

Table S9

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

Gene ID mixed annotation (+ indicates sequence confirmation)

CG12505+ unknown * CG12505 LD41905 50F6-50F6 ID:101A2
+ Ote motor_protein * 1e-174 OTE_DROME OTEFIN otefin - fruit fly (*Drosophila melanogaster* * 1e-176 DMOTEDA_2 Ote * *

CG5581 CG5581 LD41911 55C3-55C4 ID:101A4

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

CG17602+ unknown * CG17602 LD42024 20A1-20A1 ID:101B4
+ TH1 unknown * TH1(aa) * DMTH1X_3 TH1 * potential zinc-finger domains centered at aa and aa 364; kDa protein; putative(aa)

CG9984 * 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
+ grp protein_kinase * 5e-08 Ssp31 protein kinase * 2e-54 Ser/Thr kinase * 5e-13 serine/threonine kinase * 7e-27 Chk1; checkpoint

CG17161 kinase [PROTEIN_KINASE_DOM // pkinase] CG17161 LD42896 36A6-36A7 ID:101G7
+ 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
+ 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 LD43101 13F3-

CG9012 13F3 dup:1/3 ID:102A3

CG10165+ unknown * CG10165 LD43293 37F1-37F1 ID:102C2
+ 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
+ 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

CG4702 + unknown * CG4702 LD43816 88A1-88A1 ID:102F9
+ unknown * protein kinase cAMP-dependent protein kinase) unlocalised cAMP-dependent protein kinase) map_position:77F **

CG18677 CG18677 LD43873 77E8-77E8 ID:102G2
+ 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
+ unknown * 8e-74 GPI3_YEAST N-ACETYLGLUCOSAMINYL-PHOSPHATIDYLINOSITOL BIOSYNTHETIC PROTEIN (GLCN * 6e-92 similar to phosphatidylinositol biosynthetic protein; [Glycos_transf_1] CG6401 LD44262 54E7-54E7 ID:103B2

CG6401 6e-92 similar to phosphatidylinositol biosynthetic protein; [Glycos_transf_1] CG6401 LD44262 54E7-54E7 ID:103B2
+ 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 * 2e-
 CG10391 17 similar to cytochrome P450 [EP450II // p450 // P450 // MITP450 // E] CG10391 LD44491 37A3-37A3 ID:103C12
 + lswi 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
 + 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
 CG7832 + unknown * [NLS_BP // ANTIFREEZEI] CG7832 LD44696 88C10-88C10 dup:3/3 ID:103E7
 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
 + unknown * weak similarity to rat cytosolic acyl coenzyme A thioester hydrolase * acyl-CoA thioesterase(aa) * contains weak
 CG1635 similarity to rat cytosolic acyl CG1635 LD44914 100D2-100D2 ID:103G3
 + 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
 + 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
 + ion_channel * HISTIDINE-RICH GLYCOPROTEIN PRECURSOR(aa) * histidine-rich protein - Plasmodium lophurae (fragment)
 CG9411 hi * [PRO_RICH] CG9411 LD45449 12E8-12E8 ID:104C11
 CG18638+ CG18638 36A7-36A7 ID:104D7
 + up ligand_binding_or_carrier * DMTROPT_2 up * clot.789(dna)* 1e-112 troponin T - fruit fly (Drosophila melanogaster) * 4e-28
 CG7107 TRT_CAEEL TROPONIN T coded for by C. elegans cDNA yk7 [Troponin // NLS_BP] CG7107 LD45641 12A2-12A4 dup:2/2 ID:104E5
 + enzyme * BLASTX 7.5E-52 FUM1|Fumarate hydratase (fumarase) (mitochondrial and cytoplasmic), converts L-malate to
 fumarate as part of the TCA cycle(dna) * fum [DCRYSTALLIN // FUMRATELYASE // FUMARATE] CG4094 LD46083 6C7-6C7
 CG4094 ID:104H12
 + 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
 CG7627 ID:104H4
 + unknown * farnesoic acid o-methyltransferase(aa) * 2e-21 farnesoic acid o-methyltransferase farne * CG10527 LD46156
 CG10527 57B20-57B20 ID:105A6
 + receptor * protein kinase C substrate 80K-H(aa) * similar to Human protein kinase C substrate, 80KD protein, heavy chain,
 CG6453 SWISS-PROT Accession Number * similar [LDLRA_2 // ER_TARGET // EF_HAND] CG6453 LD46533 36C4-36C4 ID:105D11
 + SelD enzyme * SelD protein * 2e-93 similar to AIR synthase related proteins elegans * 1e-143 selenophosphate synthetase * 1e-
 CG8553 159 SELD_HUMAN SELENIDE,WATER DIKINAS [AIRS] CG8553 LD46437 50F-50F dup:1/2 ID:105D2
 + hep protein_kinase * MAP kinase kinase(aa) * Mkk4 * hep * 2e-46 polymyxin B resistance protein PBS2 - yeast (Saccharomyces
 CG4353 cerevisiae) [PROTEIN_KINASE_ST // PROTEIN_KINASE_DOM] CG4353 LD46661 11D5-11D6 dup:3/3 ID:105E10
 CG11567+ 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 LD46590
 28C7-26C4 dup:4/4 ID:105E4
 + structural_protein * 6e-14 CUP7_DROME PUPAL CUTICLE PROTEIN EDG-78 PRECURSOR ecdyson * 2e-28 CUD4_LOCMI
 ENDOCUTICLE STRUCTURAL GLYCOPROTEIN (ABD-4A) g * 7e-16 DMEDG78B_2 [CUTICLE // insect_cuticle] CG8505 49A3-
 CG8505 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 [RABGDIREP // RABGDI // GDI] CG4422 LD46767 30B8-
 CG4422 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 73D1-
 CG11914 73D3 dup:2/2 ID:105F4
 + nucleic_acid_binding * 2e-08 SFP1 * 3e-06 zinc-finger protein Pur-1 - mouse * 3e-06 MAZ * 3e-06 serum amyloid A-activating
 CG12054 factor SAF-8 [zf-C2H2 // ZINC_FINGER_C2H2 // ZINC_FIN] CG12054 LD46863 100B9-100B9 dup:1/2 ID:105G10
 + transporter * 3e-26 GLO3 * 4e-23 putative ARF1 GTPase activating protein * 1e-79 YQP4_CAEEL HYPOTHETICAL 127.4 KD
 PROTEIN F07F6.4 IN CHROMOSOME III (* 3e-09 ADP- [ArfGap // ZF_GCS // REVINTRACTNG] CG6838 LD46935 79F2-79F2
 CG6838 ID:105H4
 CG8320 + CG8320 ID:105H9
 + 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 43F7-43F7
 CG2916 dup:1/2 ID:106A3
 + unknown * clot.672(dna) * 7e-07 YEQ8_YEAST HYPOTHETICAL 58.0 KD PEPTIDASE IN PTP3-ILV1 INTERGENIC REGION
 CG11367 * 5e-08 similar to the peptidase family M24B * 3e-12 CG11367 LD47277 79F2-79F2 dup:2/2 ID:106B10
 + 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
 + unknown * calcium-regulated heat stable protein CRHSP-24(aa) * calcium-regulated heat stable protein CRHSP-24(aa) * RNA-
 CG9705 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
 + 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
 CG5519 ID:106C9
 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
 CG4768 + unknown * [NLS_BP] CG4768 LD47733 15A5-15A6 dup:1/2 ID:106H7
 CG1236 + enzyme * CtBP * Ygl185cp(aa) * C-terminal binding protein(aa) * 5e-31 YN14_YEAST HYPOTHETICAL 38.8 KD PROTEIN IN

MET2-SEC2 INTERGENIC REGION [D_2_HYDROXYACID_DH_3 // 2-Hacid_DH] CG1236 LD48009 83C1-83C1 dup:2/2 ID:107C3
+ shg cell_adhesion * DMDACHSOU_2 ds * EPITHELIAL-CADHERIN PRECURSOR (E-CADHERIN) (LIVER CELL ADHESION MOLECULE) (L-CAM)(aa) * DE-cadherin(aa) * DMDEC_1 shg [EGF_1 // EGF_2 // LAM_G_DOMAIN // Cadhe] CG3722 LP01248

CG3722 57B19-57B20 ID:107D10
+ 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 chitinase

CG18140 * 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
+ enzyme * cDNA EST comes from this gene; cDNA EST yk282d3.5 comes from this gene(aa) * 1e-06 CCA1_YEAST TRNA NUCLEOTIDYLTRANSFERASE PRECURSOR (TRNA ADENYLYLT [MET_TRANS // SAM_BIND] CG1239 LP01332 83C1-83C1

CG1239 dup:2/2 ID:107E5
+ 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 cDNA

CG8756 yk9e10.3; mu * 3e-07 very low dens [LDLRA_2 // ldl_recept_a // LDLRA_1] CG8756 LP01646 76C-76C ID:107F11
+ unknown * ECDYSONE-INDUCED PROTEIN 74EFA (ETS-RELATED PROTEIN E74A)(aa) * 1e-62 ecdysone-induced protein

CG6273 E74A - fruit fly (Drosophila pseudoobscura) * 5e-91 e CG6273 LP01487 74E-74E ID:107F2
+ 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 * 3e-

CG4827 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 using

CG14205 Genefinder CG14205 LP01839 18D7-18D7 ID:107G10
+ cell_adhesion * DMSCA_3 sca * 4e-15 scabrous protein precursor - fruit fly (Drosophila melanogaster) * 2e-05 coded for by C.

CG6788 elegans cDNA yk9a2.5; coded for by C. e [fibrinogen_C] CG6788 LP01858 16E2-16E2 ID:107G11
+ Lcp1 structural_protein * 9e-53 CLP1_DROME LARVAL CUTICLE PROTEIN I PRECURSOR cuticle prot * 1e-35 larval cuticle

CG11650 protein 1, LCP1=Lcp1 gene product {Y allele} miranda * 4e-53 [CUTICLE // insect_cuticle] CG11650 LP01670 44C1-44C1 ID:107G2
+ 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
 + 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_LLECTIN_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
 CG18596+ unknown * CG18596 LP02352 96D4-96D4 ID:108A7
 + 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
 CG1733 + unknown * 2e-06 inserted at base 3' end of P element Inverse PCR * * CG1733 LP02557 12A1-12A2 dup:3/5 ID:108B3
 CG10200+ unknown * CG10200 LP02570 51C5-51C5 ID:108B4
 + 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
 + nucleic_acid_binding * 2e-06 Zinc finger-AT hook protein * 2e-13 protein * 5e-09 XFIN_XENLA XFIN PROTEIN Xfin protein
 CG14438 (AA - * 2e-08 DMRNAD19A D19A [zf-C2H2 // ZINC_FINGER_C2H2 // ZINC_FIN] CG14438 LP02916 6C12-6C12 dup:2/3 ID:108C7
 + unknown * lbm * 1e-09 LBM_DROME LATE BLOOMER PROTEIN late bloomer me * 1e-11 lbm * [TM4_2] CG4471 LP02988
 CG4471 42E2-42E2 ID:108C9
 + Ald enzyme * plastidic aldolase(aa) * ALDOLASE-RELATED PROTEIN(aa) * DMALD_10 Ald * 1e-118 similar to Fructose-
 bisphosphate aldolase class-I; cDNA EST yk252e [glycolytic_enzy // ALDOLASE_CLASS_I //] CG6058 LP03138 97A6-97A6 dup:4/4
 CG6058 ID:108D12
 CG7906 + unknown * CG7906 LP03104 74E1-74E1 ID:108D7
 + 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
 + 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
 CG5904 + islet mitochondrial antigen CG5904 LP03542 ID:108F8
 + 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 finge[ZF_BBOX // NHL // ZINC_FINGER_C2H2 // Z] CG10719 LP03649 37C4-37C
 CG10719 dup:3/5 ID:108G1
 CG6234 + motor_protein * 1e-06 TRFA * * CG6234 LP04345 87C6-87C6 dup:1/2 ID:108H11
 CG11169+ unknown * CG11169 LP04006 60A1-60A2 ID:108H6
 + ligand_binding_or_carrier * ecdysone-induced membrane protein IMP-E3 - fruit fly (Drosophila melanogaster)(aa) * * CG2723
 CG2723 LP04438 84E6-84E6 ID:109A3

