Finger protein 184)(aa) * 2e-15 AZF1_YEAST ASPARAGINE-RICH ZINC

FINGER PROTEIN AZF1 fin * 8e-24 SUHW_DROME SUPPRESSO[zf-C2H2 // ZINC_FINGER_C2H2 // ZINC_FIN] CG9797
 LD30467 85B2-85B2 ID:47A9
 + translation_factor * 1e-85 NAT1_YEAST N-TERMINAL ACETYLTRANSFERASE (AMINO-TERMINAL, ALPHA-AMINO, ACETYLTR * 1e-123 N-terminal acetyltransferase * O-linked GlcNAc tran[TPR_REGION // TPR_REPEAT // NLS_BP] CG12202
 CG12202 LD30511 18C8-18D1 dup:3/6 ID:47B1
 + transcription_factor * general transcription factor IIH, polypeptide (52kD subunit)(aa) * TFIIH subunit Tfb2; has homology to
 CG7764 CAK and human IIH subunits; Tfb2p(aa) * 9e-71 CG7764 LD30622 71D3-71D4 ID:47B11
 CG9231 + * 2e-14 pIL2 hypothetical protein - rat (fragment) growth and trans * * CG9231 76B9-76B9 dup:2/2 ID:47B12
 + E(z) transcription_factor * enhancer of zeste (Drosophila) homolog 2(aa) * enhancer of zeste homolog (Drosophila)(aa) *
 CG6502 DM180_2 E(z) * ENHANCER OF ZESTE PROTEIN(aa) [SET_DOMAIN // SET // NLS_BP] CG6502 LD30505 67E4-67E4 ID:47B2
 CG3508 + unknown * HMBA-inducible(aa) * 3e-11 HIS1 protein * [NLS_BP] CG3508 LD30520 88C11-88C11 ID:47B4
 + chaperone * 1e-09 SCJ1_YEAST SCJ1 PROTEIN SCJ1 protein - yeast (Saccharomyce * 4e-11 csp29 cysteine string protein
 CG7133 * 6e-12 similar to DnaJ, prokaryotic heat sho [DnaJ // DNAJPROTEIN // DNAJ_2] CG7133 LD30543 79C3-79C3 ID:47B6
 + fzy cell_cycle_regulator * fzy * 2e-76 YGA3_YEAST HYPOTHETICAL 62.8 KD TRP-ASP REPEATS CONTAINING PROTEIN
 IN PMC1-TFG2 * Method: conceptual translation supplied by au[WD40_REGION // FIZZY_DOMAIN // WD_REPEA] CG4274
 CG4274 LD30572 35F8-35F8 dup:1/2 ID:47B7
 CG18683+ unknown * CG18683 LD30576 99C6-99C6 ID:47B8
 + chaperone * transport complex protein (90 kDa)(aa) * 6e-59 putative S transport complex 90kD subunit brain-specific isoform
 CG6549 * CG6549 LD30785 36C3-36C4 ID:47C10
 + transporter * 8e-72 contains similarity to xanthine/uracil permeases family elegan * 1e-136 yolk sac permease-like molecule *
 CG6293 1e-136 sodium-dependent vitamin C tr [xan_ur_permease // XANTH_URACIL_PERMASE] CG6293 LD30822 86A2-86A2 ID:47C11
 + FK506-bp1 ligand_binding_or_carrier * DMFKBP39_2 FK506-bp1 * KD FK506-BINDING NUCLEAR PROTEIN (PEPTIDYL-
 PROLYL CIS-TRANS ISOMERASE) (PPIASE)(aa) * 7e-24 hypothetical protein YLR4[FKBP // FKBP_PPIASE_2 //
 CG6226 FKBP_PPIASE_3] CG6226 LD30817 90E1-90E1 ID:47C12
 + unknown * predicted using Genefinder; cDNA EST comes from this gene; cDNA EST yk278a11.3 comes from this gene;
 CG4968 cDNA EST yk278a11.5 comes from this gene; cDNA CG4968 LD30683 31D6-31D6 ID:47C3
 + msl-3 tumor_suppressor * MALE-SPECIFIC LETHAL-3 PROTEIN(aa) * DMMSL3_2 msl-3 * 7e-08 hypothetical protein *
 CG8631 DMMSL3_2 msl-3 CG8631 LD30726 65E5-65E5 dup:1/2 ID:47C5
 + unknown * 4e-09 predicted using Genefinder; similar to emp24/gp25L/p24 family; cDN * 1e-08 putative T1/ST2 receptor
 CG10733 binding protein precursor * 2e-07 putative [EMP24_GP25L] CG10733 LD30746 65A3-65A3 ID:47C7
 CG11490+ unknown CG11490 dup:1/3 ID:47C9
 + unknown * xenotropic and polytropic murine leukemia virus receptor X3(aa) * polytropic murine leukemia virus receptor
 CG7536 SYG1(aa) * predicted using Genefinder; CG7536 LD30826 16F7-16F7 ID:47D1
 + transcription_factor * with similarity to Homo sapiens TAFII55 encoded by Genbank Accession Number and C. elegans
 CG2670 unknown protein encoded by Genbank Accession Number * an CG2670 LD30980 84E1-84E1 ID:47D11
 + transcription_factor * putative ring zinc finger protein NY-REN-43 antigen(aa) * putative protein(aa) * hypothetical protein,
 CG11982 similar to PRAJA1 * DMGOLTHA_3 gol [zf-C3HC4 // ZF_RING] CG11982 LD30985 85C4-85C4 dup:3/3 ID:47D12

+ unknown * 3e-05 No definition line found * 1e-32 topoisomerase I-binding RS protein * 8e-11 ring finger protein * tumor
 CG15104 protein p53-binding protein p53 bindin [zf-C3HC4 // ZINC_FINGER_C3HC4 // NLS_BP] CG15104 56A-56A dup:3/3 ID:47D3
 + cytoskeletal_structural_protein * actin-like protein; (2 actin domains)(aa) * 2e-71 ARP5_YEAST ACTIN-LIKE PROTEIN
 ARP5 probable nuclear pro * 3e-18 ACTU_DROME ACTIN-LIKE PROTEIN 13E [NLS_BP // actin] CG7940 90E5-90E6 dup:1/2
 CG7940 ID:47D6
 + Mcm3 DNA_replication_factor * Mcm3 * DNA replication factor MCM3(aa) * 1e-168 MCM3_YEAST MINICHROMOSOME
 CG4206 MAINTENANCE PROTEIN minichrom * MCM3 [MCM // MCM_1 // MCM_2] CG4206 LD30950 4F2-4F2 ID:47D8
 + transporter * DMC103B4 * 8e-09 YNM5_YEAST HYPOTHETICAL 73.8 KD PROTEIN IN SPC98-TOM70 INTERGENIC
 CG3409 REGION * 3e-37 /match=(desc;; /ma * 2e-24 similar to the monocarb CG3409 LD30953 42C6-42C1 ID:47D9
 + protein_phosphatase * 4e-25 PVH1_YEAST PROTEIN-TYROSINE PHOSPHATASE YVH1 (PTPASE YVH1) * 8e-13
 puckered protein * 1e-14 predicted using Genefinder; similar to D[PTS_HPR_SER // DSPc // TYR_PHOSPHATASE_] CG14211
 CG14211 LD31102 18D9-18D9 dup:2/2 ID:47E10
 CG7730 + unknown * CG7730 LD31138 73E4-73E4 dup:2/2 ID:47E12
 CG6506 + unknown * CG6506 LD31003 16D6-16D6 dup:3/3 ID:47E2
 + cell_adhesion THYROGLOBULIN PRECURSOR 4_DISULFIDE_CORE, ATP_GTP_A, EGF_1, THYR] CG5639 LD31017
 CG5639 dup:2/2 ID:47E4
 + tos DNA_repair_protein * DMTOSCAP1_2 tos * Tosca(aa) * 7e-47 EXO1_YEAST EXONUCLEASE I (EXO I) (DHS1 PROTEIN)
 CG10387 DHS1 pr * Tosca [53EXO_N_DOMAIN // 53EXO_I_DOMAIN // XPG] CG10387 LD31018 37A4-37A4 dup:2/2 ID:47E5
 + chaperone * 7e-25 PA10_YEAST PAC10 PROTEIN PAC10 protein - yeast (Sacchar * 7e-27 YFM9_CAEEL
 HYPOTHETICAL 20.9 KD PROTEIN T06G6.9 IN CHROMOSOME I * 2e-43 VBP1_H CG6719 LD31046 86E4-86E4 dup:4/4
 CG6719 ID:47E7
 + chaperone * 1e-10 XDJ1 protein - yeast (Saccharomyces cerevisiae) Xdj1p: H * 2e-08 DNJ1_DROME DNAJ PROTEIN
 HOMOLOG (DROJ1) droj1 * 6e-56 predicted using Genefin [DNAJ_1 // DnaJ // DNAJ_2 // NLS_BP] CG7872 LD31069 13E3-13E3
 CG7872 dup:2/2 ID:47E9
 + enzyme * 1e-109 RSP5_YEAST UBIQUITIN--PROTEIN LIGASE RSP5 hypothetical pr * 2e-48 similar to hypothetical
 proteins from yeast (YKL162) and rat (PIR: * 3e-90 [HECT_DOMAIN // HECT // WW_rsp5_WWP // C] CG4943 LD31242 54D3-
 CG4943 54D3 dup:2/3 ID:47F12
 + Cbp80 RNA_binding * cap-binding protein - human(aa) * nuclear cap binding protein, 80kD(aa) * 4e-17 GCR3_YEAST GCR3
 CG7035 PROTEIN (STO1 PROTEIN) (SUT1 PROTEIN) * by match; 1- [NLS_BP] CG7035 LD31211 4C7-4C7 ID:47F4
 + 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 CG7197 LD31204 66C5-66C5 dup:2/5 ID:47F5
 CG8440 + signal_transduction CG8440 ID:47F8
 CG5100 + unknown * [PRO_RICH // NLS_BP] CG5100 LD31243 77C4-77C4 dup:1/4 ID:47G1
 + RNA_binding * 13878, ribosomal protein S14 (not transcribed)(aa) * 9e-84 PR43_YEAST PRE-MRNA SPLICING FACTOR
 RNA HELICASE PRP43 (HELICASE JA1) * 8E-32* 5e-90 YQZN [HELICASE // NLS_BP // Ribosomal_S14 //] CG12211 LD31543
 CG12211 18C8-18C8 ID:47G11

+ motor_protein * coded for by C. elegans cDNA yk38d7.3; coded for by C. elegans cDNA cm06h5; coded for by C. elegans
 CG12301 cDNA yk38d7.5(aa) * Yml093wp(aa) * 5e-33 YMJ3_Y [NLS_BP] CG12301 LD31322 71D4-71D4 dup:1/2 ID:47G3
 CG8149 + motor_protein * CG8149 LD31448 86C1-86C1 ID:47G6
 + cell_adhesion * tip associating protein(aa) * tip associating protein(aa) * tip associating protein(aa) CG4118 LD31449 77A1-
 CG4118 73A7 dup:1/2 ID:47G7
 + enzyme * 2e-05 DMANKY_5 Ank * * [ANK_REP // ank // ANK_REP_REGION // NLS] CG10632 LD31582 69C4-69C6
 CG10632 ID:47H1
 CG18592 + * CG18592 25C3-25C3 dup:1/2 ID:47H11
 + transcription_factor * DMMLP84B_2 Mlp84B * ajuba; jub(aa) * BLASTX 7.1E-07 Human LIM protein (LPP) mRNA, partial
 CG11063 cds.(dna) * 8e-06 LRG1 [LIM_DOMAIN_1 // LIM // LIM_DOMAIN_2 //] CG11063 LD31670 12B9-12B9 ID:47H4
 + enzyme * PROCOLLAGEN-LYSINE,2-OXOGLUTARATE 5-DIOXYGENASE PRECURSOR (LYSYL HYDROXYLASE)
 (LH)(aa) * PROCOLLAGEN-LYSINE,2-OXOGLUTARATE 5-DIOXYGENASE PRECURSOR ([GLYC_TRANS //
 CG6199 HTH_LYSR_FAMILY] CG6199 LD31687 68A8-68A8 dup:3/4 ID:47H7
 CG5995 + unknown * CG5995 LD31910 97F3-97F4 dup:1/2 ID:48A2
 + enzyme * /match=(desc;; /match=(desc:(aa) * similar to Arabidopsis thaliana male sterility protein * DMC103B4 * acyl CoA
 CG8306 reductase(aa) [HELIX_LOOP_HELIX // NLS_BP] CG8306 LD31990 53C7-53C8 dup:1/3 ID:48A5
 + 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 * DMPPP_2 Arr2 * 1e-41 ARRB_DROME PHOSRESTIN I (ARRESTIN B) (ARRESTIN 2) (49 KD ARRESTIN-LIKE
 PROTEIN) * 1e-45 ARRB_CAEEL PROBABLE BETA-ARRESTIN coded [ARRESTIN // arrestin // ARRESTINS // AT] CG1487
 CG1487 LD32202 100F5-100F5 ID:48B3
 + unknown * 3e-26 YKJ5_YEAST 32.3 KD PROTEIN IN CWP1-MBR1 INTERGENIC REGION * 3e-47 similar to S. cerevisiae
 CG8435 YJU2 protein * 5e-67 unknown * 1e-35 hypothetical p CG8435 LD32459 52F5-52F5 ID:48C4
 + 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
 CG8975 48D8-48D8 ID:48D10
 + enzyme * similar to Transketolase; cDNA EST comes from this gene; cDNA EST comes from this gene; cDNA EST comes
 CG8199 from this gene; cDNA EST comes from this gene [E1_dehydrog // NLS_BP] CG8199 LD32808 85D25-85D25 dup:2/2 ID:48D12
 + transcription_factor * 5e-87 inserted at base 5' end of P element Inverse PCR * * [zf-C2H2 // ZINC_FINGER_C2H2 //
 CG8961 ZINC_FIN] CG8961 LD32631 53F5-53F5 ID:48D3
 + RNA_binding * 4e-80 DBP2_YEAST P68-LIKE PROTEIN RNA helicase DBP2 - yeast (Sac * 1e-68 RM62_DROME
 PUTATIVE ATP-DEPENDENT RNA HELICASE P62 RNA he * 1e-154 similar [helicase_C // HELICASE // DEAD // DEAD_] CG6418
 CG6418 LD32732 67F4-67F4 dup:2/2 ID:48D8
 + unknown * 1e-142 inserted at base Both 5' and 3' ends of P element Inverse PCR * * CG15893 LD32923 5E4-5E4 dup:2/2
 CG15893 ID:48E5
 + nop5 unknown * nucleolar protein NOP5/NOP58(aa) * 1e-100 NOP5_YEAST NUCLEOLAR PROTEIN NOP5 hypothetical
 CG10206 protein * 1e-119 contains similarity to S. cerevisiae Prp31 [NLS_BP] CG10206 LD32943 27C-27C dup:2/2 ID:48E7

+ BG:DS09218.3 chaperone * 8e-19 ERP5_CAEEL PROBABLE PROTEIN DISULFIDE ISOMERASE P5 PRECURSOR * 4e-21
 protein disulfide isomerase-related protein * 9e-21 ERP5_RAT PROBABLE PRO CG4455 LD33101 35F10-35F10 dup:2/3
 CG4455 ID:48F10
 + elav RNA_binding * DMELAVK_2 elav * 1e-16 polyadenylate-binding protein * ELAV_DROME ELAV PROTEIN (EMBRYONIC
 LETHAL ABNORMAL VISUAL PROTEIN) * 1e-58 Similar to the hu [RNP_1 // RBD // HUDSXL RNA // rrm] CG4262 LD33076 1B5-
 CG4262 1B5 ID:48F5
 + unknown * Yjr072cp(aa) * ATP(GTP)-binding protein(aa) * HYPOTHETICAL 39.7 KD PROTEIN C34E10.2 IN
 CG3704 CHROMOSOME III(aa) * putative protein(aa) [ATP_GTP_A] CG3704 LD33276 1D1-1D1 ID:48G10
 + ProsMA5 endopeptidase * 9e-71 PRCZ_YEAST PROTEASOME COMPONENT PUP2 (MACROPAIN SUBUNIT PUP2)
 (PROTEINASE YSCE * 1e-137 PRCZ_DROME PROTEASOME PSMA5 SUBUNIT (MULTICATALYTIC EN
 CG10938[PROTEASOME_PROTEASE // PROTEASOME_A //] CG10938 LD33318 54C1-54C1 ID:48G11
 + unknown * protein(aa) * 3e-09 PC11_YEAST PCF11 PROTEIN hypothetical protein YDR228c - * 3e-21 YRR2_CAEEL
 HYPOTHETICAL 91.1 KD PROTEIN R144.2 IN CHROMOSOME III [PRENYLATION // PRO_RICH // NLS_BP // CY] CG10228
 CG10228 LD33132 51D2-51D2 ID:48G2
 + motor_protein * kda paraneoplastic cerebellar degeneration-associated antigen Peptide, * MYOSIN HEAVY CHAIN D (MHC
 CG1962 D)(aa) * CLIP-190 * 7e-05 microtubule binding pro [NLS_BP] CG1962 38E-38E dup:3/5 ID:48G3
 + unknown * hypothetical protein(aa) * 4e-25 YMO9_YEAST HYPOTHETICAL 20.9 KD PROTEIN IN PLB1-HXT2
 CG8000 INTERGENIC REGION * 9e-21 Closely related to Arabidopsis thal [NLS_BP] CG8000 LD33361 67E4-67E4 ID:48H2
 + DNA_binding * protein(aa) * 3e-65 YEZ9_YEAST PUTATIVE 90.2 KD ZINC FINGER PROTEIN IN CCA1-ADK2
 CG15835 INTERGENIC REGION > * 2e-26 Similarity to Human XE169 protein (SW:X CG15835 LD33386 43F5-43F5 ID:48H3
 + chromatin_binding * pheromone response pathway suppressor; Srm1p(aa) * similar to RCC1 proteins(aa) * regulator of
 chromosome condensation(aa) * retinitis pigmentosa [RCC1 // RCC1_2 // RCCNDNSATION] CG9135 LD33431 26B3-26B3 dup:1/2
 CG9135 ID:48H4
 CG18124+ BG:DS01068.4 unknown * 1e-05 mtDBP protein * AAs * * CG18124 LD33443 35A1-35A1 ID:48H5
 + unknown * 5-oxo-1,2,5-tricarboxylic-3-penten acid decarboxylase/isomer(aa) * 3e-26 YNQ8_YEAST HYPOTHETICAL 28.8
 CG5793 KD PROTEIN IN PSD1-SKO1 INTERGENIC REGION * 9e CG5793 LD33646 95F1-95F1 ID:49A1
 + enzyme * 1e-10 FMS1_YEAST FMS1 PROTEIN FMS1 protein - yeast (Saccharom * 6e-11 Cs protein * 8e-33 No definition
 CG7737 line found * 2e-13 protein [ADXRDTASE // AMINEOXDASEF // NAD_BINDIN] CG7737 LD33764 47D6-47D7 dup:1/2 ID:49A10
 + transcription_factor * transcription factor 17(aa) * zinc finger protein(aa) * RENAL TRANSCRIPTION FACTOR KID-1
 CG7357 (TRANSCRIPTION FACTOR 17)(aa) * crol [zf-C2H2 // ZINC_FINGER_C2H2_2] CG7357 LD33778 93B1-93B1 ID:49A11
 CG15736+ transcription_factor * CG15736 LD33780 11A4-11A4 ID:49A12
 + enzyme * SUMO-1 activating enzyme subunit 1(aa) * Similar to ubiquitin activating proteins; Aos1p(aa) * 6e-30
 RH31_YEAST DNA DAMAGE TOLERANCE PROTEIN RHC31 ([UBA_NAD // ThiF_family] CG12276 LD33652 87B15-87B15
 CG12276 ID:49A3
 + unknown * similar to the postsynaptic membrane 43K protein from Xenopus * LGN protein(aa) * 4e-13 C10A gene product *
 CG5692 2e-29 hypothetical protein [TPR_REGION // TPR_REPEAT // NLS_BP] CG5692 LD33695 98A3-98A3 ID:49A6
 CG7878 + RNA_binding * DMRM62RH_2 Rm62 * RNA helicase(aa) * mitochondrial DEAD box protein(aa) * VASA PROTEIN(aa)

[helicase_C // KH-domain // KH_DOMAIN //] CG7878 LD33749 84F1-84F1 ID:49A7
+ Caf1 signal_transduction * Caf1 * Rack1 * CHROMATIN ASSEMBLY FACTOR P55 SUBUNIT (CAF-1 P55 SUBUNIT) (DCAF-1)(aa) * 2e-73 HAT2_YEAST HISTONE ACETYLTRANSFERASE TYPE B SUBUNIT hy [GPROTEINBRPT // WD40_REGION //
CG4236 WD_REPEA] CG4236 LD33761 88E8-88E8 ID:49A9
+ enzyme * 2e-18 probable membrane protein YDR018c - yeast (Saccharomyces cerevisiae) * 1e-17 similar to 1-acyl-glycerol-
CG4729 3-phosphate acyltransferases elegans * [GLYCEROL_ACYLTRANS] CG4729 LD34004 72F1-72F1 dup:2/2 ID:49B11
+ RNA_binding * 3e-05 NSR1_YEAST NUCLEAR LOCALIZATION SEQUENCE BINDING PROTEIN (P67) * 7e-06 protease *
CG10837 3e-05 Similarity to Bovine Poly-A binding protein II cDNA * [RNP_1 // RBD // rrm] CG10837 LD33831 cyto_unknown ID:49B3
+ unknown * 6e-97 N2,N2-dimethylguanosine tRNA methyltransferase c * 1e-105 similar to N2,N2-dimethylguanosine tRNA
CG6388 methyltransferase; cDNA ES * 1E-125 * 1e-111 [SAM_BIND] CG6388 LD33880 33D5-33E ID:49B7
+ l(3)03670 unknown * DMC507_2 anon-l * 5e-93 head-elevated expression in 0.9 kb * 8e-92 inserted at base Unknown 5' end of P
CG1715 element Plasmid rescue * CG1715 LD33960 100B-100B ID:49B8
CG1913 + CG1913 dup:6/7 ID:49B9
+ unknown * 3e-47 YKT6_YEAST HYPOTHETICAL 22.7 KD PROTEIN IN PAS1-MST1 INTERGENIC REGION * 7e-53
YMP8_CAEEL HYPOTHETICAL 82.6 KD PROTEIN IN CHROMOSOME III * 1e- [SYNAPTOBREVN // synaptobrevin] CG1515
CG1515 LD34211 7C8-7C8 ID:49C12
+ unknown * Ydl060wp(aa) * No definition line found(aa) * 8e-91 hypothetical protein YDL060w - yeast (Saccharomyces
CG7338 cerevisiae) * 0.00000000006 [NLS_BP] CG7338 LD34093 78D-78D dup:2/4 ID:49C5
+ unknown * RRM3/PIF1 helicase homolog(aa) * PIF1(aa) * putative helicase(aa) * DNA helicase homolog(aa) [NLS_BP //
CG3238 ATP_GTP_A] CG3238 LD34105 25A3-25A3 ID:49C6
+ EG:84H4.1 chaperone * by content; by match; 2-match_description=TORSINA.; 2-match_species=HOMO SAP...(aa) * 7e-55
CG3024 similarity to 35.1KD hypothetical yeast protein (Swiss [CLPPROTEASEA] CG3024 LD34179 4C7-4C7 ID:49C9
CG7869 + motor_protein * [SNF2_N // NLS_BP] CG7869 LD34474 70E1-70E1 ID:49D11
+ 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
+ peptidase * 1e-62 S2P * 2e-62 S2P * SP2 metalloprotease * S2P metalloprotease [ZINC_PROTEASE // SREBPS2PTASE]
CG8988 CG8988 LD34294 48C-48C ID:49D4
+ cell_cycle_regulator * DMUNKNOWN anon-DM192 * unknown product(aa) * 4e-05 CC27_YEAST CELL DIVISION
CONTROL PROTEIN cell division * 1e-139 unknown product [TPR_REGION // TPR_REPEAT // TPR] CG4050 57C2-57C2
CG4050 dup:3/4 ID:49D5
+ CH1-2 endopeptidase * COP9 complex homolog subunit 1-2 DCH1-2(aa) * 3e-14 YE28_CAEEL HYPOTHETICAL 47.6 KD
PROTEIN F49C12.8 IN CHROMOSOME IV * 1e-157 GPS1_HUMAN G PROTEIN [PCI_DOMAIN // PCI] CG3889 LD34304 75E2-
CG3889 75E2 dup:1/2 ID:49D6
+ motor_protein * 7e-09 by content; 1-meth * 2e-07 homeotic most like HMPB_DROME: homeotic proboscipedia protein * 9e-
CG8677 07 Williams-Beuren syndrome deletion transcript [PHD // NLS_BP // ATP_GTP_A] CG8677 LD34730 39C1-39C1 dup:5/5 ID:49E10
CG8735 + electron_transfer * 1e-11 C05E11.1 gene product * 2e-07 hypothetical protein * 3e-45 inserted at base Both 5' and 3' ends of

P element Inverse PCR * [CYTOCHROME_C] CG8735 LD34731 44D-44D2 dup:3/3 ID:49E11
 + enzyme * peptidylglycine alpha-amidating monooxygenase(aa) * 9e-38 strong similarity to the carboxyl-half of peptidylglycine alpha-amidating monoo * 7e-65 A [PAMONOXGNASE // NHL // NLS_BP] CG12130 LD34757 46C10-46C10 dup:2/2
 CG12130 ID:49E12
 + enzyme * nuclear protein methyltransferase (mono- and asymmetrically dimethylating enzyme); Hmt1p(aa) * protein N-methyltransferase 3(aa) * protein N-methyl [SAM_BIND] CG6563 LD34544 88E8-88E8 dup:2/2 ID:49E3
 CG12011 + unknown * CG12011 LD34635 62A12-62A12 dup:2/2 ID:49E7
 + TfiIS transcription_factor * 2e-20 DST1 DNA strand transferase alpha * 1e-124 TFS2_DROME TRANSCRIPTION ELONGATION FACTOR S-II (RNA POLYMERASE II ELONGATION FA * 3e-42 TFS2_CAEEL [TFIIS] CG3710 LD34766 35C1-35C1 ID:49F1
 + DNA_binding * zinc finger protein (RING finger, C3HC4 type)(aa) * 4e-34 YL23_YEAST HYPOTHETICAL 29.7 KD PROTEIN IN REC102-SFH1 INTERGENIC REGION * 5e-65 similar t [ZF_CCCH // zf-C3HC4 // ZINC_FINGER_C3HC] CG4973 LD35003
 CG4973 92C4-92C4 ID:49F12
 + DNA_binding * DNA helicase(aa) * HYPOTHETICAL 175.7 KD PROTEIN C05C10.2 IN CHROMOSOME II(aa) * DNA helicase A; Hcs1p(aa) * hypothetical helicase(aa) [ATP_GTP_A] CG6967 LD34829 53F5-53F6 ID:49F6
 CG9754 + unknown * [NLS_BP] CG9754 LD34845 57D4-57D4 ID:49F8
 + 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 dup:2/2 ID:49G2
 + unknown * 1e-146 inserted at base Unknown 5' end of P element Plasmid rescue * * [ZINC_FINGER_C2H2 // ZINC_FINGER_C2H2_2] CG5580 LD35038 55C4-55C4 ID:49G3
 + DNA_binding * 1e-125 hypothetical protein YDR334w - yeast (Saccharomyces cerevisiae) (* 1e-67 iswi protein - fruit fly (Drosophila melanogaster) ISWI p * 2e-67 p [helicase_C // DNA_LIGASE_A1 // MYB_3 //] CG9696 LD35056 57D5-57D8 dup:3/4
 CG9696 ID:49G4
 + GTP_binding * PTD004(aa) * PUTATIVE GTP-BINDING PROTEIN W08E3.3(aa) * GTP-binding protein - Methanococcus jannaschii(aa) * Similar to W08E3.3 putative GTP-binding [GTP1OBG // ATP_GTP_A] CG1354 LD35094 8F10-8F10 dup:2/2
 CG1354 ID:49G5
 + signal_transduction * vasodilator-stimulated phosphoprotein(aa) * 3e-09 Abl substrate ena (enabled) - fruit fly (Drosophila melanogaster) * 3e-08 neural variant mena+ pr [RANBP1_WASP // CYTOCHROME_C] CG10155 GH01083 51C2-51C2 dup:1/4
 CG10155 ID:54A10
 + ligand_binding_or_carrier * 2e-05 odorant-binding protein Rpal2' palmaru * * [PBP_GOBP] CG13421 GH01026 57A6-57A6
 CG13421 ID:54A2
 + unknown * 3e-80 YKL6_CAEEL HYPOTHETICAL 103.8 KD PROTEIN C03C10.6 IN CHROMOSOME III * E03A3.6 * CG5237 E03A3.7 * [AA_TRNA_LIGASE_II_2 // PRO_RICH // CYTO] CG5237 GH01039 91F10-91F11 ID:54A4
 + enzyme * 5e-19 VIT1_DROME VITELLOGENIN I PRECURSOR (YOLK PROTEIN 1) vitell * 6e-23 pancreatic lipase related CG17292 protein * 3e-25 pancreatic lipase-related protei [TAGLIPASE // ESTERASE // lipase] CG17292 GH01208 29B3-29B3 ID:54B11
 + enzyme * 2e-18 pdb|1GKY| Guanylate Kinase (E.C.2.7.4.8) Complex With Guanosine Monophosphate * 2e-70 Camguk * 2e- CG1321967 LIN2_CAEEL LIN-2 PROTEIN LIN-2A * 5e-97 D [Guanylate_kin // GUANYLATE_KINASE_1 //] CG13219 GH01140 47D7-47D7

ID:54B3

CG10671+ unknown * cDNA EST yk481g5.5 comes from this gene(aa) * * CG10671 GH01192 64C12-64C12 ID:54B9
+ enzyme * 7e-52 acyl-coenzyme A oxidase * 1e-120 similar to ACYL-COENZYME A OXIDASE, PEROXISOMAL (EC 1.3.3.6)
CG9707 (PALM * 1e-125 peroxisomal acyl-CoA oxidase * 1e CG9707 GH01226 57D11-57D11 dup:1/3 ID:54C1
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
+ BcDNA:GH07485 enzyme * 3e-55 CAO_YEAST ACYL-COENZYME A OXIDASE (ACYL-COA OXIDASE) ac * 1e-130 Similarity to
CG5009 Rat Acyl-CoA oxidase I (SW:CAO1_RAT); cDNA EST EMBL: * 1e-145 p CG5009 GH01266 54E8-54E8 dup:1/2 ID:54C6
+ odd transcription_factor * DMODDS_1 odd * transcription factor specific RNA polymerase II transcription factor) cell nucleus)
map_position:24A1-3 * Sob protein(aa) * 5e-19[zf-C2H2 // ZINC_FINGER_C2H2 // ZINC_FIN] CG3851 GH01449 25B1-25B1
CG3851 ID:54D10
+ 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
+ Diacyl glycerol kinase enzyme EDgk gene product is expressed predominantly in the embryonic CNS and adult nervous system
CG1535 and muscle DAGK, DAGKa, DAGKc, NLS_BP CG1535 GH01459 dup:2/2 ID:54D12
+ 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
+ cell_adhesion * DMARTAN_7 trn * 5e-08 tartan protein * 6e-16 5T4 oncofetal trophoblast glycoprotein * 6e-18 oncofetal
CG6959 trophoblast glycoprotein 5T4 precursor - human [LRR // LRRCT] CG6959 GH01562 86F11-86F11 dup:2/2 ID:54E11
+ endopeptidase * DMSER2_7 Ser99Db * 7e-70 serine proteinase (EC 3.4.21.-) precursor - fruit fly (*Drosophila melanogaster*) *
1e-11 similar to peptidase family S1 (tryp[trypsin // CHYMOTRYPSIN // TRYPSIN_SER] CG6483 GH01508 65A2-65A2 dup:2/2
CG6483 ID:54E6
+ defense/immunity_protein * cuticular molt protein precursor(aa) * 2e-29 peptidoglycan recognition protein precursor * 2e-31
CG8995 TNF superfamily, member (LTB)-like (peptidoglycan r CG8995 GH01554 13F1-13F1 dup:2/2 ID:54E9
CG10680+ * CG10680 38B1-38B1 dup:2/3 ID:54F11
+ protein_kinase * protein kinase(aa) * PUTATIVE SERINE/THREONINE-PROTEIN KINASE C01C4.3 IN CHROMOSOME
X(aa) * 5e-17 SNF1_YEAST CARBON CATABOLITE DEREPRESSING PROTE[PROTEIN_KINASE_ST //
CG4945 PROTEIN_KINASE_DOM] CG4945 GH01572 53C7-53C7 dup:3/4 ID:54F3
+ enzyme * long-chain-fatty-acid--CoA ligase (fadD-8)(aa) * similar to 4-coumarate-coA ligase; cDNA EST yk455e10.3 comes
CG4563 from this gene; cDNA EST yk455e10.5 c [AMP-binding] CG4563 GH01595 60D2-60D2 ID:54F5
+ endopeptidase * Cp1 * cathepsin F(aa) * 1e-59 cysteine proteinase cysteine * 9e-82 contains similarity to both a cystatin
domain and a cysteine protease domain [THIOL_PROTEASE_CYS // PAPAINE // Peptida] CG12163 GH01606 83A1-83A1 dup:2/2
CG12163 ID:54F7
CG18212+ unknown * [NLS_BP] CG18212 GH01770 90C-90C ID:54G11

+ karyopherin-alpha3 ligand_binding_or_carrier * coded for by C. elegans cDNA yk173a10.5; coded for by C. elegans cDNA
 CG9423 yk96a12.5; coded for by C. elegans cDNA cm06h1; coded for by C. elegans cDNA CG9423 GH01702 86C3-85D27 ID:54G5
 + 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
 + cell_adhesion * 1e-60 UFD4_YEAST UBIQUITIN FUSION DEGRADATION PROTEIN (UB FUSION PROTEIN 4) * 1e-169
 coded for by C. elegans cDNA yk34b1.5; coded for by C. elegans [ANK_REP // ank // HECT_DOMAIN // ANK_RE] CG5604 GH01804
 CG5604 31D1-31D3 dup:1/2 ID:54H2
 + enzyme * ODO1_YEAST 2-OXOGLUTARATE DEHYDROGENASE E1 COMPONENT PRECURSOR (ALPHA-
 KETOGLUTAR * Similar to 2-oxoglutarate dehydrogenase; coded for by C. elegans [E1_dehydrog] CG11661 73D6-73D7 dup:3/7
 CG11661 ID:54H3
 + HLHmbetatranscription_factor * 1e-108 helix-loop-helix protein m-beta - fruit fly (Drosophila melanogaster) * 2e-10 lin-22 * 3e-20
 HES1_MOUSE TRANSCRIPTION FACTOR HES-1 (HAIRY[HLH // HELIX_LOOP_HELIX // HELIX_LOOP_H] CG14548 GH01842
 CG14548 96F10-96F10 ID:54H5
 CG15217 + transmembrane_receptor * CG15217 GH01875 40C2-40C2 ID:54H7
 CG8605 + unknown * 3e-08 pi034 * * CG8605 GH01880 65F2-65F2 ID:54H8
 + unknown * ELKL motif kinase(aa) * 2e-42 serine/threonine kinase * 3e-35 KEMK_MOUSE PUTATIVE
 SERINE/THREONINE-PROTEIN KINASE EMK * 3e-40 MAP/microtubule affini [KA1] CG16701 GH01890 56D9-56D9 dup:1/2
 CG16701 ID:54H9
 CG8401 + unknown * CG8401 GH01937 52E3-52E4 ID:55A1
 + 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
 + * 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 78C7-78C7
 CG9391 dup:2/2 ID:55B1
 CG2657 + ion_channel glutamate receptor, delta-2 subunit-like SBP_GLUR CG2657 GH02344 ID:55B12
 CG11317 + transcription_factor * [ZINC_FINGER_C2H2 // ZINC_FINGER_C2H2_2] CG11317 GH02265 100B5-100B5 ID:55B5
 CG17506 + unknown smilarity to indora CG17506 GH02266 ID:55B6
 + RNA-directed_DNA_polymerase_group_II_intron_encoded * reverse transcriptase - fruit fly (Drosophila melanogaster)(aa) *
 SPAC3G9.15c; len:230aa; similarity: to YLR051C, Q120 35, unclassified protein, (21 [NLS_BP] CG1142 GH02295 85A1-85A1
 CG1142 ID:55B7
 + cell_adhesion * orphan G protein-coupled receptor FEX(aa) * BLASTX 7.5E-06 Santalum album proline rich protein mRNA,
 complete cds.(dna) * 9e-05 protein * 5e-05 kek1 [LRR // LEURICHRPT // NLS_BP // LRRCT] CG3413 GH02310 58D2-58D3
 CG3413 ID:55B8
 + transporter * DMWHITER_2 w * ORF YOL075c(aa) * putative protei(aa) * 6e-69 WHIT_DROME WHITE PROTEIN white
 CG9664 protein - fruit fly (Droso [ATP_GTP_A2 // ABC_tran // DA_BOX // ATP] CG9664 GH02377 25A1-25A1 ID:55C2

