

Table S18

List of 534 Early Zygotic Genes

Gene ID	mixed annotation (+ indicates sequence confirmation)
CG15634	+ unknown * CG15634 LD42284 25A4-25A4 ID:101D10
CG4036	+ unknown * 5e-28 F09F7.7 gene product * [NLS_BP] CG4036 LD42289 32F1-32F1 dup:1/2 ID:101D11
	+ enzyme * No definition line found(aa) * predicted secreted protein(aa) * 3e-06 predicted secreted protein * [NLS_BP]
CG1745	CG1745 LD43003 10B15-10B15 dup:1/2 ID:101G12
CG4702	+ unknown * CG4702 LD43816 88A1-88A1 ID:102F9
	+ Cyp310a1cytochrome_P450 * cytochrome P450(aa) * DMLCPM Cyt-P450-rBF6-2 * 2e-29 cytochrome P450 monooxygenase *
CG10391	2e-17 similar to cytochrome P450 [EP450II // p450 // P450 // MITP450 // E] CG10391 LD44491 37A3-37A3 ID:103C12
	+ unknown * tight junction protein (zona occludens 1)(aa) * TIGHT JUNCTION PROTEIN ZO-1 (TIGHT JUNCTION PROTEIN
CG11782	1)(aa) * 1e-05 ZO-1 MDCK * [NLS_BP] CG11782 LD44404 85B4-85B4 ID:103C6
	+ motor_protein * CLIP-190 * 6e-05 microtubule binding protein D-CLIP-190 * 3e-05 myosin * 4e-06 ORF 73, contains large
CG8621	complex repeat CR sarcoma-associated herpesv CG8621 LD44526 65E6-65E6 dup:2/2 ID:103D6
	+ neur DNA_binding * finger protein neuralized - fruit fly (Drosophila melanogaster)(aa) * DMC3HC4ZF_2 neur * 3e-89 coded for
CG11988	by C. elegans cDNA yk27g3.5; coded for by C [zf-C3HC4 // ZF_RING] CG11988 LD45505 85C4-85C5 dup:1/2 ID:104C12
	+ bl RNA_binding * hnRNP-K protein(aa) * 1e-05 YB83_YEAST HYPOTHETICAL 45.8 KD PROTEIN IN PCS60-ABD1
CG13425	INTERGENIC REGION * 4e-05 unknown * 9e-32 coded for by C. elegans CG13425 LD45549 57B1-57B1 dup:2/2 ID:104D5
	+ unknown * nucleic acid binding protein(aa) * cDNA EST comes from this gene; cDNA EST comes from this gene; cDNA
CG18426	EST yk414e4.3 comes from this gene; cDNA EST CG18426 LD45577 60A4-60A5 ID:104D9
	+ actin_binding * talin(aa) * 7e-11 cytoskeleton assembly control protein SLA2 - yeast (Saccharomyces cerevisiae) * 8e-08
CG6831	merlin * talin [BAND_41_1 // Band_41 // BAND_41_3 // PR] CG6831 LD46304 66D6-66D6 dup:1/2 ID:105B9
	+ unknown * 4e-41 protein * 1e-09 putative protein * coded for by C. elegans cDNA yk93e11.5; coded for by C. elegans cDNA
CG10473	yk103a11.5; * [NLS_BP] CG10473 LD46360 37B11-37B12 ID:105C7
	+ structural_protein * 6e-14 CUP7_DROME PUPAL CUTICLE PROTEIN EDG-78 PRECURSOR ecdyson * 2e-28
	CUD4_LOCFMI ENDOCUTICLE STRUCTURAL GLYCOPROTEIN (ABD-4A) g * 7e-16 DMEDG78B_2 [CUTICLE // insect_cuticle]
CG8505	CG8505 49A3-49A3 ID:105F10
	+ cytoskeletal_structural_protein * 1e-62 cell division cycle protein * 1e-178 SEP2_DROME SEPTIN septin * 3e-82 CDC10 *
	1e-148 SEP2_HUMAN SEPTIN HOMOLOG The gen [COPPER_BLUE // GTP_CDC // NLS_BP // ATP] CG2916 LD47044 43F7-
CG2916	43F7 dup:1/2 ID:106A3
	+ motor_protein * DMMHC95F Mhc95F * myosin-A(aa) * 1e-65 MYS2_YEAST MYOSIN-2 ISOFORM myosin MYO2 - yeast
CG10595	(Saccharo * 2e-68 myosin V [myosin_head // MYOSINHEAVY // ATP_GTP_A] CG10595 LD47348 29D1-29D1 ID:106C4
CG7269	+ RNA_binding CG7269 dup:2/2 ID:106E3
CG14954	+ unknown * CG14954 LD47625 63F4-63F4 ID:106G4
CG10283	+ unknown * CG10283 LD47881 36F8-36F9 ID:107A11
CG3722	+ 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 57B19-57B20 ID:107D10

+ LanA cell_adhesion * 7e-05 RA50_YEAST DNA REPAIR PROTEIN RAD50 (153 KD PROTEIN) RAD50 * LMA_DROME LAMININ ALPHA CHAIN PRECURSOR laminin chain A * 1e-114 similar to [RNP_1 // EGF_1 // EGFLAMININ // LAMININ] CG10236 LP01316 65A6-65A6 dup:5/5 ID:107E3

CG10236 + receptor * 4e-06 LDL receptor-like repeat; orfla * 2e-47 coded for by C. elegans cDNA yk9e10.5; coded for by C. elegans cDNA yk9e10.3; mu * 3e-07 very low dens [LDLRA_2 // ldl_recept_a // LDLRA_1] CG8756 LP01646 76C-76C ID:107F11

CG8756 + enzyme * 1e-107 ecto-5'-nucleotidase * 1e-105 5' nucleotidase (CD73) 5'-NUCLEOTID * 1e-132 putative 5'-nucleotidase * 3e-08 inserted at base 5' end of P elem [PHOSPHO_ESTER // 5_nucleotidase // 5_NU] CG4827 LP01562 54C6-54C6 ID:107F5

CG4827 + 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 LP01667 5B6-5B6 ID:107G1

CG3097 + ligand_binding_or_carrier * retinaldehyde-binding protein 1(aa) * ALPHA-TOCOPHEROL TRANSFER PROTEIN (ALPHA-TTP)(aa) * 8e-07 SC14_YEAST SEC14 CYTOSOLIC FACTOR (PHOSPHATIDYLINOSI [CRETINALDHBP // CRAL_TRIO] CG5958 LP02316 27F7-27F7 ID:108A6

CG5958 + unknown * 2e-06 inserted at base 3' end of P element Inverse PCR * * CG1733 LP02557 12A1-12A2 dup:3/5 ID:108B3

CG1733 + unknown * CG18546 LP02835 87A6-87A6 ID:108C4

CG18546 + unknown * putative DNA binding protein=son placenta, Peptide Partial, * * CG7924 LP03067 74E1-74E1 ID:108D3

CG7924 + protein_kinase * DMCDK46_3 Cdk4/6 * DMCDK5_3 Cdk5 * SNF1A * DMMAPKIN_4 rl [LDLRA_2 // RECEPTOR_TYR_KIN_II // PROTE] CG8250 LP03070 53C10-53C11 ID:108D5

CG8250 + unknown * CG7906 LP03104 74E1-74E1 ID:108D7

CG7906 + serpin * ZG-21p protein - rat(aa) * protease inhibitor (ovalbumin type)(aa) * 9e-10 Similar to serine protease inhibitor * 2e-17 PAI2_MOUSE PLASMINOGEN ACTIV [serpin] CG1342 LP03106 100A3-100A3 ID:108D8

CG1342 + Lsp1gamma larval_serum_protein * hexamerin A; arylphorin-like protein(aa) * Lsp1 bgr; * LARVAL SERUM PROTEIN BETA CHAIN PRECURSOR(aa) * 8e-06 AMYH_YEAST GLUCOAMYLASE S1/S2 PRECU[hemocyanin // HEMOCYANIN_2 // HAEMOCYAN] CG6821 LP03463 61A2-61A2 ID:108F5

CG6821 + enzyme * hydroxysteroid (17-beta) dehydrogenase 4(aa) * peroxisomal multifunctional beta-oxidation protein; Fox2p(aa) * ESTRADIOL BETA-DEHYDROGENASE (17-BETA [GDHRDH // adh_short // ADH_SHORT // THI] CG3415 LP03478 14B11-14B11 dup:2/2 ID:108F6

CG3415 + unknown * CG1806 LP03706 11A3-11A3 ID:108G2

CG1806 + transporter * renal organic cation transporter(aa) * solute carrier family (organic cation transporter), member 5(aa) * sodium-dependent carnitine transporter(aa) [sugar_tr] CG17752 LP04053 94D3-94D3 ID:108H10

CG17752 + motor_protein * 1e-06 TRFA * * CG6234 LP04345 87C6-87C6 dup:1/2 ID:108H11

CG6234 + serpin * SQUAMOUS CELL CARCINOMA ANTIGEN (SCCA-2) (LEUPIN)(aa) * ALPHA-1-ANTIPROTEINASE PRECURSOR (ALPHA-1-ANTITRYPSIN) (ALPHA-1-PROTEINASE INHIBITOR)(aa) * [serpin] CG6687 LP04383 88E7-88E7 ID:108H12

CG6687

CG14766 + unknown CG14766 LP04033 ID:108H9

CG10497 + CG10497 dup:1/2 ID:109B5

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

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

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

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

+ Neurotactin cell adhesion axon, ocellar nerve, ventral nerve cord CARBOXYLESTERASE_B_2, COesterase, ESTERA] CG9704 LP05519 ID:109D11

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

CG4818 + structural_protein * 1e-08 cuticular protein ** [insect_cuticle] CG4818 LP05492 72F1-72F1 ID:109D9

CG7953 + BG:DS00941.14 unknown * CG7953 LP05733 34D4-34D4 dup:2/2 ID:109E10

+ 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 dup:2/2 ID:109F4

CG5656 + endopeptidase * Ser12 * Ser6 * mas * DMSNAKE_2 snk [trypsin // CHYMOTRYPSIN // TRYPSIN_CATA] CG9675 LP05929 15A1-15A1 ID:109F7

CG9675 + structural_protein * Abd-5=endocuticular protein migratoria=migratory locusts, abdomen, Peptide, * Acp65Aa * 2e-12 cuticle protein ACP65A * Abd-5=endocuticular protein g [CUTICLE // insect_cuticle] CG7160 LP06660 78F1-78F1 ID:109H3

CG7160 + pbl signal_transduction * ect2 oncogene(aa) * 4e-05 regulatory protein CLS4 - yeast (Saccharomyces cerevisiae) * 3e-08 /match=(desc;; /ma * 1e-30 similar to transf[GRF_DBL // BRCT_DOMAIN // G_PROTEIN_REC] CG8114 SD01796 66A18-66A20 dup:2/4 ID:113B7

CG8114 + LanB2 cell_adhesion * DMLAMB01_2 LanB2 * LAMININ-LIKE PROTEIN C54D1.5 PRECURSOR(aa) * LAMININ GAMMA-1 CHAIN PRECURSOR (LAMININ B2 CHAIN)(aa) * 2e-06 putative [ADH_ZINC // laminin_B // laminin_EGF //] CG3322 SD01934 67B-67B ID:113C10

CG3322 + unknown * 8e-21 ERP6_YEAST ERP6 PROTEIN PRECURSOR probable membrane pro * 9e-39 similar to emp24/gp25L/p24 family * 8e-72 associated to apparatus * 2e-51 G25L [EMP24_GP25L] CG9443 SD01878 85E4-85E5 dup:1/2 ID:113C5

CG9443 + 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 ID:113E11

CG6057 none + none SD02145 ID:113F3

+ hts actin_binding * adducin homolog - fruit fly (Drosophila melanogaster)(aa) * similar to alpha-adducins(aa) * DMADDLIKE_3 hts * adducin-like(aa) [Aldolase_II] CG9325 SD02552 56D5-56D6 ID:114C12

CG9325 + motor_protein * 1e-05 microtubule binding protein D-CLIP-190 * 6e-08 Similarity with drosophila MSP-300 protein (PIR acc. no. * 5e-08 CENP-E protein * 1e-09 myosin I CG15165 SD02507 37A3-37A4 ID:114C2

CG15165

CG7434 + RpL22 ribosomal_protein Ribosomal protein L22 60S subunit ANTIFREEZE1 CG7434 SD02522 ID:114C6
+ nbA ion_channel * nbA * DMCA1_2 Ca- agr;1D * CCA1_DROME CALCIUM CHANNEL ALPHA-1 SUBUNIT (CACOPHONY PROTEIN) (NIGHTBLIND A PR * unc-2 gene product [NACHANNEL // ion_trans // CACHANNEL //] CG1522 10F10-11A1
CG1522 dup:2/2 ID:114F12
CG13868 + unknown * 0.0000000000000008* * CG13868 SD03066 56F17-57A dup:4/4 ID:115B4
+ unknown * contains a single LIM domain at the N-terminus.; cDNA EST comes from this gene; cDNA EST comes from this
CG10439 gene; cDNA EST yk357g9.5 comes from this ge [LIM_DOMAIN_1 // LIM_DOMAIN_2] CG10439 SD03168 57B1-57B1 ID:115C12
CG15319 + CG15319 SD03263 ID:115D11
+ cell_adhesion * DMDACHSOU_2 ds * contains similarity to multiple cadherin-type repeats(aa) * cadherin 18(aa) *
CG6977 DMDEC_1 shg [CADHERIN // cadherin] CG6977 SD03311 87A-87A dup:5/5 ID:115E6
+ Aac11 apoptosis_inhibitor * apoptosis inhibitor 5(aa) * Aac11(aa) * 1e-110 unknown * 1e-35 unknown protein CG6582
CG6582 SD03364 36C3-36C3 ID:115F2
+ unknown * PBK1 protein(aa) * 5e-11 predicted using Genefinder; Weak similarity to Mouse CSA-19 protei * 2e-16 PBK1
CG13096 protein * 7e-08 hypothetical protein [NLS_BP] CG13096 SD03546 29D1-29D1 ID:115H5
+ EG:100G10.8 unknown * DMC95B7 * * by content; by match; LD Drosophila melanogaster...(aa) * by content; 1-meth CG2694
CG2694 SD03887 3B5-3B5 dup:1/2 ID:116C11
+ signal_transduction * HYPOTHETICAL 94.2 KD PROTEIN C38D4.5 IN CHROMOSOME III(aa) * 2e-05 /match=(desc;; /ma
2e-05 RIP1 * 3e-12 98K GTPase-activating protein ABR, brain [RHO_GAP // RhoGAP] CG7122 SD04011 16F7-16F7 dup:4/5
CG7122 ID:116E6
CG10712 + translation_factor * 3e-06 Pdd1p Pdd1p thermoph * * [chromo // CHROMO_2] CG10712 79F5-79F5 dup:3/4 ID:116F1
+ alpha-Spec actin_binding * DMLETHAL_2 Actn * DMSPCA_2 agr;-Spec * SPECTRIN ALPHA CHAIN(aa) * 3e-15 USO1_YEAST
INTRACELLULAR PROTEIN TRANSPORT PROTEIN USO1 ([spectrin // SPEC_REPEAT // EF_HAND // S] CG1977 SD04436
CG1977 62B-62B dup:2/7 ID:117C8
+ G_protein_linked_receptor * CL3BC(aa) * protein(aa) * 4e-20 similar to G-protein coupled receptor protein; cDNA EST * 2e-
14 EMR1_MOUSE CELL SURFACE GLYCOPROTEIN[7tm_2 // RECEPTOR_PKD // GAL_LLECTIN //] CG8639 SD04590 44D2-
CG8639 44D2 dup:5/5 ID:117E6
+ cell_adhesion * robo * similar to IG (immunoglobulin) superfamily (17 domains), Low-density lipoprotein receptor domain
class A (3 domains), Laminin EGF-like (Doma[LDLRA_2 // ig // RNP_1 // EGF_1 // EGF] CG7981 SD04592 3A2-3A3 dup:4/4
CG7981 ID:117E7
+ unknown * 1e-149 inserted at base Both 5' and 3' ends of P element Inverse PCR * BLASTX 4.2E-08 Carrot gene for
CG8929 extensin.(dna) * 2e-61 inserted at base Both 5 [PRO_RICH // NLS_BP] CG8929 SD04973 57A-57A dup:2/3 ID:118B9
CG9366 + enzyme CG9366 SD05212 ID:118D6
none + none SD05284 ID:118E10
CG17148 + enzyme CG17148 SD05284 ID:118E10.2
+ 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