+ 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
 + 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
 CG9021 + unknown * Cr-P11 allergen(aa) * Cr-P11 * major allergen Per a * CG9021 LP05310 26A5-26A5 ID:109C12
 + Neurotactin cell adhesion axon, ocellar nerve, ventral nerve cord CARBOXYLESTERASE_B_2, COesterase, ESTERA] CG9704
 CG9704 LP05519 ID:109D11
 CG13598 + sba unknown * DMTF125_2 Tf125 * type I(aa) * [MBD] CG13598 LP05532 95C9-95C11 ID:109D12
 + Oscp enzyme * DMOSCPPRE_2 Oscp * ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit (oligomycin
 CG4307 sensitivity conferring protein)(aa) * coded for b [ATPASEDELTA // OSCP] CG4307 90D1-90D1 dup:2/2 ID:109D2
 CG4818 + structural_protein * 1e-08 cuticular protein ** [insect_cuticle] CG4818 LP05492 72F1-72F1 ID:109D9
 + 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
 + mas endopeptidase * mas * masquerade precursor - fruit fly (Drosophila melanogaster) * 5e-30 similar to peptidase family S1
 (trypsin family) * 4e-38 KAL_MOUSE PLASMA KA [trypsin // CHYMOTRYPSIN // TRYPSIN_HIS] CG15002 LP06006 64A12-64A12
 CG15002 ID:109F11
 + 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
 CG6968 + unknown * [NLS_BP] CG6968 LP06178 78D-78D dup:1/3 ID:109G3
 CG14455 + CG14455 LP06288 ID:109G6
 + Ag5r unknown * antigen 5-related protein(aa) * Ag5r * 1e-156 antigen 5-related * 6e-33 antigen 5-related protein CG9538
 CG9538 LP06338 12F5-12F5 ID:109G8
 + structural_protein * Abd-5=endocuticular protein migratoria=migratory locusts, abdomen, Peptide, * Acp65Aa * 2e-12 cuticle
 CG7160 protein ACP65A * Abd-5=endocuticular protein g [CUTICLE // insect_cuticle] CG7160 LP06660 78F1-78F1 ID:109H3
 CG3421 + CG3421 ID:113B12
 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 cDNA
 CG8576 CEESX42F; coded for by C. elegans cDNA CG8576 SD02002 65F5-65F5 ID:113D5

+ 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 dup:2/2
 CG6057 ID:113E11
 + 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
 + 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 37E3-37E3
 CG10026 ID:113G7
 CG9653 + brk transcription_factor * putative transcription factor(aa) * * CG9653 SD02279 7A4-7A4 dup:3/6 ID:113H5
 + signal_transduction * beta2-chimerin, cerebellar - human(aa) * beta2-chimerin, cerebellar - rat (fragment)(aa) * 2e-07
 BEM2_YEAST GTPASE ACTIVATING PROTEIN BEM2/IP[RHO_GAP // RhoGAP // DAG_PE_BINDING_DOM] CG3208 SD02309
 CG3208 5A8-5A8 dup:1/3 ID:113H7
 CG7434 + RpL22 ribosomal_protein Ribosomal protein L22 60S subunit ANTIFREEZEI CG7434 SD02522 ID:114C6
 + 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
 + signal_transduction * 5e-15 VPS9 protein - yeast (Saccharomyces cerevisiae) (Z46 * 7e-28 cDNA EST yk210c11.3 comes from
 CG9139 this gene; cDNA EST yk210c11.5 co * 3e-09 Ras inhi CG9139 SD03358 61F5-62B4 dup:3/4 ID:115F1
 CG9344 + RNA_binding CG9344 ID:116F8
 + DNA_binding * DNA (cytosine-5-)-methyltransferase 1(aa) * protein(aa) * HYPOTHETICAL 56.5 KD PROTEIN IN CAJ1-HOM3
 CG11033 INTERGENIC REGION(aa) * DNA (cytosine-5-)-methyl CG11033 SD04170 85C6-85C7 dup:1/5 ID:116H3
 CG8593 + unknown CG8593 dup:2/2 ID:116H4
 CG5953 + It has been mapped cytologically to 36A2--3 PRO_RICH CG5953 SD04335 dup:1/3 ID:117B7
 CG2818 + unknown PHO85 protein PIPLC_X_DOMAIN CG2818 SD04355 dup:1/2 ID:117B8
 CG14971 + unknown Homo sapiens CGI-15 protein CG14971 SD04505 ID:117D9
 CG18061 + CG18061 SD04793 ID:117H2
 + Mcm6 DNA_replication_factor Minichromosome maintenance 6, chromatin binding involved in pre-replicative complex formation
 CG4039 MCM, MCM_1, MCM_2 CG4039 SD04977 dup:3/3 ID:118B11
 + cytoskeletal_structural_protein homolog of human KIAA1323 protein, similar to ankyrin proteins ANK_REP,
 CG5841 ANK_REP_REGION, ZF_RING, ZF_ZZ,] CG5841 SD05267 dup:3/3 ID:118E5
 + BcDNA:GH13356 enzyme beta galactosyltransferase MITOCH_CARRIER, XYLOSE_ISOMERASE_2 CG8536 SD05469 dup:1/2
 CG8536 ID:118G11
 + transporter * Ydr205wp(aa) * 5e-09 Zn/Cd resistance gene * 1e-06 cDNA EST yk447c2.5 comes from this gene; cDNA EST co
 CG6672 * 1e-06 zinc transporter ZnT-1 - mouse ZnT-1 [KININOGEN] CG6672 86D7-86D7 dup:1/2 ID:118G3
 + 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

+ 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
 CG12016+ enzyme * [ATP_GTP_A] CG12016 SD05789 63C5-63C5 dup:1/3 ID:119D9
 CG11860+ BG:DS07851.11 unknown * CG11860 35C4-35C4 dup:2/2 ID:119H7
 + 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
 + Aph-4 enzyme * alkaline phosphatase(aa) * 3e-28 repressible alkaline phosphatase (EC 3.1.3.1) * 4e-95 PPBE_MOUSE
 ALKALINE PHOSPHATASE, EMBRYONIC PRECURSOR (EAP) e [ALKALINE_PHOSPHATASE // ALKPHPTASE //] CG1462
 CG1462 GH01338 100B-100B dup:1/2 ID:30C5
 + 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
 + enzyme * PROBABLE SUCCINYL-COA:3-KETOACID-COENZYME A TRANSFERASE PRECURSOR (3-OXOACID COA-
 TRANSFERASE)(aa) * 3-oxoacid CoA transferase precursor; succinyl-Co [COA_TRANSF_1 // COA_TRANSF_2 // CoA_tra] CG1140
 CG1140 GH01464 62B11-62B11 ID:30D6
 + BG:DS09217.1 unknown * 1e-14 predicted using Genefinder; cDNA EST comes from this g * * CG13240 GH01660 35D6-35D6
 CG13240 dup:2/2 ID:30E12
 + endopeptidase * 3e-64 cysteine proteinase cysteine * 2e-56 predicted using Genefinder; similar to cathepsin-like protease; cD *
 CG4847 1e-59 cathepsin K * 1e-59 cathepsin[THIOL_PROTEASE_CYS // PAPAINE // Peptida] CG4847 GH01592 54C9-54C9 dup:3/4 ID:30E3
 + 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
 CG14528 similar to Zinc-binding metalloprotease; cD [NEPRILYSIN // PRENYLATION // ZINC_PROTE] CG14528 GH01940 98F-98F ID:30G10
 + 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
 + endopeptidase * DMC9D2 * 8e-57 serine protease SER4 precursor * 6e-12 predicted using Genefinder; similar to
 transmembrane receptor (r * 2e-19 serine protease (BSP) [trypsin // CHYMOTRYPSIN // TRYPSIN_SER] CG8329 GH01822 67B-
 CG8329 67B ID:30G2
 + structural_protein * /match=(desc:: /match=(desc:(aa) * 2e-21 /match=(desc:: /ma * 3e-16 CU1A_TENMO LARVAL CUTICLE
 CG4791 PROTEIN A1A (TM-A1A) (TM-LCP A1A) * 6e-19 DMEDG84A_3 E [CUTICLE // insect_cuticle] CG4791 GH02089 31A1-31A1 ID:31A2
 + BcDNA:GH02431 * 2e-48 hypothetical protein YLR348c - yeast (Saccharomyces cerevisiae) (U * 1e-87 Oxoglutarate/malate carrier
 CG8790 protein - Caenorhabditis elegans * 6e-3 [mito_carr // MITOCARRIER] CG8790 87E8-87E8 dup:1/2 ID:31C11
 + Rh3 G_protein_linked_receptor * OPSIN RH3 (INNER R7 PHOTORECEPTOR CELLS OPSIN)(aa) * DMRH3A_3 Rh3 *
 CG10888 OPS3_DROME OPSIN RH3 (INNER R7 PHOTORECEPTOR CELLS OPSIN) * 5e-2[GPCRRHODOPSN // OPSIN //

G_PROTEIN_RECE] CG10888 GH02505 92C5-92C5 dup:2/2 ID:31C6
+ 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
+ Reg-2 * RHYTHMICALLY EXPRESSED GENE PROTEIN (DREG-2)(aa) * Reg-2 * 4e-16 YM14_YEAST HYPOTHETICAL 35.3 KD PROTEIN IN POM152-REC114 INTERGENIC REGION * 1e-157 [Hydrolase // HADHALOGNASE] CG3200 61C-61C dup:4/4
CG3200 ID:31E8
+ RNA_binding * probable splicing factor Cprp21 - Caenorhabditis elegans(aa) * pre-mRNA splicing factor SF3a (120 kDa subunit), similar to S. cerevisiae PRP21(aa) [SURP // ubiquitin // UBIQUITIN // UBIQU] CG16941 GH03554 92C1-92C1 ID:32A12
CG16941 + 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 GH03728 100B-CG12045 100B ID:32B12
CG4784 + structural_protein * 2e-05 DMEDG84A_3 Edg84A * * [CUTICLE // insect_cuticle] CG4784 GH03623 72F1-72F1 ID:32B4
CG7738 + CG7738 dup:2/2 ID:32C2
CG4184 + BcDNA:GH03922 unknown * CG4184 GH03922 21C3-21C dup:1/3 ID:32C9
CG10658 + Os9 unknown * Os9 * * CG10658 GH03980 38B1-38B1 ID:32D2
+ 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
+ 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
+ enzyme * PROBABLE SERYL-TRNA SYNTHETASE (SERINE--TRNA LIGASE) (SERRS)(aa) * SERYL-TRNA SYNTHETASE (SERINE--TRNA LIGASE) (SERRS)(aa) * seryl-tRNA synthetase(a [tRNA-synt_2b // TRNASYNTHSER] CG17259 GH04194 23C4-CG17259 23C5 dup:2/2 ID:32E7
CG4468 + unknown * CG4468 GH04205 92B9-92B9 dup:2/2 ID:32E8
CG6186 + CG6186 dup:2/2 ID:32G1
+ 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 dup:1/2
CG7727 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 SYNAPTOBREVIN[SYNAPTOBREVN // SYNAPTOBREVIN // synapt] CG17248 GH04664 62A10-62A10
CG17248 dup:2/2 ID:32H12
+ Motor-protein motor_protein * 1e-152 motor protein * 2e-40 coded for by C. elegans cDNA yk119d2.3; coded for by C. elegans
CG6455 cDNA yk86f8.3; c * 6e-50 motor protein * 1e-154 DMMOTPR [WD_REPEATS] CG6455 GH04666 93F14-93F14 ID:33A1
CG10233 + signal_transduction * 9e-12 hypothetical protein * unknown * phosphatidylinositol-4-phosphate 5-kinase isolog * CG10233