+ LanB1 cell_adhesion * DMLAMB01_2 LanB2 * LanB1 * LAMININ BETA-1 CHAIN PRECURSOR (LAMININ B1 CHAIN)(aa) *
 LAMININ BETA-1 CHAIN PRECURSOR (LAMININ B1 CHAIN)(aa) [laminin_EGF // EGF_1 // EGFLAMININ // L] CG7123 GH02457
 CG7123 28D-28D ID:55C7
 + 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
 + tld metalloendopeptidase DORSAL-VENTRAL PATTERNING TOLLOID PROTEIN PRECURSOR ASTACIN,ASX_HYDROXYL,
 CG6868 Astacin, CUB, EGF,] CG6868 ID:55D10
 + Dgp-1 translation_factor * 1e-07 EF1A_YEAST ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) translat * 8e-05
 EF11_DROME ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) (50 KD FEMALE-SPECIFIC PR [NLS_BP // GTP_EFTU //
 CG5729 ATP_GTP_A] CG5729 GH02692 55B9-55B9 dup:2/4 ID:55D7
 + 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
 + unknown * BLASTX 4.5E-06 YDR373W|Protein with similarity to human BDR-1 protein and other calcium binding
 CG10039 proteins(dna) * 1e-178 BLASTX 4.5E-06 YDR373W|Protei CG10039 GH02873 24D-24D dup:3/3 ID:55E7
 + actin_binding * filamin(aa) * 1e-103 similar to endothelial actin-binding protein repeats; cDNA EST EMB * 7e-11 actin binding
 CG11605 protein ABP-280 * 3e-90 gamma filamin [Filamin // FILAMIN_REPEAT] CG11605 GH03013 58F7-58F7 dup:1/3 ID:55F5
 CG16772+ unknown * CG16772 GH03035 38B1-38B1 ID:55F6
 + unknown * 2e-17 FMR2 protein * 1e-17 X mental retardation X ment * lymphoid nuclear protein related to AF4 * [HMGI_Y //
 CG8817 NLS_BP] CG8817 GH03237 23C1-23C1 dup:1/2 ID:55G11
 + Eip63F-1ligand_binding_or_carrier * Eip63F-1 * 2e-74 E631_DROME CALCIUM-BINDING PROTEIN E63-1 calcium-binding pr *
 CG15855 3e-17 similar to EF-hand calcium binding proteins; most similar to ca CG15855 GH03109 63F7-63F7 ID:55G4
 + wrapper cell_adhesion * wrapper protein(aa) * 9e-17 predicted protein contains a large number of Ig superfamily repeat * 2e-16
 CG10382 NCA1_MOUSE NEURAL CELL ADHESION MOLECULE, LAR [ig] CG10382 GH03113 58D6-58D6 ID:55G5
 + und peptidase * 1e-107 AMP2_YEAST METHIONINE AMINOPEPTIDASE (METAP 2) (PEPTIDASE M 2) (U * methionine
 aminopeptidase * 1e-38 Similarity to Rat initiation factor ass [Peptidase_M24 // MAPEPTIDASE] CG4008 GH03119 30D1-30D1
 CG4008 ID:55G6
 + 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
 + SMC2 DNA_binding * 1e-179 SMC2_YEAST CHROMOSOME SEGREGATION PROTEIN SMC2 (DA-BOX PROTEIN SMC2) *
 3e-69 Cap * 1e-136 mitotic chromosome and X-chromosome associated MIX- [ATP_GTP_A] CG10212 GH03364 51D1-51D1
 CG10212 ID:55H8
 + motor_protein * 8e-08 /motif=(desc: * 7e-11 contains similarity to a C3HC4-class zinc finger * 1e-20 mTRIP * 3e-20 hTRIP
 CG5140 [zf-C3HC4 // NLS_BP // ZF_RING] CG5140 GH03577 55B9-55B9 ID:56A7
 CG1844 + unknown * 1E-172** CG1844 GH03581 10F4-10F4 ID:56A8
 + unknown * 2e-20 coded for by C. elegans cDNA yk173c12.5 * 3e-11 unknown protein * contains similarity to Physcomitrella
 CG10509 patens glyceraldehyde 3-phosphate dehy CG10509 GH03649 57D3-57D4 dup:1/2 ID:56B3
 CG13279+ Cyt-b5 electron_transfer * CYBR_DROME PROTEIN TU-36B (CYTOCHROME B5-RELATED PROTEIN) * 9e-66 CYBR_DROVI

CYTOCHROME B5 RELATED PROTEIN cytochrome b5 * DMTU36B_4 Cyt-b5 * delta [CYTOCHROME_B5_2 // heme_1]
 CG13279 GH03691 36A9-36A9 ID:56B5
 CG18358+ unknown * CG18358 GH03717 15A3-15A3 ID:56B7
 CG2767 + enzyme aldose reductase ALDOKETO_REDUCTASE_1, ALDOKETO_REDUCTASE] CG2767 ID:56C2
 CG18597+ hypothetical protein CG18597 GH03806 ID:56C8
 CG15608+ unknown * 2e-06 CGI-62 protein * [NLS_BP] CG15608 GH03957 53F6-53F7 dup:1/3 ID:56D12
 + Pkg21D protein_kinase * Pkg21D * 1e-64 cAMP-dependent protein kinase subunit (put.); putative * protein kinase (EC 2.7.1.37),
 cGMP-dependent - fruit fly (Drosophila melanog [PROTEIN_KINASE_ST // CGMPKINASE // cNMP] CG3324 GH03852 21E1-21E1
 CG3324 ID:56D3
 + Adh storage_protein * DMADHA1_9 Adh * 3e-06 FOX2_YEAST PEROXISOMAL HYDRATASE-DEHYDROGENASE-
 EPIMERASE (HDE) (MULTIFUNCTIONAL * 1e-145 alcohol dehydrogenase (EC 1.1.1.1[ALCDHDRGNASE // GDHRDH //
 CG3481 adh_short //] CG3481 GH03875 35B3-35B3 dup:4/6 ID:56D5
 CG5433 + Klc motor_protein KINESIN LIGHT CHAIN (KLC) ATP_GTP_A, KINESINLIGHT,KINESIN_LIGHT, T] CG5433 ID:56D9
 CG18210+ unknown * CG18210 GH04075 13C5-13C5 dup:2/2 ID:56E10
 + 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 * 5e-
 CG5725 42 putative protein * coded for by C. CG5725 GH04001 77B6-77B6 dup:3/3 ID:56E4
 + unknown * dJ413H6.1.1 (hamster Androgen-dependent Expressed Protein LIKE PUTATIVE protein) (isoform 1)(aa) *
 CG3625 androgen-regulated protein FAR-17 - golden hamst CG3625 GH04039 21B5-21B5 dup:2/2 ID:56E6
 + peptidase * 5e-10 carboxypeptidase s * 3e-90 Similarity to Human aminoacylase-1 (SW:ACY1_HUMAN) * 1e-109
 aminoacylase AMINOACYLASE-1 (N-A * 1e-103 ACY1_PIG AMIN [ARGE_DAPE_CPG2_1 // ARGE_DAPE_CPG2_2] CG6465
 CG6465 GH04054 86C2-86C2 dup:2/2 ID:56E8
 CG17977+ unknown * CG17977 GH04104 44A3-44A3 ID:56F1
 + 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
 + structural_protein * Similarity to Yeast YIP1 protein cDNA EST comes from this gene; cDNA EST comes from this gene;
 CG3652 cDNA EST comes from this gene; cDNA EST comes from t CG3652 GH04132 24F1-24F1 dup:2/3 ID:56F4
 + transcription_factor * 7e-10 AZF1_YEAST ASPARAGINE-RICH ZINC FINGER PROTEIN AZF1 fin * 2e-37 transcription
 factor YY1 homolog * 1e-14 contains similarity to C2H2-type z[zf-C2H2 // ZINC_FINGER_C2H2 // ZINC_FIN] CG3445 67B4-67B4
 CG3445 dup:3/4 ID:56G10
 + unknown * secretory carrier membrane protein 2(aa) * 1e-43 partial CDS * 4e-54 SCA3_MOUSE SECRETORY CARRIER-
 ASSOCIATED MEMBRANE PROTEIN * 7e-64 SCA1_HUMAN SEC [PHOSPHOPANTETHEINE] CG9195 GH04264 13D1-13D1
 CG9195 dup:2/2 ID:56G2
 CG8993 + * DMC132E8 * similar to thioredoxin(aa) * thioredoxin - Chloroflexus aurantiacus(aa) * 4e-15 TRX1_YEAST THIOREDOXIN

I (TR-I) thioredoxin I - yeast (Sa [THIOREDOXIN // THIOREDOXIN_2 // thioered] CG8993 62E-62E ID:56G3
 + CycJ cell_cycle_regulator * CycJ * 4e-11 CG22_YEAST G2/MITOTIC-SPECIFIC CYCLIN cyclin B2 - yeast * cyclin J * 3e-05
 CG10308 Similar to cyclin [cyclin // HELIX_LOOP_HELIX // NLS_BP] CG10308 GH04281 63D2-63D2 ID:56G5
 + cell_adhesion * protein(aa) * DMCONNECTN_1 Con * 4e-18 adenylate cyclase * 1e-25 CAPRICIOUS [LRR // LEURICHRPT
 CG7896 // LRRCT] CG7896 GH04292 99D3-99D3 dup:1/2 ID:56G8
 CG3918 + NLS_BP, ZF_CCHC CG3918 ID:56H5
 + unknown * 1e-102 predicted using Genefinder; Weak similarity to elongation factors; * 1e-90 putative G-protein * 3e-90 GTP
 CG2017 binding protein putative G-protein [GTP_EFTU // ATP_GTP_A] CG2017 GH04432 83C4-83C4 dup:3/3 ID:56H9
 + RNA_binding * DOUBLE STRANDED RNA BINDING PROTEIN A (XLRBPA)(aa) * TAR (HIV) RNA-binding protein 2(aa) *
 CG6866 TAR (HIV) RNA binding protein 2(aa) * 1e-05 contains simi [dsrm // DSRBD] CG6866 GH04468 34B6-34B6 dup:1/2 ID:57A1
 + 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
 cDNA EST comes from this gene; cDNA EST * 7e-21 putative amino [AROMATIC_AA_PERMEASE_2] CG8785 GH04538 49B7-
 CG8785 49B7 ID:57A5
 + enzyme * putative nicotinate phosphoribosyltransferase(aa) * 1e-169 putative nicotinate phosphoribosyltransferase *
 CG3714 hypothetical protein * similar to nicotin CG3714 25E1-25E1 dup:2/3 ID:57A8
 CG10342 + npf signal_transduction * neuropeptide F(aa) * * CG10342 GH04563 89D5-89D5 ID:57A9
 + 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 GH04680
 CG5150 64E-64E ID:57B10
 CG4962 + unknown * CG4962 GH04593 72E2-72E2 ID:57B2
 + 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 95E1-95E1
 CG6173 ID:57B4
 + Optix unknown * transcription factor RNA polymerase II transcription factor) cell nucleus) * * CG18455 GH04859 44A2-44A2
 CG18455 ID:57C11
 + dib cytochrome_P450 * 2e-17 cytochrome P-450 - fruit fly (Drosophila melanogaster) (fragment) * 1e-10 YS45_CAEEL
 PUTATIVE CYTOCHROME P450 ZK177.5 IN CHROMOSOME II * 3e-30 [EP450II // p450 // P450 // MITP450 // C] CG12028
 CG12028 GH04745 64A5-64A5 ID:57C3
 CG7515 + CG7515 GH04814 ID:57C5
 + enzyme * ATP SYNTHASE LIPID-BINDING PROTEIN P2 PRECURSOR (PROTEIN 9) (SUBUNIT C)(aa) * 5e-12 ATP
 synthase (EC 3.6.1.-) c chain - Caenorhabditis elegans * 3e- [ATPASE_C // ATPASEC // ATP-synt_C] CG1746 GH04827 100B9-
 CG1746 100B9 ID:57C6

CG4294 + motor_protein * [PPASE // PRO_RICH // NLS_BP] CG4294 GH04951 58F1-58F1 dup:3/4 ID:57D11
 CG18004+ unknown * CG18004 GH04870 47C6-47C6 dup:2/2 ID:57D2
 + unknown * hypothetical protein - Chinese hamster (fragment)(aa) * DHFR-coamplified protein * hypothetical protein - Chinese
 CG7231 hamster (fragment)(aa) * 4e-44 ins [ACTININ_1] CG7231 GH04938 30C1-30C1 dup:2/3 ID:57D8
 + 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 GH05015
 CG17646 22F3-22F3 dup:3/3 ID:57E6
 CG13607+ unknown * CG13607 GH05104 95D10-95D10 ID:57F5
 CG9896 + unknown * [NLS_BP] CG9896 GH05301 59C1-59C1 ID:57G12
 none + none GH05253 ID:57G7
 + BcDNA:GH12504 transmembrane_receptor * 3e-07 microtubule binding protein D-CLIP-190 * 1e-06 DYNA_MOUSE DYNACTIN,
 KD ISOFORM (150 KD DYNEIN-ASSOCIATED POLYPEPTIDE) (DP- * 1e-06 DYNA_HUMAN CG9808 GH05455 85B3-85B4
 CG9808 dup:3/4 ID:57H9
 CG5783 + unknown * 3e-07 hypothetical protein ** CG5783 GH05617 36E6-36E6 ID:58A12
 + 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
 + Hrb87F RNA_binding * Rbm(aa) * similar to RNA recognition motif. (aka RRM, RBD, or RNP domain); cDNA EST yk474h4.3
 CG12749 comes from this gene; cDNA EST yk505c10.3 comes from [RNP_1 // RBD // rm] CG12749 GH05625 87F7-87F7 ID:58B2
 + Dhc64C motor_protein * DMCYTHA_2 Dhc64C * DYHC_YEAST DYNEIN HEAVY CHAIN, CYTOSOLIC (DYHC) dynein he *
 DYHC_DROME DYNEIN HEAVY CHAIN, CYTOSOLIC (DYHC) dynein h * DYHC_CA [CRYSTALLIN_BETAGAMMA //
 CG7507 THIOL_PROTEASE_] CG7507 64C-64C dup:2/3 ID:58B4
 CG9689 + unknown * CG9689 GH05731 9A2-9A2 ID:58B9
 + sm RNA_binding * DMSMOOTH_2 sm * 4e-20 homologous to human hnRNP L * 5e-22 DMSMOOTH_2 sm * [RBD] CG9218
 CG9218 GH05823 56D11-56E1 dup:1/2 ID:58C12
 CG7296 + CG7296 GH05801 ID:58C6
 + Rbf cell_cycle_regulator * DMRBFPRTN_2 Rbf * EST comes from the 3' UTR m * 3e-24 similar to retinoblastoma proteins * 1e-
 CG7413 84 RBL1_MOUSE RETINOBLASTOMA-LIKE PROTEIN (107 KD RETI CG7413 GH05946 1C2-1C2 ID:58D10
 CG10373+ unknown * gene product(aa) * 6e-19 gene product * 2e-23 JWA protein * JM4 CG10373 GH05842 37A4-37A4 ID:58D2
 + enzyme * 659aa long hypothetical 3-hydroxybutyryl-CoA dehydratase(aa) * PhaB(aa) * 9e-10 YDAK_YEAST
 CG9577 HYPOTHETICAL 56.3 KD PROTEIN IN ARO3-KRS1 INTERGENIC REGI [ECH] CG9577 GH06131 19C1-19C1 dup:2/2 ID:58E12
 + enzyme * acid phosphatase (EC 3.1.3.2) Acph-1 precursor, lysosomal - fruit fly (Drosophila melanogaster)(aa) * acid
 CG6656 phosphatase-1(aa) * PUTATIVE ACID PHOSPH [acid_phosphat] CG6656 GH06011 93F-93F dup:3/3 ID:58E4
 CG12612+ CG12612 GH06062 dup:2/2 ID:58E6
 + enzyme * lyase(aa) * lyase(aa) * lyase (EC 4.3.2.1)(aa) * [DCRYSTALLIN // FUMRATELYASE // FUMARATE] CG9510
 CG9510 GH06087 29F6-29F6 dup:2/2 ID:58E8

+ protein_kinase * Mlc-k * Lk6 * DMRSK_2 S6kII * DMDAKT1_2 Akt1 [PROTEIN_KINASE_ST // TYRKINASE // PROTE]
 CG11221 CG11221 GH06138 27A2-27A2 ID:58F2
 + unknown * predicted using Genefinder; cDNA EST yk268h6.5 comes from this gene; cDNA EST yk465f2.5 comes from this
 CG10512 gene; cDNA EST yk393g7.5 comes from this gen CG10512 GH06154 78C3-78C4 ID:58F3
 + signal_transduction * 1e-20 YMH2_YEAST HYPOTHETICAL 171.1 KD PROTEIN IN YL16A-DAK1 INTERGENIC REGION *
 2e-07 SY65_DROME SYNAPTOTAGMIN (P65) synaptotagmin - fruit fly (* [C2 // C2_DOMAIN_2] CG6643 GH06342 96A-96A
 CG6643 dup:1/2 ID:58G6
 + * 2e-19 /match=(desc;; /ma * 2e-06 No definition line found * C29F7.1 * cDNA EST yk381e5.3 comes from this gene
 CG10550 CG10550 96C8-96C8 dup:1/4 ID:58G9
 CG5089 + unknown * [NLS_BP] CG5089 GH06435 53C8-53C9 dup:2/2 ID:58H4
 CG4377 + unknown * CG4377 GH06474 58A3-58A3 ID:58H6
 CG8592 + stil unknown * 1e-171 STAND STILL (Y * 1e-173 stil * * [NLS_BP] CG8592 GH06596 49B2-49B2 ID:59A10
 CG10204 + CG10204 102B4-102B5 ID:59A6
 CG8430
 + Lrr47 actin_binding * LRR47 protein - fruit fly (Drosophila melanogaster)(aa) * DMLRR47_3 Lrr47 * 2e-05 predicted using
 CG6098 Genefinder; Similarity to Glucose-repressible alco [LRR // LEURICHRPT] CG6098 GH06740 31E6-31E6 ID:59B11
 + emp transmembrane_receptor * DMEMP_3 emp * epithelial membrane protein - fruit fly (Drosophila melanogaster)(aa) * 2e-40
 CG2727 predicted using Genefinder; similar to CD36 family; cDNA [CD36] CG2727 GH06663 60E7-60E8 ID:59B5
 + 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
 + enzyme * UTP--GLUCOSE-1-PHOSPHATE URIDYLYLTRANSFERASE (UDP-GLUCOSE PYROPHOSPHORYLASE)
 (UDPGP) (UGPASE)(aa) * similar to UTP--GLUCOSE-1-PHOSPHATE URIDYLYLTRA CG4347 GH06691 67A9-67B1 dup:1/3
 CG4347 ID:59B7
 + * VACUOLAR ATP SYNTHASE CATALYTIC SUBUNIT A (V-ATPASE KD SUBUNIT) (VAA3-1)(aa) * H+-transporting
 ATPase (EC 3.6.1.35), vacuolar, A chain, VA68 type - [ATP-synt_ab // ATP-synt_ab_C // ATPASE_] CG3762 34A4-34A4 dup:1/2
 CG3762 ID:59C4
 CG5467 + unknown * CG5467 GH07007 97B9-97B9 ID:59C8
 CG6761 + unknown * CG6761 GH07092 67B12-67B12 ID:59D1
 + transmembrane_receptor * BLASTX 4.3E-09 Mus musculus putative myelin regulatory factor mRNA, partial cds.(dna) * TPR-
 containing, SH2-binding phosphoprotein(aa) *[TPR_REGION // TPR_REPEAT // TPR // NLS_] CG2469 GH07228 62B4-62B4
 CG2469 dup:4/5 ID:59D12
 CG18512 + CG18512 GH07187 ID:59D7
 CG3588 + EG:100G7.6 structural_protein * map_position:3C5 * * * [PRO_RICH] CG3588 GH07242 3C4-3C4 dup:2/2 ID:59E3
 + transporter * solute carrier family (sodium/chloride transporters), member 3(aa) * BUMETANIDE-SENSITIVE SODIUM-
 CG4357 (POTASSIUM)-CHLORIDE COTRANSPORTER (NA-K-CL SYMPORT [AMINO_ACID_PERMEASE_2] CG4357 GH07280 69B-

69B2 dup:7/8 ID:59E7
+ Ets65A transcription_factor * ETS domain transcription factor PET-1(aa) * Friend leukemia virus integration 1(aa) * contains strong similarity to ETS domains and * DNA-BINDING [ETS_DOMAIN_1 // HSF_ETS // ETSDOMAIN //] CG7018 GH07491 65A3-
CG7018 65A3 ID:59G3
none + none GH07529 ID:59G6
+ 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
+ endopeptidase * kuz * a disintegrin and metalloprotease domain (ADAM) 10(aa) * 1e-109 kuzbanian * 1e-102 ADAM similar
CG1964 to [DISINTEGRINS_2 // ADAM_MEPRO // ZINC_PR] CG1964 GH07695 99C1-99C1 ID:59H9
CG8678 + CG8678 dup:1/2 ID:60A10
+ motor_protein * dynein light chain-A(aa) * DYNEIN LIGHT INTERMEDIATE CHAIN 1, CYTOSOLIC (LIC57/59) (DYNEIN
CG1938 LIGHT CHAIN A) (DLC-A)(aa) * 1e-38 cDNA EST comes from th [ATP_GTP_A] CG1938 GH07739 10A10-10A10 dup:2/3 ID:60A3
CG7859 + unknown * [NLS_BP] CG7859 GH07769 93D9-93D9 dup:1/2 ID:60A6
+ unknown * cDNA EST yk429e10.5 comes from this gene; cDNA EST yk431d3.5 comes * gene e1 protein - mouse * is a
CG14967 human counterpart of mouse e1 gene. * 7e-20 hypo CG14967 GH07785 63C1-64A3 dup:1/3 ID:60A7
CG11877 + unknown * protein(aa) * * CG11877 GH07807 99A1-99A1 dup:2/3 ID:60A8
CG17124 + unknown * CG17124 GH07856 32A4-32A4 dup:1/2 ID:60B6
CG8568 + unknown * 4e-05 C09D4.2 gene product * * [NLS_BP] CG8568 GH07892 16A4-16A5 dup:1/2 ID:60B9
+ 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
CG9338 + unknown * CG9338 GH07967 38F1-38F1 dup:1/2 ID:60C9
+ transporter * 8e-07 predicted using Genefinder; cDNA EST yk416g4.5 comes from this g * 2e-05 hypothetical protein - rabbit
CG4526 ORF might exte * CG4526 GH08173 73A3-73A4 dup:3/6 ID:60D10
CG11808 + unknown * [NLS_BP] CG11808 GH08125 51E9-51E9 dup:1/2 ID:60D4
+ BG:DS02780.1 cell_adhesion * Toll protein(aa) * 9e-05 cell-surface molecule connectin - fruit fly (Drosophila melanogaster) * 2e-
CG5888 06 predicted using Genefinder; Similarity to Dr [LRR] CG5888 GH08155 35F12-36A1 dup:1/2 ID:60D6
+ endopeptidase * 3e-11 TBP6_YEAST PROBABLE 26S PROTEASE SUBUNIT YTA6 (TAT-BINDING HOMOLOG 6) * 3e-08
CG14183 MEI1_CAEEL MEIOTIC SPINDLE FORMATION PROTEIN MEI-1 mei-1 * 0.000 CG14183 GH08353 76E3-76E4 dup:3/3 ID:60E12
+ Mgstl enzyme (Microsomal glutathione S-transferase-like) microsomal glutathione S-transferase-like protein [Drosophila
CG1742 melanogaster] >g MAPEG CG1742 GH08455 dup:1/2 ID:60F10
+ 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
+ unknown * A_IG002N01.31 gene product(aa) * No definition line found(aa) * C44C1.2 gene product * CG8460 GH08401
CG8460 28F1-28F1 ID:60F5

+ peptidase * carboxypeptidase D(aa) * CARBOXYPEPTIDASE PRECURSOR(aa) * * CpepE [CARBOXYPEPT_ZN_1 //
 CG4678 CARBOXYPEPT_ZN_2 //] CG4678 GH08425 15A2-15A3 dup:2/3 ID:60F8
 + ion_channel * 1e-35 VM106R.1 * 2e-06 (novel protein similar to and mouse, worm an * similar to TNF-alpha induced Protein
 CG10830 B12 * similar to human tumor necrosis fac CG10830 GH08630 93A2-93A2 dup:1/2 ID:60G10
 + cytoskeletal_structural_protein * Similarity to some phosphatases and kinases; cDNA EST comes from this gene(aa) * 2e-87
 Similarity to some phosphatases and kinases; cDNA ES[PX // RA_DOMAIN // BEM_DOMAIN] CG3138 GH08671 5B2-5B2 dup:1/2
 CG3138 ID:60G12
 + ligand_binding_or_carrier * microsomal triglyceride transfer protein large subunit precursor(aa) * 1e-51 MTP_MOUSE
 MICROSOMAL TRIGLYCERIDE TRANSFER PROTEIN, LARGE SUBUNIT PRECU [MYB_1 // ATP_GTP_A] CG9342 GH08556
 CG9342 38F4-38F4 dup:1/3 ID:60G5
 + loco signal_transduction * regulator of G-protein signalling LOCO C2(aa) * 6e-08 YTN3_CAEEL HYPOTHETICAL 33.0 KD
 PROTEIN C29H12.3 IN CHROMOSOME II (U * 6e-43 RGSE_MOUSE REGULA [GRK // RGS // NLS_BP] CG5248 GH08607
 CG5248 94B11-94C1 dup:1/3 ID:60G8
 + actin_binding * DMRCPA_X kel * The gene product is related to Drosophila melanogaster ring canel protein.(aa) * 8e-86
 CG3962 kelch protein, long form - fruit fly (Drosophi [BTB // KELCHREPEAT // Kelch] CG3962 GH08610 89E13-89E13 dup:1/3 ID:60G9
 CG3528 + unknown * CG3528 GH08765 22F-22F dup:1/2 ID:60H11
 CG14830 + * 1E-102* * CG14830 65E10-65E10 dup:2/3 ID:60H4
 + ligand_binding_or_carrier * DMC30B8 * retinaldehyde-binding protein 1(aa) * tocopherol (alpha) transfer protein (ataxia
 (Friedreich-like) with vitamin E deficiency)(aa) * 62D[CRETINALDHBP // CRAL_TRIO] CG10237 GH08711 37E3-37E3 dup:2/3
 CG10237 ID:60H5
 + enzyme * adenylosuccinate lyase (purB) homolog - Haemophilus influenzae (strain Rd KW20)(aa) * purB(aa) * probable
 membrane protein YLR359w - yeast (Sacchar [FUMRATELYASE // FUMARATE_LYASES // lyas] CG3590 GH08719 92C1-92C1
 CG3590 dup:1/2 ID:60H7
 + 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 * hypothetical protein(aa) * cDNA EST comes from this gene; cDNA EST comes from this gene; cDNA EST comes
 CG9246 from this gene; cDNA EST yk317d5.5 comes fro [NLS_BP] CG9246 GH08927 39B3-39B3 dup:1/2 ID:61B10
 CG9445 + unknown * CG9445 42C7-42C7 dup:3/3 ID:61B11
 CG13432 + unknown CG13432 GH08941 dup:1/2 ID:61B12
 + bnl signal_transduction * FGF homolog(aa) * bnl * 3e-09 LET-756 protein * 3e-14 fibroblast growth factor fibro [HBGFFGF //
 CG4608 FGF // IL1HBGF] CG4608 GH08887 92B3-94E1 dup:3/3 ID:61B2
 + chaperone * 1e-13 gene product * 1e-09 disulfide-like protein prote * [THIOREDOXIN_2] CG11790 GH08893 96B15-96B15
 CG11790 dup:1/2 ID:61B4
 + translation_factor * hypothetical translation initiation factor(aa) * HYPOTHETICAL 40.9 KD PROTEIN C01G10.9 IN
 CG11334 CHROMOSOME V(aa) * 3e-66 YP18_YEAST HYPOTHETICAL 45.0 KD P [IF-2B] CG11334 GH08894 100C-100C dup:1/2 ID:61B5
 CG12024 + signal_transduction * 5e-25 BAW protein * * [NLS_BP] CG12024 GH08896 62E3-62E3 dup:1/2 ID:61B6

+ sif signal_transduction (still life) Guanine-nucleotide dissociation stimulators CDC24 family signatur GRF_DBL, NLS_BP, PDZ,
 CG5406 PH_DOMAIN, PRO_RIC] CG5406 GH08923 dup:1/2 ID:61B8
 + 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
 + enzyme * DMGST_3 GstD1 * 7e-09 probable membrane protein YLL060c - yeast (Saccharomyces cerevisiae) * 7e-45
 CG17524 unknown * 3e-16 GTT1_MOUSE GLUTATHIONE S-TRANSFER [GST] CG17524 GH09055 55C9-55C9 dup:1/2 ID:61C11
 + Glut1 transporter * transporter glucose transporter) map_position:61E * Glut1; * transporter glucose transporter)
 map_position:61E * 2e-36 YB91_YEAST PROBABLE METABOL [SUGRTRNSPORT // SUGAR_TRANSPORT_2 // su] CG1086
 CG1086 GH08948 61E1-61E2 dup:1/2 ID:61C2
 + 26/29kD-proteinase * 26,29kDa proteinase(aa) * 8e-61 cysteine proteinase cysteine * 1e-56 predicted using Genefinder; similar
 CG8947 to cathepsin-like protease; cD * 2e-61 cath [THIOL_PROTEASE_CYS // PAPAINE // Peptida] CG8947 70C9-70C9 dup:1/2 ID:61C5
 CG7841 + unknown * CG7841 GH09068 71C4-71C4 dup:1/2 ID:61D1
 CG3987 + unknown * CG3987 GH09123 88E4-88E5 dup:2/3 ID:61D3
 + endopeptidase * TRYPSIN DELTA PRECURSOR(aa) * Ser12 * Ser6 * Dvtry-1 trypsin precursor(aa) [trypsin //
 CG4653 CHYMOTRYPSIN // TRYPSIN_HIS] CG4653 GH09333 15A1-15A1 ID:61F1
 + endopeptidase * prolyl endopeptidase(aa) * 3e-06 PPCE_PIG PROLYL ENDOPEPTIDASE (POST-PROLINE CLEAVING
 ENZYME) (PE) * prolyl oligopeptidase (EC 3.4.21.26) - human [PROLIGOPTASE // Peptidase_S9 // ESTERAS] CG2528 GH09342
 CG2528 40A6-40A6 dup:2/2 ID:61F2
 none + none GH09355 ID:61F3
 + Eip71CD enzyme * 6e-11 PMSR_YEAST PUTATIVE PEPTIDE METHIONINE SULFOXIDE REDUCTASE (PEPTIDE MET(O)
 CG7266 REDUC * 1e-123 put. Eip (aa 1-255) * 2e-29 similar to drosophila e CG7266 GH09363 71C4-71C4 dup:2/3 ID:61F4
 CG4302 + CG4302 CG11051 GH09393 ID:61F9
 CG4891 + BG:DS04095.1 unknown * CG4891 GH09478 35F1-35F1 dup:1/2 ID:61G1
 + nAcRalpha-96Ab ion_channel * DMARD1_2 nAcR bgr;-64B * DMNARAS nAcR bgr;-96A * DMDA2_2 nAcR agr;-96Ab *
 ACH2_DROME ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-LIKE CHAIN PRECU[NICOTINICR // neur_chan //
 CG6844 NEUROTR_ION_] CG6844 GH09582 96A2-96A2 dup:1/3 ID:61G11
 + Pp1alpha-96A protein_phosphatase * DMPP113C_2 Pp1-13C * 1e-153 PP12_YEAST SERINE/THREONINE PROTEIN
 PHOSPHATASE PP1-2 pho * PP11_DROME SERINE/THREONINE PROTEIN PHOSPHATASE ALPHA-[PHOSPHO_ESTER //
 CG6593 STPHPTASE // SER_THR_] CG6593 GH09488 96A5-96A5 ID:61G3
 + enzyme * sphingomyelin phosphodiesterase 1, acid lysosomal (acid sphingomyelinase)(aa) * SPHINGOMYELIN
 PHOSPHODIESTERASE PRECURSOR (ACID SPHINGOMYELINASE)(aa [PHOSPHO_ESTER // SAP_B] CG3376 GH09489
 CG3376 60C1-60C2 dup:2/5 ID:61G4
 + signal_transduction * agrin(aa) * 8e-33 similar to agrin and follistatin; egf-like repeats * 4e-13 FSA_MOUSE FOLLISTATIN
 CG7159 PRECURSOR (FS) (ACTIVIN-BINDING PROTEIN) * 4e-13 [kazal] CG7159 GH09510 66C12-66C12 ID:61G5
 + enzyme * 7e-62 SYWM_YEAST TRYPTOPHANYL-TRNA SYNTHETASE, MITOCHONDRIAL (TRYPTOPHAN--TRNA
 CG7441 LIGASE) * 1e-60 SYWM_CAEEL PROBABLE TRYPTOPHANYL-TRNA SYNTHETASE, MIT [TRNASYNTHTRP // tRNA-synt_1b //

AA_TRNA] CG7441 GH09538 75A4-75A4 dup:1/3 ID:61G8

+ cell_adhesion * 6e-05 similar to the protein kinase domain of myosin light chain kinases * 6e-05 myosin light chain kinase

CG5699 isoform * 5e-05 KMLS_CHICK MYOSIN LIGHT C CG5699 GH09541 62C3-62C3 dup:2/3 ID:61G9

CG18462+ CG18462 GH09618 dup:1/2 ID:61H1

+ G-alpha47A signal_transduction GUANINE NUCLEOTIDE-BINDING PROTEIN G(O), ALPHA SUBUNIT (CLASS-I) >gi|

CG2204 ATP_GTP_A, G-alpha, GPROTEINA, GPROTEINA] CG2204 GH09771 dup:3/4 ID:61H10

+ unknown * 2e-13 YJT6_YEAST HYPOTHETICAL 36.2 KD PROTEIN IN UBP12-CDC6 INTERGENIC REGION * 8e-18

YLF4_CAEEL HYPOTHETICAL 34.1 KD PROTEIN C40H1.4 IN CHROMOSOME CG9798 GH09808 82C1-82C2 dup:3/4

CG9798 ID:61H12

+ Galpha73B signal_transduction * GBAF_DROME GUANINE NUCLEOTIDE-BINDING PROTEIN G(F), ALPHA SUBUNIT * 4e-65

G protein a(s) subunit * 2e-69 GTP-binding regulatory protein [GPROTEINA // G-alpha // GPROTEINAQ // G] CG12232 GH09683

CG12232 77B1-77B1 dup:2/3 ID:61H4

+ transcription_factor * 3e-05 HUNB_TRICA HUNCHBACK PROTEIN hunchback * 2e-06 DMHBG_10 hb * Hunchback protein

CG9932 * [zf-C2H2 // ZINC_FINGER_C2H2 // ZINC_FIN] CG9932 GH09733 34A-34A dup:1/2 ID:61H6

CG17809+ alpha-Man-I enzyme mannosyl-oligosaccharide 1,2-alpha-mannosidase GLYHDLASE47 CG17809 GH09743 dup:1/2 ID:61H7

CG17875+ cytochrome_P450 CG17875 GH09824 dup:1/3 ID:62A2

+ TBPH RNA_binding * map_position:60A5-6 * TAR-binding protein(aa) * TBPH * 2e-16 NAB4_YEAST NUCLEAR

POLYADENYLATED RNA-BINDING PROTEIN NAB4 [RNP_1 // RBD // rrm // NLS_BP] CG10327 GH09868 60A5-60A6 dup:1/2

CG10327 ID:62A7

CG11074+ unknown * [NLS_BP] CG11074 GH09884 42F2-42F2 ID:62A8

CG1822 + CG1822 dup:2/2 ID:62B10

+ ligand_binding_or_carrier * 2e-68 62D9.a * 4e-10 cellular retinaldehyde-binding protein; CRALBP * 2e-15 alpha tocopherol

transfer protein * 1e-15 TTPA_RAT ALPHA-TOCOPHEROL TRAN [CRETINALDHBP // CRAL_TRIO] CG3823 GH10083 5E1-5E1

CG3823 ID:62B11

CG2467 + unknown * [PRO_RICH // NLS_BP] CG2467 GH09980 10F7-10F8 dup:2/2 ID:62B5

+ unknown * similar to human 5'-nucleotidase * cytosolic IMP-GMP specific 5'-nucleotidase(aa) * CYTOSOLIC PURINE 5'-

CG6247 NUCLEOTIDASE(aa) * 1e-145 similar to human 5 [NLS_BP] CG6247 GH10029 17A11-17A11 ID:62B8

+ unknown * DMRHO_2 ve * RHOMBOID PROTEIN (VEINLET PROTEIN)(aa) * 5e-32 similar to transmembrane of D.