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

CG12088 + enzyme * 3e-31 prolyl 4-hydroxylase alpha subunit * 2e-40 Similarity to Human Prolyl 4-hydroxylase alpha subunit (SW:P4HA_HU * 3e-42 P4H1_MOUSE PROLYL 4-HYDR CG12088 SD05564 99F7-99F7 dup:2/3 ID:119A3.2

CG8376 + transcription_factor CG8376 SD05618 dup:4/5 ID:119B1.2

CG7144 + enzyme * lysine ketoglutarate reductase/saccharopine dehydrogenase(aa) * similar to saccharopine dehydrogenases(aa) * lysine-ketoglutarate reductase /sacch CG7144 SD05742 28C9-28D dup:2/2 ID:119D4

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

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

CG13889 + motor_protein * 4e-05 unknown * 5e-06 Similarity with drosophila MSP-300 protein (PIR acc. no. * 2e-10 rho/rac-interacting citron kinase [PEROXIDASE_1] CG13889 SD05919 61D4-61D4 ID:119F1

CG5853 + transporter CG5853 SD06390 dup:2/3 ID:119G10.2

CG8669 + transcription_factor * ATFx(aa) * leucine-zipper protein(aa) * 7e-05 Similarity to Human transcription factor ATF-4 (SW:ATF4_HUMAN); cD * 3e-09 ATF4_MOUSE CYCLIC-AMP-DEPE[B_ZIP // bZIP // BZIP_BASIC // NLS_BP] CG8669 39D2-39D2 dup:3/3 ID:119H1

CG3879 + transporter CG3879 SD10012 dup:1/3 ID:124E12.2

CG15009 + CG15009 SD10052 dup:1/2 ID:124F9.2

CG3978 + pnr transcription_factor * GATA-BINDING FACTOR-A (TRANSCRIPTION FACTOR GATA-A) (DGATA-A) (PANNIER PROTEIN)(aa) * pnr * CG3978 89B5-89B6 dup:1/3 ID:124G11.2

CG6501 + unknown CG6501 SD10213 dup:1/2 ID:124H5.2

CG12846 + unknown CG12846 SD10395 dup:1/2 ID:125B5.2

CG5370 + endopeptidase CG5370 SD10530 dup:1/2 ID:125C11.2

CG18022 + cytoskeletal_structural_protein * 2e-21 Similarity to N.crassa ADP/ATP carrier protein (SW:ADT_NEUCR) * 7e-05 TPCC_MOUSE TROPONIN C, SLOW SKELETAL AND CARDIAC MUSCLES (TN-C) * 4e-05 CG18022 SD10992 69B3-69B3 ID:126A10

CG7262 + structural_protein * unknown(aa) * Allele: hi4(aa) * gene is related to S.cerevisiae NIC96 gene.(aa) * 7e-24 NI96_YEAST KD NUCLEOPORIN-INTERACTING COMPONENT nucle CG7262 GH01087 88D8-88D8 ID:30A8

CG1462 + 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 GH01338 100B-100B dup:1/2 ID:30C5

CG7399 + Hn enzyme * DMPAH Hn * phenylalanine 4-monooxygenase (EC 1.14.16.1) - fruit fly (Drosophila melanogaster)(aa) * phenylalanine 4-monooxygenase (EC 1.14.16.1) - f CG7399 GH01426 66A11-66A12 dup:2/2 ID:30D2

CG8230 + BcDNA:GH02536 unknown * Contains similarity to from C. elegans.(aa) * unknown(aa) * 2e-88 predicted using Genefinder; cDNA EST comes from this g * 2e-49 Contains similarity CG8230 GH02536 44F12-44F12 ID:31C8

CG12744 + transcription_factor * pleiomorphic adenoma gene-like 2; PLAG-like 2(aa) * DMZFH1_2 zfh1 * 1e-06 ZFH1_DROME ZINC-FINGER PROTEIN (ZINC-FINGER HOMEODOMAIN PROTEIN [zf-C2H2 // ZINC_FINGER_C2H2 // ZINC_FIN] CG12744 GH03826 46C1-46C1 dup:1/2 ID:32C5

CG10658 + Os9 unknown * Os9 * * CG10658 GH03980 38B1-38B1 ID:32D2

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

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

CG16758 + enzyme * i-beta-1,3-N-acetylglucosaminyltransferase(aa) * 1e-10 K09C8.4 * 8e-16 acetylglucosaminyltransferase-like protein * 5e-24 i-beta-1,3-N-acetylglucosa CG3253 GH04269 60B6-60B6 ID:32F1

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

+ enzyme * aminomethyltransferase (glycine cleavage system protein T)(aa) * 2e-68 glycine cleavage T protein * 7e-91 partia CDS, * 1e-97 GCST_HUMAN AMINOMETHY CG6415 GH04419 32A2-32A2 dup:1/2 ID:32G8

CG6415 + Mipp1 protein_phosphatase * multiple inositol polyphosphate phosphatase 1; MIPP1(aa) * Mipp1 * 1e-22 multiple inositol polyphosphate phosphatase * 2e-23 multiple inositol polyp [acid_phosphat] CG4123 GH04949 77A1-77A1 dup:4/7 ID:33C7

CG4123 + 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 GH04978 61A6-61A6 ID:33D1

CG7028 + endopeptidase * DMSER2_7 Ser99Db * 2e-45 serine proteinase (EC 3.4.21.-) precursor - fruit fly (Drosophila melanogast * 9e-24 similar to peptidase family S1 (tr[trypsin // CHYMOTRYPSIN // TRYPSIN_SER] CG10472 GH05321 65A2-65A2 dup:2/2 ID:33E11

CG10472 + enzyme * HYPOTHETICAL ALDEHYDE-DEHYDROGENASE LIKE PROTEIN F01F1.6(aa) * antiquitin=26g turgor protein homolog {C-terminal} intestinal mucosa, Peptide Partial [aldedh // ALDEHYDE_DEHYDR_GLU] CG9629 GH05218 76A3-76A3 dup:2/2 ID:33E7

CG9629 + BcDNA:GH05536 unknown * 0.0000002 * 3e-06 DMRNAPER_2 anon-3B1.2 * * CG5867 GH05588 34A10-34A11 ID:33G5

CG5867 + qkr58E-1RNA_binding * how * qkr58E-1 * QKR58E-1(aa) * 5e-10 hypothetical protein YLR116w - yeast (Saccharomyces cerevisiae) ([KH-domain // KH_DOMAIN] CG3613 GH05812 58D8-58D8 ID:33H11

CG3613 + endopeptidase * 8e-41 kuzbanian * 1e-93 coded for by C. elegans cDNA yk187d12.5; coded for by C. elegans cDNA yk187d12.3 * 1e-143 TNF-alpha converting enzyme (TACE) [DISINTEGRINS_2 // ADAM_MEPRO // ZINC_PR] CG7908 GH06244 99D3-99D3 ID:34D2

CG7908 + angel enzyme * DMANGEL_3 angel * GLUCOSE-REPRESSIBLE ALCOHOL DEHYDROGENASE TRANSCRIPTIONAL EFFECTOR (CARBON CATABOLITE REPRESSOR PROTEIN 4)(aa) * NOCTURNIN (RHYTHM CG12273 GH06351 59F4-59F4 dup:2/2 ID:34E2

CG12273 + unknown * [NLS_BP] CG5538 87C-87C dup:1/3 ID:34G11

CG5538 + mfas signal_transduction * midline fasciclin precursor * 3e-31 p68(beta ig-h3) beta-ig-h3 gene musc * 1e-29 transforming growth factor, beta-induced, 68kD TRANSFORM * 3e-29 RG [BIGH3_DOMAIN] CG3359 87A8-87A dup:3/3 ID:34H9

CG3359 + structural_protein * 7e-10 cuticular protein * * CG3672 67B2-67B2 dup:1/2 ID:35A3

CG3672 + unknown * CG5059 GH07036 77C4-77C4 ID:35A4

CG5059

+ l(2)35DfRNA_binding * MTR4_YEAST ATP-DEPENDENT RNA HELICASE DOB1 (MRNA TRANSPORT REGULATOR MTR4) ' YH27_CAEEL PUTATIVE HELICASE W08D2.7 IN CHROMOSOME IV * 1e-153 hypoth [HELICASE // DEAD // ATP_GTP_A]
 CG4152 CG4152 GH07290 35D6-35D6 ID:35C5
 CG13480 + unknown * CG13480 GH07663 70E4-70E4 dup:2/2 ID:35E7
 + BcDNA:GH07921 RNA_binding * homeobox-containing protein Wariiai(aa) * 3e-05 PEP_DROME ZINC FINGER PROTEIN ON ECDYSONE PUFFS PEP prote * 3e-05 Pep protein - fruit fly (Dr[ZINC_FINGER_C2H2 // NLS_BP // CYTOCHROM] CG8108
 CG8108 GH07921 67C3-67C3 dup:1/4 ID:35G10
 + transcription_factor * skeletal muscle LIM protein(aa) * DRAL gene product(aa) * skeletal muscle LIM-protein 1(aa) * testin(aa) [LIM] CG11916 GH07858 73D4-73D4 ID:35G5
 CG11916 + BcDNA:GH08860 * 9e-86 cif1 * 1e-37 predicted using Genefinder; similar to trehalose phosphate synthas * 4e-86 TPS1_KLULA ALPHA,ALPHA-TREHALOSE-PHOSPHATE SYNTHASE (U [TrehaloseP_syn] CG4104 24F1-24F1 dup:1/3 ID:37G7
 CG4104 + ubiquitin-protein_ligase ubiquitin-conjugating enzyme E2B (RAD6 homolog) UBIQUITIN_CONJUGAT_2 CG10536
 CG10536 GH10432 ID:37H11
 + protein_kinase * Pak * DMAURG_2 aur * MST1(aa) * SERINE/THREONINE-PROTEIN KINASE PLO1(aa) [TYRKINASE // PROTEIN_KINASE_DOM // pkin] CG11228 GH10354 56D10-56D10 ID:37H3
 CG11228 + nAcRbeta-64B ion_channel * ACH3_DROME ACETYLCHOLINE RECEPTOR PROTEIN, BETA-LIKE CHAIN PRECURSOR * 1e-97 similar to neuronal acetylcholine receptor * 1e-78 neuronal n[NICOTINICR // neur_chan // NEUROTR_ION_] CG12606
 CG12606 GH10531 64B11-64B11 dup:1/2 ID:38A12
 + BcDNA:GH10777 protein_kinase * 2e-13 KB9S_YEAST PROBABLE SERINE/THREONINE-PROTEIN KINASE YBR274W * 7e-69 tyrosine kinase * 8e-73 YWR1_CAEEL PUTATIVE TYROSINE-PROTEIN KI[UBA // PROTEIN_KINASE_TYR // TYRKINASE] CG14992
 CG14992 GH10777 64A8-64A9 dup:2/5 ID:38C12
 + endopeptidase * 5e-32 Similarity to human placental protein * 2e-42 glucocorticoid-sensitive T cell-specific protein - mouse ' 5e-41 placental protein (serine prote CG2145 GH10845 10A1-10A1 dup:2/2 ID:38D4
 CG2145 + 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
 + Acp36DE signal_transduction * 36DE accessory gland protein(aa) * 1e-156 accessory gland protein Acp36DE * 1e-124 Acp36DE * CG7157 GH11288 36F6-36F6 ID:38G8
 CG7157 + endopeptidase * encodes a-cell barrier activity on alpha factor; Bar1p(aa) * similar to eukaryotic aspartyl proteases(aa) * BLASTX 1.4E-29 PEP4|Protease A (PrA) (y [asp // ASP_PROTEASE // PEPSIN] CG13095 GH11417 29D1-29D1 ID:38H11
 CG13095 CG3624 + cell_adhesion * [ig] CG3624 GH11432 58D7-58D7 dup:2/2 ID:38H12
 + vkg cell_adhesion * DMINTGRNB_2 Cg25C * vkg * collagen type IV alpha * 7e-25 Similar to cuticular collagen; F58F6.2 [COLLAGEN_REP // Collagen // C4] CG16858 GH11516 25C1-25C1 ID:39A7
 CG16858 + transporter * 2e-50 Na(+)-dependent inorganic phosphate cotransporter mela * 7e-54 YLD2_CAEEL HYPOTHETICAL 52.7 KD PROTEIN C38C10.2 IN CHROMOSOME III * 2e-45 NPT1 [sugar_tr] CG15095 GH11849 55F1-55F1 ID:39C9
 CG15095 CG11045 + transporter * Contains similarity to equilibrative nucleoside transporter from Homo sapiens. ESTs and come from this

gene.(aa) * NBMPR-insensitive nucleoside tr [DERENTRNSPRT] CG11045 GH12067 26E2-26E2 ID:39D11

CG10841 + unknown * CG10841 GH12158 87F6-87F6 dup:2/2 ID:39E9

+ Rh4 G_protein_linked_receptor * opsin(aa) * Rh4 * OPS4_DROME OPSIN RH4 (INNER R7 PHOTORECEPTOR CELLS OPSIN) * 2e-15 YXX5_CAEEL PUTATIVE NEUROPEPTIDE Y RECEPTOR (NPY-R) simila [GPCRRHODOPSN // OPSIN // OPSINRH3RH4] CG9668 GH12673 73C5-73D1 ID:40A5

CG9668 + unknown * ABC transporter, ATP-binding protein, putative(aa) * 2e-18 conserved protein * daunorubicin resistance

CG6166 membrane protein (drrB) * CG6166 GH12746 97A9-97A9 dup:1/2 ID:40B5

+ actin_binding * 2e-12 putative actin-binding protein UNC-115 * 2e-11 protein * 2e-05 talin homologue * 5e-05 qua CG9489

CG9489 GH13330 85E5-85E5 dup:3/3 ID:40E9

+ transporter * 5e-75 Na(+)-dependent inorganic phosphate cotransporter mela * 7e-67 YLD2_CAEEL HYPOTHETICAL 52.7

CG3036 KD PROTEIN C38C10.2 IN CHROMOSOME III * 4e-46 NPT1 [NLS_BP] CG3036 GH13494 26D1-26D1 dup:3/4 ID:40F10

CG10513 + unknown * /match=(desc:; /match=(desc:(aa) * 1e-36 /match=(desc:; /ma * * CG10513 GH13495 96C7-96C7 ID:40F11

+ RNA_binding * LET 858(aa) * conserved hypothetical protein(aa) * BLASTX 7.4E-44 Caenorhabditis elegans Nucampholin

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

+ OstStt3 enzyme * STT3_YEAST OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT STT3 * STT3_CAEEL

OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT HOMOLOG * STT3_MOUSE OLIGOSACCHARYL

CG7748 [ATPASE_ALPHA_BETA] CG7748 GH13452 98F6-98F6 ID:40F6

CG7021 + Ela unknown * [COLLAGEN_REP] CG7021 GH13458 96B4-96B4 ID:40F7

CG10121 + SP1173 unknown * CG10121 GH14073 65C1-65C1 dup:2/2 ID:41B11

+ ribosomal_protein * similar to Ribosomal protein L7Ae; cDNA EST comes from this gene(aa) * 2e-18 NHP2_YEAST HIGH