GH04877 83A1-83A1 ID:33B12
 + 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
 CG3364 + unknown * CG3364 GH05668 42D5-42D6 ID:33G9
 + BcDNA:GH05741 enzyme * agr;-Est10 * 8e-48 alpha esterase * 6e-46 ACE1_CAEEL ACETYLCHOLINESTERASE PRECURSOR
 (ACHE) acetyl * 3e-54 ACES_MOUSE ACETYLCHOLINESTERASE PRECURSOR [CARBOXYLESTERASE_B_1 // ESTERASE //
 CG4757 COe] CG4757 GH05741 86D4-86D5 ID:33H7
 + transporter * solute carrier family (organic anion transporter), member 7(aa) * BLASTX 4.2E-24 Rattus organic cation
 CG9317 transporter OCT1A mRNA, complete cds.(dna) * [sugar_tr] CG9317 GH05908 38E3-38E3 dup:1/2 ID:34A5
 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
 + endopeptidase * human factor XII(aa) * 7e-31 masquerade precursor - fruit fly (Drosophila melanogaster) * 2e-05 similar to
 Trypsin * 5e-25 MCT6_MOUSE MAST CELL PRO [trypsin // CHYMOTRYPSIN // TRYPSIN_CATA] CG6639 GH06092 36C2-36C2
 CG6639 ID:34C3
 + enzyme * 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 55F1-55F1
 CG15093 ID:34G10
 CG12279+ chaperone HEAT SHOCK PROTEIN 67B2 RHODANESE, RHODANESE_2 CG12279 dup:2/2 ID:34H6
 + 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
 CG3672 + structural_protein * 7e-10 cuticular protein * * CG3672 67B2-67B2 dup:1/2 ID:35A3
 CG9921 + unknown * 6e-05 HSPC010 * 1e-05 putative protein * CG9921 GH07174 14B15-14B15 ID:35B4
 + 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
 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
 + blw enzyme * DMASSUBA blw * F1F0-ATPase alpha subunit precursor * mitochondrial ATP synthase alpha subunit precursor
 mel * similar to ATP synthase alpha and beta [ATP-synt_A-c // ATP-synt_ab // ATPASE_A] CG3612 GH08132 59A3-59A3 dup:1/2
 CG3612 ID:35H12
 CG12091+ unknown * similar to Protein phosphatase 2C (2 domains); cDNA EST yk279g8.5 comes from this gene(aa) * HYPOTHETICAL

41.2 KD PROTEIN IN ERG7-NMD2 INTERGENIC R CG12091 GH07996 62A6-62A6 ID:35H5

CG12152+ BcDNA:GH10333 unknown * 2e-91 hypothetical protein * [ALDOKETO_REDUCTASE_3] CG12152 GH10333 7B8-7B8 ID: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
+ electron_transfer * NADH-UBIQUINONE OXIDOREDUCTASE KD SUBUNIT PRECURSOR (COMPLEX I-39KD) (CI-
39KD)(aa) * 9e-70 NUEM_HUMAN NADH-UBIQUINONE OXIDOREDUCTASE KD SUBUNIT PREC CG6020 GH10437 77C3-77C3
CG6020 ID:37H12
+ unknown * /match=(desc:; /match=(desc:(aa) * 5e-21 /match=(desc:; /ma * 1e-05 predicted using Genefinder * No definition

CG10562line 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-
CG11963FORMING), BETA-CHAIN PRECURSOR (SUCCINYL-COA SYNT [ligase-CoA] CG11963 GH10480 85C1-85C2 ID:38A5
+ unknown * 1e-45 YABC_ECOLI HYPOTHETICAL 34.9 KD PROTEIN IN FRUR-FTSL INTERGENIC REGION (ORFB) >g * 1E-

CG14683170* hypothetical protein * hypothetical protein CG14683 GH10770 86C2-86C2 ID:38C10
CG9133 + unknown * CG9133 GH10732 61F4-61F4 dup:1/3 ID:38C6
+ unknown * No definition line found(aa) * putative protein(aa) * 5e-71 putative protein * hypothetical protein CG6910 GH10741
CG6910 68F7-68F7 dup:1/2 ID:38C7
+ 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 * 5e-32 Similarity to human placental protein * 2e-42 glucocorticoid-sensitive T cell-specific protein - mouse *
CG2145 5e-41 placental protein (serine prote 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
+ BcDNA:GH11322 cell_adhesion * Pxn * 6e-20 roundabout * 2e-15 hemicentin precursor * 1e-10 rig-1 protein [ig // fn3] CG16857
CG16857 GH11322 24E4-24E4 dup:2/5 ID:38G12
+ unknown * unknown(aa) * 4e-12 putative Bop-like zinc finger protein * 1e-19 DMC103B4 [IPNS_1 // CYTOCHROME_C]

CG8503 CG8503 GH11294 50E8-50E8 ID:38G9
CG3624 + cell_adhesion * [ig] CG3624 GH11432 58D7-58D7 dup:2/2 ID:38H12
+ 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
+ NaCP60E ion_channel * DMSODCHA_6 para * DMCA1_2 Ca- agr;1D * sodium channel protein - fruit fly (Drosophila melanogaster)
(fragments) * 4e-76 similar to dihydropyridine- [NACHANNEL // ion_trans // CATION_CHANNE] CG9071 GH11402 60E4-60E5
CG9071 dup:2/2 ID:38H6

+ 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
 CG12907+ unknown * 1E-145* * [PRO_RICH // NLS_BP] CG12907 GH11521 47A-47A ID:39A8
 + enzyme * contains similarity to CDP-alcohol phosphotransferases(aa) * aminoalcoholphosphotransferase(aa) * 4e-24 sn-1,2-
 CG7149 diacylglycerol cholinephosphotransf [CDP_ALCOHOL_P_TRANSF // CDP_ALCOHOL_P_T] CG7149 GH11618 28C8-28C9 ID:39B5
 + 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
 + transporter * 2e-50 Na(+)-dependent inorganic phosphate cotransporter mela * 7e-54 YLD2_CAEEL HYPOTHETICAL 52.7 KD
 CG15095 PROTEIN C38C10.2 IN CHROMOSOME III * 2e-45 NPT1 [sugar_tr] CG15095 GH11849 55F1-55F1 ID:39C9
 + 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 42B3-
 CG3174 42B3 dup:2/2 ID:39E12
 + 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 REGION
 CG4446 * 2e-57 PDXK_CAEEL PUTATIVE PYRIDOXINE KINASE (PYRIDOXAL [pfkB] CG4446 GH12231 67B1-67B1 ID:39F3
 + 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 GH12548 28E7-
 CG11236 28E7 ID:39G11
 + signal_transduction * 1e-115 disc growth factor * 2e-14 CHIT_CAEEL PUTATIVE ENDOCHITINASE coded for by C. elegans *
 CG5154 7e-26 BRP39 protein - mouse BRP39 protein m * 5e-30 Ch [Glyco_hydro_18] CG5154 GH12410 55C9-55C9 ID:39G4
 + 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
 + cell_adhesion * DMSCA_3 sca * 2e-21 sca protein * 1e-09 coded for by C. elegans cDNA yk9a2.5; coded for by C. elegans
 CG1889 cDNA yk9a2.3; simi * 5e-30 ficolin-A [fibrinogen_C] CG1889 GH12692 9A3-9A3 ID:40A10
 + Rh4 G_protein_linked_receptor * opsin(aa) * Rh4 * OPS4_DROME OPSIN RH4 (INNER R7 PHOTORECEPTOR CELLS
 CG9668 OPSIN) * 2e-15 YXX5_CAEEL PUTATIVE NEUROPEPTIDE Y RECEPTOR (NPY-R) simila [GPCRRHODOPSN // OPSIN //

OPSINRH3RH4] CG9668 GH12673 73C5-73D1 ID:40A5
 + unknown * ABC transporter, ATP-binding protein, putative(aa) * 2e-18 conserved protein * daunorubicin resistance membrane
 CG6166 protein (drrB) * CG6166 GH12746 97A9-97A9 dup:1/2 ID:40B5
 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
 + 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
 + Mipp2 protein_phosphatase * Mipp2 * multiple inositol polyphosphate phosphatase 2; MIPP2 * 1e-27 multiple inositol
 polyphosphate phosphatase * 1e-25 multiple inositol polyphosph [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 * LYSOSOMAL ACID PHOSPHATASE PRECURSOR (LAP)(aa) * acid phosphatase 2, lysosomal(aa) * 8e-60 acid
 phosphatase (EC 3.1.3.2) Acph-1 precursor, lysosomal [HIS_ACID_PHOSPHAT_1 // acid_phosphat] CG9451 GH13318 76B6-76B6
 CG9451 dup:2/2 ID:40E7
 + transporter * 5e-75 Na(+)-dependent inorganic phosphate cotransporter mela * 7e-67 YLD2_CAEEL HYPOTHETICAL 52.7 KD
 CG3036 PROTEIN C38C10.2 IN CHROMOSOME III * 4e-46 NPT1 [NLS_BP] CG3036 GH13494 26D1-26D1 dup:3/4 ID:40F10
 + 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
 + OstStt3 enzyme * STT3_YEAST OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT STT3 * STT3_CAEEL
 OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT HOMOLOG * STT3_MOUSE OLIGOSACCHARYL [ATPASE_ALPHA_BETA]
 CG7748 CG7748 GH13452 98F6-98F6 ID:40F6
 + 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
 CG8251 GH13575 44F9-44F9 ID:40G4
 + RNA_binding * 3e-16 RNA-binding protein cabeza - fruit fly (Drosophila melanogaster) (* 4e-14 EWS_MOUSE RNA-BINDING
 CG14718 PROTEIN EWS RNA-binding protein E * 2e-15 TLS [RBD // zf-RanBP // rrm // ZF_RANBP] CG14718 GH13594 86F1-86F1 ID:40G5
 + bun transcription_factor * shortsighted class 2(aa) * DMSHSA_5 bun * shortsighted class * 2e-07 protein [TSC22] CG5461
 CG5461 GH13775 33E-33E6 ID:40H5
 CG2176 + unknown * CG2176 GH14263 99E2-99E2 ID:41C11
 CG3662 + structural_protein * E25 protein(aa) * integral membrane protein 2(aa) * 2e-07 putative integral membrane pro * 1e-08