CG1697 melanogaster rhomboid protein * 9e-28 UNKNOWN rhomboid-re CG1697 GH10260 10C6-10C6 dup:1/7 ID:62C10

+ NetB cell_adhesion * extracellular extracellular) map_position:12F1 * NetB * 1e-170 NETB_DROME NETRIN-B PRECURSOR

Netrin-B melanog * 3e-67 UNC6_CAEEL UNC-6 PROTEIN P[laminin_EGF // EGFLAMININ // EGF_LAM //] CG10521 GH10173

CG10521 12F1-12F3 dup:1/2 ID:62C5

+ 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

+ unknown * similar to several putative T1/ST2receptor binding protein precursors(aa) * 3e-14 EM24_YEAST ENDOSOMAL

CG9308 P24B PROTEIN PRECURSOR (24 KD ENDOMEMBRANE P [EMP24_GP25L] CG9308 GH10235 58B9-58B9 ID:62C9

CG18069+ CaMKII protein_kinase proline rich calmodulin-dependent protein kinase PROTEIN_KINASE_DOM, pkinase CG18069 ID:62D9
 + cell_adhesion * 9e-05 tenascin-like protein precursor - fruit fly (Drosophila melanogaster) * 2e-47 C09F9.2 * 5e-06 Ten-m2 *
 CG12781 2e-05 predicted using hexExon; MAL3P2.1 [EGF_1 // EGF_2 // NLS_BP] CG12781 GH10539 59B4-59B4 dup:4/4 ID:62E10
 + 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
 + ligand_binding_or_carrier * 1e-22 YBE9_YEAST HYPOTHETICAL 16.1 KD PROTEIN IN SEC17-QCR1 INTERGENIC
 CG15309 REGION * 8e-21 putative zinc-binding protein melanogaste * 1e-18 No definitio CG15309 GH10478 9B6-9B6 dup:2/2 ID:62E4
 + tafazzin unknown * 2e-17 hypothetical protein YPR140w - yeast (Saccharomyces cerevisiae) (* 4e-39 ZK809.2 * 1e-59 tafazzin
 TFAZZIN * 2e-40 Similar to tafazzins prote [GLYCEROL_ACYLTRANS // TFAZZIN] CG8766 GH10529 49C1-49C1 dup:2/2
 CG8766 ID:62E9
 CG16979+ unknown * 3e-61 F38A5.1 gene product * 1e-40 putative protein * CG16979 GH10640 71D3-71D3 ID:62F11
 CG10433+ * [PRENYLATION] CG10433 57F3-57F3 dup:4/5 ID:62F12
 + ligand_binding_or_carrier * 2e-16 alpha tocopherol transfer protein * 1e-15 TTPA_RAT ALPHA-TOCOPHEROL TRANSFER
 CG13848 PROTEIN (ALPHA-TTP) al * tocopherol (alpha) transfer protein (ata [CRAL_TRIO] CG13848 GH10582 96E1-96E1 ID:62F2
 CG2267 + transcription_factor * CG2267 100A2-100A2 dup:2/2 ID:62F6
 + signal_transduction * protein(aa) * 1e-31 Sec7p * 2e-76 similar to S. cerevisiae protein transport protein SEC7 * 1e-38
 CG10577 cytohesin [SEC7 // Sec7 // NLS_BP] CG10577 GH10594 78B1-78B1 dup:1/2 ID:62F7
 + acj6 DNA_binding * DMIPOU_2 acj6 * POU domain transcription factor(aa) * INHIBITORY POU PROTEIN (I-POU)
 (ABNORMAL CHEMOSENSORY JUMP PROTEIN)(aa) * 1e-152 PP12_YEAST SE [HOMEBOX_1 // homeobox // HOMEBOX_2
 CG9151 //] CG9151 GH10637 13C1-13C4 ID:62F9
 + 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
 + cell_adhesion * DMARTAN_7 trn * kek1 * tartan protein(aa) * 5e-16 CYAA_YEAST ADENYLATE CYCLASE (ATP
 CG11280 PYROPHOSPHATE-LYASE) (ADENYLYL CYCLASE) [LRR // LEURICHRPT // LRRCT] CG11280 GH10871 69F5-69F5 ID:62H10
 + 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 * intermediate chain 1(aa) * nm23-H7(aa) * NUCLEOSIDE DIPHOSPHATE KINASE (NDK) (NDP KINASE)(aa) * 1e-
 CG8362 06 type nucleoside diphosphate kinase NM23-H6 CG8362 GH10857 85E4-85E4 ID:62H9
 + function_unknown * galactokinase 2(aa) * 2e-45 GAL1_YEAST GALACTOKINASE galactokinase (EC 2.7.1.6) - yea * 5e-35
 Similar to galactokinase * 2e-65 galactose kinase [GHMP_kinases // GALCTOKINASE // GHMP_KI] CG5288 GH11113 66E6-66E6
 CG5288 ID:63B10
 + 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
 CG14461+ unknown * CG14461 GH11047 79E1-79E1 ID:63B5
 CG7111 + Rack1 signal_transduction * Rack1 * GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN

(RECEPTOR OF ACTIVATED PROTEIN KINASE C HOMOLOG)(aa) * 3e-89 GBLP_YEAS[GPROTEINBRPT // WD40_REGION // WD_REPEA] CG7111 GH11320 28D2-28D2 dup:2/3 ID:63C12
 + enzyme * gamma-aminobutyric acid transaminase(aa) * PROBABLE 4-AMINO BUTYRATE AMINOTRANSFERASE, MITOCHONDRIAL PRECURSOR (GAMMA-AMINO-N-BUTYRATE TRANSAMINASE) CG7433 GH11161 76E2-76E2 dup:1/4
 CG7433 ID:63C3
 + PebIII ligand_binding_or_carrier * PebIII * 2e-48 ejaculatory bulb specific protein III * 2e-31 chemosensory protein CSP-sg1 *
 CG11390 olfactory protein CG11390 GH11257 60B1-60B1 ID:63C9
 + ion_channel * ATP-regulated potassium channel brain, Peptide Partial, * G PROTEIN-ACTIVATED INWARD RECTIFIER POTASSIUM CHANNEL (GIRK3) (POTASSIUM CHANNEL, INWARDL [CHANNEL_PORE_K // IRK] CG4370 GH11459 97D1-97D1 ID:63D11
 CG4370 97D1 ID:63D11
 + unknown * 1e-16 ERS1_YEAST TRANSMEMBRANE PROTEIN ERS1 (ERD SUPPRESSOR) ER * 6e-39 similarity to the transmembranous domains of yeast ERS1 protein; c * 5e-76 c [TONB_DEPENDENT_REC_1] CG17119 GH11342 94D12-94D12
 CG17119 ID:63D3
 + Dynein heavy chain at 93AB motor_protein DYNEIN BETA CHAIN, CILIARY ATP_GTP_A, MITOCH_CARRIER, NLS_BP,
 CG3723 THIOLE] CG3723 GH11420 ID:63D9
 + EG:25E8.1 chaperone * Similarity to HSP70's.; cDNA EST CEESD26F comes from this gene; cDNA EST CEMSB16F comes from this gene; cDNA EST CEMSB16FB comes from this gene; cDN [HEATSHOCK70 // HSP70 // HSP70_3] CG2918 GH11566 2F1-2F2 dup:2/2 ID:63E12
 CG2918 2F2 dup:2/2 ID:63E12
 + unknown * cold inducible glycoprotein 30(aa) * 5e-15 SUR4 * 8e-53 YYS3_CAEEL HYPOTHETICAL 51.5 KD PROTEIN IN CHROMOSOME IV (U * 2e-49 membrane glycoprotein CI CG3971 GH11554 73B1-77B1 dup:2/2 ID:63E9
 CG3971 73B1-77B1 dup:2/2 ID:63E9
 + unknown * cDNA EST comes from this gene; cDNA EST yk240b10.5 comes from this gene; cDNA EST yk339a6.3 comes from this gene; cDNA EST yk339a6.5 comes from this CG18176 GH11567 67C-67C ID:63F1
 CG18176 67C-67C ID:63F1
 + srp transcription_factor * GATA factor(aa) * DMGATAFAC_2 srp * 3e-12 GAT1_YEAST GAT1 PROTEIN probable membrane protein YFL02 * 2e-18 ELT1_CAEEL TRANSCRIPTION FACTOR[GATAZNFINGER // LECTIN_LEGUME_BETA // G] CG3992 GH11649 89B3-89B4 dup:2/5 ID:63F10
 CG3992 89B3-89B4 dup:2/5 ID:63F10
 + Cbp53E calcium_binding * DMCALB32A_2 Cbp53E * calbindin 2, (29kD, calretinin)(aa) * CALRETININ (CR)(aa) * CALBINDIN-32(aa) [EF_HAND // efhand // EF_HAND_2] CG6702 GH11671 53E7-53E10 ID:63F12
 CG6702 53E7-53E10 ID:63F12
 CG16959 + unknown * [EGF_2] CG16959 GH11627 71B2-71B2 dup:2/2 ID:63F7
 CG16959 71B2-71B2 dup:2/2 ID:63F7
 + 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
 CG5058 54F1-54F4 ID:63G1
 + motor_protein * 3e-08 hook1 protein * p230 peripheral membrane pr * autoantigen, subfamily a, > * CG14039 GH11749 25C3-25C3 dup:1/4 ID:63G11
 CG14039 25C3-25C3 dup:1/4 ID:63G11
 + 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 ID:63G12
 CG8815 49B2-49B3 dup:1/2 ID:63G12
 + endopeptidase * similar to the M13 or zinc metalloprotease family of peptidases(aa) * endothelin converting enzyme 1(aa) *
 CG9505 endothelin converting enzyme-2 - bovine [ZINC_PROTEASE // Peptidase_M13] CG9505 GH11680 28D1-28D1 ID:63G3

CG14355+ unknown * CG14355 GH11706 88A12-88B1 ID:63G5
 CG18107+ unknown * 1e-10 immune induced protein * 0.000000000002* 1E-141* CG18107 GH11719 55C9-55C9 ID:63G6
 + Nacalalphaunknown * 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
 + unknown * 1e-06 ectodermal (ect) - fruit fly (Drosophila melanogaster) (strain Oregon-R) * * [NLS_BP] CG6611 GH11838
 CG6611 67D2-67D2 ID:63H3
 + enzyme * DNA-DIRECTED RNA POLYMERASE II KD POLYPEPTIDE (RNA POLYMERASE II SUBUNIT 5)(aa) *
 CG6572 polymerase (RNA) II (DNA directed) polypeptide G(aa) * 7e-33 RPB7_ [S1] CG6572 GH11867 88E8-88E8 ID:63H5
 none + none GH11889 ID:63H7
 + BcDNA:GH07066 enzyme * 8e-47 PLSB_CAEEL PROBABLE GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE PRECURSOR
 (GPAT) * 6e-77 PLSB_MOUSE GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE PRECURSOR (G [GLYCEROL_ACYLTRANS]
 CG5508 CG5508 GH11892 98B2-98B2 dup:2/2 ID:63H8
 + zfh2 transcription_factor * ZINC-FINGER HOMEODOMAIN 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
 CG10286+ unknown * CG10286 GH12023 83E6-83E6 dup:1/2 ID:64A12
 + gbb signal_transduction * DM60AP * 60A PROTEIN PRECURSOR(aa) * 9e-17 contains similarity to the TGF-beta family of
 growth factors e * 3e-52 BMP7_MOUSE BONE MORPHOGENETIC PROT [TGFb_propeptide] CG5562 GH12092 60A5-60A5
 CG5562 ID:64B10
 + bnb unknown * DMBNBR_2 bnb * 1e-148 BNB_DROME BANGLES AND BEADS PROTEIN bangles and * GAP-43-related
 CG7088 protein - fruit fly (Drosophila melanogaster) * bnb gene prod CG7088 GH12078 17D6-17D6 ID:64B8
 + unknown * 1e-10 cDNA EST yk471b2.5 comes from this gene; cDNA EST yk471b2.3 come * * CG4742 GH12140 15A5-
 CG4742 15A5 ID:64C2
 + Hel89B DNA_binding * TBP-associated factor 172(aa) * Hel89B * 89B helicase(aa) * MOT1_YEAST PROBABLE HELICASE
 CG4261 MOT1 MOT1 protein - yeast (S [helicase_C // SNF2_N] CG4261 GH12153 89B3-89B3 dup:1/2 ID:64C3
 + unknown * 6e-05 transmembrane protein * 2e-12 Similarity to C.elegans cuticlin (SW:CUT1_CAEEL) * 7e-07 DMDUSKY_1
 CG3541 dy * similar to cuticlin CG3541 GH12163 60D7-60D8 dup:1/2 ID:64C4
 + emc transcription_factor * DNA-binding protein inhibitor Id-1H - human(aa) * EXTRA-MACROCHAETAE PROTEIN(aa) *
 DMEC3_3 emc * 7e-78 extramacrochaetae protein - fruit fly[HELIX_LOOP_HELIX // HELIX_LOOP_HELIX_2] CG1007 GH12170
 CG1007 61D1-61D2 dup:1/2 ID:64C5
 CG5291 + cell_adhesion CG5291 GH12331 dup:2/3 ID:64D5
 + 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
 CG4375 + unknown * CG4375 GH12486 21E2-21E2 dup:2/2 ID:64E10
 + cytoskeletal_structural_protein * putative protein transport protein sec7 homolog(aa) * DmCDS(aa) * pleckstrin and Sec7
 CG6941 domain protein(aa) * PROTEIN TRANSPORT [SPECTRINPH // PH // SEC7 // Sec7 // MIT] CG6941 GH12441 94B10-94B10

dup:2/2 ID:64E4
 + EG:100G10.1 unknown * SH3 domain-binding protein SNP70(aa) * by content; by match; LD Drosophila melanogaster...(aa) *
 CG2685 8e-06 WW domain binding protein * [PRO_RICH // NLS_BP] CG2685 GH12462 3B5-3B5 dup:3/3 ID:64E6
 + * membane-type metalloproteinase precursor(aa) * MATRIX METALLOPROTEINASE-14 PRECURSOR (MMP-14)
 (MEMBRANE-TYPE MATRIX METALLOPROTEINASE 1) (MT-MMP 1) [Peptidase_M10 // hemopexin // ZINC_PROT] CG1794
 CG1794 45F6-46A1 dup:4/5 ID:64E7
 + transporter * protein(aa) * DMATPA_2 Atp agr; * SODIUM/POTASSIUM-TRANSPORTING ATPASE ALPHA CHAIN
 (SODIUM PUMP) (NA+/K+ ATPASE)(aa) * BLASTX 3.4E-17 Rat alternativ [NAKATPASE // HATPASE // CATATPASE // E1]
 CG7651 CG7651 GH12627 79F3-79F3 ID:64F10
 + signal_transduction * 5e-23 VP27_YEAST VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS27 * 3e-10
 /match=(desc;; /ma * 9e-65 coded for by C. elegans cDNA yk21d11.3; coded [FYVE_DOMAIN // FYVE // HRS_DOMAIN] CG2903
 CG2903 GH12653 23A6-23A7 ID:64F12
 + 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
 + signal_transduction * Ras-binding protein SUR-8(aa) * 4e-25 adenylate cyclase * 9e-32 gene flightless-I protein - fruit fly
 CG5407 (Drosophila melanogaster) (* 1e-152 Ras-bindi [LRR // LEURICHRPT] CG5407 GH12617 90A6-92E12 ID:64F8
 + RNA_binding * BLASTX 2.0E-34 Arabidopsis thaliana Col-O putative RNA helicase A mRNA, complete cds.(dna) *
 DMMLE_2 mle * 1e-79 hypothetical protein YLR419w - yeas [PROTEIN_SPLICING // G_PROTEIN_RECEPTOR] CG9323
 CG9323 GH12763 38E5-38E5 ID:64G12
 + enzyme * diacylglycerol kinase(aa) * 2e-30 diacylglycerol kinase (EC 2.7.1.107) - fruit fly (Drosophila melanogaster) * 1e-57
 CG5875 alpha diacylglycerol kinase; a [DAG_PE_BINDING_DOMAIN // RA // C1 // DA] CG5875 GH12677 95D1-97F1 dup:2/5 ID:64G5
 CG10806+ transporter * protein:Na+/H+ antiporter(aa) * cdu2(aa) * cdu2 cd * CG10806 GH12682 27C-27C ID:64G6
 + 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
 + unknown * androgen-induced prostate proliferative shutoff associated protein(aa) * protein(aa) * 1e-28 unknown * 6e-40
 CG17509 cDNA EST comes from this gene elegan CG17509 GH12788 48E2-48E2 dup:3/3 ID:64H3
 CG13918+ unknown * CG13918 GH13002 62A-62A ID:65A12
 + structural_protein * 9e-09 cuticle protein LCP65Ac cuticle p * 2e-11 CUD4_LOCFMI ENDOCUTICLE STRUCTURAL
 GLYCOPROTEIN (ABD-4A) g * 1e-10 Lcp65Ac * cuticle homolog [CUTICLE // insect_cuticle] CG8511 GH12964 49A3-49A3
 CG8511 ID:65A9
 + 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
 CG7549 + unknown * [HTH_LACI_FAMILY] CG7549 GH13023 84F-84F ID:65B2
 + protein_kinase * serine/threonine kinase(aa) * predicted using Genefinder; Similarity to Arabidopsis serine/threonine protein
 kinase [PIR Acc. No. cDNA EST comes f [PROTEIN_KINASE_ST // TYRKINASE // PROTE] CG6114 GH13047 72A5-72B1
 CG6114 ID:65B6

CG6123 + unknown * [NLS_BP] CG6123 GH13094 17A7-17A7 ID:65B9
 CG18065+ unknown * CG18065 GH13245 57A8-57A8 ID:65C11
 + transcription_factor * Pcaf SPTR(aa) * CREB-BINDING PROTEIN(aa) * HAT A1(aa) * 5.9 kb fsh membrane protein(aa)
 CG7229 [BROMODOMAIN_2 // BROMODOMAIN_1 // bromo] CG7229 GH13144 56C-56C ID:65C2
 + unknown * No definition line found(aa) * 4e-06 probable membrane protein YPR091c - yeast (*Saccharomyces cerevisiae*) *
 CG5741 6e-43 No definition line found * 3e-05 h CG5741 GH13177 66E4-66E4 ID:65C6
 + enzyme * 2e-20 alpha-alpha-trehalase * 1e-102 similar to family glycosyl hydrolases; most similar to trehalase * 1e-124
 TREA_HUMAN TREHALASE PRECURSOR (ALPHA [Trehalase // TREHALASE_1 // GLHYDRLASE3] CG9364 GH13461 57B20-
 CG9364 57C dup:4/4 ID:65D10
 CG14889+ structural_protein * [COLLAGEN_REP // Collagen] CG14889 GH13492 92A1-92A1 dup:1/2 ID:65D11
 + * ribokinase(aa) * ribokinase RbsK(aa) * DMC115C2 * 1e-71 /match=(desc;; /ma [pfkB // PRO_RICH // RIBOKINASE]
 CG17010 CG17010 33D3-33D3 dup:2/2 ID:65D12
 + 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
 CG13784+ unknown * CG13784 GH13387 27E4-27E5 ID:65D3
 + enzyme * 1-PYRROLINE-5-CARBOXYLATE DEHYDROGENASE (P5C DEHYDROGENASE)(aa) * UNKNOWN(aa) *
 Similar to aldehyde dehydrogenase; coded for by *C. elegans* cDNA cm1 [aldedh // NLS_BP] CG6670 GH13449 93F-93F10 dup:2/2
 CG6670 ID:65D9
 + cytoskeletal_structural_protein * 2e-47 dystrophin * 1e-117 unnamed protein product * 1e-143 dystrobrevin dystrobrevin * 1e-
 CG8529 143 dystrobrevin B [ZF_ZZ // ZZ // CYTOCHROME_C] CG8529 GH13689 49A6-49A7 dup:2/2 ID:65E12
 + enzyme * peritrophin-95 precursor(aa) * 4e-29 triacylglycerol lipase (EC 3.1.1.3) precursor, pancreatic - mouse * 2e-29
 CG6296 lipase * 7e-31 pdb[1BU8] Rat Pancrea [DOLALLERGEN // TAGLIPASE // ESTERASE //] CG6296 100D1-100D1 dup:2/2 ID:65E4
 + Pka-C3 protein_kinase * PROTEIN KINASE DC2(aa) * DMDC2_2 Pka-C3 * 5e-88 cAMP-dependent protein kinase subunit (put.);
 CG6117 putative * 2e-99 KAPC_CAEEL CAMP-DEPENDENT PROTEIN KIN CG6117 GH13608 72B1-72B2 dup:3/3 ID:65E5
 CG18227+ CG18227 dup:2/2 ID:65E6
 + Cyp4e1 cytochrome_P450 * cytochrome P450, Cyp4e2 - fruit fly (*Drosophila melanogaster*) (U5 * 6e-79 predicted using
 Genefinder; similar to cytochrome P450 * 3e-50 CYP4B1 [EP450II // p450 // P450 // MITP450 // C] CG2062 GH13635 44C1-44C2
 CG2062 dup:2/2 ID:65E8
 + transporter * furosemide-sensitive K-Cl cotransporter(aa) * BLASTX 7.2E-55 *Rattus furosemide-sensitive K-Cl cotransporter*
 (KCC2) mRNA, complete cds.(dna) * 6e-49 [AMINO_ACID_PERMEASE_2 // KCLTRANSPORT] CG5594 GH13642 60A9-60A10
 CG5594 dup:4/5 ID:65E9
 + structural_protein * 8e-30 YLS5_CAEEL HYPOTHETICAL 55.1 KD PROTEIN F09G8.5 IN CHROMOSOME III * 2e-07 B7 *
 CG14995 6e-36 chromosome open reading frame 28.3 KD PROTEIN C21OR * 8e- [LRR] CG14995 GH13848 64A7-64A8 dup:3/3 ID:65F12
 + unknown * similar to *Arabidopsis thaliana* male sterility protein * 3e-52 /match=(desc;; /ma * 3e-32 male sterility 2-like protein
 CG1441 * 3e-54 DMC103B4 CG1441 GH13752 46C5-46C5 ID:65F4

+ unknown * SMC2orf(aa) * CD2 antigen (cytoplasmic tail)-binding protein 2(aa) * 1e-08 YHV6_YEAST HYPOTHETICAL 40.4
 CG5198 KD PROTEIN IN SPO16-REC104 INTERGENIC REGIO CG5198 GH13760 33D1-33D1 ID:65F7
 + unknown * 4e-14 probable membrane protein YOL084w - yeast (Saccharomyces cerevisiae) * 1e-103 protein * 6e-17
 CG11210 hypothetical protein * 3e-54 inserted at base Bo CG11210 GH13794 44A4-44A4 ID:65F9
 + signal_transduction * cDNA EST comes from this gene; cDNA EST comes from this gene; cDNA EST comes from this gene;
 CG8683 cDNA EST comes from this gene; cDNA EST comes from thi CG8683 GH13975 28E5-28E6 dup:2/3 ID:65G12
 + cell_adhesion * coded for by C. elegans cDNA yk9a2.5; coded for by C. elegans cDNA yk9a2.3; similar to fibrinogen-like
 CG6676 protein A precursor(aa) * 3(aa) * FIBRINOGEN [FIBRIN_AG_C_DOMAIN // fibrinogen_C] CG6676 GH13859 58C2-58C2 ID:65G3
 + enzyme * putative dehydrogenase(aa) * GLYCERATE DEHYDROGENASE (NADH-DEPENDENT HYDROXYPYRUVATE
 REDUCTASE) (HPR) (GDH) (HYDROXYPYRUVATE DEHYDROGENASE) (GLYOXYL [D_2_HYDROXYACID_DH_3 // 2-
 CG9331 Hacid_DH] CG9331 GH13879 38E9-38E9 ID:65G4
 + transporter * transmembrane transporter - electric ray (Discopyge ommata)(aa) * 1e-09 HXT3_YEAST LOW-AFFINITY
 GLUCOSE TRANSPORTER HXT3 hexose t * 2e-14 putative o [SUGAR_TRANSPORT_1 // SUGAR_TRANSPORT_2] CG3168
 CG3168 GH13883 6C9-6C10 ID:65G5
 + Cyp6a2 cytochrome_P450 * PUTATIVE CYTOCHROME P450 T10B9.7 IN CHROMOSOME II(aa) * DMCYP6A2A_5 Cyp6a2 *
 CYP6A2 * 3e-43 similar to cytochrome P450 [EP450II // MITP450 // CYTOCHROME_P450 /] CG9438 GH13965 42C5-42C5
 CG9438 ID:65G9
 CG15390+ unknown * CG15390 GH14074 22E-22E ID:65H11
 CG3372 + unknown * CG3372 GH14065 60C1-60C1 ID:65H8
 + rb chaperone * beta3 * Beta3 protein(aa) * 2e-50 beta-adaptin protein * 2e-78 cDNA EST yk288h5.5 comes from this gene;
 CG11427 cDNA EST yk288f1.5 comes CG11427 GH14079 4C4-4C4 ID:66A1
 + chaperone * hypothetical protein(aa) * 3e-22 YB96_YEAST HYPOTHETICAL 43.3 KD PROTEIN IN ALG7-ENP1
 CG3184 INTERGENIC REGION * WD-40 repeat protein * [WD40_REGION // WD40] CG3184 GH14157 6C7-6C7 ID:66A12
 + Prm motor_protein * DMSTPMY_2 Prm * 7e-13 integrin homolog - yeast (Saccharomyces cerevisiae) * MYSP_DROME
 CG5939 PARAMYOSIN, LONG FORM paramyosin, standard - f * 1e-179 Sili [NLS_BP] CG5939 GH14085 66D-66D ID:66A3
 + Gs2 enzyme * GLUTAMINE SYNTHETASE 2, CYTOPLASMIC (GLUTAMATE--AMMONIA LIGASE 2)(aa) * GLUTAMINE
 SYNTHETASE (GLUTAMATE--AMMONIA LIGASE)(aa) * glutamine synthetase [GLNA_1 // gln-synt // GLNA_ATP] CG1743
 CG1743 GH14412 10B13-10B14 dup:1/2 ID:66C10
 + Sox14 DNA_binding * DMDSOX14 Sox14 * putative(aa) * POP-1 PROTEIN(aa) * SOX-2(aa) [HMG // HMG_box // NLS_BP]
 CG3090 CG3090 GH14320 60A14-60A14 dup:1/3 ID:66C2
 + 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
 CG11871+ unknown * CG11871 GH14385 86A1-86A1 ID:66C8
 CG17919+ ligand_binding_or_carrier * 5e-13 DKA1_YEAST DKA1 PROTEIN (NSP1 PROTEIN) (TFS1 PROTEIN) DKA * 3e-44

OBA5_DROME PUTATIVE ODORANT-BINDING PROTEIN A5 PRECURSOR (ANTENNAL PROTEIN 5 [PBP] CG17919 GH14494 83E-83E ID:66D10

CG9813 + unknown * [ATPASE_ALPHA_BETA] CG9813 GH14502 87E8-87E9 dup:1/2 ID:66D11
none + none GH14469 ID:66D6
+ E(Pc) unknown * 3e-15 YFC4_YEAST HYPOTHETICAL 96.7 KD PROTEIN IN STE2-FRS2 INTERGENIC REGION * enhancer
CG7776 of polycomb * 2e-67 enhancer of polycomb * E(Pc) [NLS_BP] CG7776 GH14582 47F15-47F15 dup:5/6 ID:66E10
+ transporter * DMORCT2_2 Orct * organic cation transporter(aa) * Similarity to Rat organic cation transporter cDNA EST
CG7084 comes from this gene; cDNA EST comes from [sugar_tr] CG7084 GH14589 94A11-96D1 dup:2/2 ID:66E11
+ Con cell_adhesion * DMCONNECTN_1 Con * 1e-180 cell-surface molecule connectin - fruit fly (Drosophila melanogaster) * 3e-
CG7503 15 coded for by C. elegans cDNA yk132e5.5; coded [LRR // LRRCT] CG7503 GH14524 64C6-64C7 dup:2/2 ID:66E2
CG9321 + unknown * [ATP_GTP_A] CG9321 GH14542 29E4-29E4 dup:3/3 ID:66E4
+ unknown * 2e-24 cDNA EST CEMSE83F comes from this gene; cDNA EST comes * * CG16791 GH14545 93D6-93D6
CG16791 dup:3/3 ID:66E5
+ Rpn6 endopeptidase * 26S proteasome subunit p44.5(aa) * BLASTX 3.9E-25 YDL097C|Protein of unknown function(dna) * 2e-
CG1014990 hypothetical protein YDL097c - yeast (Saccharomyc [PCI_DOMAIN // PCI] CG10149 GH14689 51C2-51C2 ID:66F12
CG1277 + unknown * CG1277 GH14618 82E2-82E2 ID:66F2
+ signal_transduction * cAMP-dependent Rap1 guanine-nucleotide exchange factor(aa) * HYPOTHETICAL 139.4 KD
PROTEIN T20G5.5 IN CHROMOSOME III(aa) * 2e-07 KAPR_YEAST [cNMP_binding // RasGEF // DEP_DOMAIN //] CG3427
CG3427 GH14655 42C4-42D1 dup:2/3 ID:66F8
+ enzyme * 2e-15 FOX2_YEAST PEROXISOMAL HYDRATASE-DEHYDROGENASE-EPIMERASE (HDE)
(MULTIFUNCTIONAL * 4e-14 3-hydroxyacyl-CoA dehydrogenase type II * 3e-42 strong [GDHRDH // adh_short] CG3603 GH14791
CG3603 3C5-3C5 ID:66G11
CG11960+ unknown * [NLS_BP] CG11960 GH14769 56D8-56D8 dup:1/2 ID:66G8
+ transcription_factor * ZINC-FINGER PROTEIN (ZINC-FINGER HOMEODOMAIN PROTEIN 1)(aa) * DMDROSOPH_4 wdn *
transcriptional repressor(aa) * DMBTDGN_2 btd [zf-C2H2 // ZINC_FINGER_C2H2 // ZINC_FIN] CG8591 GH14774 65F4-65F4
CG8591 ID:66G9
+ unknown * hypothetical protein(aa) * similar to human 5'-nucleotidase * Unknown(aa) * 6e-46 similar to human 5'-
CG1814 nucleotidase CG1814 GH14884 45F4-45F4 ID:66H7
+ boss G_protein_linked_receptor * DMBRSEVM_5 boss * BOSS_DROME BRIDE OF SEVENLESS PROTEIN PRECURSOR
CG8285 (X558 * 4e-06 CELF35-1 * 2e-07 Unknown gene product CG8285 GH14887 96F9-96F9 dup:2/2 ID:66H8
+ * cDNA EST yk335d8.5 comes from this gene; cDNA EST yk335d8.3 comes from this gene(aa) * 2e-23 cDNA EST
CG4972 yk335d8.5 comes from this gene; cDNA EST yk335 CG4972 31D7-31D8 dup:2/2 ID:67A10
+ endopeptidase * Ypl125wp(aa) * possible RanBP7-importin-beta-Cse1p superfamily(aa) * 1e-36 hypothetical protein
YPL125w - yeast (Saccharomyces cerevisiae) (* 1e-[trypsin // CHYMOTRYPSIN // IBN_NT // TR] CG8212 GH15020 52C-52C
CG8212 dup:1/2 ID:67A11
CG15512+ unknown * CG15512 GH14951 99C7-99C7 dup:2/4 ID:67A3

+ transporter * 1e-09 myo-inositol transporter * 5e-13 GTRL_DROME GLUCOSE TRANSPORTER-LIKE PROTEIN glucose
 transpo * 1e-08 Similar to sugar transporter; coded for b [N4_MTASE // SUGRTRNSPORT // SUGAR_TRANS] CG3285 GH15136
 CG3285 25A1-25A1 ID:67B12
 + 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 // TCOMPLEX] CG7033 GH15038
 CG7033 8C13-8C13 dup:2/2 ID:67B3
 + alpha-Est2 enzyme * alpha esterase(aa) * agr;-Est2 * carboxylesterase MdaE7(aa) * alpha esterase [CHOLNESTRASE //
 CG2505 ESTERASE // COesterase] CG2505 GH15053 84D6-85A3 ID:67B5
 CG16707+ platelet glycoprotein Ib-alpha CG16707 GH15083 dup:1/2 ID:67B8
 CG18369+ unknown * CG18369 GH15231 50B9-50B9 ID:67C11
 + 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
 + transcription_factor * chromatin structural protein homolog Supt5hp(aa) * suppressor of Ty (S.cerevisiae) homolog(aa) * 9e-
 CG7626 59 SPT5_YEAST TRANSCRIPTION INITIATION PROTEIN CG7626 GH15359 56D7-56D7 dup:4/5 ID:67D10
 + transcription_factor * cDNA EST comes from this gene; cDNA EST comes from this gene; cDNA EST comes from this gene;
 cDNA EST comes from this gene; cDNA EST yk270e3.3 come [HELIX_LOOP_HELIX // LIPASE_SER] CG5455 GH15286 97B2-
 CG5455 97B2 dup:2/3 ID:67D4
 + th apoptosis_inhibitor * DMDIAP1X_3 th * APOPTOSIS INHIBITOR (INHIBITOR OF APOPTOSIS 1) (DIAP1) (THREAD
 PROTEIN)(aa) * 2e-05 similar to Zinc finger, C3HC4 type (RIN[zf-C3HC4 // BIR // BIR_REPEAT // BIR_RE] CG12284 GH15335
 CG12284 72D1-72D1 dup:2/3 ID:67D8
 CG11451+ signal_transduction * 1e-06 fimbriae-associated protein Fap1 * * [NLS_BP] CG11451 GH15349 77E-77E8 dup:1/2 ID:67D9
 + pn signal_transduction * PRUNE protein(aa) * DMPRUNEG_2 pn * 1e-16 PPX1_YEAST EXOPOLYPHOSPHATASE
 CG3461 (METAPHOSPHATASE) exopolyph * PRUNE protein CG3461 GH15456 2E1-2E1 dup:2/2 ID:67E10
 CG18437+ unknown * CG18437 GH15426 98A6-98A6 dup:2/2 ID:67E2
 + enzyme * 1e-12 FOX2_YEAST PEROXISOMAL HYDRATASE-DEHYDROGENASE-EPIMERASE (HDE)
 (MULTIFUNCTIONAL * 0.000000000000002* 2e-26 predicted using Genefinder; Similar [GDHRDH // adh_short // ADH_SHORT]
 CG17121 CG17121 GH15451 94D12-94D12 dup:2/2 ID:67E8
 + protein_kinase * Pak * 2e-89 STE20 * 2e-99 serine/threonine kinase PAK homolog DPAK * 8e-93 similar to serine/threonine-
 CG14895 protein kinase [PROTEIN_KINASE_ST // TYRKINASE // pkina] CG14895 GH15507 89C4-89C4 ID:67F10
 CG8420 + * [ER_TARGET] CG8420 85D2-85D3 dup:3/3 ID:67F12
 CG14178+ CG14178 GH15480 ID:67F6
 + receptor * kDa thyroid hormone receptor associated protein(aa) * 1e-88 thyroid hormone receptor-associated protein
 CG7999 complex component TRAP100 sa * The gene is r [NLS_BP] CG7999 GH15490 66B13-66C ID:67F8
 + transcription_factor * ash1 * polybromo protein - chicken(aa) * DMFSHA_2 fs(1)h * similar to HMG (high mobility group) box,
 CG11375 Bromodomain (5 domains), Zinc finger, C2H2 [BROMODOMAIN_2 // BAH // HMG // HMG_box] CG11375 98E1-98E1 dup:1/2