MOBILITY GROUP-LIKE NUCLEAR PROTEIN hi * 2e-27 similar [Ribosomal_L7Ae // L7ARS6FAMILY // NUCLE] CG5258

CG5258 GH14757 70F6-70F6 ID:41G10

+ HmgZ DNA_binding * 2e-07 cerevisiae mitochondrial protein gene, complete gene produc * 5e-42 HMGZ_DROME HIGH

MOBILITY GROUP PROTEIN Z (HMG-Z) high mob * 2e-11 SSRP_CAE [HMG // HMG_box // NLS_BP] CG17921 GH14749 57F8-57F9 ID:41G9

CG17921

CG2127 + unknown * [EF_HAND // NLS_BP] CG2127 GH15271 44B9-44B9 ID:42C3

+ scf ligand_binding_or_carrier * scf * 1e-110 supercoiling factor * 1e-72 coded for by C. elegans cDNA yk67a3.5; coded for by

CG9148 C. elegans cDNA yk90a3.5; co * 7e-90 calumenin [EF_HAND // EF_HAND_2] CG9148 GH15277 62B4-62B4 ID:42C4

+ signal_transduction * serine/threonine kinase with Dbl- and pleckstrin homology domains(aa) * actin-filament binding protein

Frabin(aa) * 5e-12 ROM1_YEAST RHO1 GDP-GTP E [GRF_DBL // RhoGEF // PRO_RICH // NLS_BP] CG8606 LD21492 65F2-65F2 ID:43A5

CG8606 + transcription_factor_binding * 6e-06 DIP2_YEAST DOM34 INTERACTING PROTEIN DIP2 protein - y * 2e-06 similar to beta

transducin proteins containing TRP-ASP domains el * 6e-11 ap[WD40_REGION // WD_REPEATS // WD40] CG14722 LD21659

CG14722 86F6-86F6 ID:43A8

CG8954 + unknown * [NLS_BP] CG8954 LD22235 34D6-34D6 dup:2/2 ID:43B8

CG6860 + transmembrane_receptor * protein(aa) * 4e-12 gene flightless-I protein - fruit fly (Drosophila melanogaster) (* 2e-14 Ras-

binding protein SUR-8 leuc * 2e-12 RSU1[LRR // CNMP_BINDING_3 // LEURICHRPT //] CG6860 LD26544 36C1-36C1 dup:2/2 ID:44E7

CG9506 + protein_phosphatase * CG9506 LD27991 28D1-28D1 dup:1/2 ID:45C6

CG4609 + fax failed axon connections protein CG4609 LD28084 dup:2/2 ID:45D1

CG10990 + unknown * MA3(aa) * 3e-70 apoptosis protein MA-3 - mouse apoptosis-i * 1e-69 nuclear protein H731 - human nuclear antigen H731 * nuclear antigen H731-like pr [RCC1_2 // NLS_BP] CG10990 12B8-12B8 ID:46B7

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

CG1710 + transcription_factor * host cell factor C1 (VP16-accessory protein)(aa) * HOST CELL FACTOR C1 (HCF) (VP16 ACCESSORY PROTEIN) (HFC1) (VCAF) (CFF)(aa) * host cell factor 2(a CG1710 LD29768 102B3-102B3 dup:3/3 ID:46E3

CG9107 + CG9107 LD29822 dup:3/3 ID:46E8

CG4263 + enzyme * (novel PUTATIVE protein similar to hypothetical proteins S. pombe C22F3.14C and C. elegans C16A3.8)(aa) * 1e-32 RLR1_YEAST RLR1 PROTEIN RLR1 protei [NLS_BP] CG4263 LD29940 22C3-22C3 dup:3/3 ID:46F10

CG1225 + RhoGEF3 signal_transduction RHO guanyl-nucleotide exchange factor ATP_GTP_A, GRF_DBL, RhoGEF, SH3 CG1225 LD29915 dup:1/2 ID:46F8

CG7288 + endopeptidase * hypothetical protein unp - mouse(aa) * Sad1p(aa) * putative protein(aa) * Contains similarity to Pfam domain: (UCH-1), Score=13.8, E-value=0.14, N= [UCH_2_3 // UCH-2] CG7288 LD30129 17E4-17E4 dup:1/3 ID:46G10

CG5170 + Dp1 DNA_binding * 2e-44 SCP160 * 4e-09 KH-domain putative RNA binding protein * 951003: Homology with human lipoprotein-binding protein (PIR Acc. * high density lipop [KH-domain // KH_DOMAIN // NLS_BP] CG5170 LD29992 55C10-55C11 dup:1/5 ID:46G2

CG6819 + transmembrane_receptor * nucleoporin Nup84(aa) * 6e-46 nucleoporin 88kD 88kDa nuclear * 3e-47 nucleoporin Nup84 * CG6819 LD30108 87C7-87C7 ID:46G7

CG1677 + CG1677 LD30482 ID:47A10

CG17947 + alpha-Cat actin_binding * alpha catenin(aa) * DMALPC_2 agr;-Cat * CTNA_DROME ALPHA-CATENIN cadherin-associated protein D al * HMP-1 [VINCULIN // Vinculin // ALPHACATENIN] CG17947 LD30423 80B1-80B2 ID:47A5

CG9797 + transcription_factor * b34I8.1 (Kruppel related Zinc Finger protein 184)(aa) * 2e-15 AZF1_YEAST ASPARAGINE-RICH ZINC FINGER PROTEIN AZF1 fin * 8e-24 SUHW_DROME SUPPRESSO[zf-C2H2 // ZINC_FINGER_C2H2 // ZINC_FIN] CG9797 LD30467 85B2-85B2 ID:47A9

CG6549 + chaperone * transport complex protein (90 kDa)(aa) * 6e-59 putative S transport complex 90kD subunit brain-specific isoform * CG6549 LD30785 36C3-36C4 ID:47C10

CG10997 + unknown * 2e-10 predicted using Genefinder * 9e-11 CLCP * 3e-24 chloride intracellular channel CLIC2 sapiens * 1e-22 chloride channel 64K chain - bovine CG10997 LD31682 12B9-12B9 dup:2/2 ID:47H6

CG5995 + unknown * CG5995 LD31910 97F3-97F4 dup:1/2 ID:48A2

CG8306 + enzyme * /match=(desc;; /match=(desc:(aa) * similar to Arabidopsis thaliana male sterility protein * DMC103B4 * acyl CoA reductase(aa) [HELIX_LOOP_HELIX // NLS_BP] CG8306 LD31990 53C7-53C8 dup:1/3 ID:48A5

CG10657 + ligand_binding_or_carrier * 2e-13 62D9.a * 2e-25 retinaldehyde-binding protein C * 2e-15 DMC30B8 * /match=(desc;; /ma [CRETINALDHBP // CRAL_TRIO] CG10657 LD32330 69C2-69C2 dup:2/2 ID:48B10

CG7528 + motor_protein * ARX(aa) * 1e-58 UBA2_YEAST UBIQUITIN-ACTIVATING ENZYME E1-LIKE (POLYMERASE-INTERACTING PROTEIN * 2e-28 ubiquitin activating enzyme * 1e-67 simila[UBA_NAD // ThiF_family // NAD_BINDING /] CG7528 LD33023 67E3-67E3 dup:5/5 ID:48E10

CG10206 + nop5 unknown * nucleolar protein NOP5/NOP58(aa) * 1e-100 NOP5_YEAST NUCLEOLAR PROTEIN NOP5 hypothetical protein * 1e-119 contains similarity to S. cerevisiae Prp31 [NLS_BP] CG10206 LD32943 27C-27C dup:2/2 ID:48E7
+ BG:DS09218.3 chaperone * 8e-19 ERP5_CAEEL PROBABLE PROTEIN DISULFIDE ISOMERASE P5 PRECURSOR * 4e-21 protein disulfide isomerase-related protein * 9e-21 ERP5_RAT PROBABLE PRO CG4455 LD33101 35F10-35F10 dup:2/3 ID:48F10

CG4455 + elav RNA_binding * DMELAVK_2 elav * 1e-16 polyadenylate-binding protein * ELAV_DROME ELAV PROTEIN (EMBRYONIC LETHAL ABNORMAL VISUAL PROTEIN) * 1e-58 Similar to the hu [RNP_1 // RBD // HUDSXL RNA // rrm] CG4262 LD33076 1B5-1B5 ID:48F5

CG4262 + unknown * protein(aa) * SSXT PROTEIN (SYNOVIAL SARCOMA, TRANSLOCATED TO X CHROMOSOME) (SYT PROTEIN)(aa) * synovial sarcoma, translocated to X chromosome(aa) * [PRO_RICH] CG10555 LD33241 7E2-7E3 dup:2/2 ID:48G6

CG10555 + Lac cell_adhesion * DMLACH_2 Lac * LACH_DROME LACHESIN PRECURSOR lachesin melanoga * 2e-16 predicted protein contains a large number of Ig superfamily repeat * 5e-20 c [ig] CG12369 LD33460 49A7-49A7 ID:48H6

CG12369 + unknown * 6e-97 N2,N2-dimethylguanosine tRNA methyltransferase c * 1e-105 similar to N2,N2-dimethylguanosine tRNA methyltransferase; cDNA ES * 1E-125* 1e-111 [SAM_BIND] CG6388 LD33880 33D5-33E ID:49B7

CG6388 + unknown * CG12011 LD34635 62A12-62A12 dup:2/2 ID:49E7

CG12011 + unknown * 3e-80 YKL6_CAEEL HYPOTHETICAL 103.8 KD PROTEIN C03C10.6 IN CHROMOSOME III * E03A3.6 * E03A3.7 * [AA_TRNA_LIGASE_II_2 // PRO_RICH // CYTO] CG5237 GH01039 91F10-91F11 ID:54A4

CG5237 + enzyme_inhibitor * 7B2(aa) * cDNA EST comes from this gene(aa) * 2e-22 cDNA EST comes from this gene * CG1168 GH01053 83A5-83A5 ID:54A6

CG1168 + 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 ID:54B3

CG13219 + ion_channel * Glu-RIIB * glutamate receptor precursor - human (fragment)(aa) * 9e-14 glutamate receptor DGluRIIB * 4e-17 ionotropic glutamate receptor - Caenorhab [lig_chan // ATP_GTP_A] CG17274 GH01149 93A1-93A1 ID:54B6

CG17274 + unknown * MALE STERILITY PROTEIN 2(aa) * DMC103B4 * male sterility 2-like protein(aa) * /match=(desc;; /match=(desc:(aa) CG10096 GH01346 87B13-87B14 ID:54C10

CG10096 + enzyme * similar to pig tubulin-tyrosine ligase.(aa) * 1e-41 similar to tubulin tyrosine ligase; cDNA EST comes fro * 2e-55 protein * 8e-16 TTL_BOVIN TUBULIN [NLS_BP] CG16716 GH01307 56D15-56E1 ID:54C7

CG16716 + odd transcription_factor * DMODDS_1 odd * transcription factor specific RNA polymerase II transcription factor) cell nucleus) map_position:24A1-3 * Sob protein(aa) * 5e-19[zf-C2H2 // ZINC_FINGER_C2H2 // ZINC_FIN] CG3851 GH01449 25B1-25B1 ID:54D10

CG3851 + structural_protein * Peritrophin-A * cDNA EST comes from this gene; cDNA EST yk369a9.5 comes from this gene; cDNA EST yk438c12.3 comes from this gene; cDNA EST yk438c12 CG11142 GH01453 26A-26A ID:54D11

CG11142

CG6959	+ cell_adhesion * DMARTAN_7 trn * 5e-08 tartan protein * 6e-16 5T4 oncofetal trophoblast glycoprotein * 6e-18 oncofetal trophoblast glycoprotein 5T4 precursor - human [LRR // LRRCT] CG6959 GH01562 86F11-86F11 dup:2/2 ID:54E11
CG10680	+ * CG10680 38B1-38B1 dup:2/3 ID:54F11
CG14548	+ 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 96F10-96F10 ID:54H5
CG17506	+ unknown smilarity to indora CG17506 GH02266 ID:55B6
CG3413	+ cell_adhesion * orphan G protein-coupled receptor FEX(aa) * BLASTX 7.5E-06 Santalum album proline rich protein mRNA, complete cds.(dna) * 9e-05 protein * 5e-05 kek1 [LRR // LEURICHRPT // NLS_BP // LRRCT] CG3413 GH02310 58D2-58D3 ID:55B8
CG9466	+ enzyme * DMPGMII_3 agr;-Man-II * alpha-mannosidase(aa) * alpha-mannosidase (EC 3.2.1.24) precursor - human(aa) * LYSOSOMAL ALPHA-MANNOSIDASE PRECURSOR (MANN [Glyco_hydro_38] CG9466 GH02475 29F1-29F1 ID:55C11
CG7123	+ LanB1 cell_adhesion * DMLAMB01_2 LanB2 * LanB1 * LAMININ BETA-1 CHAIN PRECURSOR (LAMININ B1 CHAIN)(aa) * LAMININ BETA-1 CHAIN PRECURSOR (LAMININ B1 CHAIN)(aa) [laminin_EGF // EGF_1 // EGFLAMININ // L] CG7123 GH02457 28D-28D ID:55C7
CG2578	+ cell_adhesion * 1e-180 odd Oz product * 8e-31 similar to tenascin * 1e-107 Ten-m4 * 1e-101 (mouse DOC4 LIKE protein) [NLS_BP] CG2578 GH02628 11B1-11B1 ID:55D3
CG7366	+ unknown * CG7366 GH02649 67E7-67E7 ID:55D4
CG4144	+ transporter * 8e-16 GPI-anchored protein - mouse (fragment) hum * 2e-16 P137_HUMAN GPI-ANCHORED PROTEIN P137 GPI-anchored prote * 2e-17 gram negative binding prot CG4144 GH02872 75D2-75D2 dup:3/3 ID:55E6
CG2681	+ EG:100G10.2 unknown * by motif; 1-match_description=ATP/GTP-binding site motif A (P-loop).; by match; 2-match_accession=SPTRE...(aa) * by motif; * 2e-10 seven-in-absentia CG2681 GH02982 3B5-3B5 ID:55F2
CG11605	+ actin_binding * filamin(aa) * 1e-103 similar to endothelial actin-binding protein repeats; cDNA EST EMB * 7e-11 actin binding protein ABP-280 * 3e-90 gamma filamin [Filamin // FILAMIN_REPEAT] CG11605 GH03013 58F7-58F7 dup:1/3 ID:55F5
CG8817	+ unknown * 2e-17 FMR2 protein * 1e-17 X mental retardation X ment * lymphoid nuclear protein related to AF4 * [HMGI_Y // NLS_BP] CG8817 GH03237 23C1-23C1 dup:1/2 ID:55G11
CG15855	+ Eip63F-1ligand_binding_or_carrier * Eip63F-1 * 2e-74 E631_DROME CALCIUM-BINDING PROTEIN E63-1 calcium-binding pr * 3e-17 similar to EF-hand calcium binding proteins; most similar to ca CG15855 GH03109 63F7-63F7 ID:55G4
CG9803	+ unknown * [PRO_RICH] CG9803 GH03629 59D6-59D6 ID:56B1
CG13279	+ Cyt-b5 electron_transfer * CYBR_DROME PROTEIN TU-36B (CYTOCHROME B5-RELATED PROTEIN) * 9e-66 CYBR_DROVI CYTOCHROME B5 RELATED PROTEIN cytochrome b5 * DMTU36B_4 Cyt-b5 * delta [CYTOCHROME_B5_2 // heme_1] CG13279 GH03691 36A9-36A9 ID:56B5
CG18358	+ unknown * CG18358 GH03717 15A3-15A3 ID:56B7
CG3523	+ BcDNA:GH07626 enzyme * p270(aa) * Similar to polyketide synthase.(aa) * FK506 polyketide synthase(aa) * [adh_zinc // Thioesterase // ACP_DOMAIN] CG3523 GH03816 23D-23D dup:4/9 ID:56C9
CG5779	+ Bc larval_serum_protein * pro-phenol oxidase A1 * pro-phenol oxidase subunit 1; proPO-p1 * DMORA_2 Bc * prophenoloxidase [TYROSINASE_2 // hemocyanin // HEMOCYANI] CG5779 GH04080 55A1-55A1 dup:2/2 ID:56E11