dJ696H22.1 (mouse E25 like protein) [NLS_BP] CG3662 GH14111 21D2-21D2 ID:41C3
+ Pdh enzyme * Pdh * 1e-08 FOX2_YEAST PEROXISOMAL HYDRATASE-DEHYDROGENASE-EPIMERASE (HDE)
(MULTIFUNCTIONAL * 1e-146 pigment cell dehydrogenase reductase * 2e-10 pr [GDHRDH // UBA_NAD // adh_short // ADH_S]
CG4899 CG4899 GH14170 72F1-72F1 ID:41C6
+ unknown * BLASTX 9.9E-08 Human mRNA for hU1-70K snRNP protein (RNP8).(dna) * * [NLS_BP] CG12239 GH14380 5B8-
CG12239 5B8 ID:41D11
+ unknown * Ylr193cp(aa) * bromodeoxyuridine-sensitive transcript protein - chicken(aa) * hypothetical protein(aa) * CGI-107
CG9131 protein(aa) CG9131 GH14384 26B2-26B3 ID:41D12
+ 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
+ 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
CG18525 + unknown * CG18525 GH14439 88E7-88E7 dup:2/2 ID:41E4
CG1552 + unknown * CG1552 GH14443 10A-10A dup:2/2 ID:41E5
+ unknown * HNK-1 sulfotransferase(aa) * 1e-20 HNK-1 sulfotransferase HN * * [NLS_BP] CG4826 GH14503 36A11-36A11
CG4826 dup:3/3 ID:41E9
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
CG11395 Antho-RFa * LWamide neuropeptide precursor protein * 33K hydroxy CG11395 GH14572 54A2-54A2 dup:2/2 ID:41F2
+ signal_transduction * 6e-05 particle 102K chain - human * 4e-05 katanin p80 subunit * 7e-05 Lis1 * coatomer protein complex,
CG9144 subunit beta (beta prime) [WD40_REGION // F-box // FBOX_DOMAIN //] CG9144 GH14636 26B3-26B3 ID:41F7
+ enzyme * NADH-ubiquinone oxidoreductase B22 subunit homolog(aa) * 6e-22 similar to NADH-ubiquinone oxidoreductase B22
CG9306 (B. taurus, SP:NI2M * 1e-26 NI2M_BOVIN CG9306 GH14794 34B6-34B6 ID:41G11
+ enzyme * 1e-103 IDH2_YEAST ISOCITRATE DEHYDROGENASE MITOCHONDRIAL SUBUNIT PRECURSOR (IS * 1e-139
IDHA_CAEEL PROBABLE ISOCITRATE DEHYDROGENASE (NAD), MITOCHON [IDH_IMDH // isodh] CG12233 GH14729 18D3-
CG12233 18D3 ID:41G6
+ unknown * 3e-06 LBM_DROME LATE BLOOMER PROTEIN late bloomer me * 4e-08 lbn * * [transmembrane4 // TMFOUR //
CG12840 TM4_2] CG12840 GH14950 42E2-42E2 ID:41H10
+ enzyme * Yjr105wp(aa) * Similarity to Human adenosine kinase cDNA EST comes from this gene; cDNA EST comes from this
CG11255 gene; cDNA EST comes from this gene; cD [PFKB_KINASES_2 // ADENOKINASE // pfkB] CG11255 GH14845 69F2-69F2 ID:41H4
+ Cyp6g1 cytochrome_P450 * CYP6-like microsomal cytochrome P450 * 1e-33 YRV5_CAEEL PUTATIVE CYTOCHROME P450
T10B9.5 IN CHROMOSOME II * 1e-59 cytochrome P450 3A11 - mouse c[EP450II // p450 // P450 // MITP450 // C] CG8453 GH14851
CG8453 48F1-48F1 dup:2/4 ID:41H5
CG9008 + BG:DS00797.2 unknown * 6e-38 YMY9_YEAST HYPOTHETICAL 34.0 KD PROTEIN IN CTF13-YPK2 INTERGENIC REGION * 3e-

35 putative protein * AAPC_PENCL POSSIBLE AOSPORY-ASSOCIATED PR CG9008 GH14910 34D1-34D1 ID:41H8
 + 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 // PNDRTASEII] CG9674 GH14941 73C-73C2 dup:4/5
 CG9674 ID:41H9
 + enzyme * stromal cell-derived factor 2(aa) * 2e-09 PMT6_YEAST DOLICHYL-PHOSPHATE-MANNOSE--PROTEIN
 CG11999 MANNOSYLTRANSFERASE * 7e-07 /match=(desc:: /ma * 3e-47 cont CG11999 GH15022 83A4-83A4 ID:42A4
 + enzyme * Adh-Finnegan(aa) * fat body protein 2(aa) * development-specific 25K protein - flesh fly (Sarcophaga peregrina)(aa) *
 CG4842 7e-09 YM71_YEAST HYPOTHETICAL [adh_short // ADH_SHORT // adh_short_C] CG4842 GH15220 72F1-72F1 ID:42B10
 + 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
 + ligand_binding_or_carrier * DMC30B8 * ALPHA-TOCOPHEROL TRANSFER PROTEIN (ALPHA-TTP)(aa) * alpha tocopherol
 CG2663 transfer protein(aa) * 62D9.a(aa) [CRETINALDHBP // CRAL_TRIO] CG2663 GH15295 83A6-83A6 ID:42C7
 CG11993+ Mst85C unknown * CG11993 LD21554 85C6-85C6 ID:43A6
 + motor_protein * 1e-34 3-hydroxyisobutyrate dehydrogenase * 1e-10 inserted at base Both 5' and 3' ends of P element Inverse
 CG4747 PCR * YKWC_BACSU HYPOTHETICAL 30.7 KD PR CG4747 LD22344 30F5-30F5 ID:43B10
 CG3510 + CycB cell_cycle_regulator G2/MITOTIC-SPECIFIC CYCLIN B CYCLINS, cyclin CG3510 dup:2/4 ID:43B3
 + noi RNA_binding * noi * noisette(aa) * 1e-30 PR09_YEAST PRE-MRNA SPLICING FACTOR PRP9 PRP9 protein - ye * noisette
 CG2925 [ZF_MATRIN] CG2925 LD22754 83B4-83B4 ID:43C11
 + Cyt-c2 electron_transfer * DMCYC4_4 Cyt-c2 * 9e-36 pdb|2YCC| Cytochrome c (Isozyme 1) (Oxidized) (Mutant With Cys
 Replaced By Thr) (C102T * 1e-59 CYC2_DROME CYTOCHROME C-2 c [CYTCHRMCIAB // cytochrome_c] CG17903 LD23501
 CG17903 36A7-36A7 ID:43F5
 + mus210 DNA_repair_protein * DNA-REPAIR PROTEIN COMPLEMENTING XP-C CELLS HOMOLOG (XERODERMA
 PIGMENTOSUM GROUP C COMPLEMENTING PROTEIN HOMOLOG) (XPCDM)(aa) * DMXPCCF_2 Xpcc * 4e- [MYB_1 //
 CG8153 NLS_BP] CG8153 51F4-51F5 dup:1/3 ID:43G11
 CG2994 + CG2994 LD26546 dup:4/4 ID:44E6
 + 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 64A3-
 CG17746 64A3 dup:4/4 ID:44F12
 + 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
 CG6564 + unknown CG6564 LD27203 ID:44H2
 + 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 dup:3/5
 CG15112 ID:45A1

+ unknown * Ser/Arg-related nuclear matrix protein (plenty of prolines 101-like)(aa) * 7e-33 cDNA EST comes from this gene;
 CG11274 cDNA EST co * 2e-43 plenty-of-prolin [RIBOSOMAL_S12 // NLS_BP] CG11274 LD28048 69F2-69F2 dup:1/2 ID:45C10
 CG4609 + fax failed axon connections protein CG4609 LD28084 dup:2/2 ID:45D1
 + 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
 + 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
 CG14657 + unknown CG14657 LD28447 ID:45F4
 CG2890 + CG2890 dup:2/3 ID:45H3
 CG16944 + sesB transporter ADP/ATP translocase ADPTRNSLCASE, MITOCARRIER CG16944 ID:46A4
 + ND42 enzyme * NADH-ubiquinone oxidoreductase kDa subunit(aa) * DMNUBO42K ND42 * NADH-UBIQUINONE
 CG6343 OXIDOREDUCTASE KD SUBUNIT PRECURSOR (COMPLEX I-42KD) (CI-42KD)(aa [ATP_GTP_A] CG6343 93F14-94A1 ID:46B3
 + unknown * 1e-07 ADRP_MOUSE ADIPOSE DIFFERENTIATION-RELATED PROTEIN (ADRP) * * [ATP_GTP_A] CG9057
 CG9057 13A11-13A11 dup:2/2 ID:46D11
 CG10928 + CG10928 LD29844 dup:3/3 ID:46E11
 + 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
 + 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
 + 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
 + 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
 CG1530 + unknown CG1530 ID:47H2
 + 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 // HTH_LYSR_FAMILY] CG6199
 CG6199 LD31687 68A8-68A8 dup:3/4 ID:47H7
 + RnrS enzyme * 1e-113 RIR2_YEAST RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE SMALL CHAIN (RIBONUCLEOTIDE R
 * 1e-107 RIR2_DROME PROBABLE RIBONUCLEOSIDE-DIPHOSPHATE REDUCTA [RIBORED_SMALL] CG8975 LD32770 48D8-
 CG8975 48D8 ID:48D10

+ enzyme * SUMO-1 activating enzyme subunit 1(aa) * Similar to ubiquitin activating proteins; Aos1p(aa) * 6e-30 RH31_YEAST
 CG12276 DNA DAMAGE TOLERANCE PROTEIN RHC31 ([UBA_NAD // ThiF_family] CG12276 LD33652 87B15-87B15 ID:49A3
 + 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-60 COXX_YEAST CYTOCHROME C OXIDASE ASSEMBLY PROTEIN COX10 PRECURSOR * 5e-94 heme A: farnesyltransferase * 4e-46 putative heme A:farnesyltransferase [COX10_ctaB_cyoE // COX10_CTAB_CYOE] CG5037 LD33876 31D9-31D9 dup:3/3 ID:49B6
 CG5037 31D9 dup:3/3 ID:49B6
 + 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
 + cell_cycle_regulator * DMUNKNOWN anon-DM192 * unknown product(aa) * 4e-05 CC27_YEAST CELL DIVISION CONTROL
 CG4050 PROTEIN cell division * 1e-139 unknown product [TPR_REGION // TPR_REPEAT // TPR] CG4050 57C2-57C2 dup:3/4 ID:49D5
 + TFIIS transcription_factor * 2e-20 DST1 DNA strand transferase alpha * 1e-124 TFS2_DROME TRANSCRIPTION ELONGATION
 CG3710 FACTOR S-II (RNA POLYMERASE II ELONGATION FA * 3e-42 TFS2_CAEEL [TFIIS] CG3710 LD34766 35C1-35C1 ID:49F1
 + unknown * 3e-80 YKL6_CAEEL HYPOTHETICAL 103.8 KD PROTEIN C03C10.6 IN CHROMOSOME III * E03A3.6 * E03A3.7
 CG5237 * [AA_TRNA_LIGASE_II_2 // PRO_RICH // CYTO] CG5237 GH01039 91F10-91F11 ID:54A4
 + enzyme_inhibitor * 7B2(aa) * cDNA EST comes from this gene(aa) * 2e-22 cDNA EST comes from this gene * CG1168
 CG1168 GH01053 83A5-83A5 ID:54A6
 + enzyme * 2e-18 pdb|1GKY| Guanylate Kinase (E.C.2.7.4.8) Complex With Guanosine Monophosphate * 2e-70 Camguk * 2e-67 LIN2_CAEEL LIN-2 PROTEIN LIN-2A * 5e-97 D [Guanylate_kin // GUANYLATE_KINASE_1 //] CG13219 GH01140 47D7-47D7
 CG13219 ID:54B3
 CG17926 + unknown * [NLS_BP] CG17926 GH01154 66D6-66D7 ID:54B7
 CG10671 + unknown * cDNA EST yk481g5.5 comes from this gene(aa) * * CG10671 GH01192 64C12-64C12 ID:54B9
 + 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 23B1-23B2 dup:1/4 ID:54C2
 CG3139 23B2 dup:1/4 ID:54C2
 + neurotransmitter_transporter * 3e-06 cocaine-sensitive serotonin transporter * 8e-11 NTGL_MOUSE SODIUM- AND CHLORIDE-DEPENDENT GLYCINE TRANSPORTER (GLYT-1) * 1e-10 NTGL_HUMAN SODI [NA_NEUROTRAN_SYMP_3]
 CG13796 CG13796 GH01326 28C2-28C2 dup:1/3 ID:54C9
 + structural_protein * Peritrophin-A * cDNA EST comes from this gene; cDNA EST yk369a9.5 comes from this gene; cDNA EST
 CG11142 yk438c12.3 comes from this gene; cDNA EST yk438c12 CG11142 GH01453 26A-26A ID:54D11
 CG5532 + unknown * CG5532 GH01442 59F7-59F7 ID:54D9
 CG1545 + unknown * CG1545 GH01560 10A-10A dup:2/2 ID:54E10
 + 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 ID:54E6
 CG6483 11 similar to peptidase family S1 (tryp[trypsin // CHYMOTRYPSIN // TRYPSIN_SER] CG6483 GH01508 65A2-65A2 dup:2/2 ID:54E6
 CG10680 + * CG10680 38B1-38B1 dup:2/3 ID:54F11