ID:67G4

+ EG:66A1.3 unknown * by match; LD Drosophila melanogaster embryo BlueScript Drosophila melanogaster cDNA clone 5prime.;
CG12184 1-match_species=Drosophil...(aa) * map_position:4 [PRO_RICH] CG12184 GH15731 4C6-4C6 dup:1/2 ID:67H9
CG7742 + unknown * [TBC // RAB_GAP] CG7742 GH15768 25C9-25C9 ID:68A4
+ enzyme * F1F0-ATP synthase g subunit(aa) * 9e-14 ATPN_CAEEL PUTATIVE ATP SYNTHASE G CHAIN,
CG6105 MITOCHONDRIAL * 3e-24 F1F0-type ATP synthase subunit g * 4e-25 AT CG6105 GH15786 32C5-32C5 dup:1/2 ID:68A6
+ transmembrane_receptor * DMEMP_3 emp * DMCD362_2 croquemort * 9e-18 epithelial membrane protein - fruit fly
CG2736 (Drosophila melanogaster) * 8e-15 mLGP85/LIMP II [CD36] CG2736 GH15894 60E7-60E7 ID:68B4
CG16820+ unknown * CG16820 GH15921 34A11-34A11 dup:2/2 ID:68B9
+ enzyme * DMACOASYN_2 AcCoAS * 6e-96 ACS1_YEAST ACETYL-COENZYME A SYNTHETASE (ACETATE--COA
LIGASE 1) (ACYL-ACTIVATI * 1e-81 acetyl-CoA synthetase - fruit fly [AMP-binding] CG6432 GH15945 98B1-98B1 dup:1/2
CG6432 ID:68C1
+ cytoskeletal_structural_protein * 8e-19 protein * sorting nexin * Y254_HUMAN HYPOTHETICAL PROTEIN KIA *
CG1514 [BEM_DOMAIN // GRK] CG1514 GH16154 7C8-7C8 ID:68C11
CG14477+ unknown * CG14477 54B16-54B17 ID:68C6
+ transporter * K05B2.5 gene product(aa) * 1e-13 YKW1_YEAST HYPOTHETICAL 52.3 KD PROTEIN IN FRE2 5'REGION *
CG8468 2e-82 /match=(desc;; /ma * 1e-40 predicted using Genefin CG8468 GH16148 50E-50E7 dup:2/5 ID:68C9
+ BG:DS03431.1 neurotransmitter_transporter * 1e-101 neurotransmitter transporter * 2e-86 similar to the sodium:neurotransmitter
symporter family (SNF) * 1e-104 NTGL_MOUSE SODIUM-[NANEUSMPORT // NA_NEUROTRAN_SYMP_3 // S] CG15279
CG15279 GH16161 35B7-35B7 ID:68D1
+ unknown * 1e-109 weak similarity to Bacillus and Pseudomonas probable glucarate transporters (G * 2e-06 conserved
CG1358 hypothetical protein * 2E-46* C05G5.1 CG1358 GH16188 43E3-43E4 dup:2/2 ID:68D3
+ * ZRP protein(aa) * 4e-10 hypothetical protein YDR299w - yeast (Saccharomyces cerevisiae) (U * 3e-26 ZRP protein * 2e-06
CG11188 inserted at base Both 5' and [NLS_BP] CG11188 27A1-27A1 dup:2/2 ID:68D6
+ unknown * 5e-08 myosin phosphatase, target subunit (A * 1e-07 PP1M M21 subunit=protein phosphatase 1M kda regulatory
CG5600 subunit * myosin phosphatase, target subu CG5600 GH16214 72D3-72D4 dup:2/4 ID:68D7
+ drongo signal_transduction * drongo * 9e-25 Drongo * 4e-12 HIV-1 Rev binding protein NUCLEOPO * 1E-151 [ArfGap // ZF_GCS
CG3365 // REVINTRACTNG] CG3365 GH16240 21D2-21E3 dup:2/2 ID:68D8
+ Anxb11 actin_binding * annexin IV(aa) * ANNEXIN IV (LIPOCORTIN IV) (36 KD ZYMOGEN GRANULE MEMBRANE
ASSOCIATED PROTEIN) (ZAP36)(aa) * DMANNIX AnniX * annexin max4(aa) [ANNEXINVI // ANNEXINIV // ANNEXIN // an]
CG9968 CG9968 GH16395 14C5-14C6 dup:3/3 ID:68E11
+ Cyp4g15 cytochrome_P450 * Cyp4e2 * CYTOCHROME P450 4C1 (CYPIVC1)(aa) * 2e-13 CP51_YEAST CYTOCHROME P450
(CYPL1) (P450-L1A1) (STEROL 14-ALPHA DEMETHYLASE) * 1E-151 [EP450II // p450 // P450 // CYTOCHROME_P] CG11715
CG11715 GH16320 10B15-10B17 dup:2/2 ID:68E2
CG18111+ unknown * 4e-10 male-specific protein * * CG18111 GH16332 99B-99B dup:2/2 ID:68E4
+ motor_protein * receptor-associated protein(aa) * 9e-14 predicted using Genefinder; Similarity to Human alpha-2-
CG8507 macroglubu * 2e-16 heparin binding protein * 5e-18 CG8507 GH16343 86D1-86D1 dup:3/3 ID:68E5

+ protein_kinase * protein kinase C, mu(aa) * DMPKC98F_2 Pkc98E * protein kinase C, mu(aa) * 6e-42 DUN1_YEAST DNA
 DAMAGE RESPONSE PROTEIN KINASE DUN1 protei [DAG_PE_BINDING_DOMAIN // PROTEIN_KINASE] CG7125 GH16373
 CG7125 90F8-90F9 dup:3/3 ID:68E7
 + * 3e-30 No definition line found * 5e-48 SCF complex protein Skp2 * 1e-42 S-phase kinase-associated protein (p45) cyclin
 CG9772 A/CDK2-associate * YKK7_CAEF FBOX_DOMAIN CG9772 ID:68F1
 CG12191 + cell_adhesion * 8e-05 adhesion molecule L1.1 * [ig] CG12191 GH16485 61D4-61D4 ID:68F12
 + unknown * 9e-36 by content; 1-meth * 1e-43 YS15_CAEEL HYPOTHETICAL 41.1 KD PROTEIN IN CHROMOSOME II * 1e-
 CG3881 42 Sqv-8-like protein * 7e-47 UDP-glucuronyltransfera CG3881 GH16433 30C2-30C2 ID:68F5
 CG15068 + CG15068 GH16622 ID:68G10
 + RNA_binding * pit * 2e-78 SPB4_YEAST ATP-DEPENDENT RRNA HELICASE SPB4 RNA helicase S * 2e-69 helicase
 pitchoune * 8e-87 YOQ2_CAEEL PUTATIVE ATP-DEPENDENT RNA HELI [helicase_C // HELICASE // DEAD // NLS_B] CG9630
 CG9630 GH16590 84F-84F ID:68G6
 + ligand_binding_or_carrier * FGF intracellular binding protein(aa) * FGF-1 intracellular binding protein * CG8660 GH16593
 CG8660 76D3-76D3 ID:68G7
 + * DMWHEELER_2 18w * DMCOP10_2 chp * 1e-20 leucine-rich motif (LRR) protein homology to interleukin receptor cy * 2e-
 CG11910 16 coded for by C. elegans cDNA yk [LRR] CG11910 96D2-96D2 dup:2/2 ID:68G8
 + enzyme * Similar to calcium channel subunit; coded for by C. elegans cDNA yk19b1.5; coded for by C. elegans cDNA
 CG6320 yk47a5.3; coded for by C. elegans cDNA yk47a [Ca_channel_B // SH3 // ATP_GTP_A] CG6320 GH16612 32D5-32D5 ID:68G9
 CG11341 + CG11341 ID:68H10
 + enzyme * pharbin(aa) * 7e-35 YNK6_YEAST HYPOTHETICAL 133.3 KD PROTEIN IN CYB5-LEU4 INTERGENIC REGION *
 CG10426 2e-31 /match=(desc;; /ma * 4e-17 similar to Inositol p [IPPC // PRENYLATION] CG10426 GH16681 69A3-69A3 ID:68H4
 chimera + chimera GH16723 ID:68H7
 CG4230 + unknown * CG4230 GH16729 25C-25C ID:68H8
 + enzyme * GLUTATHIONE S-TRANSFERASE YRS-YRS (GST 12-12) (GLUTATHIONE S-TRANSFERASE SUBUNIT 12)
 CG1681 (CLASS-THETA)(aa) * glutathione S-transferase theta 2(aa) * 5e- [GST] CG1681 GH16740 11F1-11F1 ID:68H9
 + RfaBp unknown * retinoid- and fatty acid-binding glycoprotein * 1e-15 C. elegans vitellogenin precursor, vit-5 (Spieth et al., NAR
 CG11064 * 4e-07 prepro-vWF (aa -22 to 137 [vwd // Vitellogenin_N // NLS_BP] CG11064 GH18004 102F4-102F4 ID:70A10
 + enzyme * methylenetetrahydrofolate reductase(aa) * 5e-09 YGM5_YEAST HYPOTHETICAL 68.5 KD PROTEIN IN SCS3-
 CG7560 SUP44 INTERGENIC REGION * 2e-14 methylenetetrahydro CG7560 GH18008 68C2-68C2 ID:70A11
 + 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
 CG4983 + DNA_repair_protein * CG4983 GH17939 33A5-33A5 ID:70A4
 + enzyme * MALEYLACETOACETATE ISOMERASE (MAAI)(aa) * glutathione transferase zeta 1(aa) * 6e-50 similar to
 CG9363 glutathione S-transferase * 3e-05 GTC_MOUSE GLUTATHI [GST] CG9363 GH17960 85D18-85D18 ID:70A5
 + tko ribosomal_protein * 2e-21 YN8K_YEAST PUTATIVE 40S MITOCHONDRIAL RIBOSOMAL PROTEIN YNR036C * 2e-76
 CG7925 RT12_DROME MITOCHONDRIAL 40S RIBOSOMAL PROTEIN S12 PRECURSOR (TECHNICA [RIBOSOMAL_S12 //

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
+ enzyme * 3e-53 Weak similarity to Potato alcohol dehydrogenase (SW:ADH_SULSO); cD * 7e-06 QOR_MOUSE QUINONE
CG1600 OXIDOREDUCTASE (NADPH:QUINONE REDUCTASE) (ZETA-CR [adh_zinc] CG1600 GH18014 43D3-43D3 ID:70B1
CG3835 + EG:87B1.3 actin_binding * * alkylglycerone phosphate synthase precursor(aa) * DMC87B1 CG3835 GH18028 2D4-2D6 ID:70B4
+ 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
CG18403 + very low density lipoprotein receptor - mouse CG18403 ID:70B7
+ BcDNA:GH06717 transporter * OLIGOPEPTIDE TRANSPORTER, KIDNEY ISOFORM (PEPTIDE TRANSPORTER 2) (KIDNEY
H+/PEPTIDE COTRANSPORTER)(aa) * OLIGOPEPTIDE TRANSPORTER, KIDNEY ISOFORM (P [PTR2 // PTR2_1 // PTR2_2]
CG2930 CG2930 GH18049 4A1-4A1 dup:2/3 ID:70B9
+ * 2e-09 SUR4_YEAST SUR4 PROTEIN (SRE1 PROTEIN) SUR4 protein - yea * 2e-13 predicted using Genefinder; similar to
CG12138 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 Na(+)/Cl(-
CG15444)-dependent GABA transporter (SW:NTG [NANEUSMPORT // SNF] CG15444 GH18083 24F6-24F6 ID:70C4
+ enzyme_inhibitor * RNase L inhibitor (clone 8) - human(aa) * probable membrane protein YDR091c - yeast (Saccharomyces
cerevisiae) * 3e-07 P-glycoprotein/multidrug resi [fer4 // ATP_GTP_A2 // ABC_TRANSPORTER /] CG5651 GH18088 66E5-66E5
CG5651 ID:70C5
+ 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
+ peptidase * 5e-60 putative metalloprotease; Method: conceptual translation supplied by author * 1e-23 coded for by C.
CG8196 elegans cDNA yk27b10.3; coded for by C. el [PEPDIPTASEA // Peptidase_M2] CG8196 GH18145 45A6-45A6 ID:70D1
+ msta unknown * /match=(desc:(aa) * map_position:2E3 * 7e-06 t-BOP * 5e-13 putative Bop-like zinc finger protein CG18033
CG18033 GH18166 2E2-2E2 dup:2/2 ID:70D4
+ * NADP-dependent isocitrate dehydrogenase(aa) * 1e-148 IDHP_YEAST ISOCITRATE DEHYDROGENASE (NADP),
CG7176 MITOCHONDRIAL PRECURSOR (OXALOSUCCIN * 1e-180 simil [IDH_IMDH // isodh] CG7176 66C8-66C8 dup:3/4 ID:70D6
+ actin_binding * protein(aa) * Similarity to Drosophila ring canal protein cDNA EST comes from this gene; cDNA EST comes
CG15097 from this gene(aa) * 1e-116 kelch protein, I [BTB // KELCHREPEAT // Kelch] CG15097 GH18278 55F2-55F3 dup:2/2 ID:70E1
+ defense/immunity_protein * 3e-13 peptidoglycan recognition protein precursor * 4e-17 TNF superfamily, member (LTB)-like
CG4384 (peptidoglycan recognition * 8e-17 cuticular molt prote CG4384 67A8-67A8 dup:3/3 ID:70E2
+ RNA_binding * putative RNA binding protein(aa) * 3e-05 TUD_DROME MATERNAL TUDOR PROTEIN posterior-group
protein t * 8e-07 YQK1_CAEEL HYPOTHETICAL 55.9 KD PROTEIN [KH-domain // KH_DOMAIN // TUDOR] CG7082 GH18329
CG7082 23D1-23D1 dup:3/3 ID:70E4
CG9520 + unknown CG9520 dup:5/5 ID:70E7

CG5835 + unknown * CG5835 GH18370 91F4-91F4 dup:2/2 ID:70E9
+ unknown * 4e-05 BE46_MOUSE BRAIN PROTEIN E46 gene E46 protein - mouse * * CG4975 GH18454 54E5-54E5
CG4975 ID:70F8
+ RNA_binding * mus308 * Ygr271wp(aa) * similar to Helicases conserved C-terminal domain; cDNA EST comes from this
CG5205 gene; cDNA EST yk430a5.5 comes from this gene; cD [HELICASE // DEAD // ATP_GTP_A] CG5205 GH18520 88F6-88F6 ID:70G1
+ enzyme * ubiquitin fusion degradation protein; Ufd1p(aa) * UBIQUITIN FUSION DEGRADATION PROTEIN HOMOLOG (UB
CG6233 FUSION PROTEIN 1)(aa) * 2e-47 UFD1_YEAST UBIQUITI CG6233 GH18603 70E3-70E3 ID:70G10
+ enzyme * secretory component(aa) * mollusk-derived growth factor; MDGF * AGSA_APLCA ATRIAL GLAND-SPECIFIC
CG10143 ANTIGEN PRECURSOR (AGSA) * [NLS_BP // A_deaminase] CG10143 GH18530 51B10-51B10 ID:70G4
+ Cyp28a5 cytochrome_P450 * CYP6A2(aa) * cytochrome P450 monooxygenase CYP28A1(aa) * 6e-37 YS24_CAEEL PUTATIVE
CYTOCHROME P450 IN CHROMOSOME II * 5e-40 cytochrome P450 3A[EP450II // p450 // P450 // EGF_2 // MIT] CG8864
CG8864 GH18601 34E2-34E2 dup:1/2 ID:70G9
+ 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 //
CG7995 FGG] CG7995 GH18690 62B1-62B1 dup:2/3 ID:70H9
+ unknown * GAGA-581 Adf-2 isoform(aa) * FEMALE STERILE HOMEOTIC PROTEIN (FRAGILE-CHORION MEMBRANE
CG7417 PROTEIN)(aa) * * [PRO_RICH // NLS_BP] CG7417 GH18828 56C9-56C10 dup:1/2 ID:71A2
+ 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-09 ATPK_CAEEL PUTATIVE ATP SYNTHASE F CHAIN, MITOCHONDRIAL * 3e-10 ATPK_MOUSE ATP
CG4692 SYNTHASE F CHAIN, MITOCHONDRIAL * 2e-08 F1Fo-ATPase synthase f CG4692 GH18886 60D8-60D8 dup:1/2 ID:71A7
+ transcription_factor_binding * 2e-47 WEB1_YEAST WEB1 PROTEIN (PROTEIN TRANSPORT PROTEIN SEC31) * 2e-07
fizzy-related protein * 9e-37 predicted using Genefinder; Similarity to Yeas [WD40_REGION // WD40] CG8266 GH19061 44F7-
CG8266 44F8 dup:1/3 ID:71B11
+ endopeptidase * DMSTUBBLE_1 Sb * caldecrin=serum calcium-decreasing factor pancreas, Peptide, * 7e-36
STUB_DROME SERINE PROTEINASE STUBBLE (STUBBLE-STUBBLOID PROTEIN [trypsin // CHYMOTRYPSIN // TRYPSIN_HIS
CG5390] CG5390 31D5-31D6 dup:2/2 ID:71B8
CG13124+ unknown * 1E-135* * CG13124 GH19095 33A1-33A1 dup:1/2 ID:71C3
+ enzyme * 3e-07 alpha-actinin-2 associated LIM protein * 9e-08 actinin-associated LIM protein * 4e-08 CL36_RAT LIM
CG6416 PROTEIN CLP36 LIM protein - rat * alpha-act [PDZ] CG6416 GH19182 66D9-66D ID:71D2
+ 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
+ transmembrane_receptor * patched (Drosophila) homolog(aa) * PATCHED PROTEIN HOMOLOG (PTC1) (PTC)(aa) * similar
to drosophila membrane protein PATCHED * 1e-26 probable m[PHOSPHOPANTETHEINE // 5TM_BOX] CG11212 GH19449
CG11212 42A10-42A10 dup:2/2 ID:71E10
CG15386+ unknown * 1E-132* * CG15386 GH19557 23D1-23D1 ID:71F10

+ 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
 + 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
 + transporter * unknown(aa) * anon-100EF-D3 * 1e-20 Similarity to Salmonella sodium/proline symporter (SW:PUTP_SALTY);
 CG2196 * 1e-33 sodium iodide symporter [SSF // NA_SOLUTE_SYMP_3] CG2196 GH19680 100E2-100E3 ID:71G12
 CG13319+ unknown * 1E-158** CG13319 GH19585 49E1-49E1 ID:71G2
 + unknown * 2e-22 similarity to C. elegans protein C01C10.4 * 1e-36 SH3-domain binding protein * 1e-36 SH3 binding protein
 CG14408 SH3 binding protein sapien * YKL4_CA CG14408 GH19670 12F7-13A1 ID:71G9
 + 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
 CG4186 + CG4186 77E4-77E5 ID:71H2
 + transporter * DMC171D11 * DMMDR65_2 Mdr65 * 8e-46 STE6_YEAST MATING FACTOR A SECRETION PROTEIN STE6
 (MULTIPLE DRUG RESISTANCE PROT * 4e-86 MDR4_DROME MULTIDRUG RE [ATP_GTP_A2 // ABC_TRANSPORTER //
 CG1824 ABC_tr] CG1824 GH19726 11B12-11B12 ID:71H4
 + Eaat2 neurotransmitter_transporter * EXCITATORY AMINO ACID TRANSPORTER (SEAAT1)(aa) * glutamate transporter
 2B(aa) * CeGlt-2(aa) * predicted using Genefinder; Similari[SDF // EDTRNSPORT // NA_DICARBOXYL_SYMP] CG3159 GH19729
 CG3159 21D1-21D1 dup:2/4 ID:71H5
 + enzyme * putative ribitol dehydrogenase(aa) * coded for by C. elegans cDNA CEESL70F; similar to protochlorophyllide
 CG11200 oxidoreductases(aa) * CGI-82 protein(aa) [GDHRDH // adh_short] CG11200 GH19857 56F17-56F17 ID:72A6
 + 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
 + Akap550 signal_transduction * A-kinase anchor protein DAKAP550(aa) * Akap550 * similarity with the yeast hypothetical 251.0
 KD protein YCR32W (Swiss-Prot accession number [WD40_REGION // BEACH_DOMAIN // CYTOCHRO] CG6775 GH19972 4E2-
 CG6775 4E2 dup:2/2 ID:72B5
 + peptidase * 1e-30 YHT2_YEAST HYPOTHETICAL 49.8 KD PROTEIN IN ACT3-YCK1 INTERGENIC REGION
 PRECURSOR * 7e-06 carboxypeptidase precursor * 4e-52 similar to zinc ca [CRBOXYPTASEA // Zn_carbOpept] CG8560
 CG8560 GH20109 65F7-65F8 ID:72C10
 + Hs2st enzyme * DMSD_2 Sd * SEGREGATION DISTORTER PROTEIN(aa) * 2e-74 cDNA EST yk273d10.3 comes from this
 CG10234 gene; cDNA EST yk273d10.5 come * 1e-101 heparan sulfate 2- CG10234 GH20044 37E3-37E3 ID:72C3
 CG12375+ unknown * 1e-05 hypothetical protein ** [lactamase_B] CG12375 GH20064 28E-28E ID:72C5
 CG7720 + transporter * BLASTX 2.0E-28 Human sodium iodide symporter mRNA, complete cds.(dna) * 4e-36 unknown * 2e-17

Similarity to Salmonella sodium/proline symporter (SW: [NA_SOLUTE_SYMP_3] CG7720 GH20226 93F9-91C7 ID:72D11
+ enzyme * aldehyde oxidase(aa) * DMXDH_4 ry * xanthine dehydrogenase(aa) * XANTHINE DEHYDROGENASE (XD)
CG6045 (ROSY LOCUS PROTEIN)(aa) [dehydrog_molyb // Ald_Xan_dh_C // fer2] CG6045 GH20168 88F8-88F8 ID:72D2
+ unknown * predicted using hexExon; MAL3P6.28 Hypothetical protein, len: aa; Similarity to model organism hypothetical
CG18042 proteins (C.elegans, D.melanogaster, S. CG18042 GH20177 31B1-31B1 ID:72D3
+ 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
+ Myosin-heavy-chain-like motor_protein * nonmuscle myosin II heavy chain A(aa) * nonmuscle myosin heavy chain-A(aa) *
myosin heavy chain nonmuscle form A - human(aa) * 2e-97 m[myosin_head // IQ // MYOSINHEAVY] CG10218 GH20309 89B7-
CG10218 89B7 dup:4/4 ID:72E8
+ unknown * corresponding to cDNA from BDGP EST library; undifined protein 2(aa) * anon-60Ab * 1E-87*
CG4585 [G_PROTEIN_RECEPTOR // CDP_ALCOHOL_P_TRA] CG4585 GH20310 60A6-60A6 dup:2/2 ID:72E9
+ 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
CG15688+ unknown * CG15688 GH20388 92F4-92F5 ID:72F7
CG18020+ projectin [Drosophila melanogaster] CG18020 ID:72G5
CG14021+ unknown * CG14021 GH20612 25D5-25D6 dup:2/2 ID:72H2
+ transporter * putative methyltransferase(aa) * 6e-05 probable membrane protein YDR198c - yeast (Saccharomyces
cerevisiae) * 2e-09 putative methyltransferase * F21 [ATP_GTP_A2 // ABC_TRANSPORTER // ABC_tr] CG7955 GH20617 62A-
CG7955 62A ID:72H3
CG10408+ enzyme CG10408 ID:72H5
CG1521 + transporter homology to uncharacterized human and C.elegans proteins MgtE CG1521 GH20809 ID:73A10
CG1648 + unknown * 2e-12 inserted at base 5' end of P element Inverse PCR ** CG1648 GH20817 46B10-46B10 dup:2/3 ID:73A11
+ enzyme * Similar to glycogenin.(aa) * GLYCOGENIN(aa) * 1e-27 GLG2_YEAST GLYCOGEN SYNTHESIS INITIATOR
CG9480 PROTEIN GLG2 hy * 7e-67 Similar to glycogenin. CG9480 GH20752 57C7-57C7 dup:1/2 ID:73A3
+ unknown * protein(aa) * putative glucose-induced repressor protein(aa) * Unknown protein(aa) * HYPOTHETICAL 54.9 KD
CG4221 PROTEIN C02F5.7 IN CHROMOSOME III(aa) [PHOSPHOPANTETHEINE] CG4221 GH20765 89B1-89B1 dup:3/4 ID:73A6
+ structural_protein * 4e-07 CUP8_DROME PUPAL CUTICLE PROTEIN EDG-84 PRECURSOR ecdyson * 3e-08
CU19_LOCFMI CUTICLE PROTEIN (LM-19) (LM-ACP 19) Lm-ACP1 * 5e-09 DMEDG84A_3 Ed [CUTICLE // PRO_RICH //
CG6305 insect_cuticle] CG6305 GH20904 50C9-50C11 ID:73B10
CG17736+ unknown * CG17736 GH20919 76E2-76E2 ID:73B12
- Ket cytoskeletal_structural_protein * BM KETTIN(aa) * titin(aa) * titin(aa) * Titin [ig // AA_TRNA_LIGASE_II_1 // SH3 // NLS]
CG1915 CG1915 GH20861 62C2-62C3 dup:2/2 ID:73B8
+ 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

+ BcDNA:GH02901 enzyme * hypothetical protein(aa) * 5e-11 LCFA_HAEIN LONG-CHAIN-FATTY-ACID--COA LIGASE (LONG-CHAIN ACYL-COA SYNTHETASE) > * LCFA_ECOLI LONG-CHAIN-FATTY-ACID CG9009 GH20984 13A5-13A5 dup:2/4

CG9009 ID:73C10

+ CtBP enzyme * CtBP * C-terminal binding protein CtBP2(aa) * C-terminal binding protein(aa) * similar to the D-isomer specific

CG7583 2-hydroxyacid dehydrogenases family [2-Hacid_DH] CG7583 GH20987 87D9-87D11 dup:1/2 ID:73C12

+ protein_kinase * 4e-08 Ssp31 protein kinase * 5e-11 Ca2+/calmodulin-dependent protein kinase (EC 2.7.1.123) II alpha chain - fruit * 8e-37 YQO9_CAEEL HYPOTHETICAL 1[PROTEIN_KINASE_ST // PROTEIN_KINASE_DOM] CG4523 GH20931

CG4523 6C7-6C7 dup:2/3 ID:73C2

+ peptidase * 1e-24 YBY9_YEAST PUTATIVE SERINE CARBOXYPEPTIDASE IN ESR1-IRA1 INTERGENIC REGION * 2e-83 similar to BPTI/KUNITZ inhibitor domain; cDNA EST come * 8e [ESTERASE // serine_carbpept // CRBOXYPT] CG3344 GH21114

CG3344 61C9-61C9 ID:73D10

+ 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-34A

CG12403 ID:73D11

CG1383 + unknown * 2e-74 F55A12.9 gene product * * CG1383 43E12-43E13 ID:73D4

+ Hr46 steroid_hormone_receptor * DMDHR3A_2 Hr46 * HR3_DROME PROBABLE NUCLEAR HORMONE RECEPTOR HR3 (DHR3) st * 4e-67 CHR3 gene product * 2e-71 ROR1_MOUSE NUCLEAR RECEPTOR ROR-A[STROIDFINGER // hormone_rec //

CG11823 THYROIDH] CG11823 GH21112 46F4-46F ID:73D9

+ ribosomal_protein * ribosome recycling factor(aa) * RRF_HAEIN RIBOSOME RECYCLING FACTOR (RIBOSOME RELEASING FACTOR) (RRF) * RRF_CLOPE RIBOSOME RECYCLING FACTOR (RIBOS CG4447 GH21184 67B1-67B1 dup:2/2

CG4447 ID:73E11

CG6958 + structural_protein * [GAPDH] CG6958 GH21194 94C4-94C4 dup:3/3 ID:73E12

+ unknown * weak similarity to rat TEGT protein * PTD010(aa) * Unknown(aa) * 3e-05 N-methyl-D-aspartate receptor-associated protein - fruit fly (Drosophila mela CG2076 GH21149 10A3-10A4 dup:2/2 ID:73E2

CG2076 + enzyme * 5e-12 GLO2_YEAST HYDROXYACYLGLUTATHIONE HYDROLASE ISOZYME (GLYOXALASE II) (GLX II) * 2e-62 cDNA EST yk301h4.5 comes from this gene; cDNA EST yk301h4 [lactamase_B // NLS_BP // ATP_GTP_A] CG9026 GH21160

CG9026 47F7-47F7 dup:3/3 ID:73E3

CG6740 + unknown * CG6740 GH21172 67C-67C dup:2/2 ID:73E7

+ 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

+ Gfat enzyme * glucosamine-fructose-6-phosphate aminotransferase(aa) * 1e-155 GFA1_YEAST GLUCOSAMINE--FRUCTOSE-6-PHOSPHATE AMINOTRANSFERASE (ISOMERIZING) (HEX * g [GATase_2 // SIS] CG12449 GH21229

CG12449 cyto_unknown dup:2/2 ID:73F3

+ enzyme * cAMP-specific phosphodiesterase 8B; PDE8B1; 3',5'-cyclic nucleotide phosphodiesterase(aa) * phosphodiesterase 8(aa) * 7e-16 cAMP phosphodiesterase [PDEase // PDIESTERASE1 // PAS_REPEAT //] CG5411 GH21295

CG5411 59F-59F4 dup:2/2 ID:73F7

+ ligand_binding_or_carrier * MAP-kinase activating death domain(aa) * Rab3 GDP/GTP exchange protein(aa) * regulator of presynaptic activity(aa) * 3e-12 CRAG protein [DENN_DOMAIN // PRO_RICH // ATP_GTP_A] CG5627 GH21304 13A12-13B1 ID:73F8
 CG5627 + 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
 + function_unknown * 2e-19 YBS4_YEAST HYPOTHETICAL 47.8 KD PROTEIN IN HSP26-TIF32 INTERGENIC REGION *
 CG11961 8e-90 YP67_CAEEL HYPOTHETICAL 98.3 KD PROTEIN IN CHROMOSOME II (U2 CG11961 GH21451 56D2-56D2 ID:73G2
 + unknown * 2e-06 hypothetical protein * hypothetical protein * UVS2_NEUCR UVS-2 PROTEIN uvs2 protein - Neurospora
 CG7388 crassa * [GLYCOSYL_HYDROL_F5 // zf-C3HC4 // ZINC_] CG7388 GH21463 66A12-66A12 dup:1/3 ID:73G4
 + 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
 + Acp1 structural_protein * Acp1 * ADULT CUTICLE PROTEIN PRECURSOR (DACP-1)(aa) * cuticle protein=Dacp-1
 CG7216 melanogaster, Peptide, * CG7216 GH21504 28C3-28C3 dup:1/2 ID:73G8
 + transporter * 2e-64 coded for by C. elegans cDNA yk54h9.5; coded for by C. elegans cDNA yk54h9.3; si * 4e-70
 CG7571 PGT_HUMAN PROSTAGLANDIN TRANSPORTER (PGT) prostagland CG7571 GH21536 74D1-74D1 dup:2/2 ID:73H1
 + motor_protein * 3e-05 F35D11.11 gene product * 2e-06 hyaluronan receptor - human * 3e-06 tetravalent M protein=hybrid
 CG10193 molecule containing amino-terminal subuni * Si [PRO_RICH] CG10193 GH21577 95C3-95C3 dup:2/2 ID:73H4
 + mu2 unknown * mutator 2(aa) * mutator * 4e-06 Pax transcription activation domain interacting protein PTIP * CG1960
 CG1960 GH21591 62B11-62B11 dup:2/2 ID:73H6
 + metabolism * RIBOSE-PHOSPHATE PYROPHOSPHOKINASE (PHOSPHORIBOSYL PYROPHOSPHATE SYNTHETASE)(aa) * similar to ribose-phosphate pyrophosphokinase(aa) * RIBOSE-PHOSP [Pribosyltran //
 CG6767 PRPP_SYNTHETASE] CG6767 67B11-67B12 dup:2/2 ID:73H7
 + Rpt4 endopeptidase * 26S PROTEASE REGULATORY SUBUNIT S10B (P44) (CONSERVED ATPASE DOMAIN PROTEIN
 CG3455 44)(aa) * Pros45 proteosome subunit homolog(aa) * 1e-134 SUG2_YEAST PROB CG3455 GH21618 5E1-5E1 dup:2/2 ID:73H8
 CG6652 + motor_protein * 6e-13 unknown * * [NLS_BP] CG6652 GH21622 73E4-73E4 dup:2/2 ID:73H9
 + Orct transporter * DMORCT2_2 Orct * 3e-10 YGK4_YEAST PROBABLE METABOLITE TRANSPORT PROTEIN YGL104C *
 CG6331 putative organic cation transporter [sugar_tr] CG6331 GH21655 95F2-95F2 ID:74A1
 + 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
 + corto nucleic_acid_binding * corto * CENTROSOMAL AND CHROMOSOMAL FACTOR (CCF) (CHROMOCENTROSOMIN)(aa)
 CG2530 * CP-1(aa) * inserted at base Both 5' and 3' ends of P element Inverse PCR CG2530 GH21787 82F5-82F5 ID:74B1
 + 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
 + unknown * 1e-23 hypothetical protein YDL219w - yeast (Saccharomyces cerevisiae) * 3e-32 predicted using Genefinder * 5e-
 CG5270 27 SPAC8C9.05, len:149aa; similarity: [FYVE_DOMAIN // FYVE] CG5270 GH21817 86E5-86E5 ID:74B5

+ BcDNA:GH04802 ion_channel * 5e-05 TOK1_YEAST OUTWARD-RECTIFIER POTASSIUM CHANNEL TOK1 (TWO-DOMAIN
 OUTWARD RECTIFIER * 1e-18 C24H11.8 * 8e-06 TWIK-related acid-sensitive K⁺ chann [CHANNEL_PORE_K] CG1688 46B4-
 CG1688 46B5 dup:2/2 ID:74B7
 + unknown * 2e-52 gene C35D10.2 protein - Caenorhabditis elegans similar to * 3e-81 RGS-GAIP interacting protein GIPC
 CG11546 GLUT1 * 7e-81 RGS-GAIP interacting protein [PDZ] CG11546 GH21964 44A8-44B dup:1/2 ID:74C11
 + weak homology to leucine carboxyl methyltransferase [Homo sapiens] and receptor protein kinase-like protein [Arabidopsis
 CG14768 thaliana] CG14768 GH21888 ID:74C2
 + unknown * /match=(desc:; /match=(desc:(aa) * 4e-77 /match=(desc:; /ma * 7e-06 No definition line found * No definition line
 CG7135 found CG7135 GH21891 16F7-16F7 dup:1/2 ID:74C3
 + enzyme * 7e-97 ALAM_YEAST PUTATIVE ALANINE AMINOTRANSFERASE, MITOCHONDRIAL PRECURSOR
 (GLUTAMIC * 1e-159 Similar to alanine aminotransferase; coded for by C. [aminotran_1 // ACCSYNTHASE] CG1640 GH21936
 CG1640 11E9-11E10 dup:2/3 ID:74C8
 + receptor * 3e-10 tolloid related-1 * 5e-17 similar to CUB domain (2 domains), Low-density lipoprotein recepto * 8e-15
 BMP1_MOUSE BONE MORPHOGENETIC PROTEIN PRE [LDLRA_2 // CUB // ldl_recept_a // PRO_R] CG5449 GH21941 94A3-
 CG5449 94A3 ID:74C9
 + rux unknown * CELL CYCLE NEGATIVE REGULATOR ROUGHX(aa) * rux * 1e-170 rux * [NLS_BP] CG4336 GH22074 5D1-
 CG4336 5D1 ID:74D12
 + 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
 CG10693 + CG10693 GH22026 ID:74D5
 + 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
 CG5805 dup:2/2 ID:74E10
 CG3246 + unknown * CG3246 25A3-25A3 dup:2/2 ID:74E11
 + endopeptidase * ADAMTS-1(aa) * 1e-86 Weak similarity to Eimeria thrombospondin (PIR Acc. No. c * 1e-102 secretory
 protein containing thrombospondin motifs * 2e-74 a [TSP1 // ADAM_MEPRO // RECEPTOR_CYTOKINE] CG4096 GH22104 5B1-
 CG4096 5B1 dup:3/3 ID:74E6
 + jdp chaperone * 1e-11 SCJ1_YEAST SCJ1 PROTEIN SCJ1 protein - yeast (Saccharomyce * 1e-09 DNJ1_DROME DNAJ
 PROTEIN HOMOLOG (DROJ1) droj1 * 1e-10 YRY1_CAEEL HYPOTHETIC [GRAM_POS_ANCHORING // DnaJ // DNAJPROTE]
 CG2239 CG2239 GH22106 99F8-99F10 dup:3/3 ID:74E7
 + 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
 CG8026 dup:2/2 ID:74E9
 + protein_kinase * coded for by C. elegans cDNA CEESC01F; coded for by C. elegans cDNA cm11b7; coded for by C. elegans
 CG10737 cDNA cm11b8; Similar to protein kinase.(aa) * 1e [DAG_PE_BINDING_DOMAIN // DAG_PE-bind //] CG10737 56B6-56C ID:74F1
 + cell_adhesion * Down syndrome cell adhesion molecule(aa) * 3e-66 neuroglian * 1e-58 predicted protein contains a large
 CG17800 number of Ig superfamily repeat * 2e-39 PTPT9 [ig // PRO_RICH // fn3] CG17800 GH22207 43B1-43B2 dup:3/4 ID:74F3