CG3625	+ unknown * dJ413H6.1.1 (hamster Androgen-dependent Expressed Protein LIKE PUTATIVE protein) (isoform 1)(aa) * androgen-regulated protein FAR-17 - golden hamst CG3625 GH04039 21B5-21B5 dup:2/2 ID:56E6
CG6465	+ 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 GH04054 86C2-86C2 dup:2/2 ID:56E8
CG5150	+ enzyme * DMALKPHOS_2 Aph-4 * 7e-27 PPB_YEAST REPRESSIBLE ALKALINE PHOSPHATASE PRECURSOR al * 2e-86 alkaline phosphatase * 1e-100 PPBT_MOUSE ALKALINE PHOSPHAT [ALKPHPTASE // alk_phosphatase] CG5150 GH04680 64E-64E ID:57B10
CG4962	+ unknown * CG4962 GH04593 72E2-72E2 ID:57B2
CG9398	+ unknown * tubby homolog(aa) * tub protein, testis - mouse(aa) * 3e-80 YQQ4_CAEEL HYPOTHETICAL 46.2 KD PROTEIN F10B5.4 IN CHROMOSOME III * 5e-97 tub homolog [TUB_1 // Tub // TUB_2] CG9398 GH04653 57C2-57C2 ID:57B6
CG18455	+ Optix unknown * transcription factor RNA polymerase II transcription factor) cell nucleus) * * CG18455 GH04859 44A2-44A2 ID:57C11
CG12028	+ dib cytochrome_P450 * 2e-17 cytochrome P-450 - fruit fly (Drosophila melanogaster) (fragment) * 1e-10 YS45_CAEEL PUTATIVE CYTOCHROME P450 ZK177.5 IN CHROMOSOME II * 3e-30 [EP450II // p450 // P450 // MITP450 // C] CG12028 GH04745 64A5-64A5 ID:57C3
CG4294	+ motor_protein * [PPASE // PRO_RICH // NLS_BP] CG4294 GH04951 58F1-58F1 dup:3/4 ID:57D11
CG6069	+ endopeptidase * COAGULATION FACTOR XII PRECURSOR (HAGEMAN FACTOR) (HAF)(aa) * Chain A, Coagulation Factor Xa-Trypsin Chimera Inhibited With D-Phe-Pro-Arg-Chlorometh [trypsin // TRYPSIN_CATAL] CG6069 GH04903 97A4-97A5 ID:57D5
CG13607	+ unknown * CG13607 GH05104 95D10-95D10 ID:57F5
CG6016	+ enzyme * predicted using Genefinder; cDNA EST comes from this gene; cDNA EST comes from this gene; cDNA EST yk199c3.5 comes from this gene; cDNA EST yk199c3 [CDP_ALCOHOL_P_TRANSF // CDP_ALCOHOL_P_T] CG6016 GH05229 50B1-50B1 dup:1/2 ID:57G4
none	+ none GH05253 ID:57G7
CG5783	+ unknown * 3e-07 hypothetical protein * * CG5783 GH05617 36E6-36E6 ID:58A12
CG1980	+ don juan unknown It encodes a product which is expressed in the adult (testis) NLS_BP CG1980 GH05702 ID:58B6
CG9689	+ unknown * CG9689 GH05731 9A2-9A2 ID:58B9
CG7296	+ CG7296 GH05801 ID:58C6
CG2077	+ enzyme * by content; by match; 2-match_description=4-NITROPHENYLPHOSPHATASE.; 2-match...(aa) * similar to N-acetyl-glucosamine catabolism(aa) * Similar to CG2077 GH05933 63B3-63B3 ID:58D8
CG6656	+ 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
CG12612	+ CG12612 GH06062 dup:2/2 ID:58E6
CG12529	+ Zw enzyme * 1e-129 glucose-6-phosphate dehydrogenase (ZWF1) (EC 1.1.1.49) * glucose-6-phosphate 1-dehydrogenase (EC 1.1.1.49) - fruit fly (Drosophila mela * 1e- [G6PD // G6PDHDRGNASE // G6P_DEHYDROGENA] CG12529 GH06084 18D12-

18D12 dup:3/3 ID:58E7

CG9510 + enzyme * lyase(aa) * lyase(aa) * lyase (EC 4.3.2.1)(aa) * [DCRYSTALLIN // FUMRATELYASE // FUMARATE] CG9510 GH06087 29F6-29F6 dup:2/2 ID:58E8

CG10512 + unknown * predicted using Genefinder; cDNA EST yk268h6.5 comes from this gene; cDNA EST yk465f2.5 comes from this gene; cDNA EST yk393g7.5 comes from this gen CG10512 GH06154 78C3-78C4 ID:58F3

+ signal_transduction * 1e-20 YMH2_YEAST HYPOTHETICAL 171.1 KD PROTEIN IN YL16A-DAK1 INTERGENIC REGION 2e-07 SY65_DROME SYNAPTOTAGMIN (P65) synaptotagmin - fruit fly (* [C2 // C2_DOMAIN_2] CG6643 GH06342 96A-96A dup:1/2 ID:58G6

CG6643

CG5089 + unknown * [NLS_BP] CG5089 GH06435 53C8-53C9 dup:2/2 ID:58H4

+ DNA_binding * Ser/Arg-related nuclear matrix protein (plenty of prolines 101-like)(aa) * elastic titin(aa) * 1e-11 C. elegans UNC-89 * 8e-07 MAPB_MOUSE MICROTUBU [NLS_BP] CG3950 GH06555 6B1-6B3 ID:59A3

CG3950

+ emp transmembrane_receptor * DMEMP_3 emp * epithelial membrane protein - fruit fly (Drosophila melanogaster)(aa) * 2e-40 predicted using Genefinder; similar to CD36 family; cDNA [CD36] CG2727 GH06663 60E7-60E8 ID:59B5

CG2727

+ 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 GH06666 92A1-89D4 dup:2/4 ID:59B6

CG14904

CG5467 + unknown * CG5467 GH07007 97B9-97B9 ID:59C8

CG6761 + unknown * CG6761 GH07092 67B12-67B12 ID:59D1

CG18512 + CG18512 GH07187 ID:59D7

CG3588 + EG:100G7.6 structural_protein * map_position:3C5 * * * [PRO_RICH] CG3588 GH07242 3C4-3C4 dup:2/2 ID:59E3

+ transporter * solute carrier family (sodium/chloride transporters), member 3(aa) * BUMETANIDE-SENSITIVE SODIUM-(POTASSIUM)-CHLORIDE COTRANSPORTER (NA-K-CL SYMPORT [AMINO_ACID_PERMEASE_2] CG4357 GH07280 69B-69B2 dup:7/8 ID:59E7

CG4357

+ cell_adhesion * 6e-06 CYAA_YEAST ADENYLATE CYCLASE (ATP PYROPHOSPHATE-LYASE) (ADENYLYL CYCLASE) * 1e-10 leucine-rich motif (LRR) protein homology to interleukin rec [LRR // LEURICHRPT // PRO_RICH // CYTOCH] CG15151 GH07373 36E-36E ID:59F3

CG15151

+ enzyme * similar to Gila monster phospholipase A2; similar to * PHOSPHOLIPASE A2 ISOZYMES PA2/PA4 (PHOSPHATIDYLCHOLINE 2-ACYLHYDROLASE)(aa) * 2e-21 PA2_APIME [PA2_HIS] CG3009 GH07387 4C7-4C7 ID:59F5

CG3009

+ ana unknown * ana * neuroblast proliferation inhibitor ana - Drosophila(aa) * ana * neuroblast proliferation inhibitor=ana eye disc, Peptide, [WW_DOMAIN_1] CG8084 GH07389 45A9-45A10 ID:59F6

CG8084

CG10912 + unknown * CG10912 GH07575 55B2-55B2 ID:59G12

CG14689 + unknown CG14689 GH07528 ID:59G5

none + none GH07529 ID:59G6

CG11877 + unknown * protein(aa) * * CG11877 GH07807 99A1-99A1 dup:2/3 ID:60A8

+ TM4SF unknown * TM4SF * 1e-156 belong to the membrane protein group of Transmembrane Super * 9e-07 CD53_MOUSE LEUKOCYTE SURFACE ANTIGEN CD53 (CELL SURFACE GLYCOPROT [TMFOUR // TM4_2] CG11303 GH07902 60A7-60A7

CG11303

dup:2/3 ID:60B10
 CG16887 + BG:DS00941.11 unknown * AAs(aa) * AAs(aa) * CG16887 GH07914 34D4-34D4 dup:2/3 ID:60B12
 CG17124 + unknown * CG17124 GH07856 32A4-32A4 dup:1/2 ID:60B6
 CG6332 + unknown * [NLS_BP] CG6332 GH07879 93F14-93F14 dup:1/2 ID:60B8
 CG8568 + unknown * 4e-05 C09D4.2 gene product * * [NLS_BP] CG8568 GH07892 16A4-16A5 dup:1/2 ID:60B9
 CG9338 + unknown * CG9338 GH07967 38F1-38F1 dup:1/2 ID:60C9
 + BG:DS02780.1 cell_adhesion * Toll protein(aa) * 9e-05 cell-surface molecule connectin - fruit fly (Drosophila melanogaster) * 2e-06 predicted using Genefinder; Similarity to Dr [LRR] CG5888 GH08155 35F12-36A1 dup:1/2 ID:60D6
 CG5888 + endopeptidase * 3e-11 TBP6_YEAST PROBABLE 26S PROTEASE SUBUNIT YTA6 (TAT-BINDING HOMOLOG 6) * 3e-08
 CG14183 MEI1_CAEEL MEIOTIC SPINDLE FORMATION PROTEIN MEI-1 mei-1 * 0.000 CG14183 GH08353 76E3-76E4 dup:3/3 ID:60E1
 + transporter * DMORCT2_2 Orct * putative organic cation transporter(aa) * 5e-40 Similarity to Rat organic cation transporter
 CG16727 cDNA EST * 1e-39 OCTN3 [sugar_tr] CG16727 GH08275 94D3-94D3 dup:2/2 ID:60E3
 CG7669 + unknown * [NLS_BP] CG7669 GH08407 91A-91A dup:1/2 ID:60F7
 CG11656 + unknown * CG11656 GH08448 87D9-87D9 dup:1/2 ID:60F9
 + actin_binding * DMRCPA_X kel * The gene product is related to Drosophila melanogaster ring canel protein.(aa) * 8e-86
 CG3962 kelch protein, long form - fruit fly (Drosophi [BTB // KELCHREPEAT // Kelch] CG3962 GH08610 89E13-89E13 dup:1/3 ID:60G9
 none + none GH08762 ID:60H10
 + unknown * hypothetical protein(aa) * cDNA EST comes from this gene; cDNA EST comes from this gene; cDNA EST comes
 CG9246 from this gene; cDNA EST yk317d5.5 comes fro [NLS_BP] CG9246 GH08927 39B3-39B3 dup:1/2 ID:61B10
 + bnl signal_transduction * FGF homolog(aa) * bnl * 3e-09 LET-756 protein * 3e-14 fibroblast growth factor fibro [HBGFFGF //
 CG4608 FGF // IL1HBGF] CG4608 GH08887 92B3-94E1 dup:3/3 ID:61B2
 CG3987 + unknown * CG3987 GH09123 88E4-88E5 dup:2/3 ID:61D3
 none + none GH09355 ID:61F3
 + Eip71CD enzyme * 6e-11 PMSR_YEAST PUTATIVE PEPTIDE METHIONINE SULFOXIDE REDUCTASE (PEPTIDE MET(O)
 CG7266 REDUC * 1e-123 put. Eip (aa 1-255) * 2e-29 similar to drosophila e CG7266 GH09363 71C4-71C4 dup:2/3 ID:61F4
 CG4302 CG11051 + CG4302 CG11051 GH09393 ID:61F9
 + G-alpha47A signal_transduction GUANINE NUCLEOTIDE-BINDING PROTEIN G(O), ALPHA SUBUNIT (CLASS-I) >gi|
 CG2204 ATP_GTP_A, G-alpha, GPROTEINA, GPROTEINA] CG2204 GH09771 dup:3/4 ID:61H10
 CG17875 + cytochrome_P450 CG17875 GH09824 dup:1/3 ID:62A2
 + TBPH RNA_binding * map_position:60A5-6 * TAR-binding protein(aa) * TBPH * 2e-16 NAB4_YEAST NUCLEAR
 POLYADENYLATED RNA-BINDING PROTEIN NAB4 [RNP_1 // RBD // rrm // NLS_BP] CG10327 GH09868 60A5-60A6 dup:1/2
 CG10327 ID:62A7
 CG11074 + unknown * [NLS_BP] CG11074 GH09884 42F2-42F2 ID:62A8
 + ligand_binding_or_carrier * 2e-68 62D9.a * 4e-10 cellular retinaldehyde-binding protein; CRALBP * 2e-15 alpha tocopherol
 transfer protein * 1e-15 TTPA_RAT ALPHA-TOCOPHEROL TRAN [CRETINALDHBP // CRAL_TRIO] CG3823 GH10083 5E1-5E1
 CG3823 ID:62B11