+ 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
 CG11661 * Similar to 2-oxoglutarate dehydrogenase; coded for by C. elegans [E1_dehydrog] CG11661 73D6-73D7 dup:3/7 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
 CG8401 + unknown * CG8401 GH01937 52E3-52E4 ID:55A1
 + cell_adhesion * orphan G protein-coupled receptor FEX(aa) * BLASTX 7.5E-06 Santalum album proline rich protein mRNA,
 CG3413 complete cds.(dna) * 9e-05 protein * 5e-05 kek1 [LRR // LEURICHRPT // NLS_BP // LRRCT] CG3413 GH02310 58D2-58D3 ID:55B8
 CG7506 + unknown * 2e-07 cDNA EST comes from this gene; cDNA EST co ** CG7506 GH02466 66A7-66A7 ID:55C9
 CG1537 + unknown * CG1537 GH02938 10A-10A dup:2/2 ID:55E12
 + 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
 CG9005 + cell_adhesion * 0.000000000000000003 ** CG9005 GH03037 48B1-48B2 dup:2/5 ID:55F7
 + Eip63F-1ligand_binding_or_carrier * Eip63F-1 * 2e-74 E631_DROME CALCIUM-BINDING PROTEIN E63-1 calcium-binding pr * 3e-
 CG15855 17 similar to EF-hand calcium binding proteins; most similar to ca CG15855 GH03109 63F7-63F7 ID:55G4
 + DNA_repair_protein * putative antisense basic fibroblast growth factor(aa) * antisense basic fibroblast growth factor B(aa) * 4e-
 CG8128 30 GFG_RAT PROTEIN GFG antisense basic f [MUTT // mutT // MUTTDOMAIN] CG8128 GH03273 13E13-13E14 ID:55H3
 CG4275 + moira transcription_factor chromatin modeling MYB_3, NLS_BP, myb_DNA-binding CG4275 GH03275 ID:55H4
 CG5914 + unknown * 1E-179** CG5914 GH03315 5D2-5D2 ID:55H6
 CG4782 + unknown * CG4782 GH03334 86D6-86D6 ID:55H7
 CG2767 + enzyme aldose reductase ALDOKETO_REDUCTASE_1, ALDOKETO_REDUCTASE] CG2767 ID:56C2
 + 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 // adh_short
 CG3481 //] CG3481 GH03875 35B3-35B3 dup:4/6 ID:56D5
 + Bc larval_serum_protein * pro-phenol oxidase A1 * pro-phenol oxidase subunit 1; proPO-p1 * DMORA_2 Bc * prophenoloxidase
 CG5779 [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-42
 CG5725 putative protein * coded for by C. CG5725 GH04001 77B6-77B6 dup:3/3 ID:56E4
 + 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
 CG3445 + 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 dup:3/4 ID:56G10
 + 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 49B7-49B7 ID:57A5
 CG8785 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
 CG4962 + unknown * CG4962 GH04593 72E2-72E2 ID:57B2
 CG7515 + CG7515 GH04814 ID:57C5
 CG4294 + motor_protein * [PPASE // PRO_RICH // NLS_BP] CG4294 GH04951 58F1-58F1 dup:3/4 ID:57D11
 CG9896 + unknown * [NLS_BP] CG9896 GH05301 59C1-59C1 ID:57G12
 CG11344 + unknown * CG11344 GH05223 21E2-21E2 ID:57G3
 + 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 51D2-51D2 ID:58A6
 CG10248 ID:58A6
 CG11477 + unknown * CG11477 GH05565 12E2-12E2 ID:58A7
 + Hrb87F RNA_binding * Rbm(aa) * similar to RNA recognition motif. (aka RRM, RBD, or RNP domain); cDNA EST yk474h4.3 comes from this gene; cDNA EST yk505c10.3 comes from [RNP_1 // RBD // rm] CG12749 GH05625 87F7-87F7 ID:58B2
 CG12749 comes from this gene; cDNA EST yk505c10.3 comes from [RNP_1 // RBD // rm] CG12749 GH05625 87F7-87F7 ID:58B2
 CG9689 + unknown * CG9689 GH05731 9A2-9A2 ID:58B9
 + enzyme * acid phosphatase (EC 3.1.3.2) Acph-1 precursor, lysosomal - fruit fly (Drosophila melanogaster)(aa) * acid phosphatase-1(aa) * PUTATIVE ACID PHOSPH [acid_phosphat] CG6656 GH06011 93F-93F dup:3/3 ID:58E4
 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 GH06087 29F6-29F6 dup:2/2 ID:58E8
 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
 CG11221 CG11221 GH06138 27A2-27A2 ID:58F2
 + unknown * ring finger protein 13(aa) * RING zinc finger protein(aa) * 2e-09 GOLI_DROME GOLIATH PROTEIN (G1 PROTEIN) regulatory protei * 6e-24 similar to Zinc [GRAM_POS_ANCHORING // zf-C3HC4 // CYTOC] CG10277 GH06194 84A4-84A4 dup:2/2 ID:58F6
 CG10277 ID:58F6
 + 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 dup:1/2 ID:58G6
 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

CG4377 + unknown * CG4377 GH06474 58A3-58A3 ID:58H6
 + DNA_binding * Ser/Arg-related nuclear matrix protein (plenty of prolines 101-like)(aa) * elastic titin(aa) * 1e-11 C. elegans
 CG3950 UNC-89 * 8e-07 MAPB_MOUSE MICROTUBU [NLS_BP] CG3950 GH06555 6B1-6B3 ID:59A3
 + 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
 + 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 dup:4/5
 CG2469 ID:59D12
 CG18512+ CG18512 GH07187 ID:59D7
 + 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
 CG8678 + CG8678 dup:1/2 ID:60A10
 + TM4SF unknown * TM4SF * 1e-156 belong to the membrane protein group of Transmembrane Super * 9e-07 CD53_MOUSE LEUKOCYTE SURFACE ANTIGEN CD53 (CELL SURFACE GLYCOPROT [TMFOUR // TM4_2] CG11303 GH07902 60A7-60A7
 CG11303 dup:2/3 ID:60B10
 + Rbp9 RNA_binding * 3e-14 PUB1_YEAST NUCLEAR AND CYTOPLASMIC POLYADENYLATED RNA-BINDING PROTEIN PUB1 (ARS * 1e-175 RNA-binding protein * 5e-70 Similar to the human para [RNP_1 // RBD // HUDSXL RNA // rrm] CG3151
 CG3151 GH07919 23C1-23C2 dup:1/2 ID:60C1
 + unknown * hypothetical protein(aa) * DMRNAPER_2 anon-3B1.2 * 2e-08 0.9-kb RNA transcript * 7e-10 DMRNAPER_2 anon-
 CG7096 3B1.2 CG7096 GH08336 93B5-93B5 dup:3/3 ID:60E10
 + 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
 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
 + 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
 CG4302 + CG4302 CG11051 GH09393 ID:61F9
 + enzyme * sphingomyelin phosphodiesterase 1, acid lysosomal (acid sphingomyelinase)(aa) * SPHINGOMYELIN PHOSPHODIESTERASE PRECURSOR (ACID SPHINGOMYELINASE)(aa [PHOSPHO_ESTER // SAP_B] CG3376 GH09489 60C1-
 CG3376 60C2 dup:2/5 ID:61G4

+ 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
 + unknown * 2e-13 YJT6_YEAST HYPOTHETICAL 36.2 KD PROTEIN IN UBP12-CDC6 INTERGENIC REGION * 8e-18
 CG9798 YLF4_CAEEL HYPOTHETICAL 34.1 KD PROTEIN C40H1.4 IN CHROMOSOME CG9798 GH09808 82C1-82C2 dup:3/4 ID:61H12
 CG17875+ cytochrome_P450 CG17875 GH09824 dup:1/3 ID:62A2
 CG1822 + CG1822 dup:2/2 ID:62B10
 + ligand_binding_or_carrier * 1e-22 YBE9_YEAST HYPOTHETICAL 16.1 KD PROTEIN IN SEC17-QCR1 INTERGENIC
 CG15309REGION * 8e-21 putative zinc-binding protein melanogaste * 1e-18 No definitio CG15309 GH10478 9B6-9B6 dup:2/2 ID:62E4
 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
 CG13848PROTEIN (ALPHA-TTP) al * tocopherol (alpha) transfer protein (ata [CRAL_TRIO] CG13848 GH10582 96E1-96E1 ID:62F2
 + transporter * 1e-21 putative organic cation transporter * 1e-08 similar to C. elegans protein and to rat synaptic vesicle protein
 CG4462 (PIR:S3 * 3e-14 organic cation t CG4462 GH10729 92B9-92B10 ID:62G4
 none + none GH10751 ID:62G7
 + chaperone * 6e-06 cargo selection protein TIP47 * placental protein 17b1; PP17b1 * adipose differentiation-related protein * 2e-
 CG1037406 cargo selection protein TIP47 [NLS_BP] CG10374 GH10767 95B8-95B9 ID:62G9
 + cell_adhesion * DMARTAN_7 trn * kek1 * tartan protein(aa) * 5e-16 CYAA_YEAST ADENYLATE CYCLASE (ATP
 CG11280PYROPHOSPHATE-LYASE) (ADENYLYL CYCLASE) [LRR // LEURICHRPT // LRRCT] CG11280 GH10871 69F5-69F5 ID:62H10
 + ninaC motor_protein * DMNINAC_2 ninaC * ligand binding or carrier calmodulin binding) protein kinase protein serine/threonine
 CG5125 kinase) cell non-muscle myosin) map_posit [myosin_head // PROTEIN_KINASE_TYR // IQ] CG5125 GH10824 27F5-27F6 ID:62H5
 + 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
 + 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
 CG4370 ID:63D11
 + Dynein heavy chain at 93AB motor_protein DYNEIN BETA CHAIN, CILIARY ATP_GTP_A, MITOCH_CARRIER, NLS_BP, THIOL
 CG3723 CG3723 GH11420 ID:63D9
 + unknown * cold inducible glycoprotein 30(aa) * 5e-15 SUR4 * 8e-53 YYS3_CAEEL HYPOTHETICAL 51.5 KD PROTEIN IN
 CG3971 CHROMOSOME IV (U * 2e-49 membrane glycoprotein CI CG3971 GH11554 73B1-77B1 dup:2/2 ID:63E9
 + 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
 + 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) * polymerase
 CG6572 (RNA) II (DNA directed) polypeptide G(aa) * 7e-33 RPB7_ [S1] CG6572 GH11867 88E8-88E8 ID:63H5
 CG1449 + zfh2 transcription_factor * ZINC-FINGER PROTEIN (ZINC-FINGER HOMEODOMAIN PROTEIN 2)(aa) * DMZFH2_2 zfh2 * 7e-40