+ chitinase * dJ73M23.3 * 1E-137* 9e-06 chitinase protein precursor * similar to similar to [EGF_2] CG7565 GH22222 66B6-
 CG7565 66B6 ID:74F4
 CG11737+ unknown * 3e-24 K02G10.3 gene product * * CG11737 GH22337 85A5-85A5 ID:74G2
 CG13603+ unknown * CG13603 GH22341 97F1-97F1 ID:74G3
 + unknown * 8e-13 probable membrane protein YLR427w - yeast (*Saccharomyces cerevisiae*) * 5e-05 transcription factor * 1e-
 CG12099 47 Contains C3HC4 type zinc finger sign [zf-C3HC4 // ZINC_FINGER_C3HC4 // NLS_BP] CG12099 62A7-62A7 dup:1/4 ID:74G4
 + 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
 + BcDNA:LD21403 unknown * unknown * 1e-06 tudor repeat associator with PCTAIRE * [TUDOR] CG8920 GH22439 57A-57A
 CG8920 dup:2/2 ID:74G9
 + Cyp4d8 cytochrome_P450 * DMLCYP6A9 Cyp6a9 * DMCYTO_2 Cyp4d1 * DMCYP4D2_12 Cyp4d2 * cytochrome P450(aa)
 CG4321 [EP450II // p450 // P450 // MITP450 // B] CG4321 GH22459 66A1-66A1 ID:74H1
 CG9336 + unknown * CG9336 GH22472 38F1-38F1 ID:74H4
 + enzyme * histidyl tRNA synthetase - *Caenorhabditis elegans*(aa) * HISTIDYL-TRNA SYNTHETASE HOMOLOG (HISTIDINE-
 -TRNA LIGASE HOMOLOG) (HISRS)(aa) * HISTIDYL-TRN [WHEP-TRS // tRNA-synt_2b // AA_TRNA_LIG] CG6335 GH22474
 CG6335 17B5-17B5 ID:74H5
 + acyl-CoA_dehydrogenase * Similar to acyl-CoA dehydrogenase; coded for by *C. elegans* cDNA yk122b9.5(aa) * acyl-
 Coenzyme A dehydrogenase, short/branched chain prec[Acyl-CoA_dh // ACYL_COA_DH_1 // ACYL_CO] CG3902 GH22479 75E2-
 CG3902 75E2 dup:2/2 ID:74H6
 + msl-2 DNA_binding * male-specific lethal-2(aa) * DMDNAMEL2_2 msl-2 * MSL2_DROME MALE-SPECIFIC LETHAL-2
 PROTEIN RING finger prote * 3e-38 male-specific lethal-2 [ZINC_FINGER_C3HC4 // PRO_RICH // NLS_BP] CG3241 GH22488
 CG3241 25A3-25A3 ID:74H7
 + transcription_factor * eyg * 9e-46 Eyegone * 1e-38 similar to 'Paired box' domain, homeobox protein (paired subfamily * 2e-
 41 PAX3_MOUSE PAIRED BOX PROTEIN PAX-3 pax-3 p[PAX // HOMEBOX_1 // homeobox // HOMEOB] CG10704 GH22493
 CG10704 69B3-69B4 ID:74H8
 + * DnaJ-1 * heat shock protein dnaJ homolog - human(aa) * similar to DNAJ protein; cDNA EST comes from this gene; cDNA
 CG5001 EST comes from this gene; cDNA E CG5001 ID:75A5
 + 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
 + prd transcription_factor * SEGMENTATION PROTEIN PAIRED(aa) * DMPRD_5 prd * 3e-58 similar to 'Paired box' domain,
 homeobox protein (paired subfamily * 2e-87 PAX3_MOUSE PAIRE[PAX // HOMEBOX_1 // homeobox // HOMEOB] CG6716
 CG6716 GH22686 33B14-33B14 ID:75B4
 + Abdominal B transcription_factor HOMEBOX, HOMEBOX_1, HOMEBOX_2, HTHREP] CG10291 GH22693 dup:4/5
 CG10291 ID:75B6
 + enzyme * 6e-06 YD40_YEAST HYPOTHETICAL 42.3 KD PROTEIN IN YTA2-DIT1 INTERGENIC REGION * 4e-33 predicted
 CG12177 using Genefinder; similar to Inosine-uridine preferri [IU_nuc_hydro] CG12177 GH22706 12B1-12B1 ID:75B7

+ unknown * 1e-35 probable membrane protein YOR245c - yeast (*Saccharomyces cerevisiae*) * 3e-58 K07B1.4 gene product *
 CG1942 9e-21 hypothetical protein * predicted usi CG1942 GH22719 43E11-43E11 ID:75B9
 + 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
 + unknown * BLASTX 2.0E-06 *Theileria parva* schizont/sporozyte surface protein gene, partial cds.(dna) * * [NLS_BP]
 CG12316 CG12316 GH22749 71B2-71B2 ID:75C3
 + Flo-2 unknown * 1e-176 flotillin-2 * 1e-114 epidermal surface antigen * 1e-114 flotillin epidermal surface antigen - human * 1e-
 CG11547 114 growth-associated protein [NLS_BP] CG11547 GH22754 13A3-13A4 ID:75C4
 CG8960 + unknown * CG8960 GH22765 62D2-62D2 ID:75C5
 CG8991 + transcription_factor * [PRO_RICH] CG8991 GH22790 48C-48C ID:75C6
 + 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
 + 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 //
 CG6203 KH] CG6203 GH22839 85F10-85F11 ID:75D2
 + enzyme * I(2)37Cs * Cs protein * 2e-19 No definition line found * 4e-15 protein [NAD_BINDING] CG10561 GH22841 37C1-
 CG10561 37C1 dup:2/2 ID:75D3
 + enzyme * probable membrane protein YPR184w - yeast (*Saccharomyces cerevisiae*) * similar to Alpha amylase; cDNA EST
 CG9485 yk217a9.5 comes from this gene; * amylo-1, [ISOCITRATE_LYASE] CG9485 GH22856 57D4-57D5 dup:3/4 ID:75D8
 CG11388 + unknown * CG11388 GH22974 60B1-60B1 dup:2/2 ID:75E11
 + electron_transfer * GEC-3(aa) * 3e-43 coded for by *C. elegans* cDNA yk51h9.5; coded for by *C. elegans* cDNA yk117c2.5; c
 CG17843 * 1e-64 quiescin Q6 quiescin * 2e-66 GEC-3 [THIOREDOXIN_2] CG17843 GH22889 96B6-96B6 dup:2/2 ID:75E2
 CG7905 + unknown * CG7905 GH22919 66B6-66B7 dup:2/2 ID:75E5
 + 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
 CG15658 57C7-57C7 dup:2/2 ID:75E6
 + neurotransmitter_transporter * SerT * glycine transporter type-2(aa) * SODIUM- AND CHLORIDE-DEPENDENT GABA
 TRANSPORTER 3(aa) * hypothetical protein T23G5.5 - *Caenor*[NA_NEUROTRAN_SYMP_1 // NANEUSMPORT // N] CG8380
 CG8380 GH22929 53C-53C dup:2/2 ID:75E8
 + 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
 + ligand_binding_or_carrier * calcyphosine(aa) * CRUSTACEAN CALCIUM-BINDING PROTEIN (CCBP-23 PROTEIN)(aa) *
 1e-10 predicted using Genefinder; Similarity to Human calmodulin (SW:P [EF_HAND // ehand // EF_HAND_2] CG10126 GH22994
 CG10126 87D3-87D3 ID:75F5

+ shot ligand_binding_or_carrier * Groovin(aa) * DMGROOVIN kak * 1e-09 FIMB_YEAST FIMBRIN (ABP67) fimbrin - yeast
 CG18076(Saccharomyces * Groovin [spectrin // CH] CG18076 GH23032 50C14-50C19 dup:2/7 ID:75G2
 CG6038 + unknown * CG6038 GH23035 71C2-71C2 ID:75G3
 + transporter * retinal rod Na/Ca+K exchanger(aa) * Na/Ca,K-exchanger(aa) * 2e-06 probable membrane protein YDL206w -
 CG1090 yeast (Saccharomyces cerevisiae) * 1e-05 Na/C CG1090 GH23040 82B1-82B1 ID:75G4
 + agt DNA_repair_protein * O-6-alkylguanine-DNA alkyltransferase(aa) * agt * 3e-16 MGMT_YEAST METHYLATED-DNA--
 PROTEIN-CYSTEINE METHYLTRANSFERASE (6-O-METHYLGUANINE * 2e-10 MGM [Methyltransf_1 // MGMT] CG1303
 CG1303 GH23047 84C4-84C4 ID:75G5
 + Klp68D motor_protein * Klp68D * KINESIN-LIKE PROTEIN KLP68D(aa) * 1e-38 Cin8p kinesin-related * 1e-115 Similarity to
 CG7293 urchin kinensin-2 (PIR Acc. No. cDNA EST EM [kinesin // KINESINHEAVY] CG7293 GH23075 68D2-68D2 ID:75G8
 CG2985 + CG2985 dup:1/5 ID:75H3
 + defense/immunity_protein * similar to rat autoimmune target protein p69 * 1e-39 similar to rat autoimmune target protein p69
 CG10566 * 5e-67 ICAp69 * 1e-64 diabetes mellitus type I au CG10566 GH23156 78B4-78C1 ID:75H6
 + unknown * hypothetical protein gs1.1.27.1(aa) * 6e-26 hypothetical protein YPL020c - yeast (Saccharomyces cerevisiae) (*
 CG11023 1e-29 YRW3_CAEEL HYPOTHETICAL 75.7 K CG11023 GH23213 21A3-21A3 dup:1/2 ID:75H9
 + enzyme * 5e-20 T10H10.3 gene product * 9e-07 ubiquitin protein ligase * 3e-07 WWP1 * 1e-05 S-SCAM beta
 CG13832[WW_rsp5_WWP // WW_DOMAIN_2] CG13832 GH23265 94D13-94D13 ID:76A4
 + kek1 cell_adhesion * KEK1(aa) * kek1 * 2e-11 Similarity to Rat insulin-like growth factor binding protein comple * 1e-17 leucine-
 CG12283 rich-repeat protein [ig // LRR // LEURICHRPT // LRRCT] CG12283 GH23277 34A-34A dup:1/2 ID:76A7
 CG7962 + CG7962 GH23282 ID:76A8
 + Hrb27C RNA_binding * DMHRP481_2 Hrb27C * HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN 27C (HNRNP 48)
 (HRP48.1)(aa) * 2e-36 NAB4_YEAST NUCLEAR POLYADENYLATED RNA-BINDING PROTE [RNP_1 // RBD // rrm] CG10377
 CG10377 27C-27C dup:6/8 ID:76B1
 + unknown * 2e-22 YNQ8_YEAST HYPOTHETICAL 28.8 KD PROTEIN IN PSD1-SKO1 INTERGENIC REGION * 2e-27
 YO23_CAEEL HYPOTHETICAL 23.3 KD PROTEIN ZK688.3 IN CHROMOSOME I [ATP_GTP_A] CG6028 GH23390 93F14-93F14
 CG6028 ID:76B10
 + enzyme * coded for by C. elegans cDNA yk61f5.5; coded for by C. elegans cDNA yk40b3.5; coded for by C. elegans cDNA
 yk129d12.5; coded for by C. elegans cDNA [CPSASE_2 // Carboxyl_trans // CPSase_L_] CG8723 GH23405 43F8-43F9 dup:3/4
 CG8723 ID:76B12
 + 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 96C4-96C5
 CG11856 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
 + unknown * BLASTX 7.1E-06 Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No. 4.(dna) * * [PRO_RICH]
 CG10341 CG10341 GH23387 37A4-37A4 ID:76B9

+ transporter * 3e-69 predicted using Genefinder; cDNA EST comes from this g * 3e-07 tetracycline resistance protein * similar
 CG8054 to translocase * contains similarity [PRO_RICH // NLS_BP] CG8054 GH23453 45B1-45B1 ID:76C6
 + 18w cell_adhesion * DMWHEELER_2 18w * 5e-15 CYAA_YEAST ADENYLATE CYCLASE (ATP PYROPHOSPHATE-LYASE)
 CG8896 (ADENYLATE CYCLASE) * leucine-rich motif (LRR) protein homology to int CG8896 GH23463 56F9-56F9 dup:1/4 ID:76C9
 CG13773+ enzyme * 4e-10 match to * 3e-06 hypothetical protein * [NLS_BP] CG13773 GH23590 27C3-27C3 ID:76D12
 CG13551+ GH20780 CG13551 GH23524 ID:76D4
 + Dad transcription_factor * Dad * DAD polypeptide * 2e-18 similar to ZK370.2 * 2e-40 Smad6 [Dwarfin // PRO_RICH // NLS_BP]
 CG5201 CG5201 GH23534 89E12-89E13 dup:3/4 ID:76D6
 + transporter * similar to PhoX homologous domain, present in p47phox and p40phox.(aa) * SDP8(aa) * 2e-18 hypothetical
 CG6359 protein YOR357c - yeast (Saccharomyces cerev [PX // BEM_DOMAIN] CG6359 87C5-87C5 ID:76D8
 CG4848 + transporter * 4e-12 ldlBp ** CG4848 GH23636 87B6-87B6 dup:3/3 ID:76E12
 + enzyme * fructose-1,6-bisphosphatase; Fbp1p(aa) * fructose-bisphosphatase 1(aa) * fructose-1,6-bisphosphatase
 precursor(aa) * fructose-1,6-bisphosphatase ho [FBPASE // FBPase // INFBPHPTASE // FBP] CG10611 38A-38A dup:3/3
 CG10611 ID:76F10
 + 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 * 1e-31 pdb|1SDY|A Saccharomyces cerevisiae Saccharomyces cerevisiae * 1e-34 SODC_DROME SUPEROXIDE
 DISMUTASE (CU-ZN) superoxide dismuta * 5e-38 SODE_C [CUZNDISMTASE // SOD_CU_ZN_1 // SOD_CU_Z] CG9027 47F6-
 CG9027 47F7 ID:76F8
 + transporter * Phosphate Permease(aa) * leukemia virus receptor - human(aa) * 3e-27 YB8I_YEAST PUTATIVE
 CG7628 PHOSPHATE-REPRESSIBLE PHOSPHATE PERMEASE YBR29C * 9e-52 Sim [PHO4] CG7628 GH23727 70E3-68A5 ID:76F9
 + chaperone * DMCYP1_2 Cyp1 * 4e-41 CYPH_YEAST PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE)
 (ROTAMASE) (CYCLOPHILIN) * 1e-36 CYPH_DROME PEPTIDYL-PROLYL CIS-TRANS [pro_isomerase // CSA_PPIASE_1 //
 CG1866 CSA_PP] CG1866 GH23813 98C3-98C3 dup:1/4 ID:76G11
 + Arr2 unknown * DMPPP_2 Arr2 * ARRB_DROME PHOSRESTIN I (ARRESTIN B) (ARRESTIN 2) (49 KD ARRESTIN-LIKE
 PROTEIN) * 2e-73 ARRB_CAEEL PROBABLE BETA-ARRESTIN coded for [ARRESTIN // arrestin // ARRESTINS] CG5962
 CG5962 GH23741 66D-66D dup:4/5 ID:76G2
 CG17549+ unknown * CG17549 GH23745 37E1-37E1 dup:2/2 ID:76G4
 CG6424 + BcDNA:GH05095 motor_protein * 8e-34 protein ** [NLS_BP] CG6424 GH23788 54E3-54E4 dup:1/3 ID:76G9
 CG9780 + unknown * [ABC_TRANSPORTER] CG9780 GH23891 82A4-82A4 ID:76H12
 + EG:132E8.4 motor_protein * DMC132E8 * 4e-06 USO1_YEAST INTRACELLULAR PROTEIN TRANSPORT PROTEIN USO1 (*
 CG11448 melanog * 2e-31 similar to coiled coil domains; cDNA EST yk302g12.5 com CG11448 GH23825 2A3-2A3 ID:76H2
 + Pcd enzyme * Pcd * 5e-40 pterin-4a-carbinolamine dehydratase * 1e-24 similar to 4a-carbinolamine dehydratases * 4e-22
 CG1963 pterin-4-alpha-carbinolamine dehydratase (E [RIBOSOMAL_L23 // Pterin_4a] CG1963 GH23826 99C1-99C1 dup:1/2 ID:76H3
 + unknown * HYPOTHETICAL 30.5 KD PROTEIN C30A5.3 IN CHROMOSOME III(aa) * CGI-95 protein(aa) * 2e-10
 CG3403 MOB1_YEAST MOB1 PROTEIN (MPS1 BINDER 1) * 9e-09 putative mit CG3403 GH23829 42C6-42C6 ID:76H4

+ enzyme * hexaprenyl pyrophosphate synthetase; Coq1p(aa) * 9e-26 COQ1_YEAST HEXAPRENYL PYROPHOSPHATE
 CG10585 SYNTHETASE PRECURSOR (HPS) * 9e-13 trans-prenyltransferase [ATP_GTP_A] CG10585 GH23839 78A6-78A6 ID:76H7
 CG3192 + CG3192 ID:76H8
 + unknown * 3e-05 mucin 2, intestinal/tracheal MUC1 * 3e-05 mucin precursor, intestinal - human (fragments) * 1E-157* mucin
 CG4577 CG4577 GH23863 21E-21E ID:76H9
 CG6043 + unknown * [PRO_RICH] CG6043 GH24071 34A11-34B1 ID:77B11
 + e enzyme * ebony(aa) * e * ebony * 1e-56 bacitracin synthetase 3; BacC [AMP_BINDING // ACP_DOMAIN // AMP-binding]
 CG3331 CG3331 GH24002 93D2-93D2 dup:2/2 ID:77B2
 + 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
 + unknown * UBIQUINONE BIOSYNTHESIS PROTEIN COQ4 HOMOLOG(aa) * CGI-92 protein(aa) * 4e-38 COQ4_YEAST
 CG3877 UBIQUINONE BIOSYNTHESIS PROTEIN COQ4 Coq4p * 3e-48 putative CG3877 GH24045 78A1-78A1 dup:1/2 ID:77B7
 + transcription_factor * zinc finger protein 37(aa) * hkb * 2e-17 AZF1_YEAST ASPARAGINE-RICH ZINC FINGER PROTEIN
 CG8367 AZF1 fin * 4e-47 zinc finger motif protein [zf-C2H2 // ZINC_FINGER_C2H2 // ZINC_FIN] CG8367 GH24215 50E4-50E4 ID:77C11
 + transcription_factor * DMSUHW_6 su(Hw) * crol * zf43C * 7e-08 zinc finger 30C [zf-C2H2 // ZINC_FINGER_C2H2 //
 CG7101 ZINC_FIN] CG7101 GH24178 17E1-17E1 ID:77C7
 + transporter * DMWHITER_2 w * WHITE PROTEIN HOMOLOG(aa) * hypothetical protein * 3e-39 ORF YOL075c
 CG9663 [ATP_GTP_A2 // ABC_TRANSPORTER // ABC_tr] CG9663 GH24286 25A1-25A1 ID:77D10
 + Ice endopeptidase * DMICEPROT_2 Ice * 2e-10 ETFB_YEAST PROBABLE ELECTRON TRANSFER FLAVOPROTEIN BETA-
 SUBUNIT (BETA-ETF) * ICE_DROME CASPASE PRECURSOR (DRICE) drICE pr * [CASPASE_P10 // ICE_p10 //
 CG7788 CASPASE_P20 /] CG7788 GH24292 99C4-99C4 ID:77D11
 + unknown * R01H10.7(aa) * inositol polyphosphate 4-phosphatase, type II(aa) * inositol polyphosphate 4-phosphatase type
 CG1846 II-alpha(aa) * 4e-58 inositol polypho [PH_DOMAIN] CG1846 GH24251 12E1-12E1 dup:2/2 ID:77D3
 + enzyme * flavin containing monooxygenase 3(aa) * T3P18.10(aa) * similar to Flavin-binding monooxygenase-like(aa) *
 CG3006 similar to flavin-containing monooxygenase [ADXRDTASE // FADPNR // FMO-like // PNDR] CG3006 GH24271 60A13-60A13 ID:77D7
 + transcription_factor * ORFveg132; similar to Caenorhabditis elegans ORF F59B10.1 encoded by EMBL Accession Number *
 CG3328 protein(aa) * 2e-70 similarity to a transmembranous of [CASPASE_HIS] CG3328 GH24458 60B9-60B10 dup:3/3 ID:77E12
 + phyl signal_transduction * phyl * 1e-175 phyllopod * phyllopod - fruit fly (Drosophila melanogaster) ORF * phyllopod [NLS_BP]
 CG10108 CG10108 GH24326 51A-51A2 dup:2/2 ID:77E4
 + 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
 + unknown * 6e-43 COX11 (AA 1-277) * 2e-44 cDNA EST comes from this gene; cDNA EST co * 1e-124 protein * 3e-51
 CG6922 component involved in Haem biosynthesis americana CG6922 GH24534 25E6-25E6 ID:77F11
 CG11440 + wunen * similarity to phosphatidic acid phosphatase PA_PHOSPHATASE CG11440 ID:77F12
 CG1888 + unknown * [NLS_BP] CG1888 GH24468 45F1-45F1 ID:77F2
 CG10137 + unknown * glycine-, glutamate-, thienylcyclohexylpiperidine-binding protein(aa) * 1e-59 protein * 1E-170* CG10137 37F1-

37F1 ID:77F4
+ enzyme * DMC103B4 * 1e-05 LYS2_YEAST AMINOADIPATE-SEMIALDEHYDE DEHYDROGENASE LARGE SUBUNIT (ALPHA-AMINOADI * 2e-53 /match=(desc;; /ma * 4e-75 similar to Arab [HELIX_LOOP_HELIX] CG12268 GH24480 95C13-95C13
CG12268 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
+ Cyp6d4 cytochrome_P450 * THROMBOXANE-A SYNTHASE (TXA SYNTHASE) (TXS)(aa) * Similar to cytochrome P450(aa) * cytochrome P450(aa) * CYTOCHROME P450 4A11 PRECURSOR (CYP1A11) [EP450II // p450 // P450 // MITP450 // B] CG12800
CG12800 GH24669 94C4-94C4 ID:77G11
+ endopeptidase * 2e-11 similar to Zinc-binding metalloprotease; cDNA EST come * 3e-14 NEP_MOUSE NEPRILYSIN (NEUTRAL ENDOPEPTIDASE) (NEP) (ENKEPHALINASE) (CD10) * 2e[NEPRILYSIN // PRENYLATION // ZINC_PROTE] CG3239
CG3239 GH24674 5A1-5A1 dup:1/3 ID:77G12
+ unknown * Yor243cp(aa) * 2e-79 YO43_YEAST HYPOTHETICAL 77.0 KD PROTEIN IN HES1-SEC63 INTERGENIC REGION * 3e-35 YQ4B_CAEEL HYPOTHETICAL 64.6 KD PROTEIN IN CHRO [UPF0024 // NLS_BP] CG6745 GH24787 66D4-
CG6745 66D4 ID:77H10
+ 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
CG7178 + CG7178 dup:2/2 ID:77H12
CG12120+ unknown * CG12120 GH24835 8D4-8D4 ID:78A1
CG5453
CG16719+ unknown * hypothetical protein(aa) * 3e-10 hypothetical protein * CG16719 GH24859 67B11-67B11 ID:78A4
+ unknown * ATP(GTP)-binding protein(aa) * HYPOTHETICAL 39.7 KD PROTEIN C34E10.2 IN CHROMOSOME III(aa) *
CG10222 weak similarity to ATPases(aa) * Yor262wp(aa) [ATP_GTP_A] CG10222 GH25024 70A7-70A7 ID:78B10
CG10347+ unknown * 8e-10 partial CDS ** CG10347 10F2-10F2 dup:3/3 ID:78B3
+ EG:9D2.4endopeptidase * DMC9D2 * /motif=(desc;; /motif=(desc;; /motif=(desc;; /match=(desc;; /m * 2e-20 kallikrein * 1e-28
CG3795 mesotrypsinogen mesotrypsino [trypsin // CHYMOTRYPSIN // TRYPSIN_SER] CG3795 GH24985 2B8-2B8 ID:78B4
+ SP2523 motor_protein * 1e-05 YM96_YEAST HYPOTHETICAL 113.1 KD PROTEIN IN PRE5-FET4 INTERGENIC REGION * *
CG7493 CG7493 GH25141 66A8-66A8 dup:2/3 ID:78C11
+ transporter * 3e-11 aquaporin * 4e-15 BIB_DROME NEUROGENIC PROTEIN BIG BRAIN bib protein - frui * 6e-15 similar to
CG4019 MIP protein * 1e-28 MIP_MOUSE LENS FIBER MAJOR [MINTRINSICP // MIP] CG4019 GH25142 59F1-59F2 ID:78C12
+ 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
CG17450+ unknown * CG17450 GH25094 cyto_unknown ID:78C5

+ tkv signal_transduction * DMTVP_2 tkv * transmembrane receptor type I transforming growth factor beta receptor) plasma
 membrane plasma membrane) map_position:25D6 * 2E-5[PROTEIN_KINASE_DOM // pkinase // TGFB_R] CG14026 25C10-25D
 CG14026 dup:4/7 ID:78D11
 CG8444 + CG8444 ID:78D12
 + unknown * 6e-32 antigen 5-related * 1e-19 antigen 5-related protein * 6e-34 Ag5r2 * VA3_SOLIN VENOM ALLERGEN III
 CG17210 (ALLERGEN SOL I 3) (SOL I III) CG17210 GH25284 86D8-86D8 dup:2/2 ID:78E5
 + enzyme * 8e-11 YGA1_YEAST PUTATIVE BETA-HYDROXYSTEROID DEHYDROGENASE/DELTA 5-->4-ISOMERASE (*
 CG7724 2e-12 weakly similar to dihydrokaempferol 4-reductase * 2e-21 [3Beta_HSD] CG7724 GH25466 73E5-73E5 dup:2/2 ID:78F12
 + 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
 + Pk92B protein_kinase * coded for by C. elegans cDNA CEESN53F; similar to protein kinases including CDC15 in yeast(aa) *
 DMPK92B_4 Pk92B * 8e-43 protein kinase * protei[PROTEIN_KINASE_ST // TYRKINASE // PROTE] CG4720 GH25453 92B8-
 CG4720 92B8 dup:2/3 ID:78F7
 + Pu enzyme * 4e-52 GCH1_YEAST GTP CYCLOHYDROLASE I (GTP-CH-I) GTP cyclohyd * 1e-133 GCH1_DROME GTP
 CYCLOHYDROLASE I (GTP-CH-I) (PUNCH PROTEIN) * 2e-67 GCH1_CAEEL [GTP_cyclohydrol // GTP_CYCLOHYDROL_1_1]
 CG9441 CG9441 GH25630 57C5-57C6 dup:3/3 ID:78H12
 CG5677 + CG5677 dup:2/2 ID:78H3
 + signal_transduction * actin-filament binding protein Frabin(aa) * DMD547_2 still-life * 2e-14 still life type * 1e-34 guanine
 CG7511 nucleotide exchange factor UNC-73A [GRF_DBL // RhoGEF // PH_DOMAIN] CG7511 GH25579 66A7-66A7 ID:78H4
 + 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
 + Myo61F motor_protein * Myo61F * Myo31DF * 1e-143 YMZ9_YEAST HYPOTHETICAL MYOSIN-LIKE PROTEIN IN ILV2-ADE17
 INTERGENIC REGION * myosin IB - fruit fly (Drosophila melanoga[myosin_head // IQ // MYOSINHEAVY // ATP] CG9155 GH25605
 CG9155 62B4-62B4 dup:3/3 ID:78H8
 + BcDNA:GH06348 enzyme * predicted using Genefinder; Similarity to Human pyruvate carboxylase cDNA EST comes from this
 CG1516 gene; cDNA EST comes from this gene; cDNA EST comes f [CPSase_L_chain] CG1516 GH25836 46B14-46C1 dup:5/8 ID:79B10
 CG14653+ unknown * 1E-59* * CG14653 GH25780 82D5-82D5 ID:79B5
 CG13515+ unknown * CG13515 GH25860 58F4-58F4 ID:79C4
 + 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
 + transcription_factor * 7e-05 host cell factor * inserted at base 5' end of P element Inverse PCR * similar to human host cell
 CG5186 factor * YC81_CAEEL HYPOTHETICAL 143.1 KD PR CG5186 GH26048 55C13-55C13 dup:2/2 ID:79D11
 + enzyme * 1e-09 BACR37P7.d * 8e-25 strong similarity to the insect-type alcohol/ribitol dehydrogenase family * 2e-27 cis-
 CG8888 retinol androgen dehydrogenase * 2e-3 [adh_short] CG8888 GH26015 48E4-48E6 ID:79D8
 CG3682 + enzyme phosphatidylinositol 4-phosphate 5-kinase CG3682 ID:79D9

CG17470+ unknown * CG17470 GH26094 38E-38E dup:2/2 ID:79E10
 + unknown * 3e-09 probable membrane protein YPR028w - yeast (*Saccharomyces cerevisiae*) * 4e-46 YSV4_CAEEL
 CG9848 HYPOTHETICAL 26.6 KD PROTEIN T19C3.4 IN CHROMOSOME III [PRO_RICH] CG9848 GH26090 59B4-59B6 dup:4/4 ID:79E9
 + transcription_factor * segmentation protein hairy - fruit fly (*Drosophila melanogaster*)(aa) * DMHAIRG_5 h * 3e-07 lin-22 * 2e-18 HES1_MOUSE TRANSCRIPTION FACTOR HES-1 (HAI [HLH // HELIX_LOOP_HELIX_2] CG10446 37B10-37B10 dup:2/2
 CG10446 ID:79F1
 + Cyp4p1 cytochrome_P450 * predicted using Genefinder; similar to cytochrome P450(aa) * DMCYP4D2_12 Cyp4d2 * Cyp4p1 *
 CG10842 cytochrome P450 (CYP4M2) - tobacco hornworm(aa) [EP450II // p450 // MITP450] CG10842 45C-45C dup:3/6 ID:79F11
 + motor_protein * homeotic most like HMPB_DROME: homeotic proboscipedia protein(aa) * 1e-05 neurofilament triplet H1
 CG12105 protein - rabbit (fragment) neuro * * [GRAM_POS_ANCHORING // NLS_BP] CG12105 GH26183 62A-62A dup:2/2 ID:79F12
 + transmembrane_receptor * DMCD362_2 croquemort * 2e-55 D-CD36 protein - fruit fly (*Drosophila melanogaster*) * 1e-21
 CG7227 predicted using Genefinder; similar to CD36 family; cDNA E [CD36] CG7227 GH26133 30C1-30C1 dup:3/3 ID:79F4
 + enzyme * PROBABLE ISOCITRATE DEHYDROGENASE (NAD), MITOCHONDRIAL SUBUNIT BETA PRECURSOR (ISOCITRIC DEHYDROGENASE) (NAD+-SPECIFIC ICDH)(aa) * NAD+-specific iso [isodh] CG6439 GH26270 93F14-93F14
 CG6439 ID:79G10
 CG6836 + unknown * CG6836 GH26215 75E6-75E6 ID:79G4
 + BG:DS01068.2 unknown * hypothetical protein(aa) * 1e-98 R08F11.1 gene product * 7e-50 putative protein * unknown
 CG7469 [HMG_COA_REDUCTASE_2] CG7469 GH26380 34F5-34F5 dup:2/2 ID:79H12
 + unknown * contains similarity to E. coli cation transport protein * 6e-16 YEZ3_YEAST HYPOTHETICAL 26.3 KD PROTEIN
 CG10365 IN RAD4-CHD1 INTERGENIC REGION * 3e-22 cont CG10365 GH26317 95B5-95B5 ID:79H4
 + 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
 + unknown * contains similarity to BC-2 protein * 1e-45 developmental protein * hypothetical protein * [NLS_BP] CG4108
 CG4108 GH26351 75D2-75D2 ID:79H7
 CG7300 + unknown * CG7300 GH26358 32A-32A ID:79H9
 + Sxl RNA_binding * DMSX1PS1_2 Sxl * 7e-15 PABP_YEAST POLYADENYLATE-BINDING PROTEIN, CYTOPLASMIC AND
 CG18350 NUCLEAR (PABP) (ARS CO * 1e-158 sex-lethal sex determination protei CG18350 sxl-male 6F5-6F5 dup:6/7 ID:8-31 cntrlBA10
 + da transcription_factor * TRANSCRIPTION FACTOR E2-ALPHA (IMMUNOGLOBULIN ENHANCER BINDING FACTOR E12) (TRANSCRIPTION FACTOR-3) (TCF-3) (TRANSCRIPTION FACTOR ITF-[HLH // HELIX_LOOP_HELIX // PEROXIDASE_1]
 CG5102 CG5102 da 31E1-31E1 dup:3/3 ID:8-31 cntrlBA11
 CG4694 + her CG4694 her dup:2/2 ID:8-31 cntrlBA4
 CG16724 + tra CG16724 tra dup:2/2 ID:8-31 cntrlBA5
 CG13201 + ix CG13201 ix dup:2/2 ID:8-31 cntrlBA6
 + bib transporter * pore-forming protein MIP family(aa) * NEUROGENIC PROTEIN BIG BRAIN(aa) * 1e-07 YFF4_YEAST
 HYPOTHETICAL 70.5 KD PROTEIN IN AGP3-DAK3 INTERGENIC REG[MINTRINSICP // MIP // PRO_RICH] CG4722 big brain
 CG4722 30F4-30F5 dup:2/3 ID:8-31 cntrlBB5

CG1378 + tll steroid_hormone_receptor CG1378 tll dup:2/2 ID:8-31 cntrlBC1
 + pnt transcription_factor * DMPOINT2A_2 pnt * PNT2_DROME ETS-LIKE PROTEIN POINTED P2 (D-ETS-2) gene po * 3e-12
 contains similarity to DNA-binding domain of[HSF_ETS // ETSDOMAIN // Ets // ETS_DOMA] CG17077 pnt-p1 94E12-94F1 dup:4/7
 CG17077 ID:8-31 cntrlBC10
 + ttk transcription_factor * DNA-binding protein ttk - fruit fly (Drosophila melanogaster)(aa) * DMDNABPMR_2 ttk * DNA binding
 CG1856 protein * 3e-06 contains sim[BTB // zf-C2H2 // ZINC_FINGER_C2H2 // Z] CG1856 HK or ttK 100E1-100E1 dup:5/7 ID:8-31 cntrlBC2
 + spdo actin_binding * sanpodo protein(aa) * 1e-179 sanpodo protein * 8e-47 Similar to tropomodulin; coded for by C. elegans
 CG1539 cDNA yk88e7.5; coded for by C. * 6e-47 TMOD_MO CG1539 sanpodo 100A-100A dup:3/3 ID:8-31 cntrlBC5
 CG17348 + drl CG17348 drl dup:2/2 ID:8-31 cntrlBC8
 CG1374 + tsh transcription_factor CG1374 tsh dup:3/3 ID:8-31 cntrlBD3
 + inv transcription_factor * SEGMENTATION POLARITY PROTEIN ENGRAILED(aa) * DMINVR_2 inv * INVECTED
 PROTEIN(aa) * 2e-29 HM16_CAEEL HOMEBOX PROTEIN ENGRAILED-LIKE CEH-16 homology CG17835 inv 47F17-48A
 CG17835 dup:3/4 ID:8-31 cntrlBD4
 + pros transcription_factor * DMPROS_3 pros * PRO_DROME PROTEIN PROSPERO homeotic protein prospero - f * 4e-58
 HM26_CAEEL HOMEBOX PROTEIN CEH-26 K12H4.1 protein - Caen * 2e-50 [PRO_RICH] CG17228 pros p'3' 3211 86E2-86E2
 CG17228 dup:4/4 ID:8-31 cntrlBD7
 CG4354 + slbo CG4354 slbo dup:2/2 ID:8-31 cntrlBD9
 + Antp transcription_factor * DMANTPG5_7 Antp * 1e-159 HMAN_DROME HOMEOTIC ANTENNAPEDIA PROTEIN homeotic
 protein * 7e-23 DNA-binding protein mab5 * 5e-34 HXB7_MOUSE HOMEBOX PROT CG1028 ANTP 84B-84D11 dup:3/3 ID:8-31
 CG1028 cntrlBE12
 CG4889 + Wg signal_transduction CG4889 Wg dup:2/2 ID:8-31 cntrlBE8
 CG9885 + dpp signal_transduction CG9885 dpp dup:2/2 ID:8-31 cntrlBE9
 + tup transcription_factor * isl * LIM homeobox protein(aa) * LIM homeobox protein * 4e-30 CeLIM-7 contains similarity to L
 CG10619[LIM_DOMAIN_1 // HOMEBOX_1 // homeobox] CG10619 islet 37B5-37B5 dup:3/3 ID:8-31 cntrlBF7
 CG2956 + twist transcription_factor CG2956 twist dup:3/5 ID:8-31 cntrlBG3
 CG10325 + abdA transcription_factor CG10325 abdA dup:4/4 ID:8-31 cntrlBH1
 CG1133 + opa transcription_factor CG1133 opa dup:4/4 ID:8-31 cntrlBH4
 CG2328 + eve transcription_factor CG2328 eve dup:2/2 ID:8-31 cntrlBH7
 + dMEF2 * DMMEF2_2 Mef2 * myocyte enhancer-binding factor 2(aa) * 5e-07 RLM1_YEAST TRANSCRIPTION FACTOR RLM1
 CG1429 RLM1 protein - yea * myocyte-specific enhancer f CG1429 dup:1/8 ID:8-99Cntrl IE7
 CG18253 + unknown * CG18253 GH26442 82D5-82D5 ID:80A9
 + unknown * DMANO66DB_2 anon-66Db * ANON-66Db protein * 5e-08 similar to PDZ domain (Also known as DHR or GLGF).
 CG5989 * 5e-10 hypothetical protein CG5989 GH26459 68C1-68C1 ID:80B2
 + 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
 CG8154 + unknown * [NLS_BP] CG8154 GH26521 67C2-67C2 ID:80B9