+ * APOLIPOPROTEIN D PRECURSOR(aa) * 7e-13 APD_MOUSE APOLIPOPROTEIN D PRECURSOR apolipoprotein D *
 CG4604 2e-16 apolipoprotein D APOLIPOPROTEIN D P * 2e-17 APD [lipocalin // LIPOCALIN] CG4604 49F7-49F7 dup:2/2 ID:62B12
 + enzyme * alpha-L-fucosidase(aa) * fucosidase, alpha-L- 1, tissue(aa) * 8e-28 hypothetical protein YIL106w - yeast
 CG6128 (Saccharomyces cerevisiae) * 4e-73 FUCO_CAE [Alpha_L_fucos // GLHYDRLASE29] CG6128 GH09976 68C4-68C5 ID:62B4
 CG2467 + unknown * [PRO_RICH // NLS_BP] CG2467 GH09980 10F7-10F8 dup:2/2 ID:62B5
 + NetB cell_adhesion * extracellular extracellular) map_position:12F1 * NetB * 1e-170 NETB_DROME NETRIN-B PRECURSOR
 CG10521 Netrin-B melanog * 3e-67 UNC6_CAEEL UNC-6 PROTEIN P[laminin_EGF // EGFLAMININ // EGF_LAM //] CG10521 GH10173
 12F1-12F3 dup:1/2 ID:62C5
 + transmembrane_receptor * 2e-09 /match=(desc: * 2e-52 YP84_CAEEL HYPOTHETICAL 90.9 KD PROTEIN C08B11.4 IN
 CG3106 CHROMOSOME II * predicted using Genefinder * cDNA EST comes from thi CG3106 GH10201 8F2-8F2 ID:62C6
 + motor_protein * 2e-05 cellular myosin heavy chain * 8e-07 myosin heavy chain, neuronal - rat * 1e-05 Klp68D * myosin
 CG4681 heavy chain IIb CG4681 GH10544 60D6-60D6 dup:2/2 ID:62E11
 + tafazzin unknown * 2e-17 hypothetical protein YPR140w - yeast (Saccharomyces cerevisiae) (* 4e-39 ZK809.2 * 1e-59 tafazzin
 CG8766 TFAZZIN * 2e-40 Similar to tafazzins prote [GLYCEROL_ACYLTRANS // TFAZZIN] CG8766 GH10529 49C1-49C1 dup:2/2
 ID:62E9
 CG10433 + * [PRENYLATION] CG10433 57F3-57F3 dup:4/5 ID:62F12
 CG2267 + transcription_factor * CG2267 100A2-100A2 dup:2/2 ID:62F6
 + signal_transduction * protein(aa) * 1e-31 Sec7p * 2e-76 similar to S. cerevisiae protein transport protein SEC7 * 1e-38
 CG10577 cytohesin [SEC7 // Sec7 // NLS_BP] CG10577 GH10594 78B1-78B1 dup:1/2 ID:62F7
 + enzyme * similar to chitin synthases(aa) * 9e-13 CHS3_YEAST CHITIN SYNTHASE (CHITIN-UDP ACETYL-
 CG2666 GLUCOSAMINYL TRANSFERASE 3) * 8e-06 hyaluronan synthase * 8e- CG2666 GH10726 83A5-83A5 ID:62G3
 + cell_adhesion * DMARTAN_7 trn * kek1 * tartan protein(aa) * 5e-16 CYAA_YEAST ADENYLATE CYCLASE (ATP
 CG11280 PYROPHOSPHATE-LYASE) (ADENYLYL CYCLASE) [LRR // LEURICHRPT // LRRCT] CG11280 GH10871 69F5-69F5 ID:62H10
 + EG:100G10.4 enzyme * by content; by match; 2-match_description=4-NITROPHENYLPHOSPHATASE.; 2-match...(aa) *
 CG2680 BLASTX 8.9E-14 PHO13|4-Nitrophenylphosphatase(dna) * 1e-20 4- CG2680 GH11163 3B5-3B5 ID:63C4
 + ion_channel * ATP-regulated potassium channel brain, Peptide Partial, * G PROTEIN-ACTIVATED INWARD RECTIFIER
 CG4370 POTASSIUM CHANNEL (GIRK3) (POTASSIUM CHANNEL, INWARDL [CHANNEL_PORE_K // IRK] CG4370 GH11459 97D1-
 97D1 ID:63D11
 CG18418 + unknown * CG18418 GH11346 65A10-65A10 ID:63D4
 CG6441 + unknown * CG6441 GH11511 28A1-28A1 dup:2/2 ID:63E3
 + srp transcription_factor * GATA factor(aa) * DMGATAFAC_2 srp * 3e-12 GAT1_YEAST GAT1 PROTEIN probable membrane
 CG3992 protein YFL02 * 2e-18 ELT1_CAEEL TRANSCRIPTION FACTOR[GATAZNFINGER // LECTIN_LEGUME_BETA // G] CG3992
 GH11649 89B3-89B4 dup:2/5 ID:63F10
 CG3306 + unknown * CG3306 GH11578 67B9-67B9 ID:63F3
 CG16959 + unknown * [EGF_2] CG16959 GH11627 71B2-71B2 dup:2/2 ID:63F7
 CG5058 + grh transcription_factor * DMELF1_2 grh * transcription factor NTF1 - fruit fly (Drosophila melanogaster) (fragment) * 1e-22

alpha-globin transcription factor CP2 - mouse * 9e [NLS_BP] CG5058 GH11672 54F1-54F4 ID:63G1

+ 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=[HOMEODOMAIN_1 // homeobox // ZF_MATRIN //] CG1449 GH11902

CG1449 102C1-102C3 dup:2/2 ID:63H9

+ gbb signal_transduction * DM60AP * 60A PROTEIN PRECURSOR(aa) * 9e-17 contains similarity to the TGF-beta family of growth factors e * 3e-52 BMP7_MOUSE BONE MORPHOGENETIC PROT [TGFb_propeptide] CG5562 GH12092 60A5-60A5 ID:64B10

CG5562 + bnb unknown * DMBNBR_2 bnb * 1e-148 BNB_DROME BANGLES AND BEADS PROTEIN bangles and * GAP-43-related protein - fruit fly (Drosophila melanogaster) * bnb gene prod CG7088 GH12078 17D6-17D6 ID:64B8

CG7088 + signal_transduction * 2e-15 IP63 protein * * CG7886 GH12083 88C10-88C10 ID:64B9

CG7886 + Hel89B DNA_binding * TBP-associated factor 172(aa) * Hel89B * 89B helicase(aa) * MOT1_YEAST PROBABLE HELICASE MOT1 MOT1 protein - yeast (S [helicase_C // SNF2_N] CG4261 GH12153 89B3-89B3 dup:1/2 ID:64C3

CG4261 + unknown * 6e-05 transmembrane protein * 2e-12 Similarity to C.elegans cuticulin (SW:CUT1_CAEEL) * 7e-07 DMDUSKY_ dy * similar to cuticlin CG3541 GH12163 60D7-60D8 dup:1/2 ID:64C4

CG3541 + emc transcription_factor * DNA-binding protein inhibitor Id-1H - human(aa) * EXTRA-MACROCHAETAE PROTEIN(aa) * DMEC3 emc * 7e-78 extramacrochaetae protein - fruit fly[HELIX_LOOP_HELIX // HELIX_LOOP_HELIX_2] CG1007 GH12170 61D1-61D2 dup:1/2 ID:64C5

CG1007 + endopeptidase * DMEAST_4 ea * DMSNAKE_2 snk * 2e-28 SNAK_DROME SERINE PROTEASE SNAKE PRECURSOR serine proteina * 3e-18 similar to peptidase family S1 (trypsin famil [trypsin // CHYMOTRYPSIN // TRYPSIN_SER] CG6367 GH12385 17B3-17B4 ID:64D10

CG6367 + unknown * 8e-42 YMS5_CAEEL HYPOTHETICAL 159.2 KD PROTEIN K03H1.5 IN CHROMOSOME III * 8e-17 alpha tectorin * 2e-16 tectorin alpha alpha-tectorin * 1e-15 alpha CG15560 GH12365 100B8-100B8 ID:64D8

CG15560 + unknown * CG4375 GH12486 21E2-21E2 dup:2/2 ID:64E10

CG4375 + cytoskeletal_structural_protein * putative protein transport protein sec7 homolog(aa) * DmCDS(aa) * pleckstrin and Sec7 domain protein(aa) * PROTEIN TRANSPORT [SPECTRINPH // PH // SEC7 // Sec7 // MIT] CG6941 GH12441 94B10-94B10 dup:2/2 ID:64E4

CG6941 + EG:100G10.1 unknown * SH3 domain-binding protein SNP70(aa) * by content; by match; LD Drosophila melanogaster...(aa) * 8e-06 WW domain binding protein * [PRO_RICH // NLS_BP] CG2685 GH12462 3B5-3B5 dup:3/3 ID:64E6

CG2685 + transporter * protein(aa) * DMATPA_2 Atp agr; * SODIUM/POTASSIUM-TRANSPORTING ATPASE ALPHA CHAIN (SODIUM PUMP) (NA+/K+ ATPASE)(aa) * BLASTX 3.4E-17 Rat alternativ [NAKATPASE // HATPASE // CATATPASE // E1] CG7651 GH12627 79F3-79F3 ID:64F10

CG7651 + enzyme * 2e-61 wunen * 1e-24 YSX3_CAEEL HYPOTHETICAL 39.0 KD PROTEIN T28D9.3 IN CHROMOSOME II (U2 * 6e-35 Phosphatidic acid phosphatase * 5e-36 phosphatidic [PA_PHOSPHATASE] CG11426 GH12758 79E4-79E4 ID:64G11

CG11426 + enzyme * diacylglycerol kinase(aa) * 2e-30 diacylglycerol kinase (EC 2.7.1.107) - fruit fly (Drosophila melanogaster) * 1e-57 alpha diacylglycerol kinase; a [DAG_PE_BINDING_DOMAIN // RA // C1 // DA] CG5875 GH12677 95D1-97F1 dup:2/5 ID:64G5

CG5875 + unknown * CG13918 GH13002 62A-62A ID:65A12

CG13918 + unknown * [TPR_REPEAT] CG7634 GH12875 78E2-78E2 dup:2/2 ID:65A2

CG7634

CG11509 + unknown * CG11509 GH13132 2B6-2B6 ID:65B11

CG7549 + unknown * [HTH_LACI_FAMILY] CG7549 GH13023 84F-84F ID:65B2

CG3483 + enzyme * 5e-49 IDH1_YEAST ISOCITRATE DEHYDROGENASE (NAD), MITOCHONDRIAL SUBUNIT PRECURSOR (IS * 6e-57 IDHA_CAEEL PROBABLE ISOCITRATE DEHYDROGENASE (NAD), MIT [isodh] CG3483 GH13226 60D2-60D2 ID:65C9

CG14889 + structural_protein * [COLLAGEN_REP // Collagen] CG14889 GH13492 92A1-92A1 dup:1/2 ID:65D11

CG17010 + * ribokinase(aa) * ribokinase RbsK(aa) * DMC115C2 * 1e-71 /match=(desc;; /ma [pfkB // PRO_RICH // RIBOKINASE] CG17010 33D3-33D3 dup:2/2 ID:65D12

CG13784 + unknown * CG13784 GH13387 27E4-27E5 ID:65D3

CG6117 + Pka-C3 protein_kinase * PROTEIN KINASE DC2(aa) * DMDC2_2 Pka-C3 * 5e-88 cAMP-dependent protein kinase subunit (put.); putative * 2e-99 KAPC_CAEEL CAMP-DEPENDENT PROTEIN KIN CG6117 GH13608 72B1-72B2 dup:3/3 ID:65E5

CG17022 + unknown * 3e-07 serine rich protein * SERA_ENTHI SERINE-RICH KD ANTIGEN PROTEIN (SHEHP) (SREHP) * merozoite protein Bb-1 - Babesia bovis (fragment) * CG17022 GH13755 30B10-30B10 ID:65F5

CG3168 + 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 GH13883 6C9-6C10 ID:65G5

CG11912 + endopeptidase * mas * Ser5 * Tequila * zgr;Try [trypsin // CHYMOTRYPSIN // TRYPSIN_SER] CG11912 GH13929 21B7-21B8 ID:65G7

CG1743 + Gs2 enzyme * GLUTAMINE SYNTHETASE 2, CYTOPLASMIC (GLUTAMATE--AMMONIA LIGASE 2)(aa) * GLUTAMINE SYNTHETASE (GLUTAMATE--AMMONIA LIGASE)(aa) * glutamine synthetase [GLNA_1 // gln-synt // GLNA_ATP] CG1743 GH14412 10B13-10B14 dup:1/2 ID:66C10

CG9665 + unknown * 2e-05 CU19_LOCM1 CUTICLE PROTEIN (LM-19) (LM-ACP 19) Lm-ACP1 ** [GRAM_POS_ANCHORING // insect_cuticle] CG9665 GH14349 73D-73D6 ID:66C3

CG5695 + jar motor_protein * DMMHC95F Mhc95F * 1e-116 MYS4_YEAST MYOSIN-4 ISOFORM myosin MYO4 - yeast (Saccharo * MYS9_DROME MYOSIN HEAVY CHAIN 95F (95F MHC) myosin heavy * sim [myosin_head // IQ // MYOSINHEAVY // NLS] CG5695 GH14351 95F-95F ID:66C4

CG10097 + Brassica napus 'male sterility protein 2' EMBL:X99922 CG10097 ID:66C5

CG3571 + actin_binding * DMRCPA_X kel * protein(aa) * [BTB // KELCHREPEAT // Kelch] CG3571 GH14381 87A-87A dup:2/2 ID:66C6

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

CG14723 + ion_channel * 7e-59 DrosGluCl * 1e-48 Contains similarity to Pfam domain: (neur_chan), Score=39 * 7e-67 glycine receptor subunit alpha * 8e-68 glycine receptor al [neur_chan // NEUROTR_ION_CHANNEL // NRI] CG14723 GH14445 86F9-86F9 ID:66D2

CG7503 + Con cell_adhesion * DMCONNECTN_1 Con * 1e-180 cell-surface molecule connectin - fruit fly (Drosophila melanogaster) * 3e-15 coded for by C. elegans cDNA yk132e5.5; coded [LRR // LRRCT] CG7503 GH14524 64C6-64C7 dup:2/2 ID:66E2

CG3999 + enzyme * GCSP_YEAST GLYCINE DEHYDROGENASE (DECARBOXYLATING) PRECURSOR (GLYCINE DECARBOXY * similar to glycine dehydrogenase * GCSP_HUMAN GLYCINE DEHYDROGEN CG3999 GH14537 85F16-85F16 dup:2/2

ID:66E3

CG16791 + unknown * 2e-24 cDNA EST CEMSE83F comes from this gene; cDNA EST comes * * CG16791 GH14545 93D6-93D6 dup:3/3 ID:66E5

CG3427 + signal_transduction * cAMP-dependent Rap1 guanine-nucleotide exchange factor(aa) * HYPOTHETICAL 139.4 KD PROTEIN T20G5.5 IN CHROMOSOME III(aa) * 2e-07 KAPR_YEAST [cNMP_binding // RasGEF // DEP_DOMAIN //] CG3427 GH14655 42C4-42D1 dup:2/3 ID:66F8

CG12699 + unknown * CG12699 GH14656 54B7-54B7 ID:66F9

+ transporter * 8e-59 MDL1_YEAST ATP-DEPENDENT PERMEASE MDL1 MDL1 protein - y * MDR5_DROME MULTIDRUG RESISTANCE PROTEIN HOMOLOG (P-GLYCOPROTEIN 65) * similar to mu [ATP_GTP_A2 // ABC_TRANSPORTER // ABC_tr] CG10226 GH14758 65A7-65A7 ID:66G7

CG11960 + unknown * [NLS_BP] CG11960 GH14769 56D8-56D8 dup:1/2 ID:66G8

CG2505 + alpha-Est2 enzyme * alpha esterase(aa) * agr;-Est2 * carboxylesterase MdaE7(aa) * alpha esterase [CHOLNESTRASE // ESTERASE // COesterase] CG2505 GH15053 84D6-85A3 ID:67B5

CG7626 + transcription_factor * chromatin structural protein homolog Supt5hp(aa) * suppressor of Ty (S.cerevisiae) homolog(aa) * 9e-59 SPT5_YEAST TRANSCRIPTION INITIATION PROTEIN CG7626 GH15359 56D7-56D7 dup:4/5 ID:67D10

+ th apoptosis_inhibitor * DMDIAP1X_3 th * APOPTOSIS INHIBITOR (INHIBITOR OF APOPTOSIS 1) (DIAP1) (THREAD PROTEIN)(aa) * 2e-05 similar to Zinc finger, C3HC4 type (RIN[zf-C3HC4 // BIR // BIR_REPEAT // BIR_RE] CG12284 GH15335 72D1-72D1 dup:2/3 ID:67D8

CG12284 + unknown * CG18437 GH15426 98A6-98A6 dup:2/2 ID:67E2

CG18437 + unknown * [TBC // RAB_GAP] CG7742 GH15768 25C9-25C9 ID:68A4

CG7742 + enzyme * Chain A, Crystal Structure Of Recombinant Human Brain Hexokinase Type I Complexed With Glucose And Glucose-6-Phosphate(aa) * hexokinase-like protei [HEXOKINASES // hexokinase // HEXOKINASE] CG5443 GH15883 100A5-97B2 ID:68B3

CG5443 + transmembrane_receptor * DMEMP_3 emp * DMCD362_2 croquemort * 9e-18 epithelial membrane protein - fruit fly (Drosophila melanogaster) * 8e-15 mLGP85/LIMP II [CD36] CG2736 GH15894 60E7-60E7 ID:68B4

CG2736 + unknown * CG16820 GH15921 34A11-34A11 dup:2/2 ID:68B9

CG16820 + transporter * K05B2.5 gene product(aa) * 1e-13 YKW1_YEAST HYPOTHETICAL 52.3 KD PROTEIN IN FRE2 5'REGION * 2e-82 /match=(desc;; /ma * 1e-40 predicted using Genefin CG8468 GH16148 50E-50E7 dup:2/5 ID:68C9