Contains similarity to Pfam domain: (zf-C2H2), Score=[HOMEBOX_1 // homeobox // ZF_MATRIN //] CG1449 GH11902 102C1-102C3 dup:2/2 ID:63H9

+ 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 15A5-15A5
CG4742 ID:64C2

+ unknown * 6e-05 transmembrane protein * 2e-12 Similarity to C.elegans cuticulin (SW:CUT1_CAEEL) * 7e-07 DMDUSKY_1 dy
CG3541 * 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

+ unknown * 8e-42 YMS5_CAEEL HYPOTHETICAL 159.2 KD PROTEIN K03H1.5 IN CHROMOSOME III * 8e-17 alpha tectorin *
CG15560 2e-16 tectorin alpha alpha-tectorin * 1e-15 alpha CG15560 GH12365 100B8-100B8 ID:64D8

+ EG:100G10.1 unknown * SH3 domain-binding protein SNP70(aa) * by content; by match; LD Drosophila melanogaster...(aa) * 8e-
CG2685 06 WW domain binding protein * [PRO_RICH // NLS_BP] CG2685 GH12462 3B5-3B5 dup:3/3 ID:64E6

+ 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

+ 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

+ 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

CG18065+ unknown * CG18065 GH13245 57A8-57A8 ID:65C11

+ 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

CG17108+ * cdc2MsC(aa) * cdc2MsC * CG17108 32A-32A dup:4/4 ID:65E10

+ 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

+ Cyp4e1 cytochrome_P450 * cytochrome P450, Cyp4e2 - fruit fly (Drosophila melanogaster) (U5 * 6e-79 predicted using
CG2062 Genefinder; similar to cytochrome P450 * 3e-50 CYP4B1 [EP450II // p450 // P450 // MITP450 // C] CG2062 GH13635 44C1-44C2

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 // KCLTRNSPORT] CG5594 GH13642 60A9-60A10
 CG5594 dup:4/5 ID:65E9
 + 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-Hacid_DH]
 CG9331 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
 + endopeptidase * mas * Ser5 * Tequila * zgr;Try [trypsin // CHYMOTRYPSIN // TRYPSIN_SER] CG11912 GH13929 21B7-
 CG11912 21B8 ID:65G7
 + Cyp6a2 cytochrome_P450 * PUTATIVE CYTOCHROME P450 T10B9.7 IN CHROMOSOME II(aa) * DMCYP6A2A_5 Cyp6a2 *
 CG9438 CYP6A2 * 3e-43 similar to cytochrome P450 [EP450II // MITP450 // CYTOCHROME_P450 /] CG9438 GH13965 42C5-42C5 ID:65G9
 CG15390 + unknown * CG15390 GH14074 22E-22E ID:65H11
 + structural_protein * nuclear pore protein; Seh1p(aa) * similar to WD domain, G-beta repeat (2 domains); cDNA EST yk258d4.3
 CG8722 comes from this gene; cDNA EST yk338d5.3 comes [GPROTEINBRPT // WD40] CG8722 GH14024 43F9-43F9 ID:65H2
 + 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
 + unknown * 2e-05 CU19_LOCM1 CUTICLE PROTEIN (LM-19) (LM-ACP 19) Lm-ACP1 * * [GRAM_POS_ANCHORING //
 CG9665 insect_cuticle] CG9665 GH14349 73D-73D6 ID:66C3
 CG9813 + unknown * [ATPASE_ALPHA_BETA] CG9813 GH14502 87E8-87E9 dup:1/2 ID:66D11
 + 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
 + 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-90
 CG10149 hypothetical protein YDL097c - yeast (Saccharomyc [PCI_DOMAIN // PCI] CG10149 GH14689 51C2-51C2 ID:66F12
 + cell_adhesion * 4e-06 UNC-89 * 6e-05 VGR2_MOUSE VASCULAR ENDOTHELIAL GROWTH FACTOR RECEPTOR
 CG7607 PRECURSOR (VEGFR-2) (PR * 1e-05 protein tyrosine phosphatase, receptor t [ig] CG7607 GH14648 68A8-68A8 ID:66F6
 + unknown * hypothetical protein(aa) * similar to human 5'-nucleotidase * Unknown(aa) * 6e-46 similar to human 5'-nucleotidase
 CG1814 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
 CG4972 + * cDNA EST yk335d8.5 comes from this gene; cDNA EST yk335d8.3 comes from this gene(aa) * 2e-23 cDNA EST yk335d8.5

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

+ 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

+ electron_transfer * CYTOCHROME B5 (CYTB5)(aa) * 3e-17 cytochrome b5 * 1e-25 Similarity to Human cytochrome b5 (SW:CYB5_HUMAN); cDNA EST EMBL:D * 2e-30 CYB5_MOUSE CY[Cytochrome_B5 // CYTOCHROME B5 // CYTOCH] CG2140 CG2140 GH15091 43D-43D dup:3/3 ID:67B9

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

+ Scp1 ligand_binding_or_carrier * calcium-binding protein alpha-a chain - penaeid shrimp (Penaeus sp.)(aa) * Scp1 * 5e-94 CG15848 calcium-binding protein * 2e-43 SCPB_PENSP SARCOPLASMIC CALC CG15848 GH15296 cyto_unknown ID:67D6

CG8420 + * [ER_TARGET] CG8420 85D2-85D3 dup:3/3 ID:67F12

+ enzyme * antennal-specific short-chain dehydrogenase/reductase(aa) * 1e-22 YM71_YEAST HYPOTHETICAL OXIDOREDUCTASE IN MRPL44-MTF1 INTERGENIC REGION * 1e-13 si [GDHRDH // adh_short] CG13356 20B1-20B1 dup:1/2 CG13356 ID:67G2

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

+ Hml cell_adhesion * HEMOCYTIN PRECURSOR (HUMORAL LECTIN)(aa) * 3e-13 neurexin IV * 9e-15 similar to EGF-like domain, Fibrinogen beta and gamma chains, C-te * 1e-145 o[LDLRA_2 // vwd // EGF_1 // EGF_2 // CTC] CG7002 GH15913 70C4-70C4 dup:2/3 ID:68B8

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 CG6432 1) (ACYL-ACTIVATI * 1e-81 acetyl-CoA synthetase - fruit fly [AMP-binding] CG6432 GH15945 98B1-98B1 dup:1/2 ID:68C1

+ ninaE * DMOPSA_2 ninaE * OPS1_DROME OPSIN RH1 (OUTER R1-R6 PHOTORECEPTOR CELLS OPSIN) * 1e-06 serotonin receptor * 1e-35 OPSX_MOUSE VISUAL PIGMENT-LIKE REC [OPSINRH1RH2 // GPCRRHODOPSN // OPSIN //] CG4550 92B8-92B9 dup:1/5 ID:68C2

+ 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

+ cell_adhesion * 7e-56 strong similarity to rat integral membrane glycoprotein GP120 precursor (SP:P116 * 4e-18 protein * 1e- CG7897 95 GP21_RAT INTEGRAL MEMBRANE GLYCOPROTE CG7897 GH16206 41F-41F dup:4/6 ID:68D5

+ 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

+ 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

+ 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
 + endopeptidase * chymotrypsin-like serine protease(aa) * TRYPSIN DELTA PRECURSOR(aa) * DMEAST_4 ea * Ser6 [trypsin
 CG9672 // CHYMOTRYPSIN // TRYPSIN_CATA] CG9672 GH16384 15A2-15A2 dup:2/2 ID:68E9
 CG12191+ cell_adhesion * 8e-05 adhesion molecule L1.1 * [ig] CG12191 GH16485 61D4-61D4 ID:68F12
 CG15068+ CG15068 GH16622 ID:68G10
 + Pug enzyme * Pug * C1TM_YEAST C-1-TETRAHYDROFOLATE SYNTHASE MITOCHONDRIAL PRECURSOR (C1-THF
 SYNTHAS * C1-THF synthase homolog * Contains similarity to Pfam doma [THF_DHG_CYH_2 // THFDHDRGNASE // FTHFS]
 CG4067 CG4067 GH16587 86C2-86C2 dup:2/2 ID:68G5
 + * 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
 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
 + 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
 + Taf250 transcription_factor * Taf250 * 3e-49 T145_YEAST TRANSCRIPTION INITIATION FACTOR TFIID KD SUBUNIT (TBP-
 ASSOCIATED * transcription factor * 5e-34 cDNA EST comes from this[BROMODOMAIN_2 // NLS_BP // BROMODOMAIN_] CG17603
 CG17603 GH17990 84A2-84C4 ID:70A9
 + 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 64A5-64A7
 CG14994 ID:70B5
 + 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
 + peptidase * 5e-60 putative metalloprotease; Method: conceptual translation supplied by author * 1e-23 coded for by C. elegans
 CG8196 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 23D1-23D1
 CG7082 dup:3/3 ID:70E4
 CG4975 + unknown * 4e-05 BE46_MOUSE BRAIN PROTEIN E46 gene E46 protein - mouse * * CG4975 GH18454 54E5-54E5 ID:70F8
 + 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
 + translation_factor * GTP binding protein similar to S. cerevisiae HBS1(aa) * elongation factor alpha(aa) * Elf * DMEF1AF2_8
 CG1898 Ef1 agr;100E [ELONGATNFCT // GTP_EFTU // ATP_GTP_A] CG1898 GH18819 62E3-62E3 ID:71A1
 + 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
 + endopeptidase * DMSTUBBLE_1 Sb * caldecrin=serum calcium-decreasing factor pancreas, Peptide, * 7e-36 STUB_DROME
 SERINE PROTEINASE STUBBLE (STUBBLE-STUBBLOID PROTEI [trypsin // CHYMOTRYPSIN // TRYPSIN_HIS] CG5390 31D5-
 CG5390 31D6 dup:2/2 ID:71B8
 + transmembrane_receptor * DMEMP_3 emp * 3e-53 epithelial membrane protein - fruit fly (Drosophila melanogaster) * 5e-24
 CG3829 predicted using Genefinder; similar to CD36 family; cD [CD36] CG3829 GH19047 60E8-60E8 ID:71B9
 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
 CG15386 + unknown * 1E-132* * CG15386 GH19557 23D1-23D1 ID:71F10
 + signal_transduction * 5e-30 similar to guanine-nucleotide releasing factors including BCR ele * 7e-20 transforming protein
 CG7397 (ect2) - mouse ect2 >g * 6e-17 GrfA * R02F2.2 g [GRF_DBL // RhoGEF // NLS_BP] CG7397 GH19526 90C2-90C2 ID:71F7
 CG4679 + unknown * CG4679 GH19550 49F14-49F15 ID:71F9
 + chp cell_adhesion * DMCOP10_2 chp * 2e-11 CYAA_YEAST ADENYLATE CYCLASE (ATP PYROPHOSPHATE-LYASE)
 (ADENLYL CYCLASE) * CHAO_DROME CHAOPTIN PRECURSOR (PHOTORECEPTOR CELL [ARM_REPEAT // LRR //
 CG1744 LEURICHRPT] CG1744 GH19649 100B8-100B9 ID:71G7
 + 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
 CG13458 + unknown * 1E-160* * [COPPER_BLUE] CG13458 GH20023 71B2-71B2 ID:72B12
 + enzyme * polyketide synthase(aa) * 1e-68 CEM1_YEAST SYNTHASE HOMOLOG (BETA-KETOACYL-ACP * 1e-69 similar to
 beta-ketoacyl synthase * 3e-92 putative 3-oxoacyl [B_KETOACYL_SYNTHASE // PPTA // ketoacyl] CG12170 GH20093 83B6-83B6
 CG12170 ID:72C9