+ unknown * polyporphic murine leukemia virus receptor SYG1(aa) * 3e-32 SYG1_YEAST SYG1 PROTEIN SYG1 protein -
 CG10483 yeast (Saccharomy * 1e-150 predicted using Genefin [CRYSTALLIN_BETAGAMMA] CG10483 GH26628 64F5-64F5 ID:80C8
 + actin_binding * 4e-21 alternatively spliced form * 2e-31 similar to actin binding domain of alpha-actinin and spectra beta chain
 CG3960 * 6e-30 mouse smoothelin, large iso [CH_DOMAIN // CH] CG3960 GH26714 6B3-6C1 dup:3/3 ID:80D12
 + enzyme * dihydrolipoamide S-acetyltransferase (EC 2.3.1.12) precursor - Arabidopsis thaliana (fragment)(aa) *
 CG5261 Dihydrolipoamide acetyltransferase component (E [LIPOYL // 2-oxoacid_dh // biotin_lipoyl] CG5261 27F7-27F7 ID:80D4
 CG11700+ CG11700 dup:1/2 ID:80D5
 + unknown * HYPOTHETICAL 90.9 KD PROTEIN C08B11.4 IN CHROMOSOME II(aa) * weak similarity to nodulation protein X
 CG11353 (probable sugar acetylase) (Swiss Prot accessio CG11353 GH26735 64B13-64B14 dup:3/3 ID:80E2
 + motor_protein * APXL(aa) * 2e-23 APXL * 2e-23 apical protein, Xenopus laevis-like * [PRO_RICH] CG8603 GH26744 50F6-
 CG8603 50F6 dup:4/4 ID:80E4
 CG5758 + unknown * CG5758 GH26746 36E-36E dup:2/2 ID:80E5
 + 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
 + Cyp9f2 cytochrome_P450 * CYP9 cytochrome P450(aa) * 3e-18 CYP6A2 * 2e-10 similar to cytochrome P450 * 5e-16
 CG11466 cytochrome P450 3A11 - mouse cytochrome P-45 [EP450II // p450] CG11466 GH26796 87B14-87B14 ID:80F2
 + enzyme * CGI-82 protein(aa) * 1e-16 YM71_YEAST HYPOTHETICAL OXIDOREDUCTASE IN MRPL44-MTF1
 INTERGENIC REGION * 0.000000000002 * 6e-42 predicted using Genefinde [GDHRDH // adh_short] CG7675 GH26851 91A2-
 CG7675 91A2 dup:2/4 ID:80F8
 + transporter * protein(aa) * BLASTX 3.6E-09 Plasmodium falciparum protein gene, complete cds.(dna) * rab3 effector(aa) *
 CG7321 4e-11 SY65_DROME SYNAPTOTAGMIN (P65) syna [C2 // C2_DOMAIN_2 // PDZ] CG7321 GH26867 90C7-90C7 ID:80F9
 CG7926 + Axn signal_transduction * D-Axin(aa) * 6e-15 Axin * 2e-14 axin * 1e-14 Axin [GRK] CG7926 99D5-99D5 dup:1/2 ID:80G2
 CG10965+ unknown * CG10965 GH26991 7D21-7D21 ID:80H1
 + unknown * 3e-12 YKJ5_YEAST 32.3 KD PROTEIN IN CWP1-MBR1 INTERGENIC REGION * 1e-64 YS19_CAEEL
 CG15084 HYPOTHETICAL 42.1 KD PROTEIN IN CHROMOSOME III * 1e-17 unknown * CG15084 GH26994 55F4-55F4 ID:80H2
 + cell_adhesion * DMDELTA_4 DI * DMCRPA_2 crb * Wnt inhibitory factor-1(aa) * cell communication establishment of cell
 CG3135 polarity) plasma membrane plasma membrane) ma [EGF_1 // EGF // EGF_2] CG3135 GH27042 6C12-6C13 ID:80H7
 + enzyme * 2e-08 ACH1_YEAST ACETYL-COA HYDROLASE (ACETYL-COA DEACYLASE) (ACETYL-COA ACYLASE) * 1e-
 CG7920 136 coded for by C. elegans cDNA yk20f6.3; coded for by C. el [ATP_GTP_A] CG7920 GH27164 99D4-99D4 dup:2/2 ID:81A11
 + endopeptidase * SORCIN(aa) * 8e-12 YG25_YEAST HYPOTHETICAL 38.4 KD PROTEIN IN MUP1-SPR3 INTERGENIC
 REGION * 1e-15 CAN_DROME CALPAIN (CALCIUM-ACTIVATED NEUTRAL PROTE [EF_HAND // efhand // EF_HAND_2]
 CG17765 CG17765 47A9-47A9 dup:3/3 ID:81A2
 + Vha55 enzyme * ATPase, H+ transporting, lysosomal (vacuolar proton pump), beta polypeptide, 56/58kD, isoform 2(aa) * H+-
 CG17369 ATPase beta subunit(aa) * PROBABLE VACUOLAR [ATP-synt_ab] CG17369 GH27148 87C5-87C5 dup:3/3 ID:81A7
 + yin transporter * opt1 long(aa) * 8e-17 PTR2_YEAST PEPTIDE TRANSPORTER PTR2 (PEPTIDE PERMEASE PTR2) * 8e-74
 CG2913 high-affinity peptide transporter * 2e-06 cAMP inducible p [PTR2 // PTR2_1 // PTR2_2] CG2913 GH27264 4A1-4A1 dup:2/2

ID:81B12
+ transporter * amino acid transporter chain (AmAt-L-1c) ASUR4(aa) * Similarity to Human membrane protein E16 (SW:E16_HUMAN); cDNA EST comes from this gene; cDNA ES [AROMATIC_AA_PERMEASE_2 // aa_permeases] CG1607

CG1607 GH27380 100C-100C ID:81C11

CG8861 + unknown * CG8861 GH27383 85D7-85D7 ID:81C12

CG11625+ unknown * CG11625 GH27289 92A4-92A4 dup:2/2 ID:81C4

CG2968 + CG2968 ID:81C7
+ BcDNA:GM04682 endopeptidase * MICROSOMAL SIGNAL PEPTIDASE KD SUBUNIT (SPC18)(aa) * signal peptidase complex kDa subunit(aa) * SPC 21-kDa-like(aa) * 2e-36 SC11_YEAST SIGNAL SEQUE [Peptidase_S26 // SIGNALPTASE // SPASE_I]

CG2358 CG2358 GH27340 84C4-84C4 ID:81C9
+ Cyp305a1cytochrome_P450 * CYTOCHROME P450 76C4(aa) * cytochrome P450 epoxigenase(aa) * cinnamate 4-hydroxylase(aa) * Cytochrome P-450 2A14(aa) [EP450II // p450 // P450 // MITP450 // B] CG8733 GH27419 76D3-76D3 ID:81D5

CG8733 + unknown * 2e-11 cDNA EST CEMSB78F comes from this gene; cDNA EST yk293d9.3 comes * 2e-10 Unknown * CG12118

CG12118GH27430 8D2-8D2 dup:3/4 ID:81D8
+ enzyme * phosphodiesterase 6B, cGMP-specific, rod, beta (congenital stationary night blindness 3, autosomal dominant); PDEB(aa) * 7e-45 YBJJ_CAEEL PROBABLE 3 [PDEase // PDIESTERASE1 // PDEASE_I // P] CG8279 GH27433 89E3-88C6

CG8279 dup:2/2 ID:81D9
+ protein_kinase * similar to serine/threonine kinase(aa) * 3e-37 hypothetical protein YPL236c - yeast (Saccharomyces cerevisiae) * 2e-17 SNF1A/AMP-activated protein k [PROTEIN_KINASE_ST // PROTEIN_KINASE_DOM] CG1227 84C7-84C7

CG1227 dup:3/3 ID:81E11

CG6503 + CG6503 dup:2/2 ID:81E12
+ enzyme * 1e-43 CCR4_YEAST GLUCOSE-REPRESSIBLE ALCOHOL DEHYDROGENASE TRANSCRIPTIONAL

CG5534 EFFECTOR (C * 2e-07 ANGEL * 3e-86 predicted using Genefinder; Similarity CG5534 GH27503 95E6-95E6 dup:2/2 ID:81E4
+ unknown * 1e-16 No definition line found * W06B11.1 gene product * 1e-16 No definition line found * W06B11.1 gene product

CG3967 CG3967 GH27541 67B2-67B3 dup:2/2 ID:81E6

CG11595+ unknown * CG11595 GH27568 12D5-12D5 dup:2/2 ID:81E9
+ * 1e-15 YMB8_YEAST HYPOTHETICAL 43.7 KD PROTEIN IN OST6-PSP2 INTERGENIC REGION * 7e-23 No definition

CG8195 line found * 2e-19 hypothetical protein * hypothe CG8195 52A13-52A13 ID:81F1
+ ligand_binding_or_carrier * verprolin(aa) * mucin (clone PGM-2A) - pig(aa) * Sec23-interacting protein p125(aa) *

CG8552 DMCLPTN_6 Cpn [GRAM_POS_ANCHORING] CG8552 GH27701 28E-28E9 dup:3/3 ID:81F10
+ enzyme * 2e-32 YPT6_YEAST GTP-BINDING PROTEIN YPT6 YPT6 protein - yeas * 2e-34 rab6 * 3e-53 similar to ras-related protein * 9e-34 RB17_MOUSE RAS-RELATED PRO [ALDEHYDE_DEHYDR_CYS // ras // ATP_GTP_A] CG17515

CG17515GH27649 cyto_unknown ID:81F2
+ 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 CG3567 GH27663 42D4-42D4 ID:81F6

CG15131+ unknown * CG15131 GH27691 36A10-36A10 ID:81F9
+ protein_phosphatase * similar to glycogen-binding subunit protein phosphatase-1(aa) * smooth muscle protein phosphatase
CG9619 type 1-binding subunit(aa) * protein phosphatase CG9619 GH27769 76A4-76A5 ID:81G10
+ * UDP-GLUCURONOSYLTRANSFERASE 2B13 PRECURSOR, MICROSOMAL (UDPGT)(aa) * UDP-
GLUCURONOSYLTRANSFERASE 2B20 PRECURSOR, MICROSOMAL (UDPGT)(aa) * similar t [UDPGT] CG17323 37B3-37B3
CG17323 dup:1/2 ID:81G12
+ Cyp4d20 cytochrome_P450 * /motif=(desc;; /match=(desc;; /match=(desc;; /match=(desc;; /motif=(desc:(aa) * 1e-70 similar to
cytochrome P450; cDNA EST CEMSH91R comes from this [EP450II // p450 // P450 // MITP450 // B] CG16761 GH27758 62E5-
CG16761 62E5 ID:81G8
CG5048 + unknown * CG5048 GH27783 70F1-70F1 ID:81H2
+ Gel actin_binding * DMGELS_2 Gel * gelsolin, secreted form precursor - fruit fly (Drosophila melanogaster) * 2e-73 similar to
CG1106 gelsolin; cDNA EST comes from this gene * [GELS // GELSOLIN // Gelsolin] CG1106 GH27784 82A2-82A3 ID:81H3
CG2865
+ * caltractin (20kD calcium-binding protein)(aa) * Calmodulin; Cmd1p(aa) * 7e-09 CALM_YEAST CALMODULIN calmodulin -
CG17272 yeast (Saccharomyces cere * 1e-09 C [EF_HAND_2] CG17272 92F13-92F13 dup:2/2 ID:81H6
+ 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
CG10630+ RNA_binding * CG10630 GH28067 64E-64E ID:82B10
+ unknown * 2e-19 YIC3_YEAST HYPOTHETICAL 37.4 KD PROTEIN IN IRR1-TIM44 INTERGENIC REGION * 4e-37 cDNA
CG7816 EST comes from this gene; cDNA EST co * 3e-39 KE4 * 1e-38 CG7816 GH28072 99C7-99C7 dup:2/2 ID:82B11
+ structural_protein * Gasp precursor(aa) * 1e-09 Gasp precursor * 3e-07 R02F2.4 gene product * 9e-13 insect intestinal mucin
CG4948 IIM22 CG4948 GH28017 66F4-66F4 dup:3/3 ID:82B4
+ 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
+ transcription_factor * hepatocyte nuclear factor alpha(aa) * Contains similarity to Pfam domain: (homeobox), Score=20.5,
N=1(aa) * onecut 2(aa) * coded for by C. elegans [homeobox // HOMEBOX_2 // NLS_BP] CG1922 GH28062 102C6-102C6
CG1922 ID:82B9
+ ligand_binding_or_carrier * 16k antigen precursor - nematode (Onchocerca volvulus)(aa) * phosphatidylethanolamine binding
CG6180 protein Ovd1 - nematode (Onchocerca volvulus) (fragmen [PBP] CG6180 33F2-33F2 dup:1/2 ID:82C12
+ 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
+ endopeptidase * DMSTUBBLE_1 Sb * 7e-07 T2D4_YEAST TRANSCRIPTION INITIATION FACTOR TFIID KD SUBUNIT
(TAFII-90) * 2e-26 EAST_DROME SERINE PROTEASE EASTER PRECURSOR se [trypsin // CHYMOTRYPSIN // TRYPSIN_SER
CG1773] CG1773 GH28342 46A3-46A3 ID:82C7
CG9676 + endopeptidase * Ser12 * DMEAST_4 ea * Ser6 * DMSTUBBLE_1 Sb [trypsin // CHYMOTRYPSIN // TRYPSIN_HIS]

CG9676 15A1-15A1 dup:1/3 ID:82C8

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
 + enzyme * phosphoglyceromutase - fruit fly (Drosophila melanogaster)(aa) * DMPGLY_4 Pglym78 * 3e-72 PMG1_YEAST PHOSPHOGLYCERATE MUTASE (PHOSPHOGLYCEROMUTASE 1 [PGAM // PG_MUTASE] CG17645 GH28416 87B7-87B7

CG17645 ID:82D6
 + Galpha49B signal_transduction * 7e-50 GBA2_YEAST GUANINE NUCLEOTIDE-BINDING PROTEIN ALPHA-2 SUBUNIT (GP2-ALPHA) * 1e-169 GBQ3_DROME GUANINE NUCLEOTIDE-BINDING PROTEIN G(Q), ALPH[GPROTEINA // G-alpha //

CG17759 GPROTEINAQ // G] CG17759 GH28437 49B3-49B5 ID:82D7
 + transporter * similar to C. elegans protein and to rat synaptic vesicle protein * putative integral membrane transport

CG8654 protein(aa) * HYPOTHETICAL 84.8 KD PROTEIN [sugar_tr] CG8654 GH28654 56F-56F dup:2/2 ID:82E12

CG11347 + unknown * [NLS_BP] CG11347 GH28550 64B11-64B11 dup:2/2 ID:82E4
 + unknown * cDNA EST comes from this gene; cDNA EST yk304g10.3 comes from this gene; cDNA EST yk304g10.5 comes

CG11848 from this gene(aa) * 2e-16 ankyrin repeat-contai CG11848 GH28553 96B20-96B20 dup:2/2 ID:82E5

CG7093 + unknown * [PRO_RICH] CG7093 GH28569 28D5-28D5 dup:2/2 ID:82E6

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
 + Rh5 G_protein_linked_receptor * Rh5 * DMNKDTACH_2 Takr86C * OPSIN RH4 (INNER R7 PHOTORECEPTOR CELLS OPSIN)(aa) * short wavelength-sensitive opsin; ultraviolet-sensi[GPCRRHODOPSN // OPSIN // G_PROTEIN_RECE] CG5279

CG5279 GH28578 33B10-33B10 dup:2/2 ID:82E9
 + 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
 + Chd64 actin_binding * DMMP20_6 Mp20 * predicted using Genefinder; Similarity to Human SM22 smooth muscle protein (SW:SM2H_HUMAN); cDNA EST comes from this gene; cDNA EST [SM22CALPONIN // CH] CG14996 GH28730 64A9-64A9

CG14996 dup:2/2 ID:82F12
 + transcription_factor * 8e-09 C24H11.6 * 1e-31 SRB7 SRB protein * SRB7 (suppressor of RNA polymerase B, yeast) homolog

CG17397 RNA polymerase * CG17397 GH28678 cyto_unknown ID:82F4
 + cytoskeletal_structural_protein * erythroid ankyrin(aa) * DMCACTUSB_8 cact * 1e-07 probable membrane protein YOR034c - yeast (Saccharomyces cerevisiae) [ANK_REP // ank // ANK_REP_REGION // ZF_] CG17492 GH28686 37B10-37B11 dup:5/6

CG17492 ID:82F5

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

CG17884 + Snap25 synaptosome-associated_protein Synapse protein 25 CG17884 GH28821 ID:82G10

CG17342 + Lk6 protein_kinase * 7e-51 LK6 protein kinase * 2e-06 similar to serine/threonine kinase; cDNA EST comes fro * 2e-11 map

kinase interacting kinase * 3e-12 Putative map k [PROTEIN_KINASE_ST // PROTEIN_KINASE_DOM] CG17342 GH28825 86F7-86F7 ID:82G11

+ CREG unknown * CREG * 1e-112 cellular repressor of E1A-stimulated genes CREG * 8e-25 cellular repressor of E1A-stimulated genes CREG * 2e-22 UNKNOWN cellular repressor 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 ID:82G4

CG13316+ * 0.000000002 * CG13316 3F2-3F2 ID:82G7

CG2640 + unknown * CG2640 GH28833 84C-84C ID:82H2

CG17676+ CG17676[unknown]CT39055 ID:82H3

+ unknown * 5e-05 XIAP associated factor-1 (ZAP-1) * 6e-09 SINA_DROME DEVELOPMENTAL PROTEIN SEVEN IN ABSENTIA devel * 1e-07 seven-in-absentia protein homologue- [ZF_TRAF] CG16745 GH28844 63B5-63B5 ID:82H4

+ ribosomal_protein * predicted using Genefinder; Similarity to Prototheca mitochondiral ribosomal protein S11 (SW:RT11_PROWL); cDNA EST yk372e6.3 comes from this gene; [Ribosomal_S11] CG5184 GM13519 89E13-89E13 ID:83A11

+ 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

+ enzyme * NADH:ubiquinone dehydrogenase kDa subunit(aa) * similar to NADH-ubiquinone oxidoreductase; cDNA EST comes from this gene; cDNA EST comes from this [COMPLEX1_51K_1 // COMPLEX1_51K_2] CG9140 GM14163 26B3-26B3 ID:83B12

+ protein_phosphatase * 4e-11 PVH1_YEAST PROTEIN-TYROSINE PHOSPHATASE YVH1 (PTPASE YVH1) * 5e-22 puckered protein * 3e-32 Similar to protein-tyrosine phosphatase * 1e-26 DU [DSPc] CG14080 GM13896 75F5-75F5 ID:83B6

+ * similar to Gila monster phospholipase A2; similar to * 2e-22 phospholipase A2 (EC 3.1.1.4) Pa5 - Gila monster phosph * 8e-89 inserted at base Both 5' [PA2_HIS] CG1583 7D14-7D15 dup:2/2 ID:83B8

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

+ Gr enzyme * 4e-59 glutathione reductase * GSHR_DROME GLUTATHIONE REDUCTASE (GR) (GRASE) glutathione * 1e-125 TRXB_CAEEL PROBABLE THIOREDOXIN REDUCTASE Similar t [HGRDTASE // FADPNR // pyr_redox // PYRI] CG2151 GM14215 7D18-7D18 ID:83C1

CG6544 + fau unknown * CG6544 HL07933 86C4-86C4 dup:1/2 ID:83C11

CG6050 + translation_factor CG6050 GM14682 ID:83C4

+ Elf translation_factor * Elf * elongation factor alpha-like factor(aa) * 1e-141 GST1 * elongation factor alpha-like factor [ELONGATNFCT // GTP_EFTU // EFACTOR_GTP] CG6382 GM14684 33E-33E dup:1/2 ID:83C5

CG8501 + unknown * CG8501 HL07915 48C5-48C5 ID:83C9

+ unknown * CUTICLE PROTEIN (BC-NCP1)(aa) * BLASTX 1.2E-10 Theileria parva schizont/sporozoite surface protein gene, partial cds.(dna) * CG8736 HL08183 44D-44D ID:83D10

CG6219 + unknown * anon-fe1G5 * anon1G5 * 1e-124 anon1G5 [NLS_BP] CG6219 LD21372 95E7-95E7 ID:83D11

CG7671 + chaperone * 6e-06 C09G9.2 * [WD40_REGION // WD40] CG7671 LD21432 91A-91A ID:83D12

+ Phas1 translation_factor * 2e-16 PHAS-II * 4e-16 eukaryotic translation initiation factor 4E binding protein * 1e-14 insulin-stimulated phosphoprotein PHAS-I - rat PHAS-I * in CG8846 HL08053 25A3-25A3 ID:83D4
 CG8846
 CG12251 + unknown * CG12251 HL08087 49F11-49F11 ID:83D5
 CG9578 + CG9578 ID:83D8
 + chaperone * HYPOTHETICAL 39.9 KD PROTEIN T15H9.1 IN CHROMOSOME II PRECURSOR(aa) * DNAJ PROTEIN HOMOLOG (DROJ1)(aa) * 1e-06 SCJ1_YEAST SCJ1 PROTEIN SCJ1 protein [DnaJ // DNAJ_2] CG9089 LD21896 15B4-15B4
 CG9089 dup:2/2 ID:83E11
 CG9300 + unknown * [SUGAR_TRANSPORT_2] CG9300 76B8-76B8 dup:2/2 ID:83E12
 + motor_protein * HYPOTHETICAL PROTEIN * PSD-95 binding protein(aa) * 2e-08 PSD-95/SAP90-associated protein-1 * 2e-08 CG17064 70 inserted at base Both 5' and 3' ends of P element [NLS_BP] CG17064 LD21642 50B1-50B2 dup:3/3 ID:83E2
 CG17064 + Ank cytoskeletal_structural_protein * DMANKY_5 Ank * 8e-16 YIL2_YEAST HYPOTHETICAL 123.6 KD PROTEIN IN POR2-COX5B INTERGENIC REGION * ankyrin ankyrin m * AO13 ankyrin [ank // ZU5] CG1651 LD21682 101F1-101F1 dup:3/4 ID:83E5
 CG1651 + swa RNA_binding * SWA_DROME SWALLOW PROTEIN gene swallow protein - fruit fly * DMSWAL_3 swa * * [NLS_BP]
 CG3429 CG3429 LD21771 5E6-5E7 dup:2/2 ID:83E6
 + Bsg25D motor_protein * BSG2_DROME BLASTODERM SPECIFIC PROTEIN 25D bsg25D protein * 1e-05 contains similarity to CG14025 kinesin (PFam: kinesin.hmm, score: 10.52 and 16.62) * 6e-1 CG14025 LD21844 25D2-25D2 dup:2/2 ID:83E8
 CG14025
 CG3416 + translation_factor CG3416 LD22193 dup:2/2 ID:83F10
 CG18282 + unknown * CG18282 LD22270 5E1-5E1 ID:83F11
 + Cyp4e2 cytochrome_P450 * cytochrome P450 - fruit fly (Drosophila melanogaster) (fragment)(aa) * Cyp4e2 * Cyp4e3 * 2e-12 CG2060 LD22157
 CG2060 ERG5_YEAST CYTOCHROME P450 (C-22 STEROL DESATURASE) [EP450II // p450 // P450 // MITP450 // B] CG2060 LD22157
 CG2060 44C1-44C1 ID:83F6
 + endopeptidase * valosin-containing protein homolog(aa) * Sug2p(aa) * 726aa long hypothetical transitional endoplasmic reticulum ATPase(aa) * ATPase-like protein(a [AAA // ATP_GTP_A] CG6815 89B17-89B17 dup:2/2 ID:83F7
 CG6815 + CycE cell_cycle_regulator * DMRNACE_2 CycE * 4e-20 CGS5_YEAST S-PHASE ENTRY CYCLIN cyclin B5 - yeast (Sacc * CG1E_DROME G1/S-SPECIFIC CYCLIN E cyclin E type I - fruit fly * 5e-37 c [cyclin // CYCLINS // ATP_GTP_A] CG3938 LD22682
 CG3938 35D5-35D6 dup:2/2 ID:83G5
 + par-6 ion_channel * PAR-6(aa) * PAR-6(aa) * PAR-6(aa) * dJ850H21.2 (novel protein containing a PDZ (DHR, GLGF) domain)(aa) [PDZ // ATP_GTP_A] CG5884 LD22757 16C5-16C5 ID:83G6
 CG5884 + protein_kinase mitotic checkpoint control protein kinase B-like PROTEIN_KINASE_ATP CG14030 LD22858 dup:1/2
 CG14030 ID:83H1
 CG1800 + RNA_binding double-stranded binding protein DSRBD CG1800 LD23072 dup:3/4 ID:83H11
 + zf30C transcription_factor * leukemia/lymphoma related factor cLRF(aa) * zf30C * 4e-17 YJF6_YEAST HYPOTHETICAL 98.9 KD ZINC FINGER PROTEIN IN BTN1-PEP8 INTERGENIC REG * zinc finger [zf-C2H2 // ZINC_FINGER_C2H2 // ZINC_FIN] CG3998 LD23102 30D1-30D1 ID:83H12
 CG3998 + MRG15 DNA_binding * MRG15(aa) * MORF-related gene 15(aa) * 4e-19 hypothetical protein YPR023c - yeast (Saccharomyces cerevisiae) * 4e-10 predicted using Genefinder; cDN [NLS_BP] CG6363 LD22902 88E9-88E10 dup:2/2 ID:83H4
 CG6363

+ B4 unknown * No definition line found(aa) * No definition line found * 1e-16 inserted at base 5' end of P element Inverse PCR *

CG9239 [NLS_BP] CG9239 LD22933 36D1-36D1 dup:4/5 ID:83H6

+ cell_adhesion * DMFAT_2 ft * 7e-55 adherin * 3e-43 Similarity to Drosophila Cadherin-related tumor suppressor precurs * 1e-

CG7805 58 seven-pass transmembrane receptor prec [CADHERIN // cadherin // CADHERIN_2] CG7805 LD23052 99C6-99C6 ID:83H9

+ 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

+ * Weak similarity with sea squirt nidogen precursor protein (blastp score 71); cDNA EST comes from this gene; cDNA EST

CG2221 comes from this gene; cDNA EST CG2221 9B14-9B14 dup:3/3 ID:84B2

CG6712 + unknown NLS_BP CG6712 LD23405 dup:2/2 ID:84B8

+ metastasis-associated-1-like-protein unknown * metastasis associated gene 1-like 1(aa) * 3e-74 similar to metastasis-associated

protein mta-1 (GB:U0 * 1e-128 metastasis associat[ELM2 // myb_DNA-binding // zf-C2H2 // Z] CG2244 LD24461 83B6-83B6

CG2244 ID:84C10

+ 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

CG11403+ DNA_repair_protein CG11403 LD24267 dup:2/2 ID:84C8

+ DNA_replication_factor * replication control protein 1(aa) * CDC6 protein(aa) * 7e-31 CC6_YEAST CELL DIVISION

CG5971 CONTROL PROTEIN cell division * 3e-30 recognition complex subu [AAA // ATP_GTP_A] CG5971 LD25083 66D-66D ID:84D11

+ enzyme * 1e-171 CTP synthase (EC 6.3.4.2) URA8 - yeast (Saccharomyces cerevisiae) * 1e-147 similar to CTP SYNTHASE

CG6854 (EC 6.3.4.2) (UTP--AMMONIA LIGASE) (CTP * [GATase // GATASE_TYPE_I] CG6854 LD25005 71B2-71B2 dup:2/6 ID:84D5

+ transcription_factor * TATA box binding protein (TBP)-associated factor, RNA polymerase II, E, 70/85kD(aa) * TAFII60(aa) *

CG10390 8e-48 transcription factor TFIID * 2e-15 contain CG10390 LD25013 83B2-83B2 ID:84D6

+ capu transmembrane_receptor * cappuccino(aa) * capu * 7e-16 unknown * 9e-67 FOR4_MOUSE FORMIN (LIMB DEFORMITY

CG3399 PROTEIN) formin isofo [MYB_1 // FORMIN // PRO_RICH] CG3399 LD25330 24C3-24C4 dup:5/7 ID:84F5

+ Paps enzyme * 3-prime-phosphoadenosine 5-prime-phosphosulfate synthase 1(aa) * DMPAPSSYN_2 Paps * 7e-54

KAPS_YEAST ADENYLYLSULFATE KINASE (APS KINASE) (ATP ADENOS [ATP_GTP_A] CG8363 LD25351 76D4-76D5

CG8363 ID:84F7

+ mnd transporter * minidiscs(aa) * 1e-23 MUP1_YEAST HIGH AFFINITY METHIONINE PERMEASE methionine * 1e-105 strong

similarity to Schistosoma amino acid permease * 1e-120 [aa_permeases // AMINO_ACID_PERMEASE_2] CG3297 LD25378 71A2-

CG3297 71A3 ID:84F8

+ transcription_factor * C43H6.7 gene product(aa) * HYPOTHETICAL 38.1 KD PROTEIN C2F12.15C IN CHROMOSOME

CG5880 II(aa) * hypothetical protein(aa) * 5e-15 probable membrane protei [ZF_DHHC] CG5880 LD25420 97E8-97E8 ID:84F9

CG13345+ unknown CG13345 dup:2/3 ID:84H11

+ RNA_binding * DMMLE_2 mle * protein(aa) * PUTATIVE PRE-MRNA SPLICING FACTOR RNA HELICASE C04H5.6(aa) *

PR22_YEAST PRE-MRNA SPLICING FACTOR RNA HELICASE PRP22 PRP [DEAH_ATP_HELICASE // HELICASE // ATP_GT]

CG10689 CG10689 LD25692 37C1-37C1 ID:84H6

CG3779 + numb unknown * NUMB PROTEIN(aa) * DMNUMB_2 numb * 3e-42 similar to Phosphotyrosine interaction domain (PTB/PID).;

cDNA EST * 8e-67 m-Numb [PTB_DOMAIN // PID // NLS_BP // ATP_GTP_] CG3779 LD25907 30B5-30B6 dup:1/3 ID:85A11
 CG17159+ * [NLS_BP] CG17159 cyto_unknown dup:2/3 ID:85A4
 + enzyme * glucose dehydrogenase (acceptor) (EC 1.1.99.10) - fruit fly (*Drosophila melanogaster*) (fragment)(aa) *
 DMGLDY01_11 Gld * putative benzyl alcohol deh [GMC_OXRED_1 // GMC_oxred // GMC_OXRED_2] CG9509 LD25803 13A1-
 CG9509 13A1 ID:85A6
 + 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
 + Cyp49a1 cytochrome_P450 * 7e-16 lanosterol 14-demethylase cytochrome P450 * 2e-24 cytochrome P450 cytochrome P4 * 4e-
 23 YS45_CAEEL PUTATIVE CYTOCHROME P450 ZK177.5 IN CHROMOS [EP450II // p450 // P450 // MITP450 // C] CG12894
 CG12894 LD25993 47A7-47A7 ID:85B11
 + Pros45 endopeptidase * Ug * 1e-157 PRS8_YEAST 26S PROTEASE REGULATORY SUBUNIT HOMOLOG (SUG1 PROTEIN)
 (CIM3 PROTE * Pros45 proteosome subunit homolog * 1e-176 similar to AT [AAA // ATP_GTP_A] CG1489 LD26005 19F2-19F2
 CG1489 ID:85B12
 + glu DNA_binding * 1e-123 hypothetical protein YLR086w - yeast (*Saccharomyces cerevisiae*) (* 2e-34 Cap * 1e-100 Similarity
 with the yeast chromosome segregation prot[ATP_GTP_A2 // DA_BOX // NLS_BP // ATP_G] CG11397 LD25919 36A7-36A7
 CG11397 dup:3/3 ID:85B2
 CG14233+ meso18E unknown * meso18E* CG14233 LD26007 18E2-18E3 ID:85C1
 + G-salpa60A signal_transduction * DMGNB_2 G-o agr;47A * 2e-39 GBA1_YEAST GUANINE NUCLEOTIDE-BINDING PROTEIN
 ALPHA-1 SUBUNIT (GP1-ALPHA) * GBS1_DROME GUANINE NUCLEOTIDE-BINDIN[GPROTEINA // G-alpha // GPROTEINAQ //
 CG2835 G] CG2835 LD26182 60A12-60A12 ID:85C12
 + unknown * mitochondrial and cytoplasmic fumarase (fumarate hydratase); Fum1p * FUMARATE HYDRATASE,
 CG18145 MITOCHONDRIAL PRECURSOR (FUMARASE) * Contains similarity to CG18145 31B-31B dup:2/2 ID:85C2
 CG9591 + unknown * 2e-12 inserted at base 5' end of P element Inverse PCR * * CG9591 LD26057 87F8-87F8 dup:2/2 ID:85C4
 CG7109 + mts protein_phosphatase microtubule star Ser/Thr protein phosphatase CG7109 LD26077 dup:2/2 ID:85C5
 CG17255+ unknown * 2e-05 BAT2 * 2e-05 BAT2 * CG17255 LD26094 9C2-9C2 dup:2/4 ID:85C6
 CG10591+ unknown * [COLLAGEN_REP // PRO_RICH] CG10591 LD26105 64E-64E3 ID:85C7
 CG10621+ unknown CG10621 dup:1/4 ID:85C9
 CG16989+ EG:34F3.4 unknown * /match=(desc;; /ma * * CG16989 LD26306 1C2-1C2 ID:85D12
 + EG:30B8.3 ligand_binding_or_carrier * /match=(desc;; /match=(desc:(aa) * 1e-171 62D9.a * 1e-11 cellular retinaldehyde-binding
 protein; CRALBP * 1e-11 retinaldehyde-binding protein C [CRETINALDHBP // CRAL_TRIO] CG3191 LD26231 2F1-2F1 dup:2/2
 CG3191 ID:85D2
 + signal_transduction * 3e-07 secreted polypeptide spatzle precursor - fruit fly (*Drosophila melanogaster*) * 3e-07
 CG9972 SPZ_DROME SPAETZLE PROTEIN PRECURSOR * 4e-09 spz * CG9972 LD26258 63A-63E4 ID:85D5
 + EG:34F3.1 signal_transduction * /match=(desc;; /ma * 2e-27 similar to PH (pleckstrin homology) domain; cDNA EST c * 8e-06
 CG12467 Y053_HUMAN HYPOTHETICAL PROTEIN KIAA * 7e-09 KRAC_DICDI RA [PH // PHOSPHOPANTETHEINE // PH_DOMAIN]

CG12467 LD26268 1C2-1C3 ID:85D7

CG7049 + hypothetical protein CG7049 LD26422 dup:3/3 ID:85E10

CG1646 + DNA_binding similarity to pre-mRNA processing protein NLS CG1646 LD26426 dup:3/3 ID:85E11

+ motor_protein * 7e-07 No definition line found * 1e-15 ATRX protein * 2e-15 X-linked nuclear protein * 6e-06 putative protein

CG8290 [NLS_BP // CYTOCHROME_C] CG8290 48D7-48D8 dup:3/3 ID:85E2

+ CRAG ligand_binding_or_carrier * CRAG protein * 1e-145 contains similarity to human MAP kinase-activating death domain * 1e-120 protein * 3e-16 Rab3 GDP/GTP exchange protein [DENN_DOMAIN // CYTOCHROME_C] CG12737 LD26363 7F4-7F4