CG8468 + drongo signal_transduction * drongo * 9e-25 Drongo * 4e-12 HIV-1 Rev binding protein NUCLEOPO * 1E-151 [ArfGap // ZF_GCS // REVINTRACTNG] CG3365 GH16240 21D2-21E3 dup:2/2 ID:68D8

CG3365 + Cyp4g15 cytochrome_P450 * Cyp4e2 * CYTOCHROME P450 4C1 (CYPIVC1)(aa) * 2e-13 CP51_YEAST CYTOCHROME P450 (CYPL1) (P450-L1A1) (STEROL 14-ALPHA DEMETHYLASE) * 1E-151 [EP450II // p450 // P450 // CYTOCHROME_P] CG11715 GH16320 10B15-10B17 dup:2/2 ID:68E2

CG11715 + unknown * 4e-10 male-specific protein * * CG18111 GH16332 99B-99B dup:2/2 ID:68E4

CG18111 + endopeptidase * chymotrypsin-like serine protease(aa) * TRYPSIN DELTA PRECURSOR(aa) * DMEAST_4 ea * Ser6 [trypsin // CHYMOTRYPSIN // TRYPSIN_CATA] CG9672 GH16384 15A2-15A2 dup:2/2 ID:68E9

CG9672

CG15426 + cell_adhesion * 4e-11 LAR_DROME PROTEIN-TYROSINE PHOSPHATASE DLAR PRECURSOR (PROTEIN-TYROSINE-PHOSPHAT * 1e-09 predicted protein contains a large number of Ig super [ig] CG15426 GH16705 24E1-24E3 dup:2/2 ID:68H5

CG1681 + enzyme * GLUTATHIONE S-TRANSFERASE YRS-YRS (GST 12-12) (GLUTATHIONE S-TRANSFERASE SUBUNIT 12) (CLASS-THETA)(aa) * glutathione S-transferase theta 2(aa) * 5e- [GST] CG1681 GH16740 11F1-11F1 ID:68H9

CG17603 + 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 GH17990 84A2-84C4 ID:70A9

CG1600 + enzyme * 3e-53 Weak similarity to Potato alcohol dehydrogenase (SW:ADH_SULSO); cD * 7e-06 QOR_MOUSE QUINONE OXIDOREDUCTASE (NADPH:QUINONE REDUCTASE) (ZETA-CR [adh_zinc] CG1600 GH18014 43D3-43D3 ID:70B1

CG14994 + 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 ID:70B5

CG2930 + BcDNA:GH06717 transporter * OLIGOPEPTIDE TRANSPORTER, KIDNEY ISOFORM (PEPTIDE TRANSPORTER 2) (KIDNEY H+/PEPTIDE COTRANSPORTER)(aa) * OLIGOPEPTIDE TRANSPORTER, KIDNEY ISOFORM (P [PTR2 // PTR2_1 // PTR2_2] CG2930 GH18049 4A1-4A1 dup:2/3 ID:70B9

CG7176 + * NADP-dependent isocitrate dehydrogenase(aa) * 1e-148 IDHP_YEAST ISOCITRATE DEHYDROGENASE (NADP), MITOCHONDRIAL PRECURSOR (OXALOSUCCIN * 1e-180 simil [IDH_IMDH // isodh] CG7176 66C8-66C8 dup:3/4 ID:70D6

CG9520 + unknown CG9520 dup:5/5 ID:70E7

CG11842 + endopeptidase * serine protease 18D(aa) * 4e-36 SNAK_DROME SERINE PROTEASE SNAKE PRECURSOR serine proteina * 2e-15 similar to peptidase family S1 (trypsin family) * [trypsin // CHYMOTRYPSIN // TRYPSIN_SER] CG11842 GH18608 98F10-98F10 ID:70G11

CG1468 + unknown * CG1468 GH18955 9A2-9A2 dup:2/2 ID:71A12

CG1979 + BG:DS00464.1 transmembrane_receptor * unknown(aa) * * CG1979 GH19145 84C1-84C1 dup:1/2 ID:71C10

CG6416 + enzyme * 3e-07 alpha-actinin-2 associated LIM protein * 9e-08 actinin-associated LIM protein * 4e-08 CL36_RAT LIM PROTEIN CLP36 LIM protein - rat * alpha-act [PDZ] CG6416 GH19182 66D9-66D ID:71D2

CG2082 + BcDNA:GH02439 unknown * 1e-59 cDNA EST comes from this gene; cDNA EST co * 7e-33 cytoplasmic protein Ndr1 * 5e-32 RTP nickel-specific inductio * 2e-25 development-related p CG2082 GH19206 83C-83C dup:2/2 ID:71D3

CG6385 + 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 54E7-54E8 ID:71D6

CG9130 + unknown * CG9130 GH19274 61F4-61F4 dup:2/3 ID:71D9

CG11212 + transmembrane_receptor * patched (Drosophila) homolog(aa) * PATCHED PROTEIN HOMOLOG (PTC1) (PTC)(aa) * similar to drosophila membrane protein PATCHED * 1e-26 probable m[PHOSPHOPANTETHEINE // 5TM_BOX] CG11212 GH19449 42A10-42A10 dup:2/2 ID:71E10

CG7397 + signal_transduction * 5e-30 similar to guanine-nucleotide releasing factors including BCR ele * 7e-20 transforming protein (ect2) - mouse ect2 >g * 6e-17 GrfA * R02F2.2 g [GRF_DBL // RhoGEF // NLS_BP] CG7397 GH19526 90C2-90C2 ID:71F7

CG5839 + peptidase * 3e-78 aminopeptidase yscII * 9e-93 Similarity to Human aminopeptidase N (SW:AMPN_HUMAN); cDNA EST

EMB * 1e-102 AMPN_MOUSE AMINOPEPTIDASE N (MICROSOM [ALADIPTASE // Peptidase_M1 // ZINC_PROT] CG5839
 GH19677 93F4-93F6 dup:3/7 ID:71G10
 + transporter * unknown(aa) * anon-100EF-D3 * 1e-20 Similarity to Salmonella sodium/proline symporter
 (SW:PUTP_SALTY); * 1e-33 sodium iodide symporter [SSF // NA_SOLUTE_SYMP_3] CG2196 GH19680 100E2-100E3 ID:71G11
 + chp cell_adhesion * DMCOP10_2 chp * 2e-11 CYAA_YEAST ADENYLATE CYCLASE (ATP PYROPHOSPHATE-LYASE)
 (ADENYLYL CYCLASE) * CHAO_DROME CHAOPTIN PRECURSOR (PHOTORECEPTOR CELL [ARM_REPEAT // LRR //
 LEURICHRPT] CG1744 GH19649 100B8-100B9 ID:71G7
 + Eaata2 neurotransmitter_transporter * EXCITATORY AMINO ACID TRANSPORTER (SEAAT1)(aa) * glutamate transporter
 2B(aa) * CeGlt-2(aa) * predicted using Genefinder; Similar[SDF // EDTRANSPORT // NA_DICARBOXYL_SYMP] CG3159 GH19725
 21D1-21D1 dup:2/4 ID:71H5
 + Mst98Cb unknown * CG18396 GH20038 98C2-98C2 ID:72C1
 + unknown * CG9483 GH20208 29F3-29F3 ID:72D7
 + unknown * 1e-39 /match=(desc;; /ma * 3e-06 F20D6.5 gene product * predicted using Genefinder * cDNA EST yk381e5.3
 comes from this gene [NLS_BP] CG10514 GH20308 96C7-96C7 dup:2/2 ID:72E7
 + Myosin-heavy-chain-like motor_protein * nonmuscle myosin II heavy chain A(aa) * nonmuscle myosin heavy chain-A(aa) *
 myosin heavy chain nonmuscle form A - human(aa) * 2e-97 m[myosin_head // IQ // MYOSINHEAVY] CG10218 GH20309 89B7-
 89B7 dup:4/4 ID:72E8
 + unknown * CG3557 GH20409 23E4-23E4 ID:72F9
 + transporter * 3e-19 nervous system antigen nerv * 5e-06 Similarity to Shrimp sodium/potassium-transporting ATPase beta
 cha * 7e-10 ATNB_MOUSE SODIUM/POTASSIUM-TRA CG11703 GH20514 91F10-91F10 ID:72G7
 + unknown CG5797 dup:1/3 ID:72G9
 + enzyme CG10408 ID:72H5
 + unknown * CG17111 GH20645 94D13-94D13 ID:72H6
 + enzyme * UNKNOWN(aa) * 7e-63 PUT2_YEAST DELTA-1-PYRROLINE-5-CARBOXYLATE DEHYDROGENASE
 PRECURSOR (P5C DEHYDROG * 8e-11 alternatively spliced form; /prediction [aldehyd] CG6661 GH20963 70C11-70C11 ID:73C5
 + peptidase * 1e-24 YBY9_YEAST PUTATIVE SERINE CARBOXYPEPTIDASE IN ESR1-IRA1 INTERGENIC REGION * 2e-
 83 similar to BPTI/KUNITZ inhibitor domain; cDNA EST come * 8e [ESTERASE // serine_carbpept // CRBOXYPT] CG3344
 GH21114 61C9-61C9 ID:73D10
 + defense/immunity_protein * 1e-28 peptidoglycan recognition protein precursor * 1e-28 TNF superfamily, member (LTB)-like
 (peptidoglycan recognition protein) (AF0 * 2e-28 peptid CG14704 GH21008 86E-86E ID:73D2
 + unknown * 2e-74 F55A12.9 gene product * * CG1383 43E12-43E13 ID:73D4
 + structural_protein * [GAPDH] CG6958 GH21194 94C4-94C4 dup:3/3 ID:73E12
 + enzyme * 5e-12 GLO2_YEAST HYDROXYACYLGLUTATHIONE HYDROLASE ISOZYME (GLYOXALASE II) (GLX II) * 2e-
 62 cDNA EST yk301h4.5 comes from this gene; cDNA EST yk301h4 [lactamase_B // NLS_BP // ATP_GTP_A] CG9026 GH21160
 47F7-47F7 dup:3/3 ID:73E3
 + Cyp4p2 cytochrome_P450 * DMC152A3 * DMCYP4D2_12 Cyp4d2 * 6e-09 CP56_YEAST CYTOCHROME P450-DIT2

	(CYTOCHROME P450 56) cyt * 3e-53 cytochrome P450 cytochrome P4 [EP450II // p450 // P450 // MITP450 // C] CG1944 GH21174 45C-45C dup:2/2 ID:73E8
CG8918	+ enzyme * similar to tubulin tyrosine ligase; cDNA EST comes from this gene; cDNA EST comes from this gene; cDNA EST comes from this gene; cDNA EST comes fro CG8918 GH21352 15E5-15E5 ID:73F10
CG8086	+ structural_protein * 6e-22 NSP1_YEAST NUCLEOPORIN NSP1 (NUCLEAR PORE PROTEIN NSP1) (NUCLEOSKELETAL-LIKE PRO * 5e-08 C. elegans DNA-directed RNA polymerase II large subun CG8086 GH21437 29A1-29A1 dup:3/4 ID:73F12
CG12449	+ 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 ID:73F3
CG5411	+ enzyme * cAMP-specific phosphodiesterase 8B; PDE8B1; 3',5'-cyclic nucleotide phosphodiesterase(aa) * phosphodiesterase 8(aa) * 7e-16 cAMP phosphodiesterase [PDEase // PDIESTERASE1 // PAS_REPEAT //] CG5411 GH21295 59F-59F4 dup:2/2 ID:73F7
CG7045	+ DNA_binding * DMHMGDA_2 HmgD * HIGH MOBILITY GROUP PROTEIN Z (HMG-Z)(aa) * 2e-11 HMGD_DROME HIGH MOBILITY GROUP PROTEIN D (HMG-D) high mob * 2e-05 SSRP_CAEEL PROB [HIGHMOBLTY12 // HMG_box] CG7045 GH21448 94B4-94B4 ID:73G1
CG11961	+ function_unknown * 2e-19 YBS4_YEAST HYPOTHETICAL 47.8 KD PROTEIN IN HSP26-TIF32 INTERGENIC REGION * 8e-90 YP67_CAEEL HYPOTHETICAL 98.3 KD PROTEIN IN CHROMOSOME II (U2 CG11961 GH21451 56D2-56D2 ID:73G2
CG7571	+ transporter * 2e-64 coded for by C. elegans cDNA yk54h9.5; coded for by C. elegans cDNA yk54h9.3; si * 4e-70 PGT_HUMAN PROSTAGLANDIN TRANSPORTER (PGT) prostagland CG7571 GH21536 74D1-74D1 dup:2/2 ID:73H1
CG10193	+ motor_protein * 3e-05 F35D11.11 gene product * 2e-06 hyaluronan receptor - human * 3e-06 tetravalent M protein=hybrid molecule containing amino-terminal subuni * Si [PRO_RICH] CG10193 GH21577 95C3-95C3 dup:2/2 ID:73H4
CG2530	+ corto nucleic_acid_binding * corto * CENTROSOMAL AND CHROMOSOMAL FACTOR (CCF) (CHROMOCENTROSOMIN)(aa) * CP-1(aa) * inserted at base Both 5' and 3' ends of P element Inverse PCR CG2530 GH21787 82F5-82F5 ID:74B1
CG14808	+ EG:4F1.1cell_adhesion * /match=(desc:; /match=(desc:(aa) * sarcoglycan, delta (35kD dystrophin-associated glycoprotein)(aa) * 4e-06 delta sarcoglycan * 9e-05 delta-sarcogl CG14808 GH21860 2B8-2B9 ID:74B10
CG6156	+ motor_protein * mutated in colorectal cancers(aa) * 3e-05 myosin heavy chain, MHC CCl4-cirrhotic liver fat-storing cell I * 2e-06 DMMHC_2 Mhc * myosin heavy chain I CG6156 GH21874 88F1-88F1 dup:2/2 ID:74B12
CG5539	+ unknown * POLYPOSIS LOCUS PROTEIN (TB2 PROTEIN)(aa) * pathogenicity protein(aa) * 2e-09 YSV4_CAEEL HYPOTHETICAL 26.6 KD PROTEIN T19C3.4 IN CHROMOSOME III (U CG5539 GH21788 60A2-60A2 ID:74B2
CG14768	+ weak homology to leucine carboxyl methyltransferase [Homo sapiens] and receptor protein kinase-like protein [Arabidopsis thaliana] CG14768 GH21888 ID:74C2
CG7135	+ unknown * /match=(desc:; /match=(desc:(aa) * 4e-77 /match=(desc:; /ma * 7e-06 No definition line found * No definition line found CG7135 GH21891 16F7-16F7 dup:1/2 ID:74C3
CG4336	+ rux unknown * CELL CYCLE NEGATIVE REGULATOR ROUGHSEX(aa) * rux * 1e-170 rux * [NLS_BP] CG4336 GH22074 5D1-5D1 ID:74D12
CG3246	+ unknown * CG3246 25A3-25A3 dup:2/2 ID:74E11