+ transporter * BLASTX 2.0E-28 Human sodium iodide symporter mRNA, complete cds.(dna) * 4e-36 unknown * 2e-17 Similarity
 CG7720 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) (ROSY
 CG6045 LOCUS PROTEIN)(aa) [dehydrog_molyb // Ald_Xan_dh_C // fer2] CG6045 GH20168 88F8-88F8 ID:72D2
 + serpin * 3e-34 Similar to serine protease inhibitor * 6e-38 proteinase inhibitor Spi3 - mouse serine proteinase inhib * 1e-35
 CG1865 cytoplasmic antiproteinase, CAP [serpin // SERPIN] CG1865 GH20213 42F1-42F1 ID:72D9
 + unknown * 1e-39 /match=(desc;; /ma * 3e-06 F20D6.5 gene product * predicted using Genefinder * cDNA EST yk381e5.3
 CG10514 comes from this gene [NLS_BP] CG10514 GH20308 96C7-96C7 dup:2/2 ID:72E7
 + enzyme * similar to aspartate aminotransferase(aa) * 1e-99 aspartate aminotransferase cerevisiae, Peptide Partial, * 1e-157
 CG4233 similar to aspartate aminotransferase [aminotran_1 // AA_TRANSFER_CLASS_1 // T] CG4233 GH20337 22B8-22B8 dup:2/2 ID:72F2
 CG18020 + projectin [Drosophila melanogaster] CG18020 ID:72G5
 CG17111 + unknown * CG17111 GH20645 94D13-94D13 ID:72H6
 + 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
 + structural_protein * 4e-07 CUP8_DROME PUPAL CUTICLE PROTEIN EDG-84 PRECURSOR ecdyson * 3e-08 CU19_LOCM1
 CUTICLE PROTEIN (LM-19) (LM-ACP 19) Lm-ACP1 * 5e-09 DMEDG84A_3 Ed [CUTICLE // PRO_RICH // insect_cuticle] CG6305
 CG6305 GH20904 50C9-50C11 ID:73B10
 CG1383 + unknown * 2e-74 F55A12.9 gene product * * CG1383 43E12-43E13 ID:73D4
 + 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 cyto_unknown dup:2/2
 CG12449 ID:73F3
 + 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
 CG5627 ID:73F8
 + 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 // SU] CG6484
 CG6484 GH21490 54D2-54D2 ID:73G7
 + Acp1 structural_protein * Acp1 * ADULT CUTICLE PROTEIN PRECURSOR (DACP-1)(aa) * cuticle protein=Dacp-1 melanogaster,
 CG7216 Peptide, * CG7216 GH21504 28C3-28C3 dup:1/2 ID:73G8
 + 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
 + metabolism * 3601, 14-kDa protein subunit of reductase complex(aa) * ubiquinol-cytochrome c reductase binding protein(aa) *
 CG3560 UBIQUINOL-CYTOCHROME C REDUCTASE COMP CG3560 GH21854 14B12-14B12 ID:74B9
 CG10947 + * hypothetical protein(aa) * 3e-07 hypothetical protein * * CG10947 38C9-38C9 dup:2/2 ID:74C6
 CG2457 + inaF ion_channel * INAF protein(aa) * 1e-115 INAF protein * * CG2457 GH21930 10D5-10D6 dup:1/2 ID:74C7
 + enzyme * 7e-97 ALAM_YEAST PUTATIVE ALANINE AMINOTRANSFERASE, MITOCHONDRIAL PRECURSOR (GLUTAMIC
 CG1640 * 1e-159 Similar to alanine aminotransferase; coded for by C. [aminotran_1 // ACCSYNTHASE] CG1640 GH21936 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
 + 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
 + kls unknown * klarsicht protein(aa) * 8e-06 protein * hypothetical protein * protein [NLS_BP // SUGAR_TRANSPORT_1]
 CG17046 CG17046 GH22034 61C3-61C7 dup:5/6 ID:74D8
 + 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
 + 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
 + 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 17B5-
 CG6335 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 25A3-25A3
 CG3241 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 // HOMEBOX] CG10704 GH22493 69B3-
 CG10704 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
 + 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 // HOMEBOX] CG6716
 CG6716 GH22686 33B14-33B14 ID:75B4
 + 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
 CG1479 + bt protein_kinase * projectin - fruit fly (Drosophila melanogaster)(aa) * bt * similar to Fibronectin type III domain (31 domains), IG

(immunoglobulin) superfami[ig // PROTEIN_KINASE_ST // FNTYPEIII //] CG1479 GH22863 102D6-102E1 dup:1/2 ID:75D11

+ 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

+ 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

+ transporter * 3e-69 predicted using Genefinder; cDNA EST comes from this g * 3e-07 tetracycline resistance protein * similar to

CG8054 translocase * contains similarity [PRO_RICH // NLS_BP] CG8054 GH23453 45B1-45B1 ID:76C6

+ protein_kinase * bt * hep * 8e-21 SPK1_YEAST PROTEIN KINASE SPK1 (SERINE-PROTEIN KINASE 1) * 2e-20 p90

CG1760 ribosomal S6 kinase [PROTEIN_KINASE_ST // PROTEIN_KINASE_DOM] CG1760 GH23573 10C3-10C3 ID:76D10

+ Ark unknown * 1e-05 apoptotic protease activating factor * 3e-06 apoptotic protease activating factor * 2e-34 inserted at base

CG6829 Both 5' and 3' ends of P element In [ATP_GTP_A] CG6829 GH23583 53F1-53F1 ID:76D11

+ endopeptidase * mas * DMSER1_2 Ser99Dc * 7e-61 serine proteinase (EC 3.4.21.-) precursor - fruit fly (*Drosophila melanogaster*) * 2e-29 EL2_MOUSE ELASTASE PRECURSOR pan [trypsin // CHYMOTRYPSIN // TRYPSIN_SER] CG6467 GH23808

CG6467 65A2-65A2 ID:76G10

+ 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

+ unknown * 1e-05 NIPM_BOVIN NADH-UBIQUINONE OXIDOREDUCTASE KD SUBUNIT (COMPLEX I-15 KD) (CI-15 * *

CG11455 CG11455 GH23780 21B2-21B2 ID:76G6

CG9780 + unknown * [ABC_TRANSPORTER] CG9780 GH23891 82A4-82A4 ID:76H12

+ 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

+ enzyme * 3-hydroxyacyl-CoA dehydrogenase (hbd-8)(aa) * 9e-14 HCD1_CAEEL PROBABLE 3-HYDROXYACYL-COA DEHYDROGENASE F54C8.1 * 1e-54 lambda-crystallin * 3e-74 C [3HCDH // NAD_BINDING // NLS_BP] CG10131 GH23990 51B7-

CG10131 51B7 dup:2/2 ID:77B1

CG6043 + unknown * [PRO_RICH] CG6043 GH24071 34A11-34B1 ID:77B11

+ enzyme * cDNA EST yk478b4.5 comes from this gene; cDNA EST comes from this gene; cDNA EST yk456b12.5 comes from

CG17446 this gene; cDNA EST comes from this gene(aa) [PHD] CG17446 GH24056 8D7-8D7 ID:77B9

+ unknown * 5e-11 HST2_YEAST HST2 PROTEIN (HOMOLOGOUS TO SIR2 PROTEIN 2) * 1e-09 SIR2 * 1e-48 similar to SIR;

CG3187 cDNA EST yk300f10.3 comes from this gene * 3e-49 u CG3187 GH24142 5A12-5A12 ID:77C5

+ 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

+ signal_transduction * EPHRIN-B1 PRECURSOR (EPH-RELATED RECEPTOR TYROSINE KINASE LIGAND 2) (LERK-2)

CG1862 (ELK LIGAND PRECURSOR) (ELK-L) (XLERK)(aa) * 4e-13 cek5 receptor ligand [Ephrin] CG1862 GH24276 102C5-102C5 ID:77D9

+ enzyme * DMC103B4 * 1e-05 LYS2_YEAST AMINOADIPATE-SEMIALDEHYDE DEHYDROGENASE LARGE SUBUNIT

CG12268 (ALPHA-AMINOADI * 2e-53 /match=(desc:; /ma * 4e-75 similar to Arab [HELIX_LOOP_HELIX] CG12268 GH24480 95C13-95C13

ID:77F5

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 (CYPIVA11) [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
+ inaC protein_kinase * protein kinase C (EC 2.7.1.-) beta-II - rat(aa) * DMPKCR_2 Pkc53E * DMPKC53E_2 inaC * 5e-78
KPC1_YEAST PROTEIN KINASE C-LIKE (PKC 1) serine/threoni [DAG_PE_BINDING_DOMAIN // PROTEIN_KINASE] CG6518

CG6518 GH24781 53E1-53E2 ID:77H9
+ 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
+ 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
+ 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

CG14653+ unknown * 1E-59* * CG14653 GH25780 82D5-82D5 ID:79B5
+ 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
+ enzyme * 1e-09 BACR37P7.d * 8e-25 strong similarity to the insect-type alcohol/ribitol dehydrogenase family * 2e-27 cis-retinol

CG8888 androgen dehydrogenase * 2e-3 [adh_short] CG8888 GH26015 48E4-48E6 ID:79D8
+ 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
+ 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
+ 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

CG4722 + 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
30F4-30F5 dup:2/3 ID:8-31 cntrlBB5

CG1374 + tsh transcription_factor CG1374 tsh dup:3/3 ID:8-31 cntrlBD3
CG6845 + * 2e-12 cDNA EST yk452h4.3 comes from this gene; cDNA EST yk452h4.5 comes * * CG6845 61A-61A dup:1/2 ID:80A8
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 * polytropic murine leukemia virus receptor SYG1(aa) * 3e-32 SYG1_YEAST SYG1 PROTEIN SYG1 protein - yeast
CG10483 (Saccharomy * 1e-150 predicted using Genefin [CRYSTALLIN_BETAGAMMA] CG10483 GH26628 64F5-64F5 ID:80C8
+ 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
+ fln cytoskeletal_structural_protein * DMFLIGHT_2 fln * FLIGHTIN (MUSCLE PROTEIN 27)(aa) * 2e-19 CMP-N-acetylneuraminic
CG7445 acid synthetase * myofibrillar protein flightin - fruit fly (Drosop CG7445 GH26786 76E2-76E2 dup:3/3 ID:80E9
+ Cyp9f2 cytochrome_P450 * CYP9 cytochrome P450(aa) * 3e-18 CYP6A2 * 2e-10 similar to cytochrome P450 * 5e-16 cytochrome
CG11466 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 91A2-91A2 dup:2/4
CG7675 ID:80F8
+ unknown * 1E-38* 9e-24 inserted at base Both 5' and 3' ends of P element Inverse PCR * CG13130 GH26896 30F4-30F4
CG13130 ID:80G1
CG10965+ unknown * CG10965 GH26991 7D21-7D21 ID:80H1
CG8012 + unknown * CG8012 GH26995 67E7-67E7 ID:80H3
+ 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
+ enzyme * antennal-specific short-chain dehydrogenase/reductase(aa) * BLASTX 3.5E-15 YMR226C|Protein with similarity to
CG7077 insect-type alcohol dehydrogenase, rib [adh_short] CG7077 GH27329 94A14-94A14 dup:2/2 ID:81C8
+ Cyp305a1 cytochrome_P450 * CYTOCHROME P450 76C4(aa) * cytochrome P450 epoxygenase(aa) * cinnamate 4-
CG8733 hydroxylase(aa) * Cytochrome P-450 2A14(aa) [EP450II // p450 // P450 // MITP450 // B] CG8733 GH27419 76D3-76D3 ID:81D5
+ cell_adhesion * DMARTAN_7 trn * 4e-35 KEK1 * 3e-06 contains similarity to leucine-rich repeats (LRR) * 8e-12 neurogenic
CG9431 extracellular slit protein [ig // LRR // LRRCT] CG9431 GH27420 34A10-34A10 ID:81D6
CG6503 + CG6503 dup:2/2 ID:81E12