CG12737 dup:6/6 ID:85E3

+ unknown * 2e-40 No definition line found * 2e-09 hypothetical protein * 1E-180* Hypothetical protein [NLS_BP] CG8352

CG8352 LD26402 65B4-65B5 dup:4/4 ID:85E6

+ enzyme * farnesyltransferase, CAAX box, alpha(aa) * 2e-35 RAM2_YEAST PROTEIN FARNESYLTRANSFERASE ALPHA

CG2976 SUBUNIT (CAAX FARNESYLTRANSFERASE A * 4e-58 Similar to [PPTA] CG2976 LD26412 25B-25B dup:2/2 ID:85E8

+ structural_protein * 7e-06 bK217C2.1 (Rat RTP60 (nuclear pore complex protein Np60) isolog) * 4e-11 RTP60 *

CG2158 [Ran_BP1 // RAN_BP1 // RANBP1_WASP] CG2158 LD26583 44A7-44A7 dup:3/3 ID:85F12

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

CG10609+ Or83b signal_transduction (Odorant receptor 83b) olfactory receptor CG10609 LD26485 ID:85F4

CG9925 + unknown * [PRO_RICH] CG9925 LD26515 88A4-88A4 dup:2/3 ID:85F6

+ enzyme * unknown(aa) * putative FAD synthetase(aa) * similar to FAD-1 like protein; cDNA EST yk313h1.5 comes from this

CG4407 gene; cDNA EST yk457a9.3 comes from CG4407 LD26737 11C4-11D1 ID:85G10

CG12234+ unknown exportin CG12234 LD26789 dup:1/2 ID:85G12

+ 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

CG7824 + unknown * unknown(aa) * 2e-14 unknown * * [PPASE // NLS_BP] CG7824 LD26655 99C6-99C7 ID:85G3

+ exu RNA_binding * Exuperantia (exu) protein - fruit fly (Drosophila melanogaster)(aa) * exu * 1e-158 exuperantia protein - fruit

CG8994 fly (Drosophila virilis) * exu [LECTIN_LEGUME_BETA] CG8994 LD26657 57B2-57B2 ID:85G4

+ transcription_factor * 2e-11 AZF1_YEAST ASPARAGINE-RICH ZINC FINGER PROTEIN AZF1 fin * Zinc finger-AT hook

protein * 3e-15 contains multiple of strong similarity to C2H2[zf-C2H2 // ZINC_FINGER_C2H2 // ZINC_FIN] CG10274 LD26701

CG10274 65A6-65A6 ID:85G6

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

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

+ protein_phosphatase * 3e-11 PVH1_YEAST PROTEIN-TYROSINE PHOSPHATASE YVH1 (PTPASE YVH1) * 3e-14

puckered protein * 9e-19 Similar to protein-tyrosine phosphatase * [DSPc // TYR_PHOSPHATASE_DUAL // TYR_PHO] CG6238

CG6238 LD26729 98F1-98F1 dup:1/4 ID:85G9

+ unknown * 1e-35 YNU1_YEAST HYPOTHETICAL 98.1 KD PROTEIN IN SPX19-GCR2 INTERGENIC REGION * 1e-118 No

CG9351 definition line found * 3e-51 hypothetical protein * 5e-50 [RANBP1_WASP] CG9351 LD26904 87F8-87F9 dup:3/4 ID:85H10

CG1765 + EcR steroid_hormone_receptor * ECDYSONE RECEPTOR (ECDYSTEROID RECEPTOR) (20-HYDROXY-ECDYSONE

RECEPTOR) (20E RECEPTOR)(aa) * DMECR_4 EcR * 8e-14 ecdysteroid receptor * 6e-51 [STROIDFINGER // hormone_rec // zf-C4 //] CG1765 LD26915 42A7-42A8 ID:85H12

CG10016+ transcription_factor ZINC_FINGER_C2H2, ZINC_FINGER_C2H2_2, zf CG10016 LD26791 dup:2/2 ID:85H2

CG8580 + * 1e-155 inserted at base Both 5' and 3' ends of P element Inverse PCR * * [NLS_BP] CG8580 65F4-65F5 dup:2/2 ID:85H4

+ unknown * 6e-11 hypothetical protein * hypothetical protein * YG73_SYNY3 HYPOTHETICAL TRNA/RRNA

CG14100 METHYLTRANSFERASE * [SpoU_methylase] CG14100 LD26903 76B9-76B9 dup:1/2 ID:85H9

CG9188 + unknown * [NLS_BP] CG9188 LD26930 27C7-27C7 ID:86A2

CG9201 + unknown * [THIOREDOXIN] CG9201 LD26971 13D2-13D2 ID:86A3

+ unknown * 1e-29 predicted using Genefinder * 1e-33 unknown * 1e-29 predicted using Genefinder * 1e-33 unknown

CG10038[ESTERASE] CG10038 LD26985 87B11-87B11 ID:86A6

CG9304 + unknown * 8e-42 cDNA EST comes from this gene * 2e-20 antigen * C15A7.2 * CG9304 LD26991 58B5-58B5 ID:86A7

+ bcd transcription_factor * DNA-binding-protein,transcription-factor(aa) * DMBCDG_3 bcd * 1e-125 bcd protein * 8e-52 homeotic protein bicoid - fruit fly (Drosophila ps[RNP_1 // HOMEBOX_1 // homeobox // HOME] CG1034 LD27003 84D1-84D1 dup:1/2

CG1034 ID:86A8

+ cell_cycle_regulator * protein(aa) * HYPOTHETICAL 93.9 KD PROTEIN T20B12.6 IN CHROMOSOME III(aa) * 5e-05

USF2_MOUSE UPSTREAM STIMULATORY FACTOR (UPSTREAM TRANSCRIPT[HLH // HELIX_LOOP_HELIX_2 // NLS_BP]

CG18362 CG18362 LD27073 39D1-39D2 dup:3/4 ID:86B10

CG9828 + chaperone DnaJ homolog 2 DNAJPROTEIN CG9828 LD27049 dup:2/2 ID:86B6

+ 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 CG10602 LD27070 37B4-37B5 ID:86B9

+ dnk enzyme * 1e-145 deoxynucleoside kinase * 2e-31 DCK_MOUSE DEOXYCYTIDINE KINASE (DCK) deoxycytidine kina *

CG5452 1e-49 thymidine kinase * 2e-30 DCK_RAT DEOXYCYTIDINE [ATP_GTP_A] CG5452 94A3-94A3 dup:2/2 ID:86C1

+ glutathione_transferase * 1e-24 contains similarity to glutathione S transferases * 2e-26 glutathione-S-transferase homolog *

CG6673 2e-30 glutathione-S-transferase like glutathion [GST] CG6673 LD27185 66D4-66D5 ID:86C12

+ 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

+ 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

CG9028 + unknown * 2e-15 inserted at base 5' end of P element Inverse PCR * CG9028 LD27194 70C8-70C9 dup:2/2 ID:86D1

CG6005 + NLS_BP CG6005 LD27322 dup:2/2 ID:86D10

CG7396 + unknown * [PPASE // NLS_BP] CG7396 LD27215 71E1-71E1 dup:2/2 ID:86D3

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

+ transporter * 2e-14 aquaporin * 5e-22 BIB_DROME NEUROGENIC PROTEIN BIG BRAIN bib protein - frui * 6e-22 similar to

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

+ 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
 CG8284 67B12-67B12 dup:2/2 ID:86E11
 + poly-U-binding-splicing-factor RNA_binding * siah binding protein 1(aa) * 4e-13 PABP_YEAST POLYADENYLATE-BINDING
 PROTEIN, CYTOPLASMIC AND NUCLEAR (PABP) (ARS CO * 3e-14 polyadenylate-bind[RNP_1 // RBD // rrm] CG12085 LD27486
 CG12085 62A4-62A4 dup:2/2 ID:86E12
 + Similar to a hydrophilic protein that is peripherally associated with the late Golgi in yeast. Homology to uncharacterized
 CG3338 proteins in Arabidopsis, h CG3338 LD27356 dup:3/3 ID:86E2
 + 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
 CG1444 + enzyme PUTATIVE STEROID DEHYDROGENASE ADH_SHORT, GDHRDH, adh_short CG1444 LD27387 dup:3/3 ID:86E5
 + Aats-pheenzyme * 8e-84 mitochondrial phenylalanyl-tRNA synthetase alpha subunit precursor * 1e-125 phenylalanine-tRNA
 synthetase * phenylalanyl tRNA synthetase * Aat [AA_TRNA_LIGASE_II_1 // AA_TRNA_LIGASE_I] CG13348 LD27389 50C20-
 CG13348 50C20 dup:2/2 ID:86E6
 CG5868 + CG5868 dup:2/2 ID:86E9
 CG6066 + unknown * O1(aa) * 2e-31 predicted protein of unknown function thal * * [NLS_BP] CG6066 LD27582 97E8-97E8 ID:86F10
 + transporter * 8e-11 syntaxin * 3e-17 hypothetical protein * 2e-17 syntaxin * 1e-19 inserted at base 5' end of P element
 CG11278 Inverse PCR [T_SNARE // Syntaxin] CG11278 LD27581 69F2-69F2 ID:86F9
 + protein_phosphatase * PROTEIN PHOSPHATASE 2C GAMMA ISOFORM (PP2C-GAMMA) (FIBROBLAST GROWTH
 FACTOR INDUCIBLE PROTEIN 13) (FIN13)(aa) * PROTEIN PHOSPHATASE 2C GAMMA ISOFORM [PP2C_1 // PP2C // PP2C_2]
 CG10417 CG10417 LD27655 41D1-41D1 ID:86G1
 + 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
 + transmembrane_receptor * contains similarity to M. musculus patched * 1e-21 No definition line found * [PEROXIDASE_1 //
 CG2019 5TM_BOX // NLS_BP] CG2019 LD27661 83C4-83C4 dup:3/4 ID:86G4
 CG8229 + unknown * CG8229 LD27667 44F12-45A1 dup:2/2 ID:86G5
 + 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
 CG17520 LD27706 cyto_unknown ID:86G9
 CG12030 + enzyme GALACTOWALDENASE) (UDP-GALACTOSE 4-EPIMERAS Epimerase CG12030 LD27852 dup:2/2 ID:86H11
 + 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
 CG4710 + unknown * CG4710 21E-21E dup:2/2 ID:86H5
 + GAP signal_transduction * Cdc42 GTPase-activating protein(aa) * Rga1p (Dbm1p)(aa) * DMC23E12 * ABR protein - human(aa)
 CG10538 [RHO_GAP // RhoGAP // SH3] CG10538 LD27836 38A-38A dup:2/3 ID:86H9

+ zimp nucleic_acid_binding * map_position:45A4-8 * Zimp-A(aa) * 2e-19 NFI1_YEAST NFI1 PROTEIN NFI1 protein - yeast
 CG8068 (Saccharom * 6e-43 cDNA EST comes from this gene; cDNA EST co CG8068 LD27861 45A13-45B1 dup:1/5 ID:87A1
 + protein_phosphatase * 7e-33 protein-tyrosine phosphatase; PTPase; MPTP-MEG2 * 1e-32 protein tyrosine phosphatase,
 non-receptor type * 7e-40 protein-tyrosine-phosphatase ([G_PROTEIN_RECEPTOR // CRAL_TRIO] CG3102 LD27988 8F2-8F2
 CG3102 ID:87A10
 + Rad23 DNA_repair_protein * DHR23(aa) * 2e-30 UV excision repair protein UV exci * 9e-05 ubiquitin / ribosomal protein S27a -
 CG1836 fruit fly (Drosophila melanogaster) * 4e-38 Simila [UBA // ubiquitin // UBIQUITIN_2] CG1836 102A8-102A8 dup:1/3 ID:87A11
 + ion_channel * similar to S. cerevisiae HAP4 transcriptional activator (SP:HAP4_YEAST, similar to regulatory domain of PI3-
 CG1976 kinase P85-alpha subunit (phosphatidylin [PDZ] CG1976 LD28013 100F1-100F2 ID:87A12
 + receptor * 4e-16 VTI1_YEAST VESICLE TRANSPORT V-SNARE PROTEIN VTI1 proba * 3e-27 cDNA EST yk433f11.3
 CG3279 comes from this gene; cDNA EST yk433f11.5 come * 3e-32 put CG3279 LD27967 61C9-61C9 dup:1/3 ID:87A9
 + noc transcription_factor * zinc finger protein noca - fruit fly (Drosophila melanogaster) (L1 * DMNOVA_3 noc * * [zf-C2H2 //
 CG4491 ZINC_FINGER_C2H2_2] CG4491 LD28078 35A4-35A4 ID:87B10
 + enzyme_activator * 1e-29 YQK1_CAEEL HYPOTHETICAL 55.9 KD PROTEIN C56G2.1 IN CHROMOSOME III (U * 6e-32
 CG3249 AKAP121 * 9e-33 A kinase anchor protein, 149kD * 9e-35 A-kinase a [TUDOR] CG3249 LD28079 4F8-4F9 dup:2/3 ID:87B11
 CG9924 + actin_binding CG9924 LD28030 dup:2/2 ID:87B2
 + lola transcription_factor * DMPIPSQ1_3 psq * BtbV * lola * 1e-171 LOLS_DROME LOLA PROTEIN, SHORT ISOFORM
 CG12052 (LONGITUDINALS LACKING PROTEIN) [BTB] CG12052 LD28033 47A-47A ID:87B3
 + transmembrane_receptor * InR * INSULIN RECEPTOR-RELATED PROTEIN PRECURSOR (IRR) (IR-RELATED
 RECEPTOR)(aa) * 2e-52 INSR_DROME INSULIN-LIKE RECEPTOR PRECURSOR insulin recep[Recep_L_domain // Furin-like]
 CG10702 CG10702 LD28036 37B13-37B13 dup:2/3 ID:87B4
 + unknown * splicing factor 30, survival of motor neuron-related; SPF 30(aa) * SMN gene * CG17454 LD28068 cyto_unknown
 CG17454 ID:87B8
 CG2218 + unknown * 1e-21 protein * * [ZINC_FINGER_C3HC4] CG2218 LD28173 99F6-99F6 ID:87C11
 + 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
 + DNA_repair_protein * 5e-20 predicted using Genefinder; similar to MUTT protein like; cDNA EST * 9e-05 YZGD_BACSU
 HYPOTHETICAL 45.4 KD PROTEIN IN THIAMINASE I 5'REGION * [MUTT // mutT // MUTTDOMAIN] CG10898 LD28119 86E13-
 CG10898 86E13 ID:87C5
 + BG:DS05899.1 enzyme * protein(aa) * fadD15(aa) * putative long chain fatty acid coA ligase(aa) * protein(aa) [AMP-binding]
 CG4500 CG4500 LD28132 34E4-34E4 ID:87C8
 CG15427 + cell_adhesion CG15427 LD28224 dup:1/2 ID:87D1
 + unknown * 5e-29 candidate adaptor protein CED-6 * 8e-05 m-Numb * 2e-07 E2a-Pbx1-associated protein * 3e-05 JIP-1
 CG11804 related protein [PTB_DOMAIN // PID] CG11804 LD28347 45D7-45D8 ID:87D10
 + Mcm5 DNA_replication_factor * Mcm5 * 1e-176 MCM5_YEAST MINICHROMOSOME MAINTENANCE PROTEIN (CELL
 DIVISION CONTROL PROTEIN * MCM5 homolog * MCM5_CAEEL DNA REPLICATION LICENSIN[MCM // MCM_1 // MCM_2 //
 CG4082 NLS_BP] CG4082 LD28351 86C5-86C5 dup:3/5 ID:87D11

+ unknown * * 1e-05 HR12_MOUSE HEAT-RESPONSIVE PROTEIN heat-responsive prot * 7e-05 UK14_HUMAN 14.5 KD
 TRANSLATIONAL INHIBITOR PROTEIN (P14.5) (UK114 ANTIGEN H [UPF0076 // PROTEIN_KINASE_ATP] CG1578 LD28359
 CG1578 10E3-10E4 dup:4/5 ID:87D12
 CG2061 + BcDNA:LD28247 G protein-coupled receptor 69A CRYSTALLIN_BETAGAMMA CG2061 LD28247 dup:2/3 ID:87D2
 + sn actin_binding * singed protein - fruit fly (Drosophila melanogaster)(aa) * DMSING2_2 sn * SING_DROME SINGED
 CG1536 PROTEIN singed * 2e-96 FASC_MOUSE FASCIN fasci - mouse CG1536 LD28250 7D2-7D2 ID:87D3
 + Cht2 enzyme * chitinase(aa) * 4e-66 chitinase * 3e-53 CHIT_CAEEL PUTATIVE ENDOCHITINASE coded for by C. elegans *
 CG2054 8e-60 BRP39 protein - mouse BRP39 protein m [CHITINASE_18 // Glyco_hydro_18] CG2054 LD28264 62B1-62B1 ID:87D4
 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
 + enzyme * DMUBCD1_2 eff * ben * UBIQUITIN-CONJUGATING ENZYME E2-18 KD (UBIQUITIN-PROTEIN LIGASE)
 (UBIQUITIN CARRIER PROTEIN)(aa) * ubiquitin-conjugating enzym [UBIQUITIN_CONJUGAT // UQ_con // UBIQUIT] CG4443
 CG4443 LD28310 14F2-14F2 ID:87D8
 + 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
 + Dhod enzyme * DMDHORO_3 Dhod * 2e-10 PYRD_YEAST DIHYDROOROTATE DEHYDROGENASE (DIHYDROOROTATE
 OXIDASE) (DHODEHASE) * dihydroorotate oxidase (EC 1.3.3.1), mitochond [FMN_ENZYMES // DHODEHASE_1 // DHodehase]
 CG9741 CG9741 LD28427 85A10-85A10 dup:2/2 ID:87E10
 CG16972 + motor_protein * [NLS_BP] CG16972 LD28380 34A9-34A9 dup:4/4 ID:87E5
 + G_protein_linked_receptor * Dfz2(aa) * 1e-32 transmembrane receptor * 2e-60 transmembrane receptor * 1e-43 frizzled
 CG4626 (Drosophila) homolog frizzled homo [Fz // FRIZZLED] CG4626 LD28410 6F5-6F5 dup:2/2 ID:87E9
 + Scsalphaenzyme * succinyl-CoA synthetase alpha subunit(aa) * 7e-75 SUCA_YEAST PROBABLE SUCCINYL-COA LIGASE
 CG1065 (GDP-FORMING), ALPHA-CHAIN PRECURSOR (S * 8e-41 succinyl c CG1065 64C4-64C4 dup:2/4 ID:87F1
 CG16798 + CG16798 dup:2/3 ID:87F12
 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
 + RNA_binding * dJ222E13.3.2 (PUTATIVE partial isoform 2)(aa) * DMBNBR_2 bnb * CG6961 LD28479 17D5-17D5 dup:3/4
 CG6961 ID:87F6
 + protein_kinase * 5e-49 PAN3_YEAST PAB-DEPENDENT POLY(A)-SPECIFIC RIBONUCLEASE SUBUNIT PAN3 (PAB1P-
 DEPEND * 2e-92 YOT7_CAEEL HYPOTHETICAL 76.2 KD PROTEIN ZK632.7 IN CH [AA_TRNA_LIGASE_II_2 // ANTIFREEZEI]
 CG11486 CG11486 63F4-63F4 dup:1/6 ID:87G3
 CG10346 + chaperone * CG10346 37A4-37A4 dup:1/3 ID:87G7
 CG6407 + signal_transduction CG6407 dup:3/3 ID:87H5
 CG17870 + unknown CG17870 dup:3/4 ID:87H7
 CG1218 + CG1218 ID:87H9

CG1542 + CG1542 ID:88A10
 + chaperone * 1e-14 embryonal lethal (2)13-1 (el(2)13-1) - fruit fly (*Drosophila melanogaster*) * 4e-41 similar to small heat
 CG14207 shock protein HSP20 family * 1e-12 CR [HSP20 // ACRYSTALLIN] CG14207 18D8-18D8 dup:3/4 ID:88B12
 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 melanogaster*)
 CG1826 * 7e-12 Kelch motif containing [BTB // PROTEIN_SPLICING // NLS_BP] CG1826 9E2-9E2 dup:2/2 ID:88B4
 CG9216 + unknown * [NLS_BP] CG9216 14A6-14A8 ID:88B5
 CG18041+ CG18041 ID:88B6
 CG12081+ unknown CG12081 ID:88C3
 CG12132+ unknown * 7e-30 C34G6.1 gene product * CG12132 8D8-8D8 dup:1/3 ID:88C6
 CG11177+ CG11177 ID:88C8
 CG3661
 + * 2e-47 precursor TRG1 protein * D-ERp60=protein disulphide isomerase isoform/multifunctional endoplasmic retic * 1e-136
 CG8983 predicted using Genefinder; S [THIOREDOXIN // THIOREDOXIN_2 // thioered] CG8983 48D1-48D1 dup:3/4 ID:88D12
 + * EPIDIDYMAL SECRETORY PROTEIN E1 PRECURSOR (CE1)(aa) * 4e-22 epididymal secretory protein * 9e-23
 CG7291 EP1_HUMAN EPIDIDYMAL SECRETORY PROTEIN E1 PRECURSOR CG7291 22B8-22B8 dup:2/3 ID:88D3
 CG8116 + unknown * 1e-108 inserted at base 3' end of P element Inverse PCR * * CG8116 85B2-85B2 dup:1/2 ID:88D7
 CG7407 + CG7407 dup:1/2 ID:88D9
 CG13849+ unknown CG13849 dup:2/2 ID:88E12
 + unknown * histone acetyltransferase 1(aa) * histone acetyltransferase; Hat1p(aa) * weak similarity with SINR protein (Swiss
 CG2051 Prot accession number cDNA EST co [NLS_BP] CG2051 83C-83C dup:2/3 ID:88F12
 + 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
 CG16901+ CG16901 ID:88G12
 + structural_protein * 0.000000000006* 2e-06 nonmuscle myosin-II heavy chain * 2e-07 Identity to myosin heavy chain C
 CG12702(SW:MYSC_CAEEL); cDNA EST EMBL:M8 * 0.0000001 CG12702 18F1-18F2 dup:1/3 ID:88G4
 CG1596 + CG1596[unknown|CT3517 ID:88G5
 + Rpl140 enzyme * polymerase (RNA) II (DNA directed) polypeptide B (140kD)(aa) * DNA-DIRECTED RNA POLYMERASE
 SUBUNIT B'(aa) * second largest subunit of RNA polymerase [RNA_pol_B // RNA_POL_BETA] CG3180 88A10-88A11 dup:2/3
 CG3180 ID:88G9
 CG7471 + enzyme CG7471 ID:88H1
 + EG:EG0007.12 unknown * by content; by motif; 2-match_description=ATP/GTP-binding site motif A (P-l...(aa) * by content; 1-meth
 CG4857 * by content; 1-meth * CG4857 4B1-4B2 dup:3/3 ID:88H5
 CG11723+ transcription_factor * [AA_TRNA_LIGASE_II_1] CG11723 22C3-22C3 dup:2/2 ID:88H7

CG5094 + chaperone CG5094 dup:2/2 ID:88H9
 + * 6e-24 predicted using Genefinder; similar to zinc-finger protein; cDNA E * 8e-05 DNA-binding protein BZP - golden
 CG1244 hamster DNA-binding prot * 2e-06 z [zf-C2H2 // ZINC_FINGER_C2H2 // PRO_RICH] CG1244 62F2-62F2 dup:2/5 ID:89A1
 CG9277 + betaTub56D cytoskeletal_structural_protein beta-1 tubulin TUBULIN, TUBULIN_B_AUTOREG, tubulin CG9277 ID:89A3
 + unknown * predicted using Genefinder(aa) * 3e-12 predicted using Genefinder * * [SAM_DOMAIN] CG16812 34A10-34A10
 CG16812 dup:1/4 ID:89A4
 + Ef1alpha48D ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) (50 KD FEMALE-SPECIFIC PROTEIN ATP_GTP_A,
 CG8280 EFATOR_GTP, ELONGATNFCT, GTP] CG8280 dup:2/2 ID:89B10
 CG8789 + protein_kinase CG8789 dup:2/2 ID:89B2
 CG17678 + CG17678 dup:2/2 ID:89B3
 + * C15H9.5 gene product(aa) * 5e-05 by content; 1-meth * 5e-70 C15H9.5 gene product * 1e-05 NEUM_MOUSE
 CG12121 NEUROMODULIN (AXONAL MEMBRANE PROTEIN GAP-43) (P CG12121 8D4-8D5 dup:2/3 ID:89B4
 CG2186 + homolog of a human hypothetical protein DKFZp434D1319.1 NLS_BP CG2186 LD29862 dup:1/2 ID:89C10
 + P34-ARC actin_binding PROBABLE ARP (actin related protein) 2/3 COMPLEX 34 KDA SUBUNIT CG10954 LD29815 dup:2/3
 CG10954 ID:89C2
 + transcription_factor * 4e-30 alternatively spliced form * 4e-07 BAC1_MOUSE TRANSCRIPTION REGULATOR PROTEIN
 CG8924 BACH1 (BTB AND CNC HOMOLOG 1) * 2e-07 actin binding protein MAYV [BTB] CG8924 LD29820 13F14-13F14 ID:89C4
 + * VESICLE-ASSOCIATED MEMBRANE PROTEIN/SYNAPOBREVIN BINDING PROTEIN (VAP-33)(aa) * 2e-09
 SCS2_YEAST SCS2 PROTEIN SCS2 protein - yeast (Saccharomy * 6e [MSP_domain // MSP_DOMAIN] CG5014 4A2-4A2
 CG5014 dup:2/3 ID:89D12
 + BcDNA:LD29885 unknown * coatomer protein complex, subunit epsilon(aa) * PROBABLE COATOMER EPSILON SUBUNIT
 (EPSILON-COAT PROTEIN) (EPSILON-COP)(aa) * COATOMER EPSILON SUBUNI CG9543 LD29885 26D7-26D7 dup:1/2
 CG9543 ID:89D2
 + unknown * cDNA EST comes from this gene; cDNA EST comes from this gene; cDNA EST yk228b12.5 comes from this
 CG7022 gene; cDNA EST yk273g2.5 comes from this gene; cD CG7022 LD30146 61B1-61B1 dup:2/3 ID:89F1
 + UbcD10 enzyme (Ubiquitin conjugating enzyme 10) similar to ubiquitin conjugating enzymes [Caenorhabditis elegans]
 CG5788 UBIQUITIN_CONJUGAT, UBIQUITIN_CONJUGAT_2] CG5788 LD30207 dup:3/3 ID:89F12
 + 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
 CG4602 + CG4602 dup:3/4 ID:89H6
 CG4488 + protein_kinase CG4488 ID:89H8
 CG7065 + unknown * [NLS_BP] CG7065 LD35502 8C17-8C17 ID:95A12
 + * canalicular multispecific organic anion transporter (ABC superfamily)(aa) * cadmium resistance protein YCF1 - yeast
 CG10441 (Saccharomyces cerevisiae) * 1e- [ATP_GTP_A2 // ABC_TRANSPORTER // ABC_tr] CG10441 37B9-37B9 dup:1/2 ID:95C1
 CG5456 + unknown * CG5456 LD35728 94A3-94A3 ID:95C10

+ RNA_binding * splicing factor (CC1.3)(aa) * 5e-12 polyadenylated RNA-binding protein PUB1 - yeast (Saccharomyces cerevisiae) >g * 7e-11 RNA-binding protein * 1e-1 [RNP_1 // RBD // rrm // NLS_BP] CG11266 LD35730 27D-27D3 dup:1/2
 CG11266 ID:95C11
 + E2f transcription_factor * E2f * E2F * 1e-19 predicted using Genefinder; cDNA EST comes from this * 5e-35 E2F3_MOUSE
 CG6376 TRANSCRIPTION FACTOR E2F3 (E2F-3) transcripti [NLS_BP] CG6376 LD35741 93F1-93F1 dup:2/3 ID:95C12
 + unknown * BLASTX 1.2E-22 Human YL-1 mRNA for YL-1 protein (nuclear protein with DNA-binding ability), complete
 CG4621 cds.(dna) * transcription factor-like 1(aa) * t [NLS_BP] CG4621 LD35676 34A3-34A3 ID:95C3
 CG7705 + unknown * CG7705 LD35690 91B7-91B8 ID:95C5
 + CycC cell_cycle_regulator * DMCYCLCG_2 CycC * cyclin C(aa) * cyclin C protein(aa) * cyclin C(aa) CG7281 LD35705 88D8-88D8 dup:3/3 ID:95C8
 CG7281 + Arp66B cytoskeletal_structural_protein * DMACTR66B_2 Arp66B * 1e-126 ARP3_YEAST ACTIN-LIKE PROTEIN ARP3 actin homolog YJR065 * ARP3_DROME ACTIN-LIKE PROTEIN (ACTIN-LIKE PROTEIN 66B) (ACTIN [ACTINS_ACT_LIKE // actin]
 CG7558 CG7558 LD35711 66B8-66B8 ID:95C9
 + CDC45L DNA_replication_factor * CDC45L * 2e-31 Cdc45p: assembles into a complex with Cdc46p/Mcm5p * CDC45L * 1e-30
 CG3658 predicted using Genefinder; cDNA EST yk307h3.3 comes from this ge CG3658 LD35753 1E1-1E1 ID:95D1
 + unknown * 8e-73 YIJ1_YEAST HYPOTHETICAL 84.0 KD PROTEIN IN SGA1-KTR7 INTERGENIC REGION * 1e-119
 CG3735 dJ434O14.5 (novel PUTATIVE protein similar to YIL091C yeast hy CG3735 LD35854 60A11-60A11 ID:95D10
 + RNA_binding * HYPOTHETICAL PROTEIN * 3e-23 YKB7_YEAST HYPOTHETICAL 78.3 KD PROTEIN IN RAM2-ATP7 INTERGENIC REGION * 9e-11 cDNA EST yk384f3.5 comes from this gene; [zf-CCCH] CG9425 LD35863 70F6-70F6 dup:3/3
 CG9425 ID:95D12
 + 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
 CG2856 3F2-3F2 dup:2/2 ID:95D2
 + Rad51 DNA_repair_protein * DMDMRBA_1 Rad51 * 2e-97 RA51_YEAST DNA REPAIR PROTEIN RAD51 RAD51 protein - yeast * 1e-176 RA51_DROME DNA REPAIR PROTEIN RAD51 HOMOLOG (RECA PROTEIN [HHH // RECA_1 // RECA_2 // ATP_GTP_A] CG7948 LD35801 99D5-99D6 ID:95D3
 CG7948 + Bub1 enzyme * Bub1 * 4e-75 hypothetical protein YLR419w - yeast (Saccharomyces cerevisiae) (U * DDX9_CAEEL PROBABLE ATP-DEPENDENT RNA HELICASE A (NUCLEAR DNA HEL [PROTEIN_KINASE_ST // pkinase // PROTEIN] CG7838
 CG7838 LD35813 42A1-42A1 ID:95D5
 CG15435 + nucleic_acid_binding * [ZINC_FINGER_C2H2 // ZINC_FINGER_C2H2_2] CG15435 LD35850 24F5-24F5 ID:95D9
 + lace enzyme * 1e-107 LCB2_YEAST SERINE PALMITOYLTRANSFERASE (LONG CHAIN BASE BIOSYNTHESIS PROTEIN * 2e-24 delta-aminolevulinat synthase * 1e-128 Similar to serin [aminotran_2 // AA_TRANSFER_CLASS_2 // N] CG4162 LD36009
 CG4162 35D3-35D3 dup:2/2 ID:95E11
 + protein_kinase * DMRNASTK_2 mnb * protein kinase Dyrk1B(aa) * MNB(aa) * SRPK1(aa) [PROTEIN_KINASE_ST // CG8174 PROTEIN_KINASE_DOM] CG8174 LD35909 51F11-51F11 dup:3/3 ID:95E3
 + unknown * dimethylase(aa) * 2e-97 DIM1_YEAST DIMETHYLADENOSINE TRANSFERASE (S-ADENOSYLMETHIONINE-CG11837 6-N', N'-ADENOSY * 4e-99 YQN1_CAEEL HYPOTHETICAL 34.1 KD PROT [RnaAD // RRNA_A_DIMETH // SAM_BIND] CG11837

LD35950 98F9-98F9 dup:2/2 ID:95E6
+ signal_transduction * 5e-11 CC4_YEAST CELL DIVISION CONTROL PROTEIN cell division * 8e-25 Lis1 homolog * 1e-127
YPR4_CAEEL HYPOTHETICAL 77.0 KD TRP-ASP REPEATS CO[GPROTEINBRPT // WD40_REGION // WD_REPEA] CG9062

CG9062 LD35961 47E3-47E3 dup:4/4 ID:95E7
+ motor_protein * 6e-08 F35D11.11 gene product * YL17_CAEEL HYPOTHETICAL 131.5 KD PROTEIN C02F12.7 IN

CG17081 CHROMOSOME X (* [NLS_BP] CG17081 LD35990 71B2-71B2 dup:3/3 ID:95E9
+ Eip55E enzyme * Yfr055wp(aa) * ecdysteroid-inducible polypeptide EIP40(aa) * 4e-99 CYS3_YEAST CYSTATHIONINE
GAMMA-LYASE (GAMMA-CYSTATHIONASE) * 1e-133 CGL_CAEEL PUT [Cys_Met_Meta_PP] CG5345 LD36096 55E5-55E5

CG5345 dup:2/2 ID:95F11
+ Irp-1B RNA_binding * Irp-1B * 9e-47 aconitase (ACO1) (EC 4.2.1.3) * iron regulatory protein-1B * ACOC_CAEEL PROBABLE
ACONITATE HYDRATASE, CYTOPLASMIC (CITRATE HYDRO-LYA [ACONITASE_2 // Aconitase_C // aconitase] CG6342

CG6342 LD36108 86A6-86A6 ID:95F12

CG6398 + unknown * 8e-16 coded for by C. elegans cDNA yk81c2.5 * * CG6398 LD36024 16D4-16D4 dup:2/2 ID:95F3
+ nmo protein_kinase * nmo * 2e-58 HOG1_YEAST MITOGEN-ACTIVATED PROTEIN KINASE HOG1 (MAP KINASE HOG1)
(OSMOSENSING * nemo, form I - fruit fly (Drosophila melanogaster) [PROTEIN_KINASE_ST // PROTEIN_KINASE_DOM] CG7892

CG7892 LD36031 67D9-66B4 dup:2/2 ID:95F4

CG1943 + unknown * CG1943 LD36048 84C1-84C1 ID:95F5
+ nucleic_acid_binding * castor protein - fruit fly (Drosophila sp.)(aa) * neuroblast cell lineage zinc finger protein ming - fruit fly

CG2102 (Drosophila melan * I(3)j1C2 I(3)j1C[CRYSTALLIN_BETAGAMMA // ZINC_FINGER_C2H] CG2102 LD36057 83C1-83C1 ID:95F7

CG4454 + unknown * CG4454 LD36125 32A1-32A1 dup:2/3 ID:95G2

CG5175 + CG5175 ID:95H10

CG11658+ unknown * DY3.6(aa) * * CG11658 LD36342 71C2-71C2 dup:2/2 ID:95H11
+ unknown * hormone-sensitive lipase testicular isoform(aa) * 1e-07 similar to the 'GDXG' family of lipolytic enzymes * 4e-83

CG11055 hormone-sensitive lipase * 2e-85 I [ESTERASE] CG11055 LD36294 56F15-56F15 ID:95H7
+ DNA_binding * 3e-05 HP1_DROME HETEROCHROMATIN PROTEIN (HP1) (NONHISTONE CHROMOSOMAL PROTEIN
C1A9 * 6e-06 similar to 'chromo' (CHRromatin Organization Modifier) do [chromo // CHROMO_2 // NLS_BP] CG8289 LD36501

CG8289 16B10-16B10 ID:96A10
+ unknown * 2e-10 transmembrane protein * 6e-12 weak similarity to plasminogens * 2e-12 DMDUSKY_1 dy * similar to

CG7802 cuticlin [NLS_BP] CG7802 LD36439 99C5-99C5 ID:96A7
+ enzyme * bgr;ggt-I * protein farnesyl transferase beta subunit(aa) * farnesyl protein transferase subunit B(aa) * predicted

CG17565 using Genefinder; Similarity t [prenyltrans] CG17565 LD36454 89C3-89C3 dup:1/2 ID:96A8
+ Dlc90F motor_protein * Tctex protein(aa) * DMTCTEXPR_2 Tctex * 1e-61 Tctex protein * 7e-14 predicted using Genefinder;

CG12363 cDNA EST yk460f12.5 comes from this ge CG12363 LD36705 90F7-90F7 ID:96B11
+ enzyme * GLY7(aa) * 1e-165 GLY7 * 1e-104 polypeptide GalNAc transferase-T1 * 1e-103 PAGT_HUMAN POLYPEPTIDE
N-ACETYL GALACTOSAMINYLTRANSFERASE (PROTEIN-UDP ACE [RICIN_B_LLECTIN // GLYC_TRANS // Glycos_] CG6394