+ jdp chaperone * 1e-11 SCJ1_YEAST SCJ1 PROTEIN SCJ1 protein - yeast (Saccharomyce * 1e-09 DNJ1_DROME DNAJ PROTEIN HOMOLOG (DROJ1) droj1 * 1e-10 YRY1_CAEEL HYPOTHETIC [GRAM_POS_ANCHORING // DnaJ // DNAJPROTE] CG2239 GH22106 99F8-99F10 dup:3/3 ID:74E7
 CG2239
 + Cyp4d8 cytochrome_P450 * DMCLCYP6A9 Cyp6a9 * DMCYTO_2 Cyp4d1 * DMCYP4D2_12 Cyp4d2 * cytochrome P450(aa) [EP450II // p450 // P450 // MITP450 // B] CG4321 GH22459 66A1-66A1 ID:74H1
 CG4321
 + unknown * C25E10.5 gene product(aa) * 7e-38 weak similarity to two short of multi-drug resistance proteins * No definition line found * Similarity to multidr CG8596 GH22722 65F3-65F3 ID:75B11
 CG8596
 + prd transcription_factor * SEGMENTATION PROTEIN PAIRED(aa) * DMPRD_5 prd * 3e-58 similar to 'Paired box' domain, homeobox protein (paired subfamily * 2e-87 PAX3_MOUSE PAIRE[PAX // HOMEBOX_1 // homeobox // HOMEOB] CG6716 GH22686 33B14-33B14 ID:75B4
 CG6716
 + enzyme * 6e-06 YD40_YEAST HYPOTHETICAL 42.3 KD PROTEIN IN YTA2-DIT1 INTERGENIC REGION * 4e-33 predicted using Genefinder; similar to Inosine-uridine preferri [IU_nuc_hydro] CG12177 GH22706 12B1-12B1 ID:75B7
 CG12177
 + unknown * 1e-35 probable membrane protein YOR245c - yeast (Saccharomyces cerevisiae) * 3e-58 K07B1.4 gene product * 9e-21 hypothetical protein * predicted usi CG1942 GH22719 43E11-43E11 ID:75B9
 CG1942
 CG8960
 + unknown * CG8960 GH22765 62D2-62D2 ID:75C5
 + bt protein_kinase * projectin - fruit fly (Drosophila melanogaster)(aa) * bt * similar to Fibronectin type III domain (31 domains), IG (immunoglobulin) superfamilig // PROTEIN_KINASE_ST // FNTYPEIII //] CG1479 GH22863 102D6-102E1 dup:1/2 ID:75D11
 CG1479
 CG3330
 + unknown * CG3330 GH22851 97F8-97F8 ID:75D7
 CG3770
 + unknown CG3770 dup:2/2 ID:75E10
 CG11388
 + unknown * CG11388 GH22974 60B1-60B1 dup:2/2 ID:75E11
 + electron_transfer * GEC-3(aa) * 3e-43 coded for by C. elegans cDNA yk51h9.5; coded for by C. elegans cDNA yk117c2.5; c * 1e-64 quiescin Q6 quiescin * 2e-66 GEC-3 [THIOREDOXIN_2] CG17843 GH22889 96B6-96B6 dup:2/2 ID:75E2
 CG17843
 CG2081
 + unknown * CG2081 GH22911 10A3-10A3 dup:2/2 ID:75E4
 + cell_adhesion * 2e-11 CHAO_DROME CHAOPTIN PRECURSOR (PHOTORECEPTOR CELL-SPECIFIC MEMBRANE PROTEIN) * 3e-06 Simiarity to Rat insulin-like growth factor binding prote [LRR // LEURICHRPT // NLS_BP] CG15658 GH22922 57C7-57C7 dup:2/2 ID:75E6
 CG15658
 + neurotransmitter_transporter * SerT * glycine transporter type-2(aa) * SODIUM- AND CHLORIDE-DEPENDENT GABA TRANSPORTER 3(aa) * hypothetical protein T23G5.5 - Caenor[NA_NEUROTRAN_SYMP_1 // NANEUSMPORT // N] CG8380 GH22929 53C-53C dup:2/2 ID:75E8
 CG8380
 + dei transcription_factor * DMDELILAH_2 dei * HELIX-LOOP-HELIX PROTEIN DELILAH(aa) * 2e-08 ATH2_MOUSE ATONAL PROTEIN HOMOLOG (HELIX-LOOP-HELIX PROTEIN MATH-2) (MATH2) (* 6e[HLH // HELIX_LOOP_HELIX // HELIX_LOOP_H] CG5441 GH22991 100A5-100A5 ID:75F3
 CG5441
 + ligand_binding_or_carrier * calcyphosine(aa) * CRUSTACEAN CALCIUM-BINDING PROTEIN (CCBP-23 PROTEIN)(aa) * 1e-10 predicted using Genefinder; Similarity to Human calmodulin (SW:P [EF_HAND // ehand // EF_HAND_2] CG10126 GH22994 87D3-87D3 ID:75F5
 CG10126
 + transporter * retinal rod Na/Ca+K exchanger(aa) * Na/Ca,K-exchanger(aa) * 2e-06 probable membrane protein YDL206w - yeast (Saccharomyces cerevisiae) * 1e-05 Na/C CG1090 GH23040 82B1-82B1 ID:75G4
 CG1090

CG2985 + YP1 CG2985 dup:1/5 ID:75H3

CG10566 + defense/immunity_protein * similar to rat autoimmune target protein p69 * 1e-39 similar to rat autoimmune target protein p69 * 5e-67 ICAp69 * 1e-64 diabetes mellitus type I au CG10566 GH23156 78B4-78C1 ID:75H6

CG10341 + unknown * BLASTX 7.1E-06 Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No. 4.(dna) * * [PRO_RICH] CG10341 GH23387 37A4-37A4 ID:76B9

+ cytoskeletal_structural_protein * p60 katanin(aa) * katanin p60 subunit(aa) * 4e-42 CC48_YEAST CELL DIVISION CONTROL PROTEIN cell divisi * 3e-43 transitional endoplasmic reticulum A [AAA // NLS_BP // ATP_GTP_A] CG1193 GH23455 83C-83C ID:76C7

CG1193 + 18w cell_adhesion * DMWHEELER_2 18w * 5e-15 CYAA_YEAST ADENYLATE CYCLASE (ATP PYROPHOSPHATE-LYASE) (ADENYLYL CYCLASE) * leucine-rich motif (LRR) protein homology to int CG8896 GH23463 56F9-56F9 dup:1/4 ID:76C7

CG8896 + Ark unknown * 1e-05 apoptotic protease activating factor * 3e-06 apoptotic protease activating factor * 2e-34 inserted at base Both 5' and 3' ends of P element In [ATP_GTP_A] CG6829 GH23583 53F1-53F1 ID:76D11

CG6829 + Dad transcription_factor * Dad * DAD polypeptide * 2e-18 similar to ZK370.2 * 2e-40 Smad6 [Dwarfin // PRO_RICH // NLS_BP] CG5201 GH23534 89E12-89E13 dup:3/4 ID:76D6

CG5201 + pyd enzyme * DMD477 pyd * TamA(aa) * 1e-16 coded for by C. elegans cDNA yk25e5.3; coded for by C. elegans cDNA yk25e5.5; si * 1e-138 ZO1_MOUSE TIGHT JUNCTION PRO [Guanylate_kin // GUANYLATE_KINASE_2 //] CG9763 GH23642 85B4-85B5 ID:76F2

CG9763 + chaperone * DMCYP1_2 Cyp1 * 4e-41 CYPH_YEAST PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (PPIASE) (ROTAMASE) (CYCLOPHILIN) * 1e-36 CYPH_DROME PEPTIDYL-PROLYL CIS-TRANS [pro_isomerase // CSA_PPIASE_1 // CSA_PP] CG1866 GH23813 98C3-98C3 dup:1/4 ID:76G11

CG1866 + unknown * CG17549 GH23745 37E1-37E1 dup:2/2 ID:76G4

CG17549 + transmembrane_receptor * CG7655 GH23865 90C-90C ID:76H10

CG7655 + unknown * 1E-125 * CG10570 GH23934 37B1-37B1 ID:77A3

CG10570 + 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 51B7-51B7 dup:2/2 ID:77B1

CG10131 + e enzyme * ebony(aa) * e * ebony * 1e-56 bacitracin synthetase 3; BacC [AMP_BINDING // ACP_DOMAIN // AMP-bindin] CG3331 GH24002 93D2-93D2 dup:2/2 ID:77B2

CG3331 + enzyme * DMGST_3 GstD1 * 2e-44 unknown * 1e-13 GTT1_MOUSE GLUTATHIONE S-TRANSFERASE THETA (CLASS-THETA) * 6e-16 glutathione S-transferase theta GLUTATHIONE S [GST] CG17534 55C9-55C9 dup:4/4 ID:77B3

CG17534 + unknown * UBIQUINONE BIOSYNTHESIS PROTEIN COQ4 HOMOLOG(aa) * CGI-92 protein(aa) * 4e-38 COQ4_YEAST UBIQUINONE BIOSYNTHESIS PROTEIN COQ4 Coq4p * 3e-48 putative CG3877 GH24045 78A1-78A1 dup:1/2 ID:77B7

CG3877 + enzyme * DMGLUTAC_9 Glt * LIPASE PRECURSOR(aa) * GLUTACTIN PRECURSOR(aa) * 1e-42 EST1_CAEEL GUT ESTERASE PRECURSOR (NON-SPECIFIC CARBOXYLESTERASE) [CARBOXYLESTERASE_B_1 // ESTERASE // Coe] CG7529 GH24077 78D7-78D7 ID:77C1

CG7529 + Cyp4ac1 cytochrome_P450 * 2e-75 /motif=(desc;; /ma * 3e-80 similar to Cytochrome P450 * 1e-54 cytochrome P450 Cyp4a - mouse * 2E-56 [EP450II // p450 // P450 // MITP450 // C] CG14032 GH24257 25D2-25D2 ID:77D4

CG14032

CG3006	+ enzyme * flavin containing monooxygenase 3(aa) * T3P18.10(aa) * similar to Flavin-binding monooxygenase-like(aa) * similar to flavin-containing monooxygenase [ADXRDTASE // FADPNR // FMO-like // PNDR] CG3006 GH24271 60A13-60A13 ID:77D7
CG3328	+ transcription_factor * ORFveg132; similar to Caenorhabditis elegans ORF F59B10.1 encoded by EMBL Accession Number protein(aa) * 2e-70 similarity to a transmembranous of [CASPASE_HIS] CG3328 GH24458 60B9-60B10 dup:3/3 ID:77E12
CG10108	+ phyl signal_transduction * phyl * 1e-175 phyllopod * phyllopod - fruit fly (Drosophila melanogaster) ORF * phyllopod [NLS_BP] CG10108 GH24326 51A-51A2 dup:2/2 ID:77E4
CG11440	+ wunen * similarity to phosphatidic acid phosphatase PA_PHOSPHATASE CG11440 ID:77F12
CG10137	+ unknown * glycine-, glutamate-, thienylcyclohexylpiperidine-binding protein(aa) * 1e-59 protein * 1E-170* CG10137 37F1-37F1 ID:77F4
CG12268	+ enzyme * DMC103B4 * 1e-05 LYS2_YEAST AMINOADIPATE-SEMIALDEHYDE DEHYDROGENASE LARGE SUBUNIT (ALPHA-AMINOADI * 2e-53 /match=(desc.; /ma * 4e-75 similar to Arab [HELIX_LOOP_HELIX] CG12268 GH24480 95C13-95C13 ID:77F5
CG14989	+ unknown * 1E-128* * CG14989 64A7-64A7 dup:2/2 ID:77F9
CG3239	+ 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 GH24674 5A1-5A1 dup:1/3 ID:77G12
CG7178	+ CG7178 dup:2/2 ID:77H12
CG7493	+ SP2523 motor_protein * 1e-05 YM96_YEAST HYPOTHETICAL 113.1 KD PROTEIN IN PRE5-FET4 INTERGENIC REGION * * CG7493 GH25141 66A8-66A8 dup:2/3 ID:78C11
CG17450	+ unknown * CG17450 GH25094 cyto_unknown ID:78C5
CG14026	+ tkv signal_transduction * DMTVP_2 tkv * transmembrane receptor type I transforming growth factor beta receptor) plasma membrane plasma membrane) map_position:25D6 * 2E-5[PROTEIN_KINASE_DOM // pkinase // TGFB_R] CG14026 25C10-25D6 dup:4/7 ID:78D11
CG4836	+ enzyme * 1e-19 probable membrane protein YLR070c - yeast (Saccharomyces cerevisiae) * 8e-40 sorbitol dehydrogenase * 5e-39 similar to sorbitol dehydrogenase; [adh_zinc // NLS_BP] CG4836 GH25858 92C-92C dup:1/4 ID:79C3
CG17470	+ unknown * CG17470 GH26094 38E-38E dup:2/2 ID:79E10
CG9848	+ unknown * 3e-09 probable membrane protein YPR028w - yeast (Saccharomyces cerevisiae) * 4e-46 YSV4_CAEEL HYPOTHETICAL 26.6 KD PROTEIN T19C3.4 IN CHROMOSOME III [PRO_RICH] CG9848 GH26090 59B4-59B6 dup:4/4 ID:79E9
CG7227	+ transmembrane_receptor * DMCD362_2 croquemort * 2e-55 D-CD36 protein - fruit fly (Drosophila melanogaster) * 1e-21 predicted using Genefinder; similar to CD36 family; cDNA E [CD36] CG7227 GH26133 30C1-30C1 dup:3/3 ID:79F4
CG6836	+ unknown * CG6836 GH26215 75E6-75E6 ID:79G4
CG12423	+ actin_binding * 1e-05 contains similarity to the kelch/MIPP family * 1e-06 Keap1 * 1e-07 The gene product is related to Drosophila melanogaster ri * 1e-06 kelch pro [BTB] CG12423 GH26310 cyto_unknown ID:79H3
CG18350	+ Sxl RNA_binding * DMSX1PS1_2 Sxl * 7e-15 PABP_YEAST POLYADENYLATE-BINDING PROTEIN, CYTOPLASMIC AND NUCLEAR (PABP) (ARS CO * 1e-158 sex-lethal sex determination protei CG18350 sxl-male 6F5-6F5 dup:6/7 ID:8-31 cntrlBA10

CG3772	+ Cry photoreceptor * cry * 4e-13 photolyase (EC 4.1.99.3) * blue-light receptor (AF0 * 3e-99 photolyase/blue-light receptor homolog [DNA_photolyase // DNAPHOTLYASE] CG3772 cyr 94B1-94B1 dup:4/4 ID:8-31 cntrlBB4
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[MININTRINSICP // MIP // PRO_RICH] CG4722 big brain 30F4-30F5 dup:2/3 ID:8-31 cntrlBB5
CG1378	+ tll steroid_hormone_receptor CG1378 tll dup:2/2 ID:8-31 cntrlBC1
CG17077	+ pnt transcription_factor * DMPOINT2A_2 pnt * PNT2_DROME ETS-LIKE PROTEIN POINTED P2 (D-ETS-2) gene po * 3e-12 contains similarity to DNA-binding domain of[HSF_ETS // ETSDOMAIN // Ets // ETS_DOMA] CG17077 pnt-p1 94E12-94F1 dup:4/7 ID:8-31 cntrlBC10
CG1539	+ spdo actin_binding * sanpodo protein(aa) * 1e-179 sanpodo protein * 8e-47 Similar to tropomodulin; coded for by C. elegans cDNA yk88e7.5; coded for by C. * 6e-47 TMOD_MO CG1539 sanpodo 100A-100A dup:3/3 ID:8-31 cntrlBC5
CG17348	+ drl CG17348 drl dup:2/2 ID:8-31 cntrlBC8
CG1374	+ tsh transcription_factor CG1374 tsh dup:3/3 ID:8-31 cntrlBD3
CG17835	+ inv transcription_factor * SEGMENTATION POLARITY PROTEIN ENGRAILED(aa) * DMINVR_2 inv * INVECTED PROTEIN(aa) * 2e-29 HM16_CAEEL HOMEBOX PROTEIN ENGRAILED-LIKE CEH-16 homology CG17835 inv 47F17-48A dup:3/4 ID:8-31 cntrlBD4
CG17228	+ pros transcription_factor * DMPROS_3 pros * PRO_DROME PROTEIN PROSPERO homeotic protein prospero - f * 4e-58 HM26_CAEEL HOMEBOX PROTEIN CEH-26 K12H4.1 protein - Caen * 2e-50 [PRO_RICH] CG17228 pros p'3' 3211 86E2-86E2 dup:4/4 ID:8-31 cntrlBD7
CG4354	+ slbo CG4354 slbo dup:2/2 ID:8-31 cntrlBD9
CG1028	+ Antp transcription_factor * DMANTPG5_7 Antp * 1e-159 HMAN_DROME HOMEOTIC ANTENNAPEDIA PROTEIN homeotic protein * 7e-23 DNA-binding protein mab5 * 5e-34 HXB7_MOUSE HOMEBOX PROT CG1028 ANTP 84B-84D11 dup:3/3 ID:8-31 cntrlBE12
CG4889	+ Wg signal_transduction CG4889 Wg dup:2/2 ID:8-31 cntrlBE8
CG9885	+ dpp signal_transduction CG9885 dpp dup:2/2 ID:8-31 cntrlBE9
CG10619	+ tup transcription_factor * isl * LIM homeobox protein(aa) * LIM homeobox protein * 4e-30 CeLIM-7 contains similarity to L [LIM_DOMAIN_1 // HOMEBOX_1 // homeobox] CG10619 islet 37B5-37B5 dup:3/3 ID:8-31 cntrlBF7
CG2956	+ twist transcription_factor CG2956 twist dup:3/5 ID:8-31 cntrlBG3
CG10325	+ abdA transcription_factor CG10325 abdA dup:4/4 ID:8-31 cntrlBH1
CG7902	+ Bap transcription_factor CG7902 Bap dup:6/6 ID:8-31 cntrlBH11
CG1133	+ opa transcription_factor CG1133 opa dup:4/4 ID:8-31 cntrlBH4
CG2328	+ eve transcription_factor CG2328 eve dup:2/2 ID:8-31 cntrlBH7
CG18253	+ unknown * CG18253 GH26442 82D5-82D5 ID:80A9
CG9392	+ motor_protein * BACR37P7.j(aa) * MICRONUCLEAR LINKER HISTONE POLYPROTEIN (MIC LH) LINKER HISTONE PROTEINS ALPHA, BETA, DELTA AND * * CG9392 GH26462 76C1-76C1 ID:80B3
CG8603	+ motor_protein * APXL(aa) * 2e-23 APXL * 2e-23 apical protein, Xenopus laevis-like * [PRO_RICH] CG8603 GH26744