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 62E5-62E5
CG16761 ID:81G8
+ * 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
+ 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
+ unknown * CGI-05 protein(aa) * 7e-23 YQT5_CAEEL HYPOTHETICAL 61.3 KD PROTEIN F25B5.5 IN CHROMOSOME III (U *
CG6550 1e-65 432aa long hypothetical protein * conserved [UPF0004] CG6550 GH28477 54C1-54C1 ID:82D10
+ 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 78C7-
CG9390 78C7 ID:82D4
+ 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 protein(aa)
CG8654 * 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
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 protein
CG18285 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
+ 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-
CG17342 86F7 ID:82G11
+ Hsp27 chaperone * DMHSP27G_3 Hsp27 * 1e-118 HS27_DROME HEAT SHOCK PROTEIN heat shock protein - f * 3e-13
Contains similarity to Pfam domain: (HSP20), Score=130.7, * 2 [TONB_DEPENDENT_REC_1 // HSP20 // ACRYST] CG4466
CG4466 GM13686 67B2-67B2 ID:83A12

+ 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
 CG9140 ID:83B12
 CG6544 + fau unknown * CG6544 HL07933 86C4-86C4 dup:1/2 ID:83C11
 + unknown * CUTICLE PROTEIN (BC-NCP1)(aa) * BLASTX 1.2E-10 Theileria parva schizont/sporozyte surface protein gene,
 CG8736 partial cds.(dna) * CG8736 HL08183 44D-44D ID:83D10
 + hk ion_channel * 3e-38 Hk protein * 4e-09 potassium channel beta subunit * 8e-09 potassium channel beta subunit * 4e-09
 CG2287 alpha-dendrotoxin-sensitive potassium channel CG2287 HL08167 9B7-9B8 ID:83D9
 + 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
 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 f[zf-C2H2 // ZINC_FINGER_C2H2 // ZINC_FIN] CG3998 LD23102
 CG3998 30D1-30D1 ID:83H12
 + 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
 + enzyme * 1e-82 Similar to NADH-ubiquinone oxidoreductase kd subunit; coded for by C. elegans * 4e-88 NADH
 CG12079 dehydrogenase (ubiquinone) Fe-S protein (30kD) (NAD [complex1_30Kd] CG12079 63B11-63B11 dup:2/2 ID:84H8
 + 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 13A1-13A1
 CG9509 ID:85A6
 + enzyme * Similar to carbonic anhydrase; coded for by C. elegans cDNA yk72d10.3; coded for by C. elegans cDNA yk119b1.3;
 CG6906 coded for by C. elegans cDNA cm18b8; [carb_anhydrase] CG6906 LD26647 68F7-68F7 dup:2/2 ID:85G2
 + enzyme * ACONITATE HYDRATASE, MITOCHONDRIAL PRECURSOR (CITRATE HYDRO-LYASE) (ACONITASE)(aa) *
 ACON_YEAST ACONITATE HYDRATASE, MITOCHONDRIAL PRECURSOR (CITRA [ACONITASE_2 // Aconitase_C //
 CG9244 THIOLASE_] CG9244 LD26837 39B3-39B3 dup:3/3 ID:85H6
 + RNA_binding * 2e-14 predicted using Genefinder; Similarity to Arabidopsis DNA-damage-r * 8e-43 splicing factor (45kD); SPF
 CG17540 45kDa splicing factor; SPF * 2e-17 D111 [D111_DOMAIN] CG17540 LD27025 cyto_unknown ID:86A12
 CG9304 + unknown * 8e-42 cDNA EST comes from this gene * 2e-20 antigen * C15A7.2 * CG9304 LD26991 58B5-58B5 ID:86A7
 + 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
 CG5868 + CG5868 dup:2/2 ID:86E9
 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
 CG5809 + CaBP1 chaperone protein disulfide isomerase ER_TARGET, THIOREDOXIN CG5809 LD28038 dup:2/2 ID:87B5
 CG15427+ cell_adhesion CG15427 LD28224 dup:1/2 ID:87D1
 + sn actin_binding * singed protein - fruit fly (Drosophila melanogaster)(aa) * DMSING2_2 sn * SING_DROME SINGED PROTEIN
 CG1536 singed * 2e-96 FASC_MOUSE FASCIN fascin - 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 * 8e-
 CG2054 60 BRP39 protein - mouse BRP39 protein m [CHITINASE_18 // Glyco_hydro_18] CG2054 LD28264 62B1-62B1 ID:87D4
 + Scsalphaenzyme * succinyl-CoA synthetase alpha subunit(aa) * 7e-75 SUCA_YEAST PROBABLE SUCCINYL-COA LIGASE (GDP-
 CG1065 FORMING), ALPHA-CHAIN PRECURSOR (S * 8e-41 succinyl c CG1065 64C4-64C4 dup:2/4 ID:87F1
 CG6988 + CG6988 dup:1/3 ID:87F2
 + RNA_binding * dJ222E13.3.2 (PUTATIVE partial isoform 2)(aa) * DMBNBR_2 bnb * CG6961 LD28479 17D5-17D5 dup:3/4
 CG6961 ID:87F6
 CG10627+ CG10627 ID:87F7
 CG17870+ unknown CG17870 dup:3/4 ID:87H7
 + wal electron_transfer * 2e-61 ETFA_YEAST PROBABLE ELECTRON TRANSFER FLAVOPROTEIN ALPHA-SUBUNIT
 PRECURSOR (ALP * 1e-106 ETFA_CAEEL PROBABLE ELECTRON TRANSFER FLAVOPROTEIN AL [ETF_alpha // ETF_ALPHA]
 CG8996 CG8996 48B6-48B6 dup:1/3 ID:88A12
 + chaperone * 1e-14 embryonal lethal (2)13-1 (el(2)13-1) - fruit fly (Drosophila melanogaster) * 4e-41 similar to small heat shock
 CG14207 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
 CG3661
 CG10217+ unknown * 4e-08 cDNA EST CEMSE83F comes from this gene; cDNA EST comes * * CG10217 95B7-95B8 dup:2/4 ID:88D6
 CG18858+ CG18858 ID:88F6
 CG17138+ CG17138 dup:2/2 ID:88G10
 CG1596 + CG1596|unknown|CT3517 ID:88G5
 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
 + 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
 + unknown * 1e-52 NUC1_YEAST MITOCHONDRIAL NUCLEASE nuclease NUC1 (EC 3.1.30 * 5e-77 YJ05_CAEEL
 HYPOTHETICAL 85.1 KD NUCLEASE C41D11.5 simila * 2e-68 NUCG_MOUSE [NUCLEASE_NON_SPEC // Endonuclease]
 CG8862 CG8862 LD35517 48F1-48F1 ID:95B2

+ 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

+ 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 LD35813

CG7838 42A1-42A1 ID:95D5

CG6398 + unknown * 8e-16 coded for by C. elegans cDNA yk81c2.5 * * CG6398 LD36024 16D4-16D4 dup:2/2 ID:95F3

CG5175 + CG5175 ID:95H10

+ unknown * 2e-10 transmembrane protein * 6e-12 weak similarity to plasminogens * 2e-12 DMDUSKY_1 dy * similar to cuticlin

CG7802 [NLS_BP] CG7802 LD36439 99C5-99C5 ID:96A7

+ 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

+ 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 dup:2/2

CG11128 ID:96F8

+ 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

+ 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

+ unknown * 6e-10 MLN * 1e-41 I(3)rL203 I(3)rL203 inserted at base 5' end of P element Inverse PCR * CG12878 LD37788

CG12878 98A8-98A8 dup:2/2 ID:97B3

+ ribosomal_protein * 4e-06 RM32_YEAST MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L32 PRECURSOR (YML32) * 2e-12

YLA1_CAEEL HYPOTHETICAL 19.1 KD PROTEIN C30C11.1 IN CHROMOSOME II [NLS_BP] CG12220 LD37925 100C-100C

CG12220 ID:97C1

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

CG9165 dup:2/2 ID:97D8

+ unknown * weak similarity to ATP/GTP-binding site motif A * 2e-40 weak similarity to ATP/GTP-binding site motif A elega * 1e-

CG5924 63 POM1 chabaudi * [ATP_GTP_A] CG5924 LD38710 33A1-33A1 dup:1/2 ID:97H9

+ 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 87E2-87E3

CG8483 ID:98C2

+ unknown * 3e-21 hypothetical protein YOR289w - yeast (Saccharomyces cerevisiae) * 1e-43 R166.3 * 3e-45 unknown protein *
 CG5902 Y810_METJA HYPOTHETICAL PROTEIN hypo CG5902 97F1-97F1 dup:1/6 ID:98G6
 + 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 hemocytin 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
 + 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-
 CG5505 1] CG5505 LD40339 66A5-66A5 ID:99D11
 + unknown * DIMETHYLADENOSINE TRANSFERASE (S-ADENOSYLMETHIONINE-6-N', N'-ADENOSYL(RRNA)
 DIMETHYLTRANSFERASE) (16S RRNA DIMETHYLASE) (HIGH LEVEL KASUGAMYCIN RESI [RnaAD] CG7319 LD40326 71C2-
 CG7319 71C2 dup:2/2 ID:99D9
 + unknown * Loc7p(aa) * 13S condensin XCAP-D2 subunit(aa) * gene product is related to yeast protein * 8e-38 hypothetical
 CG1911 protein YLR272c - yeast (Saccharomyce [NLS_BP] CG1911 LD40412 99B-99B dup:2/2 ID:99E3
 + unknown * 2e-49 kraken * 1e-19 dJ222E13.1 (N-terminal part of novel protein with some similarit * 6e-12 TPES_PSEPU
 TROPINESTERASE (ATROPINESTERASE) (ATROPINE [ESTERASE // EF_HAND // abhydrolase] CG11309 LD40450 78C8-78C9
 CG11309 dup:4/4 ID:99E7
 + BcDNA:LD24639 enzyme * F17F8.28(aa) * sperm associated antigen 2(aa) * UDP-N-acetylglucosamine pyrophosphorylase;
 Qri1p(aa) * 3e-88 QRI1_YEAST HYPOTHETICAL 53.5 KD PROTEIN [ATP_GTP_A] CG9535 LD24639 26D5-26D5 dup:2/3
 CG9535 ID:Farhad's BB11
 CG9432 + CG9432 G041 dup:1/4 ID:Farhad's BC7
 CG1124 + unknown CG1124 ck00336 dup:2/2 ID:Farhad's BD9
 CG15288+ CG15288 ck01592 ID:Farhad's BE4