CG6394 LD36616 17B4-17B4 dup:1/2 ID:96B8

+ Rpt1 endopeptidase * 1e-166 PRS7_YEAST 26S PROTEASE REGULATORY SUBUNIT HOMOLOG (CIM5 PROTEIN) (TAT-BINDING * 4e-48 transitional endoplasmic reticulum ATPase TER94 * PRS [AAA // ATP_GTP_A] CG1341 LD36653 43E6-43E6
 CG1341 dup:1/3 ID:96B9
 + RNA_binding * Poly(A) binding protein, cytoplasmic and nuclear; Pab1p(aa) * POLYADENYLATE-BINDING PROTEIN
 CG4612 (POLY(A) BINDING PROTEIN) (PABP)(aa) * polyadenylate bin [RNP_1 // RBD // rrm] CG4612 LD36772 60D4-60D4 ID:96C3
 + unknown * 2e-08 YHC6_CAEEL HYPOTHETICAL 81.4 KD PROTEIN ZC434.6 IN CHROMOSOME I PRECURSOR * 3e-53
 CG7012 Y253_HUMAN HYPOTHETICAL PROTEIN KIA * * CG7012 LD36812 96B2-96B3 ID:96C4
 + * similar to Arabidopsis thaliana male sterility protein * 4e-47 /match=(desc;; /ma * 6e-30 male sterility 2-like protein * 4e-49
 CG2858 DMC103B4 CG2858 60E5-60E5 dup:1/2 ID:96C7
 + Csp chaperone * cysteine string protein 1(aa) * 2e-16 MAS5_YEAST MITOCHONDRIAL PROTEIN IMPORT PROTEIN MAS5 (PROTEIN YDJ1) * 4e-19 similar to the DNA-J domain foun [4FE4S_FERREDOXIN // DNAJ_1 // DnaJ // D] CG6395 LD36856
 CG6395 79E1-79E2 dup:1/4 ID:96C8
 + unknown * Yor240wp(aa) * hypothetical protein(aa) * * 1e-56 probable membrane protein YOR240w - yeast
 CG13929 (Saccharomyces cerevisiae) [MET_TRANS // SAM_BIND] CG13929 LD36863 62A10-62A10 ID:96C9
 + 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
 CG4831 32E4-32E4 ID:96D1
 + thr unknown * three rows protein * thr * THR_DROME THREE ROWS PROTEIN chromosome disjunction prot [NLS_BP]
 CG5785 CG5785 LD37031 54F5-54F6 dup:2/2 ID:96D10
 + unknown TRAM PROTEIN (TRANSLOCATING CHAIN-ASSOCIATING MEMBRANE PROTEIN)(aa) NLS_BP CG11642
 CG11642 LD36954 dup:2/2 ID:96D3
 + I(2)k09913 unknown * 1e-22 inserted at base Both 5' and 3' ends of P element Inverse PCR * * CG3082 LD36990 59C3-59C3
 CG3082 dup:2/2 ID:96D4
 CG4877 + unknown * [NLS_BP] CG4877 LD36996 72F1-72F1 dup:2/2 ID:96D5
 CG13626 + unknown * 1e-05 No definition line found * [T_SNARE] CG13626 LD37002 96A14-96A14 ID:96D6
 + unknown * 1e-111 protein * 1e-114 UNR_RAT UNR PROTEIN probable unr protein - rat * unknown [COLD_SHOCK // CSD]
 CG7015 CG7015 LD37025 66C13-66C13 dup:2/4 ID:96D9
 + 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 // CG8637 PROTEIN_KINASE_DOM] CG8637 LD37189 76D3-76D3 dup:2/2 ID:96E10
 CG6144 + unknown * predicted using Genefinder(aa) * * CG6144 LD37206 31E4-31E4 dup:2/2 ID:96E12
 + 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
 + Noa36 nucleic_acid_binding * nucleolar protein, putative(aa) * 1e-111 cysteine-rich protein * 1e-110 Zn finger factor *
 CG10009 [NLS_BP] CG10009 LD37139 98D3-98D3 dup:2/2 ID:96E5
 CG5541 + unknown * [C_TYPE_LLECTIN_1] CG5541 LD37145 13A8-13A8 dup:3/3 ID:96E6
 CG13601 + unknown * 7e-08 No definition line found * * CG13601 LD37258 95C-95C ID:96F10

CG8825 + unknown * 3e-18 Contains similarity to Pfam domain: (PLDc), Score=13.8, * * CG8825 LD37277 23D4-23D4 ID:96F12
+ fs(1)K10DNA_binding * regulatory protein K10, oocyte-specific - fruit fly (*Drosophila melanogaster*)(aa) * DMK10G_4 fs(1)K10 *

CG3218 4e-58 K10_DROME DNA-BINDING PROTEIN K10 * 62 [PRO_RICH] CG3218 LD37240 2F1-2F1 ID:96F7
+ transporter * cationic amino acid transporter-1(aa) * solute carrier family (cationic amino acid transporter, y+ system), member 1(aa) * LOW-AFFINITY CATIONIC AMI [aa_permeases // AMINO_ACID_PERMEASE_2] CG11128 LD37241 79F5-79F6

CG11128 dup:2/2 ID:96F8
+ unknown * 8e-08 predicted using Genefinder; similar to WW domain * 1e-07 inserted at base Both 5' and 3' ends of P

CG8949 element Inverse PCR * [WW_rsp5_WWP // WW_DOMAIN_1 // NLS_BP //] CG8949 15D1-15D1 ID:96G10
+ function_unknown * 2e-05 hypothetical protein YDL115c - yeast (*Saccharomyces cerevisiae*) * 5e-09 hypothetical protein *

CG10528 2e-43 inserted at base 5' end of P element Inve CG10528 LD37329 38A-38A4 dup:1/3 ID:96G3
+ unknown * No definition line found(aa) * 3e-40 hypothetical protein YER007c-a - yeast (*Saccharomyces cerevisiae*) * 3e-58

CG5941 No definition line found * 3e-39 hypo CG5941 LD37358 5D1-5D1 ID:96G7

CG4865 + EG:EG0007.10 unknown * by content; * 1e-92 by content; 1-meth * 1E-94* CG4865 LD37360 4B1-4B1 ID:96G8
+ ion_channel * outer membrane protein(aa) * The gene product is related to adenylyl cyclase.(aa) * 1e-18 DLG1_DROME

CG5462 LETHAL(1)DISCS LARGE-1 TUMOR SUPPRESSOR PROTEIN [PDZ] CG5462 LD37377 100B1-97B9 dup:1/3 ID:96G9
+ B52 RNA_binding * transcription, DNA-dependent mRNA splicing) RNA binding RNA binding) nucleic acid binding pre-mRNA

CG10851 splicing factor) * DMB52_2 B52 * 52K active ch [RBD // rrm // NLS_BP] CG10851 LD37428 87F7-87F7 ID:96H1

CG6311 + unknown * CG6311 LD37618 74D2-74D2 dup:1/2 ID:96H12
+ enzyme * protein(aa) * 3e-37 PAN2_YEAST PAB-DEPENDENT POLY(A)-SPECIFIC RIBONUCLEASE SUBUNIT PAN2 (PAB1P-DEPE * 4e-59 YPO4_CAEEL HYPOTHETICAL 127.2 KD PROTEIN [UCH_2_3 // Exonuclease] CG8232 LD37466 44F9-

CG8232 44F11 dup:1/4 ID:96H2
+ RNA_binding * * 3e-33 cDNA EST yk500a3.3 comes from this gene; cDNA EST yk500a3.5 comes * 2e-64 inserted at base

CG2503 Unknown 5' end of P element Plasmid rescue * CG2503 LD37523 82E1-82E1 ID:96H6

CG10076 + unknown * PEM-5(aa) * * CG10076 38C6-38C7 dup:3/5 ID:96H9

CG2961 + unknown * [KININOGEN] CG2961 LD38046 9B7-9B7 ID:97C11

CG2669 + unknown * [NLS_BP] CG2669 LD38047 83A4-83A5 ID:97C12
+ enzyme * 1e-171 SYMC_YEAST METHIONYL-TRNA SYNTHETASE, CYTOPLASMIC (METHIONINE--TRNA LIGASE) (ME * 1e-08 SYEP_DROME MULTIFUNCTIONAL AMINOACYL-TRNA SYNTHETASE [tRNA-synt_1 // TRNASYNTHMET // WHEP-

CG15100 TRS] CG15100 LD37969 55F3-55F4 ID:97C3
+ transcription_factor * Cys2/His2 zinc finger protein(aa) * ovo * fruit fly STS clone SP6(dna) * zinc finger protein NY-REN-21

CG4639 antigen(aa) [zf-C2H2 // ZINC_FINGER_C2H2 // ZINC_FIN] CG4639 LD38072 94E-94E ID:97D4

CG8928 + unknown * CG8928 LD38104 13F14-13F14 ID:97D7
+ 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

CG9165 61F7-61F7 dup:2/2 ID:97D8

CG5109 + transcription_factor * DMPLYCMB_2 Pcl * BLASTX 2.1E-16 element DNA-binding protein(dna) * polycomblike nuclear

protein [PHD // PRO_RICH] CG5109 LD38218 55B5-55B7 dup:3/3 ID:97E2
 + unknown * 1e-18 hypothetical protein YDR330w - yeast (*Saccharomyces cerevisiae*) (U * 3e-35 protein * 1e-24 ubiquitin
 CG8892 regulatory domain protein * 1E-111 [UX_DOMAIN] CG8892 LD38226 25B-25B9 dup:2/2 ID:97E3
 + unknown * hypothetical protein(aa) * Hrt2p(aa) * F31D4.2(aa) * hypothetical protein(aa) CG2921 LD38241 58C1-58C1
 CG2921 dup:2/2 ID:97E5
 + Ubp64E endopeptidase * DMUBP_2 Ubp64E * 9e-55 UBPF_YEAST UBIQUITIN CARBOXYL-TERMINAL HYDROLASE
 (UBIQUITIN THIOLESTERASE * UBPE_DROME UBIQUITIN CARBOXYL-TERMINAL HYDROLASE [UCH_2_1 // UCH_2_2 //
 CG5486 UCH_2_3 // UCH-1] CG5486 LD38333 64E13-66A5 ID:97F1
 + EG:8D8.4unknown * /match=(desc:(aa) * 5e-48 hypothetical protein YDR365c - yeast (*Saccharomyces cerevisiae*) (U * 6e-34
 CG11417 cDNA EST comes from this gene * 4e-60 hypothet [NLS_BP] CG11417 LD38432 2A2-2A2 dup:2/2 ID:97F9
 + unknown * 5e-10 FIP1_YEAST FIP1 PROTEIN FIP1 protein - yeast (*Saccharom* * 3e-16 contains similarity to *S. cerevisiae*
 CG1078 FIP1 * 2e-13 YAAA_SCHPO HYPOTHETICAL 37.3 [PRO_RICH // NLS_BP] CG1078 LD38592 82C2-82C2 dup:1/3 ID:97G11
 CG8180 + unknown * 1E-178* * [ANTIFREEZEI] CG8180 LD38554 52A4-52A4 dup:1/2 ID:97G8
 + * 2e-45 sulfate permease * 1e-27 Similar to sulfate transporter. * 9e-33 DTD_MOUSE SULFATE TRANSPORTER
 (DIASTROPHIC DYSPLASIA PROTEIN HOMOLOG) (ST-OB) [Sulfate_transp // SUGAR_TRANSPORT_2] CG5002 54E7-54E7
 CG5002 ID:97G9
 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
 + DNA_binding * 7e-32 NAM7_YEAST NAM7 PROTEIN (NONSENSE-MEDIATED MRNA DECAY PROTEIN 1) (UP-
 FRAMESHIFT * 1e-27 nonsense-mediated mRNA decay trans-acting factor * 2[ZINC_FINGER_C2H2 // PRO_RICH // ATP_GTP]
 CG6701 CG6701 LD38709 50C21-50C22 dup:2/2 ID:97H8
 + unknown * weak similarity to ATP/GTP-binding site motif A * 2e-40 weak similarity to ATP/GTP-binding site motif A *elega* *
 CG5924 1e-63 POM1 chabaudi * [ATP_GTP_A] CG5924 LD38710 33A1-33A1 dup:1/2 ID:97H9
 + BcDNA:GH07910 protein_kinase * 7e-22 CC5_YEAST CELL CYCLE PROTEIN KINASE CDC5/MSD2 protein ki * 3e-12 p90
 ribosomal S6 kinase * 1e-121 YKT3_CAEEL PUTATIVE SERINE/THREONINE-[PFKB_KINASES_1 // PROTEIN_KINASE_ST //]
 CG2829 CG2829 LD38852 3F4-3F6 dup:5/6 ID:98B2
 + unknown * 4e-14 YPT2_CAEEL HYPOTHETICAL 21.6 KD PROTEIN F37A4.2 IN CHROMOSOME III * 5e-05 unknown
 CG8441 protein * * [NLS_BP] CG8441 LD38910 52F7-52F7 dup:2/2 ID:98B9
 CG18011 + nucleic_acid_binding * CG18011 LD39136 46E8-46E8 ID:98C11
 + unknown * HYPOTHETICAL 35.0 KD PROTEIN F48E8.1 IN CHROMOSOME III(aa) * Similar to plant PR-1 class of
 pathogen related proteins; Pry3p(aa) * sol i antigen(aa [SCP_AG5_PR1_SC7_2 // V5TPXLIKE // V5ALL] CG8483 LD39025 87E2-
 CG8483 87E3 ID:98C2
 + chromatin_binding * hypothetical protein - human (fragment)(aa) * UVB-resistance protein UVR8(aa) * 8e-06 RCC_YEAST
 REGULATOR OF CHROMOSOME CONDENSATION (PRP20 [RCC1 // RCC1_2 // GRF_RCC // RCCNDNSATI] CG6678 LD39062
 CG6678 93F10-93F10 dup:2/2 ID:98C4
 CG5018 + transcription_factor_binding * Ydr324cp(aa) * 1e-25 hypothetical protein YDR324c - yeast (*Saccharomyces cerevisiae*) (U *

3e-29 hypothetical protein * 7e-05 DMENHSPA_3 gro [WD40_REGION] CG5018 LD39110 72D11-72D12 ID:98C8
 + transcription_factor * 0.00000000006 * 9e-25 YMB4_CAEEL HYPOTHETICAL 104.4 KD PROTEIN F54G8.4 IN
 CG1624 CHROMOSOME III * 4e-13 TIF1 protein - mouse TIF1 isoform Pepti * 8e-24 brai [NHL] CG1624 LD39167 43C5-43C7 ID:98D2
 + unknown * 5e-40 prediabetic NOD sera-reactive autoantigen muscul * 5e-10 IVR-like protein * IVR-like protein *
 CG14444[TPR_REGION // TPR_REPEAT] CG14444 LD39177 6C1-6C1 dup:3/3 ID:98D4
 CG14764+ unknown * CG14764 LD39211 43F6-43F6 ID:98D5
 + enzyme * 9e-41 /match=(desc;; /ma * 5e-35 cDNA EST comes from this gene; cDNA EST co * 9e-06 Ubc84D * contains
 CG4502 similarity to ubiquitin-conjugatin enzymes (Pf [UQ_con // UBIQUITIN_CONJUGAT_2] CG4502 LD39243 27E4-27E4 ID:98D9
 + sli cell_adhesion * DMSLIT_2 sli * slit protein(aa) * 2e-35 contains similarity to multiple EGF-like domains * neurogenic
 CG8355 extracellular slit protein [LRR // LRRNT // EGF_1 // EGF // LEURICH] CG8355 LD39407 52D4-52D7 dup:2/2 ID:98E11
 + unknown * nucleotide binding protein (E.coli MinD like)(aa) * putative nucleotide binding protein(aa) * 7e-82 NB35_YEAST
 CG17904NBP35 PROTEIN NBP35 protein - yeast CG17904 LD39271 36A7-36A7 dup:2/2 ID:98E2
 CG6425 + unknown * CG6425 LD39291 97C3-97C3 dup:2/2 ID:98E3
 + asf1 cell_cycle_regulator * involved in silencing; Asf1p(aa) * Similarity with yeast anti-silencing protein I (Swiss Prot accession
 CG9383 number cDNA EST comes from this gene; cDNA CG9383 LD39377 76C1-76C1 dup:2/2 ID:98E8
 + unknown * inserted at base Both 5' and 3' ends of P element Inverse PCR * 6e-68 inserted at base Both 5' and 3' ends of P
 CG4699 element Inverse PCR * [AA_TRNA_LIGASE_I // NLS_BP] CG4699 LD39557 89A-89A dup:9/11 ID:98F10
 + DNA_binding * 2e-15 YJ89_YEAST HYPOTHETICAL 85.0 KD PROTEIN IN STE24-ATP2 INTERGENIC REGION * 8e-26
 Similarity to Human XE169 protein (SW:XE169_HUMAN); cDNA EST E [ARID // PRO_RICH // NLS_BP] CG3654 LD39559 67B5-
 CG3654 67B5 dup:3/3 ID:98F11
 CG1896 + unknown * [NLS_BP] CG1896 LD39576 100E2-100E2 dup:2/2 ID:98F12
 CG5194 + unknown * CG5194 LD39537 66F1-66F1 ID:98F8
 + mod DNA_binding * DNA-BINDING PROTEIN MODULO(aa) * DMLA9_4 mod * 3e-05 Similarity to Human spliceosome-
 associated protein SAP62 (PIR Acc. * 5e-05 NUCL_MOUSE NUCLEOLIN [RBD // rrm // NLS_BP // ATP_GTP_A] CG2050 100F5-
 CG2050 100F5 dup:3/3 ID:98F9
 + BcDNA:LD27873 actin_binding * 1e-06 RNA-binding protein * 1e-06 NAB2_YEAST NUCLEAR POLYADENYLATED RNA-
 CG5720 BINDING PROTEIN NAB2 * 3e-88 inserted at base Both 5' and 3' ends of P eleme [NLS_BP] CG5720 95F-98B1 dup:5/8 ID:98G12
 + cell_cycle_regulator * non-p53 regulated PA26-T1 nuclear protein(aa) * 2e-72 p53 regulated PA26-T3 nuclear protein * p53
 CG11299regulated PA26-T2 nuclear protein * CG11299 LD39604 59F5-59F6 ID:98G2
 + unknown * 3e-21 hypothetical protein YOR289w - yeast (Saccharomyces cerevisiae) * 1e-43 R166.3 * 3e-45 unknown
 CG5902 protein * Y810_METJA HYPOTHETICAL PROTEIN hypo CG5902 97F1-97F1 dup:1/6 ID:98G6
 + transporter * minidisks(aa) * 3e-26 MUP1_YEAST HIGH AFFINITY METHIONINE PERMEASE methionine * 1e-110
 Similarity to Human membrane protein E16 (SW:E16_HUMAN); cDNA [aa_permeases // AMINO_ACID_PERMEASE_2] CG12317
 CG12317LD39658 33B12-33B13 ID:98G7
 + EG:95B7.7 transcription_factor * /motif=(desc;; /motif=(desc;; /motif=(desc;; /match=(desc:(aa) * /motif=(desc;; /motif=(desc;;
 /motif=(de * 3e-29 similar to Zinc finger, C2H2 type[zf-C2H2 // ZINC_FINGER_C2H2 // ZINC_FIN] CG2712 LD39664 3B6-3B6
 CG2712 ID:98G8

+ enzyme * protein(aa) * 3e-83 predicted using Genefinder; Similarity in 3' end to Human * 5e-16 TTL_BOVIN TUBULIN--
 CG10057 TYROSINE LIGASE (TTL) * similar to tubulin [ZF_MATRIN // NLS_BP] CG10057 LD39904 96B19-96B20 dup:2/2 ID:99A1
 + su(s) RNA_binding * DMSUSG_16 su(s) * su(s) homolog; similar to Drosophila melanogaster suppressor of sable (su(s)) pro *
 CG6222 DMSUSG_16 su(s) * SUS_DROME SUPPRESSOR OF SAB [NLS_BP] CG6222 LD39941 1B10-1B10 dup:2/3 ID:99A10
 + Dp transcription_factor * DMDPRTF_2 Dp * transcription factor * 6e-59 similar to transcription factor DP-1; cDNA EST comes f
 CG4654 * 5e-72 TDP1_MOUSE TRANSCRIPTION FACTOR DP-1 (E2F CG4654 LD39905 49F13-49F13 dup:2/2 ID:99A2
 + enzyme * putative serine protease-like protein(aa) * weakly similar to human placental protein precursor
 CG3303 (SP:PP11_HUMAN)(aa) * placental protein (serine pro CG3303 LD39912 89A13-89B1 ID:99A3
 + 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
 + unknown * 4e-31 SRYA_DROME SERENDIPITY LOCUS ALPHA PROTEIN serendipity (sr * 4e-32 Drosophila simulans
 CG8247 serendipity * 4e-33 DMSRYG1_16 Sry-&agr; CG8247 LD39926 44F9-44F9 ID:99A5
 + 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
 + transporter * conserved hypothetical protein(aa) * 8e-14 conserved hypothetical protein * 7e-40 inserted at base 5' end of P
 CG8602 element Inverse PCR * [sugar_tr] CG8602 LD39967 65F2-65F2 ID:99B1
 + enzyme * 2e-45 acyl-coenzyme A oxidase * 1e-100 Similarity to Rat Acyl-CoA oxidase I (SW:CAO1_RAT); cDNA EST
 CG4586 EMBL: * 1e-116 peroxisomal acyl-CoA oxidase * 1e CG4586 LD40103 6E4-6E4 ID:99B12
 + 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
 + EG:52C10.2 signal_transduction * 1e-100 by content; 1-meth * 3e-43 YUE1_CAEEL HYPOTHETICAL 19.6 KD PROTEIN
 F16H9.1 IN CHROMOSOME X * 2e-31 RGS5_MOUSE REGULATOR OF G-PROTEIN SIGNALIN [GRK // RGS] CG5036 LD40005
 CG5036 54F1-54F1 dup:2/3 ID:99B4
 + transcription_factor * BLASTX 5.2E-13 Mus musculus glutamine repeat protein-1 mRNA, complete cds.(dna) * BLASTX
 1.1E-08 FLO11[Cell surface flocculin(dna) * 7e-09[zf-C2H2 // ZINC_FINGER_C2H2 // ZINC_FIN] CG12701 LD40013 18F2-18F2
 CG12701 dup:5/5 ID:99B5
 + chaperone * M-phase phosphoprotein 11(aa) * zuotin related factor 2(aa) * strong similarity to mouse DNAJ-like protein
 MTJ1 * 6e-41 ZUO1_YEAST ZUOTIN zuotin - [MYB_3 // DnaJ // DNAJ_2 // NLS_BP] CG10565 LD40027 78C1-78C1 dup:2/2
 CG10565 ID:99B6
 CG1726 + unknown CG1726 LD40039 ID:99B7
 CG9335 + unknown * CG9335 LD40063 38F1-38F1 ID:99B9
 + transcription_factor * 3e-09 TF3A_YEAST TRANSCRIPTION FACTOR IIIA (TFIIIA) transcriptio * 3e-15 CROL ALPHA * 2e-
 06 similar to Zinc finger, C2H2 type (3 domains)[zf-C2H2 // ZINC_FINGER_C2H2 // ZINC_FIN] CG12941 LD40262 47C6-47C6
 CG12941 dup:1/2 ID:99C12
 CG9866 + unknown * CG9866 LD40170 22E-22E ID:99C4
 CG3157 + gammaTub23C cytoskeletal_structural_protein * similar to Tubulin (2 domains); cDNA EST CEMSG51F comes from this gene(aa)

* gamma-tubulin 3(aa) * TUBULIN ALPHA-4 CHAIN(aa) * DMTUBA4_2 agr;Tub67C [TUBULIN // tubulin] CG3157 LD40196 23C2-23C2 ID:99C6

CG8374 + dmt unknown * [NLS_BP] CG8374 LD40216 85E5-85E5 ID:99C7

+ endopeptidase * 6e-15 UBPA_YEAST UBIQUITIN CARBOXYL-TERMINAL HYDROLASE (UBIQUITIN THIOLESTERASE * 2e-12 FAF_DROME PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE FAF [UCH_2_1 // UCH_2_2 // UCH_2_3 // UCH-1] CG5505 LD40339 66A5-66A5 ID:99D11

CG5505 + endopeptidase * Herpes virus-associated ubiquitin-specific protease(aa) * 1e-99 UBPF_YEAST UBIQUITIN CARBOXYL-TERMINAL HYDROLASE (UBIQUITIN THIOLESTERASE * 4e-40 UB [UCH_2_1 // UCH_2_2 // MATH // UCH_2_3 /] CG1490 LD40280 11A4-11A4 ID:99D2

CG1490 LD40280 11A4-11A4 ID:99D2

CG13840+ CG13840 LD40283 ID:99D4

+ transcription_factor * Yjr119cp(aa) * XE169 PROTEIN (SMCX PROTEIN)(aa) * T17H7.10(aa) * JUMONJI PROTEIN(aa)

CG9088 [ARID // PHD] CG9088 LD40310 26B1-26B1 dup:2/2 ID:99D7

+ enzyme * ubiquitin-conjugating enzyme E2-32k(aa) * 2e-33 UBC7_YEAST UBIQUITIN-CONJUGATING ENZYME E2-18 KD (UBIQUITIN-PROTEIN LIGASE) (UBI * 3e-24 UBC6_DROME [UBIQUITIN_CONJUGAT // UQ_con // UBIQUIT] CG7656 LD40324 71D4-71E1 dup:3/3 ID:99D8

CG7656 + unknown * DIMETHYLADENOSINE TRANSFERASE (S-ADENOSYLMETHIONINE-6-N', N'-ADENOSYL(RRNA) DIMETHYLTRANSFERASE) (16S RRNA DIMETHYLASE) (HIGH LEVEL KASUGAMYCIN RESI [RrnaAD] CG7319 LD40326 71C2-71C2 dup:2/2 ID:99D9

CG7319 + 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 64A10-64A10 dup:2/2 ID:99E11

CG14999 + fs(1)Ya cell_cycle_regulator * mitosis initiation protein fs(1)Ya - fruit fly (Drosophila melanogaster)(aa) * FSYA_DROME MITOSIS INITIATION PROTEIN FS(1)YA fs(1)Ya prote * DMFS1Y [ZINC_FINGER_C2H2] CG2707 LD40381 3B6-3B6 dup:2/2 ID:99E2

CG2707 + unknown * Loc7p(aa) * 13S condensin XCAP-D2 subunit(aa) * gene product is related to yeast protein * 8e-38 hypothetical protein YLR272c - yeast (Saccharomyce [NLS_BP] CG1911 LD40412 99B-99B dup:2/2 ID:99E3

CG1911 + RpA-70 DNA_replication_factor * DMRPA1_3 RpA-70 * REPLICATION PROTEIN A KD DNA-BINDING SUBUNIT (RP-A) (RF-A) (REPLICATION FACTOR-A PROTEIN 1) (SINGLE-STRANDED DNA-BINDING PROTEIN) CG9633 LD40420 84F-84F dup:4/4 ID:99E5

CG9633 + unknown * 5e-70 weak similarity to HSP90 * 1e-05 YXAQ_BACSU HYPOTHETICAL 37.5 KD PROTEIN IN GNTR-HTPG INTERGENIC REGION * CG2982 LD40453 4B5-4B5 dup:2/2 ID:99E8

CG2982 + M(2)21ABenzyme * 1e-88 METK_YEAST S-ADENOSYLMETHIONINE SYNTHETASE (METHIONINE ADENOSYLTRANSFERASE 1) * 1e-142 METK_DROME S-ADENOSYLMETHIONINE SYNTHETASE (METHIONINE ADENOSYLTRANSFERASE 1 // ADOMET_SYNTHETAS] CG2674 LD40460 21B-21B dup:2/2 ID:99E9

CG2674 + RNA_binding * DMB52_2 B52 * ASF/SF2 homolog(aa) * nuclear phosphoprotein SRp55 - fruit fly (Drosophila melanogaster)(aa) * dJ862K6.2.1 (splicing factor, (SRP55-1) [RBD // rm] CG6987 LD40489 89B21-89B21 dup:2/3 ID:99F1

CG6987 + ligand_binding_or_carrier * fast-twitch myosin light chain 1(aa) * DMTNC41C_2 TpnC41C * 1e-35 CC31_YEAST CELL DIVISION CONTROL PROTEIN cell division * 5e-32 CALM_DROME CALMO[EF_HAND // efhand // EF_HAND_2] CG17493

LD40645 cyto_unknown ID:99F11

+ DNA_binding * 9e-09 ssrp2 * 4e-09 contains similiarity to HMG boxes * 3e-19 mitochondrial transcription factor A * 6e-27

CG4217 transcription factor 6-like (mitochondria [HMG // HMG_box // NLS_BP] CG4217 LD40493 92E11-92E11 ID:99F2

+ unknown * No definition line found(aa) * 4e-13 No definition line found * [WW_rsp5_WWP // NLS_BP // WW_DOMAIN_2]

CG11820 CG11820 LD40504 98F6-98F6 dup:1/2 ID:99F5

+ 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 //

CG4600 THIOLASE_2 //] CG4600 LD40538 33A1-33A1 dup:1/2 ID:99F6

+ RNA_binding * 2e-16 SME1_YEAST SMALL NUCLEAR RIBONUCLEOPROTEIN E HOMOLOG SME1 * 1e-27 predicted

CG7102 using Genefinder * 1e-30 small nuclear ribonucleoprotein E * 8e-33 [BTB // Sm] CG7102 LD40565 28D5-28D5 ID:99F7

CG9839 + unknown * [CYTOCHROME_C] CG9839 LD40589 85E9-85E9 ID:99F8

+ signal_transduction * Caf1 * Nle * Taf80 * 5e-13 T2D4_YEAST TRANSCRIPTION INITIATION FACTOR TFIID KD SUBUNIT

CG6724 (TAFII-90) [GPROTEINBRPT // WD40_REGION // WD_REPEA] CG6724 LD40657 32A5-32A5 ID:99G1

+ unknown * predicted using Genefinder; similar to Acetyltransferase (GNAT) family (2 domains); cDNA EST yk466g5.3 comes

CG1969 from this gene; cDNA EST yk255h7.3 come [Acetyltransf] CG1969 LD40766 99C1-99C1 ID:99G10

+ BcDNA:LD34343 enzyme * 1e-111 SCS1 product=suppressor of chaperonin sixty-1 cerevisi * 1e-152 similar to RTS1 PROTEIN

CG5643 (SCS1 PROTEIN) * 1e-149 protein phosphatase 2A subuni CG5643 LD40774 98A3-98A3 dup:2/3 ID:99G11

+ RNA_binding * Bub3 * WD-40 repeat protein(aa) * HYPOTHETICAL 41.4 KD TRP-ASP REPEATS CONTAINING PROTEIN

F10G8.3 IN CHROMOSOME I(aa) * HYPOTHETICAL RAE1-LIKE PROTE [GPROTEINBRPT // WD40_REGION // WD_REPEA]

CG9862 CG9862 LD40776 57F6-57F6 ID:99G12

+ unknown * HYPOTHETICAL 96.2 KD PROTEIN C08B11.4 IN CHROMOSOME II(aa) * predicted using Genefinder(aa) * 3e-

CG8185 05 /match=(desc: * 7e-38 cDNA EST comes from this CG8185 LD40680 52A9-52A10 dup:1/2 ID:99G3

+ transporter * CGI-19 protein(aa) * 5e-07 probable membrane protein YPL244c - yeast (Saccharomyces cerevisiae) * 7e-83

CG7853 No definition line found * 2e-40 putative pr CG7853 LD40702 73E4-73E4 ID:99G5

+ unknown * hypothetical protein(aa) * 6e-71 inserted at base Both 5' and 3' ends of P element Inverse PCR * [NLS_BP]

CG2162 CG2162 LD40717 63B4-63B5 dup:2/2 ID:99G7

+ enzyme * Yjr084wp(aa) * acyl-protein thioesterase(aa) * 1e-22 probable membrane protein YLR118c - yeast

CG7351 (Saccharomyces cerevisiae) * 3e-67 YPI7_CAEEL HYPOTH [TNF_1] CG7351 LD40777 68C10-68C10 dup:2/3 ID:99H1

+ * BLASTX 2.3E-13 TRA1|Homolog of human TR-AP which associates with a domain of c-Myc essential for cellular

CG2905 transformation(dna) * predicted using Gen [PI3_4_KINASE_3] CG2905 41A1-41A1 ID:99H3

+ DNA_repair_protein * DMDNAPOLD_2 DNAPol- dgr; * DNA polymerase zeta subunit; Rev3p(aa) * 1e-152 DPOZ_YEAST

DNA POLYMERASE ZETA CATALYTIC SUBUNIT DNA-dire * 2e-69 DPOD_D[DNAPOLB // DNA_POLYMERASE_B // DNA_pol_]]

CG1925 CG1925 LD40801 43E16-43E17 ID:99H4

CG1404 + enzyme CG1404 ID:99H5

+ motor_protein * * similar to S. pombe phosphoprotein * BLASTX 2.1E-09 P.falciparum merozoite surface antigen (MSA-2)

CG8176 gene, complete cds.(dna) * BLASTX 5.7E-22 Homo [ZINC_PROTEASE] CG8176 LD40806 86C1-85D23 dup:3/3 ID:99H6

CG1250 + sec23 unknown * COPII protein, homolog of s. cerevisiae SEC23p(aa) * SC23_YEAST PROTEIN TRANSPORT PROTEIN

SEC23 protein transpo * S23A_MOUSE PROTEIN TRANSPORT PRO CG1250 LD40826 83B6-83B6 dup:3/4 ID:99H8

CG12758+ unknown * [NLS_BP] CG12758 trimmed 55F8-55F13 dup:2/3 ID:Farhad's BA1

CG14709+ transporter CG14709 LD21507 ID:Farhad's BA11

CG17682+ CG17682 LP04696 ID:Farhad's BB8

+ transcription_factor_binding * Fas-binding protein(aa) * ETS1 associated protein EAP1/Daxx(aa) * 2e-13 Fas-binding protein

CG9537 * 9e-09 Fas-binding protein Daxx [NLS_BP] CG9537 LD30183 26D6-26D7 dup:3/5 ID:Farhad's BB9

CG9432 + CG9432 G041 dup:1/4 ID:Farhad's BC7

CG2016 + unknown * 0.0000000007* 4e-10 0.9-kb RNA transcript * CG2016 ck01170 82E7-82E7 dup:2/3 ID:Farhad's BD11

+ enzyme * 2e-25 pancreatic lipase related protein * 1e-26 pancreatic lipase-related protein * 1e-31 phospholipase, GPL - guinea pig * LIP1_HUMAN PANCREAT[DOLALLERGEN // TAGLIPASE // ESTERASE //] CG4267 ck01198 22D3-22D3 dup:2/2

CG4267 ID:Farhad's BD12

+ BcDNA:GH02976 structural_protein * 5e-28 Gasp precursor * 9e-11 cDNA EST comes from this gene; cDNA EST yk369a9.5

CG4778 come * 4e-08 peritrophin * 6e-30 Gasp CG4778 ck00178 30F6-30F6 dup:3/3 ID:Farhad's BD2

CG1124 + unknown CG1124 ck00336 dup:2/2 ID:Farhad's BD9

+ W unknown * W * HEAD INVOLUTION DEFECTIVE PROTEIN (WRINKLED PROTEIN)(aa) * 1e-148 W * 6E-99 CG5123

CG5123 ck02091 75C-75C2 dup:2/4 ID:Farhad's BE10

CG15288+ CG15288 ck01592 ID:Farhad's BE4

+ structural_protein * 70kD peroxisomal integral membrane protein(aa) * similar to kD peroxisomal membrane protein

CG12703(PMP70), an ATP-binding transport protein(aa) * 1e-19 CG12703 ck01606 18F1-18F1 ID:Farhad's BE5

+ unknown * BLASTX 5.8E-08 Mouse proteolipid protein variant DM-20 mRNA, complete cds.(dna) * 2e-21 M6A_MOUSE

CG7540 MEMBRANE GLYCOPROTEIN M6-A membrane glycoprote * 3 [Myelin_PLP] CG7540 ck01837 78D7-78D8 ID:Farhad's BE8

CG9503 + enzyme CG9503 ck02694 ID:Farhad's BF1

CG10130+ CG10130 sec61b ID:Farhad's BF2

+ protein_kinase * DMFGFR1_2 htl * connectin/titin(aa) * flt-1(aa) * FTL4(aa) [ig // PROTEIN_KINASE_TYR // PROTEIN_KIN]

CG8222 CG8222 VEGFR 78F1 28F4-28F5 dup:9/12 ID:Path + Ctrl1 + kras305