50F6-50F6 dup:4/4 ID:80E4

CG11466 + Cyp9f2 cytochrome_P450 * CYP9 cytochrome P450(aa) * 3e-18 CYP6A2 * 2e-10 similar to cytochrome P450 * 5e-16 cytochrome P450 3A11 - mouse cytochrome P-45 [EP450II // p450] CG11466 GH26796 87B14-87B14 ID:80F2

CG2358 + BcDNA:GM04682 endopeptidase * MICROSOMAL SIGNAL PEPTIDASE KD SUBUNIT (SPC18)(aa) * signal peptidase complex kDa subunit(aa) * SPC 21-kDa-like(aa) * 2e-36 SC11_YEAST SIGNAL SEQUE [Peptidase_S26 // SIGNALPTASE // SPASE_I] CG2358 GH27340 84C4-84C4 ID:81C9

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

CG8552 + ligand_binding_or_carrier * verprolin(aa) * mucin (clone PGM-2A) - pig(aa) * Sec23-interacting protein p125(aa) * DMCLPTN_6 Cpn [GRAM_POS_ANCHORING] CG8552 GH27701 28E-28E9 dup:3/3 ID:81F10

CG15131 + unknown * CG15131 GH27691 36A10-36A10 ID:81F9

CG9619 + protein_phosphatase * similar to glycogen-binding subunit protein phosphatase-1(aa) * smooth muscle protein phosphatase type 1-binding subunit(aa) * protein phosphatase CG9619 GH27769 76A4-76A5 ID:81G10

CG4955 + RNA_binding * CG4955 GH27756 15D1-15D1 ID:81G7

CG5048 + unknown * CG5048 GH27783 70F1-70F1 ID:81H2

CG1106 + Gel actin_binding * DMGELS_2 Gel * gelsolin, secreted form precursor - fruit fly (Drosophila melanogaster) * 2e-73 similar to gelsolin; cDNA EST comes from this gene * [GELS // GELSOLIN // Gelsolin] CG1106 GH27784 82A2-82A3 ID:81H3

CG10630 + RNA_binding * CG10630 GH28067 64E-64E ID:82B10

CG1773 + endopeptidase * DMSTUBBLE_1 Sb * 7e-07 T2D4_YEAST TRANSCRIPTION INITIATION FACTOR TFIID KD SUBUNIT (TAFII-90) * 2e-26 EAST_DROME SERINE PROTEASE EASTER PRECURSOR se [trypsin // CHYMOTRYPSIN // TRYPSIN_SEF] CG1773 GH28342 46A3-46A3 ID:82C7

CG8654 + transporter * similar to C. elegans protein and to rat synaptic vesicle protein * putative integral membrane transport protein(aa) * HYPOTHETICAL 84.8 KD PROTEIN [sugar_tr] CG8654 GH28654 56F-56F dup:2/2 ID:82E12

CG11347 + unknown * [NLS_BP] CG11347 GH28550 64B11-64B11 dup:2/2 ID:82E4

CG8040 + peptidase * leucyl aminopeptidase - like protein (partial)(aa) * 1e-103 leucine aminopeptidase * 1e-105 AMPL_BOVIN CYTOSOL AMINOPEPTIDASE (LEUCINE AMINOPEPTIDASE [LAMNOPPTDASE // CRYSTALLIN_BETAGAMMA //] CG8040 GH28719 67D12-67D13 dup:3/3 ID:82F9

CG17676[unknown|CT39055] + CG17676[unknown|CT39055 ID:82H3

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

CG12775 + ribosomal_protein * 60S RIBOSOMAL PROTEIN L21(aa) * 7e-46 R21A_YEAST 60S RIBOSOMAL PROTEIN L21E A ribosomal protein * 5e-50 RL21_CAEEL PROBABLE 60S RIBOSOMAL PROTEIN L2 [RIBOSOMAL_L21E // Ribosomal_L21e] CG12775 GM14242 40D2-40D2 ID:83C2

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

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

CG8846 + Phas1 translation_factor * 2e-16 PHAS-II * 4e-16 eukaryotic translation initiation factor 4E binding protein * 1e-14 insulin-stimulated phosphoprotein PHAS-I - rat PHAS-I * in CG8846 HL08053 25A3-25A3 ID:83D4

CG14025 + Bsg25D motor_protein * BSG2_DROME BLASTODERM SPECIFIC PROTEIN 25D bsg25D protein * 1e-05 contains similarity to kinesin (PFam: kinesin.hmm, score: 10.52 and 16.62) * 6e-1 CG14025 LD21844 25D2-25D2 dup:2/2 ID:83E8

CG10390 + transcription_factor * TATA box binding protein (TBP)-associated factor, RNA polymerase II, E, 70/85kD(aa) * TAFII60(aa) * 8e-48 transcription factor TFIID * 2e-15 contain CG10390 LD25013 83B2-83B2 ID:84D6

CG9509 + 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 ID:85A6

CG2835 + G-salpa60A signal_transduction * DMGNB_2 G-o agr;47A * 2e-39 GBA1_YEAST GUANINE NUCLEOTIDE-BINDING PROTEIN ALPHA-1 SUBUNIT (GP1-ALPHA) * GBS1_DROME GUANINE NUCLEOTIDE-BINDIN[GPROTEINA // G-alpha // GPROTEINAQ // G] CG2835 LD26182 60A12-60A12 ID:85C12

CG10621 + unknown CG10621 dup:1/4 ID:85C9

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

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

CG4364 + pescadillo [Homo sapiens] (widely expressed in embryogenesis of zebrafish, high in liver) BRCT, BRCT_DOMAIN, NLS_BF CG4364 LD27336 dup:2/2 ID:86D12

CG10417 + protein_phosphatase * PROTEIN PHOSPHATASE 2C GAMMA ISOFORM (PP2C-GAMMA) (FIBROBLAST GROWTH FACTOR INDUCIBLE PROTEIN 13) (FIN13)(aa) * PROTEIN PHOSPHATASE 2C GAMMA ISOFORM [PP2C_1 // PP2C // PP2C_2] CG10417 LD27655 41D1-41D1 ID:86G1

CG4710 + unknown * CG4710 21E-21E dup:2/2 ID:86H5

CG4491 + noc transcription_factor * zinc finger protein nocA - fruit fly (Drosophila melanogaster) (L1 * DMNOVA_3 noc * * [zf-C2H2 // ZINC_FINGER_C2H2_2] CG4491 LD28078 35A4-35A4 ID:87B10

CG4500 + BG:DS05899.1 enzyme * protein(aa) * fadD15(aa) * putative long chain fatty acid coA ligase(aa) * protein(aa) [AMP-binding] CG4500 LD28132 34E4-34E4 ID:87C8

CG15427 + cell_adhesion CG15427 LD28224 dup:1/2 ID:87D1

CG6850 + Ugt enzyme * Ugt * UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (DUGT)(aa) * 8e-19 KRE5_YEAST KILLER TOXIN-RESISTANCE PROTEIN PRECURSOR * coded for by [NLS_BP] CG6850 79E3-79E3 dup:5/7 ID:88D8

CG16901 + CG16901 ID:88G12

CG3180 + Rpl140 enzyme * polymerase (RNA) II (DNA directed) polypeptide B (140kD)(aa) * DNA-DIRECTED RNA POLYMERASE SUBUNIT B'(aa) * second largest subunit of RNA polymerase [RNA_pol_B // RNA_POL_BETA] CG3180 88A10-88A11 dup:2/3 ID:88G9

CG8789 + protein_kinase CG8789 dup:2/2 ID:89B2

CG7230 + transcription_factor * fruitless protein(aa) * fruitless class I male isoform(aa) * 3e-21 LOLS_DROME LOLA PROTEIN, SHORT ISOFORM (LONGITUDINALS LACKING PROTEIN) * 2e-06 co [BTB // HTH_FIS_FAMILY // NLS_BP] CG7230 56C-56C

dup:6/10 ID:89H5

CG4602 + CG4602 dup:3/4 ID:89H6

CG5175 + CG5175 ID:95H10

+ DNA_binding * 3e-05 HP1_DROME HETEROCHROMATIN PROTEIN (HP1) (NONHISTONE CHROMOSOMAL PROTEIN C1A9 * 6e-06 similar to 'chromo' (CHRromatin Organization MODifier) do [chromo // CHROMO_2 // NLS_BP] CG8289 LD36501 16B10-16B10 ID:96A10

CG8289 + Cyp4c3 cytochrome_P450 * DMCYP4D2_12 Cyp4d2 * 1e-14 ERG5_YEAST CYTOCHROME P450 (C-22 STEROL DESATURASE) * 1e-109 cytochrome P450 cytochrome P4 * 1e-101 similar to Cytoc[EP450II // P450 // MITP450 // BP450 //] CG1438 LD37233 100B-100B2 dup:2/3 ID:96F5

CG1438 + unknown * 5e-10 FIP1_YEAST FIP1 PROTEIN FIP1 protein - yeast (Saccharom * 3e-16 contains similarity to S. cerevisiae FIP1 * 2e-13 YAAA_SCHPO HYPOTHETICAL 37.3 [PRO_RICH // NLS_BP] CG1078 LD38592 82C2-82C2 dup:1/3 ID:97G11

CG1078 + * 2e-45 sulfate permease * 1e-27 Similar to sulfate transporter. * 9e-33 DTD_MOUSE SULFATE TRANSPORTER (DIASTROPHIC DYSPLASIA PROTEIN HOMOLOG) (ST-OB) [Sulfate_transp // SUGAR_TRANSPORT_2] CG5002 54E7-54E7 ID:97G9

CG5002 + transcription_factor * hypothetical protein(aa) * 1e-19 YFJ1_YEAST HYPOTHETICAL 55.1 KD PROTEIN IN FAB1-PES4 INTERGENIC REGION * 3e-69 No definition line found * 3e-24 un [ATP_GTP_A] CG7986 LD38705 66B13-66B13 ID:97H7

CG7986 + 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 ID:98C2

CG8483 + sli cell_adhesion * DMSLIT_2 sli * slit protein(aa) * 2e-35 contains similarity to multiple EGF-like domains * neurogenic extracellular slit protein [LRR // LRRNT // EGF_1 // EGF // LEURICH] CG8355 LD39407 52D4-52D7 dup:2/2 ID:98E11

CG8355 + unknown * 3e-21 hypothetical protein YOR289w - yeast (Saccharomyces cerevisiae) * 1e-43 R166.3 * 3e-45 unknown protein * Y810_METJA HYPOTHETICAL PROTEIN hypo CG5902 97F1-97F1 dup:1/6 ID:98G6

CG5902 + Ama cell_adhesion * DMAMA_5 Ama * Immunoglobulin-C2-type-domain protein * 1e-15 hemicentin precursor * 3e-19 cell adhesion molecule (AA - 681) is 1st base in codon) [ig] CG2198 LD39923 84D1-84D1 ID:99A4

CG2198 CG9839 + unknown * [CYTOCHROME_C] CG9839 LD40589 85E9-85E9 ID:99F8

CG9839 + signal_transduction * Caf1 * Nle * Taf80 * 5e-13 T2D4_YEAST TRANSCRIPTION INITIATION FACTOR TFIID KD SUBUNIT (TAFII-90) [GPROTEINBRPT // WD40_REGION // WD_REPEA] CG6724 LD40657 32A5-32A5 ID:99G1

CG6724 CG12758 + unknown * [NLS_BP] CG12758 trimmed 55F8-55F13 dup:2/3 ID:Farhad's BA1

CG12758 CG10934 + CG10934 GH26058 dup:2/3 ID:Farhad's BA12

CG10934 CG8633 + unknown CG8633 GJB.Hx4 dup:1/2 ID:Farhad's BA5

CG8633 CG2016 + unknown * 0.0000000007* 4e-10 0.9-kb RNA transcript * CG2016 ck01170 82E7-82E7 dup:2/3 ID:Farhad's BD11

CG2016 CG5772 + transporter CG5772 ck00325 ID:Farhad's BD8

CG5772 CG1124 + unknown CG1124 ck00336 dup:2/2 ID:Farhad's BD9

CG1124 + W unknown * W * HEAD INVOLUTION DEFECTIVE PROTEIN (WRINKLED PROTEIN)(aa) * 1e-148 W * 6E-99 CG5123 ck02091 75C-75C2 dup:2/4 ID:Farhad's BE10

CG5123

CG15288	+ CG15288 ck01592 ID:Farhad's BE4
	+ structural_protein * 70kD peroxisomal integral membrane protein(aa) * similar to kD peroxisomal membrane protein
CG12703	(PMP70), an ATP-binding transport protein(aa) * 1e-19 CG12703 ck01606 18F1-18F1 ID:Farhad's BE5
	+ unknown * BLASTX 5.8E-08 Mouse proteolipid protein variant DM-20 mRNA, complete cds.(dna) * 2e-21 M6A_MOUSE
CG7540	MEMBRANE GLYCOPROTEIN M6-A membrane glycoprote * 3 [Myelin_PLP] CG7540 ck01837 78D7-78D8 ID:Farhad's BE8
CG9503	+ enzyme CG9503 ck02694 ID:Farhad's BF1
CG4859	+ unknown CG4859 dMMP dup:2/2 ID:Path + CtrL1 + kras160
	+ protein_kinase * DMFGFR1_2 htl * connectin/titin(aa) * flt-1(aa) * FTL4(aa) [ig // PROTEIN_KINASE_TYR //
CG8222	PROTEIN_KIN] CG8222 VEGFR 78F1 28F4-28F5 dup:9/12 ID:Path + CtrL1 + kras305
CG10816	+ CG10816 drosocin dup:1/3 ID:Path + CtrL1 + kras62